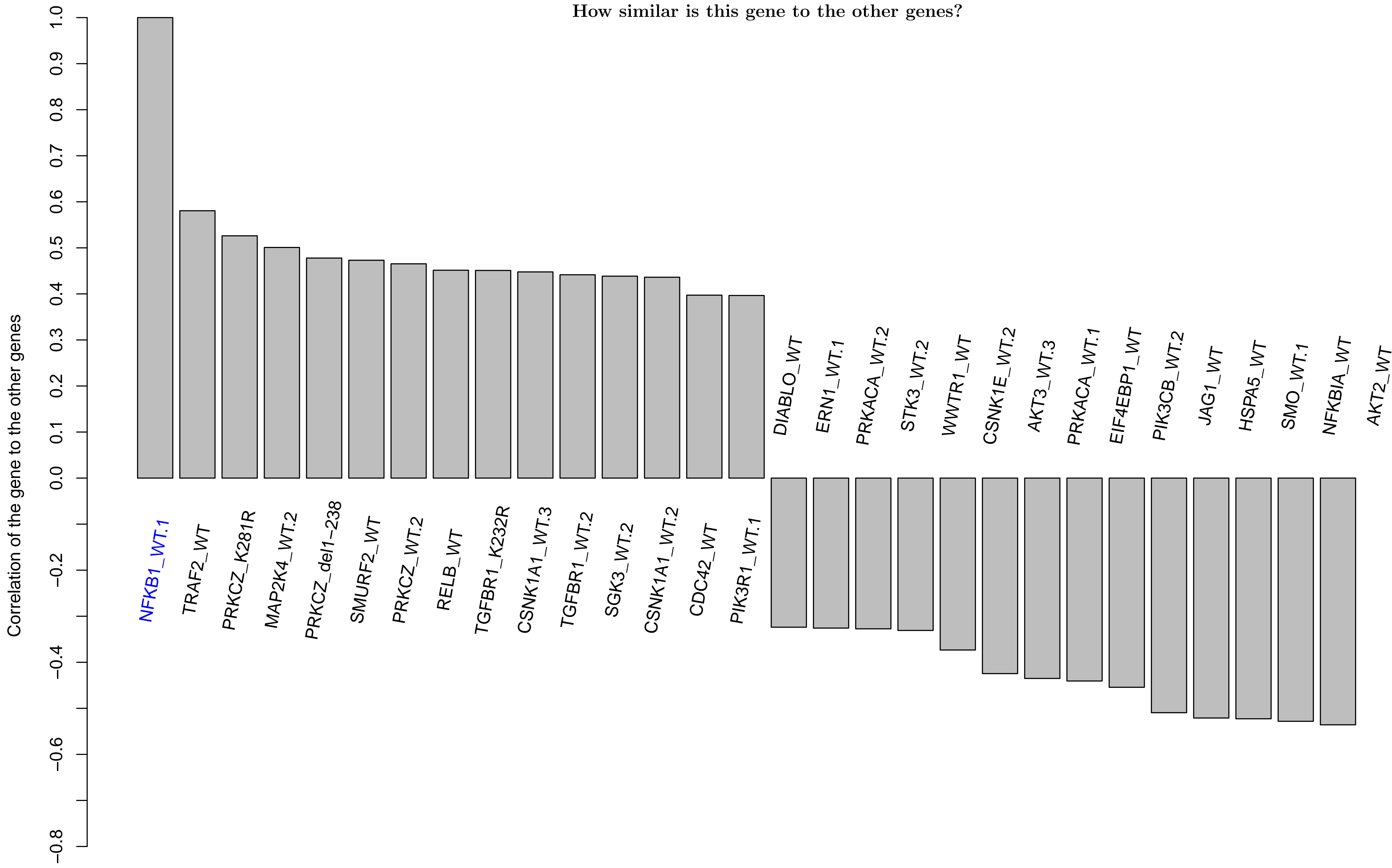
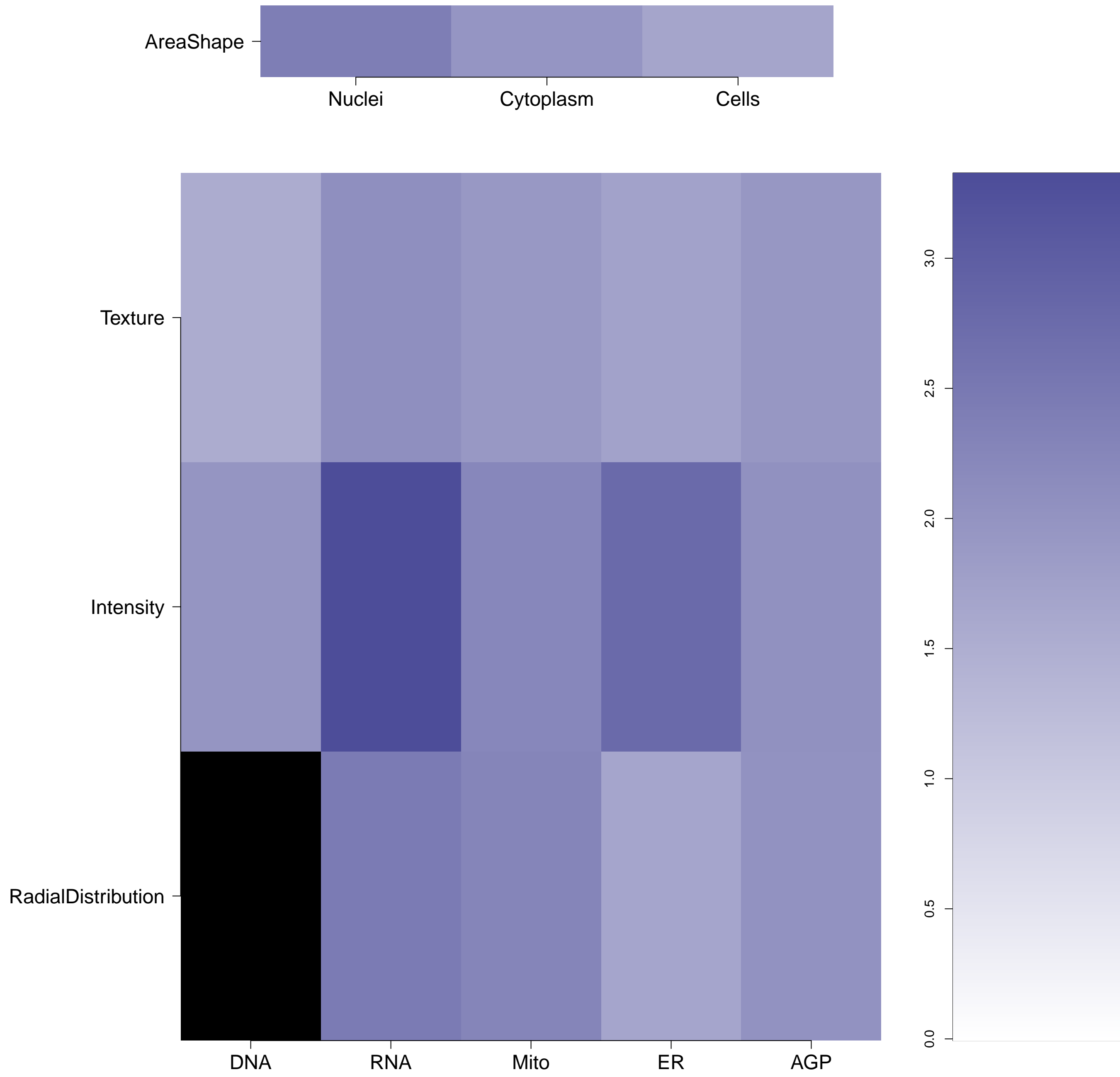


NFKB1.WT.1 - in Canonical NFkB

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

NFKB1.WT.1 (41744)

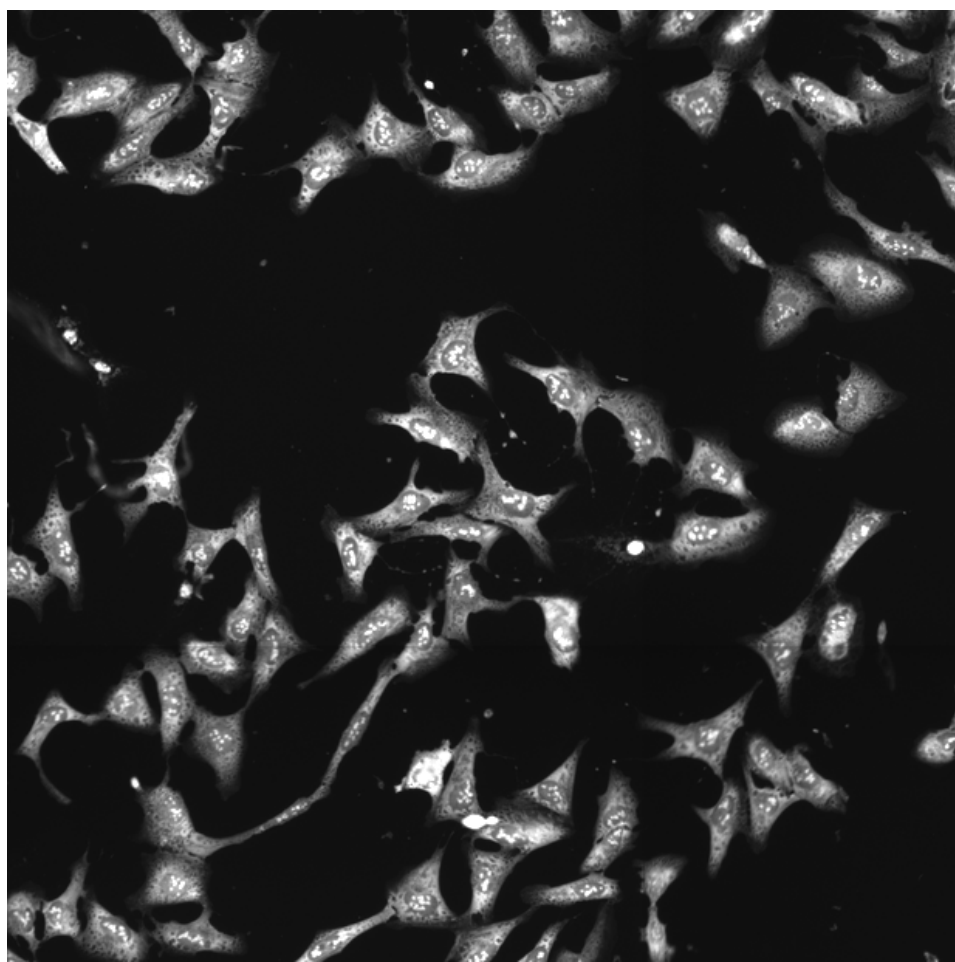
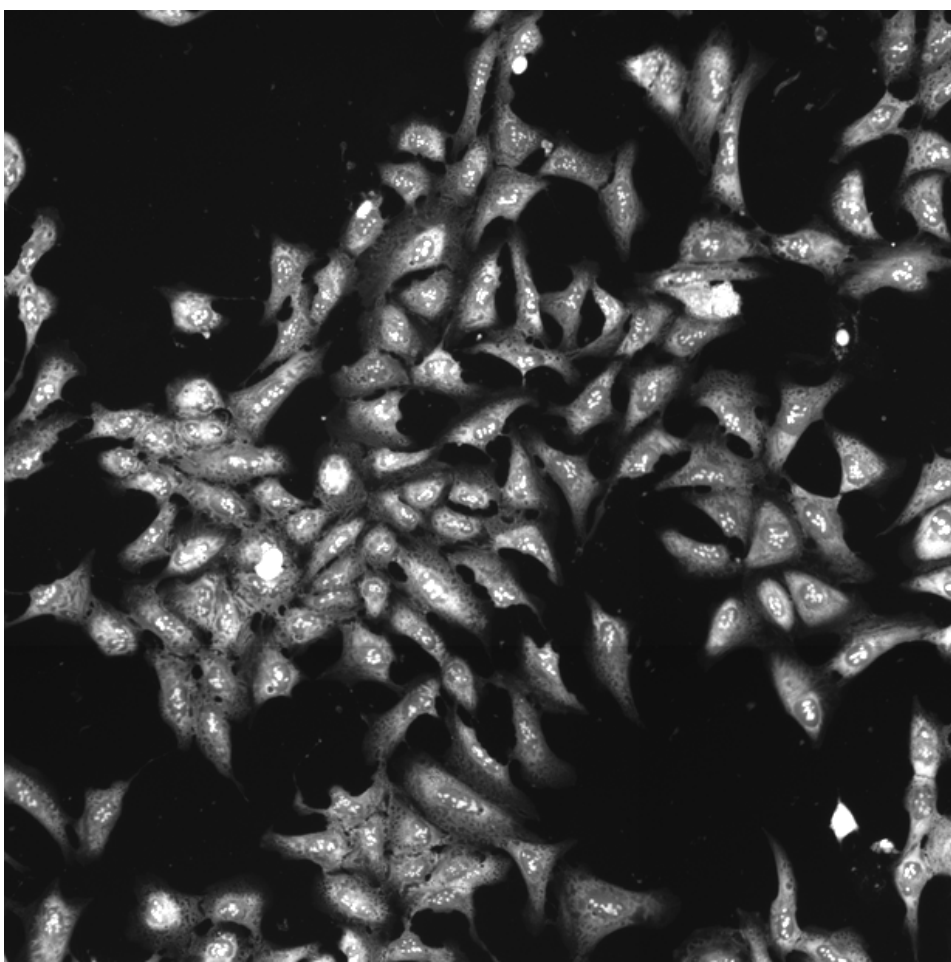
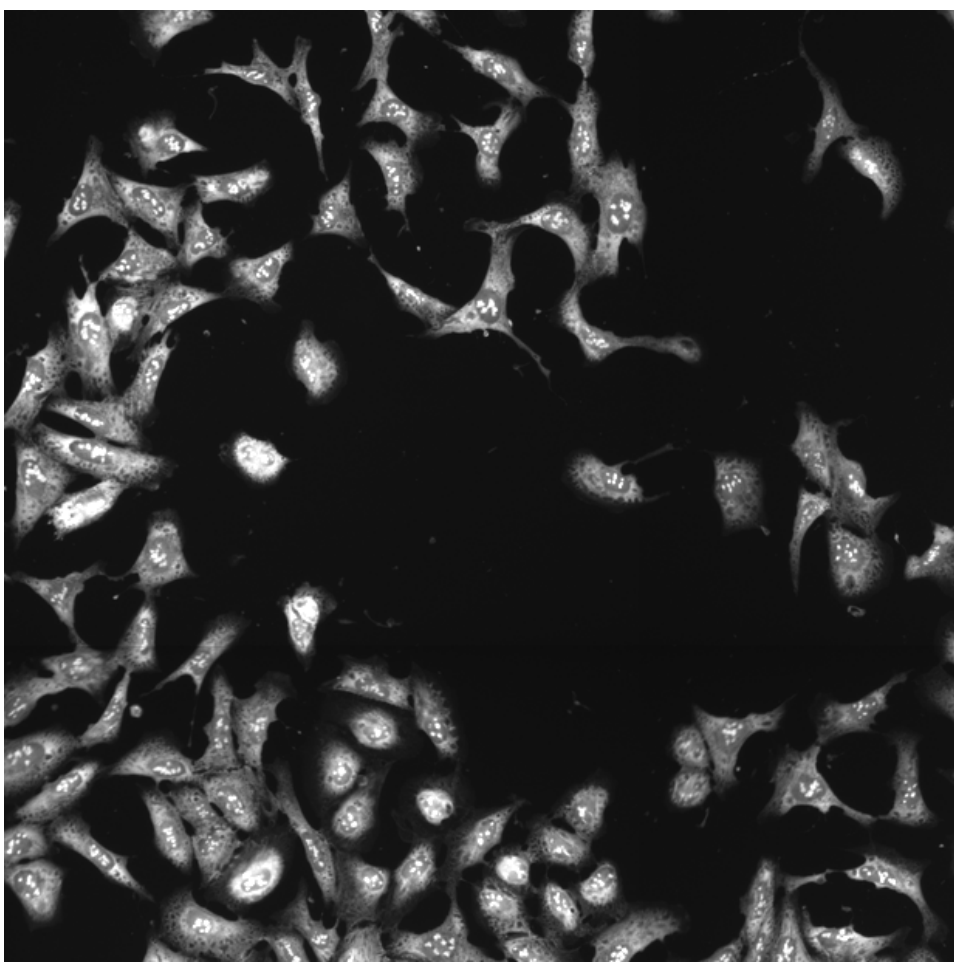
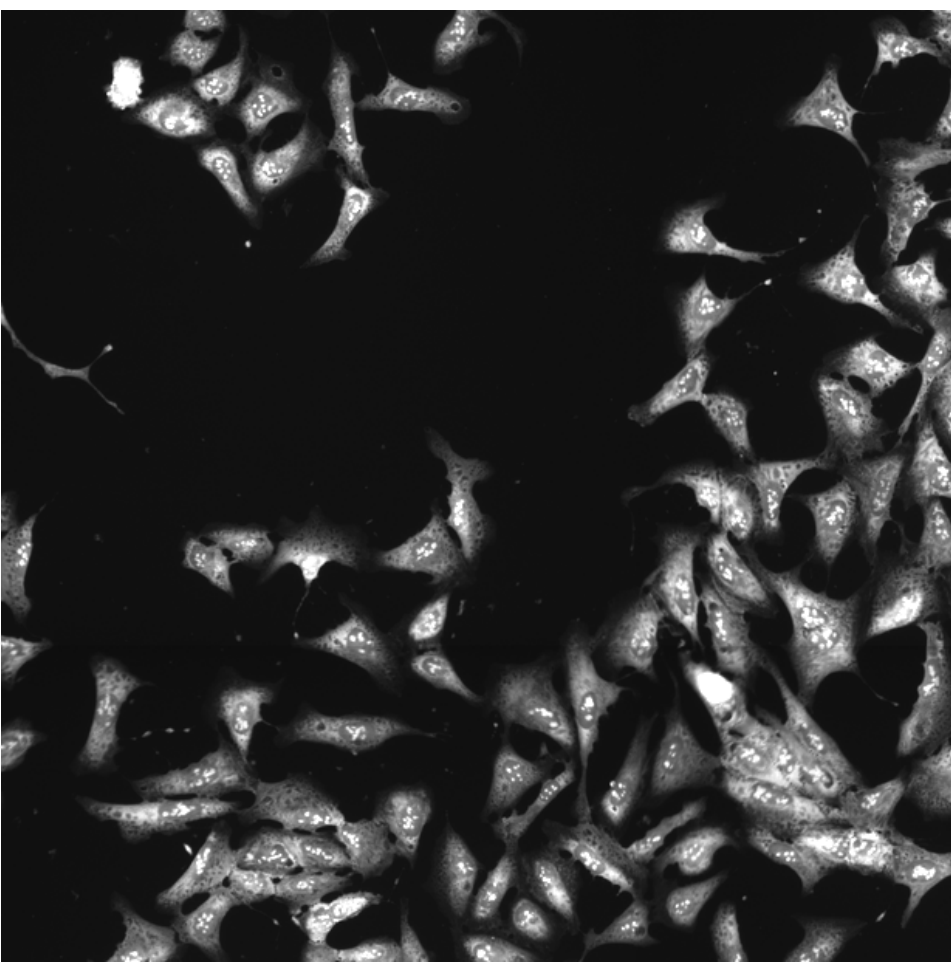
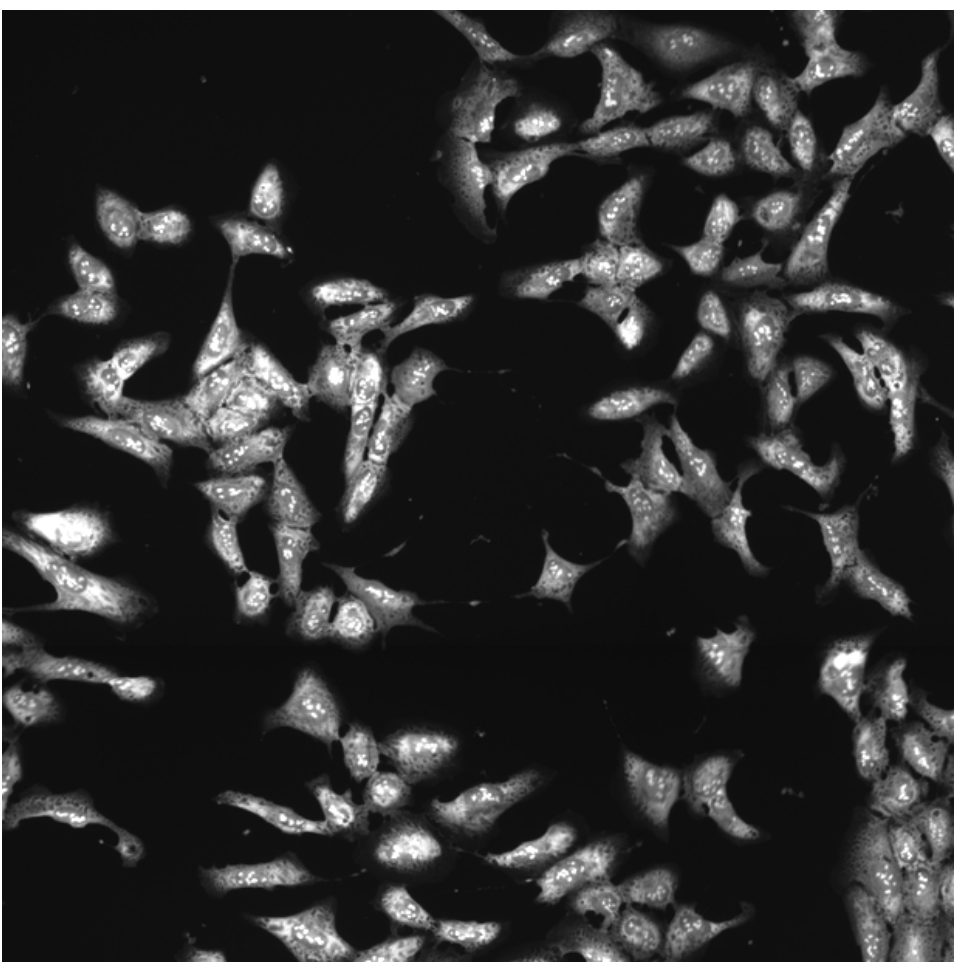
NFKB1.WT.1 (41755)

NFKB1.WT.1 (41756)

