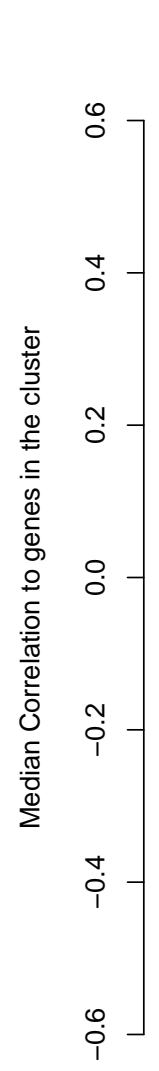


How similar is this cluster to the other clusters?

Genes in the cluster along with the pathways as annotated by experts

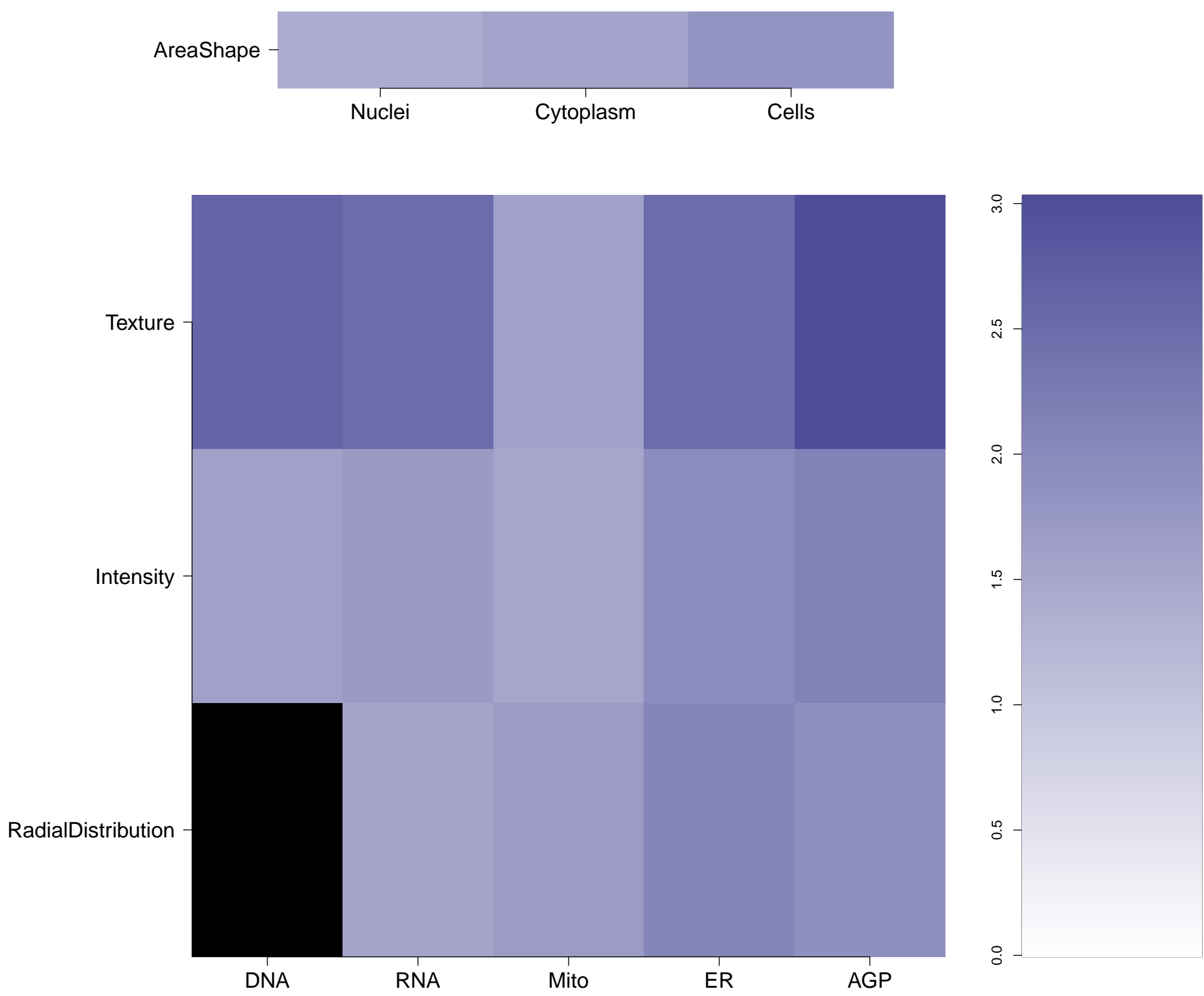
Expert Annotation		
Treatment	Pathway	Regulation Type
TGFBRI_K232R	Canonical TGFbeta	Inhibitor
TGFBRI.WT.2	Canonical TGFbeta	Activator
DVL3.WT	Canonical WNT	Activator



Top 5 genes negatively correlated to the cluster

Expert Annotation			Mean Correlation	Standard Deviation
Treatment	Pathway	Regulation Type		
SMO.WT.1	Hedgehog	Activator	-0.58	0.06
DDIT3.WT.2	Canonical ER Stress/UPR	Activator	-0.51	0.04
PRKACA.WT.2	Canonical PKA	Activator	-0.47	0.16
NFKBIA.WT	Canonical NFkB	Inhibitor	-0.47	0.21
DIABLO.WT	Canonical Apoptosis	Inhibitor	-0.43	0.10

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 cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.



How strongly are genes within the cluster correlated?

