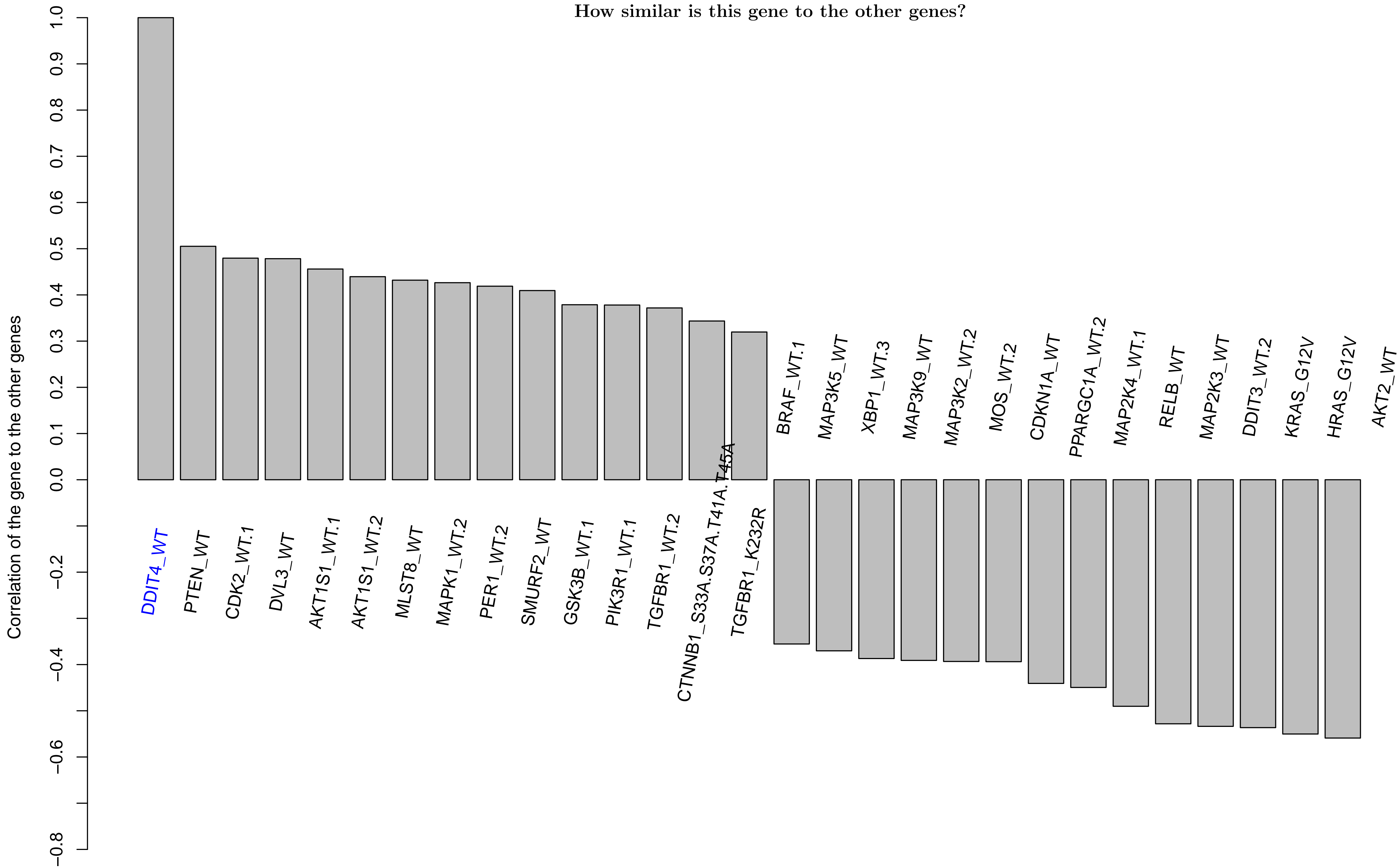
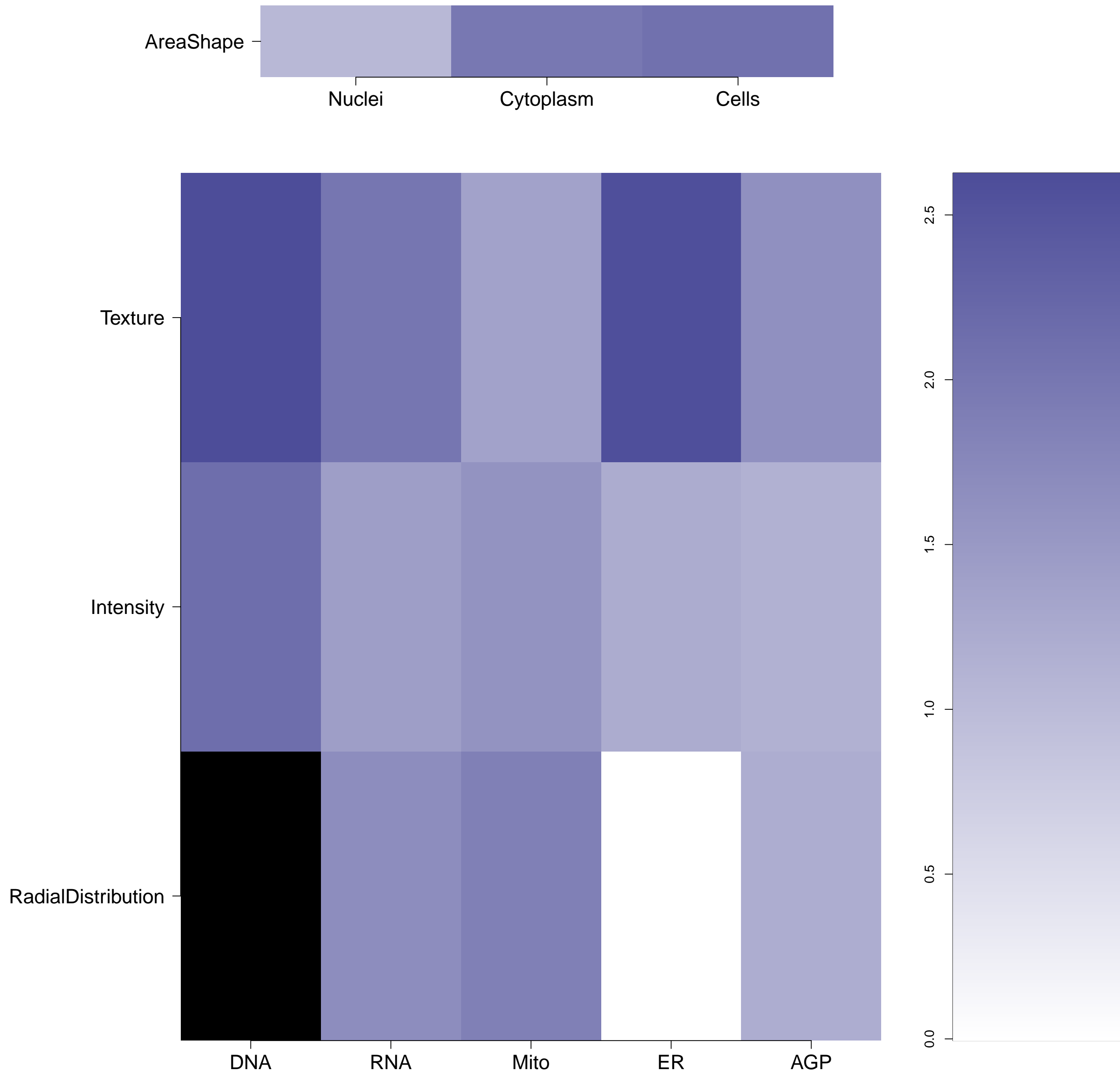


DDIT4.WT - in Canonical TOR

How similar is this gene to the other genes?



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



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.



Empty

DDIT4.WT (41744)

