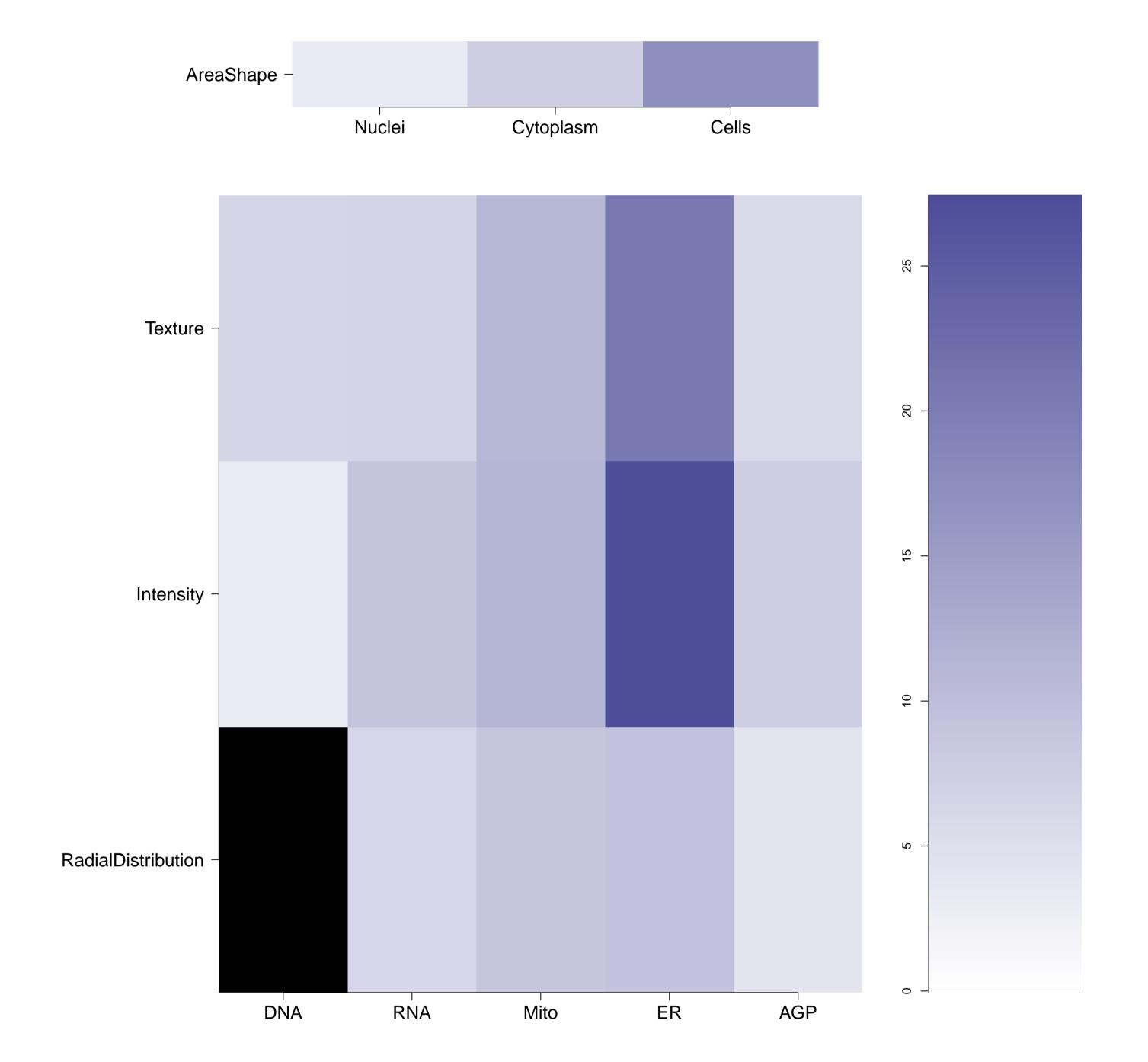
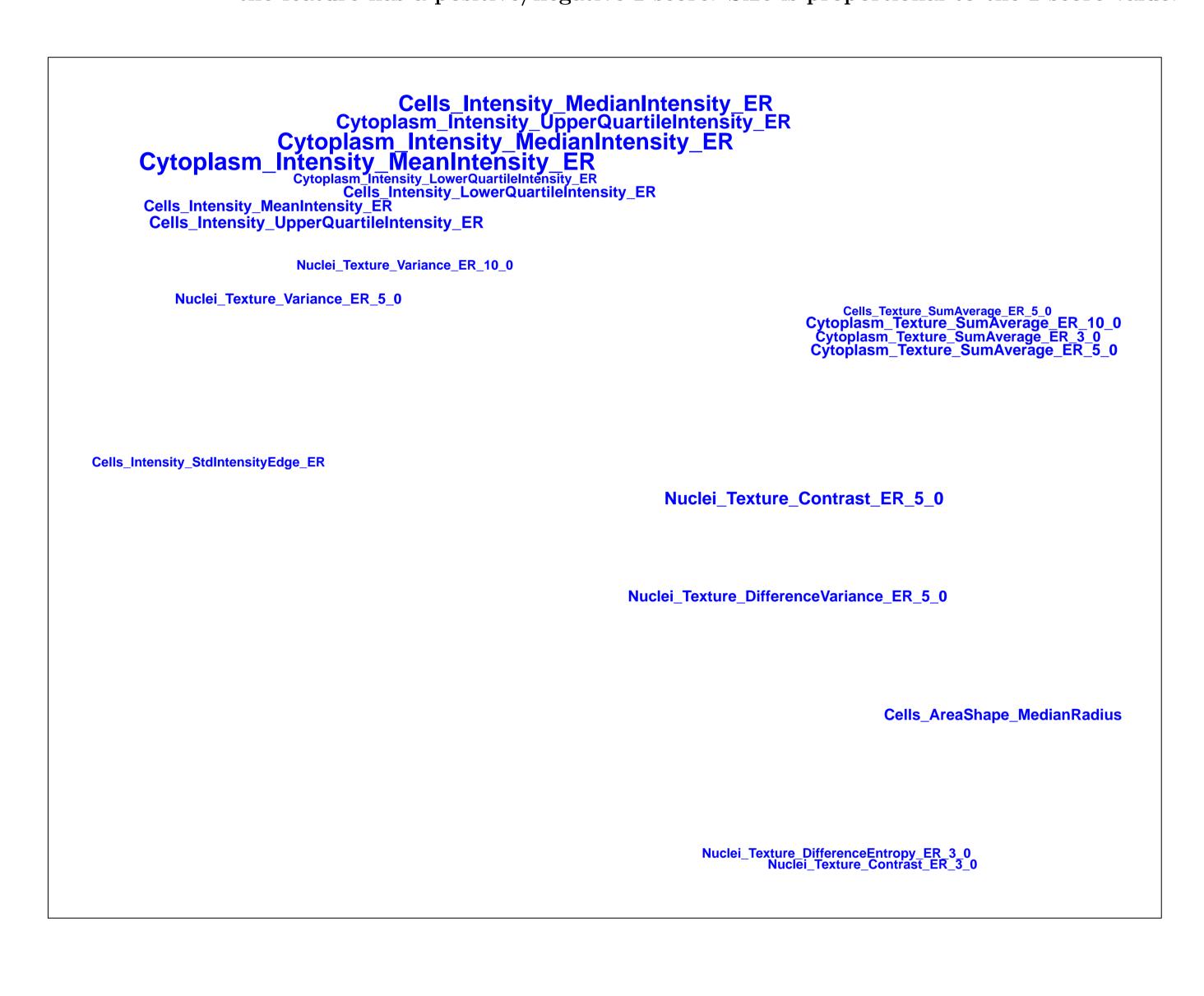
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein XBP1\_WT.3 - in Canonical ER Stress/UPR How similar is this gene to the other genes? 0.9 0.5 0.4 Correlation of the gene to the other genes TGFBR1\_K232R CSNK1E\_WT.2 TGFBR1\_WT.2 MYD88\_L265P 0.3 GRB10\_WT.2 GSK3B\_WT.1 MAP3K7\_WT AKT3\_WT.3 CASP9\_WT DDIT4\_WT E2F1\_WT 0.0 TGFB1\_WT
