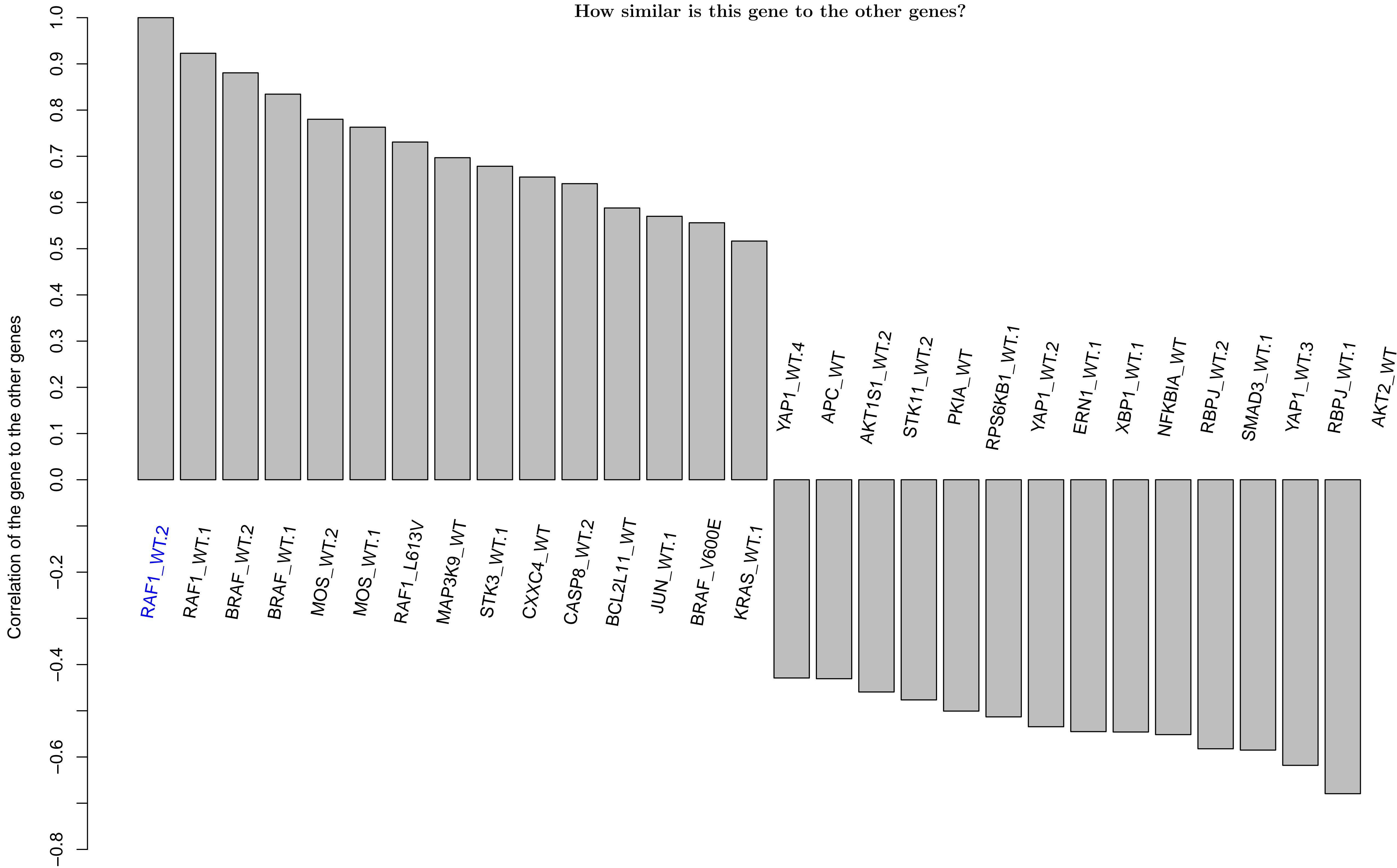
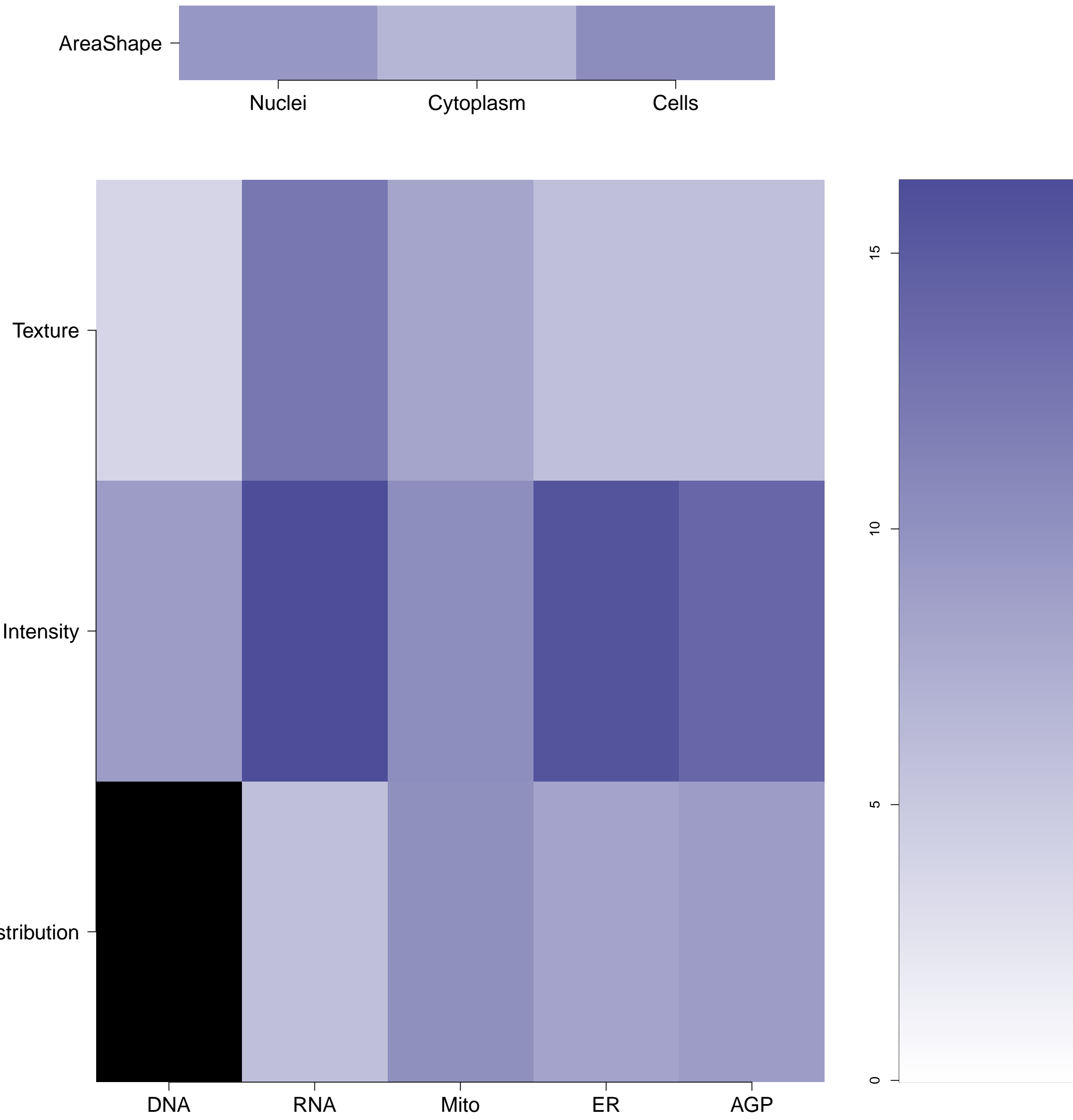


RAF1.WT.2 - in Canonical MAPK

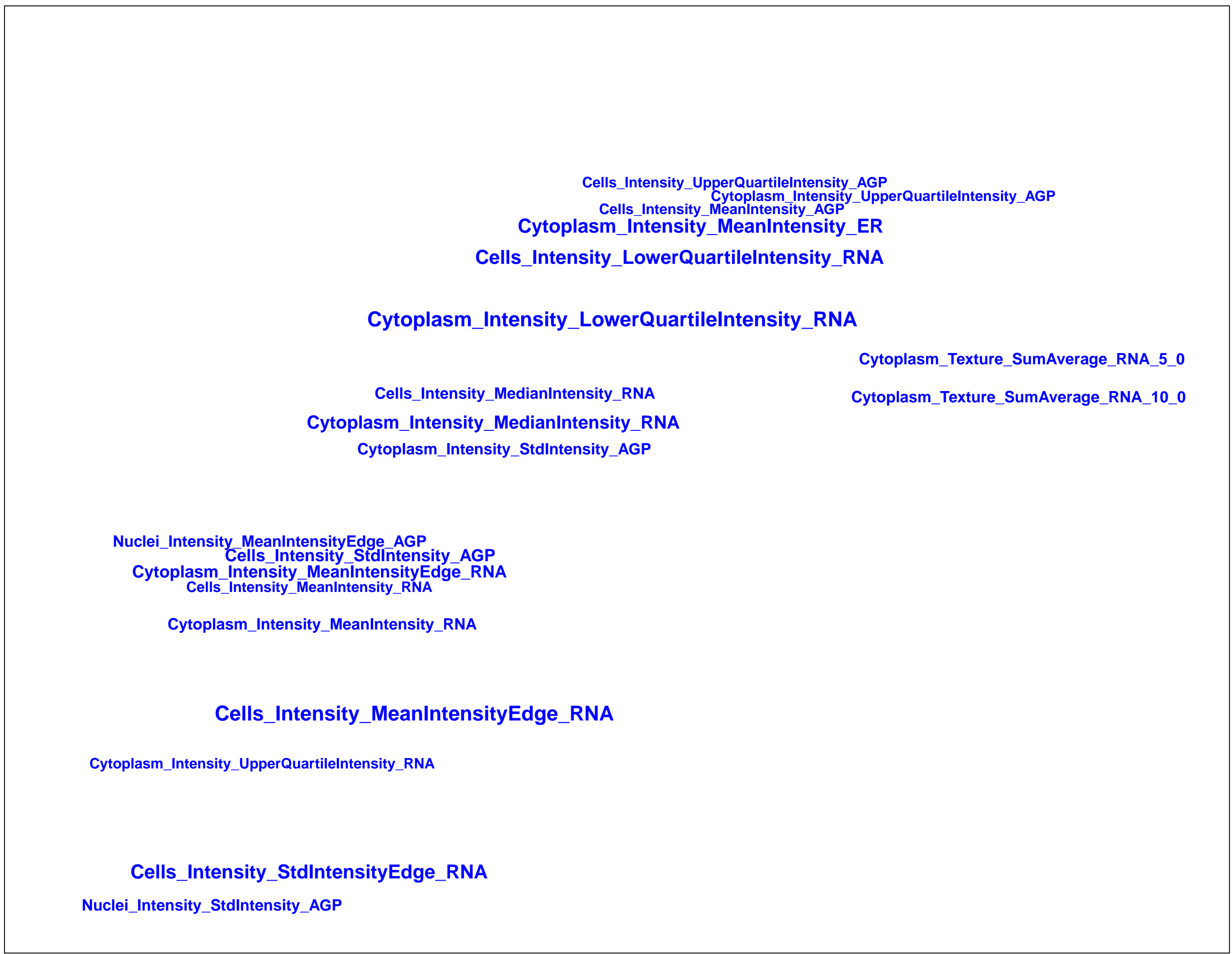
How similar is this gene to the other genes?



What groups of morphological features are distinguishing in the cluster relative to the untreated samples?
(maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the category



Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.



