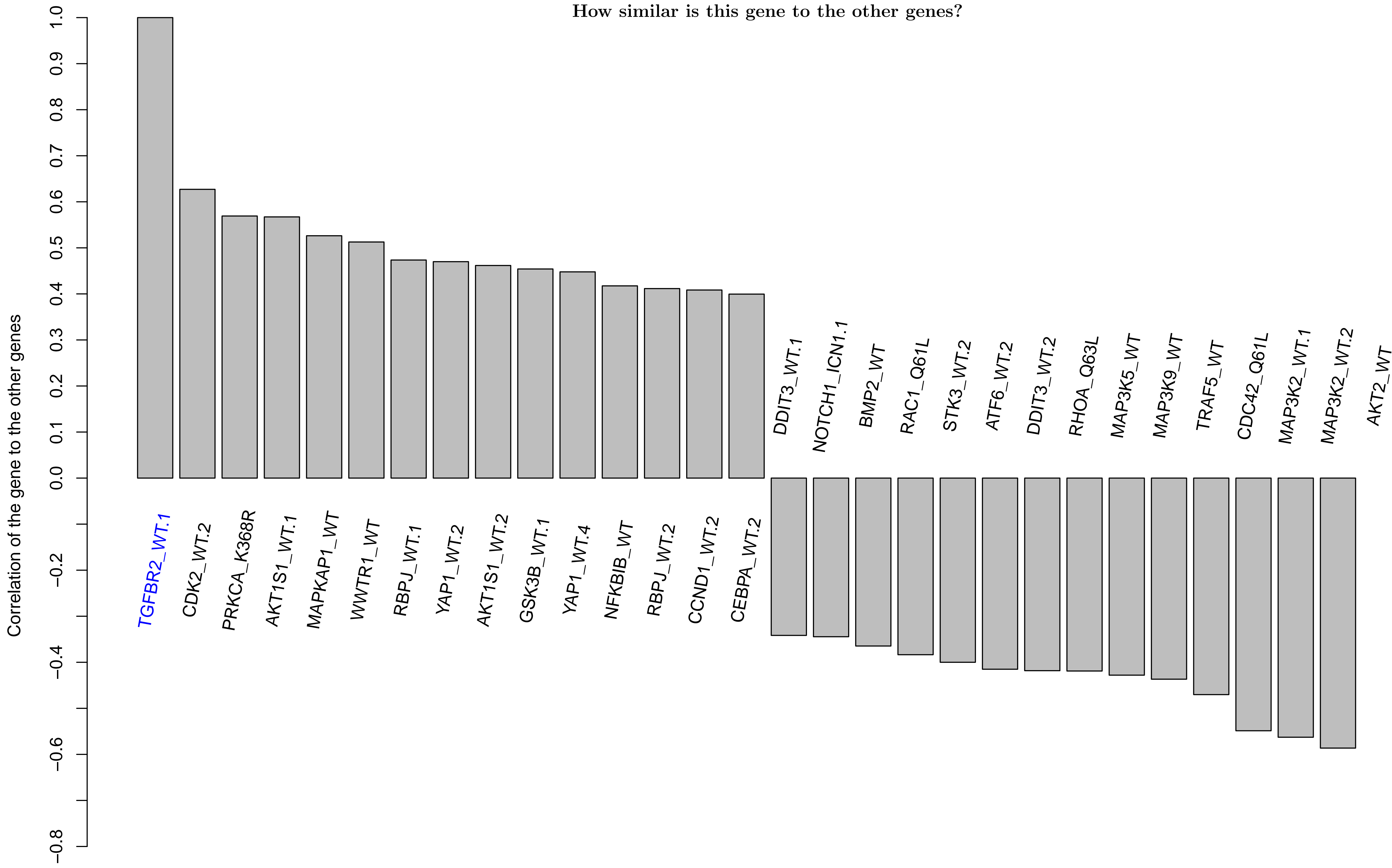
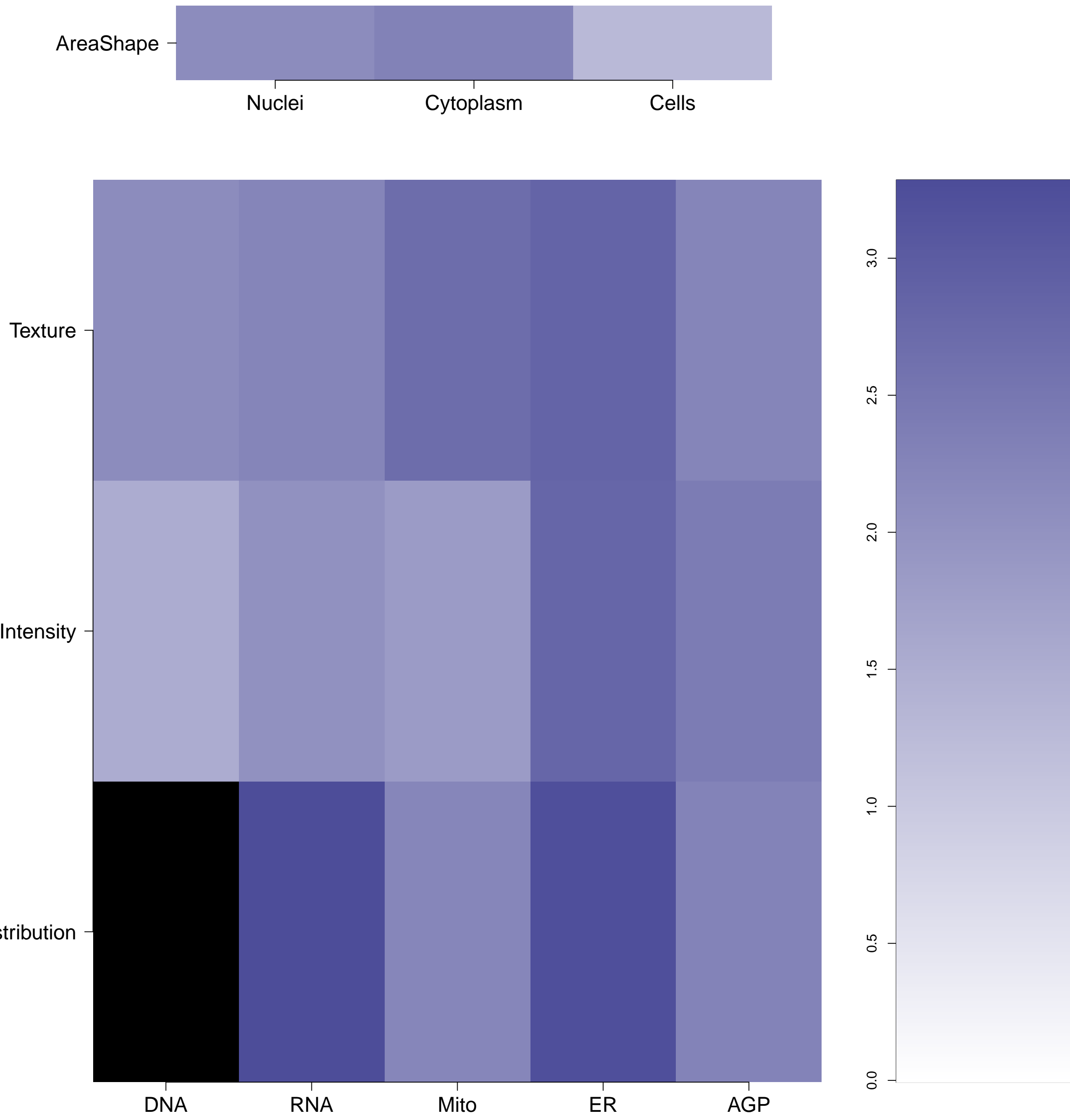


How similar is this gene to the other genes?



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

TGFBFR2.WT.1 (41744)

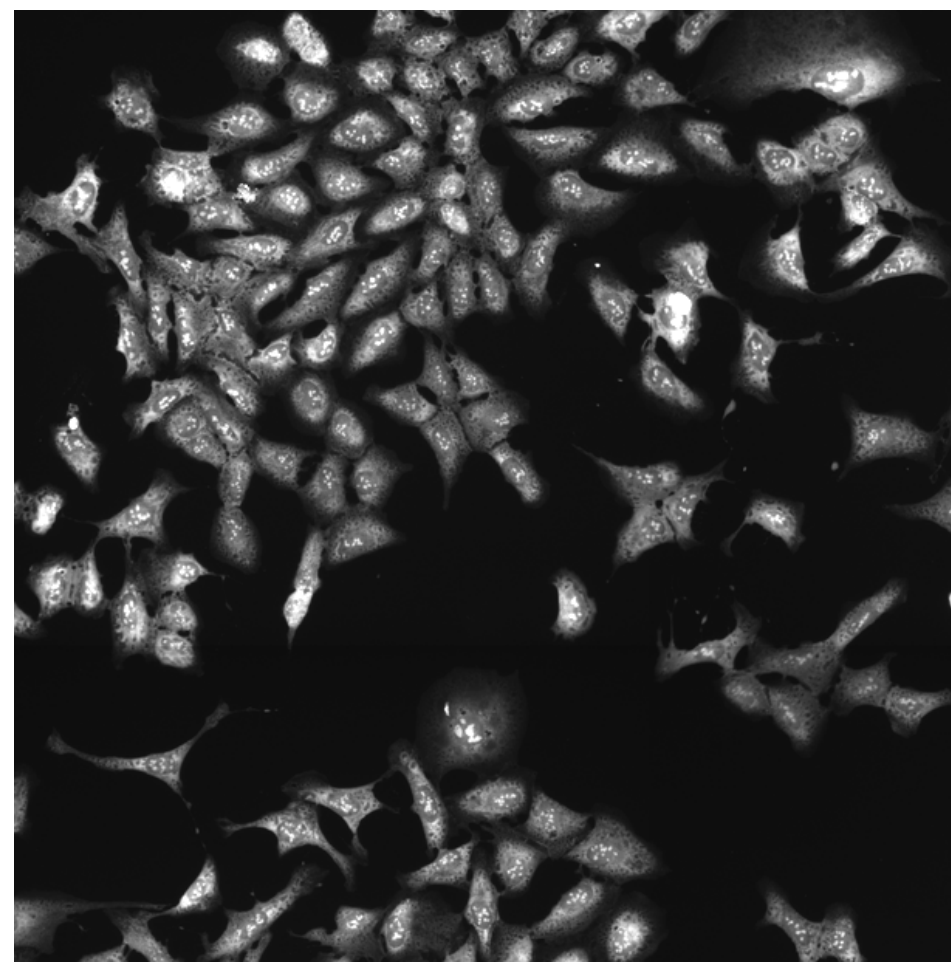
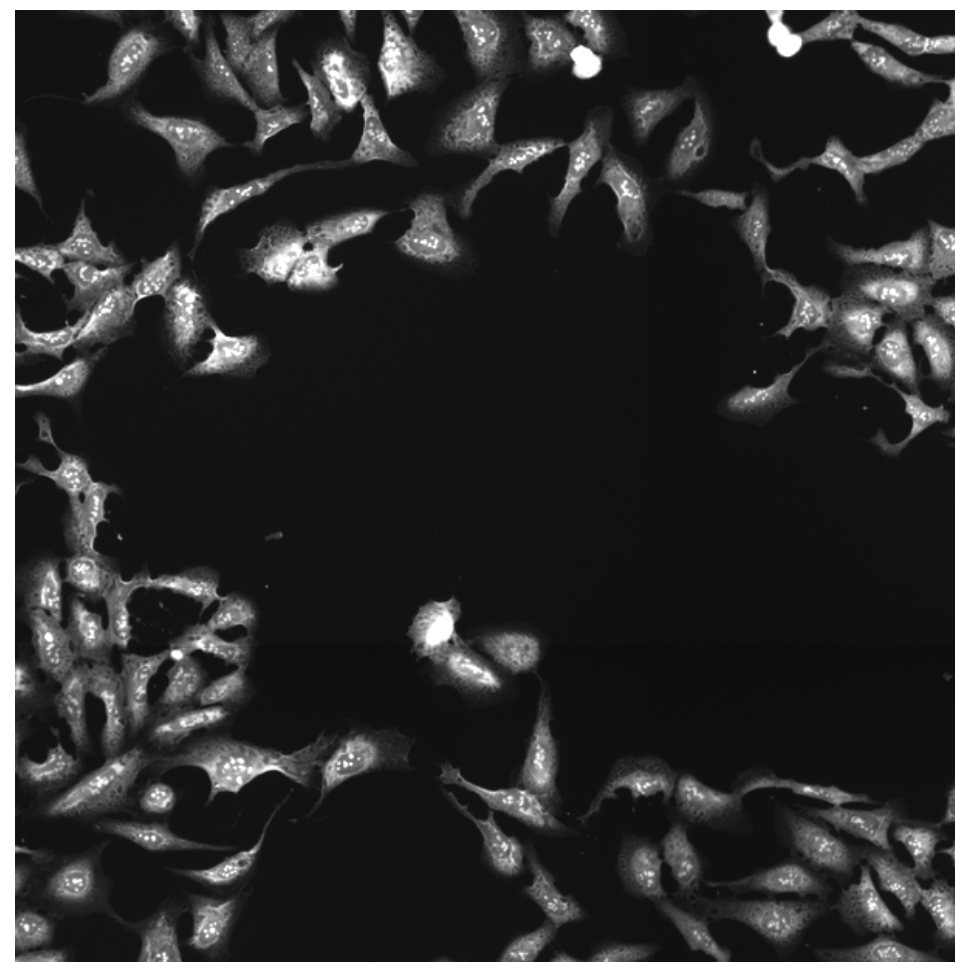
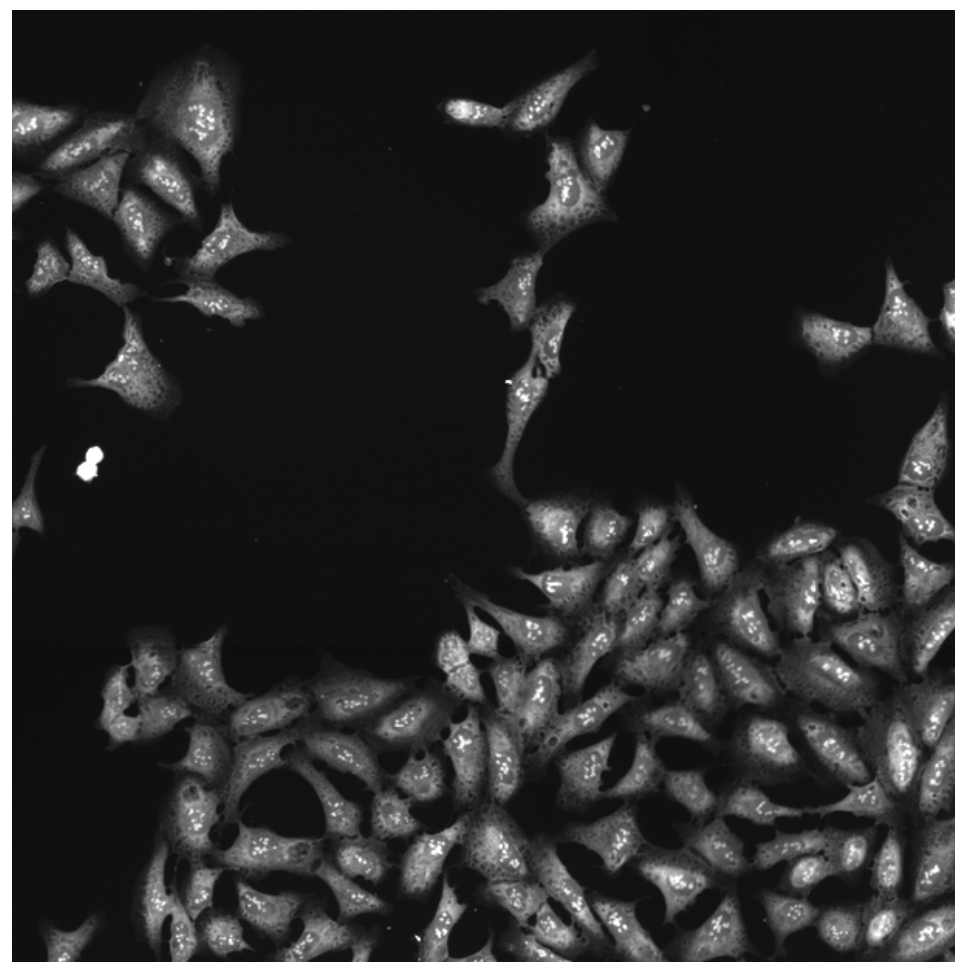
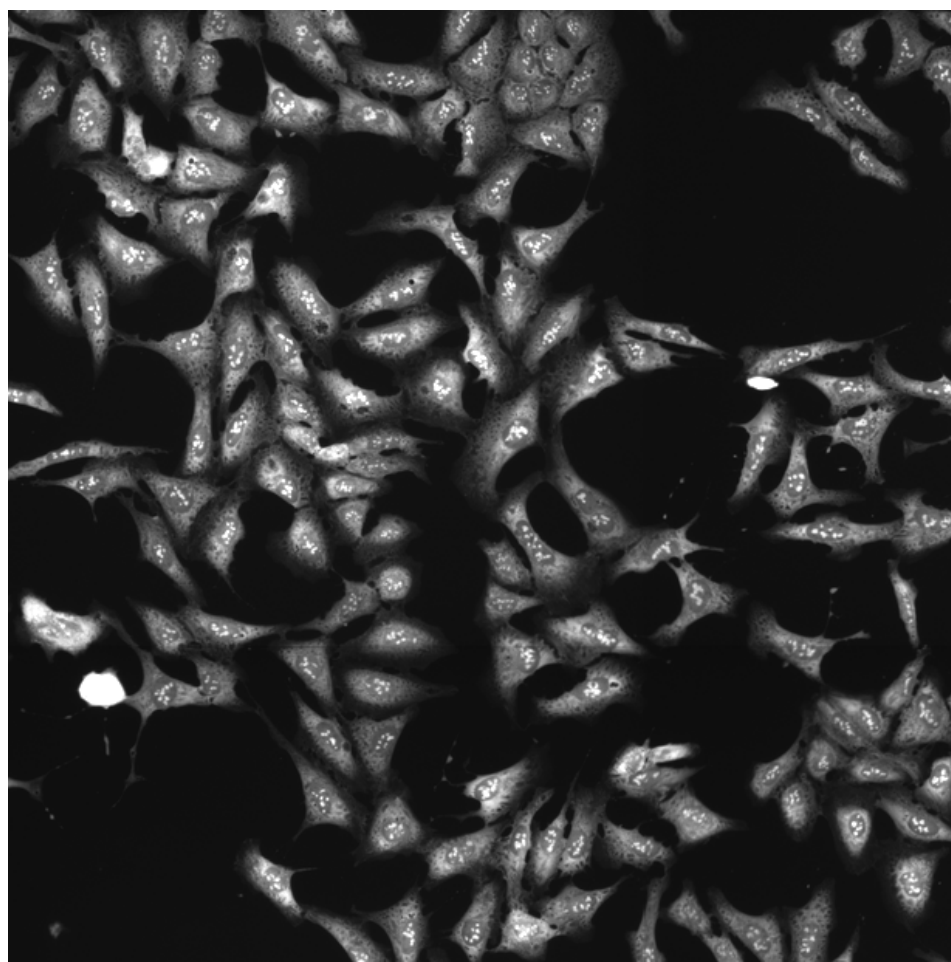
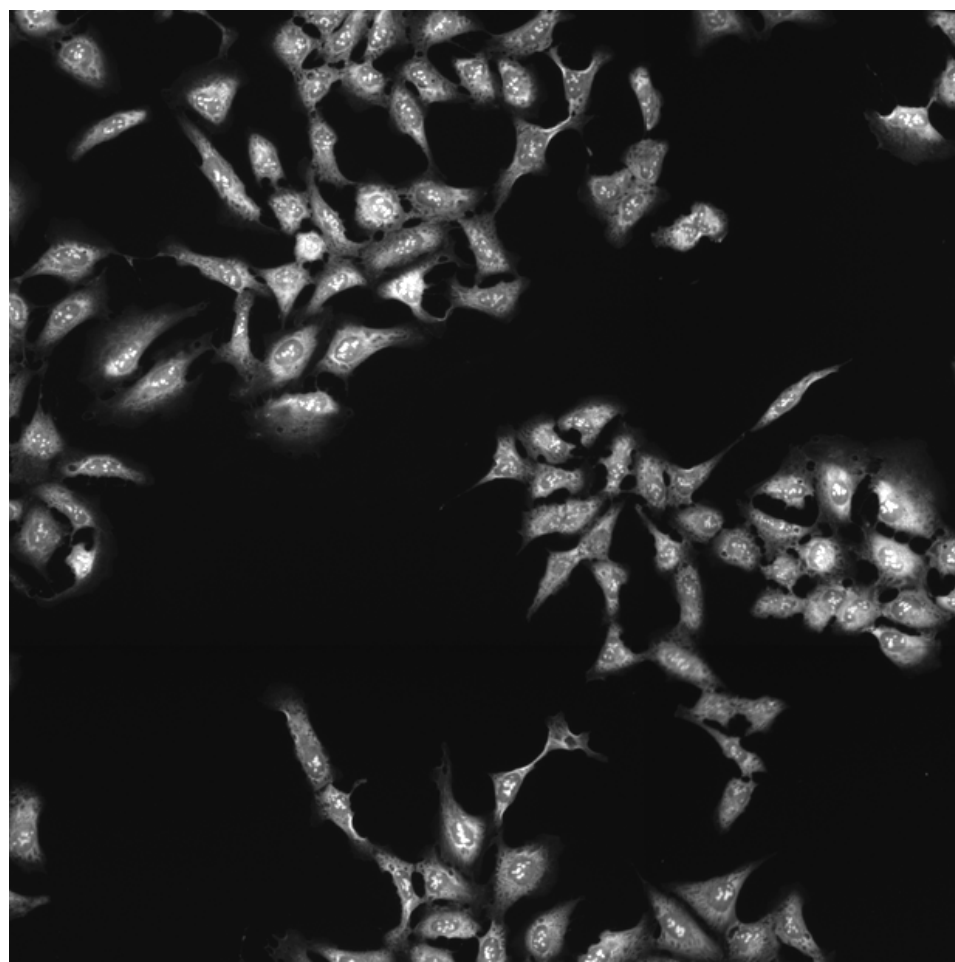
TGFBFR2.WT.1 (41755)

TGFBFR2.WT.1 (41756)

