

Correlation of the gene to the other genes

How similar is this gene to the other genes?

Gene	Correlation
CCND1_WT.2	1.00
E2F1_WT	0.82
CCND1_WT.1	0.68
AKT1S1_WT.2	0.56
AKT1S1_WT.1	0.55
CDK2_WT.2	0.55
RBPJ_WT.1	0.50
GLI1_WT	0.50
CEBPA_WT.1	0.49
ATF4_WT.2	0.48
SMAD3_WT.1	0.46
CEBPA_WT.2	0.45
PER1_WT.2	0.45
GRB10_WT.2	0.41
MAP2K4_WT.2	0.41
MOS_WT.1	-0.42
MOS_WT.2	-0.45
KRAS_WT.1	-0.51
KRAS_G12V	-0.52
MAP2K4_WT.1	-0.54
MAP3K7_WT	-0.55
TRAF5_WT	-0.55
MAP3K2_WT.1	-0.56
HRAS_G12V	-0.56
MAP2K3_WT	-0.58
MAP3K2_WT.2	-0.59
MAP3K5_WT	-0.66
TP53_WT.1	-0.67
CDKN1A_WT	-0.74
AKT2_WT	-0.75

Heatmap showing the relationship between AreaShape and various biological features. The color scale ranges from 0 (lightest) to 30 (darkest).

AreaShape	Nuclei	Cytoplasm	Cells
ure	~10	~10	~10
sity	~10	~10	~10
ion	~10	~10	~10

Cells_Texture_SumEntropy_DNA_5_0
Cells_Texture_SumEntropy_DNA_10_0
Cells_Texture_Entropy_DNA_10_0
Cells_Texture_AngularSecondMoment_DNA_10_0
Cells_Intensity_UpperQuartileIntensity_DNA
Cells_Intensity_MeanIntensity_DNA
Cells_Texture_DifferenceEntropy_DNA_5_0
Cells_Texture_AngularSecondMoment_DNA_5_0
Cells_Texture_AngularSecondMoment_DNA_3_0
Cells_Texture_DifferenceEntropy_DNA_10_0
Cells_Texture_SumEntropy_DNA_3_0
Cells_Texture_DifferenceEntropy_DNA_3_0
Cells_Texture_InverseDifferenceMoment_DNA_10_0
Cells_Texture_InverseDifferenceMoment_DNA_5_0
Cells_Texture_InverseDifferenceMoment_DNA_3_0

