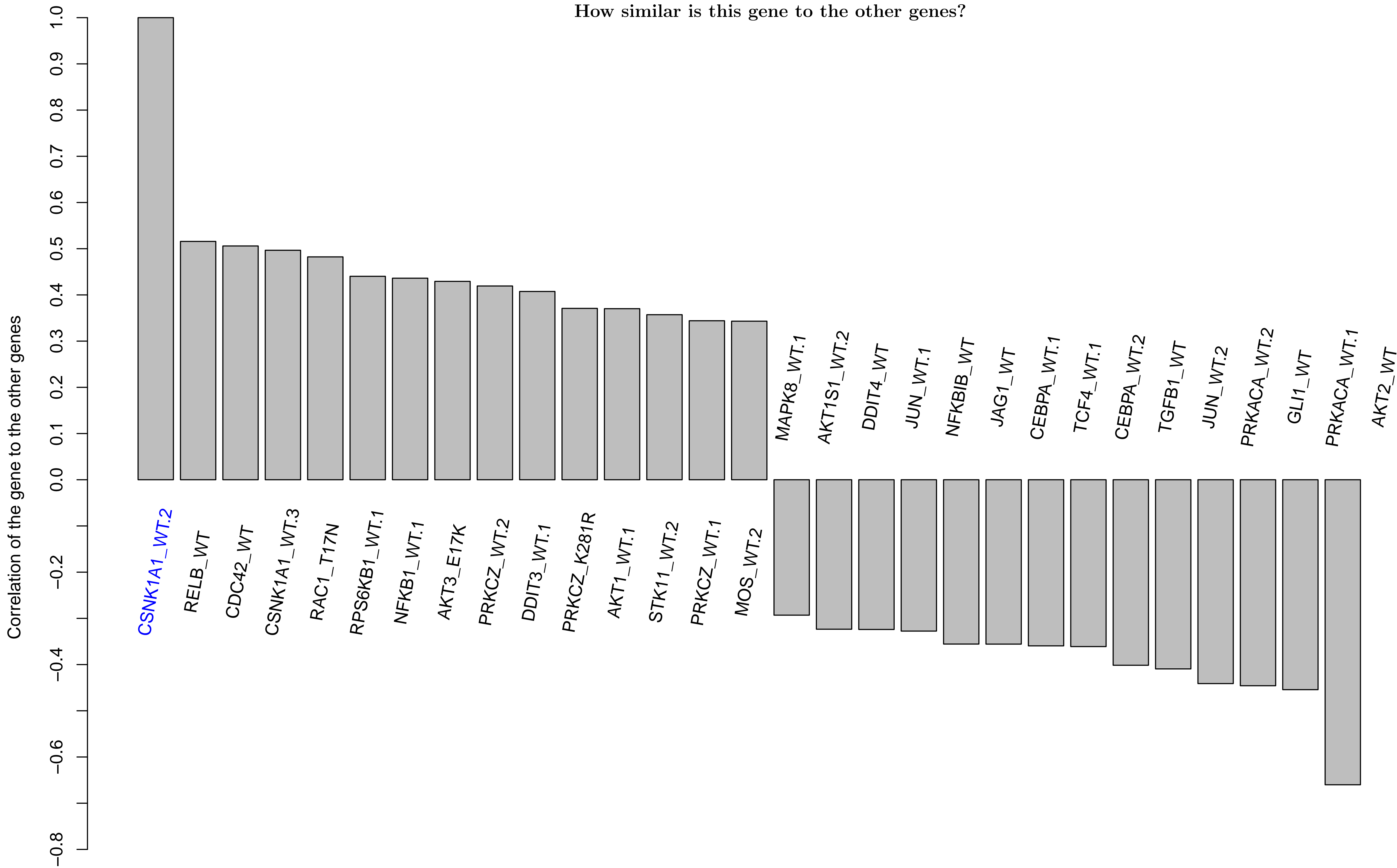
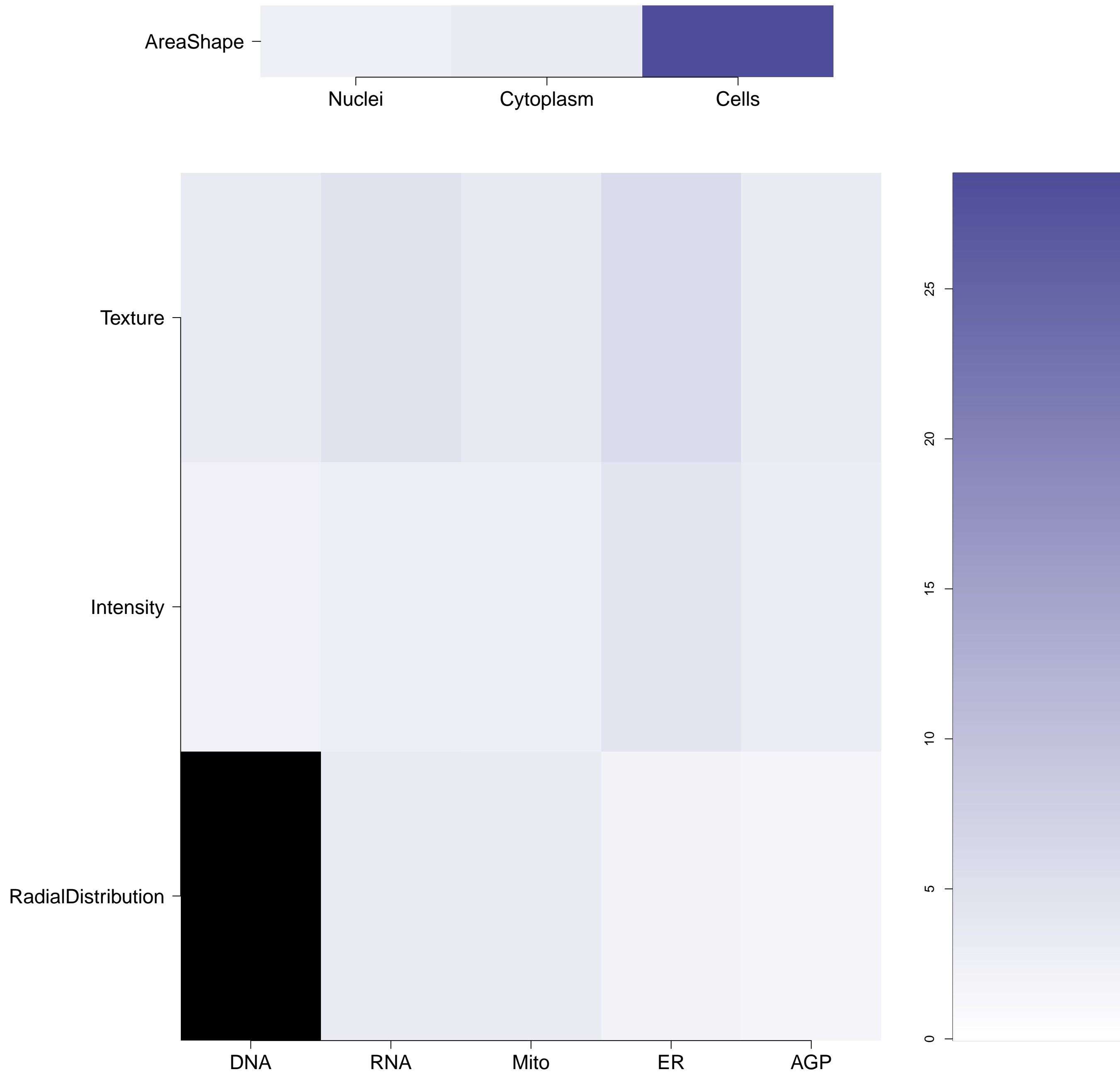


CSNK1A1.WT.2 - in Canonical WNT

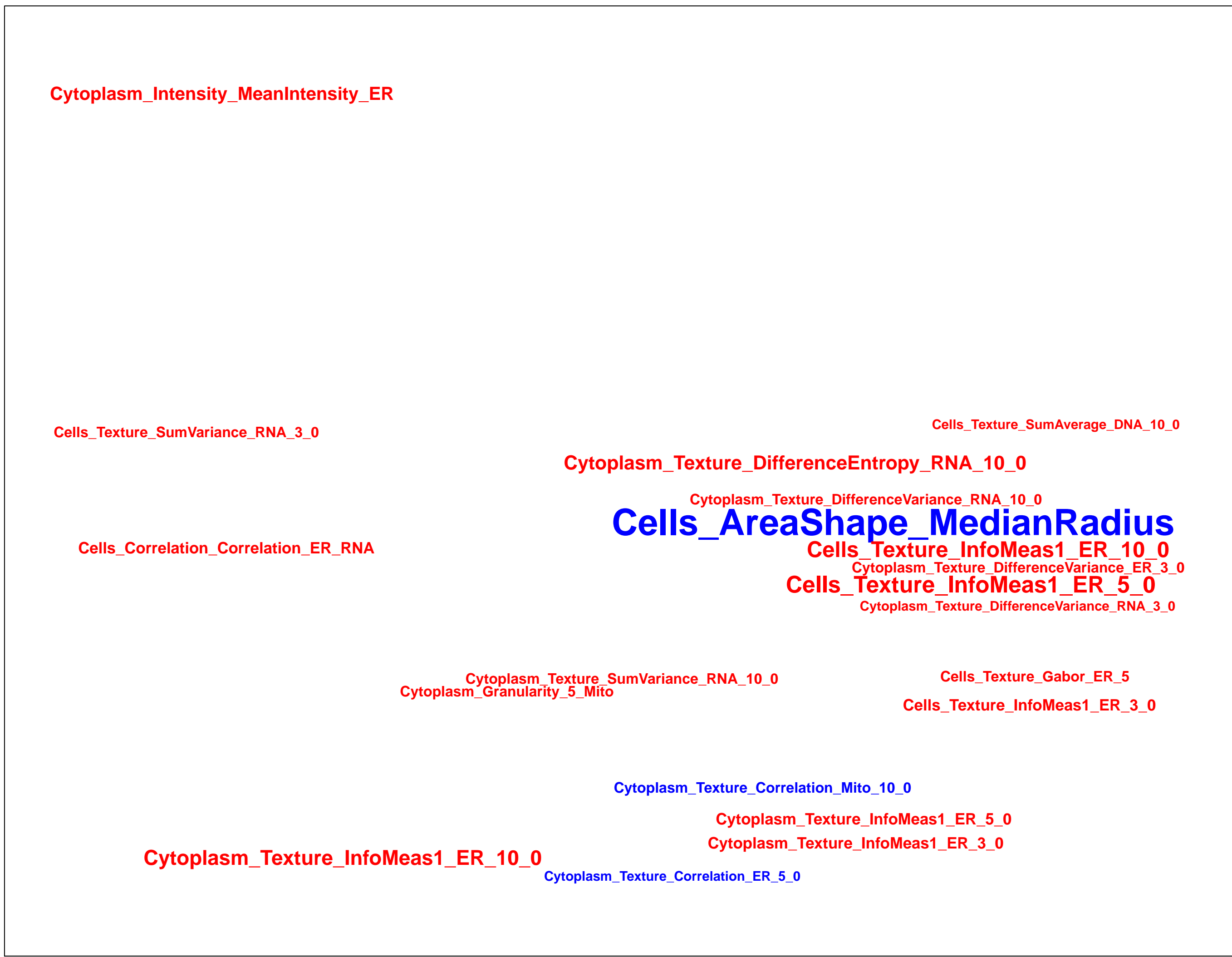
How similar is this gene to the other genes?



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

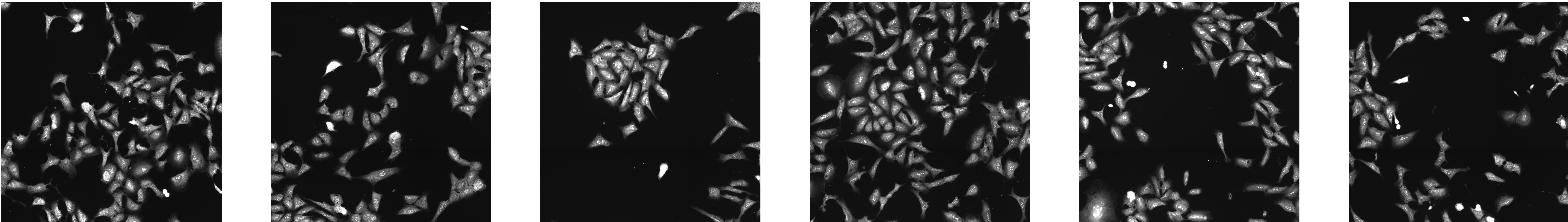


Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

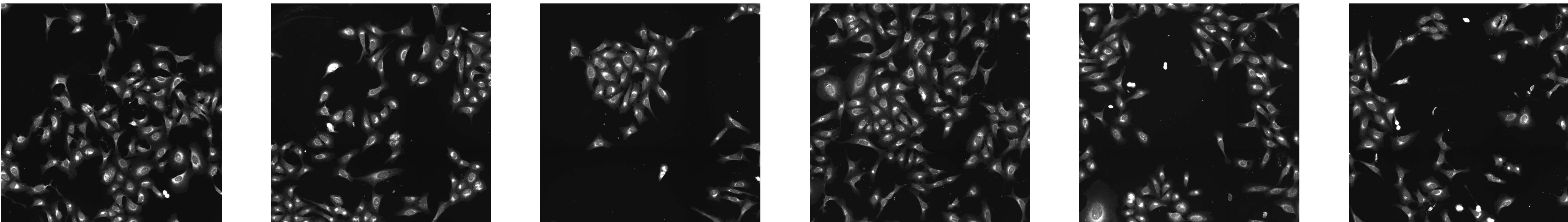


Empty CSNK1A1.WT.2 (41744) CSNK1A1.WT.2 (41755) CSNK1A1.WT.2 (41756) CSNK1A1.WT.2 (41757) CSNK1A1.WT.2 (41754)

