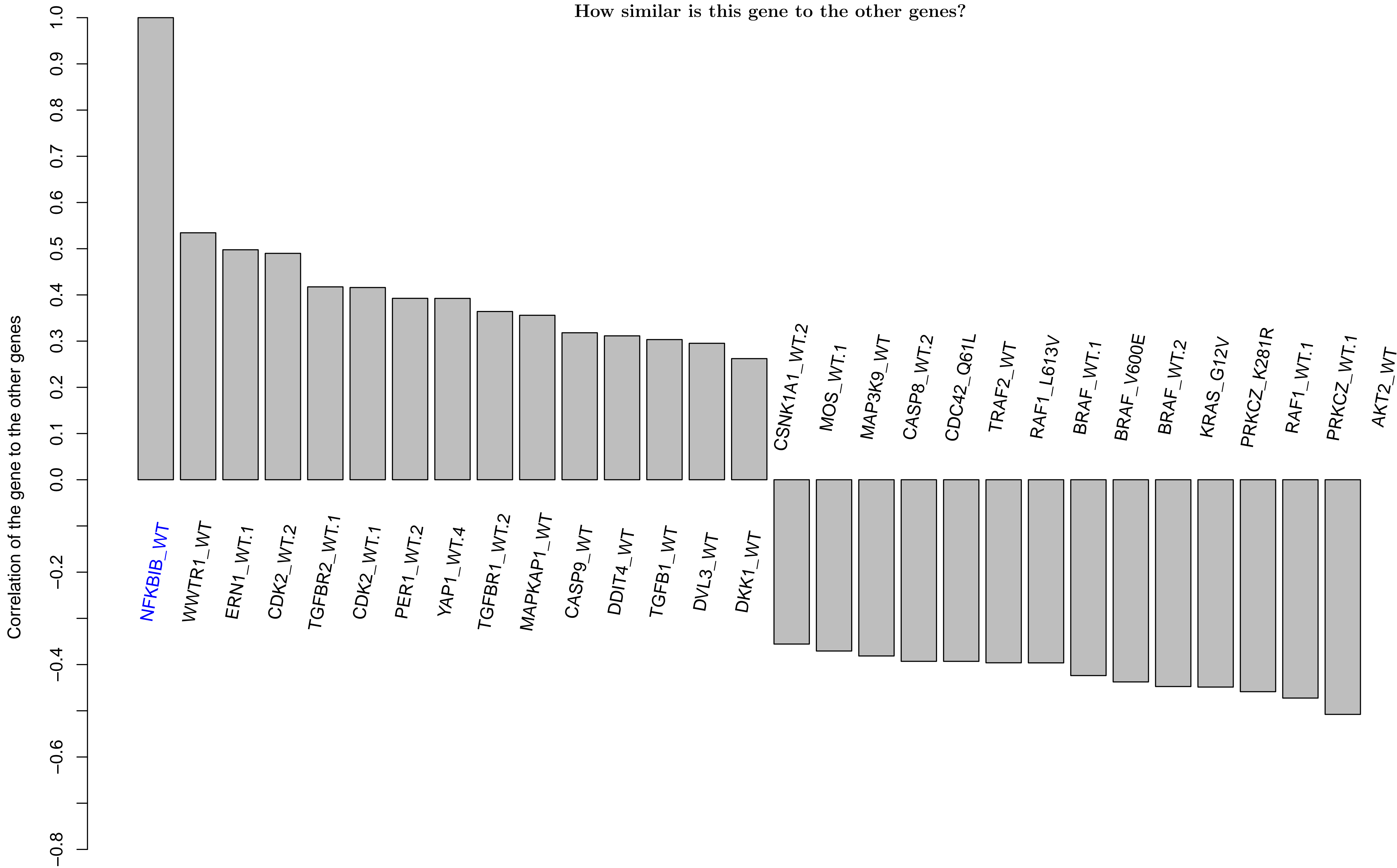
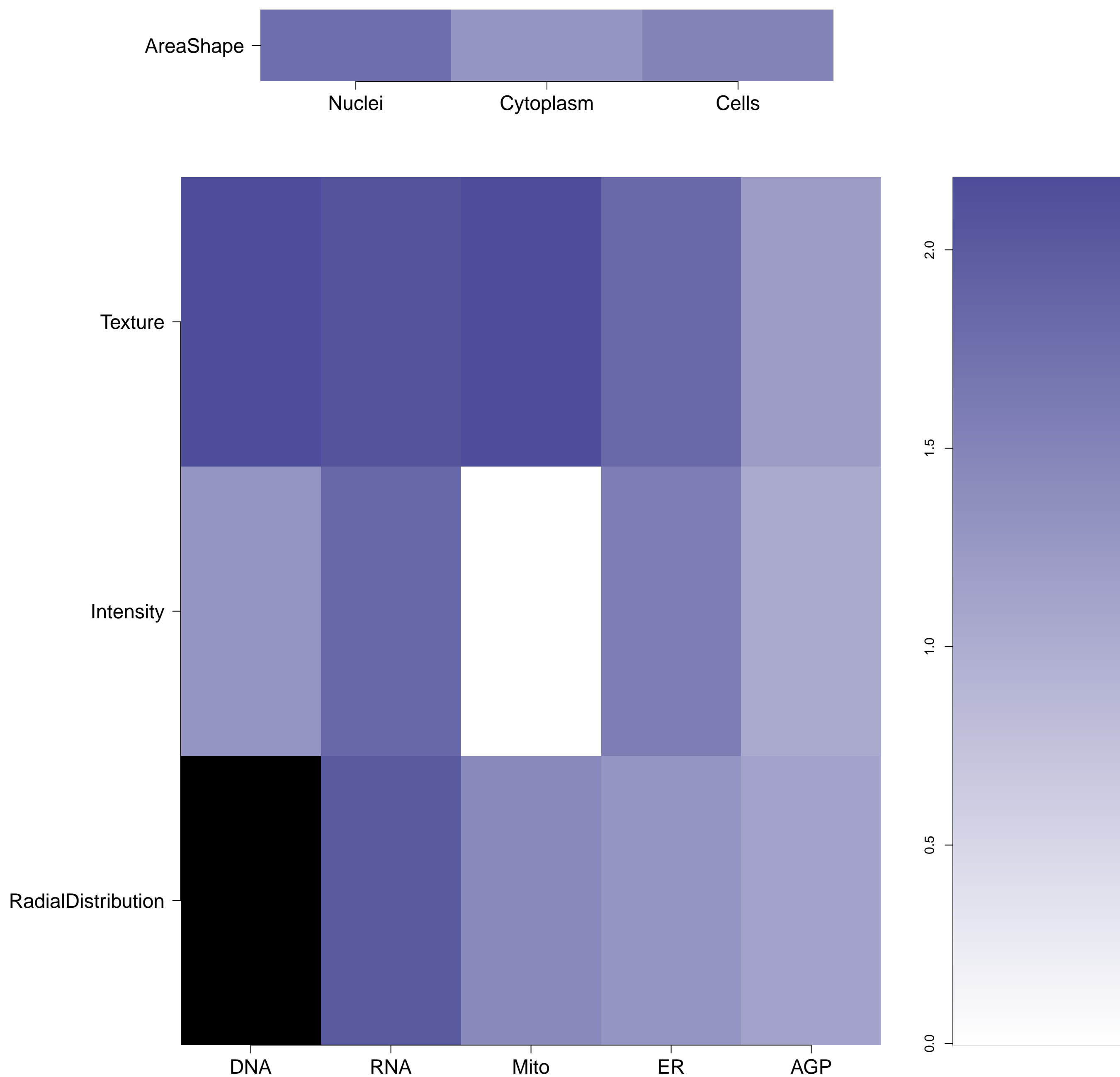


NFKBIB.WT - in Canonical NFkB

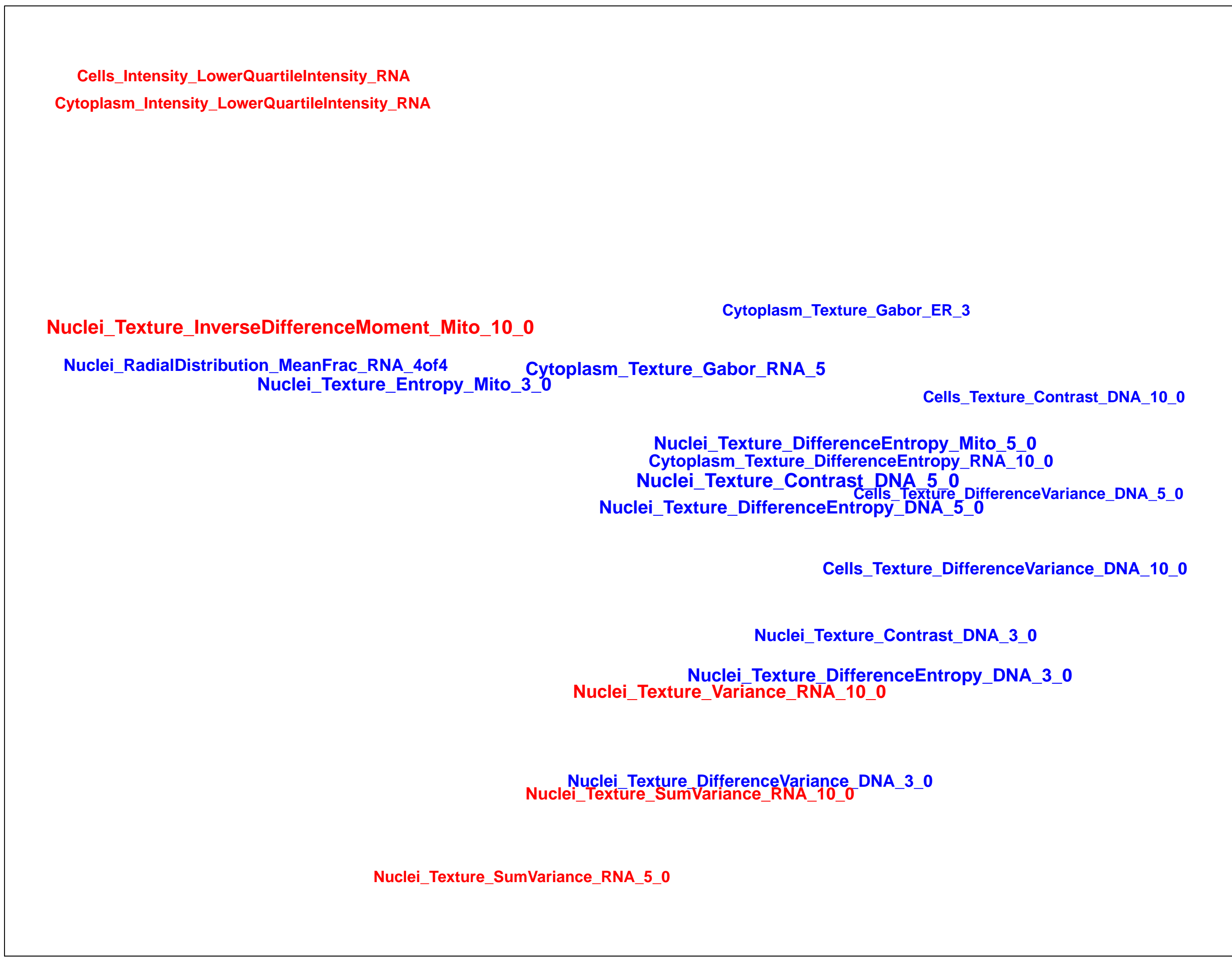
How similar is this gene to the other genes?



