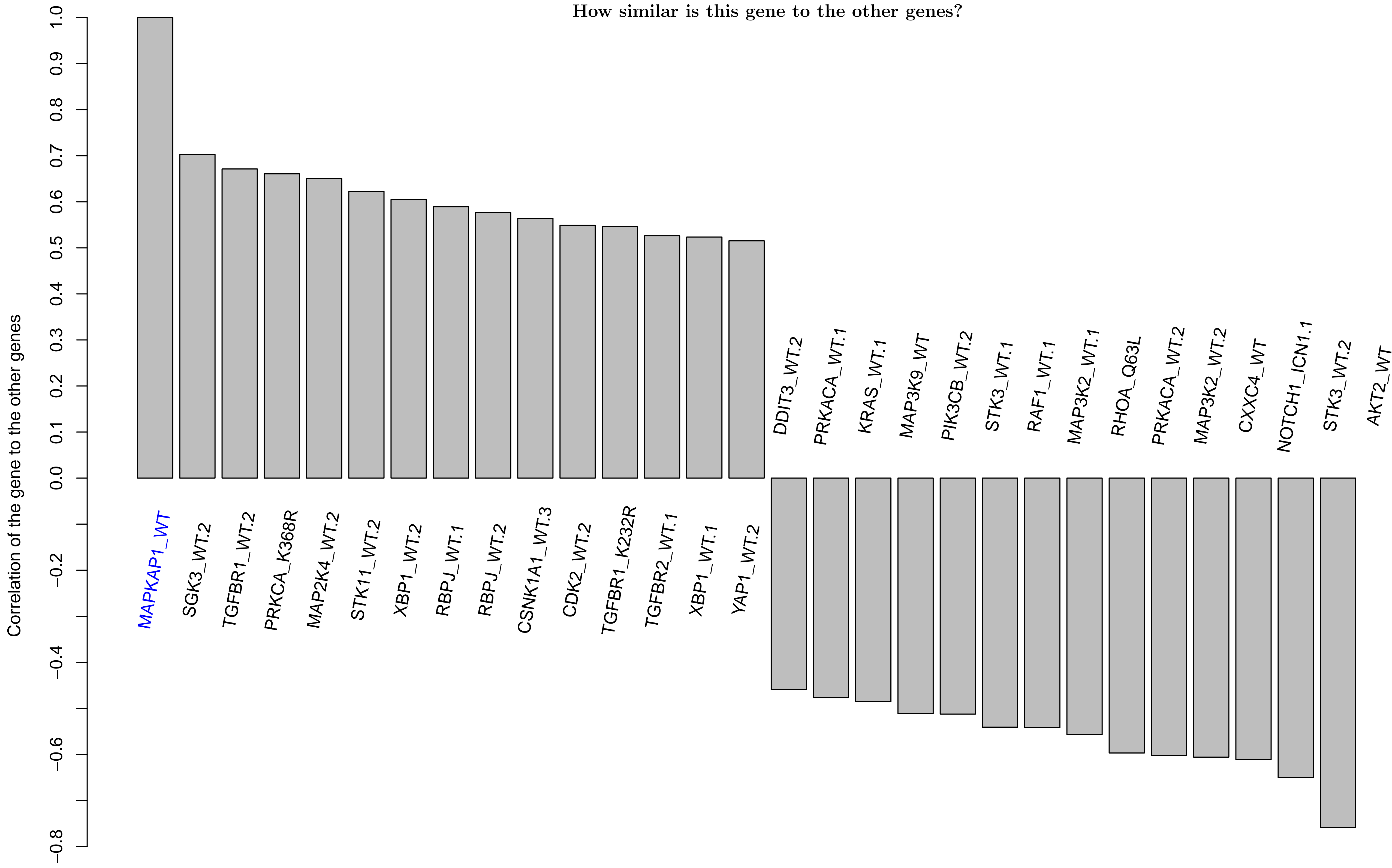
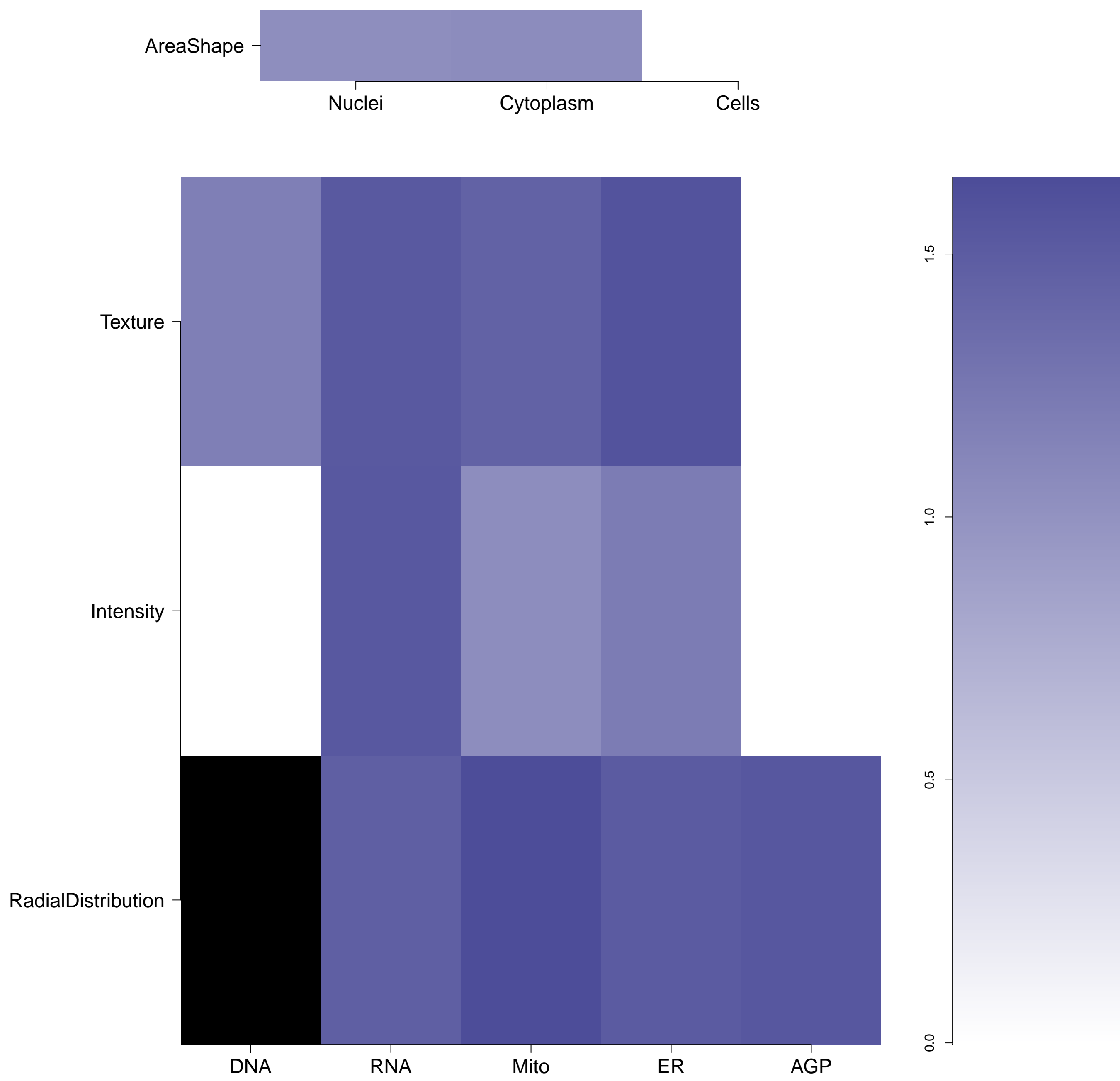


MAPKAP1.WT - in Canonical TOR

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

MAPKAP1.WT (41744)

