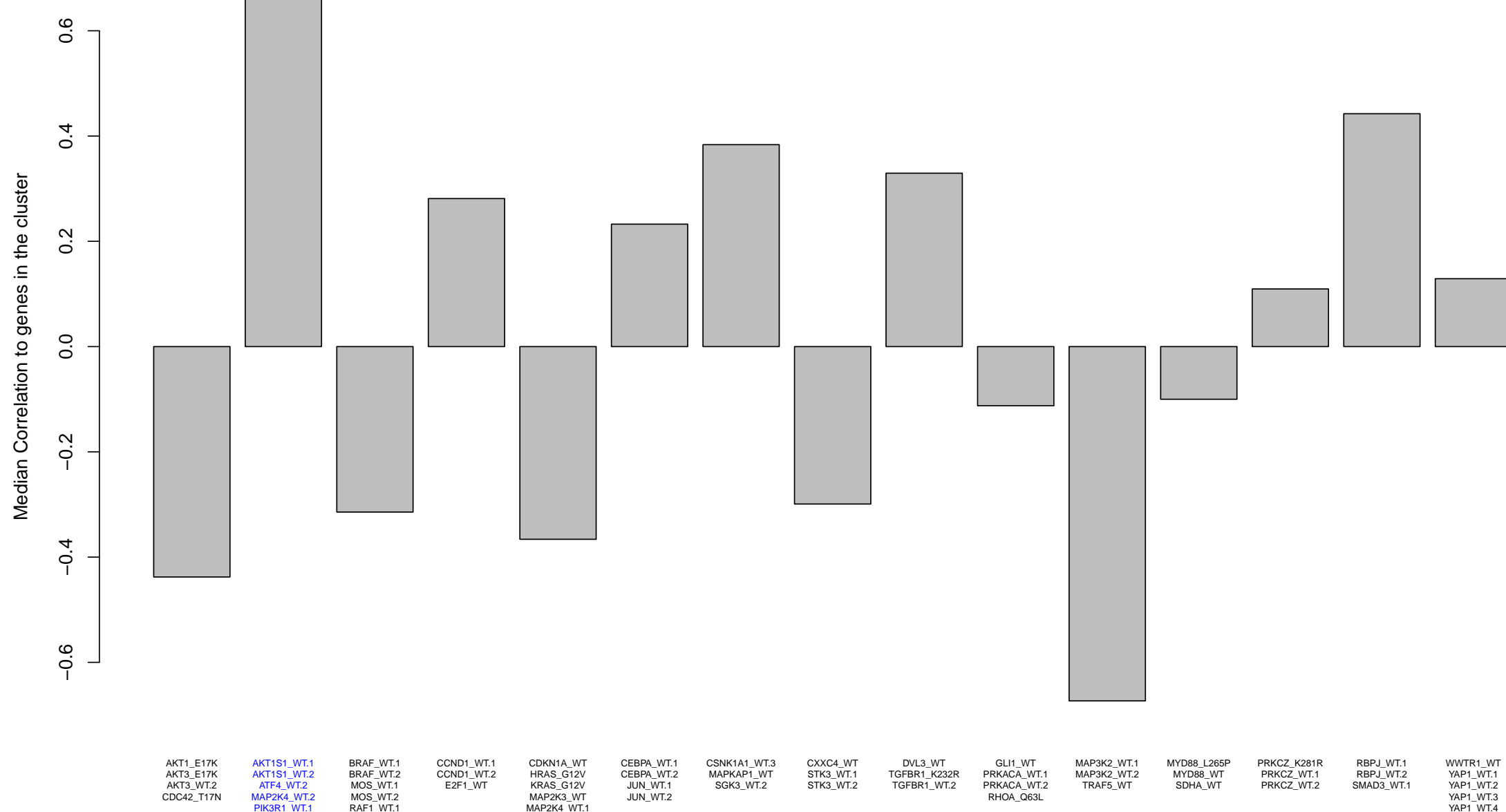


How similar is this cluster to the other clusters?