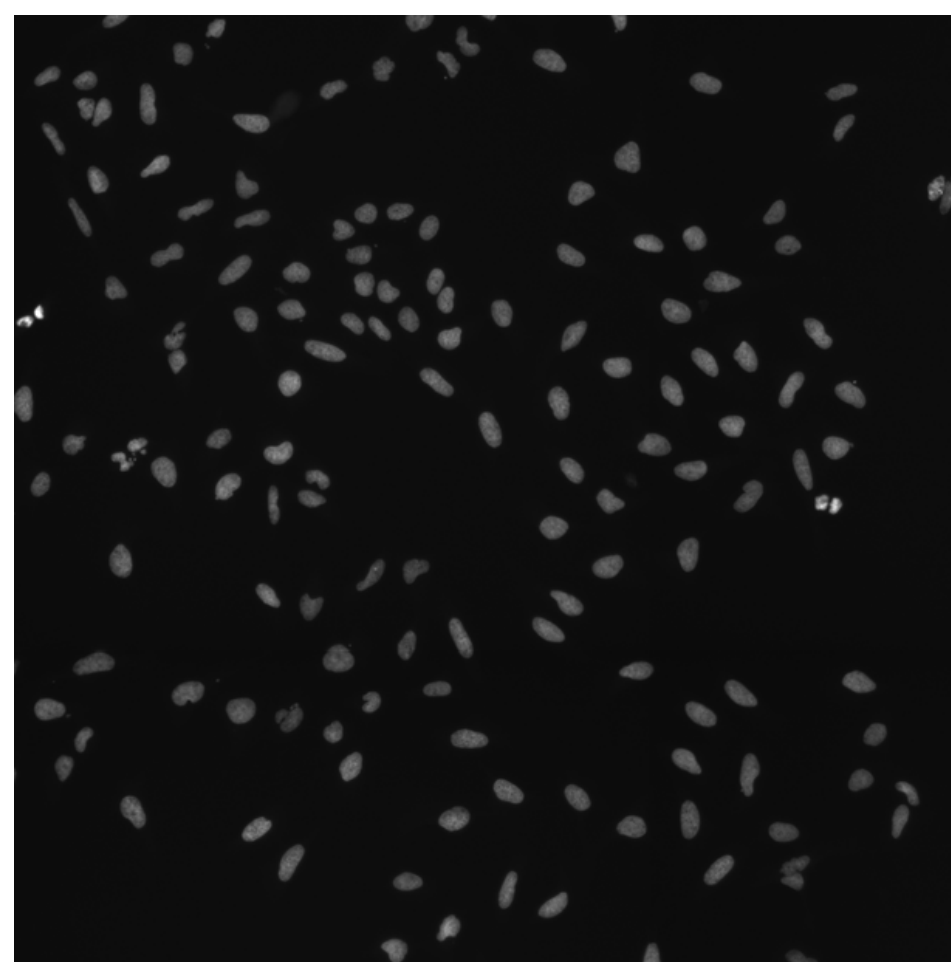
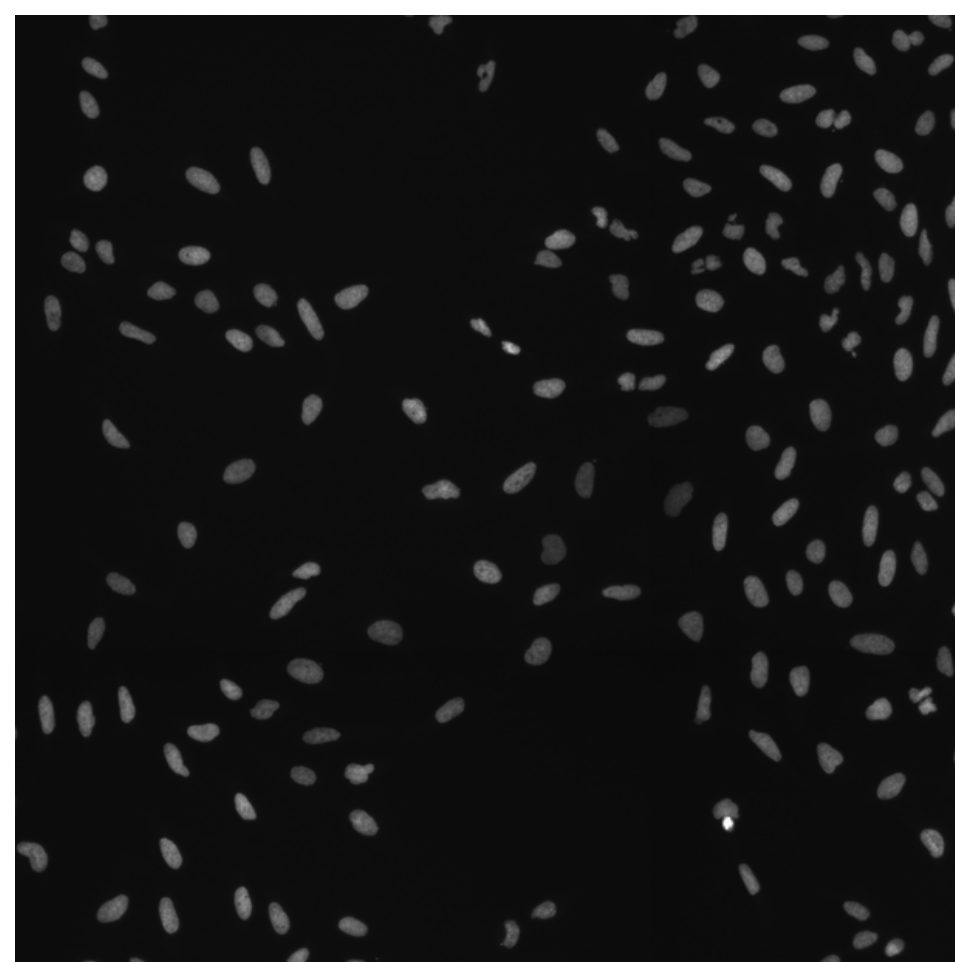
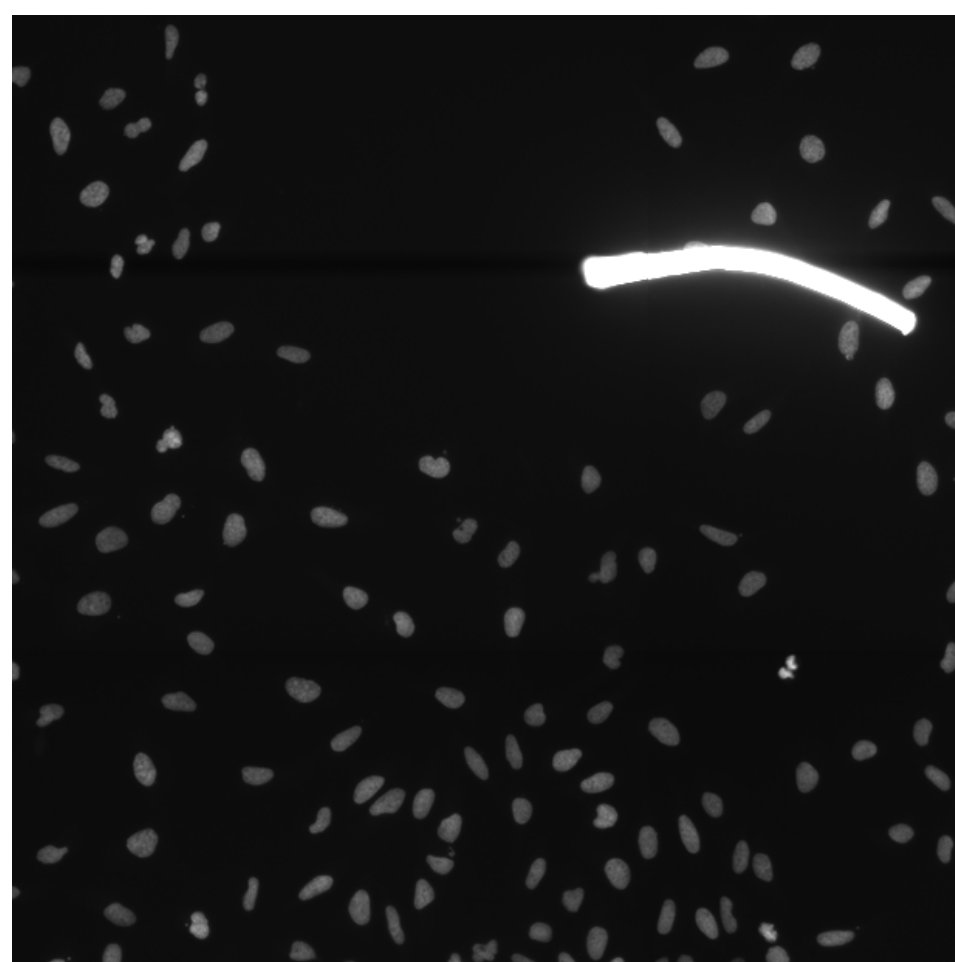
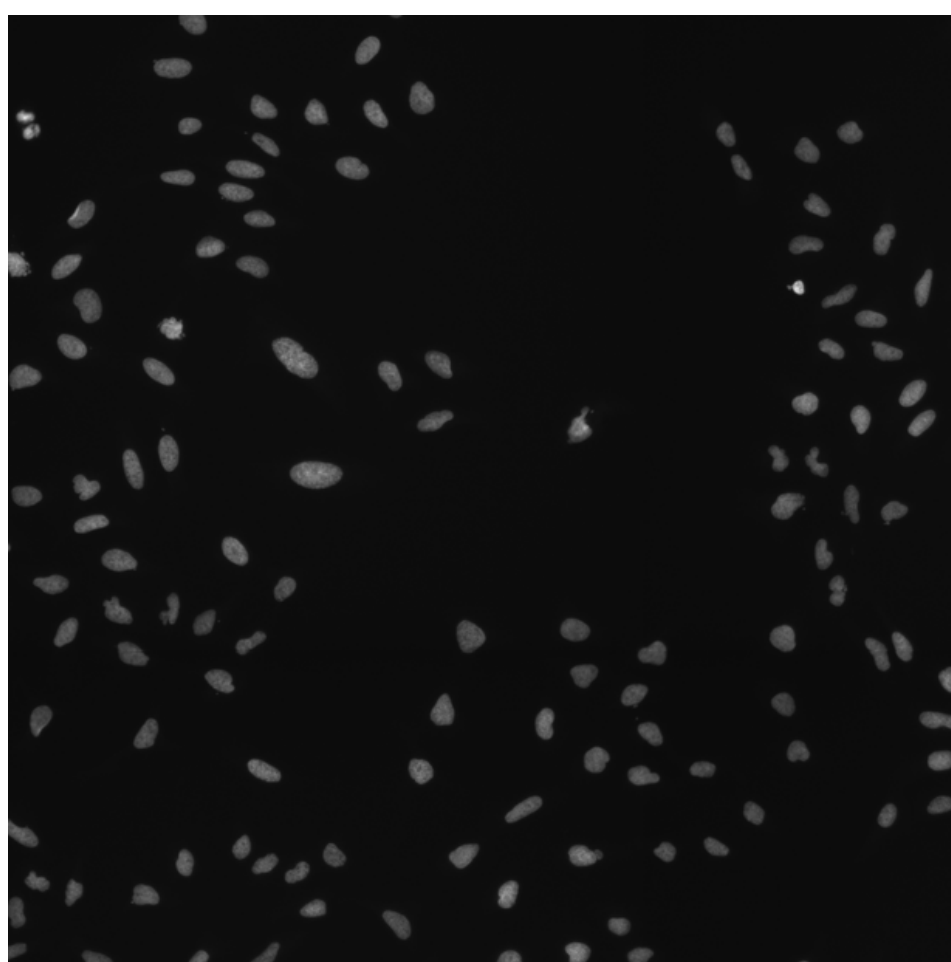
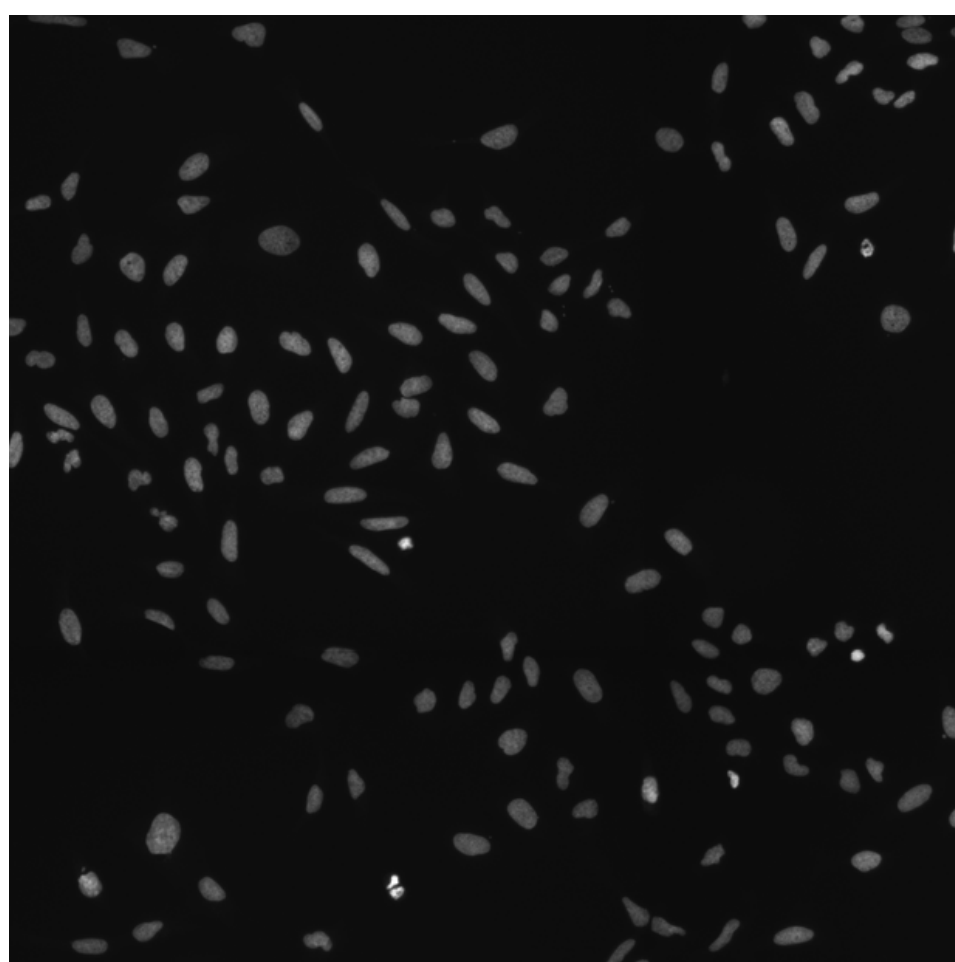
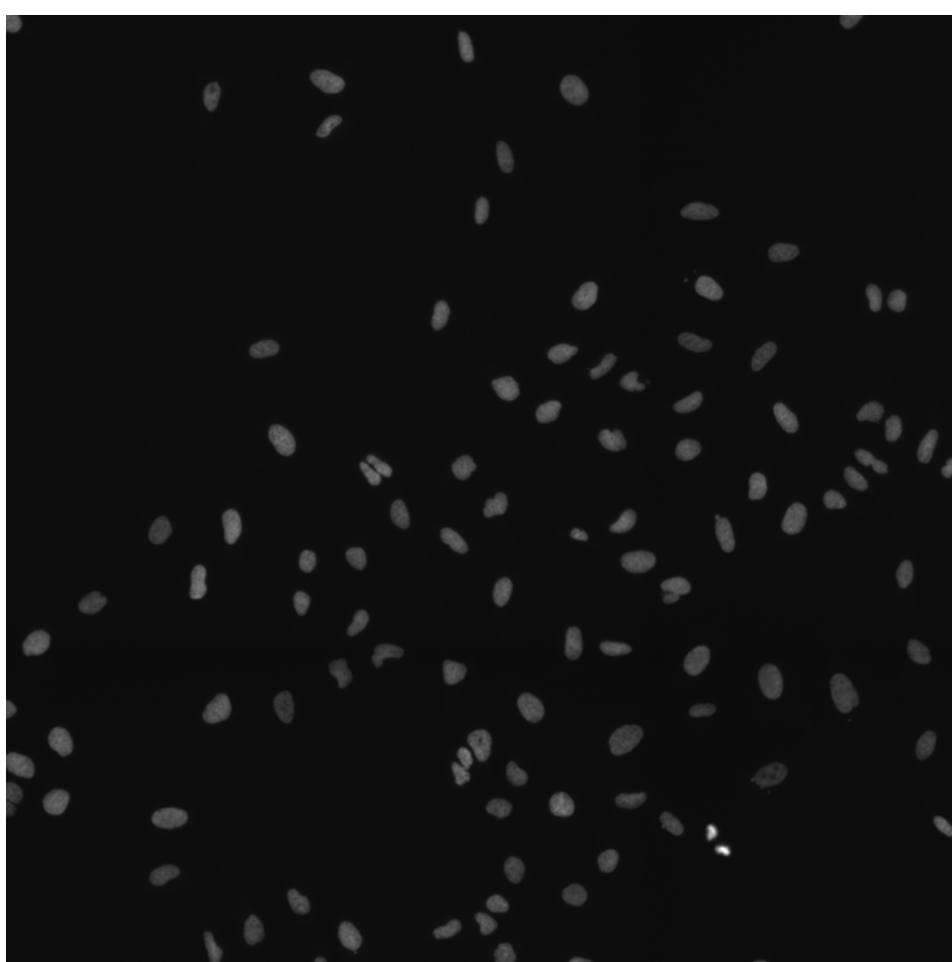
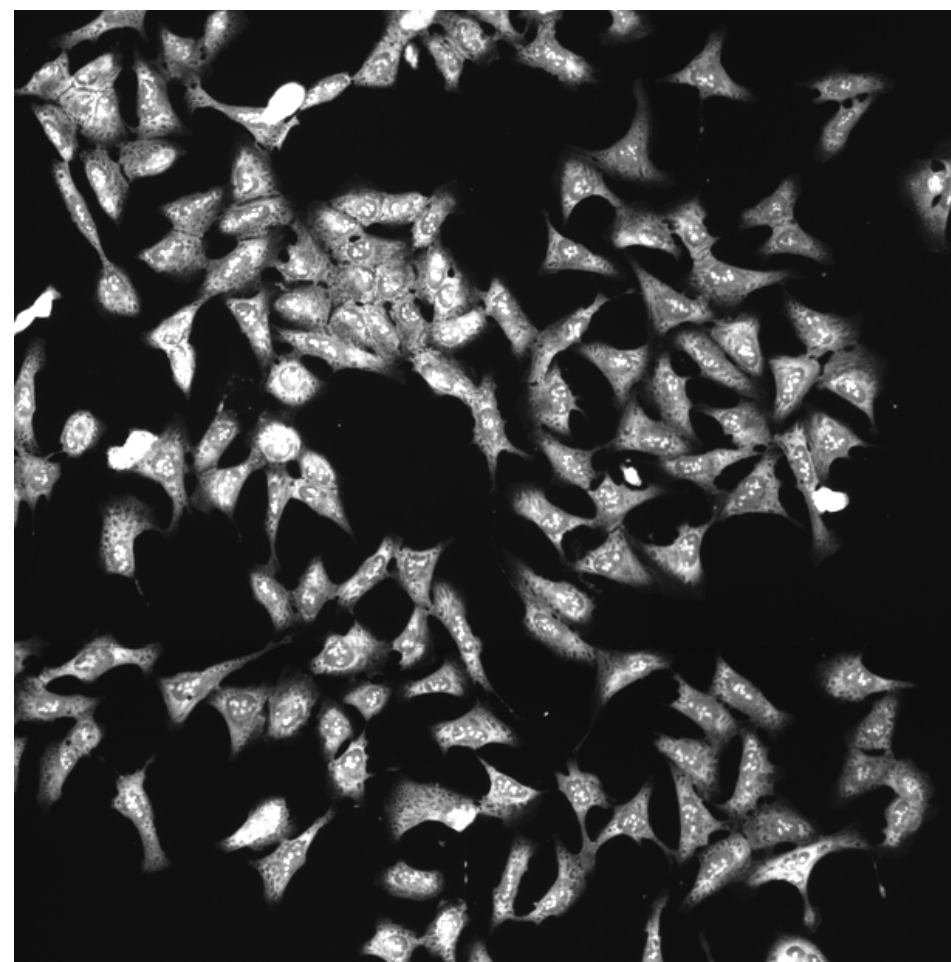
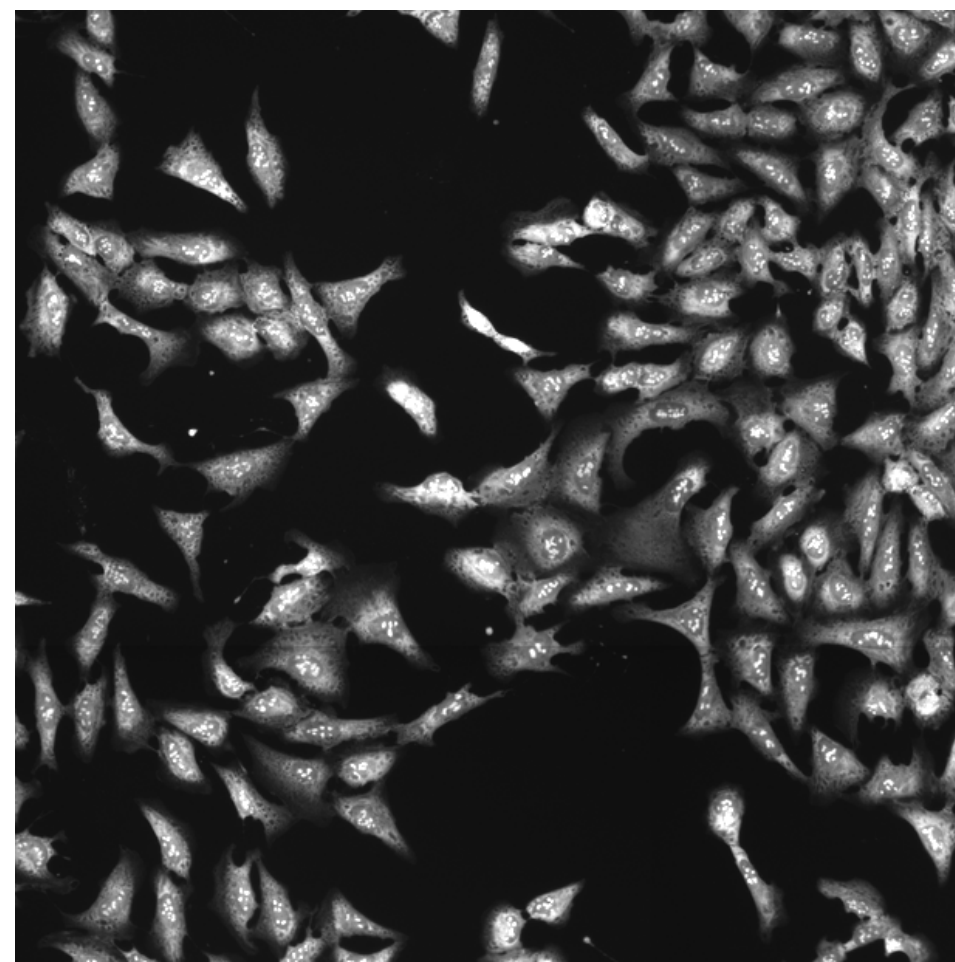
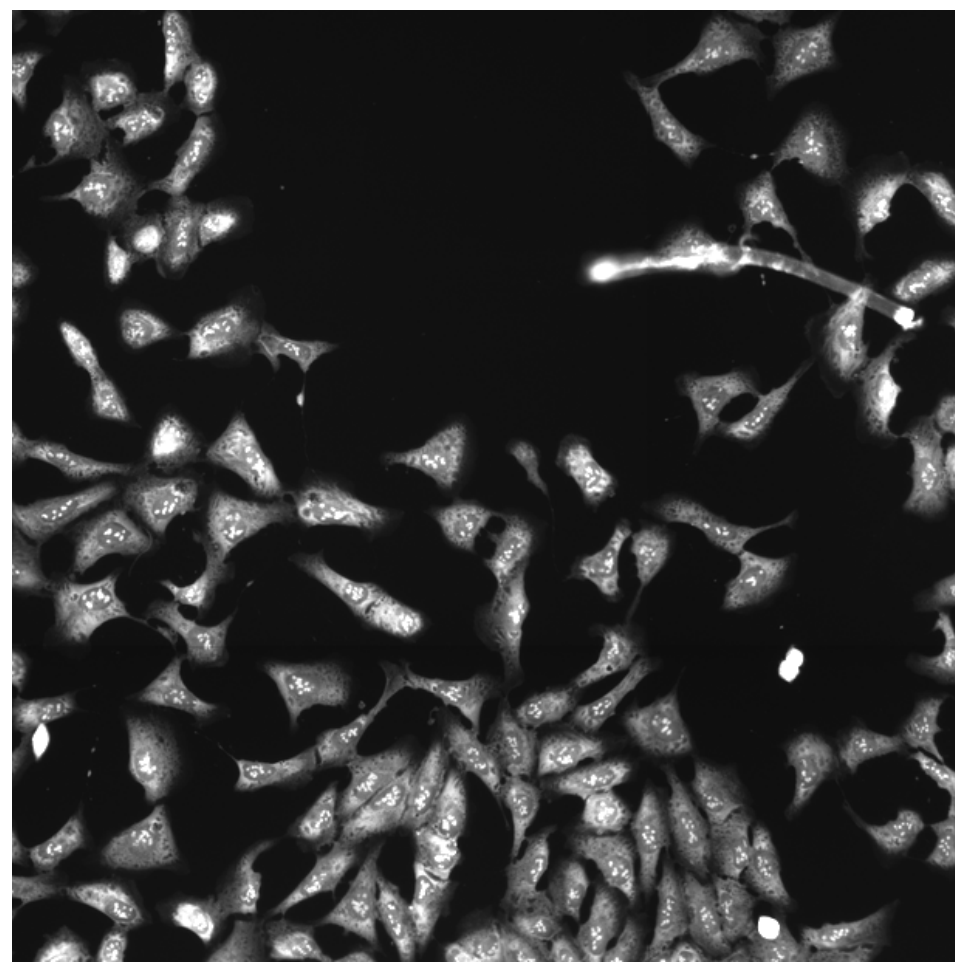
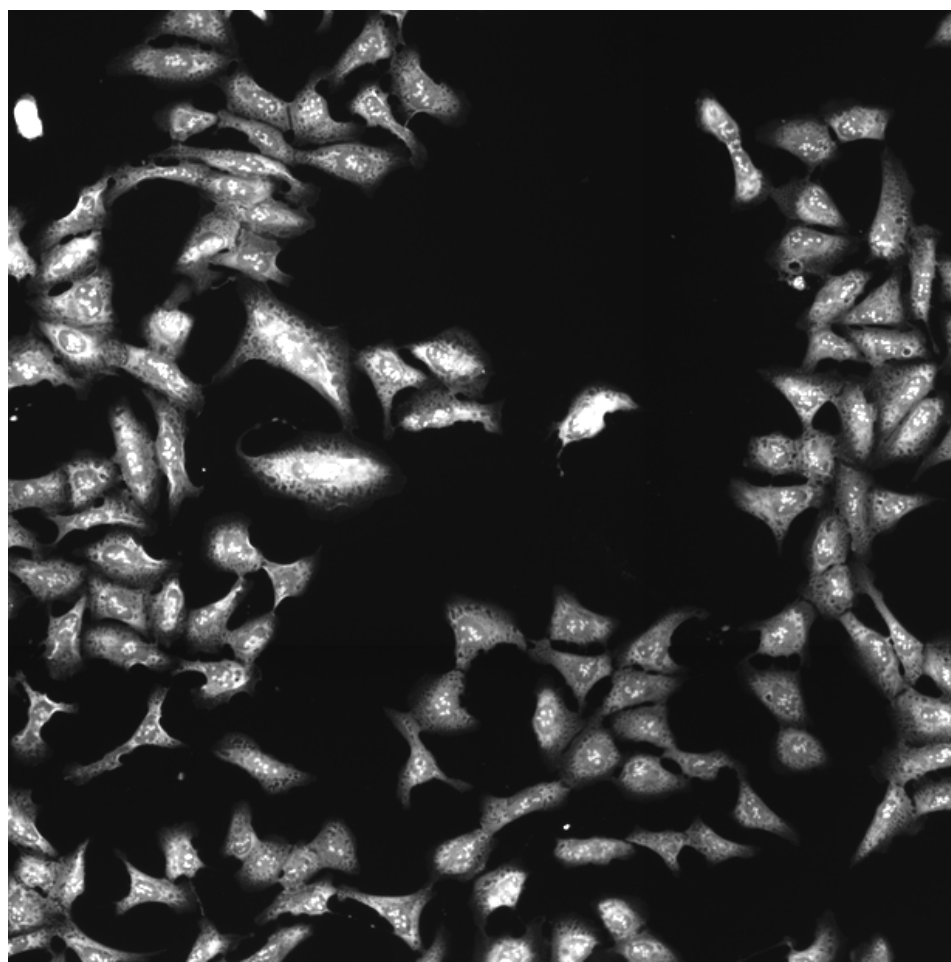
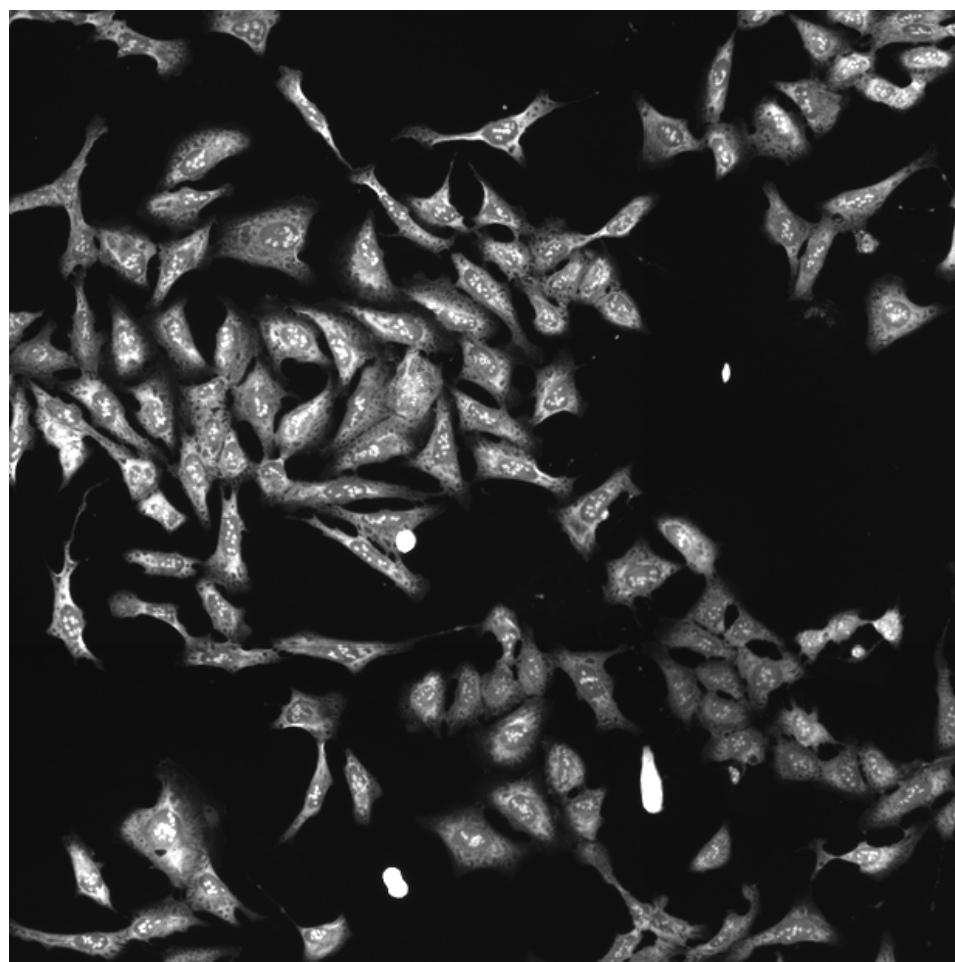
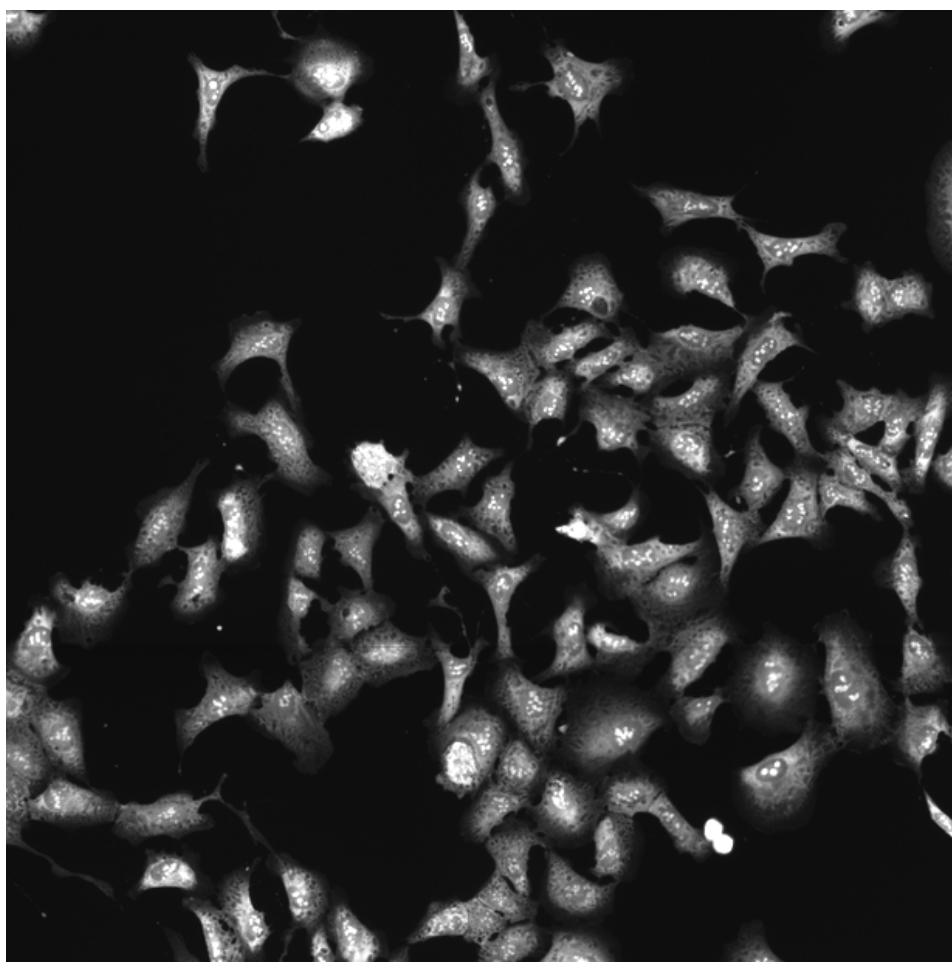
Cytoplasm_AreaShape_MeanRadius

