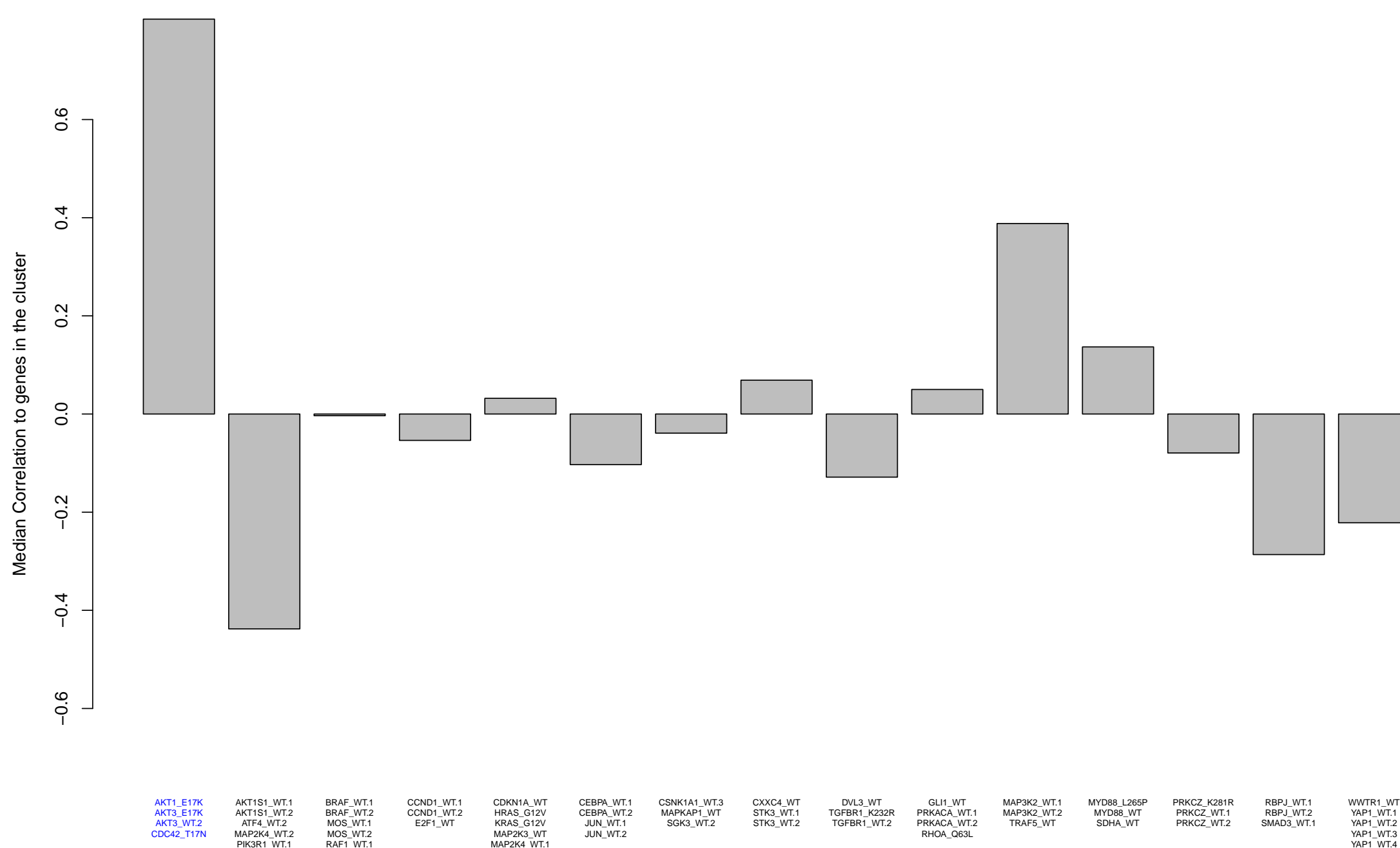


How similar is this cluster to the other clusters?

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

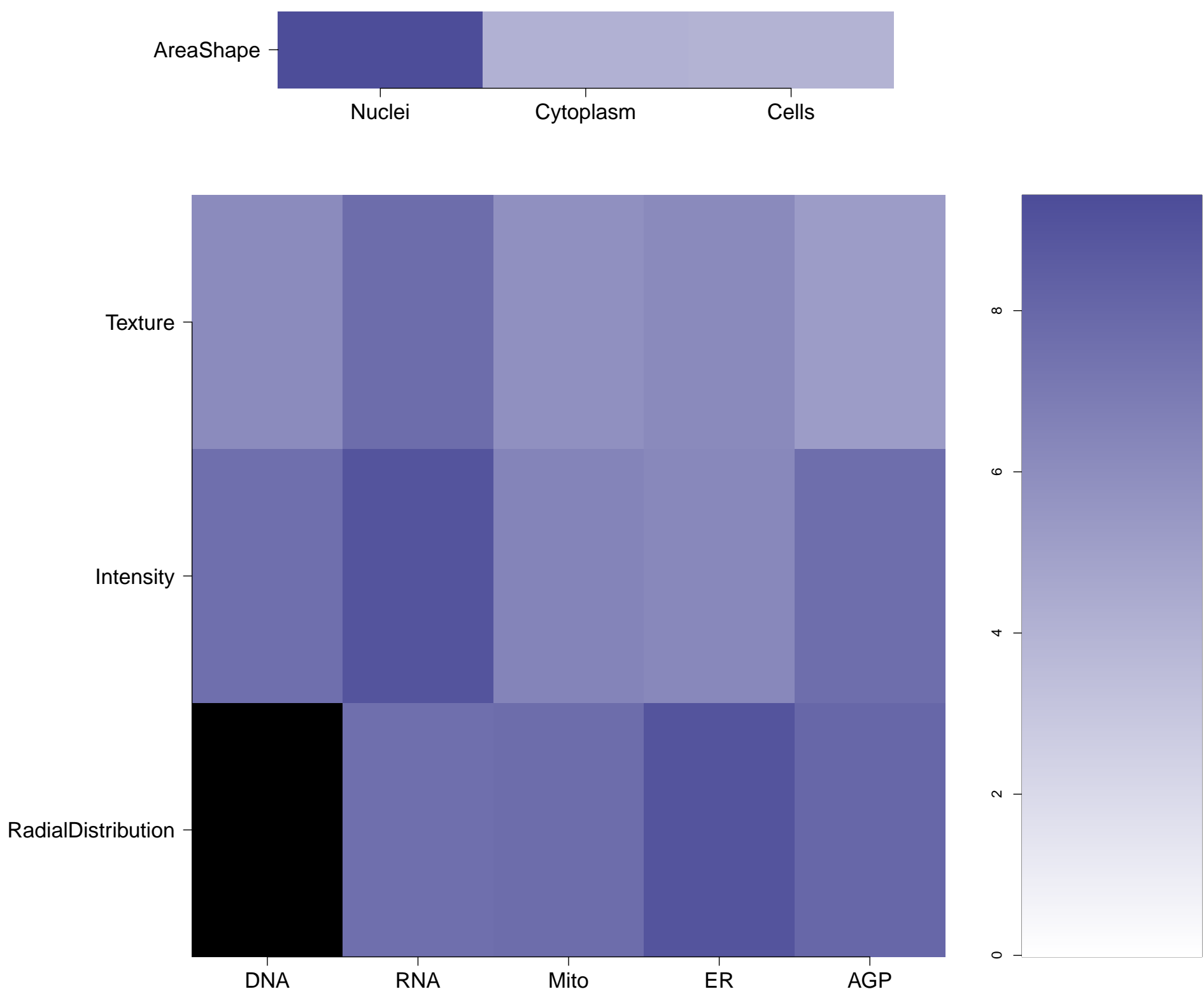
Expert Annotation		
Treatment	Pathway	Regulation Type
CDC42.T17N	Canonical Cytoskeletal Re-org	Inhibitor
AKT1.E17K	Canonical PI3K/AKT	Activator
AKT3.WT.2	Canonical PI3K/AKT	Activator
AKT3.E17K	Canonical PI3K/AKT	Activator



Top 5 genes negatively correlated to the cluster

Expert Annotation			Mean Correlation	Standard Deviation
Treatment	Pathway	Regulation Type		
PIK3R1.WT.1	Canonical PI3K/AKT	Activator	-0.48	0.14
AKT1S1.WT.2	TOR	Inhibitor	-0.47	0.04
AKT1S1.WT.1	TOR	Inhibitor	-0.43	0.05
PRKACG.WT.3	PKA	Activator	-0.42	0.09
ATF4.WT.2	Canonical ER Stress/UPR	Activator	-0.40	0.06

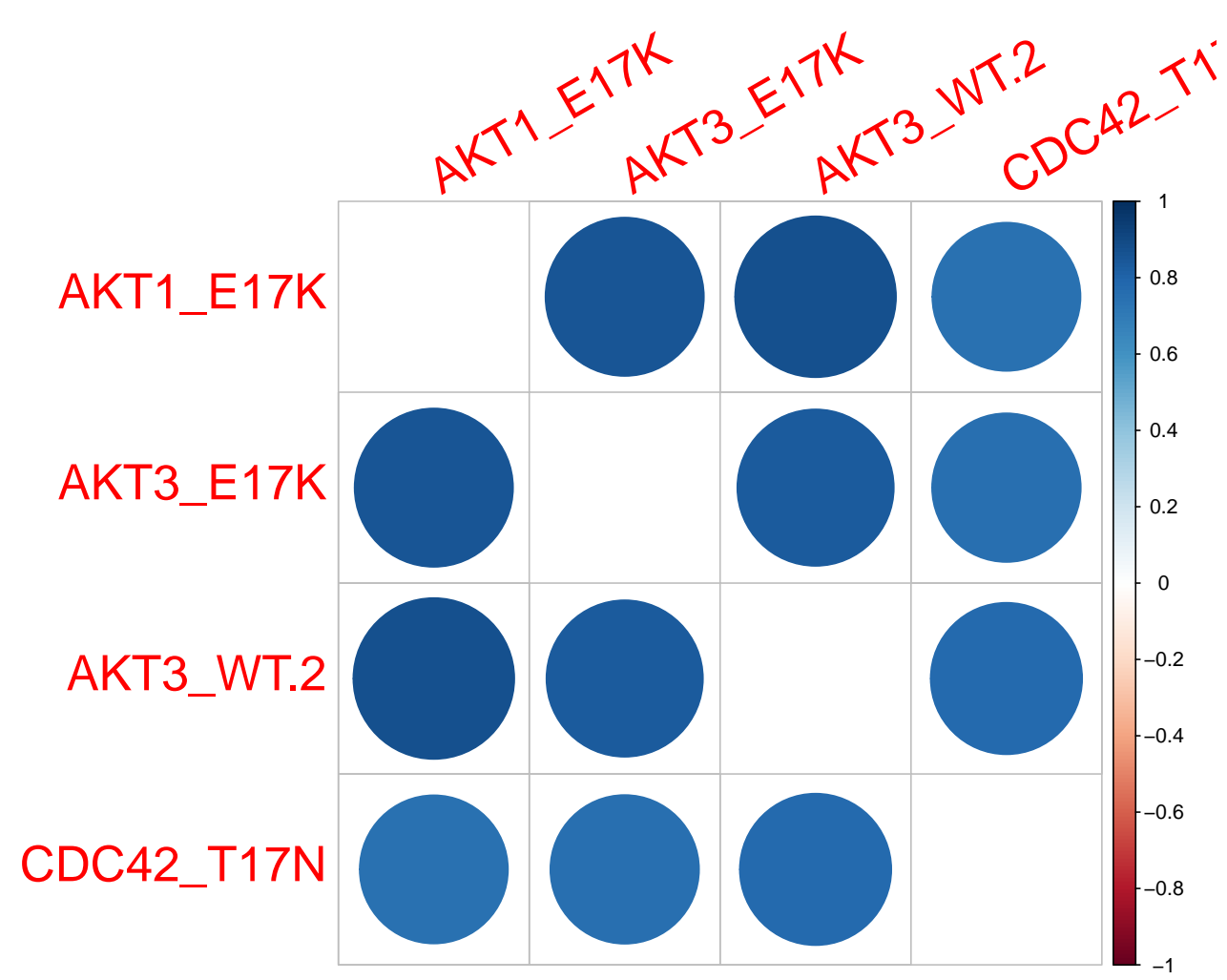
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the 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?



Empty

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

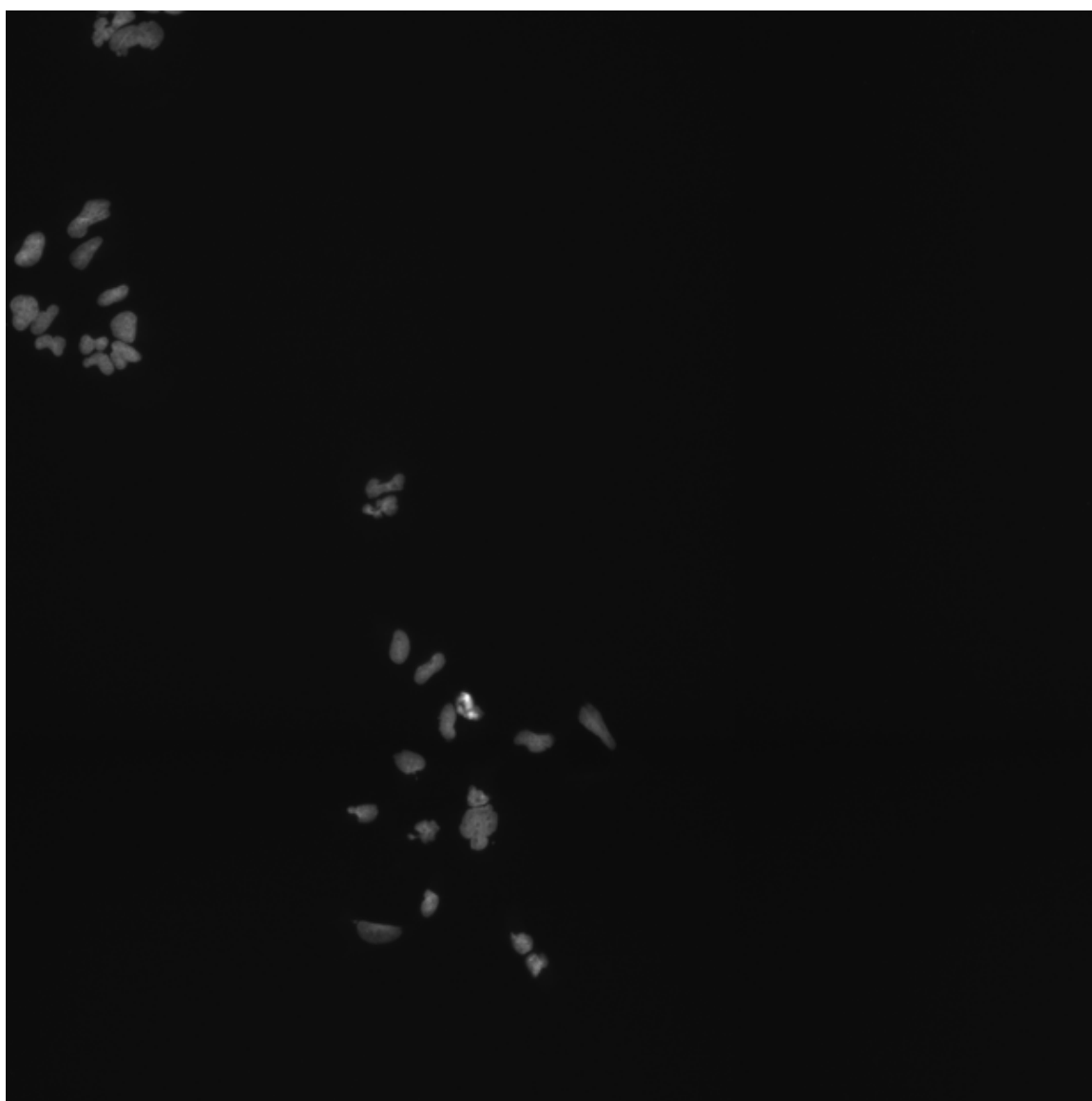
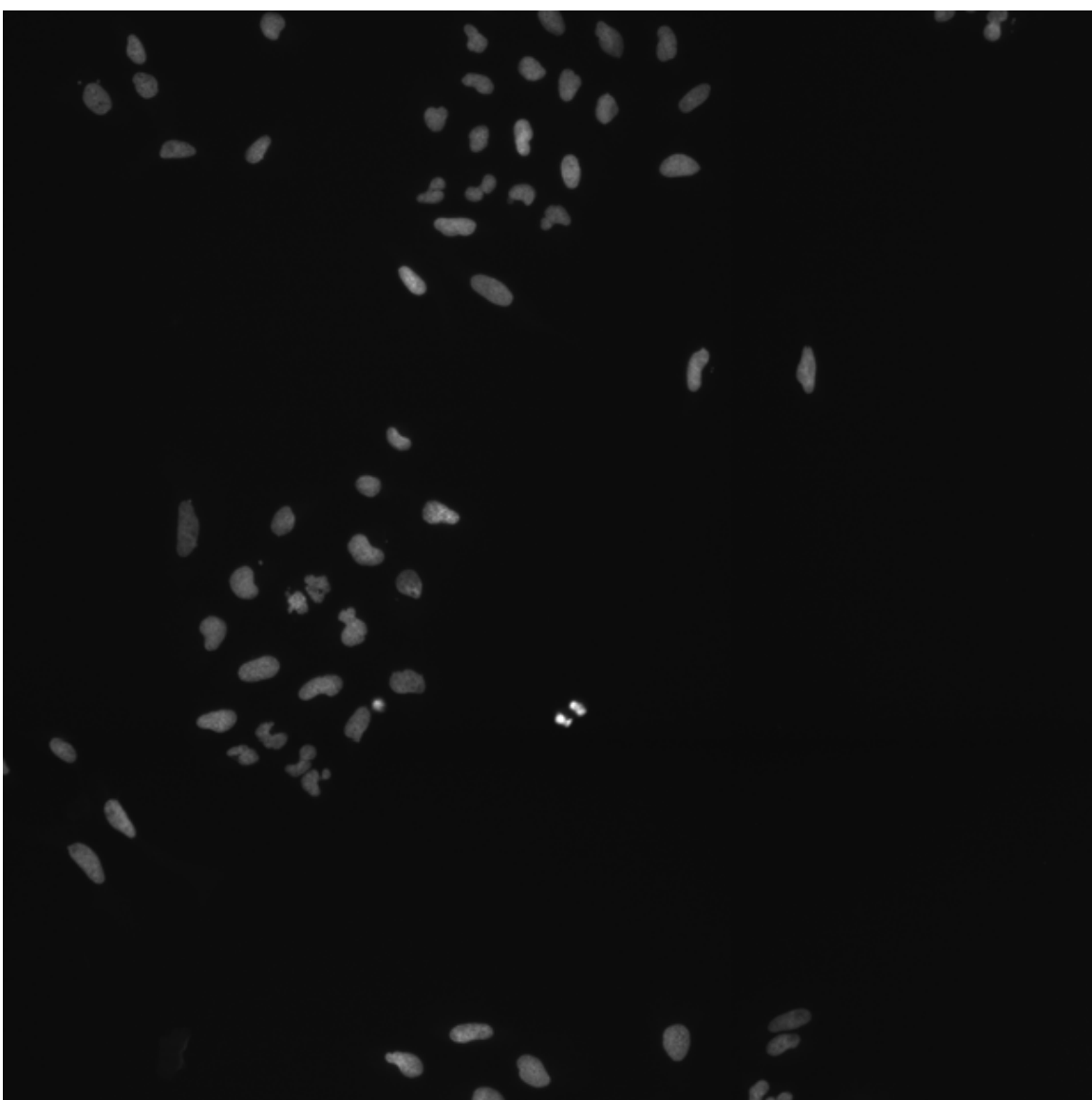
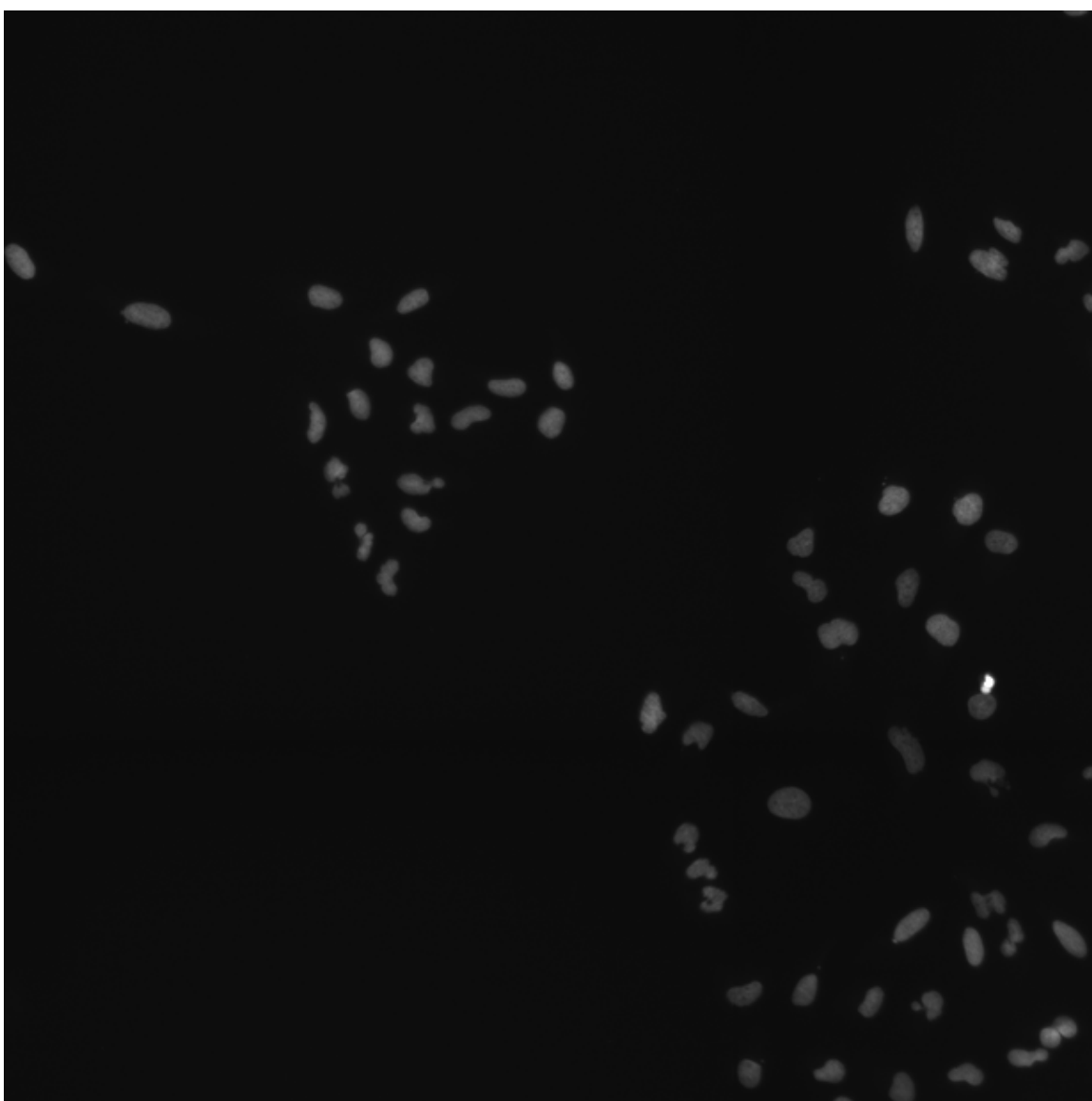
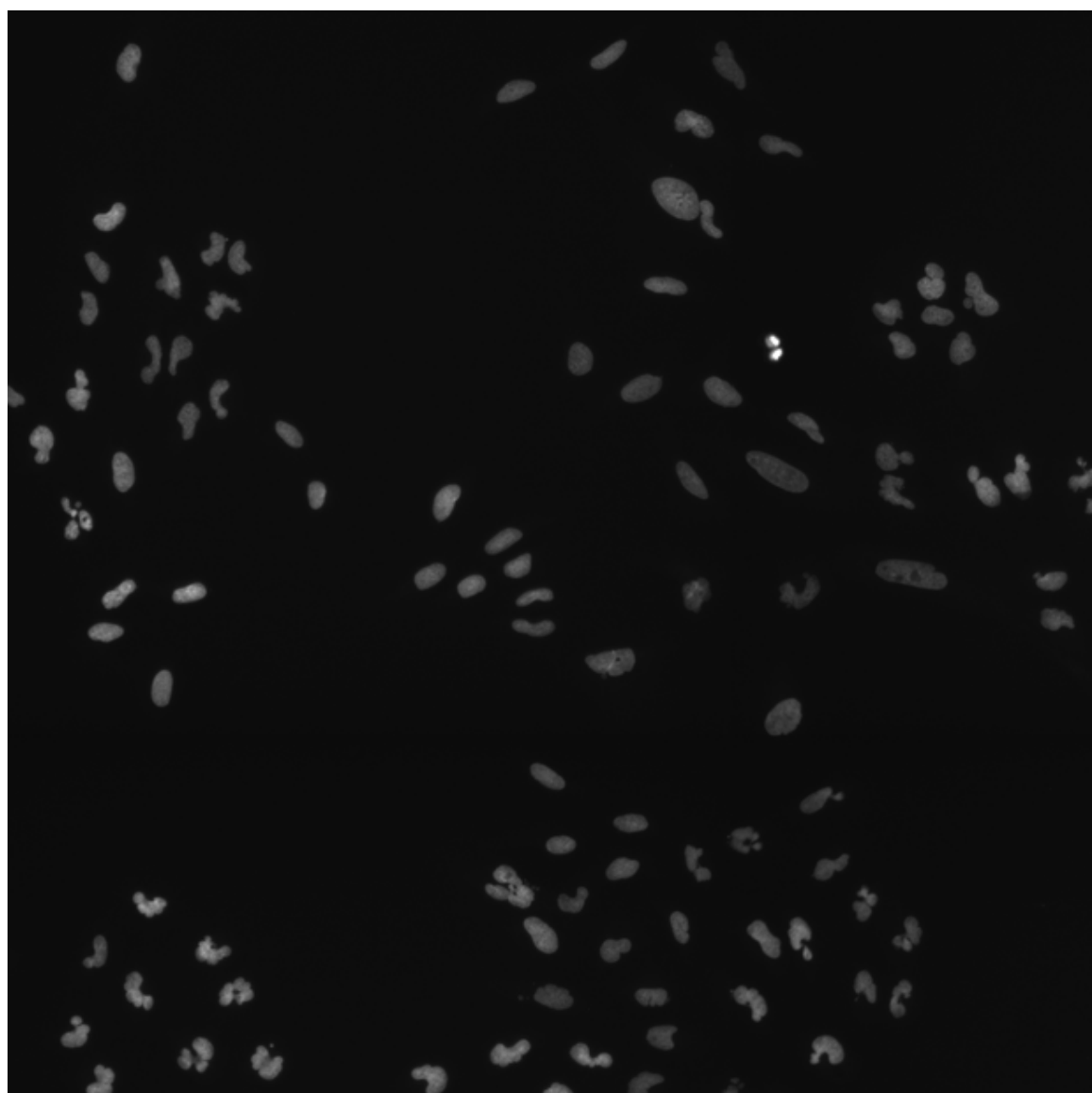
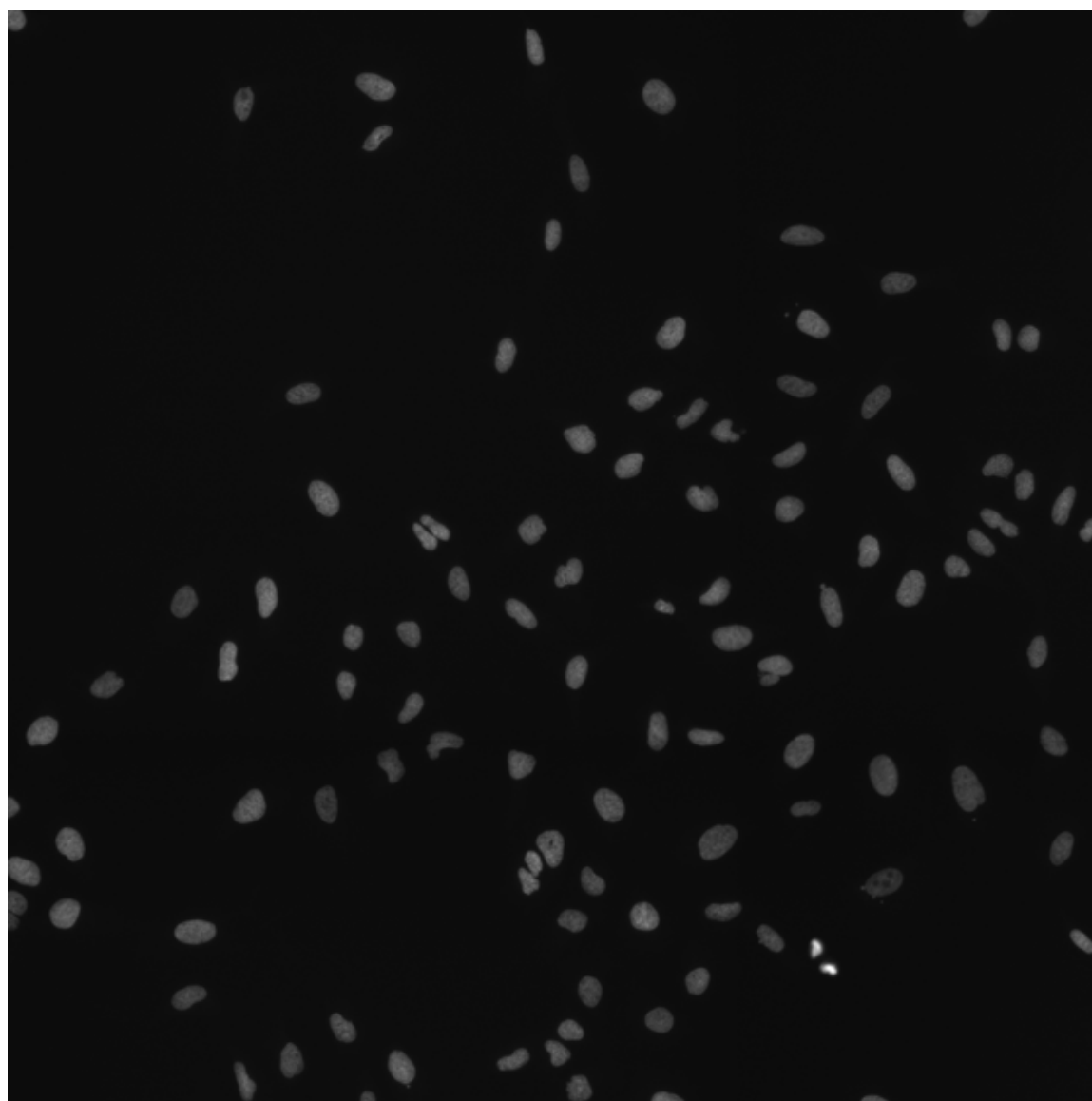
AKT1.E17K