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

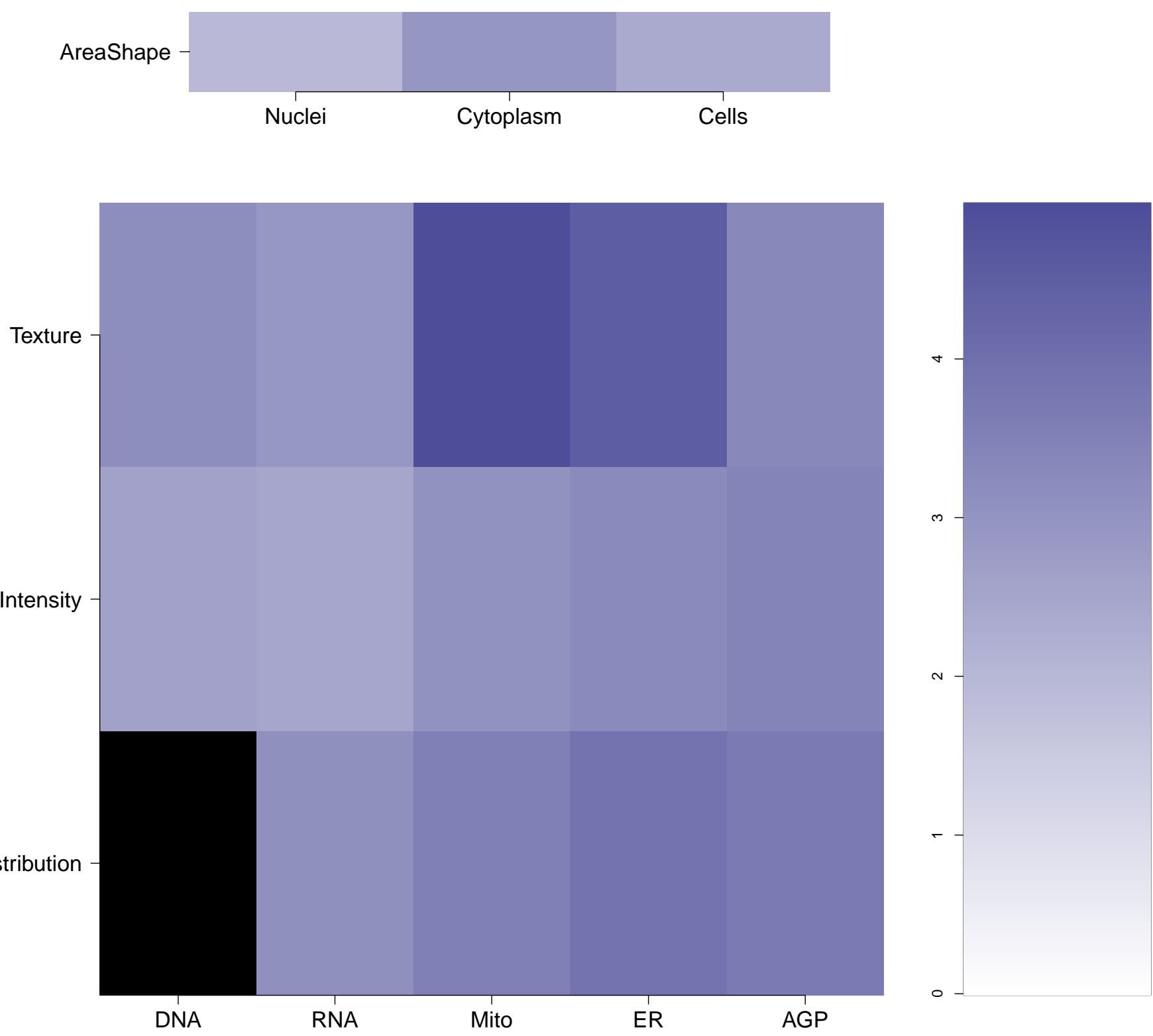
Expert Annotation		
Treatment	Pathway	Regulation Type
ATF4.WT.2	Canonical ER Stress/UPR	Activator
MAP2K4.WT.2	Canonical MAPK	Activator
PIK3R1.WT.1	Canonical PI3K/AKT	Activator
PRKCA.K368R	Canonical PKC	Inhibitor
AKT1S1.WT.1	TOR	Inhibitor
AKT1S1.WT.2	TOR	Inhibitor



