

UNIVERSIDAD DE CANTABRIA

PROGRAMA DE DOCTORADO EN BIOLOGÍA
MOLECULAR Y BIOMEDICINA



TESIS DOCTORAL

Análisis de las dinámicas de expresión génica durante las interacciones epitelio-mesenquimatosas en la extremidad. Nuevas percepciones en la función de los genes *Hoxc* durante el desarrollo del ectodermo.

PHD THESIS

Analysis of the dynamics of gene expression during epithelial-mesenchymal interactions in the limb. New insights into the function of *Hoxc* genes during the development of the ectoderm.

Realizada por Marc Fernández Guerrero

Dirigida por María A. Ros Lasierra

Escuela de Doctorado de la Universidad de Cantabria

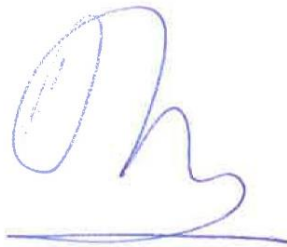
Santander 2019 Noviembre

María A. Ros Lasierra, Profesora de Investigación del Instituto de Biomedicina y Biotecnología de Cantabria (CSIC-UC-SODERCAN)

como directora de la Tesis Doctoral titulada: “Análisis de las dinámicas de expresión génica durante las interacciones epitelio-mesenquimatosas en la extremidad. Nuevas percepciones en la función de los genes *Hoxc* durante el desarrollo del ectodermo”; “Analysis^s of the dynamics of gene expression during epithelial-mesenchymal interactions in the limb. New insights into the function of *Hoxc* genes during the development of the ectoderm.”

CERTIFICA

Que dicho trabajo ha sido realizado por Don Marc Fernández Guerrero y considera que se encuentra terminado y reúne los requisitos para su presentación como memoria de doctorado por el interesado, al objeto de poder optar al grado de Doctor por la Universidad de Cantabria.



María A. Ros Lasierra

Directora y tutora de la tesis

Santander a 29 de octubre de 2019

«Hay que ser un poco vago. Solo cuando se te ocurra
un experimento que merezca la pena, te pones a
trabajar. Para trabajar a lo tonto, te vas a tu casa».

Marian Ros

«Algunos todavía no han desertado, algunos todavía
creen en una idea. Todo lo demás, es estar muerto».

Gata Cattana / Ana Sforza

INDEX

Abbreviations and Acronyms	13
INTRODUCTION	21
<i>Hox</i> genes.....	22
<i>Hox</i> genes and limb development	25
The regulation of <i>Hox</i> gene clusters	28
The limb proximo-distal axis	33
The termination of the limb outgrowth.....	40
Ectodermal organs	43
The hair follicle.....	46
The nail organ	50
Ectodermal dysplasias.....	53
AIMS OF THE PRESENT THESIS	61
MATERIALS AND METHODS	65
Mouse strains	65
Mouse Embryos	65
Genotyping.....	66
Paraffin embedding.....	67
Hematoxylin-Eosin staining.....	67
RNA probes synthesis.....	68
Whole mount in situ hybridization (WMISH)	69
In situ hybridization in paraffin sections	70
Immunohistochemistry	71
RNA-seq	72
Gene ontology analyses	74
ATAC-seq.....	74

Enhancer functional essays	75
LacZ/ β -Gal staining	76
CRISPR-Cas9	76
RESULTS	81
Temporal transcriptome analysis of the developing limb components	81
Differential gene expression analyses across stages during aging of the limb progenitor cells	85
Stage-specific transcription factor genes of the distal limb mesoderm	90
Analysis of the gene expression dynamics of AER-Fgfs in the limb ectoderm	95
The colinear activation of <i>Hoxc</i> genes in the limb ectoderm.....	98
The nail phenotype of <i>Hoxc13GFP</i> and <i>HoxCKO</i> mutant mice.....	101
The relationship between <i>Hoxc</i> genes and BMP signaling in developing hairs and nails	106
Transcriptional regulation of <i>Hoxc</i> genes in the limb ectoderm.....	108
Generation and analyses of <i>delEC1</i> and <i>delEC2</i> mutants.....	114
Generation and analyses of <i>del(EC1-EC2)</i> and <i>HoxCKO/del(EC1-EC2)</i> mutant mice	116
DISCUSSION.....	125
Gene expression profiles associated with the progressive specification of the three PD limb segments	125
The gene expression dynamics of <i>Bmp2</i> , <i>Fgfs</i> , <i>Hoxa13</i> and <i>Rprm</i> shed light into the termination of the positive feed-back loop driving limb outgrowth.....	129
The colinear expression patterns of <i>Hoxc</i> genes in the ectoderm.....	131
The role of <i>Hoxc</i> genes in the development of the nail	132
CONCLUSIONS	141
RESUMEN	145
Introducción.....	145
Objetivos.....	147

Resultados y discusión.....	147
Conclusiones	153
REFERENCES	157
AGRADECIMIENTOS.....	183
ANEX	187

Abbreviations and Acronyms

AER: Apical Ectodermal Ridge.

Alx: Cartilage Paired-Class Homeobox.

Ankrd6: Ankyrin Repeat Domain-Containing Protein 6.

ANT-C: Antennapedia Complex.

Antp: Antennapedia.

AP: Anterior-Posterior / Antero-Posterior.

ATAC-seq: Assay for Transposase Accessible Chromatin with high-throughput sequencing.

BCIP: 5-bromo-4-chloro-3-indolyl-phosphate.

Btx: Bithorax.

BX-C: Bithorax Complex.

C57BL/6: C.C. Little mice from female 57 black, line 6.

CBA: Cross from Bagg Albino.

cDNA: copy DNA.

C-DOM: Centromeric Domain.

Cdx1: Caudal Type Homeobox.

CNS: Central Nervous System.

CTNNB1: β -catenin (protein).

CYP26B1: Cytochrome P450 26 B1.

DC: Dermal Condensate.

DEGs: Differentially expressed genes.

Del: deletion.

DEPC: Diethyl pyrocarbonate.

DGEA: Differential Gene Expression Analyses.

DNA: Deoxyribonucleic acid.

DOC: sodium deoxycolate.

DP: Dermal Papilla.

DSB: double strand break.

DV: Dorsal-Ventral / Dorso-Ventral.

E9: Embryonic day 9 (the same for E10, E11,...).

EC1: Enhancer of Hoxc 1.

EC2: Enhancer of Hoxc 2.

ECM: Extra-Cellular Matrix.

ECTD: Ectodermal dysplasia.

ECT-DEGs: Differentially expressed genes in the ectoderm samples.

EDTA: Ethylenediaminetetraacetic acid.

EMBRYs: Embryonic Gene Expression Database for Biomedical Research Source.

Emx: Empty Spiracles Homeobox.

EO: Ectodermal Organ.

EtOH: Ethanol.

E coli: *Escherichia coli*

FBS: Fetal Bovine Serum.

FGF: Fibroblast Growth Factor.

FL: Forelimb.

FPKM: Fragments Per Kilobase of transcript per Million mapped reads.

FPM: Fragment Per Million mapped reads.

Fwd: Forward (primer).

GFP: Green Fluorescent Protein.

Gli1: GLI Family Zinc Finger 1.

GO: Gene Ontology.

Greml1: Gremlin1.

H₂O₂: Hydrogen Peroxide.

H3K27me3: trimethylation on lysine 27 of histone 3.

H3K4me3: trimethylation on lysine 4 of histone 3.

Hand2: Heart And Neural Crest Derivatives Expressed 2.

HCl: Hydrochloric acid.

HE: Hematoxylin Eosin.

HET: Heterozygous.

Hey1: Hes Related Family BHLH Transcription Factor With YRPW Motif 1.

HF: Hair Follicle.

HH: Hamburger and Hamilton (staging system).

Hh: Hedgehog.

HH24g: grafts of HH27 distal mesenchyme expressing cells that were made to younger HH20 limb buds, and which were left to develop for 24 hr.

HL: Hindlimb.

HOM: Homozygous.

HOM-C: Homeotic complex.

Hr: hours.

Inv: inversion.

IRS: Inner Root Sheath.

Irx: Iroquois homeobox.

ISH: In Situ Hybridization.

Kank2: KN Motif And Ankyrin Repeat Domains.

Koa mice: Koala mice.

Krt: Keratin.

KSOM: Potassium-supplemented simplex optimised medium.

KTBT: Potassium chloride + Sodium chloride + Tris-HCl buffer.

LB: Luria-Bertani (broth) or Loading Buffer.

LGR: Leucine-rich repeat-containing G-protein coupled receptor.

Lmo: LIM Domain Only.

LPM: Lateral Plate Mesoderm.

LRT: Likelihood Ratio Test.

MABT: NaCl + Maleic Acid + Tween20 buffer.

Meis: Myeloid Ecotropic Viral Integration Site.

MES-DEGs: Differentially expressed genes in the mesoderm samples.

MetOH: Methanol.

mRNA: Messenger Ribonucleic Acid.

MSX: Msh homeobox.

NaOH: Sodium Hydroxide.

NBT: Nitro Blue Tetrazolium.

Nrf2f: Nuclear Receptor Subfamily 2 Group F Member 2.

NTMT: Tris-HCl + MgCl₂ + NaCl + Triton X-100 buffer.

ON: Over Night.

ORS: Outer Root Sheath.

PBS: Phosphate-Buffered Saline.

PBT: Phosphate-Buffered Saline wit 0,1% Tween20.

PBX: Pre-B-Cell Leukemia.

PC: Principal Component.

PCA: Principal Component Analysis.

PCR: Polymerase Chain Reaction.

PD: Proximal-Distal / Proximo-Distal.

PFA: Para-formaldehyde.

PHNED: Pure Hair-Nail Ectodermal Dysplasia.

Pias1: Protein Inhibitor Of Activated STAT 1.

RA: Retinoic Acid.

RALDH: Retinaldehyde dehydrogenase.

RAR: Retinoic Acid Receptor.

Rar β : Retinoic Acid Receptor β .

RDH: Retinol Dehydrogenase.

Rev: Reverse (primer).

RNA: Ribonucleic acid.

RNA-seq: RNA sequencing.

RNP: Ribonucleoprotein.

Rprm: Reprimo

RT: Room Temperature.

RXR: Retinoid X Receptor.

Sall1: Spalt Like Transcription Factor.

SHH: Sonic Hedgehog.

SSC: NaCl + Sodium Citrate Buffer.

TAC: Transient Amplifying cells.

TBS: Tris-Buffered Saline

TBST: Tris-Buffered Saline with Tween20.

Tbx: T-Box.

T-DOM: Telomeric Domain.

TF: Transcription Factors

Tgf β : Transforming growth factor β .

Tris: tris(hidroximetil)aminomethane.

UTR: Un-Translated Region

WebGestalt: WEB-based GEne SeT AnaLysis Toolkit.

WMISH: Whole Mount In Situ Hybridization.

WT: wild type.

Zic2: Zinc Finger Protein Of The Cerebellum.

ZPA: Zone of polarizing activity.



INTRODUCTION

INTRODUCTION

The core objective of developmental biology is to understand how a single cell, the zygote, becomes a complete arranged organism. This organism is the sum of different cell types organized in the tissues and organs that are required to fulfil the vital functions of a living being. During the development of an organism, cells divide, migrate, differentiate, acquire different shapes and even die by apoptosis.

In bilaterian animals, the zygote divides and forms a mass of cells that undergoes a process of gastrulation. In this process, movements of cells result in the appearance of the three germ layers: The ectoderm (outer layer) that will give rise to the epidermis and the nervous system; the endoderm (inner layer) that will generate the digestive system and associated organs (liver, pancreas and lungs) and the mesoderm (intermediate layer) that is the origin of the heart, the gonads and the kidney, the circulatory system, bones, tendons and muscles.

The development of the different organs of the body arise when cells receive molecular cues that trigger their differentiation to a particular cell type. A cell is specified when its differentiation is reversible, but when this cell is committed to a specific fate and cannot regress, this cell is determined. Cell differentiation is fundamental for the morphogenesis of an organ, as it involves the acquisition of differential positional information, necessary to organize a 3D structure.

In the development of an organ, cells receive information of their position along the body axes. If we observe a mature bilaterian animal, three body axes are easily distinguished: the anterior-posterior (AP) axis, from the head to the tail, the dorsal-ventral (DV) axis, from the back to the chest and the proximo-distal (PD) axis, from the body wall to the tip of the digits. Positional information is transmitted through signaling pathways, consisting of ligand molecules that bind to specific receptors to activate gene expression. Some notable signaling pathways orchestrating organogenesis are the Wnt pathway, the Fibroblast Growth Factor (FGF) pathway, the Transforming Growth Factor (TGF) pathway and the Hedgehog (Hh) pathway.

The use of animal models has become an essential tool for addressing biological questions and understanding the molecular mechanisms driving a biological process *in*

vivo. In particular, the work of several developmental biologists in *Drosophila melanogaster* was key to understand the patterning and growth of organs in the early embryo (Gilbert, 2003). In organogenesis, ligands of signaling pathways can function as morphogens, a term coined by Alan Turing to refer to a diffusible molecule that can generate shape (Turing, 1952).

The use of *Drosophila* and other animal models was key to unravel many of the developmental processes common in all bilaterians. Nevertheless, if the knowledge acquired is to be translated to human, mouse is the model organism per excellence, because of the genetic and physiological similarities, simple breeding and the wide variety of genetical tools available. It is also remarkable, the use of chick embryos as a fundamental tool in developmental biology, mainly because of the possibility of direct manipulation of the embryo in the egg.

Among the processes regulating the development of a bilaterian animal, one of the main topics of this thesis is the function of homeotic genes, initially studied in the body patterning of the developing *Drosophila* egg.

***Hox* genes**

In *Drosophila*, after the establishment of the segmentary limits in the embryo, the particular structures characteristic of each body segment are specified. This process is orchestrated by the homeotic complex (HOM-C) genes, which are a family of transcription factors (Gilbert, 2003). In *Drosophila*, 8 HOM-C genes were found, organized in two clusters, the *Antennapedia* complex (*ANT-C*) and the *Bithorax* complex (*BX-C*) (E.B. Lewis, 1978). The *ANT-C* directs the specification of the anterior part of the animal, whereas the *BX-C* oversees the posterior most structures. Of particular interest is the correlation between the location of these genes in the genome and their expression domain, as the more 3' a gene is located in the chromosome, the more anteriorly it is expressed in the embryo and therefore, the more anterior is the structure specified by its function (Gilbert, 2003). This phenomenon is referred to as spatial collinearity.

These genes are not only conserved in Bilaterians but their function as homeotic selector genes and spatial collinearity are too (Gaunt et al., 1988; Graham et al., 1989). In mice, 39 homologs of *Drosophila* homeotic genes were found. *Hox* was the name given

to the vertebrate orthologs to *Drosophila* homeotic genes. They were found in 4 paralogous clusters, each one in a different chromosome, containing from 9 to 11 genes (Duboule and Dollé, 1989). The *HoxA* cluster is located in chromosome 6, the *HoxB* cluster in chromosome 11, the *HoxC* cluster in chromosome 15 and the *HoxD* cluster in chromosome 2 (Graham et al., 1989). Each *Hox* gene in one of the clusters is orthologous to a *Drosophila* homeotic gene and each *Hox* gene in a cluster is paralogous to other *Hox* genes in a different *Hox* cluster (Duboule, 2007)(Fig. 1A, B). The current explanation of this organization is a double duplication event, which could be partial and also working in combination with gene loss.

In mice, *Hox* genes were found to be activated in a sequential manner in the development of the trunk: the genes more 3' in a cluster (for example *Hoxa1* in the *HoxA* cluster) are the earliest and most anteriorly expressed and the more 5' genes in a cluster (for example *Hoxd13* in the *HoxD* cluster) are the latest and most posteriorly expressed (Izpisua-Belmonte et al., 1991). This finding did not only show the spatial collinearity of *Hox* in vertebrates, but also a temporal collinearity in the developing trunk of vertebrate embryos. The spatial collinearity of *Hox* genes in the developing trunk is the reason why 3' *Hox* are often referred to as “anterior *Hox*” and 5' *Hox* are often referred to as “posterior *Hox*” (Awgulewitsch, 2003) (Fig. 1C). Moreover, paralogous *Hox* genes show highly overlapping patterns: *In situ* hybridization experiments show *Hoxc4* and *Hoxd4* expressed at embryonic day 9.5 (E9.5) in a highly overlapping domain in the anterior part of the embryo, whereas the onset of expression of *Hoxc12* and *Hoxd12* is observed in a highly overlapping posterior domain around E10.5 (Fig. 1C).

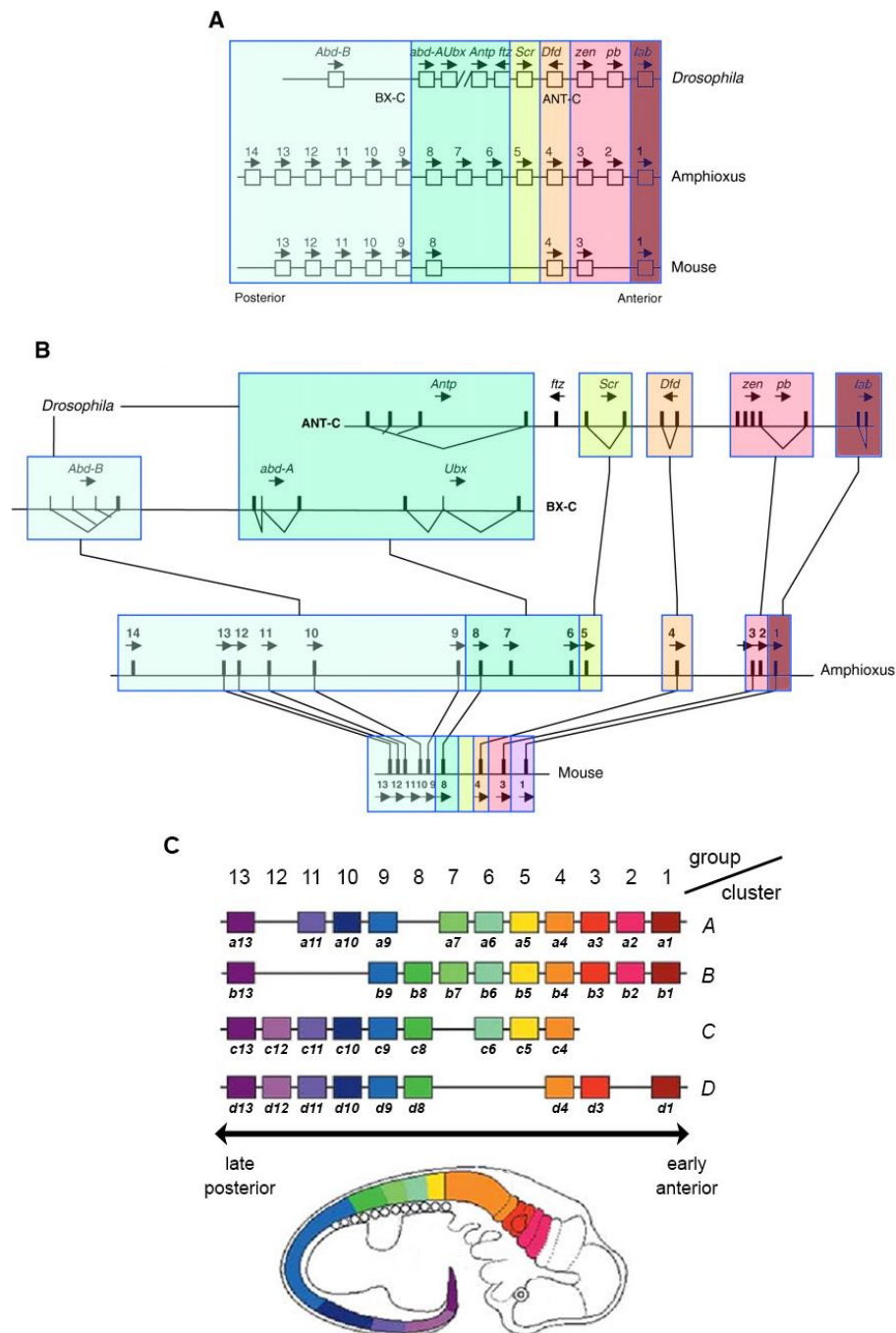


Figure1. The structural organization of *Hox* clusters and their expression along the AP axis of the developing embryo. A-B: The colored boxes correspond to the various paralogy groups, those genes that are most closely related in sequence, and hence are derived from a common ancestral *Hox* gene. **A:** Schematic depicting the *Hox* clusters as they are usually represented in the literature and textbooks. It shows the respective positions of paralogy groups 1 to 14 for the cephalochordate *amphioxus* and a vertebrate prototypic cluster, and their corresponding *Drosophila* genes located on both ANT-C and BX-C. **B:** A more precise representation of the organization within *Hox* clusters, with the correct relative distances and a clear genomic separation present between the two *Drosophila* sub-clusters (adapted from Duboule, 2007). **C:** Schematic representation of the sequential activation of *Hox* gene clusters along the anterior-posterior axis of the vertebrate embryo, starting from the 3' end of the clusters. Note that paralogy groups of *Hox* genes are activated simultaneously (Awgulewitsch, 2003).

Importantly, *Hox* genes were coopted in the evolution of vertebrates in the development of the secondary axes (Soshnikova et al., 2013). In this thesis, we focused our interest in the function of these family of genes in the development of the limb.

***Hox* genes and limb development**

Within an organism, the limb is an accessible, non-vital organ that allows a huge variety of experimental manipulations without compromising the survival of the embryos. Therefore, the limb is an ideal system to study the different mechanisms orchestrating organogenesis, which can be extrapolated to other developmental processes.

In vertebrates, limbs emerge from the flank of the embryo, as a bulge of lateral plate mesoderm cells, encased within an ectodermal hull (Bénazet et al., 2009). The patterning and growth of the limb is organized along three main spatial axes: Proximo-Distal (PD, body wall to fingertip), Antero-Posterior (AP, thumb to little finger) and Dorso-Ventral (DV, knuckle to palm).

The development of the limb is orchestrated by two main signaling centers, the Zone of polarizing activity (ZPA), a cluster of mesodermal cells located in the posterior border of the limb bud, and the Apical Ectodermal Ridge (AER), which consists of a population of distal ectodermal cells at the DV boundary (Fig. 2). These two signaling centers produce morphogens that orchestrate a variety of interlinked processes in the development of the limb: Sonic hedgehog (Shh) in the ZPA and Fgfs in the AER (reviewed in Petit et al., 2017).

The cross-talk between the AER and the ZPA is crucial for the patterning and outgrowth of the limb bud along the PD axis and the expansion of the 3 PD limb segments (Zúñiga et al., 1999): the stylopod (with one skeletal element), the zeugopod (with two skeletal segments) and the autopod (with a variable formula of skeletal elements across tetrapod species) (Fig. 3).

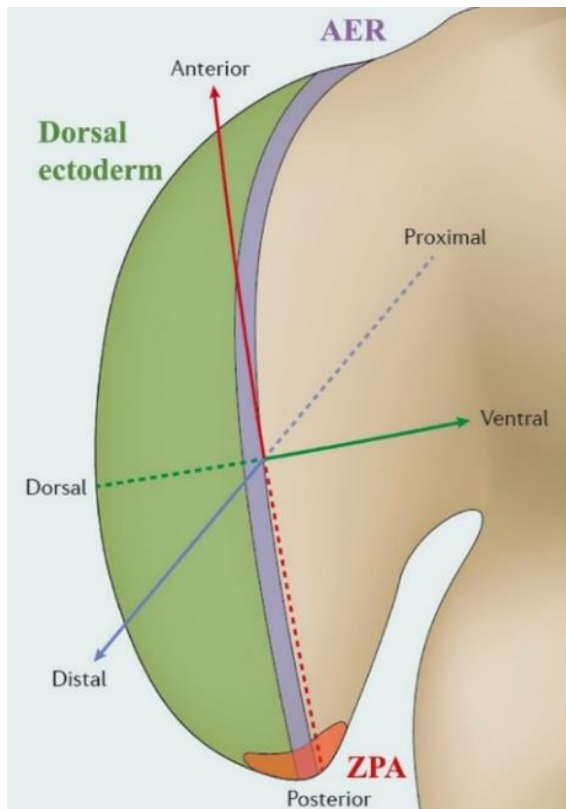


Figure 2. Overview of the three main signaling centers orchestrating limb development along the three different axes. The proximo–distal (PD) axis is controlled by the AER signaling center (purple). The anterior–posterior axis is directed by the ZPA (red). The dorsal–ventral axis is controlled by the non-AER ectoderm (green). Note that the AER is located at the DV boundary of the limb bud. From Petit et al., 2017 (Petit et al., 2017).

The *HoxA* and *HoxD* clusters are crucial in the development of the tetrapod limb, whereas *HoxB* and *HoxC* clusters are apparently dispensable (Suemori and Noguchi, 2000; Zakany and Duboule, 2007). *Hox* genes located in the 5' part of the *HoxA* and *HoxD* clusters are required for the proliferation of skeletal progenitor cells of the vertebrate limb. Specific combinations of *Hox* gene products determine the length of the upper arm (genes belonging to groups 9 and 10), the lower arm (groups 10, 11 and 12) and the digits (groups 11, 12 and 13) (Wellik and Capecchi, 2003; Zakany and Duboule, 1999). Two illustrative examples of the cooperative function of paralogous *Hoxa* and *Hoxd* genes in the development of the limb are *Hoxa11-Hoxd11* double knockout mutants that display severely truncated radius and ulna (Fromental-ramain et al., 1996a) and *Hoxa13-Hoxd13* double mutants that are unable to develop the digits (Fromental-ramain et al., 1996b)(Fig. 3). The interpretation of *Hox* mutant phenotypes is always tricky, due to the high redundancy between the function of these genes. Hence, the knock-out of one *Hox* does not have a remarkable effect in the development of the embryo, in most cases. In particular, in the autopod, it is the *Hox* gene dose rather than the *Hox* code, what has an effect in the size of the bone (Zakany et al., 1997).

The most striking phenotype in this case, occurs when *HoxA* and *HoxD* clusters are abolished in the development of the limb, giving rise to a severely truncated limb which only presents a reduced stylopod (Kmita et al., 2005; Zakany and Duboule, 2007)(Fig. 3). *HoxA*;*HoxD* double knockout limbs cannot activate the expression of *Sonic hedgehog* (*Shh*) in the ZPA which is considered a cornerstone in limb development, necessary for the patterning and growth of the limb. It is considered that *Hoxd8-13* and *Hoxa* genes are necessary for *Shh* expression in the developing limb (Tarchini et al., 2006). Mutants lacking the *HoxA* cluster and the *Hoxd8-13* genes are unable to trigger *Shh* expression in the ZPA and the limb phenotype of these animals is comparable to the loss of function of both clusters in the limb (Tarchini et al., 2006). After the onset of *Shh* expression a complex interplay between *Shh* and *Hox* genes is started to develop a full normal limb (reviewed in Pérez-gómez et al., 2018).

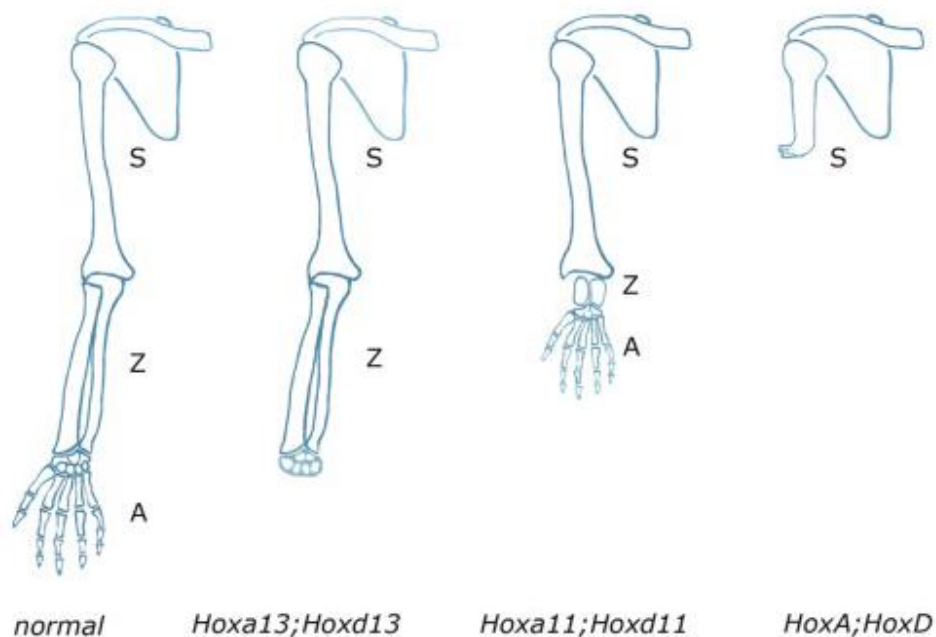


Figure 3. Combined deletions of *Hoxa* and *Hoxd* genes reveal their role in limb development. Schematic representation of the limb phenotypes of several knockouts of *Hoxa* and *Hoxd* genes. The combined deletion of *Hoxa13* & *Hoxd13* leads to the absence of digits, the combined deletion of *Hoxa11* & *Hoxd11* results in a severely truncated zeugopod and the combined deletion of *HoxA* & *HoxD* clusters results in a severely reduced limb that consist only in a truncated stylopod. Abbreviations: S=Stylopod, Z=Zeugopod and A=Autopod. (adapted from Zakany and Duboule, 2007).

The study of the function of *Hox* genes in the development of the limb is crucial to understand the development of the tetrapod limb, including the human limb. In fact, several congenital limb syndromes have been associated to human *HOX* genes. Some examples are the Hand-Foot-Genital syndrome associated to the *HOXA13* locus

(OMIM#140000)(Mortlock and Innis, 1997), Brachydactyly types D & E associated to the *HOXD13* locus (OMIM#113200, #113300)(Johnson et al., 2003) or Congenital vertical talus associated to the *HOXD10* locus (OMIM#192950)(Shrimpton et al., 2004). This information not only reflects the conservation of the function of *HOX* genes in the limb, but also highlights the importance of the study of these genes to improve our knowledge on genetic diagnostics.

The multiple roles of *Hox* genes not only in the development of the tetrapod limb, but also in other tissues, would have never been possible without a refined regulatory complex. *Hox* gene regulation has been largely studied in the recent years, nevertheless, much is still unknown about this topic.

The regulation of *Hox* gene clusters

To understand the expression dynamics of genes, modern developmental biologists have focused on the study of chromatin regulation and how cis regulatory modules are bound by transcription factors (Arnosti and Kulkarni, 2005; Furlong and Levine, 2018). These processes are key to explain how genes are expressed in a particular domain, in a discrete period of time. Extensive research of several investigators has shed light on the complex regulation of these genes in different developmental processes.

A graded switch from repressive to active chromatin marks was found to be crucial for the collinear activation of *Hox* genes in the developing trunk (Soshnikova and Duboule, 2009). Initially, *Hox* clusters are decorated with repressive histone marks, like trimethylation on lysine 27 of histone 3 (H3K27me3). As development progresses, H3K27me3 is progressively depleted from the 3' end to the 5' end of the cluster and substituted by histone marks associated to a transcription-permissive state, like trimethylation on lysine 4 of histone 3 (H3K4me3). Chromatin conformation capture experiments showed that DNA regions with a similar chromatin accessibility tend to physically interact in this process, exposing a dynamic architecture of *Hox* gene clusters during the development of the trunk (Noordermeer et al., 2011). Particularly for *Hoxd* genes, the DNA accessibility increases in time from the 3' end of the cluster to the 5' end, following the switch of chromatin marks in the developing trunk.

The activation of *Hoxd* genes during the development of the trunk was demonstrated to rely on enhancer sequences inside the cluster (Spitz et al., 2001). Conversely, distant regions located in the gene desert 5' to the cluster were reported to drive regulatory activity in the limb (Spitz et al., 2003, 2001). The *HoxD* cluster is located between two gene deserts and when chromatin conformation techniques were applied to this locus, several regulatory regions at the centromeric gene desert were proved to physically interact with *Hoxd* genes (Montavon et al., 2011). The genetic abrogation of these sequences resulted in a phenotype comparable to the loss of function of *Hoxd8-13* in the digits, attributing the activation of *Hoxd8-13* in the autopod to the regulatory regions, located in the centromeric gene desert (Montavon et al., 2011). Further research revealed that enhancers located 3' to the cluster, at the telomeric gene desert, were responsible for the activation of *Hoxd* genes in the prospective zeugopod (Andrey et al., 2013).

The study of *HoxD* regulation shed light on the mechanisms controlling the expression pattern of these genes during limb development. *Hoxd* genes are activated in a temporal colinear manner in the limb. Nevertheless, this activation is different from the one observed in the trunk: in the limb, these genes are activated in a bimodal manner, with two phases of expression. In the forelimb, the first phase occurs in early limb buds, around E9.5, with *Hoxd8-11* expressed throughout the limb bud. The second phase (starting around E11) is started by *Hoxd10-13*, with these genes expressed in the prospective autopod region. At this time point, the first phase of *Hoxd* expression remains in a proximal region of the limb, mostly associated to the prospective zeugopod (Burke et al., 1995; Nelson et al., 1996; Pérez-gómez et al., 2018; Woltering et al., 2014; Zakany and Duboule, 2007)(Fig. 4A). This results in some genes, like *Hoxd10*, expressed in two domains clearly distinguishable in the late limb bud, one proximal domain of expression (first phase) and one distal domain of expression (second phase). The two phases are separated by a transverse domain devoid of *Hoxd* transcripts that is coincident with the wrist/ankle. The discovery of the regulatory regions for the *HoxD* cluster during the development of the limb, revealed that the early phase of expression is controlled by the enhancers located 3' to the cluster, at the telomeric gene desert whereas the late phase of expression is accounted by the enhancers located 5' to the cluster, at the centromeric gene desert. This means that some *Hoxd* genes are regulated by both enhancer groups, like the previously mentioned *Hoxd10* (Fig. 4A)(Reviewed in Pérez-gómez et al.,

2018)(Woltering et al., 2014). Moreover, it is accepted that the gain of chromatin accessibility in the *HoxD* cluster associated to the first phase, is necessary for an efficient second phase (Andrey et al., 2013).

The *HoxA* cluster is the other *Hox* cluster involved in limb development with several members expressed during the development of the limb (Burke et al., 1995; Davis et al., 1995; Fromental-ramain et al., 1996b; Kmita et al., 2005). Of great interest is the expression pattern of *Hoxa11* and *Hoxa13*: the former is expressed through all the bud in early limb development and later, the distal expression of *Hoxa11* fades concomitantly with the activation of *Hoxa13* in the autopod progenitors (Fig. 4A). Of note, this is mediated by *Hoxa13* activating antisense transcription of *Hoxa11* and thus, disrupting sense transcription of *Hoxa11* (Kherdjemil et al., 2016). The mutually exclusive expressions of these genes results in *Hoxa11* confined to the zeugopod cells and *Hoxa13* confined to the autopod cells, making these two genes the best markers for the two distal segments of the limb. The activation of *Hoxa* genes in the developing limb is considered to rely on regulatory regions upstream of the *HoxA* cluster (Berlivet et al., 2013; Lehoczký et al., 2004).

Both *HoxA* and *HoxD* clusters are sitting in a boundary between topological association domains (TADs) (Dixon et al., 2012). TADs are regions of the genome that present preferential physical interaction, bringing cis-regulatory elements into proximity, such as enhancers and promoters. The boundaries of TADs are often delineated by clusters of binding motifs for insulator proteins such as CTCF or RAD21 (Dixon et al., 2012; Furlong and Levine, 2018). In the *HoxD* cluster, the 3' genes reside in the telomeric TAD (T-DOM) and the 5' genes reside into the centromeric TAD (C-DOM), thus, the cis-regulatory inputs received by these genes are significantly different depending on their location in the cluster (Fig. 4B). Telomeric T-DOM enhancers regulate 3' *Hoxd* genes preferentially, triggering the first phase of expression in early limb buds. Later, enhancers located within the C-DOM activate 5' *Hoxd* genes in the developing digits, that is, the second phase of expression (Beccari et al., 2016; Woltering et al., 2014) (Fig. 4B). Recent data showed that the TAD boundary in the *HoxD* cluster can slightly vary depending on the tissue analyzed, meaning that this boundary is dynamic (Rodríguez-carballo et al., 2017). The interpretation of this finding is that the preferential interaction

of chromatin regions can change accordingly to the transcriptional state of the genes in a cell type.

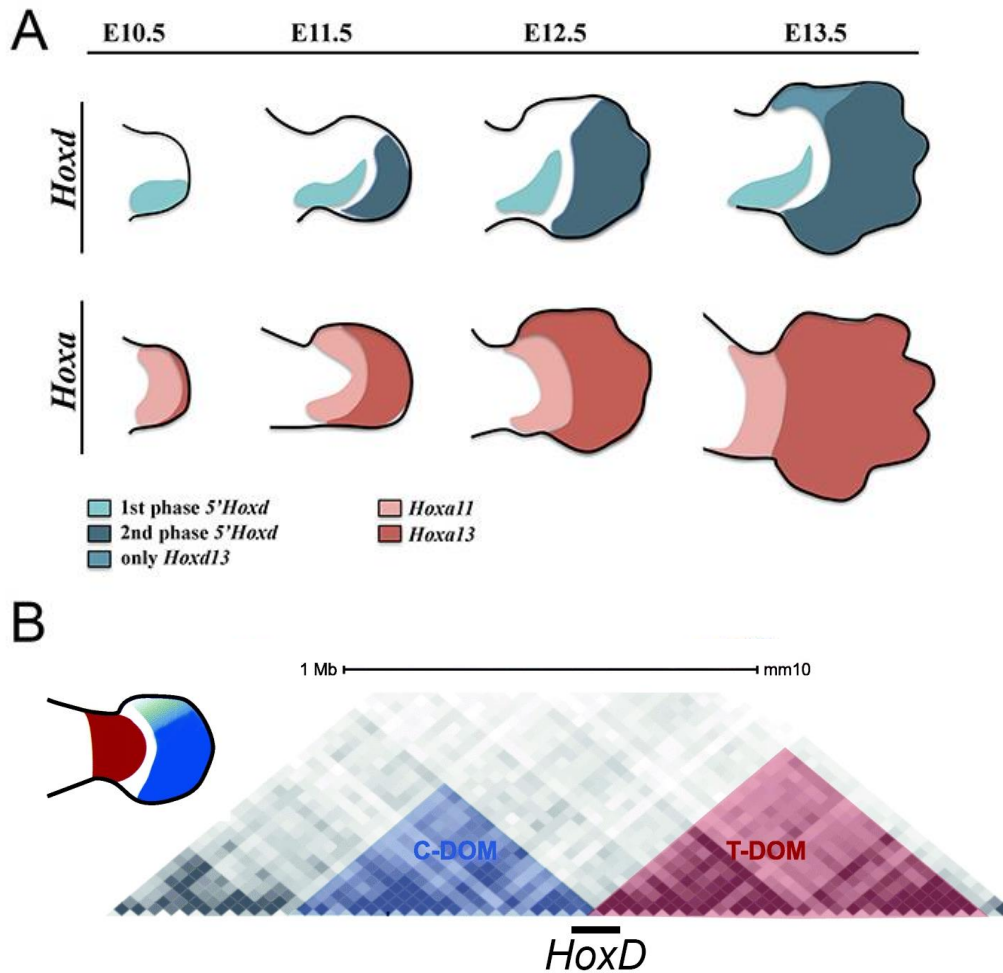


Figure 4: The expression of *Hoxa* and *Hoxd* genes in the development of the limb. A: Schematic representation of the two phases of expression of *Hoxd* genes and the expression pattern of *Hoxa11* and *Hoxa13* (from Pérez-gómez et al., 2018). **B:** Enhancers located 3' to the cluster (T-DOM enhancers) regulate the first phase of *Hoxd* expression, involved in the development of the proximal part of the limb, and enhancers located 5' to the cluster (C-DOM enhancers) regulate the second phase of *Hoxd* expression, involved in the development of the autopod (Fabre et al., 2017).

Up to this point, we have referred to the cis-inputs regulating the expression of *Hox* genes, in essence, how enhancers and promoters interact to activate the expression of *Hox* genes. Nonetheless, an essential topic to consider when studying *Hox* gene regulation is the self-regulation of *Hox* genes (Beccari et al., 2016; Kherdjemil et al., 2016; Sheth et al., 2016, 2014). The previously mentioned exclusion of *Hoxa11* from the *Hoxa13* domain is considered to be mediated by a digit enhancer located in the intron of

Hoxa11, that is bound by Hoxa13 and Hoxd13 (hereafter referred to as Hox13). Hox13 bind to this enhancer to activate the antisense transcription of *Hoxa11*. It is accepted that this antisense transcription interrupts *Hoxa11* sense transcription in distal limb cells, to facilitate correct development of the different limb segments (Kherdjemil et al., 2016). Previous to these findings it was reported that the action of Hox13 proteins are crucial for the correct segregation of Hox domains along the PD axis, as *Hoxa13;Hoxd13DKO* mutants present a distalized first phase expression of *Hoxd* genes in the developing limb (Sheth et al., 2014). This was explained when Hox13 proteins were found to play a role in the regulatory switch of the T-DOM enhancers to the C-DOM enhancers, as limbs lacking the function of *Hoxa13* and *Hoxd13* do not present the switch of chromatin marks necessary for the regulatory change in the *HoxD* locus (Beccari et al., 2016; Sheth et al., 2016). In fact, in the absence of Hox13 the T-DOM enhancers are able to act in the distal limb cells of a E13.5 mouse embryo. Collectively, these findings showed that Hox13 mediates the transition from the early to the late-distal limb program, controlling the spatial expression patterns of target genes by regulating the activity of cis-regulatory modules.

Despite the well described roles of *Hoxa* and *Hoxd* genes in the development of the limb, there is still the need of further research to comprehend their function in the precise specification of the different limb segments. Moreover, it is intriguing that the function of *Hoxb* and *Hoxc* genes in the development of the limb is apparently negligible, as several genes of these two clusters are expressed in developing limbs (Burke et al., 1995; Godwin and Capecchi, 1998; Nelson et al., 1996; Soshnikova et al., 2013; Suemori and Noguchi, 2000).

The limb proximo-distal axis

Hox genes are essential for the correct patterning of the tetrapod limb which consists of 3 PD segments. These are, from the body wall to the distal tip, the stylopod, the zeugopod and the autopod. The stylopod contains one skeletal element, the zeugopod contains two skeletal elements and the autopod is formed by the skeletal elements of the hand/foot that vary in number across tetrapod species. This variability is linked to the different evolutionary changes that allowed tetrapods to run, fly, swim, climb or even handle objects.

How the three limb segments are progressively specified is a subject of debate since the discovery of the function of the Apical Ectodermal Ridge (AER). In the 1940s a series of experiments removing the AER in chick embryos resulted in truncated wings at different levels along the PD axis (Saunders, 1948). A correlation between the truncation level and the stage of the operated embryo was observed: the earlier the AER was removed the more proximal the resulting truncation was.

The interpretation of these results was that the most distal part of the limb bud mesoderm, that is lying directly under the AER, is receiving signaling from the AER that maintains the cells in an undifferentiated state. This group of undifferentiated cells under AER influence is designated as the Progress Zone (PZ) (Summerbell et al., 1973). As cells proliferate and the limb elongates, some PZ cells will eventually fall out of AER-influence and will start differentiating to the proximal structures. Afterwards, more cells will progressively break free of the AER-influence and differentiate into the rest of the limb parts in a proximal to distal sequence. The so-called Progress Zone Model is based on the idea that cells are able to count their time spent under the influence of the AER to progressively specify the 3 limb segments (Reviewed in Tabin and Wolpert, 2007)(Fig. 5A). Thus, this model would explain why the limb is truncated at the level of the stylopod, after AER removal at stage 19/20 of Hamburger and Hamilton (HH)(Hamburger and Hamilton, 1951) but the truncation is at the level of the wrist/ankle when the AER is removed at stage 22/23HH.

X-irradiation experiments were carried out to examine the PZ model (Wolpert et al., 1979). High levels of X-rays on chick limb buds result on the loss of the proximal parts of the limb, with the more severe cases resulting in a limb composed only by digits, a condition termed as focomelia. These results were explained by stating that the X-

irradiation-induced cell death and resultantly smaller limb buds cause the proximal cells to remain within range of the AER signal for a longer time than normal, until the limb bud recovers and grows to sufficient size (Wolpert et al., 1979). Nevertheless, more recent experiments showed that the proximal cells in the limb bud, that normally give rise to proximal limb elements, do not contribute to the distal portion of the mature limb after X-irradiation. Noteworthy, the proximal truncations after X-irradiation of limb buds were explained by the depletion of the first early cartilaginous condensations in the development of the limb, which are the most proximal ones. In fact, when limb buds were irradiated at late limb bud stages, the truncations occurred in more distal parts of the limb, confirming these statements (Galloway et al., 2009).

Fgfs were identified as the diffusible molecules produced in the AER that are encountered by the distal mesoderm. *Fgf4*, *Fgf8*, *Fgf9* and *Fgf17* expression was demonstrated to be specifically in the AER (Fallon et al., 1994; Niswander et al., 1993; Sun et al., 2000). The importance of these genes was revealed when AER-extirpated limb buds supplied with exogenous Fgfs, were able to develop a mature limb with the three PD segments. Mouse genetics, revealed that *Fgf8* is the most relevant family member in the AER, as the single knockout of *Fgf8* exerts a more severe limb phenotype than the triple knockout of *Fgf4*, *Fgf9* and *Fgf17* (Mariani et al., 2008; Moon and Capecchi, 2000). Importantly, combining the deletion of *Fgf8*, in the limb bud, with increasing numbers of AER-*Fgf* knockout alleles resulted in increasingly more severe phenotypes up to the point that no limb develops (Mariani et al., 2008). Collectively, these findings indicate that the AER-Fgfs are functionally redundant.

Importantly, the conditional limb-specific knockouts of AER-*Fgfs* gave phenotypes that the PZ model could not explain. Low dose reductions of AER-Fgfs resulted in distal alterations of the limb and the genetic removal of a significant amount of AER-*Fgfs* (after a transient initial period of *Fgf* expression), yielded highly hypoplastic limbs that included the whole PD axis, with the stylopod less affected (Mariani et al., 2008; Sun et al., 2002). This was contrary to the expected in the PZ model context, as this view would predict that the removal of the AER after a short period of function would result in transverse truncations as those observed after AER removals in chick.

When mouse genetic studies started challenging the PZ model, other visions aroused to explain the specification of the limb segments. The “Early Specification (ES) Model”, was based on two ideas: first the fact that apoptosis or reduced proliferation

occurred in the distal most aspect of the limb bud, after AER removal (Rowe et al., 1982) and therefore could account for the previously mentioned truncation phenotypes. Second, the idea that the cells that are going to form the stylopod, the zeugopod and the autopod are already committed to their fate very early in limb development (Dudley et al., 2002; Tabin and Wolpert, 2007)(Fig. 5B).

Finding a consensus model to explain the PD limb patterning is a complex challenge as there are no described master regulators in the specification of each limb segment. Nevertheless, *Meis1/2*, *Hoxa11* and *Hoxa13* are taken as the best markers for the stylopod, the zeugopod and the autopod respectively (reviewed in Tabin and Wolpert, 2007). Knocking out one of these genes is not sufficient to erase one of the limb segments, however, their expression patterns are specific for each of their correspondent segments.

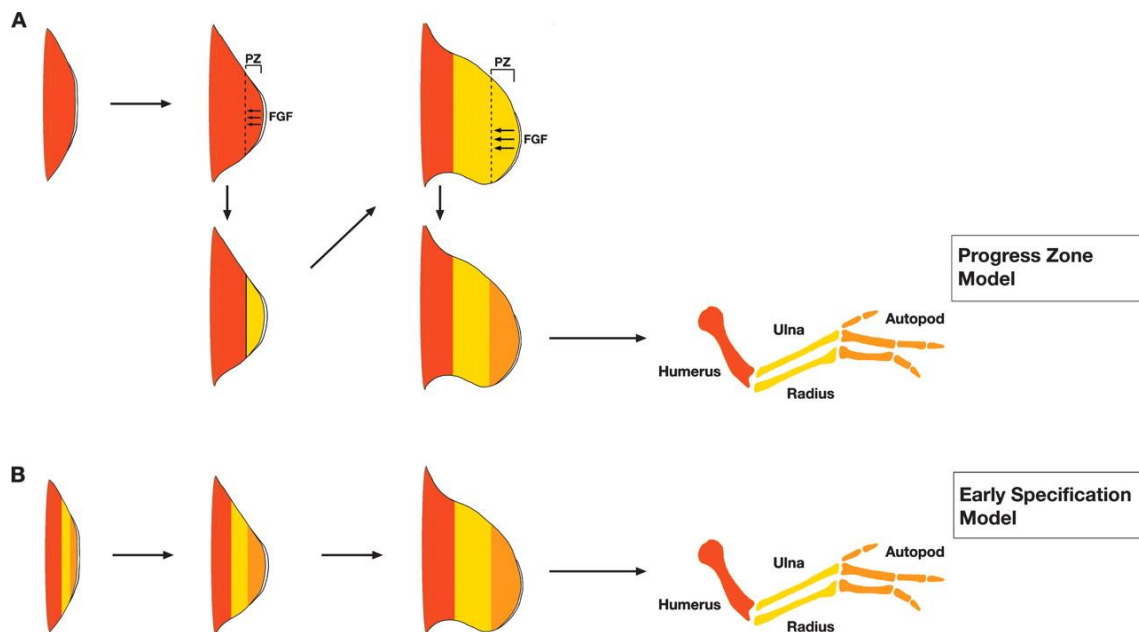


Figure 5. The first models of limb proximo-distal patterning. A: The Progress Zone model. Initially, the entire limb mesenchyme has a proximal identity (red). However, the mesenchyme at the tip of the limb bud, the progress zone (PZ), is exposed to Fgf and becomes specified at a slightly more distal, zeugopod (yellow) fate. As limb development proceeds, the progress zone cells divide, and as a result of this growth, not all of the cells remain within range of the Fgf signal. Those too far from the tip maintain their already specified fate, whereas those still in close proximity to the tip continue their specification to a still more distal, autopod (orange) fate. **B:** The Early Specification Model. All the limb segments—stylopod (red), zeugopod (yellow), and autopod (orange)—are specified in the early limb bud. These segment-specific progenitor pools expand as the limb bud grows (from Tabin and Wolpert, 2007).

The present models of limb PD specification have addressed the importance of extrinsic signals instructing the correct development of the limb segments. The idea that a signal coming from the trunk is specifying the proximal part of the limb was based on the first studies of the role of *Meis1/2* in the proximo-distal axis (Mercader et al., 2000). Retinoic Acid (RA) was found to be a suitable candidate to the signal from the trunk, as not only it induces *Meis1/2*, but also RA beads are capable of reprogramming chick limb cells to express a proximalized *Hox* gene combination (Mercader et al., 2000). Conversely, treatment of proximal limbs with Fgf8 or the inhibitor of Retinoic Acid Receptor (RAR) downregulates the expression of the proximal markers *Meis1/2*, supporting a model of RA-Fgf antagonism controlling limb proximo-distal patterning.

RA is a diffusible molecule (as Fgfs) that during the early development of vertebrate embryos is generated in the trunk mesoderm by Retinol Dehydrogenases (Rdhs) and Retinaldehyde dehydrogenases (Raldhs) (reviewed in Cunningham and Duester, 2015). Three RA receptors (RAR) ($RAR\alpha$, $RAR\beta$ and $RAR\gamma$) and three RXR ($RXR\alpha$, $RXR\beta$ and $RXR\gamma$) isotypes with differential expression patterns play a part in controlling the dynamics of RA signal transduction. While the controversy on whether RA plays a role in limb proximo-distal specification, it is considered that RA generated in the trunk by Rdh10 and Raldh2 enters the limb proximal region but is degraded distally by the action of Cytochrome P450 26 B1 (*Cyp26b1*) (reviewed in Cunningham and Duester, 2015). As a result, a RA gradient with high levels in the proximal limb bud, opposite to the Fgf gradient, is established. In fact, it has been demonstrated that AER-Fgfs induce *Cyp26b1*, what would explain the opposite trends of these gradients (Probst et al., 2011).

In the recent years, the work of two research groups using primary cell culture and recombinant limbs, evidenced that two signals were necessary for the correct development of the limb along the PD axis: Fgfs from the AER and a proximal influence from the trunk, most likely RA (Cooper et al., 2011; Rosello-Diez et al., 2011). Importantly, recombinant limbs, which are made from distal progenitor cells, are able to develop a mature limb with a complete PD axis when engrafted to the trunk of the embryo (Dudley et al., 2002; Rosello-Diez et al., 2011).

However, there is a conflict between the data described above and mouse genetic studies regarding the importance of RA in the development of the limb. *Raldh2* mutant embryos fail to grow beyond E8.5 and to observe the implication of *Raldh2* in limb

development, low doses of maternal dietary RA supplementation were used to rescue the overall development of the embryo. The forelimbs of these embryos were stunted but the hindlimbs appeared normal and the expression of *Meis2* and *Shh* was unaffected (Zhao et al., 2009). Moreover, genetic abrogation of *Rdh10* activity showed no effect in hindlimb proximo-distal patterning. Notably, after knocking out *Rdh10* the expression of *Meis1/2* remains unaffected in the forelimbs (FLs) and the hindlimbs (HLs) (Cunningham et al., 2011). These data conflict with chick studies, in which beads soaked with RAR antagonist and implanted in the limb led to *Meis1/2* downregulation (Mercader et al., 2000; Rosello-Diez et al., 2014, 2011). Reconciling findings in chicks and mice is an ongoing challenge, one possibility is that mice and chicks use different mechanisms to control *Meis1/2* activation, but this can only be resolved by genetic manipulation of chicks to eliminate RA synthesis, thus providing results that are not subject to the potential off-target effects of RA and RAR antagonist treatments.

A key division point between all models of proximo-distal (PD) patterning is whether the limb segments are specified by an intrinsic process or extrinsic signals. The first group, exemplified by the PZ model, posits that the acquisition of positional values along the proximo-distal axis is based on an autonomous clocklike mechanism inherent to the undifferentiated mesenchymal cells. The second group, exemplified by the two-signal with intercalation model, postulates that instructive cues from surrounding tissues are responsible for specifying the limb PD segments.

This unsolved question has been addressed in the recent years, taking into account fate mapping studies. Different labs devised fate mapping studies for the early limb bud, with either fluorescent dyes (Sato et al., 2007; Vargesson et al., 1997) or engraftment of GFP-fluorescent chick limb cells to non-fluorescent chick limbs (Saiz-Lopez et al., 2015). The results of these research groups, and also heterotopic recombinant limb experiments (Rosello-Diez et al., 2011), indicate that the 150um most-distal mesoderm under the AER is capable of developing the zeugopod and autopod at 19/20 HH but only the autopod at 22/23HH, and the most distal phalanges at 27HH (the equivalent stages in mice are E9.5, E10.5 and E11.5).

Homo and heterochronic transplantations of blocks of 150µm most-distal mesoderm showed that this mesenchyme is intrinsically timed in the acquisition of proximo-distal values (Saiz-Lopez et al., 2015). Blocks of distal limb mesenchyme cells expressing Green Fluorescent Protein (GFP) transplanted under the AER of older host limbs revealed that not only the transplants activated *Hoxa13* at their own pace, but also that they were able to sustain the expression of *Fgf8* in the AER for a longer period of time, when compared to non-operated limbs. The transplanted cells avoided mixing with heterochronic host cells and tend to adhere to cells of the same developmental stage.

These recent findings, combined with previously referred reports, support a model with two sequential phases: First, the proximal region of the limb (where *Meis1/2* is expressed) is dependent on instructive signals coming from the trunk, most likely RA, to specify the stylopod. Second, AER-Fgfs are a permissive influence that facilitate the clearance of RA from the distal portion of the limb bud, allowing the activation of an intrinsic programme in which *Hox* genes specify the zeugopod and the autopod. It has been published that *Hoxa13* regulates the expression of cell adhesion molecules such as *EphrinA7* (Stadler et al., 2001), therefore, it is tempting to speculate that *Hox* genes are the factors regulating cell adhesion changes that give cells a positional identity along the proximo-distal axis. Notably, the intrinsic timer of the distal mesenchyme is not affected by the age of the AER, conversely, the distal mesenchyme locally maintains the overlying AER for the appropriate duration to sustain the outgrowth of the limb (Saiz-Lopez et al., 2015)(Fig 6). A continuation of this work confirmed that *Hoxa13* activation is not dependent on the AER itself, rather than in an intrinsic timer of the distal limb mesenchyme cells, that is activated in a RA-free zone (Saiz-Lopez et al., 2017).

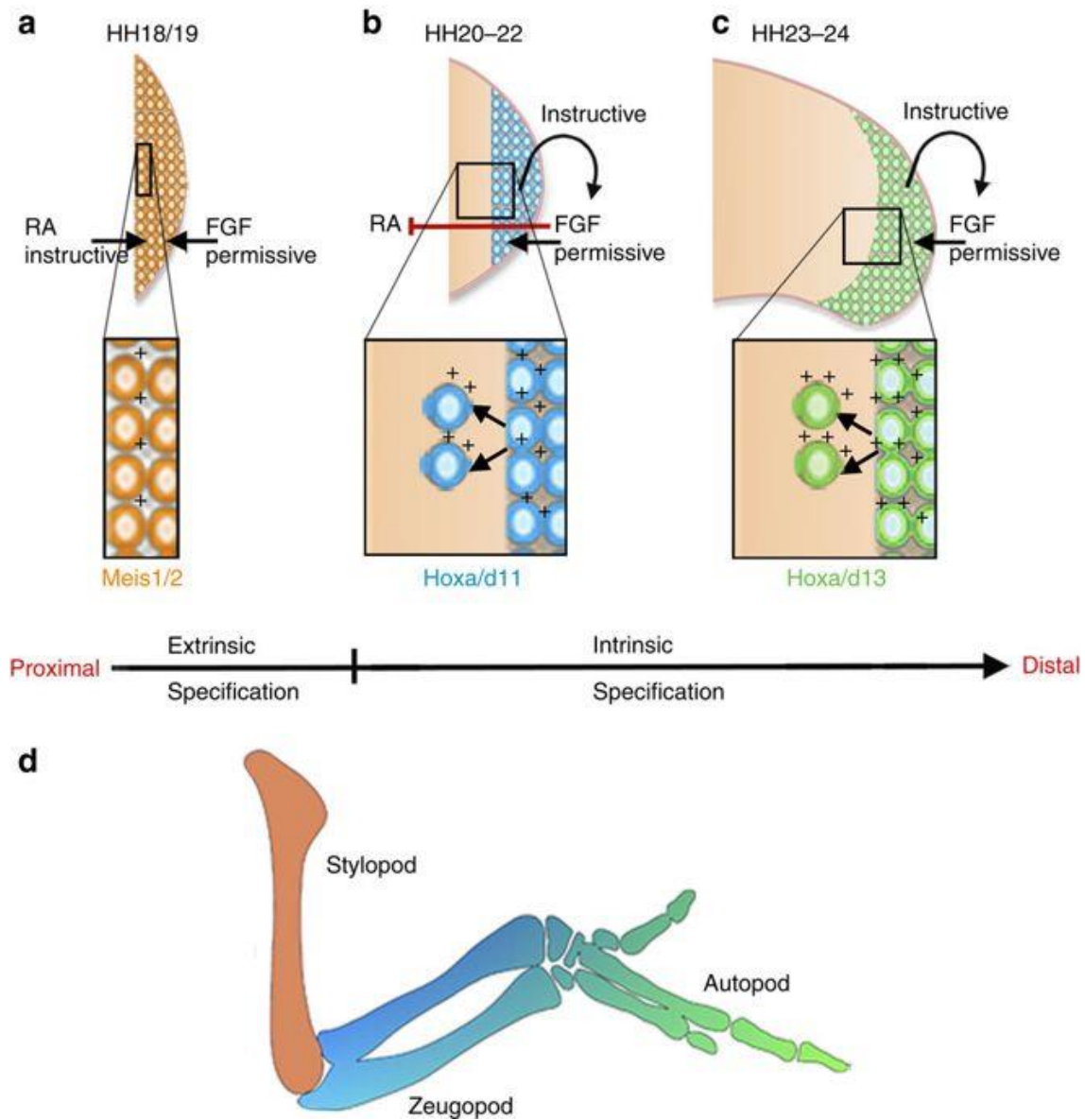


Figure 6. Instructive signals from the trunk specify the stylopod and an intrinsic timer specifies the zeugopod and the autopod. At early limb initiation stages trunk-derived retinoic acid (RA) specifies the positional value of the stylopod (humerus, **a,d**—orange) and then an intrinsic timer specifies the positional values of the zeugopod (forewing, **b,d**—blue) and the autopod (wrist/digits, **c,d**—green). AER-derived Fgfs are permissive factors that sustain growth of the limb bud and suppress the proximal program, including *Meis1/2* expression, by inducing *Cyp26b1* that degrades retinoic acid. Elimination of retinoic acid from the distal mesenchyme of the wing bud triggers the switch to intrinsic timing and mesenchyme cells express 5' *Hoxa/d* genes. This *Hoxa/d* genes maintain the expression of AER-derived Fgfs. Following the phase of proximal specification (**a**), cell adhesion properties and hence positional values intrinsically change over time (**b,c**, different adhesion properties of cells shown by additional “+” symbols in lower insets). This results in a spatial gradient of positional values along the proximo-distal axis as cells are displaced from the distal mesenchyme by an intrinsic programme of proliferation (arrows—lower insets **a–c**—graded blue/green on skeleton, **d**) (from Saiz-Lopez et al., 2015).

The termination of the limb outgrowth

Most limb developmental studies are focused in the genetic processes triggering growth or patterning. Though there is poor understanding on the mechanisms that terminate the activity of these processes.

The patterning of the limb, mediated by the specification and expansion of limb progenitors, is driven by a positive feedback loop between the ZPA/Shh and the AER/Fgfs (Laufer et al., 1994; Niswander et al., 1994). In the early limb bud, it has been reported that an initial signal of Bone Morphogenetic Proteins (Bmps) activates the expression of *Gremlin1* (*Grem1*) (Bénazet et al., 2009). In turn, *Grem1* acts as an antagonist of Bmps, preventing BMP-inhibition on AER-*Fgfs*, closing a fast negative feedback loop (Bénazet et al., 2009; Pizette and Niswander, 1999). This AER-protection permits the activation of *Shh* and thus, the upregulation of AER-*Fgfs*. Then, the activation of *Grem1* by Shh activates a second slower Shh-*Grem1*-Fgf loop (Fig. 7). Of note, it is considered that BMP signaling levels are crucial in the crosstalk between different signaling pathways regulating the patterning of the limb, mainly Fgf, Shh and Wnt (Bastida et al., 2009).

The first model that explained the termination of this explosive feedback loop was based on the increase in distance between the ZPA and the domain of expression of *Gremlin*. This model assumed that *Shh* expressing cells (from the ZPA) and their descendants were not able to express *Grem1*. With further increase in ZPA-descendants, Shh cannot further induce *Grem1*'s (Scherz et al., 2004) and the *Shh-Grem1-Fgf* loop breaks down finalizing specification (Fig 7a,b). After this point, the growth of the limb is caused mainly by the expansion of osteogenic progenitor cells in the developing bones.

An alternative view was coined some years afterwards. It was discovered that Fgf signaling inhibits expression of *Grem1*, what explains the lack of *Grem1* transcripts under the AER (Merino et al., 1999; Verheyden and Sun, 2008). Fgf-soaked beads exert a higher inhibitory effect on *Grem1* in a dosage dependent-manner. Based on these findings and the use of *Fgfr* conditional knockout models it was proposed that the maximum

expression of AER-*Fgfs* could result in *Grem1* downregulation and thus, the breaking point of the Shh-*Grem1*-Fgf loop (Verheyden and Sun, 2008)(Fig.7a',b').

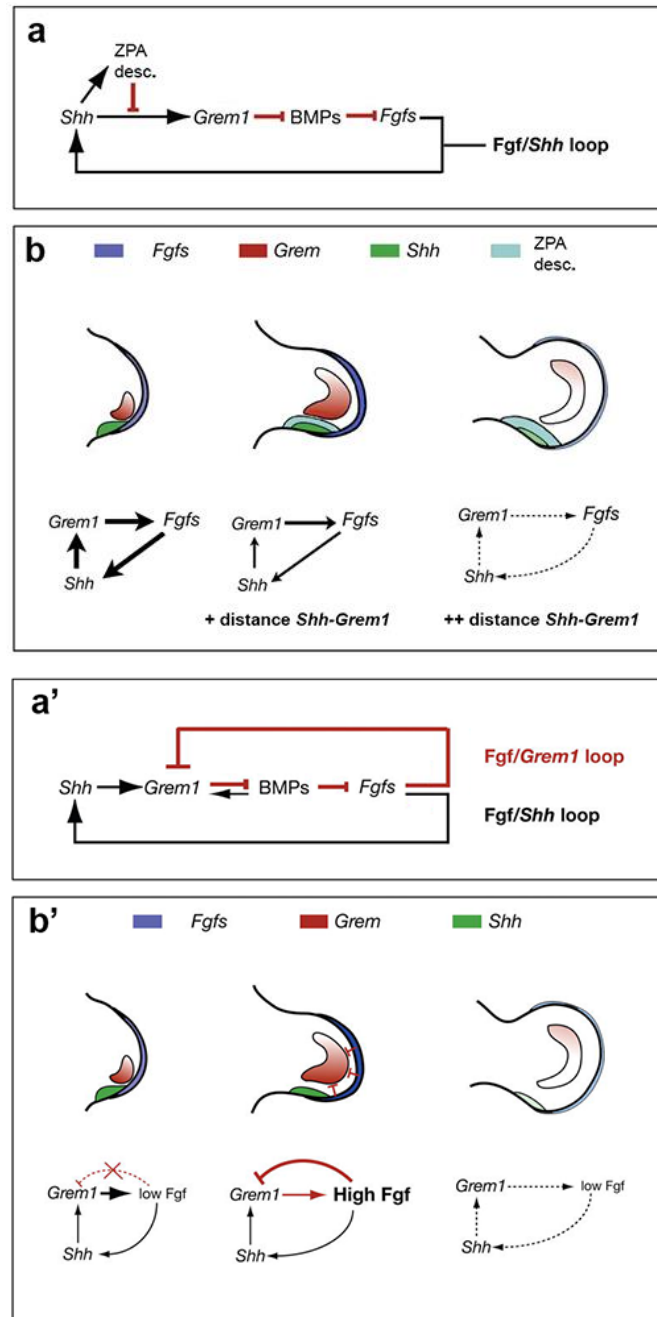


Figure 7. Two models explain the termination of limb outgrowth based on the *Fgf*-*Grem1*-*Shh* loop. a-b: First, BMPs activate *Grem1* which in turn sustains AER-*Fgfs* and these sustain *Shh* in the ZPA. This loop is broken down because the descendants of *Shh*-expressing cells cannot express *Grem1* forming a barrier for *Shh* from the ZPA to reach responding cells (Scherz et al., 2004). **a'-b':** Alternatively, the termination of limb outgrowth can be explained by progressively increased repression of *Grem1* by AER-*Fgfs*. There is a first phase in which a positive regulatory loop operates to increase all 3 signals. Afterwards, the maximum expression of AER-*Fgfs* result in the reduction of *Grem1* expression (Verheyden and Sun, 2008).

Recent investigations showed evidence of an intrinsic program mediating the deceleration of proliferation rate in the limb progenitor cells. The rate of proliferation in the distal limb mesenchyme decreases with age and interestingly, grafts of HH27 distal mesenchyme that were made to younger HH20 limb buds, left to develop for 24hr (referred to as HH24 graft or HH24g), completed their intrinsic proliferation program. Thus, these grafts were not influenced by the presence of an overlying host apical ectodermal ridge, resulting in slightly stunted limbs at the level of the autopod (Saiz-Lopez et al., 2017). An interpretation of these data is that the cells in the HH24g are intrinsically timed to terminate the proliferative outgrowth and, therefore, the termination of the limb bud growth would be an intrinsic property of limb bud progenitor cells.

Last year, the lab of Matthew Towers in collaboration with our research group, published new data that clarified these findings. In this report, the differential expression of *Bmp2* and *Bmp7* in HH24g cells in comparison with the HH24 host tissue was observed (Pickering et al., 2018). The expression of *Bmp2* and *Bmp7* in the HH24g was comparable to the expression in HH29 distal mesenchyme cells (the stage the graft would have reached if left in place), suggesting that grafted cells intrinsically time the expression of these genes, independently of the host tissue. Importantly, the grafts adapted their expression of FGF readouts *Spry2* and *Dusp6* (Chambers and Mason, 2000; Eblaghie et al., 2003) but not their expression of *Bmp* genes (Pickering et al., 2018). It is worth mentioning that the increase in BMP signaling in the grafted cells didn't result in an increase of cell death. Therefore, the stunted limb phenotype is nicely explained by excessive BMP signaling in these grafted limbs, causing the precocious decay of AER-Fgfs (Pickering et al., 2018). Furthermore, this finding points at the intrinsic increase of Bmps, overcoming the Grem1-mediated repression, as the factor mediating the breakdown of the Shh-Grem1-Fgf loop (Pickering et al., 2018). In support of this model, previous work evidenced that *Hoxa13* can activate the expression of *Bmp2* and *Bmp7* and its expression is intrinsically timed in the distal limb bud (Knosp et al., 2004; Saiz-Lopez et al., 2015).

Nevertheless, this recent communication from the Towers' lab and our lab used the chick limb model while the previous termination models were based in mouse genetics (Scherz et al., 2004; Verheyden and Sun, 2008). Therefore, a study of the precise temporal gene expression patterns of the different interplayers in the termination of limb outgrowth in mice, would be of great help to reach a consensus.

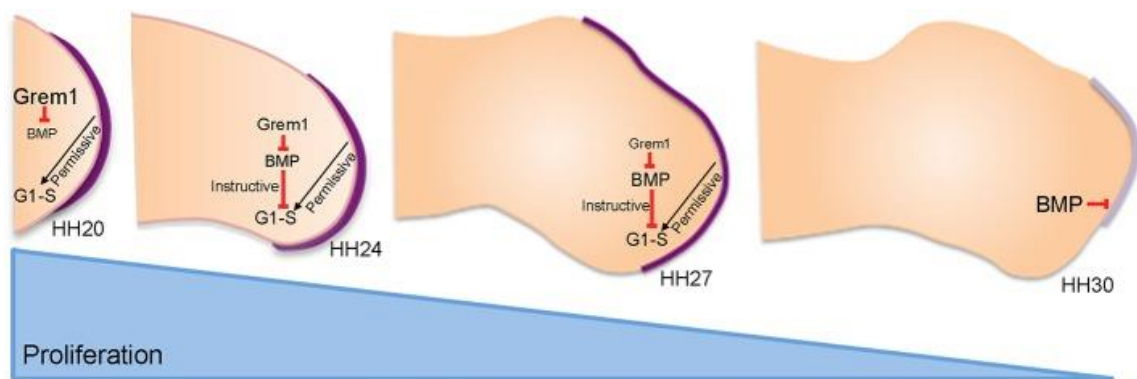


Figure 8. An intrinsic cell timer terminates limb bud outgrowth. HH20-HH24: antagonism of BMP signalling by Grem1 permits rapid mesenchyme proliferation and maintenance of the AER (purple) that permissively supports outgrowth. HH24-HH27: intrinsic rise in BMP signaling counters BMP antagonism by Grem1 and instructively decelerates mesenchyme proliferation rate. HH27-HH30: mesenchyme proliferation diminishes as patterning completes at HH28 and then BMP signalling inhibits Fgf signalling in apical ectodermal ridge that regresses (from Pickering et al., 2018).

Ectodermal organs

The limb is similar in many aspects to an ectodermal organ. Both the development of limbs and ectodermal organs require epithelial-mesenchymal cross-talking and similar developmental pathways are implicated (Biggs and Mikkola, 2014; Pispa and Thesleff, 2003).

Ectodermal organs, such as hair follicles, nails, teeth or mammary glands, arise from an epithelium and a mesenchyme separated by a basement membrane. The epithelium is derived from the ectoderm and the origin of the mesenchyme can vary. This is also the case for the skin, that surrounds many ectodermal appendages, which is composed by an ectodermal portion, the epidermis, and a mesenchymal portion, the dermis (Fig. 9). All ectodermal organs (also called ectodermal appendages) share 2 initial phases in their organogenesis: the formation of the placode and the budding. These are followed by a specialized morphogenesis phase, specific for each ectodermal organ. The placode is a local epithelial thickening that is the first morphological sign of a forming ectodermal appendage (Fig. 10). Concurrent with epithelial morphogenesis, the mesenchyme condensates as a group of cells associated to the overlying epithelium, often referred to as the dermal condensate (DC) (Fig. 10). After placode formation, the epithelium gives rise to an ingrowth, a bud (Fig. 10). In this budding phase the

internalized epithelial cells are surrounded by the dermal condensate in the tooth and the mammary gland. In the hair bud, the leading edges of the down-growing epithelium gradually engulf the dermal condensate that will become the dermal papilla (DP) (Biggs and Mikkola, 2014; Pispá and Thesleff, 2003) (Fig. 10). The classical view is that the mesenchyme gives the first signal to induce the development of the placode and then the placode signals back to the mesenchyme establishing a continuous cross-talk (Hardy, 1992; Noramly et al., 1999; Pispá and Thesleff, 2003).

Much is still unknown about the genes implicated in the development of ectodermal organs. Several members of the Fibroblast growth factor (Fgf), Hedgehog (Hh) and Transforming growth factor β (Tgf β) pathways have described roles in the development of ectodermal organs. Nevertheless, the most studied pathway in the development of ectodermal organs is probably the Wnt/ β -catenin pathway (Biggs and Mikkola, 2014).

The canonical Wnt pathway is mediated by β -catenin (CTNNB1) stabilization. β -catenin is degraded in the absence of Wnt signaling, but when Wnt ligands bind to their receptors, the transduction of the signal results in the inhibition of the β -catenin destruction complex, that marks it for degradation in the proteasome. As a result, stabilized β -catenin translocates to the nucleus and forms a complex with Tcf/Lef1 to activate gene expression (reviewed in Niehrs, 2012).

The importance of the Wnt/ β -catenin pathway in the development of ectodermal appendages was first uncovered by mouse mutants deficient in Lef1, which displayed reduced number or poorly developed hair follicles, absence of most mammary buds, and bud-stage arrested teeth (van Genderen et al., 1994). These results were complemented with the conditional deletion of β -catenin in the epithelium that resulted in the absence of all signs of hair and mammary placode, arrested tooth development at the placode-bud transition and incomplete development of the nail (Huelsenken et al., 2001; Takeo et al., 2013; Zhang et al., 2009). Conversely, forced activation of β -catenin accelerates the induction of hair placodes, fates the entire epidermis to hair follicle fate and provokes multiple ectopic invaginations in the oral cavity that give rise to supernumerary teeth (Ahn et al., 2013; Jarvinen et al., 2006; Liu et al., 2008). Moreover, mouse mutants lacking negative regulators of the Wnt canonical pathway (*Sostdc1*, *Lrp4*) display enlarged mammary placode/buds (Närhi et al., 2012). Collectively, β -catenin loss of function and gain of function experiments in the mouse epidermis reveal a central role of

Wnt signaling in the development of ectodermal organs. In fact, stabilized β -catenin is transiently found in the dermis prior to placode formation, what points to Wnt signaling as the first signal from the dermis to start the development of an ectodermal organ (Noramly et al., 1999).

Analysis of mutants for different members of the Tgf β pathway do present remarkable phenotypes in different ectodermal organs. Although none of them is probably as impressive as the loss of function of β -catenin in the ectoderm (van Genderen et al., 1994), it is possible that the importance of the Tgf β pathway in placode and bud formation is at a similar level to the Wnt signaling pathway. Several regulators of the Tgf β pathway have been linked to the early inductive events guiding hair and tooth development, but so far, mutation of Tgf β family members did not result in an early developmental arrest of other ectodermal organs (Biggs and Mikkola, 2014). Many studies have indicated that suppression of epithelial Bmp signaling is necessary for hair placode morphogenesis to take place (Botchkarev et al., 1999; Mou et al., 2006) and the dysregulation of BMP signaling in developing tooth results in the arrest of this ectodermal appendage at the lamina-placode transition (Ko et al., 2007; Wang et al., 2012). Importantly, it is well known that Wnt and Tgf β pathways interact in developmental processes (Bastida et al., 2009).

Ectodermal organs develop from the embryonic epidermis and the majority of this epidermis is going to give rise to the skin. Skin epithelium has a characteristic stratification process that is different from ectodermal appendages. Adult skin is composed by 5 layers, which are (from the most internal to the most external): the stratum basale, which is the deepest layer and is composed by cells with large nuclei (many of these are skin stem cells); the stratum spinosum, which is composed by cells that are actively producing several cytokeratin proteins and aggregating with strong desmosomal connections; the stratum granulosum, which is a thin layer of cells migrating from the stratum spinosum that contain keratohyalin granules; the stratum lucidum, which are 3 to 5 layers of dead, flattened, keratinocytes filled with eleiden (only present in palms and soles) and the stratum corneum, which is composed by several layers of corneocytes filled with different lipids (Mcgrath et al., 2004)(Fig.9). To reach a better understanding of the

processes driving the differentiation of keratinocytes in the skin and in ectodermal organs it is important to note the presence or absence of these layers in epidermal structures.

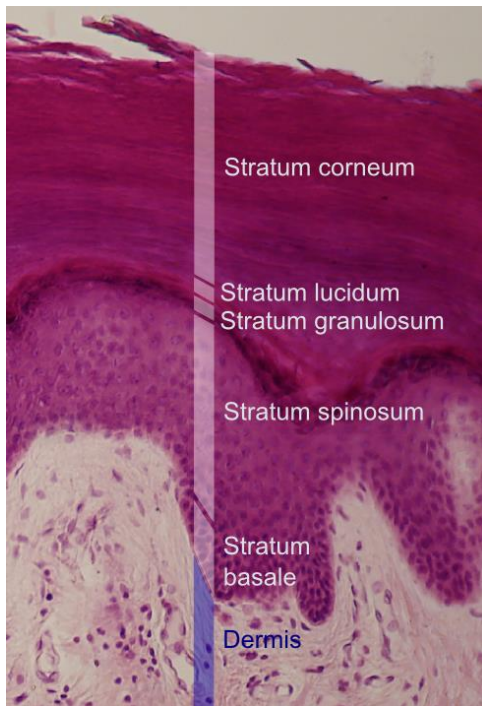


Figure 9. The different layers of the skin.

The dermis consists of different mesenchymal cell types and the epidermis is composed by 5 layers of ectodermal origin. These are from the most internal to the most external: the stratum basale, the stratum spinosum, the stratum granulosum, the stratum lucidum and the stratum corneum (image extracted from <https://commons.wikimedia.org/wiki/User:Wbensmith> online repository).

The hair follicle

The hair follicle (HF) is one of the best studied ectodermal organs and is also the most similar, in terms of immunoreactivity and genetic developmental control to the nail (De Berker et al., 2000; Mecklenburg et al., 2004; Naveau et al., 2014; Perrin et al., 2004; Potter et al., 2011), which is actually the ectodermal appendage that will be focused on in this thesis.

In the development of the HF, once the placode is established, the dermal condensate or dermal papilla becomes the permanent mesenchymal portion of the developing appendage. The dermal papilla is composed by a heterogeneous population of cells that send a variety of signals to the ectodermal portion of the HF. The bulb of the hair germ epithelium forms a cloak about the dermal papilla, and this close encounter stimulates the epithelium to proliferate. As the follicle grows downward, some epithelial germ cells lose contact with the dermal papilla, becoming the outer root sheath (ORS) cells. On the contrary, the cells that maintain their contact with the dermal papilla form the hair germ cells, which are considered as the specialized stem cell population of the

HF. As germ cells withdraw from the cell cycle, they move upward forming concentric cylinders, each of which adopts a morphologically distinct differentiation program. The three cylinders of the inner root sheath (IRS) form first and then the hair shaft appears at the center of the HF. A sebaceous gland is developed concomitantly with the end of the HF development. The sebaceous gland is directly connected to the follicle and the deposition of sebum (a mixture of lipids) is necessary for its maintenance (Fig. 10, reviewed in Fuchs et al., 2001 and Hardy, 1992).

During this developmental process a portion of the epithelial cells forms the bulge of the follicle (Fig. 10), which is a reservoir of Lgr5+ stem cells (Jaks et al., 2008), critical for the hair cycle. The hair cycle consists on 3 different phases, the first, the anagen phase, is characterized by the continuous proliferation and differentiation of hair germ cells. Once the maximum of proliferative capacity of hair germ cells is exhausted, the hair follicle enters a regression and shortening phase, called catagen. During catagen, extensive apoptosis mediates the loss of two thirds of the HF. After this, the follicle enters a resting phase known as the telogen, where the hair shaft loses its anchorage and can be liberated from its site when physically stressed. The initiation of a new hair cycle is considered to occur as a result of a signaling crosstalk between the bulge cells and the dermal papilla cells (reviewed in Fuchs, 2016 and Fuchs et al., 2001). Dermal papilla cells stimulate the bulge to produce a population of transient amplifying cells (TACs) which produce Shh to sustain dermal papilla signaling. This signaling from dermal papilla cells mediates the regeneration of the HF in the new anagen phase (Hsu et al., 2014).

The current view is that the bulge is a source of multipotent stem cells that are capable to differentiate into the hair germ cells, the specialized stem cells of the HF (Greco et al., 2009; Hsu et al., 2014; Rompolas et al., 2012).

Moreover, Shh has not only been associated with the homeostasis of the HF but also with the specification of this ectodermal appendage. *Shh* and *Noggin* were reported to activate each other in HF development and in fact, blocking Shh signaling in embryonic skin, results in the arrest of HF development at the budding stage (Mill et al., 2003; Woo et al., 2012). Further investigations exposed a crossroad in budding ectodermal appendages in the skin: in sweat gland specification, mesenchyme Bmps and Fgfs signal to the associated epithelia to block *Shh* expression. Conversely, HFs are specified when mesenchymal Bmps are blocked. This BMP inhibition allows the expression of epithelial

Shh (Lu et al., 2016). Since Noggin is a BMP antagonist, the Shh-Noggin loop described in Woo et al., 2012 is probably involved in this BMP block.

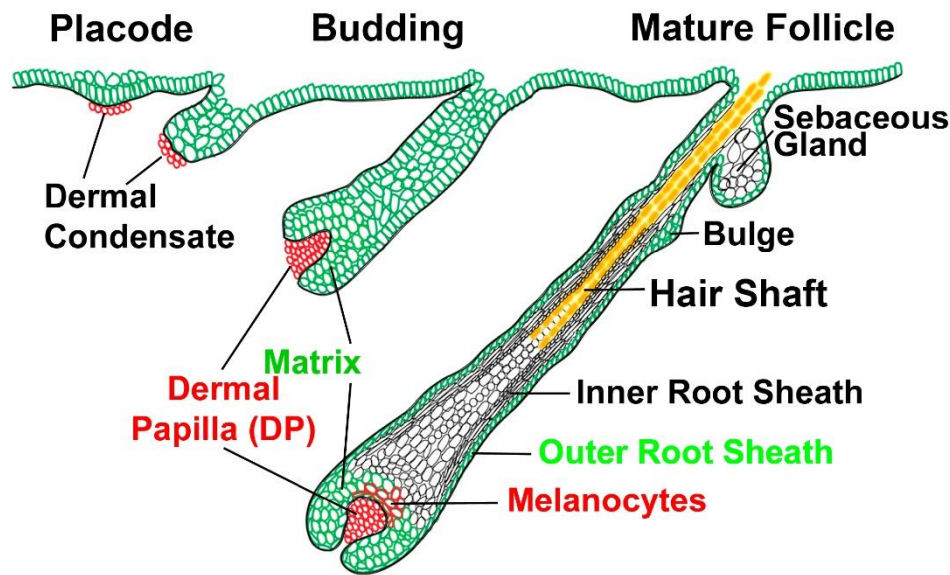


Figure 10. The development of the hair follicle. The different steps of the process of hair follicle development: the induction of the dermal condensate to form the placode, the budding (with the engulfing of the dermal papilla) and development of the mature cycling hair follicle, where epithelial cells have already differentiated into the Inner and Outer Root Sheath and the hair shaft (adapted from Rendl et al., 2005).

It is also worth mentioning the role of *Hoxc* genes in the development of the hair. Among these genes, *Hoxc13* is the best associated to the development of the HF, as *Hoxc13* mutant mice display brittle hair shafts explained by a lack of hard Keratins (Godwin and Capecchi, 1998; Mecklenburg et al., 2004; Potter et al., 2011). In fact, the current view is that *Hoxc13* binds to the *Foxn1* promoter to mediate the activation of several *Keratins* and *Keratin-associated-protein* genes, what would explain the *Foxn1* nude phenotype (Flannagan, 1966; Potter et al., 2011). Moreover, transgenic mice overexpressing *Hoxc13* in differentiating keratinocytes develop alopecia, accompanied by a progressive pathological skin condition that resembles ichthyosis (Tkatchenko et al., 2001). The importance of *Hoxc13* in mammal hair has been emphasized by the striking similar phenotypes resulting from the genetic abrogation of this gene in mice, human, rabbits and pigs (Deng et al., 2019; Godwin and Capecchi, 1998; Han et al., 2017; Lin et al., 2012). In all these species, hair differentiation is impaired in the absence of *Hoxc13* and there are obvious similarities to the ectodermal dysplasia 9 syndrome (ECTD9, OMIM #614931, see table 1).

Both *Hoxc12* and *Hoxc13* display distinct expression patterns in the ectodermal portion of the HF, associated to the hair cycle (Shang et al., 2002). Additionally *Hoxc8* transcripts have also been detected in HF epithelial cells and *Hoxc4*, *Hoxc6* and *Hoxc8* are expressed in the dermal condensate (reviewed in Awgulewitsch, 2003).

The role of *Hoxc* genes in HF regeneration has been recently studied with the *Koala* (*Koa*) mouse model (Fantauzzo et al., 2008; Katayama et al., 2009; Yu et al., 2018). In wild type mice, ear HFs remain in prolonged telogen, in contrast to dorsal skin HFs which exhibit multiple rounds of spontaneous anagen entries. The *Koa* mutant mice have an inversion on chromosome 15 that results in an increase in the proliferation of *Koa*/+ ear skin HFs compared to wild type ear skin HFs. This inversion includes the whole *HoxC* cluster and is the reason why *Hoxc* genes are overexpressed in the dermal condensate of ear skin HFs in *Koa*/+ mice. Interestingly, when the *HoxC* cluster was deleted in cis in the *Koa* inversion, the resulting *HoxCKO_Koa*/+ mice showed normal ear skin HF, arrested in prolonged telogen. In fact, *Hoxc* redundancy and the prevalence of some *Hoxc* in the HF was demonstrated when *Hoxc4KO_Koa*/+ and *Hoxc8KO_Koa*/+ mice were generated, as the first mice didn't rescue the normal phenotype but the second exhibited a partial rescue, with an intermediate level of ear skin HFs proliferation, between *Koa*/+ mice and *HoxcKO_Koa*/+ mice. The researchers working on this study also noted that the ectopic activation of *Hoxc* genes in ear skin HFs can be explained by ectopic interactions of *Hoxc* genes with distant regulatory regions, that became accessible to the *HoxC* cluster when the *Koa* inversion placed *Hoxc* genes in a different TAD. Moreover, members of the Wnt signaling pathway are upregulated in *Koa*/+ ear skin and wild type dorsal skin HFs in comparison to wild type ear skin HFs what points to *Hoxc4,6,8* as activators of Wnt signaling to mediate HF regeneration.

The nail organ

The nail is probably the less understood of the human ectodermal organs, particularly regarding the developmental cues that orchestrate its morphogenesis. It is the ectodermal organ that is most similar to the HF. In fact, some investigators have proposed that the nail unit could be seen as an unfolded form of the HF, producing a hair with no cortex, just hard cuticle, that is permanently growing at a stable rate, with no resting periods (Berker and Baran, 2012).

Mammalian nails, claws and hooves are homologous ectodermal appendages that differ in their shape and form always associated to the underlying distal phalanx. In fact, the terms “nail”, “claw” and “hoof” although useful in a general sense for referring to distal limb appendages, do not accurately describe the range of morphologies observed among living vertebrates. In general, the nail is restricted to the dorsal part of the distal phalanx, the claw expands from the dorsal and the whole lateral surface of the distal phalanx and the hoof forms a hard keratinized wall that can cover entirely the digit tip. The diversity in mammalian distal limb ectodermal appendages reflects the wide variety of adaptations to the environment using the digits to walk, climb, cut, dig and other exploratory and manipulative behaviors (reviewed in Hamrick, 2001).

Gross visual observation of the human nail unit already hints some of the different parts of the nail organ. The nail plate is surrounded and invaginates into the proximal nail fold (Fig. 11A). The cuticle, which is the stratum corneum of the tip skin and undersurface of the proximal nail fold, attaches to and seals to the dorsal surface of the nail plate (Fig. 11A). The lunula, the white semicircle extending from the proximal nail fold beneath the nail plate is the distal portion of the nail matrix (the proximal portion of the nail matrix is internalized under the proximal nail fold)(Fig. 11A). The nail bed is the red-pink area beneath the nail plate that begins where the lunula ends (Fig. 11A). An accentuated band of hyperemia beneath the nail bed results in the color differences between the lunula and the nail bed. The nail plate is attached to the bed until its free white edge (Fig. 11A). The white color of the distal nail plate is due to the light refraction of accumulated hard Keratins, different from the light refraction of the blood vessels lying beneath the nail bed. All this components of the nail can be observed in the mouse nail unit, that partially encircles the dorsal surface and sides of the distal tip, in contrast to the human nail unit that is flatter and mostly dorsal (Fig. 11B)(Fleckman et al., 2013).

The development of the nail starts around E14 in mouse embryos. First, an epithelial thickening on the dorsal surface of each digit tip appears. This thickening is less marked, in comparison to the placodes of other ectodermal organs, hindering the identification of the precise moment of the nail placode induction. Second, a transverse groove appears proximal to the placode that will finally develop into the proximal nail fold (Fig. 11C), where it is considered that the nail matrix cells are engulfed (Fig. 11C). The nail matrix produces populations of cells that differentiate to keratinocytes in the keratogenous zone (these cells produce a subset of hard Keratins characteristic of hairs and nails) that will ultimately form the nail plate (Fig. 11C). The upper layers of the nail matrix do not develop a stratum granulosum and corneum and the keratinocyte differentiation in this epithelium is different from the rest of the skin, as revealed by keratin immunoreactivity studies (Fleckman et al., 2013; Mecklenburg et al., 2004). The cells that remain under the nail plate and extend to the digit tip conform an extremely thin epithelium with no granular layer, referred as the nail bed. The volar epidermis under the free edge of the nail plate is referred as the hyponichium, which undergoes normal skin keratinization (Fig. 11C).

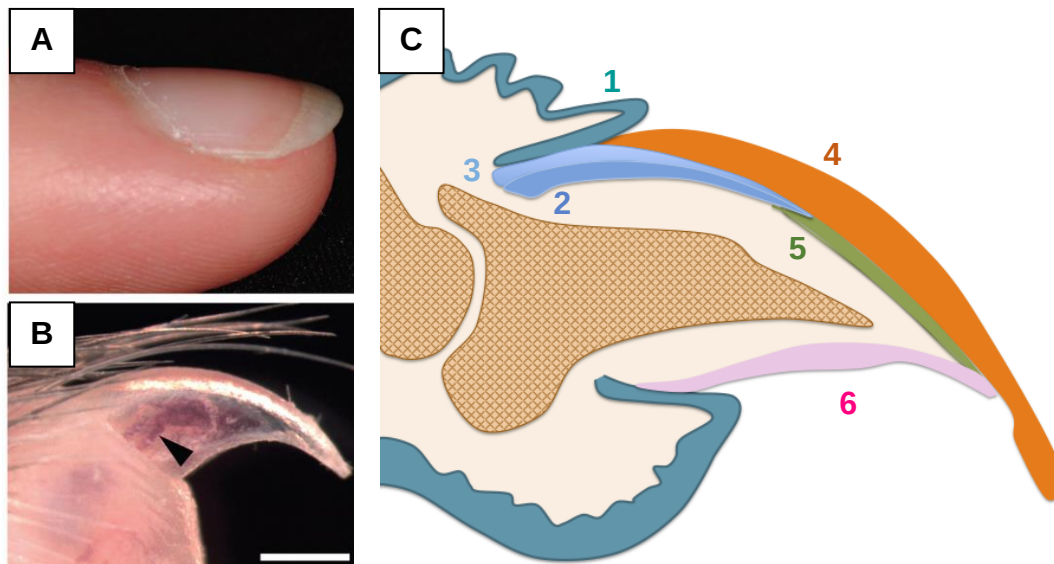


Figure 11. The nail organ. A-B: Gross observation of the human and mouse nail unit, arrowhead in B points to the distal phalanx (adapted from Fleckman et al., 2013). **C:** Schematic representation of the mouse nail organ showing the proximal nail fold (1), the nail matrix (2) (which harbors the nail stem cells), the keratogenous zone (3), the nail plate (4), the nail bed (5) and the hyponichium (6).

Currently, there is debate on where the nail stem cells are located. Some investigators have reasoned that Wnt signaling is key to shed light on this topic. It was reported that the nail matrix cell descendants were the major contributors to the nail plate and that the distal portion of the nail matrix presents differential levels of activated Wnt signaling (Takeo et al., 2013). Moreover, nail development is clearly impaired after the conditional loss of function of β -catenin in the epidermis of mice (Huelsken et al., 2001; Takeo et al., 2013). In fact, the best marker up to date of the nail matrix cells is Lgr6 (Leucine-rich repeat-containing G-protein coupled receptor 6), a receptor of R-spondin that potentiates the Wnt canonical signaling pathway (Lehoczky and Tabin, 2015). Interestingly, mutations in members of the R-spondin (Rspo) family of secreted proteins linked to the Wnt signaling pathway result in the absence of nails in mice (*Rspo2*) and in human (*RSPO4*) (Aoki et al., 2008; Ishii et al., 2008). Alternatively, a 2014 report pointed that there is a population of Keratin15-expressing cells in the proximal fold that can contribute to the nail plate (Leung et al., 2014). Although these data are seemingly in conflict with the literature mentioned above, the Keratin15+ cells identified by Leung & collaborators are multipotent and slow cycling cells whereas the Lgr6+ cells identified by Lehoczky & Tabin are seemingly specialized unipotent stem cells, therefore, it is possible that these multipotent cells could differentiate into the unipotent ones, which are the major contributors to the nail plate in normal homeostasis. Curiously, this situation would be reminiscent of the HF, as the bulge cells are comparable to the Keratin15+ cells of the proximal nail fold given its multipotency and the hair germ cells are comparable to the Lgr6+ nail matrix cells, as the unipotent stem cells of the ectodermal organ that give rise to the hair shaft/nail plate (which express a similar combination of hard acidic Keratins). It is also worth mentioning that a member of the non-canonical Wnt signaling pathway, Wnt7a, is expressed in the dorsal epidermis and required for normal Dorso-Ventral patterning. In fact, loss of function mutations of Wnt7a result in double ventral digit tips that lack nails (Parr and McMahon, 1995).

The BMP targets *Msx2* and *Foxn1* display nail phenotypes that are also widely referred in the literature (Cai and Ma, 2011; Kulesa et al., 2000; Mecklenburg et al., 2004). *Msx2* mouse mutants exhibit elongated and fragile nails, whereas *Foxn1* mice nails were thinner, shorter and easily broken (Mecklenburg et al., 2004; Satokata et al., 2000). Double *Foxn1*^{-/-};*Msx2*^{-/-} mutants exhibit a more severe phenotype with nails breaking just beyond the hyponichium. These phenotypes were explained by a downregulation of

Keratins expressed in the Keratogenous zone (Cai and Ma, 2011). In fact, a recent work showed that BMP signaling is needed for the correct development of the nail (Leung et al., 2014). The gene regulatory network in which BMPs are involved to regulate the expression of nail-associated Keratins is not yet understood, though it is known that the mesenchyme under the nail organ expresses *Bmp4* and *Msx1* which is considered a readout of BMP signaling (Allan et al., 2006; Han, 2003; Lehoczký et al., 2011)

The phenotype of *Foxn1* mice is a phenocopy of the *Hoxc13* null phenotype. In both mutants, the expression of hard Keratins is abrogated, resulting in poorly developed and fragile nails and brittle hair (Godwin and Capecchi, 1998; Mecklenburg et al., 2004; Meier et al., 1999). Histological analysis revealed that the differentiation of the nail epithelia was altered with the appearance of a granular layer in the apical nail matrix, both in *Hoxc13* and *Foxn1* mutants. Also, *Foxn1* mutants presented the nail bed and the ventral part of the proximal fold thicker than controls (Mecklenburg et al., 2004; Potter et al., 2011). These findings hint a *Hoxc13-Foxn1-Keratins* regulatory cascade in the differentiation of hair and nail keratinocytes.

Ectodermal dysplasias

One of the main reasons to study ectodermal organ development is to improve our understanding of Ectodermal dysplasias (ECTDs). ECTDs are a group of congenital disorders characterized by abnormal development of 2 or more ectodermal appendages, without other systemic findings. In all reported cases, hair development is impaired and hypotrichosis (sparse and fragile hair) is a frequent condition in ectodermal dysplasias (Table 1). The other most common clinical manifestations of ectodermal dysplasias are nail dystrophy, abnormal or missing teeth (anodontia or hypodontia) and inability to sweat (anhidrosis or hypohidrosis). The last one is caused by a dysregulation of the development of the sweat glands.

There are several animal models to study these congenital syndromes. Among them, the use of mouse models has been key to understand the development of these diseases. Some ectodermal dysplasias have been studied with other mammalian models, this is the case for ECTD1 with bovine (Drögemüller et al., 2001) and canine (Casal et

al., 2007) models or ECTD9 with pig (Han et al., 2017) and rabbit models (Deng et al., 2019).

Among the different congenital disorders included in this group of dysplasias, the pure hair-nail ectodermal dysplasias (PHNEDs) are rare congenital conditions characterized by hypotrichosis and nail dystrophy without other ectodermal or non ectodermal manifestations. The PHNEDs include ECTD4, 5, 6, 7 and 9 (Table 1).

Although it is possible to combine abnormalities in the development of ectodermal appendages together with abnormalities in the development of non-ectodermal structures, these conditions are not referred to as ectodermal dysplasias. For example, this is the case for Ectrodactyly with ectodermal dysplasia and cleft lip/palate syndrome 3 (EEC3, OMIM #604292) that is caused by mutations in the *TP63* locus (Celli et al., 1999).

In this thesis we focus our interest on ECTD9. This is defined by two characteristics: the first is that it is linked to the *HOXC13* locus and the second is that it is one of the PHNEDs (Table 1). The first well-described case was a five-generation consanguineous Chinese Hui family with three affected individuals born to healthy first-cousin parents, consistent with an autosomal-recessive mode of inheritance (Lin et al., 2012). The three affected individuals showed atrichia and severe nail dystrophy (Fig 12). Whole-exome sequencing showed that the cause of the ECTD was a point nonsense mutation in the first exon of *HOXC13*. Only homozygous individuals developed the syndrome. In this work the researchers also described the case of an Afghan female born to consanguineous first-cousin parents. She presented severe hypotrichosis and nail dystrophy. Genomic PCR assays in blood samples from the Afghan female identified a 27.6 kb homozygous microdeletion including all exon 1 and part of the *HOXC13* intron. QPCR and immunohistochemical analysis revealed a downregulation not only of *HOXC13* but also of *FOXN1*, *DSG4*, *KRT85* and *KRT35*, which are involved in the development of the hair and the nails (Potter et al., 2011).

	Location	Phenotype	P. MIM number	Inheritance	P. map key	Locus	Locus MIM number	Human case ref.
ECTD1	Xq13.1	Ectodermal dysplasia 1, <u>hypohidrotic</u> , X-linked	305100	XLR	3	EDA	300451	Zonana et al., 1993
ECTD2	13q12.11	Ectodermal dysplasia 2, Clouston type	129500	AD	3	GJB6	604418	Coulston, 1929
ECTD3	4p16.2	Ectodermal dysplasia 3, Witkop type	189500	AD	3	MSX1	142983	Freire-Maia and Pinheiro, 1979
ECTD4	12q13.13	Ectodermal dysplasia 4, hair/nail type	602032	AR	3	KRT85	602767	Witkop, 1965
ECTD5	10q24.32-q25.1	Ectodermal dysplasia 5, hair/nail type	614927	AR	2	None	None	Rafiq et al., 2005
ECTD6	17p12-q21.2	Ectodermal dysplasia 6, hair/nail type	614928	AR	2	None	None	Naeem et al., 2006
ECTD7	12q13.13	Ectodermal dysplasia 7, hair/nail type	614929	AR	3	KRT74	608248	Naeem et al., 2007
ECTD8	18q22.1-q22.3	Ectodermal dysplasia 8, hair/tooth/nail type	602401	AR	2	None	None	Fried, 1977
ECTD9	12q13.13	Ectodermal dysplasia 9, hair/nail type	614931	AR	3	HOXC13	142976	Lin et al., 2012
ECTD10A	2q13	Ectodermal dysplasia 10A, <u>hypohidrotic</u> /hair/nail type, autosomal dominant	129490	AD	3	EDAR	604095	Hout et al., 2008
ECTD10B	2q13	Ectodermal dysplasia 10B, <u>hypohidrotic</u> /hair/tooth type, autosomal recessive	224900	AR	3	EDAR	604095	Shimomura et al., 2004
ECTD11A	1q42-q43	Ectodermal dysplasia 11A, <u>hypohidrotic</u> /hair/tooth type, autosomal dominant	614940	AD	3	EDARADD	606603	Bal et al., 2007
ECTD11B	1q42-q43	Ectodermal dysplasia 11B, <u>hypohidrotic</u> /hair/tooth type, autosomal recessive	614941	AR	3	EDARADD	606603	Munoz et al., 1997
ECTD12	1p36.11	Ectodermal dysplasia 12, <u>hypohidrotic</u> /hair/tooth/nail type	617337	AD	3	KDF1	616758	Shamseldin et al., 2016
ECTD13	22q12.1	Ectodermal dysplasia 13, hair/tooth type	617392	AR	3	KREMEN1	609898	Issa et al., 2016
ECTD14	21q22.3	Ectodermal dysplasia 14, hair/tooth type with or without <u>hypohidrosis</u>	618180	AR	3	TSPEAR	612920	Peled et al., 2016

Table 1: List of the described ectodermal dysplasias, showing their linkage and inheritance in human. The information for each congenital condition was extracted from www.omim.org. P=Phenotype.

In the recent years, more cases of ECTD9 have appeared with different changes in the DNA sequence that affected *HOXC13* gene. A consanguineous Syrian family with a female having complete alopecia and nail dystrophy presented a homozygous single nucleotide deletion (c.355delC) in exon 1 of *HOXC13*, which was predicted to lead to a frameshift and a premature codon termination (Farooq et al., 2013). A Pakistani family had three children with PHNED, one boy and two girls. Sequence analysis of family members revealed that the three children carried a homozygous A to C transversion mutation in the *HOXC13* gene at nucleotide position 929 (c.929A > C. This sequence change results in substitution of Asparagine residue with Threonine at position 310 (p.Asn310Thr) of the *HOXC13* protein, affecting the portion of the second exon that codes for the homeodomain of *HOXC13* (Khan et al., 2017).

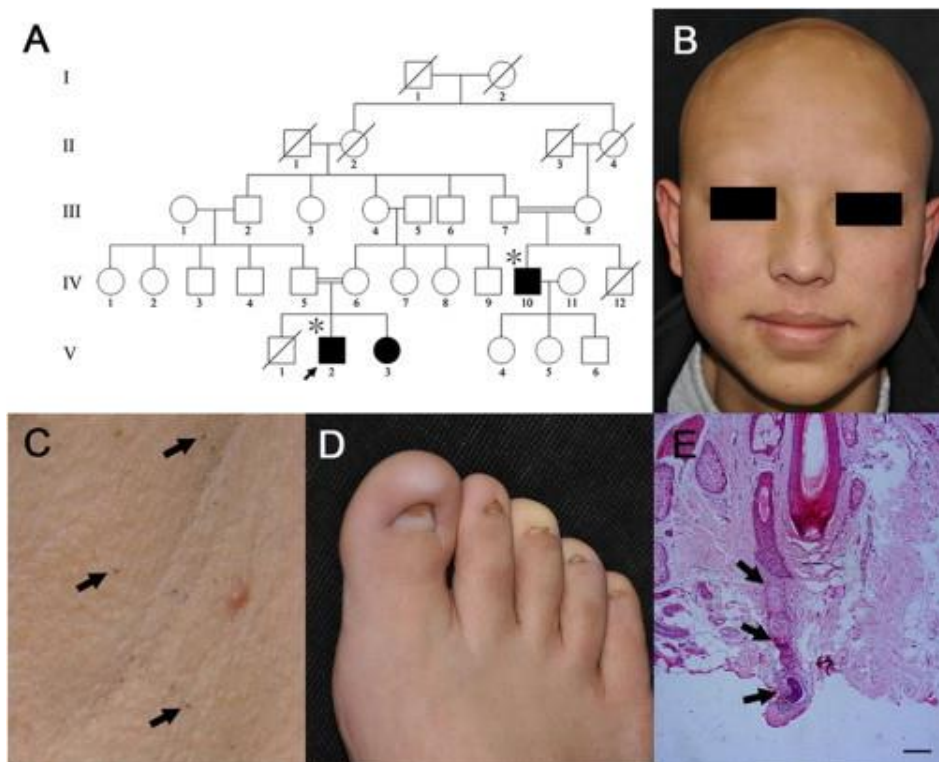


Figure 12. Ectodermal dysplasia 9 in a Chinese Hui family. **A:** Pedigree of a Chinese Hui family affected by PHNED. The arrow indicates the individual V2. Solid symbols indicate individuals with PHNED, and asterisks above pedigree symbols refer to individuals with persistent Müllerian duct syndrome. **B:** Congenital alopecia involving the scalp, beard, eyebrows, and eyelashes in individual V2. **C:** Close view of axillary area of individual V2 shows that hair shafts break off at the skin surface. Arrows show remnants of unprotruding hair. **D:** Severe nail dystrophy affecting all toenails in the individual V2. **E:** Scalp skin-biopsy section demonstrating normal epidermis and dermis. The arrow shows disorganization in a hair shaft without normal layered structure in the longitudinal section of a hair follicle. Hematoxylin-eosin staining was used. The scale bar represents 30 μ m. (from Lin et al., 2012).

The linkage of *HOXC13* with ECTD9 is of particular interest given the fact that three animal species models have been developed for this congenital syndrome (mouse, rabbit and pig) and in the three cases the phenotype was strikingly similar to the mutant condition in humans (Deng et al., 2019; Godwin and Capecchi, 1998; Han et al., 2017). These findings point to a central role for *HOXC13* in the development of the hair and the claws/nails/hoofs in mammals and possibly in other tetrapod species.



AIMS

AIMS OF THE PRESENT THESIS

Aim 1- To generate the temporal transcriptome of the AER during the development of the mouse limb. Validation, analysis and interpretation of results.

Aim 2- Generation of the temporal transcriptome of the SubAER mesoderm during the development of the mouse limb. Validation, analysis and interpretation of results.

Aim 3- To investigate the function and transcriptional regulation of *Hoxc* genes in the limb ectoderm.

3.1- To understand *Hoxc* function in the limb ectoderm.

3.2- To unravel the transcriptional regulation of *Hoxc* genes in the limb ectoderm.



MATERIALS & METHODS

MATERIALS AND METHODS

Mouse strains

Wild type mice and The *Hoxc13GFP*, *HoxCKO*, *delEC1*, *delEC2*, *del(EC1-EC2)* and *inv(EC1-EC2)* mutant mouse lines were used in this study. The *Hoxc13GFP* (Godwin et al., 1998) and *HoxCKO* (Suemori and Noguchi, 2000) lines were kindly provided by Denis Duboule (EPFL, Lausanne). The *delEC1*, *delEC2* and *del(EC1-EC2)* were generated in this study with the CRISPR-Cas9 technique. All strains were maintained in a B6CBA mixed background.

The *Hoxc13GFP* line is characterized by the insertion of an in-frame GFP reporter site at the second exon of the *Hoxc13* gene (Godwin et al., 1998). The *HoxCKO* line is characterized by a deletion spanning from the intron of *Hoxc13* to the second exon of *Hoxc4* resulting in the complete deletion of *Hoxc12*, *c11*, *c10*, *c9*, *c8* and *c6*, the loss of the second exon of *Hoxc13*, the loss of the first exon of *Hoxc4* and a partial loss of the second exon of *Hoxc4* (Suemori and Noguchi, 2000). The *delEC1* and the *delEC2* line are characterized by the complete deletion of the *EC1* and *EC2* enhancer regions, described in this study. The *del(EC1-EC2)* mouse line is characterized by the deletion of chr15:102,754,111-102,836,019 region, resulting in the loss of *EC1*, *EC2* and the genomic region between them.

All animal procedures were conducted accordingly to the EU regulations and 3R principles and reviewed and approved by the Bioethics Committee of the University of Cantabria.

Mouse Embryos

Embryonic day 0.5 was assigned to the noon of the day the vaginal plug was detected. Embryos were harvested at the desired developmental stage by cesarean section of pregnant mice, dissected in Phosphate buffered saline (PBS) and fixed overnight (ON) in 4% PFA.

Genotyping

Mutant mice and embryos were genotyped by collecting tail biopsies and yolk sac respectively. DNA extraction was carried out by alkaline lysis incubation of the tail biopsies in 25 mM NaOH;0.2 mM disodium EDTA at 95°C for 1h, followed by its neutralization (40 mM Tris-HCl) (Truett et al., 2000).

Genotype was performed following standard PCR protocols, varying the annealing temperature according to the melting temperature TM of the primers used (Table 2). The PCR was performed with 0.5µl of the extracted DNA, primer final concentration at 700 nM, and Supreme NZYTaQ II 2x MasterMix (MB35903) in a total volume of 12.5µl. PCR products were run in a 1-1.5% agarose gel containing Sybr® Safe for DNA staining and visualized in a Gel-Doc under ultraviolet light and the use of the Quantity–One software (Bio-Rad). Finally, the molecular weight of the products was determined with the use of Gene Ruler DNA Ladder (Thermo Scientific). The set of primers used to genotype each mouse strain is specified below and it is indicated into 5' to 3' orientation.

HoxCKO

Fwd-WT	CGCTCTGGGAGTGGTCTTCAGAAG	WT: 574 bp
Rev-WT	GTGCTACGATCTGTTATGTATGTG	
Fwd-MUT	GATGGAGTTTCCCCACACTGAGTG	MUT: 650 bp
Rev-MUT	CGTGAGGAAGAGTTCTTGCAGCTC	

LacZ

pBSLac-F1	GGCTGGGCATAAAAGTCAGG	Insertion: 430 bp
pBSLac-R1	GAACAAACGGCGGATTGAC	

delEC1

Ehoxc-1a	ATAGCCAGCAAGGGAAAGGGGATTG	WT: 403 bp
Ehoxc-1b	ACCCACCAAAGGAAGAAGTAAGGCTAG	
Ehoxc-1d(mut)	ACAGGAGCTGACTCAGAGACTGG	MUT: 448 bp

delEC2

Ehoxc-2a	CGTGATCCTCCAGCCTCTAACC	WT (2a-2b): 305 bp
Ehoxc-2b	GAGCCAAGGCCTACAGTCTTACC	
Ehoxc-2d(mut)	GAGAGGGAAGGAGTTGGGTGTC	MUT (2a-2d): 340 bp

del(EC1-EC2)

Ehoxc-2f	CACAAGACCCAGGCAAAGCA	WT (2f-2g): 780pb
Ehoxc-2g	GGCTTCACCCTCCCAACCTA	
Ehoxc-1h(mut)	ACAAGGGCAGGTTGATCTAGC	MUT (1h-2g): 960pb

Table 2. Primers for genotyping the mutant mouse lines used in this study.

It should be noted that the *Hoxc13GFP* samples and WT littermates were received with confirmed genotypes. Genotyping of *Hoxc13GFP* was never performed at our lab.

Paraffin embedding

After fixation in 4% PFA, samples were washed in PBS and dehydrated in increasing concentrations of ethanol until ethanol 96°. If samples were from P7 or older mice, decalcification in 9%EDTA pH=7,4 was carried out before dehydration (time depending on stage and size analyzed) and samples were washed for 24h in dH₂O, rinsing at least 3 times. Samples in ethanol 96° were stored if desired, at 4°C for days or at -20°C for longer periods or dehydration continued with two washes in absolute ethanol. Samples were then cleared twice in xylene (time depending on stage and size of the sample) before being embedded in paraffin (SIGMA, #P-3558) at 60°C for at least 1h. A Leica RM2125RT microtome was used to perform 7-10 µm sections that were placed on SuperFrostPlus slides, (LEICA, #10149870).

Hematoxylin-Eosin staining

Paraffin sections were rehydrated following standard procedures. Sections were stained with Harris Hematoxylin (Merch) for 3 minutes. Then, the sections were allowed to color differentiate in running tap H₂O for 20 minutes or more until the desired color is obtained. After rinsing with H₂O, sections were stained with Eosin (Eosin Y (SIGMA) 0.5%, 0.1725% aqueous acetic acid, 0.246% sodium acetate in dH₂O) for 30 seconds. After a quick rinse in H₂O sections were dehydrated and mounted in cytooseal60 (Richard-Allan Scientific) following routine procedures. The timing of staining in Hematoxylin and Eosin can vary after repeated uses and the recent stained sections should be observed at the scope before proceeding with the next step.

RNA probes synthesis

When the probe of interest was within a vector, plasmid DNA was transformed in *E.Coli* DH5 α competent cells (following standard procedures), plated in LB agar with antibiotic, and culture at 37°C ON. Next day, one colony was selected for inoculation in LB with antibiotic and incubated at 37°C ON in a shaker. High Pure Plasmid Isolation Kit (Roche) was used for plasmid purification. To synthesize an anti-sense transcript, specific restriction endonucleases were used to linearize the plasmids and digestion was performed following standard protocols.

Finally, the transcription of the probes was generated by in vitro transcription reaction in the presence of digoxigenin labeled nucleotides, following standard protocols and using diethylpyrocarbonate (DEPC) treated water to inhibit ribonucleases (Rnases).

In the case the probe of interest was not available, a PCR template for in vitro transcription was designed. The cDNA sequence from the gene of interest was extracted from the NCBI nucleotide repository (<https://www.ncbi.nlm.nih.gov/>) (Table 3). Primers were designed to amplify preferentially the 3'UTR of the gene of interest with Primer3 (<http://primer3.ut.ee/>), adding the DNA sequence of the SP6 promoter (ATTTAGGTGACACTATAGAA) to the 5'end of the reverse primer. RNA of embryo tissue, expressing the gene of interest, was extracted with TRI reagent (SIGMA, #T9424) following standard procedures. cDNA was synthesized with iScript cDNA synthesis kitTM (Biorad) and used for the PCR amplification of the region of interest. Then, transcription of the probe was performed in vitro with the SP6 RNA polymerase (Thermo scientific).

mHoxc8

CCGAGATGAGGAGAAGGTGGAAGAAGAAGGGAATGAGGAAGAGGAGAAA
 GAGGAGGAGGAAAAGGAAGAAAATAAGGACTAAGGAAAAAAGAGAGAG
 AAAATCAGCCCCCCCCCAGCAACTCCCTTGAAGTTTCGTTTTATGGTAGCA
 GATAAATTGAGAAGTTTACGACTGTCATTTGCTTTTATAGAGAATAGAATGA
 CACTCACAACCTCTAACTACCTGTCAGATAGTTGCAGCTCTGCTTTTATTACCT
 TTGGGCTTCCCCACTCTTTATTTGTCTGGGGGTTGGGAGGGGGAACCTGAG
 ACACAGGGAAAAGTTCTGTTCTACTCCATGCCAGCATACTCTCTTGTTC
 CTGCTCCACCTTCTGAGCCCTTCCCCATAAAGTCTAACCCTTCACACACACA
 CACACACACACACACACACACACACACACACACACACTTCTCTCC
 AACTCCCTCTTCACGGTGCTTCTCTGGTATTTATTTTAAAAGGGATTCCCCT
 GAAGATATAGAAGATGATTCTGGCTTTGCTTGTATGCTGGGAATTAGAATA
 CTGGATAAACAGTTTTTTTTTAAATGAAAAGAAAGAAAGGAAAAAACAGGAA
 AGGGGGAAATGAAAGGAAAAATTAAGAAAGAAATAAAGATAGCAAGAAG
 ATCCCCCTCCCCCTCTGAGGCTCTTCCCTTAGAAAAACCCCTTGACTTTCTC
 CAGGAATCTGCTGGAAATCAAGGAGATGTGGGTTTCTCTACCCACCTCCTTC
 CTG

mRprm

ACCGGAGGCCGTCTAAAGAGGTGGAGGCAGTGGTCGTGGGACCCTACTGA
 GTGGCCCTCGGGTCCCCCTCGGCGGGTGCTCCCTTCTGGCACCTCCAGTA
 CTCCGCCAGCCGCGATGCACCCCTCACCATCACGGACCGAGCAACGCAAA
 CCTGTGCGAGTCAGTTTTTTTCTCTTGACTTCTGCCTTTGGGGAAAAAGTGA
 CCGATTTCTGATAGCTCTTCGAAAGGCCCAAGCAAGACTGTACAGGAGG
 AGCGCCCAGACTTCGGGACACAGCAGCAGGTGGCAAAAGCAGGGCGCAG
 AACTTTGGGAGTGGCTGCTGGCGTGGGATACTGGGAGATGAACCAGGCGG
 CGAAGGCCCTTTCCACCTGCAGGTGGGCTCAGCACTGGGGACAGCTTGA
 GAGGCCGAGCAAGGCGGGGTGTGGATGGGTGTGTATTAGAGGCCCAGTG
 ACCGGAAAAAGTGAAGTGTATTCGCCACGCTGCAGACCTAATTGGGAAG
 GAACATAGATGCGTGTGGGTTTTGCGACCTACTAAGAGAGTGAACTTTGA
 TCGATAGTAACCTGTGGTTTTAGGGGATTTGTGTTAGTTTGCTTGAATACA
 AATATTTGATAAGTCTTTTGTGTCCTAGTGGCCTGTTTGCCTGCCTGCGGGT
 TAGAGTTTTTTGTCACTTCTGGGAGAACGGGTGGGGGGAGGGGAGTCTGAG
 ACTGTGAATGGGGTAAGTGCTTTCTTTTAGTGCAATTCAGCTGGGTCTTTA
 TGGGAGGCTAGCGCTCCAGCTACGCCCGGGACAAAGATCCAGAGTAGAAT
 TCTTAGCTCCTGTCTGCACGGTTTACGC

Table 3. cDNA sequence to synthesize *Hoxc8* and *Rprm* riboprobes.

Whole mount in situ hybridization (WMISH)

Samples were fixed in 4% PFA in PBS at 4°C ON. The next day, they were washed in PBS, PBS-Tween (PBT-0.1%Tween in PBS) and dehydrated in increasing concentrations of MetOH until MetOH-100% before their storage at -20°C until needed. Embryos were rehydrated in decreasing concentrations of MetOH, washed in PBT and then bleached with 6% H₂O₂ for 1h. Embryos were rinsed in PBT and digested with proteinase K (PK, 10 µg/ml) in PK buffer (50 mM Tris-HCl pH 7.4, 5 mM EDTA), adjusting the digestion time to the stage of the embryo for mesodermal expressed genes.

To examine ectodermal expressions, 5 min of PK (5 µg/ml) was used. Embryos were washed in PBT and post-fixed in 0.2% glutaraldehyde + 4% PFA before immersion in hybridization buffer (50% formamide, 5x SSC, 2% blocking powder, 0.1% Triton X-100, 0.1% CHAPS, 1 mg/ml tRNA, 50 µg/ml Heparin pH 4.5, 500 mM EDTA pH 8) at 65°C ON.

The following day, the samples were frozen at -20°C for at least 6 hours. After that, the hybridization buffer was replaced with new buffer containing the desired probe and incubated at 65°C ON. The next day, several post-hybridization washes were done to get rid of unspecific binding: three washes of 2x SSC + 0.1% CHAPS (1M NaCl, 100 mM Sodium Citrate, 0.1% Chaps) of 30 min each at 65°C, followed by three washes of 0.2x SSC + 0.1% CHAPS (10 mM NaCl, 1 mM Sodium Citrate, 0.1% Chaps) for 70 min total at 65°C. Then, two washes of KTBT buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 10 mM KCl, 1% Triton X-100) were done for 10 min at RT. Samples were blocked in 20% sheep serum (in KTBT) for 2 h at RT prior incubation with anti-Digoxigenin-Alkaline Phosphatase antibody (anti-dig-AP) diluted (1:2,000) in blocking solution at 4°C ON. After this, several washes were performed with KTBT at RT.

Finally, detection of alkaline phosphatase activity was performed by incubating the embryos in darkness in NTMT buffer (100 mM Tris-HCl pH 9.5, 50 mM MgCl₂, 100 mM NaCl, 1% Triton X-100), with NBT (3 µg/ml) and BCIP (2.3 µg/ml). Once signal level was clear and robust, reaction was stopped with several washes in KTBT and fixed in 4% PFA for analysis.

In situ hybridization in paraffin sections

A similar method to the above described for WMISH was followed in sections. Briefly, after dewaxing and rehydration, the samples were permeabilized by incubation in PK (10 µg/ml) for 7 min 30 sec. Then, samples were fixed in 4% PFA and washed with PBS, followed by an acetylation step (0.1 M triethanol-amine, 0.066 mM Acetic Anhydride) to reduce background. The sections were incubated in hybridization buffer containing the desired antisense ribonucleic acid (RNA) probe, at 65°C ON in a humid chamber.

Next day, post-hybridization washes (at 65 °C) were performed to remove unspecific binding. Slides were washed 30 min in 1x SSC/50% Formamide, 20 min in 2x SSC and two additional 20 min washes in 0.2x SSC. Finally, three washes (5 min, RT) in MABT pH 7.5 (150 mM NaCl, 100 mM Maleic Acid, 0.04% Tween) were performed before incubation with blocking solution (20% sheep serum in MABT) for 1 hour, at RT. After that, sections were incubated ON with the antibody α -DIG-AP (1:2500 in 5% sheep serum/MABT) at 4°C in a humid chamber.

The following day, and after washes in MABT at RT, the signal was revealed with NTM/NBT (3 μ l/ml)/BCIP(2.3 μ l/ml). When the desired signal level was obtained, the slides were rinsed in PBS and fixed in 4% PFA ON at 4°C. Dehydration and mounting in mounted using cytoaseal60 (Richard-Allan Scientific) following routinary procedures.

The probes used in this study were: *Bmp2*, *Cyp26b1*, *Dusp6*, *Spry2*, *Hoxb3*, *Hoxc4*, *Hoxc5*, *Hoxc8*, *Hoxc12*, *Hoxc13*, *Hoxd9*, *Hoxa13*, *Hoxd13*, *Lin28a*, *Lin28b*, *Meis1* and *Rprm*.

Immunohistochemistry

Immunoassays were performed in paraffin sections. Sections were rehydrated following standard procedures. The hydrated sections were incubated with 2% H₂O₂ in Methanol to inhibit endogenous peroxidase. After two washes in dH₂O, the sections were subject to an antigen retrieval process using Citrate buffer 10mM pH=6. After several PBS washes, the sections were incubated in blocking solution (1%BSA, 1% Goat Serum in TBST (1%Tween20 in TBS) at room temperature. Sections were rinsed in PBT (1%Tween20 in PBS) and afterwards, incubated with the desired primary antibody overnight at 4°C. After several PBS washes, sections were incubated with the desired secondary antibody, conjugated with Biotin. After several PBS washes, sections were incubated with VECTASTAIN Elite ABC HRP Kit (Vector Laboratories,) to amplify the detection of the signal, following the manufacturers procedure. The detection of the signal was realized with DAB detection solution (0.06%DAB + 0.005%H₂O₂ + Tris 0.05M pH=7.5). When the desired signal level was obtained, the slides were rinsed in PBS and fixed in 4% PFA ON at 4°C. Dehydration and mounting in mounted using cytoaseal60 (Richard-Allan Scientific) following routine procedures.

Inmunohistochemical analyses on digits of *HoxCKO* mutants, *Hoxc13GFPs* and wild type littermates were performed at least in two different animals for each genotype.

Antibodies:

- anti-Keratin 5 (SIGMA #SAB4501651).
- Anti-Keratin 10 (Biolegend #905401).
- anti-Pan-Cytokeratin (AE13) (Santa Cruz #sc-57012)

RNA-seq

The 150 distal microns of E9.5, E10.5, E11.5 and E12.5 forelimbs were dissected in cold PBS and digested in 0.25% trypsin (HyClone™ Trypsin Protease,) with soft agitation on ice. Then, to inhibit trypsin activity but avoid the serum response, the limb buds were quickly rinsed in 10% FBS and transferred to cold PBS where the separation of the ectoderm from the mesoderm was done with fine forceps (Fig. x).

The dissection of the dissected samples consisted on the 150 distal microns under the AER. It should be noted that the sectioned ectoderm corresponded to the AER, together with the distal most dorsal and the distal most ventral ectoderm.

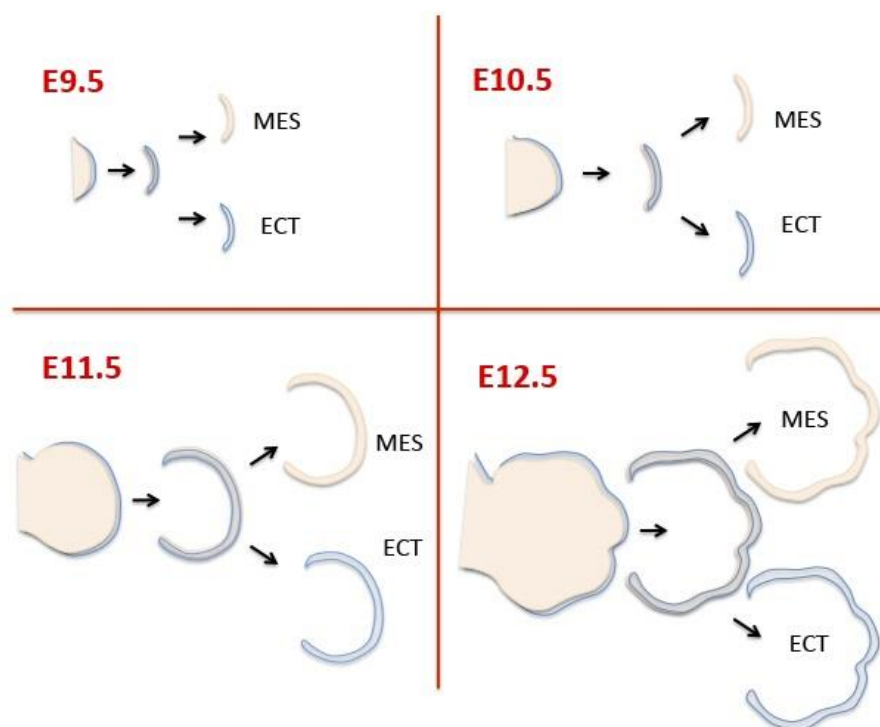


Figure 13. Schematic representation of the procedure followed to separate the distal mesoderm and ectoderm. The 150 distal microns of E9.5, E10.5, E11.5 and E12.5 forelimbs were dissected in cold PBS and digested in 0.25% trypsin on ice. Then transferred to PBS were the ectoderm was completely separated from the mesoderm with fine forceps.

Two biological replicates were prepared from two independent pools of each of the stages analyzed (E9.5, E10.5, E11.5 and E12.5) for both mesoderm and ectoderm. Total RNAs were purified using the RNeasy Mini Kit (QIAGEN) or the RNeasy Plus Mini Kit (QIAGEN). RNA libraries were prepared using the Truseq® Stranded mRNA Library Prep Library Preparation kit and 100-bp paired-end reads were generated.

The gtf from ensembl version 93 was filtered to remove readthrough transcripts and all non-coding transcripts (retained-intron, nonsense-mediated decay, etc...) from a protein-coding gene. In addition, all genes with the same gene name which overlaps were merged under the same gene id to avoid ambiguous reads. Adapters and bad-quality bases were removed with Cutadapt version 1.16 options `-m 15 -a GATCGGAAGAGCACACGTCTGAACTCCAGTCAC -q 30`. Reads were further mapped using STAR version 2.6.0c with ENCODE parameters with the gtf file described above. The counts were used for DESeq2 analyses. FPKM were computed with cufflinks version 2.2.1 omitting mitochondrial genes. For DESeq2 analyses, when there were only 2 conditions to compare, the Wald test was used. For the differential expression analysis, DESeq2 was used with options `test = "LRT", reduced = ~ 1` using only protein coding genes significant (adjusted p-value below 0.05). FPMs were uploaded to <https://genome.ucsc.edu/>.

For Hierarchical Clustering Analysis (HCA) and Principal Component Analysis (PCA) only the 500 genes with the higher variance were considered, using FPKM values. To assess the p-value associated with the number of genes driving Principal Components, a binomial test was performed. The correlation matrix was performed using Euclidean distance with ward clustering.

For heatmaps, $\log_2(\text{FPKM}+1)$ values were centered and scaled. For heatmaps generated to study differentially expressed genes (DEGs) a complete clustering was done using the Pearson correlation coefficient as distance. Six clusters were extracted for the DEGs in the ectoderm samples and seven clusters were extracted for the DEGs in the mesoderm samples. A line chart was performed with the mean of the values on the heatmap for a given cluster for each time point.

For plots showing the expression values of individual genes, red was used to represent FPKM values in the ectoderm and blue in the mesoderm. Squares were used to represent FPKM values in replicate1 and circles to represent FPKM values in replicate2.

For the analyses of stage-specific Transcription Factor (TF) genes, clusters with a peak of expression at E9.5, E10.5 and E11.5 were selected. Venn diagrams were plot with the web-based application in <http://bioinformatics.psb.ugent.be/webtools/Venn/> , using the list of mouse TFs published in Ravasi et al., 2010. Heatmaps with $\log_2(\text{FPKM}+1)$ values were centered and genes were ordered alphabetically.

Gene ontology analyses

Gene ontology analyses were performed with the WEB-based GENE SeT AnaLysis Toolkit (WebGestalt) (<http://www.webgestalt.org/>) (Liao et al., 2019; Zhang et al., 2005).

ATAC-seq

The ATAC-seq protocol is described in Buenrostro et al., 2016. Samples were collected from E14.5 forelimb digits and E14.5 hindlimb digits. The limbs from CD1 mouse embryos were dissected in cold sterile PBS 1X. 8 digits (never digit 1) were collected for each sample and incubated with 0.25% trypsin for 1h and 30 min, with soft agitation on ice. Then, to inhibit trypsin activity but avoid the serum response, the limb buds were quickly rinsed in 10% FBS and transferred to cold PBS where the separation of the ectoderm from the mesoderm was done with fine forceps (Fig. 14). The ectoderms were pipetted up-down 30 times to obtain a single cell suspension. Cells were counted in a Neubauer chamber (Zuzi) to ensure the required 50,000 cells for ATAC-seq. The cells of each sample were centrifuged and washed in cold PBS and afterwards, centrifuged with 50 μl of cold lysis buffer. The supernatant was discarded. The samples were combined with TD reaction buffer, TDE1 (Tn5 Transposase, Nextera) in nuclease-free H_2O . Transposition reactions are incubated at 37°C for 30 min and later purified with MinElute PCR Purification Kit (Qiagen). The purified DNA was stored at -20°C before continuing with the next step.

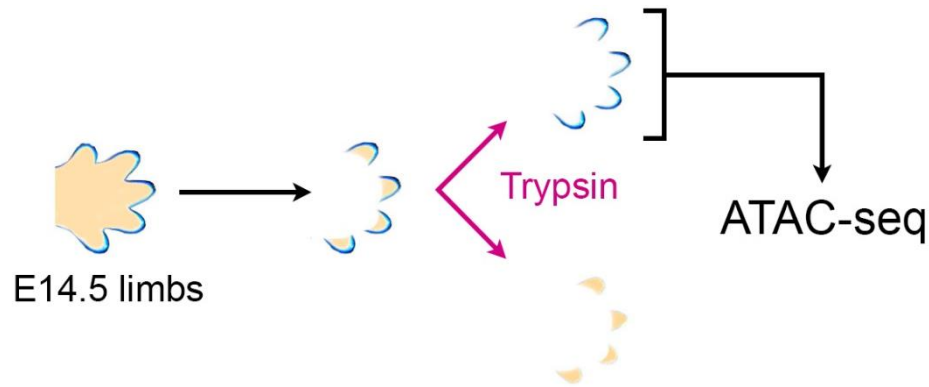


Figure 14. Schematic representation of the procedure followed to separate the digit ectoderms for ATAC-seq. E14.5 digits were dissected in cold PBS and digested in 0.25% trypsin on ice. Then transferred to PBS where the ectoderm was completely separated from the mesoderm with fine forceps. Then digit ectoderm samples were processed for ATAC-seq.

The PCR amplification to produce the ATAC-seq libraries was performed as described in Buenrostro et al., 2016, with primers listed in Buenrostro et al., 2013. The libraries were purified with MinElute PCR Purification Kit. The DNA size from the libraries was checked with gel electrophoresis and fragment analyzer.

ATAC-seq was paired-end sequenced. The generated fastqs were trimmed to 38bp. Mapping was performed with bowtie2 to mm10. Reads which mapped to chrM, or not concordant, or with a mapping quality below 30 were filtered out. Duplicates were removed using picard tool MarkDuplicates and the coverage was evaluated using an in-house tool which makes a coverage of the 5' of the read extended 20 bp each direction after the correction associated with the 9bp duplication of the Tn5.

Aligned reads were uploaded to UCSC genome browser (<https://genome.ucsc.edu/>) or to ECR browser (<https://ecrbrowser.dcode.org/>).

Enhancer functional essays

The activity of *EC1*, *EC2* and *EC1+EC2* was assayed in mouse transgenesis with the *LacZ* reporter gene. We used a vector carrying a β -globin minimal promoter and the *LacZ* coding sequence (pSK- *LacZ*; kindly provided by Denis Duboule lab).

The genomic region containing the regulatory elements of *EC1* (mm10, chromosome15: 120,754,343-102,755,452) and *EC2* (mm10, chromosome15:

102,836,392-102,840,307) were PCR-amplified using specific primers containing specific restriction enzyme target sites for its cloning into the pSK-LacZ vector 5' to the β -globin minimal promoter.

The insert carrying the putative enhancer sequence, β -globin minimal promoter, and LacZ coding sequence was excised from the vector backbone by digestion with ApaI–XbaI. The fragment was gel-purified and injected into the pronucleus of fertilized oocytes. These injected oocytes were transferred to foster CD1 females. Once the embryos reached the desired stage, foster females were euthanized and the embryos collected.

LacZ/ β -Gal staining

The embryos were dissected in cold PBS and yolk sac samples were collected for genotyping. Embryos were fixed 20 min at RT in Fix Solution (1x PBS pH=6.8, 2mM MgCl₂, 4% PFA, 0.2% Glutaraldehyde, 5mM EDTA). After rinsing in Wash solution (1x PBS pH=6.8, 2mM MgCl₂, 0.2% NP40, 0.01% sodium deoxycolate (DOC)), the embryos were washed 5x20min in Wash Solution. LacZ signal was revealed with staining solution (5mM K₃[Fe(CN)₆]^{*1}, 5mM K₄[Fe(CN)₆]^{*2}), 0.5 mg/mL X-gal/DMF) at 37°C ON. After staining samples were washed once in wash solution and fixed again in 4% PFA/PBS at 4°C ON. After this fixation, samples can be stored at 4°C in PBS for months, for longer periods, samples can be stored in Glycerol after standard dehydration and glycerol series.

To analyze the precise localization of lacZ signal in the limbs, stained limbs were processed for paraffin embed, sectioned and lightly stained in Eosin.

CRISPR-Cas9

The gRNAs used to generate *delEC1*, *delEC2*, *del(EC1-EC2)* and *inv(EC1-EC2)* mutant lines were generated with CHOPCHOP (<https://chopchop.cbu.uib.no/>) and the target regions used were chr15: 102754000-102754290 for the gRNA 5' to *EC1*, chr15:102755480-102755750 for the gRNA 3' to *EC1*, chr15: 102836000-102836365 for the gRNA 5' to *EC2* and chr15:102840330-102840600 for the gRNA 3' to *EC2*.

The CRISPR-Cas9 methodology used to generate *EC1* and *EC2* mouse lines was adapted from (Qin et al., 2015): The px330 plasmid carrying the wild-type (WT) Cas9 (Cong et al., 2013) was used as the DNA template for amplification of the Cas9 coding sequence in a polymerase chain reaction (PCR). The T7 promoter sequence was added to the forward primer and reverse primer from the coding sequence of the Cas9 gene. PCR product was amplified using the AccuPrime PCR system (Life Technologies) and purified using the QIAquick PCR purification kit (Qiagen) and in vitro transcription (IVT) performed using the mMESSAGE mMACHINE T7 ULTRA Transcription kit (Life Technologies). For sgRNA synthesis, the T7 promoter sequence was added to sgRNA template/forward primer and the IVT template generated by PCR amplification. The T7-sgRNA PCR product was purified and used as the template for IVT using MEGashortscript T7kit (Life Technologies). Both the Cas9 mRNA and the sgRNAs were purified using the MEGAclean kit (Life Technologies). Aliquots from an IVT reaction were separated on agarose gel to assess quality from a reaction. Single-stranded oligos were ordered as PAGE Ultramer from Integrated DNA Technologies.

B6CBAF1/J Fertilized eggs were collected from the oviducts of E0.5 pregnant females. The collected eggs cultured in WM medium were washed with Opti-MEM I three times to remove the serum-containing medium. The eggs were then placed in line in the electrode gap filled with Opti-MEM I solution containing Cas9 mRNA and sgRNA and electroporated. Electroporated eggs were cultured to blastocyst stage in mWM medium and transferred to pseudopregnant foster mice (for more information consult Hashimoto and Takemoto, 2015 and Qin et al., 2015).

The *del(EC1-EC2)* and *inv(EC1-EC2)* mouse lines were generated with the Alt-R® CRISPR-Cas9 System from IDT (<https://eu.idtdna.com/pages/products/crispr-genome-editing/alt-r-crispr-cas9-system>). The crRNA and tracrRNA of interest were resuspended in Nuclease-Free Duplex Buffer and mixed to form the crRNA:tracrRNA duplex. The crRNA:tracrRNA duplex was combined with the Alt-R Cas9 Nuclease 3NLS (IDT) in Opti-MEM medium to form the ribonucleoprotein (RNP) complex.

The collection of fertilized eggs and the electroporation to generate *del(EC1-EC2)* and *inv(EC1-EC2)* mouse lines were very similar to the already described for *EC1* and *EC2* mouse lines. Two steps were carried out differently: C57BL6 eggs were cultured in KSOM (Potassium-supplemented simplex optimised medium) + mineral sterile oil and

the electroporated eggs were incubated 8-9h and the eggs that reached the 2-cell stage are transferred to pseudopregnant foster mice.



RESULTS

RESULTS

Temporal transcriptome analysis of the developing limb components

To identify gene expression differences that could be involved in the acquisition of progressive proximo-distal fates, we generated the transcriptomes of the distal forelimb progenitors and of the overlying ectoderm at four sequential developmental stages in mouse embryos. Due to the progressive proximo-distal development of the limb bud, our analysis was restricted to the distal 150 microns, an approximation of the progress zone (Summerbell et al., 1973). Thus, the distal 150 microns band of the limb bud was dissected and then the mesoderm and the ectoderm components separated by mild trypsin digestion and processed separately (see Materials & Methods). It should be noted that the dissected ectoderm stripe included the AER and also the distal most dorsal and most ventral ectoderm (Fig. 13). Two biological replicates were collected per stage and each pair of ectoderm and mesoderm replicates was obtained from the same batch of embryos.

The stages selected for our study were E9.5, E10.5, E11.5 and E12.5. The E9.5 stage captures the early initiation of the limb bud. It corresponds to the stage when the AER is forming but has not yet acquired its mature morphology and position. According to cell lineage experiments in equivalent stages in chick, the E9.5 distal mesoderm is specified to form the zeugopod (Saiz-Lopez et al., 2015). In the E10.5 limb bud, the AER has adopted a mature morphology and the mesoderm, equivalent to stages HH22-23 in chick, is specified to the autopod. To incorporate further temporal information, we also included stages E11.5 and E12.5. By E11.5 the digit condensations form and by E12.5 they are clearly discernible. During E12.5 the regression of the AER has already begun over the interdigital areas, remaining only at the tips of the digits.

From each of the 16 samples, total RNA was extracted and purified using Qiagen RNeasy Mini Kit (Qiagen) and paired-end reads libraries were generated. The read length was set to 100bp in the sequencing platform. The RNA sequencing (RNA-seq) from polyadenylated transcripts yielded at least 12 million reads per sample. Nearly 86% of the reads mapped to unique loci. About 11,000 ensemble ids (hereafter referred as genes) per sample are expressed (FPKM above 1). Of the 53,837 genes present in the gtf file 13,651 (25%) were expressed in at least one of our samples. Of the 21,773 annotated protein coding genes, 12,572 (58%) are expressed in at least one of our samples.

Despite the utmost care in dissection, a few mesoderm cells occasionally remained attached to the ectoderm potentially contaminating the ectodermal samples. Thus, to evaluate the purity in our mesoderm and ectoderm samples, we analyzed the expression of genes with described domains of expression restricted to the ectoderm or mesoderm respectively, in many experimental studies. *Fgf8*, *Sp6*, *Sp8*, *Trp63*, *Perp*, *Krt14*, and *Wnt7a* were selected as ectoderm specific genes while *Prrx1*, *Tbx5*, *Hoxa9*, *Hoxd10*, *Fgf10*, *Pecam1* and *Cdh5* were selected as mesoderm specific genes. The heatmap showed that the separation of the ectoderm and the mesoderm was clean with a level of contamination between both limb components that was negligible (Fig. 15A), except in one of the E11.5 ectoderm samples that showed slight contamination with mesodermal cells.

To visually evaluate the proximity between samples we performed a principal component analysis (PCA), a linear multivariate dimension reduction technique that captures the major differences in gene expression between samples. Only the 500 genes with the higher variance were considered in the analysis, using FPKM (Fragments Per Kilobase of transcript per Million mapped reads) values. When samples were plotted along the first 2 components and in 2 dimensions, the PCA showed that replicate samples grouped together (Fig. 15B). The first dimension strongly separated the ectoderm and mesoderm samples (77% of the variance) and can be explained by the tissue factor, whereas the second dimension (12% of the variance) separated the samples according to the stage. It can also be observed that changes between E9.5 and E10.5 were as big as the changes between E10.5 and E12.5 and that the mesoderm and ectoderm samples showed parallel trajectories in the second axis.

Hierarchical cluster analysis (HCA) of the 16 samples showed a strong signal of sample clustering by tissue. The Euclidean distance between samples (Fig. 15C) revealed a positive and good correlation between replicates and between progressive stages clearly separating by tissue. It is worth mentioning, that both PCA and HCA exposed marked differences between the E9.5 samples and the rest of the samples, both in the mesoderm and the ectoderm, pointing to an important gene expression transition from E9.5 to E10.5 in distal limb bud cells.

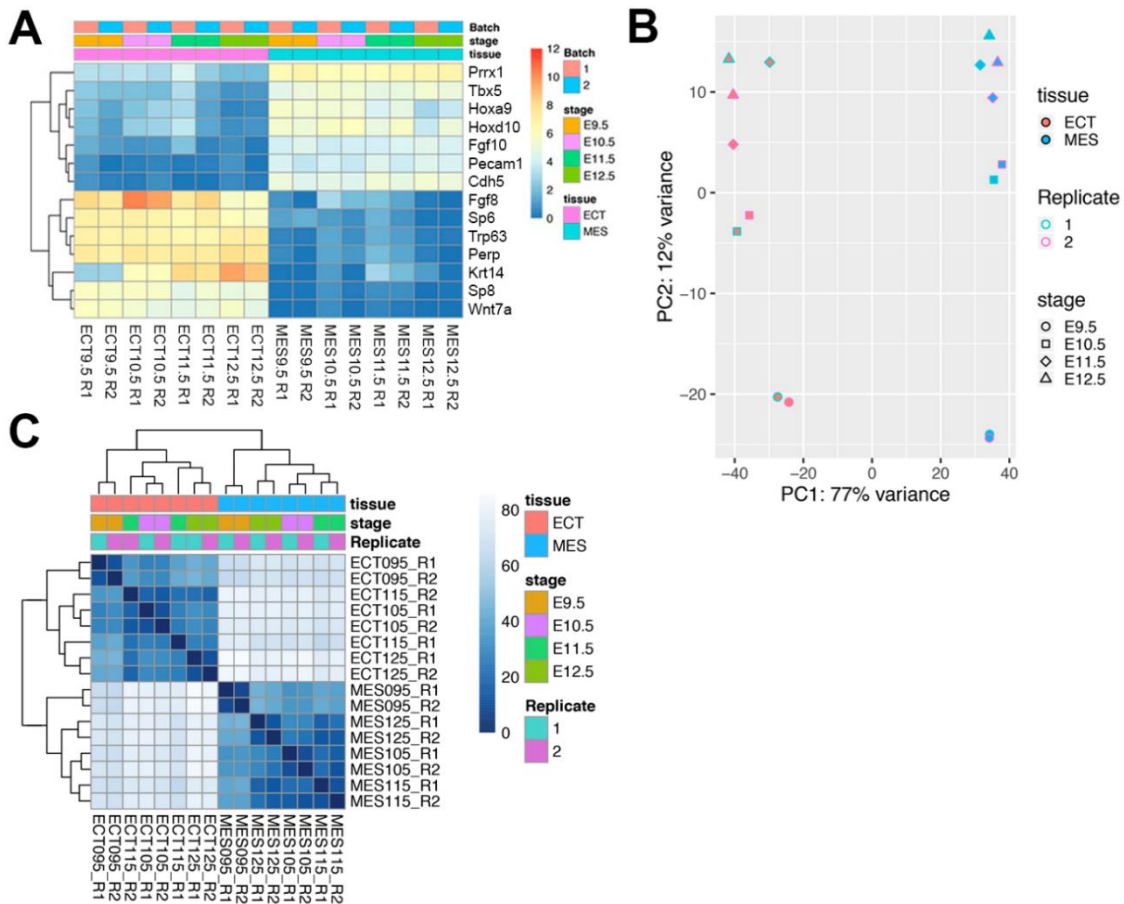


Figure 15. Preliminary analysis of the temporal transcriptome of the limb progenitors. A: Heatmap with log₂(1+FPKM) values for selected mesodermal (top cluster) and ectodermal (bottom cluster) specific expressed genes, in all samples. **B:** Principal component analysis (PCA) plot of the top500 most variable genes, using FPKM values. PC1 separates the tissues and PC2 separates the stages, these components explain 77% and 12% of the variance, respectively. **C:** Correlation matrix of the top-500 most variable genes including all experimental data, performed with Euclidean distance and hierarchical ward clustering, shows a strong signal of sample clustering by tissue.

When the top100 genes driving PC1 were considered, it could be appreciated that most genes were typical ectodermal expressed genes, such as Keratins or cadherins (Fig. 16A). We performed Gene Ontology (GO) analyses of top100 PC1 driving genes with Webgestalt (<http://www.webgestalt.org/>) that confirmed our observation, as the preferentially enriched terms were related with cell signature of ectodermal and epithelial tissues (Fig. 16C). Some of the top100 PC1 genes that were highly expressed in the mesoderm samples coded for hemoglobin chains (Fig. 16A). In this regard, it is worth mentioning that the marginal sinus runs parallel to the AER about 150 microns deep into the mesoderm and, therefore, it is likely that some blood cells are included in the mesoderm samples.

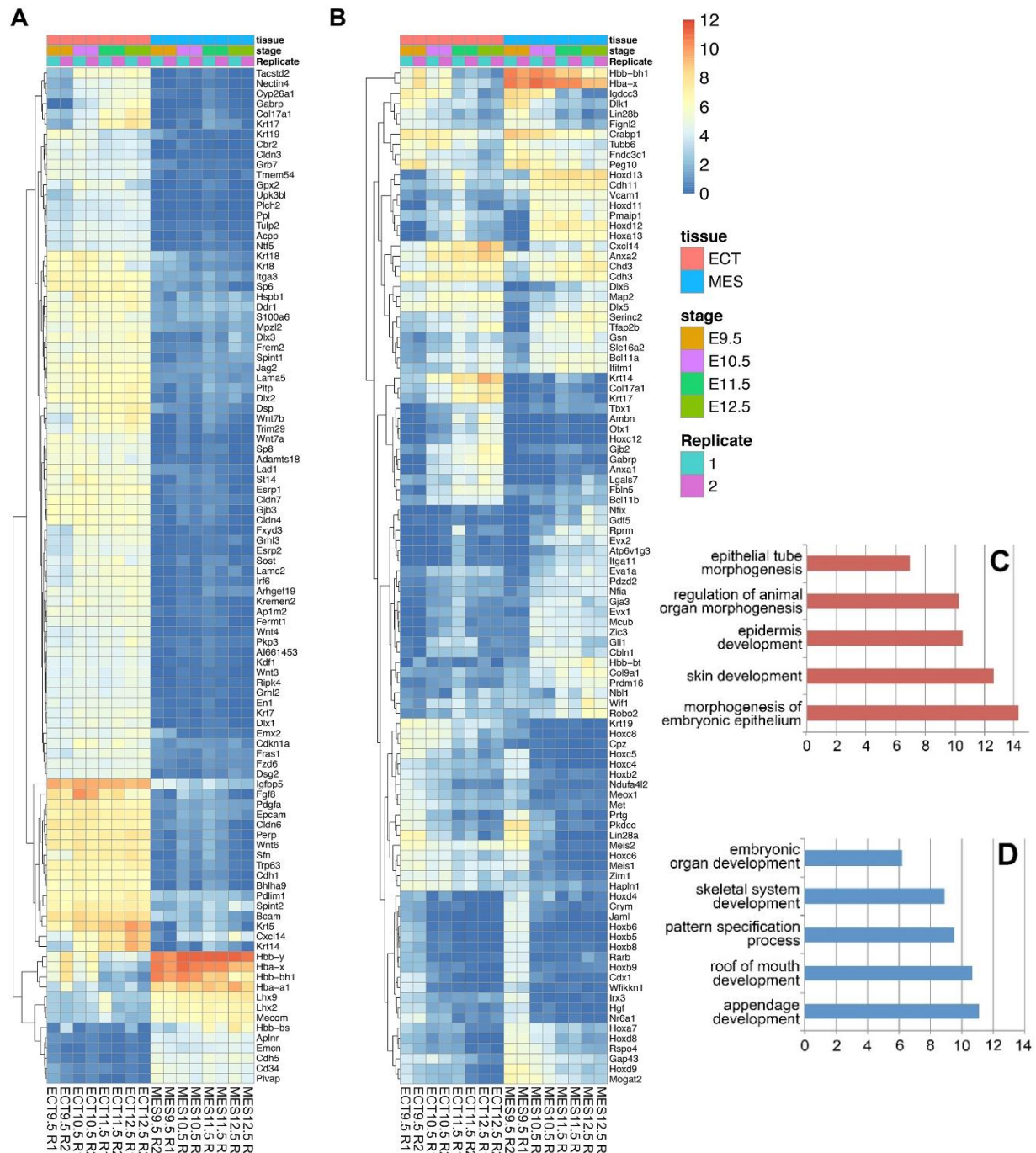


Figure 16. Analysis of the top100 PC1 and the top 100 PC2 driving genes. Heatmaps showing the $\log_2(1+\text{FPKM})$ values of the top100 PC1 (A) and top100 PC2 (B) driving genes. Note that the majority of top100 PC1 are expressed in the ectoderm samples and poorly expressed in the mesoderm samples. Enrichment ratio of selected GO categories from top100 PC1 (C) and top100 PC2 (D) driving genes. Five out of the top10 categories are shown in the plots. Note that, as expected, salient categories in C are mostly related to the development of the epidermis, while salient categories in D associate with limb development.

