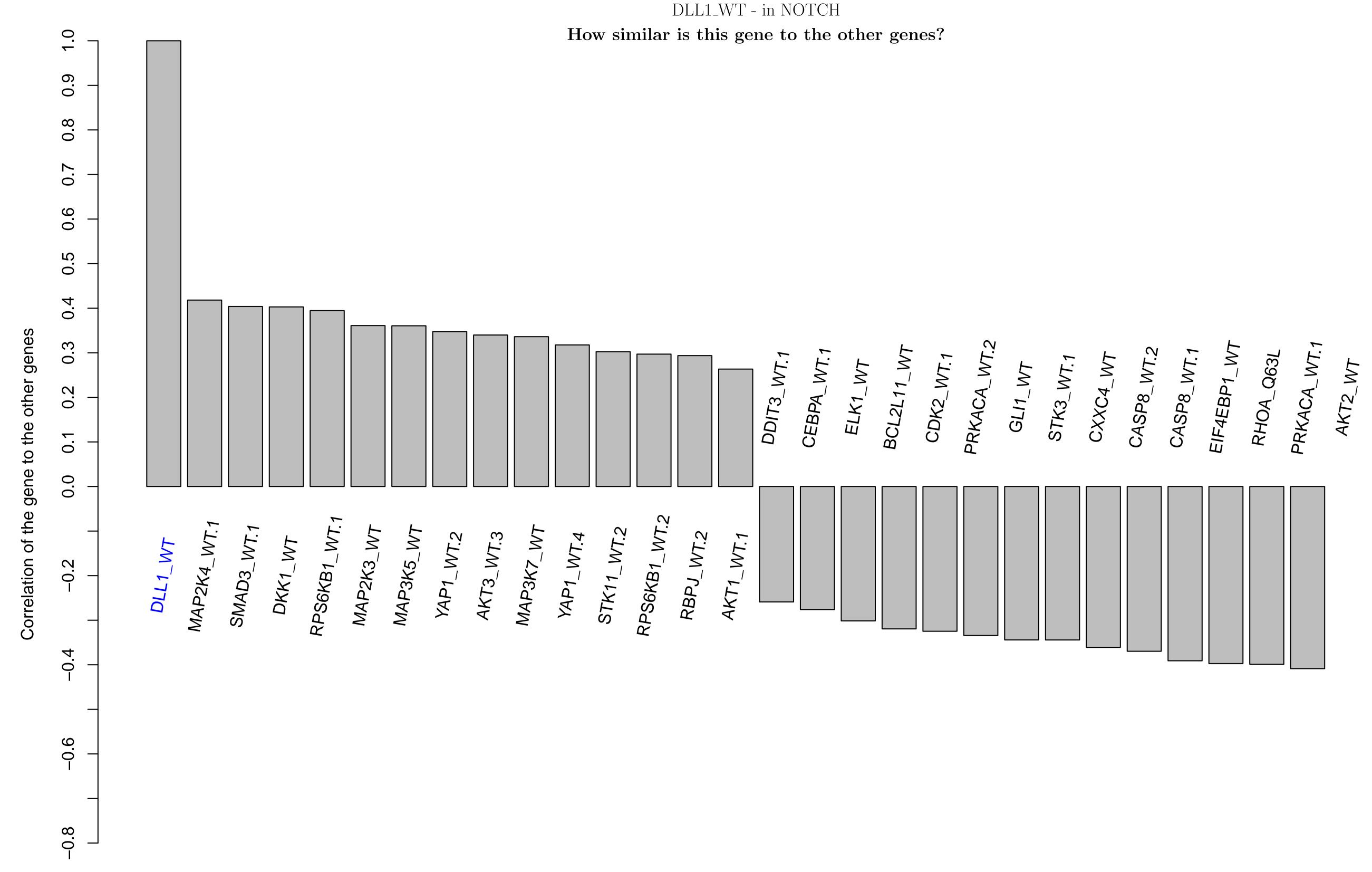
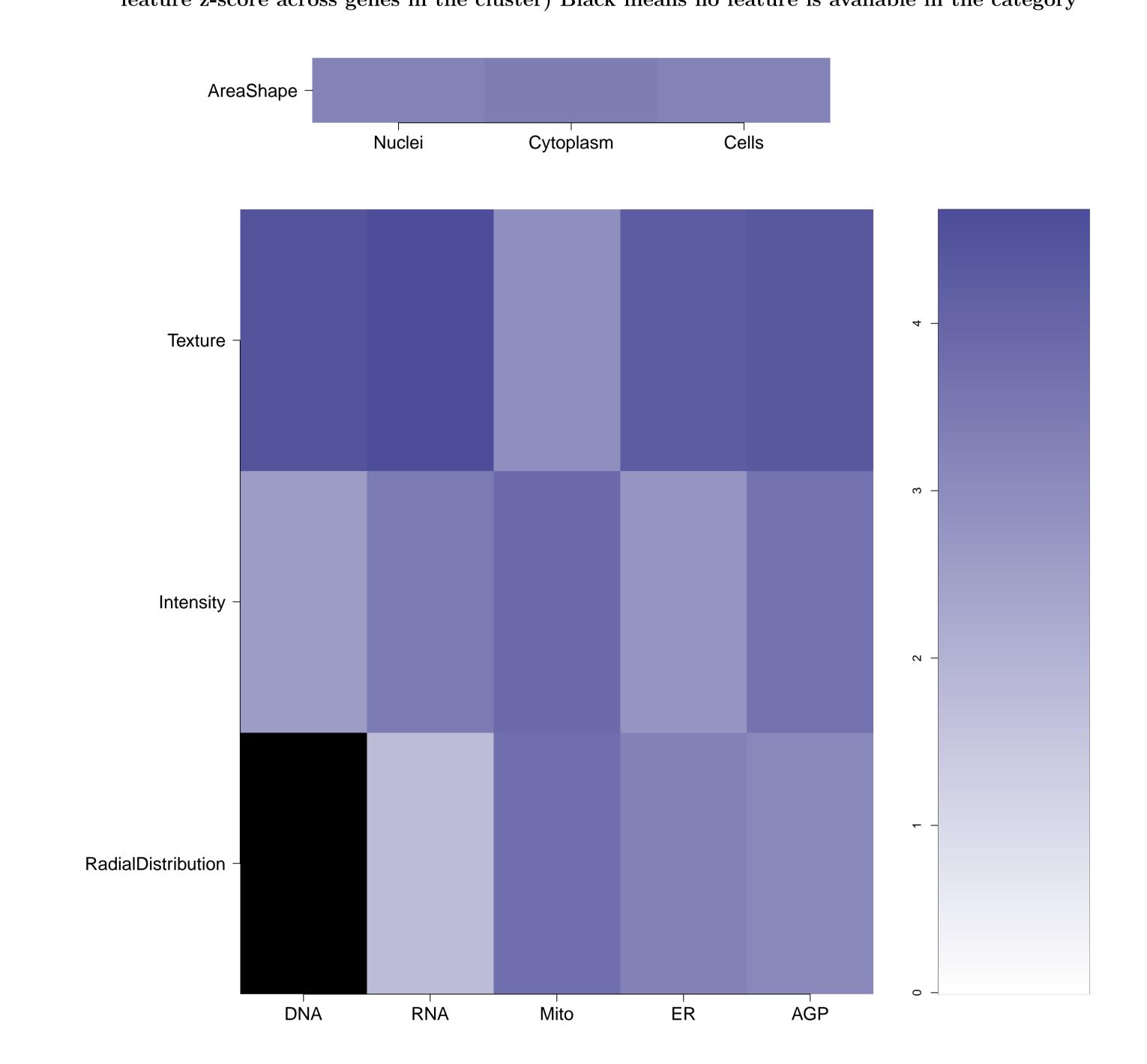
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein