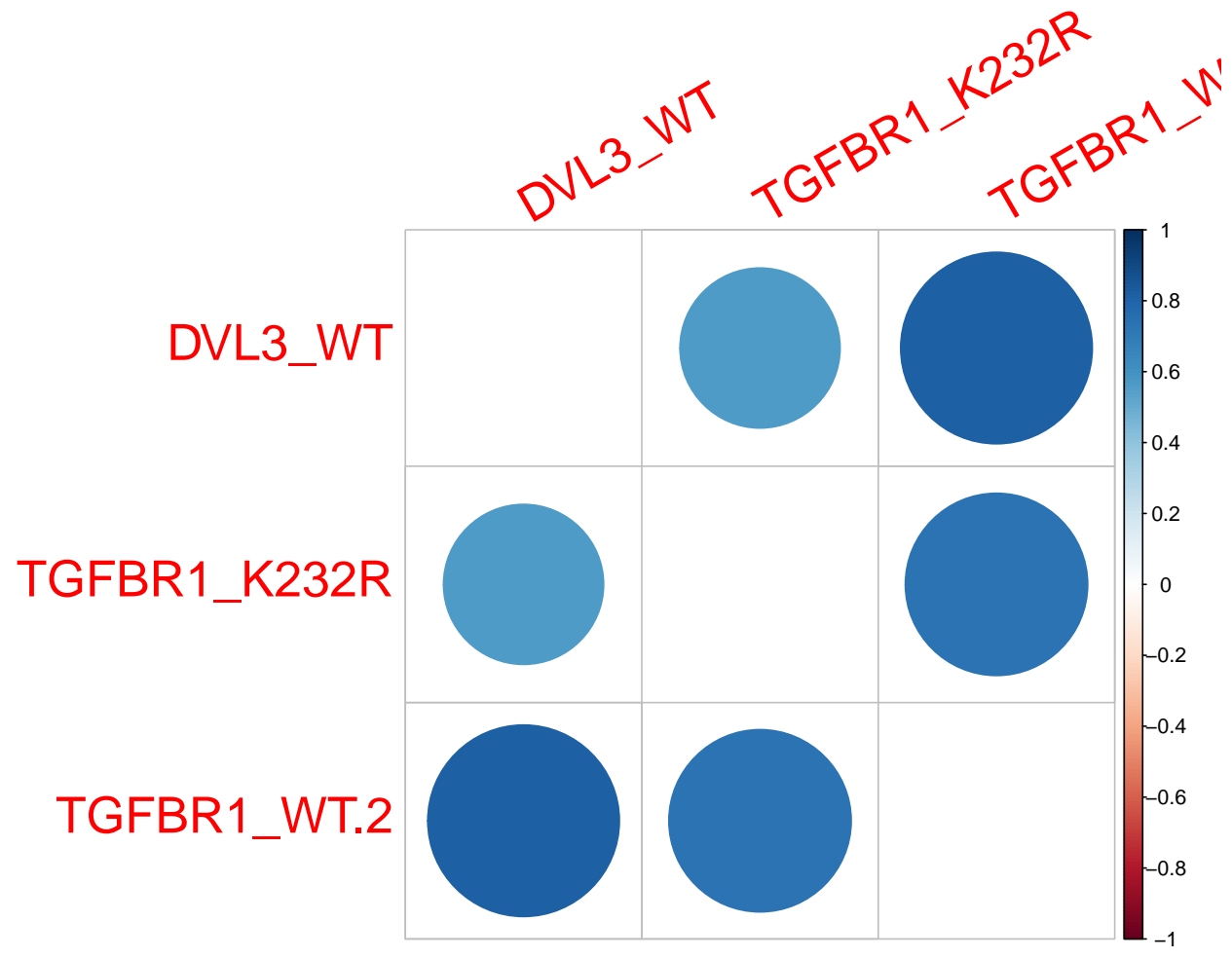


Plate : 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

Empty

DVL3.WT

