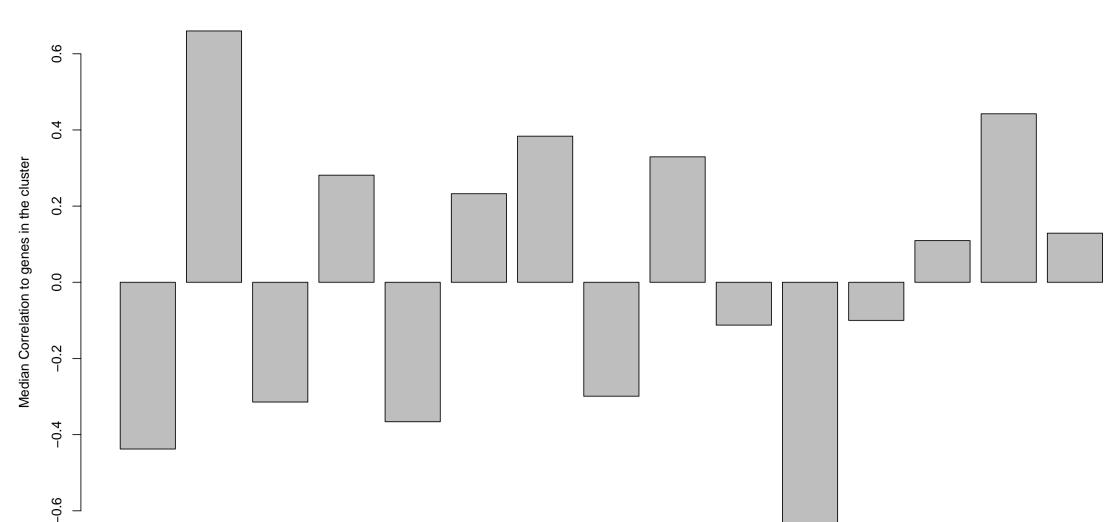
How similar is this cluster to the other clusters?

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	



AKT1_E17K AKT1S1_WT.1 BRAF_WT.1 CCND1_WT.1 CDKN1A_WT CEBPA_WT.1 CSNK1A1_WT.3 CXXC4_WT DVL3_WT GLI1_WT MAP3K2_WT.1 MYD88_L265P PRKCZ_K281R RBPJ_WT.1 WWTR1_WT AKT3_E17K AKT1S1_WT.2 BRAF_WT.2 CCND1_WT.2 HRAS_G12V CEBPA_WT.2 MAPKAP1_WT STK3_WT.1 TGFBR1_K232R PRKACA_WT.1 MAP3K2_WT.2 MYD88_WT PRKCZ_WT.1 RBPJ_WT.2 YAP1_WT.1 AKT3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PIK3R1_WT.1 MAP2K4_WT.2 MOS_WT.2 MAP2K4_WT.1 JUN_WT.2 SKS3_WT.2 STK3_WT.2 TGFBR1_WT.2 RHOA_Q63L YAP1_WT.3 PRKCA_K568R RAF1_WT.2 MAP2K4_WT.1 MAP2K5_WT WAP2K4_WT.1 MAP2K5_WT WAP2K5_WT WAP2K5_WT