Cells_Texture_SumAverage_DNA_10_0
Cells_Texture_SumAverage_DNA_3_0

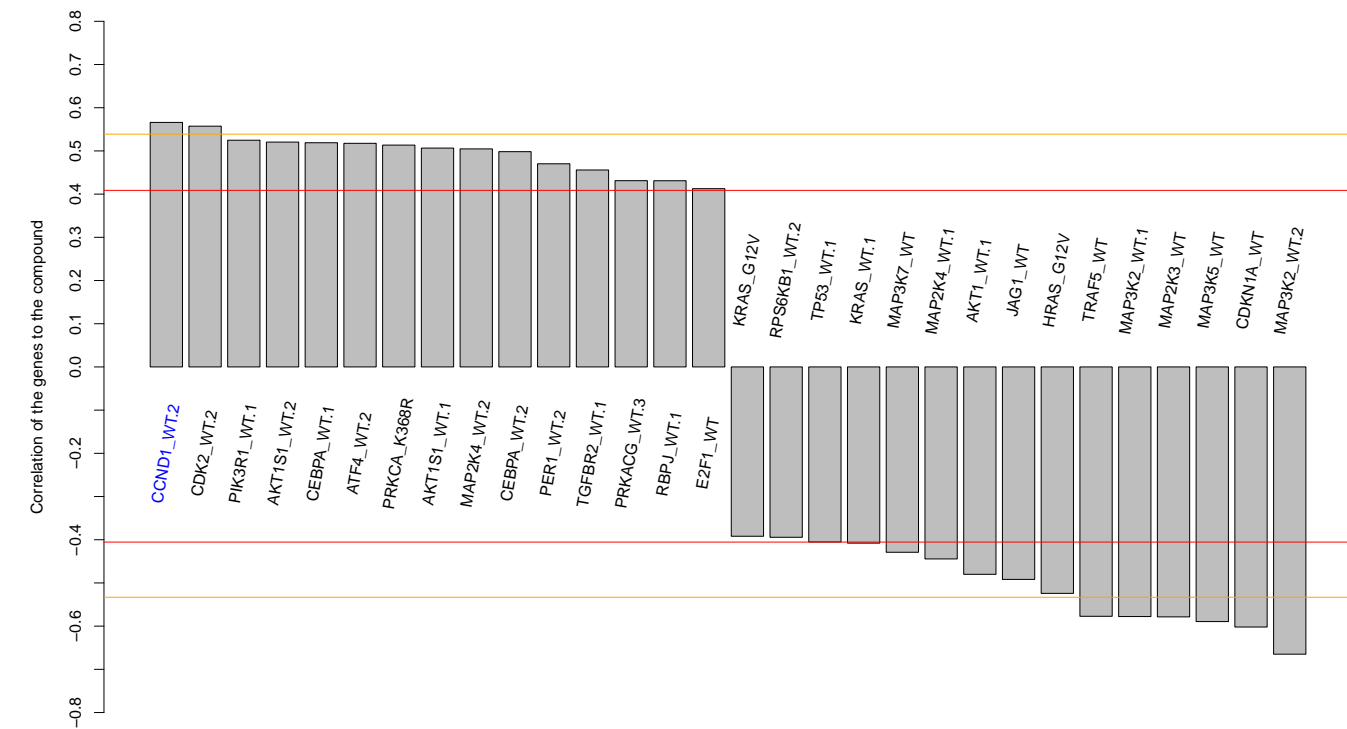
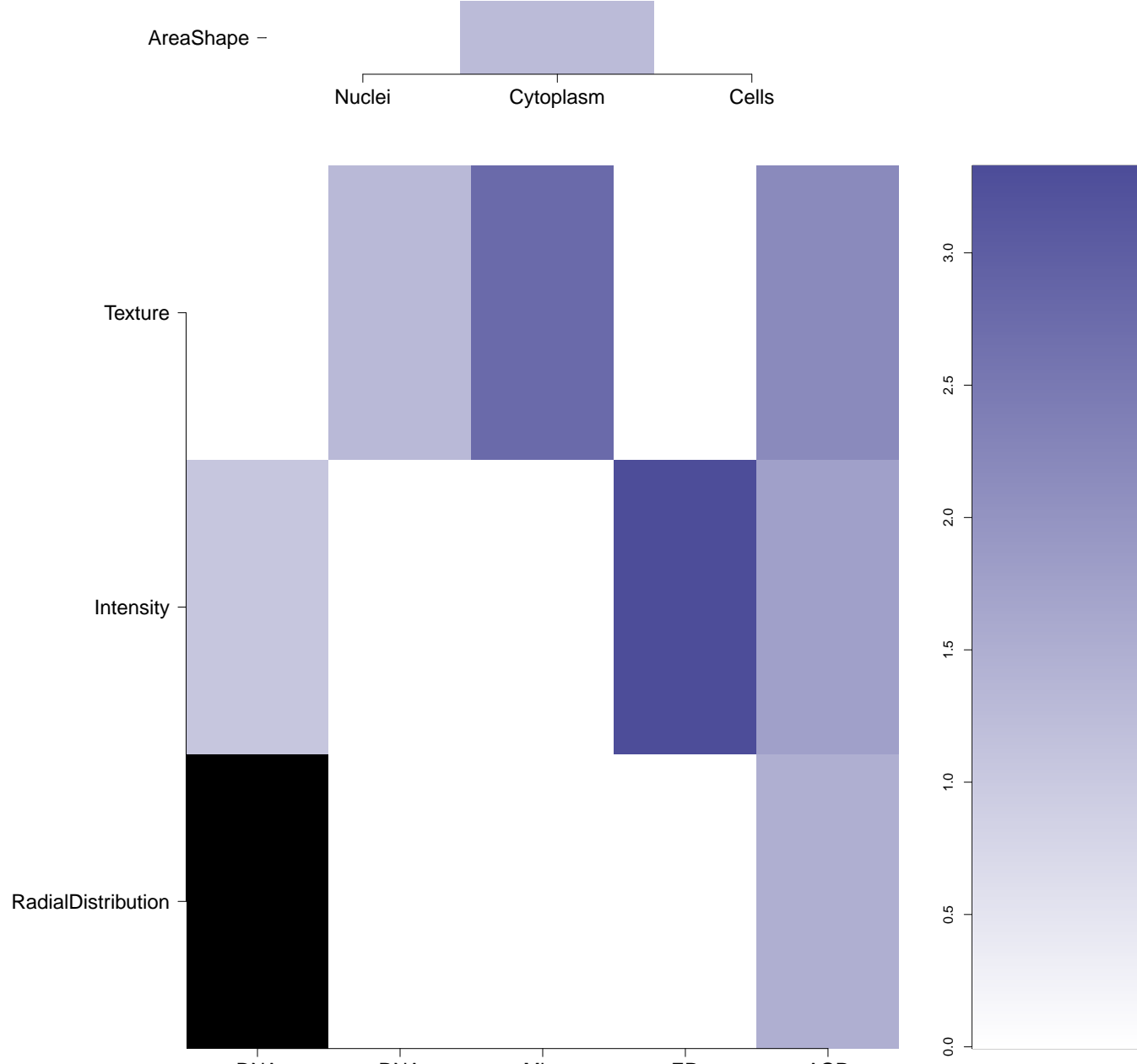
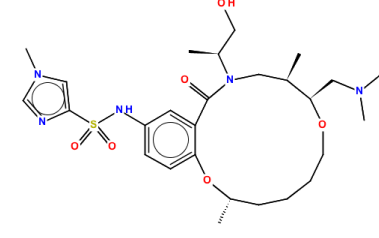
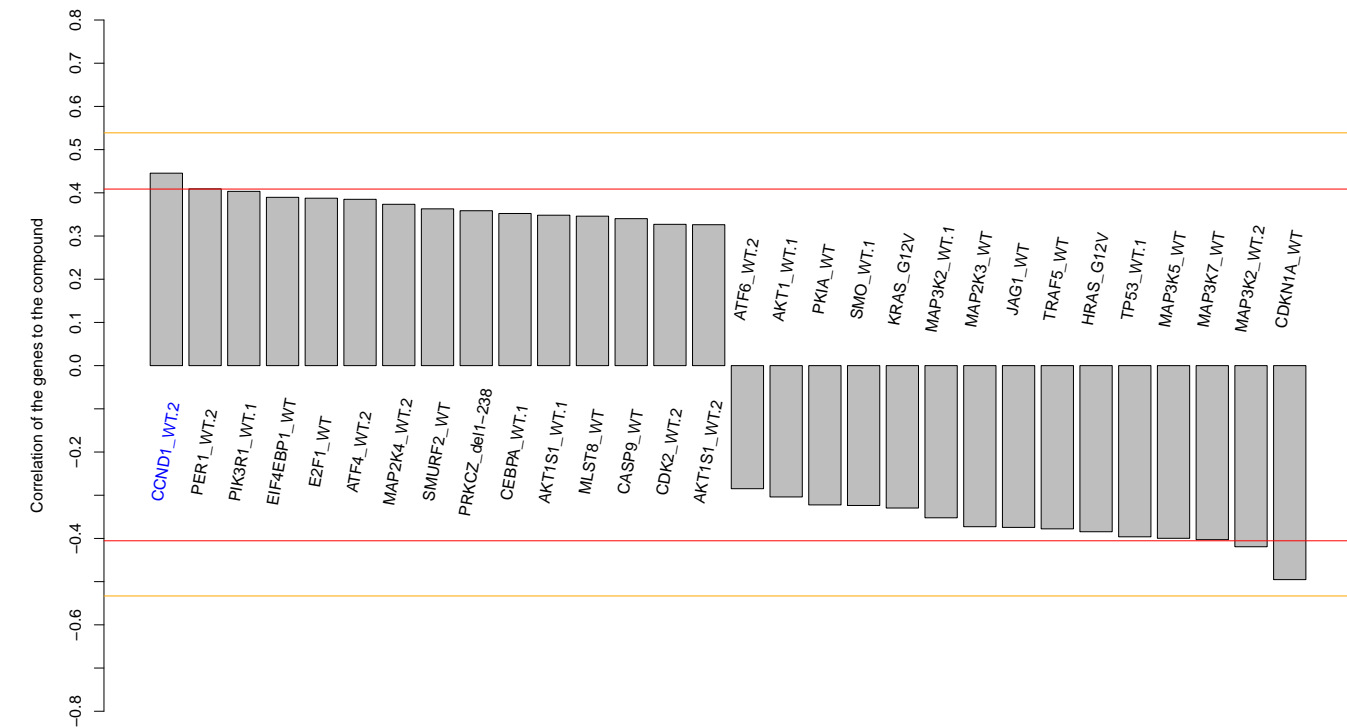
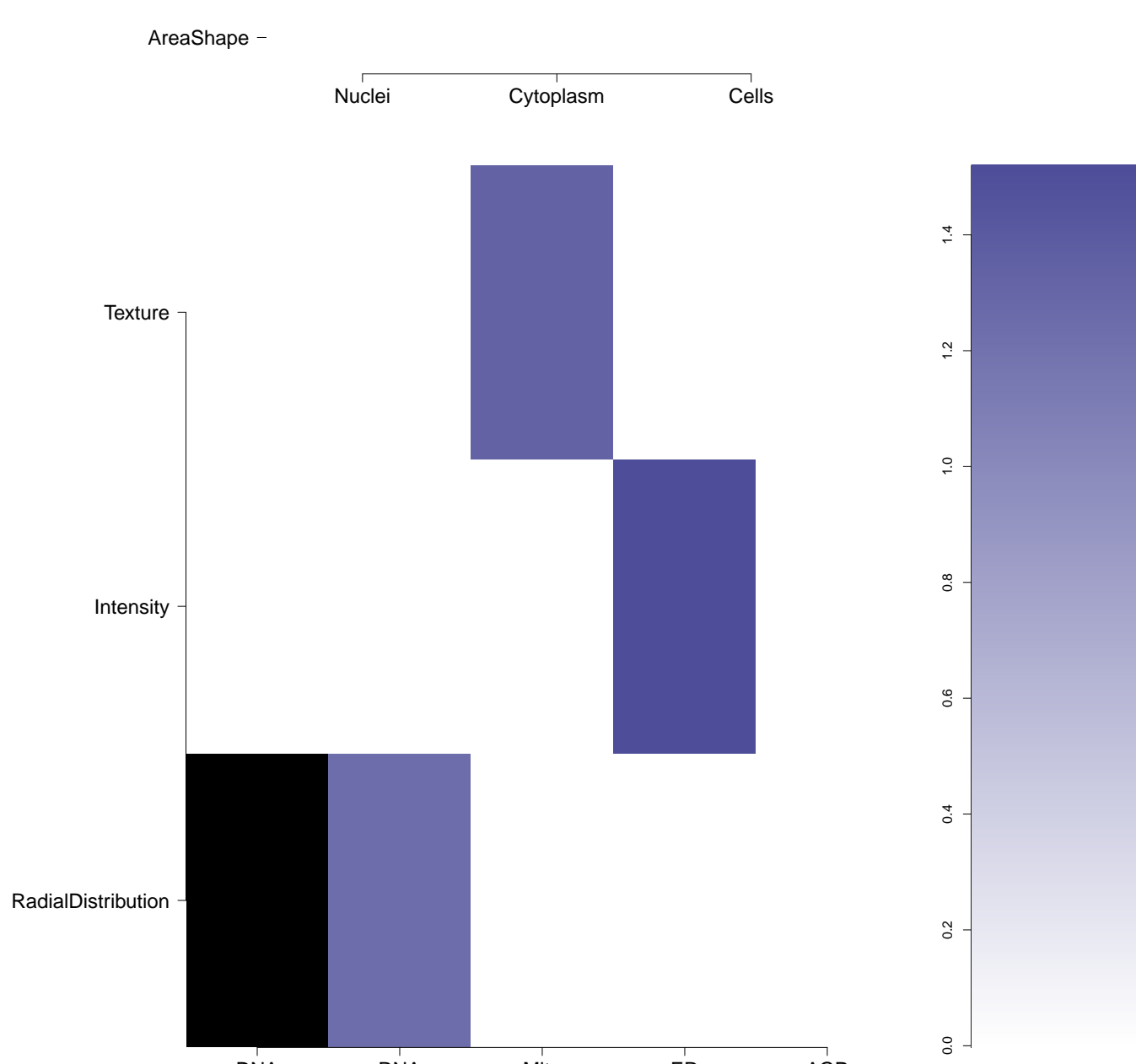

