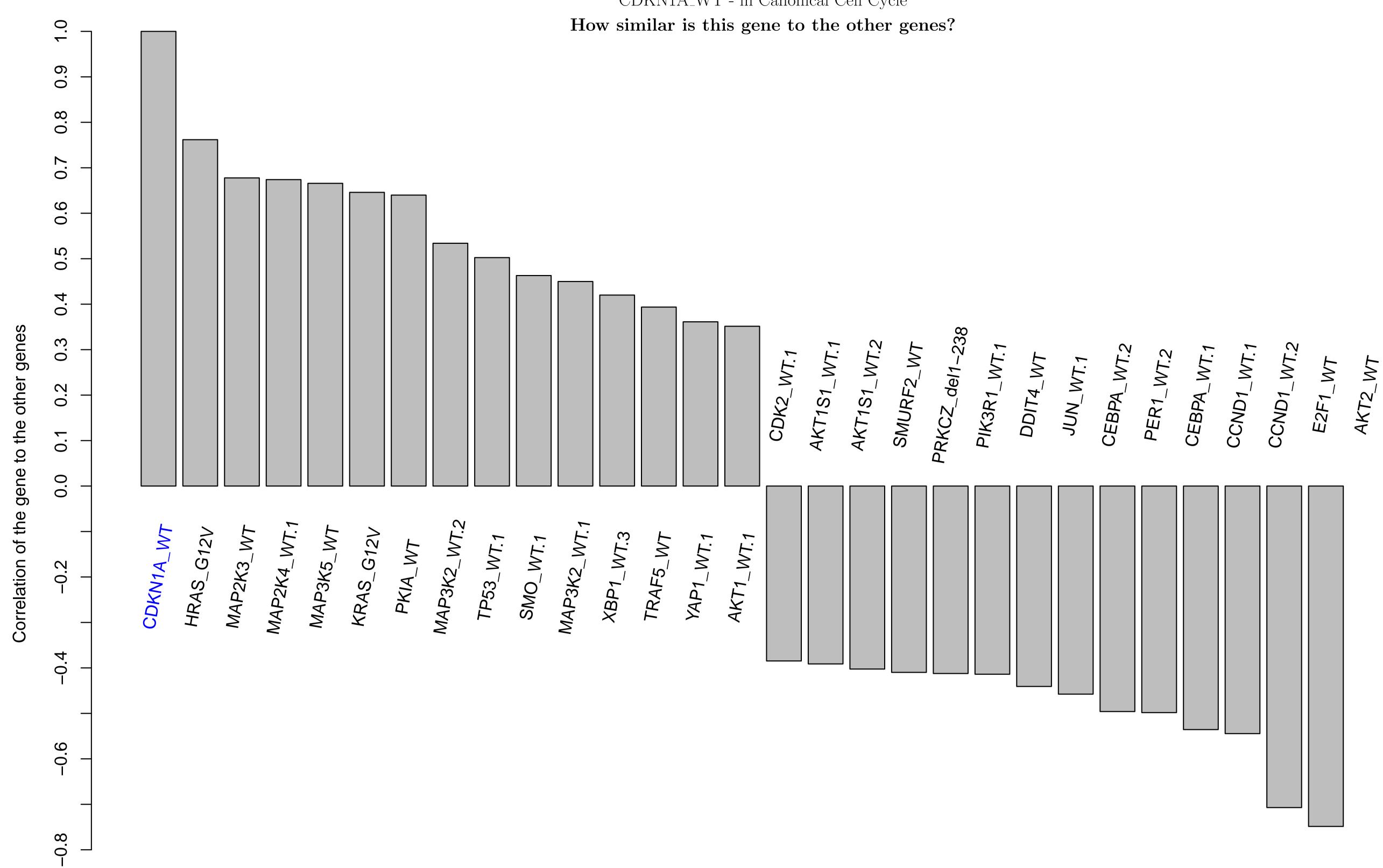
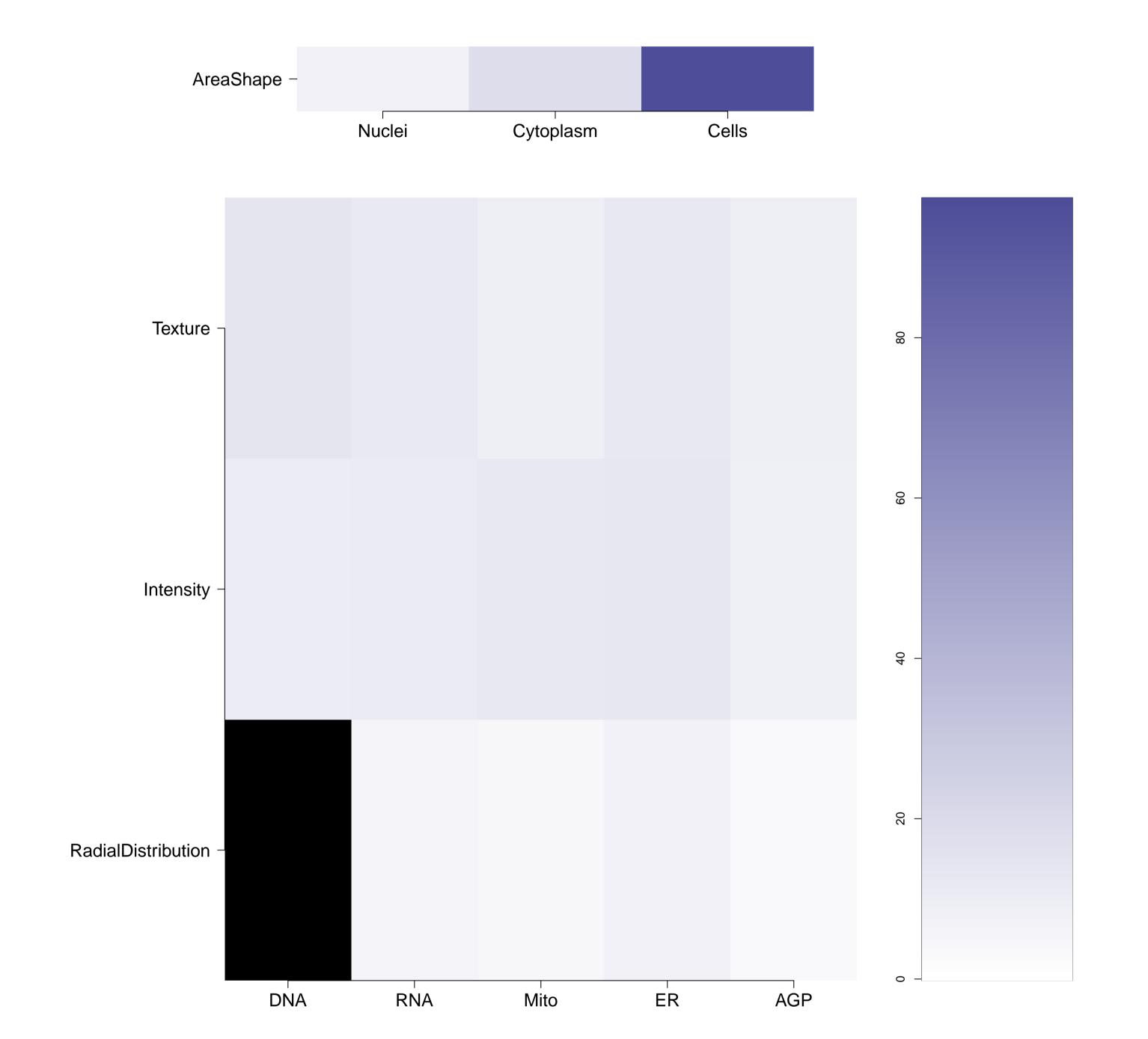
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein CDKN1A_WT - in Canonical Cell Cycle