AKT3.E17K

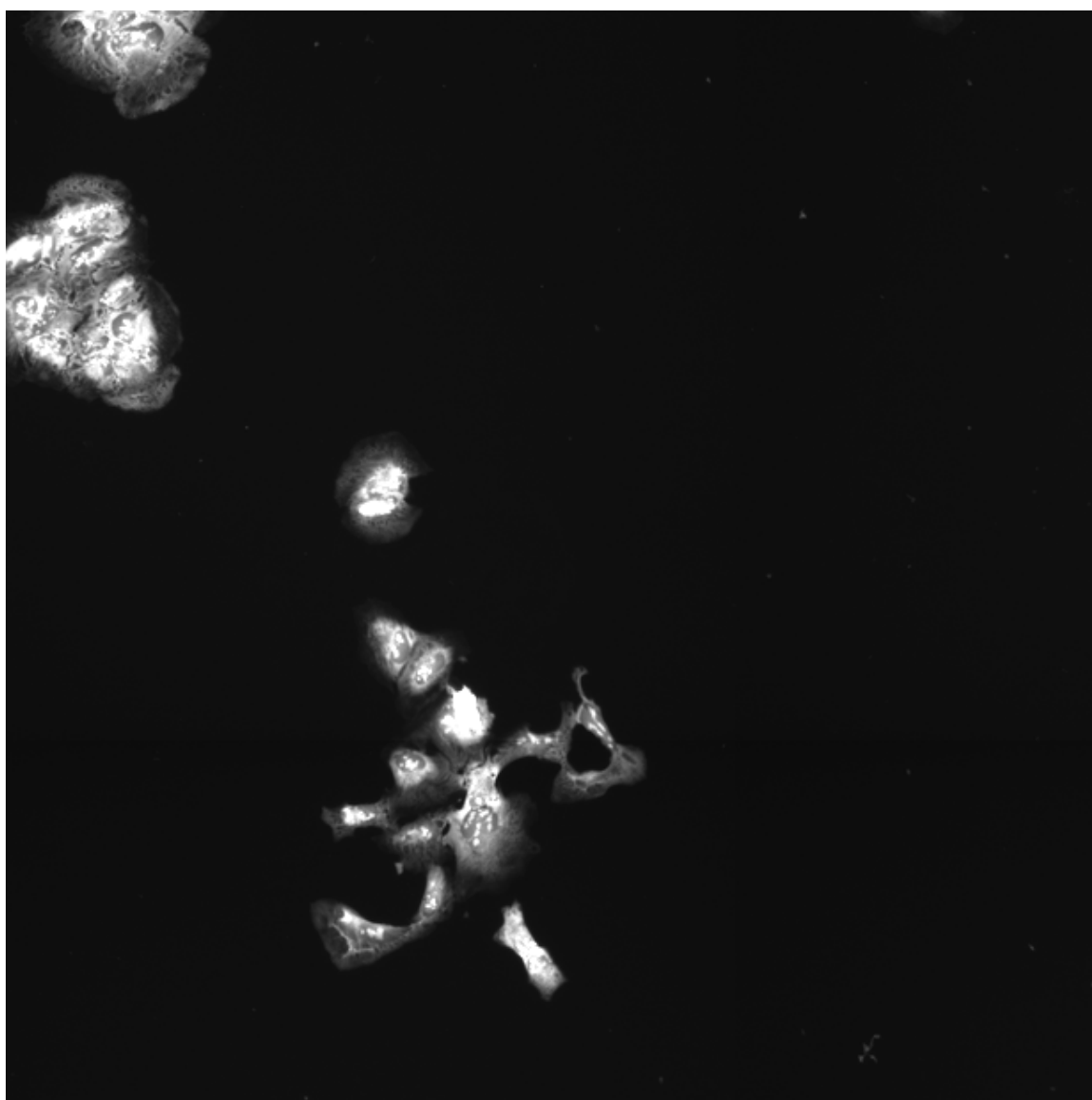
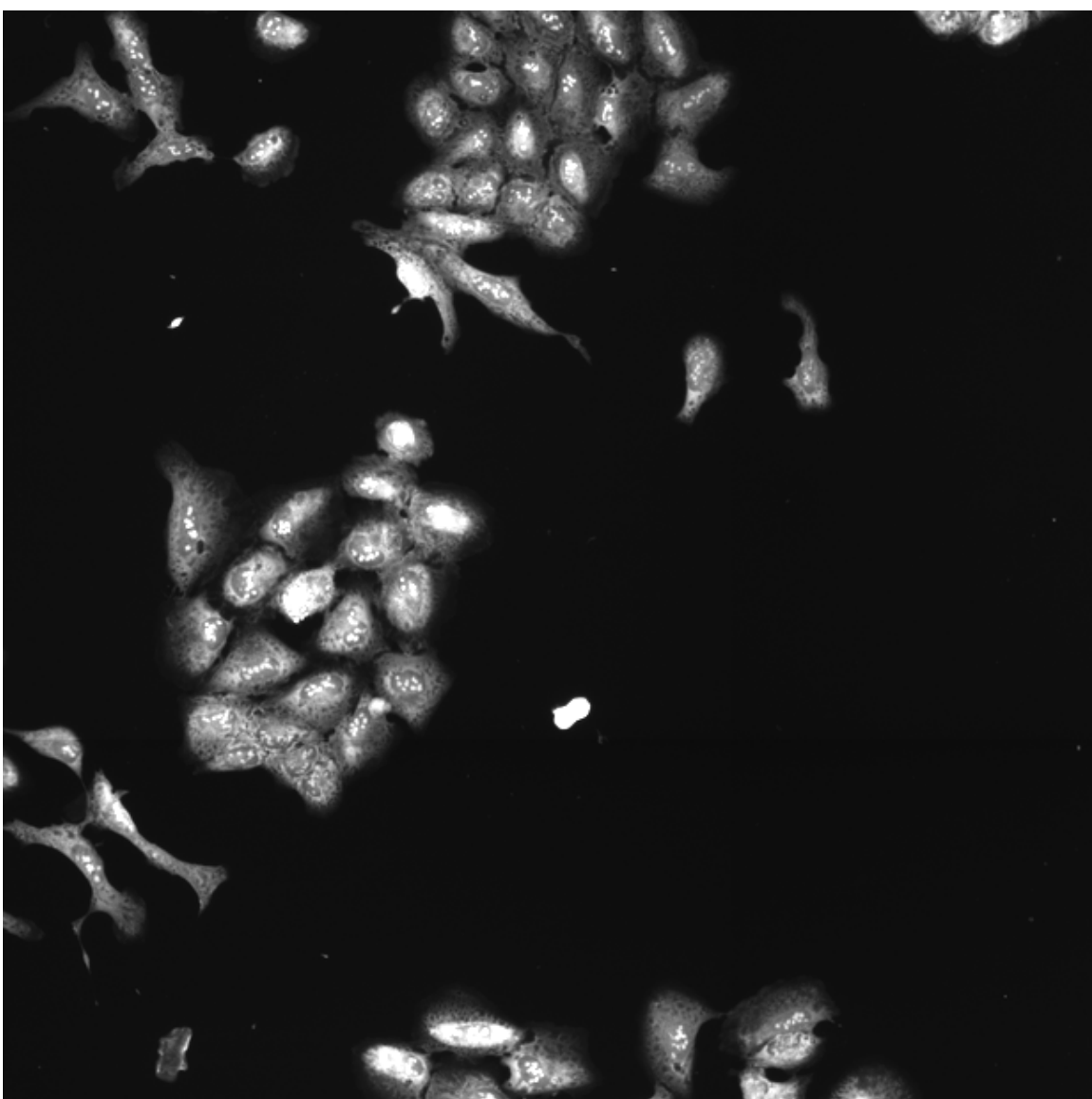
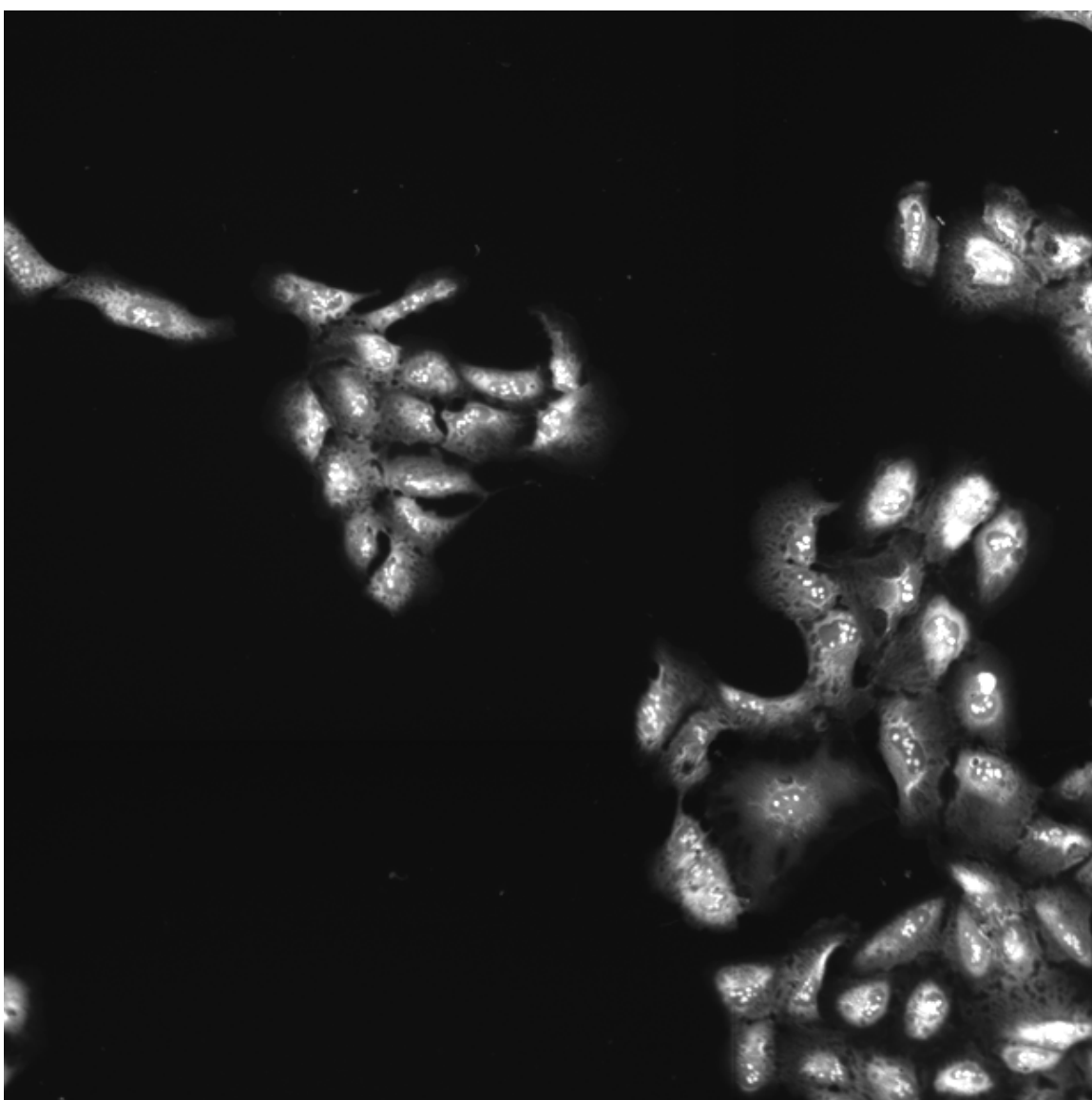
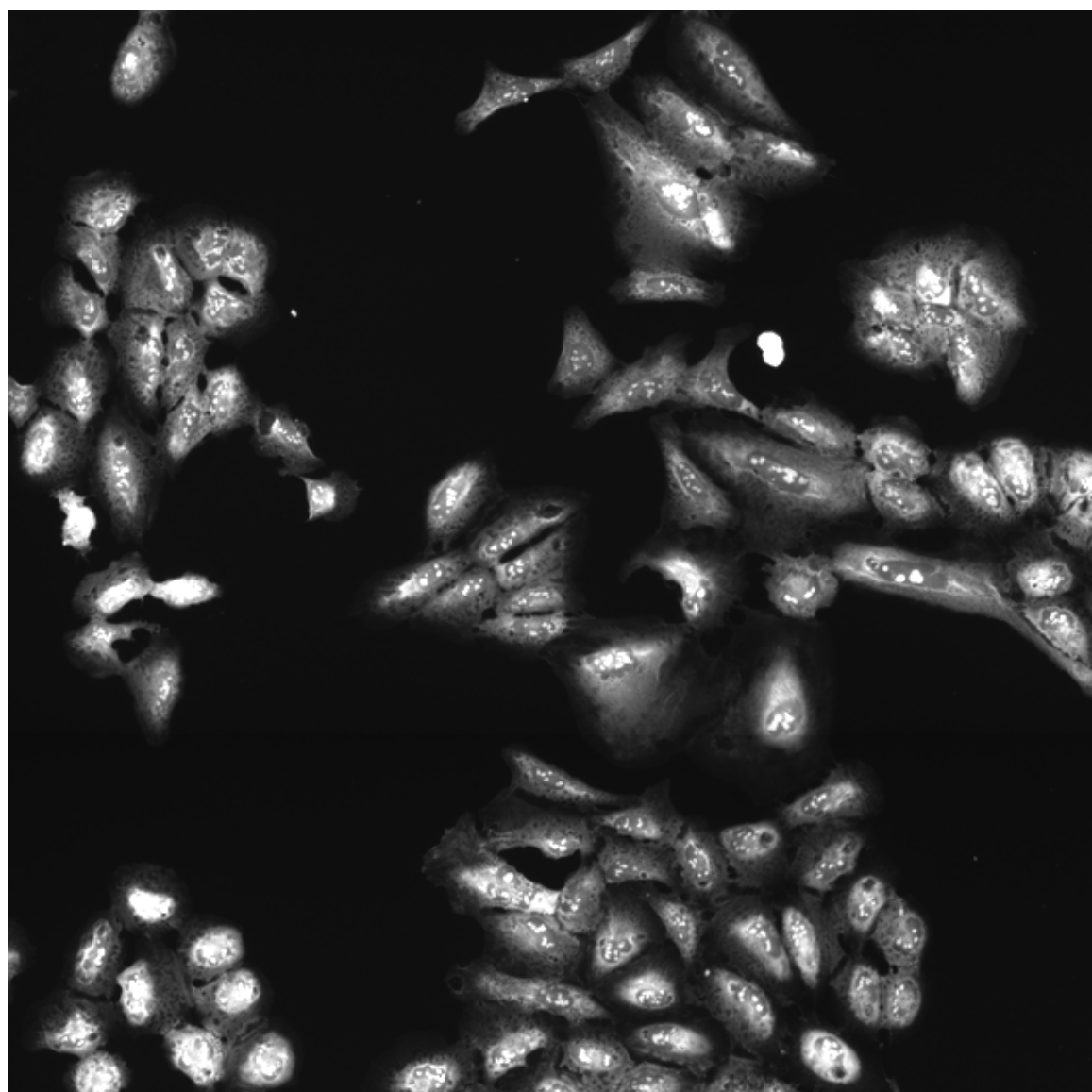
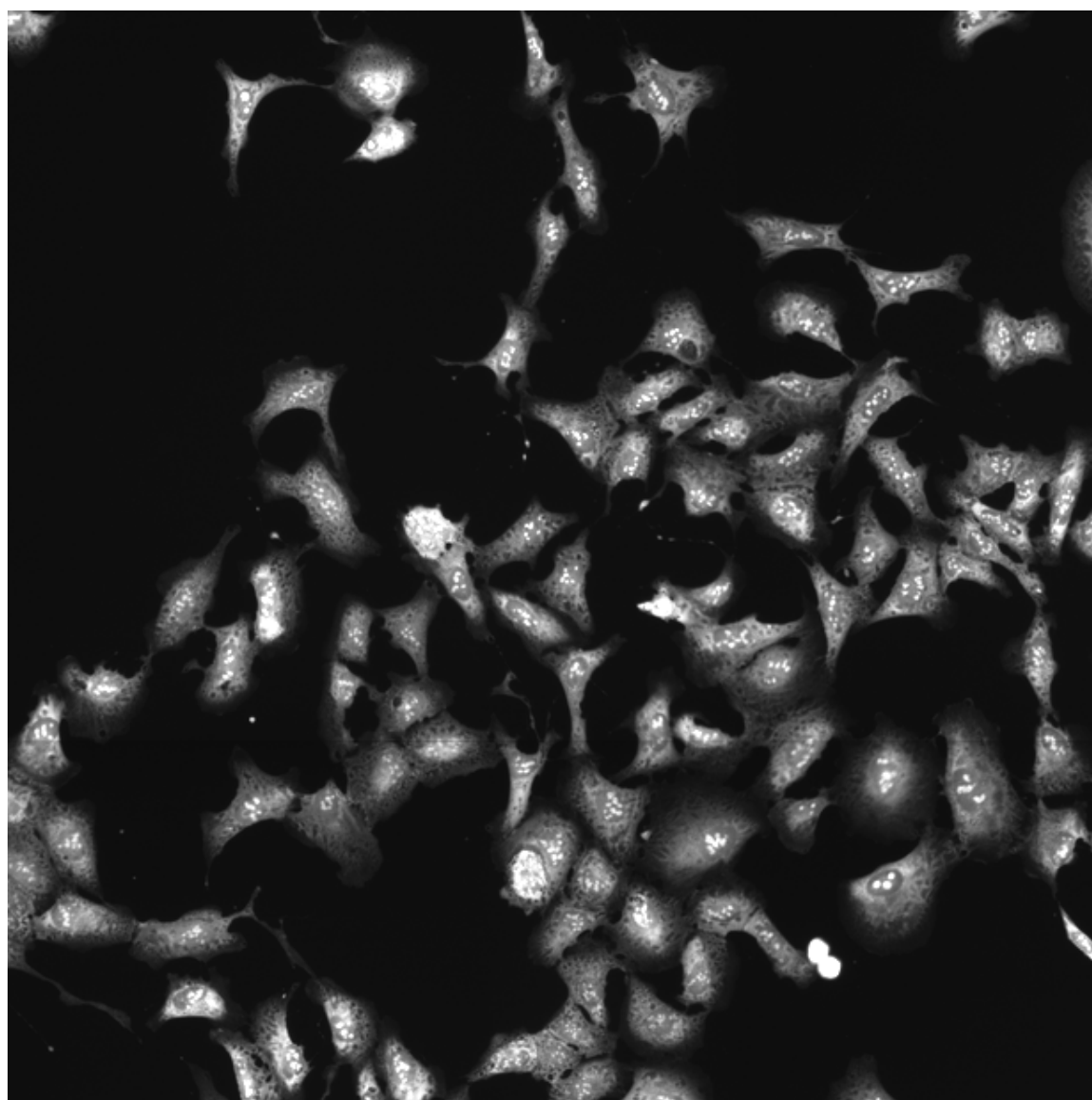
AKT3.WT.2