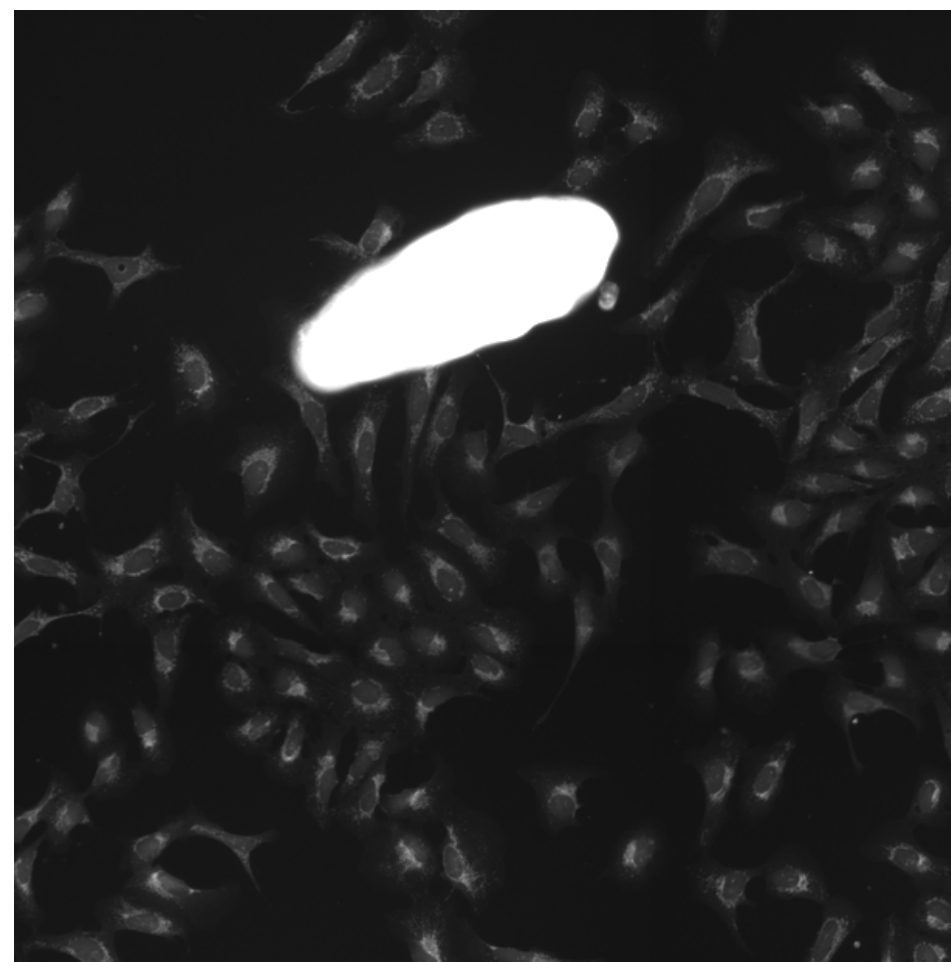
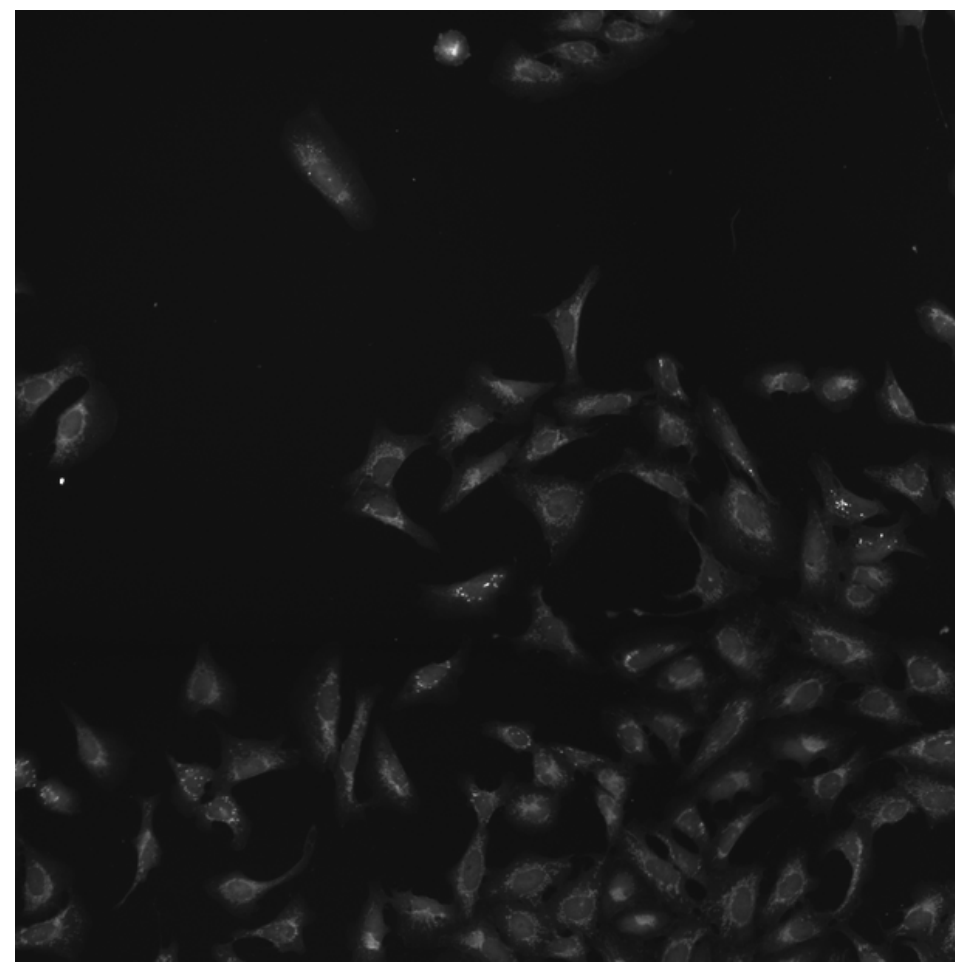
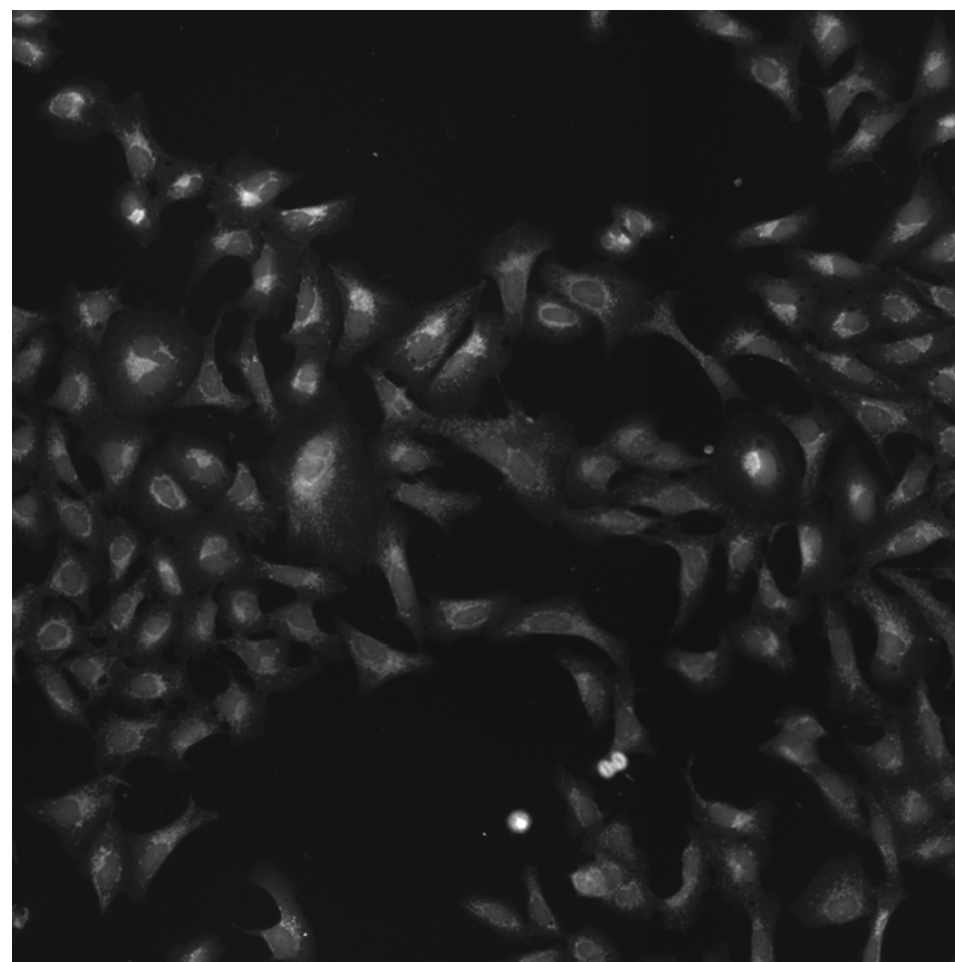