Empty

RAF1.WT.2 (41744)

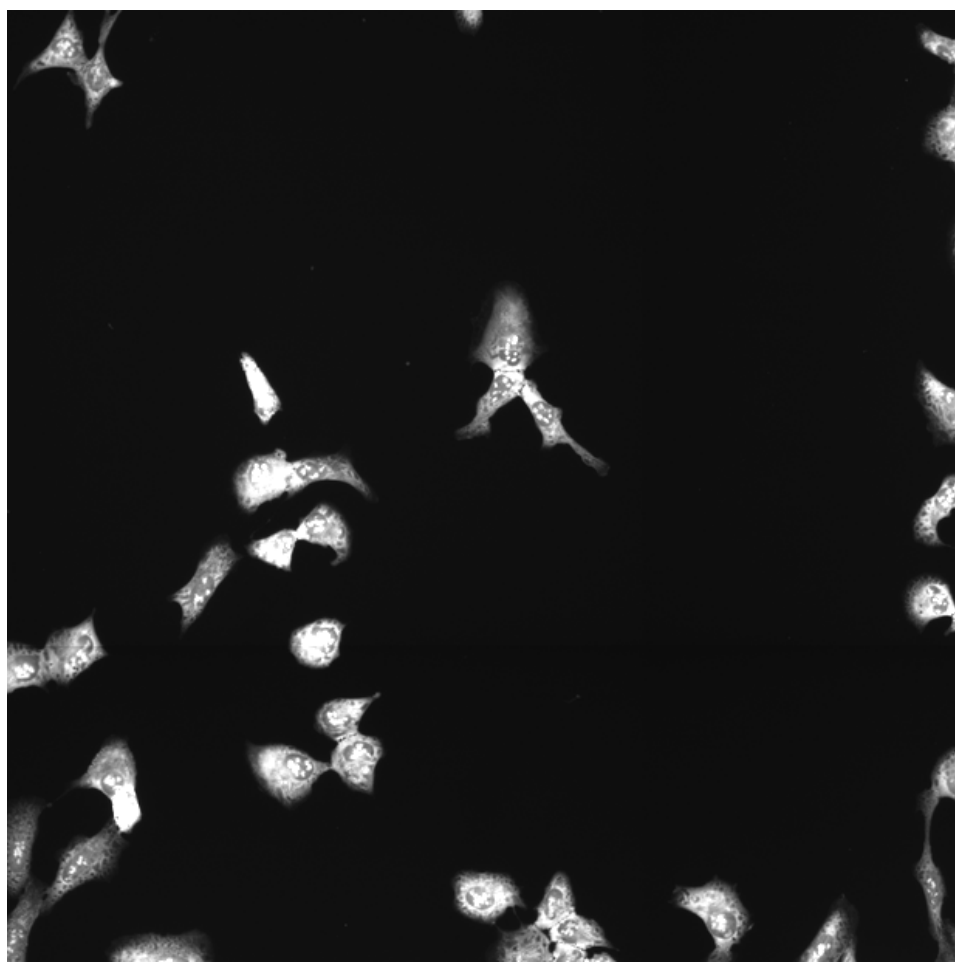