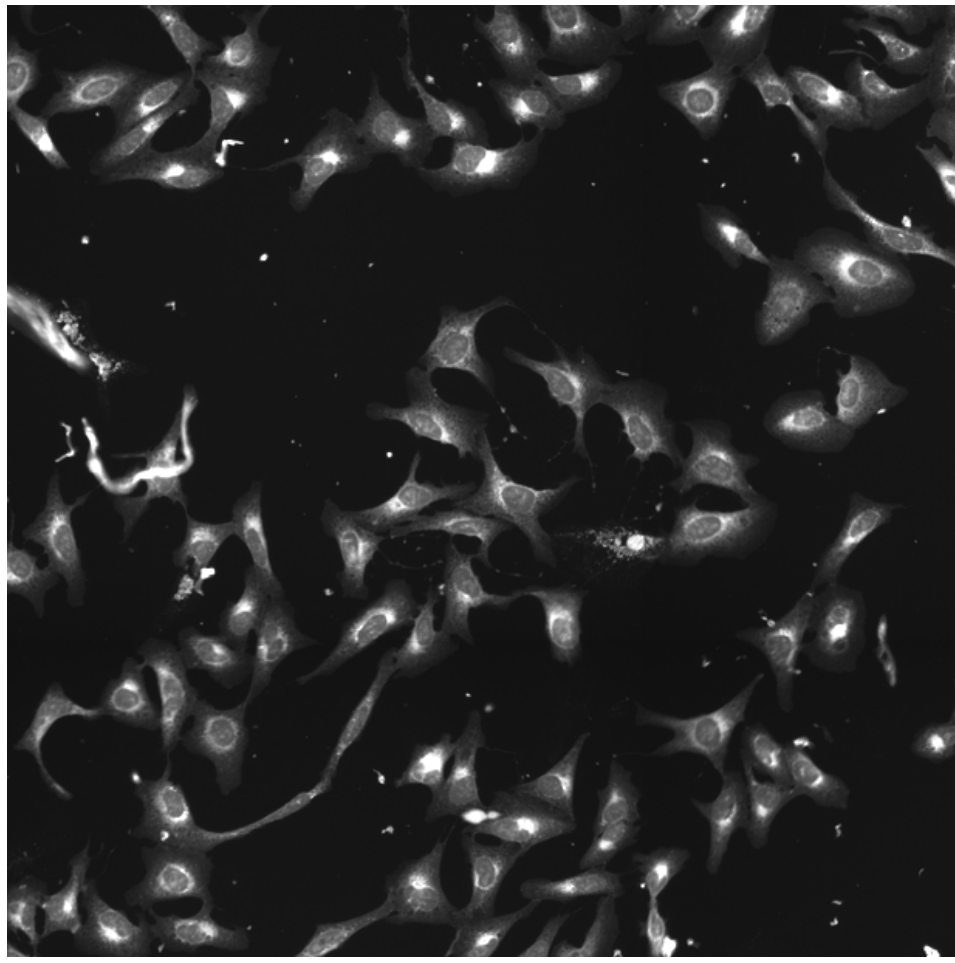
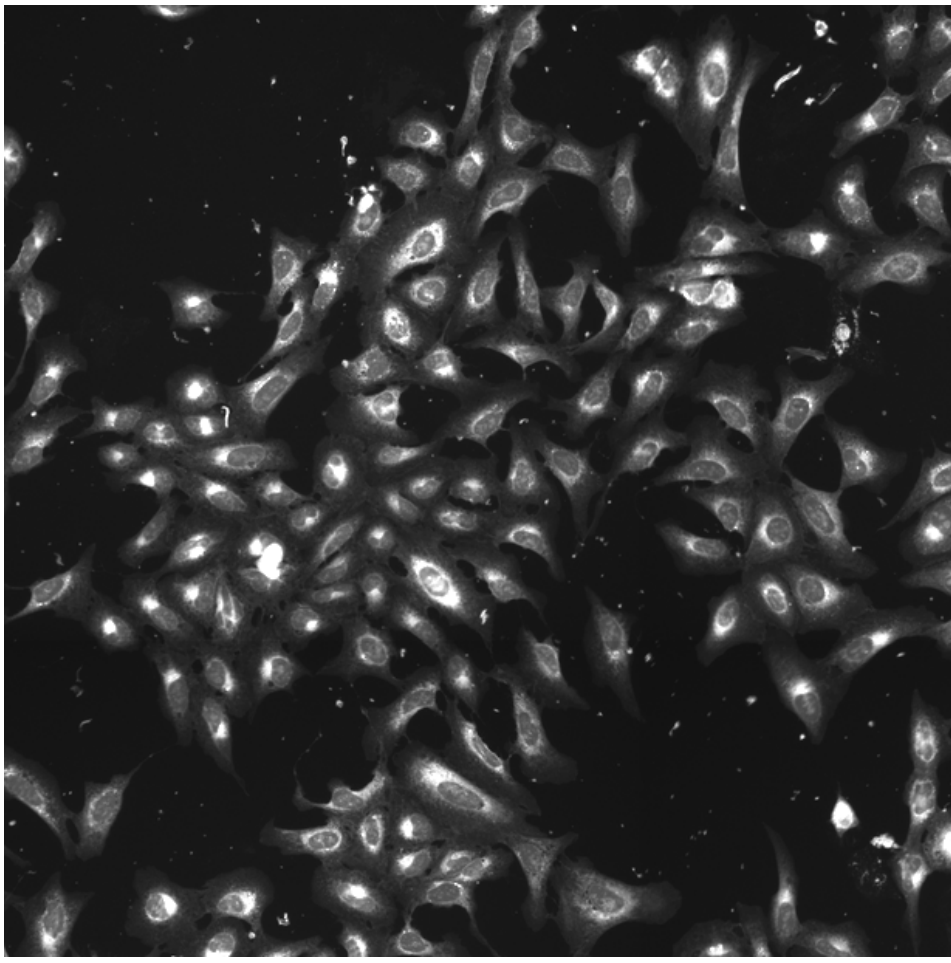
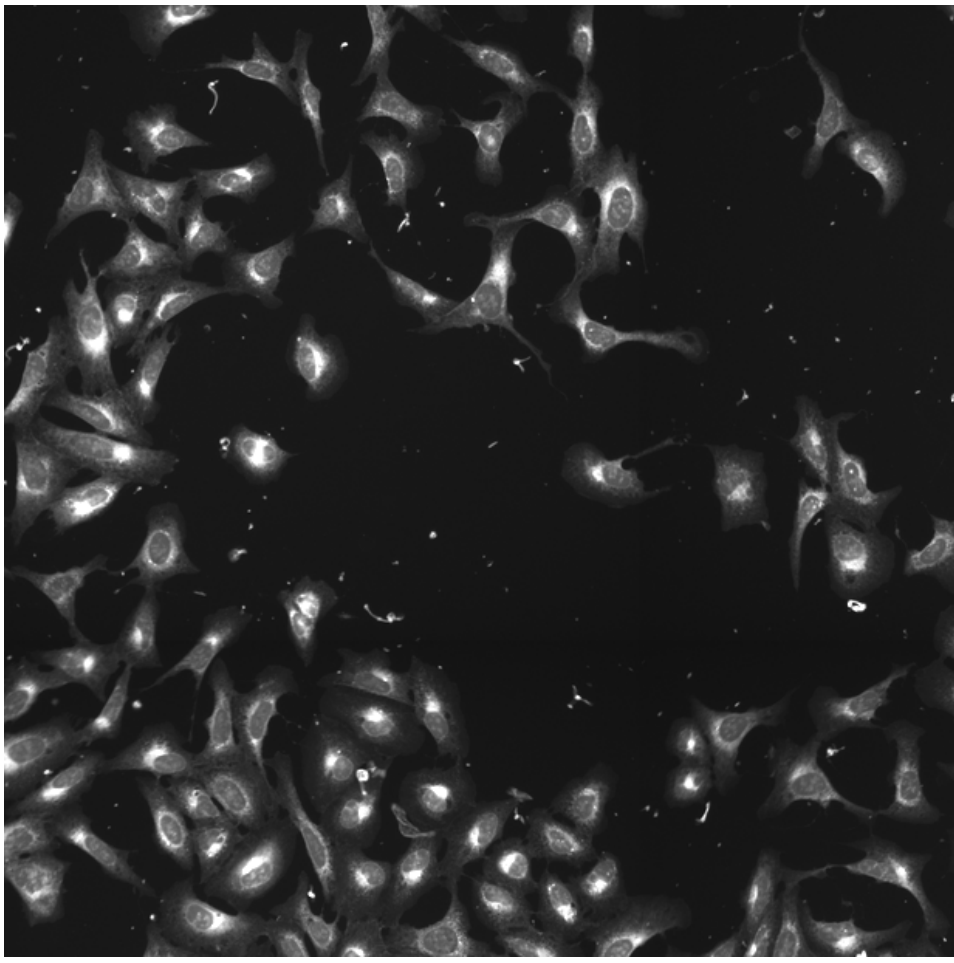
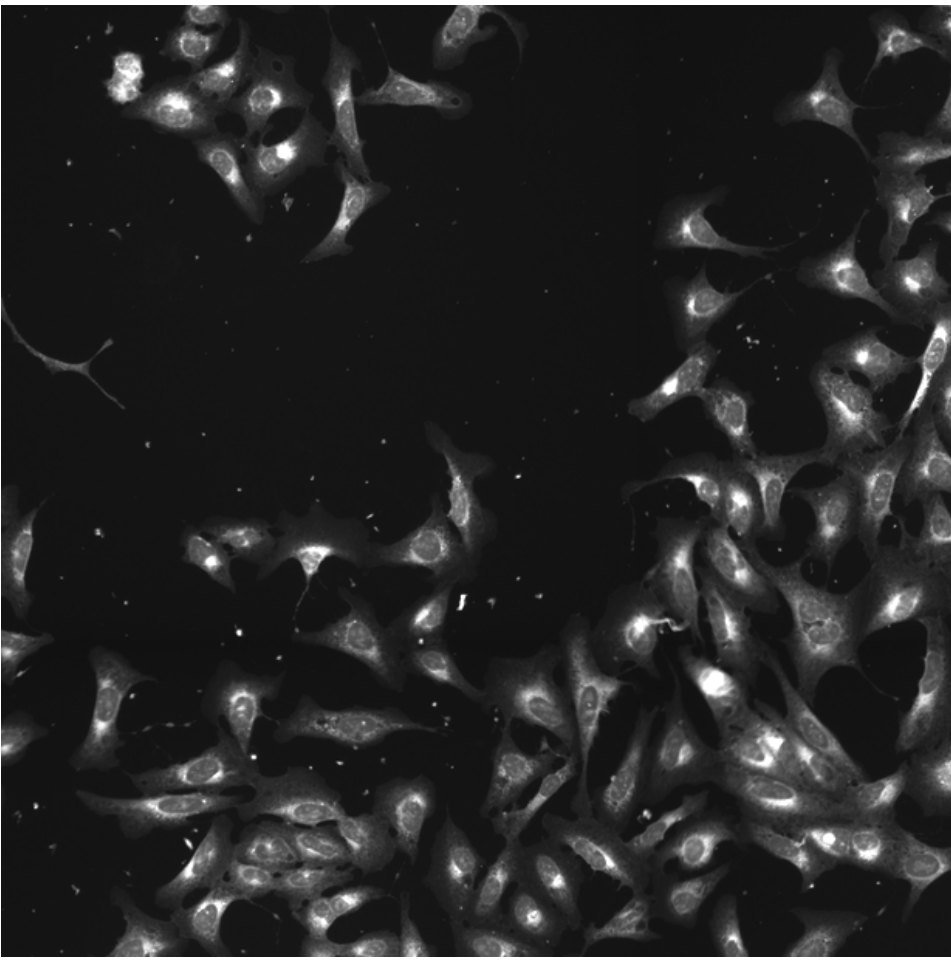
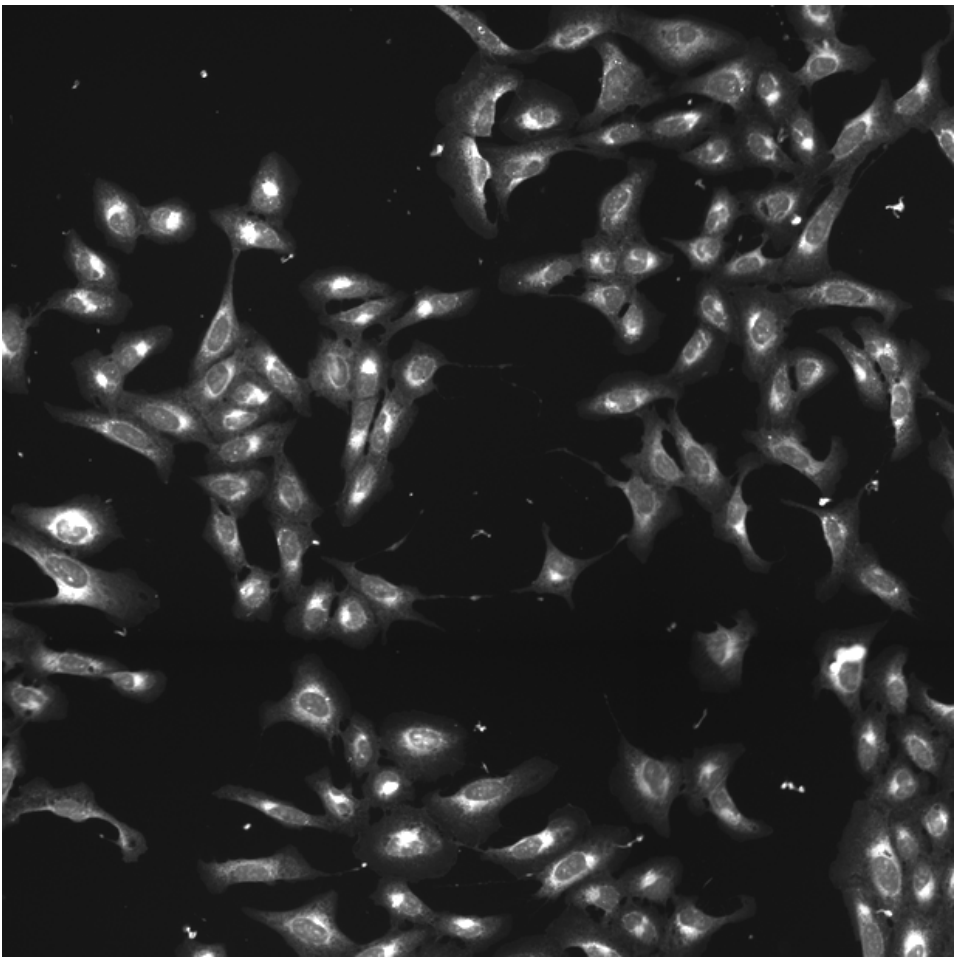
NFKB1.WT.1 (41757)

NFKB1.WT.1 (41754)

RNA

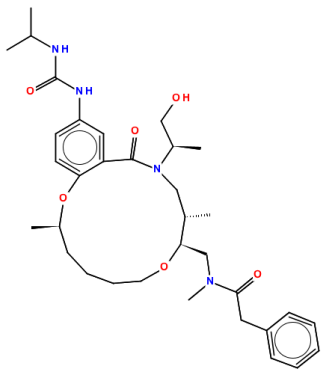
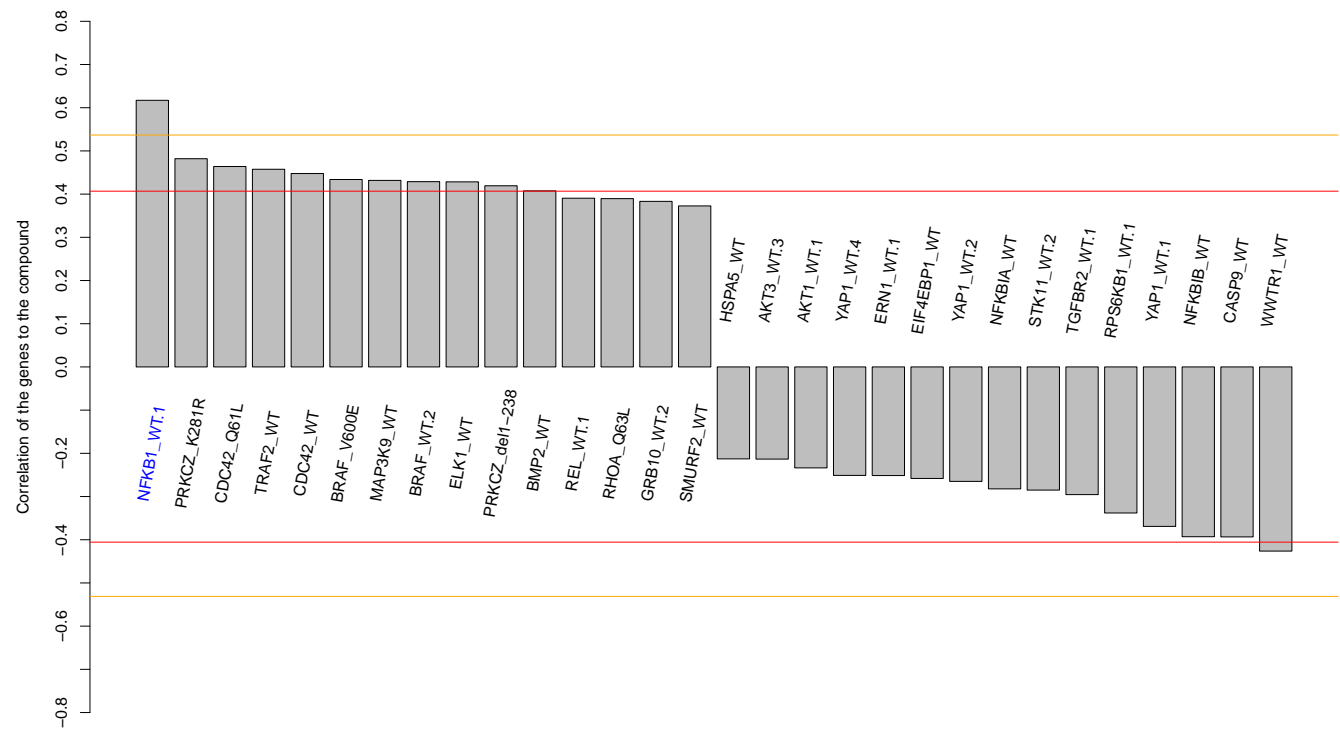
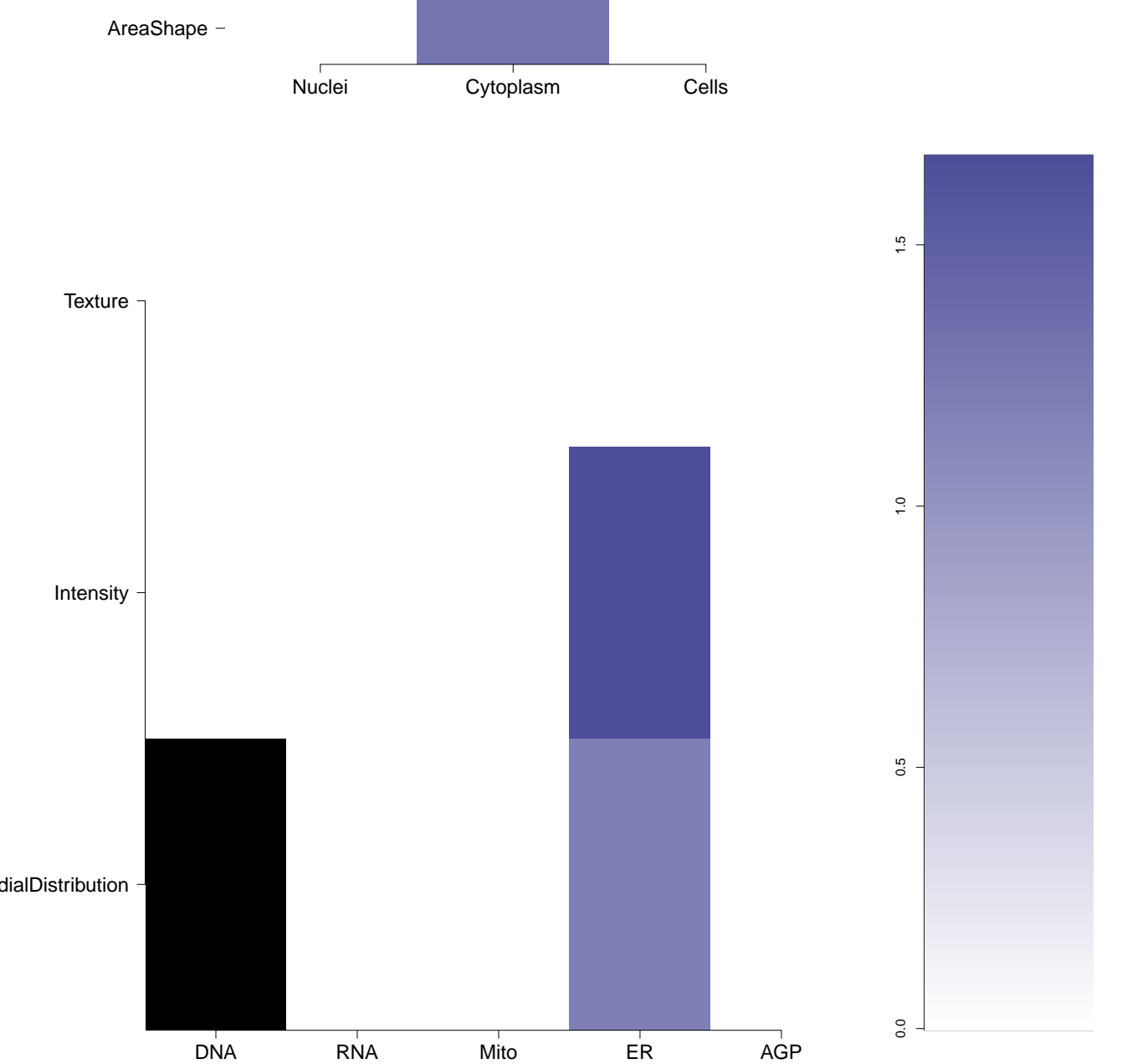
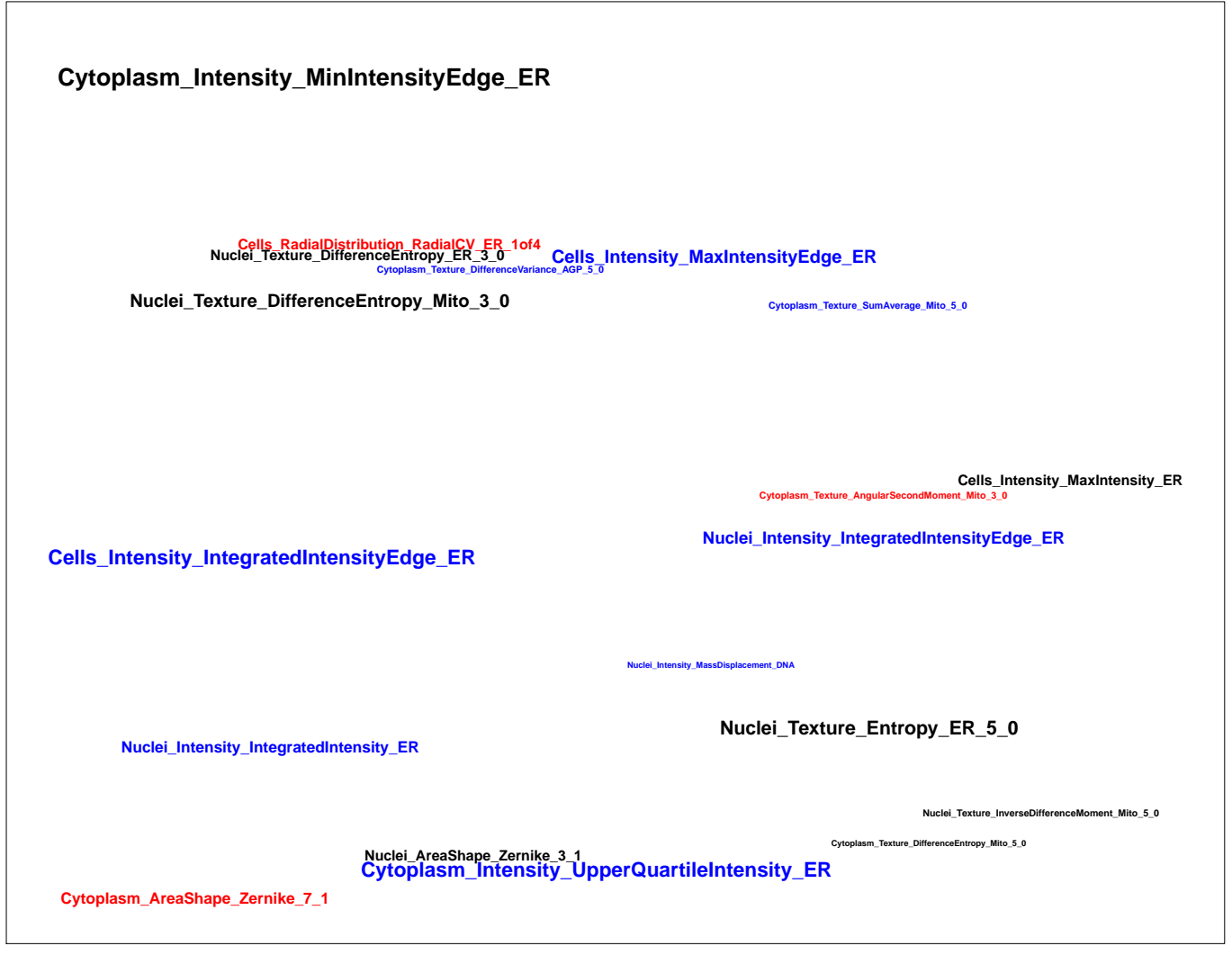
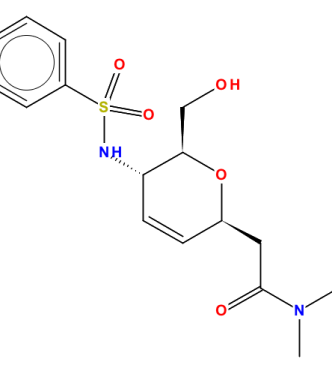
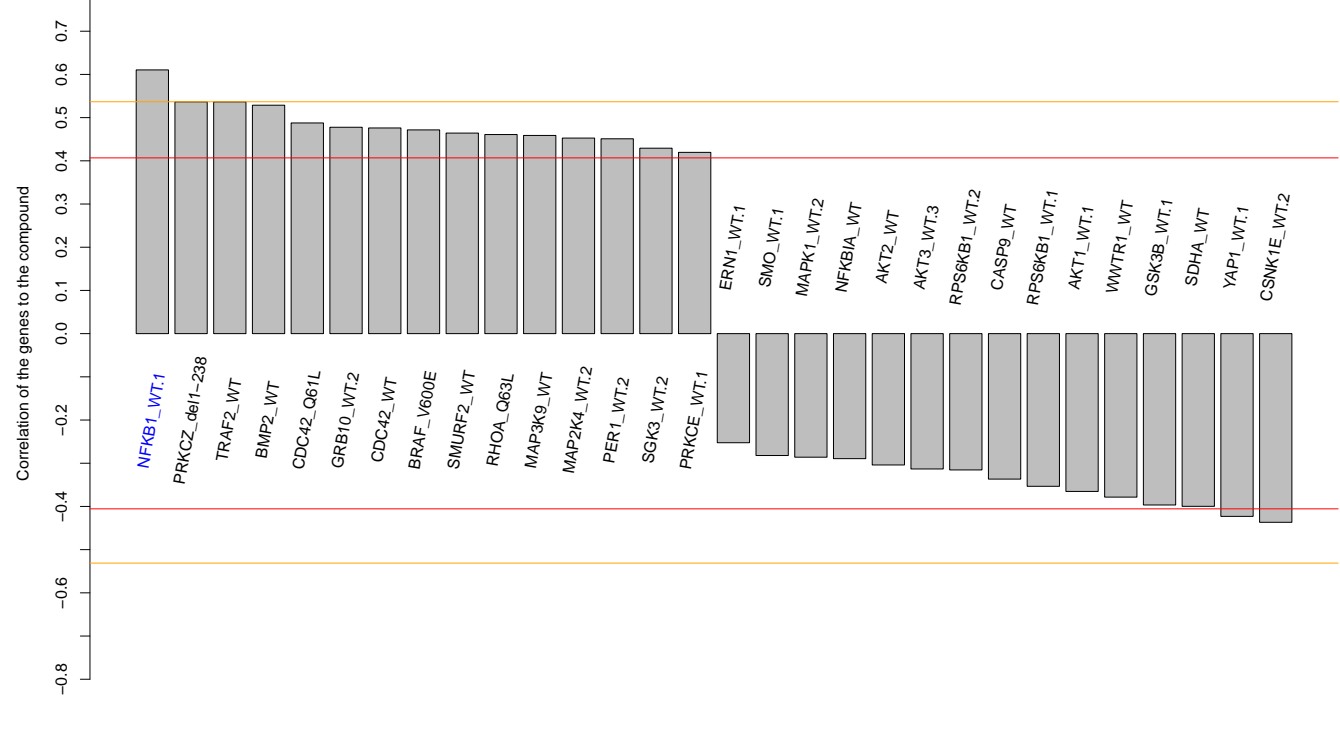
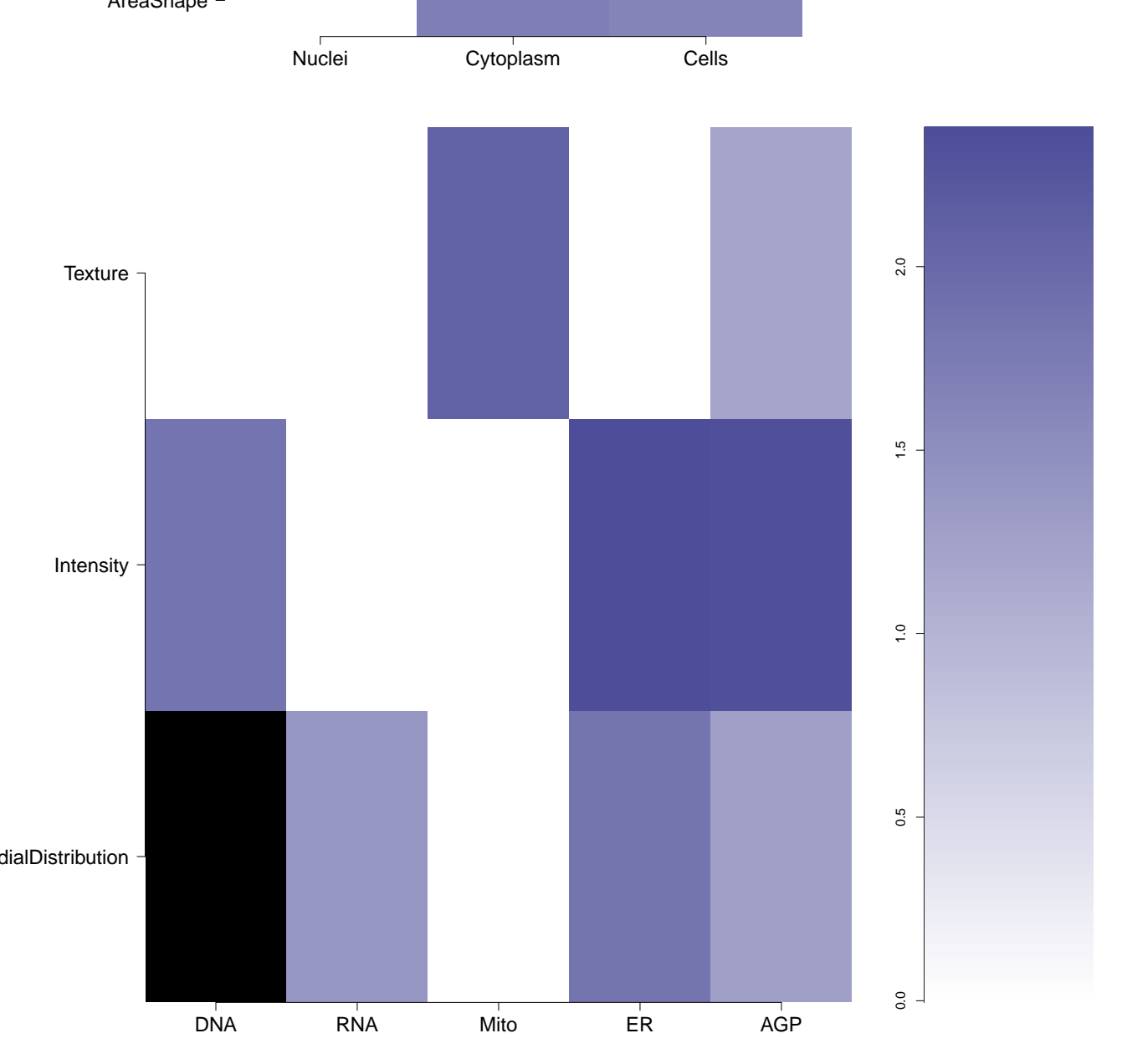

