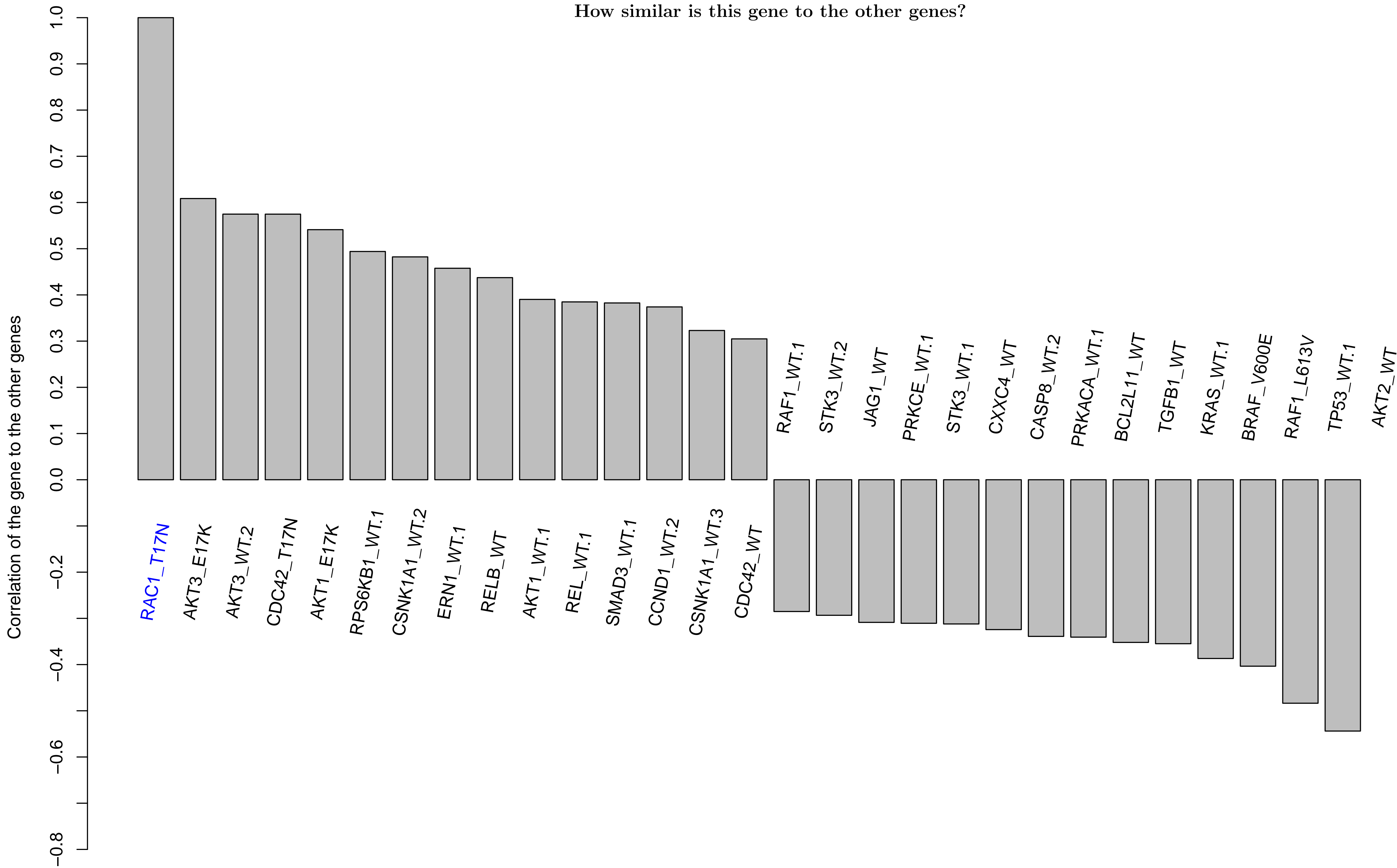
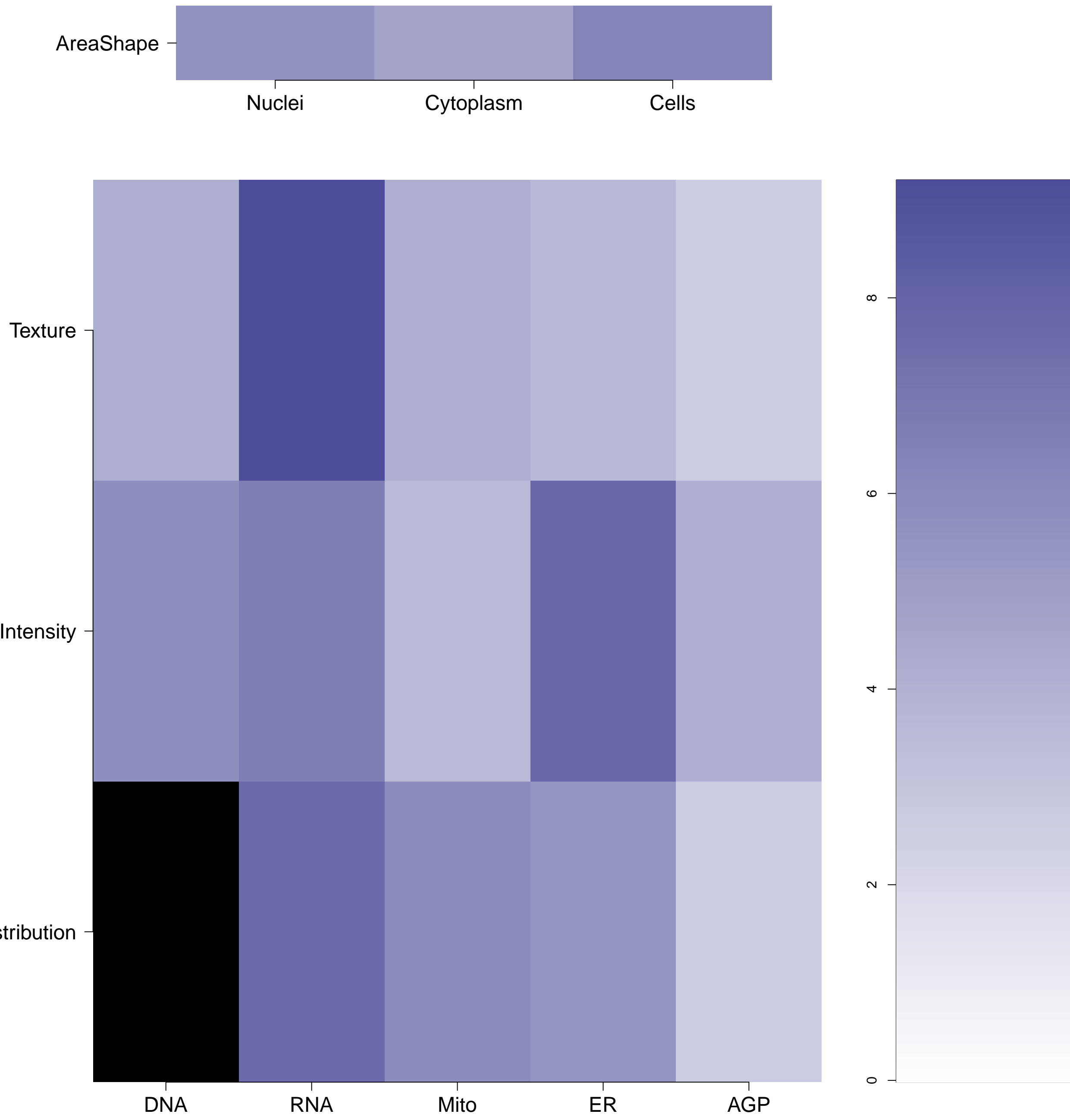


RAC1.T17N - in Canonical Cytoskeletal Re-org

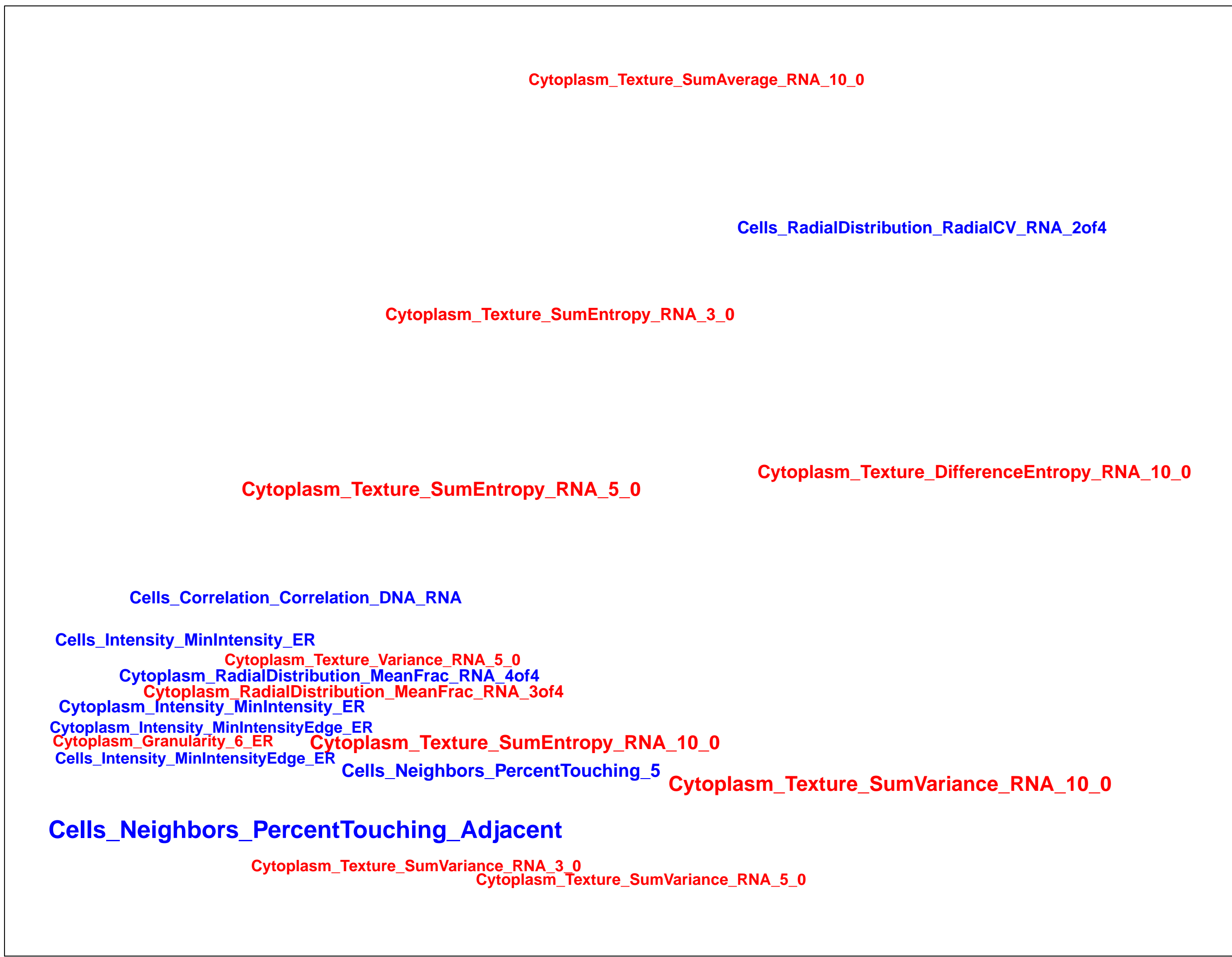
How similar is this gene to the other genes?



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

RAC1.T17N (41744)