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



box means the matching

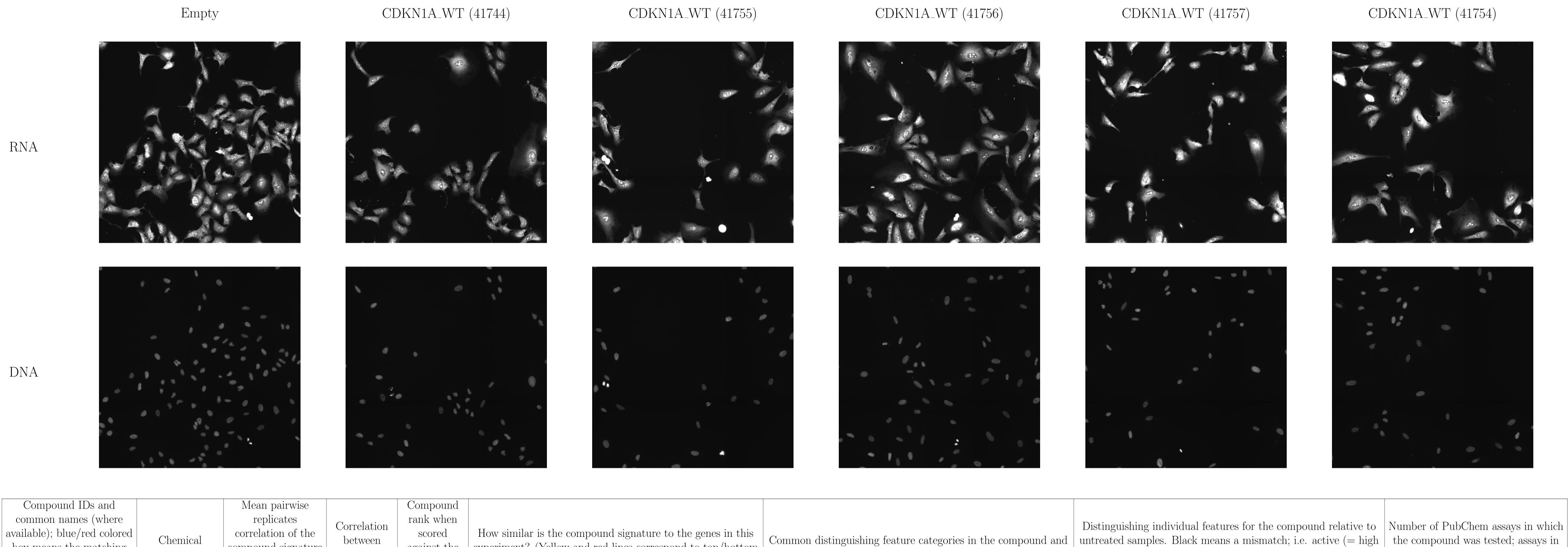
compound is

positively/negatively

correlated with the cluster

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.





the gene relative to the untreated samples

z-score in magnitude) in the compound, and either inactive (=

small z-score in magnitude) or oppositely active in the gene

which the compound was active are

itemized

experiment? (Yellow and red lines correspond to top/bottom

1st and 5th percentile DMSO correlation to all the genes)

against the

gene using

L1000

profiling

compound

the gene

compound signature

(95th DMSO

replicate correlation

is 0.52)

structure

