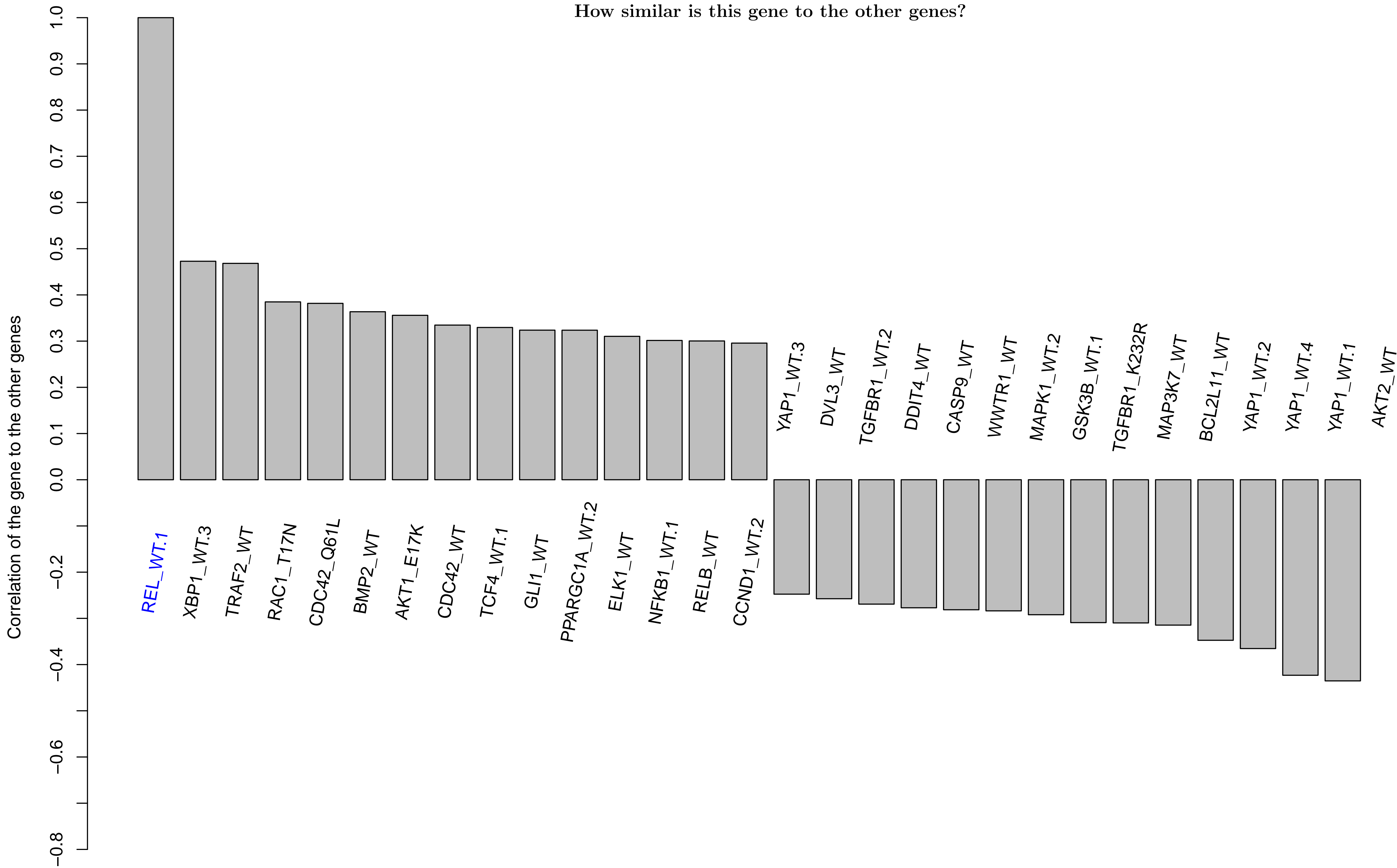
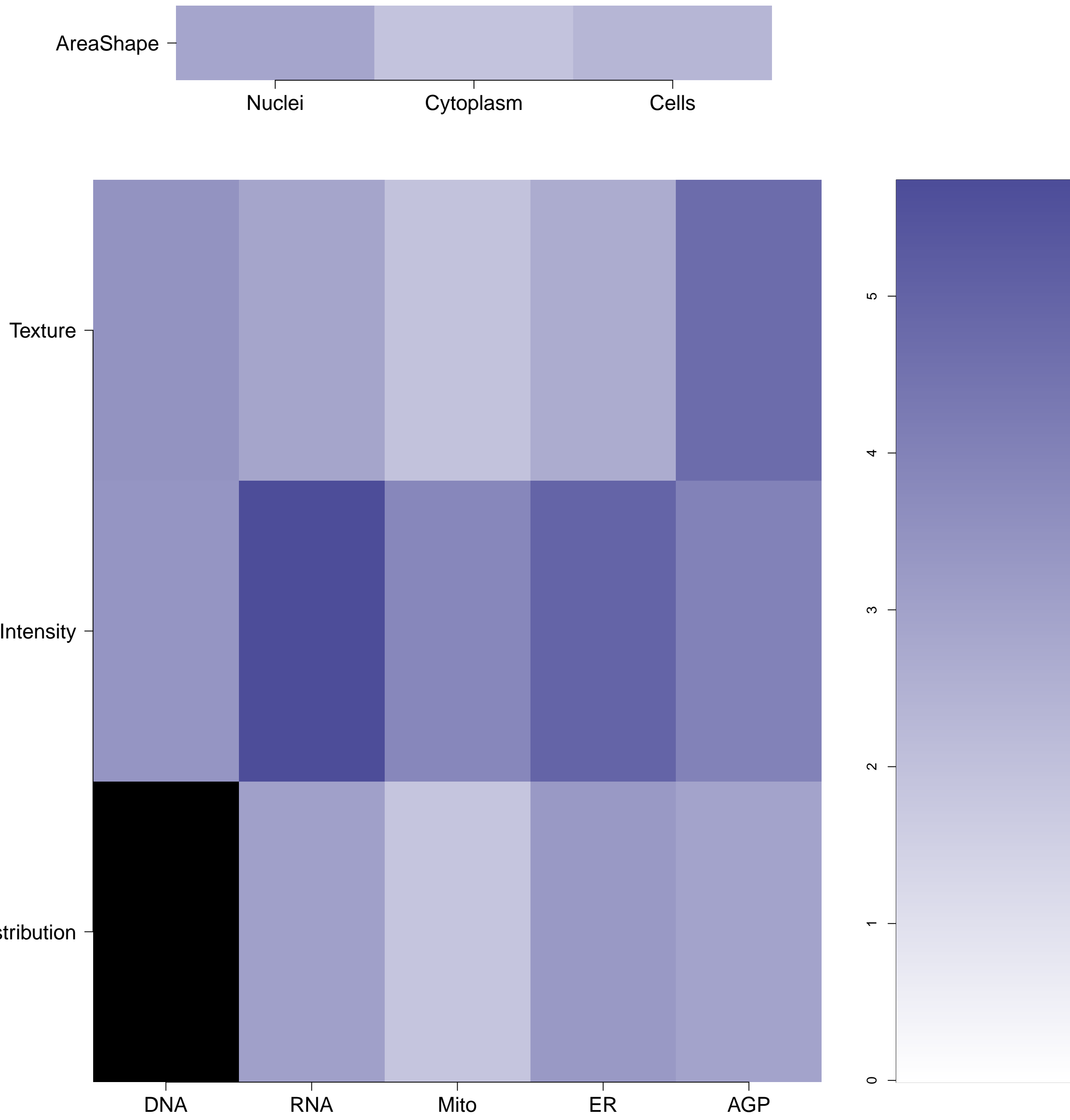


REL.WT.1 - in Canonical NFkB

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

REL.WT.1 (41744)

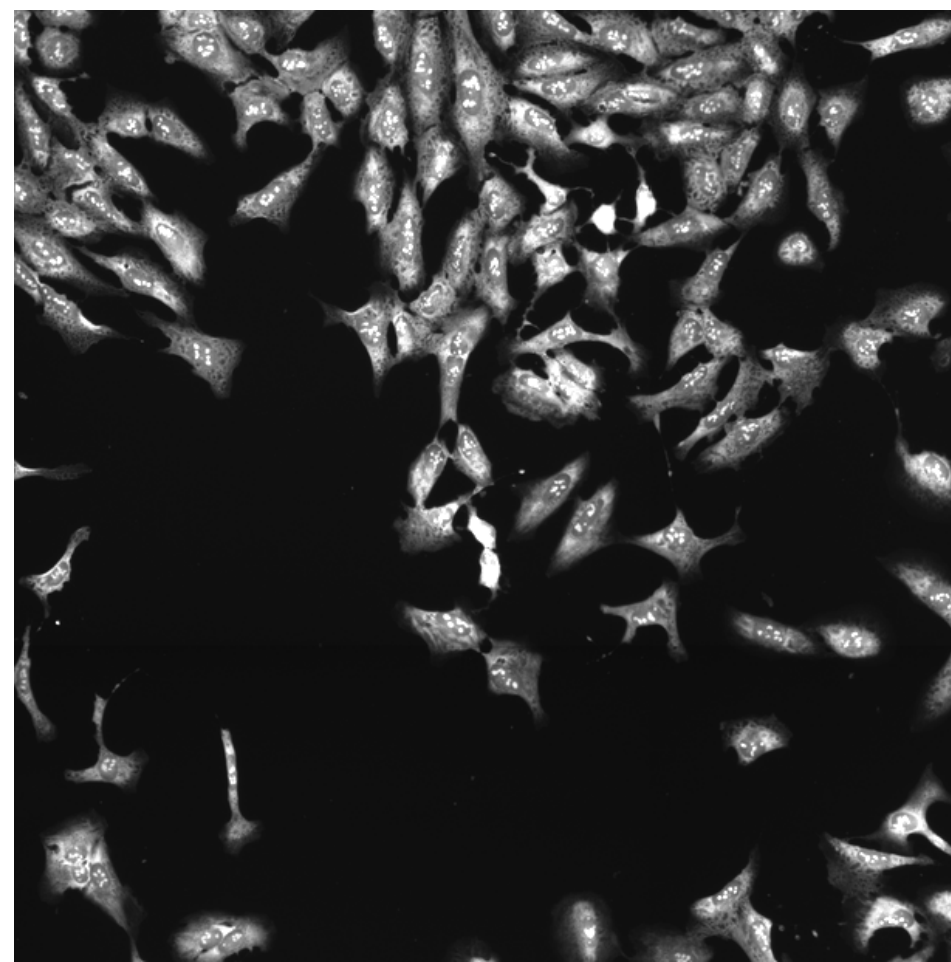
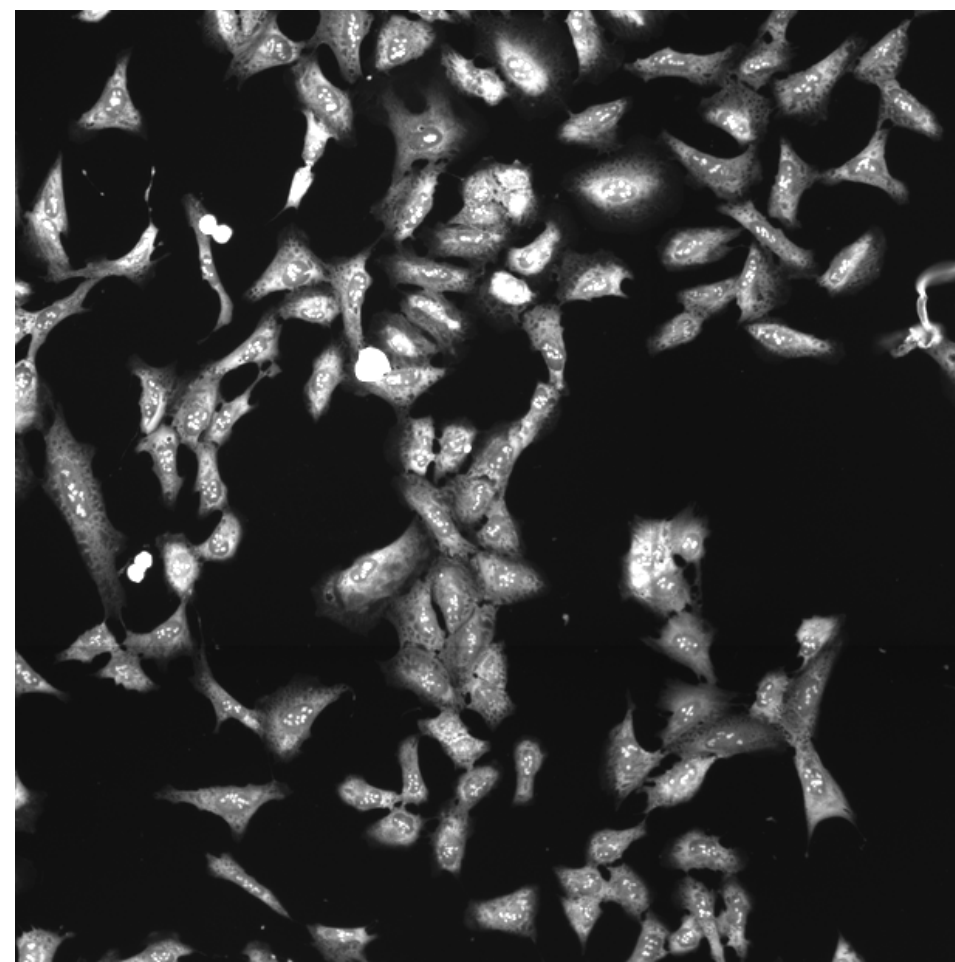
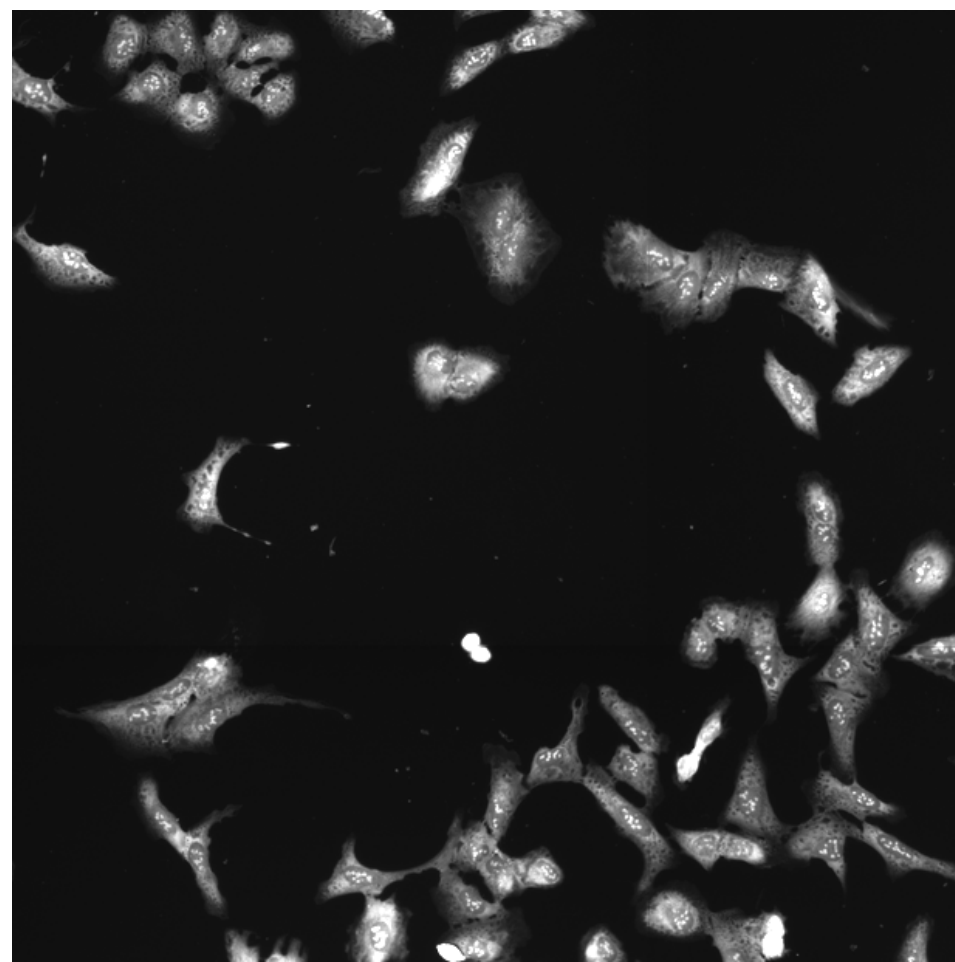
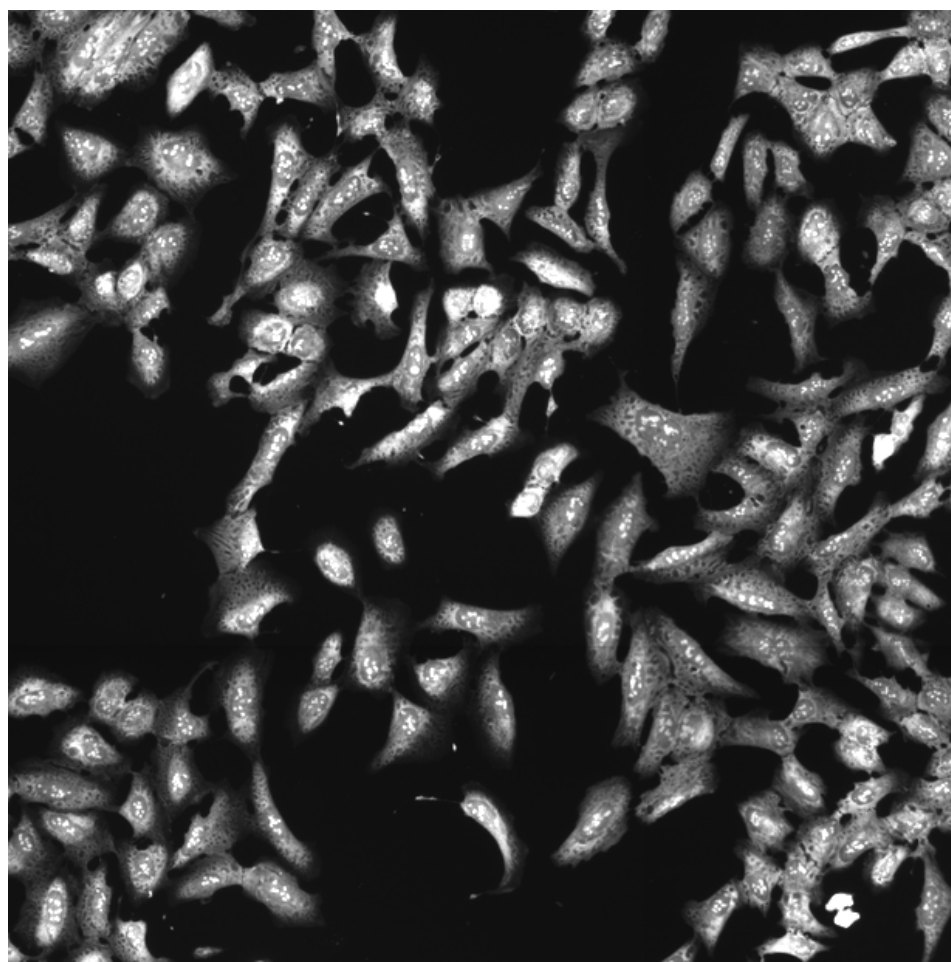
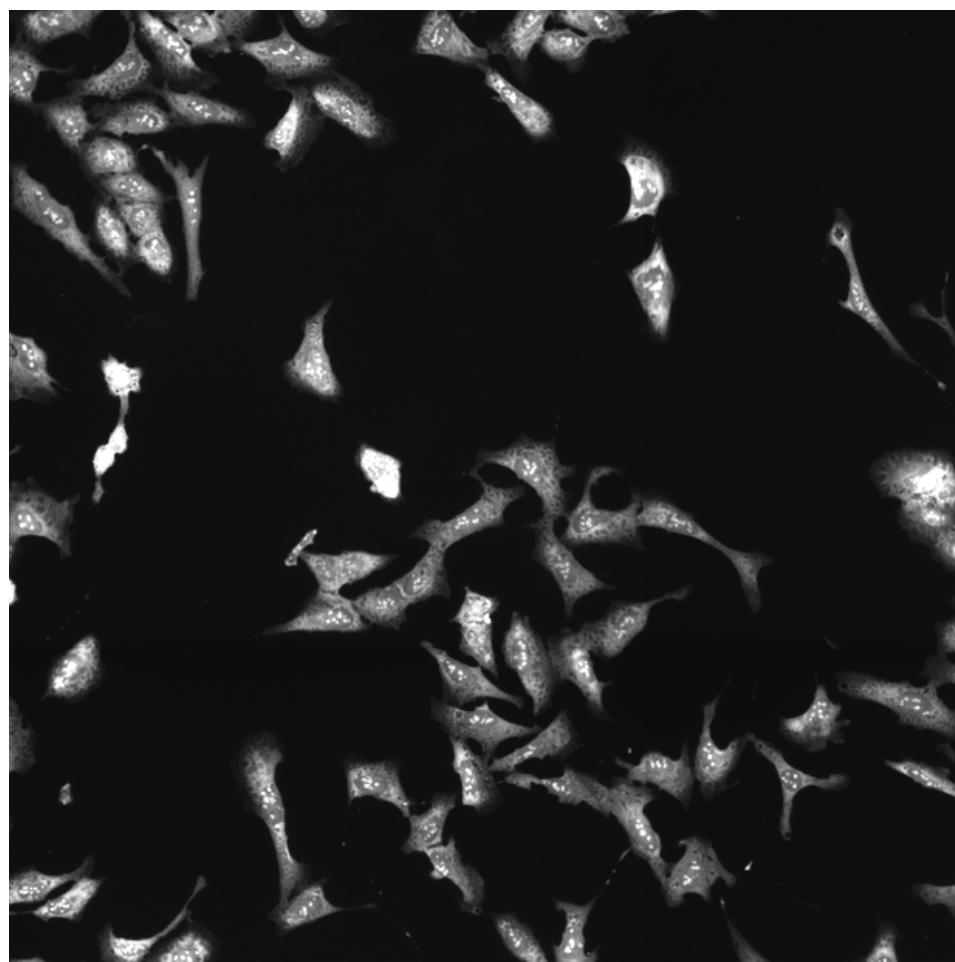
REL.WT.1 (41755)

