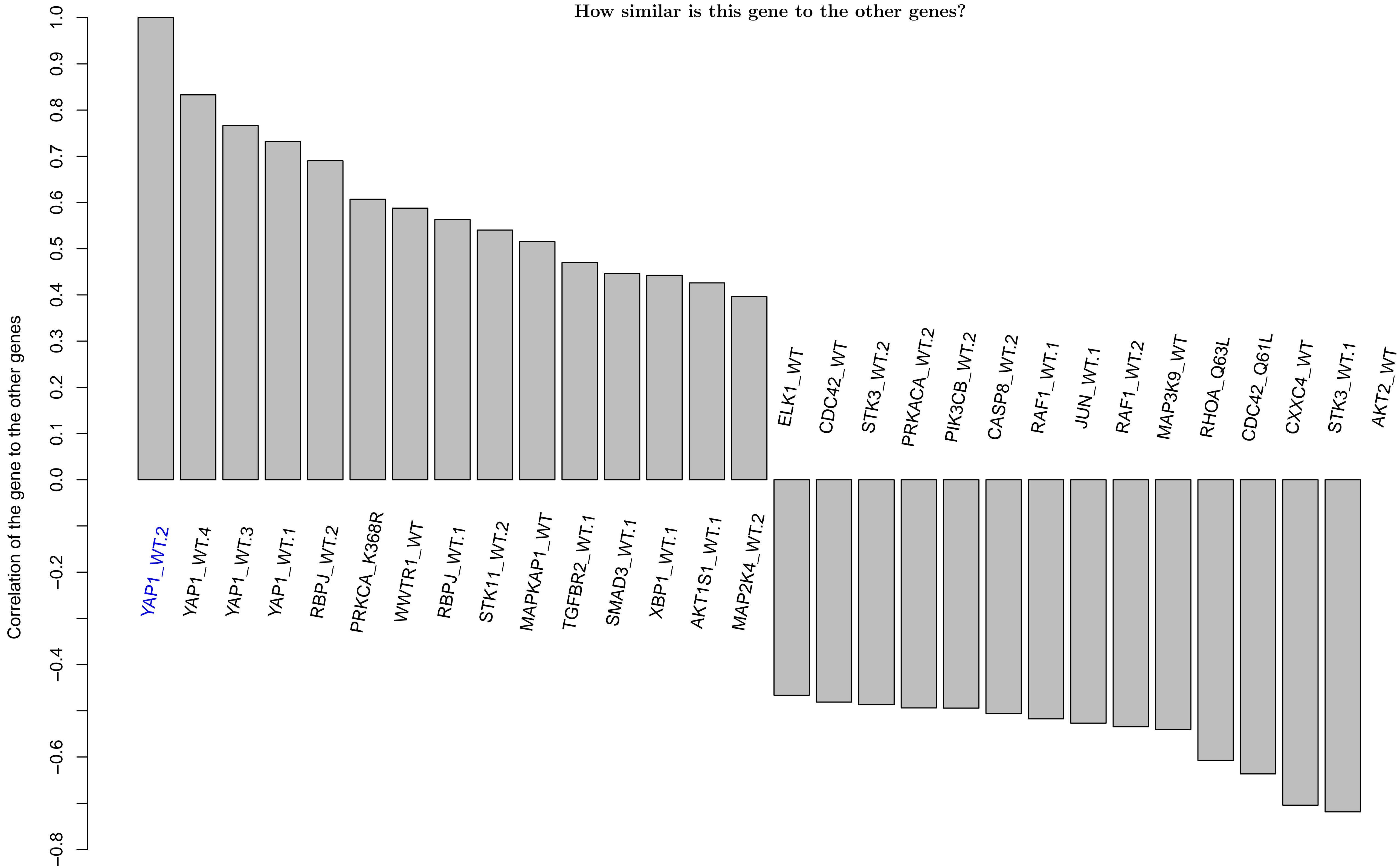
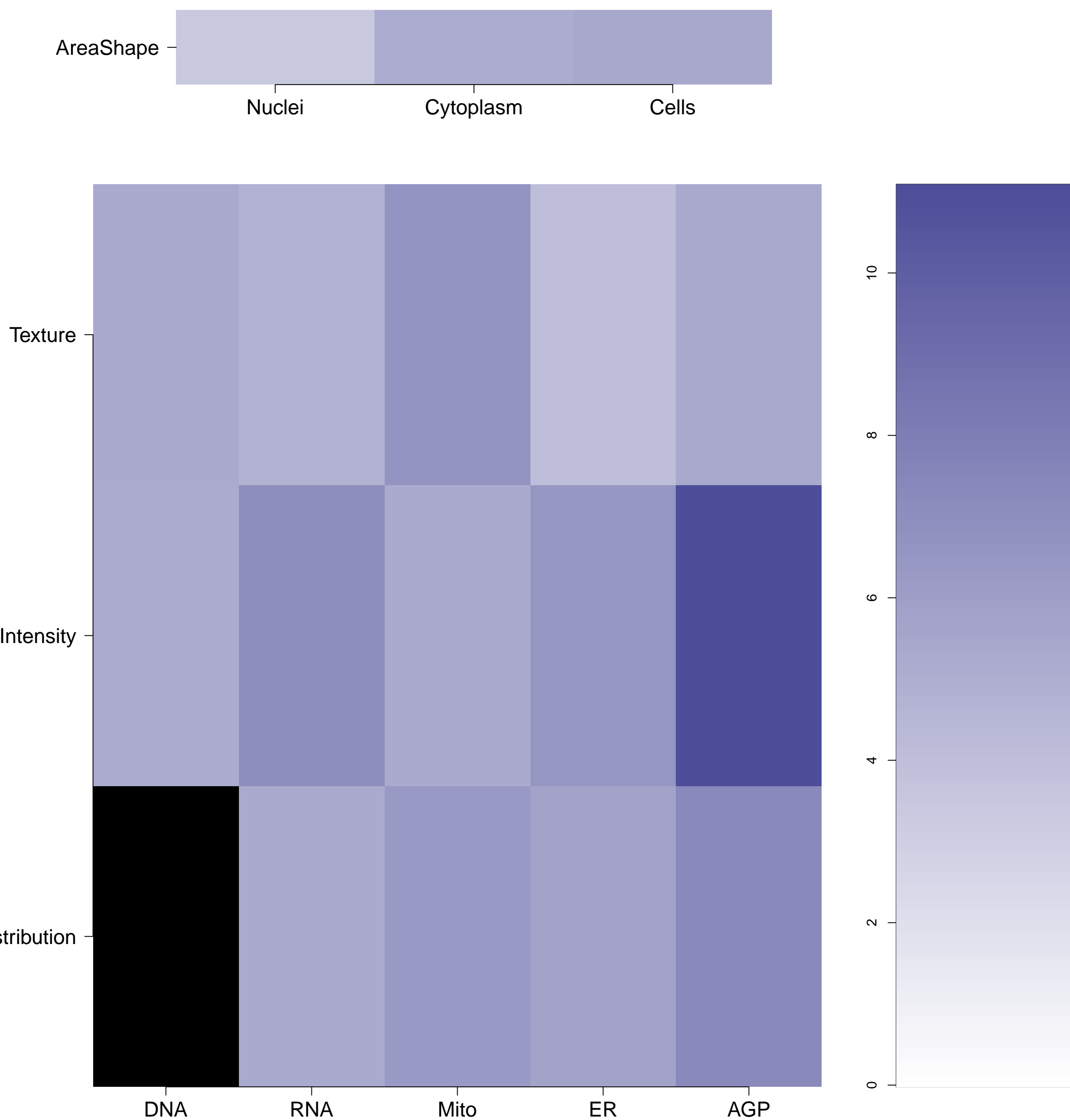


YAP1.WT.2 - in Canonical Hippo

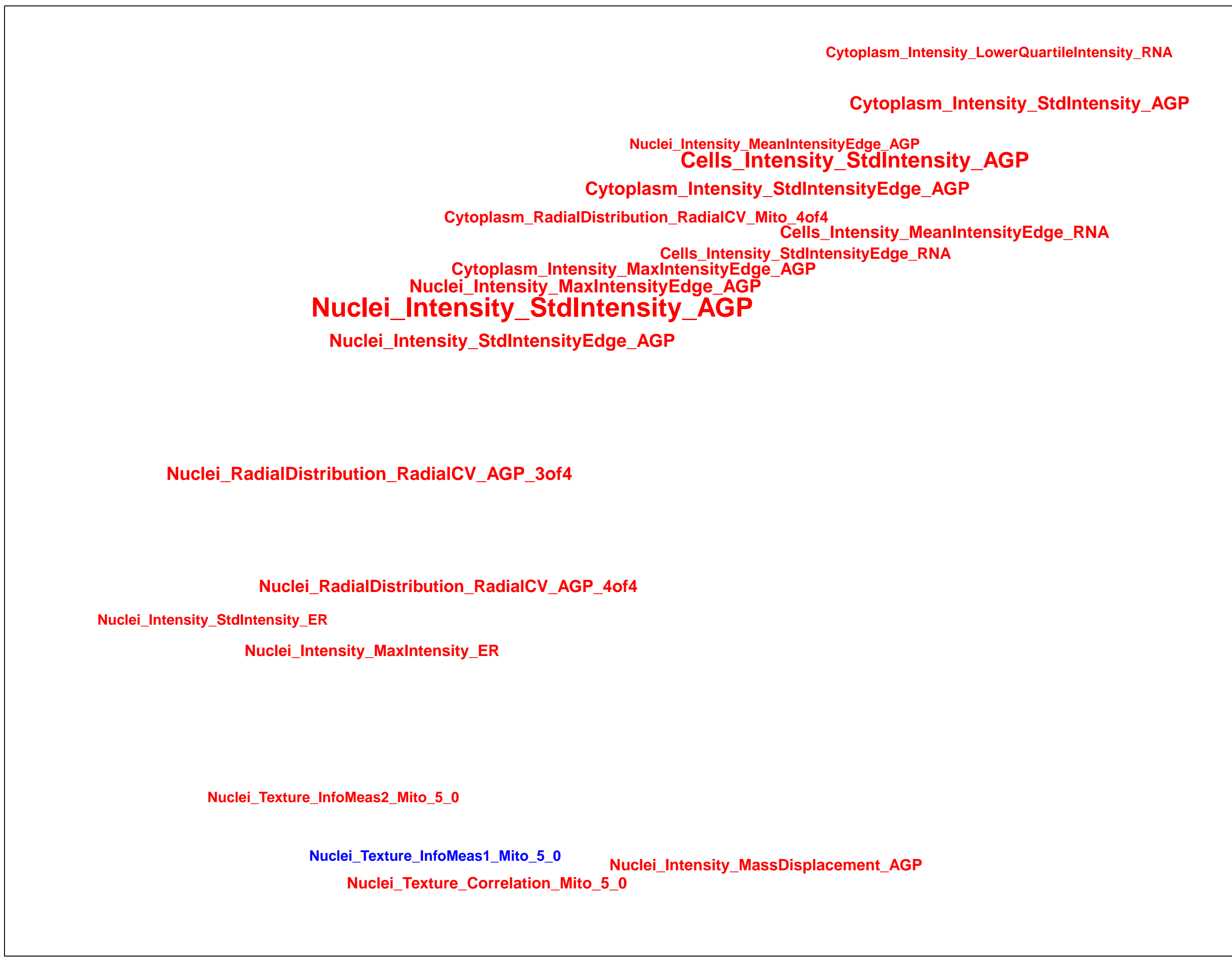
How similar is this gene to the other genes?



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

YAP1.WT.2 (41744)