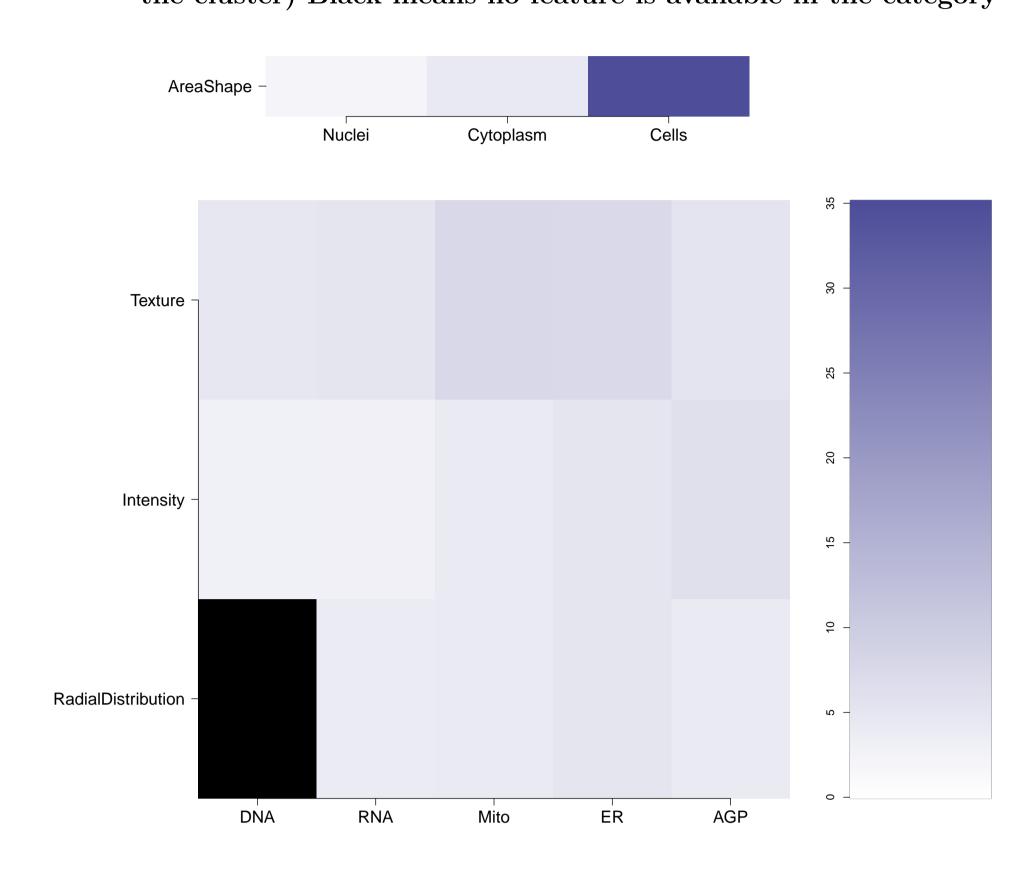
Top 5 genes	negatively	correlated	\mathbf{to}	the	cluster

	Expert Ann	otation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
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?