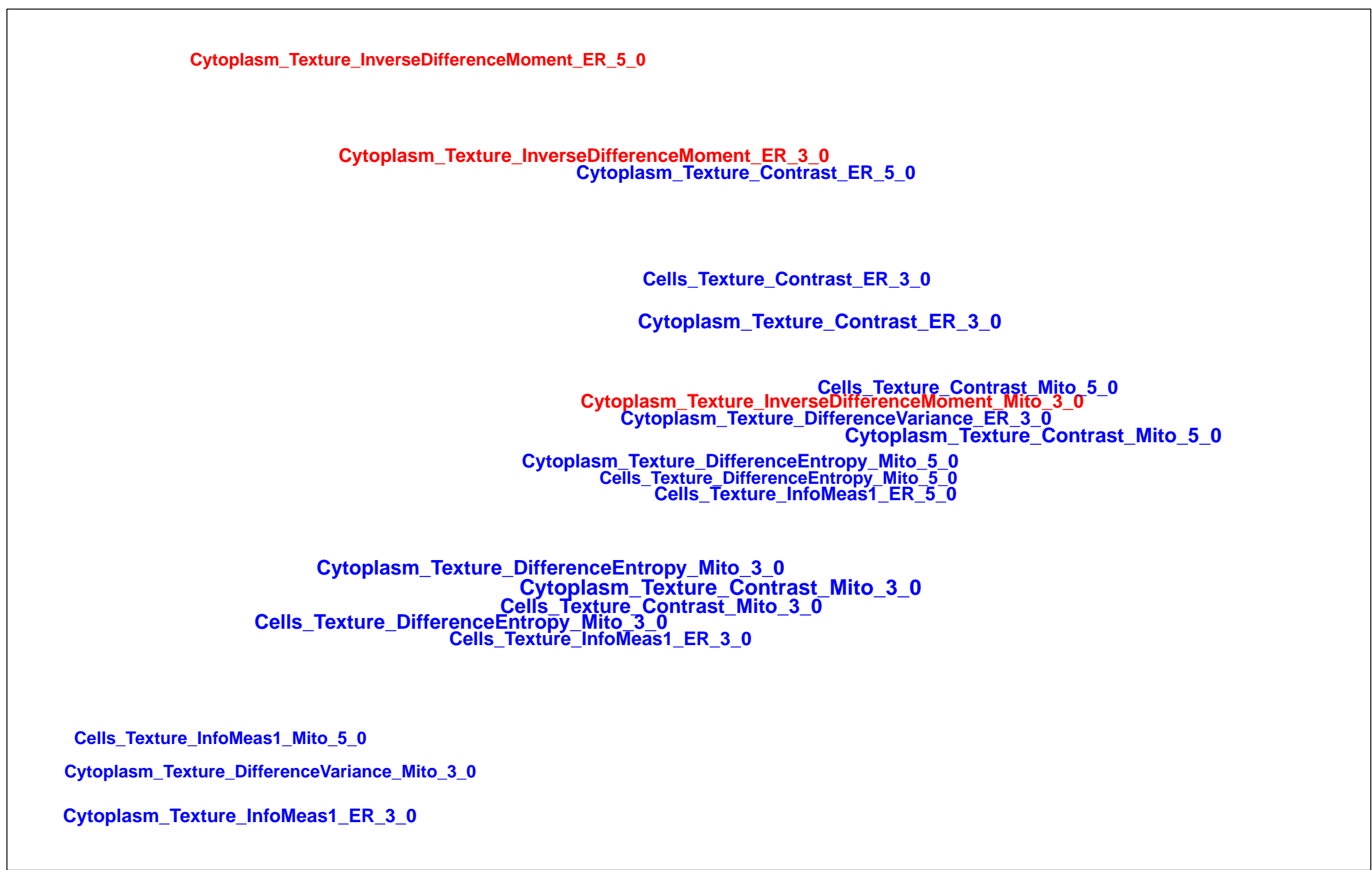
Top 5 genes negatively correlated to the cluster

Expert Annotation			Mean Correlation	Standard Deviation
Treatment	Pathway	Regulation Type		
MAP3K2.WT.1	Canonical MAPK	Activator	-0.71	0.07
MAP3K2.WT.2	Canonical MAPK	Activator	-0.71	0.07
PIK3CB.WT.2	Canonical PI3K/AKT	Activator	-0.63	0.10
TRAF5.WT	Canonical NFkB	Activator	-0.57	0.02
AKT3.WT.2	Canonical PI3K/AKT	Activator	-0.53	0.06

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?