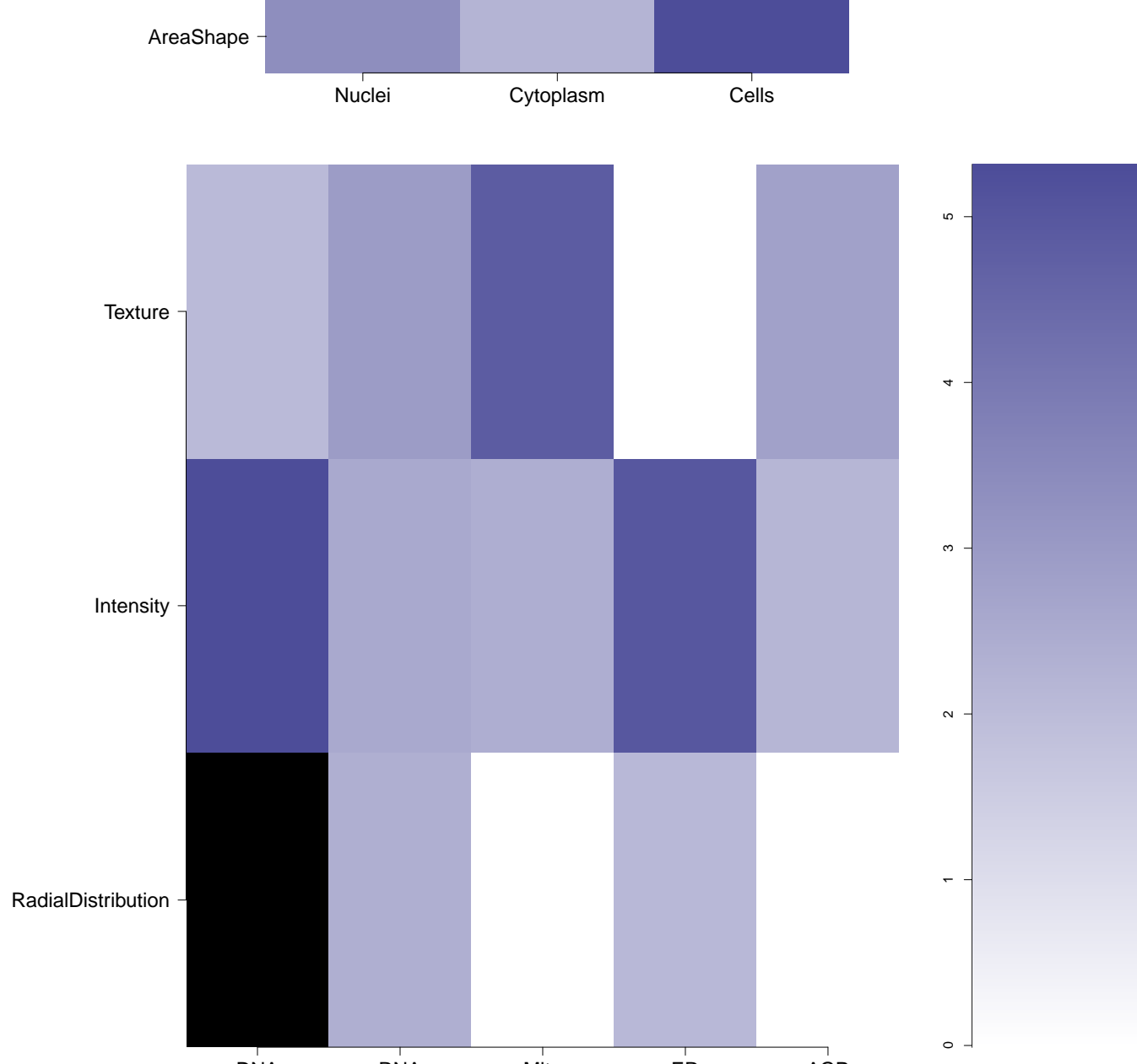
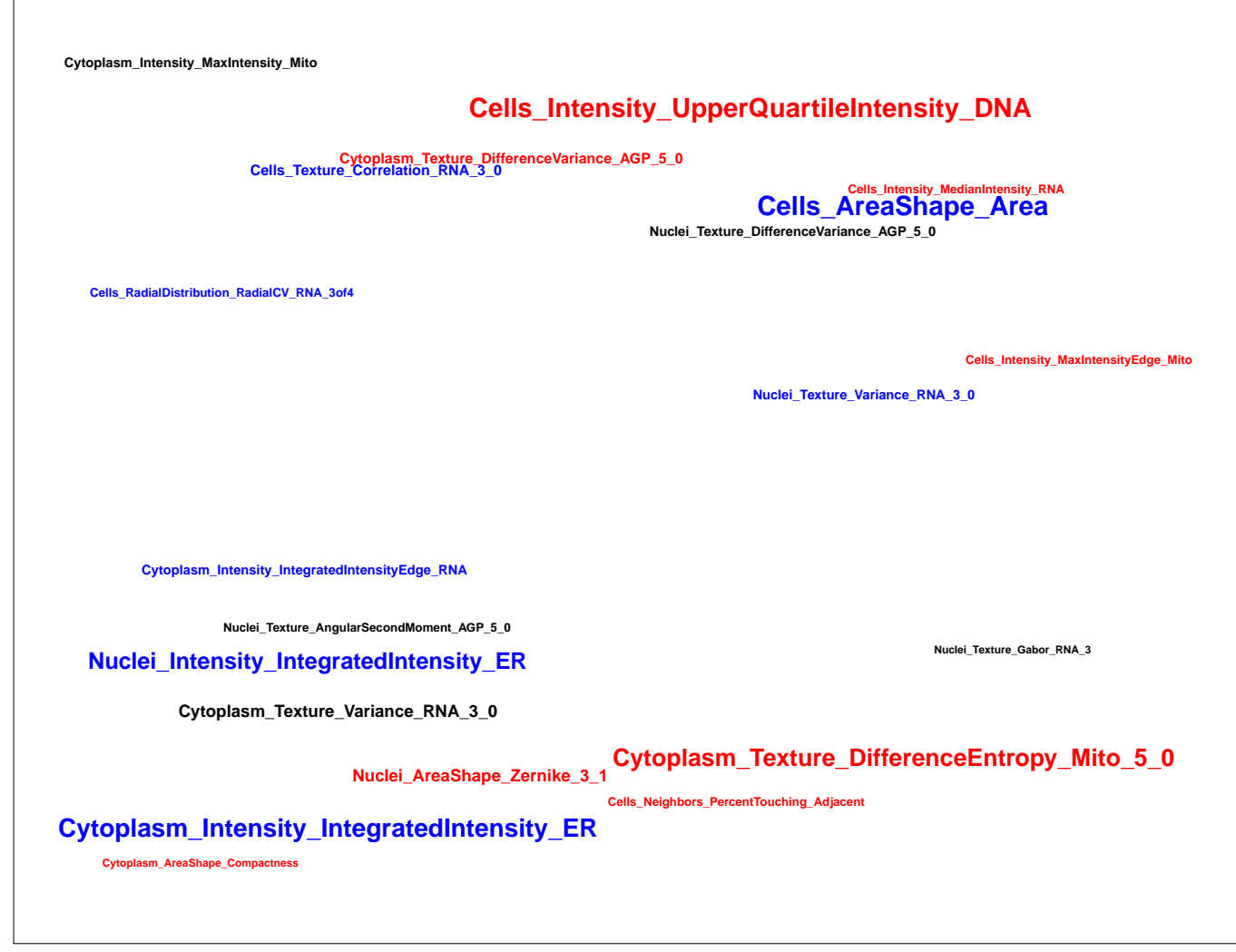
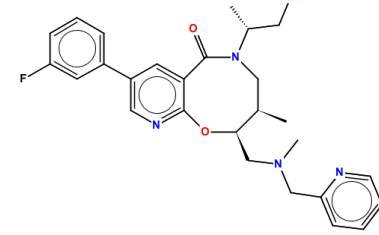
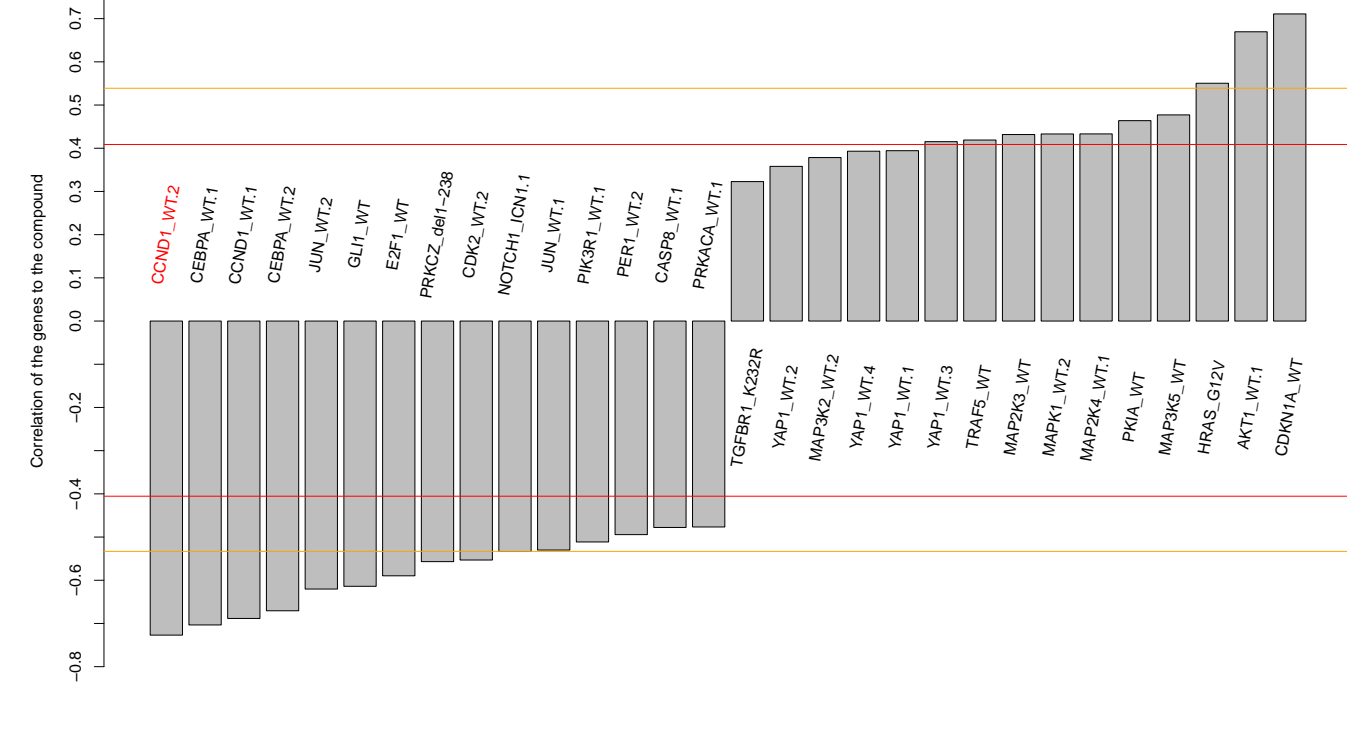
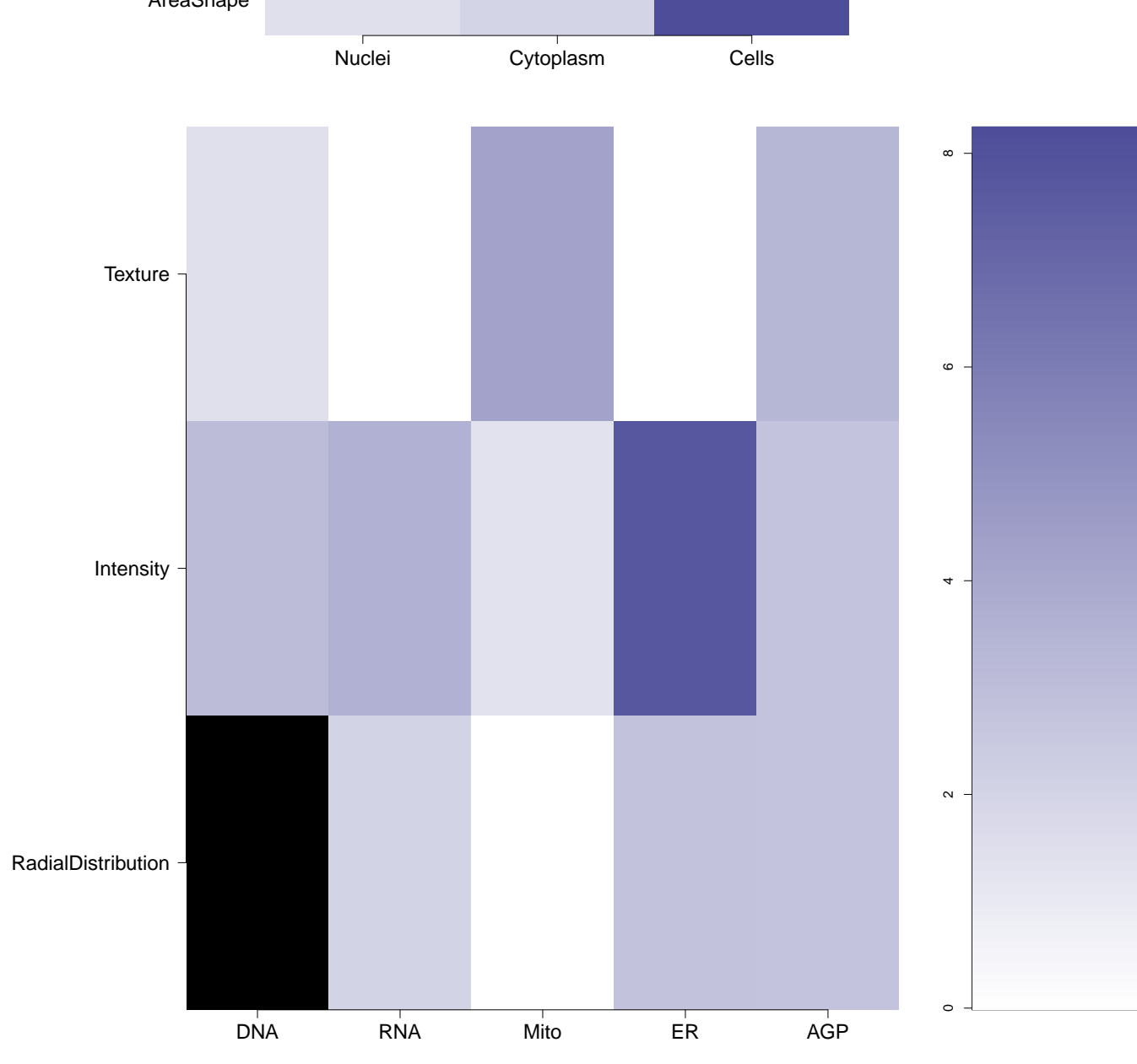
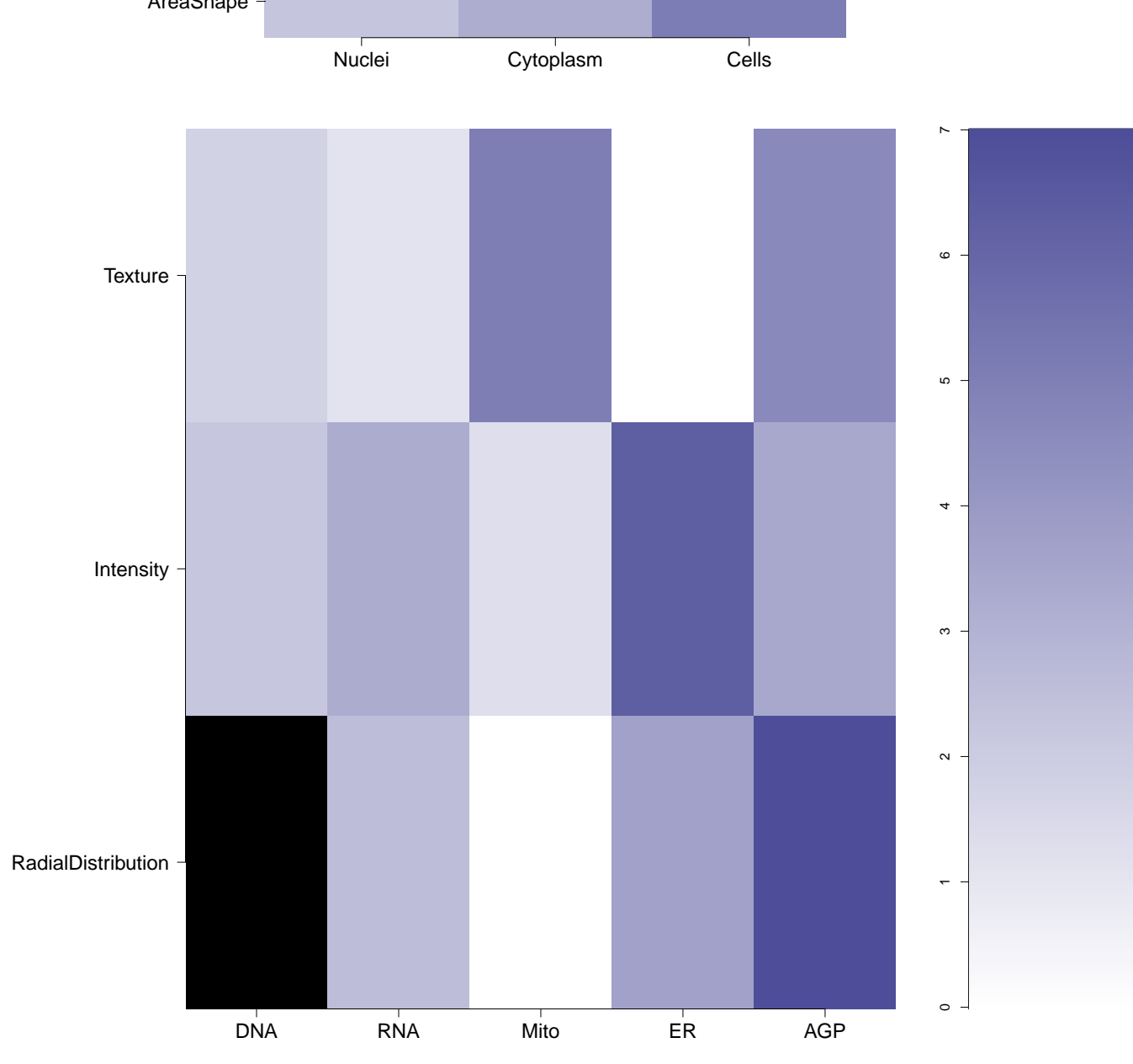

