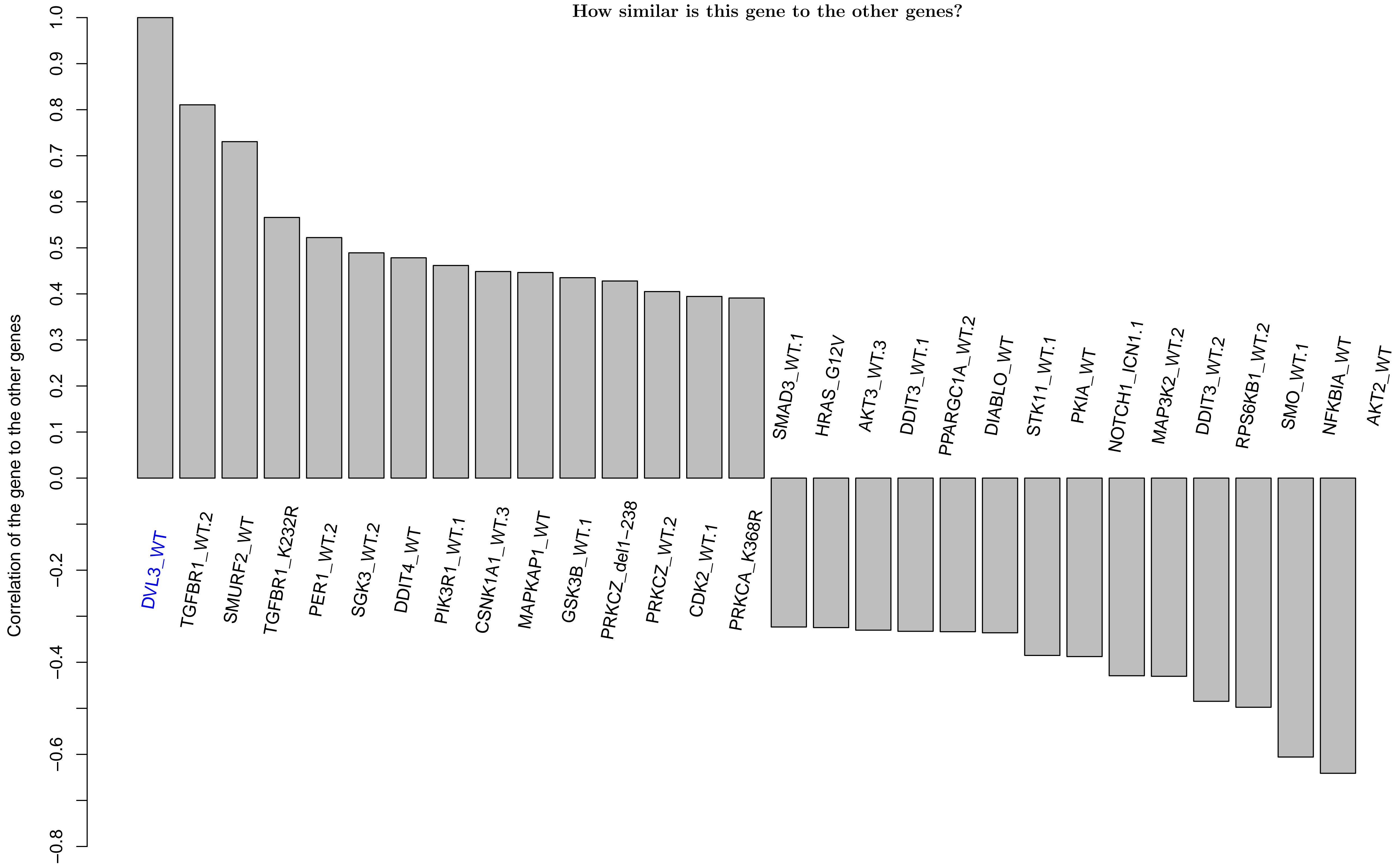
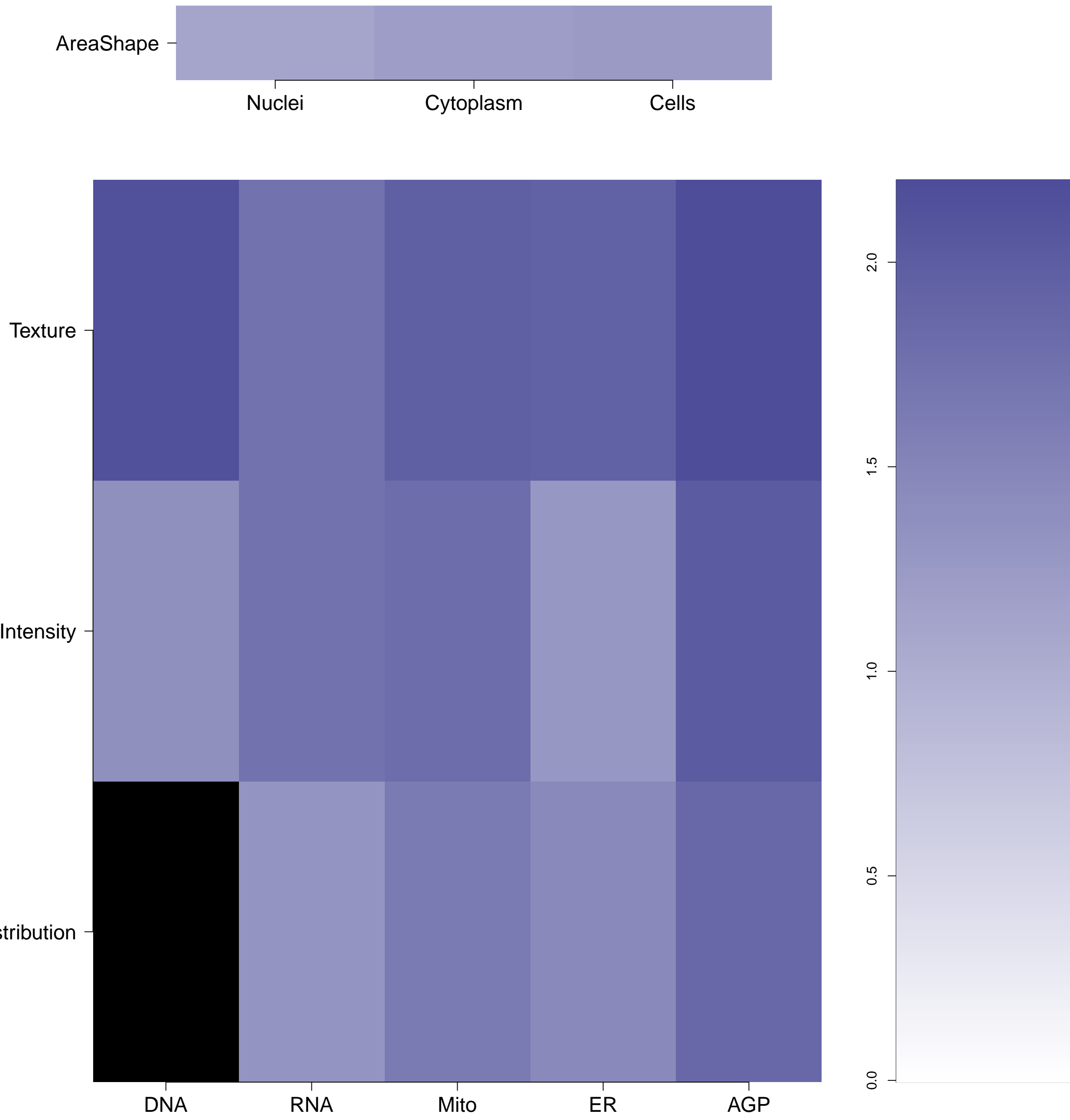


DVL3_WT - in Canonical WNT

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

DVL3.WT (41744)

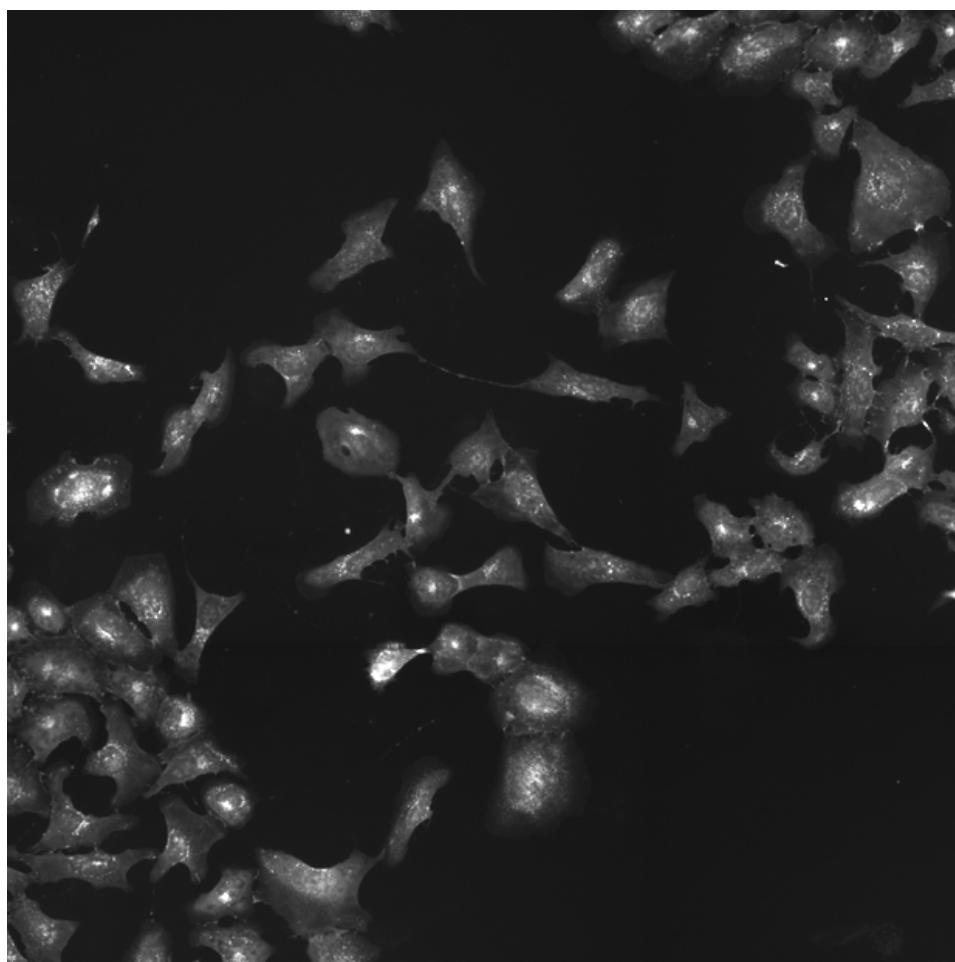
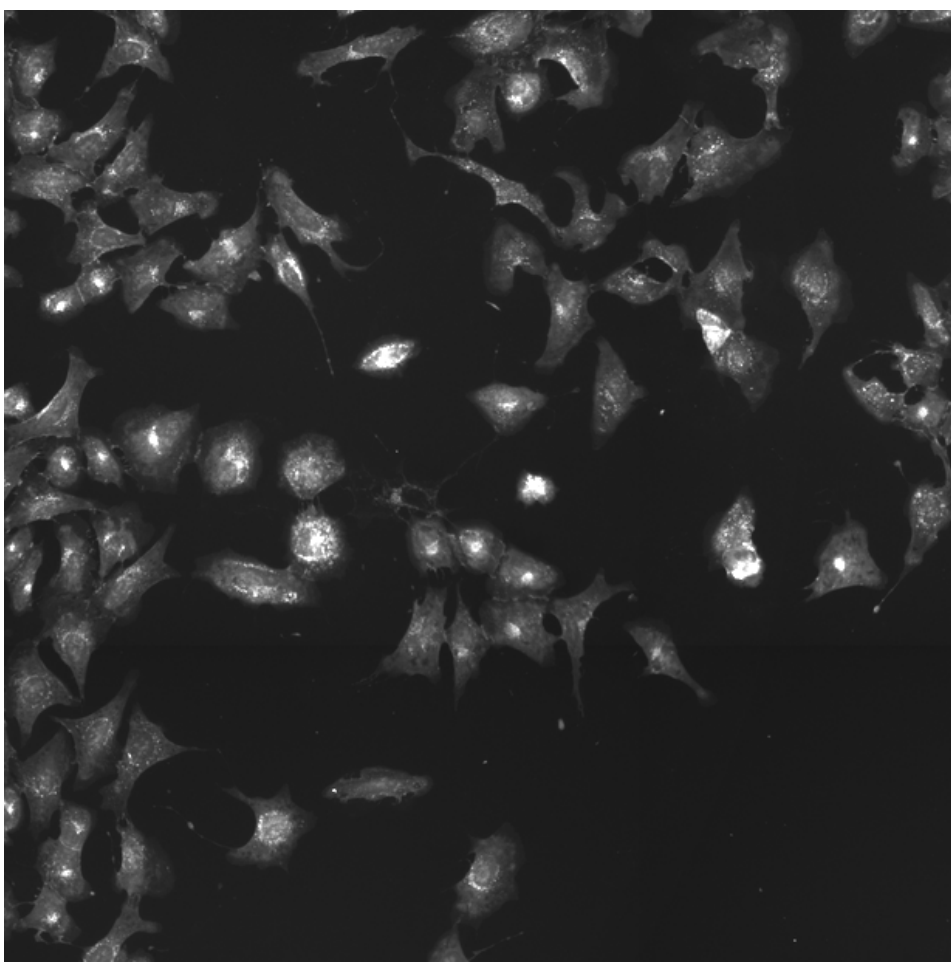
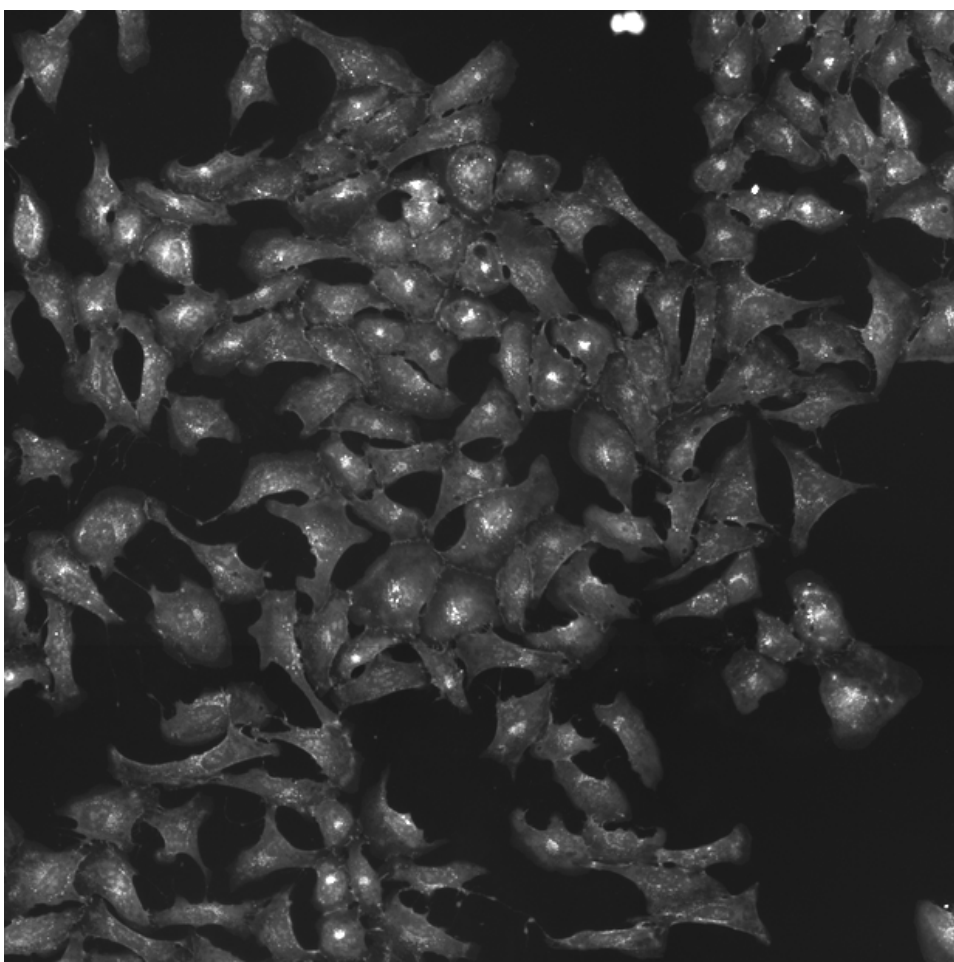
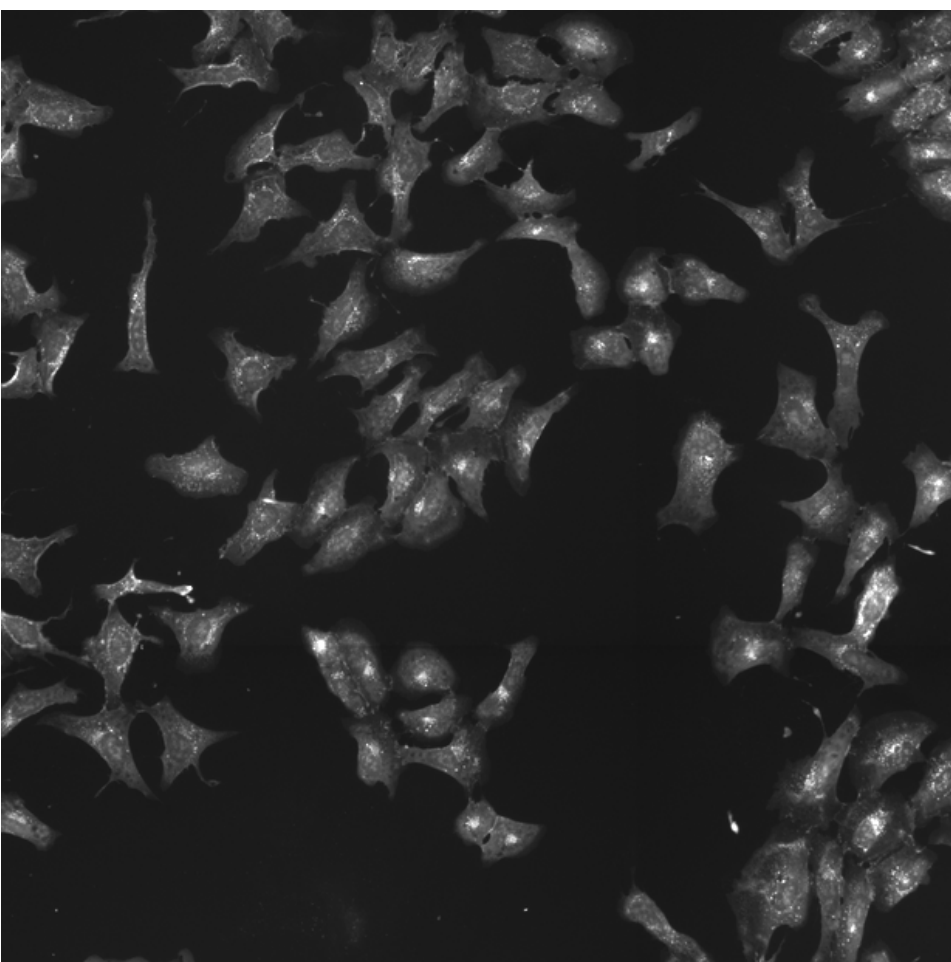
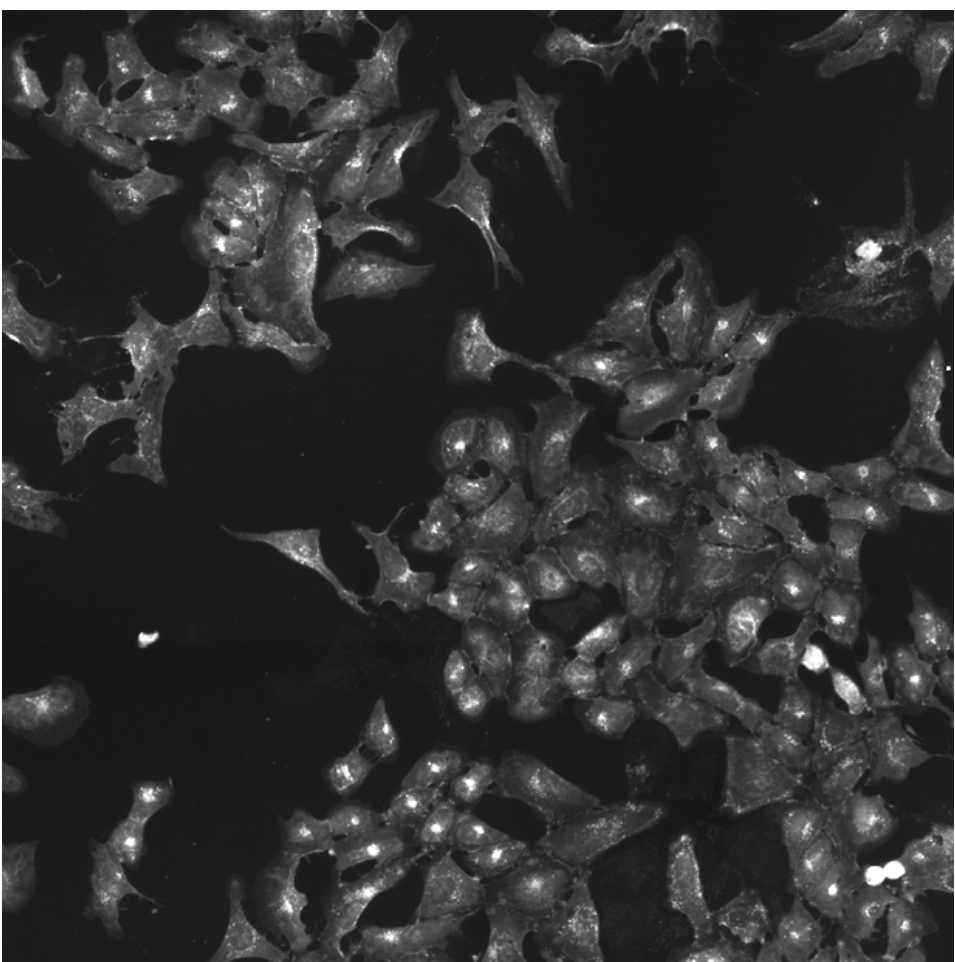
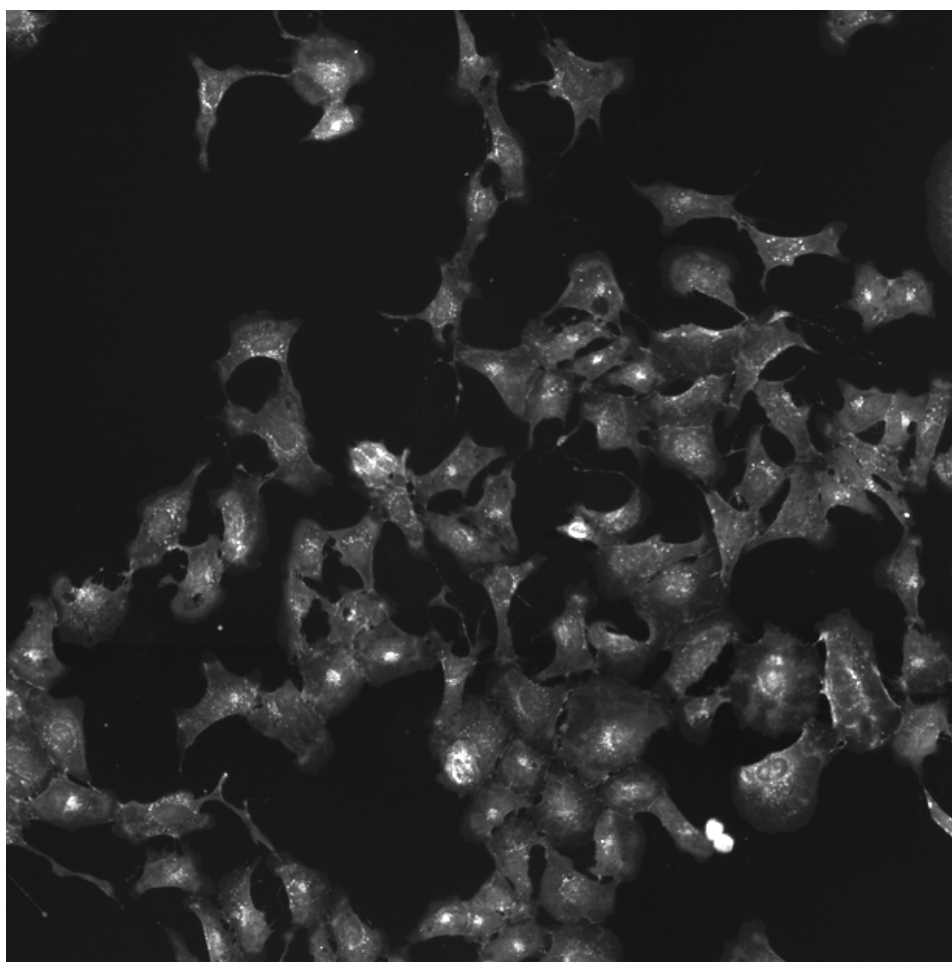
DVL3.WT (41755)

DVL3.WT (41756)

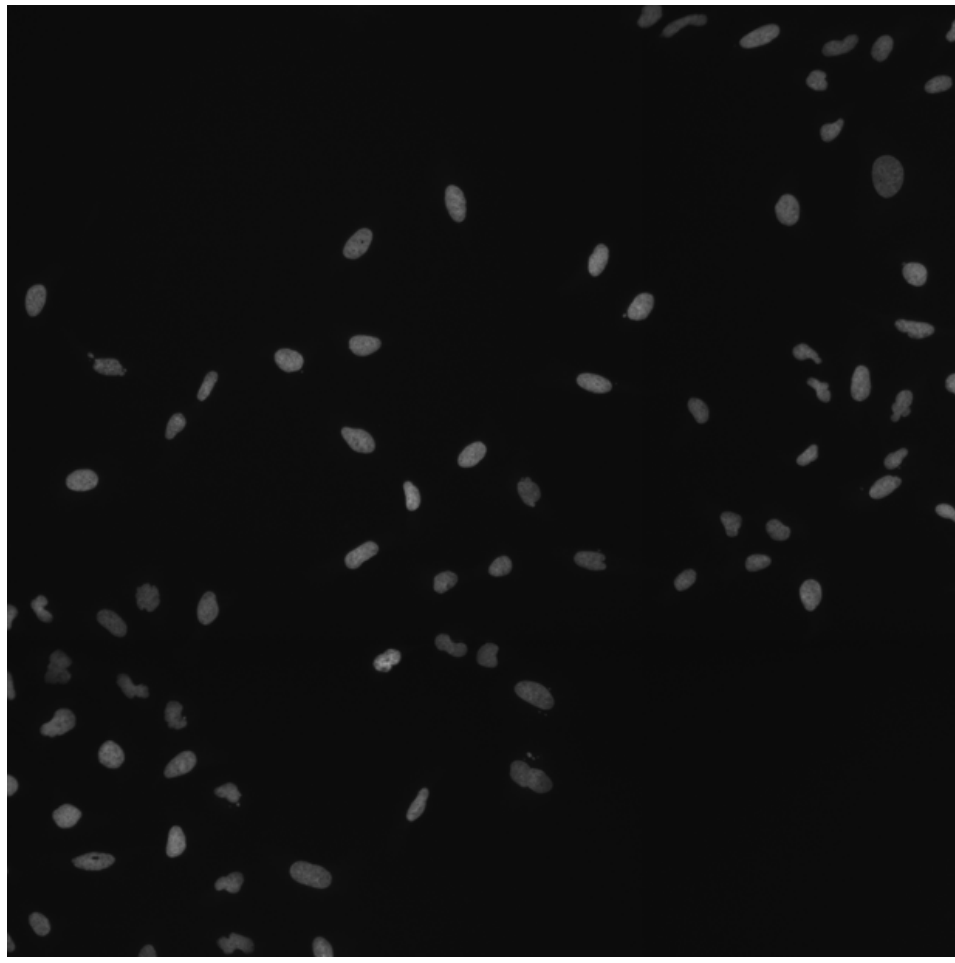
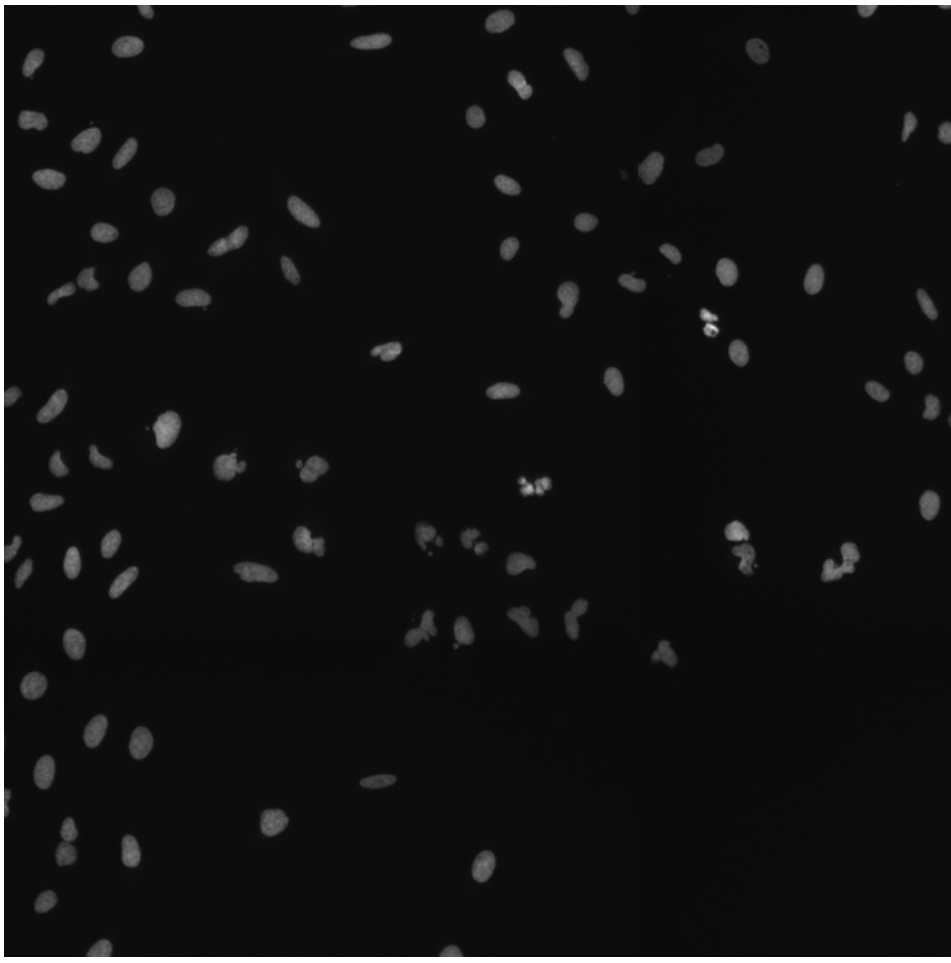
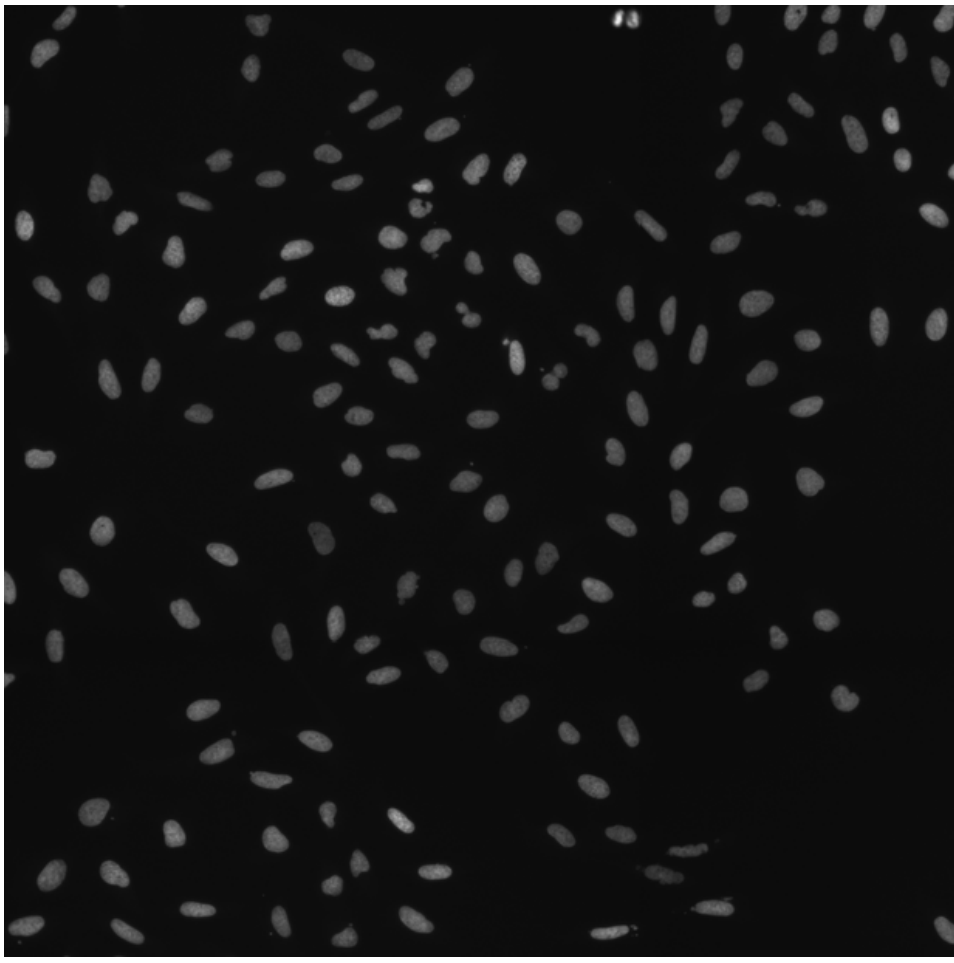