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

NFKBIB.WT (41744)

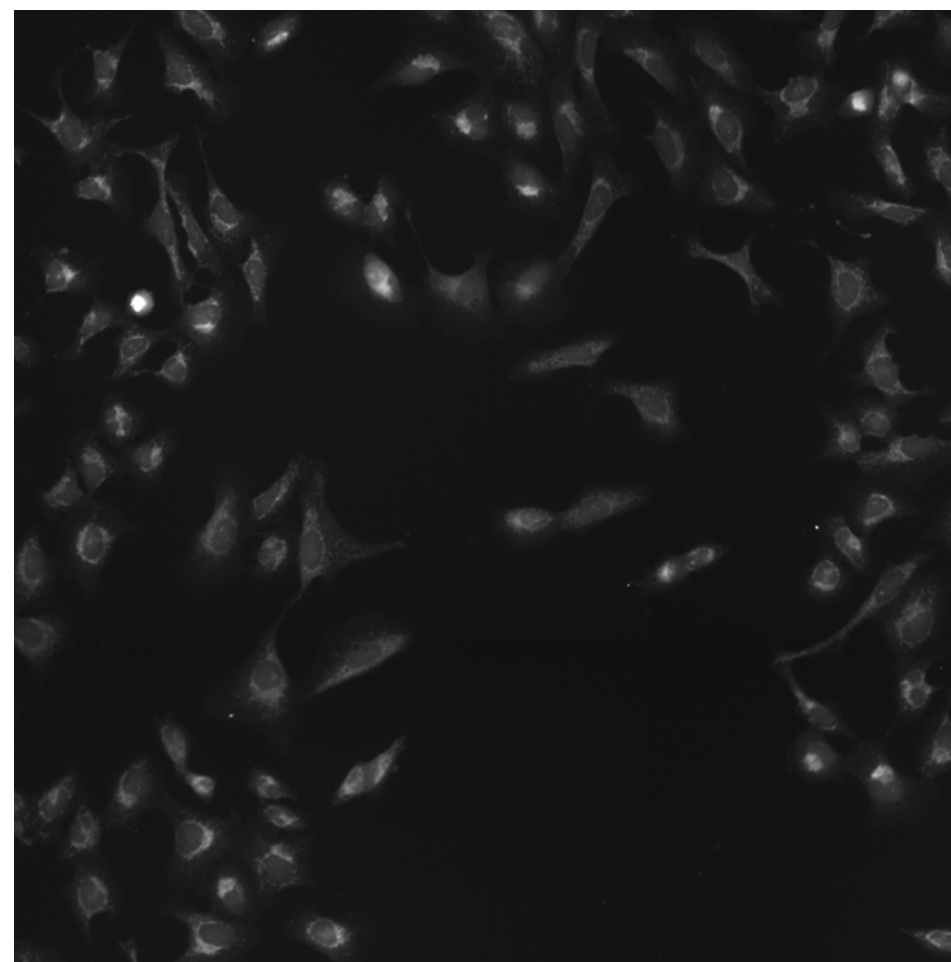
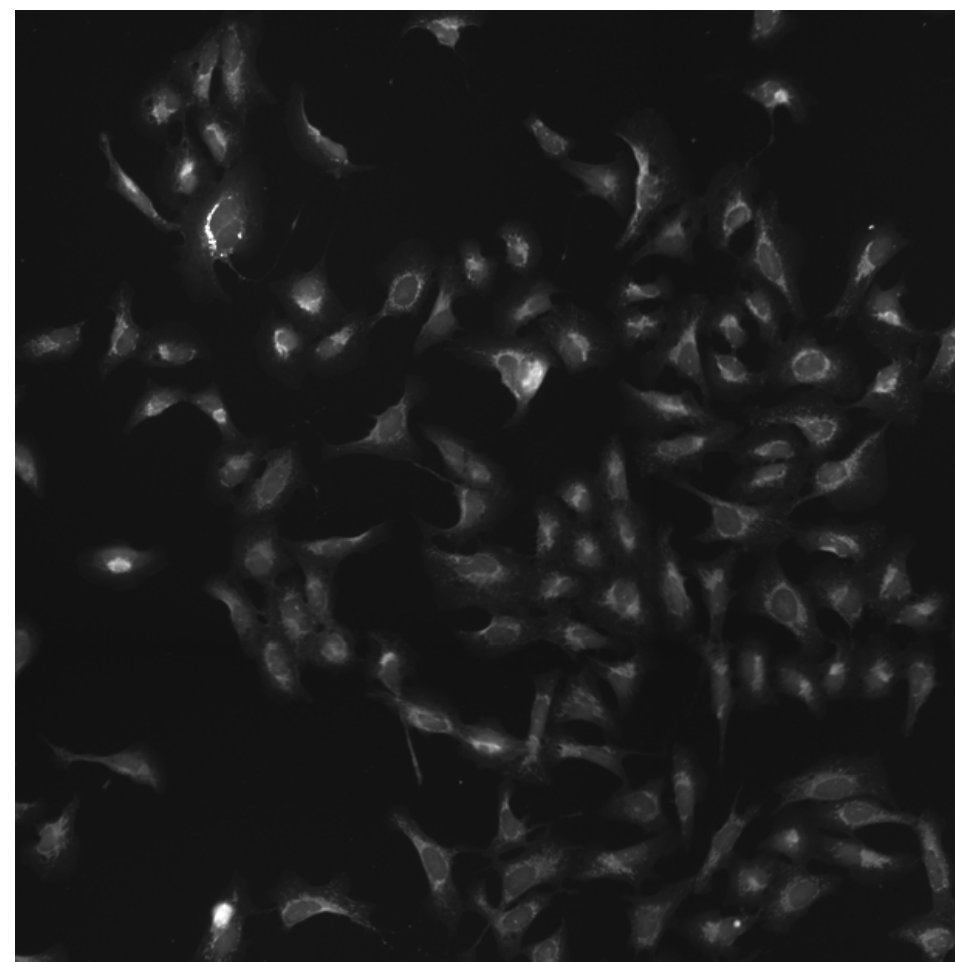
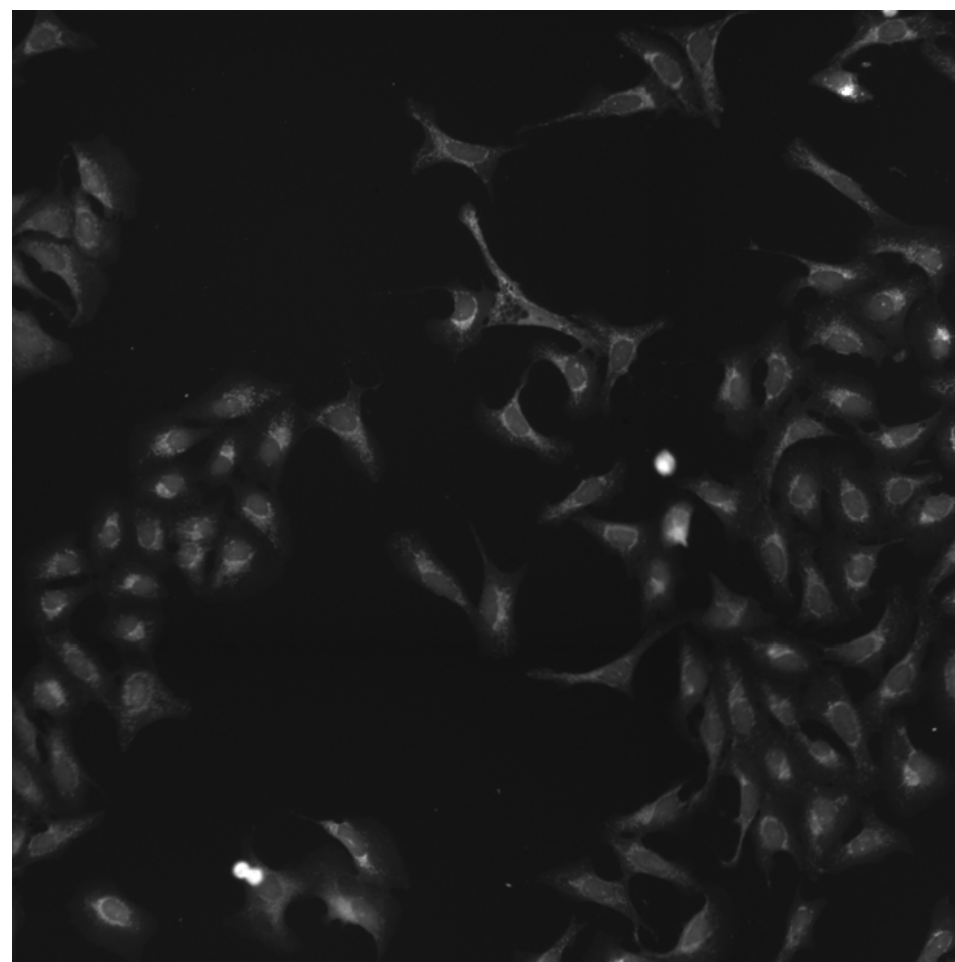
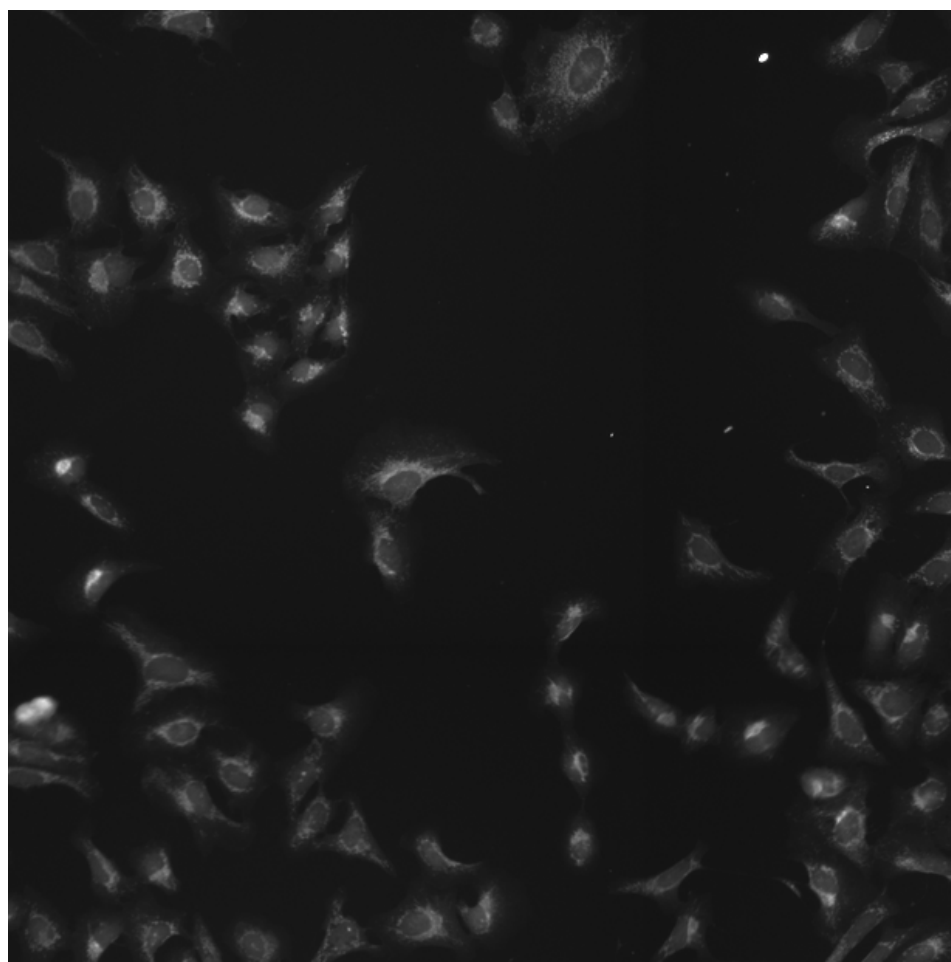
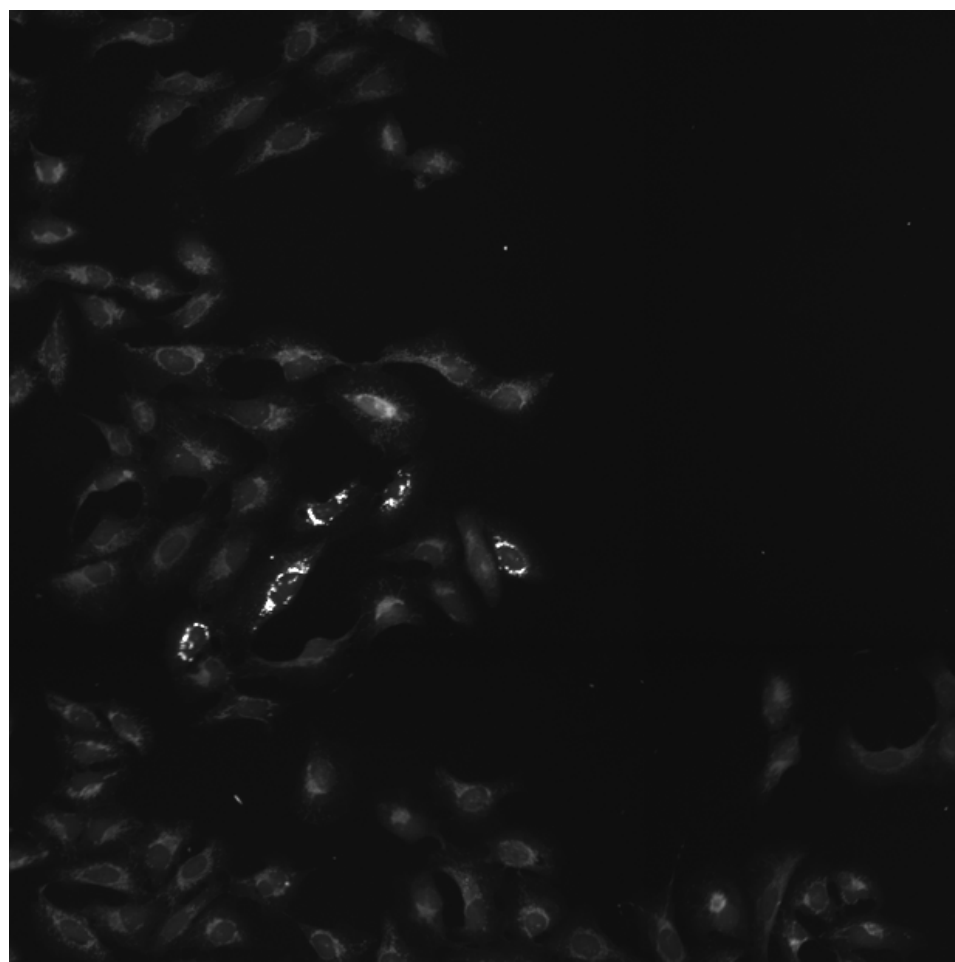
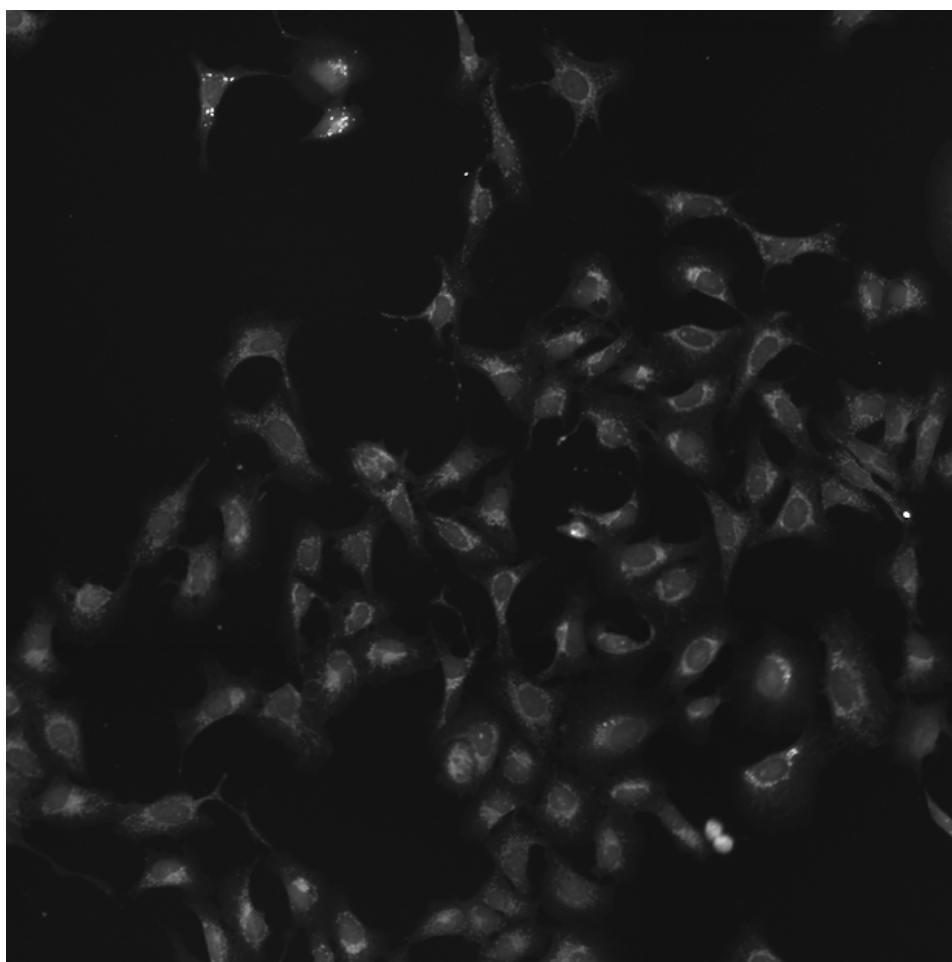
NFKBIB.WT (41755)

NFKBIB.WT (41756)

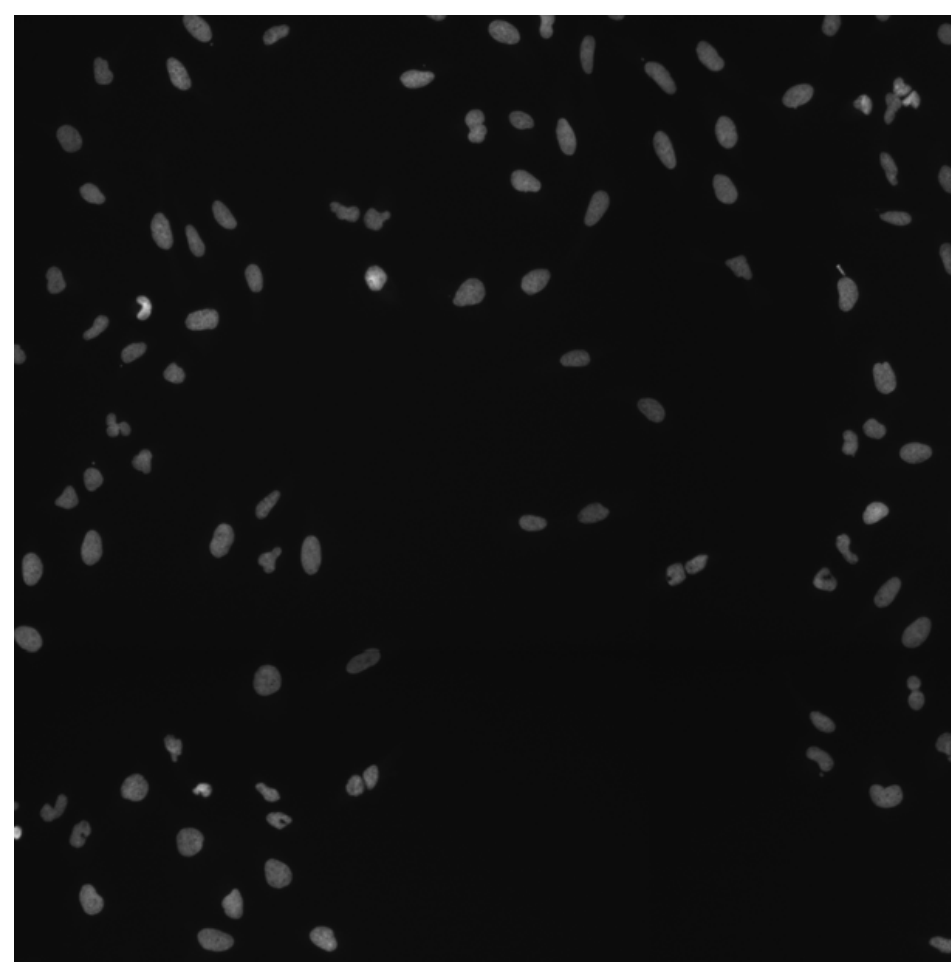
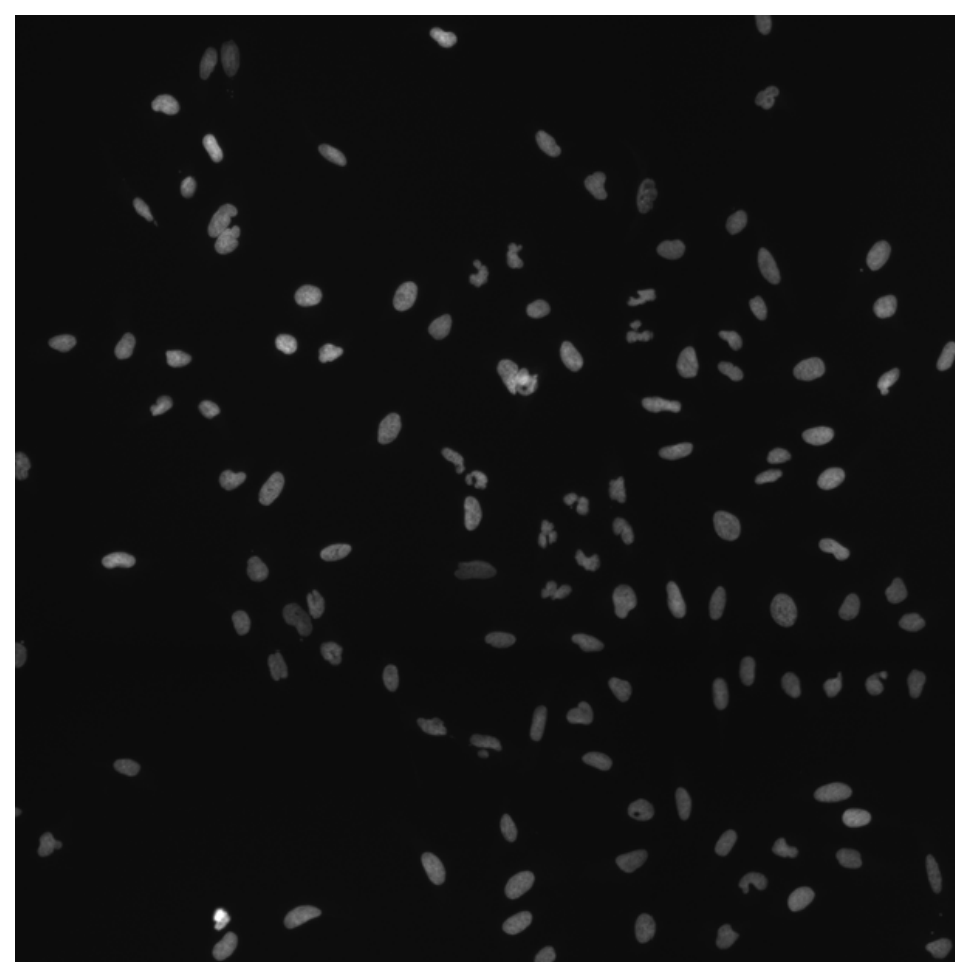
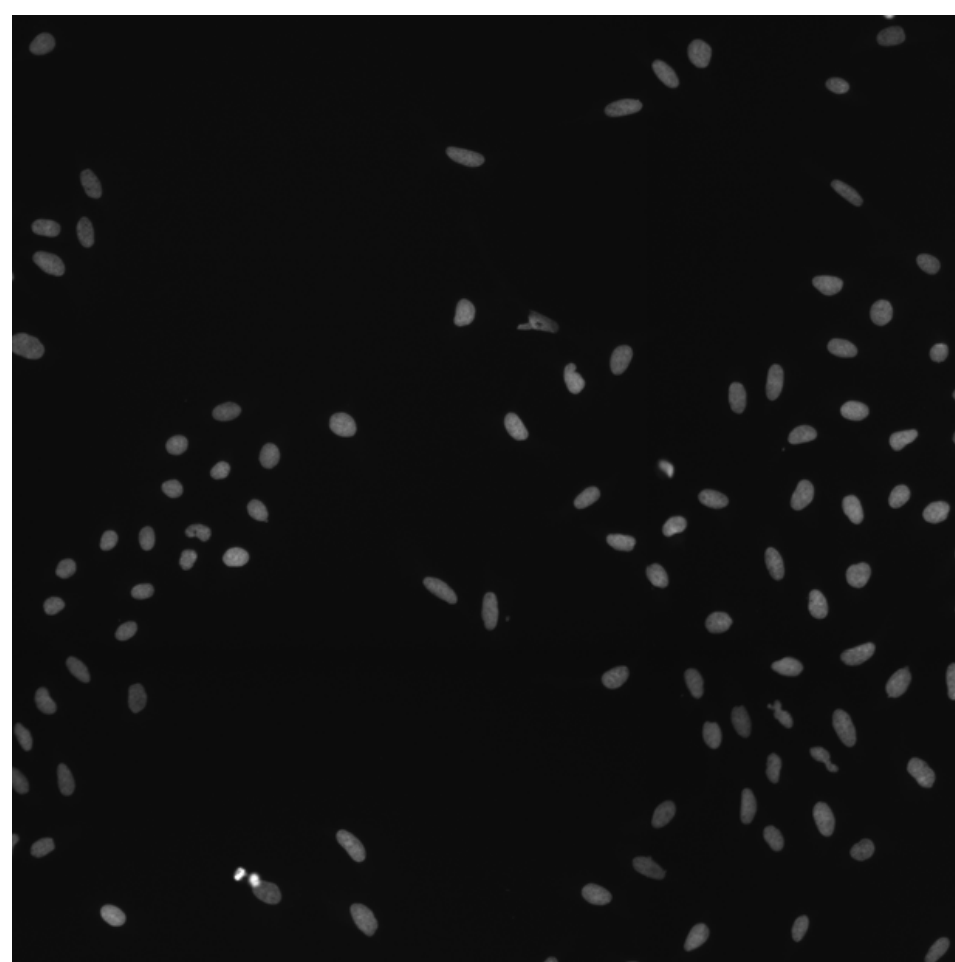
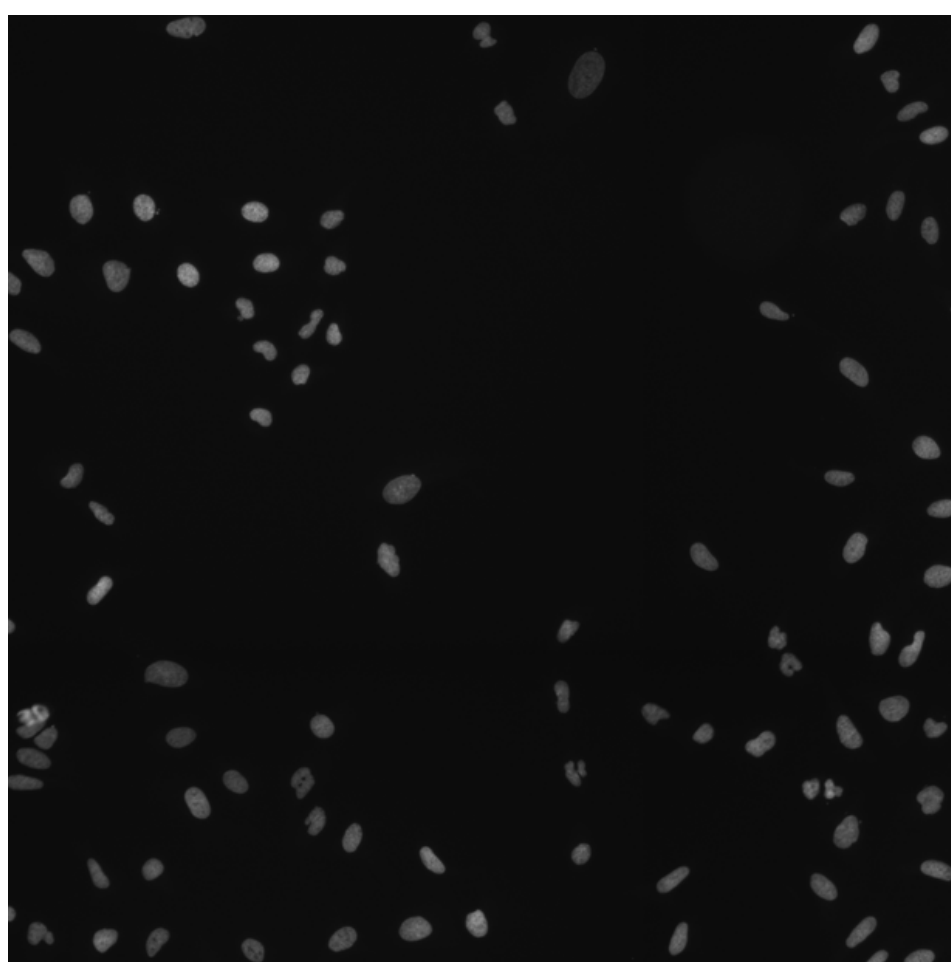
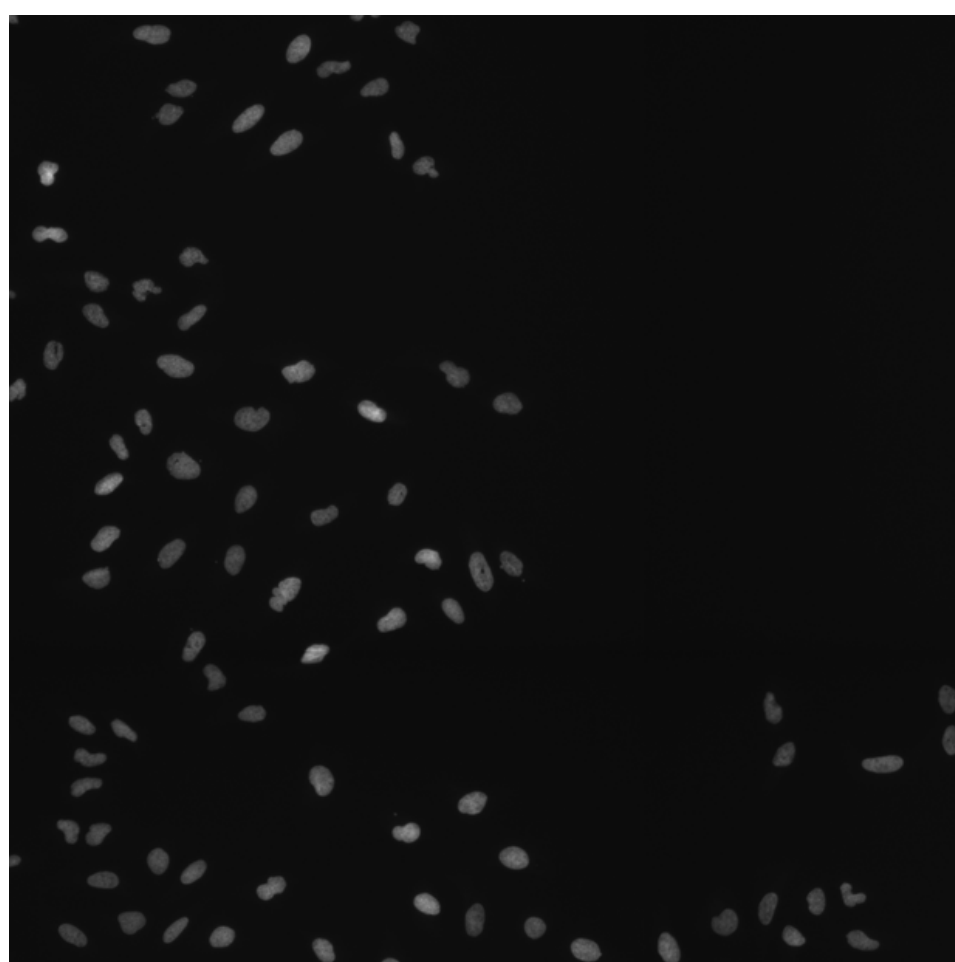
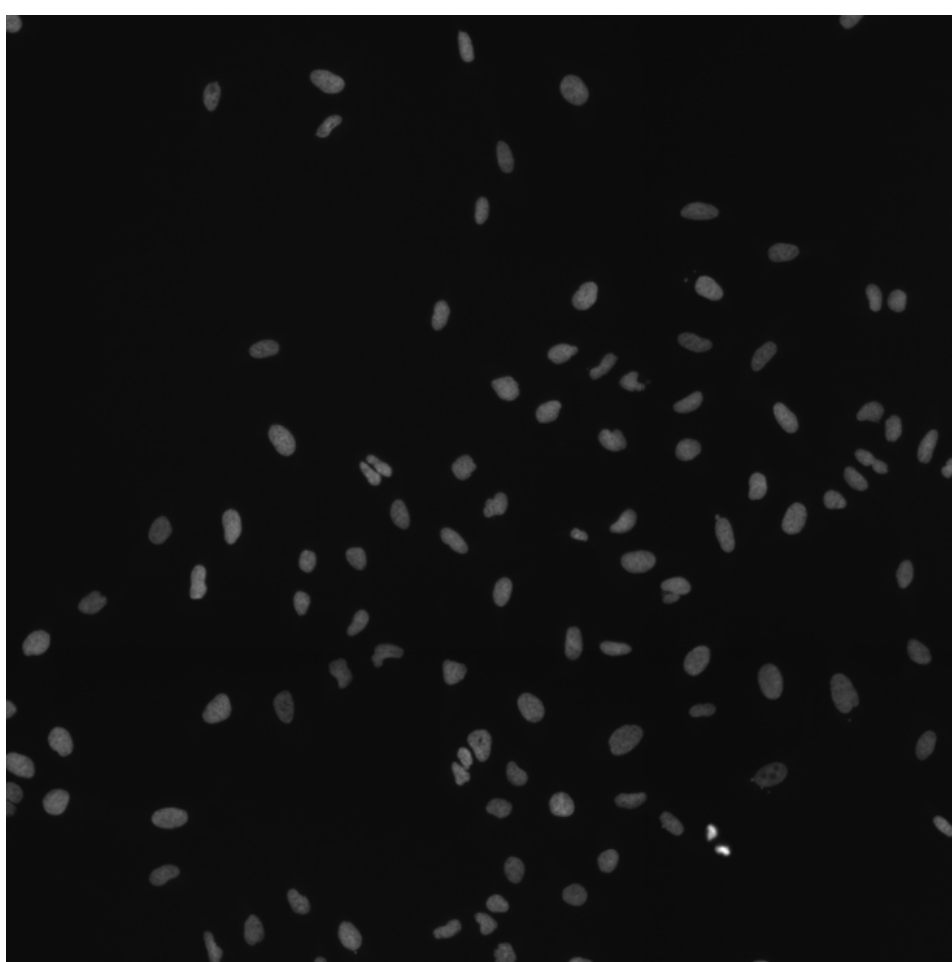
NFKBIB.WT (41757)

NFKBIB.WT (41754)

Mito



DNA

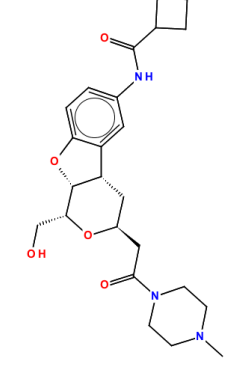
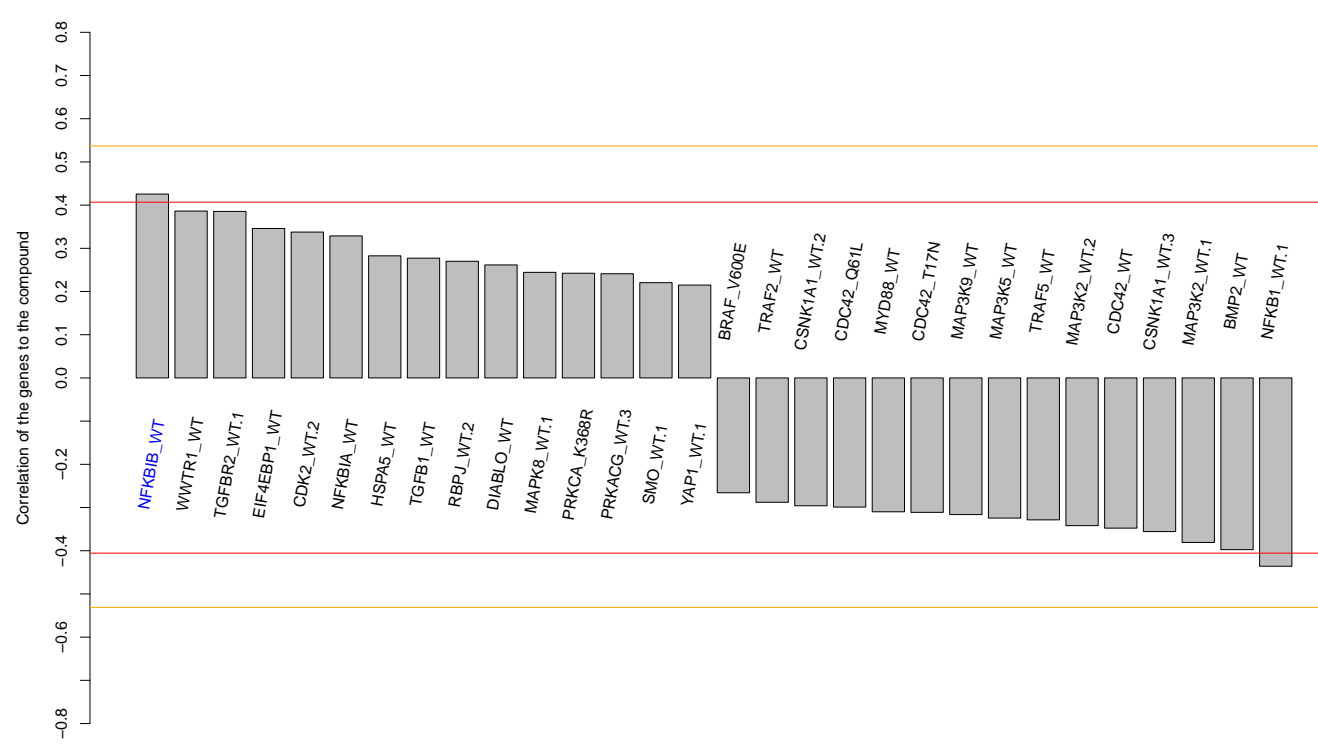