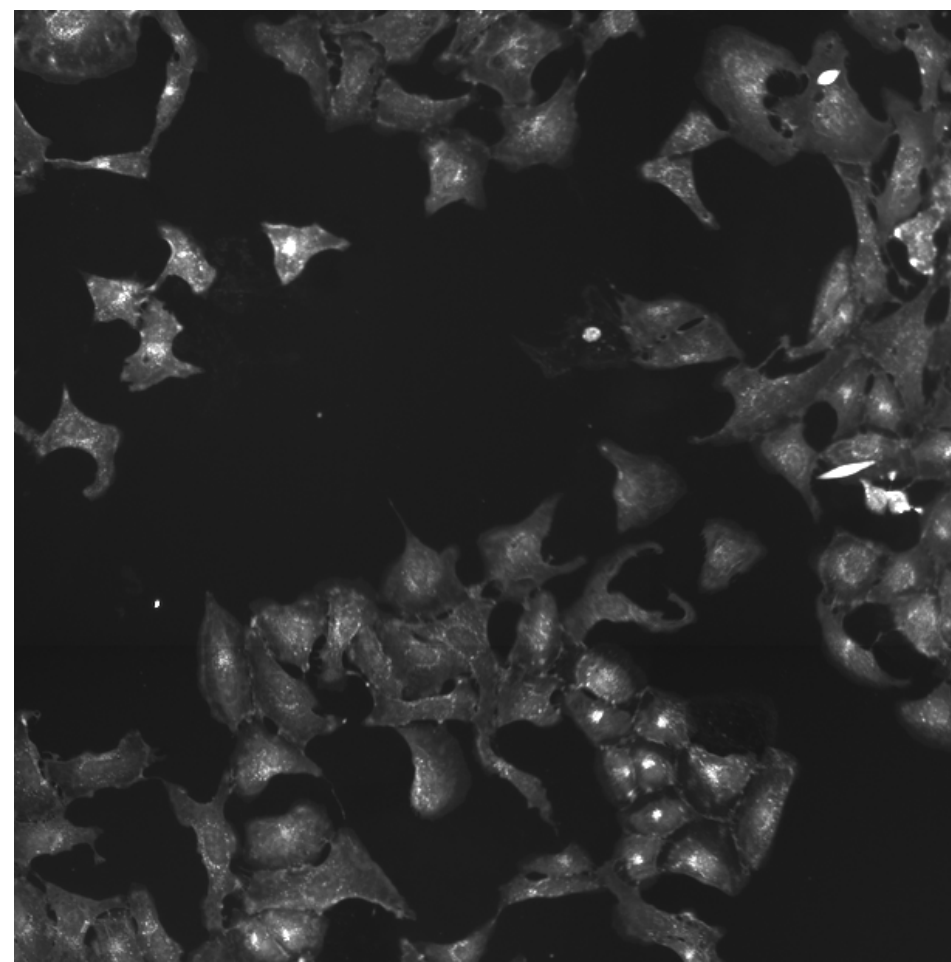
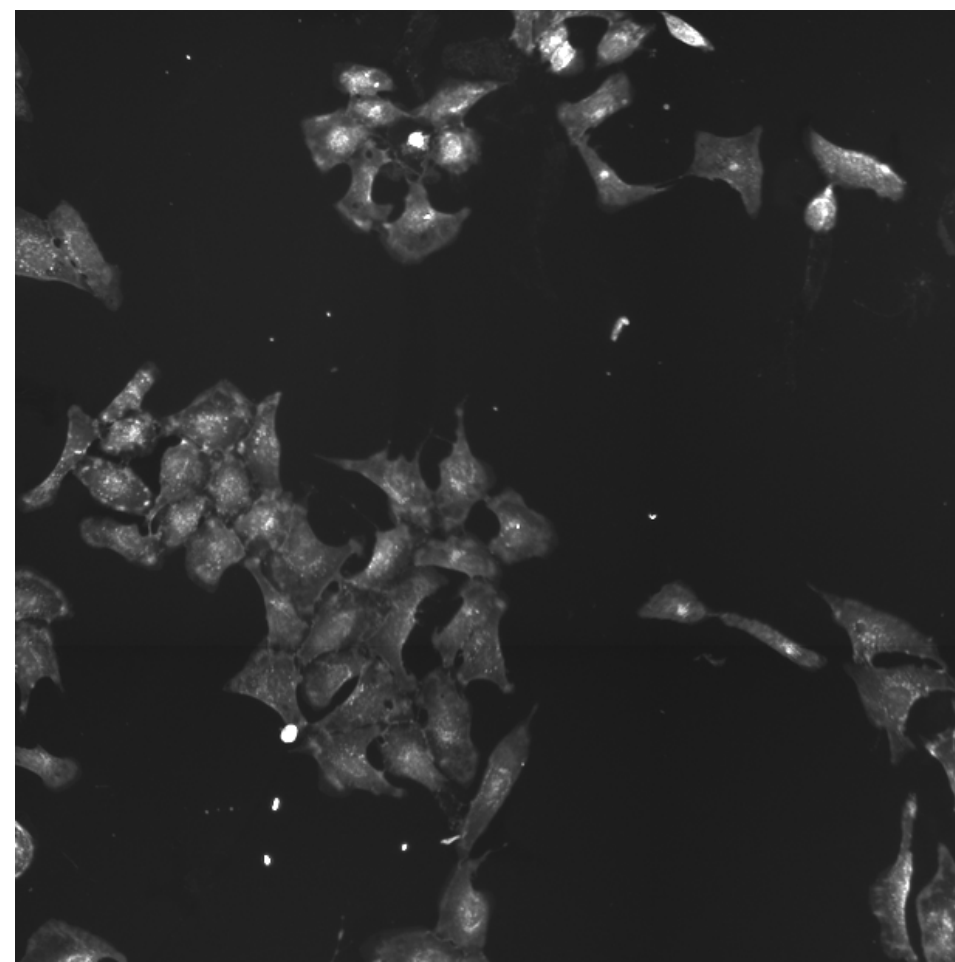
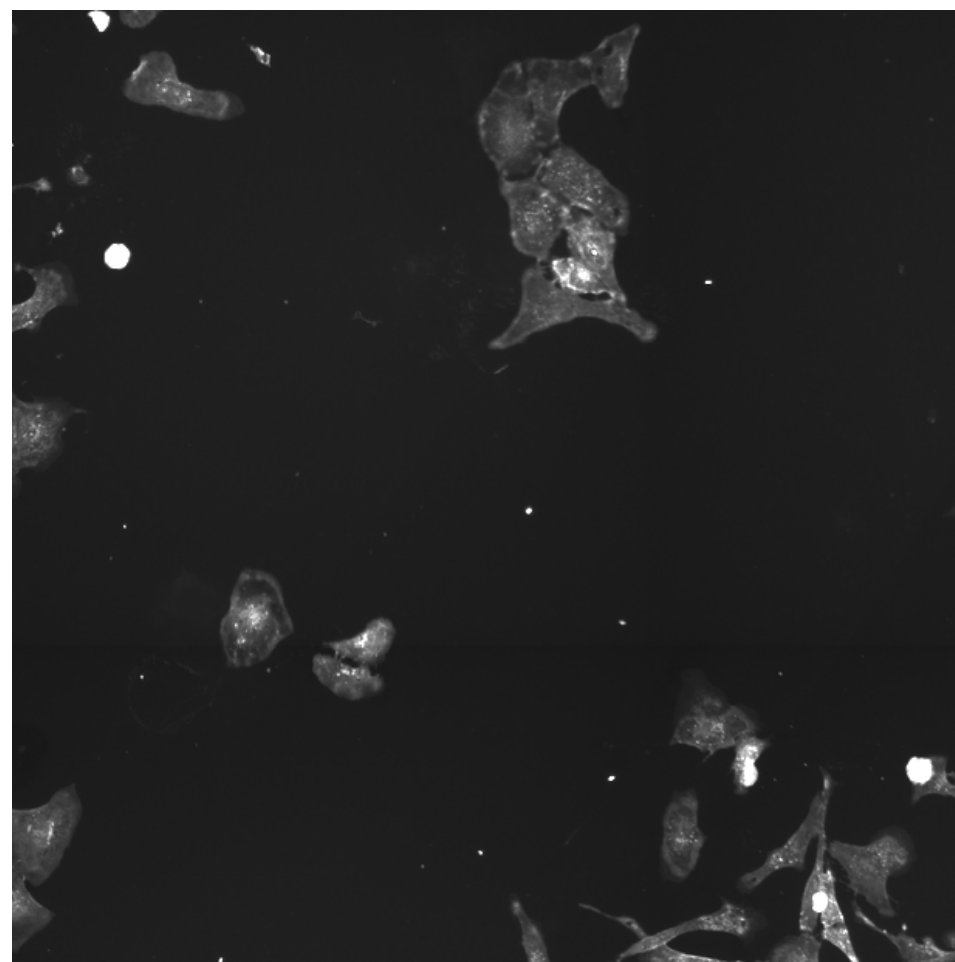
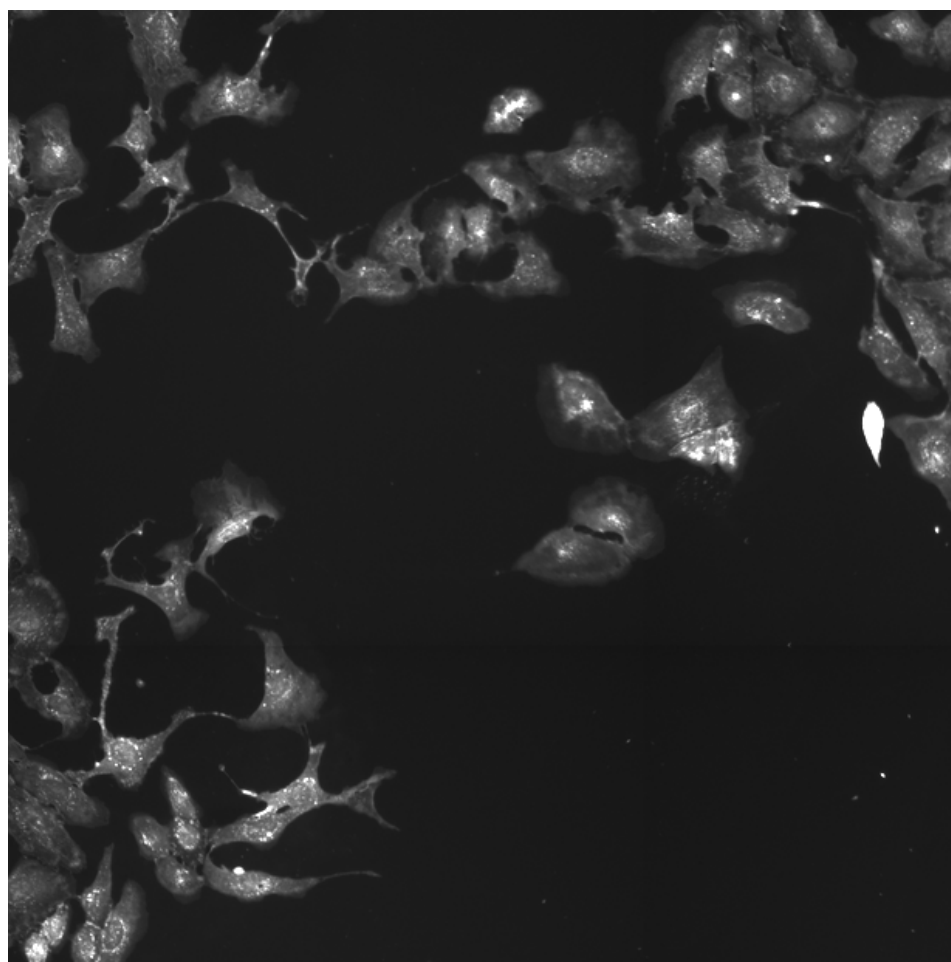
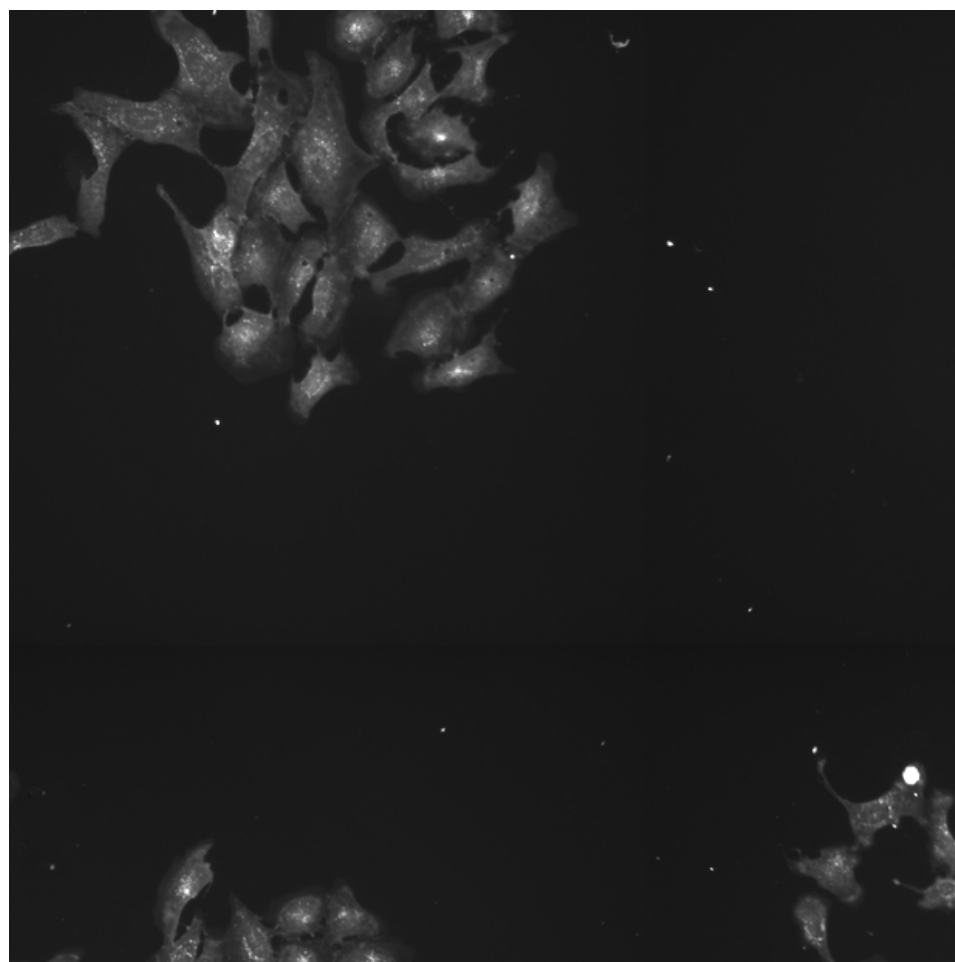
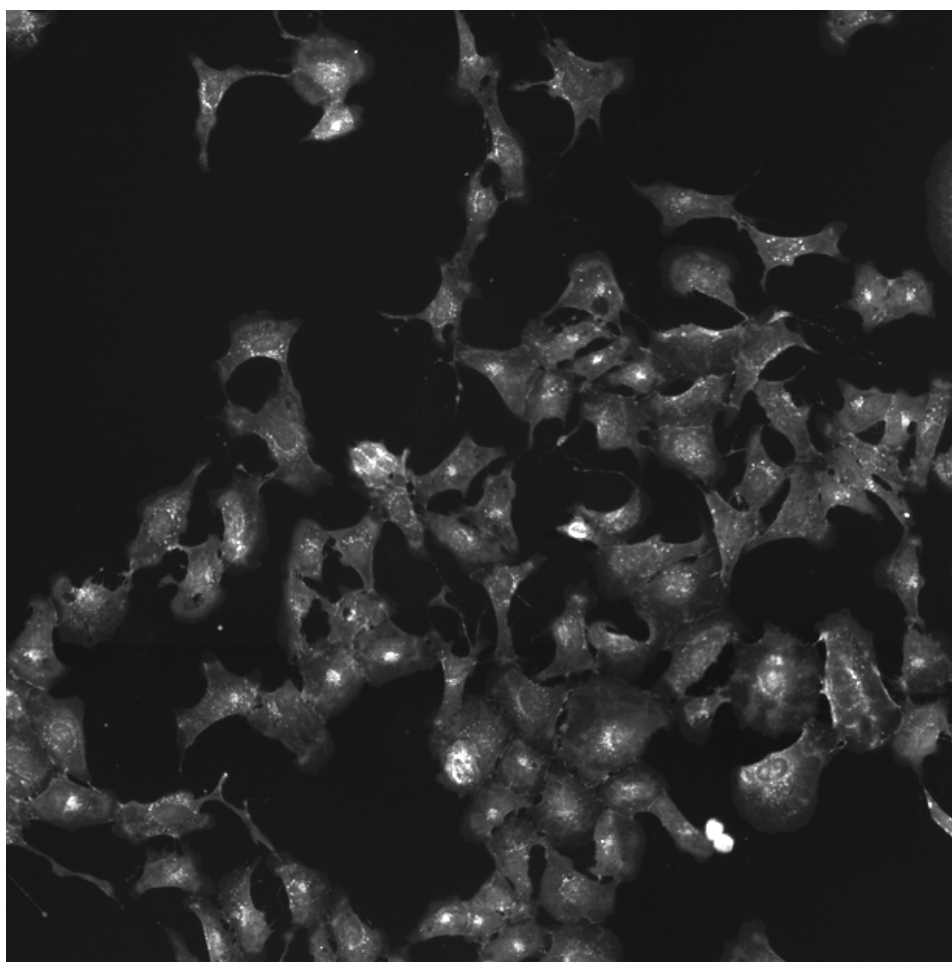
YAP1.WT.2 (41755)

YAP1.WT.2 (41756)

