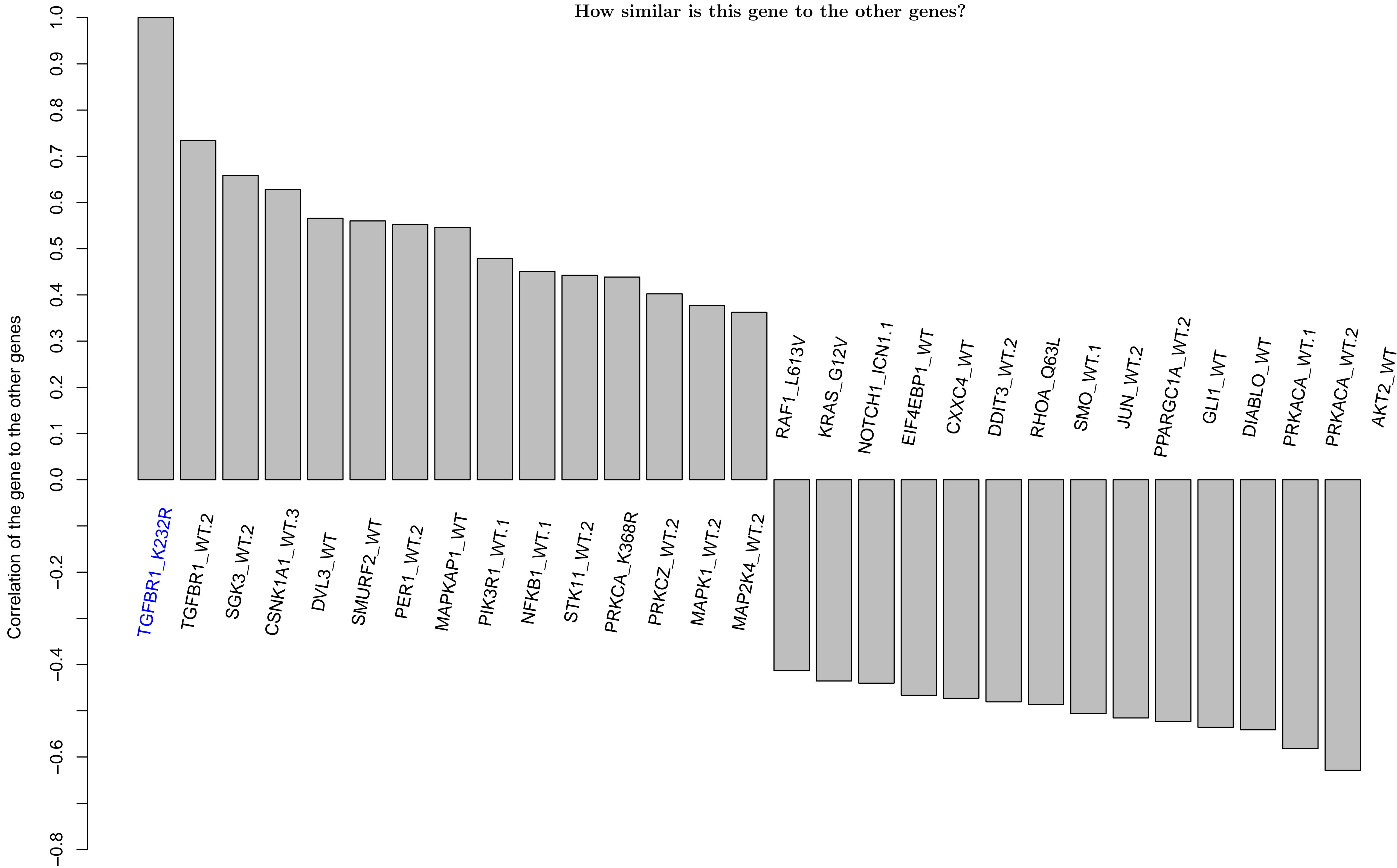
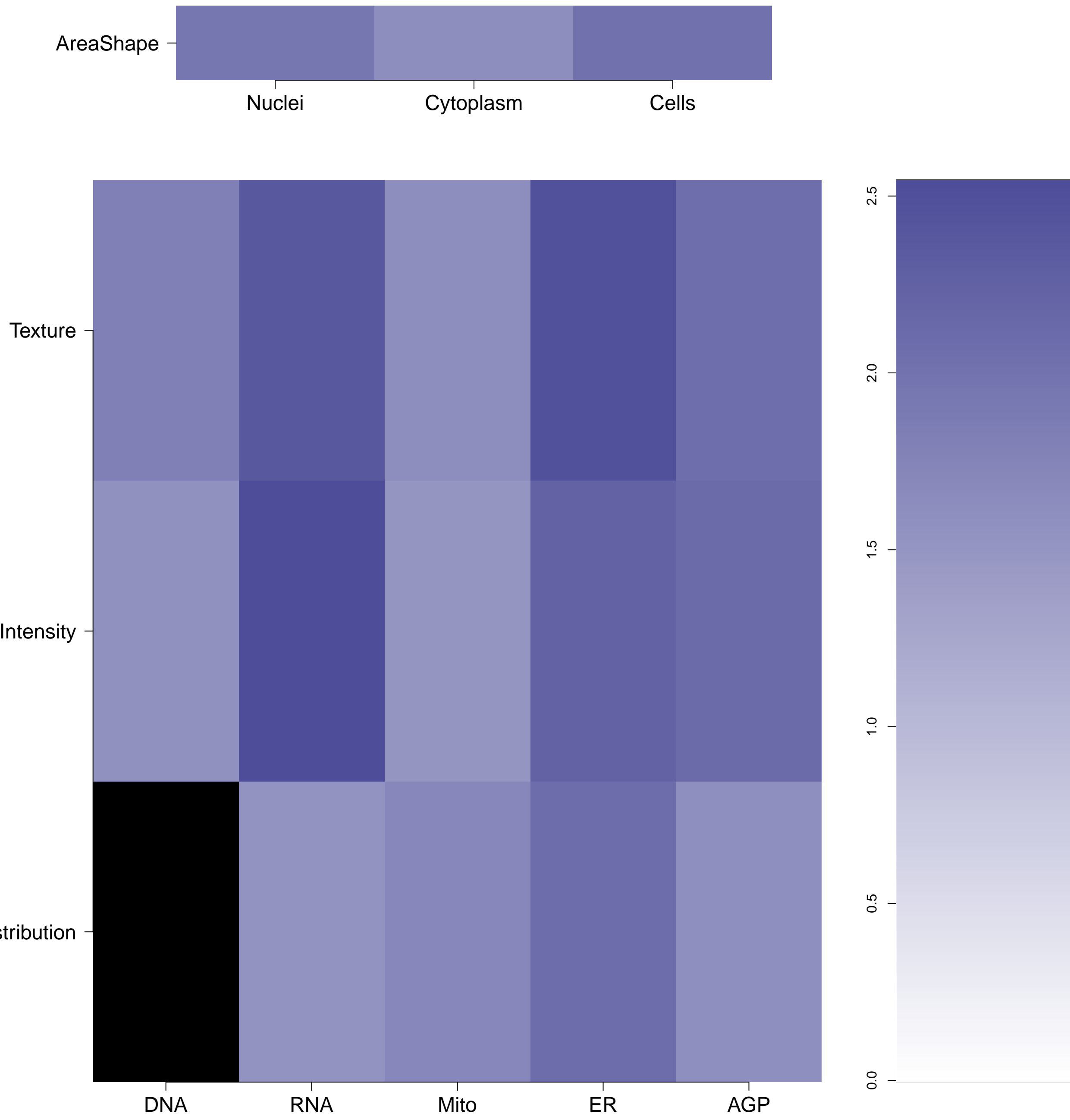


TGFBFR1.K232R - in Canonical TGFbeta

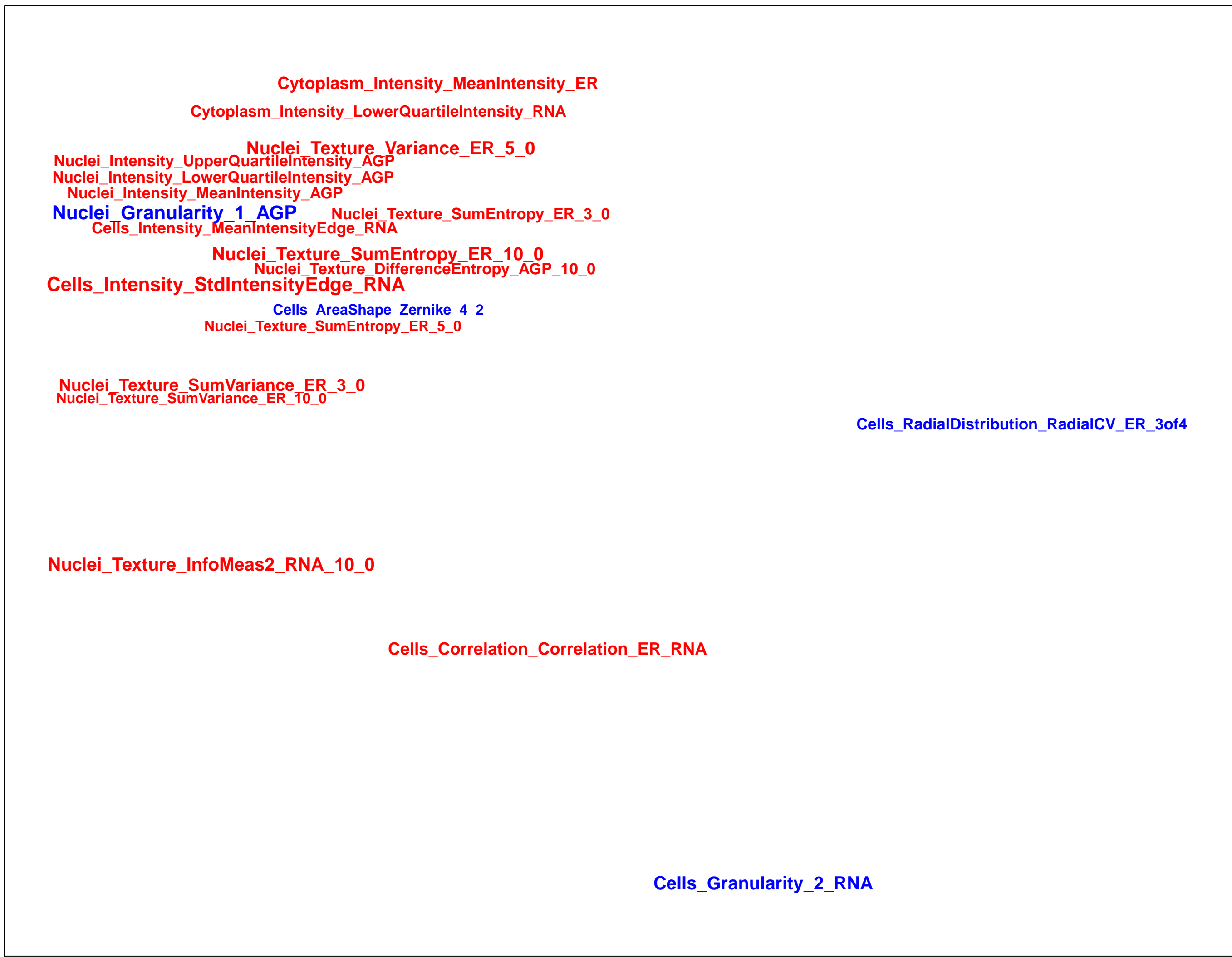
How similar is this gene to the other genes?