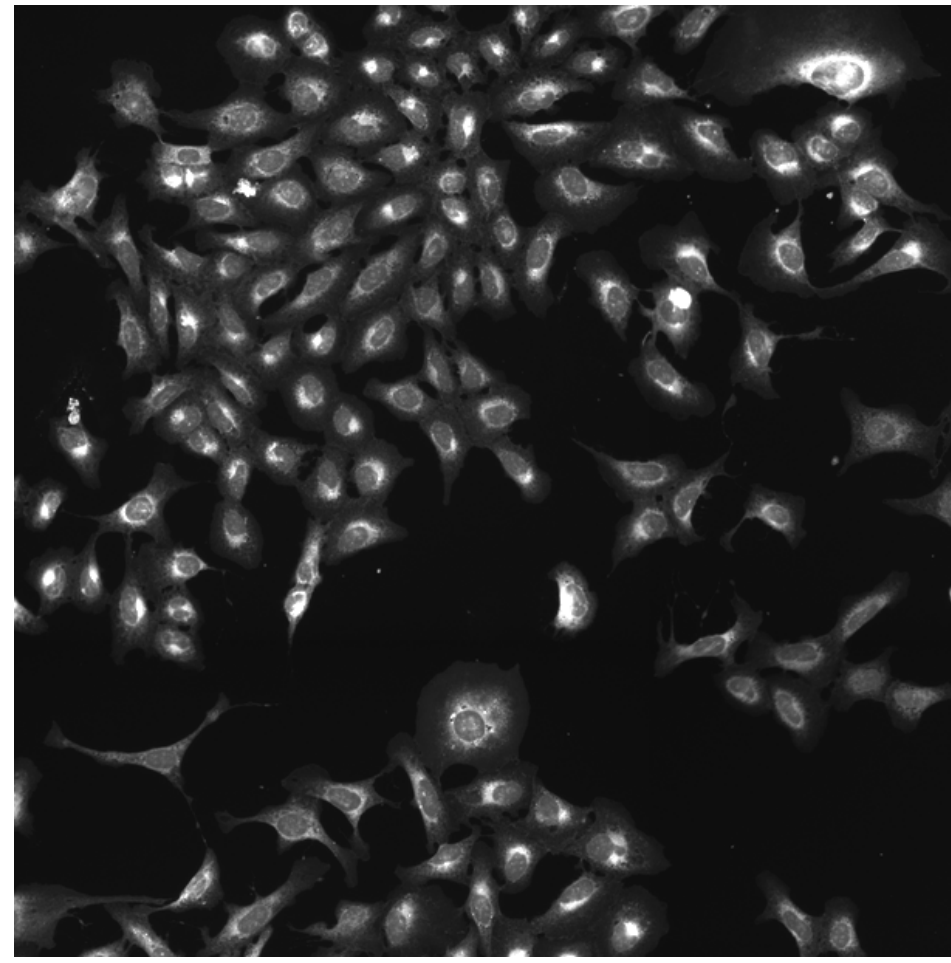
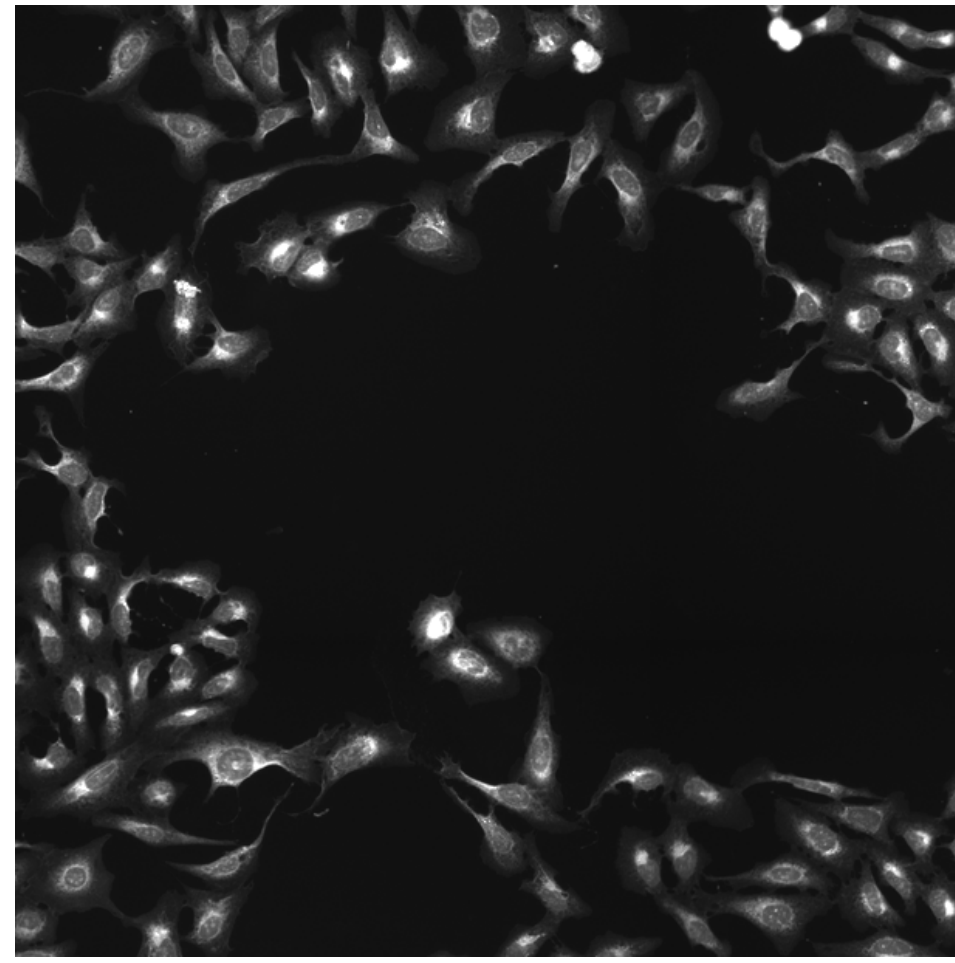
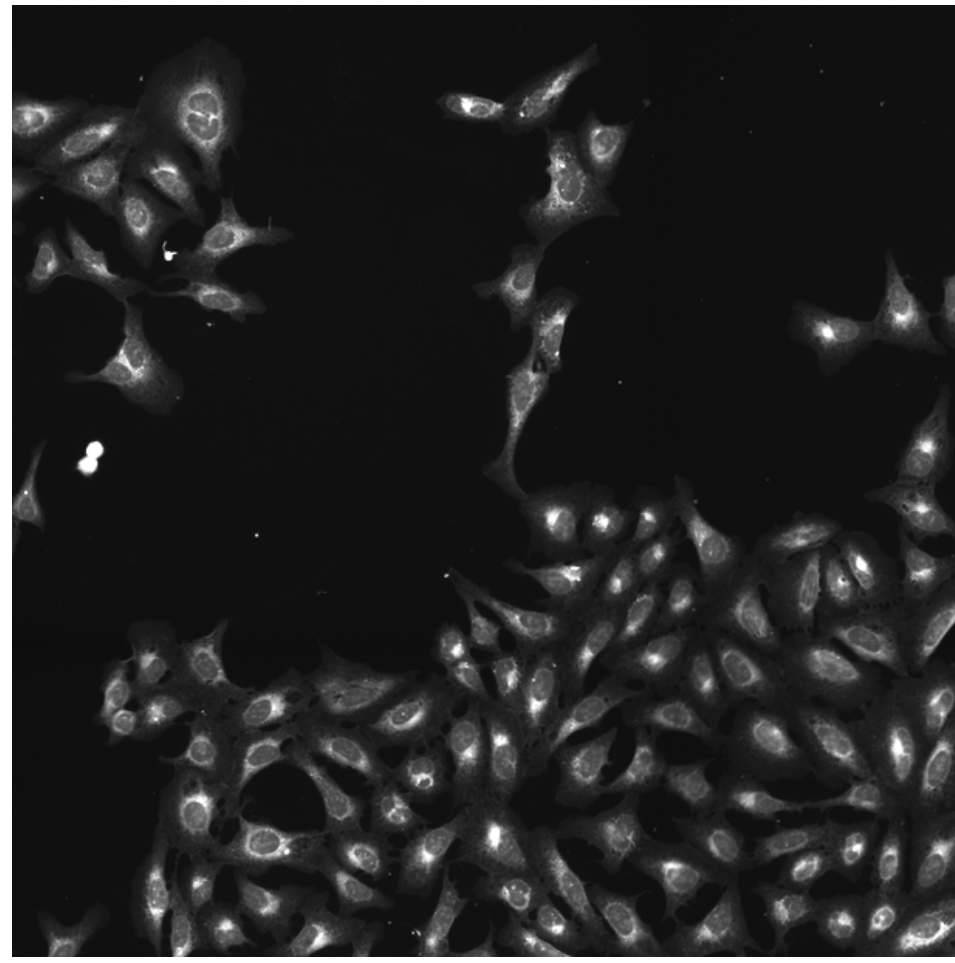
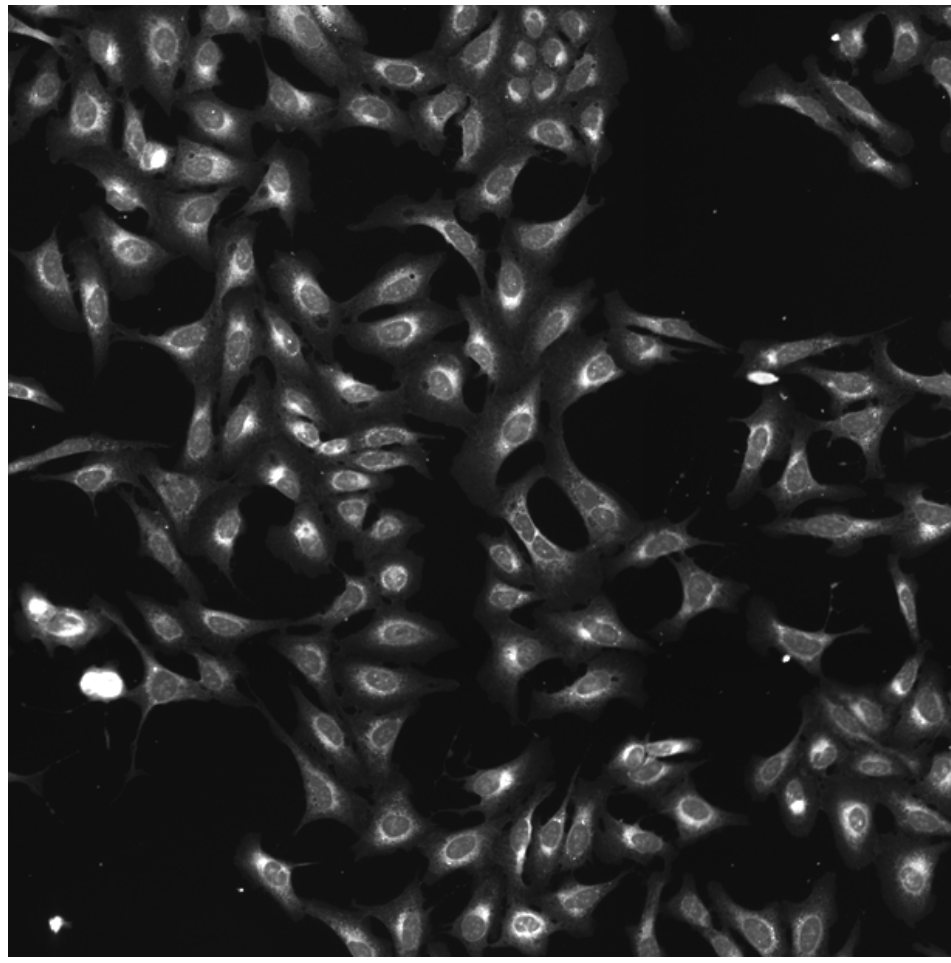
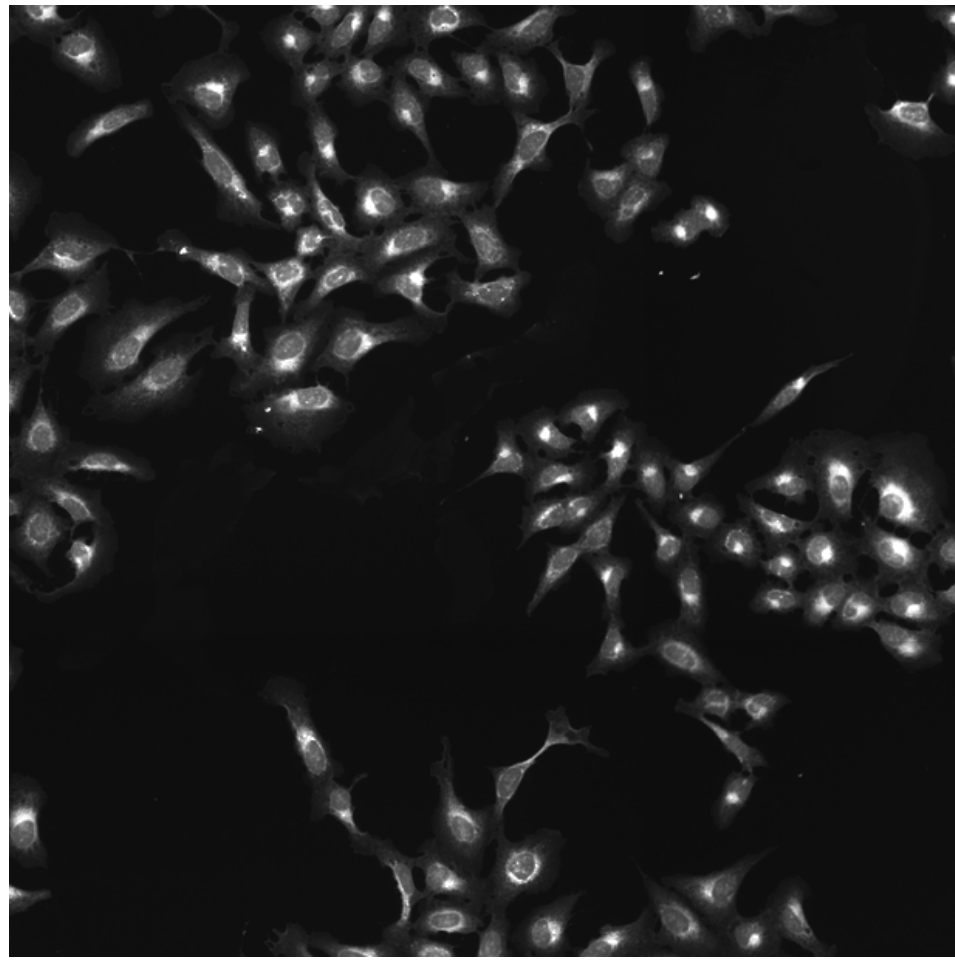
TGFBFR2.WT.1 (41757)

TGFBFR2.WT.1 (41754)

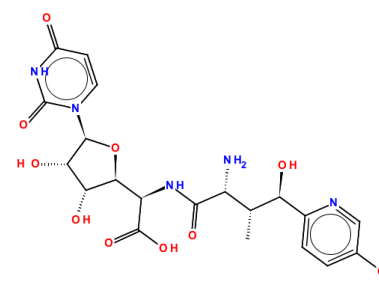
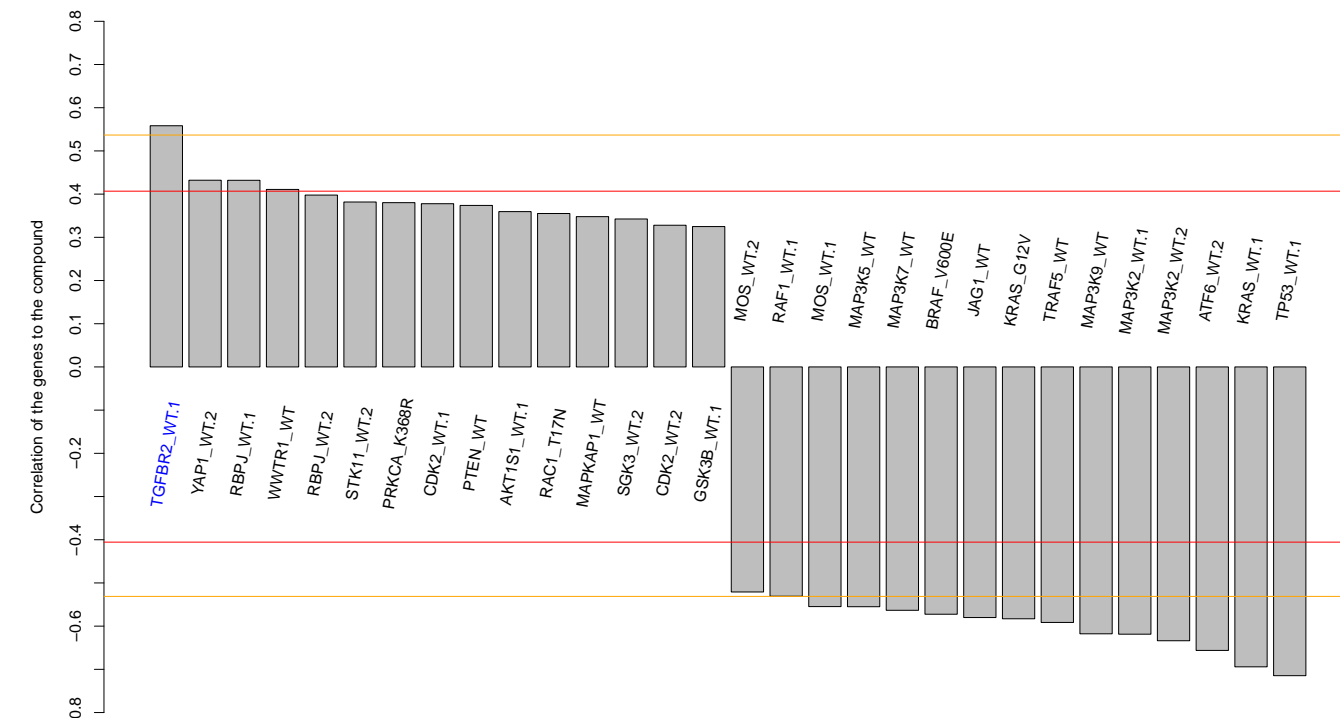
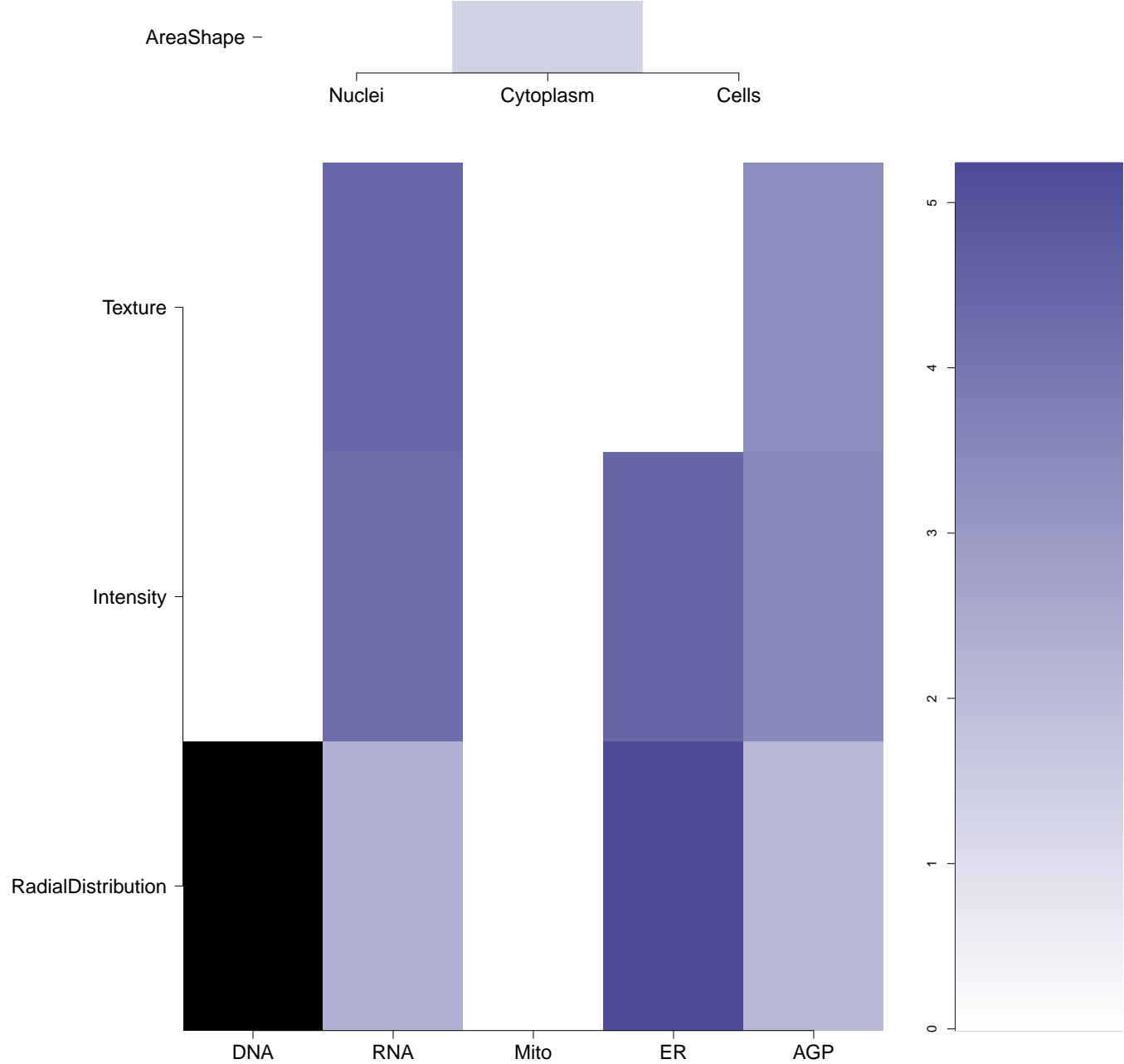

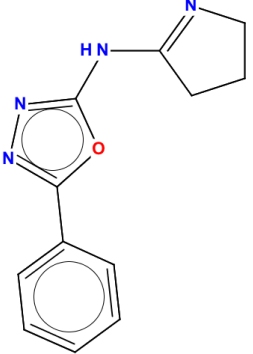
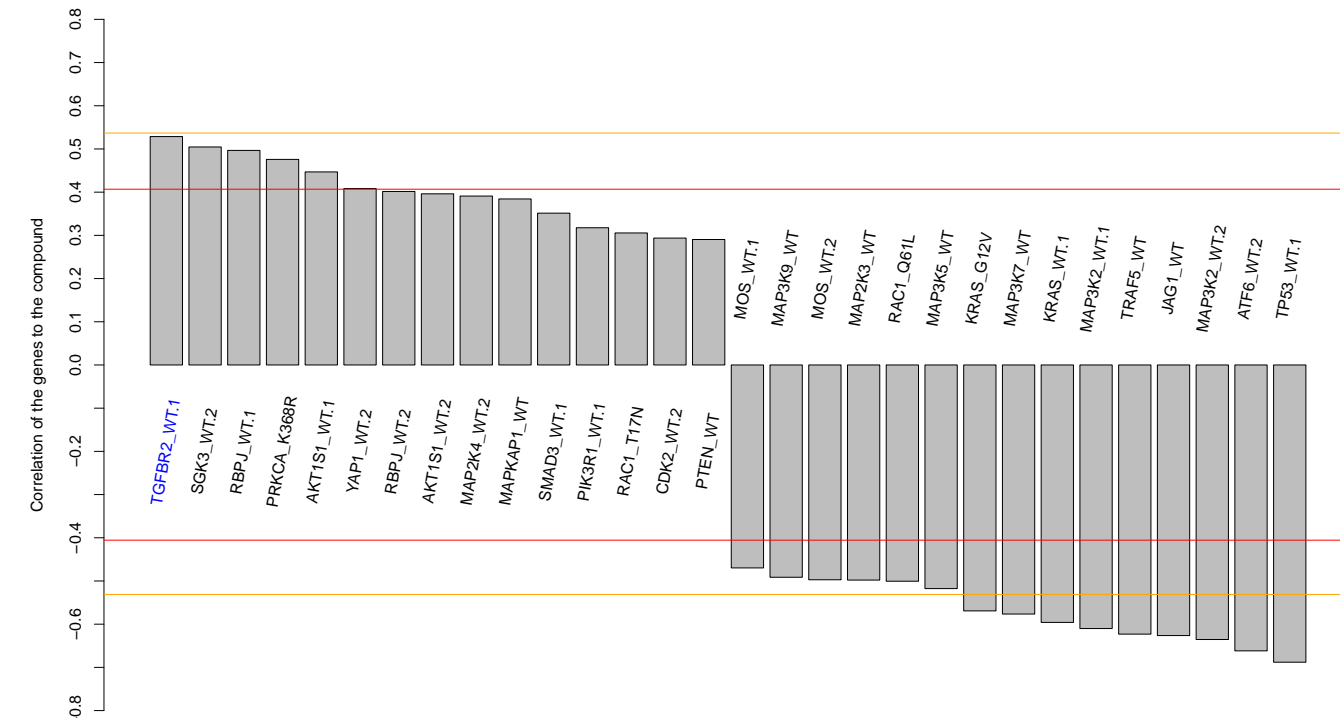
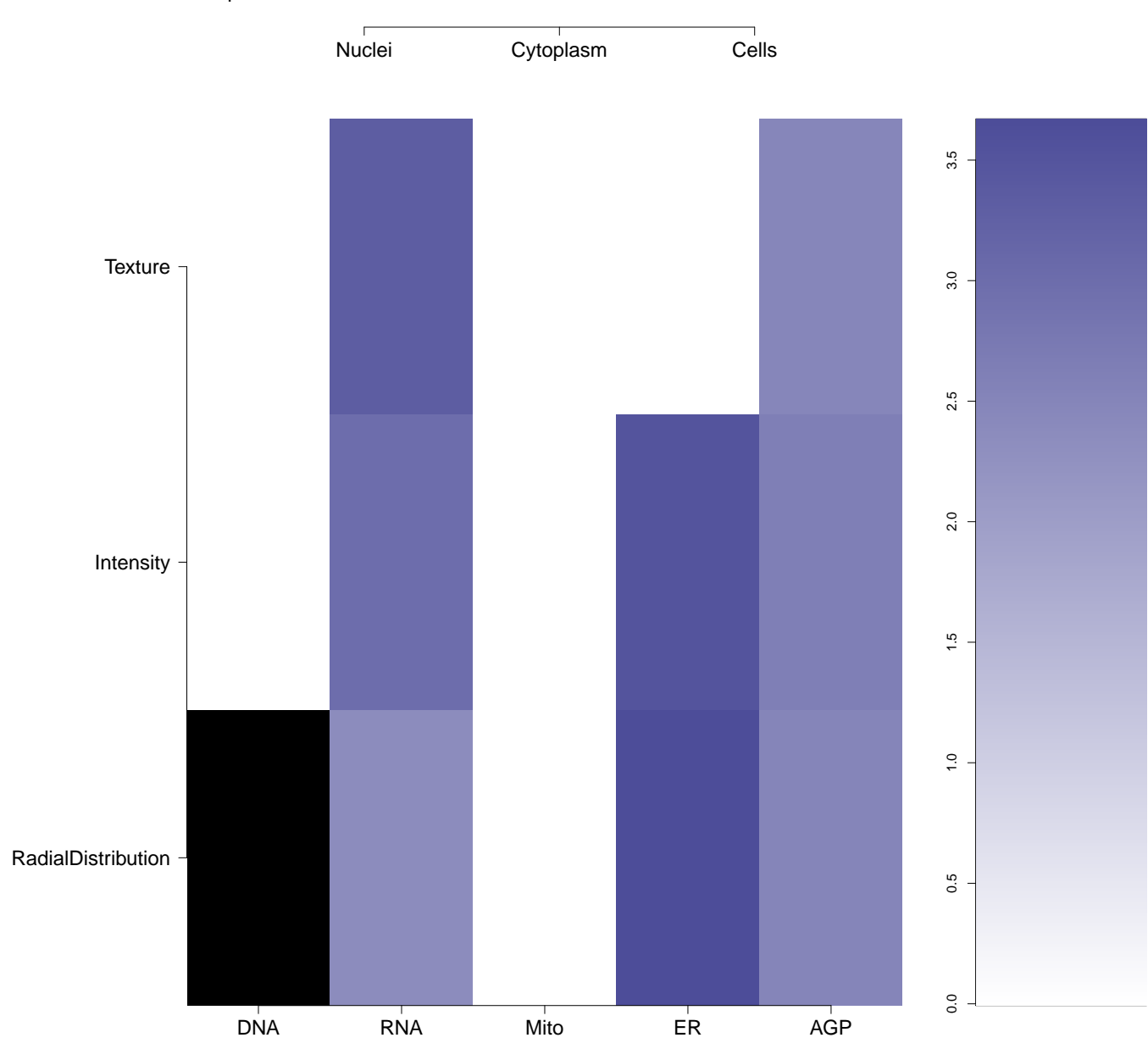