CDC42.T17N

DNA

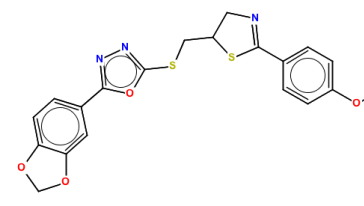


RNA



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-K03796490-001-05-1 T0509-9695 MLS001003678 HMS1763D10 ZINC6374094 SMR000347571 PubChem CID : 9622493		NA (in 1 replicates)	0.54 \pm 0.07 Treatment Score AKT1.E17K 0.48 AKT3.WT.2 0.39 CDC42.T17N 0.04	NA				Total number of assays tested in: 638. Active in the following assays: <ul style="list-style-type: none">Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Primary Screen (AID 1456)Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Secondary Assay 3 with KC22 cells (AID 1714)Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Counter-screen with HEK cells (AID 1716)Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Counter-screen 2 with HEK cells (AID 1718)VP16 counter-screen qHTS for inhibitors of ROR gamma transcriptional activity (AID 2546)qHTS for inhibitors of ROR gamma transcriptional activity (AID 2551)

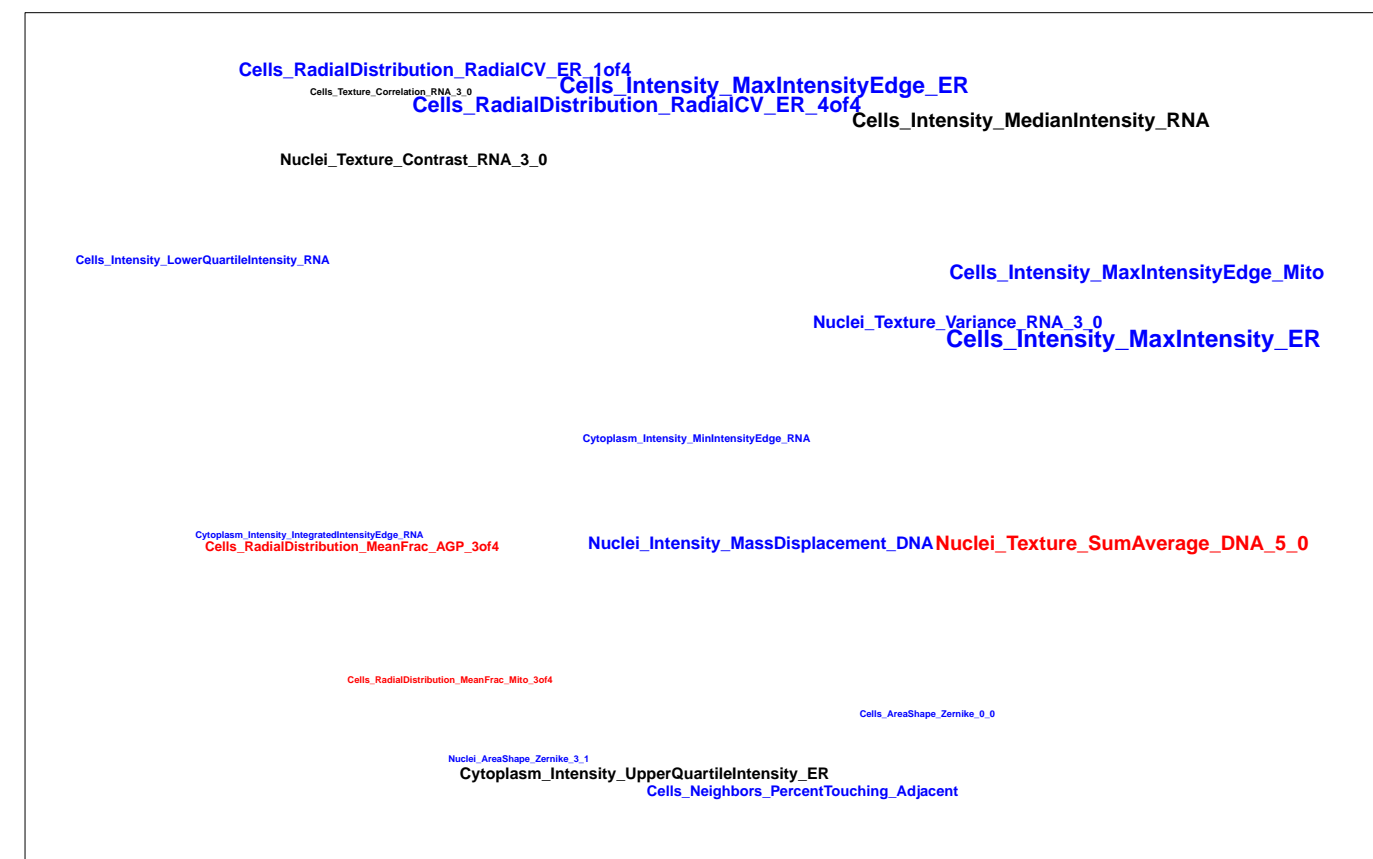
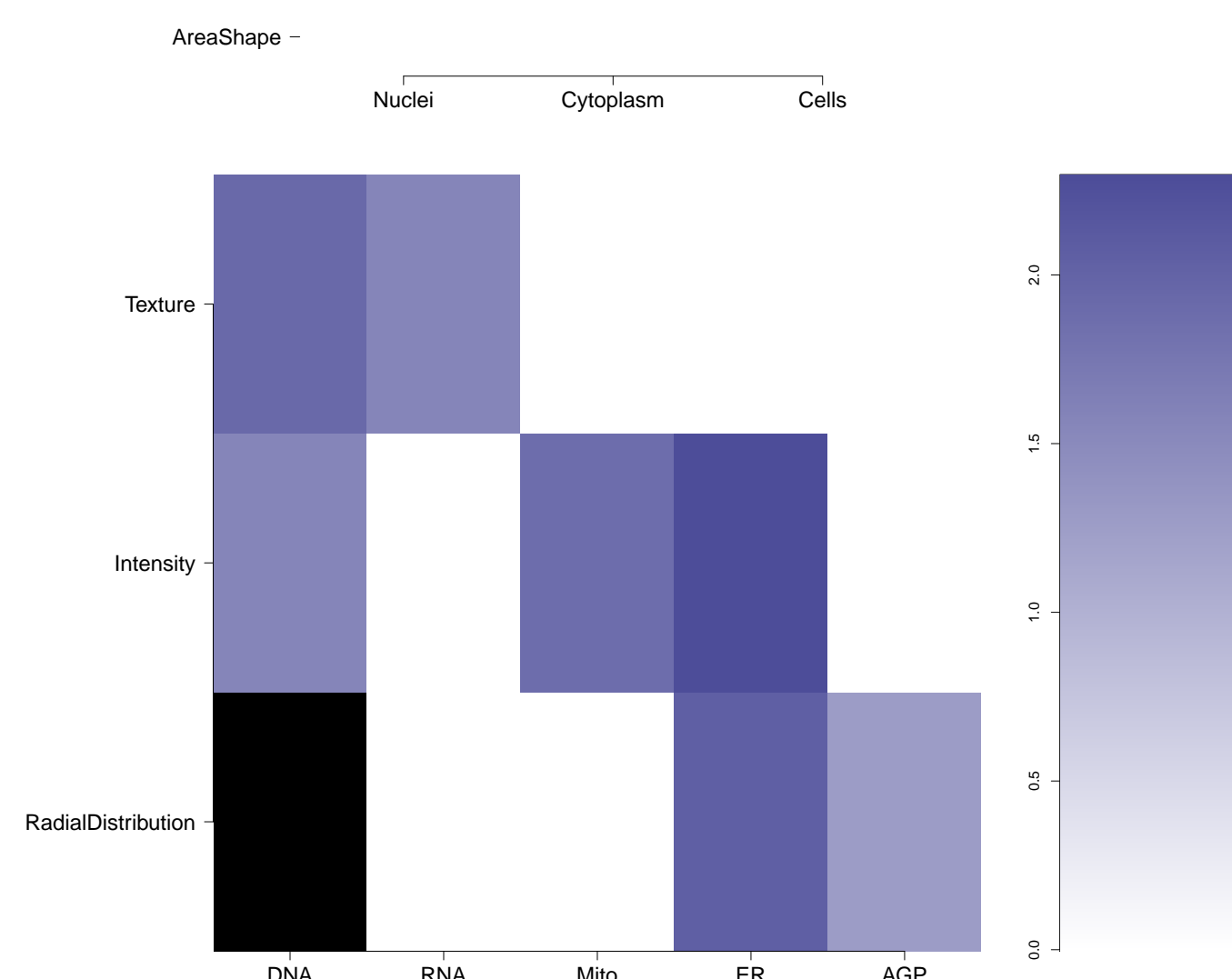
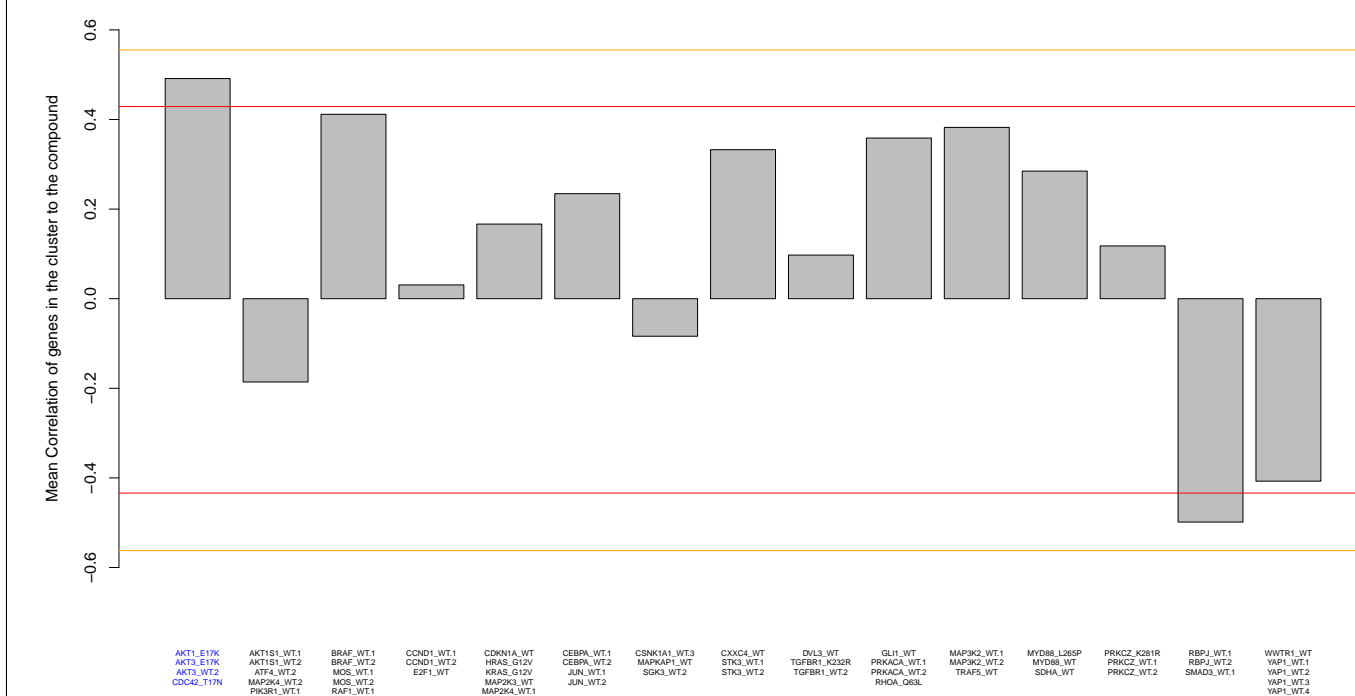
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0.66 (in 2 replicates)

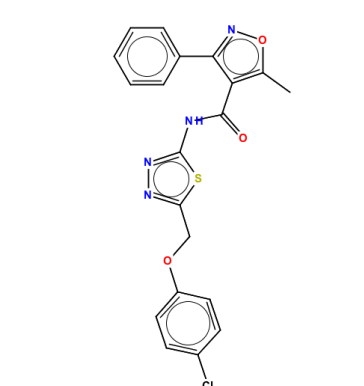
0.49 ± 0.06	
Treatment	Score
AKT1.E17K	0.54
AKT3.E17K	0.51
AKT3.WT.2	0.41
CDC42.T17N	0.50

NA



- Screening for Modulators of Post-Golgi Transport, Control Strain (AID 738)
- qHTS Assay for Inhibitors of HPGD (15-Hydroxyprostaglandin Dehydrogenase) (AID 894)
- Leishmania major promastigote HTS (AID 1063)
- Leishmania major promastigote HTS - Primary screen report 1 uM (AID 1258)
- CounterScreen for inhibitors of Janus kinase 2 mutant JAK2V617F: Cell-based high throughput assay to identify inhibitors of parental BA/P3 cell viability. (AID 1486)
- Luminescence Cell-Based/Microorganism Primary HTS to Identify Inhibitors of T.Cruzi Replication (AID 1885)
- Leishmania major promastigote EC50 determinations (AID 2008)
- Luminescence Cell-Based/Microorganism Dose Confirmation HTS to Identify Inhibitors of T.Cruzi Replication. (AID 2044)
- Fluorescence-based cell-based primary high throughput screening assay to identify antagonists of the orexin 1 receptor (OX1R; HCRTR1) (AID 435989)
- qHTS profiling assay for firefly luciferase inhibitor activator using purified enzyme and Km concentrations of substrates (counterScreen for mR-21 project) (AID 588342)
- Primary cell-based high-throughput screening for identification of compounds that inhibit bile calcium-activated chloride channels (TMEM16A) (AID 588511)
- wHTS identification of small molecule inhibitors of the mitochondrial permeability transition pore via an absorbance assay (AID 602449)
- qHTS for Antagonists of gsp, the Ethicodine Mutation Responsible for Pheochromocytoma/MidCox-Albright Syndrome qHTS (AID 624288)
- Fluorescence-based cell-based primary high throughput screening assay to identify antagonists of the human trace amine associated receptor 1 (TAAR1) (AID 642466)
- Single concentration confirmation of wHTS inhibitor hits of the mitochondrial permeability transition pore via a fluorescent based assay (AID 642504)
- Trypanosoma brucei, Primary growth inhibition assay (AID 1159557)
- TcTPY51 enzymatic inhibition (AID 1159558)
- Trypanosoma cruzi, Primary growth inhibition assay (AID 1159559)
- Leishmania donovani, Primary growth inhibition assay (AID 1159560)
- Intra-macrophage L. donovani assay (AID 1159564)
- Trypanosoma cruzi intracellular imaging assay (AID 1159565)