When the top100 genes driving PC2 were considered, we appreciated different developmental-associated genes, many of them with described roles in limb development (Fig. 16B). When we drive Webgestalt on top100 PC2 genes we retrieved several categories that can be associated with limb development (Fig. 16D).

Therefore, we have generated a valuable set of transcriptomic data that could be used to improve our understanding of the developing limb. Our temporal transcriptomic data makes possible to visualize the dynamics of key factors influencing gene expression changes in the limb progenitors and their overlying ectoderm. In fact, our data provides a collection of gene expression signatures that could be used to evaluate the ectodermal or mesodermal origin of a given sample of limb cells.

Differential gene expression analyses across stages during aging of the limb progenitor cells

To identify gene expression differences that could be involved in the acquisition of progressive proximo-distal fates, we extracted the differentially expressed genes (DEGs) across stages. First, we focused on the mesoderm samples, seeking for the identification of the gene expression dynamics responsible for the progressive restriction of their morphogenetic capacity.

We performed a likelihood ratio test (LRT) considering any gene with an adjusted p-value below 0.05 as a differentially expressed gene. We extracted 3,858 differentially expressed genes in the mesoderm samples (MES-DEGs). To characterize the dynamics of the expression changes, we performed a hierarchical clustering heatmap that revealed distinct temporal patterns of gene expression. Next, we grouped the MES-DEGs in 7 clusters, according to their temporal expression profile (Fig. 17).

The 7 clusters yielded by this approach were termed Mes1 to Mes7. The number of genes in each cluster ranged from 92 to 1135. Cluster Mes1 contained 431 genes, Mes2 contained 172 genes, Mes3 contained 1027 genes, Mes4 contained 1135 genes, Mes5 contained 882 genes, Mes6 contained 119 genes and Mes7 contained 92 genes (Fig. 17). Because of the specific profile of Mes1, Mes3, Mes4 and Mes5, we first focused our attention in these clusters.

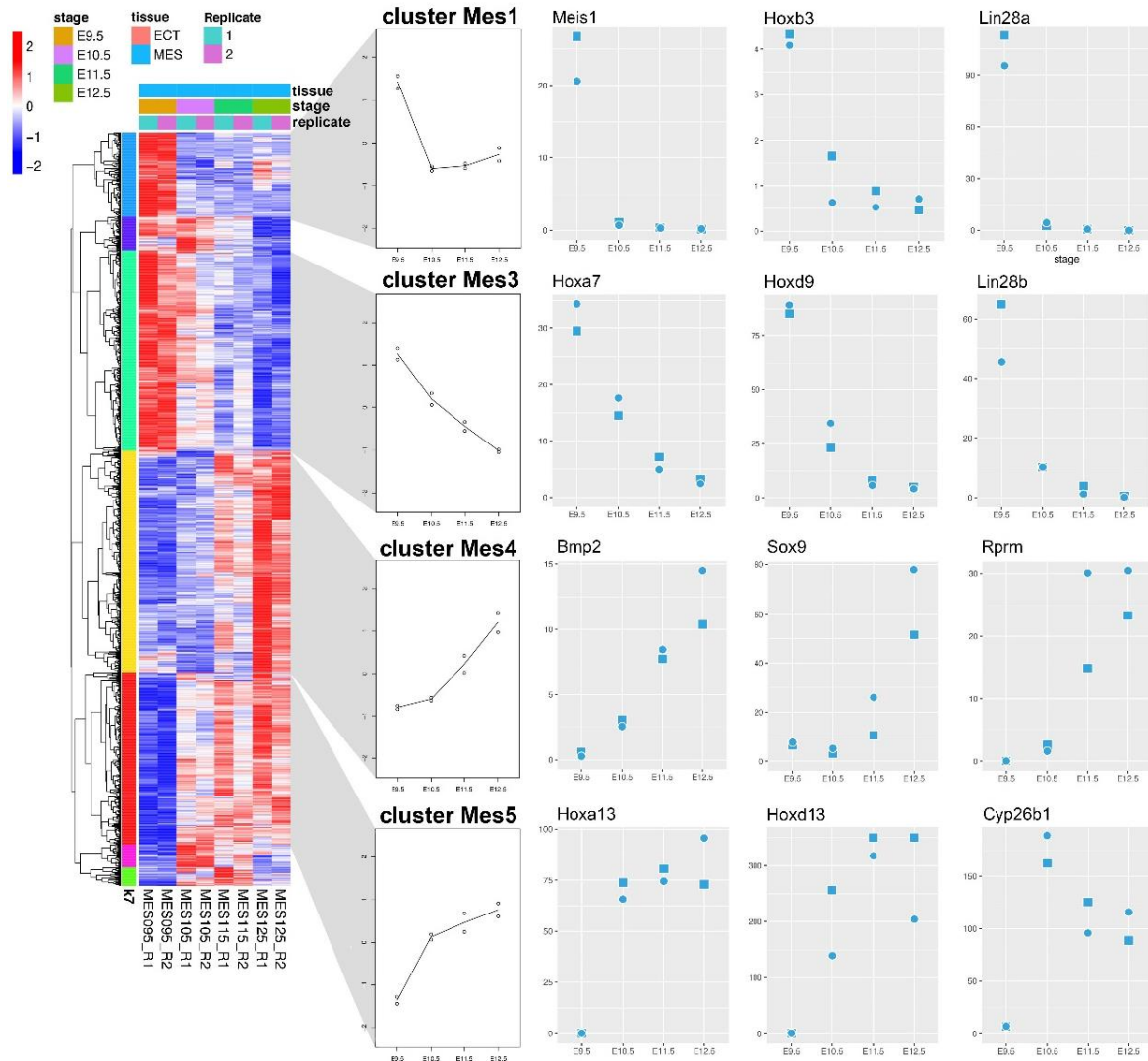


Figure 17. Temporal expression dynamics of MES-DEGs. Hierarchical clustering (Pearson correlation coefficient) with heatmap (scaled and centered) of the expression profile of MES-DEGs in $\log_2(1+\text{FPKM})$. According to the temporal dynamics of expression, seven clusters were extracted (colored on the left) and named by their order of appearance from the top to the bottom of the heatmap. Four clusters were initially selected by their specific temporal expression profile. A line chart with the mean values of the genes contained in each cluster is depicted. The expression profile, in FPKM values, of remarkable genes contained in each cluster, is depicted next to the line chart of the corresponding cluster.

Clusters Mes1 and Mes3 were characterized by genes downregulated with aging, though genes in cluster Mes1 were strongly repressed between E9.5 and E10.5 and poorly expressed in the next analyzed stages and genes in cluster Mes3 were steadily downregulated over time (top clusters in Fig. 17 and Fig. 18). In these two clusters, we found genes with described expression patterns that fit well with our data, such as *Meis1*, *Hoxb3*, *Hoxa7* and *Hoxd9* (Fig. 18).

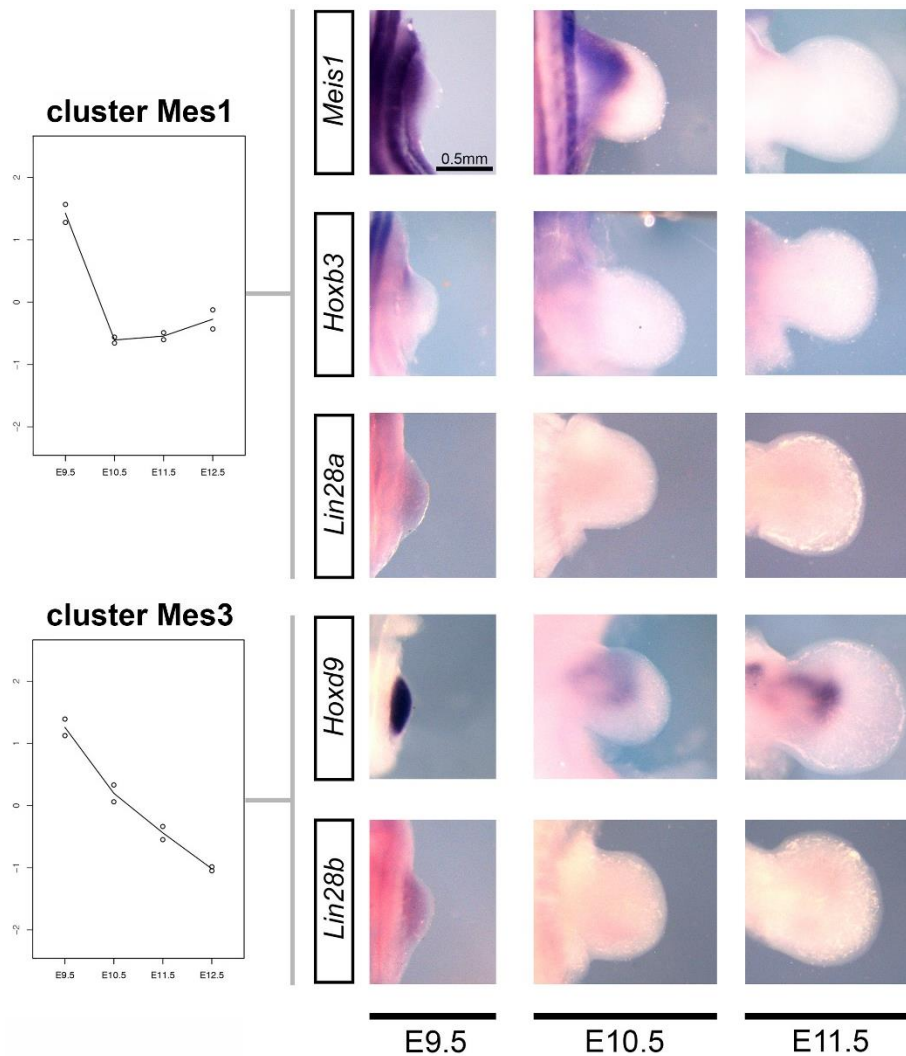


Figure 18. WMISH of temporally downregulated genes. WMISH showing the expression pattern in FL buds at E9.5, E10.5 and E11.5 of selected relevant genes (as indicated) from clusters Mes1 and Mes3. A line chart showing the mean expression values of the genes in the cluster is shown on the left. Each dot corresponds to one replicate. Genes in cluster Mes1 experience an initial abrupt downregulation and remain poorly expressed onwards. The three representative genes in cluster Mes1 are detected in E9.5 FL buds but strongly downregulated to background levels in the next studied developmental stages. Genes in cluster Mes3 are steadily downregulated over time but they show similar WMISH patterns to genes in cluster Mes1 indicating that RNA-seq is more sensitive than WMISH. All pictures are dorsal views of limb buds of the indicated stage. Anterior is at the top and distal is to the right.

Interestingly, *Lin28a* and *Lin28b* genes were also contained in Mes1 and Mes3 cluster respectively (Fig. 17). LIN-28 family proteins are RNA-binding proteins that function as posttranscriptional regulators involved in developmental timing and self-renewal in embryonic stem cells (Tsialikas and Romer-Seibert, 2015). Both *Lin28a* and *Lin28b* were expressed in E9.5 limb buds but downregulated afterwards. This expression profile had been previously described for *Lin28a* (Yokoyama et al., 2008). The difference

between *Lin28a* and *Lin28b* is that the downregulation of the latter is less abrupt than that of the former. However, this difference was not detectable by WMISH as the expression of both *Lin28* genes became undetectable from E10.5 onwards. It is worth mentioning that a recent work has linked *Lin28* genes with promoting axial progenitor expansion in the tail bud until the activation of *Hox13* genes overrides this activity (Aires et al., 2019).

Clusters Mes4 and Mes5 are characterized by genes upregulated as limb development progresses. Though the genes in cluster Mes4 are steadily upregulated over time and genes in cluster Mes5 are suddenly upregulated in the transition from E9.5 to E10.5 and steadily upregulated in the next stages (Fig. 17, bottom clusters and Fig. 19). Well-known limb developmental genes in these clusters are *Bmp2*, *Sox9*, *Hoxa13*, *Hoxd13* and *Cyp26b1*. Noteworthy, it can be observed how the onset of expression of autopod-associated *Hoxa13* and *Hoxd13* genes occurs at E10.5 in the posterior-distal limb mesoderm (Fig. 19).

The expression dynamics of *Hoxa13*, *Hoxd13* and *Lin28* genes during limb development are reminiscent of the expression of *Hoxb13*, *Hoxc13* and *Lin28* genes during tail bud expansion (Aires et al., 2019). In the tail bud the activation of *Hox13* paralogs results in repression of *Lin28* genes ending axial extension. It is tempting to speculate that a similar process occurs during limb development and therefore, the activation of *Hox13* genes could be key to silence pluripotency genes during the differentiation of the distal limb mesoderm. However, the observation that the pattern of downregulation of *Lin28* genes (Fig. 18) is not complementary to that of the activation of *Hoxa13* or *Hoxd13* genes, which is restricted to the distal-posterior border of E10.5 FL buds (Fig. 19), does not support a direct cross-regulation. Therefore, the situation in the limb bud is likely different and an alternative possibility is that *Lin28* pluripotency genes have to be silenced to facilitate the activation of *Hoxa13* and *Hoxd13* in the limb bud.

Interestingly, *Reprimo* (*Rprm*) was also found in cluster Mes4 (Fig.17, bottom clusters and Fig.19). *Rprm* is a tumor-suppressor gene implicated in p53-mediated cell cycle arrest (Ohki et al., 2000; Wichmann et al., 2016). During limb development there is a progressive deceleration of proliferation rate with stage-specific cell cycle parameters (Saiz-Lopez et al., 2015). *Rprm* transcripts were detected by WMISH at E11.5 in the distal limb mesoderm, but not in the previous analyzed stages. The coincidence of *Rprm* and *Bmp2* in the same cluster allows the speculation that there is a connection between *Bmp2*

and *Rprm*, as recent work point to an intrinsic activation of BMP signaling to terminate limb bud outgrowth (Pickering et al., 2018).

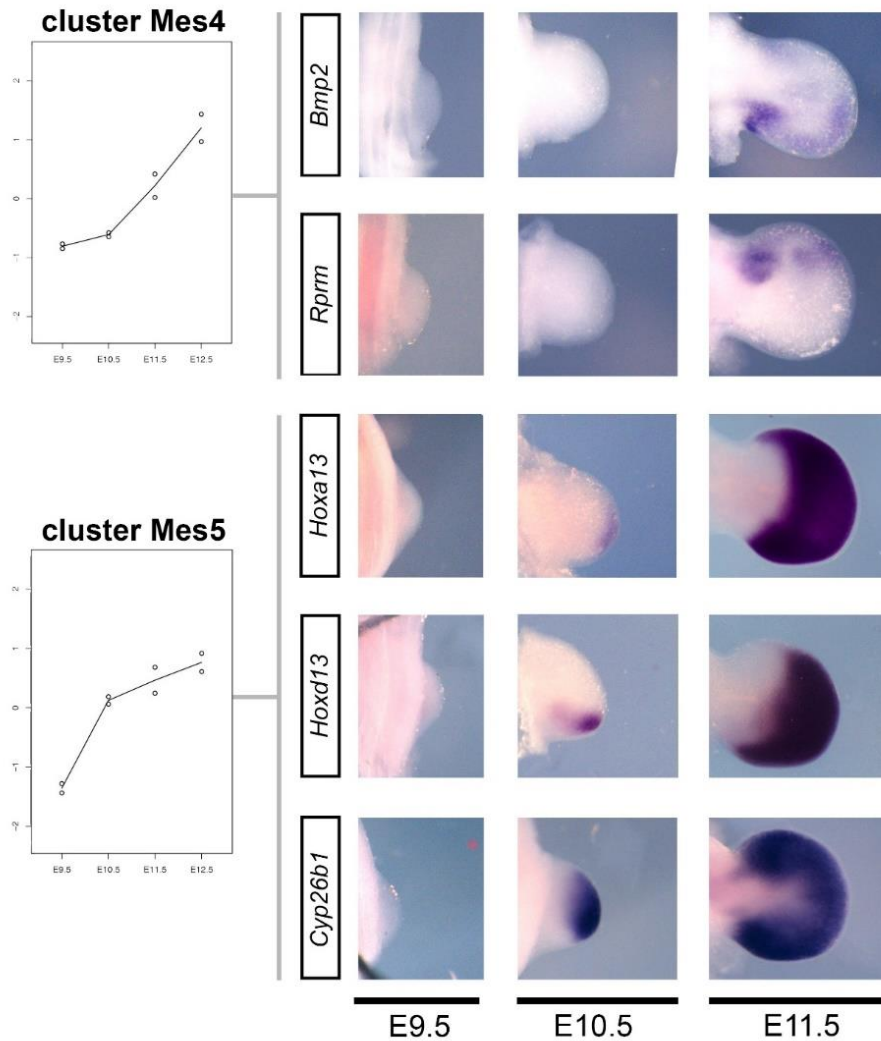


Figure 19. WMISH of temporally upregulated genes. WMISH showing the expression pattern in FL buds at E9.5, E10.5 and E11.5 of selected relevant genes (names indicated on the left) from clusters Mes4 and Mes5. A line chart showing the mean expression values of the genes in the cluster is shown on the left. Each dot corresponds to one replicate. Genes in cluster Mes4 are steadily upregulated over time while genes in cluster Mes5 are abruptly upregulated in the transition from E9.5 to E10.5 and steadily upregulated in the next stages. Note that disregarding the temporal expression profile differences detected in the RNAseq, no signal by WMISH of the selected genes is detected at E9.5 in the distal mesoderm. Orientation is as Fig. 18.

In summary, our WMISH experiments and previous publications validate our RNAseq data. Moreover, we have identified interesting expression dynamics for *Lin28b* that together with *Lin28a*, *Hoxa13* and *Hoxd13* dynamic expression patterns, could guide a path into the discovery of a relationship between *Hox13* and *Lin28* genes, in the limb

bud. We have also identified the expression pattern of *Rprm* in the limb bud, a gene with no previously identified function in the development of the limb.

Stage-specific transcription factor genes of the distal limb mesoderm

During the differential gene expression analyses of the limb progenitors and also in our preliminary analyses of the distal limb bud transcriptome, we have observed a notable gene expression transition from E9.5 to E10.5 (Fig. 15B, C; Fig. 17). We checked the number of differentially expressed genes between successive stages and observed that the amount of DEGs was larger in the E9.5vsE10.5 comparison than in the E10.5vsE11.5 or E11.5vsE12.5 comparisons, both in the ectoderm and the mesoderm samples (Fig. 20A).

Taking into consideration the current model of PD limb development (Saiz-Lopez et al., 2015), we considered that the gene expression transition occurring from E9.5 to E10.5 might be reflecting the transcriptional switch from a proximal limb specification program, regulated by extrinsic signals coming from the trunk, to an intrinsic distal limb specification program. Strongly supporting this view is the observation that both downregulation of proximal markers (*Hoxd9* and *Meis1*) and onset of distal markers (*Hoxa13* and *Hoxd13*) occurs in E10.5 distal limb progenitors (Fig. 20).

Next, we asked whether each stage of limb development had distinct transcription factor (TF) expression profiles, as TF are the best candidates to regulate cell-identity and therefore cell fate. To address this question, we extracted the set of TF genes from our list of MES-DEGs.

We concentrated on clusters Mes1, Mes6 and Mes7 as their expression profile matched best with genes with an expression peak at E9.5, E10.5 and E11.5 respectively, in limb progenitor cells (Fig. 20B, C) and that could therefore be considered as stage specific. From the 431 genes contained in cluster Mes1, 74 were included in the list of mouse TF described in Ravasi et al., 2010., from the 119 genes contained in cluster Mes6, 12 were included in this list (Fig. 20E, F) and from the 92 genes contained in cluster Mes7, 11 were included in this list (Fig. 20D, G). We selected a set of TF genes that fitted with the profile expected for each cluster and plotted heatmaps with the $\log_2(1+\text{FPKM})$ values for these genes (Fig. 20H, I).

Many of the transcription factor genes plotted in Figure 20H, can be associated to the development of the stylopod. In this analysis we found members of the TALE protein family including *Iroquois homeobox (Irx)* genes *Irx3* and *Irx5* and *Pre-B-Cell Leukemia (Pbx)* genes *Pbx1* and *Pbx3* (Bürglin, 1997; Gómez-Skarmeta and Modolell, 2002). The function of these genes has been previously explored in the limb with the combined deletion of *Irx3* and *Irx5* that results in defective limbs, in which the stylopod is mostly affected (Li et al., 2014). Reducing the genetic dose of *Pbx* in the developing limb affects first the most proximal structures, with further reduction in the *Pbx* gene dose resulting in more dramatic phenotypes finally leading to amelia in *Pbx1;Pbx2* compound mutants (Capellini, 2006). In fact, *Pbx1* has been described to genetically interact with two other genes included in cluster Mes1, *Alx1* and *Emx2*, to specify the most proximal limb parts (Capellini et al., 2010). Moreover, the best described markers for the stylopod, *Meis1* and *Meis2* genes (Capdevila et al., 1999; Mercader et al., 2000) were also found in the analysis of transcription factors of cluster Mes1. Notably, our analysis also evidenced the influence of RA coming from the trunk and reaching the distal tip at this stage. TF genes that are activated by RA signaling, *Caudal Type Homeobox 1 (Cdx1)*, *Retinoic Acid Receptor β (Rar β)* and *Nuclear Receptor Subfamily 2 Group F Member 2 (Nr2f2)* (Cunningham and Duester, 2015; Kruse et al., 2008) were also expressed at E9.5, strongly downregulated at E10.5 and poorly expressed at later stages. Of note, the conditional mutation in the developing limb bud of *Nr2f2* led to shorter limbs (Lee et al., 2004). Conjointly, these data support the notion that the E9.5 distal limb progenitors are specified to form the stylopod.

Although *Hoxa9* and *Hoxd9* are associated to development of the stylopod (Fromental-ramain et al., 1996a), they didn't appear in cluster Mes1. This was explained by the temporal profile of these genes, that are still expressed at a low level in E10.5 distal limb mesenchyme (Fig. 3, 4). Instead, we found several 3' *Hox* genes from clusters *HoxA*, *HoxC* and *HoxD* and *Hoxb2-9* genes contained in cluster Mes1. Paralogous *Hox4* and *Hox5* have been reported to be expressed at the time of limb field specification (Minguillon et al., 2012) and many of the *Hox* genes in Fig. 20H are expressed in a proximal region of the limb bud from E10.5 onwards (Burke et al., 1995; Nelson et al., 1996). It could be the case that the 3'*Hox* and *Hoxb2-9* genes in cluster Mes1 are expressed in the early limb bud to act conjointly with *Hoxa9* and *Hoxd9* in the development of the stylopod. In fact, this would explain the mild phenotype of humerus

reduction observed in *Hoxa9;Hoxd9 DKO* mutants, as more members of the *Hox* cluster would be acting in a redundant manner to develop the proximal limb segment. Also, paralogs 9 are required in the forelimb for the induction of the ZPA through the induction of *Hand2* (Xu and Wellik, 2011) indicating that at this time the program to set up *Shh* expression is already initiated.

Some of the TF genes that we extracted with the analysis of cluster Mes6 could be easily associated to the specification of distal limb parts and with the role of 5' *Hoxa,d* genes in limb development (Fig. 20I). *Spalt Like Transcription Factor 1 (Sall1)* has been described to modulate the activity of *Hox* genes in the development of the autopod (Kawakami et al., 2009). *Lmo2 (LIM Domain Only 2)*, and also *Lmo4*, are expressed in the distal limb mesoderm, under the AER (Kenny et al., 1998) and it has been suggested that the activation of these genes in the limb could rely on *Hox* genes (Calero-Nieto et al., 2013). No limb phenotype has been reported in *Lmo2* mutants (Warren et al., 1994), though this could be explained by redundancy with *Lmo4*. Interestingly we also found *Ankyrin Repeat Domain-Containing Protein 6 (Ankrd6)* and *KN Motif And Ankyrin Repeat Domains (Kank2, formerly Ankrd25)* with expression levels peaking at E10.5. It should be mentioned that proteins with Ankyrin domains are considered to play a role in cell adhesion (Bennett and Healy, 2009). This is interesting as *Hoxa13* has been described to activate the expression of adhesion molecules (Stadler et al., 2001). We consulted the Embryonic Gene Expression Database for Biomedical Research Source (EMBRY) database of (<https://www.embrys.jp/embrys/html/MainMenu.html>) WMISH experiments and found that both of these genes are expressed in the distal limb mesoderm under at E10.5 and E11.5 (Yokoyama et al., 2009). Therefore, *Ankrd25* and *Kank2* are two good candidates to study during the intrinsic specification process of the limb segments (Saiz-Lopez et al., 2015).

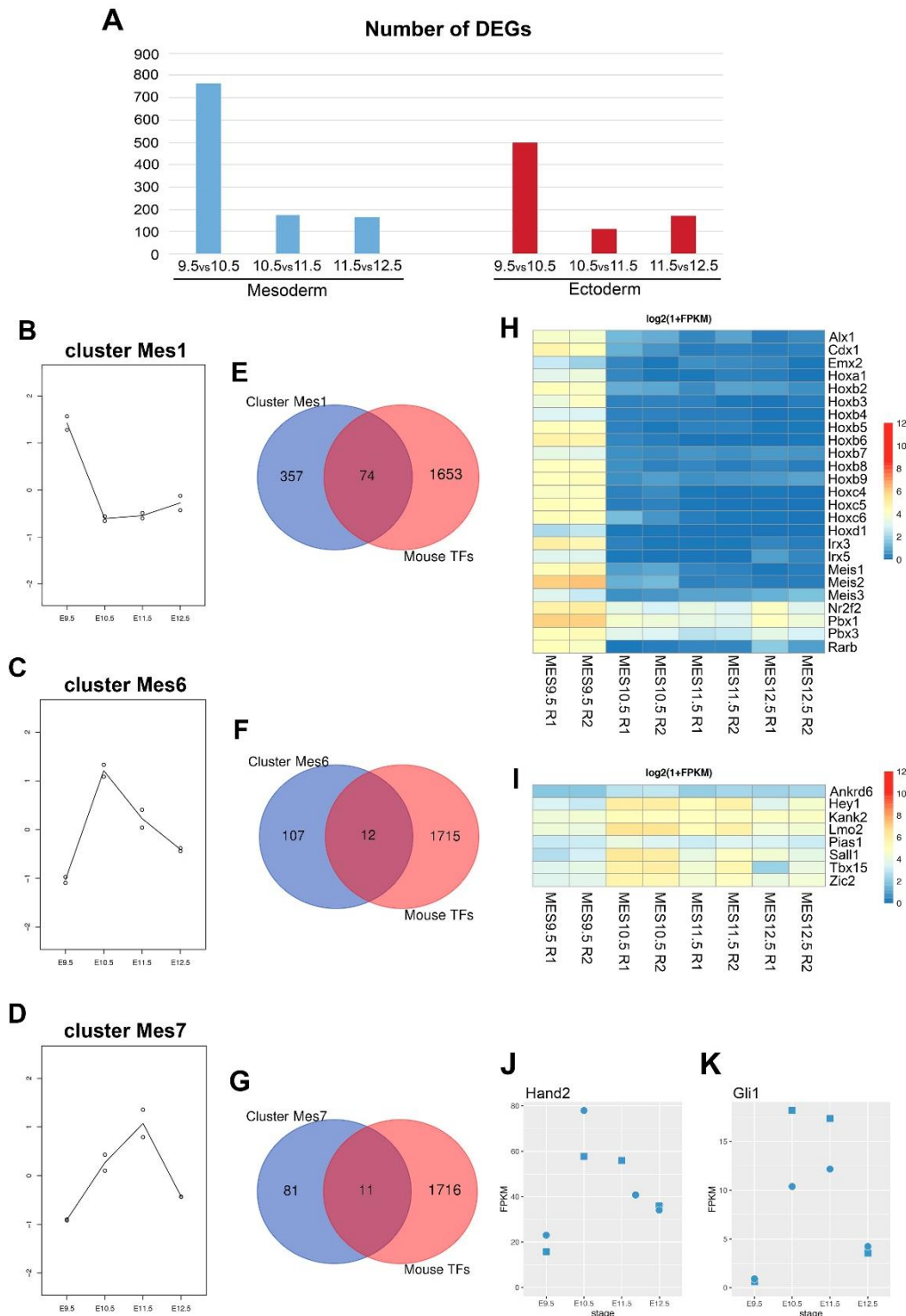


Figure 20. Analyses of stage-specific transcription factors in the limb progenitors. **A:** number of DEGs in the different contrasts. Note that the number of DEGs between E9.5 and E10.5 is larger than in the other successive-stage comparisons, both in the ectoderm and the mesoderm. **B, C, D:** line charts showing the temporal profile (mean values) of the genes contained in clusters Mes1, Mes6 and Mes7. **E, F, G:** Venn diagrams showing the number of TFs contained in each of the clusters depicted. **H, I:** Heatmap plots with $\log_2(1+FPKM)$ values showing selected transcription factor genes from clusters Mes1 and Mes6 according to minimal expression levels and low disparity between replicates. Most genes in **H** can be associated to the development of the stylopod and most genes in **I** can be associated to development of the distal limb. **J, K** show the temporal expression profiles in FPKM of *Hand2* and *Gli1*. Note that although they are included in cluster Mes7, their temporal profile does not precisely correspond to a peak at E11.5.

We also found *Hes Related Family BHLH Transcription Factor With YRPW Motif 1 (Hey1)*, *Protein Inhibitor Of Activated STAT 1(Pias1)*, *T-box15 (Tbx15)* and *Zinc Finger Protein Of The Cerebellum 2 (Zic2)* having a peak of expression at E10.5 in our data (Fig. 20I). *Hey1* is a notch effector expressed in the limb bud (Nakagawa et al., 1999). It has been reported to associate with myogenic target genes to repress myogenesis of skeletal muscle (Buas et al., 2010), therefore it is likely that it is acting in the limb to modulate the development of muscle fibers, although this would require additional investigation as myoblast are not supposed to reach the 150 distal microns at E10.5. *Pias1* is a post-transcriptional regulator through sumoylation, that is strongly expressed in the limb bud (Costa et al., 2011). It has been described as a regulator of *Tbx5* (Beketaev et al., 2014), therefore it is tempting to speculate that *Pias1* could be modulating *Tbx5* in the limb mesoderm during the specification of distal limb parts. *Tbx15* is expressed in the early limb bud and later during endochondral bone development in prehypertrophic chondrocytes of cartilaginous templates and required for proper skeletal development in the limb (Kuijper et al., 2005; Singh et al., 2005). *Tbx15* may play additional roles because chondrogenic differentiation is prevented in the distal tissue analyzed, as it is receiving the combined signal of Fgfs and Wnt signaling (ten Berge et al., 2008). *Zic2*, and also *Shh*, are associated to holoprosencephaly (Nagai et al., 2000; Taniguchi et al., 2012). In forebrain development, it is considered that *Zic2* could be modulating *Gli3* expression through *TGFB Induced Factor Homeobox 1 (Tgif1)* and *Gli3* is one of the transcriptional effectors of Shh signaling, extensively studied in limb development (Hyman et al., 2003; Ishiguro et al., 2018; Taniguchi et al., 2017, 2012; Tkatchenko et al., 2001; Towers and Tickle, 2009). *Zic2* is expressed in the distal limb mesoderm (together with *Zic3*) and the mutants of *Zic2* show disorganized skeletal elements in the proximal part of the autopod (Nagai et al., 2000, 1997). Thus, we could speculate that *Zic2* could be interacting with *Shh* signaling in the development of the autopod, given the well-known function of *Shh* in this process (Tarchini et al., 2006; Zuniga et al., 2012).

We originally intended to do this analysis to detect specific stage-markers of DEGs peaking at E11.5 and E12.5. Nevertheless, in the 7 clusters of MES-DEGs that we extracted we only obtained a cluster with genes peaking at E11.5 (cluster Mes7) and no cluster with genes peaking at E12.5 was obtained. Moreover, out of the 11 transcription factor genes that we collected in Mes7 cluster (Fig. 20G), the only genes that showed clear expression levels in the limb bud were *Heart And Neural Crest Derivatives*

Expressed 2 (Hand2) and *GLI Family Zinc Finger 1 (Gli1)*. These genes have been widely studied in the development of the limb and present remarkable roles mostly in relation with the Shh pathway (Osterwalder et al., 2014; Te Welscher et al., 2002), though none of them could be fairly stated as transcription factor genes peaking at E11.5. Furthermore, the impact of *Hand2* and *Gli1* in PD specification is difficult to assess as their peak of expression could reflect the maximum of Shh activity, understood as reaching further anterior within the distal band.

Collectively our findings support a model in which the higher amount of transcription factors regulating the progressive specification of the PD axis is functioning at E10.5 or before. Shortly after this stage, the limb segments would be already specified, in fact, our data point to a transcriptional switch between E9.5 and E10.5 that can be associated to the transition from a proximal limb specification program to a distal specification program, as many of the detected TF genes with a peak of expression at E9.5 in the distal limb progenitors can be associated to the stylopod and many of the detected TF genes with a peak of expression at E10.5 in the distal limb progenitors can be associated to the autopod.

Analysis of the gene expression dynamics of AER-Fgfs in the limb ectoderm

We applied the same workflow used to obtain MES-DEGs to the ectoderm samples. With this approach, we extracted 2,444 differentially expressed genes in the ectoderm (ECT-DEGs), across stages. We grouped ECT-DEGs in 6 clusters according to their temporal expression profile, termed Ect1 to Ect6. The number of genes in each cluster ranged from 45 to 1069. Cluster Ect1 contained 1069 genes, cluster Ect2 contained 323 genes, cluster Ect3 contained 224 genes, cluster Ect4 contained 83 genes, cluster Ect5 contained 45 genes and cluster contained Ect6 685 genes (Fig. 21, 22).

We found *Fgf* gene family members in cluster Ect3 and cluster Ect2 (Fig. 21A). Finding AER-*Fgfs* transcripts in our samples is expected, as the ectoderm samples consist of the AER and the distal most ventral ectoderm and the distal most dorsal ectoderm. Although *Fgf9* was placed in cluster Ect2 and the rest of AER-*Fgfs* (*Fgf8*, *Fgf4* and *Fgf17*) were placed in cluster Ect3, we could observe that their temporal expression

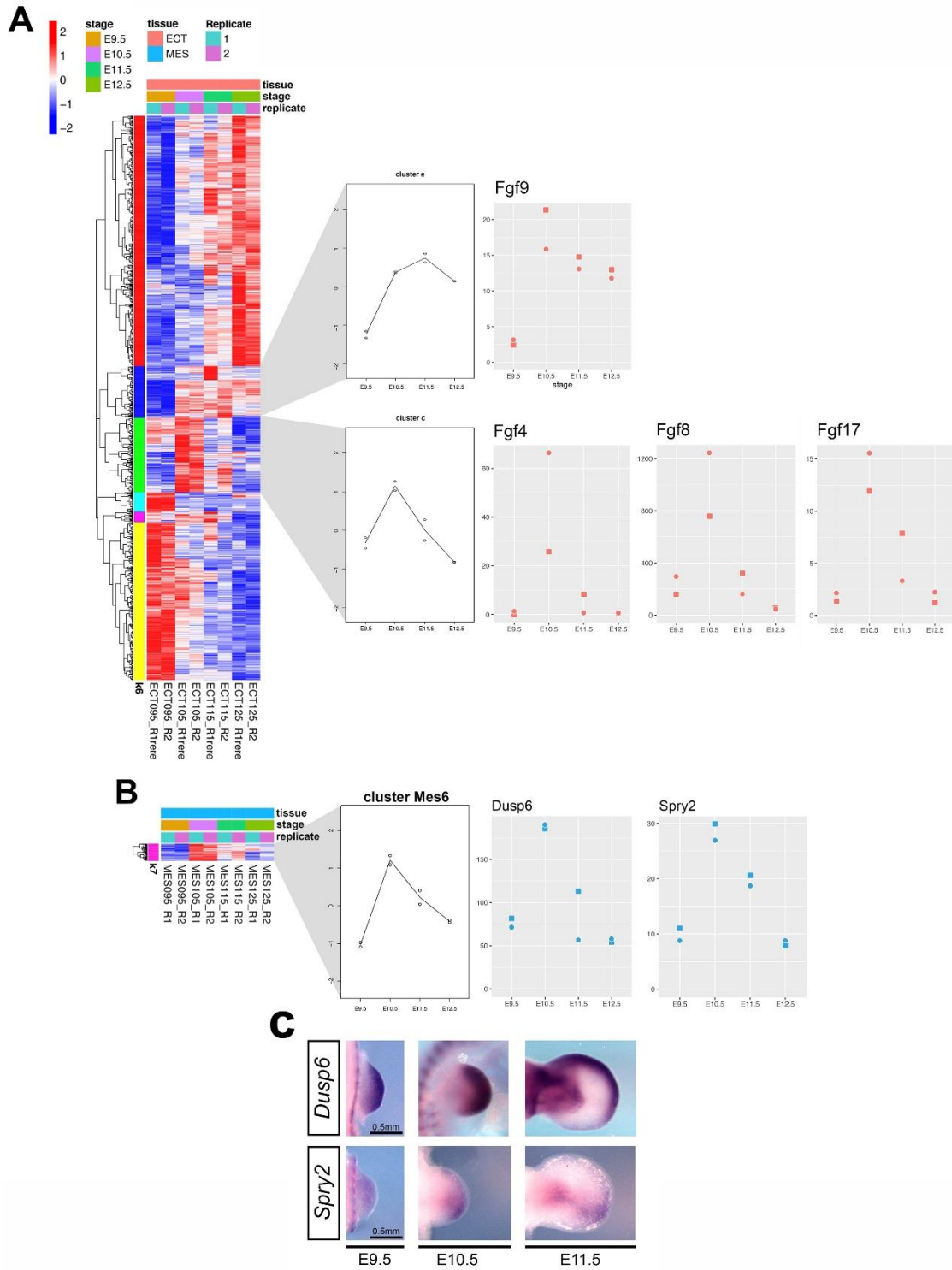


Figure 21. Temporal profiles of AER-*Fgfs* and readouts shows the peak of AER-*Fgf* activity at E10.5. Hierarchical clustering (Pearson correlation coefficient) with heatmap (scaled and centered) of the expression profile of ECT-DEGs in $\log_2(1+FPKM)$. According to the temporal dynamics of expression, six clusters were extracted (colored on the left) and named by their order of appearance from the top to the bottom of the heatmap. Line charts with the mean values of the genes contained in each cluster are depicted. *Fgf4*, *Fgf8* and *Fgf17* were found in cluster Ect3, whereas *Fgf9* was found in cluster Ect2. The expression profile, in FPKM, of AER-*Fgf* genes, is depicted in the left. Note that the maximum of expression of AER-*Fgfs* is at E10.5. **B:** Heatmap showing the expression profile, in $\log_2(1+FPKM)$ of the genes in cluster Mes6. A line chart with the mean of the values on the heatmap is depicted. *Dusp6* and *Spry2* expression profiles in FPKMs were plotted, **C:** WMISH of *Dusp6* and *Spry2* in E9.5, E10.5 and E11.5 FL buds.

profiles were very similar, with FPKM levels peaking at E10.5 and descending in the next stages. Importantly, looking again at MES-DEGs we found Fgf readouts *Dusp6* and *Spry2* in cluster Mes6 (119 genes), with a peak of expression at E10.5 indicating that not only *Fgf* transcription but also Fgf signaling peaks at E10.5 (Fig. 21B). The temporal expression profile of Fgf readouts was confirmed by WMISH (Fig. 21C). Collectively, these results show that the peak of AER-Fgf activity is occurring at E10.5.

This finding is interesting, in the context of the epithelial-mesenchymal feedback loops controlling limb outgrowth and patterning. The outgrowth of the limb bud, mediated by the expansion of limb progenitors, is based on a positive feedback loop between Shh and Fgfs that is mediated by *Grem1* (Zúñiga et al., 1999). Shh in the ZPA induces the expression of *Grem1* in a central domain of the limb bud and *Grem1*, in turn, inhibits BMPs what results in the protection of Fgfs in the AER.

The peak of AER-Fgf signaling conflicts with one of the models that explain termination of the Shh-Fgf feedback loop and that posits that the termination of the loop relies on the progressive increase of AER-Fgf levels up to E11.5 (Verheyden and Sun, 2008). Indeed, Fgfs can inhibit *Grem1* and this explains that the expression domain of *Grem1* never reaches the distal cells under the AER in wild type conditions. The model coined by Verheyden and Sun posits that progressively higher expression levels of AER-Fgfs result in *Grem1* inhibition progressively farther away from the AER eventually resulting in the impossibility of *Grem1* protection of AER-Fgfs and thus, causing the decay of the Shh-*Grem1*-Fgf loop. This is in temporal conflict with our results as our data reflected that E10.5 is the time-point of maximal AER-FGF signaling (Fig. 21) and the specification of the limb progenitors is unlikely to finish at this stage, particularly the specification of the progenitors of the autopod, which has seemingly started at E10.5. Nevertheless, the downregulation of AER-Fgfs at E11.5 matches well with the model of Pickering et al., 2018 in which, at the corresponding stage in chick, intrinsic BMP signaling overcomes *Grem1*-mediated antagonism, and therefore high BMPs could be responsible for the decay of AER-Fgfs. This intrinsic activation of BMPs is possibly mediated by *Hoxa13*, as *Hoxa13* can bind to regulatory regions of *Bmp2* and *Bmp7* and activate the expression of these genes (Knosp et al., 2004). Moreover, the strong expression of *Hoxa13* in the distal limb mesoderm at E11.5 and E12.5 (Fig 17, 19) fit well with this hypothesis.

The colinear activation of *Hoxc* genes in the limb ectoderm

The analysis of the gene expression dynamics in the distal limb ectoderm highlighted a distinctive expression of *Hoxc* genes. Centromeric *Hoxc* genes *Hoxc4*, *Hoxc5* and *Hoxc6* were found in cluster Ect1, which is characterized by genes that are steadily downregulated over time (Fig. 22, top cluster) and telomeric *Hoxc* genes *Hoxc11*, *Hoxc12* and *Hoxc13* were found in cluster Ect6, which is characterized by genes that are steadily upregulated over time (Fig. 22, bottom cluster). This particular expression dynamic of genes of the *HoxC* cluster with 3' *Hoxc* members activated earlier than 5' *Hoxc* members, suggests a colinear expression of *Hoxc* genes in the limb bud ectoderm.

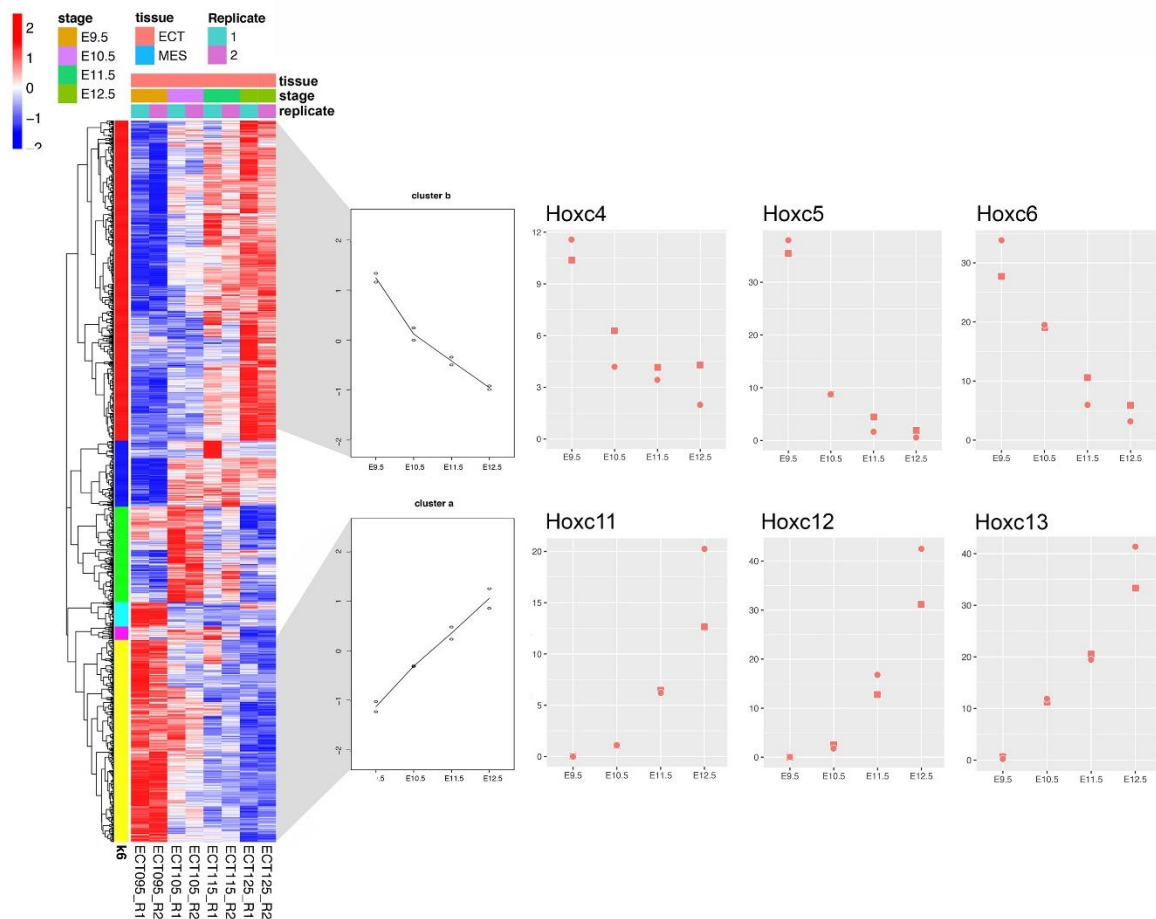


Figure 22. In the limb bud ectoderm, 3' *Hoxc* genes are progressively downregulated and 5' *Hoxc* genes are progressively upregulated over time. The same clustered heatmap of Fig. 21 is depicted here. A line chart with the mean of the values on the heatmap for clusters Ect1 and Ect6 is depicted. Expression profiles in FPKM values for *Hoxc4*, *Hoxc5*, *Hoxc6*, *Hoxc11*, *Hoxc12* and *Hoxc13* were plotted. Note that 3' *Hoxc* genes were found in cluster Ect1, characterized by a steady downregulation over time, whereas 5' *Hoxc* genes were found in cluster Ect6 characterized by a steady upregulation over time.

The expression of *Hoxc* genes in the embryonic ectoderm had been previously reported (Awgulewitsch, 2003; Reid and Gaunt, 2002). Nevertheless, their precise expression patterns and biological function in the ectoderm remain poorly studied. Hence, we decided to accomplish a more detailed analysis of *Hoxc* gene expression in our samples.

First, we generated a heatmap showing expression in $\log_2(1+\text{FPKM})$ values of all *Hox* family members. This plot showed the well-known temporal colinear activation described for *Hoxa* and *Hoxd* genes in the limb mesoderm (Fig. 23A)(reviewed in Pérez-gómez et al., 2018 and Zakany and Duboule, 2007). Interestingly, it also showed a temporal collinear activation of the *HoxC* cluster in the limb ectoderm (Fig. 23A).

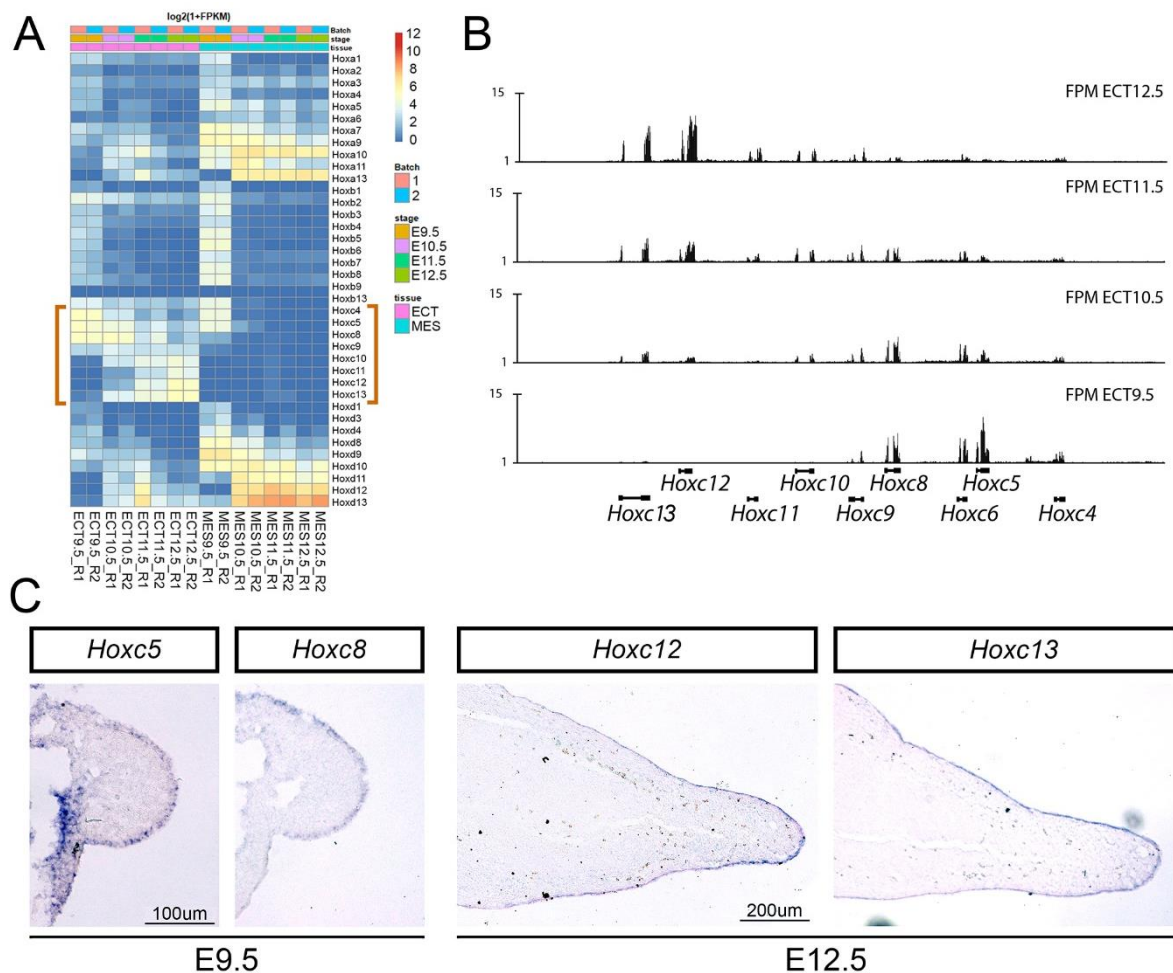


Figure 23. *Hoxc* genes are colinearly activated in the limb ectoderm. **A:** Heatmap showing $\log_2(1+\text{FPKM})$ values of all *Hox* genes across samples. Note the temporal collinear activation of the *HoxC* cluster in the ectoderm (orange brackets). **B:** Expression profile (FPM values) of the *HoxC* cluster in the different stages analyzed. Note the high expression levels of *Hoxc5* and *Hoxc8* at E9.5 and the high expression of *Hoxc12* and *Hoxc13* at E12.5. **C:** mRNA ISH for *Hoxc5*, *Hoxc8*, *Hoxc12* and *Hoxc13* in longitudinal sections of E9.5 and E12.5 FL buds, showing expression in the limb ectoderm. Dorsal is to the top and distal to the right.

Analysis of the expression values in Fragments per Million (FPM) across the *HoxC* cluster displayed high expression values of *Hoxc5*, *Hoxc6* and *Hoxc8* at E9.5 and of *Hoxc12* and *Hoxc13* at E12.5 (Fig. 23B). However, *Hoxc10* and *Hoxc11* were expressed at low levels in all stages analyzed. The *Hoxc* genes with highest expression levels could be detected by ISH in the ectoderm in limb bud sections. (Fig. 23C).

Analysis by ISH at later stages revealed that the expression of *Hoxc12* and *Hoxc13* became confined to the digit tip by E14.5 (Fig. 24A, B, C, D). Furthermore, the expression of these genes was later observed in the nail developing region at E16.5 (Fig. 10E, F) and in the nail matrix in newborn mice (Fig. 24G, H, I). It is worth mentioning that in all stages analyzed *Hoxc13* signal was stronger than the other *Hoxc* genes analyzed.

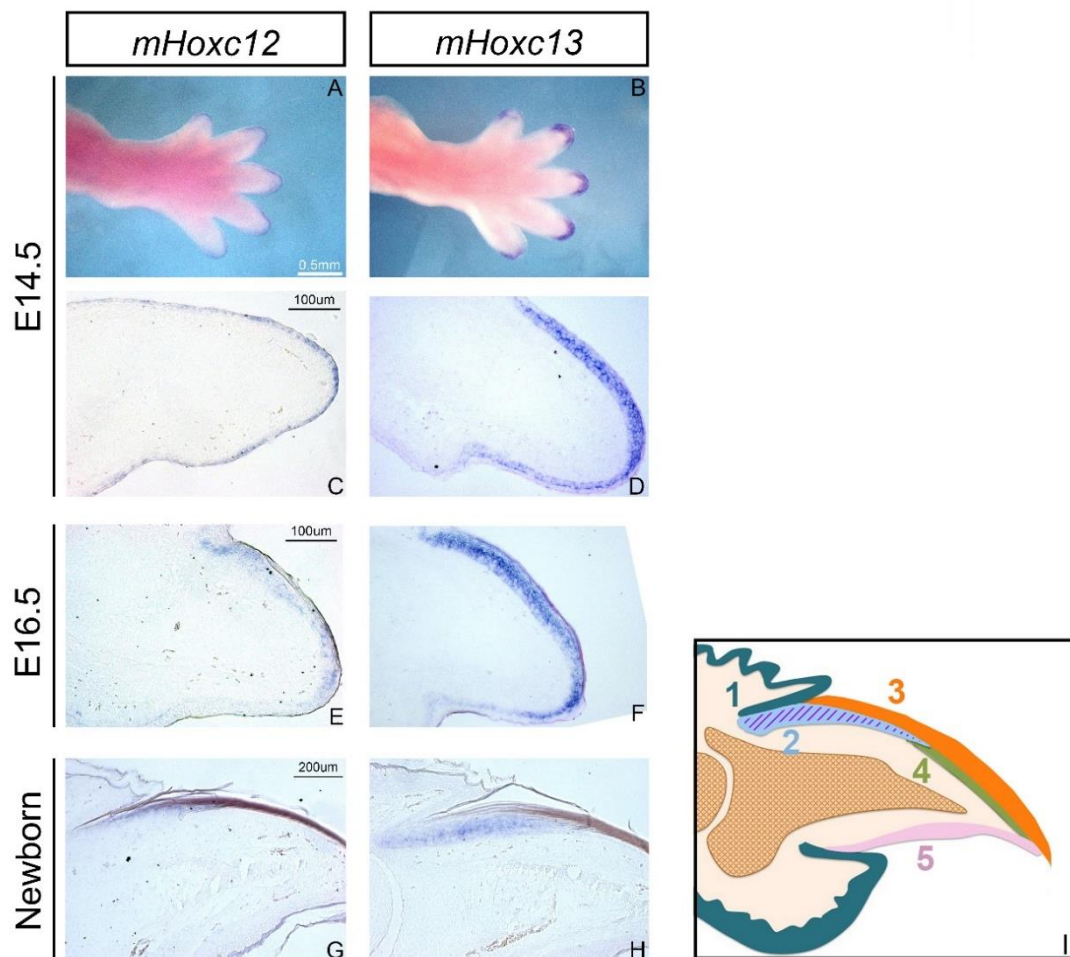


Figure 24. *Hoxc12* and *Hoxc13* become regionalized to the digit tip and the nail developing region. WMISH of E14.5 hindlimbs (A, B) and *in situ* hybridization in longitudinal sections of E14.5 (C, D), E16.5 (E, F) and newborn (G, H) forelimb digits showing the expression of *Hoxc12* and *Hoxc13* showing expression in the digit ectoderm of E14.5 FLs and in the nail unit at later stages. Note that *Hoxc13* expression is stronger in all stages analyzed. I: Schematic representation of the newborn nail organ: 1 = proximal nail fold, 2 = nail matrix, 3 = nail plate, 4 = nail bed, 5 = hyponichium. The expression domain of *Hoxc13* in the nail is marked with purple diagonal bars.

These analyses clarify the expression patterns of *Hoxc* genes in the limb ectoderm, which were dispersed and incomplete in the literature. *Hoxc* genes are activated in the limb bud ectoderm in a temporal collinear fashion and *Hoxc12* and *Hoxc13* expression persist in the digit tip ectoderm and in the nail organ at least until the newborn stage.

The nail phenotype of *Hoxc13GFP* and *HoxCKO* mutant mice

The *HoxC* cluster is considered as dispensable for the development of the limb since its complete removal didn't result in any gross alteration of limb morphology (Suemori and Noguchi, 2000). However, intrigued by its ectodermal colinear expression we decided to re-examine the limbs of mice knockout for the complete *HoxC* cluster (*HoxCKO*) (Suemori and Noguchi, 2000), focusing on ectodermal derivatives. *HoxCKO* mice die at birth due to their inability to breath, precluding analysis later than the newborn stage (Suemori and Noguchi, 2000). Visual inspection of newborn wild type forelimbs is sufficient to distinguish the nail plate, as this densely keratinized structure reflects light more intensely than the rest of the epidermis (Fig. 25A'). However, the nail plate was not observed in *HoxCKO* mutants (Fig. 25C') and poorly observed in *Hoxc13GFP* mutants (Fig. 25B'). In addition, the forelimbs of *HoxCKO* mutants displayed a strong flexion of the digits. This flexion may be related to the known expression of *Hoxc* genes in motoneurons (Dasen et al., 2003).

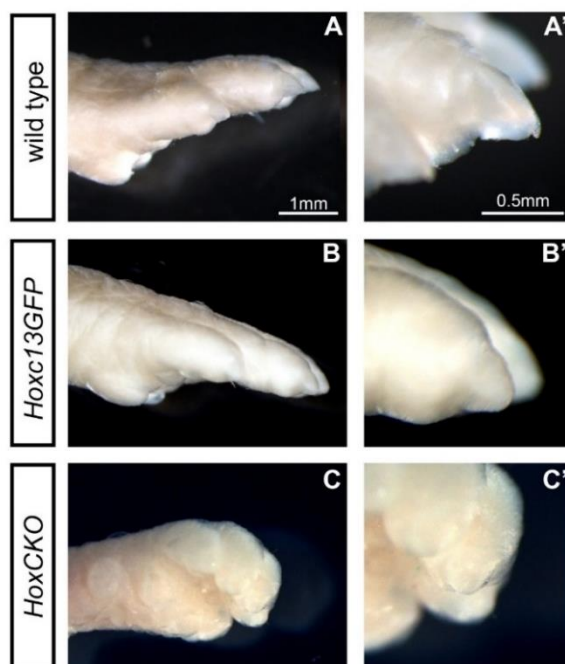


Figure 25. Nail alterations in *Hoxc13GFP* and *HoxCKO* mutant mice. Photographs of the distal tip of the FL of wild type, *Hoxc13GFP* and *HoxCKO* mutant newborn mice. A', B', C' are magnifications of A, B and C, respectively. Note the typical light reflection of the nail plate in A', is not observed in *Hoxc13GFP* (B') and *HoxCKO* (C') newborn mutants. Note also the pronounced digital flexion in *HoxCKO* mutants.

As the presence of the nail plate is not clear neither in *Hoxc13GFP* nor in *HoxCKO* mutants at birth (Fig. 25), we decided to investigate in depth the nail anatomy in these mutants. Therefore, we performed a histological analysis by hematoxylin-eosin (HE) staining of paraffin embedded longitudinal sections of the digits (Fig. 26).

At birth, all the components of the nail organ were clearly distinguished in WT digits, both in the FL and the HL (Fig. 11C, 24I, 26A', 26B'). In HE stained sections, the nail plate is the eosinophilic structure formed by a condensation of hard Keratins (Fig. 26A'', B''). The proximal nail fold is formed by a dorsal, external portion of skin epithelium that surrounds the most proximal part of the nail plate and a thin, internal epithelial layer of cells that are in direct contact with the proximal part of the nail plate (Fig. 26A'', B''). The nail matrix is located next to the proximal nail fold and is formed by several layers of cells that give rise to the nail plate. The nail bed is a thin epithelial layer of cells located distal to the nail matrix and immediately beneath the nail plate, here observed at the most distal-dorsal tip of newborn digits (Fig. 26A', B'). The volar epidermis under the free edge of the nail plate is referred as the hyponichium, which undergoes normal skin keratinization (Fig. 26A', B').

The nail plate was not clearly appreciated in *Hox13GFP* mutant mice, in comparison to wild type animals of the same stage, though the rest of the components of the nail unit were apparently present: The proximal nail fold, the nail matrix, the nail bed and the hyponichium (Fig. 26, middle panels). In contrast, the epithelial characteristics normally associated with the development of the nail were absent in *HoxCKO* mutants (Fig. 26, bottom panels). The thickening of the epithelium in these animals is mainly invariable all along the digit tip, compared to the wild type condition. The nail plate is absent, the proximal nail fold is reduced to a slight groove (more evident in the FL) and we didn't observe morphological signs of the keratogenous zone of the nail matrix nor the nail bed. This phenotype was observed both in forelimbs and hindlimbs of *HoxCKO* animals.

To determine the nail defect in *HoxCKO* mutants, we studied the expression of a battery of Keratin proteins, markers of epidermal differentiation, in the digit tip ectoderm of mutant newborn mice in comparison to wild type control littermates.

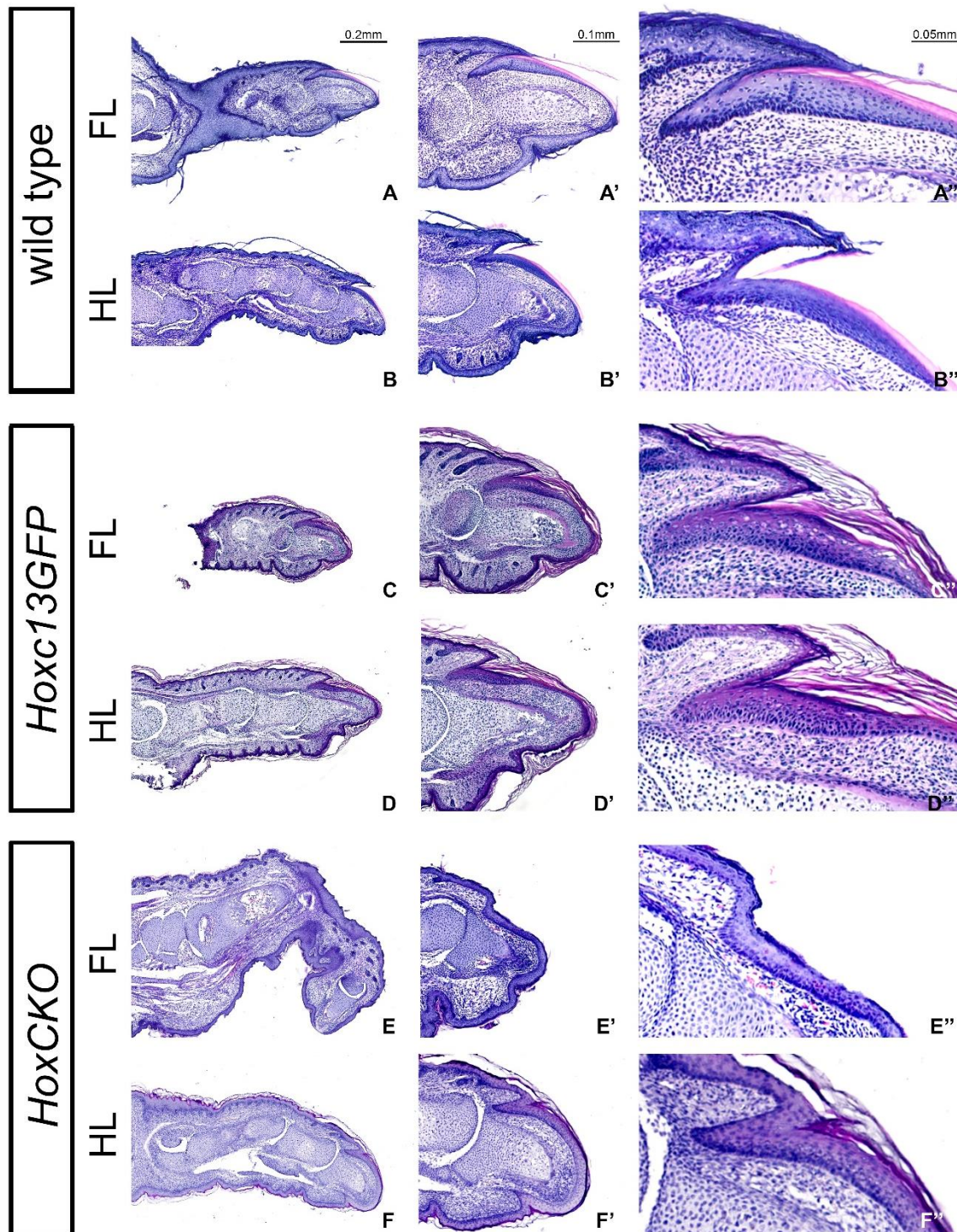


Figure 26. Histological analysis of the digits of *Hoxc13GFP* and *HoxCKO* newborn mice. Hematoxylin-Eosin stained longitudinal sections of FLs and HLs, as indicated on the left. For each section, three magnifications are shown. Note that the nail plate is only clearly appreciated in the wild type condition clearly marked by its strong eosinophilia (compare **A''-B''** with **C''-D''** and **E''-F''**). The anatomy of the nail organ is clearly lost in *HoxCKO* mutants, as there is little sign of the epithelial differentiation characteristic of the nail organ, particularly in the FL (**E', F', E'', F''**). Dorsal is to the top, distal is to the right.

Keratins are fibrous proteins that form the intermediate filaments of epithelia being the structural proteins of hair, nails, horn, hoofs, wool, feathers, and of the epithelial cells in the skin. Keratins are encoded by 54 genes (28 type I, 26 type II) and their expression marks the differentiation state of epithelial cells (Bragulla and Homberger, 2009).

The interfollicular epidermis is a stratified epithelium consisting of a proliferative basal layer (progenitor status) that gives rise to multiple suprabasal layers (spinous, granular, lucidum and cornified, Fig. 9) through a programmed differentiation process. Basal keratinocytes are mitotically active and express Keratin 5 (Krt5; type II) and Krt14. Upon their commitment to terminal differentiation, basal keratinocytes stop dividing and start expressing Krt1 (type II) and Krt10 (type I) concurrent with their migration upward into the suprabasal compartment (reviewed in Wang et al., 2016).

Therefore, we used Krt5, a marker of basal keratinocytes, Krt10 a marker of keratinocytes committed to terminal interfollicular skin differentiation and the hard Keratins that are specifically expressed in the development of the hair and the nail to determine the differentiation state of the nail organ in mutants.

At birth, Krt5 expression has not yet restricted to the basal epidermal layer except in the nail matrix where it is lost in the keratogenous zone (Fig. 27A-B)(Fleckman et al., 2013). In contrast to the wild type condition, the immunostaining of Krt5 was present throughout the epithelium of the forelimb nail region in *HoxCKO* newborn mutant mice (Fig. 27C, C'). In the hindlimb, a slightly Krt5-cleared suprabasal epithelium was observed (Fig. 27D, D'), in the region corresponding to the keratogenous zone. Krt10 expression in adult mice is detected in the stratified layers of the skin. In the nail organ, Krt10 is detected in the proximal nail fold and in the hyponichium but not in the nail matrix nor in the nail bed of wild-type mice (Fig. 27E, F)(Fleckman et al., 2013). In forelimbs and hindlimbs of *HoxCKO* mutants, the expression of Krt10 was continuous in the stratified layers of the epithelium, all along the digit tip (Fig. 27G, H) reflecting the lack of specific nail differentiation. We also performed immunostaining analyses with the AE13 antibody (Fig. 27I-L), which is a polyclonal antibody used to detect the hard Keratins that are specifically expressed in the development of the hair and the nail (De Berker et al., 2000; Lynch et al., 1986). We did not detect the expression of these hard Keratins in *HoxCKO* mutants. Collectively, these data evidence the anonychia condition

in forelimbs and hindlimbs of *HoxCKO* mutants with no obvious signs of the presence of the nail matrix.

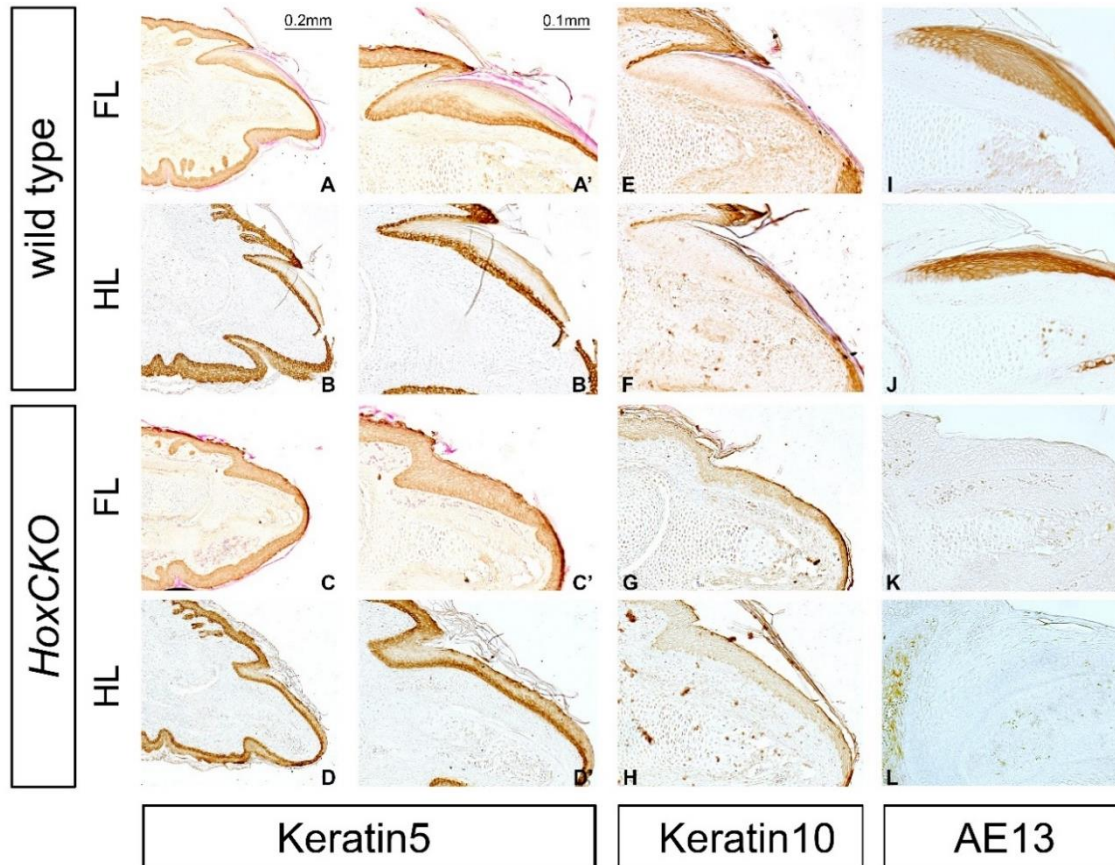


Figure 27. Immunohistochemical analysis of specific Keratins in the digit tip of *HoxCKO* mutants. Immunohistochemistry for the detection of Krt5 (A-D, A'-D'), Krt10 (E-H) and Hard Keratins (AE13 antibody; I-L) in longitudinal sections of wild type and *HoxCKO* homozygous newborn mice digit tips. For Krt5 immunostaining, two magnifications are shown. For Krt10 and AE13 immunostainings, images show the nail matrix region and surrounding tissues. Note that the expression pattern of the studied Keratins was affected both in the digit ectoderm of the forelimbs and the hindlimbs of *HoxCKO* mutants. Orientation is as in Fig. 26.

We also examined the expression of these Keratins in the digits of *Hoxc13GFP* mutant mice (Fig. 28). Krt5 expression was not affected in these mutants, but Krt10 was abnormally detected in the suprabasal layers of the proximal nail matrix. This result confirms previous findings that had reported the presence of a granular layer in the proximal nail matrix of *Hoxc13* mutants (Potter et al., 2011), a condition that is also observed in *Foxn1* mutants (Mecklenburg et al., 2004). The expression of hard Keratins is depleted in *Hoxc13GFP* mutants, as in the ECTD9, associated to the mutation of *HOXC13* (Lin et al., 2012).

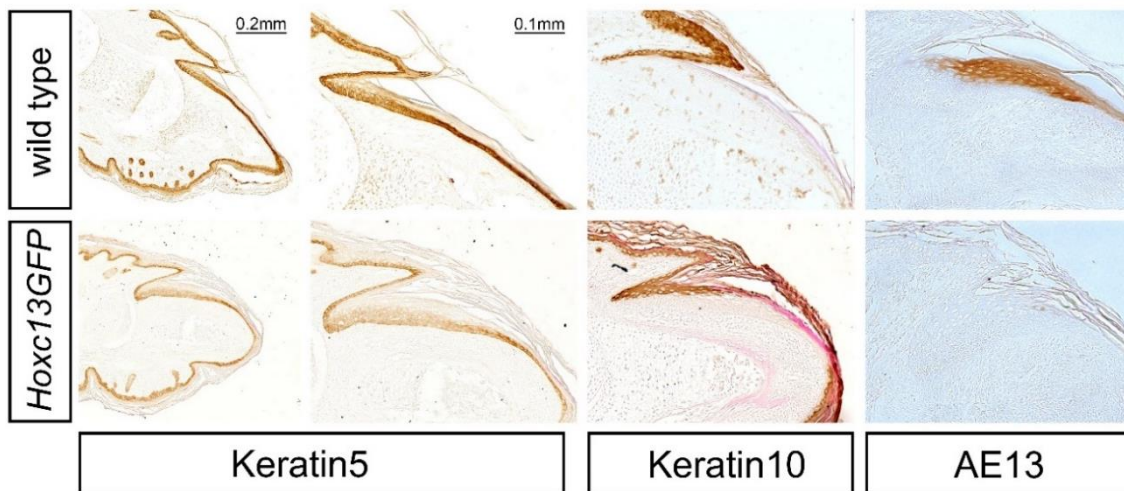


Figure 28. Immunohistochemical analysis of Keratins in the digit tip of *Hoxc13GFP* mutants. Immunohistochemistry for the detection of Krt5, Krt10 and Hard Keratins (AE13) in longitudinal sections of wild type and *Hoxc13GFP* newborn mice FL digits. Sections equivalent as in Fig. 27. The expression of Krt5 was not affected in *Hoxc13GFP* mutants. Nevertheless, Krt10 expression extended to the suprabasal layer of the nail matrix in *Hoxc13GFP* mutants and the expression of nail/hair hard Keratins, recognized by AE13 antibody was not detected in these mutants.

In summary, we have demonstrated the anonychia of *HoxCKO* newborn mice, a phenotype previously disregarded in these mutants. The knockout of the complete *HoxC* cluster results in the loss of epithelial differentiation associated to the development of the nail, as we have demonstrated in our histological analyses. In turn, *Hoxc13* mutation results in the development of twisted and fragile nails (Godwin and Capecchi, 1998). A reasonable interpretation of these results is that *Hoxc* genes are partially redundant in the development of the nail and therefore, in the *Hoxc13* mutant condition, other *Hoxc* genes can partially activate the nail differentiation program leading to a fragile nail.

The relationship between *Hoxc* genes and BMP signaling in developing hairs and nails

Then, we decided to look further into putative downstream targets of *Hoxc* genes in the developing nail organ. *Foxn1* has been described as a target of *Hoxc13* in the development of the hair and the nail. The current view is that *Hoxc13* is upstream of *Foxn1* and that *Foxn1* regulates the expression of hard acidic Keratins needed for the

development of the hair shaft and the nail plate (Potter et al., 2011). Moreover, *Foxn1* mutants (also referred as “nude mice”) lack external hair and display fragile nails.

Foxn1 has been described to be activated by BMP signaling in the development of the hair follicle, as well as *Msx2* (Andl et al., 2004). The loss of function of *Msx2* also results in impaired development of the hair and the nail (Satokata et al., 2000) and the double *Foxn1*^{-/-};*Msx2*^{-/-} mutant exhibits a more severe phenotype with nails breaking just beyond the hyponichium (Cai and Ma, 2011). Considering this information, we explored the putative role of *Hoxc* genes in mediating BMP signaling in the development of the nail and the hair.

We studied the expression of *Foxn1*, *Msx2* and *Bmp7* genes in longitudinal sections of E17.5 digits (Fig. 29). *In situ* hybridization signal of *Foxn1* in *HoxCKO* mutants was reduced to background levels. On the other hand, the expression of *Msx2* was lost in the keratogenous zone and the ventral domain of *HoxCKO* mutants. We also identified the downregulation of *Bmp7* in the digit tip of *HoxCKO* mutants, where the nail matrix should be. Moreover, *HoxCKO* digits displayed a disorganization of the *Bmp7* expression in developing hair follicles (Fi. 29D, H), though this was observed at the level of the acropodium but not in the epithelium of the metapodium (Fi. 29D', H').

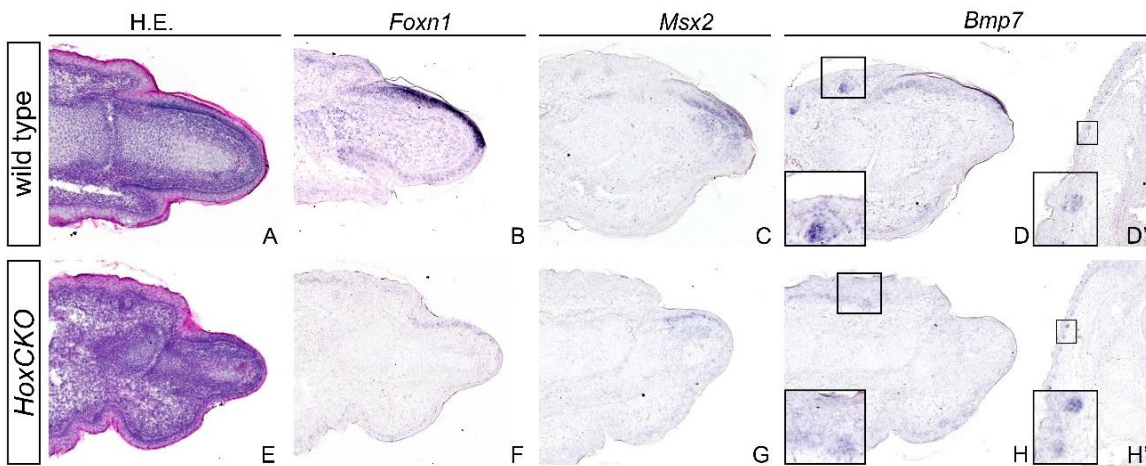


Figure 29. Analysis of the expression of *Foxn1* and *Msx2* in *HoxCKO* mutant digit tips. Longitudinal sections of E17.5 digit tips of wild type and *HoxCKO* homozygous mutant littermates **A, E** shows that the *HoxCKO* phenotype is already visible at E17.5 as the upper proximal fold and the lower proximal fold are not formed. *Foxn1* expression (**B, F**) is strongly downregulated in *HoxCKO* mutants. *Msx2* expression (**C, G**) is generally downregulated in the digit tip ectoderm and lost in the keratogenous zone in *HoxCKO* mutants. *Bmp7* expression (**D, H**) is lost in the nail matrix of *HoxCKO* mutants and de-regionalized developing HF in the acropodium (insets in **D, H**), but not in the HF in the metapodium (insets in **D', H'**). **A-C, E-H:** Digit tips. Dorsal is to the top, distal is to the right. **D', H':** Dorsal metapodium. Ventral is to the right, distal is to the top. Hematoxylin-Eosin staining.

These experiments evidence a relationship between *Hoxc* genes and BMP signaling in the development of the hair follicle and the nail organ and point to *Hoxc* genes acting upstream of *Bmp7* in the development of these ectodermal organs. Further investigations are required to examine the development of the hair follicles in *HoxCKO* mutants.

Transcriptional regulation of *Hoxc* genes in the limb ectoderm

Next, we decided to investigate the transcriptional regulation of *Hoxc* genes focusing our attention on finding the regulatory regions control their expression in the ectoderm.

The loss of function allele for *Hoxc* genes used in this study (*HoxCKO*) was generated by homologous recombination of a targeting vector. This vector contained an *EF1 α* promoter and a *puromycin* promoterless gene, substituting the *HoxC* cluster (Fig. 30A). However, the engineered recombination of this targeted mutation preserved the 3' UTR of *Hoxc4* and part of the 5' region of *Hoxc13*, therefore, we decided to use a probe that hybridizes with the 3' UTR of *Hoxc4* to check if *HoxCKO* mutants were able to express a truncated transcript containing this part of *Hoxc4*.

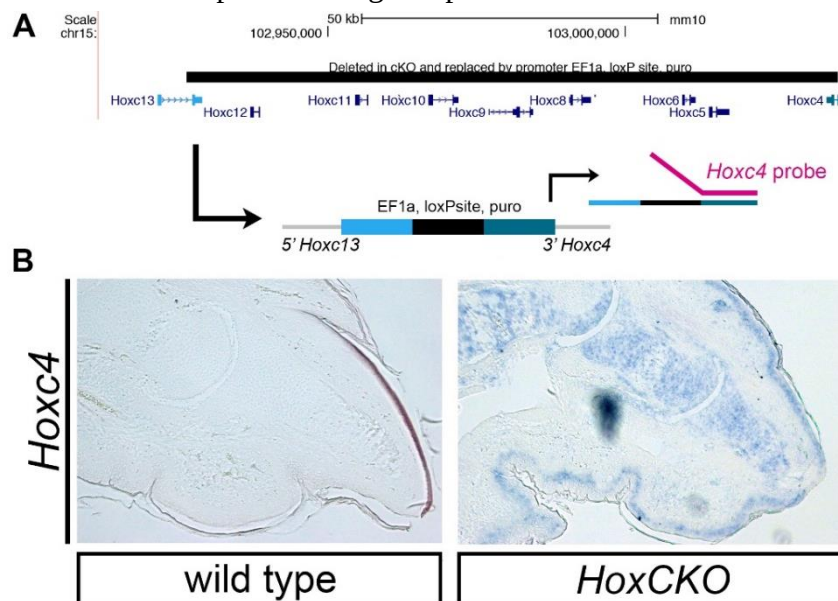


Figure 30. A transcript containing the 3'UTR of *Hoxc4* is expressed in *HoxCKO* digits. A: representation of the *HoxCKO* allele. The genomic region spanning from the *Hoxc13* intron to the second exon of *Hoxc4* was substituted by an *EF1 α* promoter and a *puromycin* promoterless gene. A transcript containing the 3' UTR of *Hoxc4* (black dashed + turquoise line) is expressed from this allele and can be detected with a *Hoxc4* probe (pink). **B:** *In situ* hybridization of *Hoxc4* of newborn mice FL digits. Note the dramatic gain of *in situ* signal in *HoxCKO* mutant digits.

In the wild type condition, *Hoxc4* expression is not detected in the digit ectoderm of newborn mice. Hence, we were surprised by the dramatic gain of *in situ* hybridization signal in *HoxcKO* mutant digits (Fig. 30B). Intriguingly, the expression domains observed in this experiment included the cartilage (Cameron et al., 2009; Yueh et al., 1998) and the limb ectoderm.

We deduced from this result, that the regulatory regions driving the expression of *Hoxc* genes in the limb ectoderm and in the cartilage could be located outside the *HoxC* cluster. It should be noted that with this experiment, we could not report whether the *EFla* promoter or the *Hoxc13* promoter were driving the expression of the transcript detected with the *Hoxc4* probe.

We focused our interest in the cis regulatory inputs regulating the activation of *Hoxc* genes in the limb ectoderm. Hence, we used ATAC-seq (Assay for Transposase Accessible Chromatin with high-throughput sequencing)(Buenrostro et al., 2016) to detect open chromatin regions in the *HoxC* locus and thus, potential regulatory regions for the activation of *Hoxc* genes in the limb ectoderm. As *Hoxc12* and *Hoxc13* show marked expression domains at the digit tip ectoderm of E14.5 limbs, we dissected E14.5 wild type digits, separated the ectoderm from the mesoderm by mild trypsin digestion and processed the collected digit ectoderms for ATAC-seq (Fig. 14).

The PCR amplification to produce the ATAC-seq libraries was performed as described in Buenrostro et al., 2016, with primers listed in Buenrostro et al., 2013. We generated ATAC-seq libraries with paired-end reads. When reads were mapped, we identified two open chromatin regions located 5' to the *HoxC* cluster in E14.5 forelimb and hindlimb samples that were not detected in the control E13.5 forebrain track (Fig. 31A). The most centromeric region, termed *EC1* (Enhancer of *HoxC* 1), was found 165kb away from the *HoxC* cluster and was conserved in placental mammals. The most telomeric region, termed *EC2* (Enhancer of *HoxC* 2) was found 81 kb away from the *HoxC* cluster and is conserved in mammals (Fig. 31B). We hypothesized that these regions could be responsible for the activation of *Hoxc* genes in the limb ectoderm, reminiscent of *Hoxa* and *Hoxd* genes, whose expression in the limb mesoderm is regulated by distant regulatory regions outside of the *HoxA* and *HoxD* clusters (Berlivet et al., 2013; Gonzalez et al., 2007; Montavon et al., 2011; Spitz et al., 2003, 2001).

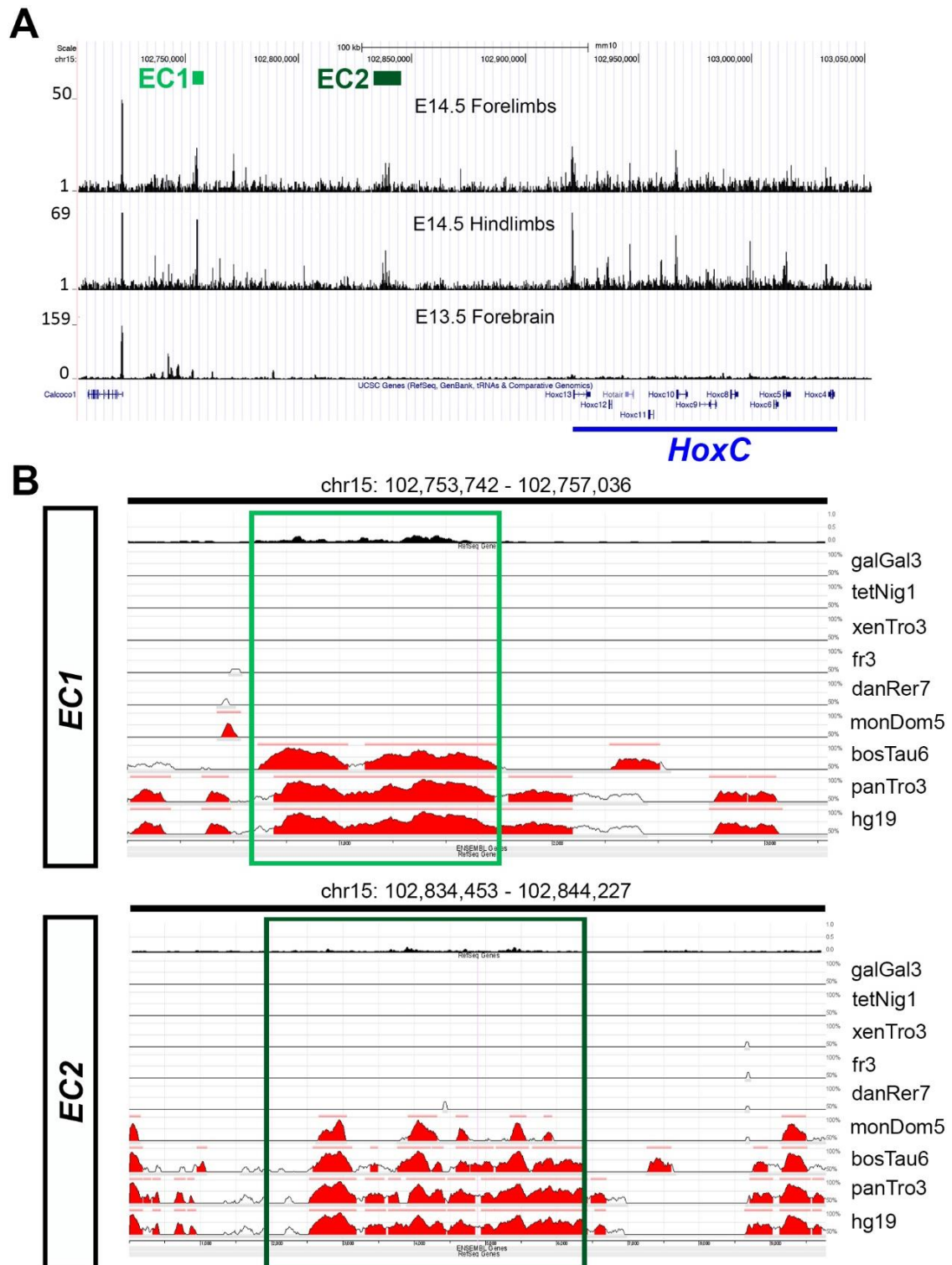


Figure 31. ATACseq on E14.5 digit ectoderms. **A:** Screenshot of UCSC browser session showing the mapped ATACseq reads in E14.5 forelimb and hindlimb digit ectoderms. Note 2 peaks of ATAC signal, termed *EC1* and *EC2*, 5' to the *HoxC* cluster that were not observed in E13.5 forebrain. **B:** Screenshot of ECR browser session showing the ATAC mapped reads in the top track and the conservation of these regions in chick (GalGal3), actinopterygian fish (tetNig1), frog (xenTro3), zebrafish (danRer7), opossum (monDom5), cow (bosTau6), chimpanzee (panTro3) and human (hg19). Note that the centromeric region of mapped reads (*EC1*) is conserved in placental mammals (light green box) and the telomeric region of mapped reads (*EC2*) is conserved in mammals (dark green box).

We limited *EC1* and *EC2* to 1.1kb and 4.1kb genomic regions, respectively, based on the overlapping between ATAC-seq signal and conservation peaks (Fig. 31B, light green and dark green boxes).

To assess their regulatory potential, these two genomic regions were cloned in tandem and assayed for enhancer activity in transgenic mouse embryos (Fig. 32). For this analysis, we used a pSK-LacZ vector that carries a β -globin minimal promoter/lacZ reporter cassette. We decided to evaluate the activity of *EC1* and *EC2* in transient transgenic E16.5 mouse embryos, as morphological signs of the development of the nail and the hair follicle are clearly appreciated at this stage.

The *EC1* and *EC2* transgenes displayed robust reporter activity in the limb ectoderm (Fig. 32D, H, K) and hair follicles (Fig. 32G) but also in many other ectodermal territories. Reporter activity was found in ectodermal cells of the head (Fig. 32A) and in the vibrissae (Fig. 32A), in the eyelashes (Fig. 32C), the dorsal midline (Fig. 32B), the ventral midline (Fig. 32E), and the genital tubercle (Fig. 32E). Notably, the *EC1+EC2* transgene also exhibited activity in the neural tube observed in the neck section (Fig. 32F). We confirmed the lacZ reporter activity in the limb ectoderm (Fig. 32N), in the hair follicle (Fig. 32O) and the developing nail region (Fig. 32P) by sectioning the limbs of stained embryos. Notably, the activity pattern in the limb ectoderm affected most ectoderm cells at distal level with a diffuse proximal boundary in the zeugopod, though hair follicles were marked all along the body.

Given the various activity domains detected with this reporter assay, we considered that *EC1* and *EC2* together could function as global ectodermal enhancers of the activity of *Hoxc* genes in the developing embryo, as the pattern of these enhancers in the neural tube could be linked to the expression of *Hoxc* genes in motoneurons (Dasen et al., 2003). Of note, a detailed study in LacZ-stained tissue sections could be considered to evaluate the ectodermal specificity of *EC1* and *EC2*.

We also evaluated the activity of the *EC1* and *EC2* sequences separately in transient transgenic E16.5 mouse embryos. *EC1* activity was observed in whiskers (Fig. 33C), the neural tube (Fig. 33D, E), hair follicles (Fig. 33F), the tail (Fig. 33A) and in the limb ectoderm (Fig. 33A, G, H). The activity pattern was highly similar to that displayed by *EC1* and *EC2* together, although with weaker intensity. Importantly, *EC1* activity was reported in the nail developing region, both in forelimbs and hindlimbs (Fig. 33G', H').

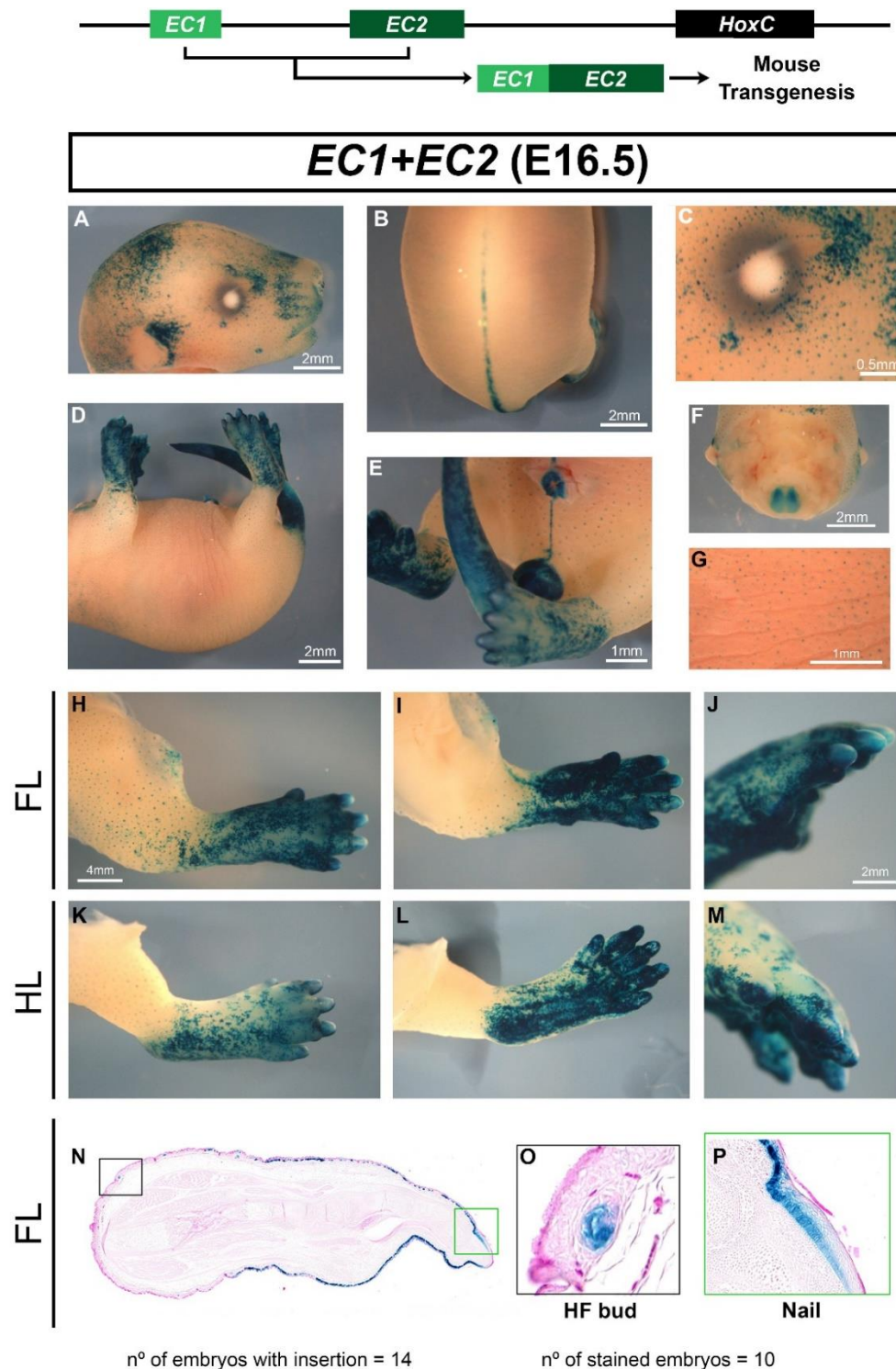


Figure 32. Representative whole-mount lacZ pattern for the *EC1-EC2* putative enhancers. Hsp68 promoter-LacZ was placed downstream of mouse *EC1* and *EC2* cloned in tandem. Reporter activity was detected in the head ectoderm including the developing whiskers (A) and eyelashes (C), in the dorsal (B) and ventral midline (E), in the genital tubercle and tail (E), in the limb ectoderm (D, H-M), in hair follicles throughout the body (G), and in the neural tube (F). Note neural tube staining in the plane of section in the neck. A longitudinal section of a stained forelimb is depicted in N with the hair bud and the nail framed magnified in (O) and (P) respectively. Note that all stained tissues are ectodermic derivatives. Of 14 embryos with insertion of the reporter transgene, 10 displayed this pattern of lacZ staining.

EC2 activity was reported in the limb ectoderm with a more scattered and distal activity pattern in comparison to *EC1* (Fig. 33, J, M, and N). Moreover, the genitalia (Fig. 33L) and the head (Fig. 33K) were only stained in *EC2* reporter mice. We generated sections of the limbs of stained embryos to confirm the reporter activity in the limb ectoderm (Fig. 33 M, N) and the nail developing region (Fig. 33M', N'). It is worth mentioning that we didn't observe a clear reporter signal in the distal part of the digit tip, though cells of the nail matrix were stained.

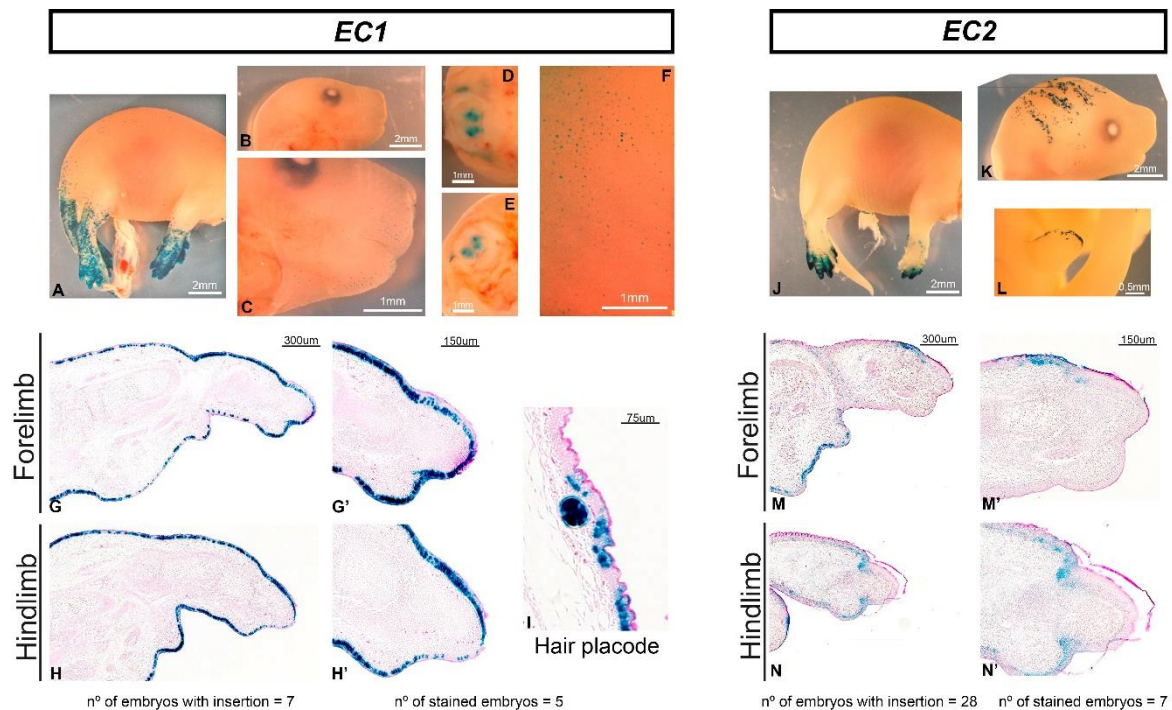


Figure 33. Representative whole-mount lacZ pattern driven by *EC1* or *EC2* putative enhancers. *Hsp68* promoter-LacZ was placed downstream of either *EC1* or *EC2*. Top images show the whole mount staining. Bottom images show longitudinal sections of limbs (dorsal is to the top, distal is to the right). *EC1* reporter activity was detected in the limb ectoderm including the nail developing region (A, G, G', H, H'), some HF's of the face (C), the neural tube (D-E) (D and E show respectively the anterior and posterior aspect of the neural tube from an embryo sectioned at the neck), and the hair follicles (F, I). *EC2* activity was observed in the limb ectoderm including the nail developing region (J, M, M', N, N')) and in ectodermal regions of the head (K) and genital tubercle (L). For *EC1* 5 of 7 embryos with insertion displayed lacZ staining. For *EC2* 7 of 28 embryos with insertion displayed lacZ staining.

In summary, we have identified two regulatory regions, *EC1* and *EC2*, with regulatory potential in several ectodermal derived structures. *EC1* is conserved in placental mammals and is capable of driving reporter activity in whiskers, the neural tube, the tail, hair follicles, the limb ectoderm and the nail developing region. *EC2* is conserved

in mammals and is capable of driving reporter activity in spotted regions in the head, the genital tubercle, the limb ectoderm and in the nail developing region. Importantly, the majority the activity domains that we observed in the analysis of *EC1* and *EC2* cloned together and separately could be associated to the expression of *Hoxc* genes (Dasen et al., 2003; Godwin and Capecchi, 1998; Shang et al., 2002; Yu et al., 2018). Therefore, it is reasonable to consider these regions as *Hoxc* enhancers that could act conjointly to regulate their expression in the developing ectoderm.

Generation and analyses of *delEC1* and *delEC2* mutants

To further investigate the functional importance of these enhancers in vivo, we used the CRISPR–Cas9 genome editing technology to individually delete these two enhancers. We followed a CRISPR-Cas9 adapted protocol (Qin et al., 3415), based on the electroporation of Cas9 mRNA and sgRNA in zygotes, to generate mutant mouse lines knockout for *EC1* (termed *delEC1*) and for *EC2* (termed *delEC2*).

We designed gRNAs with CHOPCHOP (<https://chopchop.cbu.uib.no/>) to obtain double strand breaks 5' and 3' to each regulatory region to generate the *del(EC1)* and the *del(EC2)* lines (Fig. 34A, yellow and red arrows). We designed several primers pairs, with <http://primer3.ut.ee/>, to genotype the resulting mouse lines and selected those pairs (Table 2, Fig. 34C). We generated stable lines from one sequenced F0 male for each allele.

Homozygous mutant mice for either *delEC1* or *delEC2* were viable and fertile, reached adulthood and showed no evident phenotypical abnormalities (Fig. 34B). They were similar in size to wild type littermates, their hair appeared glossy and healthy, their behavior was apparently normal and gross observation of their nails didn't reveal any remarkable alteration (Fig. 35A, B, C).

To study in detail the nails of *delEC1* and *delEC2* homozygous mice, we performed a HE histological analysis at postnatal day 9 (P9) mice. At this stage the nail plate has strongly developed and is formed by several layers of cornified keratinocytes similarly in wild type, *delEC1* and *delEC2* mice (Fig. 35D, E, F).

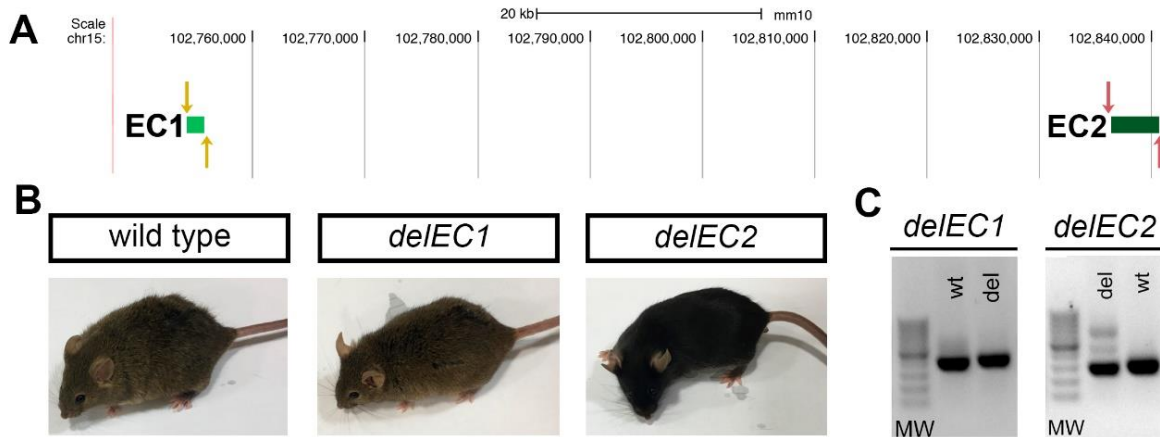


Figure 34. CRISPR-mediated individual deletion of *EC1* and of *EC2*. **A:** Screenshot of UCSC genome browser showing the position of *EC1* and *EC2* genomic regions and the cutting points of the designed gRNAs to generate *delEC1* (yellow arrows) and *delEC2* (red arrows) mouse lines. **B:** Images of adult wild type and homozygous mutant mice for *delEC1* and *delEC2*. **C:** PCR genotyping analysis of *delEC1* and *delEC2*. For each mutant line, an image showing a gel electrophoresis with a 100bp molecular weight marker and the PCR genotyping of the wild type allele and the deletion allele of a heterozygous animal is depicted. The expected amplicon size generated to detect the wild type and deletion alleles for *delEC1* are 403bp and 448bp, respectively. For the wild type and deletion alleles for *delEC2*, the expected amplicon sizes are 305bp and 340bp, respectively. The bands that run slower in the *delEC2* deletion allele PCR are nonspecific.

We checked the expression of Keratins in these digits. In accordance with the normal development of the nail plate, AE13 immunostaining didn't reveal any notable signal difference between the wild type condition and *delEC1* or *delEC2* mutants (Fig. 35 J, K, L). Nevertheless, Krt10 expression was slightly affected in *delEC2* mutants, in comparison to wild type animals of the same age, as some cells of the proximal nail matrix expressed Krt10 (Fig35. G, J). This condition was not observed in *delEC1* mutants (Fig. 35H).

These results reveal a role for *EC2* region in the keratinocyte differentiation of nail matrix cells, but not for *EC1* region. Collectively, they also indicate that, for the most part, each enhancer is dispensable for normal development and suggests redundancy between them.

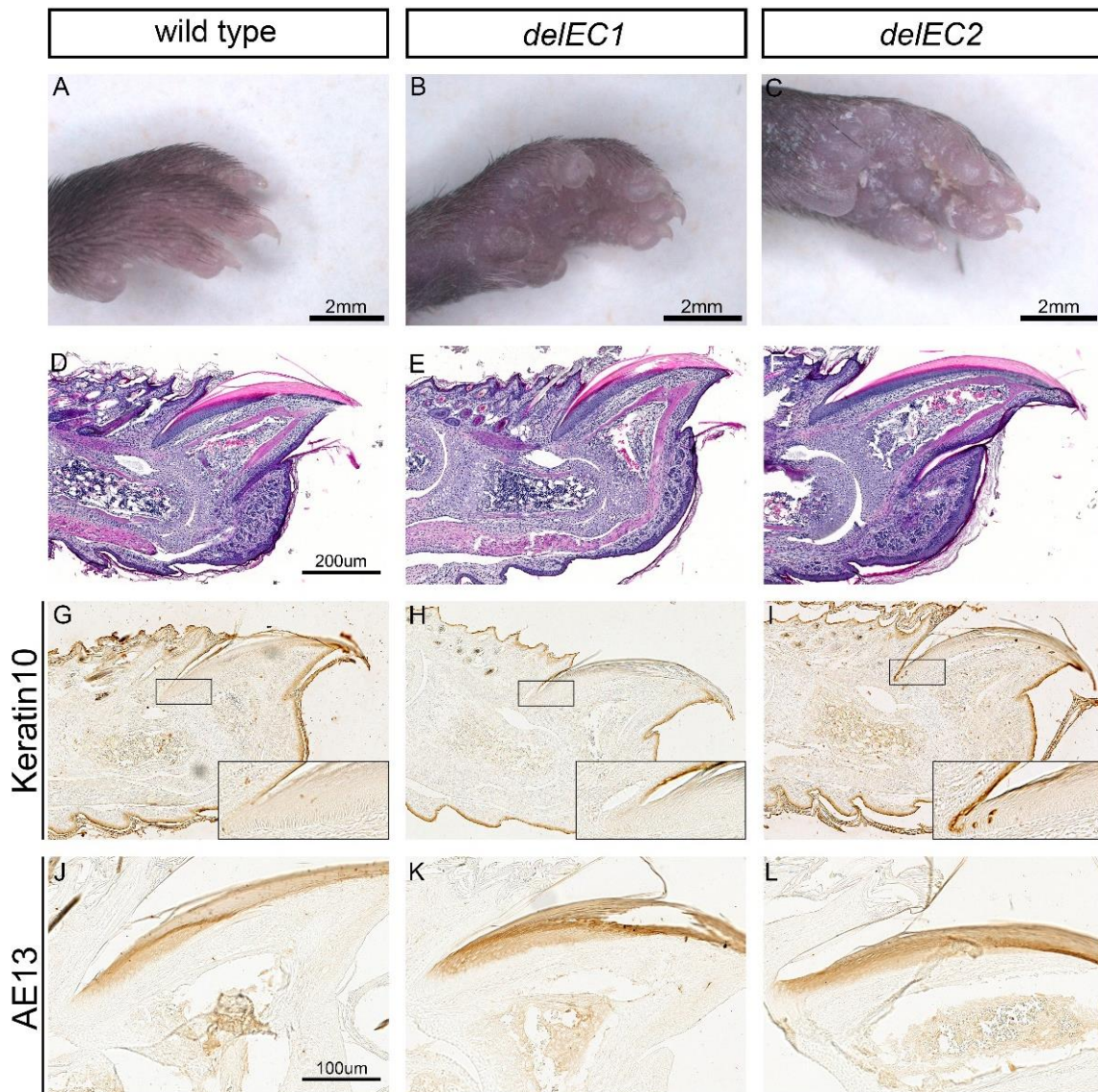


Figure 35. Phenotypic analysis of *delEC1* and *delEC2* mutant mice. **A, B** and **C** show images of the forelimb paws of P9 WT and homozygous *delEC1* and *delEC2* mice (as indicated at the top). Visual inspection of these forelimbs failed to reveal any phenotypic abnormality. **D-F** hematoxylin-eosin stained longitudinal sections of the digit tips showed no alteration in the anatomy of the nail organ. Immunohistochemistry analysis with α Krt10 antibody (**G-I**) showed some positive keratinocytes of the nail matrix exclusively in *delEC2* homozygous animals (inset in **I**). Immunohistochemistry analysis with AE13 antibody (**J-L**) failed to reveal any difference between WT and homozygous *delEC1* and *delEC2* mutants.

Generation and analyses of *del(EC1-EC2)* and *HoxCKO/del(EC1-EC2)* mutant mice

Recent investigations have emphasized that enhancers can be functionally redundant in the regulation of genes (Frankel et al., 2010; Montavon et al., 2011; Osterwalder et al., 2018). In this context, abolishing the function of one of the enhancers

participating in a cis-regulatory complex is likely to have a negligible effect in the expression of a target gene or set of target genes.

Hence, we considered that *EC1* and *EC2* could act redundantly in the regulation of *Hoxc* genes. To address this hypothesis, we used the centromeric gRNA used to generate *delEC1* mice (yellow arrow) and telomeric gRNA used to generate *delEC2* mice to excise, in mouse zygotes, the 86kb genomic region containing *EC1*, *EC2* and the genomic region in between (Fig. 36A). The mutant mouse line carrying this mutation was termed *del(EC1-EC2)*.

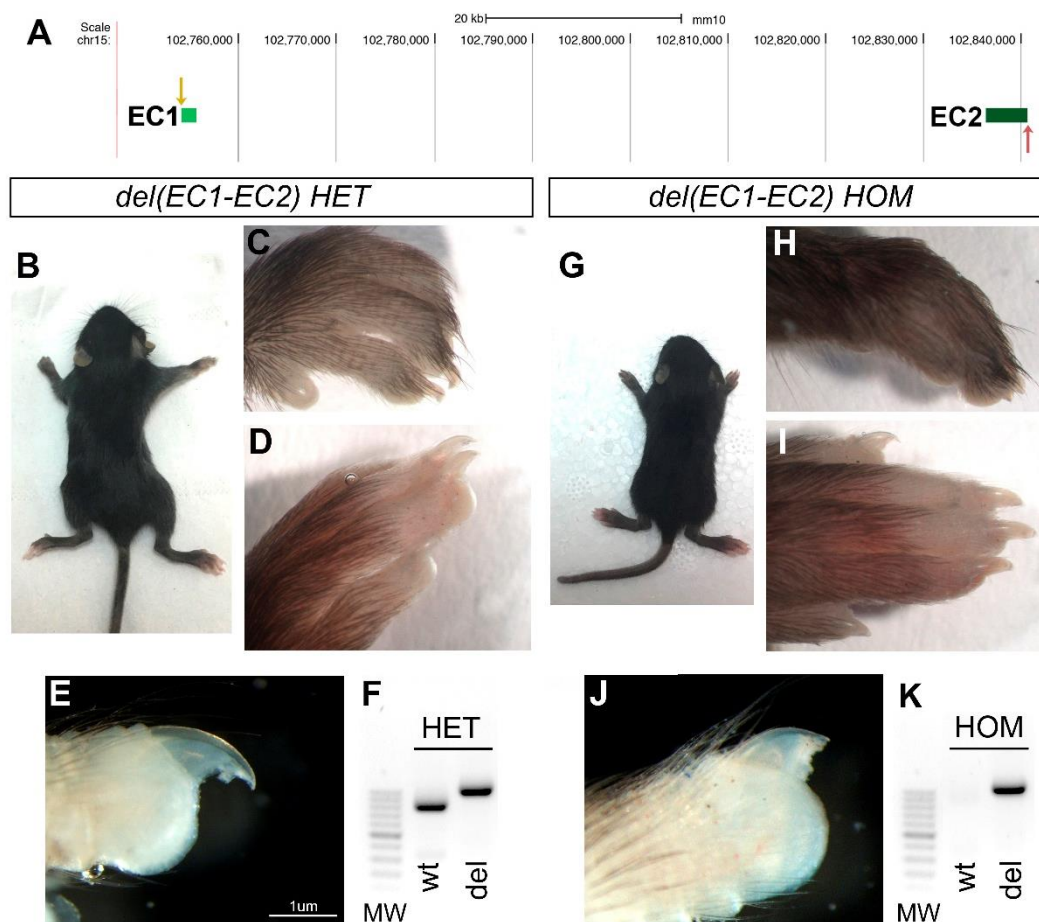


Figure 36. Generation of *del(EC1-EC2)* mice. **A:** the 3' gRNA used to generate *del(EC1)* mice (yellow arrow) and the 5' gRNA used to generate *del(EC2)* mice (red arrow) were used conjointly to excise the 86kb genomic region containing *EC1*, *EC2* and the intervening genomic region. **B** and **G** show the overall appearance of P14 heterozygous (**B**) and homozygous (**G**) mice for the *del(EC1-EC2)* deletion. Digits in **C**, **H** and **D**, **I** are from forelimbs and hindlimbs, respectively, of heterozygous and homozygous *del(EC1-EC2)* mutants. **E**, **J**: A close comparison of the digit tips of heterozygous and homozygous *del(EC1-EC2)* mutants shows a mild nail hypoplasia in homozygous animals. **F**, **K**: PCR genotyping analysis of a *del(EC1-EC2)* heterozygous mutant and a *del(EC1-EC2)* homozygous mutant with a 100bp MW marker. The size of the PCR product of the wild type allele is 780bp, of the deletion allele is 953bp.

The *del(EC1-EC2)* mutant line was generated with the Alt-R® CRISPR-Cas9 System from IDT (<https://eu.idtdna.com/pages/products/crispr-genome-editing/alt-r-crispr-cas9-system>). In this system, the crRNA:tracrRNA duplex is combined with the Alt-R® Cas9 Nuclease 3NLS (IDT) to form the ribonucleoprotein (RNP) complex. Once the RNP complex was formed, it was electroporated in C57BL6 zygotes.

Homozygous (HOM) *del(EC1-EC2)* mutants appeared smaller than their heterozygous (HET) littermates (Fig. 36B, G). We didn't observe any clear alteration in the hair of P14 HOM *del(EC1-EC2)* mutants. Notably, the nails of *del(EC1-EC2)* HOMs were apparently less developed than HET littermates, particularly in the forelimb digits (Fig. 36E, J). We decided to study this condition in more detail in longitudinal digit sections (Fig. 37).

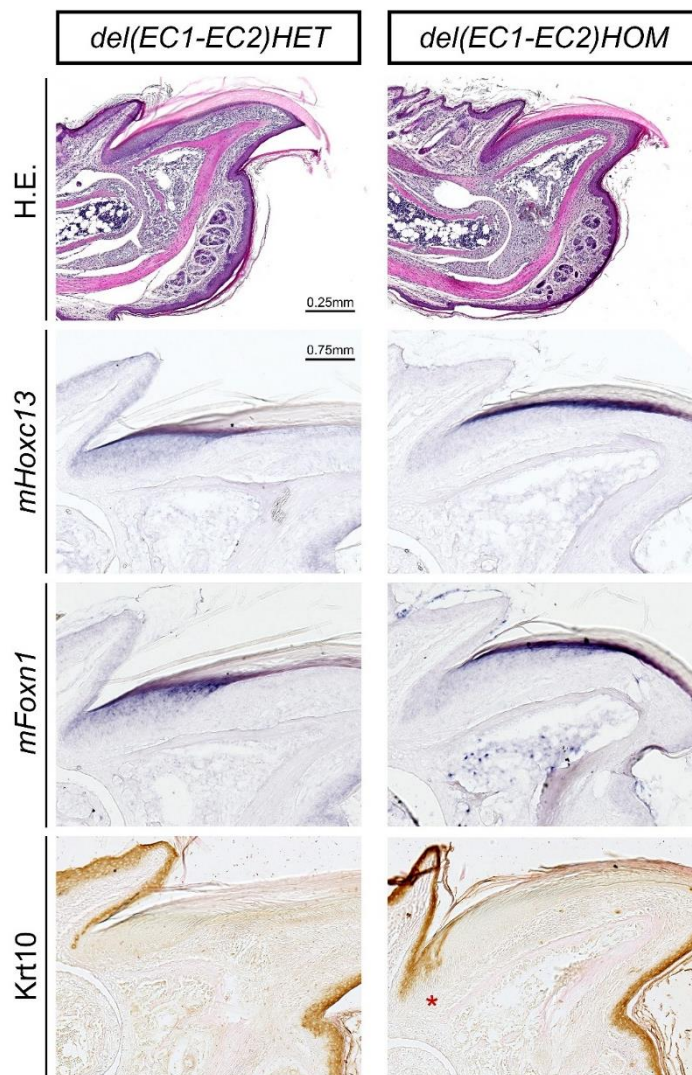


Figure 37. Histological and molecular characterization of *del(EC1-EC2)* HET and HOM forelimb digit tips. Hematoxylin-Eosin staining of longitudinal sections of HET and HOM P14 digits showing normal morphology (top row). ISH for *Hoxc13* and *Foxn1* show reduced expression in homozygous *del(EC1-EC2)* mutants in comparison to heterozygous littermates (middle rows). Staining with α Krt10 antibody revealed ectopic expression of this keratin in the proximal nail matrix of homozygous *del(EC1-EC2)* mutants (bottom row).

This phenotype was explained by the downregulation of *Hoxc13* and *Foxn1* in the nail developing region of *del(EC1-EC2)* HOM mutants in comparison to HET littermates (Fig. 37, middle rows). Of note, the epithelium of the ventral portion of the proximal nail fold of HOM *del(EC1-EC2)* mutants appeared thicker than in HET littermates. These epithelial differences could be connected to the populations of cells in the nail matrix of *del(EC1-EC2)* HOM mutants that are ectopically expressing Krt10 (Fig. 37, red asterisk).

Importantly, the overall development of the nail in *del(EC1-EC2)* HOM mutants is seemingly correct and the expression of *Hoxc13* is not completely abolished in the nail matrix of these animals (Fig. 37). Thus, we considered studying the phenotypic effect of the *EC1-EC2* deletion in a sensitized genetic background carrying and heterozygous deletion of the presumptive target genes. Therefore, we crossed animals from *del(EC1-EC2)* line with *HoxCKO* line to generate transheterozygous *HoxCKO/del(EC1-EC2)* mutants.

We obtained 5 out of 11 transheterozygous *HoxCKO/del(EC1-EC2)* mutants in 2 litters, which is above the expected mendelian rate, indicating no viability problems. *HoxCKO/del(EC1-EC2)* mutants were detected shortly after birth because of the lack of hair (Fig. 38A, B), reminiscent of the phenotype of *Hoxc13* homozygous mutants (Godwin and Capecchi, 1998). P1 *HoxCKO/+* mice presented normal nail plates (Fig. 38 C', D'), evidenced by the light reflection of condensed hard Keratins, a condition that was not observed in *HoxCKO/del(EC1-EC2)* littermates (Fig. 38 E', F').

Hematoxylin-eosin staining of longitudinally sectioned digits revealed that the development of the nail was impaired in P1 *HoxCKO/del(EC1-EC2)* mutants (Fig. 38G', H', I', J'). The proximal nail fold was less acute and the nail plate and the nail bed of these mutants were not distinguished (Fig. 38I', J'). To assess if the nail and hair phenotype is a developmental delay, further investigation in adult mice could be carried out.

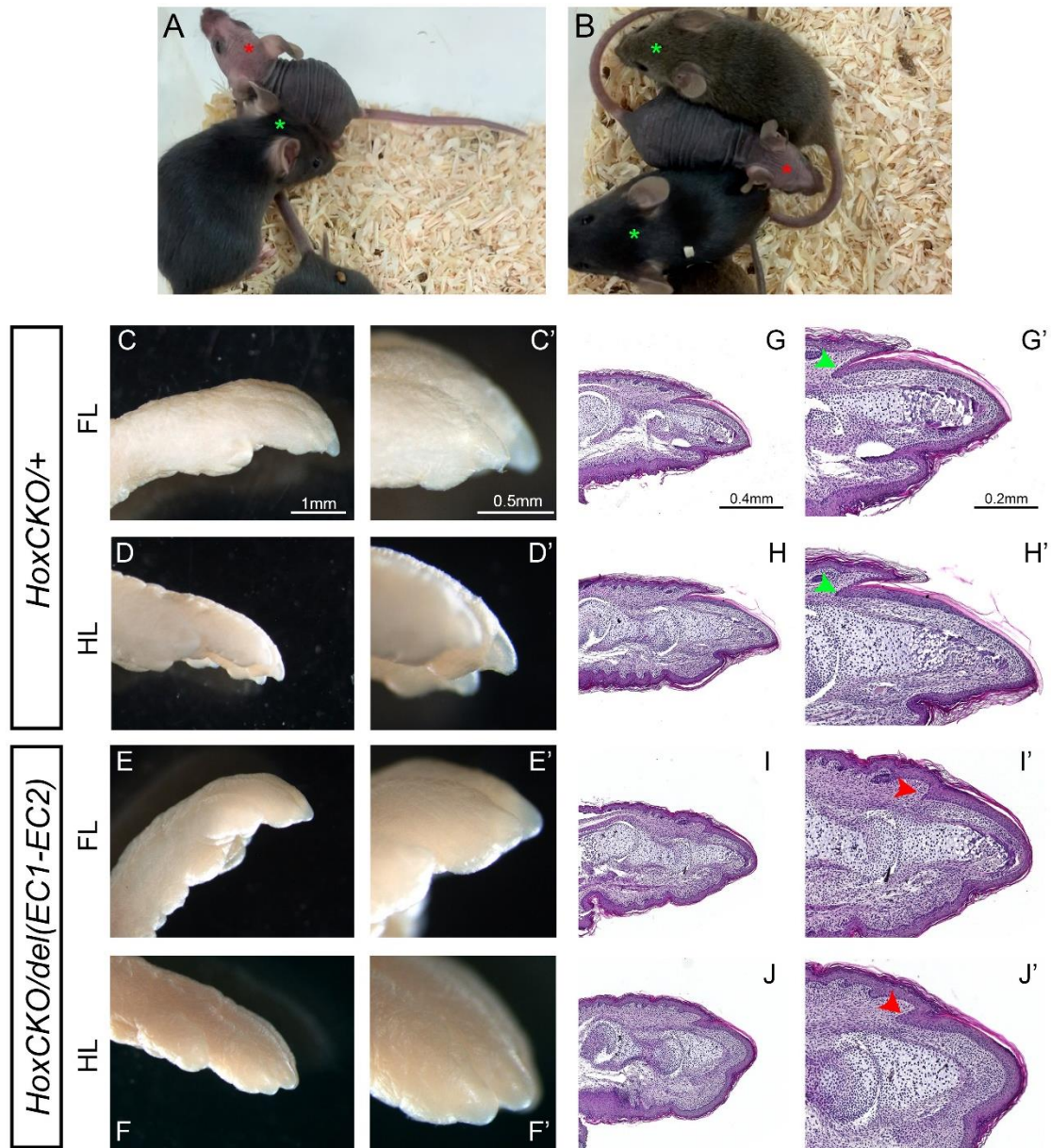


Figure 38. Evaluation of the phenotype of transheterozygous *HoxCKO/del(EC1-EC2)* mutants. **A-B:** 3-weeks-old *HoxCKO/del(EC1-EC2)* transheterozygous mutants (red asterisks) are clearly distinguished from control littermates (green asterisks) because of the dramatic loss of external hair. **C-F':** Visual observation reveals the absence of the nail plate both in FL and HL of P1 *HoxCKO/del(EC1-EC2)* transheterozygous. **(G-J'):** Hematoxylin-eosin staining of longitudinal sections of the digit tips confirms that the development of the nail is clearly affected in *HoxCKO/del(EC1-EC2)* mice as evidenced by the poorly developed nail proximal fold (green arrowheads) compared with *HoxCKO* heterozygous littermates (red arrowheads). Note also that the hair follicles close to the digit tip in *HoxCKO/del(EC1-EC2)* mice appear slightly less developed than in *HoxCKO* heterozygous. In **C-J**, dorsal is to the top, distal is to the right.

In summary, we provide evidence that enhancers located in a 86kb region spanning from the 5' end of *EC1* to the 3' end of *EC2* are regulating the expression of *Hoxc* genes in the ectoderm. Our interpretation of the results is that the correct expression of *Hoxc* genes in the ectoderm, driven by enhancers located 5' to the *HoxC* cluster, is required for the development of the hair and the nail. Furthermore, our experiments point to the existence of a threshold of *Hoxc* gene expression in ectoderm cells, below which the development of the hair and the nail is highly affected.



DISCUSSION

DISCUSSION

Here, to extend our knowledge on the mechanisms regulating the orderly and progressive differentiation of an organ, the limb, we have generated the temporal transcriptional profiles of the AER and of the subjacent mesoderm, separately but simultaneously. These transcriptomic datasets have shed light on expression profiles driving the transition along the different proximo-distal specification states and are a valuable resource for further investigations on limb development, including the interactions between the ectoderm and mesoderm components.

The temporal expression profile of the distal limb bud ectoderm revealed the collinear activation of *Hoxc* genes, a result that we have validated by in situ hybridization. Based on this observation we have investigated the biological meaning and transcriptional regulation of *Hoxc* genes in the limb ectoderm and specifically in the development of the hair and the nail.

Gene expression profiles associated with the progressive specification of the three PD limb segments

One subject of intense debate in the limb development field is how the different limb segments are progressively specified. Several PD specification models have been coined since the discovery of the limb truncation phenotypes observed after AER removal (Saunders, 1948). The first and most influential one was the Progress Zone model devised by Wolpert and collaborators (Summerbell et al., 1973). In this model, the limb progenitor cells are progressively specified to form more distal structures while remaining in a distal region under the influence of the AER, the so-called progress zone. More recently, a series of alternative models have been proposed to explain PD limb specification.

A decisive point that separates these models in two categories is whether the AER exerts an instructive or a permissive influence on the subjacent limb progenitors. Elegant tissue recombination studies in which the ectoderm and mesoderm from different stages, limb types or even different species were interchanged concluded that the AER plays a permissive role in mesenchymal differentiation. In all of these recombination experiments still a normal limb formed, indicating that AERs of distinct developmental age and origin

are functionally equivalent disregarding clear differences in morphology and gene expression (Fernandez-Teran et al., 1999; Kuhlman and Niswander, 1997; Rubin and Saunders, 1972; Zwilling, 1959). Thus, the AER provides an adequate environment necessary for the development of the whole potential of the limb progenitor cells; the AER does not alter the differentiation of the mesoderm but enables it to develop its intrinsic program. This fits nicely with the description of a permissive interaction.

This view was challenged by the phenotypes of the conditional deletion of AER-*Fgfs* in the limb ectoderm that were considered to support an instructive role of the AER. Thus, the genetic removal of a significant amount of AER-*Fgfs* after their initial activation, that is after a transient initial period of *Fgf* expression, yielded highly hypoplastic limbs that, surprisingly, included the whole PD axis. This result was surprising because, based on the AER extirpation experiments, a truncation along the PD axis was anticipated (Mariani et al., 2008; Sun et al., 2002). Because the expression domain of *Meis1* was distally expanded in these mutants, the AER-*Fgfs* were considered necessary to instruct distal fates in the limb bud. In the early limb bud, it is accepted that RA has to be cleared in the distal limb bud for the correct specification from the elbow to the digits, a role associated to the Fgf-dependent induction of *Cyp26b1* (Cunningham and Duester, 2015; Mercader et al., 2000; Probst et al., 2011). In support of this notion, *Cyp26b1* mutants present severely malformed limbs, in which the stylopod is fused to the zeugopod and the autopod is poorly developed (Yashiro et al., 2004).

If the AER function is instructive, why do the AER-exchange experiments work? Late AERs expressing higher levels of *Fgfs* should lead to the premature termination of limb outgrowth if transplanted over younger mesoderms. A possible explanation is that the AER is a very malleable structure that rapidly responds to mesodermal signals; an AER transplanted over a mesoderm of different developmental age would rapidly adapt to the new situation. In fact, it has been demonstrated, that blocks of young distal mesoderm cells, transplanted under the AER of older host limb buds causes the prolongation of *Fgf8* expression in the host AER accordingly to the age of the grafted mesoderm (Saiz-Lopez et al., 2015). In the present work, we aimed to clarify the complex gene regulatory networks specifying the different limb PD segments. Thus, our goal was to identify the gene expression signatures specific of the progenitors of the stylopod, the zeugopod and the autopod. To this end, we generated the transcriptome of the distal limb

progenitors in four successive stages selected to capture the progression through the different PD fates (Fig. 13).

A preliminary analysis confirmed the quality and reproducibility of our transcriptomic datasets, except for a minimal contamination in one of our samples. Replicate samples grouped together and both PCA and HCA analysis separated the samples by tissue (ectoderm vs mesoderm) and by stage (developmental time). GO enrichment analysis of the top contributing genes in the separation of samples by the tissue factor was enriched in categories associated with ectoderm/epidermal development. This finding reflects the presence of a set of genes, such as keratins, that are exclusive of the ectoderm while there are less genes specific of the undifferentiated limb progenitors. GO analysis of the top contributing genes in the separation of samples by stage showed significant enrichment of categories associated to limb development either ectodermal or mesodermal.

To focus on the question of how the different limb segments are progressively specified, we decided to drive differential gene expression analyses on the mesoderm samples. With this approach, we retrieved 3,858 MES-DEGs.

Seeking for gene expression signatures specific of the early limb progenitors (E9.5), we found *Hox* genes as a salient component (Fig. 17, Fig. 23A). Several 3' *Hox* genes from clusters *HoxA*, *HoxC* and *HoxD* and *Hoxb2-9* genes showed a peak of expression at E9.5 in distal mesoderm cells in accordance with previous reports (Cohn et al., 1997; Minguillon et al., 2012). Some of these *Hox* genes remain expressed in the proximal limb bud between E10.5 and E11.5 (Burke et al., 1995; Nelson et al., 1996). These findings demonstrate that *Hox* genes 3' to paralogy group 9, characteristic of the expression profile of the stylopod, are part of the expression profile characteristic of E9.5 limb progenitors.

The expression profile of the E9.5 progenitors is also characterized by the expression of the pluripotency-associated *Lin28* genes that rapidly vanish at E10.5. Recent data revealed that *Hoxb13* and *Hoxc13* genes terminate the expansion of the tail bud progenitors, at least in part by inhibiting the expression of *Lin28* genes (Aires et al., 2019). However, in the limb bud, it is likely that the operating regulatory mechanism is different since *Hox13* paralogs (in this case *Hoxa13* and *Hoxd13*) and *Lin28* genes do not display complementary patterns of gene expression, as would be expected if *Hox13* genes

repressed *Lin28a* and/or *Lin28b*, in the limb bud. Therefore, it is possible that a clearance of *Lin28* genes is needed for the activation of *Hox13* genes and subsequent specification of the autopod.

Concentrating on TF genes as responsible of cell identity, we analyzed those with an expression peak in each of the developmental stages analyzed. Among the considerable amount of TF genes peaking at E9.5, we found the genes known to be associated with the development of the proximal limb parts. These included *Irx* and *Pbx* genes, which have been associated to the development of the stylopod and whose mutation results in developmental defects in the proximal limb segment (Capellini, 2006; Li et al., 2014). *Alx1* and *Emx2*, known to interact in a signaling network with *Pbx1* (Capellini et al., 2010), also showed their maximum expression at E9.5. The best markers available for the stylopod, *Meis1* and *Meis2*, and other genes responsive to retinoic acid (which has been considered as the proximal influence specifying the stylopod) also shared this expression profile (Capdevila et al., 1999; Capellini et al., 2010; Cunningham and Duester, 2015; Kruse et al., 2008; Lee et al., 2004; Mercader et al., 2000). Together, these results indicate that E9.5 distal mesodermal cells are specified to the stylopod and that they are under RA signaling. Thus, the previously mentioned 3' *Hox* genes and *Hoxb2-9* genes could be considered as part of the specific transcriptional profile of the stylopod progenitors.

When we concentrated on TF genes with a peak of expression at E10.5 we found a set of genes associated to the development of the distal limb parts. These included *Sall1*, that acts as a modulator of *Hox* genes in the specification of autopod cells (Kawakami et al., 2009), *Zic2* which mutation presents a disorganized skeletal formula in the proximal autopod and *Lmo2*, a gene expressed in the limb subAER mesoderm between E10.5 and E11.5 (Kenny et al., 1998) that can be activated by 5' *Hox* (Calero-Nieto et al., 2013). *Ankrd6* and *Kank2*, two genes coding for proteins with ankyrin domains and associated with cell adhesion properties (Bennett and Healy, 2009) also peaked at E10.5. This was interesting as it has been proposed that changes in cell adhesion properties, some of them under *Hox* control, underly the progression along the PD developmental program (Saiz-Lopez et al., 2015; Stadler et al., 2001). Although not peaking in this stage, we also found that *Hoxa13* and *Hoxd13* were activated at E10.5 indicating initiation of the autopod program. Collectively, these data support the notion that the specification of autopod progenitors has started in the distal E10.5 mesoderm cells.

We can speculate that in the 150um of E9.5 distal mesoderm not only lie cells specified to form the stylopod, but also zeugopod progenitors. In fact, previous reports and our RNAseq data show mild expression of *Hoxa11*, the best available marker of the zeugopod progenitors at later stages (Mercader et al., 2009; Nelson et al., 1996). Moreover, in our WMISH experiments we didn't detect transcripts of *Meis1* at the most distal tip of the E9.5 limb bud. Thus, it is reasonable to assume that the transition to a zeugopod developmental program has already started in some distal tip progenitors at E9.5.

Our results indicate that the transcriptomic profile of the early E9.5 limb progenitors corresponds to that of the stylopod but, according to *in situ* data, the zeugopod profile has already started at this stage. Huge changes occur between E9.5 and E10.5 leading to a transcriptomic profile of the E10.5 limb progenitors that include transcription factors considered typical of the autopod. A more detailed temporal analysis, including intermediate points between E9 and E10.5, would be required to confirm our interpretations. Also, single cell transcriptomic of the distal cell progenitors would be instrumental to clarify how this transition in specification occurred. This information has the potential to reconcile experimental evidence regarding the specification of the limb along the PD axis.

The gene expression dynamics of *Bmp2*, *Fgfs*, *Hoxa13* and *Rprm* shed light into the termination of the positive feed-back loop driving limb outgrowth

We have identified the dynamic expression of *Reprimo*, a tumor-suppressor gene implicated in p53-mediated cell cycle arrest (Ohki et al., 2000; Wichmann et al., 2016), in the limb bud. Remarkably, *Bmp2* and *Rprm* follow a similar temporal expression pattern. Though the expression domains of these two genes in the limb bud are difficult to associate with a direct regulation between *Bmp2* and *Rprm*, the observed similarities in temporal dynamics fits nicely with the implication of both genes in the same process in the limb bud, which could be the termination of the positive feed-back loop driving limb outgrowth.

Limb development depends on the dynamic progression of signaling interactions. The *Bmp* antagonist *Grem1* is a crucial node in these interactions. Initially *Bmp4* expression in the nascent limb bud (around E9) rapidly activates its antagonist *Grem1*, which by inhibiting BMP signaling protects the AER-Fgfs (Bénazet et al., 2009). *Bmp2*, *Bmp4* and *Bmp7* are expressed in the limb bud (Robert, 2007) and these are considered to modulate the AER-Fgfs for the correct development of the limb (Selever et al., 2004). In this context, the early induction of *Grem1* by *Bmp4* is considered crucial for the initiation of the Shh-*Grem1*-Fgf positive feedback loop necessary for further progression of limb development.

Verheyden and Sun proposed a model to explain the termination of this positive feedback loop based on the progressive increase of AER-Fgfs over time causing the decay of *Grem1*. Based on elegant conditional deletions of *Fibroblast Growth Factor Receptor 1* (*Fgfr1*) and *Fgfr2* and on exogenous application of FGF8, this model posits that the break of the Shh-*Grem1*-Fgf loop occurs when the level of AER-Fgfs is high enough to restrict the *Grem1* domain far from the AER (Verheyden and Sun, 2008). However, we have identified the maximum of AER-Fgf signaling activity at E10.5, validated by Fgf readouts *Dusp6* and *Spry2*, a stage too early to terminate the expansion of the limb progenitors, specially the autopod progenitors. Further experiments as the analysis of the dynamics of AER-Fgf proteins and the dynamics of the binding of these proteins to their receptors would be necessary to clarify this topic.

In a collaboration between the lab of Matthew Towers and our lab, we found evidence that an intrinsic program in distal limb mesenchyme cells progressively increases the expression of *Bmp* family members up to the point that *Grem1* cannot exert its protective function on AER-Fgfs (Pickering et al., 2018). Notably, this progressive intrinsic activation of *Bmp* genes could be mediated by the intrinsic activation of 5' *Hox* genes (Saiz-Lopez et al., 2015). Indeed, *Hoxa13* activates transcription from the *Bmp2* and *Bmp7* enhancer regions and associates with these enhancers in vivo (Knosp et al., 2004). In this context, when BMPs reach a certain expression level, AER-Fgfs are reduced, leading to the decay of the Shh-*Grem1*-Fgf loop. The expression dynamics that we observed in our transcriptomic analysis regarding *Bmp2* and also *Rprm* are fully concordant with this model developed in chick limb buds for the termination of limb bud outgrowth.

The colinear expression patterns of *Hoxc* genes in the ectoderm

We have identified a temporal collinear activation of the *HoxC* cluster in the limb ectoderm. First, this collinearity was clearly observed in the heatmap showing the expression of all *Hox* genes in our data, in which the progressive activation of more 5' members is observed as a diagonal of high expression moving across the cluster and stages. This observation was further corroborated in the analysis of the FPM values across the *HoxC* cluster that additionally showed what *Hoxc* genes and when had the highest levels of expression. *Hoxc5*, *Hoxc6* and *Hoxc8* were highly expressed in the E9.5 limb ectoderm samples and steadily downregulated between E9.5 and E12.5 while the opposite temporal expression profile was detected for *Hoxc12* and *Hoxc13*. *Hoxc11*, *Hoxc10*, *Hoxc9* and *Hoxc4* seemed to follow the expression trend of nearby gene family members but with lower expression levels across the analyzed stages. *Hox* clusters are the most densely packed gene regions in tetrapods (Darbellay et al., 2019) therefore, it could be the case that the recruitment of transcriptional machinery activating one of the notably expressed *Hoxc* genes affects neighboring *Hoxc*. In fact, experimental data analyzing the *HoxD* cluster demonstrated that when chromatin regions are unfolded to activate gene expression, the regions with similar chromatin states tend to physically interact (Noordermeer et al., 2011).

It is remarkable the fact that the temporal collinear activation of *Hoxc* genes in the limb ectoderm is occurring at the same moment as the temporal collinear activation of *Hoxd* genes. This observation suggests the speculative idea that ancestral regulatory elements may have been partially conserved in the *HoxC* locus and the *HoxD* locus, resulting in activation of *Hoxc* genes in ectodermal cells and the activation of *Hoxd* genes in limb mesoderm cells.

It should be noted that our RNAseq analysis of the *Hoxc* expression is restricted to the 150 distal microns although the WMISH seem to support that these gene expression dynamics are occurring in the whole limb bud ectoderm. In addition, the collinear activation of the *HoxC* cluster may not be specific of the ectoderm of the limb. Several reports had previously identified the expression of *Hoxc* genes in the embryonic ectoderm (Awgulewitsch, 2003; Godwin and Capecchi, 1998; Reid and Gaunt, 2002; Shang et al., 2002), but never with this temporal accuracy. The impact of the temporal colinear activation of *Hoxc* genes in the ectoderm is unknown. One possible explanation is that it

is necessary for the progressive specification of different ectodermal structures along the AP axis of the embryonic ectoderm. Nevertheless, the reporter activity experiments of the enhancers identified in this work show remarkable and specific patterns in the limb epidermis of late stage (E16.5) mouse embryos. These findings raise the following question: Is the limb ectoderm different from the rest of the ectoderm? At least, the epidermis of the autopod is distinct in that the digit tips bear the nails and, in the mouse, is also the site where the sweat glands are located.

The role of *Hoxc* genes in the development of the nail

Interestingly, the expression of *Hoxc12* and *Hoxc13* is confined first to the digit tip in E14.5 limbs and then to the nail organ. Since both *HoxCKO* and *Hoxc13* mutants have a nail phenotype, it seems reasonable to assume that the activation of the *Hoxc* genes in the ectoderm is involved in the generation of the specialized digit tips with nails, claws or hooves.

The reader of this thesis might be surprised that from an initial analysis studying the distal limb bud, a large portion of the data addressed in these pages is dedicated to the role of *Hoxc* genes in the development of the nail/claw, a tiny part of the limb. However, the reasons to study this ectodermal appendage are numerous. First, it is indeed, a part of the limb and its shape is clearly connected to the shape of the distal phalanx, what is observed when studying the morphology of claws/nails/hoofs and distal phalanges in different species (Hamrick, 2001), therefore, there must be a crosstalk between the limb mesoderm and the limb ectoderm responsible for this shape correlation. Secondly, the nail matrix contains a population of adult stem cells and the mechanisms regulating the establishment of this population of nail stem cells are not yet understood. And last but not least, Wnt signaling originated in the nail organ is considered necessary for the regeneration of the digit tip (Takeo et al., 2013). Digit tip regeneration is considered a only example of epimorphic regeneration in mammals together with the ear in rodents and the antlers in deer (Dolan et al., 2018). Epimorphic regeneration is mediated by the formation of a blastema, which is a transient structure comprised of proliferative undifferentiated cells that undergo pattern formation, morphogenesis, and differentiation to completely regenerate structures lost by amputation. Hence, explaining the

mechanisms necessary for the development of the nail are crucial to reach a better understanding of mammalian regeneration.

In our study we have revealed the central role of *Hoxc* genes in the development of the nail/claw. The complete loss of function of the *HoxC* cluster results in digit tips with little sign of keratinocyte differentiation specific of the nail/claw. It is worth mentioning that this phenotype could involve, at least partially, a developmental delay in the differentiation of the nail organ but the perinatal death of *HoxCKO* mutants precludes further analysis. Moreover, we have been intrigued by the slight phenotypic differences between *HoxCKO* FL and HL digit tips, as the latter displayed a slightly milder phenotype. This difference could possibly rely on the expression of additional *Hox* members in the HL ectoderm, if so, this would be an interesting topic to investigate.

The importance of *Hoxc13* in the development of the nail/claw/hoof has been clearly demonstrated with the generation of animal models in several species (Deng et al., 2019; Godwin and Capecchi, 1998; Han et al., 2017) and the finding that *HOXC13* is a causative gene for the ectodermal dysplasia 9 (ECTD9) (Farooq et al., 2013; Khan et al., 2017; Lin et al., 2012). In all human and animal model cases reported so far, the loss of function mutation of *Hoxc13* leads to hypoplastic nails/claws/hooves and sparse or absent hair. In this work, we have analyzed the morphology and keratin expression patterns of *Hoxc13GFP* and *HoxCKO* mutants in the digit tip. Interestingly, immunostainings for Krt10, a marker of post-mitotic differentiated keratinocytes in the interfollicular skin, suggest that the loss of function of *Hoxc13* results in a milder version of the phenotype we reported in *HoxCKO* mutants. Hence, it is reasonable to assume that in the *Hoxc13* mutant condition other *Hoxc* genes, such as *Hoxc12*, are partially rescuing the function of *Hoxc13*. This wouldn't be surprising, given the known redundancy played by *Hox* genes in other developmental processes (Duboule, 2007; Kmita and Duboule, 2003; Zakany and Duboule, 2007).

Furthermore, *Hoxc* genes are known to play a role in the development of the hair follicle (Godwin and Capecchi, 1998; Tkatchenko et al., 2001; Yu et al., 2018) and in fact, the previously mentioned ECTD9 is a pure hair and nail ectodermal dysplasia, evidencing the implication of *Hoxc* cluster members in the development of these two ectodermal organs and suggesting common developmental programs. Hence, the gene

regulatory network in which *Hoxc* genes are involved in the development of not only the nail, but also the hair follicle is of potential interest for the hair regeneration field.

Previous investigations reported evidence of a regulatory cascade in which *Hoxc13* controls the activation of hair and nail associated Keratins through *Foxn1* (Potter et al., 2011). Moreover, *Msx2* and *Foxn1* mutants also exhibited hypoplastic nails and hair, a phenotype that was more dramatic in *Msx2;Foxn1* DKO mutants (Cai et al., 2009; Cai and Ma, 2011; Mecklenburg et al., 2004; Satokata et al., 2000). The explanation of these results was that *Msx2* and *Foxn1* were acting downstream of BMP signaling in the hair and the nail, which has been reported in several investigations to have a role in these ectodermal organs (Andl et al., 2004; Botchkarev et al., 1999; Leung et al., 2014; Mou et al., 2006). To get some insights into the implication of *Hoxc* genes in this gene regulatory network we studied the expression of components of the Bmp signaling pathway in *HoxCKO* mutants. Interestingly, we identified that *Bmp7* ligand and BMP targets *Foxn1* and *Msx2* were downregulated in the nail developing region of *HoxCKO* mutants. In addition, loss of function of *Hoxc* genes resulted in a disorganized expression pattern of *Bmp7* in the developing hair follicles. These results point at *Hoxc* genes acting upstream of BMP in the specification of the hair follicle and the nail developing region. Further experiments should be addressed in the future to confirm the epistatic relationship of these genes in the development of the hair and the nail.

In summary, we provide evidence of the implication of *Hoxc* genes in the development of the hair and the nail, in mammals. This brings an interesting question for future studies: How ancestral is the role of *Hoxc* genes in the development of the hair and the nail? Nails, claws and hair have appeared and disappeared throughout evolution and in ungulates, nails have been transformed to an extremely robust structure, surrounding the whole digit tip, the hoof. Hooves allow an extremely efficient cursorial locomotion and are considered a key evolutionary change in ungulates (Kardong V., 2007). The evaluation of the putative implication of *Hoxc* genes in the nail-claw-hoof transition would certainly be a fascinating investigation.

The regulation of *Hoxc* genes in the ectoderm

In developmental biology, the general consensus is that cis-regulatory regions and a combination of trans-factors binding these regulatory regions are responsible for the activation of a developmental gene, in a group of cells at a certain moment. Thus, we decided to look for putative regulatory regions driving the expression of *Hoxc* genes in the limb ectoderm.

It is worth mentioning that, the expression of *Hoxd* genes in the specification of the trunk segments is driven by regulatory regions inside the *HoxD* cluster and the cooption of these genes in the development of limbs is considered to be mediated by the appearance of distant regulatory regions to the cluster (Montavon et al., 2011; Soshnikova et al., 2013). Therefore, it seems reasonable to assume that a similar situation occurred to recruit *Hoxc* genes to the ectoderm. In addition, the observation that a transcript containing the 3' UTR region of *Hoxc4* conserved in the *HoxCKO* allele was upregulated, added support to our hypothesis. Accordingly, we identified two open chromatin conserved regions, termed *EC1* and *EC2*, located 165kb and 81kb respectively 5' from the *HoxC* cluster. When evaluated together, *EC1* and *EC2*, proved to drive reporter activity in broad regions of the head, tail and distal limb bud ectoderm. Also, in epidermal derivatives such as the whiskers, hair follicles and the nail. Importantly, *EC1-EC2* reporter activity was also observed in the neural tube, what could be linked to the expression of *Hoxc* genes in motoneurons (Dasen et al., 2003).

