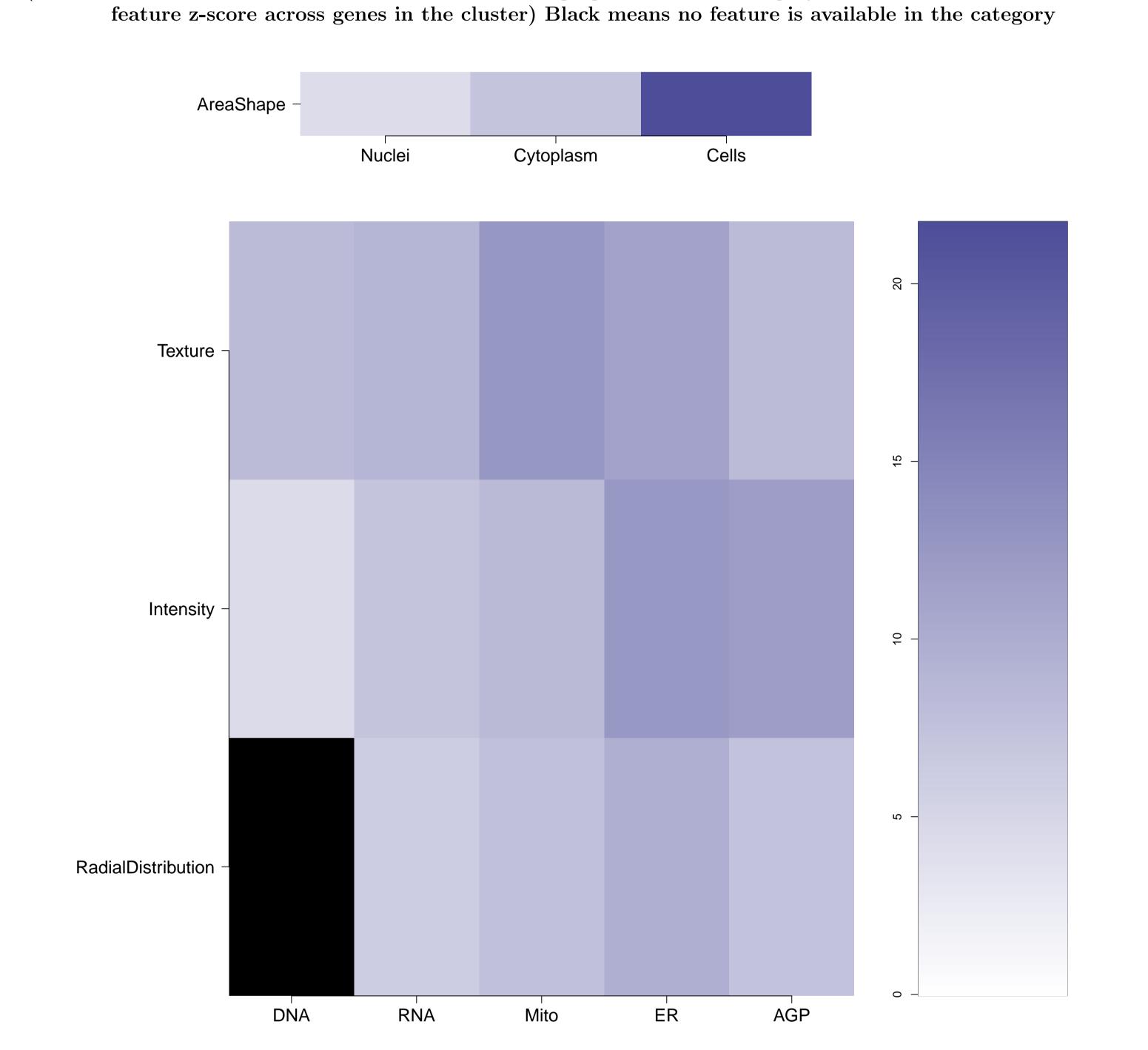


What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a