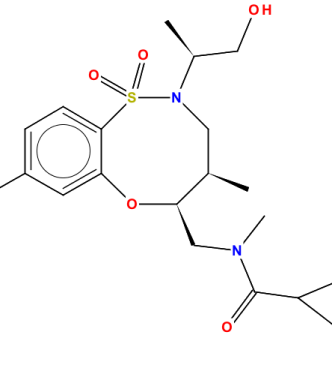
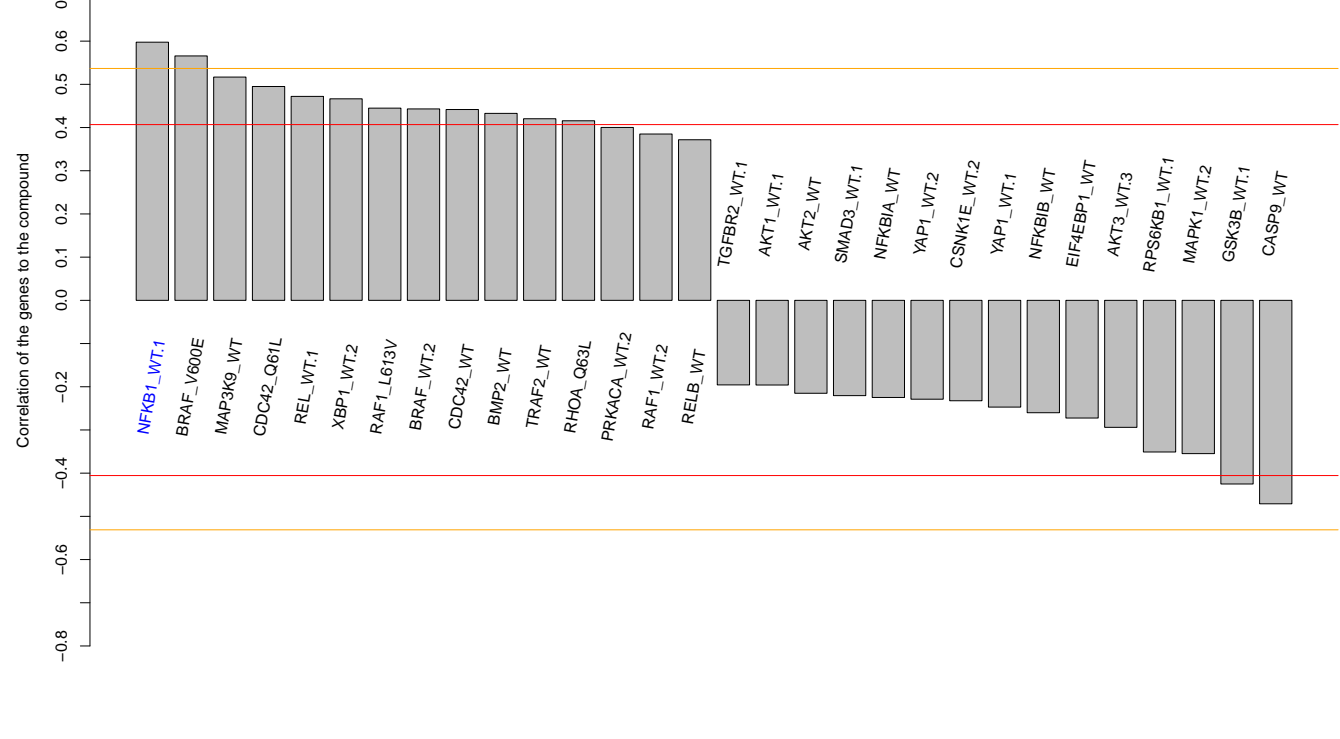
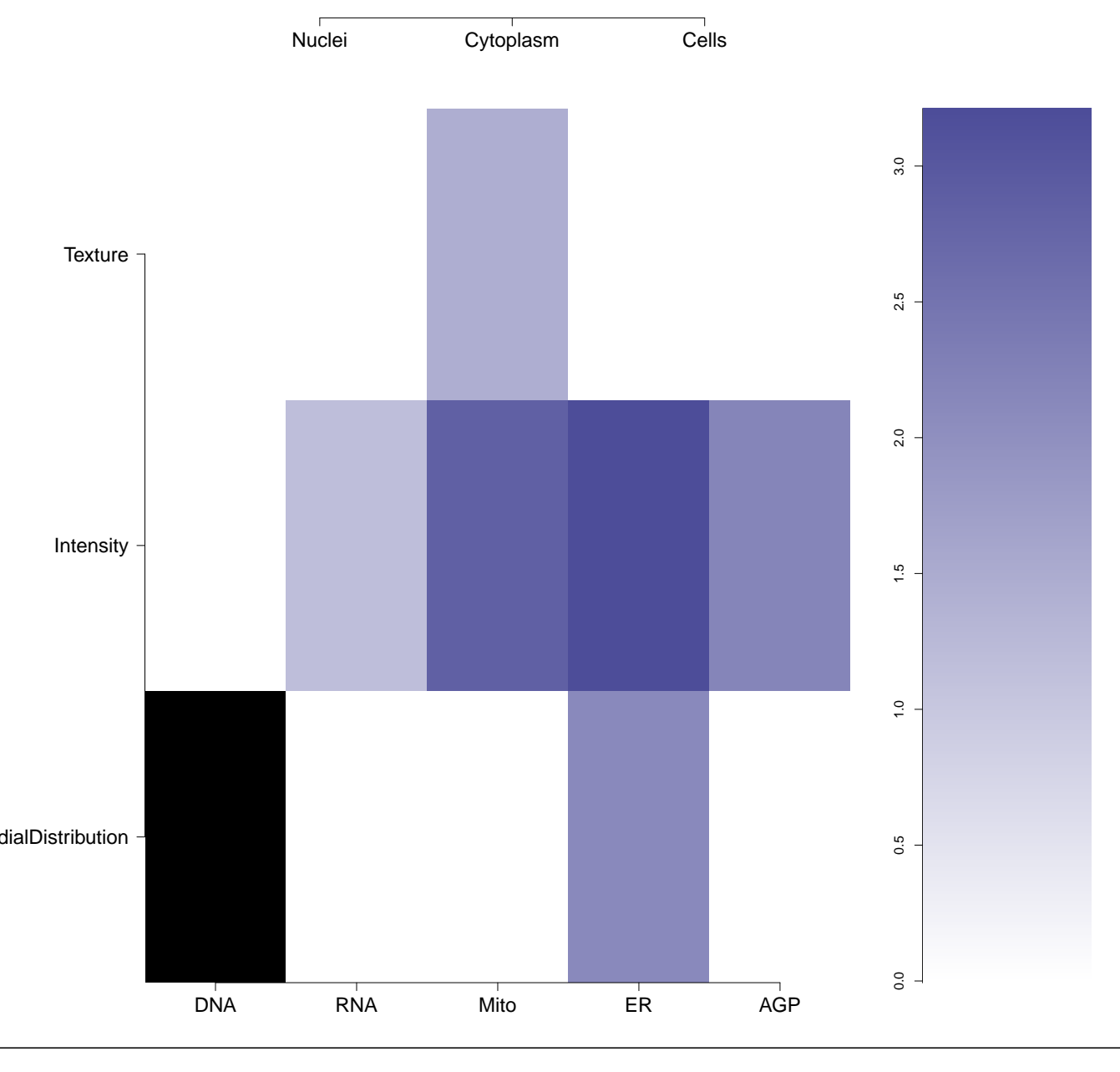