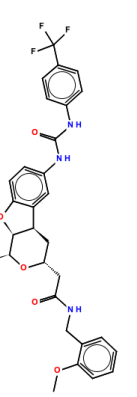
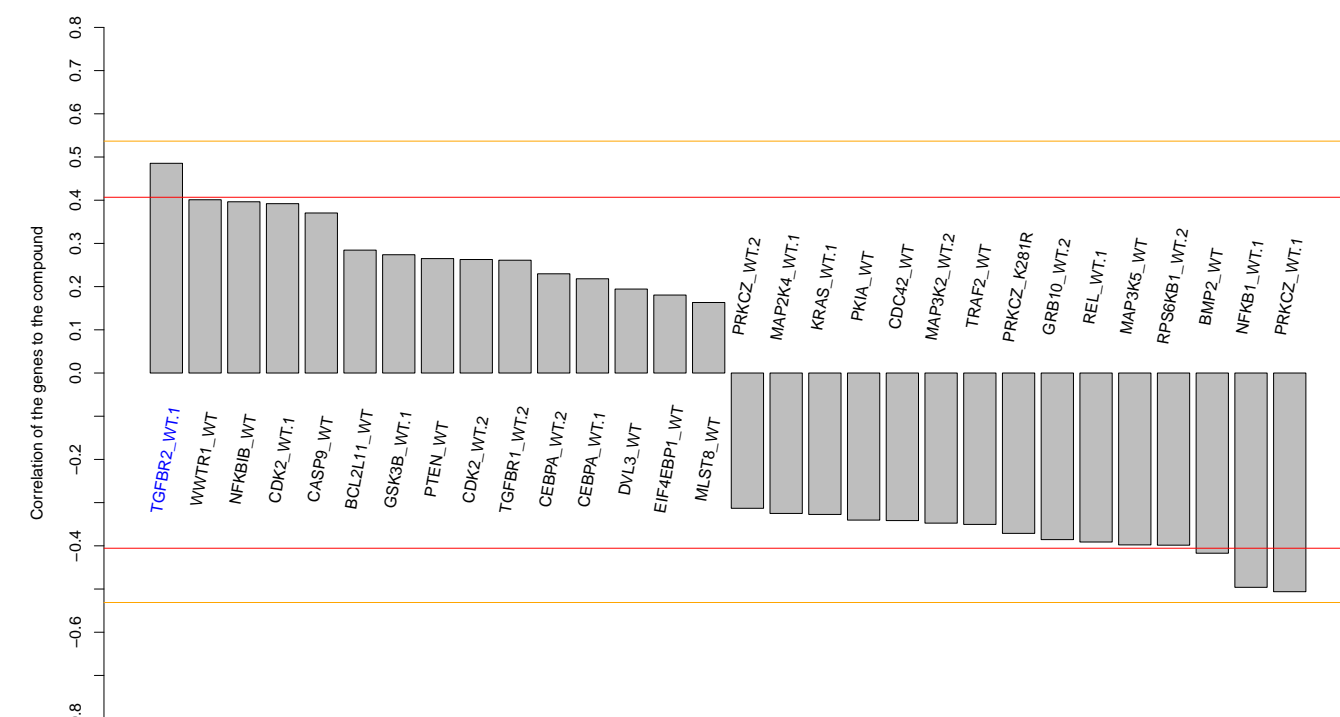
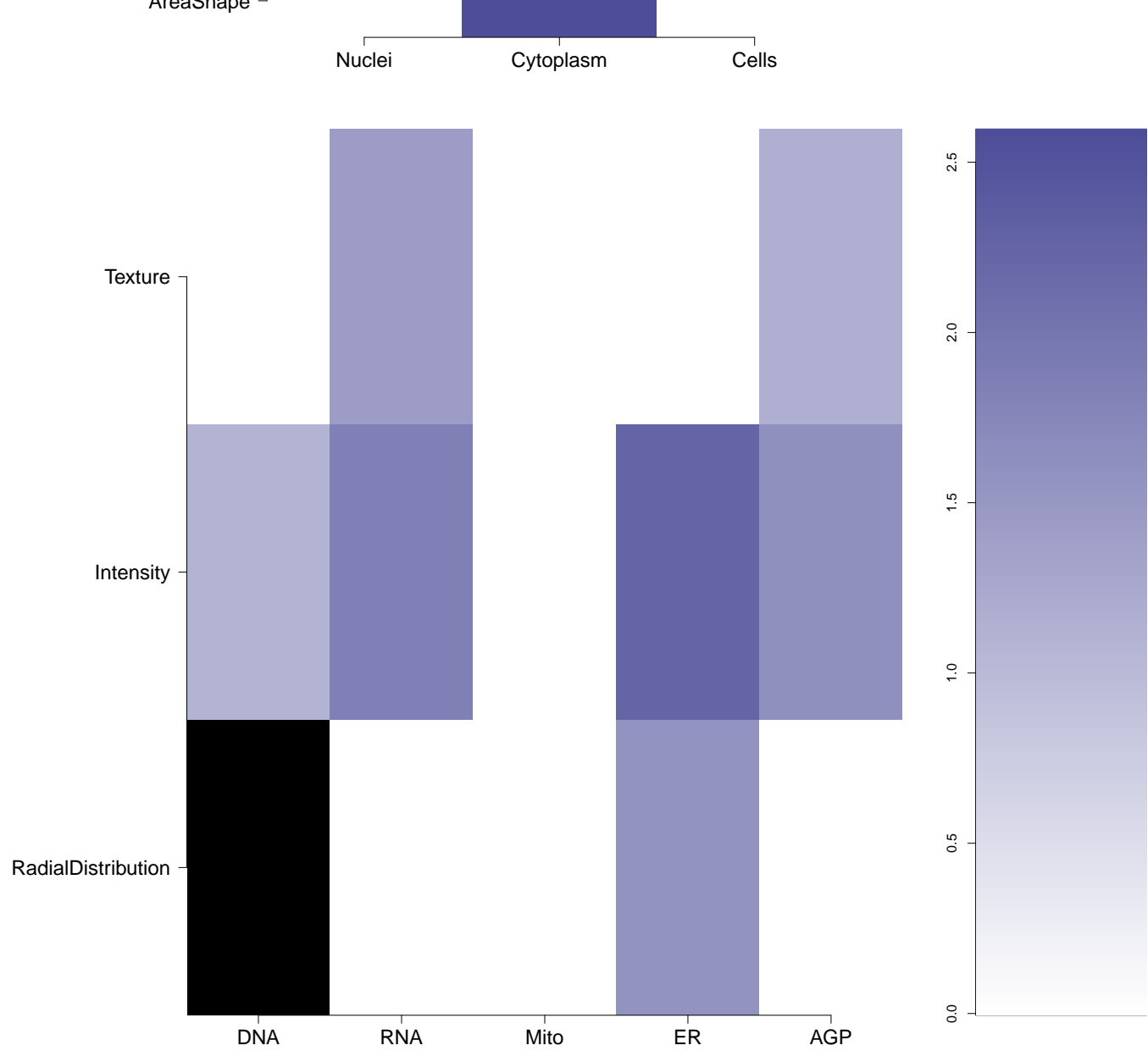
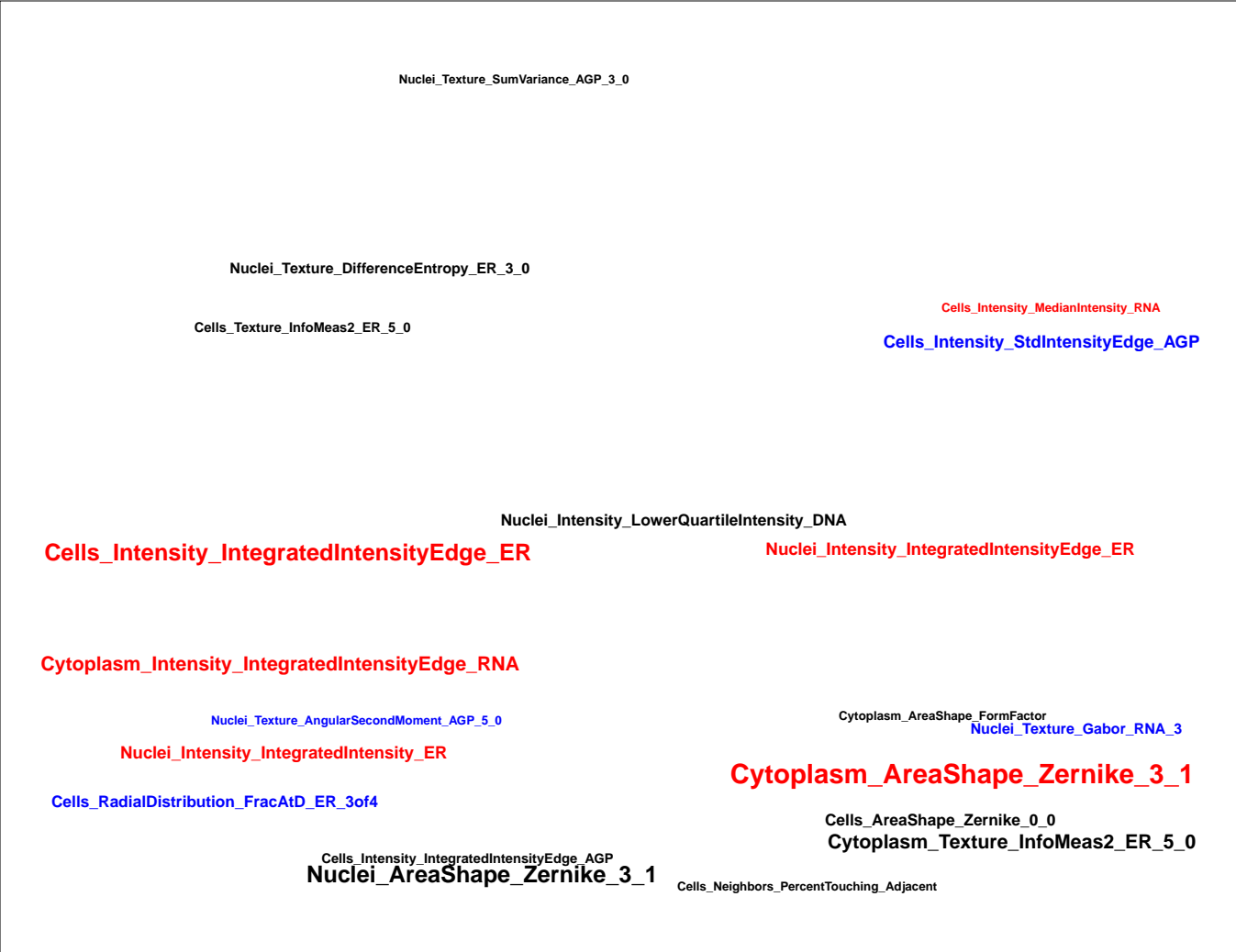
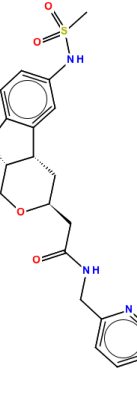
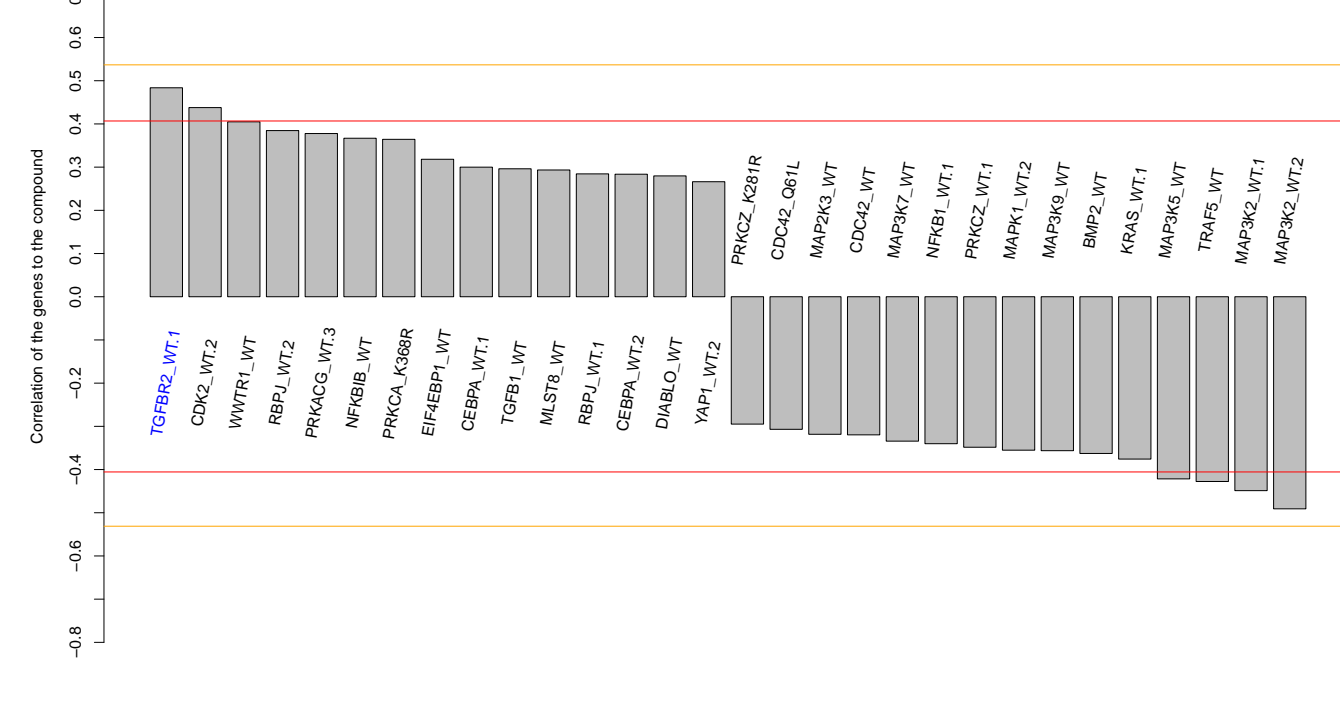
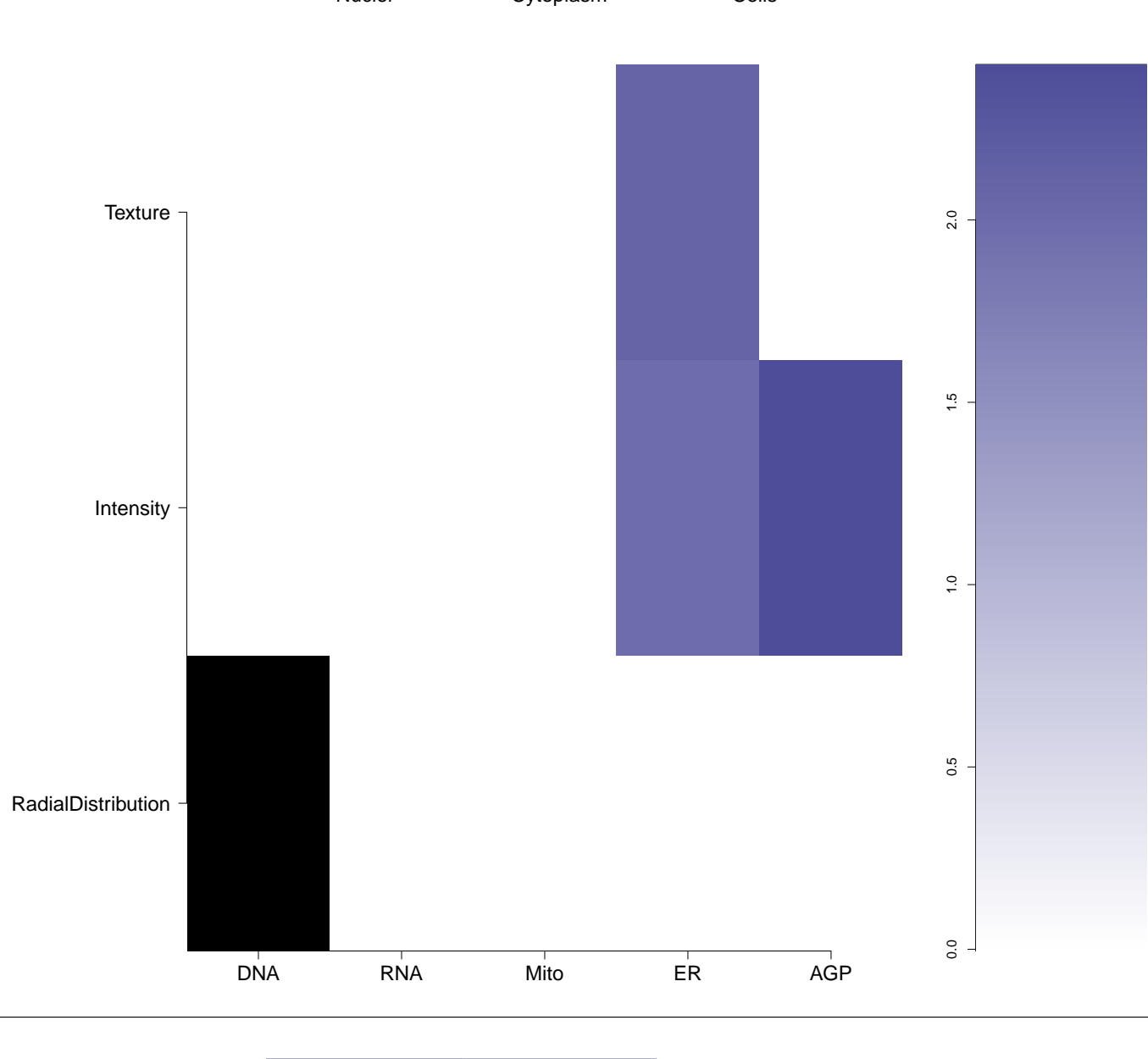
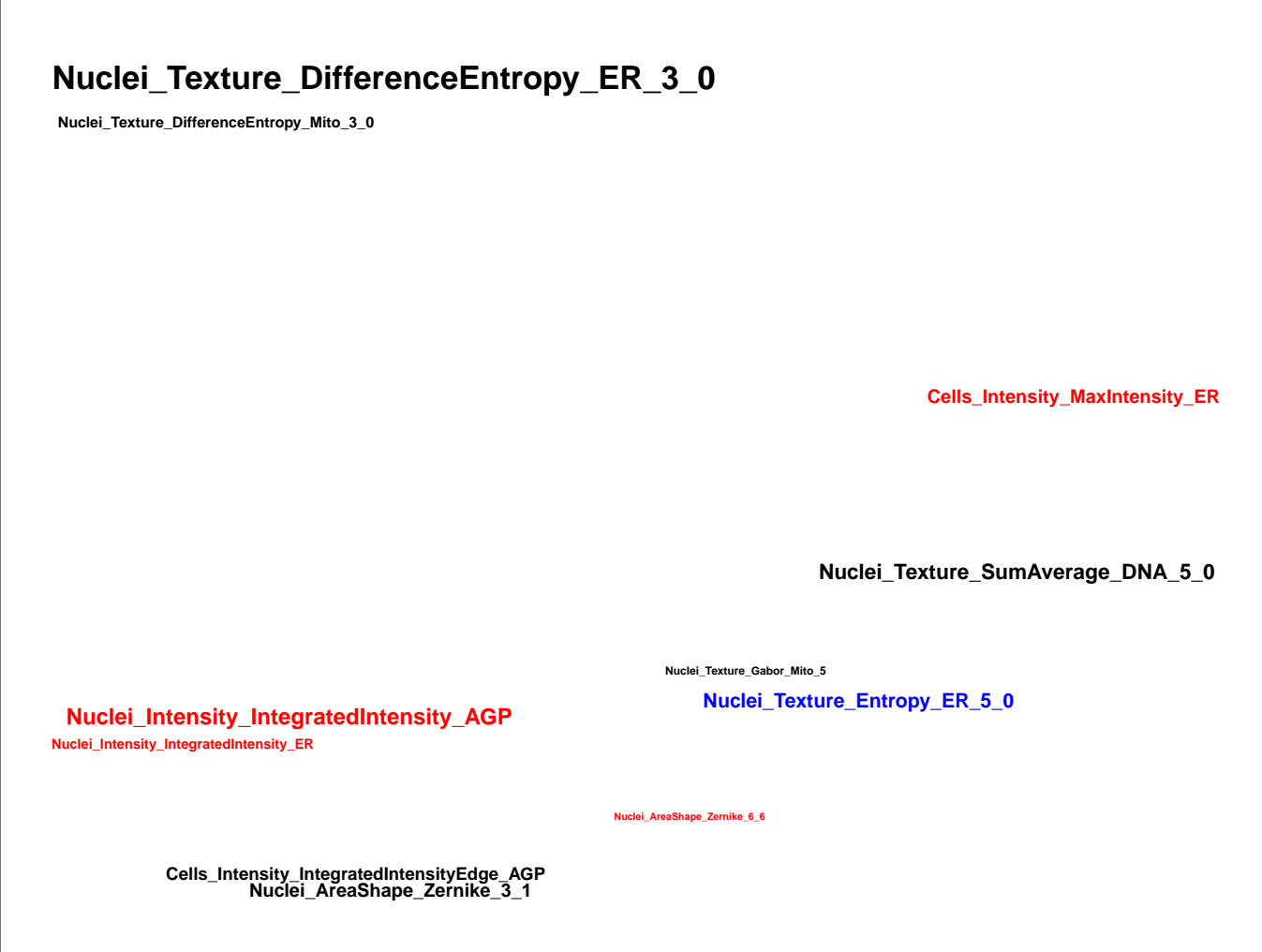
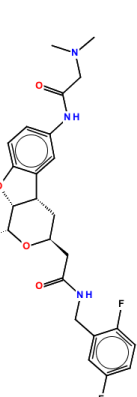
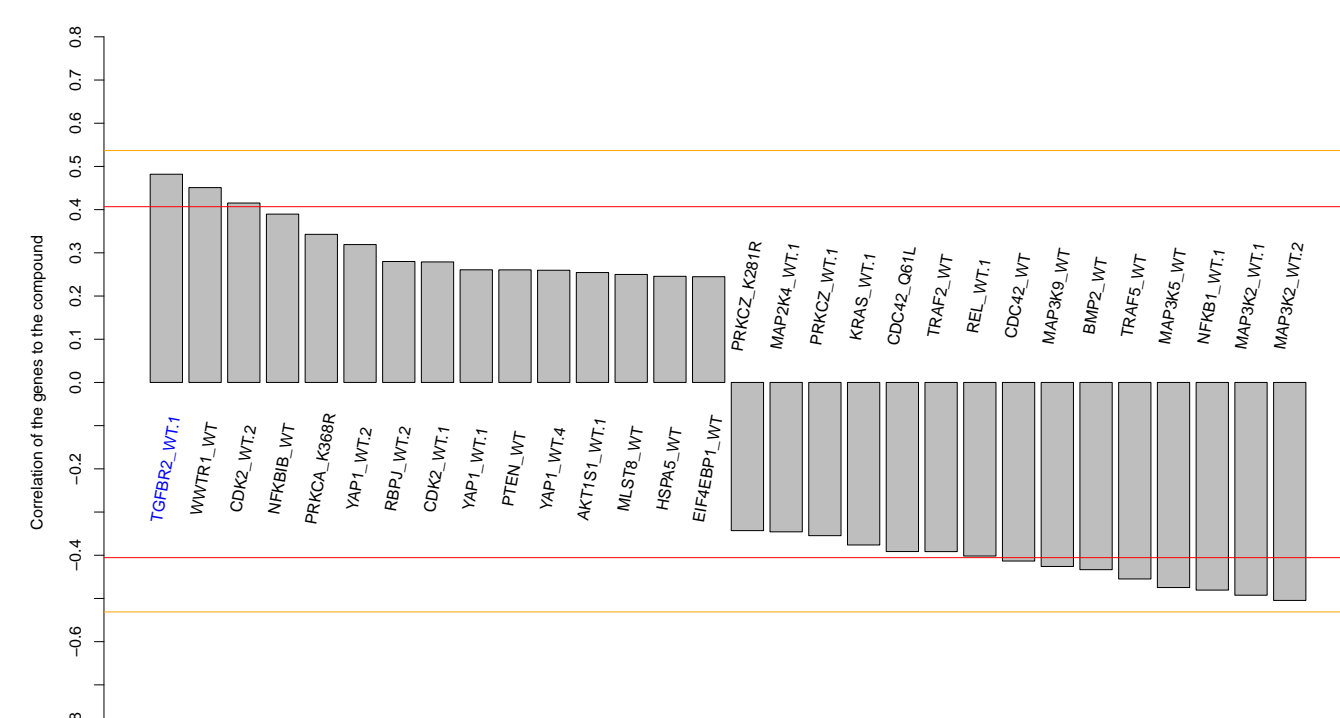
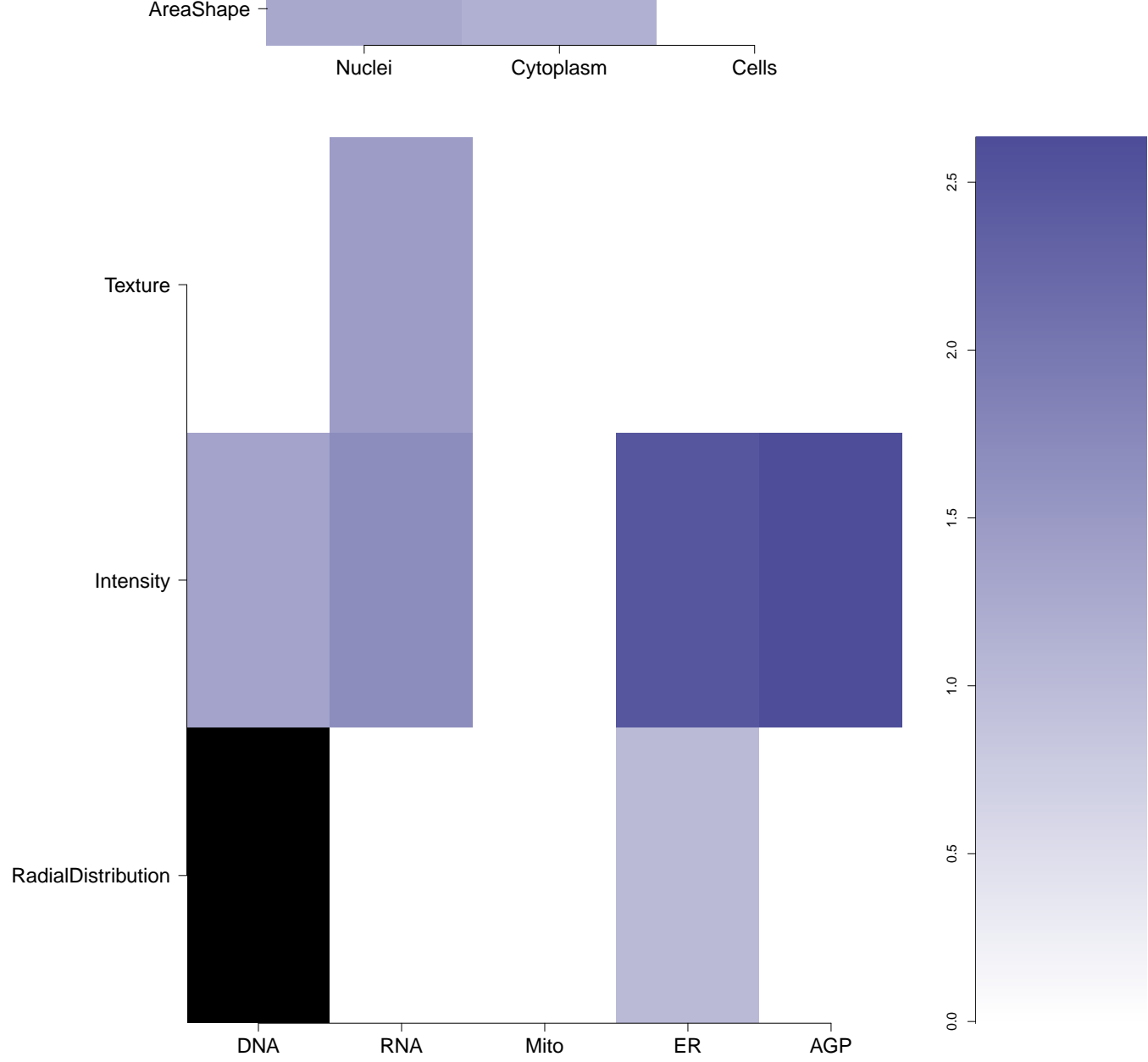
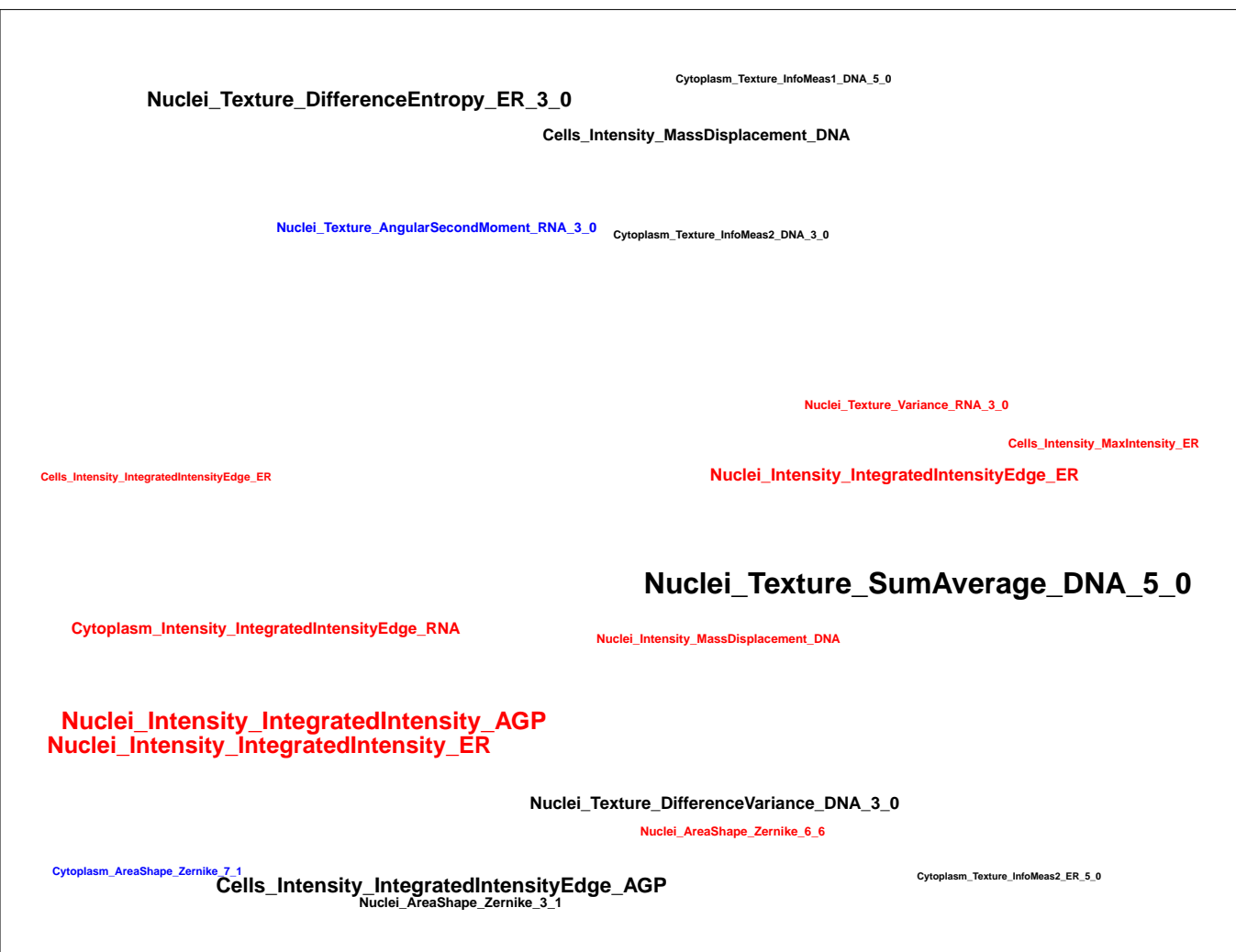
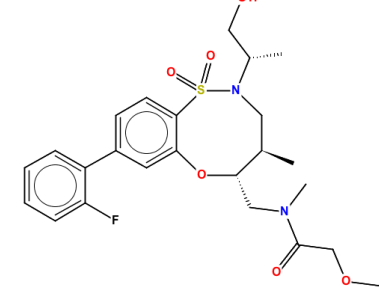
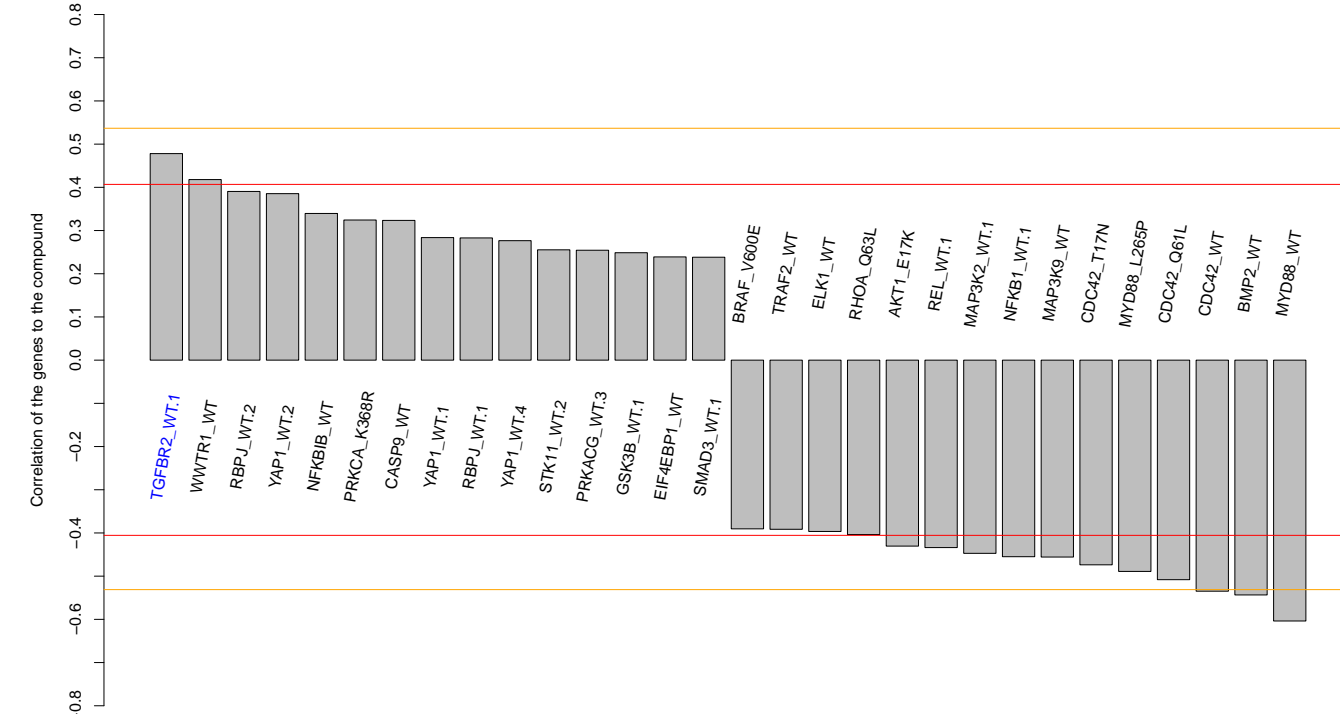
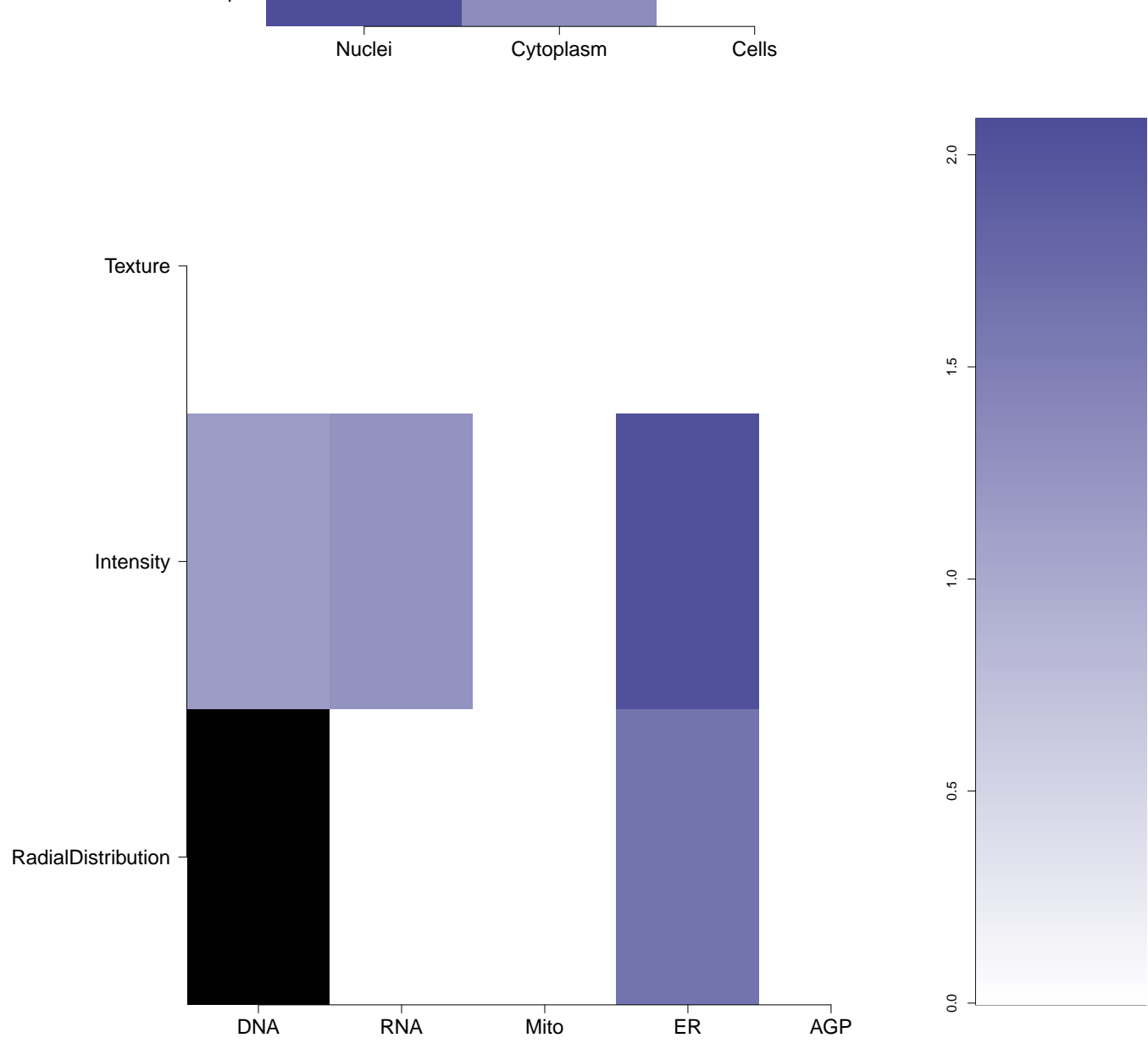

