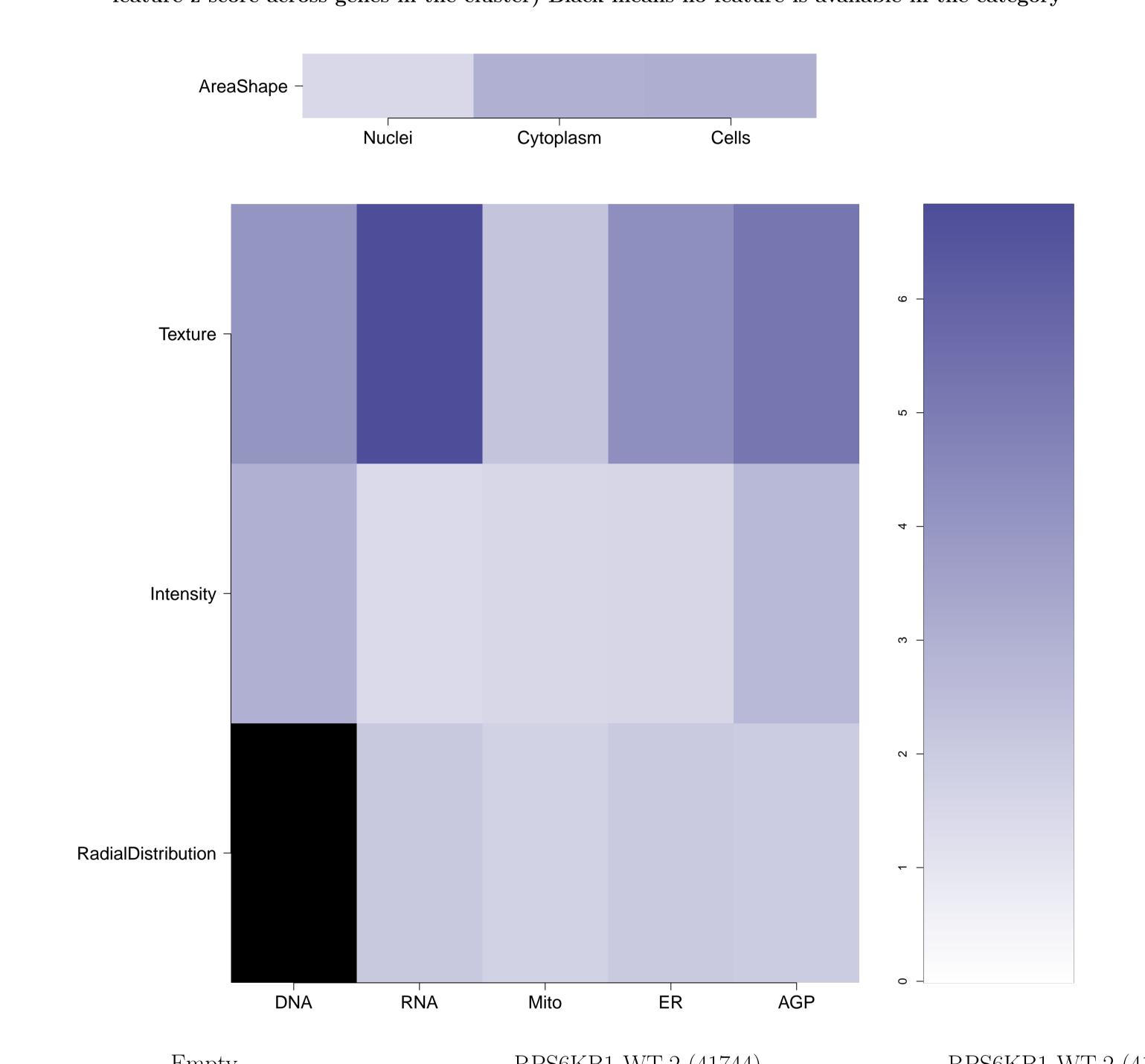
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein RPS6KB1\_WT.2 - in Canonical TOR How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes TGFBR1\_WT.2 0.3 MAPKAP1\_WT CEBPA\_WT.2 SMURF2\_WT CASP8\_WT.1 CEBPA\_WT.1 PER1\_WT.2 XBP1\_WT.2 CDK2\_WT.2 PRKCZ\_del1\_ 0.0 AKT3\_WT.3
STK3\_WT.2
SMO\_WT.1
JAG1\_WT
JAG1\_WT
JAG1\_WT
MAP3K2\_WT.1
MAP3K2\_WT.1
MAPK8\_WT.1
MAPK8\_WT.1
MAPK8\_WT.1 KRAS\_WT.1 MAP3K5\_WT

