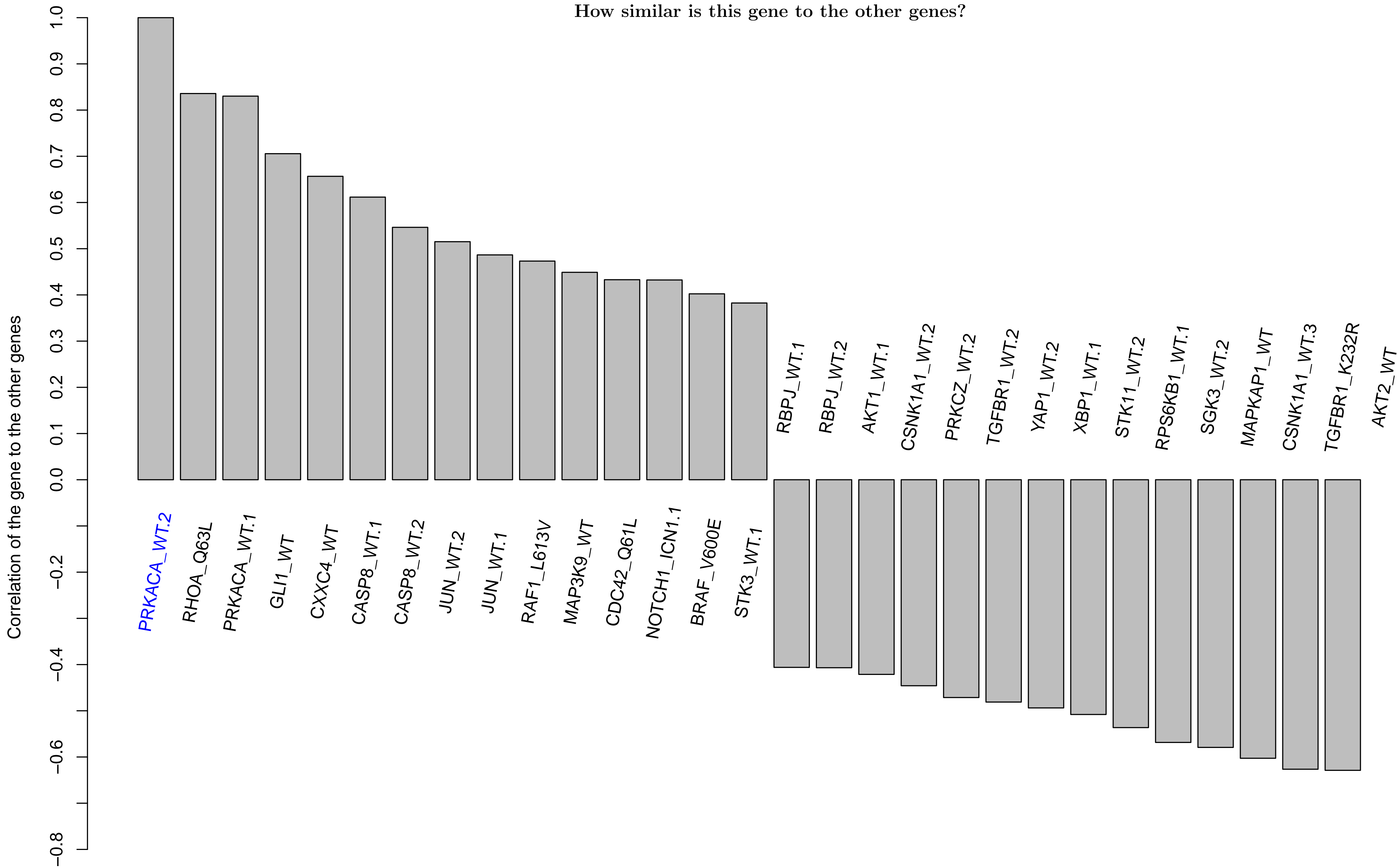
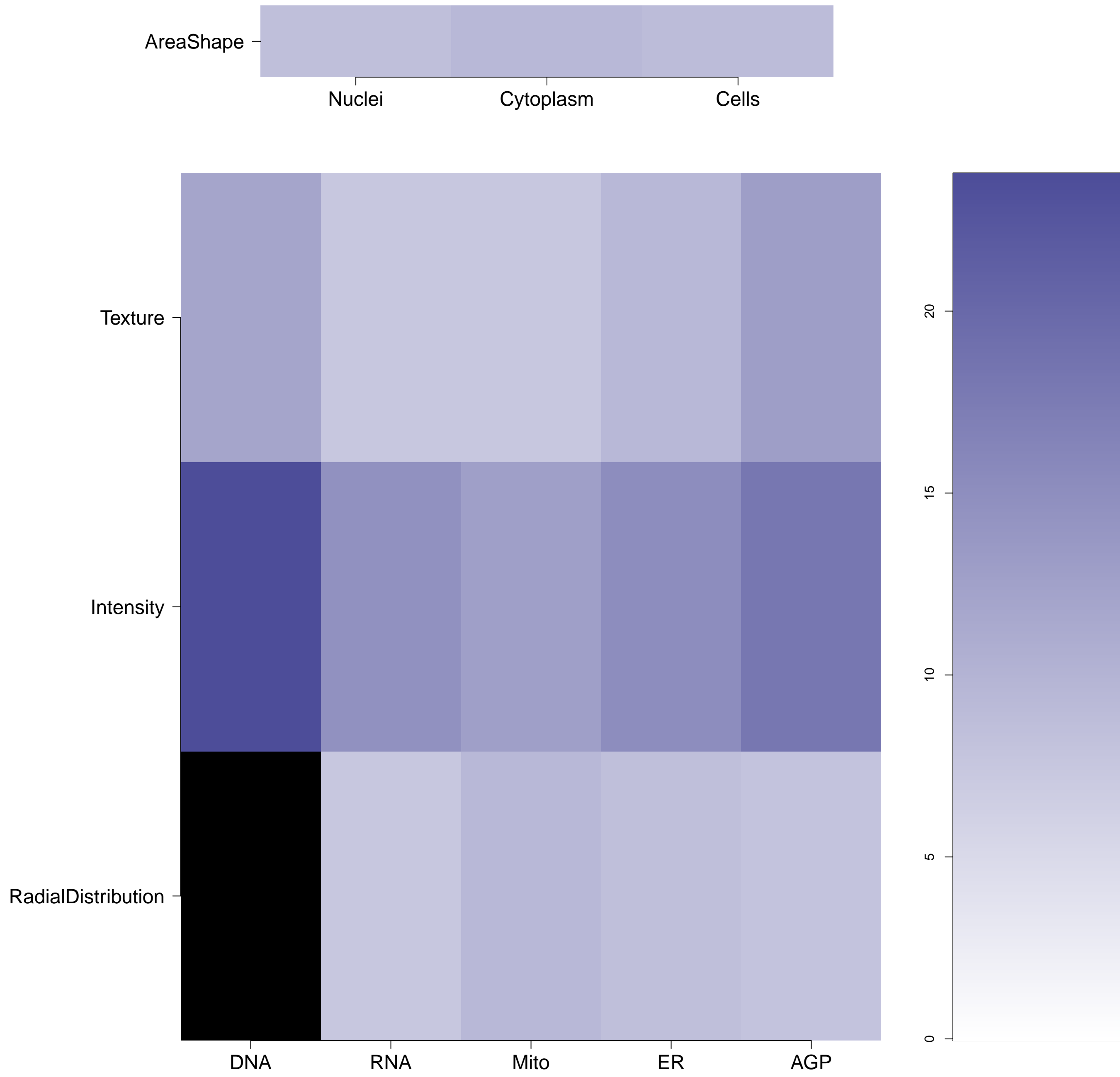


PRKACA.WT.2 - in Canonical PKA

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

PRKACA.WT.2 (41744)