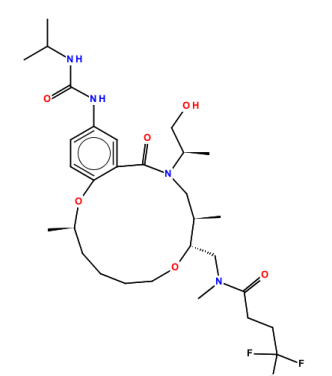
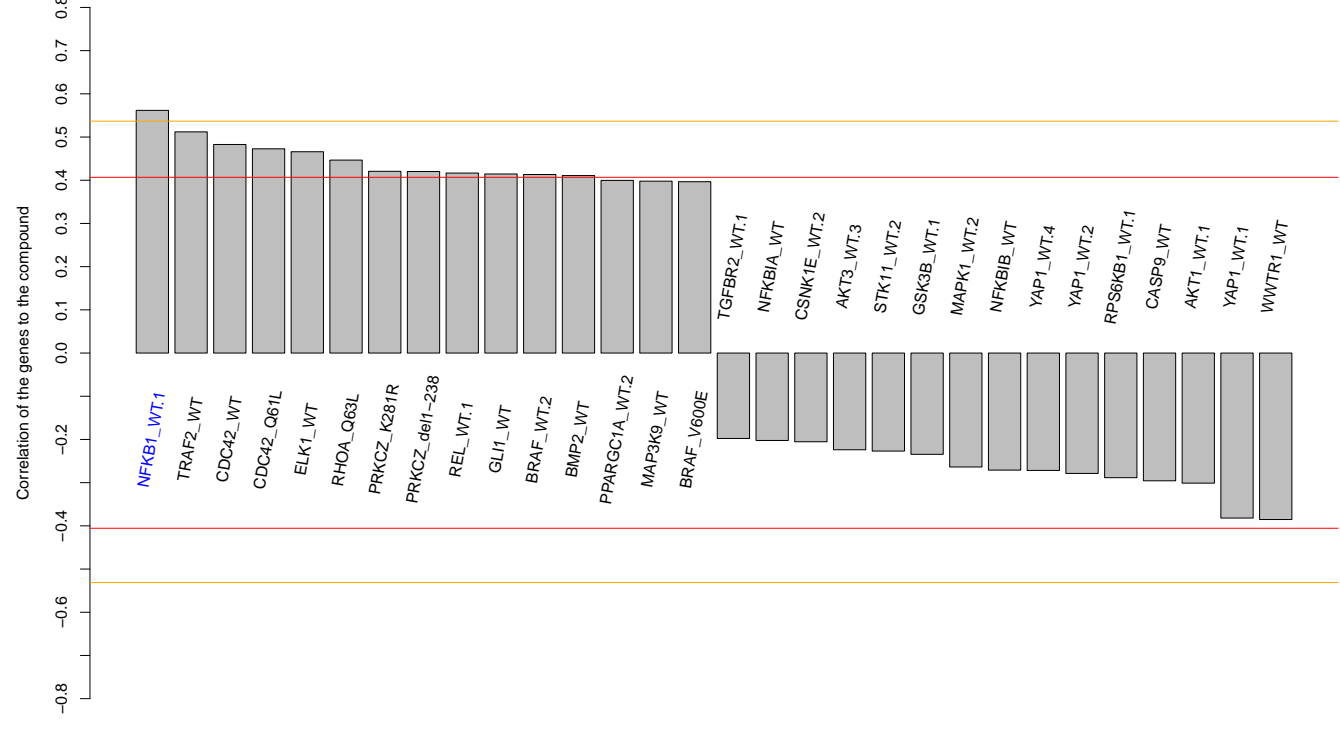
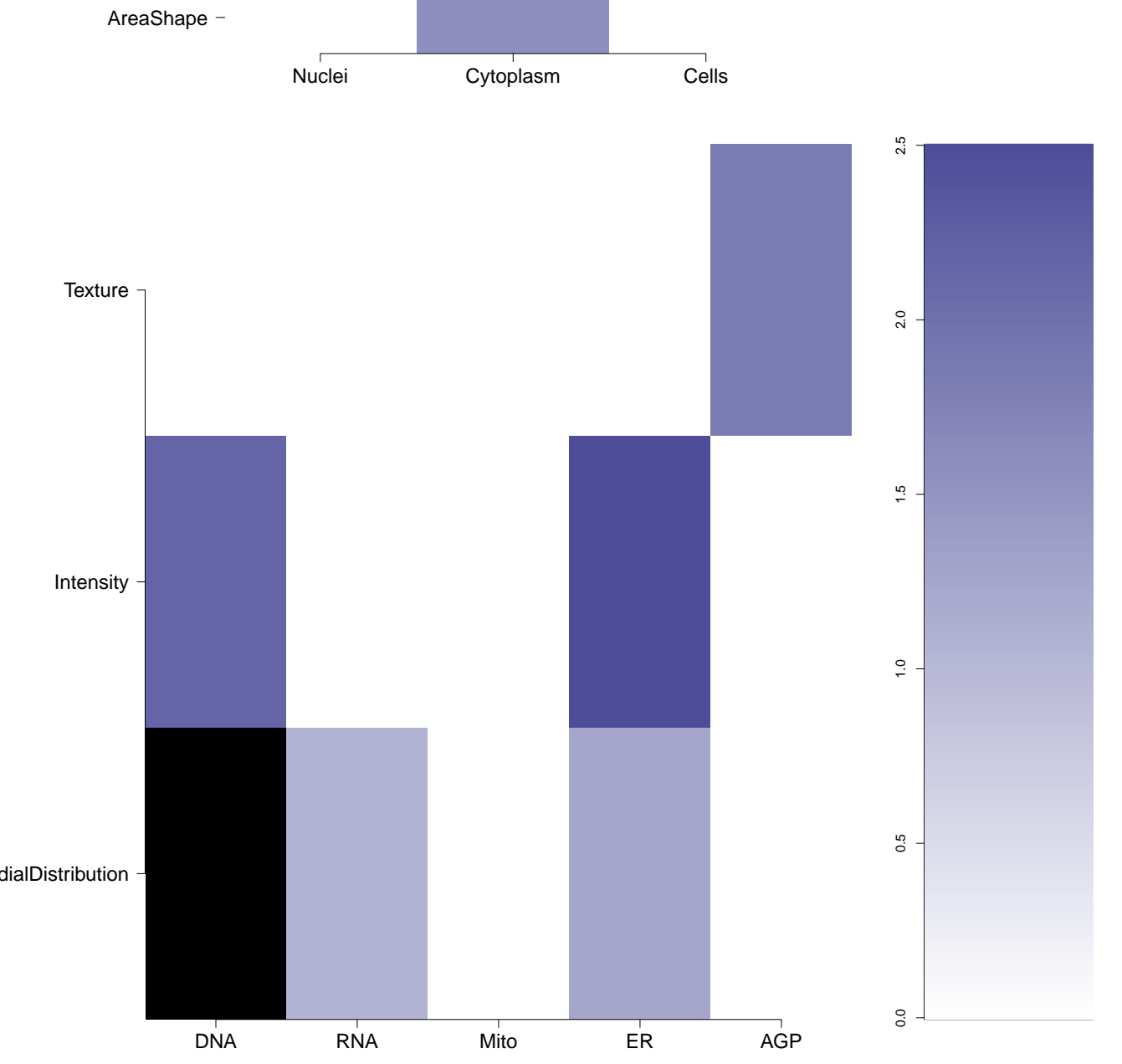
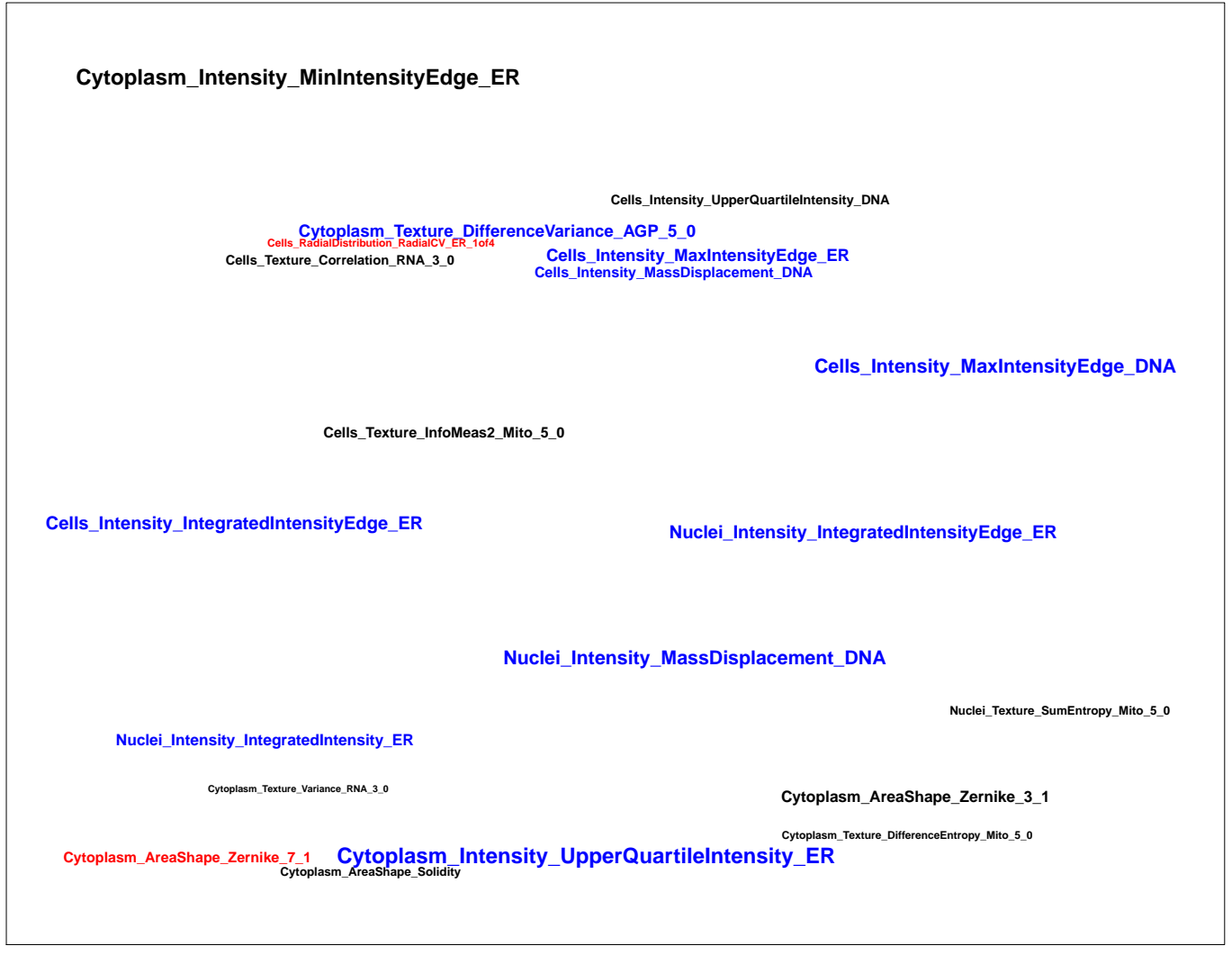
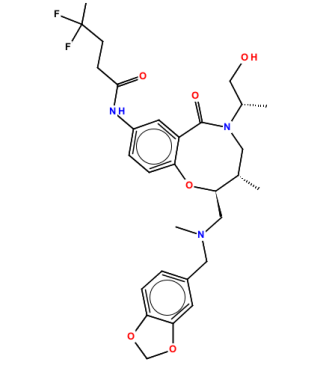
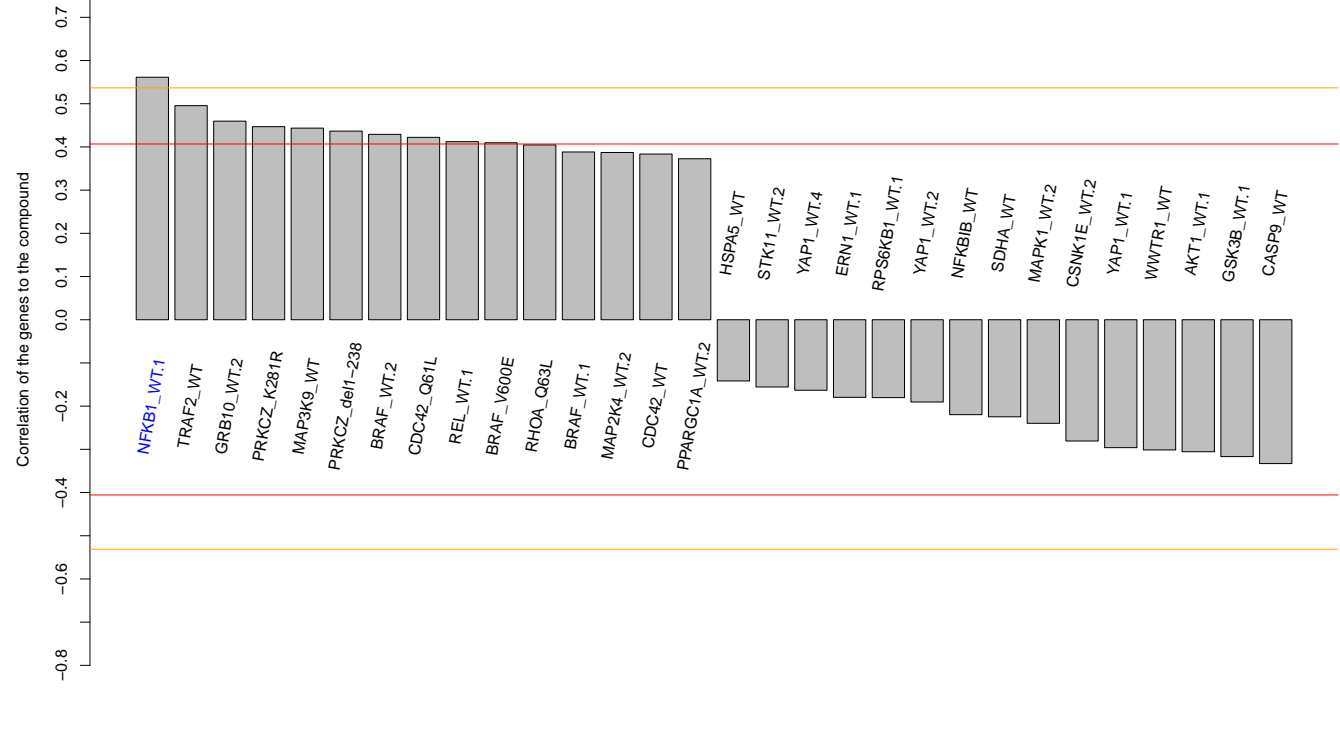
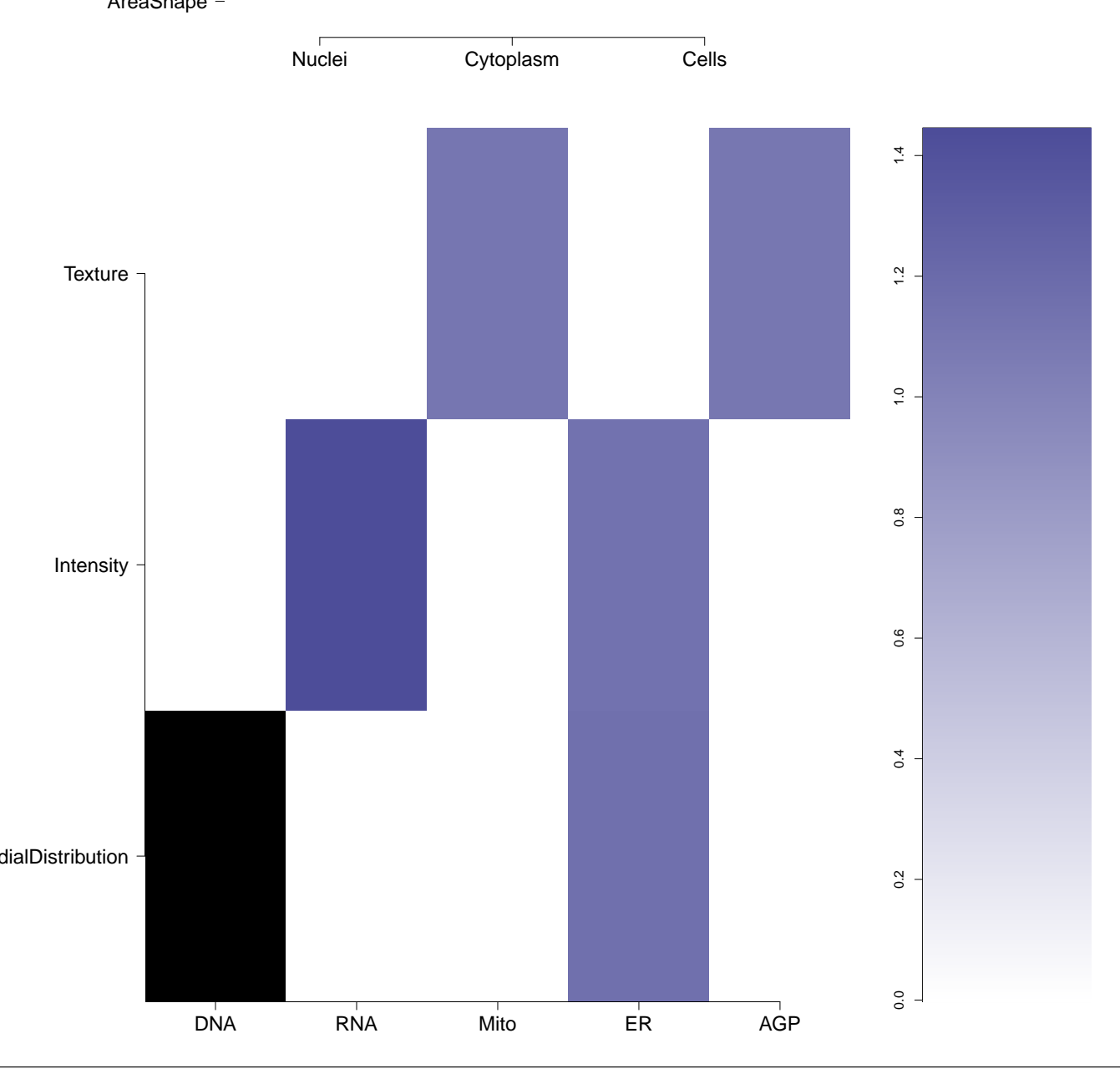
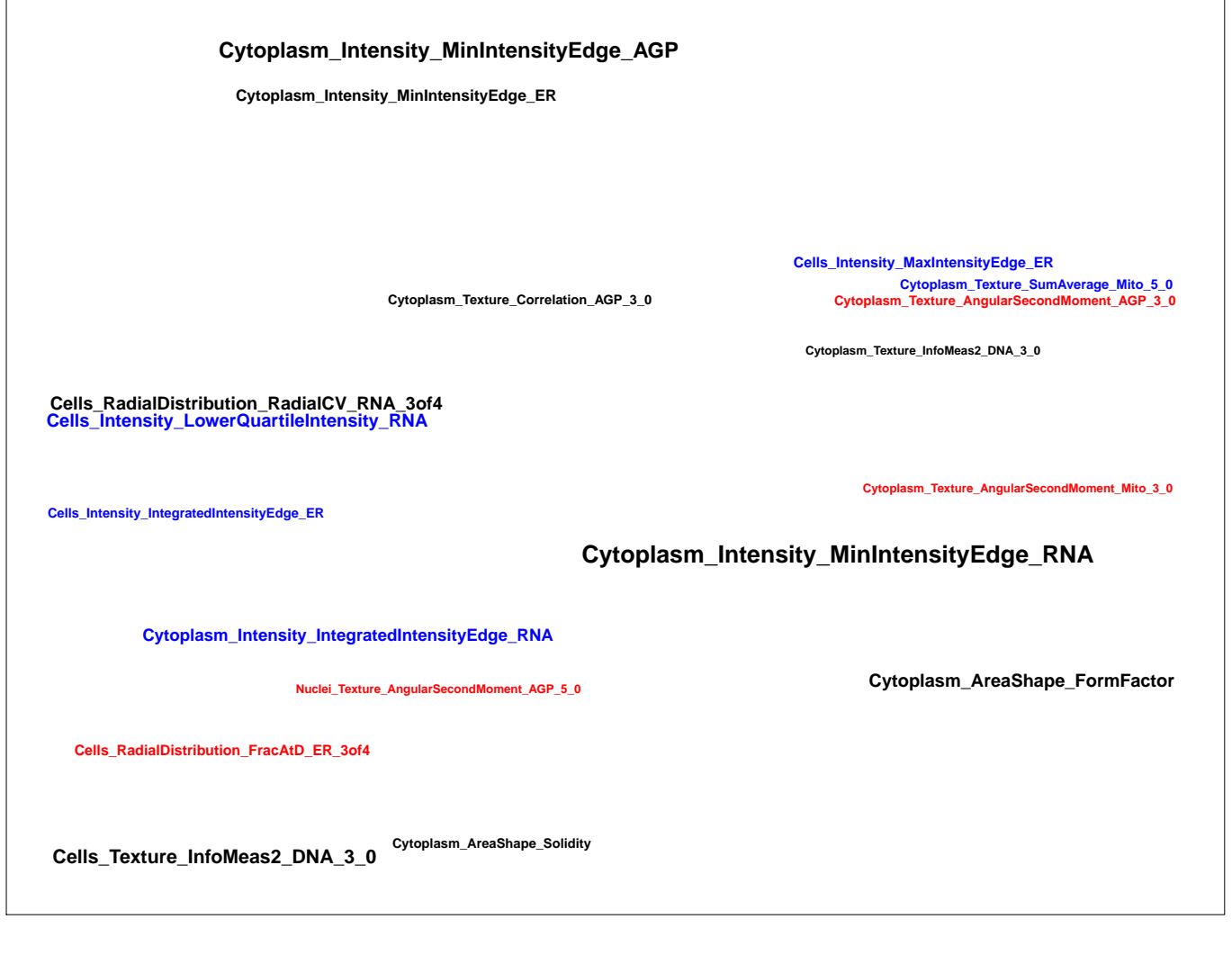
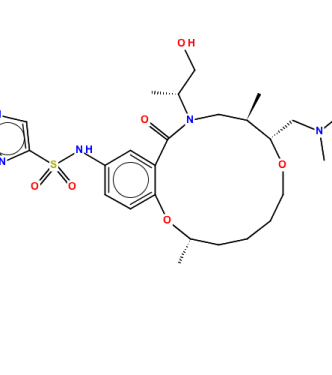
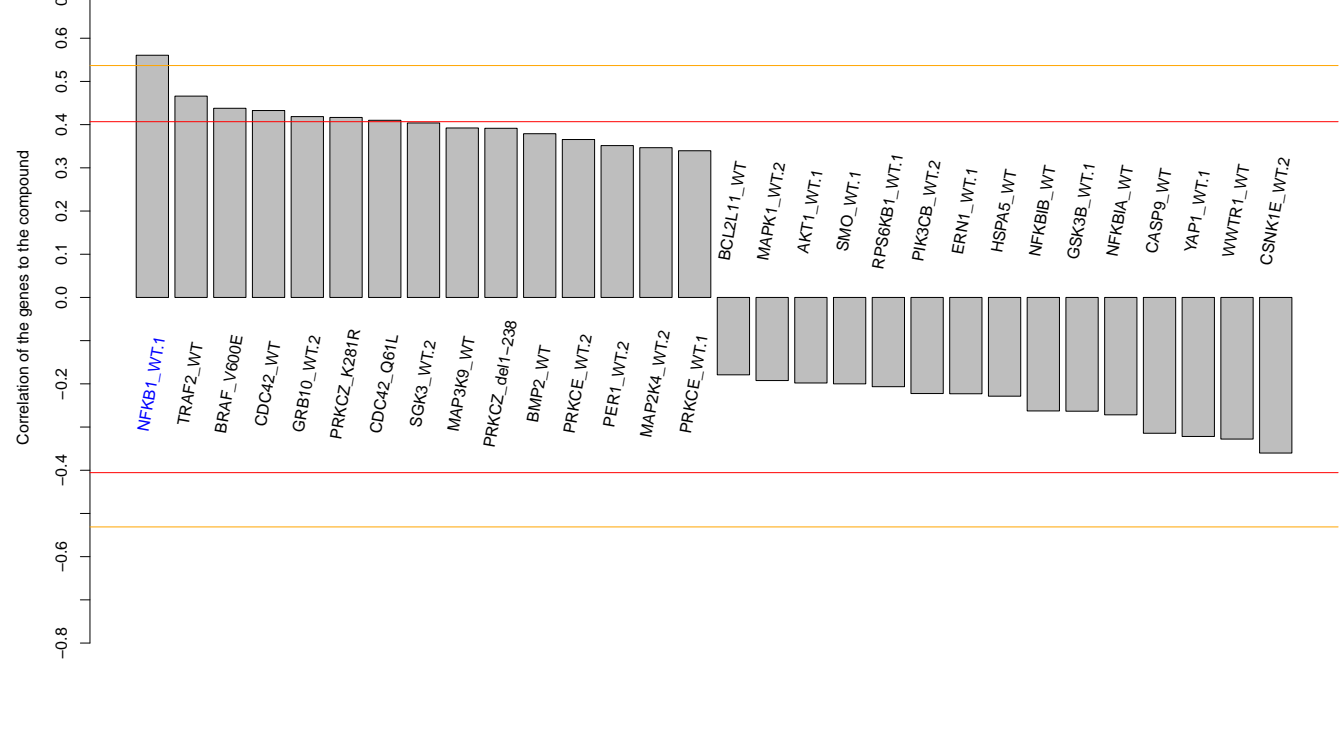
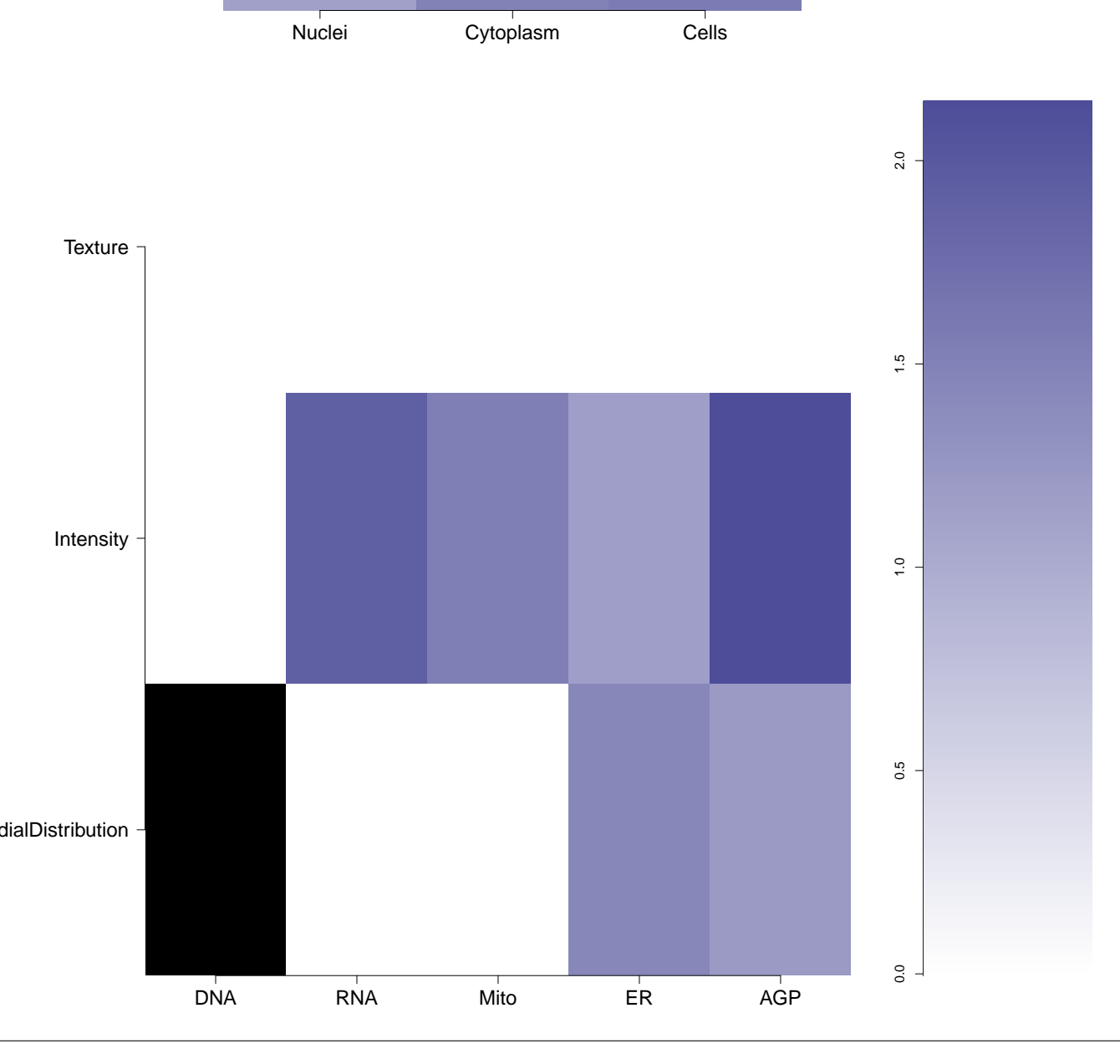



ER



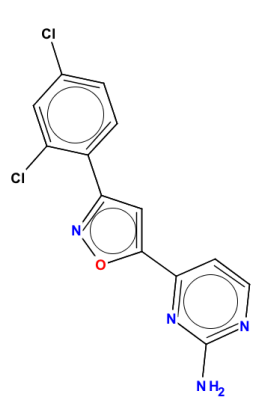
Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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-K77983109-001-01-8 PubChem CID : 44490239		0.62 (in 4 replicates)	0.62	NA				Total number of assays tested in: 50.
BRD-K83484928-001-01-8 PubChem CID : 54641192		NA (in 1 replicates)	0.61	NA				Total number of assays tested in: 38.
BRD-K90519599-001-02-8 MLS003129051 SMR001833497 PubChem CID : 46904220		0.66 (in 4 replicates)	0.60	0.227				Total number of assays tested in: 216. Active in the following assays: • HTS to Find Inhibitors of Pathogenic PempHus Antibodies (AID 588358)
BRD-K79788021-001-01-4 PubChem CID : 44620098		0.66 (in 4 replicates)	0.56	NA				Total number of assays tested in: 37.
BRD-K18763924-001-01-9 PubChem CID : 44483495		0.71 (in 3 replicates)	0.56	0.142				Total number of assays tested in: 31.
BRD-K38965110-001-01-0 PubChem CID : 44490435		0.62 (in 4 replicates)	0.56	NA				Total number of assays tested in: 48. Active in the following assays: • 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)



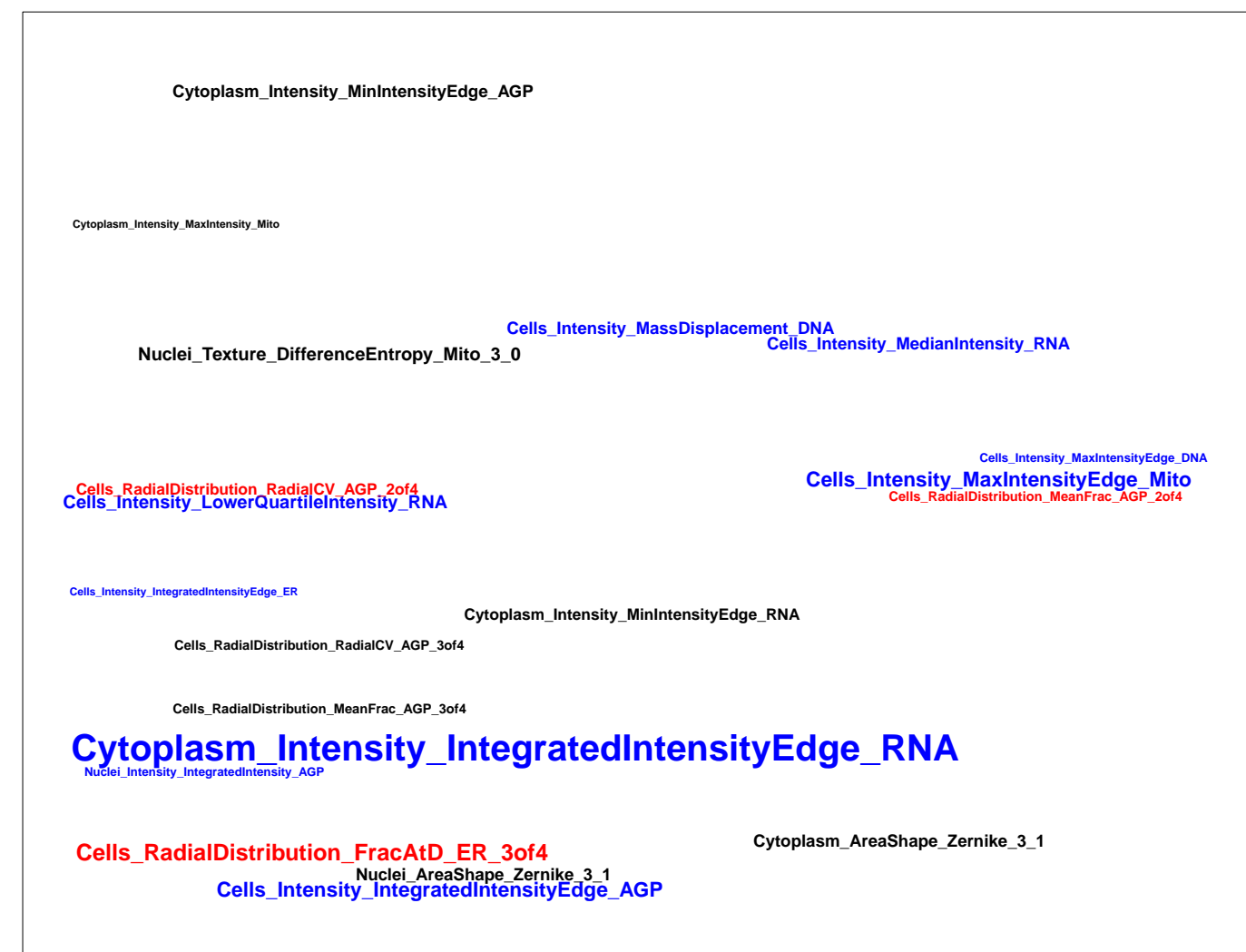
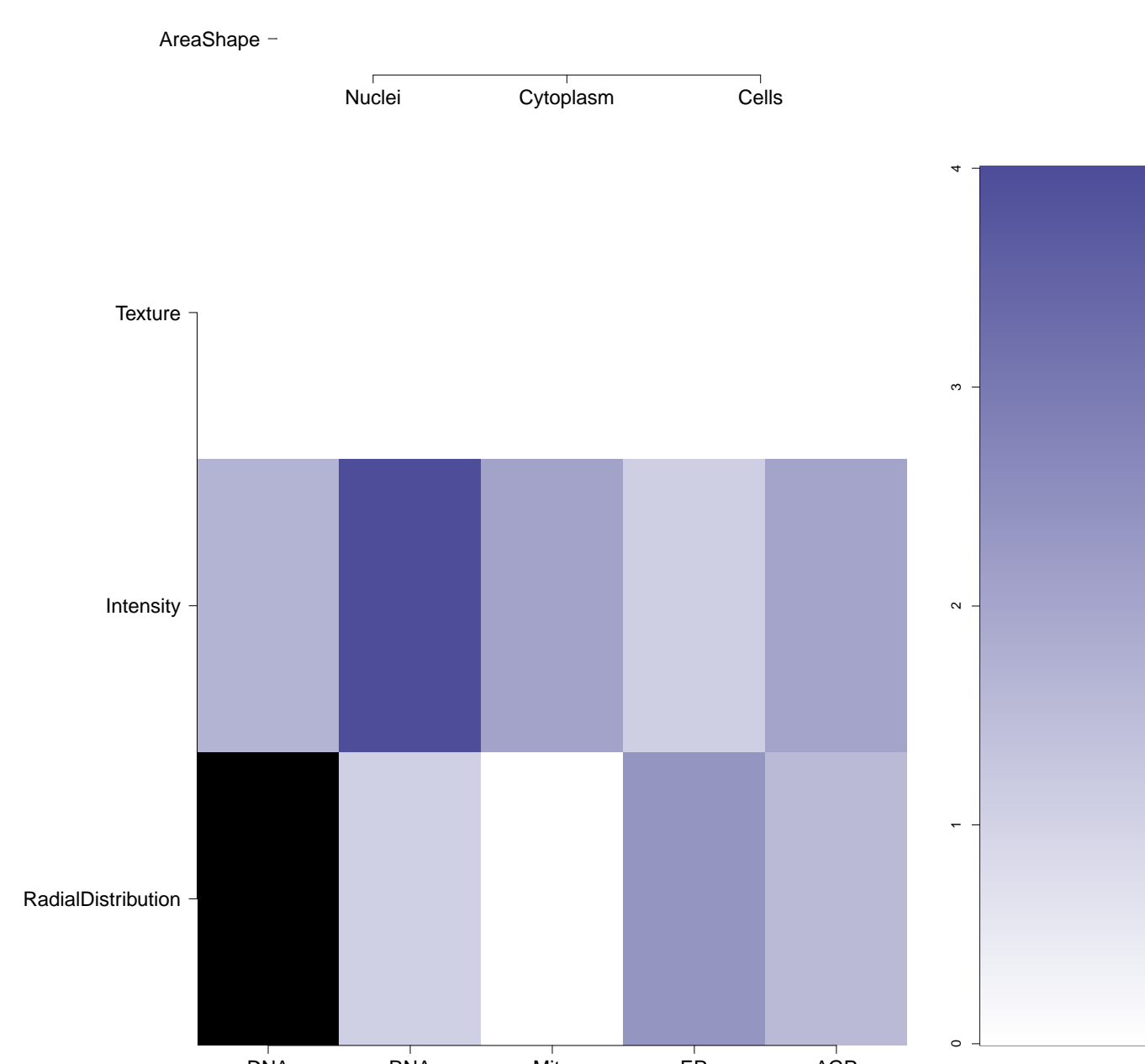
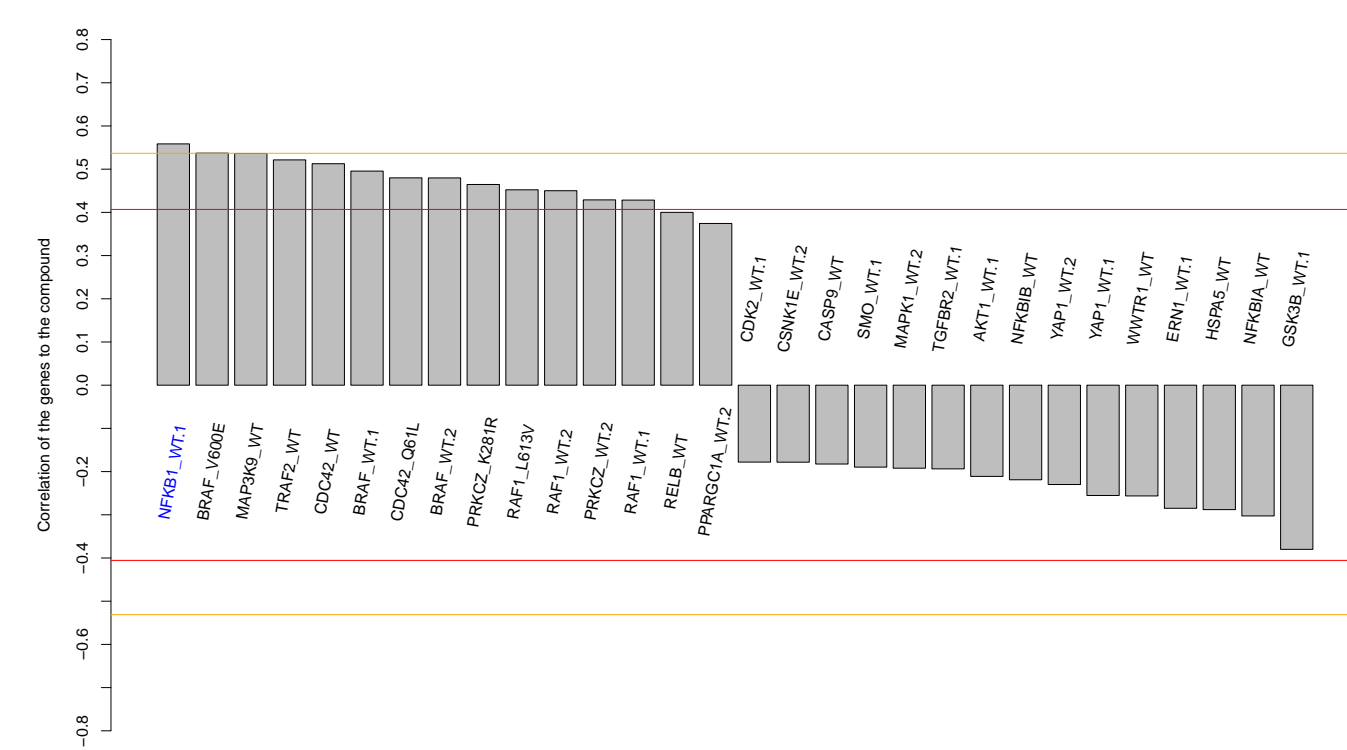
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HE019138  
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NA (in 1 replicates)