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

TGFBFR1.K232R (41744)

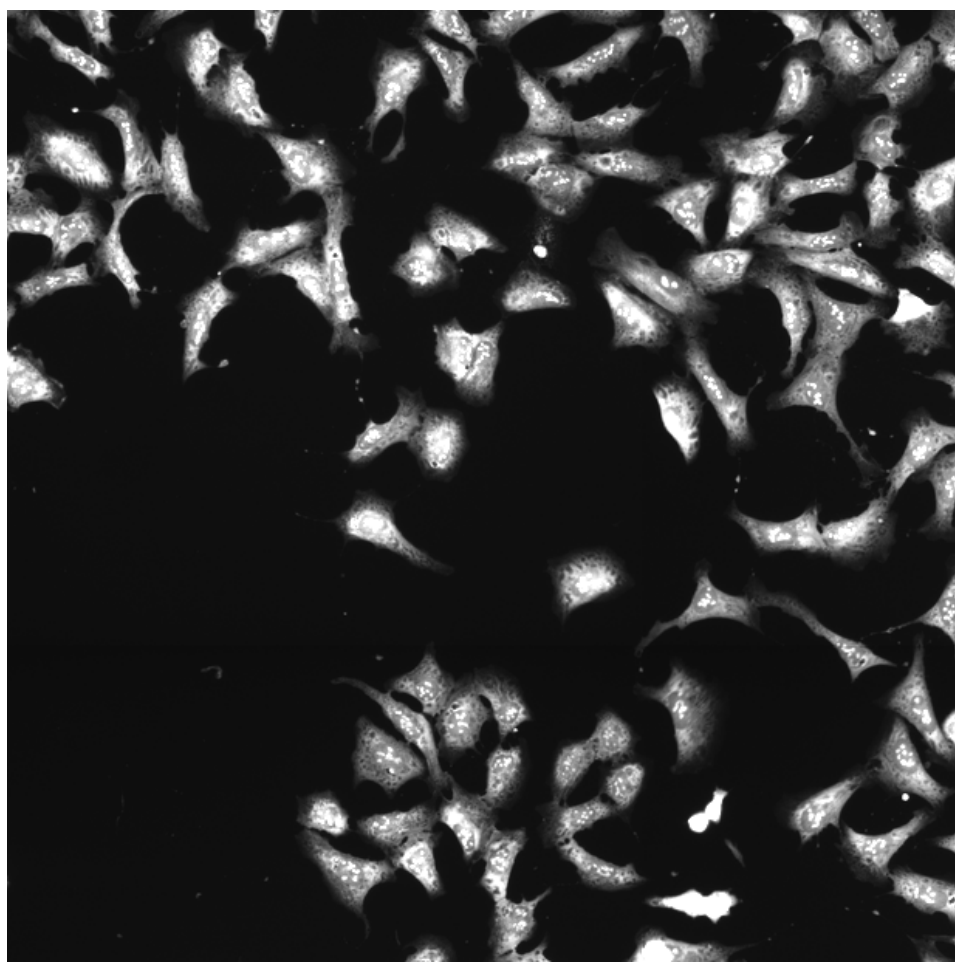
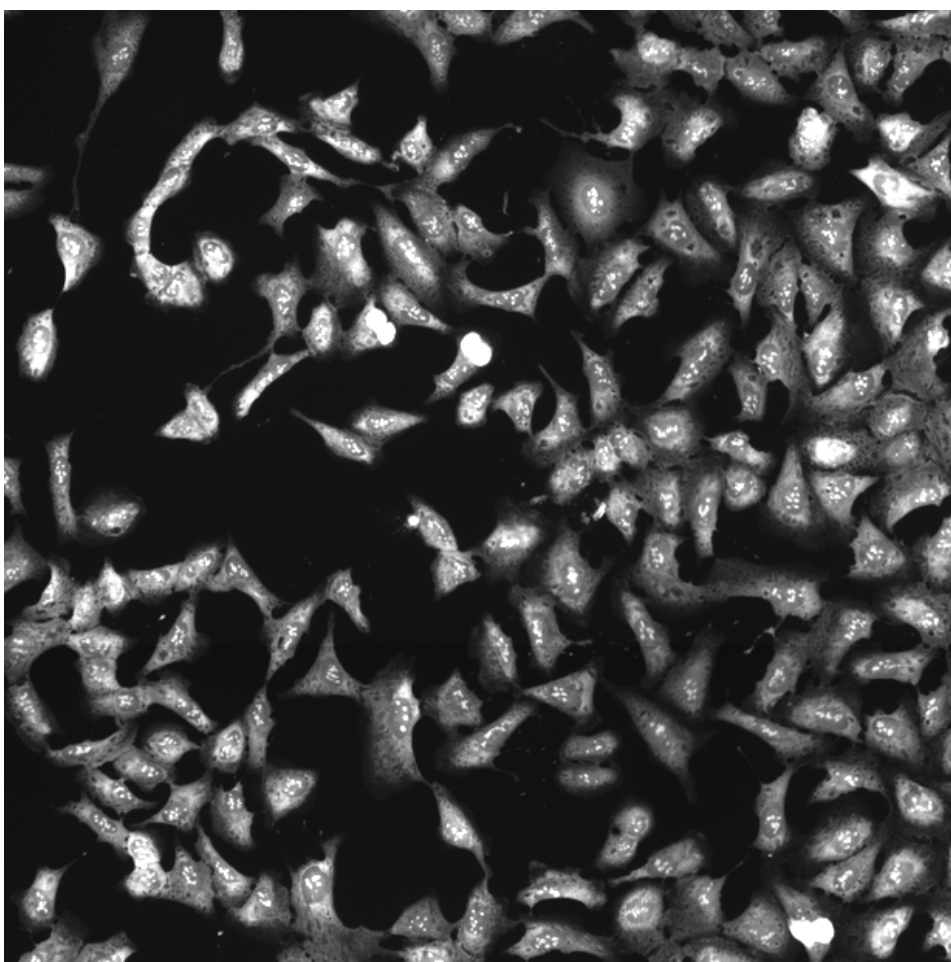
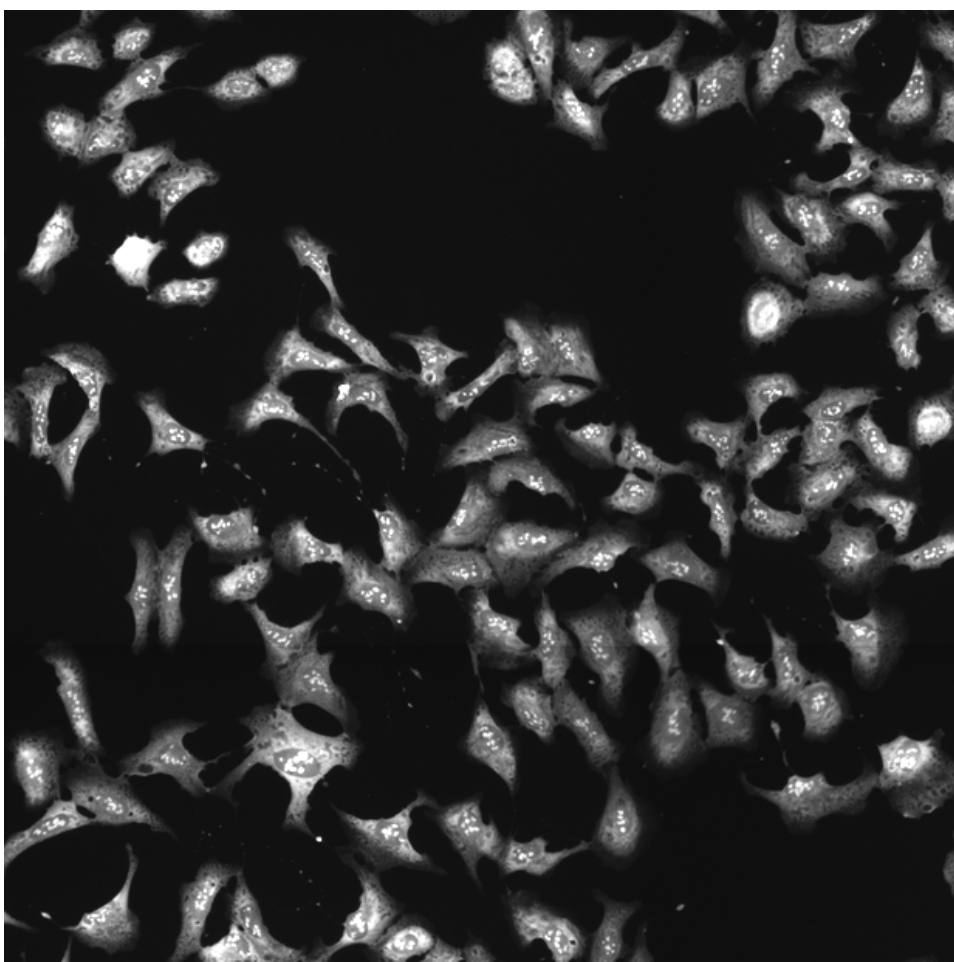
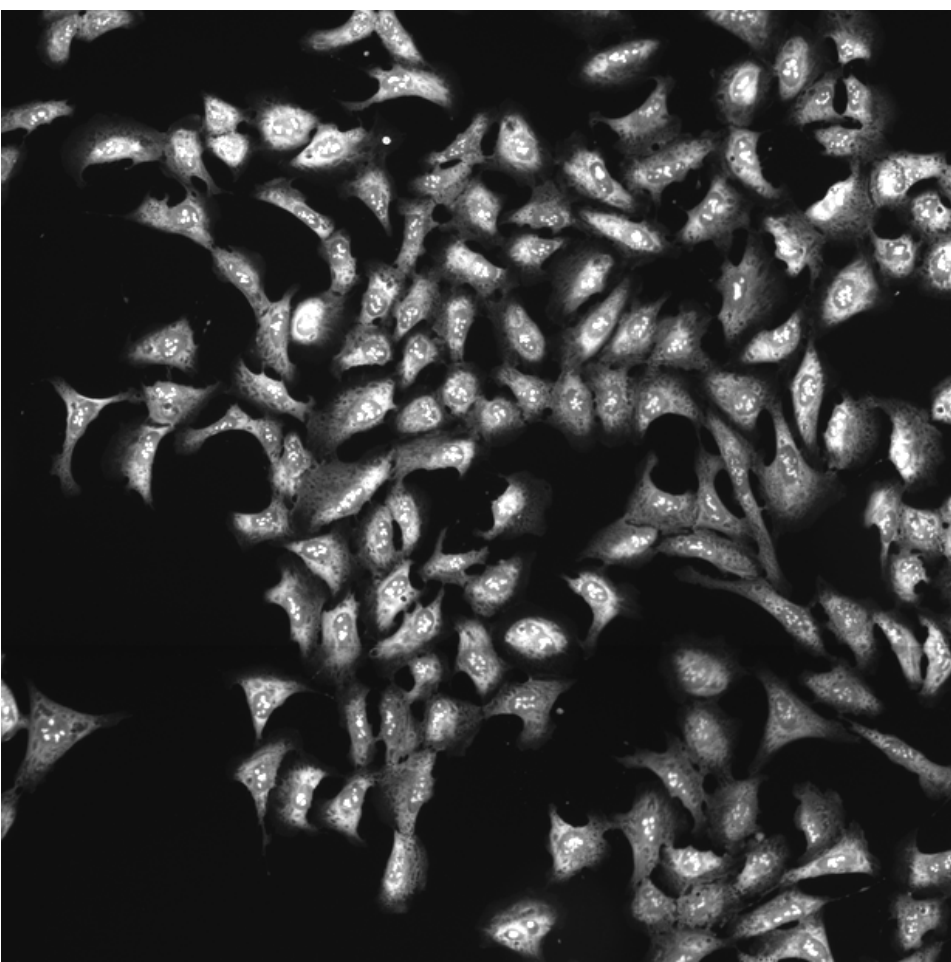
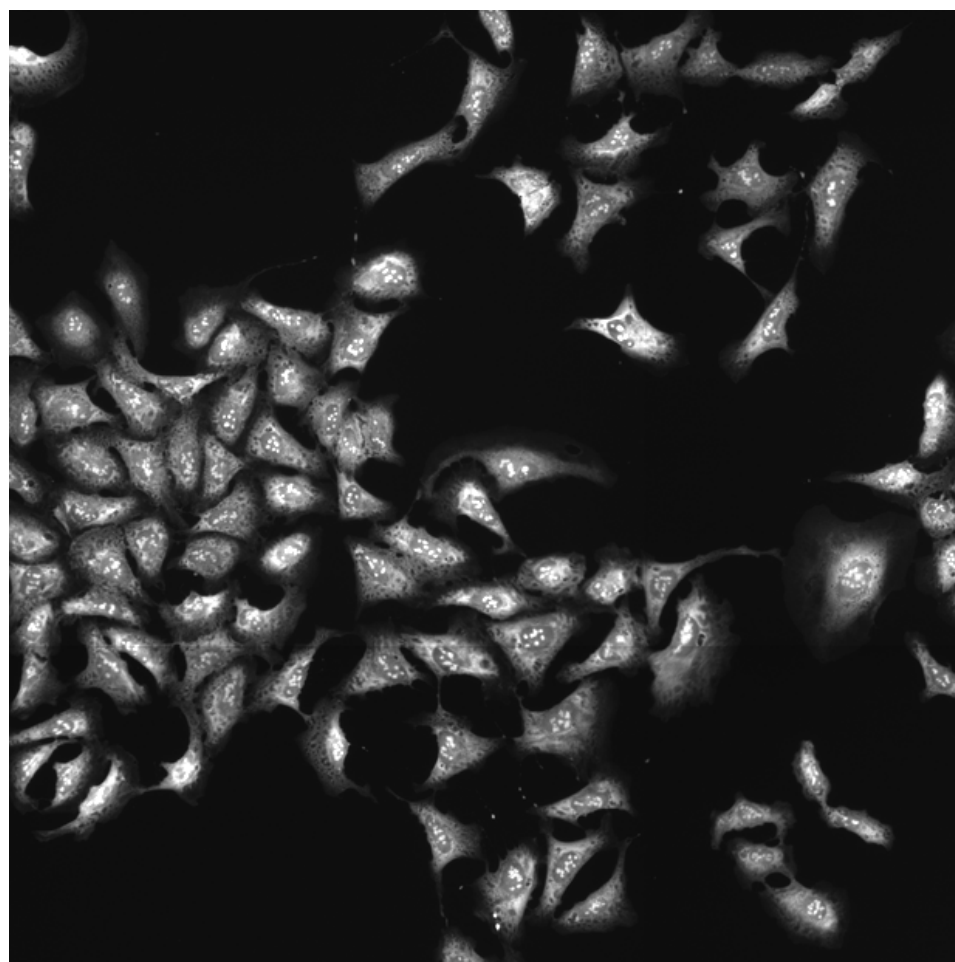
TGFBFR1.K232R (41755)

TGFBFR1.K232R (41756)

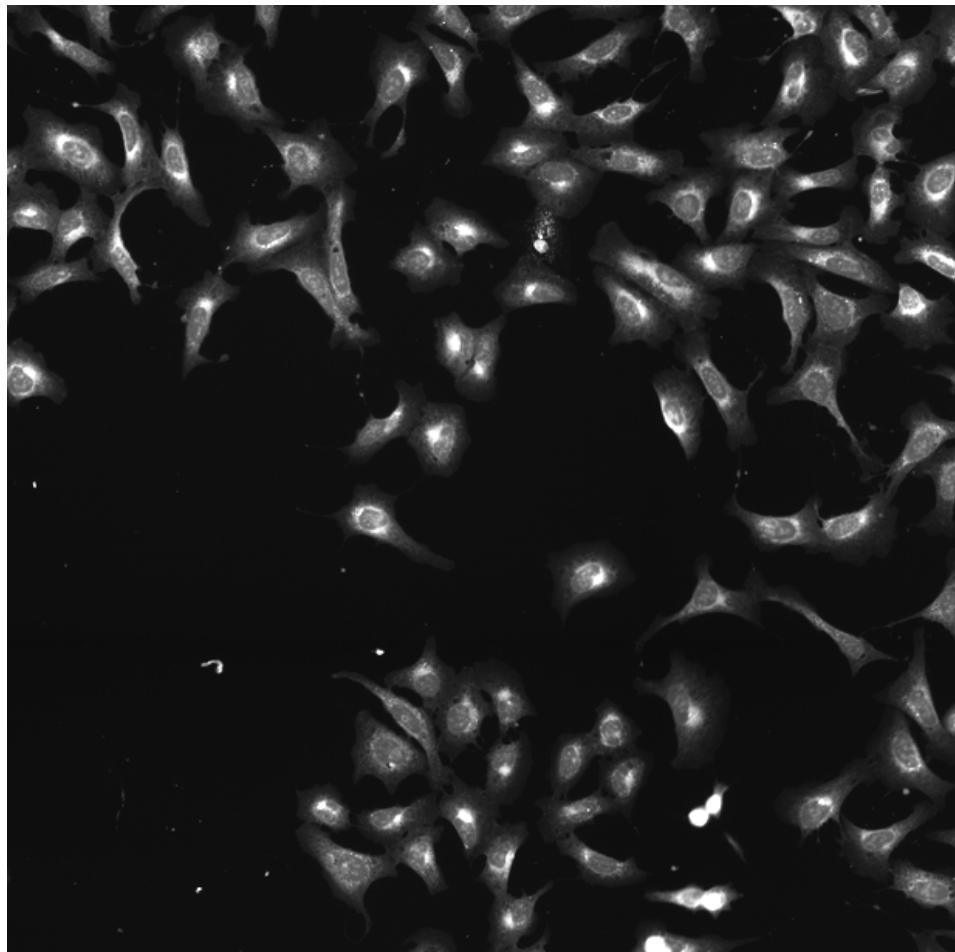
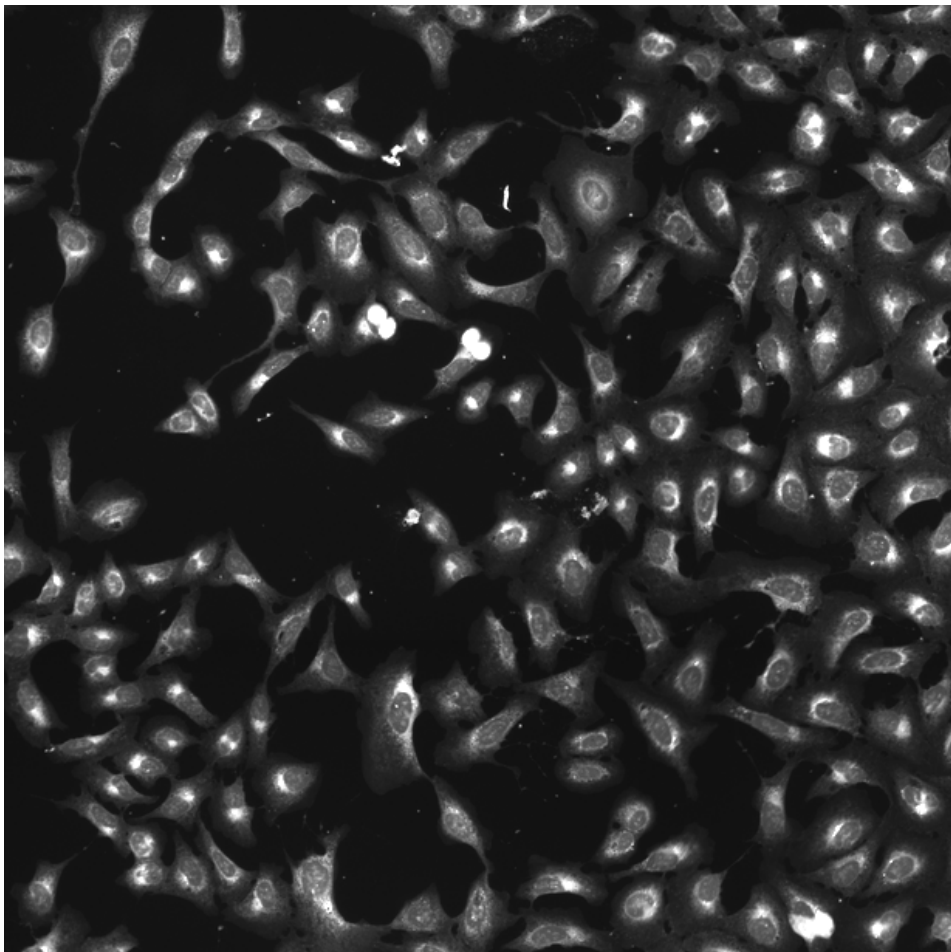
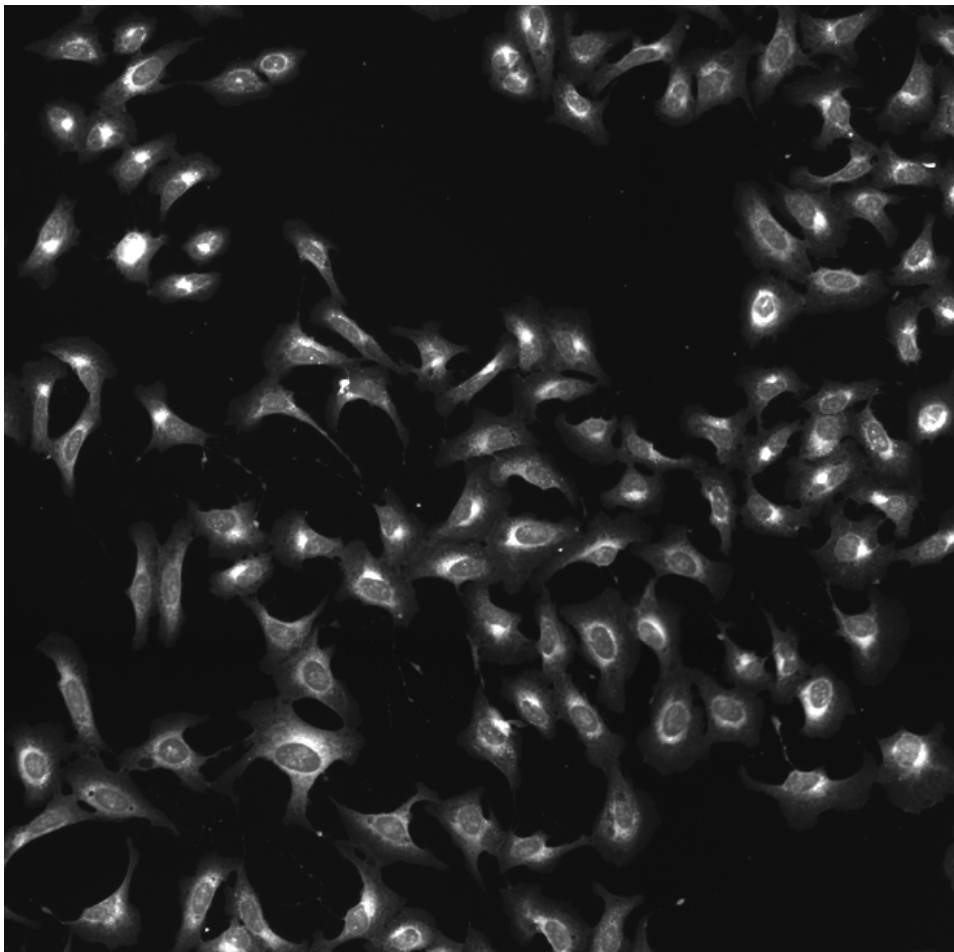
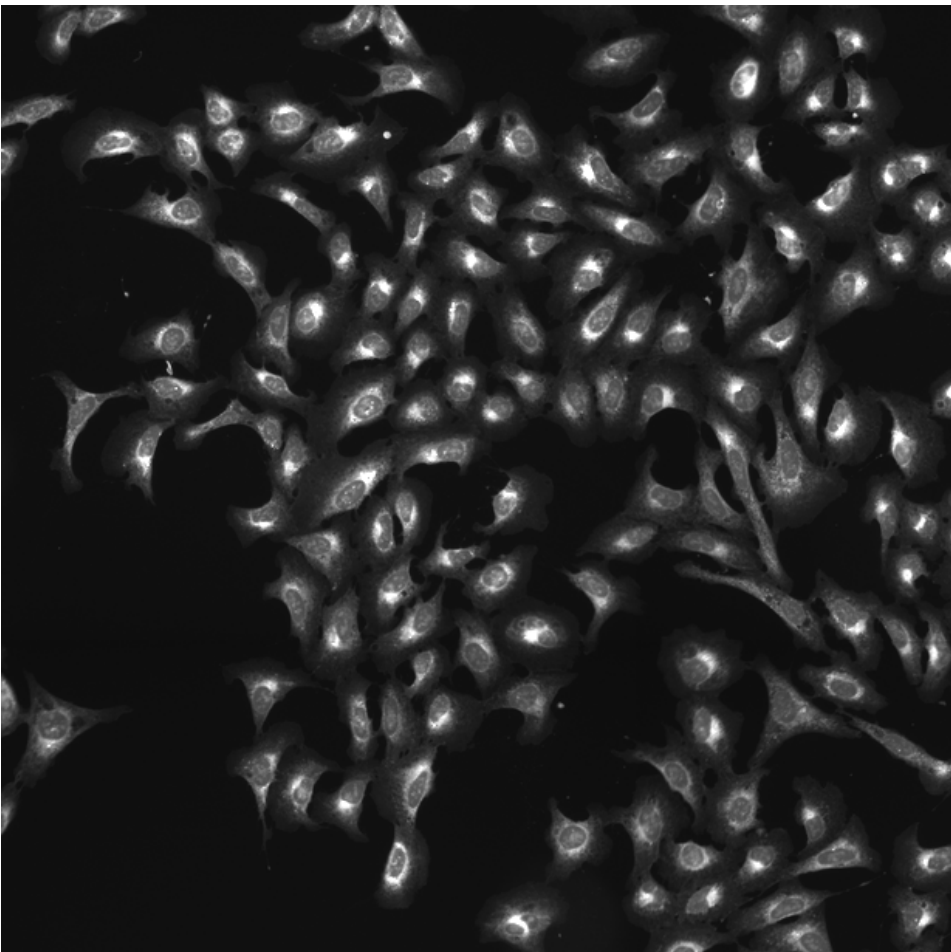
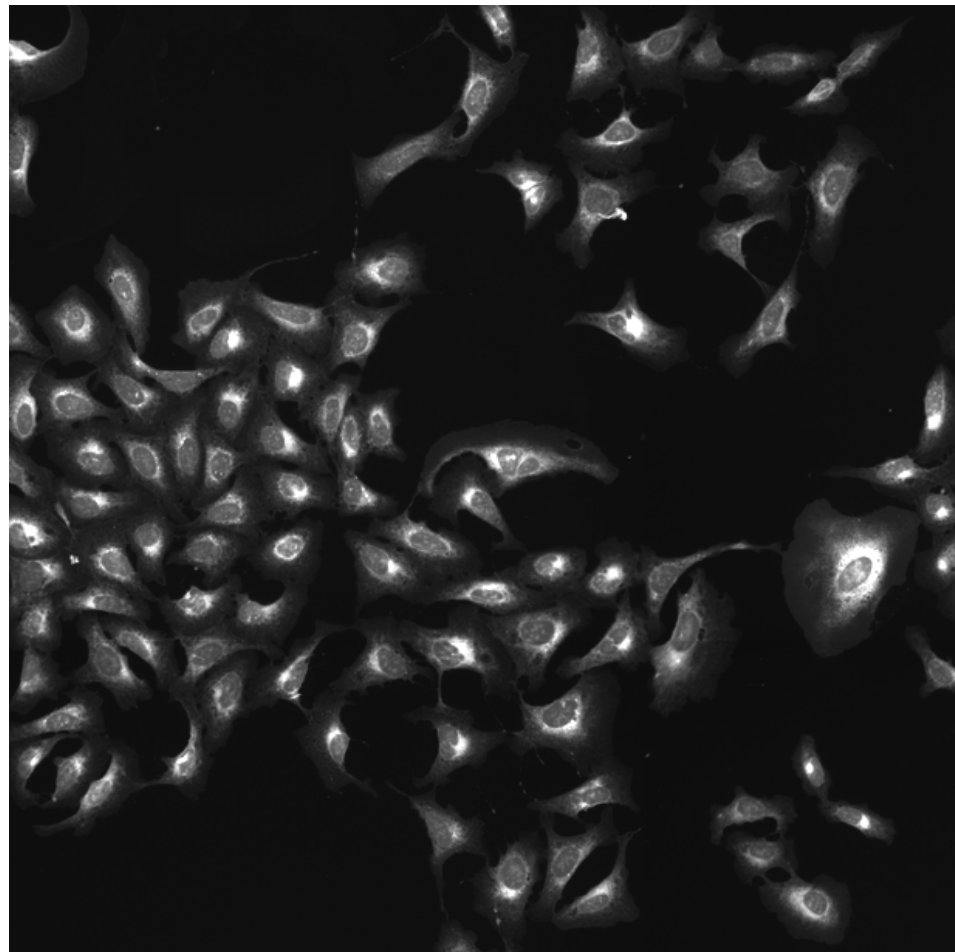
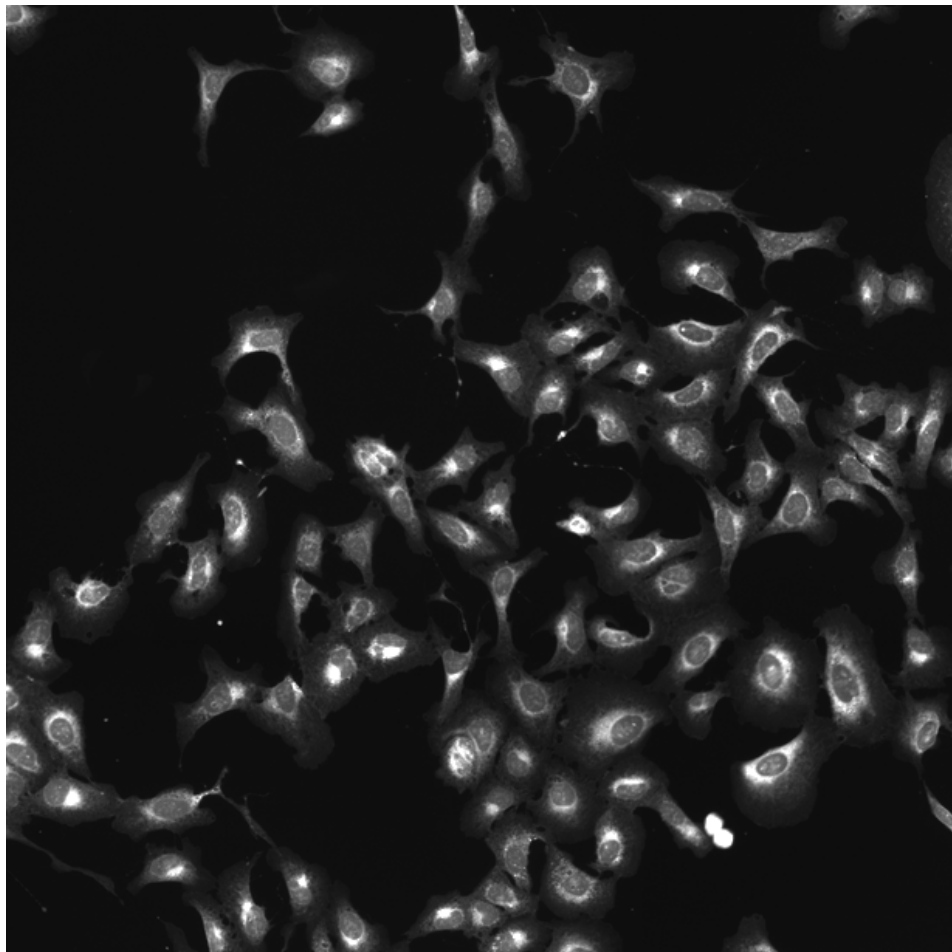
TGFBFR1.K232R (41757)

TGFBFR1.K232R (41754)

RNA