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



Compound

rank when

scored

against the

gene using

L1000

profiling

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)

Correlation

between

compound

the gene

Mean pairwise

replicates

correlation of the

compound signature

(95th DMSO

replicate correlation

is 0.52)

Chemical

structure

RNA

DNA

Compound IDs and

common names (where

available); blue/red colored

box means the matching

compound is

positively/negatively

correlated with the cluster

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.

Distinguishing individual features for the compound relative to Number of PubChem assays in which

the compound was tested; assays in

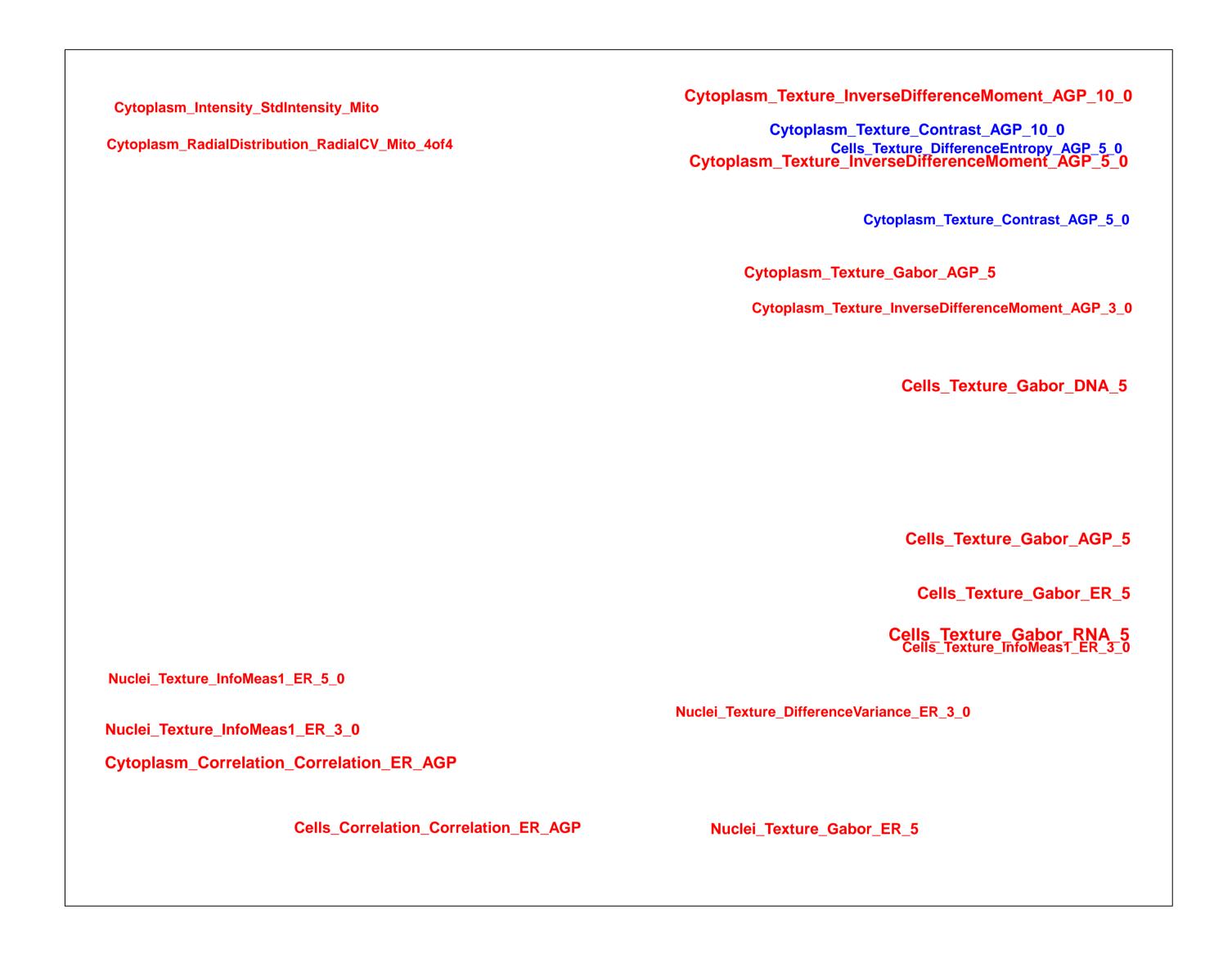
which the compound was active are

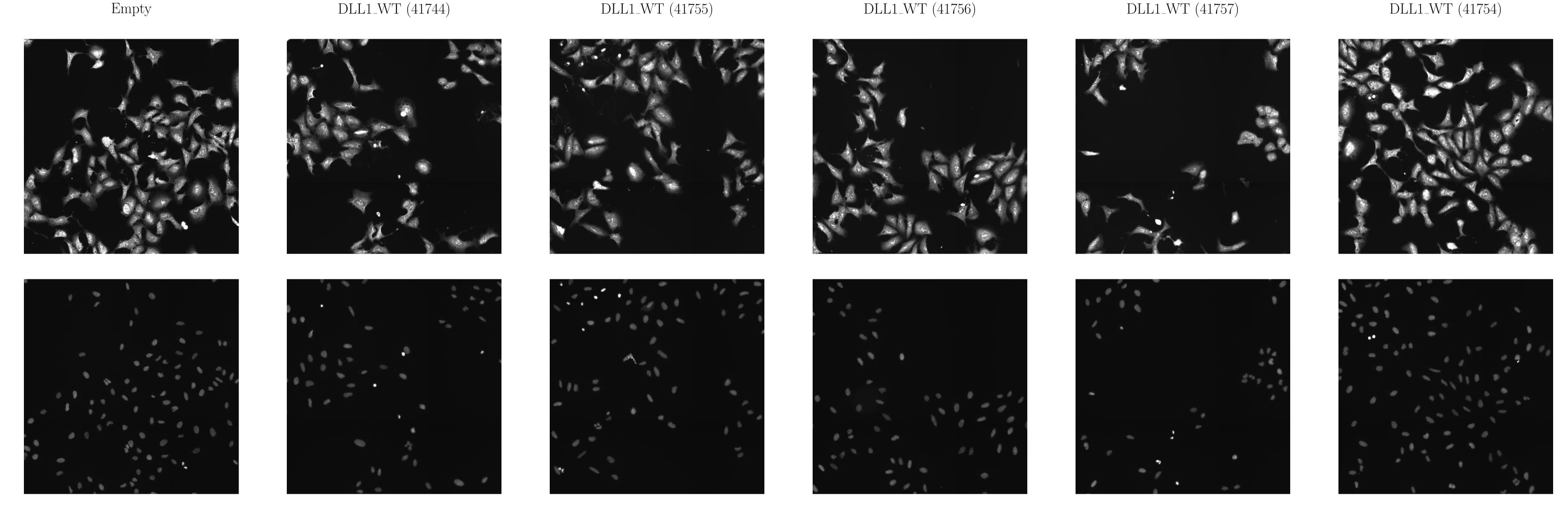
itemized

untreated samples. Black means a mismatch; i.e. active (= high

z-score in magnitude) in the compound, and either inactive (=

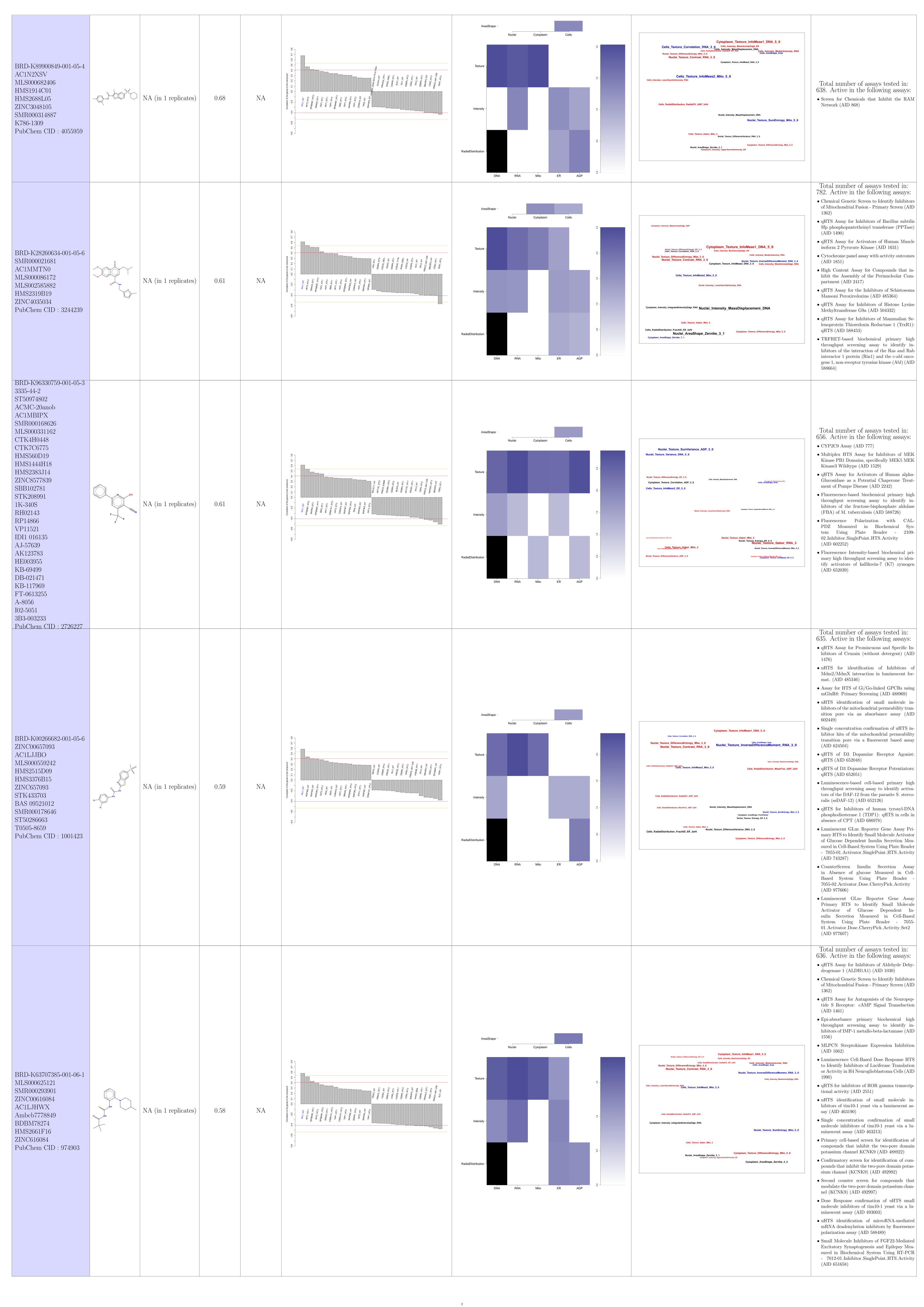
small z-score in magnitude) or oppositely active in the gene