0.56

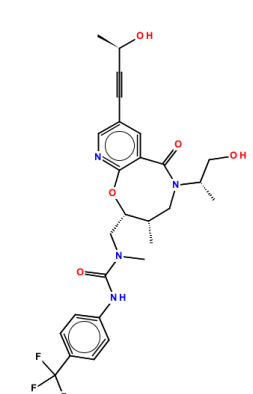
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Total number of assays tested in: 585. Active in the following assays:

- Primary Cell-based High Throughput Screening Assay for Inhibitors of West Nile Degradation (AID 13231)
- Cycloheximide CounterScreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)
- aGHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)
- HTS Luminescent assay for identification of inhibitors of Serpin-specific protease 8 (SENPS) (AID 2540)
- uHTS Luminescent assay for identification of inhibitors of Serpin-specific protease 6 (SENP6) (AID 2599)
- uHTS Luminescent assay for identification of inhibitors of Serpin-specific protease 7 (SENP7) (AID 434973)
- qHTS Assay for RalG1 Promoter Activators (AID 485297)
- qHTS Assay for NPC1 Promoter Activators (AID 485313)
- Single concentration confirmation of uHTS for inhibitors of Serpin-specific protease 8 (SENP8) using a Luminescent assay (AID 488912)
- Single concentration confirmation of uHTS for inhibitors of Serpin-specific protease 6 (SENP6) using a Luminescent assay (AID 488915)
- Single concentration confirmation of uHTS for inhibitors of Serpin-specific protease 7 (SENP7) using a Luminescent assay (AID 488917)
- Single concentration confirmation of inhibitors of Serpin-specific proteases (SENPs) using a Caspase-3 Selectivity assay (AID 488918)
- Activator for the dual FosB/delta FosB homodimer Measured in Biochemical Assays Using Plate Reader - 2072-01 Activator.SinglePoint.HTS Activity (AID 49331)
- Luminescence-based primary cell-based high throughput screening assay to identify inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1) (AID 504766)
- qHTS for inhibitors of binding or entry into cells for Marburg Virus (AID 504726)
- qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km saturating concentrations (concurrent for mR-21 project) (AID 588342)
- uHTS identification of cystic fibrosis induced NFkB inhibitors in a fluorescence assay (AID 588850)
- uHTS identification of Caspase-8 TRAIL sensitizers in a luminescence assay (AID 624354)
- 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 to identify activators of the DAF-12 from the parasite H. contortus (hDAF-12) (AID 652067)
- Luminescence-based cell-based primary high throughput screening assay to identify activators of the DAF-12 from the parasite S. stercoralis (sDAF-12) (AID 652126)
- Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glycinis (hDAF-12) (AID 687014)
- Bursicon-induced LGR2 mediated cAMP production in LGR2/CRebF-Luciferase co-transfected HEK293 cells Inhibition (AID 720647)
- Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. glycinis (hDAF-12) (AID 743950)
- Bursicon-induced LGR2 mediated cAMP production in LGR2/CRebF-Luciferase co-transfected HEK293 cells Inhibition Measured in Cell-Based System Using Plate Reader - 7011-01 Antagonist.Dose.CherryPlick.Activity.SAT (AID 743343)
- LGR2/CounterScreen with MCR Measured in Cell-Based System Using Plate Reader - 7011-02 Antagonist.Dose.CherryPlick.Activity (AID 743444)

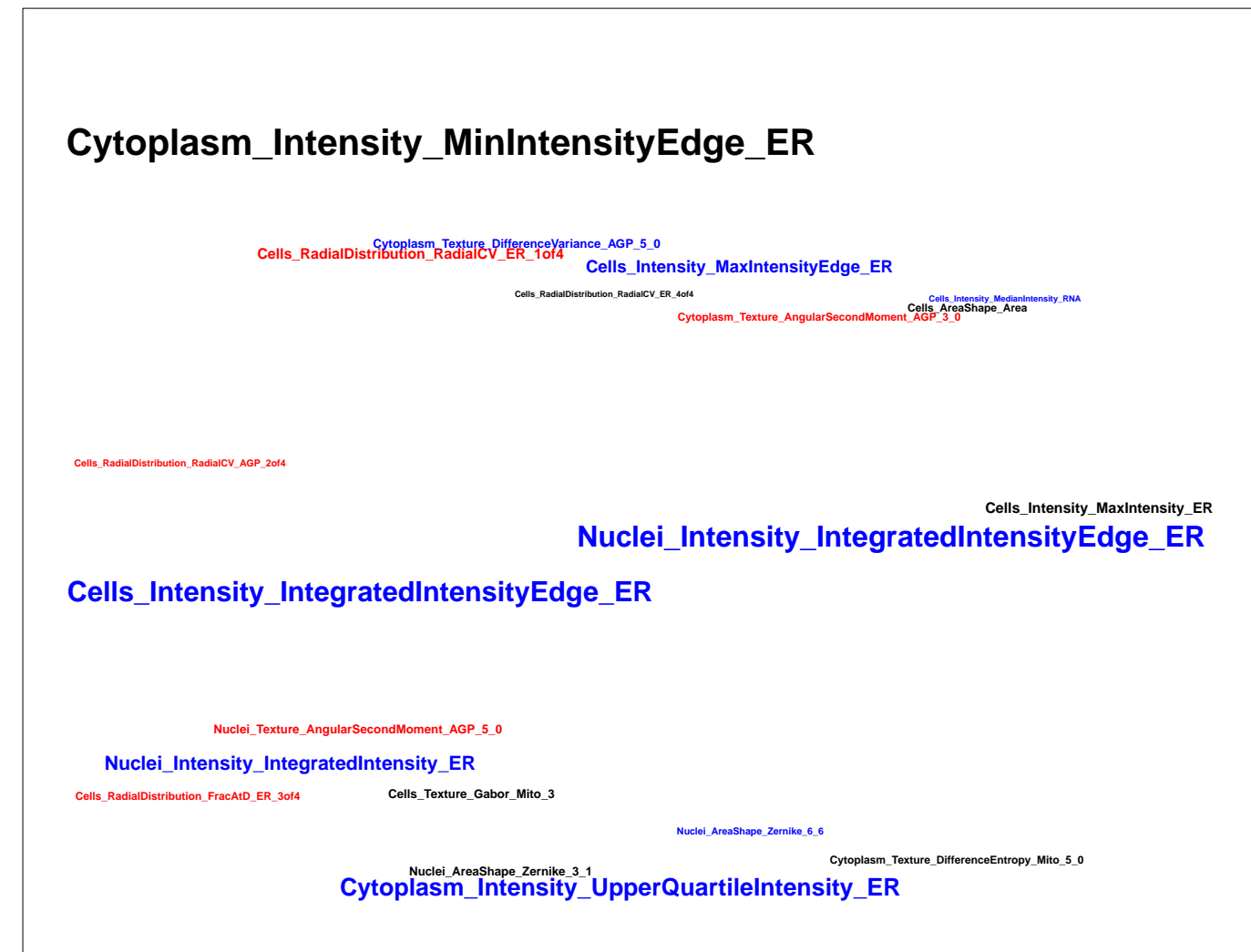
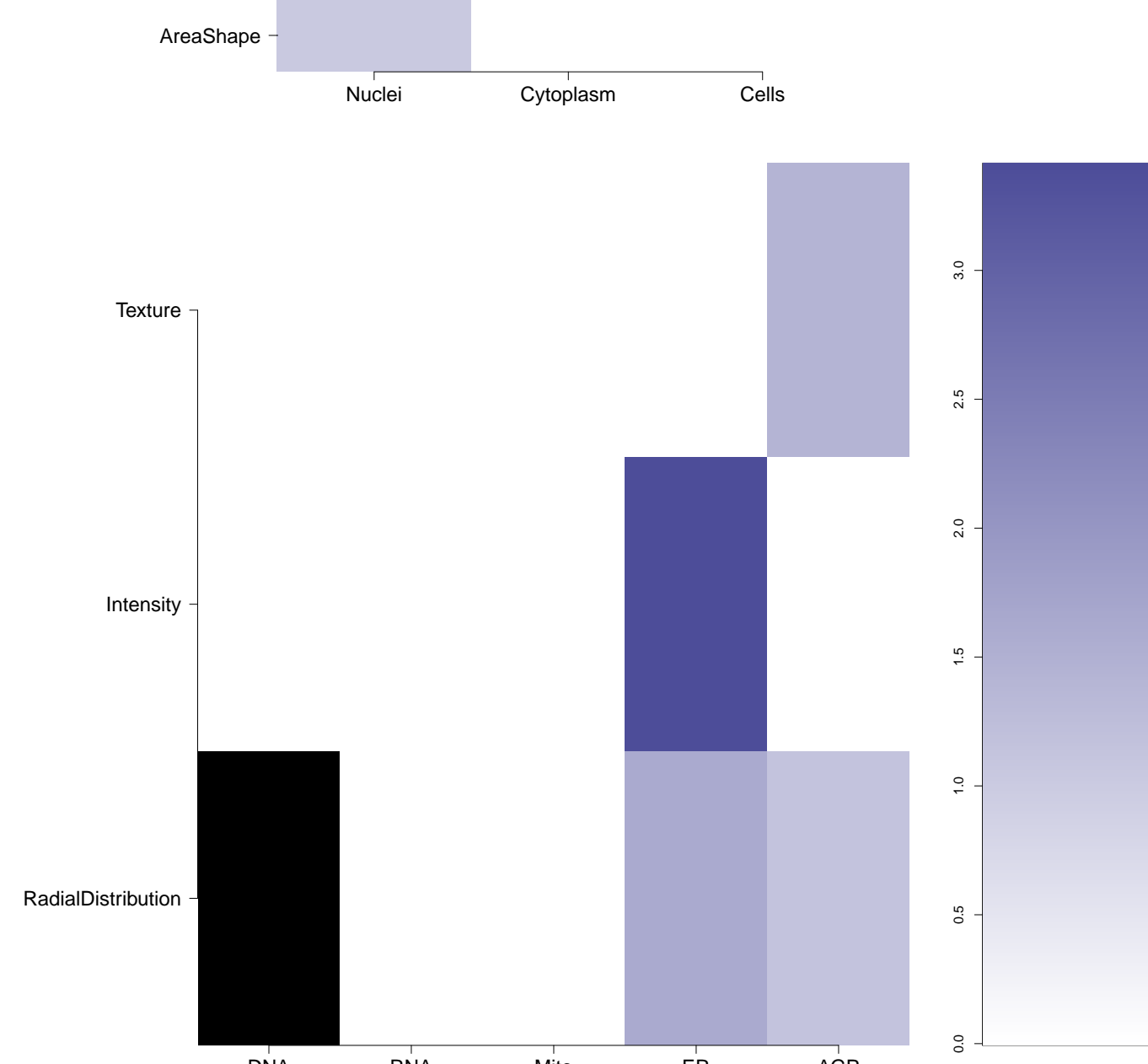
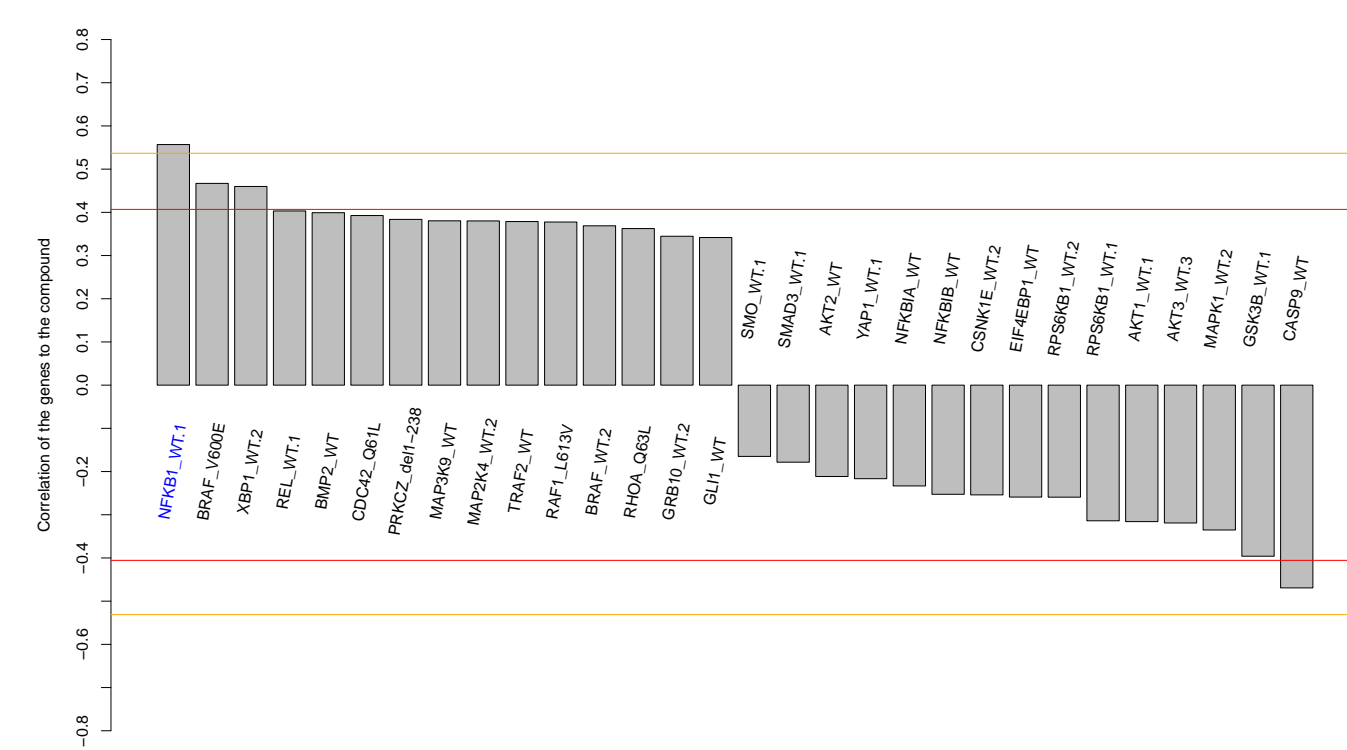
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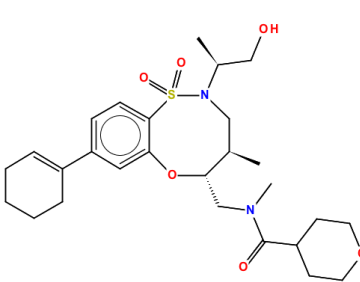
0.64 (in 4 replicates)

0.56

NA



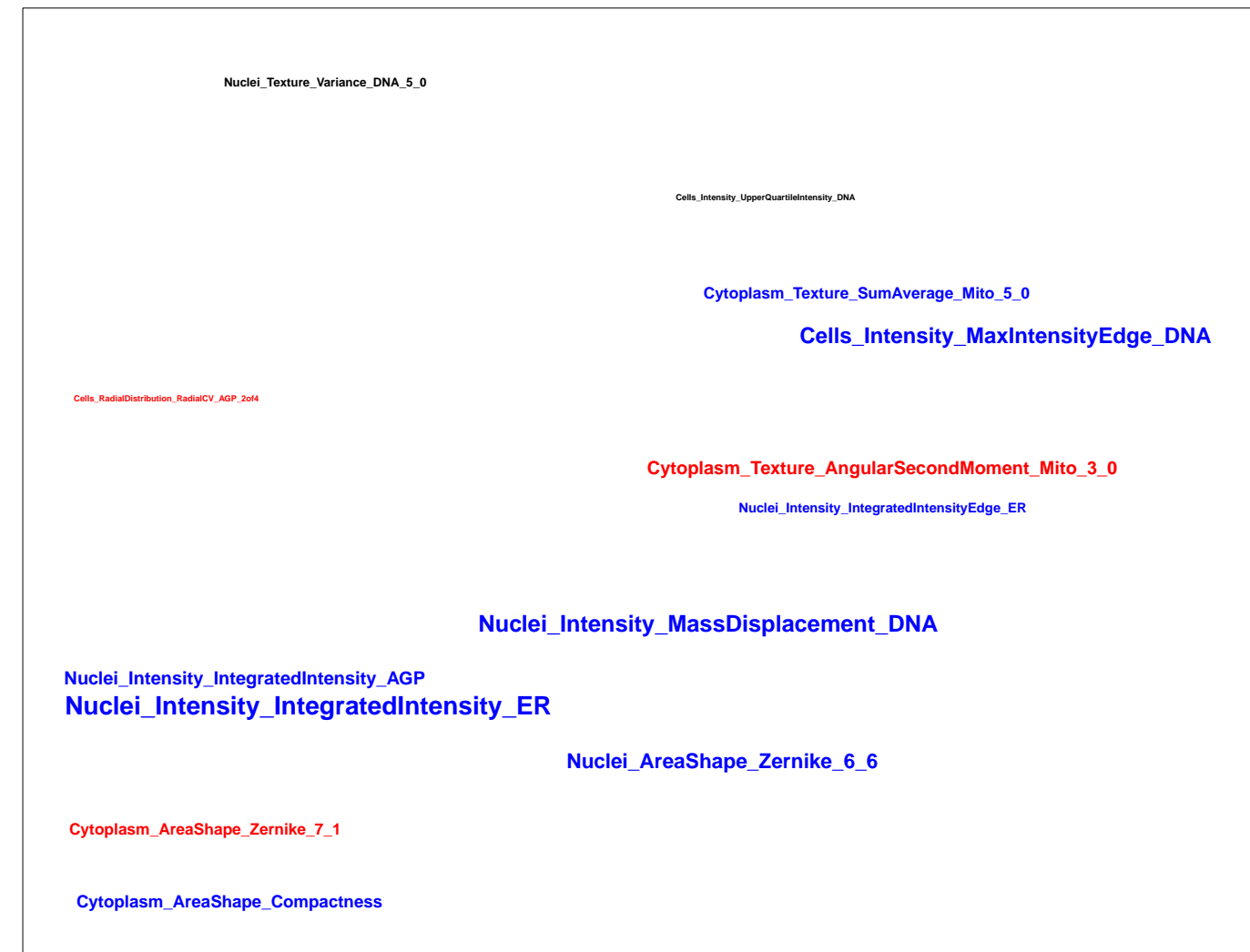
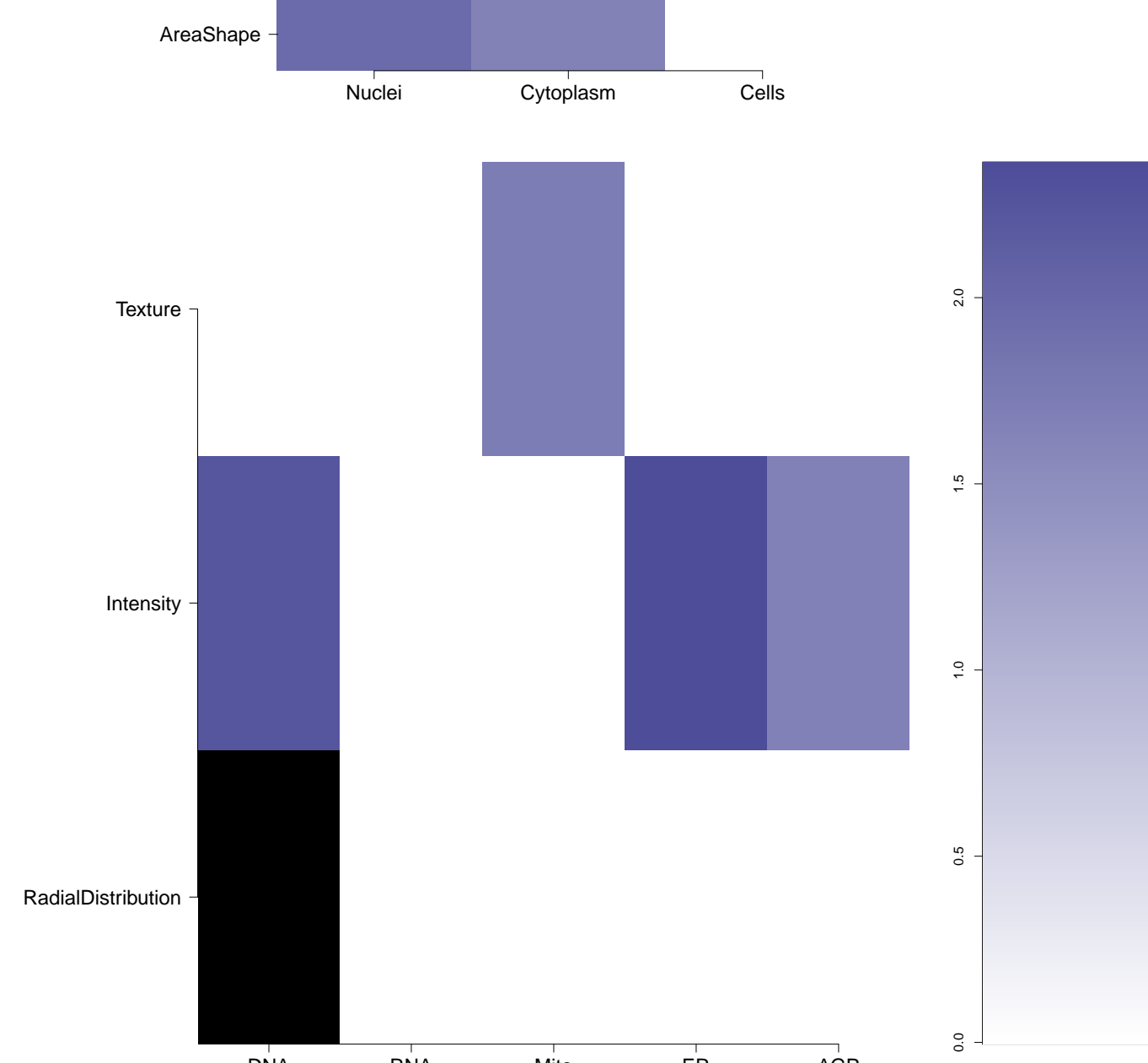
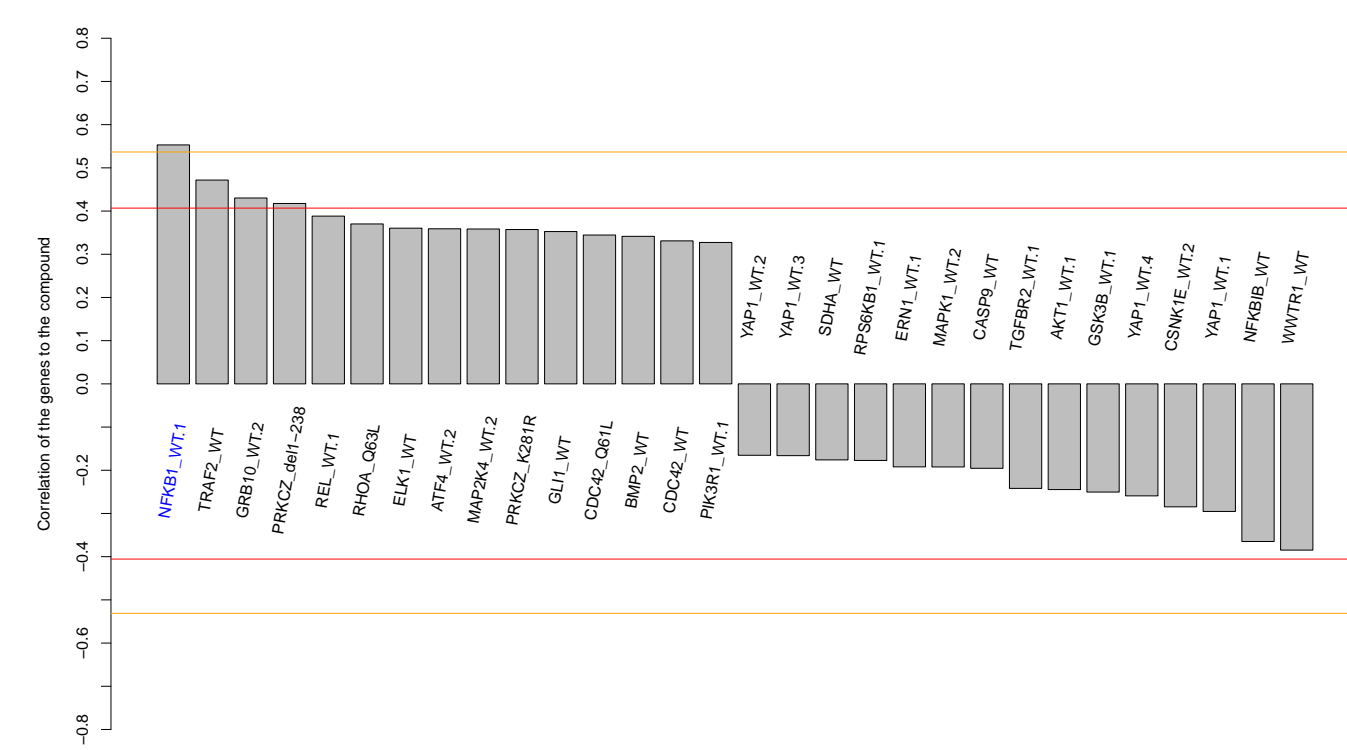
Total number of assays tested in: 31.