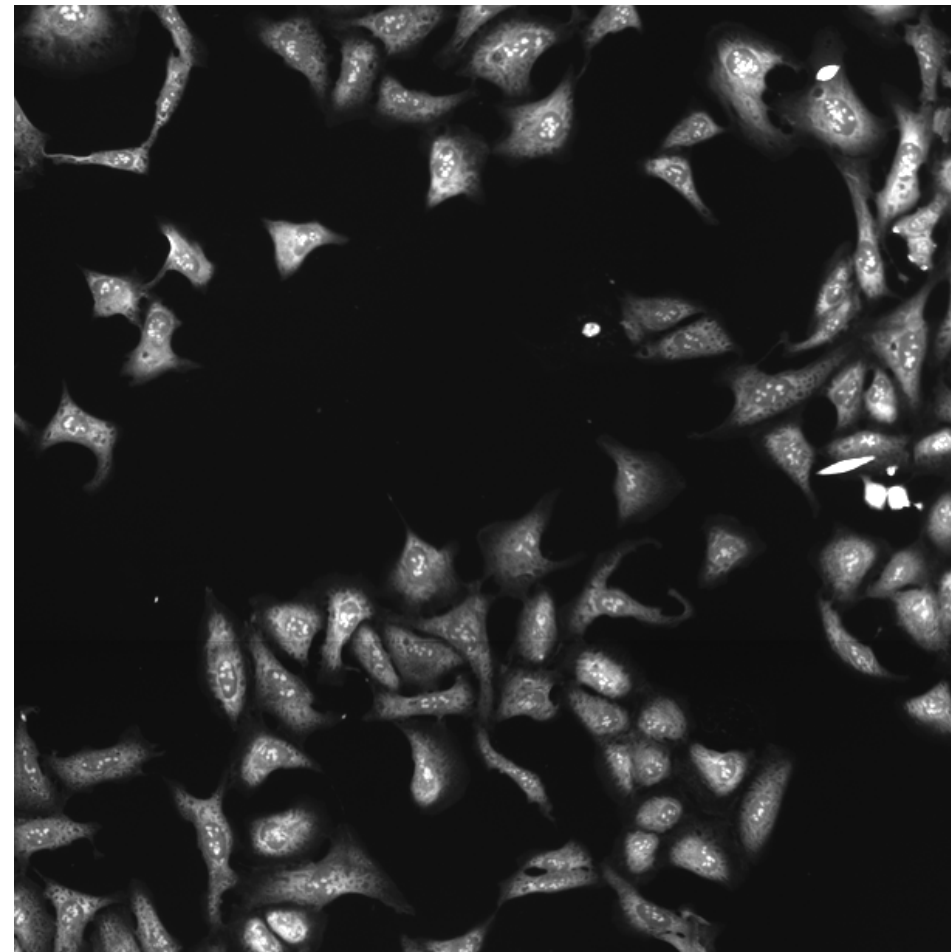
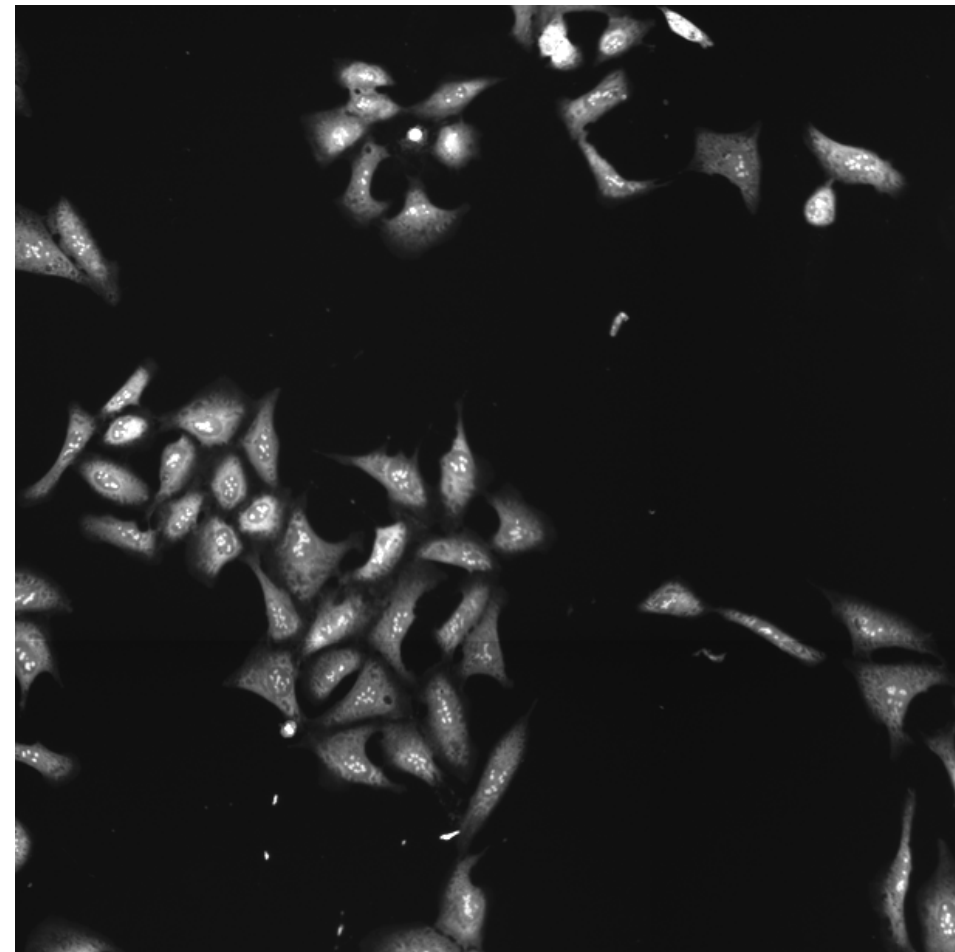
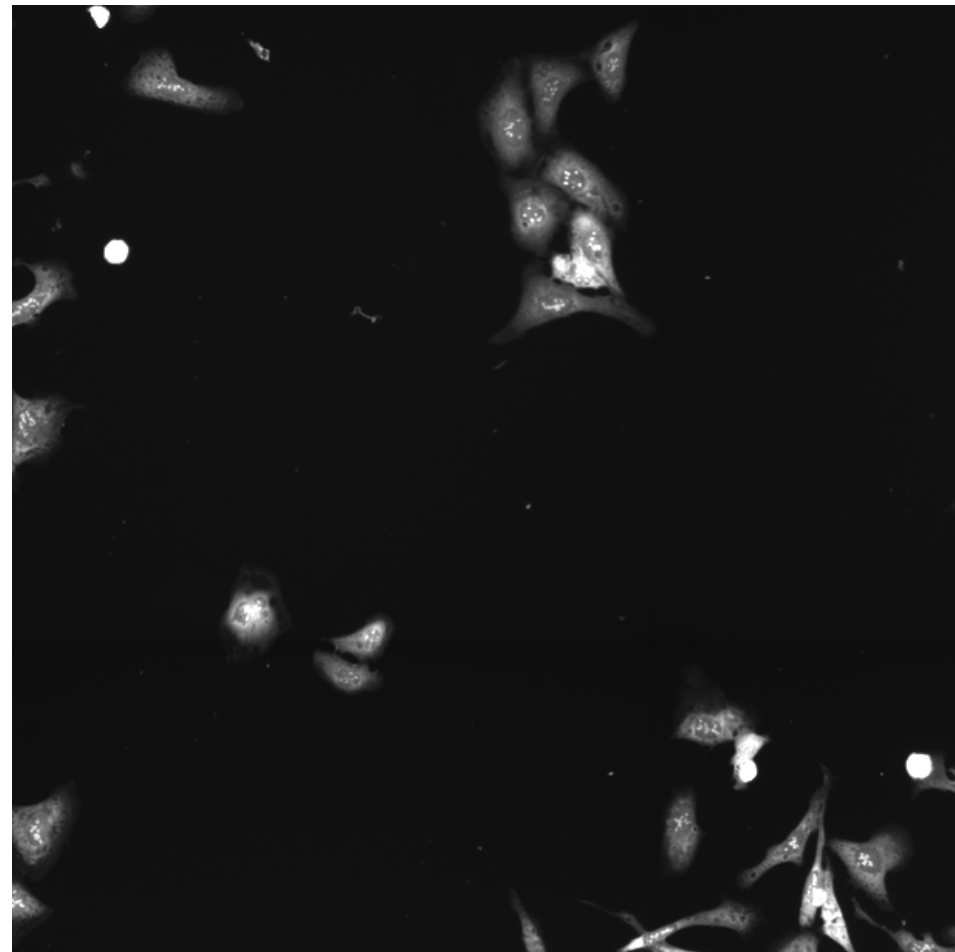
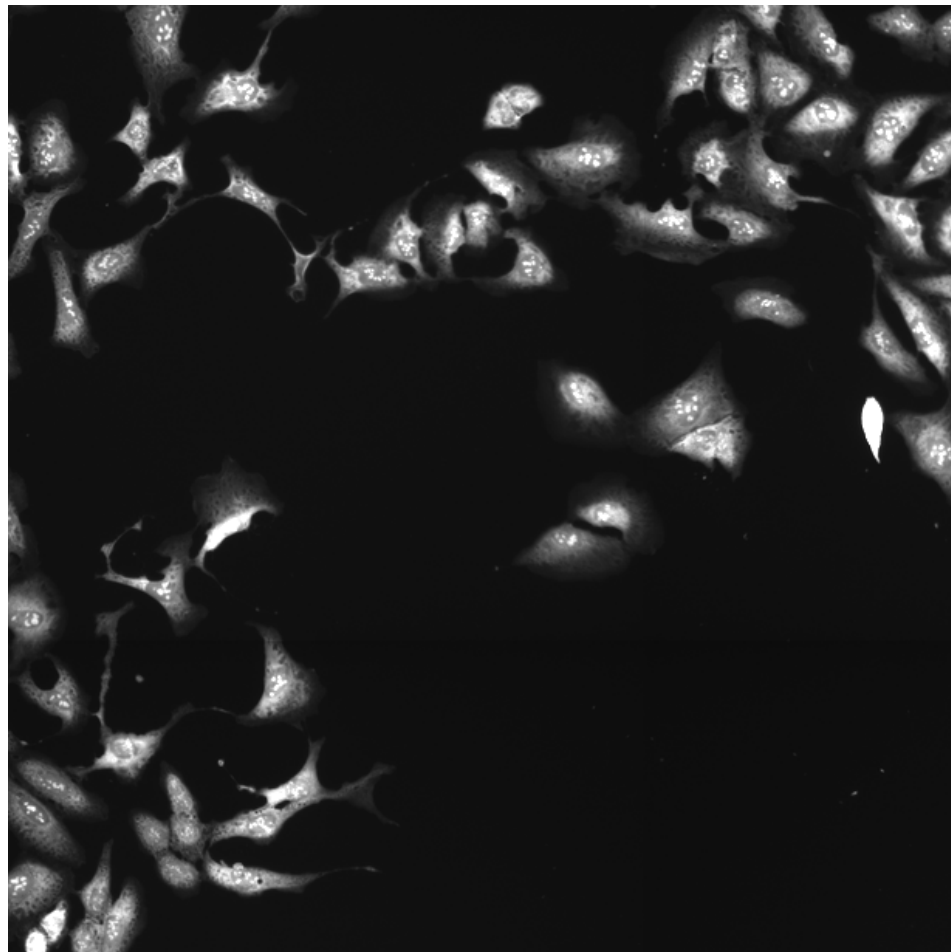
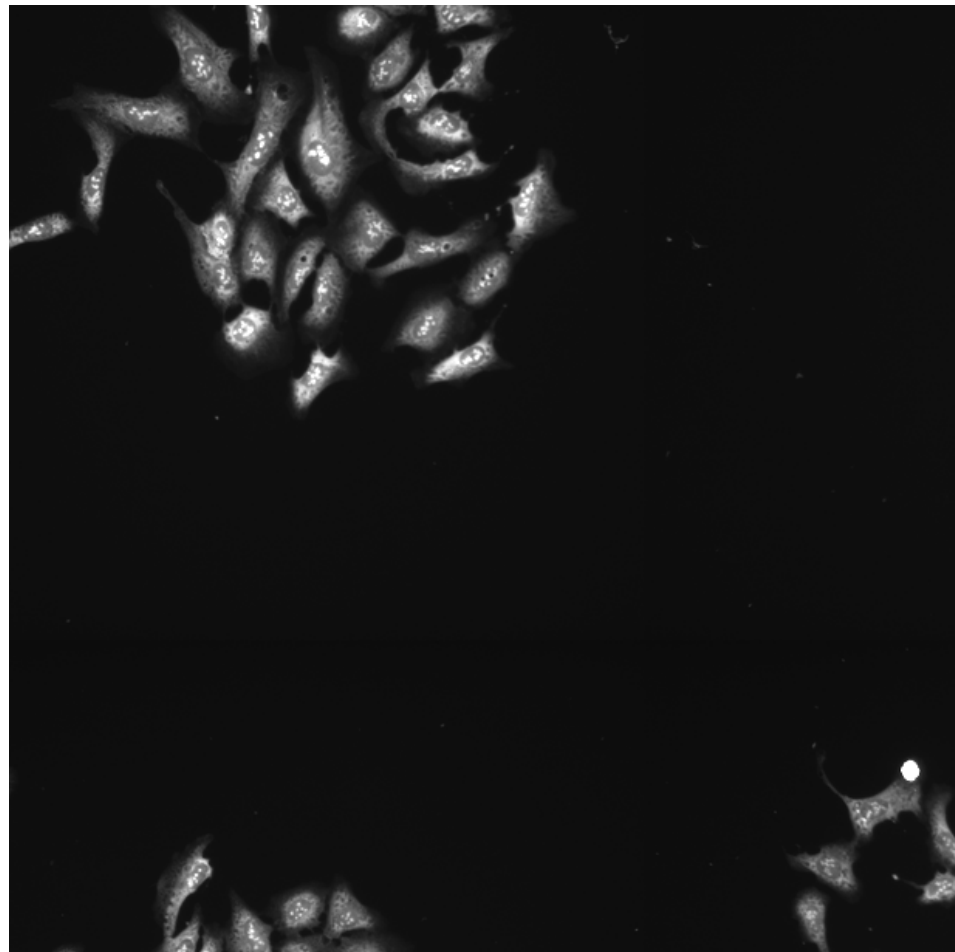
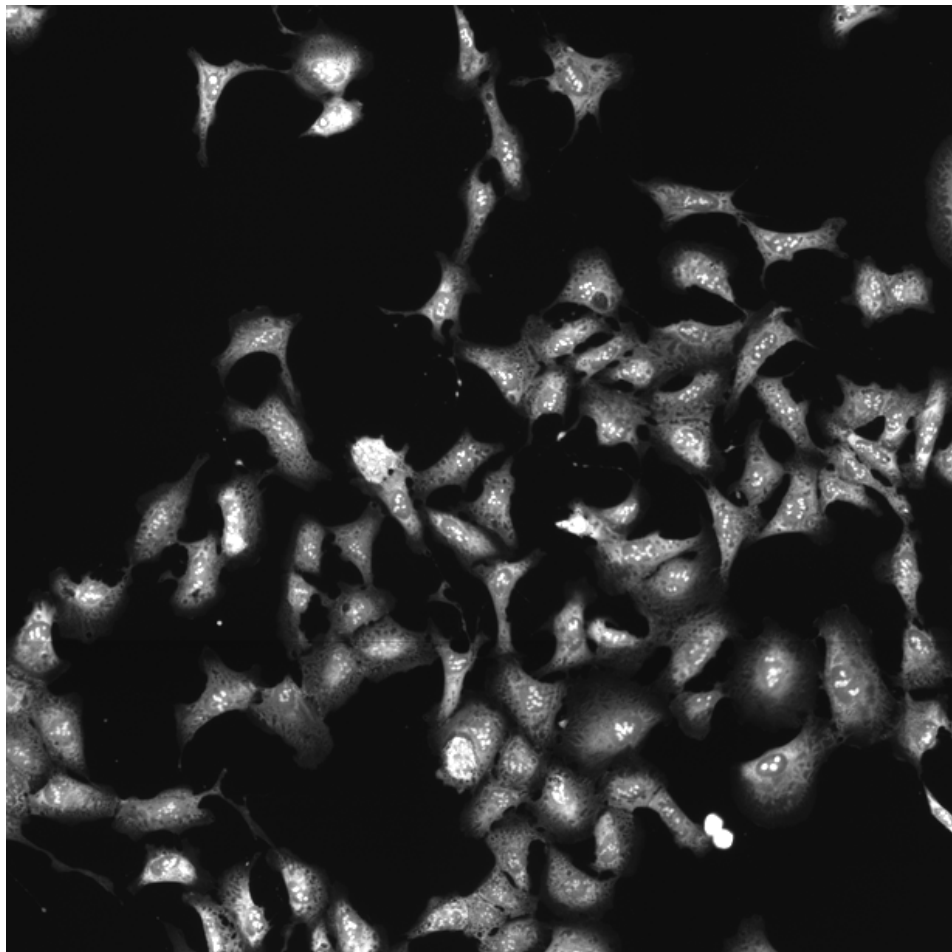
YAP1.WT.2 (41757)

YAP1.WT.2 (41754)

AGP

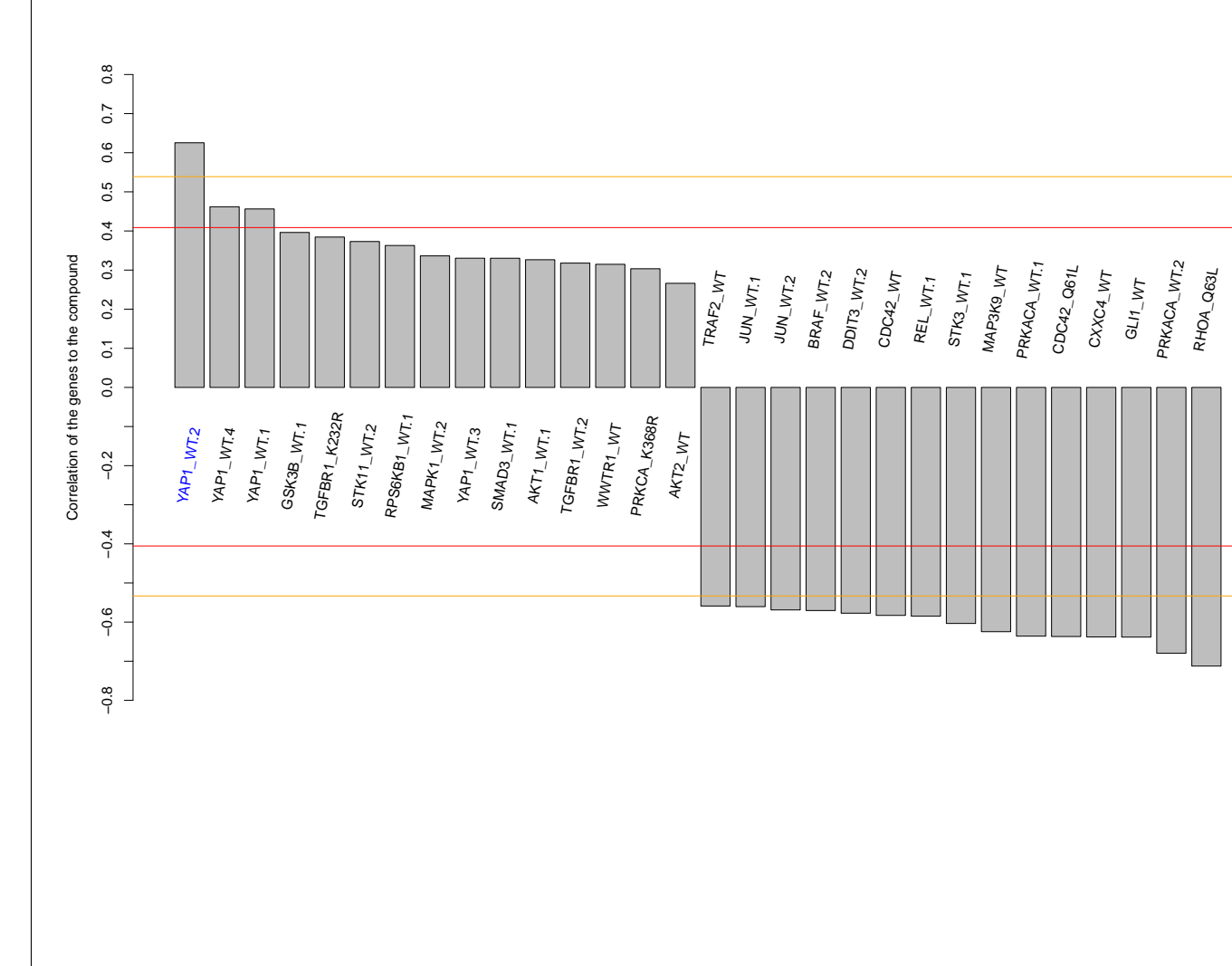
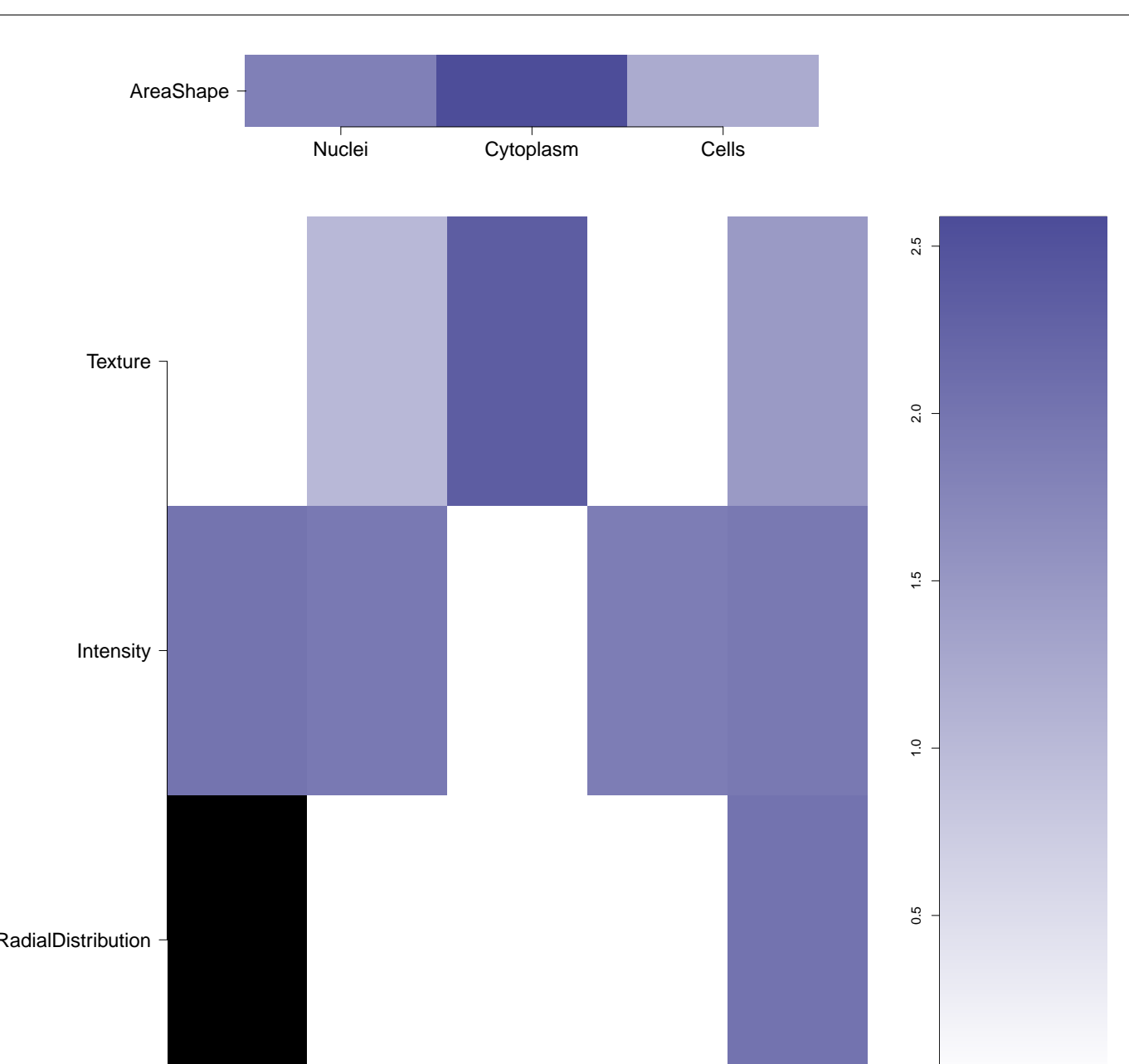