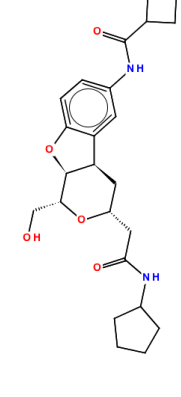
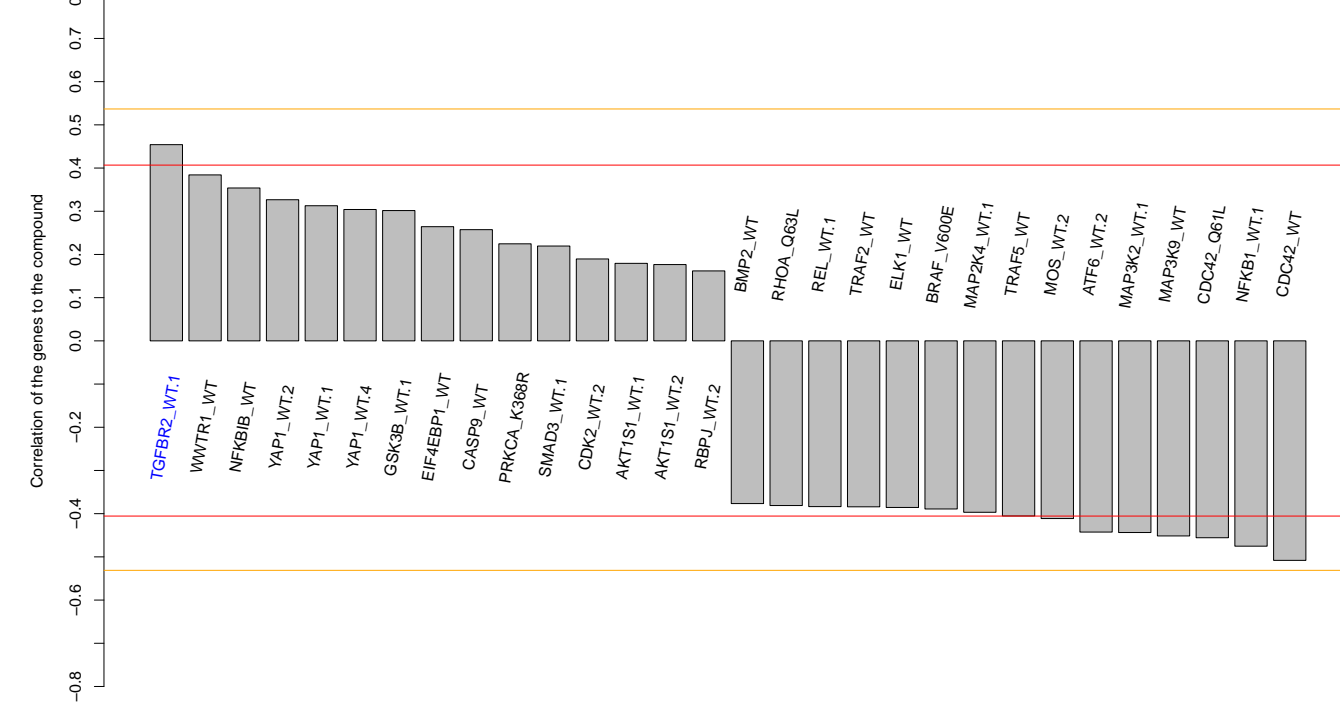
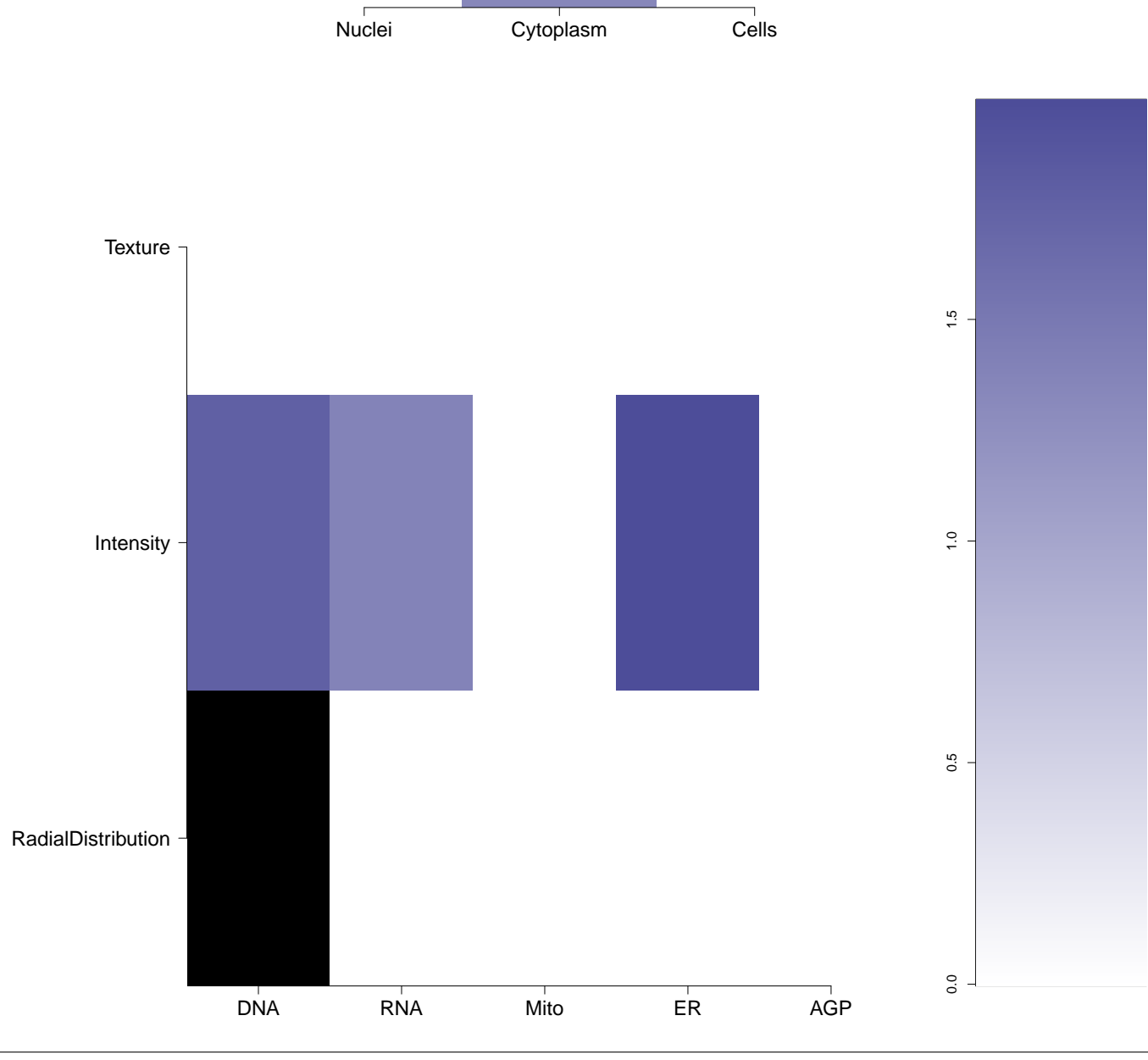
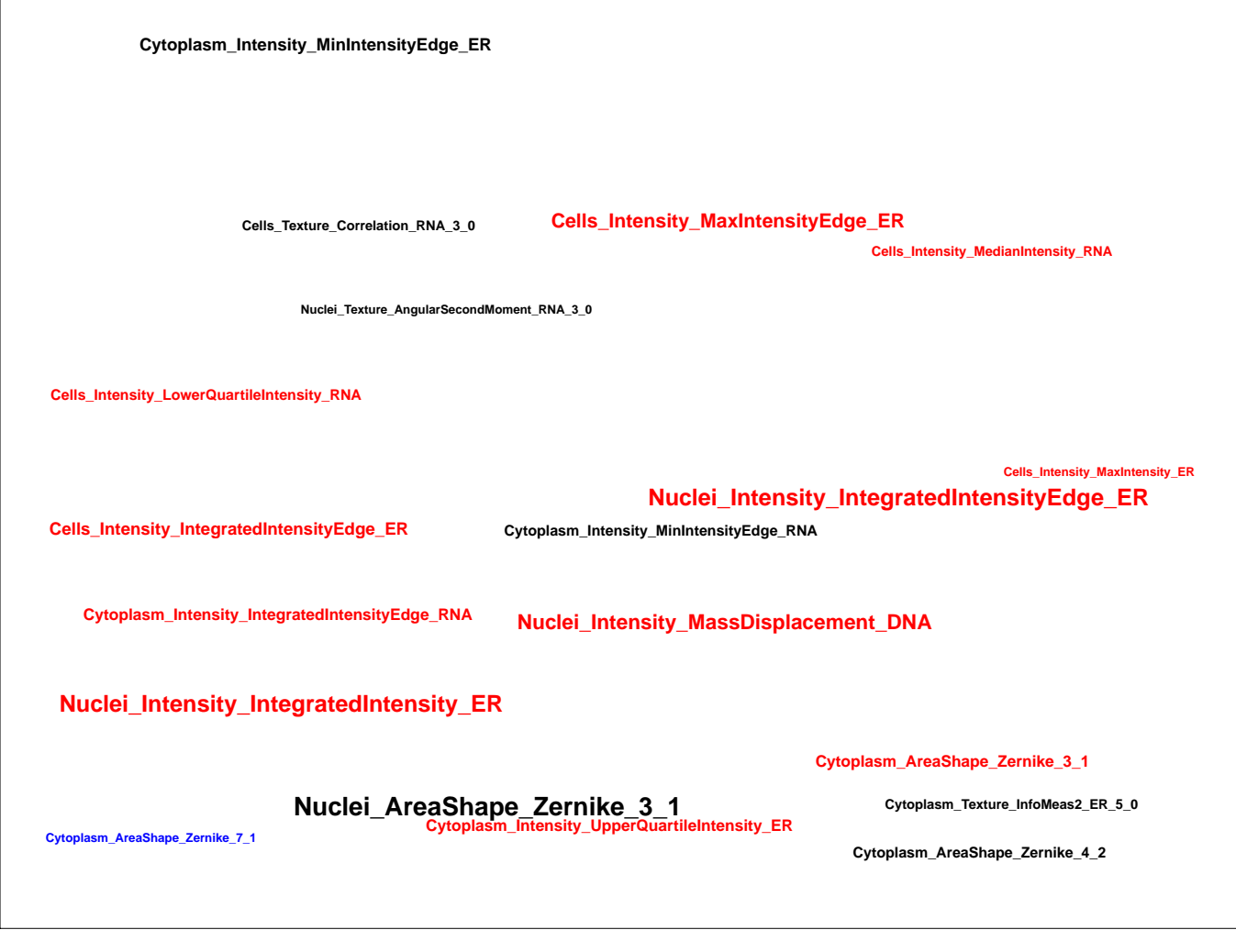
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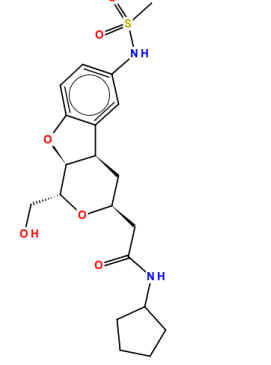
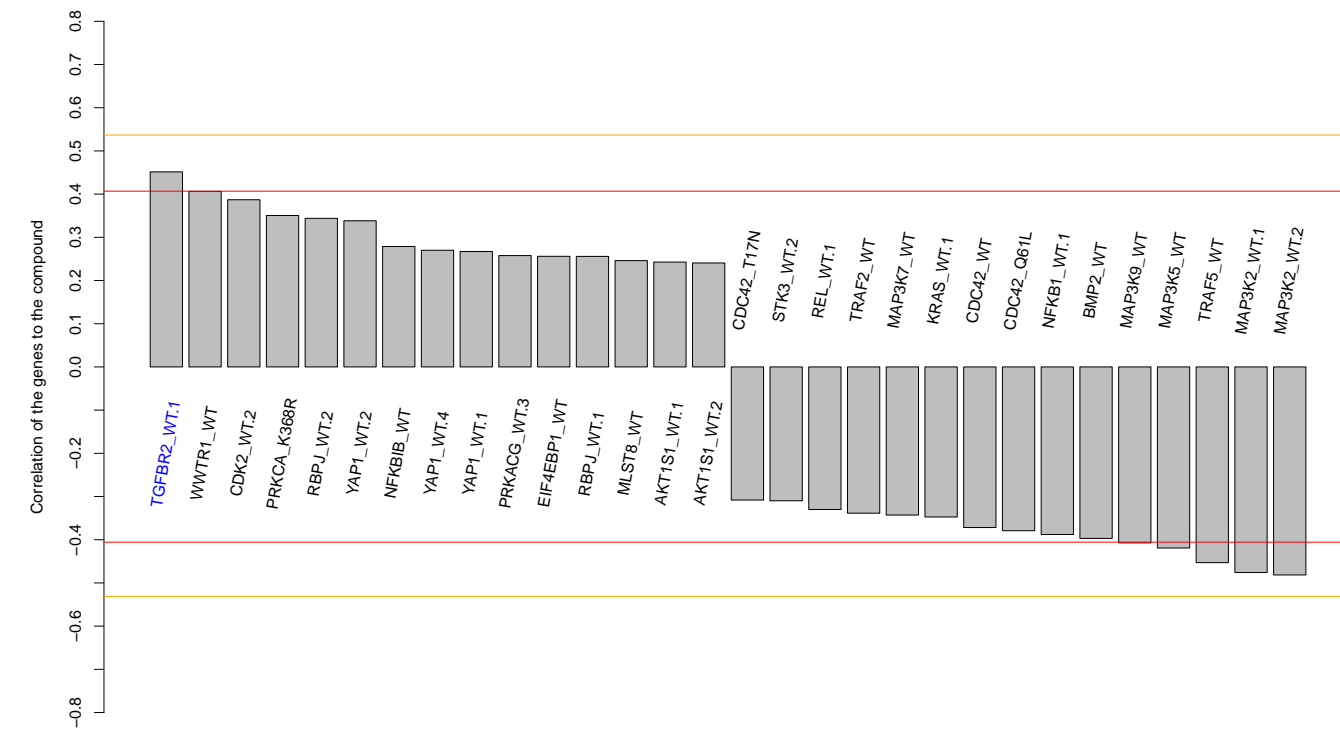
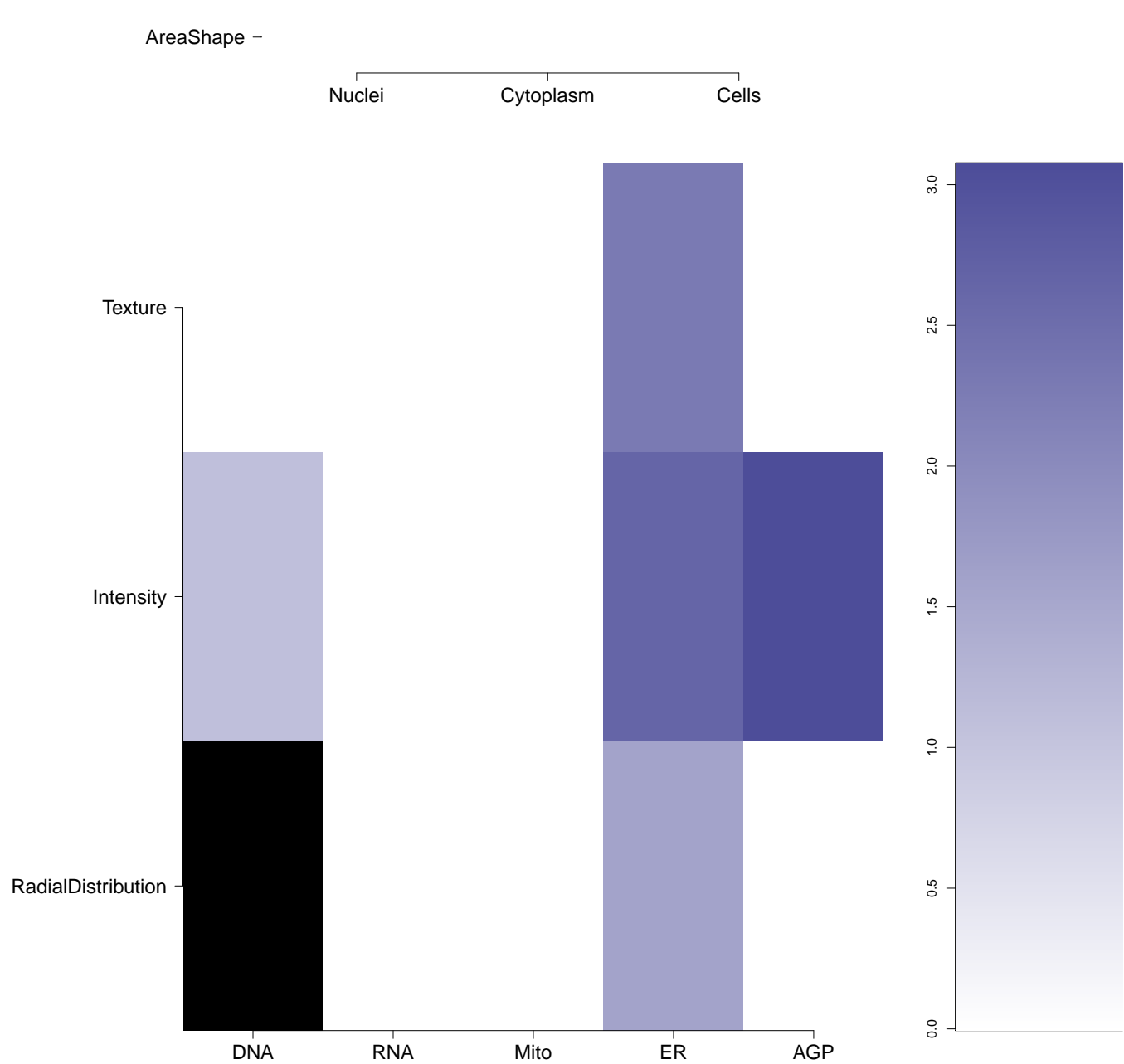
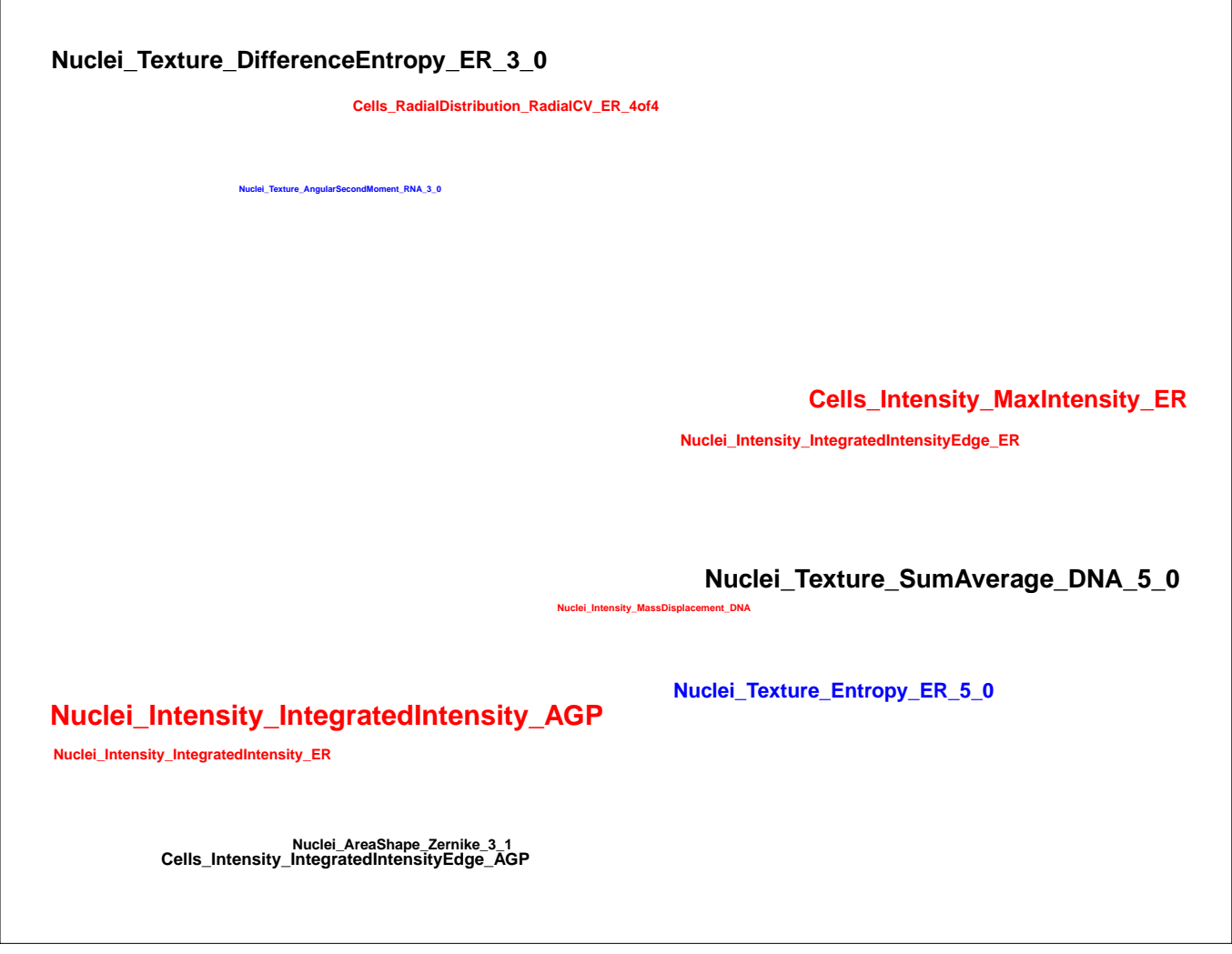
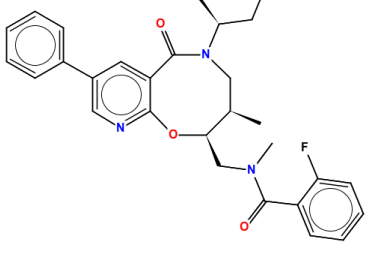
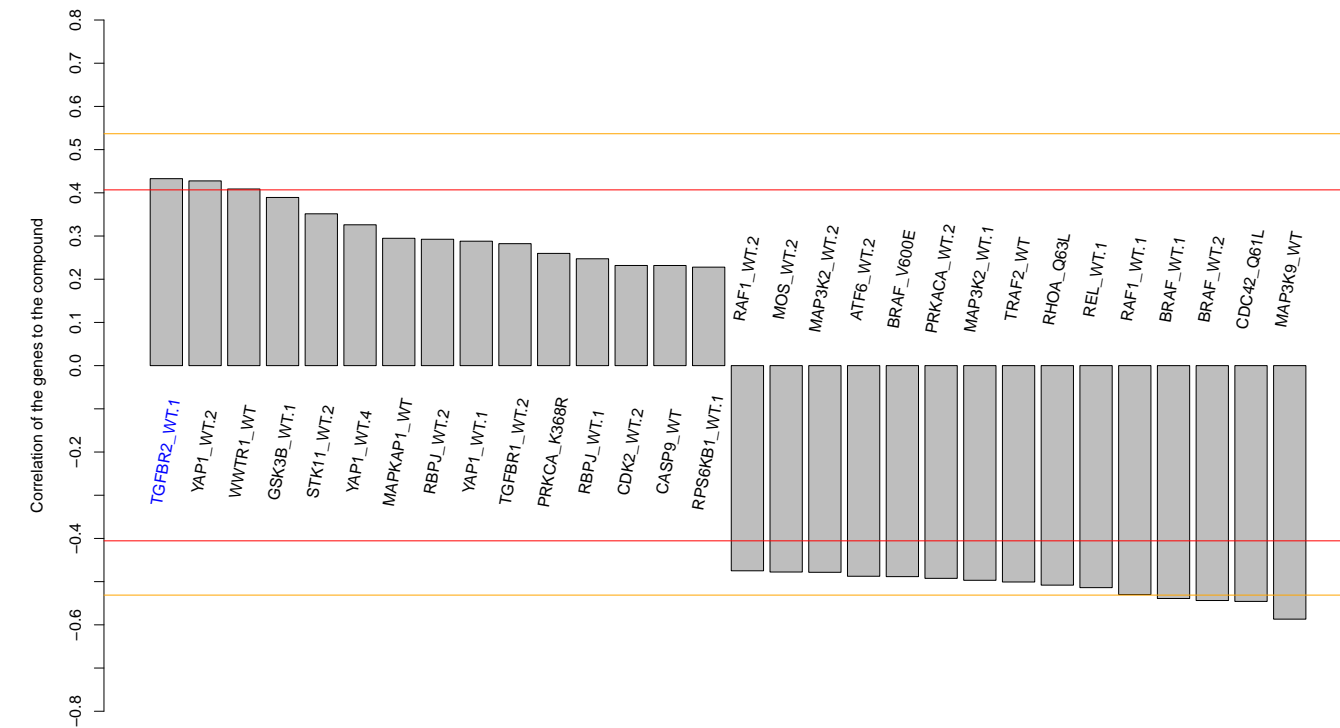
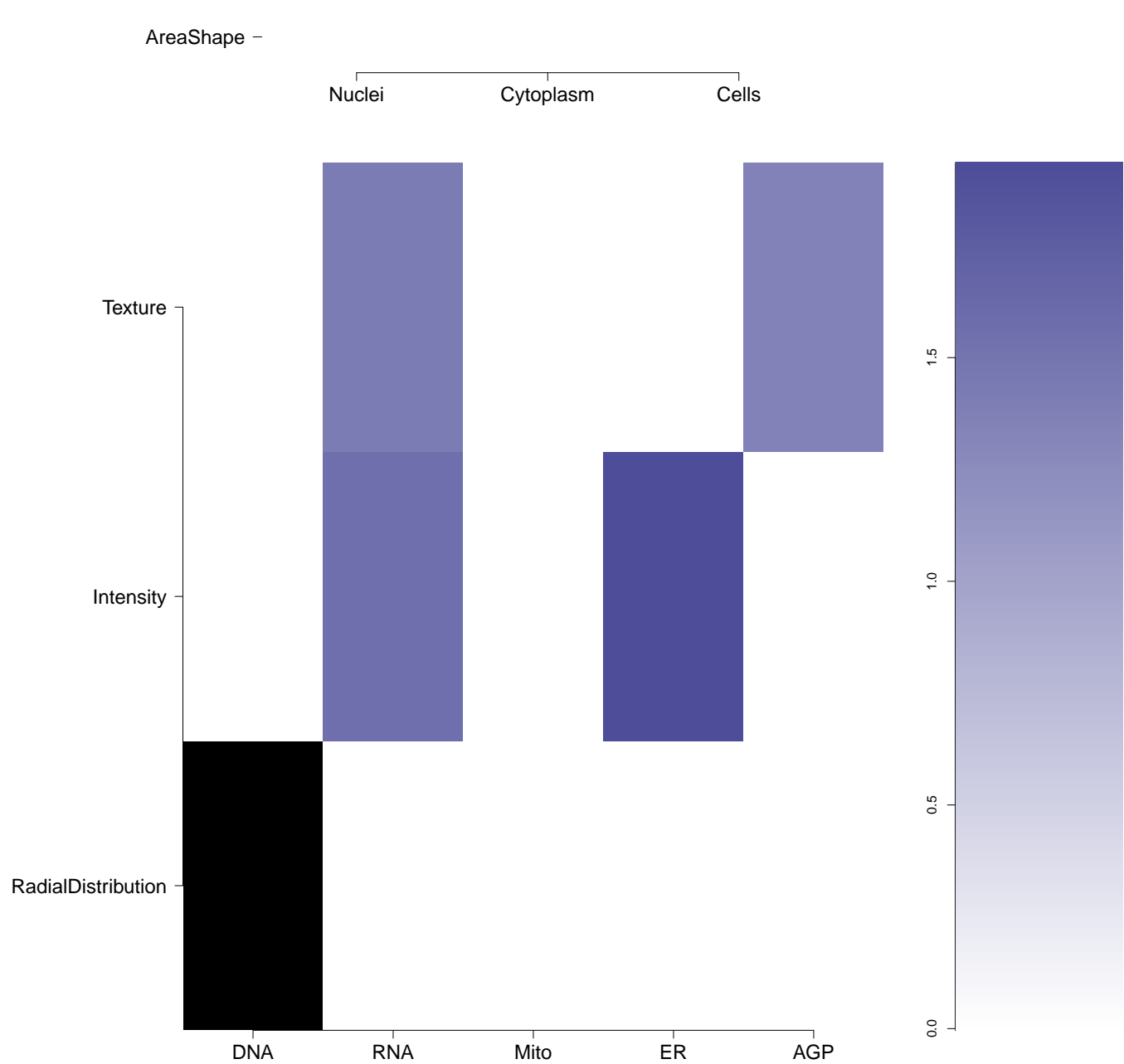