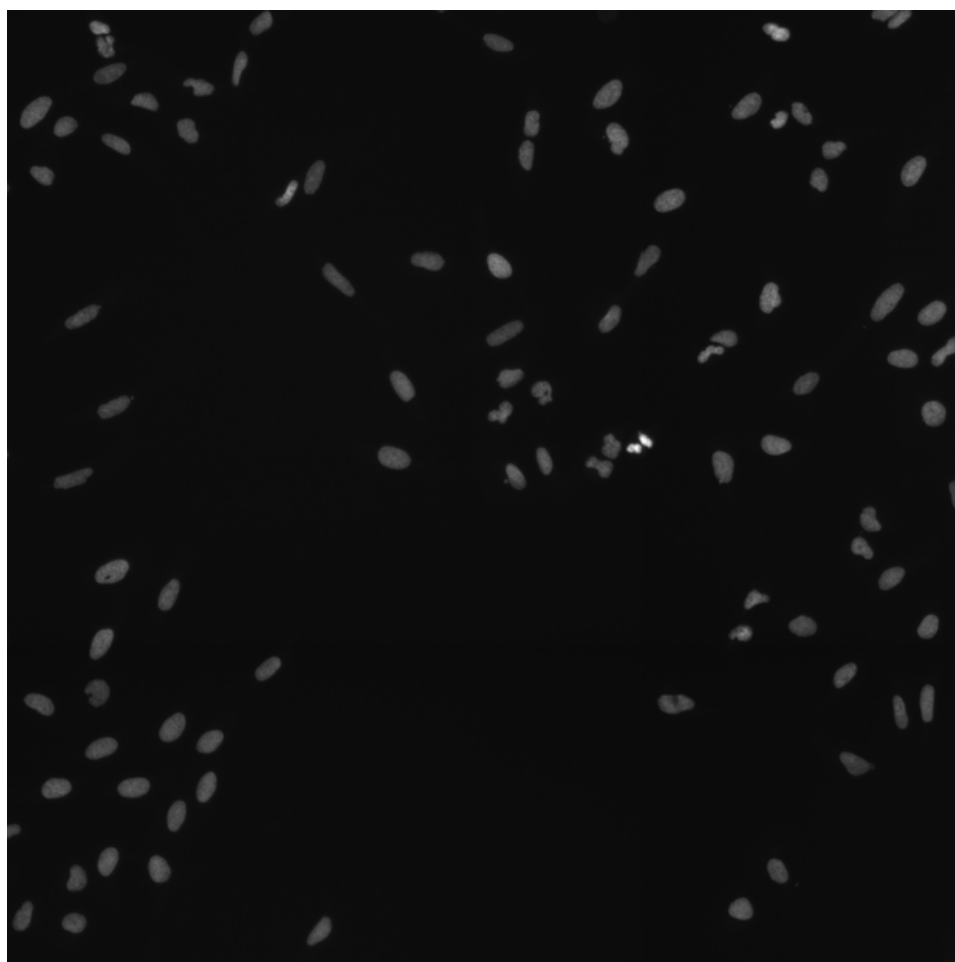
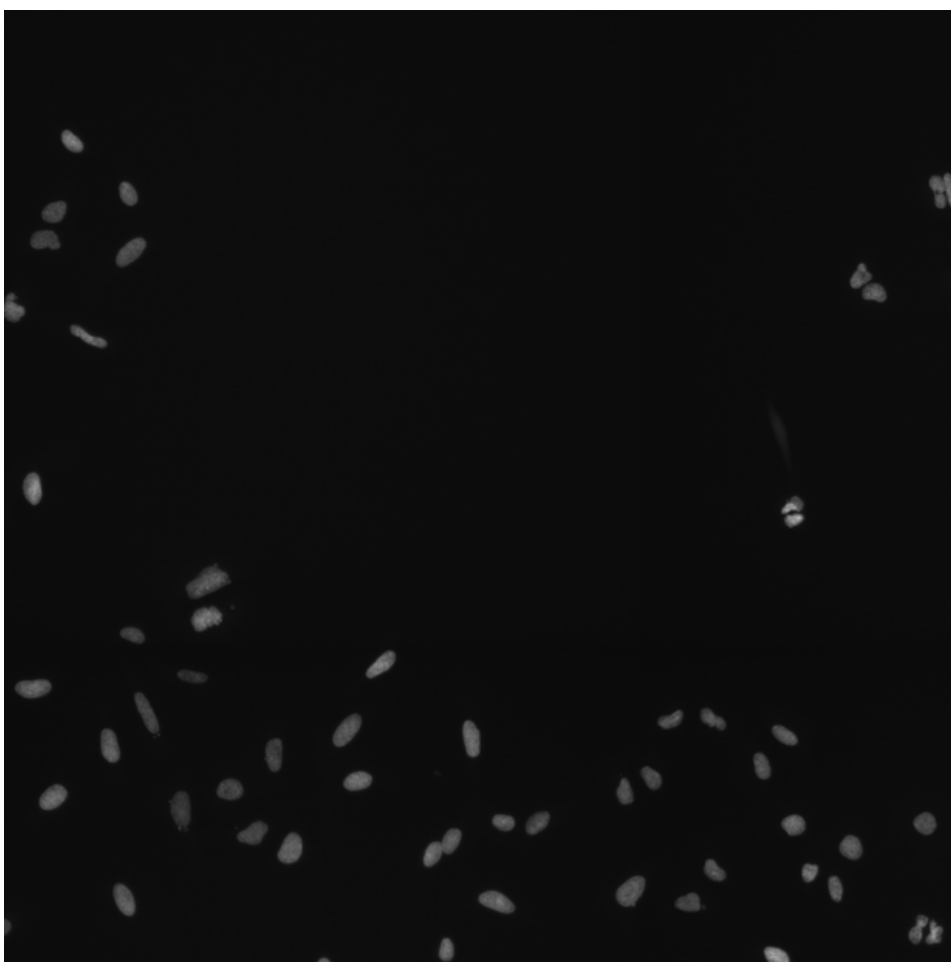
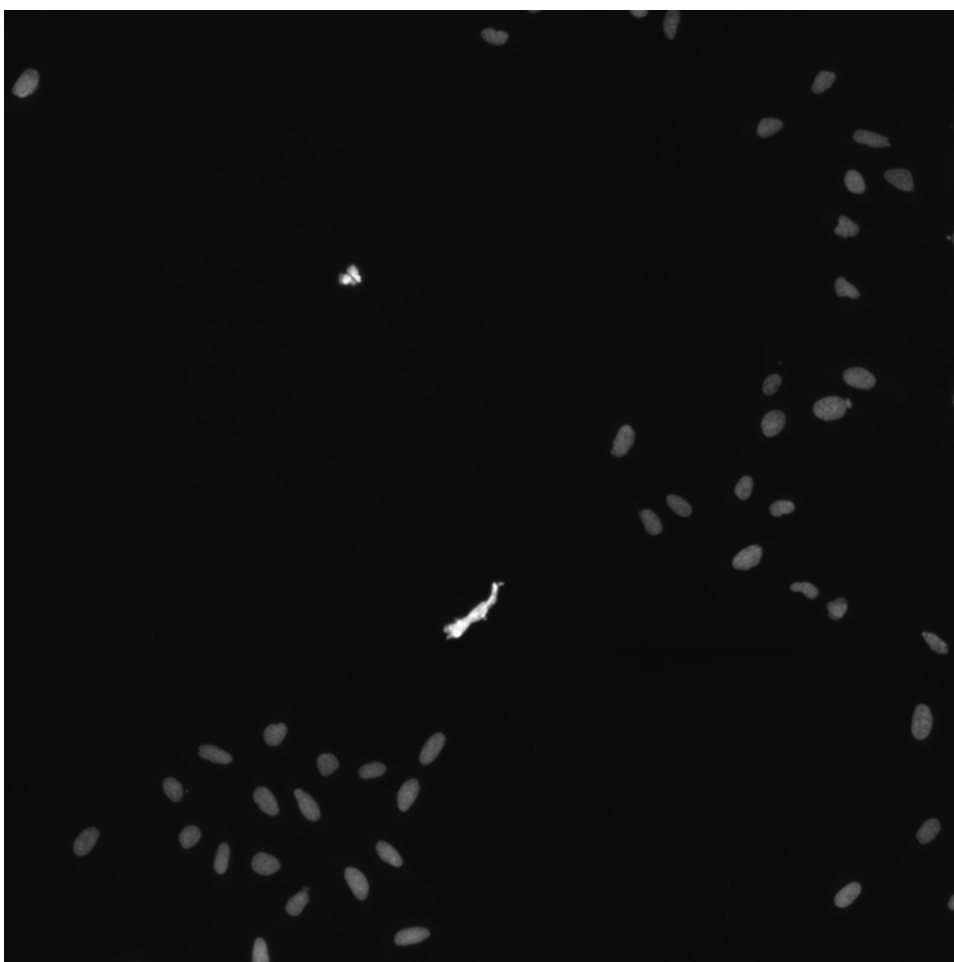