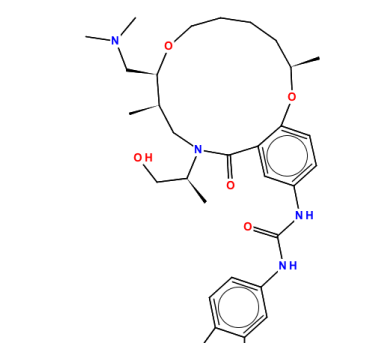
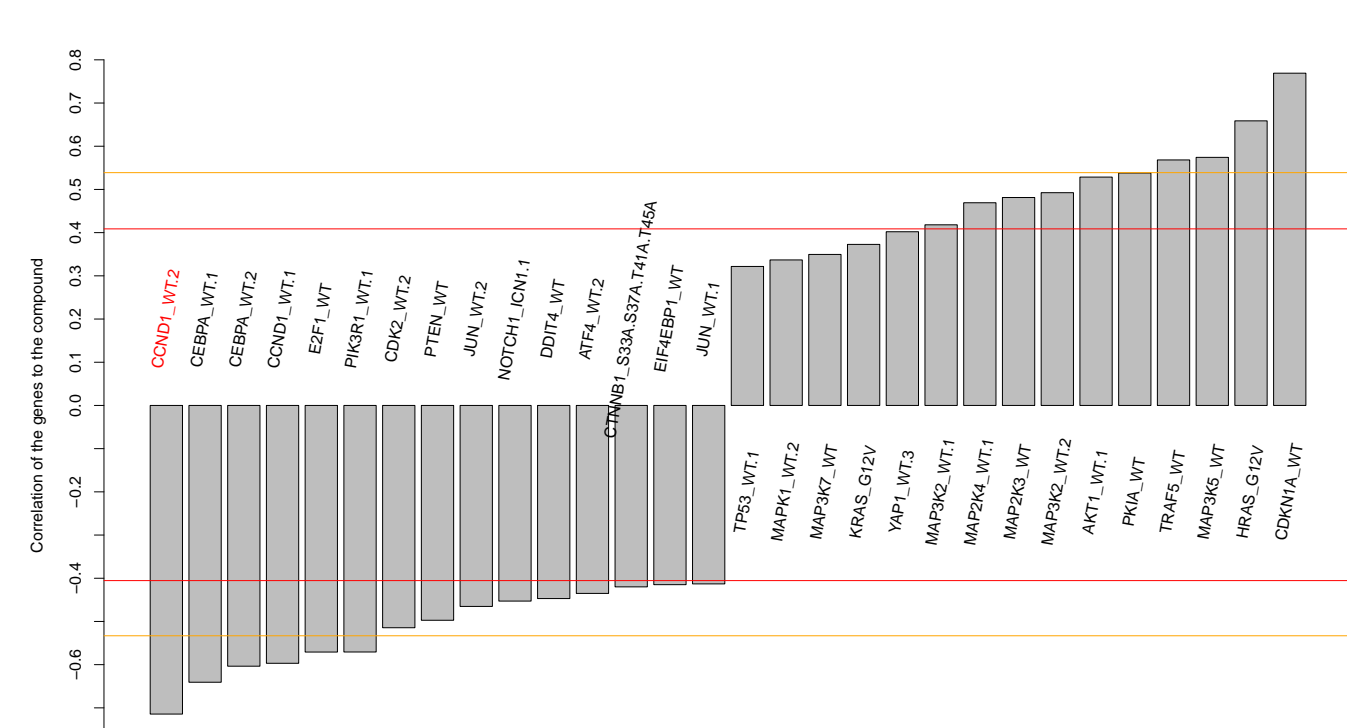
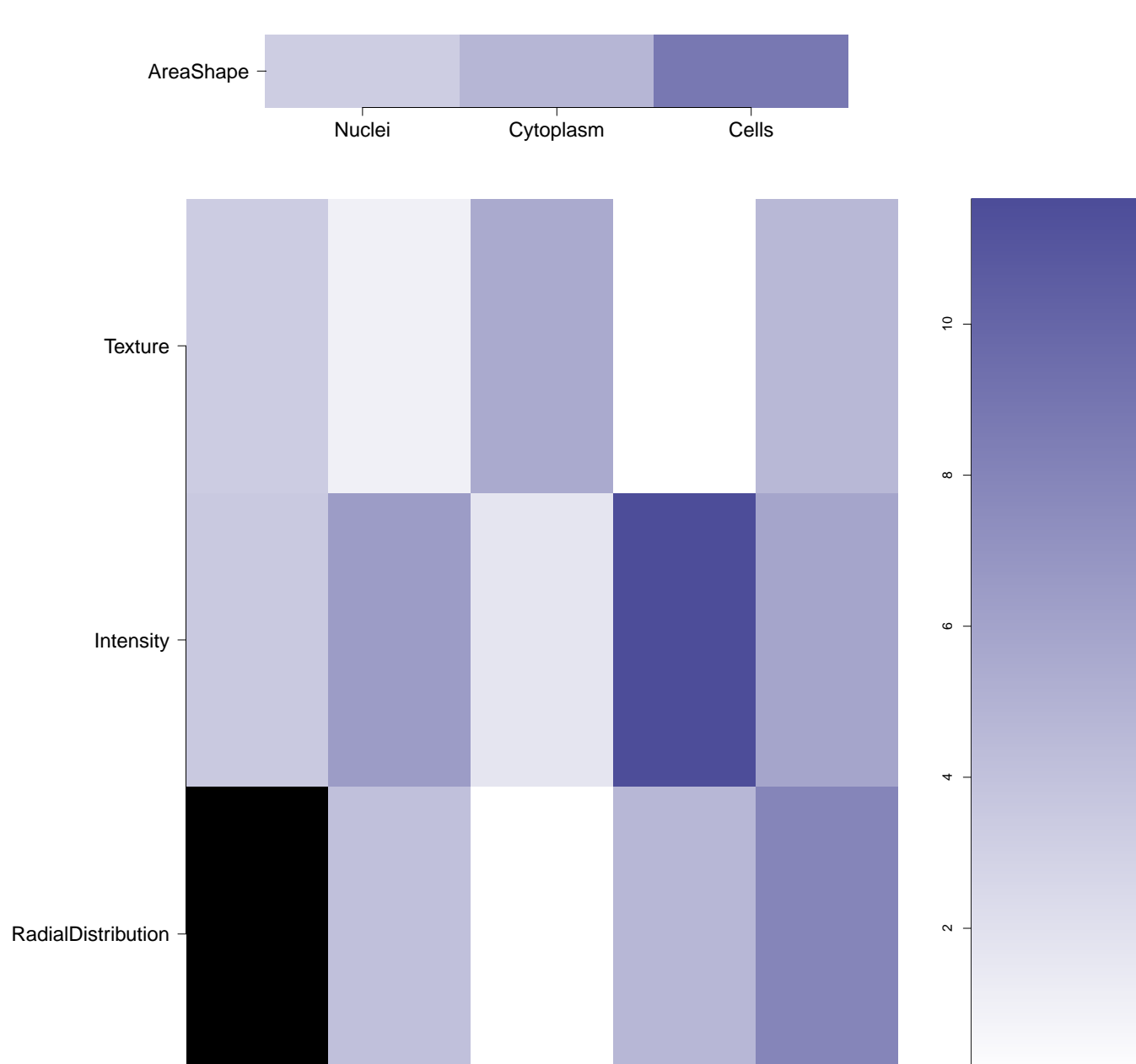

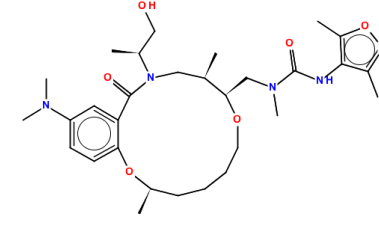
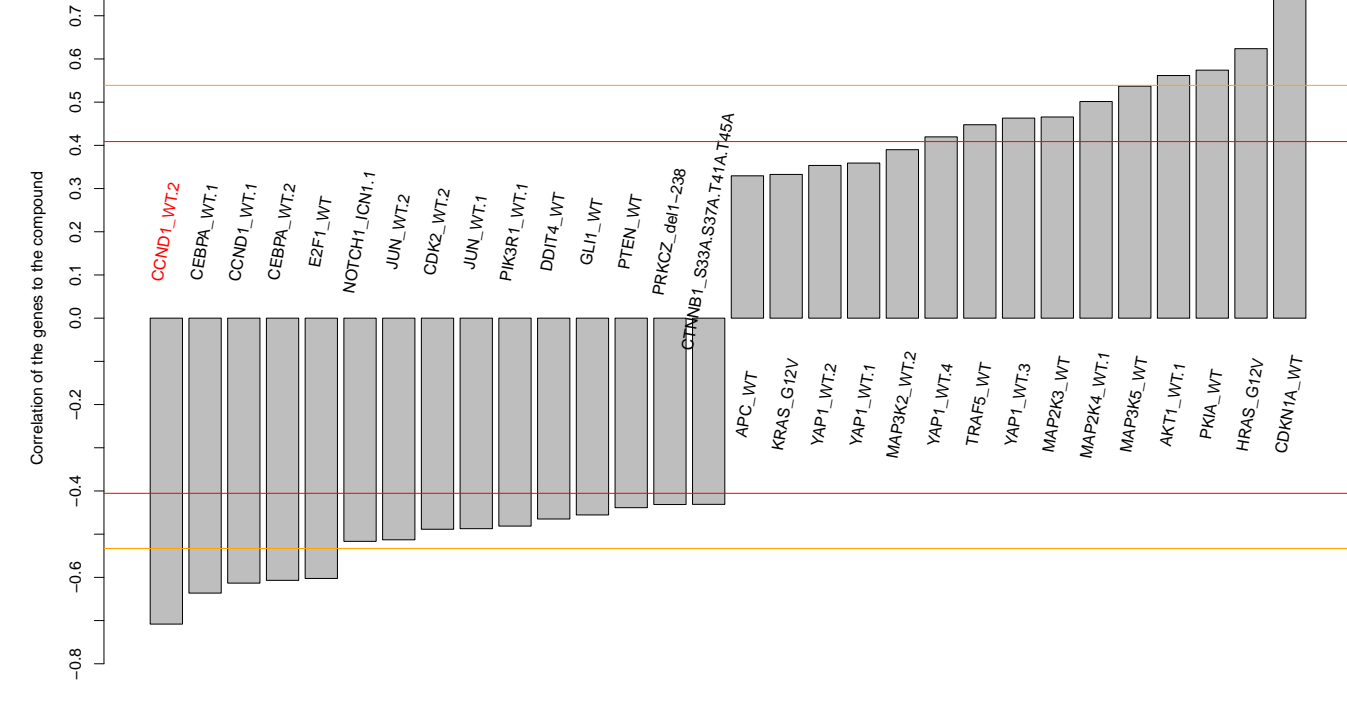
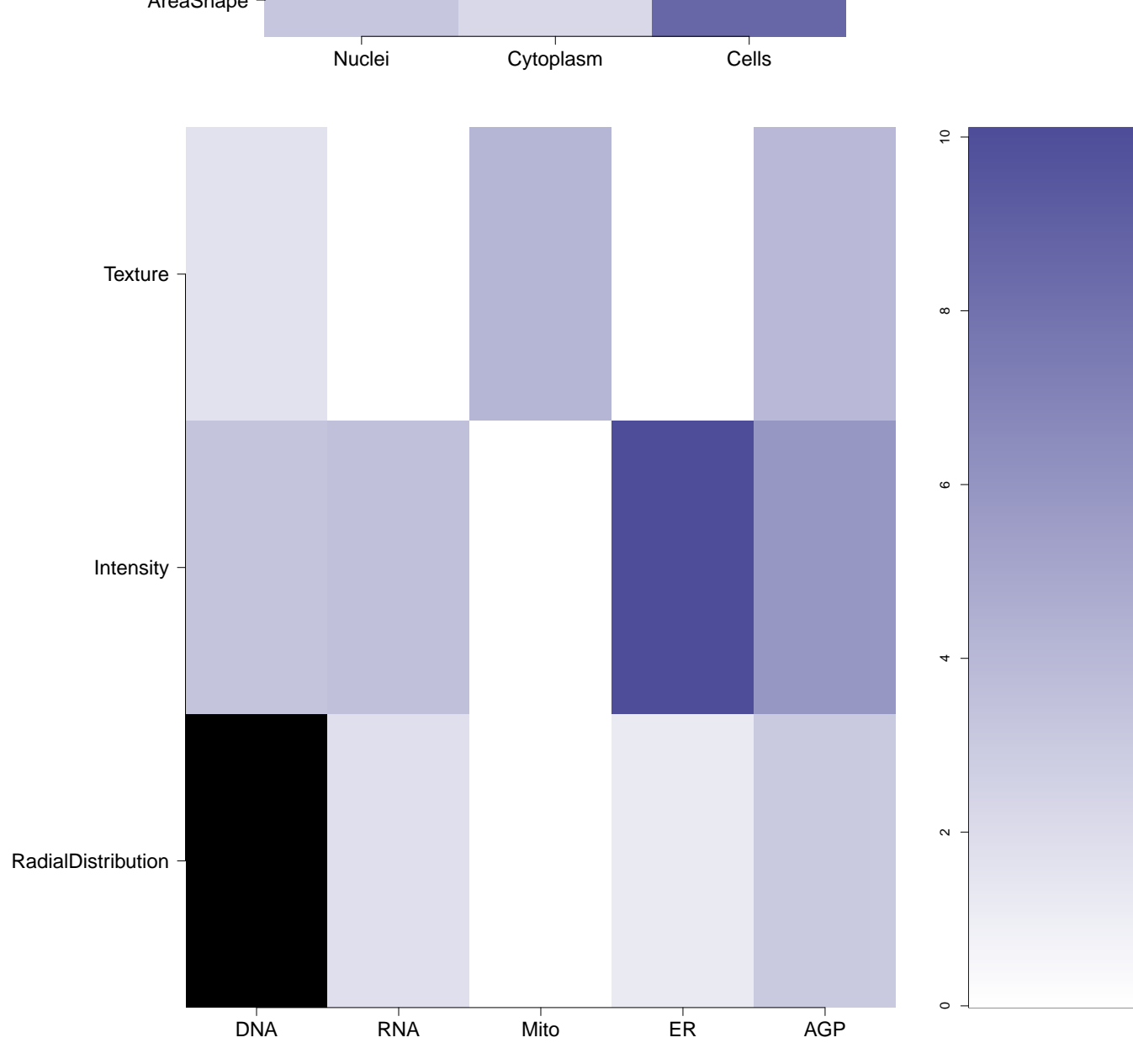
Cells_AreaShape_MedianRadius