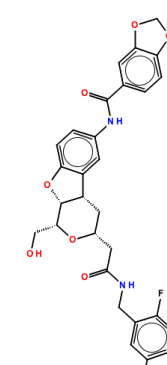
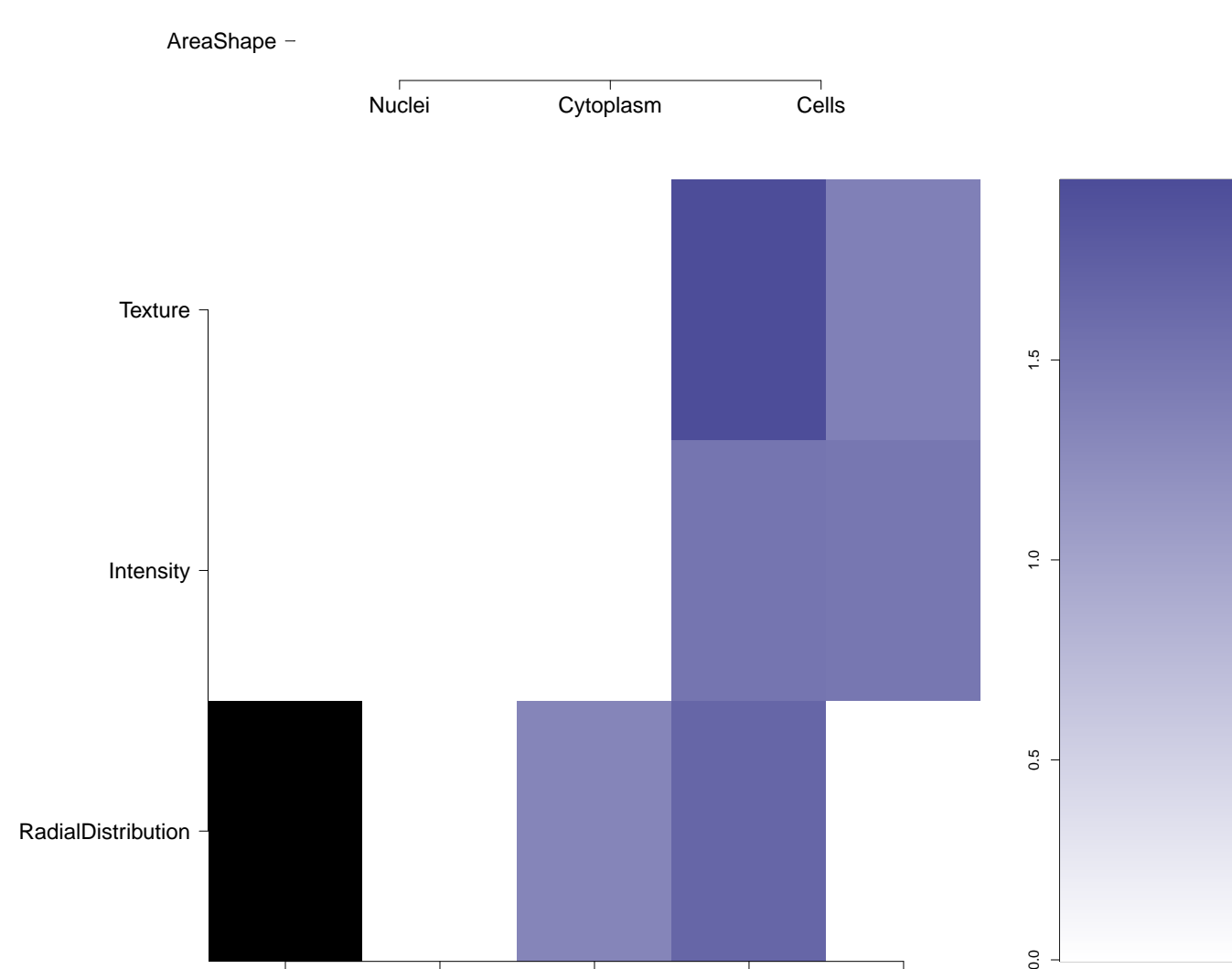
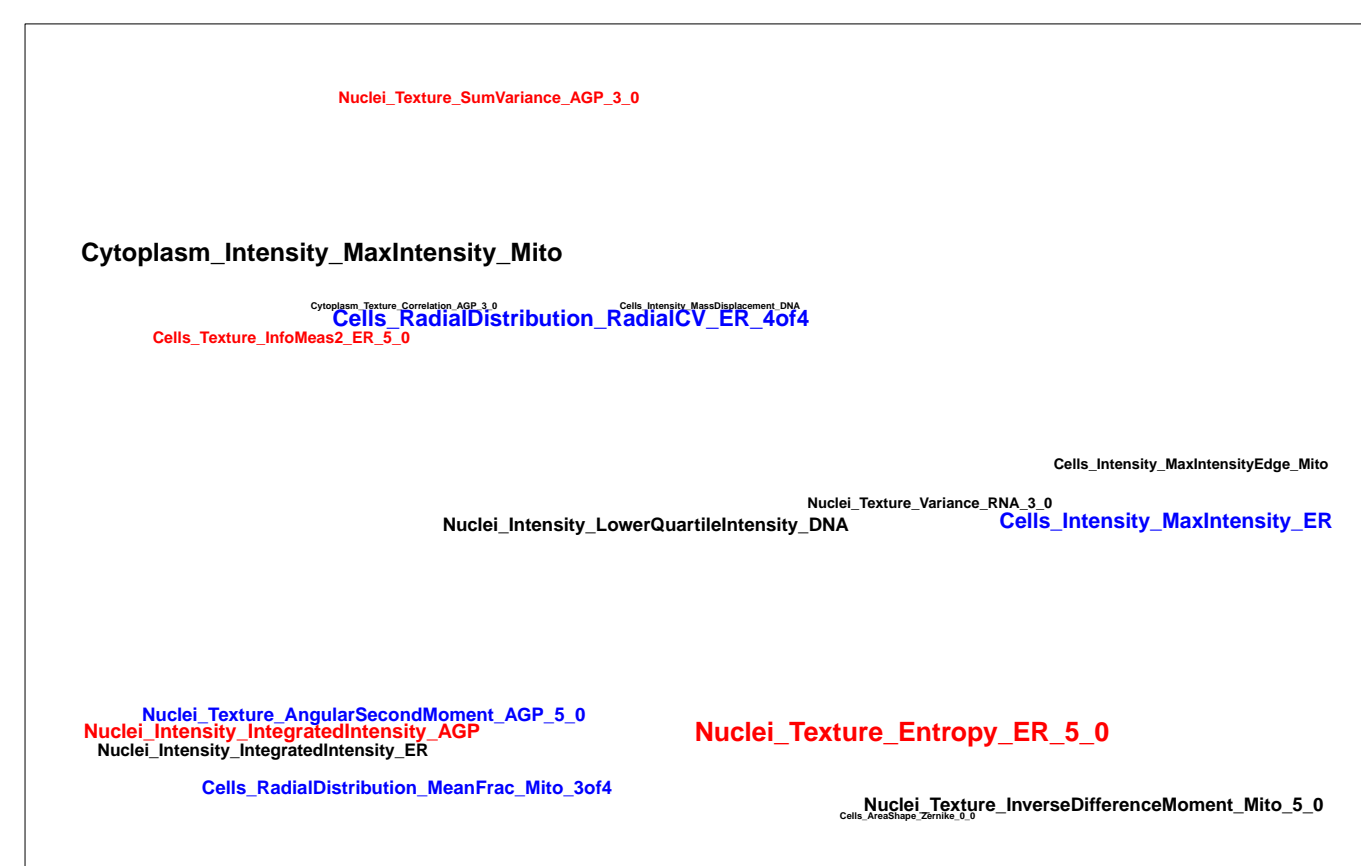
