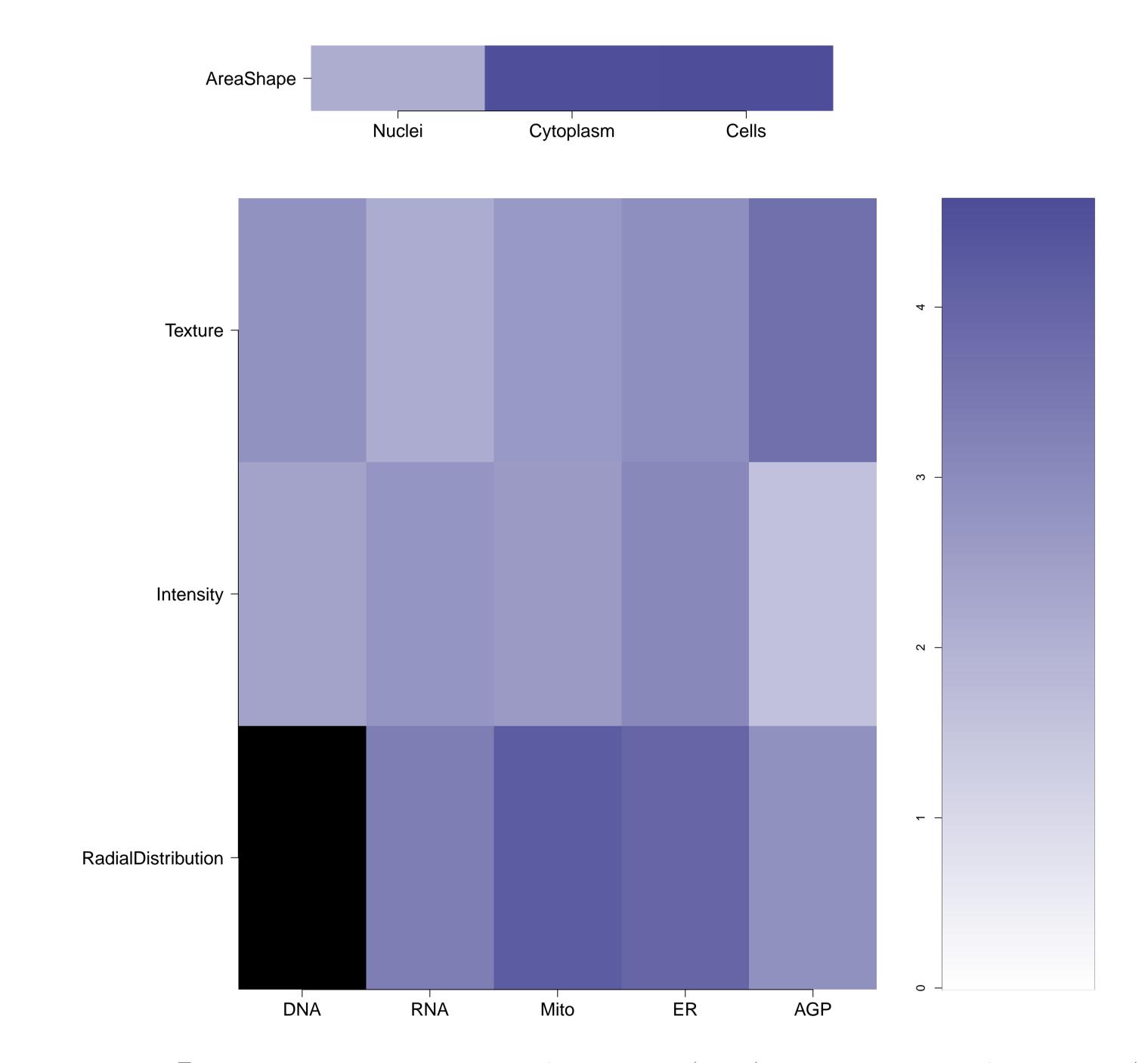
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein GRB10\_WT.2 - in Canonical Insulin Receptor Signaling How similar is this gene to the other genes? 0.9 0.5 0.4 Correlation of the gene to the other genes 0.3 PIK3CB\_WT.2 MAP2K4\_WT.1 CDKN1A\_WT HRAS\_G12V AKT3\_E17K MAP2K3\_WT AKT3\_WT.2 TRAF5\_WT MAP3K7\_I CSNK1E\_ 0.0 AKT1S1\_WT.2
AKT1S1\_WT.1
PRKCE\_WT.2
CCND1\_WT.2
CCND1\_WT.1
E2F1\_WT
E2F1\_WT
CCND1\_WT.1
PRKCZ\_K281R
PIK3R1\_WT.1
NFKB1\_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