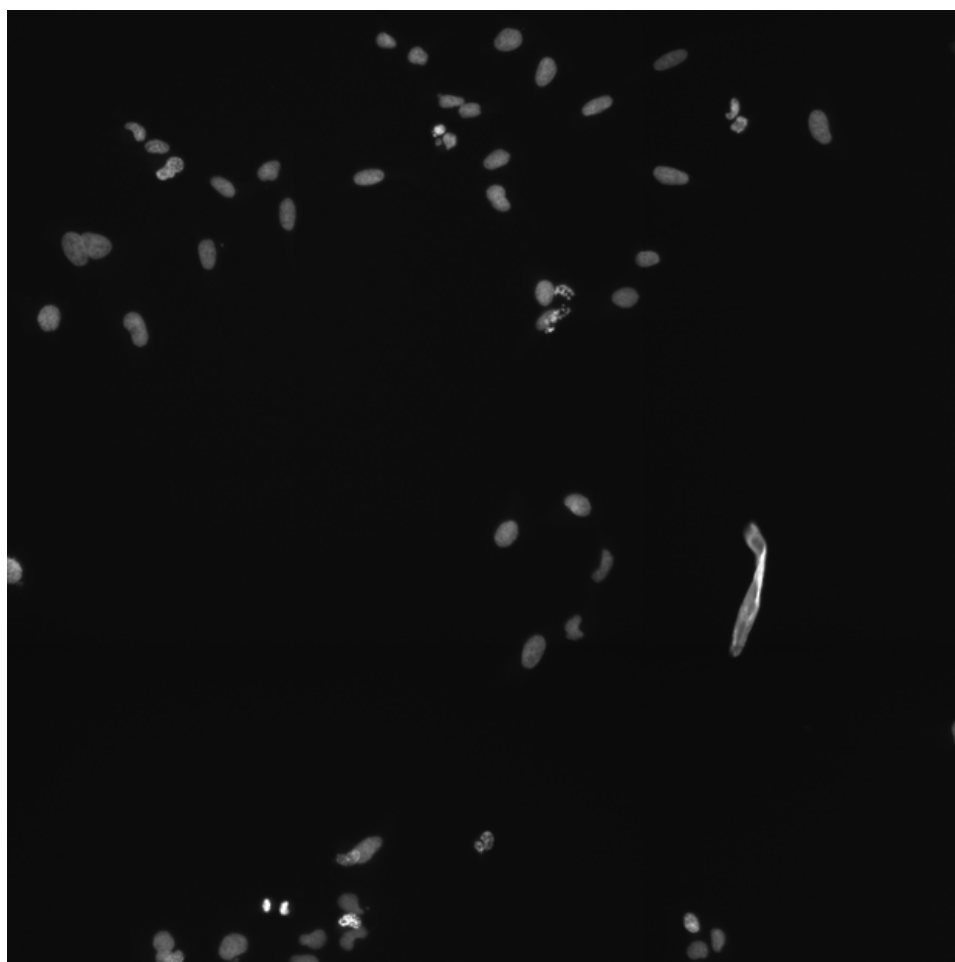
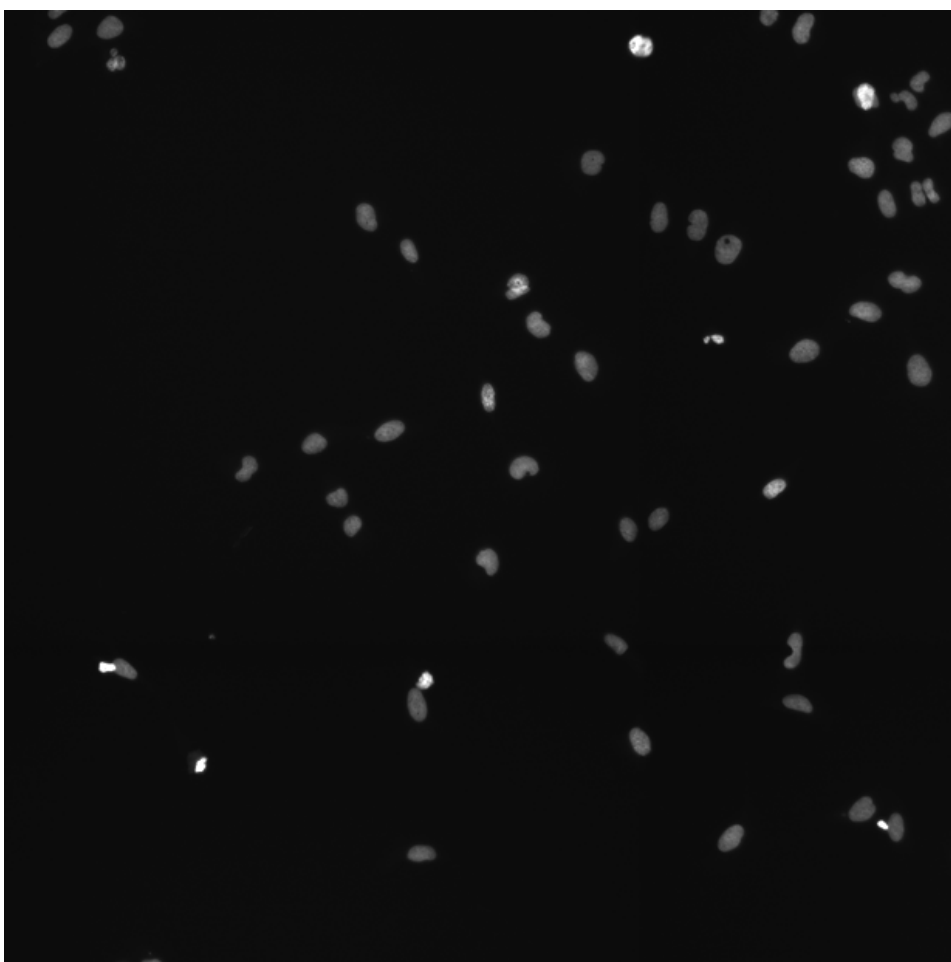
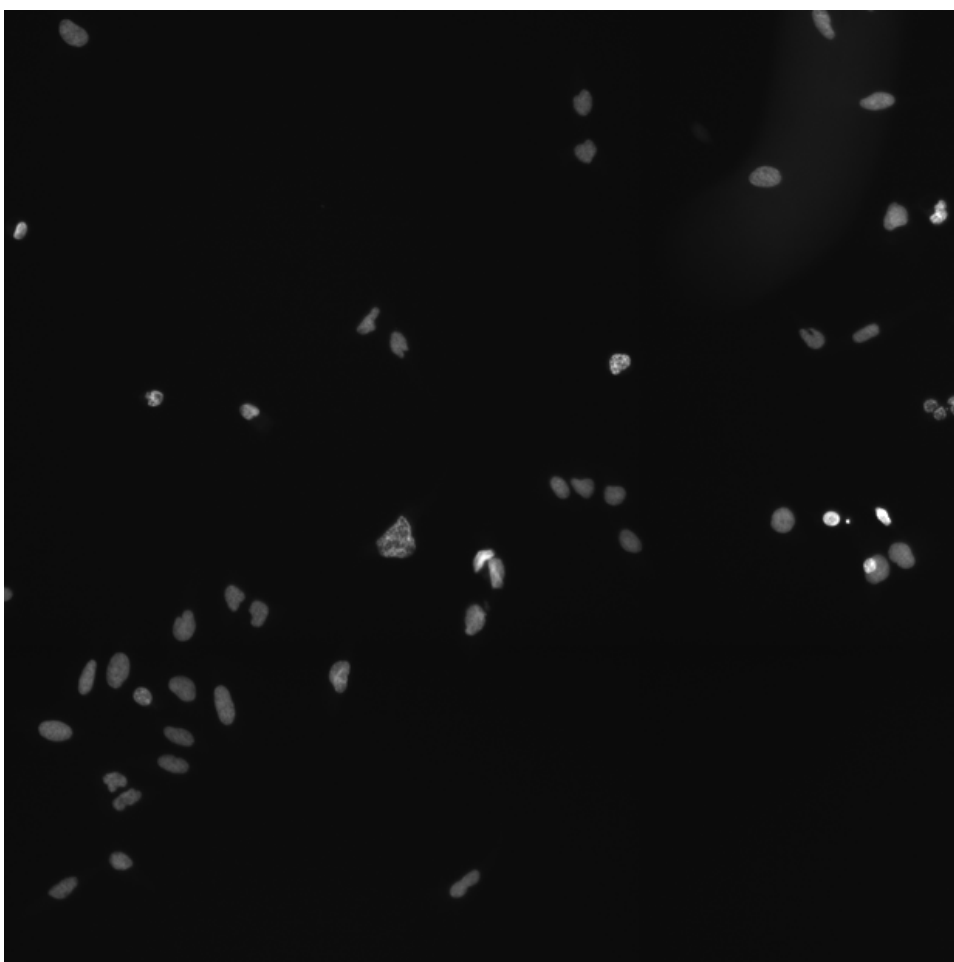
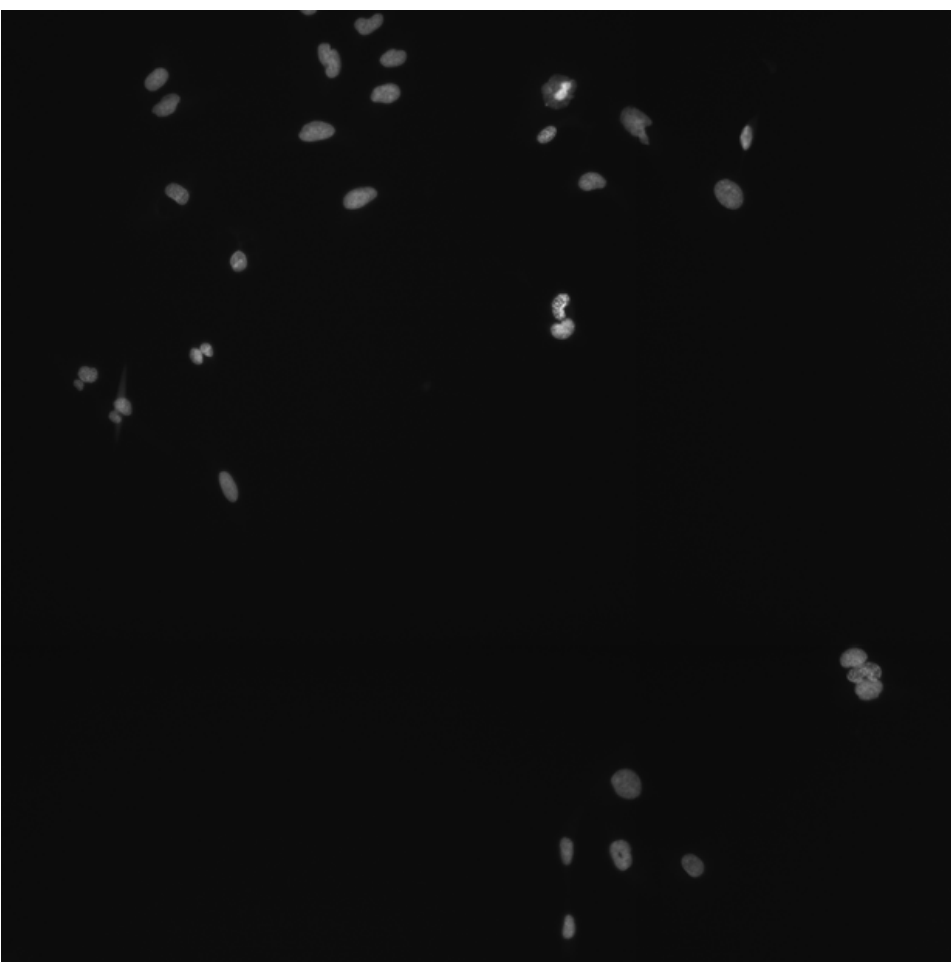
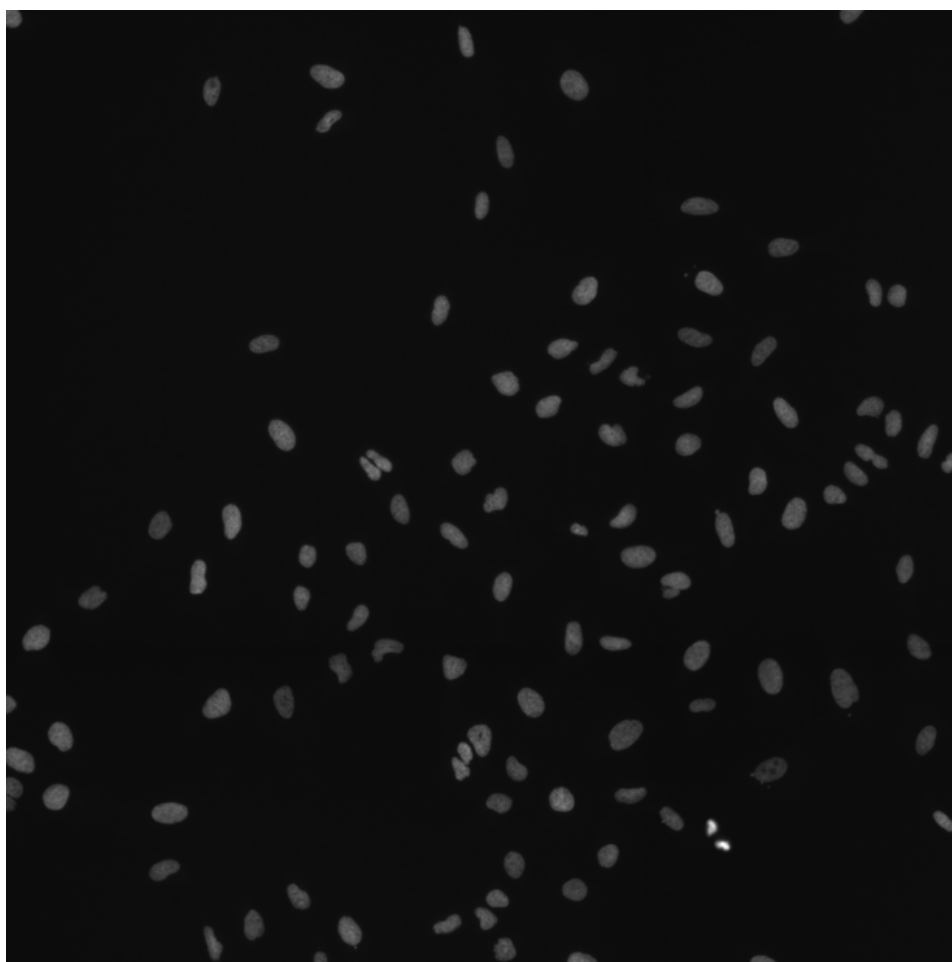
PRKACA.WT.2 (41755)

PRKACA.WT.2 (41756)