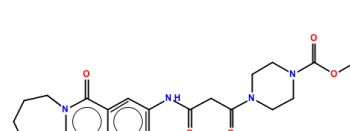
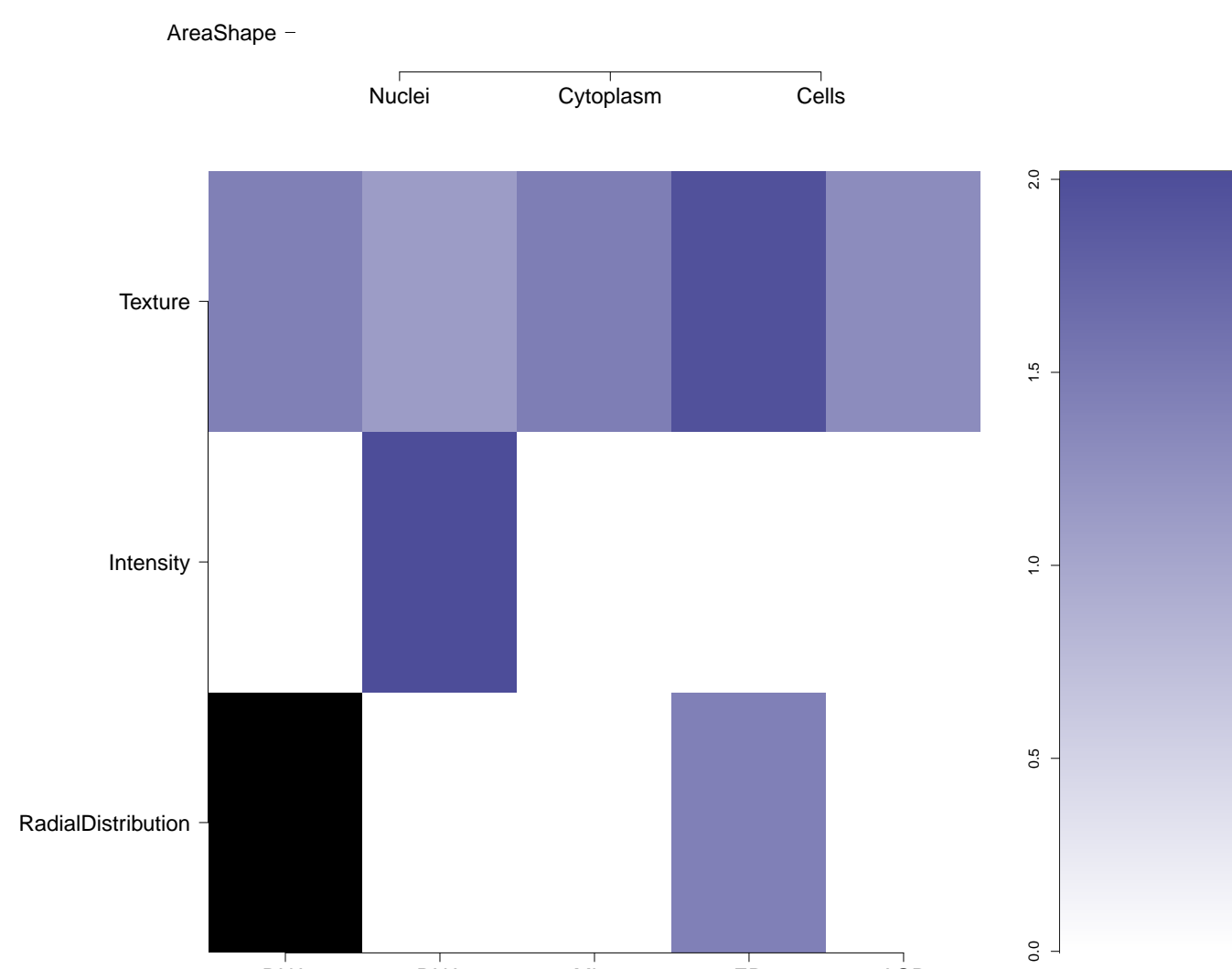
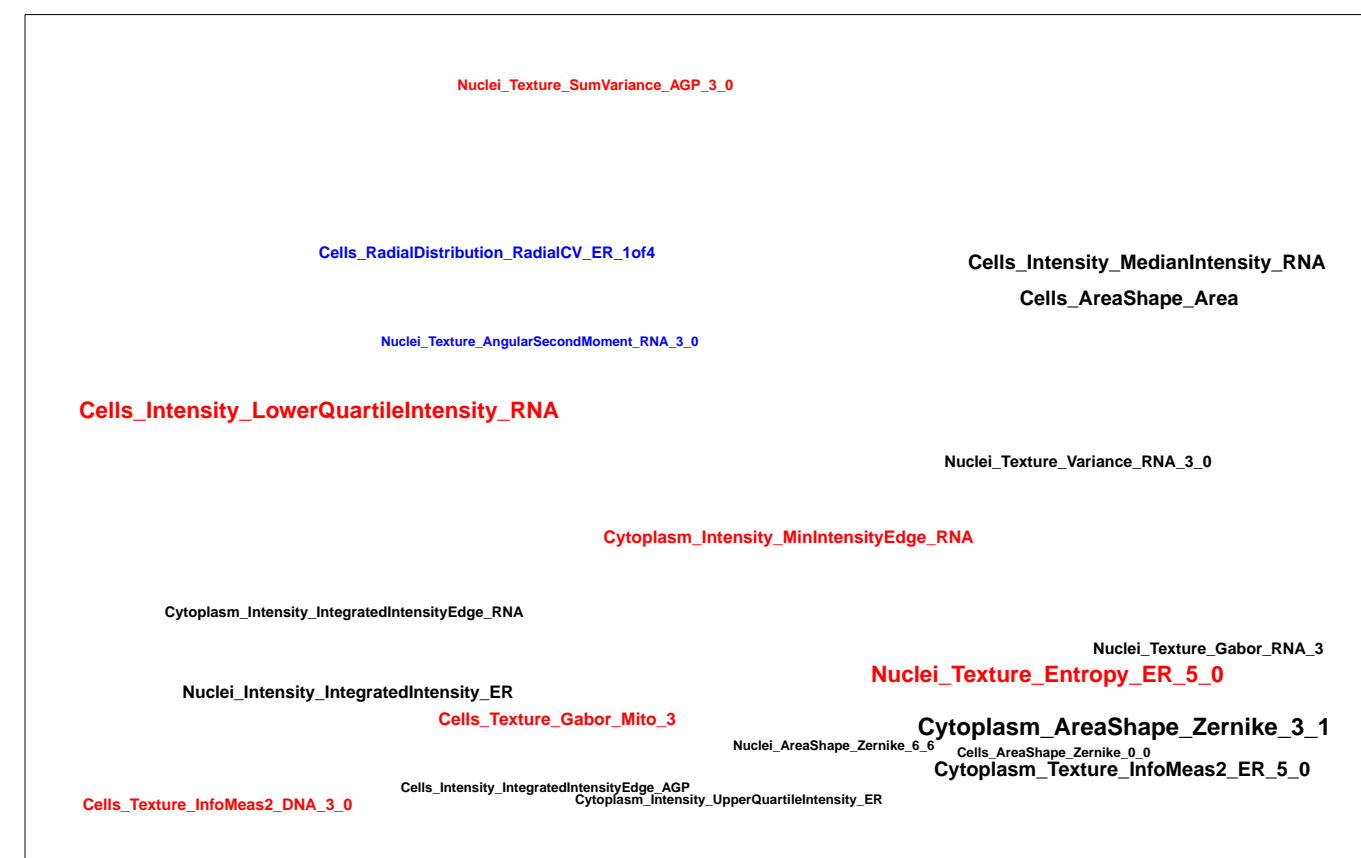