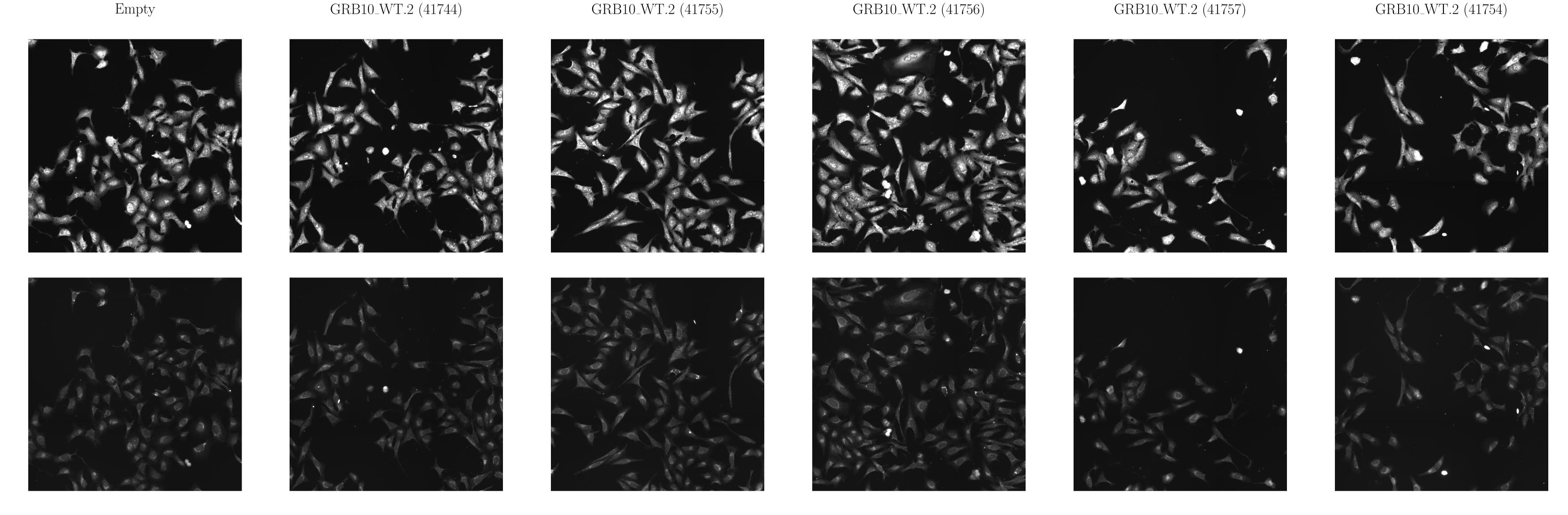


RNA

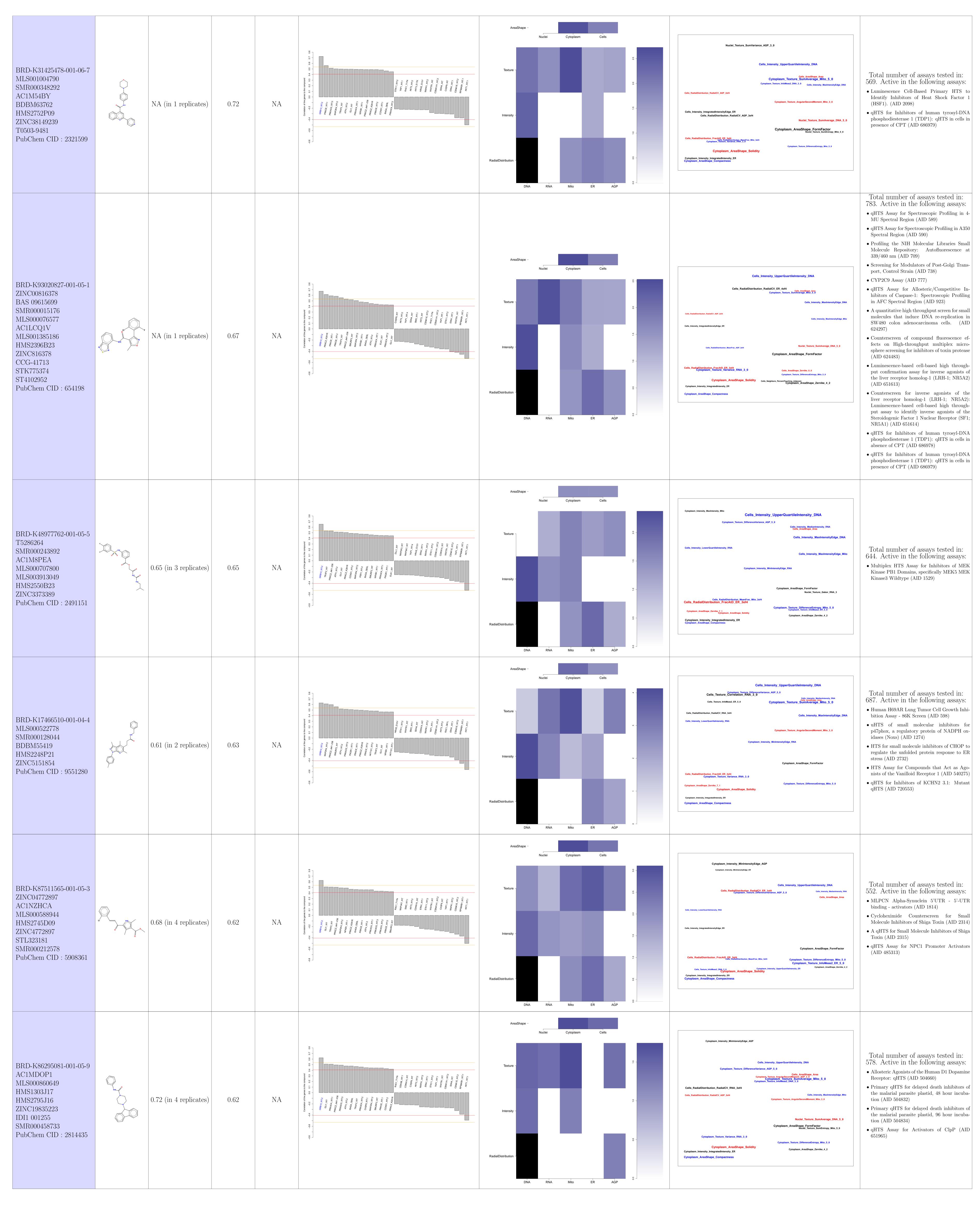
Mito