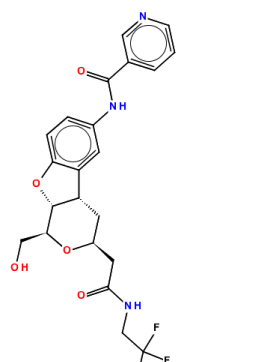
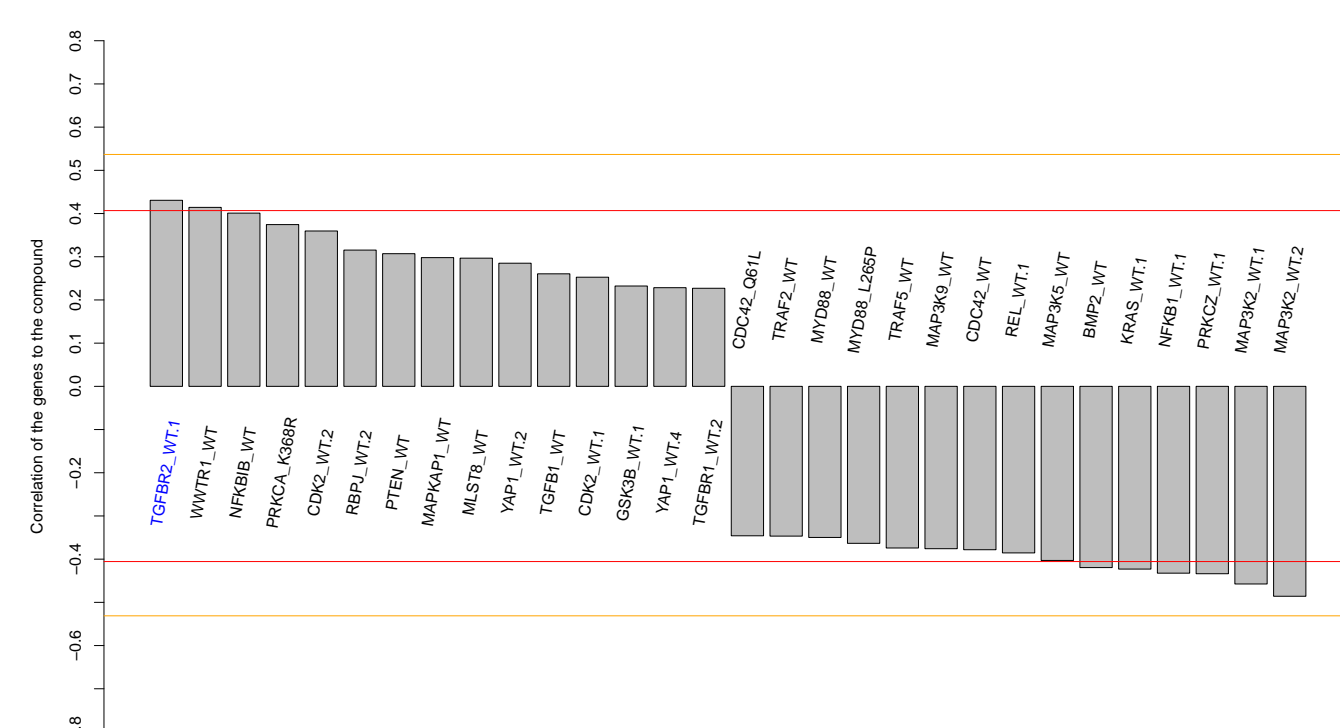
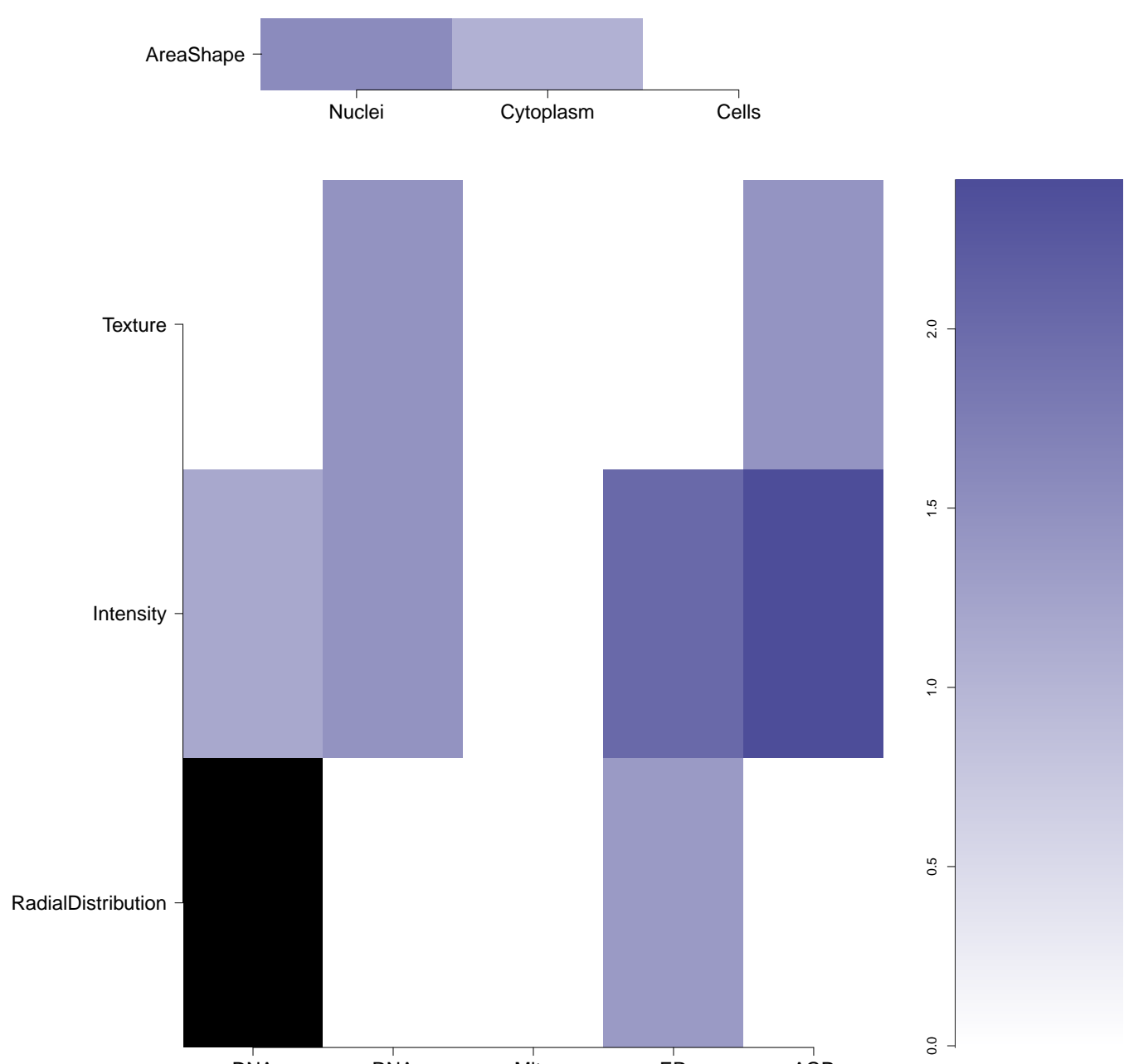
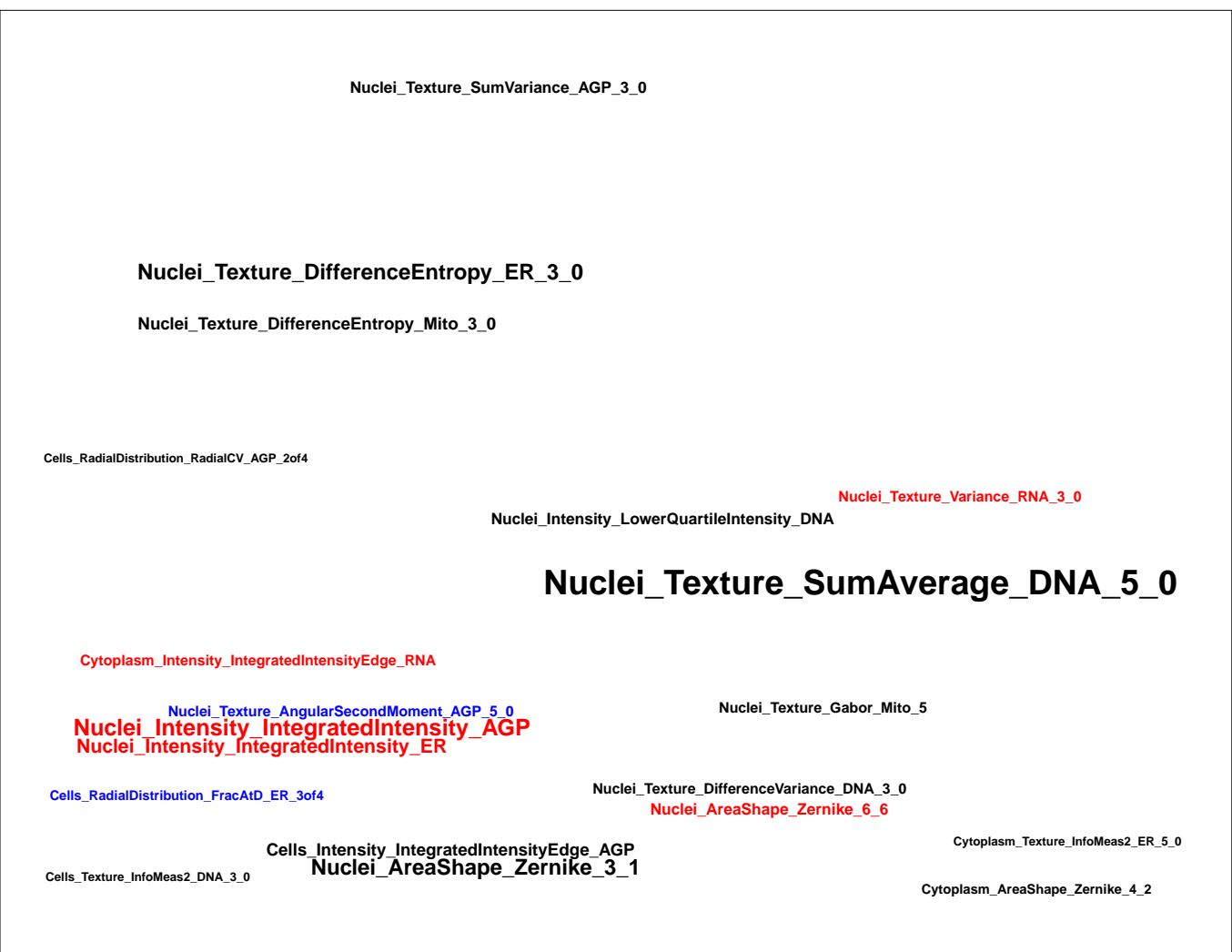
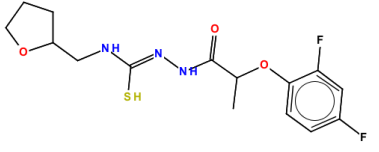
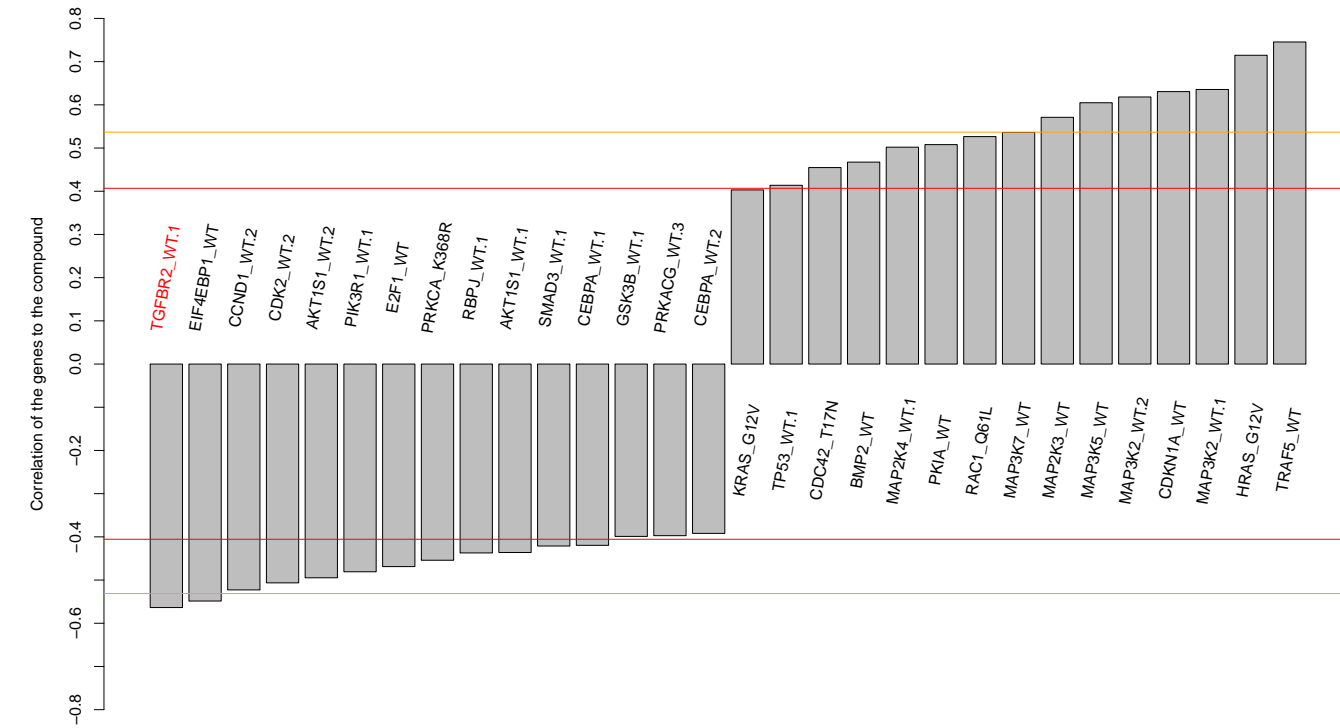
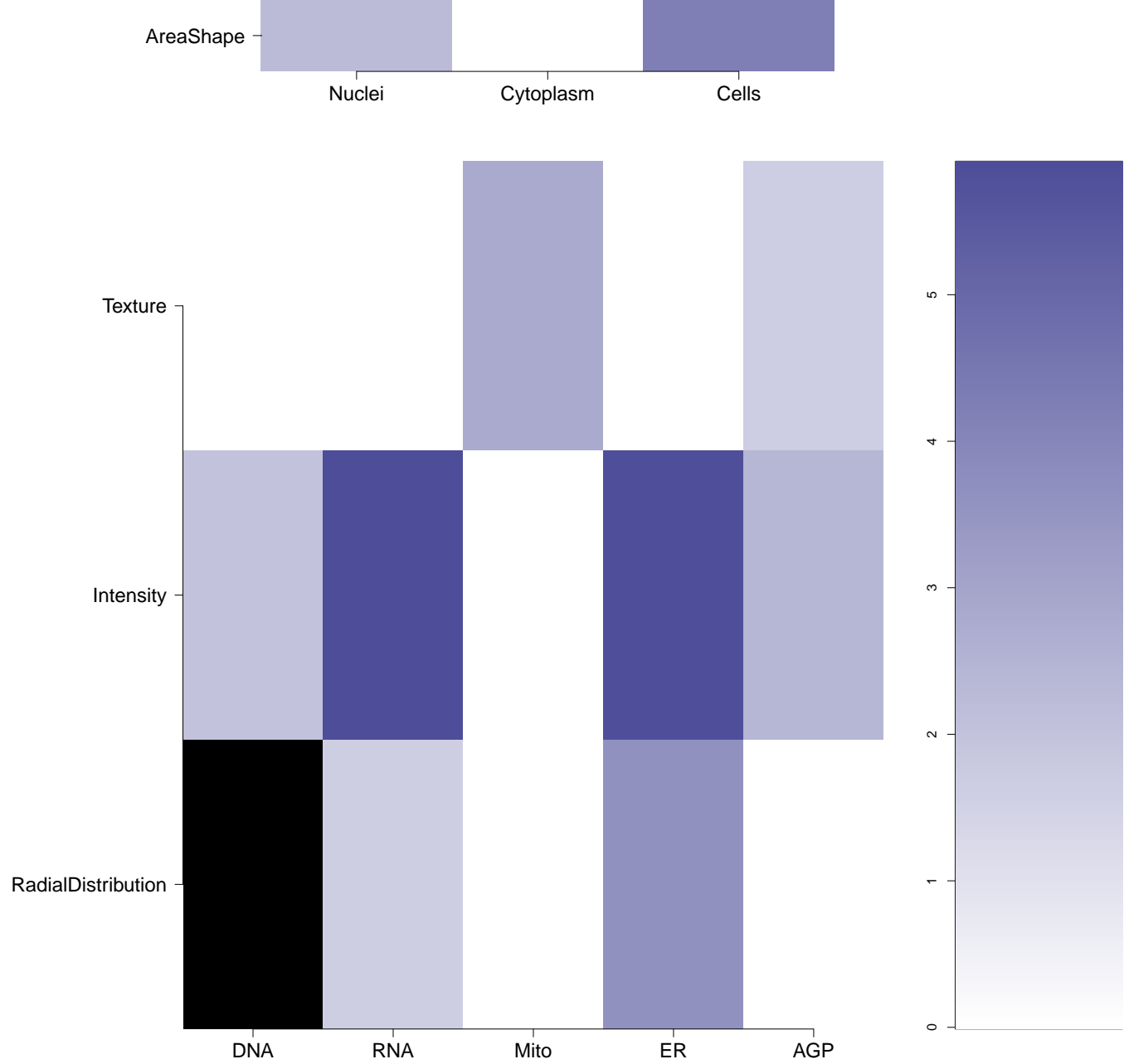
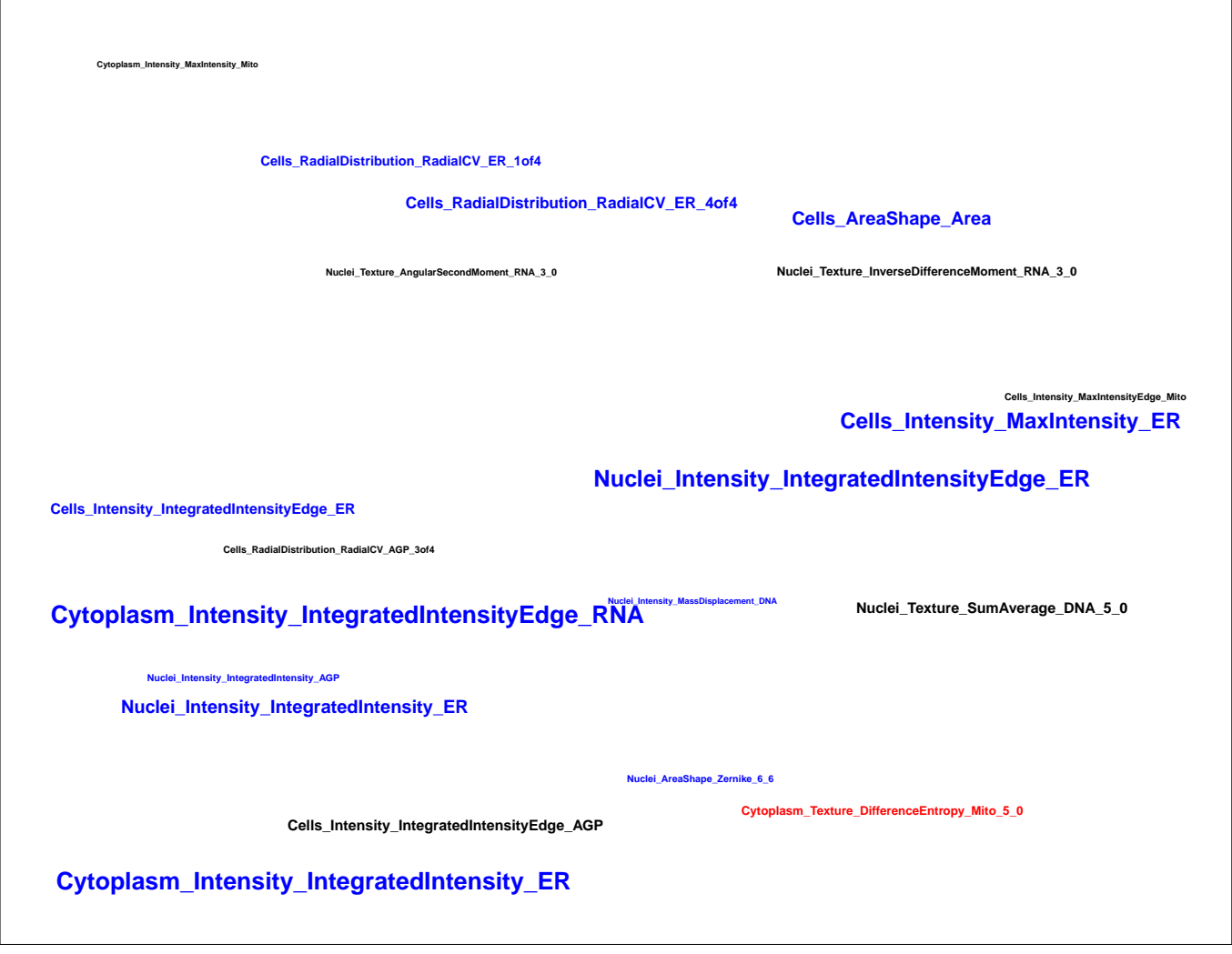
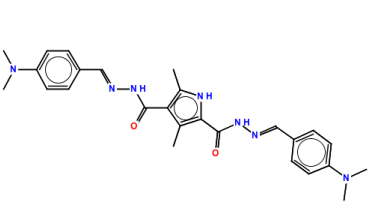
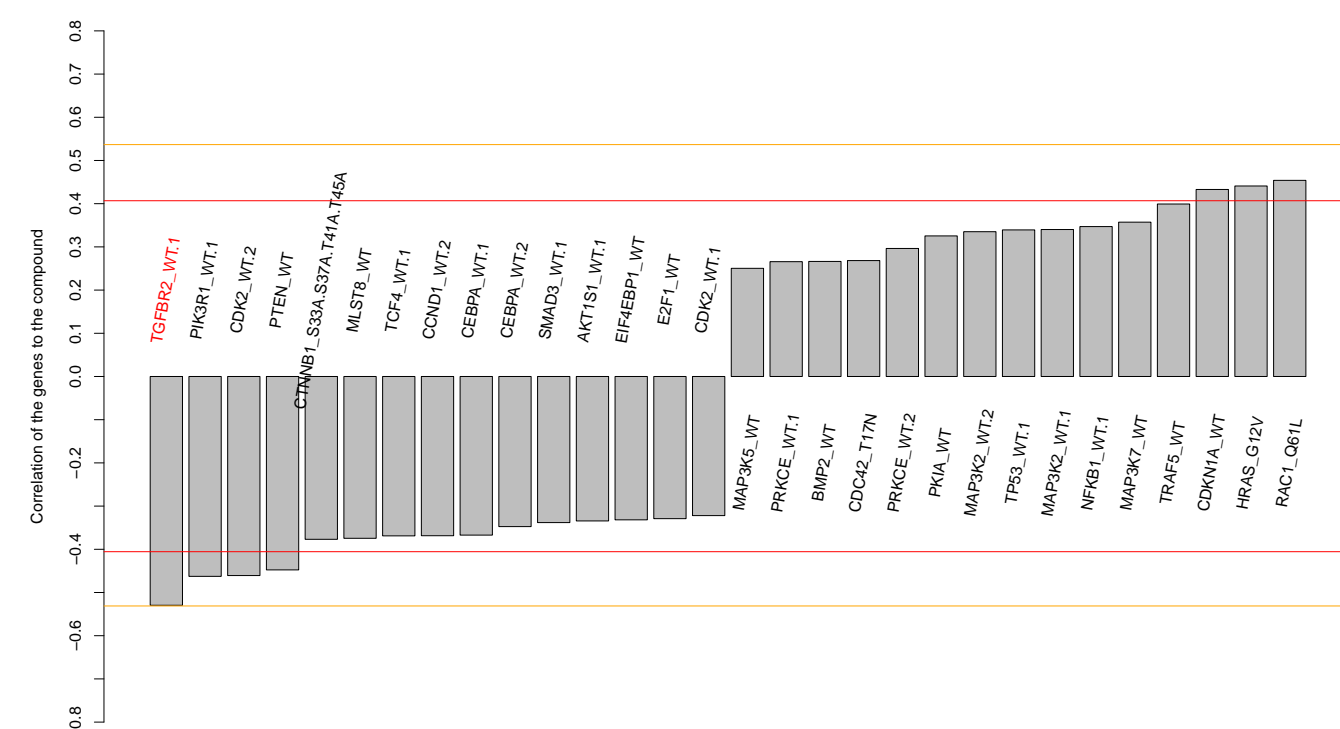
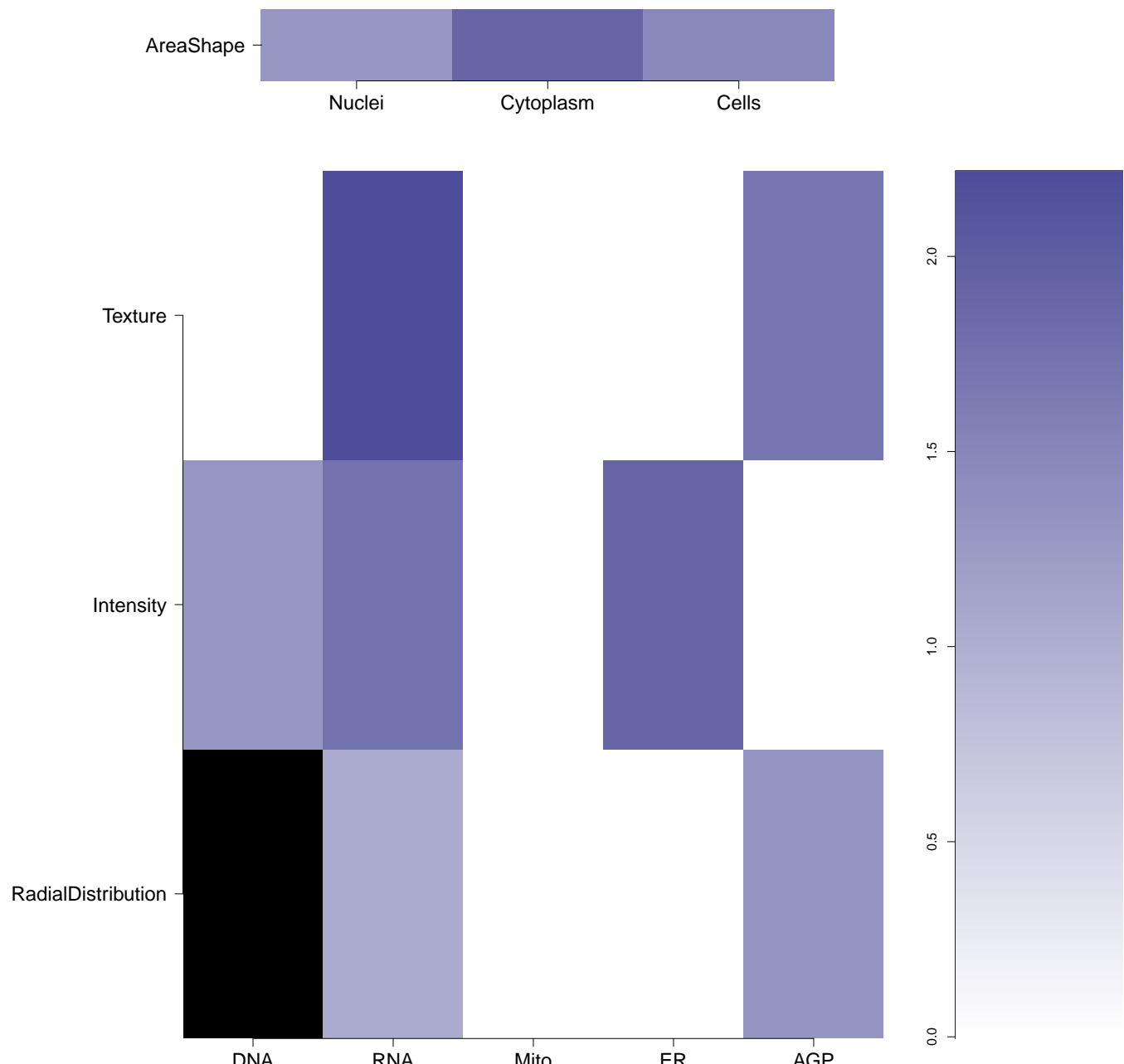