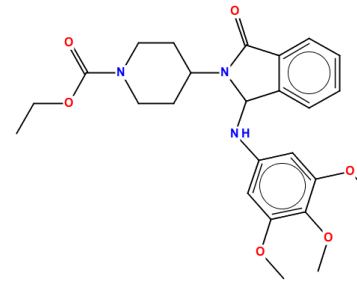
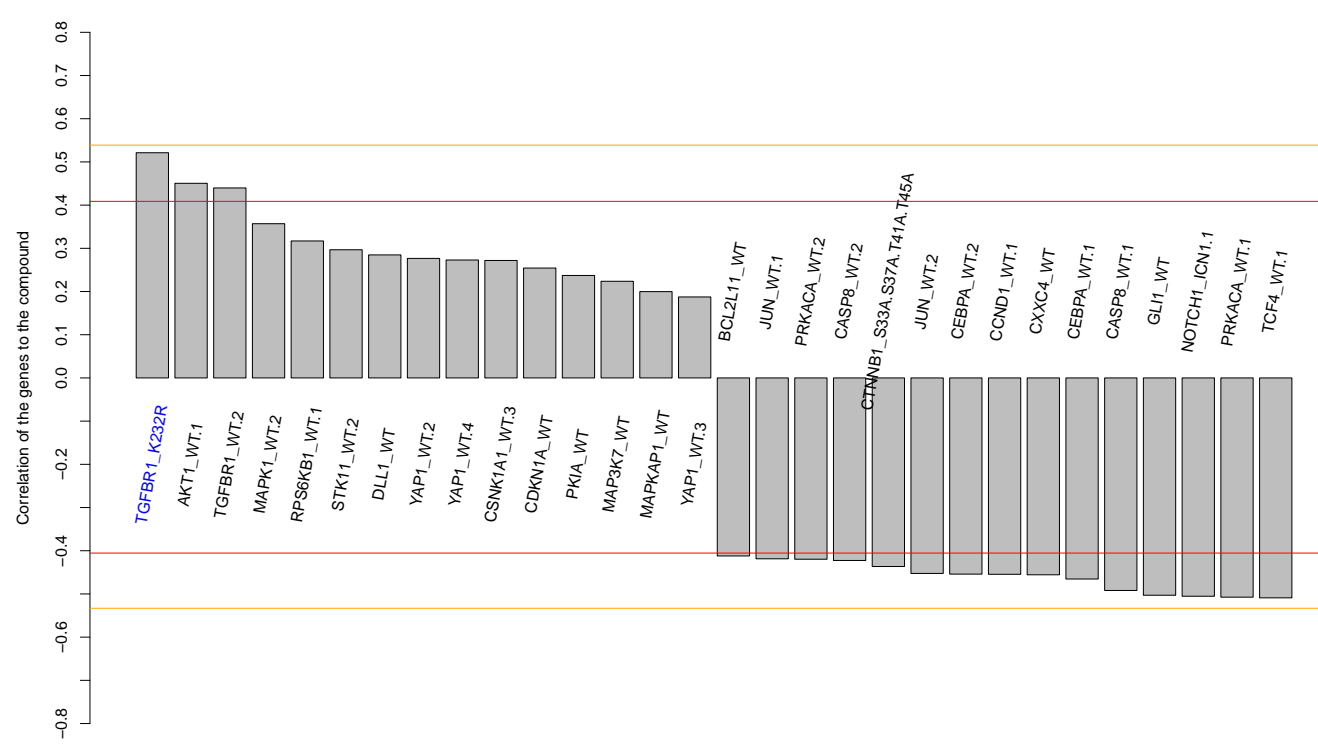
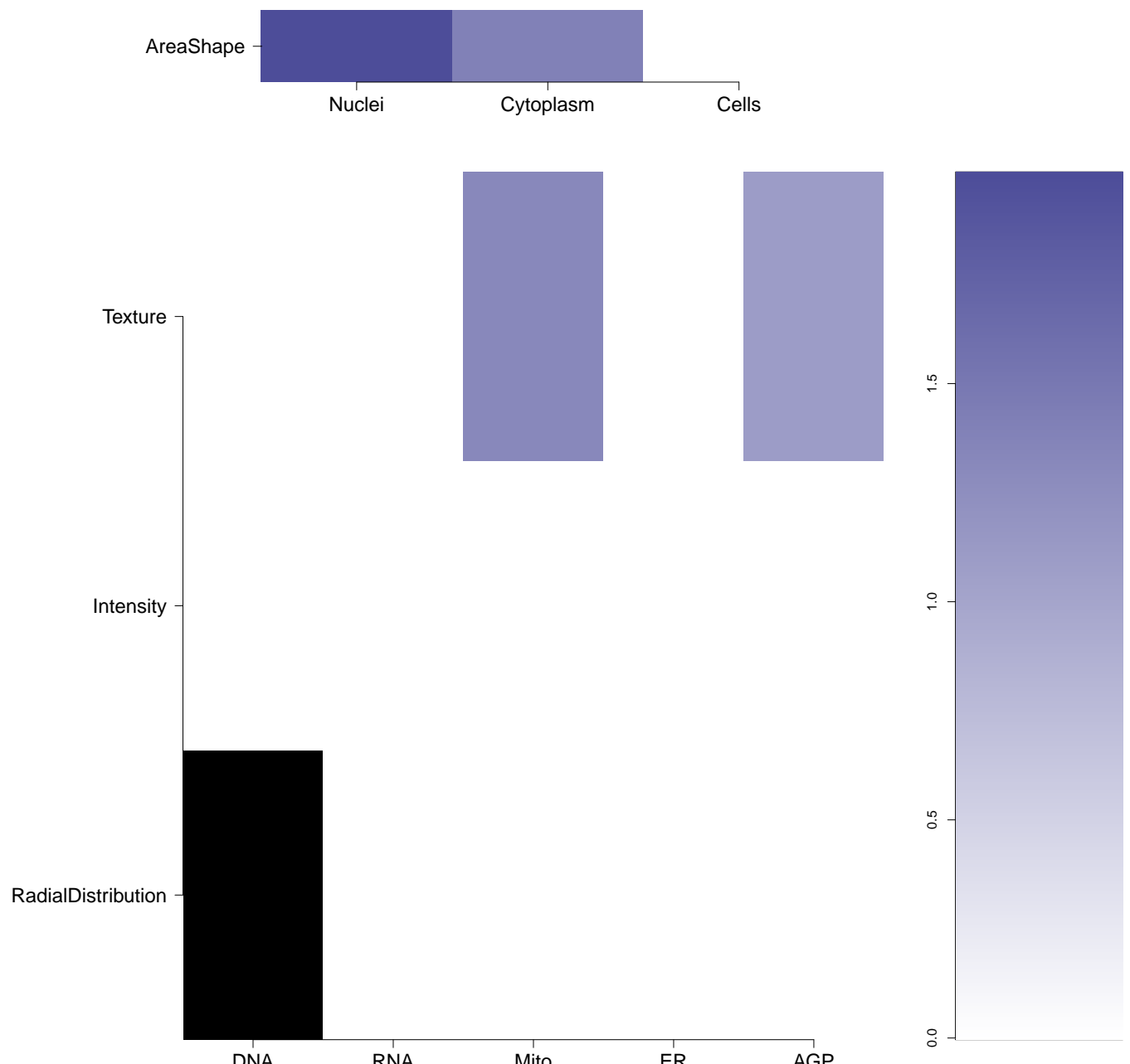

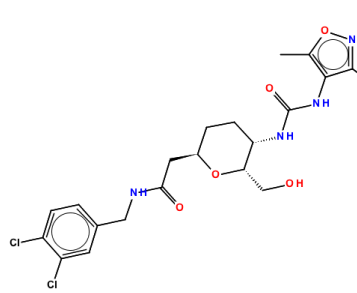
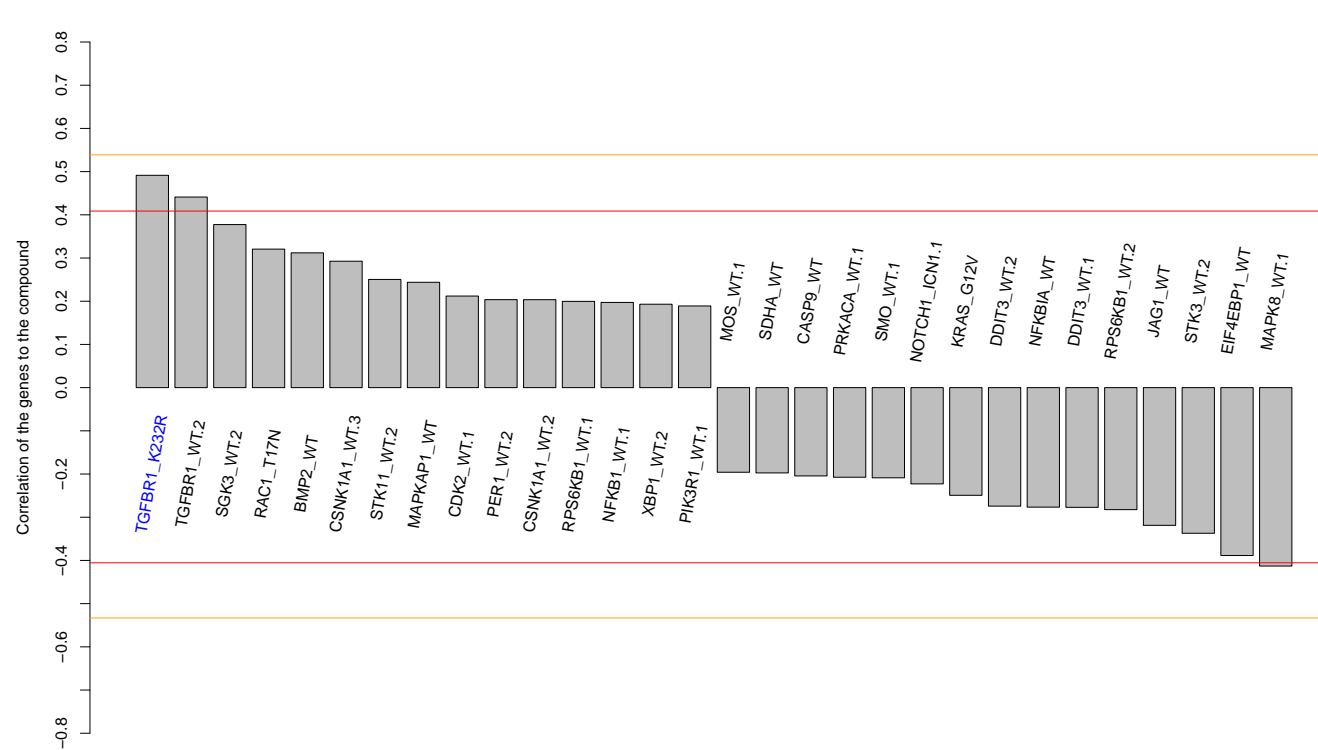
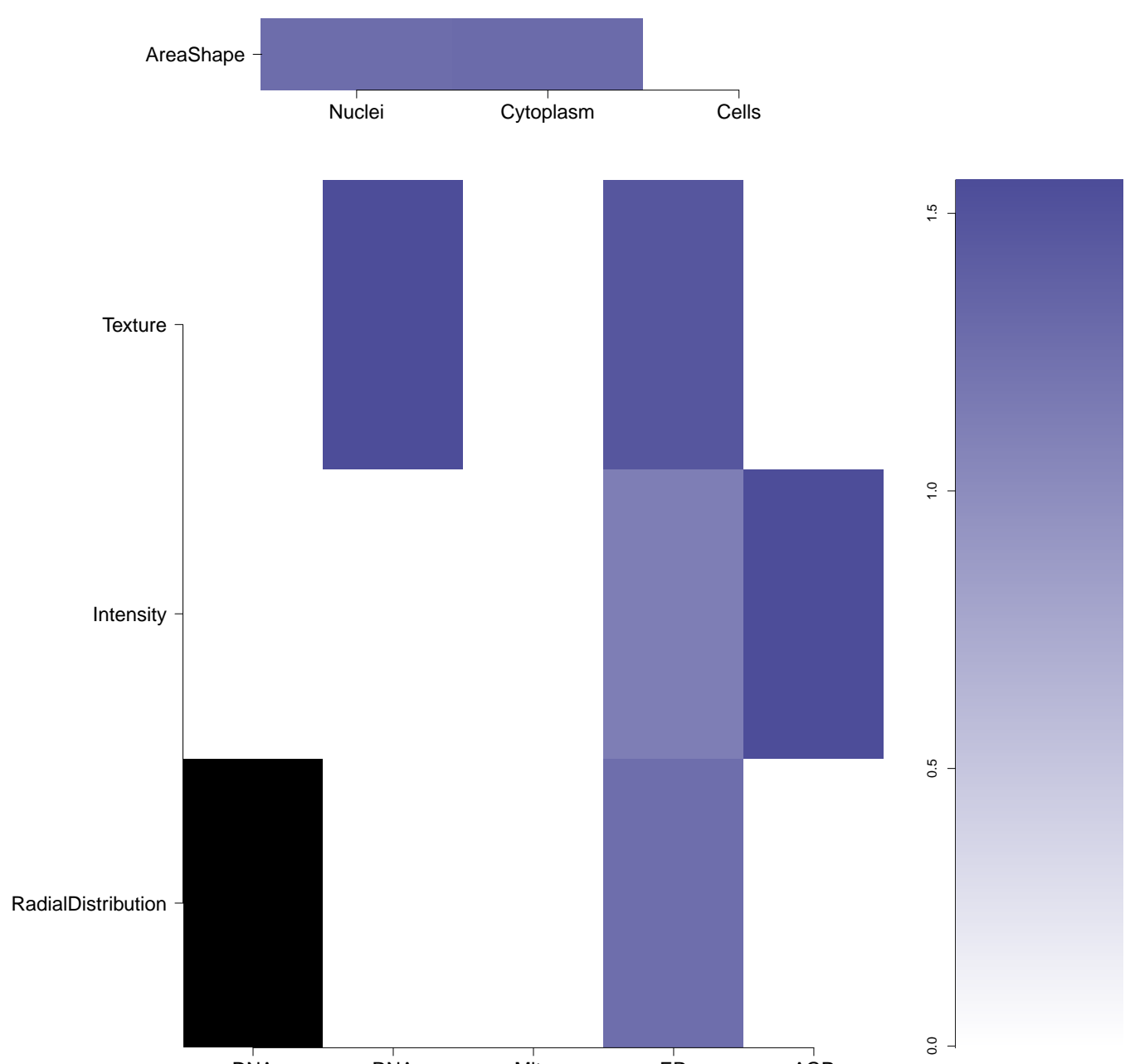
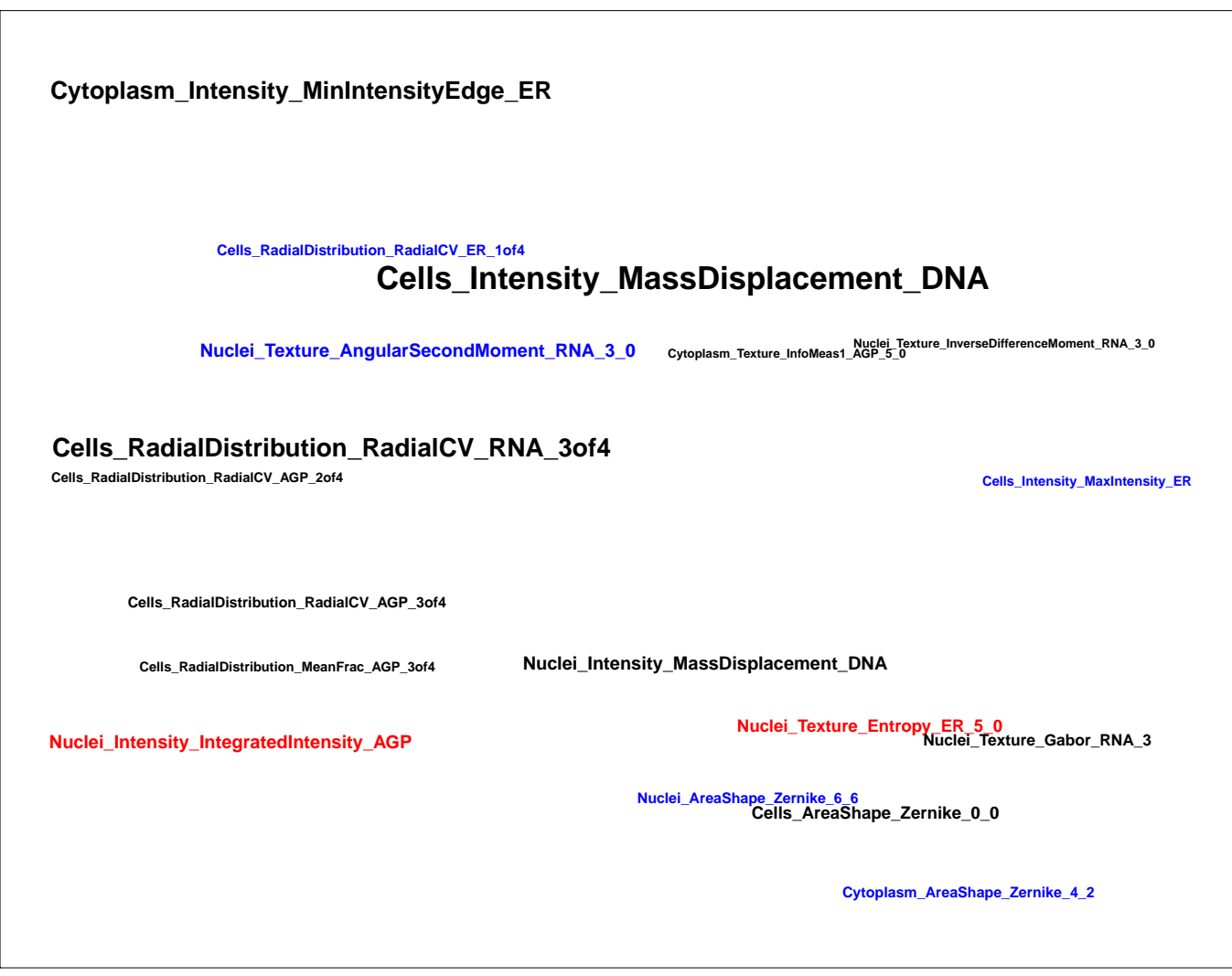
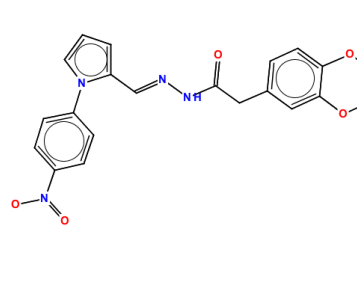
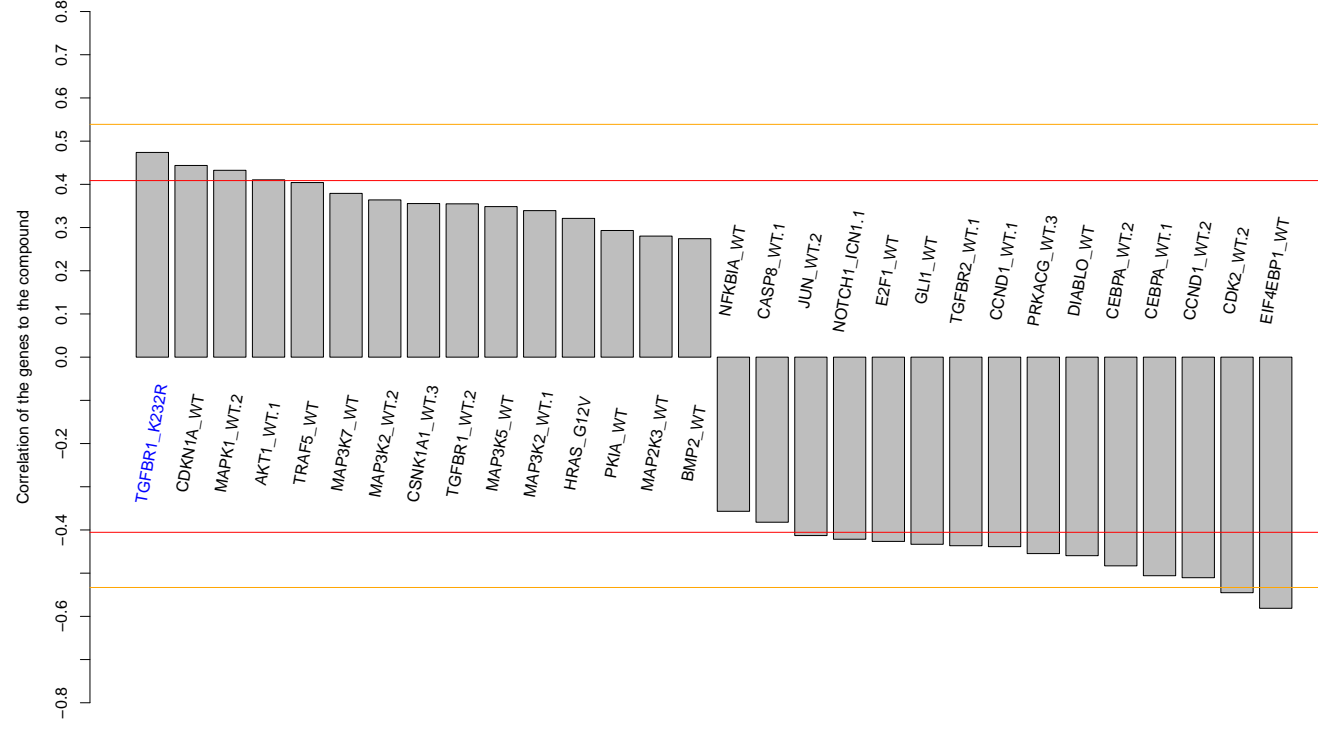
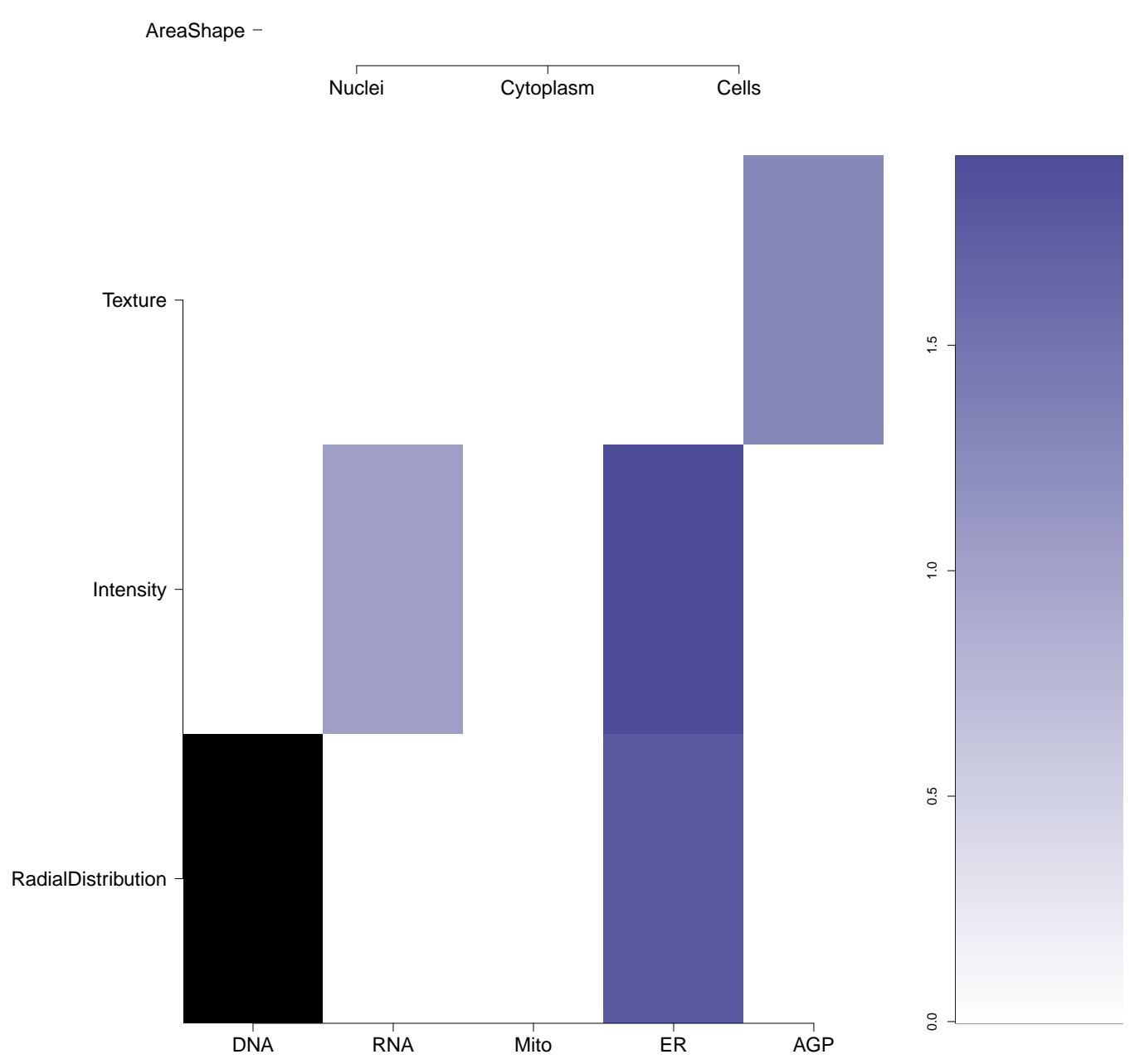
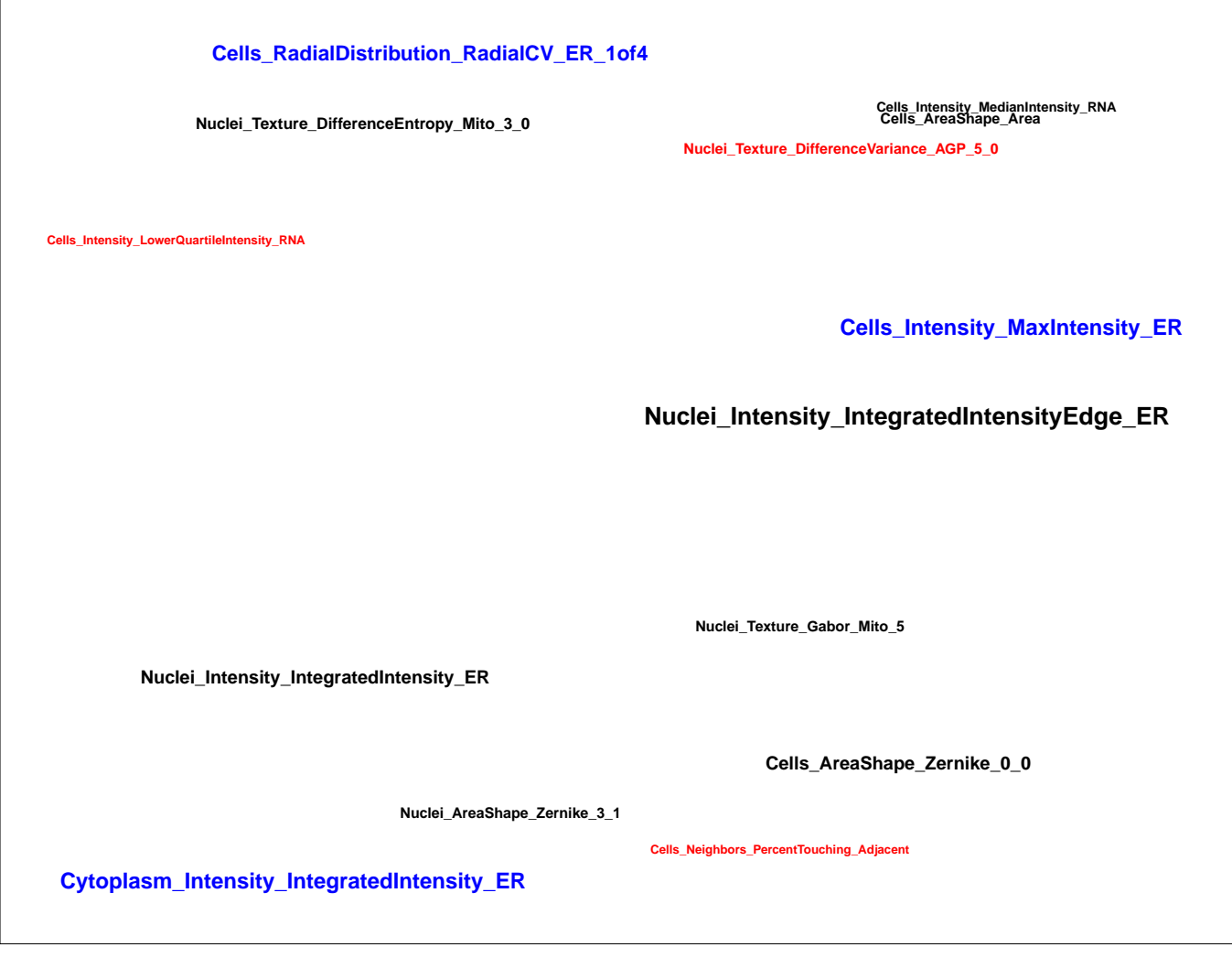
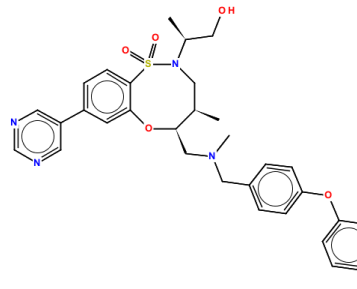
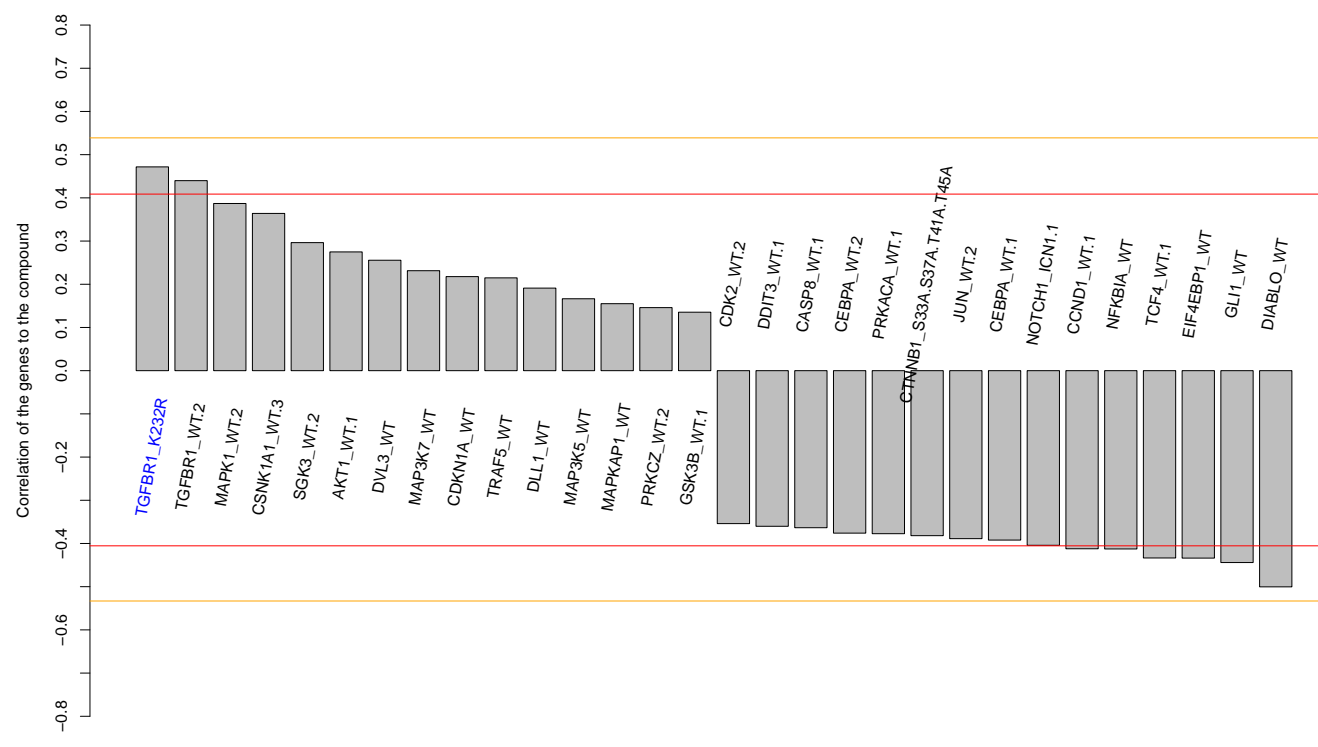
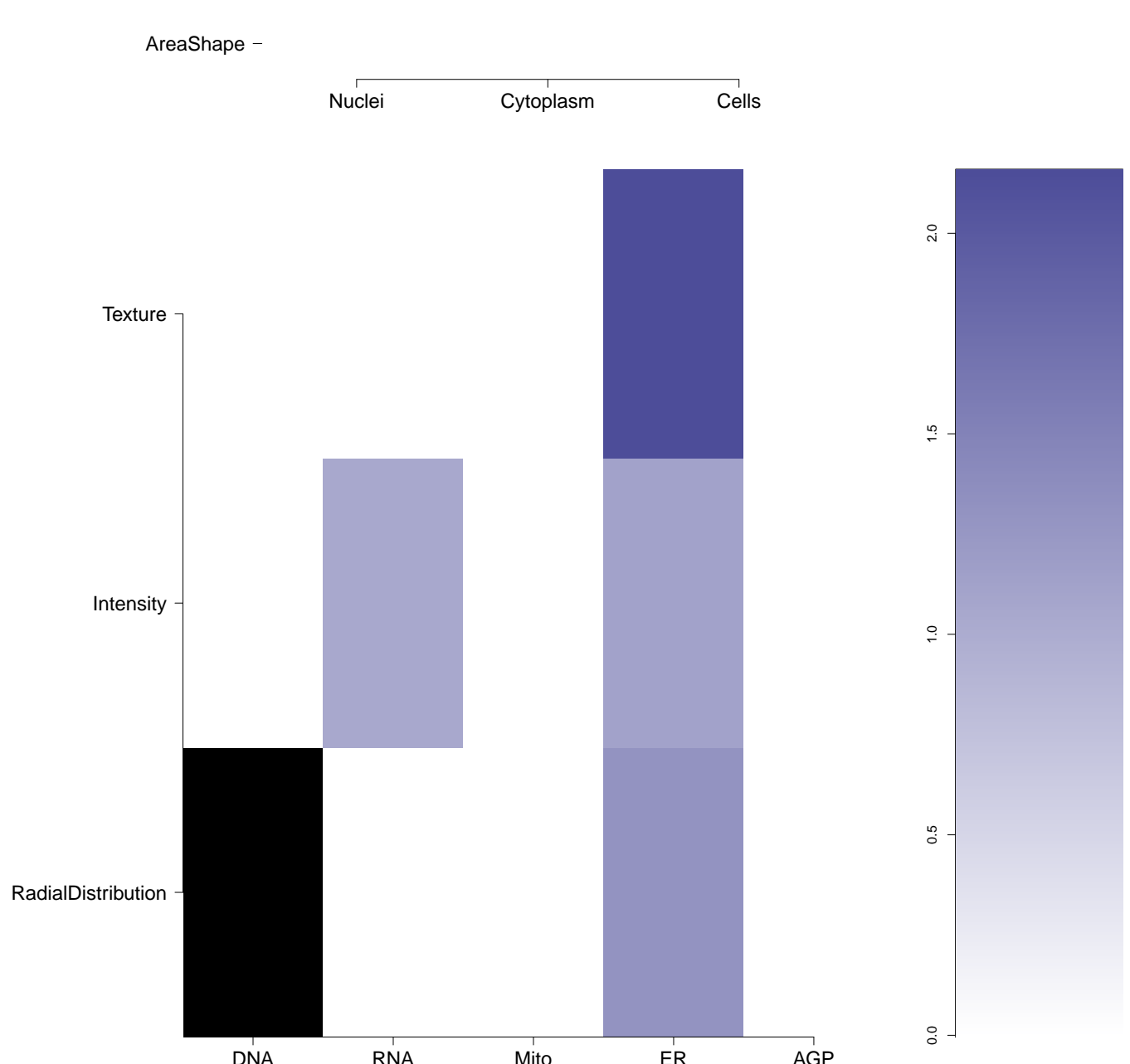
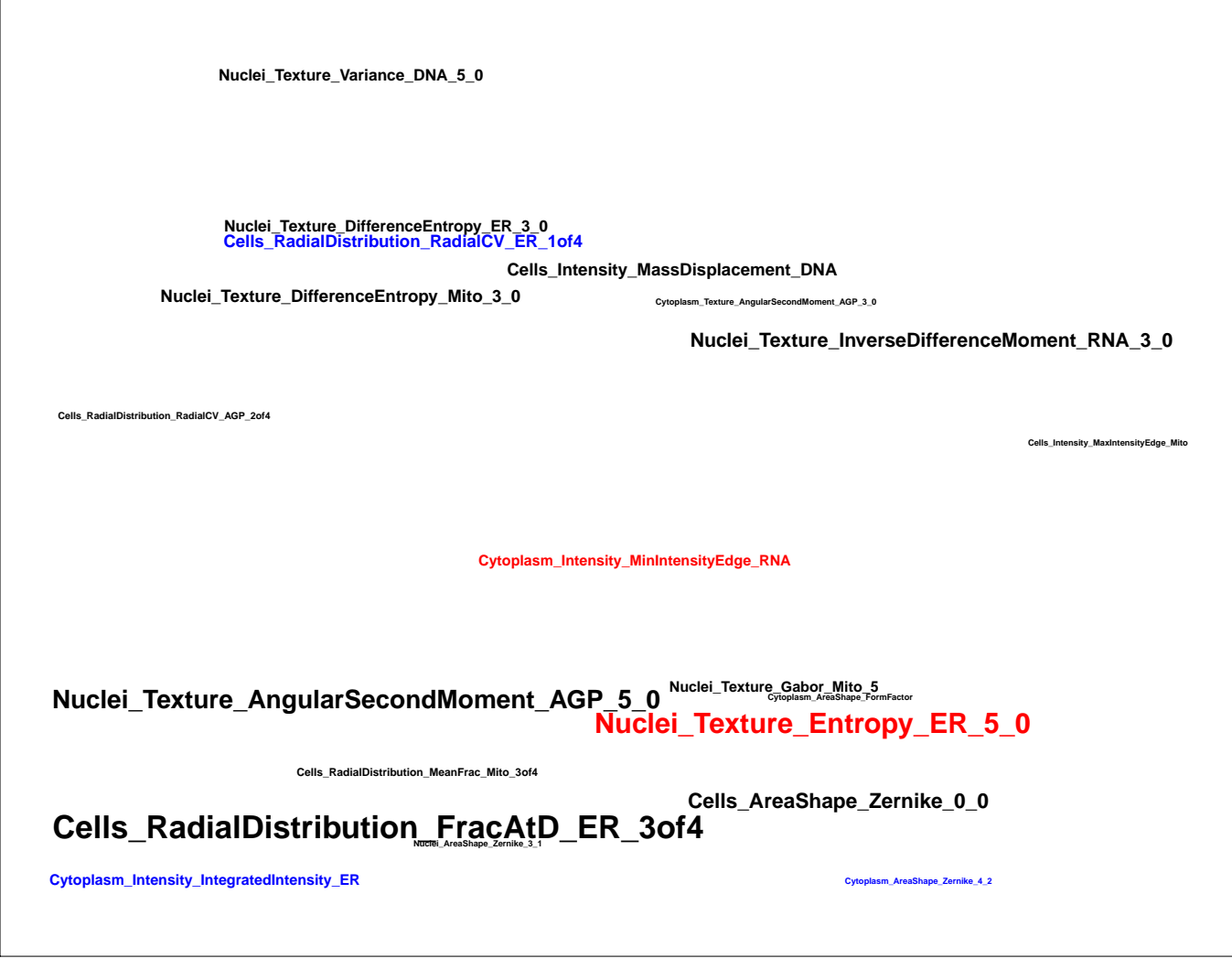
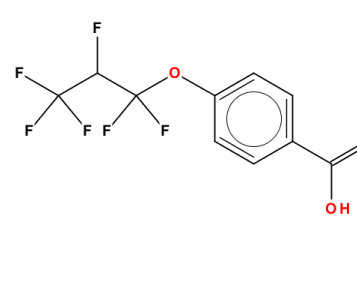