REL.WT.1 (41756)

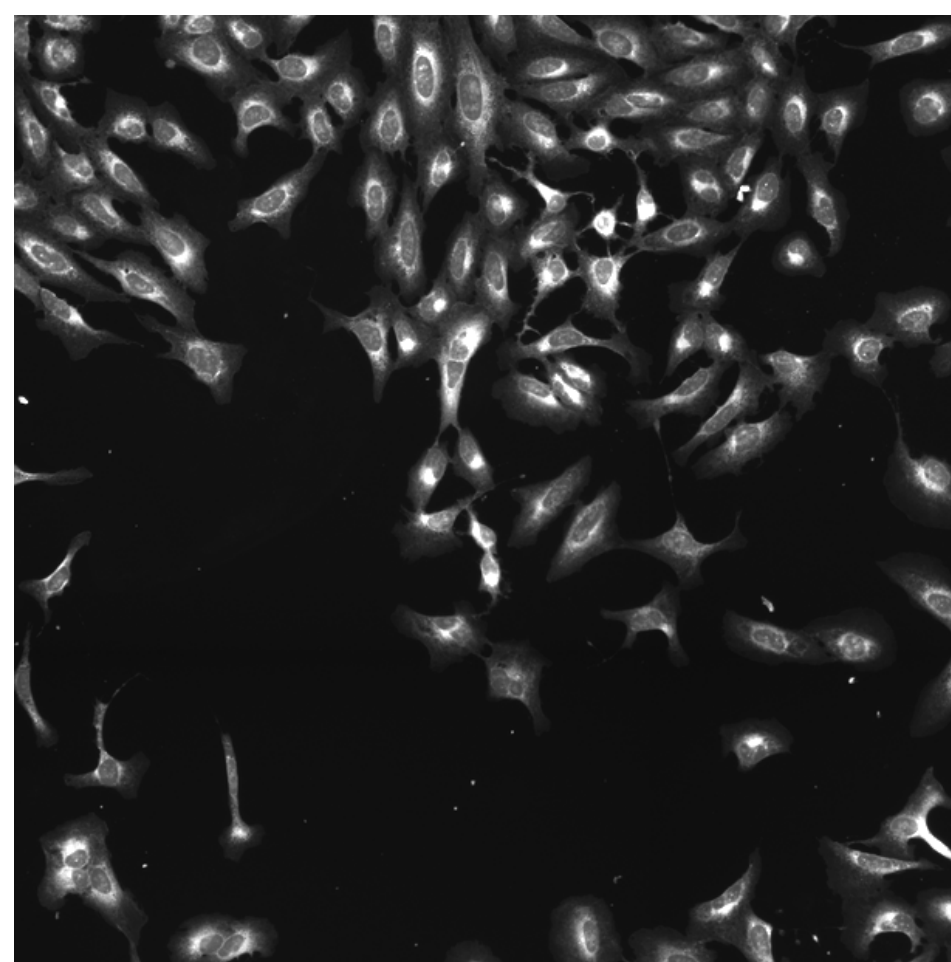
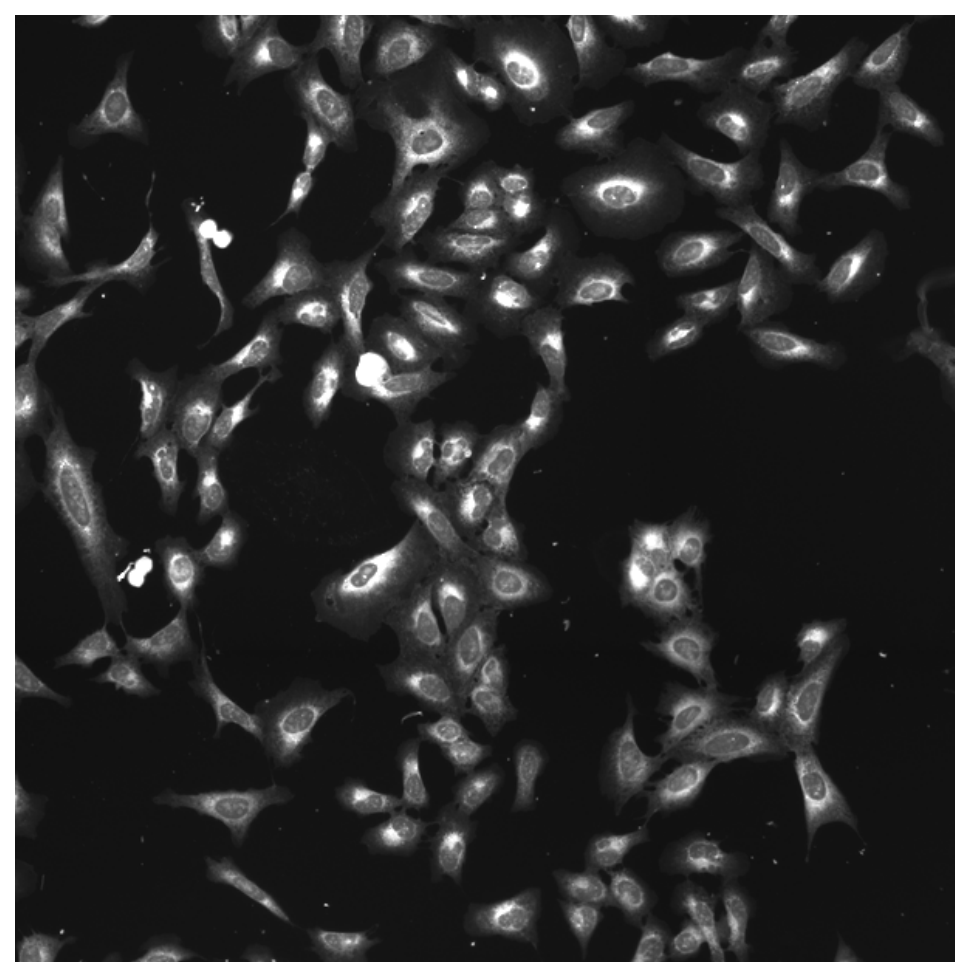
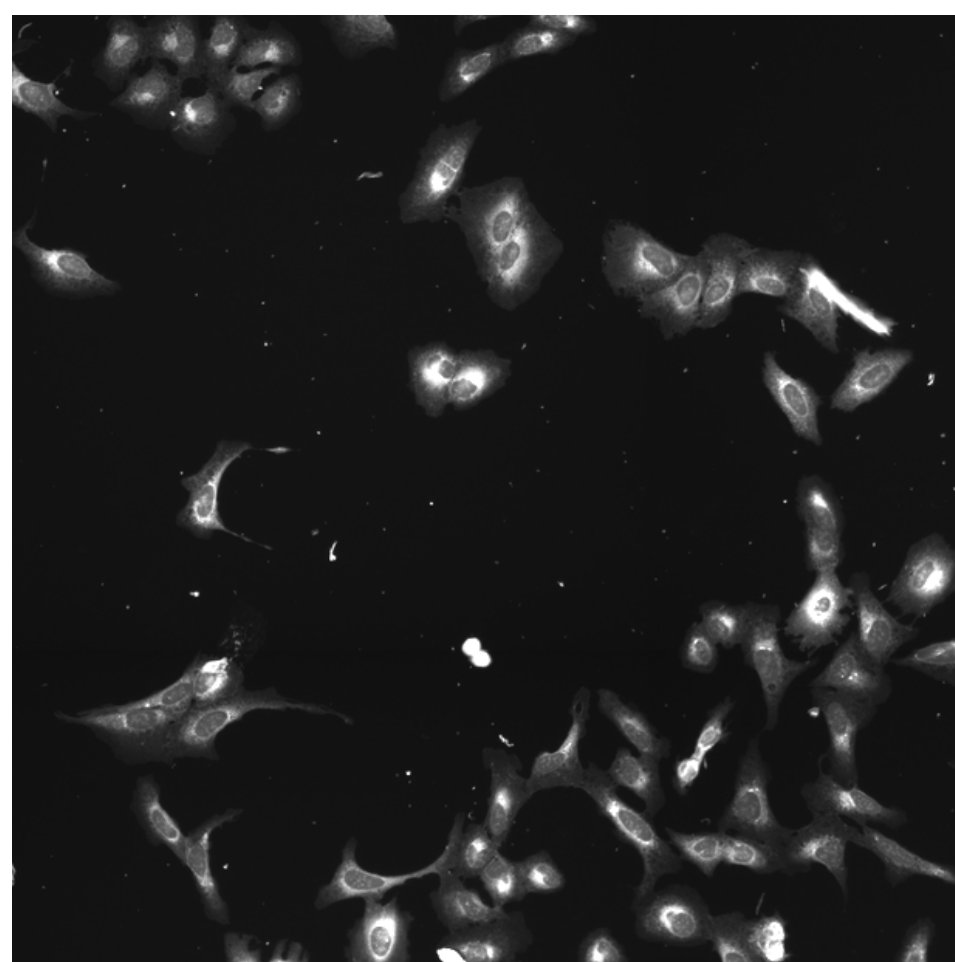
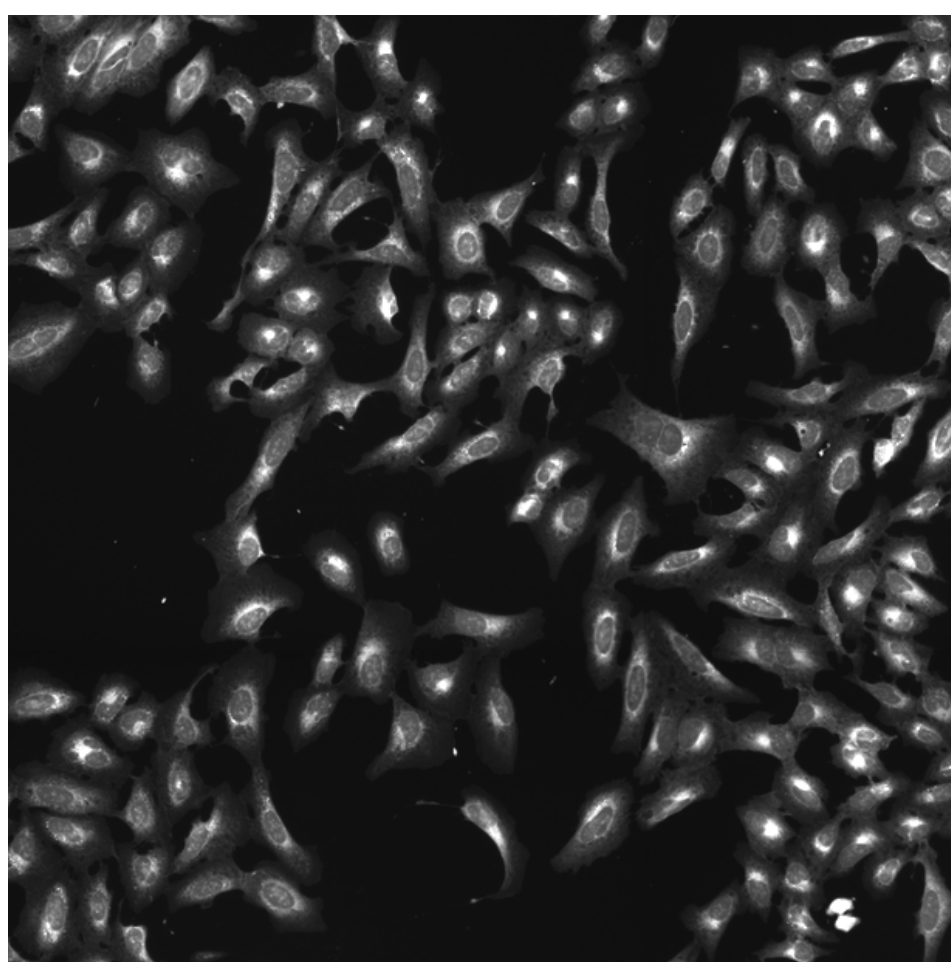
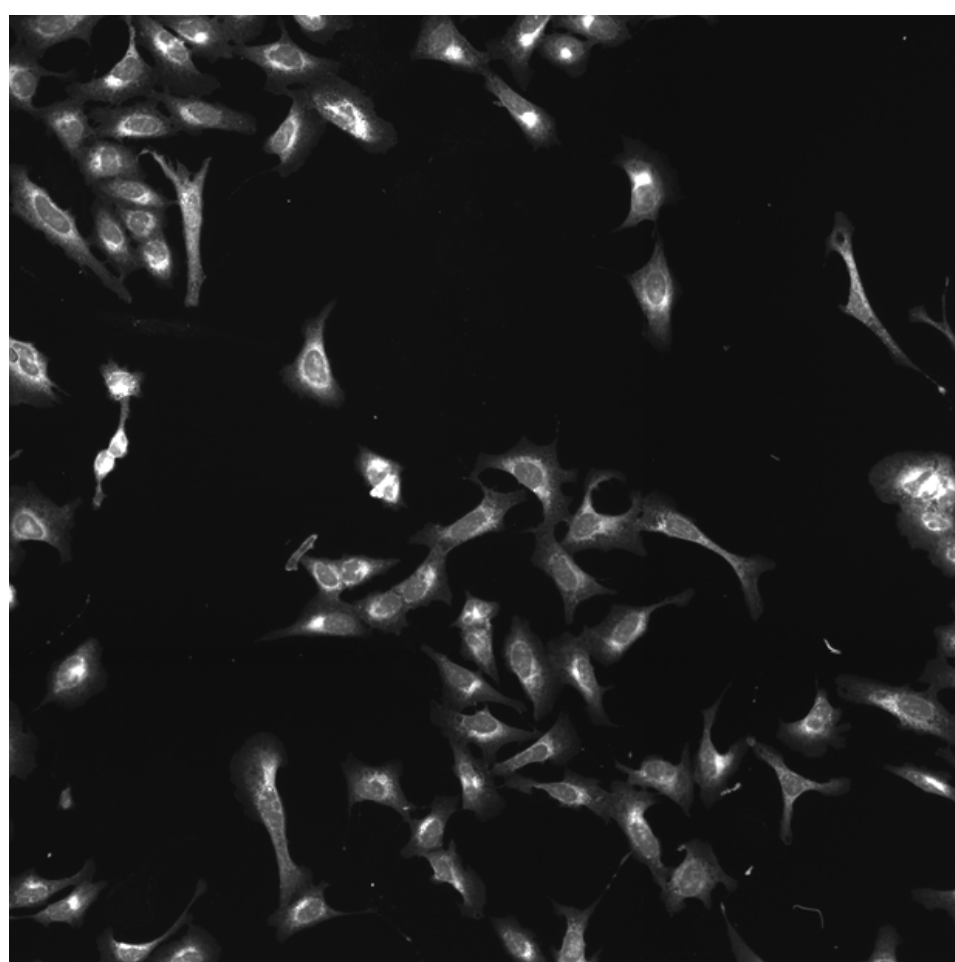
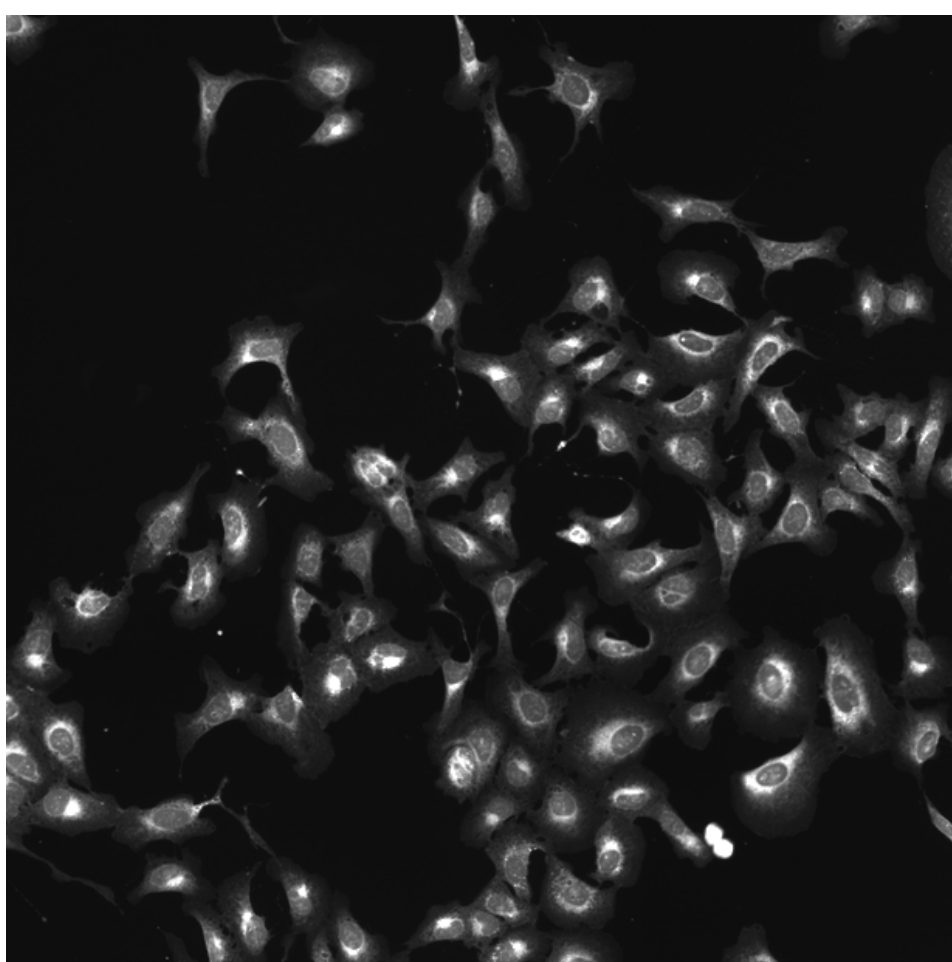
REL.WT.1 (41757)