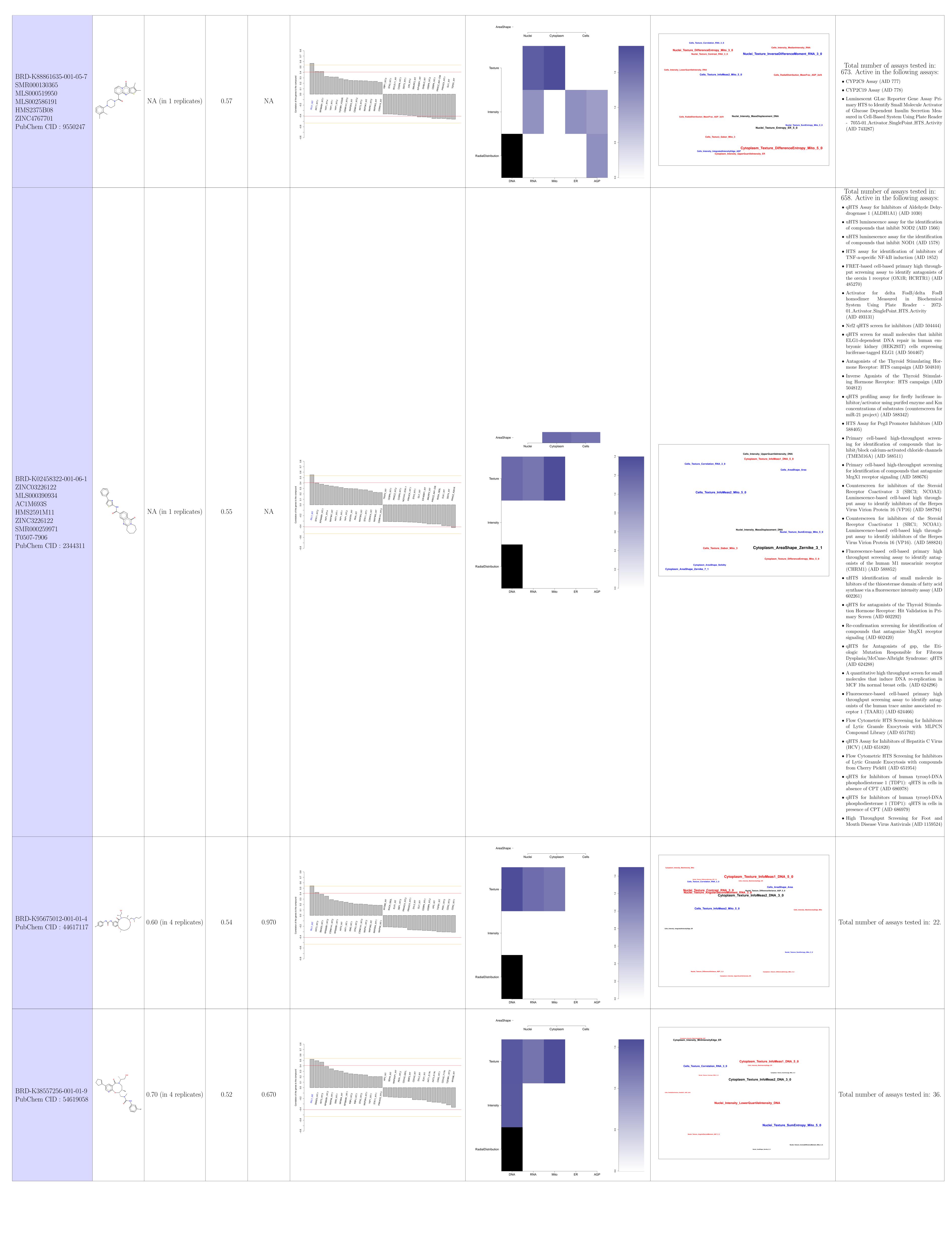


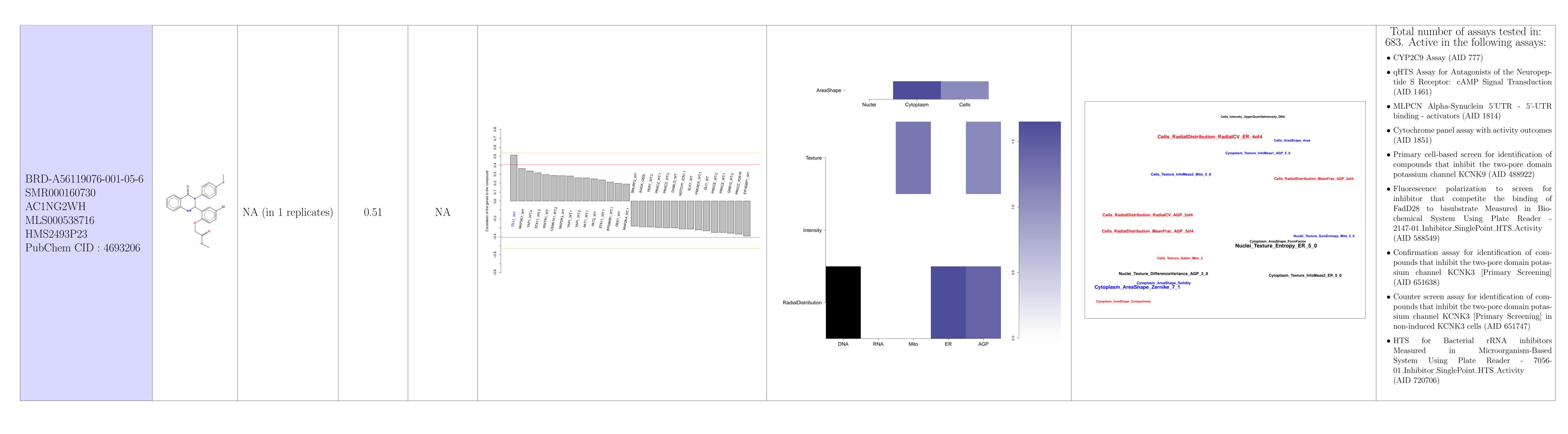


