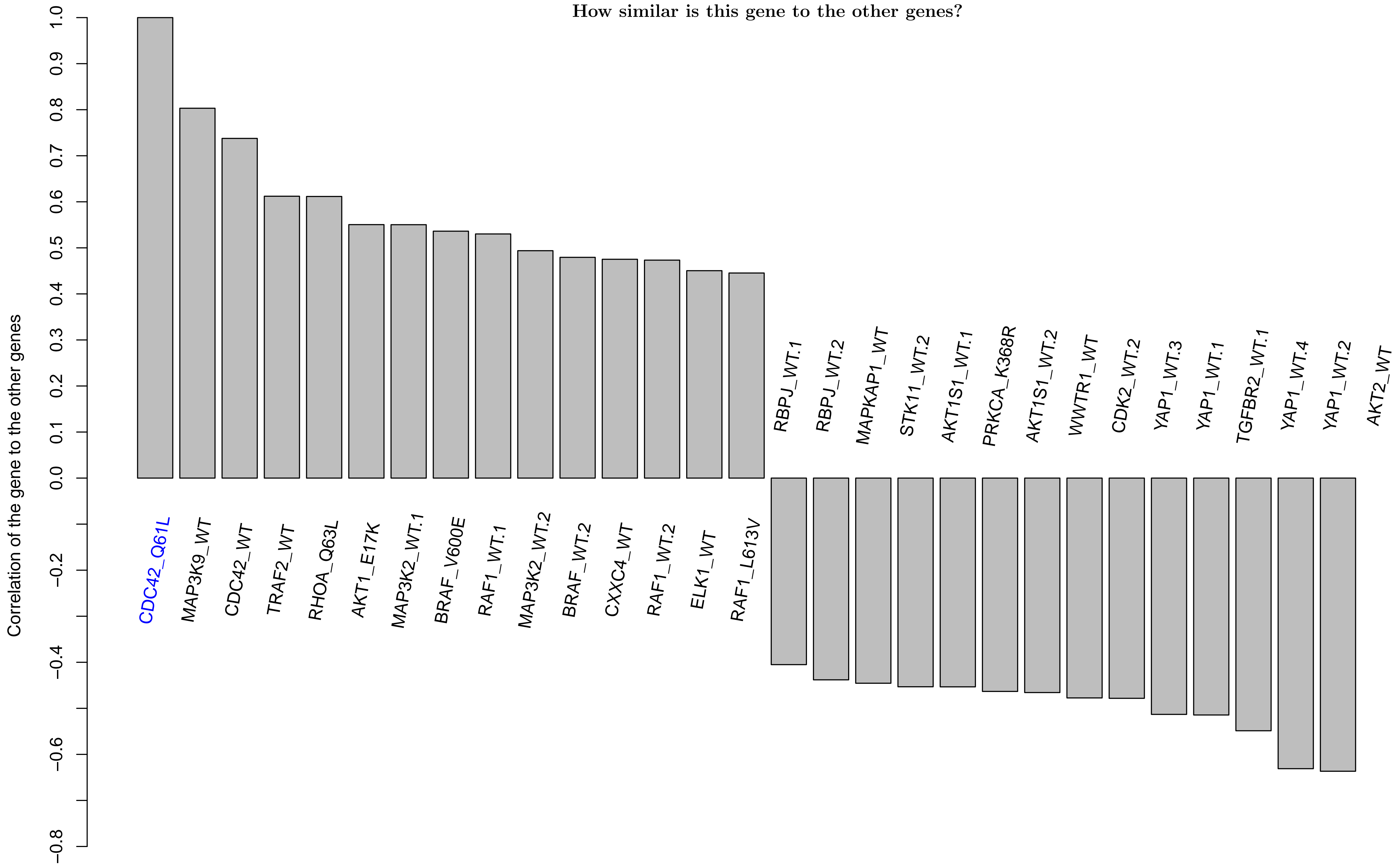
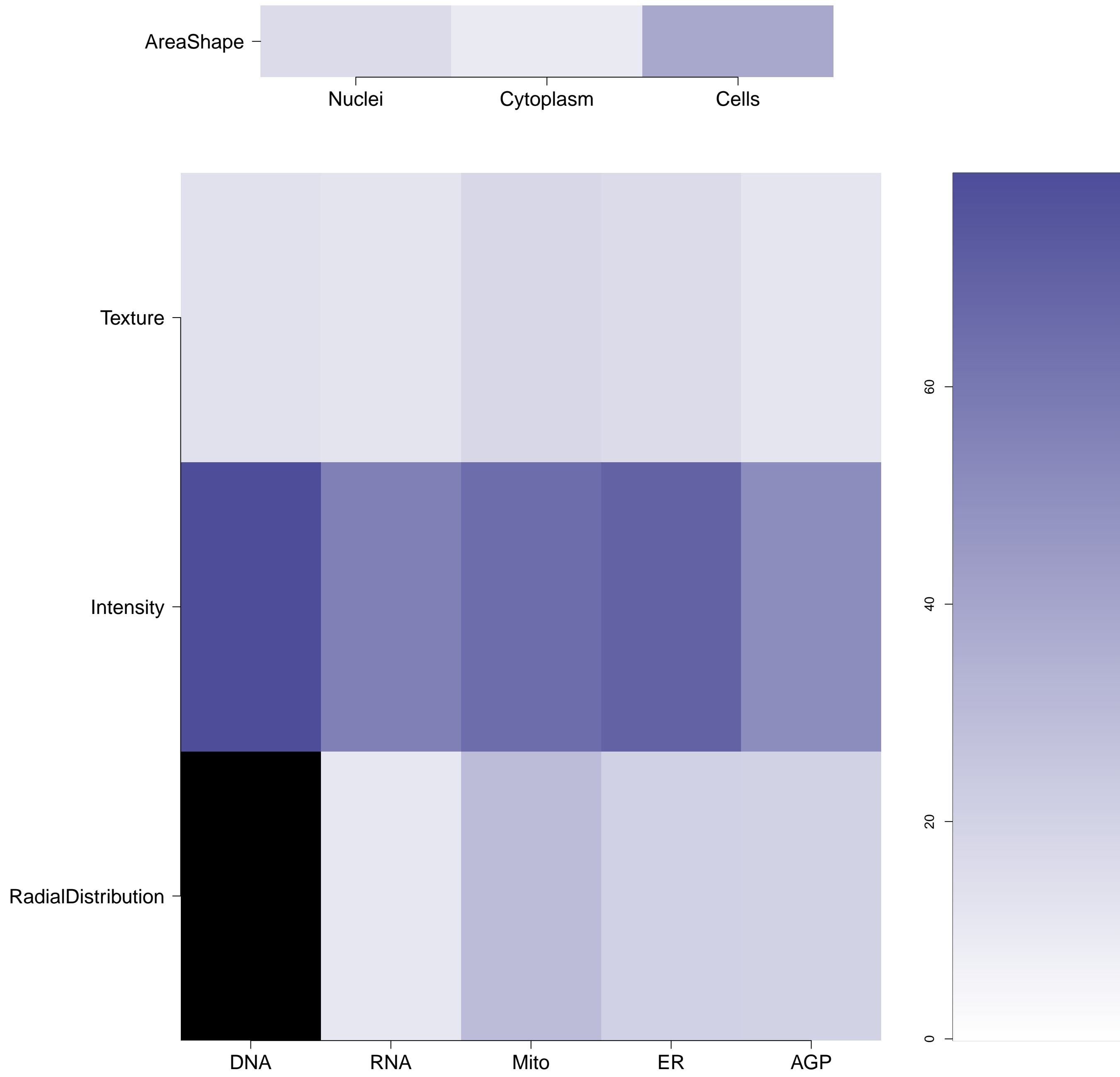


CDC42.Q61L - in Canonical Cytoskeletal Re-org

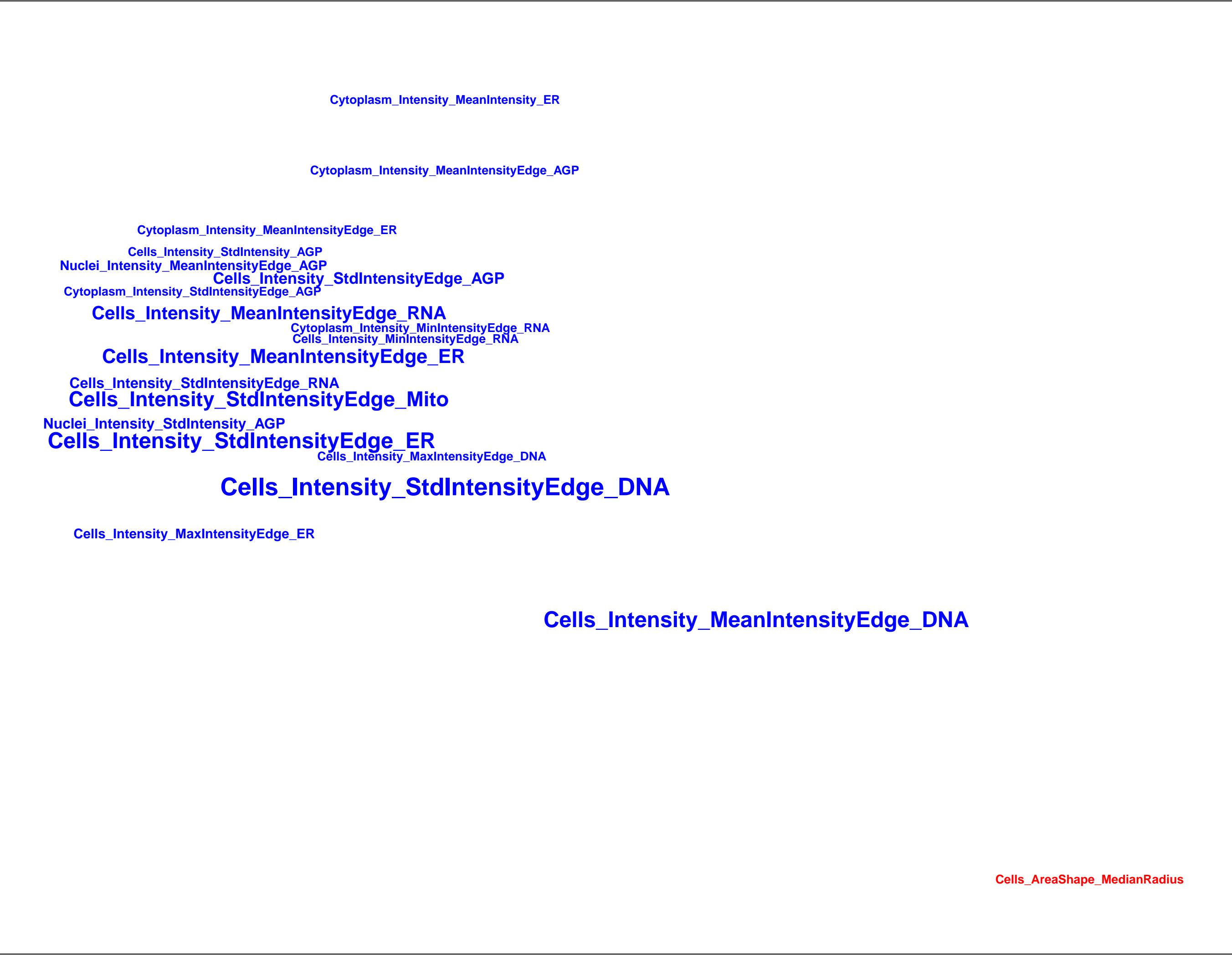
How similar is this gene to the other genes?



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

CDC42.Q61L (41744)

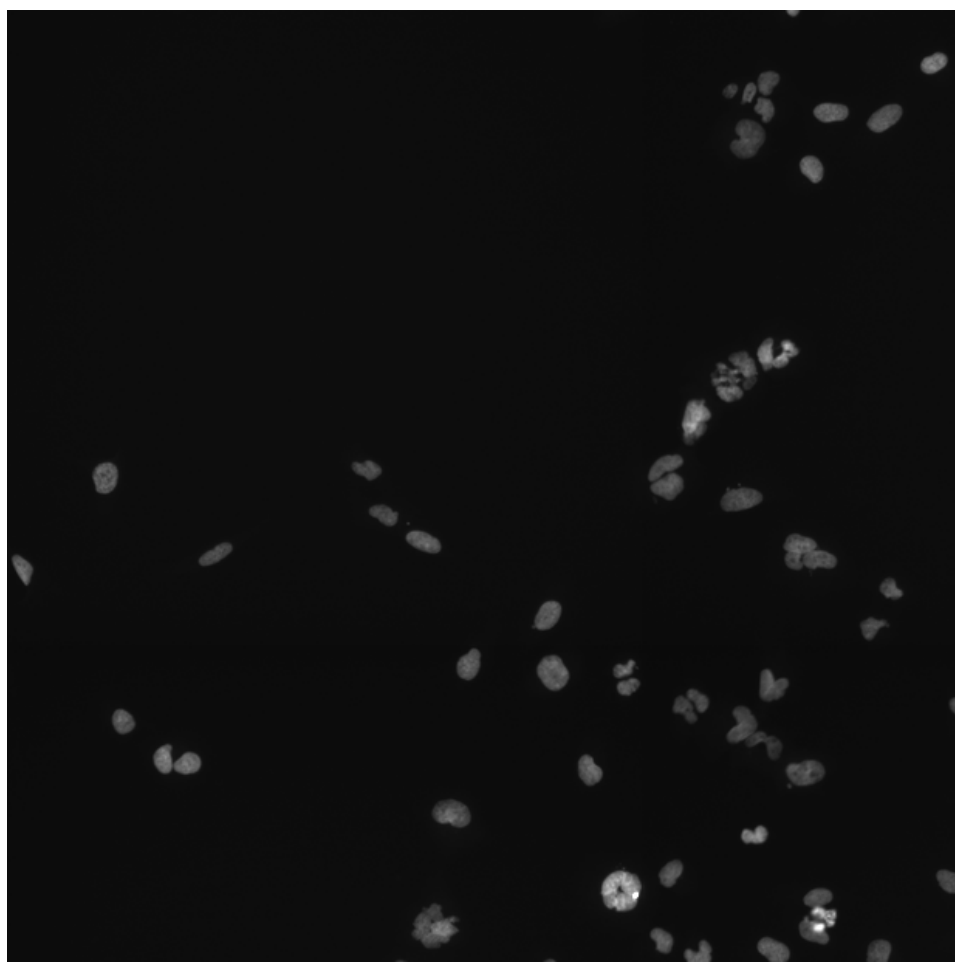
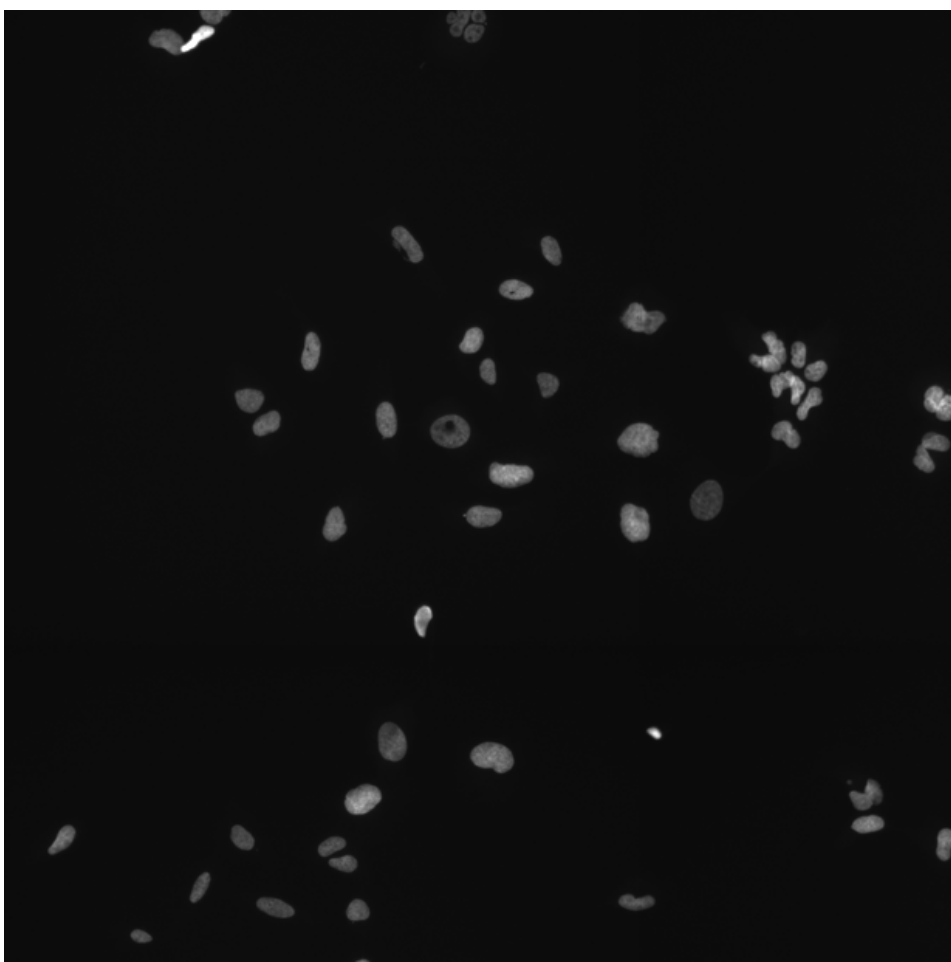
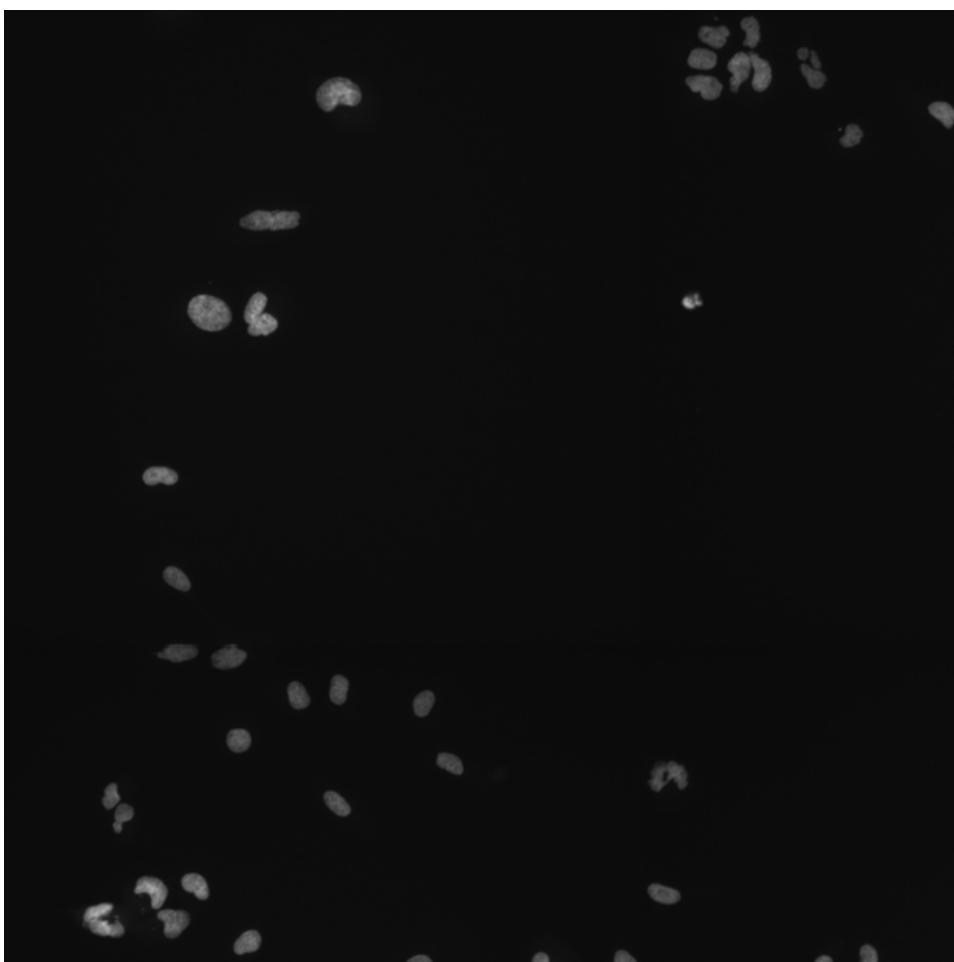
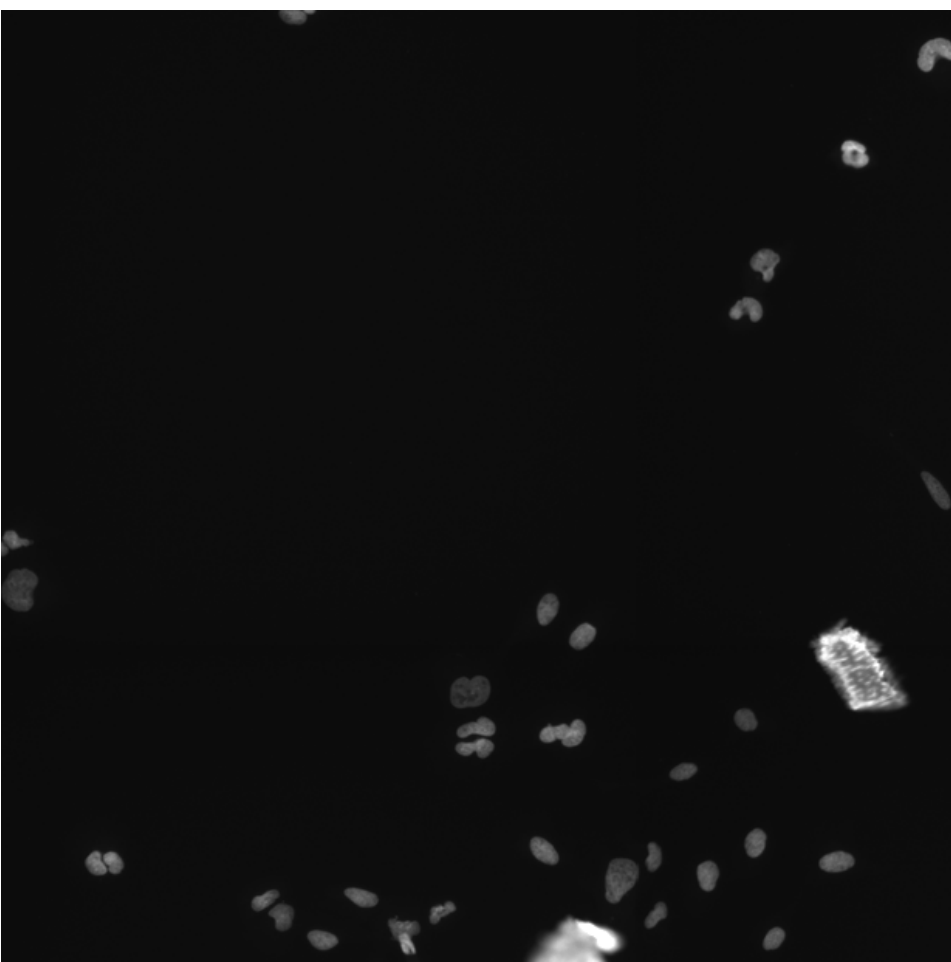
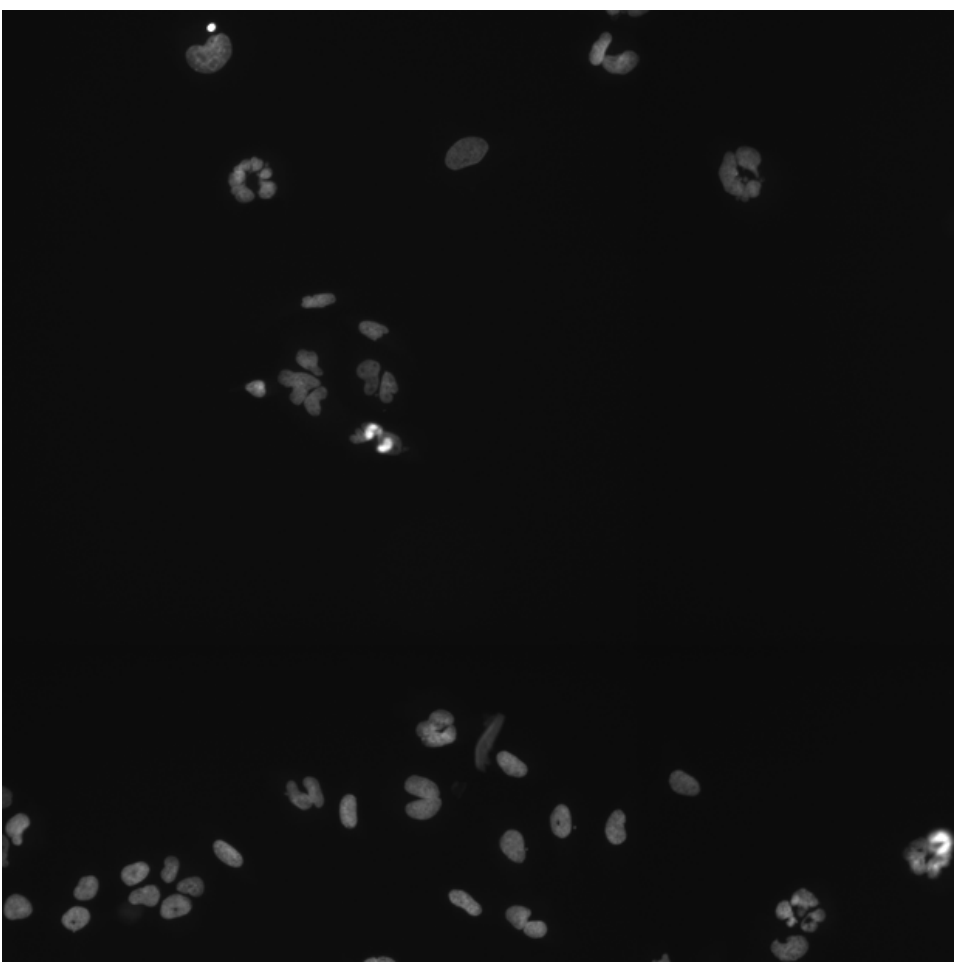
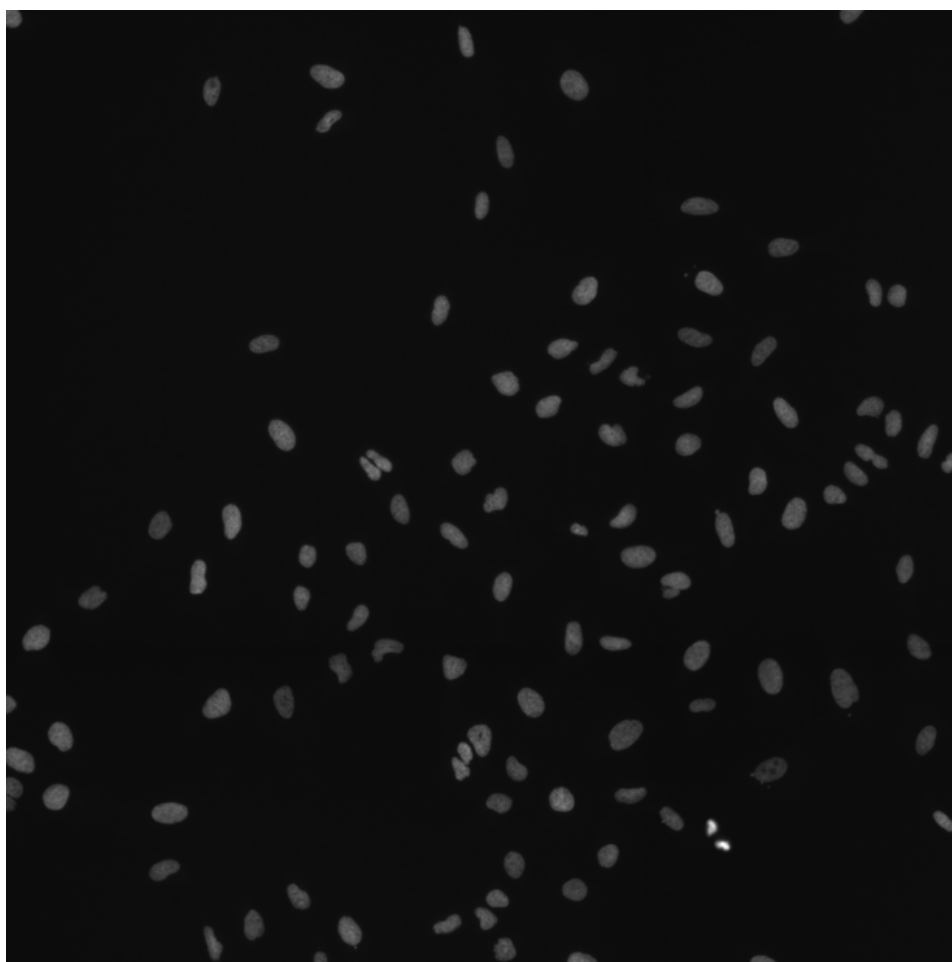
CDC42.Q61L (41755)