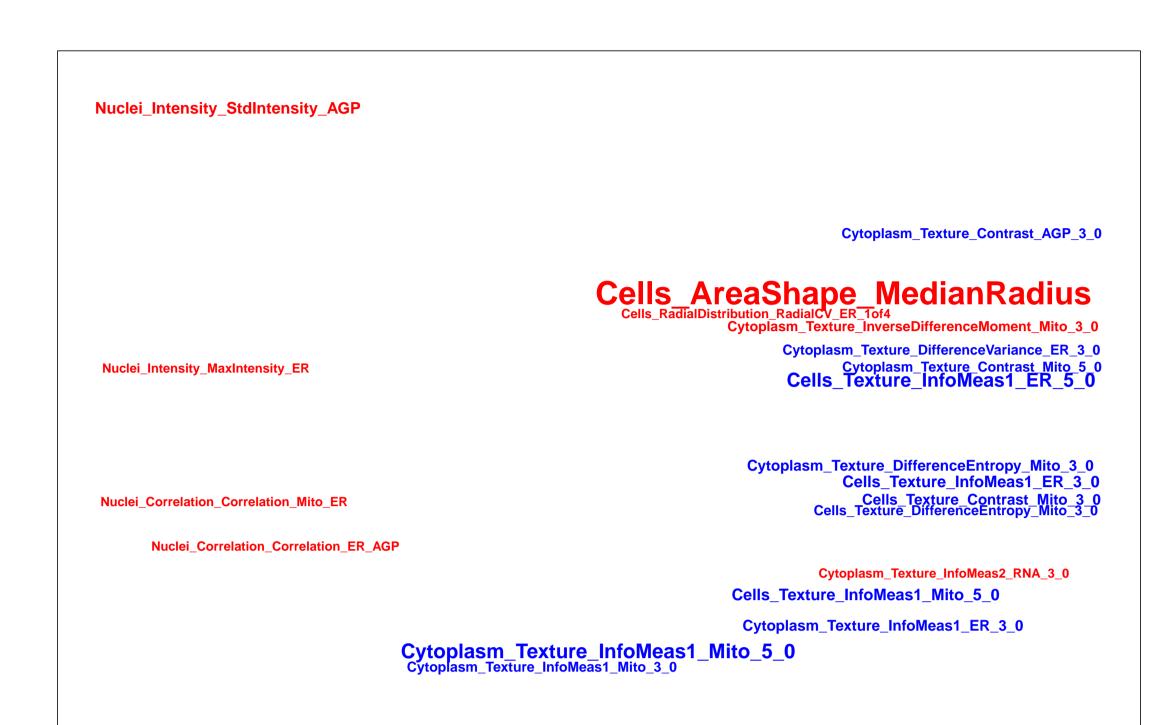
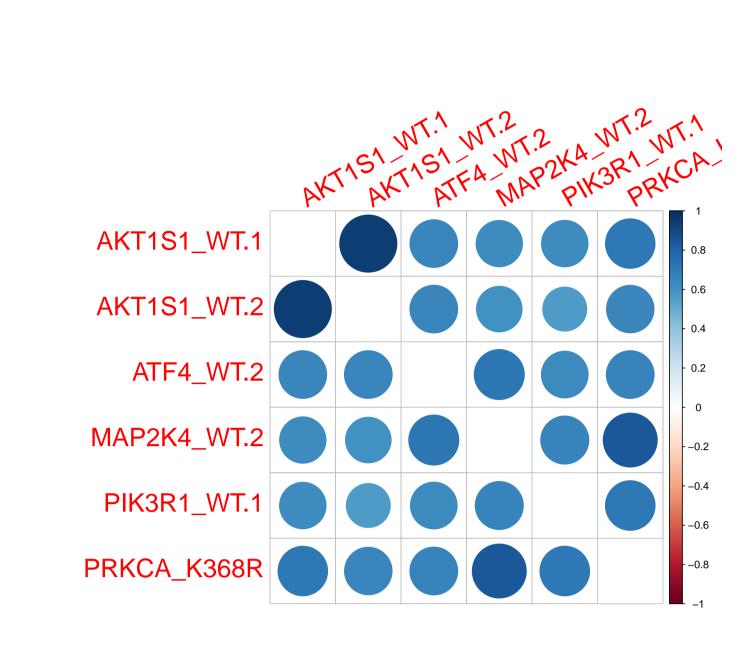
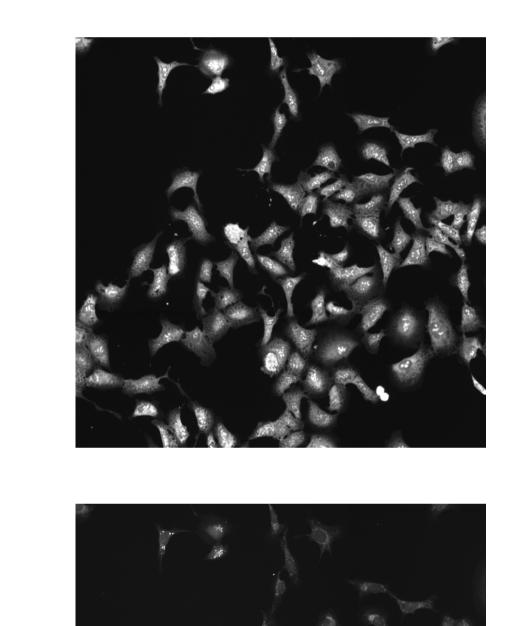


Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

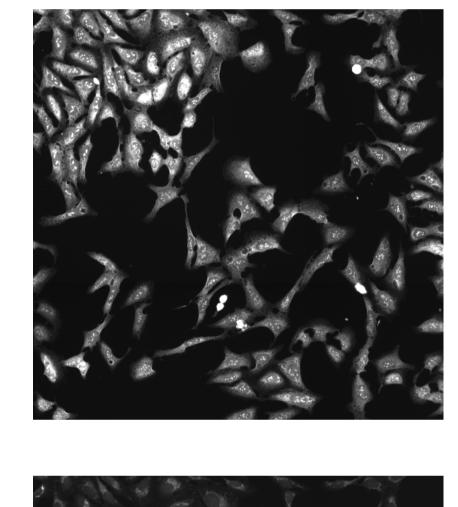




RNA

Mito

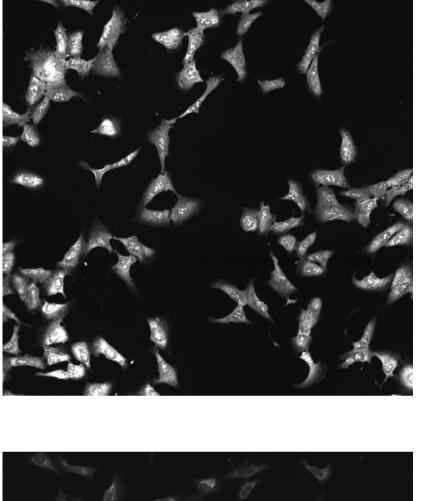
Empty



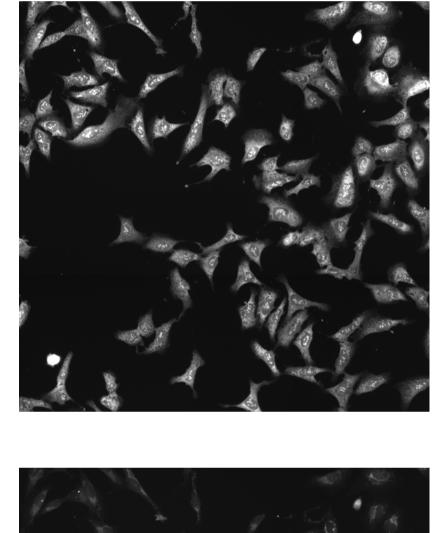
 $AKT1S1_WT.1$



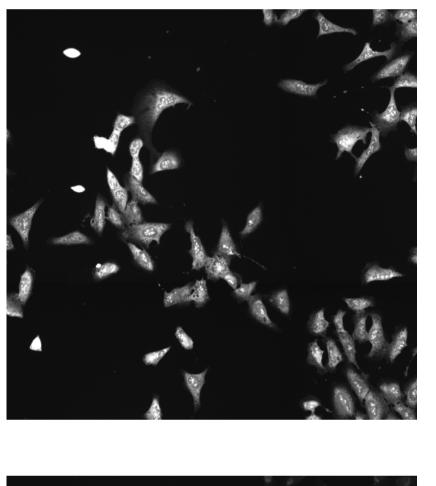
 $AKT1S1_WT.2$



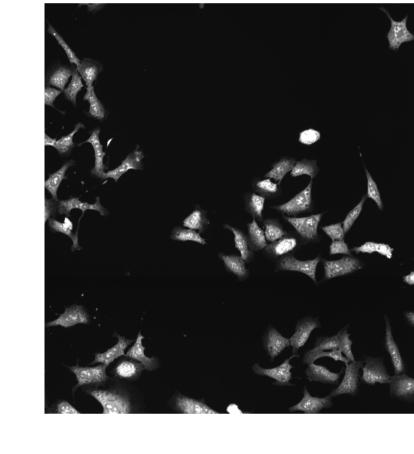
 $ATF4_WT.2$



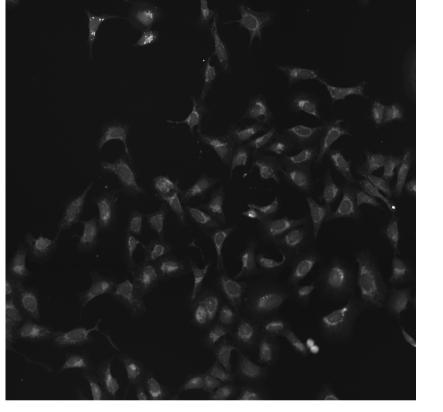
 $MAP2K4_WT.2$

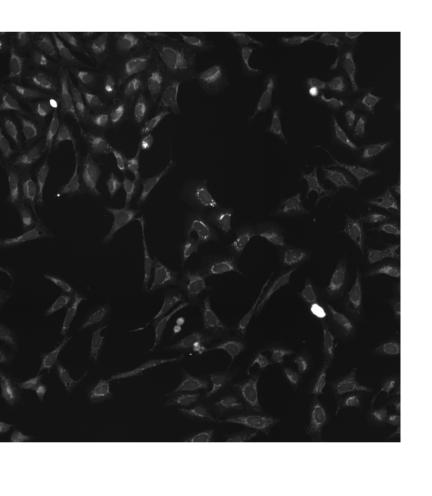


PIK3R1_WT.1



PRKCA_K368R





compound

rank when

scored

against genes

in cluster

using L1000

profiling \pm

standard

deviation;