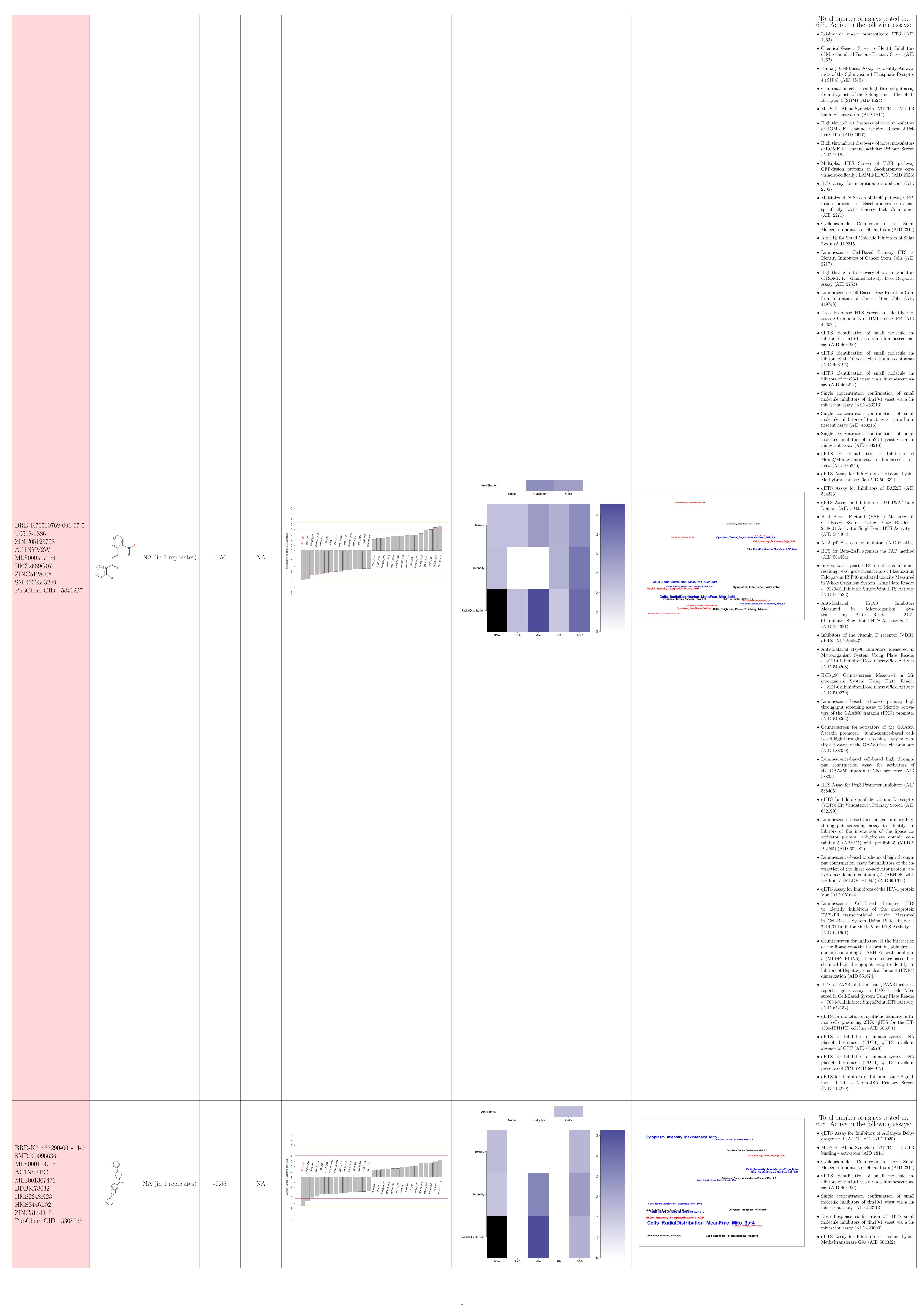
Common distinguishing feature categories in the compound and