CDC42.Q61L (41756)

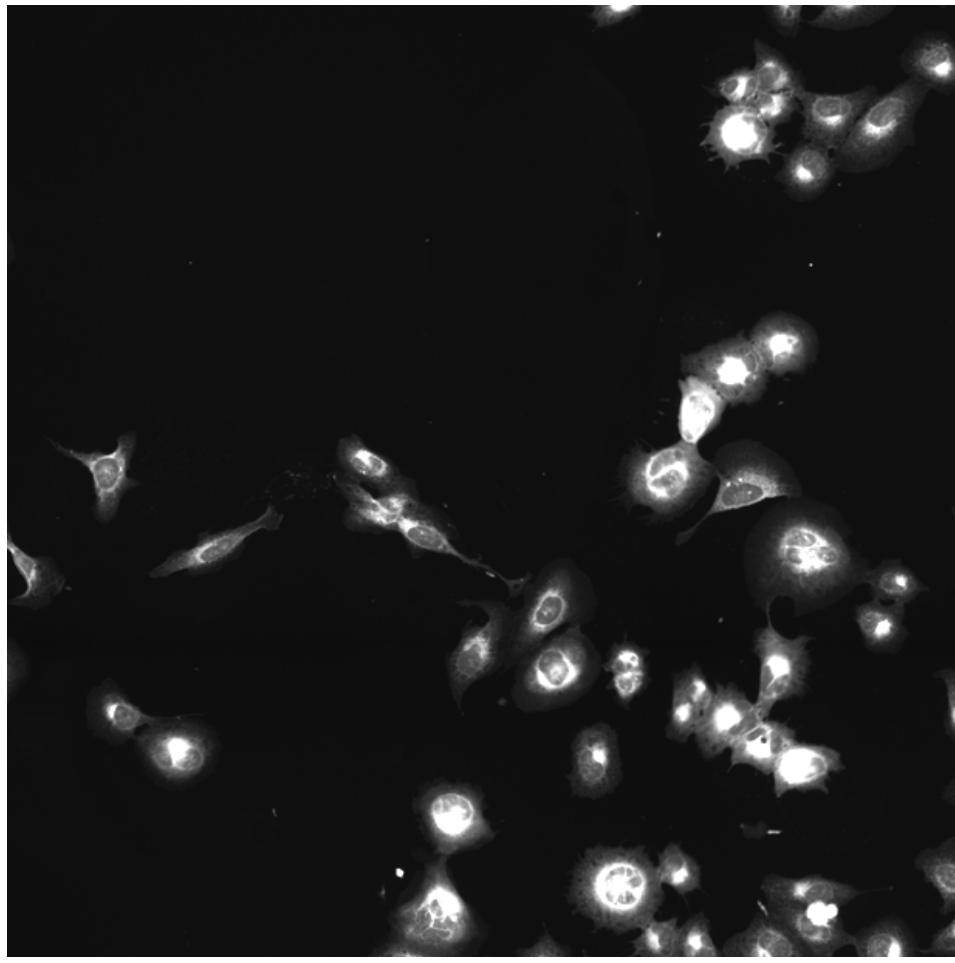
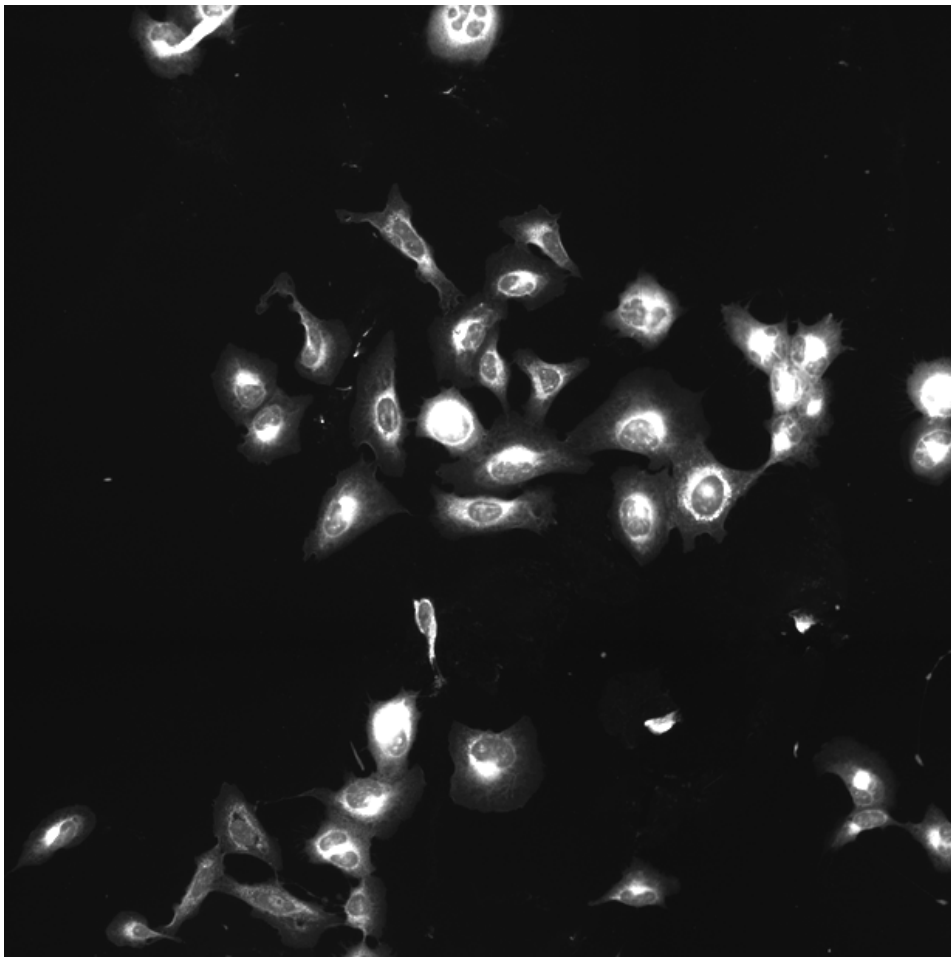
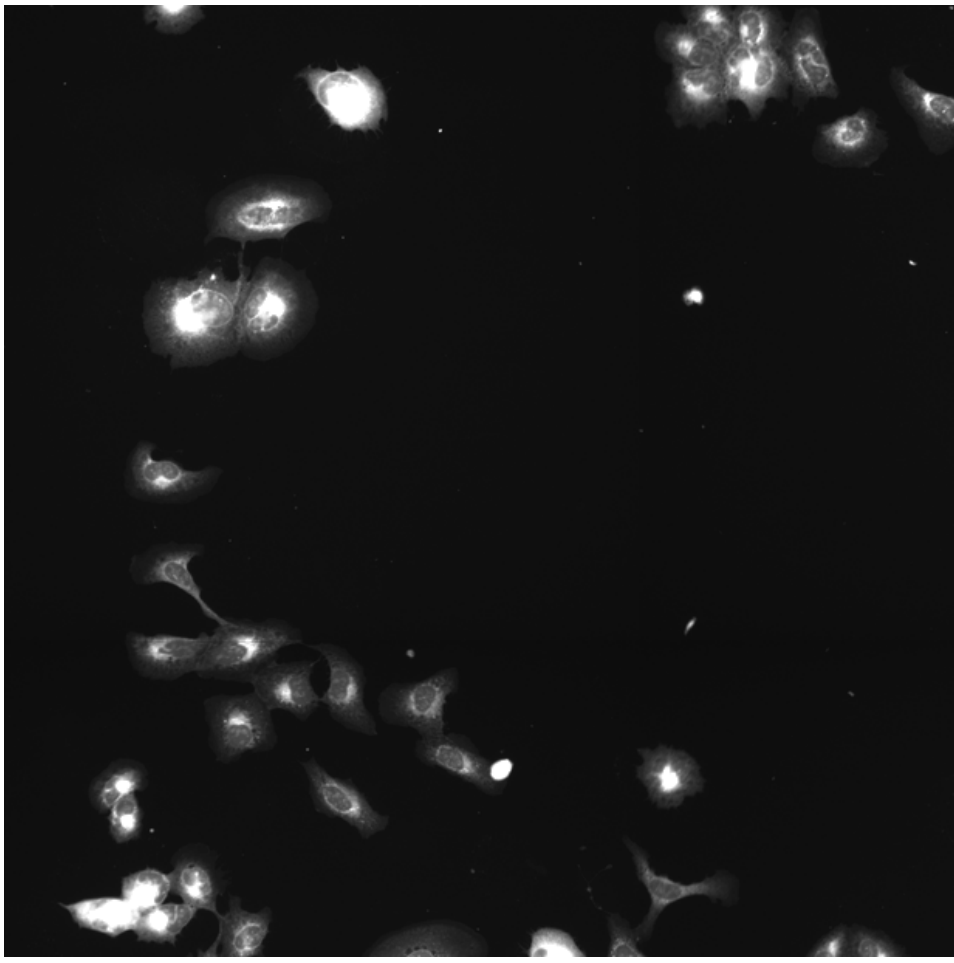
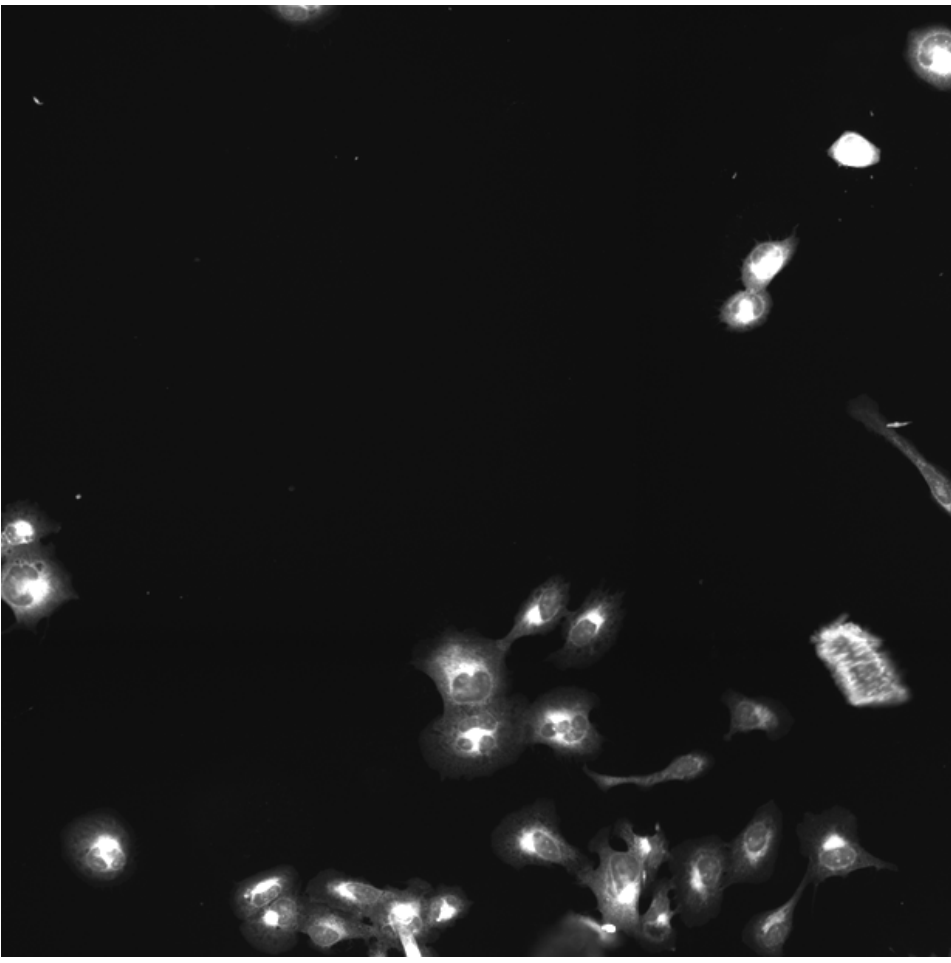
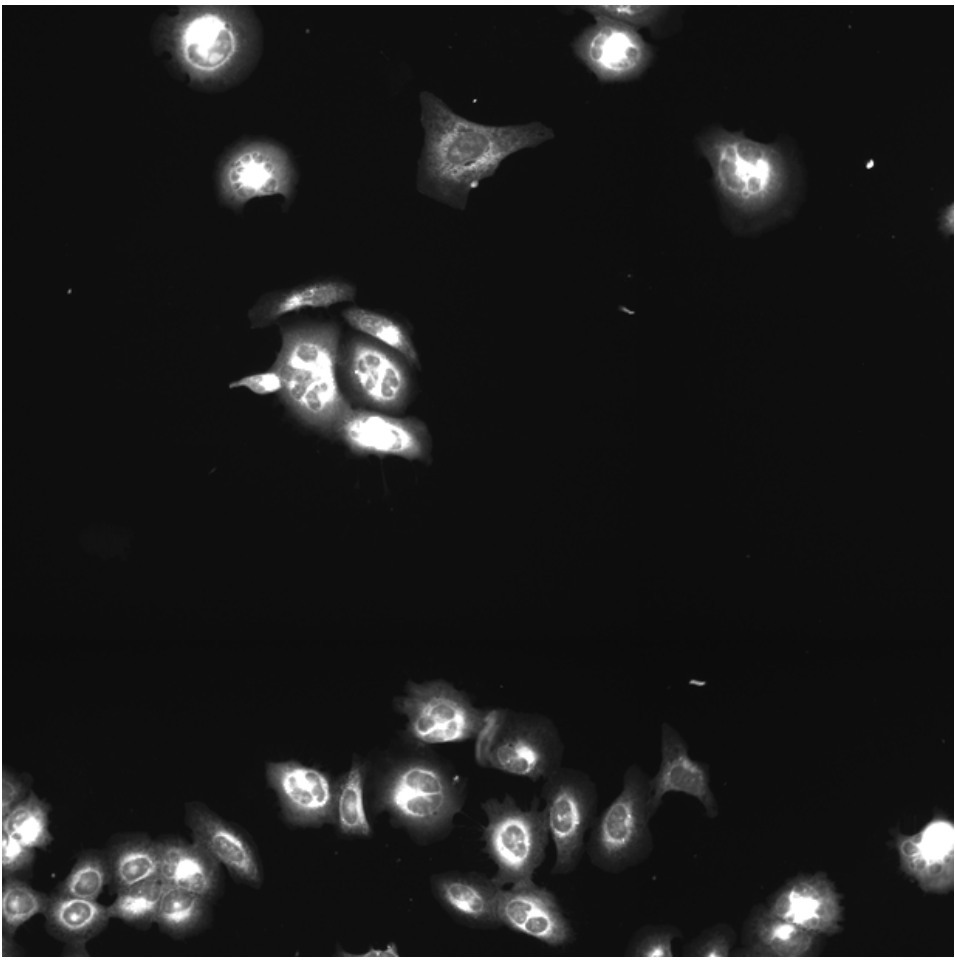
CDC42.Q61L (41757)

