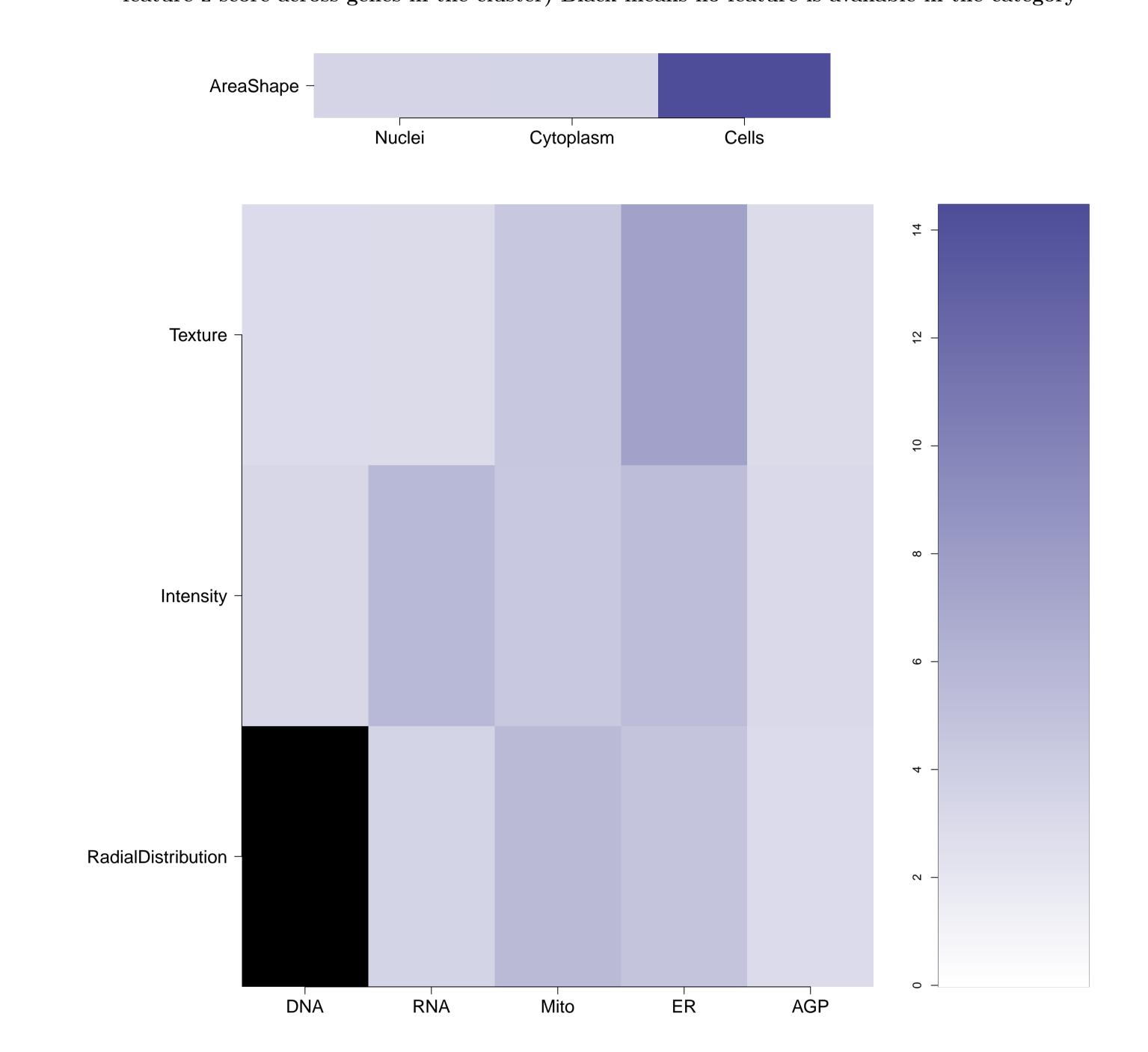
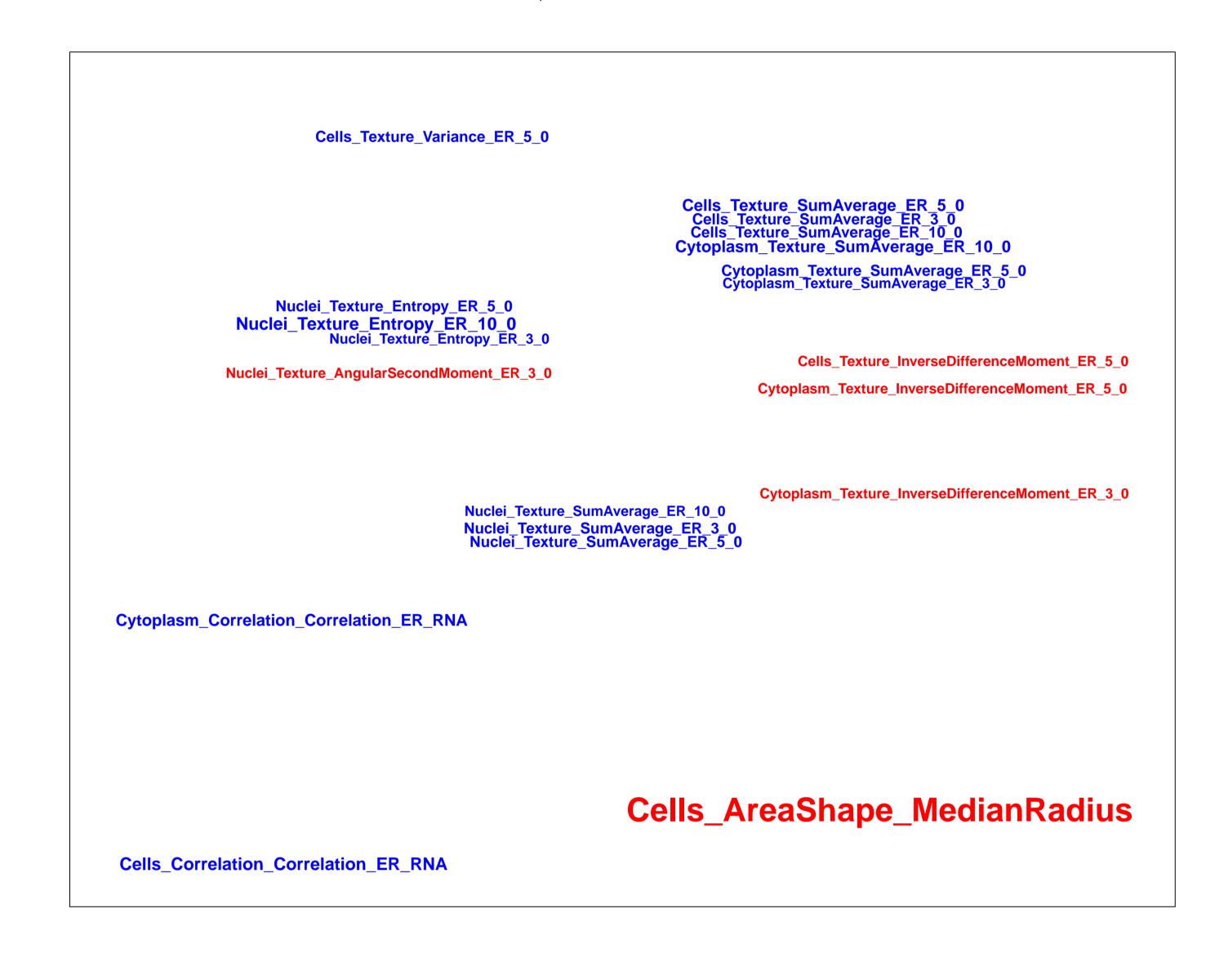
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein DIABLO\_WT - in Canonical Apoptosis How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes CSNK1A1\_WT.3 MYD88\_L265P TGFBR1\_WT.2 0.3 PRKCZ\_WT.2 MAPK1\_WT.2 PIK3R1\_WT.1 PRKCZ\_WT.1 NFKB1\_WT.1 PER1\_WT.2 MYD88\_WT DVL3\_WT 0.0 STK11\_WT.1
DDIT3\_WT.2
PRKACA\_WT.1
GLI1\_WT
GLI1\_WT
