On page 88 of the submitted thesis, Figure 7b indicates the mutational distribution by tumor tissue and by a typographic error on the x-axis labels was not clear as corrected below. (The error has no influence on any aspects in the thesis)
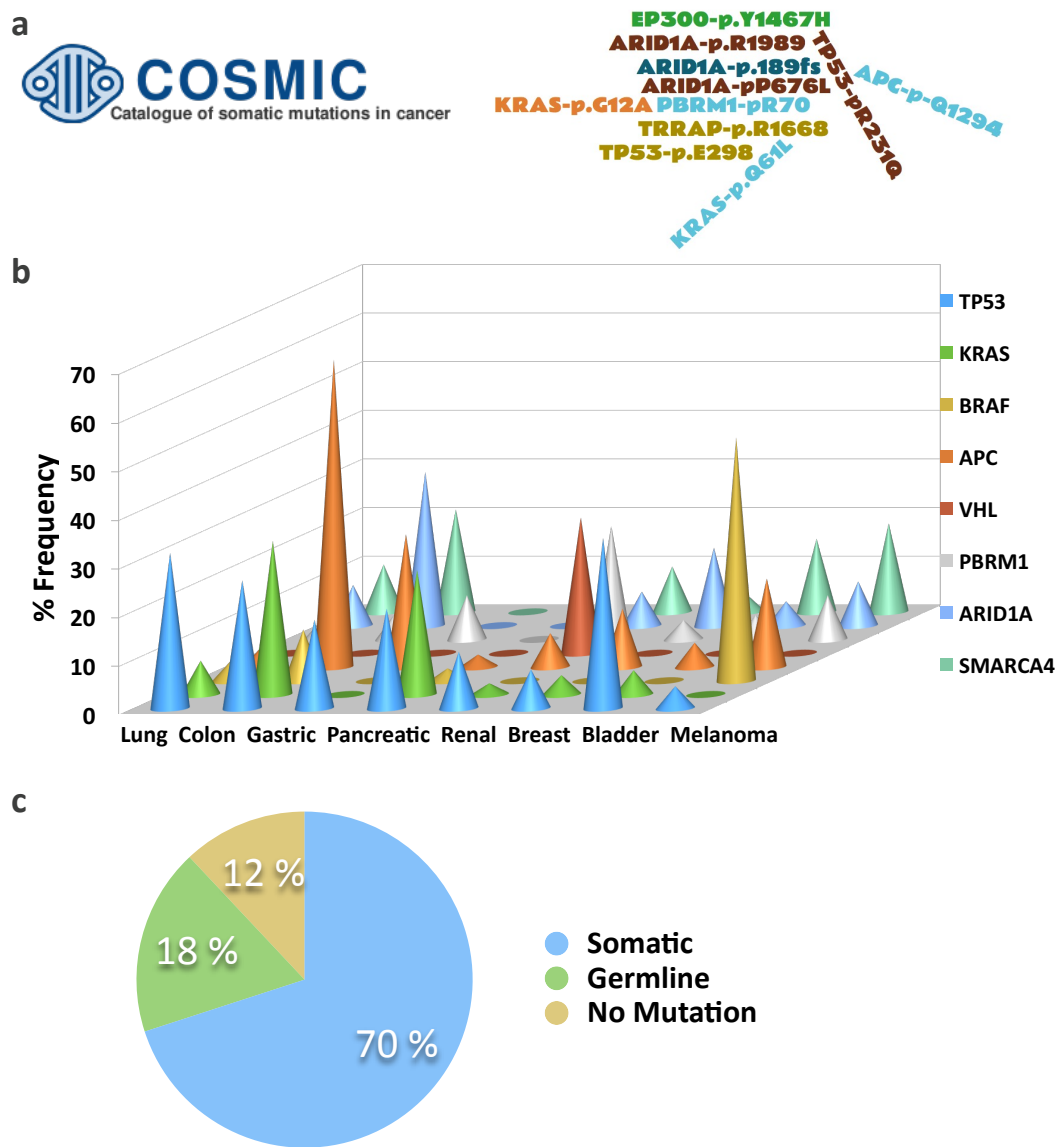

Figure 7. Sequencing/analysis strategy validation. (a) Word-cloud representing some of the identified somatic mutation already described in COSMIC database. (b) Mutated patient frequency according to the different cancer tissues of the main tumor cancer genes included in our screening. (c) Pie chart representing the distribution of results of the orthogonal validation of a random selection of identified mutations.