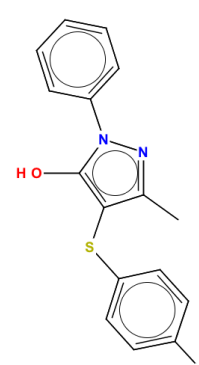
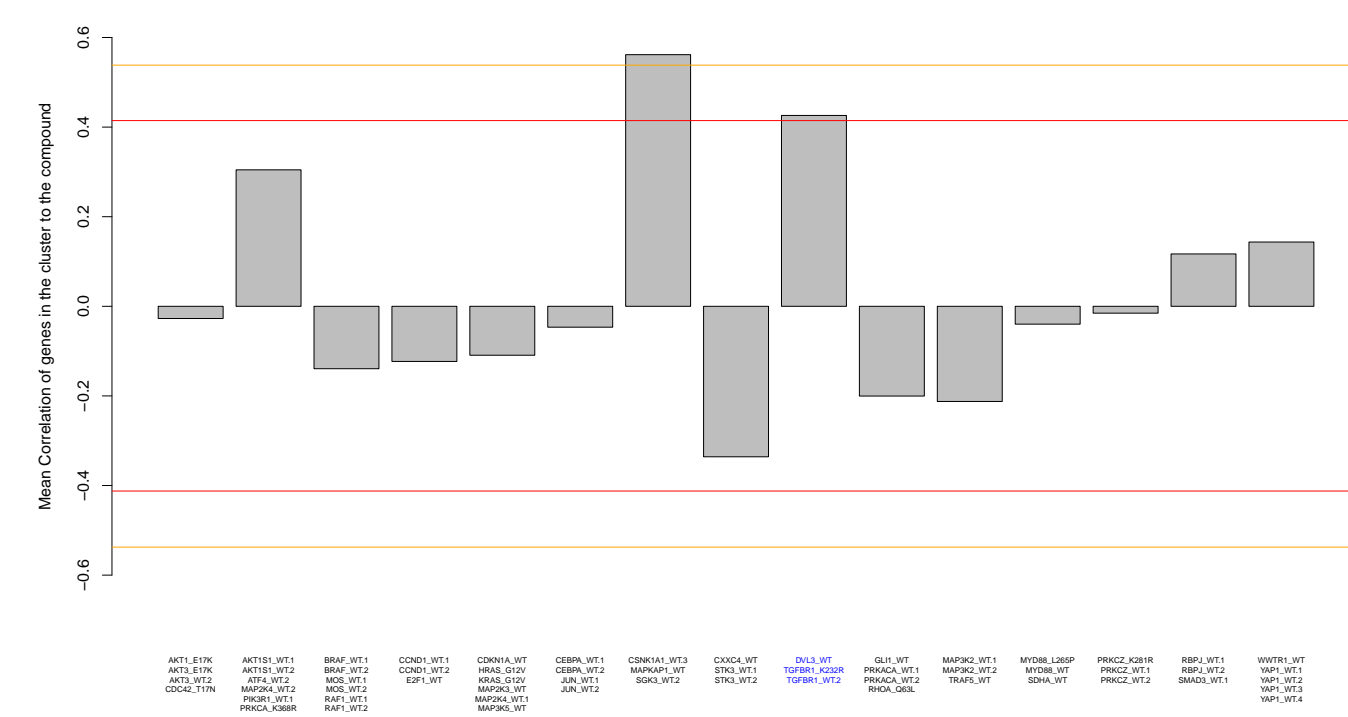
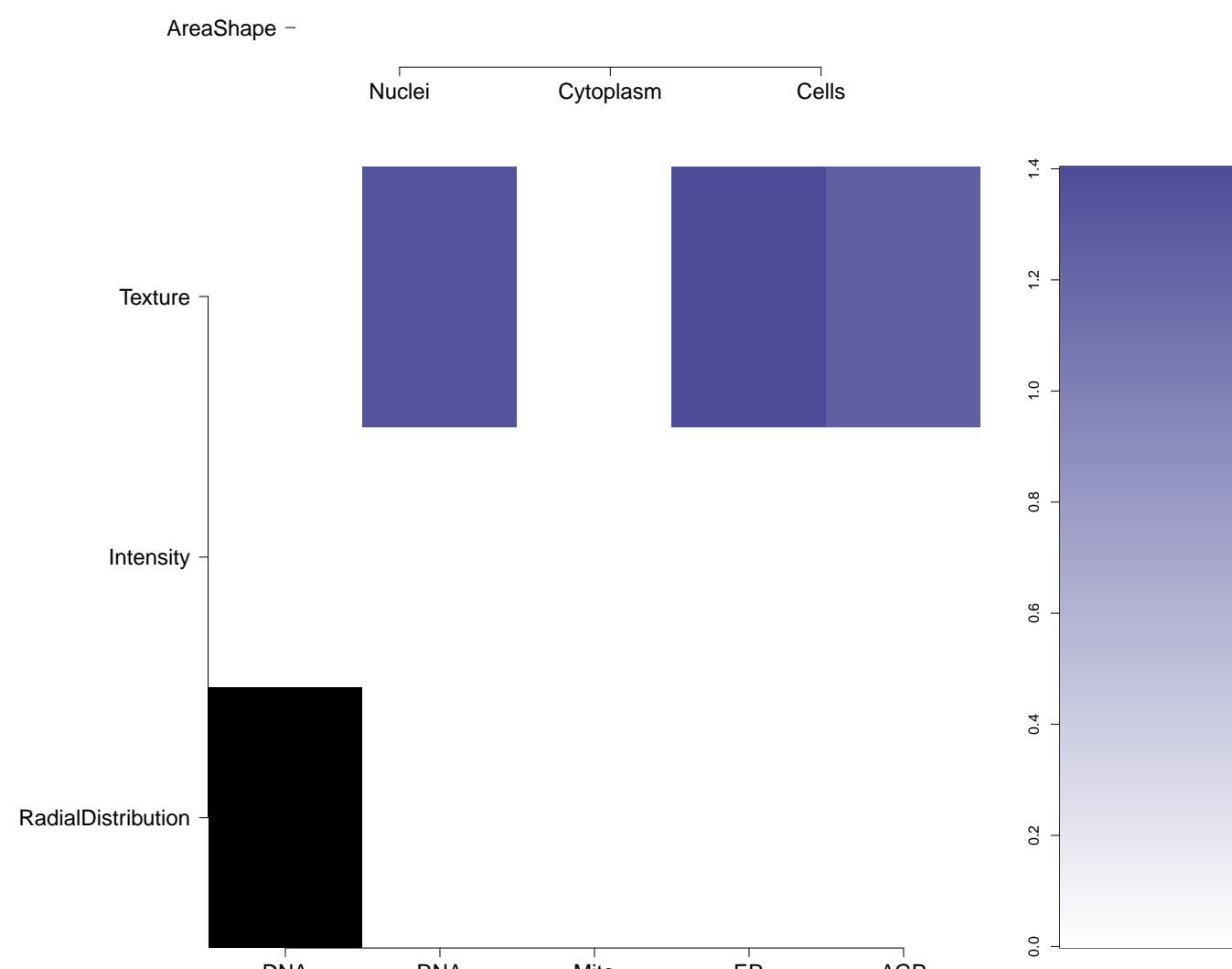