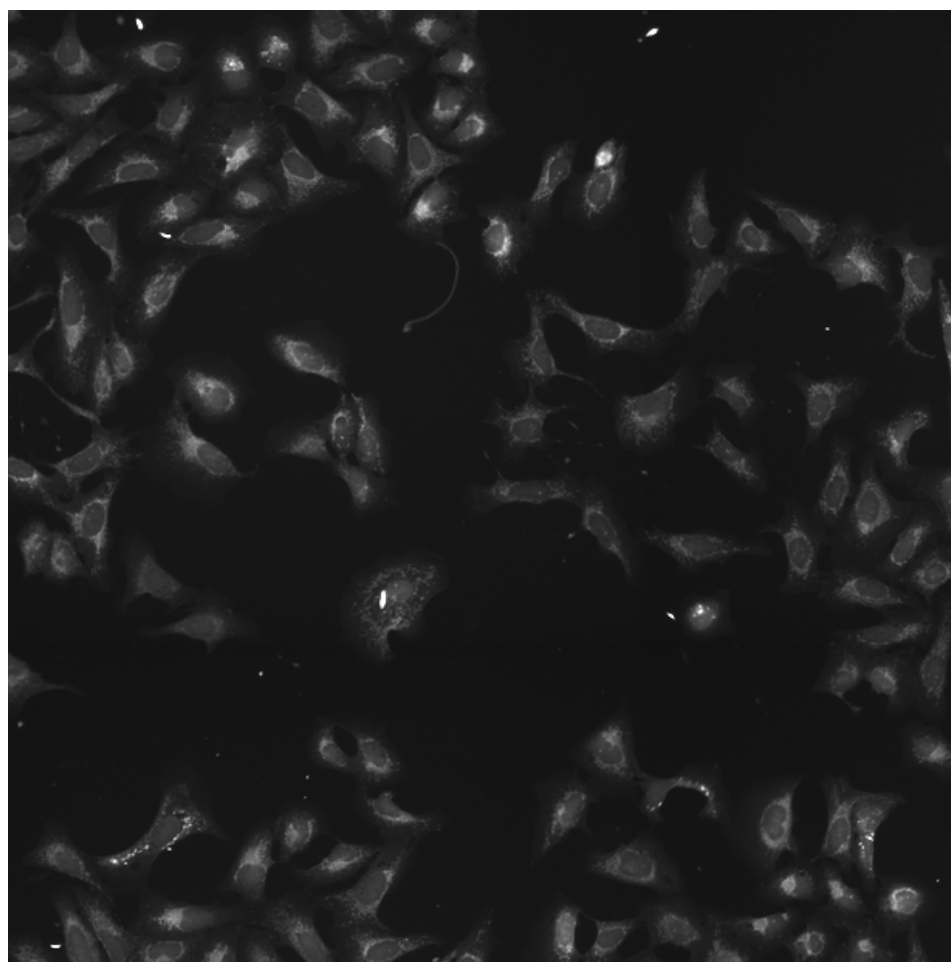
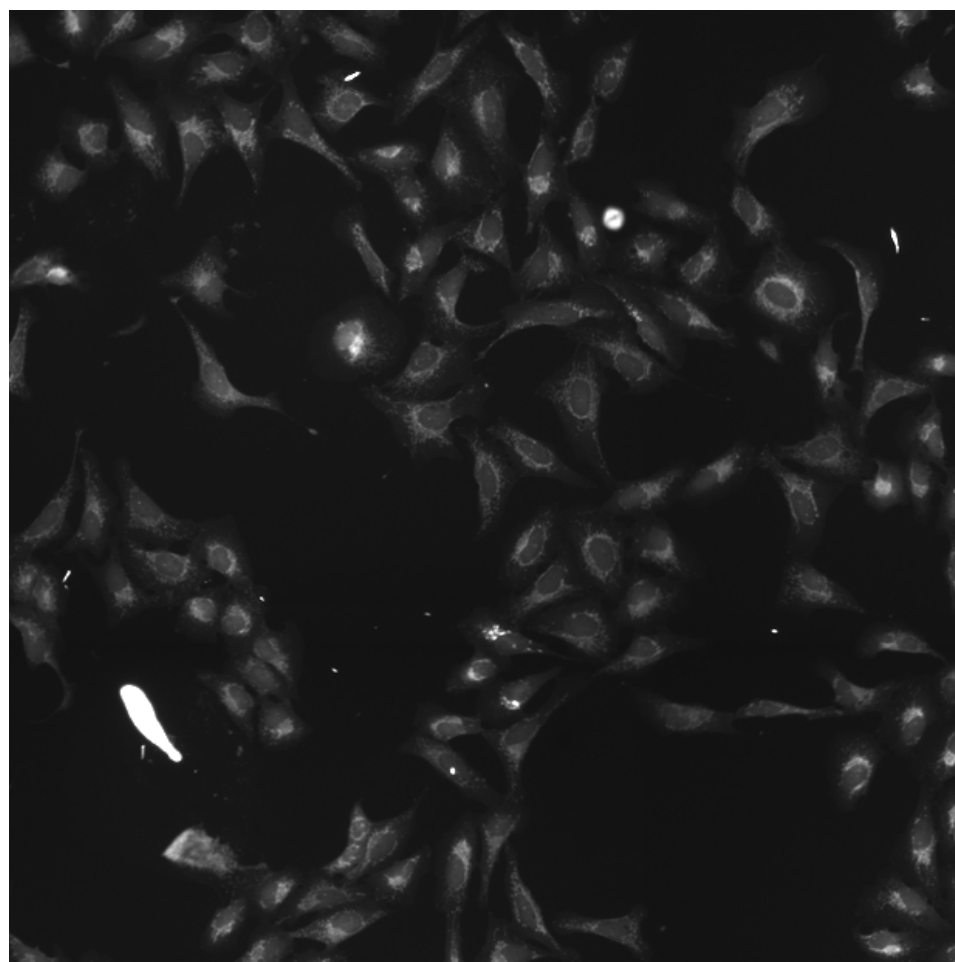
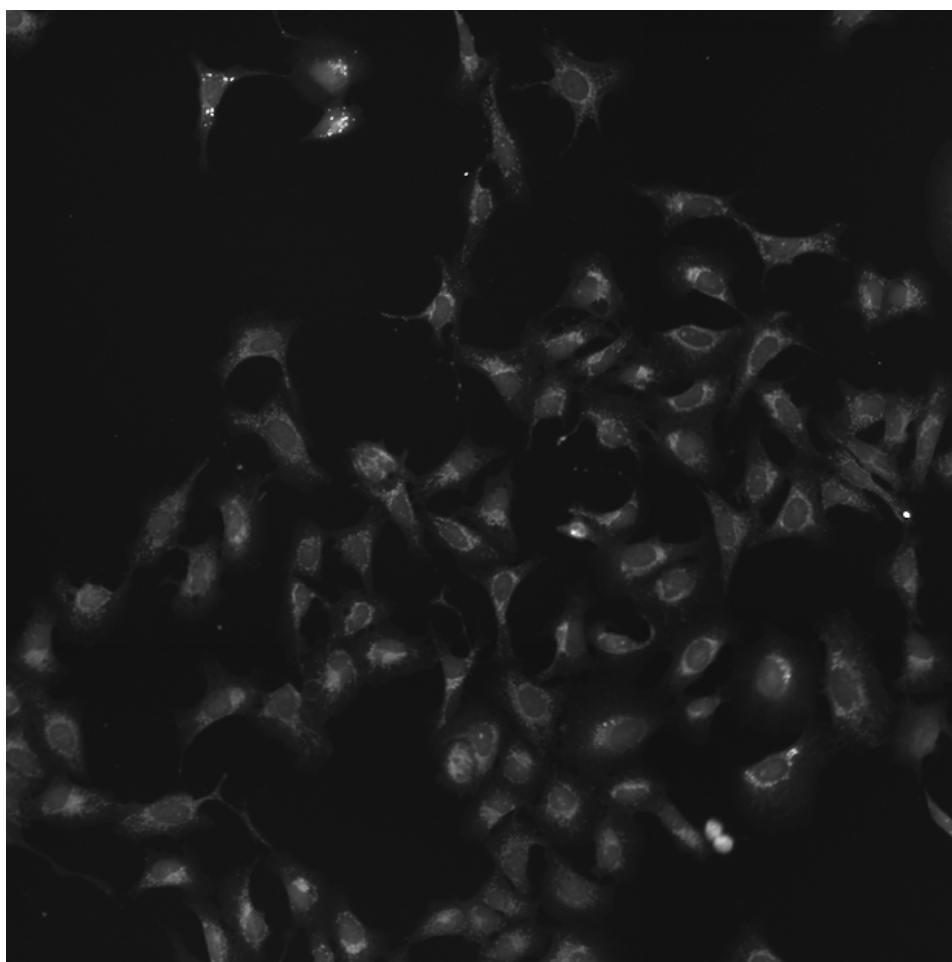
MAPKAP1.WT (41755)