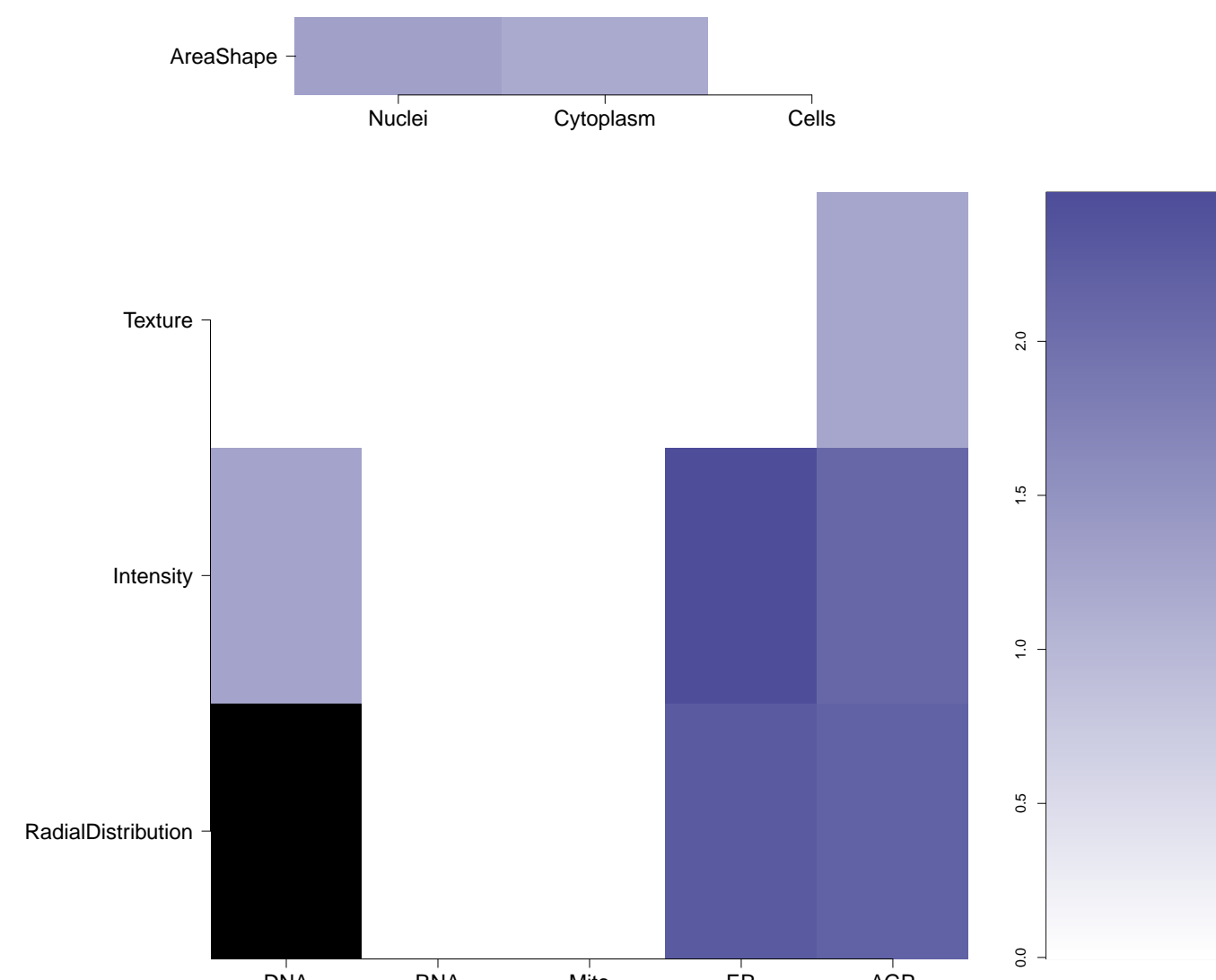
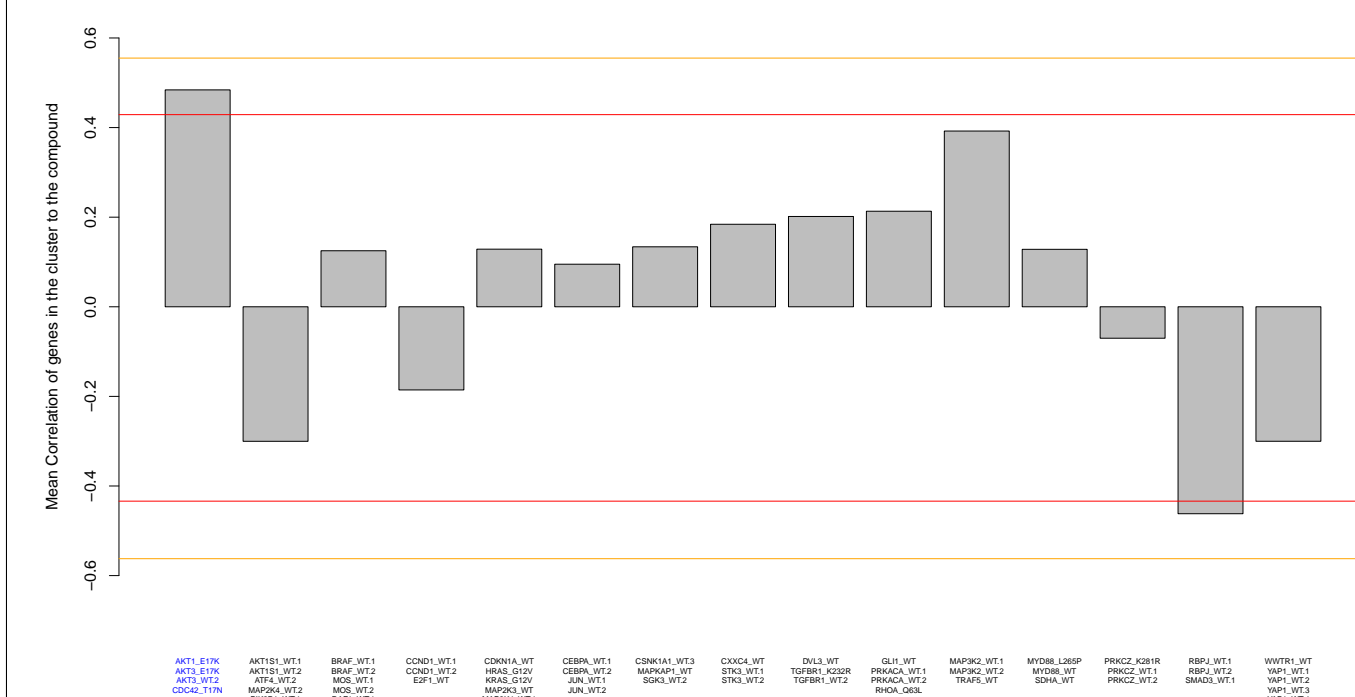
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0.57 (in 2 replicates)