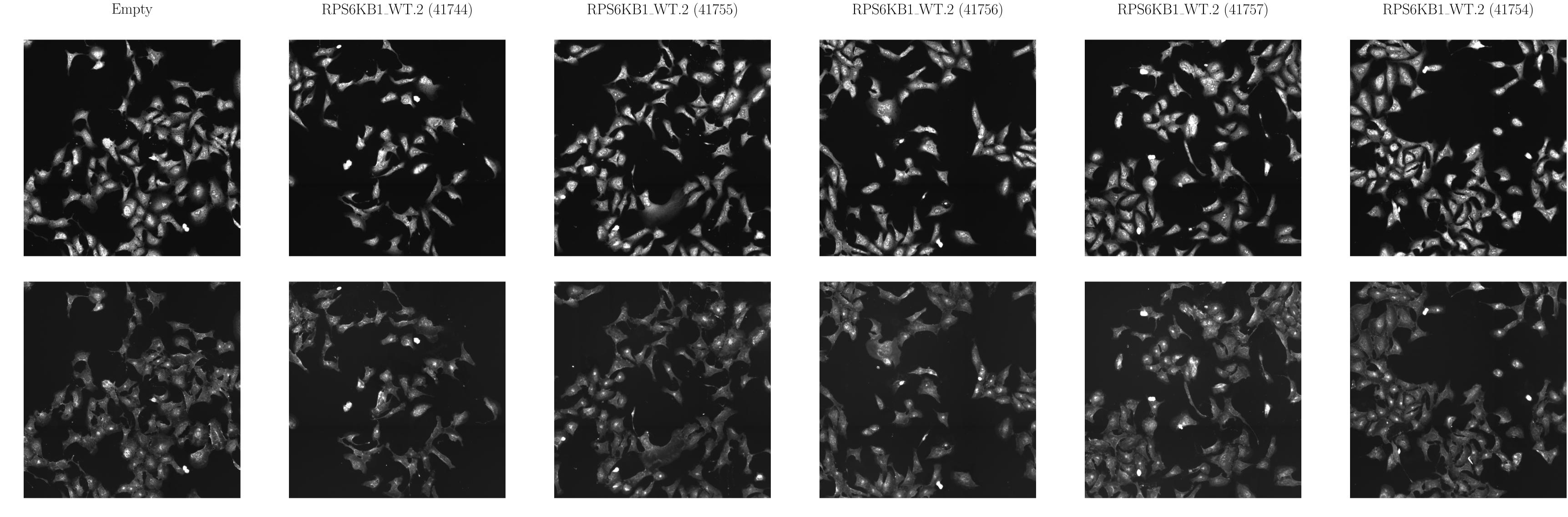
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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

0.4



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.





Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.51)	Correlation between compound the gene	against the	How similar is the compound signature to the genes in this experiment? (Yellow and red lines correspond to top/bottom 1st and 5th percentile DMSO correlation to all the genes)	Common distinguishing feature categories in the compound and the gene relative to the untreated samples	Distinguishing individual features for the compound relative to untreated samples. Black means a mismatch; i.e. active (= high z-score in magnitude) in the compound, and either inactive (= small z-score in magnitude) or oppositely active in the gene	the compound was tested; assays in
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