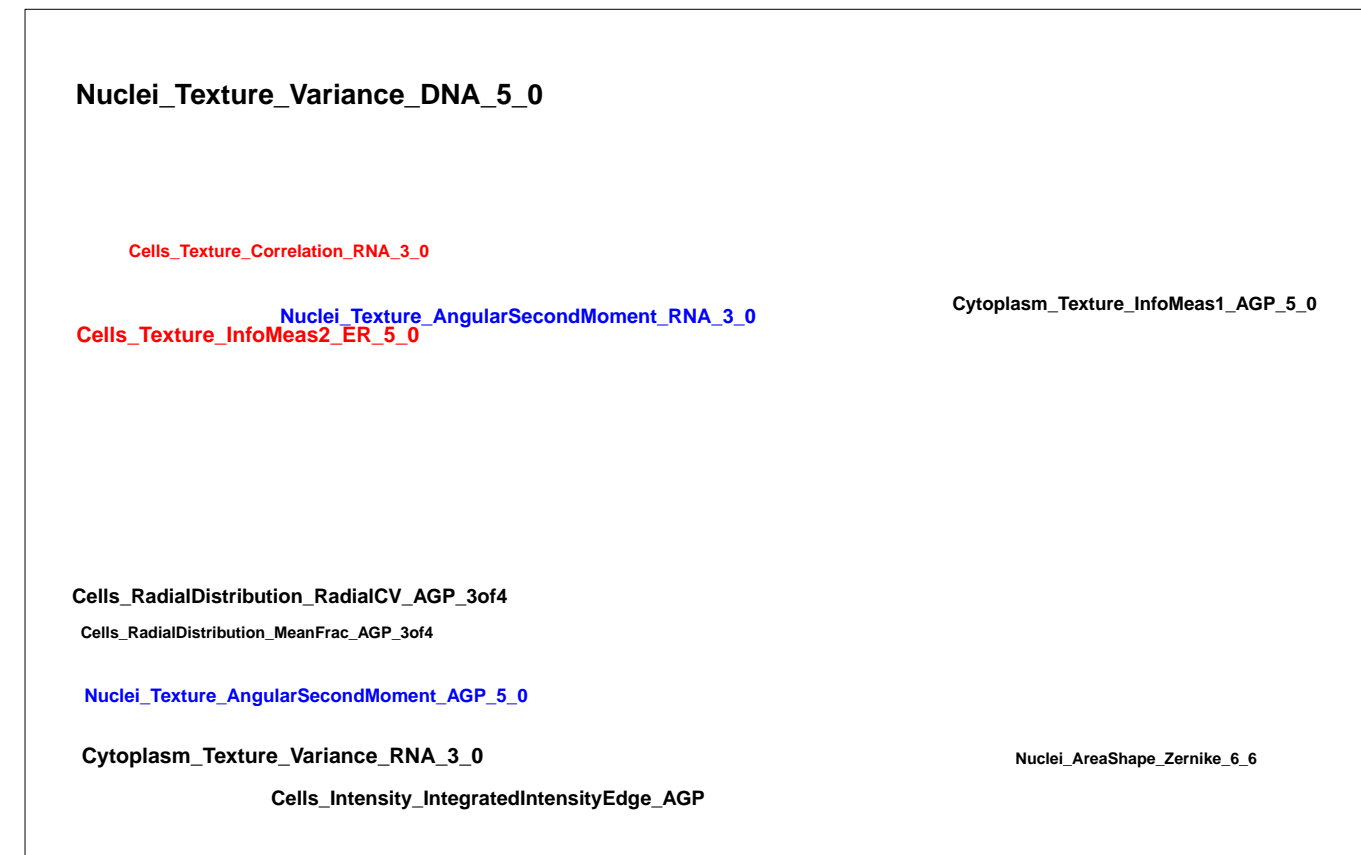
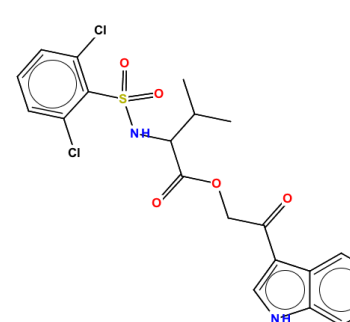