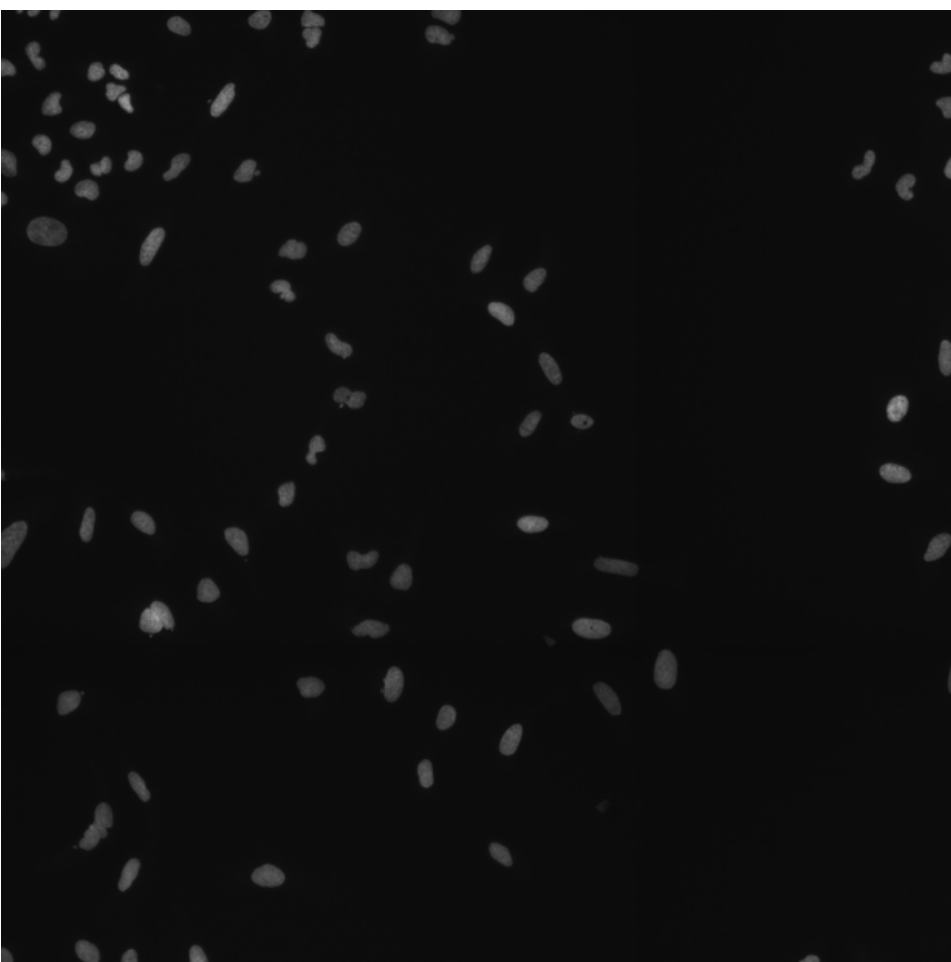
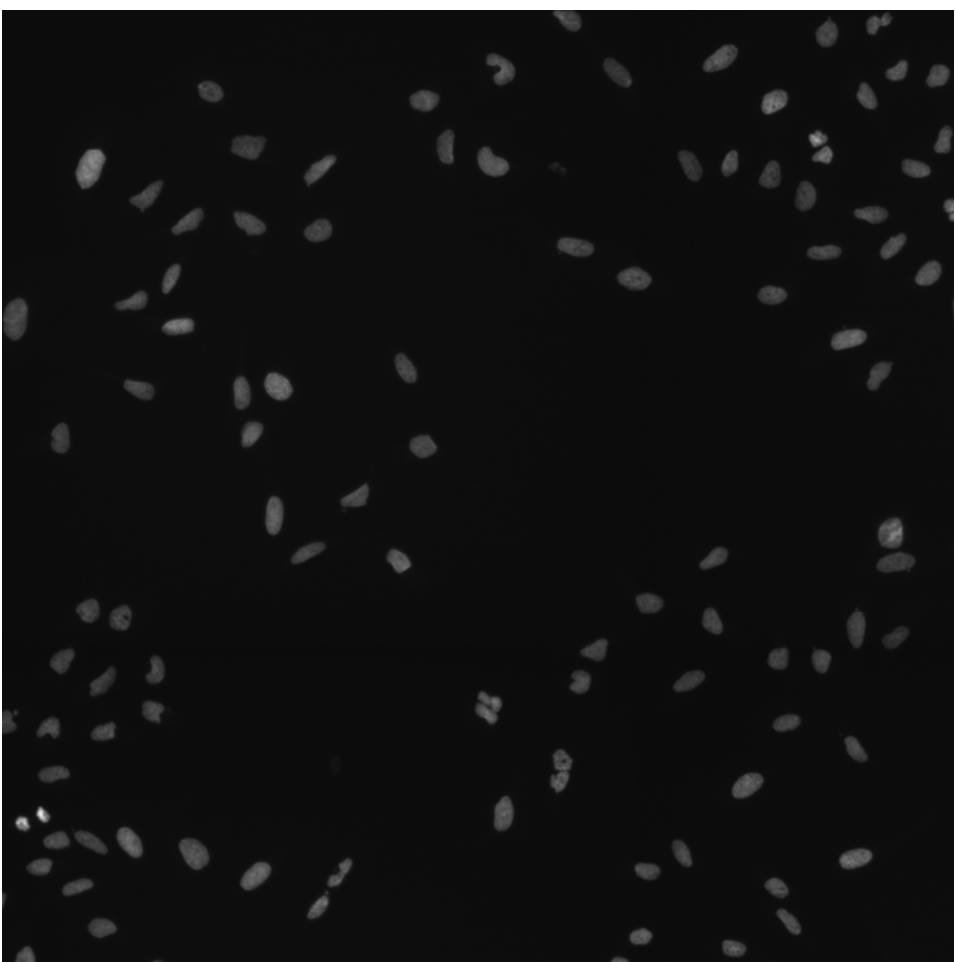
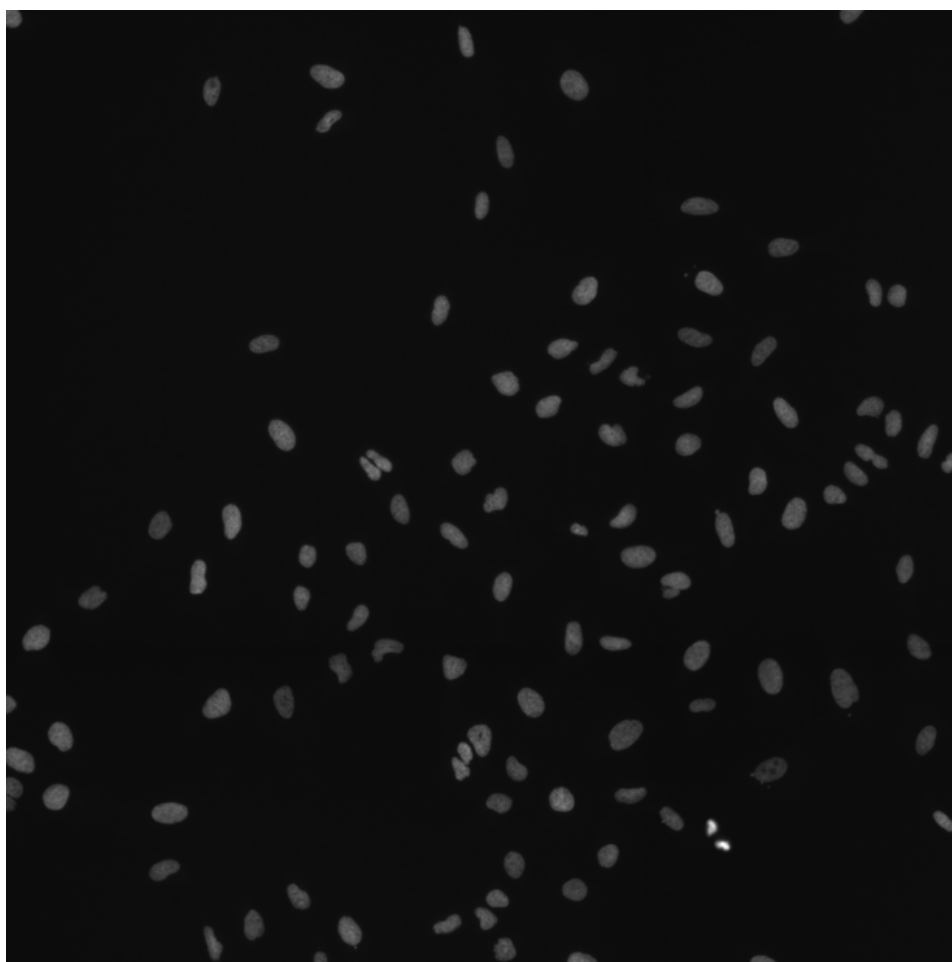
DDIT4.WT (41755)