XBP1\_WT1
SMO\_WT.1
SMO\_WT.1
KRAS\_G12V
PKIA\_WT
HRAS\_G12V
DDIT3\_WT.2 BRAF\_V600E XBP1\_WT.2 CDKN1A\_WT ATF6\_WT.2

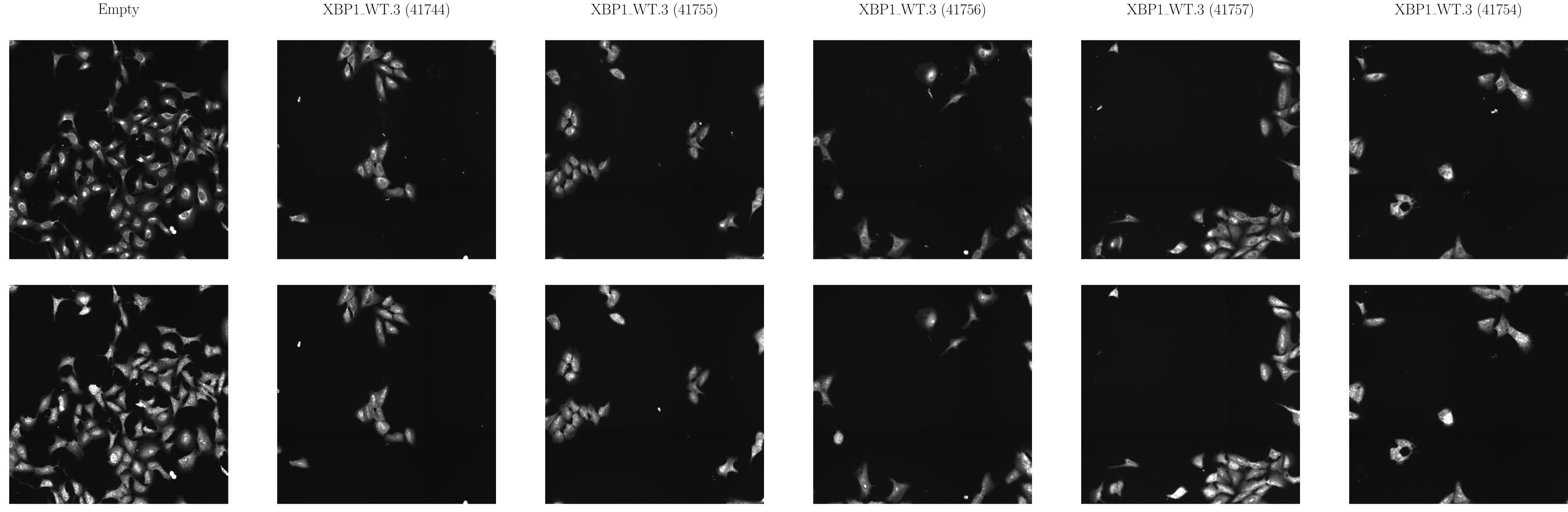
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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



RNA

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.





			I	T			
Compound IDs and		Mean pairwise		Compound			
common names (where	Chemical structure	replicates	between compound	rank when	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  Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized
available); blue/red colored		correlation of the		scored			
box means the matching		compound signature		against the			
compound is		(95th DMSO		gene using			
positively/negatively		replicate correlation	the gene	L1000			
correlated with the cluster		is 0.51)		profiling			