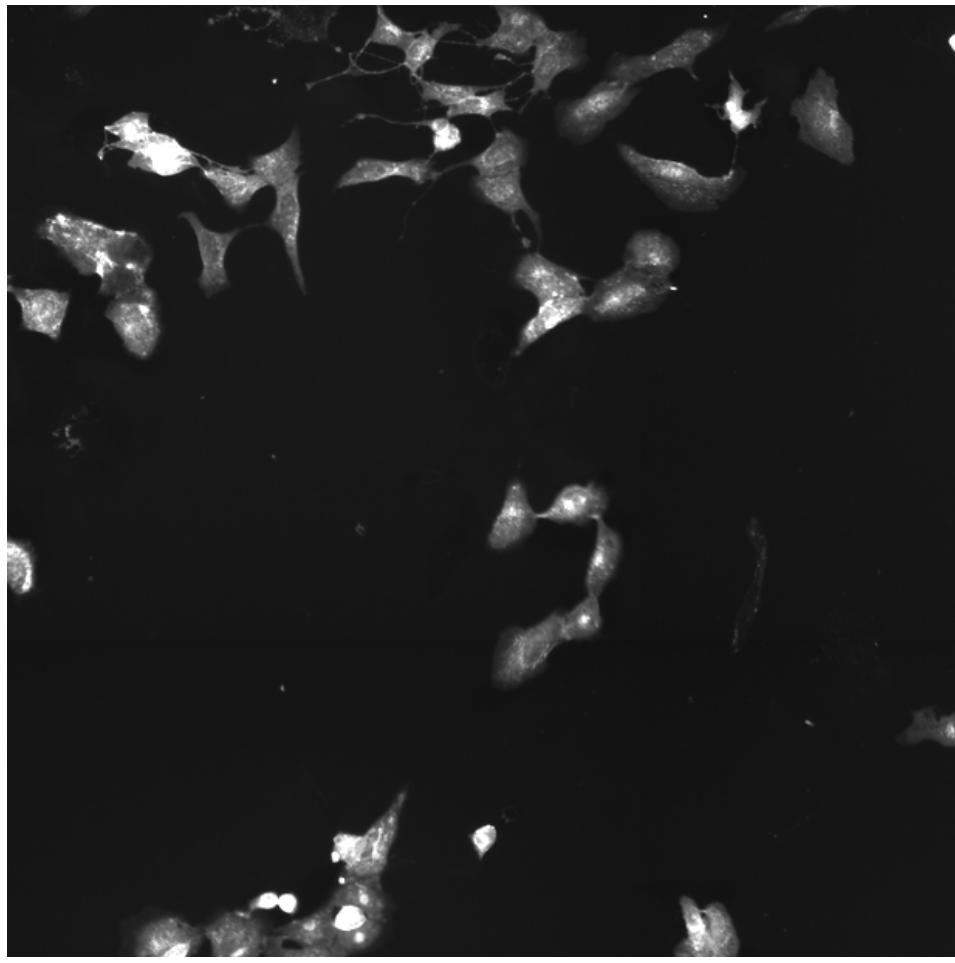
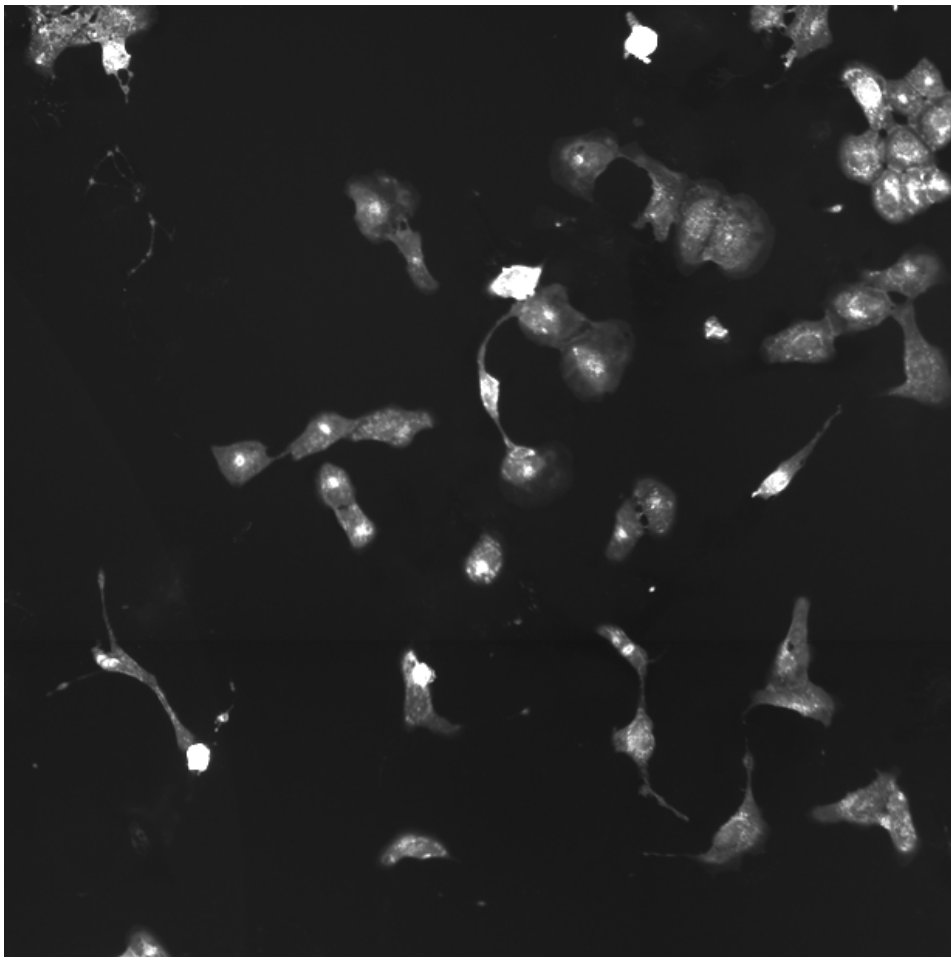
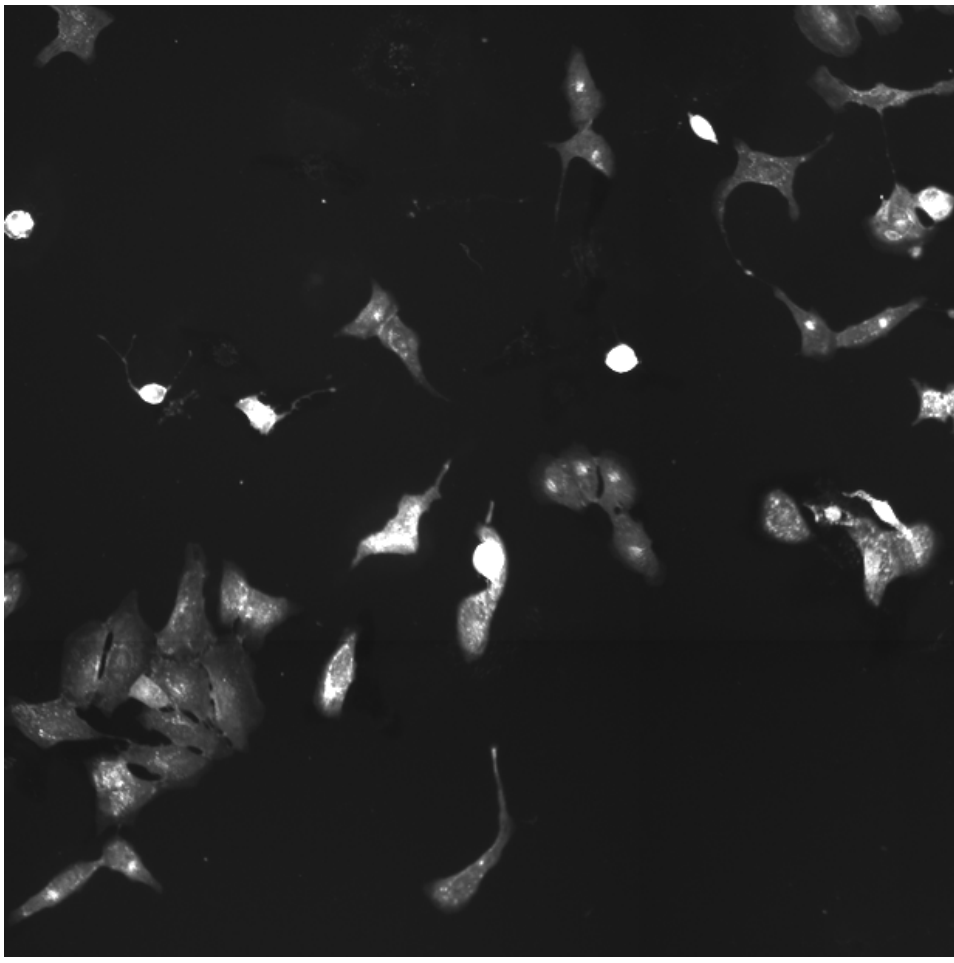
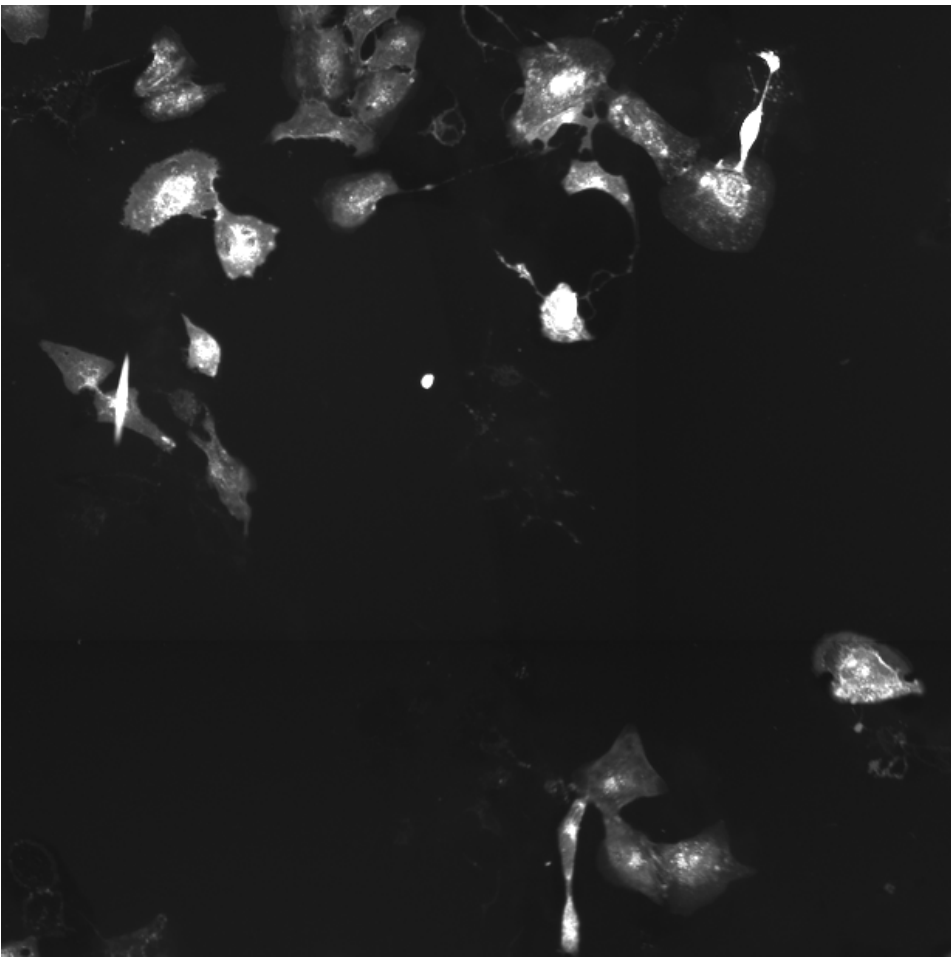
PRKACA.WT.2 (41757)

PRKACA.WT.2 (41754)

