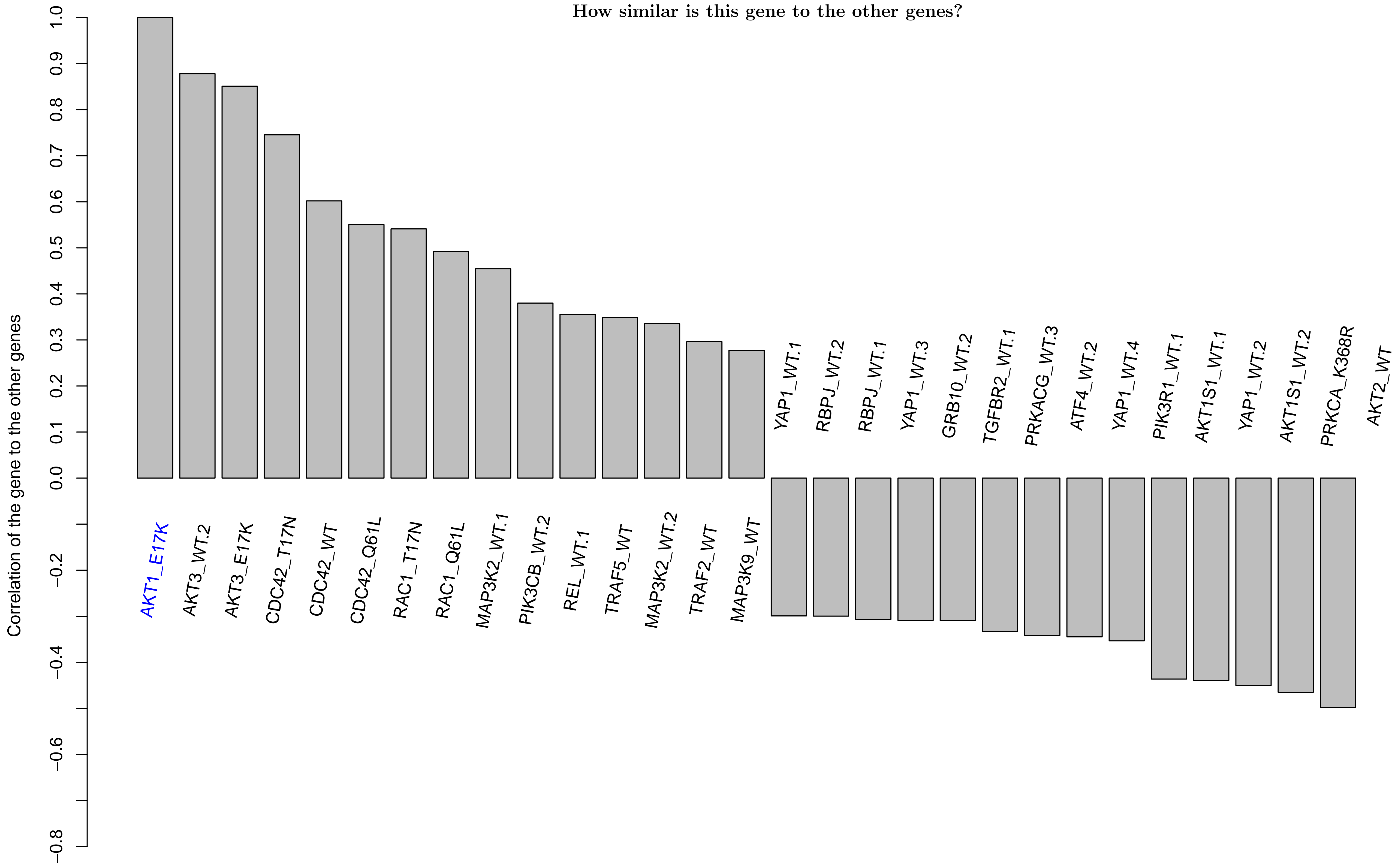
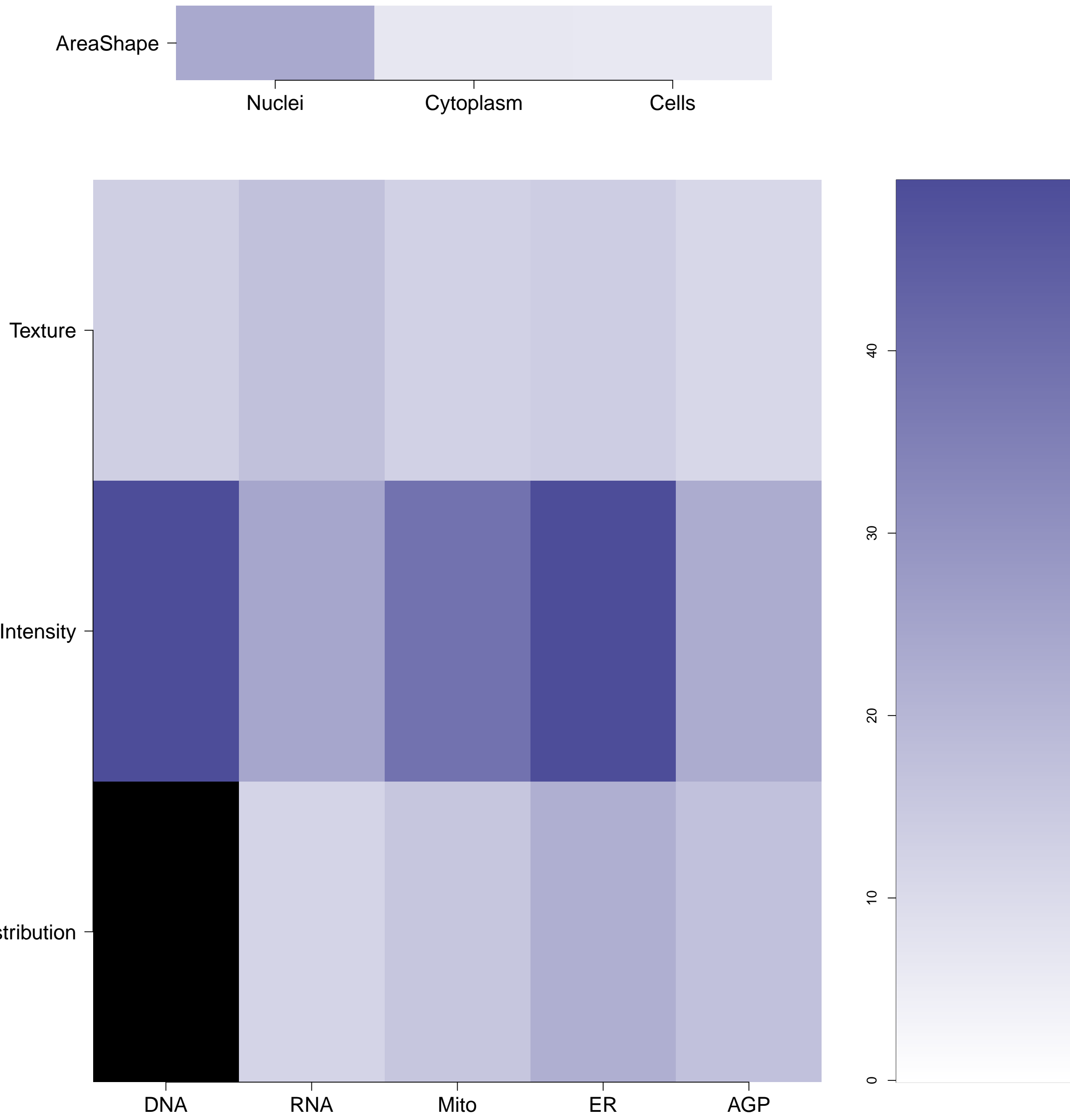