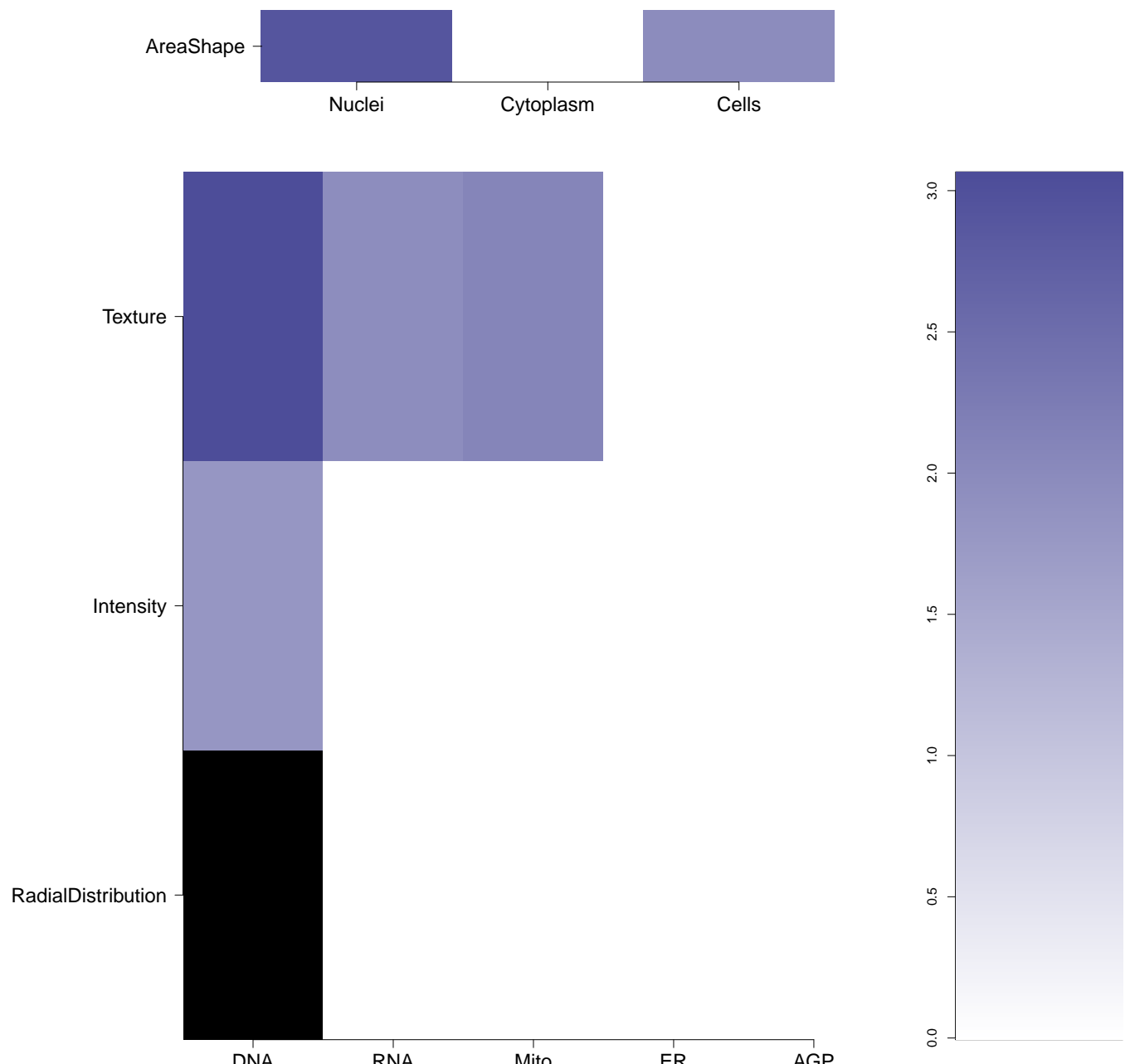
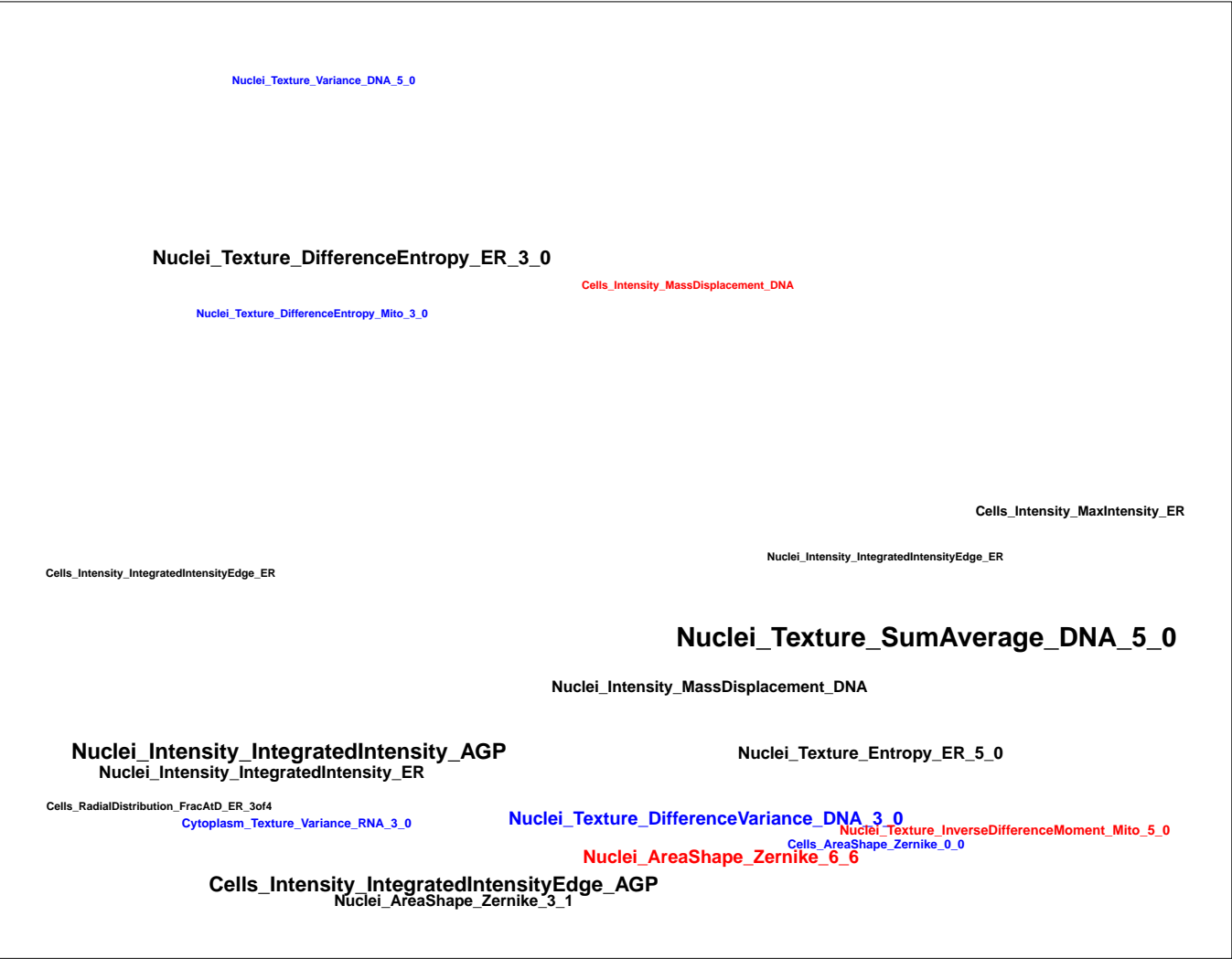
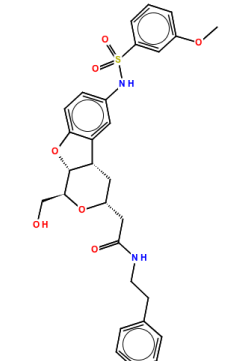
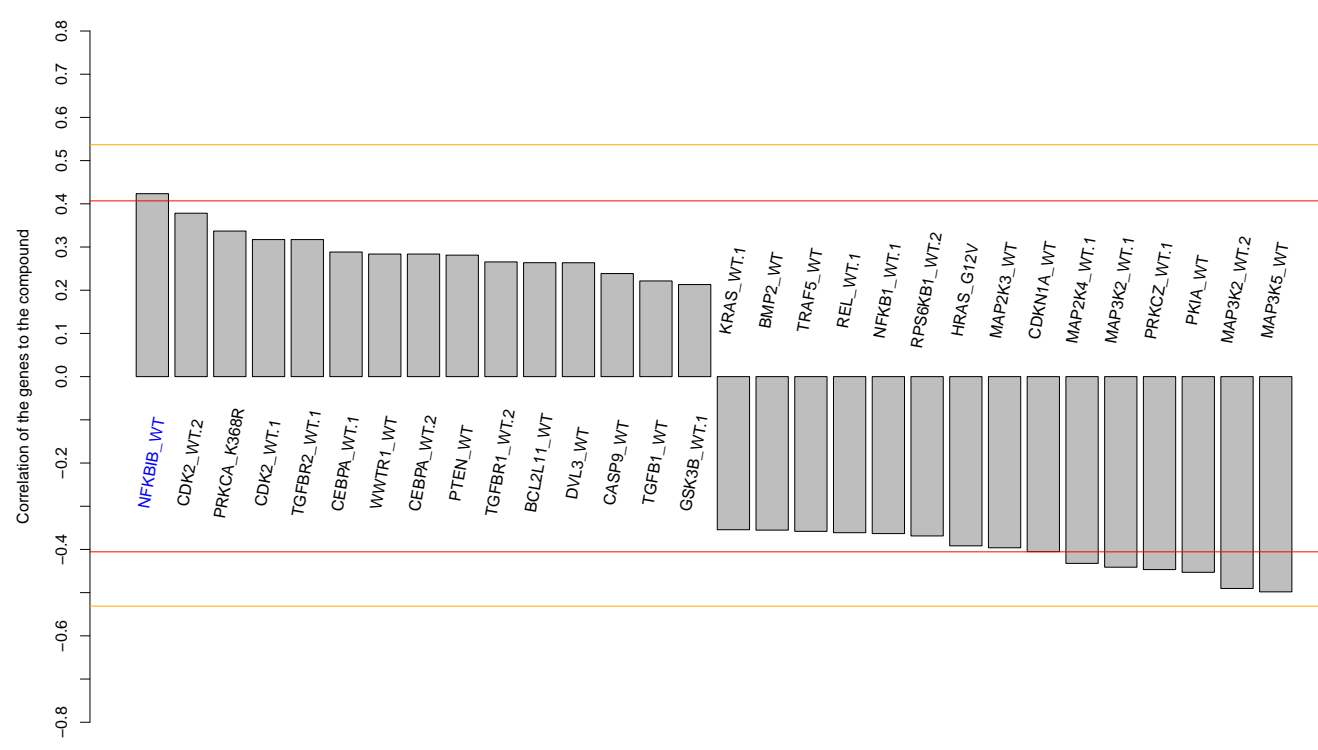
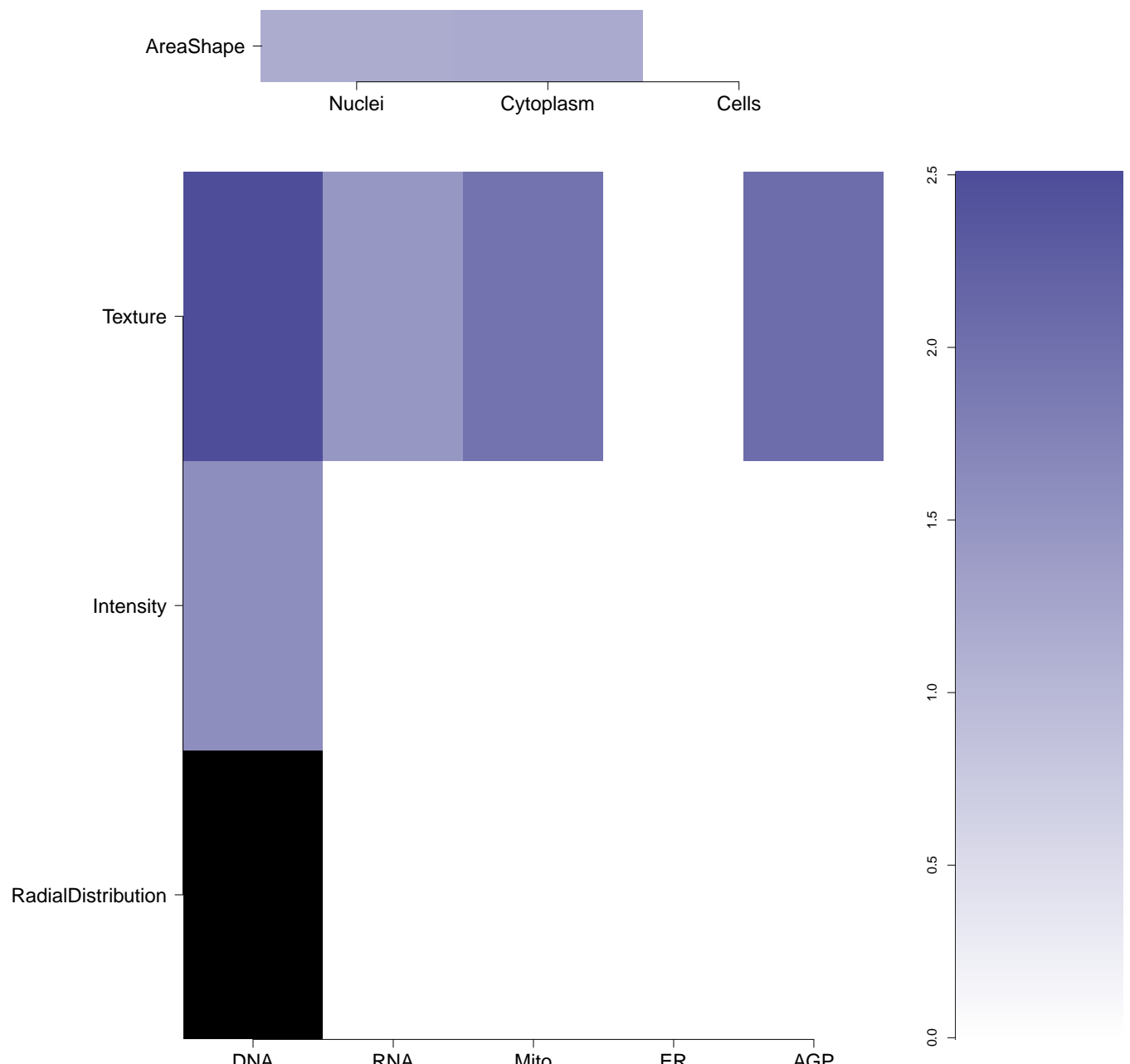
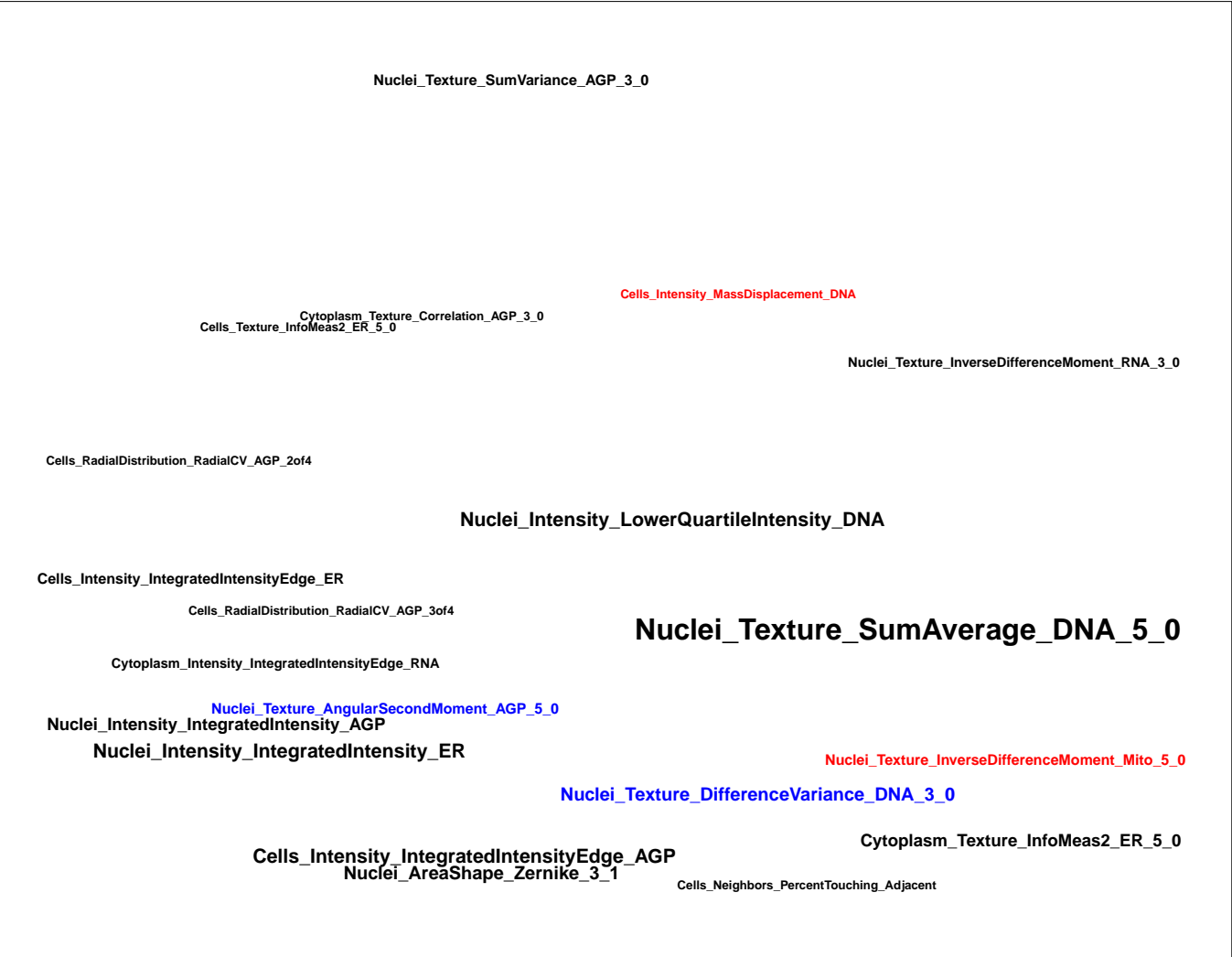
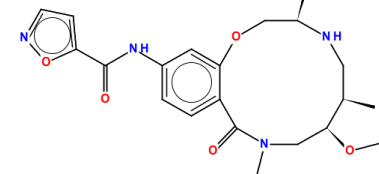
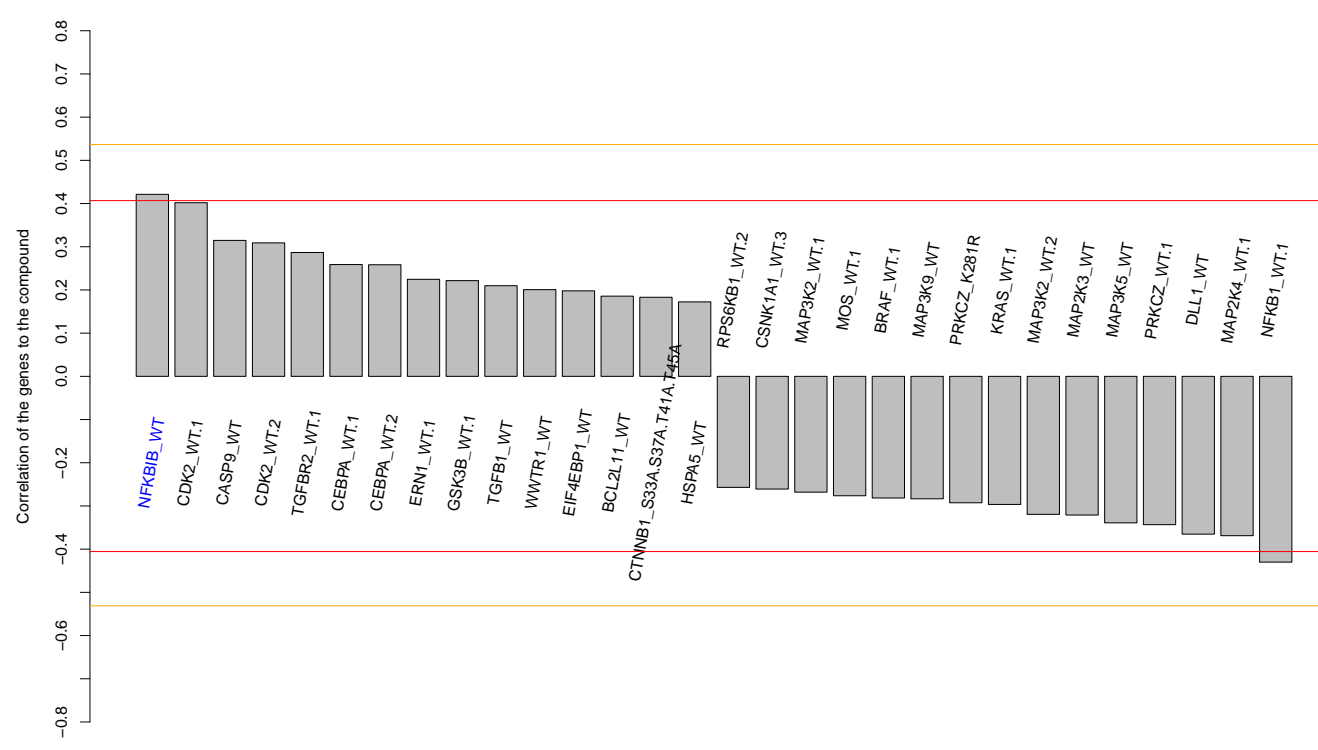
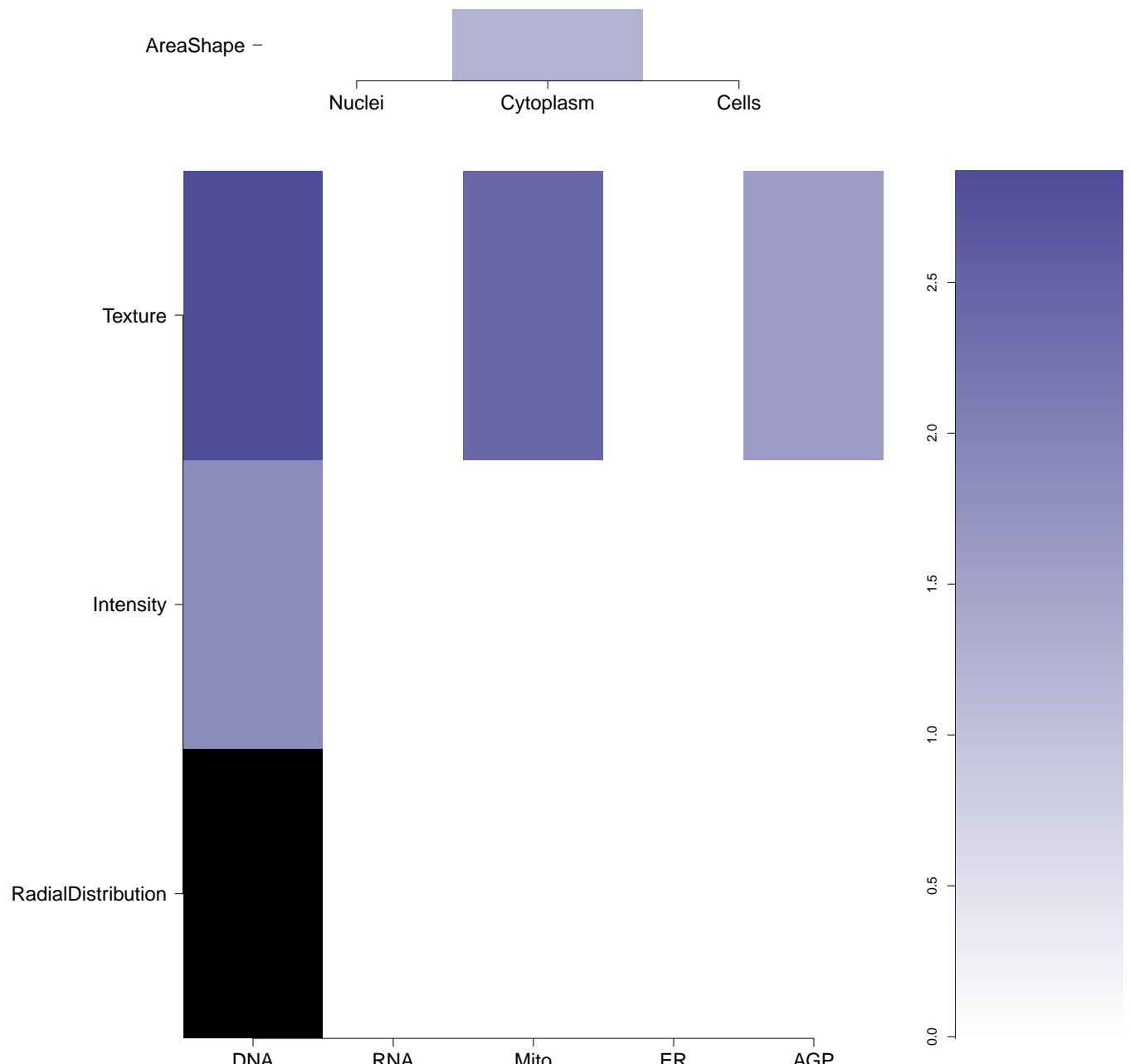

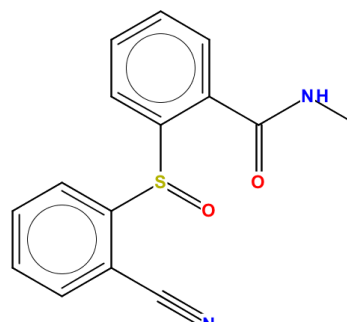
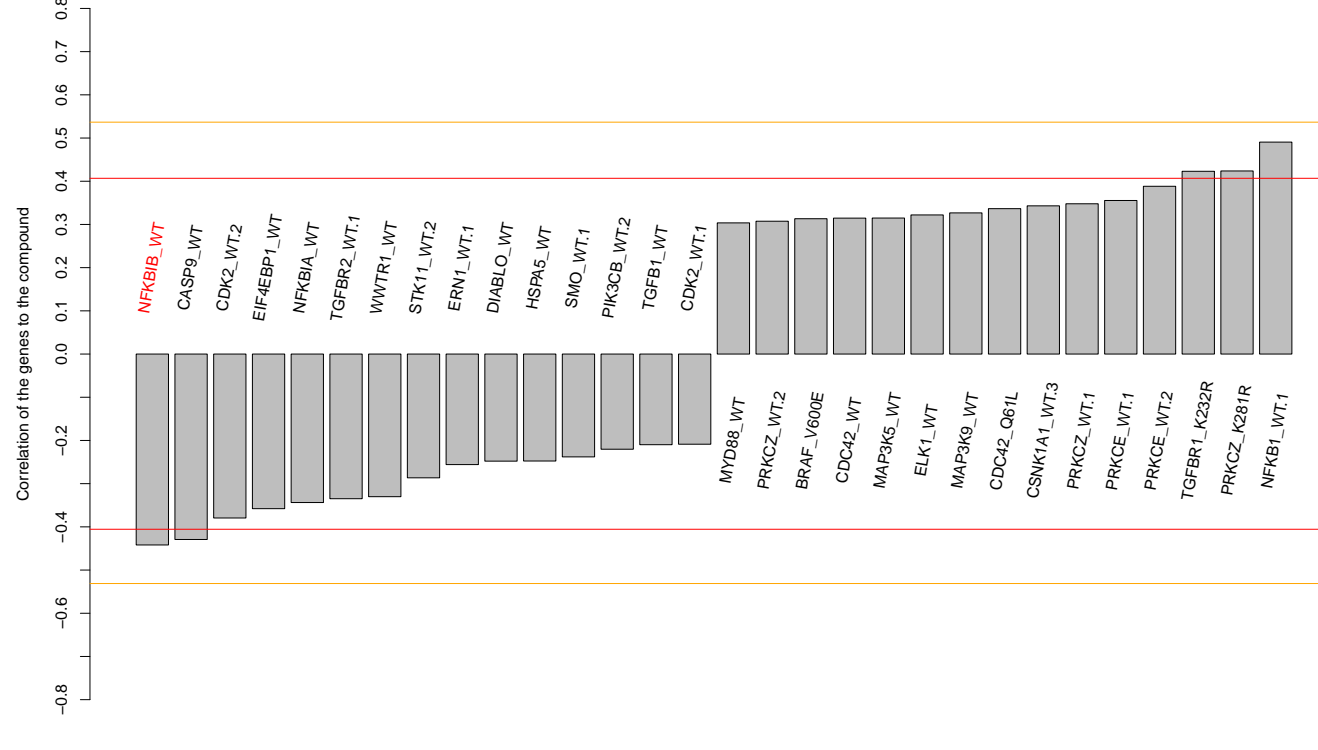
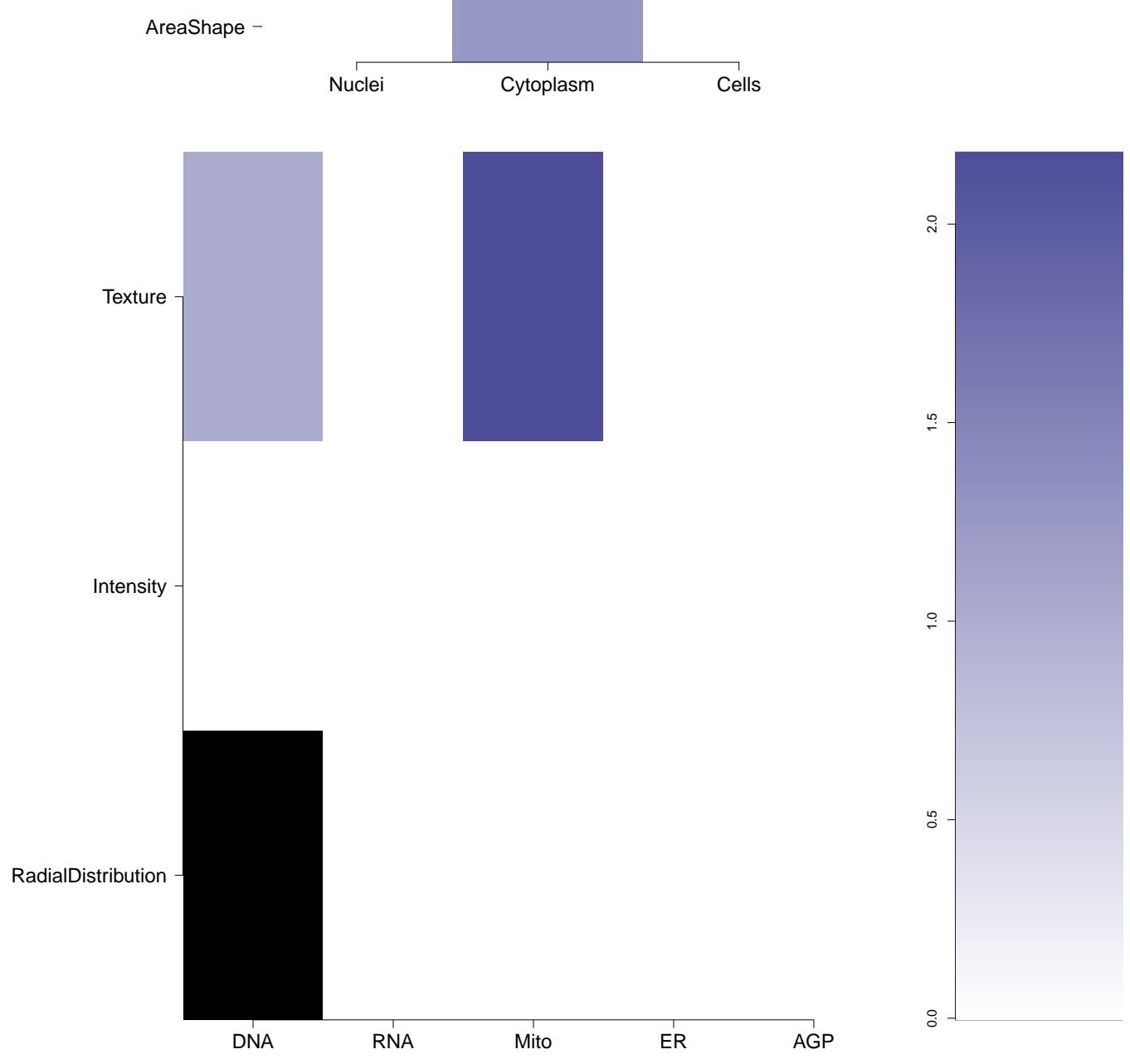
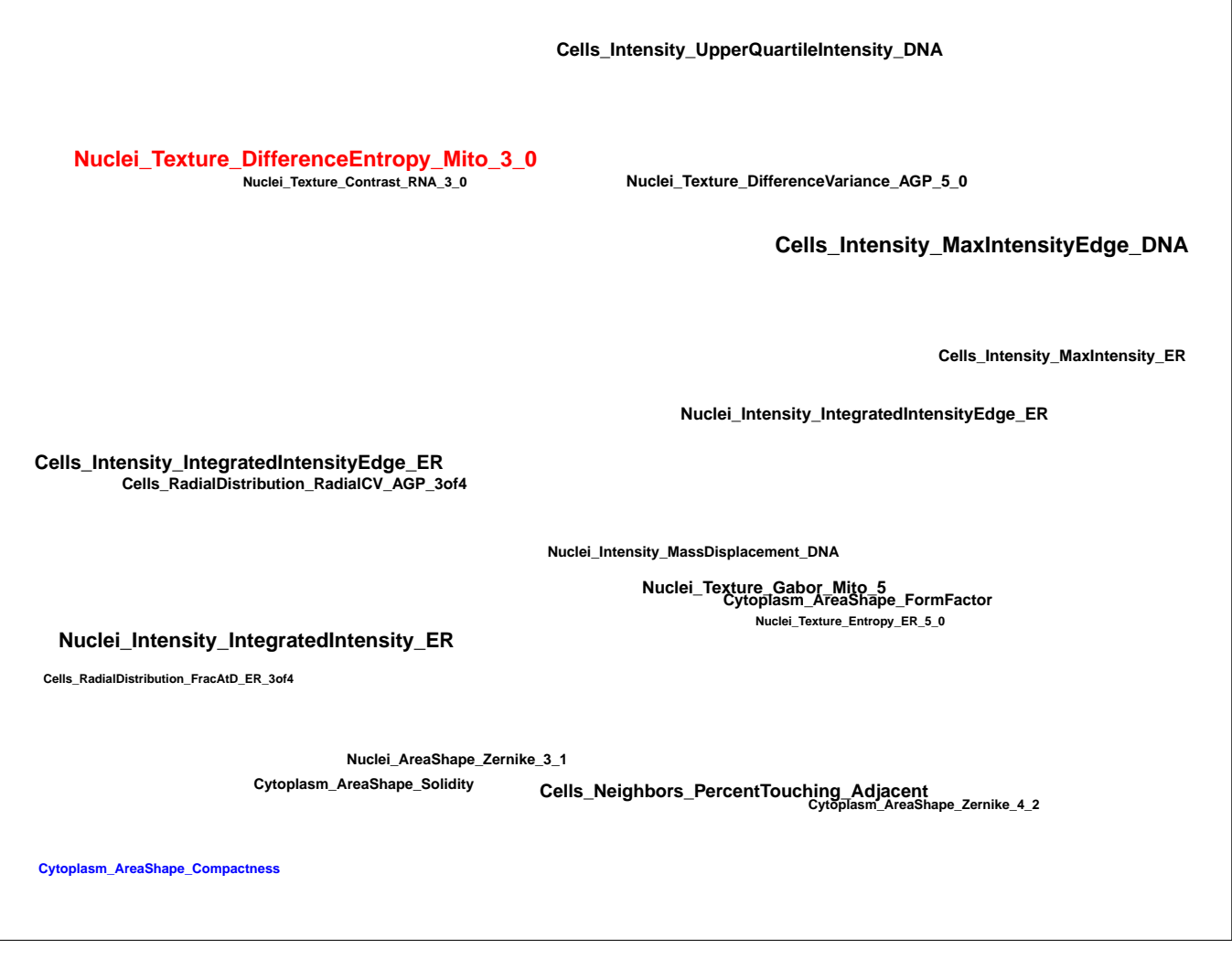
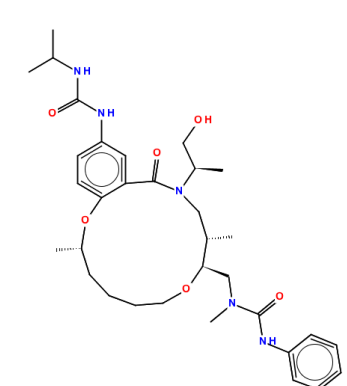
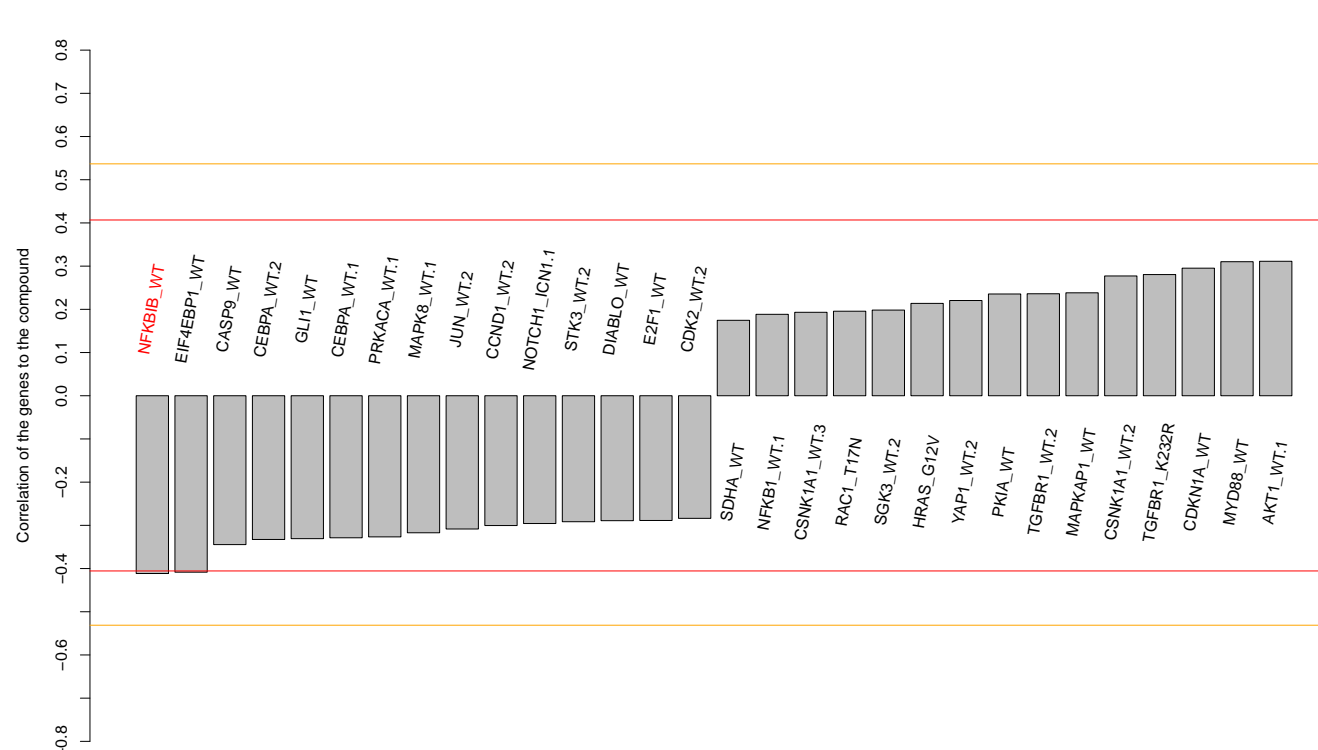
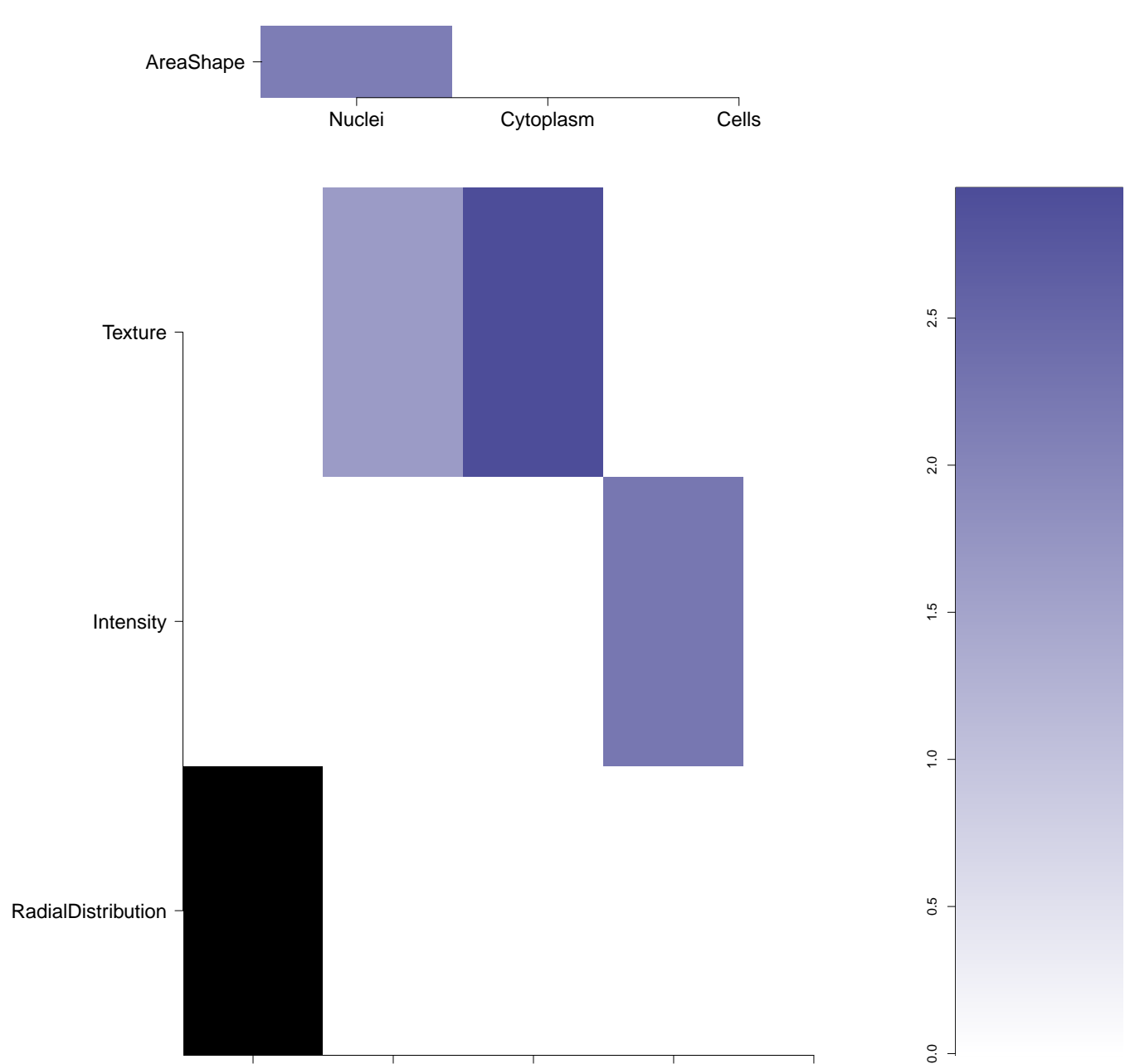