DNA

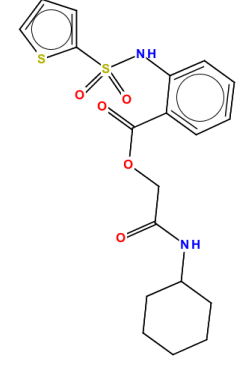
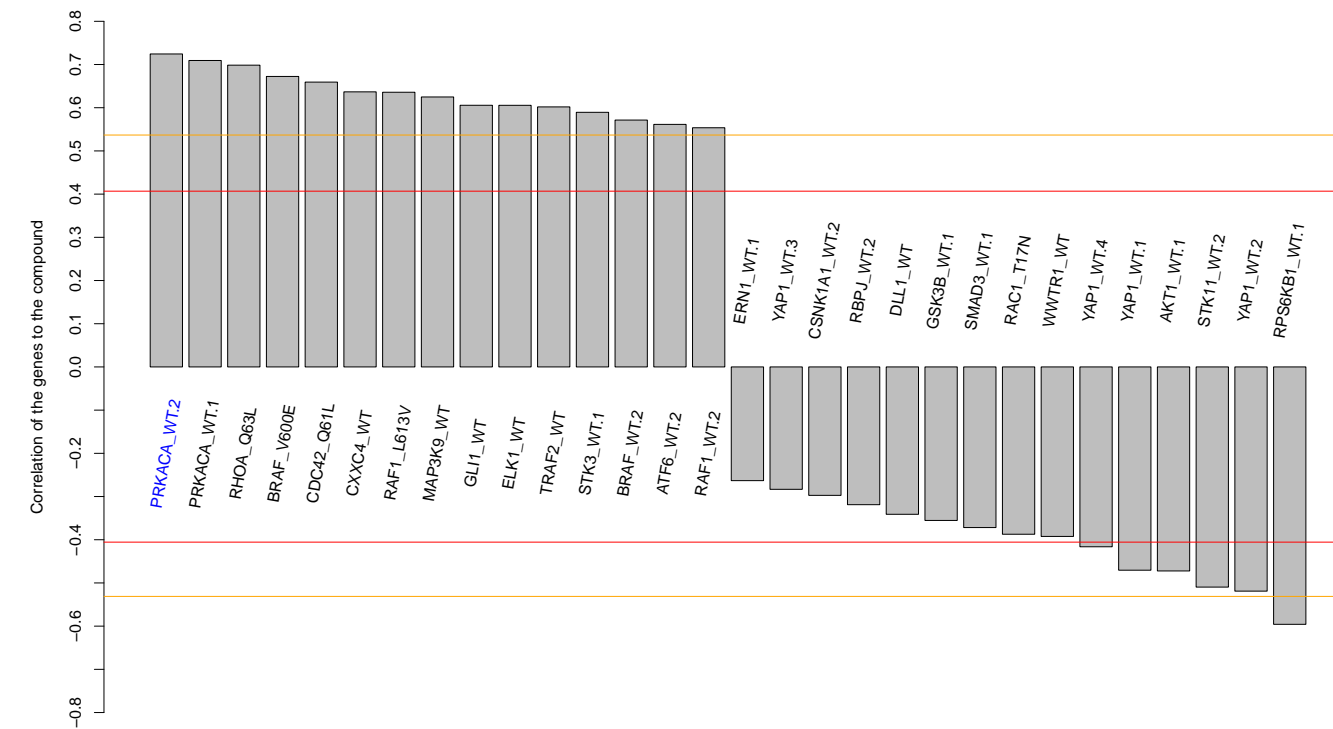
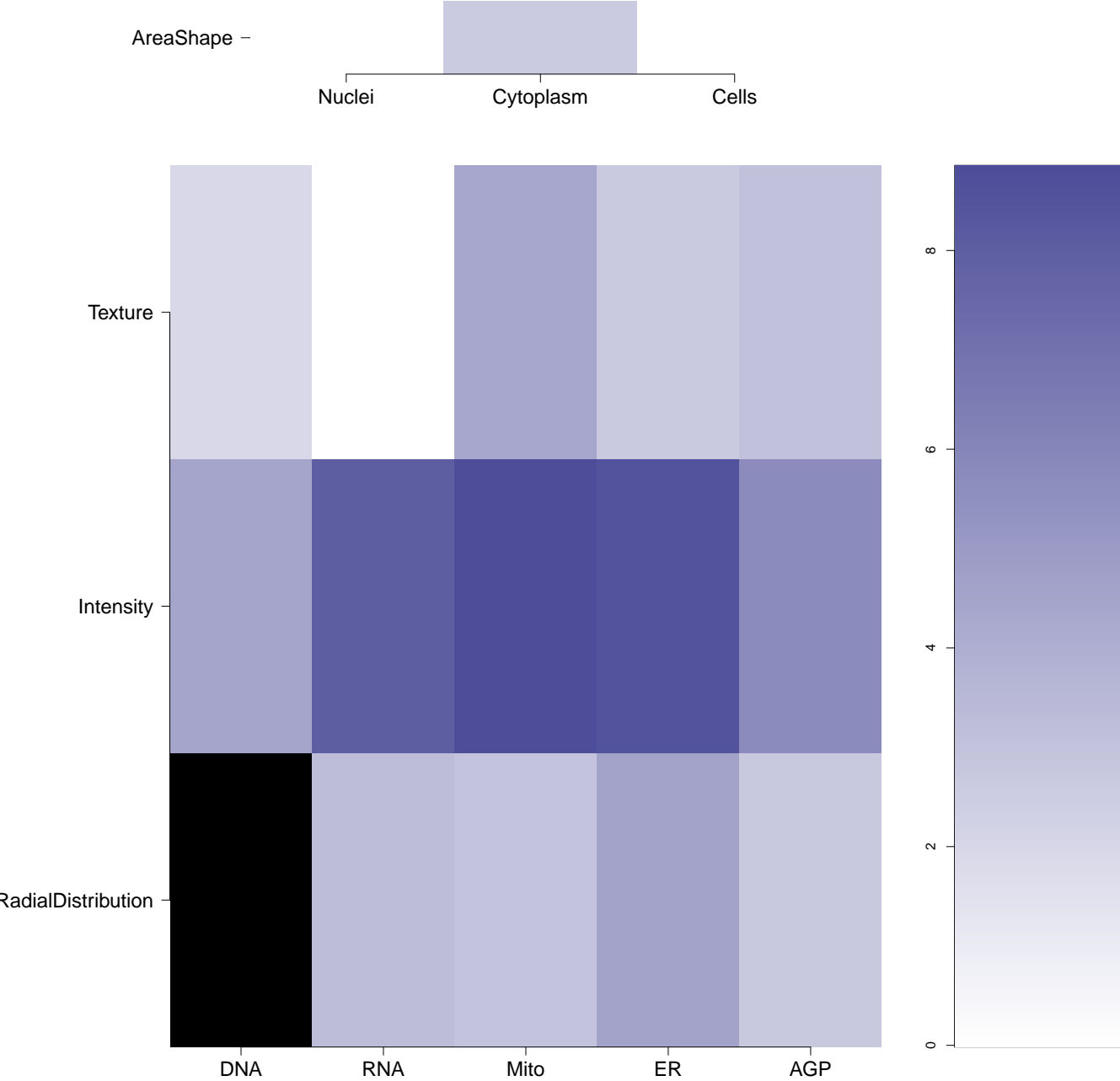
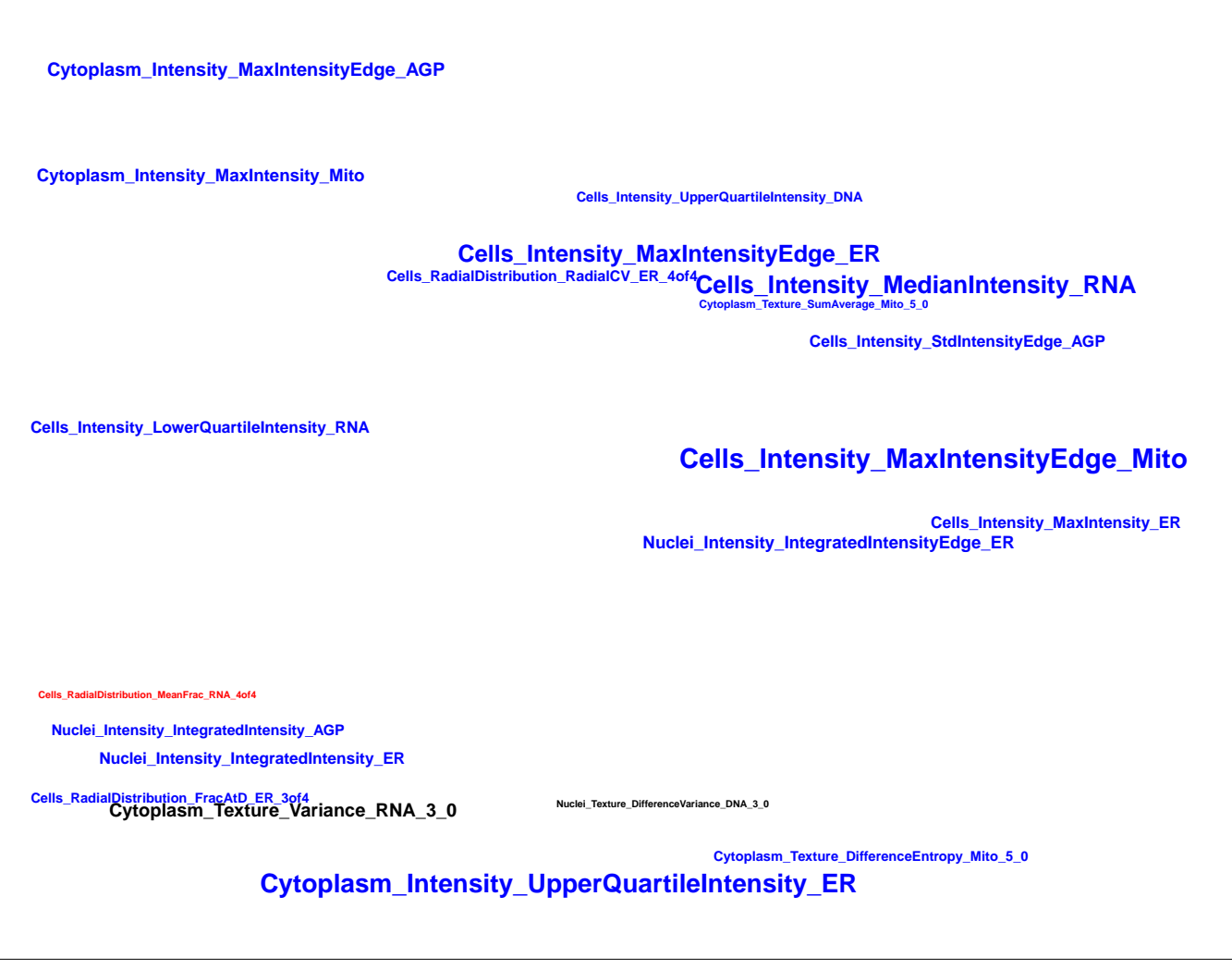
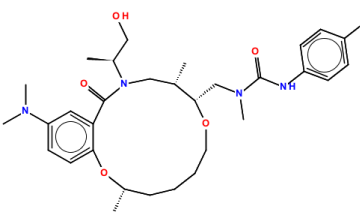
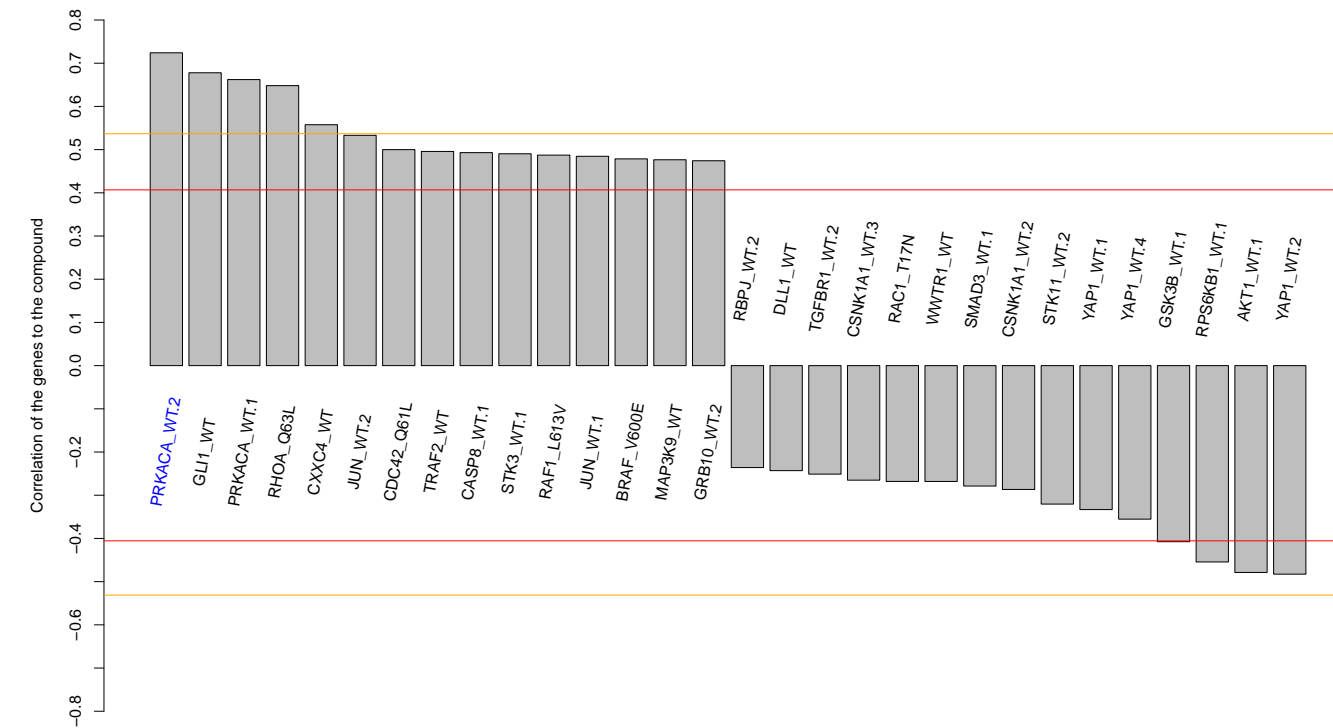
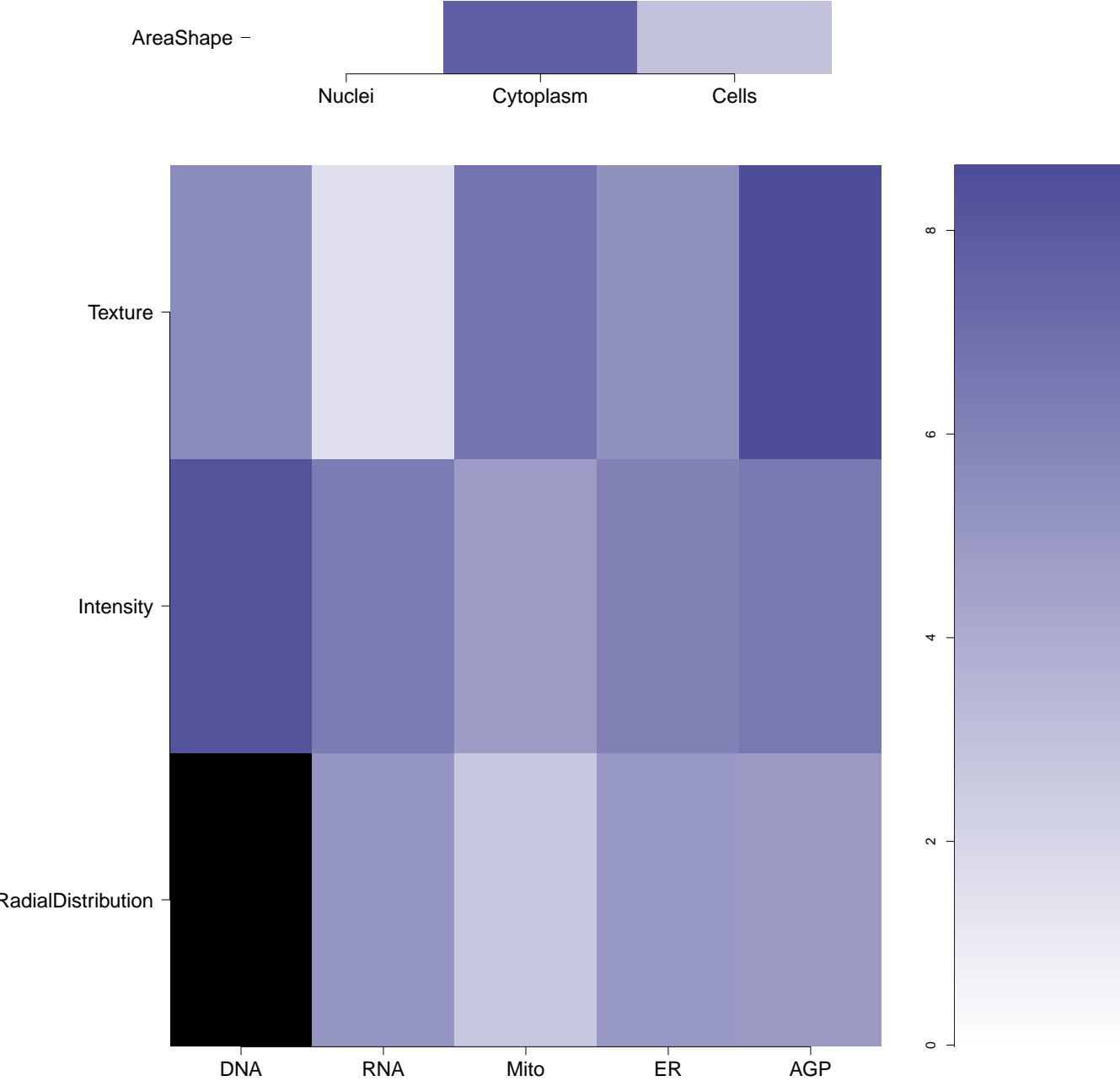