DDIT4.WT (41756)

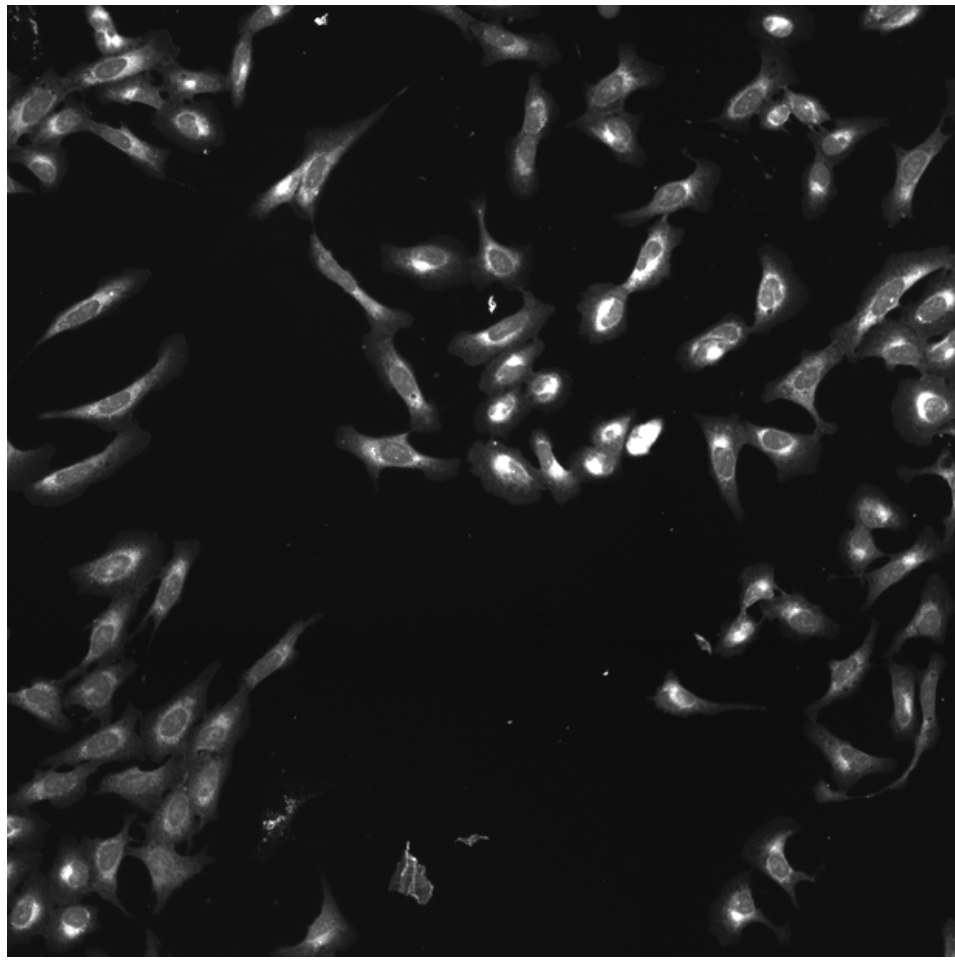
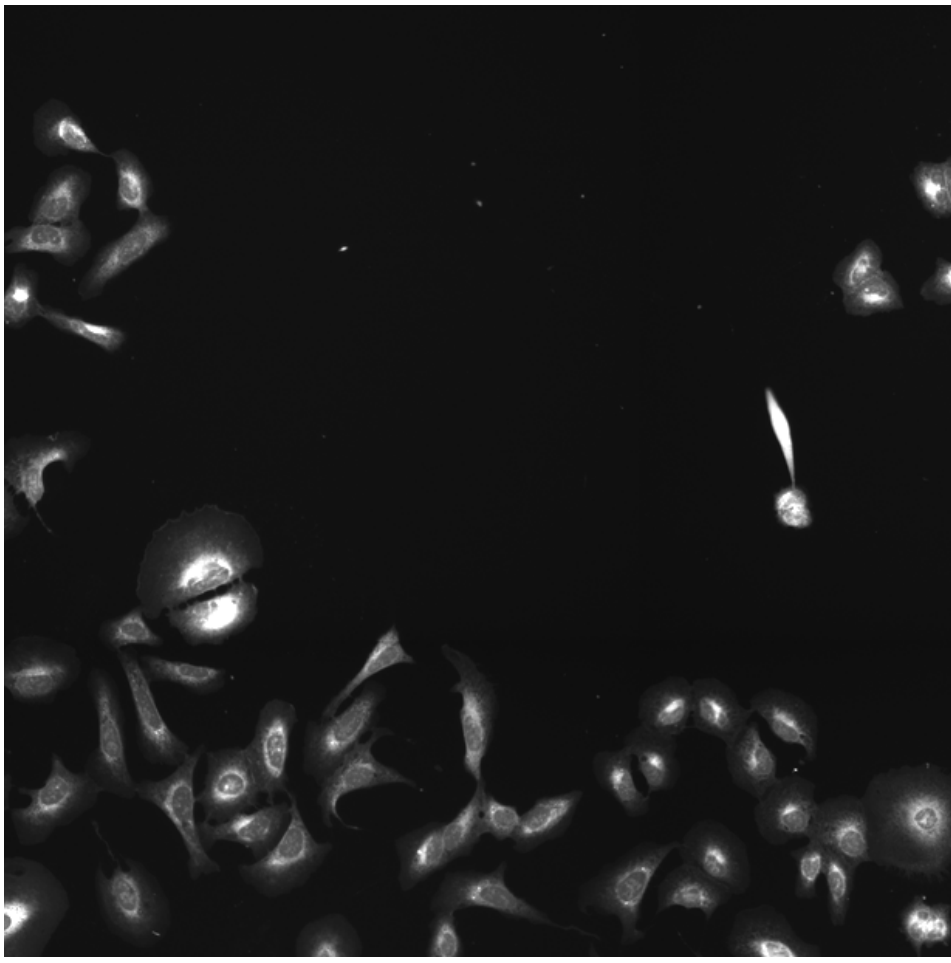
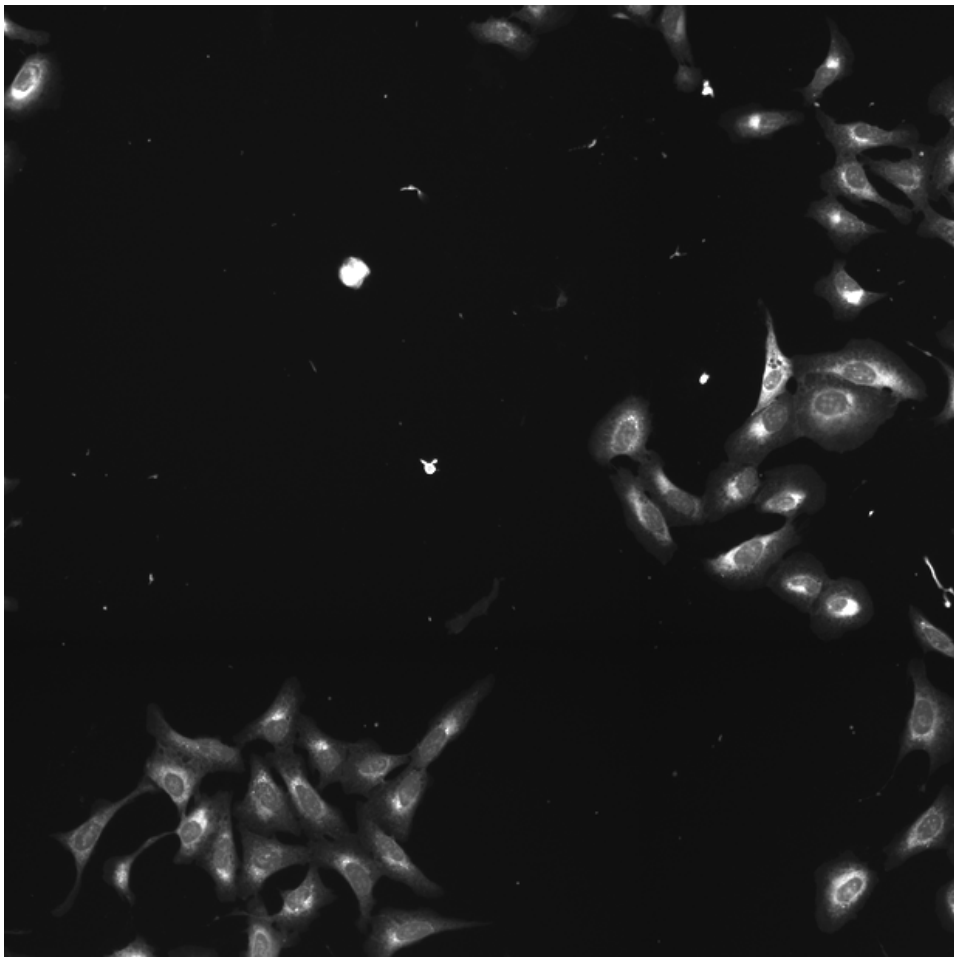
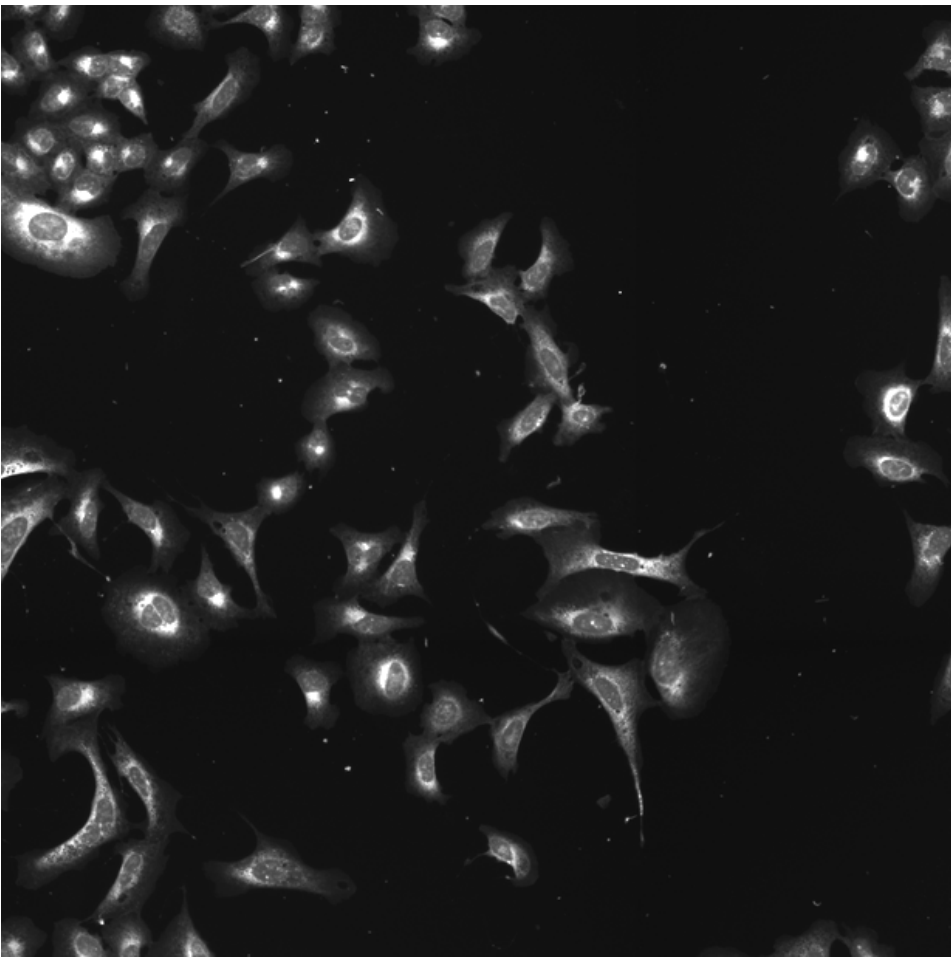
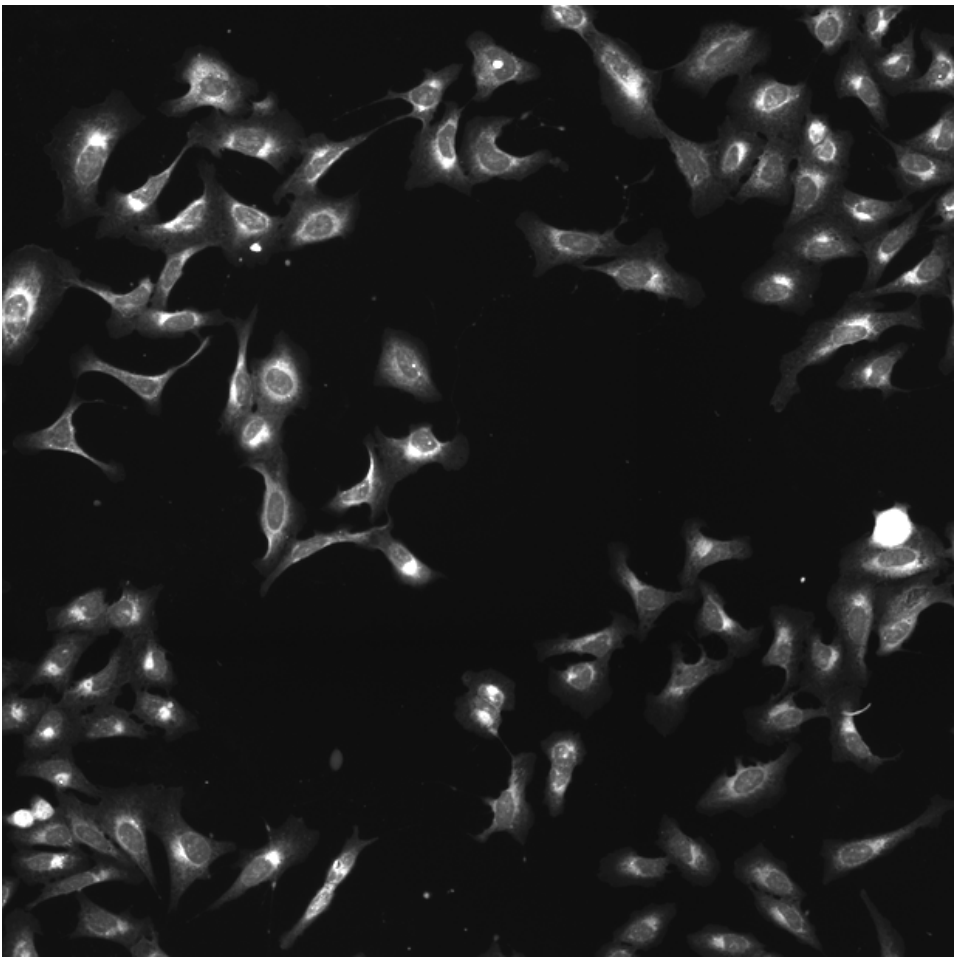
DDIT4.WT (41757)

DDIT4.WT (41754)