When evaluated individually, the *EC1* pattern of activity in the limb ectoderm of E16.5 embryos was solid up to the distal zeugopod region where it gradually restricted to hair follicles that were the only epidermal derivative observed in the rest of the limb ectoderm. When evaluated individually, the *EC2* pattern of activity in the limb was restricted to spotted regions in the digits, including the nail matrix. Nicely, most of the lacZ stained tissues with the *EC1* and *EC2* reporter constructs associate with domains of *Hoxc* gene expression. The relatively sharp transition at the zeugopod level of the pattern of activity of *EC1* suggests a temporal wave to progressively specify ectodermal structures that would be interesting to examine. Of note, a detailed study in LacZ-stained tissue sections could be considered to evaluate if *EC1* and *EC2* are capable of driving reporter activity in internal organs.

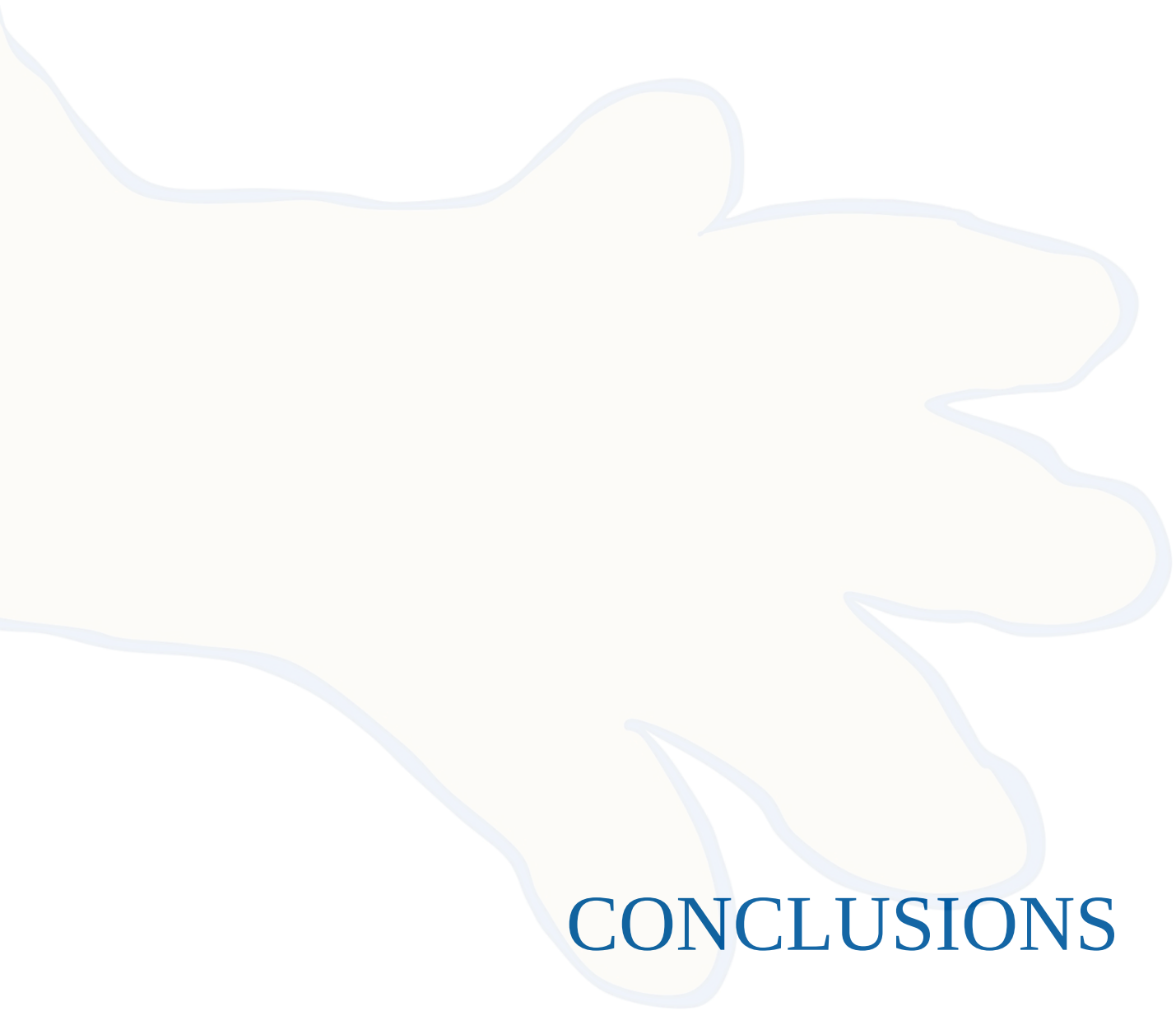
To evaluate the functional relevance of *EC1* and *EC2* regions, we used the CRISPR-Cas9 technology to delete them. Homozygous mutants for the individual deletion of each of these regulatory regions, termed *delEC1* and *delEC2*, were viable and fertile and didn't show any obvious phenotype. Nevertheless, we observed a mild alteration in *delEC2* mutants consisting in some proximal nail matrix cells expressing Krt10, a condition not observed in wild type littermates. This finding caught our attention, as in *Hoxc13* mutants Krt10 is also abnormally expressed in suprabasal layers of the proximal nail matrix.

Given the mild phenotype of the individual deletions we decided to delete the *EC1-EC2* genomic region, to clarify if the identified regulatory regions have a redundant function in the expression of *Hoxc* genes. Interestingly, homozygous *del(EC1-EC2)* mutants showed less developed nails associated with a downregulation of *Hoxc13* and *Foxn1* in the nail matrix. We also observed many cells in the proximal nail matrix of *del(EC1-EC2)* mice expressing Krt10, which reflects a defect in the differentiation of the keratinocytes in the proximal nail matrix, similar to the mutation of *Hoxc13*. It is worth mentioning that we cannot correlate the observed phenotype exclusively with the deletion of *EC1* and *EC2*, as the deletion also included the 81kb genomic region between the two enhancers. Our analysis demonstrates that the enhancer regions contained in this 86kb genomic region are not the only ones activating the expression of *Hoxc* genes in the ectoderm as low levels of expression of *Hoxc13* are still observed in *del(EC1-EC2)* homozygous mutants.

As the development of the hair of these animals showed no obvious alterations and the phenotype of the nail was quite mild, we decided to evaluate the consequences of combining the *HoxCKO* allele with the *del(EC1-EC2)* allele. Transheterozygous *del(EC1-EC2)/HoxCKO* mice showed a striking phenotype of absent nails and hairs. The aspect of these animals, resembled the hypotrichosis caused by *Hoxc13* mutation in mice and humans (Farooq et al., 2013; Godwin and Capecchi, 1998; Khan et al., 2017; Lin et al., 2012). The study of the digit tips of P1 *del(EC1-EC2)/HoxCKO*, a stage when the nail is clearly detected in healthy pups, revealed little evidence of the epithelial differentiation characteristic of nail development. The nail plate was not clearly detected, the proximal nail fold was less pronounced and the nail bed was not distinguished. The comparison of the distal tip histology of *del(EC1-EC2)/HoxCKO* and *HoxCKO* homozygous mutants indicated the formers display seemingly a milder phenotype version of the latter (similarly

to *Hoxc13* mutants), as in *HoxCKO* mutants the proximal nail fold is reduced to a slight groove and the epithelial thickening all around the digit tip is quite uniform.

Collectively, these findings provide compelling evidence of a gene dosage threshold of *Hoxc* genes, in the development of the hair and the nail. Below this threshold, presumptively below 50% considering that *HoxCKO* heterozygous mice are phenotypically normal, the development of the hair and the nail is impaired. An important difference between *del(EC1-EC2)/HoxCKO* transheterozygous and *HoxCKO* homozygous is that the former survive while the latter die perinatally because of defective lung development (Suemori and Noguchi, 2000). This strongly suggests that the *EC1* and *EC2* are probably specific enhancers of the ectoderm, at least not affecting vital organs. Moreover, we have not detected major viability problems in *del(EC1-EC2)/HoxCKO* and their behavior is indistinguishable from mice of the same litter, pointing to an absence of neural disorders. Of note, our studies point at *EC1* and *EC2* as genomic regions of interest to study in patients with PHNEDs.



CONCLUSIONS

1. We have generated the temporal transcriptional profiles of the AER and of the subjacent mesoderm, separately but simultaneously, during the development of the mouse forelimb. Our transcriptomic data provide a valuable resource to improve our understanding of limb development.

2. PCA and HCA showed that the biological replicates grouped together and that the samples separated first by tissue (ectoderm vs mesoderm) and then by stage (developmental time).

3. Differential gene expression and clustering on the mesoderm samples identified seven clusters according to the temporal gene expression patterns. Clusters showing downregulation over time included genes known to be involved in the specification of the stylopod (i.e. *Meis*) and in pluripotency (*Lin28*). Clusters showing upregulation over time included genes known to be involved in the specification of the autopod (5' *Hoxa* and *Hoxd*) and in the control of proliferation (i.e. *Bmp2* and *Rprm*).

4. The early limb bud progenitors (E9.5) are characterized by maximal expression of transcription factors known to play a role in the development of the stylopod. The expression of transcription factors specific of the autopod initiates in E10.5 limb progenitors.

5. Differential gene expression and clustering on the ectoderm samples showed that the peak of AER-Fgf activity occurs at E10.5, too early to support its implication in the termination of the positive Shh-Fgf loop.

6. The temporal expression profile of the distal limb bud ectoderm revealed the collinear activation of *Hoxc* genes, a result that we have validated by in situ hybridization.

7. *Hoxc12* and *Hoxc13* expression is restricted to the digit tip at E14.5 and persist in the nail organ at least until the newborn stage.

8. Mice null for the *HoxC* cluster lack any morphological or molecular evidence of the presence of the nail organ. *Hoxc13GFP* mutants show a milder nail phenotype.

9. BMP signaling acts downstream of *Hoxc* genes in the development of the nail.

10. ATAC-seq analysis revealed two putative regulatory regions, *EC1* and *EC2*, located 165kb and 81kb upstream of the *HoxC* cluster, respectively. When assayed in tandem, they drive reporter activity in most domains of *Hoxc* gene expression.

11. The individual deletion of *EC1* and *EC2* by CRISPR/Cas9 electroporation in mouse zygotes, yielded no obvious phenotype. However, local signs of impaired keratinocyte differentiation were detected in the proximal nail matrix of homozygous *EC2* mutants.

12. The conjoint deletion of both regulatory regions plus the intervening region *del(EC1-EC2)* resulted in hypoplastic nails with downregulation of *Hoxc13* and *Foxn1* in the nail matrix and aberrant keratinocyte differentiation.

13. Mice trans-heterozygous for the *del(EC1-EC2)* and *HoxCKO* alleles lacked nails and hair at least up to 2-3 weeks of postnatal development. This phenotype strongly suggested a dose effect of *EC1* and *EC2* in regulating *Hoxc* gene expression.



RESUMEN

Introducción

La extremidad de los vertebrados es un modelo ampliamente extendido para entender la organogénesis. Puesto que se trata de un órgano no vital, la extremidad de embriones de vertebrados permite una gran variedad de manipulaciones quirúrgicas o genéticas sin alterar la viabilidad del animal. Las extremidades emergen del flanco del embrión como un grupo de células del mesodermo de la placa lateral, cubiertas por el ectodermo. A esta estructura se le denomina “yema de la extremidad”. La adquisición de patrón y el crecimiento en la yema de la extremidad se organiza a lo largo de 3 ejes espaciales principales: Proximo-Distal (PD, desde la raíz de la extremidad hasta la punta de los dedos), Antero-Posterior (AP, desde el pulgar/hallux hasta el meñique) y Dorso-Ventral (DV, del dorso hasta la palma).

De especial interés es el proceso de especificación de los segmentos de la extremidad, en el eje próximo-distal. La extremidad de los tetrápodos se divide en 3 segmentos los cuales son, de proximal a distal, el estilopodio, el zeugopodio y el autopodio. El primero contiene 1 elemento esquelético, el segundo 2 y el tercero una fórmula de elementos esqueléticos muy variable a lo largo de las diferentes especies de tetrápodos. Esto último, se asocia a una amplia diversidad de cambios evolutivos que han permitido la adaptación de las extremidades para correr, saltar, nadar, volar o incluso manipular objetos.

El proceso progresivo de especificación de los 3 segmentos de la extremidad ha sido objeto de extenso estudio en el campo de la biología del desarrollo. Los diversos modelos que han aparecido para explicar este proceso se podrían dividir en dos categorías: la primera categoría, ejemplificada por el modelo de la zona de progreso (Summerbell et al., 1973), sostiene que existe algún tipo de mecanismo de control, tipo reloj, regulando intrínsecamente la progresiva especificación de las células de la extremidad; mientras que la segunda categoría, ejemplificada por el modelo de dos señales con intercalación (Mariani et al., 2008), sostiene que señales extrínsecas especifican los diferentes segmentos de la extremidad. El modelo mas aceptado actualmente sostiene la existencia de dos fases, una primera fase dependiente de señales (extrínseca) durante la que se especifica el estilopodio y una segunda fase en la que se activa un programa intrínseco

por el que se especifican progresivamente el zeugopodio y el autopodio (Saiz-Lopez et al., 2015). Probablemente la señal proximal durante la primera fase es el ácido retinoico, difundiendo desde el tronco del embrión. La señal distal son los FGFs que provienen del engrosamiento epitelial que se encuentra en el borde dorso-ventral de la yema de la extremidad. El nombre que se da a este engrosamiento epitelial es el de “Apical Ectodermal Ridge” (AER) y su importancia en el crecimiento y especificación de la extremidad ha sido revelada en diversos experimentos quirúrgicos en el embrión de pollo (Fernandez-Teran and Ros, 2008; Saunders, 1948). El AER envía FGFs al mesodermo subyacente manteniendo este conjunto de células en un estado proliferativo e indiferenciado.

En el proceso de especificación de los segmentos de la extremidad, es clave el papel de los genes selectores homeóticos o *Hox*. Esta familia de genes se encuentra dividida en 4 grupos o “clusters” en el genoma de los vertebrados. Estos son los clusters *HoxA*, *HoxB*, *HoxC* y *HoxD* (revisado en Duboule, 2007). Se considera que los genes que ocupan una posición mas 5’ de los clusters *HoxA* y *HoxD* son necesarios para la proliferación de los progenitores esqueléticos de la extremidad (Wellik and Capecchi, 2003; Zakany and Duboule, 1999). La relevancia de estos genes en el desarrollo de la extremidad se evidenció con la generación de ratones mutantes con pérdidas de función de estos genes. Los mutantes para la delección conjunta de *Hoxa13* y *Hoxd13* no desarrollan los dedos, la delección conjunta de *Hoxa11* y *Hoxd11* resulta en una drástica reducción del zeugopodio y los ratones mutantes con pérdida de función de los todos los genes *Hoxa* y *Hoxd* en la extremidad solo desarrollan un estilopodio reducido (Zakany and Duboule, 2007).

En el modelo de dos fases de especificación de los progenitores de la extremidad se sostiene que los genes 5’ *Hoxa,d* son elementos claves del programa de especificación intrínseca de la segunda fase (Saiz-Lopez et al., 2015). Al menos parte de la importancia de los genes 5’ *Hoxa,d* deriva de la regulación de moléculas de adhesión, resultando en la adquisición diferencial de información posicional de las células progenitores del zeugopodio y el autopodio. Notablemente, se considera que los genes *Hoxb* y *Hoxc* no participan en este proceso y que son dispensables para el desarrollo de la extremidad (Suemori and Noguchi, 2000).

Sin embargo, los genes *Hoxb* y *Hoxc* sí tienen una función en el desarrollo de otras estructuras. Esta tesis explora principalmente la función de los genes *Hoxc* en el desarrollo de estructuras ectodérmicas particularmente en el ectodermo de la extremidad.

Objetivos

Objetivo 1- Generación del transcriptoma temporal del AER durante el desarrollo de la extremidad de ratón. Incluyendo su validación, análisis e interpretación de resultados.

Objetivo 2- Generación del transcriptoma temporal del mesodermo subyacente al AER durante el desarrollo de la extremidad de ratón. Incluyendo su validación, análisis e interpretación de resultados.

Objetivo 3- Investigar la función y la regulación transcripcional de los genes *Hoxc* en el ectodermo de la extremidad

3.1- Comprender la función *Hoxc* en el ectodermo de la extremidad.

3.2- Desentrañar la regulación transcripcional de los genes *Hoxc* en el ectodermo de la extremidad.

Resultados y discusión

Análisis de las dinámicas de expresión génica en la yema de la extremidad

En este trabajo, hemos realizado un análisis del transcriptoma temporal de la yema de la extremidad con el fin de clarificar las complejas redes génicas que especifican sus diferentes segmentos. Hemos seleccionado 4 estadios clave del desarrollo de la extremidad del embrión de ratón: E9.5, E10.5, E11.5 y E12.5 y hemos diseccionado las 150 micras distales de extremidades anteriores. Las células en esta porción distal tienen el potencial para formar la extremidad desde el codo hasta la punta de los dedos en el estadio E9.5, el autopodio en E10.5 y solo las falanges más distales en E11.5 (Saiz-Lopez et al., 2015; Sato et al., 2007; Vargesson et al., 1997). Una vez diseccionada la parte distal, se separó, mediante una ligera digestión en tripsina, el ectodermo y el

mesodermo. Se obtuvieron 2 réplicas biológicas para cada estadio y se procesaron con el kit “Truseq® Stranded mRNA Library Prep Library Preparation” las muestras de ectodermo y mesodermo, por separado, para RNA-seq. El mapeo de las lecturas obtenidas en el proceso de secuenciación se realizó con el programa STAR 2.6.0c y el análisis de expresión diferencial se realizó con el programa DESeq2.

Considerando ≥ 1 FPKM como un valor de expresión significativo, de los 21.773 genes codificantes para proteína anotados, 12.572 genes (58%) se expresan en al menos 1 de nuestras muestras. El análisis de la expresión de genes específicos de ectodermo y mesodermo confirmó una separación correcta de los componentes ectodérmicos y mesodérmicos, con una leve contaminación en una de las muestras de ectodermo de E11.5. El análisis multivariable de componentes principales junto al análisis de clustering jerárquico mostró la agrupación de las réplicas y reveló una separación mucho mayor de las muestras en base al factor “tejido” que respecto al factor “estadio”.

En resumen, hemos generado el transcriptoma temporal de los progenitores de la extremidad, analizando los componentes ectodérmicos y mesodérmicos por separado. El análisis preliminar de nuestros datos demuestra la validez y calidad de los mismos y pone de manifiesto la relevancia de este material para el estudio de las dinámicas de expresión génica durante el desarrollo temprano de la extremidad.

Nuevas apreciaciones en la especificación de los progenitores de la extremidad

Para analizar la progresiva especificación de los progenitores de la extremidad, realizamos un análisis de expresión diferencial, tipo LRT, con todas las muestras de mesodermo. Los 3.855 genes diferencialmente expresados en las muestras de mesodermo se agruparon en 7 clusters, en base a su perfil de expresión temporal. A su vez, también realizamos experimentos de hibridación *in situ* para validar nuestros resultados.

Durante estos análisis observamos perfiles de expresión de genes ya descritos, como es el caso de *Meis1*, *Hoxd9* o *Cyp26b1*, que demuestran la validez de nuestros datos. Asimismo, hemos detectado altos niveles de expresión de factores de transcripción asociados al desarrollo del estilopodio (como *Irx3* y *Pbx1*) y de genes de pluripotencia (*Lin28a* y *Lin28b*) en los progenitores de la extremidad a E9.5 y expresados a muy bajo nivel en los estadios posteriores. Por otra parte, se detectó un notable incremento de la

expresión de genes asociados al desarrollo del autopodio a partir de E10.5 (como *Hoxa13* y *Hoxd13*) y a la regulación de la adhesión celular (*Kank2* y *Ankrd6*).

En conjunto, nuestro análisis transcriptómico de los progenitores de la extremidad muestra evidencias de la especificación de los progenitores del estilopodio a E9.5 y de la especificación de los progenitores de autopodio a E10.5.

Análisis de la expresión de genes implicados en la terminación de la extensión de los progenitores de la extremidad

También realizamos un análisis de expresión diferencial, tipo LRT, con todas las muestras de ectodermo. Los 2.444 genes diferencialmente expresados en las muestras de ectodermo se agruparon en 6 clusters, en base a su perfil de expresión temporal.

En este análisis encontramos a los genes *Fgf* expresados a su máximo nivel a E10.5. A su vez, el análisis de la expresión de *Dusp6* y *Spry2*, genes diana de la señalización de FGF (Chambers and Mason, 2000; Eblaghie et al., 2003), confirman el máximo de señalización de los AER-*Fgfs* en E10.5.

Notablemente, este resultado no concuerda con el modelo propuesto de terminación del patrón próximo-distal basado en un efecto inhibitorio de los *Fgfs* en el crecimiento de la extremidad (Verheyden and Sun, 2008), puesto que sería altamente improbable que la especificación de los progenitores de los segmentos de la extremidad hubiese terminado a E10.5.

Un dato que consideramos de interés es la coincidencia en los perfiles de expresión de *Bmp2* y *Rprm*, que también hemos validado con hibridación *in situ*. Un estudio reciente sostiene que el progresivo incremento autónomo de la expresión de los genes *Bmp* en la yema de la extremidad es responsable de la terminación de la extensión de los progenitores de la extremidad (Pickering et al., 2018). *Rprm* es un gen modulador del ciclo celular, por lo que esto apoyaría este modelo de terminación de la extensión de los progenitores de la extremidad.

La implicación de los genes *Hoxc* en el desarrollo de derivados ectodérmicos

Analizando las dinámicas de expresión génica en el transcriptoma del ectodermo de la extremidad observamos una activación colinear temporal de los genes *Hoxc*. Esto se confirmó mediante experimentos de hibridación *in situ* en la yema de la extremidad. Curiosamente, la expresión de los genes *Hoxc12* y *Hoxc13*, los genes situados más 5' en el cluster *HoxC*, se mantiene en estadios tardíos, siendo ésta confinada a la punta del dedo. En ratones recién nacidos, la expresión de *Hoxc12* y *Hoxc13* se observa en las células de la matriz de la uña, donde se encuentran las células madre adultas de este órgano ectodérmico. En todos los estadios analizados la expresión de *Hoxc13* es siempre mas elevada que la de *Hoxc12*.

Estas dinámicas de expresión fueron el motivo por el que decidimos estudiar las extremidades de ratones en los que el cluster *HoxC*, ha sido eliminado (*HoxCKO*), focalizándonos en los derivados ectodérmicos de estas. Notablemente, observamos que estos mutantes no presentan evidencias del desarrollo de la uña, tanto en una inspección visual externa como en tinciones de hematoxilina-eosina en secciones longitudinales de dedos incluidos en parafina. Este fenotipo se evidenció a nivel molecular mediante la inmunohistoquímica con anticuerpos específicos para diferentes Keratinas. En estos experimentos se observó como el programa de diferenciación de la uña no está actuando en la punta del dedo de los mutantes *HoxCKO*.

En estudios previos ya se hizo patente el rol de *Hoxc13* en el desarrollo de la uña, ya que los ratones mutantes para este gen presentan uñas frágiles y ausencia de pelo (Godwin and Capecchi, 1998) y mutaciones en el locus *HOXC13* están asociadas a la Displasia ectodérmica 9, una de las displasias ectodérmicas que solo afectan a la uña y al pelo (Farooq et al., 2013; Khan et al., 2017; Lin et al., 2012). Nuestros avances, en conjunto con estudios previos, ponen de manifiesto la importancia de los genes *Hoxc* en el desarrollo de la uña de los vertebrados y son de potencial interés para el diagnóstico de enfermedades congénitas afectando este órgano ectodérmico.

Análisis del control transcripcional de los genes *Hoxc* en el ectodermo de la extremidad

Nuestra hipótesis es que en la evolución de los tetrápodos, aparecieron regiones reguladoras dirigiendo la expresión de los genes *Hoxc* al ectodermo, resultando en el desarrollo de la uña/garra/pezuña.

Con este fin, realizamos un análisis del estado de la cromatina en el ectodermo del dedo de ratón a E14.5, mediante la tecnología de ATAC-Seq. Con los datos mapeados con Bowtie2, encontramos 2 regiones de cromatina abierta a 5' del cluster *HoxC* a las que denominamos *EC1* Y *EC2*. *EC1* resultó ser una región conservada en mamíferos, mientras que *EC2* resultó ser una región conservada en mamíferos placentarios. Es destacable que, mediante hibridación *in situ*, hemos observado que los ratones *HoxCKO* son capaces de expresar un transcrito con el 3'UTR remanente de *Hoxc4* (tras el evento de recombinación homóloga que generó el alelo *HoxCKO*) en el ectodermo de la extremidad, contribuyendo a la idea de que regiones situadas fuera del cluster *HoxC* dirigen esta expresión.

El potencial de *EC1* y *EC2* como regiones reguladoras fue evaluado mediante la generación de líneas reporteras transitorias en las que se insertó un constructo genético con *EC1*, *EC2* y *EC1+EC2* junto al gen reportero de la β -galactosidasa. En estos análisis ambas regiones reguladoras son capaces de dirigir la expresión reportera al ectodermo de la extremidad y a la uña, además de otras zonas donde los genes *Hoxc* se expresan. Notablemente, la mayoría de las zonas en las que se ha observado expresión reportera en los análisis de *EC1* y *EC2* (analizados conjuntamente o separados) pueden ser asociadas a la expresión de los genes *Hoxc*, como es el caso del folículo piloso. Por esto, consideramos que ambas regiones pueden estar actuando cooperativamente en la regulación de los genes *Hoxc*.

Para testar la función de estas regiones *in vivo*, hemos generado ratones mutantes con la delección de *EC1* (*delEC1*), *EC2* (*delEC2*) y la delección de ambas regiones reguladoras y el DNA intermedio (*del(EC1-EC2)*), mediante el uso de la tecnología de edición génica CRISPR-Cas9. Los ratones mutantes *delEC1* y *delEC2* no desarrollaron alteraciones fenotípicas destacables, ni problemas en la viabilidad o fertilidad. Sin embargo, se observó que los ratones homocigotos para *del(EC1-EC2)* eran más pequeños y con uñas menos desarrolladas. La alteración de las uñas de mutantes *del(EC1-EC2)* se

caracterizó mediante la tinción con hematoxilina-eosina y el análisis de expresión de *Hoxc13*, *Foxn1* y Keratina10. La expresión de *Hoxc13* y su mejor diana descrita *Foxn1* (Potter et al., 2011) resultó ser más baja en ratones homocigotos mutantes para *del(EC1-EC2)* en comparación con ratones heterocigotos para la mutación. A su vez, la alteración del patrón de Keratina10 en los queratinocitos de la uña de homocigotos *del(EC1-EC2)* evidenció el fenotipo estos mutantes.

Sin embargo, el desarrollo general de las uñas o del pelo, que también está regulado por la expresión ectodérmica de los genes *Hoxc* no está notablemente afectado en estos mutantes. Fue por esto por lo que decidimos estudiar el efecto de la mutación *del(EC1-EC2)* en un fondo genético sensibilizado, generando ratones transheterocigotos *HoxCKO/del(EC1-EC2)*. Estos mutantes se diferenciaron claramente de ratones control de la misma camada por su alopecia. Notablemente, observamos la ausencia de uñas en ratones recién nacidos *HoxCKO/del(EC1-EC2)* en tinciones de hematoxilina-eosina de secciones longitudinales.

En conjunto, nuestros análisis muestran evidencias del rol de los genes *Hoxc* en el desarrollo del pelo y la uña, además de la localización de regiones reguladoras a 5' del cluster *HoxC* implicadas en la activación de los genes *Hoxc* en el desarrollo del pelo y la uña.

Conclusiones

1. Hemos generado los perfiles transcripcionales temporales del AER y del mesodermo subyacente, por separado pero simultáneamente, durante el desarrollo de la extremidad anterior del ratón. Estos transcriptomas son un recurso valioso para mejorar nuestra comprensión del desarrollo de las extremidades.

2. El análisis de componentes principales y el análisis de clustering jerárquico mostraron la agrupación de las réplicas biológicas y la separación de las muestras primero por tejido (ectodermo vs mesodermo) y luego por estadio (tiempo de desarrollo).

3. Los análisis expresión génica diferencial y agrupación en las muestras de mesodermo identificaron siete clusters de acuerdo a los patrones temporales de expresión génica. Los clusters que mostraban una regulación negativa a lo largo del tiempo incluían genes asociados a la especificación del estilopodio (*i.e.* *Meis*) y a la pluripotencia (*Lin28*). Los clusters que mostraron regulación positiva a lo largo del tiempo incluyeron genes que están involucrados en la especificación del autopodio (5' *Hoxa* y *Hoxd*) y en el control de la proliferación (*i.e.*, *Bmp2* y *Rprm*).

4. Los progenitores tempranos de la yema de la extremidad (E9.5) se caracterizan por la máxima expresión de factores de transcripción asociados al desarrollo del estilopodio. Los factores de transcripción típicos del autopodio muestran niveles de expresión cercanos a su máximo, ya en E10.5.

5. La expresión diferencial de genes y la agrupación en las muestras de ectodermo mostraron que el pico de actividad de los AER-*Fgfs* ocurre en E10.5, demasiado temprano para respaldar su implicación en la terminación del bucle de retroalimentación positiva entre Shh y Fgf.

6. El perfil de expresión temporal del ectodermo en la parte distal de la extremidad reveló la activación colineal de los genes *Hoxc*, un resultado que hemos validado por hibridación *in situ*.

7. La expresión de *Hoxc12* y *Hoxc13* está restringida a la punta del dedo en E14.5 y persiste en la uña al menos hasta la etapa del recién nacido.

8. Los ratones nulos para los genes *Hoxc* carecen de evidencias morfológicas y moleculares de desarrollo de la uña, mientras que este fenotipo es más leve en los mutantes *Hoxc13GFP*.

9. La señalización de BMP está regulada por los genes *Hoxc* durante el desarrollo de la uña.

10. El análisis de ATAC-seq reveló dos regiones de cromatina accesible en el ectodermo de dedos en desarrollo, *EC1* y *EC2*, ubicadas 165 kb y 81 kb a 5' del cluster *HoxC*, respectivamente. Cuando se analizaron en conjunto, se demostró que son capaces de dirigir actividad reportera en la mayoría de los dominios de expresión de los genes *Hoxc*.

11. La eliminación individual de *EC1* y *EC2* mediante electroporación del sistema CRISPR/Cas9 en cigotos de ratón no produjo un fenotipo obvio. Sin embargo, se detectaron signos locales de alteración de la diferenciación de queratinocitos en la matriz de la uña en mutantes *delEC2* homocigotos.

12. La eliminación conjunta de las regiones reguladoras *EC1* y *EC2* y la región intermedia produjo un fenotipo leve restringido a la uña. Los ratones *del(EC1-EC2)* mostraron una regulación negativa de *Hoxc13* y *Foxn1* en la matriz de la uña, lo que resultó en una diferenciación de queratinocitos aberrante y uñas hipoplásicas.

13. Los ratones transheterocigotos para los alelos *del(EC1-EC2)* y *HoxCKO* no mostraron signos del desarrollo de uñas y cabello al menos hasta 2-3 semanas de desarrollo postnatal. Este fenotipo sugiere un efecto de dosis de *EC1* y *EC2* en la regulación de la expresión de los genes *Hoxc*.



REFERENCES

REFERENCES

- Ahn, Y., Sims, C., Logue, J.M., Weatherbee, S.D., Krumlauf, R., 2013. Lrp4 and Wise interplay controls the formation and patterning of mammary and other skin appendage placodes by modulating Wnt signaling. *Development* 140, 583–593. <https://doi.org/10.1242/dev.085118>
- Aires, R., de Lemos, L., Nóvoa, A., Jurberg, A.D., Mascrez, B., Duboule, D., Mallo, M., 2019. Tail Bud Progenitor Activity Relies on a Network Comprising Gdf11, Lin28, and Hox13 Genes. *Dev. Cell* 48, 383–395.e8. <https://doi.org/10.1016/j.devcel.2018.12.004>
- Allan, C.H., Fleckman, P., Fernandes, R.J., Hager, B., James, J., Wisecarver, Z., Kyle Satterstrom, F., Gutierrez, A., Norman, A., Pirrone, A., Underwood, R.A., Rubin, B.P., Zhang, M., Ramay, H.R., Clark, J.M., 2006. Tissue response and Msx1 expression after human fetal digit tip amputation in vitro. *Wound Repair Regen.* 14, 398–404. <https://doi.org/10.1111/j.1743-6109.2006.00139.x>
- Andl, T., Ahn, K., Kairo, A., Chu, E.Y., Wine-Lee, L., Reddy, S.T., Croft, N.J., Cebra-Thomas, J.A., Metzger, D., Chambon, P., Lyons, K.M., Mishina, Y., Seykora, J.T., Crenshaw, E.B., Millar, S.E., 2004. Epithelial Bmpr1a regulates differentiation and proliferation in postnatal hair follicles and is essential for tooth development. *Development* 131, 2257–2268. <https://doi.org/10.1242/dev.01125>
- Andrey, G., Montavon, T., Mascrez, B., Gonzalez, F., Noordermeer, D., Leleu, M., Trono, D., Spitz, F., Duboule, D., 2013. A Switch Between Topological Domains Underlies HoxD Genes Collinearity in Mouse Limbs. *Science* (80-.). 340. <https://doi.org/10.1038/nrg3207>
- Aoki, M., Kiyonari, H., Nakamura, H., Okamoto, H., 2008. R-spondin2 expression in the apical ectodermal ridge is essential for outgrowth and patterning in mouse limb development. *Dev. Growth Differ.* 50, 85–95. <https://doi.org/10.1111/j.1440-169X.2007.00978.x>
- Arnosti, D.N., Kulkarni, M.M., 2005. Transcriptional enhancers: Intelligent enhanceosomes or flexible billboards? *J. Cell. Biochem.* 94, 890–898. <https://doi.org/10.1002/jcb.20352>

- Awgulewitsch, A., 2003. Hox in hair growth and development. *Naturwissenschaften* 90, 193–211. <https://doi.org/10.1007/s00114-003-0417-4>
- Bastida, M.F., Sheth, R., Ros, M.A., 2009. A BMP-Shh negative-feedback loop restricts Shh expression during limb development. *Development* 136, 3779–3789. <https://doi.org/10.1242/dev.036418>
- Beccari, L., Yakushiji-Kaminatsui, N., Woltering, J.M., Necsulea, A., Lonfat, N., Rodríguez-Carballo, E., Mascrez, B., Yamamoto, S., Kuroiwa, A., Duboule, D., 2016. A role for HOX13 proteins in the regulatory switch between TADs at the HoxD locus. *Genes Dev.* 30, 1172–1186. <https://doi.org/10.1101/gad.281055.116>
- Beketaev, I., Kim, E.Y., Zhang, Y., Yu, W., Qian, L., Wang, J., 2014. Potentiation of Tbx5-mediated transactivation by SUMO conjugation and protein inhibitor of activated STAT 1 (PIAS1). *Int. J. Biochem. Cell Biol.* 50, 82–92. <https://doi.org/10.1016/j.biocel.2014.02.007>
- Bénazet, J.D., Bischofberger, M., Tiecke, E., Gonçalves, A., Martin, J.F., Zuniga, A., Naef, F., Zeller, R., 2009. A self-regulatory system of interlinked signaling feedback loops controls mouse limb patterning. *Science* (80-.). 323, 1050–1053. <https://doi.org/10.1126/science.1168755>
- Bennett, V., Healy, J., 2009. Membrane domains based on ankyrin and spectrin associated with cell-cell interactions. *Cold Spring Harb. Perspect. Biol.* 1, 1–17. <https://doi.org/10.1101/cshperspect.a003012>
- Berker, D.A.R. De, Baran, R., 2012. Science of the Nail Apparatus, in: Baran & Dawber's Diseases of the Nails and Their Management. pp. 1–50.
- Berlivet, S., Paquette, D., Langlais, D., Dostie, J., Kmita, M., 2013. Clustering of Tissue-Specific Sub-TADs Accompanies the Regulation of HoxA Genes in Developing Limbs. *PLoS Genet.* 9, 1–17. <https://doi.org/10.1371/journal.pgen.1004018>
- Biggs, L.C., Mikkola, M.L., 2014. Early inductive events in ectodermal appendage morphogenesis. *Semin. Cell Dev. Biol.* 25–26, 11–21. <https://doi.org/10.1016/j.semcdb.2014.01.007>
- Botchkarev, V.A., Botchkareva, N. V., Roth, W., Nakamura, M., Chen, L.-H., Herzog, W., Lindner, G., McMahon, J.A., Peters, C., Lauster, R., McMahon, A.P., Paus, R.,

1999. Noggin is a mesenchymally derived stimulator of hair-follicle induction. *Nat. Cell Biol.* 1, 158–164. <https://doi.org/10.1038/11078>
- Bragulla, H.H., Homberger, D.G., 2009. Structure and functions of keratin proteins in simple, stratified, keratinized and cornified epithelia. *J. Anat.* 214, 516–559. <https://doi.org/10.1111/j.1469-7580.2009.01066.x>
- Buas, M.F., Kabak, S., Kadesch, T., 2010. The notch effector Hey1 associates with myogenic target genes to repress myogenesis. *J. Biol. Chem.* 285, 1249–1258. <https://doi.org/10.1074/jbc.M109.046441>
- Buenrostro, J., Giresi, P.G., Chang, H.Y., Greenleaf, W.J., 2013. Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. *Nat. Methods* 10, 1213–1218.
- Buenrostro, J., Wu, B., Chang, H., Greenleaf, W., 2016. ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide. *Curr Protoc Mol Biol* 109, 1–21. <https://doi.org/10.1002/0471142727.mb2129s109.ATAC-seq>
- Bürglin, T.R., 1997. Analysis of TALE superclass homeobox genes (MEIS, PBC, KNOX, Iroquois, TGIF) reveals a novel domain conserved between plants and animals. *Nucl* 25, 4173–4180.
- Burke, A.C., Nelson, C.E., Morgan, B.A., Tabin, C., 1995. Hox genes and the evolution of vertebrate axial morphology. *Development* 121, 333–346. <https://doi.org/7768176>
- Cai, J., Lee, J., Kopan, R., Ma, L., 2009. Genetic interplays between Msx2 and Foxn1 are required for Notch1 expression and hair shaft differentiation. *Dev. Biol.* 326, 420–430. <https://doi.org/10.1016/j.ydbio.2008.11.021>
- Cai, J., Ma, L., 2011. Msx2 and Foxn1 regulate nail homeostasis. *Genesis* 49, 449–459. <https://doi.org/10.1002/dvg.20744>
- Calero-Nieto, F.J., Joshi, A., Bonadies, N., Kinston, S., Chan, W.I., Gudgin, E., Pridans, C., Landry, J.R., Kikuchi, J., Huntly, B.J., Gottgens, B., 2013. HOX-mediated LMO2 expression in embryonic mesoderm is recapitulated in acute leukaemias. *Oncogene* 32, 5471–5480. <https://doi.org/10.1038/onc.2013.175>
- Cameron, T.L., Belluoccio, D., Farlie, P.G., Brachvogel, B., Bateman, J.F., 2009. Global

- comparative transcriptome analysis of cartilage formation in vivo. *BMC Dev. Biol.* 9, 1–17. <https://doi.org/10.1186/1471-213X-9-20>
- Capdevila, J., Tsukui, T., Esteban, C.R., Zappavigna, V., Belmonte, J.C.I., 1999. Control of vertebrate limb outgrowth by the proximal factor *Meis2* and distal antagonism of BMPs by *Gremlin*. *Mol. Cell* 4, 839–849. [https://doi.org/10.1016/S1097-2765\(00\)80393-7](https://doi.org/10.1016/S1097-2765(00)80393-7)
- Capellini, T.D., 2006. *Pbx1/Pbx2* requirement for distal limb patterning is mediated by the hierarchical control of *Hox* gene spatial distribution and *Shh* expression. *Development* 133, 2263–2273. <https://doi.org/10.1242/dev.02395>
- Capellini, T.D., Vaccari, G., Ferretti, E., Fantini, S., He, M., Pellegrini, M., Quintana, L., Di Giacomo, G., Sharpe, J., Selleri, L., Zappavigna, V., 2010. Scapula development is governed by genetic interactions of *Pbx1* with its family members and with *Emx2* via their cooperative control of *Alx1*. *Development* 137, 2559–2569. <https://doi.org/10.1242/dev.048819>
- Casal, M.L., Lewis, J.R., Mauldin, E.A., Tardivel, A., Ingold, K., Favre, M., Paradies, F., Gaide, O., Schneider, P., 2007. Significant Correction of Disease after Postnatal Administration of Recombinant Ectodysplasin A in Canine X-Linked Ectodermal Dysplasia. *Am. J. Hum. Genet.* 81, 1050–1056. <https://doi.org/10.1086/521988>
- Celli, J., Duijf, P., Hamel, B.C.J., Bamshad, M., Kramer, B., Smits, A.P.T., Newbury-ecob, R., Hennekam, R.C.M., Buggenhout, G. Van, Haeringen, A. Van, Woods, C.G., Essen, A.J. Van, Waal, R. De, Vriend, G., Haber, D.A., Yang, A., Mckeen, F., Brunner, H.G., Bokhoven, H. Van, 1999. Heterozygous germline mutations in the *p53* homolog *p63* are the cause of EEC Syndrome. *Cell* 99, 143–153.
- Chambers, D., Mason, I., 2000. Expression of *sprouty2* during early development of the chick embryo is coincident with known sites of FGF signalling. *Mech. Dev.* 91, 361–364. [https://doi.org/10.1016/S0925-4773\(99\)00288-9](https://doi.org/10.1016/S0925-4773(99)00288-9)
- Cohn, M.J., Patel, K., Krumlauf, R., Wilkinson, D.G., Clarke, J.D.W., Tickle, C., 1997. *Hox9* genes and vertebrate limb specification. *Nature* 387, 97–100.
- Cong, L., Ran, F.A., Cox, D., Lin, S., Barretto, R., Hsu, P.D., Wu, X., Jiang, W., Marraffini, L. a, 2013. Cong, L., Ran, F. A., Cox, D., Lin, S., Barretto, R., Habib,

- N., ... Zhang, F. (2013). Multiplex Genome Engineering Using CRISPR/Cas Systems. *Science* (New York, N.Y.) 339, 819–823. <https://doi.org/10.1126/science.1231143>. Multiplex
- Cooper, K.L., Cooper, K.L., Hu, J.K., Berge, D., Fernandez-teran, M., Ros, M.A., Tabin, C.J., 2011. Initiation of Proximal-Distal Patterning in the Vertebrate Limb by Signals and Growth. *Science* (80-.). 1083, 1083–1087. <https://doi.org/10.1126/science.1199499>
- Costa, M.W., Lee, S., Furtado, M.B., Xin, L., Sparrow, D.B., Martinez, C.G., Dunwoodie, S.L., Kurtenbach, E., Mohun, T., Rosenthal, N., Harvey, R.P., 2011. Complex SUMO-1 regulation of cardiac transcription factor NKX2-5. *PLoS One* 6. <https://doi.org/10.1371/journal.pone.0024812>
- Cunningham, T.J., Chatzi, C., Sandell, L.L., Trainor, P.A., Duester, G., 2011. *Rdh10* Mutants Deficient in Limb Field Retinoic Acid Signaling Exhibit Normal Limb Patterning but Display Interdigital Webbing. *Dev. Dyn.* 240, 1142–1150. <https://doi.org/10.1177/1098300712437042>. Improving
- Cunningham, T.J., Duester, G., 2015. Mechanisms of retinoic acid signalling and its roles in organ and limb development. *Nat. Rev. Mol. Cell Biol.* 16, 110–123. <https://doi.org/10.1038/nrm3932>
- Darbellay, F., Bochaton, C., Lopez-Delisle, L., Mascrez, B., Tschopp, P., Delpretti, S., Zakany, J., Duboule, D., 2019. The constrained architecture of mammalian Hox gene clusters. *Proc. Natl. Acad. Sci. U. S. A.* 116, 13424–13433. <https://doi.org/10.1073/pnas.1904602116>
- Dasen, J.S., Liu, J.P., Jessell, T.M., 2003. Motor neuron columnar fate imposed by sequential phases of Hox-c activity. *Nature* 425, 926–933. <https://doi.org/10.1038/nature02051>
- Davis, A.P., Witte, D.P., Hsiu, M.H.-L., Potter, S.S., Capecchi, M.R., 1995. Absence of radius and ulna in mice lacking *hoxa-11* and *hoxd-11*. *Nature*.
- De Berker, D., Wojnarowska, F., Sviland, L., Westgate, G.E., Dawber, R.P.R., Leigh, I.M., 2000. Keratin expression in the normal nail unit: Markers of regional differentiation. *Br. J. Dermatol.* 142, 89–96. <https://doi.org/10.1046/j.1365-2133.2000.03246.x>

- Deng, J., Chen, M., Liu, Z., Song, Y., Sui, T., Lai, L., Li, Z., 2019. The disrupted balance between hair follicles and sebaceous glands in Hoxc13-ablated rabbits. *FASEB J.* 33, 1226–1234. <https://doi.org/10.1096/fj.201800928RR>
- Dixon, J.R., Selvaraj, S., Yue, F., Kim, A., Li, Y., Shen, Y., Hu, M., Liu, J.S., Ren, B., 2012. Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* 485, 376–380. <https://doi.org/10.1038/nature11082>
- Dolan, C.P., Dawson, L.A., Muneoka, K., 2018. Digit Tip Regeneration: Merging Regeneration Biology with Regenerative Medicine. *Stem Cells Transl. Med.* 7, 262–270. <https://doi.org/10.1002/sctm.17-0236>
- Drögemüller, C., Distl, O., Leeb, T., 2001. Partial Deletion of the Bovine ED1 Gene Causes Anhidrotic Ectodermal Dysplasia in Cattle. *Genome Res.* 11, 1699–1705. <https://doi.org/10.1101/gr.182501.reported>
- Duboule, D., 2007. The rise and fall of Hox gene clusters. *Development* 134, 2549–2560. <https://doi.org/10.1242/dev.001065>
- Duboule, D., Dollé, P., 1989. The structural and functional organization of the murine HOX gene family resembles that of Drosophila homeotic genes. *EMBO J.* 8, 1497–505. <https://doi.org/10.1002/j.1460-2075.1989.tb03534.x>
- Dudley, A.T., Ros, M.A., Tabin, C.J., 2002. A re-examination of proximodistal patterning during vertebrate limb development. *Nature* 418, 539–544. <https://doi.org/10.1038/nature00945>
- E.B. Lewis, 1978. A gene complex controlling segmentation in Drosophila. *Nature* 276, 565–570. <https://doi.org/10.1038/276565a0>
- Eblaghie, M.C., Lunn, J.S., Dickinson, R.J., Mu, A.E., Farrell, E.R., Mathers, J., Keyse, S.M., Storey, K., Tickle, C., 2003. Negative Feedback Regulation of FGF Signaling Levels by Pyst1/MKP3 in Chick Embryos. *Curr. Biol.* 13, 1009–1018. <https://doi.org/10.1016/s>
- Fabre, P.J., Leleu, M., Mormann, B.H., Lopez-Delisle, L., Noordermeer, D., Beccari, L., Duboule, D., 2017. Large scale genomic reorganization of topological domains at the HoxD locus. *Genome Biol.* 18, 1–15. <https://doi.org/10.1186/s13059-017-1278-z>

- Fallon, J., Lopez, A., Ros, M.A., Savage, M.P., Olwin, B.B., Simandl, B.K., 1994. FGF-2: apical ectodermal ridge growth signal for chick limb development. *Science* (80-.). 264, 104–107. <https://doi.org/10.1126/science.7908145>
- Fantauzzo, K.A., Tadin-Strapps, M., You, Y., Mentzer, S.E., Baumeister, F.A.M., Cianfarani, S., Van Maldergem, L., Warburton, D., Sundberg, J.P., Christiano, A.M., 2008. A position effect on TRPS1 is associated with Ambras syndrome in humans and the Koala phenotype in mice. *Hum. Mol. Genet.* 17, 3539–3551. <https://doi.org/10.1093/hmg/ddn247>
- Farooq, M., Kurban, M., Fujimoto, A., Fujikawa, H., Abbas, O., Nemer, G., Saliba, J., Sleiman, R., Tofaili, M., Kibbi, A.G., Ito, M., Shimomura, Y., 2013. A Homozygous Frameshift Mutation in the HOXC13 Gene Underlies Pure Hair and Nail Ectodermal Dysplasia in a Syrian Family. *Hum. Mutat.* 34, 578–581. <https://doi.org/10.1002/humu.22271>
- Fernandez-Teran, M., Piedra, M.E., Ros, M.A., Fallon, J.F., 1999. The recombinant limb as a model for the study of limb patterning, and its application to muscle development. *Cell Tissue Res.* 296, 121–129. <https://doi.org/10.1007/s004410051273>
- Fernandez-Teran, M., Ros, M.A., 2008. The Apical Ectodermal Ridge: Morphological aspects and signaling pathways. *Int. J. Dev. Biol.* 52, 857–871. <https://doi.org/10.1387/ijdb.072416mf>
- Flannagan, S., 1966. “Nude”, a new hairless gene with pleiotropic effects in the mouse. *Genet. Res.* 8, 295–309.
- Fleckman, P., Jaeger, K., Silva, K.A., Sundberg, J.P., 2013. Comparative Anatomy of Mouse and Human Nail Units. *Anat. Rec.* 296, 521–532. <https://doi.org/10.1002/ar.22660>
- Frankel, N., Davis, G.K., Vargas, D., Wang, S., Payre, F., Stern, D.L., 2010. Phenotypic robustness conferred by apparently redundant transcriptional enhancers. *Nature* 466, 490–493. <https://doi.org/10.1038/nature09158>
- Fromental-ramain, C., Warot, X., Lakkaraju, S., Favier, B., Haack, H., Birling, C., Dierich, A., Dollé, P., Chambon, P., 1996a. Specific and redundant functions of the paralogous Hoxa-9 and Hoxd-9 genes in forelimb and axial skeleton patterning.

- Development 122, 461–472.
- Fromental-ramain, C., Warot, X., Messadecq, N., Lemeur, M., Dollé, P., Chambon, P., 1996b. Hoxa-13 and Hoxd-13 play a crucial role in the patterning of the limb autopod. *Development* 122, 2997–3011.
- Fuchs, E., 2016. Epithelial Skin Biology. Three Decades of Developmental Biology, a Hundred Questions Answered and a Thousand New Ones to Address, 1st ed, Current Topics in Developmental Biology. Elsevier Inc. <https://doi.org/10.1016/bs.ctdb.2015.11.033>
- Fuchs, E., Merrill, B.J., Jamora, C., Dasgupta, R., 2001. At the Roots of a Never-Ending Cycle Review. *Dev. Cell* 1, 13–25.
- Furlong, E.E.M., Levine, M., 2018. Developmental enhancers and chromosome topology. *Science* (80-.). 1345, 1341–1345.
- Galloway, J.L., Delgado, I., Ros, M.A., Tabin, C.J., 2009. A reevaluation of X-irradiation-induced phocomelia and proximodistal limb patterning. *Nature* 460, 400–404. <https://doi.org/10.1038/nature08117>
- Gaunt, S.J., Sharpe, P.T., Duboule, D., 1988. Spatially restricted domains of homeo-gene transcripts in mouse embryos: relation to a segmented body plan. *Dev.* 104, 169–179.
- Gilbert, S.F., 2003. *Developmental Biology*, 7th ed. Sinauer Associates, INC. <https://doi.org/10.1016/j.scitotenv.2017.05.202>
- Godwin, A.R., Capecchi, M.R., 1998. Hoxc13 mutant mice lack external hair. *Genes Dev.* 12, 11–20. <https://doi.org/10.1101/gad.12.1.11>
- Godwin, A.R., Stadler, H.S., Nakamura, K., Capecchi, M.R., 1998. Detection of targeted GFP-Hox gene fusions during mouse embryogenesis. *Proc. Natl. Acad. Sci.* 95, 13042–13047. <https://doi.org/10.1073/pnas.95.22.13042>
- Gómez-Skarmeta, J.L., Modolell, J., 2002. Iroquois genes: Genomic organization and function in vertebrate neural development. *Curr. Opin. Genet. Dev.* 12, 403–408. [https://doi.org/10.1016/S0959-437X\(02\)00317-9](https://doi.org/10.1016/S0959-437X(02)00317-9)
- Gonzalez, F., Duboule, D., Spitz, F., 2007. Transgenic analysis of Hoxd gene regulation

- during digit development. *Dev. Biol.* 306, 847–859.
<https://doi.org/10.1016/j.ydbio.2007.03.020>
- Graham, A., Papalopulu, N., Krumlauf, R., 1989. The Murine and Drosophila Homeobox Complexes Have Common Features of Organization and Expression. *Cell* 57, 367–378.
- Greco, V., Chen, T., Rendl, M., Schober, M., Pasolli, H.A., Stokes, N., dela Cruz-Racelis, J., Fuchs, E., 2009. A Two-Step Mechanism for Stem Cell Activation during Hair Regeneration. *Cell Stem Cell* 4, 155–169.
<https://doi.org/10.1016/j.stem.2008.12.009>
- Hamburguer, V., Hamilton, H.L., 1951. A series of normal stages in the development of the chick embryo. *J. Morphol.* 88, 49–92.
- Hamrick, M.W., 2001. Development and evolution of the mammalian limb: Adaptive diversification of nails, hooves, and claws. *Evol. Dev.* 3, 355–363.
<https://doi.org/10.1046/j.1525-142X.2001.01032.x>
- Han, K., Liang, L., Li, L., Ouyang, Z., Zhao, B., Wang, Q., Liu, Z., Zhao, Y., Ren, X., Jiang, F., Lai, C., Wang, K., Yan, S., Huang, L., Guo, L., Zeng, K., Lai, L., Fan, N., 2017. Generation of Hoxc13 knockout pigs recapitulates human ectodermal dysplasia – 9. *Hum. Mol. Genet.* 26, 184–191. <https://doi.org/10.1093/hmg/ddw378>
- Han, M., 2003. Digit regeneration is regulated by Msx1 and BMP4 in fetal mice. *Development* 130, 5123–5132. <https://doi.org/10.1242/dev.00710>
- Hardy, M.H., 1992. The secret life of the hair follicle. *Trends Genet.* 8, 55–61.
[https://doi.org/10.1016/0168-9525\(92\)90350-D](https://doi.org/10.1016/0168-9525(92)90350-D)
- Hashimoto, M., Takemoto, T., 2015. Electroporation enables the efficient mRNA delivery into the mouse zygotes and facilitates CRISPR/Cas9-based genome editing. *Sci. Rep.* 5, 1–3. <https://doi.org/10.1038/srep11315>
- Hsu, Y.-C., Li, L., Fuchs, E., 2014. Transit-amplifying cells orchestrate stem cell activity and tissue regeneration. *Cell* 157, 935–49. <https://doi.org/10.1016/j.cell.2014.02.057>
- Huelsken, J., Vogel, R., Erdmann, B., Cotsarelis, G., Birchmeier, W., 2001. B-Catenin Controls Hair Follicle Morphogenesis and Stem Cell Differentiation in the Skin. *Cell* 105, 533–545.

- Hyman, C.A., Bartholin, L., Newfeld, S.J., Wotton, D., 2003. Drosophila TGIF Proteins Are Transcriptional Activators. *Mol. Cell. Biol.* 23, 9262–9274. <https://doi.org/10.1128/mcb.23.24.9262-9274.2003>
- Ishiguro, A., Hatayama, M., Otsuka, M.I., Aruga, J., 2018. Link between the causative genes of holoprosencephaly: Zic2 directly regulates Tgif1 expression. *Sci. Rep.* 8, 1–12. <https://doi.org/10.1038/s41598-018-20242-2>
- Ishii, Y., Wajid, M., Bazzi, H., Fantauzzo, K.A., Barber, A.G., Blaydon, D.C., Nam, J.S., Yoon, J.K., Kelsell, D.P., Christiano, A.M., 2008. Mutations in R-spondin 4 (RSPO4) underlie inherited anonychia. *J. Invest. Dermatol.* 128, 867–870. <https://doi.org/10.1038/sj.jid.5701078>
- Izpisúa-Belmonte, J.C., Falkenstein, H., Dollé, P., Renucci, A., Duboule, D., 1991. Murine genes related to the Drosophila AbdB homeotic genes are sequentially expressed during development of the posterior part of the body. *EMBO J.* 10, 2279–89.
- Jaks, V., Barker, N., Kasper, M., Van Es, J.H., Snippert, H.J., Clevers, H., Toftgård, R., 2008. Lgr5 marks cycling, yet long-lived, hair follicle stem cells. *Nat. Genet.* 40, 1291–1299. <https://doi.org/10.1038/ng.239>
- Jarvinen, E., Salazar-Ciudad, I., Birchmeier, W., Taketo, M.M., Jernvall, J., Thesleff, I., 2006. Continuous tooth generation in mouse is induced by activated epithelial Wnt/beta-catenin signaling. *Proc. Natl. Acad. Sci.* 103, 18627–18632. <https://doi.org/10.1073/pnas.0607289103>
- Johnson, D., Kan, S., Oldridge, M., Trembath, R.C., Roche, P., Esnouf, R.M., Giele, H., Andrew Wilkie, O.M., 2003. Missense Mutations in the Homeodomain of HOXD13 Are Associated with Brachydactyly Types D and E. *Am. J. Hum. Genet.* 72, 984–997. <https://doi.org/10.1086/374721>
- Kardong V., K., 2007. Vertebrados: Anatomía comparada, función y evolución, 4th ed. McGraw-Hill Interamericana de España S.L., 2007.
- Katayama, K., Miyamoto, S., Furuno, A., Akiyama, K., Takahashi, S., Suzuki, H., Tsuji, T., Kunieda, T., 2009. Characterization of the chromosomal inversion associated with the Koa mutation in the mouse revealed the cause of skeletal abnormalities. *BMC Genet.* 10, 60. <https://doi.org/10.1186/1471-2156-10-60>

- Kawakami, Y., Uchiyama, Y., Esteban, C.R., Inenaga, T., Koyano-Nakagawa, N., Kawakami, H., Marti, M., Kmita, M., Monaghan-Nichols, P., Nishinakamura, R., Belmonte, J.C.I., 2009. Sall genes regulate region-specific morphogenesis in the mouse limb by modulating Hox activities. *Development* 136, 585–594. <https://doi.org/10.1242/dev.027748>
- Kenny, D.A., Jurata, L.W., Saga, Y., Gill, G.N., 1998. Identification and characterization of LMO4, an LMO gene with a novel pattern of expression during embryogenesis. *Proc. Natl. Acad. Sci. U. S. A.* 95, 11257–11262. <https://doi.org/10.1073/pnas.95.19.11257>
- Khan, A.K., Muhammad, N., Aziz, A., Khan, S.A., Shah, K., Nasir, A., Khan, M.A., Khan, S., 2017. A novel mutation in homeobox DNA binding domain of HOXC13 gene underlies pure hair and nail ectodermal dysplasia (ECTD9) in a Pakistani family. *BMC Med. Genet.* 18, 1–5. <https://doi.org/10.1186/s12881-017-0402-y>
- Kherdjemil, Y., Lalonde, R.L., Sheth, R., Dumouchel, A., De Martino, G., Pineault, K.M., Wellik, D.M., Stadler, H.S., Akimenko, M.A., Kmita, M., 2016. Evolution of Hoxa11 regulation in vertebrates is linked to the pentadactyl state. *Nature* 539, 89–92. <https://doi.org/10.1038/nature19813>
- Kmita, M., Duboule, D., 2003. Organizing axes in time and space; 25 years of collinear thinking. *Science* (80-.). 301, 331–333.
- Kmita, M., Tarchini, B., Zakany, J., Logan, M.P., Tabin, C.J., Duboule, D., 2005. Early developmental arrest of mammalian limbs lacking HoxA / HoxD gene function 435, 1113–1116. <https://doi.org/10.1038/nature03648>
- Knosp, W.M., Scott, V., Bächinger, H.P., Stadler, H.S., 2004. HOXA13 regulates the expression of bone morphogenetic proteins 2 and 7 to control distal limb morphogenesis. *Development* 131, 4581–4592. <https://doi.org/10.1242/dev.01327>
- Ko, S.O., Chung, I.H., Xu, X., Oka, S., Zhao, H., Cho, E.S., Deng, C., Chai, Y., 2007. Smad4 is required to regulate the fate of cranial neural crest cells. *Dev. Biol.* 312, 435–447. <https://doi.org/10.1016/j.ydbio.2007.09.050>
- Kruse, S.W., Suino-Powell, K., Zhou, X.E., Kretschman, J.E., Reynolds, R., Vonnrhein, C., Xu, Y., Wang, L., Tsai, S.Y., Tsai, M.J., Xu, H.E., 2008. Identification of COUP-TFII orphan nuclear receptor as a retinoic acid-activated receptor. *PLoS Biol.* 6,

- 2002–2015. <https://doi.org/10.1371/journal.pbio.0060227>
- Kuhlman, J., Niswander, L., 1997. Limb deformity proteins: Role in mesodermal induction of the apical ectodermal ridge. *Development* 124, 133–139.
- Kuijper, S., Beverdam, A., Kroon, C., Brouwer, A., Candille, S., Barsh, G., Meijlink, F., 2005. Genetics of shoulder girdle formation: Roles of Tbx15 and aristaless-like genes. *Development* 132, 1601–1610. <https://doi.org/10.1242/dev.01735>
- Kulesa, H., Turk, G., Hogan, B.L.M., 2000. Inhibition of Bmp signaling affects growth and differentiation in the anagen hair follicle. *EMBO J.* 19, 6664–6674.
- Laufer, E., Nelson, C.E., Johnson, R.L., Morgan, B.A., Tabin, C., 1994. Sonic hedgehog and Fgf-4 act through a signalling cascade and feedback loop to integrate growth and patterning of the developing limb bud. *Cell* 79, 993–1003.
- Lee, C.T., Li, L., Takamoto, N., Martin, J.F., DeMayo, F.J., Tsai, M.-J., Tsai, S.Y., 2004. The Nuclear Orphan Receptor COUP-TFII Is Required for Limb and Skeletal Muscle Development. *Mol. Cell. Biol.* 24, 10835–10843. <https://doi.org/10.1128/mcb.24.24.10835-10843.2004>
- Lehoczky, J.A., Robert, B., Tabin, C.J., 2011. Mouse digit tip regeneration is mediated by fate-restricted progenitor cells. *Proc. Natl. Acad. Sci.* 108, 20609–20614. <https://doi.org/10.1073/pnas.1118017108>
- Lehoczky, J.A., Tabin, C.J., 2015. Lgr6 marks nail stem cells and is required for digit tip regeneration. *Proc. Natl. Acad. Sci.* 112, 13249–13254. <https://doi.org/10.1073/pnas.1518874112>
- Lehoczky, J.A., Williams, M.E., Innis, J.W., 2004. Conserved expression domains for genes upstream and within the HoxA and HoxD clusters suggests a long-range enhancer existed before cluster duplication. *Evol. Dev.* 6, 423–430. <https://doi.org/10.1111/j.1525-142X.2004.04050.x>
- Leung, Y., Kandyba, E., Chen, Y.-B., Ruffins, S., Chuong, C.-M., Kobiela, K., 2014. Bifunctional ectodermal stem cells around the nail display dual fate homeostasis and adaptive wounding response toward nail regeneration. *Proc. Natl. Acad. Sci.* 111, 15114–15119. <https://doi.org/10.1073/pnas.1318848111>
- Li, D., Sakuma, R., Vakili, N.A., Mo, R., Puviindran, V., Deimling, S., Zhang, X.,

- Hopyan, S., Hui, C. chung, 2014. Formation of proximal and anterior limb skeleton requires early function of *Irx3* and *Irx5* and is negatively regulated by *shh* signaling. *Dev. Cell* 29, 233–240. <https://doi.org/10.1016/j.devcel.2014.03.001>
- Liao, Y., Wang, J., Jaehnig, E.J., Shi, Z., Zhang, B., 2019. WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs. *Nucleic Acids Res.* 47, 199–205. <https://doi.org/10.1093/nar/gkz189>
- Lin, Z., Chen, Q., Shi, L., Lee, M., Giehl, K.A., Tang, Z., Wang, H., Zhang, J., Yin, J., Wu, L., Xiao, R., Liu, X., Dai, L., Zhu, X., Li, R., Betz, R.C., Zhang, X., Yang, Y., 2012. Loss-of-function mutations in *HOXC13* cause pure hair and nail ectodermal dysplasia. *Am. J. Hum. Genet.* 91, 906–911. <https://doi.org/10.1016/j.ajhg.2012.08.029>
- Liu, F., Chu, E.Y., Watt, B., Zhang, Y., Gallant, N.M., Andl, T., Yang, S.H., Lu, M.M., Piccolo, S., Schmidt-Ullrich, R., Taketo, M.M., Morrissey, E.E., Atit, R., Dlugosz, A.A., Millar, S.E., 2008. Wnt/ β -catenin signaling directs multiple stages of tooth morphogenesis. *Dev. Biol.* 313, 210–224. <https://doi.org/10.1016/j.ydbio.2007.10.016>
- Lu, C.P., Polak, L., Keyes, B.E., Fuchs, E., 2016. Spatiotemporal antagonism in mesenchymal-epithelial signaling in sweat versus hair fate decision. *Science* (80-.). 354. <https://doi.org/10.1126/science.aah6102>
- Lynch, M.H., O’Guin, W.M., Hardy, C., Mak, L., Sun, T.-T., 1986. Acidic and Basic Hair/Nail (“Hard”) Keratins: Their Colocalization in Upper Cortical and Cuticle Cells of the Human Hair Follicle and Their Relationship to “Soft” Keratins. *J. Cell Biol.* 103, 2593–2606.
- Mariani, F. V., Ahn, C.P., Martin, G.R., 2008. Genetic evidence that FGFs have an instructive role in limb proximal-distal patterning. *Nature* 453, 401–405. <https://doi.org/10.1038/nature06876>
- Mcgrath, J.A., Eady, R.A., Pope, F.M., 2004. Rook’s textbook of dermatology (Seventh Edition), Journal of the American Academy of Dermatology. <https://doi.org/10.1016/j.jaad.2006.02.022>
- Mecklenburg, L., Paus, R., Halata, Z., Bechtold, L.S., Fleckman, P., Sundberg, J.P., 2004. *FOXN1* is critical for onycholemmal terminal differentiation in nude (*Foxn1nu*)

- mice. *J. Invest. Dermatol.* 123, 1001–1011. <https://doi.org/10.1111/j.0022-202X.2004.23442.x>
- Meier, N., Dear, T.N., Boehm, T., 1999. Wnt and mHa3 are components of the genetic hierarchy controlling hair follicle differentiation. *Mech. Dev.* 89, 215–221. [https://doi.org/10.1016/S0925-4773\(99\)00218-X](https://doi.org/10.1016/S0925-4773(99)00218-X)
- Mercader, N., Leonardo, E., Piedra, M.E., Martínez-A, C., Ros, M.A., Torres, M., 2000. Opposing RA and FGF signals control proximodistal vertebrate limb development through regulation of Meis genes. *Development* 127, 3961–70.
- Mercader, N., Selleri, L., Criado, L.M., Pallares, P., Parras, C., Cleary, M.L., Torres, M., 2009. Ectopic Meis1 expression in the mouse limb bud alters P-D patterning in a Pbx1-independent manner. *Int. J. Dev. Biol.* 53, 1483–1494. <https://doi.org/10.1387/ijdb.072430nm>
- Merino, R., Rodríguez-Leon, J., Macías, D., Gañan, Y., Economides, A.N., Hurle, J.M., 1999. The BMP antagonist Gremlin regulates outgrowth, chondrogenesis and programmed cell death in the developing limb. *Development* 126, 5515–22.
- Mill, P., Mo, R., Fu, H., Grachtchouk, M., Kim, P.C.W., Dlugosz, A.A., Hui, C., 2003. Sonic hedgehog-dependent activation of Gli2 is essential for embryonic hair follicle development. *Genes Dev.* 17, 282–294. <https://doi.org/10.1101/gad.1038103.Fuchs>
- Minguillon, C., Nishimoto, S., Wood, S., Vendrell, E., Gibson-brown, J.J., Logan, M.P.O., 2012. Hox genes regulate the onset of Tbx5 expression in the forelimb. *Development* 139, 3180–3188. <https://doi.org/10.1242/dev.084814>
- Montavon, T., Soshnikova, N., Mascres, B., Joye, E., Thevenet, L., Splinter, E., De Laat, W., Spitz, F., Duboule, D., 2011. A Regulatory Archipelago Controls Hox Genes Transcription in Digits. *Cell* 147, 1132–1145. <https://doi.org/10.1016/j.cell.2011.10.023>
- Moon, A.M., Capecchi, M.R., 2000. Fgf8 is required for outgrowth and patterning of the limbs. *Nature* 403, 455–459.
- Mortlock, D.P., Innis, J.W., 1997. Mutation of HOXA13 in hand-foot-genital syndrome. *Nat. Genet.* 15, 179–180. <https://doi.org/10.1038/ng0297-179>

- Mou, C., Jackson, B., Schneider, P., Overbeek, P.A., Headon, D.J., 2006. Generation of the primary hair follicle pattern. *Proc. Natl. Acad. Sci.* 103, 9075–9080. <https://doi.org/10.1073/pnas.0600825103>
- Nagai, T., Aruga, J., Minowa, O., Sugimoto, T., Ohno, Y., Noda, T., Mikoshiba, K., 2000. *Zic2* regulates the kinetics of neurulation. *Proc. Natl. Acad. Sci. U. S. A.* 97, 1618–1623. <https://doi.org/10.1073/pnas.97.4.1618>
- Nagai, T., Aruga, J., Takada, S., Günther, T., Spörle, R., Schughart, K., Mikoshiba, K., 1997. The expression of the mouse *Zic1*, *Zic2*, and *Zic3* gene suggests an essential role for *Zic* genes in body pattern formation. *Dev. Biol.* 182, 299–313. <https://doi.org/10.1006/dbio.1996.8449>
- Nakagawa, O., Nakagawa, M., Richardson, J.A., Olson, E.N., Srivastava, D., 1999. *HRT1*, *HRT2*, and *HRT3*: A new subclass of bHLH transcription factors marking specific cardiac, somitic, and pharyngeal arch segments. *Dev. Biol.* 216, 72–84. <https://doi.org/10.1006/dbio.1999.9454>
- Närhi, K., Tummers, M., Ahtiainen, L., Itoh, N., Thesleff, I., Mikkola, M.L., 2012. *Sostdc1* defines the size and number of skin appendage placodes. *Dev. Biol.* 364, 149–161. <https://doi.org/10.1016/j.ydbio.2012.01.026>
- Naveau, A., Seidel, K., Klein, O.D., 2014. Tooth, hair and claw: Comparing epithelial stem cell niches of ectodermal appendages. *Exp. Cell Res.* 325, 96–103. <https://doi.org/10.1016/j.yexcr.2014.02.003>
- Nelson, C.E., Morgan, B. a, Burke, A.C., Laufer, E., DiMambro, E., Murtaugh, L.C., Gonzales, E., Tessarollo, L., Parada, L.F., Tabin, C., 1996. Analysis of *Hox* gene expression in the chick limb bud. *Development* 122, 1449–1466. <https://doi.org/10.1038/342767a0>
- Niehrs, C., 2012. The complex world of WNT receptor signalling. *Nat. Rev. Mol. Cell Biol.* 13, 767–779. <https://doi.org/10.1038/nrm3470>
- Niswander, L., Jeffrey, S., Martin, G.R., Tickle, C., 1994. A positive feedback loop coordinates growth and patterning in the vertebrate limb. *Nature* 371, 609–612.
- Niswander, L., Tickle, C., Vogel, A., Booth, I., Martin, G.R., 1993. FGF-4 replaces the apical ectodermal ridge and directs outgrowth and patterning of the limb. *Cell* 75,

- 579–587. [https://doi.org/10.1016/0092-8674\(93\)90391-3](https://doi.org/10.1016/0092-8674(93)90391-3)
- Noordermeer, D., Leleu, M., Splinter, E., Rougemont, J., De Laat, W., Duboule, D., 2011. The dynamic architecture of Hox gene clusters. *Science* (80-.). 334, 222–225. <https://doi.org/10.1126/science.1207194>
- Noramly, S., Freeman, A., Morgan, B.A., 1999. Beta-Catenin Signaling Can Initiate Feather Bud Development. *Development* 126, 3509–21.
- Ohki, R., Nemoto, J., Murasawa, H., Oda, E., Inazawa, J., Tanaka, N., Taniguchi, T., 2000. Reprimo, a new candidate mediator of the p53-mediated cell cycle arrest at the G2 phase. *J Biol Chem* 275, 22627–22630.
- Osterwalder, M., Barozzi, I., Tissi  res, V., Fukuda-Yuzawa, Y., Mannion, B.J., Afzal, S.Y., Lee, E.A., Zhu, Y., Plajzer-Frick, I., Pickle, C.S., Kato, M., Garvin, T.H., Pham, Q.T., Harrington, A.N., Akiyama, J.A., Afzal, V., Lopez-Rios, J., Dickel, D.E., Visel, A., Pennacchio, L.A., 2018. Enhancer redundancy provides phenotypic robustness in mammalian development. *Nature* 554, 239–243. <https://doi.org/10.1038/nature25461>
- Osterwalder, M., Speziale, D., Shoukry, M., Mohan, R., Ivanek, R., Kohler, M., Beisel, C., Wen, X., Scales, S.J., Christoffels, V.M., Visel, A., Lopez-Rios, J., Zeller, R., 2014. HAND2 Targets Define a Network of Transcriptional Regulators that Compartmentalize the Early Bud Mesenchyme. *Dev. Cell* 31, 345–357. <https://doi.org/10.1126/science.1249098>.Sleep
- Parr, B.A., McMahon, A.P., 1995. Dorsalizing signal Wnt-7a required for normal polarity and A-P axes of mouse limb.Pdf. *Nature* 374, 350–353.
- P  rez-g  mez, R., Haro, E., Fern  ndez-guerrero, M., Bastida, M.F., Ros, M.A., 2018. Role of Hox genes in regulating digit patterning. *Int. J. Dev. Biol* 805, 797–805.
- Perrin, C., Langbein, L., Schweizer, J., 2004. Expression of hair keratins in the adult nail unit: An immunohistochemical analysis of the onychogenesis in the proximal nail fold, matrix and nail bed. *Br. J. Dermatol.* 151, 362–371. <https://doi.org/10.1111/j.1365-2133.2004.06108.x>
- Petit, F., Sears, K.E., Ahituv, N., 2017. Limb development: A paradigm of gene regulation. *Nat. Rev. Genet.* 18, 245–258. <https://doi.org/10.1038/nrg.2016.167>

- Pickering, J., Rich, C.A., Stainton, H., Aceituno, C., Chinnaiya, K., Saiz-Lopez, P., Ros, M.A., Towers, M., 2018. An intrinsic cell cycle timer terminates limb bud outgrowth. *Elife* 7, 1–16. <https://doi.org/10.7554/elife.37429>
- Pispa, J., Thesleff, I., 2003. Mechanisms of ectodermal organogenesis. *Dev. Biol.* 262, 195–205. [https://doi.org/10.1016/S0012-1606\(03\)00325-7](https://doi.org/10.1016/S0012-1606(03)00325-7)
- Pizette, S., Niswander, L., 1999. BMPs negatively regulate structure and function of the limb apical ectodermal ridge. *Development* 126, 883–94. <https://doi.org/10.1126/science.276.5314.955>
- Potter, C.S., Pruett, N.D., Kern, M.J., Baybo, M.A., Godwin, A.R., Potter, K.A., Peterson, R.L., Sundberg, J.P., Awgulewitsch, A., 2011. The nude mutant gene *Foxn1* Is a *HOXC13* regulatory target during hair follicle and nail differentiation. *J. Invest. Dermatol.* 131, 828–837. <https://doi.org/10.1038/jid.2010.391>
- Probst, S., Kraemer, C., Demougin, P., Sheth, R., Martin, G.R., Shiratori, H., Hamada, H., Iber, D., Zeller, R., Zuniga, A., 2011. SHH propagates distal limb bud development by enhancing CYP26B1-mediated retinoic acid clearance via AER-FGF signalling. *Development* 138, 1913–1923. <https://doi.org/10.1242/dev.063966>
- Qin, W., Dion, S.L., Kutny, P.M., Zhang, Y., Cheng, A.W., Jillette, N.L., Malhotra, A., Geurts, A., Chen, Y.-G., Wang, H., 2015. Efficient CRISPR/Cas9-Mediated Genome Editing in Mice by Zygote Electroporation of Nuclease. *Genetics* 200, 423–430. <https://doi.org/10.1534/genetics.115.176594>
- Ravasi, T., Suzuki, H., Cannistraci, C.V., Katayama, S., Bajic, V.B., Tan, K., Akalin, A., Schmeier, S., Kanamori-katayama, M., Kamburov, A., Kaur, M., Kawaji, H., Kubosaki, A., Lassmann, T., Hazayashizaki, Y., 2010. An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. *Cell* 140, 744–752. <https://doi.org/10.1016/j.cell.2010.01.044>
- Reid, A.I., Gaunt, S.J., 2002. Colinearity and non-colinearity in the expression of Hox genes in developing chick skin. *Int. J. Dev. Biol.* 46, 209–215. <https://doi.org/10.1387/ijdb.011495>
- Rendl, M., Lewis, L., Fuchs, E., 2005. Molecular dissection of mesenchymal-epithelial interactions in the hair follicle. *PLoS Biol.* 3, 1910–1924. <https://doi.org/10.1371/journal.pbio.0030331>

- Robert, B., 2007. Bone morphogenetic protein signaling in limb outgrowth and patterning. *Dev. Growth Differ.* 49, 455–468. <https://doi.org/10.1111/j.1440-169X.2007.00946.x>
- Rodríguez-carballo, E., Lopez-delisle, L., Zhan, Y., Fabre, P.J., Beccari, L., El-idrissi, I., Hanh, T., Huynh, N., Ozadam, H., Dekker, J., Duboule, D., 2017. The HoxD cluster is a dynamic and resilient TAD boundary controlling the segregation of antagonistic regulatory landscapes 2264–2281. <https://doi.org/10.1101/gad.307769.117>.
- Rompolas, P., Deschene, E.R., Zito, G., Gonzalez, D.G., Saotome, I., Haberman, A.M., Greco, V., 2012. Live imaging of stem cell and progeny behaviour in physiological hair-follicle regeneration. *Nature* 487, 496–499. <https://doi.org/10.1038/nature11218>.Live
- Rosello-Diez, A., Arques, C.G., Delgado, I., Giovinnazzo, G., Torres, M., 2014. Diffusible signals and epigenetic timing cooperate in late proximo-distal limb patterning. *Development* 141, 1534–1543. <https://doi.org/10.1242/dev.106831>
- Rosello-Diez, A., Ros, M.A., Torres, M., 2011. Diffusible signals, not autonomous mechanisms, determine the main proximodistal limb subdivision. *Science* (80-.). 1086–1088.
- Rowe, D.A., Cairns, J.M., Fallon, J.F., 1982. Spatial and temporal patterns of cell death in limb bud mesoderm after apical ectodermal ridge removal. *Dev. Biol.* 93, 83–91. [https://doi.org/10.1016/0012-1606\(82\)90241-X](https://doi.org/10.1016/0012-1606(82)90241-X)
- Rubin, L., Saunders, J.W., 1972. Ectodermal-mesodermal interactions in the growth of limb buds in the chick embryo: constancy and temporal limits of the ectodermal induction. *Dev. Biol.* 28, 94–112.
- Saiz-Lopez, P., Chinnaiya, K., Campa, V.M., Delgado, I., Ros, M.A., Towers, M., 2015. An intrinsic timer specifies distal structures of the vertebrate limb. *Nat. Commun.* 6, 1–9. <https://doi.org/10.1038/ncomms9108>
- Saiz-Lopez, P., Chinnaiya, K., Towers, M., Ros, M.A., 2017. Intrinsic properties of limb bud cells can be differentially reset. *Development* 144, 479–486. <https://doi.org/10.1242/dev.137661>
- Sato, K., Koizumi, Y., Takahashi, M., Kuroiwa, A., Tamura, K., 2007. Specification of

- cell fate along the proximal-distal axis in the developing chick limb bud. *Development* 134, 1397–1406. <https://doi.org/10.1242/dev.02822>
- Satokata, I., Maas, R., Ma, L., Ohshima, H., Bei, M., Woo, I., Nishizawa, K., Maeda, T., Takano, Y., Uchiyama, M., Heaney, S., Peters, H., Tang, Z., Maxson, R., 2000. *Msx2* deficiency in mice causes pleiotropic defects in bone growth and ectodermal organ formation. *Nat. Genet.* 24, 391–395. <https://doi.org/10.1038/74231>
- Saunders, J.W., 1948. The Proximo-Distal Sequence of Origin of the Parts of the Chick Wing and the Role of the Ectoderm. *J. Exp. Zool.* 108, 363–404.
- Scherz, P.J., Harfe, B.D., McMahon, A.P., Tabin, C.J., 2004. The limb bud *Shh*-*Fgf* feedback loop is terminated by expansion of former ZPA cells. *Science* (80-.). 305, 396–399. <https://doi.org/10.1126/science.1096966>
- Selever, J., Liu, W., Lu, M.F., Behringer, R.R., Martin, J.F., 2004. *Bmp4* in limb bud mesoderm regulates digit pattern by controlling AER development. *Dev. Biol.* 276, 268–279. <https://doi.org/10.1016/j.ydbio.2004.08.024>
- Shang, L., Pruett, N.D., Awgulewitsch, A., 2002. *Hoxc12* expression pattern in developing and cycling murine hair follicles. *Mech. Dev.* 113, 207–210. [https://doi.org/10.1016/S0925-4773\(02\)00022-9](https://doi.org/10.1016/S0925-4773(02)00022-9)
- Sheth, R., Barozzi, I., Langlais, D., Osterwalder, M., Nemec, S., Carlson, H.L., Stadler, H.S., Visel, A., Drouin, J., Kmita, M., 2016. Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by *HOX13*. *Cell Rep.* 17, 2913–2926. <https://doi.org/10.1016/j.celrep.2016.11.039>
- Sheth, R., Bastida, M.F., Kmita, M., Ros, M., 2014. “Self-regulation,” a new facet of *Hox* genes’ function. *Dev. Dyn.* 243, 182–191. <https://doi.org/10.1002/dvdy.24019>
- Shrimpton, A.E., Levinsohn, E.M., Yozawitz, J.M., Packard, D.S., Cady, R.B., Middleton, F.A., Persico, A.M., Hootnick, D.R., 2004. A *HOX* Gene Mutation in a Family with Isolated Congenital Vertical Talus and Charcot-Marie-Tooth Disease. *Am. J. Hum. Genet.* 75, 92–96. <https://doi.org/10.1086/422015>
- Singh, M.K., Petry, M., Haenig, B., Lescher, B., Leitges, M., Kispert, A., 2005. The T-box transcription factor *Tbx15* is required for skeletal development. *Mech. Dev.* 122, 131–144. <https://doi.org/10.1016/j.mod.2004.10.011>

- Soshnikova, N., Dewaele, R., Janvier, P., Krumlauf, R., Duboule, D., 2013. Duplications of hox gene clusters and the emergence of vertebrates. *Dev. Biol.* 378, 194–199. <https://doi.org/10.1016/j.ydbio.2013.03.004>
- Soshnikova, N., Duboule, D., 2009. Epigenetic Temporal Control of Mouse Hox Genes in Vivo. *Science* (80-.). 1187, 1320–3.
- Spitz, F., Gonzalez, F., Duboule, D., 2003. a Chromosomal Regulatory Landscape Containing the HoxD Cluster *Franc. Cell* 113, 405–417.
- Spitz, F., Gonzalez, F., Peichel, C., Vogt, T.F., Duboule, D., Zákány, J., 2001. Large scale transgenic and cluster deletion analysis of the HoxD complex separate an ancestral regulatory module from evolutionary innovations. *Genes Dev.* 15, 2209–2214. <https://doi.org/10.1101/gad.205701>
- Stadler, H.S., Higgins, K.M., Capecchi, M.R., 2001. Loss of *Eph-receptor* expression correlates with loss of cell adhesion and chondrogenic capacity in *Hoxa13* mutant limbs. *Development* 128, 4177–4188.
- Suemori, H., Noguchi, S., 2000. Hox C cluster genes are dispensable for overall body plan of mouse embryonic development. *Dev. Biol.* 220, 333–342. <https://doi.org/10.1006/dbio.2000.9651>
- Summerbell, D., Lewis, J.H., Wolpert, L., 1973. Positional Information in Chick Limb Morphogenesis. *Nature* 244, 492–496. <https://doi.org/10.1038/246421a0>
- Sun, X., Lewandoski, M., Meyers, E.N., Liu, Y.H., Maxson, R.E., Martin, G.R., 2000. Conditional inactivation of *Fgf4* reveals complexity of signalling during limb bud development. *Nat. Genet.* 25, 83–86. <https://doi.org/10.1038/75644>
- Sun, X., Mariani, F. V., Martin, G.R., 2002. Functions of FGF signalling from the apical ectodermal ridge in limb development. *Nature* 418, 501–508. <https://doi.org/10.1038/nature00902>
- Tabin, C., Wolpert, L., 2007. Rethinking the proximodistal axis of the vertebrate limb in the molecular era. *Genes Dev.* 21, 1433–1442. <https://doi.org/10.1101/gad.1547407>
- Takeo, M., Chou, W.C., Sun, Q., Lee, W., Rabbani, P., Loomis, C., Mark Taketo, M., Ito, M., 2013. Wnt activation in nail epithelium couples nail growth to digit regeneration. *Nature* 499, 228–232. <https://doi.org/10.1038/nature12214>

- Taniguchi, K., Anderson, A.E., Melhuish, T.A., Carlton, A.L., Manukyan, A., Sutherland, A.E., Wotton, D., 2017. Genetic and Molecular Analyses indicate independent effects of TGIFs on Nodal and Gli3 in neural tube patterning. *Eur. J. Hum. Genet.* 25, 208–215. <https://doi.org/10.1038/ejhg.2016.164>
- Taniguchi, K., Anderson, A.E., Sutherland, A.E., Wotton, D., 2012. Loss of tgif function causes holoprosencephaly by disrupting the Shh signaling pathway. *PLoS Genet.* 8. <https://doi.org/10.1371/journal.pgen.1002524>
- Tarchini, B., Duboule, D., Kmita, M., 2006. Regulatory constraints in the evolution of the tetrapod limb anterior-posterior polarity. *Nature* 443, 985–988. <https://doi.org/10.1038/nature05247>
- Te Welscher, P., Fernandez-Teran, M., Ros, M.A., Zeller, R., 2002. Mutual genetic antagonism involving GLI3 and dHAND prepatterns the vertebrate limb bud mesenchyme prior to SHH signaling. *Genes Dev.* 16, 421–426. <https://doi.org/10.1101/gad.219202>
- ten Berge, D., Brugmann, S.A., Helms, J.A., Nusse, R., 2008. Wnt and FGF signals interact to coordinate growth with cell fate specification during limb development. *Development* 135, 3247–3257. <https://doi.org/10.1242/dev.023176>
- Tkatchenko, A. V., Visconti, R.P., Shang, L., Papenbrock, T., Pruett, N.D., Ito, T., Ogawa, M., Awgulewitsch, A., 2001. Overexpression of Hoxc13 in differentiating keratinocytes results in downregulation of a novel hair keratin gene cluster and alopecia. *Development* 128, 1547–58.
- Towers, M., Tickle, C., 2009. Growing models of vertebrate limb development. *Development* 136, 179–190. <https://doi.org/10.1242/dev.024158>
- Tsialikas, J., Romer-Seibert, J., 2015. LIN28: roles and regulation in development and beyond. *Development* 142, 2397–2404. <https://doi.org/10.1242/dev.117580>
- Turing, A.M., 1952. The chemical basis of morphogenesis. *Philos. Trans. R. Soc. London.* 237, 37–72.
- van Genderen, C., Okamura, R.M., Fariñas, I., Quo, R.-G., Parslow, T.G., Bruhn, L., Grosschedl, R., 1994. Development of several organs that require inductive epithelial-mesenchymal interactions is impaired in LEF-1-deficient mice. *Genes*

- Dev. 8, 2691–2703. <https://doi.org/10.1101/gad.8.22.2691>
- Vargesson, N., Clarke, J.D.W., Vincent, K., Coles, C., Wolpert, L., Tickle, C., 1997. Cell fate in the chick limb bud and relationship to gene expression. *Development* 124, 1909–1918.
- Verheyden, J.M., Sun, X., 2008. An Fgf/Gremlin inhibitory feedback loop triggers termination of limb bud outgrowth. *Nature* 454, 638–641. <https://doi.org/10.1038/nature07085>
- Wang, F., Ziemann, A., Coulombe, P.A., 2016. Skin Keratins. *Methods Enzymol.* 568, 303–350. <https://doi.org/10.1016/bs.mie.2015.09.032>
- Wang, Y., Li, L., Zheng, Y., Yuan, G., Yang, G., He, F., Chen, Y., 2012. BMP activity is required for tooth development from the Lamina to Bud Stage. *J. Dent. Res.* 91, 690–695. <https://doi.org/10.1177/0022034512448660>
- Warren, A.J., Colledge, W.H., Carlton, M.B.L., Evans, M.J., Smith, A.J.H., Rabbitts, T.H., 1994. The Oncogenic Cysteine-rich LIM domain protein Rbtl2 is essential for erythroid development. *Cell* 78, 45–57. [https://doi.org/10.1016/0092-8674\(94\)90571-1](https://doi.org/10.1016/0092-8674(94)90571-1)
- Wellik, D.M., Capecchi, M.R., 2003. Hox10 and Hox11 Genes Are Required to Globally Pattern the. *Science* (80-.). 301, 363–368.
- Wichmann, I.A., Zavala, K., Hoffmann, F.G., Vandeweghe, M.W., Corvalán, A.H., Amigo, J.D., Owen, G.I., Opazo, J.C., 2016. Evolutionary history of the reprimin tumor suppressor gene family in vertebrates with a description of a new reprimin gene lineage. *Gene* 592, 245–254. <https://doi.org/10.1016/j.gene.2016.07.036>
- Wolpert, L., Tickle, C., Sampford, M., 1979. The effect of cell killing by x-irradiation on pattern formation in the chick limb. *J. Embryol. Exp. Morphol.* 50, 175–93.
- Woltering, J.M., Noordermeer, D., Leleu, M., Duboule, D., 2014. Conservation and Divergence of Regulatory Strategies at Hox Loci and the Origin of Tetrapod Digits. *PLoS Biol.* 12. <https://doi.org/10.1371/journal.pbio.1001773>
- Woo, W., Zhen, H.H., Oro, A.E., 2012. Shh maintains dermal papilla identity and hair morphogenesis via a Noggin – Shh regulatory loop. *Genes Dev.* 26, 1235–1246. <https://doi.org/10.1101/gad.187401.112.as>

- Xu, B., Wellik, D.M., 2011. Axial Hox9 activity establishes the posterior field in the developing forelimb. *Proc. Natl. Acad. Sci. U. S. A.* 108, 4888–4891. <https://doi.org/10.1073/pnas.1018161108>
- Yashiro, K., Zhao, X., Uehara, M., Yamashita, K., Nishijima, M., Nishino, J., Saijoh, Y., Sakai, Y., Hamada, H., 2004. Regulation of retinoic acid distribution is required for proximodistal patterning and outgrowth of the developing mouse limb. *Dev. Cell* 6, 411–422. [https://doi.org/10.1016/S1534-5807\(04\)00062-0](https://doi.org/10.1016/S1534-5807(04)00062-0)
- Yokoyama, S., Hashimoto, M., Shimizu, H., Ueno-Kudoh, H., Uchibe, K., Kimura, I., Asahara, H., 2008. Dynamic gene expression of Lin-28 during embryonic development in mouse and chicken. *Gene Expr. Patterns* 8, 155–160. <https://doi.org/10.1016/j.gep.2007.11.001>
- Yokoyama, S., Ito, Y., Ueno-Kudoh, H., Shimizu, H., Uchibe, K., Albin, S., Mitsuoka, K., Miyaki, S., Kiso, M., Nagai, A., Hikata, T., Osada, T., Fukuda, N., Yamashita, S., Harada, D., Mezzano, V., Kasai, M., Puri, P.L., Hayashizaki, Y., Okado, H., Hashimoto, M., Asahara, H., 2009. A Systems Approach Reveals that the Myogenesis Genome Network Is Regulated by the Transcriptional Repressor RP58. *Dev. Cell* 17, 836–848. <https://doi.org/10.1016/j.devcel.2009.10.011>
- Yu, Z., Jiang, K., Xu, Z., Huang, H., Qian, N., Lu, Z., Chen, D., Di, R., Yuan, T., Du, Z., Xie, W., Lu, X., Li, H., Chai, R., Yang, Y., Zhu, B., Kunieda, T., Wang, F., Chen, T., 2018. Hoxc-Dependent Mesenchymal Niche Heterogeneity Drives Regional Hair Follicle Regeneration. *Cell Stem Cell* 23, 487–500.e6. <https://doi.org/10.1016/j.stem.2018.07.016>
- Yueh, Y.G., Gardner, D.P., Kappen, C., 1998. Evidence for regulation of cartilage differentiation by the homeobox gene Hoxc-8. *Proc. Natl. Acad. Sci.* 95, 9956–9961. <https://doi.org/10.1073/pnas.95.17.9956>
- Zakany, J., Duboule, D., 2007. The role of Hox genes during vertebrate limb development. *Curr. Opin. Genet. Dev.* 17, 359–366. <https://doi.org/10.1016/j.gde.2007.05.011>
- Zakany, J., Duboule, D., 1999. Hox genes in digit development and evolution. *Cell Tissue Res.* 296, 19–25. <https://doi.org/10.1007/s004410051262>
- Zakany, J., Fromental-ramain, C., Warot, X., Duboule, D., 1997. Regulation of number

- and size of digits by posterior Hox genes : A dose-dependent mechanism with potential. *Proc Natl Acad Sci U S A* 94, 13695–13700.
- Zhang, B., Kirov, S., Snoddy, J., 2005. WebGestalt: An integrated system for exploring gene sets in various biological contexts. *Nucleic Acids Res.* 33, 741–748. <https://doi.org/10.1093/nar/gki475>
- Zhang, Y., Tomann, P., Andl, T., Gallant, N.M., Huelsken, J., Jerchow, B., Birchmeier, W., Paus, R., Piccolo, S., Mikkola, M.L., Morrissey, E.E., Overbeek, P.A., Scheidereit, C., Millar, S.E., Schmidt-Ullrich, R., 2009. Reciprocal Requirements for EDA/EDAR/NF- κ B and Wnt/ β -Catenin Signaling Pathways in Hair Follicle Induction. *Dev. Cell* 17, 49–61. <https://doi.org/10.1016/j.devcel.2009.05.011>
- Zhao, X., Sirbu, I.O., Mic, F.A., Molotkova, N., Molotkov, A., Kumar, S., Duester, G., 2009. Retinoic Acid Promotes Limb Induction through Effects on Body Axis Extension but is Unnecessary for Limb Patterning. *Curr. Biol.* 19, 1050–1057. <https://doi.org/10.1016/j.cub.2009.04.059> Retinoic
- Zúñiga, A., Haramis, A.-P.G., McMahon, A.P., Zeller, R., 1999. Signal relay by BMP antagonism controls the SHH/FGF4 feedback loop in vertebrate limb bud. *Nature* 401, 598–602. <https://doi.org/10.1038/44157>
- Zuniga, A., Laurent, F., Lopez-Rios, J., Klasen, C., Matt, N., Zeller, R., 2012. Conserved cis-regulatory regions in a large genomic landscape control SHH and BMP-regulated Gremlin1 expression in mouse limb buds. *BMC Dev. Biol.* 12, 1–15. <https://doi.org/10.1186/1471-213X-12-23>
- Zwilling, E., 1959. Interaction between ectoderm and mesoderm in duck-chicken limb bud chimaeras. *J. Exp. Zool.* 142, 521–532.

AGRADECIMIENTOS

AGRADECIMIENTOS

Gracias al Instituto de Biomedicina y Biotecnología de Cantabria al Consejo Superior de Investigaciones Científicas y al Ministerio de Economía y Empresa por facilitar la oportunidad de realizar mi tesis.

Gracias a Ignacio Varela y Federica Bertocchini por seguir mi trabajo y potenciarlo gracias a su crítica constructiva y apoyo.

I thank Denis Duboule and their lab for accepting me at their workplace during my internship and offering us the opportunity to work together. I specially thank Lucille Delisle for Bioinformatic analysis in this work, Chase Bolt for his ATACseq of E13.5 forebrains and Nayuta Yakushiji-Kaminatsui for her help in mouse transgenic analysis and the design of the gRNAs used in this work.

Gracias al laboratorio de Alberto Gandarillas por facilitarnos maravillosos anticuerpos y por apoyarnos en nuestro trabajo.

Gracias a Víctor por su excelente apoyo desde el servicio de microscopía. Gracias a Miguel García Gómez, Mar Rodríguez y Beatriz Romero por su gran apoyo desde el servicio de estabulación y experimentación animal.

Gracias a Marta, Vincenzo, Ana y Lorena por haberme acompañado a lo largo de la tesis dentro y fuera del IBBTEC, en mi ciencia y en mi arte.

Gracias al grupo de Álvaro Rada por ser unos fantásticos vecinos y compartir sus opiniones con gran respeto y genialidad. Muchas gracias a Víctor y María por ser tan increíblemente maravillosas, nunca dejéis de ser así.

Gracias a Marta por traerme el sol de Sevilla y todo su salero.

Gracias a Jorge por darme tanto cariño y años de vida a base de risas.

Gracias a Carol y a Lolu por cuidarme y por ponerme contra las cuerdas cuando peco de soberbia.

Gracias a Jessica por rescatarme en Suiza y darme amor cuando más lo necesitaba. Descansa en paz.

Gracias a mi padre, Abel, a mi madre, Cari y a mi hermano, David. Gracias por estar siempre cuando ha hecho falta. Nunca hubiese terminado mi tesis sin su apoyo, clave en los momentos más duros, en los que la luz al final del túnel es muy difícil de ver.

Gracias a Rocío, Laura, Cristina y Sara por haber hecho del laboratorio un hogar ¡Y también a Alejandro, que lleva poquito, pero promete mucho! Gracias por aguantarme cuando no he sido el mejor de los compañeros. Gracias por cuidar y acompañar. Gracias por decir lo que pensáis. Gracias por reír y por llorar conmigo.

Gracias a Maria Félix y a Endika por las discusiones de ciencia y no de ciencia, por tener una opinión, por escuchar y contestar.

Y muchas gracias a Marián. Estoy muy orgulloso de que me brindase la oportunidad de ser parte de su laboratorio. Pocas personas he conocido tan dedicadas a su trabajo y que disfruten tanto haciéndolo. Y creo que debería hacer énfasis en el hecho de que Marián es mujer en un mundo de hombres y, aun así, ha conseguido ser referente en el campo de la biología del desarrollo, en el estado español y fuera de él. Y si hay alguna persona, seguramente muy competitiva, que considera este párrafo como un exceso de peloteo, le diré que a quien hace bien su trabajo, está bien decírselo y que se sepa.

ANEX

Differentially expressed genes in the ectoderm (ECT-DEGs), expression values are counts

Symbol	E9.5R1	E9.5R2	E10.5R1	E10.5R2	E11.5R1	E11.5R2	E12.5R1	E12.5R2	pval	padj
Hoxc13	14,56	28,31	536,62	509,12	0,00	972,33	1901,01	1607,24	1,9E-83	2,7E-79
Fbln5	21,04	3,65	443,82	475,38	1895,73	1683,07	1924,77	1722,19	6,3E-81	4,5E-77
Wfikkn1	556,69	536,94	14,79	13,29	9,66	8,11	2,10	8,14	3,6E-80	1,7E-76
Dgkk	958,02	1070,23	341,61	357,82	143,60	123,70	23,76	32,55	7,1E-79	2,5E-75
Dsg3	0,00	0,91	59,18	59,30	278,82	226,10	597,56	657,14	1,5E-78	4,2E-75
Krt14	207,14	226,47	2146,49	2224,59	9635,76	7744,13	24944,46	14270,85	2,5E-78	6,0E-75
Hoxc12	0,00	0,00	36,31	53,16	349,01	288,96	947,71	712,07	4,2E-78	8,5E-75
Gabrp	4,85	0,00	408,86	680,87	1651,68	2589,49	4361,84	4149,32	6,0E-78	1,1E-74
Krt17	77,68	53,88	551,42	673,71	3029,69	2995,05	8144,29	4850,20	1,1E-75	1,7E-72
Trp73	40,46	46,57	301,26	331,23	549,92	596,17	1901,01	1408,88	3,7E-70	5,3E-67
Hoxc11	0,00	0,00	40,35	43,96	237,61	265,64	808,63	524,90	2,5E-66	3,2E-63
Gjb2	63,11	32,87	716,84	709,50	1000,02	1341,38	5173,26	3664,10	3,0E-64	3,6E-61
Tbx1	3,24	4,57	73,97	97,12	382,49	417,72	937,92	646,96	1,9E-63	2,0E-60
Anxa1	0,00	2,74	349,68	426,31	552,49	744,20	1434,84	976,55	1,2E-62	1,2E-59
Peg10	19477,59	36464,68	2835,09	3340,97	1260,17	1332,26	369,72	642,90	5,7E-62	5,4E-59
Mest	36184,69	32736,21	14098,81	12060,42	10360,18	9434,30	4800,05	4566,39	6,3E-60	5,7E-57
Sp9	4,85	8,22	224,60	183,00	477,15	558,66	924,65	645,95	1,3E-54	1,1E-51
Otx1	6,47	3,65	30,93	64,41	559,57	281,86	1771,01	1501,45	3,8E-54	3,0E-51
Hoxc10	8,09	6,39	283,78	270,92	537,68	518,10	752,02	518,79	3,6E-53	2,7E-50
Afap1l1	313,95	328,74	702,05	694,16	1519,03	1527,94	2513,25	2135,19	1,1E-52	8,0E-50
Col17a1	616,56	365,27	1733,60	1848,37	8939,03	5508,49	19268,69	16834,30	6,7E-52	4,5E-49
Bcl11a	84,15	83,10	765,26	892,49	1553,80	1149,76	2068,75	1701,84	1,6E-51	1,0E-48
Cmklr1	401,33	384,44	52,45	28,63	17,39	16,22	4,19	5,09	4,9E-50	3,0E-47
Lama3	21,04	7,31	95,49	101,21	590,48	317,35	1829,72	1431,26	2,9E-49	1,7E-46
Gjb6	21,04	11,87	61,87	76,67	149,39	271,72	1462,10	999,95	7,0E-48	4,0E-45
Cdx1	514,61	446,54	64,56	22,49	4,51	2,03	0,00	0,00	1,5E-46	8,2E-44
Itga2	33,98	31,96	231,33	301,59	491,32	419,75	763,20	900,26	3,5E-46	1,9E-43
Tacstd2	134,32	94,97	1788,75	1466,02	1627,21	1755,05	2709,64	2000,91	4,4E-45	2,3E-42
Cxcl14	653,78	699,49	3019,35	2003,77	6584,82	5424,34	23426,45	13637,11	5,5E-44	2,7E-41
Dsc3	6,47	7,31	80,70	81,79	361,89	304,17	1722,09	711,05	1,0E-42	4,7E-40
Htra1	42,08	35,61	205,77	155,39	442,38	362,97	1717,90	1006,05	5,6E-42	2,6E-39
Alcam	532,41	424,62	866,13	1150,12	2475,91	1870,64	5254,33	5019,06	1,2E-41	5,4E-39
Dennd2c	6,47	10,04	151,98	245,36	248,56	397,45	858,25	879,91	2,7E-40	1,2E-37
Grin3a	9,71	5,48	20,17	20,45	121,06	106,46	315,90	276,69	4,0E-40	1,7E-37
Nckap5	24,27	27,40	59,18	83,83	266,59	333,57	491,33	595,09	7,3E-40	3,0E-37
Has3	105,19	93,14	519,14	707,45	1047,67	1251,15	1201,41	1147,45	1,4E-39	5,6E-37
Stc1	407,81	466,63	41,69	52,14	30,91	28,39	61,50	42,72	1,5E-39	5,7E-37
Pkp1	103,57	142,45	660,36	871,02	1072,79	1300,83	2481,80	1949,03	1,7E-39	6,4E-37
Upk1b	9,71	4,57	115,66	136,99	264,65	360,95	710,78	473,02	3,2E-39	1,2E-36
Ntn4	67,97	64,84	133,15	161,53	321,96	299,10	642,29	636,79	1,9E-38	6,8E-36
Itga9	993,62	895,82	395,41	280,12	185,45	179,46	95,75	84,43	5,0E-38	1,7E-35
Crabp1	2841,70	2139,56	2352,27	1607,10	613,66	618,48	248,81	220,74	5,0E-37	1,7E-34
Vgll3	11,33	19,18	248,81	223,89	244,69	366,02	654,87	582,88	8,0E-37	2,7E-34
Dsp	5091,10	4118,39	11352,48	10317,35	14984,24	15219,58	24632,05	23972,27	4,1E-36	1,3E-33
Mpped1	58,26	54,79	330,85	301,59	495,18	534,32	807,93	619,50	4,8E-36	1,5E-33
Col7a1	56,64	62,10	239,40	588,86	928,55	1019,98	2967,53	2755,70	6,7E-36	2,1E-33
Dpysl3	563,16	555,21	587,73	607,26	1479,75	1205,52	3191,18	2547,17	1,9E-35	5,7E-33
Bcl11b	176,39	179,89	1456,55	1587,68	1516,45	2405,97	2305,67	2297,94	2,9E-35	8,6E-33
Tfap2b	296,14	475,76	1054,42	1607,10	2782,42	2217,39	6380,26	7530,62	5,0E-35	1,5E-32
Cldn1	108,42	94,06	488,21	542,86	495,83	642,81	1256,62	1045,72	2,4E-34	6,7E-32
Zfp750	14,56	9,13	563,52	512,19	311,66	562,71	782,07	621,53	3,5E-34	9,7E-32
Rthov	12,95	3,65	494,93	493,79	294,92	519,11	594,07	594,07	3,7E-34	1,0E-31
Adgrl3	71,20	46,57	360,44	416,09	526,73	463,35	778,58	726,31	6,9E-34	1,9E-31
Fut8	1780,11	2029,06	1084,01	841,38	475,86	539,39	283,05	311,28	1,5E-33	3,9E-31
Man1c1	1152,21	1097,63	390,03	304,65	188,67	239,28	195,69	182,09	2,3E-33	6,0E-31
Hoxb5	247,60	153,41	13,45	19,42	1,29	4,06	0,00	0,00	3,7E-33	9,3E-31
Chst15	140,79	117,80	749,12	580,68	676,13	719,87	1469,09	1197,29	4,3E-33	1,1E-30
Foxj1	496,81	377,14	154,67	75,65	27,05	32,44	4,19	8,14	6,2E-33	1,5E-30
Cpt1a	63,11	31,05	435,75	399,73	653,59	661,06	691,21	701,90	1,4E-32	3,3E-30
Ldoc1	242,74	228,29	68,59	54,18	8,37	11,15	13,28	8,14	1,4E-32	3,4E-30
Anxa2	864,16	612,74	4763,71	3818,40	6496,60	5831,93	12480,27	8427,83	1,5E-32	3,6E-30

Itgb4	378,68	260,25	707,43	774,93	1510,66	1461,02	2627,17	2237,93	3,3E-32	7,6E-30
Dock8	103,57	151,59	220,57	241,27	533,82	412,66	1197,22	1099,64	3,4E-32	7,7E-30
Crb2	357,64	347,92	94,14	92,01	68,90	55,76	30,05	26,45	3,5E-32	7,8E-30
Gnai1	216,85	233,77	398,10	495,83	1066,35	813,14	1831,82	1590,96	4,0E-32	8,7E-30
Klf4	67,97	84,01	182,91	212,64	494,54	498,84	588,47	538,12	5,3E-32	1,1E-29
Pkdcc	1244,46	967,96	251,50	214,69	57,31	131,81	22,36	38,66	5,9E-32	1,3E-29
Bnip3	1551,93	1402,63	571,59	494,81	293,63	290,99	194,29	279,74	1,1E-31	2,3E-29
Npr3	29,13	47,48	21,52	43,96	37,35	46,64	705,89	443,52	2,1E-31	4,4E-29
Synpo2	37,22	47,48	260,91	203,44	804,91	376,16	2269,33	1430,24	2,4E-31	5,0E-29
Fndc1	8,09	9,13	13,45	13,29	25,11	30,42	656,27	242,10	4,6E-31	9,2E-29
Tnfaip2	21,04	9,13	675,15	770,84	421,13	830,38	834,49	896,19	4,7E-31	9,3E-29
Parvb	1351,26	978,00	392,72	311,81	243,41	199,74	115,32	144,45	1,8E-30	3,6E-28
Hgf	542,12	544,25	106,25	116,55	32,84	62,86	23,06	38,66	3,1E-30	6,0E-28
Hoxb4	229,80	250,21	45,73	46,00	21,89	17,24	15,38	18,31	3,6E-30	6,8E-28
Cavin1	45,31	18,26	149,29	128,81	498,40	316,34	2023,32	1053,86	5,1E-30	9,5E-28
Dpp4	8,09	1,83	71,28	97,12	227,95	213,93	243,92	218,71	5,8E-30	1,1E-27
Prtg	4618,56	5511,89	594,46	573,53	62,46	210,89	24,46	83,41	6,5E-30	1,2E-27
Rnf165	398,10	495,85	162,74	169,71	99,17	99,36	33,55	45,78	7,7E-30	1,4E-27
Nectin4	160,21	102,27	1276,33	1584,61	1278,20	1916,26	2297,99	1965,31	1,7E-29	3,0E-27
Rhbdl3	9,71	3,65	53,80	75,65	102,38	134,85	318,00	305,17	7,2E-29	1,3E-26
Nt5e	51,78	64,84	96,83	162,55	263,37	270,71	678,63	710,03	1,0E-28	1,7E-26
Eno3	1090,72	915,91	379,27	265,81	151,97	154,11	85,27	132,24	1,5E-28	2,5E-26
Prkch	77,68	70,31	363,13	318,97	397,95	455,24	753,41	606,27	1,8E-28	3,0E-26
AU018091	3,24	2,74	108,94	127,79	134,58	202,78	262,79	237,02	2,3E-28	3,8E-26
Dlk1	2037,41	1384,36	384,65	219,80	310,37	268,68	51,02	96,64	3,0E-28	4,9E-26
Loxl2	1755,83	1252,87	739,71	617,49	401,17	357,91	218,76	226,84	4,2E-28	6,9E-26
Cyp26a1	116,52	91,32	555,45	683,94	1016,76	1492,45	1215,39	1767,96	4,7E-28	7,7E-26
Rarb	210,38	221,90	22,86	13,29	10,95	14,19	14,68	18,31	5,2E-28	8,3E-26
Lhfpl2	755,74	668,44	501,66	440,62	179,66	254,49	83,17	67,14	7,2E-28	1,1E-25
Pid1	21,04	15,52	121,04	162,55	256,93	262,60	359,23	537,10	1,2E-27	1,9E-25
Papln	11,33	7,31	41,69	39,87	117,84	115,58	290,74	216,67	1,5E-27	2,3E-25
Mall	1,62	6,39	78,01	68,50	152,61	167,29	410,95	241,09	1,7E-27	2,6E-25
Bgn	692,62	546,08	1821,02	1754,32	3138,51	2919,00	2412,60	2193,17	1,7E-27	2,6E-25
Lmx1a	129,46	131,50	29,59	18,40	2,58	2,03	0,00	0,00	2,3E-27	3,4E-25
Cdc42ep1	456,35	361,62	104,90	93,03	65,04	65,90	53,12	38,66	2,4E-27	3,6E-25
Naaa	475,77	446,54	145,25	103,26	103,67	70,97	22,36	32,55	3,7E-27	5,5E-25
Atp2b4	318,80	305,91	771,98	729,94	1050,89	1182,20	1302,75	1417,01	4,1E-27	5,9E-25
Scube1	823,70	704,05	6006,42	5479,68	2360,65	4008,94	675,14	955,19	4,4E-27	6,3E-25
Anxa4	55,02	38,35	220,57	183,00	343,21	321,40	510,20	452,67	7,0E-27	1,0E-24
Adh1	279,96	286,74	49,76	27,60	7,73	10,14	22,36	10,17	8,3E-27	1,2E-24
Meox1	904,62	800,85	282,43	192,20	79,85	139,92	70,59	81,38	8,8E-27	1,2E-24
Hoxa11	25,89	28,31	361,78	252,52	104,32	64,89	9,78	4,07	9,4E-27	1,3E-24
Osbpl5	124,61	137,89	259,57	256,60	492,61	440,03	900,88	720,21	1,2E-26	1,6E-24
Evpl	110,04	57,53	833,85	696,21	799,76	924,67	1545,27	1169,83	1,3E-26	1,8E-24
Lrrk1	341,46	360,70	1168,74	991,66	1296,23	1567,48	1808,06	1765,93	1,5E-26	2,0E-24
Hpgd	4,85	5,48	9,41	5,11	130,72	41,57	366,22	430,29	2,4E-26	3,2E-24
Fmod	254,07	168,02	464,00	369,06	1046,39	680,32	3639,87	2163,67	3,9E-26	5,2E-24
Cyp26b1	6769,26	5516,46	6483,87	5239,44	4231,90	2442,47	595,46	526,93	4,4E-26	5,8E-24
Slc22a23	464,45	403,62	640,18	639,98	795,25	856,74	2184,06	1732,36	4,9E-26	6,3E-24
Zscan10	462,83	486,72	108,94	100,19	57,31	90,24	71,99	66,12	6,0E-26	7,7E-24
Tubb6	1937,08	1336,88	5320,51	3236,69	473,29	1072,70	137,68	128,17	6,7E-26	8,5E-24
Dcn	8,09	4,57	0,00	3,07	21,25	11,15	384,40	164,79	8,1E-26	1,0E-23
Col5a2	550,21	296,78	5620,43	6025,61	6211,99	4640,60	6067,86	4537,91	8,2E-26	1,0E-23
Col13a1	241,12	252,03	355,06	310,79	112,04	153,10	13,98	24,41	9,9E-26	1,2E-23
Fndc3c1	2857,88	3650,85	1188,91	1454,77	1032,22	865,87	148,17	287,88	1,6E-25	1,9E-23
Igdcc3	8601,15	6027,83	5629,84	3050,63	267,87	775,63	41,24	109,86	1,7E-25	2,0E-23
Tagln	51,78	57,53	578,32	487,65	388,93	527,23	333,38	303,14	1,9E-25	2,2E-23
Ambn	3,24	2,74	43,04	58,27	915,67	222,04	2910,22	837,19	1,9E-25	2,3E-23
Trabd2b	218,47	165,28	37,66	42,94	16,74	10,14	5,59	7,12	5,1E-25	6,1E-23
Rgl3	178,01	181,72	86,07	74,63	26,40	21,29	8,39	8,14	6,0E-25	7,0E-23
Btbd11	135,94	148,85	325,47	334,30	464,92	427,86	895,99	737,50	7,4E-25	8,7E-23
Met	2540,70	2573,31	1318,02	1139,90	339,99	564,74	378,80	464,88	7,7E-25	8,9E-23
Cers3	19,42	11,87	151,98	165,62	197,04	310,25	349,45	374,34	9,2E-25	1,1E-22
Car3	208,76	149,76	4,03	7,16	7,08	2,03	11,88	9,16	9,3E-25	1,1E-22

Fat4	134,32	109,58	1631,39	2301,26	1280,78	2137,29	630,41	944,00	1,3E-24	1,5E-22
Fbln2	346,31	431,02	1810,26	2083,51	1696,11	2220,43	2945,17	2373,22	1,5E-24	1,7E-22
Crim1	491,96	488,55	937,41	874,09	1291,72	1320,09	1692,74	1643,86	2,1E-24	2,3E-22
Rnf150	126,23	97,71	141,22	152,33	290,41	328,50	577,29	672,40	2,3E-24	2,5E-22
Eogt	218,47	215,51	1030,21	1525,32	1634,94	2124,11	1695,53	2298,96	3,9E-24	4,3E-22
St3gal1	1307,57	1167,94	377,92	322,03	297,50	203,79	319,40	300,09	6,2E-24	6,7E-22
Flrt2	210,38	220,99	169,46	148,24	209,28	198,72	1735,37	853,46	6,8E-24	7,3E-22
Cbx4	61,49	40,18	275,71	277,05	298,14	347,77	577,29	460,81	2,2E-23	2,3E-21
Alpl	1042,17	694,92	1791,44	1187,95	227,31	367,03	128,60	108,84	2,8E-23	3,0E-21
Oxct1	657,02	502,24	2193,57	2306,37	3425,06	2785,17	4915,37	3447,42	3,4E-23	3,6E-21
Brinp1	85,77	76,71	302,61	263,76	285,90	311,27	749,22	555,41	4,3E-23	4,5E-21
Sall4	1157,07	1205,38	399,44	313,86	383,14	179,46	44,03	68,16	5,1E-23	5,3E-21
Wnt7b	746,03	554,29	3231,85	2257,30	4295,65	4045,44	9761,54	5741,30	5,4E-23	5,6E-21
Nrxn1	3,24	0,91	20,17	10,22	54,73	46,64	180,32	157,67	7,6E-23	7,7E-21
C1s1	14,56	10,96	9,41	17,38	51,51	37,51	195,69	222,78	9,4E-23	9,6E-21
Cacng4	139,17	178,98	568,90	532,63	687,07	678,30	752,02	743,60	9,7E-23	9,8E-21
Ldlrad4	0,00	2,74	20,17	17,38	77,27	76,04	148,87	123,09	1,8E-22	1,9E-20
Chd3	1500,14	1836,38	2974,97	3768,31	8859,83	6336,85	8576,91	10346,34	2,0E-22	2,0E-20
Cbln1	12,95	1,83	180,22	146,19	191,89	215,96	25,86	27,47	2,2E-22	2,2E-20
Ankrd6	548,60	483,07	746,43	755,50	1366,42	1357,61	1596,29	1811,70	2,8E-22	2,7E-20
Gli1	17,80	14,61	430,37	892,49	493,89	1040,26	40,54	95,62	3,1E-22	3,0E-20
Sostdc1	113,28	118,71	260,91	296,48	377,34	446,11	666,05	616,45	3,1E-22	3,0E-20
Rflnb	703,95	720,49	1905,75	2077,37	1883,49	2175,82	3079,36	2618,37	6,1E-22	5,8E-20
Scel	6,47	14,61	33,62	40,89	120,41	190,61	450,79	254,31	6,6E-22	6,3E-20
Nr6a1	2202,48	3050,90	384,65	399,73	43,14	153,10	59,41	151,57	8,4E-22	8,0E-20
Ltbp4	328,51	181,72	629,42	496,85	1368,35	1079,80	3369,40	2207,41	1,0E-21	9,4E-20
Slc16a3	5280,44	3512,05	1853,30	1290,18	987,14	747,24	568,21	360,10	1,1E-21	1,1E-19
Cyp26c1	16,18	3,65	60,52	80,76	201,55	208,86	433,32	273,64	1,6E-21	1,5E-19
Rcan2	119,75	63,92	1058,45	917,03	450,75	637,74	217,36	261,43	2,1E-21	1,9E-19
Trpc4	14,56	1,83	8,07	7,16	99,81	65,90	315,20	238,03	2,3E-21	2,1E-19
Nrarp	330,13	199,07	2211,05	1766,58	1754,06	2291,40	2729,21	2137,22	2,6E-21	2,4E-19
Sema3d	945,07	1049,23	677,84	673,71	749,53	752,31	2296,59	1912,41	3,3E-21	3,0E-19
Zbtb46	179,63	201,81	78,01	69,52	38,64	36,50	9,78	14,24	3,5E-21	3,2E-19
Hoxb8	147,26	104,10	9,41	21,47	5,15	6,08	0,00	0,00	4,2E-21	3,7E-19
Figl12	2134,51	1844,60	1227,91	848,53	390,87	528,24	183,11	291,95	4,3E-21	3,9E-19
Lypd3	9,71	0,91	427,69	269,89	291,70	319,38	730,35	335,69	4,7E-21	4,2E-19
Akap2	702,33	710,45	1435,03	1466,02	2472,05	2176,83	2103,69	2486,13	7,6E-21	6,7E-19
Ret	231,41	125,10	14,79	15,33	13,52	7,10	4,89	6,10	8,2E-21	7,1E-19
Kcnip3	407,81	309,56	127,77	122,68	85,64	93,28	40,54	50,86	8,3E-21	7,2E-19
Gadd45b	8,09	6,39	84,73	130,86	167,42	217,99	184,51	233,97	8,7E-21	7,5E-19
Mmp28	195,81	151,59	56,49	34,76	2,58	5,07	6,99	1,02	8,9E-21	7,6E-19
Gap43	368,97	349,74	563,52	255,58	115,26	78,07	19,57	16,28	1,2E-20	1,0E-18
Aox3	12,95	4,57	988,52	1766,58	425,64	1225,80	154,46	346,88	1,4E-20	1,2E-18
Hoxb6	124,61	94,97	2,69	8,18	1,29	3,04	0,00	0,00	1,6E-20	1,4E-18
Penk	64,73	46,57	224,60	237,18	482,30	464,36	952,60	508,62	1,6E-20	1,4E-18
Col14a1	169,92	87,66	0,00	2,04	3,86	2,03	6,29	4,07	2,3E-20	1,9E-18
Dnmt3b	2726,80	2711,20	1804,88	1591,77	1018,05	1178,15	545,14	728,34	3,8E-20	3,2E-18
Nr2e3	4,85	4,57	24,21	28,63	45,08	33,46	236,23	145,47	4,0E-20	3,3E-18
Plekha2	1458,07	1089,41	1297,85	776,97	222,16	372,10	113,22	139,36	5,1E-20	4,2E-18
Prnp	129,46	112,32	407,51	360,88	640,71	507,96	772,98	632,72	5,4E-20	4,4E-18
Anxa8	24,27	9,13	72,63	70,54	452,04	153,10	1660,59	654,08	7,1E-20	5,7E-18
Fbxo40	420,75	394,49	160,05	131,88	28,33	76,04	8,39	16,28	7,8E-20	6,2E-18
Pcdh19	592,29	315,04	739,71	531,61	149,39	157,15	52,42	61,03	8,1E-20	6,5E-18
Glis3	234,65	231,03	69,94	84,85	37,35	52,72	22,36	20,34	8,2E-20	6,5E-18
Ndufa4l2	385,15	203,64	104,90	61,34	7,73	19,26	11,88	8,14	1,2E-19	9,4E-18
Cntn2	1495,29	1229,13	2681,77	1675,60	403,74	645,85	277,46	287,88	1,4E-19	1,1E-17
Frmpd1	45,31	59,36	103,56	86,90	174,50	179,46	349,45	335,69	1,5E-19	1,2E-17
Gpx3	933,75	586,25	523,17	345,55	262,08	205,82	63,60	71,21	1,6E-19	1,2E-17
Ptch2	43,69	22,83	884,96	1452,73	522,23	2005,48	65,00	107,83	1,8E-19	1,4E-17
Lax1	3,24	0,91	49,76	120,63	113,33	143,97	228,54	281,78	2,3E-19	1,8E-17
Snx31	3,24	2,74	60,52	63,38	79,85	129,78	189,40	151,57	3,0E-19	2,3E-17
Pla2g7	14,56	3,65	79,35	70,54	184,81	285,92	206,87	271,60	3,0E-19	2,3E-17
Pcdhb19	8,09	6,39	53,80	58,27	97,88	95,31	153,06	153,60	3,6E-19	2,8E-17
Antrr1	1000,10	641,04	1747,05	1650,04	3238,32	2969,70	4814,03	3921,46	3,8E-19	2,9E-17

Cux1	1382,01	1696,67	2940,00	3103,79	4278,91	4216,79	4934,94	5773,85	5,1E-19	3,8E-17
Cdkn2b	0,00	0,00	49,76	60,32	83,71	98,35	120,91	83,41	5,2E-19	3,9E-17
Heyl	25,89	42,92	660,36	870,00	382,49	845,59	352,94	359,09	5,5E-19	4,1E-17
Lgi2	818,85	1226,39	160,05	209,58	103,67	138,90	164,24	73,24	5,6E-19	4,2E-17
Scn4b	956,40	1042,84	377,92	307,72	166,13	265,64	208,97	223,79	7,0E-19	5,2E-17
Lama1	1186,20	1201,73	1732,26	1423,08	1017,41	735,07	228,54	305,17	7,3E-19	5,3E-17
Fam84a	48,55	48,40	184,25	224,91	186,10	323,43	1271,30	592,03	9,3E-19	6,8E-17
Cyp2w1	0,00	0,00	0,00	0,00	39,92	10,14	144,67	149,53	9,7E-19	7,1E-17
Apbb2	281,58	319,61	377,92	437,56	724,42	771,57	1011,31	1232,89	1,0E-18	7,5E-17
Fgf8	5492,43	2935,84	24212,62	13830,07	3043,21	6332,79	971,47	1139,31	1,1E-18	7,5E-17
Dgka	137,55	129,67	396,75	509,12	347,72	429,89	735,24	926,71	1,1E-18	7,8E-17
Klf5	59,88	73,97	125,08	151,30	151,97	165,26	390,69	407,91	1,1E-18	8,0E-17
Limch1	203,90	172,59	227,29	371,11	517,72	669,17	1116,14	1254,26	1,2E-18	8,7E-17
Slit2	572,87	513,20	462,65	836,27	2540,30	1795,61	2962,64	3341,63	1,4E-18	1,0E-16
Mylk	404,57	387,18	291,85	339,41	48,94	97,33	20,97	40,69	1,7E-18	1,2E-16
Car12	445,03	436,49	1070,56	1019,26	594,35	604,28	1680,86	1317,33	1,7E-18	1,2E-16
Adamts17	110,04	95,88	836,54	570,46	888,62	374,13	2950,06	1704,89	1,9E-18	1,3E-16
Ltbp3	110,04	84,92	247,47	284,21	477,15	409,61	818,41	562,53	2,3E-18	1,6E-16
Cxcl12	110,04	151,59	84,73	117,57	213,78	355,88	689,81	1082,34	2,4E-18	1,6E-16
Aox4	1,62	0,91	20,17	25,56	63,11	69,96	136,98	98,67	3,1E-18	2,1E-16
Fam196b	268,63	332,39	197,70	296,48	672,26	730,00	1042,76	1154,57	3,2E-18	2,2E-16
Cald1	2751,07	2305,75	2481,38	2825,72	4188,76	3914,65	7390,87	6676,14	4,4E-18	3,0E-16
Ptgis	632,75	385,36	270,33	151,30	146,17	140,93	30,05	35,60	4,6E-18	3,1E-16
Myl9	218,47	195,42	944,13	747,32	942,71	1007,81	1050,45	794,46	4,7E-18	3,2E-16
Ndrp2	71,20	52,96	207,12	204,47	334,20	287,95	516,49	383,50	4,9E-18	3,3E-16
Osbpl3	192,58	159,80	250,16	369,06	640,07	578,93	857,55	950,10	5,0E-18	3,3E-16
Rhbg	0,00	2,74	40,35	64,41	65,04	75,03	202,68	132,24	5,0E-18	3,3E-16
Tcf7	6235,22	6046,09	7300,23	5994,94	2499,09	3844,69	1111,95	1436,34	6,0E-18	3,9E-16
Col8a1	3,24	0,91	0,00	2,04	14,81	20,28	246,01	82,40	6,2E-18	4,0E-16
Enam	0,00	1,83	1,34	0,00	90,79	20,28	247,41	159,71	6,4E-18	4,1E-16
Fzd10	860,92	664,79	3416,10	3172,29	4198,42	2904,81	4027,76	3432,17	6,7E-18	4,4E-16
Slc27a6	1271,97	1070,23	547,38	535,70	242,76	373,11	218,06	146,48	7,3E-18	4,7E-16
Bend4	2344,88	3207,05	1527,83	1457,84	474,58	824,30	230,64	387,57	7,4E-18	4,7E-16
Sct	671,59	546,08	593,11	470,27	182,23	337,63	51,72	65,10	8,4E-18	5,4E-16
Rps6ka4	55,02	53,88	212,50	163,57	311,02	284,90	663,26	401,81	8,6E-18	5,5E-16
Greb1l	831,79	1103,11	298,57	390,53	95,30	247,39	41,24	61,03	9,4E-18	6,0E-16
Kcnma1	3,24	15,52	37,66	82,81	125,57	157,15	331,28	371,29	1,0E-17	6,5E-16
Krt35	0,00	0,00	14,79	14,31	70,19	42,58	345,26	98,67	1,5E-17	9,1E-16
Ror1	1296,24	1165,20	879,58	667,58	153,26	328,50	154,46	155,64	1,5E-17	9,3E-16
Ccdc3	347,93	315,04	1569,52	861,82	163,56	278,82	147,47	100,71	1,7E-17	1,0E-15
Hoxc5	2011,52	1945,05	472,07	475,38	88,22	245,36	32,85	110,88	1,8E-17	1,1E-15
Smpd3	443,41	206,38	2962,86	2295,13	468,14	1266,36	136,98	87,48	2,3E-17	1,4E-15
Paqr5	0,00	0,91	39,00	32,71	45,08	62,86	105,53	118,00	2,8E-17	1,7E-15
Abca12	0,00	13,70	24,21	27,60	82,42	70,97	246,71	222,78	3,3E-17	2,0E-15
Alx1	92,24	94,97	1,34	6,13	3,86	2,03	0,00	1,02	3,4E-17	2,1E-15
Gpm6b	17,80	21,00	185,60	275,01	237,61	269,70	197,09	308,22	4,0E-17	2,4E-15
Pmepa1	30,75	25,57	138,53	143,13	199,62	239,28	252,30	200,40	4,0E-17	2,4E-15
Nfib	27,51	45,66	211,15	413,02	260,15	446,11	699,60	992,83	5,2E-17	3,1E-15
Emp1	4837,03	4339,38	9741,27	9441,21	10562,37	13062,01	14166,72	16176,14	6,3E-17	3,8E-15
Crybg2	61,49	61,18	162,74	219,80	264,65	282,88	618,53	403,84	7,5E-17	4,5E-15
Capn1	344,69	262,99	470,72	402,80	1157,14	1059,52	1658,49	1103,70	7,9E-17	4,7E-15
Otof	0,00	0,00	44,38	53,16	70,19	127,75	2,10	6,10	8,7E-17	5,2E-15
Fam19a2	51,78	65,75	305,30	326,12	208,63	231,17	279,56	310,26	9,4E-17	5,6E-15
Cmpk2	8,09	11,87	28,24	31,69	148,75	103,42	187,31	133,26	9,9E-17	5,8E-15
Car2	312,33	431,02	51,11	117,57	35,42	44,61	40,54	39,67	1,0E-16	6,1E-15
Dnase2a	24,27	13,70	141,22	106,32	308,44	170,33	339,67	307,21	1,1E-16	6,3E-15
Emb	1396,57	1711,28	854,03	710,52	499,05	518,10	494,12	391,64	1,2E-16	6,8E-15
Myh14	178,01	134,24	599,84	516,28	593,70	641,80	1012,71	740,55	1,2E-16	6,8E-15
Sall3	352,78	267,56	1117,63	899,65	256,93	491,74	87,36	112,91	1,2E-16	6,8E-15
Dkk3	137,55	76,71	164,08	203,44	552,49	318,36	1051,85	849,39	1,6E-16	9,3E-15
Prr36	357,64	316,87	150,63	154,37	71,48	87,19	86,66	77,31	1,8E-16	1,0E-14
Fgfbp1	3,24	0,91	52,45	52,14	68,90	94,29	178,22	107,83	2,1E-16	1,2E-14
Scara3	457,97	356,14	1475,38	1379,12	1084,38	1405,26	595,46	528,96	2,5E-16	1,4E-14
Fosl2	181,25	263,91	338,92	396,66	333,56	458,28	1223,77	1042,67	2,7E-16	1,5E-14

Mcam	165,06	140,63	507,04	488,67	506,13	607,32	905,08	668,33	3,0E-16	1,7E-14
Krt6a	0,00	0,91	4,03	10,22	59,24	59,82	240,42	81,38	3,1E-16	1,7E-14
Sh2d4a	14,56	15,52	87,42	78,72	103,67	124,71	206,87	167,84	3,6E-16	2,0E-14
Ppp2r2c	917,56	1138,72	1058,45	562,28	28,33	147,01	27,96	32,55	3,9E-16	2,1E-14
Pcdhb17	8,09	14,61	49,76	63,38	104,96	101,39	172,63	162,76	3,9E-16	2,2E-14
Wnt3a	9,71	11,87	10,76	4,09	31,55	26,36	309,61	116,98	4,3E-16	2,4E-14
Krtap17-1	8,09	1,83	84,73	69,52	132,01	157,15	42,63	48,83	5,8E-16	3,2E-14
Slc16a2	137,55	103,19	324,13	378,26	1643,31	639,77	1575,32	1269,51	5,9E-16	3,2E-14
Fam169a	566,40	702,23	186,94	251,49	125,57	180,47	130,00	142,41	6,3E-16	3,4E-14
Trhde	0,00	3,65	262,26	338,39	29,62	113,56	25,16	12,21	6,4E-16	3,5E-14
Cadm4	116,52	70,31	325,47	333,28	518,36	482,61	449,39	505,57	7,0E-16	3,8E-14
Rab32	24,27	17,35	115,66	81,79	110,11	120,65	269,78	214,64	7,9E-16	4,3E-14
Gria3	202,28	261,17	9,41	29,65	20,61	20,28	46,83	33,57	9,1E-16	4,9E-14
Car4	58,26	82,19	0,00	1,02	0,00	0,00	0,00	0,00	9,3E-16	5,0E-14
Frzb	632,75	380,79	765,26	844,44	209,92	401,50	32,85	62,05	9,8E-16	5,2E-14
Rab3d	16,18	9,13	61,87	34,76	129,43	85,17	297,03	211,59	1,1E-15	5,7E-14
Dlk2	38,84	51,14	61,87	50,09	89,51	52,72	409,56	275,67	1,3E-15	6,7E-14
Prdm11	618,18	717,75	1174,12	1301,43	1310,40	1589,79	2186,16	2397,63	1,4E-15	7,3E-14
Pygo1	304,24	301,35	636,15	698,25	978,77	821,26	948,41	1059,96	1,6E-15	8,3E-14
Myrf	480,63	370,75	115,66	117,57	134,58	73,00	51,72	57,98	1,6E-15	8,4E-14
Gfod1	14,56	17,35	63,21	42,94	75,34	97,33	350,15	190,22	1,7E-15	8,7E-14
Col16a1	40,46	41,09	96,83	95,08	226,66	183,52	273,97	225,83	1,9E-15	1,0E-13
D430019H	291,29	219,16	465,34	545,92	1226,69	879,05	1052,54	1051,83	1,9E-15	1,0E-13
Dclk3	1,62	0,00	21,52	31,69	57,31	47,65	90,86	106,81	2,3E-15	1,2E-13
Nedd9	453,12	447,45	1175,46	1063,22	995,51	1463,05	2325,24	1918,51	2,3E-15	1,2E-13
Itm2b	3063,40	1892,09	12409,59	11050,36	8114,80	8322,05	7001,59	6895,87	2,6E-15	1,3E-13
Sfrp1	1283,29	926,87	418,27	313,86	172,57	253,47	315,20	359,09	2,7E-15	1,4E-13
Hoxb2	490,34	411,84	235,36	213,67	66,97	105,45	91,56	56,97	3,2E-15	1,6E-13
Ngf	16,18	10,96	28,24	40,89	61,17	59,82	192,20	153,60	3,3E-15	1,7E-13
Exph5	71,20	64,84	247,47	255,58	207,99	356,89	501,11	643,91	3,5E-15	1,8E-13
Pogk	1369,06	1372,49	2840,47	2805,27	2837,15	3076,16	3534,34	3241,94	3,6E-15	1,8E-13
Lin28b	2183,06	2913,92	851,34	995,75	171,29	527,23	81,07	179,03	3,6E-15	1,8E-13
Cpz	2008,28	1362,45	1281,71	901,69	176,44	494,78	53,12	107,83	3,8E-15	1,9E-13
Prss23	278,34	297,69	219,22	193,22	196,40	238,27	1018,30	656,12	3,8E-15	1,9E-13
Sult5a1	33,98	10,96	40,35	71,56	191,25	126,74	625,52	344,84	4,1E-15	2,0E-13
Grhl3	589,05	483,07	1833,13	1848,37	1316,84	1899,03	2399,33	2173,84	4,6E-15	2,3E-13
Ptpm	100,33	71,23	199,05	214,69	264,65	274,77	421,44	416,05	5,3E-15	2,6E-13
Plcd3	33,98	32,87	59,18	115,52	132,01	207,85	378,11	384,52	5,9E-15	2,9E-13
Elf1	360,88	363,44	578,32	641,00	673,55	933,80	1329,31	1473,98	6,3E-15	3,1E-13
Fry	166,68	214,59	723,57	862,85	916,96	1731,73	1374,04	2065,00	6,9E-15	3,4E-13
Itpril2	190,96	194,51	375,23	350,66	557,64	497,82	625,52	619,50	7,2E-15	3,5E-13
Sdk2	262,16	271,21	75,32	40,89	32,20	27,38	68,49	46,79	8,4E-15	4,1E-13
Arhgef3	134,32	98,62	575,63	495,83	292,99	384,27	519,28	534,05	8,8E-15	4,2E-13
Fxyd3	114,90	64,84	578,32	638,96	426,93	592,11	382,30	381,46	1,0E-14	4,8E-13
Clic6	524,32	515,94	594,46	470,27	108,82	219,00	71,99	89,52	1,1E-14	5,1E-13
Ppfia3	74,44	62,10	216,53	204,47	217,65	229,14	409,56	325,52	1,1E-14	5,3E-13
Cav1	11,33	3,65	6,72	12,27	83,07	34,47	301,93	156,65	1,2E-14	5,8E-13
Hoxa13	0,00	0,91	84,73	246,38	951,08	165,26	95,05	94,60	1,3E-14	6,2E-13
Arhgap25	19,42	24,66	32,28	28,63	25,76	32,44	243,22	142,41	1,3E-14	6,3E-13
Sema4f	33,98	21,00	33,62	26,58	215,72	84,15	397,67	290,93	1,7E-14	8,2E-13
Runx1	42,08	35,61	72,63	141,08	407,61	387,31	222,95	362,14	1,8E-14	8,5E-13
Krt15	131,08	108,67	51,11	56,23	68,90	65,90	1799,67	305,17	1,9E-14	8,6E-13
Neb1	276,73	274,86	519,14	838,31	1120,44	1517,80	1471,19	2381,36	1,9E-14	8,9E-13
Sorcs2	673,20	406,36	1564,14	1266,67	2048,98	2117,01	2734,10	2521,74	2,1E-14	9,7E-13
Fam20a	3,24	3,65	28,24	61,34	159,05	148,03	190,10	98,67	2,1E-14	9,8E-13
S1pr3	1267,11	852,90	1552,04	1357,65	1056,04	1010,85	230,64	325,52	2,3E-14	1,0E-12
Gpld1	16,18	23,74	82,04	95,08	82,42	112,54	248,81	197,34	2,7E-14	1,2E-12
Megf11	14,56	10,96	411,55	297,50	125,57	35,49	29,35	12,21	3,1E-14	1,4E-12
Efna1	440,17	476,67	720,88	734,03	1130,10	1263,31	1244,74	1105,74	3,7E-14	1,7E-12
Krt5	5267,49	3200,66	16106,78	11936,72	17912,19	18575,58	45559,93	24562,26	4,3E-14	1,9E-12
Abcg1	66,35	34,70	517,79	404,84	361,24	551,56	306,82	418,09	5,0E-14	2,3E-12
Bdh1	168,30	159,80	462,65	445,74	667,75	529,25	1162,27	719,19	5,3E-14	2,4E-12
Cln5	2608,66	3134,00	1405,44	1381,17	1269,18	1259,26	923,95	1148,46	5,4E-14	2,4E-12
Irf6	953,17	841,94	2774,57	3251,01	2565,41	3908,57	3583,96	3607,13	5,4E-14	2,4E-12

Tenm4	1110,14	842,86	2976,31	2860,48	2649,77	3120,77	3230,32	2821,82	5,7E-14	2,6E-12
Kctd12	805,90	746,06	368,51	224,91	222,80	191,63	195,69	200,40	6,1E-14	2,7E-12
Icam1	48,55	36,53	123,73	98,14	112,69	107,47	372,51	254,31	6,6E-14	2,9E-12
Gata5	89,01	48,40	2,69	4,09	1,29	0,00	0,00	0,00	6,8E-14	3,0E-12
Cyp11b1	589,05	720,49	348,33	329,19	318,75	283,89	1190,93	863,64	6,8E-14	3,0E-12
Sash1	1024,37	1036,45	1213,12	1243,15	1897,02	1710,44	2342,02	2340,67	7,8E-14	3,4E-12
Plcl2	343,07	328,74	185,60	194,24	164,20	107,47	48,22	57,98	7,9E-14	3,5E-12
Calcr	111,66	120,54	29,59	36,80	11,59	22,31	4,89	5,09	8,0E-14	3,5E-12
Cpxm2	6,47	3,65	5,38	10,22	26,40	23,32	123,71	90,53	8,1E-14	3,5E-12
Ahr	64,73	64,84	150,63	212,64	181,59	335,60	511,60	617,46	8,2E-14	3,6E-12
Spats2l	105,19	84,92	161,39	179,93	240,83	248,40	506,70	382,48	1,1E-13	4,7E-12
Wscd1	48,55	71,23	342,95	177,89	27,05	44,61	23,76	15,26	1,1E-13	4,8E-12
Prdm6	118,13	111,41	18,83	20,45	19,96	6,08	2,10	1,02	1,1E-13	4,8E-12
Espn	616,56	399,05	328,16	190,15	67,61	101,39	83,87	64,09	1,5E-13	6,4E-12
Pctp	551,83	514,11	438,44	330,21	181,59	238,27	77,58	116,98	1,6E-13	6,9E-12
Rhof	8,09	11,87	90,11	85,88	71,48	140,93	4,19	8,14	1,6E-13	6,9E-12
Syne3	4,85	2,74	73,97	102,23	83,07	165,26	21,67	24,41	1,6E-13	6,9E-12
Meis2	3569,92	3477,35	1733,60	1436,37	1199,00	1451,90	2380,46	2369,15	1,8E-13	7,5E-12
Smox	236,27	215,51	520,48	474,36	703,81	724,94	767,39	621,53	1,8E-13	7,7E-12
Sipa1l2	511,38	459,32	683,22	707,45	1213,16	1138,60	1076,31	1099,64	2,0E-13	8,4E-12
Cobl	37,22	34,70	281,09	200,38	166,13	219,00	259,29	219,72	2,1E-13	8,9E-12
Sgk3	341,46	314,13	1313,99	1694,00	1211,23	1829,07	1186,03	1581,81	2,1E-13	8,9E-12
Pianp	56,64	35,61	111,63	93,03	307,15	210,89	276,76	287,88	2,2E-13	9,2E-12
H2-T23	8,09	6,39	25,55	26,58	72,76	80,10	161,45	96,64	2,3E-13	9,6E-12
Notch1	1016,28	830,98	3835,72	4674,09	2886,09	4733,88	3883,79	4889,87	2,6E-13	1,1E-11
Mn1	59,88	97,71	118,35	145,17	155,83	254,49	532,56	500,48	2,8E-13	1,2E-11
Tmbim1	106,81	131,50	231,33	262,74	423,06	356,89	475,25	446,57	2,8E-13	1,2E-11
Eps8	281,58	242,90	953,55	847,51	538,97	579,95	338,97	228,88	3,2E-13	1,3E-11
Sfn	1093,96	847,42	5534,35	3982,99	4708,41	4358,74	7326,58	4143,22	3,2E-13	1,3E-11
Lgr6	202,28	234,68	1327,44	1042,78	294,28	469,43	1032,98	682,57	3,3E-13	1,4E-11
Rasa3	417,52	488,55	645,56	584,77	652,94	735,07	1439,74	1230,86	3,5E-13	1,4E-11
Pitpnm2	372,20	483,07	560,83	621,58	1005,82	873,98	1405,49	1269,51	3,6E-13	1,5E-11
Baiap2l1	493,57	526,90	234,02	248,43	194,47	204,81	164,94	185,14	3,8E-13	1,5E-11
Msr3	190,96	163,46	216,53	270,92	394,08	436,99	619,23	574,74	3,8E-13	1,5E-11
Lgals7	33,98	21,92	107,59	66,45	342,57	180,47	929,54	315,34	4,0E-13	1,6E-11
Mtmr11	101,95	150,67	162,74	215,71	403,74	331,54	577,99	557,45	4,1E-13	1,7E-11
Tmtc2	216,85	192,68	599,84	597,04	655,52	641,80	510,90	634,76	4,3E-13	1,7E-11
Bmp4	1927,37	1243,74	6076,36	5561,47	2935,67	3810,22	2056,86	1886,98	4,4E-13	1,8E-11
Elmo1	199,05	243,82	134,49	111,43	93,37	91,25	36,34	25,43	4,7E-13	1,9E-11
Ly75	728,22	718,66	388,68	498,90	380,56	409,61	179,62	212,60	5,1E-13	2,1E-11
Gm19410	0,00	1,83	20,17	58,27	74,05	107,47	113,92	171,91	5,3E-13	2,1E-11
Ghr	98,71	103,19	217,88	223,89	212,50	214,95	511,60	380,45	5,6E-13	2,2E-11
Iqgap2	457,97	408,19	418,27	442,67	359,31	299,10	132,09	131,22	5,8E-13	2,3E-11
Ly6g6e	14,56	2,74	99,52	101,21	169,35	125,72	255,80	155,64	5,9E-13	2,3E-11
Lipg	147,26	178,07	267,64	202,42	337,42	355,88	619,23	576,77	6,1E-13	2,4E-11
Bdkrb2	29,13	15,52	99,52	117,57	83,07	154,11	299,83	275,67	6,3E-13	2,5E-11
Abcg2	744,41	653,83	340,27	396,66	330,34	300,11	151,66	205,48	6,3E-13	2,5E-11
Slco4a1	16,18	22,83	60,52	68,50	123,63	206,83	176,82	191,24	6,7E-13	2,6E-11
Hoxa1	203,90	261,17	71,28	76,67	35,42	48,67	64,30	53,91	7,2E-13	2,8E-11
Klhl32	38,84	30,13	270,33	305,68	155,19	225,08	141,88	95,62	7,2E-13	2,8E-11
Myof	24,27	21,92	63,21	58,27	106,89	181,49	190,10	236,00	7,2E-13	2,8E-11
Unc5a	77,68	83,10	9,41	15,33	1,93	3,04	6,99	4,07	7,5E-13	2,9E-11
Tnnt3	95,48	126,02	26,90	11,25	5,80	11,15	4,19	4,07	9,0E-13	3,5E-11
Fam13c	474,16	616,39	160,05	239,23	141,66	205,82	103,44	92,57	9,4E-13	3,6E-11
Aldh1a2	80,91	61,18	0,00	0,00	7,73	5,07	11,18	15,26	9,9E-13	3,8E-11
Fam184b	77,68	52,96	43,04	53,16	120,41	97,33	396,28	242,10	1,1E-12	4,1E-11
Pls3	3877,39	3258,19	1712,09	1342,32	1754,71	1713,48	1434,14	1355,98	1,2E-12	4,5E-11
Rab27b	71,20	73,05	86,07	96,10	137,16	134,85	271,87	284,83	1,2E-12	4,5E-11
Btg1	729,84	721,40	911,86	1017,22	1193,20	1242,02	1703,22	1811,70	1,2E-12	4,6E-11
Duoxa1	0,00	3,65	53,80	60,32	54,73	79,08	112,52	82,40	1,2E-12	4,6E-11
Pde4b	40,46	52,05	40,35	48,05	79,20	92,26	199,89	228,88	1,2E-12	4,7E-11
Fap	16,18	22,83	33,62	62,36	143,60	154,11	158,65	229,90	1,3E-12	4,8E-11
Spon1	160,21	82,19	589,08	542,86	72,12	207,85	22,36	36,62	1,3E-12	5,0E-11
Colec12	1827,04	1641,88	3974,24	3403,33	1267,90	2041,99	508,10	804,64	1,5E-12	5,6E-11