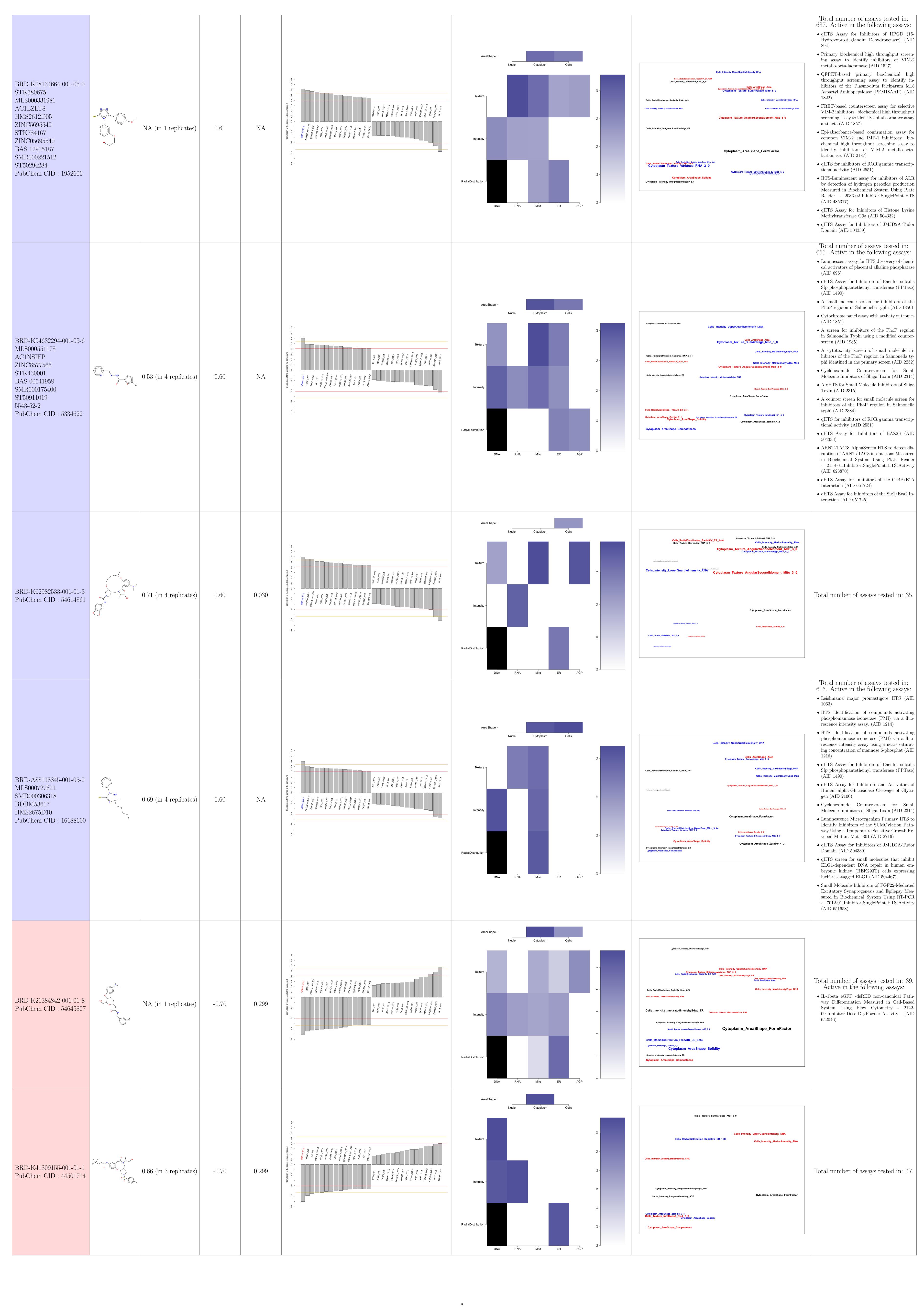
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