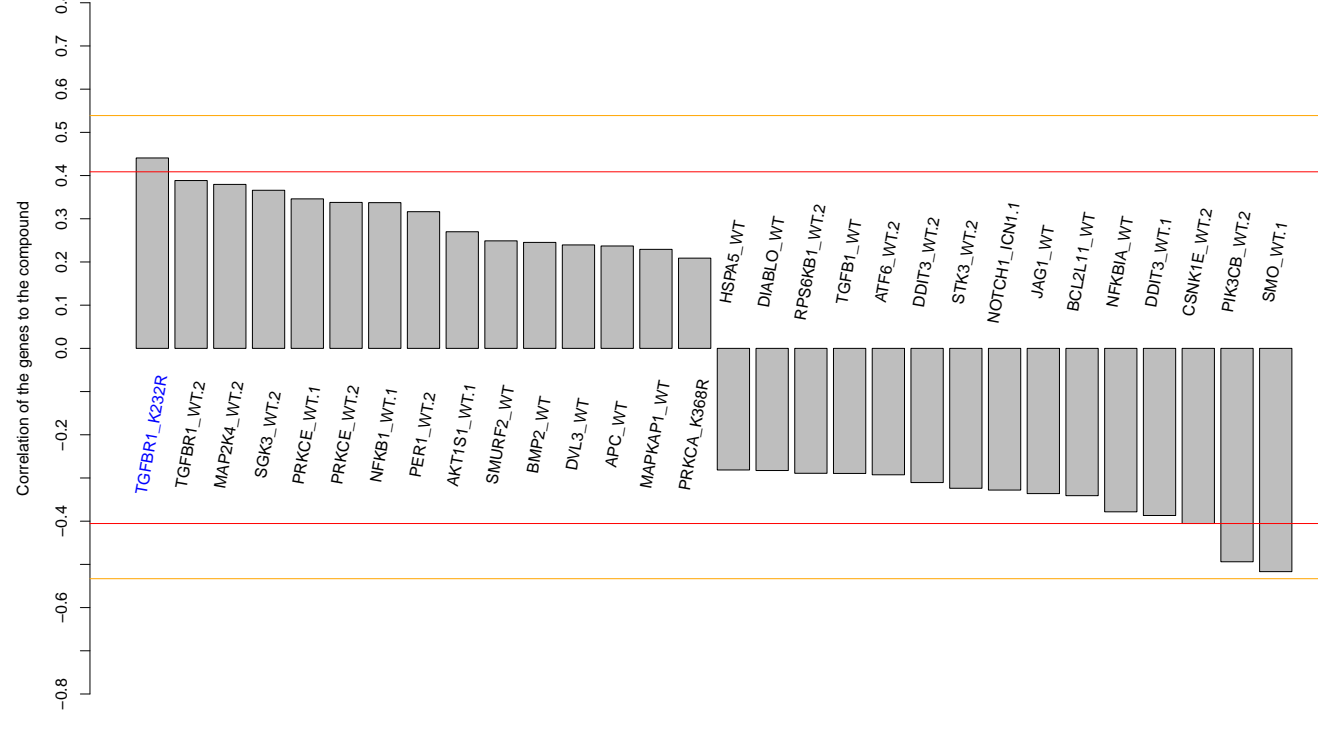
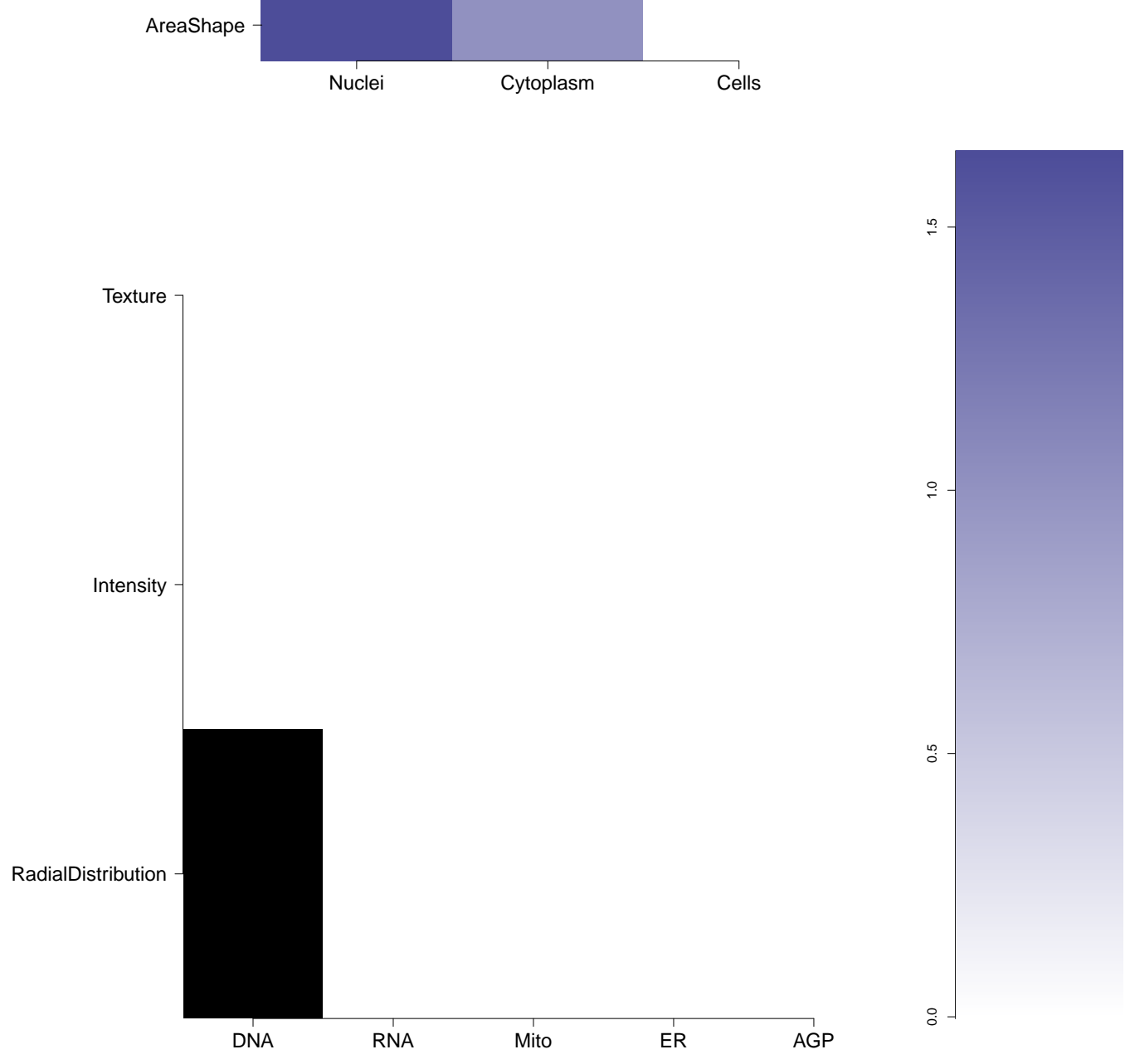



ER



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



<div>BRD-A35158877-001-05-1</div> <div>SMR000093888</div> <div>AC1NSGQ0</div> <div>MLS000116934</div> <div>MLS002586885</div> <div>HMS2245K22</div> <div>PubChem CID : 5309350</div>		NA (in 1 replicates)	0.52	NA				<div>Total number of assays tested in: 772. Active in the following assays:</div> <ul style="list-style-type: none"><li>• MLPCN Platelet Activation -Dense Granule Release (AID 1663)</li><li>• Luminescence Cell-Based Dose Confirmation HTS to Identify Inhibitors of Platelet