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PubChem CID : 54619429

0.62 (in 4 replicates)

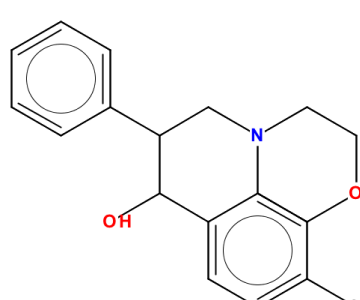
0.55

0.299



Total number of assays tested in: 36.

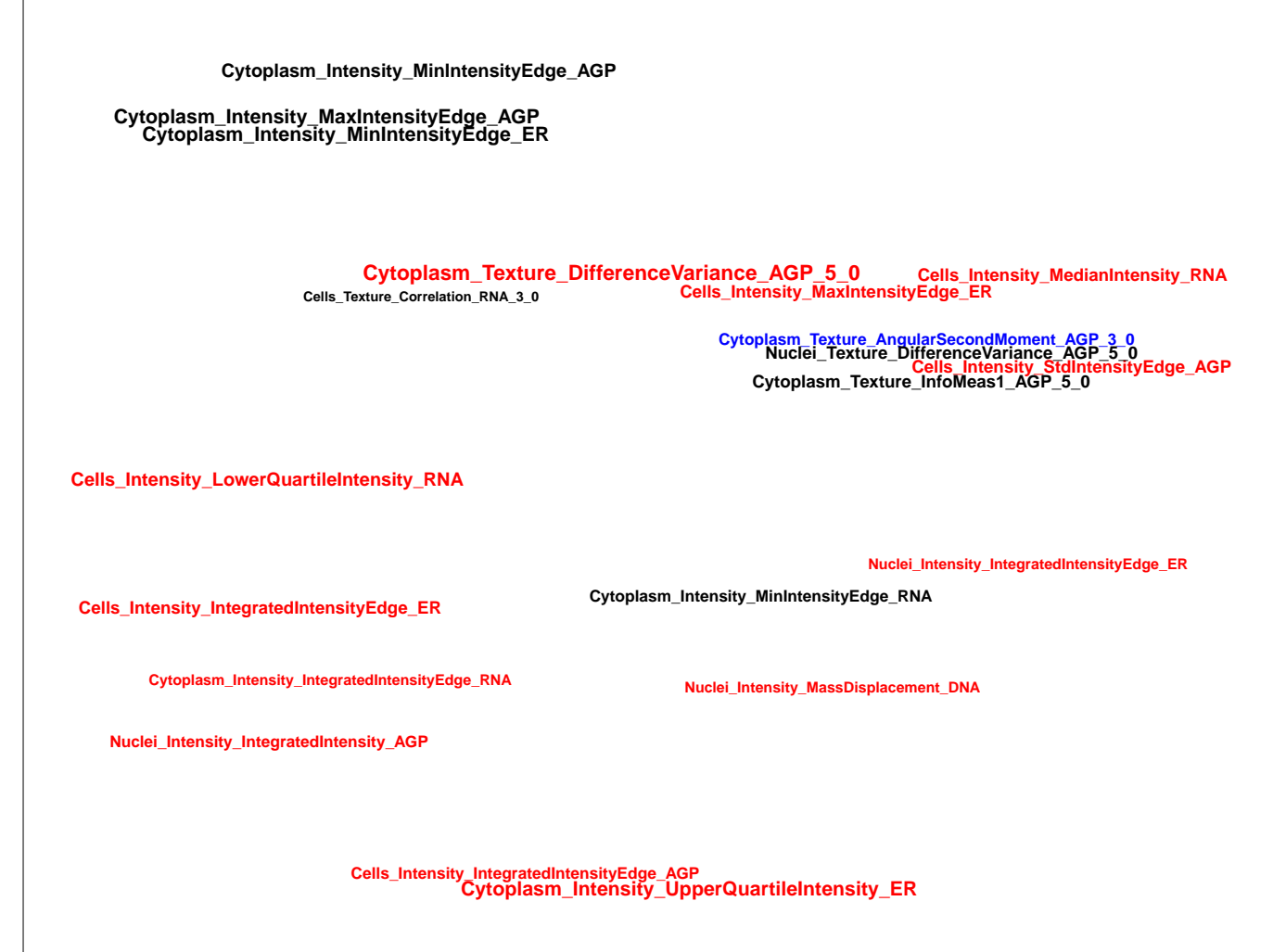
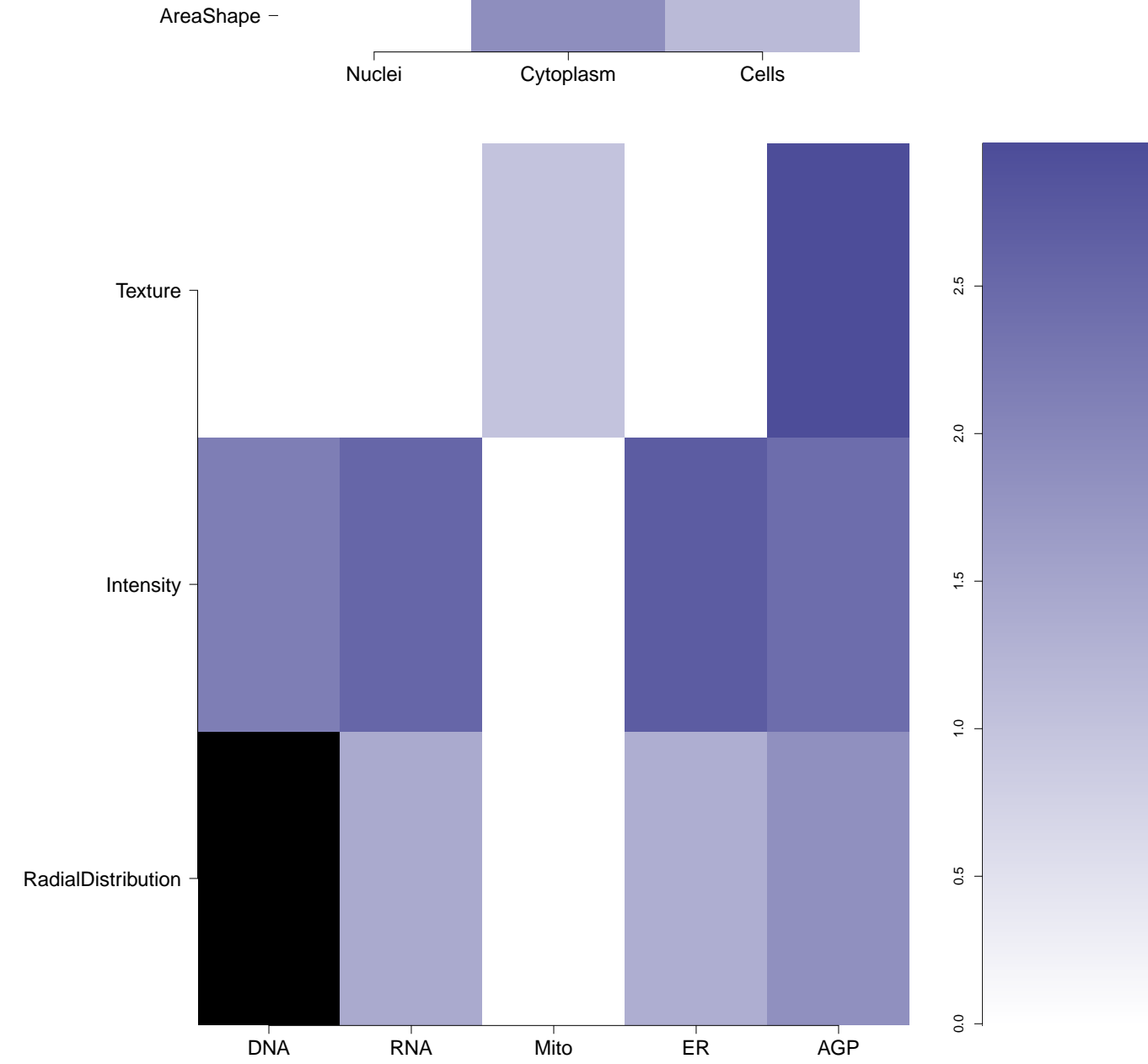
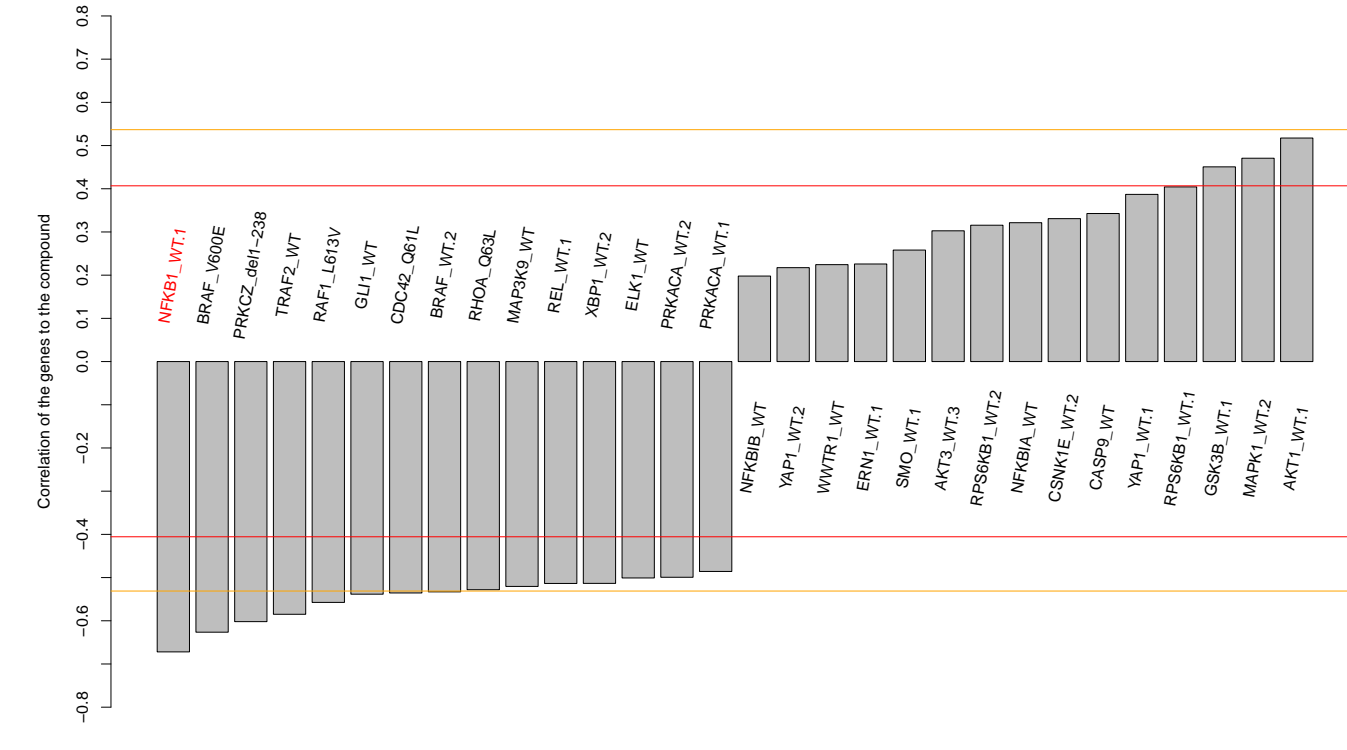
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NA (in 1 replicates)