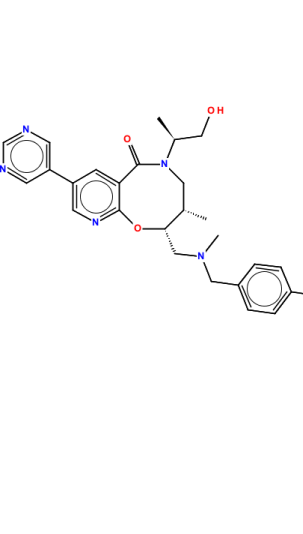
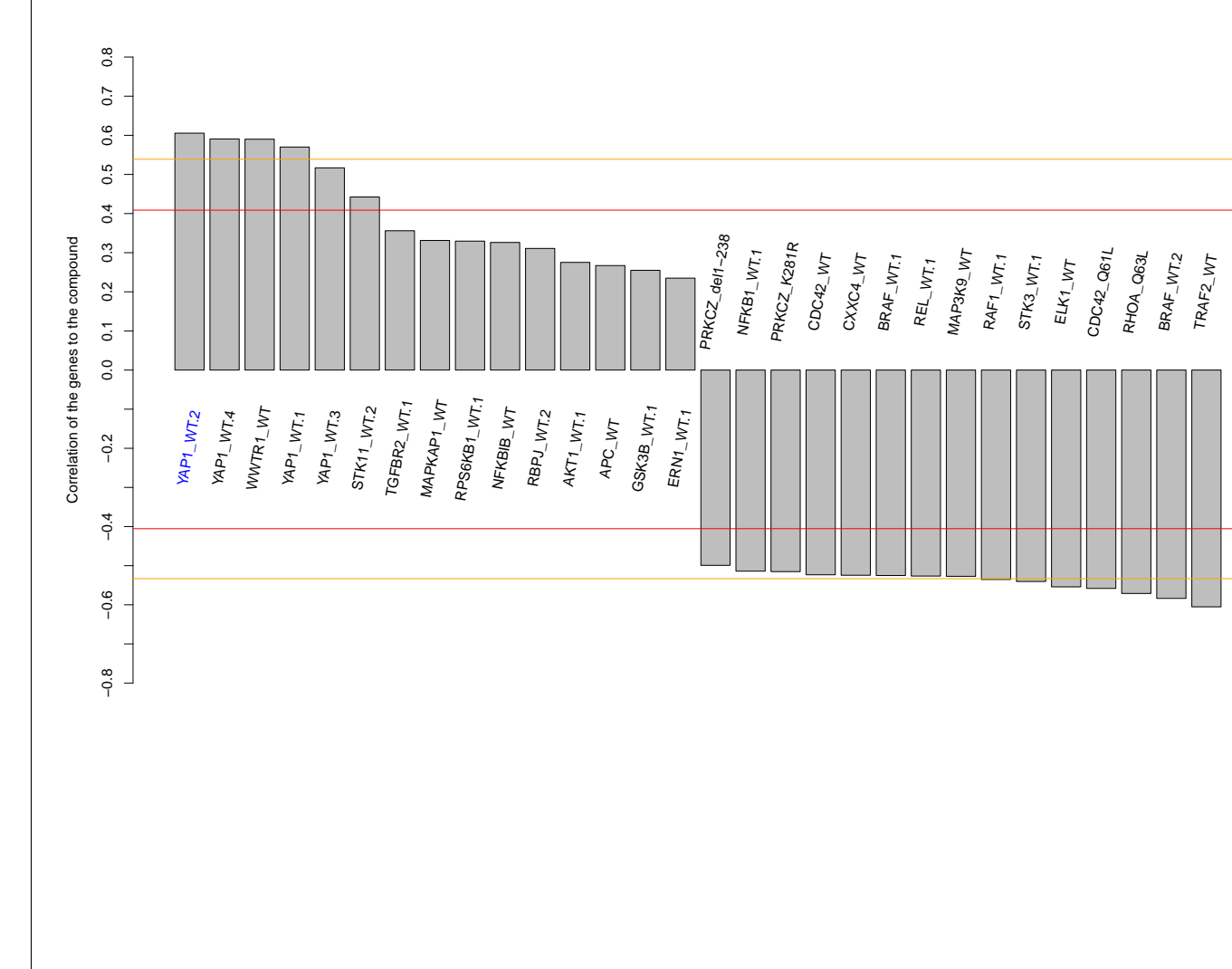
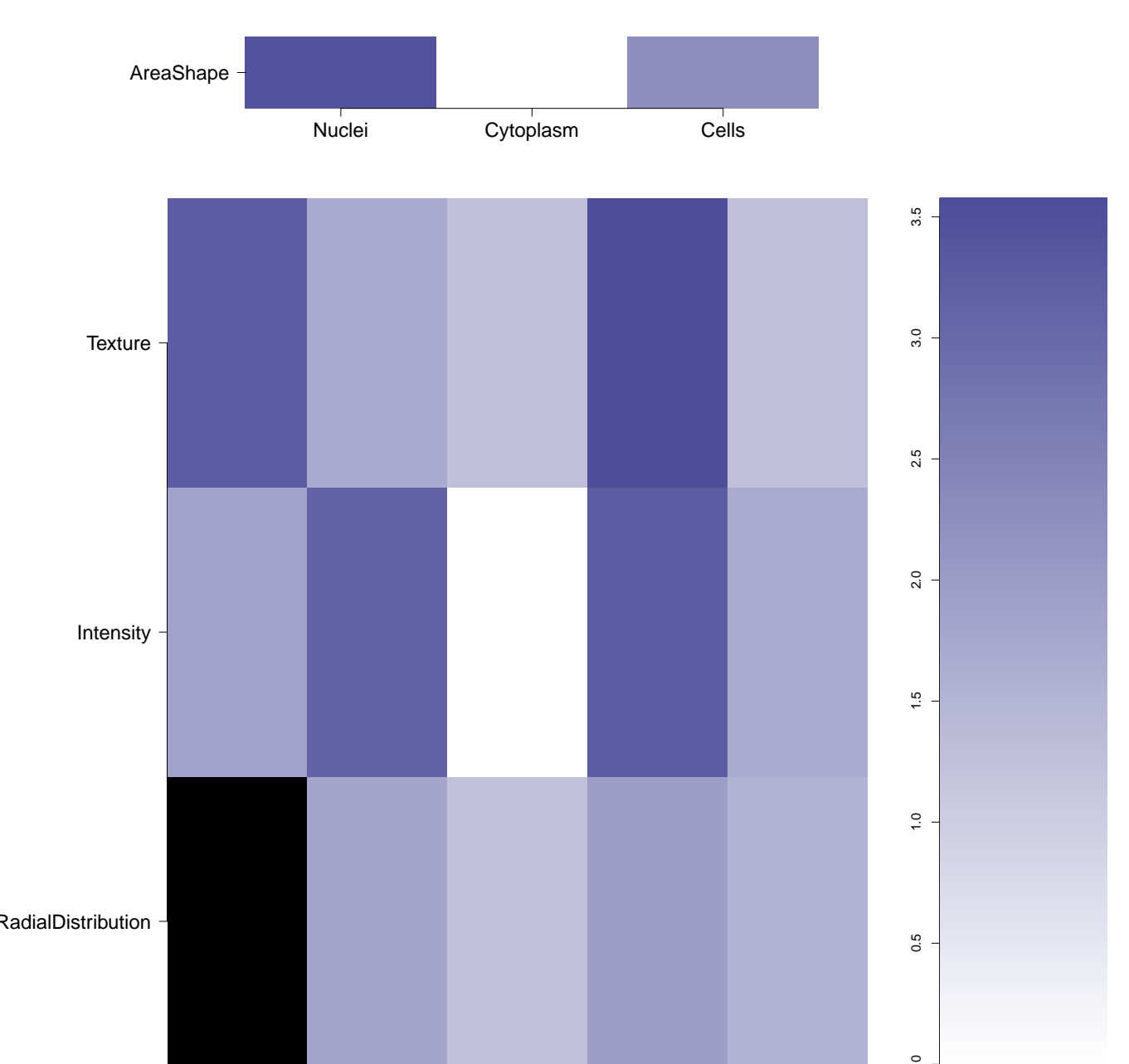
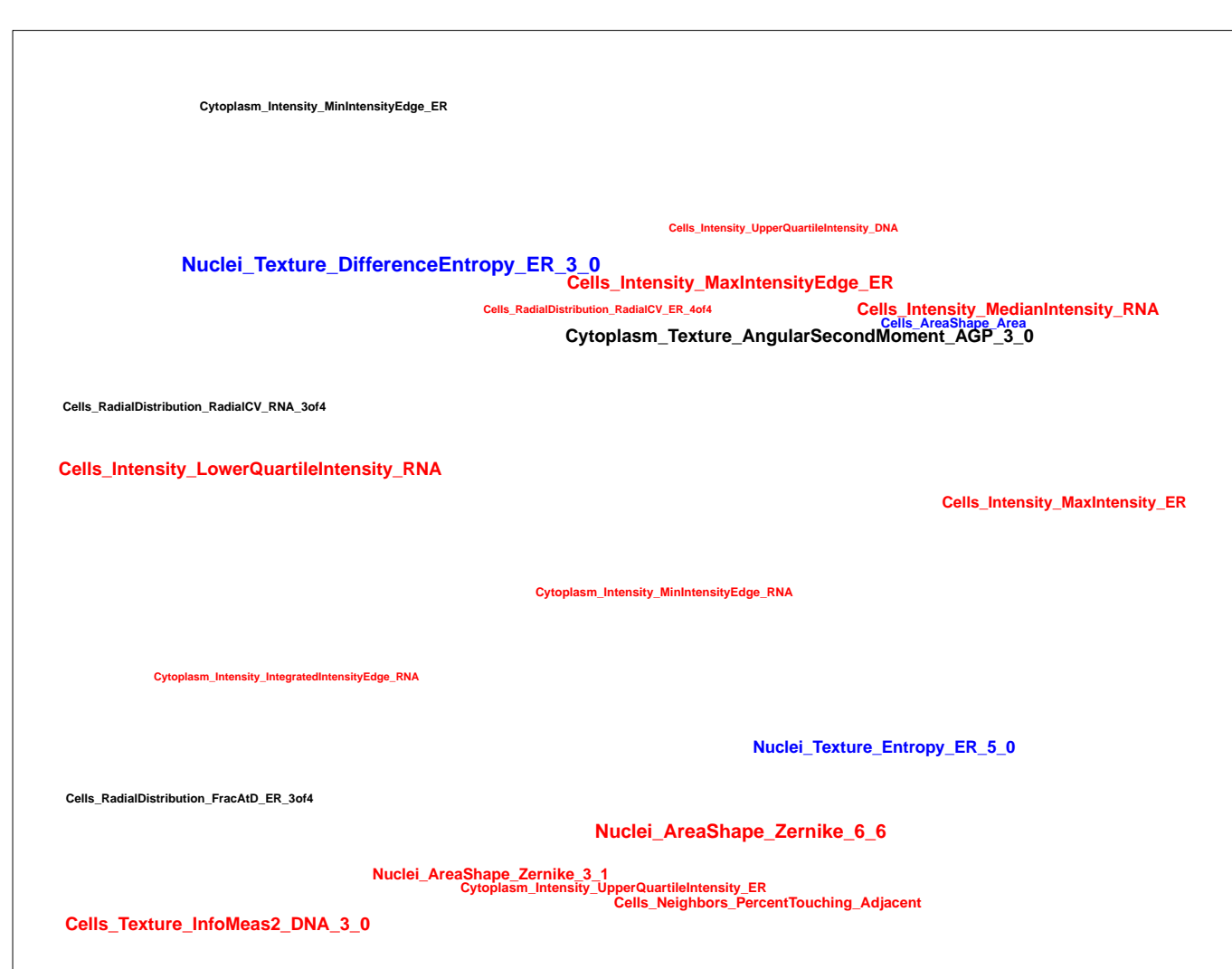
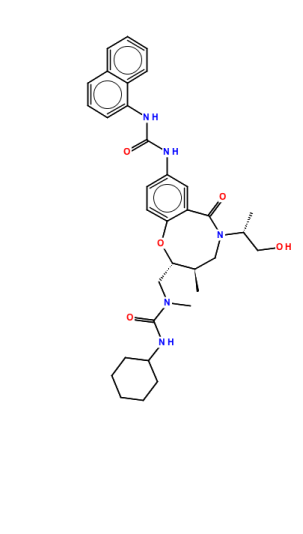
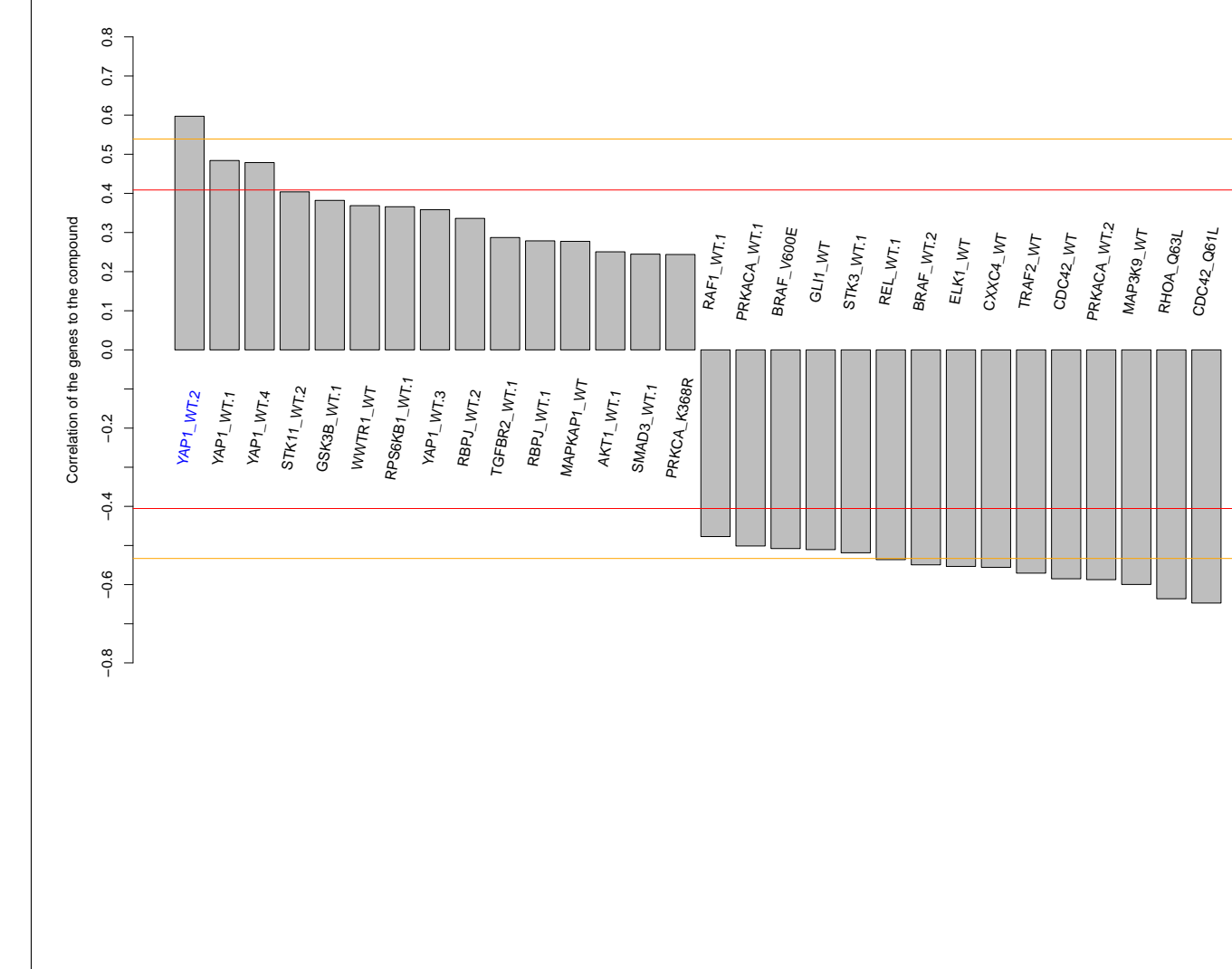
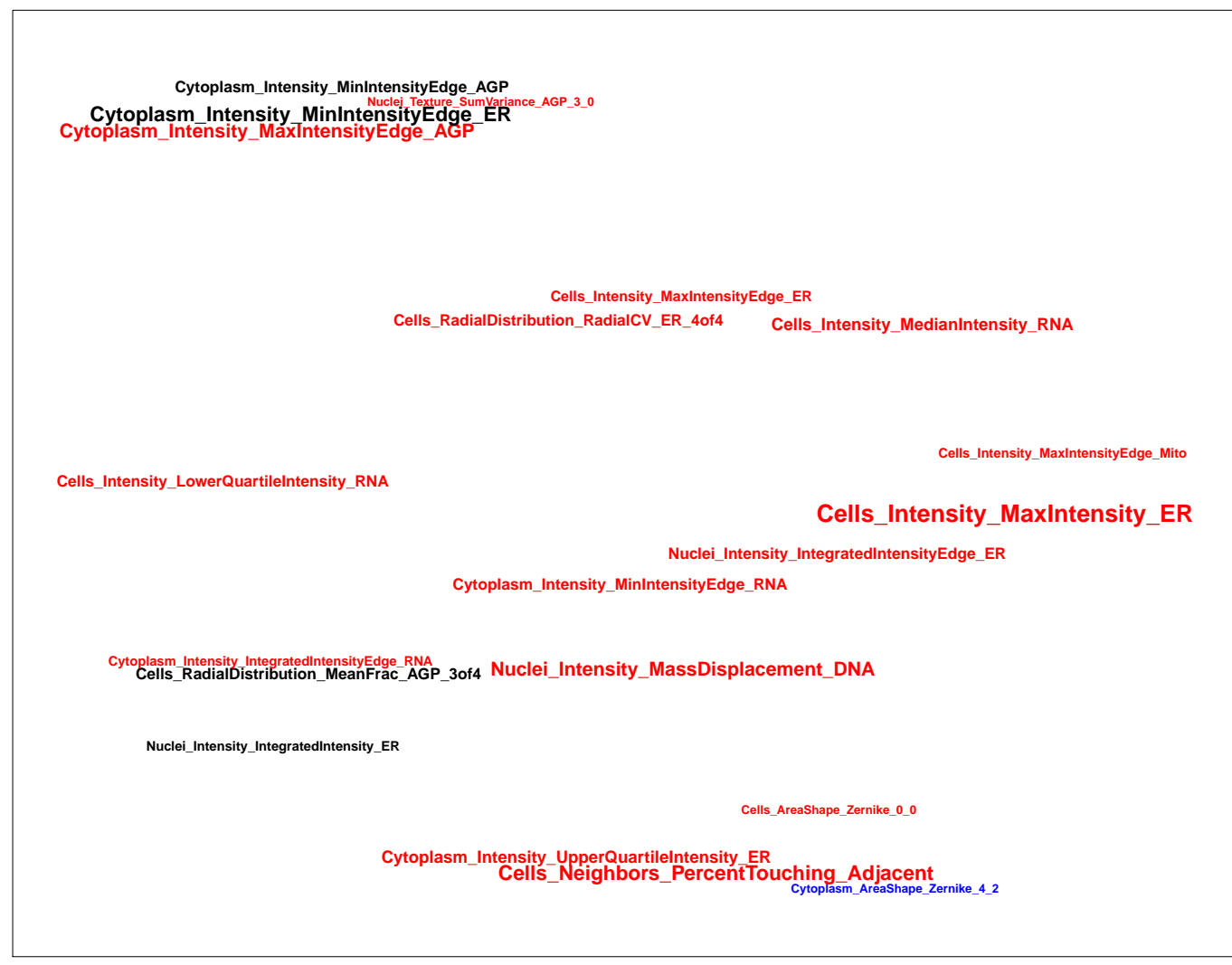
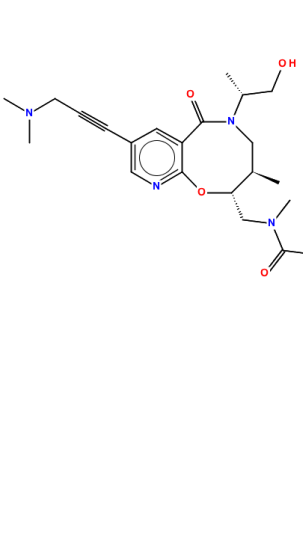
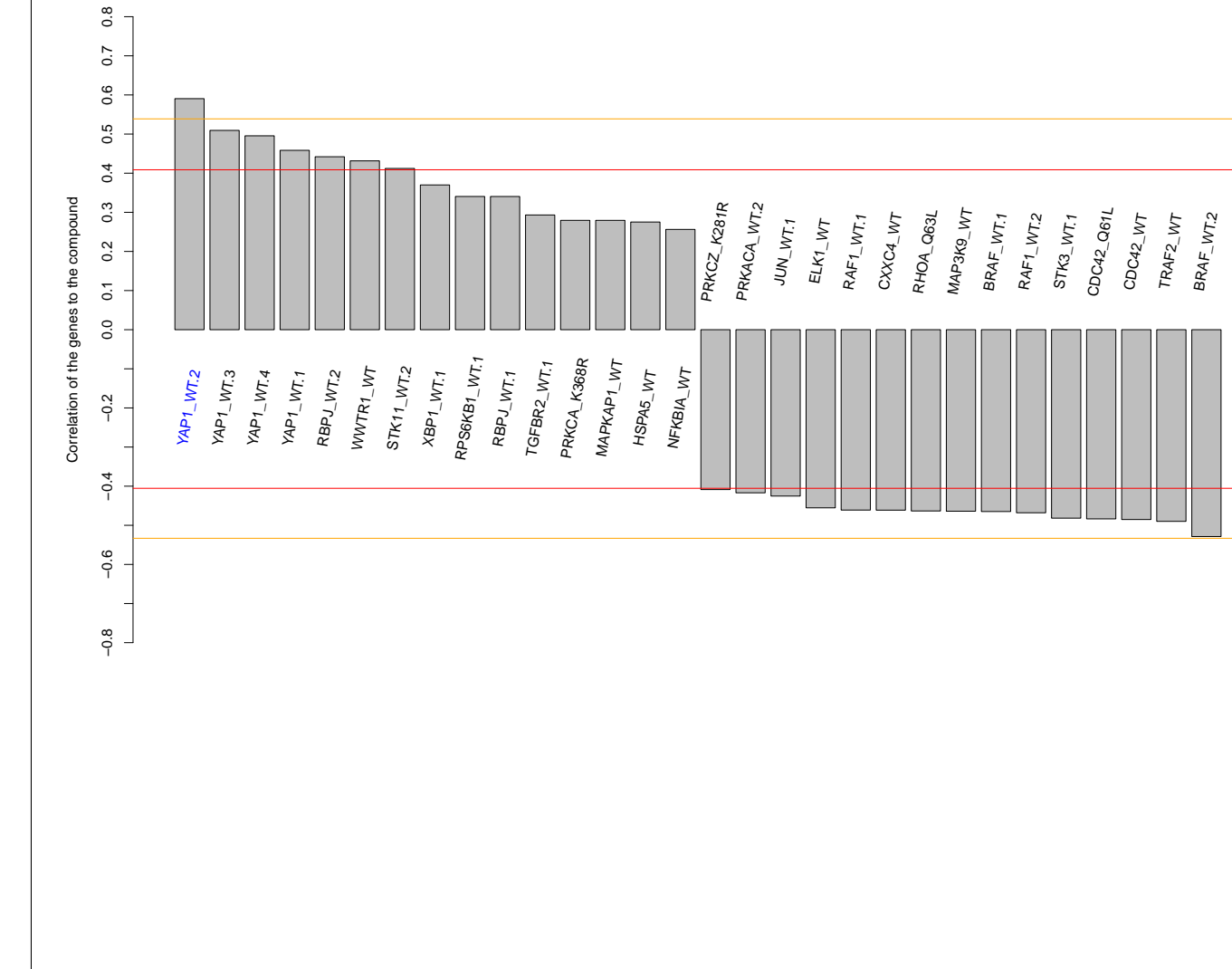