MAPKAP1.WT (41756)

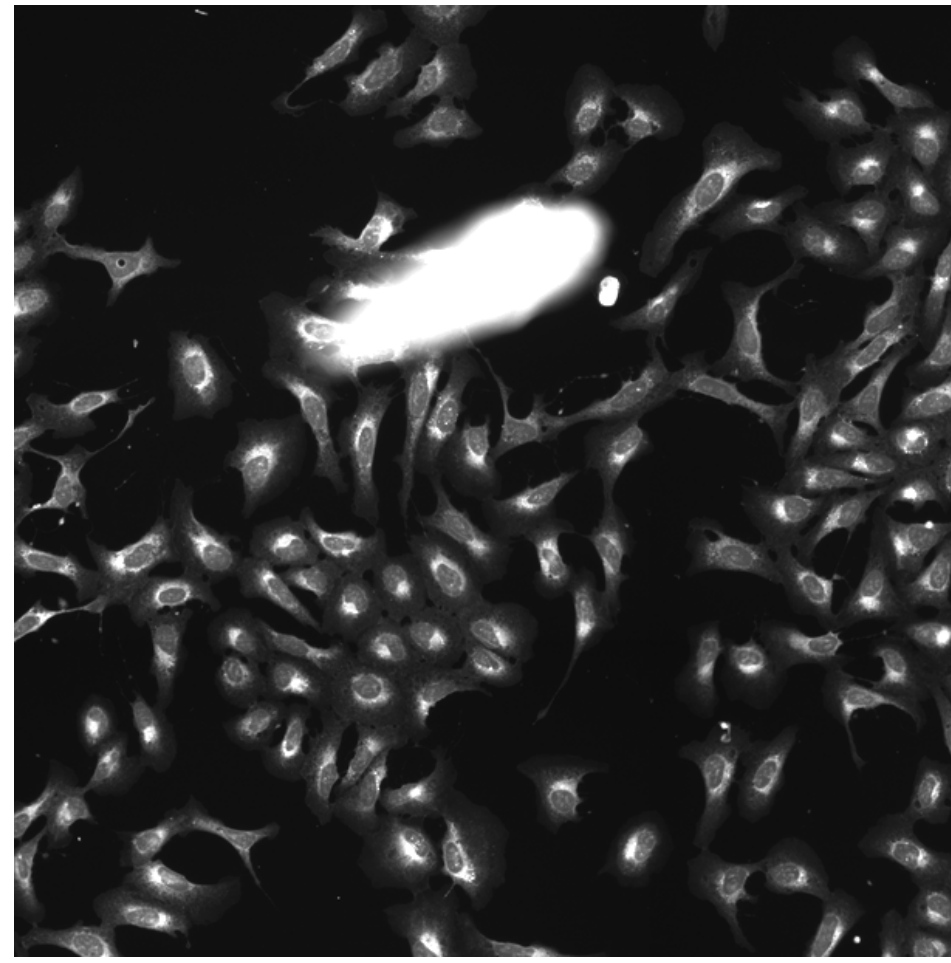
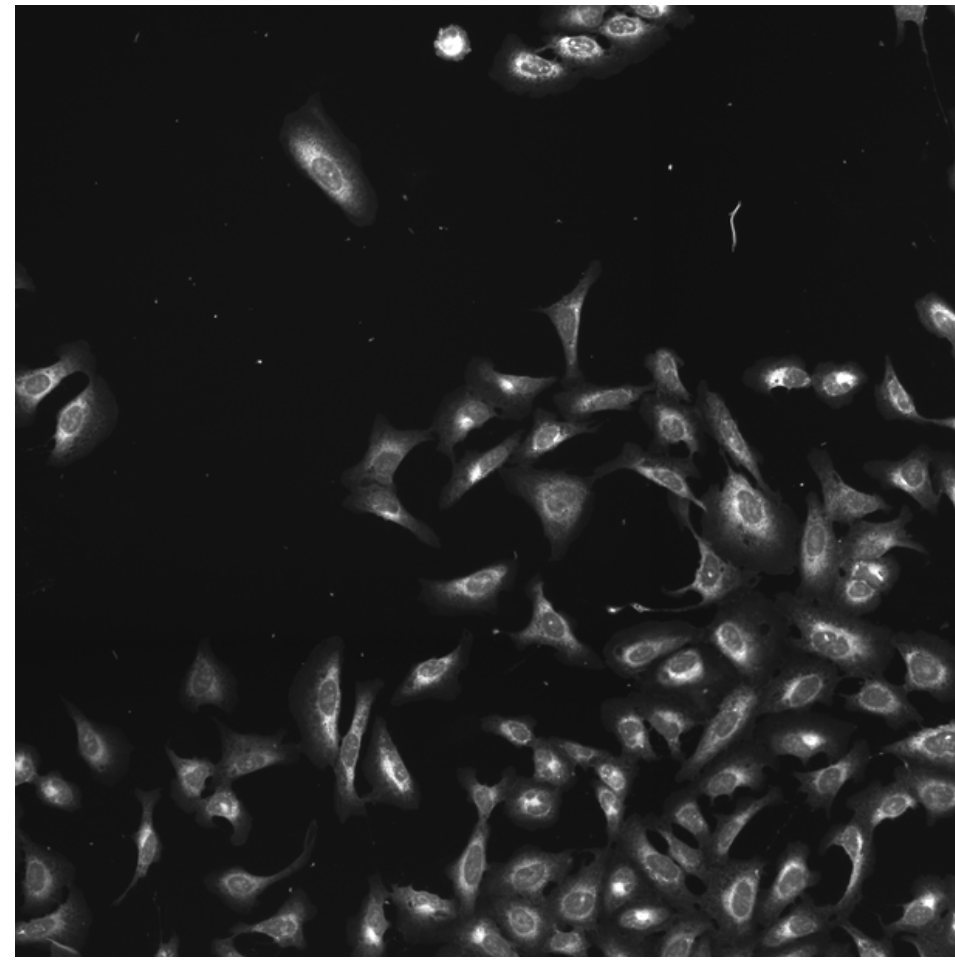
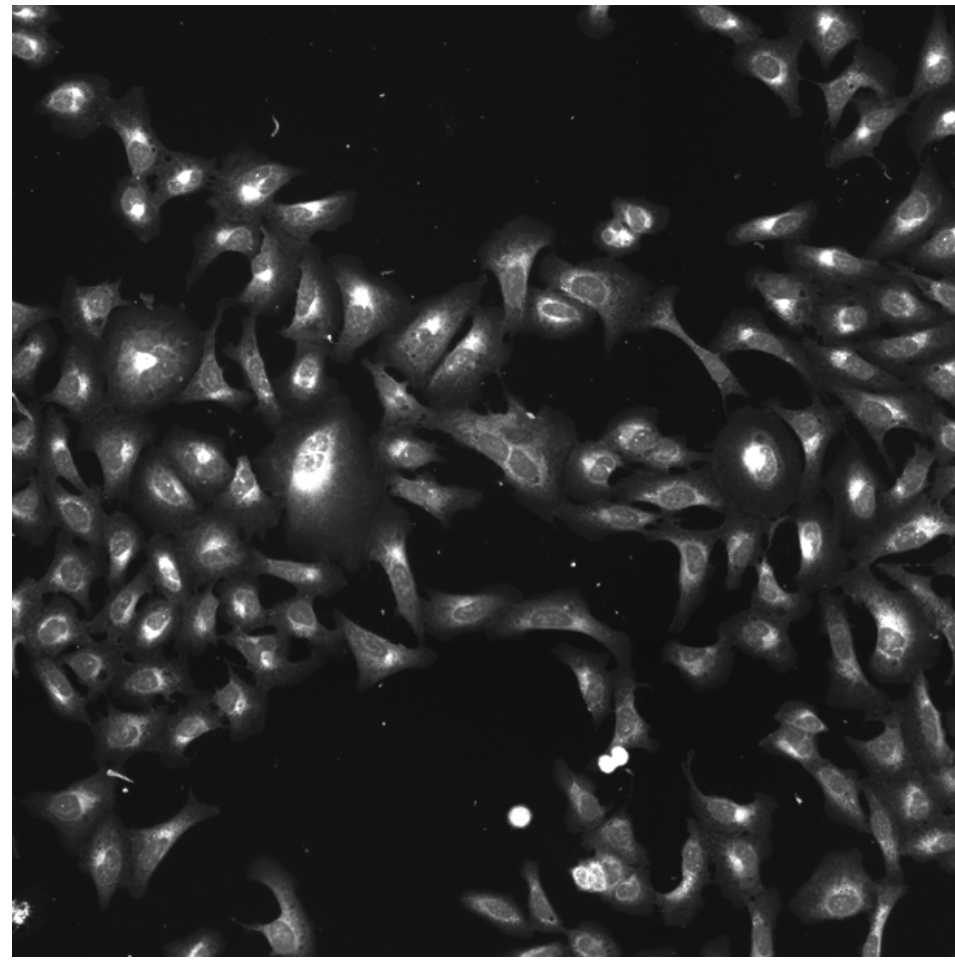
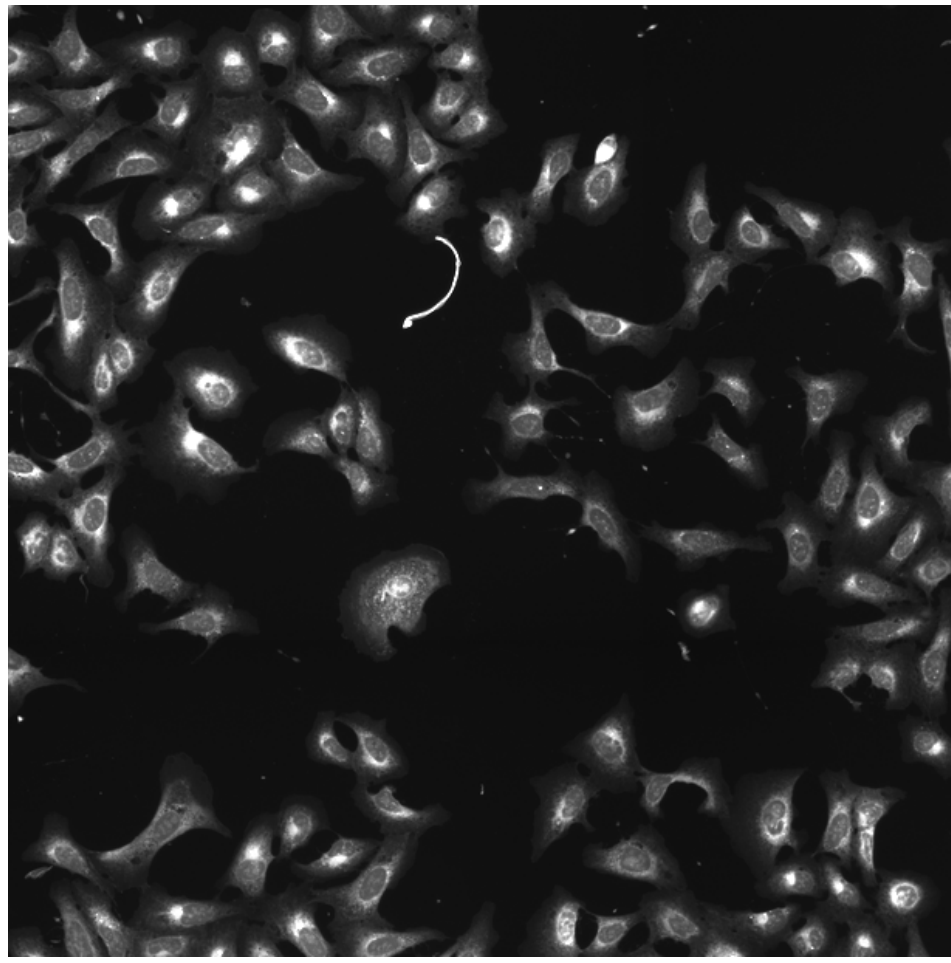
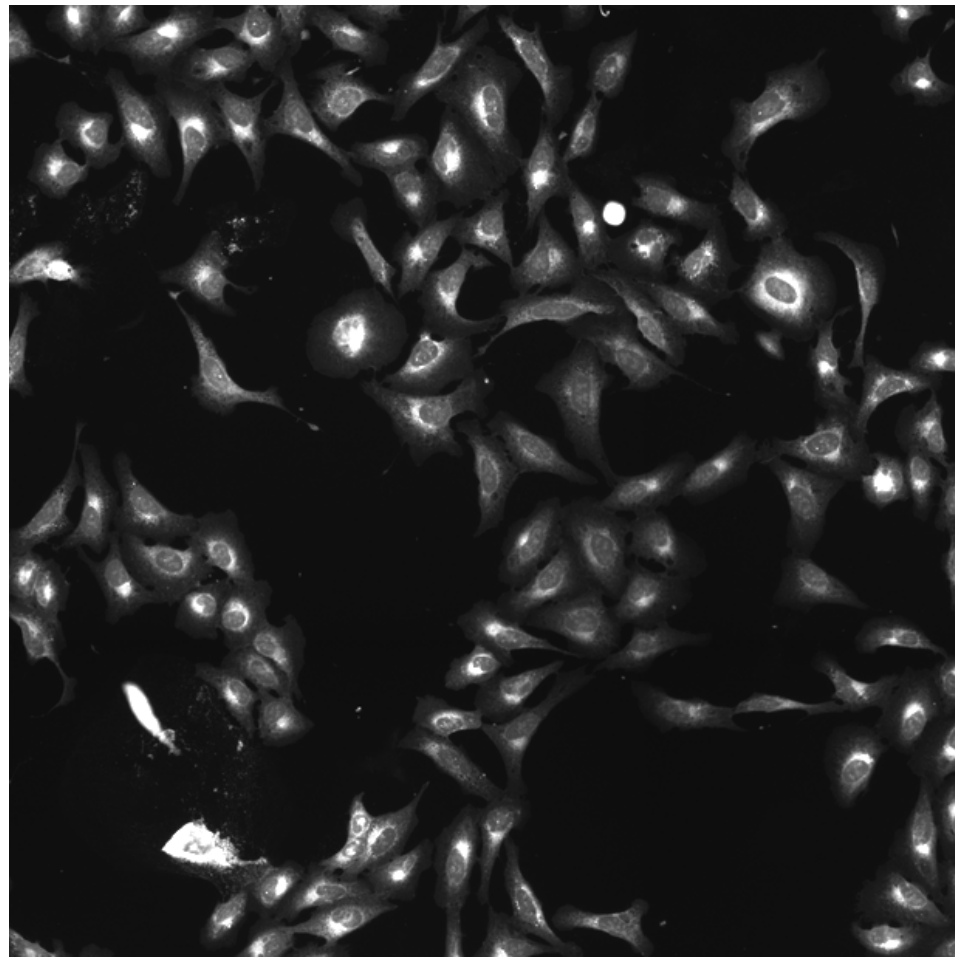
MAPKAP1.WT (41757)