CDC42.Q61L (41754)

DNA

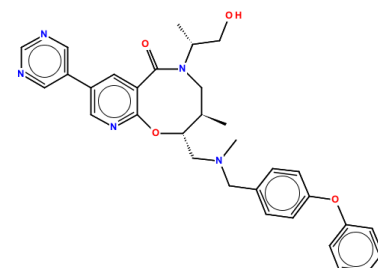
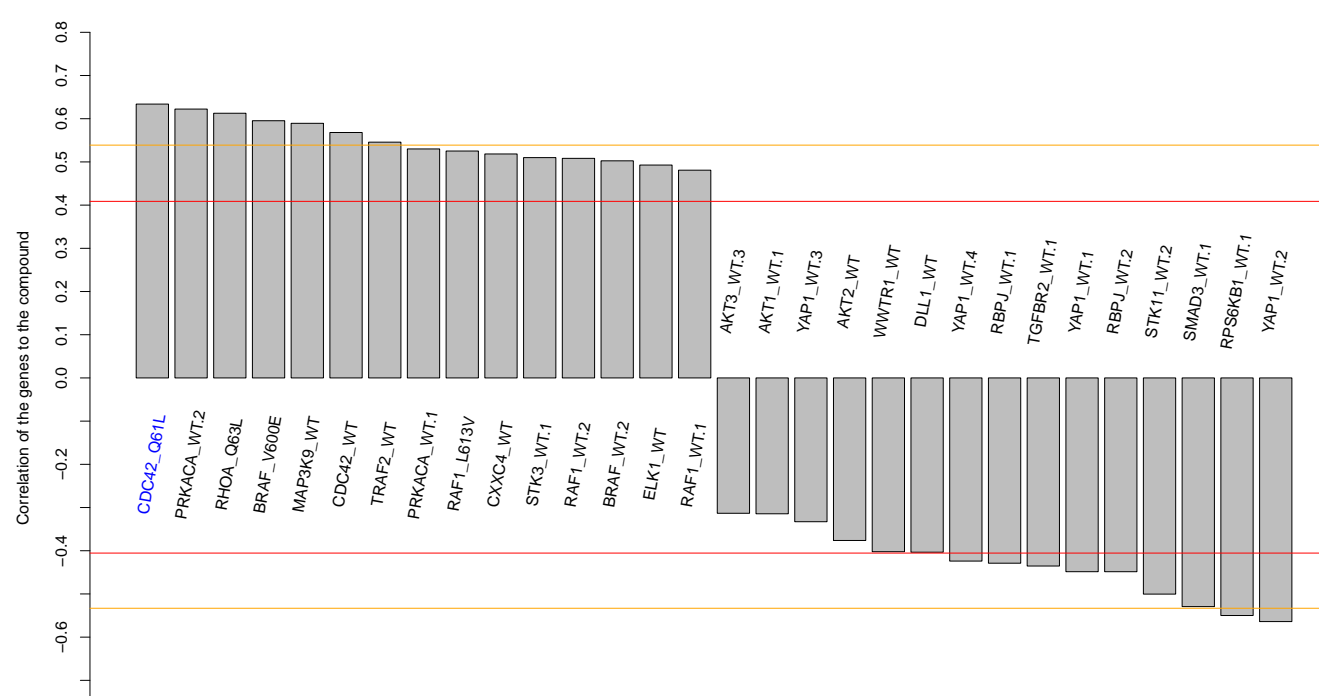
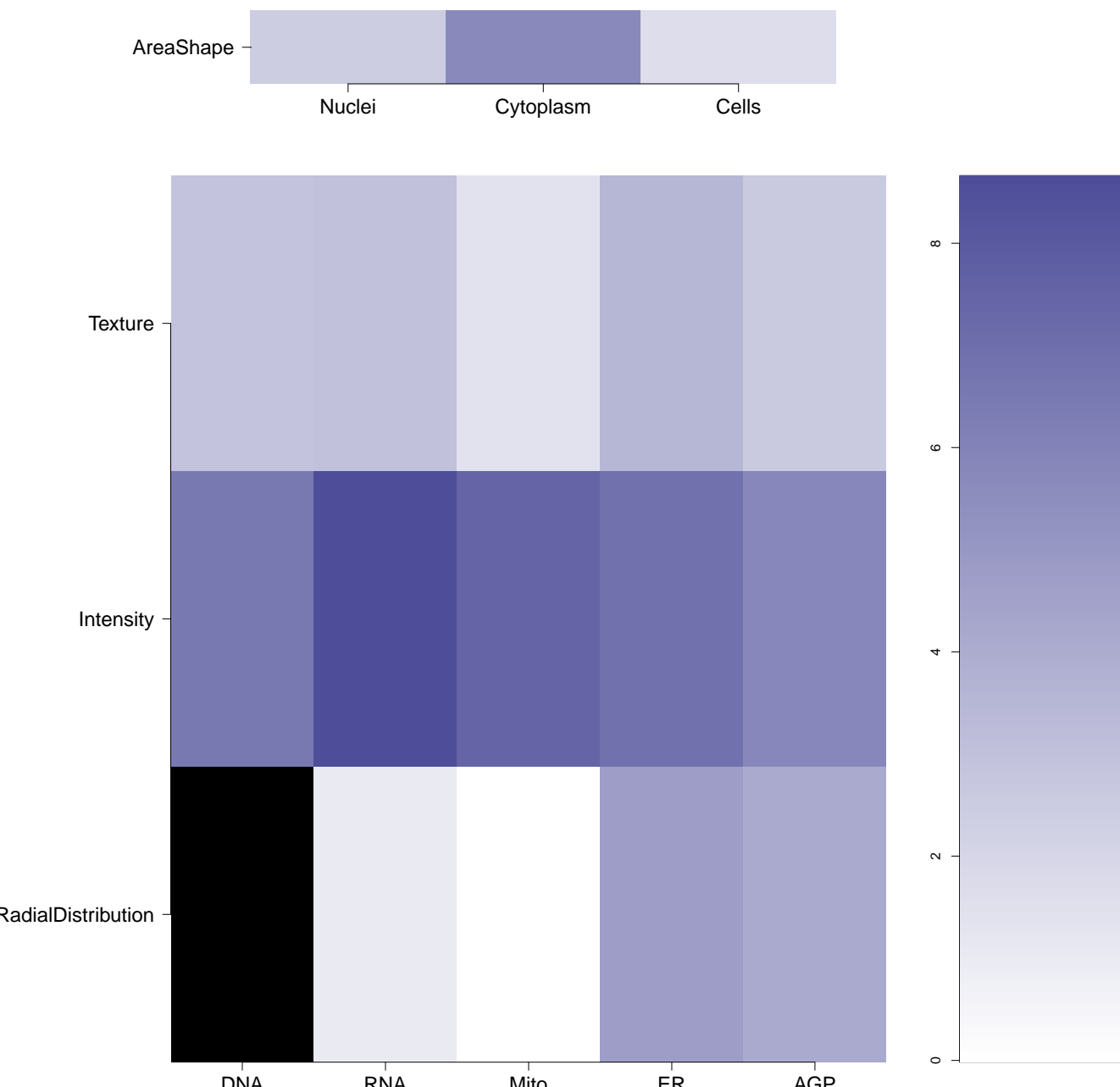

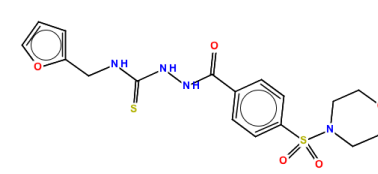
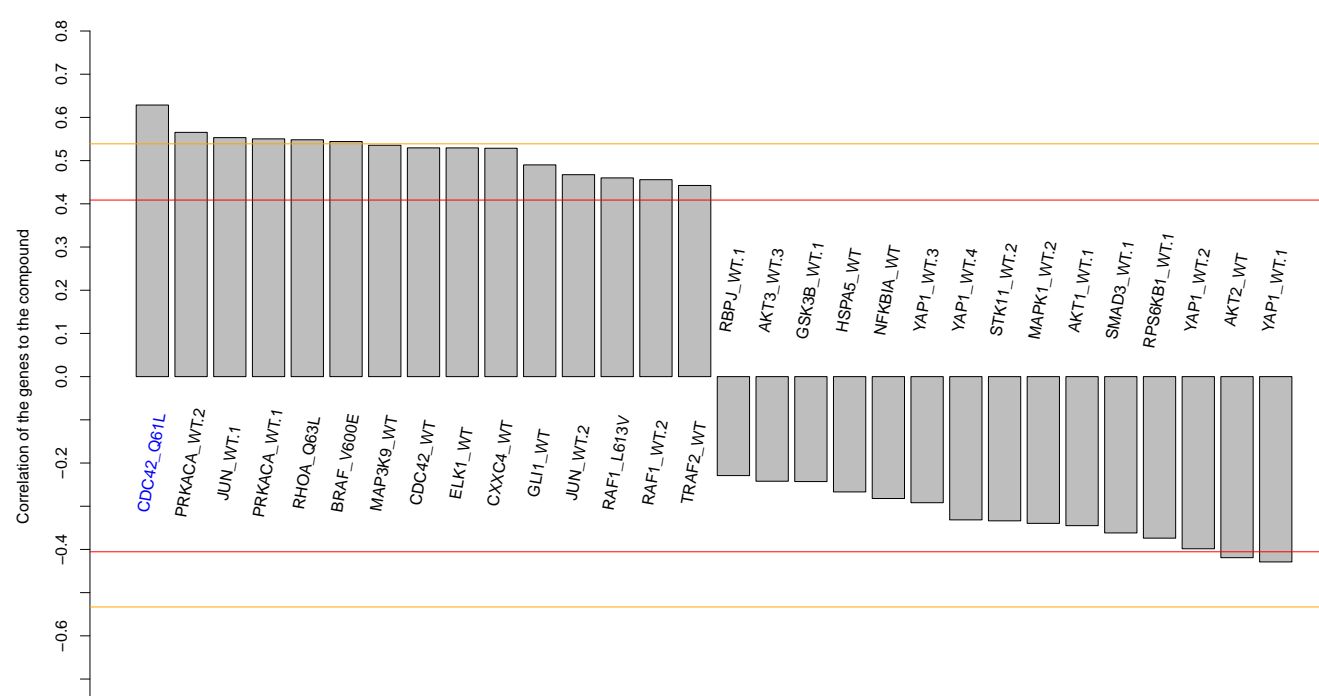
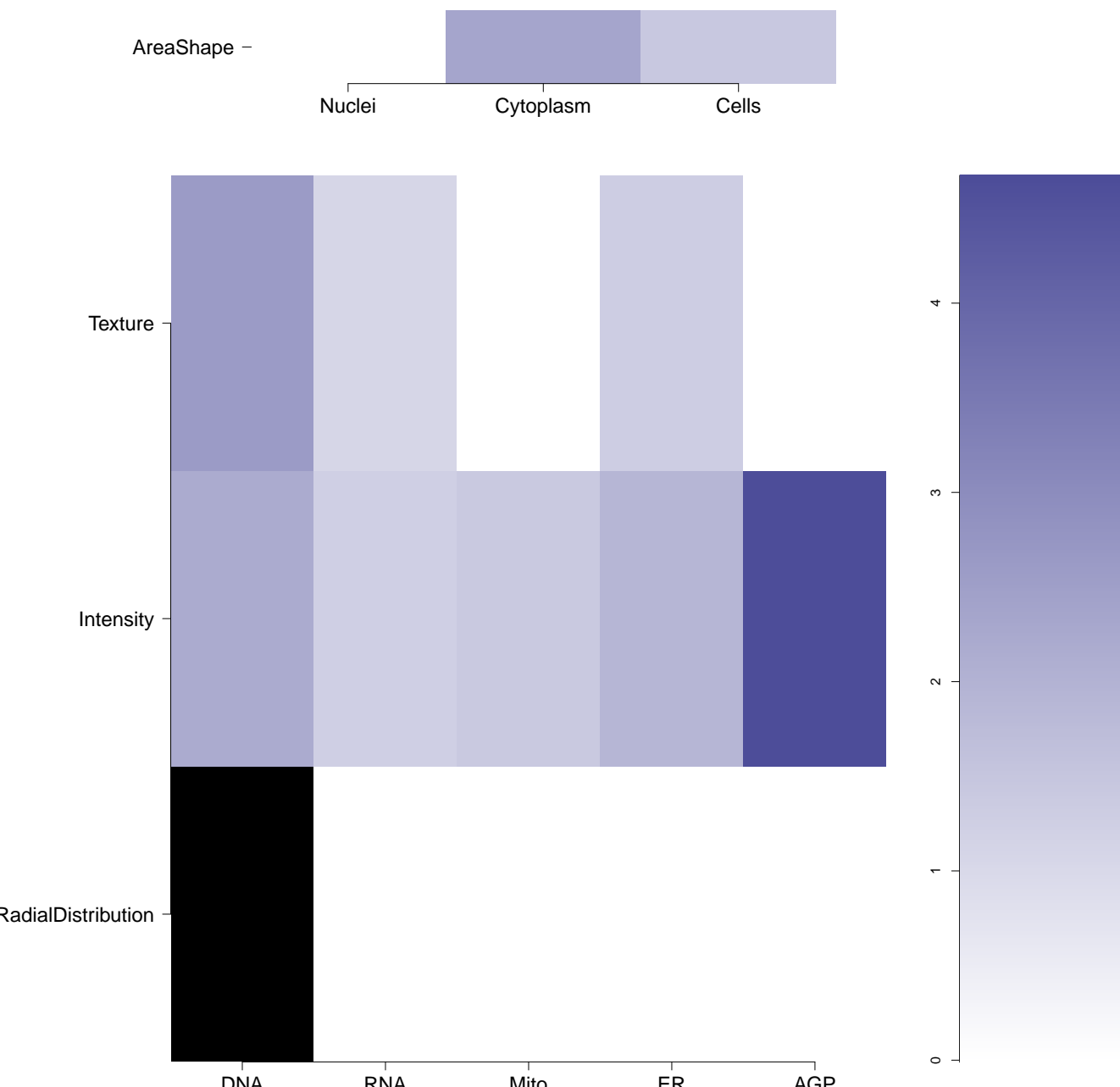
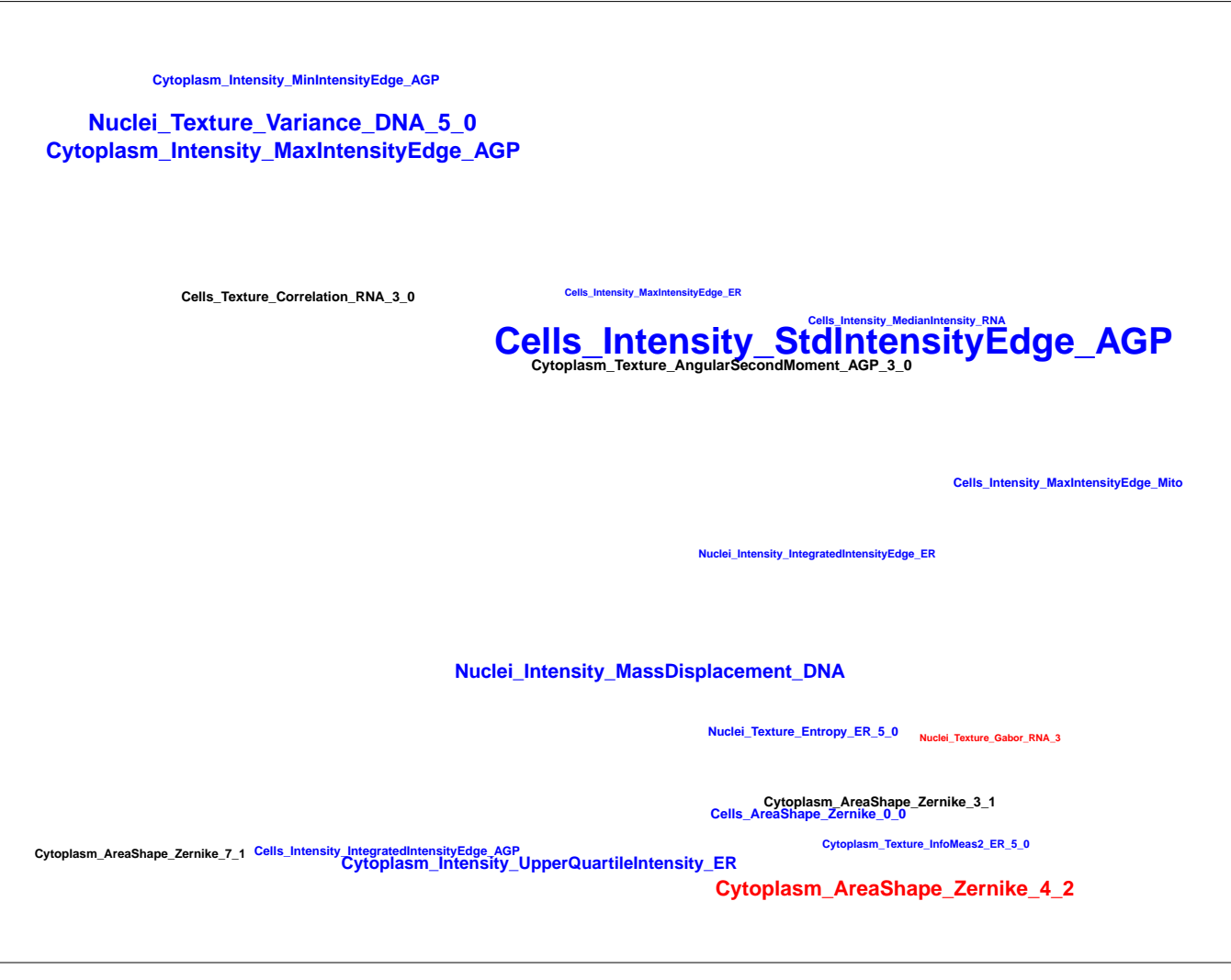
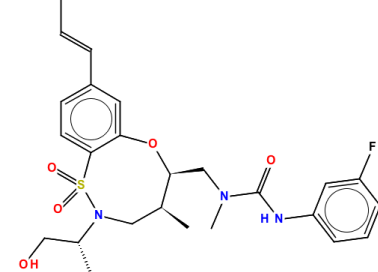
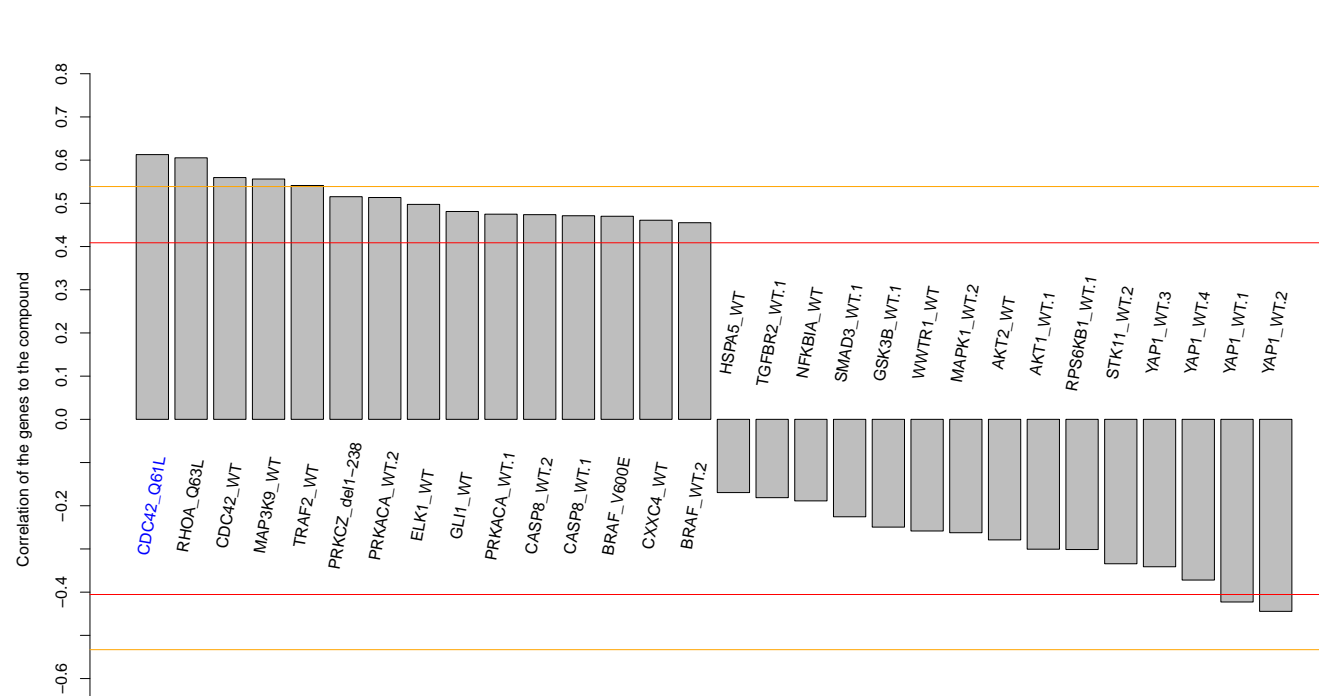
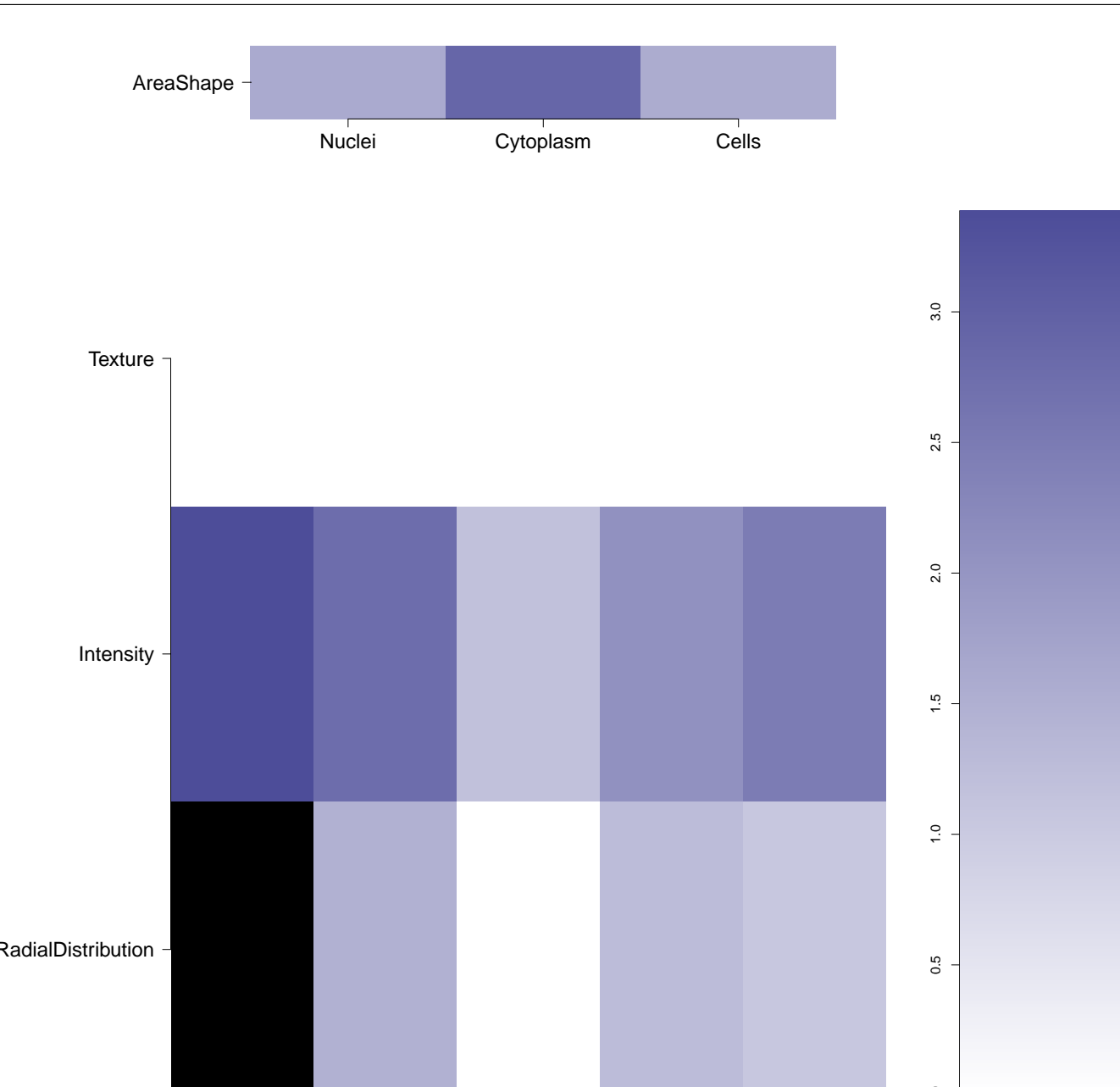