REL.WT.1 (41754)

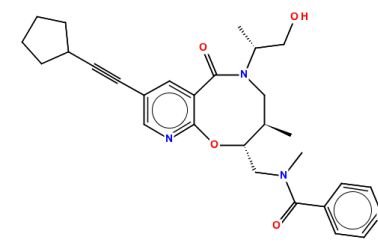
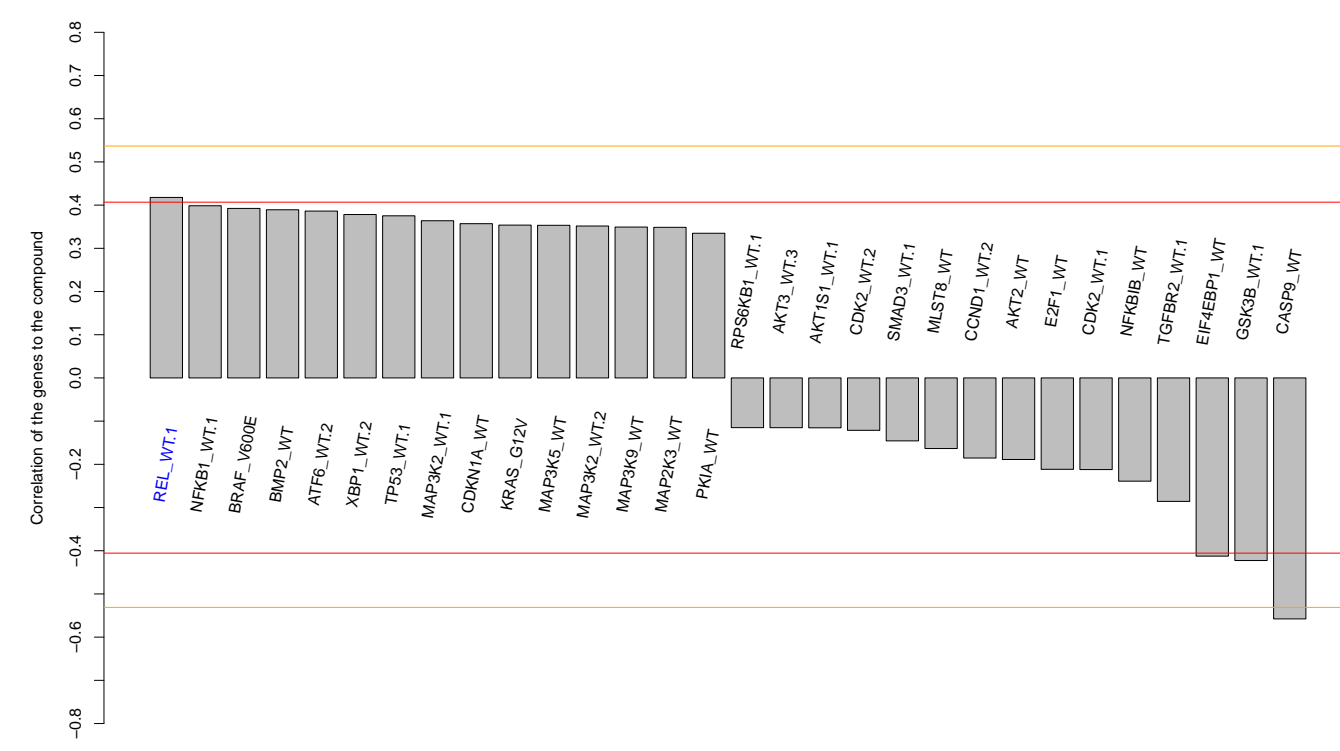
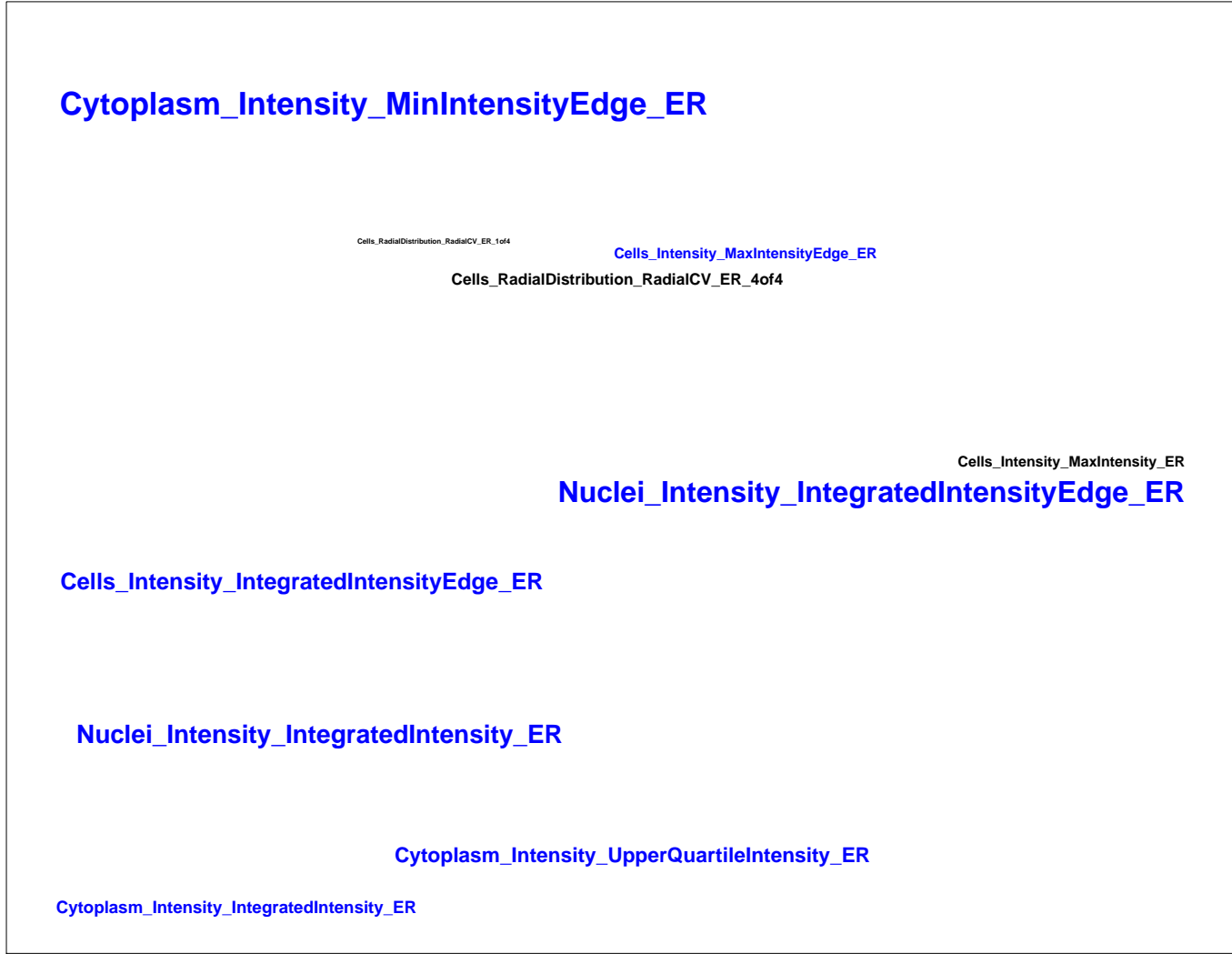
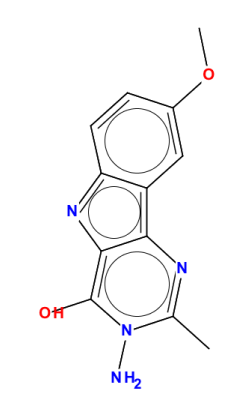
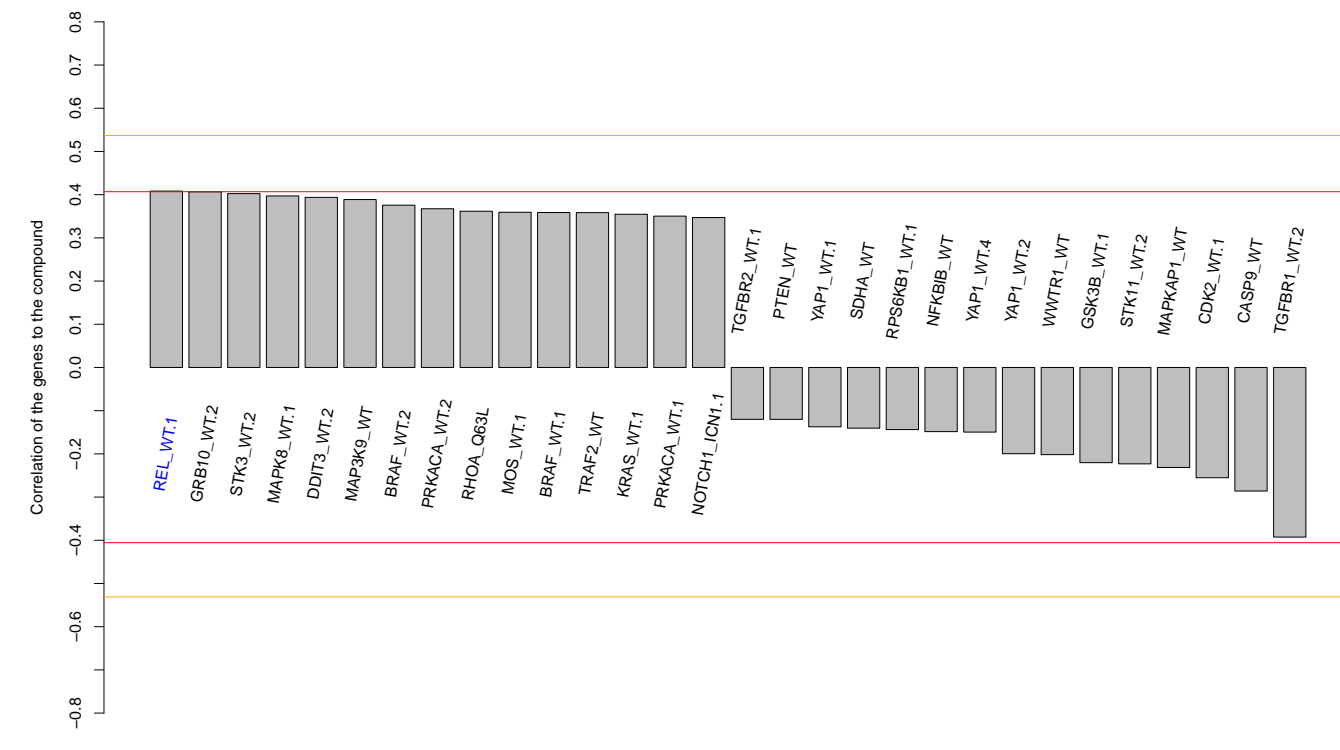
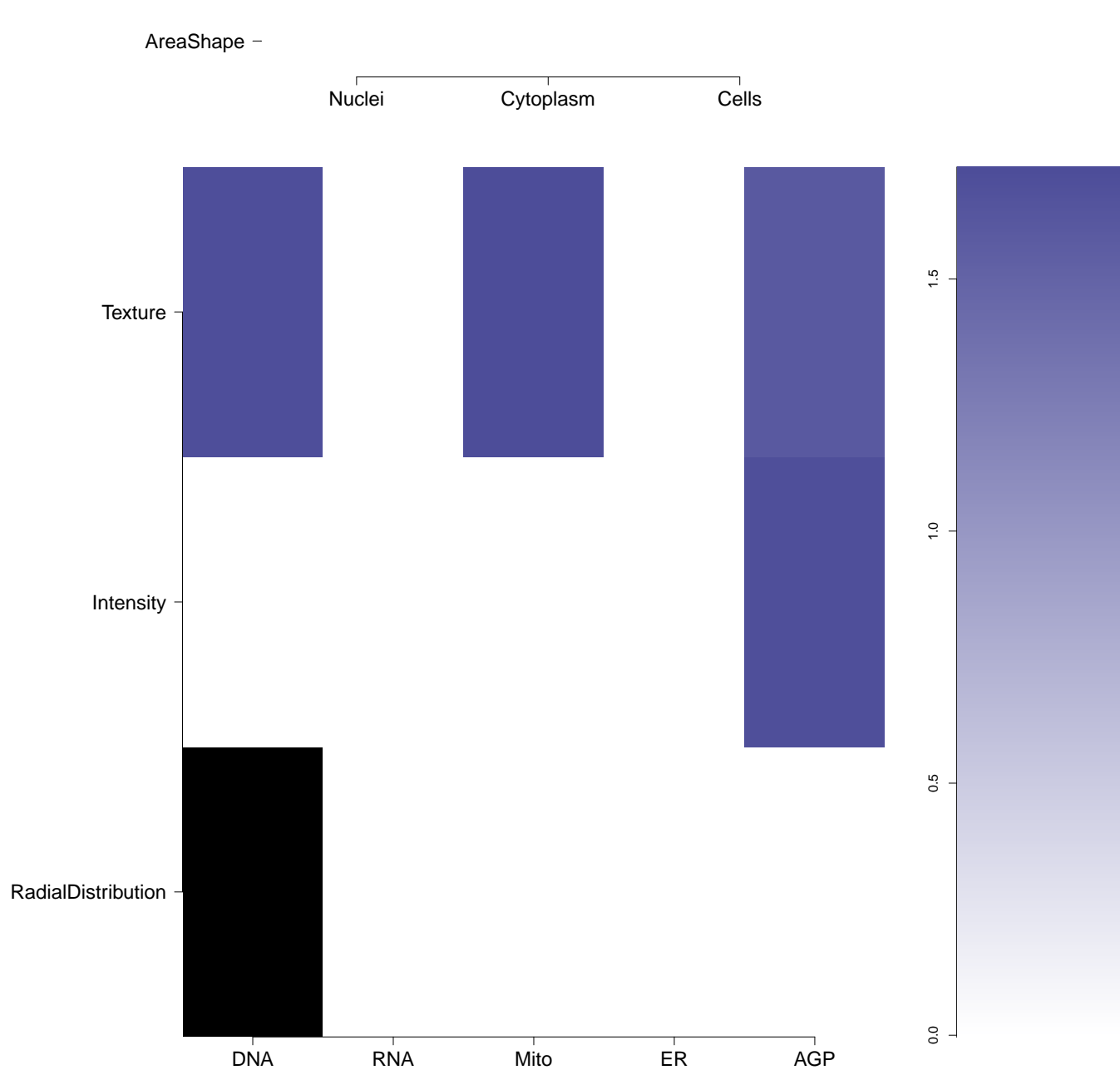