MAPKAP1.WT (41754)

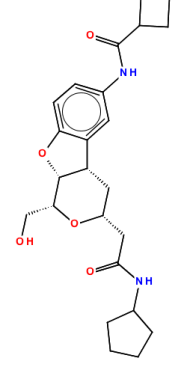
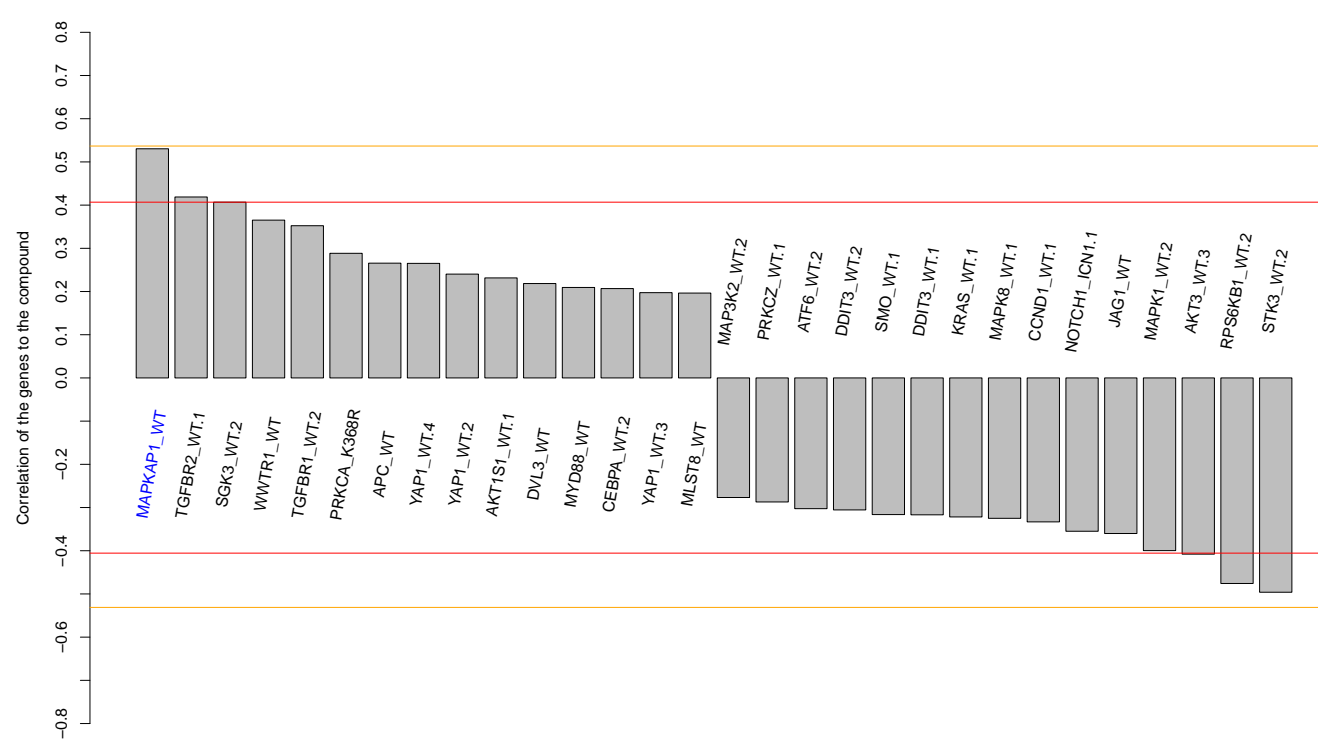
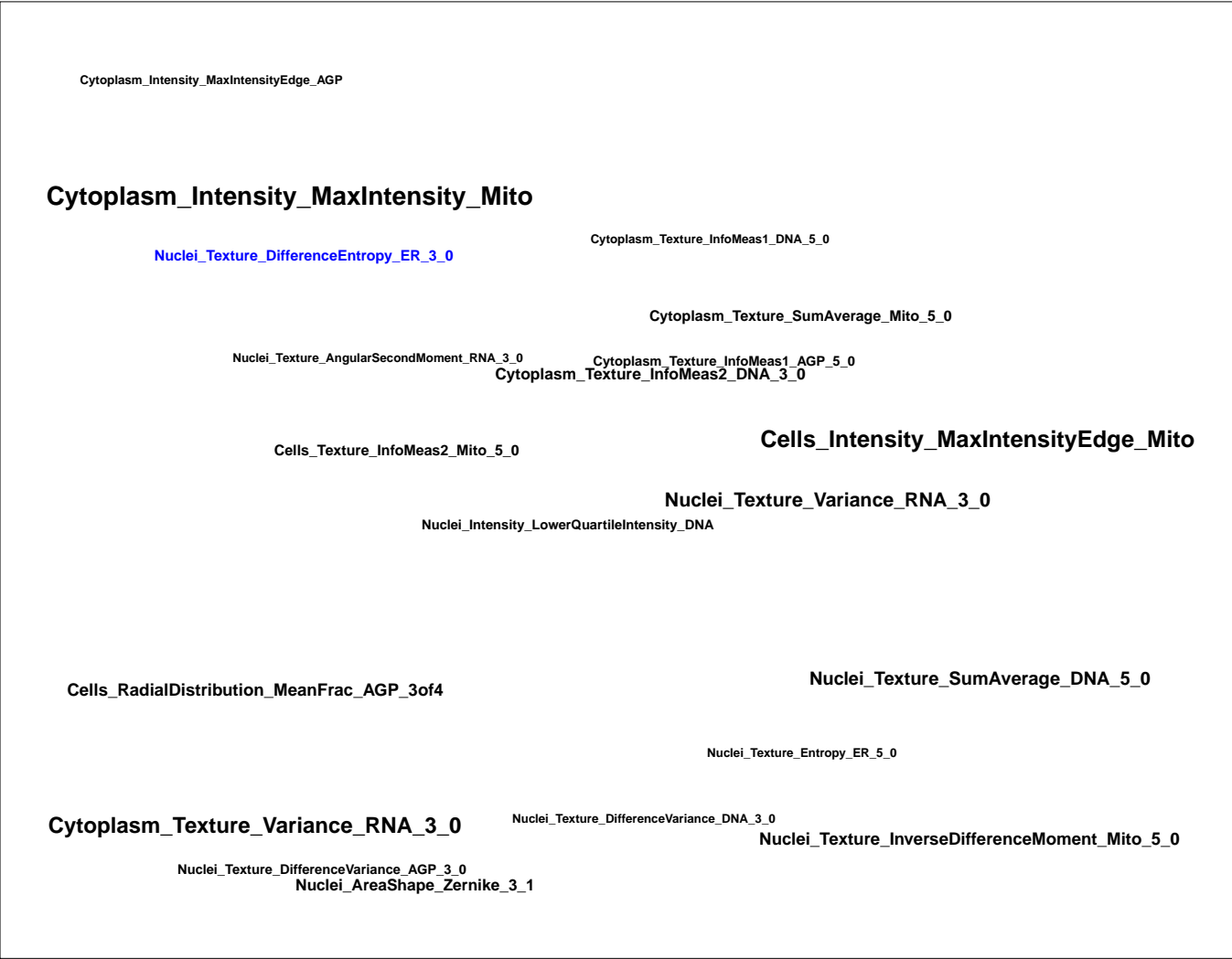