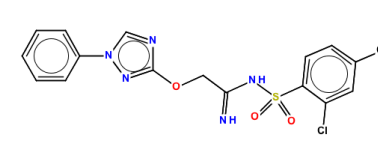
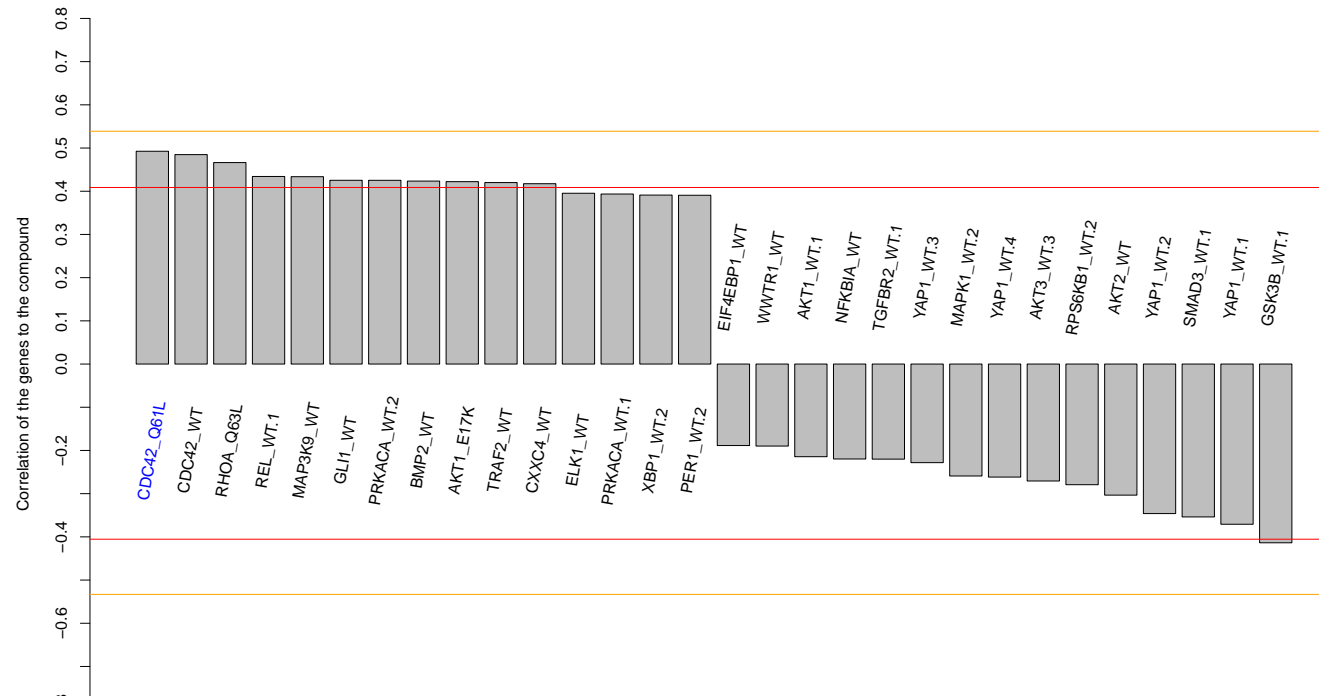
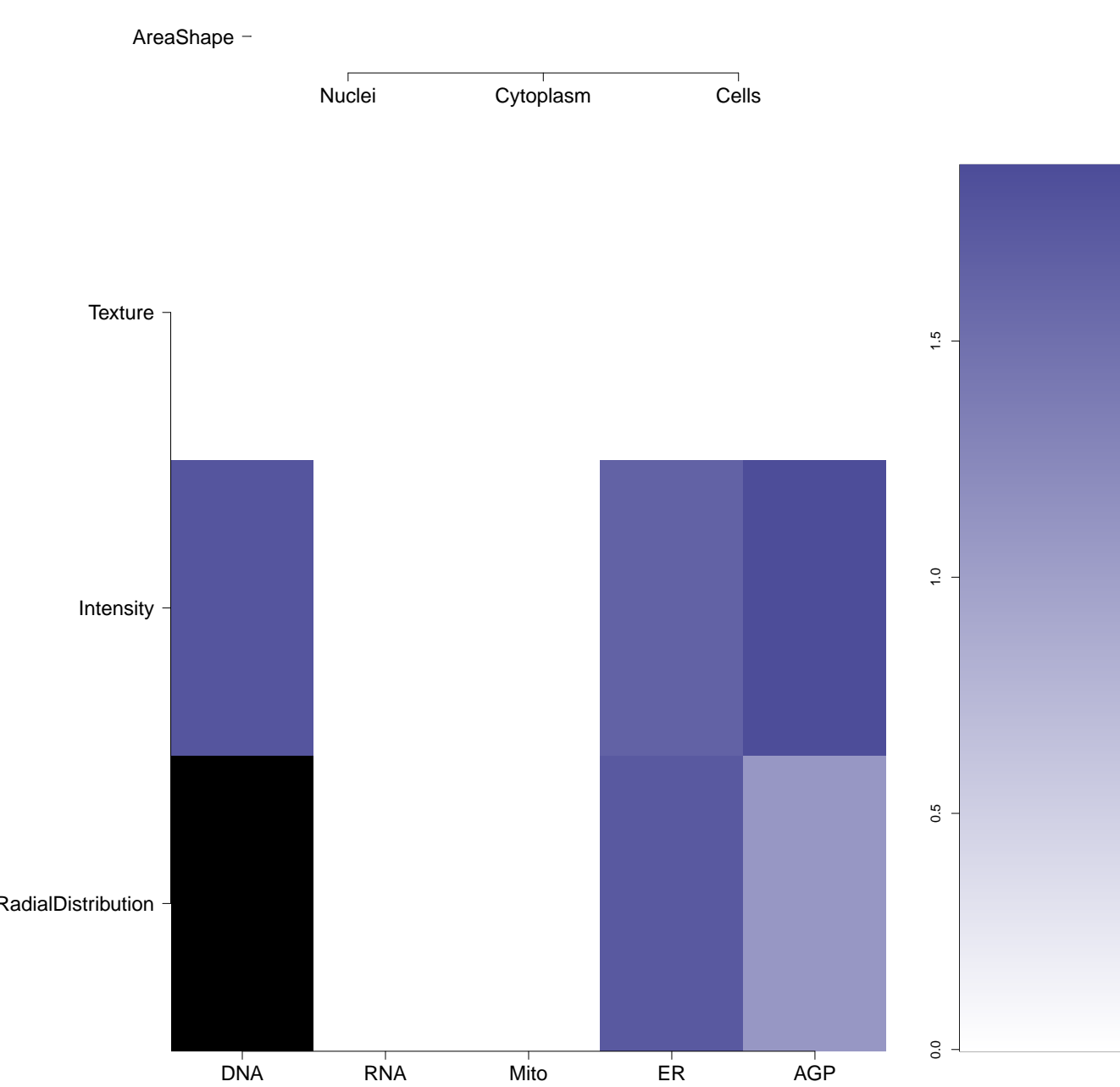
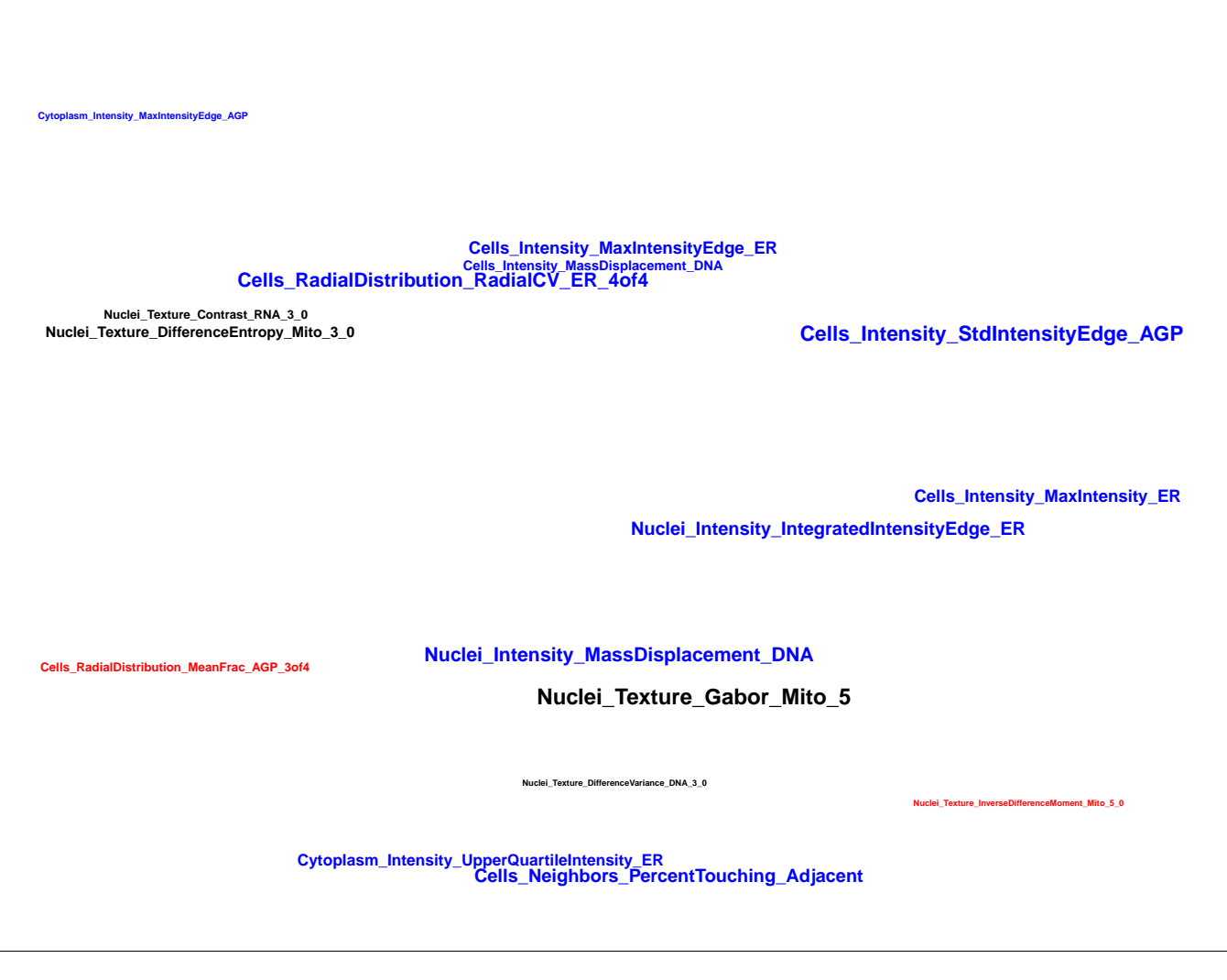
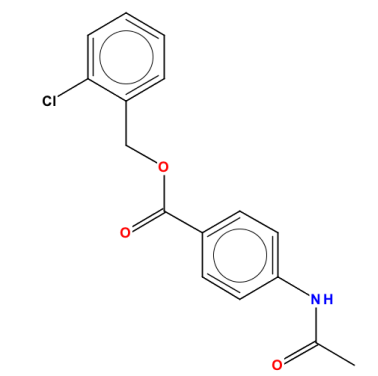
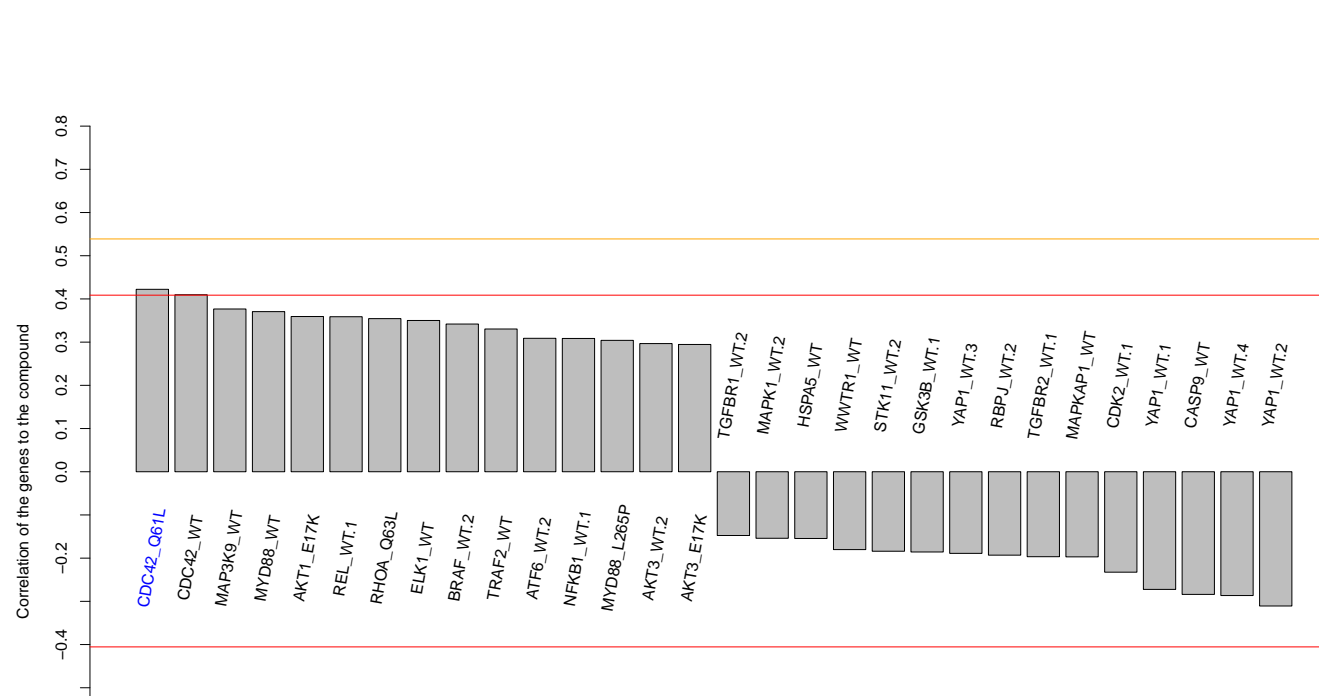
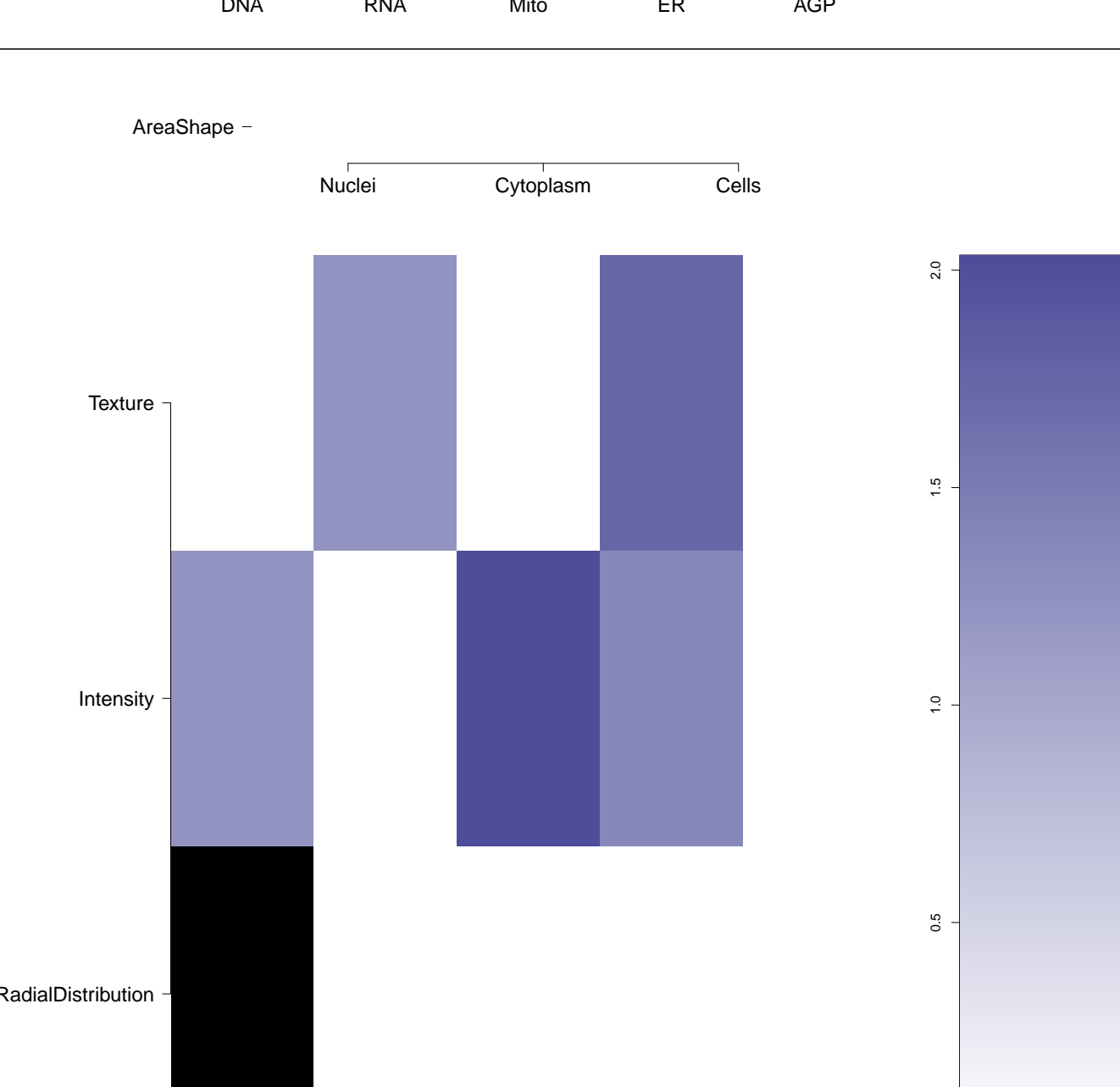