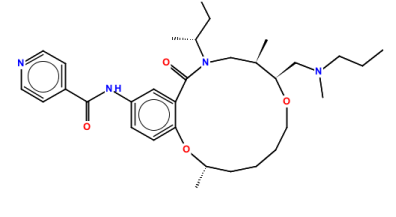
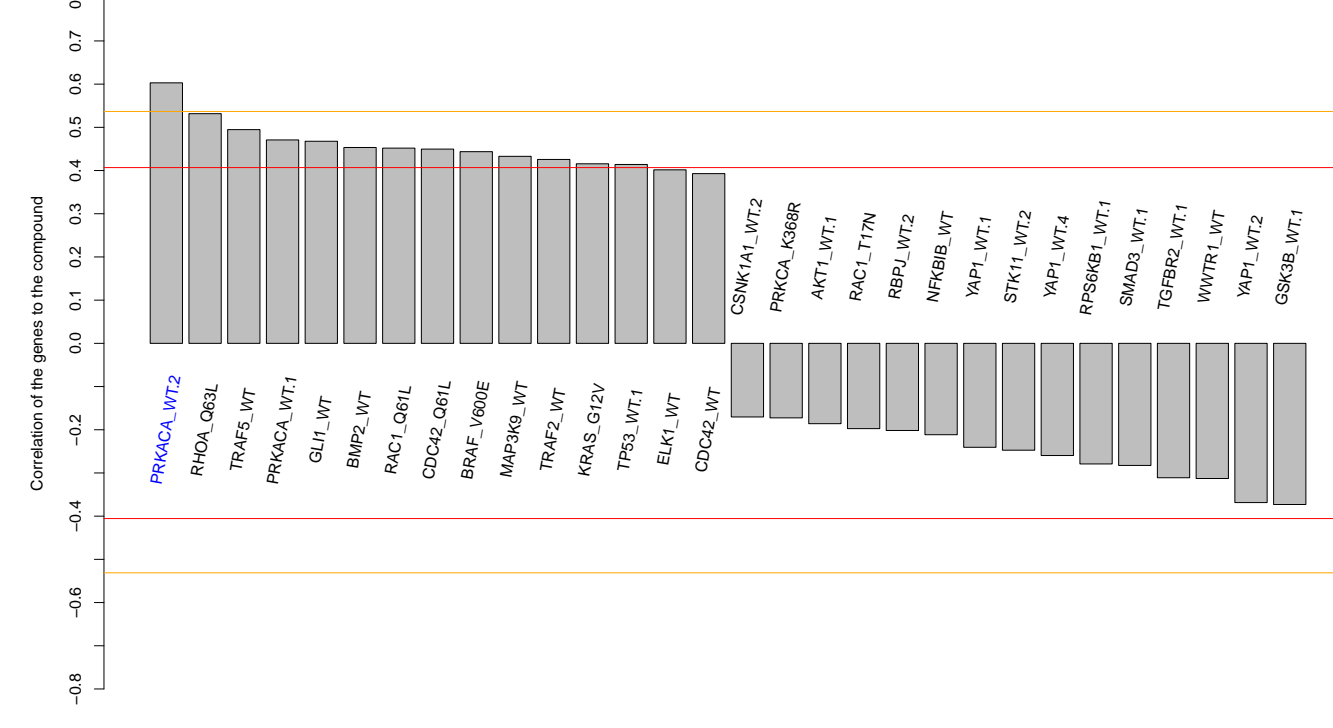
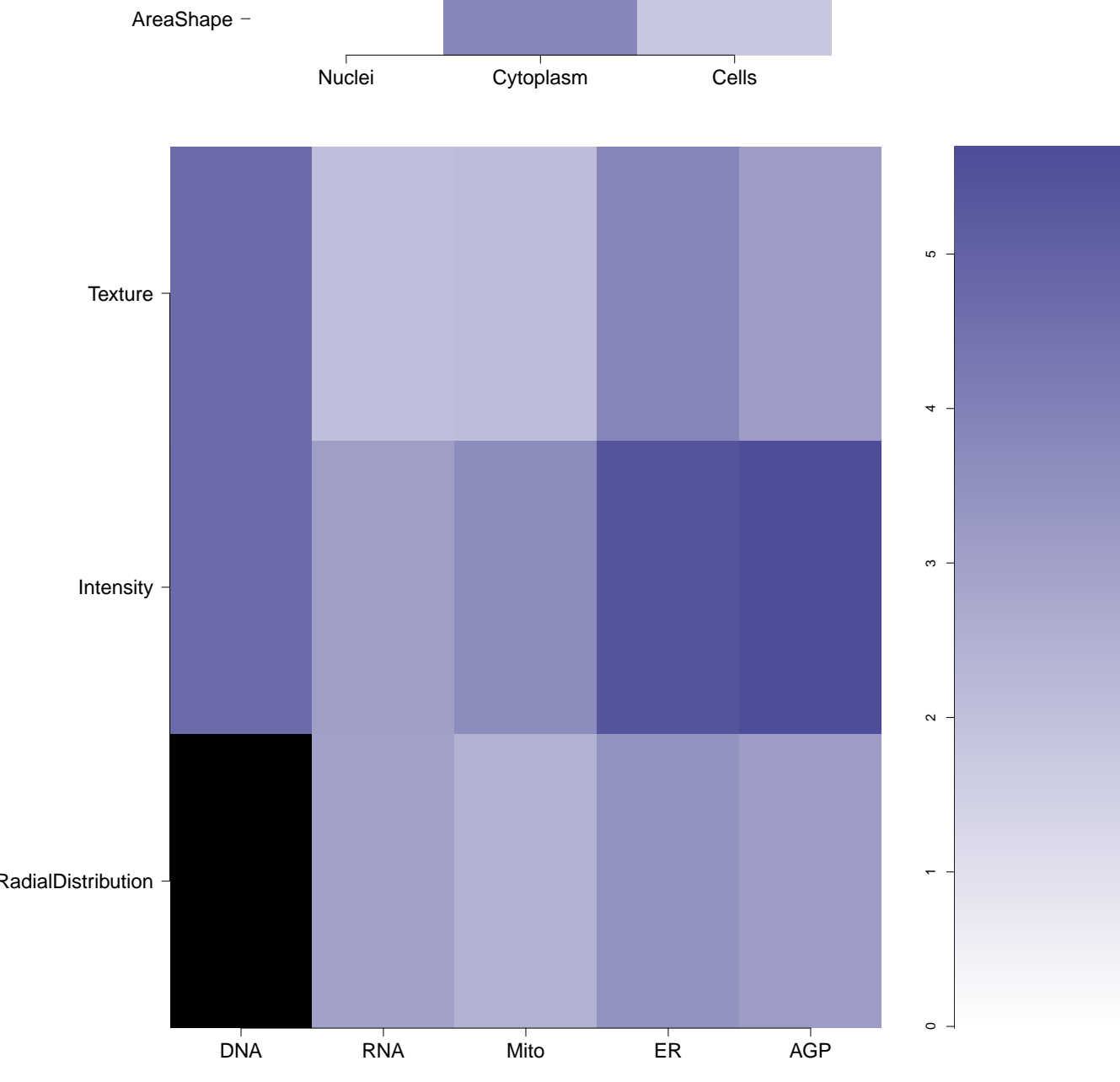