for individual

Mean \pm

standard

deviation

correlation

between

compound

and each

gene in

cluster;

Tables

contain data

for individual

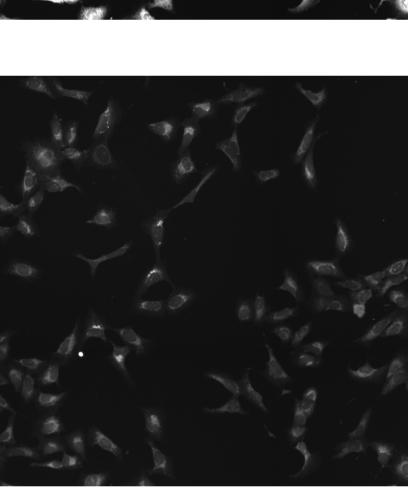


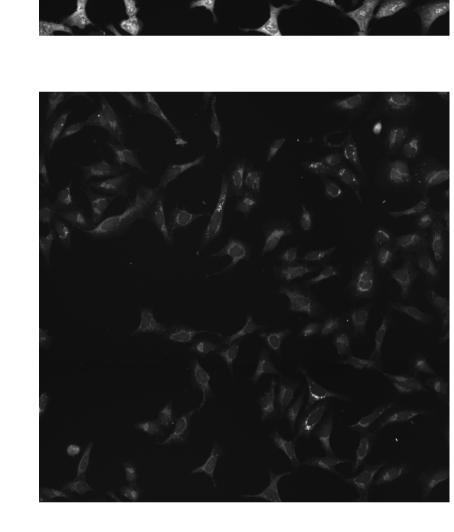
How similar is the compound signature to the gene clusters in

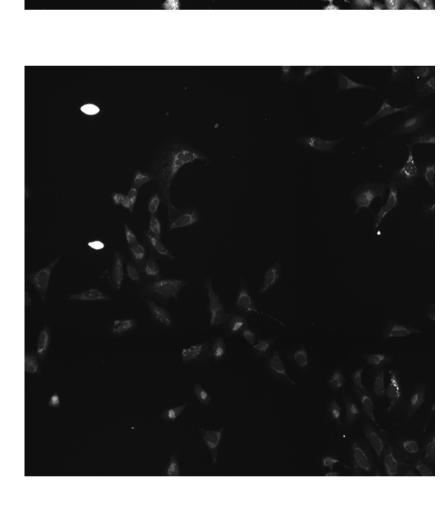
this experiment? (Yellow and red lines correspond to

top/bottom 1st and 5th percentile DMSO correlation to all

the genes)







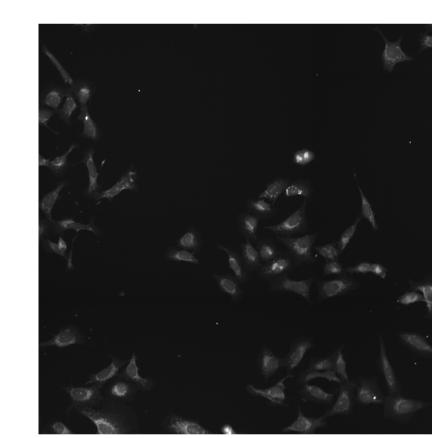
Distinguishing individual features for the compound relative to