Fut4	894,91	769,80	340,27	213,67	171,29	254,49	219,45	202,43	1,6E-12	5,8E-11
Sox10	55,02	55,70	0,00	0,00	0,00	0,00	0,70	0,00	1,6E-12	5,9E-11
Sgms2	80,91	60,27	236,71	341,46	382,49	552,57	214,56	181,07	1,6E-12	6,1E-11
Dact1	184,48	169,85	133,15	79,74	31,55	40,56	23,76	24,41	1,7E-12	6,4E-11
Bdnf	8,09	8,22	17,48	16,36	66,97	30,42	141,88	139,36	1,8E-12	6,5E-11
Crhr1	425,61	392,66	1077,28	1050,95	294,92	569,81	120,91	183,10	1,8E-12	6,5E-11
Wnt10b	90,62	101,36	975,07	1509,98	237,61	612,39	681,43	495,40	1,9E-12	6,8E-11
Tbc1d24	320,42	368,01	589,08	629,75	985,86	893,24	811,42	839,22	1,9E-12	6,9E-11
Notum	679,68	754,28	2603,77	2207,21	598,85	1079,80	617,83	444,53	2,5E-12	9,0E-11
Zhx2	398,10	389,92	552,76	535,70	625,26	652,95	1000,83	975,53	2,5E-12	9,1E-11
Metrn	1178,11	958,83	314,71	241,27	397,95	231,17	285,85	205,48	2,5E-12	9,2E-11
Calml3	1,62	2,74	9,41	13,29	50,23	36,50	119,51	70,19	2,6E-12	9,5E-11
Pdzd2	84,15	78,53	290,50	358,84	795,25	417,72	343,86	369,26	2,6E-12	9,6E-11
Zfp385c	14,56	17,35	16,14	8,18	104,32	156,14	24,46	22,38	2,7E-12	9,9E-11
Sel1l3	894,91	797,20	700,70	624,64	215,72	355,88	207,57	132,24	2,9E-12	1,0E-10
Ptpre	1,62	3,65	12,10	26,58	23,18	36,50	115,32	113,93	2,9E-12	1,0E-10
Spock2	118,13	74,88	182,91	204,47	629,12	230,15	1894,02	802,60	2,9E-12	1,0E-10
S100a3	150,50	120,54	111,63	55,21	10,30	22,31	8,39	7,12	3,2E-12	1,1E-10
Gpr4	19,42	19,18	22,86	27,60	129,43	143,97	52,42	55,95	3,2E-12	1,1E-10
Lamc2	1500,14	938,74	3222,43	2777,67	4519,10	4826,14	5201,92	4137,11	3,5E-12	1,2E-10
Sh3kbp1	275,11	308,65	184,25	180,95	123,63	126,74	66,40	78,33	3,6E-12	1,3E-10
Tnni1	169,92	111,41	170,81	101,21	33,48	46,64	13,98	9,16	4,4E-12	1,5E-10
Lamb3	383,53	166,20	492,24	402,80	1534,48	1010,85	1868,86	1640,81	4,5E-12	1,6E-10
Itm2a	381,91	254,77	338,92	322,03	505,48	472,48	997,33	937,89	5,0E-12	1,8E-10
Casr	29,13	35,61	60,52	41,92	93,37	75,03	194,99	213,62	5,2E-12	1,8E-10
Dsg1a	0,00	0,91	17,48	4,09	34,13	43,60	207,57	75,28	5,5E-12	1,9E-10
Bcl2	181,25	241,08	570,25	533,66	510,64	578,93	706,59	718,17	6,4E-12	2,2E-10
Cdh8	4,85	1,83	103,56	150,28	45,08	75,03	15,38	30,52	6,7E-12	2,3E-10
Cldn23	24,27	14,61	157,36	171,75	97,88	172,36	235,53	187,17	7,1E-12	2,5E-10
Ak4	1718,61	2194,35	835,20	952,81	419,84	692,49	556,32	603,22	7,3E-12	2,5E-10
Hsd17b14	1,62	1,83	60,52	54,18	5,15	4,06	1,40	1,02	7,9E-12	2,8E-10
Tmtc1	317,18	226,47	730,29	979,39	1099,19	1621,22	1225,17	1914,44	8,5E-12	2,9E-10
Gpa33	4,85	2,74	8,07	4,09	35,42	13,18	256,50	76,29	9,2E-12	3,2E-10
Ehbp1	365,73	400,88	423,65	540,81	782,37	726,96	1016,90	1157,62	9,8E-12	3,4E-10
Socs2	140,79	128,76	360,44	382,35	387,00	531,28	475,95	513,71	1,2E-11	4,2E-10
Ppp1r3b	97,10	121,45	103,56	125,75	159,69	191,63	446,60	350,95	1,2E-11	4,2E-10
6430548M	105,19	93,14	90,11	61,34	24,47	19,26	9,78	9,16	1,2E-11	4,2E-10
Lfng	286,44	253,86	523,17	519,34	653,59	746,23	895,29	735,46	1,3E-11	4,3E-10
Slc35d3	77,68	53,88	309,33	151,30	1,93	26,36	0,00	1,02	1,3E-11	4,4E-10
Hoxb9	150,50	166,20	51,11	27,60	38,64	11,15	3,49	4,07	1,3E-11	4,4E-10
Limk2	1738,03	1724,06	3274,88	3573,04	3417,98	4332,37	4449,90	5003,80	1,4E-11	4,6E-10
Dst	1320,51	2054,63	2638,74	4568,79	5738,70	6505,15	8038,75	12697,18	1,4E-11	4,6E-10
Hoxb3	228,18	245,64	41,69	85,88	28,98	43,60	41,24	33,57	1,4E-11	4,7E-10
3830417A	29,13	21,92	114,32	96,10	136,51	124,71	171,23	158,69	1,4E-11	4,7E-10
Ch25h	0,00	0,00	20,17	11,25	13,52	29,40	107,63	71,21	1,5E-11	5,0E-10
Tspan15	145,64	107,75	223,26	252,52	418,55	506,95	408,16	383,50	1,5E-11	5,1E-10
Prkcb	126,23	136,06	306,64	197,31	22,54	55,76	18,87	29,50	1,6E-11	5,3E-10
Dusp16	409,42	444,71	1043,66	1087,76	794,61	991,59	1238,45	1142,36	1,6E-11	5,4E-10
Hoxd11	6,47	1,83	228,64	106,32	499,69	80,10	16,77	16,28	1,7E-11	5,5E-10
Gata3	430,46	517,77	251,50	261,72	63,11	136,88	88,06	94,60	1,7E-11	5,6E-10
Crabp2	2822,28	2536,78	1032,90	746,30	890,55	264,63	272,57	172,93	1,7E-11	5,7E-10
Gpr85	51,78	39,27	252,85	301,59	149,39	213,93	169,13	165,81	1,9E-11	6,1E-10
Asb4	1318,90	1221,82	1015,42	1659,24	1620,13	514,04	50,32	102,74	1,9E-11	6,3E-10
Dab1	255,69	292,21	68,59	77,70	54,09	77,06	121,61	103,76	2,0E-11	6,5E-10
Eppk1	4,85	7,31	49,76	53,16	56,67	79,08	104,84	102,74	2,1E-11	6,9E-10
Sfxn3	37,22	32,87	39,00	61,34	166,13	96,32	319,40	216,67	2,2E-11	7,3E-10
Soga3	242,74	192,68	52,45	46,00	53,45	45,63	33,55	55,95	2,2E-11	7,3E-10
Hoxc8	1220,18	1063,84	1312,64	1095,94	260,79	584,00	76,18	178,02	2,4E-11	7,7E-10
Moxd1	233,03	247,47	1242,71	1210,44	320,68	576,91	503,91	333,65	2,4E-11	7,7E-10
Ednra	262,16	241,99	445,17	364,97	860,93	529,25	1101,47	974,52	2,5E-11	7,9E-10
Zfyve28	8,09	3,65	13,45	96,10	173,86	217,99	287,25	485,22	2,5E-11	8,0E-10
St8sia2	48,55	81,27	391,37	294,43	300,07	247,39	320,10	400,79	2,6E-11	8,5E-10
Col19a1	9,71	5,48	37,66	69,52	95,30	202,78	143,27	158,69	2,7E-11	8,7E-10
Jun	271,87	180,81	702,05	677,80	1030,93	808,07	1267,11	855,50	2,9E-11	9,4E-10

Cd59a	114,90	115,06	256,88	292,39	362,53	307,21	383,00	429,28	3,2E-11	1,0E-09
Fgf9	135,94	108,67	591,77	899,65	449,46	687,42	448,00	607,29	3,2E-11	1,0E-09
Plekha6	247,60	201,81	150,63	185,04	260,79	271,72	503,21	603,22	3,7E-11	1,2E-09
Ehd2	181,25	113,23	372,54	252,52	598,85	435,97	1605,37	761,91	3,8E-11	1,2E-09
Vsig10	113,28	95,88	278,40	395,64	403,10	587,05	448,69	547,27	3,8E-11	1,2E-09
Islr	17,80	8,22	153,32	74,63	243,41	249,42	190,80	105,79	3,9E-11	1,2E-09
Ube2ql1	155,35	64,84	1176,81	687,01	321,32	559,67	183,81	142,41	4,0E-11	1,3E-09
Rab11fip5	380,30	262,08	1358,37	1062,20	692,87	757,38	682,83	645,95	4,9E-11	1,6E-09
Hs3st2	0,00	0,00	6,72	6,13	30,91	16,22	76,18	54,93	5,1E-11	1,6E-09
Podxl2	121,37	81,27	182,91	208,56	485,52	301,13	506,70	485,22	5,3E-11	1,7E-09
Dixdc1	535,65	515,94	852,68	1024,37	755,97	737,10	325,69	374,34	5,4E-11	1,7E-09
Wnt9b	152,12	126,02	641,53	438,58	364,46	546,49	692,61	688,67	5,4E-11	1,7E-09
Slco2a1	30,75	16,44	10,76	12,27	97,23	53,74	162,14	129,19	5,5E-11	1,7E-09
Palm3	1299,48	1099,46	648,25	585,79	424,99	474,50	364,13	498,45	5,6E-11	1,7E-09
Hoxc6	975,82	838,29	581,01	586,82	180,30	329,52	97,85	192,26	6,4E-11	2,0E-09
Mapk12	213,61	231,03	112,97	222,87	64,39	75,03	20,97	32,55	6,6E-11	2,0E-09
Stat3	160,21	199,07	255,54	263,76	500,33	469,43	545,14	459,79	6,8E-11	2,1E-09
Zic3	1,62	1,83	78,01	201,40	395,37	77,06	31,45	38,66	6,9E-11	2,1E-09
Khdrbs3	2370,78	1837,30	3016,66	2026,26	1041,23	1239,99	786,26	711,05	7,1E-11	2,2E-09
Vgll1	1,62	1,83	52,45	66,45	45,72	92,26	93,65	74,26	7,6E-11	2,3E-09
Elmod1	0,00	0,00	13,45	21,47	58,60	50,69	50,32	37,64	7,7E-11	2,3E-09
Myo1c	538,89	470,28	763,92	741,19	1090,17	902,37	1829,02	1348,86	7,7E-11	2,4E-09
Chrna7	66,35	52,05	95,49	146,19	259,50	293,02	237,63	233,97	7,7E-11	2,4E-09
Kbtbd11	135,94	139,71	275,71	309,77	402,46	339,65	437,51	534,05	7,7E-11	2,4E-09
Il1r1	6,47	2,74	6,72	19,42	28,33	27,38	111,13	100,71	7,9E-11	2,4E-09
Npr1	90,62	88,58	41,69	37,83	9,02	13,18	11,18	9,16	8,1E-11	2,5E-09
Dusp27	9,71	13,70	10,76	8,18	25,11	17,24	136,98	82,40	8,4E-11	2,6E-09
Ppargc1b	8,09	10,04	16,14	35,78	41,21	46,64	155,16	114,95	8,5E-11	2,6E-09
Pmp22	186,10	195,42	5,38	15,33	31,55	6,08	8,39	14,24	8,8E-11	2,6E-09
Tdrd7	32,37	31,96	176,18	298,52	206,70	344,72	53,82	96,64	8,9E-11	2,7E-09
Papss2	35,60	25,57	130,46	128,81	457,19	180,47	292,14	271,60	9,0E-11	2,7E-09
Fgf17	64,73	42,92	484,17	375,19	99,17	244,35	72,69	42,72	9,1E-11	2,7E-09
Ada	491,96	389,01	270,33	142,10	126,21	89,22	79,67	56,97	9,7E-11	2,9E-09
Ciart	186,10	183,55	55,14	87,92	34,77	31,43	41,24	27,47	1,1E-10	3,1E-09
Cdh6	433,70	281,26	1584,32	1901,53	690,94	1178,15	570,30	657,14	1,1E-10	3,2E-09
Elk3	377,06	287,65	634,80	656,34	1360,62	954,08	1093,08	939,93	1,1E-10	3,3E-09
Kcnh2	176,39	137,89	39,00	10,22	17,39	12,17	4,19	10,17	1,1E-10	3,3E-09
Trim71	2514,80	3580,54	1439,07	1705,25	516,43	1002,74	150,26	427,24	1,2E-10	3,6E-09
Kirrel3	271,87	204,55	1609,87	1104,12	256,93	648,89	243,22	267,53	1,4E-10	4,0E-09
C1ql4	42,08	48,40	12,10	15,33	0,00	0,00	0,70	2,03	1,4E-10	4,0E-09
Rftn1	61,49	57,53	67,25	84,85	184,16	139,92	311,01	227,86	1,4E-10	4,0E-09
Tdrp	239,51	194,51	381,96	332,26	449,46	483,63	637,40	649,00	1,4E-10	4,0E-09
Dct	8,09	1,83	8,07	9,20	56,67	14,19	200,58	127,15	1,4E-10	4,1E-09
Txnip	626,27	928,69	1390,65	1403,66	1266,61	2508,38	3940,40	4029,29	1,5E-10	4,2E-09
Slc2a12	131,08	116,89	164,08	188,11	220,22	259,56	433,32	387,57	1,5E-10	4,3E-09
Duox1	0,00	1,83	57,83	60,32	45,72	92,26	63,60	54,93	1,5E-10	4,3E-09
Tubb2b	873,87	673,01	1644,84	1451,71	2725,11	2002,44	3691,59	2460,70	1,7E-10	4,8E-09
Wisp1	147,26	185,37	306,64	242,29	296,85	366,02	567,51	642,90	1,7E-10	5,0E-09
Gng4	0,00	0,00	2,69	7,16	37,99	34,47	46,83	45,78	1,8E-10	5,2E-09
Plekhh3	35,60	32,87	131,80	98,14	166,78	115,58	308,91	208,53	1,8E-10	5,3E-09
Gm42372	93,86	65,75	14,79	25,56	7,08	6,08	0,70	4,07	1,8E-10	5,3E-09
Reck	980,68	1022,75	450,55	569,44	329,69	454,23	153,76	265,50	1,8E-10	5,3E-09
Map2	1848,07	1606,26	4180,02	5589,07	3950,51	5317,88	5293,47	6480,83	1,9E-10	5,4E-09
Pgbd5	22,66	34,70	457,27	292,39	20,61	108,49	27,26	21,36	2,0E-10	5,6E-09
Adgrg1	317,18	212,77	497,62	487,65	770,78	819,23	1787,79	946,03	2,0E-10	5,8E-09
Cdc42ep3	101,95	71,23	170,81	139,04	312,95	250,43	331,98	367,22	2,1E-10	6,1E-09
Tjp3	758,97	668,44	528,55	414,04	199,62	300,11	181,71	220,74	2,2E-10	6,1E-09
Crybg3	393,24	475,76	669,77	809,68	535,11	839,51	1578,82	1578,76	2,2E-10	6,2E-09
Vim	1615,04	898,56	5750,88	4629,11	7514,66	5702,15	6844,33	4542,99	2,2E-10	6,3E-09
Tshz2	653,78	596,30	352,37	250,47	225,38	237,25	104,14	172,93	2,2E-10	6,3E-09
Hoxa3	156,97	189,03	41,69	63,38	30,26	36,50	41,24	41,71	2,2E-10	6,3E-09
Shisa3	90,62	47,48	4,03	3,07	11,59	5,07	1,40	1,02	2,3E-10	6,6E-09
Ggt1	226,56	260,25	174,84	117,57	46,36	88,21	36,34	28,48	2,5E-10	7,0E-09
Serpinb5	0,00	1,83	5,38	4,09	28,98	29,40	53,82	54,93	2,6E-10	7,2E-09

Gpx2	334,98	187,20	1086,70	637,93	552,49	863,84	164,24	118,00	2,7E-10	7,6E-09
Arhgef28	116,52	115,97	147,94	227,98	265,94	265,64	518,58	423,17	2,8E-10	7,8E-09
Krt19	1820,56	1462,90	917,24	748,35	251,13	431,92	443,80	209,55	2,8E-10	7,9E-09
Ube2e3	2477,58	2628,10	3804,78	4253,91	5816,61	6706,92	5884,74	8315,93	2,8E-10	7,9E-09
Jaml	56,64	53,88	4,03	5,11	1,93	1,01	0,70	3,05	2,9E-10	8,1E-09
St5	602,00	479,41	879,58	858,76	1334,87	1013,90	1666,18	1545,19	3,0E-10	8,2E-09
Trp53i11	1050,26	925,04	2181,46	1790,10	2135,91	2333,99	2650,23	2358,98	3,0E-10	8,4E-09
Mfsd13a	178,01	134,24	75,32	76,67	48,29	46,64	21,67	28,48	3,0E-10	8,4E-09
Cpne6	0,00	0,00	0,00	0,00	9,02	2,03	64,30	56,97	3,1E-10	8,6E-09
Palm2	122,99	103,19	185,60	180,95	317,46	360,95	306,82	357,05	3,4E-10	9,3E-09
Slc7a1	3514,90	3791,48	2960,17	2610,01	3983,99	3674,36	8644,00	6215,33	3,4E-10	9,3E-09
Ackr3	754,12	784,41	780,05	765,72	767,56	1076,76	2308,47	1754,74	3,4E-10	9,4E-09
Dnmt3a	3094,15	2619,88	4220,36	3811,24	6078,05	5324,98	6640,95	6301,80	3,5E-10	9,5E-09
Sparc	2788,29	1738,67	5219,64	4727,25	7002,73	6116,83	10891,67	7640,49	3,5E-10	9,5E-09
Pcdhb16	6,47	6,39	25,55	24,54	48,94	47,65	94,35	81,38	3,5E-10	9,5E-09
Zbtb16	93,86	109,58	32,28	25,56	10,30	12,17	0,00	6,10	3,5E-10	9,6E-09
Cdh13	27,51	32,87	147,94	80,76	127,50	102,40	262,09	225,83	3,7E-10	9,9E-09
Ppic	448,26	304,09	797,54	956,90	1382,52	1123,40	1490,76	1184,07	3,8E-10	1,0E-08
Coch	14,56	4,57	9,41	13,29	133,94	38,53	141,88	247,19	3,9E-10	1,1E-08
Ntm	79,30	96,80	177,53	168,68	24,47	54,75	20,97	15,26	4,0E-10	1,1E-08
Arid5b	1615,04	1699,41	1642,15	1812,59	1858,38	2019,68	3207,25	3226,68	4,4E-10	1,2E-08
Hoxa10	43,69	23,74	298,57	454,94	726,35	179,46	53,12	76,29	4,4E-10	1,2E-08
Arrb1	487,10	480,33	1361,06	1969,01	1210,59	3061,96	434,72	469,96	4,5E-10	1,2E-08
Pcdh7	1446,74	1330,49	2219,12	2003,77	2557,69	3005,19	3082,85	3273,48	4,6E-10	1,2E-08
Oit3	6,47	9,13	36,31	22,49	48,94	51,71	116,72	95,62	5,1E-10	1,4E-08
Bcat1	1318,90	1194,43	342,95	313,86	881,54	230,15	113,22	93,59	5,2E-10	1,4E-08
Gnaz	33,98	49,31	177,53	150,28	28,33	60,83	10,48	15,26	5,2E-10	1,4E-08
Ppp1r36	35,60	25,57	104,90	115,52	142,31	181,49	166,34	147,50	5,2E-10	1,4E-08
Pitpnm3	1,62	3,65	2,69	10,22	18,67	14,19	80,37	79,34	5,2E-10	1,4E-08
Adamts1	605,24	763,41	455,93	472,32	151,32	290,99	130,69	165,81	5,3E-10	1,4E-08
Hspa2	134,32	134,24	509,73	417,11	402,46	446,11	434,02	323,48	5,3E-10	1,4E-08
Nipal4	27,51	48,40	129,11	121,66	160,98	138,90	276,76	207,52	5,3E-10	1,4E-08
Eva1a	24,27	25,57	156,01	175,84	262,08	160,20	268,38	147,50	5,3E-10	1,4E-08
Orai2	121,37	82,19	166,77	191,18	345,79	257,53	454,98	389,60	5,5E-10	1,4E-08
Id2	2372,39	2785,17	1444,45	1473,18	1289,79	1291,70	1225,17	991,81	5,7E-10	1,5E-08
Il1rap	419,13	395,40	660,36	698,25	250,49	397,45	181,71	136,31	5,8E-10	1,5E-08
Mapk13	671,59	720,49	307,99	290,34	193,82	217,99	492,72	331,62	5,9E-10	1,5E-08
Ssh3	110,04	119,63	205,77	255,58	265,94	357,91	425,63	443,52	6,4E-10	1,7E-08
Nacc2	150,50	172,59	65,90	67,47	33,48	31,43	28,65	44,76	6,5E-10	1,7E-08
Sdf2l1	650,55	494,02	771,98	637,93	294,92	316,34	273,27	244,14	6,5E-10	1,7E-08
Aplp1	85,77	53,88	138,53	120,63	344,50	234,21	364,83	287,88	6,6E-10	1,7E-08
Igfbpl1	190,96	150,67	407,51	720,74	893,13	889,19	791,85	556,43	7,1E-10	1,8E-08
Pcsk5	1034,08	1022,75	2127,67	1988,43	768,85	1270,41	440,31	593,05	7,2E-10	1,9E-08
Vsir	176,39	134,24	28,24	23,51	27,69	22,31	36,34	16,28	7,3E-10	1,9E-08
Padi3	948,31	883,95	1433,69	1035,62	453,33	646,87	357,14	389,60	8,4E-10	2,2E-08
Pdpn	655,40	647,44	1131,08	1107,18	1015,48	1207,55	1565,54	1548,24	8,5E-10	2,2E-08
Ednrb	77,68	84,92	9,41	11,25	12,23	12,17	12,58	11,19	8,6E-10	2,2E-08
Rgs14	150,50	147,93	121,04	111,43	30,26	65,90	16,77	18,31	9,0E-10	2,3E-08
Asphd2	415,90	344,26	547,38	485,61	391,51	367,03	144,67	179,03	9,1E-10	2,3E-08
Clca2	16,18	10,96	115,66	120,63	62,46	90,24	106,23	89,52	9,6E-10	2,5E-08
Tmem114	53,40	43,83	61,87	26,58	2,58	4,06	0,00	2,03	9,8E-10	2,5E-08
Pdgfra	1398,19	858,38	6686,95	7525,37	2548,67	5389,87	1692,74	2703,82	1,0E-09	2,5E-08
Slc7a5	1869,11	1841,86	1977,03	1748,18	3158,47	2152,50	6621,38	4397,53	1,0E-09	2,6E-08
Fgf3	16,18	11,87	281,09	120,63	24,47	82,13	14,68	11,19	1,1E-09	2,7E-08
Slc6a14	0,00	0,00	6,72	14,31	30,91	46,64	48,22	53,91	1,1E-09	2,7E-08
Ifitm1	46,93	34,70	47,07	51,12	273,67	114,57	369,72	219,72	1,1E-09	2,7E-08
Arhgap22	122,99	121,45	204,43	192,20	221,51	242,32	394,88	359,09	1,1E-09	2,8E-08
Reep6	85,77	72,14	274,36	215,71	267,23	226,10	427,73	302,12	1,2E-09	2,9E-08
Krt75	17,80	27,40	29,59	27,60	83,71	34,47	445,20	139,36	1,2E-09	3,1E-08
Syt1	90,62	52,05	57,83	53,16	108,18	76,04	515,79	227,86	1,3E-09	3,2E-08
Exoc6	134,32	155,24	162,74	165,62	240,83	279,84	399,77	394,69	1,4E-09	3,4E-08
Mafb	97,10	84,01	356,40	300,56	519,01	306,20	445,20	365,19	1,4E-09	3,5E-08
Rbpms	1459,69	1549,65	1032,90	904,76	553,78	772,59	583,58	568,64	1,5E-09	3,7E-08
Pou4f1	11,33	5,48	134,49	192,20	22,54	98,35	10,48	8,14	1,5E-09	3,7E-08

Rnf144b	645,69	784,41	301,26	381,33	173,22	259,56	215,96	263,47	1,5E-09	3,8E-08
Grik4	590,67	454,76	661,70	555,12	142,31	391,36	53,82	82,40	1,5E-09	3,8E-08
Cabp7	4,85	3,65	60,52	55,21	7,08	10,14	2,80	1,02	1,6E-09	3,8E-08
Prag1	980,68	1021,84	1425,62	1272,80	1771,45	1791,55	2676,09	2128,07	1,6E-09	3,9E-08
Dhdh	147,26	188,11	75,32	95,08	51,51	46,64	20,27	33,57	1,6E-09	4,0E-08
Acvr2a	360,88	492,20	504,35	614,42	502,91	697,56	1407,59	1265,45	1,6E-09	4,0E-08
Hapln1	3908,14	4642,55	3011,28	3023,03	1009,68	2281,26	380,20	782,26	1,7E-09	4,1E-08
Des	71,20	45,66	6,72	4,09	1,93	2,03	2,80	0,00	1,7E-09	4,2E-08
Fhdc1	211,99	224,64	461,31	421,20	392,15	468,42	752,72	603,22	1,7E-09	4,2E-08
Klrg2	0,00	0,91	12,10	16,36	29,62	35,49	62,90	47,81	1,8E-09	4,3E-08
Irx3	398,10	321,44	112,97	57,25	72,12	69,96	154,46	100,71	1,8E-09	4,4E-08
Tbx15	43,69	35,61	259,57	257,63	389,58	113,56	11,88	32,55	1,9E-09	4,6E-08
Evx1	1,62	2,74	122,39	149,26	367,68	49,68	36,34	37,64	1,9E-09	4,6E-08
Hacd4	241,12	254,77	121,04	136,99	56,67	91,25	41,93	60,02	2,0E-09	4,8E-08
Dpysl5	775,15	728,71	1051,73	910,90	1271,12	1485,36	1963,91	1670,31	2,0E-09	5,0E-08
Galnt14	19,42	22,83	168,12	183,00	84,35	135,86	104,84	75,28	2,1E-09	5,1E-08
Mical2	0,00	10,96	44,38	95,08	225,38	146,00	83,17	93,59	2,1E-09	5,1E-08
Ccne1	1414,37	1474,77	967,00	734,03	749,53	609,35	553,53	539,14	2,1E-09	5,1E-08
Pax7	74,44	82,19	67,25	34,76	5,15	14,19	1,40	4,07	2,2E-09	5,3E-08
Nsg1	705,57	560,69	866,13	850,58	1622,70	1289,67	1578,82	1456,69	2,3E-09	5,5E-08
Lactb	292,91	285,82	185,60	133,93	108,18	108,49	85,27	81,38	2,4E-09	5,7E-08
Fam189a2	313,95	188,11	106,25	107,34	92,08	110,51	41,93	46,79	2,4E-09	5,7E-08
Alx3	623,04	357,96	687,25	494,81	305,22	386,29	120,91	120,03	2,4E-09	5,7E-08
Sat1	155,35	164,37	182,91	308,74	361,89	388,32	572,40	632,72	2,4E-09	5,8E-08
Gas7	50,17	41,09	95,49	120,63	198,33	189,60	271,87	179,03	2,4E-09	5,8E-08
Hoxd9	456,35	210,03	141,22	146,19	144,24	22,31	6,99	4,07	2,4E-09	5,8E-08
Ppp2r5a	661,88	822,77	536,62	556,15	347,72	346,75	322,19	322,46	2,5E-09	6,0E-08
Galnt6	152,12	136,06	262,26	196,29	74,05	84,15	58,71	38,66	2,6E-09	6,2E-08
Det1	93,86	72,14	203,08	177,89	285,90	235,22	320,10	285,84	2,6E-09	6,2E-08
Itpkb	454,74	348,83	828,47	675,76	1715,43	1042,28	1661,99	1321,39	2,7E-09	6,3E-08
Shox2	42,08	43,83	227,29	53,16	19,96	21,29	4,19	3,05	2,9E-09	6,8E-08
Trib2	477,39	548,81	965,65	932,36	1082,45	1004,77	1590,00	1224,76	2,9E-09	6,9E-08
Asap3	74,44	52,05	143,91	163,57	215,72	201,77	246,01	241,09	2,9E-09	6,9E-08
Spsb4	891,67	701,31	915,89	593,97	452,68	385,28	241,12	243,12	3,0E-09	7,0E-08
Krt8	2932,32	2054,63	4886,10	2949,42	1274,34	2642,21	524,18	651,03	3,0E-09	7,0E-08
Srms	613,33	524,16	594,46	682,92	206,06	468,42	120,21	90,53	3,0E-09	7,1E-08
Nrep	3903,29	4223,41	5351,44	6736,13	8245,52	8136,51	8739,75	10065,58	3,2E-09	7,5E-08
Gchfr	173,16	130,58	49,76	30,67	70,83	20,28	5,59	2,03	3,2E-09	7,5E-08
Tlr5	16,18	21,00	60,52	67,47	94,01	107,47	113,92	121,05	3,3E-09	7,6E-08
Esrp2	580,96	646,52	2120,94	2162,23	1237,63	2077,47	1702,52	1792,38	3,4E-09	7,9E-08
Ptpn3	255,69	278,52	429,03	498,90	347,08	497,82	907,87	803,62	3,5E-09	8,1E-08
Ddit4l	108,42	134,24	75,32	57,25	27,05	37,51	17,47	18,31	3,6E-09	8,3E-08
Pou6f2	58,26	42,01	318,75	489,70	134,58	392,38	37,74	73,24	3,7E-09	8,5E-08
Iifo2	368,97	412,75	611,94	550,01	647,15	690,46	1003,62	910,43	3,9E-09	9,1E-08
S100a14	0,00	0,91	2,69	5,11	7,73	16,22	145,37	32,55	4,5E-09	1,0E-07
Gprc5b	697,48	611,82	1410,82	1179,77	1479,75	1528,95	2358,79	1648,95	4,5E-09	1,0E-07
Camk2a	98,71	69,40	37,66	20,45	14,17	10,14	4,19	6,10	4,6E-09	1,1E-07
Itih5	165,06	147,93	59,18	77,70	16,74	33,46	14,68	28,48	4,7E-09	1,1E-07
Acsl4	2111,85	2687,46	1246,74	1319,83	523,51	978,41	454,29	698,84	4,8E-09	1,1E-07
Sytl1	95,48	76,71	259,57	223,89	236,32	234,21	312,41	270,59	4,9E-09	1,1E-07
Megf9	241,12	266,65	412,89	558,19	752,75	632,67	710,78	715,12	5,0E-09	1,1E-07
Dnajc22	76,06	94,97	21,52	23,51	21,25	20,28	8,39	9,16	5,1E-09	1,2E-07
Nr2f1	97,10	171,68	22,86	18,40	29,62	6,08	1,40	5,09	5,2E-09	1,2E-07
D930020B	16,18	12,78	71,28	149,26	111,40	172,36	148,17	296,02	5,5E-09	1,3E-07
Pdia6	11680,73	9857,66	15192,23	12262,84	7468,94	8156,79	6093,71	5122,82	5,5E-09	1,3E-07
Cavin3	42,08	32,87	57,83	40,89	157,12	76,04	392,08	193,28	5,6E-09	1,3E-07
Maob	35,60	38,35	196,36	141,08	61,17	94,29	33,55	31,53	5,6E-09	1,3E-07
Ptpu	1626,37	1546,00	1055,76	1426,15	2168,11	2375,56	2871,08	3231,77	5,7E-09	1,3E-07
Efna3	195,81	169,85	301,26	272,96	426,93	343,71	680,03	510,65	5,7E-09	1,3E-07
Clic5	0,00	1,83	25,55	47,03	31,55	38,53	60,11	66,12	5,8E-09	1,3E-07
Ak1	202,28	246,56	90,11	70,54	104,32	80,10	55,91	48,83	5,8E-09	1,3E-07
Scrn1	9,71	4,57	21,52	18,40	82,42	80,10	46,13	50,86	6,0E-09	1,3E-07
Foxq1	0,00	2,74	13,45	11,25	46,36	26,36	94,35	53,91	6,0E-09	1,4E-07
Ndrp1	1045,41	717,75	570,25	446,76	311,66	448,14	239,02	216,67	6,1E-09	1,4E-07

B3gnt8	37,22	35,61	117,01	113,48	226,02	158,17	236,93	153,60	6,3E-09	1,4E-07
Rps6ka6	2615,14	2877,40	1474,03	1568,25	1427,59	1635,41	1310,44	1440,41	6,5E-09	1,4E-07
Qrich2	64,73	53,88	22,86	13,29	3,22	5,07	3,49	1,02	6,8E-09	1,5E-07
Nampt	1799,52	2117,64	1855,99	1721,60	849,99	1197,41	749,92	826,00	6,9E-09	1,5E-07
Vcan	5466,54	5176,76	9335,10	11695,45	5832,71	7623,48	2921,40	4044,54	6,9E-09	1,5E-07
Rbp1	1409,52	1045,58	753,16	515,25	556,36	440,03	342,46	389,60	6,9E-09	1,5E-07
Acot9	124,61	94,06	201,74	195,26	235,03	249,42	371,12	339,76	7,1E-09	1,6E-07
Sox13	2123,18	2406,20	2069,83	2017,06	1209,94	1773,30	691,91	854,48	7,4E-09	1,6E-07
Hist3h2ba	38,84	24,66	80,70	64,41	189,32	115,58	283,75	173,95	7,4E-09	1,6E-07
Adcy1	202,28	221,90	282,43	313,86	403,10	439,02	522,08	667,31	8,2E-09	1,8E-07
Hr	504,90	467,54	567,56	585,79	784,95	848,63	1204,90	994,86	8,5E-09	1,9E-07
Trim29	1100,43	796,28	4158,50	2739,84	3076,05	3198,84	5399,01	3124,96	8,6E-09	1,9E-07
Adamts2	67,97	58,44	186,94	135,97	47,65	89,22	17,47	7,12	8,6E-09	1,9E-07
Sod3	50,17	31,05	1,34	2,04	0,00	1,01	0,00	0,00	8,7E-09	1,9E-07
Cebpa	48,55	50,22	264,95	159,48	196,40	141,95	490,63	261,43	8,7E-09	1,9E-07
Rai14	1071,30	1052,88	1256,16	1189,99	1210,59	943,94	431,92	525,91	8,9E-09	1,9E-07
Slco3a1	150,50	88,58	248,81	158,46	251,78	213,93	647,88	482,17	9,4E-09	2,1E-07
Cd44	1576,20	1175,25	2376,48	2687,70	848,70	1541,12	493,42	652,05	9,5E-09	2,1E-07
Kif26b	818,85	624,61	2664,29	2155,07	5427,68	2700,00	2986,40	1939,88	9,7E-09	2,1E-07
Nrn1	48,55	31,96	4,03	5,11	0,00	0,00	2,10	2,03	9,7E-09	2,1E-07
Cd109	134,32	108,67	348,33	302,61	337,42	277,81	493,42	376,38	1,0E-08	2,2E-07
Zfp467	237,89	246,56	273,02	313,86	335,49	344,72	630,41	552,36	1,0E-08	2,2E-07
Abhd15	64,73	41,09	126,42	60,32	7,08	17,24	5,59	3,05	1,0E-08	2,2E-07
Fcrl6	0,00	0,00	16,14	20,45	24,47	61,85	0,00	1,02	1,0E-08	2,2E-07
Epha3	166,68	145,19	195,01	197,31	244,05	221,03	23,76	54,93	1,1E-08	2,3E-07
Lrrc8c	145,64	123,28	82,04	88,94	216,36	117,61	545,14	336,71	1,1E-08	2,3E-07
Galnt16	169,92	105,01	630,77	495,83	341,28	438,00	476,65	409,95	1,1E-08	2,4E-07
Pde10a	621,42	685,79	480,14	472,32	236,97	320,39	258,59	281,78	1,2E-08	2,5E-07
Celsr1	1927,37	1705,80	3168,64	2660,10	3101,81	3308,34	5693,24	4179,84	1,2E-08	2,5E-07
Timp3	223,32	130,58	391,37	390,53	506,77	453,21	689,12	618,48	1,2E-08	2,5E-07
Hebp2	92,24	94,06	270,33	216,73	300,72	247,39	292,84	324,50	1,2E-08	2,6E-07
Vtcn1	0,00	0,00	22,86	19,42	30,26	32,44	38,44	39,67	1,3E-08	2,7E-07
Lin28a	5657,50	6971,13	645,56	615,44	107,54	331,54	9,09	86,47	1,3E-08	2,7E-07
Palld	911,09	817,29	1210,43	1321,87	1464,30	1328,20	1838,81	1998,88	1,3E-08	2,8E-07
Klhdc7a	205,52	199,98	134,49	110,41	43,79	71,99	11,88	33,57	1,3E-08	2,8E-07
Kifc3	213,61	223,73	328,16	437,56	479,08	542,43	603,85	631,71	1,4E-08	3,0E-07
Prex2	273,49	372,57	92,80	110,41	195,75	63,88	32,15	26,45	1,4E-08	3,0E-07
Tnfrsf19	2437,13	2293,88	3133,67	2800,16	3108,25	2819,64	5719,10	4624,37	1,5E-08	3,2E-07
Sh3rf2	1,62	10,04	76,66	70,54	42,50	54,75	85,96	81,38	1,5E-08	3,3E-07
Grhl1	30,75	43,83	112,97	158,46	96,59	167,29	262,09	243,12	1,6E-08	3,3E-07
Clca1	85,77	7,31	720,88	448,80	108,18	256,52	23,06	13,22	1,6E-08	3,3E-07
Wfikkn2	0,00	1,83	14,79	5,11	81,78	34,47	67,79	54,93	1,6E-08	3,5E-07
Fgf15	11,33	3,65	902,44	121,66	1,29	8,11	1,40	0,00	1,7E-08	3,5E-07
Fut2	74,44	64,84	64,56	41,92	9,66	15,21	8,39	5,09	1,7E-08	3,5E-07
Hoxd13	16,18	13,70	334,89	561,26	4360,05	587,05	266,28	388,59	1,7E-08	3,6E-07
Zfp703	1435,41	1231,87	1077,28	610,33	495,18	366,02	436,11	377,40	1,7E-08	3,6E-07
Dock5	228,18	326,00	142,56	174,82	148,75	109,50	57,31	63,07	1,8E-08	3,6E-07
Grem1	43,69	68,49	294,54	147,22	64,39	359,93	2,80	8,14	1,8E-08	3,7E-07
C430049E	245,98	168,94	184,25	126,77	36,06	83,14	7,69	23,40	1,8E-08	3,8E-07
Zbtb4	82,53	63,92	147,94	251,49	208,63	257,53	341,06	373,33	1,9E-08	4,0E-07
Prss8	1255,78	1070,23	743,74	544,90	238,25	410,63	445,90	354,00	2,0E-08	4,1E-07
Upk3bl	76,06	120,54	560,83	358,84	351,59	428,88	482,24	351,96	2,0E-08	4,1E-07
Nfia	16,18	30,13	84,73	218,78	343,21	204,81	207,57	279,74	2,1E-08	4,3E-07
Pcdhb20	9,71	2,74	41,69	29,65	57,31	42,58	88,76	100,71	2,1E-08	4,4E-07
Hspa5	24688,44	22557,11	25521,23	18434,64	12112,96	12370,54	11979,16	11176,41	2,2E-08	4,5E-07
Svopl	344,69	161,63	1140,49	738,12	271,74	451,18	187,31	161,74	2,2E-08	4,5E-07
Slc25a24	663,49	593,56	742,40	738,12	1054,11	1086,90	1197,22	1260,36	2,2E-08	4,5E-07
Mkx	24,27	28,31	76,66	78,72	120,41	113,56	128,60	116,98	2,2E-08	4,6E-07
Tmem64	373,82	491,29	474,76	573,53	721,84	799,96	1211,89	1032,50	2,3E-08	4,6E-07
Vwde	390,00	639,22	1842,54	2793,00	1245,36	2034,89	872,23	1040,64	2,4E-08	4,9E-07
Ly6h	21,04	21,00	63,21	54,18	73,41	92,26	155,16	115,97	2,4E-08	4,9E-07
Krt9	3,24	4,57	186,94	167,66	77,27	182,50	15,38	77,31	2,5E-08	5,0E-07
Tbc1d16	1760,69	1845,52	2131,70	2122,36	3622,75	2873,38	3879,60	3521,68	2,5E-08	5,1E-07
Slc29a3	171,54	147,02	321,44	256,60	316,17	394,41	580,79	469,96	2,5E-08	5,1E-07

Kcne1l	63,11	59,36	260,91	145,17	285,90	262,60	383,00	261,43	2,5E-08	5,1E-07
Irf2	93,86	89,49	178,87	192,20	216,36	236,24	308,91	267,53	2,5E-08	5,1E-07
Sept8	276,73	284,91	568,90	414,04	1048,96	592,11	1253,83	988,76	2,6E-08	5,3E-07
Peak1	357,64	510,46	278,40	308,74	306,51	197,71	86,66	107,83	2,6E-08	5,3E-07
Zfp827	173,16	199,07	461,31	876,14	687,72	798,95	695,41	969,43	2,7E-08	5,4E-07
Abca4	512,99	539,68	1167,39	1221,68	207,35	582,99	182,41	210,57	2,7E-08	5,5E-07
Tenm3	3016,47	2877,40	4108,74	3920,63	4821,74	4813,98	5278,10	5530,73	2,8E-08	5,7E-07
Serf1	294,53	219,16	399,44	445,74	680,63	489,71	919,75	755,81	2,9E-08	5,7E-07
Dopey2	106,81	67,57	156,01	180,95	261,44	245,36	315,90	303,14	2,9E-08	5,7E-07
Arl4a	124,61	112,32	633,46	741,19	269,16	608,34	427,03	381,46	2,9E-08	5,7E-07
Ldhh	807,52	568,90	1950,14	1664,35	2074,10	1601,95	1896,12	1768,98	2,9E-08	5,8E-07
Kcnd1	289,67	326,91	240,74	198,33	90,15	152,08	74,78	80,36	2,9E-08	5,8E-07
Hs6st2	587,43	608,17	357,75	380,31	184,81	300,11	171,93	199,38	2,9E-08	5,8E-07
Lrrc15	155,35	72,14	301,26	314,88	501,62	445,10	487,83	465,90	3,0E-08	5,9E-07
Rbpms2	323,66	207,29	154,67	159,48	182,23	57,79	21,67	19,33	3,0E-08	6,0E-07
Cpne8	35,60	56,62	110,28	131,88	101,10	156,14	350,15	226,84	3,1E-08	6,2E-07
Pich2	572,87	461,15	817,71	958,94	798,47	922,64	1411,08	1277,65	3,2E-08	6,4E-07
Fam129a	1113,37	1145,11	726,26	592,95	283,97	450,17	450,79	309,24	3,3E-08	6,5E-07
Vav3	135,94	165,28	72,63	110,41	125,57	177,43	543,05	318,40	3,3E-08	6,5E-07
Krt18	2404,76	1942,31	4147,74	2759,27	1252,44	2132,22	868,73	857,53	3,3E-08	6,6E-07
Heph	1066,44	792,63	1284,40	1192,04	2127,54	1641,50	2374,17	2331,51	3,3E-08	6,6E-07
Sdk1	336,60	273,95	532,59	454,94	578,25	546,49	1290,17	799,55	3,4E-08	6,6E-07
Slc7a11	2464,64	2618,06	1186,22	1385,26	613,02	699,59	596,86	1246,12	3,4E-08	6,6E-07
Cybrd1	48,55	42,01	65,90	65,43	115,91	108,49	172,63	163,78	3,5E-08	6,8E-07
Fras1	4456,74	3382,38	8304,89	8270,64	9924,24	9724,27	8416,16	11654,51	3,6E-08	7,0E-07
Adam19	1093,96	1106,76	1139,15	1251,33	760,48	881,08	304,02	488,27	3,6E-08	7,1E-07
Thbs1	2388,58	1644,62	3771,16	3716,17	5311,77	6558,89	4089,97	5058,73	3,8E-08	7,4E-07
Wnk2	3000,29	2911,18	3499,49	2630,45	1455,28	1731,73	1318,13	1566,55	3,9E-08	7,7E-07
Zfp423	1378,77	1405,37	1006,00	946,68	1113,35	747,24	461,97	495,40	3,9E-08	7,7E-07
Cds1	30,75	21,92	82,04	97,12	75,34	104,43	169,13	144,45	4,1E-08	7,9E-07
Amph	144,03	174,42	60,52	89,96	19,32	57,79	13,98	11,19	4,2E-08	8,1E-07
Art4	207,14	177,15	418,27	351,68	332,91	365,00	701,00	513,71	4,2E-08	8,1E-07
Fgd3	29,13	51,14	90,11	101,21	120,41	134,85	192,90	201,41	4,2E-08	8,1E-07
Pnck	51,78	43,83	86,07	89,96	132,65	135,86	178,22	174,97	4,4E-08	8,5E-07
Pik3r1	1647,41	2077,46	3867,99	4964,43	4488,83	5642,33	5231,97	8743,17	4,4E-08	8,5E-07
Nkx1-1	360,88	178,98	494,93	204,47	143,60	170,33	40,54	35,60	4,4E-08	8,6E-07
Hoxa4	64,73	75,79	9,41	11,25	9,66	5,07	9,78	5,09	4,5E-08	8,6E-07
Dlg2	1,62	2,74	8,07	12,27	27,69	18,25	55,91	66,12	4,5E-08	8,7E-07
Esyt1	275,11	166,20	340,27	303,63	645,86	491,74	796,05	676,46	4,6E-08	8,9E-07
Susd5	53,40	39,27	49,76	94,05	294,92	217,99	147,47	251,26	4,6E-08	8,9E-07
Yaf2	606,85	639,22	391,37	387,46	419,84	355,88	243,92	262,45	4,7E-08	9,0E-07
Hspd1	16877,02	15953,07	10657,16	8998,54	9241,68	8611,01	9086,41	7815,45	4,7E-08	9,1E-07
Pfkfb3	917,56	1051,06	442,48	574,55	396,66	476,53	443,10	428,26	4,8E-08	9,2E-07
Pkp3	869,02	720,49	1199,67	956,90	1380,58	1285,62	2805,39	1863,58	4,8E-08	9,2E-07
Gdnf	8,09	8,22	108,94	149,26	32,20	106,46	19,57	22,38	4,9E-08	9,4E-07
Cdk18	470,92	541,51	649,60	553,08	150,04	282,88	172,63	198,36	4,9E-08	9,4E-07
Zfp651	312,33	359,79	507,04	447,78	639,42	695,53	763,90	750,72	5,0E-08	9,6E-07
Pnma2	14,56	19,18	21,52	31,69	73,41	65,90	95,05	107,83	5,1E-08	9,7E-07
Sp5	50,17	52,05	43,04	10,22	0,64	0,00	3,49	1,02	5,3E-08	1,0E-06
Micall1	611,71	814,55	1140,49	1394,46	1577,63	1812,84	1766,12	2273,53	5,4E-08	1,0E-06
Ifitm3	1286,53	1111,33	1039,62	659,40	349,01	375,14	563,31	365,19	5,5E-08	1,0E-06
Pfkl	13388,01	11127,88	7900,07	4949,10	5172,69	4300,94	4863,65	3707,84	5,5E-08	1,0E-06
Tgfb1	357,64	182,63	723,57	532,63	1255,02	1016,94	1230,76	914,50	5,6E-08	1,1E-06
Frmd4a	456,35	545,16	929,34	1104,12	1642,66	1182,20	1138,51	1184,07	5,8E-08	1,1E-06
Nipal1	1,62	0,91	8,07	10,22	11,59	18,25	54,51	51,88	5,9E-08	1,1E-06
Agrn	11004,29	11632,86	14402,76	15753,07	15615,93	17592,10	21622,59	22908,23	6,1E-08	1,1E-06
Tgfb1	443,41	299,52	485,52	516,28	1274,98	774,62	1141,30	1151,52	6,1E-08	1,1E-06
Sema4a	210,38	136,06	320,09	308,74	452,04	416,71	935,83	534,05	6,2E-08	1,2E-06
Hsd11b2	211,99	91,32	164,08	125,75	103,67	68,94	16,07	17,29	6,2E-08	1,2E-06
Abhd12b	24,27	54,79	18,83	16,36	0,00	2,03	0,00	0,00	6,4E-08	1,2E-06
Eps8l1	29,13	21,00	83,39	101,21	106,25	152,08	124,40	161,74	6,5E-08	1,2E-06
Sptb	891,67	654,74	316,06	364,97	774,65	667,14	384,40	347,90	6,8E-08	1,3E-06
Col4a6	1171,63	1072,97	508,38	426,31	358,67	335,60	1311,84	684,60	6,8E-08	1,3E-06
Samd5	1746,12	1788,90	875,54	931,34	689,65	1010,85	2346,91	1747,62	6,8E-08	1,3E-06

Col2a1	23461,79	14983,28	29312,57	18093,18	10804,49	11876,77	7265,07	7137,97	6,8E-08	1,3E-06
Dpy19l2	0,00	0,00	6,72	3,07	19,32	12,17	48,92	39,67	6,9E-08	1,3E-06
Casz1	77,68	75,79	110,28	120,63	225,38	190,61	212,47	259,40	6,9E-08	1,3E-06
Abca1	328,51	210,03	742,40	994,73	893,77	1490,43	1017,60	1759,82	7,2E-08	1,3E-06
Stard8	2187,91	2527,65	1872,13	1416,95	736,66	1317,05	342,46	636,79	7,3E-08	1,4E-06
Wdpcp	113,28	91,32	83,39	113,48	185,45	160,20	321,49	271,60	7,4E-08	1,4E-06
Popdc2	53,40	30,13	0,00	1,02	1,29	3,04	0,70	2,03	7,4E-08	1,4E-06
Rgs5	50,17	37,44	67,25	74,63	14,17	38,53	1,40	3,05	7,5E-08	1,4E-06
Fam78b	220,09	137,89	161,39	133,93	53,45	82,13	30,05	38,66	7,7E-08	1,4E-06
Slc41a2	9,71	9,13	125,08	178,91	44,43	117,61	24,46	48,83	7,8E-08	1,4E-06
Plxnc1	87,39	87,66	377,92	379,28	70,83	286,93	37,74	32,55	7,8E-08	1,4E-06
Gria2	0,00	1,83	0,00	7,16	5,80	6,08	36,34	142,41	7,9E-08	1,5E-06
Usp43	19,42	31,05	170,81	144,15	108,18	189,60	123,71	150,55	8,0E-08	1,5E-06
Atp6v1g3	0,00	0,00	1,34	5,11	152,61	20,28	10,48	17,29	8,1E-08	1,5E-06
Cplx2	237,89	189,94	326,82	319,99	446,89	428,88	538,15	509,64	8,2E-08	1,5E-06
Mmp11	566,40	408,19	723,57	618,51	1063,77	839,51	1472,58	1251,20	8,3E-08	1,5E-06
Me2	1336,70	1213,60	902,44	734,03	817,15	808,07	574,50	529,98	8,3E-08	1,5E-06
Gcnt1	480,63	515,94	168,12	185,04	187,38	259,56	274,67	233,97	8,3E-08	1,5E-06
Rspo2	1246,07	606,34	3573,46	3741,73	1763,08	2927,12	986,15	1254,26	8,6E-08	1,6E-06
Pou3f3	8,09	8,22	61,87	121,66	66,97	81,11	68,49	96,64	8,9E-08	1,6E-06
Ntn1	318,80	333,31	1127,04	1069,36	896,99	2057,19	1273,40	1671,32	9,0E-08	1,6E-06
Fam81a	6,47	2,74	61,87	48,05	28,98	65,90	98,54	85,45	9,0E-08	1,6E-06
Sowahc	386,77	446,54	742,40	734,03	468,78	772,59	1309,74	1271,55	9,0E-08	1,6E-06
Kif1a	122,99	120,54	99,52	113,48	269,81	256,52	228,54	222,78	9,1E-08	1,6E-06
1810041L	40,46	52,05	333,54	233,09	115,91	180,47	162,14	104,78	9,4E-08	1,7E-06
Piezo2	101,95	129,67	28,24	63,38	35,42	62,86	293,54	208,53	9,4E-08	1,7E-06
Coro7	1061,59	988,96	870,16	748,35	577,60	574,88	502,51	513,71	9,4E-08	1,7E-06
Cd82	95,48	84,92	207,12	199,35	273,03	192,64	529,77	308,22	9,7E-08	1,7E-06
Phlda1	786,48	631,00	1359,72	843,42	222,80	588,06	187,31	151,57	9,8E-08	1,8E-06
Aqp4	46,93	46,57	5,38	8,18	0,64	2,03	6,99	5,09	1,0E-07	1,8E-06
Stat6	234,65	231,94	279,74	277,05	386,36	350,81	706,59	510,65	1,0E-07	1,8E-06
Rcsd1	163,45	127,84	702,05	671,67	416,62	986,52	379,50	298,05	1,0E-07	1,9E-06
Ptch1	961,26	1075,71	3761,75	4778,37	1714,14	5714,31	809,33	1075,22	1,1E-07	1,9E-06
Hoxd1	45,31	39,27	1,34	3,07	0,00	1,01	0,00	2,03	1,1E-07	2,0E-06
Amotl2	1534,13	1565,17	2059,07	2524,13	2291,10	2839,92	3607,72	3574,58	1,2E-07	2,1E-06
Prr15l	4,85	4,57	65,90	46,00	30,26	39,54	65,70	59,00	1,2E-07	2,2E-06
Map7d2	87,39	97,71	37,66	43,96	19,96	27,38	13,28	15,26	1,2E-07	2,2E-06
Bmp1	1066,44	1038,27	2030,83	2069,19	1989,10	1892,94	1610,97	1867,65	1,3E-07	2,2E-06
Acp4	19,42	14,61	78,01	110,41	93,37	93,28	11,18	27,47	1,3E-07	2,3E-06
Mogat2	485,48	206,38	130,46	110,41	151,32	18,25	9,09	7,12	1,3E-07	2,3E-06
Dkk4	76,06	53,88	68,59	37,83	0,64	6,08	4,19	0,00	1,4E-07	2,5E-06
Nkain3	8,09	4,57	2,69	2,04	25,76	12,17	54,51	64,09	1,4E-07	2,5E-06
Tmem176	179,63	111,41	369,85	285,23	711,54	406,57	1029,48	570,67	1,5E-07	2,6E-06
Olfml2a	254,07	140,63	317,40	260,69	588,55	665,12	533,26	559,48	1,5E-07	2,6E-06
Slit3	589,05	633,74	688,60	668,60	1029,64	309,24	102,74	96,64	1,5E-07	2,7E-06
Sox9	1047,03	908,60	490,90	380,31	238,90	410,63	374,61	382,48	1,5E-07	2,7E-06
Vwa5a	470,92	431,02	385,99	391,55	652,94	528,24	821,91	947,05	1,5E-07	2,7E-06
Ablim1	1844,84	2047,33	2901,00	3193,76	2895,75	3625,69	4198,99	4795,27	1,5E-07	2,7E-06
Morc4	270,25	336,96	434,41	431,42	422,42	420,77	722,66	695,79	1,6E-07	2,8E-06
Nfix	0,00	0,00	1,34	6,13	81,14	14,19	122,31	37,64	1,6E-07	2,8E-06
Arhgef37	27,51	17,35	39,00	83,83	123,63	126,74	162,84	139,36	1,6E-07	2,8E-06
Col22a1	145,64	83,10	86,07	59,30	52,16	33,46	9,78	13,22	1,6E-07	2,8E-06
Fbn1	1072,92	618,22	1987,79	1679,69	2348,41	2025,76	2771,14	2730,27	1,6E-07	2,9E-06
Cpne4	16,18	14,61	43,04	38,85	0,00	3,04	0,70	0,00	1,7E-07	2,9E-06
Lix1	322,04	253,86	238,05	341,46	391,51	80,10	14,68	22,38	1,7E-07	3,0E-06
Gpr153	271,87	275,78	86,07	114,50	123,63	83,14	85,96	88,50	1,8E-07	3,1E-06
Krt23	262,16	252,03	153,32	86,90	66,97	98,35	57,31	33,57	1,8E-07	3,1E-06
Cpm	84,15	63,92	151,98	231,05	736,01	319,38	526,27	275,67	1,8E-07	3,1E-06
Egfl6	106,81	87,66	338,92	289,32	132,65	185,54	131,39	114,95	1,8E-07	3,2E-06
Tmem100	82,53	79,45	41,69	35,78	10,30	28,39	5,59	4,07	1,8E-07	3,2E-06
Elovl7	43,69	23,74	40,35	51,12	75,34	95,31	154,46	166,83	1,9E-07	3,2E-06
Wnt4	1195,91	1086,67	1772,61	1580,52	1841,64	1612,09	3063,28	2368,13	1,9E-07	3,3E-06
Hbb-bh1	407,81	2788,82	271,67	624,64	20,61	49,68	23,06	7,12	2,0E-07	3,4E-06
Dennd2a	1155,45	1090,32	845,96	777,99	740,52	707,70	418,64	536,09	2,0E-07	3,4E-06

Pgm2	1496,91	1223,65	1093,42	622,60	498,40	441,04	525,57	420,12	2,0E-07	3,4E-06
D430041D	310,71	284,91	388,68	387,46	229,24	267,67	85,96	139,36	2,0E-07	3,4E-06
Shh	0,00	0,91	37,66	14,31	19,32	40,56	0,00	0,00	2,0E-07	3,4E-06
Trim16	21,04	42,01	135,84	180,95	110,76	167,29	218,06	172,93	2,0E-07	3,5E-06
Sirt5	108,42	122,36	180,22	169,71	261,44	249,42	378,80	290,93	2,1E-07	3,6E-06
Atp9a	441,79	249,30	728,95	512,19	1180,32	852,69	1707,41	1178,98	2,1E-07	3,6E-06
Ldha	48095,21	37620,75	24523,30	14268,65	17481,40	11241,06	14524,55	9443,03	2,2E-07	3,7E-06
Pla2g5	38,84	33,79	13,45	8,18	2,58	5,07	0,00	0,00	2,2E-07	3,8E-06
Slc25a48	0,00	1,83	10,76	13,29	12,88	14,19	57,31	42,72	2,2E-07	3,8E-06
Pcdh8	6,47	2,74	14,79	12,27	21,25	14,19	210,37	38,66	2,2E-07	3,8E-06
Tcf15	111,66	80,36	22,86	17,38	19,96	7,10	12,58	10,17	2,3E-07	3,8E-06
Chl1	51,78	33,79	251,50	234,11	276,25	440,03	168,44	467,93	2,3E-07	3,9E-06
Ptn	3043,98	3480,09	6526,90	9012,85	5497,87	6676,50	3959,97	4351,75	2,3E-07	3,9E-06
Lmo2	30,75	17,35	141,22	218,78	495,18	164,25	155,16	79,34	2,3E-07	3,9E-06
Cyr61	79,30	83,10	221,91	259,67	769,50	289,97	352,25	300,09	2,3E-07	4,0E-06
Gsn	64,73	22,83	118,35	135,97	792,68	243,33	652,07	270,59	2,4E-07	4,0E-06
Plac8	281,58	168,02	47,07	50,09	71,48	79,08	37,74	71,21	2,4E-07	4,1E-06
Pcdhb22	29,13	14,61	51,11	84,85	127,50	84,15	160,05	162,76	2,4E-07	4,1E-06
Trim47	1,62	2,74	18,83	15,33	49,58	44,61	39,14	36,62	2,5E-07	4,2E-06
Ppp2r2b	118,13	87,66	57,83	103,26	164,85	161,21	327,09	277,71	2,6E-07	4,3E-06
Mgst1	998,48	762,50	784,09	664,51	430,79	417,72	420,74	343,83	2,6E-07	4,3E-06
B4galt5	512,99	655,66	412,89	276,03	288,48	309,24	185,91	187,17	2,7E-07	4,4E-06
Elf5	8,09	13,70	99,52	115,52	71,48	159,18	67,09	93,59	2,8E-07	4,7E-06
Creb3l1	165,06	154,33	306,64	195,26	105,60	175,40	51,72	34,59	2,9E-07	4,8E-06
Fam83c	35,60	38,35	91,45	87,92	97,23	117,61	182,41	143,43	3,0E-07	5,0E-06
Acpp	1114,99	944,22	1923,24	1974,12	1969,78	2015,62	1833,92	2132,13	3,0E-07	5,0E-06
Epha8	8,09	10,96	44,38	29,65	30,91	55,76	2,10	0,00	3,0E-07	5,1E-06
Adamts12	50,17	39,27	106,25	107,34	106,89	173,38	30,05	33,57	3,1E-07	5,1E-06
Ctsh	22,66	7,31	67,25	64,41	128,14	102,40	131,39	91,55	3,1E-07	5,2E-06
Wnt5a	7188,39	5849,76	12907,21	13258,59	8985,39	11144,74	6320,86	7164,42	3,2E-07	5,3E-06
Cdh2	1401,43	961,57	1779,33	1731,83	1379,30	1471,16	234,83	532,02	3,3E-07	5,5E-06
Gja3	8,09	14,61	39,00	79,74	325,18	83,14	41,93	38,66	3,3E-07	5,5E-06
Parm1	475,77	260,25	1148,56	872,05	1045,74	1634,40	1526,40	1386,50	3,3E-07	5,5E-06
Scd1	2322,23	2553,22	1039,62	726,88	1528,69	684,38	645,09	512,69	3,4E-07	5,6E-06
Hoxb7	87,39	50,22	20,17	14,31	1,93	9,13	2,80	0,00	3,4E-07	5,6E-06
Stk39	1025,99	903,12	654,98	541,83	574,39	446,11	405,36	375,36	3,4E-07	5,6E-06
Timp2	614,95	489,46	1101,49	939,52	1693,53	1213,63	1751,44	1326,48	3,4E-07	5,7E-06
Pla2g4a	271,87	318,70	243,43	299,54	419,84	429,89	636,70	581,86	3,5E-07	5,7E-06
Sirpa	1820,56	1840,04	1393,34	1138,87	935,63	941,91	947,71	1043,69	3,5E-07	5,8E-06
Sema6d	443,41	473,93	759,88	1027,44	840,97	1385,99	1434,84	1654,03	3,6E-07	5,8E-06
Snx7	77,68	84,01	164,08	142,10	72,12	62,86	39,84	36,62	3,6E-07	5,9E-06
Myo18a	741,17	588,08	1340,89	1139,90	1768,87	1298,80	2235,78	1665,22	3,6E-07	5,9E-06
Garnl3	77,68	95,88	115,66	124,72	222,80	210,89	219,45	250,24	3,6E-07	5,9E-06
Bach2	872,25	898,56	1999,90	2256,28	1648,46	2367,45	1548,76	1600,12	3,6E-07	5,9E-06
Gcg	12,95	1,83	17,48	47,03	153,90	98,35	111,13	91,55	3,7E-07	6,0E-06
Wdr86	390,00	429,19	500,31	443,69	615,60	648,89	984,05	805,65	3,7E-07	6,0E-06
C1qtnf3	12,95	19,18	217,88	191,18	74,05	229,14	64,30	109,86	3,7E-07	6,0E-06
Il17re	69,59	46,57	172,15	165,62	138,44	203,79	229,94	258,38	3,7E-07	6,0E-06
Clu	192,58	87,66	544,69	531,61	596,28	718,85	357,84	211,59	3,7E-07	6,0E-06
Slc36a4	239,51	305,00	469,38	627,71	663,89	650,92	682,13	836,17	3,8E-07	6,1E-06
Tmc3	21,04	15,52	200,39	427,33	164,20	618,48	37,74	149,53	3,8E-07	6,2E-06
Inafm1	69,59	78,53	122,39	130,86	182,23	163,24	257,89	214,64	3,9E-07	6,3E-06
Cdk19	487,10	609,08	796,19	944,63	1232,48	1229,86	1143,40	1469,91	3,9E-07	6,3E-06
Sema6c	336,60	194,51	586,39	480,49	848,06	704,66	893,89	800,57	4,0E-07	6,5E-06
Cobll1	1592,39	1763,33	918,58	935,43	302,65	673,23	431,92	585,93	4,2E-07	6,8E-06
Pdgfrl	275,11	167,11	667,08	596,02	472,64	547,50	308,22	307,21	4,3E-07	6,9E-06
Cpne5	27,51	15,52	156,01	73,61	81,14	94,29	22,36	17,29	4,5E-07	7,3E-06
Lrp2	158,59	245,64	48,42	51,12	25,11	44,61	30,75	68,16	4,5E-07	7,3E-06
Dusp5	168,30	227,38	30,93	28,63	79,85	13,18	14,68	7,12	4,5E-07	7,3E-06
Mmrn2	144,03	62,10	48,42	27,60	16,10	17,24	11,18	9,16	4,6E-07	7,4E-06
Nrbp2	17,80	57,53	119,70	339,41	201,55	461,32	434,72	899,24	4,7E-07	7,6E-06
Plbd1	38,84	35,61	44,38	41,92	57,95	58,81	188,70	116,98	4,8E-07	7,6E-06
Il1f5	6,47	0,91	2,69	4,09	18,67	5,07	100,64	54,93	4,8E-07	7,7E-06
Susd4	1111,76	929,61	2384,55	2296,15	1596,94	2192,04	2483,89	2217,58	5,0E-07	8,1E-06

Mab21l2	84,15	42,01	355,06	180,95	168,71	128,76	10,48	37,64	5,0E-07	8,1E-06
Adam9	1246,07	1435,50	1685,19	1701,16	727,64	940,89	540,95	796,50	5,1E-07	8,1E-06
Atg10	30,75	24,66	61,87	58,27	100,45	99,36	127,90	108,84	5,2E-07	8,3E-06
Serpine2	2196,00	1843,69	3401,31	2550,71	2339,40	1744,91	1132,22	1049,79	5,2E-07	8,3E-06
Robo2	63,11	64,84	201,74	133,93	721,84	237,25	301,93	263,47	5,3E-07	8,4E-06
Fam19a4	3,24	0,00	32,28	39,87	36,06	58,81	11,88	8,14	5,3E-07	8,5E-06
Ppp1r12b	299,38	336,96	930,69	1581,54	802,98	1469,13	1090,28	1170,84	5,4E-07	8,6E-06
Crmp1	1590,77	965,22	423,65	382,35	972,98	358,92	243,92	225,83	5,4E-07	8,6E-06
Pgk1	8905,38	7417,67	5850,41	3528,06	3255,71	2784,16	3467,94	2393,56	5,4E-07	8,6E-06
Pcyt1b	317,18	311,39	363,13	332,26	652,94	513,03	673,04	631,71	5,6E-07	8,8E-06
Cyth3	700,71	643,78	849,99	822,98	1222,82	1078,78	1412,48	1245,10	5,6E-07	8,8E-06
Hoxb1	53,40	64,84	2,69	10,22	1,93	6,08	4,89	4,07	5,6E-07	8,8E-06
Fam167a	51,78	30,13	34,97	20,45	81,14	43,60	320,80	127,15	5,7E-07	8,9E-06
Tmem37	93,86	96,80	6,72	14,31	22,54	5,07	6,99	2,03	5,7E-07	8,9E-06
Nlr1	40,46	30,13	47,07	57,25	143,60	106,46	192,90	121,05	5,7E-07	9,0E-06
Ocln	74,44	63,92	203,08	208,56	135,23	275,78	364,83	320,43	5,9E-07	9,2E-06
Tmem150	93,86	62,10	29,59	23,51	9,66	13,18	13,98	10,17	5,9E-07	9,3E-06
Ccdc80	430,46	473,02	225,95	271,94	243,41	297,07	98,54	159,71	6,0E-07	9,4E-06
Hoxd4	76,06	141,54	5,38	66,45	2,58	7,10	0,00	2,03	6,2E-07	9,7E-06
Serinc2	233,03	168,94	540,66	363,95	1160,36	566,77	1185,34	731,40	6,3E-07	9,8E-06
Cx3cl1	19,42	26,48	40,35	43,96	146,17	84,15	211,07	101,72	6,5E-07	1,0E-05
Enpp1	810,76	524,16	552,76	874,09	1329,71	997,67	2230,19	1805,60	6,5E-07	1,0E-05
B4galt6	830,18	1129,59	587,73	582,73	435,94	522,16	360,63	434,36	6,5E-07	1,0E-05
Plch1	152,12	297,69	41,69	70,54	48,29	43,60	35,64	66,12	6,6E-07	1,0E-05
Map3k20	137,55	305,00	458,62	665,54	707,03	1105,15	938,62	1702,86	6,6E-07	1,0E-05
Grm8	40,46	54,79	221,91	181,97	70,19	104,43	76,88	56,97	6,7E-07	1,0E-05
Cnr1	121,37	180,81	51,11	72,59	20,61	36,50	10,48	28,48	6,9E-07	1,1E-05
Hpgds	6,47	20,09	25,55	59,30	69,54	84,15	126,50	166,83	6,9E-07	1,1E-05
Car14	676,44	597,21	338,92	349,64	711,54	160,20	59,41	64,09	6,9E-07	1,1E-05
Jak1	1603,71	1305,83	1981,07	1910,73	2458,52	2288,36	3103,82	2828,94	6,9E-07	1,1E-05
Srd5a1	349,55	332,39	482,83	447,78	673,55	607,32	989,64	706,98	7,0E-07	1,1E-05
Pam	556,69	434,67	871,51	813,77	1837,77	1151,79	916,26	863,64	7,1E-07	1,1E-05
Ctgf	113,28	78,53	387,34	376,22	279,47	577,92	342,46	339,76	7,2E-07	1,1E-05
Upk1a	270,25	96,80	364,47	295,45	39,92	97,33	46,83	41,71	7,2E-07	1,1E-05
Hoxd12	6,47	0,91	321,44	303,63	2531,93	254,49	114,62	116,98	7,3E-07	1,1E-05
Sox21	12,95	7,31	45,73	27,60	60,53	26,36	157,25	97,65	7,3E-07	1,1E-05
Ak5	32,37	19,18	138,53	72,59	19,32	28,39	13,28	6,10	7,3E-07	1,1E-05
Mapk4	142,41	159,80	345,64	344,52	311,66	525,20	475,95	621,53	7,4E-07	1,1E-05
Capn2	810,76	683,05	1125,70	1267,69	1630,43	1296,77	1878,64	1619,45	7,7E-07	1,2E-05
Rbl2	48,55	86,75	119,70	178,91	171,29	214,95	287,25	331,62	7,7E-07	1,2E-05
Adamts3	414,28	354,31	832,51	984,50	398,59	611,38	239,02	347,90	7,7E-07	1,2E-05
Hs6st3	43,69	48,40	83,39	66,45	12,88	19,26	11,18	14,24	7,8E-07	1,2E-05
Gnal	25,89	22,83	75,32	99,17	75,98	131,81	134,19	167,84	8,0E-07	1,2E-05
Atp1b1	111,66	141,54	189,63	143,13	25,76	60,83	37,04	31,53	8,2E-07	1,2E-05
Sptlc3	270,25	211,86	598,49	584,77	459,77	508,98	431,92	495,40	8,2E-07	1,2E-05
Pygb	1883,68	1554,21	2818,96	2086,57	3756,04	3104,55	6240,48	3950,96	8,2E-07	1,3E-05
Mpp6	1153,83	1147,85	750,47	715,63	768,85	629,63	570,30	517,77	8,3E-07	1,3E-05
Fn1	7989,44	6632,35	15424,91	12272,04	13289,42	11294,79	7419,53	7436,02	8,5E-07	1,3E-05
Rnase4	364,11	297,69	488,21	426,31	688,36	573,86	892,50	730,38	8,6E-07	1,3E-05
Mesd	2063,30	1620,88	2597,04	2331,93	1439,18	1563,43	1195,12	1041,65	8,6E-07	1,3E-05
Cilp	55,02	35,61	8,07	9,20	5,80	8,11	0,00	2,03	8,6E-07	1,3E-05
Grasp	42,08	49,31	121,04	103,26	230,53	137,89	292,84	175,98	8,7E-07	1,3E-05
Arhgap23	877,11	944,22	1266,92	1256,44	1278,20	1388,02	1785,69	1712,01	8,7E-07	1,3E-05
Ngfr	2505,09	2280,18	742,40	394,62	1594,37	282,88	250,91	136,31	8,8E-07	1,3E-05
Map2k1	1348,03	1272,04	919,93	834,22	767,56	720,88	741,53	712,07	9,0E-07	1,3E-05
Dsg1b	0,00	0,00	1,34	6,13	12,88	5,07	69,89	31,53	9,0E-07	1,3E-05
Tgfb2	163,45	174,42	459,96	384,40	368,33	512,02	573,80	434,36	9,1E-07	1,4E-05
Chst11	1249,31	1060,19	3707,95	3030,18	1847,43	3005,19	3471,44	2791,31	9,1E-07	1,4E-05
Npm1	40076,64	38514,74	24417,05	22622,10	25285,18	21537,16	24287,50	22112,75	9,3E-07	1,4E-05
Glrb	90,62	86,75	84,73	120,63	186,10	175,40	233,43	270,59	9,3E-07	1,4E-05
Daam1	579,34	601,78	802,92	987,57	823,59	1074,73	1371,94	1502,46	9,4E-07	1,4E-05
Slc16a6	129,46	178,98	228,64	246,38	92,08	104,43	41,93	74,26	9,7E-07	1,5E-05
Slc16a10	1286,53	826,42	3465,86	2752,11	2327,80	2404,96	2242,77	1756,77	9,8E-07	1,5E-05
Stc2	101,95	225,55	36,31	59,30	24,47	41,57	23,06	28,48	9,9E-07	1,5E-05

Syt7	247,60	251,12	82,04	108,37	85,00	70,97	127,90	89,52	1,0E-06	1,5E-05
Paccin2	2730,03	2343,19	1678,46	1566,21	1490,05	1423,51	1448,12	1290,88	1,0E-06	1,5E-05
Itgb6	3,24	5,48	16,14	37,83	43,79	102,40	64,30	125,12	1,0E-06	1,5E-05
Wnt2	127,84	52,05	4,03	17,38	7,73	6,08	12,58	11,19	1,1E-06	1,6E-05
Pdia5	469,30	335,13	590,42	442,67	319,39	293,02	183,81	162,76	1,1E-06	1,6E-05
Tinagl1	707,19	615,48	425,00	333,28	312,95	316,34	326,39	309,24	1,1E-06	1,6E-05
Raet1e	215,23	211,86	372,54	285,23	176,44	336,61	67,79	81,38	1,1E-06	1,6E-05
Cblc	119,75	89,49	156,01	146,19	209,28	194,67	339,67	273,64	1,1E-06	1,7E-05
Ebf2	37,22	23,74	2,69	2,04	0,00	0,00	0,00	1,02	1,1E-06	1,7E-05
Htr1d	1,62	1,83	0,00	3,07	19,32	24,33	29,35	48,83	1,1E-06	1,7E-05
Qsox1	380,30	313,22	886,30	709,50	721,84	842,55	652,07	613,40	1,1E-06	1,7E-05
Ica1	220,09	199,98	254,19	276,03	168,07	219,00	91,56	88,50	1,1E-06	1,7E-05
Rrbp1	7707,86	6697,18	7214,16	6474,41	4190,69	5256,03	2641,84	3634,60	1,2E-06	1,7E-05
Ssr1	4822,47	4899,15	6518,83	6174,87	3850,05	4284,72	3456,76	3738,36	1,2E-06	1,8E-05
Higd1a	671,59	638,31	482,83	419,15	403,10	366,02	311,71	292,96	1,2E-06	1,8E-05
Ago4	35,60	80,36	162,74	184,02	167,42	170,33	249,51	314,33	1,2E-06	1,8E-05
Celsr2	1415,99	1436,42	3647,43	4155,77	2041,90	3194,78	2049,88	2471,89	1,3E-06	1,9E-05
Rxra	1393,34	1237,34	2634,70	1984,34	3277,60	2451,60	4428,23	3123,94	1,3E-06	1,9E-05
Cxxc4	9,71	10,04	67,25	51,12	84,35	53,74	74,78	73,24	1,3E-06	1,9E-05
Mpzl2	1569,73	1482,07	3260,09	3111,97	2302,05	3032,56	2931,19	2858,44	1,3E-06	1,9E-05
Ppef2	40,46	42,01	6,72	6,13	0,00	2,03	0,00	2,03	1,3E-06	1,9E-05
Zic5	17,80	13,70	61,87	78,72	111,40	35,49	7,69	5,09	1,4E-06	2,0E-05
Pax2	0,00	3,65	78,01	18,40	0,64	2,03	0,70	0,00	1,4E-06	2,0E-05
Cplx1	9,71	3,65	4,03	7,16	33,48	22,31	73,38	50,86	1,4E-06	2,0E-05
Lrrn4	144,03	109,58	34,97	18,40	32,20	34,47	50,32	45,78	1,4E-06	2,0E-05
Mtus1	411,04	332,39	671,12	878,18	868,66	1140,63	889,00	1255,27	1,4E-06	2,0E-05
Tbc1d4	619,80	644,70	687,25	620,55	272,38	460,31	223,65	256,34	1,5E-06	2,1E-05
Dmd	139,17	119,63	96,83	136,99	166,13	237,25	303,32	549,31	1,5E-06	2,1E-05
Tstd3	318,80	220,99	131,80	138,01	117,20	127,75	72,69	91,55	1,5E-06	2,2E-05
Bmp8b	24,27	31,05	57,83	78,72	83,07	149,04	141,88	173,95	1,5E-06	2,2E-05
Aebp1	333,37	296,78	275,71	230,02	191,89	156,14	123,71	99,69	1,5E-06	2,2E-05
Clcn4	449,88	504,07	724,91	843,42	866,09	918,59	977,06	961,29	1,6E-06	2,3E-05
Dchs2	59,88	25,57	176,18	225,93	171,93	261,58	118,11	112,91	1,6E-06	2,3E-05
Adora2b	30,75	31,05	59,18	56,23	92,08	95,31	170,53	109,86	1,6E-06	2,3E-05
Zic2	35,60	11,87	125,08	199,35	466,20	84,15	30,75	29,50	1,6E-06	2,4E-05
Ntf3	9,71	13,70	39,00	37,83	44,43	43,60	90,16	77,31	1,6E-06	2,4E-05
Upk3b	33,98	26,48	22,86	13,29	0,00	1,01	2,10	0,00	1,7E-06	2,4E-05
Tnrc18	3951,83	3531,23	5255,95	4470,65	5819,19	5321,94	7316,79	7166,45	1,7E-06	2,4E-05
Fndc10	33,98	41,09	80,70	78,72	182,23	108,49	199,19	143,43	1,8E-06	2,5E-05
S100a10	674,82	488,55	1277,68	1143,99	1246,65	1262,30	2265,84	1384,46	1,8E-06	2,6E-05
Ogdhl	715,28	636,48	1094,77	950,77	1325,21	1304,88	1361,46	1207,46	1,8E-06	2,6E-05
Pygl	2073,01	1983,40	1987,79	1601,99	830,03	1209,58	820,51	992,83	1,8E-06	2,6E-05
Ssbp2	477,39	481,24	505,69	533,66	733,44	622,53	905,08	946,03	1,8E-06	2,6E-05
Jarid2	2205,71	2716,68	1492,86	1588,70	1173,88	1353,55	1301,35	1426,17	1,8E-06	2,6E-05
Hoxd8	152,12	129,67	41,69	80,76	61,82	5,07	2,10	2,03	1,8E-06	2,6E-05
Pcsk9	267,02	360,70	55,14	81,79	174,50	124,71	259,99	159,71	1,9E-06	2,6E-05
2310007B	97,10	79,45	234,02	197,31	59,24	113,56	51,02	37,64	1,9E-06	2,7E-05
Padi4	1,62	3,65	5,38	143,13	0,64	2,03	0,70	1,02	1,9E-06	2,7E-05
Gata6	122,99	89,49	20,17	8,18	27,05	25,35	11,18	25,43	1,9E-06	2,7E-05
Mfap4	381,91	213,68	605,21	513,21	1365,13	835,45	471,06	522,86	1,9E-06	2,7E-05
Gli2	1205,62	1174,34	1053,07	882,27	1015,48	927,71	1949,93	1673,36	1,9E-06	2,7E-05
Ccdc126	72,82	88,58	122,39	97,12	163,56	148,03	227,84	249,22	1,9E-06	2,8E-05
Rasl10b	160,21	119,63	67,25	47,03	55,38	31,43	25,86	25,43	2,0E-06	2,8E-05
Pm20d1	872,25	675,75	967,00	955,88	519,01	633,68	315,90	429,28	2,1E-06	2,9E-05
Pcdhb21	9,71	4,57	12,10	21,47	36,06	29,40	71,99	70,19	2,1E-06	2,9E-05
Pea15a	1129,56	989,88	1073,25	800,48	731,50	615,43	468,96	449,62	2,1E-06	3,0E-05
Il17rd	1969,44	1710,37	1486,14	1891,31	2186,78	1654,68	782,77	880,93	2,1E-06	3,0E-05
Gab1	911,09	893,99	1632,73	1424,10	1435,32	1784,46	1872,35	1883,93	2,2E-06	3,1E-05
1600014C	483,86	379,88	769,30	865,91	354,81	403,53	469,66	403,84	2,2E-06	3,1E-05
Sgsm1	428,84	455,67	352,37	305,68	275,60	245,36	125,10	186,15	2,3E-06	3,2E-05
Cpa2	262,16	201,81	295,88	507,08	595,63	201,77	61,50	63,07	2,4E-06	3,3E-05
Oprk1	19,42	34,70	6,72	10,22	0,64	1,01	0,00	0,00	2,4E-06	3,4E-05
St14	2624,85	1881,13	7939,07	5350,87	2741,85	3899,44	3049,30	1981,58	2,4E-06	3,4E-05
Mr1	43,69	27,40	63,21	86,90	127,50	94,29	167,04	155,64	2,5E-06	3,5E-05

Tenm2	84,15	90,40	129,11	180,95	85,64	94,29	366,22	210,57	2,5E-06	3,5E-05
Nup210	3163,73	3015,28	1825,06	1609,15	1383,80	1532,00	2121,86	1559,43	2,5E-06	3,5E-05
Rbms3	173,16	249,30	142,56	163,57	246,62	156,14	480,14	454,71	2,5E-06	3,5E-05
Chn2	122,99	122,36	26,90	37,83	39,92	28,39	41,24	29,50	2,6E-06	3,6E-05
Unc13c	0,00	8,22	65,90	109,39	39,28	84,15	74,78	64,09	2,6E-06	3,6E-05
Fgf4	77,68	23,74	3689,12	1471,13	34,13	475,52	31,45	15,26	2,6E-06	3,6E-05
Sh2b3	283,20	258,43	247,47	257,63	522,23	358,92	683,52	545,24	2,6E-06	3,7E-05
Col12a1	14,56	45,66	68,59	43,96	97,23	118,63	366,22	148,52	2,7E-06	3,7E-05
Ifngr2	187,72	166,20	289,16	236,16	634,91	373,11	564,01	450,64	2,7E-06	3,8E-05
Hspb1	631,13	377,14	2832,40	1665,37	1318,77	1428,58	1781,50	1016,22	2,8E-06	3,8E-05
Krt80	17,80	10,04	75,32	69,52	80,49	88,21	108,33	64,09	2,8E-06	3,9E-05
1110032F1	29,13	33,79	8,07	3,07	3,22	3,04	0,00	0,00	2,8E-06	3,9E-05
Tspan7	802,67	652,00	1560,11	1147,05	873,81	963,20	604,55	494,38	2,8E-06	3,9E-05
Epb41l4b	121,37	147,93	291,85	413,02	522,23	350,81	383,00	358,07	2,9E-06	4,0E-05
Lbx1	51,78	21,00	8,07	5,11	1,29	1,01	1,40	0,00	2,9E-06	4,0E-05
Psd3	273,49	384,44	571,59	937,48	779,15	1029,10	1000,83	1549,26	2,9E-06	4,0E-05
Lypd6b	393,24	260,25	771,98	694,16	779,80	998,69	701,70	780,22	2,9E-06	4,0E-05
Krt1	12,95	6,39	34,97	19,42	39,28	34,47	166,34	64,09	2,9E-06	4,0E-05
Galnt18	245,98	221,90	372,54	383,37	290,41	383,25	571,70	559,48	2,9E-06	4,0E-05
Wt1	19,42	53,88	0,00	1,02	0,64	1,01	0,00	2,03	3,0E-06	4,2E-05
H2-K1	288,05	295,87	316,06	212,64	148,75	132,82	118,81	86,47	3,2E-06	4,4E-05
Hmgn3	241,12	283,08	248,81	275,01	432,08	300,11	779,27	550,33	3,2E-06	4,4E-05
Pde3b	590,67	715,01	496,28	490,72	456,55	401,50	211,07	292,96	3,3E-06	4,5E-05
Hoxd3	30,75	66,66	4,03	20,45	2,58	0,00	0,70	0,00	3,3E-06	4,5E-05
Fam20c	360,88	179,89	898,41	650,20	361,89	407,59	241,82	254,31	3,3E-06	4,6E-05
Fat3	569,63	623,69	1927,27	2749,04	1697,40	2447,54	1095,88	2255,22	3,4E-06	4,6E-05
Smoc2	64,73	31,05	103,56	89,96	102,38	251,45	318,70	279,74	3,4E-06	4,6E-05
Ccbe1	90,62	72,14	207,12	204,47	110,11	159,18	27,26	57,98	3,6E-06	4,8E-05
Rasl11a	168,30	160,72	75,32	56,23	61,17	42,58	55,21	41,71	3,6E-06	4,9E-05
Tnfaip3	43,69	47,48	32,28	47,03	54,09	63,88	133,49	143,43	3,6E-06	4,9E-05
Rcor2	2386,96	2113,99	2137,08	1815,66	1831,34	1579,65	1068,62	1152,53	3,6E-06	4,9E-05
Fam46c	101,95	127,84	45,73	40,89	23,18	40,56	23,76	26,45	3,6E-06	4,9E-05
Hs3st6	27,51	10,04	104,90	65,43	146,17	142,96	113,22	73,24	3,7E-06	4,9E-05
Flnc	718,52	466,63	164,08	119,61	277,53	95,31	152,36	133,26	3,7E-06	5,0E-05
Apcdd1	3780,30	3164,13	7187,26	5615,65	3691,65	3983,59	3397,36	2805,55	3,8E-06	5,1E-05
Daam2	1202,38	963,39	346,99	513,21	917,60	473,49	336,87	257,36	3,8E-06	5,1E-05
Rnf213	166,68	175,33	108,94	123,70	137,80	125,72	32,15	55,95	3,8E-06	5,1E-05
Kremen2	1066,44	921,39	2580,90	1850,42	1375,43	1594,86	2290,30	1983,62	3,8E-06	5,1E-05
Asph	2367,54	2065,59	2656,22	2404,52	1727,66	1937,55	1283,18	1367,17	3,8E-06	5,1E-05
Commd3	487,10	394,49	706,08	679,85	882,83	806,05	1008,51	865,67	3,8E-06	5,2E-05
Dnajc3	1768,78	2161,47	2028,14	1582,57	1012,90	1133,53	904,38	1082,34	3,9E-06	5,3E-05
Relt	220,09	289,47	400,79	603,17	640,07	905,41	294,94	371,29	3,9E-06	5,3E-05
Bmp2	522,70	356,14	945,48	664,51	326,47	415,70	272,57	160,72	4,0E-06	5,3E-05
Grb14	61,49	54,79	61,87	73,61	103,03	123,70	171,93	169,88	4,1E-06	5,5E-05
Ptprz1	61,49	16,44	112,97	290,34	453,97	471,46	210,37	514,72	4,2E-06	5,6E-05
Arid3a	3665,40	4269,07	3921,79	3471,83	1853,87	2867,30	1005,72	1684,55	4,2E-06	5,7E-05
Me3	0,00	1,83	4,03	0,00	7,08	9,13	44,03	40,69	4,3E-06	5,7E-05
Cacna1i	35,60	73,05	135,84	127,79	6,44	58,81	2,80	3,05	4,3E-06	5,8E-05
Myh9	11146,70	9874,10	18516,88	14627,49	20627,64	18878,73	19808,94	20183,05	4,4E-06	5,8E-05
Gdf6	103,57	98,62	48,42	89,96	157,12	117,61	304,72	229,90	4,5E-06	6,0E-05
Zfp282	974,20	747,89	1447,14	1108,20	1830,69	1250,13	3364,51	2090,43	4,6E-06	6,1E-05
Cited4	385,15	193,59	642,87	379,28	191,89	334,59	99,24	82,40	4,7E-06	6,2E-05
Myo1d	168,30	162,54	309,33	259,67	350,30	316,34	465,47	373,33	4,7E-06	6,2E-05
Tmem229	278,34	401,79	275,71	276,03	103,67	124,71	241,12	192,26	4,7E-06	6,3E-05
Itga11	8,09	10,96	9,41	24,54	392,15	35,49	60,11	51,88	4,8E-06	6,3E-05
Fam163b	33,98	21,00	180,22	86,90	143,60	309,24	197,79	132,24	5,0E-06	6,6E-05
Col5a1	2605,43	1581,61	3272,19	2436,21	5293,10	3413,79	8007,30	5614,14	5,0E-06	6,7E-05
Rtn4r	17,80	12,78	36,31	21,47	62,46	54,75	121,61	75,28	5,1E-06	6,7E-05
Frem2	8114,04	5930,12	8579,25	8606,99	12707,30	11875,76	13097,40	15684,82	5,1E-06	6,7E-05
Ndnf	72,82	48,40	5,38	9,20	13,52	20,28	5,59	9,16	5,2E-06	6,9E-05
Rspo3	9,71	7,31	24,21	27,60	56,67	33,46	81,07	66,12	5,3E-06	7,0E-05
Smarca2	851,21	577,12	950,86	843,42	1388,31	1297,79	1570,43	1557,39	5,3E-06	7,0E-05
Epb41l5	1237,98	1352,40	790,81	846,49	517,72	713,78	480,84	651,03	5,3E-06	7,0E-05
Agbl5	445,03	303,17	683,22	855,69	934,99	814,16	881,31	1003,00	5,3E-06	7,0E-05

Th	50,17	73,97	64,56	49,07	3,86	16,22	6,99	8,14	5,4E-06	7,1E-05
Slc2a1	6309,66	5306,43	3464,52	2723,49	2079,89	2433,35	4309,42	2844,20	5,4E-06	7,1E-05
Il17rc	14,56	11,87	14,79	34,76	57,31	55,76	85,27	90,53	5,5E-06	7,3E-05
Gpr156	37,22	31,05	48,42	72,59	172,57	126,74	104,14	190,22	5,6E-06	7,3E-05
Bnc2	92,24	87,66	33,62	47,03	66,97	79,08	146,07	154,62	5,6E-06	7,3E-05
Tph2	3,24	2,74	26,90	38,85	16,10	31,43	1,40	2,03	5,6E-06	7,4E-05
Fndc3a	5261,02	6056,14	6529,59	7054,07	2514,54	4333,39	2029,61	2902,18	5,6E-06	7,4E-05
Phf2	1218,56	1251,96	1925,93	1904,60	2613,71	2001,43	2680,28	2357,96	5,7E-06	7,5E-05
Agap1	1747,74	1647,36	2730,19	2728,60	2876,43	4002,86	1733,27	2002,94	5,7E-06	7,5E-05
Dpf3	43,69	48,40	0,00	4,09	1,29	5,07	4,19	4,07	5,8E-06	7,5E-05
Evc	346,31	336,05	490,90	512,19	763,70	546,49	825,40	760,90	5,8E-06	7,6E-05
Gclc	469,30	651,09	438,44	591,93	687,72	774,62	1227,27	1144,39	5,9E-06	7,6E-05
Dach2	142,41	130,58	130,46	201,40	261,44	315,32	329,88	513,71	6,0E-06	7,8E-05
Slc43a1	404,57	403,62	197,70	218,78	226,66	183,52	166,34	197,34	6,1E-06	8,0E-05
Nptx2	124,61	74,88	52,45	26,58	10,95	16,22	25,86	19,33	6,2E-06	8,1E-05
Cbx6	914,33	843,77	1401,41	1276,89	1076,01	1226,81	2500,67	1675,39	6,2E-06	8,1E-05
Gbe1	491,96	446,54	426,34	288,30	234,39	259,56	173,33	191,24	6,3E-06	8,1E-05
Syt13	56,64	46,57	258,22	175,84	115,91	197,71	185,91	183,10	6,3E-06	8,2E-05
Slc13a5	27,51	38,35	82,04	136,99	36,70	59,82	15,38	18,31	6,3E-06	8,2E-05
Plcd1	296,14	227,38	679,19	583,75	466,20	545,48	501,81	464,88	6,4E-06	8,3E-05
Peg3	31305,58	27897,32	19481,19	19801,50	12756,89	16826,61	10222,82	15257,58	6,4E-06	8,3E-05
Arhgap31	179,63	172,59	185,60	258,65	435,94	315,32	438,21	449,62	6,4E-06	8,3E-05
Mgat4a	315,56	424,62	617,32	618,51	664,54	1168,01	1030,88	1210,51	6,6E-06	8,5E-05
Sp7	189,34	168,94	250,16	188,11	116,55	153,10	68,49	71,21	6,8E-06	8,8E-05
Slc6a6	1903,09	2063,76	967,00	1117,41	1244,72	1334,29	1527,80	1381,41	7,0E-06	9,0E-05
Zfp365	169,92	154,33	213,84	196,29	276,89	234,21	457,78	349,93	7,0E-06	9,0E-05
Zfpm1	352,78	284,00	139,87	87,92	91,44	103,42	154,46	91,55	7,0E-06	9,0E-05
Rnf141	427,23	401,79	429,03	398,71	478,44	570,82	800,94	750,72	7,0E-06	9,0E-05
Lmx1b	970,97	1093,06	953,55	760,61	1048,32	357,91	140,48	231,93	7,1E-06	9,0E-05
Tmem82	90,62	90,40	48,42	53,16	26,40	47,65	15,38	12,21	7,1E-06	9,1E-05
Aldoa	29201,82	19815,77	16347,52	8235,88	9089,06	6061,07	8858,57	5076,03	7,2E-06	9,2E-05
Col4a5	1814,09	1656,49	1284,40	1018,24	1183,54	1048,37	2918,61	1977,51	7,3E-06	9,3E-05
Scn3a	30,75	26,48	84,73	171,75	131,36	353,85	153,06	260,41	7,4E-06	9,4E-05
Kif3c	480,63	472,11	595,80	556,15	853,85	760,42	878,52	836,17	7,4E-06	9,4E-05
Hyou1	9628,75	8266,01	11691,40	7412,91	5285,37	5219,53	4759,51	4047,60	7,6E-06	9,7E-05
Gfra1	85,77	63,01	103,56	93,03	32,84	38,53	23,06	9,16	7,6E-06	9,7E-05
Fam46a	375,44	254,77	2135,74	2256,28	238,90	1173,08	568,91	719,19	7,7E-06	9,7E-05
Agl	602,00	626,43	720,88	695,18	831,31	883,10	1081,90	1114,89	7,7E-06	9,7E-05
Arhgef10	532,41	475,76	610,59	567,39	788,81	698,57	988,94	936,88	7,7E-06	9,7E-05
Mcf2	1098,81	1039,19	946,82	863,87	587,91	667,14	601,75	631,71	7,7E-06	9,8E-05
Dnajc6	32,37	40,18	69,94	147,22	142,31	306,20	174,73	257,36	7,7E-06	9,8E-05
Ptdss2	1161,92	918,65	923,96	747,32	627,19	614,42	489,23	490,31	7,9E-06	9,9E-05
Fgf5	1,62	4,57	49,76	24,54	12,23	54,75	0,00	1,02	8,0E-06	0,00010
Arg1	119,75	111,41	412,89	312,83	117,84	228,13	123,01	116,98	8,3E-06	0,00010
Cdh3	6992,58	5937,43	12550,81	10544,30	11203,73	12053,19	10896,56	10918,03	8,3E-06	0,00010
Hs3st1	50,17	37,44	146,60	163,57	48,29	25,35	69,89	47,81	8,3E-06	0,00010
Pcdh9	35,60	44,75	41,69	47,03	116,55	75,03	138,38	138,34	8,4E-06	0,00011
Pik3ip1	527,56	283,08	751,81	825,02	1247,94	1440,75	823,30	1184,07	8,8E-06	0,00011
Slc4a1	24,27	353,40	33,62	97,12	6,44	11,15	9,78	2,03	8,8E-06	0,00011
Endod1	145,64	116,89	344,30	334,30	264,65	316,34	275,37	227,86	8,8E-06	0,00011
Rbfox3	0,00	0,91	6,72	24,54	182,23	16,22	13,28	16,28	9,0E-06	0,00011
Cryl1	202,28	191,77	262,26	254,56	385,71	299,10	573,10	423,17	9,0E-06	0,00011
Atp7b	84,15	142,45	55,14	74,63	43,14	42,58	15,38	24,41	9,2E-06	0,00012
Cnst	815,61	744,23	523,17	525,48	418,55	393,39	488,53	426,22	9,3E-06	0,00012
B4galnt3	101,95	84,01	143,91	145,17	148,10	165,26	255,80	241,09	9,3E-06	0,00012
Adgrf4	0,00	0,91	0,00	1,02	14,17	5,07	37,74	26,45	9,4E-06	0,00012
Cav2	48,55	58,44	84,73	109,39	95,95	116,60	194,29	173,95	9,6E-06	0,00012
Nhlrc1	12,95	11,87	59,18	58,27	41,86	59,82	103,44	67,14	9,6E-06	0,00012
Smoc1	122,99	181,72	133,15	74,63	61,17	104,43	22,36	27,47	9,7E-06	0,00012
Cdc6	1260,64	1315,88	1129,73	880,23	574,39	694,52	751,32	668,33	9,8E-06	0,00012
Eps8l2	351,17	245,64	531,24	564,33	540,26	559,67	842,87	670,36	9,8E-06	0,00012
P4ha2	530,80	472,11	407,51	383,37	285,90	323,43	242,52	240,07	9,9E-06	0,00012
Skap2	402,95	550,64	243,43	241,27	151,32	233,20	140,48	195,31	9,9E-06	0,00012
Parva	2466,26	2045,50	2911,76	2482,22	3640,78	3031,55	5313,04	4234,77	1,0E-05	0,00012

Rab7b	1,62	1,83	18,83	24,54	25,76	51,71	41,93	35,60	1,0E-05	0,00013
Ssfa2	483,86	565,25	482,83	511,16	477,80	500,86	860,35	861,60	1,0E-05	0,00013
Angpt1	61,49	44,75	125,08	161,53	429,50	181,49	169,13	277,71	1,0E-05	0,00013
Hspa1b	8,09	21,00	56,49	30,67	60,53	37,51	208,27	91,55	1,0E-05	0,00013
Cyp2s1	35,60	14,61	48,42	44,98	98,52	111,53	130,00	99,69	1,1E-05	0,00013
Pwwp2b	457,97	547,90	676,50	696,21	859,00	898,31	1353,07	961,29	1,1E-05	0,00013
Kif21a	551,83	691,27	788,12	1402,64	1320,70	2098,76	1761,23	2835,05	1,1E-05	0,00013
Mchr1	0,00	0,00	2,69	2,04	1,93	4,06	33,55	24,41	1,1E-05	0,00013
Macc1	82,53	95,88	291,85	375,19	206,06	477,54	343,16	519,81	1,1E-05	0,00013
Gstk1	140,79	114,15	264,95	197,31	397,30	307,21	435,42	305,17	1,1E-05	0,00013
Nap1l1	15506,34	15371,38	11622,81	10686,41	10456,13	10165,31	9925,79	9685,14	1,1E-05	0,00013
Nr3c1	74,44	137,89	254,19	289,32	200,91	272,74	428,43	350,95	1,1E-05	0,00014
Nbl1	37,22	24,66	40,35	10,22	359,31	75,03	376,01	140,38	1,1E-05	0,00014
Hsp90aa1	19030,94	17829,63	13461,32	9835,83	11645,46	9487,02	9193,34	8058,57	1,1E-05	0,00014
Vnn1	42,08	44,75	119,70	109,39	18,67	58,81	11,88	13,22	1,2E-05	0,00014
Wwc2	1658,73	1736,85	1628,70	1613,24	2507,46	2403,95	2368,57	2590,91	1,2E-05	0,00014
Unc5b	6138,13	5501,84	7563,84	7281,03	10767,79	9492,09	9096,19	8748,26	1,2E-05	0,00015
Fzd1	7434,37	4437,09	9762,79	8105,03	5387,76	7169,25	2630,66	3348,75	1,2E-05	0,00015
Necab1	1,62	3,65	17,48	15,33	41,21	30,42	187,31	23,40	1,2E-05	0,00015
Rab39b	90,62	93,14	45,73	37,83	50,87	42,58	17,47	20,34	1,2E-05	0,00015
Hand1	171,54	84,01	2,69	2,04	48,94	2,03	5,59	0,00	1,2E-05	0,00015
Nkd2	131,08	113,23	247,47	363,95	1372,86	292,00	224,35	200,40	1,2E-05	0,00015
Anxa11	29,13	25,57	18,83	29,65	77,92	52,72	168,44	82,40	1,3E-05	0,00015
Iqgap1	2720,32	2159,65	3192,84	2541,51	3838,46	3239,40	6014,04	4703,72	1,3E-05	0,00015
Gmnn	1077,77	1128,68	831,16	794,35	755,97	706,69	624,82	597,12	1,3E-05	0,00016
Masp1	126,23	107,75	37,66	35,78	101,10	27,38	9,09	12,21	1,3E-05	0,00016
Adamtsl5	24,27	15,52	71,28	69,52	90,15	64,89	88,76	175,98	1,3E-05	0,00016
G3bp2	7560,59	8015,80	5609,67	5111,65	4900,30	5158,70	4857,36	5021,09	1,3E-05	0,00016
Slitrk4	208,76	220,07	338,92	425,29	96,59	261,58	46,83	81,38	1,4E-05	0,00016
Socs3	105,19	107,75	231,33	269,89	236,97	331,54	291,44	249,22	1,4E-05	0,00016
Fnbp1	661,88	710,45	1182,19	1292,22	1127,52	1413,37	1264,31	1387,51	1,4E-05	0,00016
Rhou	1608,57	1537,78	1342,23	1267,69	839,04	986,52	981,96	905,34	1,4E-05	0,00016
Fhl1	1746,12	1819,03	1045,00	1081,62	730,86	992,60	1086,09	1215,60	1,4E-05	0,00017
Ckb	69,59	51,14	208,46	139,04	235,03	208,86	271,87	166,83	1,4E-05	0,00017
Gpx6	51,78	55,70	21,52	18,40	6,44	9,13	10,48	10,17	1,4E-05	0,00017
Cyp4f39	1,62	0,91	6,72	8,18	4,51	7,10	51,02	26,45	1,4E-05	0,00017
Fam160a1	98,71	60,27	166,77	151,30	163,56	172,36	304,72	229,90	1,4E-05	0,00017
Csf1r	3,24	2,74	2,69	3,07	123,63	15,21	14,68	7,12	1,5E-05	0,00017
B230118H	365,73	283,08	200,39	199,35	215,07	163,24	121,61	109,86	1,5E-05	0,00018
Lmo4	891,67	999,01	1012,73	1096,96	985,21	976,38	1854,88	1521,79	1,5E-05	0,00018
Bhlha15	56,64	60,27	34,97	11,25	4,51	7,10	7,69	6,10	1,5E-05	0,00018
Ppp1r3g	74,44	60,27	30,93	20,45	12,23	10,14	16,07	14,24	1,5E-05	0,00018
Lipe	318,80	305,91	336,23	308,74	131,36	237,25	120,21	90,53	1,5E-05	0,00018
Tle6	257,31	234,68	112,97	148,24	131,36	153,10	62,90	91,55	1,5E-05	0,00018
Syk	122,99	73,97	234,02	260,69	244,69	250,43	318,70	259,40	1,5E-05	0,00018
Man2a1	2089,20	2602,53	4571,39	4312,18	1580,20	2709,13	1421,56	1907,32	1,5E-05	0,00018
Arhgap28	1296,24	1238,26	871,51	813,77	956,24	736,09	516,49	632,72	1,6E-05	0,00019
Amer2	67,97	66,66	80,70	66,45	99,81	77,06	193,60	172,93	1,6E-05	0,00019
Pcolce	865,78	394,49	1899,03	1512,02	2410,23	1828,05	1054,64	1108,79	1,6E-05	0,00019
Tfeb	32,37	36,53	87,42	78,72	185,45	107,47	141,18	111,90	1,6E-05	0,00019
Slc1a3	835,03	778,02	891,68	950,77	727,64	610,36	445,90	491,33	1,6E-05	0,00019
Stra6	365,73	354,31	496,28	197,31	269,16	227,11	92,25	76,29	1,6E-05	0,00019
Bmpr2	1110,14	1359,71	1506,31	1884,15	2200,31	2412,06	2314,76	2841,15	1,6E-05	0,00019
Etv2	42,08	17,35	2,69	4,09	1,29	1,01	0,70	1,02	1,6E-05	0,00019
Itpk1	250,83	215,51	372,54	226,96	499,69	373,11	813,52	573,72	1,6E-05	0,00020
Chst8	127,84	56,62	200,39	129,84	184,81	138,90	32,85	34,59	1,7E-05	0,00020
Ier5	809,14	857,47	1581,63	1433,31	1367,06	1864,55	2319,65	1700,82	1,7E-05	0,00020
Txnrd1	7389,06	8460,51	9604,08	9069,08	7130,87	7149,99	5075,42	5559,21	1,8E-05	0,00021
Vamp3	1773,63	1840,04	1287,09	1282,00	1275,62	1162,94	1014,80	1078,27	1,8E-05	0,00021
Dysf	140,79	141,54	279,74	212,64	394,73	198,72	72,69	90,53	1,8E-05	0,00021
Pdlim7	1127,94	1088,50	969,69	728,92	684,50	609,35	564,01	484,21	1,8E-05	0,00021
Gprn2	30,75	29,22	57,83	35,78	69,54	83,14	136,29	110,88	1,8E-05	0,00021
Ltbp1	983,91	630,09	1211,77	1146,03	3991,07	1732,75	2323,15	1853,41	1,8E-05	0,00021
Shank2	197,43	247,47	106,25	89,96	66,32	96,32	52,42	84,43	1,8E-05	0,00021

Tril	1312,42	908,60	2287,71	2058,97	2017,43	859,78	617,13	406,90	1,8E-05	0,00021
Camta1	207,14	198,16	224,60	386,44	442,38	454,23	516,49	592,03	1,8E-05	0,00021
Tuba8	82,53	14,61	129,11	51,12	7,08	19,26	3,49	2,03	1,8E-05	0,00022
2510009E	555,07	526,90	408,86	353,73	260,15	260,57	389,99	370,28	1,9E-05	0,00022
Hpn	482,25	390,84	571,59	374,17	242,76	290,99	183,81	194,29	1,9E-05	0,00022
Pear1	25,89	21,00	67,25	100,19	171,29	46,64	15,38	11,19	1,9E-05	0,00022
Creg2	8,09	4,57	76,66	44,98	41,86	103,42	60,80	54,93	2,0E-05	0,00024
Lrp12	776,77	782,59	967,00	918,05	1112,71	1181,19	1398,50	1310,20	2,0E-05	0,00024
St8sia3	43,69	28,31	24,21	4,09	0,00	2,03	0,00	0,00	2,1E-05	0,00024
Kcne1	22,66	31,05	14,79	11,25	3,22	5,07	0,70	0,00	2,1E-05	0,00024
Pdlim5	627,89	605,43	1401,41	1305,51	370,26	812,13	447,30	459,79	2,1E-05	0,00025
Slc6a17	624,66	523,25	999,28	956,90	452,04	661,06	355,04	442,50	2,1E-05	0,00025
Marveld2	336,60	295,87	410,20	419,15	378,63	464,36	628,31	706,98	2,2E-05	0,00026
Pip5k1b	79,30	60,27	52,45	57,25	15,45	14,19	27,26	21,36	2,3E-05	0,00026
Pcbd1	161,83	127,84	84,73	65,43	66,32	58,81	44,73	36,62	2,3E-05	0,00026
Wnk3	423,99	543,34	306,64	332,26	209,92	295,04	150,96	203,45	2,3E-05	0,00027
Dcblid1	2445,22	2628,10	3047,59	3176,38	1481,68	2681,75	971,47	1244,08	2,3E-05	0,00027
Tmem231	294,53	252,03	527,21	349,64	627,19	564,74	720,57	619,50	2,4E-05	0,00027
Unc13d	67,97	88,58	195,01	200,38	142,95	164,25	209,67	196,33	2,4E-05	0,00028
Astn2	40,46	40,18	55,14	68,50	75,34	51,71	242,52	116,98	2,4E-05	0,00028
Jam3	729,84	666,61	384,65	430,40	542,19	380,21	290,74	304,15	2,4E-05	0,00028
Eya2	427,23	395,40	485,52	420,18	690,94	748,25	1290,17	735,46	2,4E-05	0,00028
Tgfb2	589,05	433,76	1118,97	1288,13	1041,88	1462,04	837,28	1062,00	2,4E-05	0,00028
Rrm2	5214,09	5505,50	4361,58	4117,94	4104,41	3394,52	2813,07	3049,68	2,4E-05	0,00028
Tap1	82,53	74,88	177,53	147,22	142,31	152,08	268,38	199,38	2,5E-05	0,00029
Pou6f1	59,88	42,01	84,73	148,24	199,62	153,10	174,73	215,65	2,5E-05	0,00029
Slc2a13	8,09	8,22	8,07	11,25	21,25	13,18	58,01	53,91	2,5E-05	0,00029
Tbc1d2	203,90	229,21	384,65	360,88	306,51	462,34	539,55	600,17	2,6E-05	0,00030
Trpc5	17,80	26,48	65,90	33,74	4,51	16,22	2,10	0,00	2,6E-05	0,00030
Tm7sf2	423,99	514,11	250,16	268,87	258,22	300,11	178,92	227,86	2,6E-05	0,00030
Epb41l4a	755,74	679,40	1168,74	1068,33	960,10	1129,48	1460,70	1338,69	2,6E-05	0,00030
S100a16	103,57	64,84	741,05	350,66	258,22	361,96	485,04	194,29	2,7E-05	0,00031
C330021F	92,24	74,88	68,59	39,87	28,33	36,50	8,39	16,28	2,7E-05	0,00031
Mal2	66,35	68,49	90,11	57,25	112,04	114,57	209,67	173,95	2,8E-05	0,00031
Spsb1	129,46	132,41	271,67	224,91	318,75	601,24	306,82	245,15	2,8E-05	0,00032
H1f0	4536,03	4396,00	7255,85	7758,46	8340,17	6934,03	6692,67	7116,61	2,8E-05	0,00032
Rasef	195,81	252,03	137,18	184,02	85,00	108,49	75,48	87,48	2,8E-05	0,00032
Gal3st4	190,96	232,86	217,88	202,42	76,63	122,68	13,98	55,95	2,8E-05	0,00032
Slc35b1	1050,26	972,53	1249,43	1078,56	751,47	735,07	666,05	683,58	2,8E-05	0,00032
Serpnb6a	912,71	869,34	839,23	726,88	1146,19	1050,40	1526,40	1337,67	2,8E-05	0,00032
Spns2	30,75	61,18	98,18	183,00	102,38	160,20	323,59	210,57	2,8E-05	0,00032
Manf	2679,87	1959,66	3514,28	2198,01	1544,14	1212,62	1275,49	960,27	2,8E-05	0,00032
Prdm16	69,59	32,87	207,12	195,26	607,23	139,92	95,05	80,36	2,9E-05	0,00033
Tubb4a	106,81	105,93	51,11	31,69	33,48	26,36	27,26	32,55	2,9E-05	0,00033
Zeb1	406,19	281,26	138,53	120,63	357,38	78,07	39,14	43,74	2,9E-05	0,00033
Reps2	16,18	20,09	47,07	56,23	60,53	87,19	79,67	113,93	2,9E-05	0,00033
Plcl1	22,66	38,35	20,17	24,54	3,86	3,04	2,80	3,05	2,9E-05	0,00033
Nav2	1592,39	1798,94	3067,77	3623,13	2715,45	4146,83	3682,51	4515,53	2,9E-05	0,00033
Chmp4c	147,26	162,54	189,63	242,29	288,48	332,56	341,06	361,12	3,0E-05	0,00034
Trim9	3,24	0,00	26,90	43,96	30,26	39,54	23,76	48,83	3,0E-05	0,00034
Slc2a3	11970,40	10958,94	24610,72	21785,84	18854,90	29153,55	23446,72	23679,30	3,1E-05	0,00035
Samd4	58,26	51,14	57,83	81,79	90,79	89,22	213,16	144,45	3,1E-05	0,00035
Phactr3	46,93	31,05	63,21	43,96	35,42	11,15	3,49	2,03	3,1E-05	0,00035
Arl8a	346,31	359,79	576,97	555,12	720,56	589,07	711,48	664,26	3,2E-05	0,00036
Gng13	63,11	37,44	20,17	11,25	9,02	6,08	5,59	3,05	3,2E-05	0,00036
Fam169b	1,62	0,91	4,03	21,47	50,23	50,69	16,77	19,33	3,2E-05	0,00036
Nucb2	200,67	194,51	445,17	402,80	261,44	295,04	366,22	324,50	3,2E-05	0,00036
Abcc8	16,18	21,00	39,00	63,38	77,27	105,45	78,28	187,17	3,2E-05	0,00036
Nmnat2	626,27	750,63	341,61	276,03	601,43	605,30	601,05	874,83	3,3E-05	0,00037
Prr16	30,75	14,61	82,04	100,19	41,21	54,75	10,48	20,34	3,3E-05	0,00037
Alpk3	25,89	26,48	1,34	3,07	1,93	5,07	0,00	0,00	3,3E-05	0,00037
Dok5	323,66	377,14	174,84	175,84	139,09	216,97	110,43	141,40	3,4E-05	0,00038
Epha4	1369,06	1167,03	1784,71	2560,93	2398,64	2886,56	2614,59	2946,94	3,4E-05	0,00038
Llgl2	2085,96	1837,30	1514,38	1147,05	782,37	1040,26	1102,17	900,26	3,4E-05	0,00038

Igf2bp1	10628,85	10876,76	9704,95	8029,37	6017,52	7603,20	4631,61	5891,85	3,4E-05	0,00038
Cspg4	19,42	5,48	51,11	48,05	92,73	87,19	145,37	63,07	3,5E-05	0,00039
Ildr2	95,48	82,19	28,24	29,65	14,81	24,33	27,96	16,28	3,5E-05	0,00039
Mtmr10	373,82	374,40	583,70	604,20	542,83	668,16	781,37	734,45	3,6E-05	0,00040
Nadk2	881,96	1047,41	575,63	665,54	536,39	610,36	444,50	517,77	3,6E-05	0,00040
Mgst3	273,49	176,24	1113,60	689,05	352,87	529,25	462,67	225,83	3,6E-05	0,00040
Arfgef3	101,95	127,84	400,79	362,93	127,50	231,17	83,17	157,67	3,7E-05	0,00041
Apba2	66,35	78,53	79,35	46,00	150,68	50,69	11,88	8,14	3,7E-05	0,00041
Rbbp7	6667,30	6650,61	4860,55	4380,68	4370,99	4173,19	4467,37	4069,98	3,8E-05	0,00042
Myo5c	72,82	106,84	24,21	49,07	12,23	32,44	6,99	11,19	3,8E-05	0,00042
Hspa1a	6,47	6,39	30,93	19,42	38,64	24,33	109,03	45,78	3,8E-05	0,00042
Aldh3b2	72,82	71,23	294,54	189,13	199,62	254,49	336,87	189,21	3,8E-05	0,00042
Bhlhe40	45,31	77,62	190,98	290,34	133,94	173,38	162,84	149,53	3,8E-05	0,00043
Mme	153,74	107,75	239,40	301,59	356,09	306,20	109,03	168,86	3,9E-05	0,00043
Tom1l1	663,49	674,83	848,65	755,50	804,91	905,41	1279,69	1169,83	3,9E-05	0,00043
Hoxa2	42,08	43,83	1,34	8,18	9,66	12,17	2,80	3,05	3,9E-05	0,00043
Derl1	1972,68	1875,65	1577,59	1409,79	1111,42	1209,58	1233,56	1136,26	4,0E-05	0,00044
Ppat	2034,17	1947,79	1474,03	1139,90	1112,07	1161,92	1167,86	1045,72	4,0E-05	0,00044
Me1	338,22	352,48	181,56	198,33	151,32	188,58	142,58	177,00	4,0E-05	0,00044
Plat	163,45	165,28	117,01	102,23	61,17	70,97	152,36	165,81	4,0E-05	0,00044
Nrcam	3,24	3,65	39,00	26,58	74,70	38,53	57,31	26,45	4,1E-05	0,00045
Nsg2	42,08	31,05	36,31	64,41	95,30	206,83	139,08	142,41	4,1E-05	0,00045
Tnc	574,49	405,45	28,24	34,76	191,89	33,46	570,30	100,71	4,1E-05	0,00045
Flrt1	3,24	8,22	39,00	37,83	72,12	44,61	29,35	32,55	4,2E-05	0,00046
Pcgf5	48,55	61,18	94,14	148,24	101,10	193,65	221,55	270,59	4,2E-05	0,00046
Ppl	1100,43	1030,97	1694,60	1793,17	1349,68	1957,83	2239,98	2444,43	4,2E-05	0,00046
Bean1	0,00	0,00	9,41	10,22	30,26	15,21	29,35	18,31	4,3E-05	0,00047
Dio2	1,62	5,48	45,73	46,00	11,59	13,18	11,18	10,17	4,3E-05	0,00047
Slc35d2	30,75	19,18	57,83	73,61	94,66	173,38	48,92	63,07	4,3E-05	0,00047
Pla2g3	38,84	46,57	10,76	13,29	4,51	10,14	1,40	4,07	4,3E-05	0,00047
Lrrc8b	270,25	321,44	131,80	136,99	137,80	130,79	369,02	220,74	4,4E-05	0,00048
Grb10	24113,95	24924,96	16795,38	17271,23	16970,76	17392,36	12916,38	15669,56	4,5E-05	0,00049
Reln	25,89	26,48	9,41	19,42	37,35	31,43	83,87	76,29	4,6E-05	0,00050
Gjb5	519,47	285,82	576,97	350,66	170,64	246,38	154,46	96,64	4,6E-05	0,00050
Mgat3	174,77	196,33	252,85	198,33	478,44	317,35	468,96	400,79	4,6E-05	0,00050
Erbp3	1538,98	1155,16	1593,73	1714,45	1854,52	2400,90	2705,44	2871,67	4,6E-05	0,00050
Ski	2602,19	2473,78	3409,38	2774,60	3973,04	3442,17	6322,25	4462,63	4,7E-05	0,00051
Pmaip1	229,80	160,72	322,78	643,05	1422,44	469,43	300,53	256,34	4,8E-05	0,00052
Naip1	0,00	1,83	1,34	2,04	28,33	5,07	23,76	68,16	5,0E-05	0,00054
Tmem79	116,52	101,36	278,40	214,69	183,52	173,38	381,60	247,19	5,0E-05	0,00054
Pdzd4	148,88	159,80	213,84	214,69	283,97	300,11	345,26	301,10	5,0E-05	0,00054
Fam172a	488,72	418,23	500,31	546,95	632,34	690,46	858,25	816,84	5,0E-05	0,00054
Card14	3,24	6,39	2,69	25,56	32,20	34,47	83,17	82,40	5,1E-05	0,00055
Krt2	0,00	0,00	1,34	0,00	6,44	1,01	27,26	34,59	5,1E-05	0,00055
Syvn1	1296,24	1419,07	1209,08	1226,80	824,23	921,63	814,92	865,67	5,2E-05	0,00056
Irx4	84,15	126,93	180,22	120,63	52,80	127,75	361,33	324,50	5,2E-05	0,00056
Tmprss4	25,89	42,01	86,07	75,65	42,50	61,85	11,88	16,28	5,2E-05	0,00056
Pclaf	2429,03	2448,21	2034,87	1771,70	1746,34	1394,11	1355,87	1210,51	5,2E-05	0,00056
Lsp1	173,16	135,15	69,94	90,99	142,31	140,93	56,61	59,00	5,3E-05	0,00057
Vwa2	1186,20	1219,99	1989,14	1952,65	1699,33	2084,57	2161,70	2105,69	5,3E-05	0,00057
Emx2	945,07	1179,81	1131,08	931,34	841,62	1276,49	2101,59	2074,15	5,3E-05	0,00057
Foxp1	640,84	677,57	718,19	935,43	802,34	1086,90	1386,62	1466,86	5,4E-05	0,00057
Prr5l	299,38	369,83	507,04	442,67	948,51	584,00	895,99	729,36	5,4E-05	0,00058
C130074C	38,84	25,57	162,74	122,68	56,67	94,29	62,90	60,02	5,4E-05	0,00058
Kazn	640,84	675,75	1309,95	1385,26	1135,25	1544,16	1116,14	1439,39	5,5E-05	0,00059
Tchh	129,46	123,28	49,76	42,94	53,45	50,69	120,21	90,53	5,5E-05	0,00059
Cdx2	17,80	30,13	24,21	18,40	2,58	6,08	0,70	1,02	5,5E-05	0,00059
Galnt2	2891,86	2296,62	6327,86	4241,64	3855,85	4909,28	2779,53	2435,27	5,6E-05	0,00060
Nrp2	2691,20	2115,81	6686,95	5984,72	7927,42	4189,42	4621,83	4782,04	5,7E-05	0,00060
Nxph3	95,48	92,23	92,80	74,63	231,81	171,35	163,54	182,09	5,7E-05	0,00061
Eci1	168,30	112,32	402,13	289,32	381,21	335,60	245,31	232,95	5,7E-05	0,00061
Wsb2	419,13	365,27	788,12	650,20	898,28	793,88	1100,77	738,52	5,7E-05	0,00061
Hs6st1	1928,99	1661,05	2872,75	2361,58	3087,64	3393,51	3543,43	3060,87	5,8E-05	0,00061
Krt7	1084,25	959,74	2032,18	1568,25	1552,51	1857,46	2342,71	1980,57	5,8E-05	0,00062

Gm49394	61,49	28,31	20,17	6,13	4,51	2,03	2,80	3,05	5,8E-05	0,00062
Shtn1	12,95	21,00	63,21	47,03	71,48	135,86	100,64	71,21	5,8E-05	0,00062
Hrk	79,30	95,88	56,49	42,94	17,39	23,32	9,09	24,41	5,8E-05	0,00062
Dlx6	203,90	231,94	496,28	689,05	296,85	391,36	174,03	301,10	5,8E-05	0,00062
Wwtr1	483,86	452,93	656,32	661,45	1019,34	771,57	887,60	858,55	5,9E-05	0,00062
Hoxa7	233,03	152,50	82,04	106,32	103,67	22,31	23,76	16,28	6,0E-05	0,00063
Rasl11b	140,79	239,25	355,06	424,27	307,15	556,63	709,38	631,71	6,1E-05	0,00064
Gclm	780,01	786,24	856,72	793,33	903,43	989,56	1355,17	1262,39	6,1E-05	0,00064
Cpq	45,31	29,22	142,56	113,48	144,24	104,43	82,47	78,33	6,1E-05	0,00065
Frem1	1458,07	1369,75	2170,70	3830,67	2362,58	4424,64	731,75	1376,33	6,2E-05	0,00065
Fbxw4	398,10	371,66	782,74	626,69	434,01	508,98	375,31	356,03	6,4E-05	0,00067
Ace2	17,80	4,57	30,93	47,03	62,46	42,58	86,66	96,64	6,5E-05	0,00068
Esr1	1,62	1,83	21,52	13,29	16,74	36,50	37,74	43,74	6,6E-05	0,00070
Tdrd1	48,55	40,18	84,73	83,83	92,08	87,19	186,61	124,10	6,6E-05	0,00070
Aqp3	11,33	16,44	9,41	5,11	10,30	2,03	140,48	28,48	6,7E-05	0,00070
Nnt	1351,26	1196,25	1592,39	1409,79	1938,23	1678,00	2488,79	2178,93	6,7E-05	0,00070
Aifm1	1511,47	1448,29	1182,19	1034,60	972,98	974,35	885,51	851,43	6,7E-05	0,00070
Lor	6,47	2,74	16,14	9,20	75,98	12,17	171,93	45,78	6,7E-05	0,00071
Fermt2	1893,38	1914,00	2236,60	2584,45	2432,12	2052,12	977,76	1363,10	6,8E-05	0,00071
Fgf11	59,88	52,05	71,28	98,14	70,83	87,19	184,51	154,62	6,8E-05	0,00071
Wfdc2	508,14	295,87	334,89	224,91	142,95	148,03	174,73	143,43	7,0E-05	0,00073
Nefl	51,78	61,18	40,35	12,27	7,73	16,22	4,19	3,05	7,0E-05	0,00073
Cdkn2c	1,62	3,65	44,38	20,45	21,25	17,24	50,32	38,66	7,0E-05	0,00073
Pcdh18	2008,28	2092,98	1429,65	1523,27	1003,89	929,74	1007,12	1488,22	7,0E-05	0,00073
Ajap1	90,62	75,79	40,35	49,07	39,92	14,19	4,89	12,21	7,1E-05	0,00074
Npm3	2492,15	2274,70	3402,65	2641,70	1564,75	1920,32	1660,59	1266,46	7,1E-05	0,00074
Tspan6	2267,21	1865,60	2679,08	2369,76	1321,99	1819,94	1146,20	1286,81	7,1E-05	0,00074
Dlc1	514,61	735,10	438,44	418,13	651,66	254,49	118,11	167,84	7,3E-05	0,00076
Vwa5b2	56,64	40,18	4,03	4,09	6,44	11,15	1,40	8,14	7,4E-05	0,00077
Prickle1	713,66	852,90	1414,86	1237,02	678,06	842,55	483,64	693,76	7,4E-05	0,00077
Cbfa2t3	22,66	21,00	53,80	55,21	193,18	48,67	9,78	20,34	7,4E-05	0,00077
Tbx18	29,13	30,13	22,86	38,85	299,43	67,93	72,69	73,24	7,5E-05	0,00078
Slc25a13	4133,08	3940,33	4184,05	3039,38	2338,11	2485,06	2397,93	2069,07	7,5E-05	0,00078
Cped1	114,90	62,10	225,95	386,44	891,20	186,56	123,71	102,74	7,5E-05	0,00078
Sema3f	2085,96	1574,30	3028,76	3019,96	2918,29	3437,11	3595,84	3446,41	7,6E-05	0,00079
Pou3f1	4,85	0,91	13,45	11,25	30,91	20,28	61,50	32,55	7,6E-05	0,00079
Nfasc	59,88	41,09	65,90	47,03	16,10	30,42	8,39	8,14	7,7E-05	0,00080
Lrrtm1	381,91	261,17	595,80	525,48	349,01	379,20	211,07	257,36	7,8E-05	0,00081
Mreg	121,37	147,02	111,63	96,10	35,42	52,72	58,71	63,07	7,9E-05	0,00082
Tekt2	4,85	2,74	10,76	15,33	25,76	22,31	38,44	47,81	7,9E-05	0,00082
Clstn2	22,66	19,18	28,24	73,61	149,39	88,21	121,61	93,59	8,0E-05	0,00083
Bmp7	3602,29	3240,84	6608,94	5120,85	3536,46	4295,87	3154,14	3212,44	8,1E-05	0,00083
Cpeb2	30,75	31,05	43,04	86,90	57,31	113,56	151,66	178,02	8,0E-05	0,00083
Trim36	38,84	45,66	64,56	103,26	132,01	164,25	116,72	172,93	8,1E-05	0,00083
Erc2	79,30	110,49	115,66	124,72	238,25	237,25	178,92	261,43	8,1E-05	0,00083
Fgd5	51,78	45,66	20,17	26,58	65,68	41,57	130,00	91,55	8,2E-05	0,00084
Phactr1	110,04	133,32	53,80	39,87	19,96	43,60	35,64	30,52	8,3E-05	0,00086
Cyp51	2875,68	2841,78	2645,46	2378,96	2229,93	2392,79	1736,77	1690,65	8,4E-05	0,00086
Rec8	66,35	66,66	55,14	49,07	16,74	40,56	5,59	11,19	8,4E-05	0,00087
Slco5a1	8,09	11,87	13,45	24,54	25,76	35,49	68,49	65,10	8,6E-05	0,00088
Cyp20a1	334,98	313,22	213,84	261,72	227,95	215,96	138,38	148,52	8,6E-05	0,00088
Tns4	328,51	377,14	579,66	421,20	477,80	512,02	998,73	700,88	8,7E-05	0,00089
Kitl	760,59	1154,25	501,66	583,75	176,44	397,45	350,15	428,26	8,7E-05	0,00089
Plekhm2	475,77	535,12	706,08	757,55	789,46	828,35	883,41	942,98	9,2E-05	0,00094
Uchl1	192,58	126,02	259,57	178,91	459,12	374,13	493,42	330,60	9,2E-05	0,00094
C1qtnf12	116,52	63,01	104,90	97,12	319,39	134,85	510,90	250,24	9,3E-05	0,00095
Ssr3	6958,59	7866,95	5354,13	5728,11	4251,22	5035,00	4009,59	4578,59	9,5E-05	0,00097
Phldb3	98,71	46,57	274,36	210,60	199,62	190,61	376,01	213,62	9,6E-05	0,00098
Soat1	1369,06	1365,19	742,40	1015,17	642,00	797,94	559,82	731,40	9,7E-05	0,00098
Prom2	1148,98	1038,27	1172,77	1073,45	409,54	717,84	542,35	595,09	9,7E-05	0,00099
Txnrd2	318,80	293,13	282,43	279,10	477,80	522,16	495,52	423,17	9,8E-05	0,00099
Pdia3	15312,14	12873,86	16929,87	16195,74	12049,85	12974,82	9507,15	9908,93	9,9E-05	0,00101
Arhgap40	0,00	0,00	10,76	4,09	4,51	5,07	35,64	20,34	9,9E-05	0,00101
Mcub	1,62	0,91	26,90	43,96	166,78	12,17	23,76	13,22	0,00010	0,00103

Htra3	61,49	31,96	14,79	13,29	12,23	13,18	4,89	3,05	0,00010	0,00104
Rab11fip1	781,63	924,13	687,25	694,16	509,35	555,61	434,72	500,48	0,00010	0,00104
Shc2	645,69	589,91	381,96	333,28	399,88	293,02	314,51	271,60	0,00010	0,00106
Ttc39a	370,59	267,56	305,30	237,18	156,47	184,53	111,82	144,45	0,00010	0,00106
Gxylt2	16,18	24,66	65,90	60,32	85,64	89,22	58,01	65,10	0,00011	0,00107
Slc18a1	61,49	33,79	18,83	11,25	6,44	11,15	1,40	5,09	0,00011	0,00107
Ebf3	74,44	73,05	5,38	14,31	25,11	58,81	6,99	16,28	0,00011	0,00108
Mal	4,85	13,70	98,18	59,30	8,37	27,38	13,28	8,14	0,00011	0,00108
Fzd5	21,04	29,22	40,35	54,18	52,80	59,82	167,74	83,41	0,00011	0,00108
Gal	29,13	19,18	5,38	8,18	12,23	21,29	0,70	0,00	0,00011	0,00108
Hoxa9	153,74	90,40	150,63	317,94	221,51	71,99	16,07	35,60	0,00011	0,00108
Pik3r3	1616,66	1752,37	1603,15	1816,68	896,99	1318,06	616,43	917,55	0,00011	0,00110
Phlda2	77,68	41,09	2,69	5,11	25,11	7,10	11,18	7,12	0,00011	0,00110
Erbp2	1943,55	1567,00	2840,47	2149,96	2970,45	2735,49	4110,93	3330,44	0,00011	0,00110
Rnf149	606,85	551,55	1160,67	994,73	961,39	1244,05	842,87	860,58	0,00011	0,00110
Myk3	14,56	7,31	16,14	21,47	20,61	26,36	58,71	72,22	0,00011	0,00111
Rps6ka3	3128,13	4570,41	2310,58	2713,26	1463,01	2083,55	1181,84	1878,84	0,00011	0,00112
Gfpt1	1492,05	1766,98	1385,27	1207,37	888,62	1048,37	942,12	926,71	0,00011	0,00112
Rnf182	19,42	35,61	21,52	38,85	86,29	81,11	88,76	105,79	0,00011	0,00112
Klc3	244,36	116,89	390,03	323,06	554,42	494,78	605,25	457,76	0,00011	0,00112
Cyp4f16	90,62	131,50	263,60	141,08	25,11	52,72	74,78	105,79	0,00011	0,00113
Acat1	344,69	281,26	381,96	326,12	638,13	455,24	895,29	593,05	0,00011	0,00113
Acadl	457,97	335,13	767,95	650,20	828,09	699,59	872,23	801,58	0,00011	0,00114
Ncald	66,35	71,23	87,42	58,27	29,62	54,75	9,78	16,28	0,00011	0,00114
Barx2	37,22	54,79	203,08	176,86	38,64	50,69	104,84	34,59	0,00012	0,00115
Ccdc106	42,08	44,75	30,93	49,07	113,33	66,92	207,57	108,84	0,00012	0,00118
Mturn	129,46	115,06	147,94	212,64	329,69	281,86	236,93	312,29	0,00012	0,00118
Sowaha	19,42	18,26	16,14	4,09	0,00	0,00	0,00	0,00	0,00012	0,00118
Plscr1	229,80	245,64	161,39	105,30	175,79	83,14	59,41	53,91	0,00012	0,00118
Acad4	105,19	85,84	130,46	144,15	164,85	165,26	326,39	208,53	0,00012	0,00121
Dkk2	38,84	31,05	8,07	1,02	1,29	1,01	8,39	7,12	0,00012	0,00122
Alx4	307,47	241,08	117,01	148,24	132,01	36,50	58,01	28,48	0,00012	0,00122
Prkd1	527,56	613,65	1082,66	1240,09	328,40	642,81	301,93	501,50	0,00013	0,00125
Sost	739,55	524,16	2120,94	1567,23	1429,52	2435,38	663,26	1315,29	0,00013	0,00125
Nup62cl	263,78	287,65	139,87	160,51	88,86	179,46	70,59	88,50	0,00013	0,00126
Rassf9	121,37	177,15	188,29	177,89	86,93	111,53	37,74	68,16	0,00013	0,00128
Hey1	156,97	148,85	266,29	287,27	689,00	301,13	215,96	204,47	0,00013	0,00129
Gyg	650,55	510,46	384,65	307,72	325,83	333,57	292,84	282,79	0,00013	0,00131
Derl3	122,99	70,31	79,35	51,12	43,14	44,61	19,57	19,33	0,00013	0,00132
Pld4	98,71	73,05	48,42	57,25	36,06	47,65	11,18	21,36	0,00013	0,00133
Chst3	377,06	441,06	590,42	605,22	337,42	457,27	196,39	282,79	0,00013	0,00133
Crelid2	875,49	799,94	1178,15	699,27	511,28	440,03	478,05	406,90	0,00014	0,00136
Mbp	574,49	543,34	794,85	722,79	736,66	829,37	1077,70	976,55	0,00014	0,00136
Luzp2	21,04	10,96	103,56	156,42	81,14	134,85	16,07	66,12	0,00014	0,00137
Gstm2	244,36	230,12	212,50	157,44	314,24	208,86	666,05	388,59	0,00014	0,00137
Qprt	29,13	16,44	8,07	5,11	3,86	2,03	0,00	0,00	0,00014	0,00137
Ttc9	74,44	59,36	252,85	230,02	107,54	214,95	123,71	93,59	0,00014	0,00137
Amigo2	45,31	36,53	47,07	72,59	67,61	79,08	132,09	139,36	0,00014	0,00139
Pdia4	8186,87	6426,89	10697,51	7161,42	4830,11	5153,63	4703,60	4110,66	0,00014	0,00139
Cthrc1	103,57	84,01	26,90	55,21	16,10	19,26	39,14	27,47	0,00014	0,00140
Usp25	2647,50	3183,31	2073,87	2022,17	1483,61	1777,36	1501,24	1847,31	0,00014	0,00140
Rxfp1	0,00	0,00	0,00	1,02	0,00	4,06	16,07	63,07	0,00015	0,00143
Arhgap18	127,84	86,75	133,15	192,20	190,60	263,61	285,15	345,86	0,00015	0,00143
Shisa4	166,68	140,63	154,67	125,75	101,74	55,76	42,63	51,88	0,00015	0,00144
Spata2l	0,00	1,83	10,76	9,20	21,89	23,32	39,14	20,34	0,00015	0,00145
Pgam2	12,95	5,48	82,04	46,00	45,72	76,04	77,58	49,84	0,00015	0,00145
Tmem121l	56,64	40,18	108,94	90,99	121,06	139,92	149,56	130,21	0,00015	0,00146
Rnaset2a	43,69	22,83	197,70	115,52	121,70	79,08	75,48	61,03	0,00015	0,00147
Serinc5	1331,84	1206,30	2728,85	3180,47	1650,39	3024,45	1398,50	1599,10	0,00015	0,00148
Muc15	0,00	0,00	1,34	2,04	5,80	8,11	25,86	18,31	0,00016	0,00151
Sulf1	1534,13	1470,20	2716,74	2203,12	1117,22	1337,33	2620,88	1813,74	0,00016	0,00152
Rhob	1831,89	1523,17	2169,36	1386,28	1100,48	1283,59	875,72	604,24	0,00016	0,00152
Sorbs2	977,44	908,60	2024,11	2551,73	1415,36	2232,60	1223,77	1620,46	0,00016	0,00153
Tgm2	21,04	44,75	12,10	6,13	9,02	11,15	60,11	48,83	0,00016	0,00154

Pcsk6	352,78	344,26	1406,79	1064,24	1184,19	916,56	1430,65	564,57	0,00016	0,00155
2900026A	1964,59	1657,40	1470,00	1285,07	1436,61	1716,52	3309,99	2317,27	0,00016	0,00155
Tmed3	619,80	417,32	1304,57	1005,97	679,35	655,99	663,26	491,33	0,00016	0,00156
Atp2b3	51,78	27,40	123,73	170,73	94,01	168,31	53,82	65,10	0,00016	0,00157
Meis1	2016,37	2690,20	1069,21	1476,24	453,33	1039,24	869,43	1119,98	0,00016	0,00157
Crym	59,88	50,22	13,45	8,18	14,17	1,01	1,40	3,05	0,00017	0,00160
Pros1	1147,36	953,35	699,36	738,12	628,48	687,42	463,37	597,12	0,00017	0,00161
Pcp4l1	202,28	141,54	326,82	122,68	30,91	60,83	89,46	56,97	0,00017	0,00161
Rab6b	17,80	10,04	5,38	9,20	38,64	19,26	55,21	62,05	0,00017	0,00161
Gusb	907,85	832,81	995,24	840,35	797,83	686,41	517,19	486,24	0,00017	0,00161
Fmnl3	1305,95	1321,36	2130,36	1962,87	1834,55	1755,05	1404,09	1451,60	0,00017	0,00162
Mpp1	218,47	164,37	238,05	304,65	444,31	343,71	455,68	408,93	0,00017	0,00165
Fos	38,84	21,92	29,59	32,71	544,12	23,32	34,95	23,40	0,00017	0,00165
Hsp90b1	22392,11	22453,01	22300,14	21544,57	14349,97	16605,58	10330,45	14585,18	0,00017	0,00165
Clip2	1063,21	903,12	1429,65	1309,60	1587,29	1540,11	1639,62	1705,91	0,00017	0,00166
Stard5	417,52	330,57	808,30	665,54	679,35	892,23	615,03	603,22	0,00018	0,00168
Fam212b	12,95	11,87	22,86	21,47	13,52	18,25	77,58	47,81	0,00018	0,00171
Ero1lb	74,44	95,88	106,25	110,41	33,48	50,69	37,04	37,64	0,00018	0,00173
Sema5b	4,85	11,87	2,69	9,20	210,56	14,19	19,57	12,21	0,00018	0,00175
Pm20d2	12,95	28,31	37,66	42,94	42,50	58,81	97,85	100,71	0,00019	0,00177
Wnt10a	187,72	131,50	664,39	388,49	417,27	454,23	508,10	296,02	0,00019	0,00178
Tyro3	483,86	415,49	914,55	762,66	895,71	805,03	1117,54	795,48	0,00019	0,00180
Fam234b	436,93	389,92	632,11	610,33	725,06	685,39	679,33	752,76	0,00019	0,00181
Galr1	0,00	0,00	12,10	22,49	5,80	15,21	23,76	25,43	0,00019	0,00181
Ttc7	459,59	484,89	656,32	473,34	759,19	639,77	1017,60	907,38	0,00019	0,00181
Golm1	3993,91	3470,04	3613,80	2888,08	2561,55	2658,43	1742,36	2190,12	0,00020	0,00188
Npbwr1	25,89	44,75	13,45	9,20	7,08	14,19	1,40	2,03	0,00020	0,00188
Ppm1l	691,00	634,65	1106,87	909,87	1300,09	1083,85	1151,79	1294,95	0,00020	0,00188
Efemp1	12,95	10,96	2,69	4,09	11,59	12,17	48,22	31,53	0,00020	0,00189
Ago1	3688,05	3662,72	5133,57	4867,31	4963,41	5423,33	5985,38	5696,54	0,00020	0,00190
AW01173f	27,51	23,74	63,21	114,50	85,00	105,45	90,16	105,79	0,00020	0,00190
Gata2	59,88	98,62	14,79	8,18	27,69	4,06	8,39	3,05	0,00020	0,00193
Gsg1l	1,62	1,83	28,24	19,42	1,29	2,03	2,10	1,02	0,00020	0,00193
Jph2	92,24	57,53	56,49	54,18	32,84	39,54	16,07	16,28	0,00020	0,00193
Fam210b	241,12	169,85	162,74	180,95	298,14	268,68	420,74	346,88	0,00021	0,00195
Boc	148,88	196,33	86,07	139,04	159,69	114,57	407,46	262,45	0,00021	0,00197
Hoxa5	105,19	92,23	6,72	52,14	42,50	13,18	0,70	5,09	0,00021	0,00198
Slc35f1	89,01	98,62	24,21	30,67	48,94	26,36	22,36	26,45	0,00021	0,00198
Hba-x	503,28	3829,83	384,65	1045,84	64,39	151,07	112,52	32,55	0,00021	0,00202
Btc	0,00	0,00	2,69	5,11	13,52	17,24	13,98	28,48	0,00021	0,00202
Extl1	42,08	54,79	126,42	100,19	85,64	95,31	153,06	137,33	0,00022	0,00204
Gldc	1181,34	1010,88	1054,42	936,45	883,47	907,44	638,80	599,15	0,00022	0,00206
Inpp5b	325,27	284,00	316,06	319,99	535,75	482,61	466,87	479,12	0,00022	0,00209
Dmtn	131,08	119,63	258,22	285,23	245,34	390,35	201,98	175,98	0,00022	0,00209
Hspbap1	527,56	556,12	367,16	318,97	240,83	300,11	332,68	262,45	0,00022	0,00211
Sspn	19,42	22,83	33,62	29,65	70,19	55,76	76,18	74,26	0,00023	0,00213
Prkx	347,93	413,67	551,42	561,26	562,15	646,87	696,80	776,15	0,00023	0,00213
Ncoa1	174,77	198,16	255,54	310,79	315,53	316,34	367,62	495,40	0,00023	0,00214
Odc1	7183,53	7289,83	8074,91	6839,38	5810,82	6935,04	4524,68	4321,23	0,00023	0,00215
Selenos	631,13	626,43	632,11	609,31	405,68	414,68	349,45	427,24	0,00023	0,00215
Lmna	93,86	67,57	161,39	129,84	271,09	133,83	624,12	207,52	0,00023	0,00216
Hip1	4477,77	3756,78	3771,16	3004,63	2426,33	2743,60	2088,32	2422,05	0,00023	0,00216
Tgfb3	276,73	283,08	135,84	158,46	45,08	113,56	67,79	111,90	0,00023	0,00216
Morf4l2	5822,56	6068,01	4462,45	4619,91	4308,53	4540,22	3653,85	3935,70	0,00023	0,00217
Card10	1762,30	1515,86	1981,07	1554,96	881,54	1368,76	884,81	729,36	0,00023	0,00217
Cdh23	14,56	10,96	43,04	51,12	13,52	30,42	5,59	3,05	0,00023	0,00219
Slc25a17	1100,43	812,72	1166,05	1289,16	1497,14	1436,69	1898,91	1742,53	0,00023	0,00219
Naga	124,61	89,49	177,53	214,69	252,42	212,92	284,45	243,12	0,00023	0,00219
Baalc	11,33	16,44	13,45	17,38	12,88	16,22	88,06	42,72	0,00023	0,00219
Ifih1	1,62	3,65	2,69	19,42	36,06	57,79	31,45	54,93	0,00024	0,00220
Bcd1	315,56	324,18	122,39	164,60	59,24	134,85	57,31	120,03	0,00024	0,00220
Tspear	82,53	73,97	33,62	50,09	74,05	73,00	143,27	124,10	0,00024	0,00225
Hmmr	1513,09	1658,32	859,40	1106,16	801,05	953,06	733,15	949,08	0,00025	0,00229
Slc29a4	234,65	157,07	256,88	269,89	488,10	334,59	449,39	451,65	0,00025	0,00229

Otor	0,00	0,00	0,00	0,00	7,08	2,03	27,26	18,31	0,00025	0,00229
Cgnl1	574,49	503,16	988,52	876,14	880,90	955,09	856,15	1011,14	0,00025	0,00230
Slc48a1	294,53	224,64	437,10	342,48	656,16	460,31	784,17	534,05	0,00025	0,00230
Itpr1	587,43	745,15	267,64	382,35	228,59	346,75	185,91	314,33	0,00025	0,00232
Gpnmb	29,13	39,27	49,76	44,98	47,65	50,69	156,55	88,50	0,00025	0,00235
Pcdhb14	3,24	1,83	16,14	18,40	16,10	20,28	34,95	34,59	0,00025	0,00236
Irf2bpl	490,34	329,65	957,58	638,96	1326,49	781,71	1868,16	993,84	0,00026	0,00239
Nid2	907,85	595,39	338,92	349,64	1482,33	180,47	114,62	96,64	0,00026	0,00242
Tmem200	221,70	135,15	454,58	315,90	274,96	343,71	161,45	154,62	0,00026	0,00243
Slc16a7	97,10	73,05	263,60	361,90	146,82	252,46	141,18	230,91	0,00026	0,00245
Zbtb7a	242,74	303,17	657,67	591,93	342,57	562,71	733,15	584,91	0,00027	0,00248
Slc39a13	84,15	77,62	173,49	188,11	180,30	171,35	155,16	141,40	0,00027	0,00248
Ppp2r1b	2840,08	3051,81	2848,54	2467,90	1930,50	2002,44	1998,86	1829,00	0,00027	0,00251
Serpinc6b	16,18	30,13	20,17	39,87	64,39	49,68	93,65	108,84	0,00027	0,00251
Myb	30,75	53,88	90,11	111,43	113,98	111,53	137,68	139,36	0,00027	0,00251
Pink1	566,40	436,49	583,70	486,63	929,19	768,53	979,86	837,19	0,00028	0,00253
Mcm10	1556,78	1689,36	1420,24	1348,45	1281,42	1092,98	930,94	970,45	0,00028	0,00254
Tmem40	3,24	5,48	24,21	22,49	36,70	37,51	37,04	29,50	0,00028	0,00257
Zfp516	3518,14	3459,09	2722,12	2602,85	2383,83	2389,75	2357,39	2425,10	0,00028	0,00258
Mrc1	0,00	1,83	2,69	14,31	117,20	11,15	5,59	9,16	0,00028	0,00258
Dok4	684,53	562,51	455,93	437,56	549,92	569,81	350,15	335,69	0,00028	0,00258
Lrp11	132,70	103,19	51,11	49,07	47,65	71,99	37,04	29,50	0,00028	0,00260
Pon2	1118,23	1113,15	945,48	884,31	616,88	783,74	575,89	667,31	0,00028	0,00260
Fstl3	14,56	11,87	34,97	22,49	59,24	53,74	51,72	69,17	0,00029	0,00265
Kdr	140,79	104,10	1,34	24,54	12,88	2,03	22,36	6,10	0,00030	0,00270
Ttc22	0,00	0,00	10,76	13,29	9,02	21,29	36,34	15,26	0,00030	0,00271
Prune2	46,93	52,96	18,83	25,56	9,02	17,24	2,80	8,14	0,00030	0,00271
Jag1	490,34	594,47	1090,73	1839,17	930,48	1481,30	1195,82	1585,88	0,00030	0,00271
Sh3pxd2a	1577,82	1502,16	1803,54	2064,08	2822,34	2498,24	2048,48	2297,94	0,00030	0,00276
Tmem8b	95,48	119,63	174,84	199,35	265,94	234,21	214,56	298,05	0,00030	0,00276
Sntb1	98,71	52,05	121,04	144,15	207,35	217,99	179,62	259,40	0,00030	0,00278
Smad9	64,73	112,32	22,86	27,60	126,21	68,94	135,59	99,69	0,00031	0,00279
Tulp2	467,68	350,66	897,06	747,32	609,80	724,94	513,69	521,84	0,00031	0,00283
Ccser1	89,01	62,10	111,63	111,43	52,16	52,72	36,34	35,60	0,00031	0,00284
Rasgrp3	29,13	28,31	2,69	3,07	5,15	3,04	3,49	3,05	0,00031	0,00285
Upk2	0,00	0,00	14,79	16,36	18,67	16,22	9,78	10,17	0,00031	0,00285
Foxi2	169,92	152,50	295,88	244,34	25,76	146,00	41,93	36,62	0,00032	0,00286
Pgam1	4960,02	3913,84	3364,99	2084,53	2280,80	1664,82	2263,74	1472,96	0,00032	0,00287
1700025G	1024,37	1087,58	1687,88	1746,14	1506,15	1805,75	1677,36	1913,43	0,00032	0,00287
Cited2	1042,17	986,22	1226,57	998,82	606,58	808,07	610,84	606,27	0,00032	0,00287
Crat	563,16	404,53	1038,28	936,45	1210,59	867,89	861,74	755,81	0,00032	0,00289
Ltbp2	1,62	3,65	1,34	4,09	16,74	7,10	32,15	35,60	0,00032	0,00290
Vat1l	534,03	372,57	683,22	662,47	770,78	724,94	347,35	426,22	0,00032	0,00290
Fahd2a	85,77	111,41	165,43	183,00	182,23	171,35	241,12	228,88	0,00032	0,00293
Zhx3	318,80	351,57	521,83	559,21	328,40	478,56	234,13	258,38	0,00032	0,00293
Csn3	27,51	15,52	0,00	1,02	0,00	0,00	0,00	0,00	0,00033	0,00295
Chn1	446,64	409,10	336,23	383,37	504,84	328,50	155,16	209,55	0,00033	0,00298
Pcolce2	132,70	75,79	96,83	111,43	110,76	85,17	32,85	30,52	0,00033	0,00298
Mthfd1l	2314,14	1996,19	1210,43	879,20	1164,87	726,96	1106,36	609,33	0,00033	0,00299
Kremen1	6047,50	6565,69	7598,81	7884,20	5027,80	6477,78	3920,13	4539,94	0,00033	0,00299
Usp44	30,75	40,18	63,21	68,50	48,29	71,99	111,13	138,34	0,00033	0,00300
Map1b	587,43	483,07	806,95	884,31	953,02	953,06	747,12	776,15	0,00033	0,00300
Cbx8	77,68	69,40	161,39	189,13	95,95	189,60	278,16	219,72	0,00033	0,00301
Mindy2	92,24	123,28	190,98	224,91	173,86	282,88	302,62	312,29	0,00034	0,00301
Rprm	0,00	0,00	2,69	9,20	616,24	12,17	38,44	39,67	0,00034	0,00302
Tbc1d1	1689,48	1761,50	1291,12	1137,85	1379,94	1103,12	984,05	900,26	0,00034	0,00302
Ttc28	972,58	858,38	1222,53	935,43	1865,46	1231,88	2212,72	1736,43	0,00034	0,00308
Steap2	127,84	119,63	170,81	187,09	179,66	220,02	262,09	295,00	0,00035	0,00310
Trak1	414,28	462,06	636,15	542,86	779,15	666,13	996,63	764,96	0,00035	0,00310
Rspo4	271,87	121,45	68,59	95,08	79,20	8,11	17,47	4,07	0,00035	0,00312
Zdhhc1	90,62	77,62	127,77	195,26	162,27	209,88	243,22	223,79	0,00035	0,00312
Ati3	537,27	630,09	771,98	1060,16	850,63	1076,76	1176,25	1376,33	0,00035	0,00312
Fam19a5	483,86	399,05	352,37	300,56	234,39	259,56	241,82	198,36	0,00035	0,00312
Cbap	370,59	328,74	476,10	430,40	572,45	572,85	639,49	583,90	0,00035	0,00315