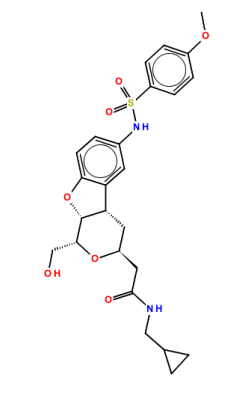
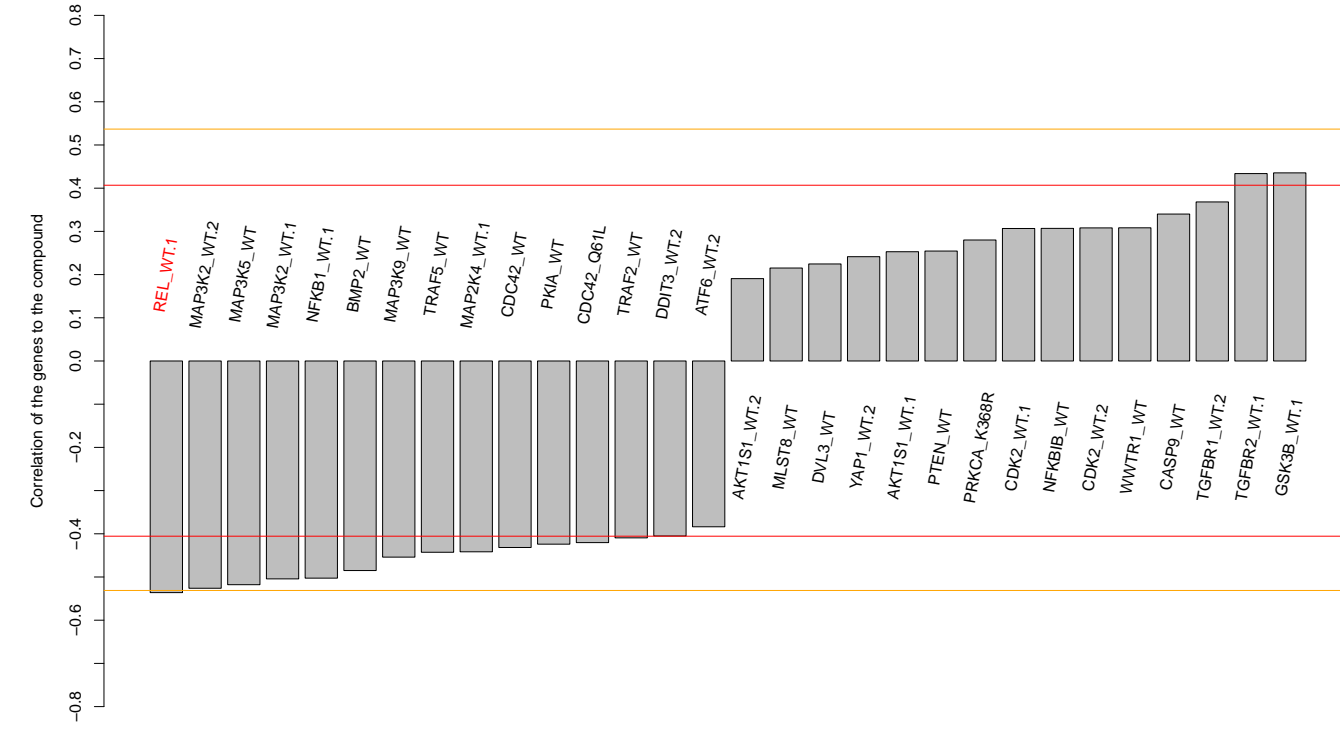