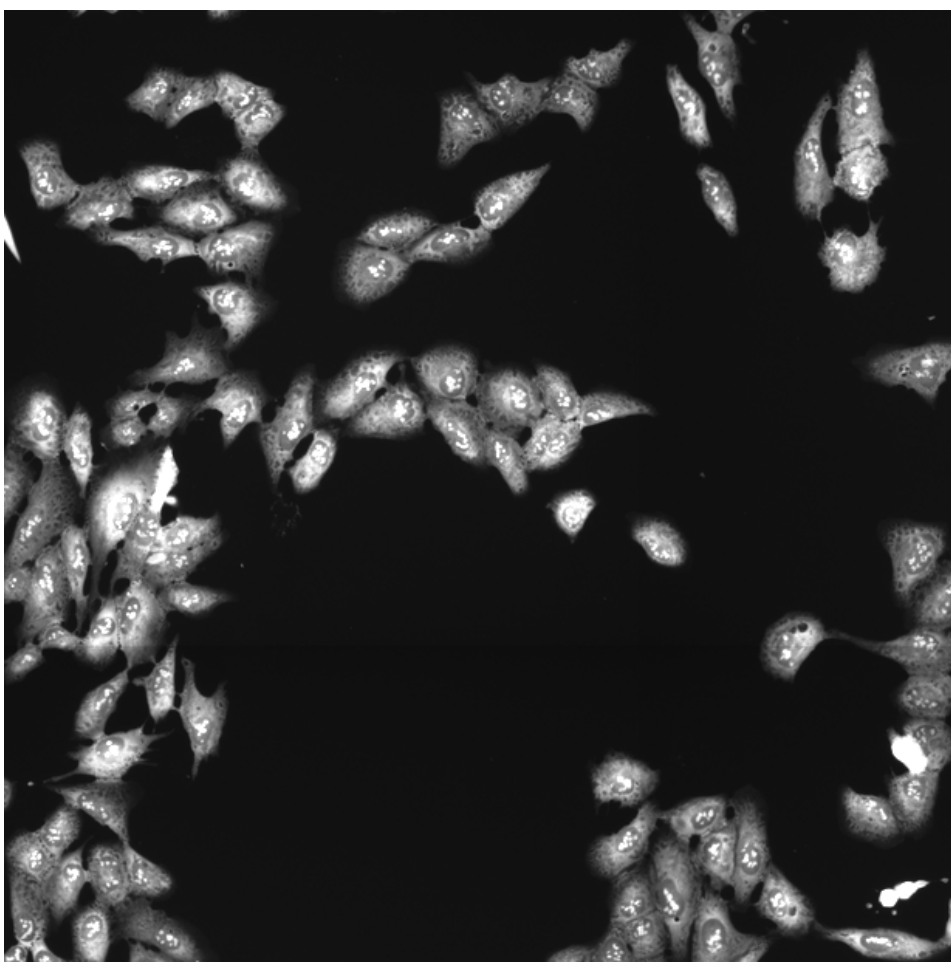
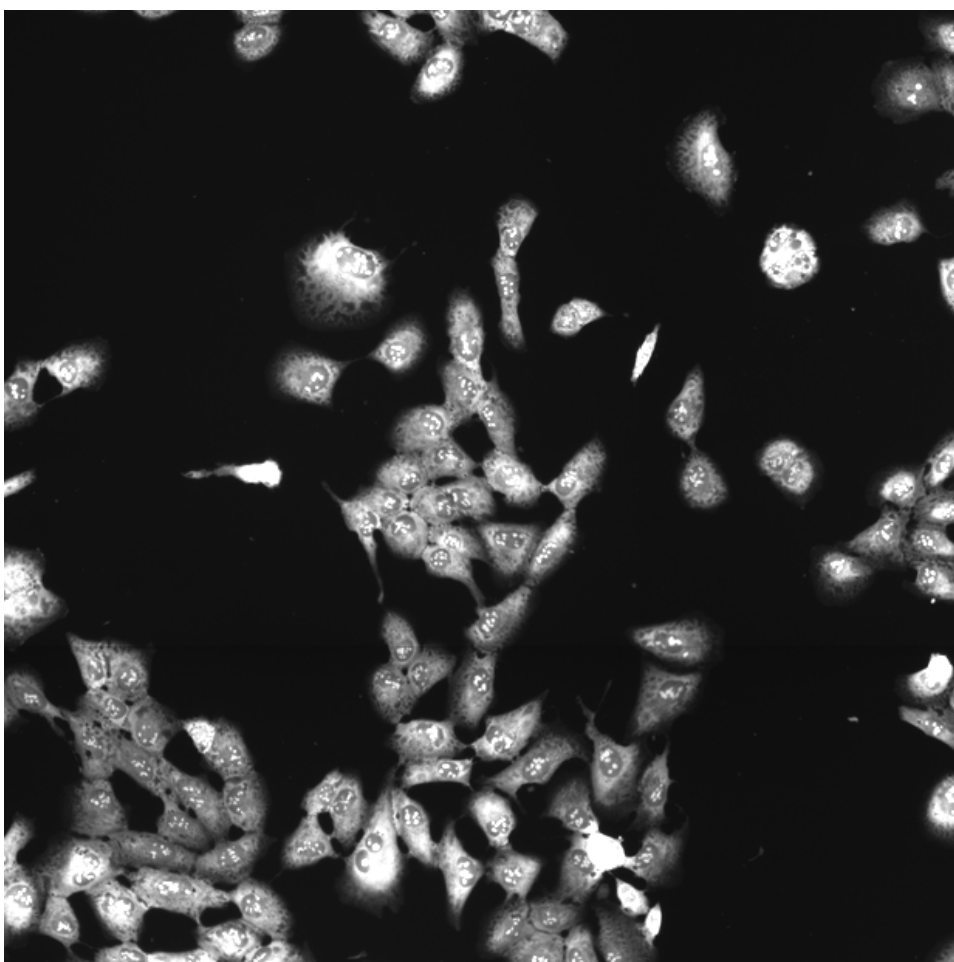
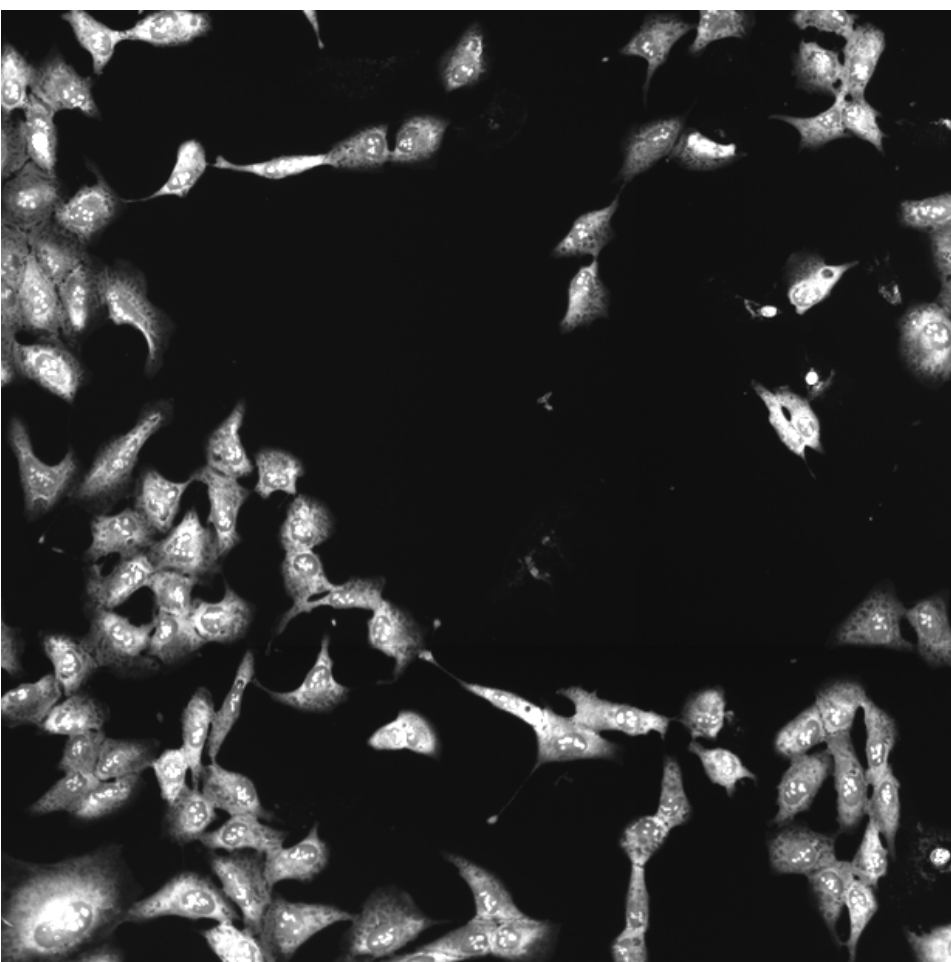