On page 110 of the submitted thesis, Figure 18b represents the number of cells in the lower chamber in migration and invasion assays and by an error was missed the second y-axis and labels and was not clear as the corrected below. In the new graph was calculated the migrating and invading relative number of cells, compared to the control. (The error has no influence on any conclusion in the thesis or either on the statistic significance of these experiments)
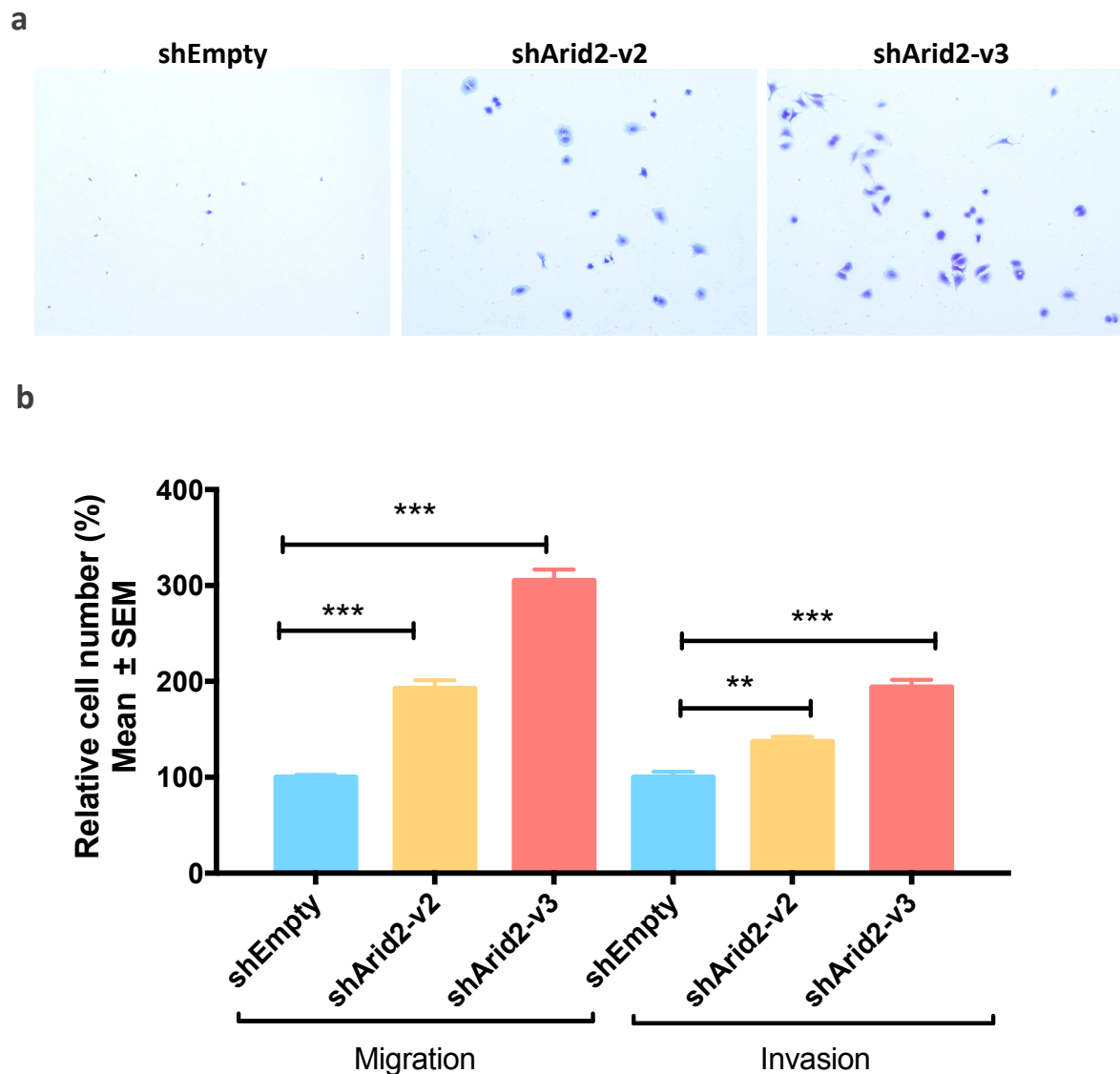

Figure 18. *In vitro* **migration and invasion assays.** (a) Representative images showing A549 cells subjected to Matrigel invasion and transwell migration that have been stained with crystal violet dye in the downer chamber. (b) Bar representation of the relative number of cells in the lower chamber in migration and invasion assays of cells transduced with either the empty vector (blue) or the different *ARID2* shRNAs (yellow and red). Data is shown as mean ± SE (standard deviation of the mean) of three independent experiments (** $p < 0.01$ and *** $p < 0.001$).