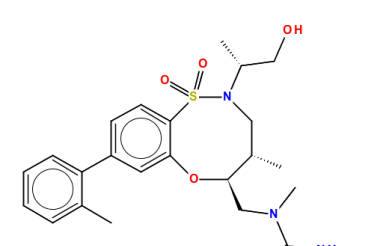
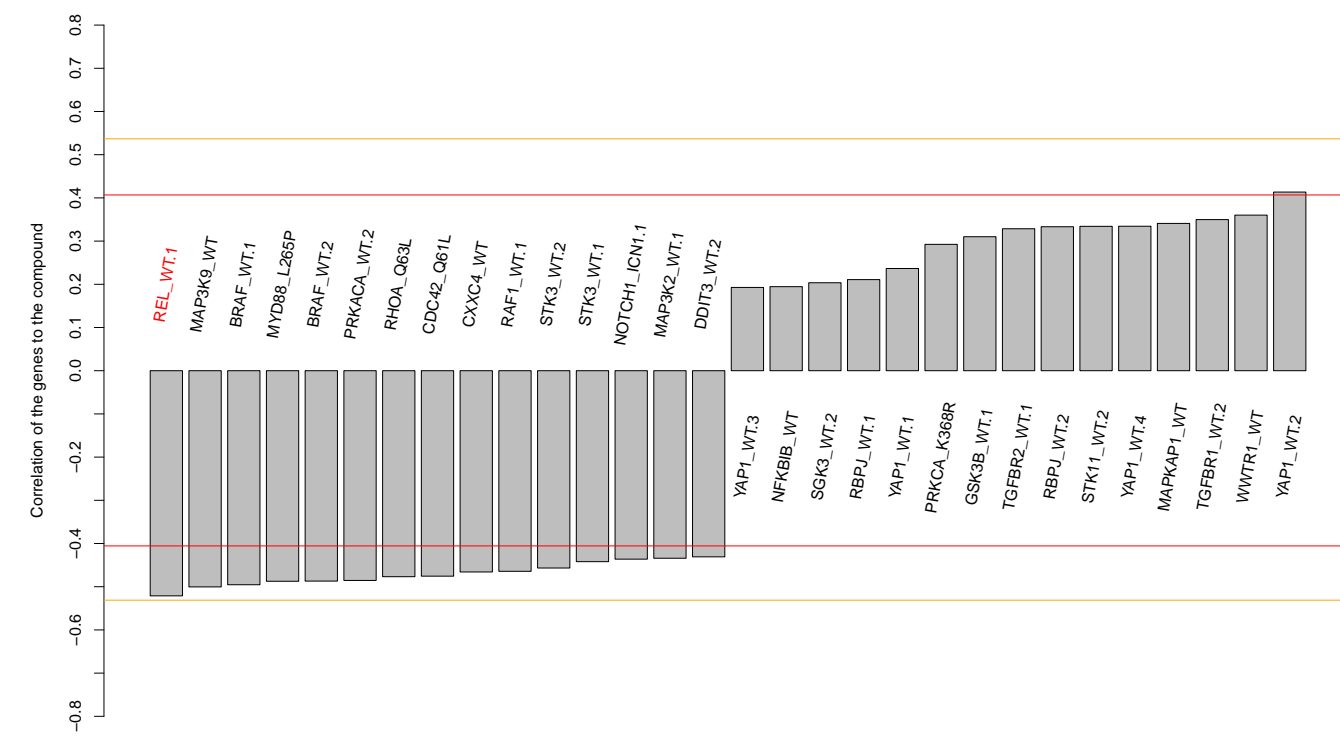
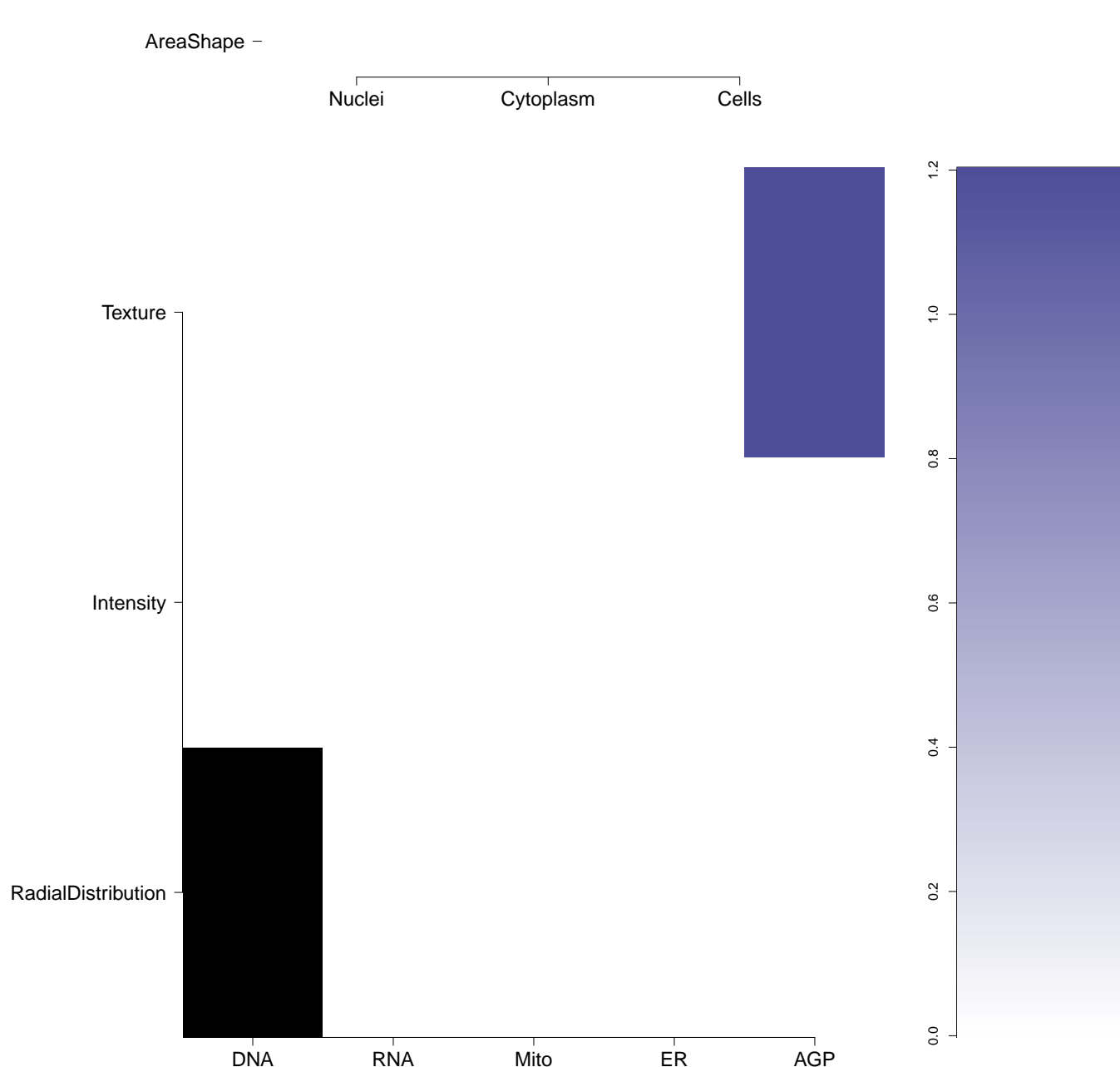
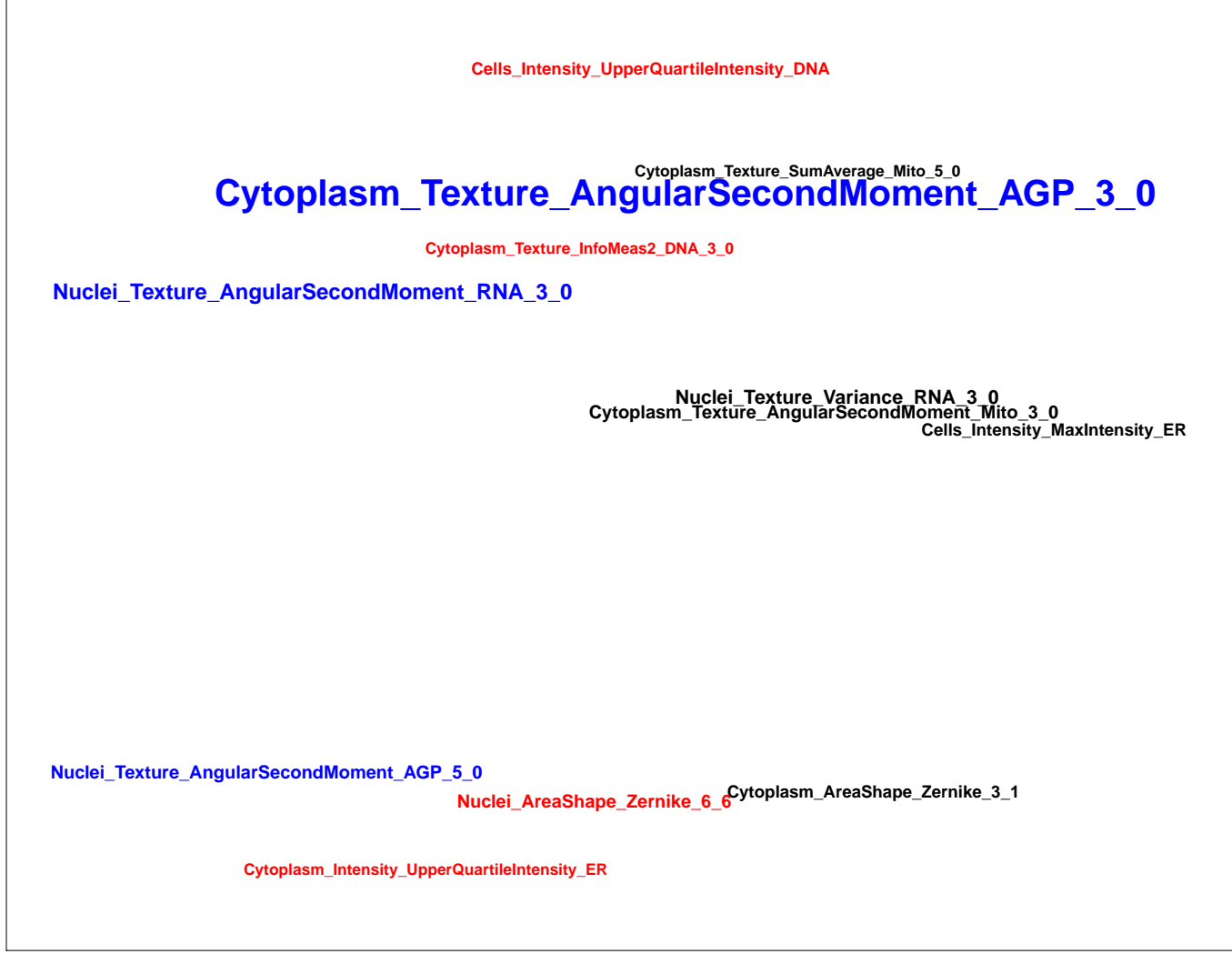
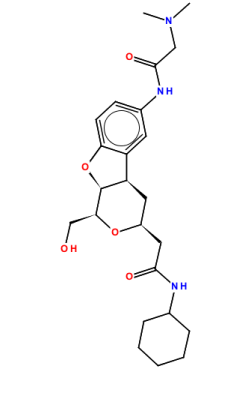
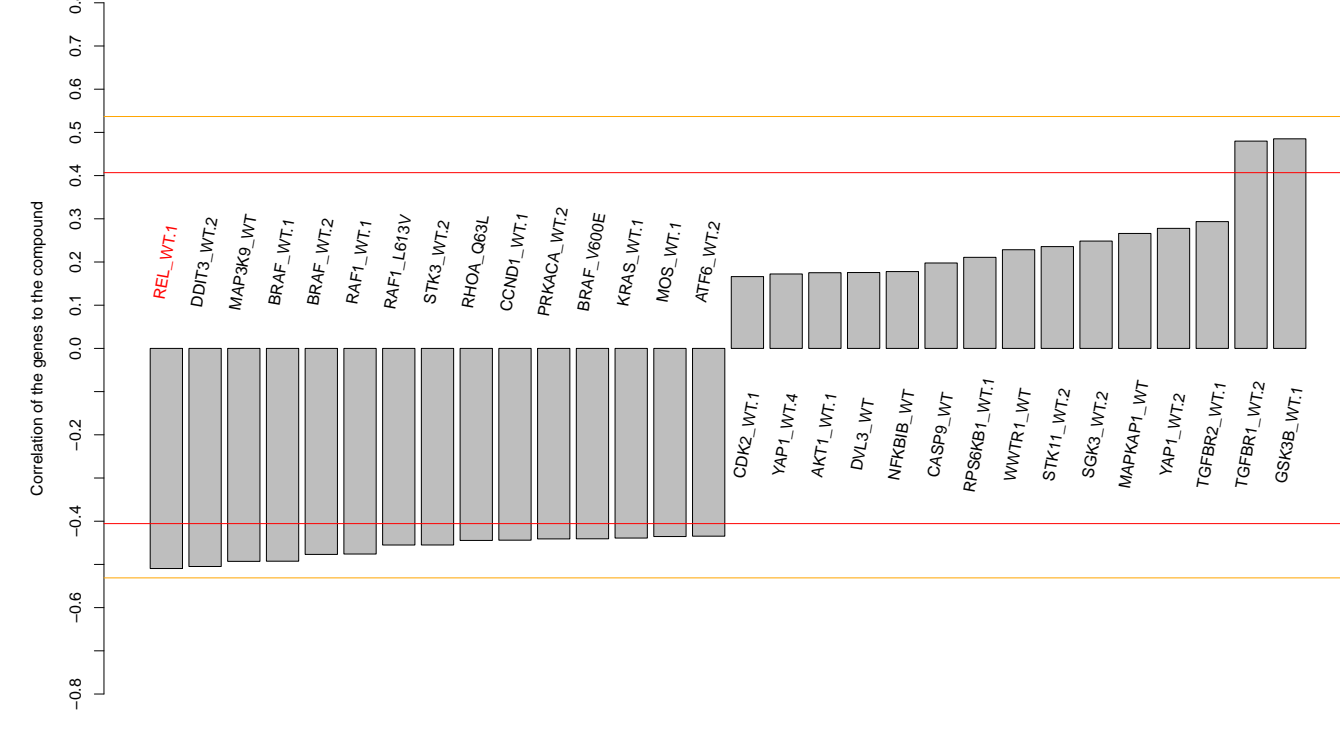
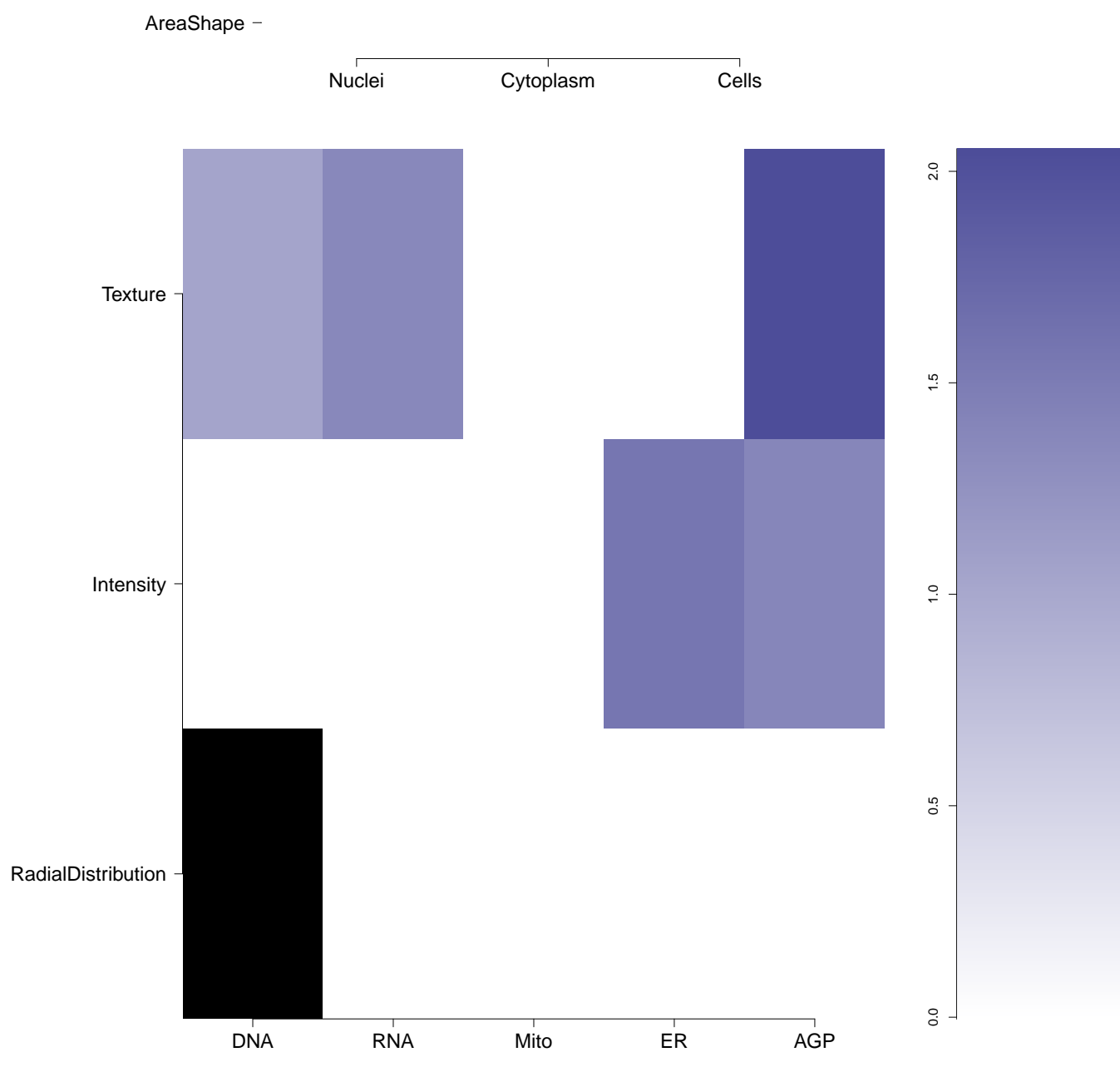
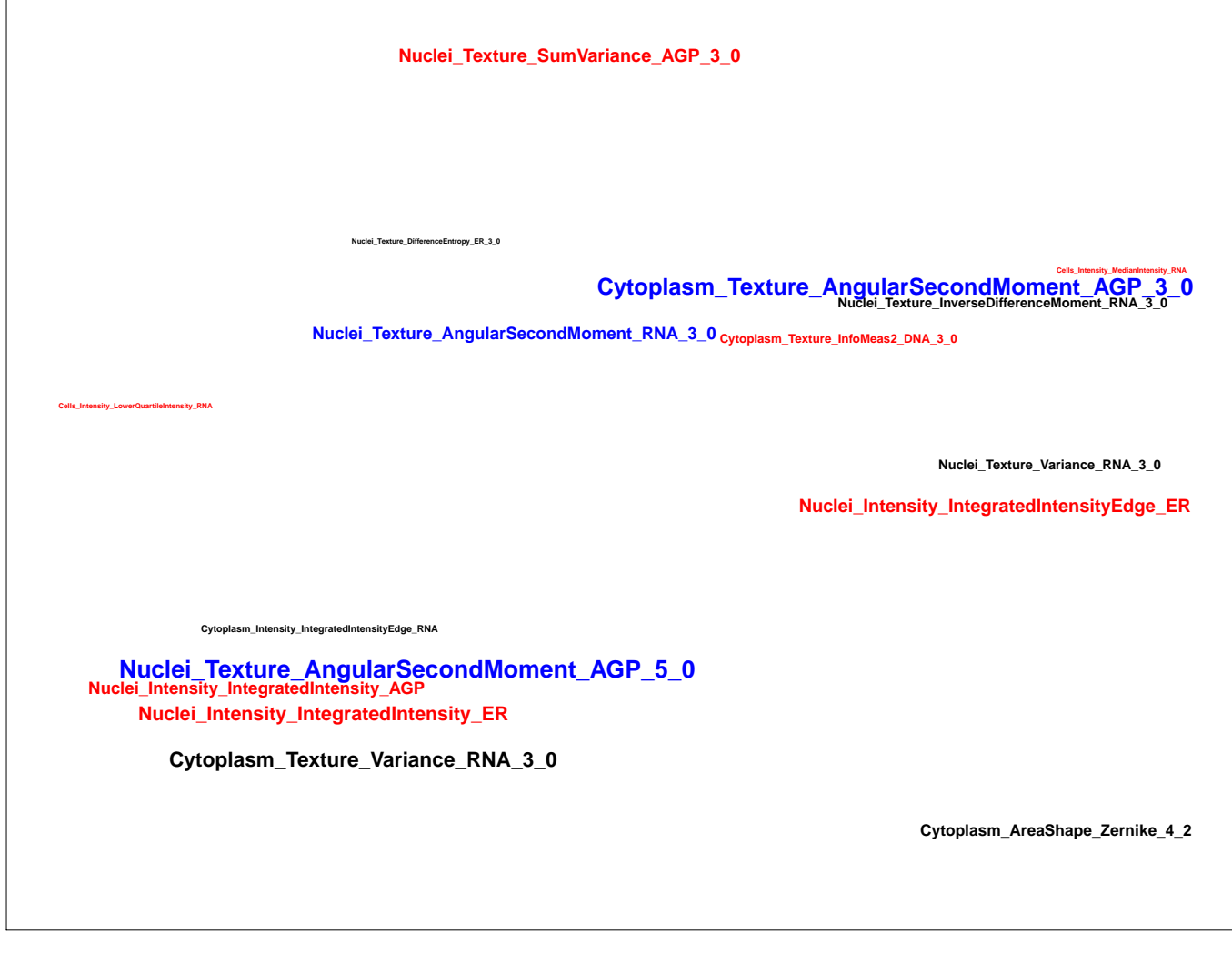
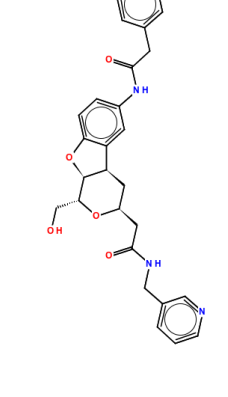
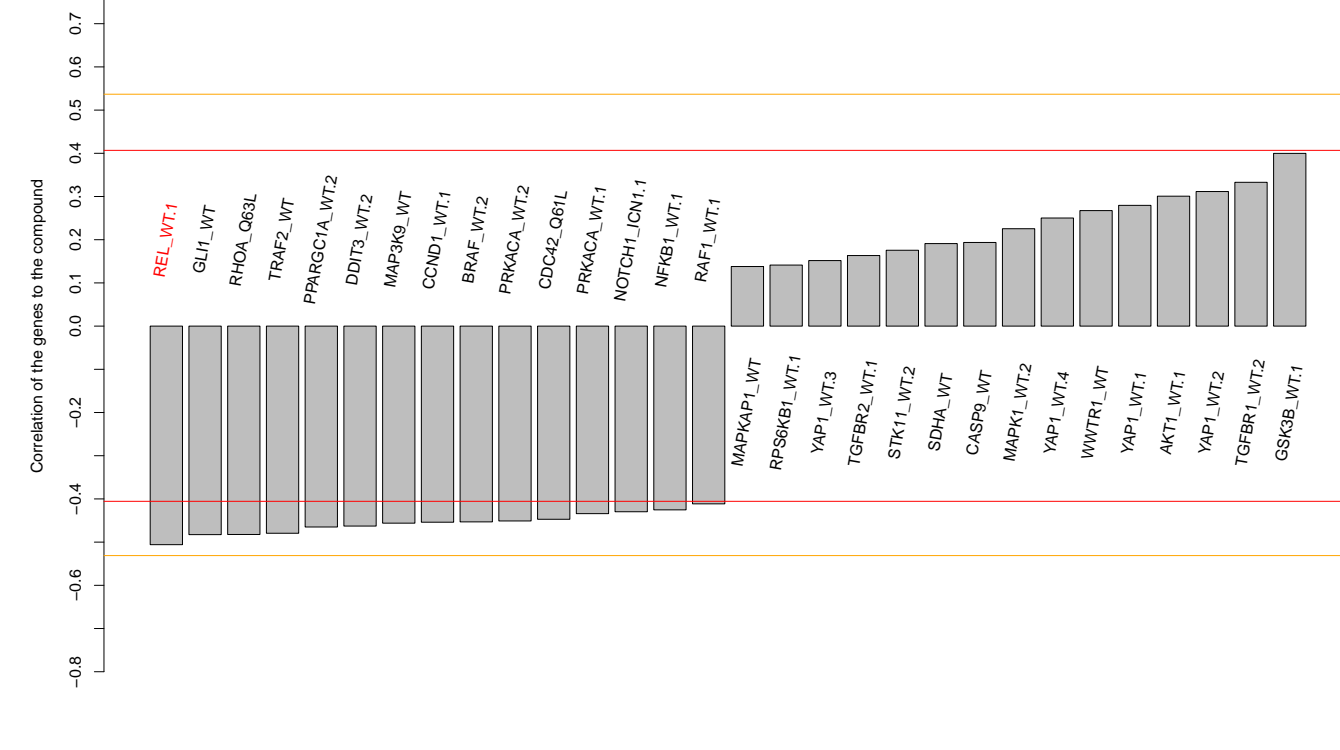
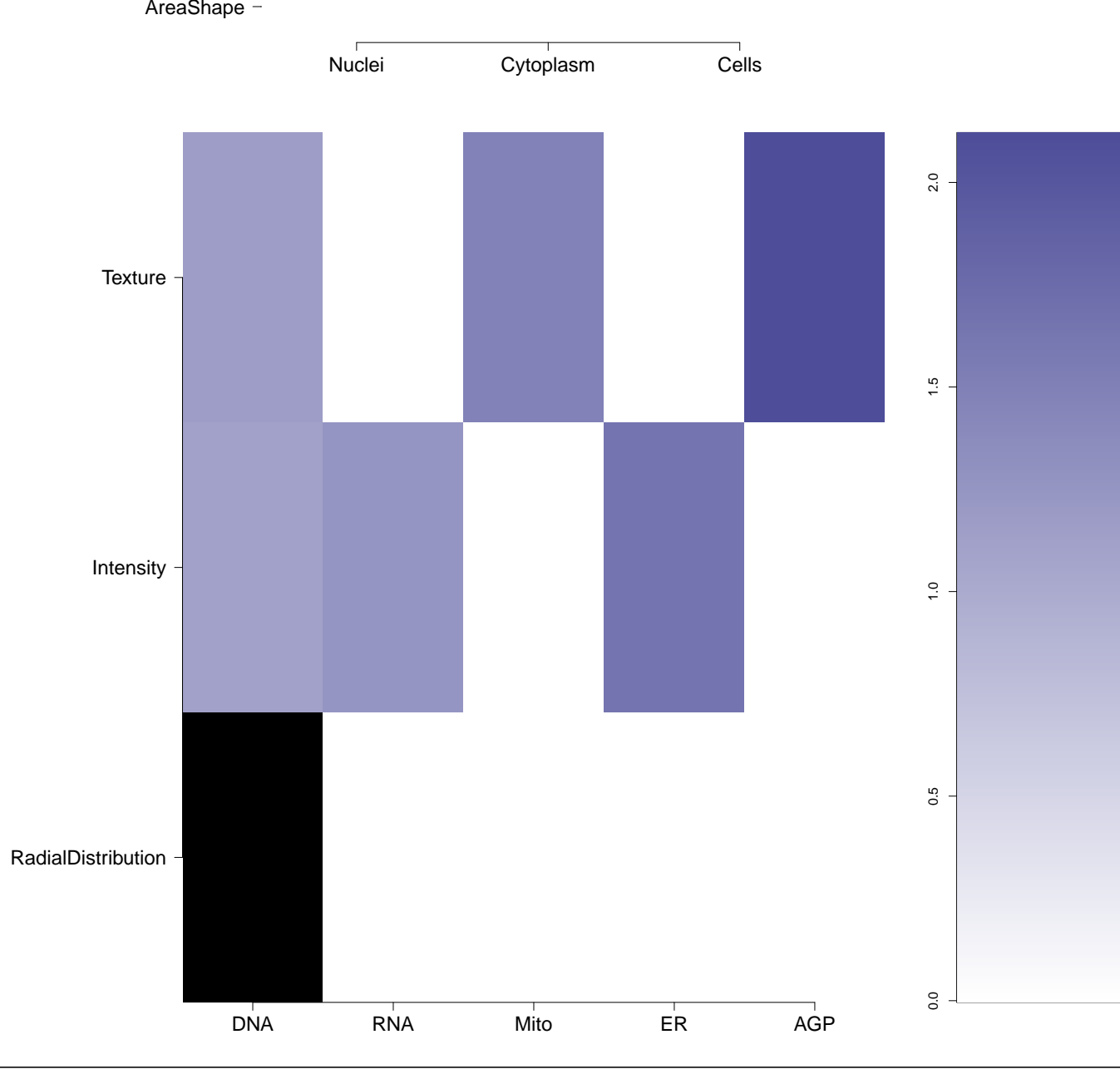
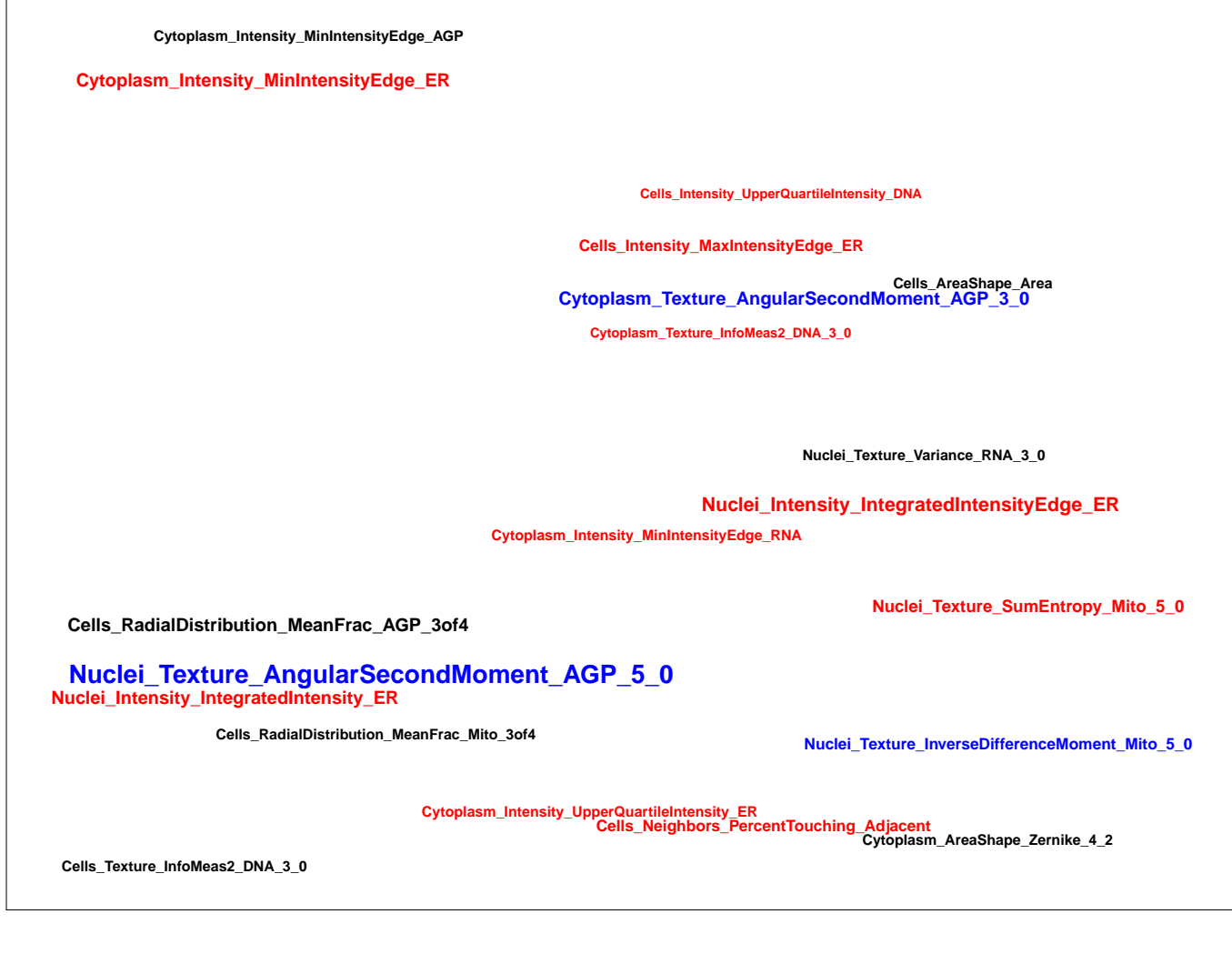
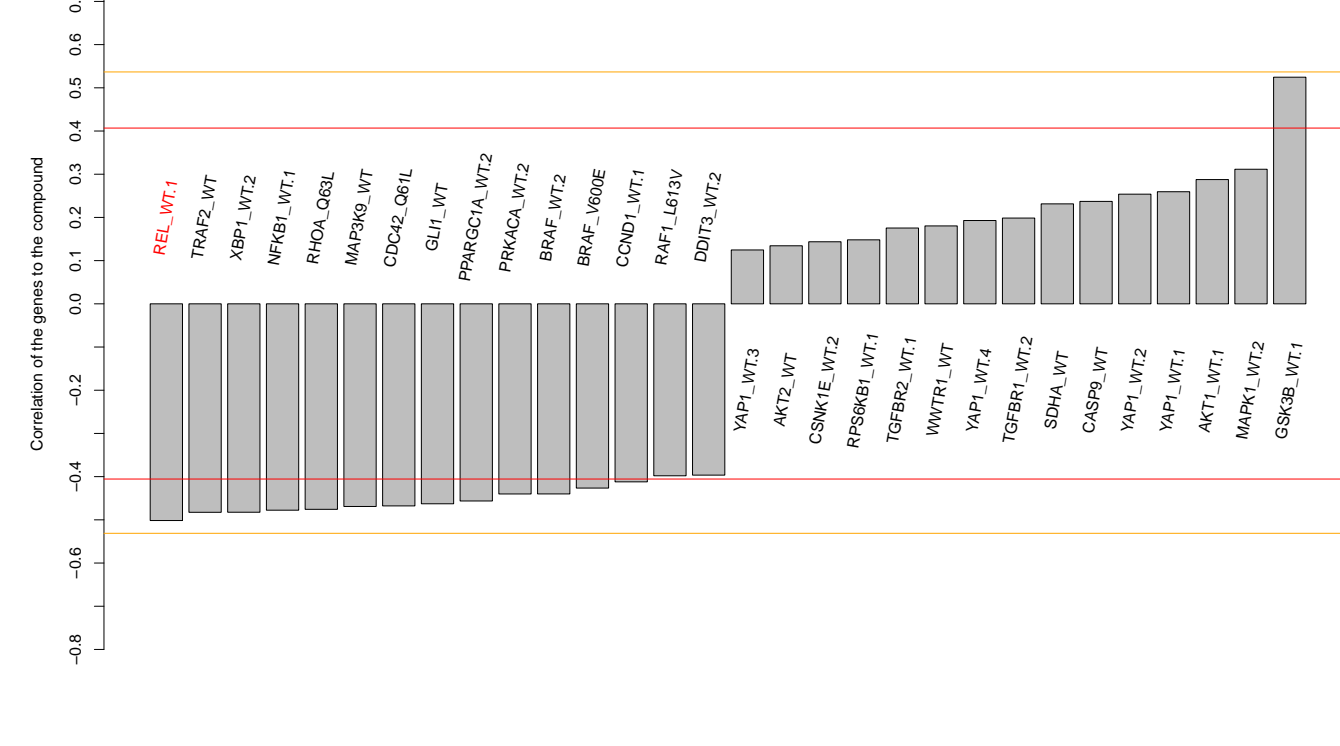
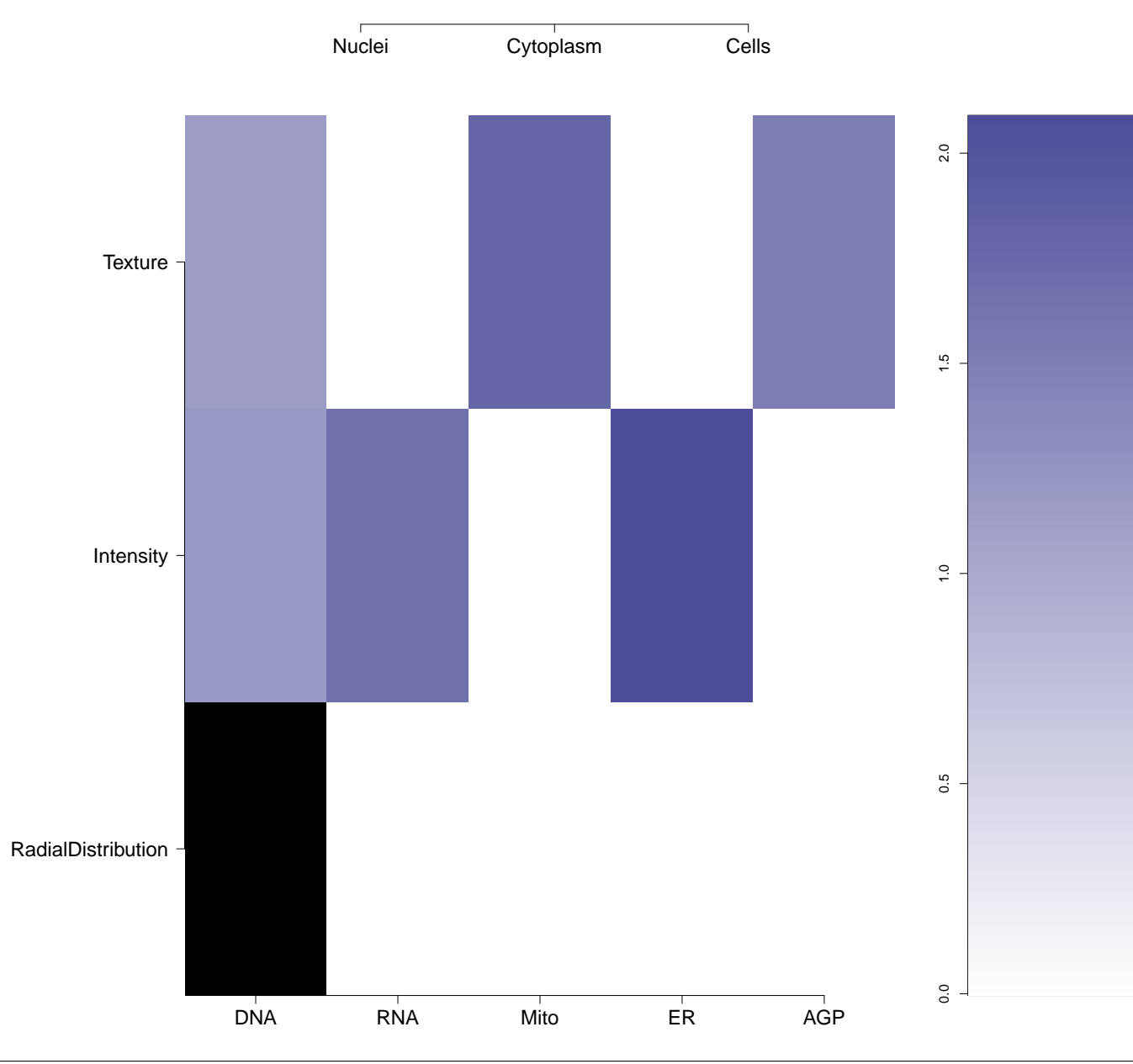
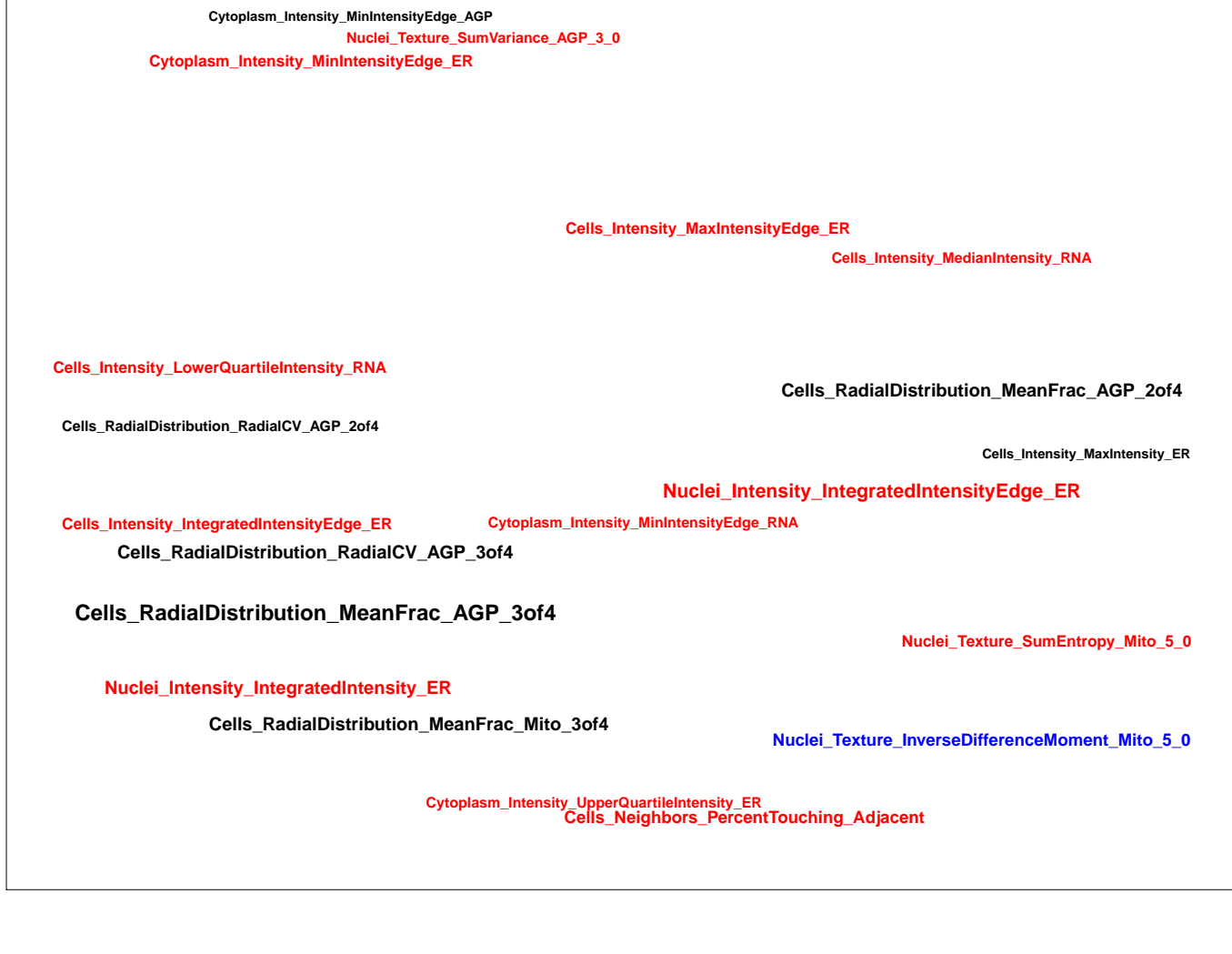
RNA