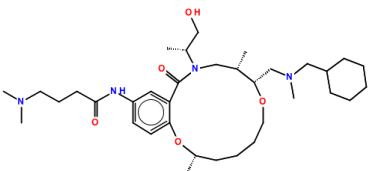
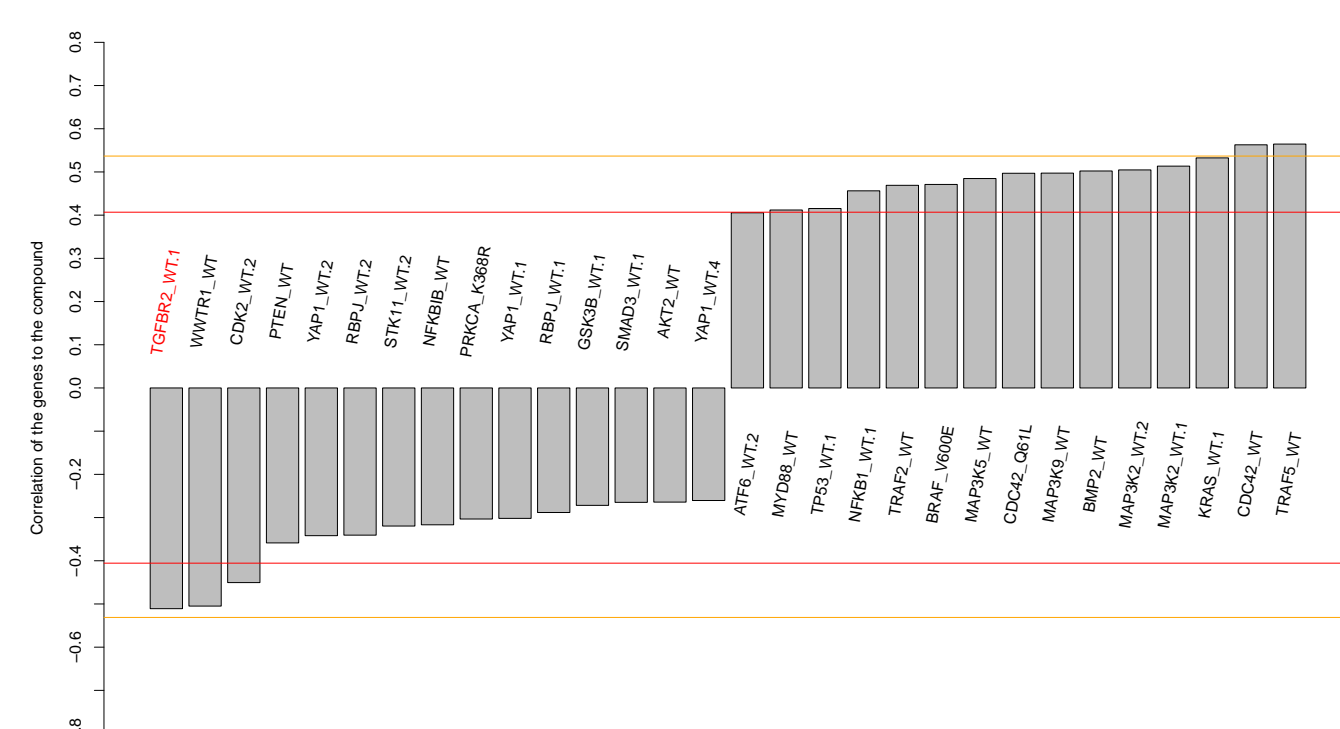
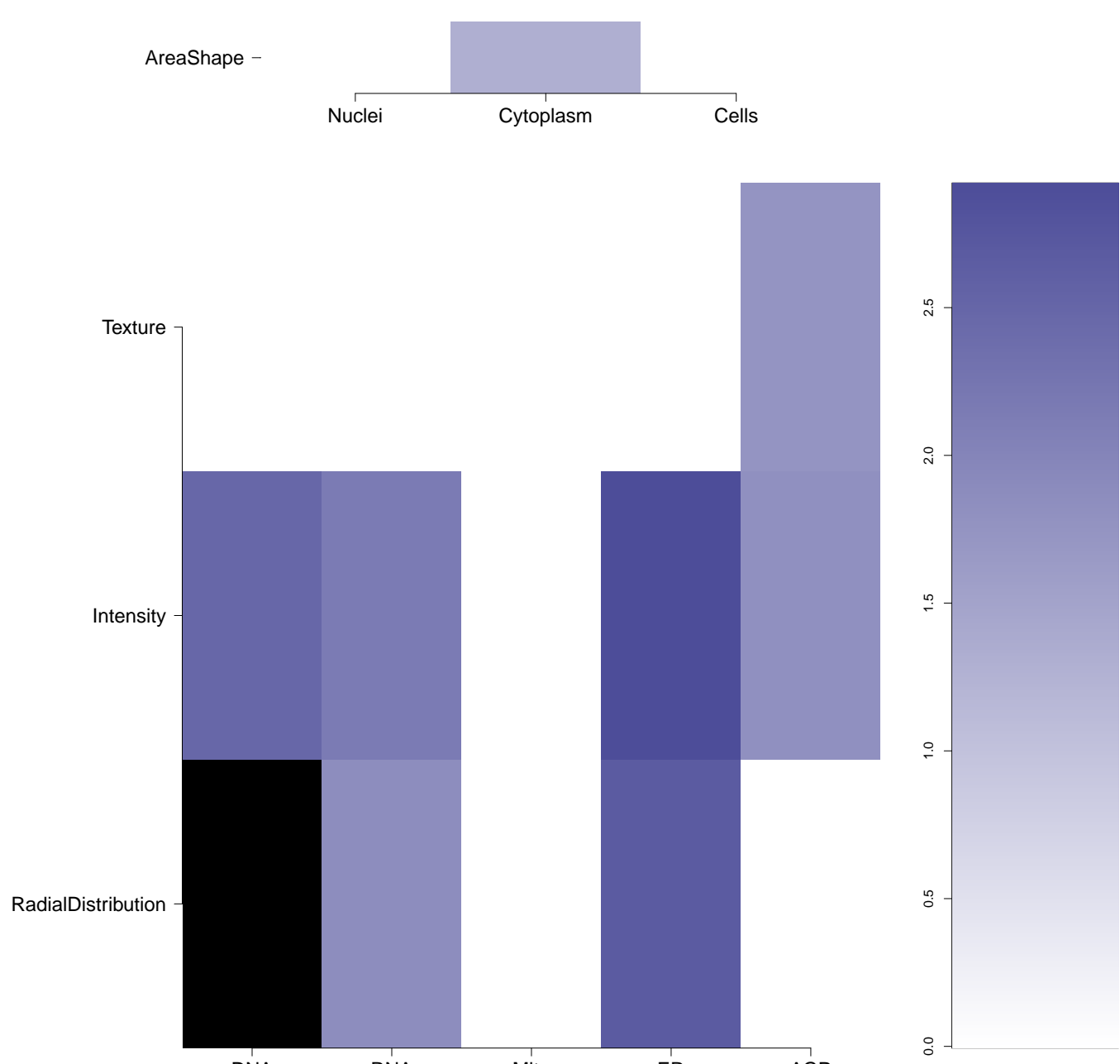
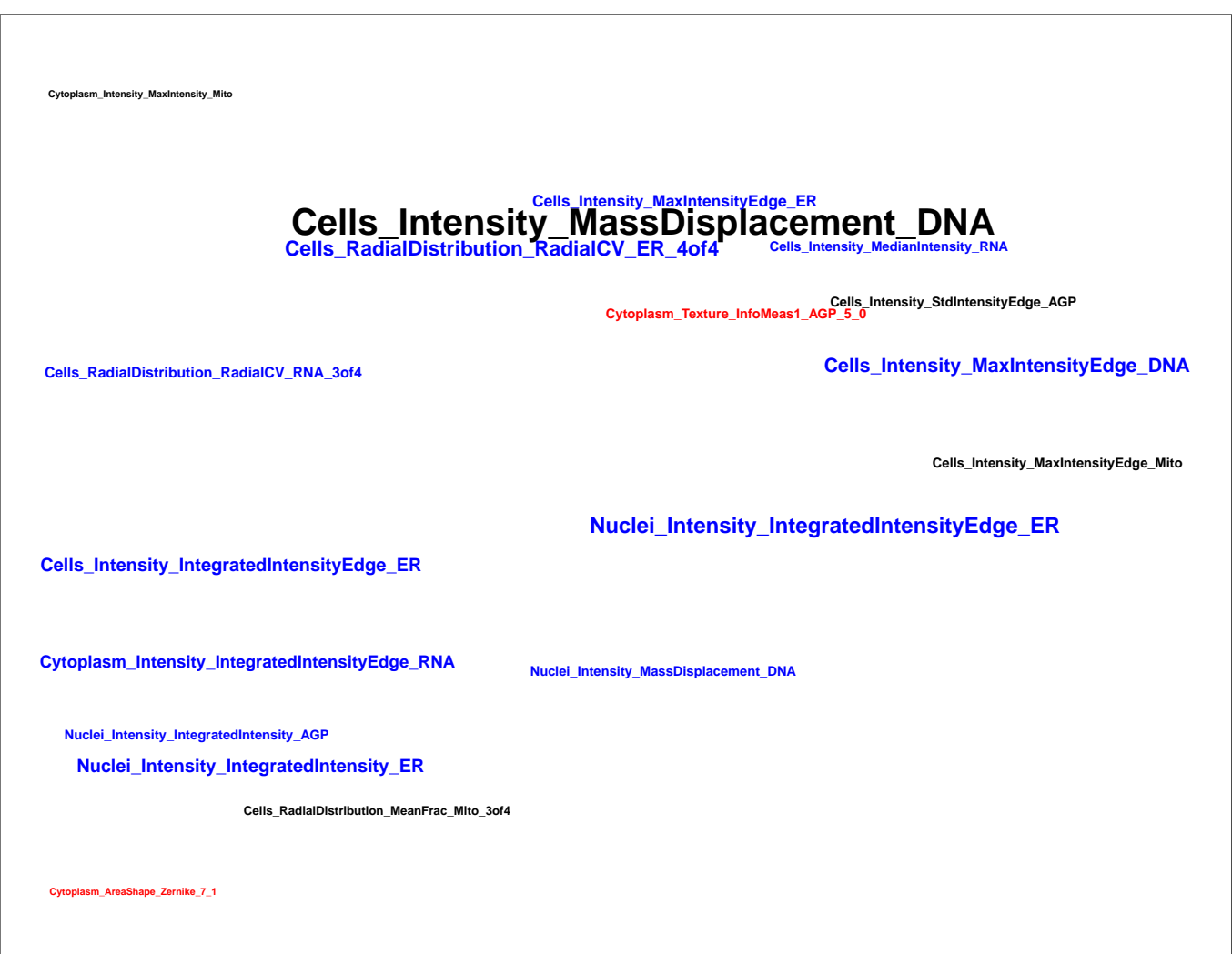