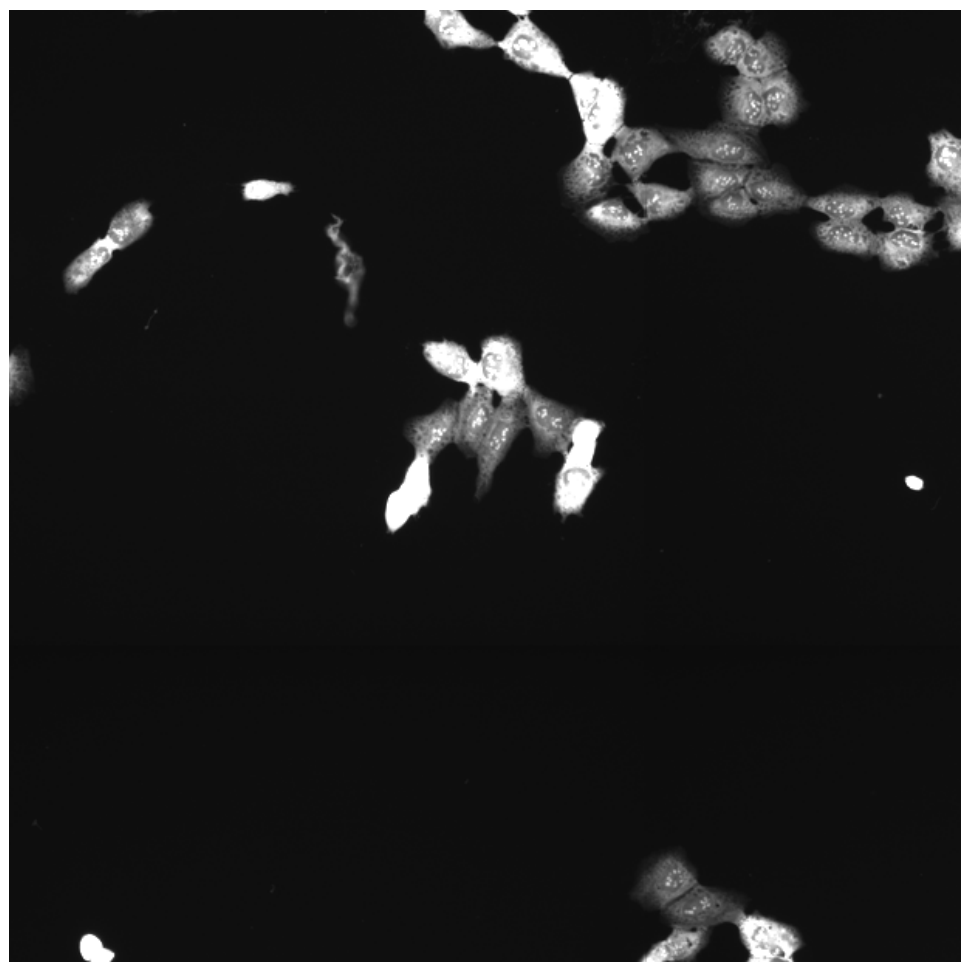
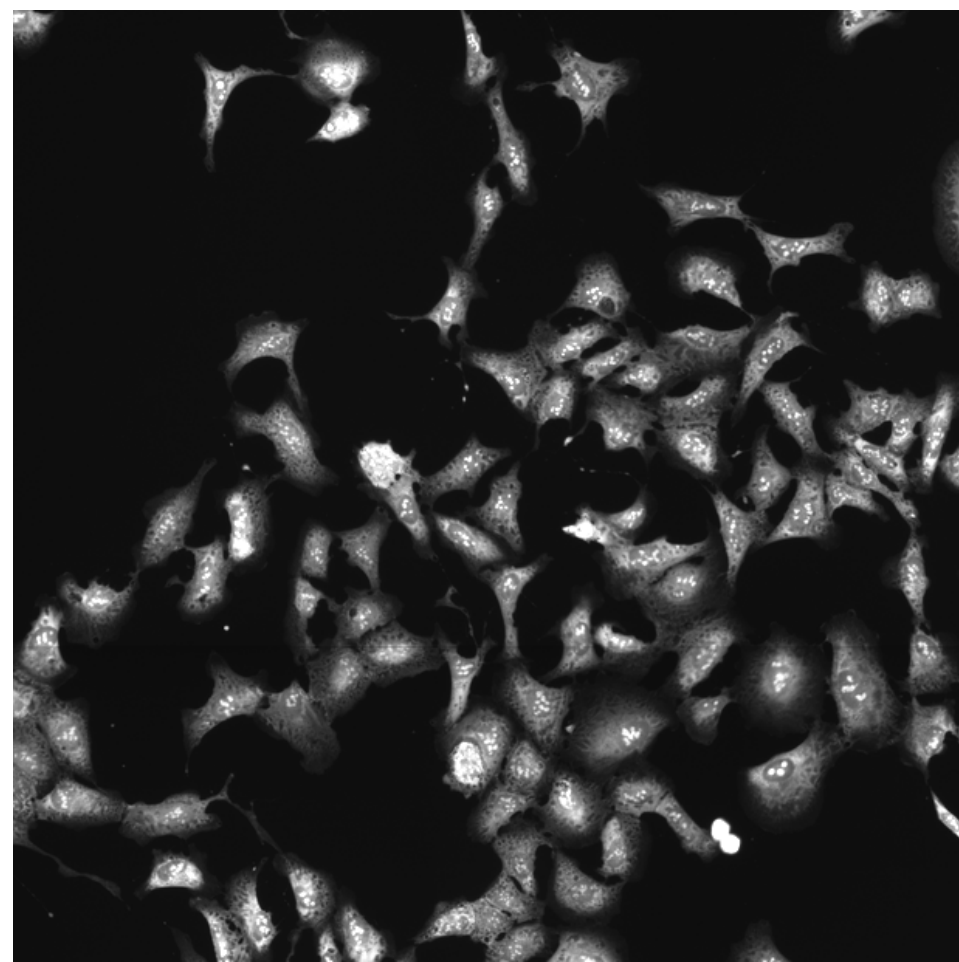
RAF1.WT.2 (41755)

RAF1.WT.2 (41756)

RAF1.WT.2 (41757)

RAF1.WT.2 (41754)

RNA



ER