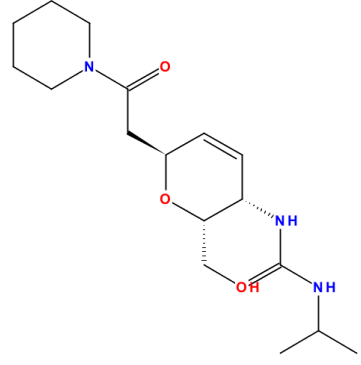
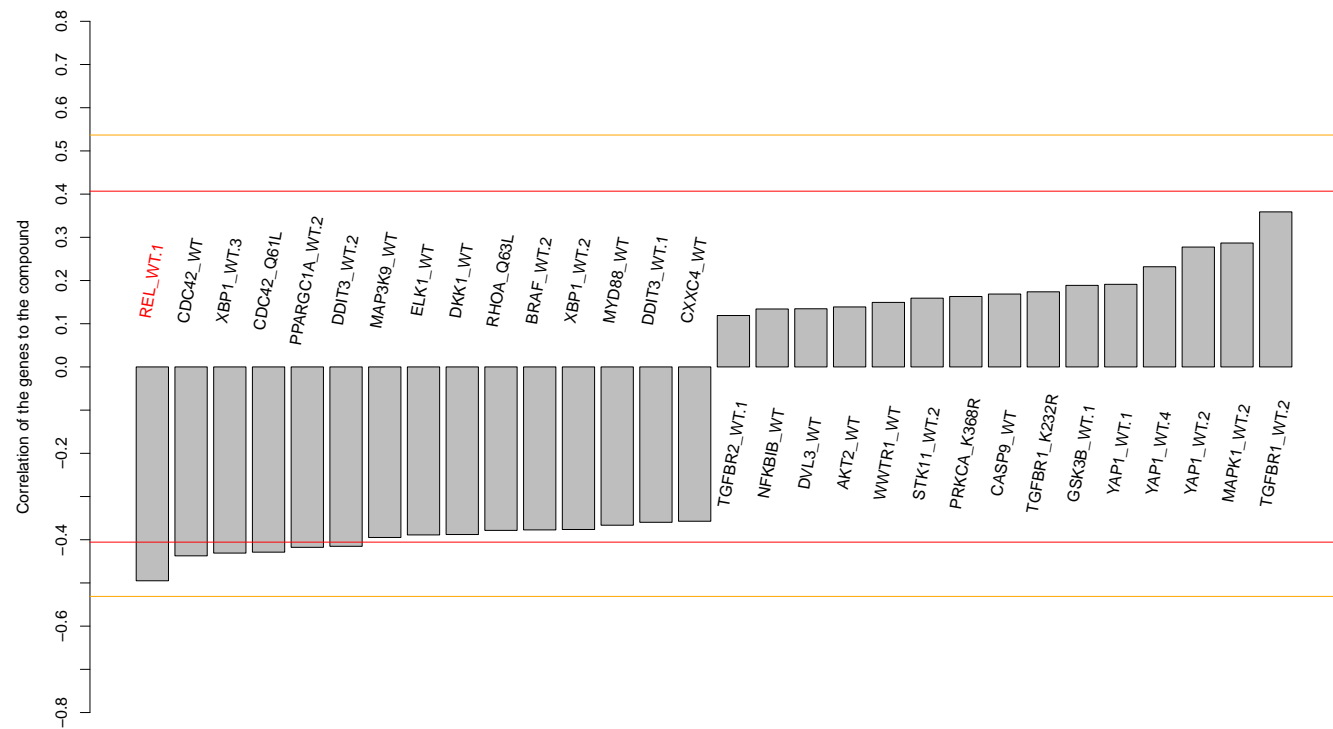
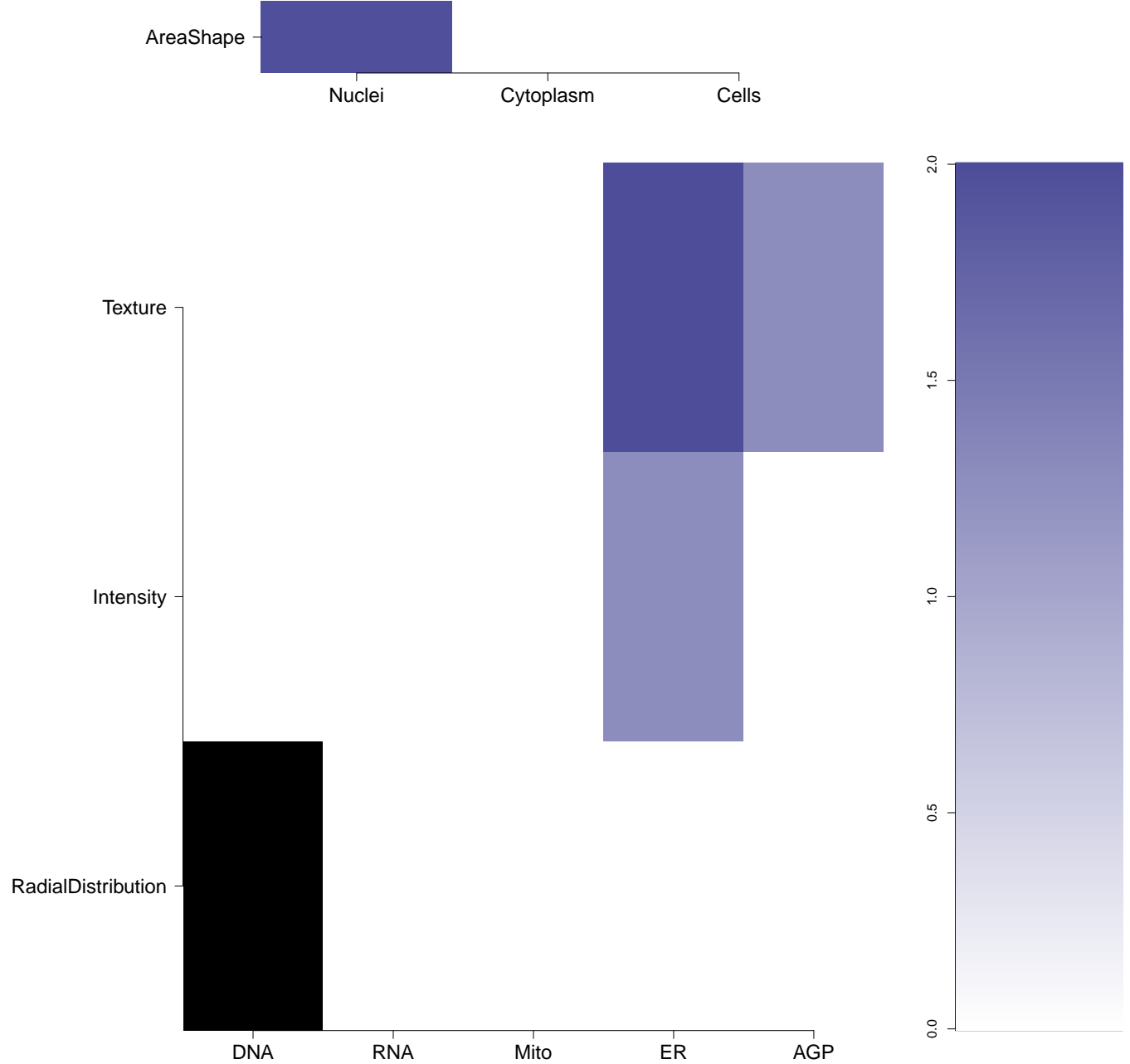