RNA

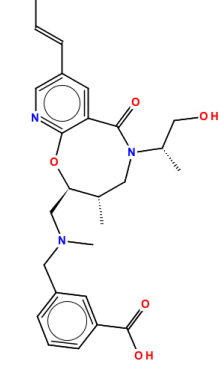
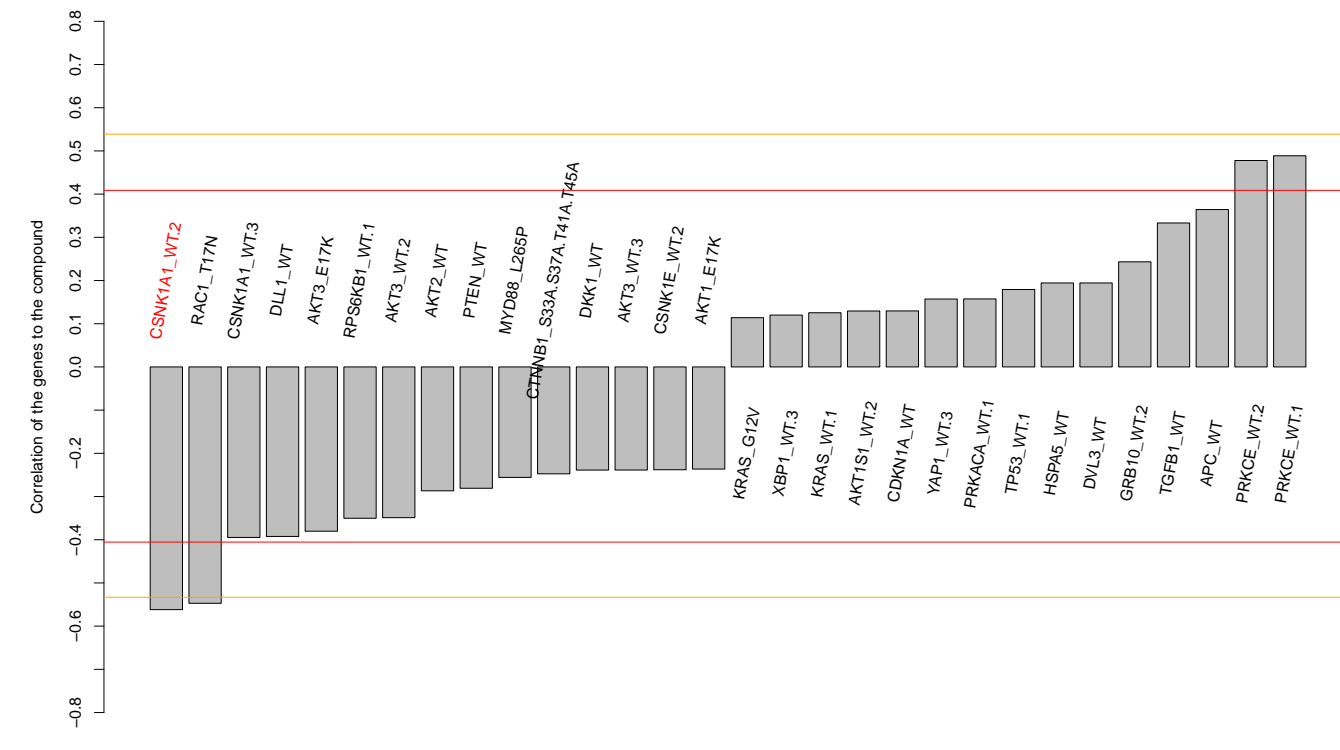
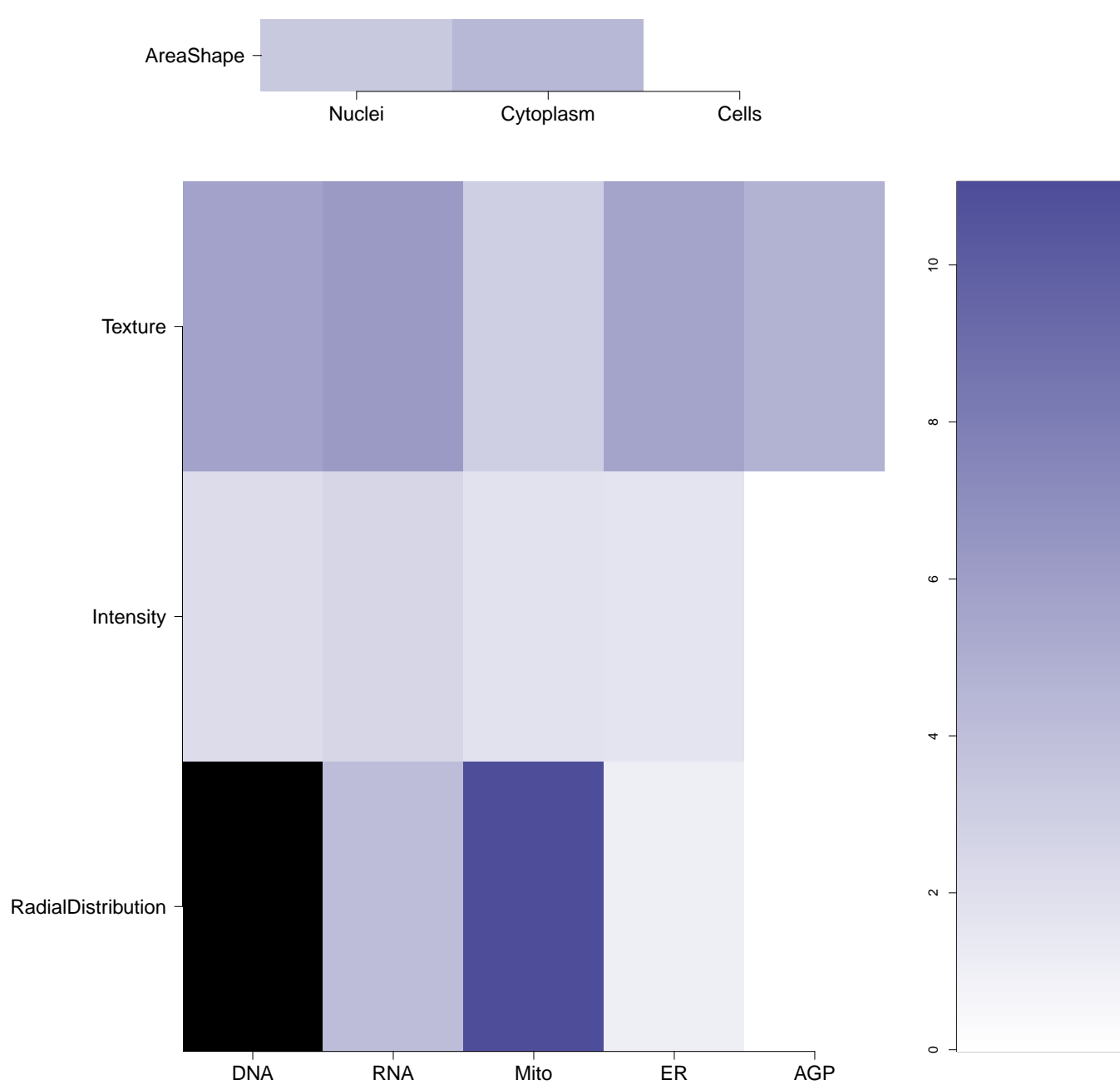

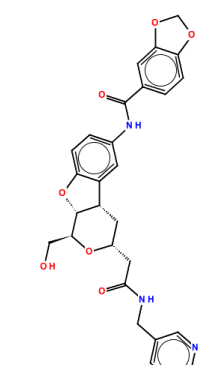
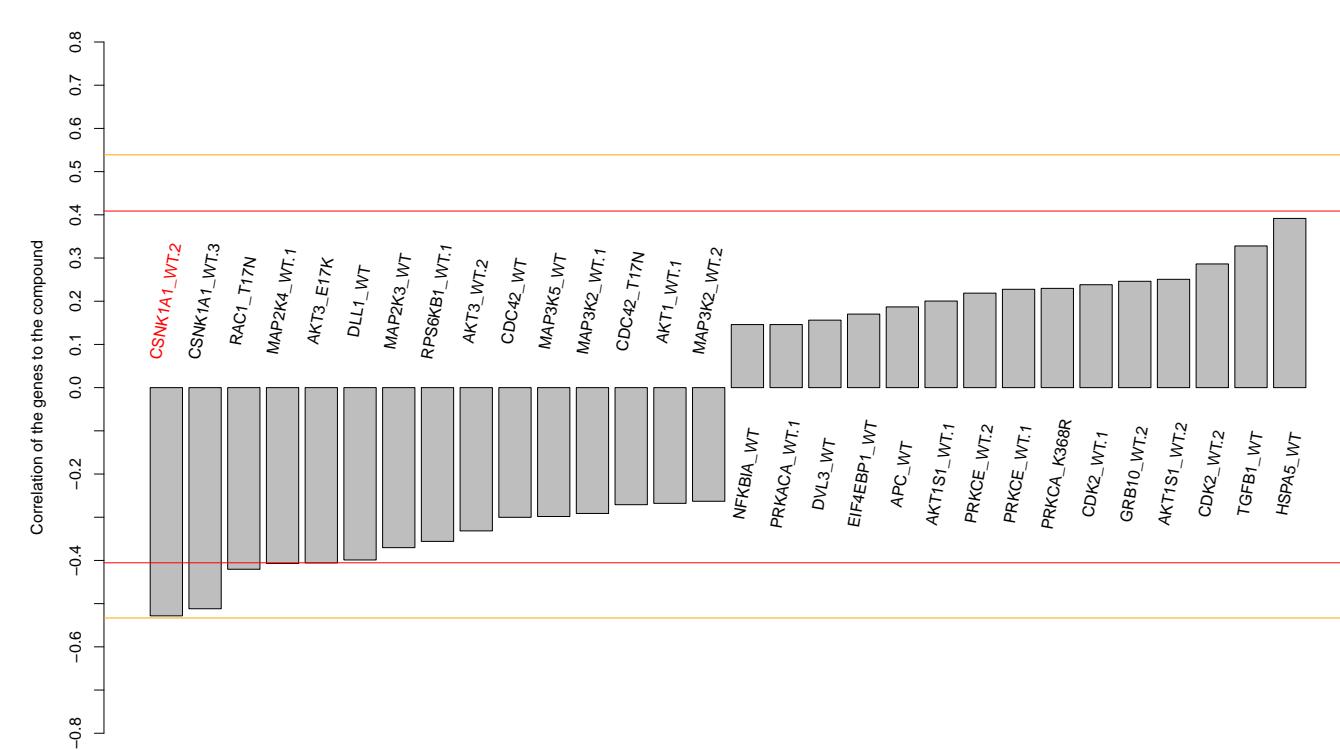
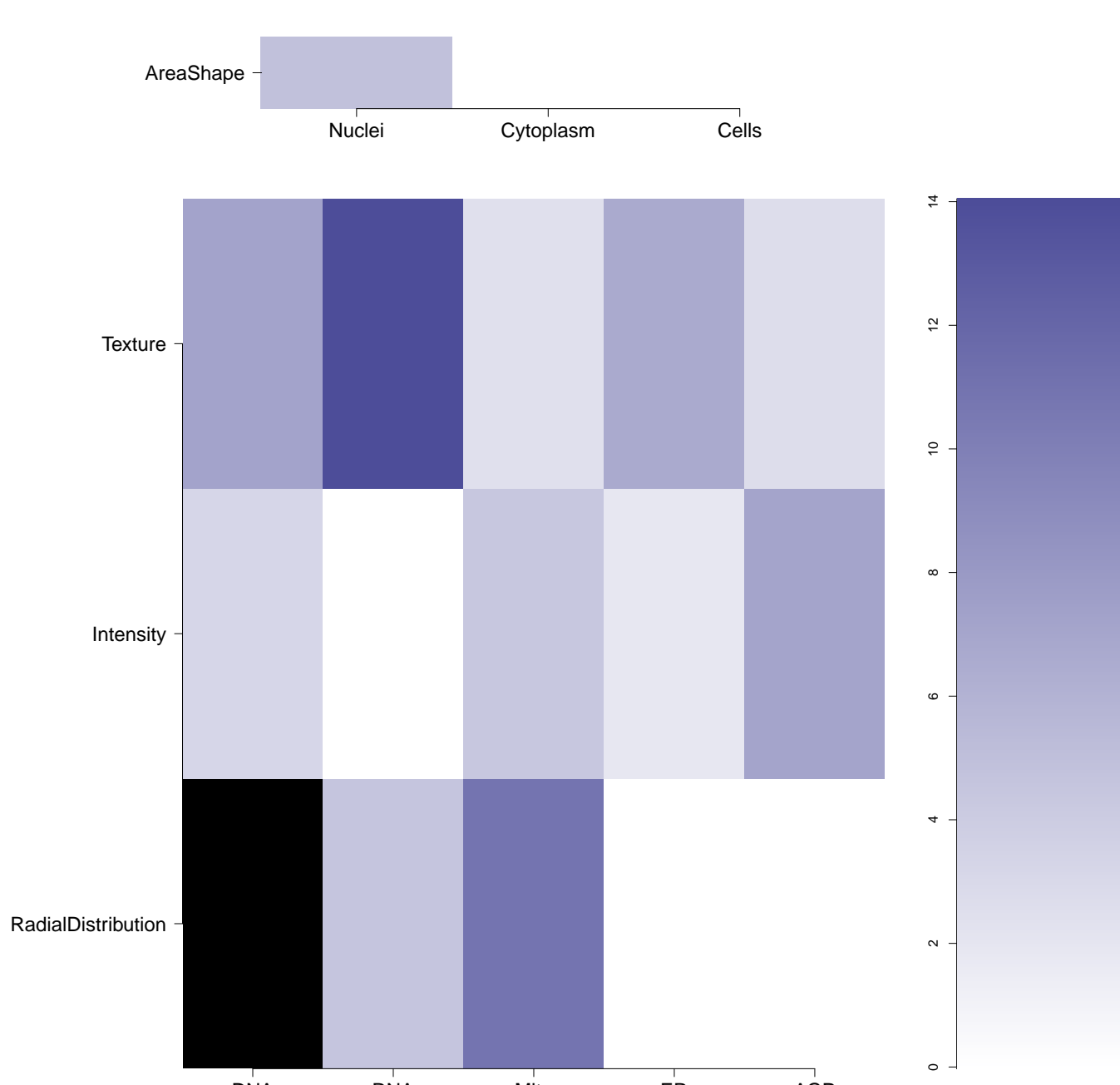