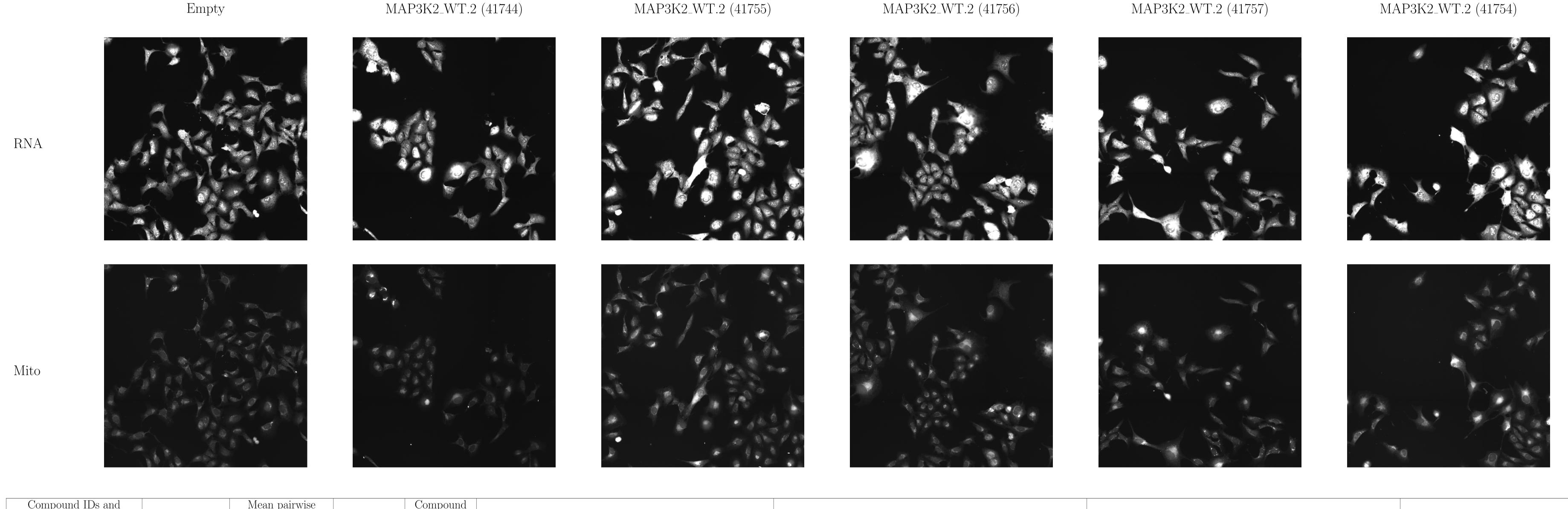


RNA

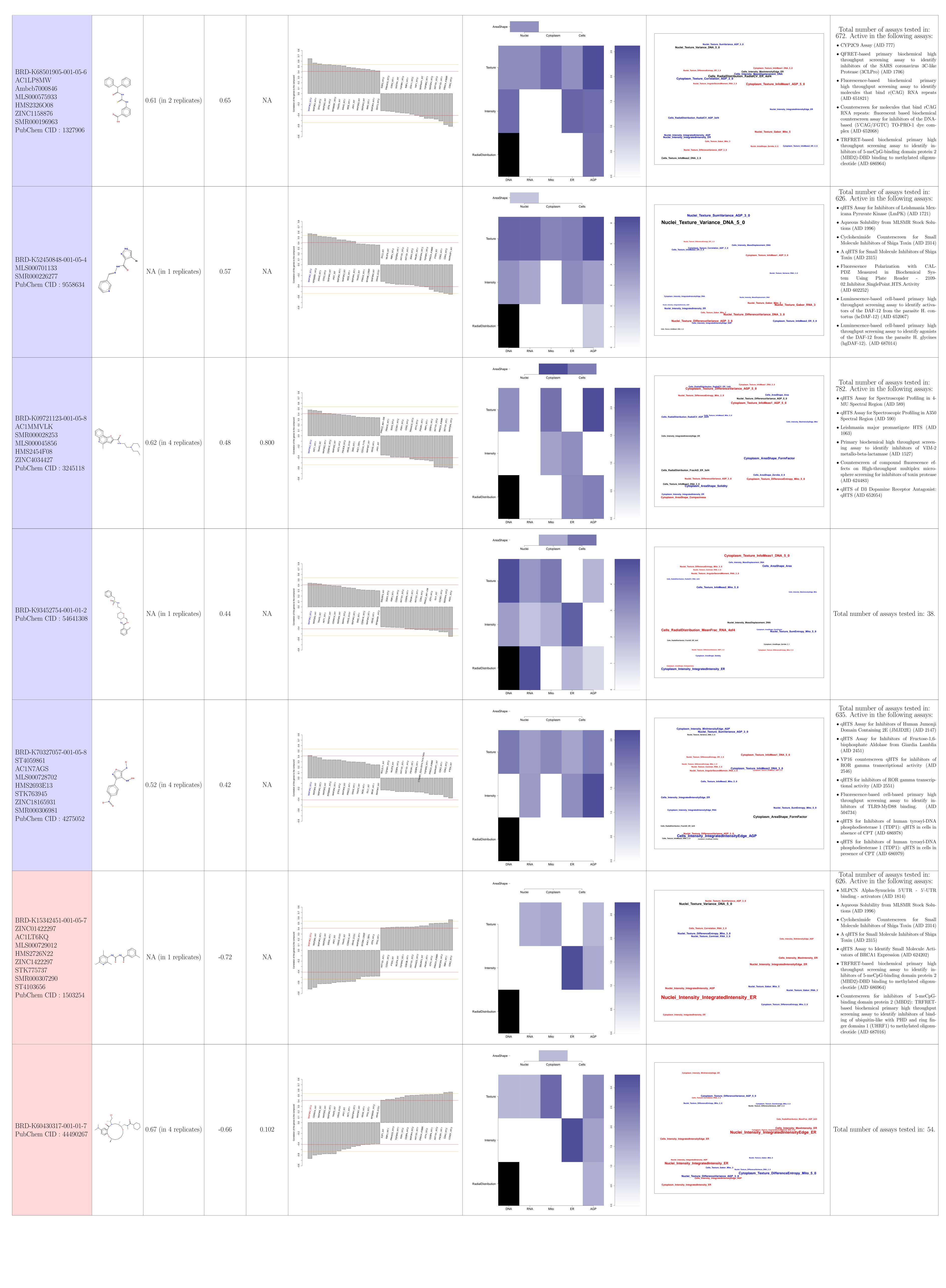
Mito