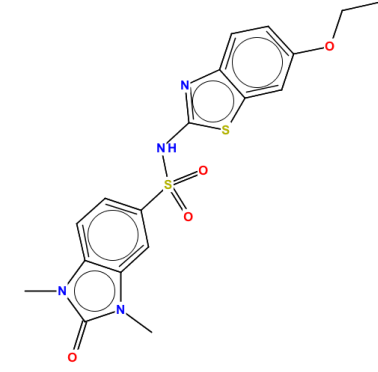
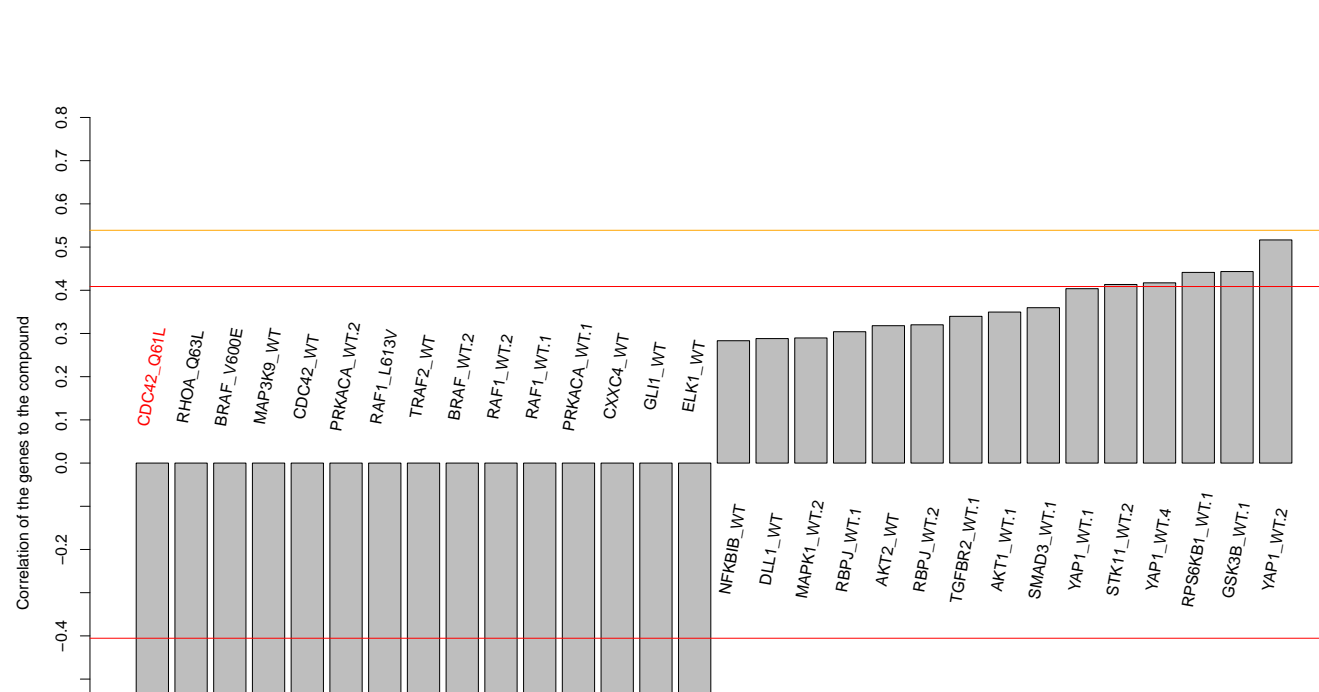
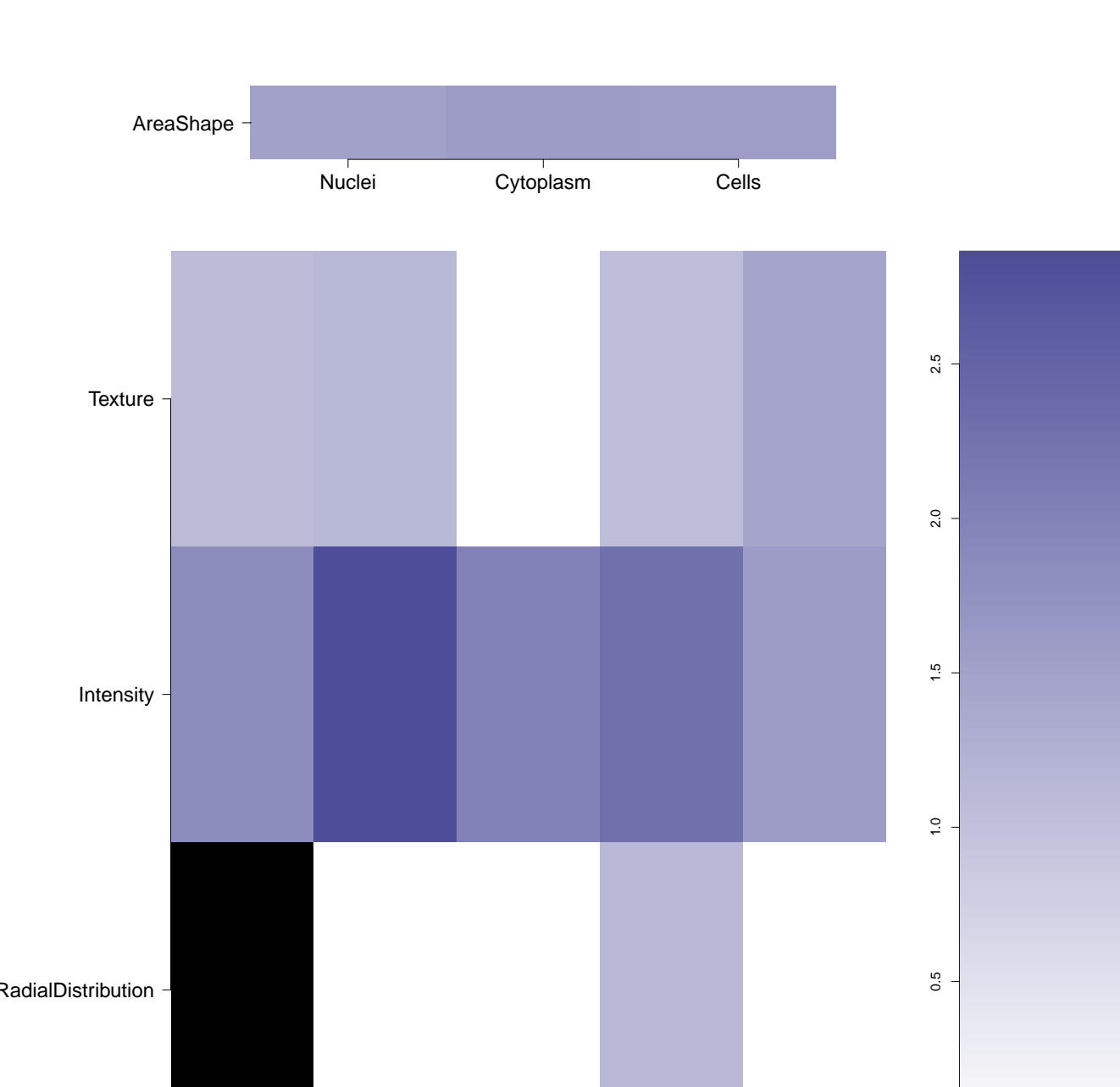

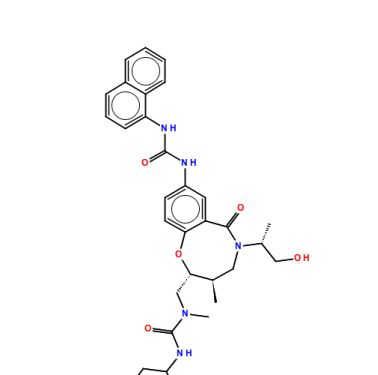
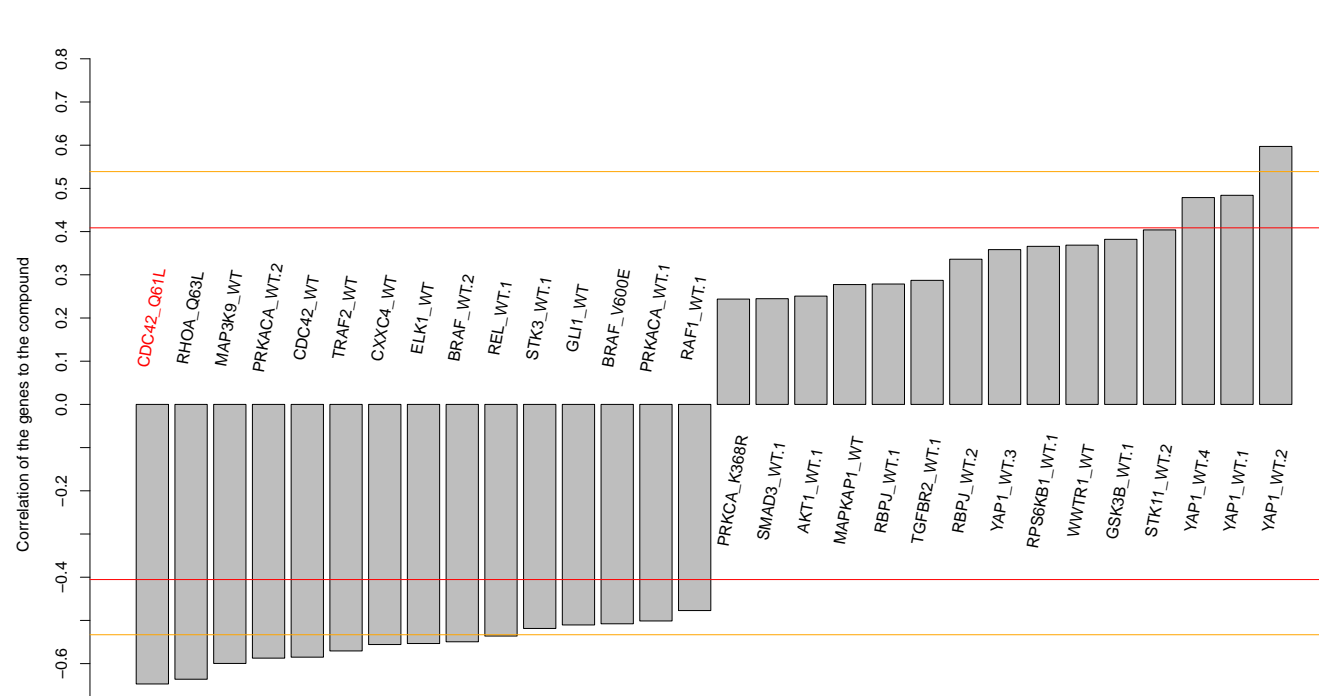
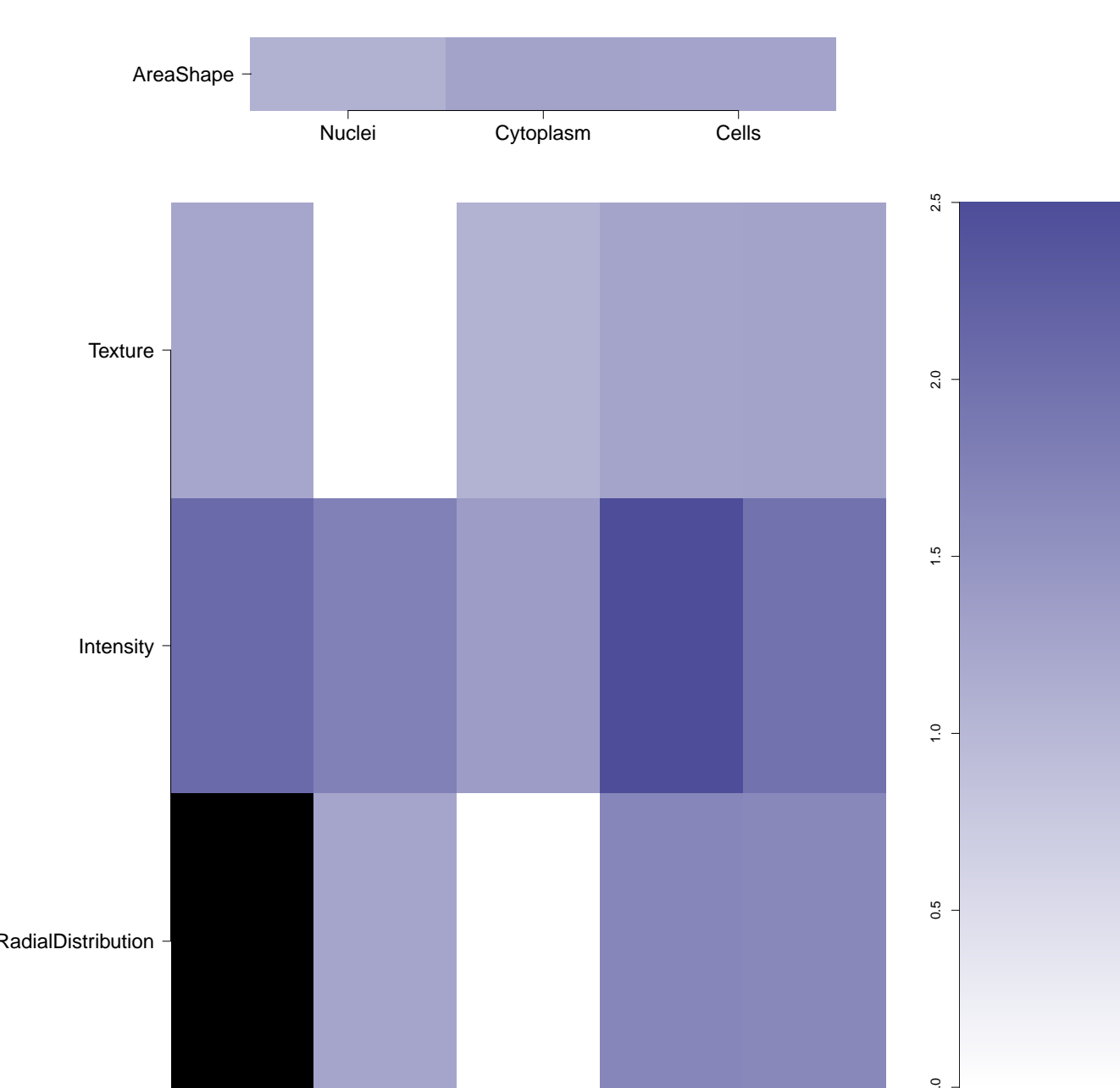
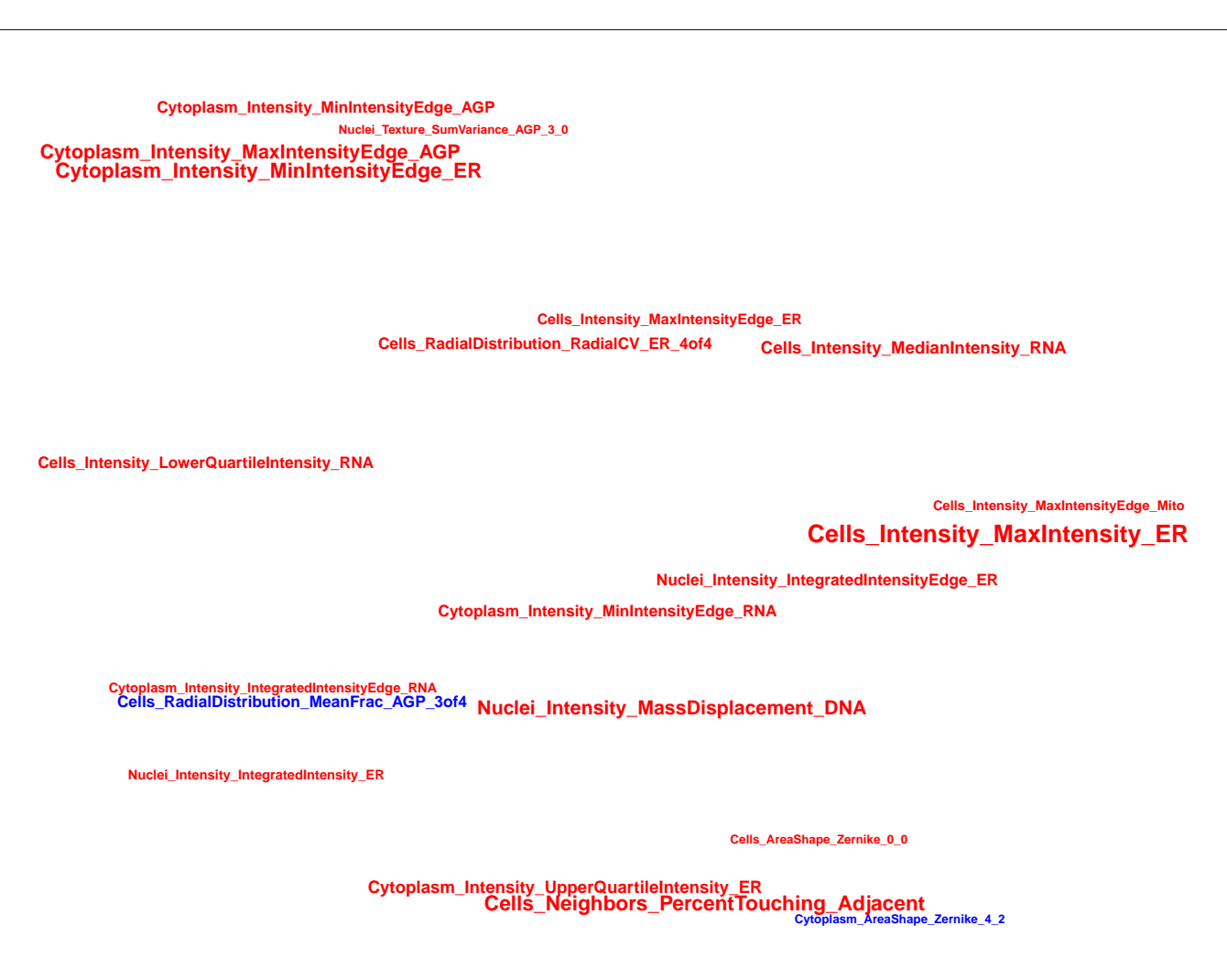