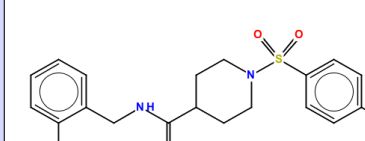
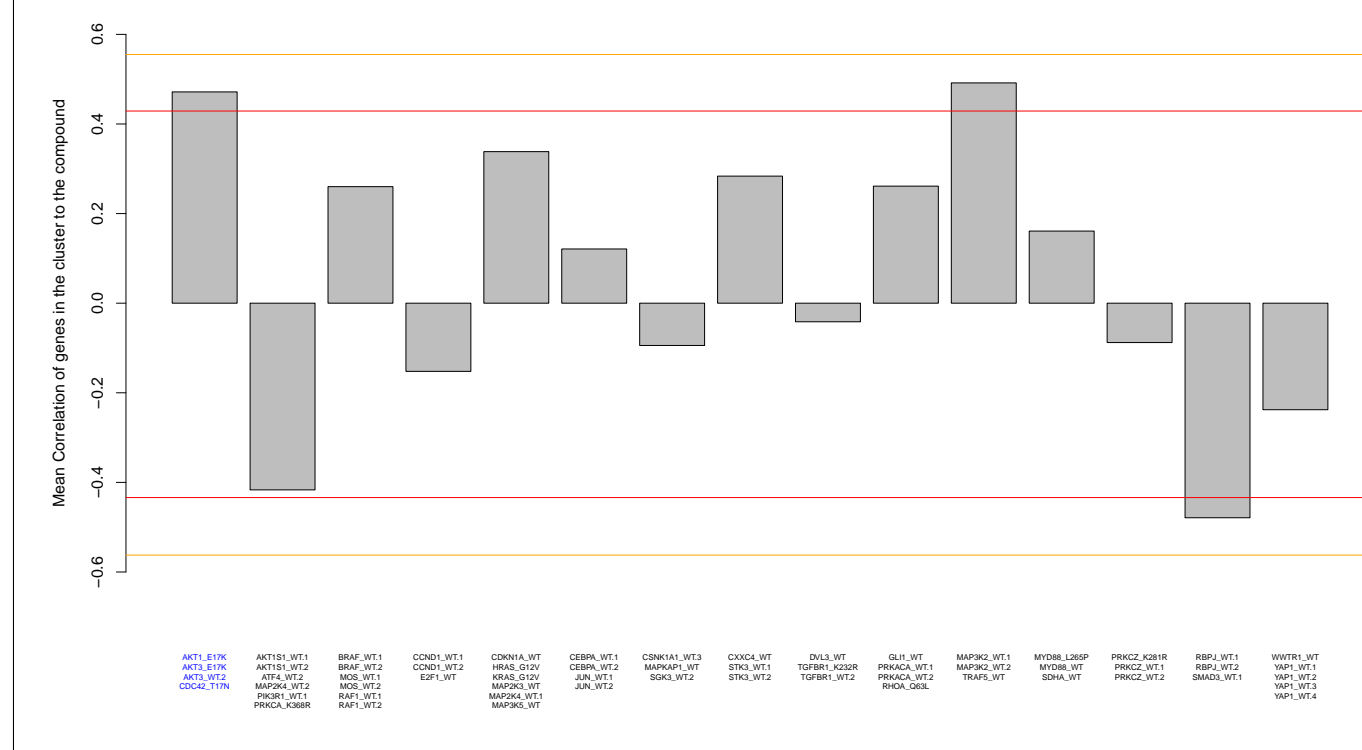
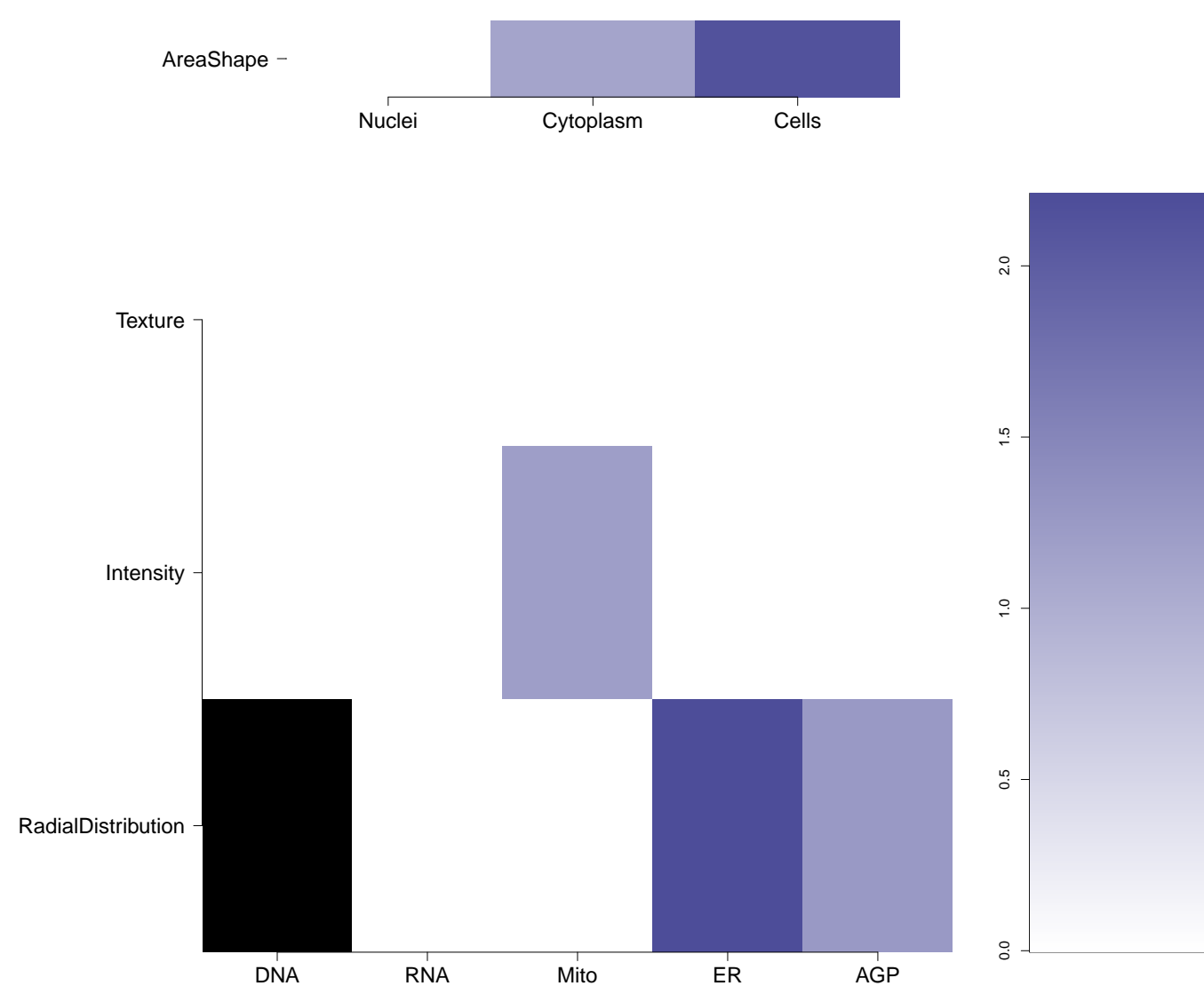
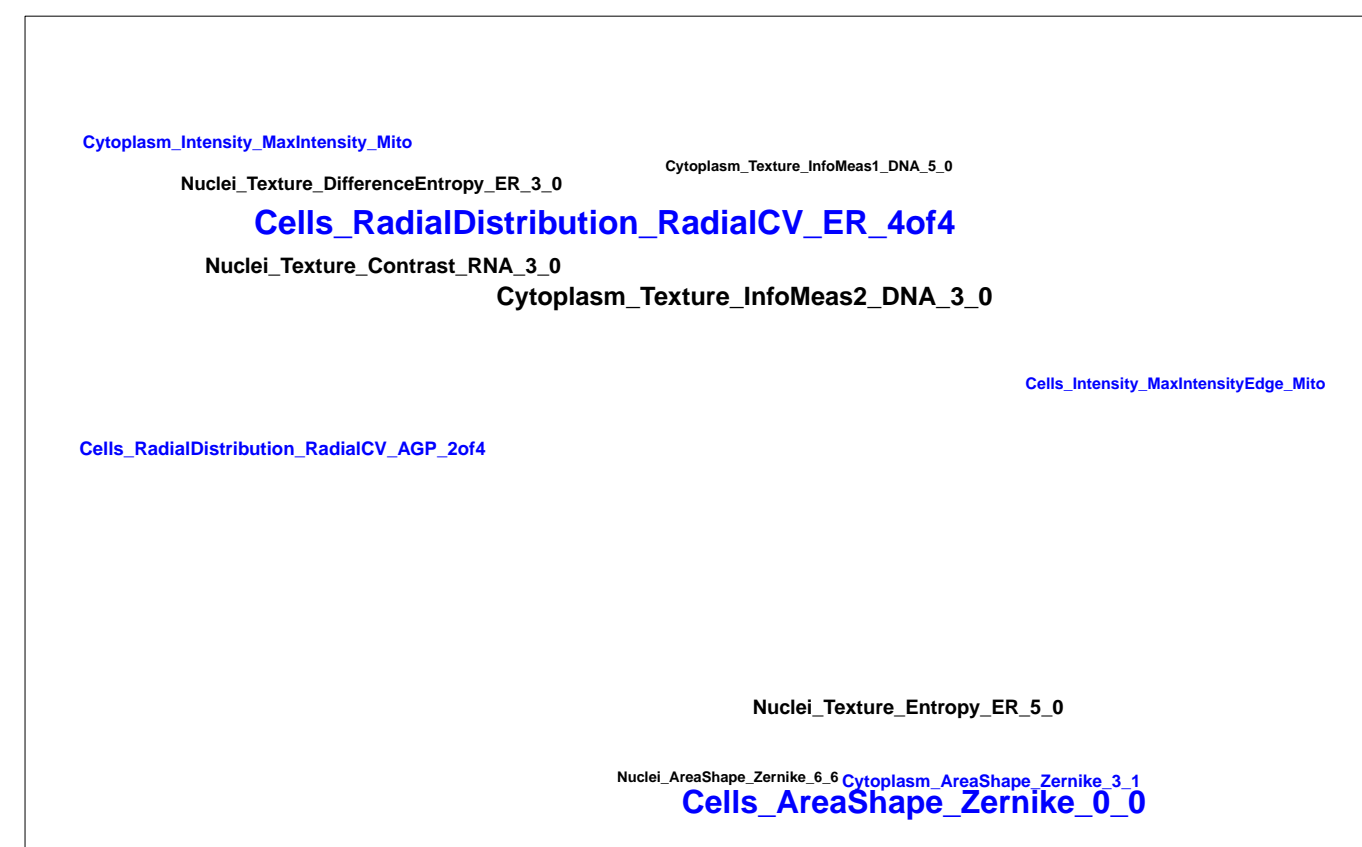
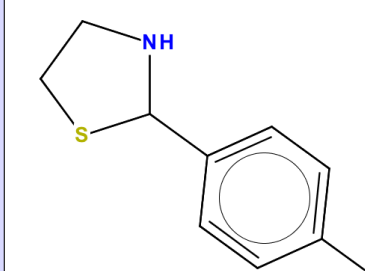
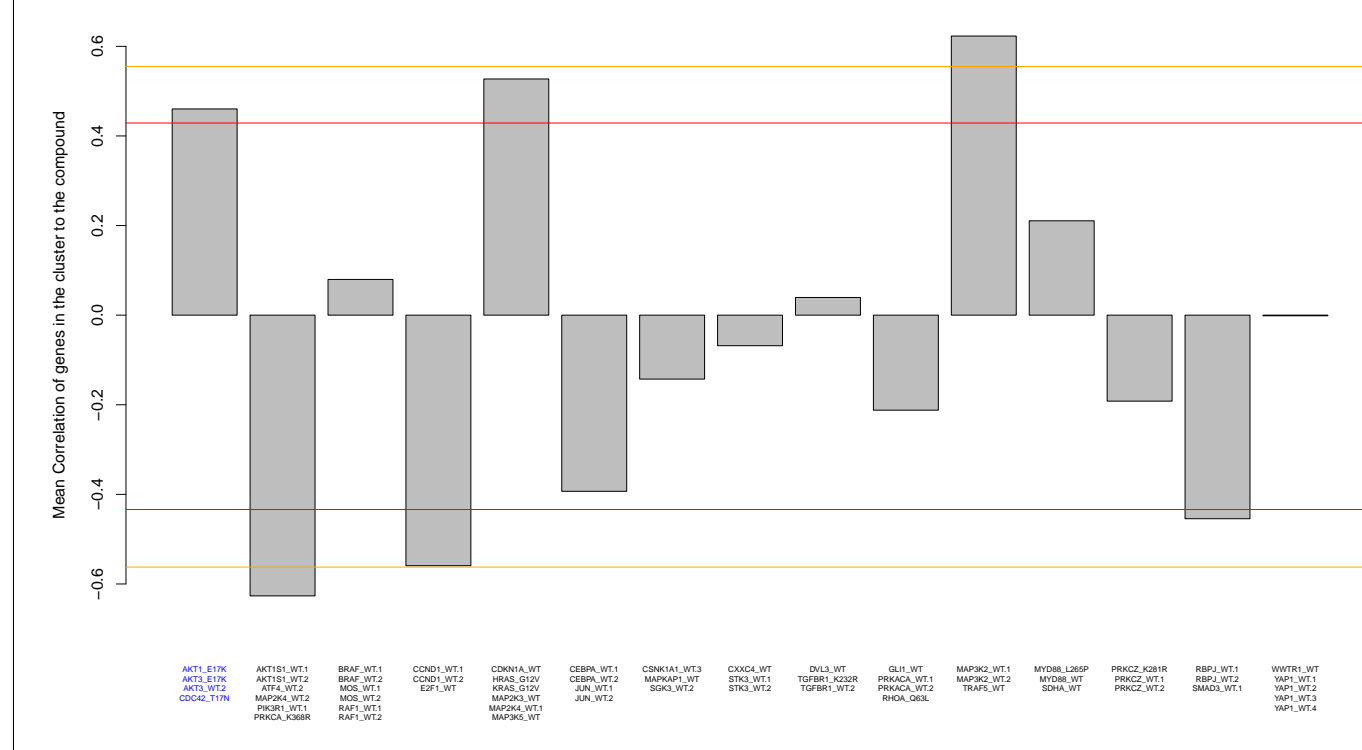
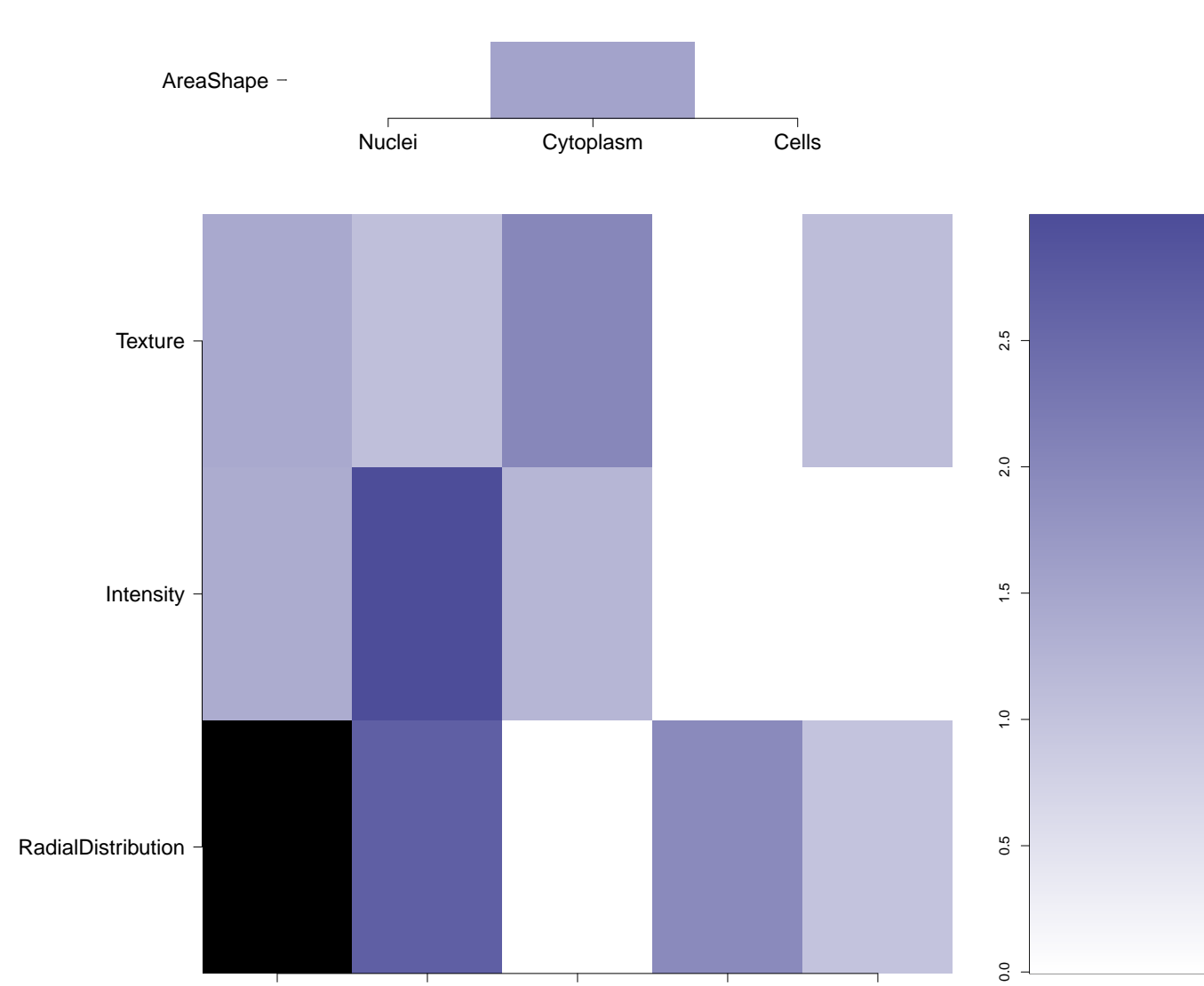
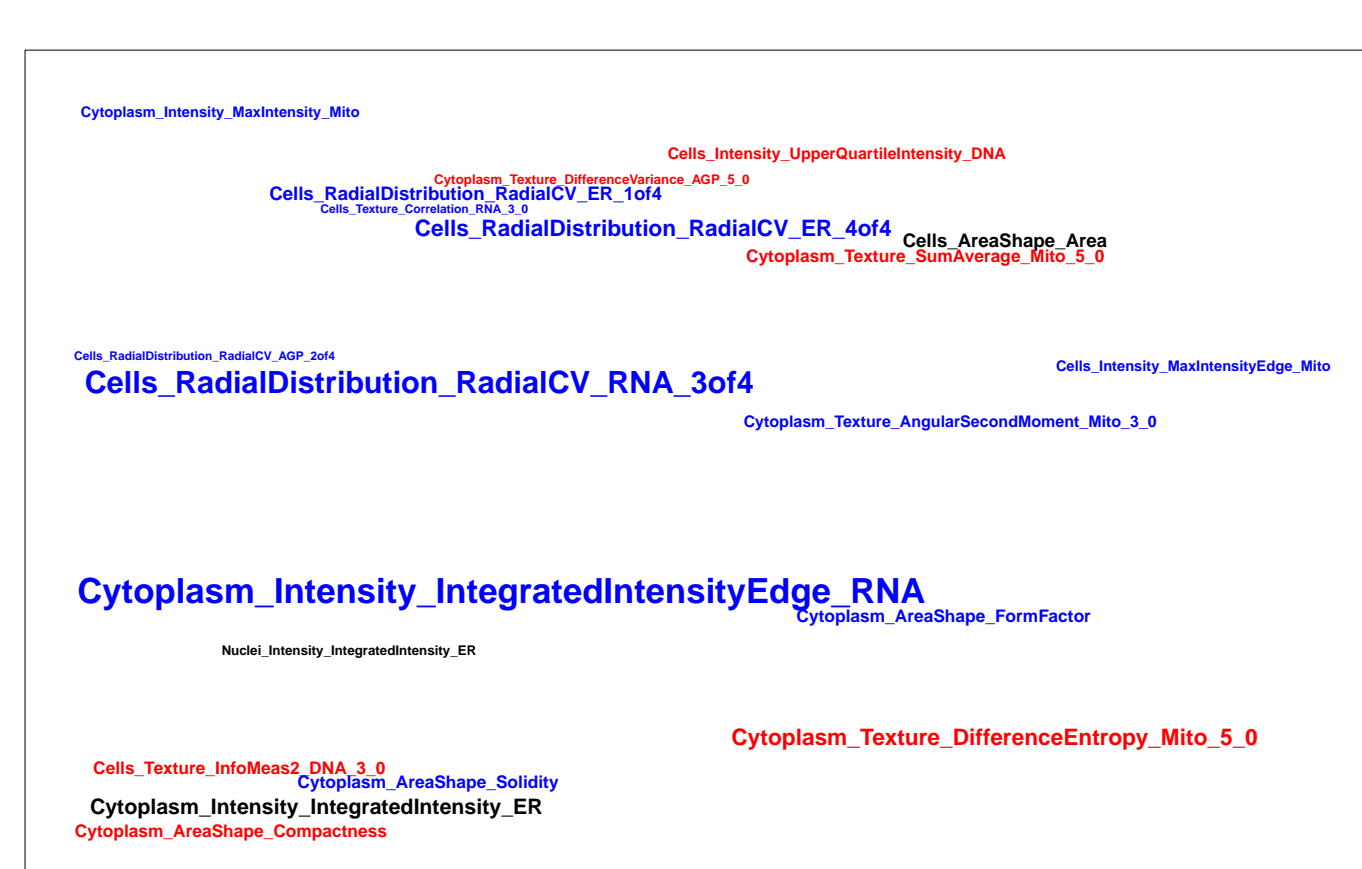
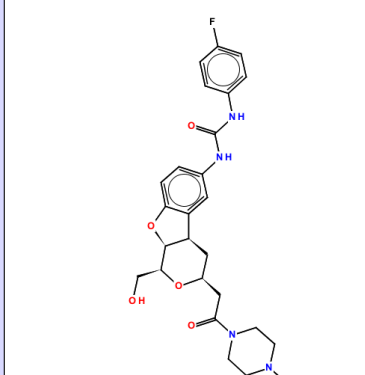
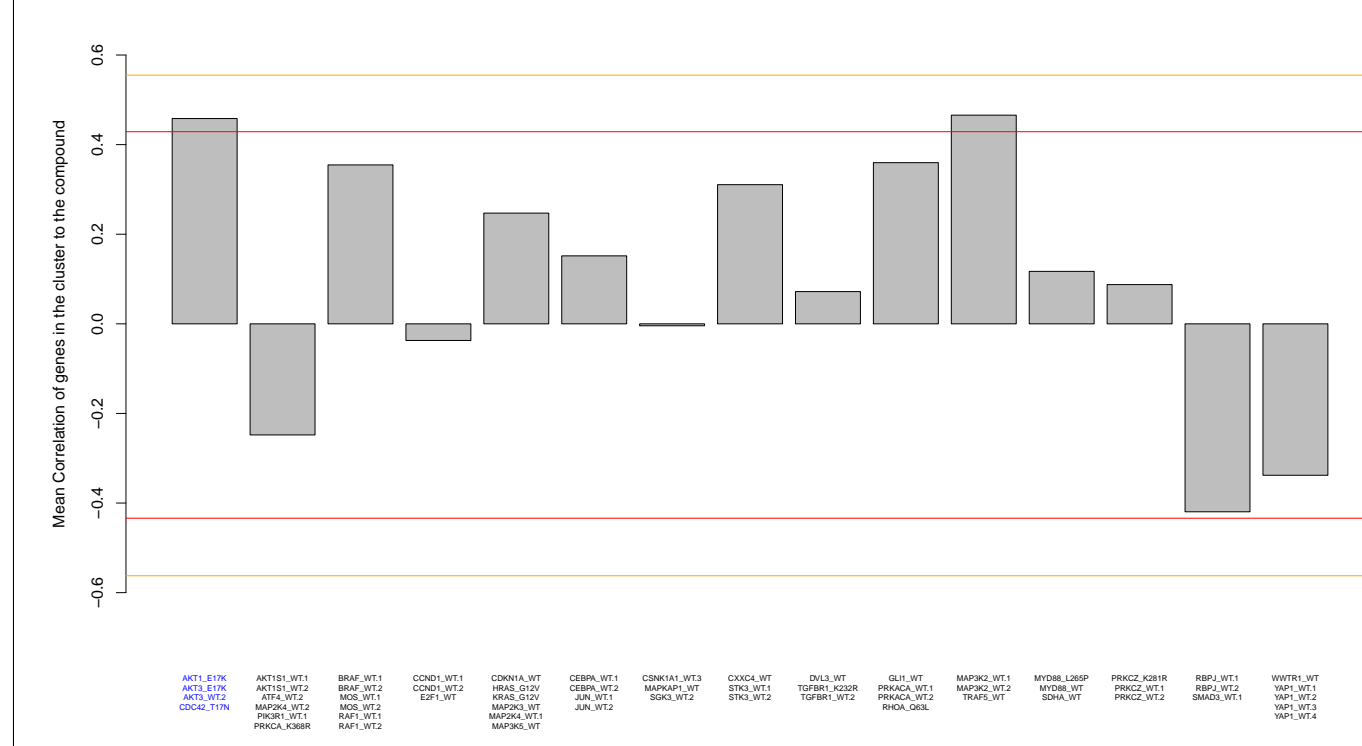
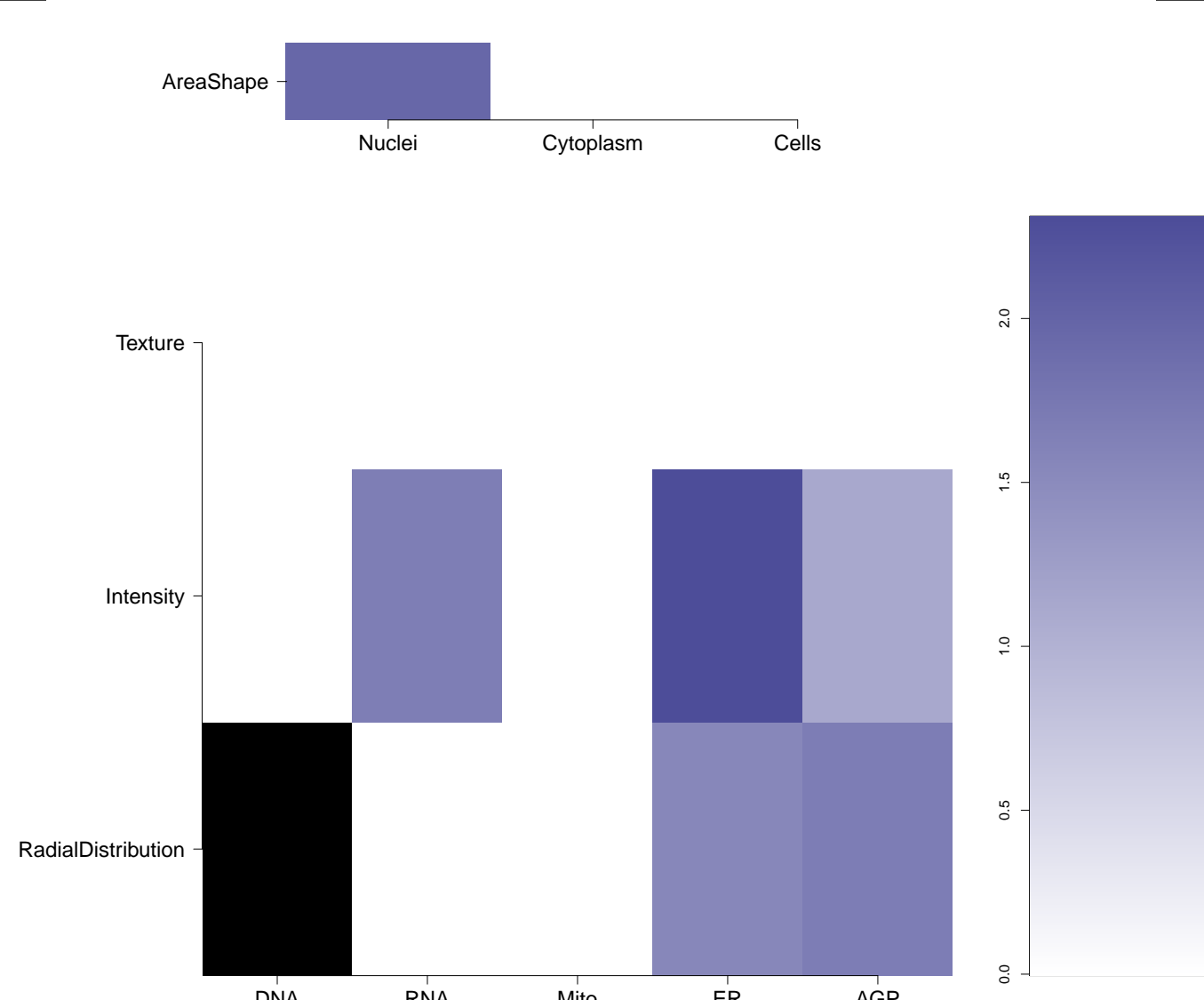
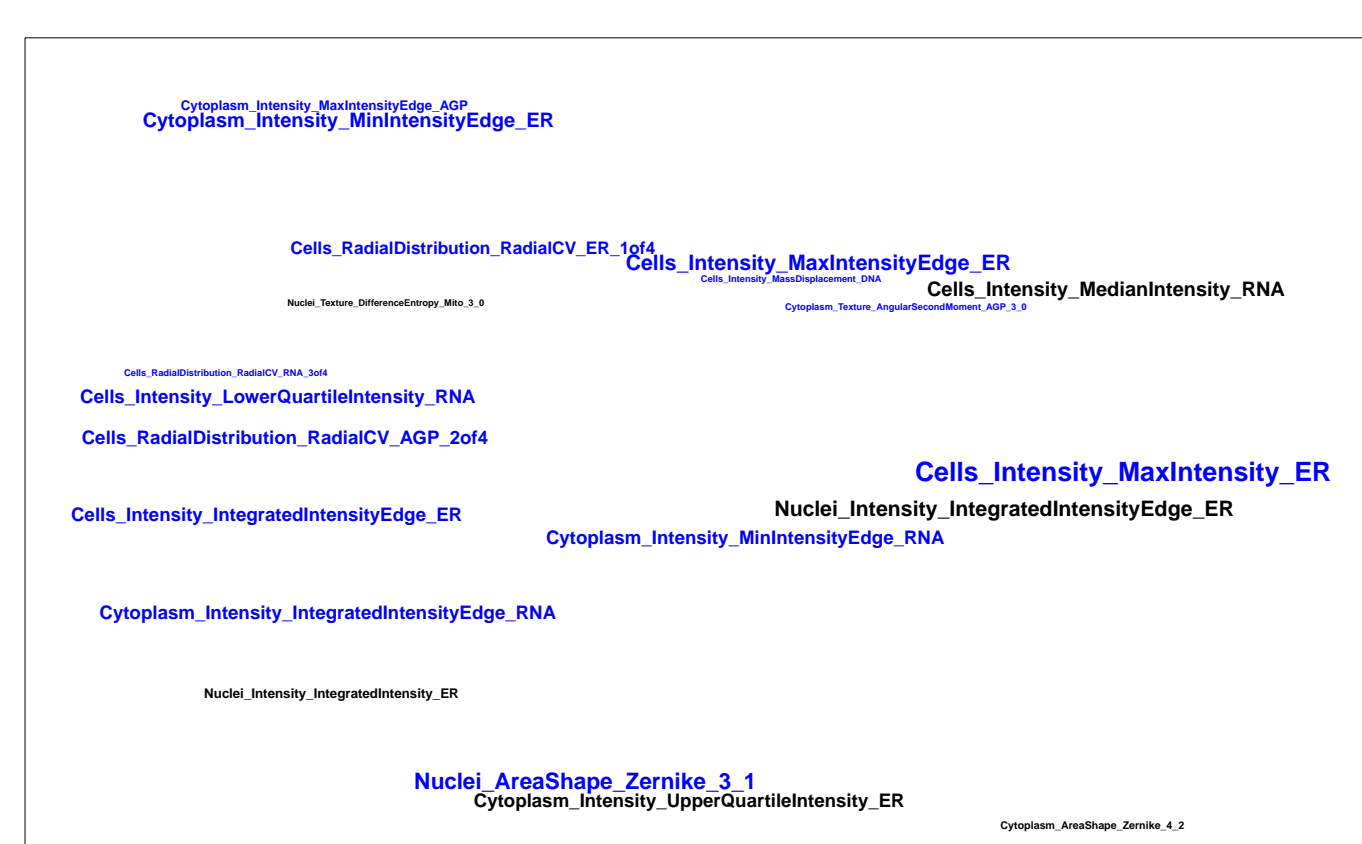
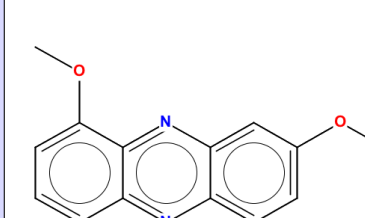
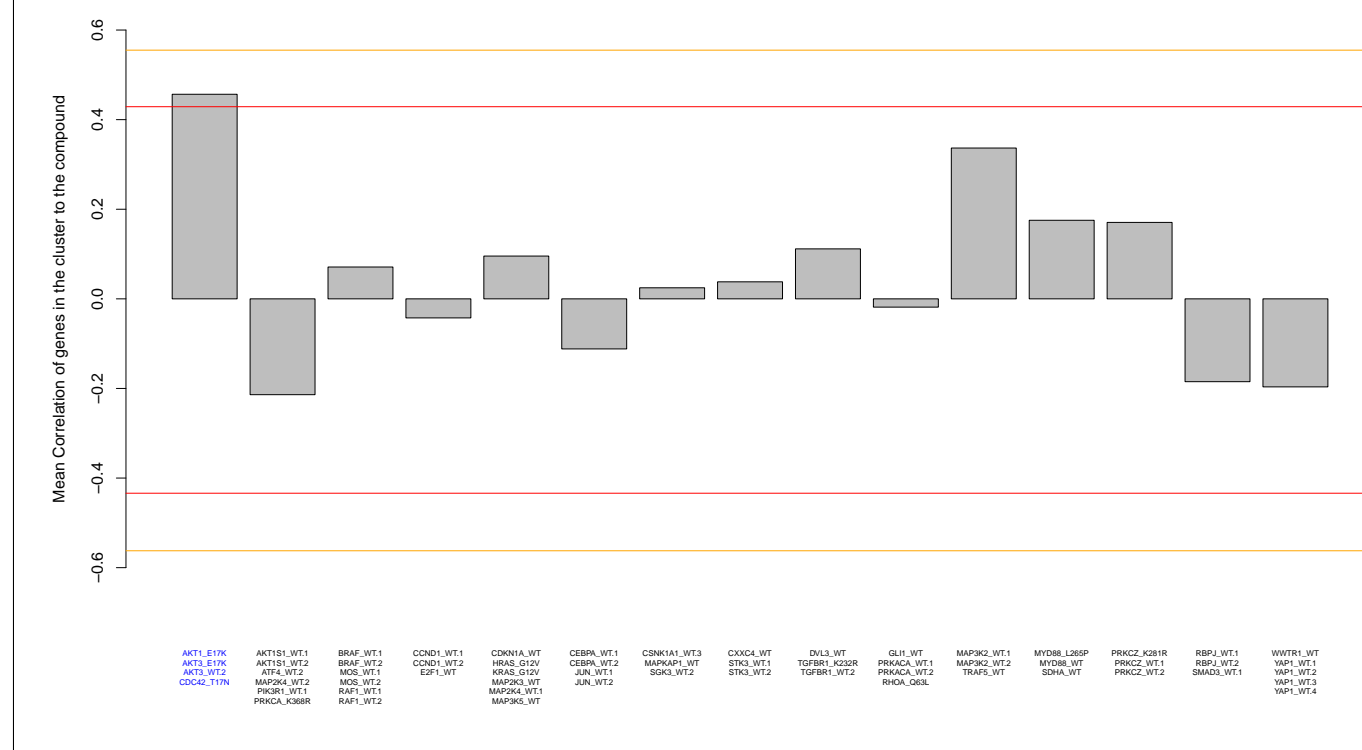
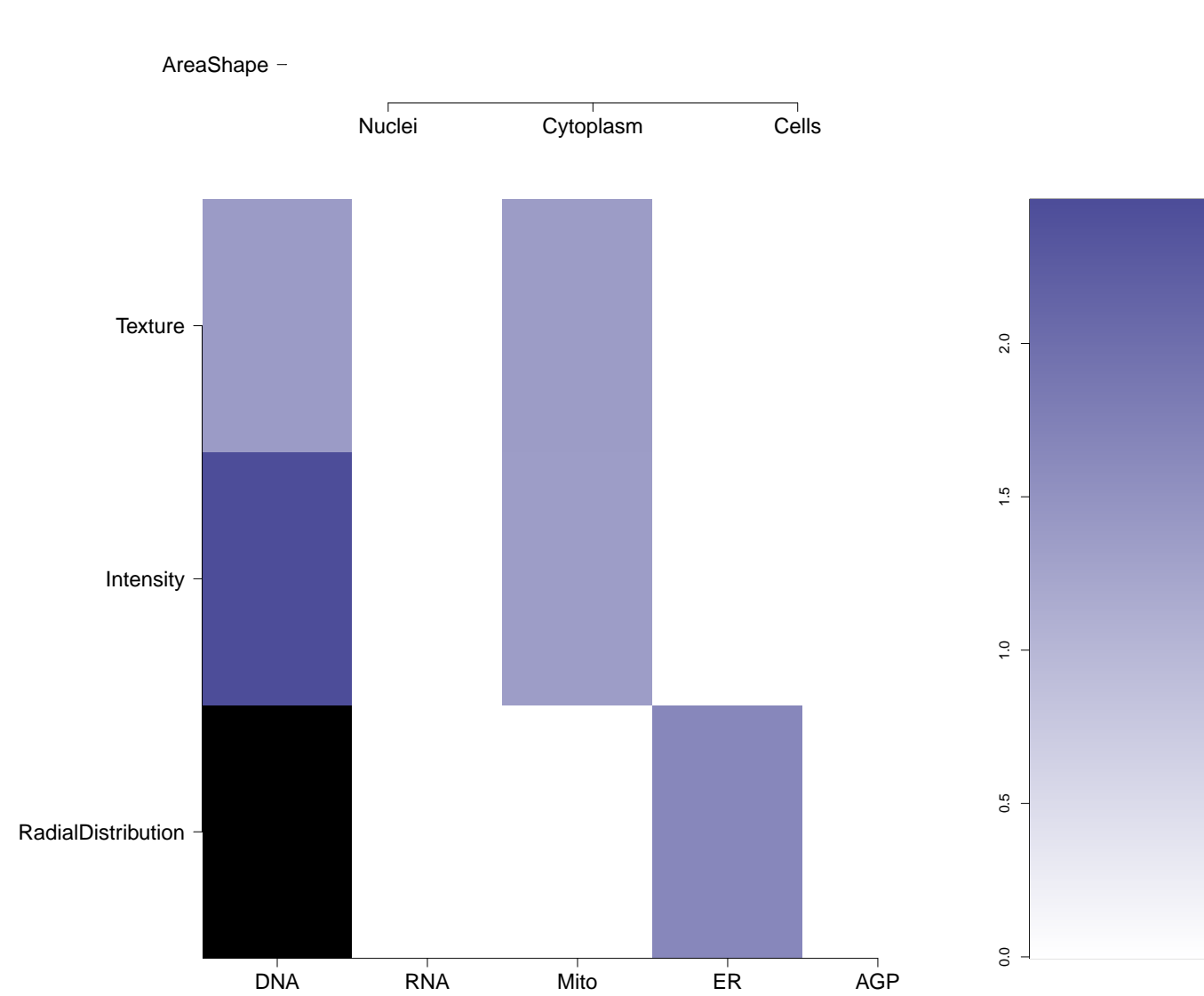
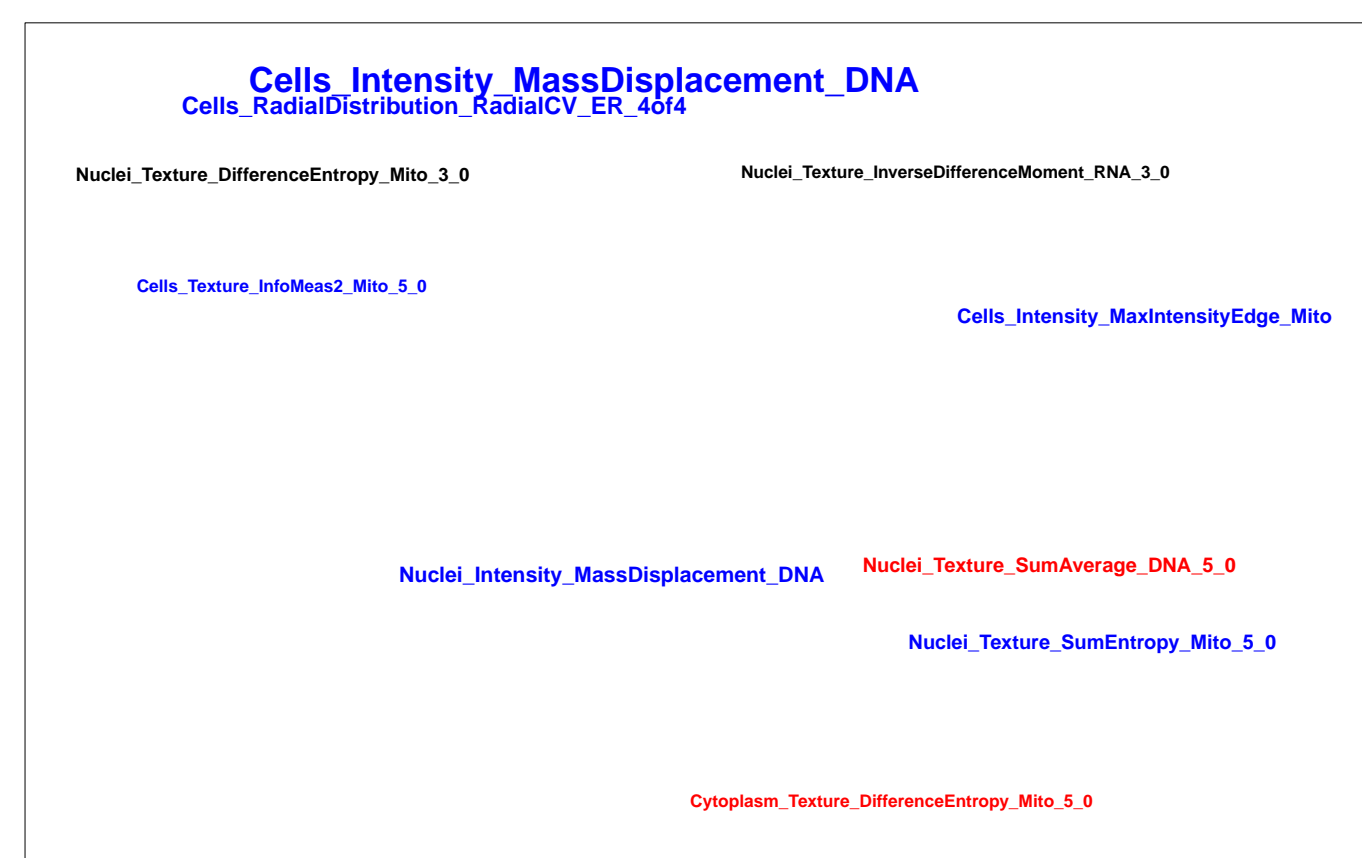
Treatment	Score
AKT1.E17K	0.47
AKT3.E17K	0.53
AKT3.WT.2	0.39
CDC42.T17N	0.54