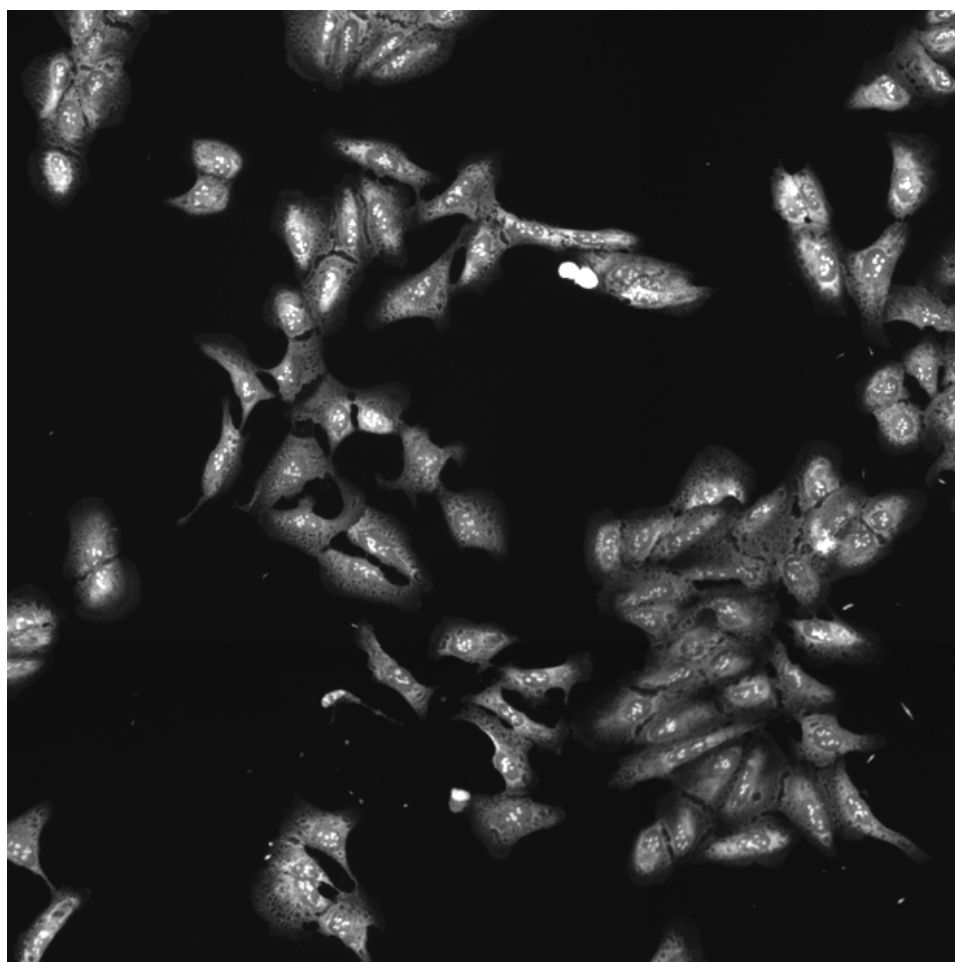
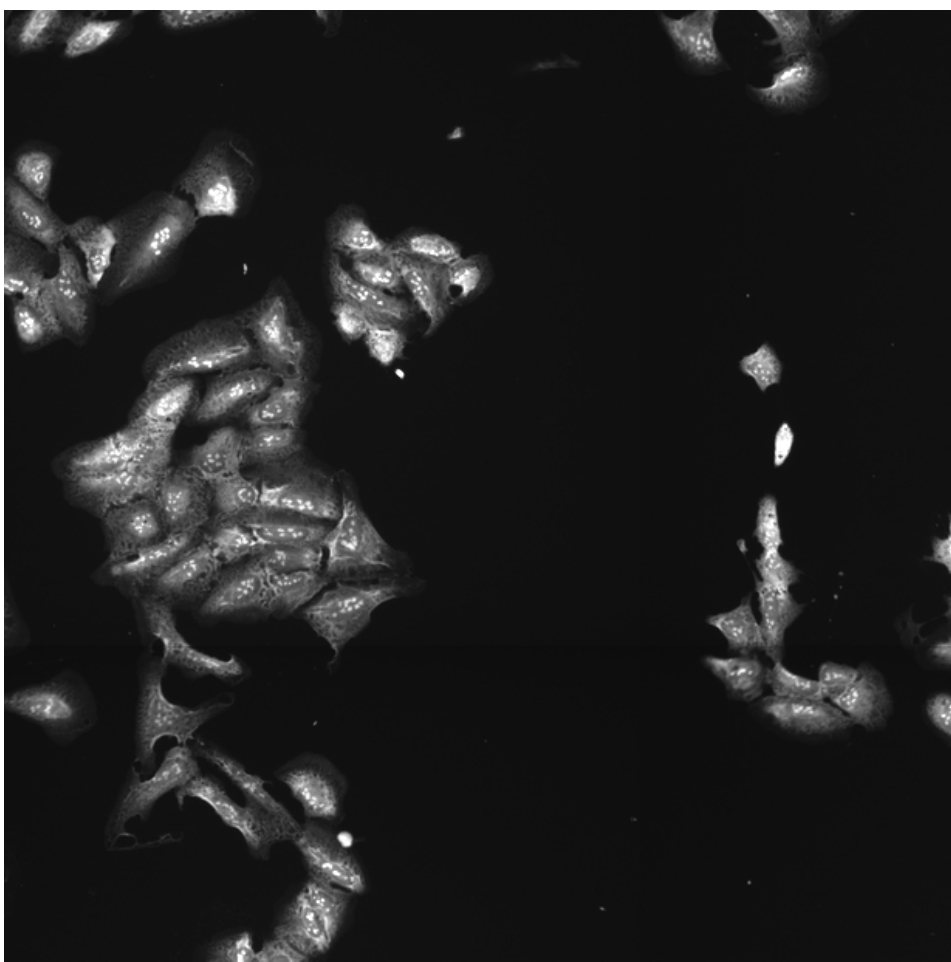
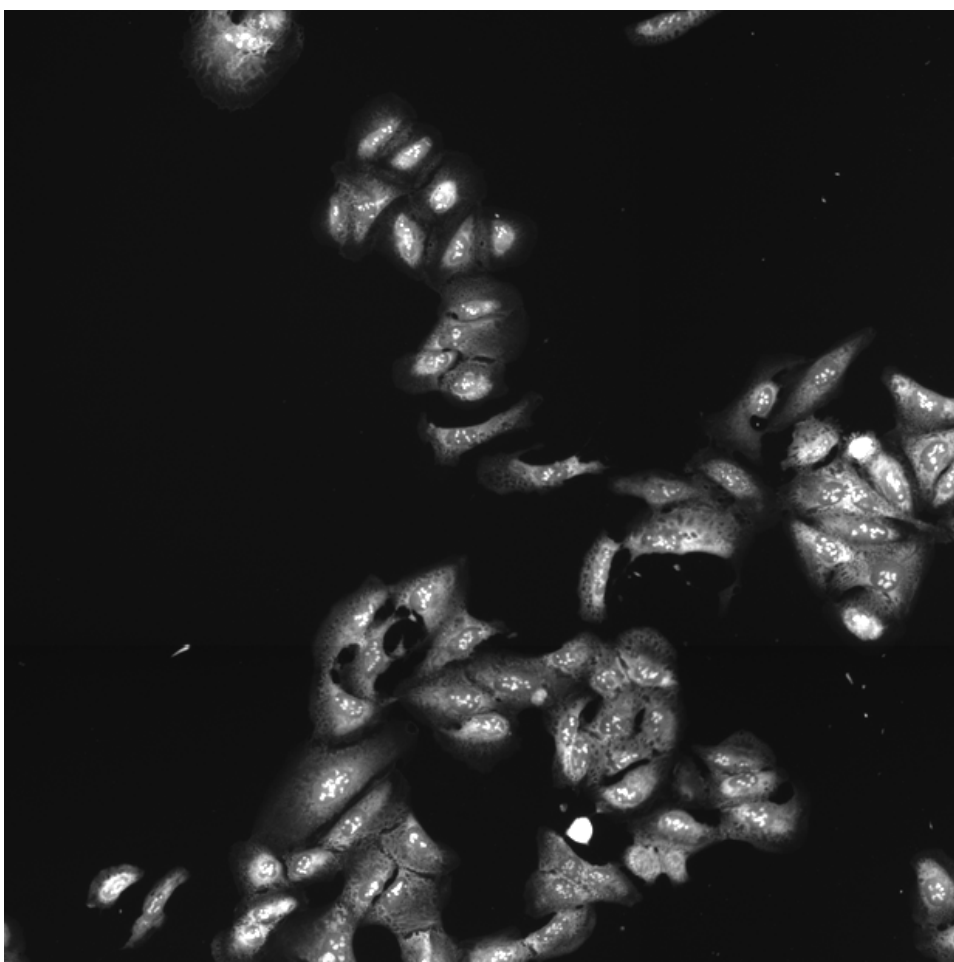
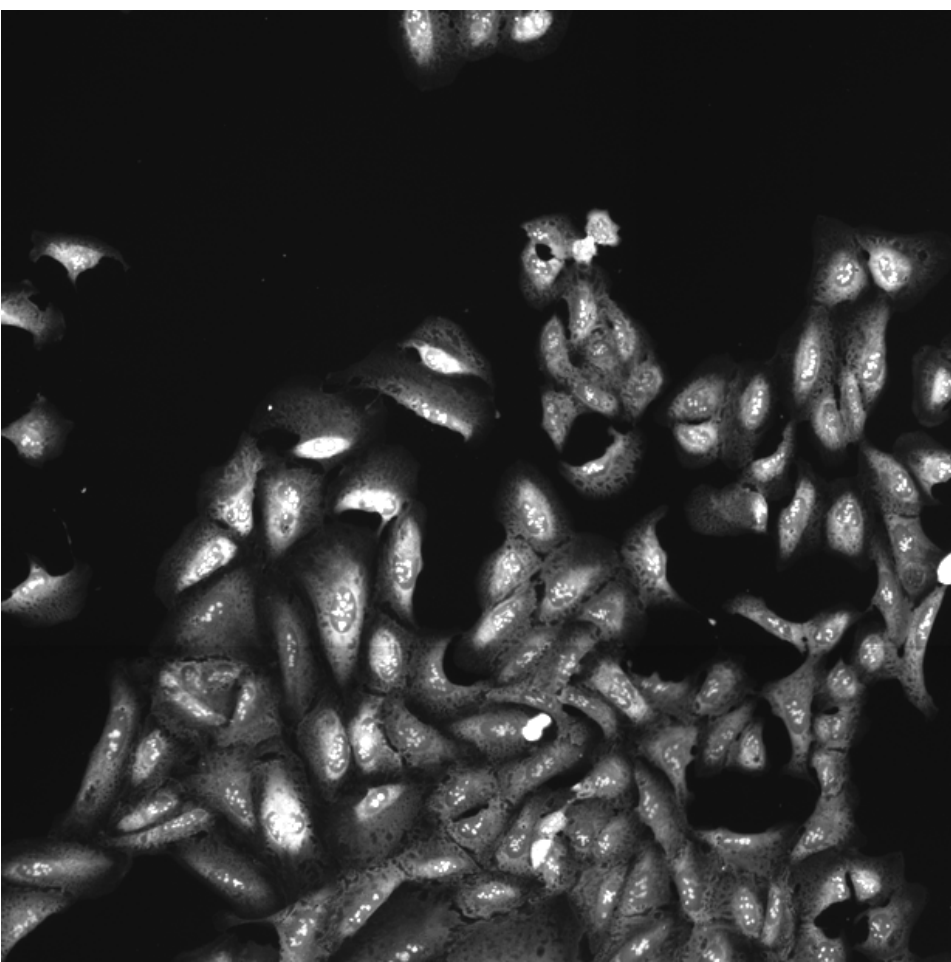
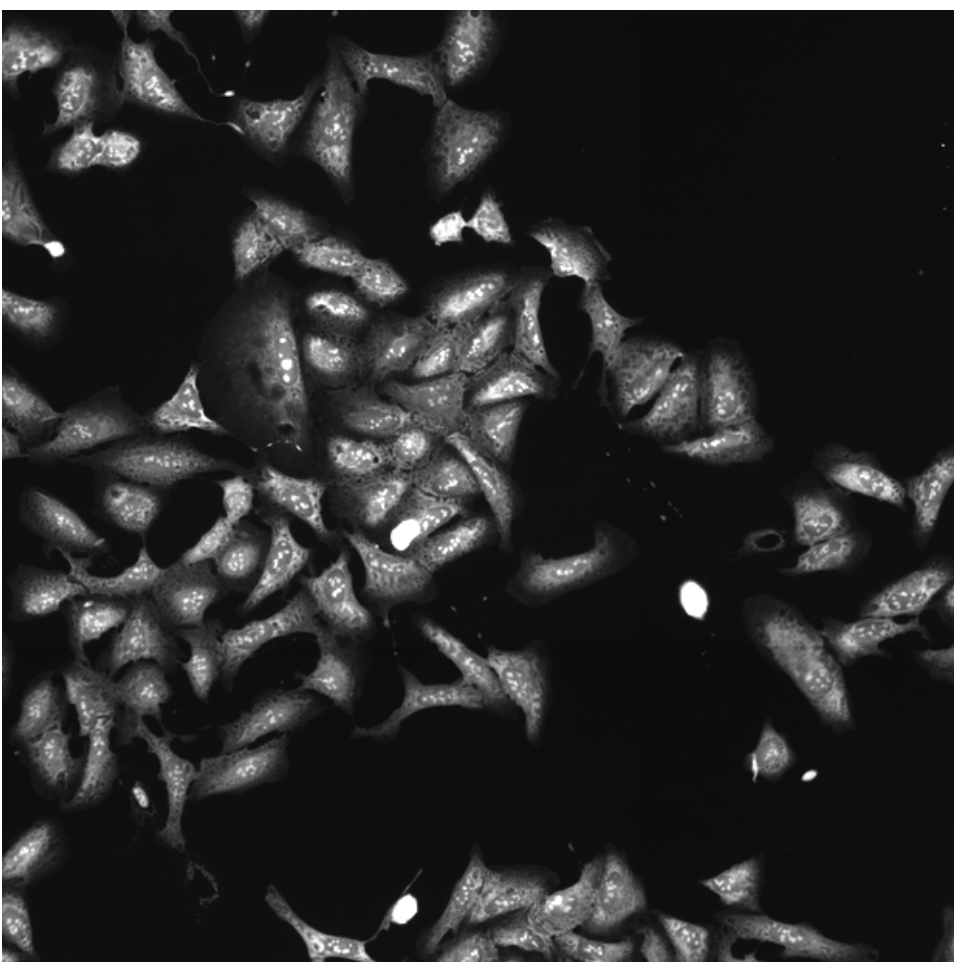
RAC1.T17N (41755)

RAC1.T17N (41756)

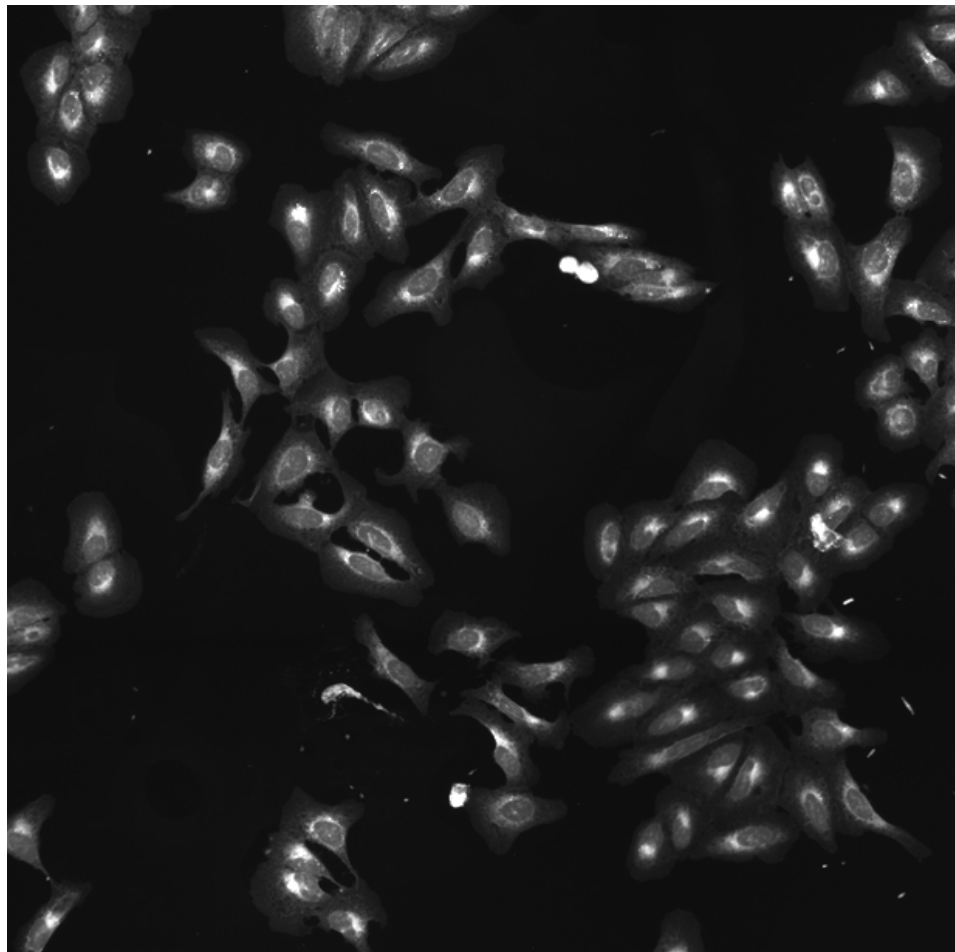
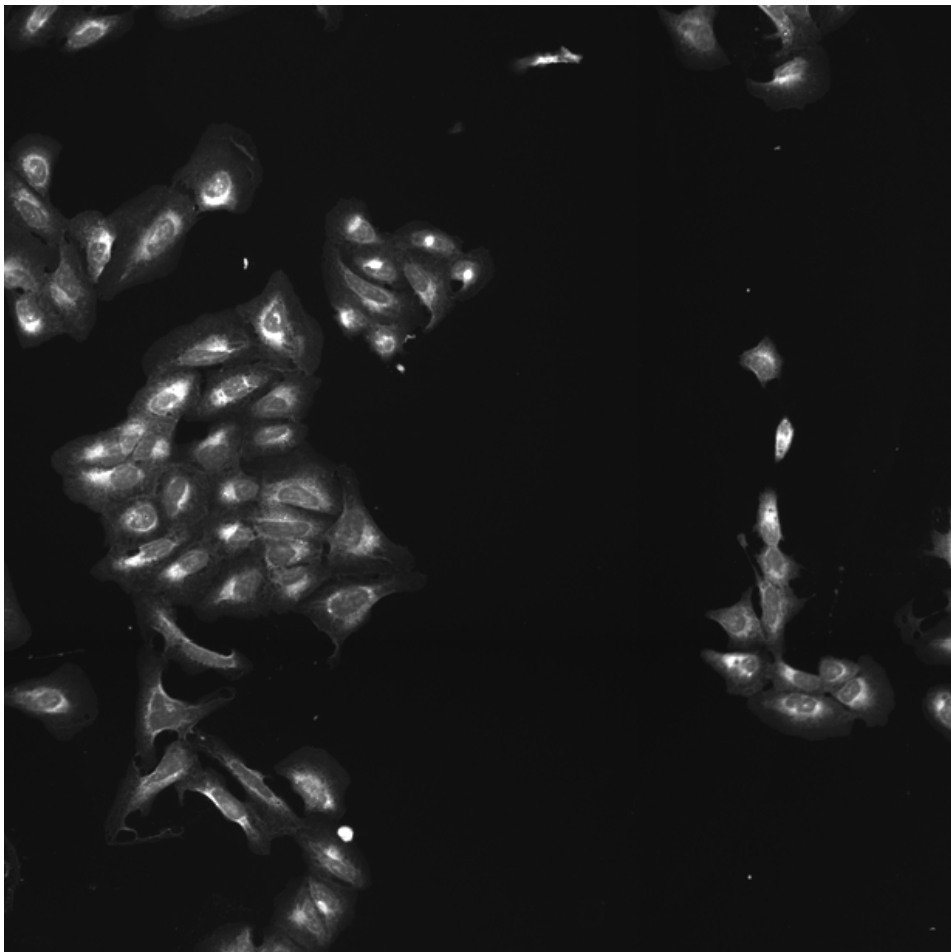
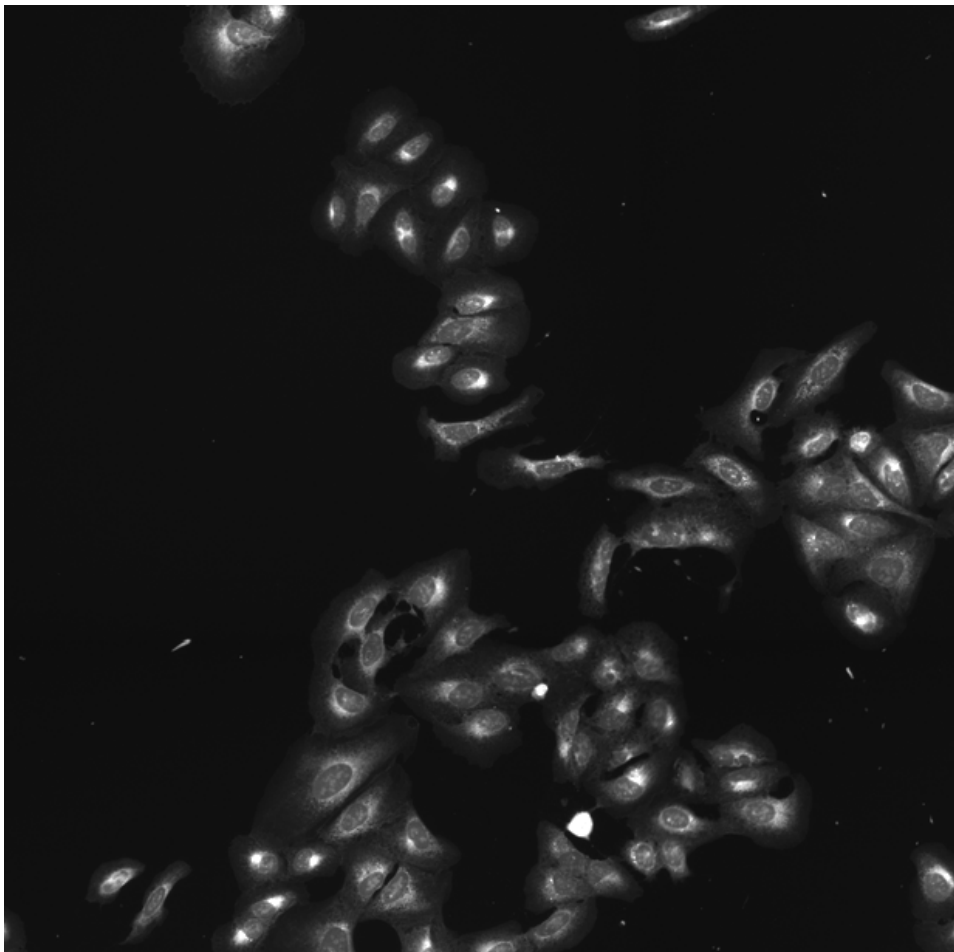
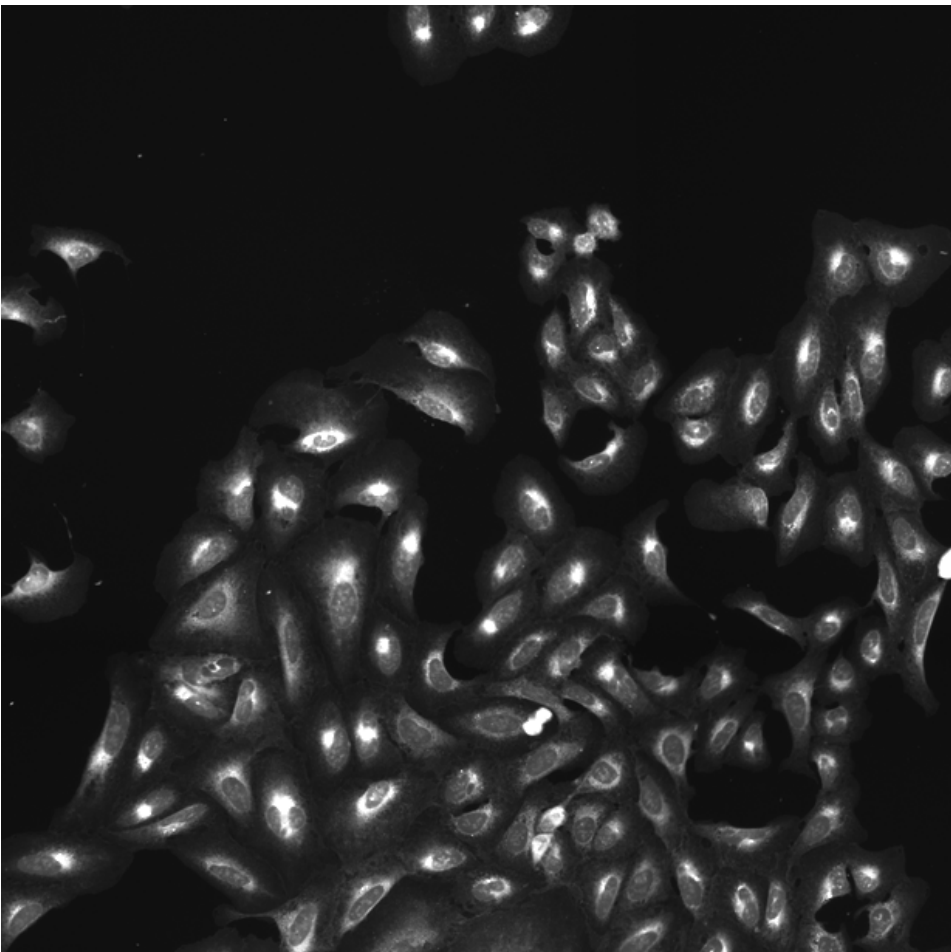
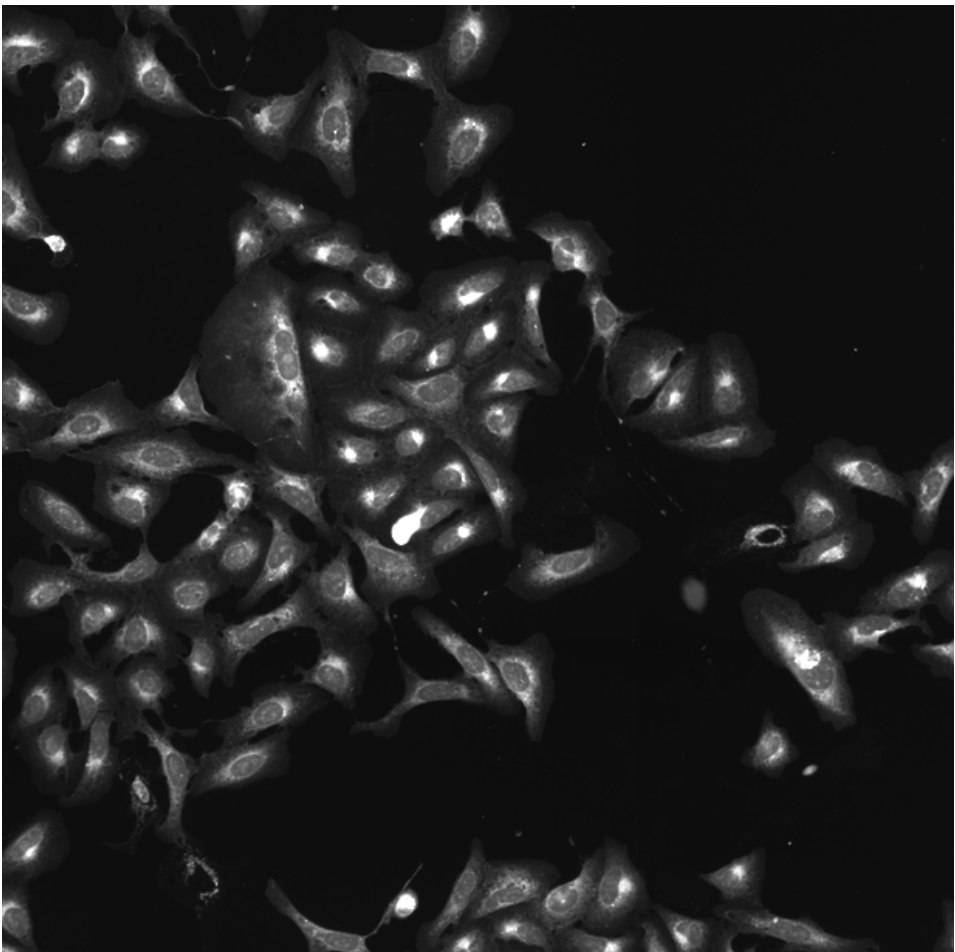
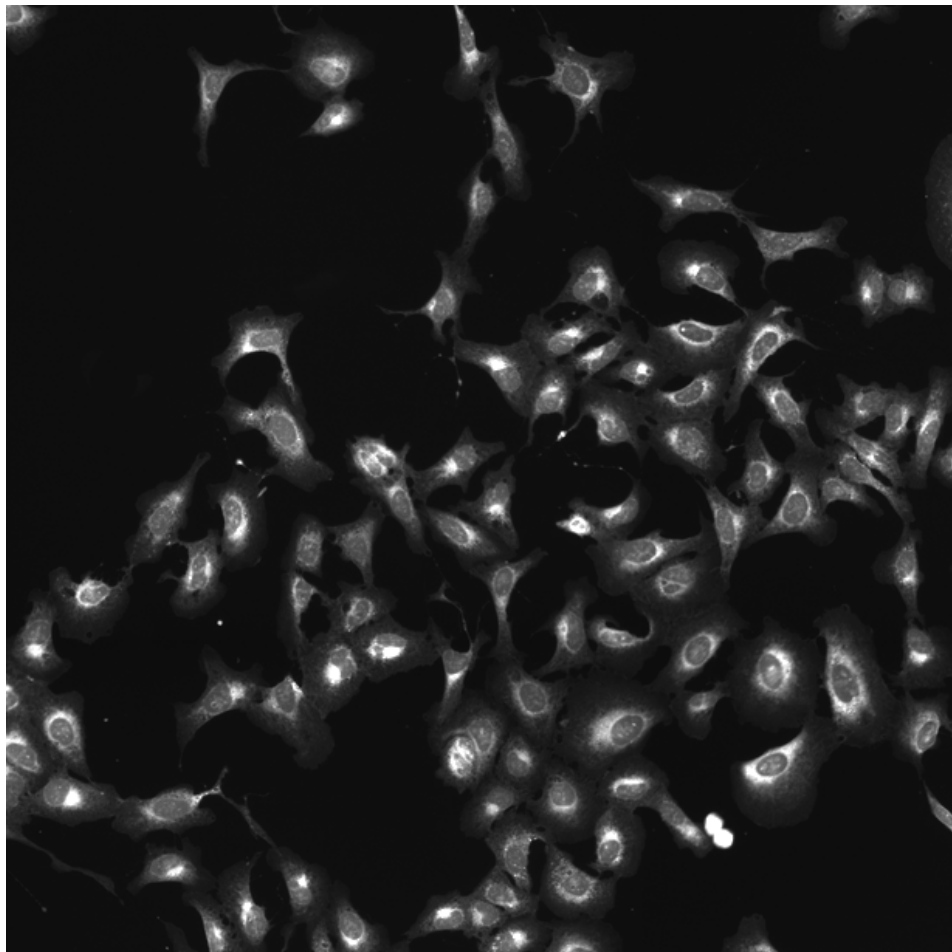
RAC1.T17N (41757)