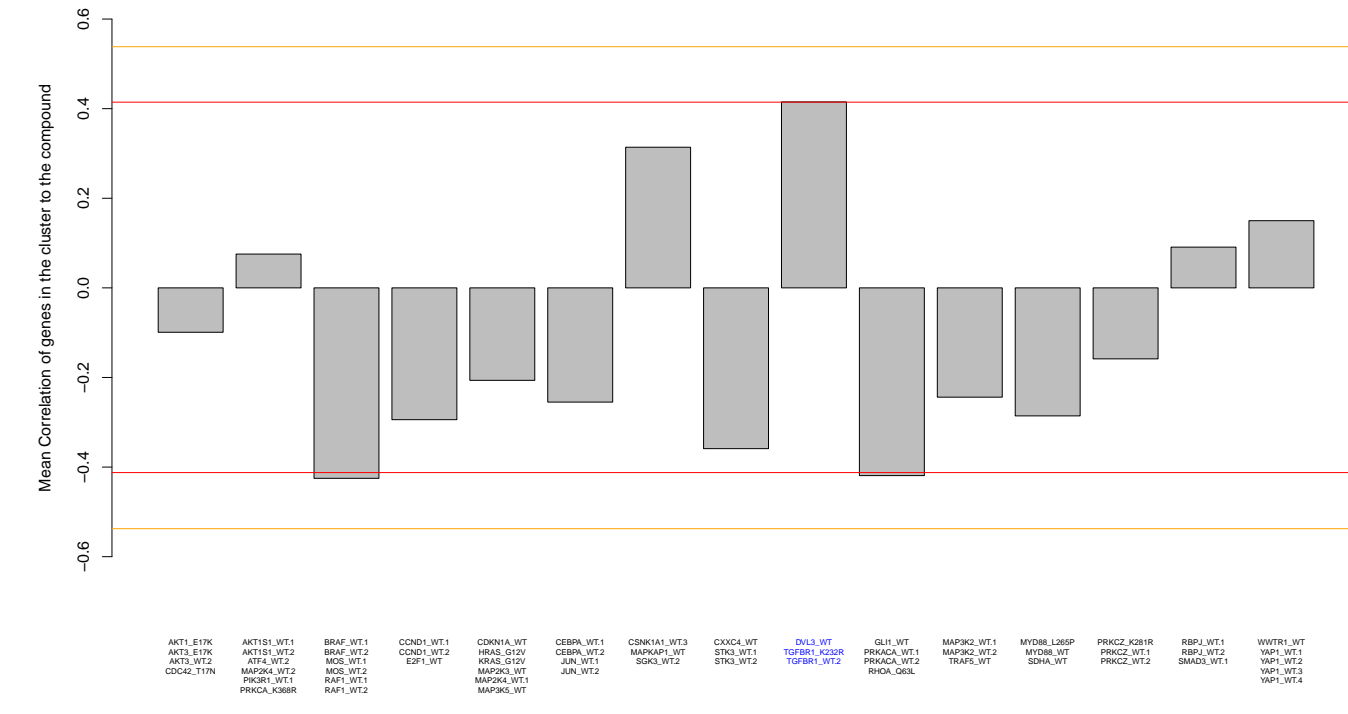
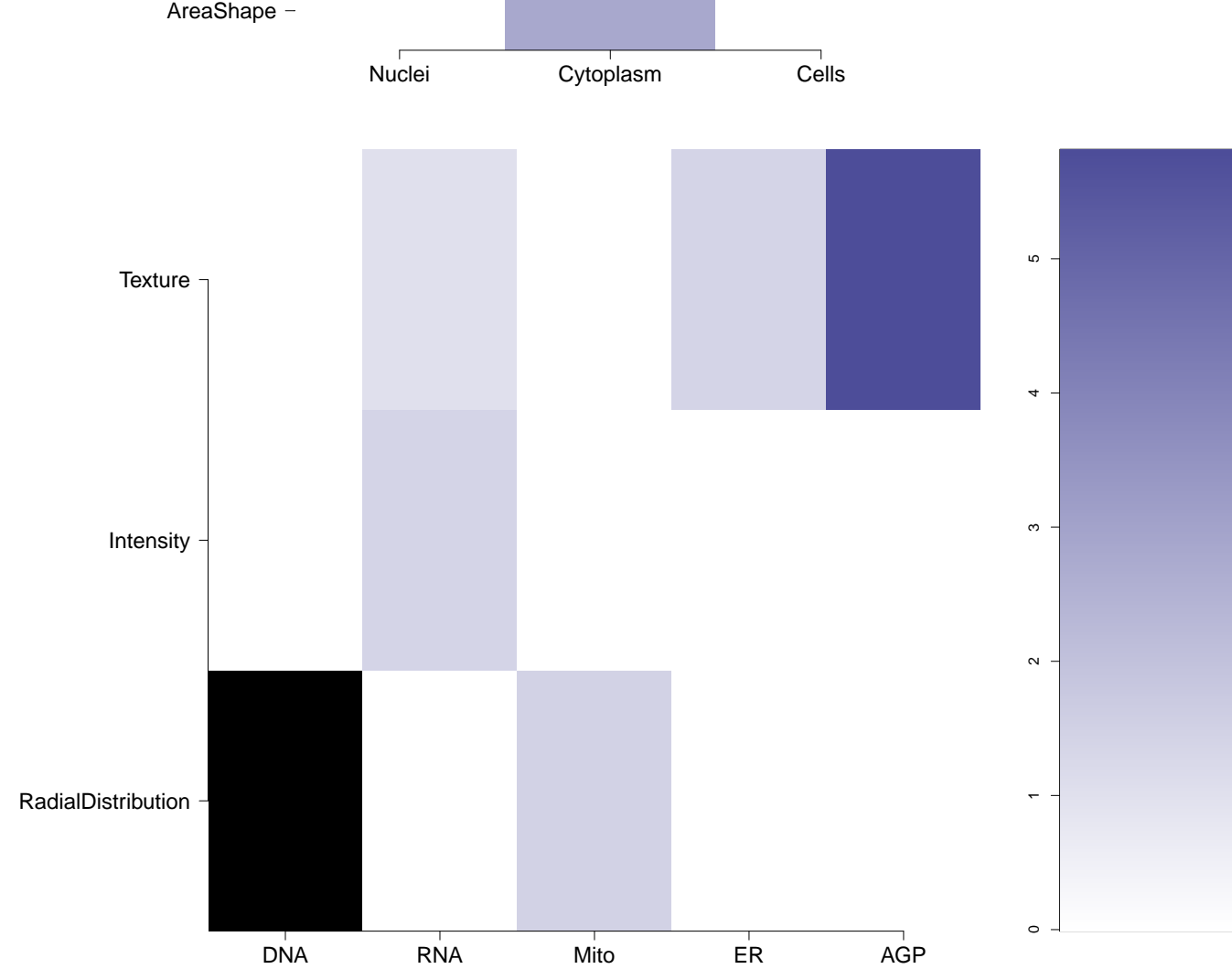
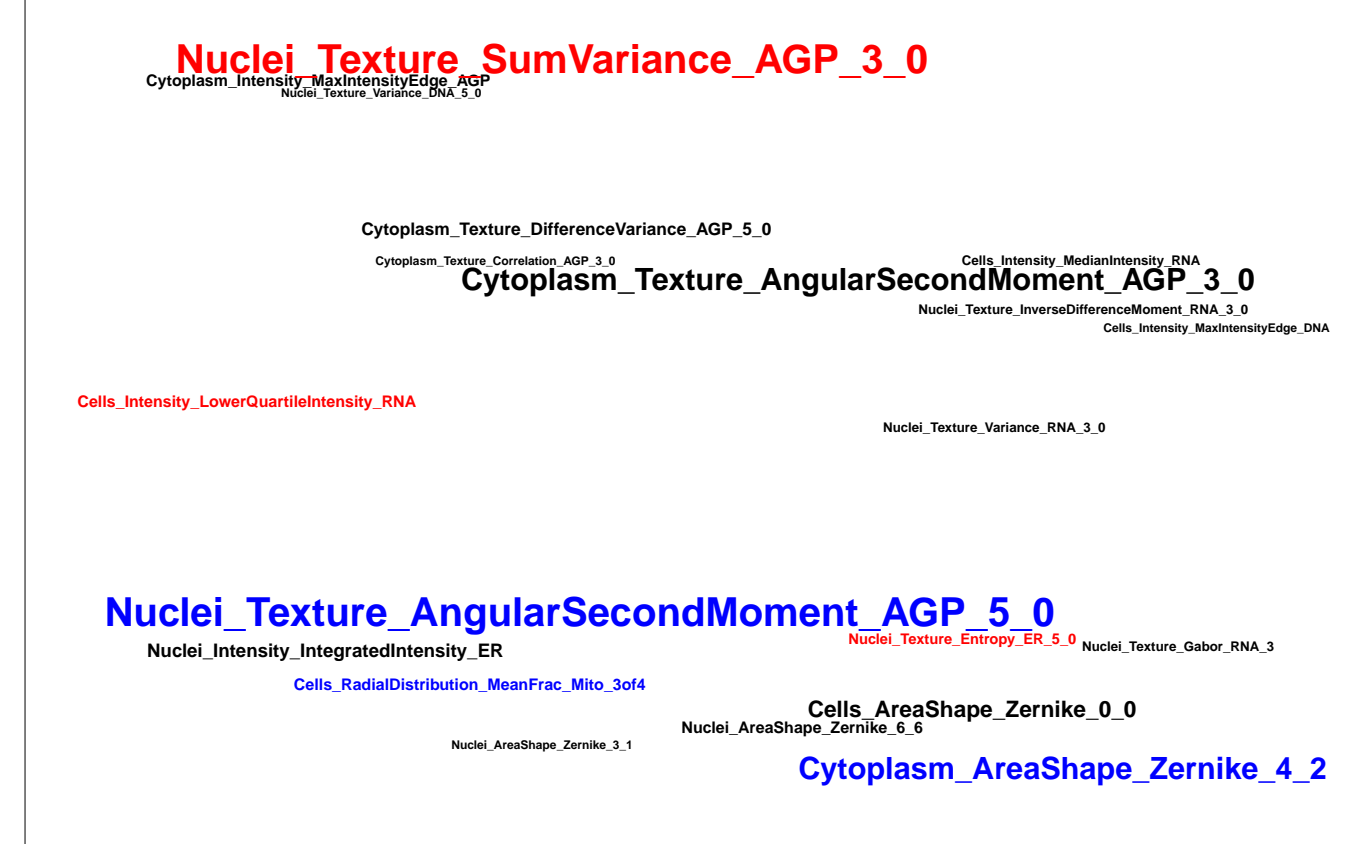
TGFBRI.K232R