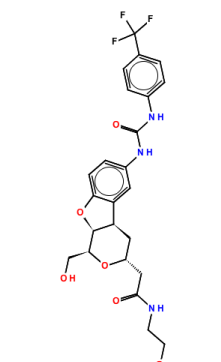
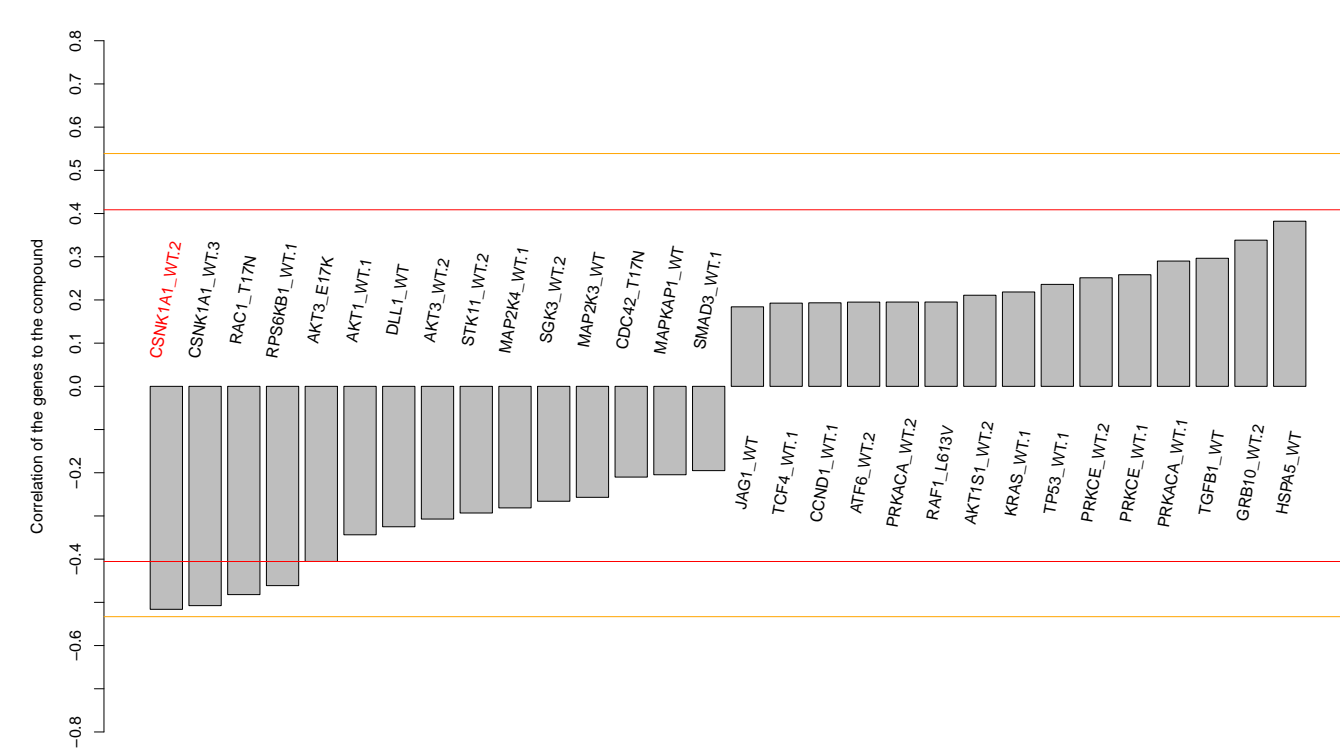
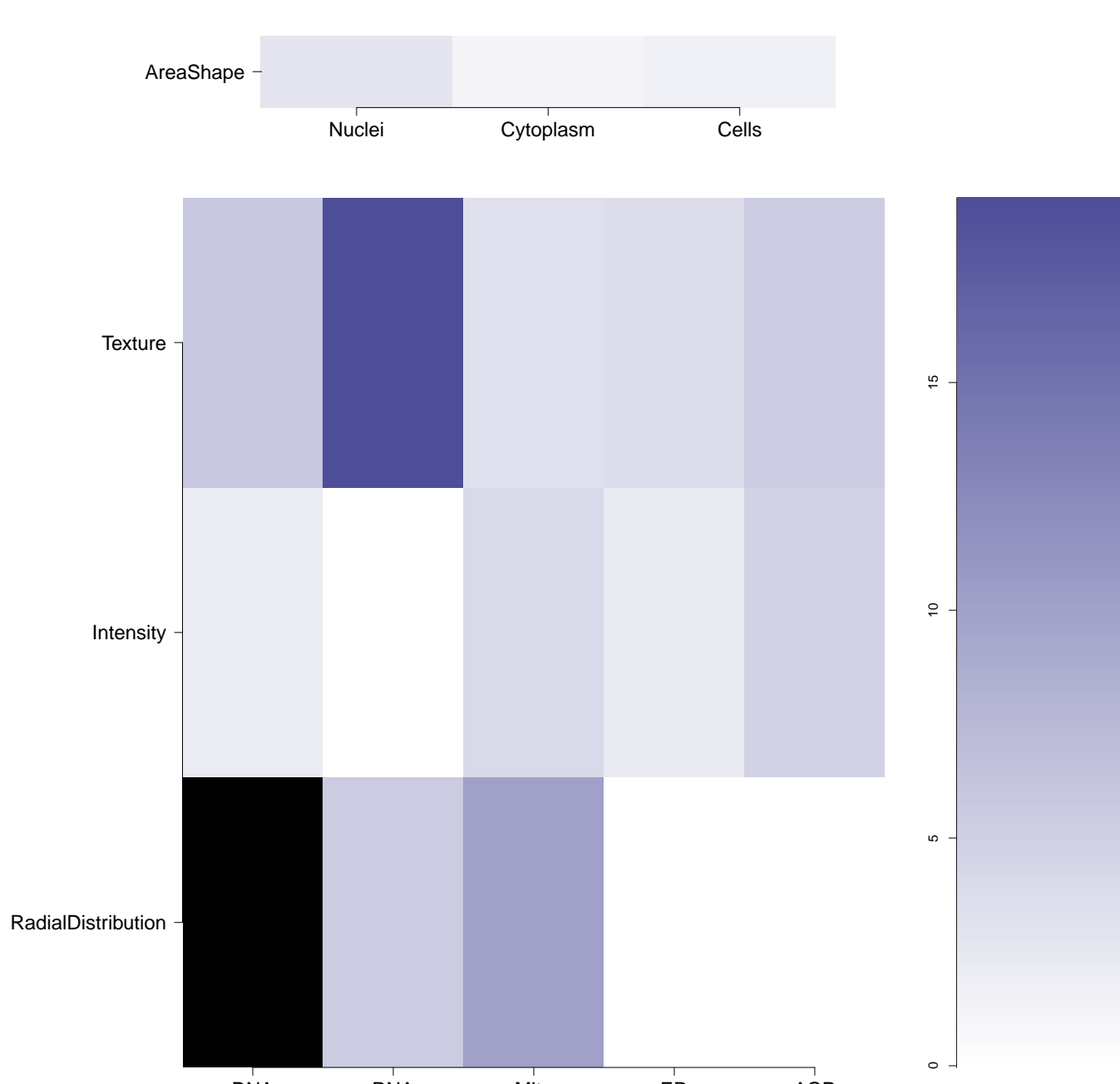
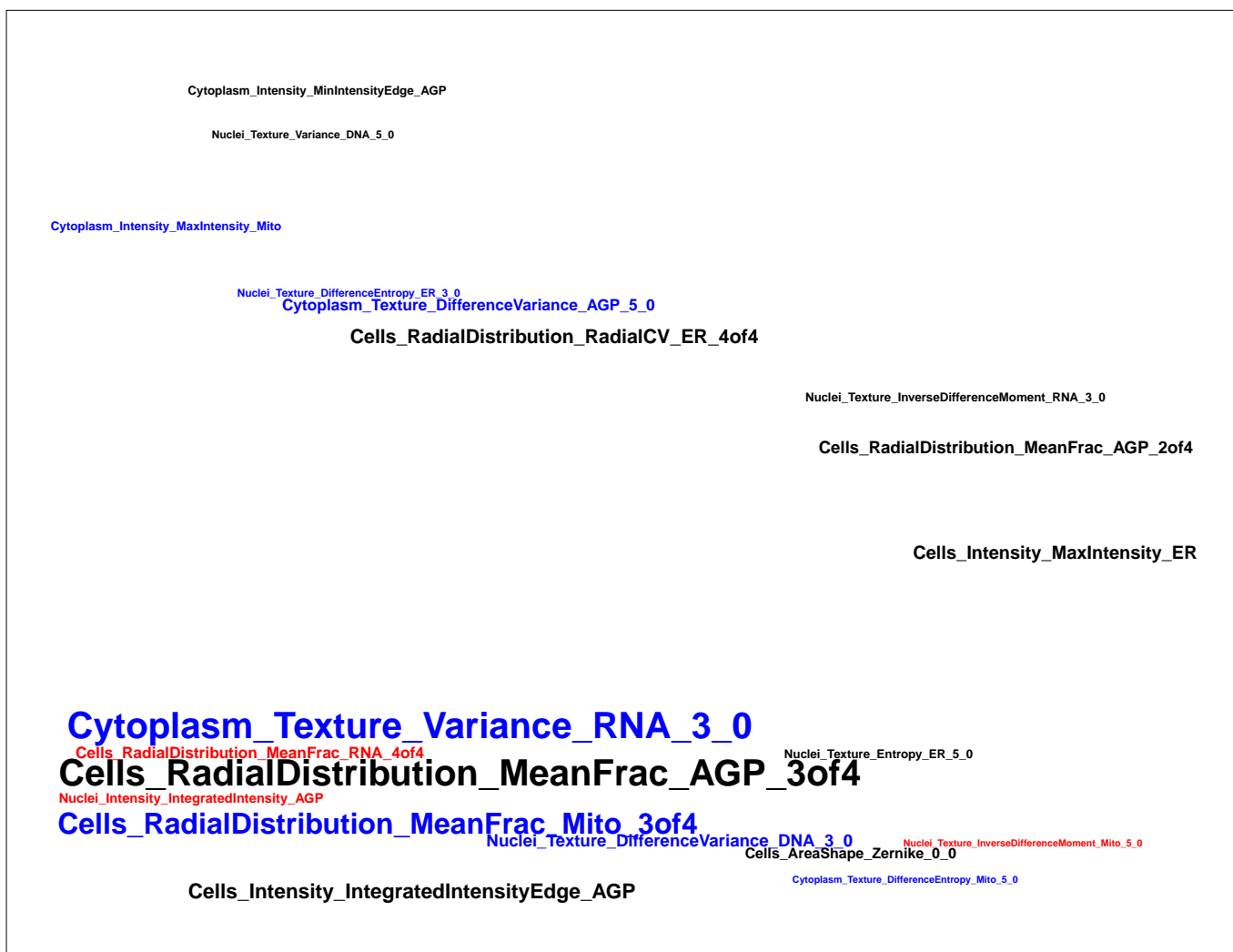
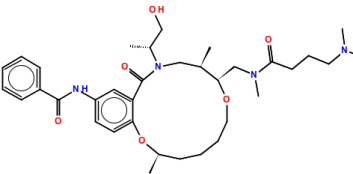