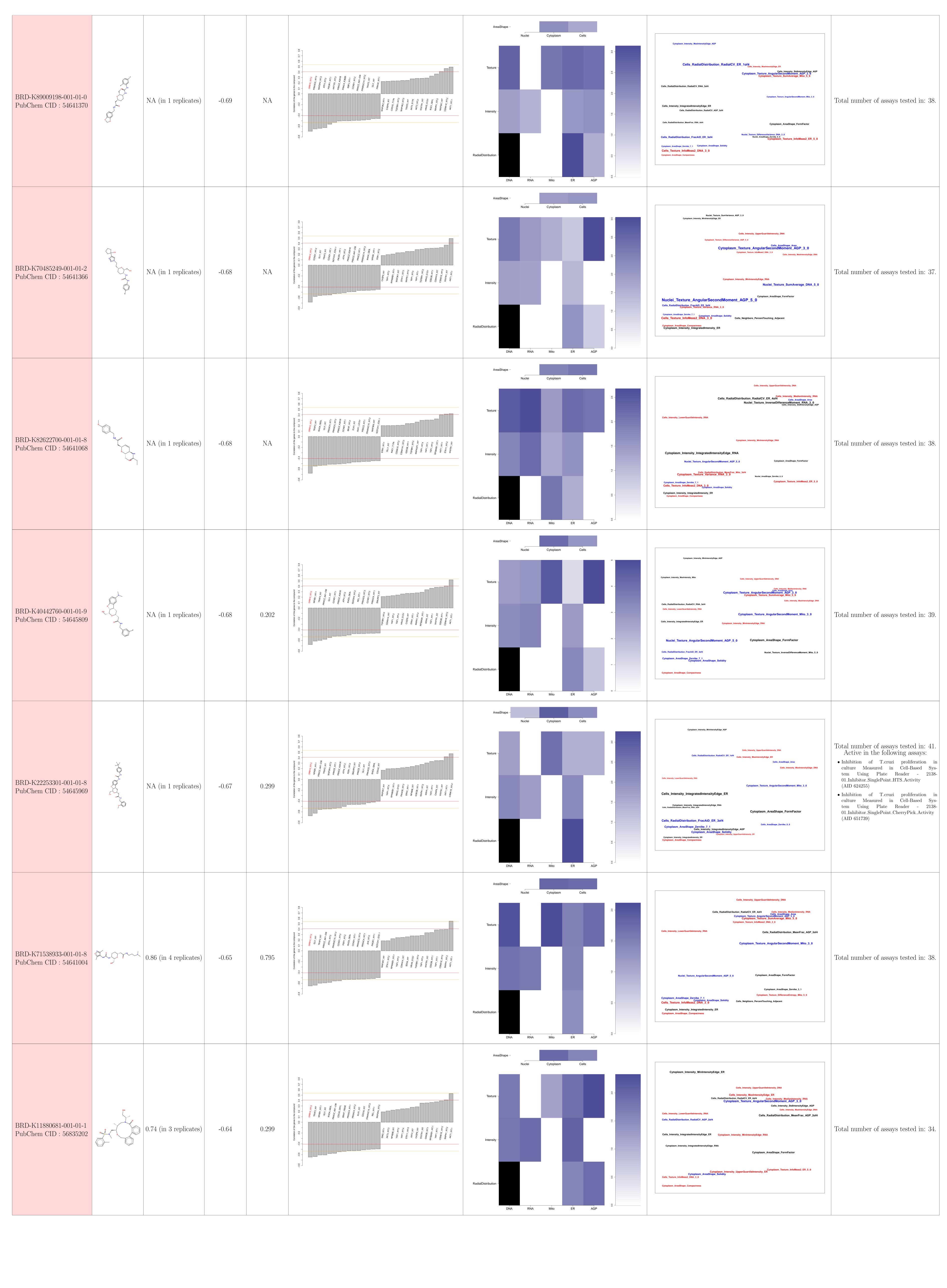




Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation	Correlation between compound the gene	gene using L1000	How similar 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	the compound was tested; assays in
correlated with the cluster		is 0.52)		profiling				







AreaShape -Cytoplasm Total number of assays tested in: 798. Active in the following assays: Cytoplasm\_Intensity\_MinIntensityEdge\_ER • Screening for Inhibitors of the Mevalonate Pathway in Streptococcus Pneumoniae - DPM-DC (AID 556) BRD-K84896953-001-04-4 Texture -Radial Distribution Radial CV\_ER\_10f4 Cytoplasm\_Texture\_Difference Variance\_AGP\_5\_0 Cells\_Intensity\_MedianIntensity\_RNA

Cytoplasm\_Texture\_Angular Second Moment\_AGP\_3\_0 SMR000094347 • HTS for small molecule inhibitors of CHOP to MLS000117397 regulate the unfolded protein response to ER stress (AID 2732) AC1NSFUV Cells\_Intensity\_LowerQuartileIntensity\_RNA Cells\_RadialDistribution\_RadialCV\_AGP\_2of4 TRAFS\_WT
ERN1\_WT.1
MAPK1\_WT.2
CDC42\_T17N