AKT1.E17K - in Canonical PI3K/AKT

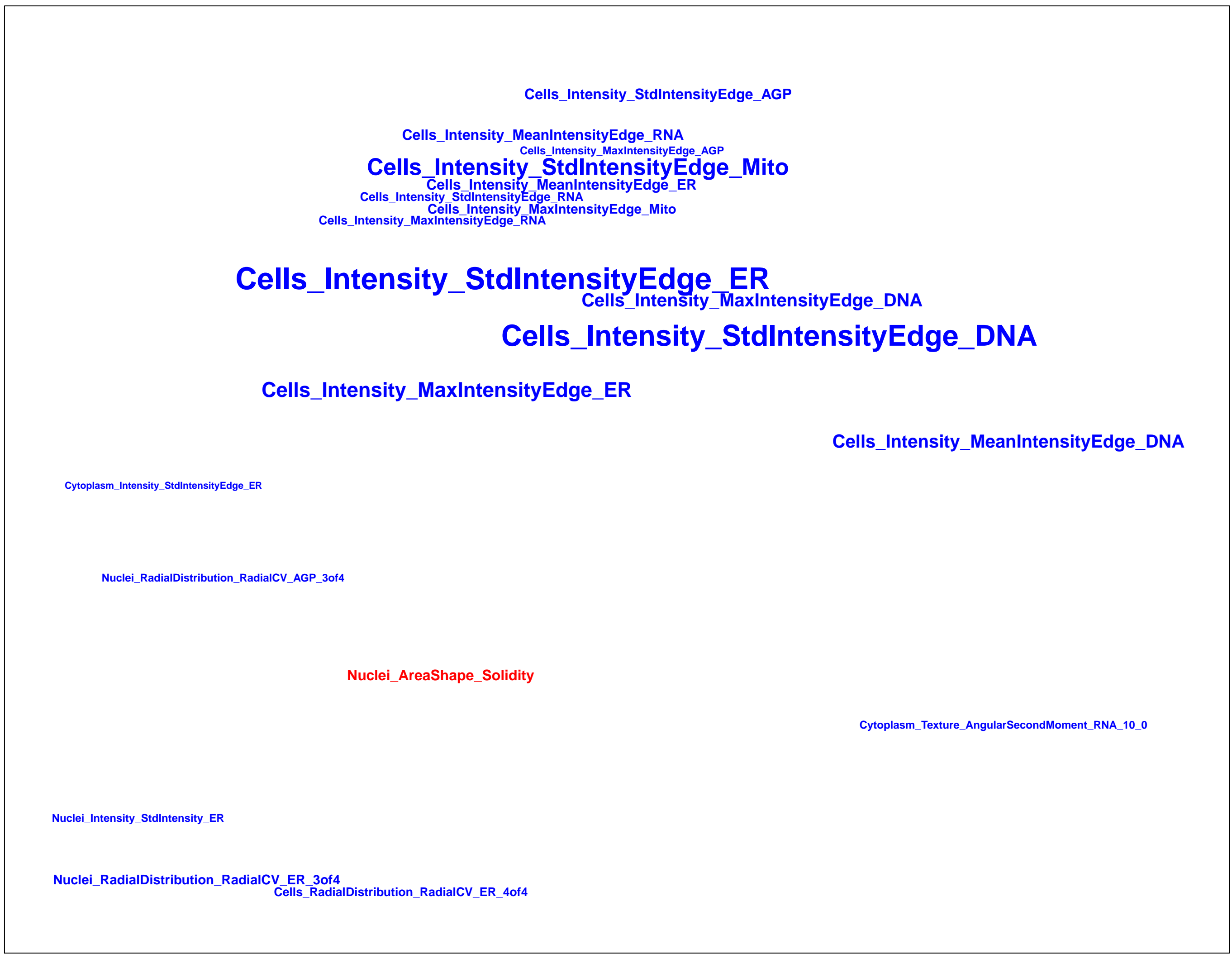
How similar is this gene to the other genes?