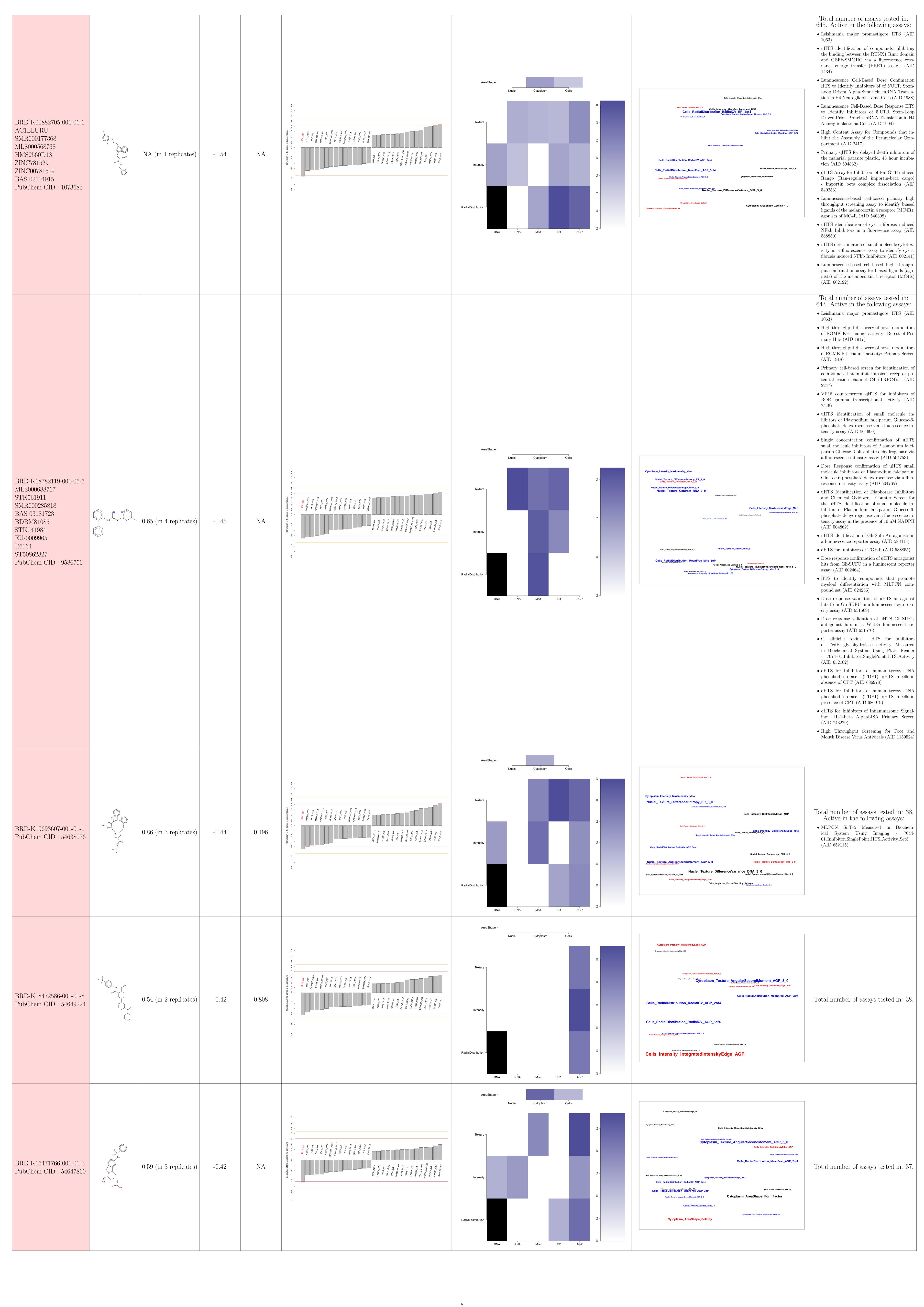
the gene relative to the untreated samples











AreaShape -Cytoplasm Cytoplasm_Intensity_MinIntensityEdge_ER BRD-K92155238-001-05-9 Texture -MLS000757144 Total number of assays tested in: 570. Active in the following assays: NSC379468 AC1L7WBA • qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 686978) MYD88_WT SGK3_WT2 SMURF2_WT ELK1_WT CDC42_WT DVL3_WT CCND1_WT2 MLST8_WT CDK2_WT1 GLI1_WT CEBPA_WT2 CEBPA_WT2 CEBPA_WT2 PER1_WT AC1Q3P47 ZINC13140245 Nuclei_Texture_Variance_RNA_3_0 Intensity -NSC-379468 SMR000529017 Nuclei_Texture_Gabor_Mito_5 Nuclei_Intensity_IntegratedIntensity_AGP PubChem CID: 342499 Nuclei_Texture_DifferenceVariance_DNA_3_0
Nuclei_AreaShape_Zernike_6_6 RadialDistribution -Mito