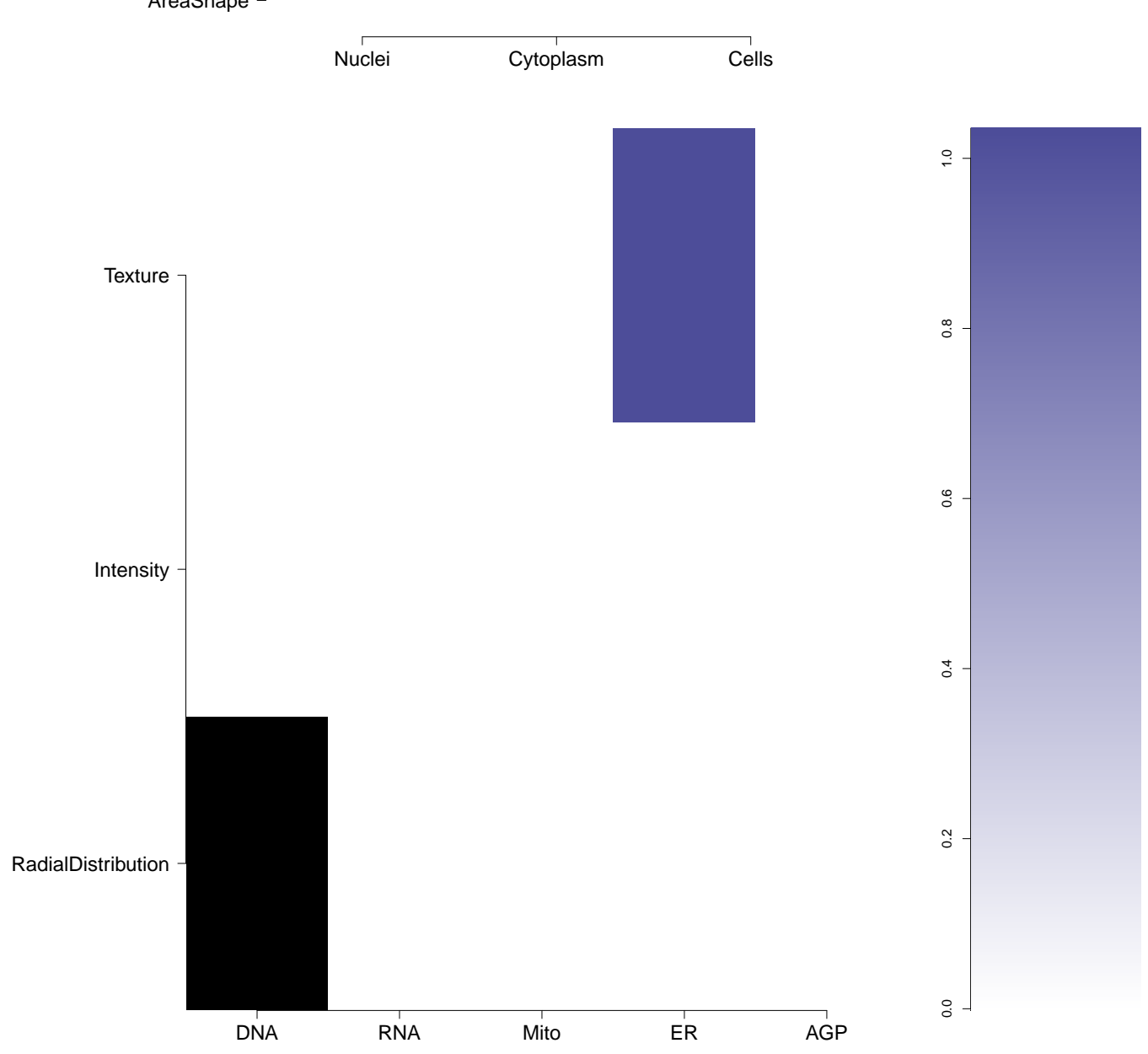
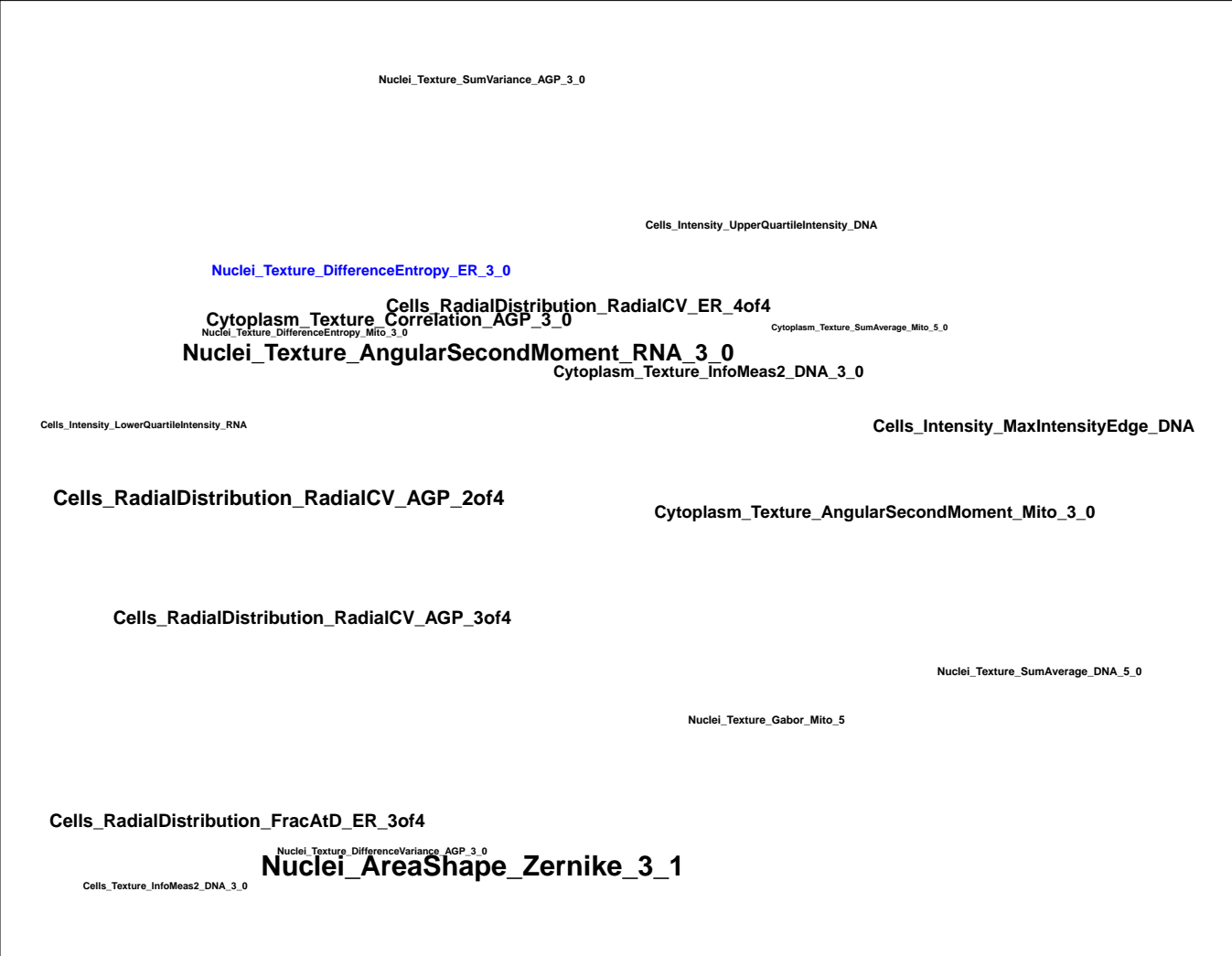
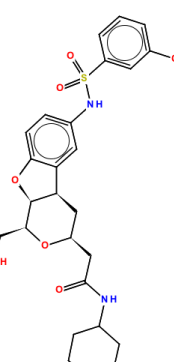