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

AKT1.E17K (41744)

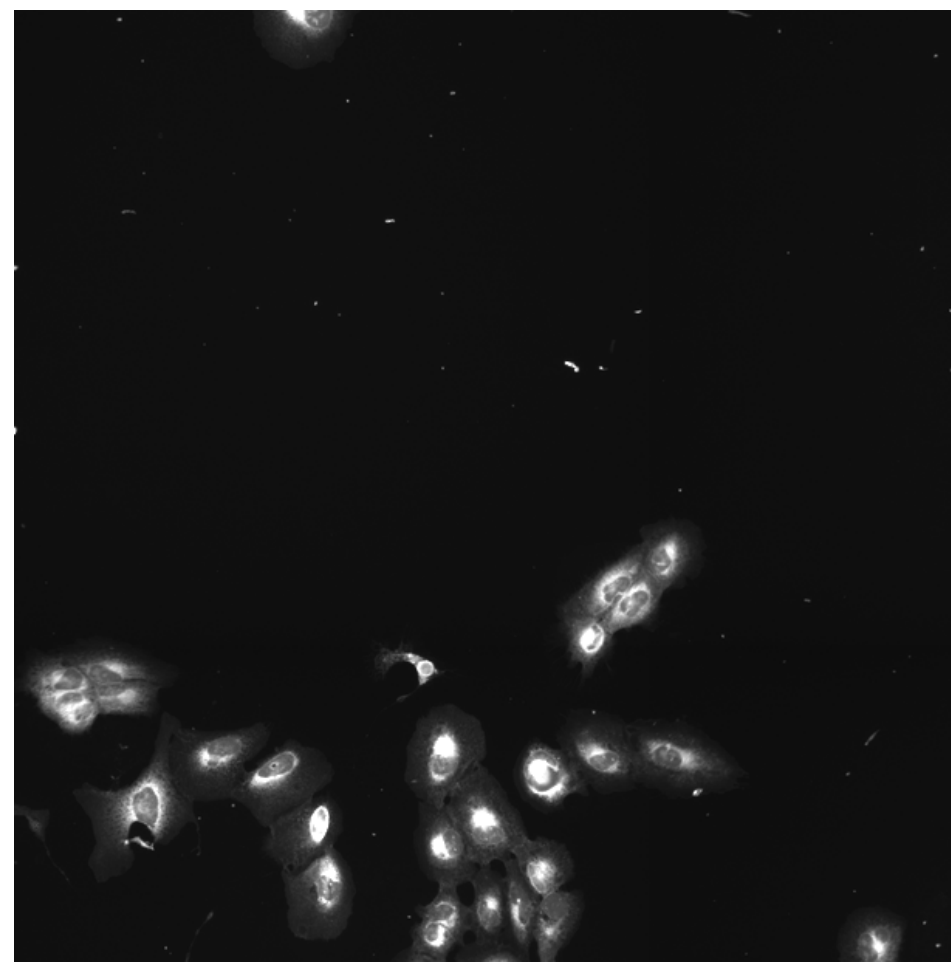
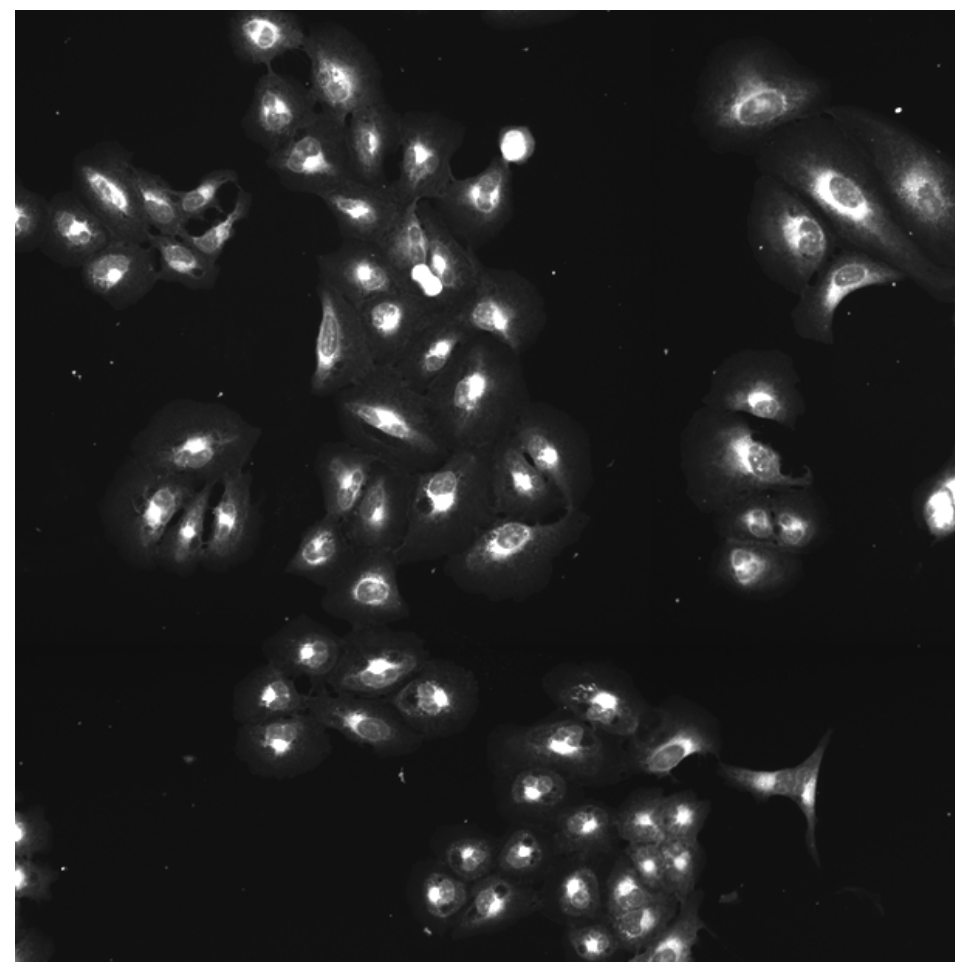
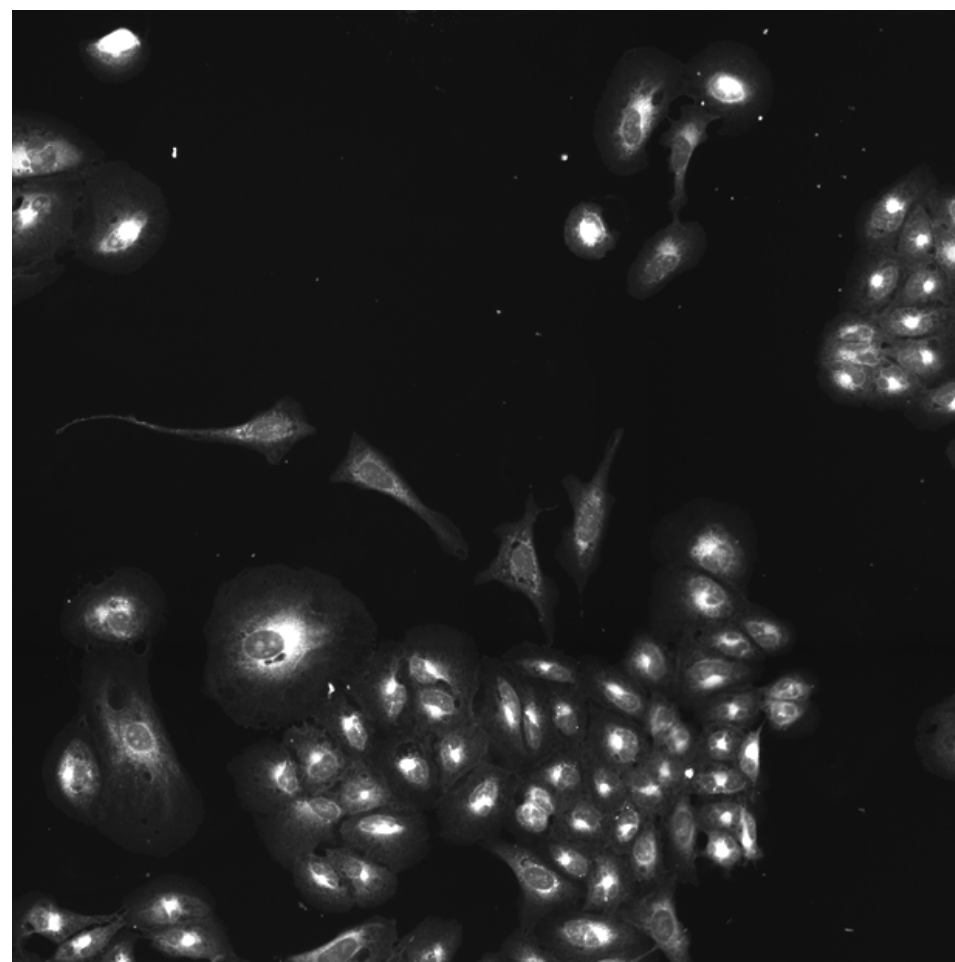