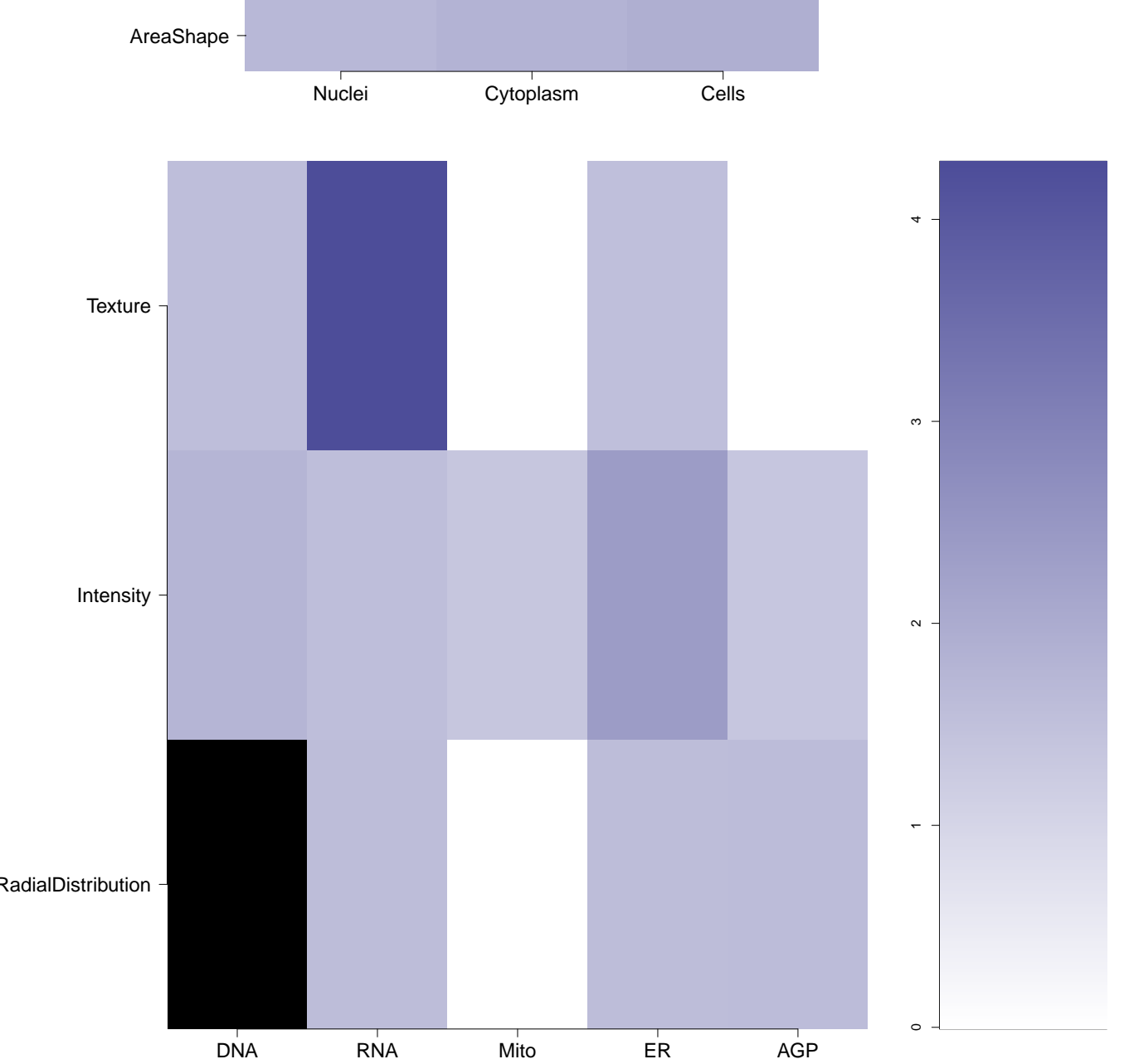
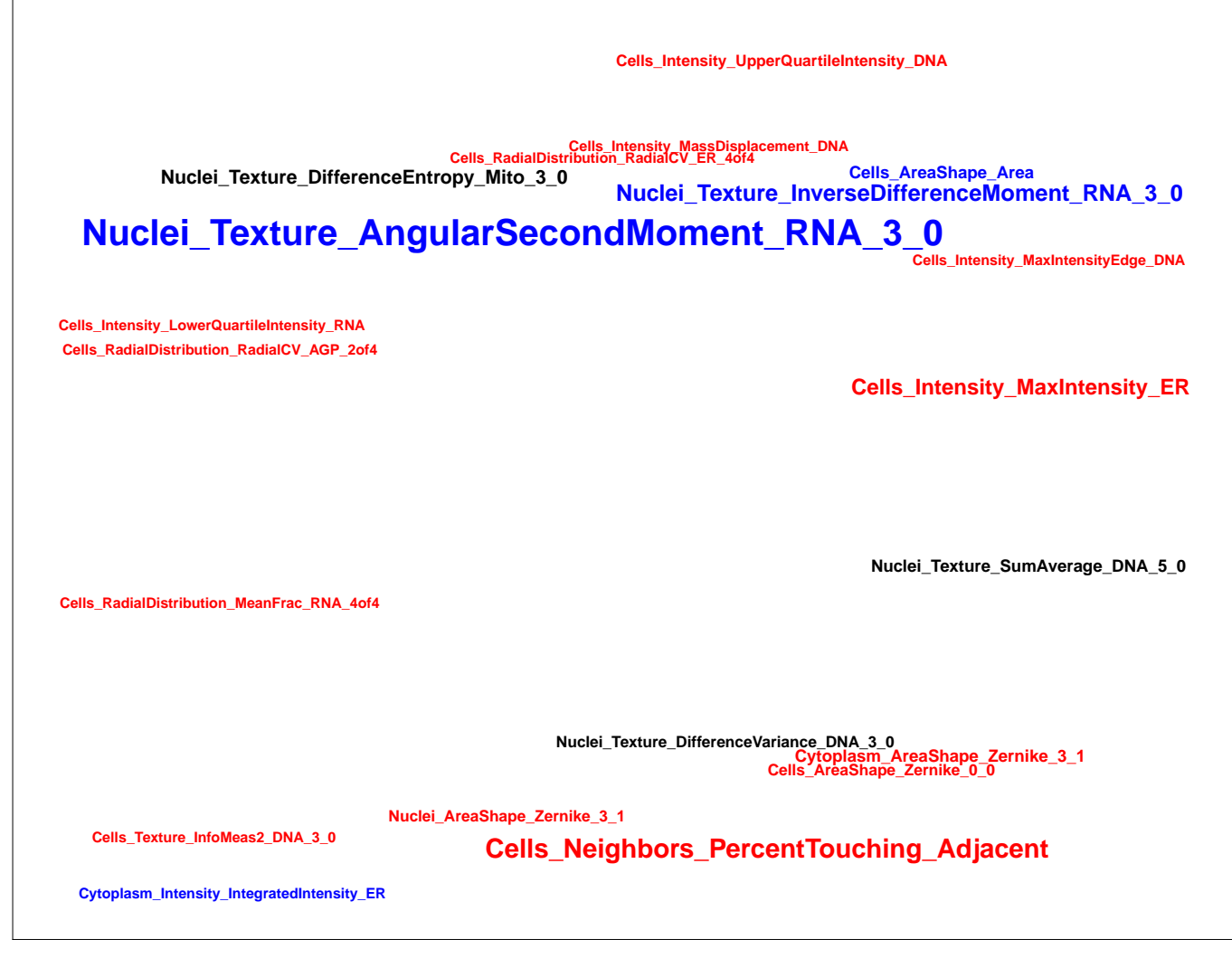
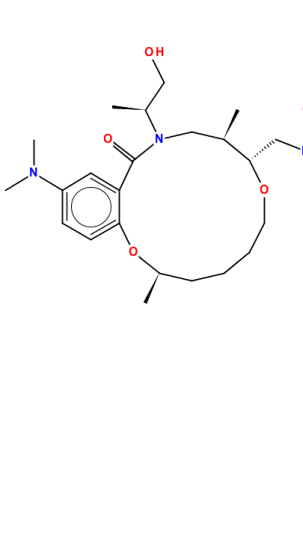
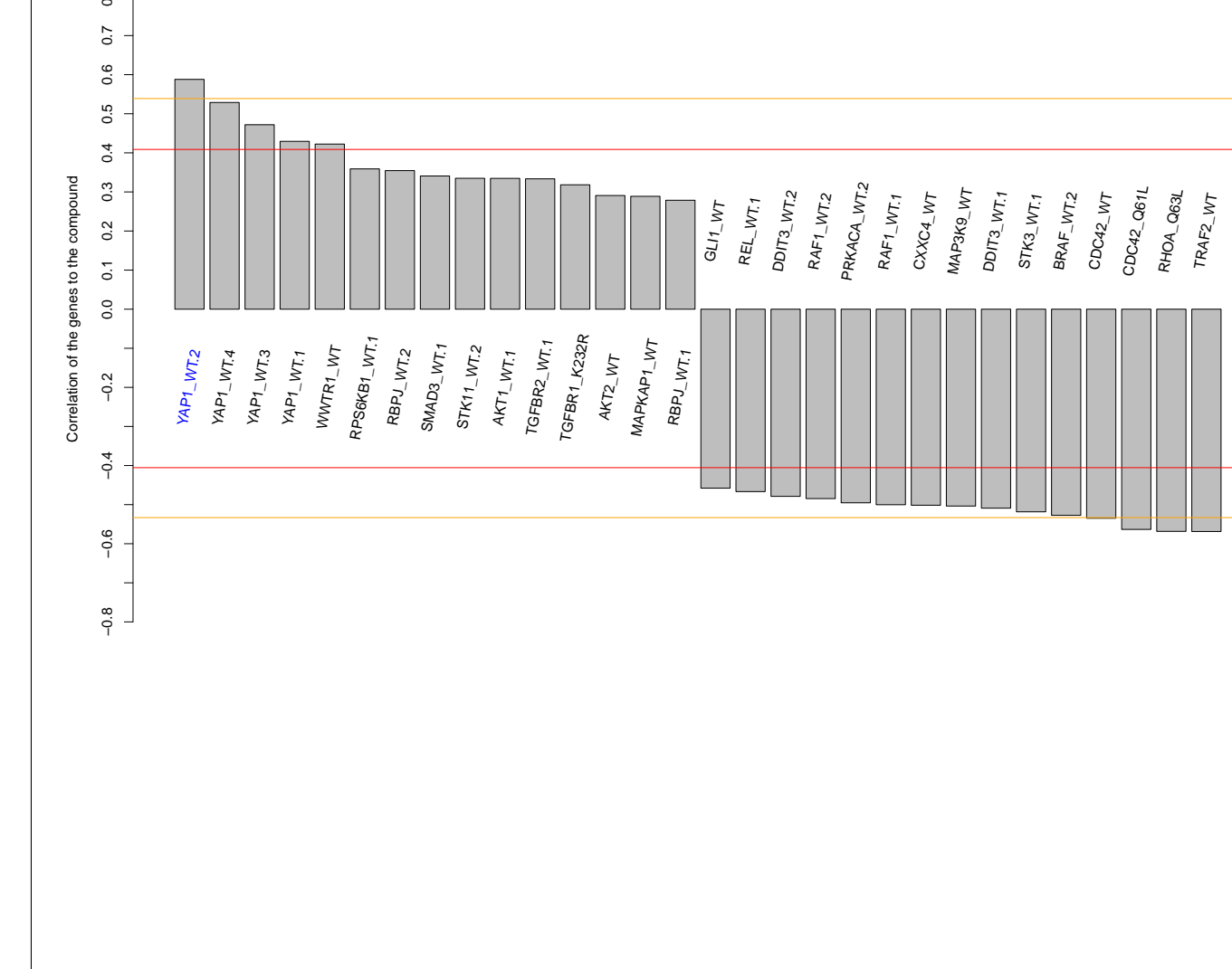
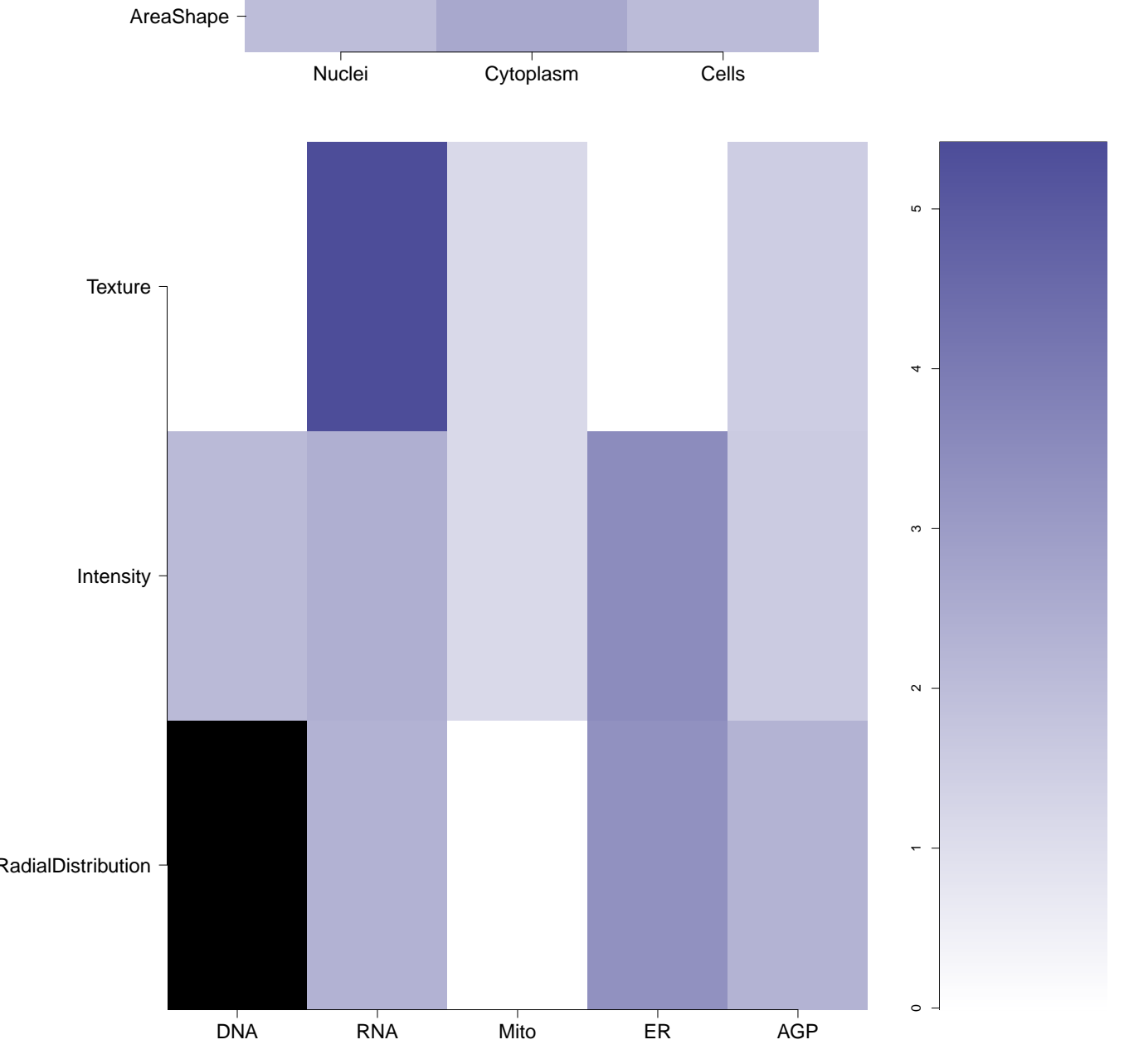
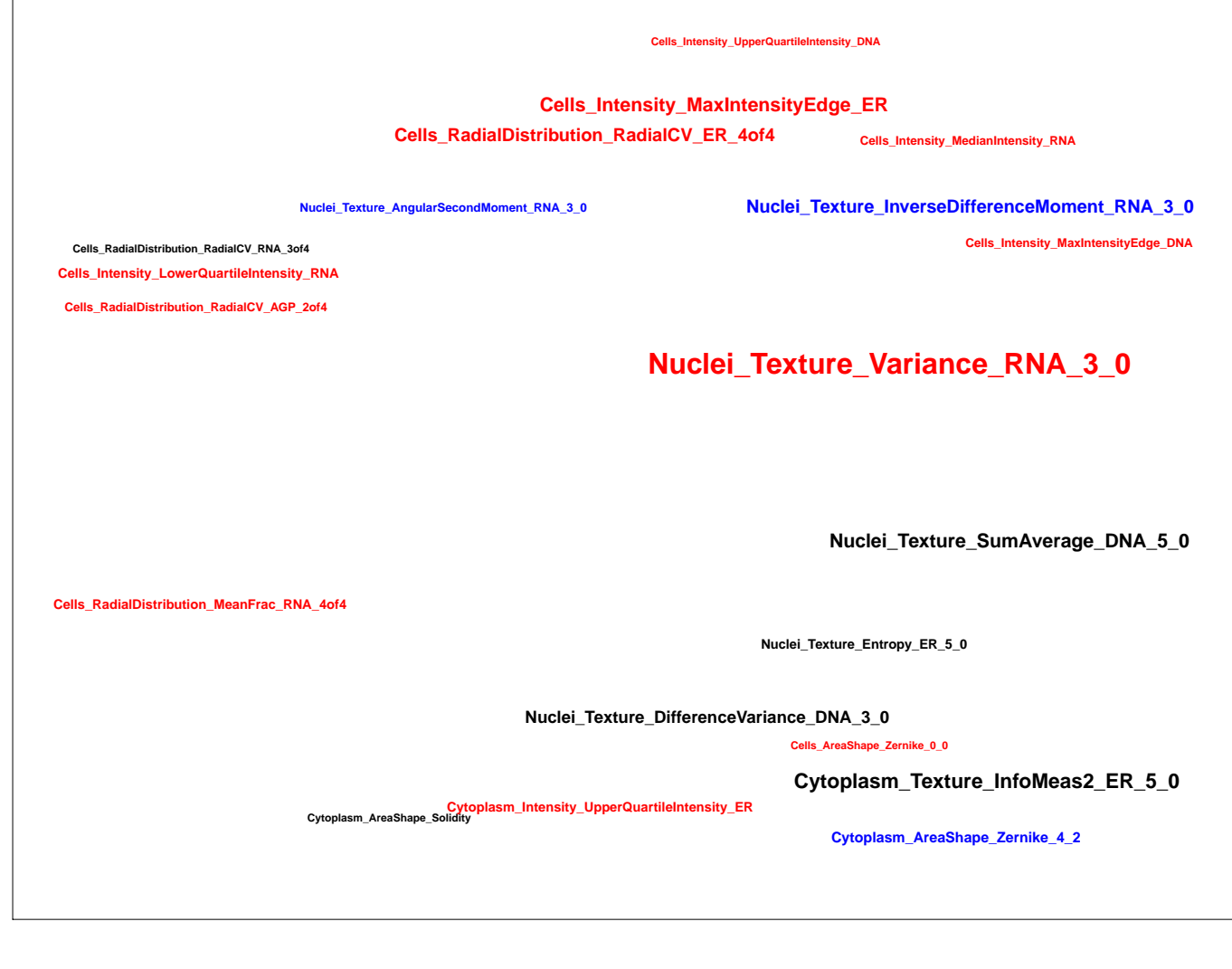
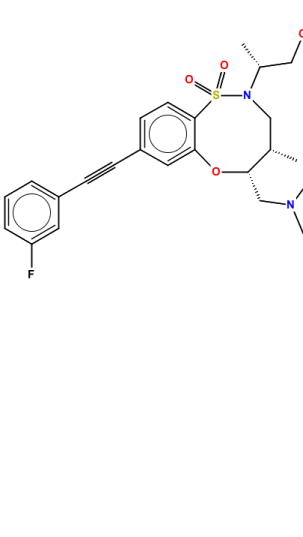
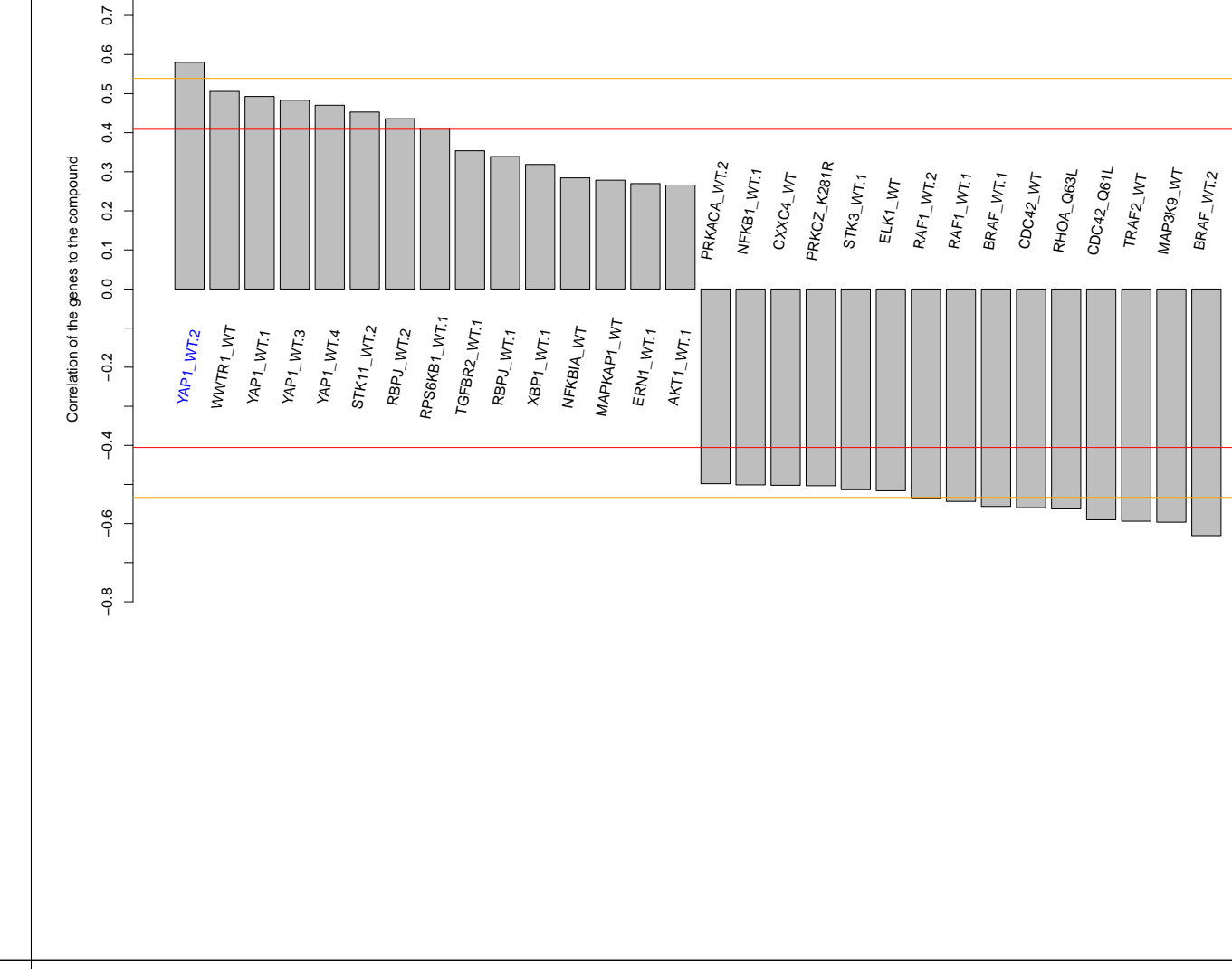
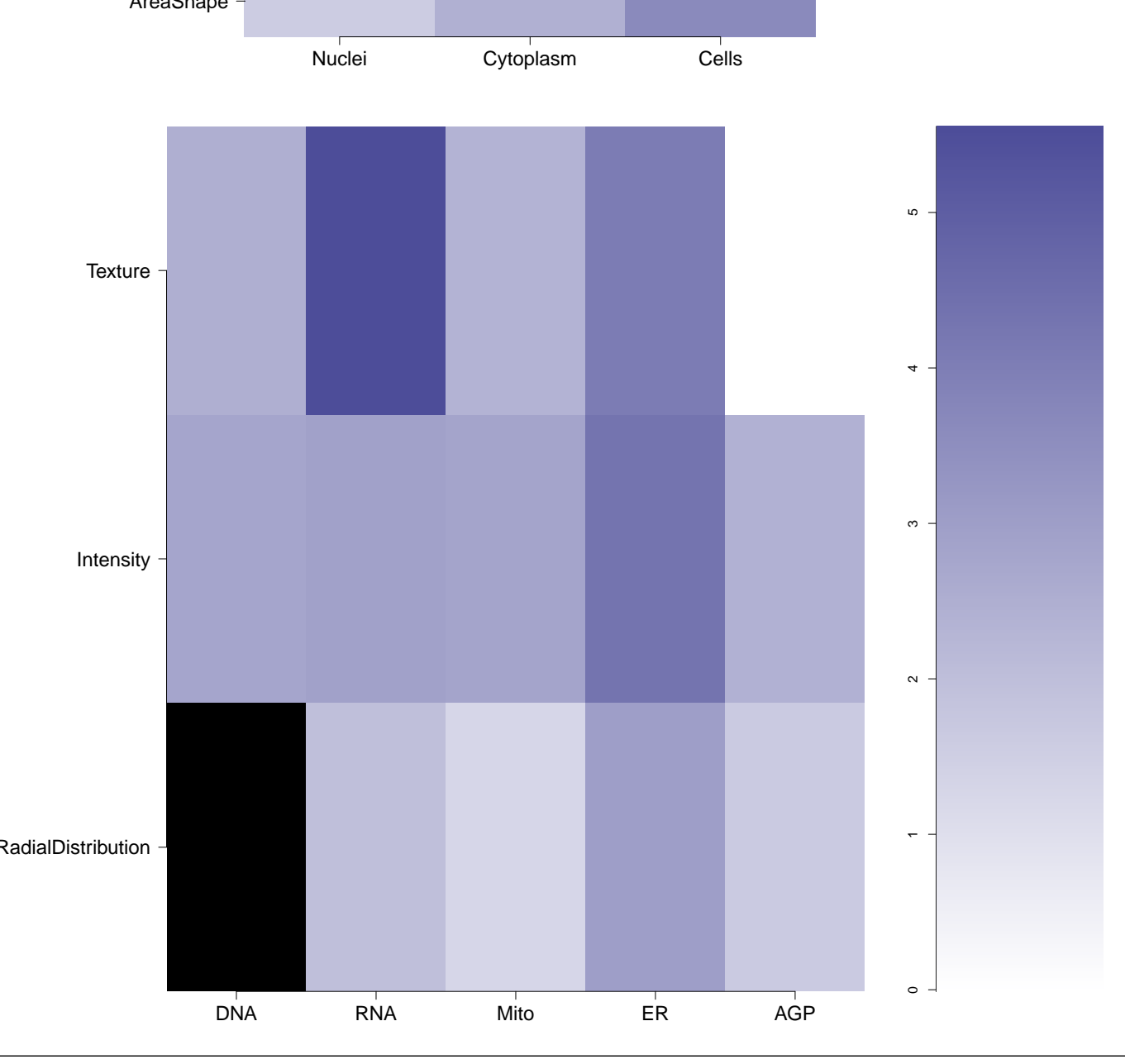