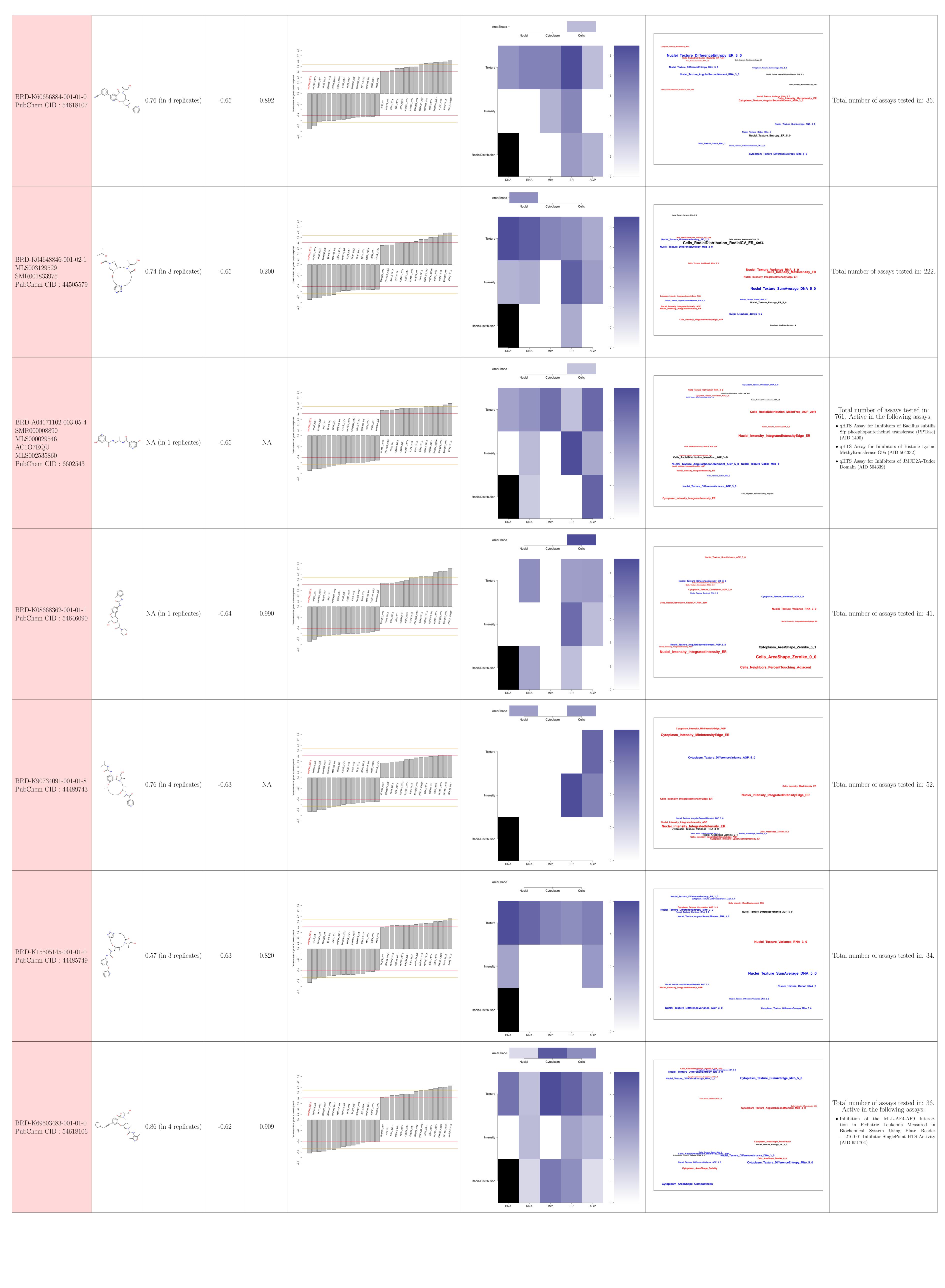
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.