Gatm	72,82	93,14	48,42	51,12	41,86	37,51	18,87	24,41	0,00036	0,00318
Palmd	22,66	14,61	14,79	12,27	28,33	22,31	112,52	43,74	0,00036	0,00320
Sema3c	1152,21	1159,72	872,85	696,21	473,93	693,50	631,81	637,81	0,00036	0,00320
Hoxc4	425,61	400,88	161,39	243,31	133,29	186,56	81,07	181,07	0,00037	0,00326
Hmox1	265,40	234,68	203,08	138,01	157,76	107,47	97,15	76,29	0,00037	0,00326
Atp8b1	27,51	18,26	71,28	98,14	37,99	99,36	116,02	144,45	0,00037	0,00327
Ist1	1865,87	1703,06	2153,22	2302,29	2397,99	2462,75	2920,01	2799,44	0,00037	0,00330
Lmod1	32,37	52,05	26,90	22,49	8,37	17,24	4,89	4,07	0,00037	0,00330
Rragd	334,98	363,44	519,14	631,80	642,00	753,32	596,16	810,74	0,00037	0,00330
Grin2c	131,08	103,19	130,46	198,33	83,07	185,54	31,45	43,74	0,00037	0,00331
Sil1	317,18	199,98	606,56	493,79	361,24	336,61	284,45	231,93	0,00038	0,00333
Adgrb2	56,64	36,53	61,87	50,09	157,12	78,07	179,62	135,29	0,00038	0,00335
L1cam	21,04	10,96	45,73	77,70	79,20	74,01	77,58	55,95	0,00039	0,00341
Igf2r	6612,28	6358,40	4049,56	4392,95	3826,23	4400,31	3386,17	4347,68	0,00039	0,00341
Scarb2	1828,65	1553,30	3141,74	2995,42	2546,10	3323,55	2531,42	2876,75	0,00039	0,00341
Slc4a11	3,24	8,22	13,45	33,74	36,70	53,74	40,54	90,53	0,00039	0,00342
Adssl1	100,33	85,84	47,07	22,49	31,55	24,33	26,56	21,36	0,00039	0,00342
Pqlc3	267,02	199,98	268,98	237,18	349,65	399,47	462,67	426,22	0,00039	0,00344
Cx3cr1	3,24	0,91	9,41	3,07	73,41	10,14	2,10	2,03	0,00040	0,00354
Fgfr3	51,78	100,45	127,77	312,83	179,01	294,03	302,62	470,98	0,00040	0,00355
Sh3rf1	1757,45	1693,93	3929,86	3091,52	2508,11	3586,15	2557,98	2779,10	0,00041	0,00358
Cmip	1014,66	892,17	1428,31	1171,59	1618,19	1499,55	1712,31	1586,89	0,00041	0,00359
Plvap	79,30	36,53	10,76	25,56	5,15	3,04	21,67	8,14	0,00041	0,00361
Vstm5	6,47	12,78	33,62	49,07	32,84	60,83	61,50	73,24	0,00041	0,00362
Chst5	92,24	44,75	166,77	139,04	164,20	186,56	243,22	194,29	0,00041	0,00364
Arid3b	5417,99	5278,12	5846,37	4324,45	2832,65	4404,36	1472,58	2670,25	0,00041	0,00364
Hoxd10	97,10	43,83	169,46	230,02	361,89	56,78	23,06	30,52	0,00042	0,00366
As3mt	343,07	356,14	325,47	308,74	279,47	260,57	193,60	175,98	0,00042	0,00367
Coa5	2420,94	2391,59	1807,57	1592,79	1576,98	1585,73	1668,97	1544,17	0,00042	0,00367
Tns1	747,64	568,90	702,05	709,50	1344,52	922,64	1276,89	1175,93	0,00042	0,00367
Tro	1665,21	1729,54	1156,63	1392,41	1171,95	1049,38	630,41	959,26	0,00042	0,00371
Syndig1	4,85	10,04	110,28	27,60	36,70	47,65	127,20	55,95	0,00043	0,00375
Mecom	488,72	364,35	540,66	633,84	1613,04	417,72	190,10	245,15	0,00043	0,00376
Gab2	203,90	233,77	320,09	267,85	128,79	221,03	100,64	112,91	0,00043	0,00376
Fam136a	1574,58	1393,50	1069,21	955,88	1068,92	967,26	916,26	821,93	0,00043	0,00376
Kcnj15	284,82	190,85	310,68	275,01	311,66	351,82	520,68	495,40	0,00043	0,00377
Arap3	487,10	533,29	279,74	354,75	194,47	308,22	159,35	240,07	0,00043	0,00379
8430408G	0,00	0,00	8,07	4,09	5,80	10,14	69,19	7,12	0,00044	0,00380
Cacnb3	1242,84	1079,37	1908,44	1707,29	1746,34	1721,59	2015,63	1825,94	0,00044	0,00385
Epha1	1712,14	1681,14	2610,49	2323,75	2390,27	2711,16	2753,67	2712,98	0,00044	0,00387
Ank2	351,17	486,72	776,02	1012,11	527,38	668,16	311,01	479,12	0,00045	0,00388
Zwint	3213,90	3345,85	2515,00	2498,57	2423,75	2467,82	2135,84	2194,19	0,00045	0,00390
Itpr3	755,74	693,10	1288,43	1574,39	1150,70	1567,48	1117,54	1347,84	0,00045	0,00390
Ntng2	29,13	36,53	4,03	8,18	3,86	6,08	3,49	4,07	0,00045	0,00390
Emp2	89,01	52,05	111,63	133,93	130,07	116,60	271,87	175,98	0,00046	0,00398
Krt39	1,62	1,83	20,17	19,42	32,20	27,38	6,29	13,22	0,00046	0,00401
Ston1	320,42	273,95	369,85	330,21	456,55	393,39	633,20	518,79	0,00047	0,00409
Fam222a	118,13	91,32	80,70	52,14	47,01	24,33	29,35	17,29	0,00047	0,00410
Abcg5	181,25	167,11	220,57	188,11	57,95	146,00	59,41	55,95	0,00047	0,00410
Plxna2	4065,11	3790,57	2189,53	2973,96	1684,52	2608,75	1273,40	1952,08	0,00048	0,00412
Lrrn1	299,38	243,82	702,05	528,54	501,62	859,78	535,36	531,00	0,00048	0,00413
Wif1	84,15	39,27	481,48	406,89	735,37	192,64	462,67	137,33	0,00049	0,00421
Bcl6	17,80	26,48	41,69	46,00	38,64	43,60	122,31	70,19	0,00049	0,00421
Desi2	657,02	574,38	381,96	410,98	368,97	320,39	392,78	333,65	0,00049	0,00421
Cep131	881,96	906,78	907,82	868,98	909,87	792,87	521,38	576,77	0,00049	0,00422
Proser2	637,60	331,48	1218,50	1080,60	813,28	952,05	577,99	627,64	0,00049	0,00422
Atp1a2	32,37	39,27	75,32	58,27	18,67	27,38	10,48	17,29	0,00049	0,00424
9330182Li	29,13	42,01	84,73	116,55	96,59	164,25	105,53	136,31	0,00050	0,00427
Acta2	135,94	30,13	231,33	328,17	341,28	800,98	246,01	372,31	0,00050	0,00430
Ano1	32,37	30,13	73,97	83,83	50,23	92,26	16,77	25,43	0,00050	0,00430
Mcph1	846,36	907,69	718,19	639,98	450,75	566,77	540,25	513,71	0,00050	0,00430
Ttc12	186,10	146,11	177,53	170,73	77,27	151,07	27,96	61,03	0,00050	0,00430
Marveld1	292,91	275,78	302,61	394,62	574,39	438,00	580,79	531,00	0,00050	0,00433
Hdac11	242,74	326,91	279,74	340,44	445,60	428,88	519,98	568,64	0,00051	0,00435

Zfp316	359,26	260,25	574,28	501,96	726,35	554,60	712,18	584,91	0,00051	0,00435
Slc45a1	45,31	23,74	20,17	8,18	7,08	8,11	2,10	2,03	0,00051	0,00437
Tep1	359,26	364,35	427,69	420,18	504,84	606,31	599,66	695,79	0,00051	0,00437
Gm2a	158,59	127,84	223,26	264,78	291,06	276,79	302,62	273,64	0,00051	0,00438
Cerk	1127,94	1067,49	1504,97	1152,17	998,09	920,62	749,92	685,62	0,00052	0,00442
Bves	46,93	33,79	16,14	3,07	4,51	8,11	2,10	3,05	0,00052	0,00449
Lss	1197,53	1653,75	855,37	741,19	962,67	850,66	844,27	764,96	0,00053	0,00450
Arrdc1	250,83	291,30	262,26	329,19	316,17	426,85	531,16	558,46	0,00053	0,00454
Lama5	10371,54	10101,48	13703,41	15465,80	14769,81	17355,86	16360,56	22222,61	0,00054	0,00457
Abcc4	76,06	77,62	115,66	74,63	108,18	122,68	229,94	173,95	0,00054	0,00457
Kctd12b	11,33	28,31	28,24	75,65	90,15	106,46	95,05	130,21	0,00054	0,00460
Olfm2	158,59	153,41	57,83	62,36	136,51	101,39	132,09	135,29	0,00054	0,00460
Dglucy	0,00	0,00	2,69	1,02	8,37	5,07	23,06	17,29	0,00054	0,00462
Sstr2	169,92	99,54	122,39	149,26	54,73	106,46	41,24	32,55	0,00054	0,00462
Lurap1l	8,09	4,57	22,86	38,85	42,50	36,50	51,72	36,62	0,00055	0,00467
Chrdl1	45,31	53,88	36,31	36,80	37,99	31,43	8,39	11,19	0,00055	0,00469
Ncs1	1161,92	1148,77	1542,63	1328,01	2206,10	1686,11	2404,22	1878,84	0,00055	0,00469
Pax8	40,46	43,83	28,24	32,71	7,08	26,36	4,19	1,02	0,00055	0,00469
Slc30a4	716,90	890,34	805,61	1040,73	957,52	1083,85	1369,85	1816,79	0,00056	0,00472
Slc4a9	1,62	1,83	9,41	16,36	22,54	22,31	24,46	30,52	0,00056	0,00476
Islr2	0,00	0,00	43,04	12,27	7,73	64,89	10,48	4,07	0,00056	0,00477
Smurf1	1037,32	1037,36	1136,46	1124,56	1415,36	1412,36	1681,55	1505,51	0,00056	0,00477
Rdh11	647,31	640,13	369,85	372,13	418,55	424,82	549,34	467,93	0,00057	0,00479
Slc7a3	30,75	41,09	36,31	46,00	52,16	58,81	102,74	106,81	0,00057	0,00480
Slc39a3	307,47	246,56	517,79	340,44	589,84	470,45	783,47	577,79	0,00057	0,00483
Pcdhb18	8,09	0,00	18,83	26,58	37,35	31,43	49,62	49,84	0,00057	0,00484
Vcam1	98,71	35,61	161,39	162,55	848,70	93,28	79,67	73,24	0,00057	0,00485
Adgra2	480,63	315,96	181,56	225,93	703,81	132,82	82,47	63,07	0,00057	0,00485
Tunar	80,91	71,23	56,49	33,74	20,61	22,31	25,86	19,33	0,00058	0,00487
Serpinf1	966,11	574,38	353,71	316,92	888,62	232,18	173,33	162,76	0,00058	0,00487
Igfbp2	3343,36	2102,12	7184,57	4170,08	5003,33	5599,74	9068,24	6150,23	0,00058	0,00488
Mt2	275,11	371,66	330,85	276,03	70,19	124,71	280,26	138,34	0,00059	0,00499
Nfatc1	40,46	35,61	121,04	136,99	383,14	111,53	172,63	76,29	0,00059	0,00500
Draxin	118,13	80,36	71,28	107,34	440,45	161,21	100,64	119,02	0,00060	0,00502
Megf6	5662,35	4567,67	6786,47	4840,73	7181,74	6194,90	11481,54	8823,54	0,00060	0,00503
6030419C	430,46	400,88	285,12	202,42	215,07	208,86	230,64	170,90	0,00060	0,00505
Hvcn1	286,44	218,25	135,84	101,21	171,93	115,58	101,34	96,64	0,00060	0,00508
Cldn8	38,84	58,44	145,25	183,00	81,78	251,45	215,26	275,67	0,00061	0,00510
Nckap1l	3,24	0,91	0,00	2,04	59,89	8,11	1,40	3,05	0,00061	0,00512
Myo7a	67,97	45,66	2,69	15,33	19,32	5,07	4,19	4,07	0,00061	0,00514
Gorasp2	4843,50	4114,74	5461,73	3576,11	2738,63	2879,46	2739,69	2036,51	0,00062	0,00517
Auts2	1242,84	1085,76	1788,75	1445,57	1882,85	1581,68	2453,84	2021,25	0,00062	0,00517
Fam84b	835,03	1051,06	1011,38	1117,41	887,33	1418,44	2040,79	1829,00	0,00064	0,00532
Chrm2	0,00	5,48	10,76	15,33	23,18	36,50	30,75	49,84	0,00064	0,00532
Nudt4	1940,31	2038,19	1642,15	1741,03	2237,65	2084,57	2676,79	2612,27	0,00064	0,00533
Jph1	82,53	67,57	18,83	30,67	27,69	35,49	9,78	20,34	0,00064	0,00533
Eml3	843,12	935,09	532,59	637,93	571,81	552,57	527,67	556,43	0,00064	0,00534
Egr3	6,47	3,65	41,69	48,05	18,03	31,43	30,75	22,38	0,00064	0,00535
Prob1	121,37	151,59	182,91	181,97	50,87	102,40	56,61	70,19	0,00065	0,00540
Cdh22	3,24	4,57	25,55	24,54	8,37	26,36	1,40	1,02	0,00065	0,00542
Slc35e4	58,26	47,48	67,25	56,23	131,36	86,18	213,86	116,98	0,00065	0,00542
Tgfb3	46,93	33,79	67,25	58,27	123,63	69,96	155,16	120,03	0,00065	0,00544
Shroom3	1168,40	997,18	839,23	592,95	797,83	498,84	473,16	429,28	0,00066	0,00546
Mrm1	100,33	84,92	154,67	141,08	164,20	161,21	234,13	194,29	0,00066	0,00548
Angptl2	498,43	441,97	728,95	767,77	1473,31	823,28	1121,74	833,12	0,00066	0,00549
Ppp3ca	496,81	452,93	556,80	578,64	1096,61	747,24	730,35	804,64	0,00066	0,00549
Homer1	650,55	839,20	560,83	616,46	395,37	464,36	362,73	443,52	0,00067	0,00553
Znrf2	401,33	397,23	435,75	495,83	495,18	635,71	781,37	701,90	0,00067	0,00553
Elovl6	2571,44	2770,56	1522,45	1723,65	2288,53	1931,47	1764,72	1843,24	0,00068	0,00565
Prss35	124,61	39,27	14,79	7,16	25,11	17,24	13,28	24,41	0,00068	0,00565
Cldn7	1560,02	1356,97	1849,27	1717,51	910,52	1412,36	875,72	879,91	0,00069	0,00571
Pcdh1	1993,72	1840,95	1468,65	1216,57	921,46	1193,35	1275,49	1203,39	0,00069	0,00571
Prrt4	111,66	111,41	37,66	14,31	25,11	20,28	40,54	11,19	0,00069	0,00571
Isl2	245,98	196,33	657,67	756,52	119,77	463,35	85,27	208,53	0,00070	0,00578

Ppp1r13l	1021,13	756,10	1621,98	1320,85	1622,70	1454,94	2109,98	1590,96	0,00070	0,00580
Ddah1	110,04	75,79	57,83	30,67	27,05	35,49	19,57	25,43	0,00070	0,00580
P3h4	383,53	301,35	641,53	556,15	774,65	599,21	501,11	527,95	0,00070	0,00581
Mapkbp1	1071,30	1229,13	1607,18	2720,42	775,93	1890,91	529,07	722,24	0,00071	0,00588
Mroh1	453,12	445,63	455,93	438,58	558,29	553,59	719,17	682,57	0,00072	0,00592
Serp1	3524,61	3686,46	3410,72	2843,10	2343,90	2431,32	2460,13	2324,39	0,00073	0,00604
Rab29	35,60	29,22	45,73	48,05	70,19	68,94	102,04	89,52	0,00074	0,00612
Dock6	616,56	631,91	891,68	1152,17	1048,32	1257,23	614,33	804,64	0,00075	0,00613
Lrrc30	11,33	4,57	28,24	24,54	1,93	13,18	0,00	0,00	0,00075	0,00614
Tubb3	1873,97	1180,73	2744,98	1435,35	1414,71	1452,91	704,49	801,58	0,00075	0,00617
Wnt11	367,35	287,65	302,61	222,87	171,93	222,04	148,87	133,26	0,00076	0,00621
Doc2b	14,56	11,87	5,38	8,18	23,83	11,15	64,30	38,66	0,00076	0,00621
Ablim2	46,93	44,75	8,07	16,36	25,11	24,33	4,19	9,16	0,00076	0,00621
Epcam	4312,71	4080,95	7436,07	7118,48	4641,44	6044,84	5120,15	5441,21	0,00076	0,00623
Dlx4	186,10	176,24	133,15	101,21	189,96	155,13	395,58	233,97	0,00076	0,00625
Zbtb8b	163,45	168,02	142,56	140,06	137,16	169,32	271,87	271,60	0,00076	0,00625
Smpdl3a	48,55	18,26	52,45	80,76	129,43	120,65	109,73	120,03	0,00077	0,00631
Racgap1	1380,39	1583,44	1437,72	1721,60	1815,24	1687,12	2507,66	2340,67	0,00077	0,00631
Gpr27	32,37	31,96	45,73	54,18	75,98	52,72	116,72	95,62	0,00077	0,00632
Tbc1d8	122,99	126,02	290,50	337,37	143,60	286,93	365,53	307,21	0,00078	0,00633
Oplah	46,93	56,62	68,59	65,43	151,32	74,01	191,50	143,43	0,00078	0,00637
Sall1	2422,56	2900,23	3130,98	3365,51	2526,14	3243,45	1418,07	1908,34	0,00079	0,00641
Snca	29,13	23,74	8,07	9,20	3,22	8,11	1,40	1,02	0,00079	0,00642
Ttc38	189,34	137,89	203,08	164,60	281,40	253,47	343,86	315,34	0,00079	0,00642
Enpp4	37,22	56,62	131,80	152,33	104,32	108,49	85,27	110,88	0,00079	0,00646
Phyh	268,63	204,55	398,10	358,84	472,64	403,53	507,40	432,33	0,00079	0,00646
Slc8a1	114,90	108,67	48,42	51,12	133,94	77,06	46,13	36,62	0,00080	0,00649
Msx2	3435,60	3659,07	3031,45	2527,20	3549,98	3662,19	5934,37	4357,85	0,00081	0,00655
Gnptab	422,37	498,59	527,21	617,49	665,18	706,69	779,27	885,00	0,00081	0,00656
Edn1	0,00	0,91	4,03	19,42	3,22	12,17	34,25	36,62	0,00081	0,00657
Rnd2	220,09	166,20	181,56	104,28	85,64	85,17	75,48	73,24	0,00081	0,00661
Slc25a30	336,60	381,70	153,32	185,04	265,30	210,89	157,25	214,64	0,00081	0,00661
Adamts1	6,47	5,48	6,72	12,27	72,76	20,28	53,12	31,53	0,00082	0,00667
Heatr5a	1160,31	1181,64	1108,22	981,44	851,92	829,37	767,39	704,95	0,00082	0,00668
lqsec2	129,46	120,54	189,63	168,68	184,16	184,53	264,18	253,29	0,00083	0,00670
Bmp6	1,62	10,96	45,73	23,51	21,25	44,61	56,61	90,53	0,00083	0,00671
Grk5	220,09	179,89	112,97	112,46	130,72	93,28	76,88	84,43	0,00083	0,00674
Cacna1h	79,30	119,63	53,80	128,81	273,03	170,33	251,60	291,95	0,00083	0,00674
Hat1	2165,26	2566,92	1886,92	2006,83	1325,21	1623,25	1511,72	1455,67	0,00083	0,00674
Spin4	93,86	98,62	137,18	93,03	177,72	178,45	197,79	227,86	0,00083	0,00674
Ankrd13d	29,13	33,79	51,11	84,85	65,04	80,10	99,94	136,31	0,00084	0,00681
Lrch1	313,95	381,70	454,58	510,14	425,64	549,53	654,17	748,69	0,00086	0,00692
Tigd5	38,84	47,48	104,90	80,76	69,54	86,18	155,16	113,93	0,00086	0,00693
Caskin2	1208,85	1236,43	1515,73	1437,39	1423,08	1493,47	2012,13	1845,27	0,00086	0,00695
Fam162a	2327,08	1867,43	1475,38	1118,43	1077,94	1004,77	1628,44	1205,43	0,00086	0,00695
Tspy14	475,77	515,03	305,30	294,43	360,60	327,49	473,16	458,78	0,00086	0,00695
Id4	61,49	74,88	129,11	143,13	139,73	334,59	195,69	199,38	0,00088	0,00709
Cecr2	2014,76	2386,11	1640,80	1948,56	886,69	1430,61	745,73	1202,38	0,00088	0,00710
Nab2	546,98	370,75	641,53	681,89	864,15	782,73	1175,55	826,00	0,00088	0,00710
Lum	69,59	9,13	4,03	4,09	6,44	8,11	2,10	0,00	0,00089	0,00717
Tiam2	286,44	310,48	790,81	855,69	348,37	850,66	366,92	392,65	0,00089	0,00717
Cdkn1c	7960,31	3789,65	4006,52	2190,85	2647,19	1667,86	2486,69	1676,41	0,00089	0,00718
Dpy19l1	1106,90	1209,95	641,53	771,86	742,45	791,85	596,16	751,74	0,00089	0,00718
Smarcc2	1679,77	1659,23	1970,31	2795,05	2853,90	2729,41	2889,26	3222,61	0,00090	0,00719
Fem1b	4003,62	4569,50	3252,02	2998,49	2399,93	2813,56	3131,07	2883,87	0,00090	0,00719
Eno1	27196,77	20229,44	16952,74	9683,50	12367,31	8527,87	12128,72	7530,62	0,00090	0,00719
Phox2a	22,66	20,09	1,34	7,16	1,29	2,03	0,70	0,00	0,00091	0,00728
Tgfa	137,55	134,24	170,81	181,97	73,41	112,54	53,12	78,33	0,00092	0,00732
Adamts5	336,60	375,31	410,20	555,12	269,16	516,07	95,75	192,26	0,00093	0,00745
Pdzrn3	637,60	603,60	433,06	414,04	317,46	395,42	308,91	386,55	0,00093	0,00745
Serpinb1b	3,24	10,04	4,03	1,02	8,37	1,01	45,43	37,64	0,00093	0,00746
Slc40a1	55,02	71,23	129,11	125,75	126,21	158,17	145,37	178,02	0,00094	0,00751
Matn4	8,09	4,57	10,76	12,27	27,05	44,61	5,59	3,05	0,00095	0,00754
Zdhhc23	38,84	51,14	110,28	118,59	86,29	123,70	139,08	119,02	0,00095	0,00756

Mad2l1	2432,27	2743,16	1983,76	2022,17	1671,64	1874,69	1548,06	1713,03	0,00096	0,00761
Lrp8	422,37	696,75	254,19	380,31	400,52	333,57	185,21	238,03	0,00096	0,00762
Sept11	6552,41	7992,06	4564,66	4584,12	6441,87	4258,36	3440,69	3903,15	0,00096	0,00762
Atxn1	87,39	162,54	435,75	708,47	229,24	521,14	237,63	476,07	0,00096	0,00764
Nek6	597,14	636,48	610,59	576,59	985,86	717,84	1062,33	987,74	0,00097	0,00768
Mogs	3189,63	2450,95	4543,15	3148,77	2073,45	2101,81	2253,95	1662,17	0,00097	0,00774
Plcb1	69,59	76,71	151,98	202,42	150,04	223,06	47,53	100,71	0,00098	0,00777
Grm4	236,27	112,32	509,73	316,92	197,69	248,40	98,54	156,65	0,00098	0,00777
Padi1	4,85	2,74	12,10	17,38	13,52	19,26	46,83	30,52	0,00098	0,00778
Rab15	1645,79	1307,66	3265,47	2100,89	2435,34	2694,93	3349,83	2856,41	0,00098	0,00778
Lym9	197,43	254,77	225,95	248,43	123,63	172,36	83,87	120,03	0,00099	0,00780
Ccm2	825,32	708,62	731,64	675,76	560,86	539,39	483,64	428,26	0,00099	0,00784
Mocos	6,47	7,31	52,45	41,92	32,84	35,49	41,24	22,38	0,00100	0,00787
Cct8	9572,11	9876,84	7382,27	7068,38	7358,83	7123,63	6945,67	6567,30	0,00100	0,00789
Kpnb1	22142,89	20559,09	17013,26	13841,32	14586,93	12418,19	13871,08	11568,05	0,00100	0,00791
Srcin1	30,75	47,48	24,21	63,38	49,58	65,90	148,17	130,21	0,00101	0,00797
Ociad2	90,62	65,75	73,97	90,99	125,57	156,14	164,24	181,07	0,00101	0,00801
Psat1	2467,87	2555,05	1283,06	1016,20	1765,65	775,63	1121,74	685,62	0,00102	0,00804
Kcng1	42,08	44,75	8,07	12,27	42,50	8,11	2,80	3,05	0,00102	0,00806
Upp1	22,66	15,52	1,34	2,04	1,93	0,00	0,00	0,00	0,00103	0,00814
Cd9	566,40	559,77	816,37	801,51	629,12	833,42	1459,30	944,00	0,00104	0,00823
Mtx2	970,97	984,40	741,05	771,86	576,96	687,42	616,43	607,29	0,00105	0,00823
Pard6b	600,38	590,82	473,41	431,42	353,52	441,04	341,06	298,05	0,00105	0,00823
Dnajb11	1618,28	1507,64	1950,14	1445,57	1277,56	983,48	972,17	895,17	0,00105	0,00827
Fcho1	45,31	66,66	56,49	99,17	104,96	132,82	150,96	194,29	0,00106	0,00831
Apoc1	163,45	101,36	286,47	219,80	153,26	184,53	107,63	79,34	0,00106	0,00832
Smarca1	517,85	514,11	395,41	456,98	767,56	554,60	782,77	816,84	0,00107	0,00836
Paqr7	17,80	11,87	32,28	22,49	41,21	33,46	83,17	54,93	0,00108	0,00845
P3h3	155,35	121,45	176,18	218,78	356,74	234,21	307,52	305,17	0,00108	0,00846
Acot7	279,96	195,42	203,08	128,81	465,56	241,31	607,34	407,91	0,00108	0,00846
Ipo11	2524,51	2341,37	1861,37	1583,59	1591,79	1623,25	1670,37	1566,55	0,00108	0,00846
Alkbh5	3031,03	3384,21	2383,20	2400,43	2175,19	2070,37	2349,70	2173,84	0,00108	0,00847
Prrx1	899,76	794,46	957,58	719,72	1777,25	524,18	295,63	299,07	0,00109	0,00852
Prkcz	291,29	232,86	275,71	224,91	128,14	186,56	109,73	131,22	0,00109	0,00852
Kif5c	781,63	840,12	531,24	621,58	811,35	812,13	941,42	1317,33	0,00110	0,00856
Rims2	69,59	78,53	22,86	44,98	34,13	20,28	11,88	17,29	0,00110	0,00859
Laptm5	3,24	3,65	5,38	5,11	83,71	10,14	8,39	5,09	0,00110	0,00859
Hdac7	723,37	729,62	977,76	1080,60	1206,72	1030,12	1181,14	1197,29	0,00112	0,00873
Sgpp2	46,93	38,35	119,70	56,23	32,84	19,26	20,27	20,34	0,00112	0,00877
Uroc1	6,47	10,04	43,04	51,12	23,18	37,51	14,68	14,24	0,00113	0,00882
Ppfibp1	1506,62	1748,72	1465,96	1711,38	1792,06	2324,86	2525,83	2941,86	0,00114	0,00884
Lzts1	45,31	31,96	84,73	81,79	103,03	71,99	148,17	105,79	0,00114	0,00884
Lnx1	257,31	206,38	468,03	455,96	119,13	351,82	98,54	143,43	0,00115	0,00893
Pdk1	2857,88	2468,30	1812,95	1934,25	1580,20	1762,15	1947,84	2003,96	0,00115	0,00894
Rai2	21,04	29,22	6,72	2,04	0,64	2,03	2,10	4,07	0,00116	0,00899
Mgll	14,56	12,78	40,35	78,72	59,24	64,89	46,83	81,38	0,00116	0,00901
Pdlim4	299,38	253,86	289,16	232,07	913,09	368,04	662,56	515,74	0,00116	0,00901
Krt90	71,20	67,57	119,70	75,65	38,64	43,60	35,64	23,40	0,00116	0,00904
Cib2	331,75	222,81	529,90	358,84	678,70	556,63	840,08	539,14	0,00117	0,00904
Hand2	254,07	121,45	363,13	164,60	626,54	173,38	30,75	79,34	0,00117	0,00906
Snx25	101,95	148,85	215,19	283,19	264,65	330,53	244,62	272,62	0,00117	0,00907
Eno1b	4620,18	3232,62	2797,44	1662,31	2099,21	1410,33	1981,38	1259,34	0,00117	0,00908
Nox4	37,22	62,10	80,70	102,23	107,54	165,26	127,20	251,26	0,00117	0,00909
Bcl7a	1281,68	1718,58	1985,10	2594,67	2636,25	2768,95	2567,06	3121,91	0,00118	0,00909
Stx11	4,85	8,22	24,21	21,47	19,96	28,39	53,82	39,67	0,00118	0,00915
Eda2r	126,23	146,11	75,32	113,48	27,05	82,13	30,05	30,52	0,00120	0,00930
Rusc2	33,98	26,48	22,86	48,05	86,29	74,01	85,96	96,64	0,00120	0,00930
Tspan18	148,88	130,58	57,83	78,72	673,55	123,70	213,86	154,62	0,00121	0,00933
Lypd6	375,44	413,67	798,88	1157,28	664,54	1256,22	738,74	939,93	0,00123	0,00946
Lrig1	158,59	183,55	301,26	322,03	239,54	435,97	464,07	415,03	0,00123	0,00946
Ttyh1	11,33	10,04	69,94	48,05	28,98	29,40	32,85	21,36	0,00123	0,00949
Gpr87	35,60	19,18	64,56	88,94	75,98	116,60	87,36	97,65	0,00124	0,00953
Aldh1a3	0,00	0,91	5,38	9,20	10,30	20,28	41,24	13,22	0,00125	0,00960
Gpr160	3,24	2,74	10,76	12,27	15,45	18,25	27,96	35,60	0,00125	0,00962

Nedd4l	226,56	230,12	236,71	304,65	366,40	318,36	516,49	397,74	0,00126	0,00967
Adcy5	24,27	21,92	129,11	70,54	76,63	82,13	34,95	67,14	0,00126	0,00970
Ltbr	644,07	414,58	948,17	810,71	614,31	648,89	457,78	394,69	0,00127	0,00977
Ncl	31488,45	33977,20	22487,09	21938,16	25976,11	21537,16	22200,58	21607,18	0,00128	0,00986
Mpv17l	32,37	30,13	17,48	33,74	43,79	61,85	99,24	80,36	0,00129	0,00987
Ssc5d	29,13	25,57	41,69	37,83	97,88	92,26	43,33	77,31	0,00129	0,00987
Fam171a2	407,81	218,25	392,72	388,49	924,04	501,88	991,04	651,03	0,00133	0,01023
Ankrd45	145,64	252,95	63,21	81,79	75,98	71,99	34,95	87,48	0,00134	0,01023
P3h2	275,11	311,39	229,98	183,00	137,16	184,53	145,37	134,28	0,00134	0,01024
Zfp618	1043,79	1381,63	1359,72	1797,25	2025,16	2117,01	2074,34	2336,60	0,00134	0,01027
Abcd2	92,24	76,71	32,28	53,16	52,16	34,47	5,59	20,34	0,00134	0,01027
Gstm7	77,68	37,44	164,08	110,41	226,66	117,61	273,27	185,14	0,00135	0,01032
Slc18b1	111,66	84,01	189,63	199,35	216,36	194,67	167,04	183,10	0,00136	0,01041
Gbx2	19,42	10,04	22,86	8,18	2,58	1,01	0,70	0,00	0,00137	0,01045
Plce1	129,46	134,24	68,59	39,87	51,51	35,49	106,93	74,26	0,00137	0,01046
Plekhf2	322,04	409,10	455,93	521,39	460,41	682,35	773,68	765,98	0,00137	0,01046
Figl1	1623,13	2050,07	1398,72	1342,32	944,00	1225,80	1126,63	1052,84	0,00137	0,01047
Insig1	597,14	1022,75	490,90	527,52	551,85	594,14	345,26	381,46	0,00137	0,01047
Mdfi	758,97	610,91	828,47	574,55	1533,84	1074,73	1510,32	1037,58	0,00138	0,01049
Snrk	462,83	448,37	513,76	472,32	600,14	571,84	782,77	697,83	0,00139	0,01057
Ntrk2	16,18	16,44	0,00	0,00	0,64	0,00	2,10	1,02	0,00139	0,01061
Tcf19	801,05	673,92	398,10	335,32	457,19	253,47	407,46	322,46	0,00140	0,01063
Sv2a	116,52	106,84	61,87	101,21	61,17	48,67	16,77	38,66	0,00140	0,01067
Dpep1	17,80	16,44	5,38	1,02	0,00	0,00	0,00	0,00	0,00141	0,01070
Agps	2671,78	3075,55	1916,51	2093,73	1566,68	2185,96	1425,76	1668,27	0,00141	0,01070
Zmat4	38,84	31,05	12,10	15,33	14,81	21,29	2,80	5,09	0,00141	0,01070
Gipt2	234,65	249,30	121,04	133,93	166,13	124,71	125,80	110,88	0,00142	0,01075
Gldn	17,80	9,13	26,90	47,03	4,51	25,35	1,40	1,02	0,00142	0,01077
5730596B	14,56	24,66	2,69	9,20	0,64	2,03	0,70	0,00	0,00142	0,01077
Emp3	42,08	20,09	65,90	76,67	113,33	83,14	109,03	94,60	0,00142	0,01077
Slc39a14	1089,10	908,60	1888,27	1992,52	927,26	1786,48	719,87	955,19	0,00143	0,01080
Plscr3	1482,34	1241,00	1904,41	1798,28	2287,88	1903,08	2626,47	2180,96	0,00143	0,01084
Clic3	0,00	0,00	0,00	2,04	10,95	9,13	21,67	11,19	0,00144	0,01089
Zfp185	202,28	209,12	279,74	394,62	335,49	465,38	406,76	594,07	0,00145	0,01096
Irak4	25,89	27,40	60,52	36,80	71,48	73,00	88,76	85,45	0,00145	0,01096
Clmp	241,12	280,34	238,05	251,49	876,39	208,86	120,21	123,09	0,00146	0,01104
Poir3b	2090,81	1847,34	1492,86	1473,18	1432,10	1372,81	1316,73	1226,79	0,00146	0,01104
Wwc1	1351,26	1475,68	2431,62	2316,60	1922,77	2654,38	2312,66	2600,06	0,00147	0,01110
Batf3	63,11	73,97	47,07	34,76	42,50	18,25	13,98	4,07	0,00148	0,01115
Igsf8	600,38	407,27	1050,38	819,91	1252,44	925,69	1351,67	922,64	0,00148	0,01115
Cars	1081,01	1215,43	973,72	1011,08	859,00	758,39	728,25	719,19	0,00149	0,01119
9330159F	33,98	42,92	9,41	15,33	9,66	12,17	5,59	6,10	0,00149	0,01121
Rragc	566,40	617,30	601,18	698,25	862,22	858,77	888,30	979,60	0,00149	0,01121
Gdf10	8,09	10,04	1,34	1,02	104,32	5,07	20,97	19,33	0,00150	0,01125
P4hb	21649,32	15751,26	24261,04	17478,76	13654,52	12118,08	12473,98	9675,98	0,00150	0,01128
Rps6ka2	1799,52	1460,16	1810,26	1659,24	1470,73	1231,88	1029,48	1027,41	0,00151	0,01130
Ripply3	108,42	72,14	45,73	20,45	26,40	25,35	30,05	23,40	0,00151	0,01131
Snx5	6588,01	7056,97	4633,25	4904,11	4072,21	5156,67	3674,12	4428,04	0,00151	0,01131
Mmp23	33,98	36,53	68,59	71,56	83,07	112,54	88,06	102,74	0,00152	0,01140
Tanc1	1207,24	1459,24	1669,05	1939,36	2150,08	2193,06	2017,73	2235,89	0,00152	0,01140
Metrl1	11,33	23,74	69,94	35,78	28,98	46,64	109,73	76,29	0,00152	0,01142
Pbx1	4126,61	4124,79	3482,00	3457,52	3582,18	4149,87	5115,25	5526,66	0,00153	0,01146
Mtcl1	1134,41	1042,84	1776,64	1872,91	1384,45	1727,68	1660,59	2050,75	0,00154	0,01155
2610318N	783,25	611,82	446,51	410,98	511,92	340,67	356,44	297,03	0,00155	0,01157
P4ha1	2717,09	1907,61	4001,14	2802,20	1886,71	1930,46	1912,89	1488,22	0,00156	0,01166
Cpt2	697,48	579,86	494,93	421,20	354,81	388,32	365,53	403,84	0,00157	0,01169
Ppt1	904,62	767,06	1408,13	1383,21	1077,29	1210,59	1094,48	1117,95	0,00157	0,01170
2200002D	61,49	63,92	39,00	31,69	16,10	28,39	14,68	16,28	0,00157	0,01173
C77080	595,53	487,63	657,67	478,45	721,20	650,92	1265,01	864,65	0,00159	0,01182
Tmem200	95,48	67,57	2,69	5,11	8,37	2,03	25,86	0,00	0,00160	0,01190
Anpep	213,61	151,59	203,08	173,80	396,66	243,33	418,64	354,00	0,00160	0,01196
Tmed9	3006,76	2943,14	4097,98	3573,04	2813,33	2784,16	2588,73	2445,44	0,00162	0,01209
Tcerg1l	24,27	25,57	2,69	7,16	3,22	2,03	2,80	2,03	0,00163	0,01209
Arhgef9	76,06	92,23	78,01	94,05	133,29	161,21	158,65	185,14	0,00163	0,01212

C1qtnf7	1,62	0,91	1,34	0,00	77,92	2,03	13,98	9,16	0,00163	0,01212
Sesn2	1341,55	1230,04	1137,80	1067,31	853,21	997,67	826,10	697,83	0,00163	0,01215
Plcxd3	12,95	24,66	99,52	110,41	41,21	153,10	37,74	48,83	0,00164	0,01218
Nup50	3220,37	3218,01	2773,23	2175,52	1947,24	2038,94	2210,62	1875,79	0,00164	0,01219
Thbs4	29,13	16,44	6,72	7,16	1,93	3,04	2,10	1,02	0,00165	0,01219
Rgs2	50,17	41,09	84,73	117,57	117,20	120,65	102,04	105,79	0,00165	0,01219
Inhba	0,00	0,00	0,00	4,09	2,58	1,01	23,06	21,36	0,00165	0,01219
Syt9	74,44	72,14	106,25	145,17	142,95	183,52	188,00	160,72	0,00165	0,01222
Il1rl2	16,18	24,66	10,76	30,67	30,26	20,28	87,36	72,22	0,00166	0,01225
N4bp3	692,62	508,64	546,04	317,94	304,58	387,31	268,38	163,78	0,00166	0,01226
Ucn2	0,00	0,00	4,03	12,27	5,15	14,19	11,88	42,72	0,00166	0,01231
Bnip1	100,33	74,88	177,53	134,95	155,83	156,14	285,15	184,12	0,00167	0,01233
PKlr	6,47	45,66	1,34	11,25	0,64	0,00	0,00	1,02	0,00168	0,01243
Nhsl2	616,56	523,25	325,47	298,52	337,42	408,60	406,06	377,40	0,00168	0,01243
Hacd1	122,99	99,54	162,74	128,81	133,94	106,46	62,90	38,66	0,00169	0,01248
Ctdspl	1540,60	1614,48	1730,91	1586,66	1473,31	1578,64	2555,88	2134,17	0,00170	0,01250
Cldn9	95,48	78,53	61,87	44,98	14,81	37,51	25,86	15,26	0,00170	0,01250
Klf3	1474,25	1975,19	1065,18	1365,83	621,39	1042,28	645,78	933,83	0,00170	0,01251
Fip1l1	2228,37	2148,69	2923,86	2873,77	2305,91	2428,28	1840,21	2002,94	0,00170	0,01254
Snap91	903,00	904,04	925,31	1358,68	496,47	1060,53	109,03	398,76	0,00173	0,01275
Vstm2b	40,46	33,79	45,73	79,74	14,17	39,54	9,09	9,16	0,00175	0,01288
Npr2	19,42	29,22	41,69	89,96	129,43	110,51	62,90	170,90	0,00176	0,01293
Slc16a12	139,17	123,28	326,82	397,69	251,78	483,63	134,19	268,55	0,00177	0,01299
Mpeg1	0,00	0,00	0,00	8,18	41,21	18,25	23,76	8,14	0,00177	0,01299
Inf2	297,76	227,38	337,58	520,37	442,38	468,42	754,11	515,74	0,00178	0,01306
Ifi202b	0,00	0,00	0,00	1,02	12,23	12,17	11,18	9,16	0,00181	0,01327
Prps2	1352,88	1778,85	1648,87	1508,96	888,62	1035,19	1025,99	1186,10	0,00182	0,01336
Trim37	1657,12	1917,66	1188,91	1250,31	1150,06	1244,05	1228,67	1277,65	0,00182	0,01336
Nr4a2	32,37	85,84	142,56	233,09	48,94	102,40	31,45	54,93	0,00182	0,01337
Zfp579	139,17	124,19	221,91	309,77	228,59	295,04	259,29	356,03	0,00183	0,01338
Dkk1	368,97	446,54	426,34	553,08	359,96	763,46	210,37	205,48	0,00183	0,01339
Slc25a35	27,51	20,09	64,56	65,43	26,40	27,38	19,57	20,34	0,00184	0,01344
Cnrip1	32,37	46,57	4,03	12,27	25,11	6,08	2,80	2,03	0,00184	0,01344
Cbr2	530,80	420,97	785,43	491,74	255,64	320,39	394,88	321,45	0,00186	0,01356
Foxo4	2581,15	2663,71	2423,55	1988,43	2068,95	1966,96	1564,14	1664,20	0,00187	0,01363
Lhfp	97,10	93,14	59,18	83,83	229,24	133,83	197,09	145,47	0,00187	0,01366
Manea	878,72	906,78	730,29	742,21	483,59	675,25	377,41	524,90	0,00187	0,01366
Npnt	2272,06	2515,78	4373,68	4252,89	2687,12	3723,02	2715,93	3158,53	0,00188	0,01374
Stac2	45,31	48,40	36,31	36,80	20,61	26,36	10,48	11,19	0,00189	0,01376
Pkm	65750,62	52643,30	45388,41	27164,31	34711,02	23478,77	31639,23	21173,84	0,00189	0,01376
Fam83b	406,19	424,62	373,89	308,74	213,14	337,63	708,69	510,65	0,00189	0,01376
Mppd2	244,36	169,85	195,01	214,69	412,11	226,10	684,22	367,22	0,00190	0,01386
Plec	3129,75	2308,49	3613,80	3554,64	3818,50	4047,47	4667,26	4698,63	0,00190	0,01386
Nexmif	4,85	2,74	13,45	10,22	55,38	21,29	20,97	22,38	0,00191	0,01391
Otud1	63,11	77,62	169,46	177,89	109,47	213,93	190,10	217,69	0,00192	0,01392
Nrxn3	17,80	15,52	65,90	176,86	18,67	139,92	6,29	23,40	0,00192	0,01394
Smarcd3	103,57	115,97	92,80	115,52	238,90	138,90	228,54	234,98	0,00193	0,01399
Tmem266	63,11	40,18	176,18	132,90	75,34	104,43	62,90	86,47	0,00193	0,01399
Rcbtb1	1734,79	1943,22	1347,61	1592,79	1207,37	1345,44	793,25	1137,27	0,00193	0,01402
Rbms2	1108,52	936,00	1143,18	1074,47	1482,97	1274,47	1882,14	1537,05	0,00194	0,01407
Mycbp	338,22	303,17	240,74	241,27	216,36	214,95	169,13	178,02	0,00195	0,01410
Pcdhgb6	51,78	33,79	72,63	87,92	134,58	101,39	109,73	102,74	0,00195	0,01411
Padi2	11,33	21,00	5,38	7,16	0,64	1,01	0,70	1,02	0,00195	0,01415
Calr	22212,48	16465,36	30400,61	20171,58	15773,70	13190,78	14235,91	11322,89	0,00196	0,01416
Adamts15	124,61	58,44	30,93	35,78	9,02	10,14	42,63	6,10	0,00196	0,01417
Dlx3	2406,38	2742,25	2036,21	1631,64	2072,81	2498,24	4554,04	2907,27	0,00197	0,01422
Rxrg	9,71	4,57	18,83	19,42	3,22	4,06	0,00	1,02	0,00199	0,01440
Rab6a	2684,72	2591,57	4131,60	3756,04	3002,00	3658,13	2680,28	2522,75	0,00200	0,01446
Cadps2	9,71	7,31	18,83	28,63	122,35	27,38	30,75	33,57	0,00202	0,01455
Spata33	21,04	20,09	28,24	41,92	72,76	67,93	51,02	67,14	0,00202	0,01457
Dclk1	25,89	25,57	65,90	60,32	112,04	55,76	25,86	33,57	0,00203	0,01462
Adam23	63,11	63,01	13,45	35,78	18,67	7,10	4,89	13,22	0,00204	0,01469
Epha5	0,00	0,00	18,83	18,40	18,67	8,11	4,89	14,24	0,00205	0,01476
Fam49a	378,68	495,85	1036,93	1062,20	667,11	1247,09	733,15	982,65	0,00208	0,01493

Hes1	415,90	533,29	948,17	975,30	516,43	1149,76	1482,37	1137,27	0,00207	0,01493
Nxf7	21,04	20,09	9,41	3,07	0,64	1,01	2,80	3,05	0,00209	0,01502
Adam22	48,55	83,10	170,81	261,72	119,77	209,88	55,21	110,88	0,00210	0,01506
Snai1	344,69	211,86	95,49	119,61	252,42	30,42	41,93	16,28	0,00210	0,01511
Zfp362	1658,73	1567,91	2141,12	1896,42	3259,57	2215,36	3083,55	2642,79	0,00211	0,01514
Adam12	22,66	16,44	18,83	19,42	11,59	6,08	0,70	2,03	0,00211	0,01514
Sipa1	283,20	262,99	174,84	164,60	239,54	166,28	125,80	128,17	0,00216	0,01547
Npc1	932,13	859,29	590,42	600,11	705,75	652,95	566,81	602,21	0,00216	0,01548
Bdh2	8,09	1,83	20,17	13,29	37,35	24,33	41,24	35,60	0,00217	0,01553
Wasf1	954,78	1099,46	665,74	658,38	757,90	536,35	559,12	595,09	0,00220	0,01574
Parp12	6,47	7,31	16,14	28,63	41,86	32,44	38,44	38,66	0,00221	0,01580
Cadm3	163,45	132,41	157,36	103,26	93,37	113,56	58,01	55,95	0,00221	0,01581
Cdkn1a	801,05	741,49	2424,89	1858,59	847,41	2198,13	1163,67	818,88	0,00222	0,01586
Hspa12b	160,21	136,06	231,33	187,09	439,80	255,50	278,16	299,07	0,00222	0,01589
Slitrk6	21,04	10,96	21,52	33,74	22,54	58,81	76,88	92,57	0,00223	0,01590
Sdc2	234,65	267,56	371,20	359,86	1227,97	403,53	561,22	415,03	0,00225	0,01606
Fat2	1102,05	1154,25	1617,94	1407,75	906,01	1069,66	1468,39	1473,98	0,00227	0,01617
Ppp1r26	449,88	543,34	758,54	713,59	733,44	794,89	798,14	872,79	0,00230	0,01637
Tbc1d30	11,33	6,39	56,49	83,83	14,17	49,68	51,02	35,60	0,00232	0,01651
Hsd17b11	89,01	32,87	185,60	176,86	182,88	180,47	157,25	133,26	0,00232	0,01655
Efcab1	131,08	150,67	87,42	132,90	133,29	164,25	245,31	250,24	0,00233	0,01659
Tmem131	1624,75	1561,52	1682,50	1799,30	1737,32	1950,73	2485,29	2338,63	0,00234	0,01662
Uaca	1069,68	1069,32	831,16	885,34	830,67	790,84	506,00	686,64	0,00234	0,01662
Fhl2	24,27	36,53	121,04	109,39	71,48	124,71	57,31	99,69	0,00237	0,01683
Rgs9	87,39	123,28	71,28	99,17	109,47	64,89	34,95	28,48	0,00237	0,01683
Pcdhb8	1,62	0,91	9,41	6,13	23,18	16,22	16,07	21,36	0,00238	0,01687
Dip2a	297,76	384,44	529,90	682,92	538,33	733,05	635,30	743,60	0,00238	0,01687
Srgap3	267,02	275,78	271,67	243,31	271,74	281,86	390,69	490,31	0,00238	0,01688
Stac	19,42	16,44	192,32	128,81	18,03	67,93	91,56	15,26	0,00238	0,01688
Stim1	255,69	236,51	438,44	349,64	371,55	373,11	494,12	424,19	0,00239	0,01694
Mrap2	0,00	0,00	12,10	7,16	11,59	16,22	9,78	17,29	0,00239	0,01694
Adcy2	9,71	13,70	25,55	17,38	52,16	54,75	29,35	31,53	0,00240	0,01699
Ampd3	19,42	22,83	51,11	22,49	23,18	24,33	83,17	70,19	0,00240	0,01700
Cpne2	365,73	317,78	287,81	334,30	171,93	242,32	129,30	193,28	0,00240	0,01701
Immt	4265,78	3780,52	3175,36	2845,14	3086,35	2730,42	2660,02	2406,79	0,00241	0,01704
Lama2	6,47	6,39	26,90	30,67	51,51	27,38	15,38	10,17	0,00242	0,01711
Lpin2	805,90	1037,36	1067,87	1366,85	1160,36	1419,45	1712,31	1753,72	0,00243	0,01716
Map7	362,49	319,61	411,55	471,29	372,19	530,27	706,59	629,67	0,00243	0,01717
Ctnnd2	283,20	345,18	458,62	500,94	463,63	609,35	553,53	690,71	0,00243	0,01717
Slc26a2	448,26	530,55	512,42	446,76	535,11	589,07	716,37	930,77	0,00246	0,01735
Tbc1d14	1927,37	2144,12	1347,61	1380,14	1461,72	1453,93	1630,54	1524,84	0,00246	0,01737
Mras	140,79	135,15	193,67	195,26	359,96	224,07	283,75	264,48	0,00247	0,01742
Tmeff1	2102,14	2134,08	1326,09	1445,57	1527,40	1614,12	1278,99	1549,26	0,00247	0,01742
Snph	64,73	40,18	40,35	27,60	14,81	9,13	13,28	17,29	0,00250	0,01762
Tnik	315,56	315,04	342,95	395,64	444,31	498,84	492,72	802,60	0,00251	0,01763
Fam3c	749,26	716,84	926,65	855,69	560,22	775,63	448,00	508,62	0,00251	0,01763
Kiz	305,85	326,91	301,26	338,39	504,84	448,14	457,78	502,52	0,00251	0,01765
Tead4	245,98	261,17	567,56	376,22	390,22	469,43	503,91	514,72	0,00251	0,01766
Gadd45g	25,89	49,31	131,80	112,46	74,05	97,33	67,09	73,24	0,00252	0,01769
Naf1	648,93	630,09	484,17	404,84	361,89	409,61	418,64	423,17	0,00254	0,01781
Pcyox1l	540,50	444,71	878,23	806,62	658,10	684,38	795,35	697,83	0,00254	0,01781
Iffo1	90,62	76,71	61,87	102,23	81,78	39,54	19,57	24,41	0,00254	0,01781
Foxj2	139,17	172,59	212,50	229,00	292,34	242,32	290,04	332,64	0,00255	0,01785
Pla2g6	584,20	562,51	312,02	402,80	304,58	344,72	424,23	377,40	0,00261	0,01826
Prkar1b	155,35	89,49	112,97	83,83	173,86	133,83	295,63	214,64	0,00264	0,01849
Plppr3	422,37	546,99	668,43	1089,80	953,02	1279,54	884,11	1523,82	0,00264	0,01849
Hes6	359,26	313,22	587,73	426,31	568,59	600,23	377,41	307,21	0,00266	0,01859
Stx19	0,00	0,00	9,41	12,27	9,02	20,28	13,98	10,17	0,00267	0,01869
Arhgef2	2173,35	1902,13	1573,56	1639,82	1517,74	1470,15	1320,22	1349,88	0,00268	0,01873
Klk5	0,00	0,00	5,38	11,25	16,10	15,21	16,77	8,14	0,00268	0,01873
Apc2	16,18	7,31	16,14	16,36	62,46	25,35	66,40	47,81	0,00271	0,01893
Ush1c	25,89	34,70	21,52	8,18	22,54	8,11	1,40	2,03	0,00272	0,01900
R3hdm4	1147,36	1124,11	1361,06	1470,11	1713,50	1523,88	1805,26	1684,55	0,00274	0,01912
Def6	134,32	86,75	258,22	237,18	280,11	189,60	317,30	224,81	0,00275	0,01917

F13a1	0,00	1,83	1,34	5,11	48,29	8,11	2,10	3,05	0,00275	0,01917
201011110	1147,36	1060,19	1292,47	1671,51	1817,81	1873,68	1614,46	1861,55	0,00276	0,01922
Pcsk1	43,69	42,01	52,45	37,83	21,89	20,28	0,70	10,17	0,00279	0,01942
Arhgap24	29,13	37,44	149,29	83,83	52,16	65,90	107,63	69,17	0,00280	0,01949
Rsl1d1	3901,67	3872,75	2786,68	2817,54	3099,23	2720,28	2646,74	2738,41	0,00282	0,01963
Sox14	194,19	120,54	359,09	271,94	113,33	178,45	94,35	149,53	0,00285	0,01980
Flnb	2362,69	1819,95	2856,61	2831,85	4191,98	3238,38	3078,66	3390,46	0,00285	0,01981
Srpx	17,80	19,18	33,62	31,69	62,46	44,61	76,88	54,93	0,00287	0,01990
Kit	448,26	467,54	359,09	313,86	280,11	245,36	314,51	287,88	0,00287	0,01993
Lamb1	9787,34	7711,71	12166,16	10447,18	12474,20	12338,09	14405,04	14395,97	0,00289	0,02007
Elavl2	152,12	166,20	143,91	178,91	66,97	109,50	63,60	83,41	0,00289	0,02007
Plxna4	888,43	971,61	543,35	694,16	538,97	562,71	586,38	674,43	0,00290	0,02008
Fyn	412,66	408,19	492,24	526,50	695,44	663,09	598,26	527,95	0,00290	0,02012
Rerg	3,24	1,83	2,69	10,22	44,43	12,17	75,48	14,24	0,00292	0,02022
Lrrc1	509,76	500,42	646,91	634,87	616,24	737,10	940,72	797,52	0,00294	0,02033
Axin2	1495,29	2245,48	3312,54	3240,78	1211,88	2098,76	1580,91	1797,46	0,00295	0,02042
Bex1	2819,04	2389,76	1862,72	1224,75	1499,71	1362,68	1661,99	1174,91	0,00296	0,02046
Sp6	7900,43	7817,64	8412,48	7117,46	5385,83	8585,67	4605,76	3741,41	0,00298	0,02058
Tmprss6	27,51	11,87	8,07	1,02	0,00	1,01	0,70	0,00	0,00302	0,02085
Itgb3	21,04	37,44	8,07	2,04	3,86	6,08	3,49	3,05	0,00302	0,02085
Tulp1	29,13	42,92	65,90	69,52	105,60	78,07	130,00	89,52	0,00302	0,02085
Slc29a1	93,86	91,32	102,21	118,59	206,70	102,40	311,71	197,34	0,00303	0,02087
Gpc3	10992,96	8652,28	9718,40	8321,76	13906,94	12437,45	13526,52	14483,46	0,00303	0,02091
Mmp17	211,99	117,80	117,01	112,46	126,21	75,03	57,31	39,67	0,00306	0,02111
Vgll4	1464,54	1369,75	1968,97	1796,23	1851,30	1890,91	2721,52	2092,46	0,00307	0,02111
Trnfaip6	42,08	42,92	72,63	58,27	66,97	59,82	18,87	25,43	0,00306	0,02111
Rpn2	7031,42	5511,89	9729,16	7752,32	5938,96	5614,95	5499,65	4363,96	0,00307	0,02112
Kcnmb4	127,84	119,63	161,39	138,01	387,00	208,86	246,01	191,24	0,00309	0,02127
Impdh1	1226,65	1148,77	890,34	636,91	797,18	523,17	654,87	457,76	0,00310	0,02134
Kcnu1	1,62	0,91	4,03	8,18	14,17	9,13	23,76	22,38	0,00311	0,02137
Col9a1	137,55	88,58	90,11	82,81	376,05	126,74	88,06	70,19	0,00312	0,02140
Arhgap19	1875,58	2134,08	1258,85	1564,16	1055,40	1332,26	1211,19	1335,64	0,00312	0,02140
Mtss1	508,14	578,04	757,19	1032,55	1871,26	927,71	702,40	963,33	0,00312	0,02141
Parp14	0,00	0,00	4,03	8,18	10,30	4,06	13,98	24,41	0,00313	0,02144
Fcrls	0,00	0,00	0,00	1,02	49,58	2,03	4,89	3,05	0,00313	0,02147
Cks2	932,13	973,44	692,63	744,26	746,96	705,67	612,24	606,27	0,00313	0,02147
S100a6	451,50	325,09	761,23	564,33	422,42	639,77	288,65	328,57	0,00320	0,02188
Cacybp	2451,69	2518,52	1960,90	1558,03	1830,05	1501,58	1578,82	1315,29	0,00320	0,02188
Ccdc129	3,24	0,91	2,69	7,16	11,59	13,18	18,87	36,62	0,00320	0,02188
Hist2h2be	30,75	40,18	48,42	87,92	121,06	87,19	143,97	92,57	0,00320	0,02188
Igf2	9908,71	6061,62	6724,61	3372,66	3975,62	3384,38	3964,16	2836,06	0,00321	0,02193
Fgfr4	22,66	25,57	2,69	1,02	4,51	7,10	0,70	4,07	0,00323	0,02204
Foxh1	21,04	29,22	9,41	0,00	0,64	1,01	0,00	1,02	0,00324	0,02211
Alas2	14,56	118,71	6,72	31,69	1,93	8,11	6,99	1,02	0,00325	0,02219
Dlgap1	3,24	9,13	26,90	8,18	25,11	110,51	35,64	60,02	0,00326	0,02225
Plekhh1	733,08	808,15	669,77	628,73	402,46	576,91	330,58	460,81	0,00328	0,02239
Ctsl	2726,80	2213,52	3219,74	2962,71	3237,68	3038,64	4503,02	3759,72	0,00331	0,02257
Rin3	42,08	23,74	84,73	59,30	89,51	56,78	122,31	106,81	0,00333	0,02268
Nlrp9b	0,00	0,00	13,45	13,29	4,51	28,39	15,38	19,33	0,00334	0,02276
Nell1	19,42	12,78	10,76	6,13	1,93	1,01	0,70	1,02	0,00336	0,02289
Itgav	2768,87	2513,04	4036,11	4313,21	4148,84	4901,17	3685,30	5244,89	0,00337	0,02291
Adcyap1r1	80,91	50,22	90,11	66,45	41,21	46,64	17,47	27,47	0,00338	0,02297
L3hypdh	67,97	94,97	115,66	96,10	113,98	141,95	204,78	174,97	0,00339	0,02302
Ctf1	108,42	115,06	142,56	128,81	159,05	161,21	211,07	222,78	0,00339	0,02302
Tbx5	281,58	246,56	236,71	219,80	559,57	120,65	69,89	78,33	0,00342	0,02322
Prss22	124,61	95,88	185,60	236,16	177,72	265,64	116,72	127,15	0,00342	0,02322
Erg	74,44	64,84	10,76	7,16	37,99	9,13	10,48	26,45	0,00342	0,02323
Tmem154	0,00	0,91	6,72	6,13	10,95	14,19	19,57	15,26	0,00346	0,02345
Syt17	50,17	43,83	45,73	40,89	25,76	31,43	11,18	14,24	0,00346	0,02345
Slc39a6	1896,62	1650,10	2114,22	2083,51	2439,20	2162,64	2817,97	2693,65	0,00347	0,02348
Sdad1	1998,57	2282,92	1242,71	1559,05	1300,09	1440,75	1510,32	1535,01	0,00347	0,02348
Ovol1	93,86	115,06	173,49	160,51	147,46	158,17	289,34	193,28	0,00349	0,02359
Ppid	2383,72	2361,46	1740,33	1647,99	1790,77	1569,51	1710,91	1616,39	0,00349	0,02359
Plet1	17,80	11,87	5,38	4,09	3,22	6,08	0,00	0,00	0,00351	0,02374

Mmd	443,41	504,07	307,99	348,61	280,75	375,14	223,65	263,47	0,00352	0,02375
Radil	30,75	25,57	34,97	25,56	39,28	21,29	96,45	70,19	0,00352	0,02378
Podxl	2553,64	2919,40	1900,37	1940,38	1363,20	1838,19	2123,26	1991,75	0,00353	0,02384
Arhgap27	271,87	210,94	259,57	248,43	252,42	270,71	473,16	374,34	0,00355	0,02393
Stt3a	4320,80	4238,02	4036,11	3624,16	2689,05	3191,74	3036,02	2986,62	0,00355	0,02396
Dscaml1	6,47	10,96	39,00	32,71	13,52	28,39	4,89	6,10	0,00356	0,02396
Nav1	2022,85	1995,27	1587,01	1473,18	1824,25	1667,86	2232,29	2294,89	0,00359	0,02417
Fabp4	16,18	18,26	0,00	2,04	0,00	0,00	0,00	0,00	0,00361	0,02429
Wdsub1	197,43	220,99	381,96	348,61	307,15	362,97	350,85	347,90	0,00363	0,02443
Fhod3	139,17	175,33	166,77	193,22	179,66	100,38	72,69	65,10	0,00366	0,02460
Pvr	140,79	145,19	92,80	116,55	54,73	79,08	65,70	68,16	0,00366	0,02461
Tusc5	9,71	10,96	21,52	24,54	50,87	37,51	34,25	49,84	0,00367	0,02466
Ddt	762,21	557,03	430,37	350,66	453,97	343,71	371,82	304,15	0,00369	0,02476
Fam83f	111,66	102,27	271,67	232,07	139,73	171,35	263,49	157,67	0,00369	0,02476
Acvr1b	1424,08	1518,60	2279,64	2547,64	1741,19	2567,18	2545,40	2739,43	0,00371	0,02488
Cacna1c	32,37	69,40	86,07	216,73	424,35	113,56	76,88	98,67	0,00371	0,02488
Hip1r	875,49	625,52	854,03	860,80	918,89	839,51	1414,57	1200,34	0,00373	0,02500
Axl	1453,21	1204,47	1537,25	1260,53	2141,71	1833,12	2641,15	1895,12	0,00373	0,02500
Slc17a5	121,37	126,93	174,84	193,22	222,16	230,15	213,16	237,02	0,00373	0,02500
Irx5	98,71	85,84	49,76	37,83	41,86	23,32	97,85	70,19	0,00374	0,02505
Ano6	1521,18	1314,96	1683,84	1752,27	2085,69	2072,40	2033,80	2038,55	0,00374	0,02505
Csrnp1	126,23	157,98	64,56	66,45	81,14	48,67	65,70	46,79	0,00376	0,02513
Eln	69,59	27,40	126,42	119,61	202,84	139,92	224,35	111,90	0,00376	0,02514
Slc39a2	4,85	5,48	4,03	18,40	9,66	18,25	44,03	44,76	0,00378	0,02527
Bnip3l	2958,21	2997,93	2142,46	1946,51	1718,00	2138,31	1942,94	2190,12	0,00379	0,02531
Evi5l	234,65	222,81	355,06	359,86	507,42	335,60	451,49	427,24	0,00379	0,02534
Tmem51	189,34	144,28	185,60	164,60	244,69	233,20	431,22	262,45	0,00380	0,02535
Slc7a10	9,71	12,78	6,72	7,16	14,81	18,25	34,25	41,71	0,00382	0,02547
Slc12a4	1218,56	1153,33	1468,65	1929,14	1751,49	2150,47	1890,53	2242,00	0,00382	0,02549
Elmo3	189,34	145,19	201,74	224,91	230,53	318,36	323,59	354,00	0,00383	0,02550
Cdk20	79,30	125,10	112,97	144,15	231,81	153,10	298,43	212,60	0,00385	0,02563
Pcdhb3	4,85	0,91	14,79	11,25	16,74	26,36	33,55	24,41	0,00388	0,02584
Crtc3	181,25	155,24	287,81	244,34	302,65	241,31	454,98	299,07	0,00390	0,02597
Spint2	2582,77	1969,71	4851,13	3697,76	3247,34	3457,38	3970,45	3111,74	0,00392	0,02607
Atp2b1	3176,68	3194,27	3767,13	4817,22	2111,44	3420,88	1750,75	2360,00	0,00394	0,02618
Mapk1ip1l	4924,42	4602,37	3685,09	3319,50	3571,23	3288,06	3379,88	2875,74	0,00398	0,02645
Pitpnc1	349,55	483,98	399,44	539,79	579,54	564,74	703,09	906,36	0,00399	0,02649
Kyat3	161,83	125,10	112,97	126,77	172,57	158,17	311,01	208,53	0,00402	0,02670
Lamp5	8,09	7,31	10,76	10,22	0,00	1,01	0,00	0,00	0,00405	0,02687
Plekhg5	279,96	347,00	511,07	610,33	475,86	651,93	533,96	619,50	0,00406	0,02692
Tnks1bp1	1114,99	971,61	1164,70	986,55	1338,09	1194,37	1857,68	1508,57	0,00407	0,02699
Matn3	30,75	36,53	12,10	12,27	18,03	12,17	3,49	6,10	0,00408	0,02704
Itgb8	194,19	160,72	498,97	677,80	138,44	426,85	243,92	339,76	0,00408	0,02705
Tmx1	1199,14	1407,19	1313,99	1303,47	964,61	1029,10	840,08	936,88	0,00409	0,02709
Magt1	2119,94	2126,77	2298,47	2509,82	1705,77	1920,32	1560,65	1662,17	0,00410	0,02714
Ccser2	525,94	548,81	511,07	715,63	730,22	878,03	863,14	1116,93	0,00411	0,02716
Capg	920,80	521,42	1283,06	907,83	1502,93	1315,02	2404,22	1307,15	0,00411	0,02720
Tmprss2	33,98	37,44	83,39	125,75	58,60	128,76	116,02	136,31	0,00414	0,02733
Adamts20	205,52	365,27	607,90	1250,31	169,35	605,30	134,89	325,52	0,00414	0,02737
Hspa13	1181,34	1245,56	1296,50	1216,57	840,33	982,46	879,22	867,71	0,00415	0,02743
Fbxo32	113,28	126,02	112,97	113,48	157,76	184,53	192,20	236,00	0,00418	0,02754
Mid1	244,36	377,14	398,10	326,12	414,05	463,35	560,52	673,41	0,00418	0,02754
BC052040	678,06	565,25	531,24	349,64	289,77	315,32	414,45	299,07	0,00417	0,02754
Npepl1	516,23	465,72	525,86	499,92	747,60	641,80	735,94	733,43	0,00419	0,02765
Bag2	671,59	612,74	708,77	510,14	376,05	372,10	454,29	328,57	0,00421	0,02771
Tmbim6	6445,60	5270,81	7237,02	5218,99	4175,24	4228,96	4116,52	3240,93	0,00422	0,02779
Zfhx2	684,53	661,13	759,88	893,52	1003,24	883,10	1070,02	1095,57	0,00422	0,02779
Sec23a	1163,54	1074,80	738,36	749,37	878,32	665,12	552,83	708,00	0,00424	0,02789
Hic1	1,62	2,74	0,00	1,02	0,00	1,01	34,25	5,09	0,00424	0,02789
Prx	110,04	151,59	174,84	212,64	329,05	197,71	280,96	339,76	0,00426	0,02799
Pcdhb11	0,00	0,00	6,72	4,09	14,81	9,13	18,87	9,16	0,00426	0,02800
Cnnm2	199,05	134,24	267,64	221,85	120,41	164,25	109,73	102,74	0,00427	0,02807
Gsta3	1,62	0,00	0,00	3,07	4,51	8,11	25,16	17,29	0,00428	0,02808
Lgals3	6,47	2,74	10,76	3,07	21,25	13,18	52,42	24,41	0,00428	0,02808

Sema3e	179,63	192,68	156,01	150,28	216,36	207,85	521,38	236,00	0,00428	0,02808
Stk26	801,05	1040,10	732,98	800,48	732,15	935,83	1262,21	1361,07	0,00429	0,02810
Lrrc17	17,80	10,04	16,14	9,20	102,38	24,33	48,22	48,83	0,00429	0,02810
Ndufaf4	674,82	881,21	1172,77	1280,98	568,59	908,45	402,57	661,21	0,00435	0,02847
Lingo1	69,59	69,40	28,24	25,56	43,14	18,25	18,87	10,17	0,00435	0,02848
Krt42	8,09	13,70	64,56	36,80	10,30	30,42	9,78	5,09	0,00435	0,02848
Uchl3	844,74	889,43	810,99	666,56	496,47	577,92	610,84	541,17	0,00436	0,02850
Egln3	153,74	104,10	94,14	90,99	114,62	116,60	358,54	155,64	0,00436	0,02850
Edem1	1100,43	1440,07	1042,31	1290,18	621,39	922,64	427,73	749,71	0,00437	0,02854
Phyhipl	59,88	53,88	39,00	28,63	9,02	20,28	19,57	16,28	0,00440	0,02871
Col1a2	10973,54	4617,90	15045,64	9516,86	21607,70	12710,19	5614,97	7234,61	0,00441	0,02879
Fign	466,06	881,21	427,69	536,72	202,19	421,78	174,73	290,93	0,00442	0,02881
Fam117a	584,20	562,51	708,77	626,69	908,58	813,14	1010,61	822,95	0,00445	0,02902
Rdh14	108,42	82,19	157,36	156,42	160,98	187,57	224,35	182,09	0,00446	0,02904
Tor3a	84,15	44,75	199,05	146,19	153,26	154,11	185,91	125,12	0,00446	0,02906
Ahnak	3197,72	3814,31	3523,69	5231,26	4569,32	6598,43	5884,04	9262,98	0,00448	0,02916
Speg	373,82	443,80	180,22	239,23	161,63	186,56	144,67	287,88	0,00451	0,02935
Clcn3	1174,87	1349,66	657,67	923,16	373,48	799,96	450,79	629,67	0,00451	0,02937
Pde4d	160,21	164,37	239,40	265,81	231,17	310,25	297,73	352,98	0,00452	0,02940
Mif	9852,07	7771,07	6485,21	3536,24	5067,72	2985,92	4611,35	2552,25	0,00455	0,02955
Ntf5	459,59	356,14	780,05	535,70	676,13	700,60	854,76	732,41	0,00455	0,02959
Pdgfrb	1004,95	784,41	699,36	596,02	1348,39	632,67	441,01	402,83	0,00457	0,02969
Mthfd2	812,38	809,07	512,42	445,74	616,88	332,56	416,54	276,69	0,00461	0,02992
Id3	2723,56	2758,68	1648,87	1509,98	3264,72	2225,50	4895,10	2531,91	0,00462	0,03000
Ybx2	55,02	61,18	145,25	227,98	92,73	160,20	99,24	159,71	0,00465	0,03013
Trnfaip8l3	25,89	31,96	10,76	14,31	4,51	8,11	3,49	5,09	0,00465	0,03018
Endou	1,62	0,91	29,59	21,47	8,37	22,31	18,17	9,16	0,00466	0,03018
Strbp	1348,03	1652,84	1258,85	1657,20	1009,04	1147,73	710,08	975,53	0,00466	0,03018
Spag16	50,17	68,49	36,31	38,85	30,26	25,35	11,88	19,33	0,00466	0,03018
Camk4	474,16	530,55	664,39	809,68	672,26	897,30	857,55	1022,33	0,00470	0,03043
Hba-a1	100,33	571,64	98,18	204,47	39,28	42,58	143,27	21,36	0,00471	0,03046
Fkbp2	351,17	336,05	564,87	454,94	345,79	297,07	316,60	270,59	0,00472	0,03050
Csf2ra	37,22	53,88	98,18	143,13	104,32	123,70	95,75	139,36	0,00472	0,03050
Sulf2	10123,94	7500,77	6768,99	5040,08	6868,80	4767,34	4832,20	3829,91	0,00473	0,03052
Fam171b	234,65	173,50	112,97	229,00	277,53	138,90	48,22	79,34	0,00472	0,03052
Mgp	6,47	2,74	1,34	3,07	30,26	8,11	32,15	21,36	0,00474	0,03062
Tfg	1749,36	1928,61	1582,97	1607,10	1432,74	1549,23	1208,40	1230,86	0,00478	0,03084
Wnt3	966,11	924,13	1591,04	1384,23	839,68	1388,02	2005,84	1619,45	0,00479	0,03088
Sh3pxd2b	1089,10	1041,93	1011,38	1060,16	1982,01	1277,51	1945,04	1536,03	0,00482	0,03107
Wrb	587,43	626,43	325,47	399,73	381,21	392,38	263,49	394,69	0,00486	0,03128
Fabp5	4521,47	3829,83	3147,12	2462,79	2564,13	2263,01	3147,15	2404,75	0,00489	0,03151
Trip10	616,56	641,96	583,70	548,99	403,10	425,84	463,37	440,46	0,00490	0,03151
Meis3	271,87	214,59	185,60	148,24	278,18	263,61	317,30	322,46	0,00492	0,03166
Cysltrl1	17,80	18,26	1,34	0,00	4,51	4,06	7,69	9,16	0,00493	0,03170
Socs5	339,84	350,66	357,75	324,08	408,25	367,03	587,08	499,46	0,00494	0,03173
Kbtbd8	234,65	399,05	161,39	205,49	63,75	153,10	97,85	150,55	0,00495	0,03178
Irs1	2225,13	2765,99	4878,03	6436,58	3043,21	5154,64	3439,29	4904,11	0,00495	0,03179
Rab38	110,04	126,93	239,40	236,16	204,13	179,46	297,03	196,33	0,00495	0,03180
Ncoa3	1021,13	1167,03	1515,73	1725,69	1329,71	1652,65	1745,85	1897,15	0,00498	0,03193
Marveld3	29,13	27,40	69,94	93,03	45,72	87,19	94,35	89,52	0,00498	0,03194
Synrg	784,86	609,08	785,43	847,51	1000,67	988,55	1151,09	1092,52	0,00498	0,03194
H2-T22	92,24	52,05	51,11	36,80	138,44	77,06	222,25	104,78	0,00500	0,03201
Bambi	5439,03	4724,74	6226,99	6104,33	3711,61	4725,77	3929,92	4043,53	0,00500	0,03201
Thra	479,01	378,05	611,94	575,57	1099,83	598,20	989,64	797,52	0,00507	0,03248
Cdc42se2	2793,15	3080,12	2439,69	2153,03	2126,90	1954,79	2079,93	1893,08	0,00508	0,03249
Serhl	93,86	76,71	102,21	104,28	140,38	153,10	161,45	169,88	0,00509	0,03255
Gpd2	733,08	809,07	464,00	558,19	495,83	497,82	528,37	563,55	0,00515	0,03292
Ksr1	89,01	115,06	95,49	104,28	126,85	108,49	196,39	186,15	0,00517	0,03302
Acp2	893,29	822,77	1030,21	975,30	838,40	831,39	598,96	675,45	0,00517	0,03303
Zswim5	362,49	368,92	289,16	269,89	207,99	260,57	207,57	212,60	0,00517	0,03303
Pramef12	12,95	4,57	41,69	30,67	33,48	51,71	40,54	37,64	0,00519	0,03309
1190002N	511,38	497,68	412,89	537,75	743,74	530,27	877,12	808,71	0,00519	0,03310
Adcy8	8,09	4,57	13,45	24,54	19,96	22,31	44,03	35,60	0,00520	0,03314
Ccnb1	2906,43	2879,22	1944,76	2252,19	2313,64	2219,42	2025,41	1908,34	0,00520	0,03314

Svep1	82,53	71,23	40,35	49,07	661,32	34,47	104,14	116,98	0,00521	0,03317
Fam109b	87,39	101,36	79,35	124,72	189,96	140,93	220,15	183,10	0,00521	0,03317
Adamts18	4217,23	4945,72	5077,08	6163,62	2509,39	5037,03	1793,38	2827,93	0,00522	0,03322
Canx	10924,99	10649,38	11647,02	9836,85	7676,93	8612,03	6880,68	8009,74	0,00523	0,03327
Dsg2	2205,71	1825,43	3112,15	2789,94	2484,92	3435,08	3634,98	3485,06	0,00528	0,03360
Ipcef1	1,62	2,74	1,34	5,11	7,73	8,11	24,46	22,38	0,00529	0,03362
St8sia6	27,51	34,70	86,07	110,41	56,02	103,42	143,27	77,31	0,00530	0,03366
Ric3	161,83	139,71	49,76	84,85	46,36	99,36	30,75	53,91	0,00531	0,03372
Net1	1658,73	1741,41	2134,39	1722,62	2002,62	1838,19	3193,98	2439,34	0,00532	0,03375
Krtdap	0,00	0,00	0,00	0,00	0,64	1,01	32,85	3,05	0,00532	0,03375
Ddr2	419,13	327,83	238,05	336,35	1094,68	198,72	106,23	162,76	0,00535	0,03392
Trim6	182,87	268,47	115,66	157,44	32,20	131,81	21,67	64,09	0,00535	0,03393
Rnf208	46,93	36,53	47,07	38,85	78,56	51,71	157,25	80,36	0,00536	0,03395
Piga	487,10	584,43	473,41	597,04	290,41	371,09	286,55	372,31	0,00538	0,03403
Kank4	116,52	98,62	146,60	202,42	513,86	124,71	85,27	94,60	0,00538	0,03403
Ctdsp2	5188,20	4766,74	6296,92	5446,97	7545,57	6279,05	9066,84	7264,11	0,00540	0,03417
Twist1	713,66	513,20	250,16	302,61	1669,71	224,07	247,41	203,45	0,00541	0,03425
Clcf1	19,42	10,96	63,21	101,21	16,74	47,65	27,26	43,74	0,00543	0,03430
Uchl5	789,72	907,69	638,84	714,61	587,26	565,75	538,85	565,59	0,00543	0,03435
Wdfy2	1068,06	1149,68	825,78	994,73	714,12	846,60	609,44	715,12	0,00546	0,03448
Abhd14b	53,40	44,75	73,97	107,34	86,93	94,29	118,11	134,28	0,00547	0,03454
Hkdc1	0,00	0,00	5,38	4,09	28,33	7,10	2,10	4,07	0,00550	0,03472
Gfra2	8,09	6,39	1,34	3,07	64,39	8,11	6,99	7,12	0,00551	0,03479
Mapre2	2123,18	1841,86	2202,98	1967,98	3458,54	2312,70	3521,76	3131,06	0,00557	0,03510
Pgghg	330,13	270,30	376,58	399,73	526,09	430,91	565,41	484,21	0,00557	0,03510
Tubg2	14,56	21,00	24,21	24,54	57,95	24,33	88,06	59,00	0,00561	0,03532
Ndfip1	1341,55	1318,62	1374,51	1287,11	1104,34	1277,51	806,53	941,96	0,00563	0,03544
Tsc22d3	425,61	468,46	330,85	403,82	491,32	466,39	612,24	622,55	0,00563	0,03545
Rep15	1,62	1,83	18,83	21,47	16,10	11,15	17,47	17,29	0,00564	0,03546
Adgrg6	93,86	110,49	251,50	271,94	182,88	346,75	96,45	196,33	0,00568	0,03569
Ulk2	501,67	535,12	570,25	718,70	866,09	854,71	747,12	1038,60	0,00569	0,03577
Traf3ip2	200,67	179,89	244,78	263,76	206,06	253,47	398,37	315,34	0,00570	0,03579
Slit1	17,80	16,44	6,72	5,11	1,93	5,07	0,00	1,02	0,00571	0,03586
Prelid2	249,21	172,59	103,56	103,26	132,65	96,32	101,34	110,88	0,00575	0,03608
Polr3gl	66,35	42,01	68,59	166,64	192,53	138,90	176,12	155,64	0,00576	0,03614
Nyap1	101,95	121,45	160,05	196,29	220,87	225,08	188,00	250,24	0,00577	0,03619
Slc4a4	139,17	142,45	146,60	184,02	90,79	92,26	45,43	89,52	0,00577	0,03619
Fkbp7	42,08	32,87	63,21	75,65	79,20	69,96	93,65	104,78	0,00580	0,03633
Sun2	810,76	634,65	870,16	945,65	1382,52	995,65	1311,14	1188,14	0,00580	0,03633
Nrip1	822,09	1135,98	609,25	637,93	552,49	662,07	857,55	879,91	0,00581	0,03636
Tmed10	2262,35	1546,00	3473,93	2635,56	1947,24	1746,94	1880,04	1359,03	0,00587	0,03672
Zfp710	1194,29	1247,39	1807,57	1759,43	1660,69	1947,69	1155,28	1447,53	0,00592	0,03704
Rnf180	71,20	66,66	91,45	92,01	108,82	123,70	139,08	152,59	0,00594	0,03714
Aff1	404,57	476,67	310,68	291,36	364,46	284,90	208,97	258,38	0,00595	0,03716
Rtn4ip1	325,27	318,70	360,44	318,97	359,31	353,85	530,47	481,15	0,00597	0,03730
Tmem246	56,64	63,01	96,83	82,81	165,49	128,76	157,25	98,67	0,00598	0,03736
Rtl1	24,27	13,70	4,03	0,00	0,00	0,00	0,00	0,00	0,00604	0,03768
Apbb1ip	4,85	5,48	6,72	14,31	28,98	34,47	28,65	20,34	0,00606	0,03779
Znrf1	739,55	854,73	1100,15	1403,66	1271,12	1391,06	1162,97	1475,00	0,00608	0,03789
Itga8	87,39	64,84	64,56	87,92	307,15	95,31	60,80	68,16	0,00609	0,03795
Slc25a38	454,74	481,24	365,82	279,10	349,65	269,70	255,10	247,19	0,00612	0,03808
Cep85	610,09	735,10	400,79	508,10	481,66	374,13	328,48	399,78	0,00611	0,03808
Nexn	27,51	25,57	16,14	34,76	39,28	82,13	67,09	109,86	0,00612	0,03808
Ino80c	521,09	490,37	376,58	374,17	467,49	415,70	297,73	324,50	0,00614	0,03820
Pgd	3634,65	2990,63	2774,57	2003,77	2564,13	1787,50	1876,55	1428,20	0,00615	0,03821
Ryk	1990,48	1581,61	2313,27	1854,51	2611,13	2078,49	4051,53	2722,13	0,00614	0,03821
Msi1	2875,68	3295,63	2890,24	2938,17	2007,13	2416,11	1671,07	2200,29	0,00615	0,03821
Ptpn14	3094,15	3601,54	4463,79	4253,91	3360,67	4568,61	5635,93	5526,66	0,00617	0,03831
Evc2	577,73	504,98	576,97	614,42	898,93	762,45	798,84	748,69	0,00618	0,03839
Crispld2	37,22	28,31	8,07	10,22	133,94	21,29	29,35	23,40	0,00619	0,03841
Ppp2r3a	496,81	509,55	445,17	472,32	612,38	548,52	677,23	770,05	0,00619	0,03841
Ahi1	409,42	424,62	235,36	286,25	390,22	297,07	215,26	251,26	0,00620	0,03843
Tpi1	17156,98	12402,67	10798,38	5968,36	8009,84	5456,78	8751,63	5146,21	0,00620	0,03846
Srebf1	2908,04	2455,51	2976,31	2387,14	1959,48	2047,05	1820,64	1809,67	0,00622	0,03857

Rnf181	1058,35	1020,92	837,89	805,60	738,59	740,14	721,27	725,29	0,00624	0,03863
Pcdhga7	105,19	82,19	174,84	147,22	213,78	176,42	204,78	161,74	0,00624	0,03863
Mycl	2733,27	2288,40	3521,00	2817,54	3791,46	3488,81	4629,52	3804,48	0,00627	0,03882
Fgf12	3,24	11,87	0,00	1,02	9,66	4,06	40,54	11,19	0,00629	0,03891
Arhgap29	1985,63	2343,19	3242,61	3804,09	2194,51	4361,78	4155,66	6016,97	0,00631	0,03903
Susd6	550,21	529,64	1088,04	1180,79	564,73	1014,91	998,73	833,12	0,00634	0,03917
Ydjc	59,88	64,84	65,90	56,23	92,08	68,94	224,35	98,67	0,00634	0,03917
Nfkb1a	187,72	231,94	243,43	215,71	396,66	278,82	568,21	326,53	0,00635	0,03919
Baiap2	428,84	423,71	660,36	726,88	629,12	873,98	633,20	754,79	0,00636	0,03926
Tmem238	37,22	25,57	108,94	75,65	91,44	70,97	119,51	69,17	0,00638	0,03934
Lclat1	1139,27	1135,07	1148,56	1015,17	669,69	931,77	668,15	734,45	0,00638	0,03935
Pax3	19,42	60,27	14,79	20,45	7,08	9,13	2,10	8,14	0,00639	0,03940
Dusp8	17,80	10,04	52,45	38,85	37,99	44,61	83,17	41,71	0,00640	0,03944
Cdc25b	613,33	577,12	595,80	572,50	931,12	749,27	905,08	806,67	0,00642	0,03952
Ptx3	21,04	21,00	5,38	10,22	1,29	3,04	17,47	15,26	0,00643	0,03956
Enpp3	118,13	92,23	200,39	219,80	200,91	257,53	157,25	231,93	0,00643	0,03959
Nfe2l2	896,53	933,26	741,05	784,13	365,11	621,52	566,81	550,33	0,00646	0,03973
Frmd4b	2801,24	2852,74	3385,17	3544,42	3688,43	4504,74	4017,28	4510,44	0,00646	0,03973
Psd4	71,20	94,97	147,94	213,67	182,23	168,31	227,14	154,62	0,00648	0,03981
Kcna1	27,51	26,48	102,21	75,65	32,84	74,01	32,85	30,52	0,00649	0,03985
Fuom	19,42	10,96	63,21	40,89	68,90	33,46	68,49	62,05	0,00652	0,04002
Has2	195,81	116,89	52,45	92,01	263,37	103,42	34,25	71,21	0,00652	0,04002
Elovl5	1568,11	1751,46	1366,44	1255,42	1098,54	1190,31	1172,06	1161,69	0,00654	0,04011
Lrrc4	37,22	42,01	76,66	64,41	72,76	107,47	113,22	97,65	0,00656	0,04024
Egfr	2074,63	1794,38	1903,06	2168,36	1229,91	1986,22	2912,32	3063,93	0,00657	0,04025
Sgms1	160,21	199,98	212,50	294,43	232,46	348,78	364,13	433,34	0,00660	0,04046
Isl1	50,17	35,61	17,48	46,00	5,80	15,21	7,69	9,16	0,00661	0,04048
Klf11	176,39	239,25	277,05	314,88	308,44	413,67	378,11	446,57	0,00667	0,04081
Tinf2	867,40	830,07	781,40	820,93	696,09	640,78	549,34	586,95	0,00669	0,04092
Zfp799	506,52	596,30	679,19	796,39	561,51	774,62	949,81	1027,41	0,00670	0,04099
Phf19	56,64	30,13	12,10	13,29	6,44	11,15	15,38	9,16	0,00672	0,04106
Med4	1021,13	960,65	812,33	818,89	764,34	787,80	613,63	676,46	0,00672	0,04107
Med8	1042,17	1073,89	856,72	776,97	766,92	697,56	742,23	689,69	0,00673	0,04109
Jmjd6	915,95	886,69	646,91	619,53	720,56	541,42	563,31	511,67	0,00673	0,04109
Ankrd29	19,42	18,26	9,41	18,40	66,32	21,29	63,60	64,09	0,00678	0,04138
Gipc2	43,69	34,70	88,76	106,32	63,11	92,26	97,15	95,62	0,00680	0,04145
Rab11fip4	1118,23	1435,50	1448,48	1374,01	1754,71	1871,65	1915,69	1936,82	0,00682	0,04157
Ephb6	273,49	181,72	337,58	361,90	473,29	361,96	452,89	419,10	0,00683	0,04157
Myo6	532,41	349,74	332,20	360,88	251,78	408,60	146,07	215,65	0,00682	0,04157
Olfml1	29,13	27,40	49,76	57,25	71,48	93,28	46,83	48,83	0,00682	0,04157
4931428F1	223,32	264,82	295,88	393,60	455,26	445,10	366,22	428,26	0,00688	0,04189
Xbp1	1221,80	1212,69	1584,32	1123,54	702,53	733,05	1131,52	742,58	0,00689	0,04191
Mppe1	110,04	112,32	201,74	199,35	185,45	191,63	180,32	206,50	0,00691	0,04202
Srpk2	786,48	632,83	1054,42	1257,46	1281,42	1075,74	1085,39	1587,91	0,00694	0,04219
Tmem176	173,16	100,45	286,47	195,26	359,96	236,24	441,71	286,86	0,00699	0,04248
Gmps	3435,60	3743,08	2918,48	2828,79	2370,30	2714,20	2312,66	2599,05	0,00701	0,04258
Slc45a3	199,05	218,25	180,22	237,18	69,54	163,24	82,47	90,53	0,00701	0,04258
Kif16b	534,03	561,60	665,74	641,00	647,15	761,44	825,40	958,24	0,00702	0,04261
Chrn1	12,95	14,61	41,69	79,74	36,70	93,28	48,22	71,21	0,00702	0,04261
Gm20219	1,62	2,74	13,45	53,16	7,73	28,39	24,46	39,67	0,00704	0,04267
Unc79	53,40	85,84	29,59	24,54	21,89	13,18	6,99	25,43	0,00705	0,04273
Frk	211,99	203,64	238,05	305,68	218,94	362,97	397,67	503,53	0,00712	0,04316
Msmo1	1152,21	1363,36	917,24	674,74	833,24	839,51	833,79	784,29	0,00713	0,04317
Arhgap10	890,05	901,30	1444,45	1132,74	1817,17	1286,63	1685,75	1425,15	0,00713	0,04317
Cd34	121,37	51,14	25,55	42,94	37,35	16,22	22,36	10,17	0,00715	0,04326
Trim21	126,23	134,24	67,25	82,81	56,67	61,85	76,18	83,41	0,00720	0,04353
Tmed4	1074,54	889,43	891,68	952,81	739,87	789,82	636,00	638,83	0,00721	0,04357
Lrrn3	1,62	2,74	2,69	10,22	36,06	14,19	18,87	23,40	0,00721	0,04357
Klhdc9	9,71	5,48	12,10	3,07	27,05	30,42	37,74	28,48	0,00723	0,04365
Sparcl1	40,46	25,57	4,03	12,27	3,86	0,00	9,78	4,07	0,00727	0,04389
Cacnb2	53,40	60,27	138,53	198,33	117,84	189,60	60,80	131,22	0,00727	0,04389
Zfp398	205,52	231,03	306,64	319,99	227,31	357,91	393,48	526,93	0,00728	0,04389
Foxd1	12,95	12,78	1,34	2,04	0,00	1,01	0,00	0,00	0,00728	0,04389
Baz1a	1294,62	1329,57	954,89	1036,64	937,56	1030,12	1317,43	1365,14	0,00728	0,04391

Nradd	294,53	194,51	321,44	288,30	477,80	355,88	601,75	414,02	0,00729	0,04395
Twist2	63,11	37,44	78,01	26,58	159,05	25,35	9,78	9,16	0,00733	0,04414
Nup37	640,84	628,26	470,72	471,29	417,27	452,20	408,86	438,43	0,00734	0,04414
Inpp4b	16,18	15,52	18,83	33,74	71,48	49,68	28,65	28,48	0,00734	0,04414
Sept9	10916,90	9137,17	7633,77	5513,42	8183,70	5603,80	5714,91	4918,35	0,00733	0,04414
Pof1b	42,08	39,27	72,63	106,32	78,56	142,96	95,05	188,19	0,00737	0,04430
A930004D	129,46	144,28	225,95	221,85	119,13	193,65	287,95	256,34	0,00738	0,04433
Rgma	613,33	503,16	667,08	460,05	253,06	345,74	404,66	258,38	0,00739	0,04441
Syngr1	22,66	19,18	39,00	43,96	49,58	60,83	55,91	76,29	0,00744	0,04468
Cd55	48,55	31,05	94,14	187,09	85,64	113,56	38,44	84,43	0,00744	0,04468
Nxt2	121,37	123,28	106,25	114,50	154,54	191,63	200,58	200,40	0,00745	0,04472
Arhgdib	273,49	174,42	248,81	244,34	358,67	350,81	493,42	357,05	0,00748	0,04486
St3gal6	43,69	42,92	14,79	28,63	57,31	41,57	109,73	60,02	0,00750	0,04499
Nes	3437,22	2664,63	2972,28	2381,00	2388,33	2046,04	1934,56	1615,38	0,00752	0,04504
Homer3	1937,08	1674,75	1565,49	1300,40	1444,33	1137,59	1130,12	979,60	0,00754	0,04514
Ehd4	2665,30	2698,42	2174,74	1697,07	1721,22	2127,15	1663,38	1623,51	0,00754	0,04515
Nefm	24,27	15,52	4,03	2,04	6,44	8,11	1,40	2,03	0,00757	0,04528
Fkbp11	135,94	130,58	123,73	129,84	99,17	71,99	70,59	41,71	0,00757	0,04528
Cox4i2	661,88	472,11	839,23	599,08	410,18	415,70	427,73	260,41	0,00758	0,04531
Tiam1	3524,61	3272,80	5959,35	5194,45	3641,42	5087,73	3542,73	3869,58	0,00759	0,04535
Dennd5b	454,74	546,08	767,95	825,02	327,12	589,07	225,74	419,10	0,00759	0,04536
Zfp687	2598,95	2381,55	2305,20	1904,60	1810,73	1639,47	1741,66	1578,76	0,00762	0,04549
Perp	5426,08	4026,16	6132,84	4973,63	5331,09	5519,65	9033,29	7122,71	0,00765	0,04568
Fancd2	773,54	932,35	576,97	677,80	576,32	701,62	431,22	525,91	0,00765	0,04568
F5	27,51	19,18	20,17	8,18	1,93	3,04	0,70	5,09	0,00766	0,04570
Prss50	21,04	12,78	21,52	7,16	5,80	5,07	1,40	0,00	0,00768	0,04582
Pcdhb13	0,00	0,00	0,00	1,02	5,80	3,04	13,98	12,21	0,00769	0,04585
Schip1	273,49	447,45	377,92	444,71	598,85	655,99	563,31	833,12	0,00770	0,04586
Arhgef19	1568,11	1178,90	1807,57	1639,82	1599,52	1764,18	2599,21	2102,63	0,00770	0,04586
Cltc	7638,27	8134,51	6187,98	6151,36	5356,85	5979,95	5377,34	5952,89	0,00772	0,04594
Itga6	6439,13	5890,85	6100,56	5671,88	3626,61	4921,45	3800,62	4368,03	0,00774	0,04605
Dsc1	0,00	0,00	2,69	5,11	7,73	15,21	12,58	10,17	0,00774	0,04605
Plod3	1314,04	1135,98	1784,71	1657,20	1334,22	1286,63	1217,48	1093,53	0,00775	0,04610
Arhgap32	1273,58	1539,60	1486,14	1520,20	1445,62	1799,66	2192,45	2195,20	0,00778	0,04622
Tcf15	14,56	14,61	8,07	4,09	1,93	0,00	0,70	0,00	0,00783	0,04649
Tmem178	419,13	354,31	642,87	435,51	408,25	335,60	280,96	267,53	0,00785	0,04659
Mcm4	5935,84	6161,15	5159,12	4411,35	4654,32	4025,16	4168,94	4009,96	0,00786	0,04663
Smtnl2	406,19	378,05	492,24	487,65	397,30	557,64	784,87	632,72	0,00786	0,04666
Mrc2	2014,76	1484,81	1215,81	1240,09	2774,05	1790,54	2176,38	2051,77	0,00787	0,04667
Zfp784	46,93	40,18	63,21	63,38	91,44	77,06	92,25	122,07	0,00789	0,04676
Emc2	613,33	570,73	391,37	401,78	392,15	369,06	346,65	433,34	0,00790	0,04679
Ccnjl	1064,83	1237,34	1190,26	914,98	631,69	818,21	741,53	746,65	0,00791	0,04686
Coro2a	307,47	336,96	732,98	528,54	435,94	605,30	449,39	488,27	0,00792	0,04692
Twistnb	503,28	538,77	422,31	382,35	306,51	348,78	362,73	338,74	0,00793	0,04692
Epb41l1	423,99	399,97	330,85	416,09	534,46	517,09	633,20	564,57	0,00793	0,04692
Calu	6892,24	6019,61	8039,94	7251,38	5772,18	6164,48	5032,08	5254,04	0,00795	0,04701
Sorl1	1912,80	1774,29	1591,04	1544,74	1119,79	1307,92	1473,98	1453,64	0,00798	0,04715
Il3ra	85,77	86,75	156,01	184,02	130,72	150,06	105,53	107,83	0,00798	0,04715
Agap3	1806,00	1999,84	2387,24	2498,57	2716,74	2453,63	2869,69	2739,43	0,00801	0,04730
Ccdc117	888,43	1132,33	864,78	836,27	480,37	663,09	744,33	675,45	0,00806	0,04758
Impact	1019,51	1067,49	480,14	691,09	621,39	630,64	487,83	739,53	0,00810	0,04777
Pdgfa	5701,19	6941,91	6045,42	5981,65	3000,71	5032,98	3465,85	3959,10	0,00810	0,04777
Wnt8a	16,18	12,78	36,31	24,54	7,73	14,19	4,89	3,05	0,00811	0,04779
Rap1a	427,23	423,71	352,37	338,39	259,50	309,24	235,53	275,67	0,00811	0,04779
Dennd2d	98,71	125,10	147,94	157,44	148,75	175,40	199,89	280,76	0,00812	0,04782
Arhgef40	846,36	901,30	1055,76	1485,44	2057,35	1371,80	1241,95	1382,43	0,00813	0,04787
Tfap2a	1632,84	1818,12	2166,67	2292,06	1810,73	2313,71	2648,83	2899,13	0,00813	0,04787
Bmp8a	58,26	31,05	48,42	69,52	125,57	81,11	112,52	124,10	0,00814	0,04787
Kirrel2	1,62	0,00	14,79	14,31	0,00	1,01	1,40	1,02	0,00815	0,04792
Syt2	4,85	10,04	43,04	73,61	21,25	54,75	15,38	39,67	0,00818	0,04798
Adcy7	46,93	71,23	57,83	112,46	106,25	195,68	155,16	178,02	0,00817	0,04798
Bex4	733,08	609,08	399,44	285,23	388,93	337,63	456,38	253,29	0,00817	0,04798
Sec23ip	1721,85	1712,19	1401,41	1304,49	1269,18	1311,98	1207,00	1208,48	0,00817	0,04798
E430018J	105,19	122,36	197,70	148,24	186,74	184,53	282,36	206,50	0,00817	0,04798

Epb41l3	1755,83	1166,12	2680,43	2423,94	1613,69	1744,91	2171,48	1858,50	0,00823	0,04829
Dars2	1029,22	834,64	644,22	554,10	723,13	620,50	568,91	608,31	0,00823	0,04829
Atp2c2	563,16	631,00	560,83	581,71	260,79	468,42	324,99	335,69	0,00825	0,04834
Ggt5	50,17	33,79	91,45	111,43	74,70	136,88	42,63	59,00	0,00826	0,04842
Bard1	432,08	668,44	599,84	1150,12	770,14	1073,72	1072,11	1898,17	0,00827	0,04844
Map4k5	1040,55	1415,41	1051,73	1548,83	1660,05	2110,93	1888,43	2697,72	0,00832	0,04869
Dirc2	435,32	317,78	446,51	356,79	688,36	507,96	757,61	587,96	0,00833	0,04872
Fgf1	42,08	44,75	117,01	185,04	76,63	192,64	78,98	120,03	0,00833	0,04872
Elovl4	93,86	101,36	193,67	148,24	186,10	216,97	139,78	160,72	0,00835	0,04885
Capn5	493,57	313,22	381,96	270,92	197,04	195,68	257,89	230,91	0,00839	0,04906
Gucy1b1	14,56	5,48	5,38	10,22	15,45	20,28	37,74	41,71	0,00841	0,04910
Plcx1	92,24	83,10	45,73	27,60	33,48	31,43	25,86	44,76	0,00840	0,04910
Ildr1	101,95	52,05	119,70	117,57	151,97	171,35	176,82	175,98	0,00850	0,04960
Decr1	768,68	584,43	579,66	460,05	556,36	446,11	380,20	332,64	0,00850	0,04962
Fam118a	461,21	502,24	380,61	408,93	390,22	368,04	269,78	309,24	0,00855	0,04988

Differentially expressed genes in the mesoderm (MES-DEGs), expression values are counts

Symbol	E9.5R1	E9.5R2	E10.5R1	E10.5R2	E11.5R1	E11.5R2	E12.5R1	E12.5R2	pval	padj
Lin28a	7060,66	8793,16	210,51	174,57	3,33	6,39	0,81	1,15	5,95E-276	8,72E-272
Meis2	4582,96	5371,43	82,89	119,02	21,62	25,55	12,19	16,16	6,49E-210	4,76E-206
Hoxc5	1263,16	1203,64	11,84	14,55	7,48	3,83	0,00	1,15	1,16E-163	5,69E-160
Pkdcc	9813,56	8881,83	164,46	193,08	14,97	30,66	25,20	6,92	4,43E-130	1,62E-126
Hoxb6	812,75	844,20	9,21	5,29	4,16	1,28	0,81	2,31	7,04E-124	2,07E-120
Hoxb5	762,30	799,27	10,53	5,29	8,32	8,94	4,88	3,46	4,41E-115	1,08E-111
Hoxa13	11,01	5,91	3142,59	3917,19	3505,34	4352,06	4540,39	3939,77	1,13E-113	2,38E-110
Meis1	1375,99	1884,67	55,92	72,74	22,45	14,05	6,50	13,85	7,59E-104	1,39E-100
Hoxc4	694,42	804,00	11,84	18,51	3,33	1,28	3,25	0,00	2,19E-102	3,56E-99
Irx3	1784,20	1380,99	13,82	3,97	4,99	3,83	19,51	9,23	8,36E-101	1,226E-97
Hoxd12	8,26	9,46	6041,12	6592,57	10992,56	8557,23	4800,54	7595,65	1,191E-98	1,588E-95
Jaml	832,02	744,88	38,16	30,42	9,98	3,83	5,69	2,31	7,522E-97	9,194E-94
Hoxb9	943,01	1138,61	24,34	37,03	24,12	26,83	33,33	45,01	8,245E-91	9,303E-88
Dlk1	9407,19	6135,23	529,58	347,81	163,00	155,84	68,29	113,09	2,191E-87	2,295E-84
Hoxb3	776,06	1263,94	18,42	17,19	14,97	7,66	3,25	9,23	6,88E-78	6,728E-75
Hoxb8	776,06	845,38	19,74	13,22	13,31	11,50	19,51	6,92	8,525E-78	7,815E-75
Rspo2	755,88	759,07	60,52	43,64	45,74	31,93	13,82	9,23	1,267E-73	1,093E-70
Hoxb4	401,79	423,28	13,82	11,90	9,15	7,66	3,25	4,62	1,622E-73	1,322E-70
Inhba	0,00	0,00	0,66	2,64	58,21	33,21	575,58	530,84	2,312E-73	1,785E-70
Dlx5	7,34	7,09	244,72	302,85	686,10	456,03	1663,32	1417,12	1,177E-68	8,635E-66
Hgf	748,54	772,08	20,39	42,32	8,32	12,77	6,50	10,39	1,433E-68	1,001E-65
Cdx1	1007,22	757,89	51,31	21,16	7,48	8,94	7,32	8,08	2,609E-65	1,74E-62
Sema3a	4171,09	6265,29	399,32	342,52	403,34	439,42	664,19	534,30	3,813E-63	2,432E-60
Evx1	12,84	14,19	1450,58	1282,81	784,23	1039,79	563,38	416,60	5,155E-63	3,151E-60
Col14a1	985,21	809,91	2,63	3,97	4,16	2,55	43,90	13,85	7,019E-62	4,118E-59
Sema6a	226,58	293,22	452,61	506,51	1437,90	1149,65	4372,92	3653,58	2,503E-60	1,412E-57
Hoxc6	699,00	701,14	61,18	23,80	5,82	3,83	2,44	1,15	5,042E-59	2,739E-56
Crym	808,16	637,29	42,10	31,74	16,63	3,83	18,70	16,16	8,258E-58	4,326E-55
Cyp26b1	570,58	448,11	18266,11	16094,59	9207,87	12400,89	11375,77	8871,98	1,364E-56	6,9E-54
Nr6a1	1910,79	3142,69	46,71	84,64	13,31	44,71	17,07	21,93	4,12E-54	2,014E-51
Serinc2	22,02	17,74	703,25	933,67	2994,72	1831,78	4399,75	2725,76	1,383E-52	6,543E-50
Hoxb1	207,32	274,31	0,00	0,00	0,00	0,00	0,00	0,00	3,049E-52	1,398E-49
Itga11	18,35	21,28	301,30	440,39	1165,95	823,92	1459,27	1246,32	1,427E-51	6,344E-49
Wnt5a	1289,76	1570,16	9105,42	10664,48	10840,37	12550,34	21748,35	18632,54	2,91E-51	1,255E-48
Slc38a4	6096,55	6417,81	2287,38	2057,78	1139,34	1357,86	1117,01	1077,84	9,041E-50	3,789E-47
Slit3	443,99	406,73	4024,12	3496,64	2848,35	2640,36	2207,19	2021,81	6,92E-49	2,82E-46
Papss2	38,53	22,46	209,20	275,08	780,07	569,72	1696,65	1352,49	9,432E-49	3,739E-46
Tfap2b	6,42	2,36	2295,93	4866,73	2919,87	5108,28	6269,56	4967,99	1,743E-48	6,729E-46
Bcl11b	20,18	16,55	274,33	267,14	395,86	415,15	439,81	490,45	2,456E-48	9,236E-46
Scn4b	522,88	634,92	149,99	112,41	47,40	58,76	15,45	20,77	2,751E-47	1,009E-44
Gabrb3	288,04	331,06	34,87	30,42	16,63	14,05	4,88	6,92	3,3E-47	1,181E-44
Gata5	207,32	196,27	0,66	0,00	0,00	1,28	0,81	0,00	3,56E-47	1,243E-44
Des	545,81	354,71	34,21	17,19	8,32	3,83	3,25	3,46	9,848E-47	3,359E-44
Dlx6	0,00	2,36	26,31	37,03	185,45	107,30	471,52	528,53	2,298E-46	7,661E-44
Mdga1	61,46	41,38	466,42	484,03	938,92	783,04	941,41	890,89	2,379E-46	7,756E-44
Plcg2	1333,79	1346,70	290,12	216,89	211,24	183,94	141,46	110,78	2,502E-46	7,977E-44
Cdh11	3450,98	3117,86	13792,01	13293,58	17609,88	15987,79	19303,78	19173,77	3,153E-46	9,839E-44
Bmp2	22,93	37,84	198,67	243,34	652,83	619,53	1138,96	838,96	1,065E-45	3,254E-43

Rasl11b	125,67	151,34	348,01	413,94	854,09	720,45	1534,06	1554,44	2,707E-45	8,103E-43
Igdcc3	24739,39	22424,50	14473,55	6429,90	137,22	509,68	34,14	36,93	1,481E-44	4,343E-42
Tmem26	72,47	61,48	240,78	331,94	957,21	735,78	1500,73	1277,48	2,992E-44	8,606E-42
Chd3	621,95	780,35	5659,56	6961,54	14297,48	9393,92	16615,31	20551,65	5,964E-44	1,682E-41
Hoxd9	4183,93	4192,62	1631,49	1159,82	303,55	431,76	169,91	264,27	6,182E-44	1,711E-41
Zic3	44,95	54,39	1872,92	1996,95	1060,34	1779,40	991,00	1103,23	6,91E-44	1,877E-41
Rarb	1343,88	1171,71	7,89	7,93	19,96	15,33	158,53	46,16	8,684E-44	2,316E-41
Atp6v1g3	0,00	0,00	38,81	60,83	428,29	292,52	356,89	570,08	9,603E-44	2,515E-41
Nr2f1	960,44	981,35	22,37	22,48	94,81	58,76	60,97	120,02	1,092E-43	2,81E-41
Rprm	5,50	4,73	48,02	84,64	943,07	481,58	977,18	777,80	3,99E-43	1,009E-40
Lbx1	592,59	243,56	1,97	6,61	1,66	0,00	0,00	0,00	1,513E-42	3,762E-40
Hoxb2	676,07	605,36	37,50	35,71	13,31	34,49	28,45	16,16	2,516E-42	6,15E-40
Bcl11a	168,79	95,77	1795,30	2213,83	3228,41	2973,76	3623,37	3175,82	3,57E-42	8,585E-40
Hoxa1	385,28	522,60	16,45	5,29	4,16	10,22	6,50	2,31	4,333E-42	1,025E-39
Prtg	4936,14	7786,98	543,39	502,54	40,75	126,46	8,94	33,47	1,148E-41	2,672E-39
Hoxd13	194,47	160,80	7643,66	14449,42	17188,24	19615,58	11323,74	19724,23	1,401E-41	3,212E-39
Emp1	449,49	436,29	641,41	788,20	2334,40	2077,03	3703,04	2923,09	3,426E-40	7,731E-38
Plxna2	1405,34	1762,89	438,79	362,36	175,48	238,87	179,66	192,72	1,093E-39	2,43E-37
Cep170b	190,80	159,62	1480,84	1392,57	2304,46	1693,82	2751,06	2244,54	1,553E-39	3,4E-37
Mme	82,56	69,76	486,82	522,38	1265,75	852,02	1492,60	1996,43	2,504E-39	5,401E-37
Cbln1	28,44	30,74	1313,74	1444,15	1059,50	1241,62	243,08	480,07	6,563E-39	1,395E-36
Map2	111,91	121,78	451,29	495,93	978,83	961,87	1790,14	1257,86	6,693E-39	1,402E-36
Hoxb7	272,45	242,38	13,16	10,58	16,63	14,05	18,70	16,16	8,105E-39	1,674E-36
Fat4	206,40	232,92	847,98	1136,01	3256,68	2042,54	4016,03	4183,26	3,475E-38	7,08E-36
Ror1	879,72	840,65	51,97	23,80	19,96	12,77	147,96	79,63	8,578E-38	1,724E-35
Creb5	22,02	39,02	6,58	10,58	305,21	98,36	1210,50	1767,93	2,132E-37	4,226E-35
Hoxd1	143,10	208,09	3,95	3,97	0,00	0,00	0,00	1,15	4,438E-37	8,68E-35
Nrp2	2279,56	1684,85	16253,06	17196,22	10320,60	11390,47	9497,83	9099,32	2,164E-36	4,177E-34
Robo2	165,12	178,54	622,33	654,63	2257,06	1027,02	5155,80	5160,70	2,286E-36	4,355E-34
Wfikkn1	443,99	250,66	10,53	10,58	13,31	15,33	2,44	9,23	2,92E-36	5,491E-34
Nfix	5,50	3,55	37,50	31,74	392,53	145,62	3173,80	1023,60	7,741E-36	1,437E-33
Col9a3	11,01	13,01	29,60	39,67	368,41	113,69	1641,37	1163,24	8,551E-36	1,568E-33
Irx5	404,54	436,29	5,92	0,00	1,66	0,00	43,90	16,16	5,819E-35	1,054E-32
Hopx	194,47	245,93	8,55	5,29	5,82	1,28	4,88	2,31	6,99E-35	1,25E-32
Nlgn3	8,26	9,46	105,92	121,67	273,61	199,27	442,25	345,05	8,674E-35	1,533E-32
Prdm16	715,51	604,18	2323,56	2141,10	4976,51	3701,87	5436,28	6367,79	1,306E-34	2,28E-32
Mrc1	6,42	7,09	171,70	215,56	306,87	278,47	522,73	335,82	2,183E-34	3,768E-32
Meox1	412,80	269,58	11,18	9,26	26,61	22,99	39,84	25,39	6,943E-34	1,184E-31
Cpt1a	46,78	35,47	407,21	374,26	683,60	493,07	1053,60	776,64	7,157E-34	1,207E-31
Crb2	839,35	664,48	200,65	215,56	163,00	176,28	48,78	71,55	1,241E-33	2,068E-31
Cadps2	16,51	8,28	77,63	103,15	297,73	200,55	588,58	478,91	1,384E-33	2,281E-31
Pbx1	7393,65	8297,75	1760,43	1467,95	1110,23	1094,72	2329,95	1565,98	2,371E-33	3,864E-31
Myc	1613,58	2232,28	315,77	252,59	82,33	112,41	173,16	77,32	2,464E-33	3,972E-31
Rspo4	2539,16	2000,54	1370,32	703,56	203,75	240,15	135,76	110,78	3,921E-33	6,251E-31
Spock2	54,12	48,48	316,43	326,65	888,19	555,66	864,99	837,81	7,093E-33	1,119E-30
Lgi2	521,04	799,27	47,37	62,16	81,50	120,07	44,71	53,08	7,83E-33	1,222E-30
Dpyd	1,83	3,55	48,68	43,64	66,53	57,48	236,57	216,95	2,67E-32	4,122E-30
Col9a2	6,42	2,36	13,16	6,61	81,50	28,10	629,23	450,06	3,131E-32	4,784E-30
Upk3b	271,53	115,87	0,00	0,00	0,83	0,00	0,81	0,00	3,912E-32	5,916E-30
Sdk2	699,00	828,83	142,10	84,64	84,83	65,15	90,24	76,16	4,02E-32	6,017E-30

Sp9	2,75	1,18	10,53	19,84	203,75	79,20	733,29	435,06	6,229E-32	9,23E-30
Mab2112	147,69	108,78	3559,67	2184,74	1259,10	1861,16	593,46	662,40	6,484E-32	9,51E-30
Maf	26,60	21,28	68,42	99,19	268,62	168,62	556,88	595,47	4,746E-31	6,893E-29
Sfrp1	2466,69	1962,71	200,65	169,28	246,16	222,27	625,98	325,43	7,849E-31	1,129E-28
Sgms2	10,09	13,01	163,15	141,51	227,87	186,50	815,40	435,06	1,316E-30	1,874E-28
Kif26b	1407,18	1662,39	6643,72	5475,07	11381,76	8106,31	14142,28	13334,51	1,835E-30	2,587E-28
Wfikkn2	1,83	2,36	50,66	44,96	398,35	152,01	552,81	441,98	3,423E-30	4,782E-28
Mest	82907,08	79810,00	54139,81	46597,61	19810,39	25266,74	18157,50	17311,21	4,805E-30	6,649E-28
Ahnak	295,38	448,11	574,97	708,85	2628,80	1716,81	4652,58	3865,91	1,599E-29	2,192E-27
Fam19a5	469,67	428,01	161,18	113,73	35,76	56,21	34,96	32,31	1,718E-29	2,334E-27
Tmem178	10,09	5,91	108,55	128,28	148,86	148,18	250,39	238,88	5,821E-29	7,834E-27
Pdzd2	59,63	92,22	1285,46	2250,86	2281,18	3524,31	2374,66	3347,76	6,046E-29	8,062E-27
Hoxa7	1427,36	1289,95	721,67	592,47	198,76	310,41	99,99	137,33	7,216E-29	9,45E-27
Cdh3	596,26	394,91	4887,23	4147,30	9113,89	6223,44	12770,00	8281,13	7,202E-29	9,45E-27
Ltbp3	55,96	43,75	161,83	201,02	582,14	357,67	1668,20	938,21	1,907E-28	2,475E-26
Rin2	184,38	214,01	108,55	178,53	656,16	489,24	1358,46	1329,41	2,062E-28	2,653E-26
Slc16a2	132,10	73,31	2656,43	1991,66	2093,23	1652,94	2817,73	1886,80	3,503E-28	4,468E-26
Gldc	1193,44	1242,65	3416,92	2069,68	676,12	875,01	177,23	215,80	3,898E-28	4,929E-26
Hoxa4	315,56	269,58	20,39	43,64	16,63	20,44	11,38	12,69	4,666E-28	5,849E-26
Matn4	3,67	2,36	0,66	0,00	1,66	1,28	274,78	105,01	5,217E-28	6,485E-26
Eya1	273,36	236,47	7,24	14,55	20,79	15,33	22,76	12,69	6,031E-28	7,434E-26
Cacna1h	233,92	264,85	480,89	714,14	1259,93	1038,52	2099,07	2508,80	6,09E-28	7,444E-26
Alx1	641,21	699,95	67,10	56,87	12,47	43,43	8,94	21,93	1,006E-27	1,219E-25
Gdf5	1,83	2,36	88,15	51,58	259,47	131,57	1625,11	508,92	1,066E-27	1,282E-25
Ccne1	4322,44	3873,39	2007,79	1780,06	1325,63	1443,45	1066,61	982,06	1,54E-27	1,837E-25
Pmaip1	14,68	8,28	2651,17	6179,95	3463,76	6642,42	944,66	2496,11	1,646E-27	1,947E-25
Flnc	3872,95	3487,94	1492,02	953,51	652,00	522,45	608,10	526,23	2,247E-27	2,637E-25
Prr5l	418,30	424,46	437,48	424,52	1388,00	889,06	3956,68	2611,51	2,306E-27	2,685E-25
Lin28b	5352,60	8083,75	1182,83	1216,68	155,52	459,86	33,33	101,55	2,936E-27	3,391E-25
Pianp	33,94	55,57	248,67	207,63	608,76	461,14	644,68	898,97	4,06E-27	4,652E-25
Zfp536	0,92	1,18	3,95	3,97	67,36	21,72	248,77	251,57	5,009E-27	5,695E-25
Hs6st2	1401,68	1317,14	249,99	357,07	281,92	334,68	273,97	230,80	1,149E-26	1,296E-24
Mtus1	72,47	65,03	914,42	890,03	251,99	493,07	110,56	116,55	2,079E-26	2,328E-24
Dusp5	520,12	580,54	153,28	161,34	148,03	121,35	91,05	76,16	2,657E-26	2,953E-24
Thsd4	384,36	398,45	732,20	1143,95	3165,20	3096,39	5652,52	3366,23	4,272E-26	4,711E-24
Dmrta1	133,93	150,16	30,26	18,51	0,00	2,55	0,81	1,15	5,893E-26	6,45E-24
Rundc3b	26,60	24,83	48,68	85,96	160,51	148,18	539,81	392,36	6,5E-26	7,063E-24
Lrrn3	5,50	4,73	31,58	41,00	468,21	213,32	261,77	480,07	8,5E-26	9,168E-24
Tfeb	12,84	15,37	120,39	142,83	293,57	232,48	195,92	192,72	9,739E-26	1,043E-23
Gli1	80,72	69,76	868,37	1650,46	1078,63	1470,27	398,35	320,81	1,055E-25	1,121E-23
Gfra1	188,97	199,82	14,47	11,90	14,14	11,50	99,18	75,01	1,461E-25	1,542E-23
Ntrk2	204,56	139,52	2,63	3,97	25,78	17,88	8,94	9,23	1,478E-25	1,549E-23
Mcub	34,86	13,01	717,07	501,22	530,58	494,35	367,46	378,51	1,534E-25	1,595E-23
Cux2	75,22	76,85	182,88	267,14	780,07	491,79	895,07	1089,38	2,32E-25	2,396E-23
Meis3	301,80	214,01	17,76	19,84	28,28	28,10	51,22	60,01	3,808E-25	3,906E-23
Ndnf	305,47	480,04	13,82	18,51	49,07	76,64	91,86	77,32	4,823E-25	4,912E-23
Synpo2	8,26	13,01	167,75	255,24	503,97	275,92	452,01	586,23	5,931E-25	5,999E-23
Rasgef1b	104,58	122,96	643,39	720,75	824,98	1035,96	898,32	1291,33	6,192E-25	6,221E-23
Tnik	311,89	386,63	71,05	67,45	64,04	57,48	37,40	49,62	6,341E-25	6,327E-23
Adcy5	22,93	36,65	57,89	51,58	201,26	139,24	391,03	363,51	9,055E-25	8,974E-23

Sall3	1054,93	1713,23	4399,76	2619,83	562,19	840,52	195,11	197,33	1,523E-24	1,499E-22
Pear1	226,58	157,25	1553,86	1411,09	576,32	711,51	502,41	568,92	2,815E-24	2,753E-22
C1qtnf7	7,34	11,82	9,87	23,80	145,54	97,08	304,86	256,19	3,115E-24	3,026E-22
Stc2	213,74	244,75	25,66	43,64	10,81	15,33	18,70	13,85	3,23E-24	3,117E-22
D430019H1	569,66	621,92	1532,15	1522,18	1968,48	1765,35	2478,72	2309,16	3,252E-24	3,118E-22
St8sia2	155,95	154,89	860,48	882,09	692,75	932,49	1582,02	1154,00	3,344E-24	3,185E-22
Smad9	56,87	96,95	21,05	23,80	243,67	167,34	432,50	402,75	3,965E-24	3,752E-22
Cysltr1	151,36	210,46	13,16	15,87	3,33	10,22	4,88	6,92	4,152E-24	3,904E-22
Dock6	1381,49	1336,06	4621,46	4872,02	2485,76	2973,76	1658,44	1711,39	4,282E-24	4,001E-22
Crybg1	23,85	15,37	38,16	34,38	424,97	126,46	923,52	760,49	4,399E-24	4,084E-22
Mtmr11	55,96	52,02	210,51	290,95	350,12	302,74	556,07	519,30	5,219E-24	4,814E-22
Sox9	641,21	584,08	396,03	244,66	2302,80	1028,30	7050,82	4783,35	6,453E-24	5,916E-22
Nrep	2470,36	2430,92	3590,59	4931,53	6761,20	6421,43	12934,22	11534,27	7,031E-24	6,406E-22
Eva1a	14,68	7,09	144,73	244,66	565,51	399,82	1098,31	514,69	1,036E-23	9,376E-22
Pax9	0,00	1,18	48,02	60,83	133,06	297,63	186,17	276,96	1,495E-23	1,345E-21
Tgfb3	107,33	92,22	519,71	468,16	441,60	420,26	686,14	575,85	1,531E-23	1,369E-21
Atp8a2	15,59	14,19	64,47	84,64	171,32	160,95	235,76	215,80	2,455E-23	2,182E-21
Pax3	354,09	218,74	3,29	18,51	3,33	3,83	5,69	9,23	2,832E-23	2,502E-21
H2-Q4	52,29	49,66	211,83	187,79	387,54	332,12	365,02	335,82	2,915E-23	2,56E-21
Nsun2	8599,02	8601,62	4724,08	4589,01	3956,92	4177,06	2510,43	2788,07	3,428E-23	2,993E-21
Enpp1	7,34	3,55	113,15	208,95	261,13	277,19	407,29	260,80	4,022E-23	3,491E-21
Gprn2	12,84	7,09	46,05	43,64	76,51	62,59	217,87	214,64	4,117E-23	3,553E-21
Efr3b	231,17	261,30	762,46	897,96	1007,11	958,04	1128,39	1245,17	4,583E-23	3,931E-21
Gata6	333,91	249,48	41,45	31,74	7,48	25,55	7,32	3,46	4,951E-23	4,222E-21
Fgf13	114,67	89,86	198,67	253,92	622,06	450,92	799,95	777,80	5,55E-23	4,706E-21
Dclk1	140,35	157,25	478,92	551,47	538,90	662,96	927,59	877,04	5,688E-23	4,795E-21
Sulf1	253,18	262,48	98,68	169,28	2365,17	1265,89	1485,28	2689,98	6,776E-23	5,68E-21
Arg1	349,50	257,75	11,84	14,55	4,16	3,83	23,58	3,46	6,967E-23	5,807E-21
Slain1	11,93	5,91	30,26	42,32	190,44	200,55	117,88	125,79	7,529E-23	6,24E-21
Gfra2	11,93	9,46	7,89	10,58	245,33	94,53	283,72	257,34	7,704E-23	6,349E-21
Slc1a3	312,81	232,92	1194,01	1375,38	1244,96	1497,10	1608,04	1562,52	1,022E-22	8,374E-21
Rffl	89,90	126,51	173,67	248,63	631,21	401,10	1064,98	1196,70	1,3E-22	1,06E-20
Scn2b	1283,34	1682,49	486,16	375,58	347,62	306,57	328,44	366,97	1,48E-22	1,199E-20
Figl2	3698,66	3409,91	2547,89	1948,01	388,37	647,64	134,95	298,89	1,704E-22	1,373E-20
Cacna1g	794,41	917,51	2228,17	2642,32	2299,47	2443,64	4972,07	3995,16	1,786E-22	1,431E-20
Scn11a	0,00	0,00	195,38	346,49	126,41	281,03	150,40	115,40	1,859E-22	1,482E-20
Nup210	837,52	863,12	259,85	256,56	297,73	288,69	255,27	212,34	2,061E-22	1,634E-20
Dmd	949,43	1305,32	372,35	376,91	107,28	229,93	75,61	86,55	2,262E-22	1,784E-20
Trib2	220,16	284,95	1635,44	2261,44	1624,18	2263,53	2640,50	2104,90	2,499E-22	1,96E-20
Pklr	255,02	287,31	256,56	177,21	44,08	83,03	6,50	10,39	3,028E-22	2,363E-20
Mturn	56,87	41,38	186,17	215,56	419,98	287,41	527,61	530,84	3,066E-22	2,38E-20
Skap2	657,72	694,04	159,86	149,44	141,38	172,45	108,94	159,25	3,425E-22	2,644E-20
Mr1	7,34	3,55	38,16	30,42	91,48	67,70	252,83	176,56	4,242E-22	3,258E-20
Evx2	3,67	4,73	383,53	1274,87	1205,87	1821,56	764,18	1794,48	4,35E-22	3,323E-20
Trp53inp1	80,72	93,41	240,78	345,17	580,48	503,29	812,96	1330,57	4,659E-22	3,541E-20
Kcnab1	18,35	15,37	5,26	9,26	61,54	35,77	323,56	182,33	4,913E-22	3,714E-20
Hspd1	32186,25	34433,66	17535,89	15498,15	10837,04	13910,76	7523,15	8330,75	5,066E-22	3,81E-20
Gatsl2	211,90	262,48	963,76	1231,23	1325,63	1566,08	1017,83	1113,61	7,894E-22	5,908E-20
Adamts5	44,95	56,75	169,73	183,82	197,93	80,48	831,66	888,58	8,728E-22	6,499E-20
Runx1	22,02	21,28	43,42	54,22	223,71	231,21	249,58	504,30	9,564E-22	7,085E-20

Fgf2	37,61	30,74	159,86	286,98	277,77	314,24	939,78	580,46	1,239E-21	9,131E-20
Lmo2	632,04	556,89	2516,31	2752,08	1140,17	1606,95	634,11	699,33	1,376E-21	1,009E-19
Gbx2	129,34	158,44	178,94	78,03	2,49	8,94	0,81	0,00	1,475E-21	1,076E-19
Amph	133,93	141,88	12,50	11,90	11,64	8,94	8,13	4,62	1,658E-21	1,204E-19
Itga9	2464,86	2436,83	1082,84	793,49	765,10	804,75	512,17	594,31	2,015E-21	1,456E-19
Hoxd11	119,25	52,02	2566,97	1844,86	1753,09	1590,35	757,68	1259,02	2,63E-21	1,891E-19
Unc5c	988,88	943,52	321,04	424,52	1557,65	1080,67	6293,95	3143,51	3,043E-21	2,177E-19
Cdon	3039,10	3343,69	981,53	994,51	1748,10	1646,55	5028,98	3691,66	3,113E-21	2,217E-19
Pdk1	3583,08	2613,00	897,32	1002,44	765,94	841,80	1020,27	1010,91	3,833E-21	2,716E-19
Plekha2	656,81	438,65	48,02	66,12	92,31	95,80	143,08	93,47	4,226E-21	2,98E-19
Sorbs2	33,02	18,92	99,99	107,12	260,30	231,21	248,77	268,88	4,603E-21	3,231E-19
Sdc2	365,10	266,03	995,34	876,80	1915,26	1378,30	4626,57	2641,51	6,224E-21	4,348E-19
Zbtb16	921,00	1324,24	410,50	271,11	56,55	76,64	51,22	130,40	6,421E-21	4,463E-19
Ifitm1	41,28	53,21	342,09	357,07	817,50	489,24	670,69	476,60	6,467E-21	4,474E-19
Efnb2	3344,57	4256,47	1169,67	1415,05	889,85	1099,83	985,31	812,42	7,185E-21	4,948E-19
Shh	15,59	10,64	901,92	978,64	34,93	302,74	0,81	3,46	7,611E-21	5,216E-19
Epha1	85,31	109,96	717,07	559,41	271,94	263,14	191,86	155,79	8,116E-21	5,537E-19
Tcf7	3712,42	4734,14	2319,61	1970,50	1322,30	1499,65	878,81	1013,22	8,865E-21	6,02E-19
Megf11	2,75	4,73	37,50	75,38	291,90	213,32	141,46	103,86	8,914E-21	6,025E-19
Il1rap	581,59	772,08	162,49	165,31	167,16	183,94	180,48	192,72	1,043E-20	7,02E-19
Hoxd8	1600,74	1975,71	626,94	694,30	88,15	246,54	42,27	88,86	1,077E-20	7,214E-19
Prokr2	7,34	5,91	36,18	92,57	252,82	235,04	260,15	283,88	1,272E-20	8,481E-19
Ptprz1	30,27	37,84	46,71	59,51	93,14	107,30	360,96	265,42	1,291E-20	8,572E-19
Cybrd1	10,09	11,82	25,66	21,16	156,35	84,31	409,73	213,49	1,42E-20	9,382E-19
Kcnd2	0,00	2,36	7,24	13,22	54,06	56,21	121,94	111,94	1,926E-20	1,267E-18
Asic2	81,64	86,31	1,97	2,64	0,83	0,00	0,00	0,00	2,177E-20	1,425E-18
Abca4	35,78	41,38	102,63	132,25	176,31	169,89	346,32	317,35	2,306E-20	1,504E-18
Mpeg1	0,00	0,00	25,66	56,87	119,76	84,31	417,86	165,02	3,212E-20	2,085E-18
Cpm	276,12	204,55	974,29	1110,88	1152,65	1313,16	1257,65	1089,38	3,554E-20	2,287E-18
Ppm1h	24,77	36,65	215,78	182,50	323,51	334,68	299,98	460,45	3,555E-20	2,287E-18
Unc5b	2367,62	2241,74	7354,20	6931,12	10029,52	7859,77	7867,84	8698,88	3,612E-20	2,314E-18
Rnf180	22,93	20,10	36,18	37,03	90,65	67,70	247,95	208,87	3,945E-20	2,509E-18
Card11	0,00	0,00	9,87	9,26	103,12	72,81	61,79	84,24	3,951E-20	2,509E-18
Nkd2	734,78	835,92	2261,06	2725,63	2853,34	3482,16	3314,44	3232,36	3,97E-20	2,51E-18
Col9a1	264,19	197,45	1082,18	731,33	2762,69	1216,07	4522,51	3891,30	4,681E-20	2,947E-18
Celsr2	75,22	91,04	232,22	247,30	367,58	381,94	422,74	426,98	7,884E-20	4,942E-18
Pcsk6	341,25	277,85	628,91	827,87	3180,17	2036,16	7291,45	3002,72	8,802E-20	5,494E-18
Trim62	287,12	273,12	866,40	773,65	1177,60	1000,20	1077,99	1022,45	1,07E-19	6,648E-18
Hsd11b2	682,49	495,41	3054,44	1807,83	621,23	753,66	330,06	339,28	1,281E-19	7,927E-18
Nefl	218,32	131,24	13,82	7,93	11,64	7,66	17,07	12,69	1,338E-19	8,248E-18
Runx1t1	52,29	99,32	19,74	41,00	118,09	113,69	494,28	466,22	1,369E-19	8,402E-18
Cacng4	66,96	89,86	146,70	153,41	797,54	360,22	1050,35	870,12	1,433E-19	8,76E-18
Cx3cr1	5,50	3,55	71,71	133,57	253,65	180,11	459,32	228,49	1,535E-19	9,344E-18
Scube3	3093,23	3318,86	1101,91	864,90	931,43	762,60	1669,01	1523,28	1,561E-19	9,462E-18
Camk1d	17,43	13,01	240,12	222,18	98,96	126,46	95,93	77,32	1,724E-19	1,041E-17
Epb41l2	2244,70	2503,04	4547,78	4943,43	7482,22	6717,79	7878,41	7205,60	2,068E-19	1,243E-17
Nyap1	44,95	53,21	217,75	271,11	328,50	301,46	313,80	362,36	2,14E-19	1,281E-17
Mogat2	4039,91	2408,45	2229,48	1076,50	610,42	503,29	241,45	256,19	2,284E-19	1,362E-17
Parvb	2677,68	2384,81	936,13	777,62	803,36	600,37	659,31	516,99	2,514E-19	1,493E-17
Cxcl12	554,07	332,24	31,58	31,74	21,62	40,88	76,42	33,47	2,644E-19	1,564E-17

Slc35f2	135,76	130,06	652,60	585,86	470,71	510,96	406,48	460,45	2,878E-19	1,696E-17
Kcnh2	456,83	281,40	101,97	79,35	65,70	65,15	40,65	41,54	3,188E-19	1,87E-17
Nebi	159,61	205,73	14,47	6,61	38,26	35,77	12,19	18,46	4,198E-19	2,453E-17
Ssh3	7,34	3,55	32,24	23,80	80,67	63,87	178,04	144,25	5,364E-19	3,122E-17
Kcnq5	138,52	183,26	7,24	3,97	7,48	6,39	16,26	34,62	5,589E-19	3,24E-17
Gdf10	29,35	30,74	34,21	21,16	554,70	154,56	1384,47	580,46	6,236E-19	3,601E-17
Pou6f1	40,36	27,19	48,02	58,19	229,53	114,96	495,91	385,44	8,316E-19	4,783E-17
Dach1	1430,11	1668,30	1074,28	1740,38	4794,38	3383,80	8311,72	7282,92	1,005E-18	5,757E-17
Prdm1	452,24	1055,84	173,67	171,92	64,04	70,26	101,62	107,32	1,018E-18	5,81E-17
Vcam1	591,68	332,24	3194,56	2855,24	2968,94	2856,24	3585,16	3080,04	1,112E-18	6,322E-17
Sox8	534,80	390,18	71,05	62,16	30,77	28,10	195,92	90,01	1,195E-18	6,769E-17
Fgfr2	1154,00	1673,03	140,12	149,44	785,90	398,55	1555,20	1569,45	1,31E-18	7,374E-17
Sox5	243,09	292,04	742,06	736,62	853,26	776,65	1306,43	1892,57	1,312E-18	7,374E-17
Cpa4	115,58	95,77	4,61	7,93	7,48	2,55	0,81	1,15	1,461E-18	8,179E-17
Peg3	38950,62	48297,93	24426,96	17038,84	7188,66	7642,62	11418,05	7098,28	1,484E-18	8,277E-17
Hapln1	1284,26	1206,00	292,75	370,29	206,25	418,98	110,56	135,02	1,493E-18	8,295E-17
Slc26a7	0,92	1,18	0,00	0,00	4,99	3,83	178,85	57,70	1,74E-18	9,632E-17
Adamts17	163,28	122,96	1128,89	855,64	875,71	601,65	1060,10	992,44	1,762E-18	9,714E-17
Stk32b	11,93	14,19	39,47	46,29	152,19	80,48	602,40	249,26	1,821E-18	1,001E-16
Tiam2	88,98	138,34	163,15	165,31	219,55	218,43	1099,12	632,39	1,923E-18	1,052E-16
Pard3b	27,52	33,11	105,92	107,12	119,76	149,45	261,77	281,58	1,943E-18	1,059E-16
Jazf1	13,76	17,74	121,70	195,73	129,74	157,12	357,70	257,34	2,57E-18	1,396E-16
Nexmif	40,36	53,21	159,20	167,96	226,20	254,20	321,93	417,75	2,598E-18	1,405E-16
Rab11fip5	56,87	65,03	288,14	234,08	661,15	388,33	1016,20	624,32	2,605E-18	1,405E-16
Prickle1	645,80	800,45	1373,61	1196,84	1455,36	1235,23	3487,61	2850,39	2,776E-18	1,492E-16
Emx2	264,19	165,53	15,13	6,61	19,96	22,99	14,63	4,62	3,039E-18	1,627E-16
Hbb-bh1	20588,48	12362,68	19844,97	14292,05	5506,26	6759,94	1026,77	1912,18	3,253E-18	1,735E-16
Sema5b	26,60	13,01	38,81	91,25	647,01	353,84	424,37	812,42	3,309E-18	1,758E-16
BC067074	323,82	286,13	806,53	715,46	1177,60	947,82	1808,03	1387,11	3,473E-18	1,833E-16
Lmo7	195,39	280,22	196,70	293,59	1476,15	1099,83	1038,97	1600,60	3,466E-18	1,833E-16
Hmga2	17355,82	21654,79	13474,92	10950,14	3749,01	6514,68	2853,50	3191,97	3,865E-18	2,032E-16
Tnni1	186,22	157,25	13,16	18,51	21,62	11,50	6,50	13,85	4,48E-18	2,347E-16
Bmper	23,85	7,09	15,79	7,93	184,62	83,03	460,14	306,97	5,141E-18	2,684E-16
Slc16a7	16,51	9,46	67,10	67,45	71,52	102,19	226,82	207,72	5,315E-18	2,764E-16
Zic5	269,69	284,95	1067,70	999,80	321,01	479,02	230,07	242,34	5,503E-18	2,852E-16
Epha4	839,35	879,67	8125,21	8646,38	4275,44	8113,97	3463,22	4766,04	5,597E-18	2,891E-16
Prnp	133,93	68,58	394,72	420,55	1035,39	703,84	1183,67	969,36	5,888E-18	3,03E-16
Mamdc2	25,69	33,11	456,55	321,36	65,70	116,24	24,39	49,62	6,781E-18	3,478E-16
Serpine2	1293,43	1055,84	2484,08	2734,89	3826,35	3888,37	3668,90	3562,41	7,274E-18	3,704E-16
Thra	436,65	379,54	1009,81	875,48	1848,73	1301,66	2701,47	2061,05	7,249E-18	3,704E-16
Npr3	284,37	329,88	73,02	55,54	44,91	49,82	34,14	57,70	7,675E-18	3,895E-16
Prrt4	566,91	456,39	94,73	38,35	32,43	52,37	44,71	20,77	8,723E-18	4,412E-16
Thsd7a	25,69	27,19	25,00	31,74	104,79	57,48	486,96	237,72	8,91E-18	4,491E-16
Flrt1	1,83	2,36	41,45	108,44	242,01	323,18	153,65	325,43	9,134E-18	4,588E-16
Adamts1	10,09	13,01	22,37	39,67	103,12	111,13	249,58	165,02	9,874E-18	4,943E-16
Arhgef5	248,60	257,75	833,51	743,23	920,62	803,48	854,42	885,12	1,073E-17	5,355E-16
Aatk	11,01	3,55	18,42	29,09	113,10	86,86	172,35	159,25	1,187E-17	5,903E-16
Myrf	1329,21	1113,78	423,66	432,45	334,32	323,18	199,18	313,89	1,212E-17	6,004E-16
Npm1	72660,54	64135,55	37221,00	36751,74	27419,02	32118,66	22170,28	23781,71	1,269E-17	6,268E-16
Tgm2	414,63	307,41	136,18	108,44	81,50	83,03	56,09	61,16	1,367E-17	6,728E-16

Npnt	122,92	143,06	144,07	111,09	252,82	183,94	1133,27	613,93	1,427E-17	7,001E-16
Ldlrad4	8,26	1,18	8,55	14,55	61,54	42,15	289,41	147,71	1,935E-17	9,463E-16
Tfap2a	90,82	59,12	1045,34	1247,10	744,31	941,44	1960,86	852,81	2,065E-17	1,007E-15
Wt1	113,75	62,66	0,00	1,32	0,00	1,28	0,00	1,15	2,809E-17	1,364E-15
Prkg2	116,50	130,06	2,63	2,64	16,63	15,33	14,63	27,70	3,489E-17	1,689E-15
Col25a1	270,61	283,76	1286,11	1351,58	805,02	1154,76	1601,53	2497,26	4,243E-17	2,047E-15
Islr	42,20	31,92	336,82	214,24	653,67	319,35	1216,19	677,40	4,351E-17	2,093E-15
Unc13b	47,70	56,75	113,15	117,70	192,94	185,22	288,60	343,89	6,466E-17	3,099E-15
Ppat	3927,08	3871,02	2133,44	2108,03	1254,94	1686,15	973,93	1134,39	6,615E-17	3,161E-15
Clstn2	14,68	18,92	148,02	231,43	240,34	376,83	154,46	189,26	6,704E-17	3,193E-15
Rbfox3	18,35	13,01	149,99	166,63	412,49	371,72	164,22	385,44	6,964E-17	3,306E-15
Gja5	164,20	96,95	5,26	1,32	7,48	2,55	6,50	9,23	7,426E-17	3,514E-15
Plekha6	290,79	469,39	13,16	14,55	61,54	29,38	27,64	70,39	7,616E-17	3,592E-15
Pbx3	1118,22	1324,24	497,34	423,19	248,66	286,14	527,61	392,36	1,112E-16	5,209E-15
Eno3	1952,07	1222,55	505,24	339,88	441,60	333,40	263,40	248,11	1,109E-16	5,209E-15
Shroom1	22,02	26,01	78,94	84,64	158,84	118,80	229,26	216,95	1,269E-16	5,927E-15
Lrrn1	64,21	53,21	194,07	121,67	637,86	266,97	1367,40	805,49	1,339E-16	6,236E-15
Tgm3	0,00	2,36	174,33	235,40	14,97	54,93	3,25	9,23	1,368E-16	6,351E-15
Iglon5	98,15	87,49	327,61	298,88	705,23	508,40	1030,02	597,77	1,404E-16	6,497E-15
Patj	192,64	195,09	454,58	445,68	706,06	570,99	1229,20	864,35	1,433E-16	6,609E-15
Kif1a	62,38	44,93	97,36	99,19	404,17	235,04	630,05	402,75	1,489E-16	6,846E-15
Itih5	332,99	380,72	174,33	169,28	66,53	104,75	57,72	55,39	2,042E-16	9,33E-15
Fibin	135,76	74,49	9,21	3,97	24,12	16,61	517,86	168,48	2,039E-16	9,33E-15
Nusap1	1138,40	1015,64	1986,73	2020,75	2952,31	2810,25	2778,70	2846,93	2,074E-16	9,45E-15
Oxct1	1220,04	968,35	3125,49	3102,54	4016,80	3661,00	4767,21	3772,44	2,167E-16	9,84E-15
Tgfbr3	501,78	796,91	336,82	222,18	61,54	117,52	47,96	68,09	2,362E-16	1,07E-14
Kcnmb4	122,92	75,67	190,12	175,89	995,47	438,14	972,30	1139,00	2,558E-16	1,154E-14
Csf1r	16,51	4,73	183,54	202,34	385,05	238,87	830,85	333,51	2,632E-16	1,184E-14
Bcat1	6102,98	5361,97	3597,17	3267,85	2040,83	2585,43	1683,64	1399,81	2,672E-16	1,199E-14
Scrn1	13,76	5,91	8,55	15,87	333,49	81,75	309,74	470,83	2,686E-16	1,201E-14
Mafb	96,32	47,29	210,51	161,34	707,72	378,11	2292,55	919,74	2,955E-16	1,317E-14
Sox13	1375,99	1936,69	667,73	563,38	496,49	392,16	356,08	428,14	3,096E-16	1,376E-14
Nfatc2	21,10	28,38	17,10	22,48	80,67	49,82	239,01	180,02	3,118E-16	1,381E-14
Epb41l3	937,51	792,18	619,70	597,76	1743,11	1213,52	3495,74	2494,96	3,192E-16	1,41E-14
Phactr3	86,23	70,94	546,02	267,14	108,11	130,29	30,08	35,77	3,268E-16	1,44E-14
Angptl2	701,76	668,03	2014,36	1949,34	2943,16	2625,03	3484,35	2391,10	3,511E-16	1,542E-14
Slc27a6	40,36	44,93	299,98	253,92	69,86	104,75	52,03	39,24	4,07E-16	1,782E-14
Abca1	344,91	244,75	407,87	435,10	706,06	549,28	1395,04	1253,25	4,1E-16	1,79E-14
Hbb-bt	27,52	24,83	274,99	333,27	568,01	582,49	1873,06	481,22	4,308E-16	1,875E-14
Fbxl2	128,43	178,54	10,53	17,19	16,63	16,61	31,71	30,00	4,398E-16	1,909E-14
Peli3	31,19	29,56	214,46	257,88	99,80	113,69	79,67	81,93	4,968E-16	2,15E-14
Ptprt	21,10	8,28	324,98	177,21	165,50	121,35	311,36	409,67	5,357E-16	2,311E-14
Rbpms	1105,38	1104,32	724,30	555,44	462,39	439,42	279,66	302,35	5,712E-16	2,457E-14
Wif1	379,77	334,61	243,41	245,98	1314,82	587,60	6545,97	1984,89	5,769E-16	2,474E-14
Metrn	3891,30	2747,79	829,56	591,15	825,81	509,68	861,74	649,70	6,472E-16	2,768E-14
Pam	696,25	774,44	1556,49	1634,59	2173,06	2027,22	2428,32	3195,44	6,936E-16	2,958E-14
Naaa	126,59	115,87	532,87	667,85	164,66	252,92	73,17	114,25	8,375E-16	3,554E-14
Cdh22	4,59	2,36	185,52	122,99	37,42	43,43	21,14	39,24	8,384E-16	3,554E-14
Rtn4r	11,93	13,01	63,81	62,16	202,09	139,24	117,07	153,48	8,62E-16	3,644E-14
Filip1l	151,36	218,74	371,69	486,67	568,84	528,84	1006,45	1470,20	8,8E-16	3,709E-14

Rrad	6,42	11,82	111,18	104,48	165,50	120,07	107,31	110,78	8,861E-16	3,724E-14
Tnc	905,40	728,33	53,94	88,61	155,52	98,36	4775,34	797,42	9,194E-16	3,853E-14
Smarca1	571,49	634,92	1063,76	1199,49	1396,32	1382,13	1978,75	1833,71	1,036E-15	4,331E-14
Ppp1r3b	23,85	24,83	33,55	35,71	60,71	93,25	254,46	185,79	1,078E-15	4,491E-14
Pmepa1	44,03	33,11	127,62	170,60	190,44	162,23	460,14	308,12	1,137E-15	4,723E-14
Chchd4	1650,27	1312,41	872,98	710,17	415,82	556,94	352,83	328,89	1,178E-15	4,88E-14
Sspn	27,52	31,92	57,89	44,96	122,25	84,31	295,92	223,88	1,234E-15	5,098E-14
Hoxc8	78,89	76,85	11,84	7,93	7,48	5,11	0,00	0,00	1,363E-15	5,615E-14
Nfib	37,61	113,51	151,31	301,53	371,74	435,59	1473,90	1332,87	1,896E-15	7,791E-14
Greb1l	753,13	1308,86	277,62	300,20	103,95	182,67	95,93	163,87	2,405E-15	9,855E-14
Reep1	569,66	569,89	123,02	145,47	287,75	238,87	452,82	390,05	2,64E-15	1,079E-13
Neurl1b	1,83	4,73	17,76	31,74	65,70	58,76	108,94	160,41	2,913E-15	1,187E-13
Axl	316,48	217,55	453,26	429,81	1546,84	822,64	2497,42	1676,77	2,942E-15	1,195E-13
Mmp9	94,48	93,41	7,24	2,64	5,82	6,39	5,69	5,77	3,141E-15	1,273E-13
Car4	50,45	88,68	0,66	0,00	0,00	0,00	0,00	0,00	3,159E-15	1,277E-13
Odc1	13364,53	10053,55	5941,78	5982,90	4343,63	5084,01	3267,29	3593,57	3,231E-15	1,302E-13
Calml4	6,42	11,82	103,94	103,15	73,18	102,19	8,94	12,69	3,304E-15	1,328E-13
Podxl	1483,32	1647,02	467,08	361,04	563,85	493,07	631,67	467,37	3,34E-15	1,331E-13
Crabp1	8523,80	6692,12	5673,37	2802,34	1145,16	1124,10	1269,85	661,24	3,338E-15	1,331E-13
Lix1	3702,33	3374,43	4102,41	3583,92	755,12	1742,36	236,57	422,37	3,335E-15	1,331E-13
Noc2l	6367,17	6064,29	3999,78	3700,30	3450,46	3175,59	2316,13	2031,05	3,587E-15	1,426E-13
Kctd12	3470,25	4539,05	603,26	818,62	580,48	1053,85	1325,94	983,21	4,002E-15	1,586E-13
Cacnb3	321,98	276,67	572,34	732,65	1397,15	1081,95	2020,21	1343,26	4,053E-15	1,603E-13
Paqr8	77,97	74,49	192,09	211,60	276,93	241,43	395,91	351,97	4,068E-15	1,604E-13
Sparcl1	192,64	223,46	595,36	407,32	948,90	606,76	1444,63	1315,56	4,499E-15	1,769E-13
Mmp28	25,69	24,83	71,71	56,87	188,78	100,91	292,67	270,04	4,585E-15	1,798E-13
Adgrb2	144,94	98,14	129,60	108,44	505,63	298,91	1491,78	670,48	5,306E-15	2,076E-13
Ltbp1	718,27	444,56	2024,89	3884,13	5912,10	5655,00	5150,11	3945,54	5,734E-15	2,237E-13
Tns3	2916,18	3474,93	4387,26	4065,31	6923,37	6360,12	10511,60	8795,82	6,038E-15	2,349E-13
Mid1ip1	142,19	115,87	716,41	535,60	517,28	486,69	447,94	504,30	6,116E-15	2,373E-13
Irf2bpl	407,29	386,63	1315,06	998,47	1978,46	1333,59	3246,97	2159,14	6,461E-15	2,501E-13
Dgkk	96,32	87,49	661,81	993,18	438,27	708,95	118,69	222,72	6,643E-15	2,564E-13
Gja3	66,05	62,66	630,89	962,77	898,17	1260,78	191,86	489,30	7,075E-15	2,724E-13
Ddit4	633,87	333,42	361,82	341,20	828,31	661,69	1949,48	1994,12	7,698E-15	2,956E-13
Gpc4	299,97	318,05	176,96	167,96	682,77	470,08	1186,11	788,18	8,015E-15	3,069E-13
Arhgef28	123,84	85,13	204,59	178,53	509,79	306,57	720,28	670,48	8,157E-15	3,116E-13
Nfatc1	285,29	359,44	1336,77	953,51	1263,25	1052,57	3310,38	1897,18	8,291E-15	3,159E-13
Dnah1	37,61	44,93	198,67	167,96	272,78	201,83	407,29	286,19	8,781E-15	3,337E-13
Slc16a10	146,77	158,44	249,99	460,22	948,90	1029,58	778,82	1098,61	8,851E-15	3,355E-13
Ndrp2	51,37	14,19	134,86	140,18	341,80	208,21	869,06	577,00	9,512E-15	3,596E-13
Cpa2	2001,61	1447,20	6189,79	6068,86	965,53	2879,23	230,07	380,82	1,015E-14	3,828E-13
Lrrc17	104,58	63,85	86,18	119,02	487,34	311,68	535,74	466,22	1,084E-14	4,075E-13
Plcd1	128,43	80,40	549,31	569,99	383,38	399,82	447,94	408,52	1,145E-14	4,295E-13
Cul9	42,20	49,66	75,00	63,48	133,06	111,13	247,14	261,96	1,484E-14	5,551E-13
Jag1	172,46	180,90	2687,35	4078,53	1416,28	3284,17	474,77	1118,23	1,525E-14	5,693E-13
Lrp11	253,18	164,35	31,58	33,06	40,75	29,38	37,40	28,85	1,544E-14	5,747E-13
Entpd1	34,86	20,10	57,23	71,41	188,78	131,57	491,84	251,57	1,572E-14	5,838E-13
Etv2	100,91	118,24	37,50	17,19	0,00	3,83	1,63	3,46	1,64E-14	6,075E-13
Mras	213,74	184,45	378,27	370,29	621,23	509,68	956,86	743,18	1,667E-14	6,161E-13
Myh15	0,00	2,36	1,97	0,00	23,29	8,94	217,87	71,55	1,734E-14	6,39E-13