KRAS\_G12V
KRAS\_G12V
CASP8\_WT.1 PRKACG\_WT.3 XBP1\_WT.3 SMO\_WT.1

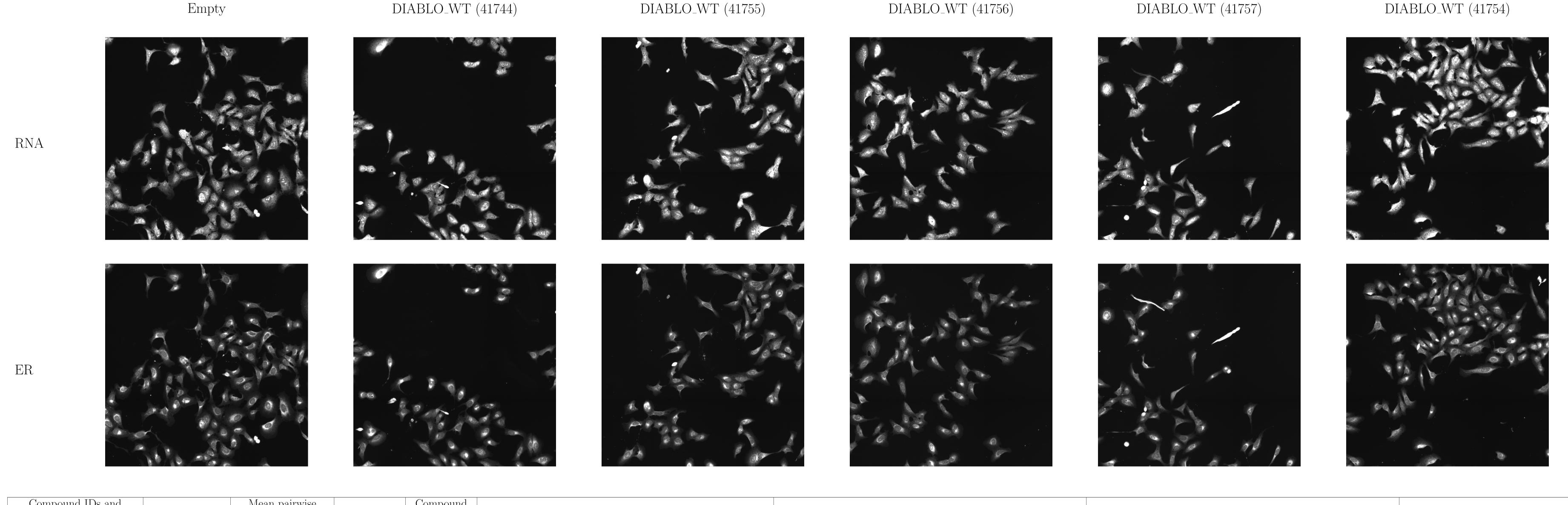
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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



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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		Mean pairwise		Compound				
common names (where available); blue/red colored		replicates correlation of the	ce Correlation between aga	rank when scored	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	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 itemized	
box means the matching compound is		compound signature (95th DMSO		against the gene using				
positively/negatively correlated with the cluster		replicate correlation is 0.51)	the gene	L1000 profiling			sman z-score in magnitude) of oppositely active in the gene	nemzea