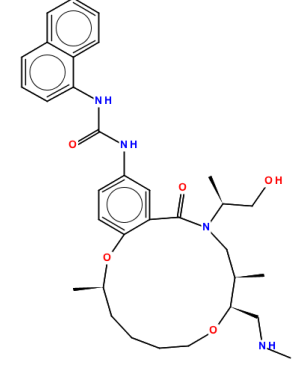
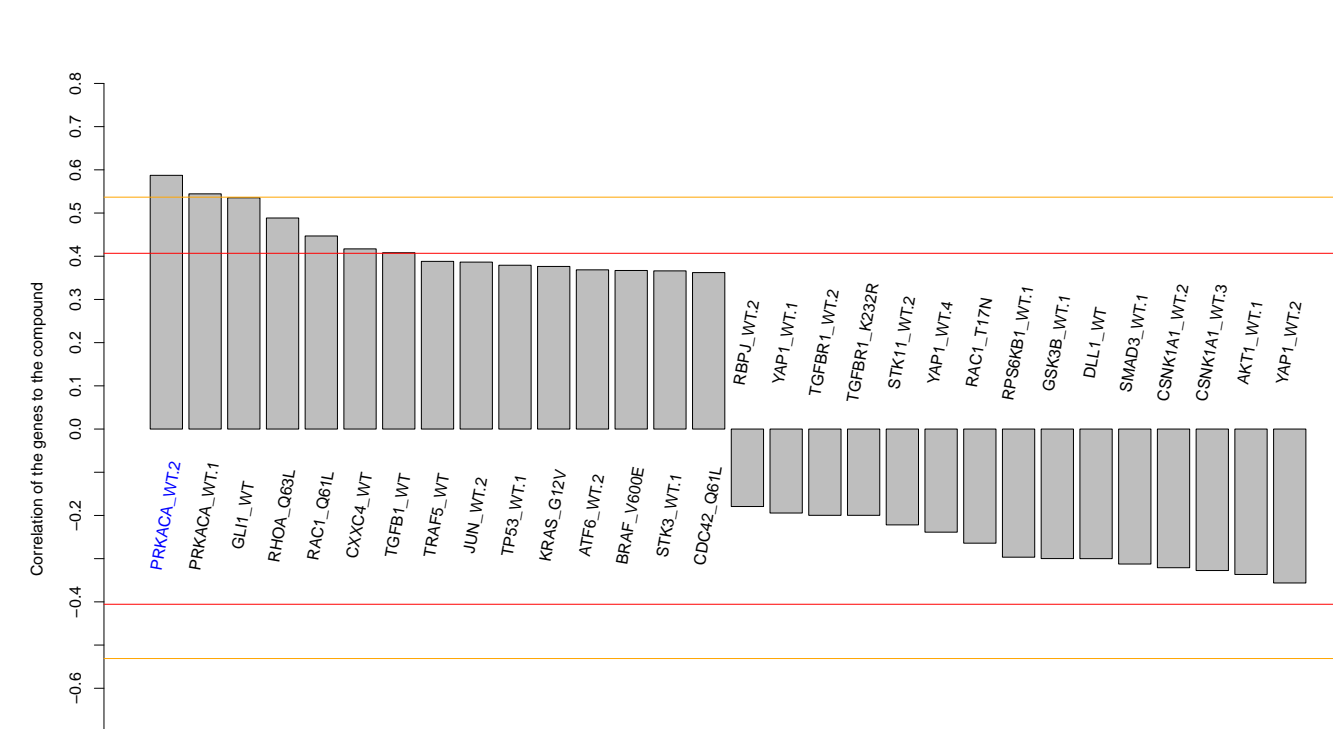
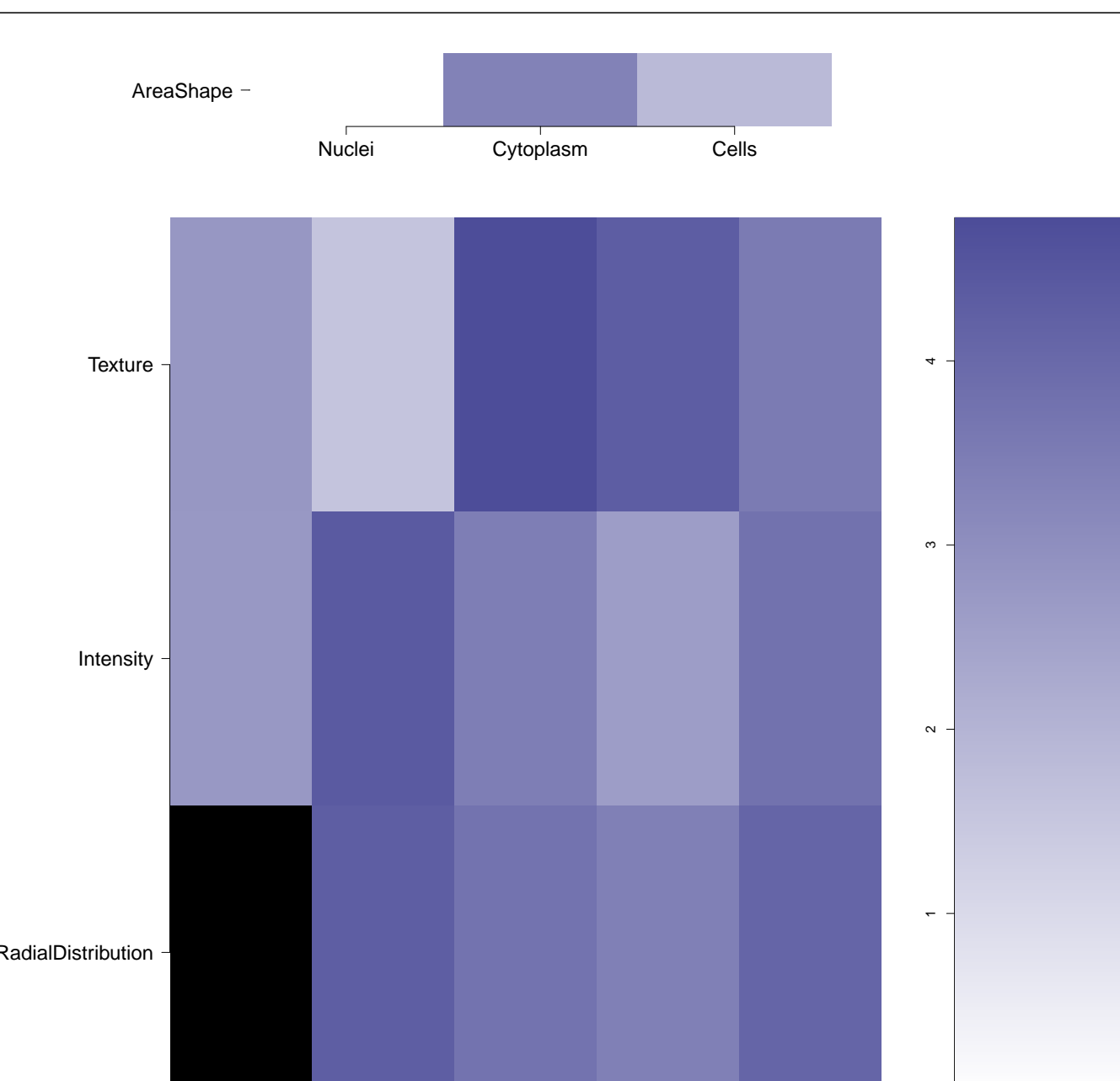
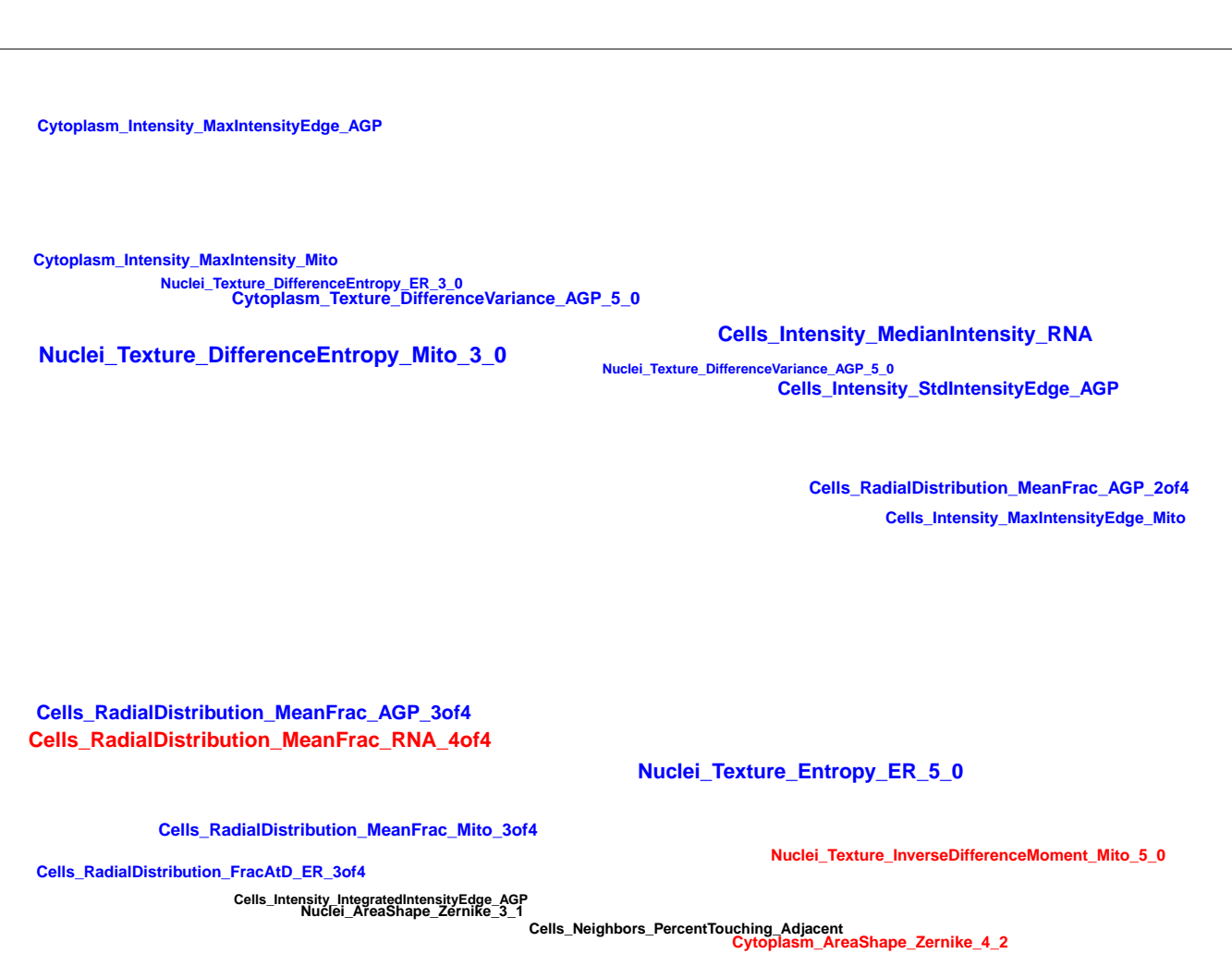
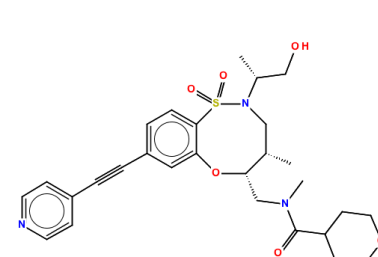
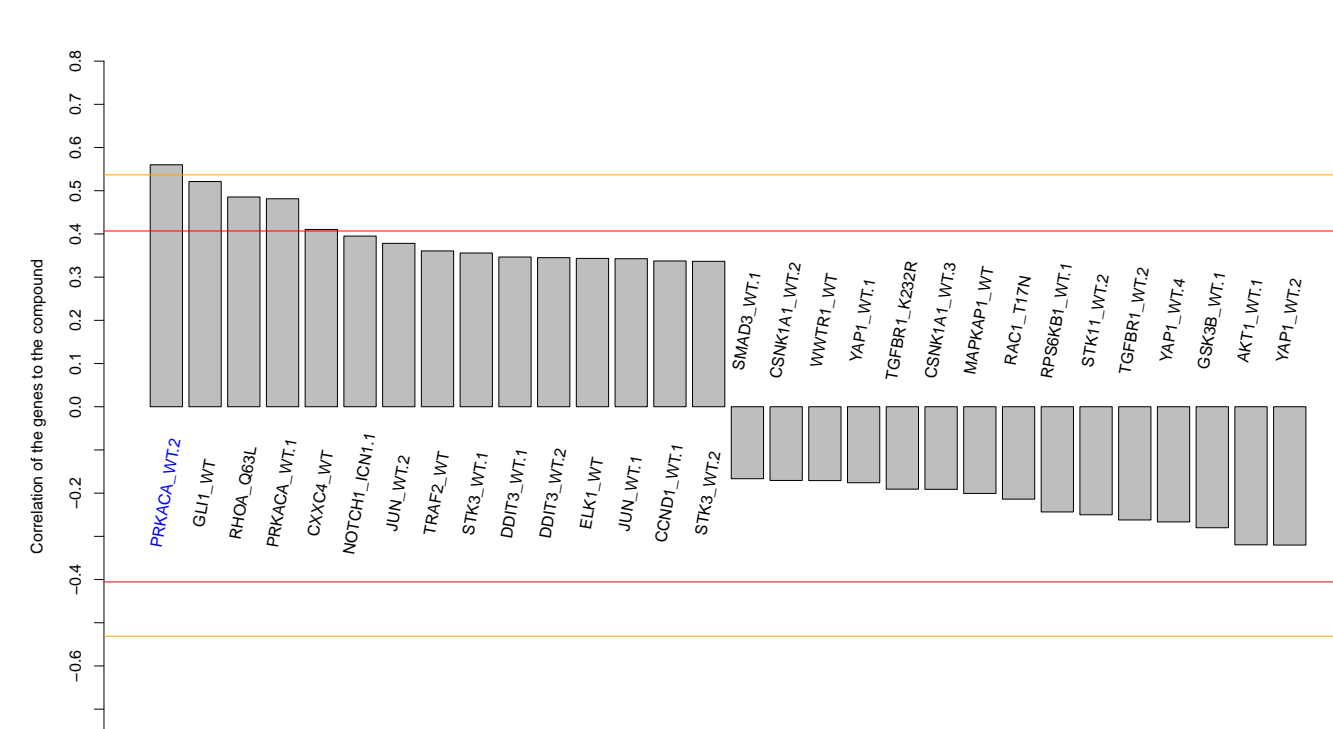
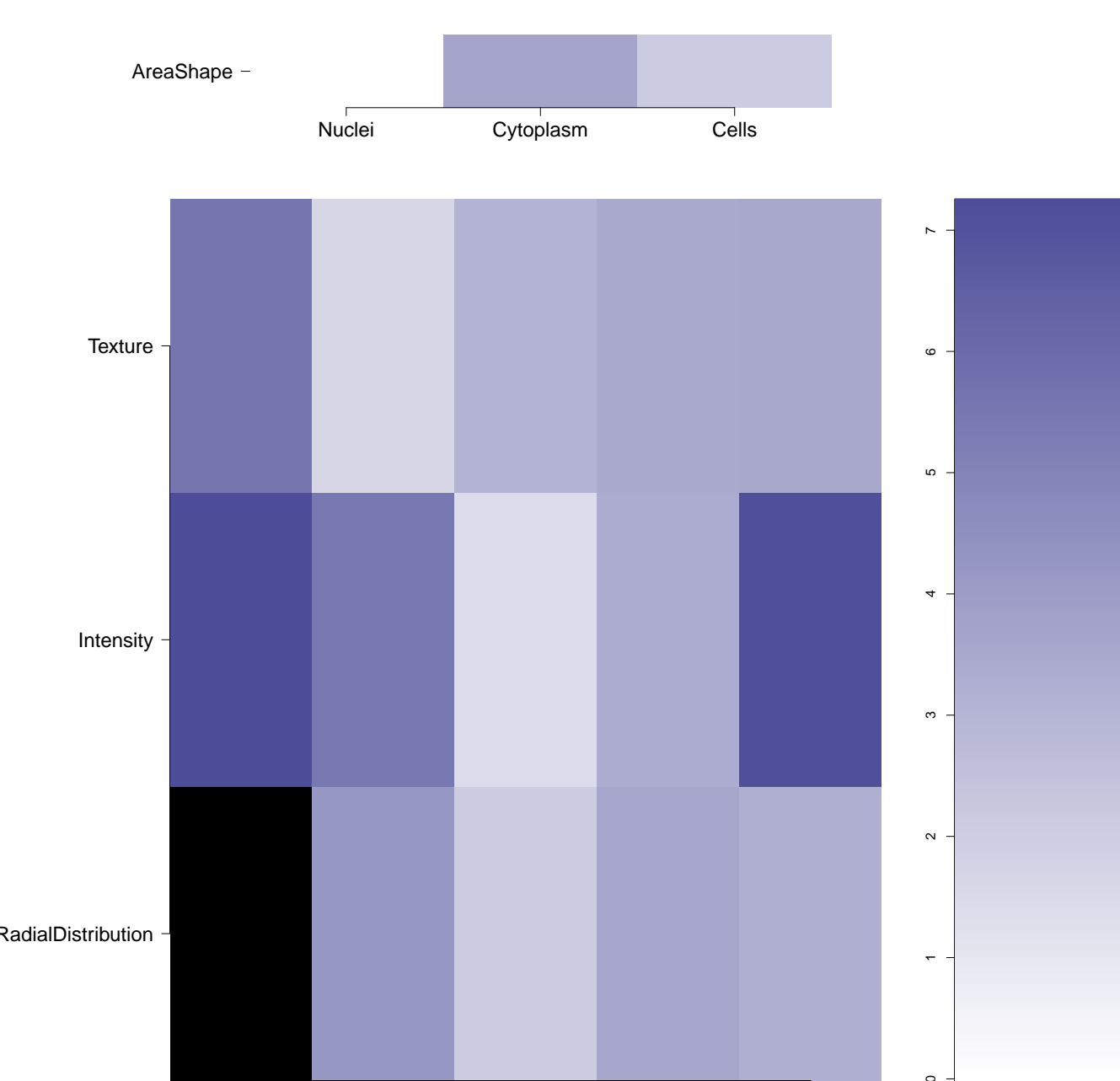
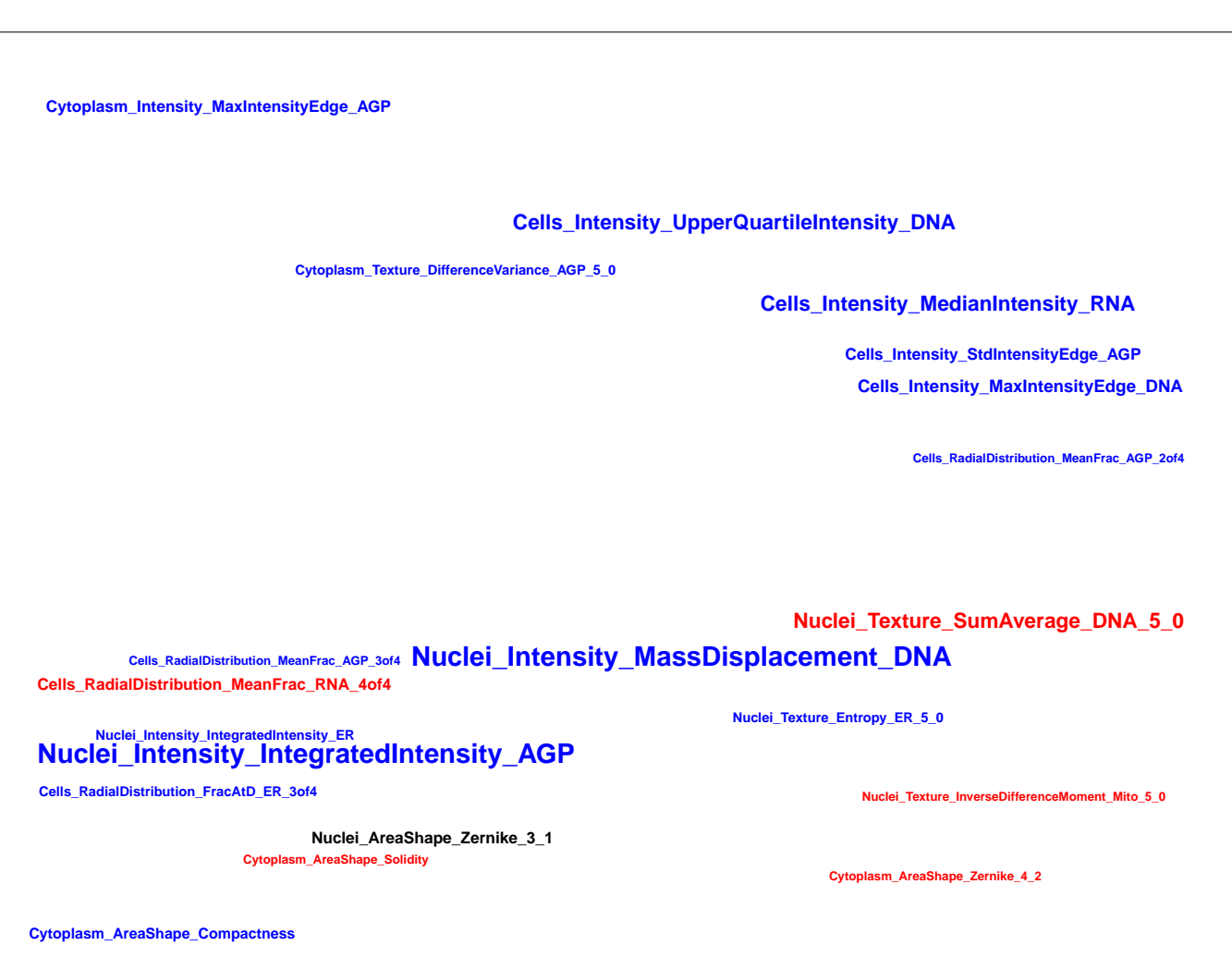
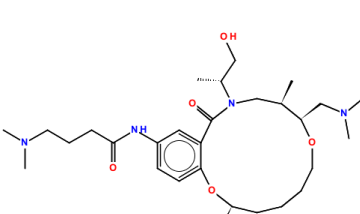
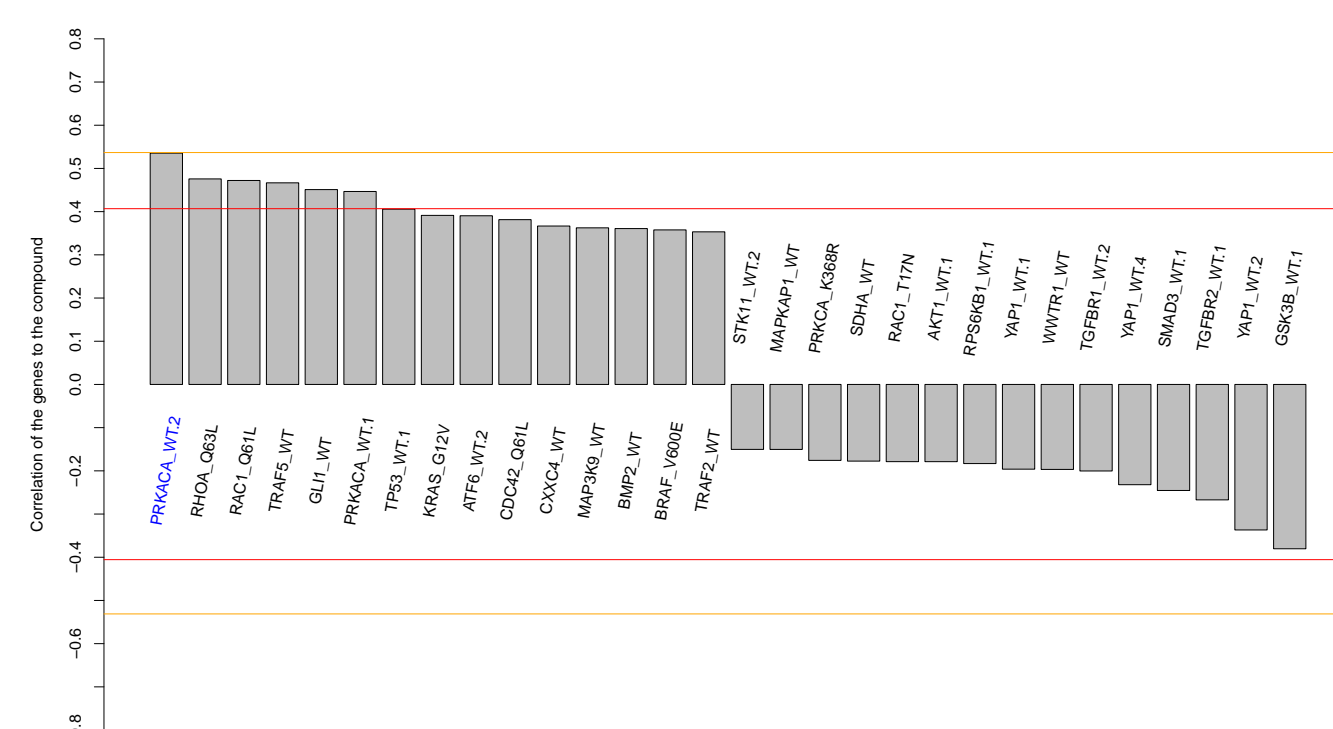
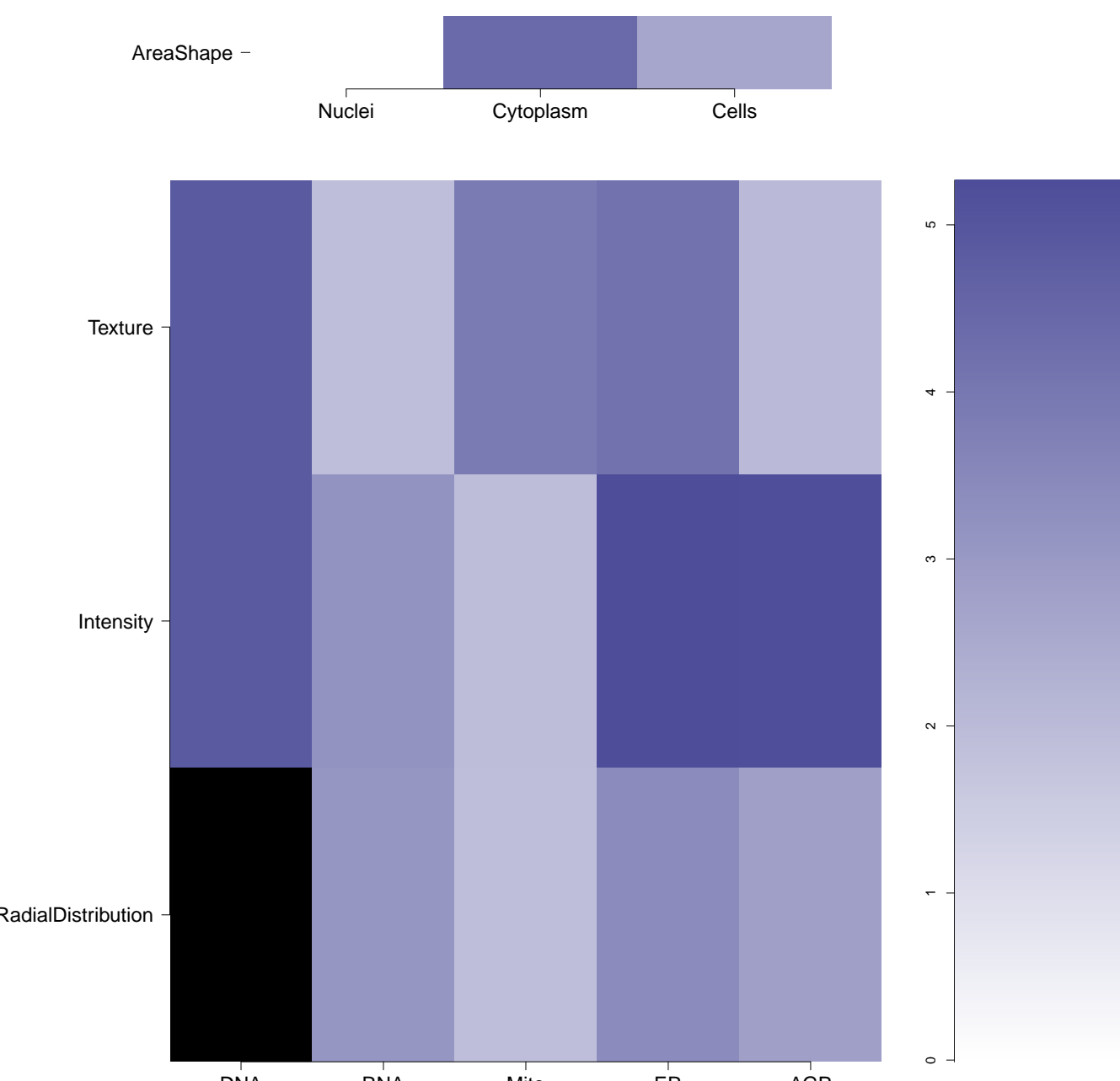