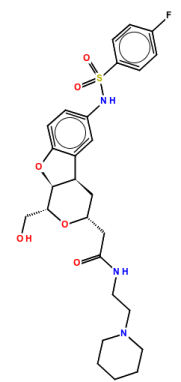
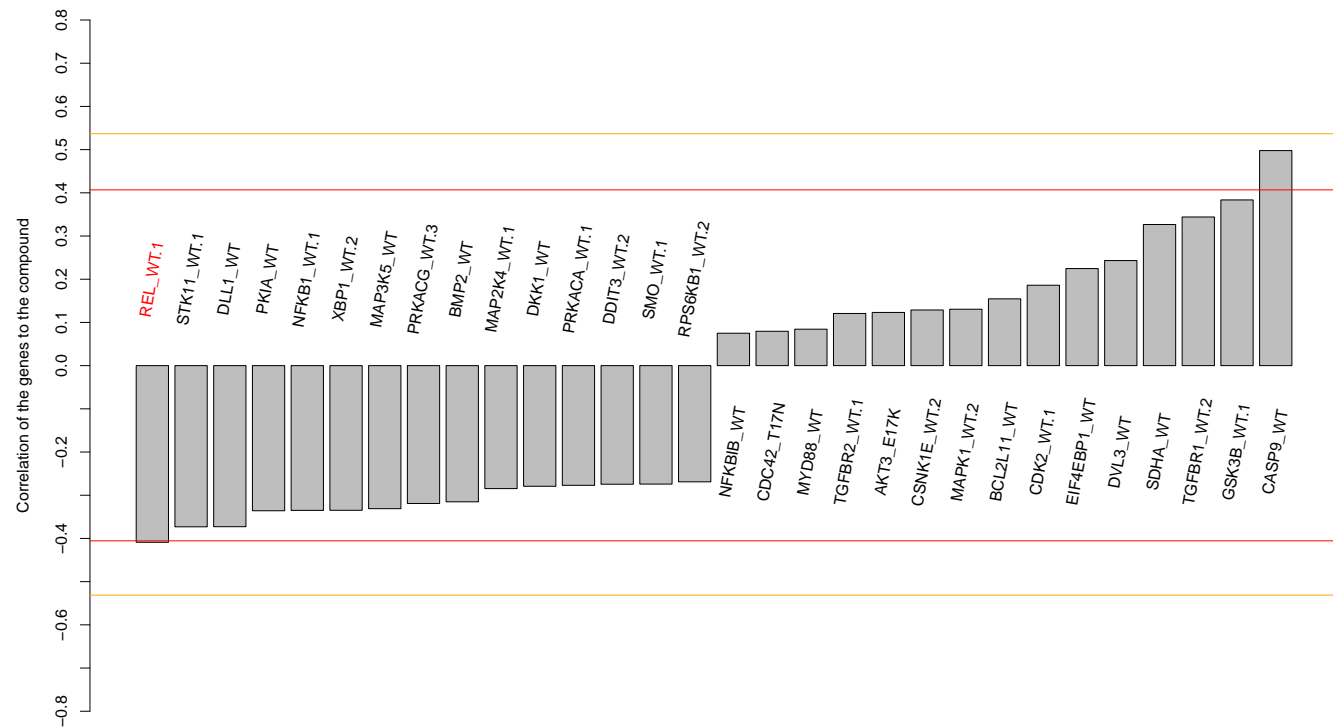
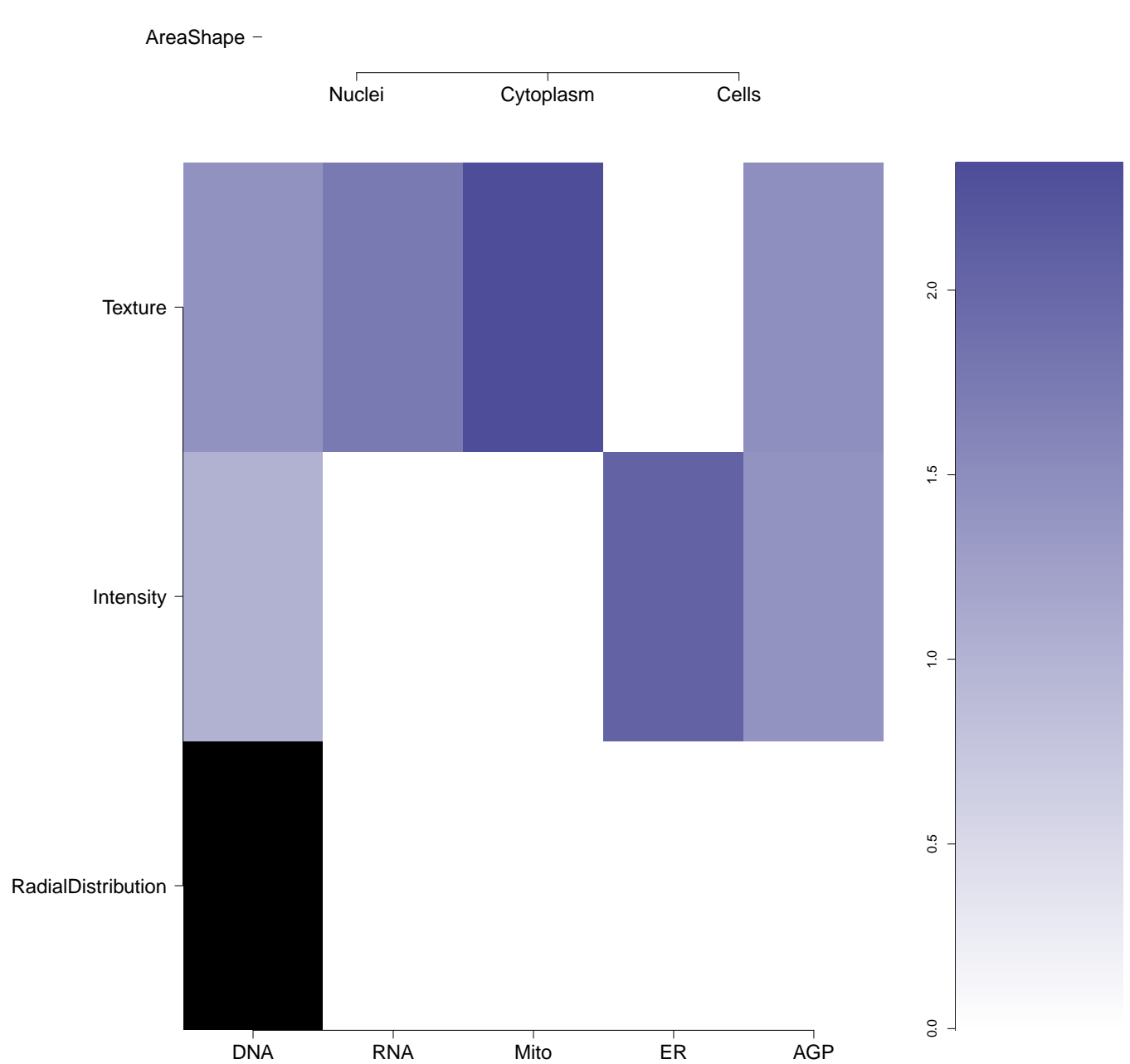