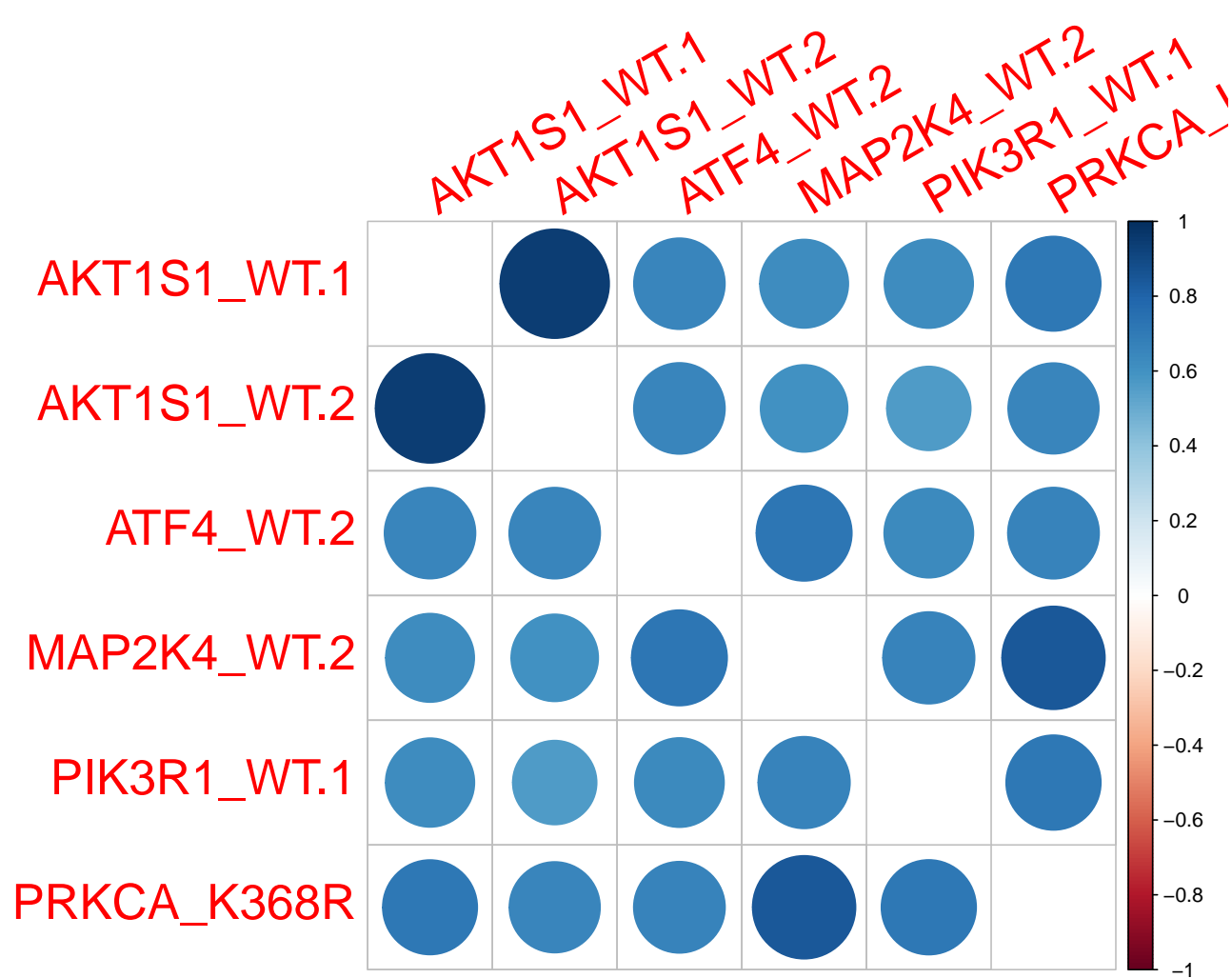


Plate : 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