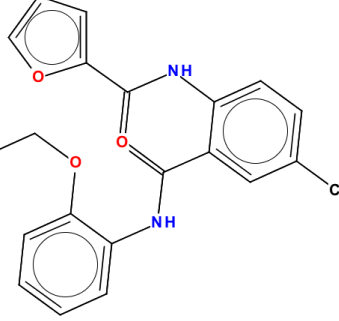
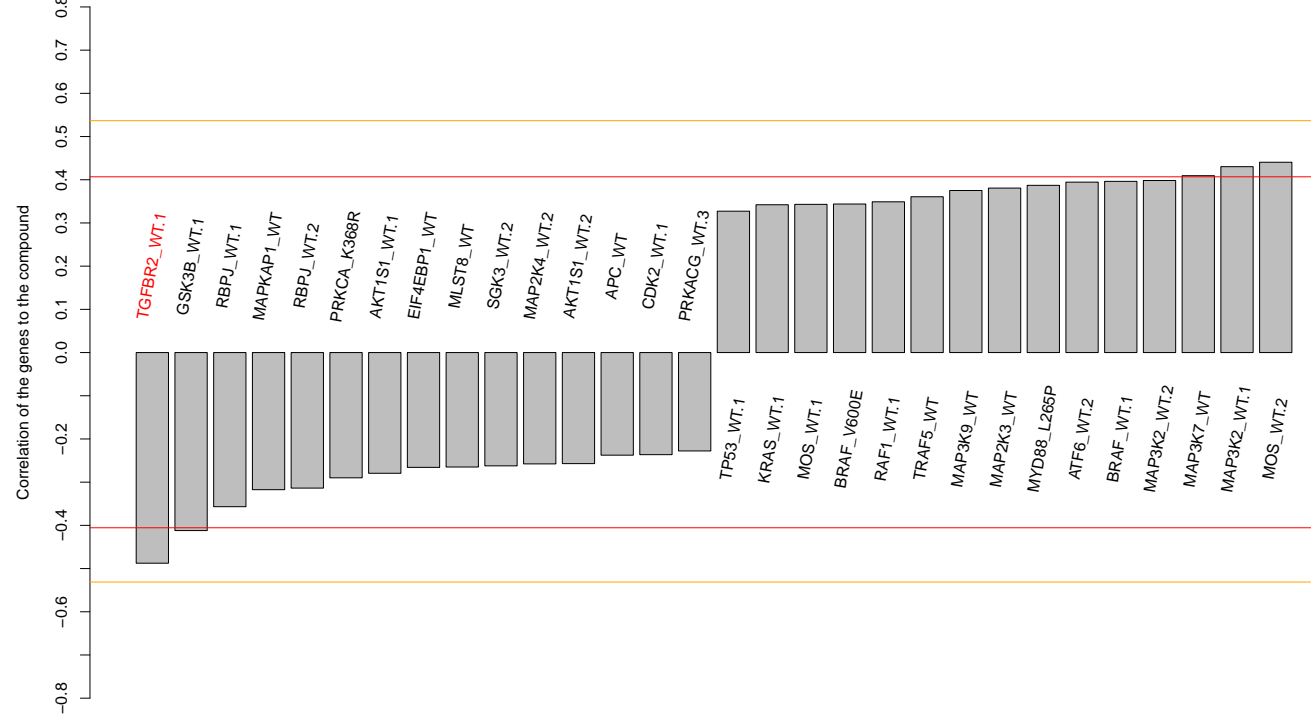
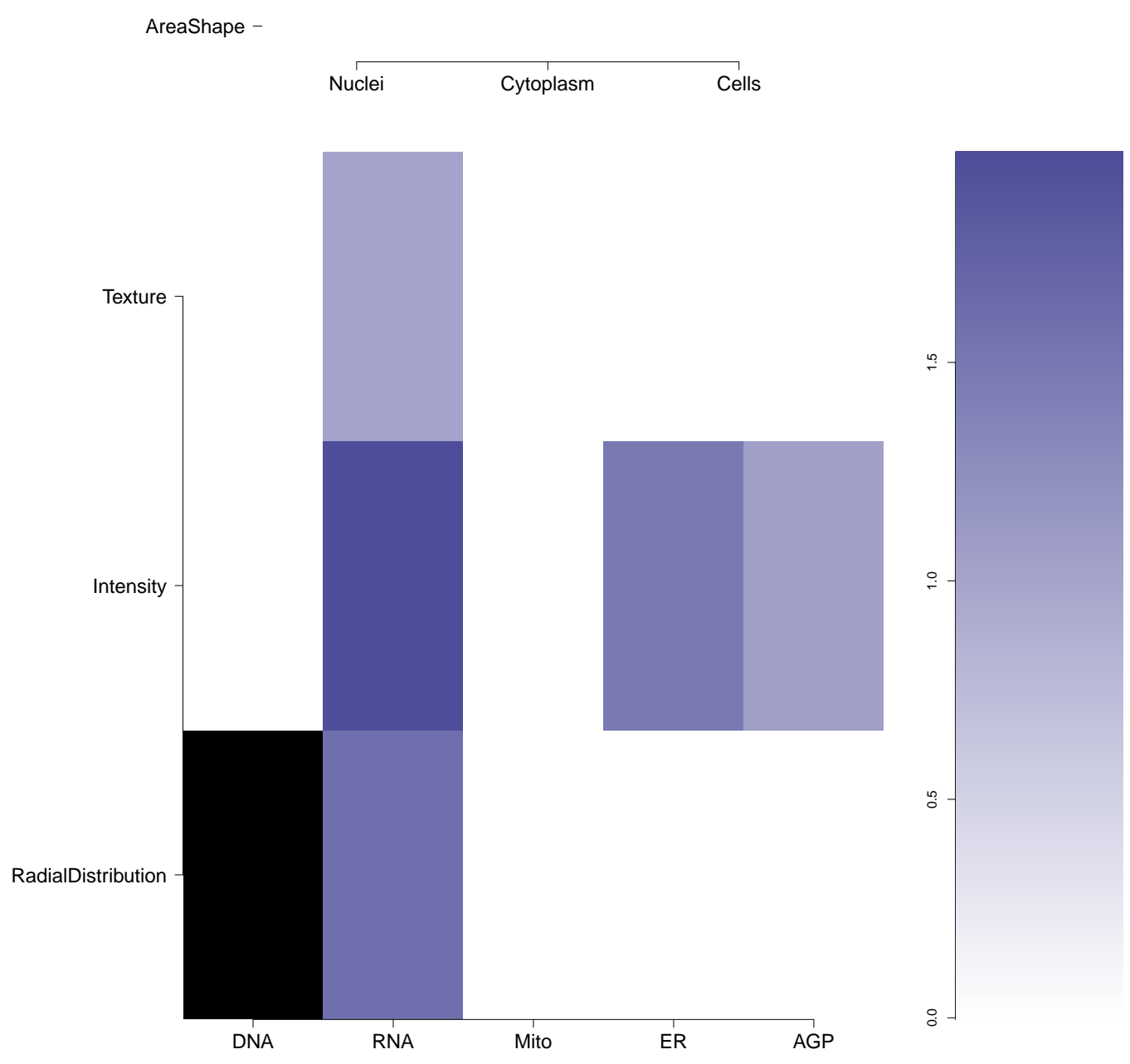
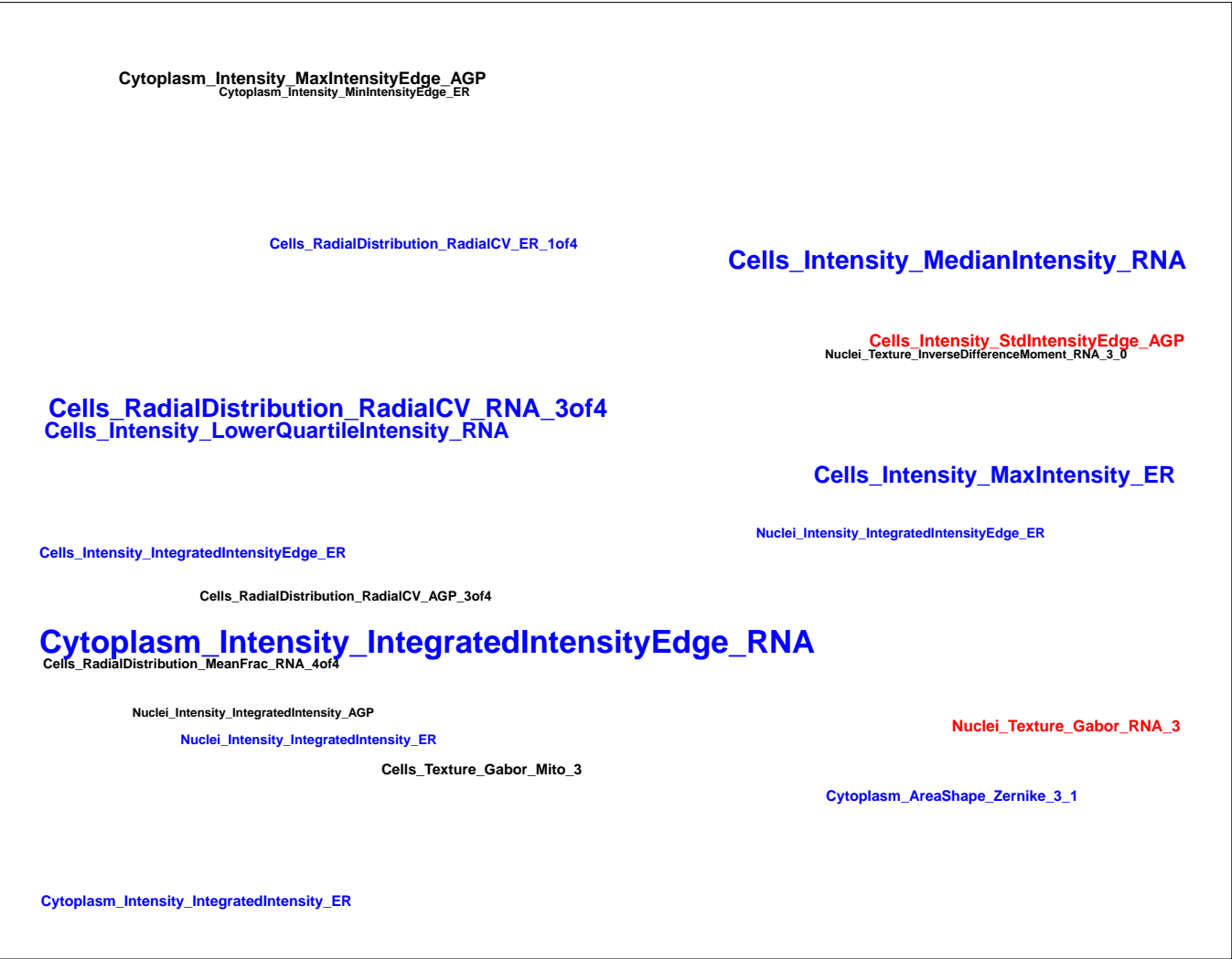
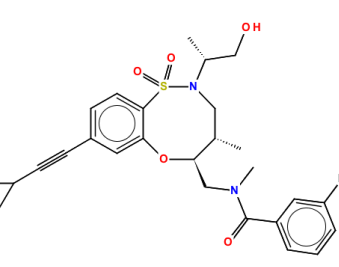
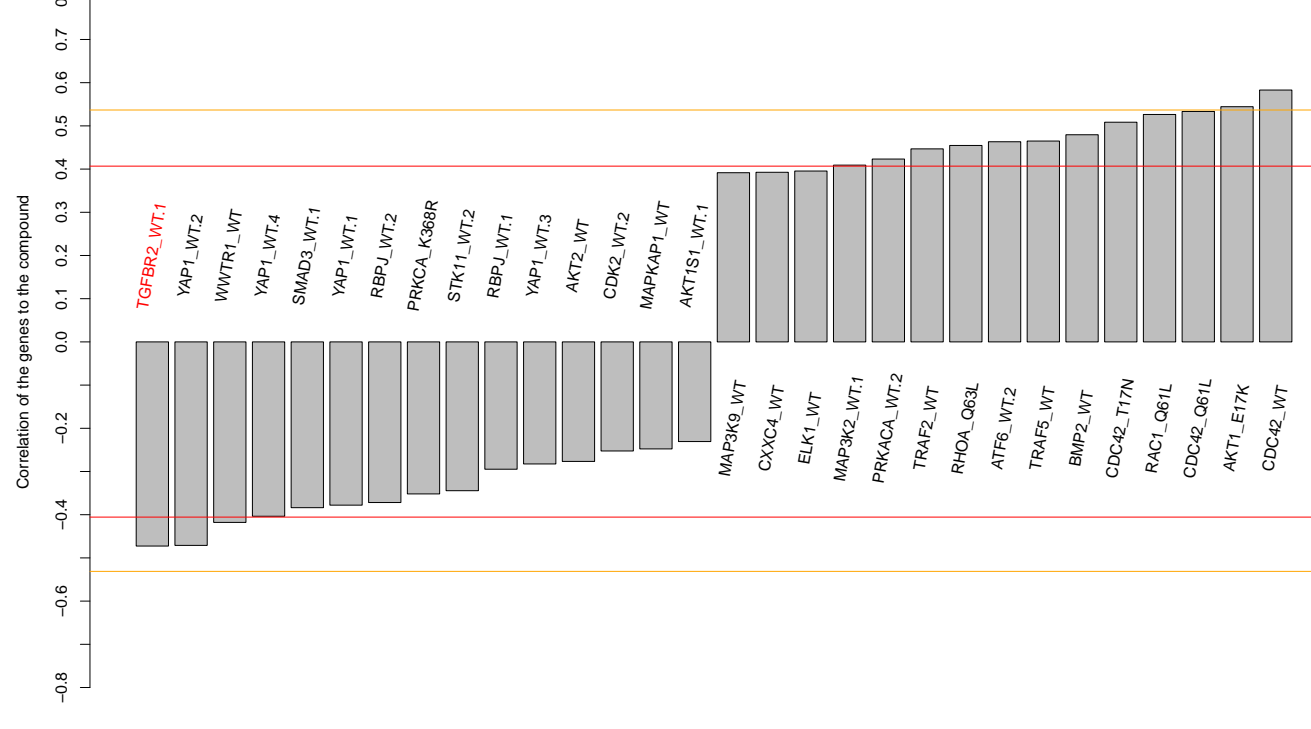
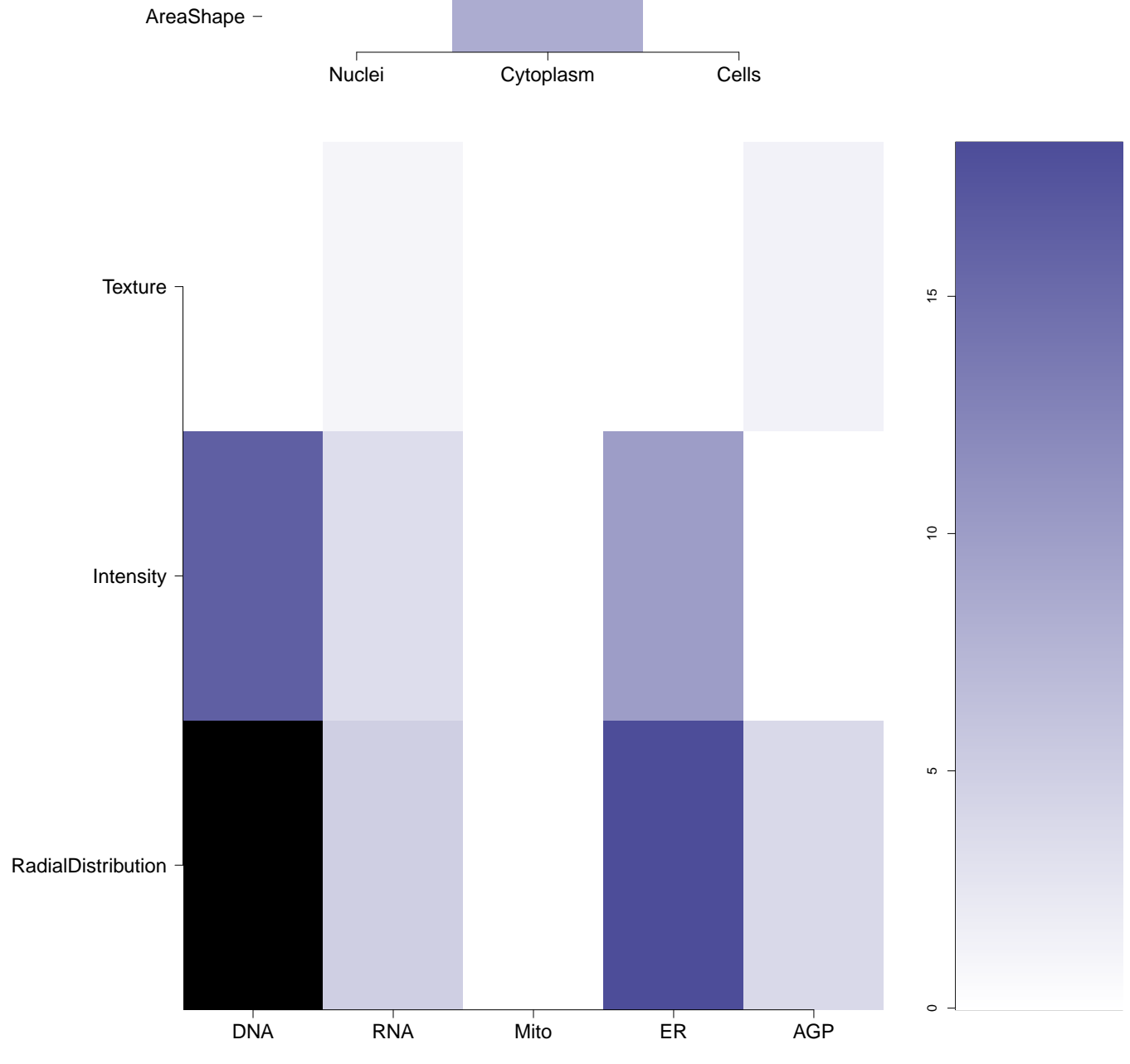
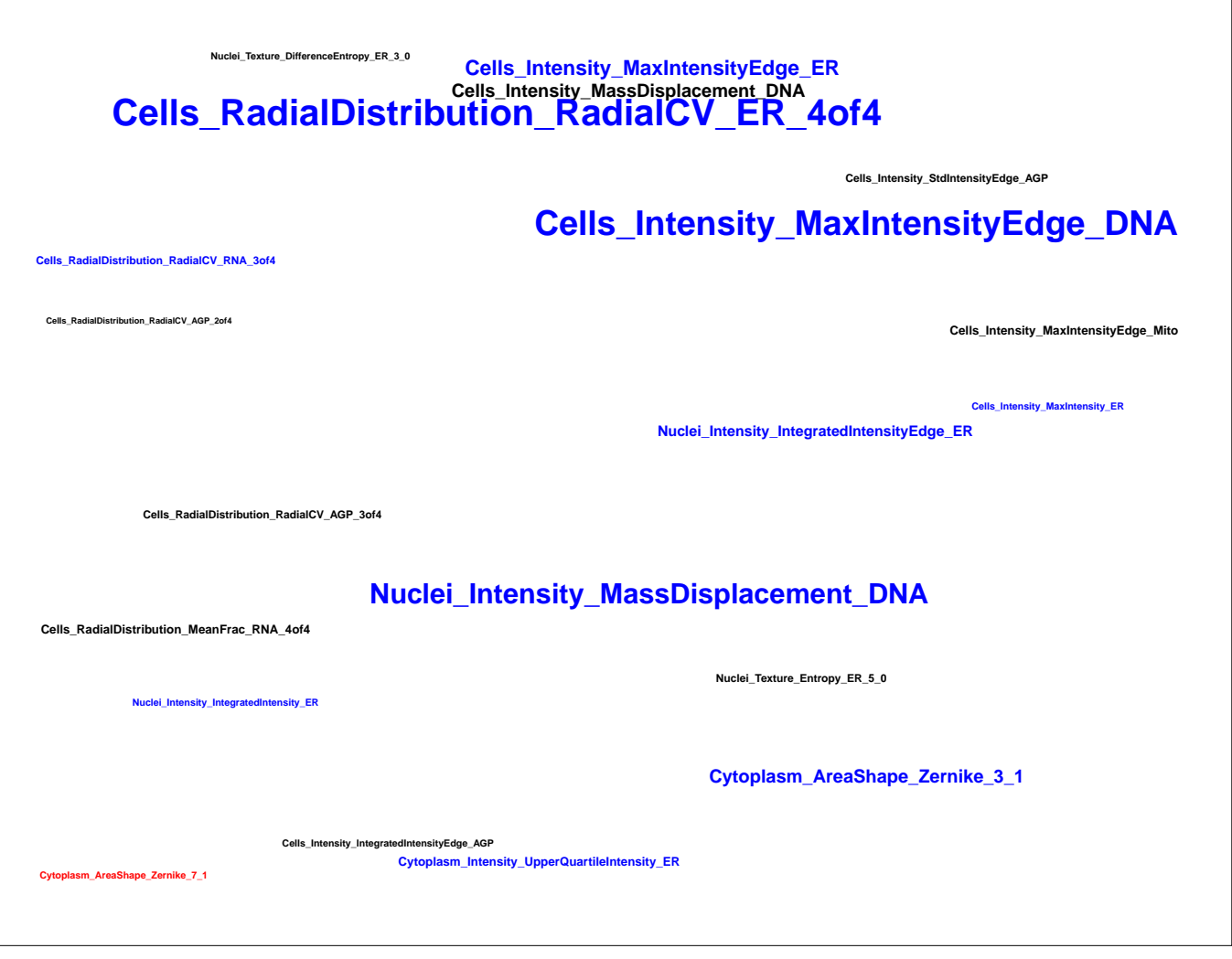
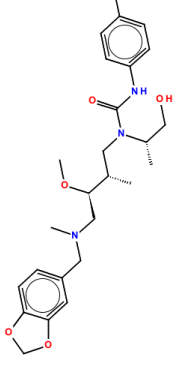
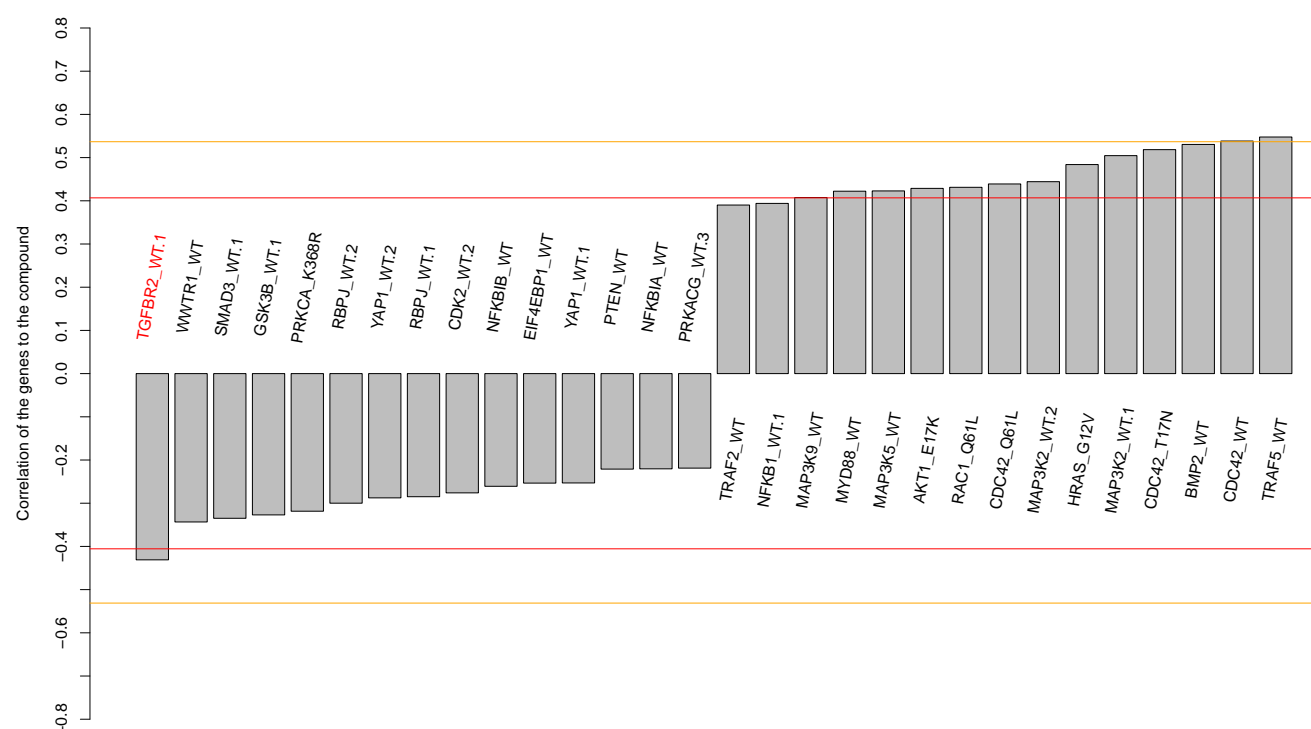
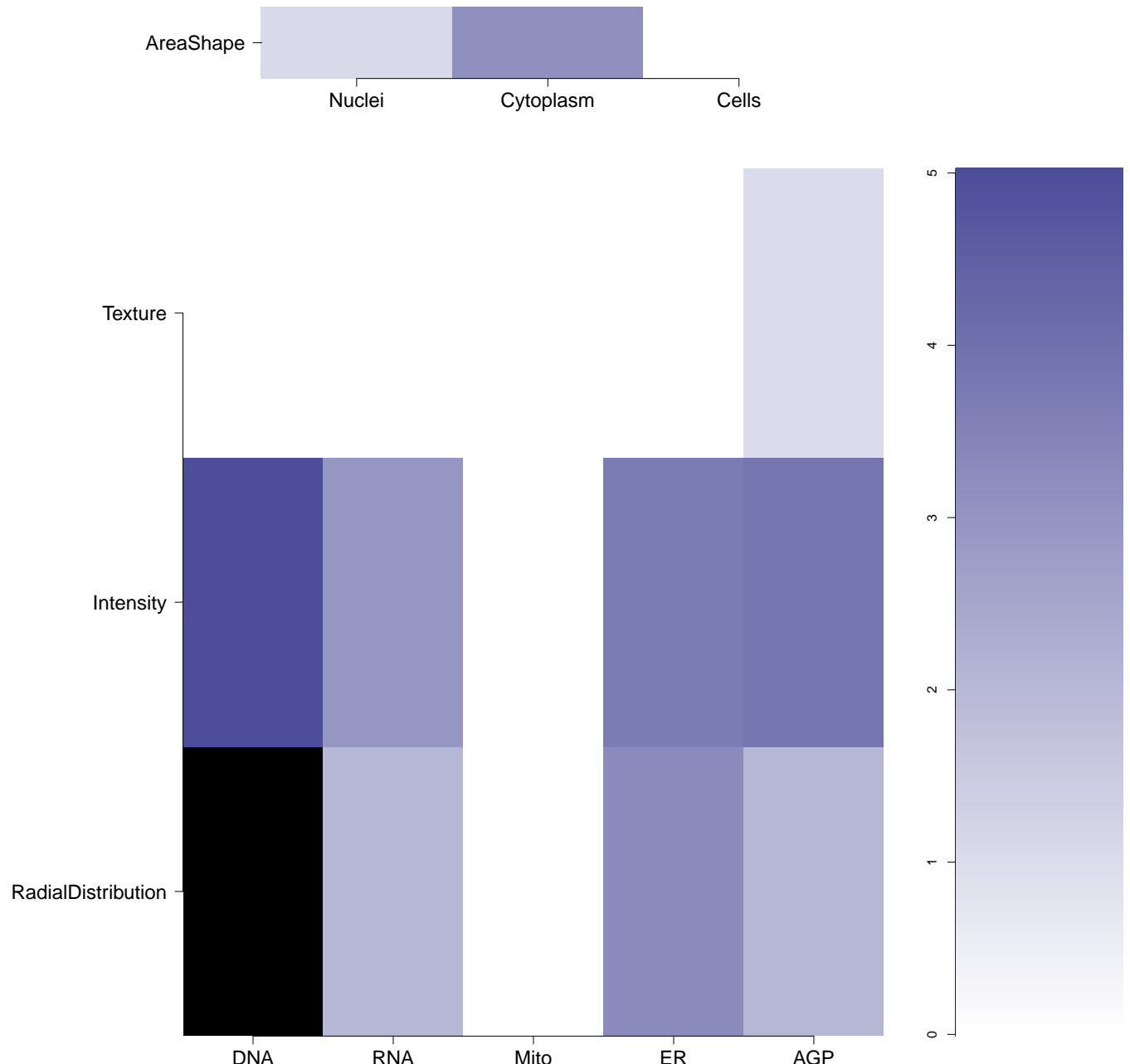