DNA

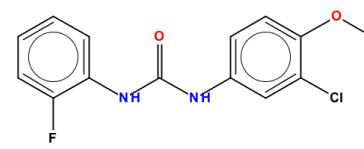


ER



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound the gene	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)	Common distinguishing feature categories in the compound and the gene relative to the untreated samples	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
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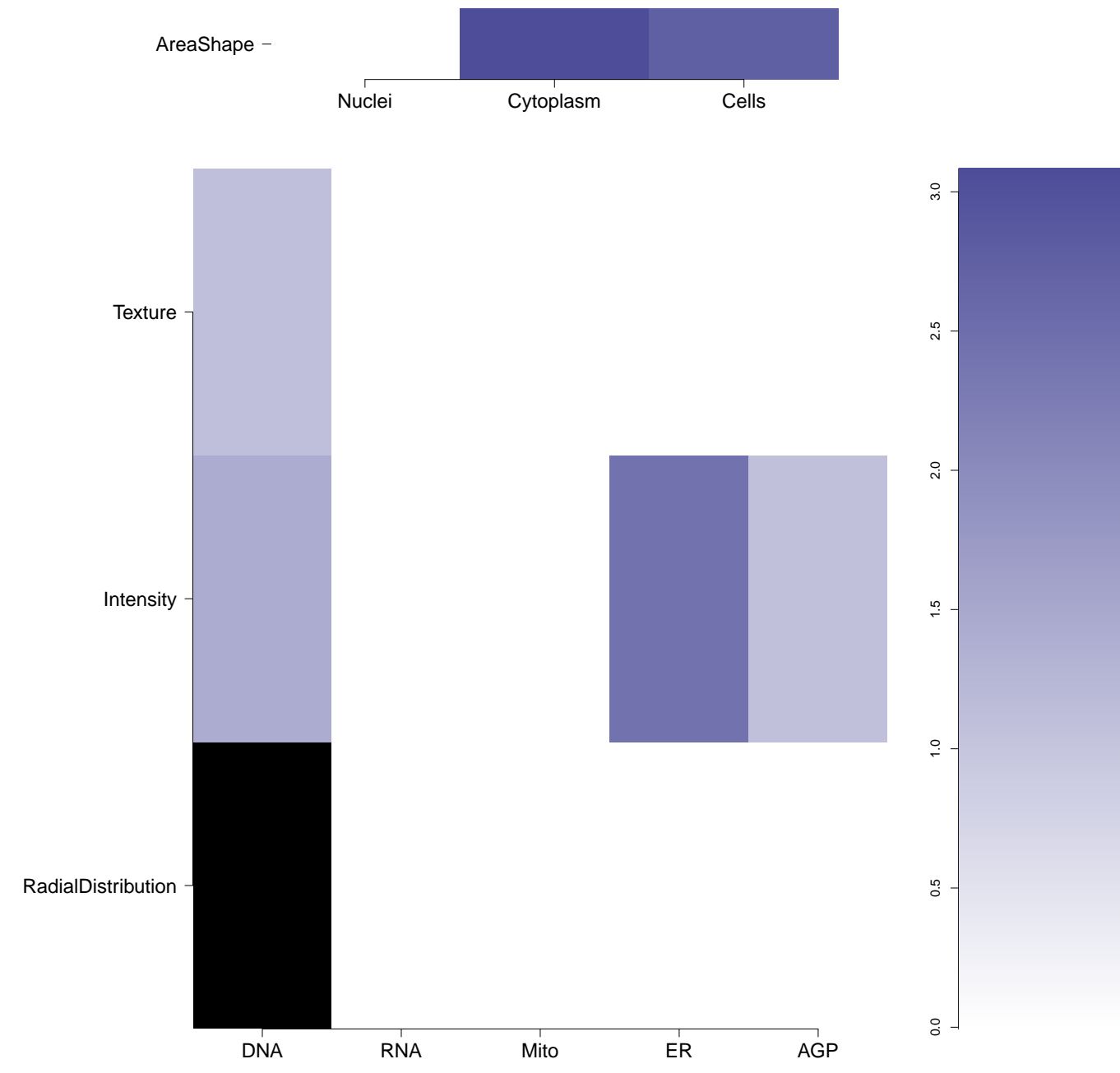
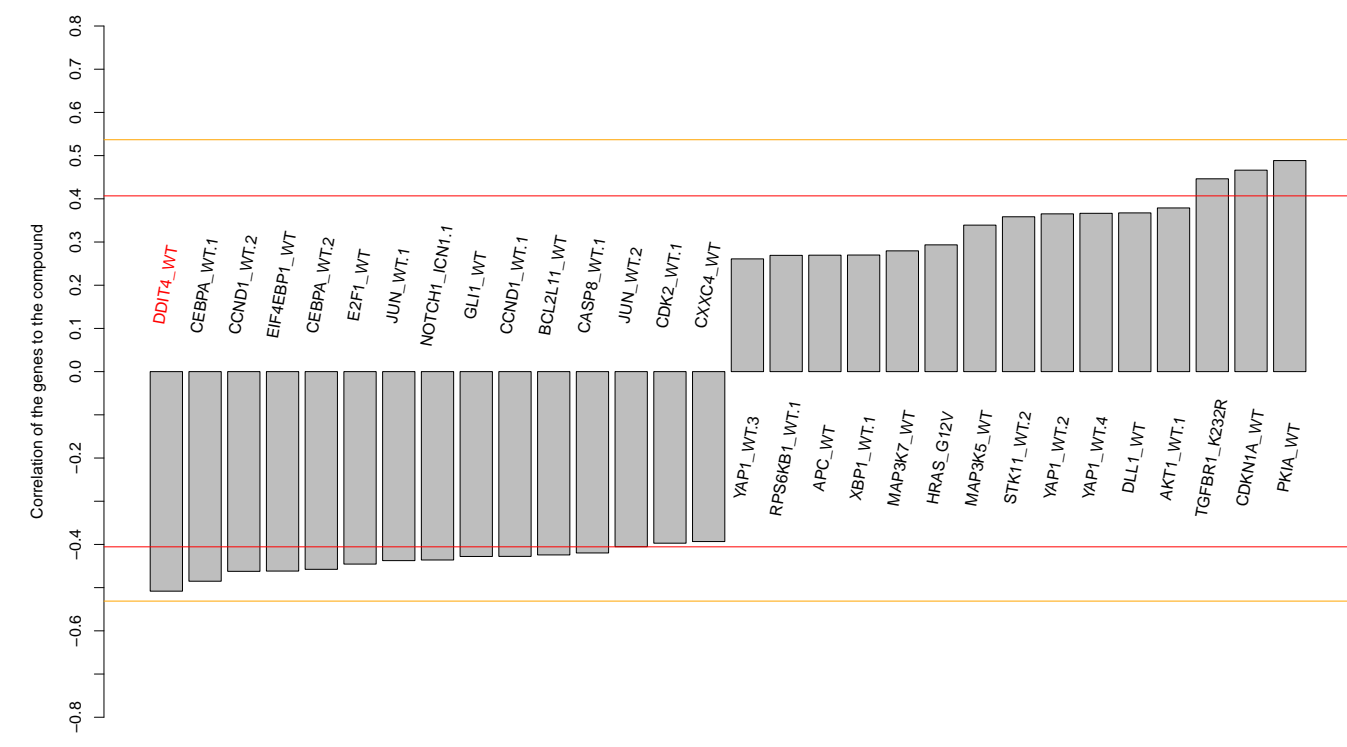
BRD-K67856310-001-06-2
ST50864543
AC1NAZU1
MLS000679238
HMS2623E16
ZINC6457869
STK476143
ZINC06457869
SMR000297513
PubChem CID : 4460240



NA (in 1 replicates)

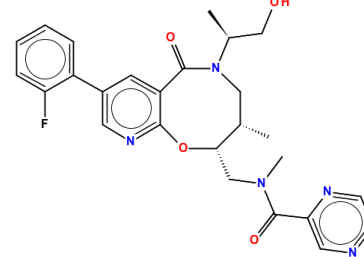
-0.51

NA



- Total number of assays tested in: 643. Active in the following assays:
- Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932)
 - Confirmation cell-based high throughput screening assay to measure STAT1 activation (AID 1262)
 - Primary screen for compounds that activate Alzheimer's amyloid precursor (AID 1276)
 - qHTS Assay for Enhancers of SMN2 Splice Variant Expression (AID 1458)
 - MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814)
 - Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of the Epstein-Barr virus nuclear antigen 1 (EBNA-1). (AID 1950)
 - qHTS Assay for Modulators of miRNAs and/or Inhibitors of miR-21 (AID 2289)
 - Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)
 - A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)
 - HTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 8 (SEN8) (AID 2540)
 - uHTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 6 (SEN6) (AID 2599)
 - uHTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 7 (SEN7) (AID 434973)
 - qHTS Assay for Rab9 Promoter Activators (AID 485297)
 - qHTS Assay for NPC1 Promoter Activators (AID 485313)
 - Single concentration confirmation of uHTS for inhibitors of Sentrin-specific protease 7 (SEN7) using a Luminescent assay (AID 488917)
 - Single concentration confirmation of inhibitors of Sentrin-specific proteases (SENPs) using a Caspase-3 Selectivity assay (AID 488918)
 - Activator for delta FosB/delta FosB homodimer Measured in Biochemical System Using Plate Reader - 2072-01-Activator SinglePoint HTS Activity (AID 493131)
 - qHTS screen for small molecules that induce genotoxicity in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1 (AID 504466)
 - Luminescence-based cell-based primary high throughput screening assay for inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1): repression of SF-1 (NR5A1) activated StAR promoter by full-length DAX-1 (AID 652010)
 - Luminescence-based cell-based primary high throughput screening assay to identify activators of the DAF-12 from the parasite H. contortus (hcDAF-12) (AID 652067)
 - Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12). (AID 687014)
 - Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12). (AID 743050)