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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-K48818351-001-01-7 PubChem CID : 54641364		NA (in 1 replicates)	0.50	NA				Total number of assays tested in: 37.
BRD-K18713590-001-01-7 PubChem CID : 54646201		0.88 (in 4 replicates)	0.46	0.300				Total number of assays tested in: 37.
BRD-K07787963-001-05-4 MLS000042070 AC1N1W7G HMS2183L15 STL057077 ZINC20326393 SMR000058149 PubChem CID : 5389638		NA (in 1 replicates)	0.45	NA				Total number of assays tested in: 768. Active in the following assays: <ul style="list-style-type: none"> <li>Primary Antimicrobial Assay for E. coli BW25113 and 8710:tolC::kan Protocol for 384-well HTS (AID 573)</li> <li>Antimicrobial Assay for E. coli BW25113 and 8710:tolC::kan - Dose Response (AID 617)</li> <li>Allotesteric Modulators of D1 Receptors: Primary Screen (AID 641)</li> <li>Allotesteric Modulators of D1 Receptors: Confirmation Screen (AID 642)</li> <li>Allotesteric Modulators of D1 Receptors: Secondary Assay 2 (AID 647)</li> <li>Cell signaling CRE-BLA (Fak stim) (AID 662)</li> <li>Screening for Modulators of Post-Golgi Transport, Control Strain (AID 738)</li> <li>CYP2C9 Assay (AID 777)</li> <li>Fluorescence-based cell-based primary high throughput screening assay to identify antagonists of the human trace amine associated receptor 1 (TAAR1) (AID 624466)</li> <li>Fluorescence-based cell-based primary high throughput screening assay to identify agonists of the human trace amine associated receptor 