RAC1.T17N (41754)

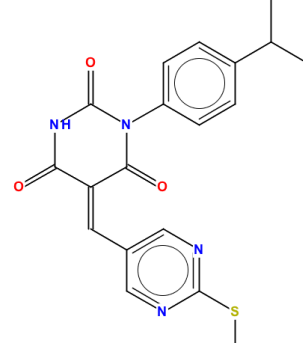
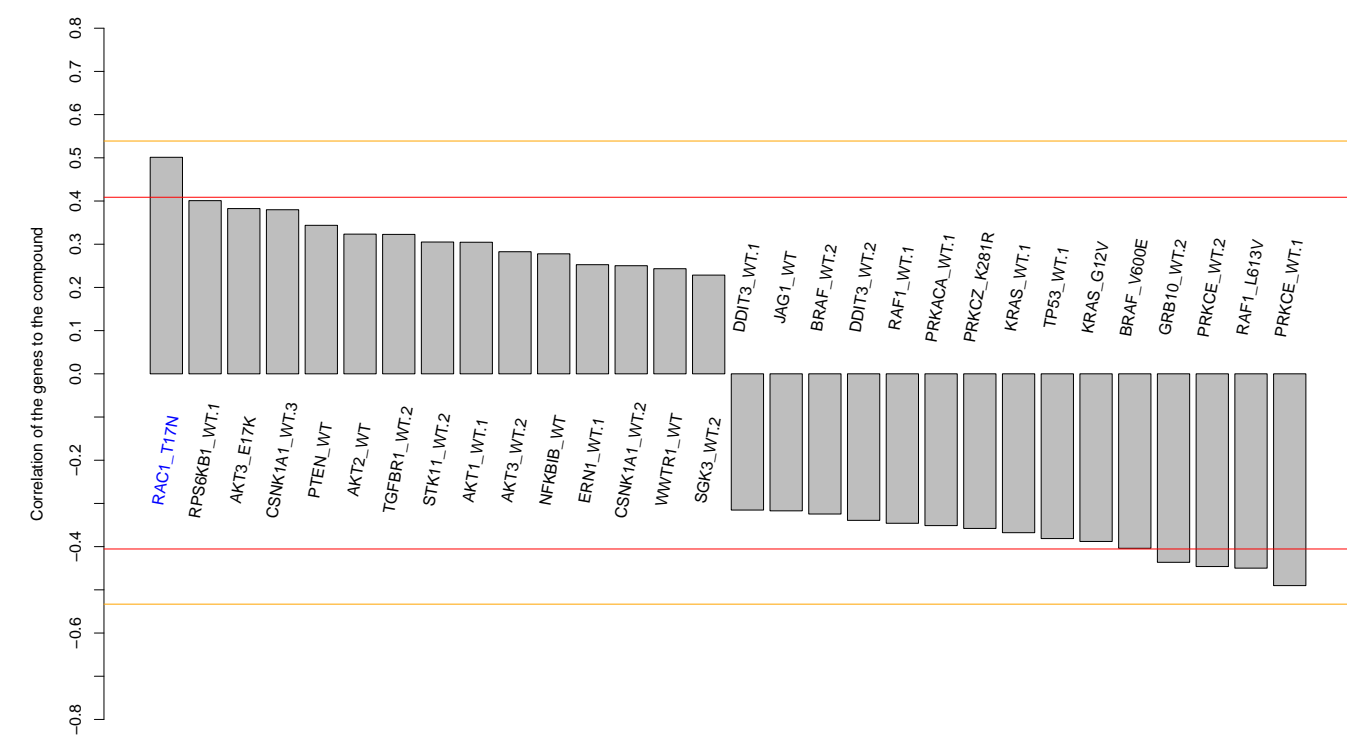
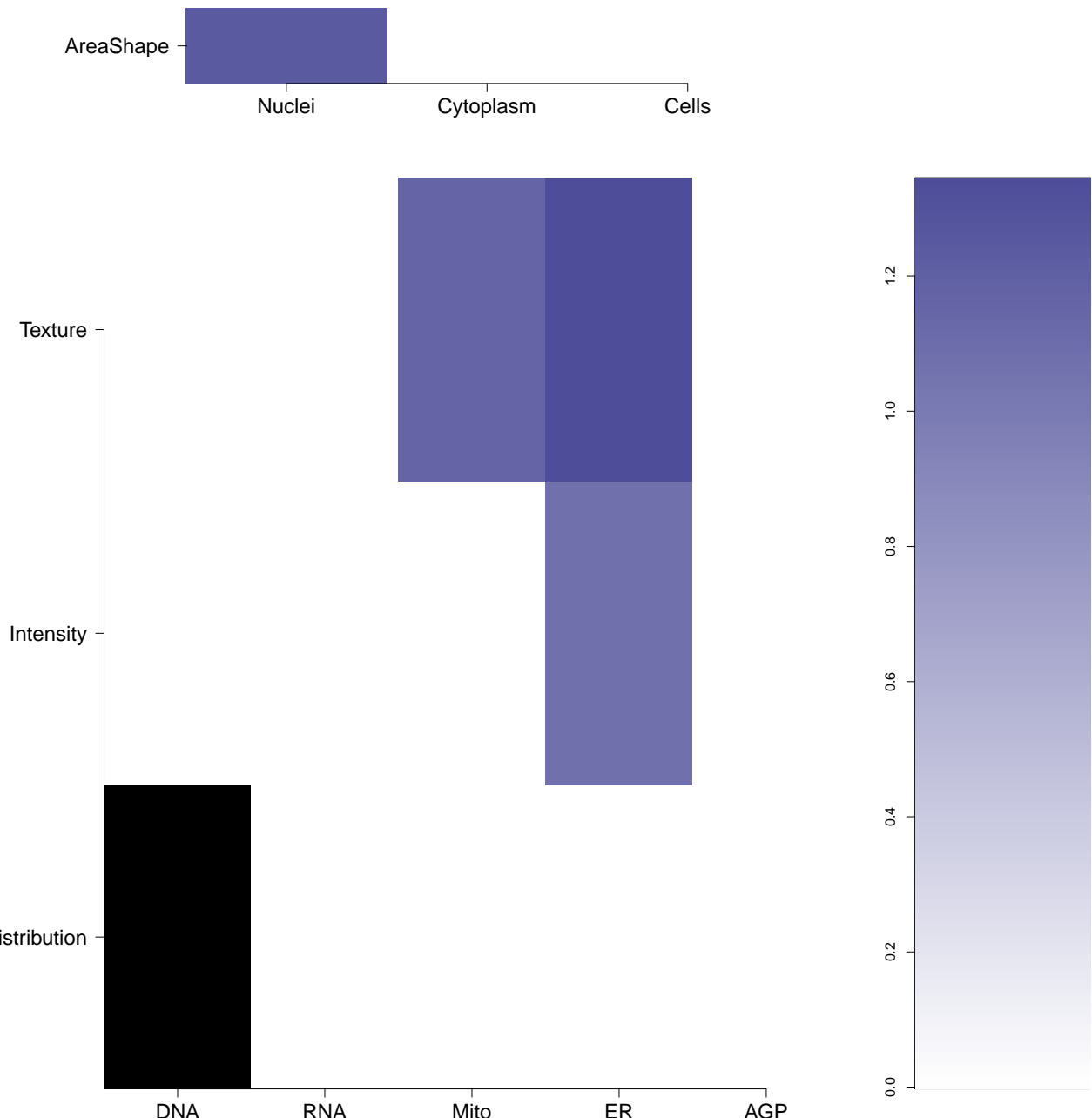
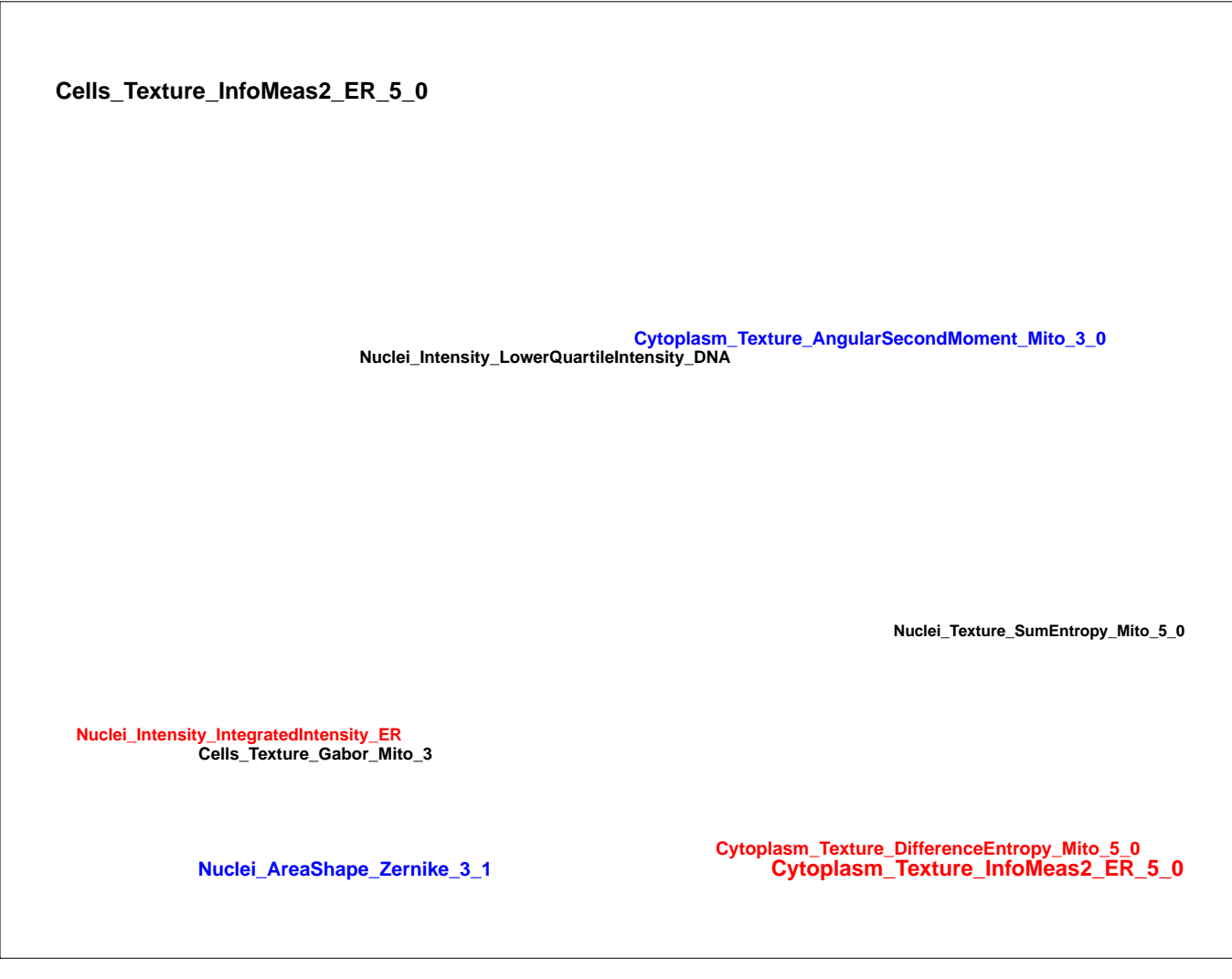
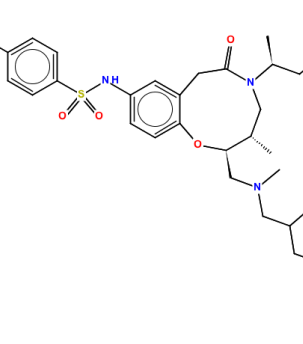
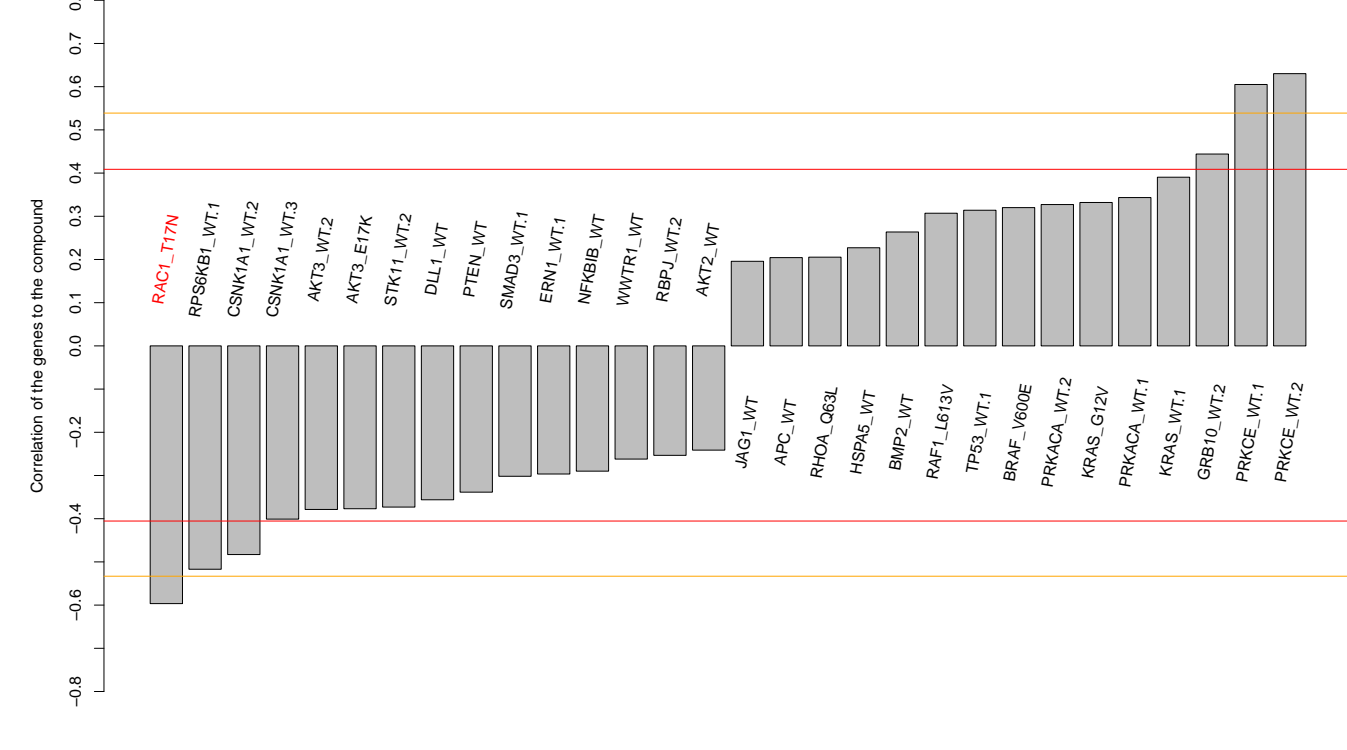
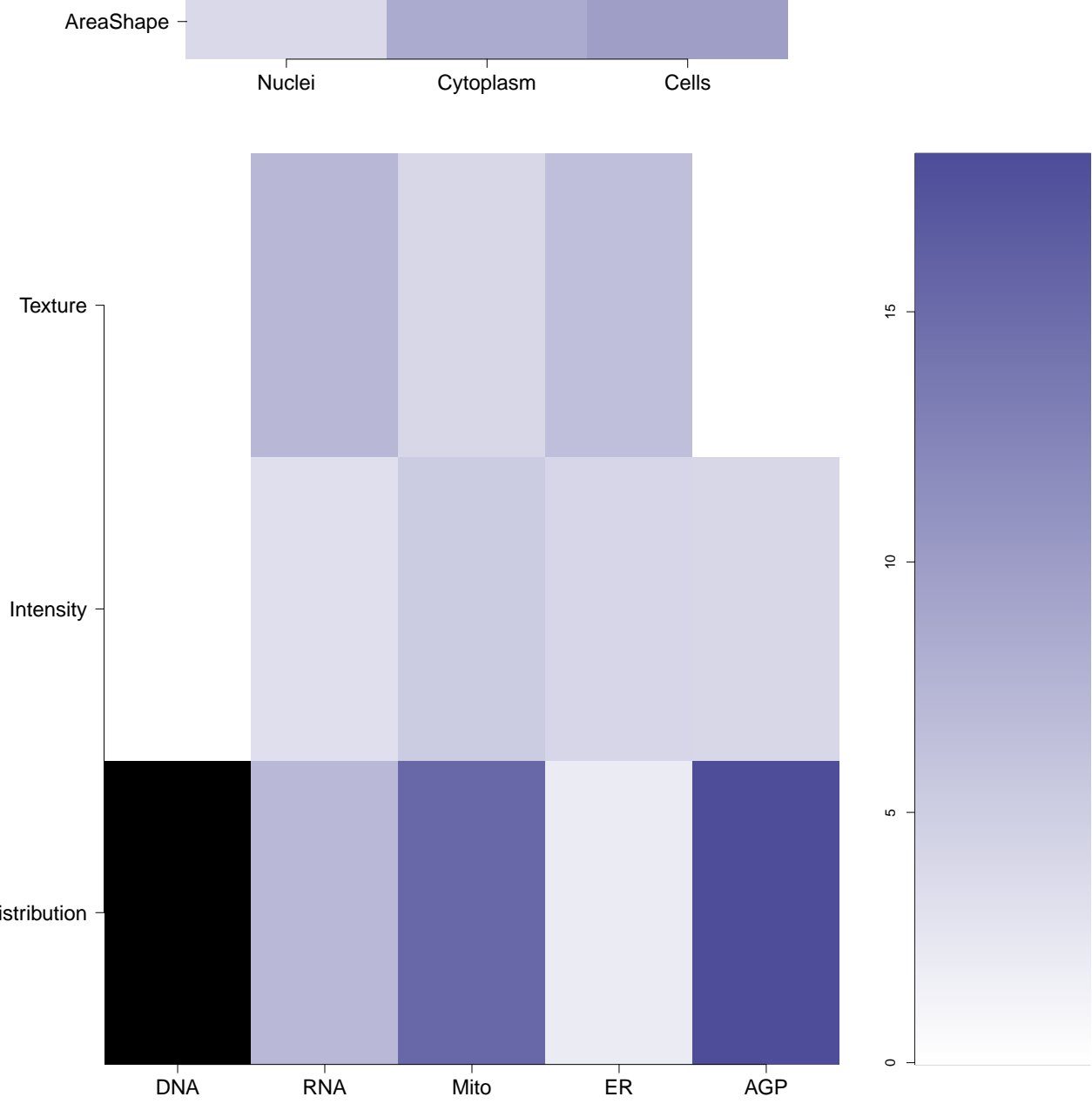