-0.67

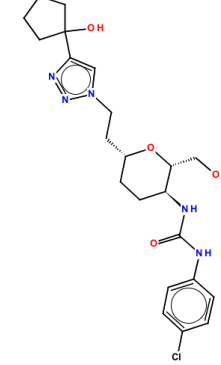
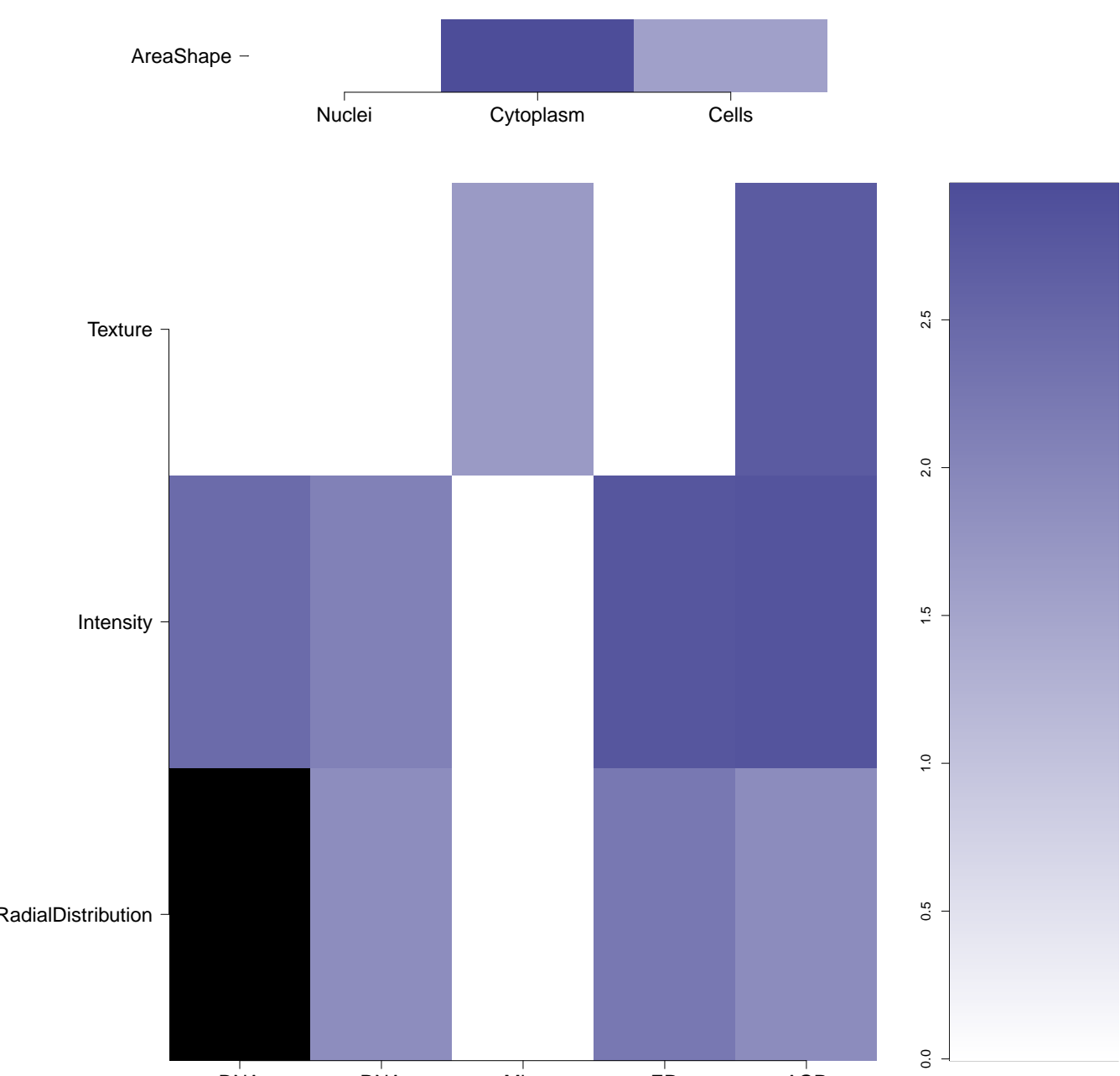
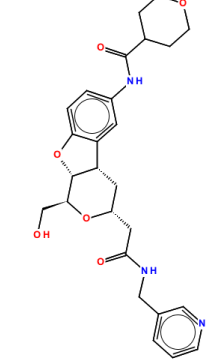
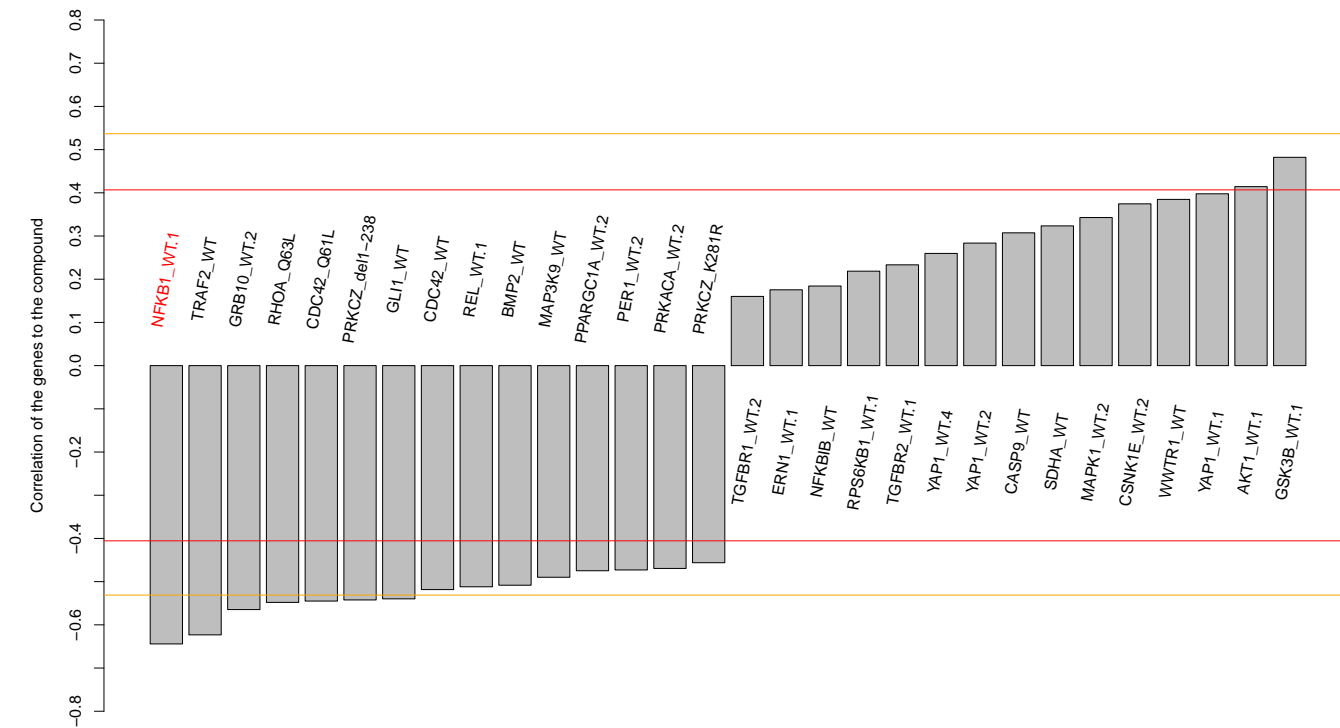
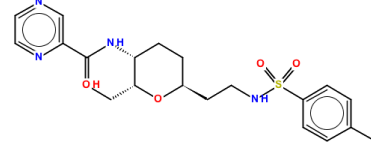
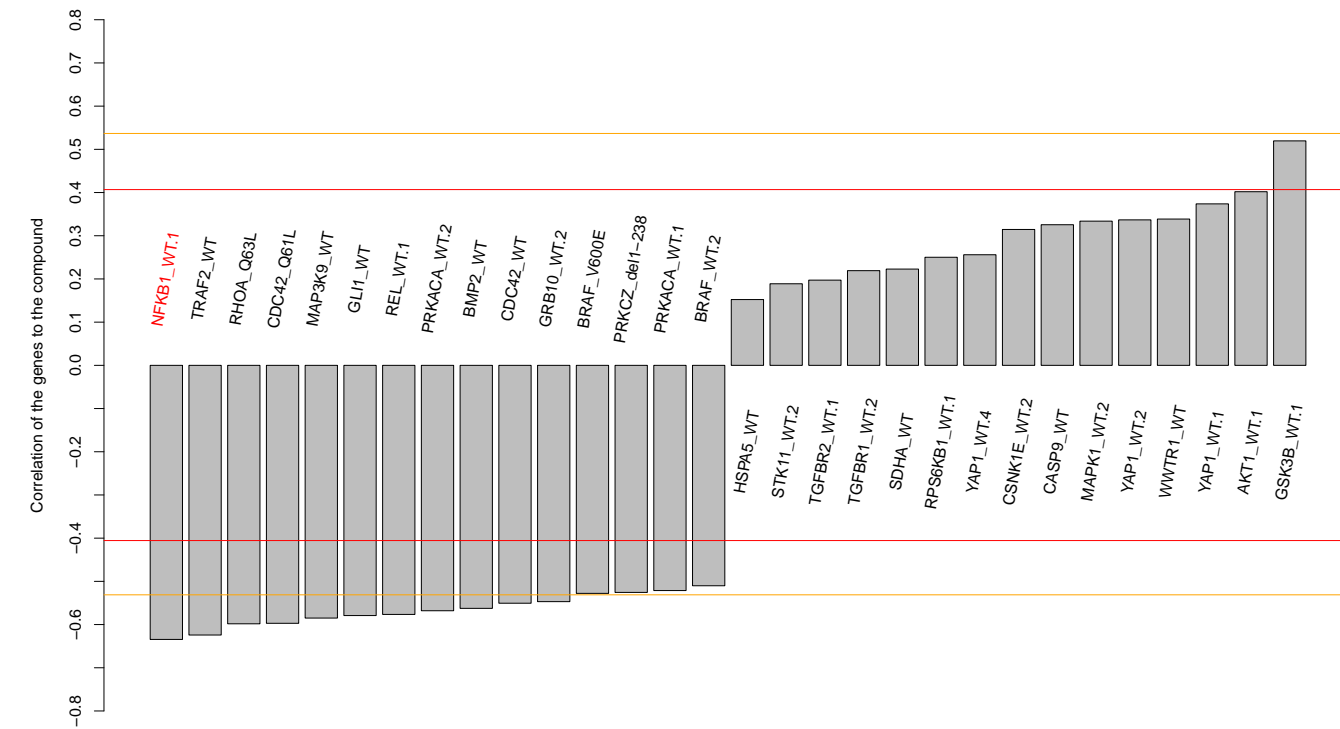
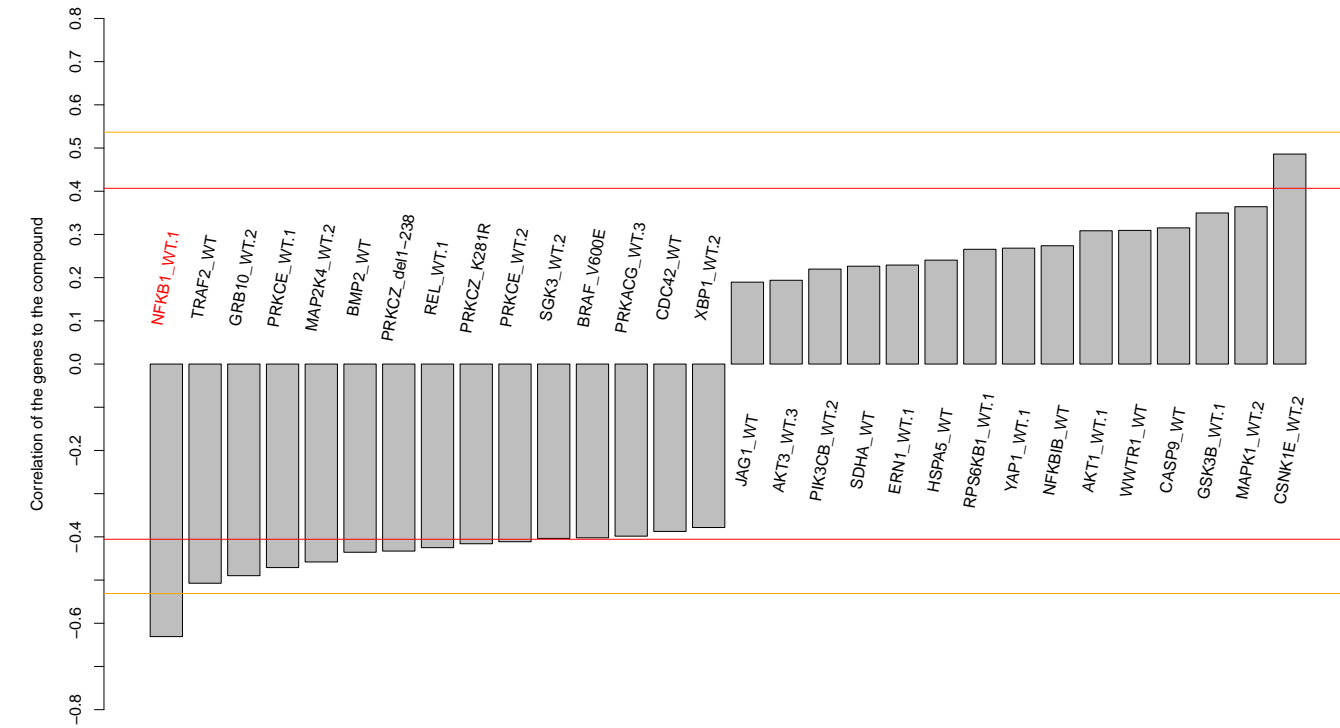
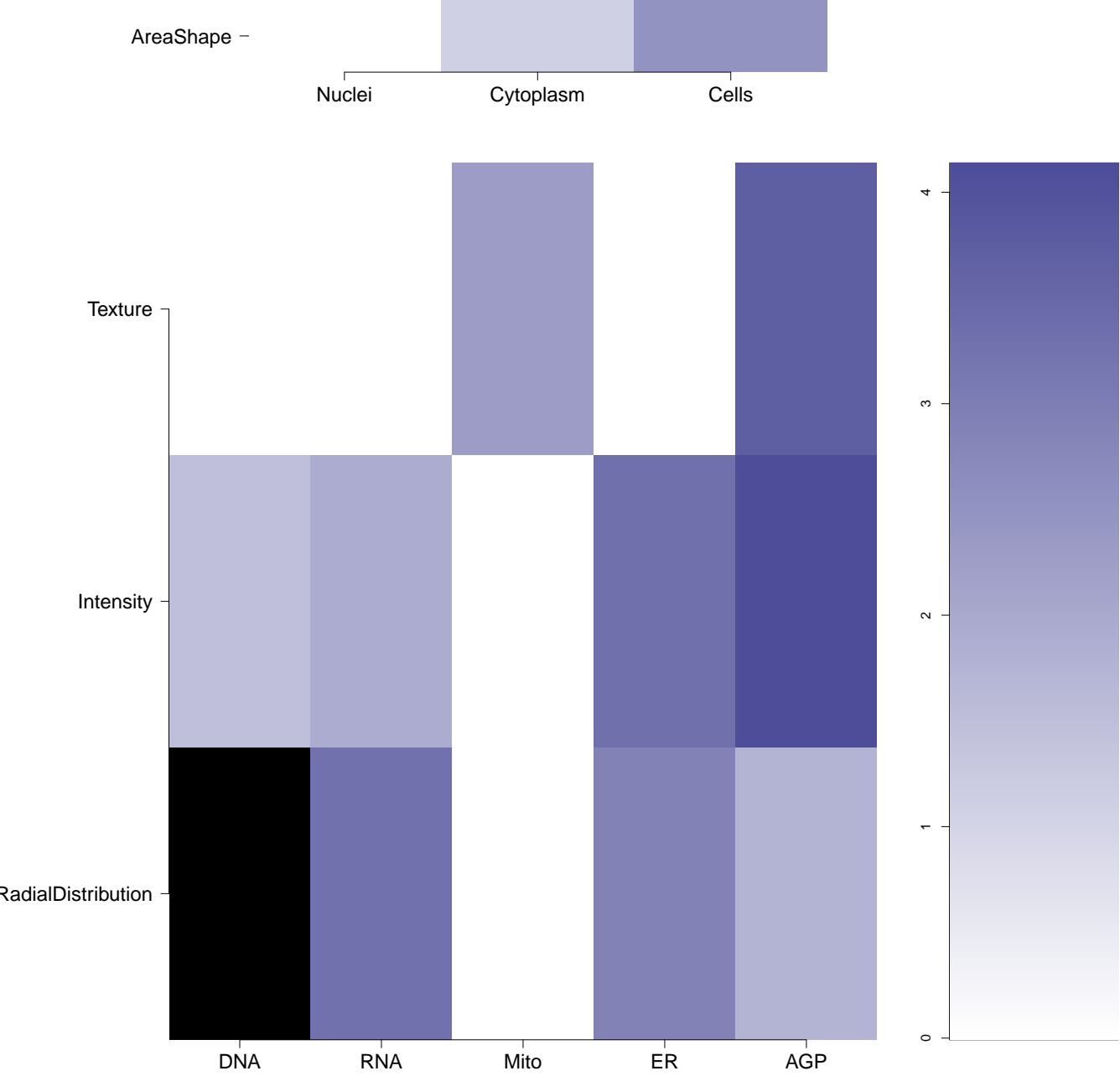
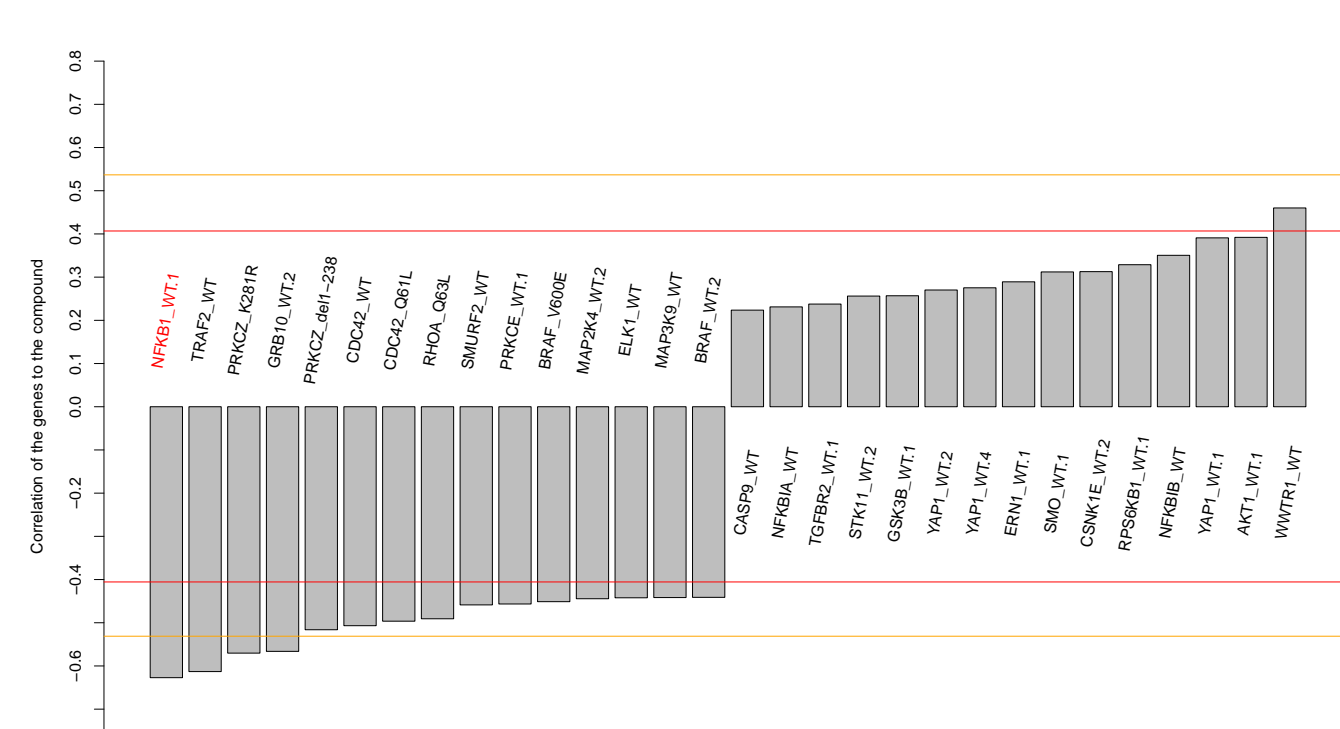
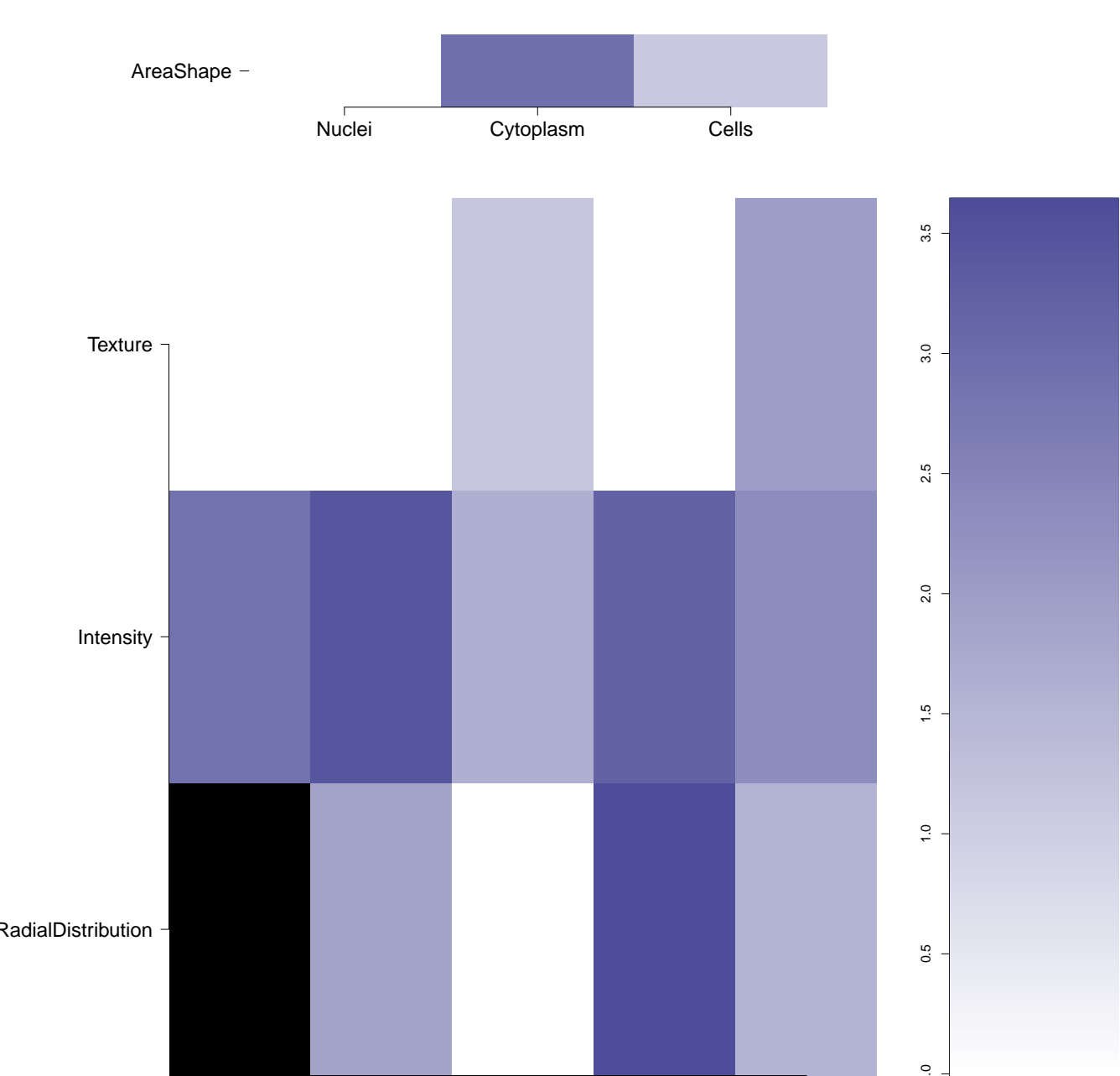
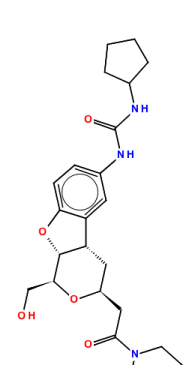
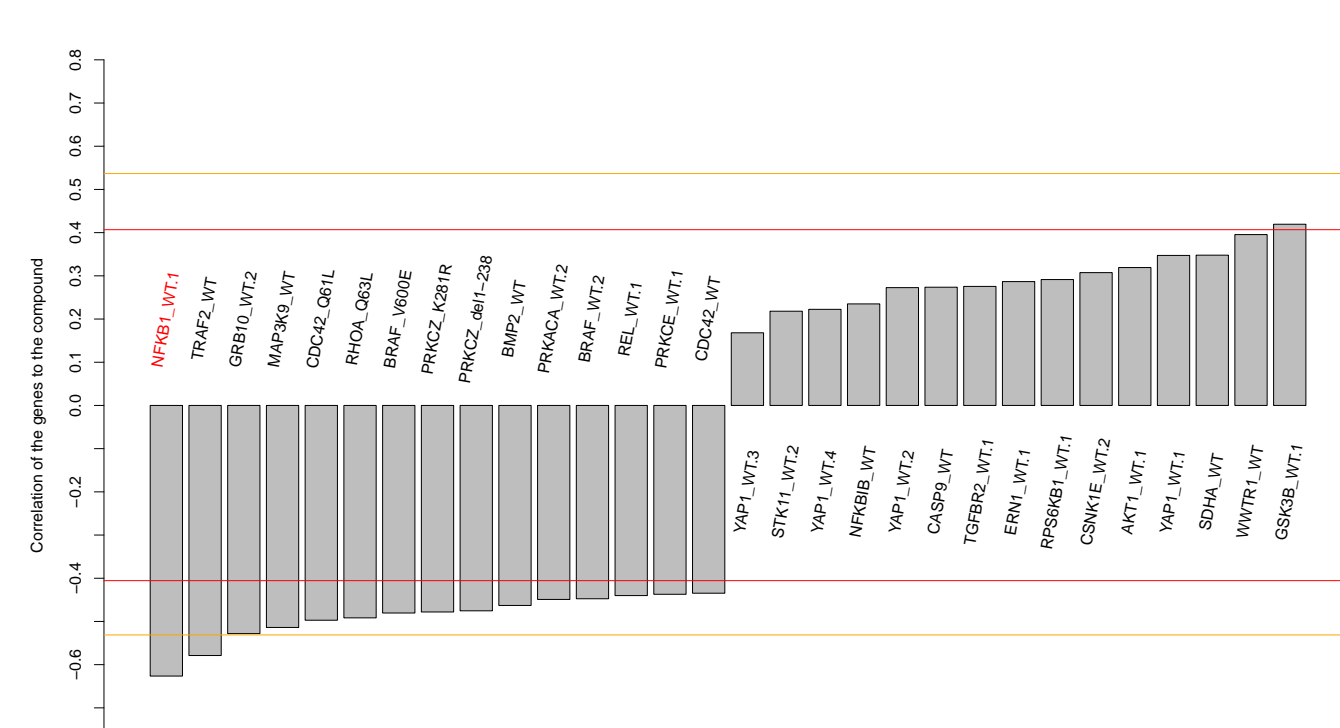
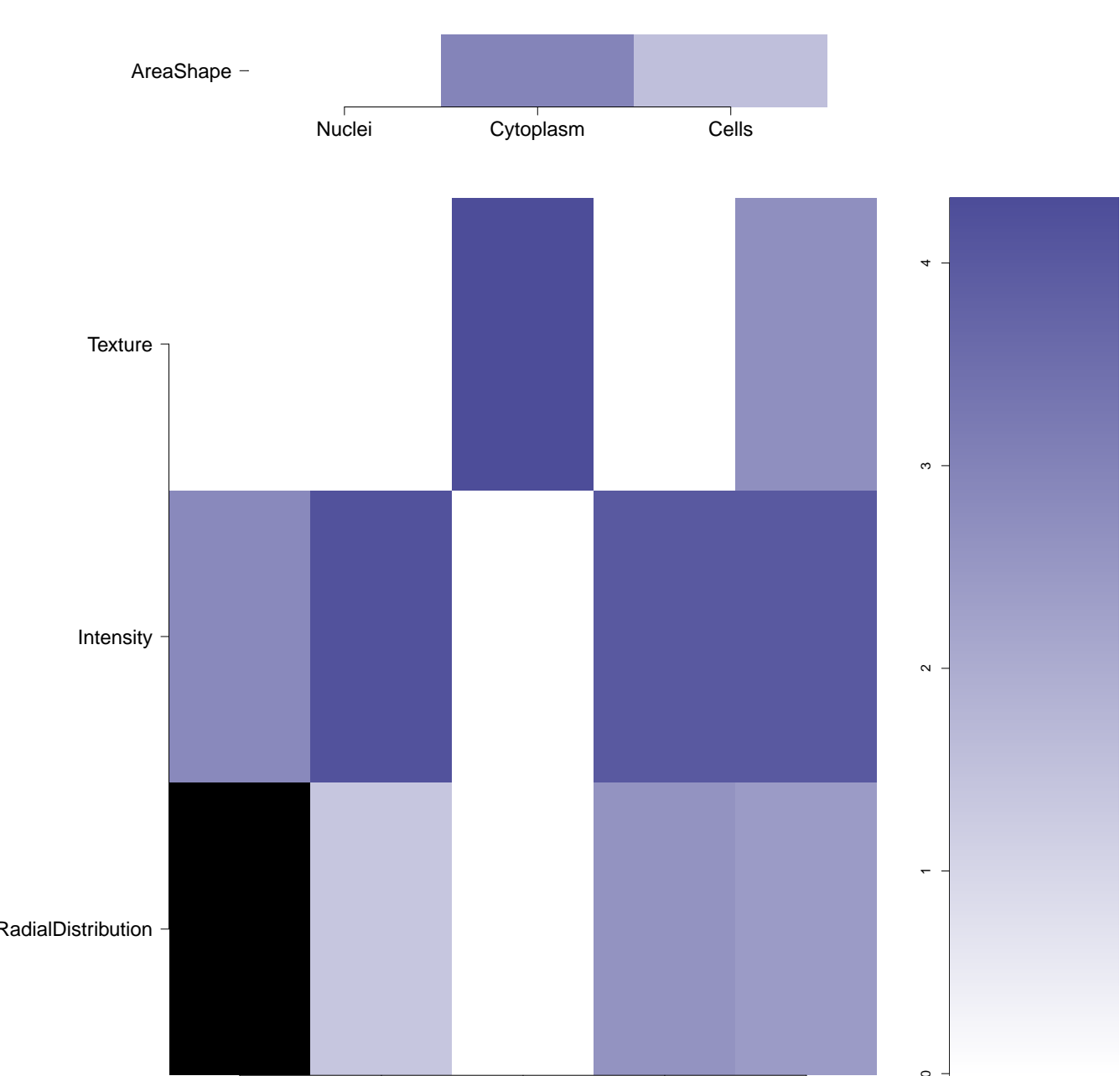
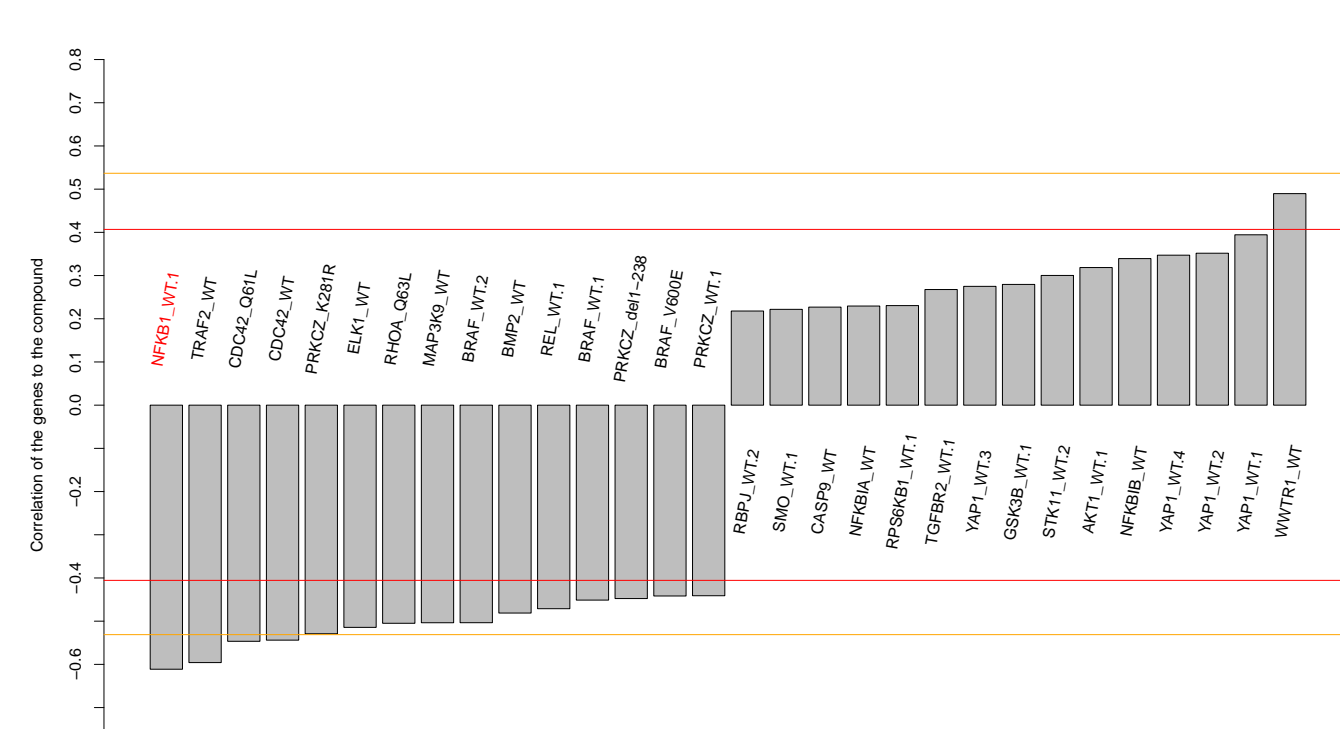
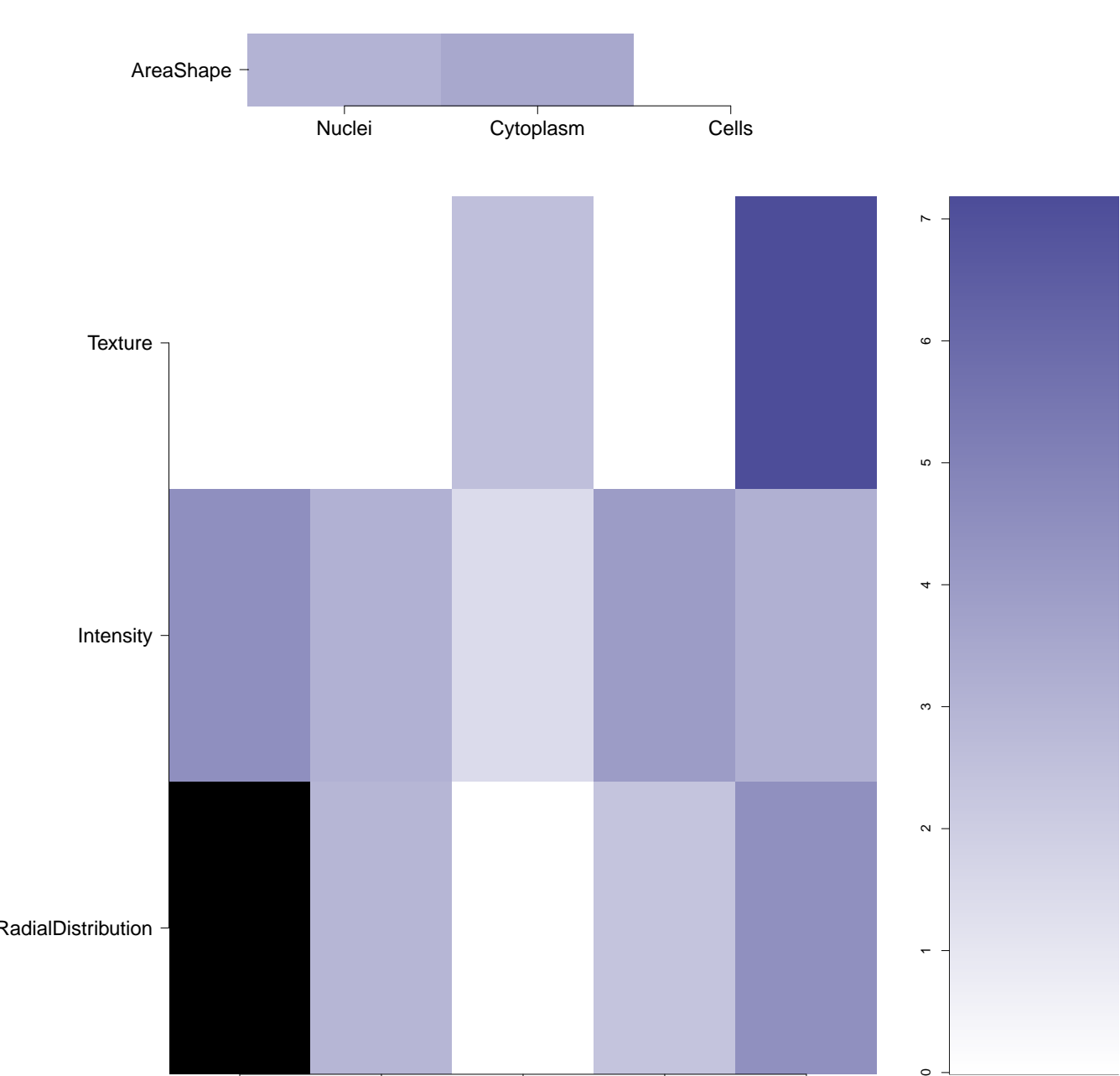
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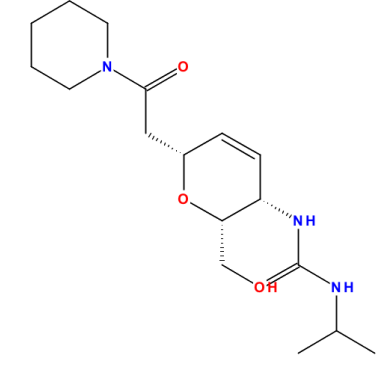
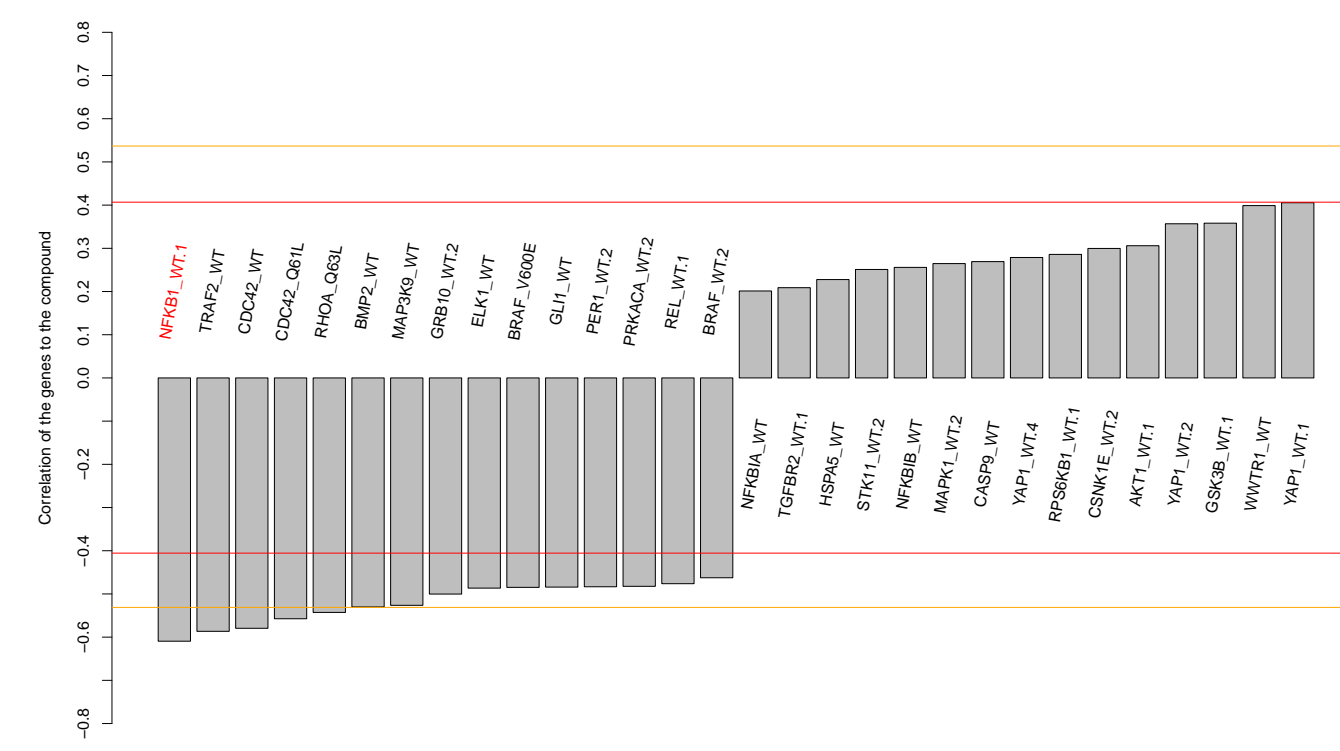
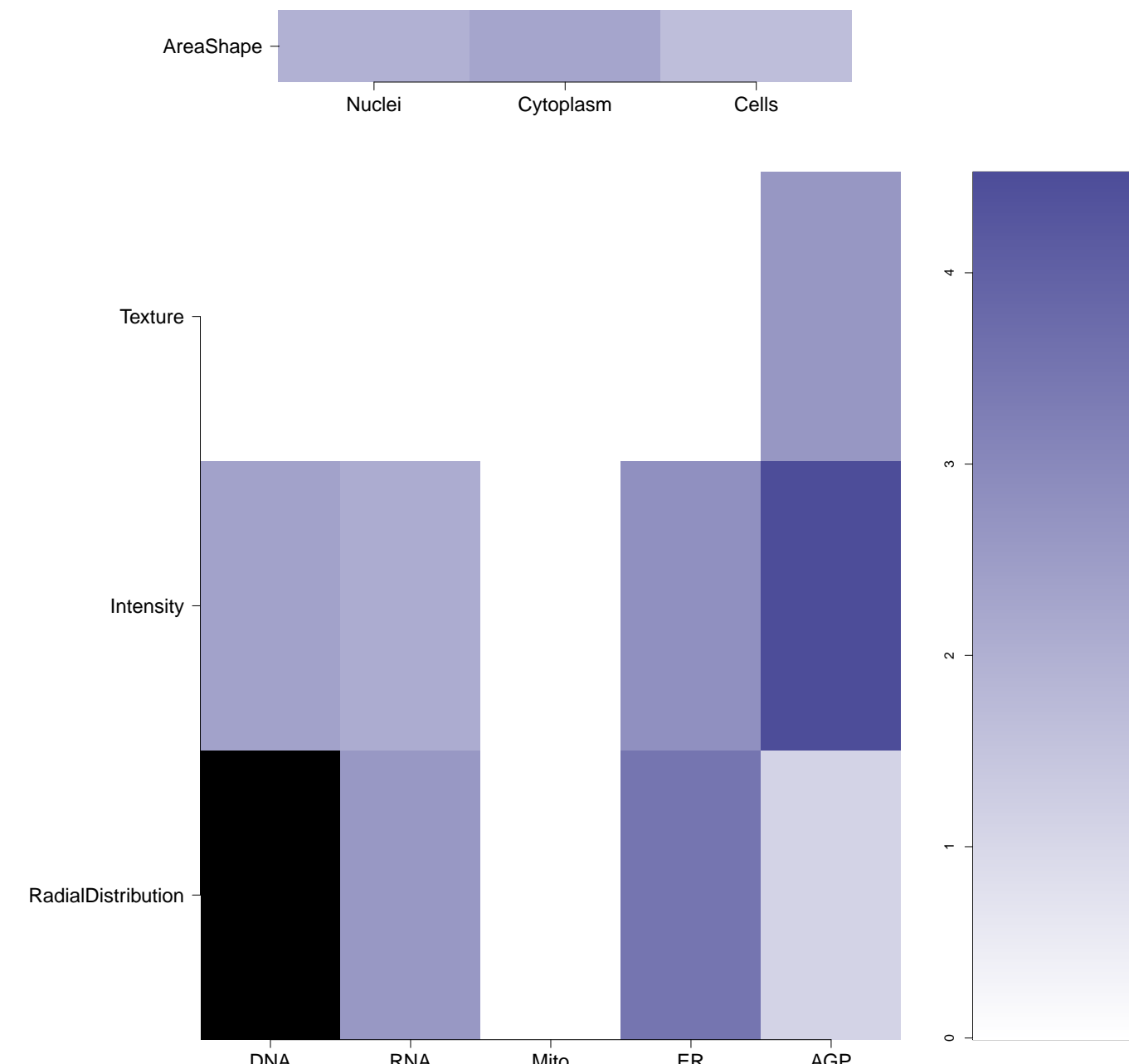
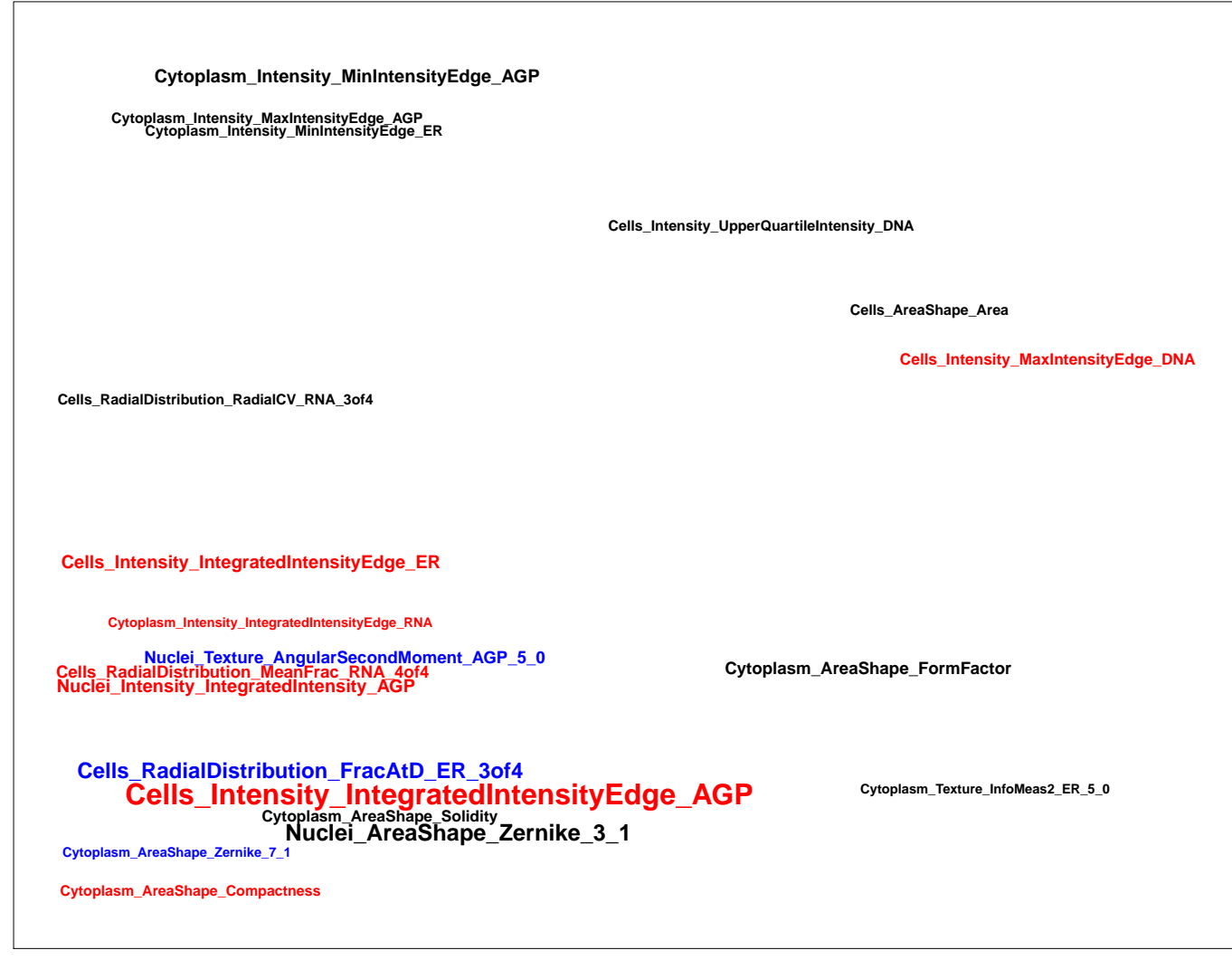
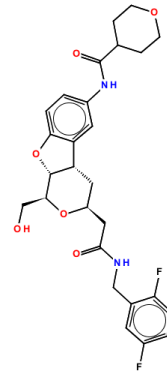
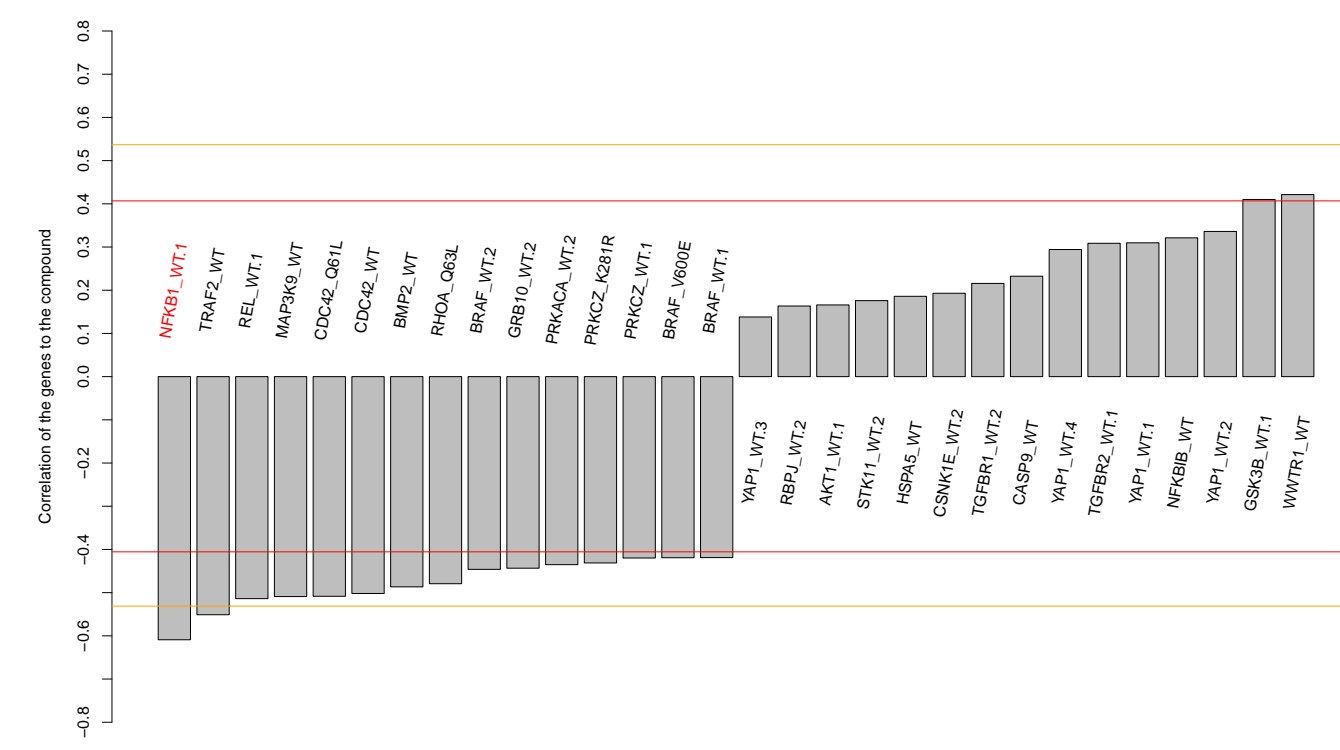
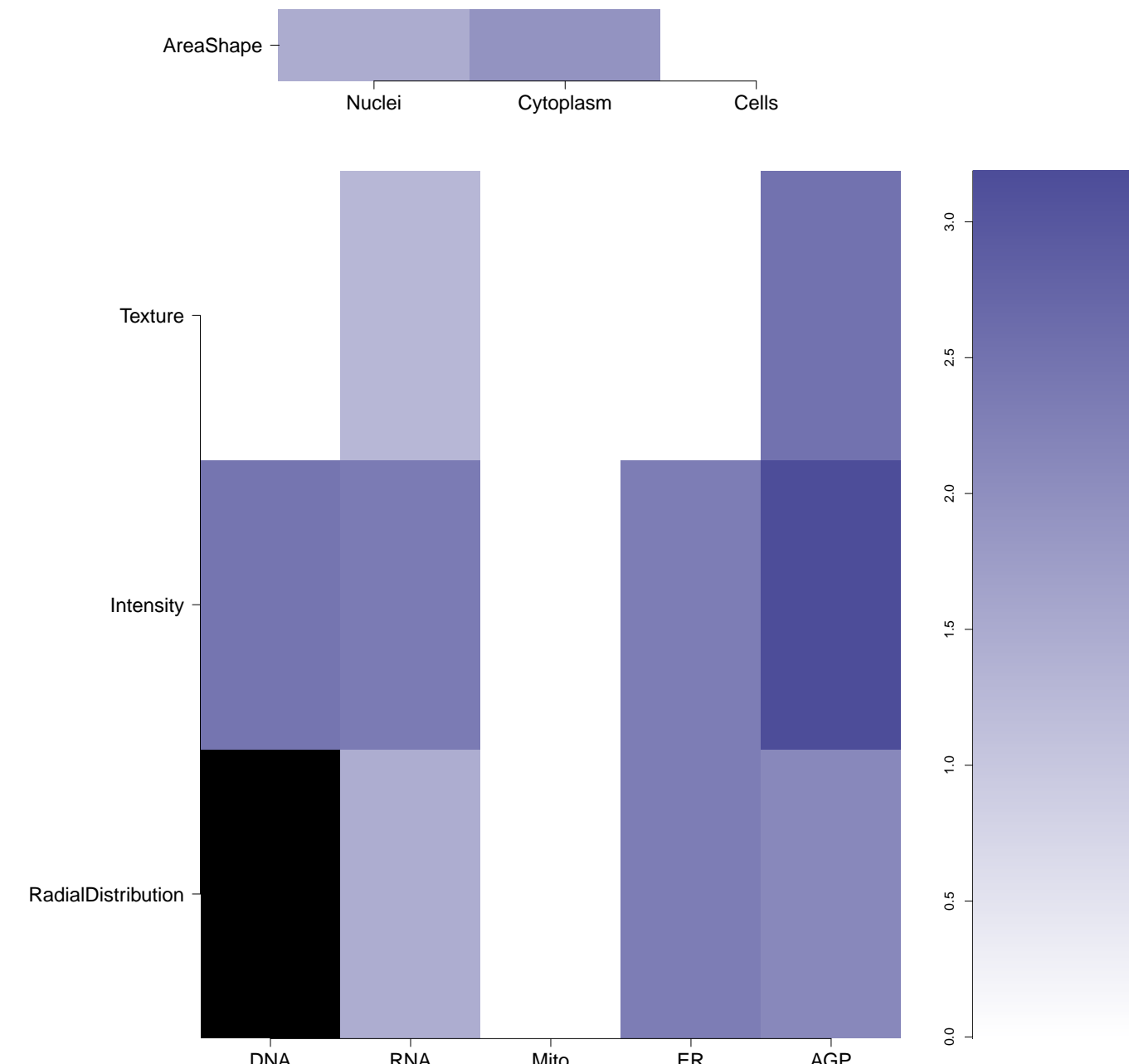
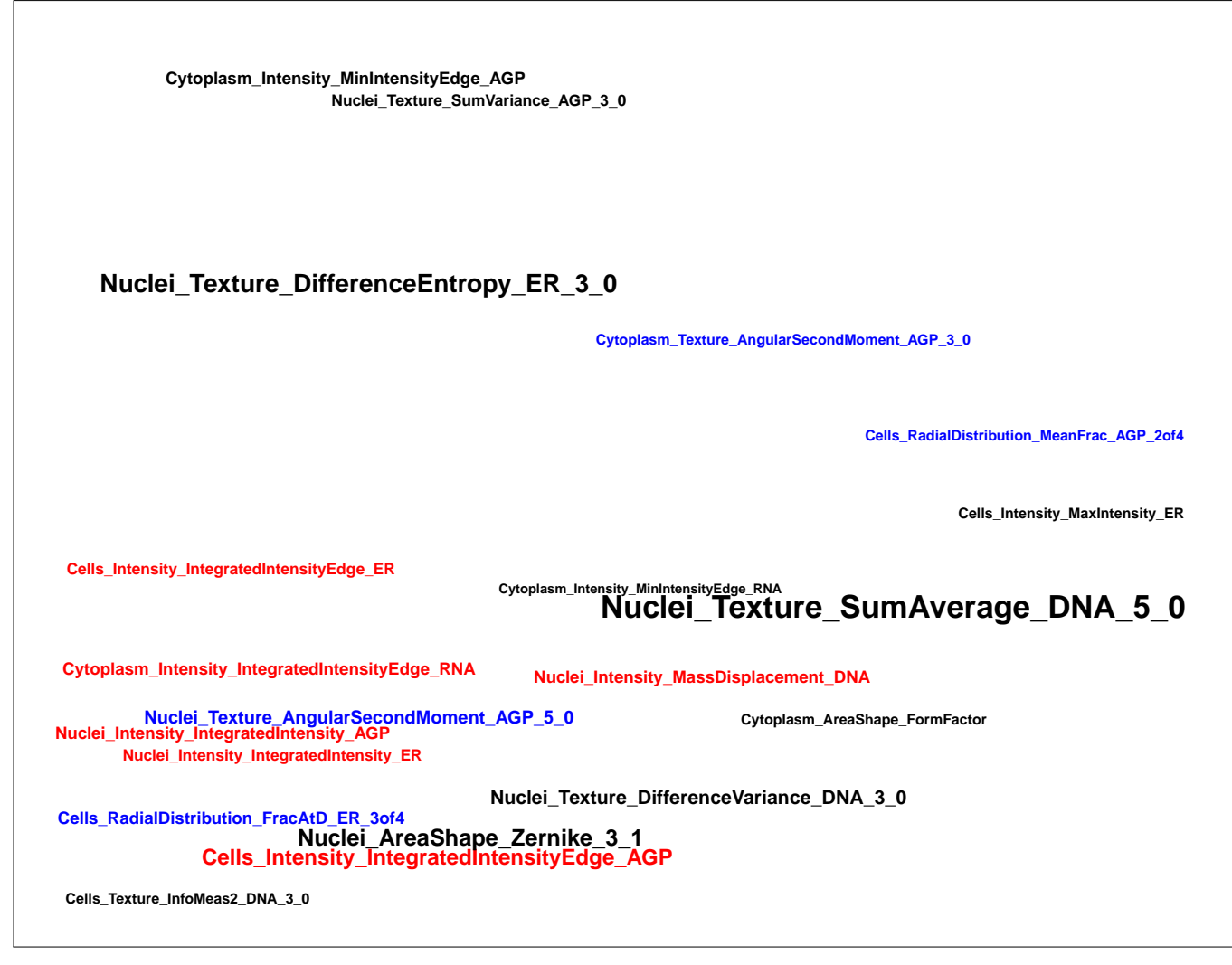