Empty

AKT1S1.WT.1

AKT1S1.WT.2

ATF4.WT.2

MAP2K4.WT.2

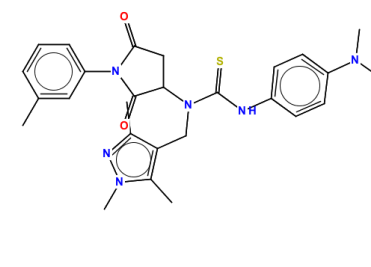
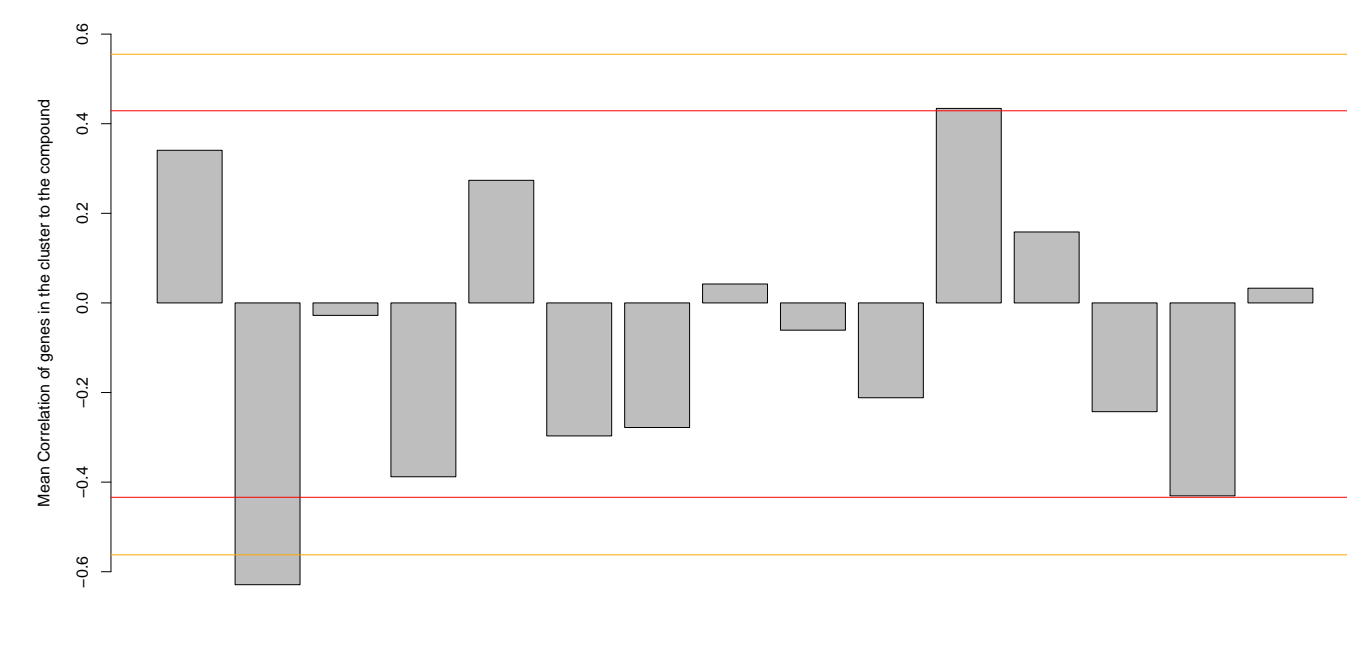
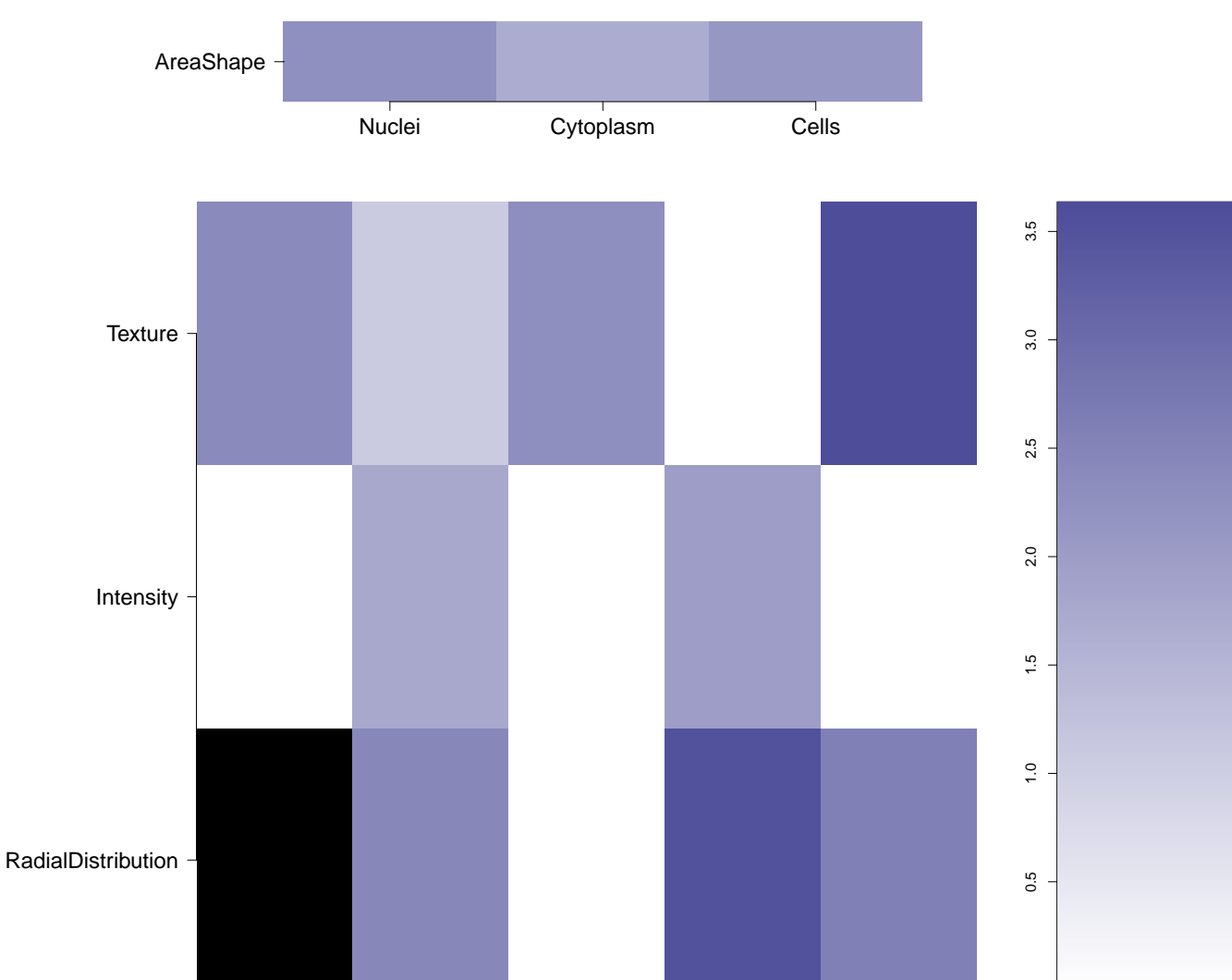
PIK3R1.WT.1