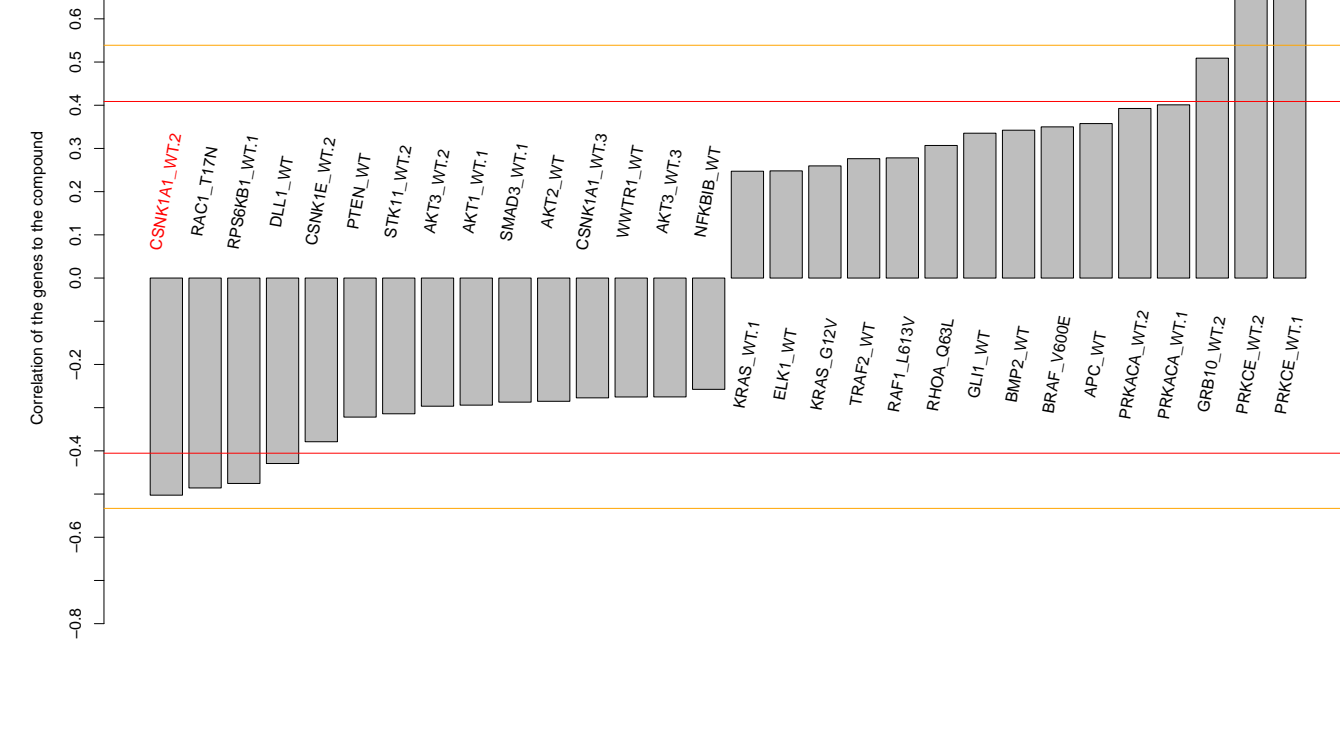
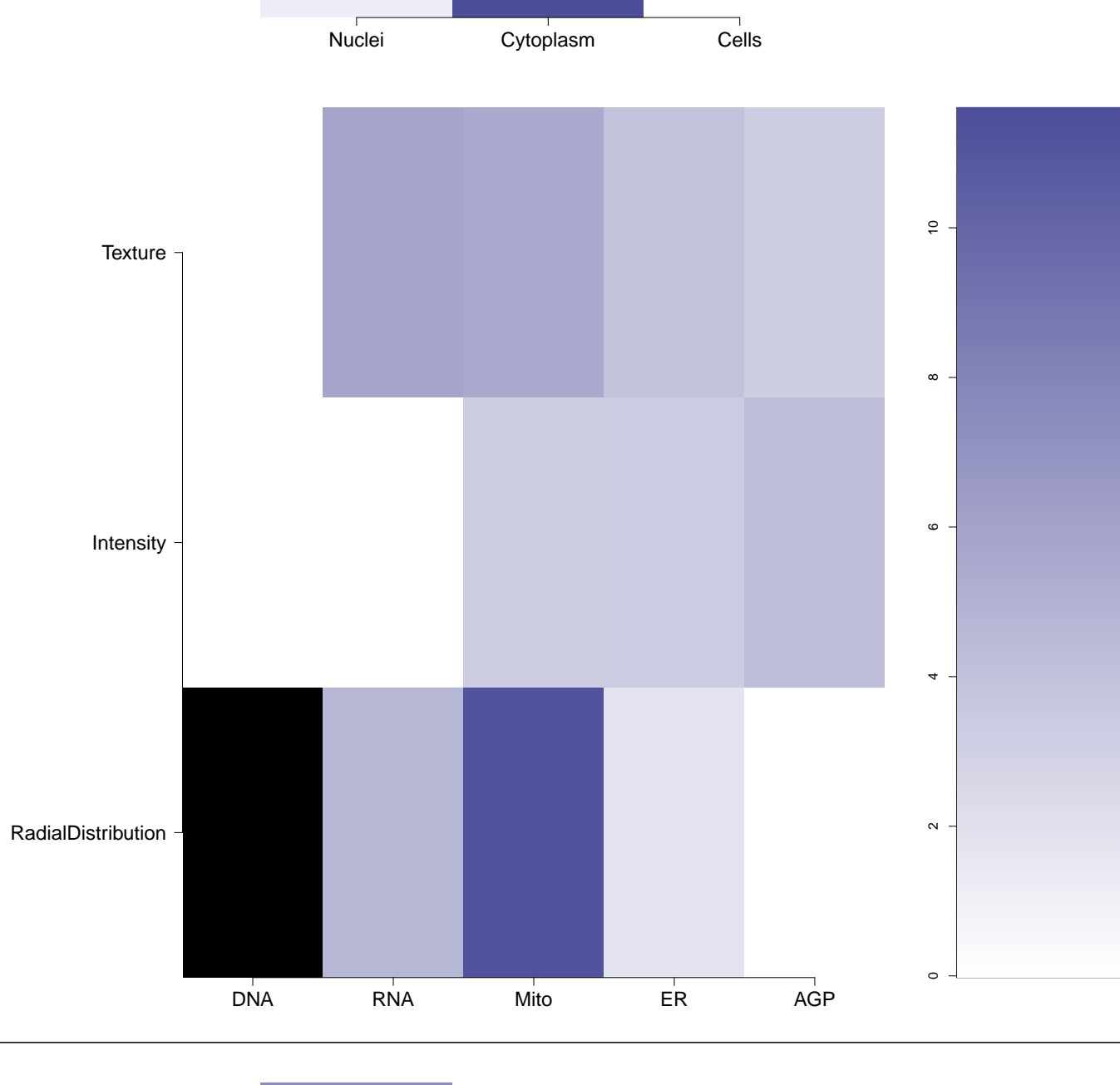
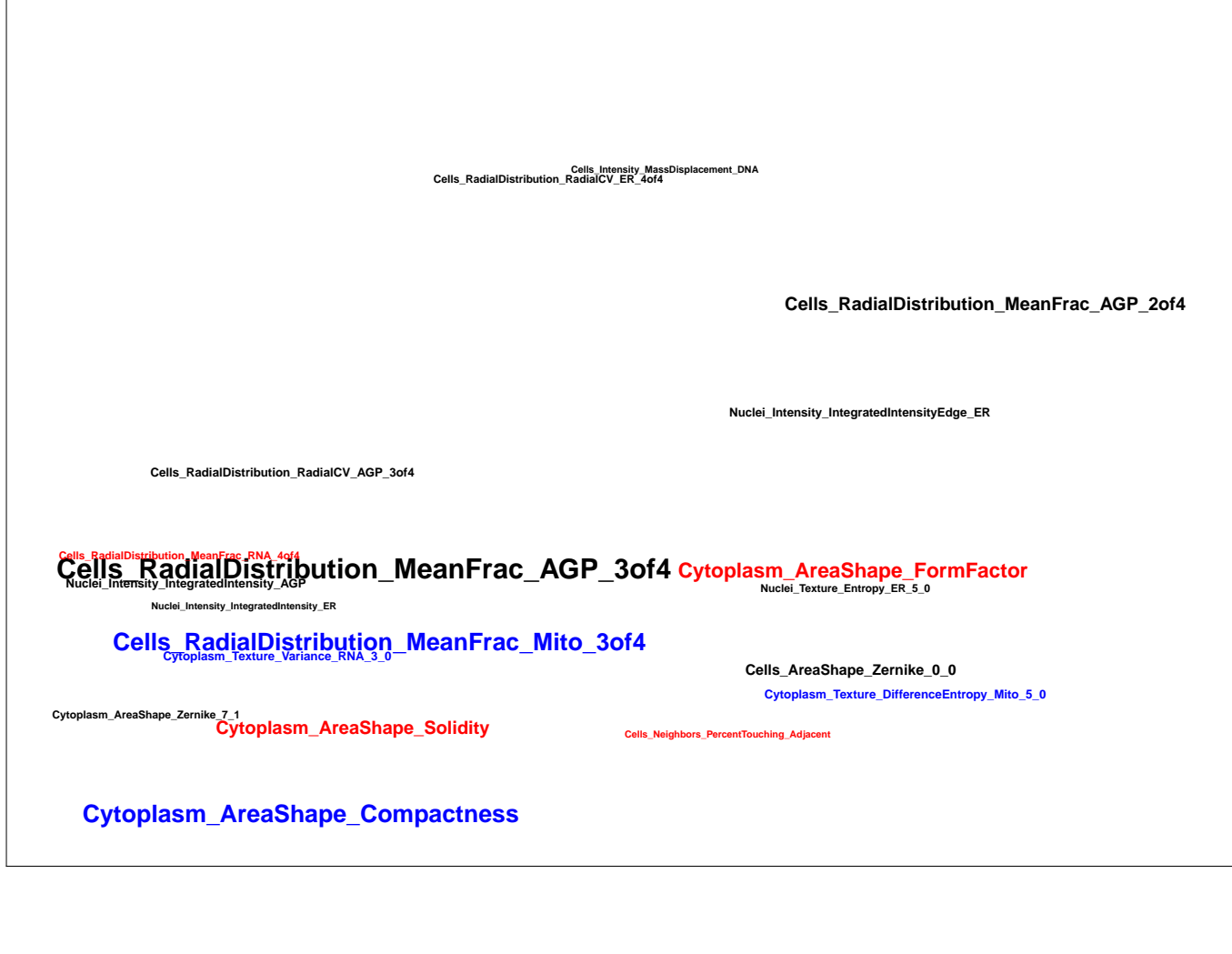
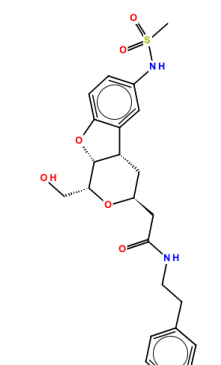
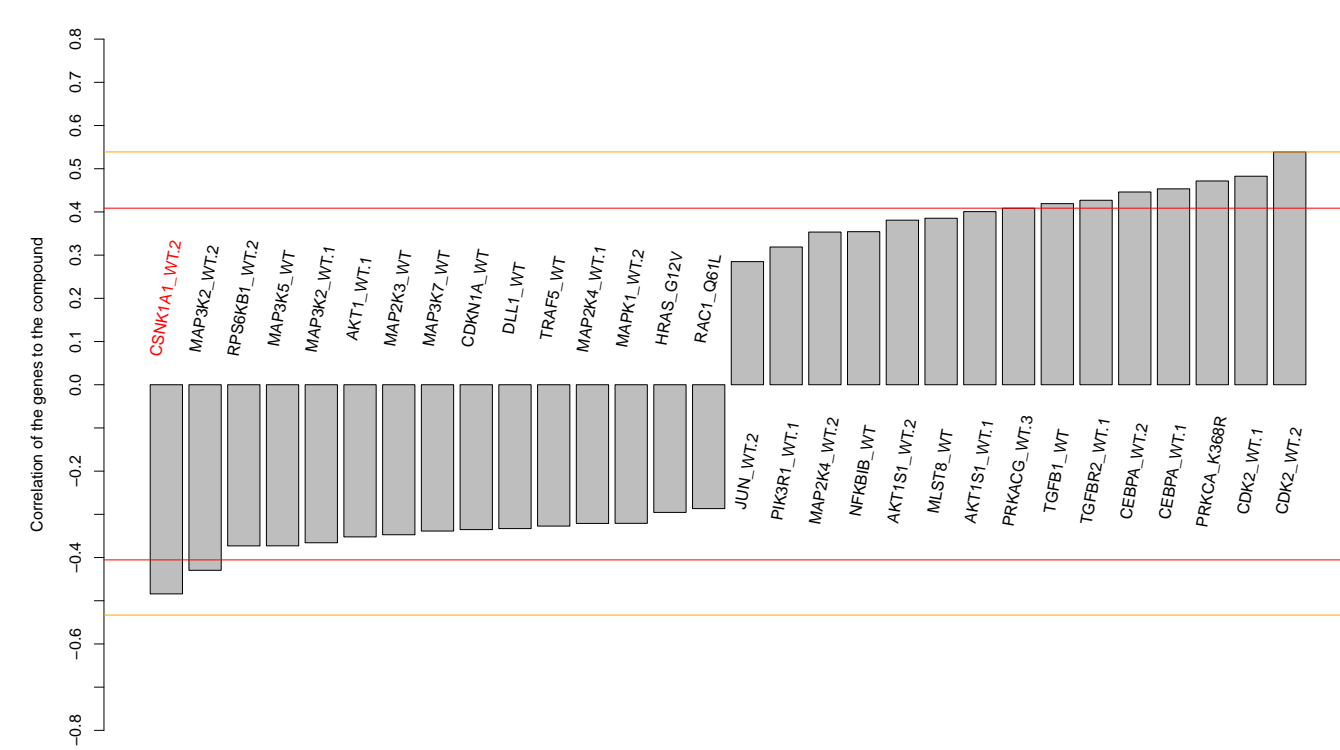
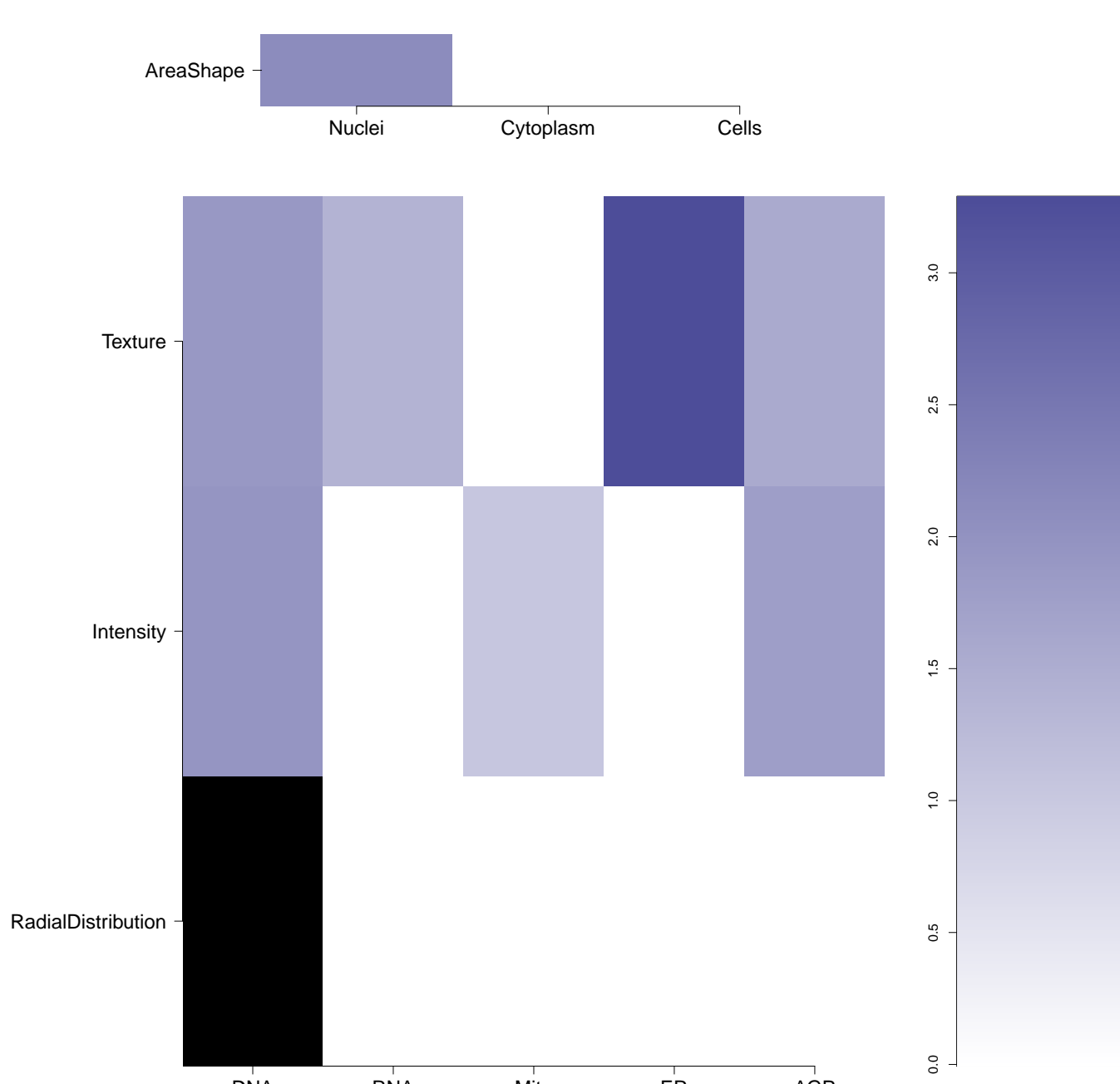