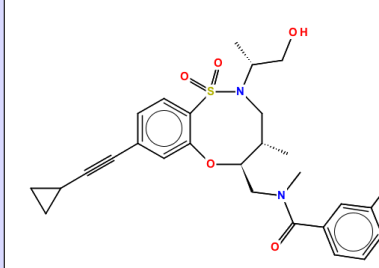
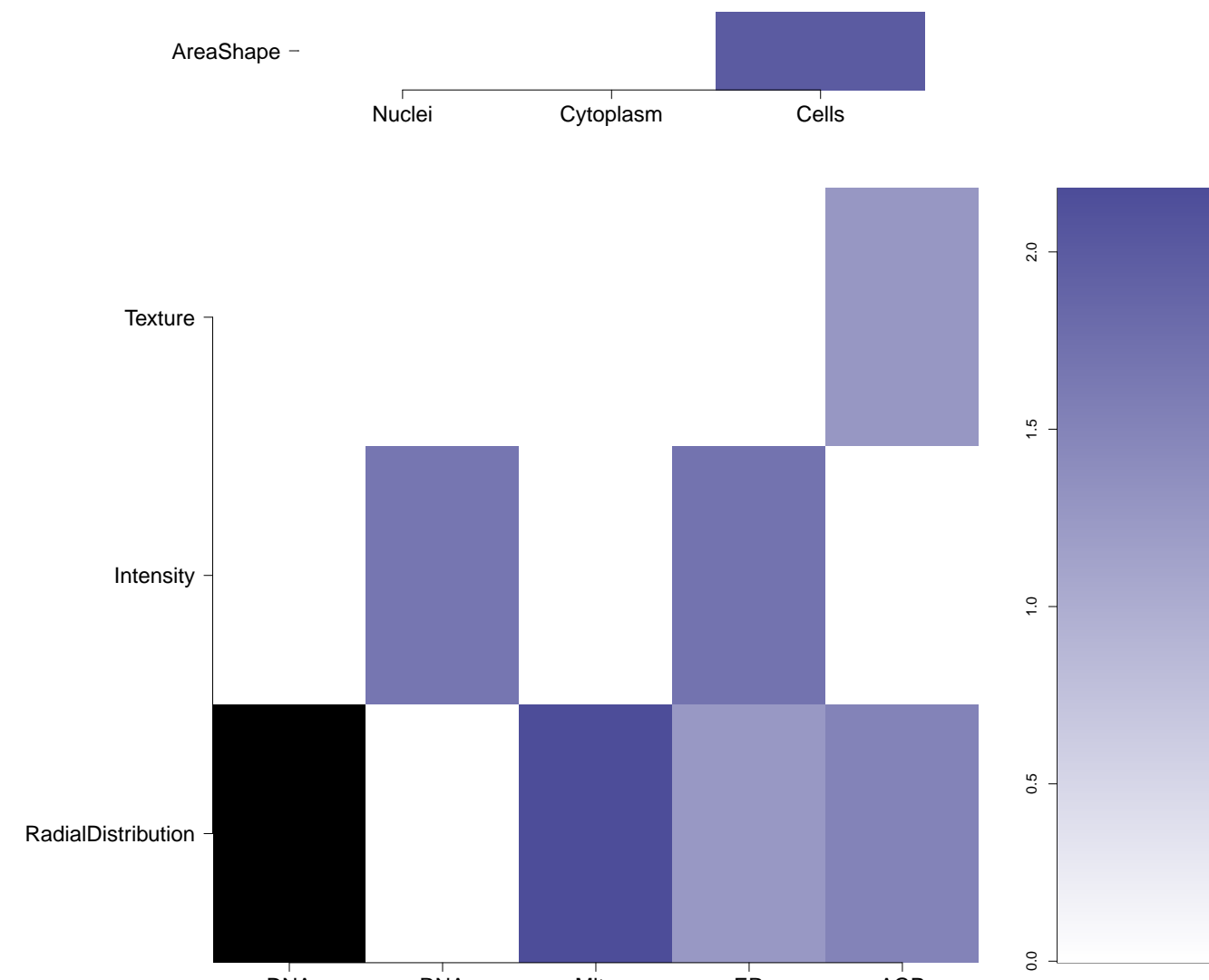
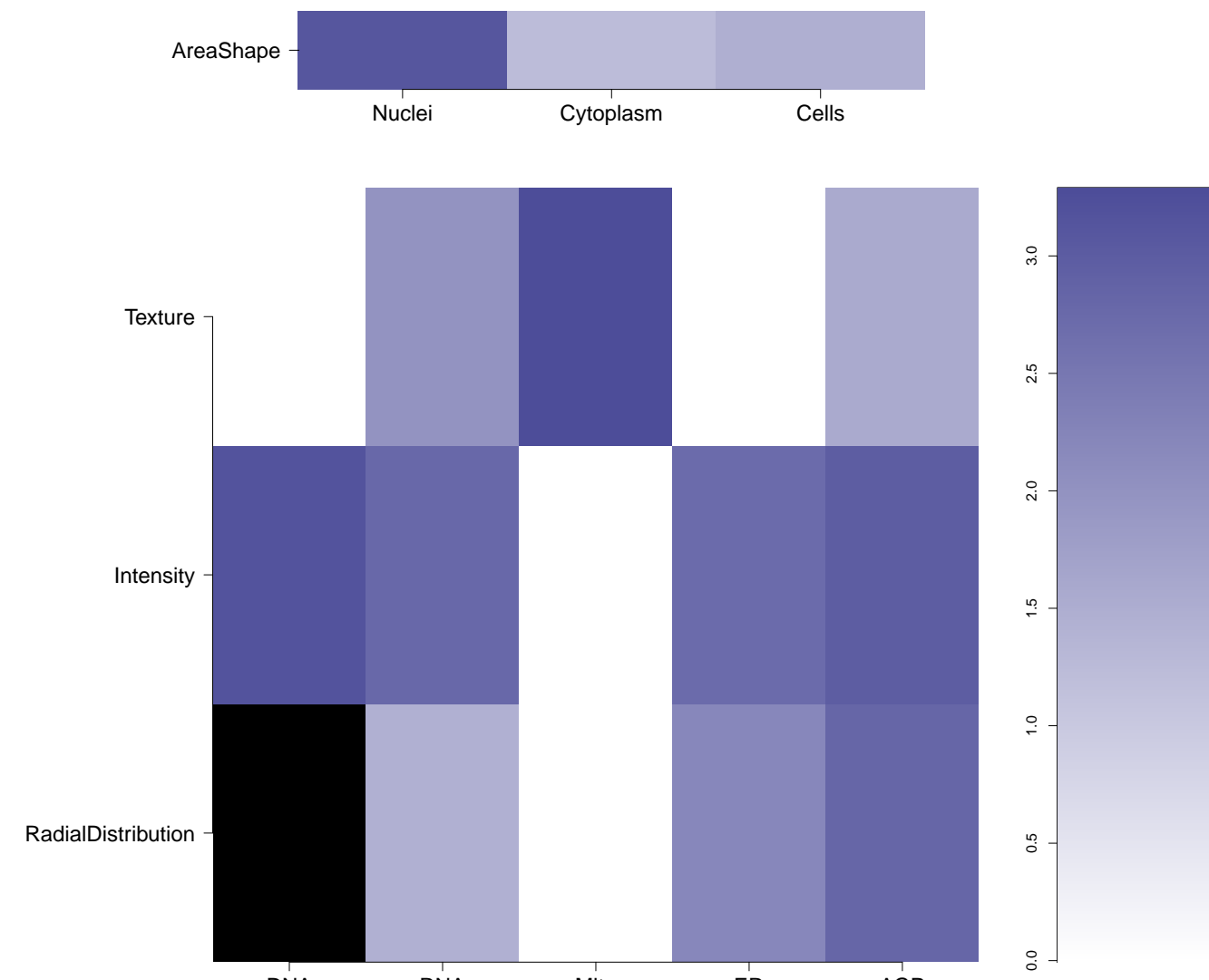
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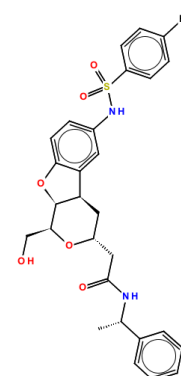
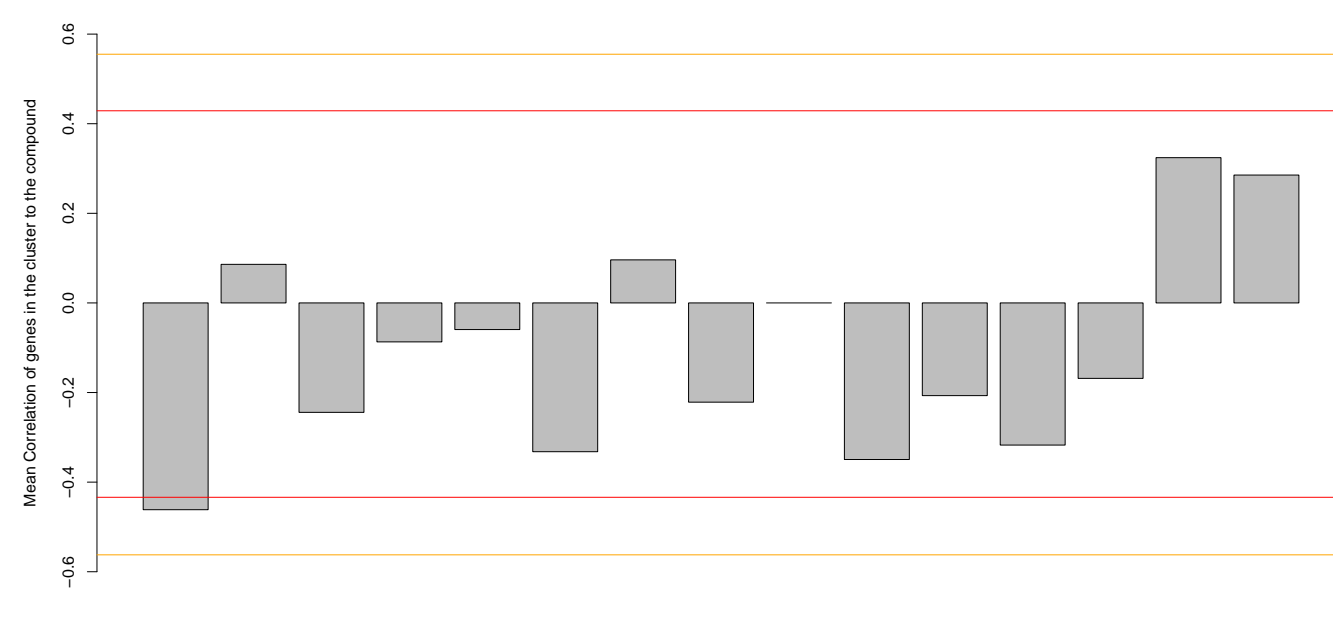
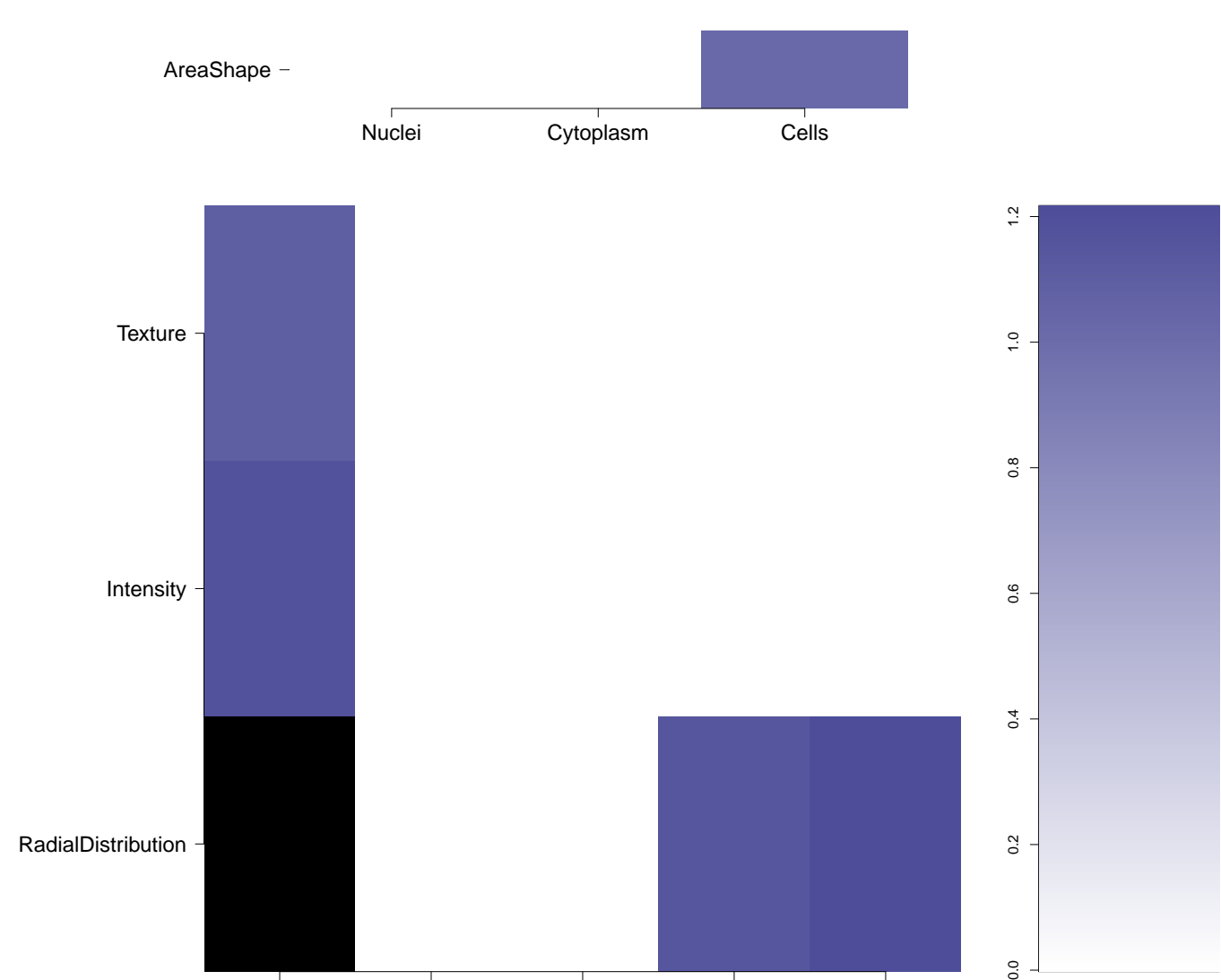
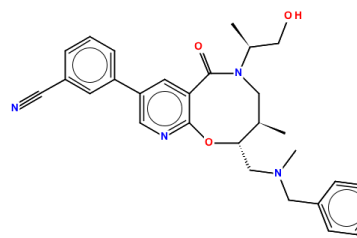
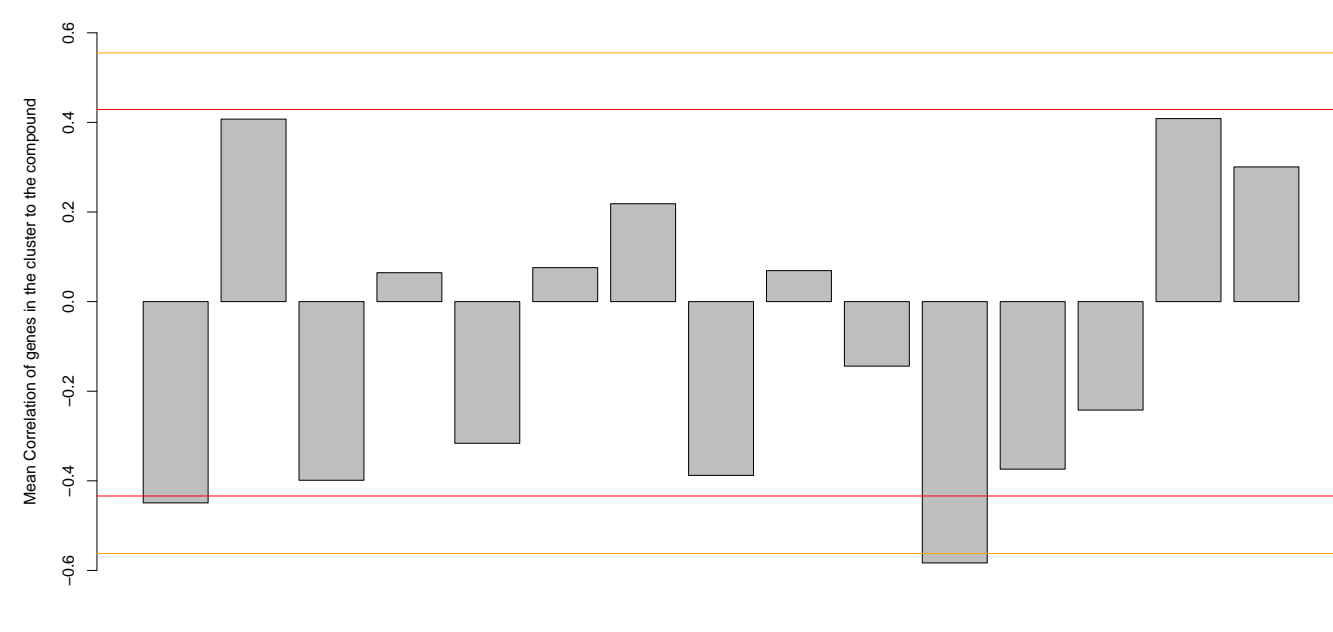
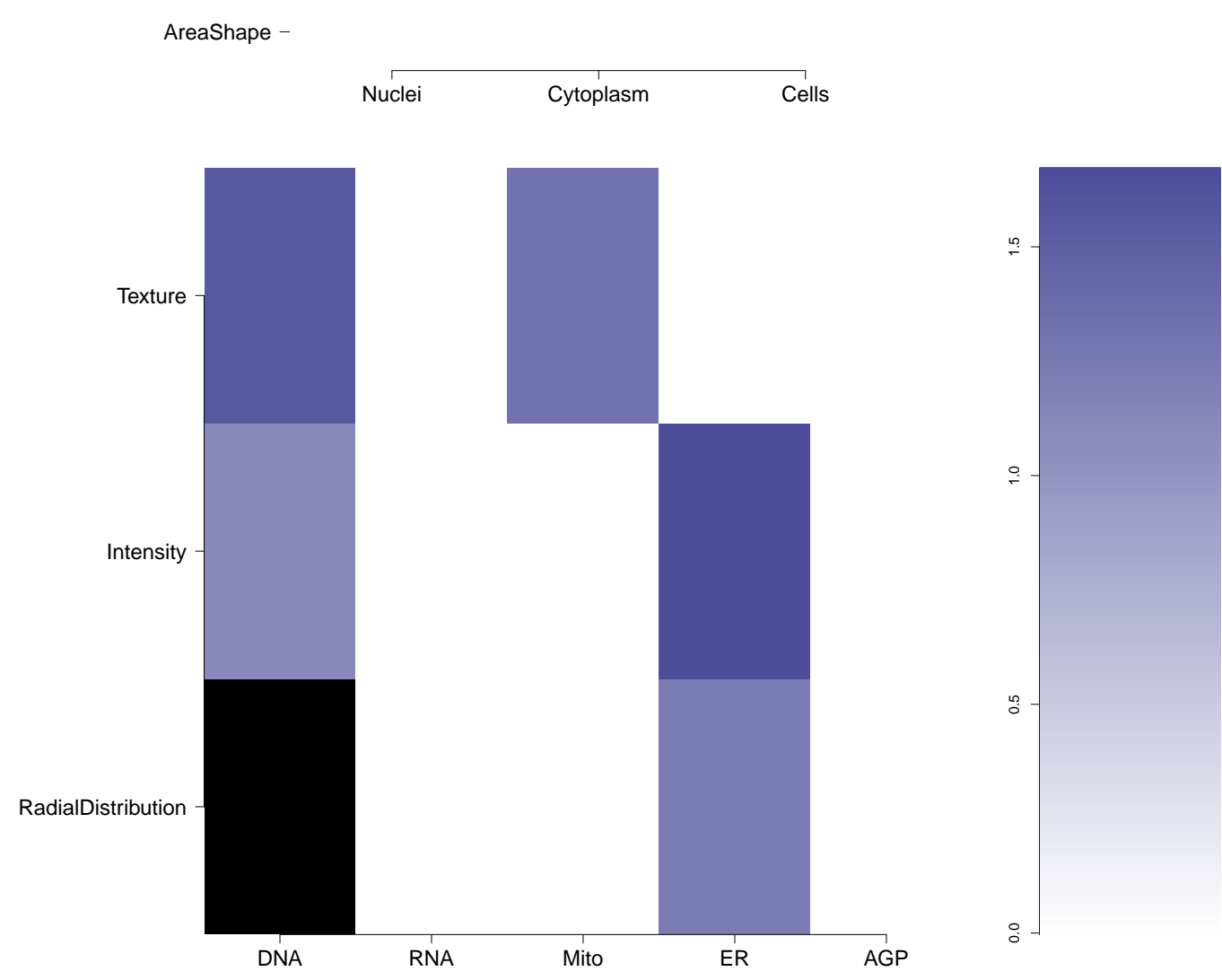
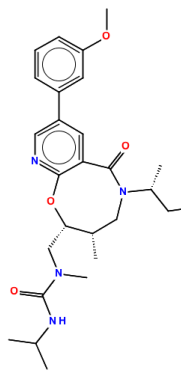
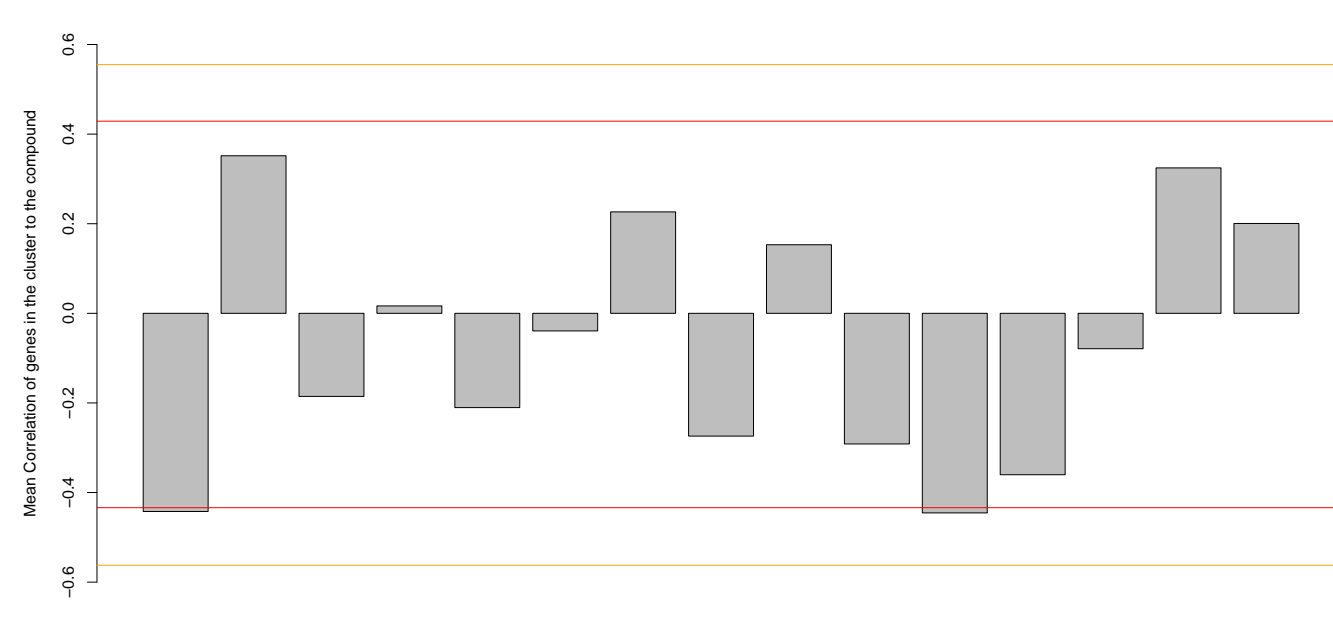
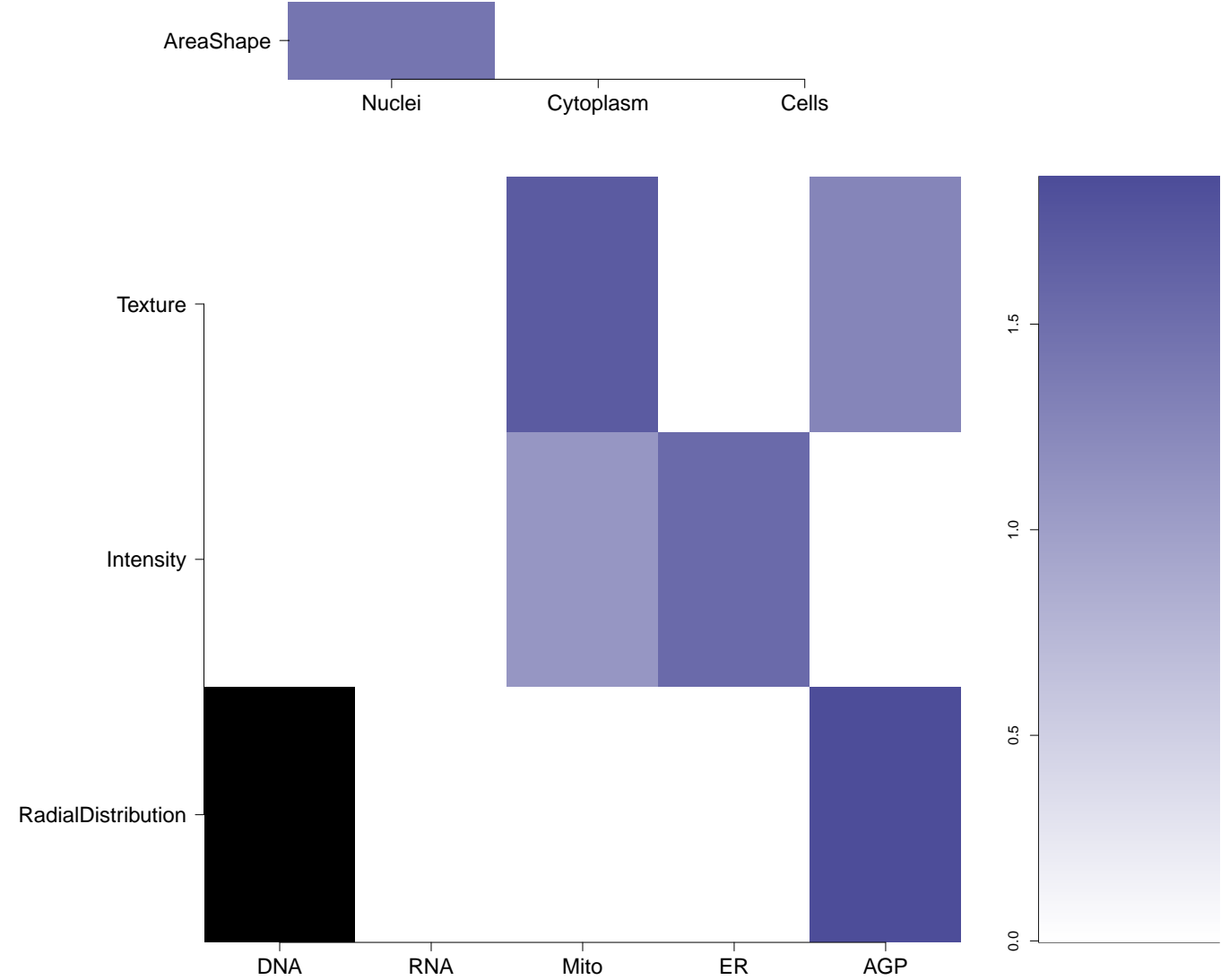
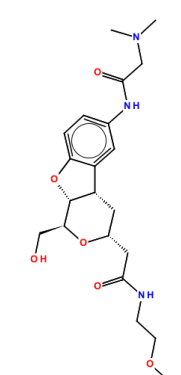
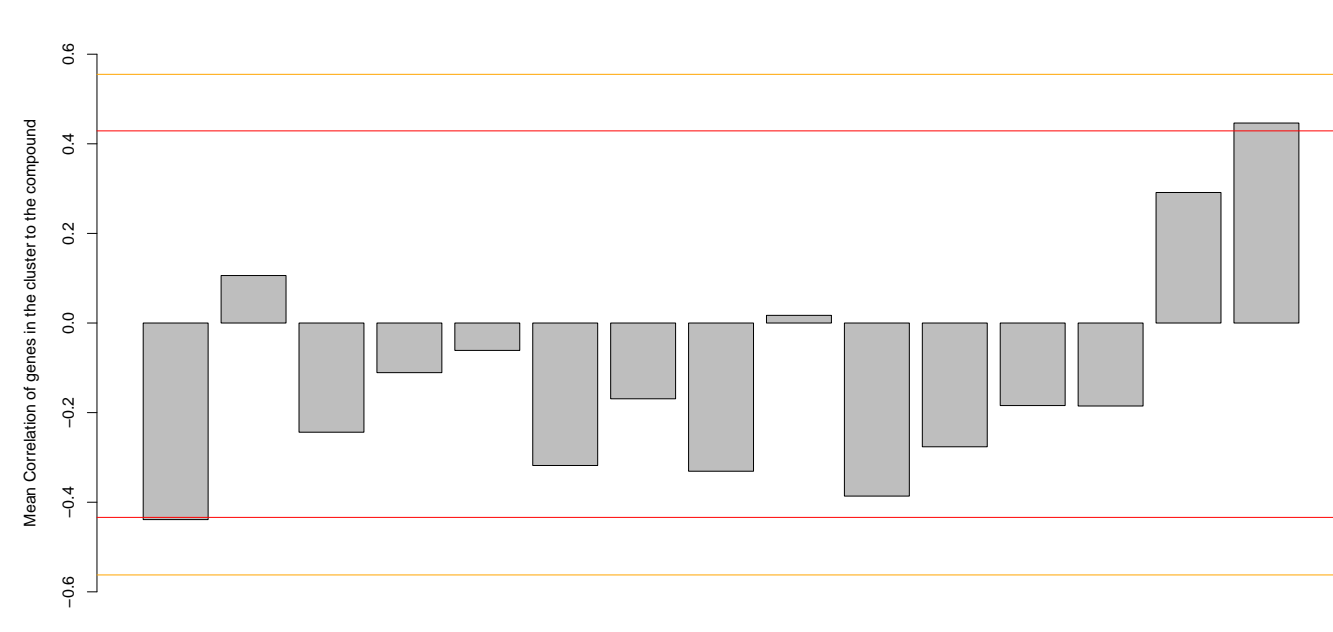
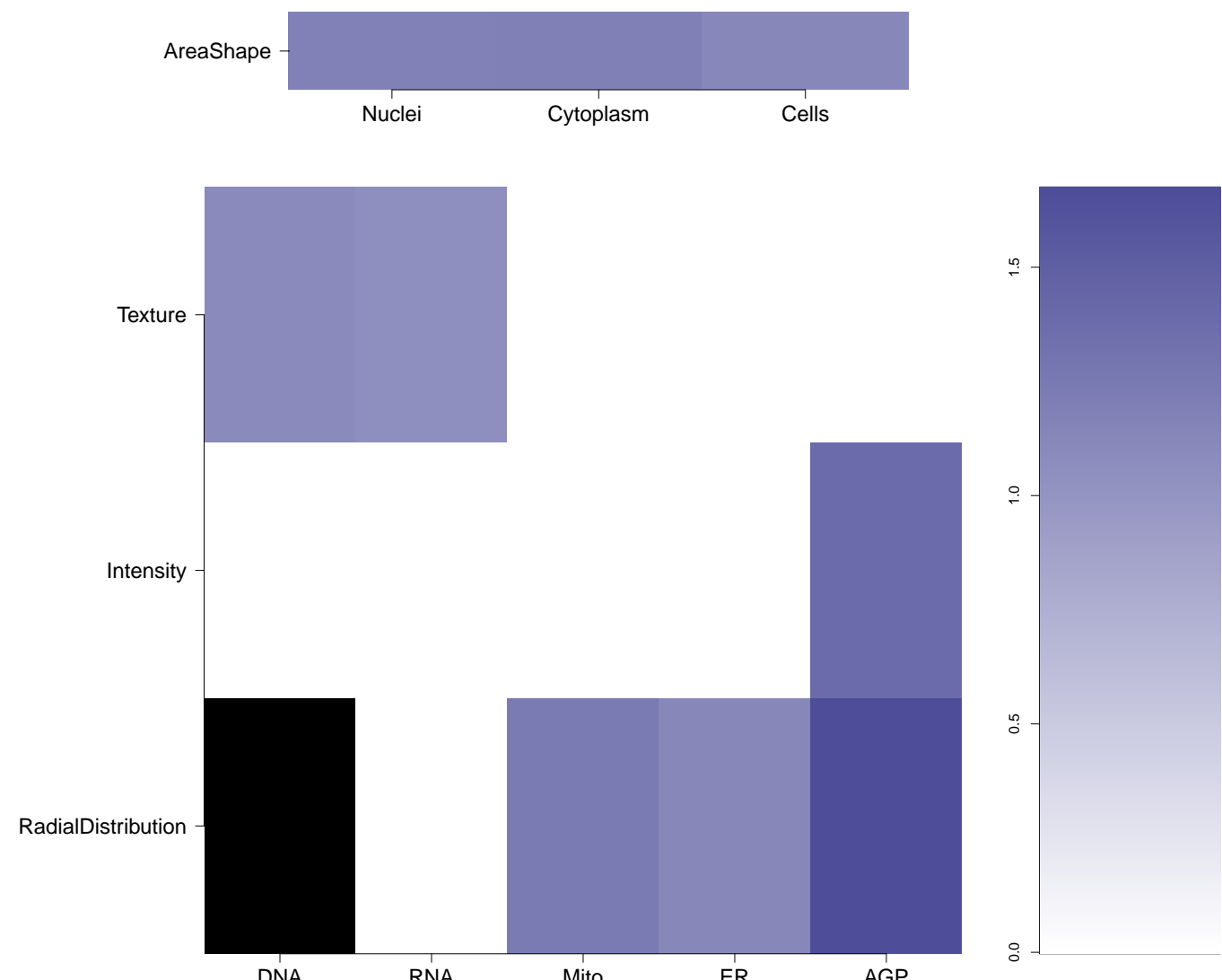


