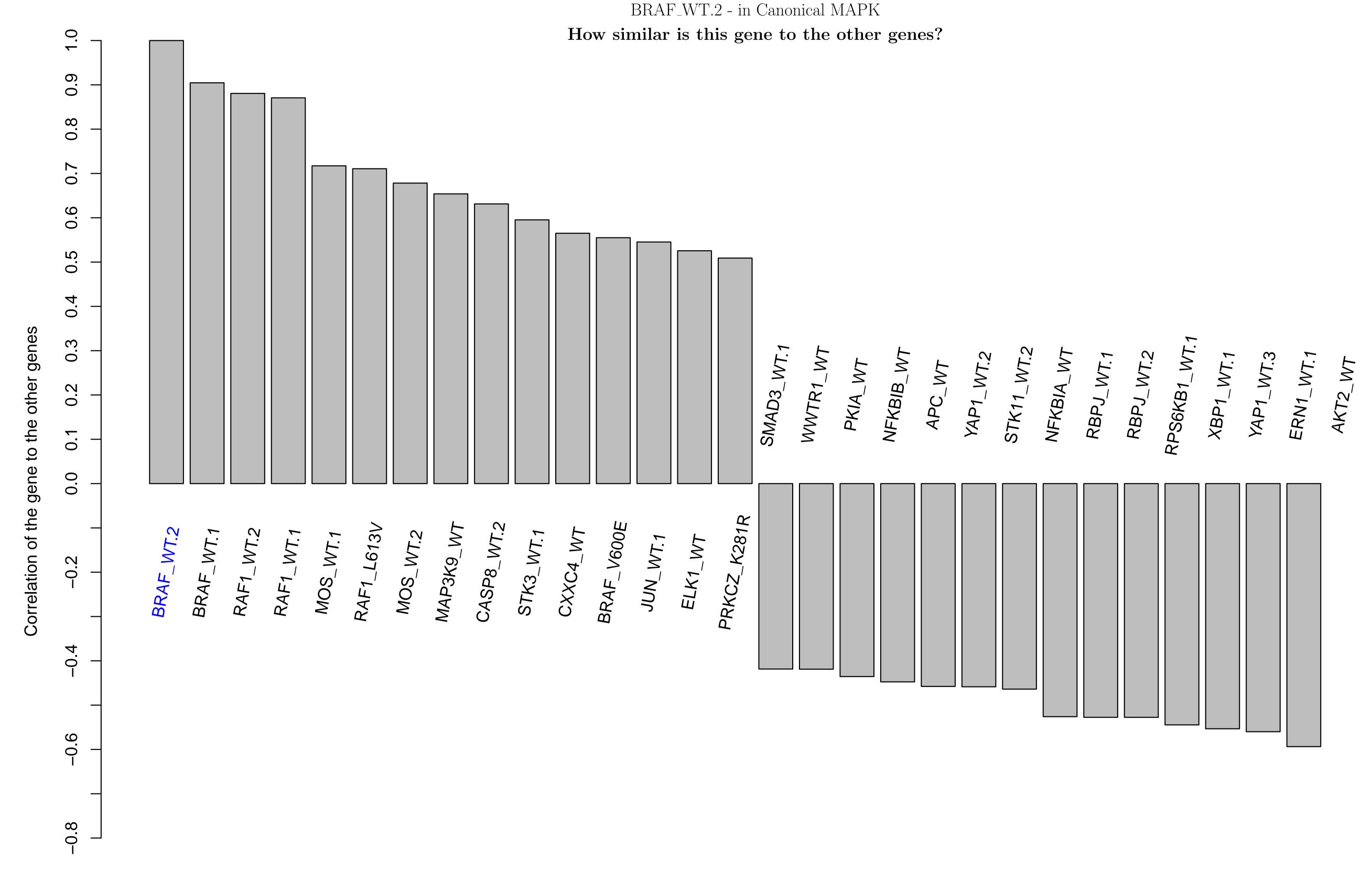
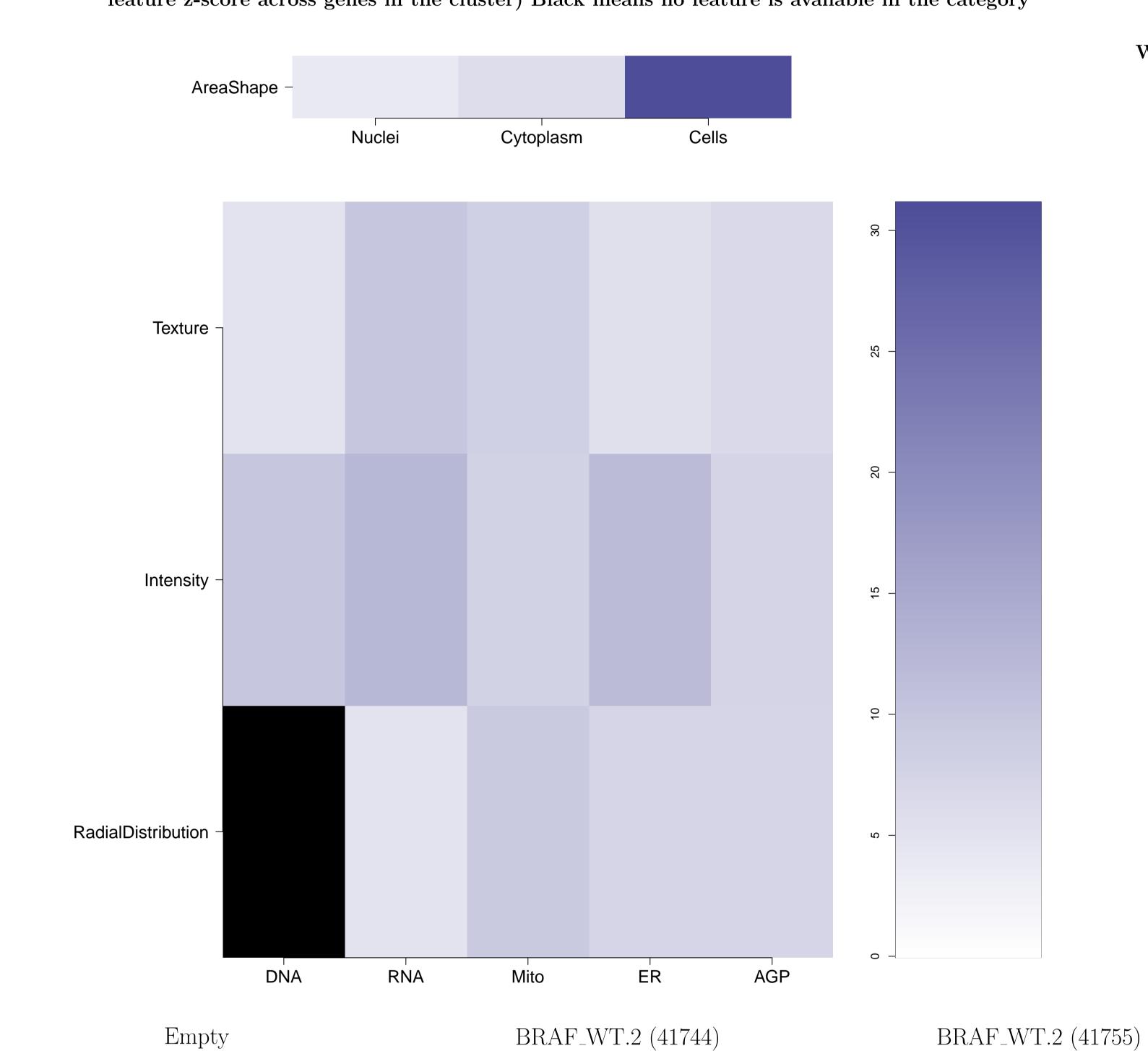
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein