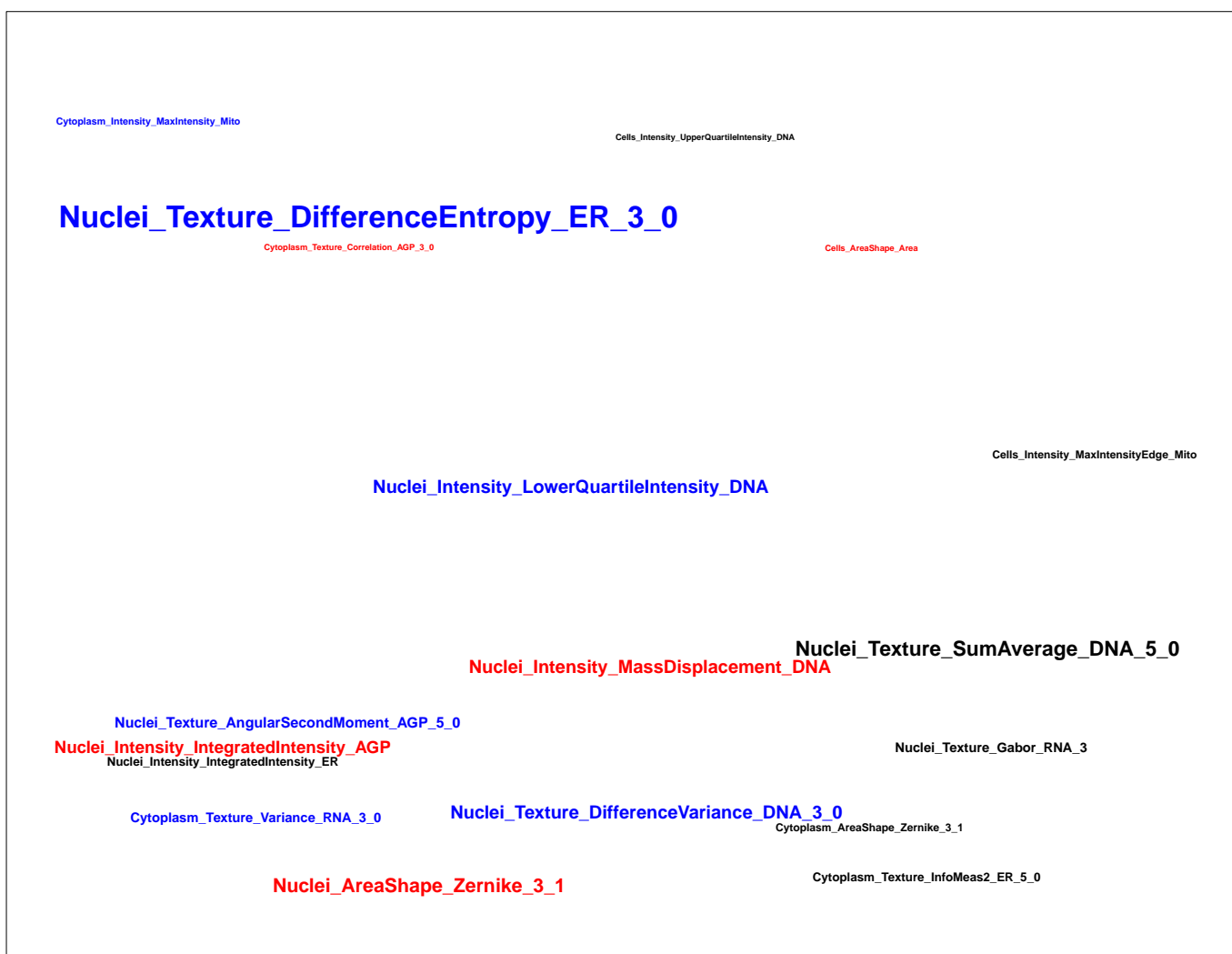
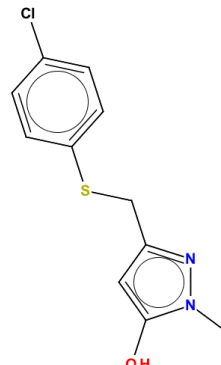
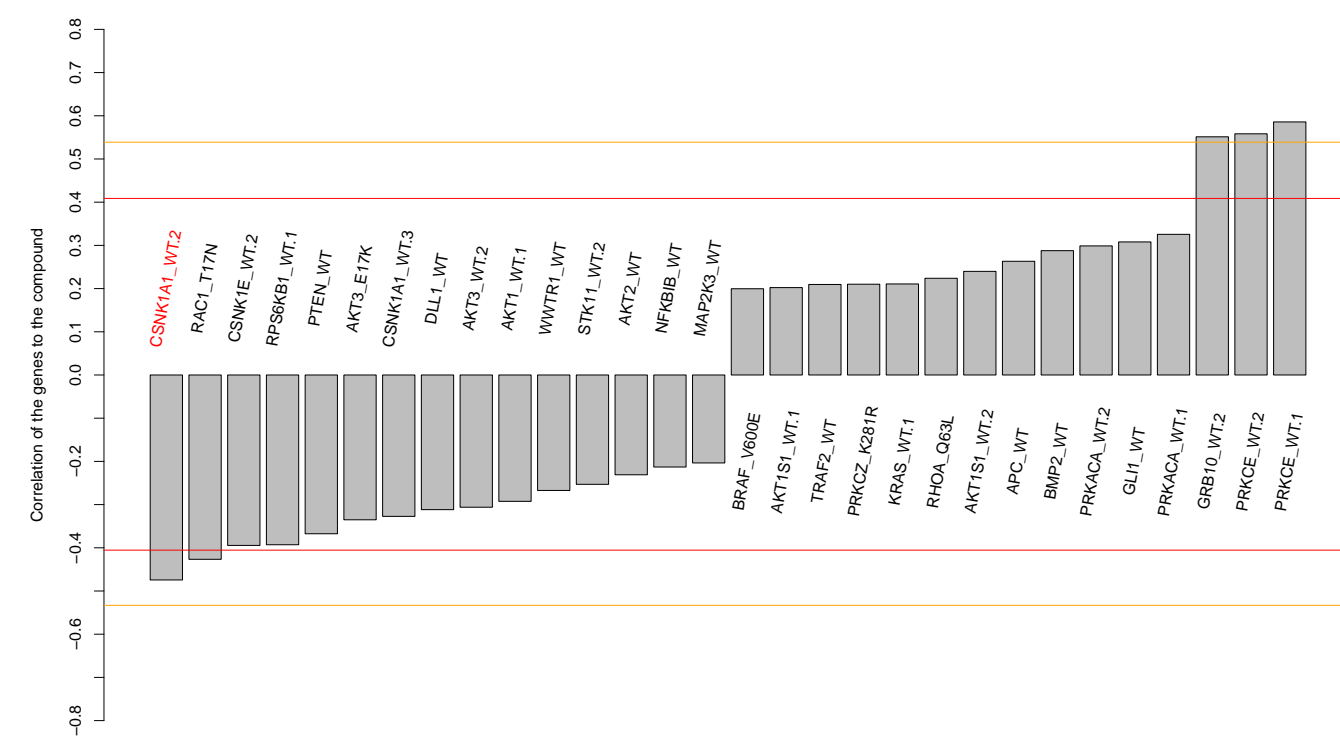
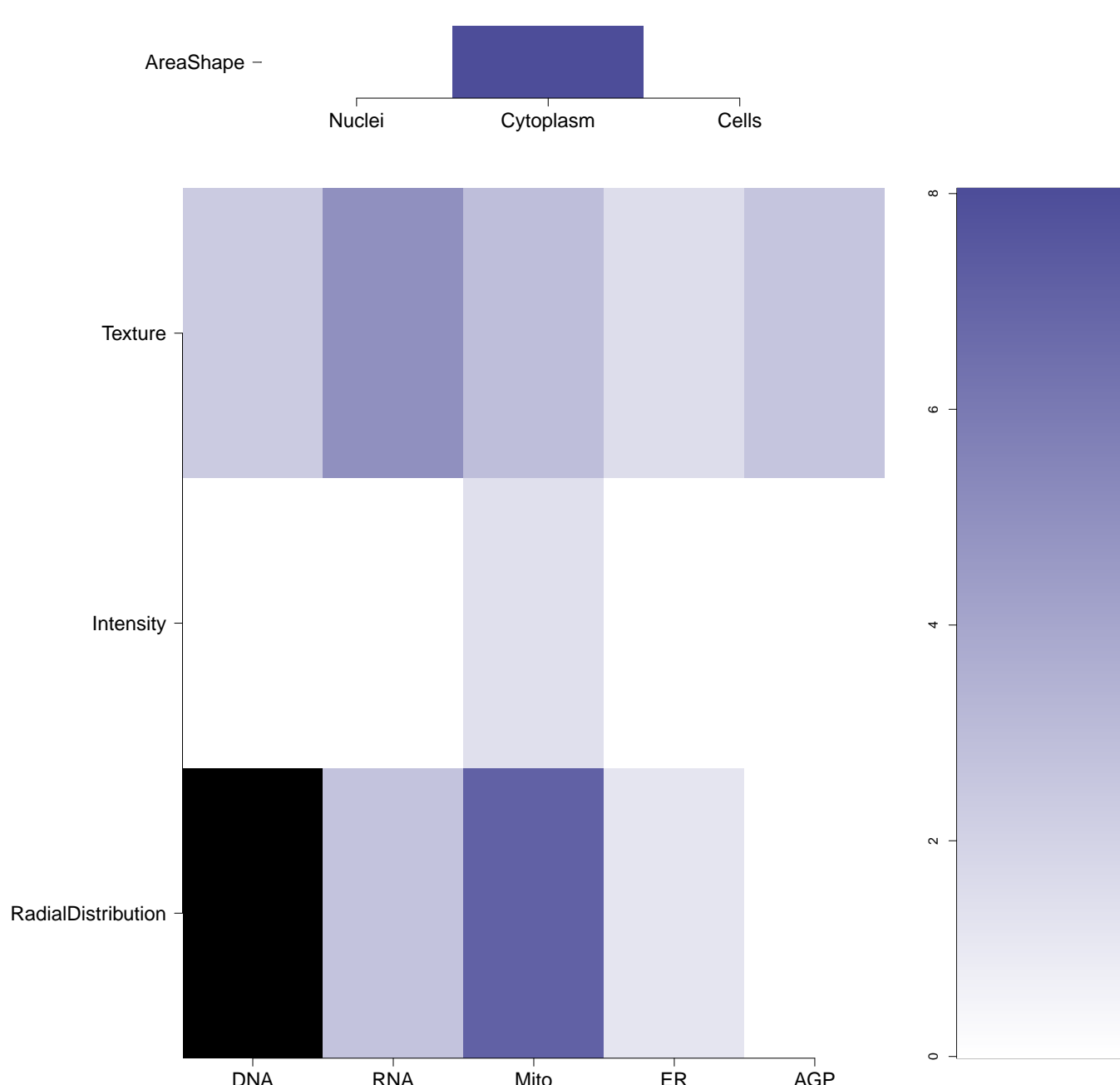
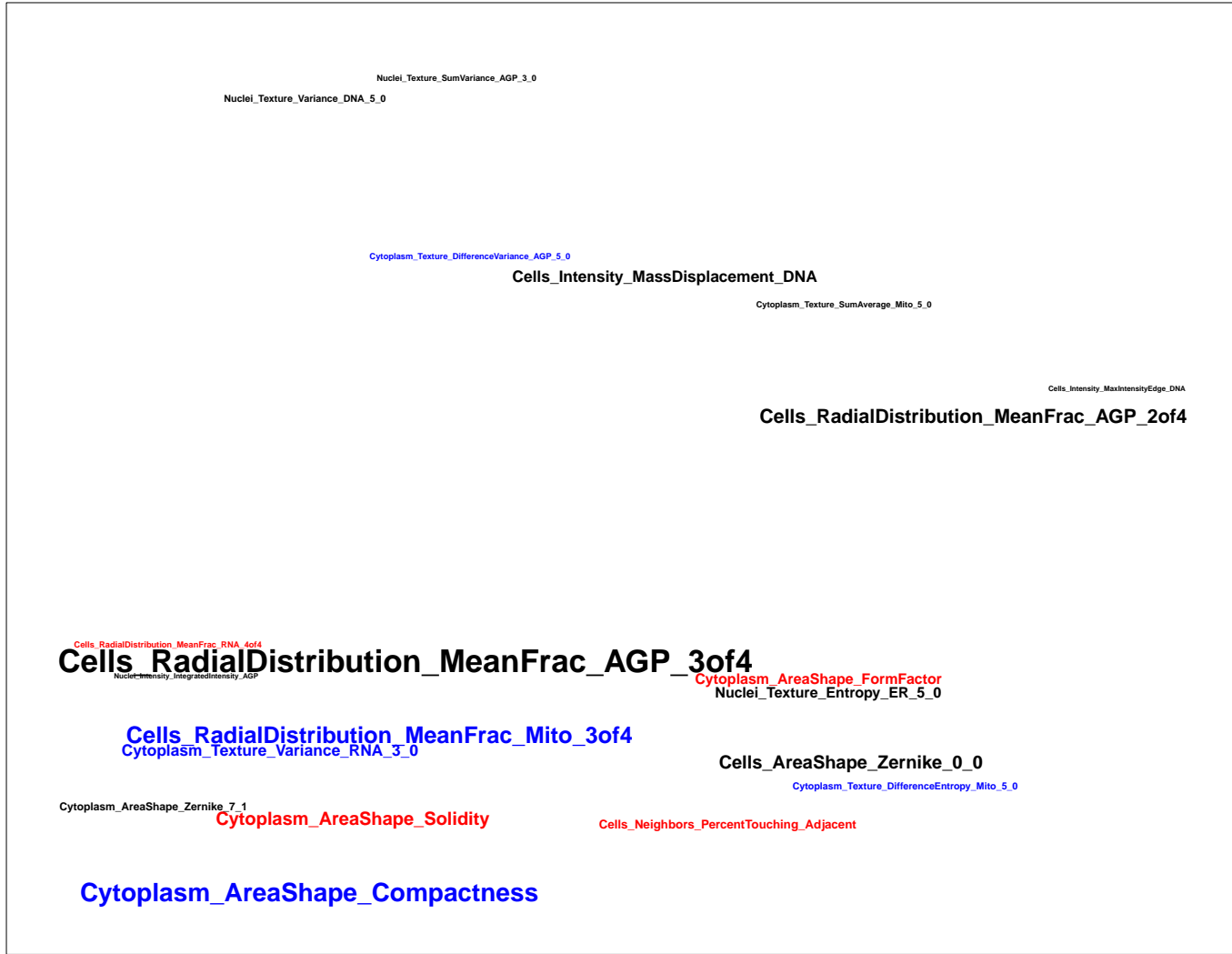