| | | Wicali Pali Wisc | | | | | | |
|------------------------------|-----------|-----------------------|--|-------------|--|--|--|--|
| common names (where | | replicates | Completion | rank when | | | Distinguishing individual factures for the common dupletive to | Number of DulcCham agains in which |
| available); blue/red colored | Cl: 1 | correlation of the | | scored | How similar is the compound signature to the genes in this | | Distinguishing individual features for the compound relative to Number of Pu | |
| box means the matching | Chemical | compound signature | between | against the | experiment? (Yellow and red lines correspond to top/bottom | | untreated samples. Black means a mismatch; i.e. active (= high | 7 |
| compound is | structure | (95th DMSO | the gene using the gene using the gene using the second that the secon | gene using | 1st and 5th percentile DMSO correlation to all the genes) | the gene relative to the untreated samples | z-score in magnitude) in the compound, and either inactive (= w small z-score in magnitude) or oppositely active in the gene | which the compound was active are itemized |
| positively/negatively | | replicate correlation | | L1000 | | | | |
| correlated with the cluster | | is 0.51 | | profiling | | | | |





AreaShape -Cytoplasm Cells_Intensity_UpperQuartileIntensity_DNA Cytoplasm_Texture_Correlation_AGP_3_0

Cytoplasm_Texture_AngularSecondMoment_AGP_3_0

Cytoplasm_Texture_SumAverage_Mito_5_0 Texture -Cells_RadialDistribution_RadialCV_RNA_3of4 MAP3K2 WT2
JAG1_WT
MAP3K2_WT2
JAG1_WT
MAP2K3_WT
CDKN1A_WT
MAP3K5_WT
AKT1_WT1
HRAS_G12V
TRAF6_WT
MAP3K2_WT1
FPSS_WT11
FPSS_WT11 Nuclei_Texture_Variance_RNA_3_0
Cytoplasm_Texture_AngularSecondMoment_Mito_3_0 BRD-K18001731-001-01-7 NA (in 1 replicates) Total number of assays tested in: 41. 0.985-0.61 PubChem CID : 54646091 Intensity -Cells_RadialDistribution_MeanFrac_RNA_4of4 Cytoplasm_AreaShape_FormFactor Nuclei_Intensity_IntegratedIntensity_ER Cytoplasm_Texture_DifferenceEntropy_Mito_5_0 Cytoplasm_AreaShape_Zernike_7_1 Cytoplasm_AreaShape_Solidity Cytoplasm_AreaShape_Zernike_4_2 Cytoplasm_Intensity_IntegratedIntensity_ER
Cytoplasm_AreaShape_Compactness RadialDistribution -DNA RNA Mito