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



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

replicates

correlation of the

compound signature

(95th DMSO

replicate correlation

is 0.51)

Chemical

structure

RNA

ER

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

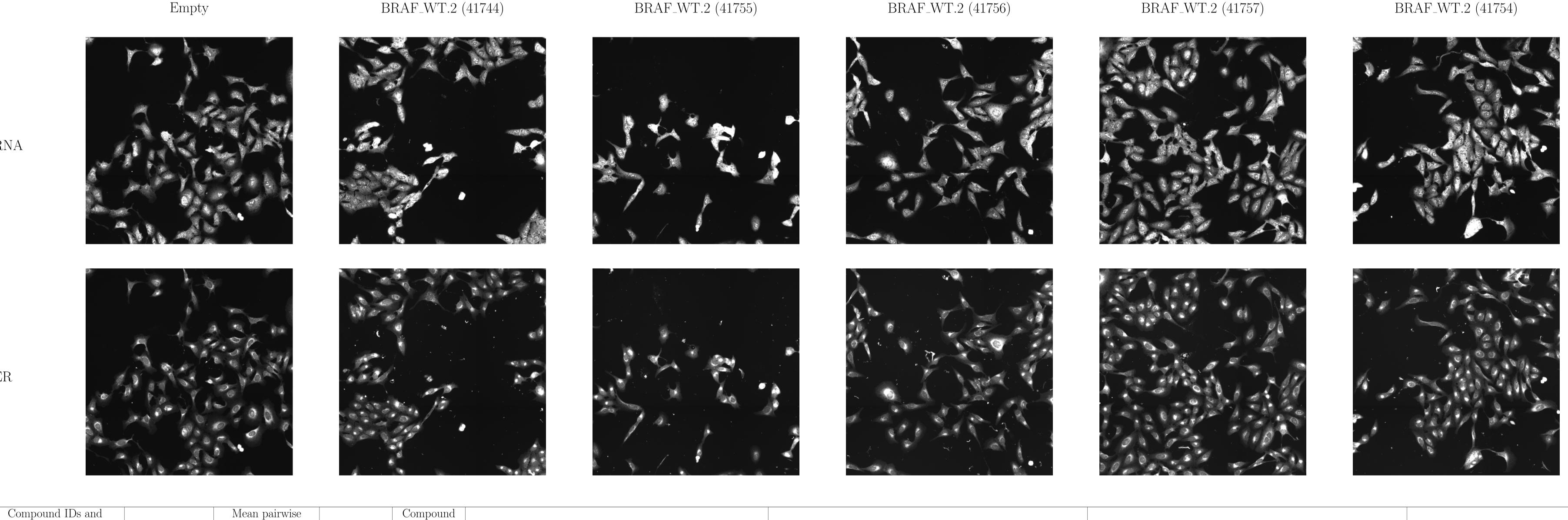
itemized

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

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

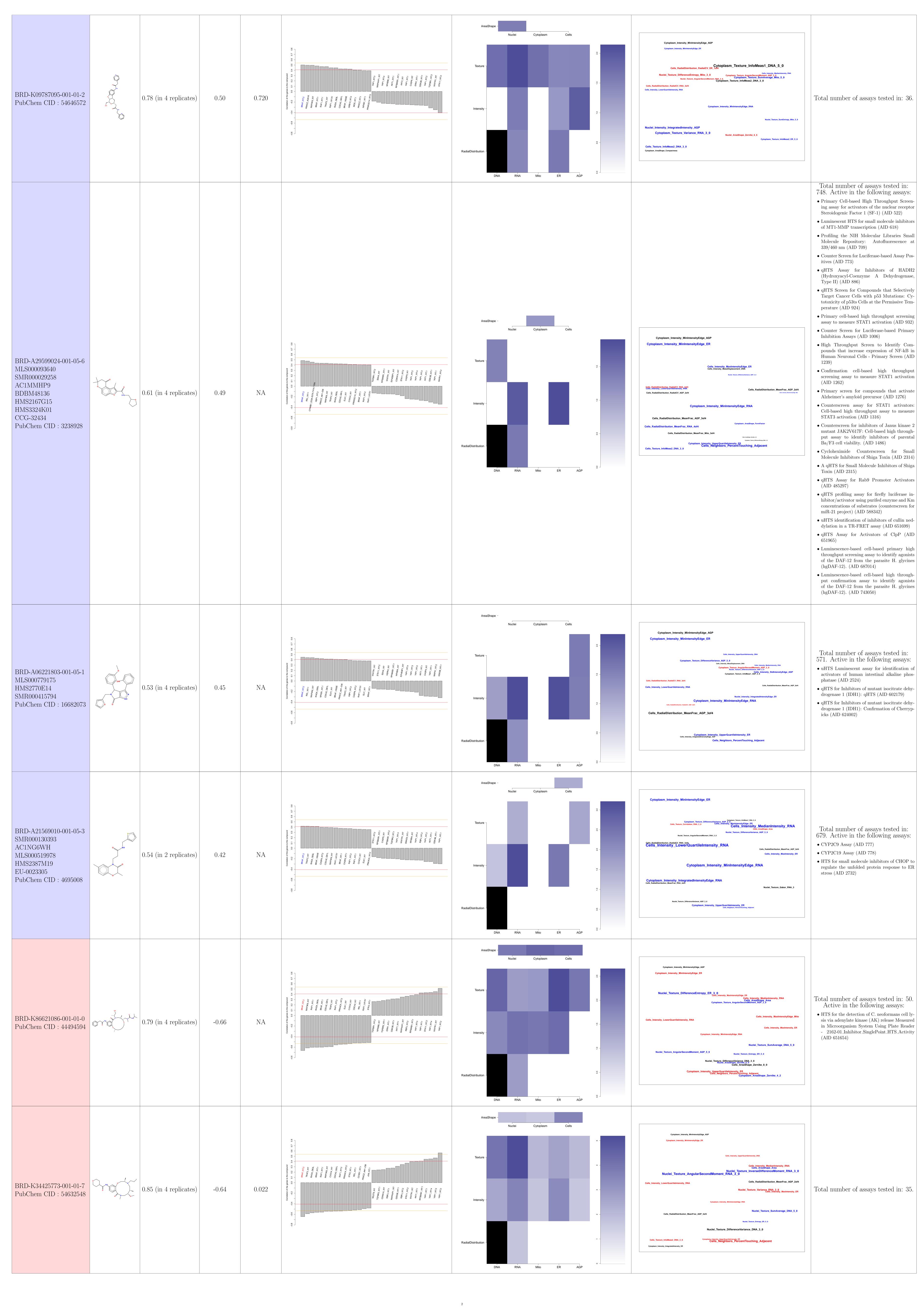
small z-score in magnitude) or oppositely active in the gene





Common distinguishing feature categories in the compound and

the gene relative to the untreated samples





Cytoplasm Nuclei_Texture_DifferenceEntropy_ER_3_0 Nuclei_Texture_AngularSecondMoment_RNA_3_0 Nuclei_Texture_InverseDifferenceMoment_RNA_3_0 Texture -Cells_Intensity_LowerQuartileIntensity_RNA Cells_RadialDistribution_MeanFrac_AGP_2of4 Nuclei_Texture_Variance_RNA_3_0 Cells_Intensity_MaxIntensity_ER BRD-K72464155-001-01-7
PubChem CID: 54632230

0.82 (in 4 replicates) Cytoplasm_Intensity_MinIntensityEdge_RNA Total number of assays tested in: 35. 0.280Intensity -Nuclei_Texture_SumAverage_DNA_5_0 Cells_RadialDistribution_MeanFrac_AGP_3of4 Nuclei_Texture_Entropy_ER_5_0 Cells_RadialDistribution_MeanFrac_Mito_30f4_Nuclei_Texture_DifferenceVariance_DNA_3_0
Nuclei_AreaShape_Zernike_6_6_Cells_AreaShape_Zernike_0_0 Cells_Neighbors_PercentTouching_Adjacent RadialDistribution -Cytoplasm_Intensity_IntegratedIntensity_ER Mito

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