ER

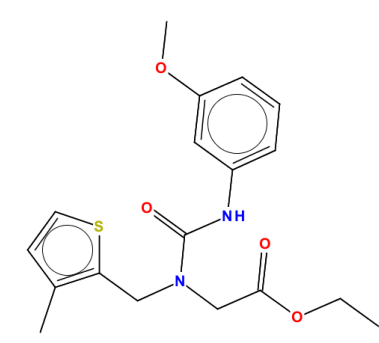
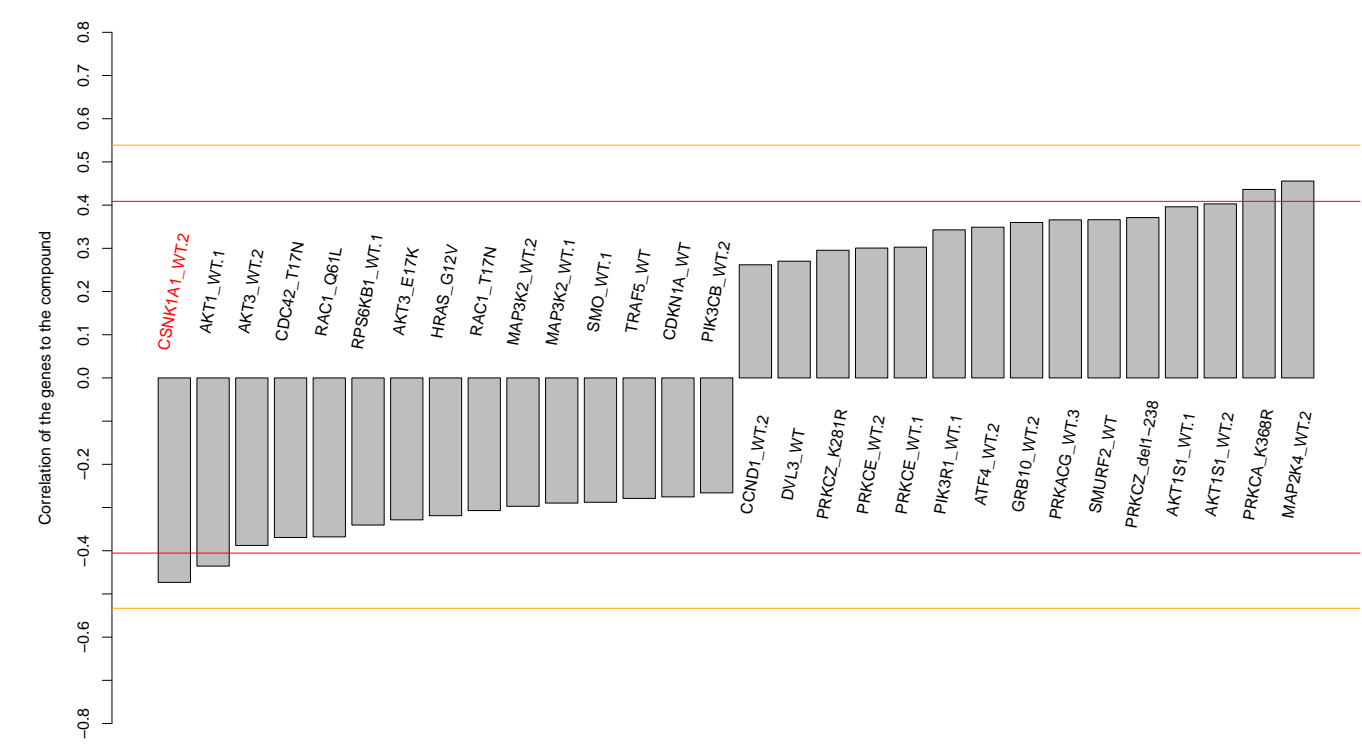
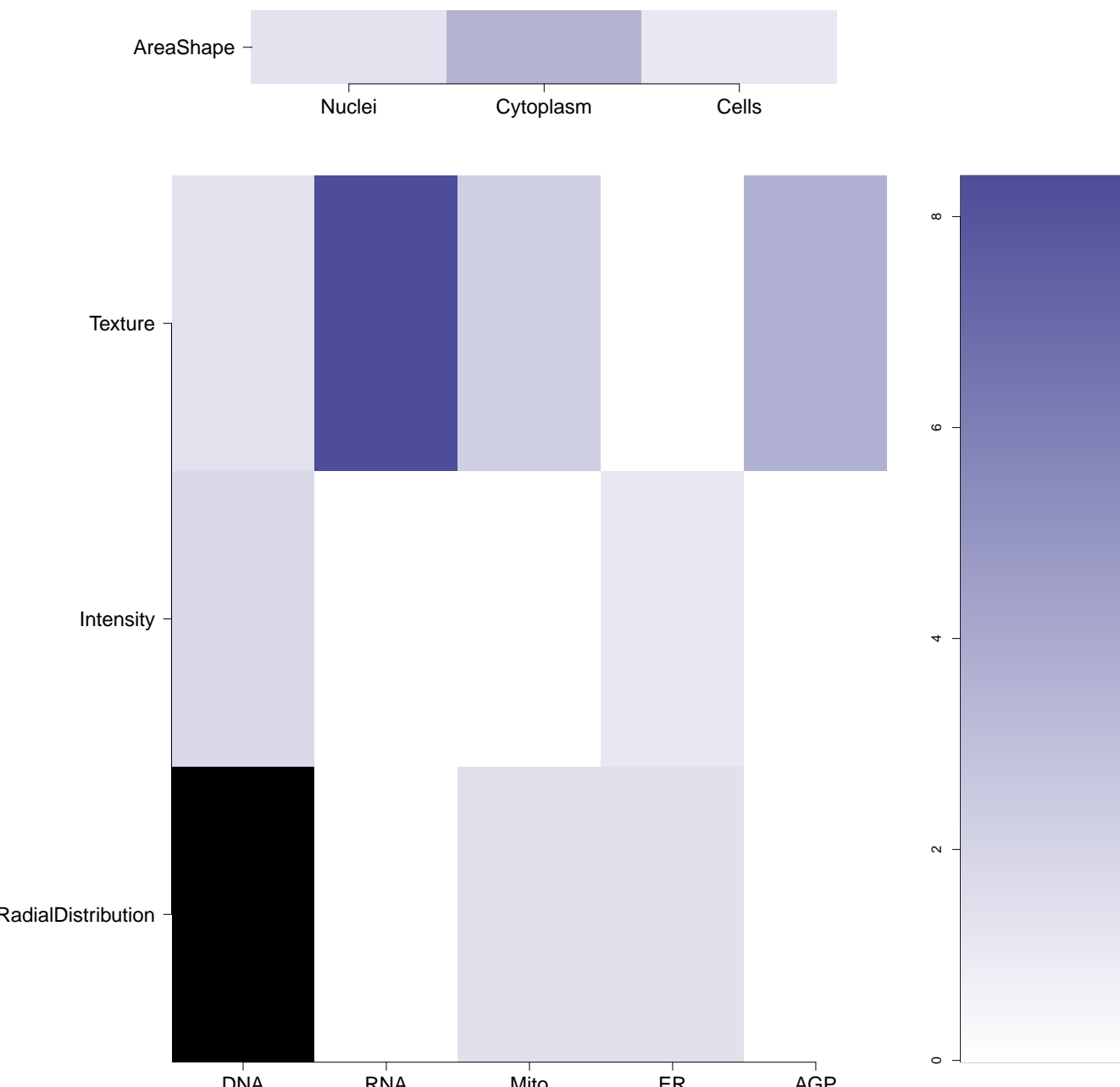
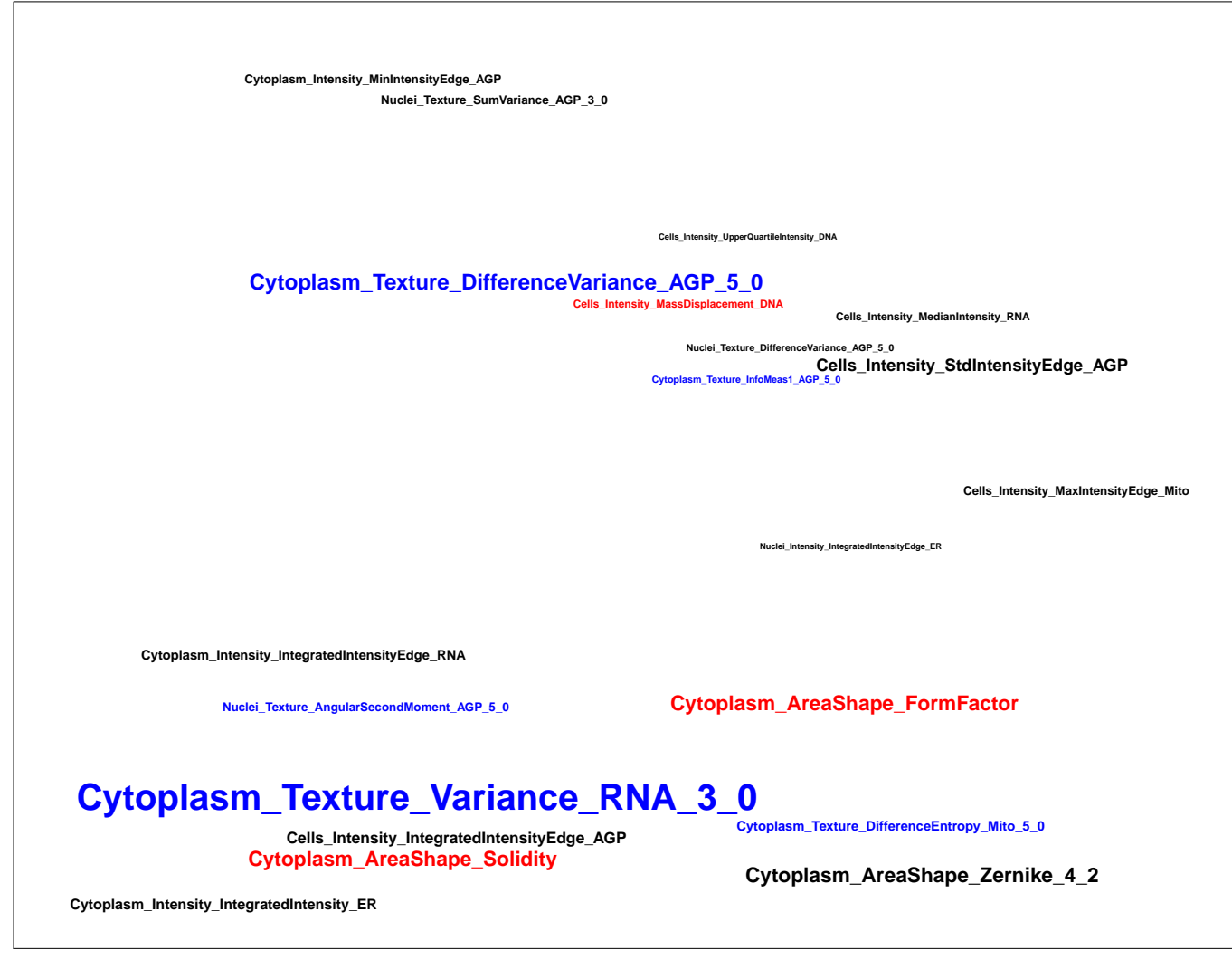
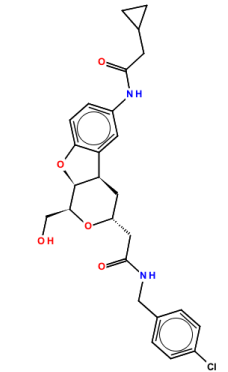
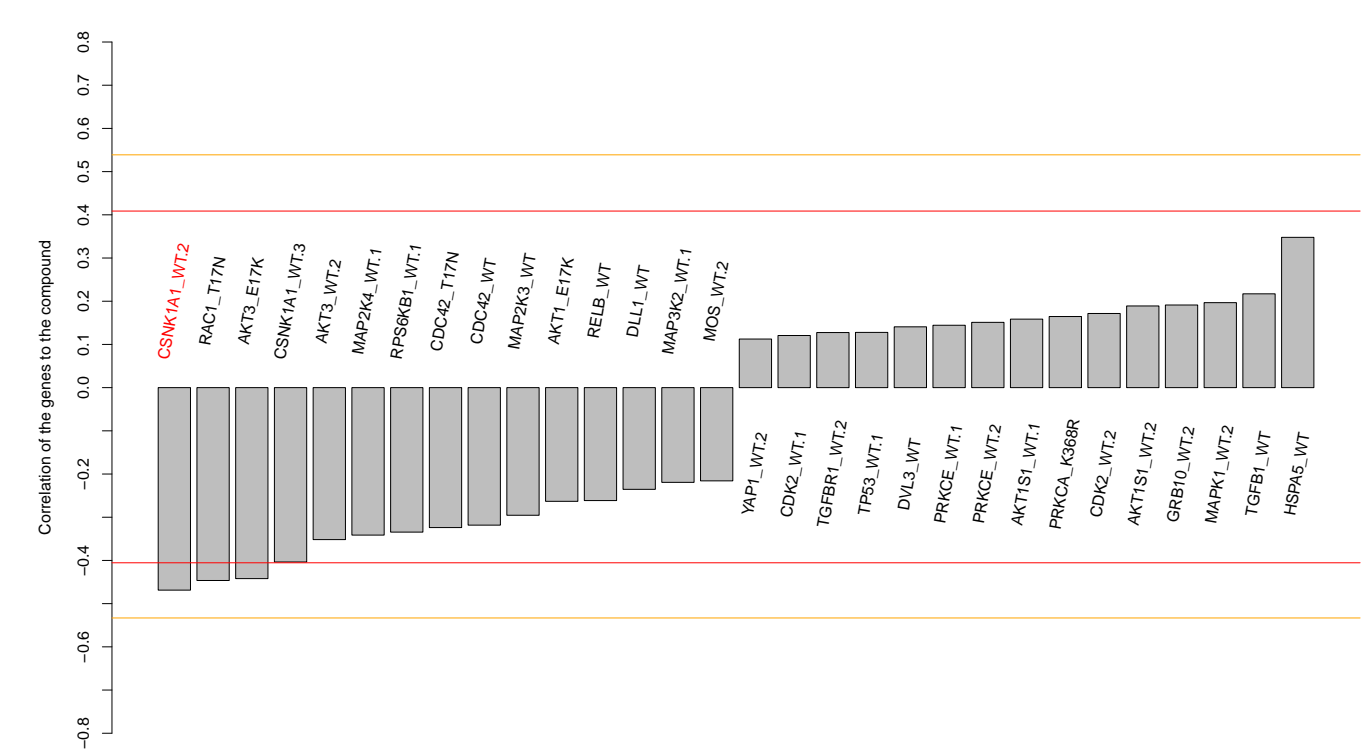
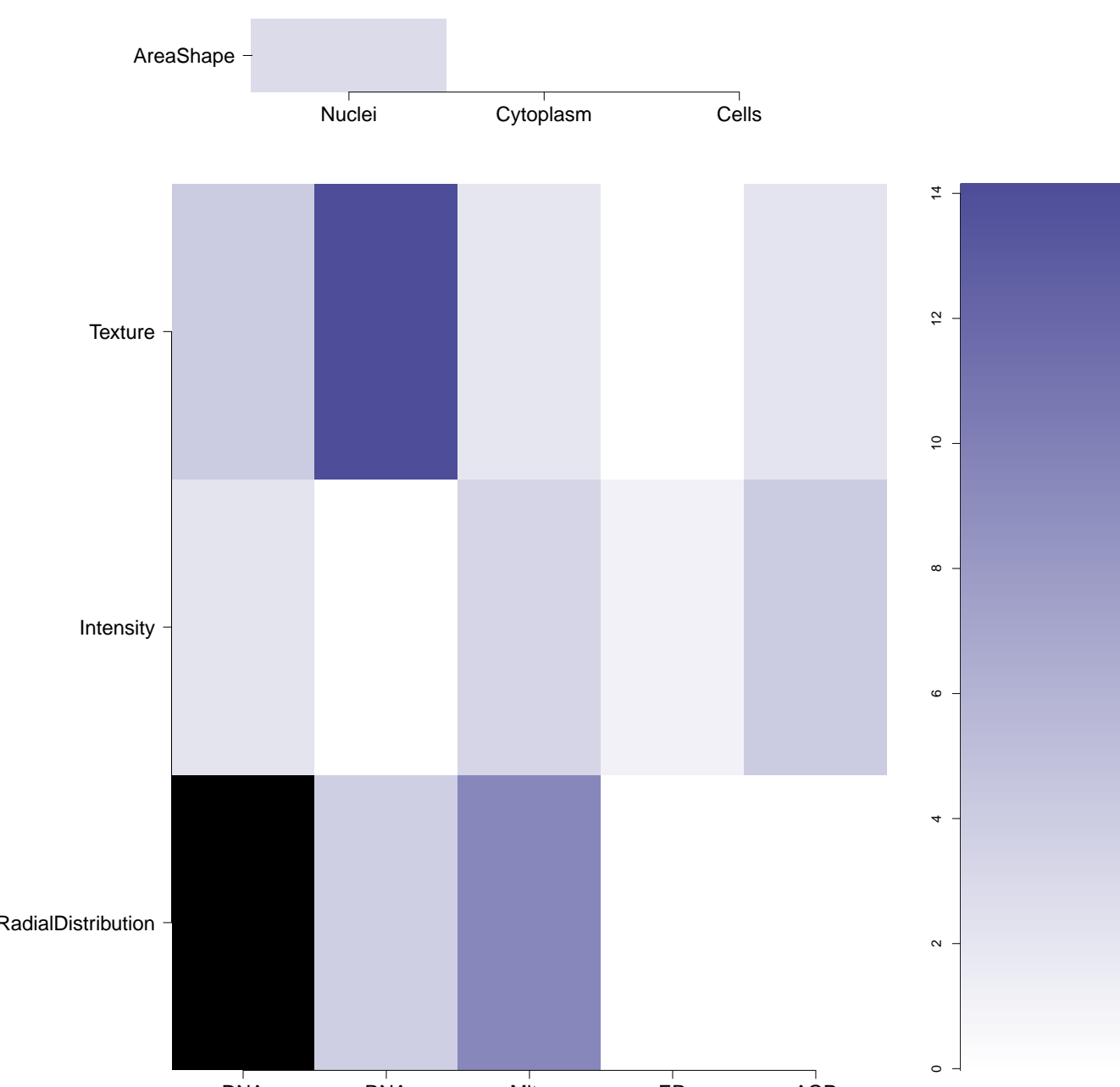