untreated samples. Black means a mismatch; i.e. active (= high

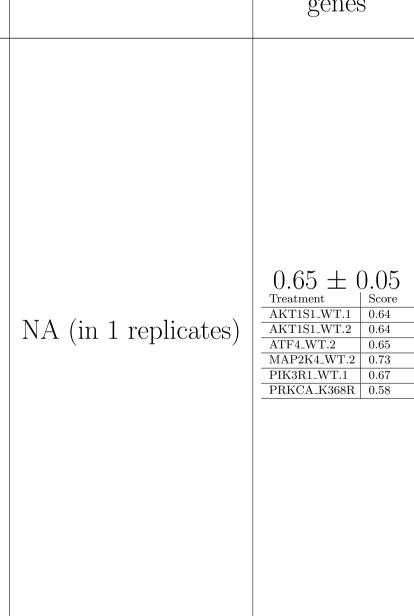
z-score in magnitude) in the compound, and either inactive (=

small z-score in magnitude) or oppositely active in the gene

cluster



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure
BRD-K59496950-001-06-2 SMR000008290 AC1LDHEO ASN 08222509 MLS000068187 MLS002538128 HMS2502P09 ZINC1337997 ZINC01337997 PubChem CID: 648117	



Mean pairwise

replicates

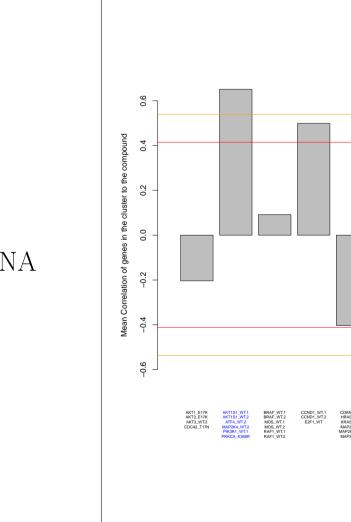
correlation of the

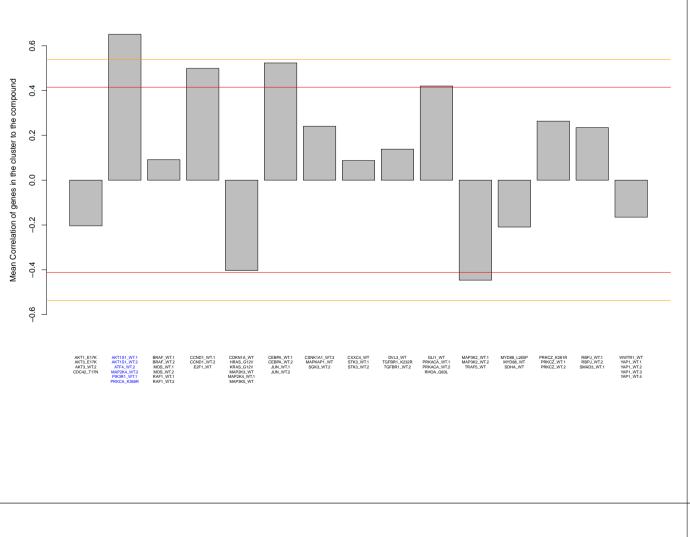
compound signature

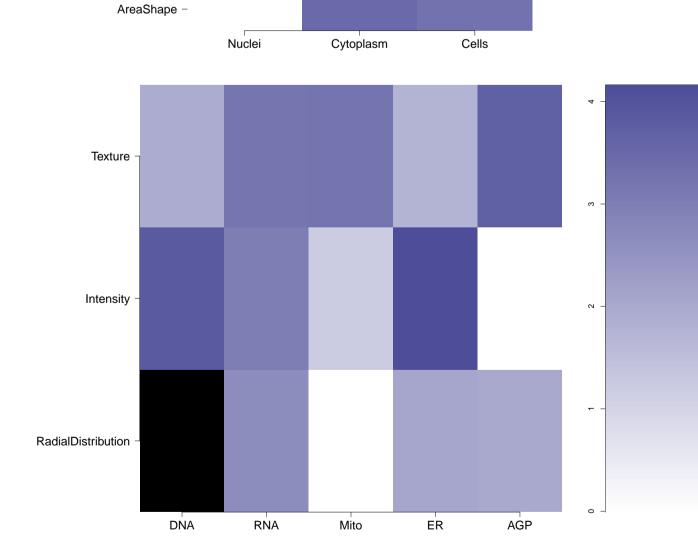
(95th DMSO

replicate correlation

is 0.52)