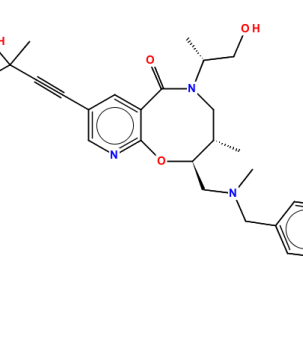
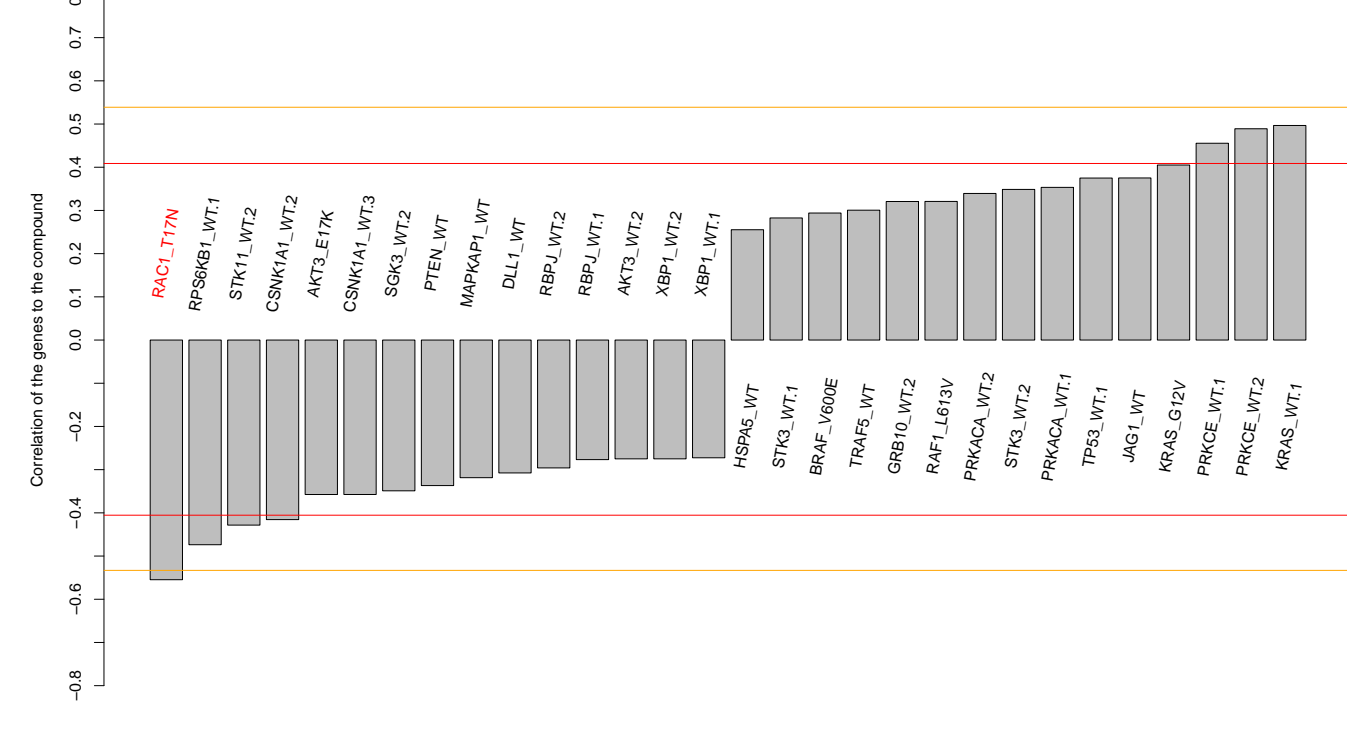
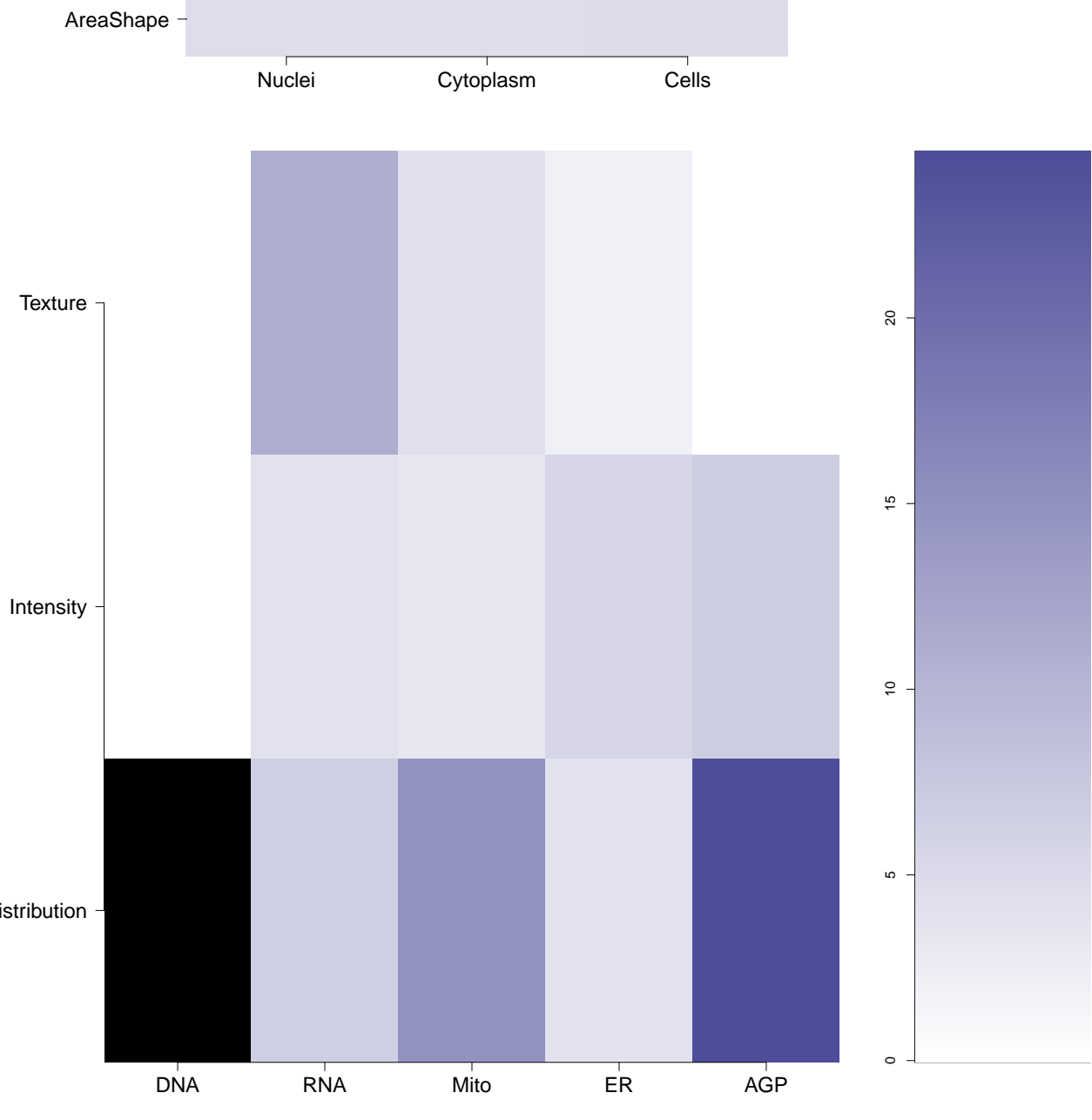
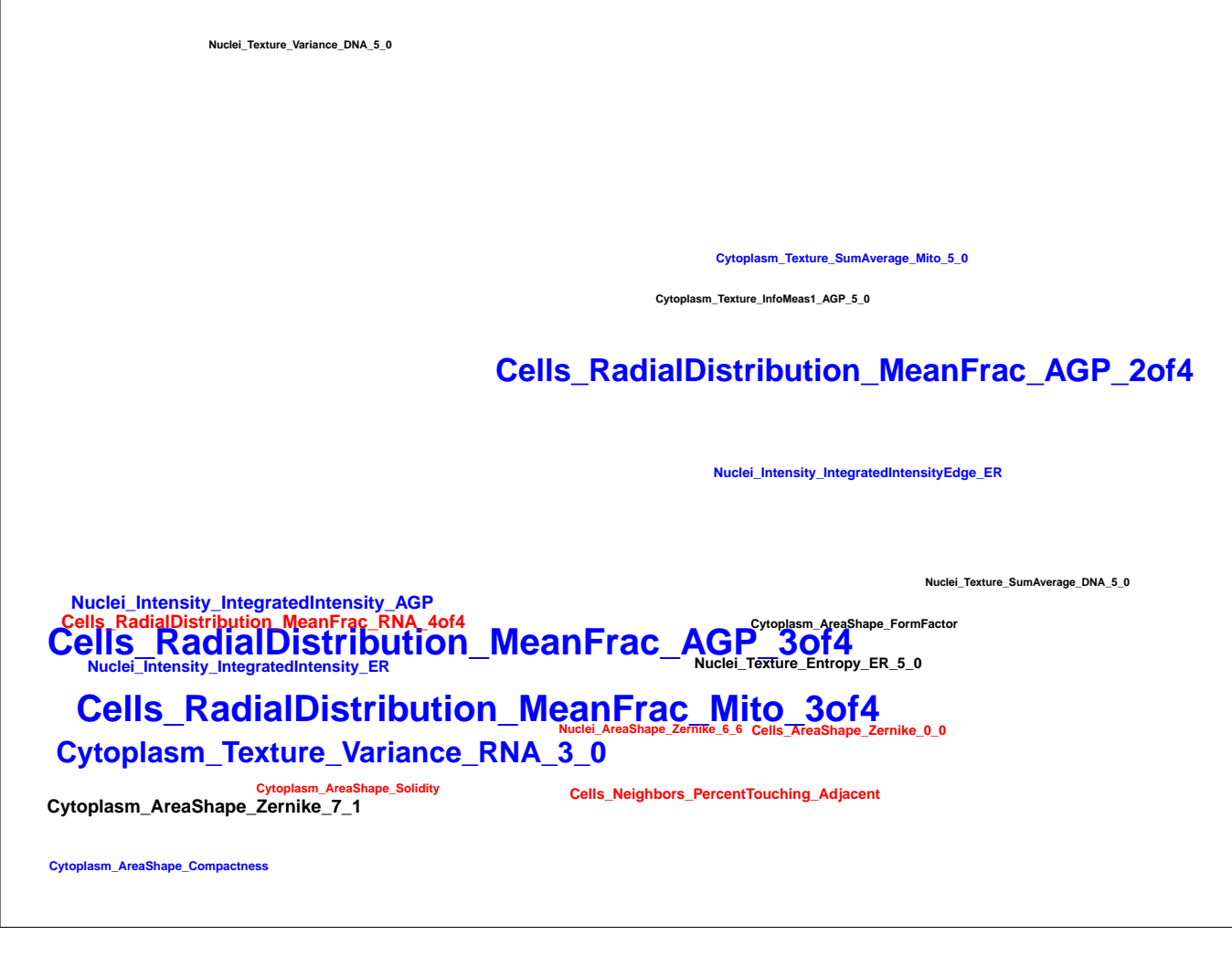
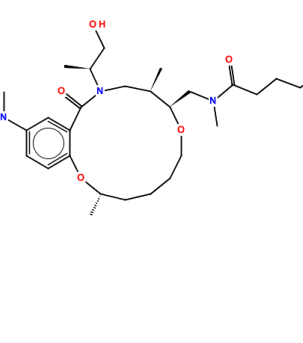
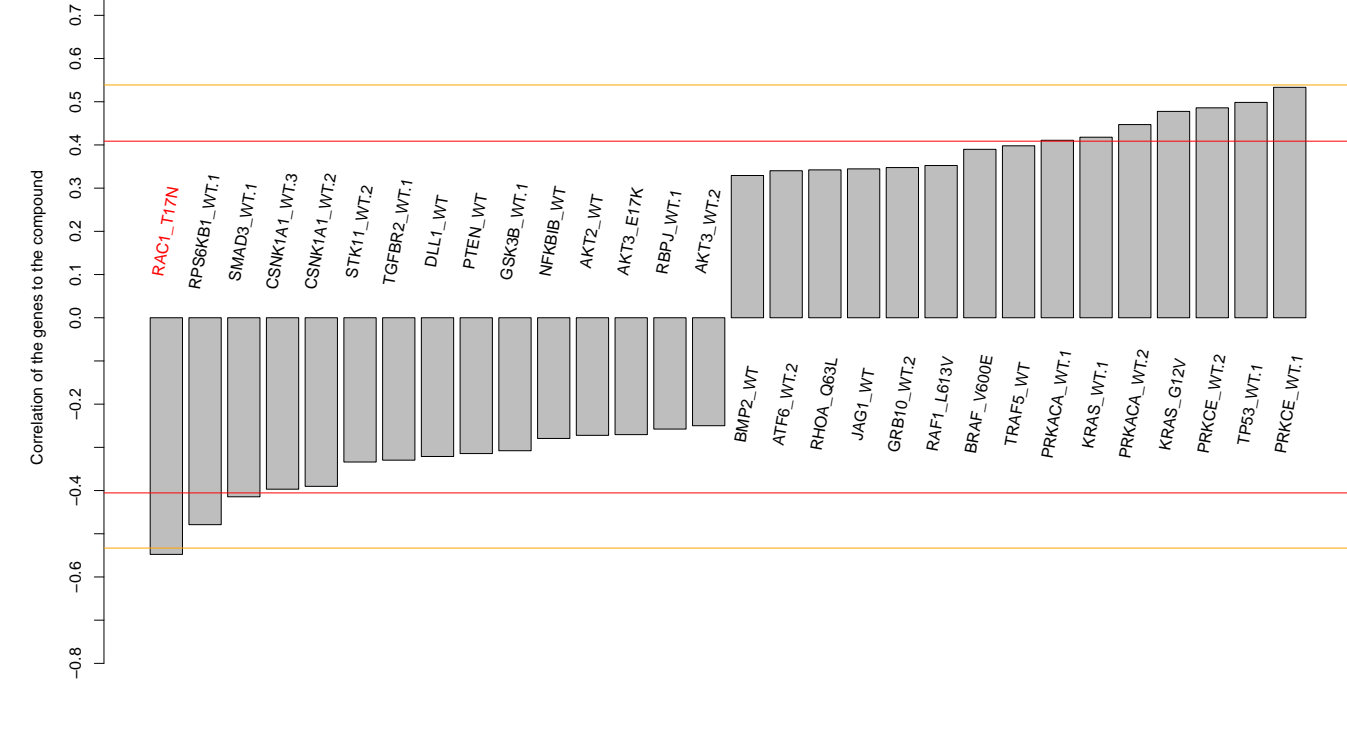
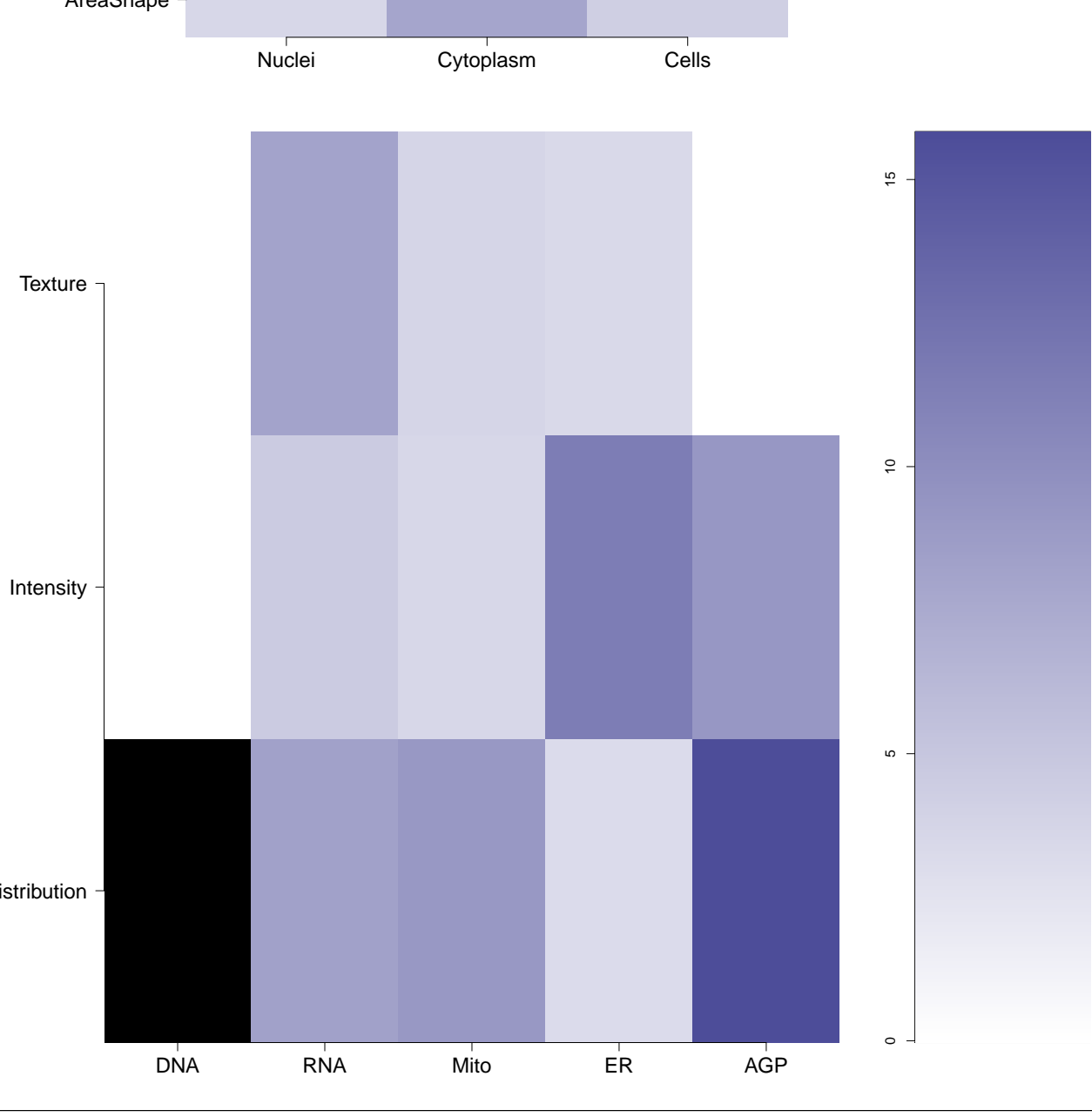