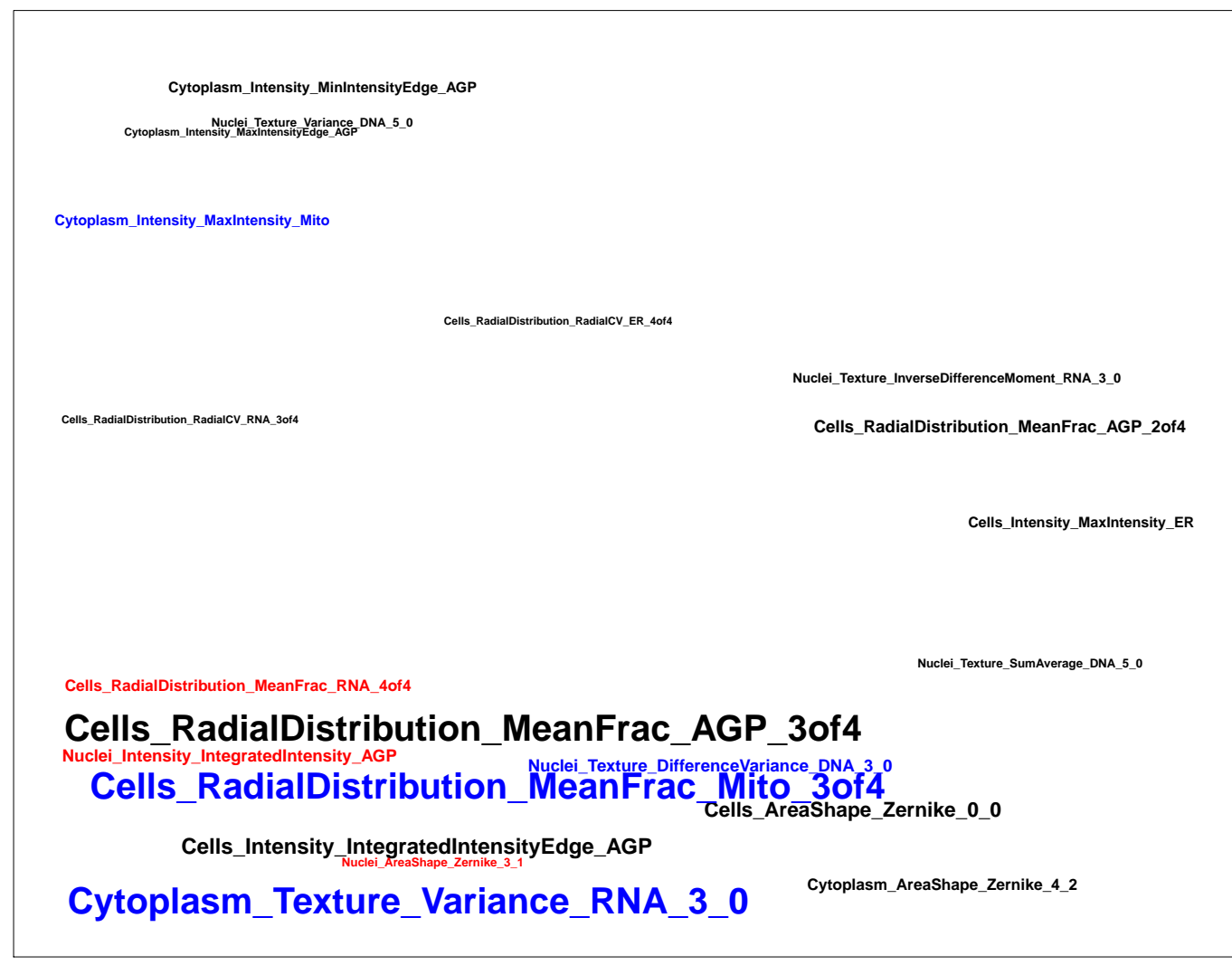
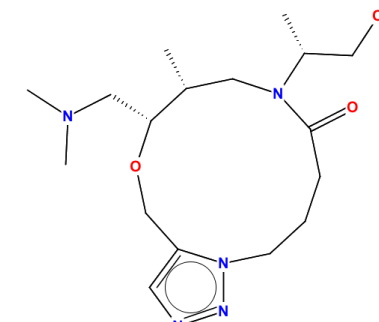
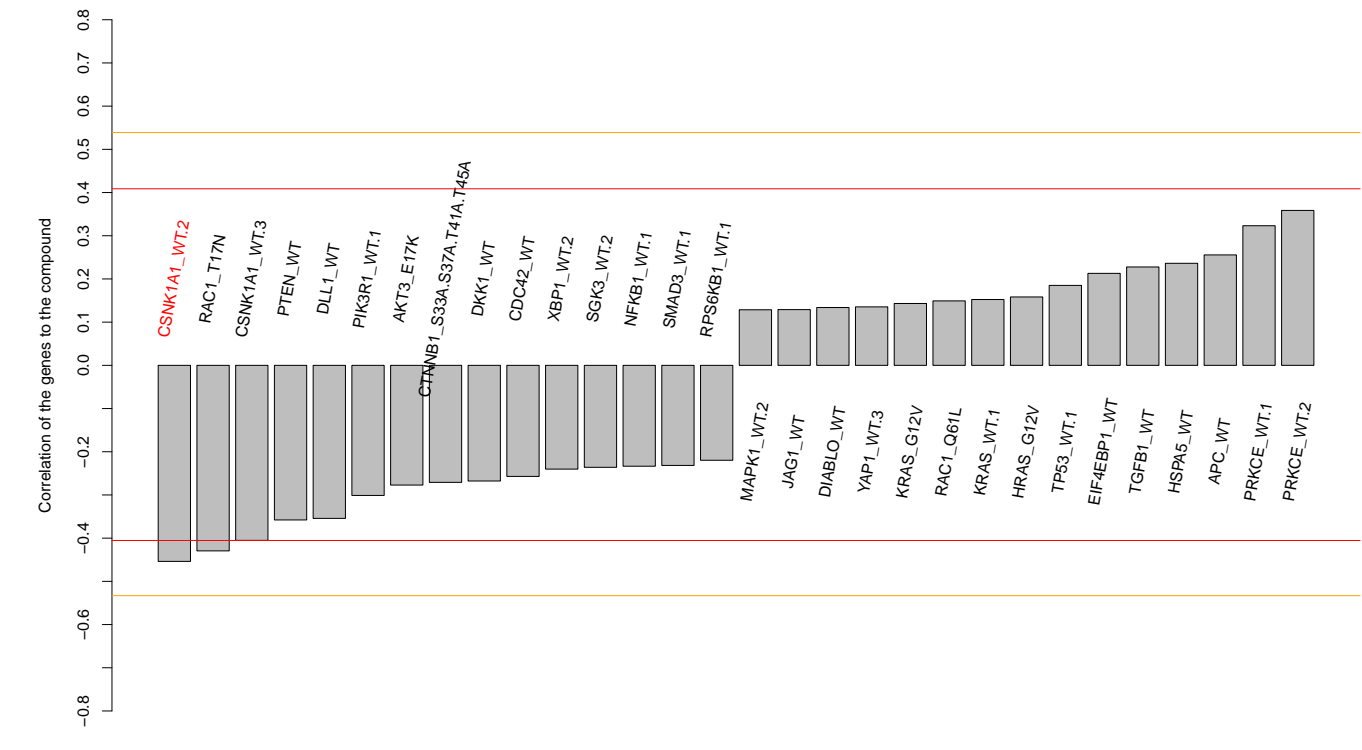
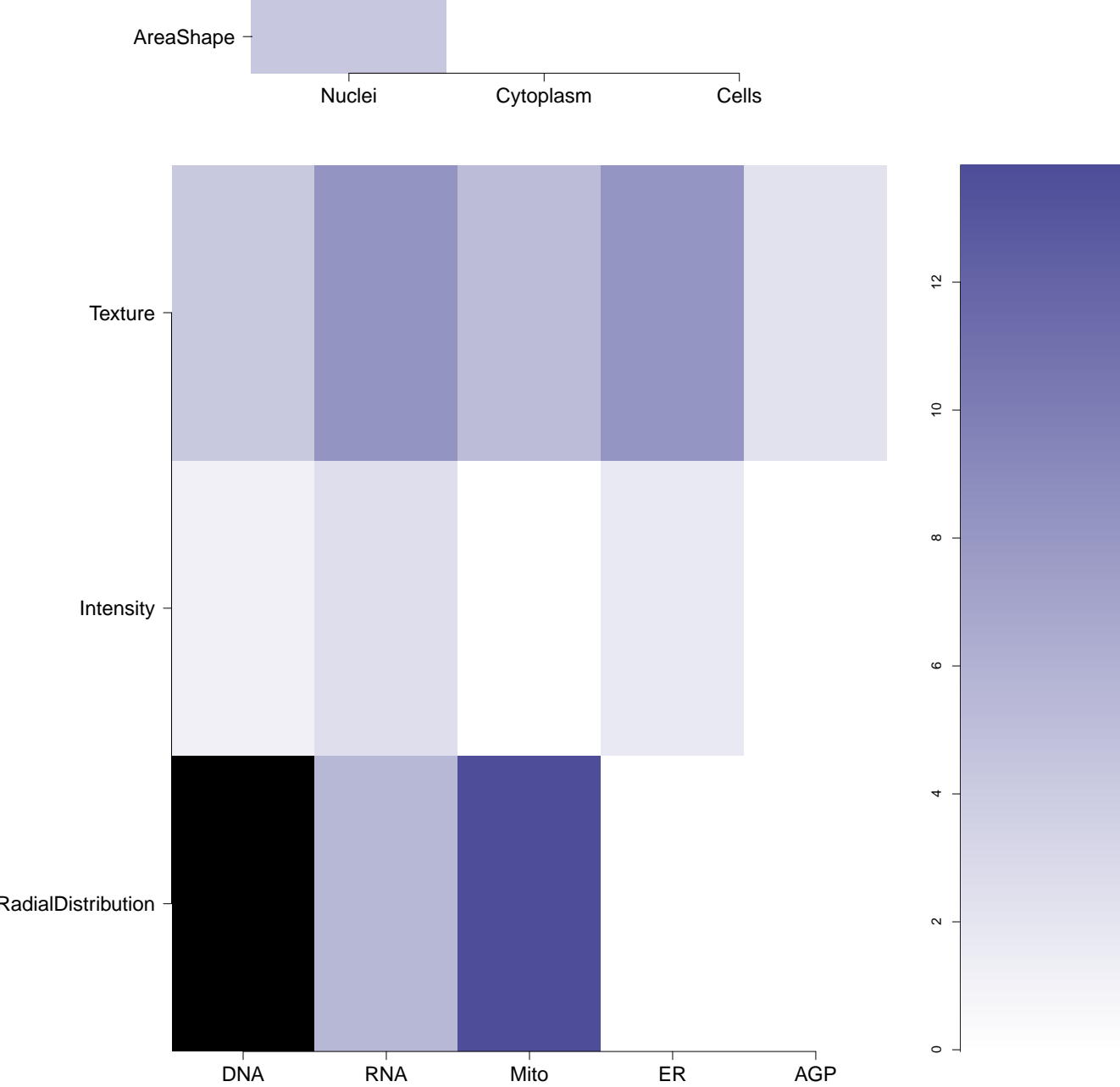
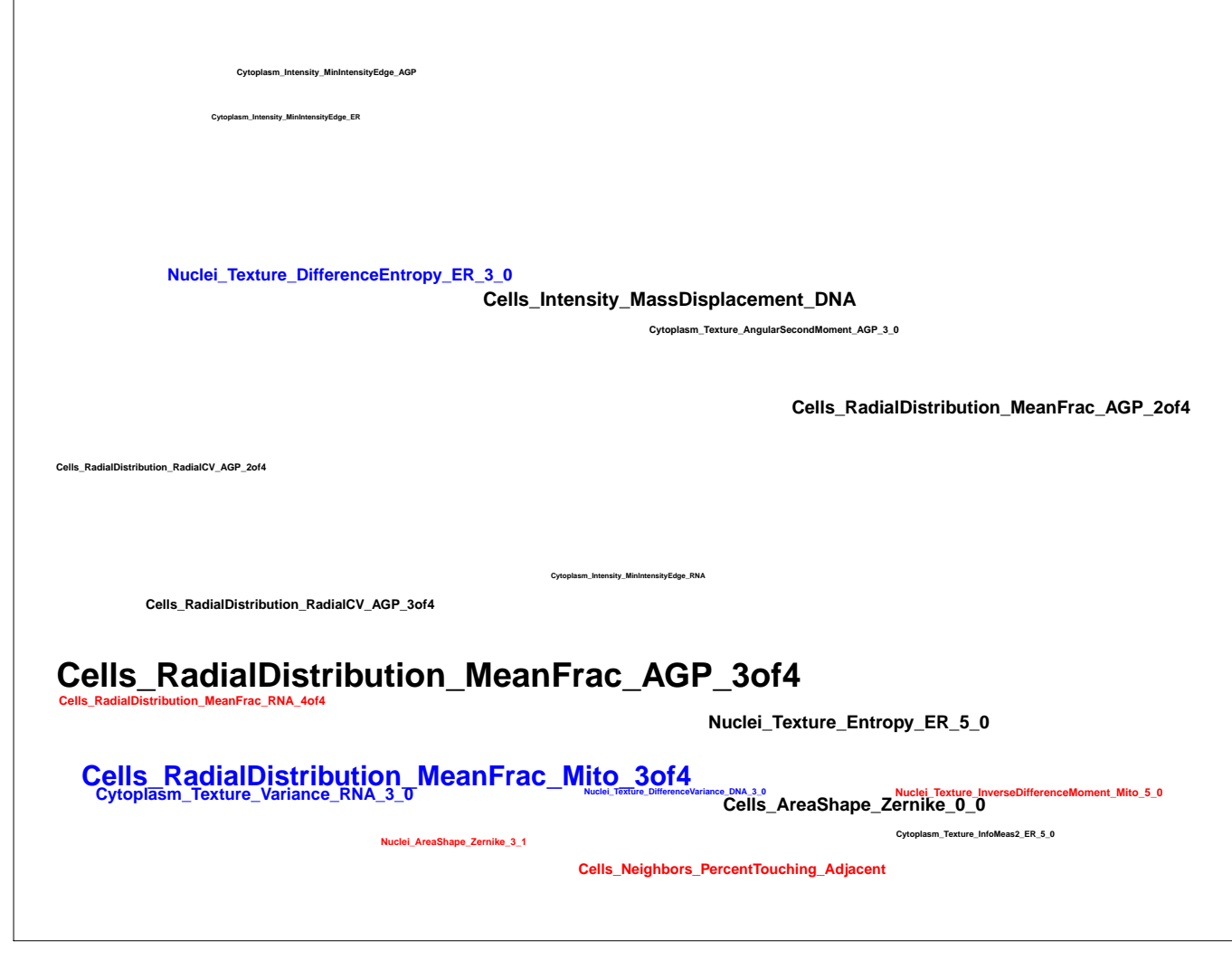
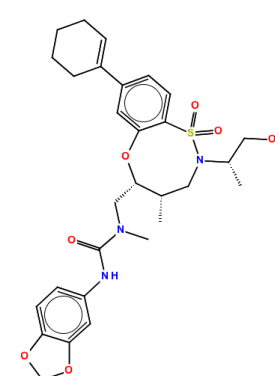
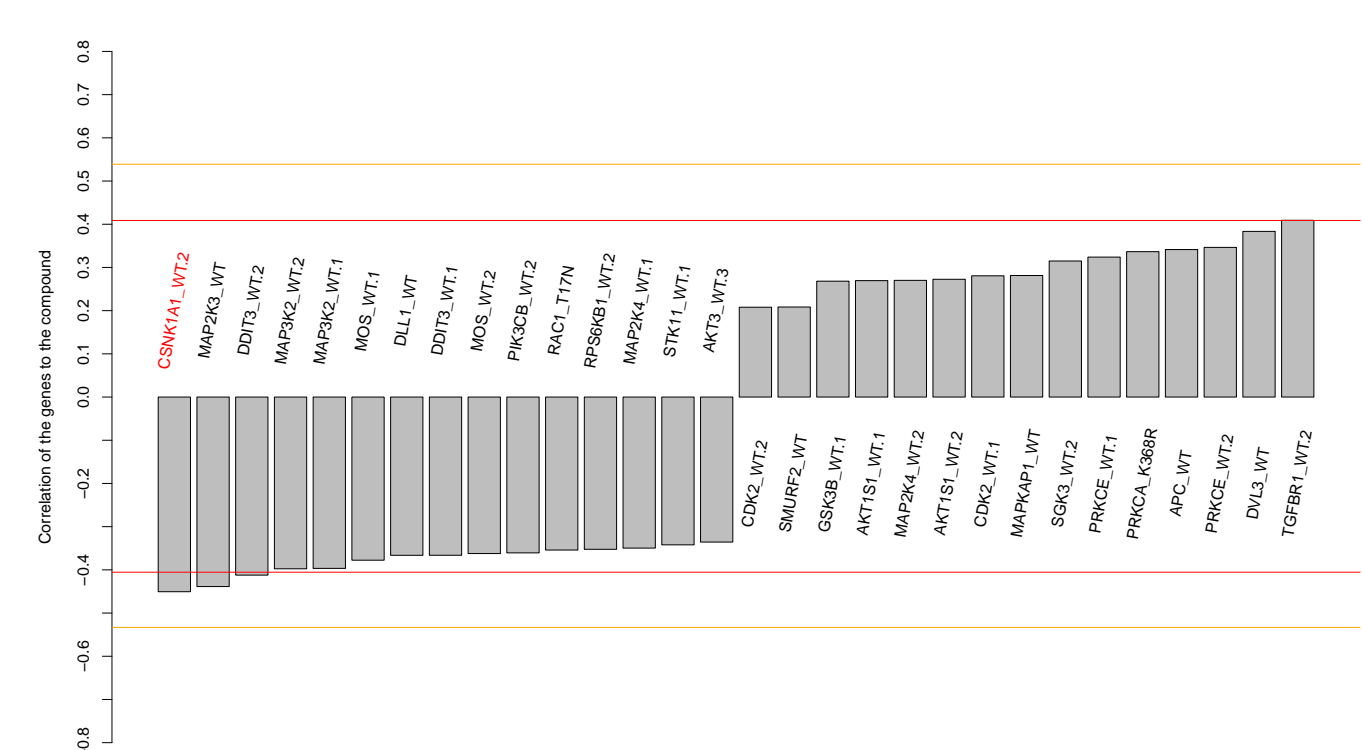
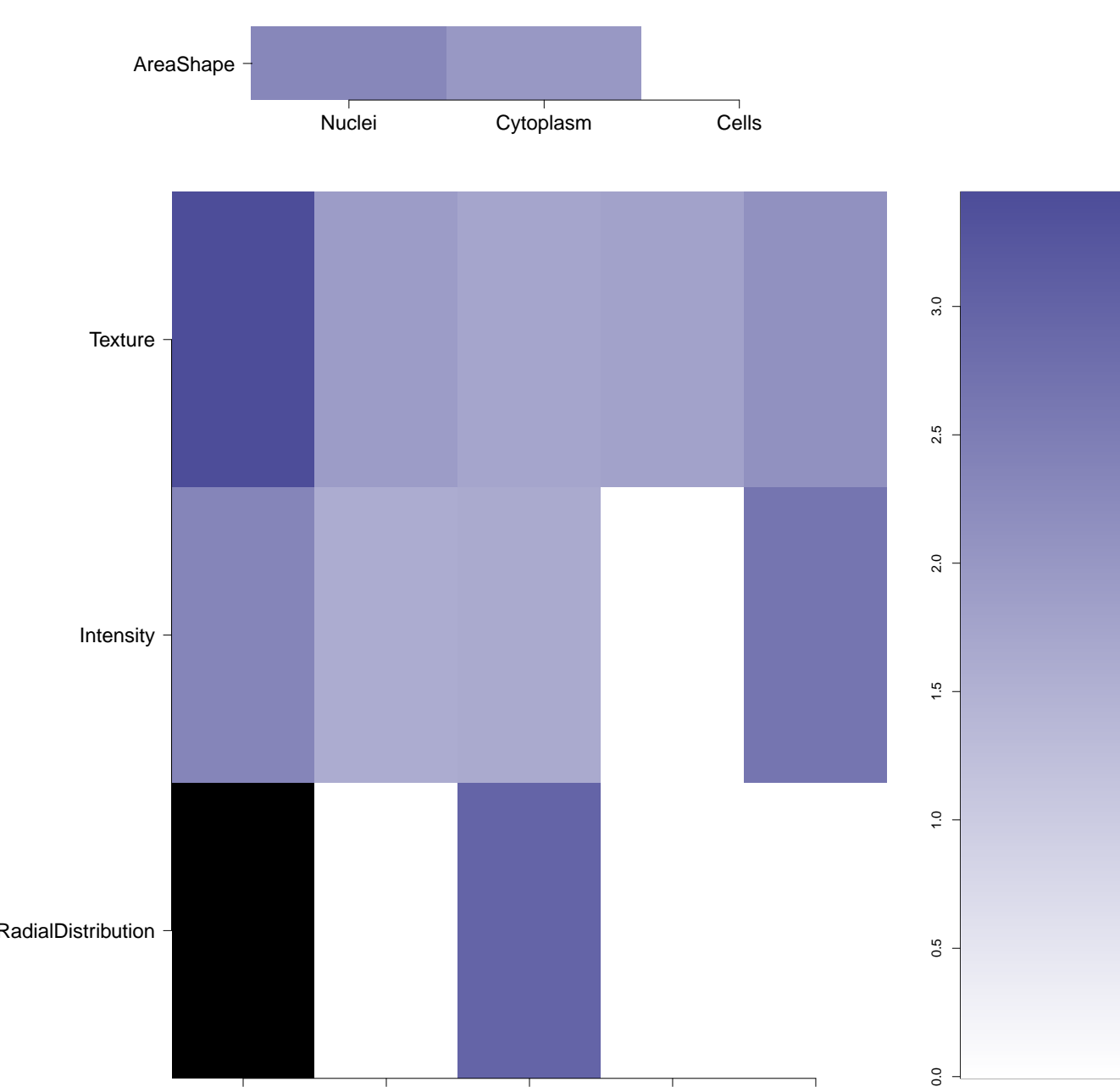