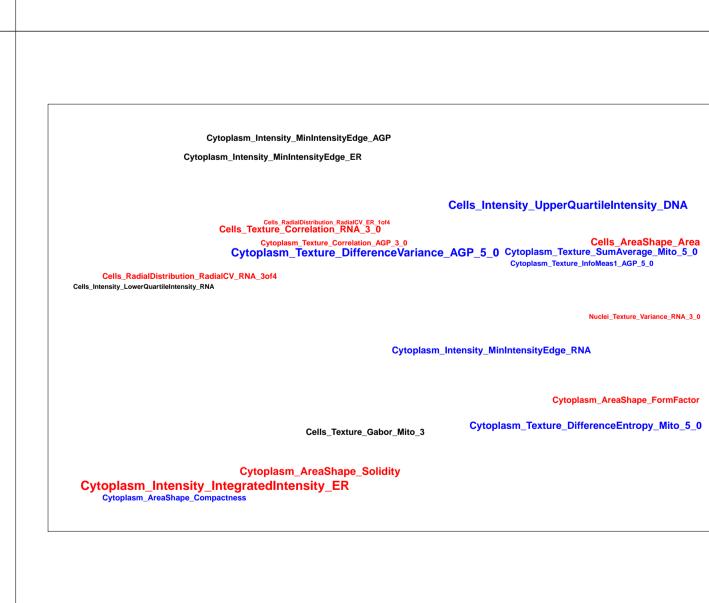


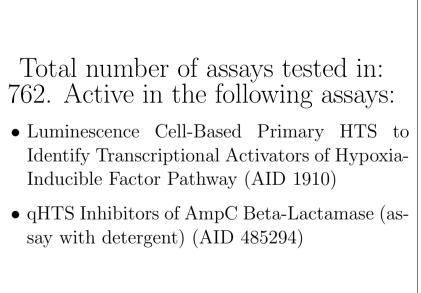




Common distinguishing feature categories in the compound and

genes in the cluster relative to the untreated samples



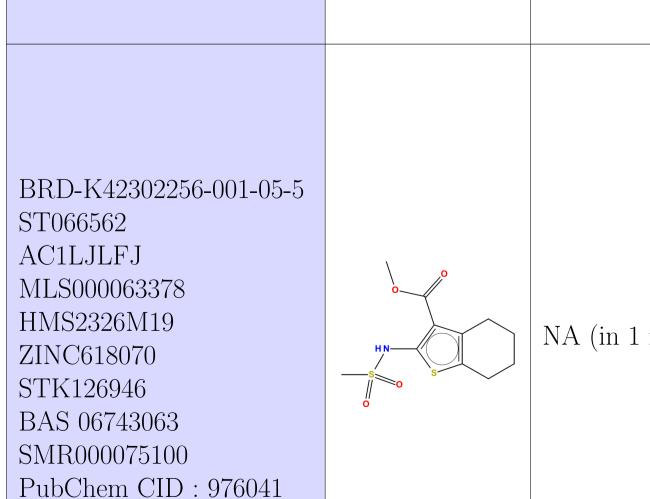


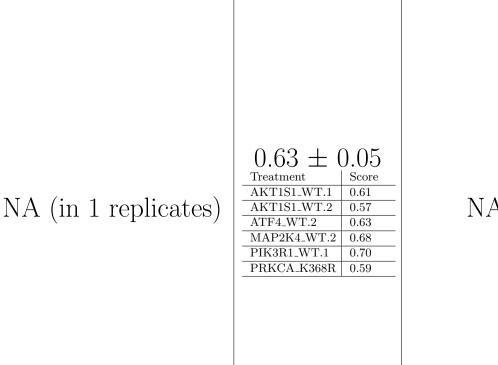
Number of PubChem assays in which

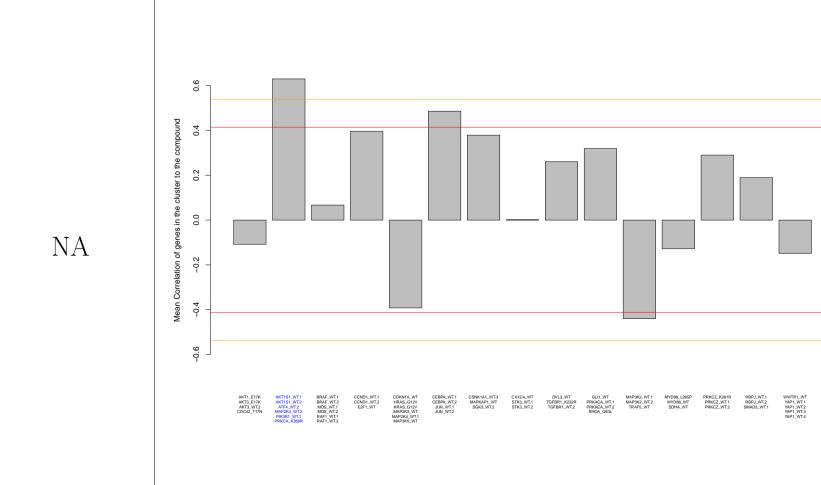
the compound was tested; assays in

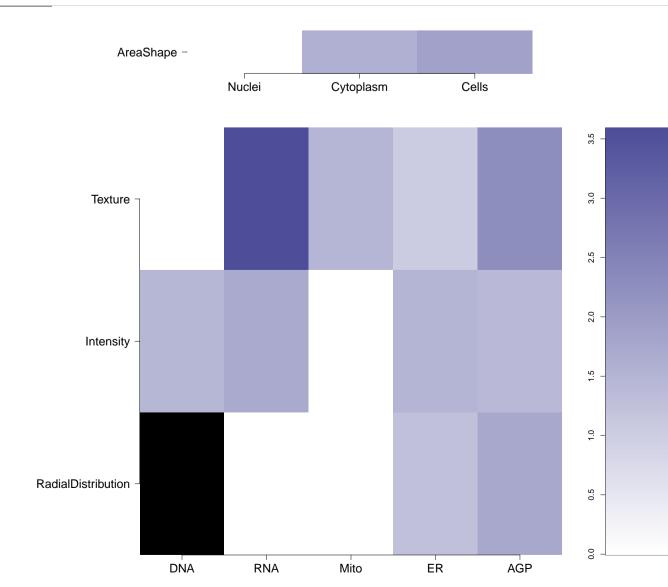