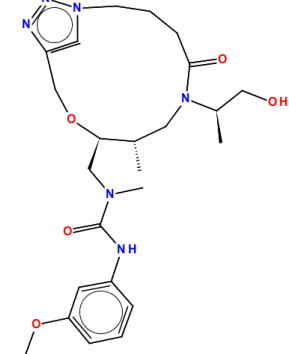
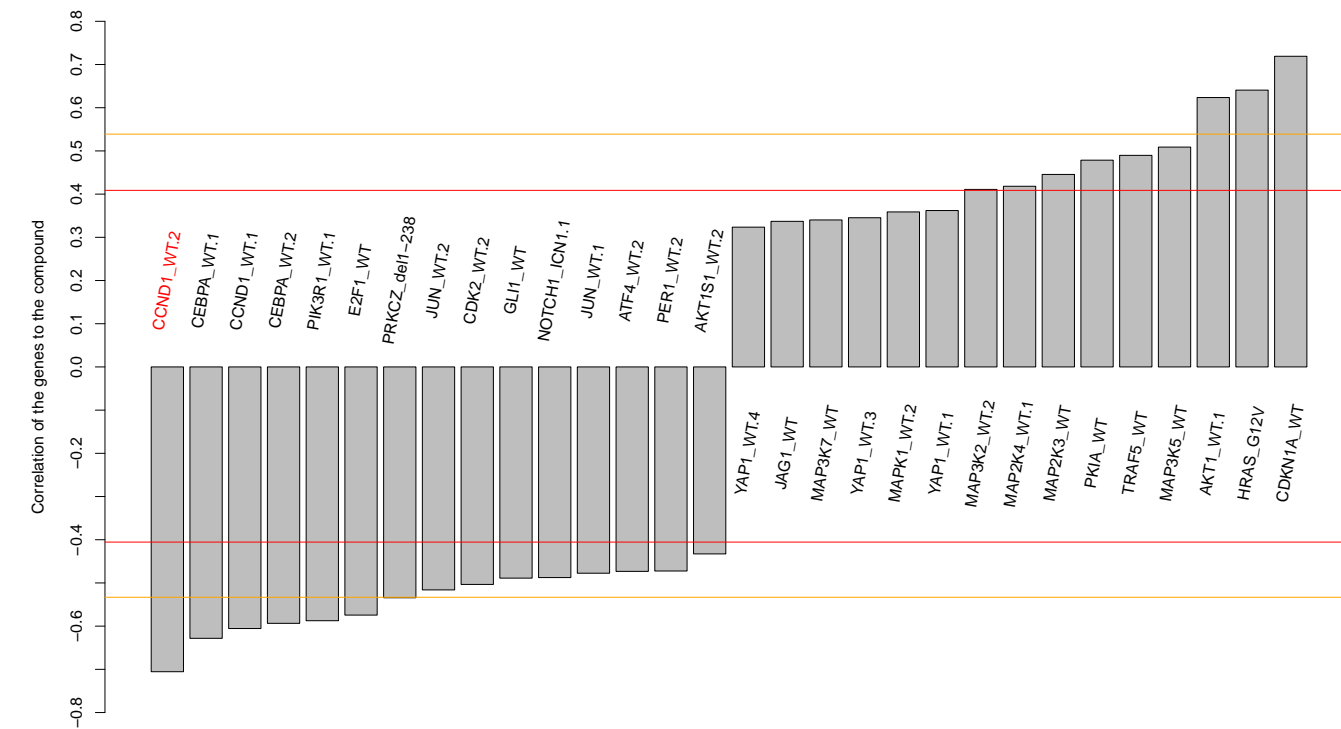
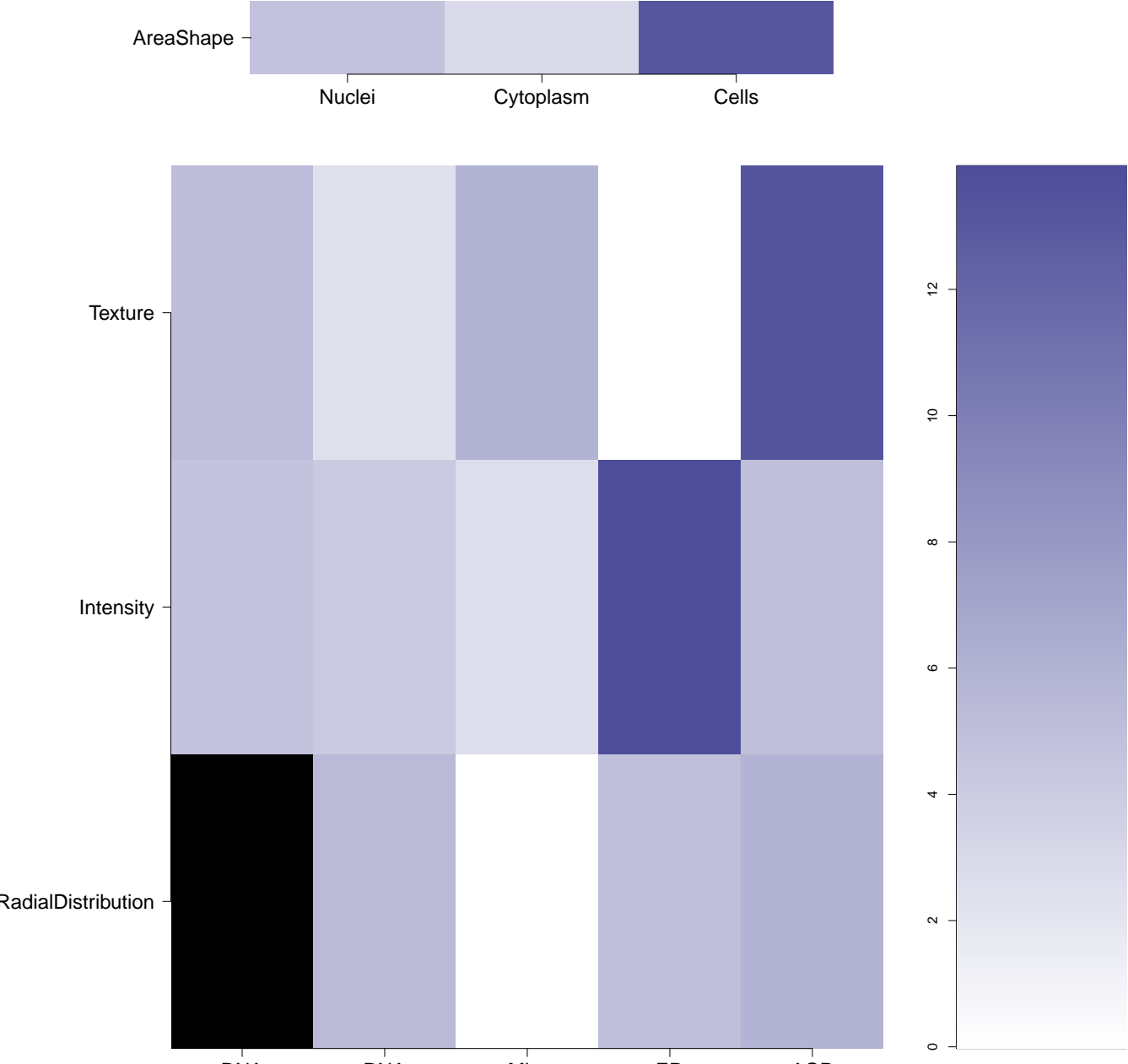
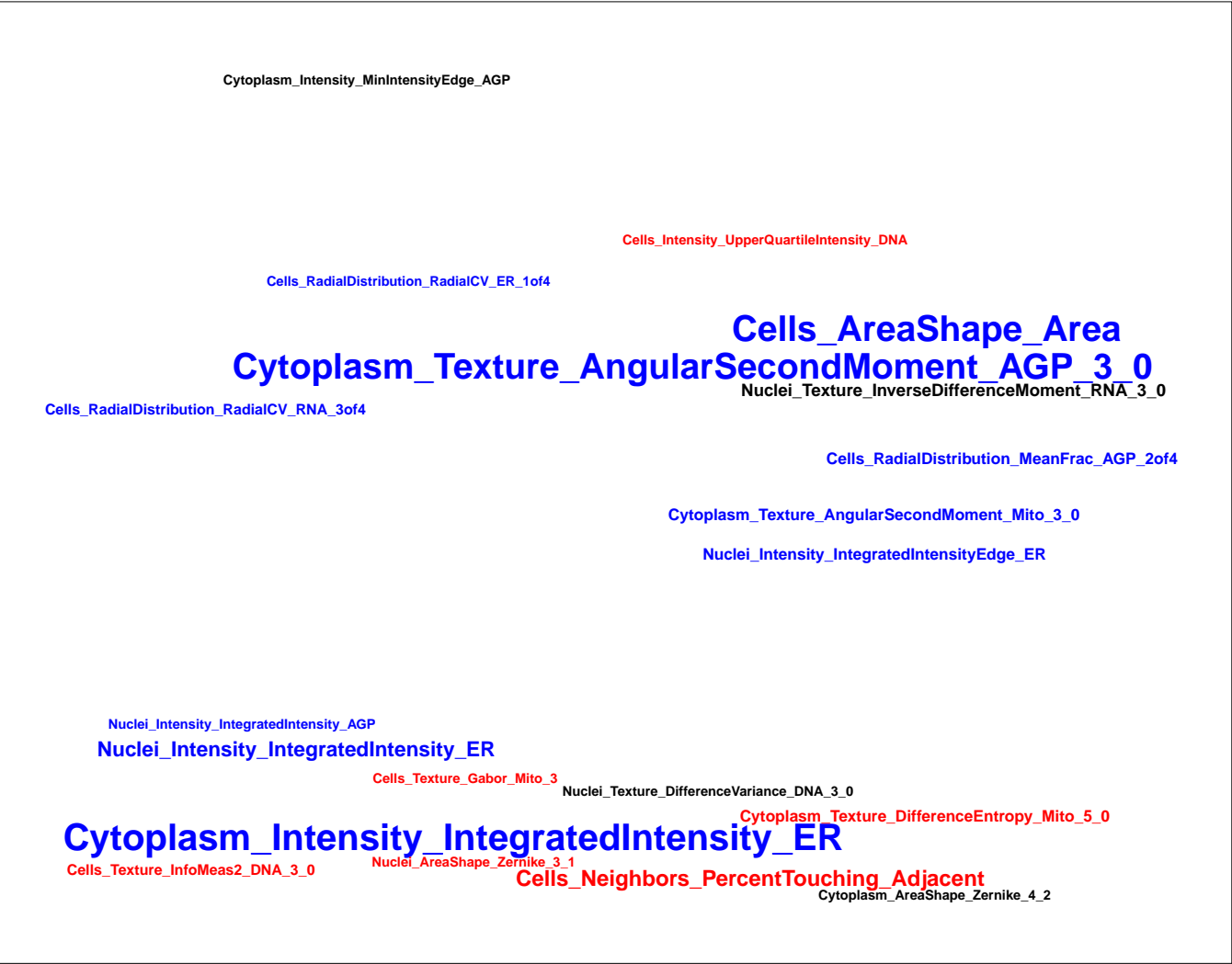
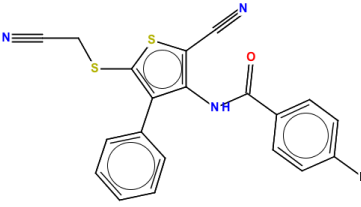
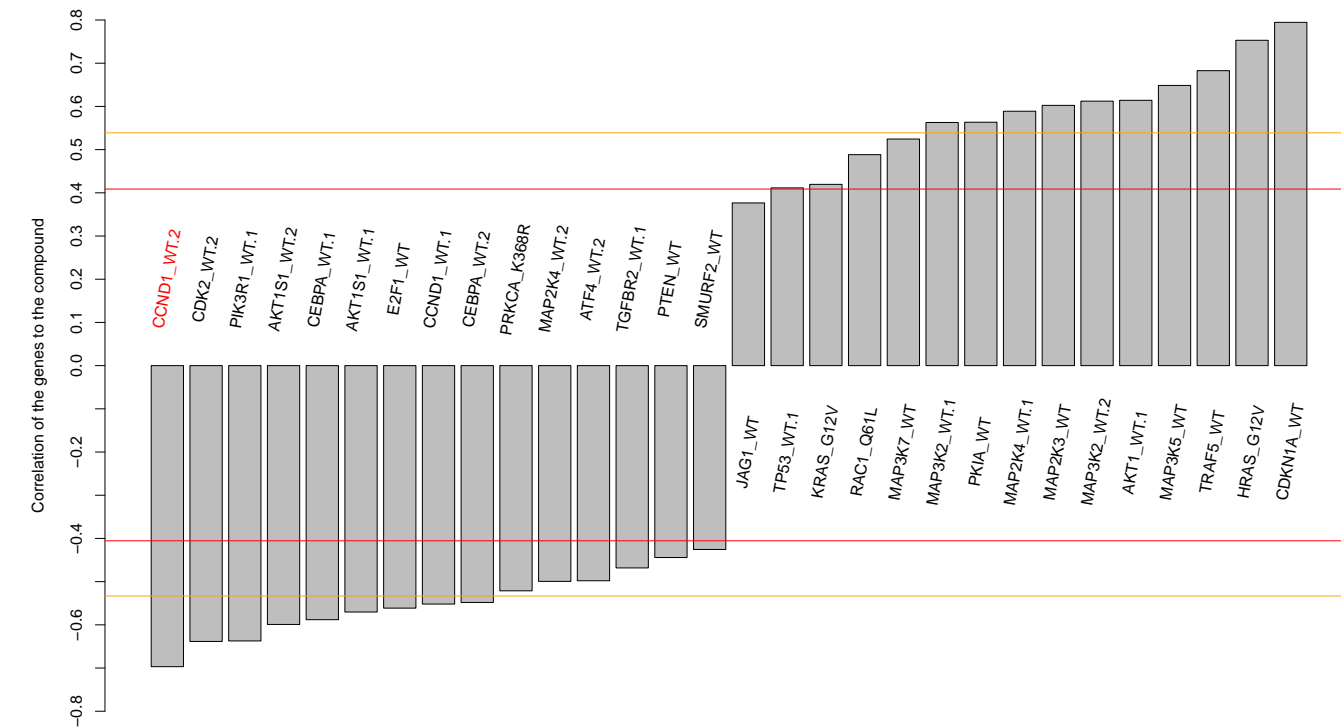
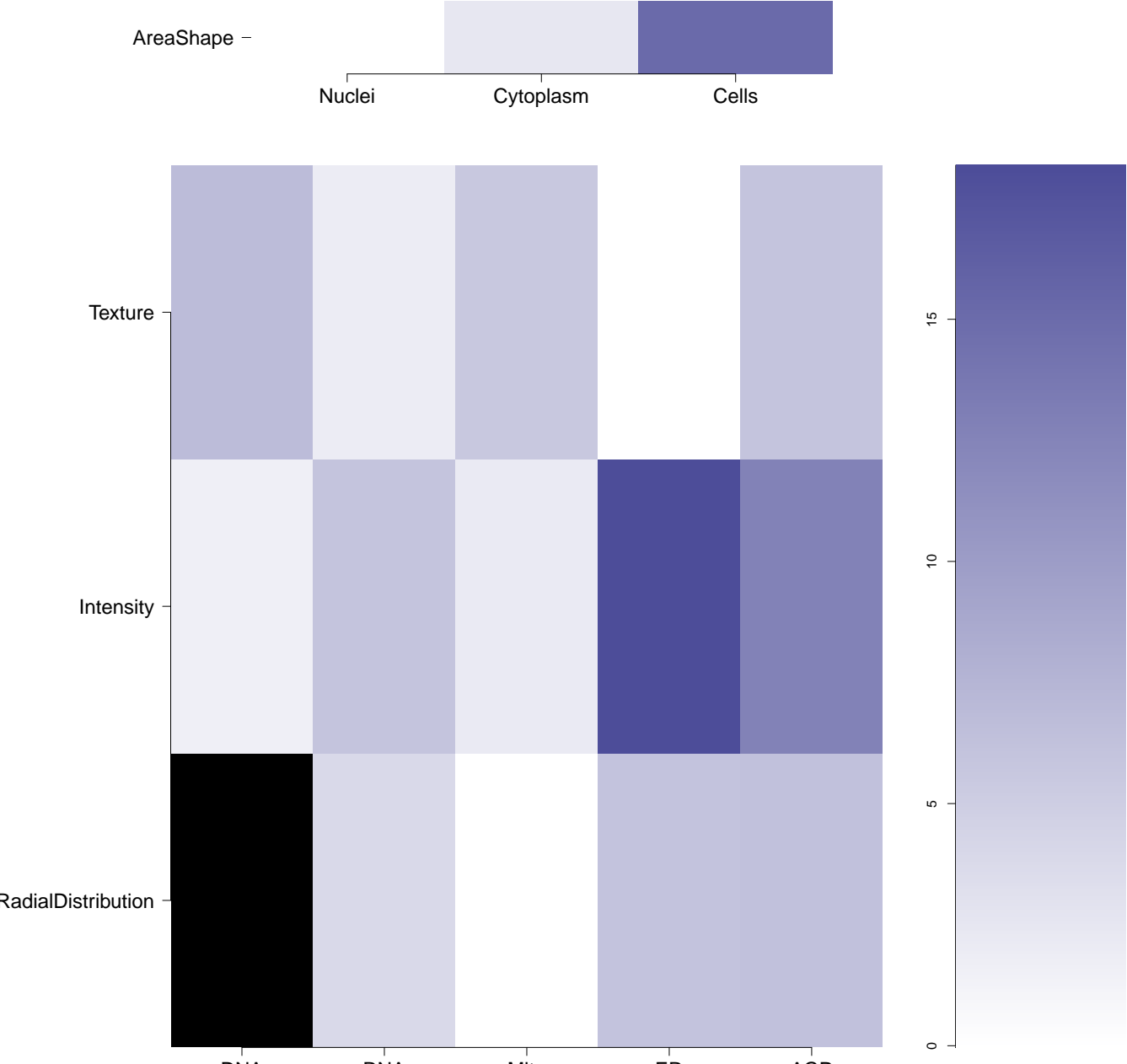
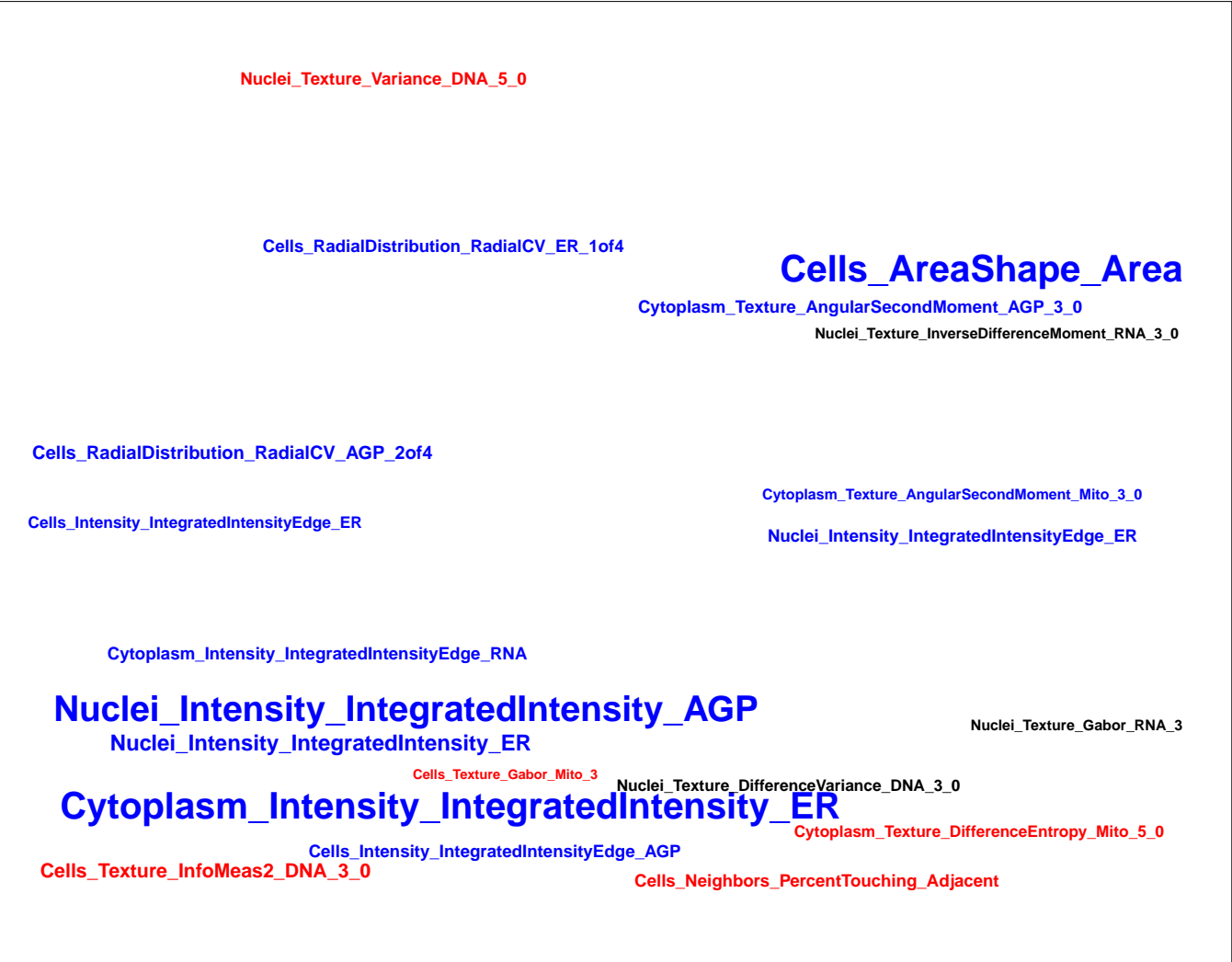
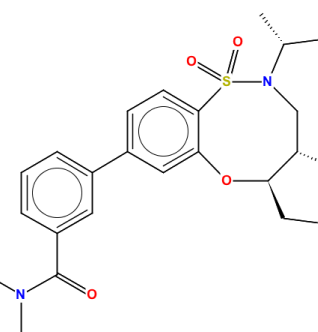
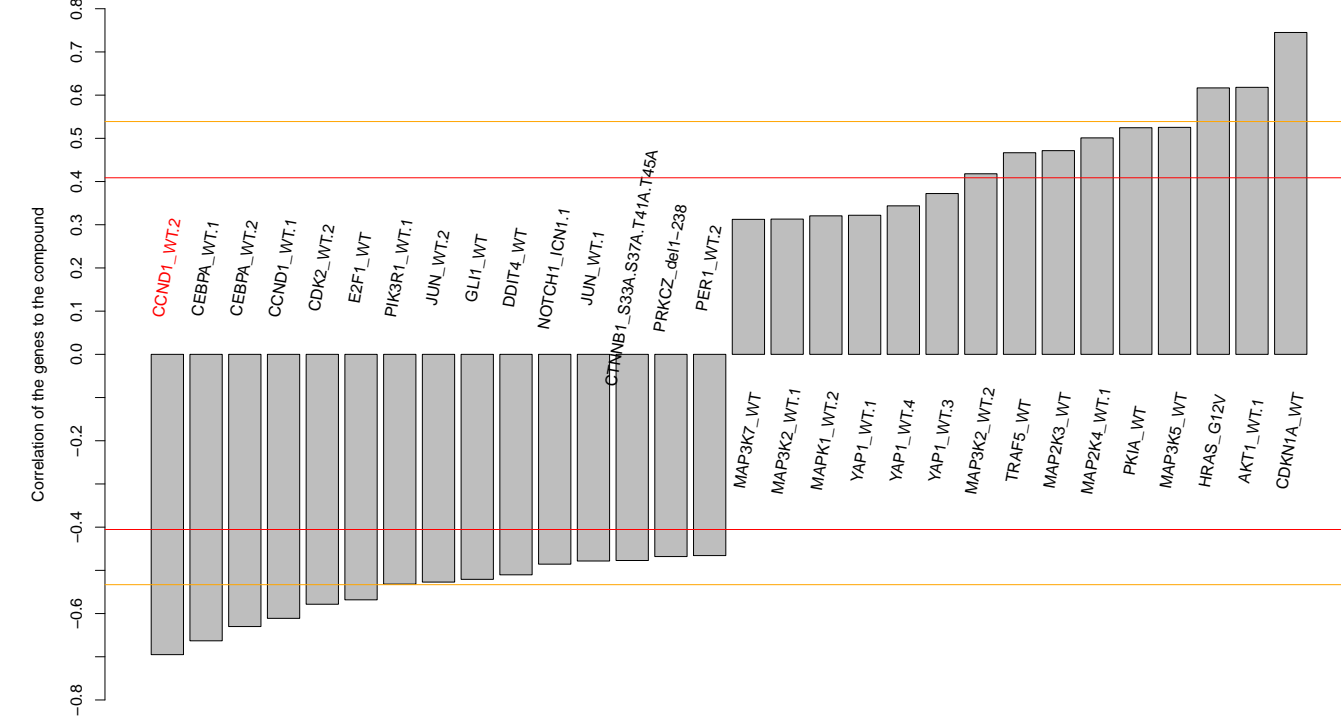
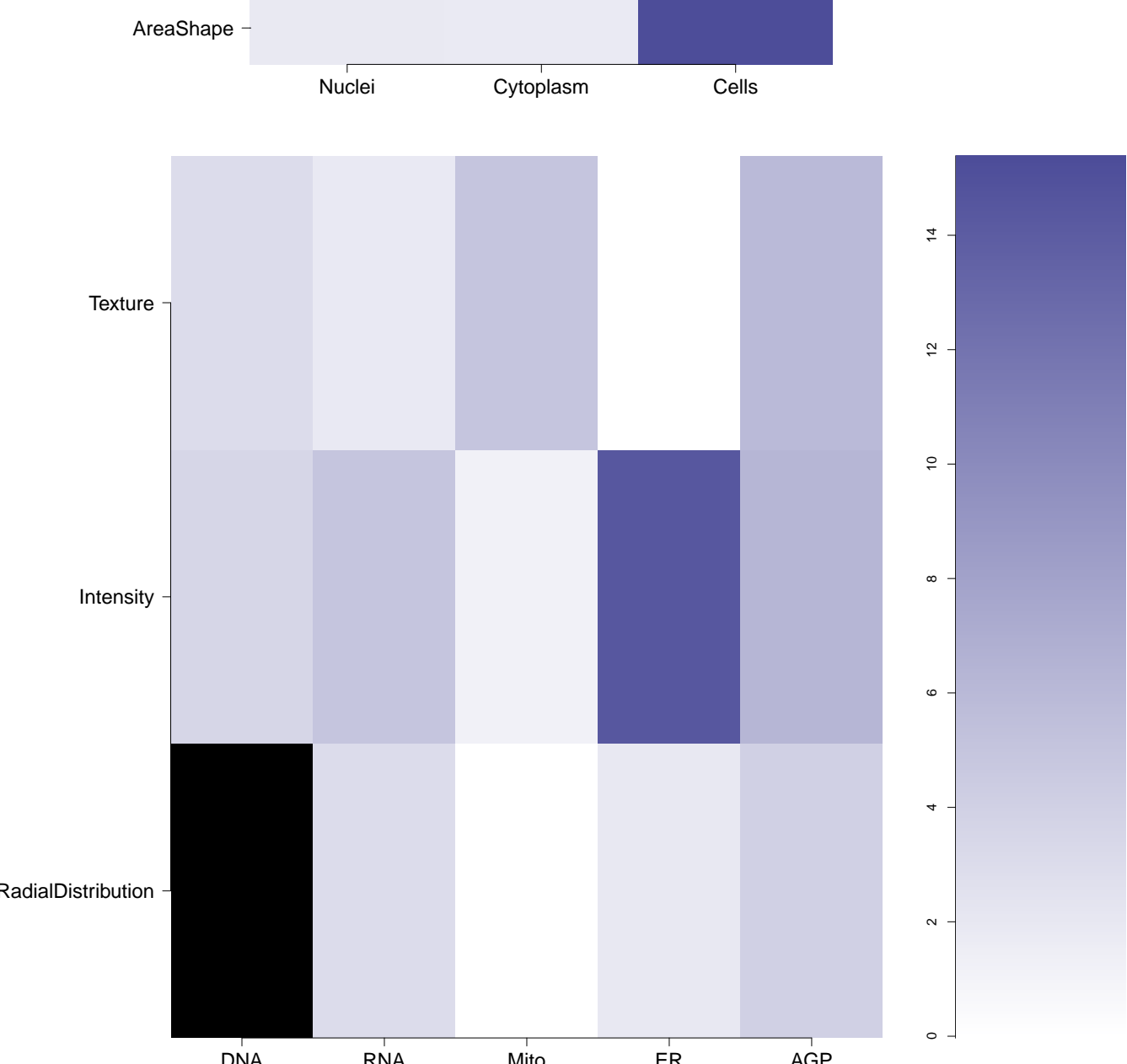