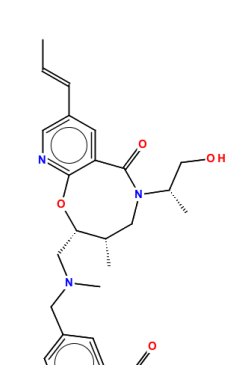
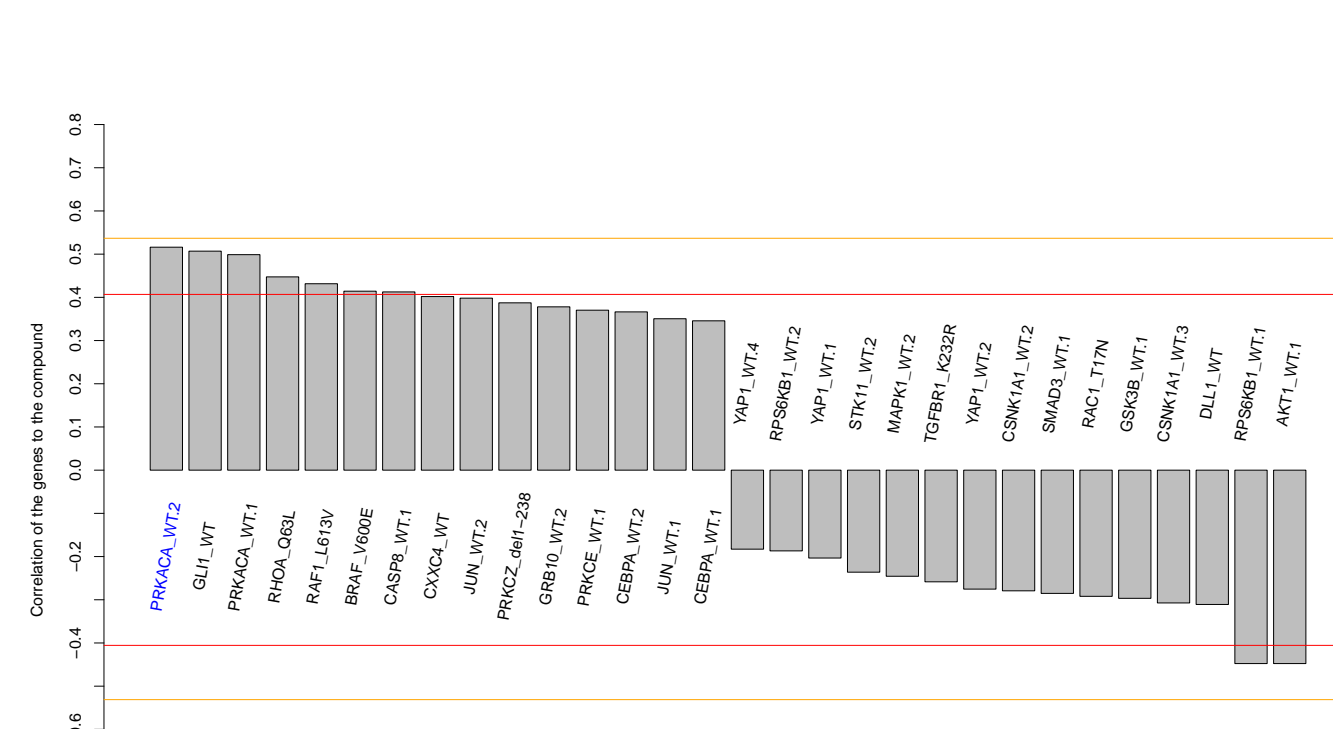
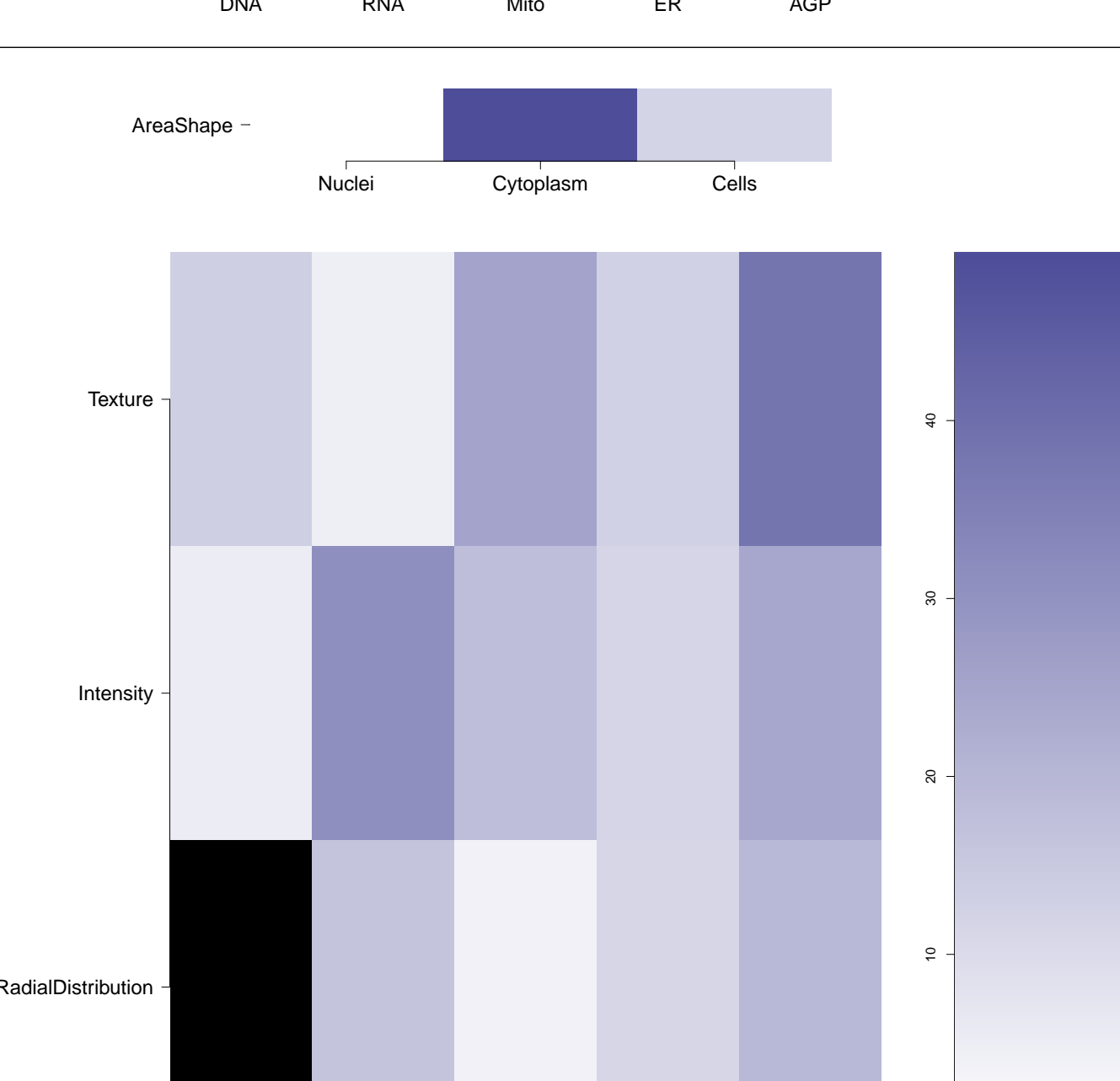
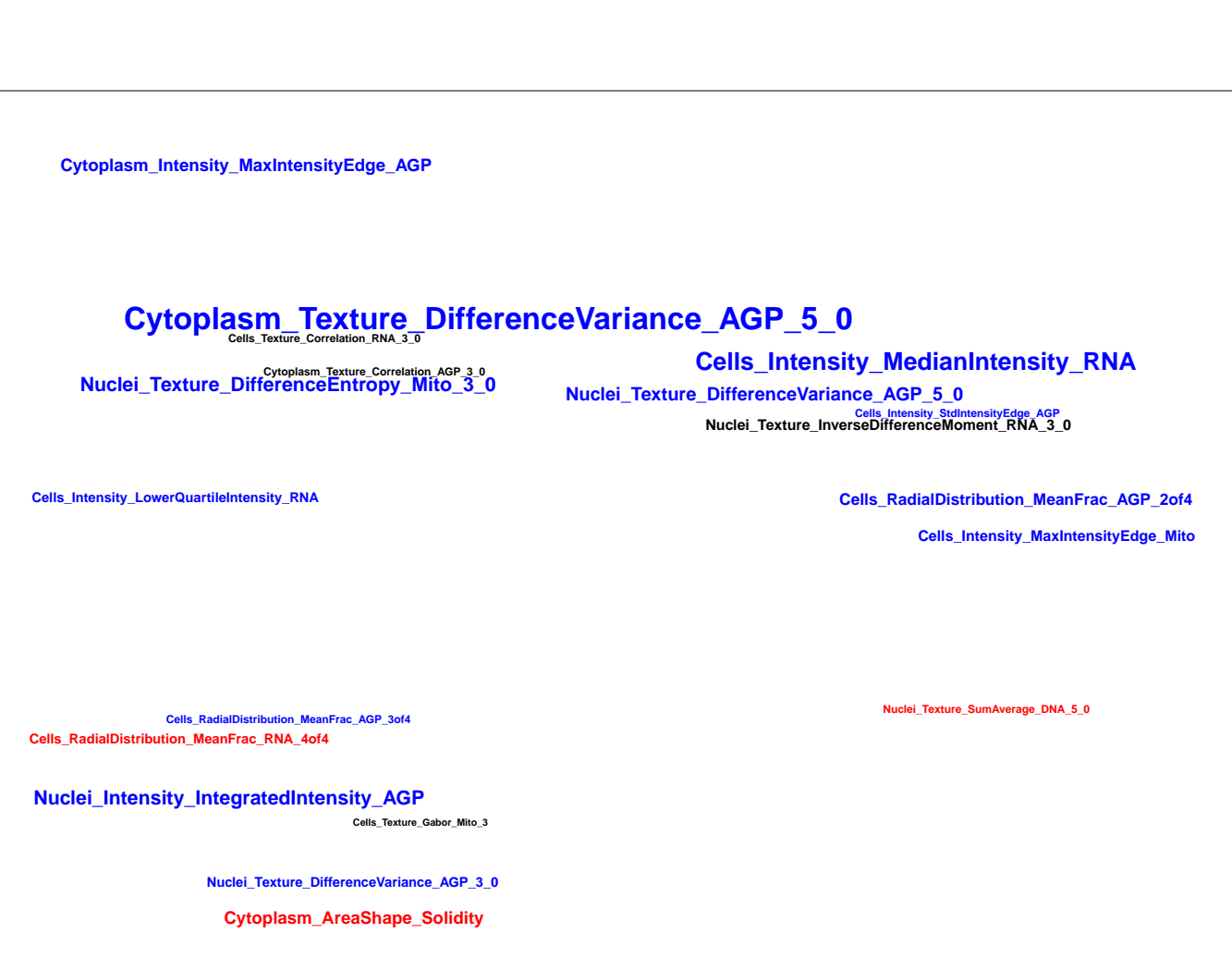