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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-K29799191-001-01-6 PubChem CID : 54618149		0.83 (in 4 replicates)	-0.56	0.342				Total number of assays tested in: 35.
BRD-K09444102-001-01-1 PubChem CID : 54646618		0.94 (in 4 replicates)	-0.53	0.330				Total number of assays tested in: 36.
BRD-K56916068-001-01-2 PubChem CID : 54646507		0.97 (in 3 replicates)	-0.52	0.067				Total number of assays tested in: 37.
BRD-K65891102-001-01-4 PubChem CID : 44620287		0.88 (in 4 replicates)	-0.50	0.201				Total number of assays tested in: 37.
BRD-K96165286-001-01-4 PubChem CID : 54645911		0.54 (in 2 replicates)	-0.48	0.275				Total number of assays tested in: 40.
BRD-K04488512-001-06-6 3L-577S AC1MZ5IC MLS000755130 HMS2596120 HMS3380G02 ZINC13140601 SMR000337998 PubChem CID : 3842739		0.77 (in 4 replicates)	-0.47	0.342				<p>Total number of assays tested in: 636. Active in the following assays:</p> <ul style="list-style-type: none"> <li>qHTS Assay for Inhibitors of Aldehyde Dehydrogenase 1 (ALDH1A1) (AID 1030)</li> <li>Fluorescence polarization-based countercreen for RBBP9 inhibitors: primary biochemical high throughput screening assay to identify inhibitors of the oxidoreductase glutathione S-transferase omega 1(GSTO1). (AID 1974)</li> <li>Fluorescence Cell-Free Homogenous Primary HTS to Identify Inhibitors of RecA Intein Splicing Activity (AID 2221)</li> <li>Fluorescence Cell-Free Homogeneous Counter Screen to Identify Inhibitors of GFP Chromophore Formation (AID 434968)</li> <li>Fluorescence Cell-Free Homogeneous Secondary Screen to Identify Inhibitors of DnaB-Intein Splicing Activity (AID 449749)</li> <li>Fluorescence Cell-Free Homogeneous Secondary Screen to Identify Non-Covalent Inhibitors of RecA-Intein Splicing Activity (AID 449750)</li> <li>Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of Protein Arginine Deiminase 4 (PAD4) (1536 HTS) (AID 485272)</li> <li>Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of human platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (PAFAH1B2) (AID 492953)</li> <li>Fluorescence polarization-based biochemical high throughput confirmation assay for inhibitors of human platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (PAFAH1B2) (AID 493034)</li> <li>Inhibition of SOD1 G33A mutant aggregation in rat PC12 cells by cytotoxicity protection assay (AID 551238)</li> <li>Epi Absorbance-based biochemical primary high throughput screening assay to identify inhibitors of human tyrosyl-DNA phosphodiesterase 2 (TDP2) (AID 720702)</li> </ul>



BRD-K52871910-001-05-4 MLS000583915 AC1N51HE HMS2539106 SMR000206901 PubChem CID : 4187953		NA (in 1 replicates)	-0.47	NA				Total number of assays tested in: 640. Active in the following assays: <ul style="list-style-type: none"> <li>Cyclodextride CounterScreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)</li> <li>A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)</li> <li>Antagonist of Human D 1 Dopamine Receptor: qHTS (AID 504652)</li> </ul>
BRD-K53046450-001-01-7 PubChem CID : 54646719		0.92 (in 4 replicates)	-0.47	0.342				Total number of assays tested in: 37.
BRD-K48241951-001-01-6 PubChem CID : 44491463		0.93 (in 2 replicates)	-0.45	0.342				Total number of assays tested in: 49.
BRD-K04278887-001-01-9 PubChem CID : 54618150		0.71 (in 4 replicates)	-0.45	0.342				Total number of assays tested in: 33.