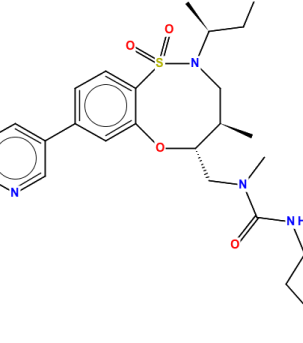
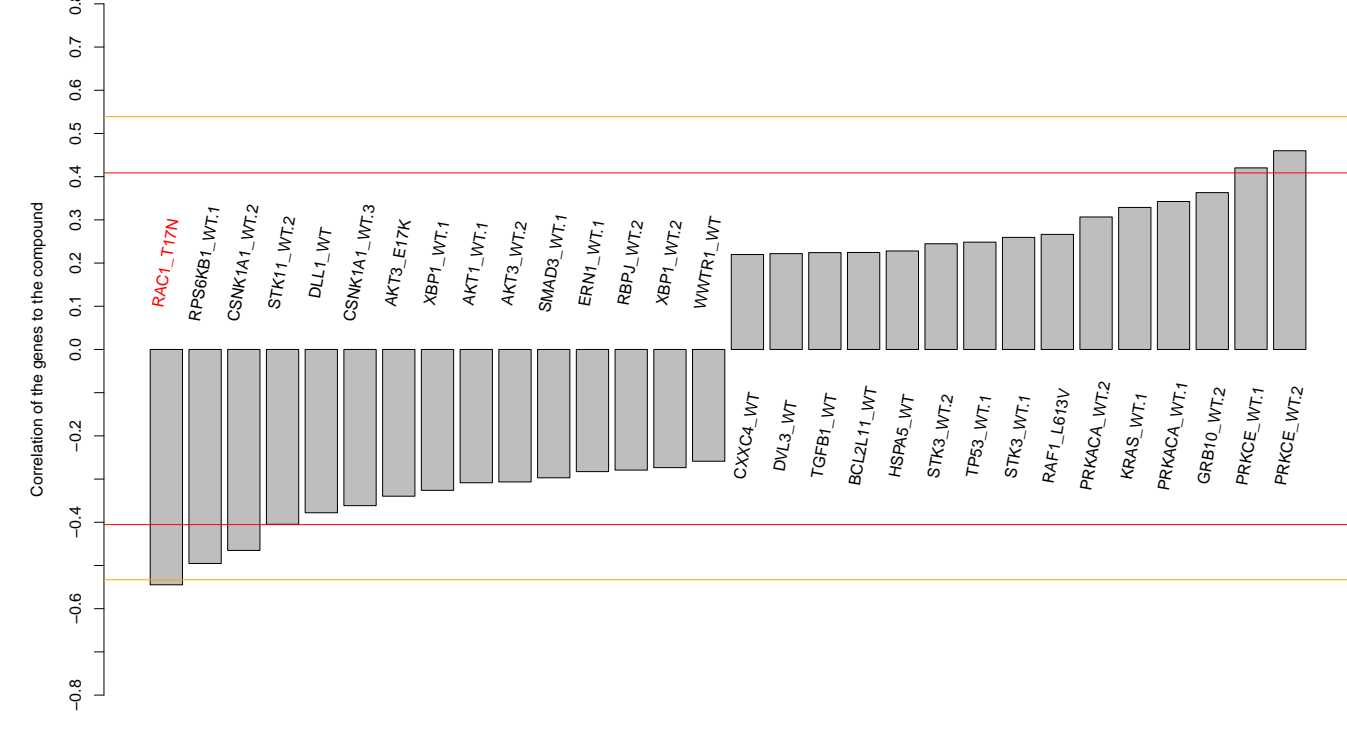
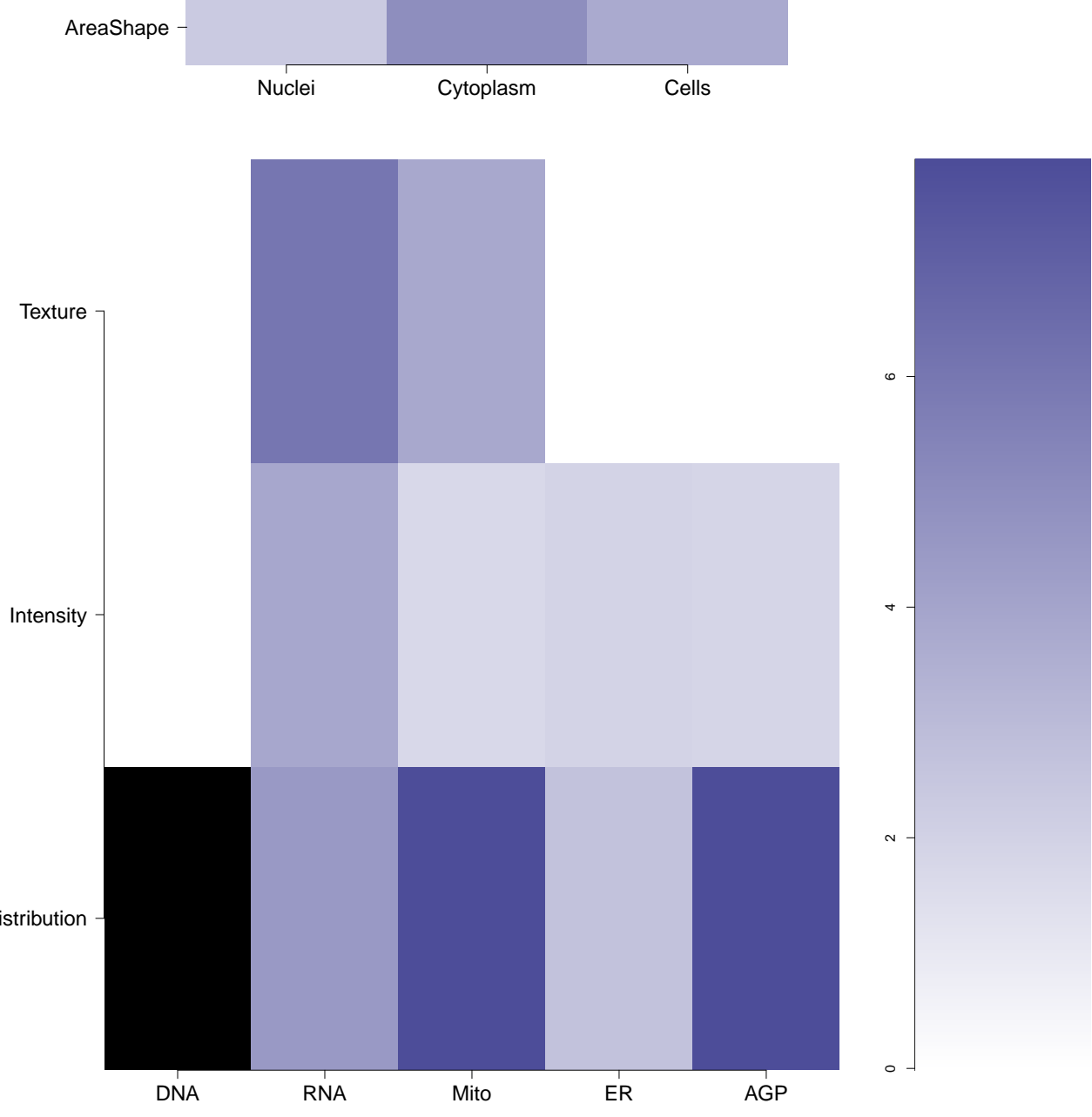