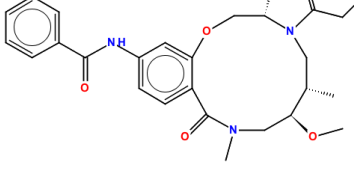
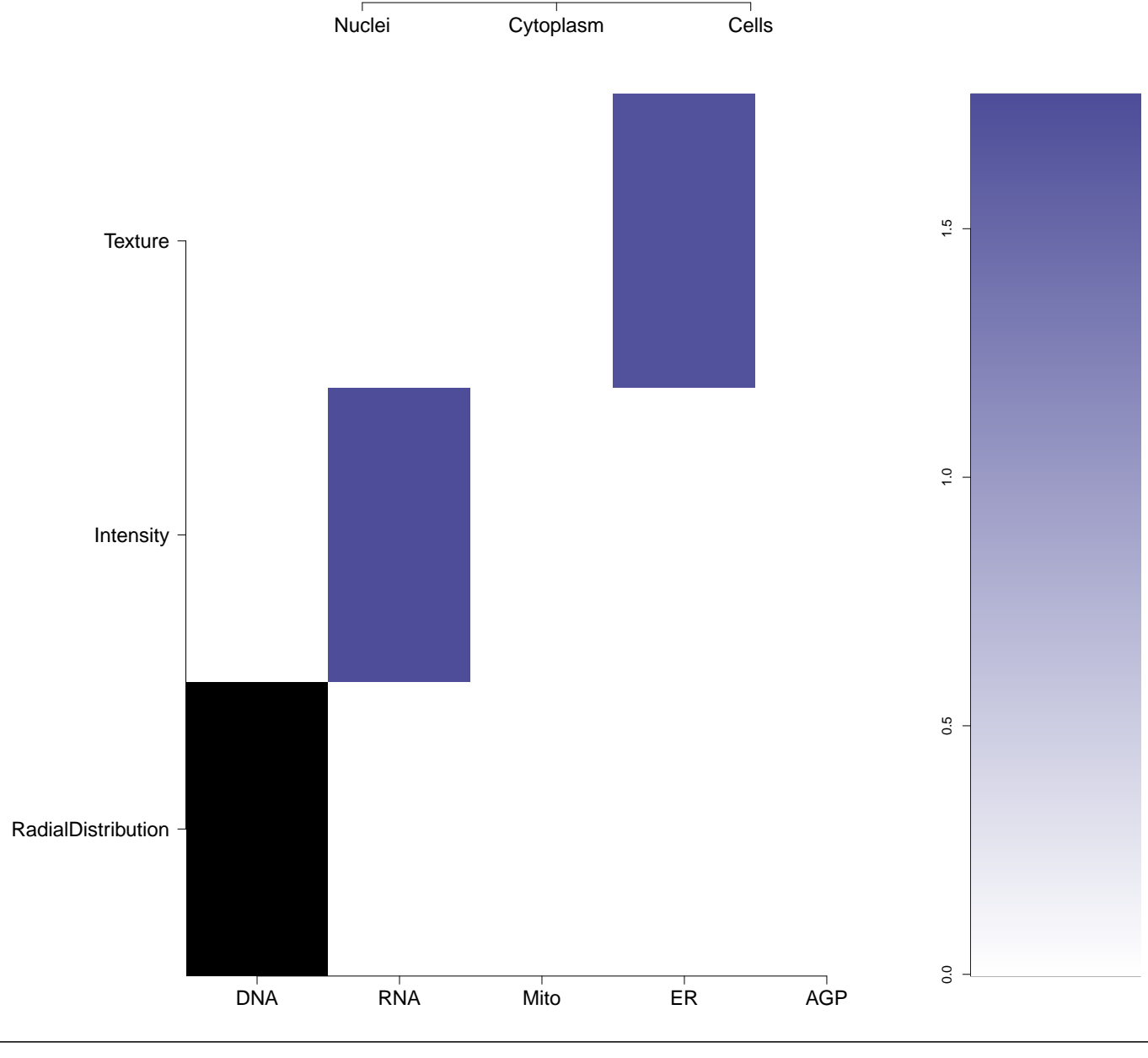
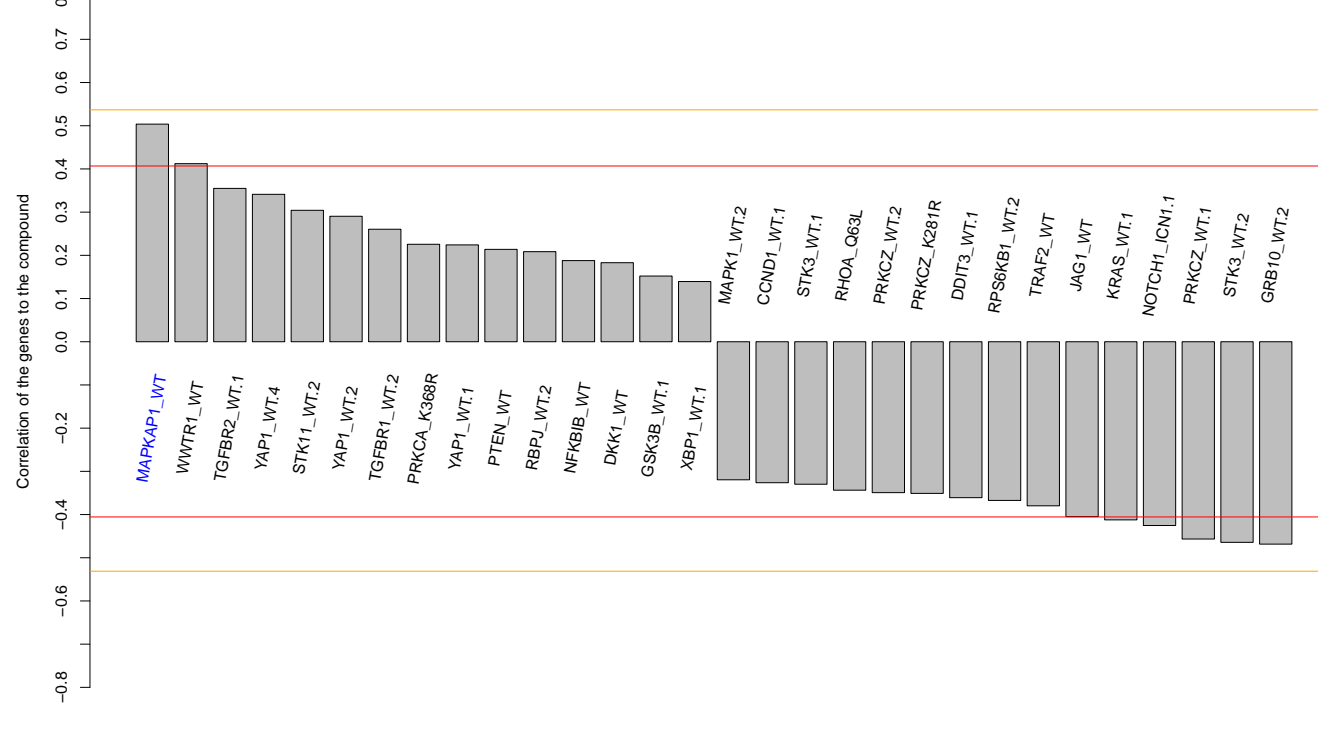
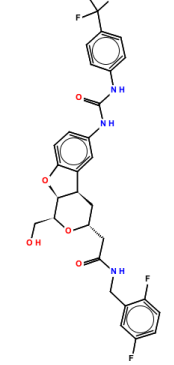
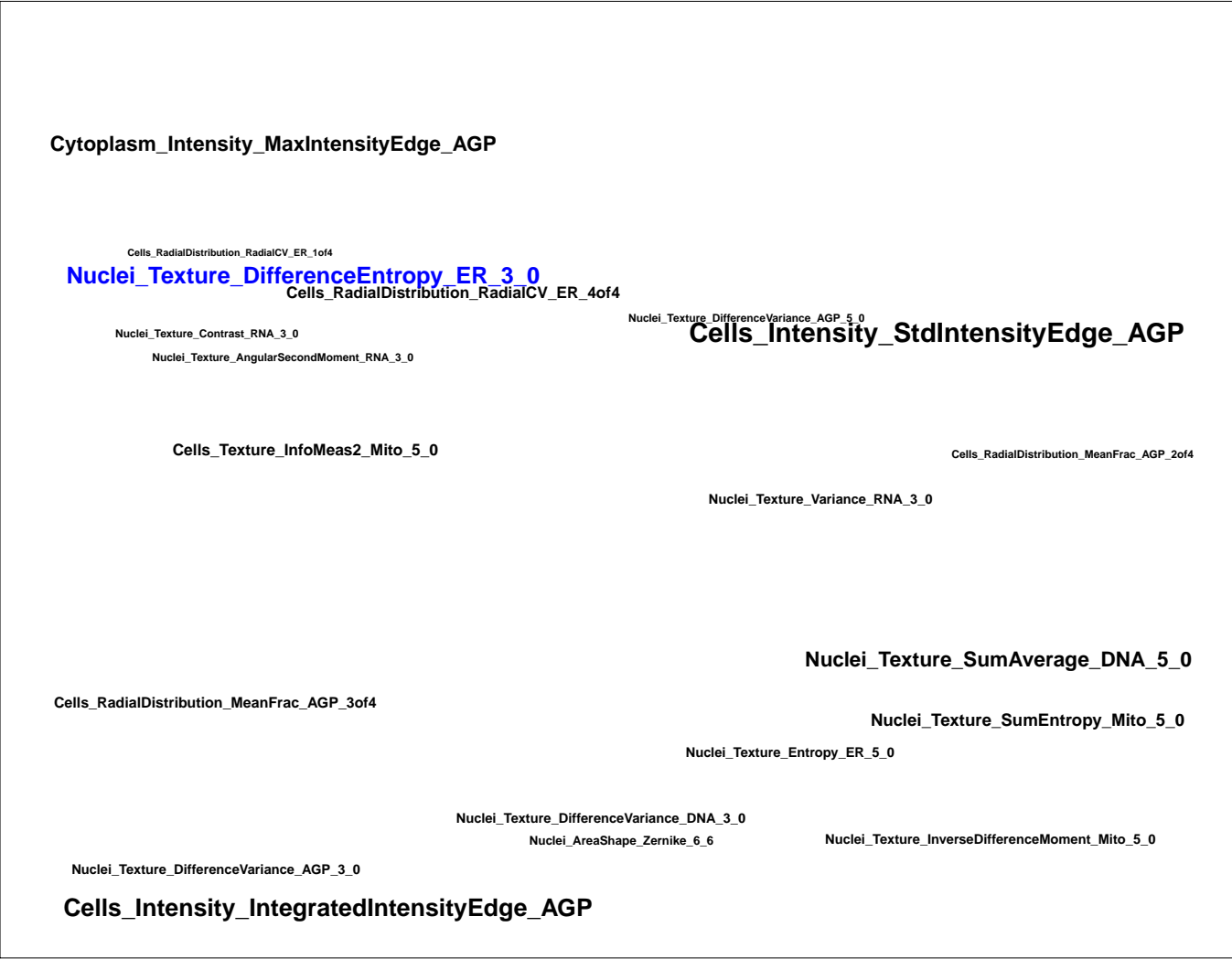
Mito