Eps8	65,13	83,95	413,14	526,35	495,65	660,41	333,31	521,61	1,781E-14	6,548E-13
Tmem8b	163,28	141,88	296,04	285,66	399,19	325,73	656,06	594,31	1,857E-14	6,809E-13
Asap3	30,27	13,01	52,63	50,25	248,66	121,35	463,39	282,73	1,898E-14	6,942E-13
Zcchc18	66,96	30,74	393,40	330,62	493,16	375,55	791,01	490,45	1,964E-14	7,167E-13
Tgfb2	1382,41	1441,29	291,43	231,43	443,26	228,65	881,25	912,82	2,082E-14	7,577E-13
Adam22	33,94	44,93	46,05	111,09	198,76	176,28	384,53	558,54	2,363E-14	8,579E-13
Slc44a1	424,72	432,74	580,23	749,85	1422,10	1366,81	1360,08	1912,18	2,421E-14	8,768E-13
E2f2	297,21	266,03	556,55	579,25	702,73	743,44	966,61	860,89	2,542E-14	9,186E-13
Spry2	403,62	537,97	1244,01	1457,37	862,41	995,09	415,42	387,75	2,613E-14	9,416E-13
Nfia	40,36	96,95	422,35	1100,30	897,33	1320,82	1741,36	2202,99	2,946E-14	1,059E-12
Mtss1	624,70	891,49	2232,12	2680,67	2693,67	2692,73	2895,77	3350,07	3,131E-14	1,123E-12
Stmn2	15,59	16,55	12,50	38,35	438,27	218,43	60,97	99,24	3,389E-14	1,212E-12
Dars	5022,36	4107,49	2190,01	2199,29	1951,85	2029,77	1802,34	1586,76	3,661E-14	1,307E-12
Rhof	21,10	13,01	102,63	171,92	206,25	252,92	18,70	40,39	3,909E-14	1,392E-12
Ctsc	429,31	432,74	669,04	812,00	1265,75	1067,90	1621,86	1373,26	3,96E-14	1,406E-12
Sgk1	257,77	195,09	98,68	160,02	708,55	390,88	910,52	1100,92	3,991E-14	1,414E-12
Pippr3	584,34	695,22	1465,71	1789,32	1595,91	1654,22	2325,07	2103,75	3,999E-14	1,414E-12
Cdk19	189,89	307,41	526,29	831,84	1305,67	1253,12	1492,60	1982,58	4,109E-14	1,449E-12
Emb	1074,19	1162,25	2288,03	1967,85	836,63	956,76	533,30	691,25	4,764E-14	1,676E-12
Sft2d2	264,19	203,36	451,29	458,90	796,71	625,92	911,33	941,67	5,035E-14	1,767E-12
Tbc1d24	654,05	703,50	1217,70	1210,07	1560,15	1421,73	1899,89	1825,63	5,119E-14	1,792E-12
Palm2	38,53	37,84	55,92	51,58	272,78	139,24	256,90	331,20	5,26E-14	1,837E-12
Cyfp2	650,38	649,11	1518,34	1089,72	2308,62	1527,76	6611,00	3406,62	6,025E-14	2,099E-12
C1ql3	3,67	2,36	3,95	5,29	10,81	5,11	104,06	72,70	6,115E-14	2,126E-12
Mnx1	0,00	0,00	90,78	109,77	6,65	31,93	0,81	0,00	6,151E-14	2,133E-12
Nptx2	238,50	124,15	76,31	35,71	14,14	12,77	8,13	2,31	6,332E-14	2,19E-12
Dtx3l	33,94	44,93	79,60	133,57	197,10	186,50	298,36	323,12	6,358E-14	2,195E-12
Cbfa2t3	173,37	177,35	1051,92	1202,13	576,32	908,22	312,99	489,30	6,835E-14	2,353E-12
Padi3	12,84	13,01	267,75	154,73	51,56	90,69	8,13	21,93	7,064E-14	2,421E-12
Cthrc1	20,18	8,28	6,58	6,61	27,44	19,16	198,36	107,32	7,048E-14	2,421E-12
Tbx2	532,97	430,38	681,54	735,30	1989,27	1415,35	1609,66	1449,43	7,429E-14	2,538E-12
Islr2	0,00	2,36	1,32	0,00	10,81	2,55	162,59	66,93	7,44E-14	2,538E-12
Utp4	3231,74	3168,71	1927,53	1750,96	1359,72	1508,60	1370,65	1282,10	7,733E-14	2,632E-12
Pcdh10	37,61	49,66	167,75	99,19	94,81	98,36	521,11	310,43	7,825E-14	2,657E-12
C3ar1	0,92	0,00	9,21	19,84	44,08	43,43	136,58	71,55	7,853E-14	2,66E-12
Efnb1	998,97	756,71	3985,97	3169,99	4608,92	3325,04	3891,65	3290,06	7,972E-14	2,691E-12
Ccdc106	40,36	24,83	111,84	92,57	181,30	167,34	387,78	242,34	7,981E-14	2,691E-12
Hoxa11	1009,06	614,82	3846,50	2088,20	425,80	876,29	245,51	293,12	8,173E-14	2,75E-12
Kank4	727,44	662,12	3392,58	2223,09	1466,17	1485,60	1080,43	931,28	8,434E-14	2,831E-12
Tspan18	678,82	702,32	1542,02	1978,43	3789,76	3314,82	1917,78	3025,80	8,826E-14	2,956E-12
Tekt2	0,92	3,55	7,89	18,51	62,37	44,71	160,15	92,32	9,062E-14	3,028E-12
Rftn2	166,04	134,79	529,58	484,03	844,94	479,02	1885,26	1044,37	9,275E-14	3,092E-12
Rrp15	1643,85	1683,67	1107,83	1108,24	783,40	867,35	656,06	612,78	9,57E-14	3,183E-12
Stac	10,09	10,64	3,95	5,29	20,79	12,77	182,92	78,47	9,714E-14	3,224E-12
Col12a1	160,53	164,35	136,18	51,58	117,26	34,49	2862,44	732,79	9,766E-14	3,234E-12
Gpm6b	11,93	11,82	128,94	169,28	109,78	176,28	125,20	161,56	9,954E-14	3,289E-12
Fut4	441,23	422,10	77,63	117,70	155,52	183,94	96,74	118,86	1,037E-13	3,417E-12
Gpr156	2,75	8,28	17,10	51,58	229,53	159,67	142,27	223,88	1,096E-13	3,605E-12
Peg10	25086,14	47173,51	12511,82	14003,75	4940,75	9073,29	1801,52	3940,92	1,135E-13	3,725E-12
Col17a1	5,50	10,64	39,47	43,64	258,64	111,13	25,20	18,46	1,144E-13	3,746E-12

Gadd45b	10,09	15,37	19,08	26,45	78,17	85,59	115,44	182,33	1,151E-13	3,759E-12
Shd	66,96	37,84	196,04	264,50	378,39	283,58	398,35	438,52	1,222E-13	3,984E-12
Col2a1	1054,01	655,02	779,56	394,10	2254,56	857,13	10254,70	5171,09	1,312E-13	4,269E-12
Gyg	1685,13	1454,29	765,09	625,53	546,38	568,44	582,08	466,22	1,347E-13	4,371E-12
Slc18b1	158,70	150,16	356,56	409,97	421,64	412,60	572,33	532,00	1,538E-13	4,98E-12
Fbln2	637,54	578,17	1732,14	1411,09	2350,20	1790,90	5354,98	2893,09	1,556E-13	5,027E-12
Pmp22	212,82	238,84	59,87	58,19	280,26	145,62	617,85	461,60	1,587E-13	5,117E-12
Hhip	15,59	20,10	21,71	18,51	61,54	43,43	137,39	151,17	1,81E-13	5,823E-12
Hk2	3772,97	4550,88	2291,32	2283,92	1163,46	1575,02	1470,65	1235,94	1,89E-13	6,066E-12
Klhdc8b	33,94	48,48	82,23	111,09	294,40	175,00	311,36	349,66	1,913E-13	6,128E-12
Nomo1	4168,33	3415,82	2412,37	1961,24	1801,32	1627,39	1215,38	1111,31	1,919E-13	6,132E-12
Chst11	204,56	225,83	189,46	170,60	420,81	352,56	650,37	556,23	1,926E-13	6,142E-12
Syt11	288,96	258,94	630,89	519,73	833,30	729,39	911,33	986,67	1,977E-13	6,292E-12
Pcdhb19	13,76	15,37	62,50	71,41	88,98	60,04	174,79	160,41	2,081E-13	6,606E-12
Kcna6	160,53	151,34	518,39	412,61	564,68	436,87	756,87	658,94	2,108E-13	6,679E-12
Plce1	208,23	308,59	75,65	66,12	170,49	98,36	625,98	460,45	2,186E-13	6,909E-12
Ltbp4	109,16	72,12	230,91	212,92	490,66	291,24	950,35	601,24	2,273E-13	7,169E-12
Plxnbl	1650,27	1605,64	3782,03	4659,10	4178,97	4456,81	4267,24	4813,35	2,279E-13	7,172E-12
Gata4	90,82	85,13	2,63	0,00	2,49	0,00	3,25	0,00	2,287E-13	7,184E-12
Tpbp	278,87	313,32	565,10	655,95	786,73	765,16	947,10	901,28	2,3E-13	7,207E-12
Snai2	240,34	361,80	646,02	771,01	1017,92	1187,97	1403,98	1265,94	2,327E-13	7,278E-12
Ptpcr	1,83	2,36	21,05	35,71	63,20	86,86	81,30	86,55	2,556E-13	7,977E-12
Abca8b	203,65	287,31	28,95	33,06	44,91	49,82	60,97	101,55	2,565E-13	7,988E-12
Ptpdc1	165,12	163,16	275,64	294,91	350,12	375,55	538,99	639,32	2,573E-13	7,995E-12
Tle1	704,51	589,99	2012,39	2003,56	1355,57	1539,25	1577,96	1442,50	2,615E-13	8,11E-12
Cacybp	6085,55	4794,44	2826,82	3035,09	2155,60	2713,17	1650,31	1656,00	2,683E-13	8,303E-12
Pnmal2	51,37	31,92	435,50	240,69	410,83	296,35	589,40	416,60	2,694E-13	8,319E-12
Dctd	2960,21	2443,92	1855,16	1622,68	1185,08	1208,41	984,50	866,66	2,952E-13	9,097E-12
Crmp1	5703,94	4438,55	5204,32	3917,19	2278,68	2470,47	1508,04	1137,85	3,003E-13	9,234E-12
Epha2	272,45	261,30	1625,57	1449,44	613,75	894,17	686,14	422,37	3,24E-13	9,943E-12
Kif26a	1154,91	1254,48	2258,43	2896,23	4269,62	3994,39	3216,08	2719,99	3,408E-13	1,044E-11
Pnck	7,34	1,18	26,97	46,29	87,32	54,93	168,28	140,79	3,646E-13	1,114E-11
Syne2	1331,96	1363,25	3990,57	3626,24	3849,64	3793,84	3220,14	4199,42	3,747E-13	1,143E-11
Pde3a	379,77	398,45	103,28	210,27	1010,44	624,64	1250,34	1224,40	3,773E-13	1,148E-11
Alx3	2385,97	1598,54	850,61	523,70	271,94	255,48	469,08	215,80	3,849E-13	1,169E-11
Ephb2	1614,50	1216,64	4089,91	3956,86	4534,91	4220,49	4454,22	3862,45	3,896E-13	1,181E-11
Trp53i11	268,78	148,98	878,90	882,09	1245,79	1015,52	2012,08	1263,63	3,919E-13	1,185E-11
Tgfb1	652,22	430,38	1232,17	860,93	2694,50	1189,25	5913,48	4174,03	4,025E-13	1,215E-11
Pcyt1b	113,75	146,61	169,73	223,50	700,24	516,06	481,27	733,95	4,056E-13	1,222E-11
Slc16a3	8681,58	4923,32	2457,10	1809,15	1431,24	1471,55	1684,46	1038,60	4,163E-13	1,251E-11
Tfap2c	1437,45	1671,85	1772,27	1590,94	299,39	595,26	91,86	229,65	4,263E-13	1,279E-11
Adora1	1,83	2,36	7,89	17,19	49,07	57,48	82,11	81,93	4,556E-13	1,364E-11
Alcam	959,52	1354,98	102,63	113,73	610,42	323,18	510,54	874,73	4,579E-13	1,368E-11
Hmga1	11075,80	9475,38	6412,81	4622,07	4306,21	3782,35	2603,10	1728,70	4,651E-13	1,386E-11
Tmtc2	260,52	257,75	352,61	528,99	691,09	895,45	1177,98	1083,61	4,666E-13	1,388E-11
Mical1	904,48	792,18	2125,54	2232,35	2620,48	2208,60	1831,60	1758,70	4,944E-13	1,468E-11
Anxa4	40,36	30,74	74,34	80,67	188,78	104,75	456,88	268,88	5,262E-13	1,559E-11
Bves	199,06	205,73	36,84	35,71	54,89	62,59	92,68	110,78	5,335E-13	1,578E-11
Emp2	58,71	52,02	52,63	87,28	281,09	163,51	425,18	331,20	5,45E-13	1,608E-11
Asb4	11570,24	11756,13	21181,08	15659,49	6292,15	9308,33	1934,04	3423,93	5,508E-13	1,622E-11

Smarca2	624,70	632,56	1292,03	1208,75	1630,01	1552,03	2016,15	1644,46	6,089E-13	1,79E-11
Azin2	28,44	21,28	68,42	66,12	128,90	103,47	226,82	170,79	6,482E-13	1,898E-11
Alpk3	59,63	82,76	0,66	1,32	7,48	2,55	2,44	3,46	6,483E-13	1,898E-11
Gpc5	114,67	68,58	38,81	31,74	0,83	6,39	2,44	1,15	6,908E-13	2,018E-11
Agrn	2785,00	3233,73	4085,96	5164,29	6968,27	5786,57	10206,73	9397,05	7,54E-13	2,199E-11
Sp5	62,38	66,21	26,31	17,19	1,66	0,00	2,44	1,15	7,586E-13	2,208E-11
Tmem63a	46,78	22,46	90,78	100,51	211,24	162,23	350,39	265,42	7,802E-13	2,266E-11
Fermt1	12,84	8,28	40,13	34,38	84,83	68,98	2,44	1,15	8,392E-13	2,433E-11
Rarres2	73,39	44,93	1,32	1,32	1,66	0,00	0,81	1,15	8,543E-13	2,472E-11
Itga8	233,92	170,26	620,36	760,43	1278,22	901,84	944,66	1425,19	9,397E-13	2,713E-11
Cpq	45,87	39,02	132,89	120,35	199,59	139,24	652,00	296,58	9,493E-13	2,736E-11
Rusc2	77,97	65,03	152,62	132,25	265,29	213,32	386,97	315,04	9,589E-13	2,758E-11
C1qb	4,59	3,55	58,55	85,96	162,17	86,86	355,26	125,79	1,004E-12	2,882E-11
Eya4	131,18	204,55	21,05	31,74	30,77	38,32	139,83	155,79	1,044E-12	2,991E-11
Tbc1d4	724,69	885,58	303,27	302,85	291,07	327,01	341,44	336,97	1,059E-12	3,029E-11
Abat	481,60	429,19	815,74	686,37	1631,67	1010,41	2268,98	1874,10	1,106E-12	3,157E-11
Rps6ka6	5766,32	6318,49	2336,71	2783,82	1992,60	2641,64	1685,27	2125,67	1,133E-12	3,222E-11
Gpr155	18,35	27,19	31,58	72,74	207,08	196,72	195,11	214,64	1,132E-12	3,222E-11
Col6a3	232,08	228,19	592,73	509,16	878,21	659,13	3282,74	1229,01	1,157E-12	3,282E-11
Tenm2	16,51	8,28	10,53	6,61	34,10	25,55	445,50	91,17	1,178E-12	3,336E-11
Cdh6	817,34	989,63	215,78	160,02	256,14	260,59	630,05	388,90	1,212E-12	3,425E-11
Hoxd3	172,46	461,12	28,95	68,77	2,49	21,72	2,44	4,62	1,227E-12	3,462E-11
Ssbp2	576,08	581,72	945,34	891,35	1715,66	1269,72	1891,76	1749,47	1,24E-12	3,49E-11
Rab11fip4	405,46	523,78	947,32	1141,30	1287,37	1402,57	1613,73	1531,36	1,256E-12	3,531E-11
Parp9	16,51	21,28	51,31	66,12	114,77	108,58	141,46	159,25	1,274E-12	3,574E-11
Nckap1l	1,83	4,73	51,31	91,25	118,92	99,64	211,37	96,94	1,375E-12	3,849E-11
Actc1	55,04	69,76	2,63	5,29	1,66	1,28	1,63	0,00	1,402E-12	3,918E-11
Sv2b	0,00	1,18	184,20	375,58	35,76	217,16	12,19	30,00	1,423E-12	3,969E-11
Csf1	63,30	69,76	176,31	214,24	323,51	269,53	280,47	261,96	1,485E-12	4,132E-11
Vill	70,63	48,48	278,27	269,79	319,35	228,65	316,24	333,51	1,561E-12	4,321E-11
Bcor	1632,84	1791,26	3494,55	3492,67	4063,37	3636,73	4099,77	4104,79	1,56E-12	4,321E-11
Pid1	12,84	13,01	26,97	60,83	237,02	122,63	176,41	252,73	1,556E-12	4,321E-11
Tspan11	48,62	18,92	117,76	111,09	485,68	195,44	922,71	478,91	1,605E-12	4,433E-11
Slc35f1	30,27	29,56	49,34	33,06	130,57	91,97	225,19	181,18	1,707E-12	4,707E-11
Msx2	729,27	569,89	826,93	489,32	2480,77	1117,71	6642,71	3480,48	1,764E-12	4,855E-11
Maml2	128,43	222,28	95,39	111,09	237,85	173,72	543,06	656,63	1,782E-12	4,895E-11
Sfxn3	92,65	89,86	163,81	167,96	378,39	237,59	597,53	429,29	1,843E-12	5,044E-11
Sall1	601,77	1075,94	8395,59	6995,92	1723,98	3496,21	2553,51	1684,85	1,843E-12	5,044E-11
Cygb	411,88	267,21	176,31	150,76	54,89	60,04	73,17	39,24	1,854E-12	5,065E-11
Hey1	538,47	407,91	3119,57	3401,42	1843,74	2922,66	677,20	1328,26	1,885E-12	5,139E-11
F13a1	11,01	4,73	83,55	138,86	173,81	112,41	239,82	141,94	2,184E-12	5,942E-11
Cerk	508,20	468,21	1015,73	974,67	1241,63	1204,58	1135,71	1208,24	2,188E-12	5,944E-11
Tbx4	25,69	16,55	200,65	252,59	123,91	195,44	273,97	171,95	2,43E-12	6,589E-11
Dpysl5	125,67	126,51	335,51	244,66	545,55	417,71	794,26	552,77	2,48E-12	6,712E-11
Adgre1	0,92	0,00	16,45	38,35	64,04	43,43	200,80	77,32	2,515E-12	6,793E-11
Mapk12	539,39	456,39	378,27	456,26	187,95	245,26	72,35	116,55	2,546E-12	6,864E-11
Rtl1	96,32	89,86	6,58	0,00	0,83	3,83	0,81	0,00	2,627E-12	7,071E-11
Dnmbp	785,23	880,85	1207,17	1526,14	2485,76	2239,26	2331,57	2964,64	2,651E-12	7,121E-11
Mpzl3	236,67	199,82	57,23	66,12	65,70	74,09	49,59	48,47	2,737E-12	7,339E-11
Smpd5	7,34	4,73	25,00	26,45	73,18	72,81	88,61	78,47	2,812E-12	7,527E-11

St6galnac2	11,01	8,28	34,21	42,32	98,96	76,64	105,69	113,09	2,88E-12	7,696E-11
Ano1	128,43	201,00	226,30	228,79	33,27	63,87	28,45	16,16	2,967E-12	7,913E-11
H1f0	4206,86	4210,36	6848,97	8578,93	11711,92	10220,39	11203,43	12634,03	3,013E-12	8,021E-11
Zfp467	204,56	210,46	473,00	423,19	578,82	441,98	872,31	740,87	3,04E-12	8,077E-11
Il17d	0,00	2,36	10,53	10,58	70,69	45,99	81,30	51,93	3,362E-12	8,918E-11
Adamts7	224,75	219,92	353,27	317,40	528,92	433,03	1039,78	727,02	3,381E-12	8,951E-11
Ankrd29	42,20	39,02	51,31	63,48	102,29	106,02	294,29	190,41	3,481E-12	9,201E-11
Zfhx4	1604,40	2240,56	1189,41	956,15	1383,84	1242,90	3655,89	3398,54	3,623E-12	9,557E-11
Epha7	675,15	909,23	281,56	220,85	144,70	186,50	457,70	327,74	3,72E-12	9,796E-11
Frzb	1134,73	735,42	4304,37	3864,29	1257,43	2633,98	88,61	302,35	3,939E-12	1,035E-10
Myof	9,17	22,46	16,45	17,19	79,84	44,71	234,13	141,94	3,952E-12	1,037E-10
Tmem28	394,45	478,85	136,18	85,96	103,95	100,91	157,71	120,02	4,005E-12	1,049E-10
Lhx1	54,12	72,12	15,79	15,87	14,14	17,88	0,00	0,00	4,069E-12	1,064E-10
S1pr3	1511,75	1379,81	1167,70	1048,73	2688,68	1817,72	5873,65	3700,89	4,167E-12	1,088E-10
Ybx2	20,18	20,10	96,05	142,83	158,84	135,40	149,58	189,26	4,197E-12	1,094E-10
Arid3b	1475,98	1545,34	3261,01	2377,82	726,85	1191,80	188,61	415,44	4,348E-12	1,131E-10
Frmf5	27,52	23,65	38,81	64,80	135,56	98,36	186,17	267,73	4,512E-12	1,171E-10
Hand2	1156,75	846,56	4007,68	3058,90	2854,17	2972,48	1758,44	1908,72	4,667E-12	1,209E-10
Gria3	90,82	156,07	11,18	9,26	14,97	19,16	67,48	55,39	4,904E-12	1,269E-10
Lgr4	610,94	852,48	298,67	436,42	432,45	537,78	1621,05	1427,50	5,002E-12	1,292E-10
Tcf15	91,73	101,68	23,03	18,51	12,47	11,50	8,13	10,39	5,219E-12	1,345E-10
Pde7b	22,02	36,65	25,66	13,22	103,95	56,21	195,11	237,72	5,595E-12	1,44E-10
Afdn	3067,54	4189,08	1850,56	1851,47	1352,24	1571,19	944,66	1197,86	5,751E-12	1,477E-10
Slco2a1	0,00	0,00	8,55	2,64	38,26	26,83	122,76	50,78	5,88E-12	1,508E-10
Nlgn2	552,23	663,30	671,67	862,26	1350,58	1108,77	1881,19	1919,11	5,97E-12	1,528E-10
Mn1	246,76	336,97	114,47	107,12	138,88	187,78	488,59	453,52	6,634E-12	1,695E-10
Wdr77	5113,18	5159,79	3224,82	3314,14	2161,42	2779,60	1885,26	1957,19	6,755E-12	1,723E-10
Grina	174,29	108,78	598,65	550,15	945,57	606,76	1166,60	793,95	6,78E-12	1,727E-10
Myliip	111,91	218,74	353,27	427,16	326,00	463,69	1186,92	994,75	7,356E-12	1,87E-10
Daam1	486,18	630,19	634,83	608,34	992,14	742,16	1651,94	1812,94	7,731E-12	1,962E-10
Lyar	3052,86	3292,85	2093,96	2112,00	1753,92	1815,17	1102,38	1316,72	8,274E-12	2,096E-10
Samd12	13,76	8,28	8,55	18,51	182,13	139,24	82,11	267,73	9,275E-12	2,346E-10
Zfhx2	210,07	230,56	654,57	476,09	1038,71	664,24	1140,59	1027,06	9,783E-12	2,47E-10
Trpm4	46,78	43,75	120,39	117,70	177,14	136,68	283,72	226,18	1,025E-11	2,584E-10
Gprn3	0,92	2,36	5,92	10,58	18,30	25,55	85,36	66,93	1,036E-11	2,607E-10
Pik3ip1	7,34	14,19	83,55	70,09	170,49	86,86	164,22	165,02	1,039E-11	2,609E-10
Ipo5	20839,83	19837,52	13017,05	12128,47	11494,87	11520,77	9690,50	9265,50	1,057E-11	2,651E-10
Popdc2	117,42	80,40	3,29	11,90	4,16	5,11	1,63	5,77	1,078E-11	2,698E-10
P3h2	400,87	422,10	185,52	175,89	128,07	123,91	199,18	175,41	1,106E-11	2,764E-10
Atad3a	3306,05	3029,19	2116,33	1828,99	1774,71	1684,88	1208,06	1276,33	1,13E-11	2,819E-10
BC052040	702,67	588,81	331,56	226,14	198,76	233,76	173,97	165,02	1,16E-11	2,889E-10
Dsc3	3,67	0,00	4,61	13,22	182,13	80,48	65,85	191,56	1,176E-11	2,924E-10
Mmp11	197,23	144,25	267,75	207,63	670,30	335,95	1501,54	882,81	1,26E-11	3,126E-10
Nckap5	11,01	7,09	19,74	33,06	48,23	63,87	151,21	110,78	1,297E-11	3,213E-10
Rasgrp3	656,81	643,20	242,09	227,47	303,55	327,01	239,82	290,81	1,361E-11	3,366E-10
P3h3	340,33	413,82	780,88	956,15	979,67	966,98	1156,03	1186,32	1,378E-11	3,404E-10
Plk2	1910,79	2737,15	601,28	694,30	806,69	794,54	2064,92	1422,89	1,466E-11	3,614E-10
Pitx2	111,00	95,77	2,63	18,51	1,66	0,00	1,63	0,00	1,472E-11	3,622E-10
Ebf2	104,58	105,23	21,05	17,19	11,64	15,33	12,19	17,31	1,668E-11	4,097E-10
Slc8a1	456,83	474,12	125,65	124,31	387,54	204,38	907,27	663,55	1,697E-11	4,162E-10

Nfic	288,04	243,56	786,14	536,93	1135,18	726,83	2012,08	1328,26	1,715E-11	4,2E-10
Fam163a	13,76	10,64	5,92	17,19	50,73	30,66	201,61	115,40	1,83E-11	4,465E-10
Fam13a	46,78	28,38	107,23	112,41	195,43	152,01	230,07	234,26	1,827E-11	4,465E-10
Hoxa10	1012,73	886,76	3609,67	4676,29	2479,11	3858,99	2565,71	2711,91	1,863E-11	4,54E-10
Chrdl1	22,93	28,38	140,78	112,41	210,40	231,21	142,27	258,50	1,877E-11	4,566E-10
Pla2g4a	112,83	120,60	153,28	193,08	413,32	256,76	507,29	553,92	1,891E-11	4,591E-10
Rgs5	36,69	40,20	180,91	120,35	29,11	45,99	12,19	16,16	1,94E-11	4,702E-10
Rnf150	608,19	760,25	203,94	185,15	266,95	263,14	491,03	371,59	1,95E-11	4,72E-10
Gpr153	87,15	75,67	137,49	104,48	324,34	198,00	523,55	379,67	1,976E-11	4,774E-10
Rdh10	839,35	919,87	84,86	149,44	192,94	228,65	828,41	376,21	2,016E-11	4,864E-10
Trmt61a	780,65	822,92	508,52	505,19	412,49	448,36	234,13	288,50	2,023E-11	4,872E-10
Coro1a	110,08	63,85	517,08	425,84	676,95	510,96	758,49	454,68	2,03E-11	4,88E-10
Ptgrn	2027,29	1836,19	2741,30	3062,87	4280,43	3768,30	5237,10	4682,95	2,182E-11	5,239E-10
Syn2	2,75	2,36	2,63	11,90	95,64	71,53	55,28	105,01	2,244E-11	5,378E-10
Crispld2	83,48	49,66	88,81	100,51	447,42	235,04	359,33	398,13	2,42E-11	5,791E-10
Cluh	4111,46	4375,89	3156,41	2896,23	2278,68	2384,88	1671,45	1887,95	2,549E-11	6,089E-10
Snx5	9761,27	9429,26	3888,60	4680,26	3218,43	4441,48	2753,50	3458,55	2,583E-11	6,161E-10
Cdc42ep1	1242,98	1285,22	693,38	488,00	398,35	311,68	405,67	272,34	2,665E-11	6,345E-10
Tapbp	74,30	88,68	161,18	238,05	385,88	255,48	512,17	437,37	2,981E-11	7,086E-10
Zfpn1	999,89	1065,30	535,50	333,27	301,05	264,42	297,54	198,49	3,001E-11	7,123E-10
Mthfd1l	5440,67	3937,23	2398,55	2093,49	1832,92	1514,98	1541,38	1113,61	3,088E-11	7,318E-10
Mgp	0,92	0,00	7,24	3,97	37,42	26,83	71,54	47,31	3,209E-11	7,591E-10
Trpm5	0,00	0,00	2,63	5,29	11,64	10,22	95,12	40,39	3,274E-11	7,734E-10
Fam169b	1,83	0,00	42,10	78,03	61,54	75,37	37,40	39,24	3,28E-11	7,735E-10
Plppr1	26,60	22,46	47,37	55,54	117,26	120,07	140,64	130,40	3,61E-11	8,5E-10
Trpm1	129,34	95,77	26,31	22,48	14,14	8,94	19,51	20,77	3,769E-11	8,861E-10
D630003M2	28,44	8,28	139,47	91,25	491,50	152,01	747,11	445,45	3,921E-11	9,202E-10
Riox2	918,24	910,41	502,60	501,22	456,57	421,54	389,41	351,97	4,028E-11	9,439E-10
Mef2c	341,25	378,35	226,96	313,43	391,70	351,28	1538,94	845,88	4,19E-11	9,802E-10
Zim1	420,14	986,08	99,99	226,14	56,55	95,80	32,52	73,86	4,206E-11	9,824E-10
Plcl2	1098,96	1252,11	934,16	862,26	415,82	572,27	400,79	407,36	4,238E-11	9,882E-10
Dach2	125,67	133,61	60,52	56,87	68,19	66,42	291,04	206,57	4,368E-11	1,017E-09
Lhfp	526,55	433,92	123,68	149,44	282,76	249,09	1051,16	545,84	4,377E-11	1,017E-09
Tbx18	596,26	775,62	338,14	576,60	1098,59	1260,78	1868,19	2066,82	4,548E-11	1,056E-09
Creb3l2	898,06	1126,78	1304,53	1173,04	2031,69	1567,36	3590,85	2835,39	4,61E-11	1,068E-09
Ypel5	100,91	88,68	178,94	207,63	239,51	227,38	381,28	341,59	4,964E-11	1,148E-09
Tox	18,35	11,82	50,66	46,29	66,53	43,43	174,79	136,17	5,022E-11	1,16E-09
Wdr12	1961,24	2080,94	1144,02	1153,20	874,88	1085,78	758,49	815,88	5,055E-11	1,166E-09
Slc6a8	395,37	418,55	780,22	798,78	1036,22	875,01	1188,55	1066,30	5,214E-11	1,201E-09
Gpm6a	9,17	13,01	9,87	21,16	19,13	21,72	213,81	88,86	5,331E-11	1,226E-09
Hmgcs2	0,00	0,00	1,97	5,29	20,79	14,05	53,66	57,70	5,363E-11	1,231E-09
Enpp5	20,18	11,82	36,84	42,32	85,66	65,15	136,58	141,94	5,5E-11	1,261E-09
Rrs1	2015,37	2324,51	1770,30	1452,08	978,00	1106,22	834,10	745,49	5,527E-11	1,265E-09
Tagln	279,78	156,07	24,34	17,19	34,10	15,33	44,71	20,77	5,769E-11	1,318E-09
Sema4d	207,32	251,84	736,14	790,84	502,31	608,04	447,94	491,61	5,948E-11	1,357E-09
Apc2	11,93	3,55	82,89	39,67	229,53	111,13	301,61	168,48	6,14E-11	1,398E-09
Clmp	1176,01	1357,34	2467,63	2733,57	3072,89	3148,76	2816,10	3196,59	6,394E-11	1,453E-09
Tbc1d8b	18,35	34,29	72,36	126,96	129,74	217,16	269,90	336,97	6,399E-11	1,453E-09
Lrrn4	94,48	78,04	6,58	6,61	7,48	14,05	14,63	11,54	6,478E-11	1,469E-09
Nhs1	565,07	729,51	1167,04	1155,85	1136,01	1076,84	1886,07	1832,56	6,822E-11	1,544E-09

Eogt	689,83	747,25	2848,53	3226,85	850,76	1788,34	403,23	661,24	7,146E-11	1,615E-09
Foxp1	396,29	501,32	187,49	170,60	243,67	305,30	578,02	665,86	7,279E-11	1,643E-09
Rsl1d1	7754,16	8061,28	4893,81	4827,05	3531,96	4175,78	2568,96	3277,37	7,383E-11	1,661E-09
Gja4	317,40	143,06	31,58	15,87	38,26	15,33	25,20	20,77	7,376E-11	1,661E-09
Disp1	1605,32	1840,92	1202,57	957,48	644,52	675,74	768,25	716,64	7,537E-11	1,693E-09
Mthfd2	2734,55	2631,92	1957,79	1949,34	1200,88	1563,52	1027,58	964,75	8,162E-11	1,83E-09
Synpo	691,66	484,76	1251,25	764,39	1904,45	1122,82	5059,87	2904,63	8,226E-11	1,842E-09
Wipi1	396,29	547,43	1510,44	1583,01	849,93	943,99	1016,20	1110,15	8,283E-11	1,852E-09
Ddx21	10816,20	13711,75	7629,85	7039,56	5333,28	6164,68	4506,25	4846,82	8,53E-11	1,904E-09
Fhdc1	5,50	13,01	17,10	25,13	140,55	42,15	184,54	211,18	8,592E-11	1,915E-09
Slc16a12	66,05	78,04	5,92	5,29	8,32	11,50	0,81	4,62	8,726E-11	1,942E-09
Nxph3	26,60	5,91	27,63	34,38	272,78	111,13	243,89	258,50	8,786E-11	1,953E-09
Pdzrn3	776,06	974,26	431,56	215,56	181,30	218,43	186,17	210,03	9,168E-11	2,034E-09
Dopey2	99,99	65,03	199,33	197,05	360,10	233,76	535,74	422,37	9,368E-11	2,076E-09
Gsn	87,15	82,76	744,70	1461,34	1589,26	1894,37	3371,35	790,49	9,543E-11	2,111E-09
Bgn	369,68	316,87	2378,16	1446,79	1826,27	1378,30	3908,72	1862,56	9,606E-11	2,122E-09
Dnaaf3	36,69	31,92	167,10	203,66	153,85	130,29	129,26	137,33	9,629E-11	2,124E-09
Fcrls	5,50	0,00	19,08	46,29	166,33	65,15	522,73	137,33	9,712E-11	2,139E-09
Thbs3	105,49	134,79	262,49	367,65	335,15	399,82	553,63	511,22	9,956E-11	2,189E-09
Hif3a	379,77	281,40	863,11	685,04	1497,78	822,64	2128,33	1683,69	1,004E-10	2,204E-09
Gal	39,45	95,77	3,29	0,00	1,66	1,28	0,00	1,15	1,031E-10	2,26E-09
Atp1a2	2,75	5,91	111,84	55,54	71,52	38,32	139,83	120,02	1,053E-10	2,306E-09
Pitrm1	5284,72	5184,62	6533,20	7028,98	7534,62	8787,16	2355,15	3164,28	1,107E-10	2,419E-09
Pygo1	575,16	682,22	968,37	1161,14	1331,45	1350,20	1709,66	1779,47	1,113E-10	2,429E-09
Fgfr3	48,62	95,77	55,92	104,48	360,93	296,35	360,96	763,95	1,168E-10	2,545E-09
Tubb6	2792,34	1788,90	1029,55	741,91	789,22	652,75	549,56	326,58	1,196E-10	2,603E-09
Oplah	61,46	43,75	118,41	107,12	362,59	166,06	435,75	363,51	1,206E-10	2,62E-09
Erc2	40,36	55,57	61,18	59,51	136,39	129,02	233,32	185,79	1,228E-10	2,664E-09
Cmpk2	30,27	37,84	63,15	50,25	191,28	97,08	468,27	215,80	1,244E-10	2,696E-09
Astn1	135,76	85,13	147,36	158,70	462,39	227,38	1087,74	571,23	1,252E-10	2,708E-09
Nr2f2	1130,15	1887,04	352,61	337,23	352,61	443,25	642,24	387,75	1,29E-10	2,787E-09
Alx4	2365,79	2510,13	1517,02	1026,24	370,91	456,03	956,04	456,99	1,312E-10	2,83E-09
1110032F0	121,09	132,42	20,39	18,51	37,42	28,10	20,32	28,85	1,316E-10	2,834E-09
Masp1	94,48	60,30	33,55	87,28	314,36	272,08	453,63	362,36	1,376E-10	2,959E-09
Lgals7	0,00	0,00	2,63	1,32	19,96	11,50	122,76	32,31	1,384E-10	2,973E-09
Ddx39	6333,22	4829,91	3643,22	3266,53	2903,24	2875,40	2080,37	1875,26	1,423E-10	3,05E-09
Pgk1	14761,62	10637,63	7235,79	5111,39	3999,33	3738,92	4227,40	2874,62	1,424E-10	3,05E-09
Ngfr	1448,46	1279,31	296,04	543,54	2712,79	1693,82	3533,94	2276,85	1,504E-10	3,216E-09
Ak4	1563,12	2091,58	339,46	610,99	206,25	459,86	120,32	270,04	1,52E-10	3,245E-09
Smyd5	2944,62	2629,55	2339,35	1789,32	1555,99	1378,30	999,94	880,50	1,565E-10	3,337E-09
Dpep1	136,68	75,67	10,53	14,55	4,99	1,28	8,94	1,15	1,58E-10	3,364E-09
Gap43	1344,80	1275,76	953,90	641,40	439,94	357,67	343,88	188,10	1,597E-10	3,396E-09
Tbrg4	2260,29	2401,36	1759,11	1555,24	1257,43	1382,13	878,81	982,06	1,621E-10	3,44E-09
Gstt1	4,59	3,55	15,13	6,61	57,38	19,16	222,75	90,01	1,671E-10	3,537E-09
Slitrk2	5,50	1,18	2,63	10,58	115,60	38,32	111,38	137,33	1,67E-10	3,537E-09
Smox	247,68	184,45	630,89	644,05	898,17	659,13	1130,02	796,26	1,677E-10	3,539E-09
Rnf152	11,01	22,46	13,16	21,16	97,30	70,26	110,56	255,03	1,676E-10	3,539E-09
Rorc	3,67	1,18	0,66	1,32	18,30	7,66	68,29	57,70	1,684E-10	3,55E-09
Pabpc4	7382,65	6066,65	3518,23	3077,41	3051,27	2679,96	2797,40	2171,84	1,694E-10	3,564E-09
Cpox	1111,80	1042,84	674,31	780,26	410,83	554,39	352,83	364,67	1,712E-10	3,599E-09

Bnip3	1941,98	1156,34	470,37	490,64	370,91	540,34	397,54	482,37	1,726E-10	3,622E-09
Mgat3	444,90	507,23	729,57	843,74	1177,60	1071,73	1305,62	1187,47	1,77E-10	3,708E-09
Ap1p1	84,39	39,02	239,46	201,02	656,16	279,75	994,25	590,85	1,844E-10	3,859E-09
Hsp90aa1	34326,37	29902,88	23826,99	17548,00	15133,27	17455,51	10833,53	10693,00	1,856E-10	3,877E-09
Cux1	710,93	1051,11	1770,30	2065,71	2946,48	2817,92	2558,39	2962,33	1,945E-10	4,059E-09
Smim14	145,85	102,86	226,30	211,60	394,20	281,03	723,54	497,38	1,98E-10	4,126E-09
Slc22a23	200,89	204,55	122,36	107,12	244,50	218,43	386,16	385,44	1,996E-10	4,152E-09
Aff2	397,20	457,57	1369,66	1089,72	957,21	1025,74	1022,71	1024,76	2,023E-10	4,204E-09
Dnase2a	27,52	21,28	101,31	78,03	133,06	108,58	175,60	152,33	2,092E-10	4,34E-09
Col24a1	56,87	102,86	52,63	93,90	118,09	93,25	1573,89	283,88	2,095E-10	4,34E-09
P4ha3	0,00	0,00	7,24	23,80	54,06	34,49	102,43	58,85	2,145E-10	4,438E-09
Cdc42ep3	97,24	68,58	292,75	559,41	729,34	871,18	430,87	867,81	2,149E-10	4,44E-09
Dnmt3a	3720,68	2597,63	9746,18	8224,51	10531,83	8879,13	9382,39	10286,79	2,154E-10	4,443E-09
Ctso	11,93	10,64	34,87	50,25	68,19	84,31	104,87	123,48	2,167E-10	4,464E-09
Itpr3	475,18	578,17	1522,29	1403,15	928,11	854,57	918,65	987,83	2,174E-10	4,472E-09
Fam131b	109,16	100,50	396,03	368,97	256,14	305,30	231,69	193,87	2,211E-10	4,542E-09
Dnmt3b	1468,64	1437,74	2124,23	1847,51	1082,79	1173,92	573,14	760,49	2,247E-10	4,609E-09
Tcp11l2	18,35	15,37	23,68	22,48	150,53	44,71	186,98	236,57	2,277E-10	4,665E-09
Caln1	4,59	4,73	2,63	11,90	32,43	45,99	119,51	80,78	2,429E-10	4,97E-09
Ackr3	136,68	108,78	52,63	80,67	211,24	183,94	665,82	312,74	2,46E-10	5,026E-09
Slc7a1	2034,63	2164,89	1234,14	1204,78	1074,47	1116,44	851,98	988,98	2,549E-10	5,201E-09
Lrba	470,59	431,56	1067,05	1196,84	1620,86	1752,58	866,62	1313,26	2,693E-10	5,486E-09
Cyp4v3	8,26	4,73	10,53	10,58	40,75	25,55	101,62	76,16	2,893E-10	5,885E-09
Pdcd4	555,90	542,70	713,12	681,08	1012,93	835,41	1331,63	1535,98	2,911E-10	5,915E-09
Mpped2	422,89	362,98	524,97	498,58	906,48	697,45	2018,58	1169,01	2,95E-10	5,985E-09
Pth1r	660,48	470,58	536,15	466,84	1564,31	932,49	2625,87	1713,70	2,977E-10	6,032E-09
Nap1l1	26383,24	25908,90	13386,77	14680,86	12417,98	14917,34	11500,97	12279,75	3,135E-10	6,343E-09
Cacna2d3	13,76	5,91	15,13	25,13	63,20	66,42	100,81	109,63	3,319E-10	6,707E-09
Rcc1	5887,40	5229,55	4047,81	3573,34	3223,42	3165,37	2422,63	2392,25	3,329E-10	6,716E-09
Bambi	1111,80	968,35	1086,12	1124,11	1812,97	1400,02	3201,44	2483,42	3,434E-10	6,919E-09
Chst3	203,65	211,64	326,96	361,04	373,40	439,42	649,56	595,47	3,47E-10	6,981E-09
Met	660,48	281,40	40,79	70,09	74,02	140,51	85,36	71,55	3,525E-10	7,083E-09
Drp2	41,28	48,48	143,41	194,40	117,26	132,85	221,94	222,72	3,605E-10	7,234E-09
Glis1	49,54	46,11	73,02	68,77	315,19	141,79	276,41	289,65	3,623E-10	7,261E-09
Syndig1	0,00	1,18	16,45	10,58	57,38	28,10	117,88	50,78	3,675E-10	7,353E-09
4930402H2	307,30	292,04	451,29	603,05	755,96	703,84	891,82	1132,08	3,684E-10	7,363E-09
Smarcc2	1542,03	1822,01	3324,82	3386,87	4503,31	3554,97	4609,49	4404,83	3,832E-10	7,648E-09
Gstm7	76,14	47,29	261,83	166,63	495,65	245,26	837,35	482,37	4,004E-10	7,979E-09
Trpm3	7,34	3,55	22,37	37,03	34,93	56,21	90,24	205,41	4,158E-10	8,264E-09
Nav2	126,59	205,73	703,25	786,88	485,68	639,97	444,69	474,30	4,153E-10	8,264E-09
Srm	6423,12	5043,92	3335,34	2504,78	2345,21	2180,50	1955,99	1367,49	4,378E-10	8,689E-09
Pus1	1310,86	1196,54	977,58	854,32	706,06	752,38	505,66	480,07	4,484E-10	8,888E-09
Cav1	138,52	85,13	145,39	185,15	376,73	269,53	881,25	474,30	4,701E-10	9,305E-09
Irs2	560,49	565,16	1846,61	1502,34	1428,75	1406,40	2542,13	1643,30	4,825E-10	9,538E-09
Grik5	446,74	569,89	892,06	876,80	1383,84	1101,11	1494,22	1473,66	5,028E-10	9,926E-09
Hspa5	25871,37	24084,53	20419,94	16316,77	10208,32	11016,20	11660,31	9237,80	5,055E-10	9,965E-09
Mxd4	462,33	347,61	776,93	662,56	1815,46	937,60	1893,39	2024,12	5,071E-10	9,971E-09
Bmf	346,75	160,80	492,74	259,21	1638,32	680,85	2047,85	2543,42	5,064E-10	9,971E-09
Tmem176b	143,10	111,14	531,55	365,00	1054,51	459,86	1990,13	918,59	5,097E-10	1,001E-08
Myo1f	2,75	1,18	31,58	39,67	64,04	29,38	117,07	73,86	5,135E-10	1,007E-08

Ftsj3	4953,56	5137,32	3730,72	3177,92	2759,37	2902,23	2265,72	2132,60	5,392E-10	1,055E-08
Adamts9	499,03	573,44	167,75	165,31	348,46	212,05	931,65	612,78	5,409E-10	1,055E-08
Sema3d	43,11	21,28	26,31	19,84	210,40	44,71	336,57	432,75	5,401E-10	1,055E-08
Klh5	473,34	549,79	293,41	314,75	1215,02	685,96	1177,98	1867,18	5,407E-10	1,055E-08
Pdzd4	133,01	148,98	140,78	174,57	360,10	247,81	537,37	446,60	5,569E-10	1,085E-08
Atp2a2	12924,22	13490,65	10067,21	9931,83	5763,23	7355,20	5704,55	5894,65	5,59E-10	1,087E-08
Mak16	2475,87	2475,85	1689,38	1552,59	1034,55	1334,87	864,18	1002,83	5,682E-10	1,104E-08
Ddx18	3205,14	3167,52	2364,34	2008,85	1578,44	1894,37	1286,92	1195,55	5,763E-10	1,118E-08
Txnip	449,49	536,79	788,77	739,27	591,29	956,76	1702,34	1836,02	5,915E-10	1,146E-08
Phlda1	429,31	326,33	348,67	272,43	129,74	145,62	124,38	109,63	5,938E-10	1,149E-08
Ctss	0,92	0,00	9,87	38,35	51,56	39,60	159,34	72,70	6,028E-10	1,165E-08
Sned1	29,35	88,68	97,36	355,75	758,45	703,84	847,11	2336,86	6,276E-10	1,211E-08
Ebf4	21,10	29,56	18,42	17,19	59,05	30,66	160,97	128,09	6,326E-10	1,219E-08
Trp63	24,77	16,55	125,65	68,77	182,13	121,35	25,20	16,16	6,337E-10	1,22E-08
Fam214a	55,04	57,94	113,15	130,93	174,64	163,51	217,87	281,58	6,467E-10	1,243E-08
Btg1	580,67	528,51	728,91	1046,08	1482,81	1253,12	1676,33	2069,13	6,61E-10	1,267E-08
Pcdhb17	23,85	20,10	43,42	50,25	85,66	75,37	176,41	123,48	6,605E-10	1,267E-08
Nrxn1	25,69	16,55	3,95	5,29	54,06	7,66	165,84	215,80	6,718E-10	1,286E-08
Prkcd	328,40	387,81	671,02	813,33	974,68	900,56	930,03	971,67	6,879E-10	1,315E-08
Prkg1	123,84	163,16	44,73	42,32	20,79	30,66	31,71	32,31	7,044E-10	1,345E-08
Cxcl14	40,36	5,91	491,42	358,39	691,92	402,38	2169,79	568,92	7,192E-10	1,372E-08
C1qa	4,59	1,18	49,34	67,45	140,55	63,87	405,67	90,01	7,503E-10	1,429E-08
Clcf1	4,59	5,91	51,97	84,64	34,10	94,53	155,28	145,40	7,55E-10	1,436E-08
Itm2b	1057,68	741,34	1799,24	1612,10	2963,12	2189,44	4828,99	3100,81	7,781E-10	1,478E-08
Arsb	120,17	105,23	300,64	243,34	405,01	314,24	580,45	413,13	7,885E-10	1,496E-08
Ezr	498,11	442,20	622,99	592,47	2054,14	1057,68	1898,27	1610,99	7,998E-10	1,516E-08
Cnbp	20077,53	17141,75	11267,81	11874,55	9151,32	10815,65	7580,06	8015,71	8,085E-10	1,53E-08
Stk39	2182,32	1910,68	1851,87	1721,87	942,24	1328,48	525,99	702,79	8,171E-10	1,544E-08
Pum3	3762,87	4261,20	3549,15	3179,24	2352,70	2665,91	1654,38	1733,31	8,334E-10	1,573E-08
Dil4	534,80	433,92	175,65	126,96	164,66	127,74	207,31	170,79	8,482E-10	1,598E-08
Ldhb	1013,65	715,32	2923,52	2605,29	3390,58	2573,94	4049,36	2825,00	8,486E-10	1,598E-08
Cybb	0,00	0,00	10,53	23,80	55,72	34,49	60,16	45,01	8,504E-10	1,599E-08
Chrdl2	1,83	0,00	0,00	0,00	16,63	6,39	41,46	65,78	8,59E-10	1,613E-08
Tmem151b	282,54	163,16	667,73	599,08	1076,14	731,94	1588,53	1042,07	8,732E-10	1,638E-08
Col1a2	3173,03	1777,08	16758,30	9103,96	19476,90	10305,97	52063,69	20040,43	8,876E-10	1,663E-08
Postn	95,40	114,69	1,32	2,64	54,06	14,05	82,92	65,78	9,284E-10	1,737E-08
Hs3st3b1	728,36	1320,69	69,08	93,90	45,74	143,07	354,45	103,86	9,319E-10	1,741E-08
Zic2	635,71	780,35	2793,93	2430,72	1165,95	1727,03	925,15	1231,32	9,459E-10	1,765E-08
Slc25a13	3080,38	2913,32	2116,33	1912,31	1430,41	1729,58	994,25	1225,55	9,857E-10	1,837E-08
Olfml3	171,54	159,62	153,94	202,34	1020,42	444,53	921,09	597,77	1,017E-09	1,893E-08
Yaf2	1362,23	1148,06	835,48	819,94	683,60	763,88	486,15	483,53	1,045E-09	1,942E-08
Cntnap3	0,00	0,00	0,00	0,00	96,47	25,55	17,07	70,39	1,048E-09	1,945E-08
Gpr157	9,17	14,19	30,92	33,06	71,52	67,70	95,93	93,47	1,064E-09	1,973E-08
Rcan3	178,88	138,34	207,88	239,37	422,47	320,62	505,66	643,93	1,067E-09	1,976E-08
Hkdc1	3,67	10,64	17,76	43,64	128,07	77,92	239,01	113,09	1,113E-09	2,059E-08
Parp12	36,69	35,47	57,89	60,83	111,44	103,47	176,41	151,17	1,151E-09	2,126E-08
Fam109b	108,24	89,86	159,20	156,05	261,13	241,43	480,46	319,66	1,161E-09	2,142E-08
Synpr	3,67	2,36	12,50	11,90	34,93	24,27	79,67	60,01	1,19E-09	2,193E-08
Chrna1	32,11	31,92	69,08	38,35	3,33	8,94	0,81	0,00	1,21E-09	2,228E-08
Lrrc8b	456,83	547,43	170,39	175,89	237,85	217,16	287,79	316,20	1,253E-09	2,303E-08

Mcoln3	294,46	320,42	205,25	222,18	127,24	125,18	108,12	93,47	1,263E-09	2,318E-08
Hpse	14,68	17,74	23,03	27,77	67,36	40,88	178,85	106,17	1,266E-09	2,32E-08
Ppp2r1b	4575,63	4751,88	3311,66	3181,89	2359,35	2796,20	2121,02	2078,36	1,269E-09	2,324E-08
Nlrp10	0,00	2,36	19,08	23,80	64,04	58,76	26,01	36,93	1,423E-09	2,602E-08
Fbxo41	4,59	5,91	78,94	93,90	169,65	261,86	30,89	130,40	1,439E-09	2,628E-08
Rnase4	20,18	18,92	40,79	56,87	156,35	94,53	288,60	131,56	1,442E-09	2,631E-08
Trim71	2640,98	5443,55	1811,74	2289,21	385,05	935,05	73,98	325,43	1,449E-09	2,64E-08
Rab38	44,03	48,48	25,66	21,16	167,99	71,53	189,42	207,72	1,511E-09	2,751E-08
Nbl1	238,50	179,72	80,26	31,74	671,96	229,93	1499,10	632,39	1,531E-09	2,783E-08
Acta2	100,91	78,04	5,26	1,32	14,97	16,61	6,50	0,00	1,561E-09	2,834E-08
Tead3	218,32	306,23	586,15	612,31	694,42	613,15	974,74	812,42	1,565E-09	2,837E-08
Tm4sf1	11,01	7,09	23,68	22,48	37,42	26,83	182,92	79,63	1,574E-09	2,851E-08
Ppan	2215,34	2122,32	1520,31	1362,16	825,81	1186,69	754,43	758,18	1,721E-09	3,104E-08
Kcnab3	2,75	8,28	72,36	108,44	86,49	94,53	47,15	81,93	1,722E-09	3,104E-08
Angpt1	119,25	117,05	109,20	222,18	331,82	457,31	532,49	609,31	1,722E-09	3,104E-08
Wdr3	2771,24	2981,89	2063,05	1942,72	1396,32	1627,39	1317,00	1313,26	1,719E-09	3,104E-08
Aes	721,94	354,71	2848,53	2215,16	4475,86	2561,16	5726,50	3296,99	1,755E-09	3,158E-08
Asic4	45,87	41,38	0,66	2,64	0,00	0,00	0,00	0,00	1,76E-09	3,164E-08
Gabra4	34,86	31,92	11,84	22,48	98,96	66,42	118,69	162,71	1,768E-09	3,173E-08
Zfp651	204,56	245,93	372,35	355,75	510,62	449,64	644,68	620,85	1,796E-09	3,216E-08
Dhrs3	142,19	109,96	149,33	167,96	178,80	173,72	964,17	385,44	1,794E-09	3,216E-08
Adcy2	36,69	33,11	11,18	26,45	99,80	65,15	191,05	141,94	1,828E-09	3,271E-08
Slc9a3r1	769,64	529,69	462,47	224,82	204,58	164,78	111,38	115,40	1,843E-09	3,293E-08
C1qbp	7290,91	6065,47	4578,04	3495,32	3086,20	3175,59	2611,23	2145,29	1,859E-09	3,318E-08
Chst15	361,43	464,66	596,02	569,99	577,15	540,34	1514,55	1058,22	1,867E-09	3,327E-08
Hsph1	10808,86	10246,27	10211,29	6970,80	5082,96	5126,16	4063,18	3804,75	1,897E-09	3,376E-08
Spint2	53,20	55,57	138,15	79,35	280,26	140,51	767,44	326,58	1,92E-09	3,413E-08
Timp2	1031,99	782,72	1469,00	1401,83	2498,23	1848,38	3934,73	2702,68	1,926E-09	3,42E-08
Evc	553,15	516,69	1036,79	1014,34	1449,54	1136,88	1401,55	1321,33	1,966E-09	3,486E-08
Slc2a4	169,71	140,70	263,80	350,46	394,20	378,11	509,73	550,46	2,004E-09	3,55E-08
Rapgef1	24,77	35,47	84,21	107,12	158,84	131,57	160,97	256,19	2,03E-09	3,592E-08
Ptch2	77,97	54,39	613,78	663,89	153,02	530,12	114,63	126,94	2,131E-09	3,767E-08
Wdr43	5084,74	5716,68	3093,25	3372,33	2272,86	2964,82	1801,52	2169,53	2,144E-09	3,784E-08
Nudt19	914,57	624,28	407,87	331,94	303,55	279,75	249,58	221,57	2,216E-09	3,906E-08
2510009E0	204,56	263,66	206,57	240,69	419,98	292,52	738,17	654,32	2,232E-09	3,929E-08
Higd1a	1262,24	987,26	614,44	587,18	474,86	523,73	469,08	460,45	2,266E-09	3,985E-08
Hba-x	24623,80	17277,72	33743,55	24690,71	19351,32	20378,18	8744,22	8236,12	2,268E-09	3,985E-08
G430095P1	6,42	1,18	30,92	41,00	66,53	71,53	63,41	61,16	2,276E-09	3,993E-08
Cxadr	658,64	721,24	933,50	1288,10	1407,13	1525,20	1945,42	2029,89	2,286E-09	4,006E-08
Rragd	229,33	219,92	1026,26	1457,37	703,56	1133,04	593,46	946,28	2,303E-09	4,031E-08
Pitx1	15,59	11,82	11,18	7,93	55,72	16,61	308,11	90,01	2,315E-09	4,047E-08
Ahsa1	4454,54	4142,96	3397,18	3050,96	2998,05	2920,11	1886,88	1973,35	2,321E-09	4,053E-08
Kank1	569,66	636,11	1184,15	1116,17	1310,66	1043,63	1595,84	1924,88	2,412E-09	4,207E-08
Lrrc4b	4,59	13,01	42,76	46,29	46,57	66,42	185,36	100,40	2,483E-09	4,325E-08
Gar1	1524,60	1673,03	1282,17	1161,14	1011,27	956,76	618,66	701,63	2,489E-09	4,331E-08
Nog	17,43	17,74	15,13	14,55	17,46	6,39	185,36	77,32	2,585E-09	4,493E-08
Pde4a	150,44	165,53	314,46	267,14	100,63	118,80	92,68	81,93	2,689E-09	4,668E-08
Edn3	104,58	91,04	121,70	132,25	285,25	198,00	375,59	319,66	2,694E-09	4,671E-08
Prdm6	204,56	235,29	130,26	79,35	37,42	67,70	33,33	18,46	2,737E-09	4,74E-08
Map2k1	2465,77	2128,24	1477,55	1456,05	1136,01	1333,59	868,24	984,37	2,762E-09	4,777E-08

Dab1	29,35	26,01	29,60	13,22	34,10	22,99	233,32	115,40	2,778E-09	4,8E-08
Dut	4789,36	3699,58	2793,93	2482,30	2084,08	2169,01	1755,18	1614,45	2,785E-09	4,806E-08
Enpp2	58,71	69,76	271,70	156,05	49,90	43,43	52,84	47,31	2,862E-09	4,932E-08
Smim10l2a	58,71	29,56	187,49	160,02	376,73	233,76	382,90	251,57	2,933E-09	5,044E-08
Hist2h2be	18,35	7,09	34,87	63,48	181,30	89,42	175,60	168,48	2,932E-09	5,044E-08
Runx2	24,77	54,39	42,10	132,25	210,40	265,70	446,32	445,45	2,954E-09	5,074E-08
Fndc10	49,54	37,84	103,28	96,54	216,23	130,29	321,12	219,26	3,148E-09	5,4E-08
Cacna1d	6,42	8,28	46,71	103,15	135,56	307,85	53,66	121,17	3,207E-09	5,496E-08
Spock1	29,35	16,55	7,89	22,48	64,87	16,61	446,32	155,79	3,227E-09	5,523E-08
Crim1	299,97	306,23	412,48	423,19	544,72	578,66	754,43	700,48	3,235E-09	5,531E-08
Ap3m2	30,27	31,92	63,15	80,67	93,14	116,24	165,03	162,71	3,807E-09	6,501E-08
Adamtsl2	57,79	42,56	373,66	530,31	242,84	518,62	324,37	191,56	3,891E-09	6,636E-08
Ppid	4677,45	4873,66	2891,95	3054,93	2051,64	2711,90	1759,25	2004,50	3,898E-09	6,641E-08
Cdc25b	604,52	586,45	1051,26	1296,03	1653,29	1434,51	1822,66	1447,12	3,966E-09	6,749E-08
Ppp2r2b	49,54	62,66	4,61	5,29	4,16	1,28	4,88	5,77	4,009E-09	6,813E-08
Klhl14	1,83	0,00	76,31	105,80	39,92	72,81	12,19	39,24	4,126E-09	7,005E-08
Cth	898,06	930,51	562,47	658,60	380,06	484,13	337,38	351,97	4,214E-09	7,145E-08
Shc2	798,07	785,08	296,69	286,98	479,85	353,84	360,96	364,67	4,236E-09	7,176E-08
Fbxo32	37,61	34,29	53,29	56,87	127,24	84,31	161,78	207,72	4,483E-09	7,585E-08
Yrdc	831,10	809,91	486,82	552,80	397,52	434,31	339,01	351,97	4,505E-09	7,613E-08
Mcrip2	230,25	119,42	46,05	46,29	36,59	25,55	33,33	24,23	4,53E-09	7,646E-08
Vcan	3791,31	3512,77	5311,55	4746,38	4419,31	4373,78	10676,63	7760,68	4,657E-09	7,851E-08
Htra2	1245,73	1059,39	714,43	728,69	624,56	533,95	462,58	481,22	4,663E-09	7,853E-08
Exosc7	987,04	926,96	613,12	575,28	338,48	498,18	296,73	333,51	4,729E-09	7,945E-08
Frmd4a	1674,12	2422,64	6923,31	6872,93	3966,90	5557,92	6638,65	5786,17	4,723E-09	7,945E-08
Podxl2	222,91	247,11	530,89	456,26	684,44	491,79	908,08	739,72	4,794E-09	8,046E-08
Itga1	204,56	210,46	626,28	585,86	218,72	286,14	130,07	215,80	4,858E-09	8,144E-08
Nrcam	2,75	0,00	11,18	17,19	81,50	29,38	87,80	65,78	5,153E-09	8,628E-08
Cdkn2c	11,01	3,55	27,63	25,13	62,37	21,72	185,36	120,02	5,237E-09	8,749E-08
Lzts1	92,65	61,48	349,98	285,66	181,30	200,55	238,20	240,03	5,231E-09	8,749E-08
Cib2	50,45	30,74	135,52	92,57	335,15	164,78	508,91	272,34	5,284E-09	8,818E-08
Gpd1l	997,13	830,01	615,10	592,47	468,21	417,71	353,64	384,28	5,298E-09	8,831E-08
Mpp1	255,93	232,92	498,00	462,87	686,93	585,04	874,75	646,24	5,389E-09	8,972E-08
Clstn3	59,63	28,38	133,55	134,89	372,57	159,67	492,65	357,74	5,564E-09	9,253E-08
Rab43	249,51	231,74	509,84	439,06	682,77	568,44	889,38	661,24	5,758E-09	9,565E-08
Fam19a2	7,34	5,91	3,95	3,97	18,30	8,94	72,35	60,01	6,175E-09	1,025E-07
Sema3c	330,24	489,49	46,71	89,93	148,03	199,27	289,41	264,27	6,204E-09	1,028E-07
Ebna1bp2	2835,46	2514,86	1955,16	1576,40	1587,59	1462,61	1038,97	1091,69	6,224E-09	1,03E-07
Kif21a	82,56	133,61	190,78	301,53	380,89	510,96	495,09	822,80	6,254E-09	1,034E-07
Ppif	1443,87	1336,06	1381,50	1195,52	860,74	965,71	593,46	620,85	6,273E-09	1,036E-07
Apcdd1	3214,31	4699,85	1792,67	2057,78	1348,91	1871,37	1239,77	1290,18	6,426E-09	1,06E-07
Hbb-bs	117,42	59,12	194,07	314,75	1232,48	370,44	2861,63	768,57	6,524E-09	1,075E-07
Ptpn3	30,27	37,84	73,02	66,12	113,10	107,30	147,96	174,25	6,612E-09	1,088E-07
Ldha	86222,30	54370,49	37167,05	23448,90	24202,25	19429,08	21418,29	15767,15	6,661E-09	1,095E-07
Arhgef40	2454,77	3210,09	7779,18	7362,25	5026,40	5888,76	5715,12	5637,31	6,681E-09	1,097E-07
Akap1	1748,42	1792,45	1001,92	1001,12	938,92	1044,90	862,55	894,35	6,684E-09	1,097E-07
Col13a1	87,15	113,51	198,02	161,34	64,04	65,15	26,83	40,39	6,775E-09	1,11E-07
Fam168a	1173,26	1565,44	2753,14	3173,95	3324,88	3641,83	3440,45	4071,33	6,822E-09	1,117E-07
Lpar1	2035,55	1879,94	3766,24	3934,38	3421,35	3758,08	3895,71	4193,65	7,1E-09	1,161E-07
Evi5l	265,11	218,74	458,53	415,26	784,23	541,61	813,77	753,56	7,172E-09	1,172E-07

Syngn3	5,50	8,28	76,97	60,83	69,86	61,31	119,51	65,78	7,225E-09	1,179E-07
Tcf19	352,25	335,79	590,76	587,18	957,21	774,10	896,70	776,64	7,475E-09	1,218E-07
Adgrg2	0,00	2,36	0,66	9,26	17,46	24,27	133,33	70,39	7,538E-09	1,227E-07
Fam13c	85,31	65,03	198,67	199,69	203,75	263,14	277,22	358,90	7,675E-09	1,248E-07
Olfml1	59,63	85,13	165,78	153,41	248,66	215,88	671,51	300,04	7,695E-09	1,25E-07
Slc38a5	55,04	50,84	73,68	64,80	28,28	47,26	4,88	3,46	7,755E-09	1,258E-07
Frem2	208,23	165,53	263,80	216,89	803,36	370,44	1593,40	745,49	7,883E-09	1,276E-07
Tshz2	1460,38	2525,51	1291,38	782,91	410,00	318,07	375,59	673,94	7,878E-09	1,276E-07
Ppp3ca	971,45	976,62	894,69	1110,88	2017,55	1792,18	2042,16	2909,24	7,996E-09	1,293E-07
Ier5	273,36	249,48	753,25	576,60	599,61	641,25	1080,43	765,10	8,03E-09	1,297E-07
Trabd2b	133,01	218,74	42,10	37,03	33,27	38,32	65,85	76,16	8,091E-09	1,306E-07
Kpnb1	35822,53	36981,63	28863,56	25880,95	21220,01	23690,45	16983,58	17674,72	8,685E-09	1,4E-07
Ddah1	498,11	559,25	261,83	189,11	160,51	190,33	230,88	195,03	8,808E-09	1,417E-07
Nrip1	1347,55	2245,29	657,20	694,30	648,68	623,37	636,55	745,49	8,805E-09	1,417E-07
Mcm10	3262,01	3451,29	3281,40	2860,53	2134,81	2368,28	1465,77	1605,22	8,932E-09	1,435E-07
Umps	4607,73	4339,23	3601,12	3039,06	2505,72	2545,84	2129,96	1915,65	9,046E-09	1,452E-07
Tnrc18	2724,46	3169,89	6700,29	4922,27	7689,30	5805,73	10725,40	8844,28	9,707E-09	1,556E-07
Vwa2	26,60	14,19	107,23	138,86	117,26	162,23	105,69	106,17	9,886E-09	1,583E-07
Npr2	47,70	100,50	103,28	204,98	323,51	284,86	449,57	608,16	1,009E-08	1,614E-07
Arid5b	753,13	960,07	1355,85	1277,52	2178,05	1776,85	2294,99	2079,51	1,013E-08	1,618E-07
Chadl	1,83	3,55	7,89	7,93	14,97	15,33	130,07	39,24	1,014E-08	1,618E-07
Hist1h1c	85,31	74,49	132,89	173,24	380,06	223,54	388,60	324,28	1,029E-08	1,64E-07
Armc2	7,34	2,36	37,50	44,96	74,02	56,21	61,79	80,78	1,092E-08	1,74E-07
Cbln4	0,92	1,18	11,84	85,96	251,15	508,40	15,45	137,33	1,101E-08	1,752E-07
Slco2b1	18,35	14,19	38,81	30,42	78,17	51,10	134,95	110,78	1,124E-08	1,786E-07
Sncaip	187,13	230,56	293,41	675,79	948,06	1136,88	1004,01	1021,29	1,13E-08	1,794E-07
Lrp2	21,10	132,42	1,32	3,97	0,00	0,00	0,00	2,31	1,134E-08	1,798E-07
Kit	445,82	555,71	342,74	351,78	782,57	679,57	853,61	954,36	1,165E-08	1,844E-07
Bend3	3042,77	3661,75	2432,76	2197,96	1213,36	1760,24	999,94	1242,86	1,165E-08	1,844E-07
Fst	68,80	43,75	1,97	1,32	4,16	0,00	7,32	5,77	1,195E-08	1,889E-07
Ncald	243,09	187,99	78,29	48,93	59,05	56,21	64,22	58,85	1,199E-08	1,893E-07
Tmem30b	14,68	18,92	6,58	30,42	363,42	387,05	14,63	109,63	1,247E-08	1,966E-07
Bmp1	1488,82	1119,69	3172,20	3242,72	3106,16	2729,78	3884,33	3173,51	1,295E-08	2,039E-07
Bnc2	155,95	301,50	42,76	48,93	150,53	79,20	313,80	341,59	1,296E-08	2,039E-07
Prmt3	1501,66	1286,40	758,51	773,65	755,12	683,40	665,00	604,70	1,308E-08	2,056E-07
Rtn4rl1	16,51	21,28	110,52	55,54	7,48	8,94	9,76	6,92	1,335E-08	2,096E-07
Gxylt2	78,89	81,58	71,71	63,48	67,36	71,53	609,72	186,95	1,348E-08	2,115E-07
Pou3f3	1,83	0,00	0,66	6,61	29,11	15,33	111,38	51,93	1,369E-08	2,145E-07
Pcdhgc4	27,52	34,29	153,94	111,09	204,58	123,91	291,04	180,02	1,397E-08	2,187E-07
Hdac6	867,79	906,86	1676,88	1791,96	1993,43	1744,91	2045,41	1812,94	1,431E-08	2,237E-07
Hs3st3a1	219,24	208,09	8,55	9,26	10,81	33,21	381,28	56,55	1,458E-08	2,278E-07
Nedd4l	323,82	321,60	318,40	361,04	641,19	441,98	1043,84	808,96	1,465E-08	2,286E-07
Itga4	269,69	267,21	75,00	132,25	224,54	302,74	59,35	73,86	1,472E-08	2,295E-07
Vax2	6,42	2,36	83,55	30,42	3,33	1,28	0,00	1,15	1,491E-08	2,321E-07
Grin3a	20,18	24,83	9,21	5,29	24,12	16,61	259,33	57,70	1,506E-08	2,342E-07
Slc40a1	51,37	66,21	84,21	166,63	138,05	162,23	374,78	308,12	1,508E-08	2,343E-07
Apobec3	48,62	31,92	86,18	88,61	136,39	153,29	203,24	166,18	1,52E-08	2,359E-07
Zcchc24	567,83	586,45	522,34	489,32	847,44	707,67	1356,83	1100,92	1,534E-08	2,378E-07
Scn5a	52,29	42,56	7,24	5,29	4,99	3,83	1,63	1,15	1,549E-08	2,399E-07
Glis3	25,69	43,75	76,31	74,06	92,31	79,20	208,93	168,48	1,555E-08	2,406E-07

Cbx8	78,89	75,67	232,88	244,66	164,66	295,08	360,96	396,98	1,563E-08	2,415E-07
Stard8	543,06	725,96	231,57	181,18	247,00	208,21	295,92	216,95	1,576E-08	2,433E-07
Mybbp1a	19725,28	20647,43	16256,35	12355,94	11296,10	10598,49	8701,94	7460,63	1,613E-08	2,488E-07
Mamld1	6,42	9,46	3,95	10,58	47,40	19,16	77,23	131,56	1,618E-08	2,492E-07
Kcnn1	61,46	62,66	175,65	245,98	295,23	324,46	204,05	346,20	1,668E-08	2,567E-07
Lamb2	354,09	404,36	447,34	558,09	822,49	587,60	1609,66	1060,53	1,672E-08	2,57E-07
Hspe1	3493,18	2866,02	2140,01	1504,98	1299,85	1742,36	973,93	991,29	1,682E-08	2,583E-07
Lbh	412,80	309,78	1193,36	1030,21	990,48	878,84	913,77	721,25	1,688E-08	2,59E-07
Ndufa4l2	99,07	62,66	17,10	6,61	7,48	3,83	4,06	8,08	1,719E-08	2,635E-07
Sfxn1	3093,23	2965,34	1584,12	1703,36	2002,58	1894,37	1638,12	1538,29	1,727E-08	2,645E-07
Hspa8	41810,84	44451,74	41800,35	32370,36	20158,84	19354,99	22547,49	17797,05	1,734E-08	2,652E-07
Slc1a4	1311,78	1331,33	714,43	677,11	577,15	712,78	631,67	649,70	1,854E-08	2,832E-07
Flt1	1091,62	991,99	495,37	458,90	537,24	459,86	576,39	507,76	1,863E-08	2,844E-07
Mapre3	33,94	49,66	114,47	132,25	161,34	143,07	173,16	198,49	1,932E-08	2,946E-07
P2ry6	0,92	0,00	19,08	23,80	49,07	34,49	58,53	31,16	1,935E-08	2,948E-07
Heatr1	4655,43	4997,81	3319,56	3207,02	2395,11	2637,81	2545,38	2174,14	1,961E-08	2,984E-07
Cspg4	34,86	17,74	164,46	85,96	275,27	130,29	527,61	250,42	1,996E-08	3,034E-07
Erbp3	93,57	48,48	26,31	22,48	100,63	34,49	228,44	324,28	2,01E-08	3,051E-07
Dio3	68,80	52,02	0,00	1,32	0,83	2,55	0,00	4,62	2,04E-08	3,094E-07
Pcdhac2	3,67	3,55	1,32	1,32	20,79	2,55	116,25	51,93	2,059E-08	3,12E-07
Hprt	2067,65	1552,43	793,38	942,93	577,99	840,52	649,56	603,54	2,065E-08	3,126E-07
Ipo11	4458,21	4404,26	2892,61	2950,45	2026,70	2702,95	1806,40	1881,03	2,07E-08	3,13E-07
Fgf12	22,93	14,19	3,29	1,32	28,28	2,55	149,58	115,40	2,077E-08	3,138E-07
Igfbp7	0,00	1,18	6,58	2,64	5,82	6,39	76,42	33,47	2,089E-08	3,153E-07
Gtpbp4	4121,55	4385,35	2972,21	2662,15	1816,29	2409,15	1806,40	1774,86	2,124E-08	3,202E-07
Ablim2	0,00	0,00	49,34	83,32	24,95	61,31	8,94	26,54	2,139E-08	3,221E-07
Cln6	458,66	392,54	1147,96	950,86	736,00	708,95	547,94	565,46	2,148E-08	3,23E-07
Ntng1	118,34	182,08	12,50	17,19	44,08	37,04	108,94	51,93	2,149E-08	3,23E-07
Metap2	7112,95	7321,13	5101,04	5045,26	4507,46	4689,29	3711,17	3819,75	2,167E-08	3,253E-07
Pamr1	0,00	0,00	0,66	0,00	4,16	1,28	46,34	32,31	2,263E-08	3,394E-07
Hspa9	15393,66	16557,67	11336,88	10895,92	9458,19	10377,50	7143,49	8038,79	2,298E-08	3,443E-07
Eef1e1	1222,80	905,68	626,94	596,44	527,26	522,45	419,49	358,90	2,314E-08	3,464E-07
Nat10	2946,45	2623,64	1980,81	1814,44	1597,57	1523,92	1357,65	1194,39	2,354E-08	3,52E-07
Fgf8	17,43	2,36	173,02	64,80	66,53	39,60	3,25	1,15	2,38E-08	3,555E-07
Zmym3	1097,12	1020,37	1557,81	1823,70	2589,71	2037,43	2584,41	2557,27	2,413E-08	3,601E-07
Mtap	4504,99	3990,44	2814,32	2442,62	2086,57	2202,22	2202,31	2019,51	2,441E-08	3,638E-07
Slc6a6	3683,07	4734,14	1918,32	2064,39	1907,77	2041,27	2208,82	1839,48	2,505E-08	3,73E-07
Mtx2	1946,57	1879,94	1060,47	1194,20	670,30	992,53	718,66	723,56	2,559E-08	3,806E-07
Ankrd34a	11,93	13,01	34,21	27,77	78,17	65,15	162,59	78,47	2,59E-08	3,849E-07
Chd3os	116,50	108,78	242,75	300,20	279,43	297,63	338,19	331,20	2,645E-08	3,927E-07
Tmem35a	21,10	11,82	33,55	30,42	100,63	43,43	208,12	128,09	2,69E-08	3,989E-07
Ebf3	356,84	498,95	140,78	153,41	540,56	592,71	442,25	731,64	2,709E-08	4,014E-07
Hpgds	0,00	0,00	3,95	17,19	26,61	49,82	52,03	61,16	2,799E-08	4,142E-07
Foxp2	147,69	271,94	19,08	30,42	80,67	67,70	67,48	106,17	2,806E-08	4,149E-07
Eif2s1	5609,45	4838,19	3581,38	3487,38	2488,25	3164,09	2179,55	2245,69	2,865E-08	4,232E-07
Zmat4	35,78	39,02	1,97	3,97	0,83	0,00	0,81	1,15	2,93E-08	4,324E-07
Ncam1	265,11	352,34	721,67	730,01	677,78	679,57	755,24	808,96	2,971E-08	4,379E-07
Ctf1	39,45	34,29	53,94	78,03	90,65	102,19	182,92	165,02	3,025E-08	4,455E-07
Rcl1	2263,05	1749,88	1440,05	1272,23	939,75	1102,39	797,52	785,88	3,046E-08	4,481E-07
C1s1	1,83	11,82	5,26	6,61	39,09	26,83	112,19	70,39	3,059E-08	4,496E-07

Tmem173	941,18	848,93	1699,91	1401,83	865,73	1043,63	621,10	571,23	3,087E-08	4,533E-07
Rpf2	1591,56	1351,43	931,53	802,75	587,97	784,32	575,58	548,15	3,109E-08	4,56E-07
Srpx	1,83	4,73	17,10	14,55	56,55	42,15	78,86	45,01	3,139E-08	4,6E-07
Hdc	0,00	0,00	0,00	0,00	14,14	3,83	52,03	33,47	3,154E-08	4,617E-07
Fzd7	3165,69	3210,09	1776,22	1445,47	1039,54	1346,37	1762,50	1384,80	3,161E-08	4,622E-07
Ccdc80	107,33	172,62	99,99	92,57	276,10	150,73	512,17	417,75	3,253E-08	4,753E-07
Jmjd6	2011,70	1779,44	1532,81	1321,16	1134,35	1117,71	785,32	868,96	3,328E-08	4,857E-07
Ms4a6c	0,92	0,00	10,53	15,87	27,44	30,66	47,15	36,93	3,372E-08	4,916E-07
Nell2	91,73	72,12	75,00	41,00	117,26	54,93	1012,14	213,49	3,389E-08	4,936E-07
Nrbp2	14,68	21,28	25,66	47,61	49,90	67,70	130,89	140,79	3,431E-08	4,993E-07
Nfkbia	239,42	212,82	335,51	354,42	583,81	499,46	934,91	588,54	3,491E-08	5,074E-07
Atat1	370,60	371,26	836,80	845,07	892,34	797,09	1134,08	843,58	3,599E-08	5,227E-07
Itpkb	1147,58	1080,67	3944,52	2722,99	3151,90	2742,55	4915,98	3165,43	3,657E-08	5,306E-07
Mycbp	628,37	517,87	375,64	321,36	249,49	288,69	173,16	215,80	3,705E-08	5,37E-07
Cd200	41,28	22,46	15,79	14,55	93,97	66,42	113,00	105,01	3,758E-08	5,442E-07
Zfr2	8,26	3,55	16,45	18,51	39,92	34,49	70,73	72,70	3,768E-08	5,45E-07
Slc48a1	277,03	183,26	442,08	390,13	782,57	559,50	1187,74	761,64	3,862E-08	5,581E-07
Adam11	197,23	184,45	491,42	440,39	538,07	406,21	591,84	518,15	4,008E-08	5,781E-07
Sall4	1739,25	2514,86	1890,69	1700,71	651,17	941,44	126,82	416,60	4,007E-08	5,781E-07
Fign	697,17	1378,62	367,09	482,71	142,21	347,45	33,33	113,09	4,023E-08	5,796E-07
Cbx4	127,51	100,50	224,33	169,28	305,21	214,60	537,37	400,44	4,223E-08	6,079E-07
Pipp3	1064,10	916,32	2863,66	2318,31	2756,04	2167,73	3765,64	2627,67	4,244E-08	6,103E-07
Spint1	16,51	14,19	65,79	51,58	142,21	80,48	108,94	103,86	4,262E-08	6,122E-07
Hcn1	0,92	3,55	2,63	5,29	34,93	8,94	70,73	75,01	4,319E-08	6,198E-07
Mycl	432,06	342,88	853,24	743,23	1279,06	972,09	1208,06	973,98	4,354E-08	6,237E-07
Plekhg5	207,32	216,37	288,14	341,20	508,96	397,27	611,35	564,31	4,352E-08	6,237E-07
Hgh1	569,66	578,17	411,16	379,55	235,35	320,62	209,74	208,87	4,492E-08	6,428E-07
Nip7	3090,47	2149,52	1477,55	1426,96	1078,63	1262,06	1060,10	915,12	4,705E-08	6,727E-07
Sp7	11,93	20,10	92,76	80,67	84,83	66,42	153,65	99,24	4,91E-08	7,013E-07
9930012K1	106,41	80,40	386,82	277,72	141,38	144,34	159,34	147,71	5E-08	7,135E-07
Dtx1	11,01	4,73	15,79	19,84	74,02	25,55	125,20	108,48	5,021E-08	7,157E-07
Pcdhb20	10,09	7,09	25,66	26,45	50,73	31,93	90,24	84,24	5,117E-08	7,288E-07
Garnl3	81,64	75,67	136,83	137,54	237,85	181,39	265,84	251,57	5,206E-08	7,406E-07
Letmd1	728,36	646,75	321,04	327,98	340,97	327,01	386,97	349,66	5,225E-08	7,426E-07
Prrg3	361,43	261,30	311,83	341,20	664,48	505,85	981,24	767,41	5,288E-08	7,509E-07
Fndc3c1	7075,34	13431,53	4680,01	6010,67	2346,04	3851,33	1643,81	2576,89	5,341E-08	7,577E-07
Camta1	189,89	230,56	333,53	441,71	577,99	546,72	555,25	677,40	5,357E-08	7,588E-07
Kdr	3786,73	2986,62	1625,57	1362,16	1760,57	1601,85	1802,34	1589,06	5,364E-08	7,588E-07
Tcf15	154,11	66,21	30,26	15,87	4,99	7,66	13,82	3,46	5,365E-08	7,588E-07
Pcdhb7	4,59	8,28	28,95	15,87	49,90	33,21	102,43	77,32	5,376E-08	7,596E-07
Nefm	155,03	92,22	28,29	34,38	14,97	24,27	16,26	26,54	5,501E-08	7,766E-07
Usp29	230,25	370,08	136,18	167,96	56,55	83,03	86,99	96,94	5,611E-08	7,914E-07
Nipal3	97,24	53,21	157,23	129,60	341,80	195,44	403,23	386,59	5,648E-08	7,958E-07
S1pr1	344,00	357,07	262,49	286,98	468,21	402,38	809,71	633,55	5,657E-08	7,963E-07
Aqp3	61,46	75,67	41,45	37,03	14,97	17,88	4,06	8,08	5,665E-08	7,966E-07
Lama3	3,67	2,36	1,32	1,32	19,13	6,39	217,06	18,46	5,695E-08	7,993E-07
Ncl	49476,94	68147,27	37782,81	35499,35	29526,38	33412,65	18172,95	23465,51	5,69E-08	7,993E-07
St14	9,17	8,28	96,05	54,22	89,82	38,32	8,94	4,62	5,7E-08	7,993E-07
Hbp1	1122,81	981,35	1345,98	1421,67	1492,79	1684,88	2316,94	2283,77	5,772E-08	8,086E-07
Larp6	4,59	7,09	23,03	19,84	75,68	38,32	78,04	71,55	5,797E-08	8,114E-07

Csrnp3	118,34	156,07	106,57	138,86	133,89	171,17	346,32	396,98	5,823E-08	8,142E-07
Scn9a	0,92	0,00	0,00	0,00	13,31	0,00	69,10	80,78	5,959E-08	8,324E-07
Fcho1	5,50	8,28	26,31	26,45	57,38	60,04	74,79	55,39	6,119E-08	8,54E-07
Cyp39a1	199,06	209,28	341,43	355,75	515,61	450,92	462,58	470,83	6,254E-08	8,72E-07
Slc16a1	3588,58	4194,99	1999,23	2437,33	1593,41	2062,98	1521,86	1671,00	6,294E-08	8,768E-07
Bahd1	444,90	461,12	734,17	728,69	920,62	845,63	1027,58	942,82	6,361E-08	8,852E-07
Antxr1	1271,42	1474,39	2033,44	1953,30	2342,72	2117,91	3796,53	2988,87	6,441E-08	8,955E-07
Smarcd3	215,57	196,27	421,69	297,56	670,30	462,41	787,76	655,47	6,575E-08	9,132E-07
Apba2	91,73	81,58	174,33	212,92	287,75	305,30	186,17	222,72	6,581E-08	9,132E-07
Sptbn2	1348,47	1647,02	1436,76	921,77	755,96	656,58	487,78	508,92	6,745E-08	9,351E-07
Ppp2r5a	1247,56	1328,96	716,41	767,04	670,30	599,10	540,62	656,63	6,785E-08	9,398E-07
4931428F04	347,67	349,98	582,21	600,41	795,88	687,24	756,87	796,26	6,85E-08	9,478E-07
Cdc25a	3986,70	4107,49	3431,39	3143,54	2259,55	2722,11	1841,36	1935,26	6,871E-08	9,498E-07
Slc2a1	5980,97	4135,87	3078,78	2323,60	1954,34	1894,37	2156,79	1773,70	6,895E-08	9,523E-07
Rcsd1	306,39	224,65	774,96	544,86	339,31	335,95	227,63	203,10	7,175E-08	9,901E-07
Fhl1	954,94	1075,94	383,53	481,38	419,98	499,46	523,55	579,31	7,434E-08	1,025E-06
Eif2s2	6899,22	5486,12	3893,87	3688,40	2970,60	3618,84	2706,35	2368,02	7,526E-08	1,036E-06
Msantd3	1022,82	926,96	373,01	462,87	414,99	398,55	558,50	420,06	7,927E-08	1,091E-06
Mpp6	2511,64	2297,31	1551,23	1793,28	1142,67	1507,32	983,68	925,51	7,962E-08	1,095E-06
Ptn	5733,29	5947,23	1750,56	2443,94	3678,32	3280,33	3337,21	4037,86	7,99E-08	1,097E-06
Arnt2	1098,96	1409,36	1972,92	2123,90	2491,58	2485,80	3230,71	2825,00	8,237E-08	1,13E-06
Chrna4	99,99	122,96	13,82	6,61	31,60	21,72	52,03	28,85	8,505E-08	1,166E-06
Calb2	44,95	29,56	8,55	6,61	3,33	2,55	0,00	0,00	8,545E-08	1,17E-06
Rnf157	425,64	493,04	922,32	650,66	1101,09	887,79	1512,92	1315,56	8,553E-08	1,17E-06
Parp14	0,92	1,18	7,89	14,55	16,63	29,38	57,72	47,31	8,6E-08	1,176E-06
Mctp2	57,79	95,77	9,87	17,19	9,15	8,94	11,38	8,08	8,624E-08	1,178E-06
Gata1	125,67	92,22	92,76	93,90	63,20	48,54	17,07	20,77	8,646E-08	1,18E-06
Cct8	17055,86	17340,39	12028,95	11721,15	9451,54	11565,48	7910,93	8283,44	8,887E-08	1,211E-06
Wnt2b	70,63	55,57	13,16	1,32	1,66	1,28	3,25	2,31	9,006E-08	1,227E-06
Uchl3	1418,19	1104,32	744,70	731,33	558,03	654,02	547,12	538,92	9,048E-08	1,231E-06
Krt18	214,65	173,81	75,65	30,42	69,03	49,82	28,45	19,62	9,16E-08	1,245E-06
Itpril2	405,46	485,95	631,54	846,39	877,38	986,14	1275,54	1189,78	9,214E-08	1,251E-06
Dnaja2	6101,14	6338,59	4549,09	4346,99	3493,70	3761,91	3026,66	3392,77	9,308E-08	1,263E-06
Slit2	667,81	522,60	471,03	511,80	937,25	776,65	3634,75	1253,25	9,359E-08	1,269E-06
Fcgr3	2,75	3,55	25,66	41,00	56,55	40,88	114,63	49,62	9,393E-08	1,272E-06
Loxl1	58,71	23,65	104,60	47,61	212,90	114,96	888,57	246,96	9,417E-08	1,274E-06
Atp1b3	3381,27	3180,53	2505,78	2541,81	1718,16	2112,80	1382,85	1568,29	9,556E-08	1,292E-06
Gpatch4	950,35	1259,21	726,28	744,56	520,60	633,58	382,90	429,29	9,638E-08	1,302E-06
Svopl	34,86	31,92	52,63	44,96	184,62	85,59	178,85	176,56	9,691E-08	1,308E-06
Epha8	14,68	10,64	84,86	104,48	59,05	137,96	13,82	24,23	1,006E-07	1,356E-06
Wipf3	2,75	1,18	15,13	10,58	37,42	19,16	121,94	42,70	1,016E-07	1,368E-06
Frk	33,02	28,38	49,34	80,67	77,34	126,46	269,90	160,41	1,037E-07	1,396E-06
Padi2	59,63	53,21	50,00	26,45	17,46	12,77	3,25	1,15	1,05E-07	1,411E-06
Fam198b	466,92	604,18	359,85	325,33	216,23	136,68	182,92	123,48	1,052E-07	1,413E-06
Dus1l	1815,39	1561,89	1363,08	1220,65	1071,98	991,25	738,17	776,64	1,058E-07	1,419E-06
Strip2	32,11	26,01	25,66	37,03	56,55	33,21	236,57	113,09	1,061E-07	1,423E-06
Col5a2	2032,80	1474,39	5089,85	3910,58	6245,58	3876,87	15149,54	6501,66	1,078E-07	1,444E-06
Syn3	6,42	11,82	92,10	78,03	57,38	88,14	47,15	61,16	1,09E-07	1,459E-06
Ccdc136	246,76	360,62	830,88	872,84	1004,62	807,31	835,72	1174,78	1,093E-07	1,46E-06
Mtmr7	29,35	24,83	129,60	103,15	101,46	121,35	129,26	108,48	1,093E-07	1,46E-06

Fam46c	90,82	83,95	65,79	124,31	212,07	220,99	298,36	303,50	1,104E-07	1,474E-06
Arl4c	622,86	595,91	276,30	286,98	298,56	232,48	326,81	313,89	1,108E-07	1,477E-06
Aen	1428,28	1682,49	1447,29	1178,33	755,12	914,61	678,82	637,01	1,129E-07	1,504E-06
Speg	705,42	822,92	248,01	263,17	369,25	319,35	305,67	459,29	1,137E-07	1,513E-06
Megf10	144,02	53,21	5,26	7,93	36,59	11,50	139,02	99,24	1,174E-07	1,561E-06
Shank1	18,35	18,92	20,39	26,45	43,25	33,21	112,19	91,17	1,175E-07	1,561E-06
Draxin	454,08	387,81	534,84	548,83	1518,57	1098,55	912,96	1653,69	1,207E-07	1,603E-06
Gfm2	1362,23	1450,75	1084,15	1034,18	797,54	876,29	645,49	700,48	1,231E-07	1,633E-06
Cped1	971,45	1377,44	3859,66	4919,63	2778,49	4654,80	3493,30	4079,40	1,238E-07	1,64E-06
C1qc	6,42	0,00	72,36	74,06	193,77	56,21	423,55	98,09	1,284E-07	1,699E-06
Dok4	1731,00	1363,25	628,91	587,18	875,71	633,58	751,99	687,79	1,297E-07	1,716E-06
Loxl3	111,00	56,75	237,49	199,69	311,86	249,09	467,45	360,05	1,337E-07	1,767E-06
Kctd8	0,92	0,00	17,10	13,22	14,14	25,55	70,73	35,77	1,36E-07	1,796E-06
Sardh	14,68	10,64	96,71	89,93	115,60	65,15	155,28	86,55	1,371E-07	1,808E-06
Mdfic	215,57	258,94	107,89	150,76	165,50	190,33	502,41	369,28	1,374E-07	1,81E-06
March9	48,62	31,92	115,13	96,54	234,52	103,47	421,93	236,57	1,377E-07	1,814E-06
Chpf	1775,94	1370,35	1065,07	609,66	551,37	381,94	508,10	354,28	1,395E-07	1,835E-06
Unc5a	32,11	50,84	57,23	27,77	4,16	5,11	3,25	2,31	1,413E-07	1,855E-06
Arrdc1	24,77	15,37	44,73	52,90	92,31	72,81	112,19	122,32	1,411E-07	1,855E-06
Eif4ebp1	2404,31	1479,12	1073,63	749,85	790,05	668,07	637,36	495,07	1,426E-07	1,871E-06
Dbx2	0,00	0,00	2,63	0,00	79,01	24,27	835,72	158,10	1,442E-07	1,89E-06
Laptm5	75,22	60,30	206,57	228,79	388,37	258,03	634,92	272,34	1,447E-07	1,896E-06
Id4	32,11	29,56	36,18	51,58	77,34	77,92	169,91	121,17	1,456E-07	1,905E-06
Inpp4b	44,03	27,19	188,81	269,79	171,32	378,11	187,79	270,04	1,463E-07	1,913E-06
Me2	2677,68	2417,91	1618,33	1527,47	1363,88	1748,74	1092,62	1069,76	1,472E-07	1,922E-06
Limch1	779,73	879,67	372,35	358,39	523,93	457,31	752,80	667,01	1,478E-07	1,928E-06
Mtus2	68,80	92,22	5,26	2,64	17,46	3,83	40,65	32,31	1,488E-07	1,94E-06
Madcam1	7,34	4,73	52,63	38,35	70,69	49,82	93,49	58,85	1,519E-07	1,979E-06
Myb	71,55	81,58	145,39	161,34	177,14	265,70	313,80	265,42	1,53E-07	1,988E-06
Acpp	0,00	2,36	34,21	17,19	78,17	45,99	13,82	19,62	1,529E-07	1,988E-06
Klc3	4,59	3,55	27,63	18,51	85,66	37,04	95,93	58,85	1,53E-07	1,988E-06
Sirpa	498,11	574,62	383,53	431,13	1012,93	641,25	1230,01	1158,62	1,574E-07	2,043E-06
Dct	1,83	1,18	16,45	17,19	52,39	30,66	41,46	39,24	1,624E-07	2,106E-06
Fat3	101,82	105,23	173,02	136,22	325,17	201,83	386,97	355,43	1,628E-07	2,11E-06
Phyh	231,17	187,99	517,73	425,84	600,44	487,96	626,79	547,00	1,645E-07	2,13E-06
Tmem200b	454,99	290,86	45,39	25,13	21,62	19,16	587,77	57,70	1,657E-07	2,143E-06
Dlx3	18,35	17,74	32,89	15,87	114,77	38,32	395,91	110,78	1,659E-07	2,145E-06
Msx1	4663,69	4161,88	8136,40	6260,62	7365,80	6392,05	24534,37	11243,46	1,676E-07	2,164E-06
Fam241b	26,60	21,28	150,65	117,70	137,22	106,02	110,56	72,70	1,719E-07	2,218E-06
Dact1	405,46	501,32	144,07	140,18	108,94	154,56	343,07	205,41	1,745E-07	2,25E-06
Cdca7l	1442,04	1398,72	1313,09	1296,03	943,07	1103,66	500,78	664,71	1,766E-07	2,275E-06
Pik3cd	38,53	41,38	105,26	120,35	153,85	121,35	170,72	147,71	1,768E-07	2,275E-06
Nfatc4	2350,19	2054,93	3700,46	3201,73	5445,55	3903,70	6111,85	5450,36	1,782E-07	2,29E-06
Rfx2	68,80	53,21	203,28	166,63	259,47	201,83	178,04	216,95	1,786E-07	2,293E-06
Imp4	3674,81	3069,39	2868,26	2609,25	1999,25	2170,28	1547,07	1614,45	1,787E-07	2,293E-06
Prkar1b	53,20	39,02	58,55	41,00	224,54	90,69	425,18	198,49	1,813E-07	2,324E-06
Msr1	0,00	0,00	19,08	29,09	28,28	33,21	39,02	21,93	1,819E-07	2,33E-06
Matn2	188,05	158,44	43,42	52,90	191,28	85,59	369,90	263,11	1,828E-07	2,339E-06
Ablim1	374,27	372,44	250,64	269,79	557,20	415,15	746,30	653,17	1,834E-07	2,345E-06
Igf2bp1	14070,88	16438,25	14791,96	12997,34	6604,02	9741,36	4216,83	6118,53	1,853E-07	2,367E-06

Grik1	2,75	4,73	39,47	55,54	49,90	107,30	36,58	50,78	1,856E-07	2,369E-06
Wnt11	167,87	107,59	17,76	5,29	44,08	30,66	59,35	40,39	1,865E-07	2,379E-06
Foxo4	927,42	1038,11	2440,66	2343,44	3029,65	2524,12	1576,33	2326,47	1,868E-07	2,381E-06
Runx3	6,42	4,73	32,89	31,74	69,86	53,65	370,71	47,31	1,889E-07	2,405E-06
Polr1b	3145,51	3018,55	2252,51	1938,76	1468,67	1560,97	1639,74	1306,33	1,906E-07	2,425E-06
Slit1	39,45	40,20	4,61	6,61	1,66	2,55	1,63	2,31	1,953E-07	2,482E-06
Ctps	5543,41	5663,47	4201,74	4057,37	2929,02	3577,97	2794,15	2685,37	1,956E-07	2,482E-06
Cnrip1	193,56	223,46	48,68	88,61	69,86	65,15	47,15	55,39	1,956E-07	2,482E-06
Mycbpap	4,59	8,28	45,39	51,58	52,39	70,26	52,84	72,70	1,976E-07	2,505E-06
Srp19	1245,73	1179,99	849,30	862,26	630,38	697,45	457,70	585,08	2,029E-07	2,57E-06
Tcf4	2891,41	4359,33	4783,29	6079,44	6648,93	7581,30	9880,74	12125,12	2,047E-07	2,591E-06
E2f4	2973,97	3048,11	2593,94	2515,36	2257,89	2236,71	1589,34	1578,68	2,089E-07	2,641E-06
Narf	987,04	867,85	1544,65	1432,25	1889,48	1637,61	2008,02	1999,89	2,096E-07	2,645E-06
Polr1e	1171,43	1135,06	907,19	735,30	530,58	605,48	544,68	458,14	2,095E-07	2,645E-06
Ndst4	0,00	1,18	3,95	2,64	80,67	30,66	9,76	28,85	2,1E-07	2,649E-06
Aqp1	24,77	52,02	7,89	6,61	34,93	14,05	312,18	64,62	2,102E-07	2,649E-06
Cars	1965,83	2077,39	1621,62	1501,02	1171,77	1296,55	795,08	986,67	2,129E-07	2,68E-06
Pogk	1206,28	1587,90	2113,70	2634,38	2806,77	3179,42	3489,23	3732,05	2,146E-07	2,7E-06
Pde10a	246,76	328,69	92,10	126,96	277,77	265,70	354,45	508,92	2,158E-07	2,712E-06
Wdr36	3203,31	3200,63	1918,97	1981,08	1565,97	1954,40	1456,01	1600,60	2,251E-07	2,827E-06
Oxr1	488,94	517,87	559,18	813,33	948,90	1033,41	1267,41	1375,57	2,259E-07	2,833E-06
Pcdhb8	1,83	1,18	9,21	13,22	41,58	17,88	76,42	42,70	2,26E-07	2,833E-06
Tstd3	393,53	256,57	212,49	183,82	169,65	163,51	71,54	92,32	2,322E-07	2,908E-06
Gfm1	2066,74	2193,26	1567,02	1588,30	1224,17	1374,47	1087,74	1047,84	2,342E-07	2,931E-06
Map3k11	2175,90	1745,15	1601,23	1276,19	1053,68	918,44	839,79	670,48	2,401E-07	3,002E-06
Gcnt4	31,19	34,29	163,15	157,38	61,54	84,31	33,33	58,85	2,405E-07	3,005E-06
Adgrl2	6881,79	8399,43	4286,61	4333,77	2704,48	3561,36	4017,66	3158,51	2,413E-07	3,01E-06
Gas6	34,86	24,83	38,81	62,16	101,46	71,53	201,61	140,79	2,412E-07	3,01E-06
Edil3	97,24	94,59	19,08	17,19	22,45	16,61	27,64	15,00	2,427E-07	3,024E-06
D10Wsu10%	2855,64	3106,04	2314,35	2261,44	1809,64	1958,24	1559,26	1442,50	2,434E-07	3,03E-06
Sema6c	460,50	244,75	1551,23	1281,48	1173,44	1002,75	1812,09	1159,77	2,438E-07	3,033E-06
Angptl4	302,72	191,54	655,89	449,64	844,11	632,31	1020,27	902,43	2,486E-07	3,089E-06
Igsf3	1725,49	1547,70	3307,71	2701,83	3263,34	2748,94	3881,08	3846,29	2,487E-07	3,089E-06
Pip5kl1	2,75	3,55	25,66	26,45	39,92	33,21	50,40	49,62	2,521E-07	3,129E-06
Selenop	385,28	352,34	517,08	559,41	1160,13	643,80	1595,84	1103,23	2,542E-07	3,151E-06
Tspan5	782,48	870,21	290,77	420,55	286,08	416,43	283,72	288,50	2,558E-07	3,169E-06
Ccr1	0,00	0,00	7,24	7,93	30,77	21,72	30,89	25,39	2,571E-07	3,182E-06
Crif1	233,92	127,69	2116,33	999,80	641,19	539,06	1040,59	433,91	2,579E-07	3,189E-06
Dock10	273,36	351,16	73,02	137,54	43,25	81,75	86,17	92,32	2,624E-07	3,243E-06
Cdh4	50,45	35,47	211,83	146,80	259,47	137,96	291,04	229,65	2,668E-07	3,294E-06
Spock3	15,59	18,92	88,81	88,61	84,83	141,79	49,59	60,01	2,705E-07	3,337E-06
Trhde	0,92	2,36	0,66	5,29	45,74	44,71	22,76	49,62	2,742E-07	3,38E-06
Ppfia3	33,02	36,65	96,71	58,19	184,62	109,86	205,68	176,56	2,747E-07	3,383E-06
Efna5	444,90	763,80	182,88	207,63	131,40	191,61	556,07	360,05	2,815E-07	3,464E-06
Selenbp1	56,87	29,56	59,87	56,87	240,34	102,19	369,90	208,87	2,86E-07	3,516E-06
Slc18a1	136,68	67,39	19,08	3,97	14,97	5,11	5,69	5,77	2,897E-07	3,559E-06
Edar	28,44	26,01	225,65	391,45	104,79	333,40	158,53	190,41	2,909E-07	3,571E-06
Stra6	1650,27	1314,78	342,09	171,92	783,40	347,45	1825,10	1065,15	3,039E-07	3,727E-06
Shisa3	268,78	225,83	73,68	153,41	87,32	149,45	17,89	35,77	3,056E-07	3,745E-06
Tcaf2	174,29	134,79	309,19	306,82	386,71	343,62	400,79	437,37	3,136E-07	3,839E-06

Bdh1	185,30	165,53	396,69	411,29	453,24	373,00	493,47	413,13	3,211E-07	3,928E-06
Ust	217,41	210,46	210,51	208,95	191,28	217,16	84,55	70,39	3,261E-07	3,986E-06
Bhlhe40	162,37	137,15	32,89	52,90	23,29	42,15	39,02	35,77	3,298E-07	4,028E-06
Zbtb8a	88,98	72,12	176,31	150,76	157,18	178,83	438,19	255,03	3,358E-07	4,098E-06
Ttll7	28,44	18,92	55,26	55,54	123,08	93,25	108,94	226,18	3,404E-07	4,151E-06
2010111101	732,94	517,87	738,78	825,23	1252,44	992,53	1802,34	1550,98	3,41E-07	4,155E-06
Irx1	60,54	55,57	2,63	1,32	126,41	3,83	334,94	274,65	3,416E-07	4,158E-06
Cd40	113,75	104,05	342,09	365,00	93,14	203,10	68,29	87,70	3,435E-07	4,178E-06
Ebf1	83,48	107,59	153,94	133,57	311,86	374,27	228,44	405,06	3,577E-07	4,347E-06
Med8	1675,04	1475,58	1258,48	1150,56	984,66	1046,18	757,68	728,18	3,592E-07	4,361E-06
Cldn6	23,85	44,93	72,36	50,25	94,81	42,15	4,06	1,15	3,598E-07	4,365E-06
Nsg1	968,70	749,61	1183,49	1244,45	1734,79	1571,19	1901,52	1954,88	3,606E-07	4,369E-06
Plch1	321,06	244,75	94,07	122,99	89,82	111,13	58,53	93,47	3,607E-07	4,369E-06
Zfp956	80,72	99,32	189,46	207,63	235,35	206,94	296,73	257,34	3,739E-07	4,525E-06
Klf8	14,68	23,65	38,81	63,48	90,65	86,86	104,87	168,48	3,751E-07	4,535E-06
Iars	7908,27	7533,95	6498,99	5926,04	4676,29	4999,70	4225,78	4124,41	3,776E-07	4,562E-06
Slc27a1	95,40	73,31	146,04	255,24	187,12	236,32	374,78	379,67	3,782E-07	4,566E-06
Tyrobp	1,83	3,55	34,21	55,54	74,85	45,99	157,71	43,85	3,791E-07	4,573E-06
Jakmip2	55,04	60,30	157,23	161,34	211,24	192,89	134,14	177,72	3,832E-07	4,618E-06
Rap1gds1	2855,64	3357,88	1889,37	2056,46	1088,61	1725,75	1075,55	1178,24	3,85E-07	4,637E-06
Sp6	101,82	165,53	99,34	62,16	175,48	70,26	7,32	13,85	3,859E-07	4,644E-06
Shisa2	447,66	310,96	705,88	685,04	541,39	565,88	990,19	1001,68	3,878E-07	4,663E-06
Tmem198b	251,35	240,02	355,90	398,07	574,66	504,57	525,99	611,62	3,887E-07	4,669E-06
Naa25	2726,30	3140,33	1848,58	1922,89	1195,06	1661,88	1219,44	1298,25	3,97E-07	4,766E-06
Phyhip	7,34	3,55	48,02	47,61	106,45	56,21	281,28	58,85	4,098E-07	4,915E-06
Elovl7	39,45	56,75	5,26	1,32	6,65	6,39	3,25	2,31	4,154E-07	4,977E-06
Slitrk6	144,94	174,99	70,39	58,19	8,32	14,05	154,46	46,16	4,174E-07	4,998E-06
Ildr2	122,92	141,88	70,39	62,16	44,91	54,93	27,64	32,31	4,203E-07	5,029E-06
Apela	3,67	3,55	6,58	6,61	27,44	6,39	92,68	55,39	4,218E-07	5,042E-06
Psd2	59,63	205,73	8,55	19,84	24,12	19,16	15,45	13,85	4,277E-07	5,109E-06
Magee2	48,62	44,93	273,67	165,31	181,30	158,40	221,13	153,48	4,283E-07	5,112E-06
Emp3	28,44	21,28	103,94	58,19	169,65	91,97	328,44	152,33	4,293E-07	5,119E-06
Cic	1718,15	2234,65	2834,71	3021,87	4267,95	3429,79	5096,46	4581,39	4,311E-07	5,136E-06
Nolc1	8415,56	10596,25	8396,25	6058,28	5443,05	5261,56	3722,55	3815,14	4,344E-07	5,172E-06
Rbpms2	729,27	591,18	945,34	833,16	464,88	535,23	356,89	249,26	4,362E-07	5,189E-06
Igfbp5	2978,56	2712,32	1253,88	595,12	1910,27	848,19	543,06	455,83	4,414E-07	5,246E-06
Pitpnm1	168,79	166,71	264,46	343,84	622,06	431,76	434,12	596,62	4,422E-07	5,252E-06
Sorcs2	409,13	224,65	161,83	107,12	538,90	254,20	1747,05	620,85	4,441E-07	5,27E-06
Barx2	1,83	0,00	3,29	2,64	0,00	0,00	113,81	10,39	4,467E-07	5,293E-06
Agtr2	0,00	0,00	6,58	1,32	18,30	10,22	34,96	50,78	4,467E-07	5,293E-06
Atl3	548,56	782,72	711,15	946,90	1051,19	1156,04	1683,64	1979,12	4,52E-07	5,351E-06
Pwp1	3313,38	3140,33	2444,60	2168,87	1781,36	1991,45	1674,70	1505,97	4,533E-07	5,358E-06
Clec1b	147,69	79,22	46,71	39,67	32,43	33,21	8,94	17,31	4,532E-07	5,358E-06
Osr1	75,22	42,56	16,45	27,77	5,82	3,83	252,02	46,16	4,558E-07	5,383E-06
Foxd2	68,80	18,92	3,29	2,64	1,66	2,55	0,00	1,15	4,579E-07	5,404E-06
Zfp365	68,80	61,48	107,23	133,57	156,35	223,54	242,26	223,88	4,605E-07	5,43E-06
Plekkg3	451,32	558,07	1223,62	1097,66	1277,39	1064,06	1138,96	988,98	4,66E-07	5,49E-06
Celsr1	421,05	303,86	454,58	460,22	920,62	725,56	911,33	822,80	4,79E-07	5,639E-06
Tshz3	365,10	711,78	246,04	306,82	203,75	200,55	109,75	143,10	4,82E-07	5,669E-06
Sfn	3,67	4,73	73,02	21,16	113,93	47,26	8,13	3,46	5,04E-07	5,924E-06

Zeb2	285,29	463,48	98,02	122,99	83,16	99,64	195,92	111,94	5,13E-07	6,024E-06
Trmt6	1892,45	1883,49	1028,23	1196,84	928,11	1235,23	699,15	814,73	5,152E-07	6,045E-06
C77080	243,09	219,92	549,97	415,26	757,62	500,74	1011,32	701,63	5,164E-07	6,055E-06
Coro2a	8,26	14,19	34,21	38,35	70,69	71,53	73,17	64,62	5,213E-07	6,108E-06
Foxj2	151,36	225,83	269,06	346,49	473,20	389,60	615,41	579,31	5,285E-07	6,186E-06
Ppp1r26	206,40	300,32	376,95	370,29	638,70	452,20	730,85	826,27	5,393E-07	6,303E-06
Zdhhc2	190,80	209,28	42,76	60,83	74,02	99,64	73,98	88,86	5,39E-07	6,303E-06
Fam169a	615,53	705,86	191,44	245,98	167,99	281,03	204,87	298,89	5,554E-07	6,486E-06
Nos1	75,22	79,22	13,16	6,61	12,47	7,66	24,39	13,85	5,708E-07	6,66E-06
Krt19	82,56	34,29	9,87	7,93	11,64	10,22	1,63	3,46	5,729E-07	6,675E-06
Cacna1c	163,28	358,25	534,18	1149,24	1154,31	2070,65	1479,59	2651,90	5,728E-07	6,675E-06
Klf5	7,34	9,46	17,76	25,13	39,92	37,04	73,17	68,09	5,739E-07	6,681E-06
Rap1gap	58,71	52,02	82,23	75,38	136,39	108,58	228,44	170,79	5,757E-07	6,697E-06
Gse1	731,11	1105,50	901,27	950,86	1937,71	1447,28	2204,75	2278,00	5,795E-07	6,735E-06
Bche	272,45	270,76	65,13	108,44	90,65	100,91	54,47	91,17	5,804E-07	6,736E-06
Utp18	1723,66	1768,80	1157,83	1215,36	904,82	1159,87	766,62	793,95	5,804E-07	6,736E-06
Timp3	752,21	683,40	2561,70	2192,67	1450,37	1794,73	2477,91	1457,51	5,874E-07	6,811E-06
Ero1l	998,05	1171,71	559,18	760,43	345,13	600,37	193,48	311,58	5,879E-07	6,811E-06
Hfe	4,59	4,73	18,42	21,16	55,72	33,21	56,91	55,39	5,908E-07	6,836E-06
Glr3	104,58	122,96	88,15	156,05	227,87	277,19	337,38	386,59	5,909E-07	6,836E-06
Samd9l	0,00	1,18	15,79	17,19	14,97	11,50	36,58	41,54	5,981E-07	6,913E-06
Mxd3	145,85	78,04	315,11	298,88	633,71	371,72	628,42	430,44	6,35E-07	7,334E-06
Agbl5	506,36	384,26	734,17	769,68	1223,34	877,57	1151,97	1284,41	6,499E-07	7,499E-06
Tceal8	3638,12	2669,75	1918,32	1700,71	1535,20	1474,11	1453,58	1119,38	6,503E-07	7,499E-06
Ppm1l	558,65	759,07	806,53	1035,50	1437,07	1291,44	1663,32	1644,46	6,542E-07	7,538E-06
Slc25a23	135,76	140,70	226,96	175,89	332,65	265,70	546,31	366,97	6,618E-07	7,62E-06
Gng12	2610,71	2594,08	1810,43	1805,19	1687,39	2115,36	886,13	1170,16	6,745E-07	7,76E-06
Wdr72	1,83	1,18	1,97	11,90	59,05	47,26	30,08	63,47	6,769E-07	7,782E-06
Tcp11l1	165,12	248,29	383,53	452,29	493,99	608,04	587,77	718,94	6,776E-07	7,783E-06
Cct4	14952,43	12323,66	8757,42	8314,44	7336,69	7751,19	7270,32	6229,31	6,814E-07	7,82E-06
Tmem200c	33,94	20,10	25,66	10,58	104,79	20,44	209,74	255,03	6,82E-07	7,822E-06
Thumpd3	1313,61	1297,04	786,14	896,64	461,56	728,11	374,78	497,38	6,834E-07	7,831E-06
Lama2	55,04	31,92	260,51	157,38	176,31	109,86	299,98	221,57	6,974E-07	7,986E-06
Casz1	25,69	23,65	132,89	132,25	197,93	220,99	71,54	201,95	6,994E-07	8,002E-06
Degs1	1420,94	1313,59	832,19	757,78	793,38	825,19	740,61	708,56	7,215E-07	8,249E-06
Psmd12	3833,51	3860,38	3168,91	2968,97	2457,48	2774,49	1884,45	2019,51	7,26E-07	8,274E-06
Srfbp1	965,95	915,14	749,96	625,53	419,98	484,13	485,34	426,98	7,254E-07	8,274E-06
Fam234b	293,54	334,61	462,47	491,96	651,17	533,95	746,30	739,72	7,26E-07	8,274E-06
Grem1	506,36	616,01	1190,07	1024,92	261,97	1191,80	40,65	106,17	7,246E-07	8,274E-06
Lor	0,00	1,18	57,89	23,80	46,57	26,83	111,38	32,31	7,358E-07	8,379E-06
Spel1	46,78	73,31	138,81	257,88	254,48	328,29	260,96	436,21	7,368E-07	8,385E-06
Mrpl44	1024,65	854,84	779,56	700,91	484,84	513,51	467,45	414,29	7,396E-07	8,41E-06
Rgs9	63,30	60,30	380,24	612,31	242,01	479,02	85,36	241,19	7,448E-07	8,462E-06
1190002N1	447,66	655,02	609,84	1306,61	1960,16	2863,91	1742,99	2520,34	7,467E-07	8,478E-06
Casd1	4099,53	5814,81	1508,47	2441,30	1096,10	1972,29	1104,00	1609,84	7,568E-07	8,577E-06
Rab27a	33,94	48,48	115,78	97,86	107,28	90,69	188,61	160,41	7,569E-07	8,577E-06
Spsb4	1227,38	1048,75	405,24	402,03	632,87	390,88	503,22	593,16	7,572E-07	8,577E-06
Ism1	79,81	98,14	154,60	228,79	258,64	355,11	628,42	305,81	7,632E-07	8,638E-06
Sdf2l1	771,47	533,24	595,36	454,93	284,42	265,70	269,09	249,26	7,749E-07	8,763E-06
Dennd3	33,94	22,46	38,81	39,67	87,32	57,48	156,90	118,86	7,774E-07	8,785E-06

Amt	626,53	449,29	1034,15	867,55	530,58	587,60	304,86	366,97	7,783E-07	8,788E-06
Zfp316	285,29	261,30	563,79	428,48	758,45	539,06	791,82	788,18	7,791E-07	8,79E-06
Cdo1	1827,32	1247,38	517,08	252,59	306,87	204,38	899,95	364,67	7,853E-07	8,854E-06
Hsd3b6	44,95	13,01	44,08	33,06	118,09	63,87	410,55	152,33	7,979E-07	8,989E-06
Ccbe1	21,10	16,55	1,97	0,00	65,70	26,83	34,14	61,16	8,14E-07	9,163E-06
Ptprg	2699,69	3110,77	4562,91	4546,69	2054,14	2780,87	2001,51	2050,66	8,252E-07	9,282E-06
Cadm4	123,84	114,69	217,09	201,02	308,54	187,78	476,40	381,98	8,325E-07	9,357E-06
Lrrc3	66,05	66,21	89,47	91,25	238,68	140,51	255,27	207,72	8,504E-07	9,551E-06
Ldlrap1	405,46	300,32	598,65	550,15	868,23	762,60	948,73	803,19	8,574E-07	9,622E-06
Pacsin3	134,85	150,16	234,86	202,34	454,90	304,02	439,00	378,51	8,602E-07	9,646E-06
Igf2bp2	8867,80	9445,82	9321,20	7568,56	5813,96	6711,40	3538,01	4482,15	8,729E-07	9,781E-06
Entpd6	862,29	689,31	669,70	539,57	493,99	481,58	312,99	298,89	8,742E-07	9,789E-06
Arsi	5,50	3,55	5,26	9,26	15,80	3,83	334,13	16,16	8,762E-07	9,804E-06
Mertk	197,23	242,38	515,76	511,80	457,40	624,64	602,40	925,51	8,822E-07	9,863E-06
Pgap1	198,14	240,02	227,62	216,89	311,86	315,51	452,82	512,38	8,874E-07	9,914E-06
Cpxm2	0,00	3,55	1,97	1,32	7,48	2,55	94,30	26,54	9,039E-07	1,008E-05
Slc2a13	21,10	20,10	25,00	30,42	26,61	51,10	117,88	106,17	9,04E-07	1,008E-05
Daam2	938,43	1256,84	3441,92	2672,73	1472,83	1449,84	1991,76	1409,04	9,109E-07	1,015E-05
Cmklr1	220,16	300,32	94,07	72,74	92,31	68,98	135,76	107,32	9,134E-07	1,017E-05
Zbtb4	17,43	33,11	55,92	70,09	91,48	76,64	126,82	156,94	9,166E-07	1,02E-05
Tmem51	38,53	31,92	53,29	62,16	148,03	77,92	234,13	147,71	9,235E-07	1,027E-05
Nop2	4737,99	4588,71	3504,41	2722,99	2046,65	2252,04	2273,04	1593,68	9,289E-07	1,032E-05
Ptcd3	2845,55	2914,50	1680,83	1883,21	1307,33	1783,23	1183,67	1309,79	9,565E-07	1,062E-05
Parp4	59,63	42,56	75,65	100,51	154,68	140,51	178,85	185,79	9,694E-07	1,076E-05
Wisp1	157,78	219,92	32,89	42,32	68,19	51,10	176,41	92,32	9,939E-07	1,102E-05
Colec12	850,36	1048,75	251,30	222,18	280,26	288,69	831,66	339,28	9,956E-07	1,103E-05
Nol9	3351,91	3340,15	2537,36	2246,89	1809,64	1932,69	1917,78	1735,62	1,003E-06	1,11E-05
Wdsub1	112,83	113,51	223,01	256,56	299,39	270,81	276,41	266,57	1,004E-06	1,111E-05
Sptb	600,85	763,80	885,48	954,83	408,33	611,87	69,91	210,03	1,008E-06	1,114E-05
Mad2l1	4397,66	4183,16	2383,42	2695,22	2123,17	2762,99	1576,33	1982,58	1,011E-06	1,117E-05
Col5a1	2197,00	1551,25	1751,22	1374,06	5013,93	2275,03	10380,71	4719,88	1,016E-06	1,122E-05
Vamp3	3581,24	3194,72	1902,53	2273,34	1942,70	2133,24	1539,75	1692,92	1,046E-06	1,154E-05
Stx2	304,55	258,94	468,40	460,22	732,67	562,05	654,43	670,48	1,047E-06	1,154E-05
Atp2b4	150,44	114,69	519,05	411,29	505,63	421,54	1335,70	461,60	1,069E-06	1,177E-05
Mapk1ip1l	7619,32	8290,66	6861,47	6435,19	4798,54	5467,22	4292,44	4073,63	1,079E-06	1,188E-05
Wdr73	1185,19	1114,96	968,37	827,87	596,28	671,91	556,88	583,93	1,08E-06	1,188E-05
Fry	16,51	13,01	32,24	27,77	86,49	84,31	50,40	50,78	1,087E-06	1,194E-05
Shmt1	3445,48	3109,59	2784,72	2250,86	2183,87	2179,22	1481,22	1561,37	1,097E-06	1,204E-05
Mcf2l	44,95	44,93	48,02	64,80	87,32	117,52	146,33	195,03	1,123E-06	1,233E-05
Fchsd1	107,33	105,23	205,91	165,31	230,36	222,27	295,92	297,73	1,145E-06	1,256E-05
Sms	2442,84	2343,42	1168,36	1516,89	884,86	1370,64	669,07	897,81	1,155E-06	1,265E-05
Mecom	5137,95	6364,61	7691,03	7608,23	9676,91	8638,98	11579,01	13382,98	1,156E-06	1,266E-05
St8sia1	79,81	101,68	132,89	177,21	217,06	259,31	262,59	325,43	1,167E-06	1,276E-05
Pde9a	122,92	73,31	207,23	227,47	265,29	229,93	399,16	324,28	1,17E-06	1,278E-05
Epha3	1204,45	1334,88	296,69	531,64	1695,70	1962,07	563,38	1087,07	1,172E-06	1,28E-05
Csdc2	47,70	22,46	197,36	170,60	158,01	113,69	191,05	140,79	1,193E-06	1,302E-05
Ctps2	573,33	391,36	1109,15	896,64	1279,06	1135,60	1603,16	1241,71	1,209E-06	1,318E-05
Erg	733,86	841,84	216,44	186,47	666,97	348,73	583,71	790,49	1,211E-06	1,319E-05
Smoc2	87,15	85,13	7,24	1,32	4,99	10,22	75,61	19,62	1,253E-06	1,365E-05
C330018D2	97,24	107,59	21,71	23,80	84,00	54,93	97,56	114,25	1,26E-06	1,371E-05

Bbs9	264,19	211,64	292,09	308,14	502,31	417,71	561,76	545,84	1,272E-06	1,383E-05
Mrps18b	819,17	672,76	542,08	372,94	285,25	311,68	321,93	255,03	1,288E-06	1,399E-05
Epha5	6,42	10,64	64,47	163,99	69,03	134,13	60,16	81,93	1,288E-06	1,399E-05
Rassf9	50,45	65,03	344,06	372,94	227,87	304,02	50,40	162,71	1,298E-06	1,409E-05
Hpse2	57,79	53,21	250,64	154,73	186,29	252,92	105,69	129,25	1,306E-06	1,415E-05
Peli2	466,00	519,05	444,71	371,62	848,27	472,63	1149,53	1344,41	1,325E-06	1,434E-05
Naga	100,91	85,13	192,75	201,02	340,14	224,82	384,53	276,96	1,325E-06	1,434E-05
Ptpn13	1844,74	1929,60	915,74	938,96	1323,96	1189,25	1219,44	1369,80	1,329E-06	1,437E-05
Lmo1	545,81	253,02	940,08	592,47	661,15	588,88	152,84	173,10	1,342E-06	1,451E-05
Pdgfc	987,96	1101,95	1631,49	1725,84	2137,30	2243,09	2863,25	2057,59	1,348E-06	1,456E-05
Eln	33,94	17,74	133,55	68,77	245,33	113,69	383,72	177,72	1,362E-06	1,47E-05
Polr3gl	120,17	101,68	203,94	186,47	285,25	214,60	330,06	323,12	1,366E-06	1,473E-05
Dlx1	3,67	1,18	26,97	14,55	42,41	38,32	3,25	2,31	1,411E-06	1,52E-05
Zpld1	0,00	0,00	0,66	1,32	30,77	39,60	2,44	10,39	1,412E-06	1,521E-05
Rab11fip1	632,04	631,38	724,96	644,05	431,62	485,41	248,77	328,89	1,428E-06	1,537E-05
Prr16	0,00	2,36	3,29	11,90	24,12	20,44	81,30	36,93	1,439E-06	1,546E-05
Psme3	7421,17	7074,02	5284,58	5414,24	4712,88	4787,65	4186,75	3994,01	1,439E-06	1,546E-05
Vstm2b	49,54	59,12	1,97	6,61	2,49	1,28	8,13	1,15	1,45E-06	1,557E-05
Tmem169	22,02	11,82	54,60	62,16	93,14	67,70	95,12	115,40	1,457E-06	1,563E-05
Csn3	32,11	31,92	0,00	0,00	0,00	0,00	1,63	0,00	1,458E-06	1,564E-05
Arid3a	2337,35	3523,41	3252,45	3035,09	1120,21	1756,41	383,72	942,82	1,478E-06	1,583E-05
Camsap3	73,39	37,84	211,17	120,35	366,75	235,04	352,01	250,42	1,489E-06	1,594E-05
Flnb	4538,93	3010,27	4209,64	3709,56	11039,96	5805,73	14747,13	9971,75	1,507E-06	1,612E-05
Tiparp	1165,01	1922,51	892,71	1199,49	245,33	628,48	350,39	348,51	1,518E-06	1,623E-05
Lap3	4905,86	3426,46	2987,99	2307,73	1960,16	2006,78	1769,82	1437,89	1,533E-06	1,638E-05
Hdac8	199,06	218,74	393,40	402,03	464,88	365,33	523,55	516,99	1,535E-06	1,639E-05
Prdx3	1967,67	1695,49	1031,52	1047,40	992,14	1073,01	998,32	829,73	1,547E-06	1,651E-05
Tmem176a	144,94	98,14	432,21	286,98	554,70	325,73	645,49	475,45	1,555E-06	1,658E-05
P2ry12	0,00	0,00	1,97	2,64	14,97	10,22	37,40	21,93	1,585E-06	1,689E-05
Yars2	873,30	814,64	507,21	523,70	417,48	500,74	329,25	407,36	1,604E-06	1,707E-05
Dusp6	4278,41	5191,71	11588,18	11656,34	3348,16	7067,79	3552,64	3381,23	1,632E-06	1,736E-05
Mdfi	564,16	261,30	917,71	833,16	2329,41	1278,67	1846,24	1537,13	1,645E-06	1,748E-05
Bicc1	285,29	435,11	444,05	540,89	672,79	790,70	1067,42	935,90	1,647E-06	1,749E-05
Pfkl	13448,93	11399,06	10425,09	6470,90	6351,20	5481,27	4861,51	4264,04	1,67E-06	1,772E-05
Pde8b	3,67	2,36	11,18	3,97	19,13	15,33	94,30	36,93	1,671E-06	1,772E-05
Pgm2	2320,84	1618,64	1600,57	899,29	667,80	522,45	765,00	511,22	1,688E-06	1,789E-05
Tlr1	0,00	1,18	5,26	2,64	6,65	12,77	43,09	33,47	1,721E-06	1,823E-05
Pcdhb14	7,34	4,73	14,47	17,19	35,76	33,21	72,35	48,47	1,749E-06	1,849E-05
Sarm1	12,84	18,92	35,52	44,96	59,88	45,99	120,32	85,40	1,748E-06	1,849E-05
Fzd1	1104,46	861,94	1390,71	1095,01	2097,38	1751,30	2678,71	2141,83	1,763E-06	1,864E-05
Slc35e3	306,39	386,63	367,74	505,19	531,42	576,10	911,33	847,04	1,774E-06	1,874E-05
Ruvbl1	2711,62	2501,86	2142,65	1855,44	1580,11	1477,94	1405,61	1267,10	1,782E-06	1,88E-05
Cadm1	2168,56	2200,36	1164,41	1084,43	1593,41	1525,20	1614,54	1749,47	1,792E-06	1,89E-05
Etv1	121,09	161,98	115,78	165,31	202,09	242,70	445,50	347,36	1,819E-06	1,916E-05
P4ha1	3140,93	2432,10	1611,75	1407,12	1126,03	1301,66	1547,07	1201,32	1,83E-06	1,926E-05
Zfp185	24,77	35,47	21,05	23,80	51,56	54,93	115,44	91,17	1,833E-06	1,928E-05
Nudt10	213,74	208,09	94,73	111,09	54,06	88,14	69,10	63,47	1,838E-06	1,933E-05
Rprml	1,83	0,00	74,34	18,51	1,66	6,39	0,81	0,00	1,866E-06	1,96E-05
Aff3	1936,48	2635,46	1734,77	937,64	454,90	494,35	1921,03	1033,99	1,886E-06	1,981E-05
Nmi	6,42	11,82	22,37	30,42	54,89	43,43	73,17	69,24	1,896E-06	1,989E-05

Pgf	11,01	8,28	19,74	13,22	60,71	48,54	54,47	64,62	1,911E-06	2,003E-05
Lrrc56	144,02	81,58	444,05	312,11	464,88	337,23	522,73	400,44	1,92E-06	2,011E-05
Notch2	2189,66	2017,09	2389,34	2410,88	2641,27	2292,91	6582,55	3930,54	1,944E-06	2,036E-05
Gucy2c	0,00	0,00	44,73	64,80	4,99	29,38	0,00	3,46	2,032E-06	2,126E-05
Hcn4	130,26	108,78	19,74	15,87	36,59	19,16	79,67	41,54	2,036E-06	2,128E-05
Cpne8	17,43	16,55	8,55	13,22	24,12	38,32	121,13	58,85	2,078E-06	2,171E-05
Cdv3	6185,53	7576,52	3974,78	4423,70	3079,55	4131,07	2434,82	3090,42	2,1E-06	2,192E-05
Dock2	4,59	2,36	30,26	26,45	60,71	42,15	79,67	35,77	2,144E-06	2,237E-05
Chd7	3737,19	6151,78	5130,64	4862,76	1768,06	3206,25	743,05	1516,36	2,15E-06	2,242E-05
Shb	280,70	268,39	725,62	592,47	503,14	398,55	317,87	353,13	2,161E-06	2,251E-05
Utrn	2421,74	3588,44	1495,31	978,64	943,07	873,73	1764,13	1128,62	2,166E-06	2,253E-05
Col4a6	172,46	186,81	40,13	27,77	71,52	30,66	83,74	91,17	2,165E-06	2,253E-05
Bend4	1761,27	2945,24	1058,49	1211,39	646,18	1043,63	375,59	717,79	2,177E-06	2,264E-05
Gspt1	9390,67	10106,75	8464,67	7499,79	5275,06	6521,07	4561,53	5024,53	2,23E-06	2,317E-05
Aldh6a1	266,94	266,03	238,14	281,69	417,48	379,38	565,01	511,22	2,241E-06	2,326E-05
Ddx58	18,35	21,28	53,94	55,54	81,50	70,26	97,56	88,86	2,246E-06	2,33E-05
Pias3	342,16	359,44	492,08	687,69	916,46	712,78	879,62	935,90	2,291E-06	2,375E-05
Ankrd6	293,54	292,04	658,52	733,98	355,11	454,75	440,63	466,22	2,302E-06	2,385E-05
Ubl4b	54,12	55,57	36,84	25,13	9,15	6,39	8,94	6,92	2,311E-06	2,392E-05
Epb41l5	1256,74	1673,03	896,66	837,13	433,28	804,75	352,01	474,30	2,335E-06	2,415E-05
Scin	1,83	1,18	0,00	0,00	23,29	1,28	24,39	113,09	2,499E-06	2,583E-05
Cxxc4	66,05	70,94	359,19	439,06	235,35	395,99	182,10	426,98	2,507E-06	2,588E-05
Gm2115	0,00	0,00	0,00	0,00	0,83	1,28	76,42	8,08	2,507E-06	2,588E-05
Slc6a15	76,14	147,79	19,08	31,74	24,95	24,27	13,01	23,08	2,521E-06	2,6E-05
Dars2	1248,48	1071,21	936,79	856,97	780,91	761,32	464,20	565,46	2,565E-06	2,644E-05
Hemgn	188,97	164,35	241,43	396,74	115,60	307,85	4,88	31,16	2,571E-06	2,649E-05
Znhit6	943,93	1052,29	665,75	763,07	547,22	532,67	514,60	519,30	2,592E-06	2,668E-05
Acsl5	888,89	820,55	394,72	433,77	568,01	512,23	498,35	431,60	2,61E-06	2,685E-05
Eml3	1392,50	1246,20	1080,86	1028,89	782,57	809,86	682,07	718,94	2,638E-06	2,711E-05
Car3	77,06	46,11	13,16	14,55	12,47	8,94	1,63	6,92	2,644E-06	2,716E-05
Gbe1	649,47	562,80	659,83	535,60	279,43	403,65	250,39	250,42	2,65E-06	2,72E-05
Klf14	47,70	53,21	7,24	5,29	2,49	6,39	11,38	6,92	2,689E-06	2,759E-05
Acsl6	45,87	70,94	0,66	6,61	11,64	10,22	4,88	5,77	2,697E-06	2,764E-05
Prdx6	12232,55	9156,14	8465,99	6408,74	5523,72	5089,12	4778,59	3631,65	2,712E-06	2,778E-05
Nifk	3686,74	2985,44	2395,26	1863,38	1671,59	1679,77	1612,92	1276,33	2,775E-06	2,839E-05
Sun2	852,20	755,52	1324,27	1280,16	2082,42	1567,36	1880,38	1583,29	2,776E-06	2,839E-05
Gdpd1	162,37	132,42	179,60	160,02	262,80	232,48	356,08	351,97	2,787E-06	2,849E-05
Tlnrd1	1914,46	1404,64	4310,95	2979,55	2372,66	2392,55	1562,51	1400,96	2,806E-06	2,866E-05
Klf1	174,29	135,97	140,78	111,09	59,88	72,81	16,26	40,39	2,812E-06	2,871E-05
Lgals9	7,34	0,00	19,74	18,51	42,41	24,27	198,36	50,78	2,816E-06	2,873E-05
Dgkz	6020,42	4958,79	3311,66	2396,33	2981,41	2174,12	2351,90	1920,26	2,821E-06	2,875E-05
Ncan	11,01	21,28	57,89	50,25	70,69	63,87	96,74	91,17	2,848E-06	2,901E-05
Slc19a1	847,61	919,87	634,83	560,73	499,81	503,29	433,31	454,68	2,859E-06	2,91E-05
Cyp2d22	7,34	11,82	21,71	33,06	44,91	52,37	69,91	73,86	2,861E-06	2,911E-05
Zmiz1	4301,35	6215,63	12026,32	11541,29	11224,58	11966,58	9225,49	8446,15	2,9E-06	2,948E-05
Pcdh18	2894,17	4126,41	2853,13	3160,73	2073,27	2421,93	6273,63	5060,31	2,937E-06	2,982E-05
Tmem119	1920,88	954,16	5686,53	4046,79	6655,58	4893,68	5185,07	4066,71	2,937E-06	2,982E-05
Clec14a	138,52	105,23	143,41	122,99	233,69	155,84	534,93	306,97	2,947E-06	2,99E-05
Pcdh9	0,00	3,55	11,84	10,58	25,78	11,50	60,16	48,47	2,964E-06	3,004E-05
Arhgap33	271,53	302,68	500,63	826,55	1160,13	941,44	660,94	1043,22	2,981E-06	3,019E-05

Ptch1	674,24	968,35	2884,05	3647,40	1410,45	3355,70	873,93	1250,94	2,991E-06	3,028E-05
Lmna	148,61	85,13	288,14	191,76	610,42	232,48	1411,30	515,84	2,998E-06	3,032E-05
Elk3	1676,87	1819,64	3581,38	3250,66	2788,47	3049,13	3189,25	2848,08	3,047E-06	3,08E-05
Palld	665,98	611,28	1392,03	1285,45	1459,52	1053,85	2138,90	1502,51	3,049E-06	3,08E-05
Wdr55	1630,09	1159,89	960,47	724,72	714,37	627,20	569,07	500,84	3,062E-06	3,091E-05
Arpc1b	738,45	620,74	1468,34	1389,93	1312,32	1118,99	926,78	811,26	3,07E-06	3,097E-05
Plscr1	675,15	607,73	514,45	457,58	463,22	430,48	295,92	267,73	3,085E-06	3,106E-05
Slnf5	7,34	3,55	23,03	17,19	19,13	38,32	61,79	81,93	3,083E-06	3,106E-05
Tac1	9,17	2,36	11,84	22,48	64,04	38,32	268,28	42,70	3,086E-06	3,106E-05
Armcx6	122,00	93,41	135,52	140,18	271,94	214,60	264,21	303,50	3,166E-06	3,185E-05
Ypel2	39,45	68,58	48,02	81,99	82,33	100,91	182,10	301,19	3,185E-06	3,202E-05
Acvr2b	1704,39	1768,80	1801,88	1352,90	893,18	1135,60	412,98	713,17	3,188E-06	3,203E-05
2810408A1	91,73	112,32	217,75	289,62	301,88	272,08	264,21	353,13	3,196E-06	3,209E-05
Prkd1	436,65	455,21	244,07	178,53	143,04	175,00	271,53	212,34	3,211E-06	3,221E-05
Col16a1	251,35	250,66	320,38	202,34	443,26	288,69	1064,17	609,31	3,238E-06	3,246E-05
Csrnp1	196,31	240,02	221,04	185,15	97,30	88,14	98,37	99,24	3,252E-06	3,258E-05
Cd53	0,92	1,18	7,89	17,19	24,12	17,88	44,71	38,08	3,286E-06	3,29E-05
Pdgfrl	17,43	15,37	165,12	119,02	119,76	99,64	137,39	49,62	3,294E-06	3,296E-05
Gpd2	1274,17	1358,52	965,08	958,80	785,06	860,96	659,31	703,94	3,309E-06	3,307E-05
Polr3g	732,03	878,49	484,18	525,02	312,69	407,49	225,19	347,36	3,31E-06	3,307E-05
Rgcc	46,78	44,93	3,29	2,64	11,64	7,66	59,35	23,08	3,332E-06	3,327E-05
Arhgef19	5,50	3,55	33,55	18,51	70,69	40,88	69,91	46,16	3,404E-06	3,397E-05
Set	19569,33	20098,82	15572,18	15176,79	11989,69	13680,83	9045,01	10903,03	3,5E-06	3,49E-05
Plat	306,39	156,07	38,16	39,67	74,02	45,99	119,51	58,85	3,517E-06	3,505E-05
Dysf	576,08	527,33	1401,24	1239,16	1632,50	1235,23	1853,55	1196,70	3,524E-06	3,509E-05
Cdk20	80,72	79,22	185,52	204,98	251,15	200,55	179,66	183,49	3,53E-06	3,512E-05
Ell3	3,67	2,36	13,16	10,58	37,42	25,55	47,96	39,24	3,586E-06	3,563E-05
Sox7	414,63	332,24	117,10	95,22	179,63	116,24	217,87	146,56	3,583E-06	3,563E-05
Vegfc	289,88	353,52	265,12	245,98	98,13	206,94	75,61	80,78	3,62E-06	3,595E-05
Sfrp2	1086,11	1086,58	557,21	538,25	689,43	639,97	831,66	733,95	3,625E-06	3,598E-05
Rps6ka4	77,06	53,21	65,13	63,48	166,33	109,86	311,36	174,25	3,629E-06	3,599E-05
Polr3h	992,55	715,32	519,05	523,70	531,42	482,85	352,83	338,12	3,701E-06	3,668E-05
Pdk2	121,09	66,21	260,51	165,31	587,97	245,26	704,84	458,14	3,738E-06	3,702E-05
Nsg2	61,46	79,22	3,95	3,97	28,28	19,16	43,90	16,16	3,774E-06	3,736E-05
Cxcl16	0,00	1,18	3,29	1,32	11,64	7,66	39,02	27,70	3,778E-06	3,737E-05
Zfp503	1906,21	2046,65	1631,49	1129,40	2953,97	1769,18	5052,56	3768,98	3,809E-06	3,765E-05
Ago4	31,19	48,48	46,71	95,22	136,39	163,51	160,15	267,73	3,817E-06	3,771E-05
Itgav	1286,09	1350,25	3077,46	2629,09	1570,13	1979,95	1525,93	1750,62	3,851E-06	3,801E-05
C2cd3	1186,10	1357,34	2249,88	2006,20	2646,26	2166,45	2646,19	2670,36	3,856E-06	3,803E-05
Map6	353,17	379,54	252,62	145,47	126,41	137,96	128,45	88,86	3,861E-06	3,806E-05
Nup37	1051,26	943,52	597,99	692,98	564,68	639,97	478,02	458,14	3,872E-06	3,815E-05
Pno1	2533,66	1772,35	1550,57	1118,82	916,46	1000,20	899,95	669,32	3,897E-06	3,837E-05
Rflna	5,50	3,55	3,29	1,32	12,47	3,83	53,66	41,54	3,906E-06	3,843E-05
Tma16	926,50	898,59	592,07	730,01	472,37	546,72	395,10	438,52	3,931E-06	3,864E-05
Lmx1b	4882,01	7737,32	4499,10	4599,59	2656,24	2814,09	3073,00	2685,37	3,972E-06	3,902E-05
Wdr74	2015,37	1464,94	1296,64	983,93	855,75	783,04	766,62	610,47	3,999E-06	3,927E-05
Sim2	112,83	30,74	0,00	9,26	0,00	0,00	2,44	1,15	4,029E-06	3,953E-05
Enpep	35,78	44,93	1,32	1,32	4,16	0,00	11,38	6,92	4,07E-06	3,991E-05
C2cd5	838,44	1002,64	1775,56	2063,07	616,24	1176,47	326,81	585,08	4,081E-06	3,999E-05
Naf1	835,68	1097,22	603,91	535,60	252,82	417,71	421,93	309,27	4,133E-06	4,047E-05

Eps8l2	7,34	14,19	13,16	14,55	76,51	33,21	98,37	63,47	4,141E-06	4,052E-05
Rasa4	12,84	4,73	7,89	18,51	61,54	39,60	69,10	80,78	4,188E-06	4,096E-05
Ahr	31,19	40,20	41,45	68,77	74,02	79,20	154,46	143,10	4,201E-06	4,102E-05
Rbl2	49,54	98,14	68,42	144,15	198,76	195,44	317,06	378,51	4,2E-06	4,102E-05
Cited2	1697,05	2174,35	2277,51	1683,52	1130,19	1240,34	869,06	940,51	4,206E-06	4,104E-05
Gstm6	2,75	3,55	7,89	1,32	40,75	19,16	113,81	32,31	4,22E-06	4,116E-05
Stim2	752,21	1093,68	549,97	560,73	307,71	452,20	333,31	370,44	4,244E-06	4,137E-05
Igf1r	2330,01	3145,06	5310,24	5432,75	4679,61	5239,85	5748,45	6295,09	4,248E-06	4,137E-05
Vwa5a	98,15	42,56	135,52	132,25	266,95	178,83	395,91	288,50	4,292E-06	4,175E-05
Desi2	1393,42	1306,50	797,32	884,74	657,82	777,93	751,18	730,48	4,292E-06	4,175E-05
Gsc	68,80	28,38	17,76	11,90	0,00	1,28	1,63	8,08	4,303E-06	4,18E-05
AF529169	4,59	23,65	9,87	31,74	203,75	150,73	69,10	282,73	4,302E-06	4,18E-05
Ptpru	345,83	257,75	871,66	809,36	769,26	700,01	1866,56	813,57	4,313E-06	4,186E-05
Eif2b3	1198,03	1174,08	907,19	827,87	666,14	756,21	622,73	549,31	4,317E-06	4,188E-05
Capn6	15982,59	17131,11	22532,32	15089,50	7473,08	8817,81	10533,55	7983,40	4,325E-06	4,193E-05
Sema3g	240,34	216,37	92,76	79,35	110,61	71,53	66,66	85,40	4,331E-06	4,196E-05
Lactb	391,70	411,46	286,17	281,69	183,79	223,54	175,60	185,79	4,336E-06	4,198E-05
Reln	233,00	163,16	66,44	91,25	35,76	63,87	17,89	46,16	4,357E-06	4,216E-05
Smpdl3a	24,77	18,92	30,26	42,32	93,14	48,54	122,76	117,71	4,387E-06	4,242E-05
Lhx9	5144,37	6284,21	7536,43	8811,69	9273,57	10986,82	12081,42	17838,59	4,406E-06	4,258E-05
Heatr3	2815,28	2709,95	1757,80	1881,89	1733,96	1838,16	1386,10	1569,45	4,492E-06	4,338E-05
Negr1	13,76	10,64	15,79	10,58	33,27	29,38	79,67	60,01	4,499E-06	4,342E-05
Rnft2	47,70	92,22	134,20	242,01	288,58	226,10	315,43	385,44	4,528E-06	4,366E-05
Ms4a6b	0,00	0,00	11,18	19,84	18,30	21,72	34,96	21,93	4,571E-06	4,405E-05
Klf9	17,43	30,74	140,78	156,05	65,70	90,69	56,91	99,24	4,589E-06	4,419E-05
Rtkn2	119,25	100,50	160,52	199,69	266,12	254,20	280,47	275,81	4,647E-06	4,472E-05
Btg2	99,99	93,41	133,55	163,99	179,63	201,83	299,17	249,26	4,658E-06	4,48E-05
Ptx3	103,66	111,14	27,63	15,87	24,12	14,05	307,30	58,85	4,669E-06	4,488E-05
Cd83	18,35	10,64	7,24	17,19	30,77	26,83	94,30	70,39	4,692E-06	4,507E-05
Psat1	8406,38	6660,19	3782,69	4015,05	3743,19	3856,44	4228,21	3051,19	4,704E-06	4,515E-05
Las1l	2416,24	2650,83	2148,57	1948,01	1641,65	1712,98	1318,62	1384,80	4,739E-06	4,546E-05
Mvb12b	763,22	839,47	714,43	569,99	1339,76	919,72	1712,10	1501,36	4,778E-06	4,58E-05
Hand1	53,20	68,58	26,31	15,87	102,29	60,04	248,77	105,01	4,784E-06	4,583E-05
Snrpa1	4425,18	3459,56	2814,32	2523,29	2346,88	2306,96	1974,68	1776,01	4,808E-06	4,604E-05
Nudt18	22,02	20,10	34,87	37,03	91,48	53,65	120,32	92,32	4,896E-06	4,685E-05
Cinp	1374,16	1012,09	884,16	788,20	738,49	659,13	521,92	435,06	4,936E-06	4,72E-05
Cntn4	0,00	0,00	20,39	5,29	34,10	7,66	34,96	98,09	4,972E-06	4,751E-05
Fbrsl1	399,04	529,69	951,92	897,96	1175,93	1069,17	864,99	1095,15	4,981E-06	4,757E-05
Surf2	766,89	733,06	491,42	563,38	449,08	502,01	332,50	360,05	4,986E-06	4,759E-05
Zfp72	94,48	105,23	24,34	27,77	31,60	44,71	80,48	79,63	5,034E-06	4,801E-05
Kctd6	99,99	135,97	241,43	457,58	387,54	611,87	439,81	439,68	5,144E-06	4,902E-05
Sostdc1	7,34	1,18	17,10	9,26	11,64	11,50	296,73	18,46	5,15E-06	4,902E-05
Frem1	543,06	774,44	1870,29	2738,86	1216,68	2032,33	598,34	1020,14	5,149E-06	4,902E-05
Bmp4	1349,39	1289,95	2684,72	2972,94	1584,27	2717,01	1122,70	1099,77	5,272E-06	5,015E-05
Ugdh	1432,86	1403,45	1203,88	1278,84	1660,78	1550,75	2335,64	2168,37	5,28E-06	5,02E-05
Ccl6	32,11	59,12	8,55	11,90	3,33	5,11	2,44	4,62	5,319E-06	5,05E-05
B4galnt3	7,34	11,82	3,29	3,97	18,30	14,05	54,47	41,54	5,315E-06	5,05E-05
Rab3d	45,87	36,65	144,07	64,80	212,07	116,24	253,64	244,65	5,336E-06	5,063E-05
Jade2	17,43	34,29	16,45	14,55	55,72	26,83	117,88	99,24	5,35E-06	5,07E-05
Ccng2	332,07	344,06	478,92	860,93	516,45	1084,50	1457,64	1561,37	5,351E-06	5,07E-05