PRKCA.K368R

Mito

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 0.54)	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-K59496950-001-06-2 SMR000008290 AC1LDHEO ASN 08222509 MLS000068187 MLS002538128 HMS2502P09 ZINC1337997 ZINC01337997 PubChem CID : 648117		NA (in 1 replicates)	0.68 \pm 0.05 Treatment Score AKT1S1.WT.1 0.05 AKT1S1.WT.2 0.04 ATF4.WT.2 0.05 MAP2K4.WT.2 0.09 PIK3R1.WT.1 0.09 PRKCA.K368R 0.09	NA				Total number of assays tested in: 762. Active in the following assays: <ul style="list-style-type: none">• Luminescence Cell-Based Primary HTS to Identify Transcriptional Activators of Hypoxia-Inducible Factor Pathway (AID 1910)• qHTS Inhibitors of AmpC Beta-Lactamase (assay with detergent) (AID 485294)
BRD-A04599535-003-05-3 SMR00004833 AC1O7EWO MLS000029919 MLS002534451 PubChem CID : 6602651		NA (in 1 replicates)	0.66 \pm 0.06 Treatment Score AKT1S1.WT.1 0.08 AKT1S1.WT.2 0.05 ATF4.WT.2 0.08 MAP2K4.WT.2 0.24 PIK3R1.WT.1 0.20 PRKCA.K368R 0.27	NA				Total number of assays tested in: 752. Active in the following assays: <ul style="list-style-type: none">• CYP2C19 Assay (AID 778)• qHTS Assay for Agonists of the Thyroid Stimulating Hormone Receptor: Activators of Intracellular cAMP Concentrations in Parental HEK 293 (AID 938)• qHTS of Mel-1/Bid interaction inhibitors (AID 1021)• Fluorescence-based primary cell-based high throughput screening assay to identify antagonists of the G-protein coupled receptor 7 (GPR7). (AID 1861)

<div>BRD-A57762296-001-05-6</div> <div>AC1NMVVZ</div> <div>MLS000698218</div> <div>HMS2519113</div> <div>STL400806</div> <div>SMR000227890</div> <div>ST50709480</div> <div>PubChem CID : 5016927</div>	<div></div>	<div>0.72 (in 4 replicates)</div>	<div><div>-0.63 ± 0.04</div><table><tr><th>Treatment</th><th>Score</th></tr><tr><td>ARTISI.WT.1</td><td>-0.60</td></tr><tr><td>ARTISI.WT.2</td><td>-0.61</td></tr><tr><td>ATPL.WT.2</td><td>-0.65</td></tr><tr><td>MAPK1.WT.1</td><td>-0.70</td></tr><tr><td>PI3KB.WT.1</td><td>-0.59</td></tr><tr><td>PRKCA.K66R1</td><td>-0.63</td></tr></table></div> <div><div>0.357 ± 0.247</div><table><tr><th>Treatment</th><th>Score</th></tr><tr><td>ARTISI.WT.1</td><td>0.340</td></tr><tr><td>ARTISI.WT.2</td><td>0.155</td></tr><tr><td>ATPL.WT.2</td><td>0.336</td></tr><tr><td>MAPK1.WT.1</td><td>0.211</td></tr><tr><td>PI3KB.WT.1</td><td>0.236</td></tr><tr><td>PRKCA.K66R1</td><td>0.302</td></tr></table></div>	Treatment	Score	ARTISI.WT.1	-0.60	ARTISI.WT.2	-0.61	ATPL.WT.2	-0.65	MAPK1.WT.1	-0.70	PI3KB.WT.1	-0.59	PRKCA.K66R1	-0.63	Treatment	Score	ARTISI.WT.1	0.340	ARTISI.WT.2	0.155	ATPL.WT.2	0.336	MAPK1.WT.1	0.211	PI3KB.WT.1	0.236	PRKCA.K66R1	0.302	<div></div>	<div><div><div>AreaShape</div><div>NucleiCytoplasmCells</div></div><div><div>Texture</div><div>Intensity</div><div>RadialDistribution</div></div><div><div>DNA</div><div>RNA</div><div>Mito</div><div>ER</div><div>AGP</div></div><div></div></div> <div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div><div>Cytoplasm_Intensity_MeanIntensityEdge_AGP</div><div>Cytoplasm_Intensity_MeanIntensity_Mito</div><div>Cells_RadialDistribution_RadialCV_ER_104</div><div>Cytoplasm_Texture_AngularSecon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Treatment	Score																																
ARTISI.WT.1	-0.60																																
ARTISI.WT.2	-0.61																																
ATPL.WT.2	-0.65																																
MAPK1.WT.1	-0.70																																
PI3KB.WT.1	-0.59																																
PRKCA.K66R1	-0.63																																
Treatment	Score																																
ARTISI.WT.1	0.340																																
ARTISI.WT.2	0.155																																
ATPL.WT.2	0.336																																
MAPK1.WT.1	0.211																																
PI3KB.WT.1	0.236																																
PRKCA.K66R1	0.302																																

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