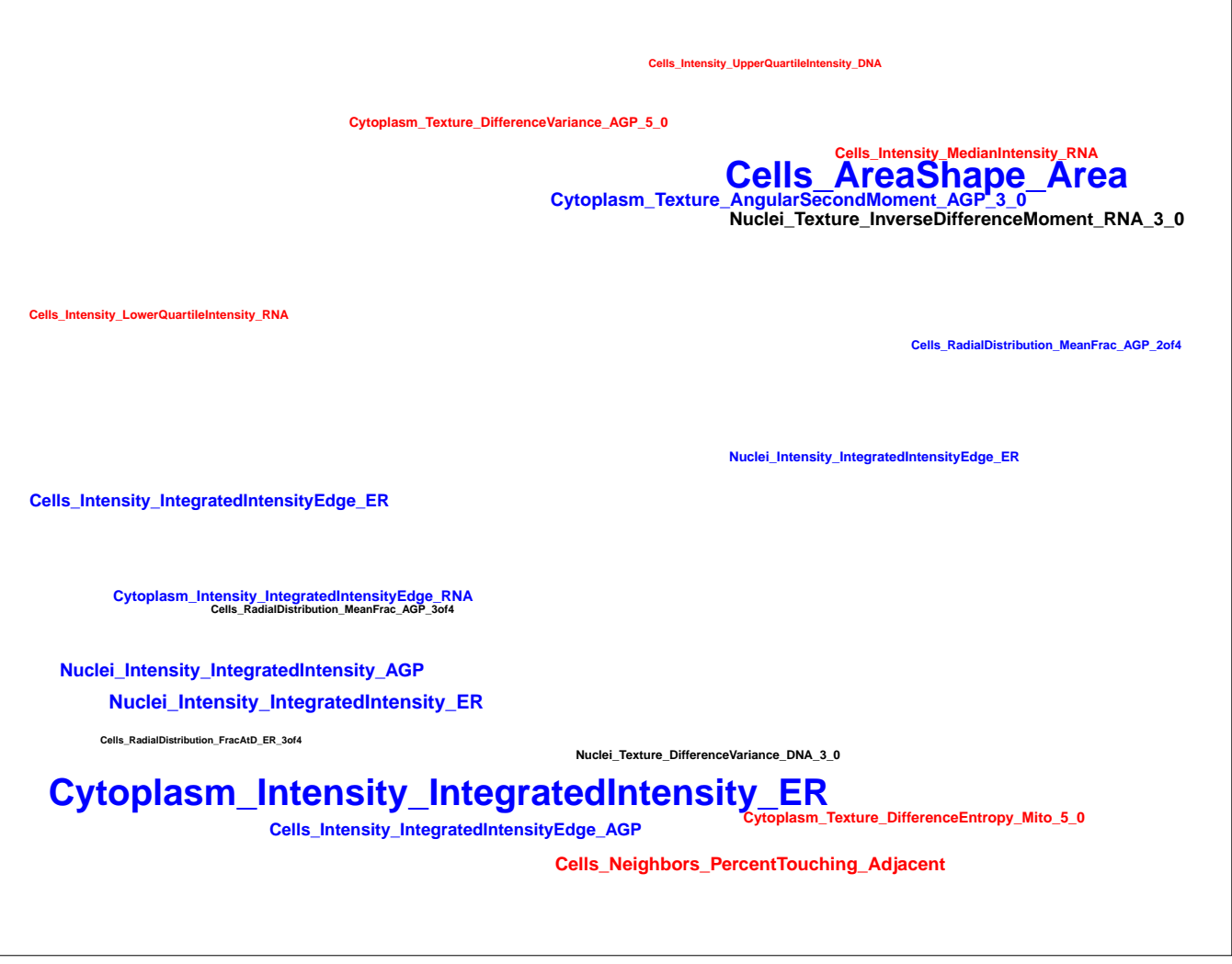
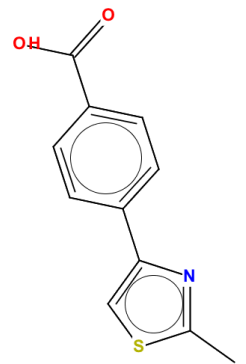
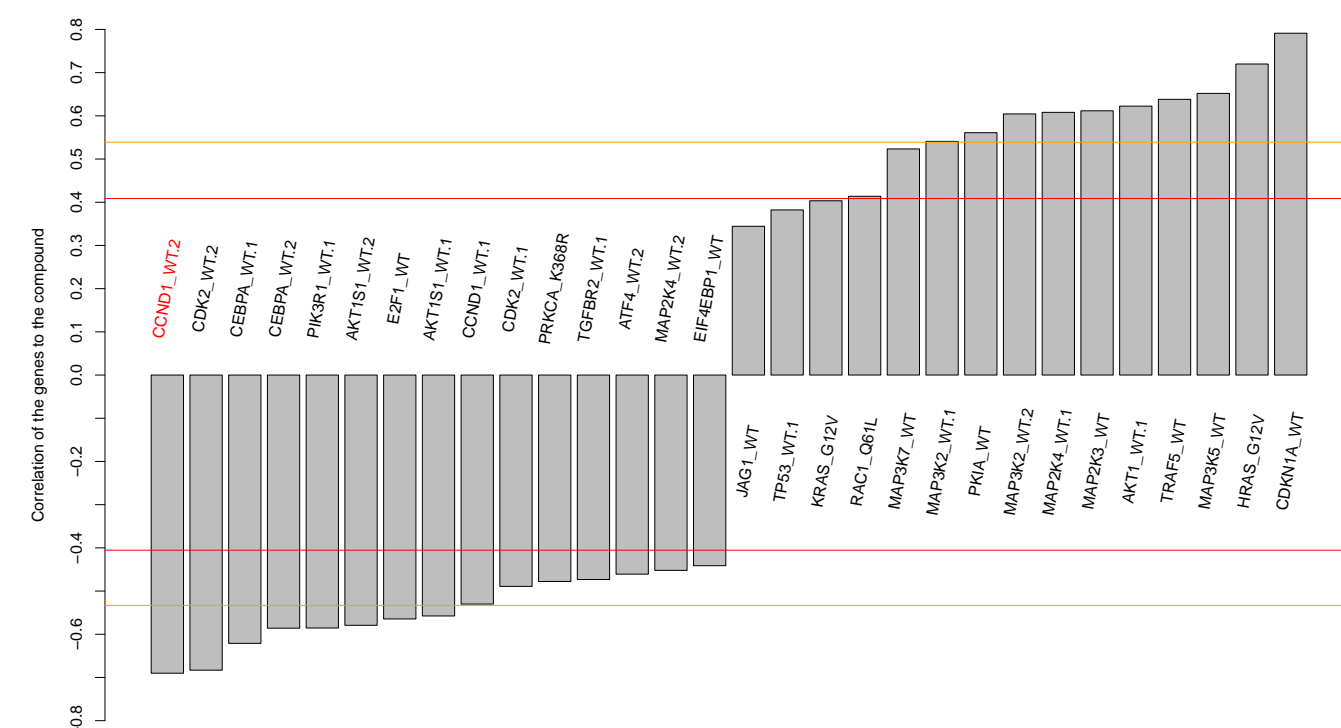
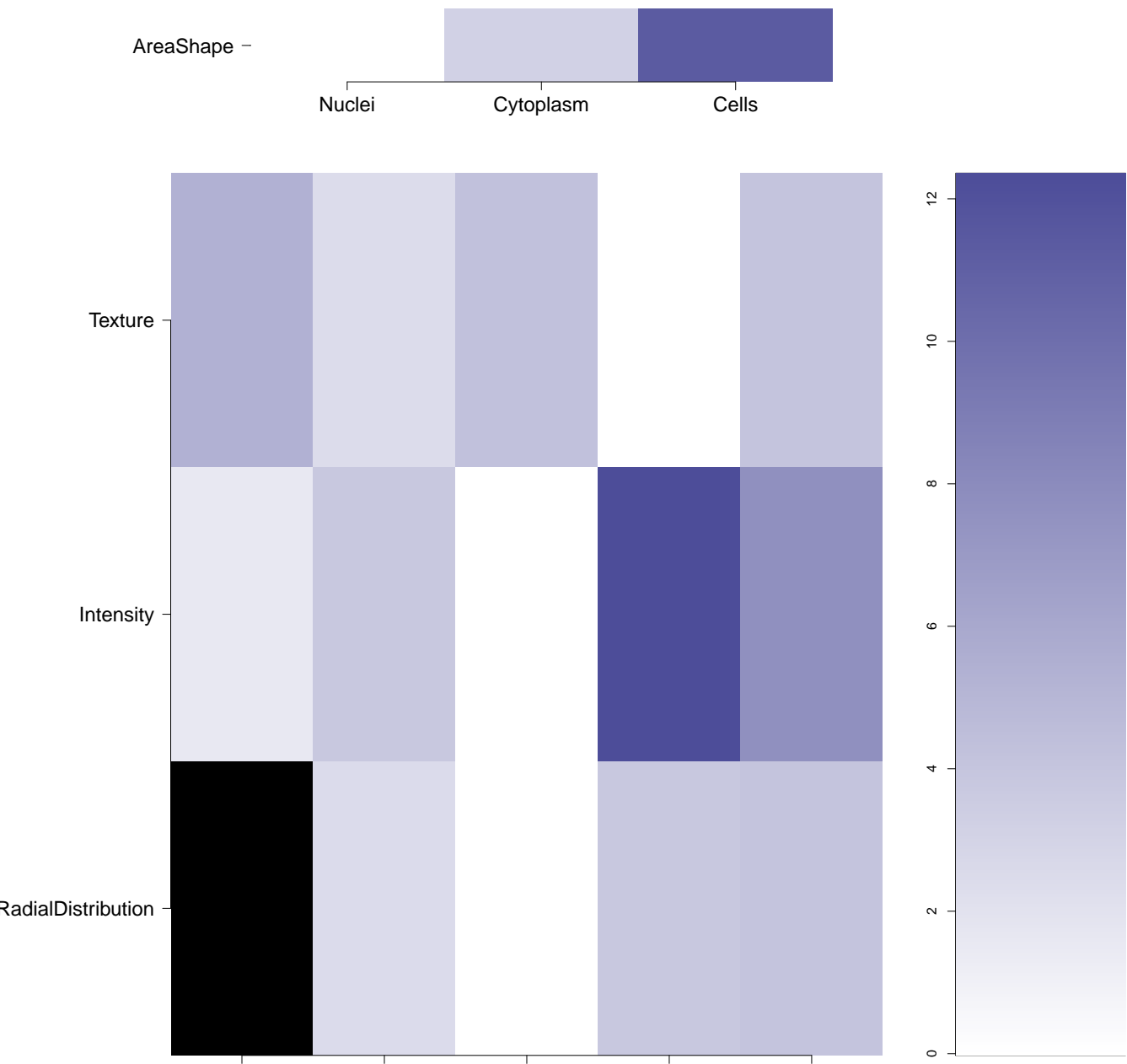
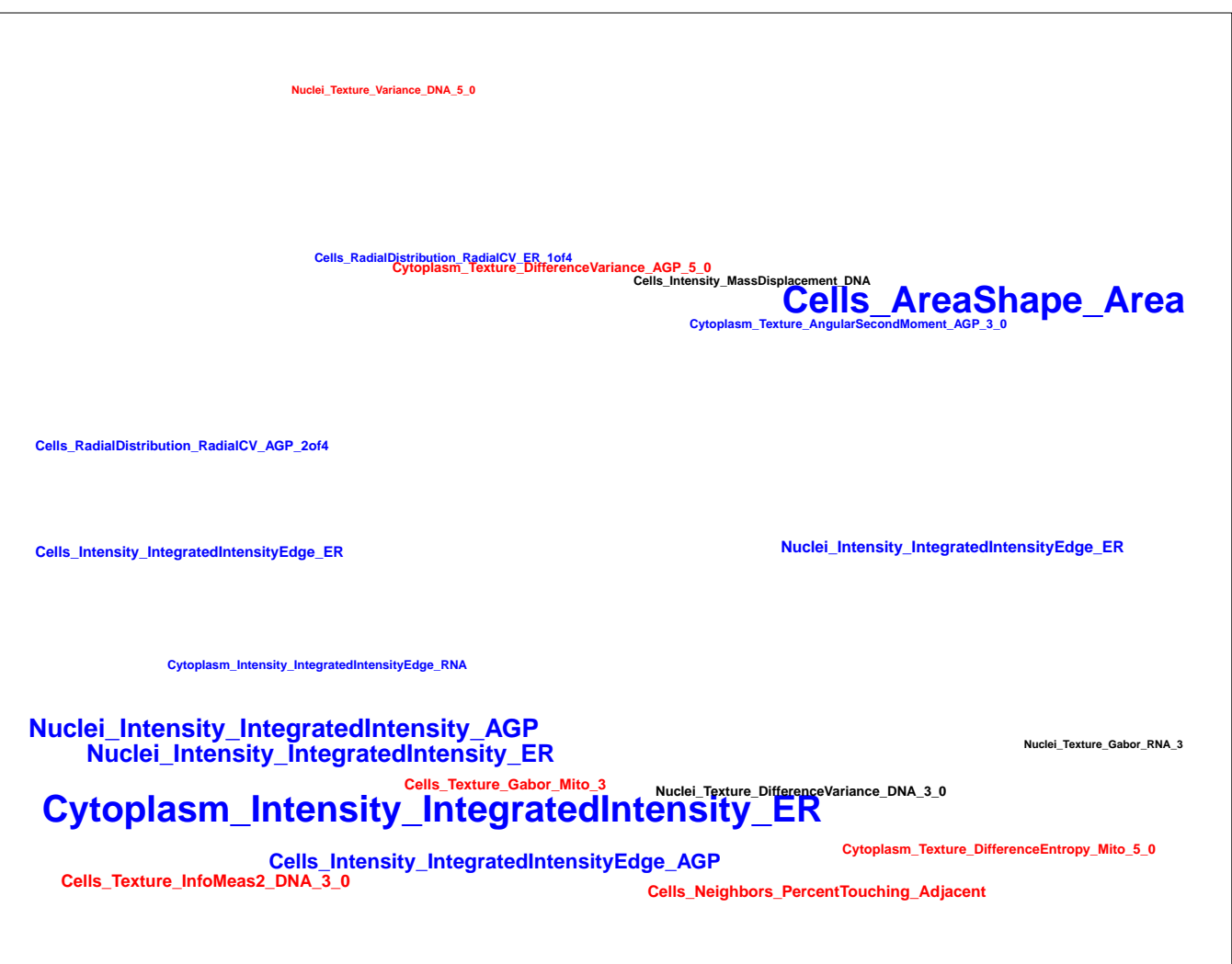
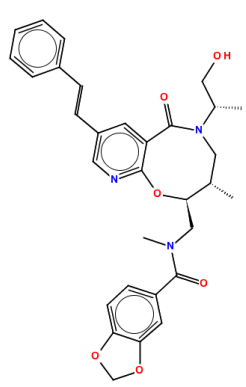
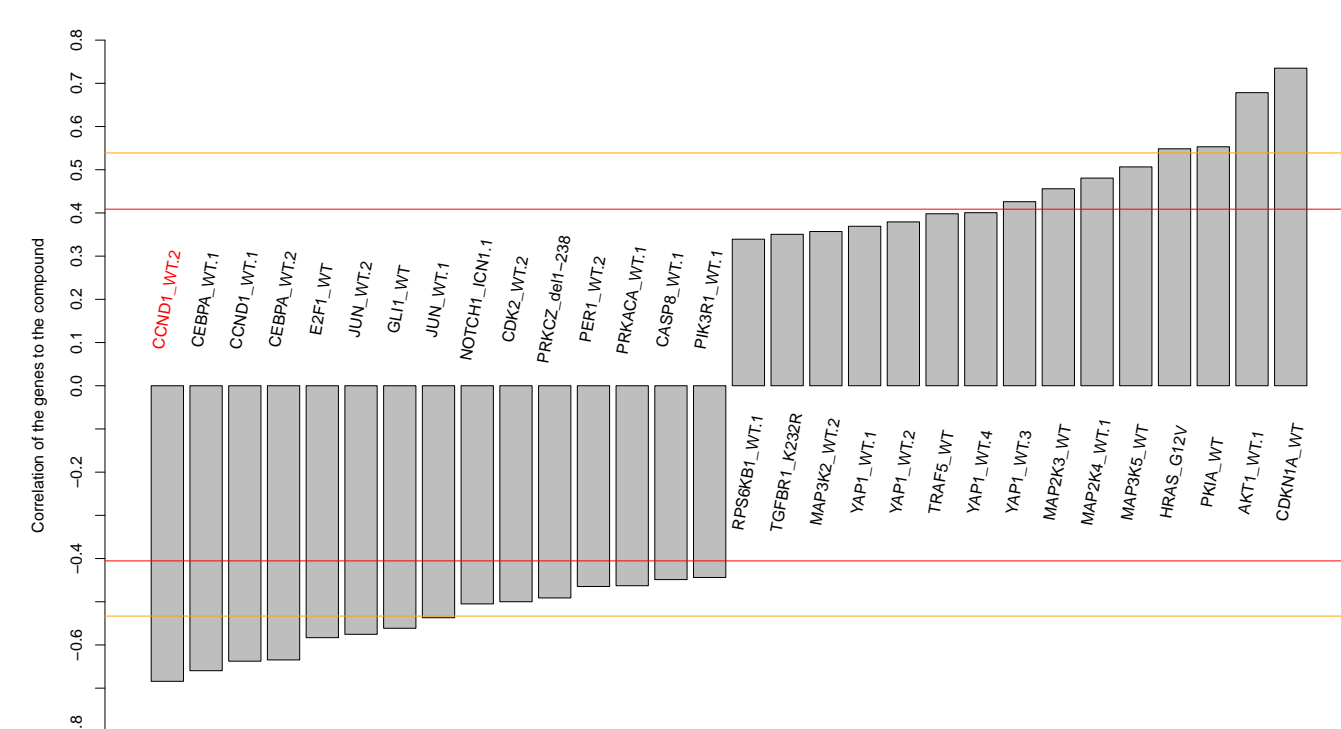
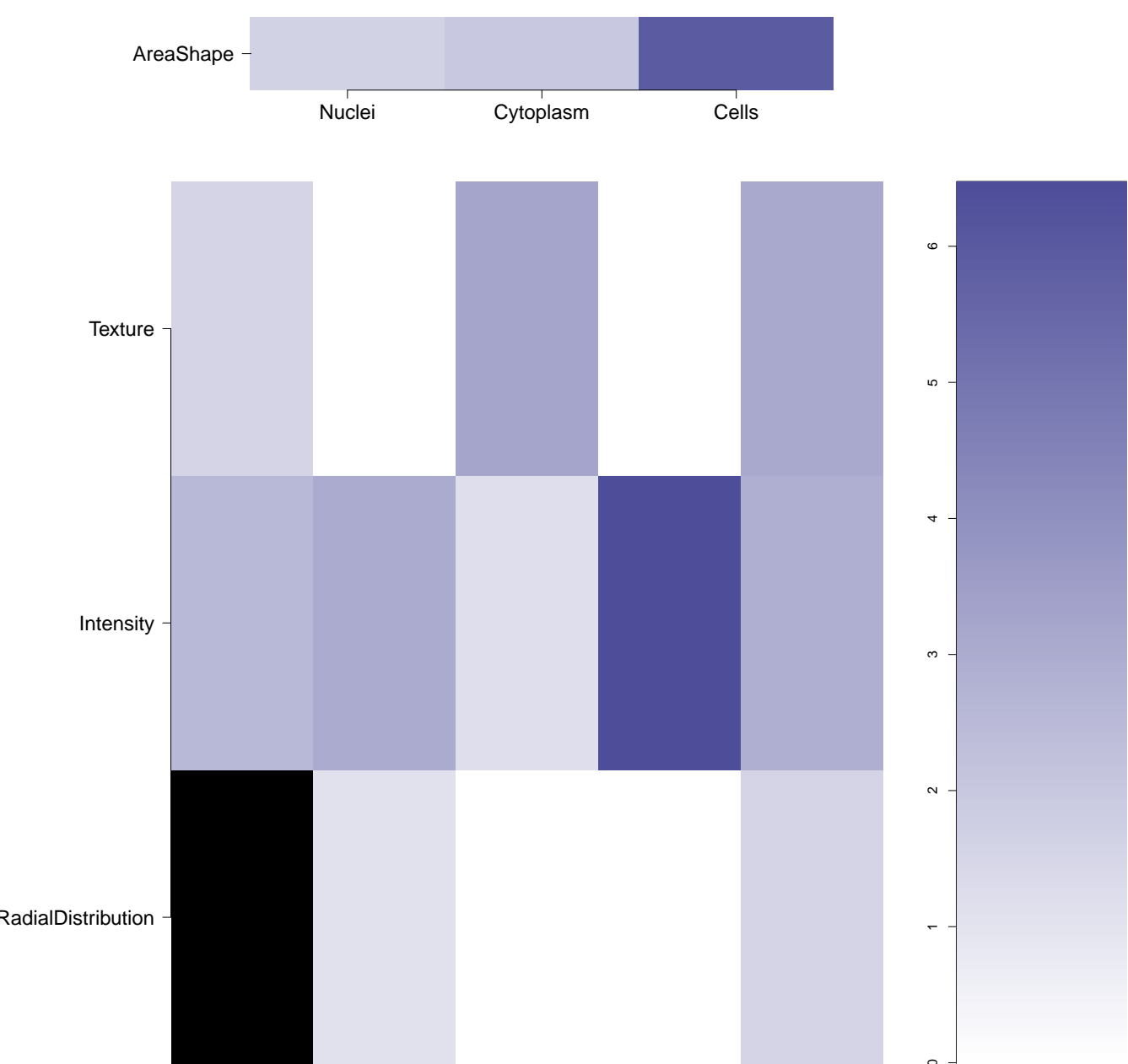
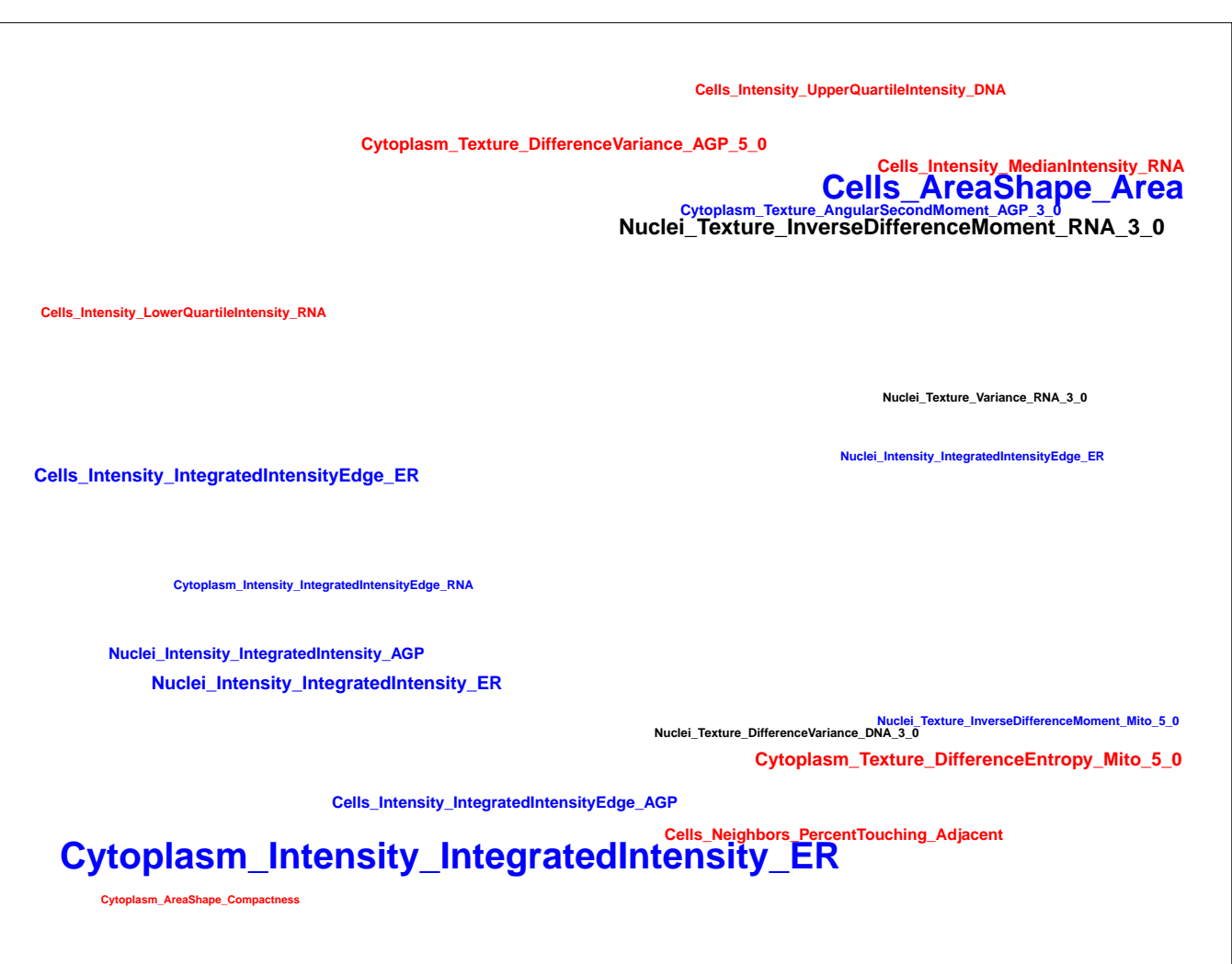
Cytoplasm_Intensity_IntegratedIntensity_ER