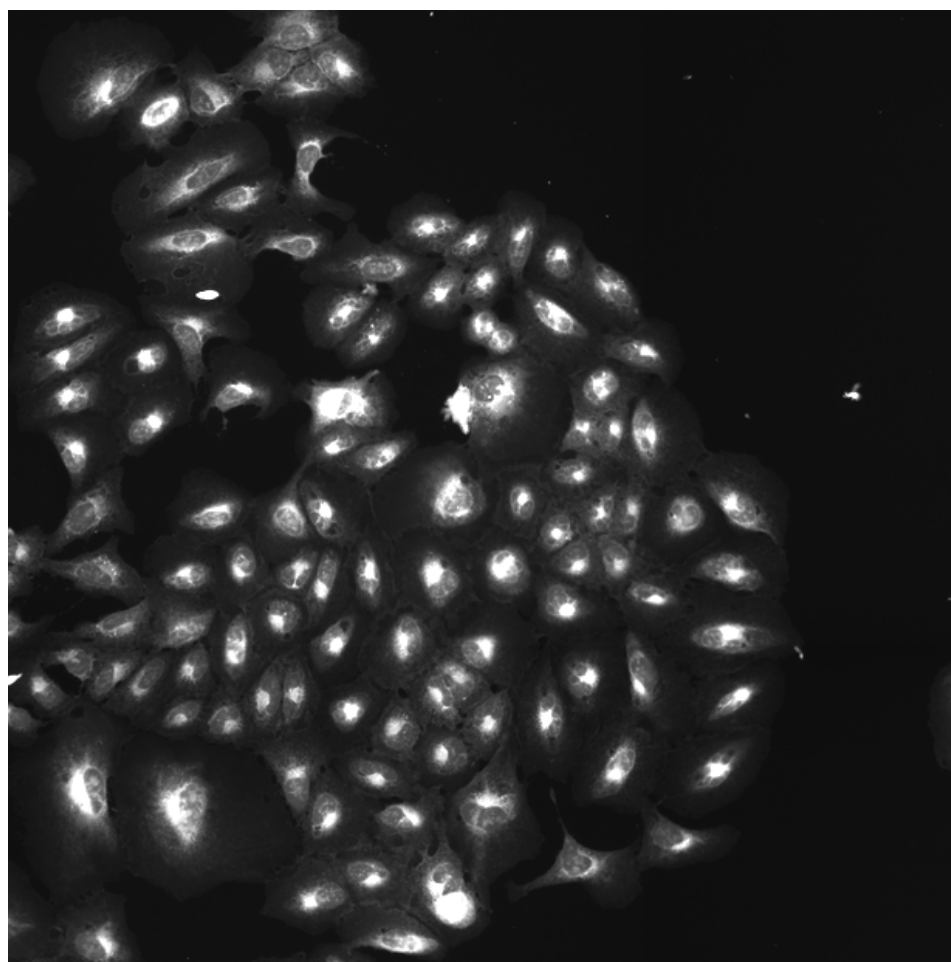
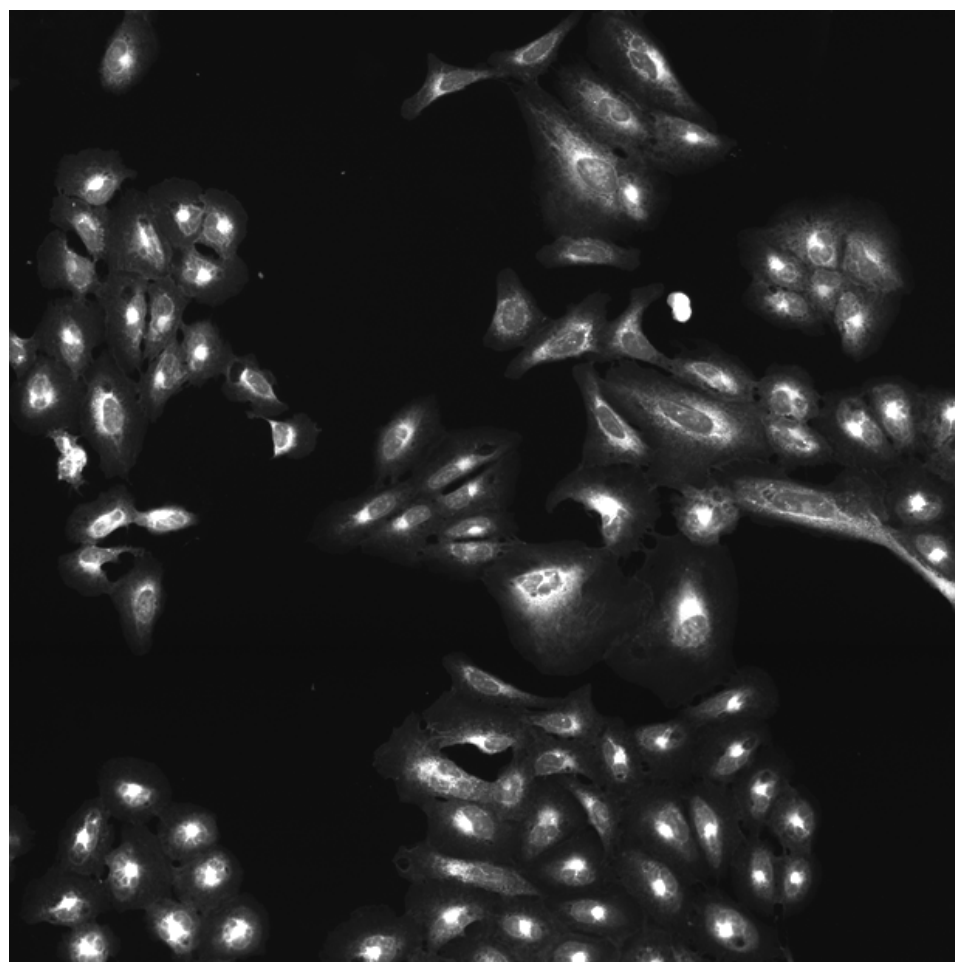
AKT1.E17K (41755)

AKT1.E17K (41756)

AKT1.E17K (41757)

AKT1.E17K (41754)

ER



DNA