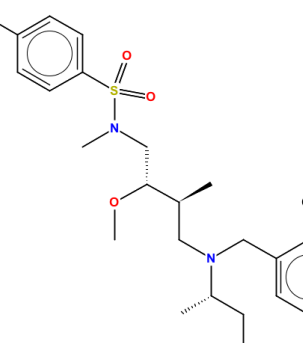
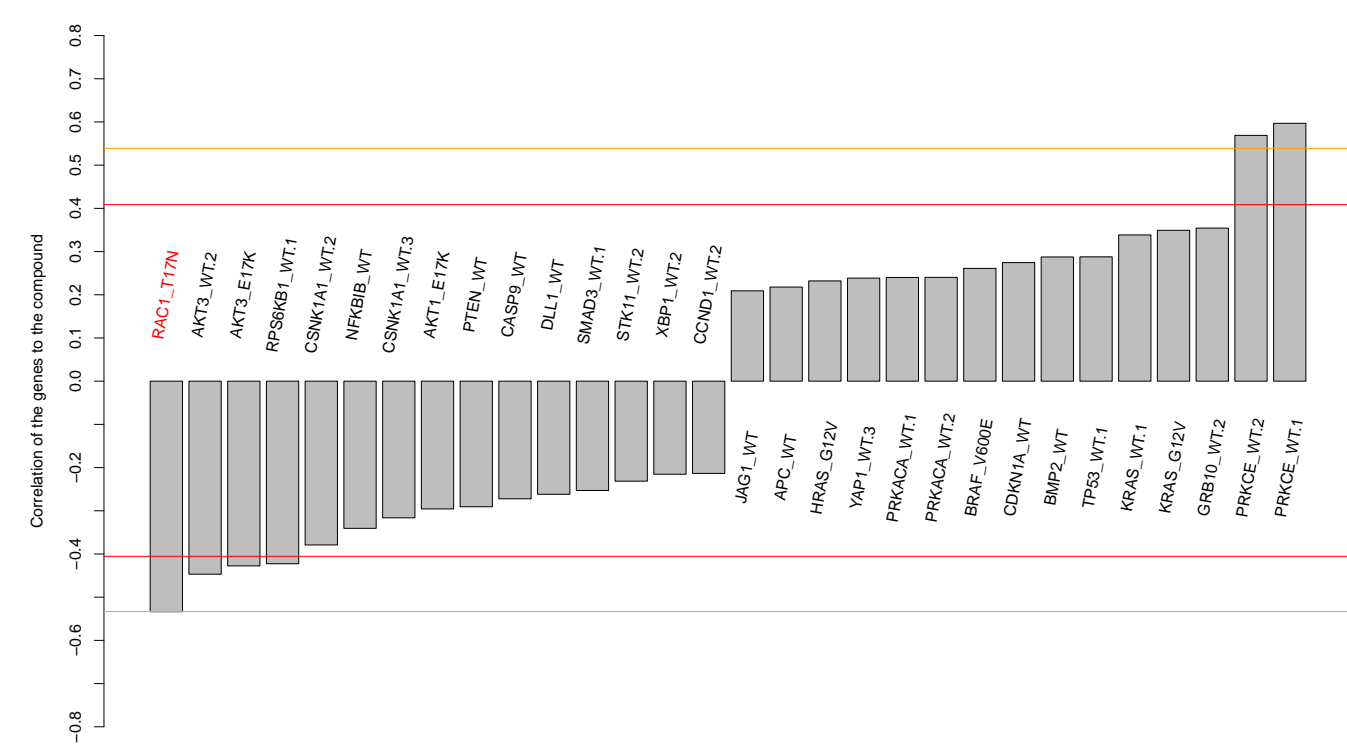

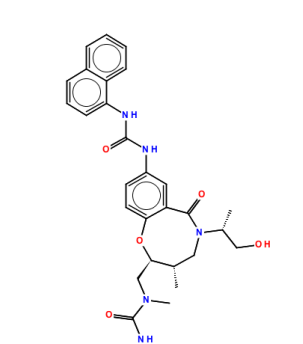
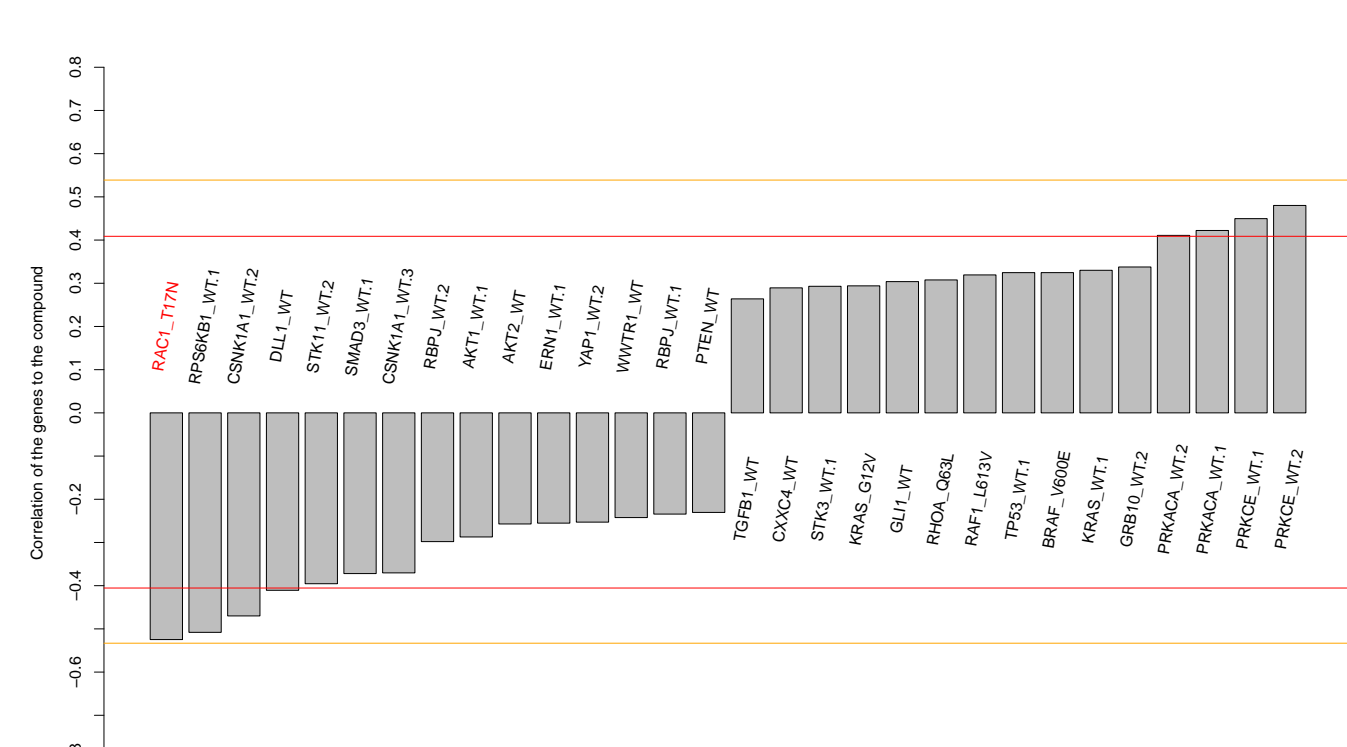
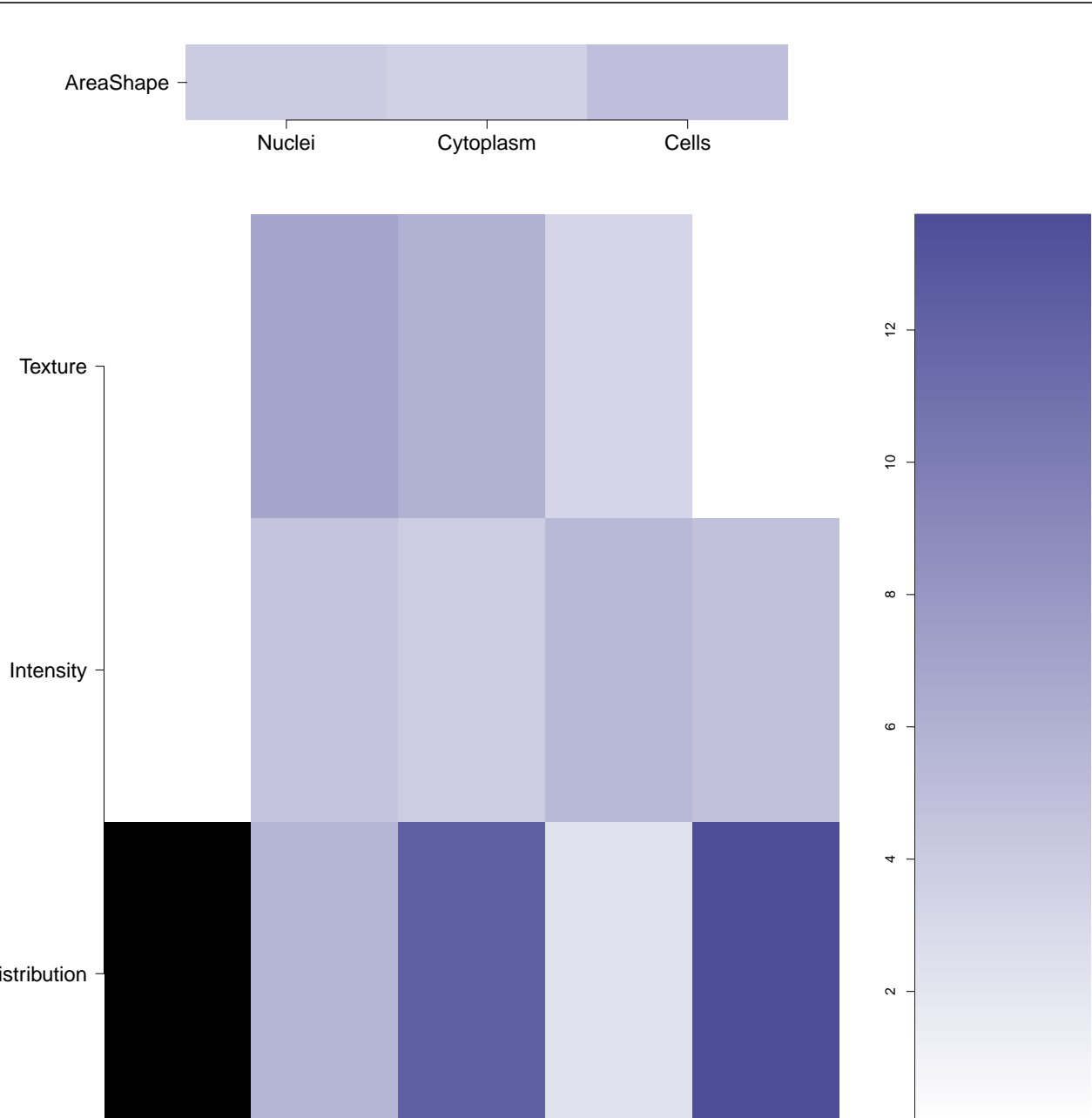
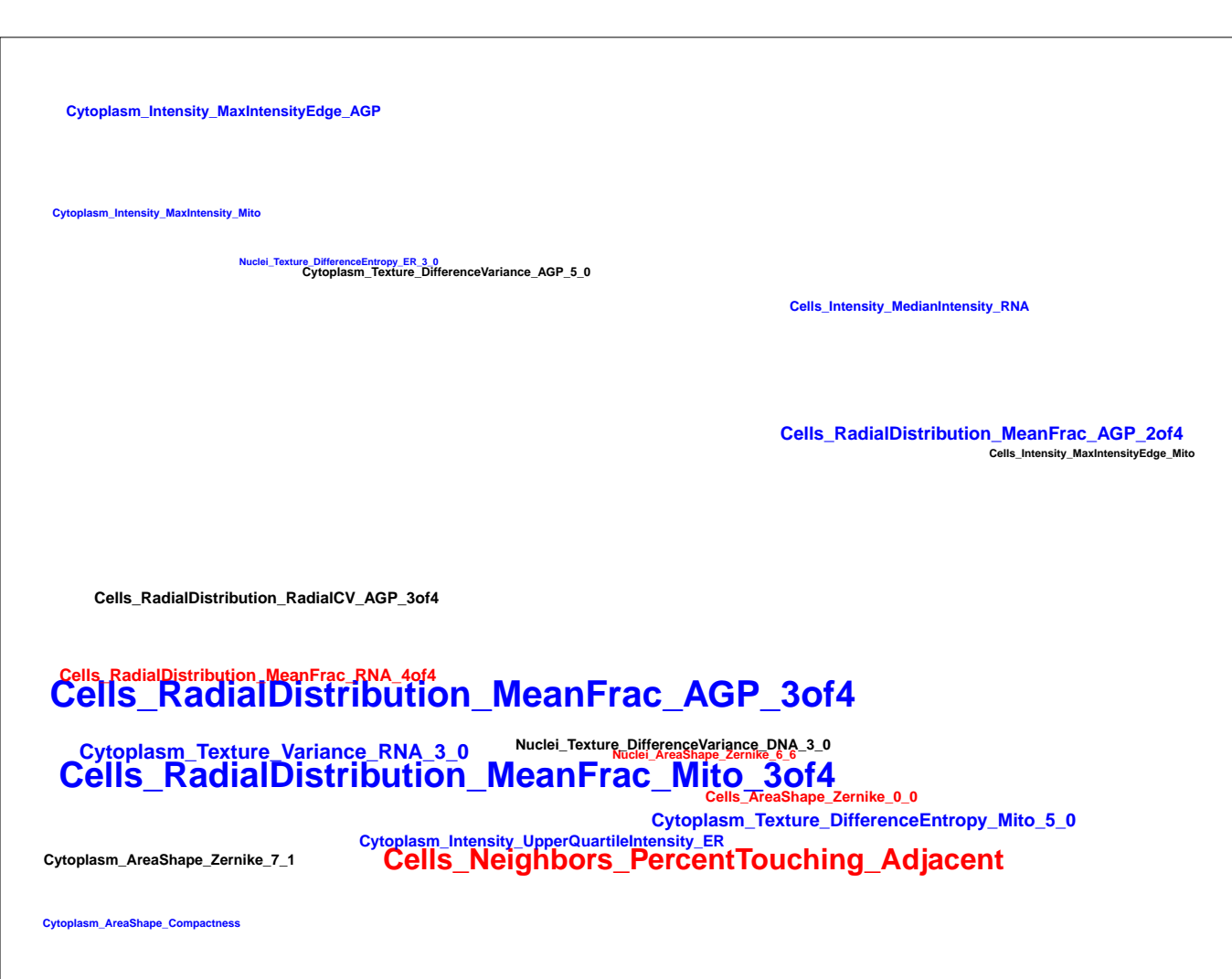
RNA