Col8a2	5,50	4,73	23,68	14,55	40,75	19,16	209,74	36,93	5,424E-06	5,136E-05
Ddx10	1664,95	1752,25	1274,27	1219,33	1034,55	1116,44	760,12	923,20	5,434E-06	5,143E-05
Tmem50b	174,29	222,28	348,67	444,35	468,21	404,93	512,98	506,61	5,528E-06	5,228E-05
Acox3	167,87	202,18	251,96	238,05	330,16	318,07	406,48	441,98	5,538E-06	5,234E-05
Epb41l1	401,79	477,67	480,89	453,61	839,95	650,19	878,81	926,67	5,568E-06	5,259E-05
Ybx3	9513,60	7014,90	4634,62	3443,74	3912,84	3100,22	3538,82	2159,14	5,606E-06	5,288E-05
Nostrin	48,62	89,86	14,47	22,48	11,64	11,50	4,88	10,39	5,605E-06	5,288E-05
Greb1	778,81	1185,90	3661,64	4108,95	1588,42	3271,39	449,57	1210,55	5,614E-06	5,292E-05
Dzip1	336,66	598,27	361,82	522,38	1011,27	832,86	1108,07	1526,75	5,68E-06	5,351E-05
Wipf1	1097,12	1390,45	2120,94	2008,85	2287,83	2100,03	2739,68	2529,58	5,712E-06	5,378E-05
Sept3	1002,64	1137,42	1655,83	2040,59	1927,73	2165,17	2156,79	2366,86	5,738E-06	5,399E-05
Ccdc112	133,01	163,16	248,01	341,20	353,45	425,37	378,03	501,99	5,75E-06	5,406E-05
Wnt7b	8,26	2,36	69,73	19,84	139,71	76,64	20,32	6,92	5,827E-06	5,472E-05
Col7a1	27,52	63,85	167,10	305,49	138,88	213,32	316,24	245,80	5,825E-06	5,472E-05
Apoe	153,19	251,84	274,99	290,95	749,30	304,02	1998,26	628,93	5,836E-06	5,477E-05
Lrrc32	122,92	120,60	26,97	35,71	44,08	19,16	25,20	31,16	5,89E-06	5,524E-05
Epn3	15,59	7,09	34,21	19,84	69,03	40,88	127,63	77,32	6,007E-06	5,623E-05
Car2	763,22	893,86	709,83	764,39	449,08	605,48	337,38	373,90	6,01E-06	5,623E-05
Cstf2	3796,82	3653,47	2889,32	2830,11	2360,18	2600,76	2077,93	2086,44	6,004E-06	5,623E-05
Ift172	748,54	780,35	1566,36	1315,87	1709,01	1341,26	1848,67	1589,06	6,009E-06	5,623E-05
Esrrg	36,69	85,13	7,24	6,61	6,65	8,94	34,96	26,54	6,055E-06	5,66E-05
Akap5	23,85	29,56	72,36	97,86	108,11	109,86	90,24	117,71	6,065E-06	5,666E-05
Aagab	1884,19	1878,76	1663,73	1507,63	1021,25	1355,31	742,23	912,82	6,096E-06	5,692E-05
Zfp827	195,39	509,59	594,05	1130,72	996,30	1305,49	1973,87	1996,43	6,139E-06	5,728E-05
Rab32	38,53	56,75	32,24	44,96	98,13	90,69	217,87	117,71	6,201E-06	5,782E-05
Klf15	155,03	161,98	57,23	66,12	16,63	33,21	38,21	9,23	6,21E-06	5,787E-05
Galnt7	1755,76	1988,72	1330,85	1450,76	646,18	1209,69	347,13	618,55	6,49E-06	6,044E-05
Nfe2l2	1039,33	1055,84	898,64	812,00	403,34	597,82	504,04	493,91	6,599E-06	6,142E-05
Asph	3430,80	3600,26	2305,14	2237,64	1991,77	2359,34	1873,88	1958,34	6,781E-06	6,307E-05
Dkk1	172,46	150,16	255,91	174,57	118,92	181,39	738,17	354,28	6,871E-06	6,384E-05
Tubb3	94,48	34,29	244,72	276,40	591,29	338,51	654,43	273,50	6,872E-06	6,384E-05
Ino80c	850,36	821,74	561,81	567,34	605,43	546,72	364,21	425,83	6,913E-06	6,418E-05
Lyz2	0,92	3,55	30,92	100,51	57,38	53,65	81,30	32,31	6,982E-06	6,478E-05
Pip4k2a	446,74	521,42	459,19	522,38	287,75	380,66	190,23	221,57	6,993E-06	6,483E-05
Gas2	331,15	302,68	246,04	335,91	469,87	457,31	657,69	613,93	7,01E-06	6,496E-05
Bysl	2907,93	2691,03	2266,32	1539,37	1442,06	1345,09	1282,04	961,29	7,019E-06	6,497E-05
Lgals12	0,00	1,18	21,71	50,25	29,94	44,71	15,45	35,77	7,025E-06	6,497E-05
Pgpep1	542,14	468,21	651,94	596,44	794,21	608,04	1412,93	1044,37	7,025E-06	6,497E-05
Unc5d	19,26	26,01	5,92	17,19	21,62	15,33	78,86	88,86	7,066E-06	6,531E-05
Six1	185,30	131,24	19,08	22,48	126,41	154,56	47,15	139,63	7,08E-06	6,54E-05
Trim29	1,83	2,36	57,23	11,90	88,15	38,32	7,32	2,31	7,132E-06	6,583E-05
Sdk1	130,26	100,50	254,59	167,96	337,64	247,81	568,26	346,20	7,154E-06	6,6E-05
Cbx6	592,59	594,72	658,52	834,49	740,16	1014,25	1814,53	1286,71	7,262E-06	6,696E-05
Gpnmb	1,83	2,36	1,32	1,32	14,97	6,39	52,03	23,08	7,393E-06	6,812E-05
Sema4b	140,35	193,91	371,03	314,75	261,97	301,46	589,40	420,06	7,412E-06	6,825E-05
Fes	110,08	98,14	224,99	236,72	256,14	220,99	266,65	240,03	7,612E-06	7,004E-05
Kdm2b	3337,24	3774,07	4868,81	4012,41	2790,14	2812,81	2329,95	2248,00	7,655E-06	7,04E-05
Nampt	2655,66	2543,24	1129,54	1463,99	875,71	1447,28	821,90	1078,99	7,67E-06	7,045E-05
AW551984	92,65	88,68	42,10	56,87	123,08	68,98	242,26	180,02	7,671E-06	7,045E-05
Rrp8	1652,11	1405,82	1176,91	1035,50	923,12	894,17	764,18	793,95	7,726E-06	7,092E-05

Npc1	879,72	729,51	999,29	936,32	1282,38	1053,85	2033,22	1586,76	7,749E-06	7,109E-05
Trem2	0,92	0,00	3,29	6,61	14,97	8,94	74,79	18,46	7,781E-06	7,133E-05
Tbc1d2b	497,19	633,74	980,21	942,93	1076,97	1060,23	1134,08	1293,64	7,944E-06	7,278E-05
Cd109	414,63	322,78	303,93	331,94	628,72	461,14	784,51	721,25	7,97E-06	7,297E-05
Galnt17	131,18	137,15	39,47	34,38	66,53	39,60	21,95	39,24	7,978E-06	7,3E-05
Syne1	78,89	108,78	178,28	183,82	228,70	238,87	247,14	384,28	7,987E-06	7,304E-05
Eif1a	2929,02	3813,09	1892,00	2283,92	1038,71	1787,07	1164,97	1308,64	7,995E-06	7,306E-05
Fbxo44	21,10	5,91	42,76	25,13	66,53	34,49	125,20	132,71	8,062E-06	7,363E-05
Fam210b	219,24	197,45	324,32	302,85	446,59	365,33	683,70	465,06	8,113E-06	7,405E-05
Pa2g4	13444,34	12301,20	9929,06	7482,60	7551,25	6989,87	6497,19	5428,43	8,145E-06	7,425E-05
Nudt11	419,22	573,44	214,46	267,14	166,33	219,71	161,78	220,41	8,141E-06	7,425E-05
Hoxa5	728,36	929,33	251,30	462,87	109,78	292,52	52,84	162,71	8,204E-06	7,474E-05
Pcdh19	467,84	342,88	315,11	202,34	139,71	152,01	952,79	409,67	8,347E-06	7,6E-05
Nav3	99,99	85,13	14,47	25,13	20,79	29,38	49,59	58,85	8,398E-06	7,642E-05
Ddx56	3617,94	2887,31	2422,24	1651,78	1761,40	1529,03	1399,11	1254,40	8,511E-06	7,74E-05
Rrp1b	2748,31	3469,02	2357,77	2339,47	1565,14	2023,38	1108,07	1455,20	8,814E-06	8,01E-05
Fkbp7	61,46	57,94	117,76	100,51	134,72	144,34	248,77	166,18	8,82E-06	8,01E-05
Abhd14b	17,43	21,28	39,47	81,99	134,72	74,09	163,41	111,94	8,924E-06	8,098E-05
Dlg2	2,75	7,09	10,53	26,45	72,35	70,26	32,52	80,78	8,928E-06	8,098E-05
Ncoa1	98,15	192,72	221,70	236,72	350,95	369,17	425,18	611,62	8,992E-06	8,151E-05
Dnm1	1054,01	1184,72	2034,76	1602,85	2125,66	1742,36	2545,38	2518,04	9,311E-06	8,436E-05
Col4a5	316,48	303,86	216,44	206,31	394,20	258,03	611,35	532,00	9,342E-06	8,459E-05
Fam162a	2890,50	1664,75	1314,40	957,48	953,05	895,45	916,21	728,18	9,379E-06	8,487E-05
Esyt1	400,87	223,46	780,88	584,54	1138,51	733,22	1395,86	1022,45	9,431E-06	8,523E-05
Fam214b	120,17	111,14	183,54	224,82	316,02	242,70	287,79	331,20	9,43E-06	8,523E-05
Arhgdig	99,07	50,84	2,63	11,90	9,98	7,66	13,82	5,77	9,565E-06	8,639E-05
Slc4a4	309,14	357,07	538,13	567,34	153,85	404,93	47,15	111,94	9,578E-06	8,645E-05
Mapkbp1	332,07	462,30	682,86	846,39	875,71	963,15	903,20	1163,24	9,584E-06	8,645E-05
Frmf6	1986,01	2537,33	1191,38	1342,32	1407,13	1364,25	2498,23	2187,99	9,595E-06	8,65E-05
Ctns	235,75	253,02	391,43	375,58	439,10	436,87	495,09	529,69	9,601E-06	8,651E-05
Hspa4	15210,20	17232,79	12071,05	11959,19	9769,22	11339,38	7896,30	8871,98	9,674E-06	8,711E-05
Lrrc75b	18,35	17,74	92,76	126,96	110,61	116,24	52,84	125,79	9,685E-06	8,715E-05
Fam163b	3,67	13,01	76,97	75,38	19,13	38,32	13,82	11,54	9,751E-06	8,768E-05
Tspy15	66,05	78,04	103,28	137,54	124,75	171,17	273,16	216,95	9,756E-06	8,768E-05
Ssc5d	152,28	100,50	47,37	55,54	59,88	63,87	21,14	32,31	9,777E-06	8,782E-05
Ndufaf4	937,51	1104,32	501,29	690,33	361,76	551,83	350,39	403,90	9,889E-06	8,877E-05
Gabra5	20,18	30,74	1,32	2,64	0,00	0,00	0,00	0,00	9,901E-06	8,882E-05
Krt14	4,59	2,36	50,66	6,61	274,44	120,07	48,78	4,62	9,983E-06	8,95E-05
Serpini1	8,26	21,28	59,21	63,48	85,66	88,14	73,17	128,09	9,995E-06	8,956E-05
Vgll4	1082,45	1048,75	1610,44	1445,47	1430,41	1371,92	2136,46	1935,26	1,007E-05	9,02E-05
Abca9	43,11	30,74	30,92	54,22	75,68	54,93	171,53	130,40	1,014E-05	9,079E-05
Mbnl2	404,54	608,91	340,11	539,57	627,88	665,52	1190,99	1192,09	1,02E-05	9,118E-05
Slitrk5	111,00	163,16	78,94	56,87	205,41	75,37	396,73	345,05	1,026E-05	9,167E-05
L3mbtl2	1766,77	1541,79	1490,05	1237,84	1152,65	1075,56	771,50	834,34	1,031E-05	9,208E-05
Spats2l	285,29	287,31	178,28	170,60	213,73	187,78	385,34	358,90	1,034E-05	9,232E-05
Zfp362	1896,11	2109,32	3970,84	3528,38	4769,43	3542,20	4494,87	3981,31	1,044E-05	9,315E-05
Ubash3b	233,00	251,84	616,41	587,18	351,78	481,58	332,50	380,82	1,058E-05	9,428E-05
Tlr13	1,83	2,36	5,26	6,61	29,94	29,38	50,40	20,77	1,058E-05	9,428E-05
Psd3	133,01	268,39	430,24	706,20	546,38	875,01	787,76	1496,74	1,068E-05	9,515E-05
Sdad1	2962,05	4034,19	2604,46	2968,97	1587,59	2034,88	1177,17	1632,92	1,079E-05	9,604E-05

Rspo1	33,02	31,92	1,32	0,00	0,83	5,11	1,63	1,15	1,085E-05	9,652E-05
Nhsl2	631,12	934,06	303,93	342,52	738,49	532,67	1073,92	842,42	1,092E-05	9,711E-05
Slc36a4	513,70	595,91	784,83	1262,97	1228,33	1428,12	1386,91	1681,38	1,121E-05	9,962E-05
Hic2	1780,53	1875,21	1947,26	1733,77	1071,98	1389,80	614,60	923,20	1,129E-05	0,0001002
Irx2	49,54	87,49	9,87	13,22	24,12	12,77	102,43	53,08	1,14E-05	0,0001012
Tspan15	101,82	52,02	157,23	153,41	315,19	222,27	300,80	246,96	1,152E-05	0,0001021
Ampd2	1952,07	1983,99	2063,70	1969,17	1495,28	1506,04	1199,12	1219,78	1,157E-05	0,0001025
Aff1	300,88	534,42	886,14	1093,69	1063,66	1310,60	1142,21	1429,81	1,157E-05	0,0001025
Rae1	2684,10	2560,98	2044,63	1950,66	1760,57	1798,56	1516,99	1380,19	1,169E-05	0,0001035
Tmem199	773,31	681,04	521,02	523,70	292,74	435,59	236,57	316,20	1,175E-05	0,000104
Ccnd2	7877,09	11026,62	10924,40	12447,19	16221,88	14608,21	19772,04	21398,69	1,187E-05	0,000105
Pag1	565,99	616,01	380,90	444,35	180,46	291,24	247,14	272,34	1,198E-05	0,0001059
Atic	10000,70	7466,56	5696,40	5128,58	4105,78	3819,39	4534,70	3006,18	1,22E-05	0,0001078
Kidins220	936,59	1057,02	1049,28	1009,05	1496,11	1315,71	1709,66	1907,57	1,239E-05	0,0001094
Pappa2	48,62	80,40	77,63	39,67	102,29	72,81	361,77	175,41	1,255E-05	0,0001107
Spred3	89,90	68,58	174,33	263,17	220,38	297,63	230,07	274,65	1,259E-05	0,000111
Rac2	6,42	5,91	51,97	60,83	108,11	45,99	129,26	45,01	1,276E-05	0,0001124
Cpe	770,55	774,44	661,15	612,31	908,98	747,27	1507,23	1195,55	1,307E-05	0,000115
Ccdc58	949,43	764,98	535,50	573,96	448,25	527,56	374,78	413,13	1,344E-05	0,0001182
Fgd3	13,76	28,38	133,55	117,70	76,51	103,47	61,79	103,86	1,364E-05	0,0001199
Gm2a	66,96	60,30	97,36	96,54	223,71	98,36	367,46	222,72	1,368E-05	0,0001202
Efemp1	89,90	59,12	10,53	17,19	32,43	21,72	60,16	125,79	1,396E-05	0,0001226
Dcx	486,18	822,92	913,11	867,55	547,22	687,24	2034,84	1353,65	1,406E-05	0,0001234
Adamts1	1488,82	2095,13	1509,79	1331,74	815,83	804,75	1673,08	1679,08	1,41E-05	0,0001237
Myo6	210,99	241,20	201,30	195,73	339,31	270,81	431,68	444,29	1,417E-05	0,0001242
Map3k13	38,53	68,58	163,81	206,31	105,62	178,83	217,87	250,42	1,433E-05	0,0001256
Atp1b2	39,45	36,65	55,92	50,25	114,77	68,98	133,33	153,48	1,435E-05	0,0001256
Shox2	891,64	755,52	694,04	696,95	108,11	269,53	374,78	166,18	1,436E-05	0,0001257
Nufip1	1212,71	1105,50	903,24	859,61	548,88	687,24	542,25	637,01	1,466E-05	0,0001282
Ccdc141	134,85	221,10	28,29	85,96	19,13	38,32	9,76	28,85	1,469E-05	0,0001284
Srpk2	807,25	736,61	1145,33	1442,83	1752,26	1452,39	1572,27	2056,43	1,472E-05	0,0001286
Cited4	264,19	154,89	218,41	72,74	87,32	45,99	14,63	30,00	1,476E-05	0,0001289
Zbtb46	461,42	656,21	304,59	398,07	160,51	250,37	121,13	206,57	1,492E-05	0,0001302
Brd3os	42,20	26,01	116,44	91,25	153,85	102,19	178,85	131,56	1,493E-05	0,0001302
Nop16	2402,48	1874,03	1551,23	1280,16	1360,56	1202,02	995,88	949,75	1,495E-05	0,0001303
Cuedc1	489,85	433,92	905,21	830,52	1027,07	875,01	1045,47	849,35	1,5E-05	0,0001306
Gfpt2	879,72	911,59	600,63	575,28	425,80	508,40	454,45	519,30	1,499E-05	0,0001306
Il1r1	0,92	8,28	28,95	18,51	31,60	38,32	58,53	73,86	1,501E-05	0,0001306
Pabpc1	50895,13	40907,04	25576,24	19812,08	23907,86	18376,51	24288,04	17406,99	1,512E-05	0,0001314
Mphosph6	765,05	627,83	448,66	472,13	399,19	438,14	336,57	316,20	1,549E-05	0,0001346
Unc93b1	36,69	14,19	64,47	100,51	152,19	118,80	231,69	121,17	1,56E-05	0,0001355
Ppm1e	124,76	120,60	63,15	91,25	35,76	49,82	24,39	35,77	1,567E-05	0,000136
Kcnk2	72,47	56,75	9,21	15,87	10,81	12,77	26,83	34,62	1,569E-05	0,0001361
Ltv1	1743,84	1864,57	1172,30	1319,84	911,47	1216,07	799,14	871,27	1,59E-05	0,0001378
Kcnj8	0,00	1,18	2,63	1,32	0,83	2,55	183,73	1,15	1,593E-05	0,000138
Tm7sf2	161,45	178,54	261,83	264,50	406,67	358,95	403,23	324,28	1,607E-05	0,0001391
Lgi3	0,92	1,18	5,26	9,26	20,79	6,39	58,53	31,16	1,612E-05	0,0001395
Hexb	209,15	167,89	157,89	148,12	229,53	252,92	470,70	330,05	1,622E-05	0,0001403
Socs2	451,32	598,27	906,53	744,56	181,30	346,17	352,01	246,96	1,633E-05	0,0001411
Adam12	338,49	335,79	157,89	130,93	187,95	158,40	235,76	223,88	1,653E-05	0,0001428

Cacnb1	41,28	66,21	78,94	119,02	128,07	164,78	186,98	238,88	1,665E-05	0,0001437
Tceal3	13,76	22,46	27,63	31,74	46,57	40,88	88,61	85,40	1,679E-05	0,0001449
Ankrd13d	18,35	22,46	41,45	78,03	80,67	76,64	99,99	121,17	1,704E-05	0,0001469
Dnajc3	1807,13	2125,87	1240,72	1494,40	913,97	1180,31	778,00	962,44	1,706E-05	0,0001469
Bnc1	89,90	82,76	20,39	15,87	27,44	34,49	10,57	24,23	1,706E-05	0,0001469
Id1	1747,51	1378,62	1728,85	1392,57	4130,73	2480,69	7480,06	3137,74	1,719E-05	0,000148
Fbln5	100,91	55,57	96,71	41,00	176,31	103,47	627,61	214,64	1,723E-05	0,0001482
Llgl2	212,82	197,45	151,97	108,44	59,05	83,03	65,85	83,09	1,779E-05	0,000153
Sertad4	1098,96	1438,92	2919,58	3397,45	1243,29	2093,64	1425,93	1304,02	1,783E-05	0,0001532
Hsp90b1	20064,69	22571,11	16970,79	17930,19	11850,80	14632,49	9850,66	11695,83	1,797E-05	0,0001543
Fos	21,10	14,19	15,79	14,55	442,43	21,72	31,71	17,31	1,798E-05	0,0001543
Ddx31	724,69	772,08	553,92	566,02	443,26	521,17	315,43	378,51	1,802E-05	0,0001546
Fastkd2	938,43	987,26	573,00	702,24	375,07	583,77	293,48	399,29	1,804E-05	0,0001547
Coro1c	6588,24	6845,82	5540,49	4702,74	4435,94	4304,80	3800,60	3331,61	1,81E-05	0,0001551
Impdh1	2335,51	2014,73	1727,54	1354,22	1155,97	1104,94	1170,66	931,28	1,832E-05	0,0001569
Mettl16	2130,03	2376,53	1492,02	1544,66	1253,27	1448,56	943,04	1211,70	1,836E-05	0,0001571
Tmem260	302,72	296,77	459,84	407,32	532,25	495,63	591,02	667,01	1,839E-05	0,0001573
Ccnh	993,46	935,24	669,70	670,50	561,35	611,87	518,67	536,61	1,847E-05	0,0001578
Serbp1	24958,63	23259,24	18472,02	14118,80	15121,63	13385,75	12476,52	10957,27	1,85E-05	0,000158
Zc3h12d	0,92	1,18	3,29	3,97	6,65	6,39	30,08	30,00	1,853E-05	0,0001582
Chordc1	2989,57	3103,68	2122,91	2311,70	1388,83	1904,59	1425,12	1584,45	1,869E-05	0,0001594
Dse	1408,10	1587,90	863,77	966,73	799,20	881,40	895,88	882,81	1,869E-05	0,0001594
Zfp36l2	1834,65	2005,27	1068,36	972,02	1011,27	1065,34	1972,25	1442,50	1,876E-05	0,0001599
Hspb8	265,11	164,35	740,09	527,67	791,72	585,04	528,43	403,90	1,877E-05	0,0001599
Rax	0,00	0,00	3,29	0,00	25,78	15,33	22,76	20,77	1,888E-05	0,0001607
Txn1	4519,67	3823,73	2601,17	2797,05	2146,45	2760,44	2101,51	1996,43	1,892E-05	0,0001609
Timm9	613,69	527,33	338,80	402,03	305,21	361,50	221,94	261,96	1,9E-05	0,0001615
Rap1gap2	74,30	107,59	14,47	22,48	37,42	33,21	30,08	26,54	1,903E-05	0,0001617
Egfr	29,35	20,10	32,24	38,35	52,39	71,53	8,94	4,62	1,934E-05	0,0001642
Pgam1	6606,59	4536,69	3534,68	2332,86	2627,97	2087,25	2381,98	1701,00	1,971E-05	0,0001673
Cntfr	491,69	398,45	126,31	88,61	262,80	118,80	222,75	214,64	1,973E-05	0,0001673
Arhgef3	145,85	169,08	181,57	320,04	266,12	357,67	508,10	515,84	2,011E-05	0,0001705
Sox10	0,00	1,18	0,66	0,00	1,66	0,00	41,46	16,16	2,014E-05	0,0001707
Trp53inp2	493,52	420,92	836,14	839,78	957,21	829,03	1044,66	857,42	2,034E-05	0,0001722
Rnasel	28,44	49,66	81,57	150,76	130,57	191,61	167,47	283,88	2,034E-05	0,0001722
Iqgap2	553,15	651,48	719,70	745,88	943,07	977,20	1471,46	1103,23	2,042E-05	0,0001728
Hk3	0,00	0,00	13,16	14,55	18,30	12,77	46,34	16,16	2,047E-05	0,000173
Aldoa	44709,59	27449,50	23496,09	12009,45	13955,67	9511,43	12333,44	7175,60	2,061E-05	0,0001742
Ms4a6d	0,00	0,00	9,21	7,93	14,14	12,77	40,65	17,31	2,065E-05	0,0001744
Nrarp	190,80	141,88	584,18	390,13	337,64	328,29	273,97	211,18	2,076E-05	0,0001752
Emilin3	164,20	138,34	201,30	182,50	464,88	327,01	397,54	282,73	2,083E-05	0,0001757
Sema4f	21,10	15,37	51,97	37,03	92,31	56,21	115,44	86,55	2,119E-05	0,0001786
Nptxr	81,64	50,84	38,16	30,42	121,42	70,26	190,23	141,94	2,125E-05	0,000179
Uncx	41,28	13,01	0,66	0,00	0,00	0,00	0,81	0,00	2,129E-05	0,0001793
Zfp579	130,26	147,79	302,62	260,53	259,47	274,64	354,45	306,97	2,131E-05	0,0001794
Kcnf1	51,37	62,66	9,21	3,97	28,28	16,61	60,16	41,54	2,144E-05	0,0001803
Sdr39u1	178,88	161,98	326,96	273,75	459,89	337,23	586,96	400,44	2,146E-05	0,0001804
Zdhhc1	50,45	92,22	167,10	226,14	182,96	164,78	276,41	244,65	2,15E-05	0,0001806
Dbt	758,63	753,16	519,05	534,28	421,64	416,43	371,52	441,98	2,192E-05	0,000184
Slc35g1	219,24	293,22	41,45	112,41	77,34	61,31	65,04	72,70	2,2E-05	0,0001846

Adamts16	34,86	21,28	0,66	3,97	0,00	0,00	0,00	0,00	2,216E-05	0,0001858
Fam78b	204,56	196,27	84,21	96,54	52,39	85,59	83,74	69,24	2,217E-05	0,0001858
Fbn1	1436,53	952,98	456,55	283,01	1062,83	499,46	2716,11	1250,94	2,229E-05	0,0001867
Cited1	357,76	268,39	630,23	277,72	184,62	118,80	122,76	113,09	2,263E-05	0,0001895
Slc25a5	15983,50	11324,58	11442,80	8971,71	7270,99	7162,32	6445,97	4628,71	2,271E-05	0,00019
Zfhx3	337,58	802,82	536,15	480,06	861,57	804,75	1532,43	1679,08	2,289E-05	0,0001914
Ctbp2	3829,84	3538,78	3549,81	3181,89	2572,25	2562,44	2092,56	2207,61	2,292E-05	0,0001916
Spns2	380,69	362,98	224,99	251,27	200,42	210,77	175,60	175,41	2,305E-05	0,0001925
Snx33	402,71	435,11	690,75	663,89	680,28	641,25	989,37	796,26	2,318E-05	0,0001935
E2f5	1122,81	1285,22	853,24	1147,91	380,89	749,83	230,88	414,29	2,323E-05	0,0001938
Cdc34	5130,61	3056,38	3308,37	2203,25	2341,89	1813,89	1429,19	1144,77	2,345E-05	0,0001955
Emc2	1010,89	936,42	549,31	621,57	544,72	582,49	545,50	572,39	2,346E-05	0,0001955
Gjb3	8,26	2,36	47,37	18,51	51,56	28,10	2,44	0,00	2,366E-05	0,0001971
Chrn4	52,29	41,38	8,55	10,58	8,32	5,11	4,06	8,08	2,386E-05	0,0001987
Tnfrsf19	1320,95	1440,11	738,12	870,19	848,27	936,33	412,17	650,86	2,396E-05	0,0001994
Tspoap1	10,09	4,73	3,95	7,93	7,48	8,94	37,40	64,62	2,446E-05	0,0002034
Gprc5b	622,86	571,08	843,38	765,72	1131,02	906,95	1473,90	1162,08	2,451E-05	0,0002037
Chn1	981,54	961,25	1759,11	1916,27	1323,13	1576,30	1206,44	1192,09	2,458E-05	0,0002041
Sox6	407,29	668,03	366,43	309,46	367,58	247,81	731,67	1097,46	2,468E-05	0,0002049
Cdh2	2750,15	2960,61	2094,62	1548,62	1290,70	1355,31	1716,98	1345,57	2,471E-05	0,000205
Fmn1	6,42	7,09	27,63	44,96	57,38	47,26	68,29	41,54	2,484E-05	0,000206
Vsig10	52,29	35,47	98,02	134,89	156,35	150,73	129,26	183,49	2,489E-05	0,0002063
Neo1	3306,96	3214,82	4407,00	4017,70	5332,45	4707,18	7435,35	5776,94	2,518E-05	0,0002086
Dusp4	1231,97	1156,34	1173,62	962,77	563,85	685,96	717,03	596,62	2,546E-05	0,0002107
Gpr12	32,11	18,92	0,66	0,00	0,00	0,00	0,00	0,00	2,555E-05	0,0002114
Mmp17	226,58	185,63	448,00	413,94	293,57	245,26	216,25	189,26	2,581E-05	0,0002134
Dnaaf5	1229,22	1242,65	1492,68	1076,50	855,75	950,38	633,30	592,00	2,584E-05	0,0002135
Rpl22l1	3165,69	2090,40	1330,85	1366,12	1113,56	1240,34	1492,60	1172,47	2,611E-05	0,0002156
Abcg4	31,19	43,75	65,79	119,02	123,91	99,64	174,79	159,25	2,615E-05	0,0002158
Rbp1	466,92	236,47	274,33	226,14	577,15	309,13	2294,18	613,93	2,621E-05	0,0002163
Epop	2772,16	2093,95	2227,51	1293,39	1095,26	924,83	1025,96	677,40	2,671E-05	0,0002202
Adssl1	45,87	21,28	35,52	17,19	143,87	53,65	191,86	148,87	2,686E-05	0,0002214
Ifngr2	454,99	431,56	487,47	476,09	896,50	656,58	818,65	1006,29	2,72E-05	0,000224
Oasl2	11,01	5,91	114,47	97,86	14,97	66,42	24,39	13,85	2,727E-05	0,0002244
Cnp	136,68	65,03	262,49	174,57	493,16	223,54	652,81	445,45	2,731E-05	0,0002247
Rars	4675,61	4484,66	3643,22	3009,97	2975,59	2807,70	2546,20	2181,07	2,75E-05	0,0002261
Ercc2	1899,78	1773,53	1875,56	1668,97	1285,71	1428,12	916,21	1066,30	2,764E-05	0,0002272
Nedd9	335,74	348,79	201,96	167,96	251,99	227,38	701,59	387,75	2,823E-05	0,0002319
Gmps	6169,02	6278,29	4990,52	5049,23	3348,16	4215,38	3485,98	3458,55	2,831E-05	0,0002324
Neurl1a	114,67	87,49	213,15	187,79	251,99	212,05	286,98	251,57	2,84E-05	0,000233
Cxcr4	87,15	59,12	15,79	18,51	16,63	15,33	38,21	31,16	2,865E-05	0,0002349
Prss35	13,76	8,28	1,97	3,97	10,81	7,66	79,67	26,54	2,868E-05	0,000235
A430033K0	92,65	121,78	203,28	195,73	182,96	205,66	310,55	264,27	2,884E-05	0,0002362
Ptgr1	238,50	174,99	417,74	367,65	638,70	387,05	795,89	560,85	2,887E-05	0,0002363
Rgma	588,92	548,61	325,64	318,72	452,41	445,81	691,02	588,54	2,907E-05	0,0002378
Nsun5	691,66	644,38	525,63	507,83	385,88	404,93	362,58	368,13	2,924E-05	0,000239
Mfap3l	27,52	44,93	23,03	59,51	213,73	187,78	84,55	274,65	2,924E-05	0,000239
Ifrd2	2166,73	1534,69	1353,22	978,64	988,81	735,78	785,32	623,16	2,935E-05	0,0002396
Sirt5	123,84	101,68	213,80	189,11	253,65	203,10	338,19	278,11	2,936E-05	0,0002396
Celf5	4,59	8,28	35,52	23,80	51,56	40,88	45,53	56,55	2,98E-05	0,0002431

Hyal1	11,93	20,10	59,87	75,38	76,51	48,54	99,18	79,63	3,003E-05	0,0002449
Tanc1	2010,78	2445,11	4249,11	4262,36	3411,37	3972,68	4229,03	3835,91	3,051E-05	0,0002486
1110004E0i	584,34	454,02	394,06	365,00	329,33	307,85	225,19	234,26	3,068E-05	0,0002498
Map1b	1472,31	1321,87	5120,12	2942,52	2840,04	2171,56	3207,95	2875,78	3,068E-05	0,0002498
5730596B2i	19,26	33,11	0,00	1,32	0,00	0,00	0,81	0,00	3,121E-05	0,0002539
Kcng1	191,72	276,67	135,52	152,09	69,03	158,40	47,96	47,31	3,131E-05	0,0002546
Loxl2	1949,32	1401,09	663,12	624,21	1049,52	673,18	1725,92	1242,86	3,135E-05	0,0002547
Tap1	11,93	3,55	21,71	19,84	46,57	28,10	107,31	54,24	3,141E-05	0,0002551
Hspa14	1798,88	1733,33	1251,25	1348,93	1253,27	1269,72	948,73	1009,75	3,161E-05	0,0002566
Eif1ad	1746,59	1675,39	1433,47	1347,61	1064,49	1139,43	883,69	1013,22	3,169E-05	0,000257
Tulp1	27,52	8,28	111,84	70,09	148,86	94,53	176,41	102,71	3,169E-05	0,000257
Dnah2	18,35	20,10	26,31	42,32	40,75	40,88	86,17	95,78	3,173E-05	0,000257
Cdh8	2,75	22,46	1,32	1,32	25,78	1,28	104,06	98,09	3,173E-05	0,000257
Wdr86	230,25	172,62	220,38	212,92	423,30	316,79	636,55	410,83	3,19E-05	0,0002582
Ssbp1	1396,17	1327,78	869,03	1015,67	742,65	867,35	615,41	732,79	3,204E-05	0,0002592
Irs1	244,93	555,71	1395,32	1785,35	920,62	1262,06	999,13	1203,63	3,215E-05	0,00026
Anp32b	13082,00	12959,77	10778,36	10282,29	9702,69	9719,65	7017,49	7892,23	3,222E-05	0,0002604
Cycs	2059,40	1518,14	1383,48	1161,14	966,36	975,92	882,06	677,40	3,226E-05	0,0002606
Hoxa9	2107,10	2253,56	1631,49	2367,24	757,62	1530,31	343,07	721,25	3,243E-05	0,0002618
Polr2h	1674,12	1217,82	1116,39	994,51	820,82	875,01	690,20	646,24	3,252E-05	0,0002624
Specc1	744,87	766,16	1593,33	1306,61	1371,37	1332,32	1167,41	1297,10	3,27E-05	0,0002637
Esr1	0,00	1,18	2,63	10,58	12,47	29,38	56,91	26,54	3,276E-05	0,000264
Tex15	43,11	134,79	71,05	157,38	296,89	302,74	336,57	660,09	3,282E-05	0,0002644
Cdh20	56,87	68,58	9,21	2,64	13,31	5,11	4,88	12,69	3,286E-05	0,0002645
Ciart	195,39	171,44	61,18	87,28	40,75	67,70	85,36	76,16	3,374E-05	0,0002714
Tspan33	110,08	88,68	219,07	227,47	99,80	154,56	51,22	77,32	3,377E-05	0,0002716
Ric3	166,04	230,56	58,55	91,25	40,75	63,87	31,71	66,93	3,383E-05	0,0002719
Ndrg4	74,30	50,84	105,92	140,18	187,12	157,12	206,49	183,49	3,397E-05	0,0002729
Srr	165,12	157,25	236,83	251,27	358,43	250,37	500,78	376,21	3,407E-05	0,0002734
Prkar2b	862,29	987,26	465,76	448,32	785,90	748,55	692,64	810,11	3,407E-05	0,0002734
Slc15a3	0,00	2,36	12,50	13,22	19,96	21,72	49,59	24,23	3,418E-05	0,0002741
Cavin2	33,02	27,19	9,87	14,55	39,09	40,88	118,69	55,39	3,42E-05	0,0002741
Phf2	1416,35	1974,53	2654,46	2689,93	3170,19	2939,27	3725,80	3502,40	3,439E-05	0,0002755
Arhgap30	2,75	7,09	22,37	43,64	50,73	56,21	53,66	35,77	3,447E-05	0,000276
Spi1	5,50	4,73	34,87	33,06	59,05	38,32	75,61	33,47	3,45E-05	0,0002761
Gemin5	4551,78	4289,58	3567,57	2897,56	2677,03	2416,82	2540,51	2246,85	3,506E-05	0,0002804
Tsr2	1504,42	1144,52	959,16	897,96	836,63	766,43	631,67	645,09	3,509E-05	0,0002804
Macrocl1	11,93	5,91	28,95	18,51	52,39	21,72	115,44	65,78	3,51E-05	0,0002804
Igf2bp3	9170,52	7914,67	7252,89	5073,04	4598,11	4413,38	4389,18	3818,60	3,551E-05	0,0002835
Nrp1	973,28	794,54	2054,49	1813,12	1533,54	2088,53	2225,89	1758,70	3,563E-05	0,0002844
Adgrl3	247,68	347,61	611,15	646,69	563,85	743,44	695,90	694,71	3,57E-05	0,0002847
Tbx15	920,08	1103,14	3903,08	4656,45	1641,65	3500,04	300,80	1260,17	3,601E-05	0,000287
Diexf	1317,28	1401,09	1076,91	1076,50	676,95	853,30	774,75	725,87	3,619E-05	0,0002882
Il17rd	4228,88	5124,32	9335,02	9061,64	4613,08	6159,57	5220,03	5446,90	3,618E-05	0,0002882
Tmcc3	27,52	37,84	48,02	34,38	100,63	99,64	156,09	87,70	3,686E-05	0,0002934
Acat1	598,10	465,85	861,80	763,07	1086,12	853,30	1610,48	1135,54	3,733E-05	0,0002969
Plekhh1	462,33	597,09	260,51	215,56	165,50	203,10	56,91	173,10	3,752E-05	0,0002983
Tbc1d8	33,02	36,65	60,52	55,54	45,74	63,87	131,70	115,40	3,802E-05	0,0003021
Cldn34c1	15,59	15,37	30,26	31,74	50,73	54,93	65,85	77,32	3,814E-05	0,0003029
Kctd12b	144,94	150,16	117,76	149,44	161,34	218,43	299,17	354,28	3,821E-05	0,0003033

Tob1	99,99	137,15	188,15	203,66	203,75	277,19	399,16	302,35	3,825E-05	0,0003034
Dgat2	425,64	454,02	357,22	286,98	235,35	209,49	222,75	182,33	3,829E-05	0,0003036
Dgka	70,63	63,85	98,68	100,51	124,75	136,68	172,35	190,41	3,893E-05	0,0003085
Sdc4	111,91	121,78	139,47	117,70	284,42	166,06	429,24	276,96	3,909E-05	0,0003096
Lrrc20	396,29	327,51	666,41	614,95	778,41	651,47	765,81	706,25	3,945E-05	0,0003123
Trak1	559,57	552,16	969,03	953,51	1065,32	979,76	1088,56	909,35	4,02E-05	0,0003181
Ddit4l	11,93	13,01	37,50	35,71	41,58	66,42	71,54	69,24	4,031E-05	0,0003186
Lrrtm4	17,43	7,09	61,84	46,29	3,33	16,61	1,63	2,31	4,031E-05	0,0003186
Pcsk9	126,59	167,89	66,44	59,51	163,83	141,79	53,66	73,86	4,036E-05	0,0003188
Nup160	3480,34	3544,69	2619,59	2658,19	1691,55	2321,01	1795,02	1825,63	4,044E-05	0,0003193
G3bp2	10049,32	10563,14	7335,78	8438,75	5438,06	7270,90	4420,89	5294,57	4,092E-05	0,0003229
Nr3c1	53,20	67,39	93,42	138,86	104,79	160,95	251,21	201,95	4,097E-05	0,0003229
Tpd52	58,71	65,03	152,62	206,31	172,15	190,33	162,59	120,02	4,097E-05	0,0003229
Slc9a9	11,01	9,46	27,63	18,51	89,82	38,32	86,17	57,70	4,109E-05	0,0003237
Vars	9165,93	8440,82	6871,99	5251,57	5206,87	4515,57	4721,68	3767,82	4,118E-05	0,0003242
Nacc1	5514,97	5753,33	5986,52	4975,17	4686,27	4649,69	3179,49	3242,75	4,206E-05	0,000331
Camkk1	71,55	73,31	88,81	92,57	141,38	153,29	162,59	206,57	4,213E-05	0,0003314
Mmp23	27,52	16,55	28,95	27,77	70,69	44,71	99,99	90,01	4,216E-05	0,0003314
Lix1l	1088,87	1027,46	1116,39	1469,28	1778,87	1589,07	2126,71	2080,67	4,249E-05	0,0003338
Iqsec2	102,74	86,31	121,70	112,41	233,69	144,34	337,38	236,57	4,252E-05	0,0003339
Klf11	193,56	245,93	339,46	365,00	365,09	427,93	478,02	553,92	4,281E-05	0,000336
Myh9	5522,31	5156,24	15226,80	11910,26	14780,66	10053,05	12482,21	8895,06	4,289E-05	0,0003364
Kdm4a	2933,61	2754,88	4181,35	3689,72	6159,92	4297,13	6767,09	5735,40	4,297E-05	0,0003369
Crtc3	334,82	370,08	390,77	388,81	514,78	427,93	699,96	669,32	4,358E-05	0,0003415
Ipcef1	0,00	0,00	12,50	21,16	14,97	17,88	17,89	19,62	4,403E-05	0,0003448
Txndc16	276,12	237,65	349,32	432,45	507,30	502,01	514,60	622,01	4,436E-05	0,0003472
Slc4a1	1957,58	1922,51	2597,88	2709,76	1843,74	2298,02	544,68	1121,69	4,488E-05	0,0003511
Dhx32	449,49	448,11	330,25	285,66	342,63	296,35	209,74	192,72	4,506E-05	0,0003523
Ptprd	887,06	1226,10	1706,49	1836,93	1753,92	1873,93	2365,72	2193,76	4,524E-05	0,0003535
Galnt16	188,97	139,52	97,36	43,64	53,22	58,76	39,84	33,47	4,535E-05	0,0003542
Mlph	1,83	2,36	18,42	15,87	24,95	33,21	27,64	33,47	4,547E-05	0,0003549
Fbxo17	104,58	66,21	173,67	146,80	261,13	203,10	251,21	238,88	4,569E-05	0,0003563
C1qtnf2	58,71	35,47	4,61	5,29	2,49	5,11	8,94	1,15	4,566E-05	0,0003563
Otor	3,67	0,00	1,32	0,00	31,60	10,22	31,71	31,16	4,589E-05	0,0003577
Psmd6	4244,47	3420,55	2707,75	2311,70	2149,78	2156,23	2179,55	1857,95	4,615E-05	0,0003595
Wwtr1	871,46	822,92	1025,60	1129,40	1423,76	1259,51	2163,29	1531,36	4,629E-05	0,0003604
Retreg1	31,19	22,46	41,45	29,09	78,17	58,76	105,69	99,24	4,638E-05	0,0003609
Timm10	617,36	441,02	378,93	316,07	257,81	264,42	242,26	184,64	4,648E-05	0,0003615
Tifab	0,92	1,18	15,13	35,71	29,94	31,93	35,77	19,62	4,674E-05	0,0003633
Coa5	2944,62	3172,25	1836,74	2020,75	1862,03	2039,99	1771,44	1900,64	4,677E-05	0,0003633
Tmem255a	1004,47	910,41	517,08	540,89	564,68	634,86	490,22	579,31	4,758E-05	0,0003695
Bex4	538,47	377,17	256,56	197,05	210,40	201,83	198,36	129,25	4,761E-05	0,0003695
Desi1	2273,14	2183,81	1653,86	1261,65	1229,16	1111,33	1236,51	969,36	4,769E-05	0,0003699
Tyro3	942,09	681,04	2174,88	1649,13	1877,00	1679,77	2054,35	1574,06	4,775E-05	0,0003702
Adamts12	128,43	158,44	76,97	50,25	139,71	94,53	291,85	196,18	4,793E-05	0,0003714
Ucp2	589,84	362,98	1751,22	1142,62	2135,64	1264,61	2532,38	1369,80	4,817E-05	0,000373
Gars	7256,97	6206,17	5276,03	4294,09	4184,79	3920,31	3685,97	3088,11	4,942E-05	0,0003826
Eif3j1	719,18	796,91	384,85	502,54	310,20	445,81	282,10	341,59	4,964E-05	0,000384
Mpo	18,35	5,91	100,65	67,45	59,05	54,93	35,77	27,70	4,968E-05	0,0003841
Zfp128	147,69	154,89	195,38	177,21	148,03	206,94	351,20	342,74	4,984E-05	0,0003852

Esrp1	8,26	37,84	62,50	38,35	84,83	65,15	4,88	5,77	5,039E-05	0,0003892
Rusc1	166,04	114,69	185,52	173,24	308,54	198,00	689,39	331,20	5,127E-05	0,0003958
Klf4	25,69	21,28	15,79	14,55	51,56	51,10	117,88	53,08	5,141E-05	0,0003967
Ttc39c	212,82	125,33	211,17	228,79	357,60	342,34	491,03	399,29	5,15E-05	0,0003971
Stim1	223,83	237,65	307,22	335,91	547,22	376,83	541,43	514,69	5,175E-05	0,0003989
Manf	3496,85	2583,44	3061,68	2197,96	1462,02	1420,46	1629,99	1107,84	5,186E-05	0,0003995
Aldh1a2	679,74	476,49	2,63	27,77	781,74	335,95	4934,68	879,35	5,241E-05	0,0004033
Prmt6	1145,74	1151,61	1001,26	815,97	630,38	747,27	585,33	598,93	5,239E-05	0,0004033
Slc29a4	275,20	205,73	641,41	580,57	573,83	540,34	728,41	462,76	5,259E-05	0,0004045
Pink1	333,91	240,02	621,68	494,61	825,81	502,01	1033,27	780,11	5,273E-05	0,0004054
Igfbp3	1627,34	1310,05	584,84	413,94	789,22	656,58	1520,24	832,04	5,316E-05	0,0004083
Lrrc42	1131,06	865,48	1290,06	1303,97	2074,93	1756,41	2169,79	1788,71	5,317E-05	0,0004083
Six5	442,15	353,52	634,18	613,63	1008,77	654,02	1046,28	932,44	5,42E-05	0,000416
Lrrc8c	355,92	342,88	313,14	338,56	449,08	415,15	812,96	571,23	5,433E-05	0,0004168
Mtch2	2695,11	2332,78	1590,70	1778,74	1543,52	1566,08	1480,40	1337,49	5,494E-05	0,0004211
2610528A1	17,43	7,09	38,81	42,32	43,25	62,59	4,06	9,23	5,493E-05	0,0004211
Vps13d	661,39	768,53	949,29	953,51	1215,02	1084,50	1289,36	1480,59	5,507E-05	0,0004216
Gnl3	3367,51	4312,04	1720,96	2487,59	1033,72	2002,95	732,48	1355,95	5,504E-05	0,0004216
Trip13	2003,44	1748,70	1387,42	1352,90	1187,58	1438,34	873,93	988,98	5,52E-05	0,0004224
Nudc	6151,59	5579,52	5835,21	4257,07	4746,14	3857,71	2804,72	2557,27	5,542E-05	0,0004238
Erap1	79,81	76,85	82,23	93,90	143,04	130,29	213,81	171,95	5,565E-05	0,0004253
Pik3cg	21,10	18,92	25,00	42,32	80,67	56,21	94,30	83,09	5,576E-05	0,000426
Fblim1	1089,78	997,91	2048,57	2096,13	2015,88	1872,65	2377,10	1713,70	5,606E-05	0,000428
Pwwp2b	83,48	91,04	105,92	116,38	217,06	157,12	343,88	197,33	5,614E-05	0,0004285
Atp9a	361,43	282,58	352,61	230,11	491,50	302,74	1088,56	658,94	5,618E-05	0,0004285
Tsr1	3354,66	4213,91	2571,57	2593,38	1401,31	2304,41	1353,58	1698,69	5,649E-05	0,0004306
Eif4a1	38499,29	33857,85	26661,70	26875,45	24458,40	26352,52	21403,66	19288,02	5,715E-05	0,0004354
Lrsam1	113,75	147,79	111,18	129,60	195,43	201,83	275,59	263,11	5,727E-05	0,0004361
Trim25	578,83	686,95	317,75	345,17	361,76	307,85	410,55	388,90	5,743E-05	0,0004372
Stab2	45,87	41,38	15,79	23,80	8,32	3,83	5,69	5,77	5,858E-05	0,0004457
Aig1	121,09	91,04	25,66	21,16	39,09	24,27	52,03	31,16	5,868E-05	0,0004462
Flywch2	88,06	61,48	230,25	150,76	301,05	190,33	372,34	233,11	5,899E-05	0,0004483
Hspb6	52,29	36,65	76,97	68,77	123,08	88,14	215,43	131,56	5,938E-05	0,0004511
Ptpn1	2606,13	2646,11	2411,05	2010,17	1934,38	1835,61	1478,78	1312,10	5,944E-05	0,0004513
Ccdc42	33,02	34,29	10,53	3,97	5,82	5,11	1,63	1,15	5,971E-05	0,0004531
Arhgef6	17,43	15,37	35,52	56,87	51,56	80,48	99,18	79,63	5,976E-05	0,0004532
Utp20	3905,06	4394,81	3211,67	3139,57	2363,51	2769,38	2421,81	2349,55	6,017E-05	0,0004561
Acsf2	508,20	405,55	1413,08	1026,24	1510,25	959,32	1121,07	866,66	6,034E-05	0,0004571
Cx3cl1	80,72	48,48	218,41	142,83	370,91	194,16	239,01	213,49	6,049E-05	0,000458
Mkx	36,69	50,84	172,36	223,50	113,93	263,14	389,41	168,48	6,094E-05	0,0004613
Ism2	21,10	24,83	24,34	18,51	84,00	68,98	65,85	50,78	6,164E-05	0,0004663
Arhgap24	73,39	44,93	358,53	253,92	128,07	199,27	316,24	139,63	6,181E-05	0,0004673
Tex10	2666,67	3191,17	1932,79	2146,39	1168,45	1825,39	1256,03	1343,26	6,192E-05	0,0004679
Arhgef9	139,43	186,81	142,76	230,11	285,25	321,90	390,22	455,83	6,202E-05	0,0004685
6030419C1	169,71	138,34	258,54	187,79	353,45	238,87	534,12	386,59	6,261E-05	0,0004727
Magel1	392,62	292,04	539,44	450,97	648,68	539,06	1267,41	732,79	6,267E-05	0,0004729
Arhgef10l	505,45	393,72	824,30	714,14	1086,12	817,53	947,91	1068,61	6,299E-05	0,000475
Btbd11	376,10	435,11	290,12	255,24	425,80	376,83	721,91	547,00	6,321E-05	0,0004764
Hes1	348,58	302,68	613,78	669,18	383,38	666,80	961,73	848,19	6,364E-05	0,0004794
Ppl	6,42	3,55	30,92	14,55	39,09	34,49	4,06	1,15	6,476E-05	0,0004876

Arxes1	381,61	331,06	206,57	239,37	191,28	210,77	156,90	167,33	6,585E-05	0,0004956
2310030G0	19,26	15,37	63,15	55,54	73,18	80,48	56,09	81,93	6,59E-05	0,0004957
Mboat1	44,03	31,92	15,13	31,74	63,20	47,26	105,69	114,25	6,616E-05	0,0004974
Fam217b	303,64	328,69	242,75	243,34	140,55	189,05	148,77	126,94	6,666E-05	0,0005009
Zcchc3	2924,44	2998,45	2399,87	2106,71	1856,21	1868,82	1813,72	1770,24	6,697E-05	0,000503
Zfpm2	24,77	21,28	28,29	37,03	39,09	30,66	231,69	58,85	6,704E-05	0,0005032
Sash1	1153,08	1416,46	2719,59	2458,49	1825,44	2032,33	1403,98	1735,62	6,753E-05	0,0005067
Cnnm1	50,45	85,13	12,50	22,48	11,64	12,77	15,45	17,31	6,766E-05	0,0005074
Fhod3	248,60	260,12	107,89	138,86	226,20	223,54	269,09	300,04	6,8E-05	0,0005097
Stat3	533,88	678,67	922,32	1024,92	1344,75	1316,99	1033,27	1409,04	6,816E-05	0,0005105
Boc	696,25	734,24	1200,59	946,90	800,86	852,02	2109,64	1298,25	6,818E-05	0,0005105
Dcaf13	1473,23	1385,72	988,76	1014,34	849,93	1001,47	783,70	787,03	6,837E-05	0,0005117
Sema5a	2613,46	4432,64	2278,17	2309,05	1699,86	1985,06	6576,05	3848,60	6,916E-05	0,0005171
Cfl2	1831,90	2040,74	876,93	1162,46	684,44	1182,86	692,64	807,80	6,913E-05	0,0005171
Grik3	36,69	31,92	5,92	3,97	0,83	1,28	12,19	3,46	6,971E-05	0,0005206
Klhdc10	5036,12	5630,36	3562,96	3866,93	2805,94	3331,43	3177,05	3279,68	6,968E-05	0,0005206
Pigc	284,37	240,02	294,72	289,62	336,81	338,51	521,92	496,22	7,034E-05	0,0005251
Lima1	2440,09	2447,47	4825,39	4040,18	3964,41	3451,50	5557,41	4325,21	7,056E-05	0,0005256
Mad2l2	552,23	380,72	727,59	649,34	1248,28	825,19	1356,02	1072,07	7,054E-05	0,0005256
Adcyap1r1	75,22	94,59	31,58	31,74	35,76	24,27	17,07	21,93	7,053E-05	0,0005256
Rrp9	2430,92	1829,10	1707,80	1265,61	1267,41	965,71	969,86	746,64	7,046E-05	0,0005256
Esm1	153,19	104,05	87,50	47,61	32,43	20,44	47,96	40,39	7,063E-05	0,0005259
Enpp4	86,23	101,68	68,42	80,67	181,30	166,06	152,84	184,64	7,124E-05	0,0005302
Kcnab2	54,12	20,10	161,18	120,35	208,74	129,02	244,70	161,56	7,147E-05	0,0005316
Eno1	45851,66	30271,78	28738,56	16337,93	15883,41	11695,77	15524,32	8615,79	7,191E-05	0,0005346
Pmpca	3653,71	3730,32	3013,65	3078,73	2630,46	2854,96	1797,46	2183,38	7,205E-05	0,0005354
Fkbp3	5518,64	4605,26	3815,58	3558,80	3093,68	3392,74	2726,67	2880,39	7,238E-05	0,0005376
Trmt10a	817,34	949,43	653,91	715,46	470,71	641,25	282,91	410,83	7,303E-05	0,0005418
BC034090	250,43	279,04	428,27	507,83	558,03	568,44	472,33	605,85	7,299E-05	0,0005418
Pltp	23,85	7,09	59,21	37,03	155,52	86,86	117,07	69,24	7,395E-05	0,0005484
Pdgfra	3802,32	4559,15	4137,93	4120,85	3332,36	4972,87	8519,03	7464,10	7,405E-05	0,0005488
Fam102b	788,90	1260,39	342,74	489,32	343,47	471,36	629,23	579,31	7,426E-05	0,0005502
Cacnb2	34,86	44,93	92,10	129,60	128,90	183,94	106,50	162,71	7,508E-05	0,0005559
Syt3	11,93	11,82	30,26	23,80	68,19	37,04	107,31	55,39	7,529E-05	0,0005569
Npm3	2596,03	1707,32	1144,67	1034,18	1085,28	855,85	1143,84	843,58	7,527E-05	0,0005569
2010300C0	60,54	59,12	126,31	119,02	79,01	63,87	37,40	39,24	7,649E-05	0,0005655
Rsl24d1	2052,06	2017,09	1374,27	1626,65	1097,76	1374,47	1021,89	1083,61	7,689E-05	0,0005682
Mybpc3	22,02	22,46	6,58	6,61	7,48	7,66	0,00	0,00	7,734E-05	0,0005712
Sp8	12,84	11,82	71,05	27,77	54,06	74,09	4,06	12,69	7,795E-05	0,0005754
Stk32a	0,92	0,00	0,66	2,64	12,47	16,61	27,64	16,16	7,799E-05	0,0005754
Polr3d	1200,78	1226,10	1126,91	1163,78	782,57	974,65	669,88	653,17	7,851E-05	0,000579
Slc25a33	422,89	328,69	711,80	925,74	899,00	988,70	636,55	912,82	7,885E-05	0,0005812
Srms	3,67	4,73	30,26	17,19	4,99	7,66	0,00	0,00	7,935E-05	0,000584
Rrp12	3366,59	2941,69	2666,30	1765,51	1745,60	1429,40	1500,73	1065,15	7,932E-05	0,000584
Ppp1r2	1437,45	1169,35	1121,65	977,31	793,38	915,89	652,00	648,55	7,929E-05	0,000584
2810004N2	2753,82	2052,56	1818,32	1641,20	1653,29	1488,16	1082,87	1200,16	7,965E-05	0,0005859
Dab2ip	1428,28	2171,98	2991,28	3000,71	2983,08	3180,70	4162,36	4003,24	8,085E-05	0,0005944
Pcdhgb6	87,15	65,03	122,36	107,12	168,82	103,47	388,60	199,64	8,099E-05	0,0005952
Ddr1	152,28	114,69	274,99	194,40	381,72	268,25	424,37	349,66	8,118E-05	0,0005956
Enpp3	87,15	49,66	118,41	150,76	251,99	160,95	379,65	207,72	8,111E-05	0,0005956

Prps1	2581,36	2372,98	1960,42	2022,07	1392,16	1774,29	1325,94	1321,33	8,116E-05	0,0005956
Mreg	100,91	119,42	34,87	31,74	44,08	62,59	38,21	40,39	8,185E-05	0,0006003
Sntb1	93,57	102,86	53,29	71,41	123,08	114,96	158,53	234,26	8,206E-05	0,0006015
Mrto4	3476,67	2266,57	2235,40	1679,55	1560,98	1365,53	1292,61	982,06	8,211E-05	0,0006016
Myo1d	89,90	82,76	153,94	148,12	223,71	173,72	273,97	199,64	8,218E-05	0,0006018
Tspan4	556,82	399,64	319,06	220,85	191,28	155,84	226,82	143,10	8,309E-05	0,0006082
Mical2	64,21	81,58	73,02	76,70	275,27	140,51	160,15	361,20	8,341E-05	0,0006102
Fam114a1	294,46	208,09	206,57	185,15	461,56	240,15	788,57	504,30	8,353E-05	0,0006108
Dusp9	7548,68	4743,60	6920,68	4902,44	4247,16	3609,90	2721,80	2220,30	8,388E-05	0,000613
Ston1	494,44	475,31	568,39	499,90	610,42	536,50	1096,69	830,88	8,394E-05	0,0006132
Ncbp1	5675,50	5307,58	4359,63	4505,69	3786,44	4217,94	3203,07	3194,28	8,406E-05	0,0006137
Itgam	0,92	0,00	13,16	35,71	28,28	37,04	25,20	10,39	8,469E-05	0,000618
Rnf135	25,69	24,83	72,36	70,09	88,98	66,42	88,61	95,78	8,49E-05	0,0006193
Mcu	265,11	262,48	376,30	384,84	409,16	468,80	538,99	511,22	8,529E-05	0,0006218
Acbd4	29,35	31,92	63,81	42,32	103,95	68,98	133,33	108,48	8,544E-05	0,0006226
Pcdhb3	1,83	8,28	23,03	11,90	40,75	26,83	68,29	49,62	8,584E-05	0,0006252
Chst2	1287,93	1479,12	621,68	626,86	1560,15	968,26	1374,72	1646,76	8,659E-05	0,0006303
Lsg1	1796,13	1822,01	1569,65	1519,53	1313,98	1323,37	1001,57	1102,07	8,666E-05	0,0006305
Zfp532	1053,09	1563,07	2709,72	2752,08	2426,71	2741,28	2553,51	3141,20	8,768E-05	0,0006376
Abtb2	396,29	318,05	330,25	281,69	348,46	334,68	899,14	549,31	8,833E-05	0,000642
Cdhr4	7,34	18,92	53,29	83,32	39,09	79,20	89,43	109,63	8,856E-05	0,0006434
Gnaz	31,19	26,01	54,60	54,22	91,48	85,59	83,74	105,01	8,958E-05	0,0006505
Prkca	132,10	205,73	161,18	173,24	248,66	252,92	403,23	353,13	9,015E-05	0,0006543
Htr5b	5,50	4,73	33,55	33,06	38,26	44,71	35,77	25,39	9,081E-05	0,0006588
Osbpl5	213,74	235,29	407,87	337,23	407,50	343,62	653,62	469,68	9,096E-05	0,0006595
Synrg	333,91	325,15	363,80	292,27	617,91	394,71	692,64	755,87	9,114E-05	0,0006605
Nup50	4871,01	4956,42	3932,02	3623,60	3087,03	3408,07	2794,15	3026,95	9,132E-05	0,0006615
Slc22a17	96,32	190,36	223,67	592,47	408,33	632,31	657,69	945,13	9,14E-05	0,0006617
Fam83h	40,36	37,84	120,39	92,57	128,07	109,86	99,18	109,63	9,194E-05	0,0006653
Nup43	1714,48	1349,06	1078,23	1084,43	775,08	938,88	812,15	624,32	9,235E-05	0,0006679
Mansc4	1,83	2,36	3,29	5,29	27,44	17,88	21,95	30,00	9,285E-05	0,0006712
Ralgds	2363,95	2644,92	1520,97	1282,81	1494,45	1286,33	1742,99	1489,82	9,399E-05	0,0006791
Npas3	7,34	14,19	26,97	27,77	45,74	54,93	49,59	86,55	9,466E-05	0,0006837
Trim6	179,80	260,12	199,99	230,11	32,43	158,40	11,38	34,62	9,483E-05	0,0006846
Pus7	1680,54	2380,08	1139,41	1454,73	862,41	1271,00	550,38	838,96	9,548E-05	0,0006889
Ddc	103,66	53,21	13,16	22,48	16,63	20,44	18,70	20,77	9,568E-05	0,00069
Rbbp7	8155,95	8200,80	6277,29	6014,64	5555,32	6075,26	4983,46	4913,75	9,583E-05	0,0006908
Fam174b	363,26	372,44	131,57	141,51	134,72	104,75	309,74	146,56	9,591E-05	0,000691
Slc11a1	0,00	2,36	19,08	23,80	32,43	28,10	39,84	16,16	9,613E-05	0,0006922
Atrnl1	1086,11	1068,85	1128,89	1235,20	1431,24	1475,38	1783,64	1794,48	9,693E-05	0,0006977
Gm11110	35,78	18,92	46,05	38,35	73,18	84,31	115,44	95,78	9,718E-05	0,0006991
Prodh	467,84	484,76	324,32	289,62	281,92	255,48	199,99	253,88	9,725E-05	0,0006993
Nop58	6204,80	7212,35	3991,23	4811,18	3392,24	4507,90	2716,11	3419,31	9,802E-05	0,0007045
Bpnt1	683,41	708,23	521,02	511,80	287,75	421,54	302,42	357,74	9,811E-05	0,0007048
Trim26	524,71	552,16	874,95	829,20	1193,40	912,06	1000,76	986,67	9,864E-05	0,0007082
Rrm2	12399,51	12084,83	11334,91	11194,80	7450,62	10302,14	6121,60	6514,35	9,91E-05	0,0007111
Tars2	1525,51	1384,54	1115,07	1236,52	961,37	950,38	856,86	759,33	9,955E-05	0,0007141
Msto1	1420,94	1259,21	1144,02	990,54	960,54	843,08	715,41	688,94	0,00010	0,00072
Hr	7,34	3,55	19,74	5,29	34,10	26,83	73,17	48,47	0,00010	0,00072
Memo1	1509,92	1310,05	888,77	929,70	699,41	887,79	690,20	793,95	0,00010	0,00072

Aatf	1523,68	1395,18	1194,01	863,58	716,87	783,04	753,62	813,57	0,00010	0,00073
Cpa5	29,35	16,55	0,66	0,00	0,00	0,00	0,00	0,00	0,00010	0,00073
Nap1l5	77,06	134,79	57,89	63,48	47,40	74,09	11,38	23,08	0,00010	0,00073
Megf9	388,03	517,87	576,28	884,74	903,16	960,60	1040,59	1291,33	0,00010	0,00073
Dscr3	1384,25	1228,46	872,98	923,09	754,29	826,47	718,66	785,88	0,00010	0,00073
Nfam1	240,34	334,61	127,62	122,99	143,04	125,18	98,37	140,79	0,00010	0,00073
Apobec1	0,92	5,91	9,21	17,19	20,79	15,33	48,78	47,31	0,00010	0,00074
Itga2	173,37	161,98	83,55	56,87	160,51	113,69	212,18	213,49	0,00010	0,00074
Col1a1	2842,80	1758,16	2064,36	1265,61	4919,96	2032,33	16757,58	3618,96	0,00010	0,00074
Ms4a4a	0,00	0,00	1,97	7,93	6,65	10,22	26,83	26,54	0,00011	0,00075
Nudcd1	1407,18	1429,46	942,05	1097,66	741,82	942,71	683,70	765,10	0,00011	0,00075
Ttc7b	1186,10	1054,66	882,85	796,13	686,10	768,99	523,55	619,70	0,00011	0,00075
Eml1	757,71	799,27	1087,44	1038,15	763,44	892,89	475,58	580,46	0,00011	0,00075
Mthfd1	4793,03	4435,01	3839,26	2958,39	3273,32	2857,52	2421,81	2133,75	0,00011	0,00076
Creb3l1	71,55	63,85	11,18	11,90	20,79	11,50	64,22	28,85	0,00011	0,00076
Lurap1	28,44	22,46	34,87	34,38	46,57	65,15	95,93	91,17	0,00011	0,00076
Col6a2	324,73	221,10	742,72	449,64	1077,80	499,46	1922,65	851,65	0,00011	0,00076
Tril	7700,04	8413,62	10236,28	7629,39	3442,97	4578,16	5687,48	3696,27	0,00011	0,00076
Arg2	0,00	3,55	1,32	0,00	17,46	3,83	56,91	25,39	0,00011	0,00077
Samd4	347,67	475,31	242,09	216,89	158,01	192,89	342,26	303,50	0,00011	0,00077
Pnpla2	138,52	96,95	175,65	161,34	273,61	192,89	352,83	294,27	0,00011	0,00077
B630019K0	111,00	108,78	190,78	187,79	177,97	245,26	303,23	261,96	0,00011	0,00077
Pcdhga6	26,60	29,56	46,71	30,42	76,51	40,88	128,45	108,48	0,00011	0,00078
Fkbp1a	9370,49	7747,96	6268,74	5411,59	5051,35	4845,13	4973,70	3865,91	0,00011	0,00078
Acot1	158,70	109,96	244,07	171,92	384,22	223,54	604,03	365,82	0,00011	0,00078
Aif1	0,00	0,00	2,63	9,26	22,45	10,22	43,90	16,16	0,00011	0,00079
Ajap1	48,62	46,11	136,83	133,57	114,77	145,62	38,21	72,70	0,00011	0,00080
Rnf182	53,20	43,75	83,55	108,44	127,24	117,52	170,72	131,56	0,00011	0,00080
Commd3	420,14	283,76	664,44	622,89	923,95	702,56	1062,54	762,80	0,00011	0,00080
Zfyve1	479,76	475,31	763,77	703,56	743,48	725,56	855,24	866,66	0,00011	0,00080
Snx29	110,08	119,42	240,12	203,66	232,86	190,33	273,16	274,65	0,00011	0,00080
Elac2	2432,75	2338,69	1854,50	1318,51	1442,06	1232,68	1230,01	1066,30	0,00011	0,00080
Tmem44	151,36	164,35	198,67	232,76	312,69	260,59	339,82	345,05	0,00011	0,00081
Abcb1b	27,52	30,74	22,37	34,38	34,93	28,10	144,71	70,39	0,00012	0,00081
St5	949,43	1124,42	1993,31	1754,93	1680,74	1621,01	1738,11	1716,00	0,00012	0,00082
Lcp2	15,59	9,46	38,16	47,61	72,35	56,21	72,35	50,78	0,00012	0,00082
Otud6b	1953,91	2186,17	1084,81	1411,09	820,82	1278,67	786,95	956,67	0,00012	0,00082
3110082l17	933,84	751,98	697,99	477,42	533,08	463,69	370,71	315,04	0,00012	0,00082
Grwd1	3473,00	2674,48	2761,03	1732,45	1615,04	1512,43	1402,36	949,75	0,00012	0,00082
Cecr2	1766,77	3181,71	2891,95	3412,00	592,96	1655,50	388,60	910,51	0,00012	0,00082
Mindy3	652,22	652,66	502,60	525,02	410,00	410,04	360,96	376,21	0,00012	0,00082
Ddx1	7035,90	6737,05	5590,48	5258,18	4761,11	5174,70	4160,74	4077,10	0,00012	0,00082
Nup107	3092,31	3456,02	2348,56	2511,39	2030,85	2432,15	1728,36	1818,71	0,00012	0,00082
Dapl1	0,00	0,00	1,32	2,64	12,47	6,39	17,07	25,39	0,00012	0,00083
Slc14a2	1,83	0,00	26,97	15,87	13,31	19,16	24,39	32,31	0,00012	0,00083
Eif3e	8333,91	6571,52	4424,76	4030,92	3767,31	4209,00	5050,12	4041,32	0,00012	0,00083
Grsf1	3195,97	3208,91	2445,92	2514,04	2079,92	2305,69	1941,35	1915,65	0,00012	0,00084
Foxp4	2730,88	2240,56	986,79	812,00	2470,79	1098,55	5497,25	2410,71	0,00012	0,00084
Tbxa2r	112,83	81,58	31,58	15,87	32,43	14,05	23,58	21,93	0,00012	0,00085
Tle4	738,45	1087,76	1463,74	1962,56	1678,24	2258,42	2181,99	2484,57	0,00012	0,00085

Dkk3	86,23	83,95	139,47	121,67	235,35	166,06	303,23	196,18	0,00012	0,00085
Rhbdf2	109,16	137,15	317,75	337,23	186,29	270,81	182,92	205,41	0,00012	0,00085
Pop1	871,46	1001,45	746,67	737,94	574,66	564,61	558,50	498,53	0,00012	0,00085
Dnajc11	4399,50	4038,92	4074,78	3082,70	2860,83	2626,31	2316,13	1966,42	0,00012	0,00085
Cdc6	2813,44	2630,73	2497,89	2018,11	1329,79	1787,07	1468,21	1332,87	0,00012	0,00086
Figl1	2417,16	2568,07	1590,04	1601,52	1201,71	1710,42	1277,16	1232,48	0,00012	0,00086
Madd	255,02	267,21	277,62	350,46	429,96	381,94	499,16	618,55	0,00012	0,00086
Camk2n1	76,14	140,70	20,39	37,03	31,60	30,66	82,11	73,86	0,00012	0,00086
Orc5	947,60	1010,91	585,49	633,47	449,91	614,42	382,09	511,22	0,00012	0,00087
Raver2	591,68	465,85	641,41	659,92	982,16	869,90	1170,66	933,59	0,00013	0,00087
Rerg	52,29	24,83	11,18	18,51	49,07	51,10	132,51	69,24	0,00013	0,00087
3632451O0	174,29	106,41	153,28	141,51	335,98	228,65	343,88	342,74	0,00013	0,00088
Pcdh15	0,00	0,00	0,66	3,97	14,14	12,77	17,89	23,08	0,00013	0,00088
Fam189b	377,94	379,54	536,15	559,41	706,89	595,26	722,72	699,33	0,00013	0,00088
Nop14	1797,96	2351,70	1580,18	1415,05	1183,42	1309,32	984,50	1111,31	0,00013	0,00088
S100a13	27,52	28,38	44,73	38,35	98,13	79,20	82,92	75,01	0,00013	0,00089
Trps1	1076,94	1697,86	2084,75	2457,17	1415,44	2443,64	3965,63	3807,06	0,00013	0,00089
Oasl1	0,92	0,00	10,53	9,26	20,79	8,94	33,33	23,08	0,00013	0,00089
Ube2f	1325,54	1242,65	922,32	1064,60	647,01	886,51	578,83	657,78	0,00013	0,00090
Mapk14	3028,10	3148,61	2216,33	2294,50	2078,26	2183,06	1821,85	1936,42	0,00013	0,00090
Trim46	34,86	53,21	92,10	112,41	113,10	103,47	145,52	136,17	0,00013	0,00092
Dnajb4	122,92	165,53	140,12	156,05	148,86	199,27	324,37	316,20	0,00013	0,00092
Fmo2	0,92	1,18	3,95	46,29	46,57	98,36	17,07	5,77	0,00013	0,00092
Psmg2	972,37	943,52	716,41	756,46	592,96	670,63	515,42	545,84	0,00013	0,00093
Ptchd4	0,92	2,36	3,95	5,29	43,25	15,33	13,82	76,16	0,00014	0,00093
Cmb1	32,11	35,47	1,97	3,97	5,82	3,83	7,32	3,46	0,00014	0,00094
Rnf39	0,00	0,00	19,08	18,51	10,81	14,05	4,06	2,31	0,00014	0,00094
Elfn1	9,17	4,73	13,82	18,51	54,06	16,61	74,79	61,16	0,00014	0,00094
Gfi1b	48,62	42,56	41,45	51,58	30,77	22,99	7,32	9,23	0,00014	0,00094
Abcb4	2,75	2,36	0,00	0,00	9,15	2,55	31,71	17,31	0,00014	0,00094
Csnk2a2	2576,77	2660,29	2084,10	2049,84	1768,89	1880,32	1593,40	1598,30	0,00014	0,00095
Pcdhb11	1,83	3,55	9,21	9,26	18,30	8,94	65,04	25,39	0,00014	0,00095
Metap1	1829,15	1773,53	1375,58	1489,11	978,83	1209,69	1005,63	1052,45	0,00014	0,00096
Chst8	64,21	44,93	37,50	18,51	218,72	90,69	95,93	116,55	0,00014	0,00096
Srd5a1	162,37	134,79	228,93	206,31	363,42	270,81	349,57	316,20	0,00014	0,00097
Fzd8	108,24	78,04	82,89	76,70	125,58	109,86	278,03	175,41	0,00014	0,00098
Zfp92	1,83	0,00	7,24	3,97	18,30	19,16	21,14	31,16	0,00014	0,00098
Caskin1	20,18	42,56	55,26	56,87	51,56	84,31	130,07	145,40	0,00014	0,00098
Bmp7	2179,57	2315,05	2623,54	2065,71	1669,92	1758,96	1331,63	1294,79	0,00014	0,00099
Kifc2	6,42	9,46	11,84	29,09	27,44	35,77	49,59	91,17	0,00014	0,00099
Nkx1-2	6,42	2,36	45,39	29,09	0,00	3,83	4,06	2,31	0,00014	0,00099
Kcnn4	68,80	54,39	49,34	51,58	29,11	28,10	9,76	16,16	0,00015	0,00100
Vat1l	170,62	87,49	26,31	11,90	67,36	39,60	79,67	55,39	0,00015	0,00101
Wdr89	519,21	457,57	359,85	263,17	232,03	237,59	262,59	226,18	0,00015	0,00101
Zfp593	681,57	510,78	496,68	421,87	312,69	302,74	321,12	274,65	0,00015	0,00101
Herc3	52,29	101,68	144,73	202,34	245,33	310,41	208,12	378,51	0,00015	0,00101
Cend1	53,20	48,48	132,89	100,51	96,47	106,02	46,34	43,85	0,00015	0,00101
Gpsm1	2234,61	2266,57	2442,63	2361,95	1842,07	1968,46	1339,76	1511,74	0,00015	0,00101
Mylk	167,87	161,98	159,86	140,18	561,35	245,26	343,07	451,22	0,00015	0,00101
Akna	521,04	663,30	1327,56	1113,53	913,97	832,86	925,96	919,74	0,00015	0,00101

Fcgr1	1,83	0,00	19,08	23,80	26,61	17,88	51,22	17,31	0,00015	0,00101
Etf1	9231,98	10679,01	5469,44	7105,69	4671,30	6614,32	3889,21	4859,51	0,00015	0,00102
Csad	275,20	206,91	359,19	371,62	534,74	381,94	656,87	534,30	0,00015	0,00103
Pfkfb3	1128,31	1512,23	772,98	839,78	508,96	685,96	821,09	747,79	0,00015	0,00104
Grb7	56,87	60,30	14,47	22,48	18,30	19,16	12,19	5,77	0,00015	0,00104
Tcaf1	2446,51	2140,06	3422,84	3442,42	3509,50	3239,46	4126,59	3868,22	0,00015	0,00105
Cct7	18994,17	15032,43	14437,37	11682,79	11602,98	10830,98	9072,65	7691,44	0,00015	0,00105
Arhgap22	27,52	20,10	82,23	107,12	54,06	68,98	42,27	41,54	0,00015	0,00105
Gnl2	2055,73	2167,25	1726,22	1649,13	1524,39	1534,14	1130,83	1285,56	0,00015	0,00105
Bag2	932,92	688,13	501,29	375,58	429,96	355,11	417,05	357,74	0,00016	0,00107
Lrrc40	2287,81	2171,98	1494,66	1731,13	1259,93	1532,87	1171,48	1252,09	0,00016	0,00107
Smug1	615,53	568,71	334,19	350,46	330,16	351,28	387,78	342,74	0,00016	0,00107
Lmf1	718,27	481,22	211,17	167,96	292,74	183,94	526,80	288,50	0,00016	0,00109
Ids	288,04	426,83	309,85	407,32	507,30	510,96	722,72	788,18	0,00016	0,00110
Epcam	26,60	29,56	126,31	83,32	167,16	100,91	73,17	33,47	0,00016	0,00110
Dsg2	31,19	53,21	42,10	13,22	114,77	83,03	165,84	120,02	0,00016	0,00110
Pcdhb22	77,06	53,21	76,97	93,90	141,38	118,80	191,86	167,33	0,00016	0,00111
Slc12a4	845,78	759,07	1261,77	1196,84	675,29	794,54	734,92	641,63	0,00016	0,00111
Dact2	109,16	82,76	40,13	15,87	23,29	10,22	24,39	24,23	0,00017	0,00112
Mapk11	309,14	279,04	640,10	551,47	640,36	578,66	376,40	510,07	0,00017	0,00112
Parl	1427,36	1211,91	1119,02	1114,85	772,59	895,45	767,44	632,39	0,00017	0,00113
Mfap4	1430,11	1139,79	2332,11	1512,92	3481,23	1981,23	4694,04	3167,74	0,00017	0,00113
Nck2	723,77	783,90	1229,54	1391,25	1337,27	1461,33	934,09	1141,31	0,00017	0,00113
Zpr1	1819,06	1489,76	1357,16	1067,24	1094,43	968,26	838,16	799,72	0,00017	0,00115
Ednrb	82,56	62,66	29,60	37,03	52,39	60,04	139,02	99,24	0,00017	0,00116
Vapb	2243,78	1891,76	1442,03	1416,38	1323,96	1328,48	1246,27	1177,08	0,00017	0,00116
Morf4l2	9117,31	8990,61	5451,68	6466,93	5292,53	6330,74	5033,86	5281,88	0,00017	0,00116
Pdlim2	22,93	16,55	112,49	79,35	118,09	54,93	104,06	79,63	0,00017	0,00117
Ccdc86	2181,40	1900,04	2021,60	1278,84	1156,80	993,81	1008,07	730,48	0,00018	0,00118
Apbb2	421,05	683,40	548,00	534,28	534,74	567,16	1308,87	971,67	0,00018	0,00119
Krt35	0,00	0,00	1,97	3,97	34,10	14,05	6,50	17,31	0,00018	0,00119
Zfp46	640,29	676,31	821,01	789,52	859,91	775,37	1327,57	1106,69	0,00018	0,00119
Man1a	175,21	196,27	142,76	156,05	219,55	204,38	305,67	321,97	0,00018	0,00120
Pfdn4	1085,20	718,87	701,94	641,40	525,59	517,34	427,62	378,51	0,00018	0,00120
Cpt1c	99,07	98,14	127,62	198,37	199,59	275,92	243,89	379,67	0,00018	0,00120
Ggta1	404,54	411,46	192,09	222,18	173,81	220,99	258,52	203,10	0,00018	0,00121
Dync1i1	95,40	59,12	208,54	214,24	176,31	183,94	151,21	165,02	0,00018	0,00121
Pgr	0,00	0,00	2,63	2,64	10,81	10,22	18,70	17,31	0,00018	0,00121
Sertad2	528,38	624,28	618,39	625,53	658,66	765,16	1004,82	1076,69	0,00018	0,00122
Cyb561	14,68	7,09	42,10	42,32	39,09	56,21	58,53	68,09	0,00018	0,00124
Mapre1	7560,61	6648,37	5118,14	4905,08	4998,96	5099,33	4387,55	4168,26	0,00019	0,00125
Fam81a	86,23	43,75	23,03	17,19	14,14	21,72	10,57	10,39	0,00019	0,00126
Ms4a7	0,00	1,18	0,00	1,32	6,65	1,28	34,96	19,62	0,00019	0,00126
Galns	119,25	78,04	192,09	154,73	301,88	231,21	261,77	227,34	0,00019	0,00126
Baiap2l1	183,47	253,02	207,23	195,73	113,93	109,86	85,36	109,63	0,00019	0,00128
Nop9	2710,70	2430,92	2120,94	1706,00	1620,03	1467,72	1454,39	1129,77	0,00019	0,00129
Ppp1r36	5,50	1,18	15,79	11,90	48,23	33,21	22,76	33,47	0,00019	0,00129
Col22a1	246,76	184,45	264,46	163,99	133,06	111,13	69,10	87,70	0,00019	0,00130
Hoxa2	144,94	165,53	15,79	31,74	18,30	51,10	7,32	39,24	0,00019	0,00130
Senp8	409,13	377,17	359,19	386,16	179,63	255,48	143,89	208,87	0,00019	0,00130

Pcdhb16	22,02	3,55	20,39	37,03	52,39	42,15	111,38	99,24	0,00020	0,00131
Zdhhc9	349,50	403,18	712,46	645,37	700,24	588,88	930,03	703,94	0,00020	0,00131
Gm7694	55,96	70,94	67,76	51,58	72,35	58,76	299,17	115,40	0,00020	0,00131
Wdr4	1634,68	1508,68	1384,14	1208,75	1047,86	1171,37	814,59	901,28	0,00020	0,00131
Epb41l4b	146,77	112,32	239,46	445,68	475,70	771,54	180,48	426,98	0,00020	0,00132
Ltbp2	7,34	5,91	6,58	5,29	4,99	6,39	85,36	17,31	0,00020	0,00133
Ddx27	2396,98	2711,13	2245,27	1830,31	1783,03	1812,61	1358,46	1402,11	0,00020	0,00133
Reps2	8,26	8,28	7,24	3,97	15,80	21,72	42,27	40,39	0,00020	0,00133
Bcas3	394,45	328,69	539,44	454,93	1048,69	605,48	1000,76	775,49	0,00020	0,00134
Slc39a13	127,51	166,71	236,17	256,56	291,07	264,42	341,44	317,35	0,00020	0,00134
Pkp2	77,06	70,94	15,13	3,97	31,60	15,33	82,11	43,85	0,00020	0,00134
Tm9sf2	2454,77	2868,39	1759,11	1770,80	1197,56	1581,41	1677,95	1661,77	0,00020	0,00136
Plppr2	165,12	134,79	434,19	281,69	495,65	321,90	517,86	372,74	0,00020	0,00136
Cacng8	13,76	17,74	71,05	58,19	98,96	42,15	105,69	77,32	0,00021	0,00136
Stxbp6	194,47	186,81	262,49	409,97	402,51	527,56	427,62	481,22	0,00021	0,00136
Syt5	8,26	7,09	35,52	23,80	38,26	20,44	92,68	45,01	0,00021	0,00137
Osbpl3	268,78	342,88	211,83	236,72	398,35	348,73	556,07	445,45	0,00021	0,00138
Uhrf1	13768,16	13523,75	16558,97	13591,13	11823,36	12372,79	8832,02	8567,32	0,00021	0,00138
Thumpd1	2817,11	2902,68	2057,78	1934,79	1339,76	1890,53	1478,78	1559,06	0,00021	0,00139
Slc16a6	234,84	340,52	238,14	305,49	108,94	194,16	35,77	95,78	0,00021	0,00139
Atp2b1	2772,16	3854,47	2035,42	2286,57	1348,08	2005,50	1306,43	1602,91	0,00021	0,00139
Rxra	2173,15	2135,33	3095,88	2525,94	3980,21	2975,04	5117,59	4013,63	0,00021	0,00140
Cnn2	7173,50	4842,92	4828,68	3591,86	2138,97	1925,02	3404,68	1548,67	0,00021	0,00140
Sh3rf3	4,59	11,82	44,08	103,15	44,91	47,26	25,20	38,08	0,00021	0,00140
Rhd	64,21	28,38	132,23	130,93	88,15	127,74	19,51	40,39	0,00021	0,00141
Cebpz	2836,37	3315,32	2450,52	2429,40	1955,17	2190,72	1434,06	1793,32	0,00021	0,00141
Pigq	1985,10	1701,41	1710,43	1803,86	1529,38	1439,62	1002,38	1112,46	0,00021	0,00142
Dnajb11	2029,13	1804,27	1794,64	1704,68	1378,85	1474,11	1172,29	1059,38	0,00022	0,00142
Sh3d21	37,61	26,01	52,63	47,61	124,75	57,48	126,01	136,17	0,00022	0,00142
Ptms	2766,66	1656,48	7264,74	4741,09	11069,07	5221,96	11705,02	6185,46	0,00022	0,00143
Pde4dip	659,56	942,34	1592,68	1945,37	1447,05	1986,34	1612,92	1975,65	0,00022	0,00145
Cct3	21795,69	16688,91	15317,59	12285,85	12036,26	11119,67	10347,38	8224,58	0,00022	0,00146
C1d	1370,49	967,16	521,68	576,60	701,90	646,36	794,26	652,01	0,00022	0,00146
Hpgd	22,02	14,19	28,95	51,58	91,48	63,87	70,73	94,63	0,00022	0,00146
Aunip	454,08	431,56	358,53	316,07	261,13	304,02	169,91	227,34	0,00022	0,00146
Auts2	1093,45	1499,22	2478,81	2037,94	2646,26	2119,19	3433,95	2642,67	0,00022	0,00147
Pcdhb18	11,93	8,28	18,42	22,48	54,89	21,72	73,98	63,47	0,00022	0,00147
H2-Ke6	143,10	105,23	138,15	194,40	241,17	215,88	312,18	304,66	0,00022	0,00147
Kif3c	574,25	568,71	1028,89	891,35	1034,55	898,00	1016,20	985,52	0,00023	0,00148
Mapk13	31,19	23,65	7,24	6,61	40,75	11,50	77,23	61,16	0,00023	0,00149
Acss2	141,27	101,68	120,39	117,70	189,61	169,89	334,13	230,80	0,00023	0,00149
Rassf2	186,22	211,64	361,82	359,71	402,51	415,15	342,26	451,22	0,00023	0,00150
Nectin3	1142,99	1534,69	693,38	954,83	592,96	777,93	456,07	631,24	0,00023	0,00151
Susd5	33,94	34,29	3,95	1,32	12,47	3,83	59,35	20,77	0,00023	0,00151
Cubn	11,93	753,16	5,26	2,64	17,46	7,66	17,07	6,92	0,00023	0,00151
Zfp523	642,13	695,22	1039,42	1034,18	1162,63	1065,34	1069,04	1103,23	0,00023	0,00153
Usp10	4837,98	5285,12	4647,12	3909,25	3520,31	3501,32	2939,67	2993,49	0,00023	0,00153
Fap	52,29	44,93	1,97	2,64	4,16	0,00	42,27	4,62	0,00023	0,00153
Kif5a	18,35	40,20	34,21	60,83	98,96	79,20	134,14	115,40	0,00024	0,00153
Cck	1,83	2,36	30,26	30,42	12,47	6,39	4,88	2,31	0,00024	0,00154

Ppt1	627,45	614,82	732,20	737,94	1136,01	882,68	1153,59	1084,76	0,00024	0,00154
Bcl9l	1091,62	1287,58	2407,11	1733,77	2898,25	1839,44	3837,18	2700,37	0,00024	0,00154
Zfp703	1629,17	1700,22	2459,73	1498,37	889,85	896,73	1212,94	943,98	0,00024	0,00154
Cfh	0,00	0,00	8,55	21,16	12,47	22,99	13,82	27,70	0,00024	0,00155
Hspa2	17,43	39,02	55,26	63,48	119,76	83,03	105,69	116,55	0,00024	0,00155
Perp	22,93	7,09	69,73	47,61	128,90	67,70	15,45	1,15	0,00024	0,00155
Gper1	0,00	0,00	1,32	0,00	17,46	3,83	22,76	19,62	0,00024	0,00156
Prnd	46,78	15,37	80,92	84,64	87,32	83,03	224,38	122,32	0,00024	0,00157
Abcb1a	11,93	8,28	4,61	1,32	12,47	2,55	58,53	35,77	0,00024	0,00157
Gtf2h3	2048,39	1807,82	1395,32	1508,95	1400,47	1341,26	1070,67	1132,08	0,00024	0,00157
Urb2	1891,53	2296,13	1362,43	1456,05	721,86	1222,46	932,47	1035,14	0,00024	0,00159
Rgs12	1401,68	1422,37	2651,17	2248,22	2594,70	2133,24	2493,35	2398,02	0,00025	0,00160
Krt23	67,88	81,58	40,13	13,22	4,99	14,05	13,01	3,46	0,00025	0,00160
Nmrk1	54,12	30,74	40,79	38,35	49,90	65,15	250,39	87,70	0,00025	0,00160
Dennd2c	40,36	61,48	60,52	93,90	94,81	107,30	147,15	196,18	0,00025	0,00161
Gstt3	19,26	10,64	26,97	19,84	52,39	25,55	134,95	58,85	0,00025	0,00161
Cldn12	1267,75	1324,24	722,33	946,90	619,57	837,97	521,92	658,94	0,00025	0,00165
Mroh1	336,66	305,05	617,73	464,19	655,33	472,63	813,77	714,33	0,00026	0,00166
Dph5	368,77	387,81	258,54	260,53	174,64	204,38	148,77	211,18	0,00026	0,00166
Scara5	21,10	9,46	3,29	1,32	14,97	6,39	35,77	47,31	0,00026	0,00168
Amigo1	163,28	171,44	434,19	384,84	271,11	325,73	440,63	287,35	0,00026	0,00168
Mrpl16	1014,56	734,24	833,51	625,53	464,88	438,14	467,45	347,36	0,00026	0,00169
Exosc1	817,34	780,35	593,39	566,02	477,36	578,66	412,98	436,21	0,00026	0,00169
Fam185a	321,98	381,90	146,04	228,79	160,51	212,05	116,25	143,10	0,00026	0,00169
Amd1	2764,82	2957,06	1445,97	1949,34	991,31	1730,86	1165,79	1274,02	0,00026	0,00169
Adm	68,80	33,11	20,39	9,26	5,82	6,39	10,57	8,08	0,00026	0,00169
Elf1	150,44	153,71	136,83	173,24	217,89	212,05	287,79	317,35	0,00026	0,00169
Fam117a	489,85	448,11	544,05	646,69	911,47	811,14	776,38	750,10	0,00026	0,00169
Tdrd1	41,28	68,58	7,24	19,84	46,57	52,37	95,93	71,55	0,00026	0,00170
Sesn1	446,74	415,01	461,16	448,32	726,85	637,42	676,38	720,10	0,00026	0,00170
Ptgis	917,33	468,21	379,58	333,27	350,12	189,05	242,26	167,33	0,00026	0,00170
Cd33	0,92	0,00	5,92	2,64	16,63	15,33	26,83	16,16	0,00026	0,00170
Myo10	1893,36	2434,46	4102,41	3574,67	2543,14	2885,62	3711,17	3822,06	0,00027	0,00171
Serpinb6a	488,94	341,70	606,55	666,53	928,94	740,89	1020,27	833,19	0,00027	0,00171
Acer2	131,18	154,89	28,29	56,87	58,21	49,82	76,42	90,01	0,00027	0,00173
Atg16l2	78,89	118,24	250,64	335,91	197,93	266,97	139,83	193,87	0,00027	0,00173
Nop56	5026,03	6093,85	4275,42	4668,36	2776,00	3823,22	2384,42	3015,41	0,00027	0,00174
Tead4	135,76	190,36	69,73	60,83	79,01	61,31	69,10	47,31	0,00027	0,00174
Ctsh	36,69	68,58	38,81	23,80	106,45	47,26	199,99	128,09	0,00027	0,00174
Artn	8,26	5,91	18,42	14,55	34,10	31,93	49,59	39,24	0,00027	0,00174
Plec	1079,69	954,16	2184,09	1818,41	2380,97	1520,09	3110,39	2155,68	0,00027	0,00175
Upp1	137,60	62,66	34,21	27,77	17,46	22,99	38,21	20,77	0,00027	0,00176
Rhobtb1	365,10	403,18	627,60	641,40	566,34	767,71	761,75	835,50	0,00028	0,00177
A430105119	0,00	0,00	0,00	1,32	8,32	1,28	20,32	30,00	0,00028	0,00177
Elovl2	799,91	870,21	535,50	607,02	360,10	502,01	281,28	429,29	0,00028	0,00177
Serhl	88,06	87,49	119,07	140,18	184,62	134,13	227,63	218,11	0,00028	0,00178
Smn1	2048,39	1502,77	1523,60	1137,33	1089,44	1011,69	882,06	747,79	0,00028	0,00178
Kifc3	146,77	144,25	355,24	316,07	237,02	339,79	284,54	320,81	0,00028	0,00178
Sbk1	4153,66	3465,48	8384,41	6166,73	8386,21	6365,23	9515,72	7503,33	0,00028	0,00178
Tcp1	19056,55	16435,89	13515,71	12174,76	10952,64	11543,76	11068,47	9272,42	0,00028	0,00178

Bop1	4455,46	3902,95	3577,44	2494,20	2482,43	2272,47	2190,12	1577,52	0,00028	0,00179
Selenos	762,30	631,38	423,00	498,58	379,23	416,43	386,97	328,89	0,00028	0,00181
MsrB3	510,95	530,88	279,59	271,11	370,91	385,77	657,69	465,06	0,00028	0,00181
Cd84	0,92	0,00	7,24	7,93	9,15	12,77	33,33	17,31	0,00029	0,00182
1810041L15	70,63	55,57	20,39	10,58	9,98	6,39	103,25	25,39	0,00029	0,00182
Itpr2	162,37	146,61	63,15	80,67	195,43	117,52	221,13	212,34	0,00029	0,00183
Tars	4037,16	4119,32	3453,10	3047,00	2830,06	2737,44	2568,96	2332,24	0,00029	0,00183
Coq2	838,44	731,88	359,85	505,19	374,24	420,26	462,58	475,45	0,00029	0,00185
RimKlb	577,92	698,77	854,56	1261,65	946,40	1258,23	1542,19	1519,82	0,00029	0,00185
Kyat3	381,61	373,62	209,86	167,96	211,24	177,56	254,46	222,72	0,00029	0,00187
Bmpr1b	258,69	250,66	81,57	146,80	217,06	268,25	289,41	490,45	0,00030	0,00188
Adgrl1	1280,59	2318,59	3522,18	5193,38	4685,43	5534,92	4015,22	6412,80	0,00030	0,00188
Tmem126a	819,17	587,63	534,84	473,45	330,16	406,21	348,76	343,89	0,00030	0,00189
Zfp853	1,83	2,36	15,13	15,87	19,13	21,72	30,08	26,54	0,00030	0,00190
Slc6a4	1,83	2,36	10,53	22,48	49,07	21,72	24,39	32,31	0,00030	0,00191
Eno1b	7395,49	4880,75	5052,36	2819,53	2799,28	2041,27	2573,84	1336,34	0,00030	0,00191
Smim1	132,10	108,78	65,13	54,22	54,06	33,21	42,27	31,16	0,00030	0,00191
Kcne1l	22,93	13,01	22,37	18,51	82,33	43,43	129,26	53,08	0,00030	0,00192
Ralgs1	26,60	47,29	47,37	93,90	114,77	127,74	120,32	208,87	0,00030	0,00193
1500011B01	233,00	223,46	140,12	152,09	88,98	116,24	120,32	103,86	0,00030	0,00193
Gprin1	122,00	94,59	157,23	95,22	79,84	70,26	30,89	41,54	0,00031	0,00193
Usp25	1367,73	1550,06	965,74	1048,73	725,19	1000,20	596,71	769,72	0,00031	0,00193
Enoph1	1430,11	1036,92	1002,58	850,36	708,55	728,11	652,81	571,23	0,00031	0,00194
Pdss1	311,89	314,51	124,34	187,79	141,38	167,34	147,15	147,71	0,00031	0,00194
Ccdc160	50,45	28,38	20,39	13,22	13,31	14,05	3,25	3,46	0,00031	0,00195
Kcnd3	40,36	76,85	0,00	7,93	9,98	5,11	5,69	4,62	0,00031	0,00195
Mphosph10	1765,85	1949,70	1295,32	1389,93	918,96	1263,34	656,87	970,52	0,00031	0,00195
Peg12	1249,40	1126,78	1500,58	1307,93	999,63	989,98	786,13	821,65	0,00031	0,00196
Ntn1	310,97	335,79	73,02	37,03	58,21	83,03	166,66	30,00	0,00031	0,00196
Akr1b8	129,34	169,08	278,27	203,66	426,63	315,51	326,00	311,58	0,00031	0,00197
Tle3	4540,77	5635,09	5825,34	5572,93	8632,38	6747,17	10074,22	8780,81	0,00032	0,00198
Ptges	187,13	145,43	286,17	261,85	439,94	295,08	496,72	363,51	0,00032	0,00199
Kbtbd8	399,04	697,59	247,35	327,98	44,91	205,66	60,97	133,86	0,00032	0,00200
Lrrc3b	39,45	26,01	7,89	5,29	7,48	3,83	3,25	1,15	0,00032	0,00200
Stra6l	3,67	1,18	20,39	37,03	13,31	40,88	4,06	2,31	0,00032	0,00202
Scara3	446,74	326,33	272,35	238,05	599,61	323,18	972,30	619,70	0,00032	0,00203
Ppp1r13b	256,85	244,75	267,09	235,40	539,73	327,01	648,74	473,14	0,00032	0,00203
Pcdhb5	2,75	5,91	18,42	7,93	39,09	11,50	79,67	42,70	0,00033	0,00207
Timm17a	2091,51	1456,66	1366,37	1270,90	1049,52	1175,20	893,44	822,80	0,00033	0,00207
Cd82	74,30	49,66	59,21	50,25	164,66	74,09	273,16	147,71	0,00033	0,00208
Cntn1	0,00	2,36	1,32	0,00	15,80	5,11	26,01	25,39	0,00033	0,00208
Rcor2	4195,85	3748,06	4603,04	3888,09	3122,79	3275,22	2155,16	2594,20	0,00033	0,00208
Plxnc1	40,36	29,56	61,84	74,06	100,63	91,97	110,56	99,24	0,00033	0,00209
Arhgef26	77,97	86,31	78,94	71,41	108,94	75,37	301,61	147,71	0,00033	0,00209
Max	1558,54	1567,80	1219,01	1251,07	925,61	1090,89	937,34	940,51	0,00033	0,00210
Pcbp4	8860,46	6829,27	8153,50	6499,99	6253,07	5246,23	4188,38	3790,90	0,00034	0,00210
Nr4a2	36,69	56,75	77,63	117,70	76,51	120,07	163,41	184,64	0,00034	0,00210
Xpnpep2	30,27	13,01	18,42	6,61	29,94	28,10	120,32	58,85	0,00034	0,00211
Cct5	22924,92	18214,14	15843,87	12115,25	11844,98	11009,81	11471,70	8344,60	0,00034	0,00213
Sp4	279,78	359,44	517,73	587,18	565,51	770,27	634,11	805,49	0,00034	0,00214

Hmbs	2094,26	1451,93	1424,92	1315,87	1266,58	1157,31	878,00	811,26	0,00034	0,00215
Pcdh8	22,02	5,91	8,55	11,90	29,94	22,99	214,62	25,39	0,00035	0,00216
Gab1	795,32	990,81	824,96	785,55	1263,25	952,93	1660,88	1473,66	0,00035	0,00216
Styk1	0,92	2,36	21,71	26,45	17,46	30,66	3,25	8,08	0,00035	0,00216
Tmem64	448,57	495,41	530,23	681,08	728,51	791,98	885,32	916,28	0,00035	0,00216
Smoc1	541,22	601,82	434,84	242,01	189,61	269,53	153,65	248,11	0,00035	0,00217
Stard13	63,30	75,67	124,34	132,25	106,45	166,06	203,24	197,33	0,00035	0,00218
Igsf10	424,72	433,92	586,81	514,44	681,11	549,28	954,42	778,95	0,00035	0,00218
Slc16a13	216,49	154,89	431,56	376,91	478,19	361,50	439,81	361,20	0,00035	0,00218
Havcr2	0,00	0,00	0,00	0,00	9,15	6,39	21,14	10,39	0,00035	0,00218
Tcf7l2	352,25	591,18	462,47	601,73	559,69	703,84	1044,66	1170,16	0,00036	0,00221
Plekhg1	177,04	241,20	148,02	152,09	212,90	159,67	433,31	309,27	0,00036	0,00221
Mfsd12	165,12	165,53	325,64	242,01	333,49	251,65	422,74	376,21	0,00036	0,00224
Mmp14	1957,58	1664,75	3309,69	2512,71	4144,87	2796,20	5559,03	3725,12	0,00036	0,00224
Spry1	828,35	962,44	2470,26	2596,03	1077,80	1622,28	2468,15	1272,87	0,00036	0,00226
Dhx57	551,31	690,49	980,21	1077,82	1035,39	1090,89	1083,68	1287,87	0,00037	0,00228
Cyth4	37,61	18,92	48,68	55,54	103,12	95,80	167,47	79,63	0,00037	0,00229
Gdf11	1193,44	1350,25	2224,88	2799,69	2683,69	2875,40	1876,32	2849,24	0,00037	0,00229
Nmd3	1558,54	1959,16	911,13	1302,64	692,75	1070,45	618,66	803,19	0,00037	0,00230
Myo1e	441,23	387,81	816,40	642,73	989,65	714,06	1247,08	832,04	0,00037	0,00231
H2-T23	5,50	0,00	5,92	7,93	40,75	11,50	60,16	38,08	0,00038	0,00232
Palmd	60,54	74,49	19,08	15,87	49,07	20,44	189,42	58,85	0,00038	0,00233
Rassf3	1379,66	1603,27	1312,43	1540,69	796,71	1147,09	663,38	807,80	0,00038	0,00233
Twsg1	1883,27	1829,10	2328,16	2808,95	2914,88	3128,32	3071,37	3203,51	0,00038	0,00235
Lanc13	1,83	3,55	9,21	10,58	11,64	16,61	32,52	33,47	0,00038	0,00235
Gstk1	50,45	37,84	144,07	120,35	205,41	100,91	186,98	135,02	0,00038	0,00235
Arhgap6	42,20	47,29	34,21	46,29	113,93	98,36	78,86	90,01	0,00038	0,00235
F830016B0	0,00	0,00	0,66	0,00	2,49	3,83	11,38	26,54	0,00038	0,00236
Kirrel3	6,42	5,91	25,66	30,42	17,46	24,27	139,02	24,23	0,00039	0,00238
Rspo3	62,38	30,74	342,09	316,07	363,42	441,98	23,58	213,49	0,00039	0,00238
Xpot	4638,00	5484,93	3301,14	3665,92	2855,00	3420,85	2335,64	2954,25	0,00039	0,00238
Arhgef37	0,92	1,18	8,55	21,16	22,45	20,44	39,84	18,46	0,00039	0,00238
Foxd1	32,11	8,28	0,00	0,00	0,83	1,28	0,00	0,00	0,00039	0,00238
Rnf125	49,54	37,84	144,73	103,15	29,11	62,59	28,45	36,93	0,00039	0,00241
Cyb5r4	976,95	701,14	486,16	454,93	497,32	417,71	468,27	430,44	0,00039	0,00242
Fam136a	2772,16	2012,36	1749,90	1544,66	1489,46	1470,27	1247,90	1246,32	0,00039	0,00242
Cse1l	9962,17	9799,34	7288,42	7341,09	5931,22	7679,66	5207,02	5671,93	0,00040	0,00244
Bcam	512,79	273,12	292,75	112,41	464,88	195,44	84,55	40,39	0,00040	0,00245
Camk1g	111,91	102,86	275,64	186,47	340,14	229,93	376,40	250,42	0,00040	0,00246
St13	9749,35	8158,23	7008,17	6232,85	5984,45	5988,40	5419,20	4719,88	0,00040	0,00246
Ly6h	49,54	27,19	5,26	3,97	7,48	12,77	7,32	4,62	0,00040	0,00246
Map3k1	852,20	1357,34	711,15	704,88	315,19	548,00	391,03	535,46	0,00040	0,00248
Rabl3	757,71	697,59	597,99	571,31	471,54	493,07	353,64	431,60	0,00041	0,00251
Hif1an	3168,45	3167,52	3213,64	3033,77	1865,36	2393,83	1901,52	2031,05	0,00041	0,00252
Plekhj1	1226,47	873,76	815,09	716,78	642,02	655,30	448,75	543,54	0,00041	0,00254
Casp8	210,99	167,89	265,12	260,53	330,99	347,45	499,16	355,43	0,00042	0,00256
Clns1a	4332,53	3263,29	2907,74	2479,65	2362,68	2152,40	2122,64	1676,77	0,00042	0,00256
Tmem231	307,30	270,76	692,07	470,80	695,25	531,39	653,62	613,93	0,00042	0,00257
Tacstd2	0,92	1,18	24,34	9,26	31,60	12,77	2,44	1,15	0,00042	0,00259
Copg2	1196,19	1261,57	1503,87	1404,47	1970,98	1761,52	1934,85	2019,51	0,00043	0,00261

Eif2s3x	2081,41	2157,79	1269,67	1449,44	1235,81	1541,81	1003,19	1232,48	0,00043	0,00261
Exosc8	1637,43	1508,68	1083,49	1170,40	963,87	1103,66	935,72	931,28	0,00043	0,00265
Herpud1	688,91	645,56	638,78	538,25	397,52	398,55	409,73	417,75	0,00043	0,00265
Trim16	87,15	75,67	65,13	85,96	120,59	117,52	182,10	165,02	0,00044	0,00267
Fat1	4428,85	4073,21	6330,58	6827,97	8093,48	6508,29	8185,71	6947,10	0,00044	0,00270
Dcaf6	111,00	160,80	186,17	248,63	291,07	270,81	299,98	406,21	0,00044	0,00271
Mxd1	202,73	234,11	265,12	333,27	346,79	351,28	417,05	567,77	0,00045	0,00272
Dcaf12l1	97,24	54,39	67,10	67,45	93,14	68,98	229,26	156,94	0,00045	0,00272
Lox	77,97	52,02	2,63	7,93	19,96	10,22	122,76	17,31	0,00045	0,00273
Apoa1	5,50	237,65	7,89	5,29	14,97	2,55	8,13	6,92	0,00045	0,00273
Hsf1	1284,26	1454,29	1466,37	1335,71	1032,06	1044,90	852,80	883,97	0,00045	0,00273
Snrpn	630,20	420,92	1309,14	1098,98	1096,93	988,70	859,30	603,54	0,00045	0,00273
1700001O2	36,69	21,28	49,34	48,93	79,01	80,48	105,69	87,70	0,00045	0,00276
Hs3st2	0,00	0,00	0,00	0,00	0,83	1,28	68,29	1,15	0,00046	0,00277
Wdr45	166,95	150,16	181,57	203,66	255,31	237,59	328,44	304,66	0,00046	0,00279
Casp6	602,68	496,59	1131,52	961,44	854,09	808,59	776,38	739,72	0,00046	0,00280
Atxn7l2	396,29	435,11	765,75	781,59	706,06	622,09	776,38	640,47	0,00046	0,00280
Sqor	34,86	17,74	96,71	62,16	144,70	84,31	115,44	95,78	0,00046	0,00282
Fyb	11,01	4,73	19,74	43,64	57,38	48,54	61,79	45,01	0,00047	0,00285
Urb1	1673,20	1960,34	1395,32	1424,31	999,63	1235,23	1067,42	1002,83	0,00047	0,00285
Fam160a1	5,50	3,55	10,53	5,29	27,44	10,22	44,71	42,70	0,00047	0,00287
Lactb2	238,50	263,66	148,02	179,86	140,55	134,13	121,13	114,25	0,00048	0,00288
Prex2	1394,34	2272,48	982,18	1187,59	538,90	977,20	480,46	782,41	0,00048	0,00288
Gprc5a	133,93	79,22	32,24	26,45	18,30	17,88	41,46	9,23	0,00048	0,00290
Adamts2	53,20	40,20	13,16	11,90	35,76	17,88	98,37	50,78	0,00048	0,00290
Jdp2	48,62	49,66	34,87	35,71	68,19	51,10	194,30	83,09	0,00049	0,00294
Col19a1	0,00	0,00	1,32	1,32	10,81	8,94	13,82	15,00	0,00049	0,00296
Cyp2u1	6,42	7,09	20,39	18,51	23,29	34,49	43,09	46,16	0,00049	0,00299
Ophn1	163,28	218,74	217,09	202,34	294,40	228,65	400,79	396,98	0,00050	0,00302
Cd300a	0,92	5,91	13,16	33,06	28,28	25,55	56,91	38,08	0,00050	0,00303
A930004D1	79,81	78,04	109,86	99,19	81,50	109,86	228,44	166,18	0,00050	0,00304
Ak6	810,92	507,23	467,08	448,32	384,22	389,60	302,42	270,04	0,00051	0,00308
Sapcd2	517,37	461,12	876,93	886,06	829,14	763,88	562,57	685,48	0,00051	0,00308
Lrrk2	156,86	172,62	63,81	112,41	152,19	158,40	218,69	311,58	0,00051	0,00308
Nhp2	4392,16	2382,44	2136,73	1401,83	1716,50	1194,36	1381,22	774,34	0,00051	0,00310
Grid2ip	0,92	0,00	4,61	5,29	6,65	6,39	26,01	18,46	0,00052	0,00312
Stc1	118,34	143,06	62,50	63,48	116,43	97,08	152,84	166,18	0,00052	0,00312
Gpn1	1996,10	1712,05	1720,96	1561,85	1346,42	1333,59	1059,29	1127,46	0,00052	0,00312
Sec24d	340,33	224,65	317,75	484,03	638,70	551,83	809,71	611,62	0,00052	0,00312
Bach2	1168,67	1790,08	812,46	891,35	693,58	767,71	1155,22	1212,86	0,00052	0,00313
Hdac5	708,18	444,56	1182,83	954,83	1525,22	1052,57	1590,97	1309,79	0,00052	0,00314
Gkap1	115,58	118,24	81,57	93,90	157,18	137,96	183,73	229,65	0,00052	0,00314
Ecsit	782,48	711,78	555,89	431,13	484,01	411,32	403,23	341,59	0,00053	0,00317
Cd99l2	812,75	630,19	918,37	802,75	1437,90	1048,74	1463,33	1367,49	0,00053	0,00317
Abcf2	6380,93	5483,75	5068,80	3907,93	4075,01	3695,48	3335,58	2886,16	0,00053	0,00320
Bzw2	7532,17	6335,05	5368,13	4477,92	4217,22	4157,90	4229,03	3306,22	0,00054	0,00322
Lgals3	0,00	0,00	11,18	11,90	18,30	15,33	12,19	6,92	0,00054	0,00323
Lsm2	1882,35	1669,48	1552,55	1190,23	1190,90	1159,87	985,31	905,89	0,00054	0,00323
Ippk	578,83	619,55	350,64	417,90	260,30	381,94	270,72	303,50	0,00054	0,00324
Evi2a	0,00	0,00	5,26	11,90	12,47	12,77	26,01	12,69	0,00054	0,00324

Ano4	24,77	26,01	0,66	2,64	0,00	2,55	1,63	0,00	0,00055	0,00328
Tiam1	1071,44	1564,25	2322,24	2398,98	2133,14	2547,11	2584,41	2716,52	0,00055	0,00330
Pla2g16	29,35	23,65	59,21	63,48	153,02	68,98	99,18	85,40	0,00055	0,00331
Tmbim1	225,66	215,19	281,56	312,11	395,03	385,77	463,39	376,21	0,00056	0,00332
Ypel3	112,83	119,42	215,12	272,43	339,31	205,66	288,60	302,35	0,00056	0,00334
Chrd	15,59	18,92	28,95	55,54	63,20	49,82	73,98	87,70	0,00056	0,00336
Rgl1	1380,58	1650,56	2232,77	1953,30	1299,85	1302,94	1242,21	1279,79	0,00056	0,00336
Slc8a2	80,72	41,38	83,55	70,09	163,83	103,47	237,38	165,02	0,00057	0,00338
Cyp4f16	36,69	52,02	151,97	125,64	24,95	66,42	133,33	107,32	0,00057	0,00339
Fbxl7	343,08	410,28	244,72	271,11	264,46	314,24	584,52	453,52	0,00057	0,00341
Cyp26a1	17,43	13,01	9,87	5,29	40,75	19,16	0,00	2,31	0,00057	0,00342
Tom1l1	188,05	190,36	160,52	144,15	138,05	150,73	86,99	76,16	0,00058	0,00345
Exosc2	2154,80	1928,42	1724,25	1658,39	1575,95	1512,43	1115,38	1263,63	0,00058	0,00345
Calcr1	235,75	286,13	122,36	121,67	121,42	132,85	283,72	180,02	0,00058	0,00345
Slc4a11	2,75	2,36	4,61	7,93	15,80	30,66	40,65	19,62	0,00058	0,00345
Sgpl1	2355,70	2020,64	3168,91	2803,66	3537,78	2963,54	4624,94	3775,90	0,00058	0,00346
Ptpro	0,00	1,18	0,00	2,64	14,97	20,44	24,39	11,54	0,00058	0,00347
Reck	1059,51	1207,18	615,10	702,24	594,62	711,51	630,05	758,18	0,00058	0,00347
Tpm4	15964,24	13514,29	11996,71	11369,37	9602,06	9628,95	9571,81	8268,44	0,00058	0,00347
Gltp	522,88	461,12	886,14	671,82	966,36	845,63	1149,53	898,97	0,00058	0,00347
Tagap	0,00	0,00	17,76	3,97	1,66	0,00	88,61	2,31	0,00059	0,00348
Rimbp2	9,17	14,19	52,63	30,42	10,81	12,77	0,81	5,77	0,00059	0,00348
Asf1b	1564,04	1369,16	1714,38	1311,90	1215,02	1121,55	853,61	810,11	0,00059	0,00350
Zfp30	166,95	150,16	186,17	152,09	273,61	223,54	312,99	312,74	0,00059	0,00351
Rnf44	4604,06	6500,58	6306,24	6193,18	3416,36	4658,64	2576,28	3311,99	0,00059	0,00352
Rnf165	500,86	912,78	492,74	539,57	229,53	410,04	183,73	278,11	0,00059	0,00352
Lrpprc	4320,61	3931,32	3178,77	2726,96	2461,64	2668,46	2694,97	2399,17	0,00059	0,00352
Prps2	676,99	857,21	601,28	708,85	453,24	475,19	390,22	444,29	0,00059	0,00352
Klhdc4	649,47	662,12	763,12	673,14	534,74	459,86	390,22	426,98	0,00059	0,00352
Crat	739,37	585,26	1195,99	968,06	1669,09	1131,77	1652,75	1297,10	0,00060	0,00353
Gal3st3	44,03	62,66	136,83	107,12	86,49	95,80	168,28	133,86	0,00060	0,00353
Afap1l1	654,05	545,06	394,72	380,87	486,51	401,10	308,11	308,12	0,00060	0,00353
Txnrd3	452,24	405,55	280,25	248,63	234,52	228,65	282,91	264,27	0,00060	0,00355
Atf3	126,59	107,59	47,37	46,29	71,52	65,15	50,40	49,62	0,00060	0,00355
Ogfrl1	192,64	211,64	271,70	387,49	353,45	424,09	417,86	529,69	0,00060	0,00356
Myl2	22,93	21,28	0,66	0,00	0,00	0,00	3,25	0,00	0,00060	0,00357
Rcc1l	1265,91	938,79	957,84	771,01	672,79	680,85	586,96	513,53	0,00060	0,00357
Sh3pxd2b	2540,08	3137,96	4452,39	4017,70	4774,42	4318,85	5178,57	4842,20	0,00061	0,00357
Arfgap3	288,04	270,76	439,45	375,58	528,09	454,75	546,31	503,15	0,00061	0,00357
Ppp5c	3113,41	2903,86	3274,82	3377,62	3017,17	3147,49	1847,86	2175,30	0,00061	0,00359
Ktn1	2826,28	4277,75	1900,55	2375,18	1114,39	1857,32	699,96	1535,98	0,00061	0,00360
Nptn	1087,95	1014,46	679,57	802,75	624,56	688,51	621,10	490,45	0,00061	0,00361
Pbdc1	2464,86	2010,00	1884,77	1671,62	1508,59	1682,32	1262,53	1185,16	0,00061	0,00361
Pcdh11x	33,94	20,10	1,32	2,64	1,66	2,55	4,06	11,54	0,00062	0,00364
Asgr1	3,67	3,55	0,00	0,00	14,14	10,22	11,38	17,31	0,00062	0,00364
Nle1	1079,69	899,77	868,37	642,73	671,96	611,87	511,35	454,68	0,00062	0,00364
Tsen2	821,92	618,37	608,52	465,51	463,22	450,92	336,57	346,20	0,00062	0,00364
Capn2	1597,07	1472,03	1990,68	1727,16	2815,92	2221,38	3091,69	2523,81	0,00062	0,00366
Art4	39,45	41,38	32,24	26,45	21,62	20,44	2,44	8,08	0,00062	0,00366
Gpx2	0,92	0,00	7,89	3,97	20,79	12,77	0,00	0,00	0,00063	0,00368

Gnl3l	2619,89	2746,61	2129,49	2073,65	1723,15	1928,86	1509,67	1724,08	0,00063	0,00371
Nqo1	83,48	56,75	122,36	96,54	215,39	121,35	319,49	178,87	0,00063	0,00372
Pld4	6,42	1,18	19,08	50,25	82,33	44,71	69,10	23,08	0,00063	0,00372
Ddx51	1527,35	1604,45	1182,83	1301,32	879,04	1139,43	729,23	902,43	0,00064	0,00374
Pard3	2303,41	2912,13	4929,34	4328,48	3951,10	3962,46	3129,90	3388,16	0,00064	0,00375
S100a11	157,78	113,51	236,17	219,53	569,67	314,24	729,23	272,34	0,00064	0,00378
Itgb8	5,50	16,55	20,39	43,64	33,27	90,69	68,29	132,71	0,00065	0,00378
Csf2ra	38,53	42,56	77,63	89,93	125,58	93,25	152,02	100,40	0,00065	0,00379
Cyyr1	196,31	244,75	129,60	116,38	130,57	140,51	103,25	86,55	0,00065	0,00380
Psma3	3396,86	2754,88	2178,17	2242,93	1858,71	2175,39	1790,14	1691,77	0,00065	0,00380
Glis2	1681,46	2089,22	1269,67	1244,45	1222,50	1129,21	1017,02	1169,01	0,00065	0,00382
Csta1	0,00	0,00	0,66	3,97	15,80	25,55	2,44	2,31	0,00066	0,00384
Rac3	137,60	81,58	187,49	181,18	335,15	213,32	328,44	273,50	0,00066	0,00385
Selplg	0,00	0,00	5,26	9,26	19,13	14,05	19,51	9,23	0,00066	0,00386
Apex1	7747,74	5727,32	6506,88	4704,06	4381,06	4132,35	3552,64	3021,18	0,00067	0,00391
Zmpste24	1142,99	1087,76	797,98	760,43	658,66	757,49	696,71	685,48	0,00067	0,00392
Tubb2b	1116,39	681,04	1053,89	1052,69	2361,84	1673,38	2695,78	1532,52	0,00068	0,00395
Tlr7	1,83	2,36	9,21	15,87	20,79	10,22	46,34	24,23	0,00068	0,00396
Kremen2	2,75	0,00	34,87	18,51	33,27	12,77	5,69	4,62	0,00068	0,00396
Trmt2b	144,02	89,86	147,36	145,47	260,30	185,22	338,19	260,80	0,00068	0,00398
Tmem241	58,71	47,29	93,42	99,19	113,10	127,74	143,08	126,94	0,00068	0,00398
Ulk2	610,02	812,28	882,19	1105,59	1196,72	1393,63	1298,30	1754,09	0,00069	0,00402
Mast4	592,59	827,65	827,59	784,23	611,25	766,43	1440,57	1194,39	0,00069	0,00402
Cmtr2	425,64	469,39	222,36	272,43	117,26	219,71	273,16	271,19	0,00069	0,00402
Tg	26,60	14,19	1,32	3,97	0,83	0,00	1,63	1,15	0,00069	0,00402
Dchs2	33,02	14,19	3,29	2,64	9,15	10,22	41,46	25,39	0,00069	0,00402
Pcdhb9	0,92	1,18	3,95	2,64	9,98	5,11	37,40	15,00	0,00069	0,00403
Ephb3	1380,58	1250,93	2100,54	2027,36	1817,12	2176,67	3238,84	2243,38	0,00069	0,00403
Trmt5	647,63	539,15	441,42	448,32	306,04	375,55	337,38	317,35	0,00070	0,00407
Plekhh2	190,80	279,04	262,49	390,13	492,33	541,61	462,58	706,25	0,00070	0,00407
Dirc2	518,29	370,08	323,01	310,78	626,22	527,56	613,79	677,40	0,00070	0,00408
Nup54	1636,51	1811,36	1590,04	1532,76	1157,64	1428,12	925,96	1025,91	0,00070	0,00409
Baz1a	1920,88	2829,37	1742,01	1750,96	1025,41	1485,60	1038,15	1205,93	0,00071	0,00410
Rnmt	1824,56	1991,08	1167,70	1469,28	965,53	1219,91	825,97	1094,00	0,00071	0,00411
Mrap	26,60	17,74	11,18	2,64	0,00	1,28	0,00	1,15	0,00071	0,00411
Vdac2	6005,74	5186,98	4772,77	4729,19	3753,17	4175,78	3525,82	3209,28	0,00071	0,00412
Nnt	1604,40	1376,26	2192,64	1818,41	2544,80	2088,53	3911,16	2608,05	0,00071	0,00412
Pik3r3	703,59	922,24	1361,11	1483,82	1335,61	1483,05	1416,18	1876,41	0,00071	0,00412
Ly86	0,92	1,18	11,84	13,22	25,78	12,77	43,09	15,00	0,00071	0,00413
Serf1	344,00	201,00	671,67	534,28	616,24	587,60	838,16	578,16	0,00071	0,00413
Pkm	96815,59	77693,58	76314,92	46103,00	49977,96	38563,08	43037,38	29744,45	0,00072	0,00413
Lss	1740,17	1792,45	1393,35	1118,82	1328,12	1397,46	989,37	1001,68	0,00072	0,00413
Ptprn	34,86	40,20	13,82	19,84	16,63	5,11	3,25	2,31	0,00072	0,00415
Pex26	99,07	140,70	196,70	212,92	234,52	246,54	247,95	312,74	0,00072	0,00416
Psmd14	3981,20	2949,97	2280,14	2289,21	1962,66	2146,01	2103,94	1855,64	0,00072	0,00416
Ptgr	36,69	52,02	0,00	2,64	3,33	2,55	18,70	1,15	0,00073	0,00420
Aldh3a2	329,32	320,42	324,98	345,17	513,12	452,20	525,17	533,15	0,00073	0,00420
Stx1b	176,13	148,98	267,75	331,94	260,30	287,41	329,25	347,36	0,00073	0,00420
Pdia3	15423,93	14500,37	14207,78	12742,10	11112,31	12333,19	9337,68	9203,18	0,00073	0,00421
Gprasp2	447,66	520,24	628,26	739,27	720,20	756,21	853,61	967,06	0,00073	0,00421

Sv2c	15,59	36,65	34,87	29,09	10,81	10,22	89,43	49,62	0,00073	0,00421
Cd1d1	45,87	49,66	37,50	78,03	85,66	122,63	146,33	153,48	0,00073	0,00422
Rad23b	7719,31	8791,98	6297,68	6515,86	5627,68	6167,23	4454,22	5189,55	0,00073	0,00422
Rfx5	162,37	250,66	346,69	419,23	372,57	468,80	446,32	657,78	0,00074	0,00423
Adcyap1	0,00	1,18	0,00	1,32	16,63	1,28	35,77	21,93	0,00074	0,00423
Samd5	57,79	75,67	119,73	150,76	123,08	109,86	186,17	161,56	0,00074	0,00424
1810046K0	0,00	1,18	0,00	0,00	0,83	0,00	57,72	2,31	0,00074	0,00426
Appbp2	4005,97	4651,38	2964,31	3048,32	1941,87	2797,48	2047,04	2526,11	0,00074	0,00426
Jun	376,10	314,51	313,80	261,85	239,51	194,16	601,59	409,67	0,00074	0,00427
Lrrc49	614,61	594,72	960,47	870,19	844,94	827,75	548,75	611,62	0,00075	0,00428
Mrpl37	2800,60	2131,78	1760,43	1416,38	1472,83	1254,40	1389,35	1002,83	0,00075	0,00431
Sphkap	22,02	15,37	0,66	0,00	0,83	0,00	1,63	0,00	0,00075	0,00431
Glrx3	4243,55	3108,41	2715,64	2597,35	2378,48	2447,48	2077,12	1847,56	0,00075	0,00431
Anpep	385,28	339,34	540,10	412,61	671,13	518,62	973,12	679,71	0,00076	0,00434
Wnk2	115,58	108,78	224,99	166,63	231,19	178,83	421,93	241,19	0,00076	0,00434
Kif13b	308,22	342,88	498,00	402,03	525,59	388,33	760,12	639,32	0,00076	0,00435
Srsf12	55,04	44,93	84,86	72,74	100,63	99,64	122,76	148,87	0,00076	0,00435
Nid1	7295,50	5864,47	8108,77	5976,29	4242,17	4327,79	4294,88	3172,36	0,00076	0,00436
Immt	5215,92	5227,18	4644,48	4037,53	4149,86	3899,87	3181,12	3172,36	0,00076	0,00437
Phf21a	705,42	957,71	1053,89	1460,02	1824,61	1849,66	1436,50	2198,38	0,00077	0,00438
Zfand4	65,13	63,85	71,05	109,77	142,21	146,90	147,96	169,64	0,00077	0,00438
Etv4	1841,07	1466,12	3729,40	2828,79	2431,70	2397,66	1908,83	1165,54	0,00077	0,00439
Card10	179,80	171,44	411,82	269,79	190,44	134,13	160,15	117,71	0,00077	0,00439
Car7	8,26	54,39	0,00	2,64	2,49	1,28	1,63	1,15	0,00077	0,00439
Pls3	1486,07	1228,46	1357,82	1202,13	2187,20	1675,93	2857,56	2084,13	0,00077	0,00441
Sf3a3	4695,80	4741,23	4733,95	4177,72	3842,99	3741,47	3040,48	2972,71	0,00078	0,00443
Tal2	4,59	1,18	1,32	0,00	2,49	1,28	75,61	3,46	0,00078	0,00446
Rpusd2	574,25	643,20	567,07	404,68	212,07	374,27	265,03	267,73	0,00079	0,00450
Grm4	4,59	9,46	11,18	6,61	10,81	5,11	74,79	25,39	0,00079	0,00452
Fgf5	20,18	13,01	0,66	1,32	0,00	0,00	0,81	0,00	0,00080	0,00455
Sypl	1140,24	1506,32	799,96	944,25	589,63	780,48	738,17	730,48	0,00081	0,00459
Irgq	598,10	593,54	847,32	747,20	998,79	749,83	1403,98	1066,30	0,00081	0,00460
5730409E0	84,39	101,68	130,26	136,22	201,26	175,00	182,92	222,72	0,00081	0,00460
Pbbp	31,19	14,19	57,89	95,22	211,24	103,47	46,34	120,02	0,00081	0,00462
Arhgap29	1686,05	1813,73	984,16	1178,33	1136,01	1246,73	1643,00	1576,37	0,00082	0,00465
Als2cl	10,09	13,01	30,92	38,35	45,74	40,88	49,59	53,08	0,00082	0,00466
Canx	12871,01	13221,07	11255,31	10967,33	8015,30	9745,20	8208,47	8163,42	0,00083	0,00469
Ggn	7,34	8,28	20,39	17,19	44,91	24,27	54,47	40,39	0,00083	0,00472
Pld3	371,52	261,30	678,91	473,45	963,03	512,23	1210,50	784,72	0,00083	0,00472
Cpne2	263,27	251,84	201,96	239,37	148,03	146,90	143,08	126,94	0,00083	0,00472
Gchfr	77,06	37,84	87,50	63,48	227,04	114,96	183,73	180,02	0,00083	0,00473
Pcdhb13	0,00	0,00	4,61	1,32	9,15	3,83	21,14	19,62	0,00084	0,00474
Pdzk1ip1	16,51	8,28	45,39	39,67	57,38	52,37	49,59	47,31	0,00084	0,00477
Rnf149	709,09	640,84	413,14	378,23	444,92	408,76	395,91	453,52	0,00085	0,00482
Mgst1	439,40	179,72	185,52	138,86	424,13	195,44	821,09	544,69	0,00085	0,00482
Mb21d2	632,96	644,38	455,24	445,68	286,08	402,38	365,02	285,04	0,00085	0,00483
Nek2	1799,80	1812,55	1500,58	1810,48	1310,66	1614,62	864,99	1057,07	0,00086	0,00485
Fam43a	425,64	316,87	416,42	286,98	214,56	166,06	191,05	183,49	0,00086	0,00486
Acsl4	887,06	1357,34	615,76	834,49	385,88	776,65	321,12	410,83	0,00086	0,00486
Steap3	202,73	154,89	498,66	322,69	243,67	176,28	182,92	96,94	0,00086	0,00488

Npepl1	435,73	397,27	414,45	404,68	729,34	468,80	903,20	731,64	0,00087	0,00490
Fgd1	2137,37	1940,24	4414,89	3081,38	2574,74	2188,17	2235,64	1995,27	0,00087	0,00490
Lama1	1238,39	937,61	1458,47	1622,68	1145,16	1145,82	855,24	747,79	0,00087	0,00490
Pigw	162,37	257,75	88,81	137,54	89,82	130,29	41,46	71,55	0,00087	0,00490
Limk1	746,70	681,04	1466,37	1128,08	1650,80	1199,47	1690,15	1292,48	0,00087	0,00490
Entpd5	163,28	167,89	213,80	248,63	360,93	275,92	308,11	385,44	0,00087	0,00491
Wars	4836,15	4050,74	4025,44	3062,87	3091,19	2840,91	2515,30	2052,97	0,00088	0,00493
Ets1	3353,75	2702,86	1749,90	1719,22	2281,18	2094,92	2347,02	2349,55	0,00088	0,00493
Fcer1g	10,09	4,73	21,05	54,22	59,05	35,77	80,48	47,31	0,00088	0,00493
Lpcat1	3025,34	2620,09	2317,64	2031,33	1812,13	1879,04	1776,32	1510,59	0,00088	0,00495
Hoxc9	26,60	20,10	6,58	5,29	9,98	1,28	0,00	0,00	0,00088	0,00495
Zfp568	3543,63	4620,63	3055,75	3353,81	2003,41	2691,46	1048,72	2051,82	0,00088	0,00495
Cyp2j9	1,83	2,36	2,63	2,64	23,29	11,50	26,01	16,16	0,00090	0,00503
Shmt2	6933,16	5552,33	5323,39	3646,08	3700,78	2838,36	3359,97	2471,88	0,00090	0,00505
Timm44	1660,36	1600,91	1299,93	1249,74	1239,14	1311,88	930,84	1027,06	0,00090	0,00505
Khynyn	2402,48	2395,45	1907,79	1780,06	1205,87	1587,79	979,62	1425,19	0,00090	0,00505
Fam98a	1258,57	1721,51	1181,51	1108,24	815,00	950,38	683,70	849,35	0,00090	0,00506
Fbxl20	524,71	541,52	709,83	870,19	1013,76	945,27	899,14	1365,19	0,00090	0,00506
Zfp672	221,99	204,55	196,04	214,24	251,99	250,37	371,52	356,59	0,00090	0,00506
Cers1	22,93	31,92	45,39	43,64	55,72	67,70	82,11	98,09	0,00090	0,00507
Pvr	111,00	94,59	44,08	44,96	28,28	40,88	52,84	39,24	0,00091	0,00508
Exoc6b	666,90	821,74	940,08	819,94	1144,33	995,09	1515,36	1265,94	0,00091	0,00509
Lamb3	2,75	2,36	1,97	5,29	45,74	12,77	2,44	0,00	0,00091	0,00511
Saa2	0,92	0,00	23,68	11,90	0,83	0,00	0,00	0,00	0,00092	0,00513
Elf4	203,65	182,08	234,86	243,34	355,11	261,86	395,91	386,59	0,00092	0,00515
Itga6	653,14	572,26	888,77	858,29	1046,20	950,38	1503,17	1027,06	0,00092	0,00516
Cntn3	6,42	13,01	0,00	0,00	14,14	3,83	26,83	15,00	0,00092	0,00517
Kcnu1	0,00	0,00	9,21	6,61	19,96	8,94	17,07	12,69	0,00092	0,00517
Clcn3	574,25	833,56	193,41	318,72	124,75	306,57	103,25	273,50	0,00093	0,00519
Vwce	24,77	34,29	19,74	23,80	49,07	30,66	100,81	66,93	0,00093	0,00519
Pak1ip1	1310,86	1292,31	983,50	1075,18	701,07	983,59	575,58	718,94	0,00094	0,00523
Msi1	2797,85	3749,24	3272,19	2803,66	1971,81	2200,94	1890,95	1946,80	0,00094	0,00523
Id3	3154,69	2111,68	3028,12	2335,50	5675,08	3290,55	8461,31	4790,27	0,00094	0,00526
Thoc3	3207,89	2741,88	2418,29	2127,87	2252,90	2041,27	1747,05	1682,54	0,00095	0,00527
Cox4i2	94,48	37,84	118,41	71,41	257,81	100,91	479,65	203,10	0,00095	0,00527
Pygl	100,91	89,86	107,89	67,45	163,83	60,04	331,69	240,03	0,00095	0,00531
Mettl24	56,87	34,29	7,24	6,61	9,15	11,50	21,95	10,39	0,00096	0,00533
Mettl2	1242,06	978,99	859,16	856,97	687,76	806,03	567,45	620,85	0,00096	0,00533
Acss3	7,34	11,82	28,29	19,84	52,39	35,77	41,46	57,70	0,00096	0,00533
Wdr75	2563,01	3297,58	1707,80	2098,78	1074,47	1872,65	1108,07	1407,88	0,00096	0,00535
Esrp2	5,50	8,28	26,31	22,48	33,27	24,27	5,69	2,31	0,00097	0,00541
Kcnk6	98,15	122,96	42,76	63,48	34,93	43,43	46,34	39,24	0,00098	0,00542
Mnd1	137,60	127,69	138,81	129,60	69,03	81,75	69,91	58,85	0,00098	0,00543
Orc1	956,77	949,43	784,83	878,13	424,13	673,18	424,37	520,46	0,00099	0,00552
Nudt5	2791,43	2174,35	2080,81	1969,17	1644,97	1689,98	1482,03	1372,11	0,00100	0,00553
Samd14	1158,58	1006,18	2116,99	1605,49	2400,10	1682,32	2833,17	2082,98	0,00100	0,00553
Mtrr	780,65	910,41	681,54	691,66	497,32	650,19	423,55	460,45	0,00100	0,00554
Mcph1	1097,12	1320,69	989,42	977,31	660,32	802,20	538,99	728,18	0,00101	0,00559
Gabrb1	0,00	0,00	0,00	1,32	7,48	3,83	20,32	13,85	0,00101	0,00559
Nrk	211,90	270,76	277,62	214,24	321,84	205,66	842,23	398,13	0,00101	0,00560

Cercam	166,95	100,50	210,51	167,96	368,41	238,87	444,69	300,04	0,00101	0,00561
Rarg	2613,46	2131,78	5309,58	3901,32	6066,78	3788,73	7523,15	4859,51	0,00102	0,00564
Kcnma1	8,26	14,19	30,92	55,54	21,62	21,72	113,81	38,08	0,00102	0,00566
Soat1	1758,52	2239,38	1120,99	1412,41	877,38	1140,71	1115,38	1282,10	0,00103	0,00568
Txndc5	6816,66	5246,10	4655,67	3578,63	3551,91	3213,91	3464,03	2460,34	0,00103	0,00568
Ppm1g	7713,80	7572,97	6778,58	5561,03	5826,44	5156,82	4643,64	4094,41	0,00103	0,00569
Glt8d2	19,26	24,83	40,79	29,09	75,68	39,60	95,93	80,78	0,00103	0,00569
Tpd52l1	81,64	50,84	196,04	158,70	181,30	178,83	177,23	117,71	0,00103	0,00570
Ipo4	5127,86	4566,25	4199,11	3251,98	3196,81	2801,31	2863,25	2151,06	0,00103	0,00570
St8sia3	15,59	24,83	1,97	0,00	0,00	0,00	0,00	0,00	0,00103	0,00570
Tns2	834,77	909,23	1080,86	833,16	491,50	408,76	725,97	467,37	0,00104	0,00574
Col11a1	1079,69	795,72	1964,37	1411,09	2308,62	1549,47	3412,00	1930,65	0,00104	0,00575
Mns1	879,72	1047,56	1172,96	994,51	800,03	830,30	453,63	631,24	0,00104	0,00576
Denr	2693,27	2595,26	1815,03	2073,65	1650,80	1986,34	1446,26	1597,14	0,00105	0,00580
Cnnm4	335,74	306,23	446,03	427,16	507,30	507,12	797,52	542,38	0,00106	0,00581
Lsamp	47,70	83,95	15,79	14,55	24,12	17,88	32,52	35,77	0,00106	0,00581
Cpsf4	1253,99	1399,91	1150,60	1206,10	1099,42	1089,61	669,07	830,88	0,00107	0,00587
Gabrp	0,00	1,18	6,58	0,00	51,56	39,60	7,32	0,00	0,00107	0,00587
Snx8	934,76	866,66	776,93	648,02	605,43	586,32	508,91	534,30	0,00107	0,00589
Carmil1	261,44	326,33	401,29	484,03	523,10	523,73	534,12	563,15	0,00108	0,00593
Drd4	3,67	5,91	5,26	1,32	19,13	10,22	39,84	26,54	0,00108	0,00595
Gpr83	0,00	1,18	7,89	2,64	7,48	5,11	47,96	11,54	0,00108	0,00595
Tnfaip6	708,18	480,04	346,03	245,98	153,85	223,54	398,35	196,18	0,00109	0,00600
Nnat	15896,36	9705,93	30112,17	16011,27	9832,43	7505,93	11383,90	6574,36	0,00110	0,00602
Orc6	1778,70	1461,39	1262,43	1301,32	1025,41	1244,18	753,62	934,74	0,00110	0,00606
Pqlc3	9,17	13,01	16,45	13,22	52,39	29,38	46,34	46,16	0,00111	0,00608
Lrrc15	8,26	4,73	22,37	19,84	66,53	58,76	14,63	61,16	0,00111	0,00609
Hnrnpab	32142,22	27693,07	26997,87	23226,73	20897,34	20739,68	19016,80	16173,36	0,00111	0,00611
Ubqln1	5258,12	5735,59	5099,06	4942,11	3958,58	4406,99	3587,60	3428,55	0,00112	0,00612
Fjx1	419,22	303,86	827,59	535,60	478,19	459,86	1286,92	675,09	0,00112	0,00612
Zeb1	2454,77	3659,38	2232,12	2007,53	1393,82	1661,88	1914,52	1771,40	0,00112	0,00612
Ctsf	116,50	89,86	246,70	150,76	249,49	149,45	358,52	286,19	0,00112	0,00613
Zfp219	1098,04	950,61	1627,54	1315,87	2444,18	1613,34	2068,99	1932,96	0,00112	0,00615
Psmd1	8802,67	8463,28	6964,75	6257,98	5759,91	6025,44	5721,62	4770,65	0,00113	0,00615
Fkbp1b	27,52	10,64	70,39	51,58	72,35	61,31	115,44	71,55	0,00113	0,00616
Dmbx1	3,67	3,55	13,16	59,51	23,29	49,82	0,81	6,92	0,00113	0,00616
Supv3l1	1062,26	1065,30	908,50	796,13	603,77	744,72	594,28	640,47	0,00113	0,00616
Uchl1	202,73	94,59	151,31	85,96	286,08	190,33	612,16	281,58	0,00113	0,00616
H2afv	1669,53	1112,59	2904,45	2432,04	3694,12	2493,46	4163,99	2751,14	0,00113	0,00616
Utp15	2071,32	2429,73	1734,12	1777,41	1099,42	1599,29	1160,10	1226,71	0,00113	0,00618
Lrrc25	0,92	1,18	19,08	22,48	32,43	14,05	42,27	11,54	0,00113	0,00618
Itpr1	1168,67	1803,09	666,41	913,83	415,82	762,60	658,50	737,41	0,00114	0,00621
Vstm4	21,10	13,01	5,26	11,90	35,76	29,38	41,46	57,70	0,00114	0,00621
Tmem263	553,15	580,54	438,13	657,27	676,95	809,86	1162,54	971,67	0,00115	0,00625
Hacd1	322,90	192,72	159,86	150,76	121,42	113,69	117,07	75,01	0,00115	0,00625
St8sia6	41,28	113,51	14,47	2,64	14,14	14,05	19,51	4,62	0,00115	0,00625
Igf2r	7734,90	6317,31	4343,84	4554,62	4459,23	3975,23	4840,37	3875,14	0,00115	0,00626
Pex2	795,32	633,74	399,98	445,68	401,68	387,05	408,11	498,53	0,00115	0,00627
Parvg	5,50	10,64	17,76	41,00	45,74	48,54	99,99	35,77	0,00116	0,00629
Mdn1	3507,86	5132,59	2632,75	3210,98	1449,54	2662,08	1174,73	1968,73	0,00116	0,00629

Traf3ip2	154,11	117,05	74,34	67,45	74,02	58,76	53,66	51,93	0,00117	0,00636
Ncf1	12,84	5,91	31,58	38,35	45,74	42,15	75,61	38,08	0,00117	0,00637
Amn	9,17	24,83	3,29	2,64	0,83	0,00	0,00	0,00	0,00118	0,00639
Pus7l	521,04	464,66	327,61	272,43	268,62	292,52	291,04	215,80	0,00118	0,00639
Faf1	1975,00	1961,52	1411,11	1538,04	1264,92	1460,06	1092,62	1240,55	0,00118	0,00641
Lingo1	66,96	79,22	21,71	9,26	60,71	34,49	62,60	66,93	0,00119	0,00644
Nim1k	38,53	27,19	190,78	92,57	69,86	93,25	53,66	87,70	0,00119	0,00644
Heph	843,94	729,51	1224,93	1228,58	1487,80	1099,83	1948,67	1403,27	0,00119	0,00644
Cdh1	37,61	35,47	160,52	42,32	122,25	81,75	23,58	5,77	0,00119	0,00645
Espn	44,03	33,11	11,18	5,29	7,48	1,28	4,06	6,92	0,00119	0,00646
Fzd4	716,43	640,84	473,00	862,26	844,11	1269,72	2207,19	1223,24	0,00120	0,00648
Dus4l	293,54	295,59	207,23	202,34	157,18	199,27	129,26	154,64	0,00121	0,00655
Adamts4	135,76	104,05	207,88	222,18	290,24	237,59	265,84	216,95	0,00121	0,00656
Ttyh2	233,00	235,29	609,84	454,93	268,62	296,35	449,57	280,42	0,00122	0,00659
Tmem246	141,27	89,86	146,04	122,99	375,07	213,32	339,82	216,95	0,00123	0,00665
A730017C2	16,51	15,37	36,18	46,29	75,68	40,88	177,23	47,31	0,00123	0,00665
Sema3b	70,63	37,84	44,08	50,25	160,51	93,25	118,69	133,86	0,00123	0,00665
Mars	5602,12	4625,36	4541,20	3544,25	3364,80	3161,54	3033,97	2408,41	0,00124	0,00670
Tomm5	1077,86	580,54	477,61	358,39	446,59	291,24	365,83	281,58	0,00124	0,00671
Slc20a2	1988,76	1936,69	1639,38	1404,47	1294,86	1305,49	1278,79	1160,93	0,00125	0,00673
Eif5a	45262,74	30126,35	32194,30	23058,77	23889,56	19793,13	19034,69	13850,35	0,00125	0,00674
Hyou1	10452,94	8120,40	9631,05	6718,20	4598,11	4874,51	5881,78	3727,43	0,00125	0,00675
Aldh1l2	19,26	33,11	27,63	55,54	70,69	61,31	91,86	111,94	0,00126	0,00681
Rpl7l1	6113,98	4861,83	4110,30	3480,77	3698,28	3286,72	3277,05	3055,80	0,00127	0,00684
Ints14	2369,46	2224,01	2128,17	1992,98	1871,18	1850,94	1445,45	1470,20	0,00127	0,00686
Nacad	4,59	1,18	1,97	7,93	14,14	5,11	60,16	23,08	0,00128	0,00687
Pcca	547,64	556,89	971,00	899,29	755,96	790,70	765,00	707,40	0,00128	0,00687
Tnks1bp1	1160,42	1106,68	1967,66	1573,75	2014,22	1589,07	2990,89	1997,58	0,00128	0,00688
Bhlha9	7,34	2,36	45,39	3,97	54,06	38,32	3,25	1,15	0,00128	0,00688
Acadvl	512,79	348,79	769,04	655,95	953,05	716,61	1072,30	859,73	0,00128	0,00688
Tbx3	618,28	1133,88	528,92	452,29	463,22	645,08	1356,83	993,60	0,00128	0,00688
Kitl	443,07	568,71	144,73	247,30	153,85	282,30	422,74	340,43	0,00128	0,00690
Scarf2	899,90	908,05	1096,65	1203,46	966,36	914,61	1930,78	1338,64	0,00129	0,00691
Slc29a3	233,92	215,19	306,56	265,82	451,58	261,86	663,38	456,99	0,00129	0,00691
Tesk2	151,36	128,88	230,25	281,69	277,77	332,12	242,26	311,58	0,00129	0,00691
Nab1	488,94	595,91	239,46	317,40	379,23	458,58	543,87	516,99	0,00129	0,00693
Thop1	4945,31	3495,03	4136,62	2631,74	2904,90	2142,18	1986,88	1534,83	0,00130	0,00695
Pgam2	0,92	2,36	3,95	9,26	28,28	16,61	34,14	15,00	0,00130	0,00696
Dcun1d5	1692,47	1463,75	842,06	1064,60	771,76	1048,74	720,28	904,74	0,00130	0,00696
Cebpa	14,68	9,46	29,60	22,48	71,52	31,93	87,80	48,47	0,00130	0,00696
Usp2	78,89	60,30	127,62	150,76	158,01	149,45	258,52	148,87	0,00130	0,00697
Anxa1	3,67	4,73	4,61	6,61	24,95	17,88	43,90	18,46	0,00130	0,00698
Emc6	1505,33	993,18	966,39	736,62	688,59	679,57	653,62	512,38	0,00131	0,00698
Ptpnb	182,55	218,74	106,57	115,06	223,71	177,56	224,38	293,12	0,00131	0,00699
Timm8a1	134,85	124,15	68,42	103,15	48,23	70,26	34,96	49,62	0,00131	0,00699
Tnfrsf11a	35,78	81,58	5,92	9,26	6,65	20,44	34,14	21,93	0,00131	0,00702
Agpat5	1101,71	1049,93	654,57	802,75	512,29	702,56	573,95	615,08	0,00131	0,00702
Pabpc4l	220,16	236,47	178,94	236,72	244,50	304,02	377,21	462,76	0,00132	0,00707
Nat6	156,86	156,07	271,04	259,21	344,30	246,54	363,39	305,81	0,00132	0,00707
Ran	26984,09	16821,33	16207,67	12875,67	12992,64	11814,57	11393,66	9013,92	0,00133	0,00708