total number of assays tested in: 749. Active in the following assays:

- HIV-1 RT-RNase H MLCSEN HTS MH077605 (AID 565)
- Primary Anticellular Assay for E. coli BW25131 and 8710:tol(C)can. Probe for 384-well HTS (AID 573)
- Anticellular Assay for E. coli BW25131 and 8710:tol(C)can - Dose Response (AID 617)
- HIV-1 RT-RNase H MLCSEN HTS MH077605 Confirmation Assay (AID 651)
- HIV-1 RT-RNase H MLCSEN MH077605 Probe Assay: Dose response Assay (AID 652)
- CYP2C9 Assay (AID 777)
- CYP2C19 Assay (AID 778)
- qHTS Assay for Inhibitors of HADH2 Hydroxyacyl-Coenzyme A Dehydrogenase, type II) (AID 886)
- qHTS Assay for Inhibitors of 15-lipoO (15-lumen lipocycogenase) (AID 887)
- qHTS Assay for Inhibitors of HSD17B4, hydroxysteroid (17-beta) dehydrogenase 4 (AID 893)
- qHTS Assay for Inhibitors of HPGD (15-Hydroxyprostaglandin Dehydrogenase) (AID 894)
- qHTS Assay for Inhibitors of Aldehyde Dehydrogenase 1 (ALDH1A1) (AID 1030)
- HTS identification of compounds inhibiting phosphomannose isomerase (PMI) via a fluorescence intensity assay (AID 1209)
- Chemical Genetic Screen to Identify Inhibitors of Mitochondrial Fusion - Primary Screen (AID 1362)
- qHTS Assay for Inhibitors of Bacillus subtilis *pp* phosphatohistidine transferase (PPTase) (AID 1190)
- HTS for small molecule inhibitors of CHOP to regulate the unfolded protein response to ER stress (AID 2732)
- HTS Assay for Allosteric Antagonists of the Human D2 Dopamine Receptor: Primary Screen for Antagonists (AID 48344)
- Elucidation of physiology of non-replicating, drug-tolerant Mycobacterium tuberculosis (AID 48890)
- A Cell Based Secondary Assay to Explore Compounds that Modulate Non-Replicating, Drug-tolerant Compounds in Replicating H37Rv TB of Mycobacterium tuberculosis (AID 492652)
- Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of human platelet-activating factor acetylcholinesterase 1b, catalytic subunit 2 (PFAH1B2) (AID 492953)
- HTS identification of APOBEC3G DNA Deaminase Inhibitors via a fluorescence-based single-stranded DNA deaminase assay (AID 493012)
- Fluorescence polarization-based biochemical high throughput confirmation assay for inhibitors of human platelet-activating factor acetylcholinesterase 1b, catalytic subunit 2 (PFAH1B2) (AID 493034)
- Single concentration confirmation of qHTS for APOBEC3G DNA Deaminase Inhibitors via a fluorescence-based single-stranded DNA deaminase assay (AID 493152)
- HTS identification of small molecule inhibitors of Plasmodium falciparum Glucose-6-phosphate dehydrogenase via a fluorescence intensity assay (AID 504690)
- Inhibitors of the vitamin D receptor (VDR): qHTS (AID 504847)
- qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9b: Hit Confirmation (AID 58814)
- qHTS for Inhibitors of the Vitamin D receptor (VDR): Hit Validation in Primary Screen (AID 602199)
- Fluorescence-based cell-based primary high throughput screening assay to identify inhibitors of the interaction of nucleotide-binding oligomerization domain containing 2 (NOD2) and the receptor-interacting serine-threonine kinase 2 (RIPK2) (AID 612407)
- qHTS for Inhibitors of WRN Helicase (AID 651708)
- qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 680678)
- qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in presence of CPT (AID 680679)
- qHTS for Inhibitors of FLK1-PDB (polo-like kinase 1 - polo-box domain): Primary Screen (AID 720504)