TGFBRI.WT.2

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 0.52)	Mean \pm standard deviation correlation between compound and each gene in cluster; Tables contain data for individual genes	Mean compound rank when scored against genes in cluster using L1000 profiling \pm standard deviation; Tables contain data for individual genes	How similar is the compound signature to the gene clusters 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 genes in the cluster 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 cluster	Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized
BRD-K29073962-001-01-3 PubChem CID : 54641201		NA (in 1 replicates)	0.48 \pm 0.12 Treatment Score DVL3.WT 0.36 TGFBRI_K232R 0.37 TGFBRI.WT.2 0.03	NA				Total number of assays tested in: 38.

<div>BRD-K04267190-001-01-4</div> <div>PubChem CID : 54646512</div>		0.67 (in 4 replicates)	<div>0.45 ± 0.13</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>DVLS.WT</td><td>0.46</td></tr><tr><td>TFPBRL.K202H</td><td>0.39</td></tr><tr><td>TFPBRL.WT.2</td><td>0.58</td></tr></table>	Treatment	Score	DVLS.WT	0.46	TFPBRL.K202H	0.39	TFPBRL.WT.2	0.58	<div>0.705 ± 0.049</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>DVLS.WT</td><td>0.682</td></tr><tr><td>TFPBRL.K202H</td><td>0.631</td></tr><tr><td>TFPBRL.WT.2</td><td>0.761</td></tr></table>	Treatment	Score	DVLS.WT	0.682	TFPBRL.K202H	0.631	TFPBRL.WT.2	0.761				Total number of assays tested in: 37.
Treatment	Score																							
DVLS.WT	0.46																							
TFPBRL.K202H	0.39																							
TFPBRL.WT.2	0.58																							
Treatment	Score																							
DVLS.WT	0.682																							
TFPBRL.K202H	0.631																							
TFPBRL.WT.2	0.761																							
<div>BRD-K24588660-001-05-1</div> <div>SMR000029508</div> <div>AC1MMPHI</div> <div>MLS000093894</div> <div>MLS002588230</div> <div>HMS2172A20</div> <div>HMS3307J08</div> <div>ZINC4077675</div> <div>PubChem CID : 3242390</div>		NA (in 1 replicates)	<div>0.43 ± 0.20</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>DVLS.WT</td><td>0.29</td></tr><tr><td>TFPBRL.K202H</td><td>0.27</td></tr><tr><td>TFPBRL.WT.2</td><td>0.69</td></tr></table>	Treatment	Score	DVLS.WT	0.29	TFPBRL.K202H	0.27	TFPBRL.WT.2	0.69	NA				Total number of assays tested in: 758. Active in the following assays: <ul style="list-style-type: none">Factor XIIa Mixture HTS (AID 684)CYP2C9 Assay (AID 777)Primary qHTS for delayed death inhibitors of the malarial parasite plasid, 48 hour incubation (AID 504832)								
Treatment	Score																							
DVLS.WT	0.29																							
TFPBRL.K202H	0.27																							
TFPBRL.WT.2	0.69																							
<div>BRD-K05950645-001-07-2</div> <div>MLS000536739</div> <div>SMR000155669</div> <div>AC1LGWR5</div> <div>BDBM48497</div> <div>HMS1485K04</div> <div>HMS2379O21</div> <div>ID11_022358</div> <div>F1386-0259</div> <div>T0500-8534</div> <div>PubChem CID : 828338</div>		NA (in 1 replicates)	<div>0.43 ± 0.12</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>DVLS.WT</td><td>0.39</td></tr><tr><td>TFPBRL.K202H</td><td>0.31</td></tr><tr><td>TFPBRL.WT.2</td><td>0.55</td></tr></table>	Treatment	Score	DVLS.WT	0.39	TFPBRL.K202H	0.31	TFPBRL.WT.2	0.55	NA				Total number of assays tested in: 701. Active in the following assays: <ul style="list-style-type: none">HTS for Estrogen Receptor-beta Coactivator Binding inhibitors (AID 633)Screening for Modulators of Post-Golgi Transport, Control Strain (AID 738)CYP2C9 Assay (AID 777)CYP2C19 Assay (AID 778)Inhibitors of Plasmodium falciparum ML7-Family Leucine Aminopeptidase (M17LAP) (AID 1619)Fluorescence Cell-Free Homogenous Primary HTS to Identify Inhibitors of RecA Intein Splicing Activity (AID 2221)Fluorescence Cell-Free Homogeneous Counter Screen to Identify Inhibitors of GFP Chromophore Formation (AID 434968)Fluorescence Cell-Free Homogeneous Dose Retest to Identify Inhibitors of RecA-Intein Splicing Activity (AID 435010)Fluorescence Cell-Free Homogeneous Secondary Screen to Identify Inhibitors of DnaB-Intein Splicing Activity (AID 449749)Fluorescence Cell-Free Homogeneous Secondary Screen to Identify Non-Covalent Inhibitors of RecA-Intein Splicing Activity (AID 449750)								
Treatment	Score																							
DVLS.WT	0.39																							
TFPBRL.K202H	0.31																							
TFPBRL.WT.2	0.55																							
<div>BRD-A47393232-001-05-0</div> <div>MLS000409274</div> <div>SMR000243613</div> <div>AC1NIO3E</div> <div>MLS003912484</div> <div>BDBM114051</div> <div>HMS2575L04</div> <div>T5304168</div> <div>PubChem CID : 4834110</div>		NA (in 1 replicates)	<div>0.42 ± 0.09</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>DVLS.WT</td><td>0.34</td></tr><tr><td>TFPBRL.K202H</td><td>0.38</td></tr><tr><td>TFPBRL.WT.2</td><td>0.92</td></tr></table>	Treatment	Score	DVLS.WT	0.34	TFPBRL.K202H	0.38	TFPBRL.WT.2	0.92	NA				Total number of assays tested in: 639. Active in the following assays: <ul style="list-style-type: none">qHTS Assay for Inhibitors of the ERK Signaling Pathway using a Homogeneous Screening Assay; Stimulation with EGF (AID 1454)Counterscreen qHTS for Inhibitors of Tau Fibril Formation, Fluorescence Polarization (AID 1463)qHTS Assay for Promiscuous and Specific Inhibitors of Cruzain (without detergent) (AID 1476)Multiplex HTS Assay for Inhibitors of MEK Kinase PB1 Domains, specifically MEK5 MEK Kinase 2 mutant (AID 1530)Multiplex HTS Assay for Inhibitors of MEK Kinase PB1 Domains, specifically MEK5 binding to MEK Kinase 2 Wildtype (AID 1531)Nrf2 qHTS screen for inhibitors (AID 504444)Primary qHTS for delayed death inhibitors of the malarial parasite plasid, 48 hour incubation (AID 504832)Nrf2 qHTS screen for inhibitors (AID 504444)Primary qHTS for delayed death inhibitors of the malarial parasite plasid, 96 hour incubation (AID 504834)High-throughput multiplex microsphere screening for inhibitors of toxin protease, specifically Botulinum neurotoxin light chain A protease, MLPCN compound set (AID 588499)HTS to identify compounds that promote myeloid differentiation with MLPCN compound set (AID 624256)QFRET-based biochemical primary high throughput screening assay to identify exosite inhibitors of ADAM10. (AID 720582)QFRET-based biochemical primary high throughput screening assay to identify exosite inhibitors of ADAM17. (AID 720648)QFRET-based biochemical high throughput confirmation assay to identify exosite inhibitors of ADAM17 (AID 743257)Counterscreen for exosite inhibitors of ADAM17: Fluorescence resonance energy transfer (FRET)-based biochemical high throughput dose response assay to identify inhibitors of ADAM10 (AID 743259)								
Treatment	Score																							
DVLS.WT	0.34																							
TFPBRL.K202H	0.38																							
TFPBRL.WT.2	0.92																							