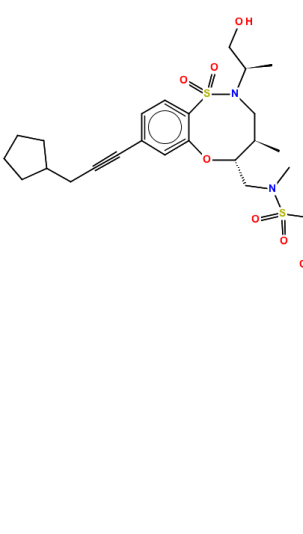
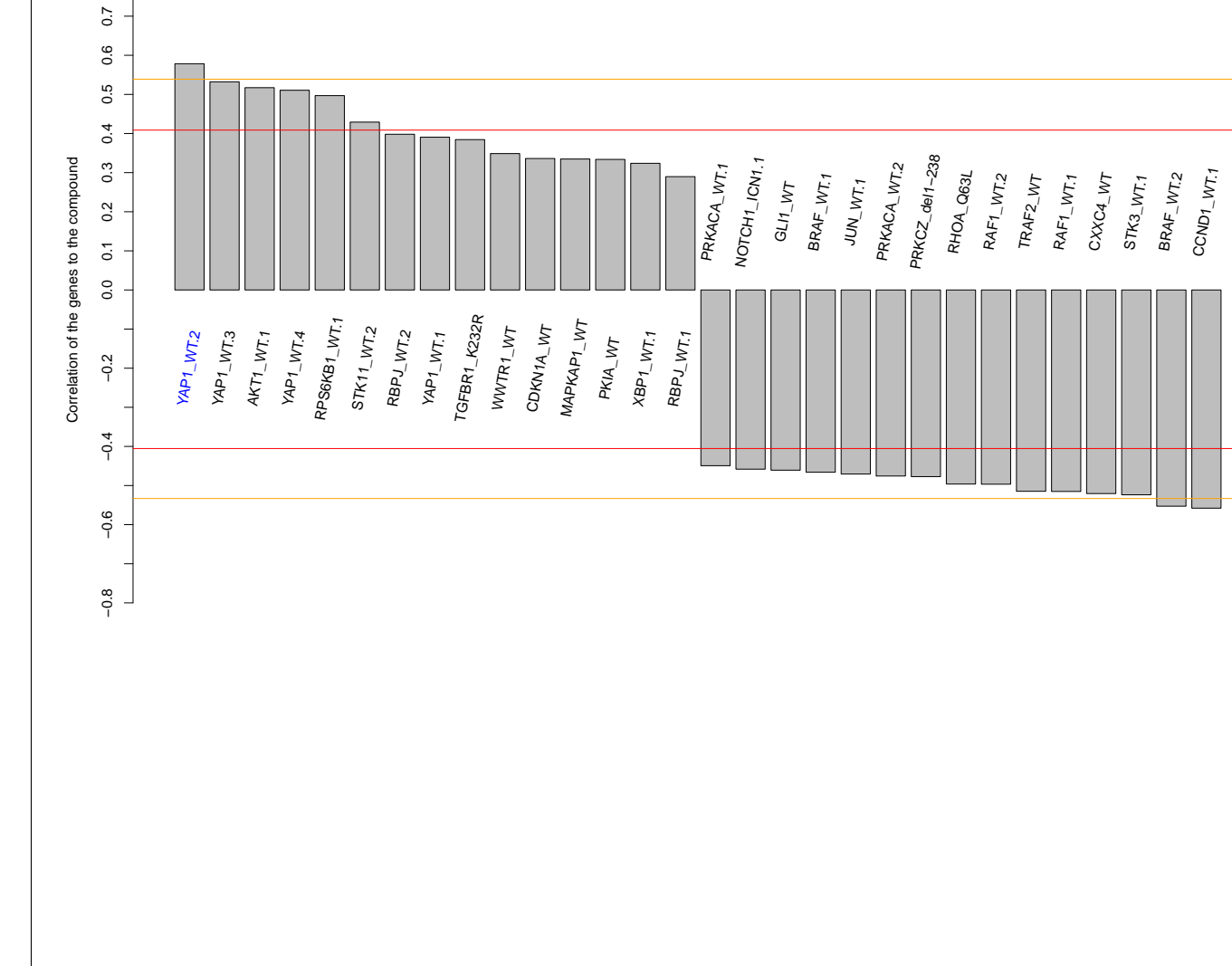
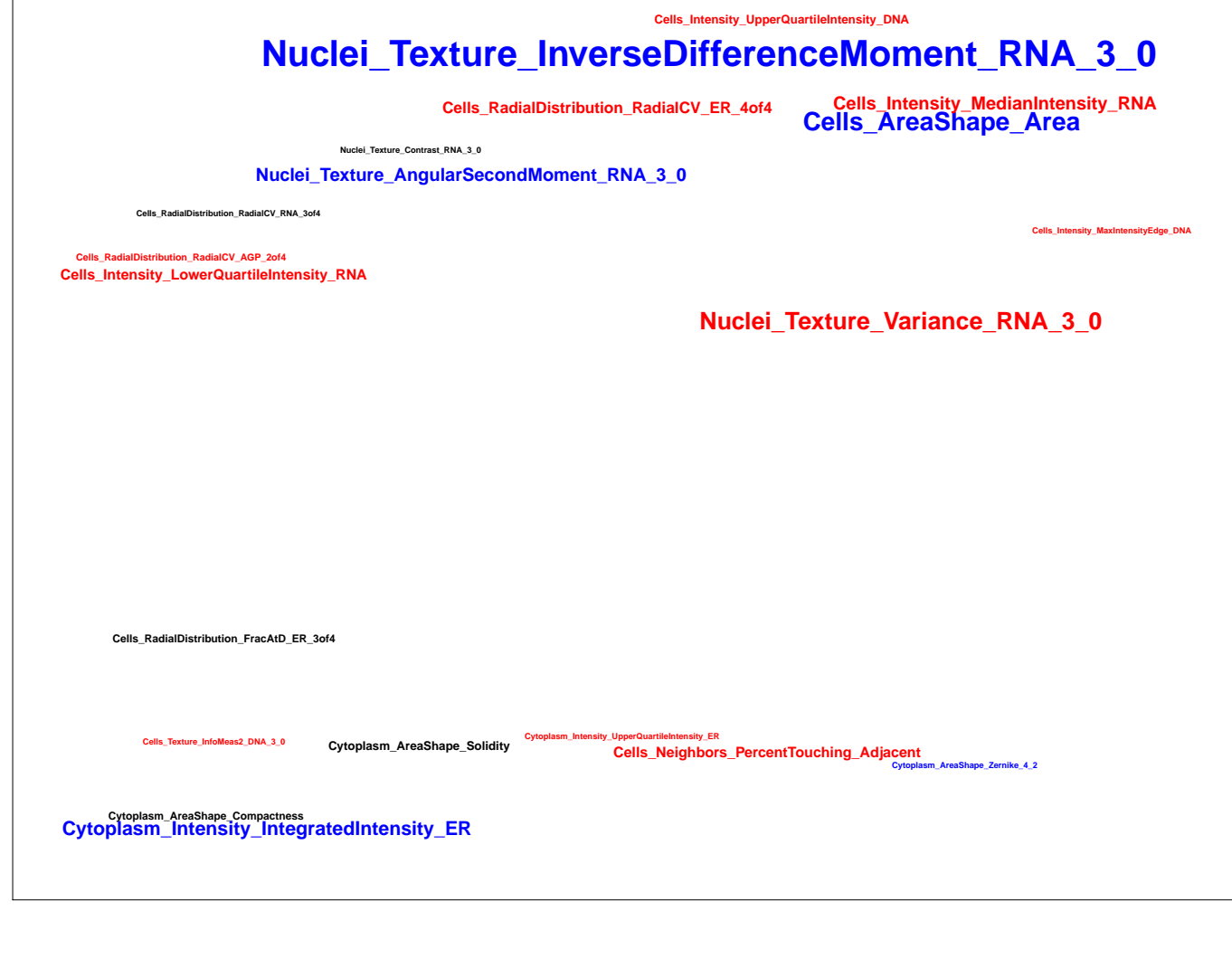