1 (TAAR1) (AID 624467)</li> <li>Fluorescence-based cell-based primary high throughput confirmation assay to identify agonists of the human trace amine associated receptor 1 (TAAR1) (AID 651783)</li> <li>Counter-screen for agonists of the human trace amine associated receptor 1 (hTAAR1): Fluorescence-based cell-based high throughput screening assay to identify nonselective Ga16 antagonists (AID 651952)</li> <li>Fluorescence-based biochemical high throughput primary assay to identify inhibitors of phospholipase C isozymes (PLC-gamma1). (AID 720700)</li> </ul>
BRD-K24992635-001-01-6 PubChem CID : 54646413		0.77 (in 4 replicates)	0.45	0.586				Total number of assays tested in: 38.
BRD-K51201721-001-01-3 PubChem CID : 54646146		0.83 (in 4 replicates)	0.45	0.325				Total number of assays tested in: 37.
BRD-K10210954-001-01-2 PubChem CID : 54646564		0.89 (in 4 replicates)	0.44	0.725				Total number of assays tested in: 36.
BRD-K06237859-001-01-7 PubChem CID : 44496596		0.56 (in 3 replicates)	0.43	0.018				Total number of assays tested in: 54. Active in the following assays: <ul style="list-style-type: none"> <li>Fluorescence Cell-Based Primary HTS to Identify Reactive Oxygen Species Inducers in Cancer Cells Measured in Cell-Based System Using Plate Reader and Imaging Combination - 2044-01 Activator.SinglePoint.HTS Activity (AID 624156)</li> <li>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)</li> <li>Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader (AID 1159554)</li> </ul>



BRD-K34015625-001-01-6 PubChem CID : 54646168		0.64 (in 4 replicates)	0.43	0.165				Total number of assays tested in: 37.
BRD-K80362711-001-01-0 PubChem CID : 54646591		0.80 (in 4 replicates)	0.42	0.586				Total number of assays tested in: 37.
BRD-K07937631-001-01-6 PubChem CID : 54632048		0.72 (in 4 replicates)	0.42	0.838				Total number of assays tested in: 31.
BRD-A32792984-001-05-0 2L-351S AC1MV3JU MLS000326124 HMS2304C23 OR010317 SMR000170250 3B3-047746 PubChem CID : 3726662		NA (in 1 replicates)	-0.44	NA				Total number of assays tested in: 663.
BRD-K22854900-001-01-8 PubChem CID : 44487478		0.60 (in 4 replicates)	-0.41	NA				Total number of assays tested in: 38.