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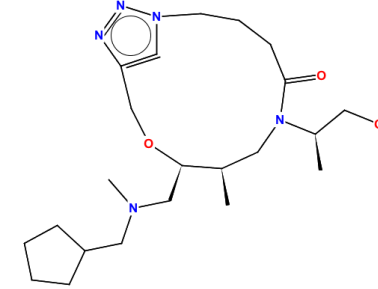
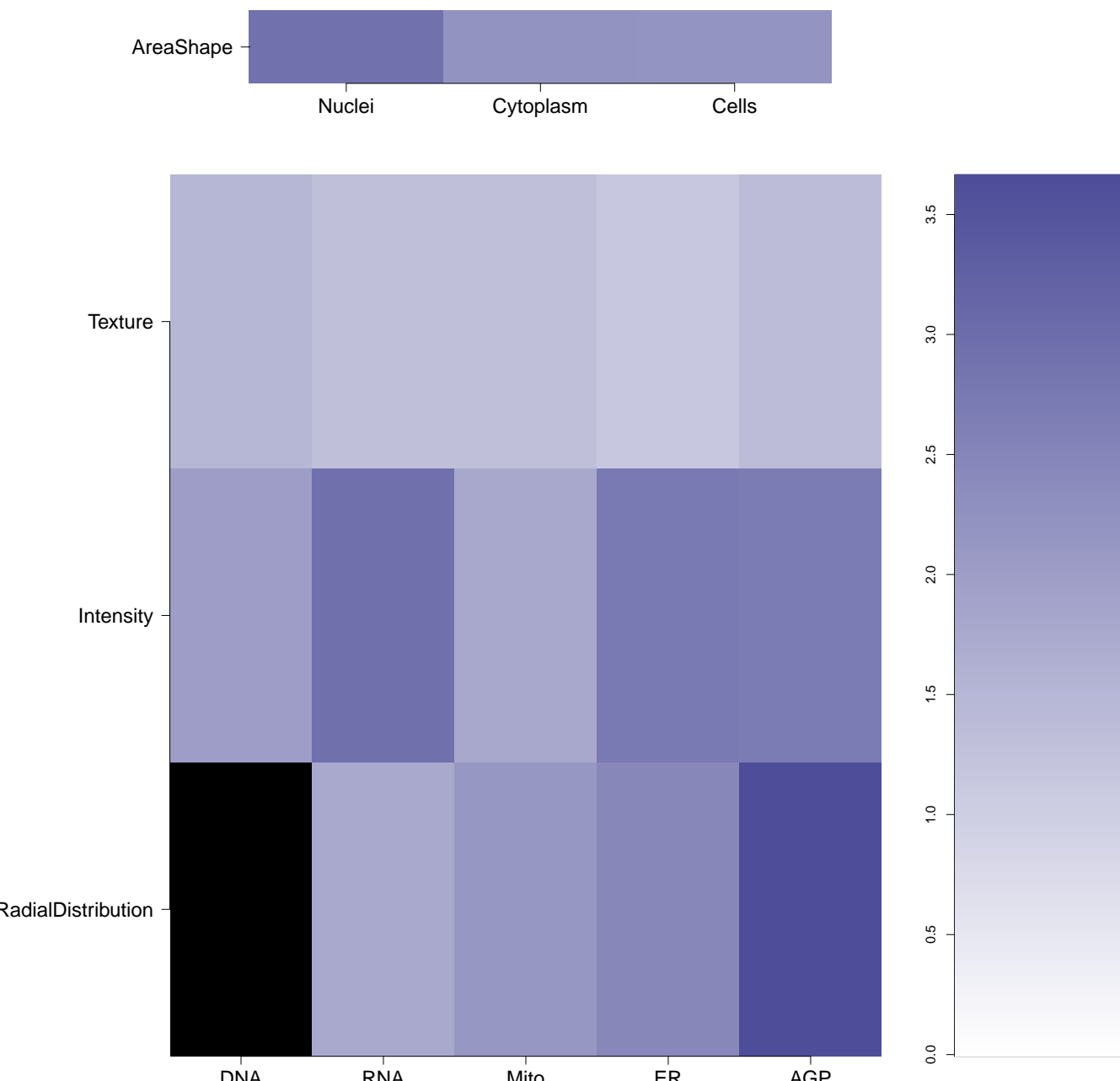
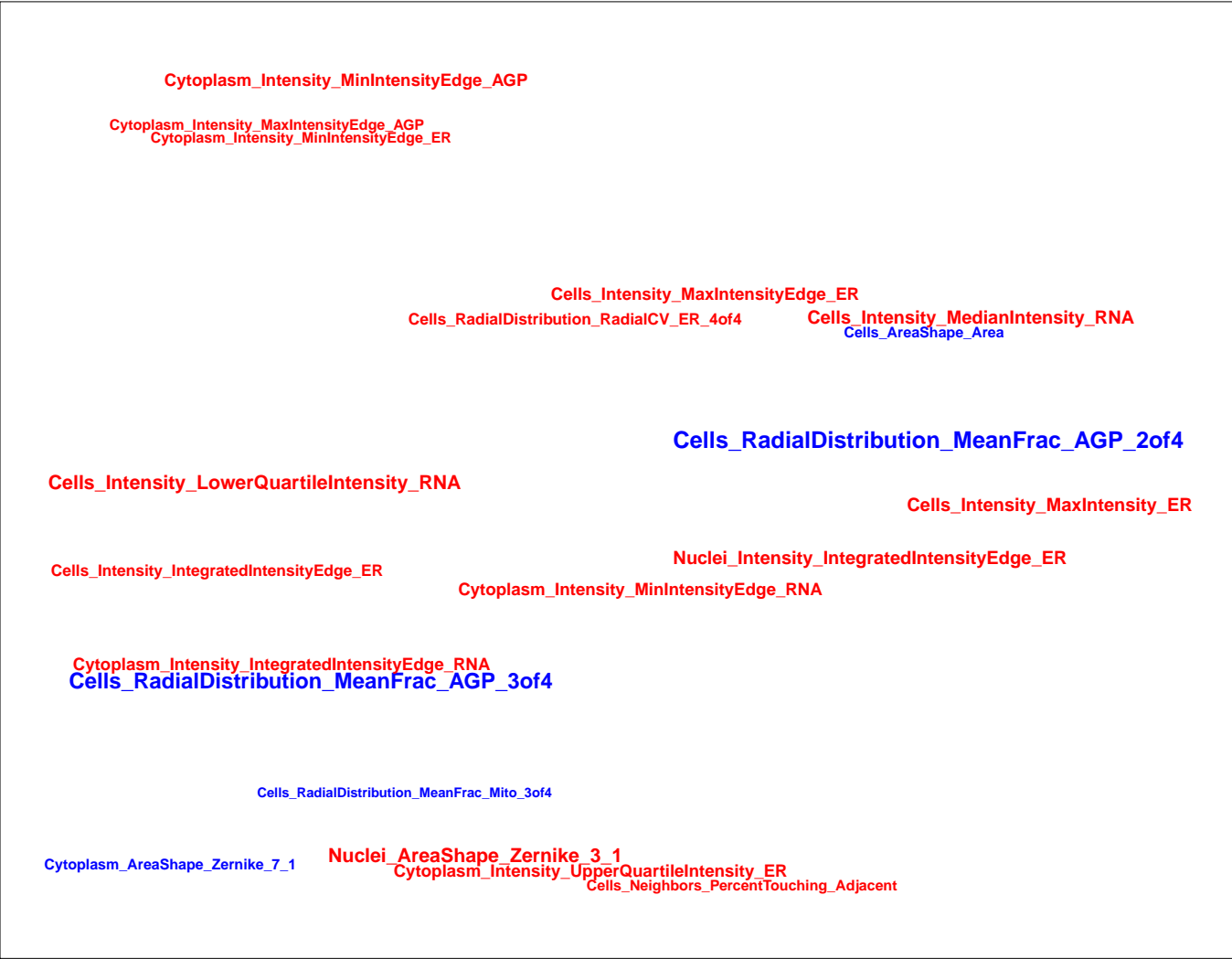
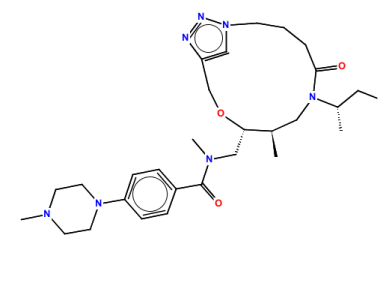
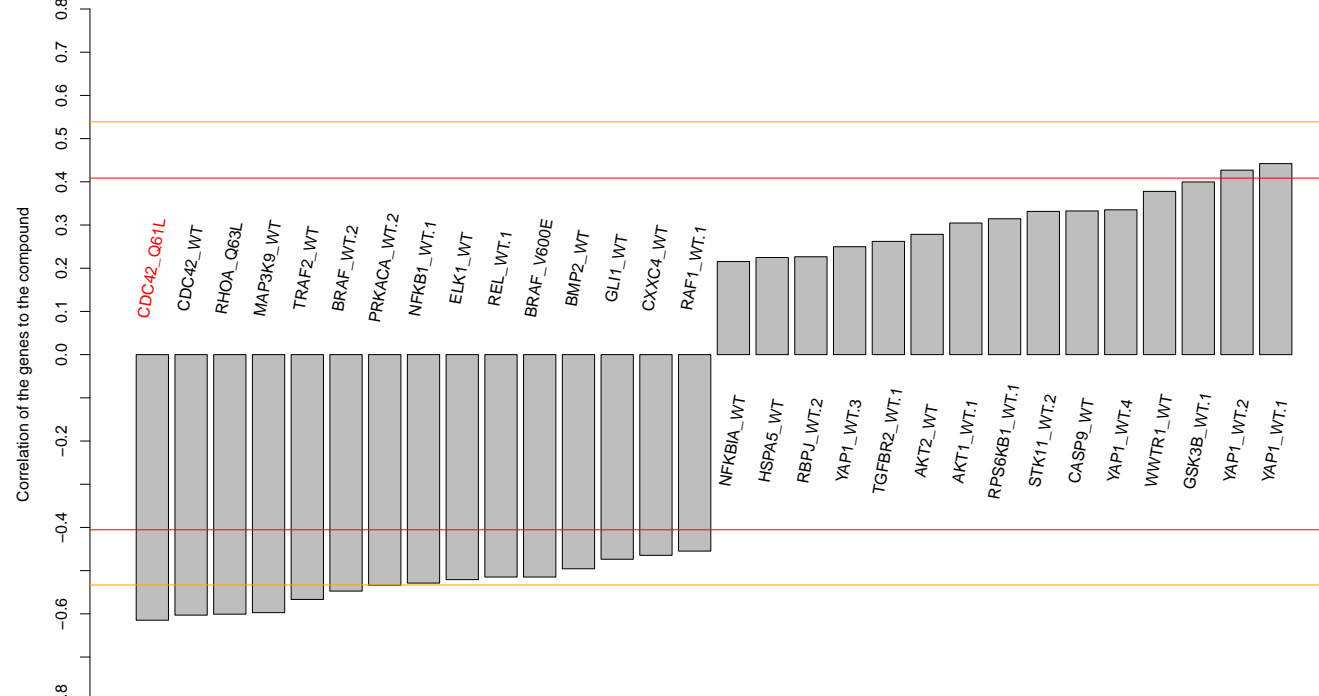
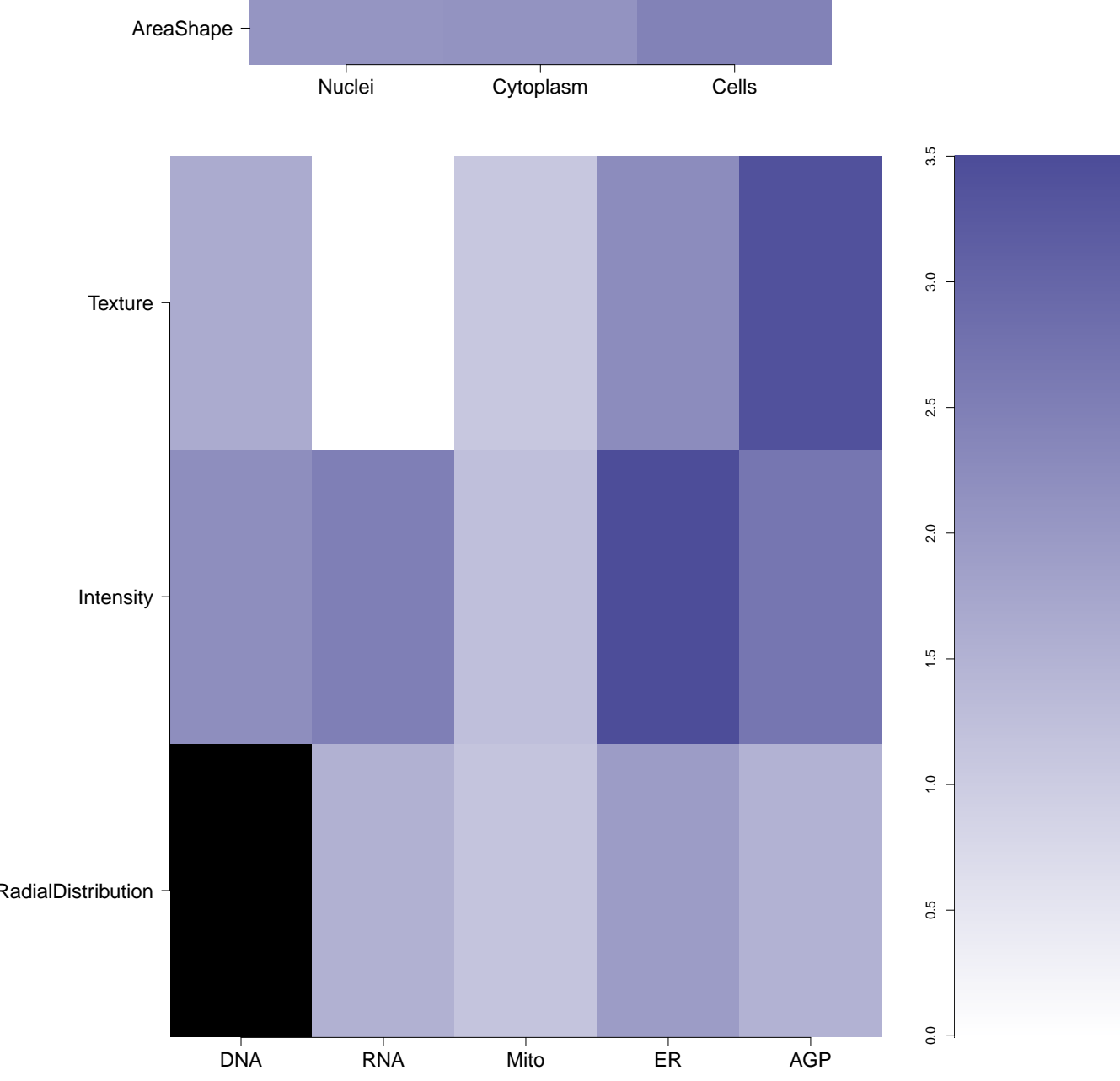
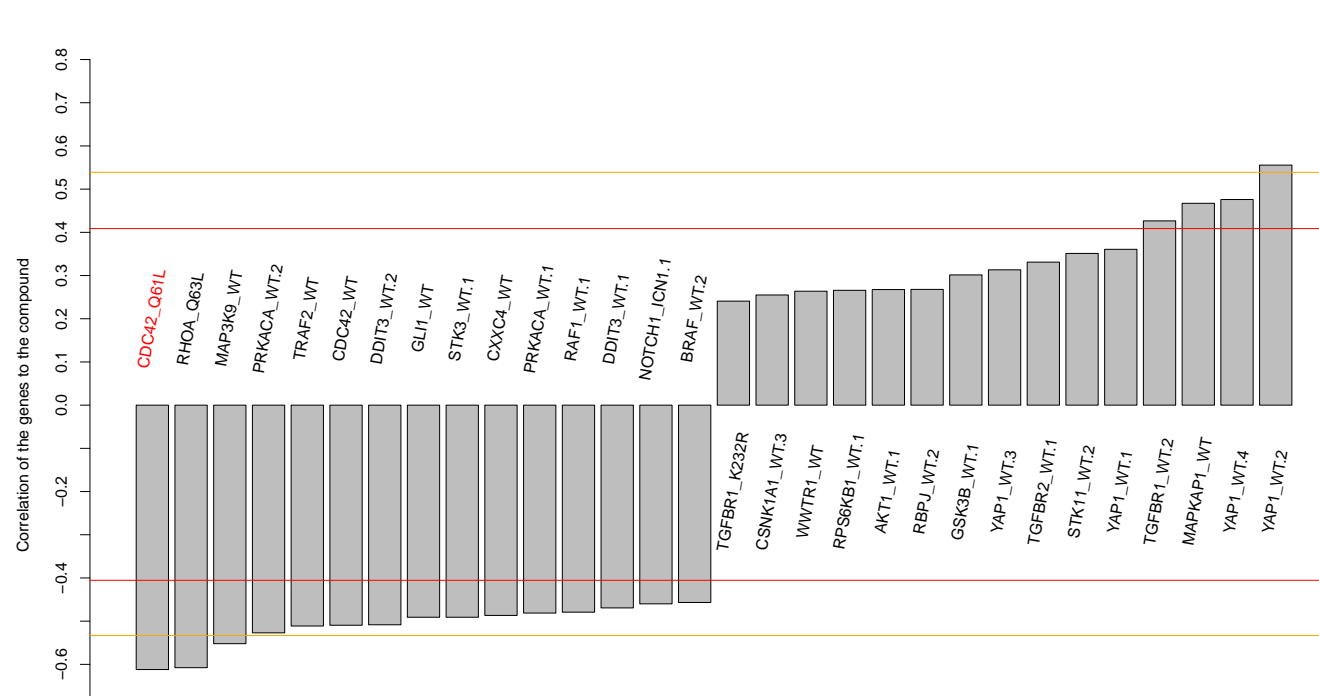
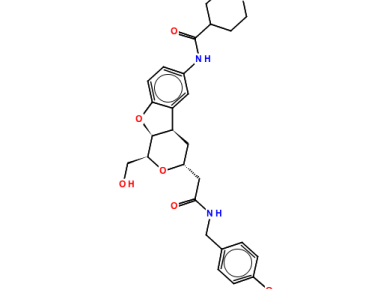
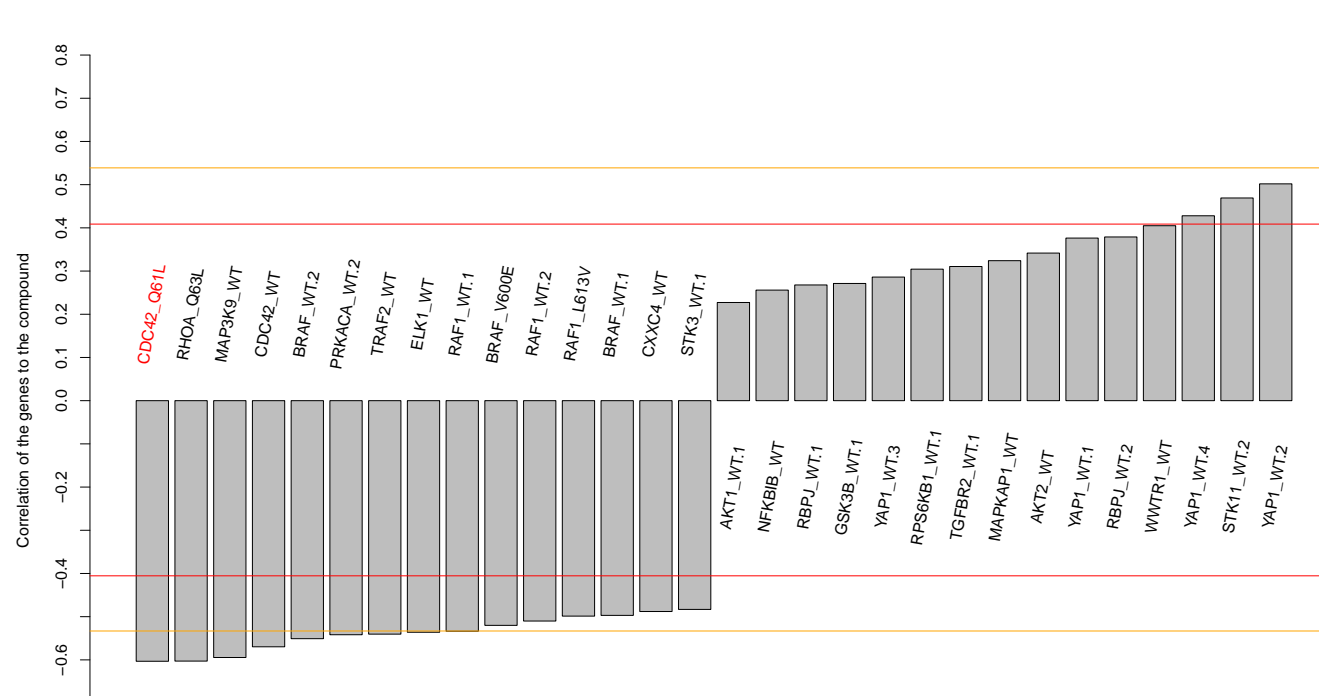
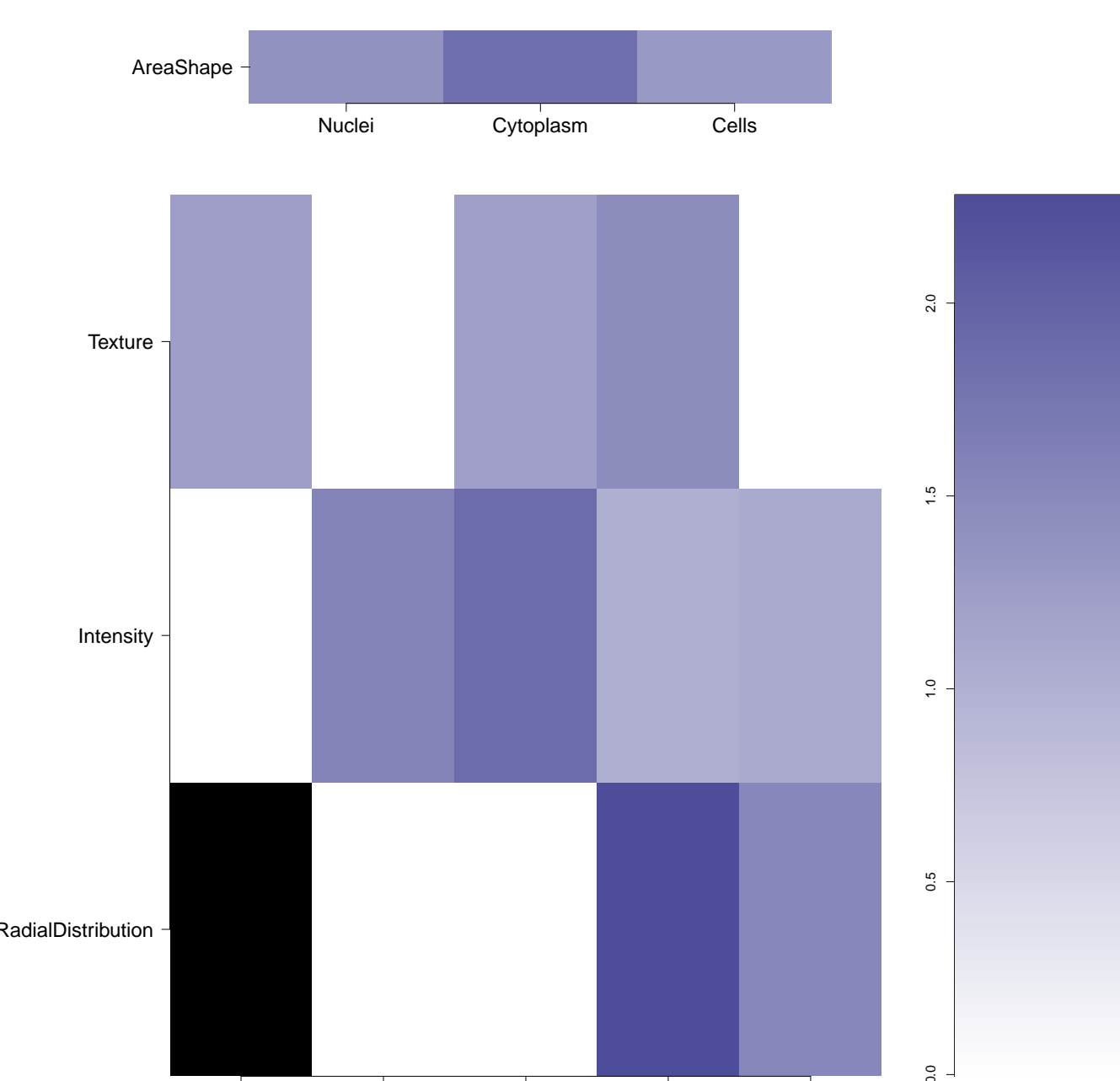
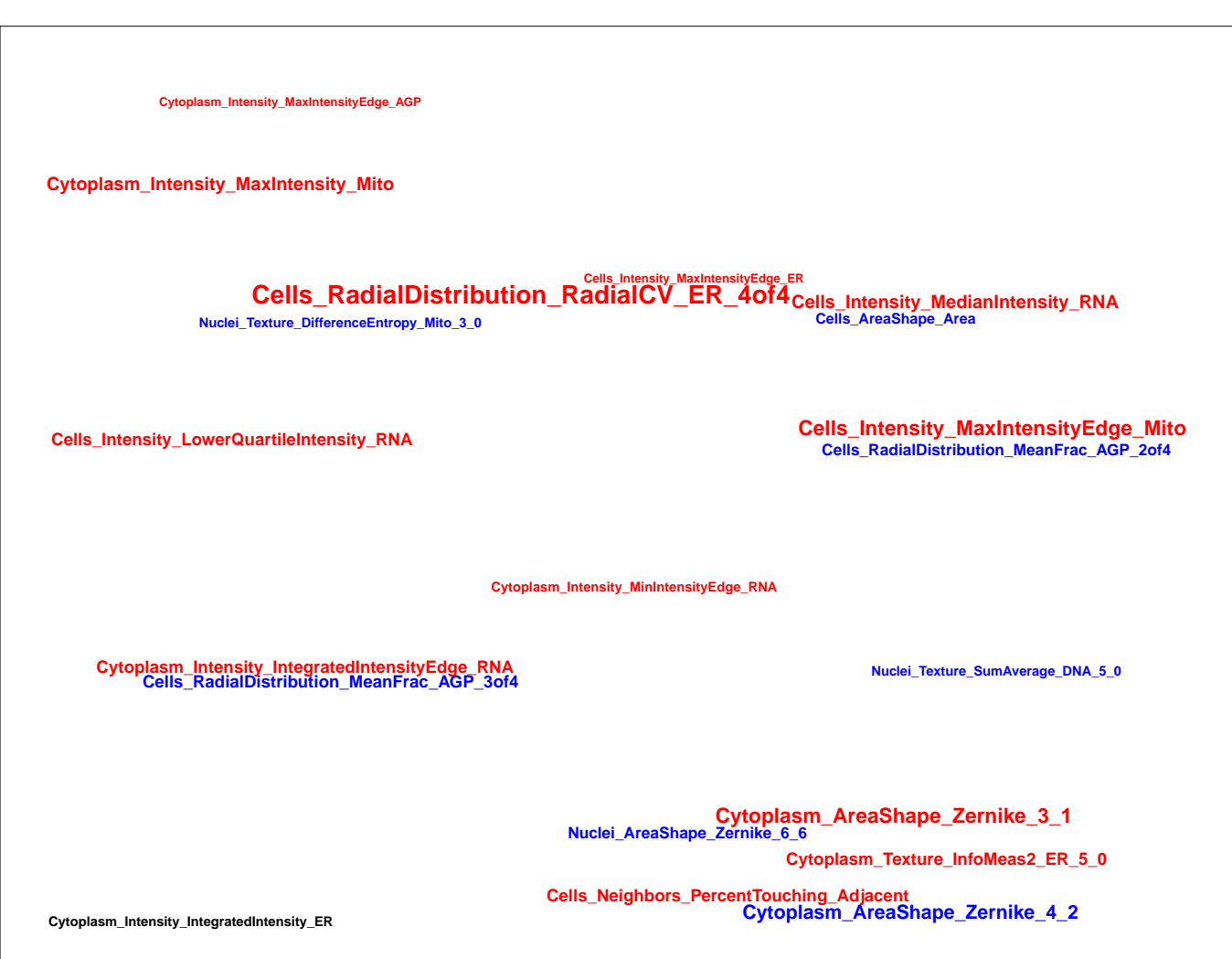
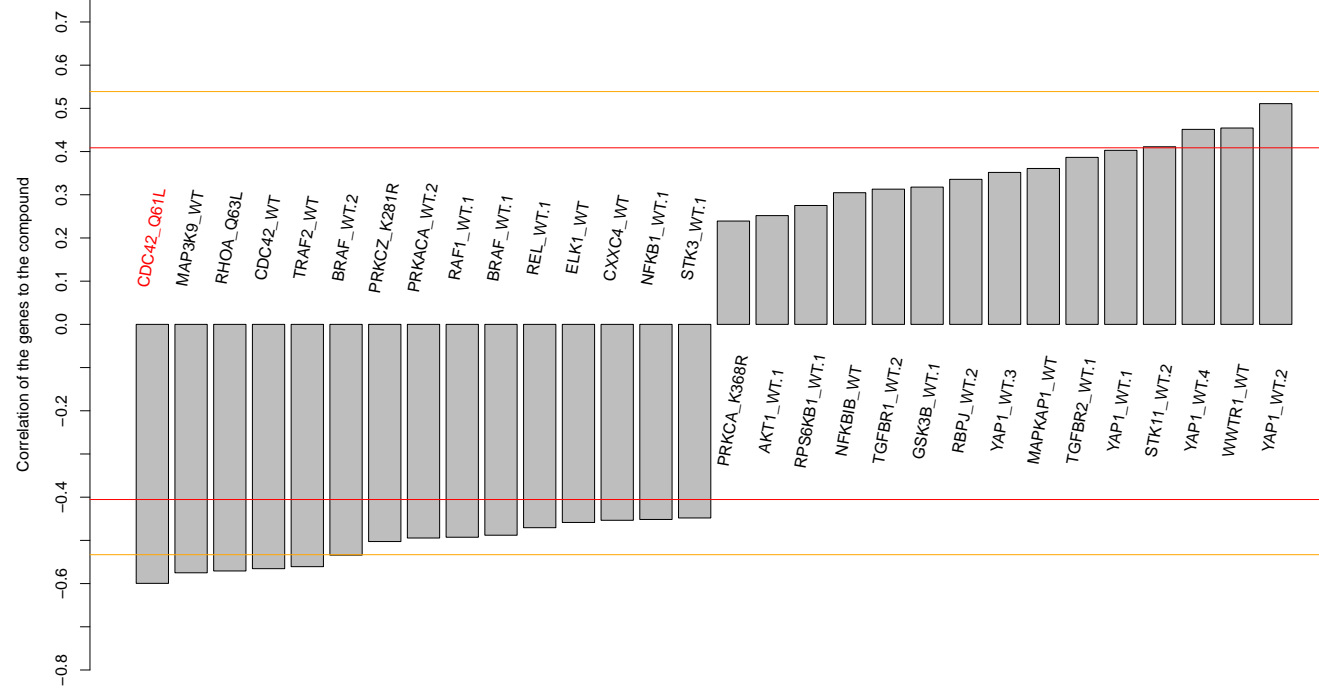
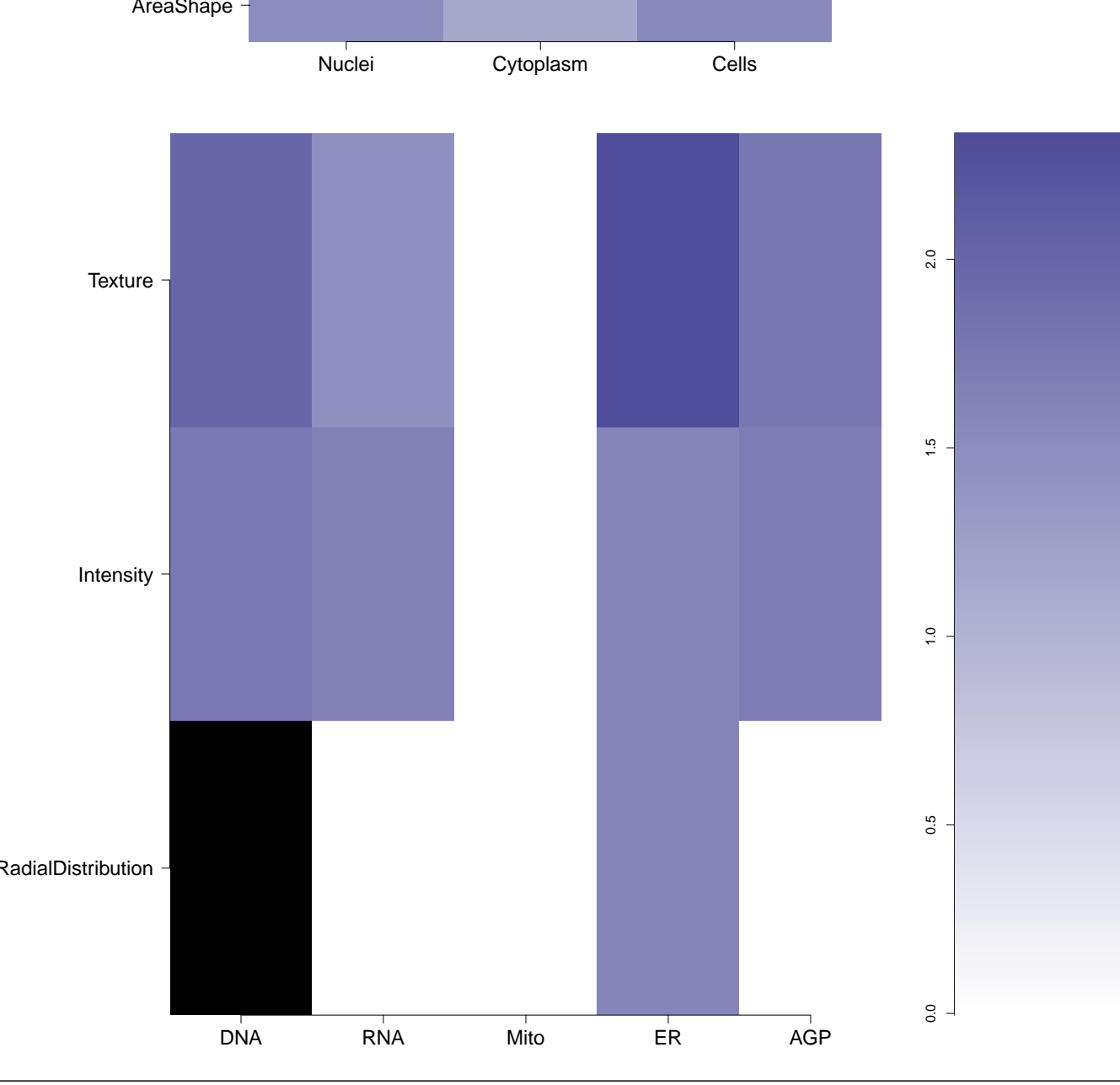