RNA



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
--	--------------------	--	---------------------------------------	--	---	---	---	---

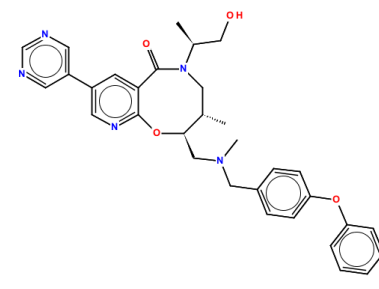
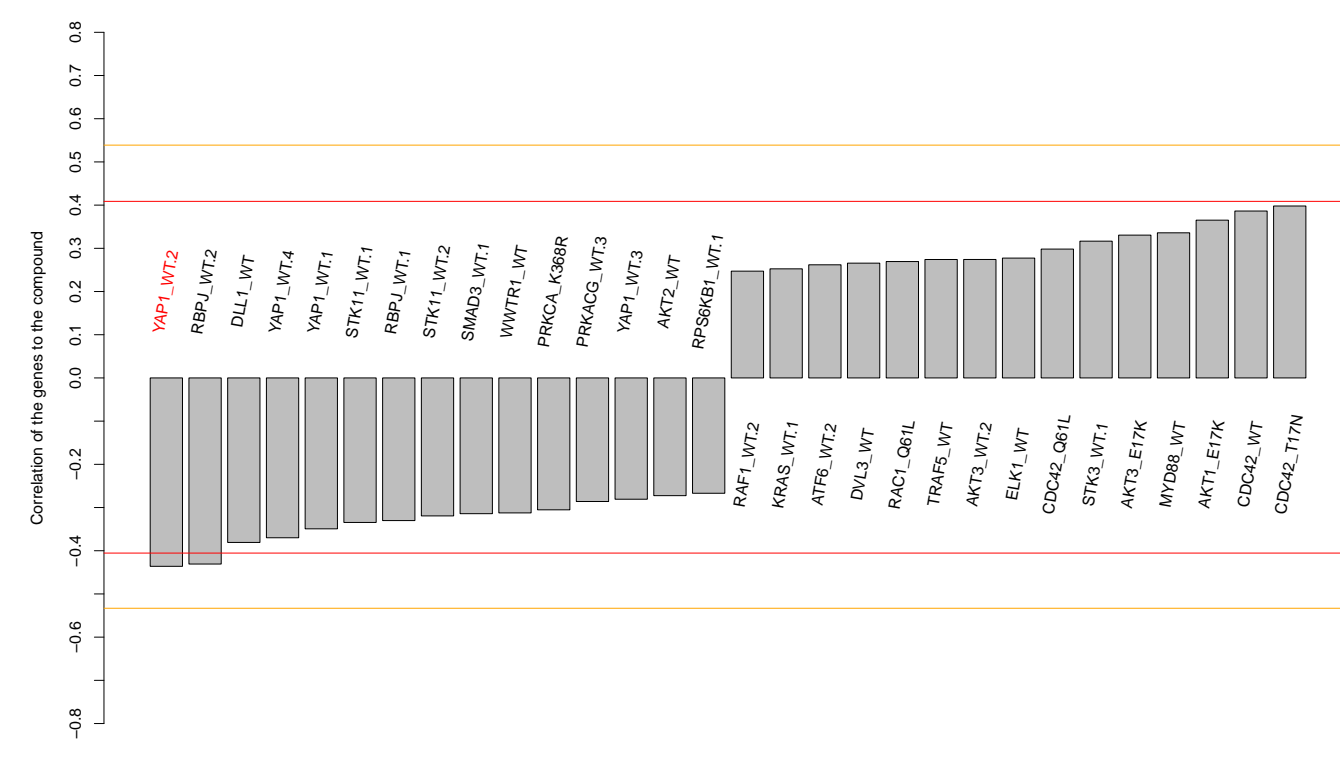
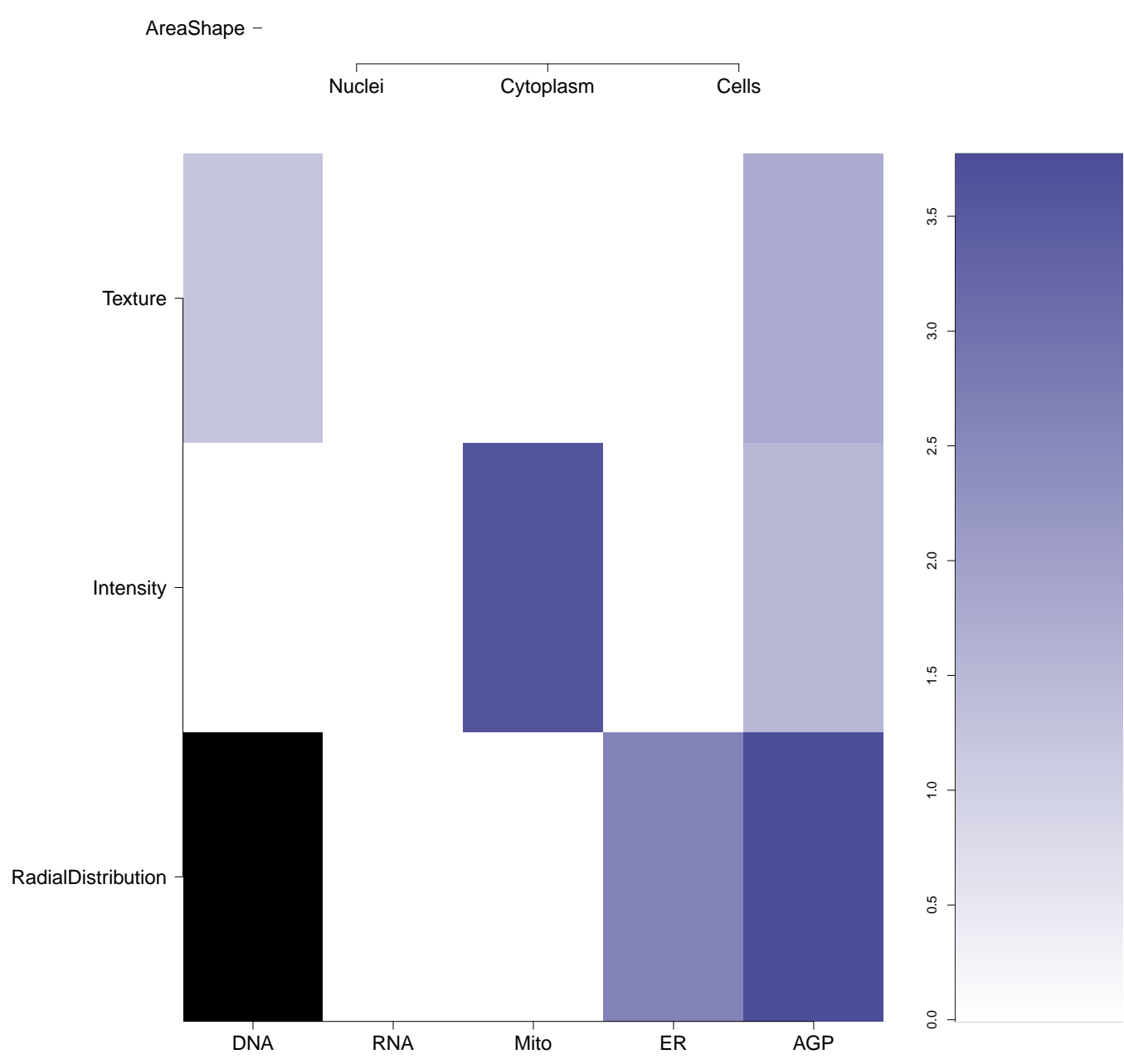
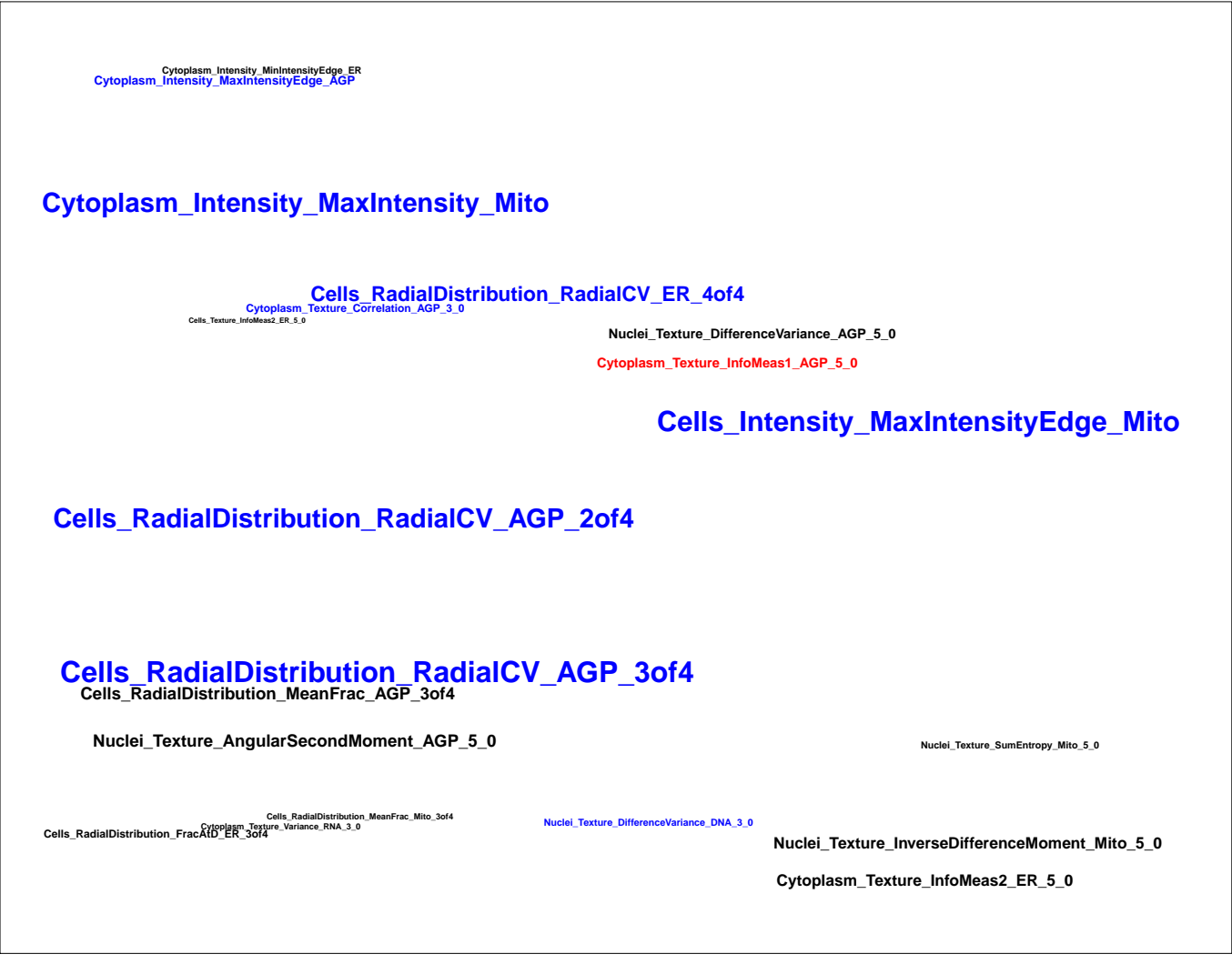
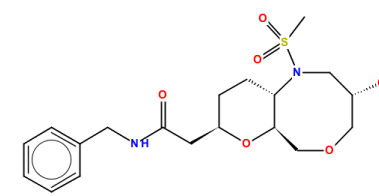
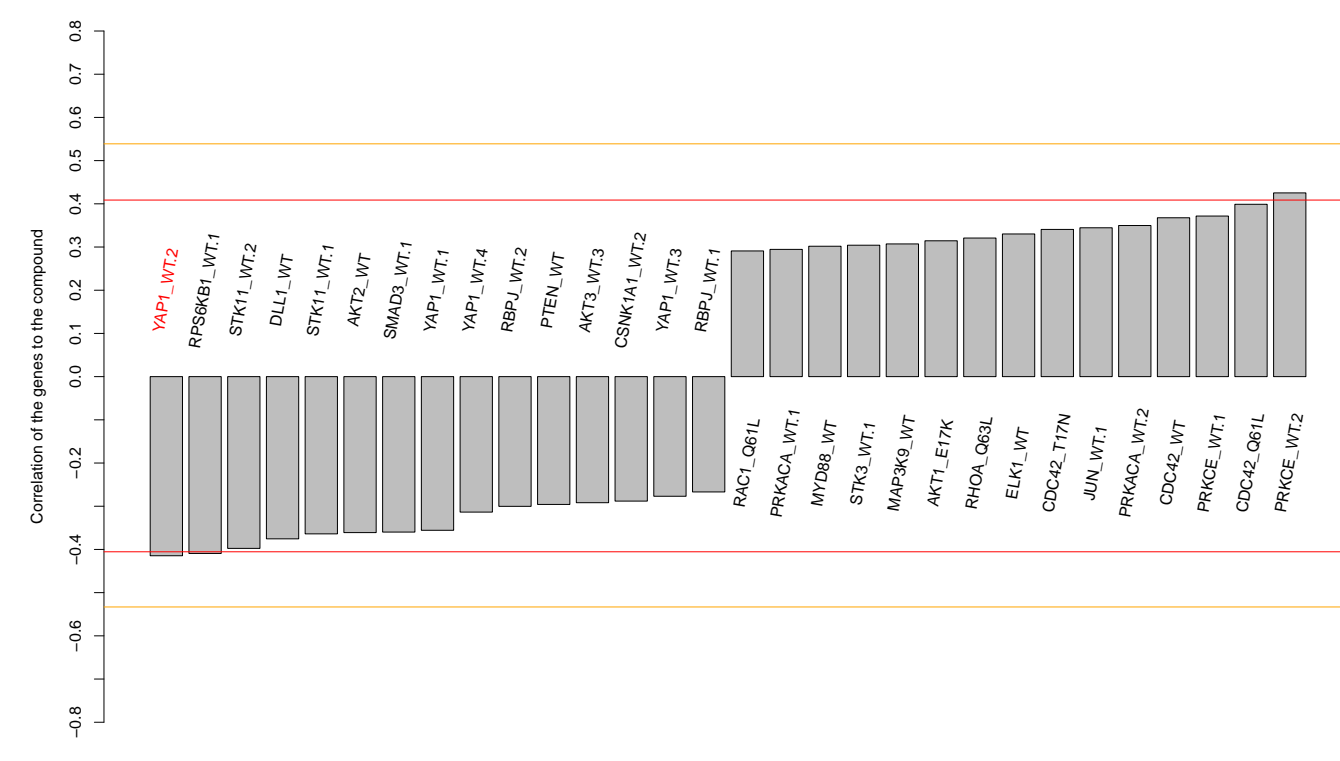
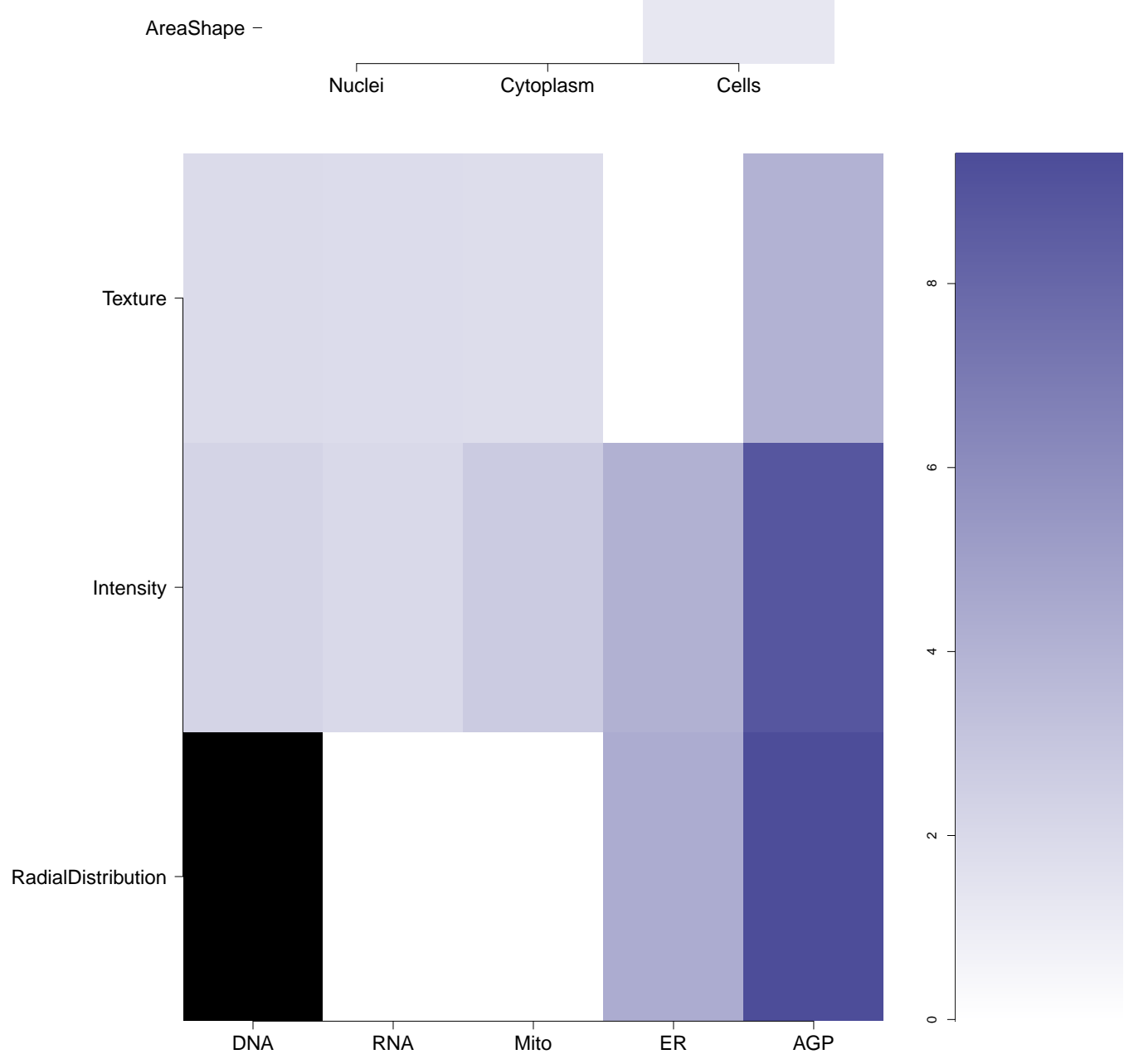
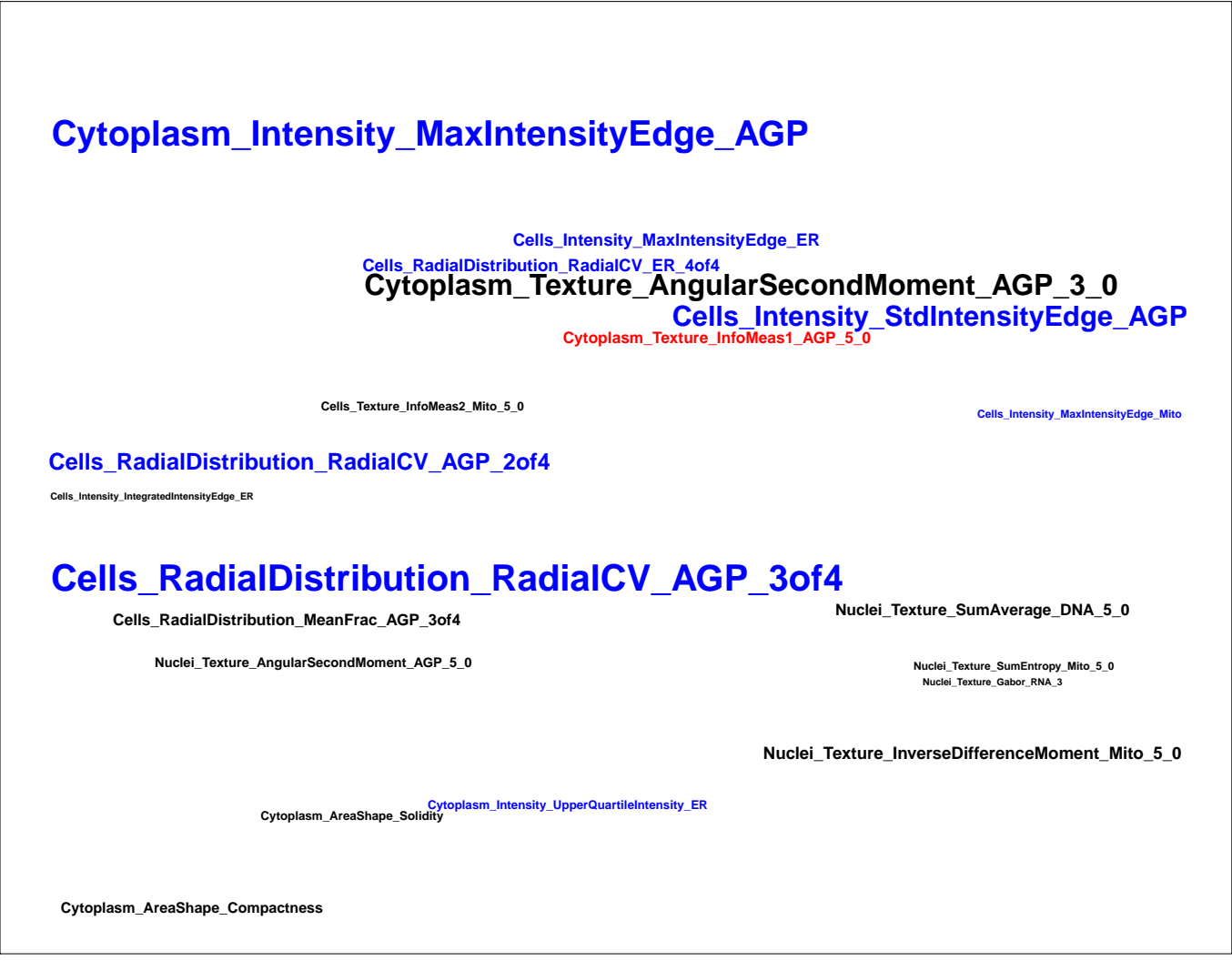
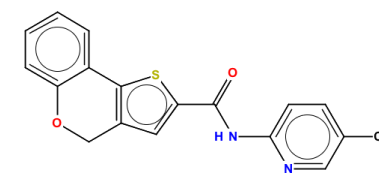
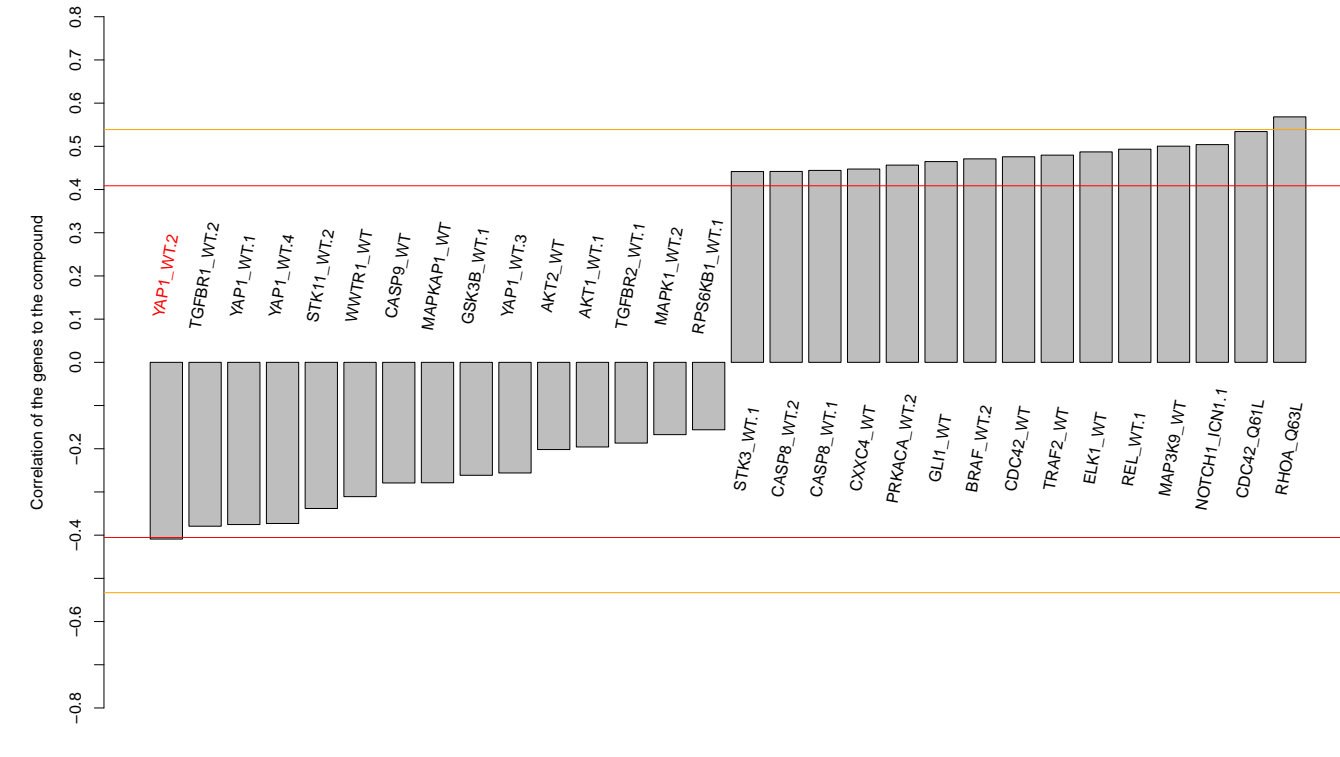
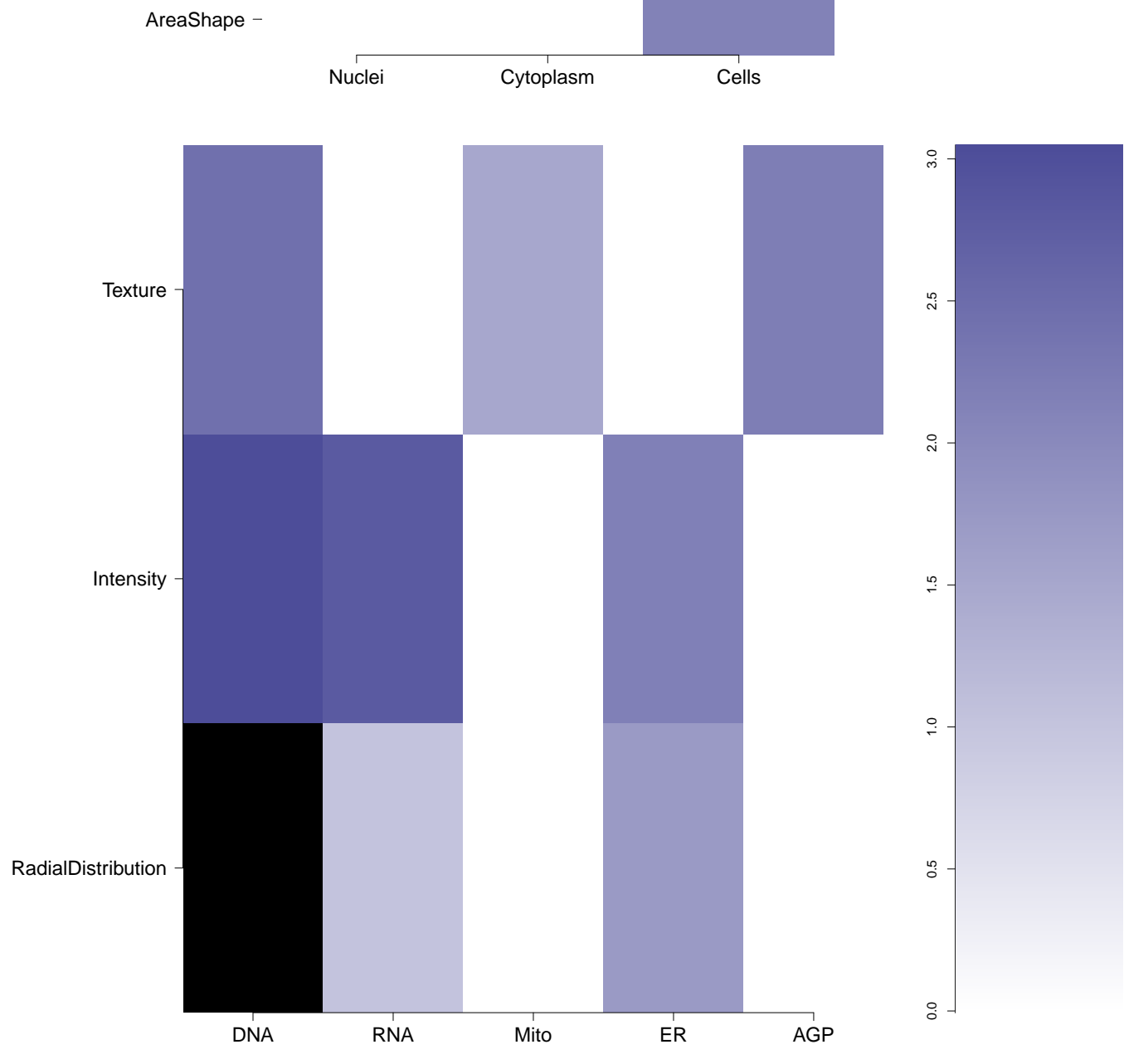
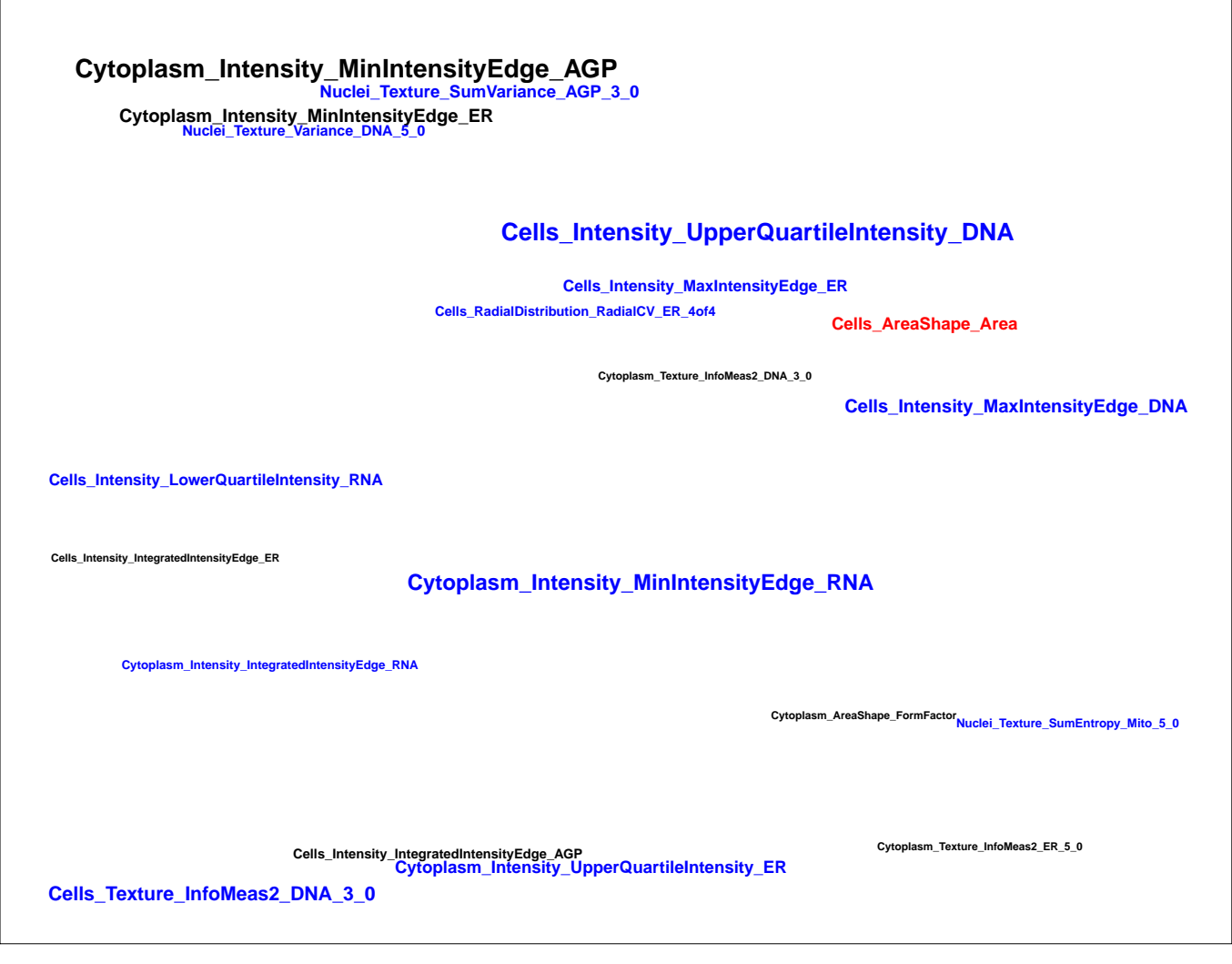