Dense Granule Release (AID 1889)</li><li>• qHTS identification of small molecule modulators of myocardial damage (AID 588492)</li></ul>
<div>BRD-K93783788-001-01-0</div> <div>PubChem CID : 54641130</div>		NA (in 1 replicates)	0.49	NA				<div>Total number of assays tested in: 38.</div>
<div>BRD-K15994694-001-05-2</div> <div>AC1OBOXE</div> <div>MLS000587960</div> <div>STK745321</div> <div>ZINC33352338</div> <div>SMR000211968</div> <div>PubChem CID : 6882959</div>		0.57 (in 3 replicates)	0.47	NA				<div>Total number of assays tested in: 635. Active in the following assays:</div> <ul style="list-style-type: none"><li>• qHTS Assay for Inhibitors of Bacillus subtilis Sfp phosphopantetheinyl transferase (PPTase) (AID 1490)</li><li>• qHTS Assay for Inhibitors of BAZ2B (AID 504333)</li><li>• qHTS Assay for Inhibitors of JMJD2A-Tudor Domain (AID 504339)</li><li>• Primary cell-based high-throughput screening for identification of compounds that activate/potentiate calcium-activated chloride channels (TMEM16A) (AID 623877)</li><li>• qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1); qHTS in cells in absence of CPT (AID 686978)</li><li>• qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1); qHTS in cells in presence of CPT (AID 686979)</li><li>• QFRET-based biochemical