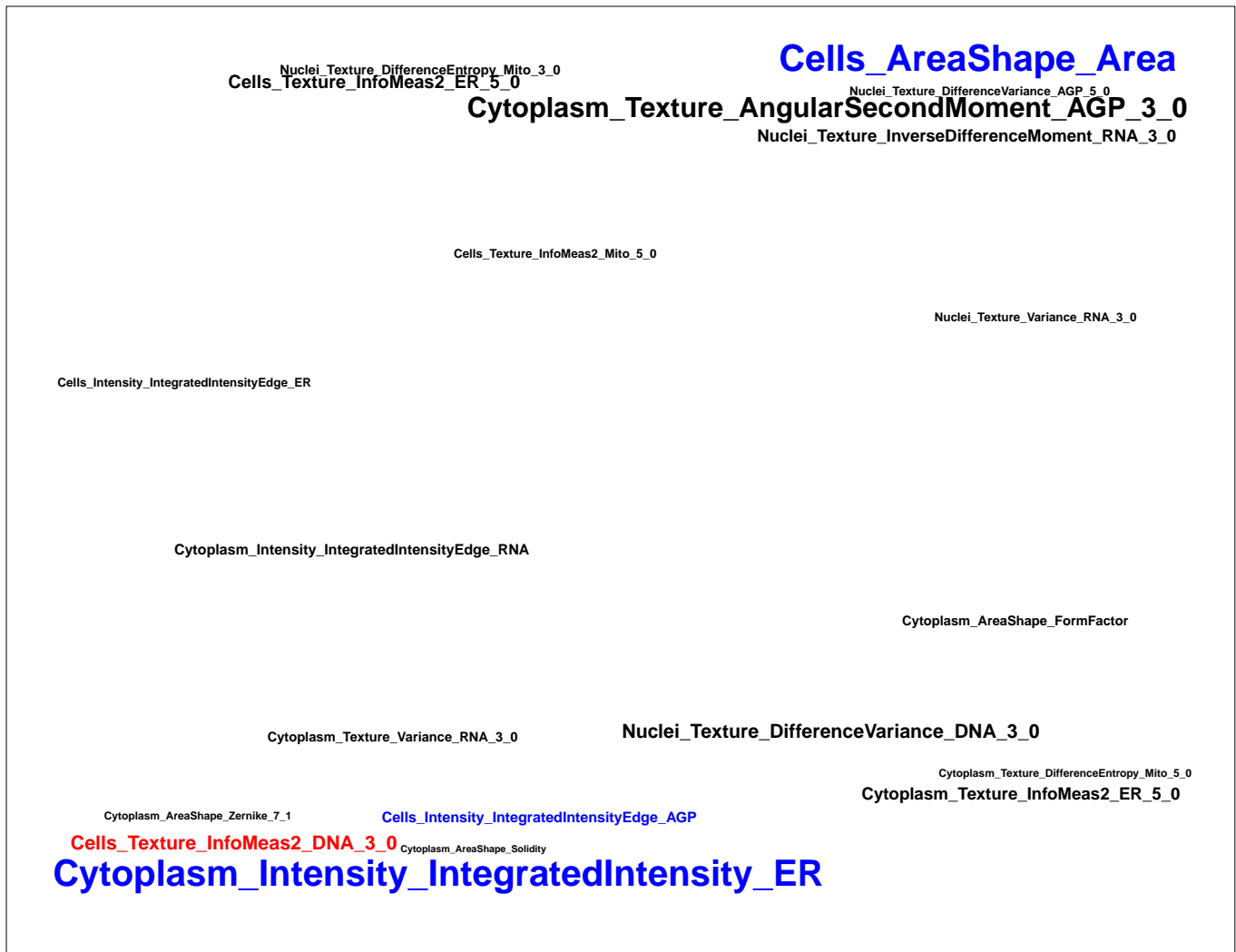
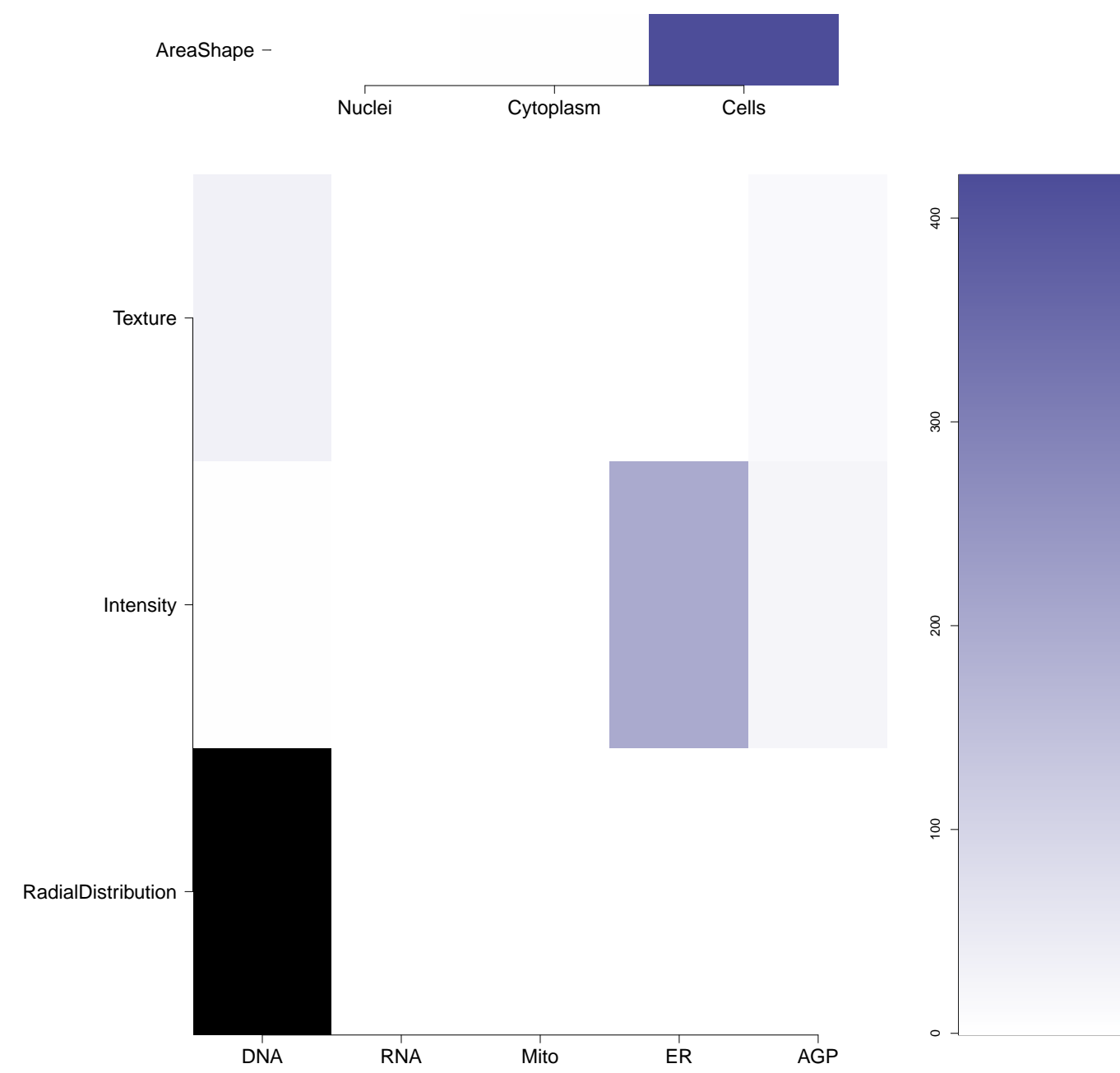
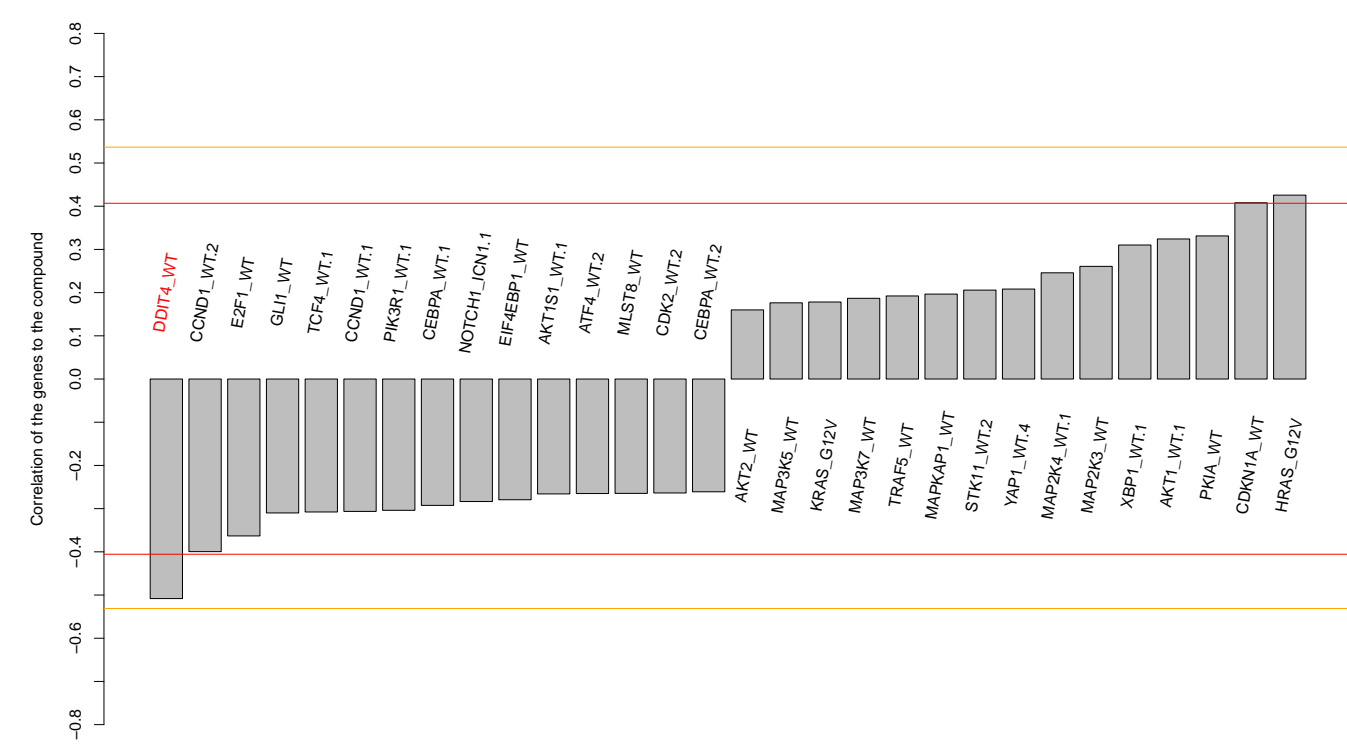
BRD-K06042430-001-01-9
PubChem CID : 54618127



0.99 (in 4 replicates)

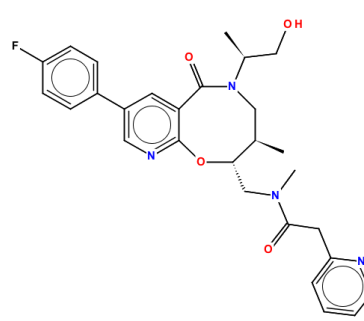
-0.51

0.916



Total number of assays tested in: 36.