Total number of assays tested in: 493. Active in the following assays:

- Aqueous Solubility from MLSMR Stock Solutions (ADT 1996)
- Primary qHTS for delayed death inhibitors of the malarial parasite plasmodium, 48 hour incubation (ADT 504832)
- Primary qHTS for delayed death inhibitors of the malarial parasite plasmodium, 96 hour incubation (ADT 504834)
- High-throughput multiplex microsphere screening for inhibitors of toxin protease, specifically Lactoferrin Proteinase, MLPCPN compound set (ADT 585801)
- Luminescent Gluc Reporter Gene Assay Primary HTS to Identify Small Molecule Activators of the *Gluc* Reporter Gene Insertion Sequence. Measured in Cell-Based System Using Plate Reader - 7055-01 Activator Single-Point HTS Activity (ADT 743287)



BRD-K04830910-001-01-8 PubChem CID : 54641362		NA (in 1 replicates)	-0.66	NA			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cells_Intensity_UpperQuartIntensity_RNA</div> <div>Cells_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Nuclei_Intensity_MassDisplacement_DNA</div> <div>Nuclei_Texture_SumAverage_DNA_5.0</div> <div>Nuclei_Intensity_MassDisplacement_DNA</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Nuclei_Intensity_IntegratedIntensityEdge_ER</div> <div>Nuclei_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 37.
BRD-K37255594-001-01-2 PubChem CID : 54645900		0.91 (in 2 replicates)	-0.64	0.017			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cells_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_SumAverage_Mito_3.0</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_MeanFrac_AGP_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cells_RadiolDistribution_FracAD_ER_304</div> <div>Cells_RadiolDistribution_FracAD_ER_304</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Solidity</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 42.
BRD-K84760360-001-01-5 PubChem CID : 54641098		NA (in 1 replicates)	-0.63	NA			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_FormFactor</div> <div>Cells_Intensity_IntegratedIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 37.
BRD-K40048343-001-01-0 PubChem CID : 54641179		0.70 (in 2 replicates)	-0.63	NA			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_FormFactor</div> <div>Cells_Intensity_IntegratedIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 40.
BRD-K44341698-001-01-6 PubChem CID : 54645988		0.83 (in 2 replicates)	-0.63	0.839			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_FormFactor</div> <div>Cells_Intensity_IntegratedIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 47. Active in the following assays: <ul style="list-style-type: none"> <li>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)</li> </ul>
BRD-K01326303-001-01-5 PubChem CID : 54646023		0.79 (in 2 replicates)	-0.63	0.276			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_FormFactor</div> <div>Cells_Intensity_IntegratedIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 38.
BRD-K92925409-001-01-7 PubChem CID : 54646095		0.82 (in 3 replicates)	-0.61	0.344			<div> <div>Cytoplasm_Intensity_MinIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiolDistribution_RadiACV_ER_304</div> <div>Cells_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_IntegratedIntensityEdge_ER</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cytoplasm_AreaShape_FormFactor</div> <div>Cells_Intensity_IntegratedIntensityEdge_AGP</div> <div>Cytoplasm_Intensity_MinIntensityEdge_ER</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cytoplasm_AreaShape_Compactness</div> </div>	Total number of assays tested in: 39.

BRD-K20152345-001-01-2 PubChem CID : 54641316		0.82 (in 2 replicates)	-0.61	NA				Total number of assays tested in: 38.
BRD-K52012504-001-01-6 PubChem CID : 54646337		0.88 (in 4 replicates)	-0.61	0.883				Total number of assays tested in: 39.