primary high throughput screening assay to identify exosite inhibitors of ADAM10. (AID 720582)</li><li>• Fluorescence-based biochemical high throughput primary assay to identify inhibitors of phospholipase C isozymes (PLC-gamma1). (AID 720700)</li></ul>
<div>BRD-K09244864-001-01-3</div> <div>PubChem CID : 54618567</div>		0.64 (in 4 replicates)	0.47	0.615				<div>Total number of assays tested in: 24. Active in the following assays:</div> <ul style="list-style-type: none"><li>• Cytotoxicity Assay Measured in Cell-Based System Using Plate Reader - 2144-02 Activator Dose CherryPick Activity (AID 720690)</li><li>• Cytotoxicity Assay Measured in Cell-Based System Using Plate Reader - 2144-02 Inhibitor Dose CherryPick Activity Set2 (AID 720697)</li></ul>
<div>BRD-A76935636-001-05-4</div> <div>SBB018443</div> <div>MLS000099001</div> <div>AC1MH9ZK</div> <div>HMS2319L21</div> <div>BBL015123</div> <div>STK664101</div> <div>SMR000062989</div> <div>ST4129256</div> <div>R2327</div> <div>T0517-2252</div> <div>PubChem CID : 2998630</div>		NA (in 1 replicates)	0.44	NA				<div>Total number of assays tested in: 782. Active in the following assays:</div> <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>• RNA aptamer-based HTS for inhibitors of GRK2 (AID 488847)</li></ul>