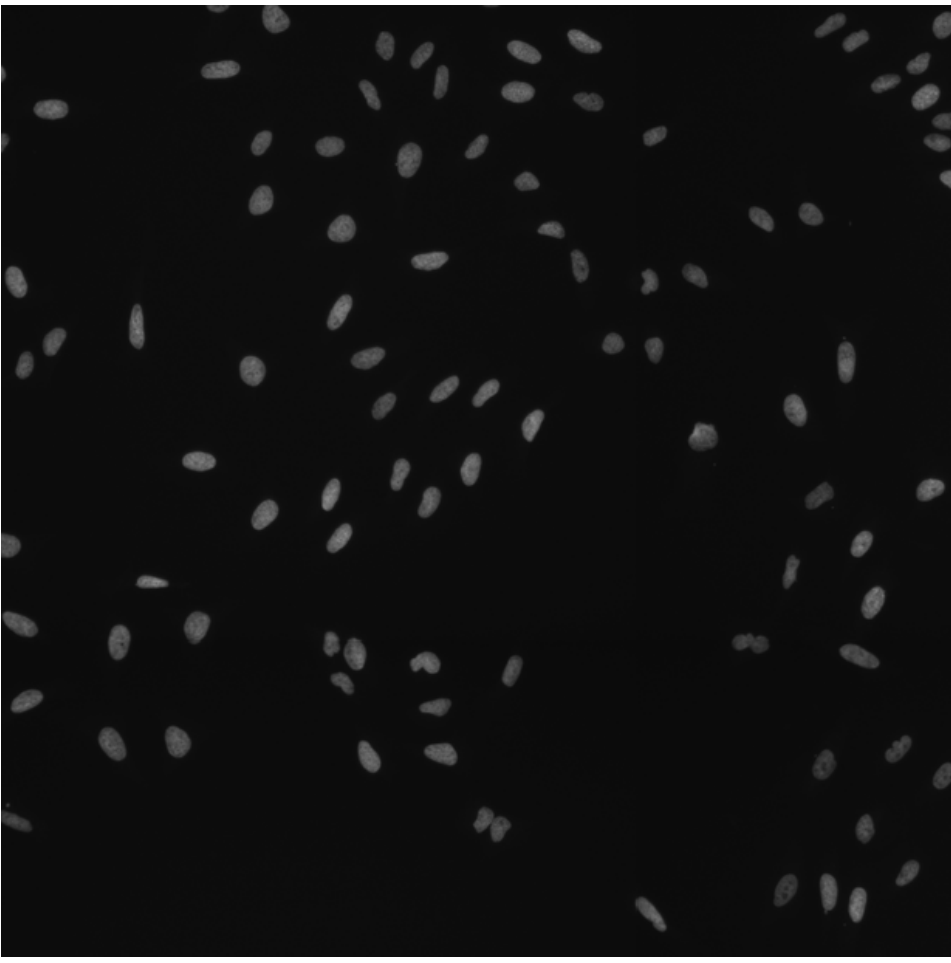
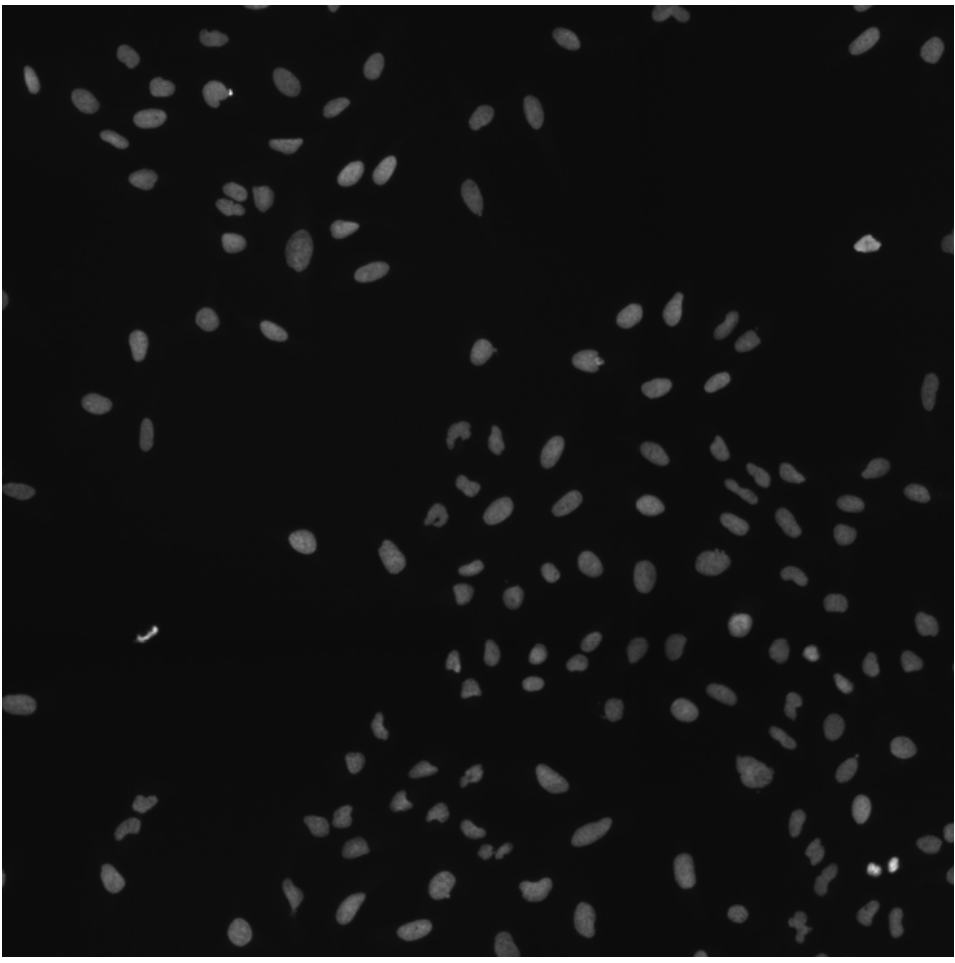
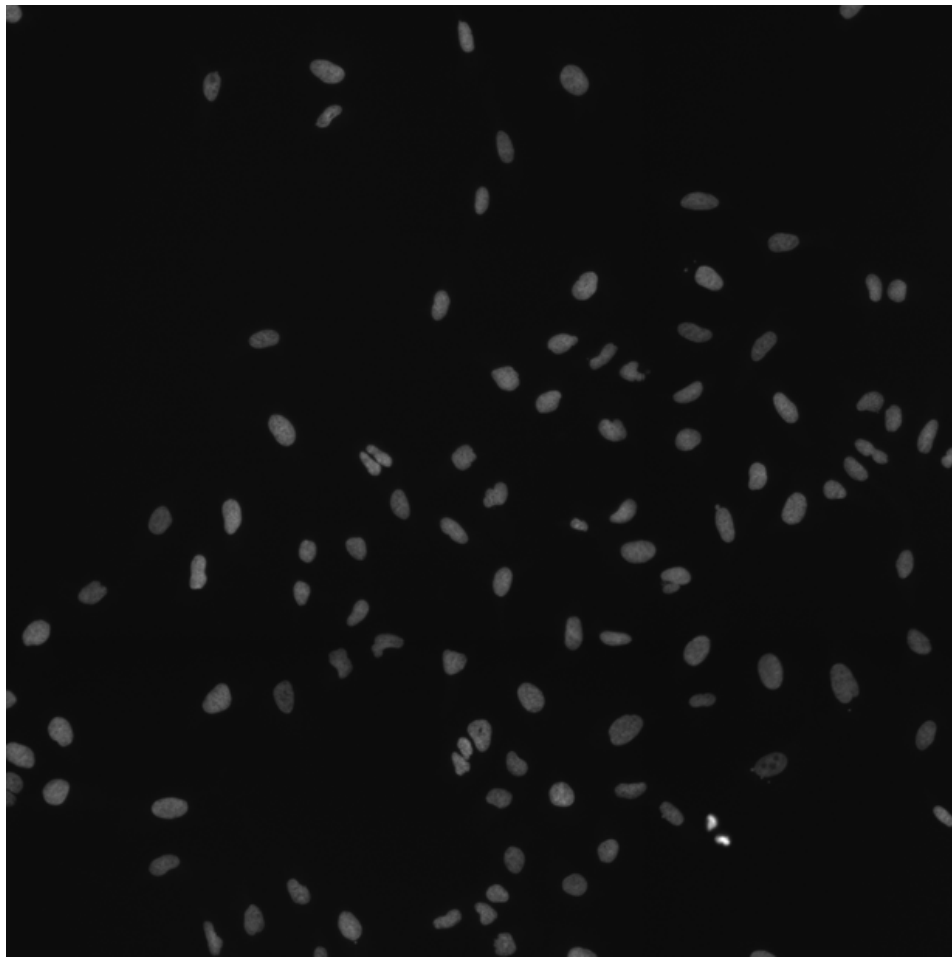
DVL3.WT (41757)

DVL3.WT (41754)

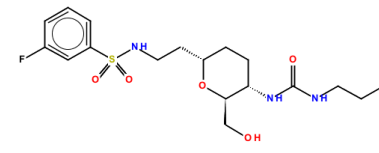
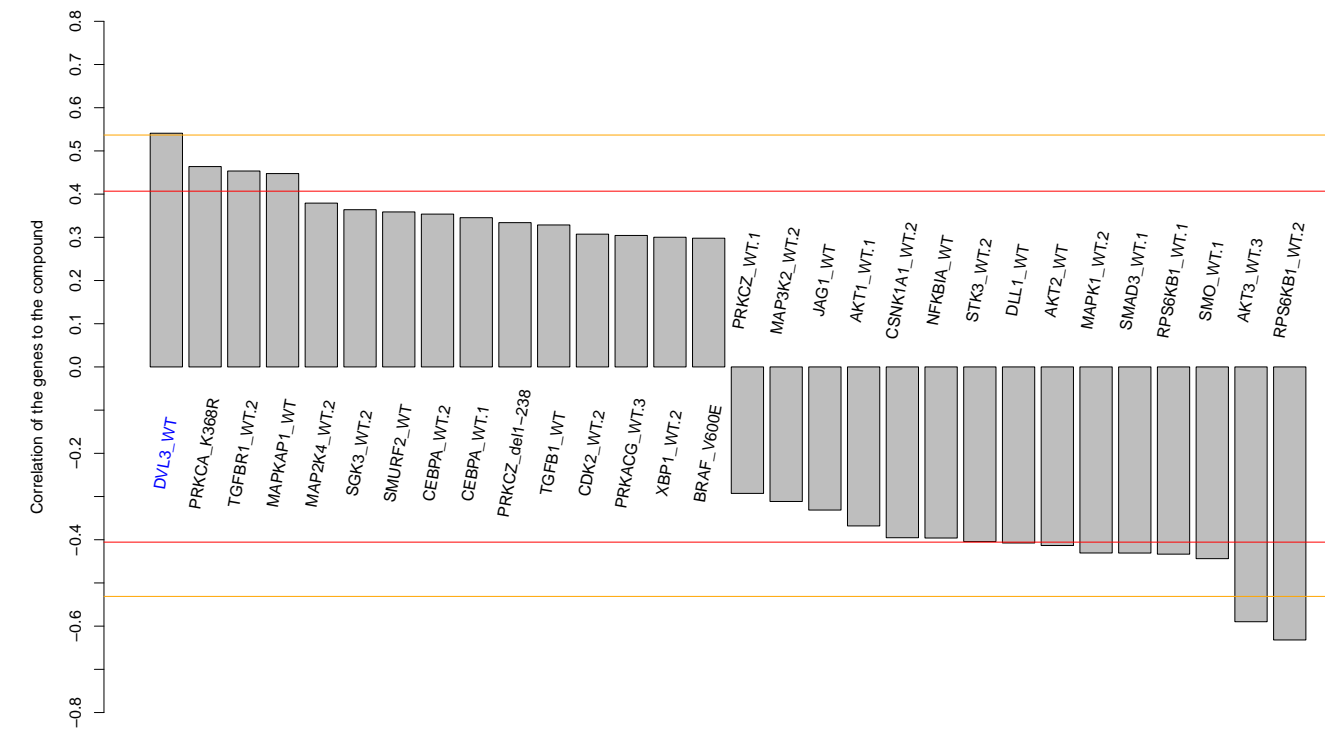
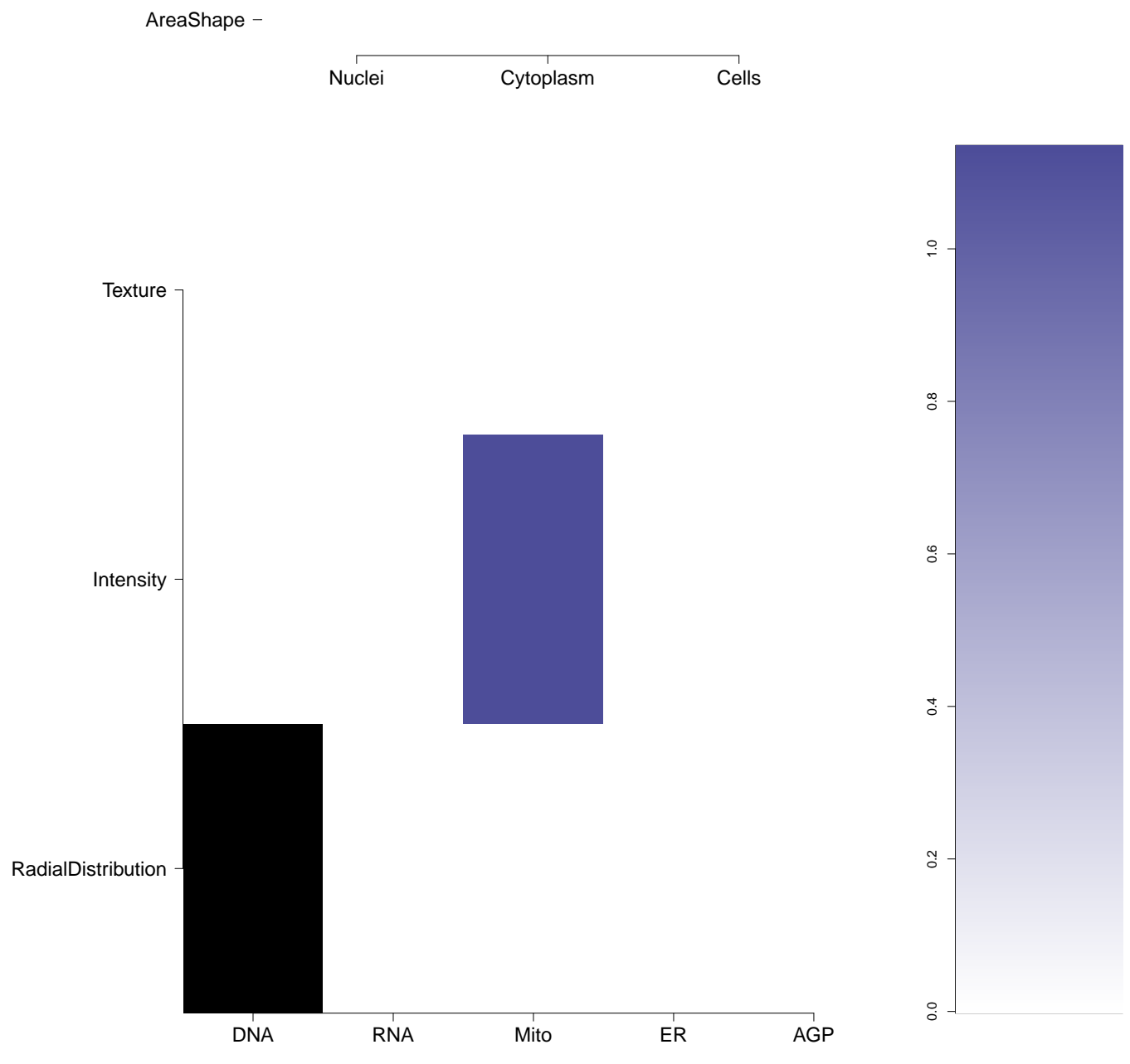
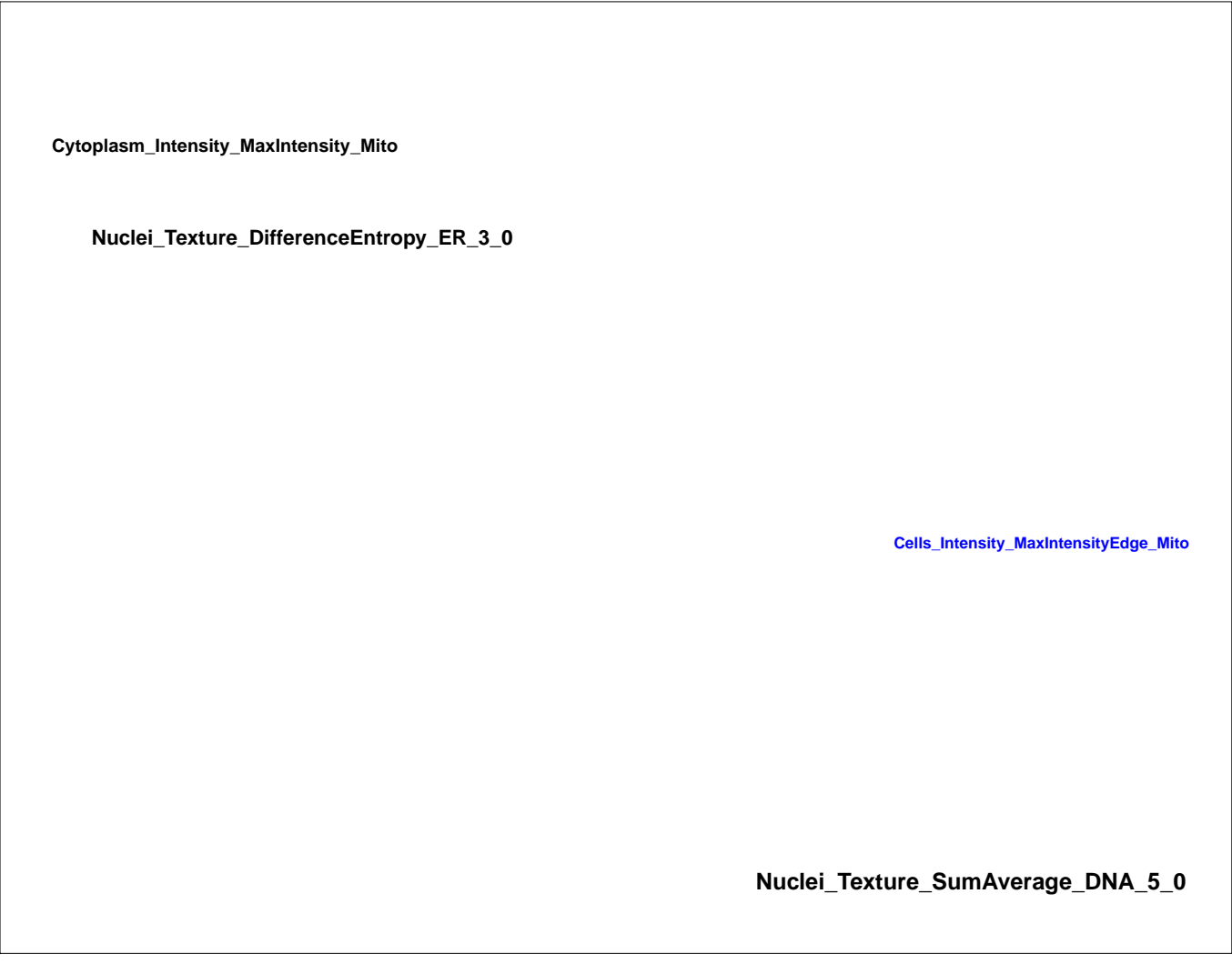
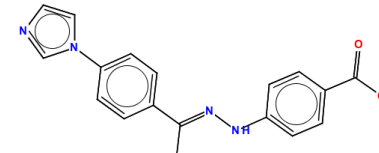
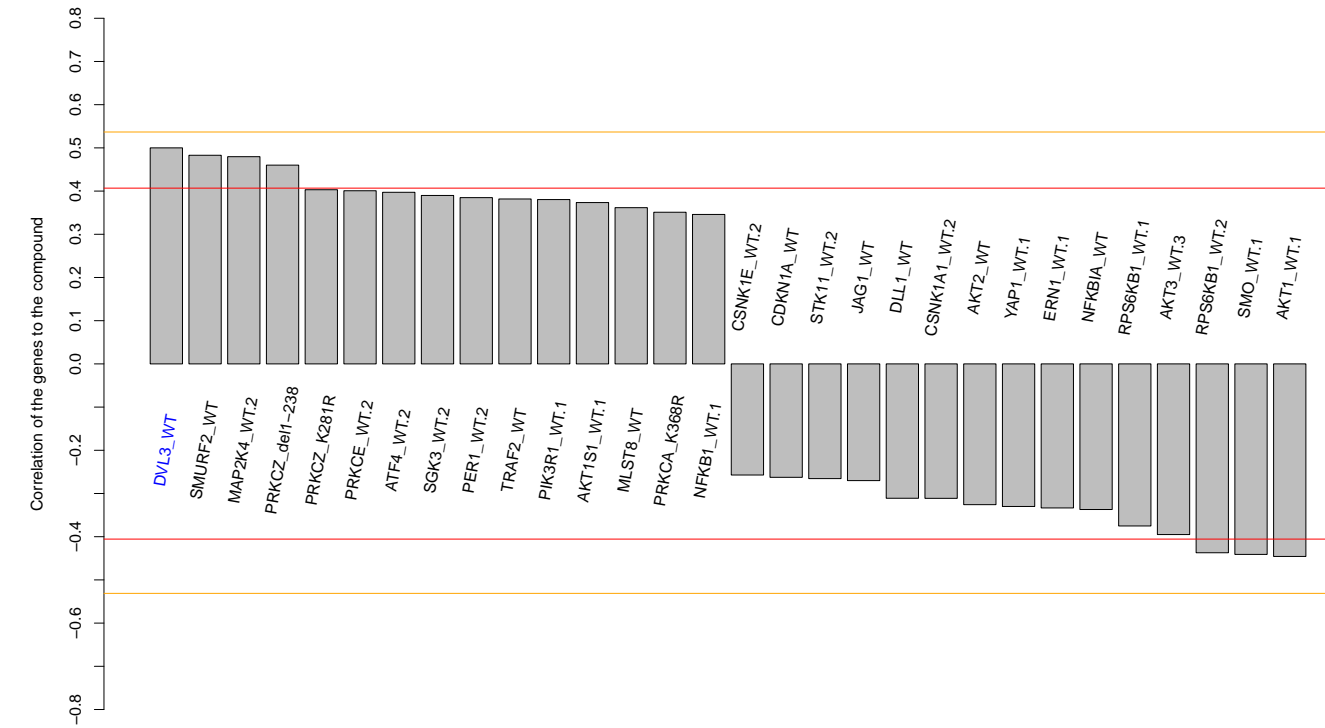
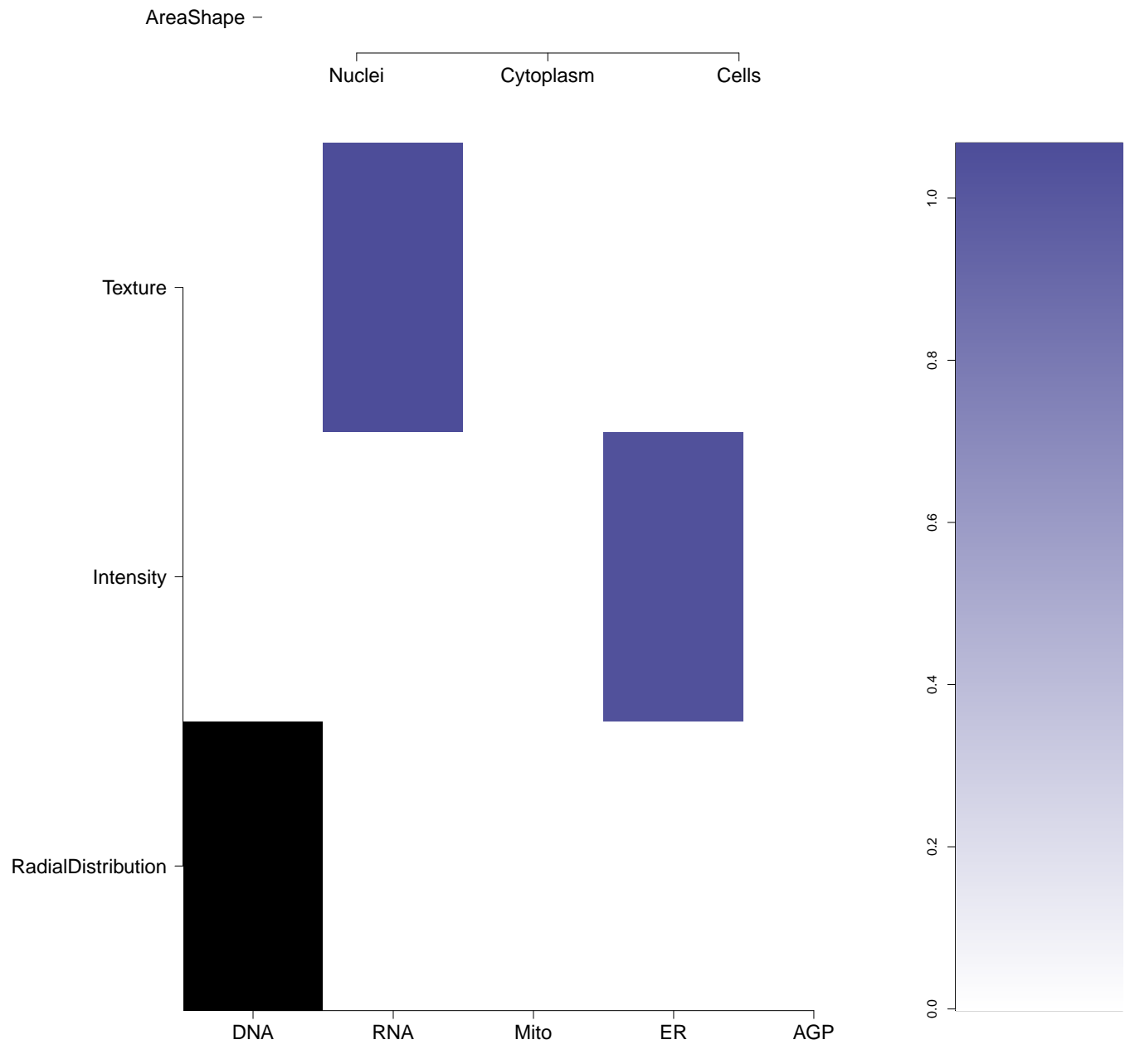
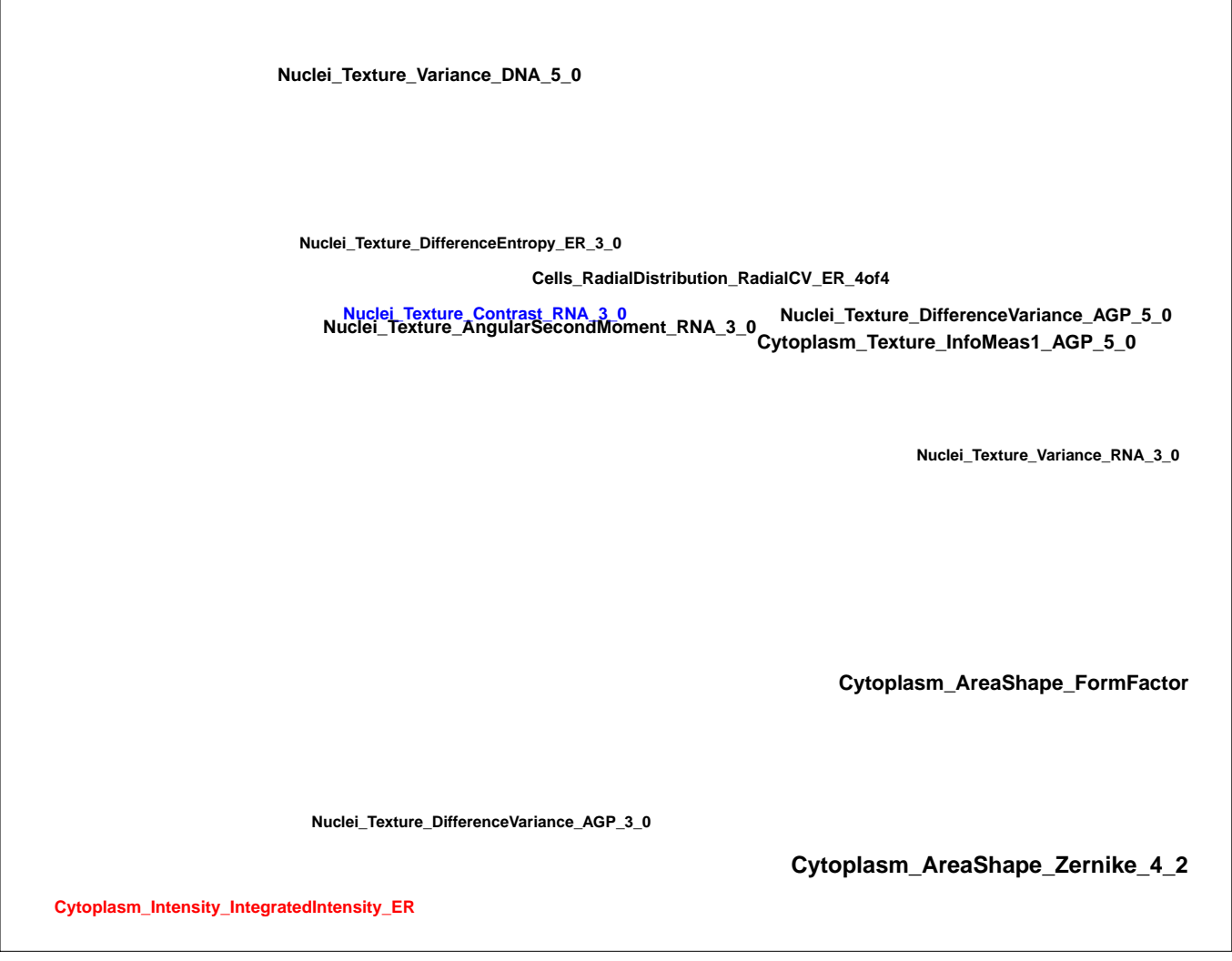
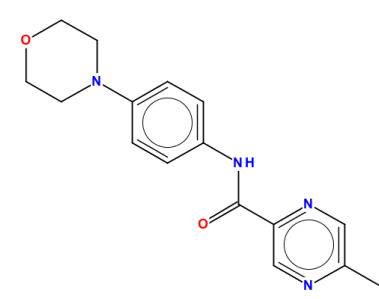
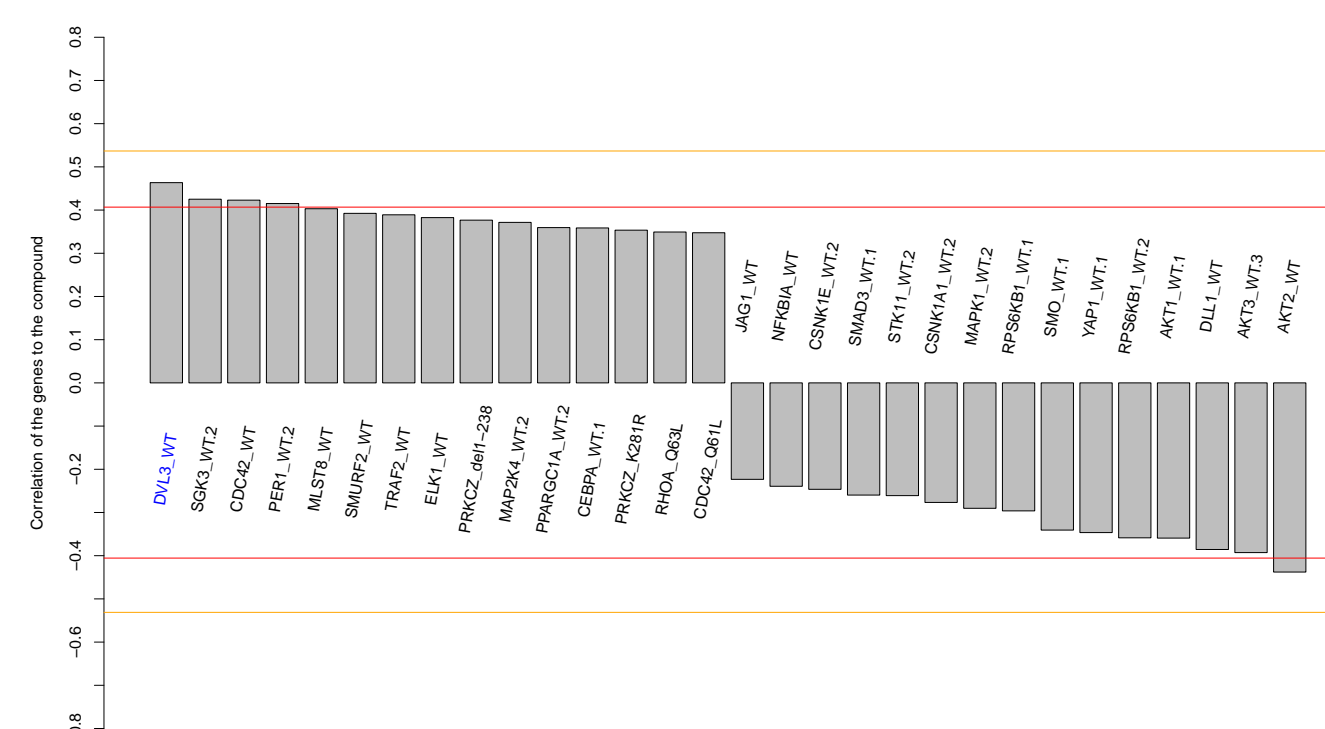