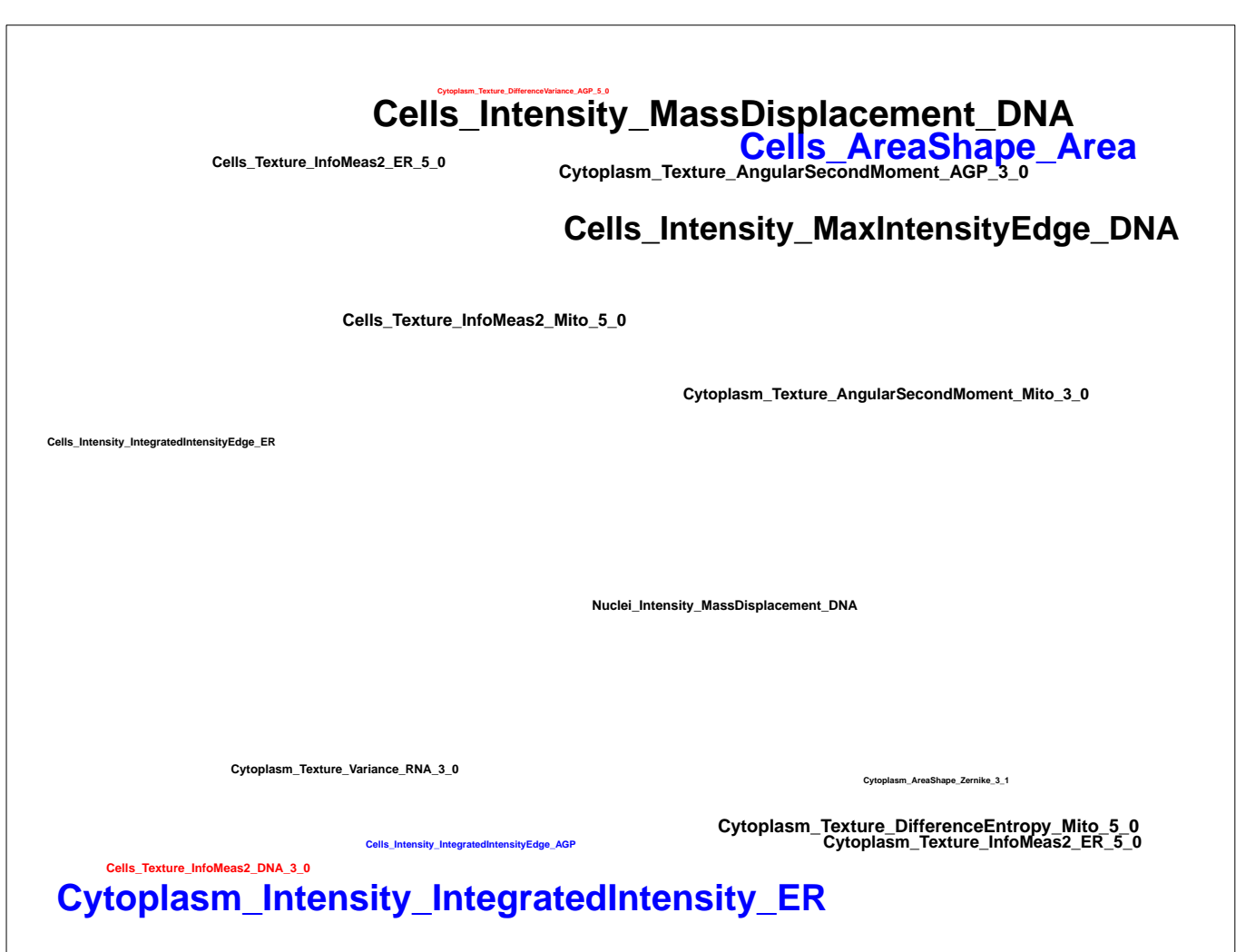
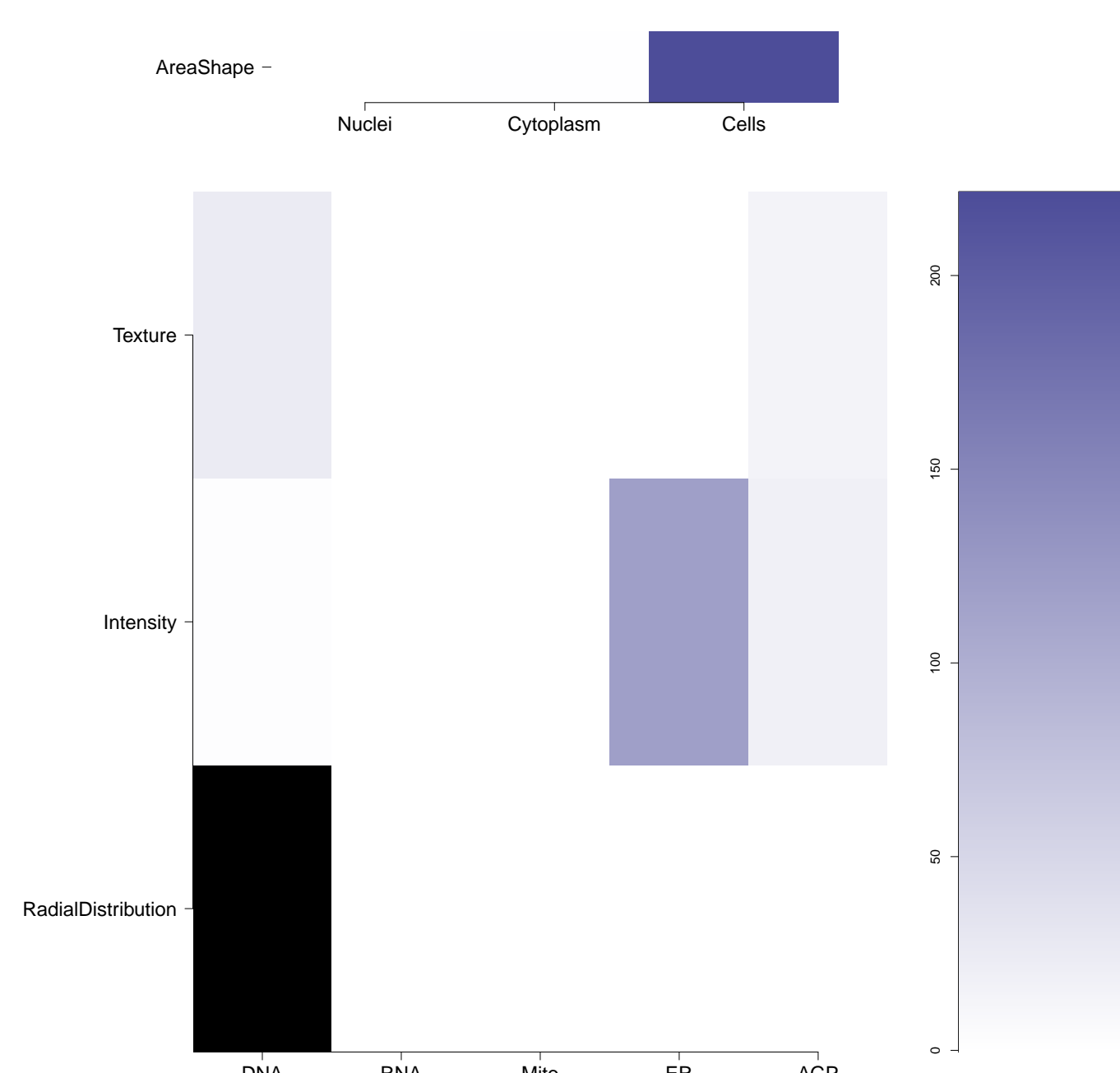
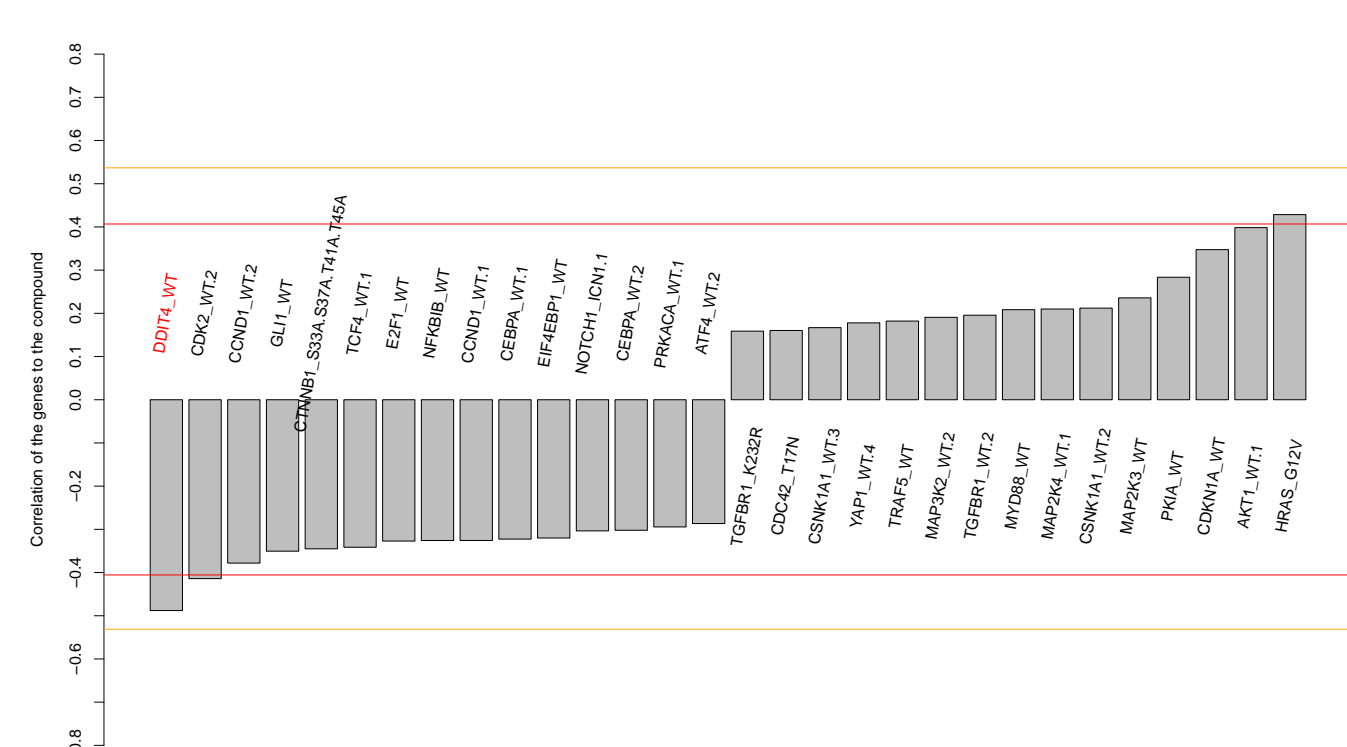
BRD-K87062384-001-01-5
PubChem CID : 54618426



NA (in 1 replicates)

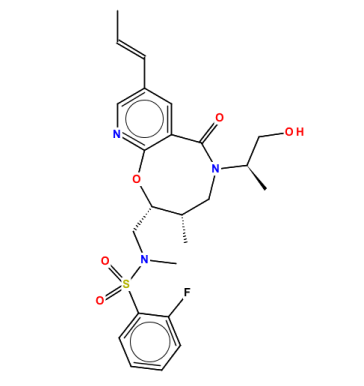
-0.49

0.315



Total number of assays tested in: 37.