<div>BRD-K43089177-001-06-1</div> <div>SMR000123694</div> <div>MLS000123058</div> <div>STK178377</div> <div>AC1LL2IR</div> <div>BDBM73383</div> <div>HMS1914K05</div> <div>HMS2437P20</div> <div>ZINC789542</div> <div>ZINC00789542</div> <div>BAS 05018824</div> <div>ST50276881</div> <div>K786-1645</div> <div>PubChem CID : 1077699</div>	<div></div>	NA (in 1 replicates)	<div>0.47 ± 0.06</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1E9K</td><td>0.43</td></tr><tr><td>AKT5E9K</td><td>0.48</td></tr><tr><td>AKT5W12</td><td>0.43</td></tr><tr><td>CDG2T1N</td><td>0.45</td></tr></table>	Treatment	Score	AKT1E9K	0.43	AKT5E9K	0.48	AKT5W12	0.43	CDG2T1N	0.45	NA	<div></div>	<div></div>	<div></div>	<div>Total number of assays tested in: 700. Active in the following assays:</div> <ul style="list-style-type: none">Leishmania major promastigote HTS (AID 1063)Primary screen for compounds that activate Insulin promoter activity in TRM-6 cells (AID 1296)Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Primary Screen (AID 1456)Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Retesting of RCC2 cells with Ouabain (AID 1717)Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of Protein Phosphatase Methyltransferase 1 (PME-1). (AID 2130)Fluorescence polarization-based biochemical high throughput confirmation assay for inhibitors of Protein Phosphatase Methyltransferase 1 (PME-1). (AID 2171)Fluorescence Polarization Cell-Free Homogeneous Primary HTS to Identify Inhibitors of the LANA Histone H2A/H2B Interaction (AID 2629)uHTS fluorescent assay for identification of inhibitors of ATG4B (AID 504462)Dose response confirmation of the uHTS fluorescent assay for identification of inhibitors of ATG4B. (AID 504756)Single concentration confirmation of inhibitors of ATG4B via a fluorescent assay (AID 504757)Primary qHTS for delayed death inhibitors of the malarial parasite plasmod, 96 hour incubation (AID 504834)Dose response counterscreen of uHTS hits for ATG4B inhibitors in a Phospholipase A2 assay (AID 588400)
Treatment	Score																	
AKT1E9K	0.43																	
AKT5E9K	0.48																	
AKT5W12	0.43																	
CDG2T1N	0.45																	
<div>BRD-A4148464-001-06-0</div> <div>BRN 1211793</div> <div>67086-S1-1</div> <div>F1912-0001</div> <div>AC1MCJDX</div> <div>MLS000678441</div> <div>CTK517353</div> <div>HMS2721O10</div> <div>HE088600</div> <div>KB-92026</div> <div>SMR000323916</div> <div>KB-323361</div> <div>LS-151122</div> <div>PubChem CID : 2771064</div>	<div></div>	NA (in 1 replicates)	<div>0.46 ± 0.06</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1E9K</td><td>0.38</td></tr><tr><td>AKT5E9K</td><td>0.50</td></tr><tr><td>AKT5W12</td><td>0.45</td></tr><tr><td>CDG2T1N</td><td>0.51</td></tr></table>	Treatment	Score	AKT1E9K	0.38	AKT5E9K	0.50	AKT5W12	0.45	CDG2T1N	0.51	NA	<div></div>	<div></div>	<div></div>	<div>Total number of assays tested in: 617. Active in the following assays:</div> <ul style="list-style-type: none">uHTS identification of TNAP inhibitors in the absence of phosphate acceptor performed in luminescent assay (AID 1012)Aqueous Solubility from MLSMR Stock Solutions (AID 1996)Primary biochemical fluorescence polarization-based high throughput screening assay to identify inhibitors of protein arginine methyltransferase 1 (PRMT1) (AID 652257)
Treatment	Score																	
AKT1E9K	0.38																	
AKT5E9K	0.50																	
AKT5W12	0.45																	
CDG2T1N	0.51																	
<div>BRD-K85264253-001-01-7</div> <div>PubChem CID : 54647901</div>	<div></div>	0.62 (in 2 replicates)	<div>0.46 ± 0.08</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1E9K</td><td>0.45</td></tr><tr><td>AKT5E9K</td><td>0.46</td></tr><tr><td>AKT5W12</td><td>0.47</td></tr><tr><td>CDG2T1N</td><td>0.46</td></tr></table>	Treatment	Score	AKT1E9K	0.45	AKT5E9K	0.46	AKT5W12	0.47	CDG2T1N	0.46	NA	<div></div>	<div></div>	<div></div>	<div>Total number of assays tested in: 36.</div>
Treatment	Score																	
AKT1E9K	0.45																	
AKT5E9K	0.46																	
AKT5W12	0.47																	
CDG2T1N	0.46																	
<div>BRD-K71919342-001-06-4</div> <div>AC1N4ZAA</div> <div>MLS001003683</div> <div>CTK0B5719</div> <div>HMS2685K03</div> <div>ZINC5257101</div> <div>PL045918</div> <div>SMR000347522</div> <div>14265-35-1</div> <div>PubChem CID : 4136929</div>	<div></div>	NA (in 1 replicates)	<div>0.46 ± 0.04</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1E9K</td><td>0.48</td></tr><tr><td>AKT5E9K</td><td>0.50</td></tr><tr><td>AKT5W12</td><td>0.41</td></tr><tr><td>CDG2T1N</td><td>0.43</td></tr></table>	Treatment	Score	AKT1E9K	0.48	AKT5E9K	0.50	AKT5W12	0.41	CDG2T1N	0.43	NA	<div></div>	<div></div>	<div></div>	<div>Total number of assays tested in: 652. Active in the following assays:</div> <ul style="list-style-type: none">Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932)Counter Screen for Glucose-6-Phosphate Dehydrogenase-based Primary Assay (AID 1020)qHTS for Inhibitors of Tau Fibril Formation, Thioflavin T Binding (AID 1460)Primary biochemical high throughput screening assay to identify inhibitors of VIM-2 metallo-beta-lactamase (AID 1527)MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814)QFRET-based counterscreen for PFM18AAP inhibitors: biochemical high throughput screening assay to identify inhibitors of the Cathepsin L proteinase (CTSL1). (AID 1906)Fluorescence polarization-based counterscreen for RBBP9 inhibitors: primary biochemical high throughput screening assay to identify inhibitors of the oxidoreductase glutathione S-transferase omega 1(GSTO1). (AID 1974)Homogeneous Time-Resolved Fluorescence Resonance Energy Transfer (HTRF) Assay (AID 2073)Primary biochemical high throughput screening assay to identify inhibitors of BCL2-related protein, long isoform (BCLXL). (AID 2129)Fluorescence polarization-based biochemical high throughput confirmation assay for inhibitors of the oxidoreductase glutathione S-transferase omega 1(GSTO1). (AID 2176)Fluorescence Cell-Free Homogenous Primary HTS to Identify Inhibitors of RecA Intein Splicing Activity (AID 2221)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 Inhibitors of Fructose-1,6-bisphosphate Aldolase from Giardia Lamblia (AID 2451)qHTS Assay for Inhibitors of Fructose-1,6-bisphosphate Aldolase from Giardia Lamblia: Coupling assay counterscreen (AID 2472)qHTS Assay for Inhibitors of Bloom's syndrome helicase (BLM) (AID 2528)uHTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 6 (SENp6) (AID 2599)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 Non-Covalent Inhibitors of RecA-Intein Splicing Activity (AID 449750)FRET-based cell-based primary high throughput screening assay to identify antagonists of the orexin 1 receptor (OX1R; HCRTR1) (AID 485270)qHTS Assay for Inhibitors of DNA Polymerase Beta (AID 485314)qHTS Assay for the Inhibitors of Schistosoma Mansonii Peroxisomeoxins (AID 485364)Single concentration confirmation of inhibitors of Sentrin-specific proteases (SENPs) using a Caspase-3 Selectivity assay (AID 488918)uHTS Fluorescent assay for identification of inhibitors of Apaf-1 (AID 489030)qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)uHTS identification of small molecule modulators of myocardial damage (AID 588492)Primary and Confirmatory Screening for Flavivirus Genomic Capping Enzyme Inhibition (AID 588689)uHTS identification of modulators of interaction between CendR and NRP-1 using Fluorescence Polarization assay (AID 602438)A quantitative high throughput screen for small molecules that induce DNA re-replication in MCF 10a normal breast cells. (AID 624296)qHTS of TDP-43 Inhibitors (AID 652104)VEID(2) R110 Enzymatic Primary HTS to identify Inhibitors of Caspase 6 Measured in Biochemical System Using Plate Reader - 7052-01.Inhibitor.SinglePoint.HTS.Activity.Set2 (AID 686996)VEID(2) R110 Enzymatic Primary HTS to identify Inhibitors of Caspase 6 Measured in Biochemical System Using Plate Reader - 7052-01.Inhibitor.Dose.CherryPick.Activity (AID 720632)Development of Small Molecule Probes of the Histone Methyltransferase, NSD2 Measured in Biochemical System Using Plate Reader - 7053-01.Inhibitor.SinglePoint.HTS.Activity.Set2 (AID 743445)
Treatment	Score																	
AKT1E9K	0.48																	
AKT5E9K	0.50																	
AKT5W12	0.41																	
CDG2T1N	0.43																	

BRD-K65196043-001-01-0 PubChem CID : 54618158		0.92 (in 4 replicates)	<div>0.45 ± 0.10</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.55</td></tr><tr><td>AKT1.E0K</td><td>0.58</td></tr><tr><td>AKT1.WT.2</td><td>0.45</td></tr><tr><td>CDK2.T1N</td><td>0.52</td></tr></table>	Treatment	Score	AKT1.E0K	0.55	AKT1.E0K	0.58	AKT1.WT.2	0.45	CDK2.T1N	0.52	<div>0.725 ± 0.112</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.60</td></tr><tr><td>AKT1.E0K</td><td>0.602</td></tr><tr><td>AKT1.WT.2</td><td>0.683</td></tr><tr><td>CDK2.T1N</td><td>0.665</td></tr></table>	Treatment	Score	AKT1.E0K	0.60	AKT1.E0K	0.602	AKT1.WT.2	0.683	CDK2.T1N	0.665				Total number of assays tested in: 33.
Treatment	Score																											
AKT1.E0K	0.55																											
AKT1.E0K	0.58																											
AKT1.WT.2	0.45																											
CDK2.T1N	0.52																											
Treatment	Score																											
AKT1.E0K	0.60																											
AKT1.E0K	0.602																											
AKT1.WT.2	0.683																											
CDK2.T1N	0.665																											
BRD-K16535949-001-01-4 PubChem CID : 44488211		0.60 (in 4 replicates)	<div>0.44 ± 0.08</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.47</td></tr><tr><td>AKT1.E0K</td><td>0.45</td></tr><tr><td>AKT1.WT.2</td><td>0.53</td></tr><tr><td>CDK2.T1N</td><td>0.52</td></tr></table>	Treatment	Score	AKT1.E0K	0.47	AKT1.E0K	0.45	AKT1.WT.2	0.53	CDK2.T1N	0.52	NA				Total number of assays tested in: 43.										
Treatment	Score																											
AKT1.E0K	0.47																											
AKT1.E0K	0.45																											
AKT1.WT.2	0.53																											
CDK2.T1N	0.52																											
BRD-K32464623-001-06-9 MLS000775327 HMS2753L15 ZINC13637891 SMR000368401 PubChem CID : 9614758		NA (in 1 replicates)	<div>0.44 ± 0.07</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.41</td></tr><tr><td>AKT1.E0K</td><td>0.41</td></tr><tr><td>AKT1.WT.2</td><td>0.37</td></tr><tr><td>CDK2.T1N</td><td>0.53</td></tr></table>	Treatment	Score	AKT1.E0K	0.41	AKT1.E0K	0.41	AKT1.WT.2	0.37	CDK2.T1N	0.53	NA				Total number of assays tested in: 570. Active in the following assays: <ul style="list-style-type: none">Luminescence Microorganism Primary HTS to Identify Inhibitors of the SUMOylation Pathway Using a Temperature Sensitive Growth Reversal Mutant Mot1-301 (AID 2716)qHTS Assay for Inhibitors of BAZ2B (AID 504333)uHTS fluorescent assay for identification of inhibitors of ATG4B (AID 504462)uHTS Fluorescent Assay Using Nedd8 Protein Substrate for Identification of Inhibitors of Sentrin-Specific Protease 8 (SENPs) (AID 602440)Fluorescence polarization-based biochemical primary high throughput screening assay to identify inhibitors of ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1) (AID 651572)qHTS Assay for Inhibitors of Hepatitis C Virus (HCV) (AID 651820)qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDPI): qHTS in cells in absence of CPT (AID 686978)qHTS for Inhibitors of Inflammasome Signaling: IL-1-beta AlphaISA Primary Screen (AID 743279)										
Treatment	Score																											
AKT1.E0K	0.41																											
AKT1.E0K	0.41																											
AKT1.WT.2	0.37																											
CDK2.T1N	0.53																											
BRD-K67411319-001-01-8 PubChem CID : 44501932		0.88 (in 3 replicates)	<div>-0.55 ± 0.05</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>-0.48</td></tr><tr><td>AKT1.E0K</td><td>-0.56</td></tr><tr><td>AKT1.WT.2</td><td>-0.56</td></tr><tr><td>CDK2.T1N</td><td>-0.56</td></tr></table>	Treatment	Score	AKT1.E0K	-0.48	AKT1.E0K	-0.56	AKT1.WT.2	-0.56	CDK2.T1N	-0.56	<div>0.440 ± 0.229</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.389</td></tr><tr><td>AKT1.E0K</td><td>0.402</td></tr><tr><td>AKT1.WT.2</td><td>0.317</td></tr><tr><td>CDK2.T1N</td><td>0.562</td></tr></table>	Treatment	Score	AKT1.E0K	0.389	AKT1.E0K	0.402	AKT1.WT.2	0.317	CDK2.T1N	0.562				Total number of assays tested in: 47.
Treatment	Score																											
AKT1.E0K	-0.48																											
AKT1.E0K	-0.56																											
AKT1.WT.2	-0.56																											
CDK2.T1N	-0.56																											
Treatment	Score																											
AKT1.E0K	0.389																											
AKT1.E0K	0.402																											
AKT1.WT.2	0.317																											
CDK2.T1N	0.562																											
BRD-K27824357-001-01-4 PubChem CID : 54618409		0.76 (in 4 replicates)	<div>-0.52 ± 0.03</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>-0.49</td></tr><tr><td>AKT1.E0K</td><td>-0.53</td></tr><tr><td>AKT1.WT.2</td><td>-0.51</td></tr><tr><td>CDK2.T1N</td><td>-0.56</td></tr></table>	Treatment	Score	AKT1.E0K	-0.49	AKT1.E0K	-0.53	AKT1.WT.2	-0.51	CDK2.T1N	-0.56	<div>0.325 ± 0.352</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>0.339</td></tr><tr><td>AKT1.E0K</td><td>0.362</td></tr><tr><td>AKT1.WT.2</td><td>0.316</td></tr><tr><td>CDK2.T1N</td><td>0.642</td></tr></table>	Treatment	Score	AKT1.E0K	0.339	AKT1.E0K	0.362	AKT1.WT.2	0.316	CDK2.T1N	0.642				Total number of assays tested in: 37.
Treatment	Score																											
AKT1.E0K	-0.49																											
AKT1.E0K	-0.53																											
AKT1.WT.2	-0.51																											
CDK2.T1N	-0.56																											
Treatment	Score																											
AKT1.E0K	0.339																											
AKT1.E0K	0.362																											
AKT1.WT.2	0.316																											
CDK2.T1N	0.642																											
BRD-K48693155-001-01-2 PubChem CID : 54618096		0.88 (in 4 replicates)	<div>-0.52 ± 0.04</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>-0.48</td></tr><tr><td>AKT1.E0K</td><td>-0.54</td></tr><tr><td>AKT1.WT.2</td><td>-0.50</td></tr><tr><td>CDK2.T1N</td><td>-0.56</td></tr></table>	Treatment	Score	AKT1.E0K	-0.48	AKT1.E0K	-0.54	AKT1.WT.2	-0.50	CDK2.T1N	-0.56	NA				Total number of assays tested in: 37.										
Treatment	Score																											
AKT1.E0K	-0.48																											
AKT1.E0K	-0.54																											
AKT1.WT.2	-0.50																											
CDK2.T1N	-0.56																											
BRD-K04968712-001-05-7 MLS000858711 SMR000458790 AC1MDPY6 BDBM45738 HMS2811A04 ZINC1034543 PubChem CID : 2814981		NA (in 1 replicates)	<div>-0.51 ± 0.10</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>-0.46</td></tr><tr><td>AKT1.E0K</td><td>-0.49</td></tr><tr><td>AKT1.WT.2</td><td>-0.42</td></tr><tr><td>CDK2.T1N</td><td>-0.64</td></tr></table>	Treatment	Score	AKT1.E0K	-0.46	AKT1.E0K	-0.49	AKT1.WT.2	-0.42	CDK2.T1N	-0.64	NA				Total number of assays tested in: 545. Active in the following assays: <ul style="list-style-type: none">Factor XIla 1536 HTS (AID 800)Primary qHTS for delayed death inhibitors of the malarial parasite plasid, 48 hour incubation (AID 504832)Primary qHTS for delayed death inhibitors of the malarial parasite plasid, 96 hour incubation (AID 504834)Confirmation screen for delayed death inhibitors of the malarial parasite plasid, 96 hour incubation (AID 504848)Confirmation screen for delayed death inhibitors of the malarial parasite plasid, 48 hour incubation (AID 504850)qHTS for induction of synthetic lethality in tumor cells producing 2HG: qHTS for the HT-1080-IDH1KD cell line (AID 686971)										
Treatment	Score																											
AKT1.E0K	-0.46																											
AKT1.E0K	-0.49																											
AKT1.WT.2	-0.42																											
CDK2.T1N	-0.64																											
BRD-K89505656-001-01-2 PubChem CID : 44494377		0.70 (in 4 replicates)	<div>-0.47 ± 0.10</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E0K</td><td>-0.49</td></tr><tr><td>AKT1.E0K</td><td>-0.43</td></tr><tr><td>AKT1.WT.2</td><td>-0.36</td></tr><tr><td>CDK2.T1N</td><td>-0.39</td></tr></table>	Treatment	Score	AKT1.E0K	-0.49	AKT1.E0K	-0.43	AKT1.WT.2	-0.36	CDK2.T1N	-0.39	NA				Total number of assays tested in: 51.										
Treatment	Score																											
AKT1.E0K	-0.49																											
AKT1.E0K	-0.43																											
AKT1.WT.2	-0.36																											
CDK2.T1N	-0.39																											

BRD-K08306736-001-01-7 PubChem CID : 54645948		NA (in 1 replicates)	<div>-0.46 ± 0.09</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>-0.46</td></tr><tr><td>AKT1.E19K</td><td>-0.45</td></tr><tr><td>AKT1.WT.2</td><td>-0.36</td></tr><tr><td>CDC42.T1N</td><td>-0.97</td></tr></table>	Treatment	Score	AKT1.E19K	-0.46	AKT1.E19K	-0.45	AKT1.WT.2	-0.36	CDC42.T1N	-0.97	<div>0.220 ± 0.132</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>0.177</td></tr><tr><td>AKT1.E19K</td><td>0.062</td></tr><tr><td>AKT1.WT.2</td><td>0.317</td></tr><tr><td>CDC42.T1N</td><td>0.335</td></tr></table>	Treatment	Score	AKT1.E19K	0.177	AKT1.E19K	0.062	AKT1.WT.2	0.317	CDC42.T1N	0.335			<div>Cells_RadialDistribution_RadialCV_ER_A04 Nuclei_Texture_AngularSecondMoment_RNA_3_0 Nuclei_Texture_InverseDifferenceMoment_RNA_3_0 Cytoplasm_Texture_Intensity_DNA_3_0 Cells_RadialDistribution_RadialCV_AGP_204 Cells_RadialDistribution_RadialCV_AGP_204 Nuclei_Texture_SumAverage_DNA_3_0 Nuclei_Intensity_MeanDisplacement_DNA Nuclei_AreaShape_Zernike_0_0 Cells_AreaShape_Zernike_0_0 Cytoplasm_AreaShape_Zernike_7_1</div>	Total number of assays tested in: 40.
Treatment	Score																											
AKT1.E19K	-0.46																											
AKT1.E19K	-0.45																											
AKT1.WT.2	-0.36																											
CDC42.T1N	-0.97																											
Treatment	Score																											
AKT1.E19K	0.177																											
AKT1.E19K	0.062																											
AKT1.WT.2	0.317																											
CDC42.T1N	0.335																											
BRD-K60656884-001-01-0 PubChem CID : 54618107		0.76 (in 4 replicates)	<div>-0.45 ± 0.03</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>-0.44</td></tr><tr><td>AKT1.E19K</td><td>-0.41</td></tr><tr><td>AKT1.WT.2</td><td>-0.44</td></tr><tr><td>CDC42.T1N</td><td>-0.50</td></tr></table>	Treatment	Score	AKT1.E19K	-0.44	AKT1.E19K	-0.41	AKT1.WT.2	-0.44	CDC42.T1N	-0.50	<div>0.565 ± 0.277</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>0.567</td></tr><tr><td>AKT1.E19K</td><td>0.765</td></tr><tr><td>AKT1.WT.2</td><td>0.317</td></tr><tr><td>CDC42.T1N</td><td>0.335</td></tr></table>	Treatment	Score	AKT1.E19K	0.567	AKT1.E19K	0.765	AKT1.WT.2	0.317	CDC42.T1N	0.335			<div>Cytoplasm_Intensity_MinIntensityEdge_ER Cells_RadialDistribution_RadialCV_ER_A04 Nuclei_Texture_DifferenceEntropy_ER_3_0 Cells_Intensity_MaxIntensityEdge_ER Nuclei_Texture_AngularSecondMoment_Mito_3_0 Cells_Intensity_MaxIntensity_ER Nuclei_Texture_SumAverage_DNA_3_0 Nuclei_Texture_Gabor_Mito_3 Nuclei_Texture_Entropy_ER_3_0 Cytoplasm_Texture_DifferenceEntropy_Mito_3_0</div>	Total number of assays tested in: 36.
Treatment	Score																											
AKT1.E19K	-0.44																											
AKT1.E19K	-0.41																											
AKT1.WT.2	-0.44																											
CDC42.T1N	-0.50																											
Treatment	Score																											
AKT1.E19K	0.567																											
AKT1.E19K	0.765																											
AKT1.WT.2	0.317																											
CDC42.T1N	0.335																											
BRD-K33903208-001-01-9 PubChem CID : 44506100		0.59 (in 4 replicates)	<div>-0.44 ± 0.07</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>-0.41</td></tr><tr><td>AKT1.E19K</td><td>-0.30</td></tr><tr><td>AKT1.WT.2</td><td>-0.42</td></tr><tr><td>CDC42.T1N</td><td>-0.44</td></tr></table>	Treatment	Score	AKT1.E19K	-0.41	AKT1.E19K	-0.30	AKT1.WT.2	-0.42	CDC42.T1N	-0.44	<div>0.597 ± 0.370</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>0.214</td></tr><tr><td>AKT1.E19K</td><td>0.565</td></tr><tr><td>AKT1.WT.2</td><td>0.317</td></tr><tr><td>CDC42.T1N</td><td>0.360</td></tr></table>	Treatment	Score	AKT1.E19K	0.214	AKT1.E19K	0.565	AKT1.WT.2	0.317	CDC42.T1N	0.360			<div>Nuclei_Intensity_MaxIntensityEdge_AGP Nuclei_Texture_AngularSecondMoment_AGP_3_0 Cytoplasm_Intensity_MinIntensityEdge_AGP Cytoplasm_Intensity_MaxIntensity_Mito Cells_Intensity_MaxIntensityEdge_DNA Cells_Texture_SumAverage_Mito_3_0 Cytoplasm_Texture_Correlation_AGP_3_0 Cytoplasm_Texture_SumAverage_Mito_3_0 Cells_RadialDistribution_RadialCV_AGP_204 Cells_Intensity_MaxIntensity_ER Cytoplasm_Texture_AngularSecondMoment_Mito_3_0 Cells_RadialDistribution_RadialCV_AGP_204 Nuclei_AreaShape_Zernike_3_1 Cytoplasm_Texture_DifferenceEntropy_Mito_3_0</div>	Total number of assays tested in: 27.
Treatment	Score																											
AKT1.E19K	-0.41																											
AKT1.E19K	-0.30																											
AKT1.WT.2	-0.42																											
CDC42.T1N	-0.44																											
Treatment	Score																											
AKT1.E19K	0.214																											
AKT1.E19K	0.565																											
AKT1.WT.2	0.317																											
CDC42.T1N	0.360																											
BRD-K45440108-001-01-9 PubChem CID : 54646043		NA (in 1 replicates)	<div>-0.44 ± 0.08</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>-0.42</td></tr><tr><td>AKT1.E19K</td><td>-0.47</td></tr><tr><td>AKT1.WT.2</td><td>-0.44</td></tr><tr><td>CDC42.T1N</td><td>-0.53</td></tr></table>	Treatment	Score	AKT1.E19K	-0.42	AKT1.E19K	-0.47	AKT1.WT.2	-0.44	CDC42.T1N	-0.53	<div>0.608 ± 0.326</div> <table><tr><th>Treatment</th><th>Score</th></tr><tr><td>AKT1.E19K</td><td>0.553</td></tr><tr><td>AKT1.E19K</td><td>0.230</td></tr><tr><td>AKT1.WT.2</td><td>0.543</td></tr><tr><td>CDC42.T1N</td><td>0.335</td></tr></table>	Treatment	Score	AKT1.E19K	0.553	AKT1.E19K	0.230	AKT1.WT.2	0.543	CDC42.T1N	0.335			<div>Cytoplasm_Intensity_MaxIntensityEdge_AGP Cells_Texture_Correlation_DNA_3_0 Cells_RadialDistribution_RadialCV_ER_A04 Cells_Intensity_MinIntensityEdge_AGP Cells_Texture_Intensity_Mito_5_0 Cells_RadialDistribution_RadialCV_AGP_204 Cells_Texture_SumAverage_DNA_3_0 Nuclei_Intensity_IntegratedIntensity_AGP Cells_RadialDistribution_RadialCV_Mito_Frac_Mito_204 Nuclei_AreaShape_Zernike_3_1 Cells_AngularSecondMoment_AGP Nuclei_AreaShape_Zernike_3_1 Cells_AngularSecondMoment_AGP Cytoplasm_AreaShape_Zernike_4_2</div>	Total number of assays tested in: 41.
Treatment	Score																											
AKT1.E19K	-0.42																											
AKT1.E19K	-0.47																											
AKT1.WT.2	-0.44																											
CDC42.T1N	-0.53																											
Treatment	Score																											
AKT1.E19K	0.553																											
AKT1.E19K	0.230																											
AKT1.WT.2	0.543																											
CDC42.T1N	0.335																											