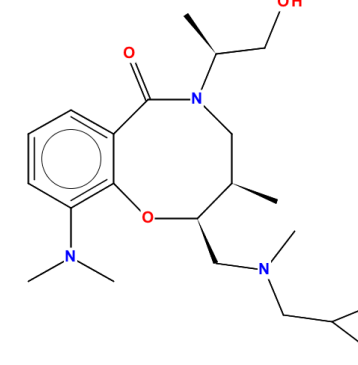
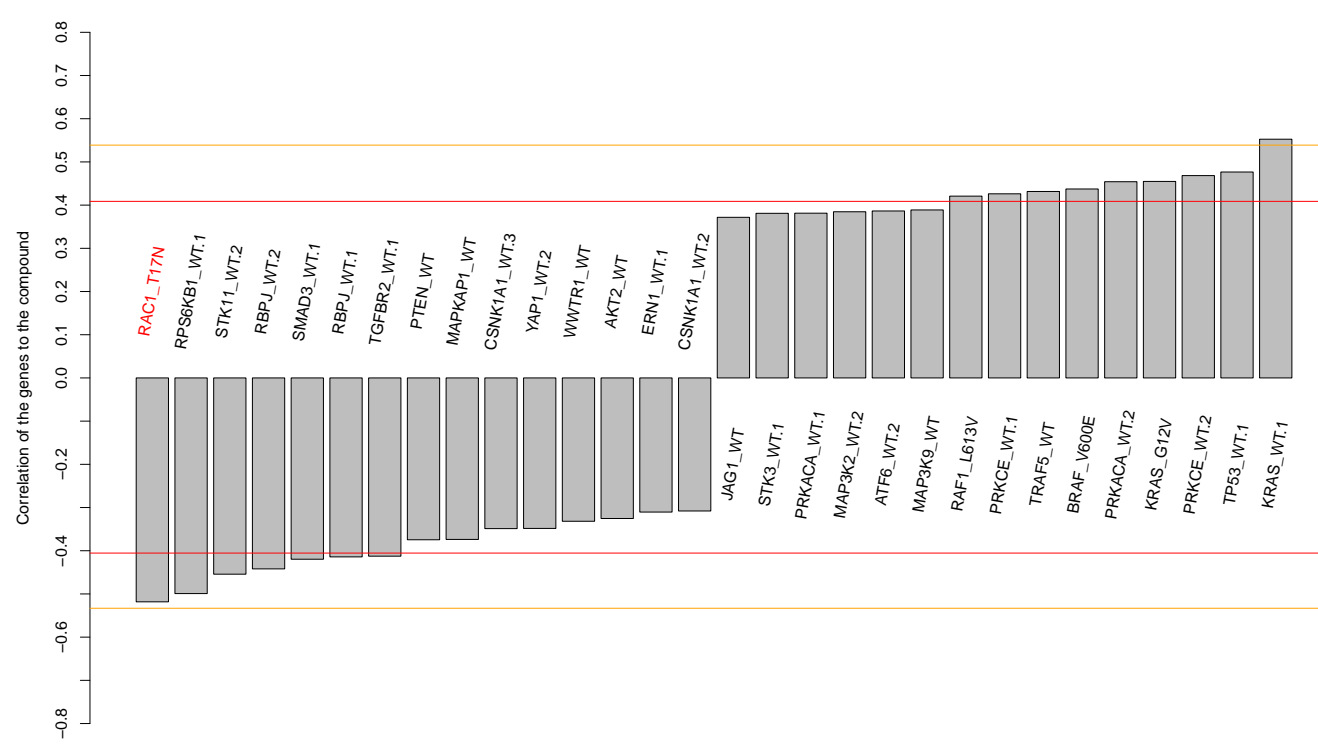
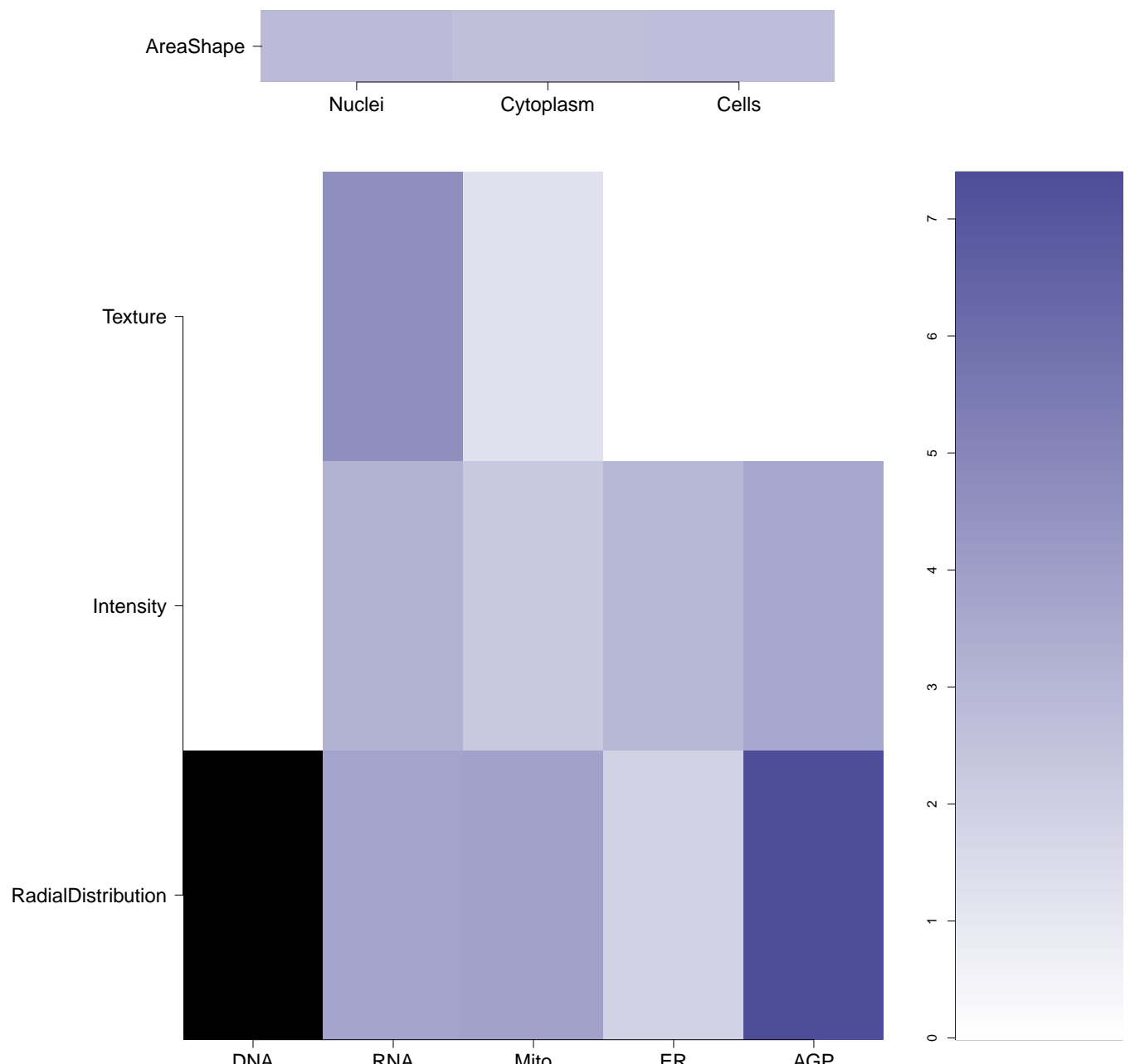
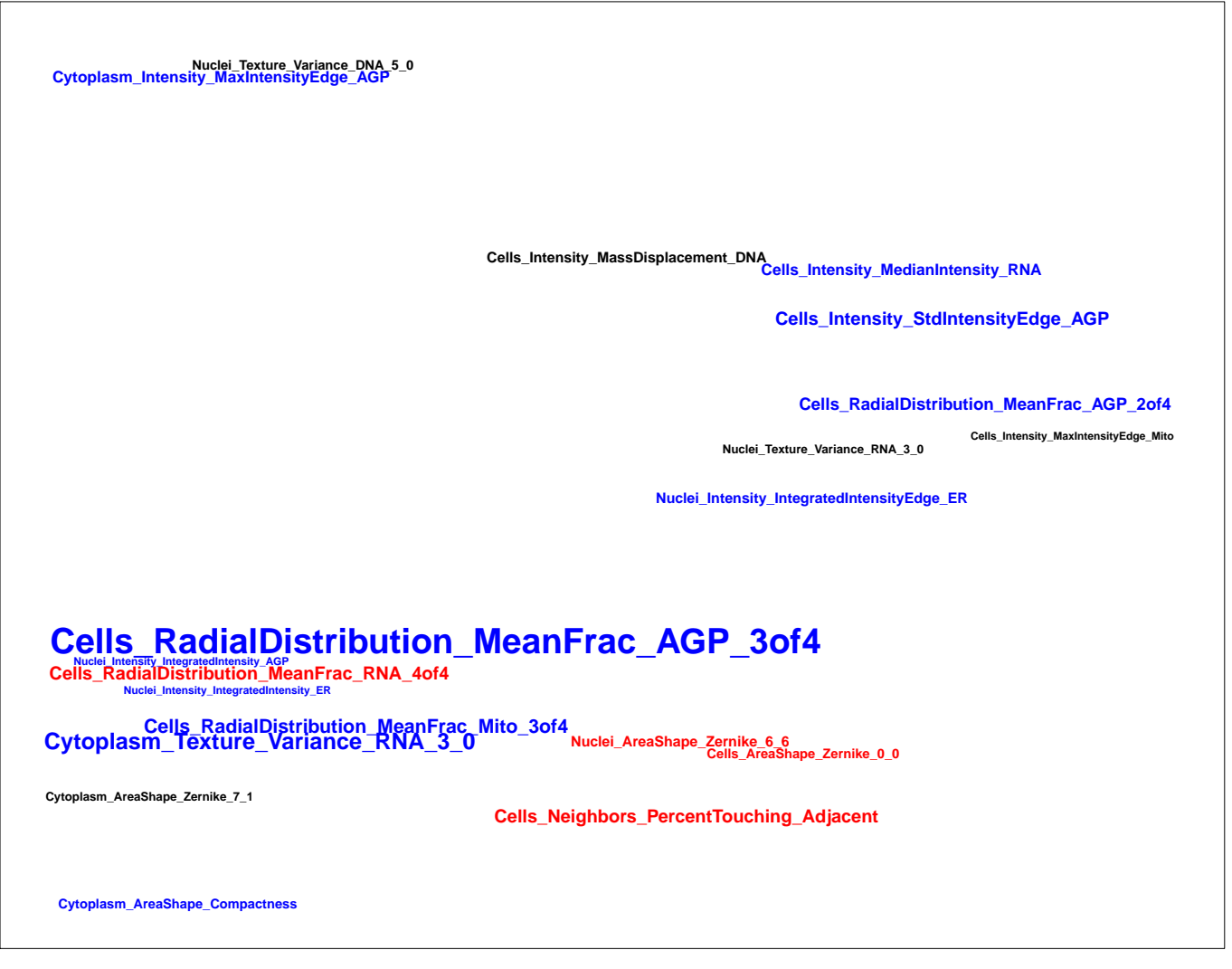
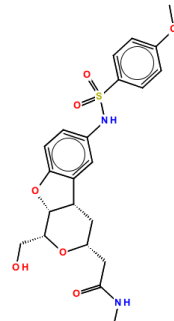
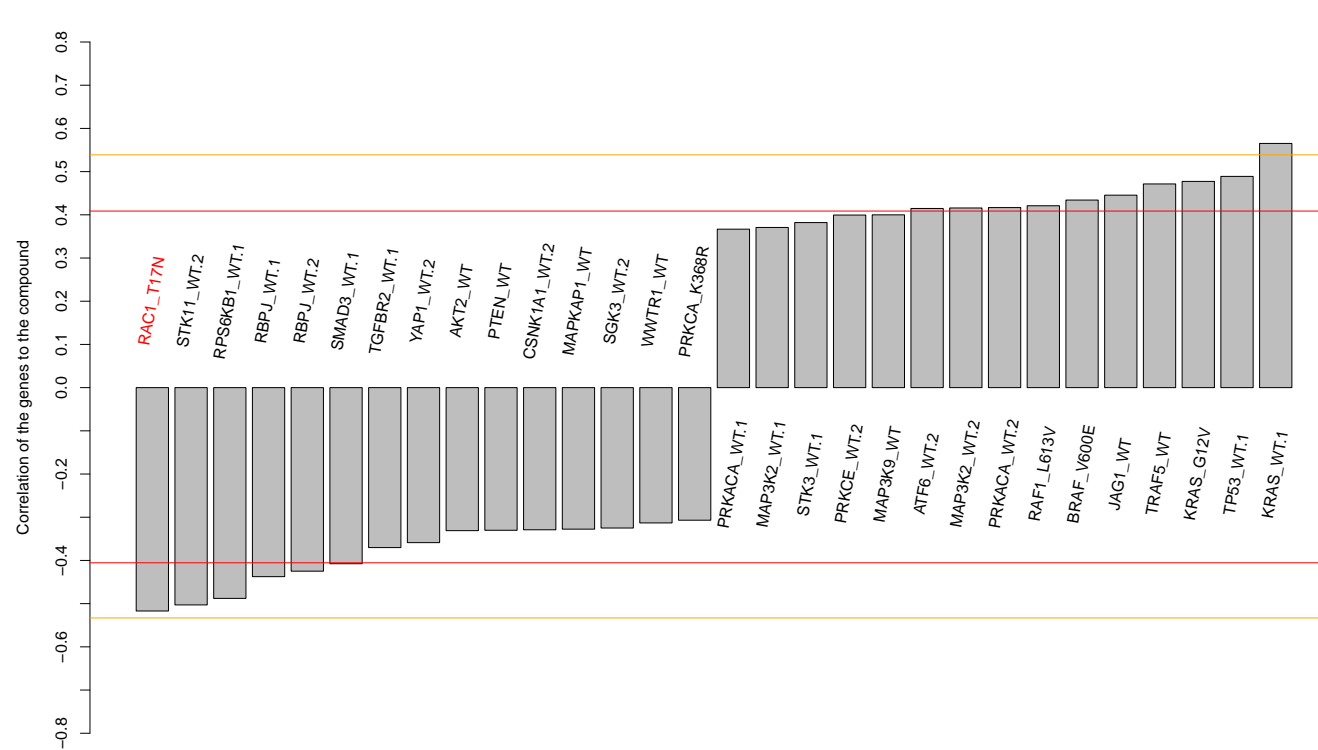
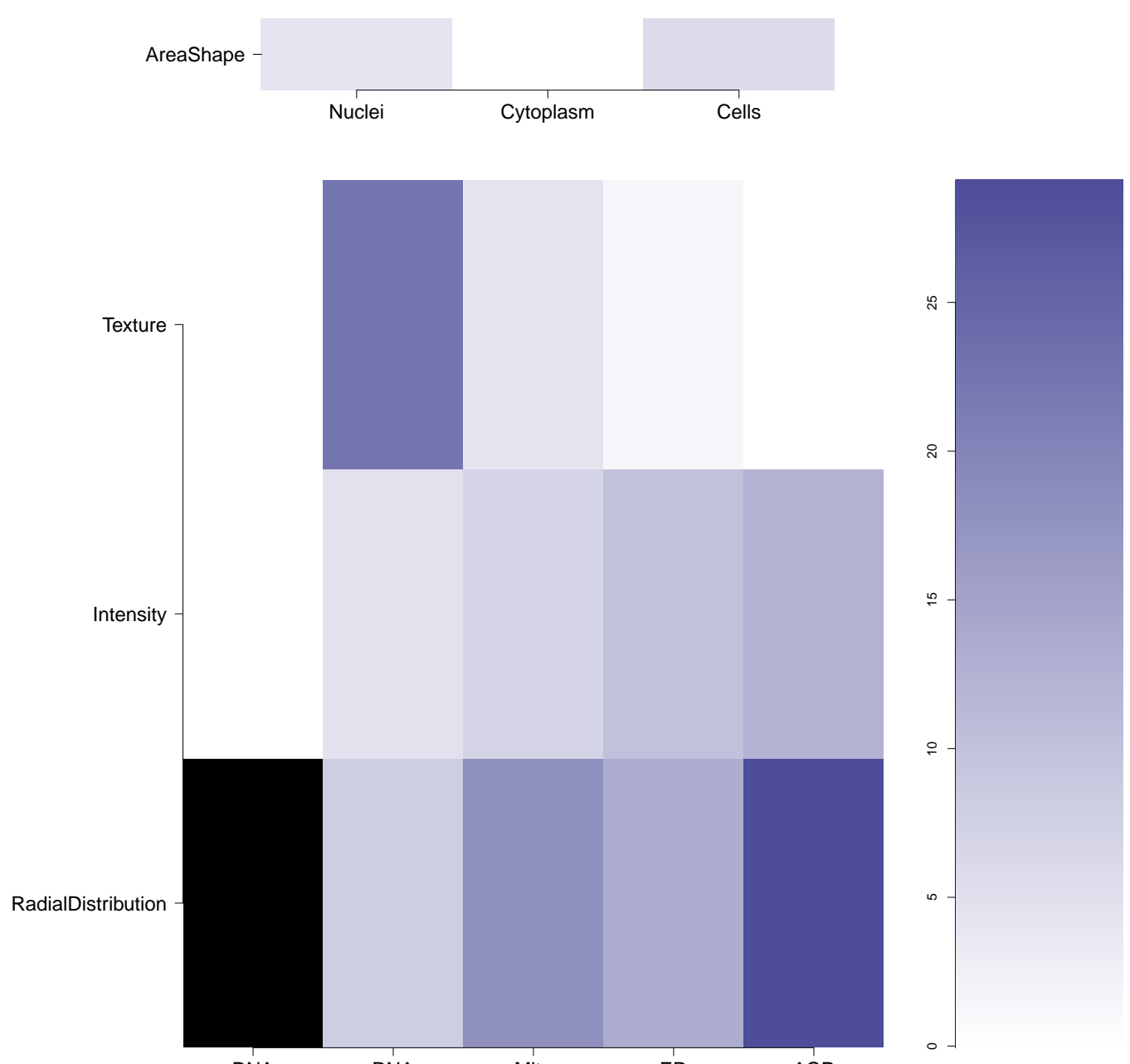
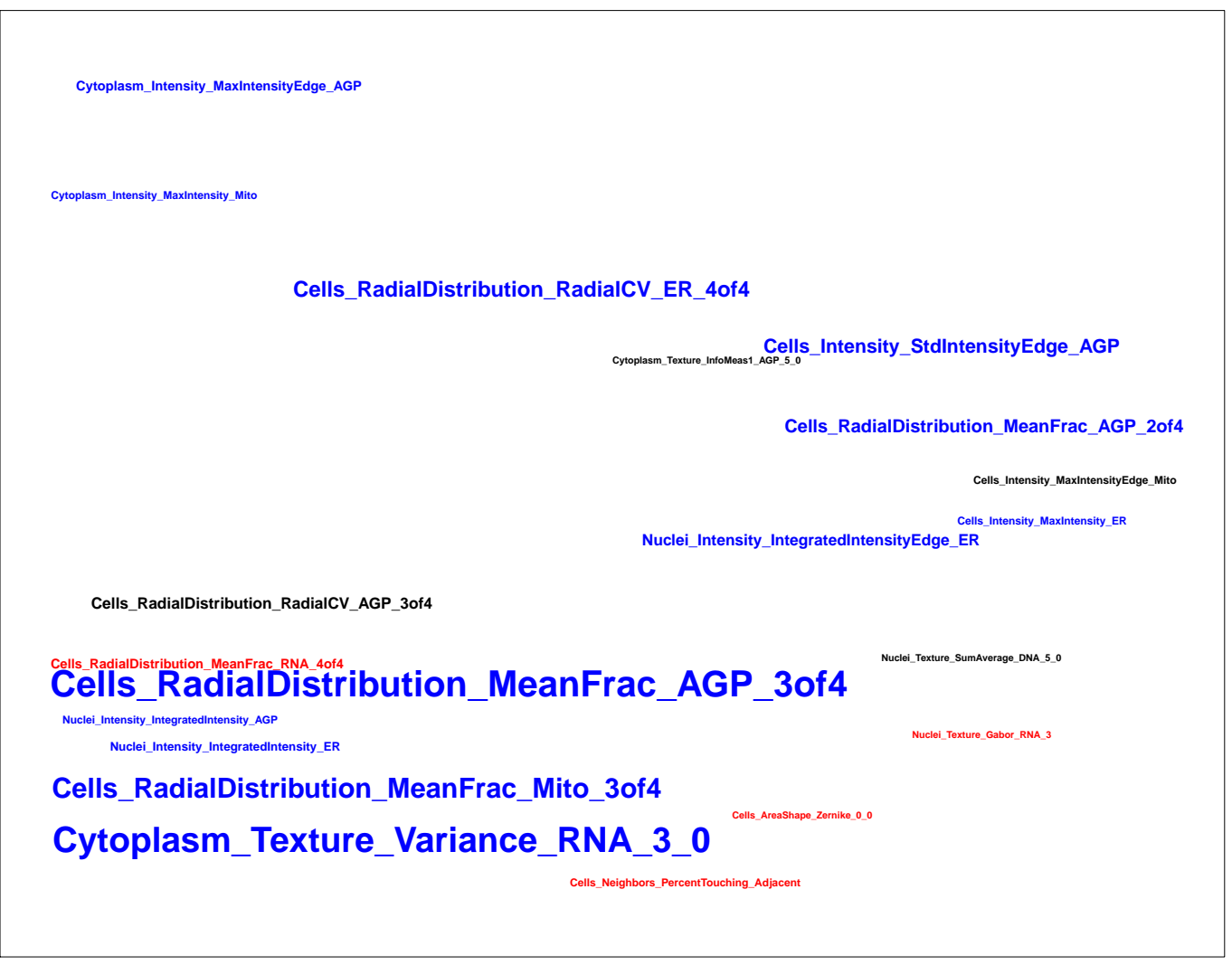
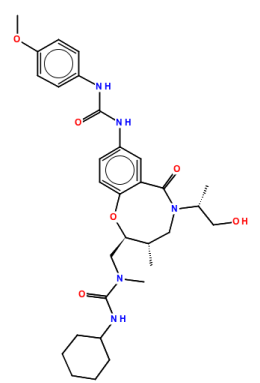
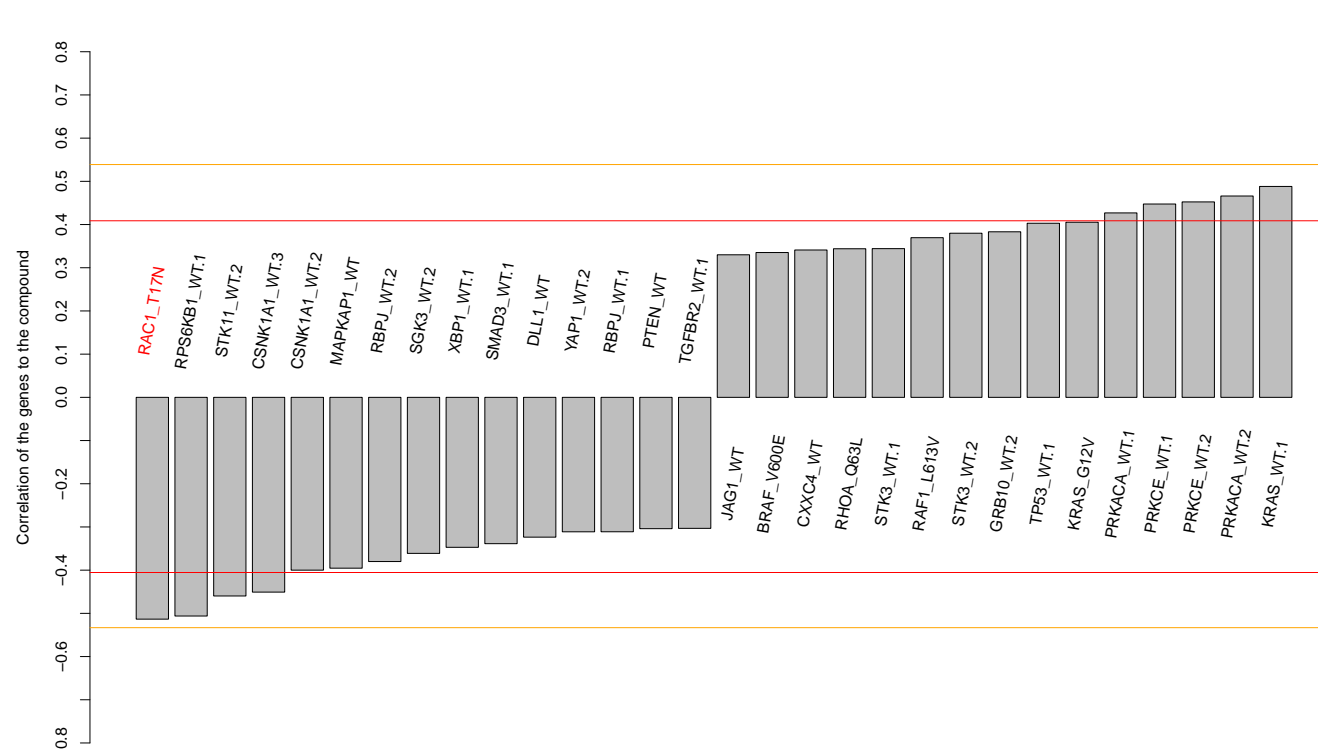
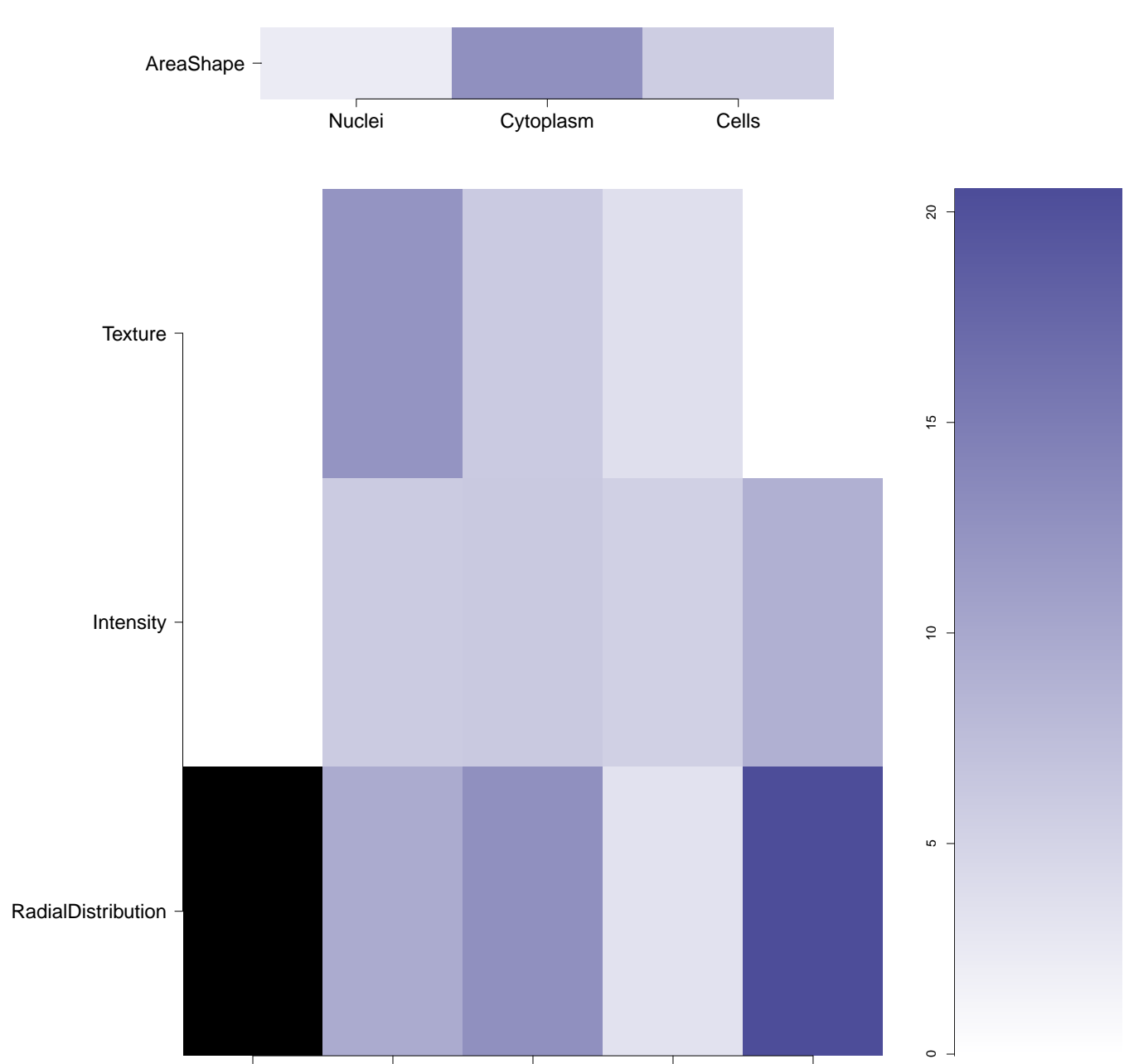