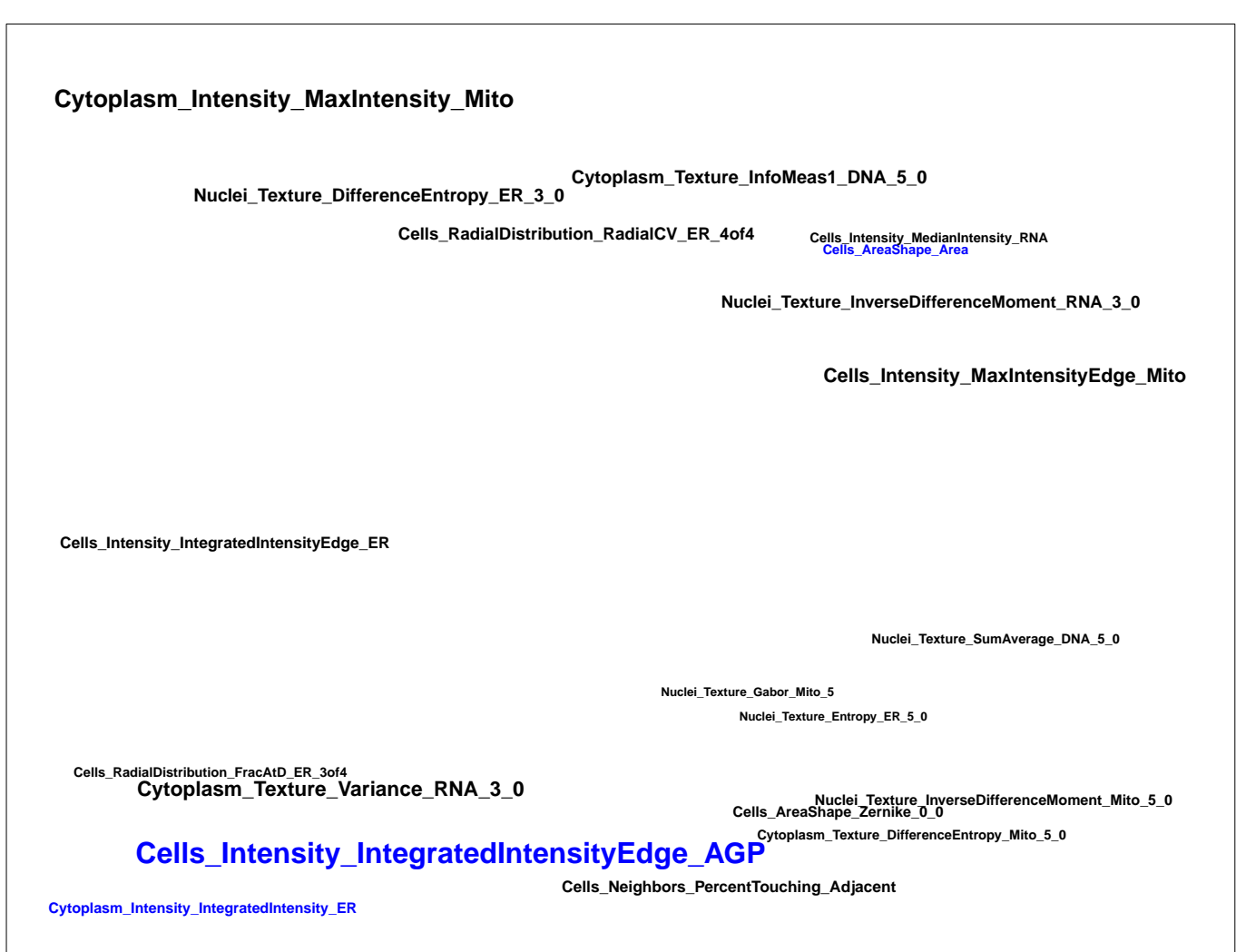
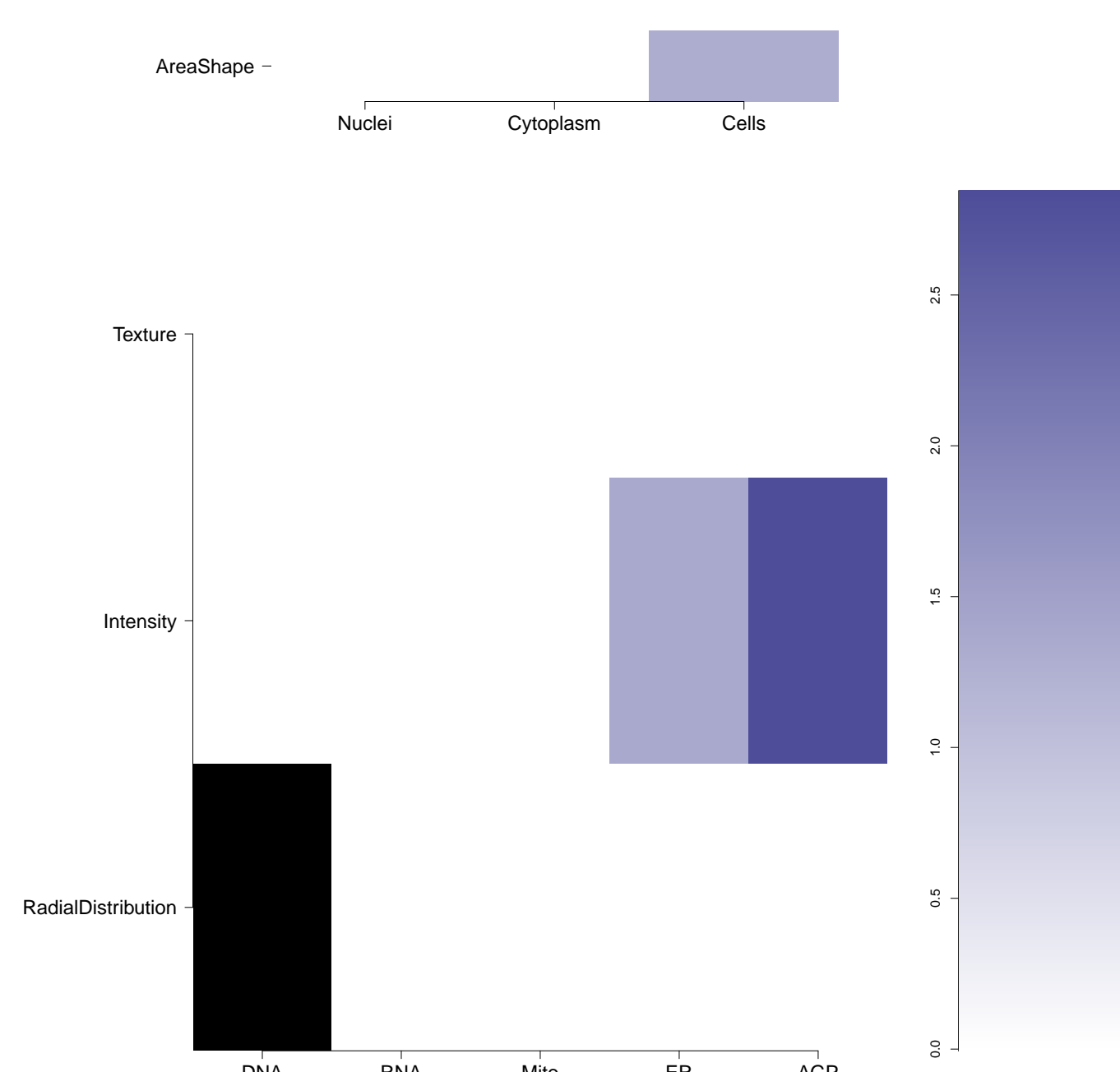
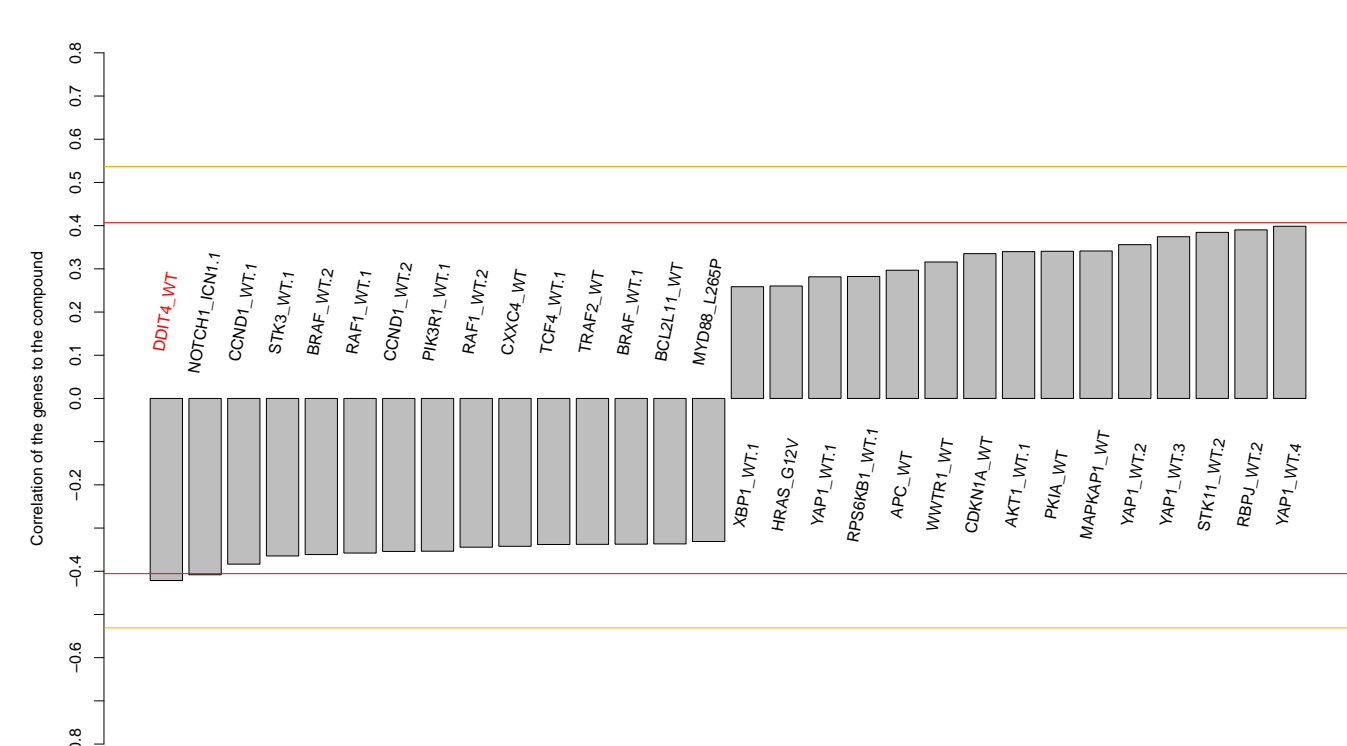
BRD-K61505971-001-01-2
PubChem CID : 54619345



0.61 (in 4 replicates)

-0.42

0.315



Total number of assays tested in: 38.