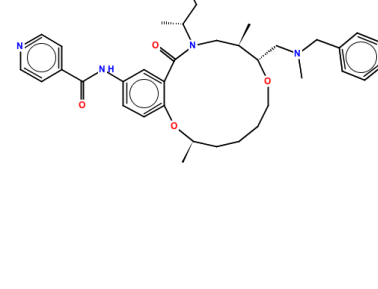
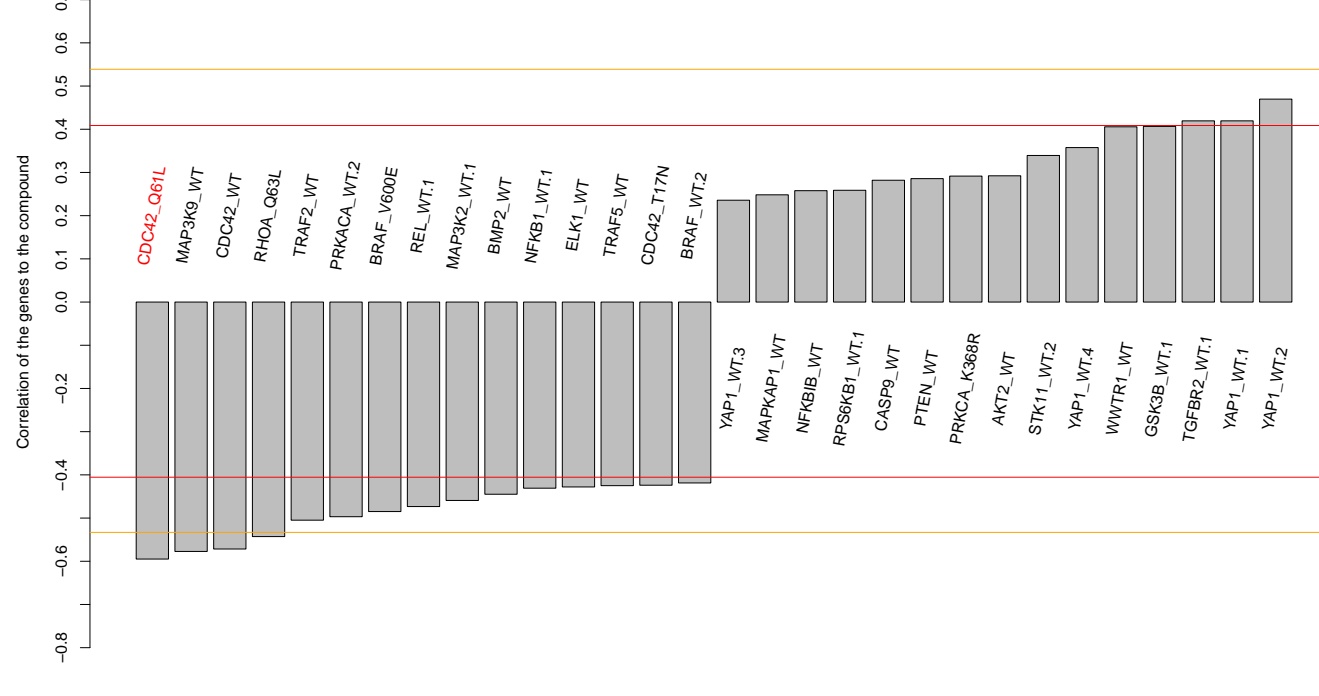
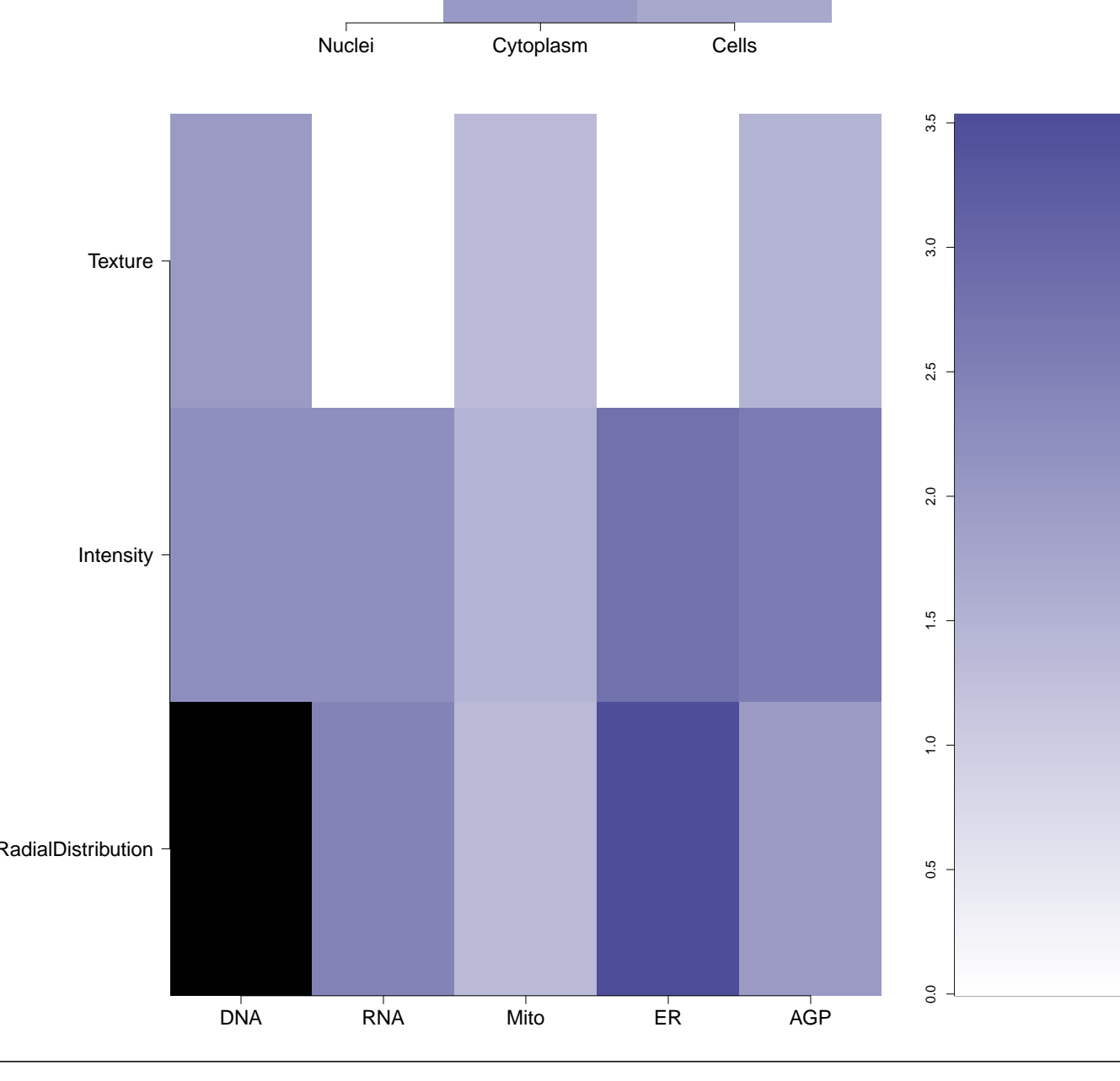
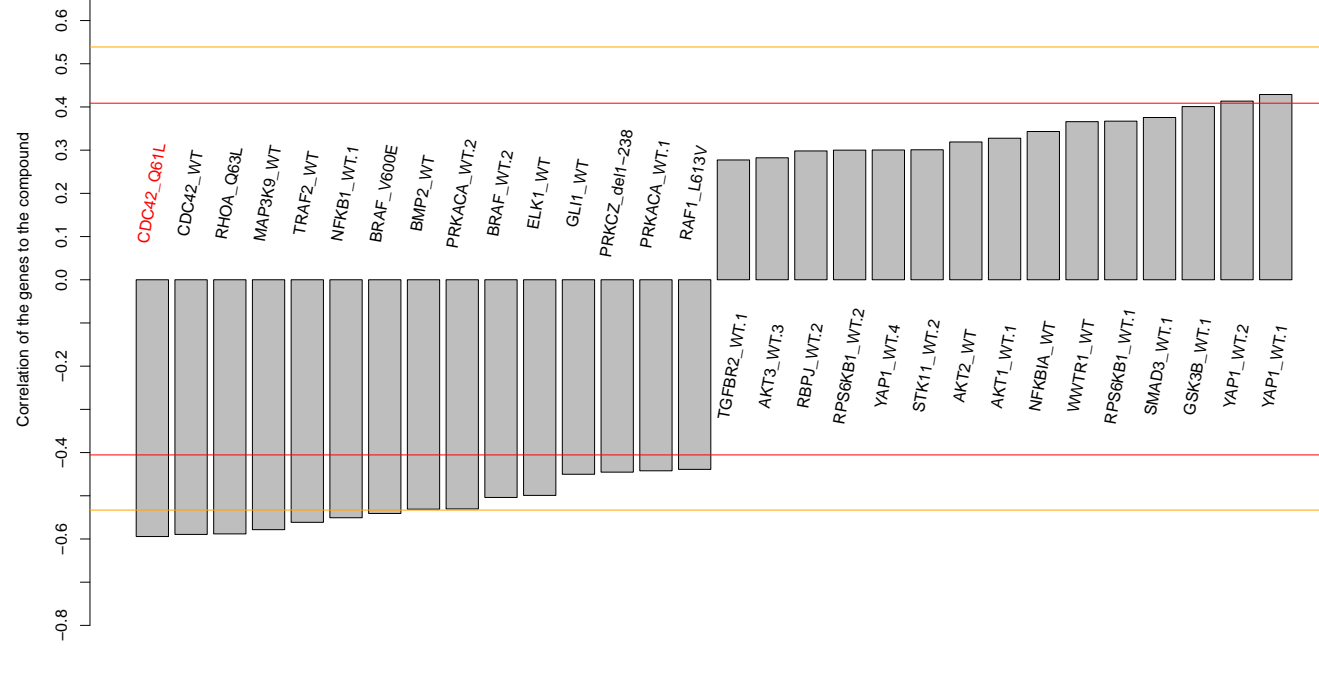
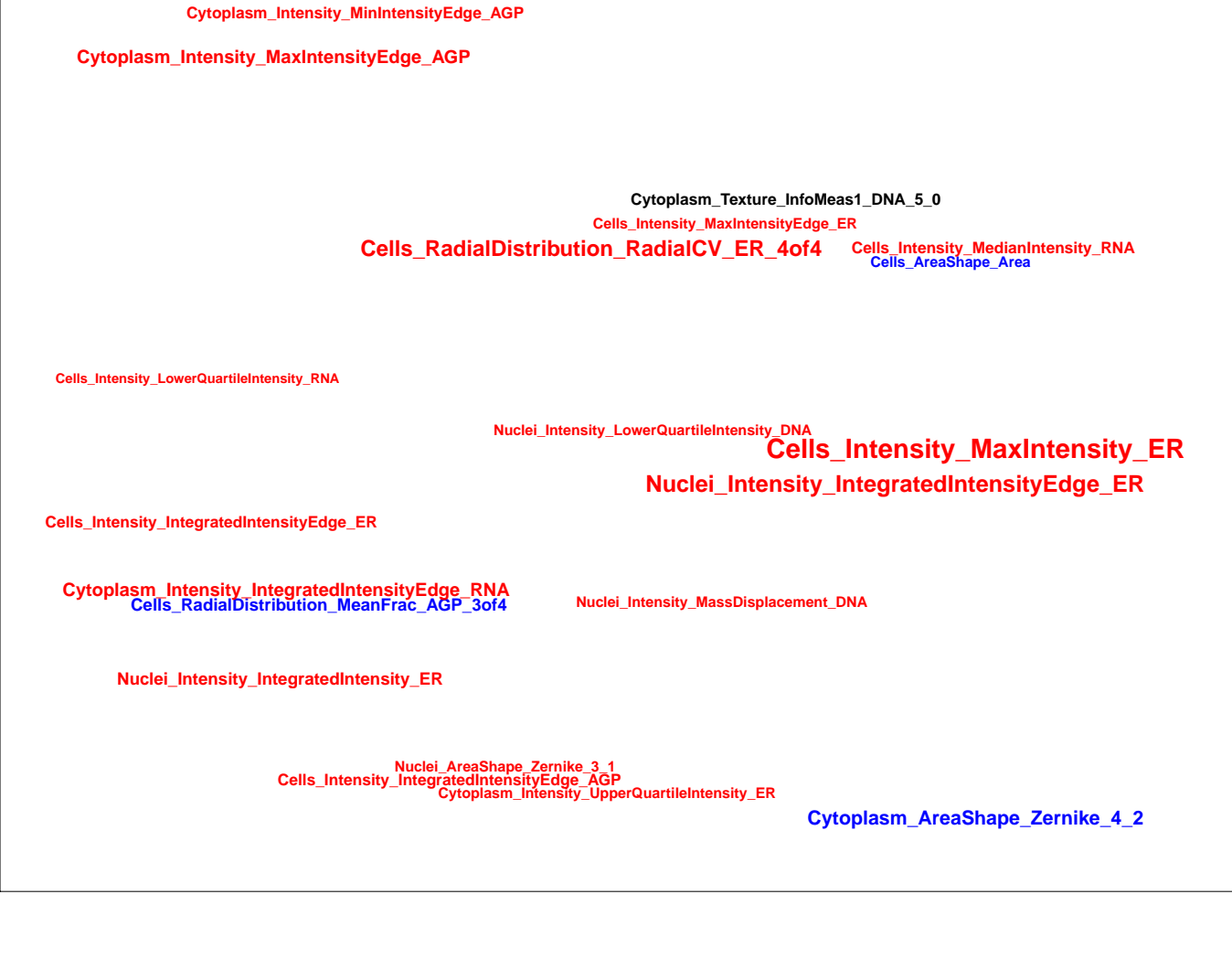


Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Correlation between compound 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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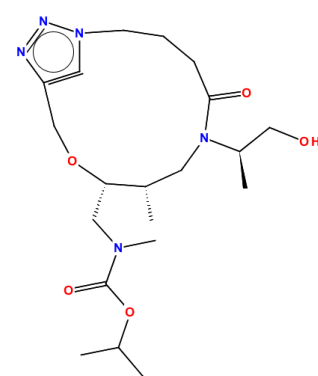


BRD-K29290722-001-01-4 PubChem CID : 54618609		0.68 (in 4 replicates)	0.63	0.720				Total number of assays tested in: 23. Active in the following assays: <ul style="list-style-type: none"> <li>Small molecule inhibitors of mR122 Measured in Cell-Based System Using Plate Reader - 2144-01_Activator_SinglePoint.HTS_Activity (AID 623001)</li> <li>Small molecule inhibitors of mR122 Measured in Cell-Based System Using Plate Reader - 2144-01_Activator_Dose_CherryPick_Activity (AID 651956)</li> </ul>
BRD-K48929882-001-05-1 ASN 03067318 AC1ML71R MLS000715091 HMS2711E13 ZINC12496877 SMR000275070 PubChem CID : 3169072		NA (in 1 replicates)	0.63	NA				Total number of assays tested in: 622.
BRD-K43419088-001-01-9 PubChem CID : 54618842		0.56 (in 3 replicates)	0.61	0.121				Total number of assays tested in: 37.
BRD-K2833890-001-05-9 3F-052 MLS000755458 HMS2593G05 SMR000337858 PubChem CID : 16195129		0.56 (in 4 replicates)	0.49	NA				Total number of assays tested in: 627. Active in the following assays: <ul style="list-style-type: none"> <li>uHTS identification of TNAP inhibitors in the absence of phosphate acceptor performed in luminescent assay (AID 1012)</li> <li>uHTS Identification of Diaphorase Inhibitors and Chemical Oxidizers: Counter Screen for Diaphorase-based Primary Assays (AID 1217)</li> <li>HTS Assay for Positive Allosteric Modulators of the Human D2 Dopamine Receptor: Primary Screen for Potentiators (AID 485347)</li> <li>qHTS screen for small molecules that inhibit ELG1-dependent DNA repair in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1 (AID 504467)</li> </ul>
BRD-K13311495-001-05-2 ZINC00471339 AC1LHXLB MLS000579407 HMS2609D22 ZINC471339 SMR000198841 ST45132445 ST50671527 PubChem CID : 894589		0.63 (in 4 replicates)	0.42	NA				Total number of assays tested in: 644. Active in the following assays: <ul style="list-style-type: none"> <li>qHTS Assay for Spectroscopic Profiling in 4-MU Spectral Region (AID 589)</li> <li>qHTS Assay for Spectroscopic Profiling in A350 Spectral Region (AID 590)</li> <li>CYP2C9 Assay (AID 777)</li> <li>qHTS Assay for Inhibitors of HPGD (15-Hydroxyprostaglandin Dehydrogenase) (AID 894)</li> <li>qHTS Assay for Inhibitors of BAZ2B (AID 304333)</li> <li>Full deck counterscreen for antagonists of the human M1 muscarinic receptor (CHRM1): Fluorescence-based cell-based high throughput screening assay to identify nonselective inhibitors and assay artifacts using the parental CHO-K1 cell line (AID 602250)</li> <li>Fluorescence-based biochemical primary high throughput screening assay to identify molecules that bind r(CAG) RNA repeats (AID 651821)</li> <li>Counterscreen for molecules that bind rCAG RNA repeats: fluorescent based biochemical counterscreen assay for inhibitors of the DNA-based (5'CAG/3'GTC) TO-PRO-1 dye complex (AID 652068)</li> </ul>
BRD-K15058425-001-05-2 ZINC01113695 F1560-0786 SMR000075891 AC1LPQHO MLS000097314 MLS002546301 HMS2326N09 ZINC1113695 PubChem CID : 1291706		NA (in 1 replicates)	-0.72	NA				Total number of assays tested in: 781. Active in the following assays: <ul style="list-style-type: none"> <li>qHTS Assay for Spectroscopic Profiling in 4-MU Spectral Region (AID 589)</li> <li>qHTS Assay for Spectroscopic Profiling in A350 Spectral Region (AID 590)</li> <li>CYP2C9 Assay (AID 777)</li> <li>qHTS Assay for Inhibitors of HPGD (15-Hydroxyprostaglandin Dehydrogenase) (AID 894)</li> <li>qHTS Assay for Inhibitors of BAZ2B (AID 304333)</li> <li>Full deck counterscreen for antagonists of the human M1 muscarinic receptor (CHRM1): Fluorescence-based cell-based high throughput screening assay to identify nonselective inhibitors and assay artifacts using the parental CHO-K1 cell line (AID 602250)</li> <li>Fluorescence-based biochemical primary high throughput screening assay to identify molecules that bind r(CAG) RNA repeats (AID 651821)</li> <li>Counterscreen for molecules that bind rCAG RNA repeats: fluorescent based biochemical counterscreen assay for inhibitors of the DNA-based (5'CAG/3'GTC) TO-PRO-1 dye complex (AID 652068)</li> </ul>
BRD-K91399333-001-01-7 PubChem CID : 44490007		0.66 (in 3 replicates)	-0.65	0.248				Total number of assays tested in: 57.



BRD-K95369587-001-01-9 PubChem CID : 44505050		0.73 (in 3 replicates)	-0.64	0.280				Total number of assays tested in: 43.
BRD-K17360472-001-02-9 MLS003129709 SMR001834155 PubChem CID : 44485743		0.74 (in 3 replicates)	-0.61	0.280				Total number of assays tested in: 96. Active in the following assays: <ul style="list-style-type: none"> <li>SMM ID4 Measured in Biochemical System Using Small Molecule MicroArray 2128-01 Other.SinglePoint.HTS Activity (AID 624137)</li> </ul>
BRD-K3366264-001-05-4 AC1OAWT1 MLS000588555 STL148557 ZINC15986304 SMR000219977 PubChem CID : 6867852		NA (in 1 replicates)	-0.61	NA				Total number of assays tested in: 628. Active in the following assays: <ul style="list-style-type: none"> <li>Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)</li> <li>HTS Luminescent assay for identification of inhibitors of Senrin-specific protease 8 (SEN8) (AID 2540)</li> <li>uHTS Luminescent assay for identification of inhibitors of Senrin-specific protease 6 (SEN6) (AID 2599)</li> <li>uHTS Luminescent assay for identification of inhibitors of Senrin-specific protease 7 (SEN7) (AID 434973)</li> <li>Single concentration confirmation of uHTS for inhibitors of Senrin-specific protease 6 (SEN6) using a Luminescent assay (AID 488915)</li> <li>Single concentration confirmation of uHTS for inhibitors of Senrin-specific protease 7 (SEN7) using a Luminescent assay (AID 488917)</li> <li>Single concentration confirmation of inhibitors of Senrin-specific proteases (SENPs) using a Caspase-3 Selectivity assay (AID 488918)</li> <li>Single concentration confirmation of inhibitors of Senrin-specific proteases (SENPs) using a Luminescent Interference Counterscreen assay (AID 488919)</li> <li>qHTS Assay for Inhibitors of JMJD2A-Tudor Domain (AID 504339)</li> <li>qHTS for Inhibitors of PLK1-PDB (polo-like kinase 1 - polo-box domain): Primary Screen (AID 720504)</li> <li>qHTS for Inhibitors of Inflammasome Signaling: IL-1-beta AlphaLisa Primary Screen (AID 743279)</li> </ul>
BRD-K34898609-001-01-5 PubChem CID : 54646445		0.68 (in 4 replicates)	-0.60	0.280				Total number of assays tested in: 37.
BRD-K33287655-001-01-3 PubChem CID : 54633138		0.65 (in 4 replicates)	-0.60	0.280				Total number of assays tested in: 20. Active in the following assays: <ul style="list-style-type: none"> <li>Small molecule inhibitors of miR122 Measured in Cell-Based System Using Plate Reader - 2144-01 Activator.SinglePoint.HTS Activity (AID 623901)</li> <li>Cytotoxicity Assay Measured in Cell-Based System Using Plate Reader - 2144-02 Inhibitor.Dose.CherryPick.Activity.Set2 (AID 720697)</li> </ul>
BRD-K41520544-001-01-4 PubChem CID : 4944602		0.58 (in 4 replicates)	-0.59	NA				Total number of assays tested in: 43.
BRD-K19056919-001-01-4 PubChem CID : 54646755		0.82 (in 4 replicates)	-0.59	0.280				Total number of assays tested in: 37.

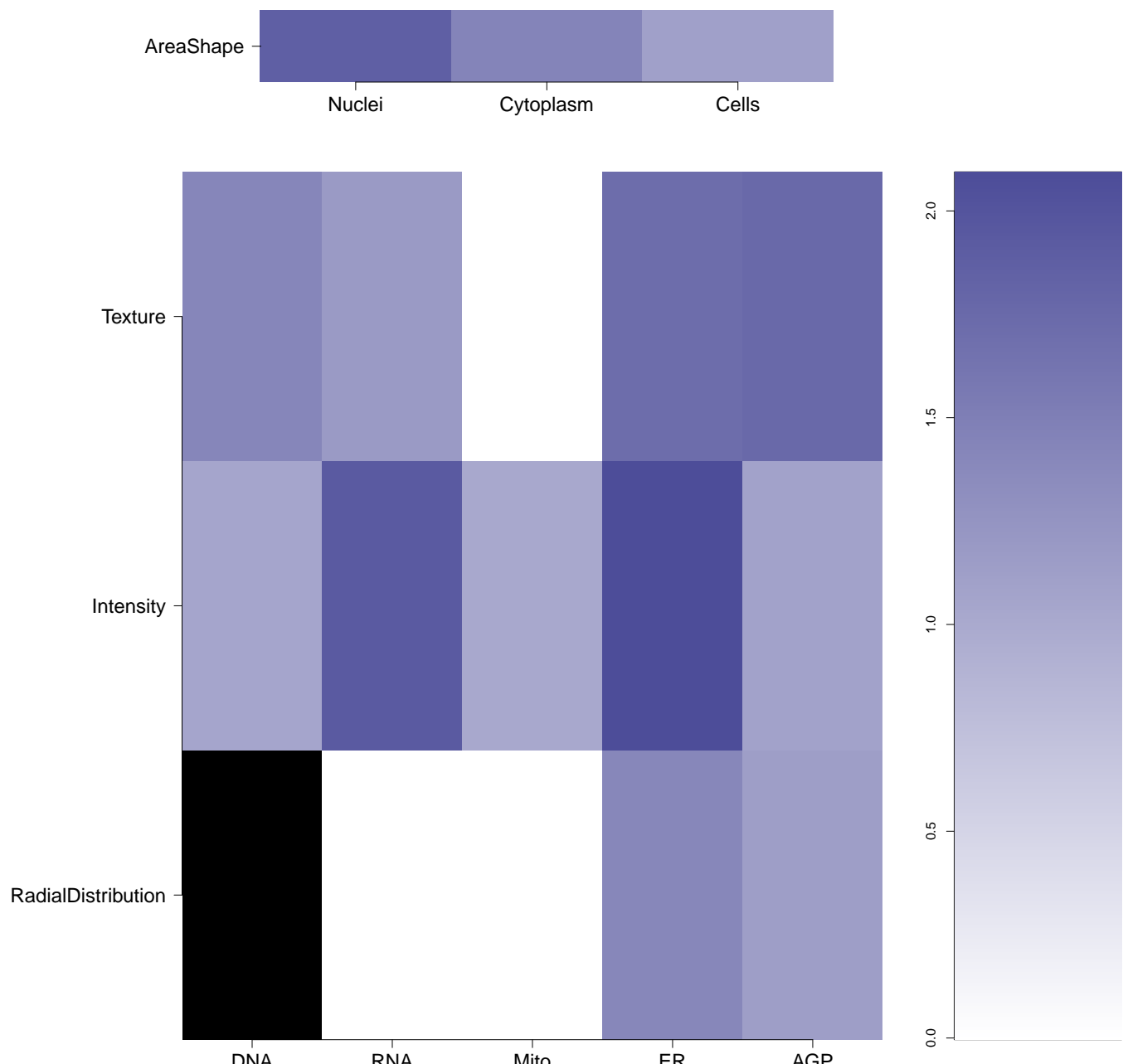
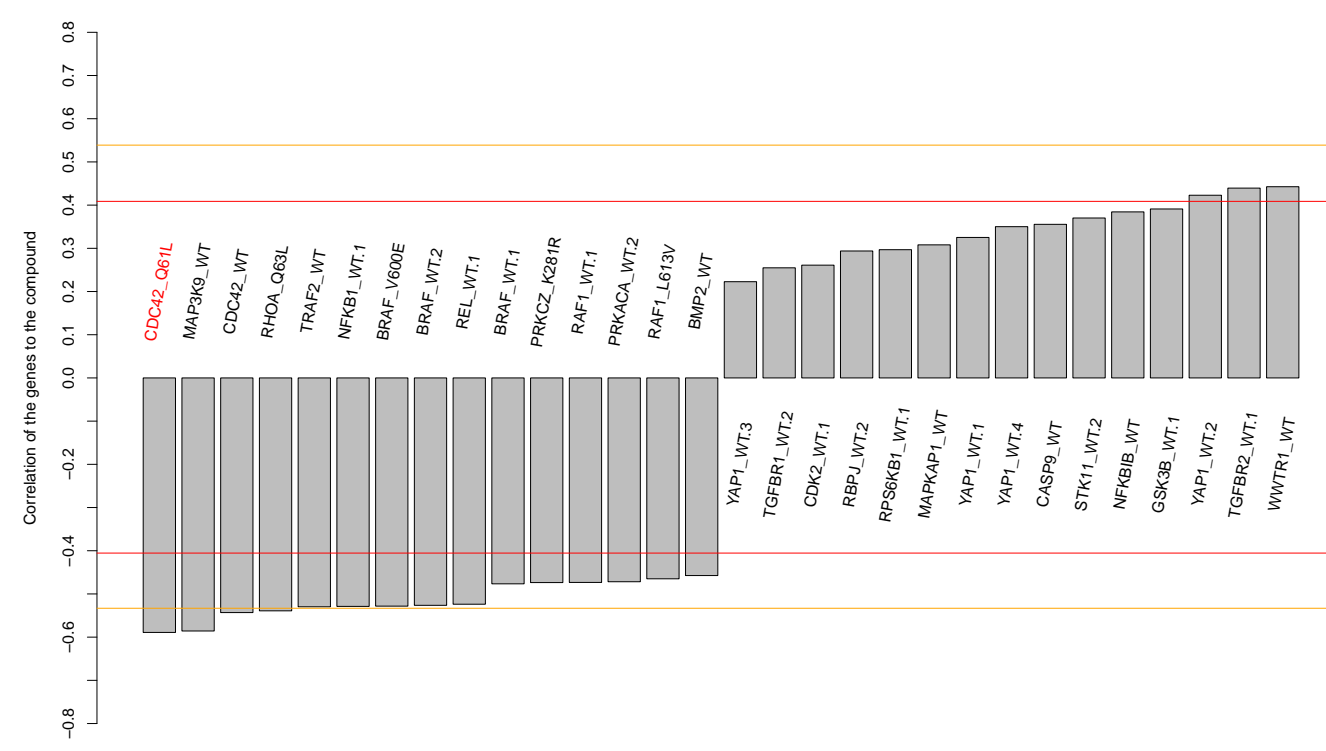
BRD-K53241640-001-01-5  
PubChem CID : 44505765



0.54 (in 3 replicates)

-0.59

0.280



Total number of assays tested in: 43.  
Active in the following assays:  
• DENV2 CPE-Based HTS Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2149-01.Other SinglePoint.HTS.Activity (AID 651640)