ER

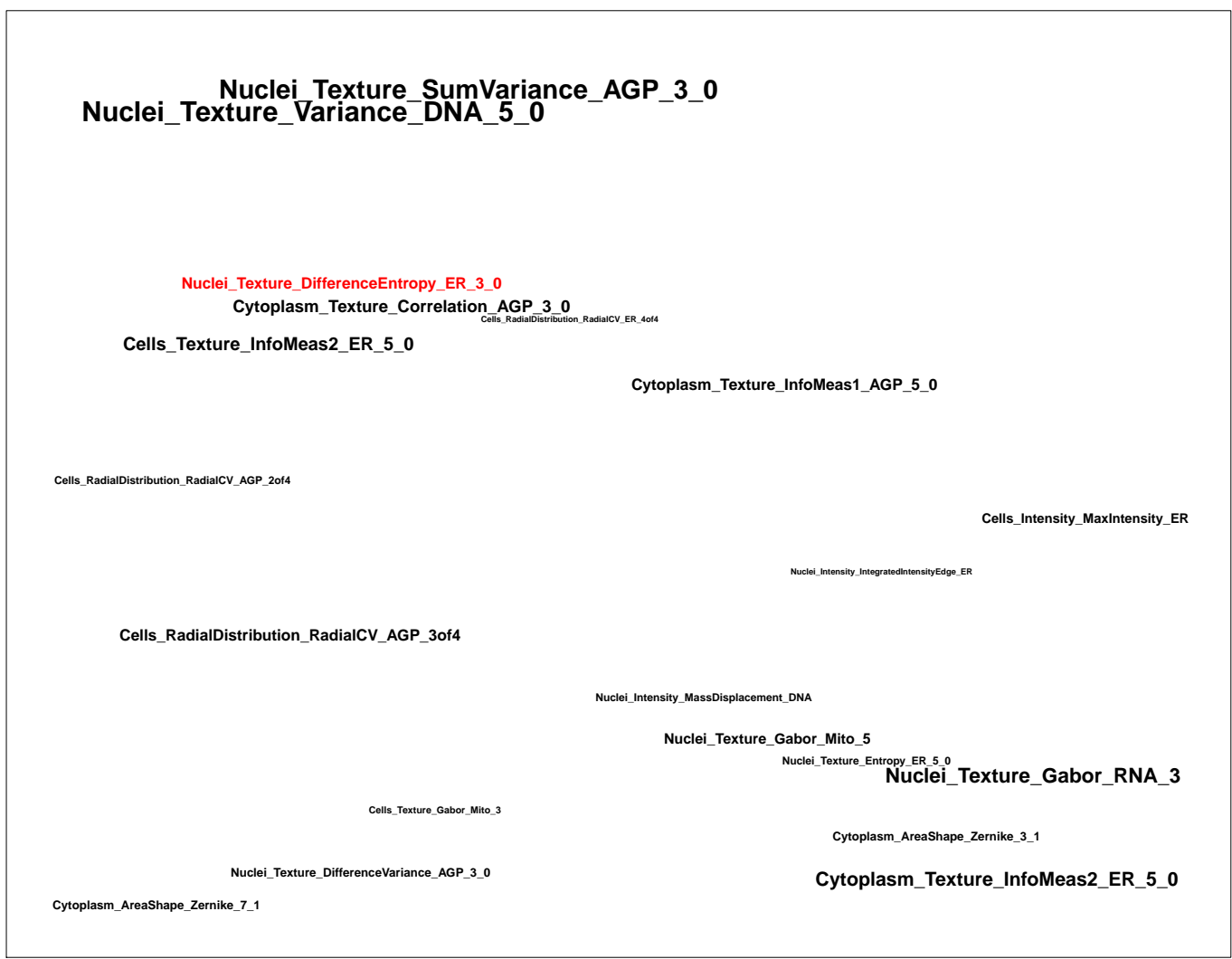
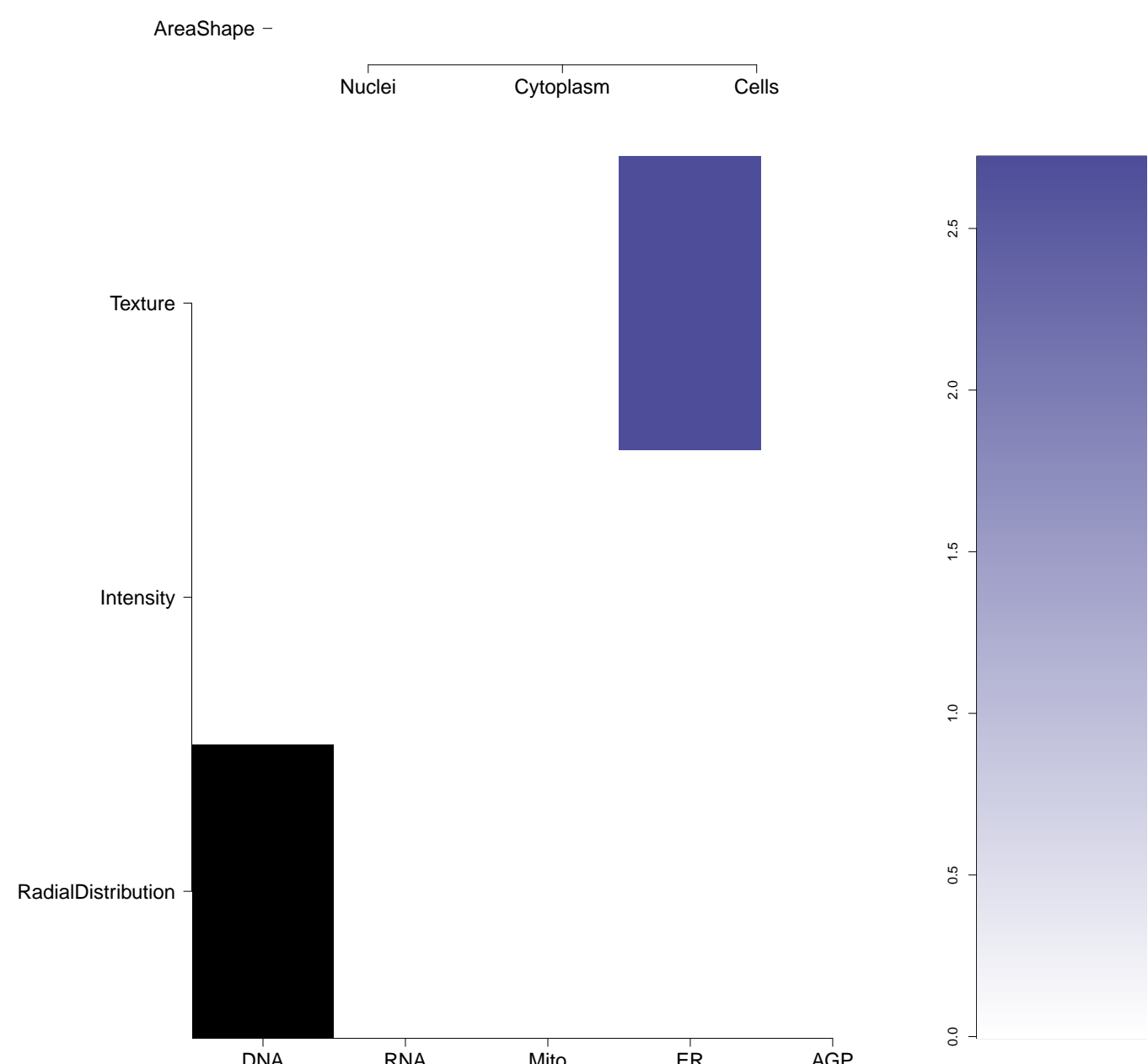
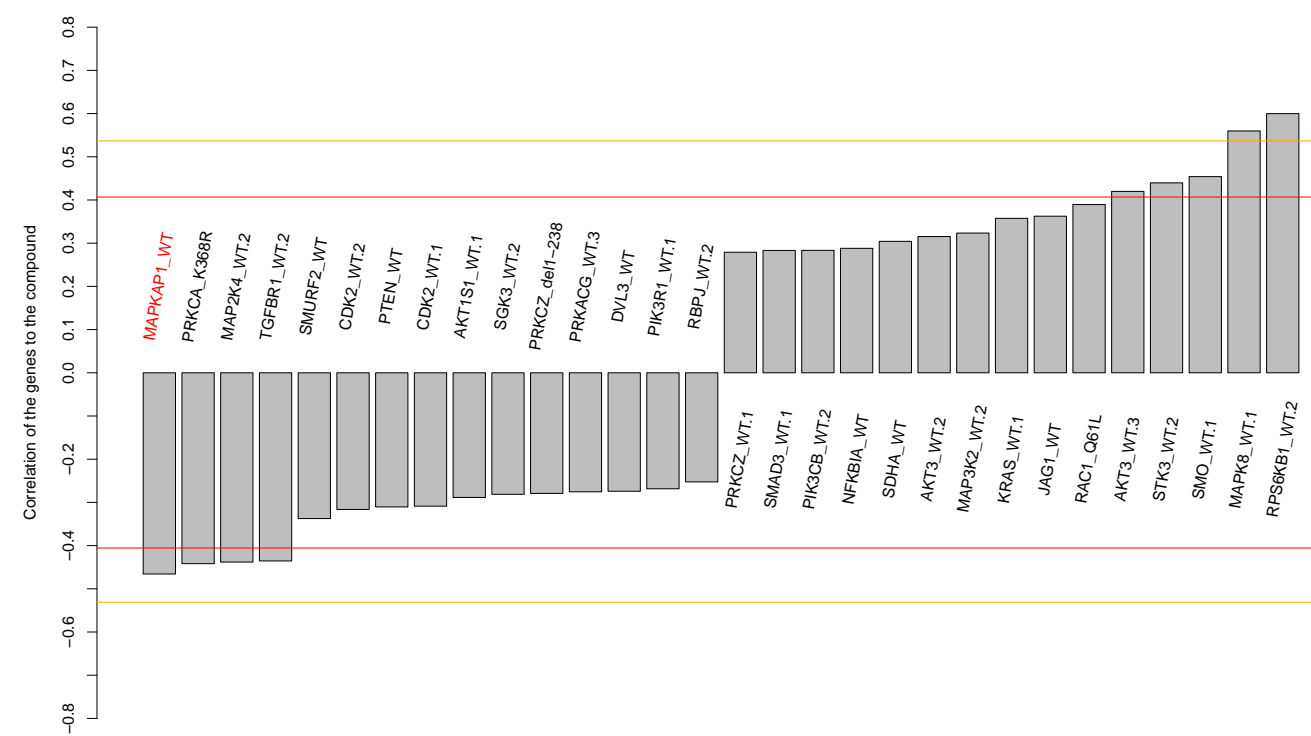


Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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-K00347265-001-01-8 PubChem CID : 54645953		NA (in 1 replicates)	0.53	0.621				Total number of assays tested in: 40.
BRD-K48782834-001-01-2 PubChem CID : 54619202		0.80 (in 4 replicates)	0.53	0.717				Total number of assays tested in: 38.
BRD-K49434056-001-01-0 PubChem CID : 54645999		0.71 (in 2 replicates)	0.51	0.621				Total number of assays tested in: 47. Active in the following assays: <ul style="list-style-type: none"> HTS for the detection of C. neoformans cell lysis via adenylate kinase (AK) release Measured in Microorganism System Using Plate Reader - 2162-01.Inhibitor.SinglePoint.HTS.Activity (AID 651654) IC50 with Alamar Blue Measured in Microorganism System Using Plate Reader - 2162-02.Inhibitor.Dose.CherryPick.Activity (AID 686998)
BRD-K43048602-001-01-3 PubChem CID : 54631933		0.55 (in 4 replicates)	0.50	0.621				Total number of assays tested in: 39. Active in the following assays: <ul style="list-style-type: none"> Inhibition of T.cruzi proliferation in culture Measured in Cell-Based System Using Plate Reader - 2162-01.Inhibitor.SinglePoint.HTS.Activity (AID 624255)
BRD-K37032043-001-01-2 PubChem CID : 54641078		NA (in 1 replicates)	0.50	NA				Total number of assays tested in: 45. Active in the following assays: <ul style="list-style-type: none"> HTS for the detection of C. neoformans cell lysis via adenylate kinase (AK) release Measured in Microorganism System Using Plate Reader - 2162-01.Inhibitor.SinglePoint.HTS.Activity (AID 651654)
BRD-K37753453-001-01-6 PubChem CID : 54646437		0.83 (in 4 replicates)	0.49	NA				Total number of assays tested in: 37.

-0.47

NA



Total number of assays tested in: 367. Active in the following assays:

- Primary cell-based high throughput screening assay to measure STAT3 inhibition (AID 862)
- Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932)
- Leishmaniana major promastigote HTS (AID 1063)
- 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)
- Cycloheximide Counter screen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)
- a qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)
- qHTS for inhibitors of BOR gamma transcription factor (AID 2351)
- qHTS Assay for RhoA Promoter Activators (AID 482927)
- qHTS screen for small molecules that increase activity in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1 (AID 504466)
- qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counter screen for mR-21 project) (AID 588342)
- qHTS identification of Caspase-8 TRAIL sensitizers in a luminescence assay (AID 62354)
- Single concentration confirmation of Caspase-8 TRAIL sensitizer hits in a luminescence panel assay (AID 651596)
- Luminescence-based cell-based primary high throughput screening assay for inhibitors of the orphan nuclear receptor subfamily 1, group B, member 1 (DAX-1/NR0B1): repression of SF-1 (NR5A1) activated SREBP 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 (hGDAF-12) (AID 652067)
- Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glyemes (hGDAF-12) (AID 687014)
- Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. contortus (hGDAF-12) (AID 738932)
- Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. glyemes (hGDAF-12) (AID 743950)