YAP1\_WT.1
STK11\_WT.2
HRAS\_G12V
AKT3\_E17K
WWTR1\_WT
CASP9\_WT
RAC1\_G61L
AKT3\_WT.2
RPSGKB1\_WT.1
CSNK1E\_WT.2
AKT1\_WT.1 0.77 (in 4 replicates) • Luminescence-based primary cell-based high -0.64 MLS000878377 Cytoplasm\_Texture\_AngularSecondMoment\_Mito\_3\_0 throughput screening assay to identify in-BDBM38473 hibitors of the orphan nuclear receptor sub-Intensity -Cells\_Intensity\_IntegratedIntensityEdge\_ER Cytoplasm\_Intensity\_MinIntensityEdge\_RNA HMS2259A05 family 0, group B, member 1 (DAX1; NR0B1) (AID 504766) ZINC6577386 Cytoplasm\_AreaShape\_FormFactor • Luminescence-based cell-based primary high PubChem CID: 5308954 throughput screening assay to identify biased ligands of the melanocortin 4 receptor (MC4R): agonists of MC4R (AID 540308) Cells\_RadialDistribution\_FracAtD\_ER\_3of4 Cytoplasm\_Texture\_DifferenceEntropy\_Mito\_5\_0 Cells\_Texture\_InfoMeas2\_DNA\_3\_0 Cytoplasm\_Intensity\_UpperQuartileIntensity\_ER Cytoplasm\_AreaShape\_Solidity

Cytoplasm\_Intensity\_IntegratedIntensity\_ER RadialDistribution -ER AGP Mito