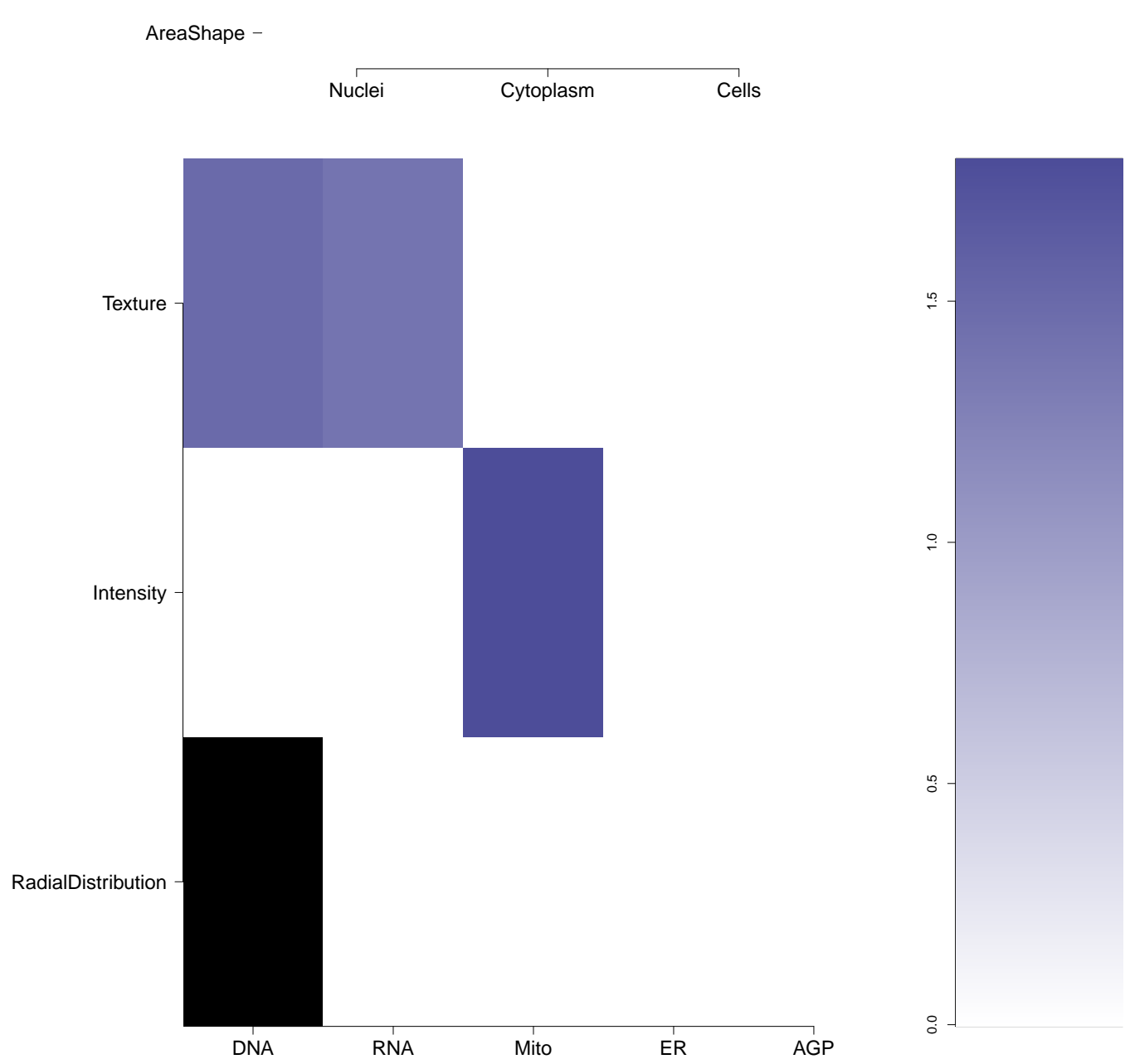
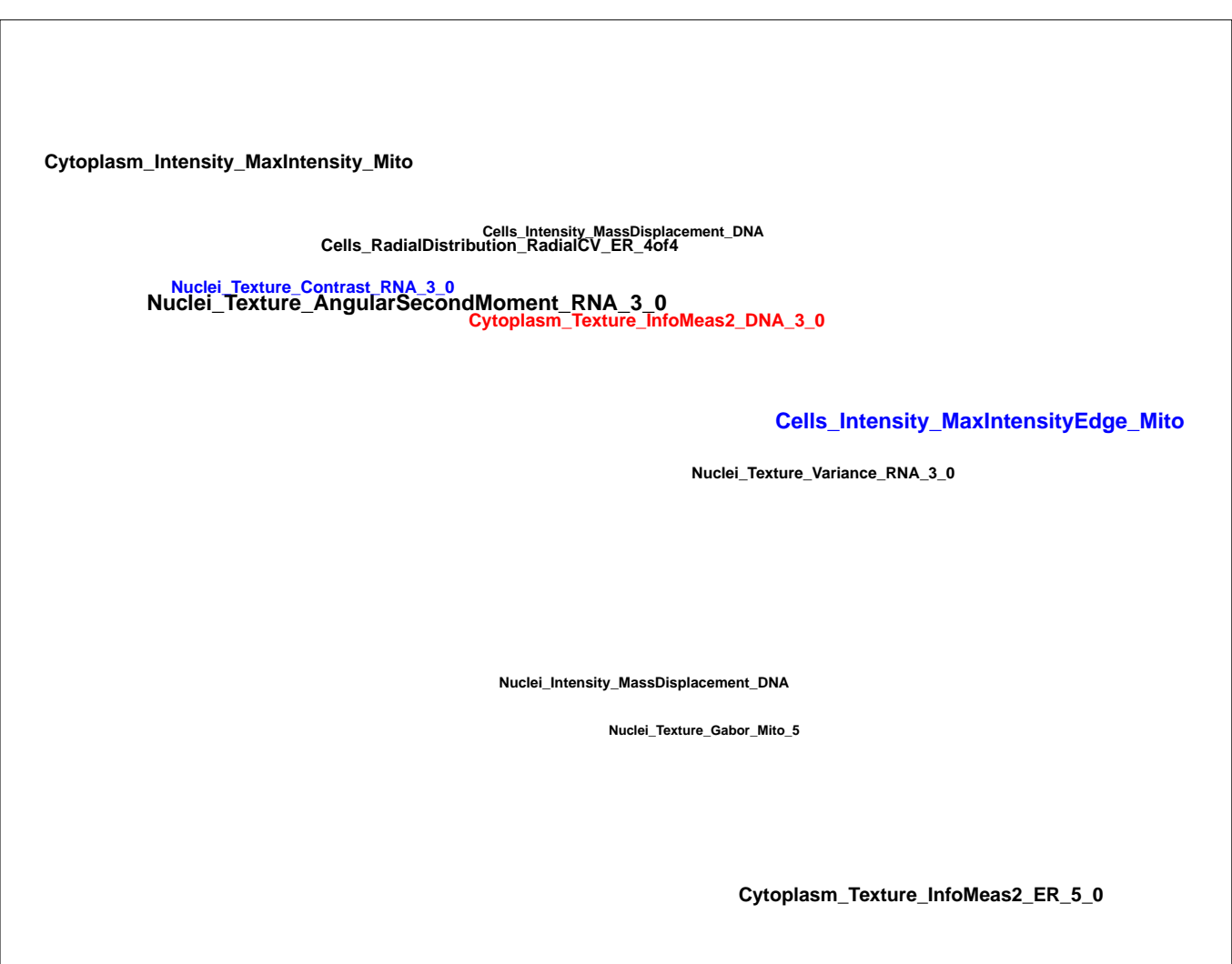
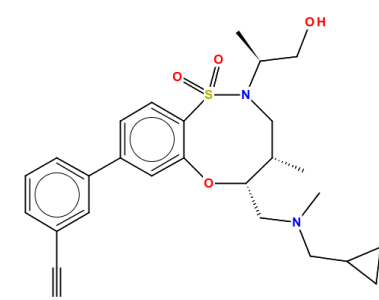
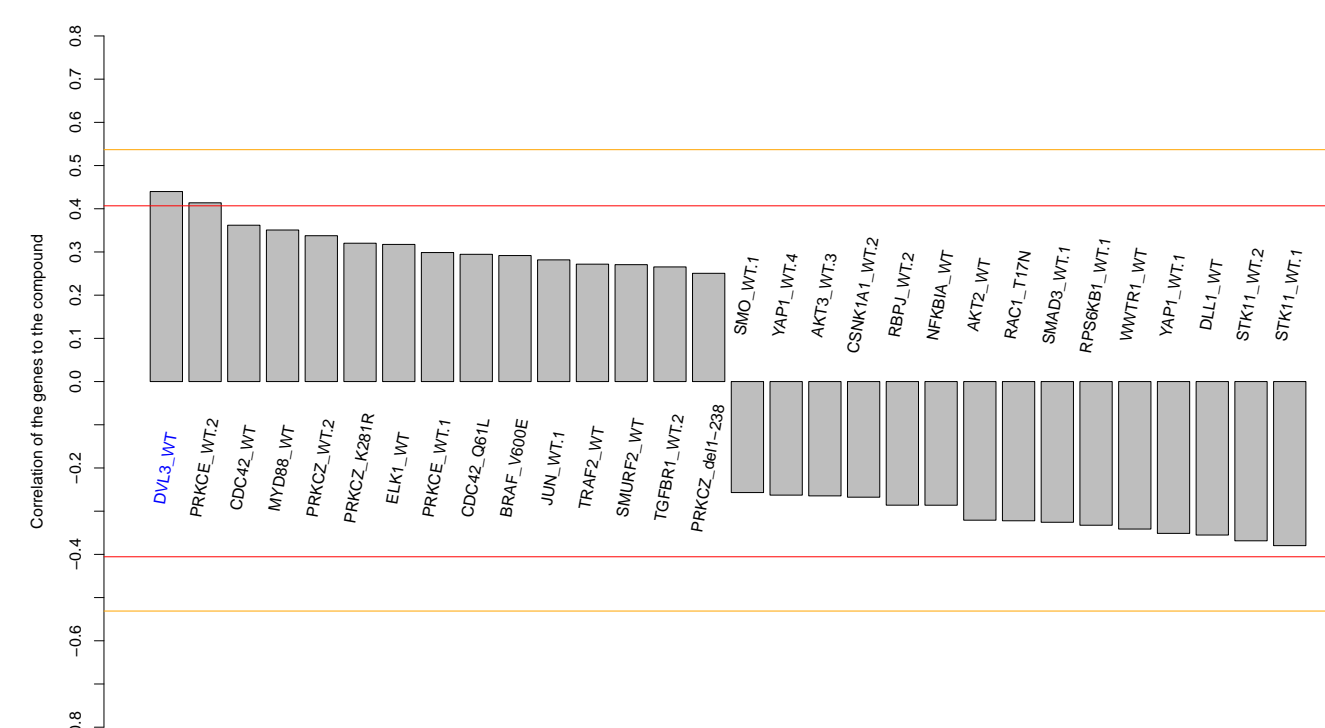
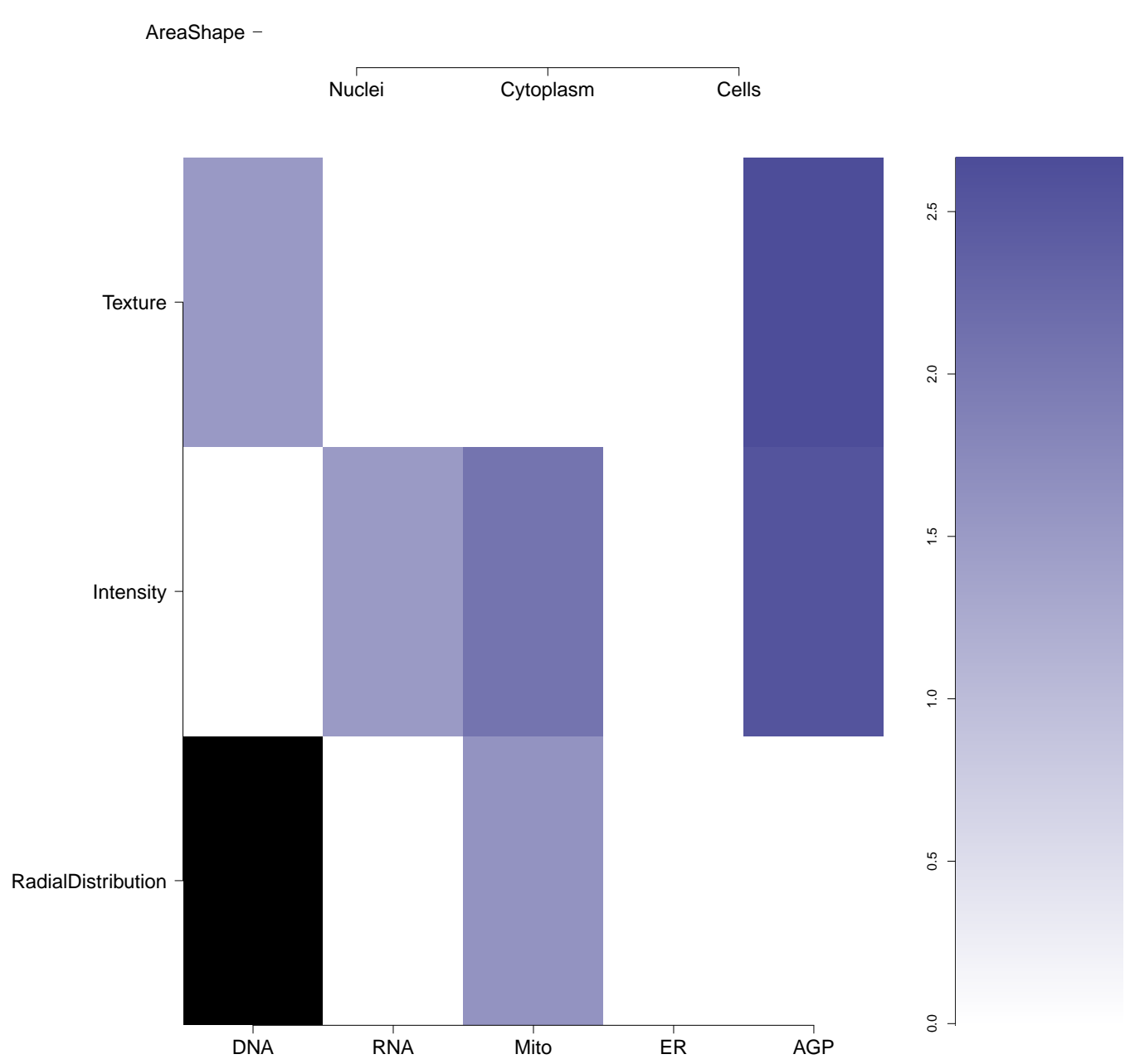

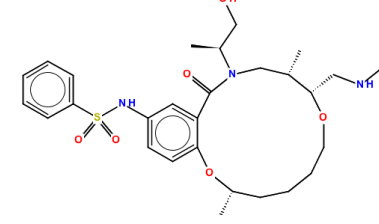
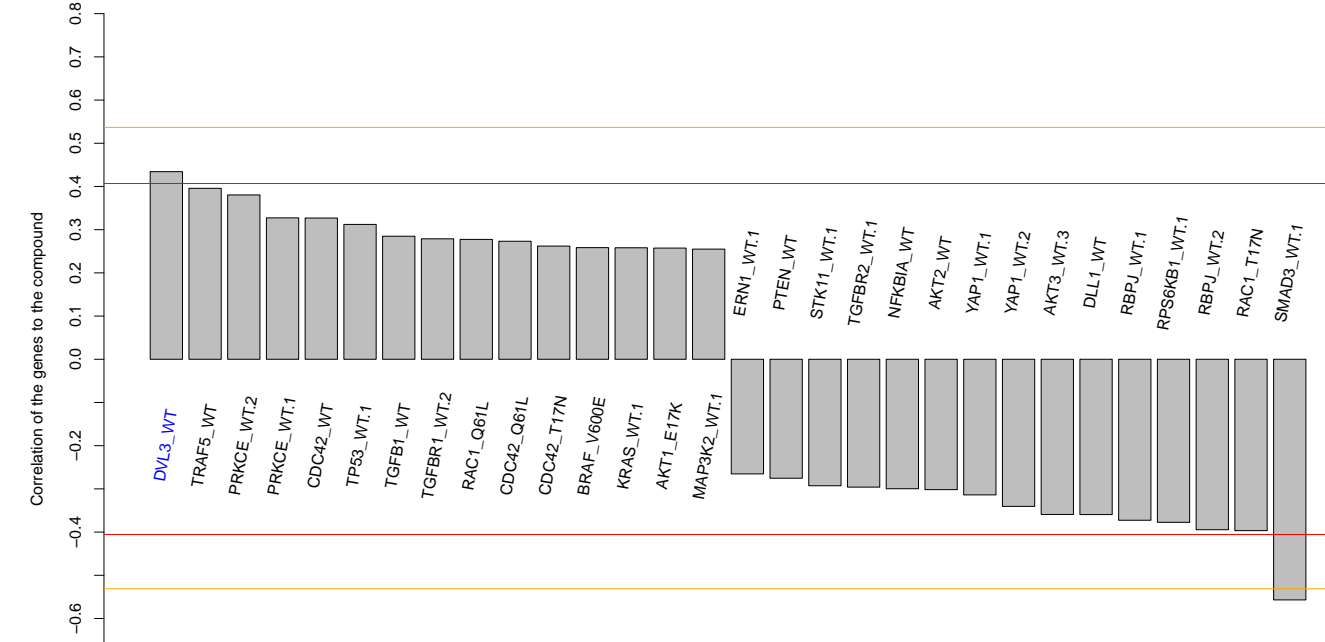
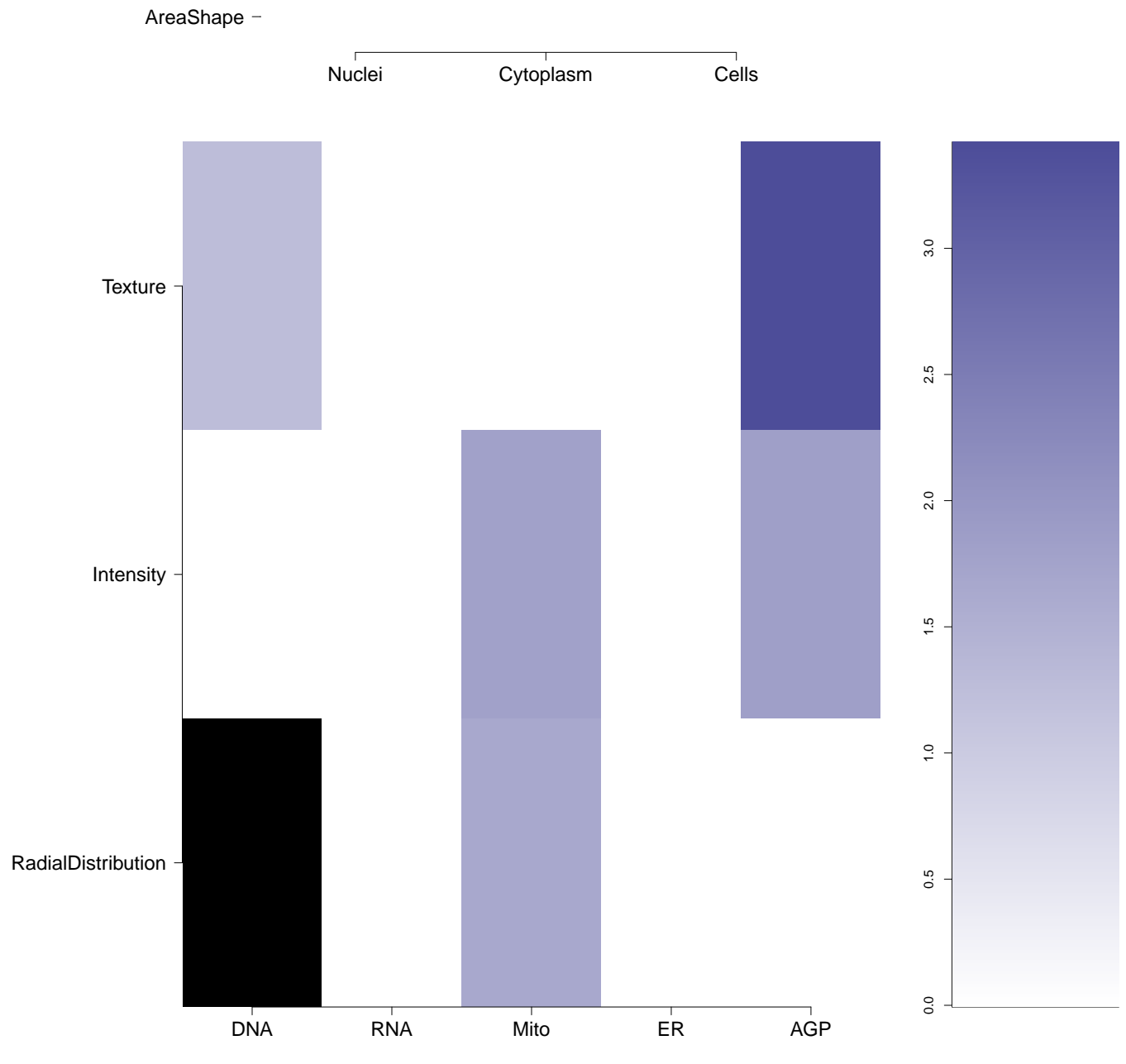
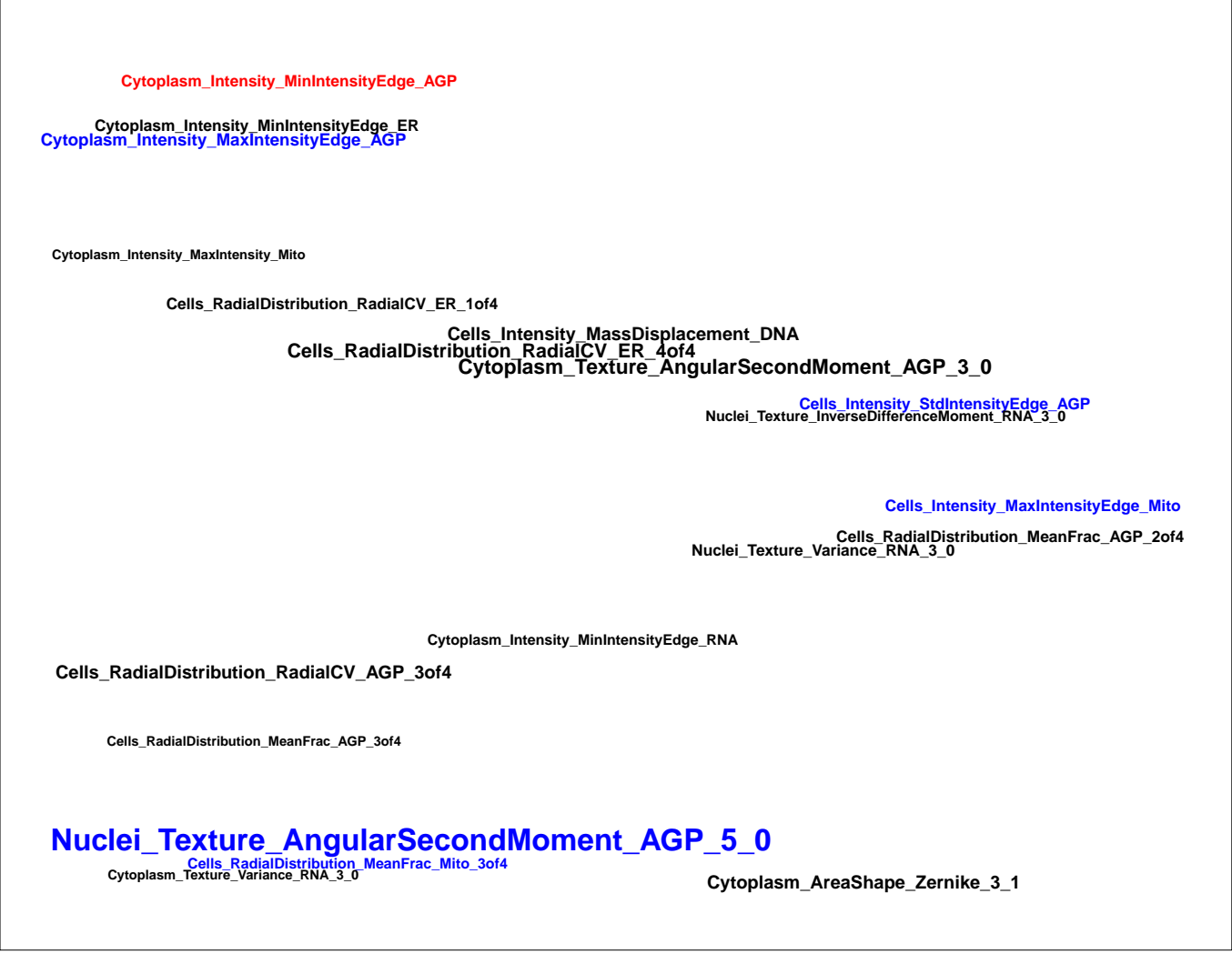
AGP



DNA



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 0.53)	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-K95882018-001-01-0 PubChem CID : 54641157		NA (in 1 replicates)	0.54	NA				Total number of assays tested in: 38.