AGP

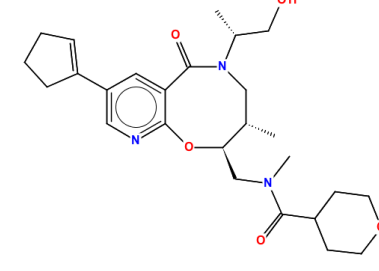
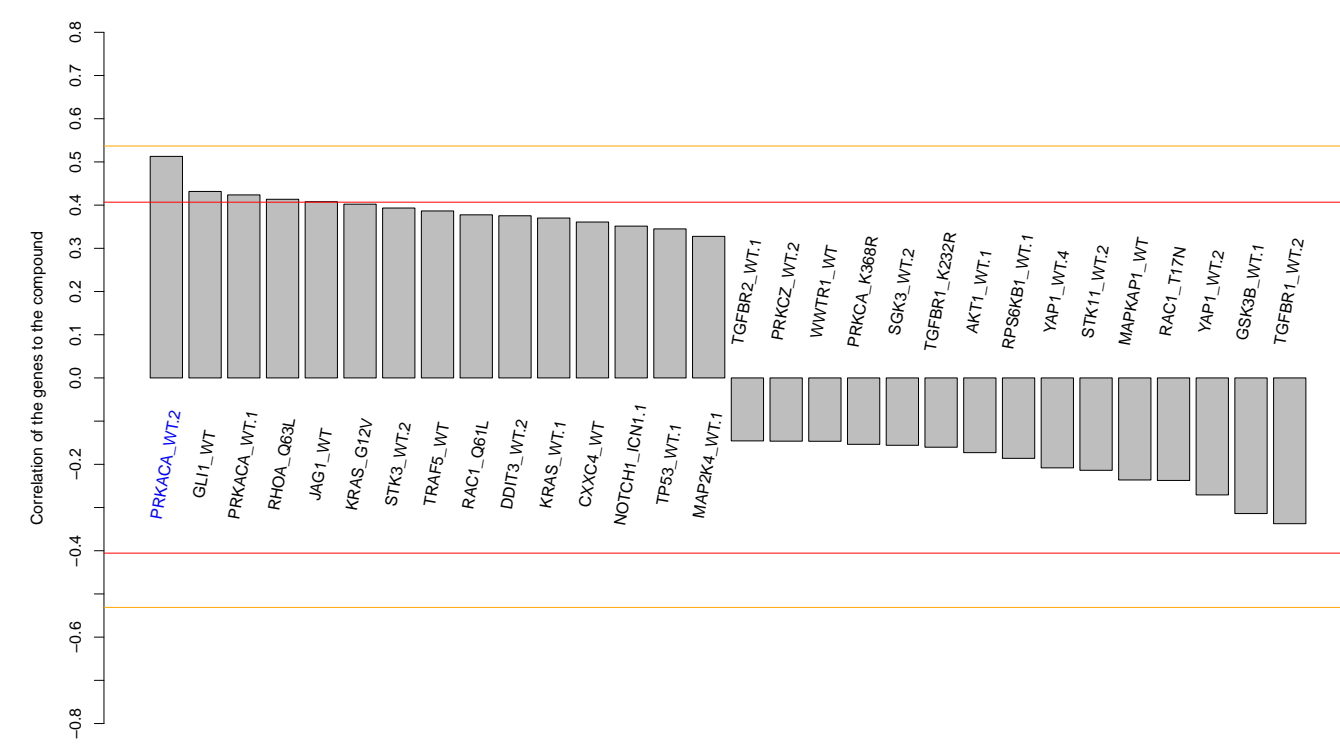


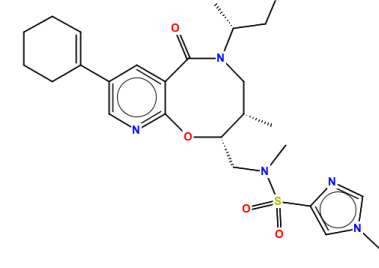
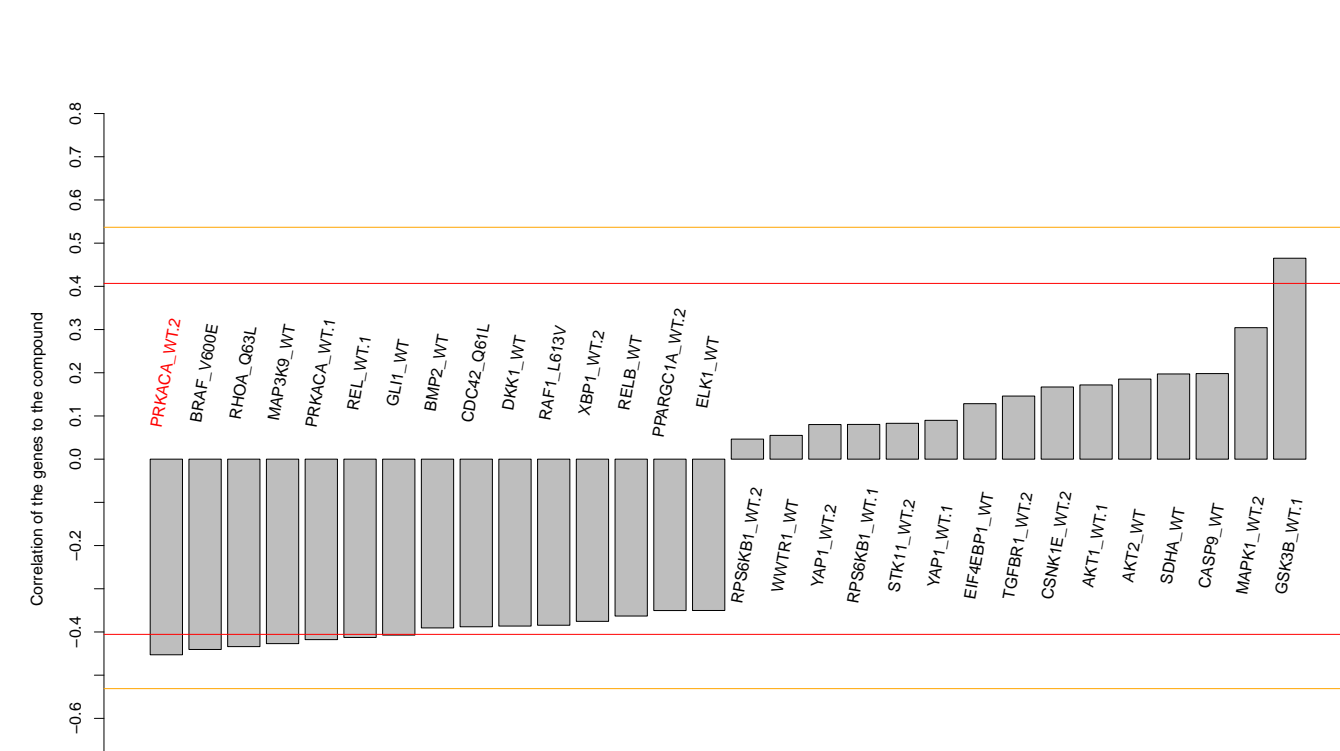


Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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-K52251545-001-05-2 AC1M5VPS MLS000418615 HMS2531C16 ZINC3270008 SMR000247565 T0510-7581 PubChem CID : 2386323		0.83 (in 4 replicates)	0.72	NA				<p>Total number of assays tested in: 629. Active in the following assays:</p> <ul style="list-style-type: none"> <li>• Total Fluorescence Counterscreen for Inhibitors of the Interaction of Thyroid Hormone Receptor and Steroid Receptor Coregulator 2 (AID 1479)</li> <li>• Antagonist of Human D 1 Dopamine Receptor: qHTS (AID 504652)</li> <li>• High-throughput multiplex microsphere screening for inhibitors of toxin proteases, specifically Botulinum neurotoxin light chain F protease, MLPCN compound set (AID 588497)</li> </ul>
BRD-K86981519-001-01-5 PubChem CID : 44496872		0.89 (in 4 replicates)	0.72	0.763				Total number of assays tested in: 29.
BRD-K95264594-001-01-3 PubChem CID : 54614949		0.89 (in 4 replicates)	0.60	0.958				<p>Total number of assays tested in: 19. Active in the following assays:</p> <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 (AID 1159554)</li> </ul>
BRD-K21740361-001-01-2 PubChem CID : 44494140		0.83 (in 4 replicates)	0.59	0.601				<p>Total number of assays tested in: 51. Active in the following assays:</p> <ul style="list-style-type: none"> <li>• HTS for Bacterial rRNA inhibitors Measured in Microorganism-Based System Using Plate Reader - 7056-01.Inhibitor.SinglePoint.HTS.Activity (AID 720706)</li> </ul>
BRD-K70116395-001-01-5 PubChem CID : 54619000		0.68 (in 4 replicates)	0.56	0.897				<p>Total number of assays tested in: 43. Active in the following assays:</p> <ul style="list-style-type: none"> <li>• Whole cell Yeast HTS to identify compounds modulating the fidelity of the start codon recognition in eukaryotes. Measured in Whole Organism System Using Plate Reader - 2155-01.Other.SinglePoint.HTS.Activity (AID 602393)</li> <li>• Small molecule inhibitors of mR122 Measured in Cell-Based System Using Plate Reader - 2144-01.Activator.Dose.DryPowder.Activity (AID 743399)</li> </ul>
BRD-K96106084-001-01-2 PubChem CID : 44486430		0.75 (in 4 replicates)	0.54	0.605				Total number of assays tested in: 30.
BRD-K87990527-001-01-5 PubChem CID : 54618135		0.80 (in 4 replicates)	0.52	0.631				Total number of assays tested in: 37.



BRD-K97620396-001-01-4 PubChem CID : 54619002		0.80 (in 4 replicates)	0.51	0.701				Total number of assays tested in: 35.
BRD-K47647527-001-01-0 PubChem CID : 54618834		0.65 (in 3 replicates)	0.50	0.656				Total number of assays tested in: 25.
BRD-K99901517-001-01-0 PubChem CID : 54614965		0.60 (in 4 replicates)	0.50	0.589				Total number of assays tested in: 19.
BRD-K83684822-001-01-0 PubChem CID : 54632651		0.55 (in 4 replicates)	-0.57	0.411				Total number of assays tested in: 35.
BRD-K79355010-001-01-5 PubChem CID : 44493589		0.55 (in 4 replicates)	-0.53	NA				Total number of assays tested in: 43.
BRD-K54470262-001-01-6 PubChem CID : 54619082		0.56 (in 4 replicates)	-0.52	0.711				Total number of assays tested in: 39.
BRD-K42605934-001-01-0 PubChem CID : 54649241		0.56 (in 2 replicates)	-0.45	0.884				Total number of assays tested in: 36.