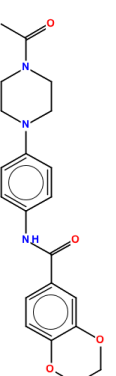
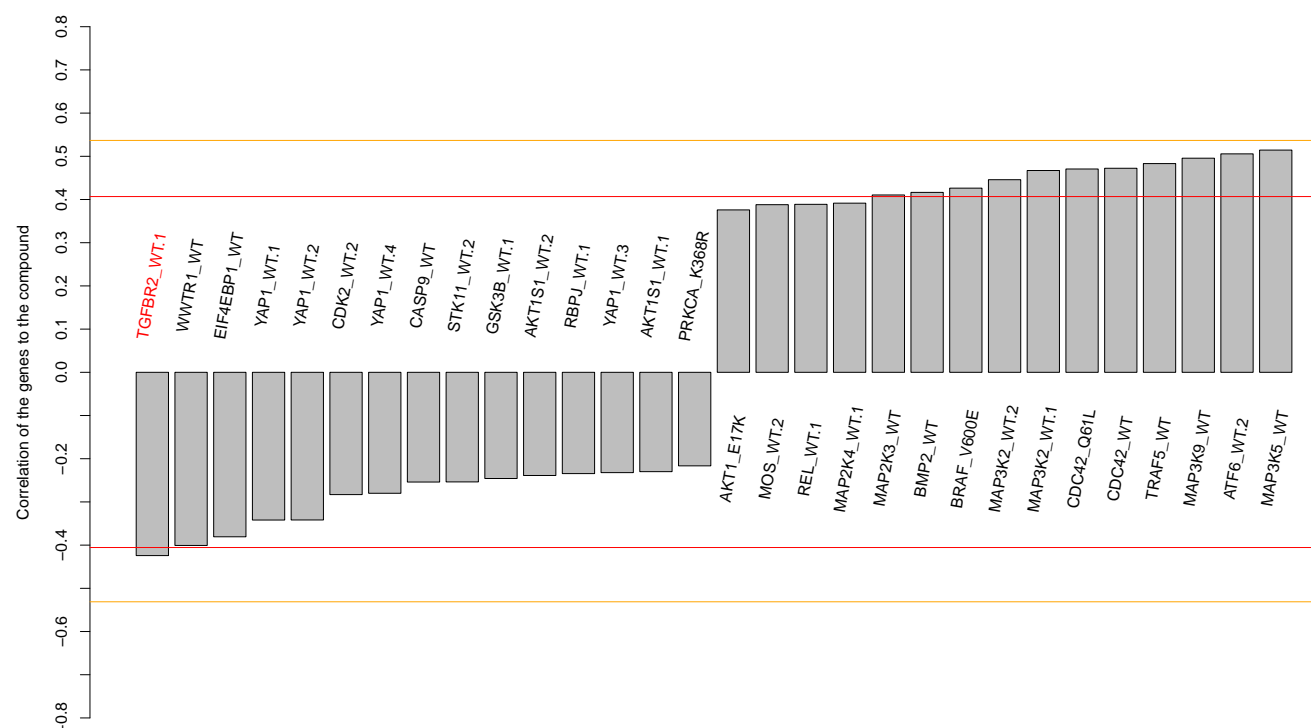
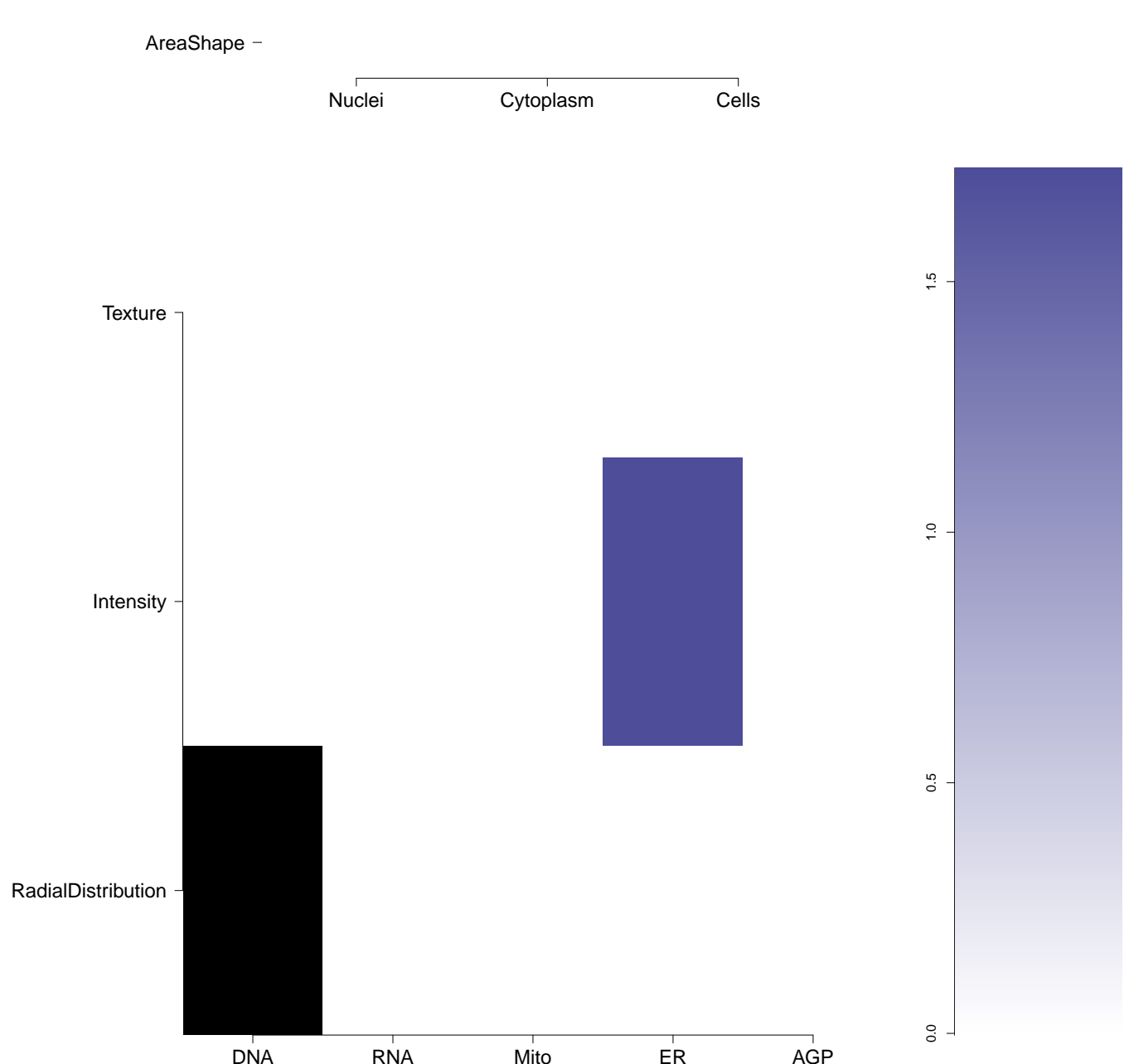
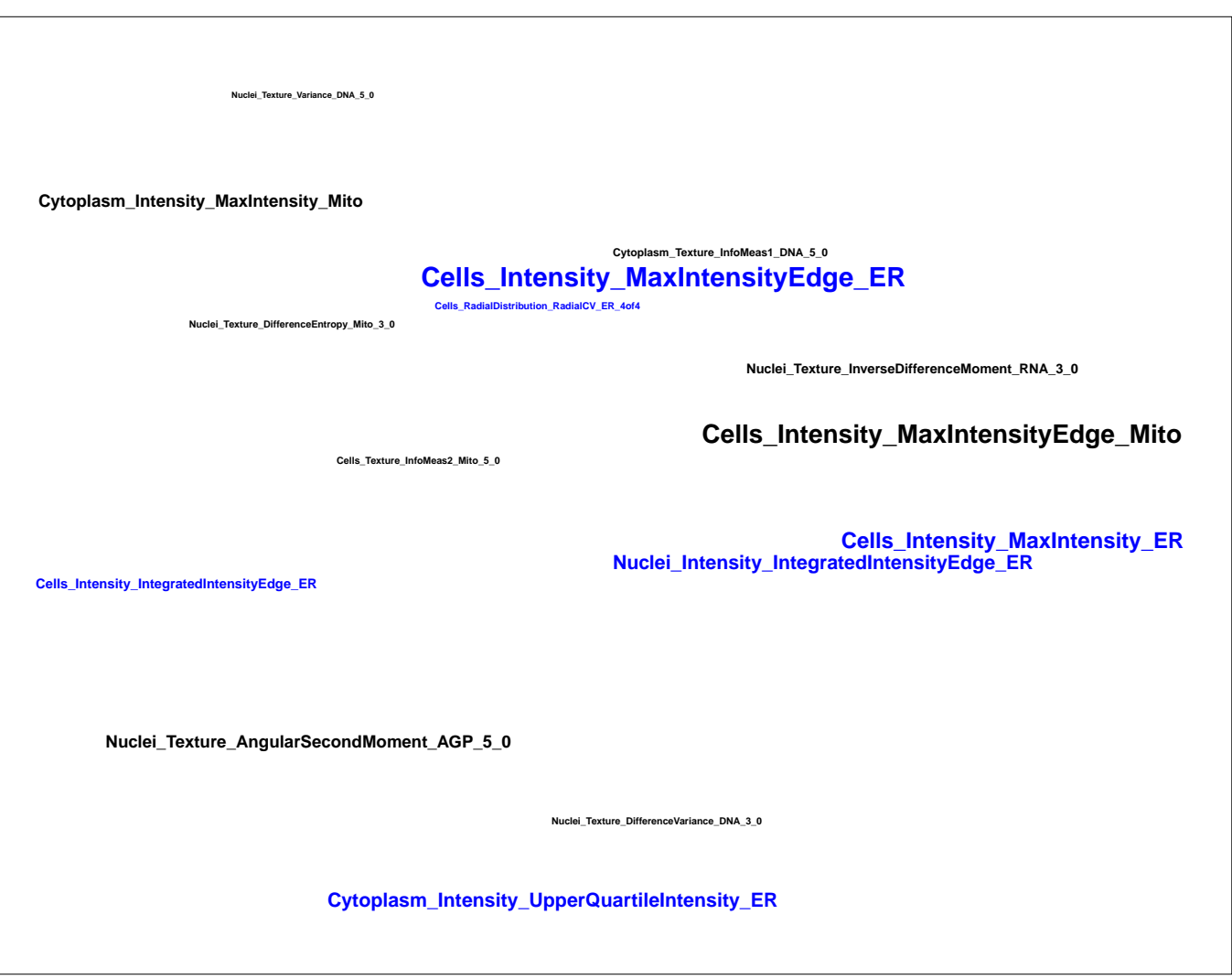
ER



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-K76218980-001-11-3 nikkomycin z AC1NUQ0P MLS000028371 HMS2233C10 SMR000058642 PubChem CID : 5458181		NA (in 1 replicates)	0.56	NA				Total number of assays tested in: 698. Active in the following assays: <ul style="list-style-type: none"> qHTS Assay for Inhibitors of Bacillus subtilis Sfp phosphopantetheinyl transferase (PPTase) (AID 1490) Fluorescence Cell-Based Secondary Assay to Identify Inhibitors of Resistant C. albicans Growth in the Presence of Fluconazole (AID 2423) Fluorescence Cell-Based Retest of C. albicans Growth in the Presence of Fluconazole (AID 2467) qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332) qHTS of TDP-43 Inhibitors (AID 652104)
BRD-K15827540-001-05-0 T5250099 AC1M2QX1 MLS001010624 HMS1774C11 HMS2718E22 ZINC12531006 SMR000352827 PubChem CID : 2123280		NA (in 1 replicates)	0.53	NA				Total number of assays tested in: 643. Active in the following assays: <ul style="list-style-type: none"> Primary cell-based high throughput screening assay to measure STAT3 inhibition (AID 862) Counter Screen for Luciferase-based Primary Inhibition Assays (AID 1006) qHTS Assay for Enhancers of SMN2 Splice Variant Expression (AID 1458) qHTS Assay for Inhibitors of Leishmania Mexicana Pyruvate Kinase (LmPK) (AID 1721) Luminescence-based primary biochemical high throughput screening assay to identify inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1789) qHTS for inhibitors of ROR gamma transcriptional activity (AID 2551) qHTS Assay for Rab9 Promoter Activators (AID 485297) qHTS screen for small molecules that induce genotoxicity in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1 (AID 504466) qHTS for Inhibitors of binding or entry into cells for Lassa Virus (AID 540256) qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342) 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 StatR promoter by full-length DAX-1 (AID 652010) qHTS for Inhibitors of PLK1-PDB (polo-like kinase 1 - polo-box domain): Primary Screen (AID 72604)
BRD-K76662562-001-01-9 PubChem CID : 54645971		NA (in 1 replicates)	0.49	0.651				Total number of assays tested in: 39. Active in the following assays: <ul style="list-style-type: none"> Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2153-05 Inhibitor.Dose.CherryPick Activity (AID 1159567)
BRD-K10768305-001-01-5 PubChem CID : 54646206		0.63 (in 4 replicates)	0.48	0.831				Total number of assays tested in: 36.
BRD-K83933044-001-01-3 PubChem CID : 54646579		0.64 (in 4 replicates)	0.48	0.758				Total number of assays tested in: 36.
BRD-K33894111-001-01-6 PubChem CID : 54618688		0.74 (in 4 replicates)	0.48	0.295				Total number of assays tested in: 37.
BRD-K06228572-001-01-2 PubChem CID : 54645949		NA (in 1 replicates)	0.45	0.651				Total number of assays tested in: 41.

<div>BRD-K96707093-001-01-6</div> <div>PubChem CID : 54646144</div>		0.64 (in 4 replicates)	0.45	0.801				Total number of assays tested in: 37.
<div>BRD-K11230389-001-01-4</div> <div>PubChem CID : 54620166</div>		0.63 (in 4 replicates)	0.43	NA				Total number of assays tested in: 33.
<div>BRD-K35589880-001-01-9</div> <div>PubChem CID : 54646630</div>		0.79 (in 4 replicates)	0.43	0.738				Total number of assays tested in: 38.
<div>BRD-A50921700-001-05-5</div> <div>ST50843211</div> <div>AC1MG1XY</div> <div>MLS001035763</div> <div>HMS2980J20</div> <div>STK436533</div> <div>SMR000666319</div> <div>PubChem CID : 2954221</div>		NA (in 1 replicates)	-0.56	NA				Total number of assays tested in: 491. Active in the following assays: <ul style="list-style-type: none">• qHTS for Inhibitors of Tau Fibril Formation, Thioflavin T Binding (AID 1460)• HTS using Di-HDL to assay lipid transfer in [4A]SR-BI cells Measured in Cell-Based System Using Plate Reader - 2085-01.Inhibitor.SinglePoint.HTS.Activity (AID 488896)• Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Absorbance-based biochemical high throughput Glycerophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) full deck assay to identify assay artifacts (AID 588335)• Fluorescence-based biochemical primary high throughput screening assay to identify inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 588726)• Fluorescence-based biochemical high throughput confirmation assay for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 651616)• Absorbance-based biochemical primary high throughput screening assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651718)• Absorbance-based biochemical high throughput confirmation assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651822)• Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Fluorescence-based biochemical high throughput Glycerophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) assay to identify assay artifacts (AID 652141)
<div>BRD-K24842996-001-05-7</div> <div>MLS000724518</div> <div>SMR000306111</div> <div>BDBM51728</div> <div>ZINC60230669</div> <div>PubChem CID : 45037793</div>		NA (in 1 replicates)	-0.53	NA				Total number of assays tested in: 625. Active in the following assays: <ul style="list-style-type: none">• qHTS for Inhibitors of Tau Fibril Formation, Thioflavin T Binding (AID 1460)• HTS using Di-HDL to assay lipid transfer in [4A]SR-BI cells Measured in Cell-Based System Using Plate Reader - 2085-01.Inhibitor.SinglePoint.HTS.Activity (AID 488896)• Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Absorbance-based biochemical high throughput Glycerophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) full deck assay to identify assay artifacts (AID 588335)• Fluorescence-based biochemical primary high throughput screening assay to identify inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 588726)• Fluorescence-based biochemical high throughput confirmation assay for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 651616)• Absorbance-based biochemical primary high throughput screening assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651718)• Absorbance-based biochemical high throughput confirmation assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651822)• Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Fluorescence-based biochemical high throughput Glycerophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) assay to identify assay artifacts (AID 652141)
<div>BRD-K60719499-001-01-3</div> <div>PubChem CID : 44616972</div>		0.78 (in 4 replicates)	-0.51	0.349				Total number of assays tested in: 38.

BRD-K49416011-001-05-2 AC1LLBP1 BAS 06021781 MLS000089225 HMS2433D04 ZINC797151 STK115082 ZINC00797151 SMR000072981 PubChem CID : 1081839		0.54 (in 2 replicates)	-0.49	NA				Total number of assays tested in: 781. Active in the following assays: <ul style="list-style-type: none"> • qHTS Assay for Spectroscopic Profiling in 4-MU Spectral Region (AID 589) • qHTS Assay for Spectroscopic Profiling in A350 Spectral Region (AID 590) • Human H69AR Lung Tumor Cell Growth Inhibition Assay - 86K Screen (AID 598) • qHTS Assay for Agonists of the Thyroid Stimulating Hormone Receptor: Activators of Intracellular cAMP Concentrations in Parental HEK 293 (AID 938) • HTS using DiI-HDL to assay lipid transfer in IdIA[SR-BI] cells Measured in Cell-Based System Using Plate Reader - 2085-01 Inhibitor.SinglePoint.HTS.Activity (AID 488896) • Primary cell-based high-throughput screening for identification of compounds that antagonize MrgX1 receptor signaling (AID 588676) • Counterscreen of compound fluorescence effects on High-throughput multiplex microsphere screening for inhibitors of toxin protease (AID 624483) • Luminescence-based cell-based primary high throughput screening assay to identify activators of Transthyretin (TTR) transcription (AID 1117267)
BRD-K65196043-001-01-0 PubChem CID : 54618158		0.91 (in 4 replicates)	-0.47	0.307				Total number of assays tested in: 33.
BRD-K58023987-001-01-3 PubChem CID : 54649023		0.67 (in 2 replicates)	-0.43	0.011				Total number of assays tested in: 36.
BRD-K93301753-001-05-3 AC1LCRMW SMR000011224 Ambcb6191699 MLS000070503 HMS2506C17 SMSF0016921 ZINC04092174 ZINC04092174 CB07122 BAS 02244189 PubChem CID : 654919		0.73 (in 4 replicates)	-0.42	NA				Total number of assays tested in: 777.