BRD-K26925032-065-05-9 T0506-6599 MLS000775143 SMR000364886 PubChem CID : 16237932		NA (in 1 replicates)	0.50	NA				Total number of assays tested in: 624. Active in the following assays: <ul style="list-style-type: none">Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932)HTS identification of compounds activating phosphomannose isomerase (PMI) via a fluorescence intensity assay using a near- saturating concentration of mannose 6-phosphat (AID 1216)qHTS Assay for Enhancers of SMN2 Splice Variant Expression (AID 1458)Luminescence-based primary biochemical high throughput screening assay to identify inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1789)MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814)Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)qHTS Assay for Rab9 Promoter Activators (AID 485297)qHTS Assay for NPC1 Promoter Activators (AID 485313)qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342)Absorbance-based biochemical primary high throughput screening assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651718)Absorbance-based biochemical high throughput confirmation assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651822)Luminescence-based cell-based primary high throughput screening assay for inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1): repression of SF-1 (NR5A1) activated SAr promoter by full-length DAX-1 (AID 652010)Luminescence-based cell-based primary high throughput confirmation assay for inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1): repression of SF-1 (NR5A1) activated SAr promoter by full-length DAX-1 (AID 652134)Counterscreen for inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1): Luminescence-based cell-based high throughput assay for nonselective inhibitors/assay artifacts using AP2 mutant SF-1 (NR5A1) Transactivation Assay (AID 652136)Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12; AID 687014)
BRD-K61396432-001-05-0 F5791-2458 606132-22-3 ACILDDAG ASN 06977449 MLS000032170 CTK&J6174 HMS2433106 ZINC1367592 ZINC01367592 HE360420 SMR000007544 KB-292807 T6621342 PubChem CID : 646264		NA (in 1 replicates)	0.46	NA				Total number of assays tested in: 791. Active in the following assays: <ul style="list-style-type: none">MLPCN Alpha-Synuclein 5'UTR - 5'UTR binding - activators (AID 1814)Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)High Content Assay for Compounds that inhibit the Assembly of the Perinuclear Compartment (AID 2417)
BRD-K00799745-001-01-0 PubChem CID : 54618981		0.60 (in 3 replicates)	0.44	0.969				Total number of assays tested in: 36. Active in the following assays: <ul style="list-style-type: none">Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader (AID 1159554)
BRD-K57969466-001-01-8 PubChem CID : 44489309		0.70 (in 4 replicates)	0.43	0.218				Total number of assays tested in: 46.