Lhx2	3530,79	3236,10	5317,47	4594,30	6133,31	4680,35	6276,88	5959,28	0,00133	0,00711
Glb1l2	20,18	31,92	40,13	72,74	76,51	83,03	82,92	118,86	0,00134	0,00714
Bmp3	11,01	2,36	32,24	14,55	0,00	0,00	4,88	1,15	0,00134	0,00715
Gmnc	0,92	0,00	7,24	26,45	14,97	29,38	2,44	5,77	0,00135	0,00717
Id2	2027,29	1604,45	1195,33	1121,46	1672,42	1665,71	2673,83	1931,80	0,00135	0,00717
Ptdss2	1863,09	1492,13	1320,32	1084,43	1106,08	945,27	974,74	807,80	0,00135	0,00718
Cd36	7,34	10,64	5,26	19,84	15,80	28,10	79,67	43,85	0,00135	0,00718
Sema6d	368,77	567,53	323,67	409,97	543,89	576,10	872,31	729,33	0,00136	0,00721
Celf2	188,05	277,85	123,02	201,02	351,78	287,41	370,71	460,45	0,00136	0,00722
Hcfc1r1	186,22	126,51	443,40	259,21	501,48	316,79	709,72	377,36	0,00137	0,00729
Trim36	46,78	59,12	39,47	51,58	80,67	120,07	96,74	189,26	0,00137	0,00729
Ahcyl2	678,82	722,42	981,53	1055,34	858,25	979,76	1237,33	1147,08	0,00138	0,00731
Caprin1	28495,84	29202,93	25355,20	23608,92	20035,76	22185,68	18294,89	19184,16	0,00138	0,00731
Cryl1	105,49	76,85	173,02	178,53	266,95	158,40	291,04	216,95	0,00138	0,00732
Extl1	0,92	2,36	3,29	3,97	9,15	8,94	32,52	16,16	0,00139	0,00735
Wscd2	37,61	48,48	7,89	6,61	17,46	8,94	23,58	27,70	0,00139	0,00737
Trub1	700,84	725,96	541,42	571,31	451,58	454,75	430,06	467,37	0,00139	0,00738
Ccdc3	160,53	128,88	209,86	141,51	29,94	38,32	95,12	17,31	0,00139	0,00738
Gart	9316,37	6947,51	6493,72	4550,66	4846,77	4002,06	4452,59	3308,53	0,00139	0,00739
Cct2	20274,76	16678,27	14155,15	11853,39	11356,81	10685,35	11735,10	8809,66	0,00140	0,00740
Ttc28	1464,97	1823,19	2749,19	1748,32	3432,16	2235,43	5289,13	3296,99	0,00140	0,00742
Wdr61	1914,46	1701,41	1349,27	1429,60	1247,45	1396,19	1086,12	1085,92	0,00140	0,00743
Pdgfd	17,43	35,47	36,84	52,90	92,31	74,09	76,42	111,94	0,00141	0,00746
Farsb	3115,24	3025,64	2466,31	2220,44	1881,16	2138,35	2010,45	1658,30	0,00142	0,00749
Eif4g1	29979,16	40632,74	33335,02	30443,50	26776,17	28747,63	16680,35	20896,70	0,00142	0,00751
Klhl24	889,81	1003,82	1019,68	1366,12	1081,96	1269,72	1708,03	1846,41	0,00142	0,00753
Cd9	113,75	67,39	101,97	105,80	196,27	146,90	401,60	171,95	0,00143	0,00755
Vav1	5,50	8,28	24,34	44,96	56,55	33,21	73,17	31,16	0,00143	0,00756
Kank2	2085,08	2409,64	4014,91	3482,09	3434,65	3276,50	3324,20	3129,66	0,00143	0,00757
Orc2	2321,75	2748,97	1459,79	1936,11	1235,81	1756,41	985,31	1334,03	0,00143	0,00757
Pcdhb21	20,18	14,19	38,81	35,71	56,55	30,66	73,17	77,32	0,00144	0,00758
Sar1b	1131,98	712,96	565,10	559,41	489,00	503,29	501,60	461,60	0,00144	0,00758
Ywhag	9511,76	10294,75	8867,94	8079,03	6739,57	7268,34	6618,32	6310,09	0,00144	0,00759
Tut1	1663,11	1464,94	1494,66	1121,46	726,85	853,30	1121,07	823,96	0,00144	0,00759
Slc12a2	1744,76	2051,38	969,03	1344,96	900,66	1337,43	821,90	948,59	0,00144	0,00759
Grip2	17,43	27,19	2,63	2,64	0,83	5,11	0,81	1,15	0,00145	0,00766
Fam105a	42,20	49,66	75,65	100,51	118,09	86,86	129,26	128,09	0,00145	0,00766
Utp11	1277,84	1044,02	904,56	794,81	723,52	729,39	714,59	650,86	0,00146	0,00768
Mgrn1	1332,88	1279,31	1983,44	1662,36	2511,54	1942,91	2471,40	2184,53	0,00146	0,00769
Lrrk1	346,75	385,45	510,50	441,71	646,18	489,24	831,66	654,32	0,00146	0,00770
Cps1	0,00	1,18	1,32	7,93	16,63	31,93	37,40	9,23	0,00147	0,00771
Ctu2	859,54	831,19	764,43	658,60	583,81	563,33	515,42	510,07	0,00147	0,00773
Dkc1	4138,06	5780,52	3068,25	3495,32	2484,93	3245,84	1609,66	2624,20	0,00148	0,00776
Armc6	629,29	556,89	524,31	407,32	360,93	365,33	340,63	308,12	0,00148	0,00778
Baz2a	3303,29	4366,43	3874,13	3878,84	2005,90	3018,47	1303,99	2178,76	0,00148	0,00779
Sema4a	31,19	28,38	130,91	58,19	117,26	94,53	113,81	91,17	0,00148	0,00779
Fam196b	0,92	3,55	16,45	7,93	39,92	24,27	13,82	15,00	0,00149	0,00780
Capn1	147,69	109,96	167,75	162,67	430,79	164,78	446,32	342,74	0,00149	0,00780
Slc26a1	2,75	1,18	7,89	10,58	24,12	15,33	30,89	19,62	0,00149	0,00780
Rbfox1	0,92	4,73	1,32	2,64	7,48	11,50	26,83	23,08	0,00149	0,00781

Qtrt1	732,03	606,55	618,39	472,13	407,50	435,59	360,96	353,13	0,00149	0,00782
Polr2d	2032,80	1675,39	1588,07	1421,67	1417,11	1400,02	1099,12	1033,99	0,00150	0,00786
Tbx1	21,10	21,28	70,39	39,67	111,44	70,26	56,91	90,01	0,00150	0,00787
Unc13c	11,93	20,10	0,00	0,00	1,66	2,55	0,00	1,15	0,00150	0,00787
Idh3a	2244,70	1830,28	1809,11	1610,78	1385,50	1457,50	1240,58	1139,00	0,00151	0,00789
Dnajc2	1979,59	2445,11	1505,18	1840,89	1332,28	1687,43	829,22	1202,47	0,00151	0,00789
Gemin6	573,33	390,18	392,08	357,07	300,22	324,46	239,82	212,34	0,00151	0,00789
Rap1a	818,26	738,97	426,95	563,38	350,95	484,13	417,05	424,67	0,00151	0,00789
St3gal1	790,74	887,95	622,99	601,73	726,02	666,80	1125,95	957,82	0,00152	0,00792
Sfn2	1,83	1,18	9,87	11,90	11,64	8,94	29,27	20,77	0,00152	0,00792
Dcl3	0,00	0,00	1,32	1,32	1,66	3,83	21,14	11,54	0,00152	0,00792
Mrps6	677,90	490,68	396,03	294,91	356,77	323,18	288,60	288,50	0,00153	0,00797
Tmem248	2113,52	2257,11	1668,33	1925,53	1446,21	1590,35	1309,68	1377,88	0,00153	0,00797
Arhgef10	463,25	444,56	609,18	552,80	756,79	639,97	761,75	814,73	0,00153	0,00797
Nos1ap	11,01	20,10	25,66	14,55	33,27	40,88	93,49	49,62	0,00153	0,00797
Lxn	412,80	276,67	1091,39	749,85	837,46	564,61	708,90	511,22	0,00153	0,00797
Col8a1	2,75	0,00	0,00	1,32	14,97	31,93	62,60	3,46	0,00153	0,00800
Itpr1p1	261,44	274,31	269,72	261,85	370,91	289,97	494,28	445,45	0,00154	0,00800
Rfc5	2671,26	1943,79	1882,79	1702,03	1728,14	1606,95	1247,90	1208,24	0,00154	0,00801
Inha	9,17	17,74	25,00	39,67	29,94	35,77	60,16	70,39	0,00154	0,00801
Telo2	956,77	1003,82	797,98	792,17	650,34	790,70	461,76	585,08	0,00155	0,00806
Sowahb	49,54	16,55	5,26	7,93	9,15	5,11	0,81	3,46	0,00157	0,00815
Isy1	2266,71	1961,52	1845,29	1504,98	1432,91	1486,88	1157,66	1269,40	0,00157	0,00818
Magi2	16,51	22,46	15,13	22,48	29,11	24,27	85,36	49,62	0,00158	0,00819
Abcc1	1263,16	1125,60	822,98	920,45	647,01	836,69	682,89	679,71	0,00158	0,00819
Il17rc	16,51	7,09	58,55	46,29	68,19	43,43	34,14	35,77	0,00158	0,00821
Srgap3	202,73	216,37	193,41	210,27	331,82	265,70	329,25	481,22	0,00158	0,00822
Snx7	176,13	165,53	263,14	267,14	167,99	163,51	124,38	146,56	0,00159	0,00827
Ube2n	2580,44	2364,71	1997,26	2134,48	1686,56	2000,39	1490,97	1470,20	0,00159	0,00827
6030468B1	15,59	10,64	12,50	27,77	3,33	3,83	0,81	1,15	0,00160	0,00828
Taf5l	1738,33	1476,76	1311,11	1166,43	1135,18	1042,35	982,06	919,74	0,00160	0,00830
Ptcd2	1061,35	957,71	811,14	651,98	629,55	579,93	630,05	528,53	0,00160	0,00831
Man2b1	567,83	464,66	742,72	888,71	896,50	802,20	1228,39	895,51	0,00161	0,00832
Myom1	10,09	21,28	13,16	23,80	24,95	31,93	70,73	60,01	0,00161	0,00836
Cd300c2	0,00	0,00	1,32	6,61	13,31	10,22	17,89	15,00	0,00161	0,00836
Ephx2	6,42	14,19	15,13	13,22	54,89	15,33	108,12	41,54	0,00164	0,00850
Il18	0,00	0,00	4,61	5,29	5,82	12,77	25,20	10,39	0,00165	0,00855
Tprkb	789,82	790,99	382,87	518,41	454,90	453,47	234,95	426,98	0,00165	0,00856
Chmp2b	708,18	692,86	598,65	679,76	732,67	763,88	1070,67	999,37	0,00166	0,00857
Adsl	3488,59	2611,82	2547,23	1949,34	2033,35	1755,13	1677,95	1422,89	0,00166	0,00859
Eif2b1	2324,51	1567,80	1508,47	1301,32	1241,63	1093,44	1060,10	864,35	0,00166	0,00859
Chrna3	16,51	13,01	1,97	2,64	0,00	0,00	0,00	0,00	0,00166	0,00859
Ptp4a1	1345,72	1812,55	761,14	1063,27	679,45	986,14	718,66	813,57	0,00167	0,00861
Necab1	0,92	3,55	4,61	3,97	8,32	3,83	39,02	18,46	0,00167	0,00864
Pcdhgb7	166,04	113,51	311,83	218,21	400,02	222,27	616,22	333,51	0,00167	0,00864
Gpr146	15,59	11,82	48,02	67,45	44,08	45,99	35,77	42,70	0,00168	0,00867
Rps27l	3169,36	1950,88	1726,88	1460,02	1244,96	1313,16	1405,61	880,50	0,00169	0,00869
Hat1	2700,61	2779,71	2049,23	2310,37	1491,12	2230,32	1119,45	1489,82	0,00169	0,00869
Ccnj1	1084,28	1161,07	1088,10	1036,82	684,44	795,81	783,70	732,79	0,00169	0,00869
Arhgap18	633,87	643,20	353,93	391,45	493,99	413,87	592,65	564,31	0,00169	0,00869

Creb3l4	29,35	9,46	46,71	39,67	108,11	60,04	97,56	76,16	0,00169	0,00871
Klf3	816,42	1146,88	382,22	575,28	540,56	588,88	776,38	948,59	0,00170	0,00874
Slc7a2	366,01	412,64	254,59	277,72	151,36	220,99	226,82	240,03	0,00170	0,00875
Gli2	2150,21	3102,49	1805,16	1142,62	1254,11	993,81	2595,79	1791,01	0,00170	0,00876
Lrig1	384,36	396,09	961,13	880,77	350,95	761,32	400,79	428,14	0,00170	0,00876
Entpd3	0,00	0,00	1,32	0,00	1,66	3,83	29,27	8,08	0,00171	0,00878
Shq1	601,77	511,96	449,98	361,04	330,16	328,29	326,81	281,58	0,00171	0,00880
Tlr6	2,75	2,36	4,61	5,29	13,31	15,33	34,96	17,31	0,00171	0,00880
Trafd1	565,07	536,79	692,07	682,40	826,65	758,77	899,14	902,43	0,00172	0,00881
Fam83g	69,72	49,66	174,33	133,57	124,75	134,13	129,26	109,63	0,00172	0,00883
Dimt1	497,19	471,76	319,06	350,46	185,45	311,68	178,04	246,96	0,00172	0,00884
Ikbkap	6287,36	6031,18	5774,03	5067,75	4465,88	4477,25	4122,53	3940,92	0,00173	0,00887
St6gal1	1126,48	1085,40	1613,07	1493,08	1675,75	1442,17	1875,50	1800,25	0,00174	0,00890
Arl5c	2,75	5,91	5,92	2,64	27,44	8,94	34,14	33,47	0,00175	0,00896
Cyp4f17	30,27	37,84	53,29	80,67	93,97	68,98	96,74	130,40	0,00175	0,00896
Tpm1	3478,50	2876,66	2090,02	1989,01	1759,74	1635,06	2352,71	1639,84	0,00175	0,00896
Tnfaip8l2	0,00	0,00	3,95	7,93	10,81	8,94	22,76	10,39	0,00175	0,00898
Tle2	12,84	27,19	19,08	70,09	53,22	75,37	87,80	183,49	0,00176	0,00900
Pes1	5503,04	4576,89	4403,71	3323,39	3418,02	3113,00	2941,30	2486,88	0,00176	0,00901
Lrch1	155,95	177,35	226,30	249,95	194,60	270,81	344,70	363,51	0,00176	0,00903
Tfam	2470,36	2326,87	1538,73	1795,93	1344,75	1735,97	1279,60	1444,81	0,00177	0,00907
Usp15	2230,02	2698,13	1843,32	1873,96	1171,77	1746,19	1170,66	1369,80	0,00178	0,00907
Fcgr2b	0,00	0,00	3,29	5,29	6,65	16,61	21,95	10,39	0,00178	0,00911
Rbp4	43,11	222,28	50,00	35,71	47,40	39,60	21,95	5,77	0,00179	0,00913
Slc43a1	838,44	760,25	807,85	831,84	477,36	637,42	323,56	496,22	0,00179	0,00913
Vipr2	21,10	23,65	15,13	26,45	57,38	48,54	57,72	64,62	0,00179	0,00913
Nfil3	932,92	799,27	551,94	367,65	439,10	439,42	721,10	550,46	0,00179	0,00913
Xdh	5,50	3,55	0,00	2,64	4,16	1,28	29,27	21,93	0,00179	0,00913
Rnf43	5,50	7,09	17,76	11,90	28,28	16,61	53,66	33,47	0,00180	0,00918
Fut10	357,76	295,59	501,95	425,84	682,77	535,23	576,39	602,39	0,00180	0,00918
Fcgrt	42,20	24,83	38,16	37,03	85,66	44,71	219,50	71,55	0,00180	0,00919
Gtse1	1692,47	1792,45	2126,86	1842,22	1539,36	1628,67	1229,20	1202,47	0,00181	0,00921
Zdhhc8	874,21	851,29	1351,24	1190,23	1494,45	1249,29	1652,75	1389,42	0,00181	0,00921
Rbm38	1323,70	969,53	1339,40	945,57	904,82	843,08	600,78	580,46	0,00181	0,00923
Dnaja1	3384,94	3789,44	3229,43	3200,40	2152,27	2655,69	1777,95	2326,47	0,00182	0,00925
Endod1	103,66	85,13	209,86	226,14	187,95	171,17	231,69	159,25	0,00182	0,00925
Mettl27	57,79	41,38	100,65	71,41	174,64	95,80	143,08	156,94	0,00182	0,00925
Ttc27	1568,63	1269,85	1178,23	1007,73	930,60	923,55	857,67	770,87	0,00182	0,00926
Hspbap1	483,43	418,55	359,85	305,49	207,91	298,91	234,13	215,80	0,00183	0,00928
2410004B1	546,73	423,28	315,11	361,04	301,88	329,57	249,58	251,57	0,00183	0,00930
Vps37d	133,93	83,95	212,49	178,53	340,97	203,10	354,45	252,73	0,00183	0,00930
Slc39a10	4939,81	5920,04	3793,87	3848,42	2899,08	3606,07	2966,50	3561,26	0,00183	0,00931
Tarbp2	1387,00	869,03	1076,91	747,20	800,86	646,36	497,53	469,68	0,00186	0,00941
Plscr3	1292,51	1105,50	2221,59	1826,35	2331,91	1859,88	2848,62	2028,74	0,00187	0,00946
Asns	3438,14	2970,07	3072,20	2770,60	1965,15	2097,47	2138,09	1458,66	0,00189	0,00958
Krt8	135,76	157,25	107,23	26,45	57,38	47,26	33,33	19,62	0,00190	0,00960
Ppp2cb	2317,17	1916,59	1837,40	1665,00	1437,07	1543,09	1299,11	1229,01	0,00190	0,00962
Abcd2	139,43	152,52	51,31	74,06	104,79	100,91	136,58	130,40	0,00190	0,00962
Ano6	1258,57	1096,04	1466,37	1335,71	1776,37	1407,68	2550,26	1909,88	0,00190	0,00962
Cers4	112,83	100,50	228,93	259,21	237,85	283,58	140,64	241,19	0,00190	0,00963

Lin7c	2585,94	3444,19	1706,49	2281,28	1145,99	1950,57	1129,20	1478,28	0,00190	0,00964
St8sia4	255,02	247,11	69,73	129,60	91,48	153,29	83,74	110,78	0,00191	0,00964
Get4	1893,36	1328,96	1237,43	1060,63	1100,25	868,62	853,61	750,10	0,00191	0,00966
Brms1	904,48	740,15	980,87	673,14	643,69	532,67	441,44	417,75	0,00191	0,00967
Gsdmd	9,17	1,18	20,39	18,51	32,43	17,88	54,47	42,70	0,00192	0,00969
Aifm3	2,75	2,36	30,26	47,61	0,83	12,77	5,69	2,31	0,00192	0,00970
Fzd6	87,15	70,94	29,60	42,32	108,94	85,59	98,37	88,86	0,00193	0,00975
Stambpl1	366,93	378,35	209,86	197,05	77,34	108,58	323,56	101,55	0,00193	0,00976
Grhpr	1753,01	1148,06	1272,30	837,13	807,52	637,42	734,10	475,45	0,00194	0,00977
Nepro	1072,36	1235,56	735,49	838,45	487,34	738,33	504,85	662,40	0,00194	0,00979
Timm23	1387,92	783,90	788,77	490,64	558,86	445,81	495,91	330,05	0,00194	0,00980
Tspo	171,54	98,14	482,21	297,56	519,77	264,42	512,98	357,74	0,00194	0,00980
Fam212a	1274,17	943,52	1399,27	946,90	667,80	651,47	710,53	512,38	0,00195	0,00980
Slco3a1	317,40	260,12	120,39	99,19	153,85	164,78	295,11	156,94	0,00195	0,00981
Hnrnpf	5196,66	4218,63	3743,87	3173,95	3274,15	2915,00	2875,45	2486,88	0,00196	0,00985
Nol3	5,50	5,91	10,53	7,93	38,26	11,50	47,96	35,77	0,00196	0,00989
Pdxdp	957,69	822,92	837,45	974,67	704,40	688,51	547,94	557,38	0,00197	0,00989
P2ry13	1,83	0,00	4,61	7,93	12,47	17,88	28,45	15,00	0,00197	0,00989
Lypd6b	1,83	3,55	11,18	10,58	43,25	12,77	30,89	26,54	0,00197	0,00990
Stoml2	4033,49	2970,07	3061,02	2357,98	2465,80	2204,77	1910,46	1650,23	0,00197	0,00991
Dner	27,52	3,55	1,97	3,97	26,61	37,04	43,09	41,54	0,00197	0,00991
Nipsnap2	811,83	798,09	1173,62	997,15	1408,79	1070,45	1699,09	1383,65	0,00198	0,00993
Amer2	99,99	117,05	251,30	235,40	191,28	206,94	151,21	211,18	0,00198	0,00994
Cyp20a1	642,13	573,44	321,04	400,71	374,24	445,81	349,57	338,12	0,00198	0,00994
C1qtnf4	14,68	2,36	40,13	19,84	51,56	17,88	141,46	54,24	0,00198	0,00995
Tgjf1	964,11	952,98	1500,58	1401,83	1063,66	1352,75	1887,70	1547,52	0,00198	0,00995
Ehd3	869,63	724,78	748,64	584,54	556,36	553,11	382,09	455,83	0,00198	0,00995
Nek3	378,86	364,16	672,33	437,74	433,28	375,55	266,65	245,80	0,00199	0,01000
Dpp6	38,53	27,19	12,50	9,26	14,14	7,66	70,73	31,16	0,00200	0,01003
Zfp706	4926,96	4576,89	3612,96	3643,43	3026,32	3561,36	3102,26	2891,93	0,00201	0,01004
Myo18a	1634,68	1809,00	3812,95	2905,49	3321,55	2384,88	3096,57	2859,62	0,00201	0,01006
Ppp1r7	2800,60	2899,13	2554,47	2145,06	2094,06	2198,39	1508,04	1801,40	0,00201	0,01006
Tcim	179,80	182,08	84,86	99,19	105,62	118,80	162,59	165,02	0,00201	0,01008
Tefm	426,56	268,39	250,64	234,08	154,68	185,22	175,60	163,87	0,00202	0,01009
Numbl	187,13	135,97	323,01	234,08	504,80	284,86	478,83	363,51	0,00202	0,01010
Plgrkt	156,86	151,34	117,76	124,31	209,57	143,07	348,76	230,80	0,00203	0,01013
Acot11	256,85	257,75	273,01	273,75	207,91	186,50	154,46	146,56	0,00203	0,01014
Plekhn2	575,16	671,58	901,92	897,96	1053,68	918,44	1043,03	1028,22	0,00203	0,01016
Pcdhga10	33,02	43,75	55,92	38,35	73,18	74,09	141,46	87,70	0,00204	0,01019
Dip2a	415,55	511,96	630,89	773,65	721,86	840,52	813,77	969,36	0,00205	0,01025
Creld2	1165,92	825,28	1004,55	798,78	660,32	583,77	569,07	482,37	0,00206	0,01026
Impact	1487,90	1930,78	1003,89	1247,10	929,77	1144,54	581,27	928,97	0,00206	0,01026
Arl8a	433,90	417,37	519,05	591,15	701,07	599,10	784,51	710,87	0,00206	0,01027
Ints3	5750,72	5185,80	5743,77	4626,04	4446,75	4097,86	3395,74	3275,06	0,00206	0,01027
Pnmal1	4,59	7,09	33,55	41,00	17,46	26,83	5,69	12,69	0,00206	0,01027
Ddx25	412,80	329,88	236,83	216,89	263,63	228,65	203,24	165,02	0,00207	0,01030
Tigar	409,13	383,08	269,72	275,08	216,23	246,54	247,14	231,95	0,00207	0,01031
Nup205	7648,67	7306,94	6343,08	5981,58	5275,06	5628,17	5090,77	4767,19	0,00208	0,01035
Trmt1	1795,21	1481,49	1209,80	1169,07	1136,01	932,49	1008,07	827,42	0,00208	0,01036
Ln timer	489,85	731,88	442,74	941,61	1214,19	1509,87	1123,51	2183,38	0,00209	0,01039

Pdk4	20,18	17,74	11,84	14,55	15,80	20,44	65,04	41,54	0,00209	0,01040
Dcbld2	2684,10	3699,58	1864,37	2387,08	1585,10	2273,75	1016,20	1608,68	0,00211	0,01047
Sifn9	411,88	558,07	743,38	978,64	1197,56	1116,44	686,95	1126,31	0,00211	0,01047
Bmpr2	788,90	1434,19	1756,48	2159,61	2063,29	2490,91	2290,93	3228,90	0,00211	0,01048
Abca3	127,51	134,79	116,44	93,90	219,55	134,13	287,79	225,03	0,00212	0,01052
Adgrg3	152,28	122,96	72,36	68,77	84,00	86,86	63,41	43,85	0,00212	0,01053
Nutf2	1182,43	1124,42	885,48	933,67	727,68	858,41	724,35	610,47	0,00213	0,01056
Fbl	3771,13	3305,86	3106,41	2315,66	2323,59	2028,49	2133,21	1702,16	0,00213	0,01058
Mfsd6	13,76	8,28	6,58	7,93	22,45	16,61	37,40	41,54	0,00214	0,01060
Ptgdr	0,00	0,00	2,63	0,00	28,28	10,22	4,06	30,00	0,00214	0,01060
Nars	5964,46	5302,85	4722,77	3841,81	4095,80	3598,40	3438,83	3181,59	0,00215	0,01068
Abcc8	21,10	22,46	3,95	14,55	6,65	8,94	0,81	0,00	0,00216	0,01069
Tap2	1,83	1,18	7,89	7,93	18,30	8,94	27,64	20,77	0,00217	0,01073
Myo7a	188,97	140,70	87,50	85,96	99,80	83,03	76,42	65,78	0,00217	0,01073
Ranbp1	11063,88	7815,35	8239,68	6760,52	6717,95	6324,35	5298,07	4163,65	0,00217	0,01076
Rasal3	0,00	0,00	5,92	5,29	13,31	11,50	23,58	6,92	0,00218	0,01078
Tceal5	19,26	17,74	26,97	17,19	60,71	47,26	56,09	53,08	0,00218	0,01080
Trim65	33,94	57,94	69,08	76,70	88,98	83,03	121,13	139,63	0,00219	0,01083
Shkbp1	557,73	399,64	933,50	644,05	1195,89	804,75	1643,81	950,90	0,00220	0,01088
Plxdc2	277,95	374,81	683,52	763,07	784,23	1046,18	251,21	624,32	0,00222	0,01095
Tmem229b	55,96	40,20	46,05	51,58	93,14	63,87	152,02	101,55	0,00222	0,01095
Dyrk1b	328,40	236,47	731,54	443,03	572,17	449,64	863,37	601,24	0,00223	0,01099
Asah1	414,63	375,99	423,66	494,61	577,99	643,80	639,80	673,94	0,00224	0,01106
Grasp	223,83	173,81	336,17	290,95	326,83	316,79	464,20	364,67	0,00225	0,01112
Crip1	36,69	18,92	109,20	46,29	158,84	58,76	203,24	124,63	0,00225	0,01112
Apod	26,60	17,74	132,23	97,86	40,75	43,43	275,59	34,62	0,00226	0,01115
Pdia6	11923,41	9516,76	10428,38	7507,72	6870,97	7072,90	6253,30	4681,79	0,00226	0,01116
Slc1a5	1996,10	1728,60	1642,02	1273,55	1172,61	1156,04	1162,54	992,44	0,00227	0,01120
Mst1r	13,76	18,92	10,53	17,19	24,12	37,04	51,22	57,70	0,00228	0,01125
Gli3	5529,65	8742,32	6852,26	6550,25	5369,87	5405,91	11844,85	9650,93	0,00229	0,01125
Cdk8	1811,72	1950,88	1313,09	1571,11	1125,20	1384,69	781,26	1111,31	0,00229	0,01125
Pwp2	2394,22	2051,38	1829,51	1552,59	1345,59	1369,36	1452,76	1100,92	0,00229	0,01127
Jph2	55,96	59,12	34,21	25,13	19,13	11,50	16,26	19,62	0,00230	0,01133
Themis2	4,59	4,73	16,45	37,03	42,41	34,49	43,90	20,77	0,00232	0,01143
Ghitm	3200,55	3032,73	2028,84	2461,14	2134,81	2276,31	1755,18	1987,19	0,00233	0,01145
Dlst	5053,55	4806,26	4197,80	3795,52	3299,10	3460,45	3376,23	2831,93	0,00233	0,01145
Foxo3	865,96	1177,62	1372,95	1162,46	1865,36	1329,76	1986,07	2073,74	0,00233	0,01146
Sec24c	5525,98	5610,26	5345,10	4750,35	4512,45	4284,36	3645,32	3623,57	0,00235	0,01154
Mogs	3545,47	2802,18	2514,34	1839,57	2131,48	1665,71	1755,18	1359,42	0,00236	0,01156
Gjb2	3,67	23,65	48,02	42,32	79,01	98,36	30,89	39,24	0,00235	0,01156
Dhfr	2585,94	2034,83	2095,94	1883,21	1727,31	1839,44	1298,30	1367,49	0,00237	0,01162
Hdac9	662,31	795,72	241,43	400,71	521,44	615,70	517,04	583,93	0,00237	0,01163
Anxa6	1760,35	1112,59	2673,54	1711,29	3459,60	1798,56	7051,63	2906,94	0,00237	0,01164
Kcnj2	52,29	117,05	378,93	727,36	69,03	415,15	106,50	204,26	0,00238	0,01167
Kti12	1788,79	1172,89	1248,62	806,71	843,28	697,45	743,86	516,99	0,00238	0,01167
Def6	98,15	61,48	348,67	191,76	220,38	136,68	221,13	160,41	0,00239	0,01171
Fuca1	307,30	197,45	395,37	379,55	541,39	402,38	747,92	493,91	0,00241	0,01178
Nr3c2	1,83	3,55	3,95	1,32	17,46	11,50	21,95	21,93	0,00241	0,01178
Ctdsp2	4457,29	4315,59	5561,54	5001,62	6690,51	5533,65	7930,44	6814,39	0,00241	0,01178
Grrp1	307,30	132,42	277,62	146,80	79,01	89,42	95,93	60,01	0,00241	0,01180

Nphp4	142,19	143,06	299,98	242,01	270,28	258,03	199,99	228,49	0,00243	0,01186
Irgm1	25,69	11,82	11,84	7,93	22,45	14,05	66,66	43,85	0,00243	0,01188
Mettl1	1109,97	808,73	712,46	605,70	642,02	572,27	536,55	423,52	0,00243	0,01190
Txnrd2	415,55	448,11	428,27	394,10	342,63	316,79	239,82	264,27	0,00243	0,01190
Trnt1	1309,03	1437,74	725,62	960,12	626,22	989,98	503,22	708,56	0,00244	0,01192
Serinc5	515,54	487,13	867,72	1072,53	564,68	730,67	360,14	585,08	0,00245	0,01196
Gtf2e1	1549,37	1576,08	1367,69	1342,32	1039,54	1168,81	1032,46	1016,68	0,00246	0,01203
Pcdhb6	2,75	0,00	3,95	2,64	10,81	6,39	25,20	21,93	0,00247	0,01203
Asnsd1	2266,71	1917,78	1254,54	1362,16	1344,75	1403,85	1589,34	1387,11	0,00248	0,01211
Rfx1	478,84	547,43	822,98	825,23	713,54	742,16	826,78	778,95	0,00248	0,01211
Homer1	951,27	1219,01	650,62	773,65	428,29	742,16	465,01	520,46	0,00249	0,01214
Mfsd2a	133,01	95,77	283,54	314,75	123,91	220,99	221,94	201,95	0,00249	0,01215
Selenot	2459,35	2825,82	1339,40	1998,27	1175,10	1793,45	894,26	1338,64	0,00249	0,01215
Klhl13	505,45	472,94	771,01	692,98	785,90	674,46	947,91	799,72	0,00250	0,01216
Ddx52	2122,69	2106,95	1700,57	1762,87	1365,55	1756,41	1153,59	1280,94	0,00250	0,01216
Ube2h	1020,98	1049,93	1310,45	1329,09	1393,82	1276,11	1751,12	1591,37	0,00250	0,01216
Nqo2	614,61	559,25	443,40	457,58	413,32	438,14	331,69	351,97	0,00250	0,01218
Eif2a	2228,19	2144,79	1492,68	1642,52	1563,47	1641,44	1465,77	1388,27	0,00251	0,01221
Crocc	755,88	879,67	1604,52	1219,33	1617,53	1332,32	1316,19	1270,56	0,00251	0,01222
Lrrc59	10087,84	7681,75	7216,71	5628,48	5823,11	5158,09	5175,31	3727,43	0,00253	0,01228
Exosc3	1025,57	690,49	754,56	617,60	513,12	500,74	472,33	413,13	0,00253	0,01231
Rab33a	1,83	3,55	16,45	15,87	20,79	15,33	38,21	19,62	0,00253	0,01231
Atp7a	1520,01	1813,73	1251,91	1073,85	890,68	1033,41	1689,33	1381,34	0,00257	0,01245
Zbtb7b	20,18	13,01	42,10	46,29	58,21	30,66	84,55	63,47	0,00257	0,01247
Iigp1	1,83	4,73	0,00	0,00	0,83	1,28	26,01	6,92	0,00257	0,01247
Esrrb	3,67	4,73	4,61	1,32	24,12	6,39	29,27	33,47	0,00257	0,01247
Robo1	1531,02	1999,36	1855,82	1337,03	1252,44	1310,60	3371,35	2162,60	0,00257	0,01247
Fosl2	85,31	148,98	63,81	67,45	46,57	40,88	204,05	93,47	0,00258	0,01249
Mlh1	1023,74	916,32	812,46	789,52	740,99	786,87	512,17	610,47	0,00259	0,01253
Ifitm3	232,08	153,71	180,91	126,96	306,87	176,28	563,38	320,81	0,00259	0,01254
Lrig3	616,44	556,89	1007,84	874,16	517,28	799,65	1133,27	1063,99	0,00260	0,01256
Rogdi	301,80	237,65	511,81	394,10	681,11	479,02	769,87	493,91	0,00260	0,01256
Abcd1	280,70	264,85	638,78	448,32	816,67	467,52	741,42	547,00	0,00261	0,01263
Trappc9	495,36	426,83	1060,47	658,60	1181,75	729,39	1642,18	958,98	0,00262	0,01265
Noa1	1232,89	923,42	785,48	593,79	686,93	532,67	595,09	482,37	0,00263	0,01271
Gm49394	42,20	11,82	3,95	0,00	0,00	2,55	0,00	0,00	0,00263	0,01273
Igf1	96,32	101,68	69,73	128,28	32,43	31,93	106,50	72,70	0,00264	0,01275
Nmnat1	226,58	190,36	283,54	240,69	191,28	190,33	117,07	137,33	0,00265	0,01282
Egr1	233,00	289,68	140,78	125,64	1006,28	83,03	92,68	49,62	0,00268	0,01293
Mab21l1	87,15	62,66	291,43	252,59	103,12	316,79	247,14	249,26	0,00268	0,01293
Dagla	94,48	92,22	190,12	187,79	162,17	187,78	155,28	182,33	0,00268	0,01294
Plagl1	955,85	1820,82	729,57	962,77	964,70	1426,84	2233,21	2067,97	0,00269	0,01298
Stard10	105,49	83,95	304,59	183,82	373,40	214,60	520,30	206,57	0,00269	0,01298
Mif	15580,80	10520,58	11633,58	6370,39	6943,32	5055,90	6460,61	3849,76	0,00269	0,01298
Sipa1	1650,27	1537,06	1303,22	1054,02	1328,12	1029,58	863,37	863,19	0,00269	0,01298
Was	8,26	5,91	33,55	34,38	30,77	34,49	26,01	28,85	0,00271	0,01305
Tvp23a	293,54	318,05	335,51	346,49	552,21	435,59	552,81	476,60	0,00271	0,01305
Tomm40	4839,82	3484,39	3447,18	2096,13	2683,69	1831,78	1980,37	1244,02	0,00273	0,01313
Col15a1	904,48	790,99	1541,36	1019,63	2398,44	1346,37	2690,90	1650,23	0,00273	0,01313
Slc45a4	955,85	1026,28	1021,65	806,71	693,58	637,42	613,79	613,93	0,00273	0,01315

Racgap1	2100,68	2205,09	2057,12	2531,23	2904,07	3262,45	3318,51	3318,91	0,00274	0,01317
Trip10	780,65	828,83	913,11	855,64	493,99	652,75	556,07	519,30	0,00274	0,01318
Anxa2	1170,51	689,31	1094,02	696,95	1623,35	891,62	4287,56	1409,04	0,00274	0,01319
Dcxr	63,30	41,38	103,28	59,51	118,92	89,42	203,24	135,02	0,00276	0,01325
Xpr1	943,01	980,17	972,97	1063,27	1318,14	1139,43	1438,13	1645,61	0,00277	0,01329
Zfp330	1063,18	1005,00	856,53	830,52	635,37	771,54	639,80	619,70	0,00277	0,01330
Cd151	1238,39	859,57	895,35	826,55	672,79	646,36	551,19	600,08	0,00277	0,01331
Myl6b	60,54	30,74	88,81	81,99	136,39	57,48	254,46	136,17	0,00277	0,01332
Nol10	1610,83	2325,69	1528,21	1495,73	1278,22	1704,04	997,50	938,21	0,00280	0,01344
Irf7	0,00	1,18	2,63	1,32	10,81	1,28	27,64	18,46	0,00281	0,01346
Npr1	416,47	238,84	90,13	95,22	167,99	91,97	245,51	102,71	0,00281	0,01346
Scml4	16,51	23,65	0,66	2,64	3,33	1,28	24,39	8,08	0,00282	0,01351
Naprt	11,01	21,28	30,26	26,45	37,42	38,32	86,99	50,78	0,00282	0,01351
Gal3st1	2,75	0,00	2,63	5,29	12,47	5,11	26,83	24,23	0,00282	0,01352
Fmo1	11,01	41,38	1,32	1,32	6,65	10,22	17,89	15,00	0,00283	0,01353
Fam111a	601,77	522,60	807,19	950,86	900,66	997,64	869,87	1020,14	0,00283	0,01356
Ldb2	387,11	379,54	311,83	298,88	387,54	463,69	521,92	562,00	0,00283	0,01357
Dis3	2980,39	3657,02	2351,85	2613,22	1971,81	2458,97	1684,46	1998,73	0,00284	0,01360
Dnajc28	37,61	43,75	83,55	68,77	96,47	85,59	108,12	99,24	0,00284	0,01360
Psd4	7,34	4,73	25,66	34,38	43,25	34,49	39,84	19,62	0,00286	0,01367
Pla2g7	20,18	8,28	19,08	11,90	69,86	37,04	45,53	55,39	0,00288	0,01378
Cd3eap	1049,42	993,18	1014,42	733,98	803,36	756,21	480,46	588,54	0,00289	0,01379
Ccdc59	747,62	637,29	571,02	587,18	439,94	510,96	389,41	417,75	0,00289	0,01379
Ly75	886,14	897,41	624,31	692,98	568,84	692,34	518,67	520,46	0,00289	0,01379
Cables1	377,02	283,76	469,05	424,52	643,69	531,39	581,27	605,85	0,00289	0,01380
Noc3l	1153,08	1475,58	876,27	985,25	705,23	878,84	647,93	791,65	0,00290	0,01382
Plaur	38,53	22,46	54,60	21,16	9,15	10,22	4,88	8,08	0,00290	0,01382
Steap2	104,58	115,87	121,05	130,93	154,68	167,34	201,61	229,65	0,00290	0,01385
Sipa1l2	1022,82	1241,47	1390,06	1220,65	1561,81	1172,64	2792,52	1785,24	0,00291	0,01389
Marveld1	709,09	774,44	983,50	969,38	1101,92	998,92	1171,48	1230,17	0,00294	0,01400
Mllt1	2946,45	3132,05	4523,44	4190,94	6164,08	4585,82	5675,29	4596,40	0,00294	0,01402
Etfa	921,00	809,91	1080,86	1276,19	1453,70	1435,78	1265,78	1259,02	0,00295	0,01406
Ubfd1	4949,90	5923,59	3826,77	4528,17	3260,01	3865,38	2871,38	3391,62	0,00295	0,01407
Smtnl2	208,23	133,61	94,73	50,25	80,67	75,37	69,91	53,08	0,00297	0,01413
Egln3	261,44	150,16	71,71	96,54	99,80	94,53	115,44	102,71	0,00297	0,01415
Plaa	2916,18	3426,46	2091,33	2576,19	1649,13	2304,41	1378,78	1807,17	0,00298	0,01416
Micalcl	4,59	2,36	6,58	6,61	38,26	16,61	15,45	40,39	0,00298	0,01419
Olfml2a	9,17	11,82	27,63	13,22	59,88	44,71	66,66	30,00	0,00298	0,01419
Cdkn1b	430,23	449,29	444,05	774,97	645,35	921,00	894,26	1241,71	0,00301	0,01432
Ints11	2888,66	2138,88	2254,48	1928,18	1818,79	1619,73	1484,47	1192,09	0,00302	0,01435
Tmem41a	551,31	455,21	539,44	485,35	410,83	435,59	280,47	312,74	0,00303	0,01438
Epas1	299,05	279,04	423,66	379,55	611,25	462,41	468,27	610,47	0,00303	0,01438
Dab2	561,40	861,94	359,19	552,80	652,00	623,37	1477,96	858,58	0,00303	0,01439
Foxo1	328,40	482,40	672,33	723,40	584,64	637,42	763,37	780,11	0,00303	0,01439
Kctd7	63,30	83,95	95,39	116,38	141,38	144,34	174,79	152,33	0,00304	0,01442
Zbtb38	102,74	139,52	205,91	203,66	255,31	236,32	208,93	240,03	0,00304	0,01443
Kif21b	1209,95	2007,64	3470,86	3308,85	3096,18	3415,74	1893,39	2814,62	0,00305	0,01444
Cnih2	252,26	135,97	732,85	450,97	709,39	389,60	628,42	410,83	0,00305	0,01444
Hoxd4	343,08	980,17	73,02	313,43	5,82	85,59	4,06	20,77	0,00306	0,01449
Kif6	30,27	46,11	98,68	89,93	39,92	43,43	32,52	43,85	0,00306	0,01449

Tsc22d1	4574,71	4490,58	6434,52	5391,75	5581,94	5370,14	10885,56	6810,93	0,00306	0,01450
Gypa	156,86	208,09	124,99	227,47	70,69	171,17	21,14	58,85	0,00307	0,01452
Rbm19	2695,11	2771,43	2746,56	1789,32	2029,19	1581,41	1458,45	1274,02	0,00309	0,01461
Nadk	3580,33	3224,28	2529,47	2283,92	2289,49	2070,65	2455,96	2141,83	0,00309	0,01462
Chrna5	41,28	35,47	5,92	6,61	8,32	16,61	19,51	15,00	0,00309	0,01462
Adh5	5252,61	3718,50	3634,01	2937,23	2663,73	2204,77	2699,85	1834,87	0,00310	0,01467
Slc16a9	11,01	27,19	0,00	1,32	1,66	2,55	6,50	4,62	0,00312	0,01474
Gsr	1120,97	1057,02	646,02	749,85	688,59	780,48	738,17	694,71	0,00313	0,01479
Micu1	667,81	489,49	934,16	769,68	1349,74	1034,68	1612,92	960,13	0,00313	0,01480
Sox17	163,28	107,59	61,18	41,00	64,04	52,37	78,04	66,93	0,00314	0,01483
Dhx33	2202,50	2947,61	2140,67	2164,90	1308,16	1852,21	947,91	1470,20	0,00315	0,01487
Tmem200a	3,67	5,91	5,92	11,90	48,23	7,66	43,09	49,62	0,00315	0,01487
Gfra3	47,70	49,66	21,71	7,93	62,37	52,37	69,10	53,08	0,00316	0,01492
Dusp2	128,43	120,60	69,73	88,61	84,83	84,31	54,47	39,24	0,00316	0,01492
Vwa5b1	11,01	16,55	2,63	2,64	0,00	0,00	0,81	0,00	0,00321	0,01512
Nell1	11,01	18,92	1,97	1,32	0,83	0,00	0,81	0,00	0,00321	0,01512
Rnf141	509,12	503,68	288,14	417,90	259,47	319,35	246,33	273,50	0,00321	0,01514
Ccl9	0,00	0,00	9,87	15,87	5,82	7,66	17,89	6,92	0,00322	0,01515
Gm266	207,32	135,97	55,26	58,19	66,53	45,99	86,99	27,70	0,00323	0,01520
Frmd4b	561,40	581,72	891,40	733,98	666,14	613,15	404,85	497,38	0,00323	0,01520
Dhps	802,66	809,91	693,38	564,70	533,91	586,32	450,38	483,53	0,00323	0,01521
Slc7a8	8,26	33,11	26,97	29,09	63,20	52,37	126,01	65,78	0,00324	0,01521
Tomm22	3075,80	2050,20	1953,84	1642,52	1667,43	1498,38	1432,44	1132,08	0,00324	0,01521
Scx	34,86	22,46	102,63	52,90	62,37	52,37	134,14	85,40	0,00325	0,01526
Paqr7	21,10	16,55	28,29	25,13	55,72	34,49	87,80	53,08	0,00325	0,01526
Fam69b	256,85	153,71	391,43	276,40	617,91	337,23	656,06	484,68	0,00325	0,01528
Mrpl15	2167,64	1500,41	1417,69	1100,30	1164,29	1046,18	1011,32	898,97	0,00327	0,01533
Akap6	19,26	27,19	47,37	56,87	89,82	66,42	49,59	45,01	0,00328	0,01538
Zwint	3980,28	4222,18	4574,09	4956,66	3773,13	4504,07	2229,95	3047,72	0,00328	0,01539
Pcdh7	364,18	457,57	413,14	354,42	271,94	281,03	247,95	199,64	0,00328	0,01539
Gdnf	46,78	22,46	3,29	6,61	10,81	2,55	57,72	17,31	0,00329	0,01540
Acacb	77,97	62,66	136,18	117,70	145,54	136,68	143,08	171,95	0,00329	0,01540
Sipa1l1	1841,07	2643,74	2927,47	2426,75	1470,33	1790,90	1465,77	1501,36	0,00329	0,01543
Wwc2	1213,62	1454,29	2079,49	2316,99	2018,38	2388,72	1582,84	1862,56	0,00330	0,01544
Slco5a1	6,42	20,10	7,24	7,93	17,46	14,05	39,84	51,93	0,00330	0,01547
Tsen15	1073,27	692,86	703,25	632,15	641,19	567,16	397,54	453,52	0,00331	0,01550
Tmem2	1735,58	2015,91	3521,52	3558,80	2623,81	3216,46	2029,15	2878,09	0,00332	0,01555
Nlk	849,44	1340,79	545,37	915,16	375,90	725,56	258,52	441,98	0,00333	0,01558
Tspan13	628,37	530,88	316,43	380,87	622,06	477,74	744,67	620,85	0,00333	0,01558
Cmtm6	835,68	896,22	588,78	629,50	553,87	655,30	512,98	534,30	0,00333	0,01558
Wbp1	1101,71	672,76	2056,47	1518,21	2483,26	1651,66	2681,15	1714,85	0,00335	0,01564
Chrm4	63,30	72,12	5,26	13,22	25,78	25,55	0,00	12,69	0,00335	0,01564
Ctnnal1	397,20	455,21	550,63	694,30	714,37	809,86	678,82	842,42	0,00335	0,01564
Prom2	4,59	0,00	18,42	15,87	21,62	8,94	0,81	0,00	0,00335	0,01564
Clec4a2	0,00	0,00	5,26	9,26	17,46	11,50	5,69	8,08	0,00335	0,01564
Fkbp14	227,50	158,44	199,99	255,24	341,80	291,24	404,04	370,44	0,00335	0,01564
Cpa3	0,00	1,18	0,00	10,58	17,46	8,94	39,84	35,77	0,00336	0,01567
Ywhab	11127,17	9879,74	8736,37	8633,15	7782,44	8010,50	7074,39	6793,62	0,00336	0,01568
Kif16b	304,55	384,26	576,94	641,40	663,65	685,96	534,12	828,57	0,00337	0,01569
Kcmf1	1983,26	1881,12	1324,93	1630,62	1118,55	1394,91	1065,79	1181,70	0,00338	0,01577

Dph6	836,60	981,35	559,18	535,60	619,57	668,07	625,17	669,32	0,00339	0,01578
Klhl21	643,05	707,05	441,42	474,77	327,66	424,09	475,58	500,84	0,00339	0,01581
Ifi207	0,92	0,00	5,26	13,22	13,31	20,44	13,01	15,00	0,00341	0,01588
Kctd10	3692,24	2927,51	2978,13	2479,65	2089,07	1992,73	2161,67	1644,46	0,00342	0,01588
Syne4	68,80	56,75	126,97	152,09	158,84	123,91	121,13	107,32	0,00341	0,01588
Igsf6	0,92	0,00	5,26	9,26	19,13	14,05	13,01	10,39	0,00342	0,01588
Calhm2	40,36	18,92	46,71	34,38	52,39	52,37	154,46	72,70	0,00342	0,01588
Uba2	8233,01	7194,62	5816,79	6224,92	5767,39	6108,47	4842,81	5010,68	0,00342	0,01589
Pgs1	940,26	880,85	907,19	875,48	739,32	770,27	605,66	578,16	0,00343	0,01595
Dlat	1834,65	1609,18	1547,28	1346,29	1274,07	1239,07	1038,15	1089,38	0,00343	0,01595
Stmn1	2784,09	2075,03	3955,71	3258,59	5689,22	3806,62	6312,65	4246,73	0,00344	0,01596
Stk25	1259,49	1274,58	1535,44	1695,42	1743,94	1686,15	1917,78	2078,36	0,00346	0,01604
Il6ra	6,42	0,00	17,76	34,38	28,28	39,60	39,02	25,39	0,00346	0,01604
Eda	144,02	135,97	65,13	56,87	94,81	70,26	123,57	109,63	0,00346	0,01607
Radil	56,87	50,84	23,03	17,19	18,30	19,16	17,89	15,00	0,00347	0,01609
Wdr19	273,36	264,85	333,53	345,17	389,21	356,39	439,81	522,76	0,00347	0,01609
Sorcs1	6,42	4,73	4,61	15,87	49,90	72,81	4,06	32,31	0,00350	0,01621
Pctp	342,16	406,73	524,31	350,46	275,27	284,86	136,58	231,95	0,00350	0,01623
Exph5	1,83	0,00	5,92	14,55	19,13	14,05	18,70	20,77	0,00352	0,01632
Vbp1	1816,31	1621,01	1111,78	1338,35	875,71	1299,10	851,98	931,28	0,00353	0,01632
Baiap2l2	89,90	81,58	28,29	22,48	64,04	39,60	60,16	50,78	0,00353	0,01633
Depdc1b	773,31	734,24	695,36	710,17	602,10	632,31	470,70	481,22	0,00354	0,01637
Usp14	3417,04	4207,99	2097,25	2876,40	1568,46	2587,99	1489,35	1991,81	0,00357	0,01651
Arhgap4	13,76	26,01	38,81	80,67	74,02	90,69	60,97	70,39	0,00357	0,01652
Adgrg1	81,64	73,31	192,75	165,31	146,37	144,34	122,76	76,16	0,00357	0,01652
Plpp6	55,04	53,21	90,78	68,77	100,63	98,36	115,44	166,18	0,00357	0,01652
Prkcq	47,70	24,83	24,34	29,09	74,02	48,54	97,56	79,63	0,00359	0,01656
Otx1	0,00	0,00	0,66	1,32	19,13	8,94	0,81	0,00	0,00359	0,01658
Zfp618	890,72	1444,84	1530,84	1948,01	2533,99	2286,53	2003,95	3153,89	0,00360	0,01661
Ctif	582,50	606,55	1145,33	780,26	1178,43	935,05	1271,47	1078,99	0,00362	0,01672
Enc1	502,70	746,06	774,30	1044,76	661,15	1318,26	1721,04	1526,75	0,00364	0,01678
Rtl6	784,31	694,04	1186,78	901,93	1361,39	981,03	1683,64	1337,49	0,00364	0,01679
Selenom	169,71	72,12	286,17	175,89	433,28	203,10	763,37	310,43	0,00364	0,01680
Dpf3	40,36	36,65	8,55	2,64	14,97	14,05	13,01	15,00	0,00365	0,01681
Dlg5	2379,55	3042,19	4881,31	3615,66	5028,07	3816,84	5266,37	5378,81	0,00365	0,01681
Pla2g6	724,69	652,66	544,71	415,26	391,70	407,49	439,81	370,44	0,00365	0,01683
Panx2	1,83	4,73	2,63	1,32	26,61	8,94	26,83	16,16	0,00366	0,01686
Eef2kmt	221,08	231,74	230,25	212,92	192,94	167,34	110,56	130,40	0,00367	0,01691
Ntng2	22,02	78,04	5,26	7,93	6,65	5,11	37,40	8,08	0,00367	0,01691
Tnfrsf12a	13,76	17,74	53,29	51,58	13,31	19,16	30,08	24,23	0,00368	0,01692
Bcl7b	624,70	502,50	332,22	272,43	372,57	266,97	345,51	348,51	0,00370	0,01701
Exosc9	1319,12	1460,21	815,09	1175,69	839,12	969,54	665,82	781,26	0,00370	0,01703
Tbl3	4881,10	3730,32	4115,57	2775,89	2725,27	2411,71	2463,27	1727,54	0,00373	0,01714
Gfra4	35,78	35,47	42,76	47,61	81,50	57,48	124,38	78,47	0,00373	0,01715
Porcn	55,04	73,31	103,94	129,60	138,88	131,57	134,14	162,71	0,00373	0,01715
Slc17a5	200,89	221,10	215,78	275,08	303,55	307,85	370,71	395,82	0,00375	0,01724
Prdm11	288,96	468,21	492,74	624,21	523,10	646,36	773,94	924,36	0,00377	0,01733
Cep112	116,50	105,23	179,60	177,21	187,12	191,61	206,49	222,72	0,00378	0,01735
Nabp2	1887,86	1305,32	1501,23	1120,14	1222,50	984,87	841,42	667,01	0,00379	0,01739
Vwde	0,92	1,18	20,39	6,61	24,12	16,61	17,07	15,00	0,00380	0,01741

Clip3	2174,98	1677,76	4066,88	2663,48	5054,68	3084,89	6185,83	3753,97	0,00381	0,01746
Dok2	11,01	16,55	34,87	44,96	61,54	51,10	46,34	32,31	0,00382	0,01750
Nacc2	67,88	66,21	75,00	64,80	84,00	81,75	144,71	131,56	0,00383	0,01753
Sfxn5	102,74	126,51	132,89	163,99	207,08	208,21	209,74	230,80	0,00384	0,01758
Al661453	15,59	7,09	57,23	27,77	56,55	34,49	14,63	6,92	0,00384	0,01758
Rpf1	1305,36	1187,08	929,55	989,22	474,86	829,03	675,57	672,78	0,00385	0,01762
Nod1	16,51	14,19	14,47	30,42	43,25	35,77	63,41	55,39	0,00385	0,01764
Rflnb	898,06	789,81	514,45	550,15	557,20	577,38	825,16	693,56	0,00386	0,01766
Ikzf4	105,49	150,16	102,63	161,34	167,99	205,66	260,96	290,81	0,00386	0,01767
Slc30a10	38,53	79,22	38,16	93,90	27,44	51,10	7,32	13,85	0,00388	0,01776
Prpf3	1875,93	1903,59	1736,75	1743,03	1432,08	1534,14	1158,47	1306,33	0,00389	0,01778
Tert	199,98	290,86	475,63	477,42	360,10	449,64	436,56	471,99	0,00390	0,01784
Kmt5a	3172,12	3383,89	2634,07	2814,24	2746,06	2955,88	1877,13	2201,84	0,00391	0,01785
Hook1	54,12	98,14	135,52	267,14	148,03	264,42	286,16	237,72	0,00391	0,01786
Tmem106b	497,19	578,17	453,26	645,37	711,88	774,10	869,87	1036,30	0,00391	0,01787
Cox15	1416,35	1360,89	1081,52	1007,73	972,18	949,10	842,23	956,67	0,00393	0,01791
Ruvbl2	6958,84	5217,72	5810,87	3739,98	4078,34	3265,01	3274,61	2257,23	0,00393	0,01793
Hist3h2a	5,50	11,82	17,10	18,51	29,94	35,77	36,58	43,85	0,00395	0,01800
Tmem100	86,23	66,21	86,18	38,35	16,63	24,27	35,77	30,00	0,00395	0,01801
Kifap3	1999,77	1785,35	1805,82	1688,81	2445,01	2154,95	2743,75	2626,51	0,00395	0,01801
Krtcap3	0,92	3,55	11,18	27,77	20,79	20,44	17,89	43,85	0,00397	0,01808
Foxh1	32,11	24,83	5,92	5,29	0,83	2,55	0,00	5,77	0,00398	0,01811
Rbm17	2936,36	3082,39	2388,03	2491,55	2278,68	2335,07	1567,39	2011,43	0,00398	0,01814
Vmac	130,26	80,40	228,28	161,34	273,61	166,06	358,52	255,03	0,00398	0,01814
Gga3	1247,56	1508,68	1149,94	1214,04	583,81	1032,13	534,93	747,79	0,00400	0,01820
Dennd1a	1038,41	1143,34	1529,52	1371,41	1817,12	1581,41	1696,65	1674,46	0,00400	0,01821
Gsap	7,34	4,73	9,21	11,90	19,96	24,27	25,20	47,31	0,00400	0,01821
Pias1	557,73	691,68	1284,80	1154,53	705,23	1020,63	963,36	949,75	0,00401	0,01822
Kansl1l	120,17	185,63	222,36	358,39	293,57	481,58	330,88	574,69	0,00401	0,01824
Dtx4	124,76	127,69	85,52	76,70	111,44	99,64	173,16	166,18	0,00401	0,01824
Cox18	373,35	392,54	264,46	269,79	231,19	208,21	243,08	175,41	0,00402	0,01826
Thy1	6,42	4,73	16,45	7,93	15,80	21,72	103,25	15,00	0,00405	0,01841
Relt	174,29	159,62	188,15	296,24	162,17	229,93	96,74	99,24	0,00406	0,01843
Rassf8	549,48	729,51	704,57	886,06	958,04	1157,31	1407,24	1061,68	0,00406	0,01843
Gen1	893,48	1503,95	844,69	968,06	439,94	772,82	391,03	582,77	0,00406	0,01843
Sipa1l3	1065,93	1269,85	2424,21	1883,21	2137,30	1647,83	1829,98	1808,32	0,00408	0,01851
Itm2a	833,85	487,13	330,25	406,00	409,16	315,51	923,52	583,93	0,00409	0,01853
Foxred1	740,28	743,70	546,02	610,99	501,48	496,90	487,78	429,29	0,00411	0,01865
Ago1	1884,19	2359,98	3028,12	3480,77	3744,02	3705,70	2923,41	3678,96	0,00412	0,01867
Abca2	224,75	391,36	254,59	300,20	450,75	407,49	532,49	616,24	0,00414	0,01877
Stk32c	11,01	16,55	18,42	10,58	40,75	29,38	45,53	51,93	0,00415	0,01881
Ppp2r2a	3552,81	4170,16	3190,62	2959,71	1917,75	2722,11	2343,77	2282,62	0,00416	0,01885
Hsp90ab1	157386,68	130681,91	126996,37	92936,00	101724,82	87103,85	85693,48	68822,48	0,00417	0,01886
Phldb1	1518,18	1485,04	2678,80	2274,67	2927,36	2135,79	2624,24	2385,33	0,00417	0,01889
Shoc2	1529,18	1555,98	1026,92	1253,71	823,32	1097,28	925,15	875,89	0,00420	0,01899
Strap	7684,45	6048,92	5064,86	4906,40	4729,51	4845,13	4468,04	3891,30	0,00420	0,01899
Cplx1	16,51	18,92	3,29	7,93	4,99	5,11	0,81	0,00	0,00420	0,01899
Iffo1	155,95	204,55	282,22	350,46	296,89	358,95	330,88	388,90	0,00421	0,01903
Slfn14	0,92	2,36	15,13	14,55	25,78	40,88	5,69	34,62	0,00422	0,01905
Fgd2	7,34	2,36	26,31	23,80	47,40	22,99	29,27	26,54	0,00424	0,01916

Polr3b	2420,83	2325,69	1824,90	1557,88	1641,65	1549,47	1585,28	1659,46	0,00426	0,01923
Pcdhb4	1,83	5,91	11,18	13,22	28,28	16,61	31,71	27,70	0,00426	0,01924
Pthlh	0,00	0,00	4,61	7,93	10,81	14,05	6,50	17,31	0,00428	0,01930
Hus1	1402,59	1655,29	1040,73	1221,97	504,80	986,14	721,91	795,11	0,00428	0,01932
Ramp3	17,43	14,19	13,82	10,58	33,27	14,05	96,74	33,47	0,00429	0,01934
Rtl5	68,80	125,33	189,46	346,49	208,74	362,78	237,38	466,22	0,00429	0,01934
Prtn3	17,43	10,64	53,94	34,38	74,02	33,21	86,99	55,39	0,00429	0,01934
Pcdhb15	1,83	0,00	6,58	6,61	12,47	7,66	27,64	15,00	0,00430	0,01936
Me1	160,53	124,15	46,05	75,38	63,20	66,42	82,11	83,09	0,00431	0,01939
Adss	3407,87	3130,87	2235,40	2287,89	2019,21	2349,12	2340,52	2017,20	0,00431	0,01940
Tes	1112,72	607,73	1701,22	1651,78	1991,77	1652,94	2142,15	1565,98	0,00435	0,01957
Wnt6	26,60	13,01	128,94	47,61	153,02	48,54	17,89	0,00	0,00435	0,01958
Kcnh1	21,10	24,83	1,97	0,00	4,99	8,94	12,19	5,77	0,00439	0,01973
Cast	392,62	399,64	353,93	408,65	523,93	484,13	586,15	626,62	0,00439	0,01975
C5ar1	0,92	1,18	15,79	19,84	14,14	14,05	5,69	10,39	0,00440	0,01978
Lbp	21,10	48,48	40,13	60,83	85,66	148,18	99,99	88,86	0,00441	0,01981
Adgrg6	0,00	1,18	5,26	7,93	7,48	7,66	20,32	15,00	0,00441	0,01982
Slc35a1	948,52	910,41	601,28	616,28	449,08	638,69	487,78	590,85	0,00442	0,01986
U2af1	3884,88	3677,12	3293,90	3077,41	2973,93	3143,65	2521,81	2439,56	0,00442	0,01986
Jph4	0,92	2,36	9,21	3,97	17,46	14,05	30,89	15,00	0,00443	0,01988
Mall	15,59	14,19	3,95	5,29	9,98	5,11	48,78	19,62	0,00446	0,01999
Gm14403	153,19	147,79	111,84	112,41	58,21	83,03	52,84	81,93	0,00446	0,01999
Sfrp5	20,18	10,64	0,00	0,00	0,00	0,00	0,81	0,00	0,00446	0,02000
Cntnap2	26,60	29,56	86,84	39,67	26,61	21,72	235,76	36,93	0,00447	0,02003
Rasa3	853,11	880,85	778,90	694,30	718,53	688,51	483,71	556,23	0,00447	0,02003
Cdkn1c	2988,65	1836,19	4978,02	2729,60	9658,61	3382,52	9525,47	6397,80	0,00447	0,02004
Fam167b	3,67	1,18	7,89	1,32	15,80	14,05	43,90	17,31	0,00448	0,02005
Parva	2396,06	2012,36	2391,32	1966,53	3334,86	2306,96	5064,75	3331,61	0,00448	0,02006
Dnrtip2	2607,04	3035,10	2005,81	2155,64	1530,21	2126,85	1273,10	1689,46	0,00449	0,02007
Stat2	101,82	171,44	285,51	353,10	187,95	385,77	390,22	391,21	0,00449	0,02007
Hoxc13	0,92	0,00	7,24	1,32	21,62	19,16	2,44	0,00	0,00449	0,02009
Lrrfip1	711,85	1003,82	685,49	723,40	478,19	643,80	309,74	473,14	0,00449	0,02009
Mrpl47	822,84	689,31	587,47	567,34	523,10	514,79	465,01	456,99	0,00449	0,02009
Ispd	92,65	119,42	67,76	55,54	49,90	66,42	41,46	33,47	0,00449	0,02009
Slc14a1	28,44	11,82	25,00	29,09	49,90	25,55	4,06	5,77	0,00451	0,02015
Adamts18	22,02	40,20	53,94	21,16	76,51	44,71	11,38	6,92	0,00454	0,02026
Tor3a	88,98	72,12	200,65	161,34	148,86	125,18	122,76	103,86	0,00458	0,02044
Lad1	82,56	88,68	75,65	29,09	64,87	33,21	20,32	8,08	0,00462	0,02063
P4htm	29,35	15,37	15,13	30,42	59,05	42,15	66,66	78,47	0,00463	0,02064
Qsox1	460,50	340,52	772,98	642,73	790,05	593,99	868,24	720,10	0,00463	0,02067
Mt2	113,75	49,66	128,28	124,31	30,77	54,93	47,96	27,70	0,00464	0,02069
Spry4	727,44	1619,82	2855,11	3544,25	1037,88	2073,20	1654,38	1177,08	0,00465	0,02071
Abcg1	123,84	126,51	147,36	132,25	144,70	118,80	307,30	198,49	0,00465	0,02074
Car5b	8,26	8,28	10,53	13,22	19,13	19,16	43,90	32,31	0,00466	0,02076
Ak1	144,02	128,88	167,75	132,25	330,99	172,45	311,36	290,81	0,00466	0,02076
Gadd45g	14,68	20,10	69,08	113,73	39,92	47,26	25,20	76,16	0,00466	0,02077
Wdr6	7666,10	5786,43	12399,32	9454,41	15917,50	10617,65	17156,74	11812,38	0,00471	0,02099
Sh3tc2	126,59	153,71	147,36	130,93	72,35	140,51	45,53	58,85	0,00473	0,02103
Ung	1576,88	1326,60	1342,03	1101,63	1061,17	1145,82	775,57	889,74	0,00476	0,02116
Sh3kbp1	431,14	488,31	270,38	285,66	360,10	325,73	469,89	417,75	0,00478	0,02127

Dnaja3	1317,28	1422,37	1132,83	1129,40	799,20	997,64	902,39	847,04	0,00479	0,02132
Susd2	7,34	16,55	15,79	11,90	34,93	21,72	78,86	34,62	0,00482	0,02143
Spata18	2,75	0,00	2,63	1,32	9,15	1,28	20,32	31,16	0,00483	0,02148
Aldh2	2077,75	1929,60	4430,02	2737,53	4677,95	2869,01	6768,72	3854,37	0,00484	0,02148
Igdcc4	623,78	751,98	406,56	432,45	289,41	378,11	320,31	503,15	0,00484	0,02150
Siah1b	606,35	632,56	440,11	568,67	365,92	454,75	286,16	363,51	0,00485	0,02151
Ctxn1	902,65	600,64	1640,70	1270,90	1901,12	1313,16	1890,14	1316,72	0,00486	0,02159
Srgn	3,67	3,55	15,13	26,45	30,77	20,44	22,76	24,23	0,00489	0,02167
Slc2a10	74,30	72,12	107,23	96,54	118,09	112,41	246,33	132,71	0,00489	0,02167
Aard	83,48	66,21	48,02	44,96	35,76	44,71	18,70	27,70	0,00489	0,02167
Adam7	6,42	5,91	36,18	13,22	3,33	0,00	3,25	1,15	0,00491	0,02178
Stx5a	878,80	772,08	1156,52	1261,65	1364,71	1213,52	1254,40	1237,09	0,00493	0,02183
Ifit2	154,11	157,25	138,15	142,83	237,02	163,51	332,50	244,65	0,00493	0,02183
Helb	262,36	297,95	367,74	365,00	414,99	350,00	553,63	466,22	0,00493	0,02183
Zfp629	1774,11	2018,28	3088,65	2729,60	2361,01	2369,56	2884,39	2691,14	0,00493	0,02183
Cox17	536,64	403,18	381,56	317,40	309,37	251,65	262,59	182,33	0,00494	0,02188
Trmo	219,24	151,34	144,73	141,51	77,34	90,69	113,81	106,17	0,00495	0,02189
Prx	143,10	196,27	267,09	284,33	393,36	314,24	278,85	394,67	0,00496	0,02196
Pitpnb	3349,16	3517,50	2486,05	2760,02	2461,64	2663,36	2069,80	2326,47	0,00498	0,02203
Sorbs3	833,85	506,05	1591,36	1069,89	1878,66	1216,07	2375,47	1319,03	0,00499	0,02205
Gtf2e2	1875,93	1645,84	1377,56	1520,85	1084,45	1277,39	1043,84	1165,54	0,00499	0,02205
Iqgap1	1990,60	1655,29	2326,85	1839,57	3803,07	2446,20	3990,02	2981,95	0,00501	0,02213
Wnt7a	5,50	5,91	50,00	3,97	31,60	15,33	1,63	0,00	0,00501	0,02213
Nek7	1676,87	1762,89	1459,79	2064,39	2582,23	2801,31	2436,45	3245,06	0,00503	0,02220
Gclc	898,98	1164,62	556,55	763,07	477,36	656,58	475,58	592,00	0,00506	0,02235
Kdelc1	1483,32	1611,55	1265,06	1378,02	914,80	1090,89	986,12	1083,61	0,00506	0,02235
Ptger1	0,00	4,73	1,97	5,29	8,32	1,28	56,09	18,46	0,00508	0,02240
Hbb-y	23362,48	17205,60	35638,19	34321,02	34228,45	35023,44	35990,63	27451,44	0,00508	0,02241
Sept5	88,06	52,02	217,09	156,05	242,84	146,90	286,16	151,17	0,00508	0,02241
Bms1	4375,65	5146,78	4416,21	3648,72	3350,66	3171,76	3148,60	2755,76	0,00509	0,02242
Ngly1	194,47	225,83	187,49	181,18	267,79	245,26	330,06	318,51	0,00510	0,02246
9330182L06	22,02	59,12	36,84	37,03	67,36	88,14	116,25	105,01	0,00511	0,02252
Rhot2	1907,12	1853,93	1561,76	1750,96	1533,54	1439,62	1096,69	1262,48	0,00511	0,02252
Lmcd1	12,84	8,28	2,63	3,97	13,31	6,39	36,58	23,08	0,00512	0,02252
Six2	22,02	10,64	21,71	7,93	12,47	39,60	130,89	42,70	0,00512	0,02254
Lasp1	3500,52	3158,06	8092,98	5687,99	6320,43	5150,43	8226,36	5023,38	0,00513	0,02255
Tmem184a	54,12	16,55	21,71	33,06	15,80	22,99	4,88	2,31	0,00513	0,02258
Rnf138	731,11	884,40	399,32	624,21	306,04	482,85	383,72	424,67	0,00514	0,02260
Ppp1r14a	179,80	62,66	23,68	15,87	61,54	16,61	50,40	24,23	0,00515	0,02261
Utp3	2324,51	2154,25	2043,97	1672,94	1728,97	1670,82	1425,93	1306,33	0,00514	0,02261
Phlda2	49,54	35,47	20,39	30,42	115,60	61,31	101,62	56,55	0,00516	0,02265
Slbp	2704,28	2595,26	1982,79	2096,13	1879,50	2065,54	1729,98	1789,86	0,00516	0,02266
Xpo5	5411,31	5473,11	5055,65	4128,78	3922,82	4030,16	3614,43	3243,90	0,00520	0,02282
Prps1l3	1273,25	1321,87	1011,13	1031,53	680,28	849,46	1015,39	882,81	0,00521	0,02285
Cox6b2	39,45	26,01	125,65	76,70	107,28	52,37	186,98	90,01	0,00521	0,02287
Dlx2	20,18	10,64	68,42	27,77	118,92	77,92	152,02	35,77	0,00521	0,02287
Ttyh3	5153,54	5272,11	9122,53	7155,94	10673,21	7405,02	12026,96	8741,58	0,00522	0,02288
Coq5	1256,74	963,62	1020,34	772,33	806,69	737,05	627,61	552,77	0,00522	0,02290
Ppa2	965,03	707,05	521,68	548,83	510,62	528,84	533,30	471,99	0,00523	0,02291
Smim12	897,15	575,81	666,41	400,71	447,42	402,38	355,26	251,57	0,00525	0,02298

Adarb2	2,75	0,00	0,00	2,64	9,98	3,83	22,76	25,39	0,00525	0,02298
Pclaf	5316,83	4382,98	3735,32	3819,32	2840,87	3617,56	3063,24	2731,53	0,00525	0,02300
Akap2	1678,71	1858,66	3137,99	2801,01	3115,31	2488,35	2534,00	3155,05	0,00526	0,02302
Gpr137c	11,01	7,09	22,37	25,13	24,12	45,99	34,14	70,39	0,00526	0,02304
Med17	1374,16	1386,90	1132,83	1043,44	928,94	1044,90	874,75	908,20	0,00527	0,02306
Alpl	194,47	192,72	101,97	46,29	67,36	74,09	112,19	57,70	0,00531	0,02320
Shisa8	28,44	14,19	1,32	1,32	4,16	0,00	3,25	2,31	0,00531	0,02320
Arnt	1276,92	1436,56	1567,02	1639,88	1968,48	1729,58	2126,71	2108,36	0,00532	0,02323
Prmt7	2793,26	2253,56	2115,67	1662,36	1655,79	1456,22	1600,72	1269,40	0,00534	0,02331
Blcap	969,61	976,62	793,38	736,62	678,61	687,24	594,28	660,09	0,00534	0,02331
Stx18	887,97	629,01	799,30	702,24	1013,76	766,43	1777,13	1143,62	0,00534	0,02333
Fam221a	35,78	29,56	55,92	67,45	75,68	76,64	83,74	84,24	0,00535	0,02334
Sssca1	1528,27	978,99	1052,57	579,25	697,74	523,73	612,16	408,52	0,00536	0,02339
Lepr	11,93	17,74	3,29	13,22	29,94	22,99	48,78	43,85	0,00540	0,02356
Csf3r	2,75	2,36	4,61	11,90	18,30	15,33	34,14	18,46	0,00540	0,02357
Zfp791	29,35	31,92	75,65	68,77	24,95	77,92	130,89	107,32	0,00542	0,02363
Mrpl12	5292,98	2654,38	3020,89	2151,68	2548,96	1779,40	1807,21	1289,02	0,00544	0,02370
Sbspon	5,50	4,73	0,66	0,00	7,48	0,00	55,28	6,92	0,00545	0,02377
Chad	1,83	1,18	2,63	2,64	4,16	0,00	39,84	9,23	0,00546	0,02377
Flrt2	737,53	956,52	451,29	519,73	468,21	697,45	1085,30	806,65	0,00547	0,02382
Comtd1	244,01	152,52	92,76	67,45	77,34	80,48	118,69	57,70	0,00549	0,02389
Ccdc85c	1844,74	1933,15	1682,15	1617,39	1718,16	1560,97	1216,19	1244,02	0,00553	0,02405
Rrn3	2896,00	3619,18	2413,68	2713,73	1877,00	2478,13	1721,04	1946,80	0,00554	0,02411
Zfp398	210,07	344,06	367,09	390,13	238,68	410,04	632,48	612,78	0,00554	0,02411
Mlxipl	4,59	11,82	17,10	31,74	25,78	49,82	43,90	51,93	0,00555	0,02413
Aldh3a1	0,00	0,00	0,66	0,00	17,46	5,11	4,06	15,00	0,00562	0,02441
Mpped1	98,15	75,67	129,60	80,67	154,68	127,74	208,93	192,72	0,00564	0,02449
Spsb1	211,90	221,10	421,69	308,14	251,99	279,75	365,83	410,83	0,00565	0,02456
Selenbp2	0,92	1,18	3,29	3,97	10,81	8,94	26,83	10,39	0,00566	0,02457
Nob1	2192,41	1695,49	1591,36	1329,09	1236,64	1166,26	1255,21	986,67	0,00566	0,02458
Rtca	1628,26	1273,39	1190,72	1122,79	839,95	964,43	958,48	757,03	0,00568	0,02467
Llph	458,66	334,61	311,83	210,27	220,38	218,43	199,18	197,33	0,00571	0,02478
Timp4	0,00	0,00	0,00	1,32	15,80	11,50	2,44	3,46	0,00573	0,02486
Tdh	4,59	30,74	0,66	0,00	0,00	0,00	1,63	0,00	0,00577	0,02501
Gatad2b	1566,79	2183,81	2754,46	2816,88	2524,85	2760,44	3242,90	3313,14	0,00577	0,02502
Prom1	1479,65	1618,64	2528,15	3019,22	2239,59	3060,62	1945,42	2437,26	0,00579	0,02509
Cops7a	2729,05	2131,78	1851,21	1666,33	1765,56	1571,19	1533,25	1297,10	0,00580	0,02515
Tom1l2	436,65	498,95	564,44	494,61	775,08	583,77	810,52	802,03	0,00581	0,02516
Efs	1004,47	1016,82	1685,43	1539,37	1988,44	1474,11	1563,33	1387,11	0,00581	0,02516
Gulp1	361,43	345,25	444,71	630,82	548,05	703,84	620,29	800,88	0,00581	0,02516
Ankrd27	1597,98	1782,99	1295,32	1294,71	1220,01	1143,26	906,45	1144,77	0,00583	0,02525
Urgcp	356,84	314,51	467,74	329,30	679,45	467,52	855,24	568,92	0,00587	0,02541
Rpp40	432,98	403,18	334,85	259,21	225,37	269,53	244,70	233,11	0,00589	0,02549
Prkrip1	690,75	560,44	558,52	506,51	420,81	427,93	390,22	363,51	0,00590	0,02552
Rexo2	954,02	742,52	713,78	675,79	563,02	599,10	495,09	515,84	0,00590	0,02552
Sptssb	18,35	9,46	1,32	1,32	1,66	0,00	0,00	0,00	0,00593	0,02564
Smyd2	1544,78	1207,18	946,00	858,29	947,23	780,48	892,63	767,41	0,00595	0,02572
Gpr173	146,77	139,52	146,04	187,79	225,37	229,93	239,82	301,19	0,00596	0,02574
Apln	370,60	412,64	555,89	518,41	388,37	462,41	802,39	585,08	0,00598	0,02582
B3gnt8	6,42	3,55	15,79	6,61	54,06	22,99	21,14	19,62	0,00598	0,02582

Siah2	210,99	225,83	140,78	109,77	178,80	93,25	430,87	219,26	0,00598	0,02583
Corin	11,93	11,82	8,55	11,90	10,81	12,77	34,96	41,54	0,00600	0,02587
Cbln2	10,09	8,28	0,00	5,29	41,58	29,38	5,69	12,69	0,00600	0,02587
Hdac11	263,27	273,12	294,72	368,97	472,37	429,20	412,17	555,08	0,00601	0,02592
Atf7ip	2319,00	2711,13	4067,54	2978,23	3401,39	3022,30	5498,87	4058,63	0,00602	0,02594
Iqch	5,50	1,18	35,52	34,38	8,32	19,16	2,44	10,39	0,00604	0,02601
Wasf3	931,09	1282,85	541,42	728,69	576,32	679,57	424,37	663,55	0,00604	0,02603
Gpc2	621,03	874,94	1299,93	2085,55	1308,99	1852,21	1272,29	1923,72	0,00604	0,02603
Lamc2	8,26	7,09	56,58	15,87	138,88	47,26	148,77	17,31	0,00605	0,02604
Kif27	30,27	55,57	134,20	85,96	114,77	127,74	85,36	101,55	0,00607	0,02611
Ywhaq	4012,39	3350,79	2841,95	2598,67	2488,25	2589,27	2508,80	2283,77	0,00607	0,02613
Minpp1	2103,43	1902,41	1829,51	1654,42	1488,63	1614,62	1290,98	1290,18	0,00608	0,02617
Tmem74b	41,28	28,38	10,53	6,61	8,32	3,83	21,95	15,00	0,00610	0,02625
Dph1	603,60	481,22	524,31	423,19	394,20	397,27	322,75	238,88	0,00612	0,02629
Rhox5	11,01	39,02	5,26	1,32	5,82	5,11	0,81	2,31	0,00612	0,02629
Uck2	8739,37	8212,62	7684,45	7372,83	7259,35	7214,69	5411,89	5943,12	0,00612	0,02630
Tbc1d30	1,83	4,73	3,29	7,93	5,82	11,50	27,64	27,70	0,00612	0,02631
Emilin2	2030,96	1833,83	1255,85	707,53	1256,60	839,24	2134,02	1541,75	0,00613	0,02631
Zfp707	89,90	95,77	155,25	146,80	79,84	122,63	232,51	165,02	0,00613	0,02633
Haghl	102,74	171,44	177,62	351,78	259,47	297,63	347,13	422,37	0,00615	0,02637
Wnt9a	4,59	3,55	3,29	3,97	12,47	10,22	25,20	20,77	0,00615	0,02639
Mylk3	7,34	3,55	10,53	13,22	34,93	30,66	17,07	26,54	0,00616	0,02640
Snx1	2667,59	1980,44	1803,85	1498,37	1673,25	1402,57	1339,76	1278,64	0,00616	0,02641
Rtp4	1,83	1,18	1,32	2,64	2,49	3,83	22,76	12,69	0,00616	0,02641
Gcsh	3109,74	2201,54	1993,31	1668,97	1763,07	1714,26	1599,91	1344,41	0,00617	0,02642
Svep1	287,12	329,88	478,92	706,20	1036,22	757,49	263,40	669,32	0,00619	0,02650
Mb21d1	19,26	24,83	17,10	11,90	19,96	31,93	56,09	54,24	0,00619	0,02650
Atp6v0e2	62,38	42,56	81,57	47,61	103,12	75,37	146,33	135,02	0,00619	0,02650
Eprs	10777,67	10306,57	8909,38	7482,60	7557,07	6798,26	7218,29	5905,04	0,00620	0,02655
Piga	803,58	887,95	635,49	814,65	333,49	593,99	369,08	474,30	0,00624	0,02669
Pbxip1	371,52	300,32	559,18	396,74	954,72	468,80	811,34	751,26	0,00625	0,02674
Trim47	42,20	27,19	31,58	35,71	74,02	49,82	149,58	63,47	0,00627	0,02679
Glpr1	0,00	0,00	1,32	6,61	15,80	11,50	7,32	12,69	0,00627	0,02679
Glyctk	50,45	42,56	39,47	35,71	75,68	68,98	106,50	78,47	0,00628	0,02685
Exo1	2177,73	2396,63	2227,51	2163,58	1790,51	2106,41	1286,11	1557,91	0,00628	0,02685
Foxc1	92,65	76,85	46,71	51,58	68,19	67,70	170,72	94,63	0,00629	0,02688
Rmnd5b	364,18	333,42	671,67	589,83	571,33	487,96	669,88	501,99	0,00630	0,02691
Blzf1	528,38	490,68	508,52	462,87	279,43	375,55	299,17	334,66	0,00635	0,02711
Akap13	765,97	1346,70	1501,89	1760,22	1662,44	1996,56	2097,44	2418,79	0,00636	0,02716
Pprc1	4568,29	6150,60	5091,17	4307,32	1885,32	3572,86	3131,53	2590,74	0,00639	0,02724
Psmg1	1493,41	1022,74	949,29	692,98	793,38	678,29	711,34	563,15	0,00641	0,02735
Pou3f1	3,67	2,36	9,21	5,29	23,29	5,11	50,40	20,77	0,00641	0,02735
Ihh	0,92	4,73	3,95	3,97	1,66	3,83	36,58	12,69	0,00645	0,02748
Hmgn3	238,50	203,36	325,64	378,23	370,91	383,22	555,25	360,05	0,00645	0,02748
Rbms3	296,30	489,49	703,25	886,06	489,00	775,37	786,13	1097,46	0,00647	0,02758
Tspan6	2721,71	2260,66	1846,61	1998,27	1447,05	1723,20	1683,64	1608,68	0,00647	0,02758
Pin1	2940,03	1864,57	2020,94	1478,53	1611,71	1236,51	1278,79	938,21	0,00648	0,02758
Atn1	2180,49	2430,92	4128,06	3413,32	4731,17	3222,85	5020,85	3826,68	0,00648	0,02760
Ece2	23,85	24,83	32,89	64,80	46,57	72,81	82,92	92,32	0,00649	0,02762
Rexo4	1182,43	1401,09	1168,36	1157,17	859,08	1073,01	717,85	817,03	0,00651	0,02768

Rnf144a	2214,43	2310,32	2538,68	2748,11	2785,98	3047,85	3678,65	3280,83	0,00651	0,02769
Trim56	235,75	417,37	683,52	716,78	688,59	767,71	546,31	988,98	0,00654	0,02782
Gpx3	911,82	708,23	496,03	341,20	649,51	443,25	453,63	381,98	0,00655	0,02783
Irf1	57,79	43,75	63,81	67,45	59,88	112,41	136,58	136,17	0,00655	0,02783
Rasef	8,26	8,28	44,08	51,58	21,62	33,21	8,94	26,54	0,00658	0,02795
Slc52a2	651,30	552,16	496,03	488,00	488,17	385,77	352,83	319,66	0,00660	0,02801
Ebi3	0,00	2,36	6,58	3,97	13,31	7,66	24,39	17,31	0,00661	0,02808
Vim	8119,26	5421,09	9654,74	7247,19	14913,72	8333,68	31206,35	10218,70	0,00662	0,02812
Gtf2f2	1171,43	1027,46	982,18	849,03	760,11	723,00	697,52	728,18	0,00664	0,02817
Pdlr3	5,50	5,91	42,76	38,35	24,12	34,49	107,31	13,85	0,00667	0,02827
Slc37a4	235,75	167,89	88,15	92,57	128,90	114,96	90,24	131,56	0,00668	0,02833
Glicc1	404,54	738,97	829,56	1248,42	948,90	1554,58	1271,47	1717,16	0,00669	0,02835
Polr1d	2050,23	1239,11	1121,65	859,61	938,08	766,43	950,35	640,47	0,00669	0,02835
Vps13a	277,95	372,44	423,00	437,74	493,16	532,67	535,74	641,63	0,00670	0,02838
Pgghg	443,07	419,74	326,30	305,49	555,53	412,60	649,56	530,84	0,00678	0,02873
Lpcat2	7,34	13,01	26,31	75,38	39,92	81,75	36,58	49,62	0,00680	0,02879
Acaa1b	0,00	1,18	10,53	10,58	15,80	14,05	20,32	6,92	0,00682	0,02885
Wdr5	3723,43	3674,75	3119,57	3544,25	2709,47	3090,00	2259,22	2498,42	0,00684	0,02896
Wnt2	253,18	132,42	0,00	0,00	0,00	1,28	8,94	0,00	0,00686	0,02902
Nol11	3013,42	2705,22	2289,35	1961,24	1931,06	2025,94	1962,49	1727,54	0,00687	0,02905
Kcnk5	307,30	286,13	244,07	222,18	184,62	218,43	165,03	161,56	0,00690	0,02918
Scube1	3513,36	4083,85	4466,86	3597,15	3230,90	2838,36	807,27	2226,07	0,00692	0,02924
Brix1	2307,99	2610,63	1718,33	1884,53	1210,03	1856,05	1195,05	1445,97	0,00696	0,02940
Tmie	0,00	1,18	3,29	3,97	8,32	6,39	29,27	8,08	0,00696	0,02940
Smyd1	19,26	23,65	1,97	2,64	4,99	2,55	8,13	5,77	0,00699	0,02951
1700030J2	33,94	28,38	64,47	62,16	74,85	81,75	67,48	85,40	0,00701	0,02959
Nxn12	0,00	0,00	0,66	2,64	13,31	6,39	17,89	5,77	0,00701	0,02961
Gtf3c5	2571,27	2253,56	2124,23	1661,04	1729,80	1615,90	1528,37	1366,34	0,00702	0,02962
Cdh13	17,43	16,55	24,34	13,22	30,77	19,16	68,29	49,62	0,00704	0,02968
Cdyl	793,49	928,15	749,96	794,81	502,31	682,13	512,17	499,68	0,00704	0,02968
Manba	34,86	35,47	40,13	39,67	50,73	48,54	87,80	80,78	0,00705	0,02971
Sema6b	183,47	132,42	88,15	55,54	71,52	57,48	94,30	63,47	0,00707	0,02978
Wdr18	4342,63	3178,16	3078,12	2256,15	2618,82	2050,21	2147,84	1516,36	0,00707	0,02980
Rps6ka3	3155,60	5330,05	2136,73	2880,36	1660,78	2596,93	1397,48	2253,77	0,00712	0,03001
Slc25a22	790,74	1087,76	657,20	789,52	433,28	643,80	458,51	522,76	0,00713	0,03001
Arih2	1695,22	1700,22	1107,83	1404,47	1192,57	1214,80	933,28	1103,23	0,00715	0,03011
Kpna3	3440,89	3856,83	2332,77	2562,97	1880,33	2708,06	1927,53	2297,62	0,00716	0,03014
Atp1a1	10740,98	8874,74	9278,44	7296,13	6959,13	6389,50	6373,62	5469,98	0,00717	0,03019
Abce1	7374,39	9591,25	4481,99	6203,76	3936,96	6148,07	3577,84	4637,94	0,00721	0,03032
Ppp2r2d	1475,06	1194,18	1107,18	1092,37	967,19	1000,20	817,84	840,11	0,00723	0,03039
Clec16a	702,67	812,28	1173,62	999,80	1328,95	1094,72	1208,06	1255,56	0,00728	0,03059
Pm20d1	34,86	42,56	113,81	97,86	140,55	74,09	68,29	91,17	0,00728	0,03060
Ccm2	1103,54	955,34	1022,97	1016,99	844,11	740,89	711,34	623,16	0,00729	0,03061
Chst10	316,48	205,73	351,95	424,52	500,64	545,44	651,18	430,44	0,00730	0,03065
Ppa1	5412,23	4275,39	4109,64	3278,43	3315,73	3239,46	3031,53	2166,07	0,00730	0,03067
Alyref	3459,24	3323,59	3444,55	3315,46	3118,63	3235,63	2039,72	2485,72	0,00730	0,03067
St6galnac6	344,00	281,40	300,64	330,62	468,21	425,37	556,88	455,83	0,00731	0,03069
Utp6	4004,13	4119,32	3530,73	3278,43	2953,97	3185,81	2694,97	2815,77	0,00734	0,03078
Echdc1	364,18	392,54	230,91	244,66	223,71	278,47	178,85	233,11	0,00734	0,03079
Al464131	182,55	101,68	69,73	55,54	49,90	45,99	108,94	60,01	0,00735	0,03083

Psmb9	0,00	0,00	3,95	2,64	9,98	5,11	10,57	13,85	0,00736	0,03087
Cdk18	166,95	176,17	124,99	145,47	80,67	116,24	85,36	78,47	0,00738	0,03093
Cc2d1a	453,16	507,23	634,18	633,47	751,80	668,07	770,69	753,56	0,00739	0,03096
Ing1	1775,94	1923,69	1467,03	1497,05	1414,61	1420,46	1201,56	1261,33	0,00741	0,03104
Car15	16,51	14,19	33,55	44,96	39,92	53,65	48,78	55,39	0,00743	0,03111
Ggt7	37,61	24,83	44,73	58,19	60,71	74,09	89,43	86,55	0,00743	0,03112
Gmfb	4568,29	5914,13	2576,83	3925,12	2072,44	3452,78	2091,75	2820,39	0,00746	0,03121
Mib2	439,40	373,62	554,58	514,44	670,30	541,61	678,82	730,48	0,00746	0,03123
Lsr	406,38	247,11	682,86	650,66	851,59	544,17	1108,07	600,08	0,00749	0,03130
Lcp1	505,45	361,80	584,84	510,48	912,30	553,11	1047,09	800,88	0,00749	0,03130
Rasl11a	340,33	305,05	301,30	219,53	112,27	167,34	209,74	110,78	0,00749	0,03130
Tbc1d2	10,09	14,19	32,89	27,77	43,25	38,32	39,02	47,31	0,00749	0,03130
Lfng	49,54	34,29	110,52	103,15	94,81	79,20	130,89	81,93	0,00750	0,03133
Prep	5158,13	4793,26	4208,32	2968,97	3072,89	2635,25	3470,53	3098,50	0,00751	0,03135
Hpcal1	493,52	463,48	721,01	595,12	375,90	422,82	439,81	336,97	0,00751	0,03135
Fam129a	3,67	5,91	17,76	19,84	37,42	21,72	26,83	20,77	0,00751	0,03135
Uchl5	920,08	1146,88	684,83	764,39	549,71	747,27	508,10	623,16	0,00752	0,03140
Rpp30	630,20	527,33	395,37	433,77	330,16	435,59	307,30	334,66	0,00757	0,03160
Wnk4	70,63	92,22	124,99	125,64	109,78	81,75	153,65	203,10	0,00759	0,03164
Trappc5	1135,65	986,08	1000,60	928,38	804,19	776,65	686,95	699,33	0,00760	0,03167
Trove2	1186,10	1267,48	988,76	1192,88	1215,02	1446,00	1721,04	1808,32	0,00762	0,03176
Ier2	2471,28	1691,95	3407,71	2172,84	2598,86	1604,40	1269,85	1094,00	0,00762	0,03176
Irf6	2,75	14,19	39,47	19,84	77,34	43,43	34,96	24,23	0,00763	0,03177
Pinx1	633,87	681,04	668,38	503,87	375,07	426,65	443,88	339,28	0,00765	0,03185
N4bp3	569,66	400,82	905,21	610,99	469,87	425,37	408,92	365,82	0,00766	0,03189
Lbr	3317,05	3281,03	2964,97	3150,15	2495,74	2824,31	2281,98	2138,37	0,00767	0,03194
Slc37a2	16,51	16,55	67,10	66,12	14,97	39,60	43,90	34,62	0,00770	0,03202
Lhpp	741,20	565,16	786,80	637,44	508,96	365,33	435,75	353,13	0,00770	0,03204
Lgr6	22,93	34,29	20,39	6,61	7,48	5,11	3,25	3,46	0,00772	0,03209
Tnfaip8l3	0,00	0,00	4,61	5,29	9,15	2,55	18,70	10,39	0,00772	0,03211
Rab28	796,24	755,52	523,00	498,58	533,08	558,22	573,14	588,54	0,00775	0,03221
Snx4	1840,16	1566,62	1209,14	1239,16	1164,29	1214,80	1186,11	1115,92	0,00775	0,03221
Zkscan2	94,48	140,70	70,39	117,70	119,76	177,56	202,43	278,11	0,00775	0,03221
Dcaf15	2151,13	1937,88	2443,95	2074,97	1936,05	1973,57	1489,35	1390,57	0,00776	0,03222
Hbs1l	2288,73	2014,73	1551,89	1702,03	1496,11	1674,66	1317,00	1426,35	0,00778	0,03231
5730559C1	542,14	524,96	971,66	838,45	1128,53	789,43	1300,74	855,12	0,00780	0,03237
Eef1d	11596,85	7898,12	7726,55	5563,68	6269,70	4980,54	5569,60	3519,71	0,00782	0,03243
Tlcd2	94,48	56,75	151,97	95,22	217,06	111,13	273,97	193,87	0,00785	0,03258
Clec4a1	0,92	0,00	3,29	18,51	16,63	14,05	14,63	19,62	0,00786	0,03258
Zfp521	1697,97	1993,45	2647,88	2340,79	2949,81	2602,04	2763,26	3385,85	0,00786	0,03259
Maff	163,28	184,45	165,78	178,53	64,87	106,02	110,56	63,47	0,00787	0,03260
Dap	228,41	294,41	437,48	337,23	466,55	310,41	659,31	493,91	0,00787	0,03262
Trmt10c	810,92	846,56	505,24	588,50	229,53	518,62	386,97	418,90	0,00790	0,03273
Slc4a5	17,43	11,82	38,81	43,64	49,90	48,54	38,21	65,78	0,00790	0,03274
Ccdc117	1420,02	1552,43	1129,54	1297,35	692,75	1021,91	908,89	965,90	0,00794	0,03286
Atg9b	49,54	49,66	63,15	72,74	38,26	56,21	16,26	25,39	0,00795	0,03290
Ahrr	11,01	22,46	17,10	34,38	40,75	49,82	51,22	83,09	0,00795	0,03290
Tmem164	4024,31	4341,60	3041,94	3376,29	2620,48	2906,06	3163,23	3217,36	0,00797	0,03295
Nox4	46,78	56,75	65,13	84,64	83,16	154,56	113,00	173,10	0,00798	0,03300
Plcl1	44,03	55,57	19,08	14,55	21,62	10,22	47,15	36,93	0,00799	0,03303

Nars2	402,71	415,01	234,86	296,24	227,87	245,26	199,99	270,04	0,00800	0,03306
Sptlc3	1,83	1,18	5,26	3,97	16,63	6,39	24,39	16,16	0,00801	0,03308
Timm21	774,22	563,98	398,00	478,74	363,42	425,37	312,99	410,83	0,00802	0,03314
Noc4l	2252,04	2082,12	1880,16	1364,80	1606,72	1359,14	1317,81	1002,83	0,00802	0,03314
Slc6a9	164,20	250,66	319,72	383,52	321,84	323,18	424,37	399,29	0,00803	0,03317
Gpr27	121,09	126,51	62,50	55,54	68,19	72,81	103,25	91,17	0,00804	0,03318
Mtmr4	3862,86	4144,15	4457,65	4270,29	3112,81	3353,14	3135,59	3113,50	0,00805	0,03323
Twink	1602,57	1833,83	1479,52	1272,23	1088,61	1228,85	1057,66	1148,23	0,00808	0,03331
Elf3	39,45	31,92	140,12	80,67	116,43	70,26	82,92	64,62	0,00808	0,03333
Zfp799	542,14	701,14	723,64	812,00	598,78	854,57	1298,30	1038,60	0,00809	0,03334
2900026A0:	261,44	290,86	309,85	236,72	580,48	335,95	529,24	483,53	0,00809	0,03335
Fam19a1	28,44	16,55	1,97	6,61	2,49	1,28	12,19	8,08	0,00809	0,03335
Evi2b	1,83	0,00	2,63	15,87	20,79	25,55	16,26	15,00	0,00812	0,03346
Hs6st1	661,39	650,29	612,47	473,45	912,30	593,99	1317,00	912,82	0,00813	0,03347
Slc16a4	3,67	0,00	3,29	0,00	2,49	0,00	33,33	19,62	0,00816	0,03361
Ptgs1	42,20	28,38	37,50	46,29	93,97	54,93	122,76	77,32	0,00817	0,03363
G6pc2	0,00	0,00	3,29	15,87	10,81	17,88	4,06	5,77	0,00818	0,03364
Mettl13	1295,27	1356,16	1162,44	945,57	876,54	933,77	869,87	830,88	0,00819	0,03367
Nup133	4089,44	3915,95	3897,16	3565,41	3192,65	3296,94	2853,50	2479,95	0,00819	0,03367
Osbpl2	328,40	352,34	449,98	462,87	515,61	487,96	612,97	518,15	0,00820	0,03370
Dnm3	30,27	28,38	37,50	26,45	48,23	24,27	107,31	66,93	0,00821	0,03375
Agtr1a	20,18	31,92	8,55	5,29	14,97	3,83	51,22	28,85	0,00824	0,03384
Pde1a	0,92	0,00	9,21	7,93	11,64	8,94	11,38	16,16	0,00824	0,03385
Hck	3,67	0,00	8,55	14,55	22,45	14,05	36,58	16,16	0,00825	0,03387
Numa1	5653,49	7128,41	10804,67	8388,49	13046,70	9125,66	12014,76	11333,47	0,00834	0,03423
Tuba4a	100,91	67,39	155,25	141,51	215,39	150,73	104,87	98,09	0,00839	0,03443
Ccdc60	0,92	2,36	8,55	9,26	11,64	10,22	15,45	26,54	0,00839	0,03443
Bdnf	11,93	20,10	34,87	43,64	32,43	53,65	50,40	80,78	0,00839	0,03443
Abcg2	1233,80	1217,82	897,98	1048,73	712,71	873,73	670,69	825,11	0,00843	0,03457
Crebrf	22,93	48,48	49,34	95,22	49,07	81,75	111,38	155,79	0,00843	0,03457
Bin2	39,45	28,38	65,13	78,03	139,71	71,53	47,96	58,85	0,00843	0,03457
Pxk	189,89	243,56	307,22	317,40	381,72	380,66	334,94	340,43	0,00844	0,03457
Bcl2	321,06	474,12	436,16	536,93	600,44	687,24	713,78	737,41	0,00844	0,03459
Crtac1	1,83	8,28	15,13	18,51	31,60	15,33	64,22	24,23	0,00846	0,03464
Pdap1	6038,76	5646,92	5274,71	4988,40	5115,39	4366,11	3920,10	3670,89	0,00847	0,03468
Spata2l	8,26	5,91	11,84	7,93	36,59	17,88	29,27	35,77	0,00847	0,03468
Adam5	0,00	2,36	7,89	2,64	16,63	16,61	15,45	17,31	0,00848	0,03471
Mgat5	565,07	712,96	940,74	940,28	825,81	942,71	1001,57	1276,33	0,00852	0,03487
Naa50	5266,37	7074,02	3123,51	4542,72	2613,83	4254,98	2516,12	3343,15	0,00855	0,03497
Spryd7	320,15	318,05	104,60	173,24	123,08	218,43	130,89	176,56	0,00856	0,03499
Sertad3	122,00	114,69	159,20	152,09	133,06	181,39	251,21	221,57	0,00857	0,03501
Eif3b	19170,30	14931,93	15447,18	10455,53	11273,65	9170,37	10207,55	7183,67	0,00858	0,03504
Banp	632,96	840,65	935,48	745,88	519,77	499,46	552,81	515,84	0,00864	0,03528
Gdpc3	11,01	11,82	54,60	72,74	34,10	63,87	19,51	62,32	0,00865	0,03531
Pde5a	288,96	480,04	747,99	1051,37	696,08	975,92	587,77	918,59	0,00867	0,03541
Gprasp1	1638,35	2023,01	2577,49	2511,39	2852,51	2713,17	2701,47	3614,34	0,00869	0,03548
Larp4	2303,41	3489,12	1511,76	2090,84	861,57	1812,61	910,52	1454,04	0,00870	0,03548
Plcx3	2,75	0,00	27,63	27,77	15,80	22,99	5,69	33,47	0,00870	0,03548
Actl6a	4885,68	3964,43	4345,82	4192,26	3692,46	3778,52	2984,38	2828,46	0,00870	0,03548
Slc7a6	3187,71	3309,41	2814,98	2931,94	2115,68	2669,74	1818,60	2190,30	0,00874	0,03562

Prmt5	7841,31	5628,00	6027,96	4253,10	4507,46	3603,51	3949,37	3053,49	0,00876	0,03572
Ppargc1a	7,34	3,55	9,21	22,48	9,15	22,99	34,14	50,78	0,00878	0,03578
Blnk	0,00	0,00	0,66	1,32	10,81	6,39	14,63	4,62	0,00880	0,03584
Arpc5l	1214,54	983,72	811,80	768,36	791,72	751,10	699,96	693,56	0,00880	0,03584
Senp7	427,47	494,22	498,66	581,89	522,27	563,33	721,10	799,72	0,00882	0,03592
Efnb3	1334,71	1104,32	1763,72	1381,99	2047,49	1396,19	2611,23	2132,60	0,00883	0,03592
Cops7b	1681,46	1476,76	1592,02	1329,09	1251,61	1230,13	1032,46	979,75	0,00883	0,03592
Lrp1	3672,06	3616,82	4008,33	4282,19	5985,28	4385,27	5923,24	5751,55	0,00884	0,03594
Fmn13	1734,67	1858,66	2822,87	2602,64	2520,69	2351,67	2486,85	2298,78	0,00885	0,03596
L1td1	17,43	35,47	84,86	63,48	60,71	51,10	104,87	66,93	0,00885	0,03596
Cops5	3132,67	2452,20	2316,98	2098,78	2038,34	2065,54	1802,34	1527,90	0,00885	0,03597
Clybl	268,78	141,88	315,77	231,43	185,45	194,16	113,00	106,17	0,00887	0,03602
Eif4e	4537,10	4569,79	3052,47	4112,91	2580,56	3508,99	2348,65	2711,91	0,00887	0,03602
Ogfod1	837,52	1060,57	720,36	657,27	580,48	688,51	570,70	565,46	0,00887	0,03602
Aox3	0,92	0,00	7,89	9,26	10,81	5,11	0,00	0,00	0,00888	0,03605
Rnf126	2215,34	1678,94	1691,36	1383,31	1582,60	1286,33	1143,84	963,59	0,00889	0,03609
Hs6st3	4,59	2,36	0,00	1,32	9,98	7,66	15,45	13,85	0,00890	0,03611
Whrn	265,11	335,79	501,29	675,79	266,95	401,10	415,42	398,13	0,00891	0,03615
Fen1	4374,73	3398,08	4305,69	3175,28	3023,83	2792,37	2448,64	2086,44	0,00892	0,03618
Gpsm3	184,38	87,49	99,99	62,16	54,06	44,71	57,72	32,31	0,00896	0,03630
Ikzf5	755,88	870,21	729,57	782,91	400,85	656,58	425,99	467,37	0,00895	0,03630
Mki67	7567,03	9249,55	11594,10	11378,62	12944,41	12901,62	11474,95	12892,53	0,00900	0,03646
Bst2	33,02	13,01	15,79	18,51	38,26	30,66	101,62	43,85	0,00903	0,03659
Arhgef17	2513,48	3090,67	4017,54	3714,85	4145,70	3775,96	4495,68	4348,29	0,00905	0,03666
Tmem59l	300,88	193,91	388,79	160,02	141,38	107,30	128,45	77,32	0,00908	0,03678
Pik3cb	167,87	183,26	112,49	116,38	69,03	118,80	77,23	79,63	0,00911	0,03688
D430042OC	440,32	556,89	793,38	759,10	923,12	742,16	782,88	787,03	0,00912	0,03691
Snx22	3,67	10,64	6,58	18,51	33,27	31,93	30,89	42,70	0,00914	0,03697
Gng5	2219,93	1403,45	2291,32	1514,24	1417,11	1168,81	1059,29	807,80	0,00914	0,03697
Phka2	502,70	534,42	761,80	663,89	836,63	708,95	865,80	820,50	0,00915	0,03701
Shroom3	1515,42	1552,43	972,97	814,65	1117,72	767,71	1679,58	1199,01	0,00919	0,03716
Adgrl4	174,29	144,25	52,63	81,99	99,80	75,37	113,00	94,63	0,00922	0,03726
Kctd5	2287,81	2156,61	2002,52	1989,01	1610,05	1877,76	1447,88	1489,82	0,00924	0,03733
Smurf1	1131,06	1353,79	2138,04	2048,52	1349,74	1705,31	1247,08	1535,98	0,00925	0,03735
Lypd1	33,02	29,56	10,53	11,90	4,99	3,83	13,82	4,62	0,00926	0,03737
Sgcd	52,29	60,30	36,18	26,45	4,99	20,44	18,70	15,00	0,00926	0,03739
Selenoo	194,47	195,09	190,12	194,40	276,10	210,77	334,94	317,35	0,00927	0,03741
Wls	2432,75	2329,24	2393,95	2790,43	2905,73	2921,39	3651,01	3443,55	0,00927	0,03741
Btd	261,44	172,62	348,67	257,88	536,40	362,78	574,76	381,98	0,00929	0,03748
Dsc2	111,00	73,31	30,92	56,87	147,20	144,34	70,73	146,56	0,00938	0,03781
Map3k5	57,79	85,13	40,79	48,93	61,54	74,09	93,49	159,25	0,00939	0,03784
Aacs	1486,07	1492,13	1461,76	1182,30	1137,68	1210,96	945,47	931,28	0,00940	0,03786
Tnfrsf10b	190,80	190,36	234,86	264,50	262,80	228,65	393,47	310,43	0,00940	0,03788
Ppp1r21	365,10	379,54	403,93	398,07	598,78	472,63	596,71	573,54	0,00941	0,03789
Mcf2	1124,64	948,25	796,67	776,30	698,57	715,34	695,08	680,86	0,00943	0,03797
Dpp9	2204,34	2164,89	2340,66	1948,01	1911,10	1668,27	1452,76	1419,42	0,00946	0,03807
Dennd2a	1883,27	2259,48	2531,44	1924,21	1574,29	1516,26	1343,01	1469,05	0,00947	0,03811
Wnt3	5,50	3,55	28,29	15,87	24,12	24,27	1,63	8,08	0,00948	0,03811
Psmg3	943,01	523,78	584,18	383,52	418,31	342,34	367,46	286,19	0,00948	0,03811
Zdhc7	994,38	780,35	611,15	464,19	516,45	415,15	623,54	428,14	0,00949	0,03812

Ldah	1664,03	1408,18	1218,35	1051,37	1045,37	988,70	1056,85	917,43	0,00949	0,03812
Piezo2	296,30	336,97	224,33	247,30	339,31	358,95	373,15	500,84	0,00948	0,03812
Rnd2	147,69	92,22	78,29	85,96	168,82	122,63	239,01	167,33	0,00955	0,03836
Kbtbd11	419,22	364,16	591,42	675,79	556,36	710,23	616,22	698,17	0,00955	0,03836
Scarb2	1199,86	1293,49	1022,31	1132,04	1309,83	1279,94	1586,90	1691,77	0,00955	0,03837
Rpap3	1049,42	1146,88	1076,91	1048,73	980,50	1052,57	698,33	765,10	0,00959	0,03849
Synpo2l	3,67	2,36	9,21	3,97	7,48	7,66	43,90	13,85	0,00959	0,03849
Cep128	354,09	457,57	588,78	573,96	720,20	781,76	518,67	695,86	0,00959	0,03849
Rpp38	280,70	225,83	191,44	166,63	81,50	153,29	134,14	115,40	0,00960	0,03849
Ydjc	142,19	115,87	57,89	55,54	98,96	83,03	87,80	76,16	0,00961	0,03855
Diaph3	684,33	774,44	717,72	711,49	478,19	628,48	437,37	463,91	0,00962	0,03857
Zcchc12	184,38	74,49	34,87	39,67	99,80	66,42	166,66	85,40	0,00964	0,03864
Sncg	15,59	5,91	4,61	3,97	30,77	11,50	56,09	20,77	0,00966	0,03868
Sik1	786,15	1038,11	830,88	810,68	473,20	708,95	521,92	495,07	0,00966	0,03868
Ctse	8,26	15,37	98,68	39,67	118,92	24,27	76,42	66,93	0,00970	0,03884
Rpusd4	859,54	662,12	527,60	513,12	566,34	544,17	422,74	480,07	0,00972	0,03889
Sox18	593,51	417,37	363,80	249,95	239,51	236,32	441,44	316,20	0,00973	0,03894
Dcc	2,75	11,82	0,00	0,00	0,00	0,00	12,19	6,92	0,00974	0,03895
Optc	0,92	2,36	28,29	15,87	0,00	3,83	5,69	2,31	0,00975	0,03901
Sp110	0,00	0,00	5,92	7,93	10,81	8,94	12,19	5,77	0,00976	0,03904
Rara	968,70	974,26	1030,86	896,64	1543,52	1067,90	1805,59	1442,50	0,00977	0,03905
Junb	346,75	254,21	506,55	294,91	473,20	180,11	144,71	106,17	0,00977	0,03906
Unc80	0,00	1,18	0,00	0,00	4,99	14,05	7,32	8,08	0,00978	0,03908
Plpp4	3,67	0,00	0,66	0,00	1,66	3,83	30,08	8,08	0,00981	0,03917
Pdcd5	1568,63	1099,59	1007,18	760,43	949,73	800,92	752,80	667,01	0,00981	0,03918
Emg1	3735,35	2648,47	2753,80	2256,15	2142,29	1996,56	1988,50	1512,90	0,00982	0,03921
Ank3	1311,78	1559,52	909,16	1005,09	1292,36	1154,76	1761,69	1413,65	0,00988	0,03943
Flvcr1	458,66	670,39	208,54	312,11	218,72	342,34	291,04	402,75	0,00990	0,03948
Tmem209	1634,68	1586,72	1231,51	1265,61	1040,38	1214,80	906,45	1114,77	0,00997	0,03976
Wdfy4	19,26	3,55	47,37	42,32	60,71	40,88	84,55	43,85	0,00997	0,03976
E2f7	1190,69	1424,74	2161,72	1945,37	1783,03	1916,08	1714,54	1748,32	0,00998	0,03979
Rsad2	11,01	4,73	7,89	2,64	7,48	2,55	42,27	23,08	0,00998	0,03980
Nudt13	53,20	36,65	63,15	112,41	127,24	117,52	95,12	124,63	0,00999	0,03981
Ctnnbip1	1291,60	942,34	2212,38	1702,03	2468,29	1739,80	2557,58	1846,41	0,01000	0,03982
Ank1	251,35	467,03	352,61	411,29	175,48	275,92	43,09	167,33	0,01000	0,03983
Tfdp1	4147,23	4727,05	2443,29	3495,32	2431,70	3294,38	2078,74	2624,20	0,01006	0,04004
Trim27	5015,94	3954,97	3990,57	3091,96	2886,61	2792,37	2968,94	2297,62	0,01007	0,04008
C1ra	1,83	2,36	1,97	1,32	19,13	2,55	34,14	11,54	0,01007	0,04009
Bcl2l1	1061,35	874,94	1736,75	1359,51	2124,83	1495,82	2273,85	1538,29	0,01012	0,04026
Ssx2ip	557,73	738,97	523,66	630,82	444,09	526,28	332,50	381,98	0,01014	0,04033
P3h4	499,03	358,25	570,36	552,80	894,84	636,14	769,06	732,79	0,01015	0,04034
Zfp385b	16,51	14,19	38,81	58,19	52,39	56,21	29,27	48,47	0,01016	0,04040
Gpi1	13389,30	10337,31	8904,12	5502,84	6840,20	5181,09	7515,02	4875,67	0,01021	0,04054
Tifa	18,35	20,10	21,05	78,03	64,04	42,15	100,81	87,70	0,01020	0,04054
Cops2	4426,10	4990,71	2773,53	3622,27	2542,31	3515,37	2212,07	2898,86	0,01024	0,04067
Pcdhb10	0,92	0,00	3,29	1,32	8,32	7,66	13,01	13,85	0,01024	0,04068
Prr5	476,09	351,16	509,84	342,52	267,79	249,09	265,84	181,18	0,01026	0,04071
Nop10	1722,74	1098,41	1011,79	806,71	903,99	697,45	820,28	617,39	0,01026	0,04072
Slc7a4	4,59	0,00	1,97	0,00	6,65	5,11	28,45	16,16	0,01029	0,04080
Eme1	954,94	1029,83	1229,54	1206,10	1021,25	1180,31	633,30	825,11	0,01029	0,04080

Cxcl13	18,35	13,01	0,00	0,00	0,00	0,00	0,00	0,00	0,01029	0,04081
Adcy4	255,93	183,26	331,56	309,46	323,51	307,85	418,68	399,29	0,01030	0,04082
Pdgfa	44,03	39,02	96,71	66,12	119,76	91,97	63,41	65,78	0,01030	0,04082
Plekhf2	241,26	271,94	222,36	327,98	345,96	361,50	410,55	548,15	0,01032	0,04088
Pak7	9,17	4,73	15,79	17,19	27,44	26,83	28,45	38,08	0,01036	0,04102
Arc	15,59	26,01	42,76	25,13	9,98	15,33	7,32	3,46	0,01037	0,04105
Pde3b	1324,62	1695,49	1226,25	1433,57	886,52	1219,91	641,43	923,20	0,01040	0,04114
Slc9a6	412,80	467,03	238,14	329,30	350,12	475,19	497,53	676,25	0,01039	0,04114
Gm42372	99,07	164,35	98,68	105,80	30,77	85,59	26,83	48,47	0,01040	0,04117
Aimp2	2328,18	1402,27	1475,58	975,99	988,81	878,84	1091,81	700,48	0,01041	0,04119
9530077C0	43,11	34,29	48,68	64,80	98,96	85,59	89,43	76,16	0,01046	0,04138
Cd34	2527,24	1668,30	1181,51	1063,27	1546,84	1221,18	1408,86	1032,83	0,01050	0,04153
Fpgs	917,33	879,67	753,91	621,57	668,63	548,00	573,14	438,52	0,01052	0,04156
Erlin2	1678,71	1702,59	1244,67	1330,42	1323,13	1361,70	834,10	1149,39	0,01052	0,04156
Fzd9	9,17	5,91	7,89	9,26	20,79	14,05	42,27	25,39	0,01056	0,04173
Siglec1	0,00	1,18	0,66	5,29	5,82	3,83	31,71	9,23	0,01058	0,04178
Zfp286	221,99	184,45	244,07	261,85	277,77	300,19	352,83	354,28	0,01059	0,04181
Plekhg2	2036,47	2858,93	4485,94	4074,56	3335,69	3353,14	3822,55	3246,21	0,01065	0,04204
Marc2	432,98	299,14	471,03	404,68	651,17	458,58	871,49	622,01	0,01065	0,04204
Adpgk	1336,55	1407,00	961,79	1208,75	859,91	1011,69	751,18	893,20	0,01066	0,04204
Impdh2	7818,38	6117,49	5427,34	4132,75	4527,42	3736,36	4609,49	3440,09	0,01067	0,04208
Zfp493	85,31	98,14	69,08	84,64	38,26	47,26	39,84	49,62	0,01067	0,04208
Snrpb2	1960,33	1814,91	1411,77	1575,07	1234,98	1465,16	1100,75	1269,40	0,01069	0,04213
Agps	2991,40	3124,96	1918,32	2524,62	1863,70	2404,05	1507,23	1891,41	0,01070	0,04216
Snx18	2023,62	2116,41	1736,09	1518,21	1293,19	1461,33	2133,21	1879,87	0,01073	0,04227
Ptges3	3915,15	4672,66	2674,85	3483,41	1896,96	3054,24	2112,89	2491,49	0,01073	0,04227
Cep164	1044,84	1428,28	2072,26	1790,64	2328,58	1936,52	1837,29	1980,27	0,01074	0,04229
Clint1	3905,06	4368,79	3447,84	3336,62	3179,34	3487,27	2725,05	2775,38	0,01078	0,04242
Ipo7	7825,72	10954,50	5154,32	6874,25	4172,31	6719,06	3949,37	5218,41	0,01080	0,04252
Rtl3	1,83	0,00	1,32	2,64	1,66	0,00	21,95	10,39	0,01082	0,04258
Gucy1a1	36,69	13,01	9,87	18,51	9,98	10,22	109,75	21,93	0,01086	0,04271
Zfp354c	877,88	1210,73	992,05	1143,95	847,44	1382,13	1881,19	1867,18	0,01089	0,04282
Proser3	375,19	470,58	753,25	670,50	651,17	579,93	617,04	616,24	0,01093	0,04297
Manea	1029,24	1062,94	799,30	880,77	367,58	753,66	404,85	580,46	0,01096	0,04306
Lilrb4a	0,00	0,00	5,92	10,58	4,16	3,83	13,01	8,08	0,01097	0,04310
Smc6	3612,43	6649,55	2439,34	3422,58	2054,14	3165,37	1447,88	2677,29	0,01098	0,04312
Lypla1	1864,01	1605,64	1301,90	1132,04	1199,22	1305,49	1182,86	1058,22	0,01099	0,04317
Etl4	300,88	603,00	176,96	232,76	251,99	250,37	235,76	253,88	0,01101	0,04321
Pnma3	4,59	2,36	3,29	7,93	18,30	26,83	23,58	13,85	0,01101	0,04321
Senp3	4147,23	3736,23	3634,67	3397,45	3403,88	3121,94	2704,72	2541,12	0,01103	0,04328
Eif3m	5382,87	4011,72	3393,24	3394,81	3050,44	3114,27	3215,26	2717,68	0,01104	0,04330
Acap1	6,42	13,01	22,37	39,67	21,62	28,10	3,25	8,08	0,01105	0,04333
Acvr2a	487,10	658,57	479,58	696,95	666,97	873,73	936,53	1204,78	0,01105	0,04333
Stk24	2421,74	2330,42	2077,52	1930,82	1891,14	1838,16	1612,10	1630,61	0,01106	0,04334
Fzd5	28,44	43,75	92,76	58,19	30,77	38,32	134,95	61,16	0,01106	0,04336
Hbegf	173,37	163,16	76,31	87,28	57,38	89,42	126,01	77,32	0,01107	0,04339
Fermt3	82,56	81,58	113,81	167,96	262,80	150,73	142,27	141,94	0,01111	0,04351
Socs5	445,82	471,76	469,71	473,45	536,40	591,43	856,05	635,86	0,01112	0,04355
Eid1	3222,57	2912,13	2893,26	2679,35	3341,51	3033,80	4585,10	3901,69	0,01112	0,04355
Tfpi	368,77	303,86	154,60	238,05	182,13	217,16	176,41	178,87	0,01119	0,04378

Tnip2	12,84	16,55	31,58	34,38	26,61	34,49	45,53	60,01	0,01120	0,04382
Fam234a	477,01	365,35	558,52	427,16	819,99	513,51	964,99	738,56	0,01121	0,04384
Tomm70a	5575,51	7371,97	3301,79	4869,37	2761,03	4644,58	2186,87	3482,78	0,01123	0,04392
Adap2	0,00	0,00	3,29	2,64	8,32	7,66	8,94	10,39	0,01127	0,04406
Pou4f1	14,68	22,46	18,42	19,84	2,49	8,94	0,81	3,46	0,01127	0,04406
Usp36	1362,23	1991,08	1269,01	1327,77	902,32	1066,62	817,03	1098,61	0,01130	0,04416
Tmem5	580,67	522,60	342,09	367,65	397,52	365,33	395,10	356,59	0,01131	0,04418
Ift22	402,71	305,05	624,31	507,83	509,79	433,03	334,13	334,66	0,01133	0,04423
Pde12	1025,57	980,17	865,08	843,74	610,42	717,89	722,72	589,70	0,01134	0,04427
Hdx	376,10	604,18	203,28	326,65	83,16	252,92	121,13	219,26	0,01136	0,04435
Kdm5b	4455,46	4834,64	6071,38	5714,44	4770,26	4997,14	8150,75	6203,92	0,01138	0,04439
Iivbl	286,21	156,07	263,14	232,76	375,07	269,53	530,86	420,06	0,01138	0,04439
Ccdc115	647,63	631,38	400,64	526,35	461,56	493,07	294,29	395,82	0,01139	0,04444
Dkk2	44,95	61,48	16,45	17,19	29,11	20,44	56,91	35,77	0,01144	0,04458
Pskh1	1144,82	1009,73	1585,44	1397,86	1858,71	1497,10	1712,10	1653,69	0,01144	0,04458
Aph1b	308,22	366,53	611,15	748,52	493,16	716,61	464,20	657,78	0,01148	0,04475
Tube1	391,70	413,82	285,51	330,62	175,48	265,70	155,28	245,80	0,01150	0,04480
Baalc	14,68	10,64	1,97	1,32	16,63	5,11	32,52	15,00	0,01150	0,04480
Trim13	105,49	111,14	119,07	99,19	108,11	137,96	217,87	180,02	0,01153	0,04489
Crhbp	0,92	0,00	18,42	7,93	2,49	2,55	0,00	1,15	0,01154	0,04494
Slc25a21	13,76	10,64	32,24	38,35	11,64	10,22	0,00	6,92	0,01155	0,04494
Fstl1	7202,85	5622,09	7796,94	6211,69	9413,28	7384,58	13882,13	9537,84	0,01156	0,04498
Hnrnp1l	4047,25	4232,82	3284,69	3554,83	2693,67	3328,87	2651,07	2744,22	0,01156	0,04498
Sgsm1	380,69	345,25	428,27	403,36	429,96	443,25	222,75	291,96	0,01157	0,04500
Veph1	10,09	2,36	0,00	0,00	2,49	1,28	25,20	4,62	0,01159	0,04506
Thns12	45,87	43,75	80,92	68,77	141,38	84,31	121,13	87,70	0,01160	0,04507
Dock9	278,87	312,14	221,70	232,76	407,50	301,46	377,21	458,14	0,01160	0,04508
Prmt1	14103,90	11519,66	11681,60	10676,39	11005,86	9612,35	8464,56	7469,87	0,01161	0,04508
Hmgcll1	22,93	34,29	55,26	108,44	69,86	123,91	69,91	88,86	0,01165	0,04522
Tmem33	2156,64	2472,30	1514,39	1809,15	1197,56	1605,68	1312,93	1572,91	0,01166	0,04525
Cisd1	928,33	660,94	757,20	567,34	604,60	525,01	455,26	358,90	0,01169	0,04537
Erfe	33,02	34,29	46,71	52,90	83,16	81,75	60,16	73,86	0,01172	0,04548
Rbfa	492,60	445,75	300,64	206,31	314,36	218,43	278,85	178,87	0,01174	0,04553
Bzw1	14702,91	15229,89	11096,76	12051,77	9567,97	12151,80	9437,67	9843,65	0,01174	0,04555
Sgpp2	6,42	16,55	50,00	58,19	39,92	106,02	20,32	62,32	0,01176	0,04558
Homer2	456,83	384,26	257,22	284,33	345,13	454,75	528,43	458,14	0,01181	0,04578
Mesd	2532,74	1892,95	2138,04	2036,62	1559,32	1747,47	1324,31	1450,58	0,01182	0,04580
Zhx2	281,62	305,05	337,48	347,81	533,91	366,61	462,58	646,24	0,01184	0,04586
Yars	3888,55	3133,23	3129,43	2323,60	2479,94	1979,95	2198,25	1661,77	0,01187	0,04596
Zfp623	505,45	510,78	351,30	343,84	242,84	337,23	427,62	390,05	0,01187	0,04596
Rorb	11,01	23,65	0,66	5,29	14,97	22,99	21,95	35,77	0,01191	0,04610
Ecm2	0,00	1,18	0,66	6,61	12,47	11,50	17,07	15,00	0,01191	0,04610
Adat1	488,94	581,72	545,37	510,48	360,93	398,55	313,80	378,51	0,01192	0,04611
Adamts15	139,43	114,69	57,89	47,61	52,39	37,04	239,01	56,55	0,01192	0,04611
Twistnb	1101,71	1138,61	747,99	833,16	489,83	806,03	651,18	626,62	0,01193	0,04615
Xbp1	2020,87	1464,94	1928,18	1465,31	833,30	878,84	1643,81	924,36	0,01194	0,04615
Homer3	3145,51	2538,51	3206,40	2409,56	2084,91	1948,02	1947,04	1656,00	0,01195	0,04618
Apob	5,50	1025,10	0,00	0,00	0,00	1,28	0,81	0,00	0,01196	0,04621
Rgs2	241,26	180,90	226,96	212,92	315,19	275,92	441,44	320,81	0,01196	0,04621
Egln1	2762,99	2145,97	1707,80	1396,54	1547,67	1500,93	1878,75	1522,13	0,01197	0,04621

Krt17	3,67	2,36	23,68	1,32	80,67	49,82	44,71	3,46	0,01197	0,04621
Elov14	329,32	368,89	201,30	232,76	207,08	242,70	227,63	205,41	0,01198	0,04624
Abca7	43,11	108,78	109,20	189,11	231,19	191,61	194,30	227,34	0,01198	0,04624
Sesn3	1408,10	1790,08	2072,91	2257,47	2649,59	2775,77	2261,66	3526,64	0,01202	0,04636
Aspg	26,60	30,74	45,39	130,93	90,65	162,23	54,47	102,71	0,01202	0,04637
Coq7	894,39	711,78	617,07	569,99	607,09	471,36	494,28	376,21	0,01206	0,04652
Tomm20	4184,85	2513,68	2170,93	1978,43	2158,09	1942,91	2036,47	1621,38	0,01208	0,04658
Tmem80	109,16	114,69	149,99	191,76	197,93	181,39	211,37	210,03	0,01210	0,04663
Bicral	135,76	268,39	327,61	411,29	344,30	464,97	404,04	628,93	0,01211	0,04666
Sept11	17977,77	25485,61	14118,31	17639,25	12649,18	15562,42	9791,31	13252,58	0,01213	0,04671
Usp28	1315,45	1457,84	1144,02	1080,47	726,85	972,09	888,57	984,37	0,01214	0,04676
Mettl3	1102,63	1094,86	971,00	905,90	791,72	812,42	666,63	780,11	0,01217	0,04684
Atp6v1a	2985,90	2604,72	2018,97	1999,59	1753,09	2001,67	2110,45	1860,25	0,01219	0,04692
Gmnn	1550,28	1263,94	1047,31	1175,69	975,51	1328,48	658,50	853,96	0,01222	0,04700
Fahd2a	77,97	70,94	130,91	109,77	94,81	90,69	152,84	141,94	0,01224	0,04707
Ndfip1	968,70	788,63	1240,72	1296,03	1194,23	1277,39	1346,26	1381,34	0,01227	0,04719
Snai1	1951,15	2186,17	2224,88	1557,88	835,79	1285,05	1454,39	819,34	0,01234	0,04745
Tmem97	1565,88	1119,69	1186,78	772,33	854,92	740,89	771,50	585,08	0,01235	0,04747
Ulbp1	33,94	56,75	55,92	46,29	103,95	104,75	73,98	113,09	0,01237	0,04753
Mast3	506,36	588,81	765,09	860,93	772,59	714,06	830,03	902,43	0,01240	0,04763
Sema7a	98,15	88,68	121,70	116,38	63,20	67,70	65,85	48,47	0,01240	0,04763
Tmx4	422,89	424,46	597,99	944,25	777,58	1051,29	657,69	1149,39	0,01242	0,04770
Zfp395	1034,74	921,05	1293,35	1125,43	1527,71	1346,37	1436,50	1591,37	0,01243	0,04773
Agfg2	250,43	247,11	406,56	392,78	327,66	416,43	442,25	393,52	0,01247	0,04785
Cd86	0,00	0,00	2,63	6,61	9,98	12,77	8,13	5,77	0,01250	0,04796
Pfn1	24618,30	16898,19	21002,80	13843,73	13023,41	11141,38	12796,83	8277,67	0,01256	0,04818
Slc25a15	681,57	710,59	482,21	585,86	405,01	527,56	300,80	431,60	0,01257	0,04821
Nipsnap3b	500,86	433,92	354,59	384,84	271,11	365,33	265,03	263,11	0,01259	0,04827
Ppp1r9a	1194,36	2402,54	471,03	911,19	569,67	1126,66	439,00	900,12	0,01259	0,04827
Chd1	3381,27	5989,80	3284,69	3900,00	1669,09	3022,30	1917,78	2538,81	0,01263	0,04840
Src	1734,67	1747,52	2833,40	2450,56	2652,92	2269,92	2466,53	2406,10	0,01264	0,04840
Smu1	3927,99	3691,31	3139,30	3197,76	2899,08	3166,65	2532,38	2657,67	0,01267	0,04851
Klhl29	293,54	384,26	569,71	740,59	510,62	731,94	474,77	578,16	0,01268	0,04856
Ifi202b	0,00	1,18	7,24	18,51	19,13	8,94	8,94	10,39	0,01270	0,04858
Pbx2	6257,09	4797,99	4416,21	3737,33	4482,52	3667,38	2864,88	3434,32	0,01270	0,04858
Abhd4	705,42	578,17	913,77	667,85	1181,75	762,60	1509,67	1100,92	0,01270	0,04858
Phb2	11200,56	7278,56	8173,90	5039,97	5961,99	4580,72	5083,45	3358,15	0,01274	0,04872
Twist1	5221,42	4893,76	3372,84	3328,68	4638,03	3765,74	6694,74	4730,26	0,01274	0,04872
Lars	4255,48	4408,99	3689,93	3482,09	3216,77	3189,64	3199,82	2970,41	0,01275	0,04873
Dus3l	990,71	991,99	797,32	796,13	765,94	747,27	638,99	683,17	0,01276	0,04875
Otop1	0,00	2,36	13,82	21,16	6,65	12,77	0,81	3,46	0,01277	0,04878
Adam23	75,22	86,31	70,39	76,70	75,68	71,53	157,71	121,17	0,01279	0,04886
Timeless	3555,56	3557,70	4649,09	4128,78	4109,94	3958,63	2654,32	3150,43	0,01280	0,04888
Uspl1	1897,95	2176,71	1568,99	1650,46	1033,72	1458,78	1282,04	1358,26	0,01281	0,04890
Tchp	377,94	449,29	589,44	638,76	676,95	588,88	428,43	480,07	0,01282	0,04894
Cd68	16,51	35,47	32,24	78,03	59,05	75,37	158,53	71,55	0,01283	0,04894
Wdr1	5115,01	4758,97	4860,92	4591,65	3313,24	3505,15	3983,51	3135,43	0,01287	0,04908
Polr1a	4936,14	4829,91	4082,01	3392,16	3624,27	3012,08	3363,22	2815,77	0,01287	0,04909
Tpm2	396,29	250,66	546,68	424,52	766,77	463,69	1000,76	589,70	0,01288	0,04909
Rnf17	54,12	82,76	30,26	50,25	14,97	34,49	20,32	17,31	0,01289	0,04912

Tnfrsf11b	12,84	8,28	53,29	34,38	18,30	16,61	28,45	19,62	0,01296	0,04939
Fam49a	112,83	147,79	149,33	212,92	255,31	292,52	200,80	310,43	0,01298	0,04944
Nkrf	569,66	853,66	481,55	525,02	265,29	466,25	319,49	392,36	0,01303	0,04962
Ccdc88b	4,59	3,55	16,45	15,87	30,77	19,16	33,33	16,16	0,01304	0,04966
Slc6a12	2,75	1,18	21,71	3,97	0,00	0,00	0,00	0,00	0,01306	0,04971
Clec5a	0,00	0,00	0,66	0,00	9,15	7,66	6,50	5,77	0,01310	0,04987
Nsmf	492,60	573,44	657,20	810,68	822,49	793,26	842,23	872,43	0,01312	0,04990
Rab22a	783,40	1018,01	859,82	1261,65	1224,17	1614,62	1486,09	1921,42	0,01311	0,04990
Cd93	1405,34	1239,11	876,27	682,40	1192,57	885,23	1539,75	1201,32	0,01315	0,05000
Arhgap23	440,32	458,75	780,22	629,50	611,25	606,76	924,34	665,86	0,01315	0,05000

Gene contribution to the PCA (only most 500 most variant genes were considered)

Symbol	PC1	PC2	Symbol	PC1	PC2	Symbol	PC1	PC2
Krt5	0,00968	0,00193	Vwde	0,00238	0,00006	Celsr2	0,00153	0,00034
Fgf8	0,00849	0,00073	Hoxc10	0,00181	0,00211	Arhgap8	0,00165	0,00002
Krt14	0,00682	0,00754	Cpa2	0,00128	0,00051	Crabp1	0,00031	0,00631
Hbb-bh1	0,00606	0,00952	Prrx1	0,00240	0,00000	Lcp1	0,00155	0,00050
Perp	0,00832	0,00000	Nid2	0,00223	0,00013	Wif1	0,00026	0,00393
Wnt6	0,00806	0,00008	Prrx2	0,00217	0,00013	Bnc1	0,00163	0,00008
Hba-x	0,00690	0,00290	Zic2	0,00196	0,00100	Robo4	0,00156	0,00012
Igfbp5	0,00748	0,00159	Fbln5	0,00088	0,00599	Cdh3	0,00056	0,00467
Sfn	0,00752	0,00084	Hoxa11	0,00143	0,00009	Rcan2	0,00121	0,00042
Cldn6	0,00740	0,00069	Zic3	0,00104	0,00603	Wwc1	0,00163	0,00004
Hbb-y	0,00684	0,00017	Erbp3	0,00235	0,00014	Mbp	0,00164	0,00000
Bcam	0,00712	0,00068	Sorbs2	0,00220	0,00071	Slc16a2	0,00008	0,00905
Trp63	0,00717	0,00002	Serinc2	0,00001	0,01348	Capn6	0,00143	0,00007
Bhlha9	0,00671	0,00000	Ramp2	0,00232	0,00004	Wfikkn1	0,00000	0,00864
Epcam	0,00670	0,00002	Otx1	0,00115	0,00293	Tmcc3	0,00159	0,00005
Cdh1	0,00662	0,00014	Capg	0,00225	0,00046	Tmem255a	0,00156	0,00001
Hba-a1	0,00615	0,00002	Twist1	0,00213	0,00000	Phlda3	0,00149	0,00027
Hoxd13	0,00237	0,02304	Lypd3	0,00170	0,00178	Gli1	0,00009	0,00304
Pdgfa	0,00637	0,00017	Igfbp2	0,00215	0,00053	Klc3	0,00142	0,00107
Igdcc3	0,00006	0,03136	Dlx5	0,00085	0,00472	Hoxc9	0,00159	0,00008
Hoxd12	0,00177	0,02322	Col15a1	0,00221	0,00070	Arl4c	0,00153	0,00051
Sp6	0,00617	0,00101	Alas2	0,00229	0,00007	Kirrel3	0,00123	0,00002
Krt17	0,00451	0,00629	Cped1	0,00193	0,00174	Col26a1	0,00141	0,00003
Cldn4	0,00590	0,00010	Hand2	0,00190	0,00043	Krt15	0,00088	0,00004
Gjb3	0,00561	0,00022	Anxa8	0,00140	0,00215	Emilin1	0,00145	0,00000
Trim29	0,00564	0,00042	Crhr1	0,00199	0,00031	Alcam	0,00067	0,00028
Esrp1	0,00573	0,00002	Hoxa9	0,00178	0,00071	Nfix	0,00030	0,00403
Dlx2	0,00562	0,00012	Proser2	0,00224	0,00010	Shox2	0,00103	0,00113
Wnt7b	0,00531	0,00156	Cacna1b	0,00229	0,00010	Jaml	0,00020	0,00706
Dsp	0,00552	0,00010	Lin28b	0,00001	0,01364	Prss22	0,00153	0,00000
St14	0,00540	0,00002	Itgb4	0,00211	0,00069	Coro1a	0,00097	0,00252
Cldn7	0,00538	0,00023	Tgm1	0,00232	0,00000	Stx3	0,00152	0,00010
Col17a1	0,00442	0,00346	Cdx1	0,00003	0,01375	Tbx18	0,00123	0,00106
Tacstd2	0,00473	0,00189	Penk	0,00184	0,00093	Gimap4	0,00153	0,00001
Hoxa13	0,00162	0,01909	Eya2	0,00224	0,00008	Ablim1	0,00152	0,00018
Lin28a	0,00010	0,03187	Cyp26b1	0,00017	0,00130	Tubb6	0,00001	0,00457
Wnt7a	0,00487	0,00036	Arhgef16	0,00224	0,00014	Bcl11b	0,00090	0,00379
Pltp	0,00491	0,00032	Evx2	0,00102	0,00577	Gap43	0,00057	0,00376
Fxyd3	0,00476	0,00028	Col9a1	0,00134	0,00375	Ifitm1	0,00023	0,00764
Kremen2	0,00493	0,00002	Cbln1	0,00065	0,00448	Hoxa7	0,00079	0,00356
Sp8	0,00473	0,00031	Adgra2	0,00212	0,00005	Gng11	0,00145	0,00003
Cxcl14	0,00287	0,01119	Sparcl1	0,00192	0,00100	Lmx1b	0,00121	0,00099
Itga3	0,00459	0,00057	A730017C2f	0,00210	0,00019	Nbl1	0,00023	0,00293
Adamts18	0,00451	0,00048	Pik3r1	0,00214	0,00038	Lama4	0,00144	0,00036
Lad1	0,00455	0,00061	Nr6a1	0,00007	0,01325	Crb3	0,00151	0,00009
Lama5	0,00468	0,00000	Fgfr2	0,00172	0,00013	Hr	0,00151	0,00015
Gabrp	0,00291	0,00521	Snap91	0,00180	0,00055	Ackr3	0,00125	0,00047

Dlx3	0,00430	0,00024	Lmo2	0,00137	0,00192	Sh3rf1	0,00152	0,00001
Jag2	0,00461	0,00000	Mab21l2	0,00107	0,00172	Tfap2a	0,00077	0,00247
Fermt1	0,00454	0,00001	Zim1	0,00158	0,00323	Alpl	0,00078	0,00232
Irf6	0,00450	0,00038	Prdm16	0,00159	0,00311	Chd3	0,00000	0,00915
Ap1m2	0,00447	0,00012	Epha1	0,00198	0,00018	Itga11	0,00060	0,00478
Krt7	0,00453	0,00000	Ddr2	0,00205	0,00005	Gdf5	0,00049	0,00322
Hspb1	0,00420	0,00063	Kcne3	0,00217	0,00002	Pcdh7	0,00148	0,00000
Krt18	0,00390	0,00253	Cldn5	0,00206	0,00007	Stard10	0,00132	0,00048
Hbb-bs	0,00295	0,00259	Smpd3	0,00137	0,00015	Pcdh12	0,00148	0,00001
Lamc2	0,00425	0,00066	Gjb6	0,00131	0,00172	Samd5	0,00137	0,00000
Meis2	0,00186	0,01187	Tbx5	0,00206	0,00001	Lypd6	0,00148	0,00011
Pkdcc	0,00005	0,02529	Rspo4	0,00107	0,00491	Dnm1	0,00136	0,00028
Krt8	0,00364	0,00240	S100a11	0,00190	0,00079	Nfatc1	0,00098	0,00278
Spint2	0,00388	0,00099	Ets1	0,00208	0,00002	Etl4	0,00141	0,00048
Dlx1	0,00425	0,00000	Fgf9	0,00187	0,00065	Eps8l2	0,00144	0,00034
Sost	0,00398	0,00004	Slc9a3r1	0,00178	0,00187	Met	0,00081	0,00344
Spint1	0,00400	0,00018	Htra1	0,00138	0,00244	Ntn1	0,00125	0,00000
Arhgef19	0,00400	0,00016	Kcnk1	0,00211	0,00000	Cgn	0,00148	0,00001
Cdh5	0,00390	0,00013	Map2	0,00157	0,00307	Fam83b	0,00145	0,00003
En1	0,00395	0,00005	Sptlc3	0,00211	0,00006	Crym	0,00025	0,00602
Hbb-bt	0,00255	0,00492	Fam89a	0,00200	0,00062	Hoxb8	0,00010	0,00744
Grhl3	0,00380	0,00040	Esam	0,00206	0,00001	Sema3d	0,00120	0,00031
Gjb2	0,00258	0,00439	Ston2	0,00212	0,00002	Tdrp	0,00144	0,00021
Pkp3	0,00374	0,00012	Pik3ip1	0,00184	0,00145	Apoe	0,00093	0,00117
Al661453	0,00372	0,00002	Prom2	0,00197	0,00036	Art4	0,00143	0,00000
Gpx2	0,00329	0,00001	Pygl	0,00183	0,00013	Hoxa5	0,00089	0,00277
Wnt3	0,00377	0,00000	Evx1	0,00065	0,00526	Stab1	0,00138	0,00027
Grhl2	0,00373	0,00002	Mcub	0,00101	0,00487	Twist2	0,00117	0,00012
Cyp26a1	0,00326	0,00108	Isl2	0,00178	0,00019	Dlc1	0,00136	0,00004
Sct	0,00274	0,00184	Robo2	0,00057	0,00800	Sgk1	0,00101	0,00091
Pdlim1	0,00360	0,00003	Epb41l4a	0,00210	0,00002	Rarb	0,00013	0,00574
Nectin4	0,00322	0,00129	Hoxd8	0,00098	0,00523	Lama3	0,00066	0,00205
Esrp2	0,00362	0,00008	Hoxb6	0,00011	0,01054	Pdzd2	0,00043	0,00549
Wnt4	0,00363	0,00004	Lgals1	0,00151	0,00053	Tbx2	0,00096	0,00069
Emx2	0,00331	0,00109	Crabp2	0,00141	0,00225	Rasip1	0,00135	0,00002
Frem2	0,00341	0,00056	Dsc2	0,00204	0,00001	Hoxd4	0,00027	0,00599
Tmem54	0,00343	0,00028	Nid1	0,00190	0,00004	Heyl	0,00107	0,00041
Kdf1	0,00355	0,00000	F11r	0,00192	0,00023	Hoxb2	0,00017	0,00750
Ripk4	0,00353	0,00004	Sostdc1	0,00157	0,00129	Fgf17	0,00104	0,00000
Rspo2	0,00265	0,00250	Moxd1	0,00185	0,00000	Lrrtm1	0,00128	0,00000
Krt19	0,00280	0,00320	Tspan18	0,00155	0,00216	Col25a1	0,00108	0,00150
Hoxd11	0,00160	0,00621	Rnf43	0,00201	0,00002	Flt4	0,00138	0,00003
Plvap	0,00335	0,00006	Cd248	0,00169	0,00009	Vegfd	0,00126	0,00000
Cbr2	0,00332	0,00024	Fgf10	0,00193	0,00001	Crmp1	0,00100	0,00142
Asb4	0,00239	0,00176	Pf4	0,00189	0,00024	Meox1	0,00036	0,00584
Cdkn1a	0,00335	0,00001	Fam46a	0,00170	0,00000	Hgf	0,00002	0,00852
Ambn	0,00169	0,00409	Tie1	0,00193	0,00007	Edar	0,00114	0,00010
Hoxc13	0,00255	0,00273	Igfbpl1	0,00183	0,00016	Dst	0,00108	0,00100
Grb7	0,00328	0,00073	Mapk13	0,00166	0,00022	Cd9	0,00127	0,00048
Dsg2	0,00340	0,00005	Pdpr	0,00194	0,00031	Pla2r1	0,00140	0,00000

Hmga1b	0,00001	0,00157	Wnt10a	0,00191	0,00008	S100a3	0,00070	0,00172
Acpp	0,00336	0,00010	Lmo7	0,00157	0,00109	Evpl	0,00111	0,00070
Hoxa10	0,00235	0,00284	Dlx6	0,00076	0,00298	Pqlc3	0,00137	0,00022
Lhx9	0,00287	0,00141	Llgl2	0,00177	0,00109	Fam20c	0,00129	0,00002
Lhx2	0,00282	0,00097	Pth1r	0,00150	0,00102	Cblc	0,00138	0,00007
Cdh11	0,00242	0,00395	Gsn	0,00037	0,00903	Ptch2	0,00009	0,00083
Hoxc8	0,00222	0,00404	Zfp750	0,00143	0,00117	Tmem132c	0,00127	0,00003
Cldn3	0,00305	0,00023	Aox3	0,00118	0,00043	Camsap3	0,00125	0,00031
Col2a1	0,00216	0,00005	Lix1l	0,00178	0,00043	Fry	0,00112	0,00099
Meis1	0,00161	0,00896	Col3a1	0,00137	0,00004	Arg1	0,00063	0,00259
Cpz	0,00197	0,00324	Nkx1-1	0,00142	0,00071	Fjx1	0,00126	0,00017
Tmem119	0,00243	0,00199	Plekhg1	0,00189	0,00000	Notum	0,00111	0,00015
Anxa1	0,00197	0,00400	Col18a1	0,00185	0,00004	Itga6	0,00128	0,00000
Cd34	0,00306	0,00018	Cntn2	0,00146	0,00075	Bnpl	0,00138	0,00005
Mpzl2	0,00315	0,00000	Frzb	0,00046	0,00104	Hey1	0,00079	0,00153
Pmaip1	0,00032	0,01000	Bcl11a	0,00006	0,01128	Gpc4	0,00110	0,00004
Dlk1	0,00005	0,01759	Hsd11b2	0,00135	0,00022	Gprc5c	0,00122	0,00002
Aldh1a2	0,00148	0,00003	Parm1	0,00181	0,00031	Rftn2	0,00094	0,00221
Mecom	0,00282	0,00065	Srms	0,00148	0,00077	Wnt9b	0,00131	0,00021
Upk3bl	0,00292	0,00028	Padi3	0,00147	0,00021	Tbx1	0,00042	0,00391
Hoxc12	0,00165	0,00362	Bcat1	0,00137	0,00206	Fam196b	0,00122	0,00028
Tulp2	0,00301	0,00001	Wnk2	0,00168	0,00008	Kank4	0,00108	0,00049
Tfap2b	0,00005	0,01685	Cldn1	0,00162	0,00057	Frmd4b	0,00135	0,00000
Aplnr	0,00289	0,00009	Car14	0,00149	0,00041	Tpd52	0,00120	0,00005
Rprm	0,00059	0,01053	S100a10	0,00176	0,00003	Cep170b	0,00079	0,00186
Fzd6	0,00291	0,00007	Upk1b	0,00125	0,00179	Tmem200b	0,00039	0,00171
Ddr1	0,00285	0,00029	Tagln	0,00110	0,00004	Cacna1g	0,00110	0,00135
Fmod	0,00245	0,00143	Large2	0,00178	0,00002	Map7	0,00137	0,00004
Ntf5	0,00294	0,00006	Irx3	0,00004	0,00821	Shh	0,00028	0,00017
S100a6	0,00278	0,00000	Icam2	0,00175	0,00000	Eva1a	0,00002	0,00764
Hoxc5	0,00045	0,01494	Hpn	0,00164	0,00056	Lgr6	0,00123	0,00000
Plch2	0,00291	0,00004	Fam83h	0,00180	0,00006	Cobll1	0,00105	0,00126
Peg10	0,00064	0,01203	Nmnat2	0,00170	0,00009	Arid3b	0,00068	0,00174
Slc4a1	0,00260	0,00035	Ppp2r2c	0,00077	0,00239	Emilin2	0,00115	0,00000
Emcn	0,00280	0,00003	Erg	0,00159	0,00009	Pmp22	0,00066	0,00026
Fras1	0,00283	0,00007	Plekha7	0,00178	0,00003	Krtap17-1	0,00094	0,00063
Prss8	0,00250	0,00094	Sox18	0,00169	0,00000	Rassf10	0,00132	0,00001
Mogat2	0,00168	0,00506	Has3	0,00151	0,00091	Vwa1	0,00129	0,00000
Ppl	0,00283	0,00002	Cd93	0,00174	0,00000	Ndufa4l2	0,00017	0,00604
Hoxd9	0,00142	0,00690	Atp2c2	0,00169	0,00028	Tom1l1	0,00129	0,00007
Rab15	0,00271	0,00029	Nebi	0,00150	0,00000	Alx4	0,00096	0,00167
Vcam1	0,00194	0,00379	Emx1	0,00174	0,00002	Thbs1	0,00124	0,00029
Prtg	0,00000	0,01734	Lmo1	0,00127	0,00013	Vgll3	0,00094	0,00109
Wnt10b	0,00239	0,00026	Hapln1	0,00086	0,00479	Atp6v1g3	0,00037	0,00418
Slc2a3	0,00273	0,00015	Hist3h2ba	0,00131	0,00179	Figln2	0,00003	0,00660
Rhov	0,00200	0,00189	Cd44	0,00149	0,00028	Espn	0,00079	0,00216
Hoxd10	0,00226	0,00001	Tubb3	0,00121	0,00045	Hoxb9	0,00011	0,00628
Hoxc6	0,00097	0,01058	Trp73	0,00128	0,00139	Adgrf5	0,00128	0,00006
Lbh	0,00251	0,00006	Hoxb5	0,00006	0,00962	Pear1	0,00093	0,00064
Rab25	0,00266	0,00006	Tjp3	0,00149	0,00055	Slit3	0,00060	0,00065

Vwa2	0,00263	0,00025	Gja3	0,00072	0,00378	Synpo	0,00086	0,00164
Itga4	0,00253	0,00012	Hoxc4	0,00038	0,00741	Gsg1	0,00122	0,00001
Kdr	0,00258	0,00036	Hoxc11	0,00091	0,00215	Plxna2	0,00088	0,00263
Cdcp1	0,00266	0,00001	Prss23	0,00152	0,00000	Sox14	0,00121	0,00012
Tbx15	0,00185	0,00018	Rhpn2	0,00167	0,00030	Tmem173	0,00109	0,00010
Npnt	0,00234	0,00026	Nkd2	0,00115	0,00272	Ccdc68	0,00128	0,00010
Snai1	0,00228	0,00082	Acta2	0,00130	0,00000	Tmtc1	0,00116	0,00052
Lgals7	0,00157	0,00427	Anxa2	0,00084	0,00323	Sytl1	0,00127	0,00016
Fgf4	0,00097	0,00010	Rnase4	0,00138	0,00151	Tmem26	0,00071	0,00274
Lypd6b	0,00255	0,00025	Chst11	0,00157	0,00045	Nav2	0,00120	0,00038
Eng	0,00254	0,00006	Zeb1	0,00160	0,00032	Colec12	0,00075	0,00123
Apoc1	0,00241	0,00001	Clmp	0,00148	0,00061	Nfia	0,00042	0,00533
Pkp1	0,00217	0,00126	Ass1	0,00165	0,00000	Sulf1	0,00051	0,00111
Emp1	0,00203	0,00263	Marveld2	0,00169	0,00003	Palm3	0,00102	0,00064
Plxnd1	0,00249	0,00002	Gjb5	0,00139	0,00067	Card10	0,00112	0,00033
Pecam1	0,00247	0,00010	Gimap6	0,00164	0,00001	Aldh3b2	0,00124	0,00014
Egfr	0,00255	0,00001	Lpar1	0,00156	0,00035	Trim2	0,00126	0,00001
Lix1	0,00151	0,00255	Nrarp	0,00114	0,00170	Itgb5	0,00123	0,00007
Susd4	0,00253	0,00001	Fndc3c1	0,00080	0,00425	Laptm5	0,00092	0,00178
Lamb3	0,00226	0,00072	Ly6g6e	0,00127	0,00121			