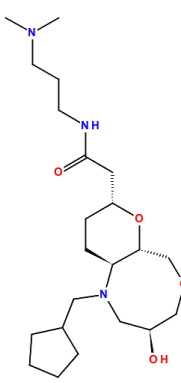
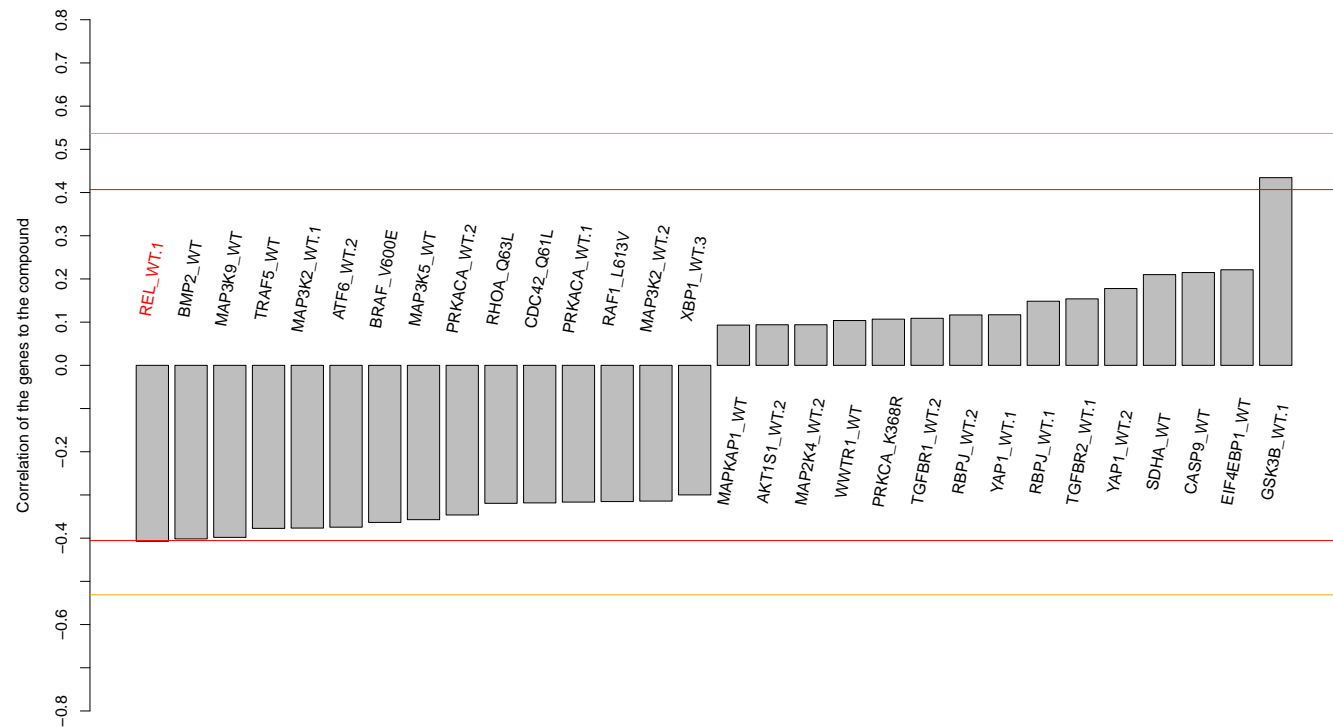
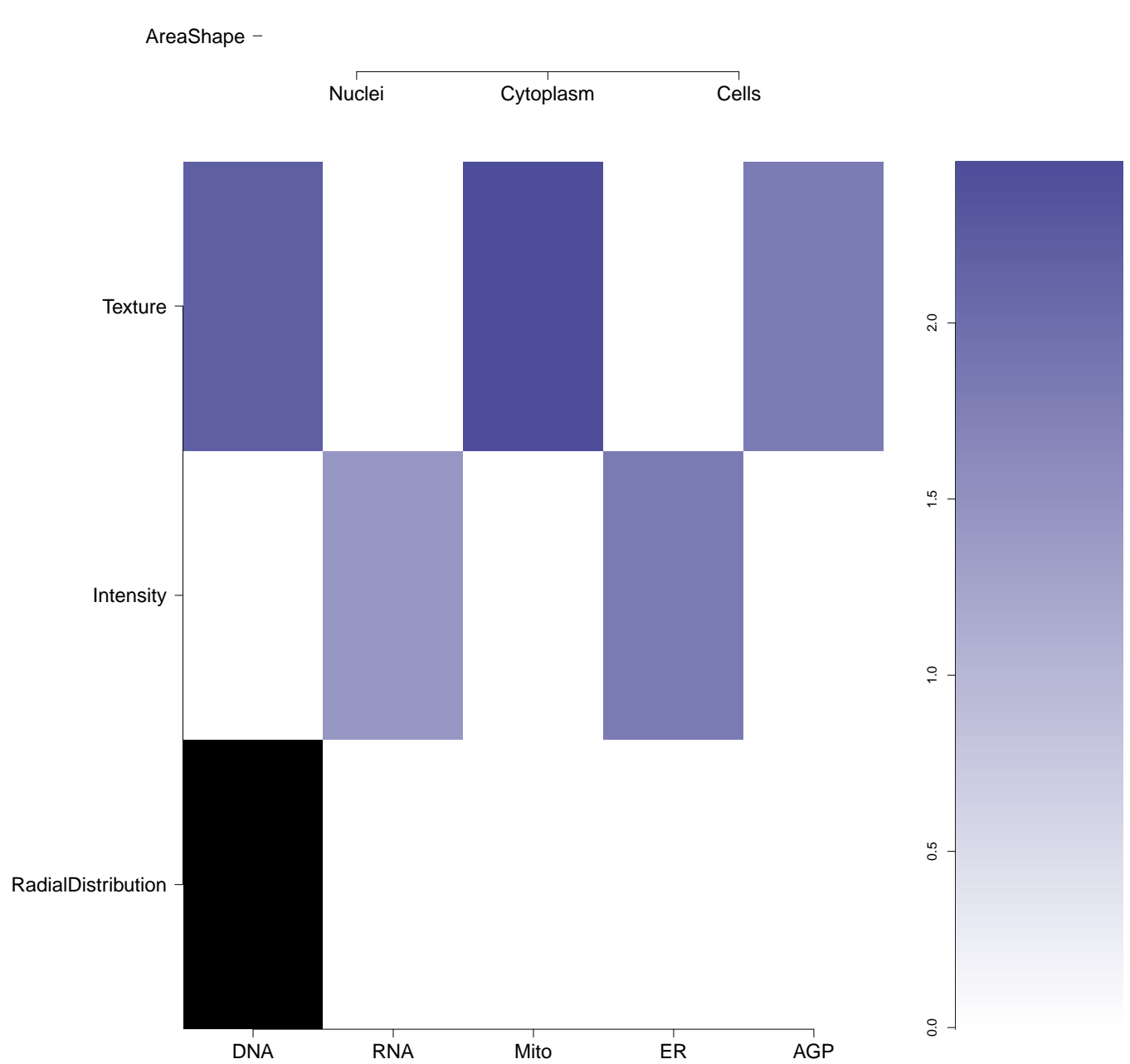
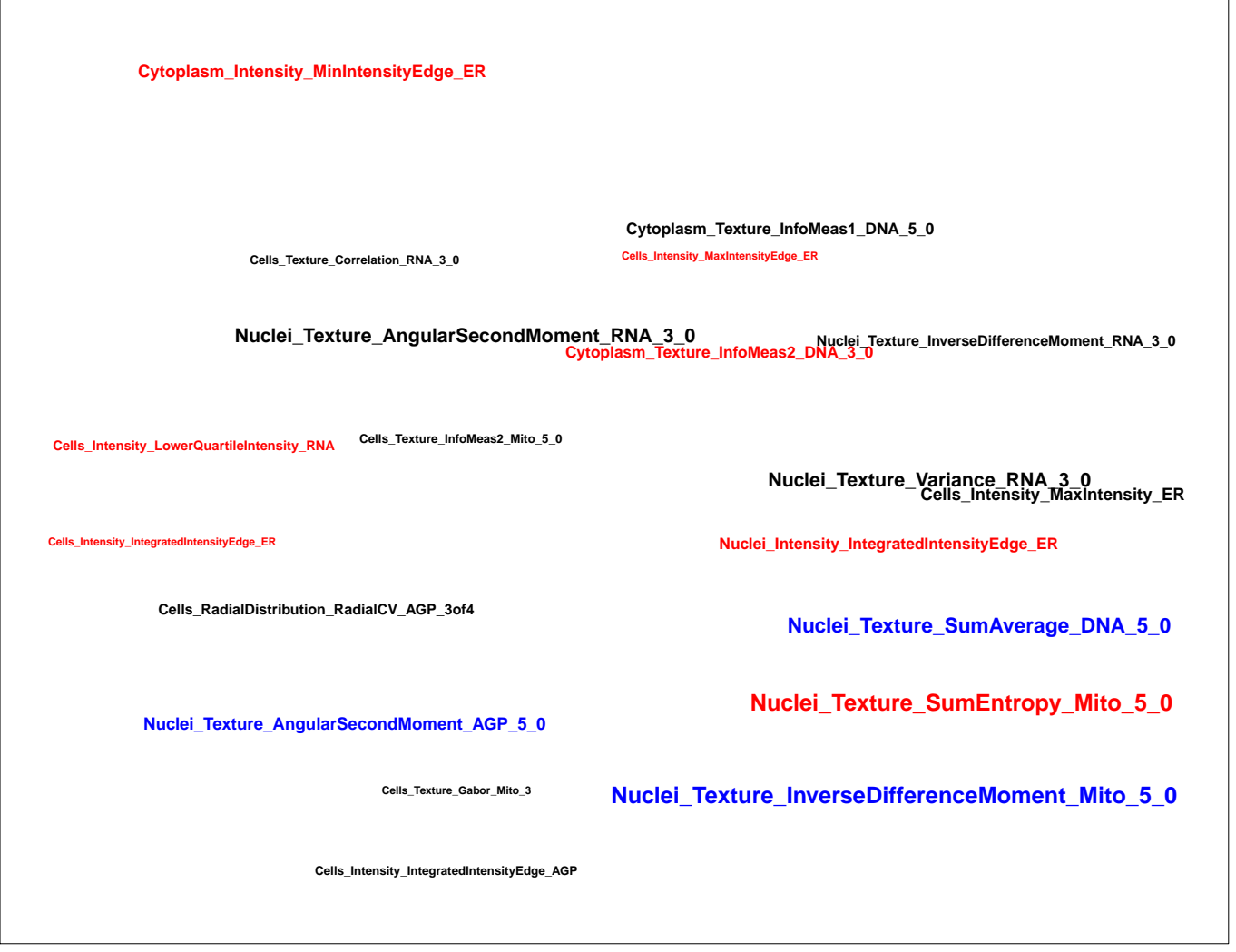


ER



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-K68980973-001-01-8 PubChem CID : 54619802		0.59 (in 4 replicates)	0.42	0.602				Total number of assays tested in: 36.
BRD-K48965155-001-06-3 BAS 00411398 AC1LG4QK MLS000590405 HMS2560H18 ZINC8691724 STK830429 ZINC08691724 SMR000217342 PubChem CID : 814510		0.55 (in 4 replicates)	0.41	NA				Total number of assays tested in: 650. Active in the following assays: <ul style="list-style-type: none"> Primary screen for compounds that inhibit Insulin promoter activity in TRM-6 cells (AID 1273) Multiplex HTS Assay for Inhibitors of MEK Kinase PBI Domains, specifically MEK5 MEK Kinase3 Wildtype (AID 1529) Dyrk1 A HTS Measured in Biochemical System Using Plate Reader - 2124-01 Inhibitor.SinglePoint.HTS Activity (AID 50441) MLPCN Dyrk1A Kinase Measured in Biochemical System Using Plate Reader - 2124-01 Inhibitor.Dose.CherryPick Activity (AID 588345) 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) Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Fluorescence-based biochemical high throughput Glycerophosphate Dehydrogenase-Trisphosphate Isomerase (GDH-TPI) assay to identify assay artifacts (AID 652141)
BRD-K59755197-001-01-5 PubChem CID : 54646601		0.79 (in 3 replicates)	-0.54	0.382				Total number of assays tested in: 36.
BRD-K90445273-001-01-1 PubChem CID : 54618522		0.54 (in 4 replicates)	-0.52	0.398				Total number of assays tested in: 28.
BRD-K10666842-001-01-1 PubChem CID : 54646497		0.66 (in 4 replicates)	-0.51	0.386				Total number of assays tested in: 36.
BRD-K56708236-001-01-0 PubChem CID : 54647370		0.55 (in 4 replicates)	-0.51	0.353				Total number of assays tested in: 39.
BRD-K76885311-001-01-0 PubChem CID : 54632584		0.58 (in 4 replicates)	-0.50	0.940				Total number of assays tested in: 35.

BRD-K33337505-001-01-0 PubChem CID : 54641315		0.54 (in 2 replicates)	-0.49	NA				Total number of assays tested in: 38.
BRD-K62014585-001-01-2 PubChem CID : 54645921		NA (in 1 replicates)	-0.41	0.829				Total number of assays tested in: 43.
BRD-K18767302-001-01-2 PubChem CID : 54657795		0.56 (in 5 replicates)	-0.41	0.240				Total number of assays tested in: 36.