which the compound was active are

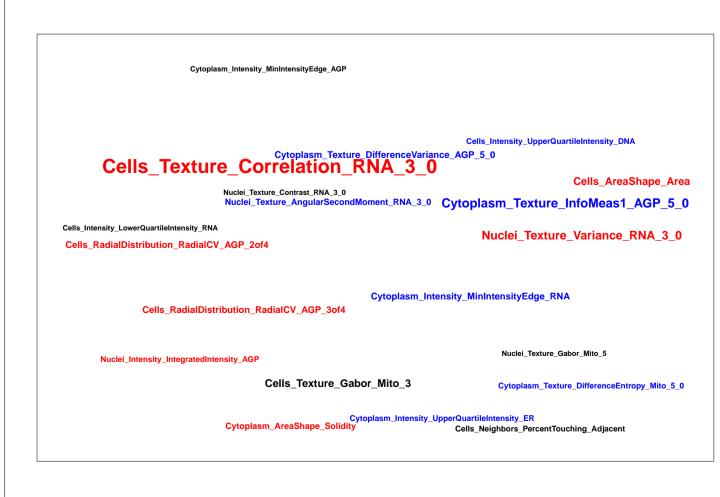
itemized











Total number of assays tested in: 777. Active in the following assays:
• qHTS Assay for Inhibitors of HADH2 (Hydroxyacyl-Coenzyme A Dehydrogenase, Type II) (AID 886)
• qHTS Assay for Inhibitors of Bacillus subtilis

Sfp phosphopantetheinyl transferase (PPTase) (AID 1490)• A qHTS for Small Molecule Inhibitors of Shiga

Toxin (AID 2315)