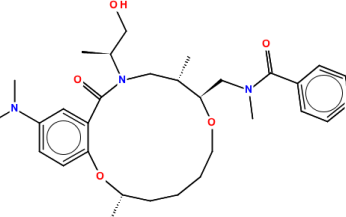
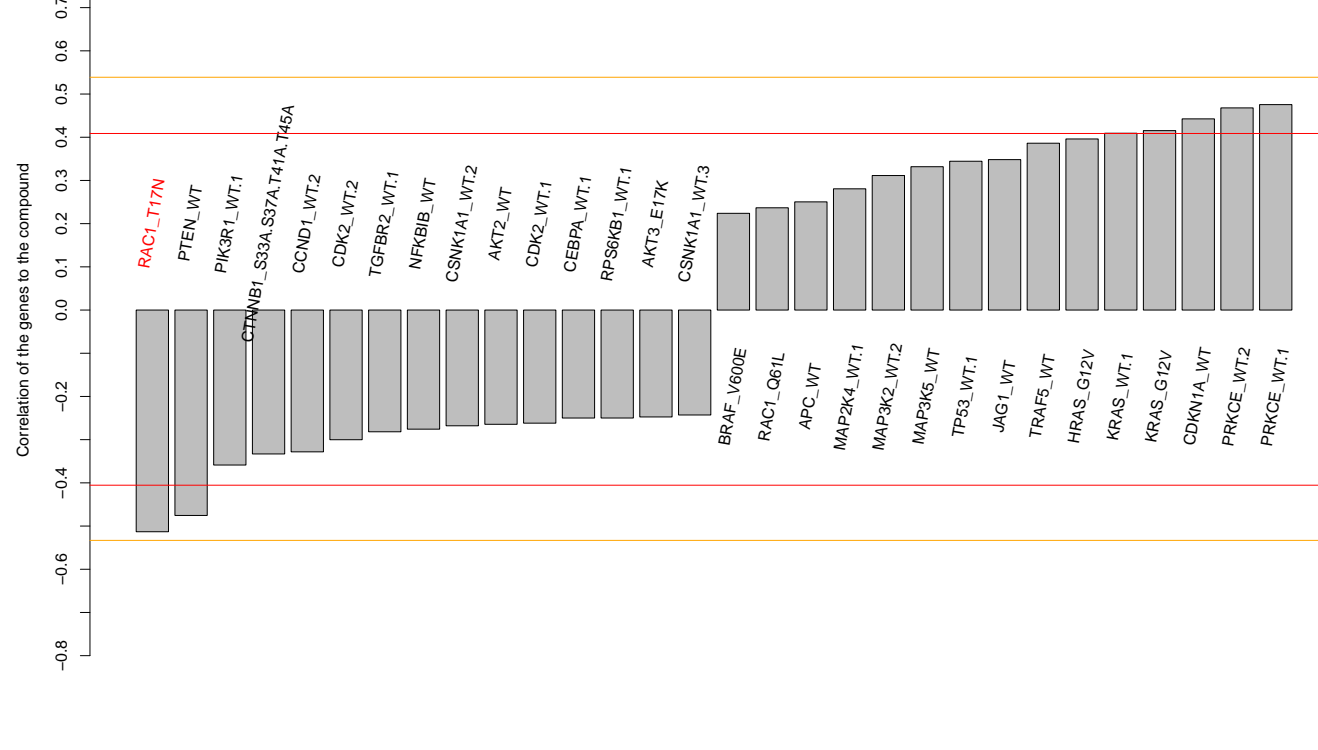
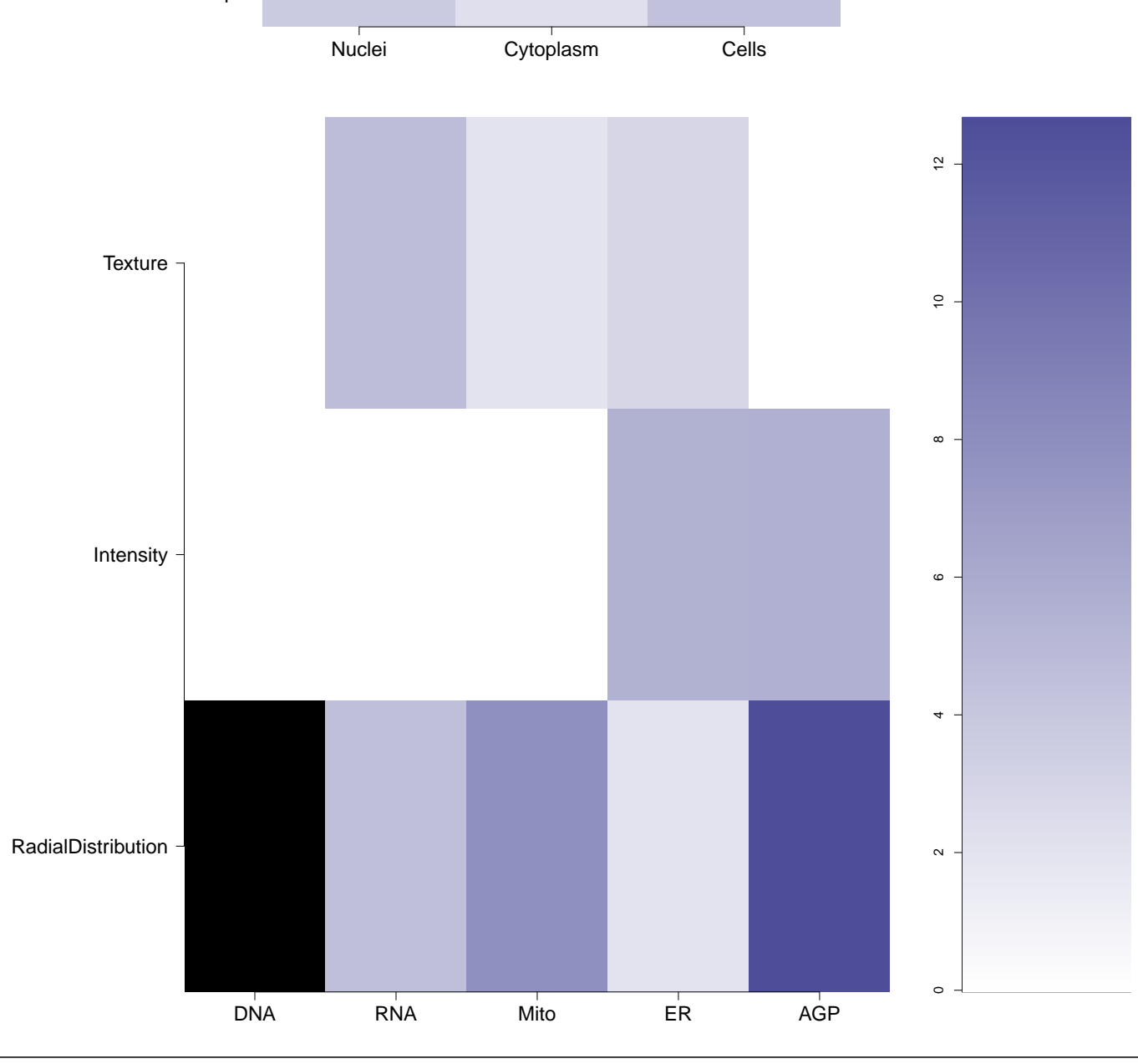



ER



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-K84767166-001-05-7 AC1M3GKX Ambcb6585282 MLS000680947 HMS2566M09 ZINC12382993 SMR000269607 PubChem CID : 2189681		NA (in 1 replicates)	0.50	NA				<p>Total number of assays tested in: 640. Active in the following assays:</p> <ul style="list-style-type: none"> Primary cell-based high-throughput screening assay to identify agonists of Galanin Receptor 2 (GALR2) (AID 803) qHTS Assay for Inhibitors of Aldehyde Dehydrogenase 1 (ALDH1A1) (AID 1030) qHTS for Inhibitors of Tau Fibril Formation, Thioflavin T Binding (AID 1460) qHTS Assay for Inhibitors of Bacillus subtilis Sfp phosphopantetheinyl transferase (PPTase) (AID 1490) qHTS Assay for the Inhibitors of Schistosoma Mansoni Peroxidoxins (AID 485364) qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332) qHTS Assay for Inhibitors of Mammalian Selenoprotein Thioredoxin Reductase 1 (TrxR1): qHTS (AID 588453) qHTS for Inhibitors of WRN Helicase (AID 651768) 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) qHTS for Inhibitors of PLK1-PDB (polo-like kinase 1 - polo-box domain): Primary Screen (AID 720504)
BRD-K47783463-001-01-9 PubChem CID : 44485701		0.95 (in 3 replicates)	-0.60	0.897				<p>Total number of assays tested in: 41. Active in the following assays:</p> <ul style="list-style-type: none"> Luminescence Cell-Based Primary HTS to Identify Inhibitors of STK33 (AID 2330) HTS for suppressors of simvastatin-induced myotoxicity in differentiated C2C12 cells Measured in Cell-Based System Using Plate Reader - 2112-01.Suppressor.SinglePoint.HTS.Activity (AID 602340) mutant P53 Measured in Biochemical System Using Small Molecule MicroArray - 2077-01.Other.SinglePoint.HTS.Activity (AID 624136) NF-KappaB Measured in Biochemical System Using Small Molecule MicroArray - 2080-01.Other.SinglePoint.HTS.Activity (AID 624139) SMM c-myc Measured in Biochemical System Using Small Molecule MicroArray - 2081-01.Other.SinglePoint.HTS.Activity (AID 624141) HTS for suppressors of simvastatin-induced myotoxicity in differentiated C2C12 cells Measured in Cell-Based System Using Plate Reader - 2112-01.Other.Dose.CherryPick.Activity (AID 624405)
BRD-K62780697-001-01-3 PubChem CID : 54618446		0.85 (in 4 replicates)	-0.55	0.939				<p>Total number of assays tested in: 23.</p>
BRD-K89110518-001-01-9 PubChem CID : 44492642		0.84 (in 4 replicates)	-0.55	0.052				<p>Total number of assays tested in: 28.</p>
BRD-K23002629-001-01-3 PubChem CID : 54619021		0.70 (in 4 replicates)	-0.54	0.745				<p>Total number of assays tested in: 38.</p>
BRD-K55522920-001-01-7 PubChem CID : 54648993		NA (in 1 replicates)	-0.53	0.923				<p>Total number of assays tested in: 35.</p>
BRD-K10704442-001-01-4 PubChem CID : 44492151		0.70 (in 3 replicates)	-0.52	0.836				<p>Total number of assays tested in: 51.</p>

BRD-K65963096-001-01-9 PubChem CID : 44486854		0.84 (in 3 replicates)	-0.52	0.877				Total number of assays tested in: 54.
BRD-K60861723-001-01-1 PubChem CID : 54646599		0.89 (in 4 replicates)	-0.52	0.673				Total number of assays tested in: 38.
BRD-K82157325-001-02-8 MLS002474370 SMR001398531 PubChem CID : 44202021		0.93 (in 3 replicates)	-0.51	0.849				Total number of assays tested in: 372. Active in the following assays: <ul style="list-style-type: none">• HTS for Identification of VLA-4 Allosteric Modulators from MLPCN library (AID 2557)• oHTS Luminescent assay for identification of activators of mouse intestinal alkaline phosphatase (AID 2805)• DENV2 CPE-Based HTS Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2149-01-Other.SinglePoint-HTS.Activity (AID 651640)
BRD-K49673270-001-01-3 PubChem CID : 44485812		0.81 (in 4 replicates)	-0.51	0.016				Total number of assays tested in: 46.