CCND1_WT.2 (41754)



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 0.51)	Correlation between compound and 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-K60430317-001-01-7 PubChem CID : 44490267		0.67 (in 4 replicates)	0.57	0.630				Total number of assays tested in: 54.
BRD-K52827598-001-01-4 PubChem CID : 44495977		0.52 (in 4 replicates)	0.45	NA				Total number of assays tested in: 43.
BRD-K99447049-001-04-5 ZINC00815361 SMR000092393 AC1LM009 MLS000115228 MLS001368098 HMS2251007 ZINC815361 STK961361 CCG-117641 BAS 09530694 ST50718758 PubChem CID : 1094029		NA (in 1 replicates)	-0.74	NA				Total number of assays tested in: 783.
BRD-K70412800-001-01-7 PubChem CID : 54619125		0.87 (in 4 replicates)	-0.73	0.690				Total number of assays tested in: 37.
BRD-K37906141-001-01-8 PubChem CID : 44617686		0.92 (in 4 replicates)	-0.72	0.161				Total number of assays tested in: 40.
BRD-K90061492-001-01-1 PubChem CID : 44483968		0.90 (in 3 replicates)	-0.71	0.394				Total number of assays tested in: 28.
BRD-K36176998-001-01-3 PubChem CID : 44486403		0.89 (in 4 replicates)	-0.71	0.394				Total number of assays tested in: 46.

<div>BRD-K80711156-001-02-8</div> <div>MLS003129217</div> <div>SMR001833663</div> <div>PubChem CID : 44505852</div>		0.93 (in 3 replicates)	-0.71	0.394				Total number of assays tested in: 77.
<div>BRD-K46976183-001-05-0</div> <div>10P-378S</div> <div>AC1MCBYB</div> <div>SMR000180621</div> <div>MLS000327655</div> <div>HMS2404B20</div> <div>ZINC4014200</div> <div>PubChem CID : 2765899</div>		0.90 (in 3 replicates)	-0.70	NA				Total number of assays tested in: 637. 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-Free Homogeneous Primary HTS to Identify Inhibitors of the RanGTP-Importin-beta complex (AID 2216)• qHTS of D3 Dopamine Receptor Antagonist: qHTS (AID 652054)
<div>BRD-K53978514-001-01-5</div> <div>PubChem CID : 54619300</div>		0.89 (in 4 replicates)	-0.70	0.241				Total number of assays tested in: 39.
<div>BRD-K68607418-004-05-5</div> <div>MLS000068649</div> <div>AC1O7FQT</div> <div>CTK717840</div> <div>SMR000010792</div> <div>TR-041126</div> <div>Z-2138</div> <div>PubChem CID : 6603383</div>		0.89 (in 3 replicates)	-0.69	NA				Total number of assays tested in: 766. Active in the following assays: <ul style="list-style-type: none">• qHTS Assay for Inhibitors of DNA Polymerase Beta (AID 485314)
<div>BRD-K34942615-001-01-3</div> <div>PubChem CID : 54619217</div>		0.87 (in 4 replicates)	-0.68	0.815				Total number of assays tested in: 38.