BRD-K58469266-001-01-0 PubChem CID : 54646063		NA (in 1 replicates)	0.63	0.767				Total number of assays tested in: 39.
BRD-K88597074-001-01-4 PubChem CID : 54618422		0.81 (in 4 replicates)	0.61	0.767				Total number of assays tested in: 36.
BRD-K91399333-001-01-7 PubChem CID : 44490007		0.66 (in 3 replicates)	0.60	0.862				Total number of assays tested in: 57.
BRD-K03331449-001-01-8 PubChem CID : 54619602		0.68 (in 4 replicates)	0.59	0.767				Total number of assays tested in: 39.
BRD-K45378289-001-01-2 PubChem CID : 44617810		0.76 (in 4 replicates)	0.59	0.767				Total number of assays tested in: 39.
BRD-K13462310-001-01-5 PubChem CID : 54619306		0.88 (in 4 replicates)	0.58	NA				Total number of assays tested in: 40.
BRD-K17923226-001-01-5 PubChem CID : 54619100		0.85 (in 4 replicates)	0.58	0.132				Total number of assays tested in: 38. Active in the following assays: <ul style="list-style-type: none"> <li>MLPCN SirT-5 Measured in Biochemical System Using Imaging - 7044-01.Inhibitor.SinglePoint.HTS.Activity.Set5 (AID 652115)</li> <li>Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2153-01.Inhibitor.Dose.DryPowder.Activity (AID 1159566)</li> <li>Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2153-02.Inhibitor.Dose.CherryPick.Activity (AID 1159567)</li> <li>HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader - 2153-03.Inhibitor.Dose.DryPowder.Activity (AID 1159569)</li> <li>Plasmodium falciparum 3D7-ScDHODH Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2153-02.Inhibitor.Dose.CherryPick.Activity (AID 1159570)</li> <li>Plasmodium falciparum PNITD609-resistant ATP4 D1247Y Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2153-03.Inhibitor.Dose.DryPowder.Activity (AID 1159571)</li> <li>HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader - 2153-03.Inhibitor.Dose.CherryPick.Activity (AID 1159577)</li> </ul>







BRD-K72980834-001-01-1 PubChem CID : 54618539		0.70 (in 4 replicates)	-0.44	0.929				Total number of assays tested in: 36.
BRD-K89056622-001-01-7 PubChem CID : 54657476		0.74 (in 4 replicates)	-0.41	0.233				Total number of assays tested in: 39.
BRD-K23940360-001-05-8 MLS000731532 HMS2744D15 ZINC5050928 CCG-136395 SMR000309807 PubChem CID : 16195347		0.63 (in 2 replicates)	-0.41	NA				Total number of assays tested in: 576. Active in the following assays: <ul style="list-style-type: none"><li>• MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814)</li><li>• Fluorescence Cell-Free Homogeneous Primary HTS to Identify Inhibitors of the RanGTP-Importin-beta complex (AID 2216)</li><li>• Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)</li><li>• qHTS Assay for Identifying a Potential Treatment of Ataxia-Telangiectasia (AID 485349)</li><li>• Luminescence-based cell-based primary high throughput screening assay to identify biased ligands of the melanocortin 4 receptor (MC4R): agonists of MC4R (AID 540308)</li><li>• uHTS identification of DNMT1 inhibitors in a Fluorescent Molecular Beacon assay (AID 588458)</li><li>• Fluorescence-based biochemical primary high throughput screening assay to identify inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 588726)</li><li>• Luminescence-based cell-based high throughput confirmation assay for biased ligands (agonists) of the melanocortin 4 receptor (MC4R) (AID 602192)</li><li>• qHTS Assay to Identify Small Molecule Activators of BRCA1 Expression (AID 624202)</li><li>• uHTS identification of SKN-1 Inhibitors in a fluorescence assay (AID 624304)</li><li>• Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Fluorescence-based biochemical high throughput Glycophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) assay to identify assay artifacts (AID 652141)</li><li>• HTS for Bacterial rRNA inhibitors Measured in Microorganism-Based System Using Plate Reader - 7056-01 Inhibitor.SinglePoint.HTS Activity (AID 720706)</li></ul>