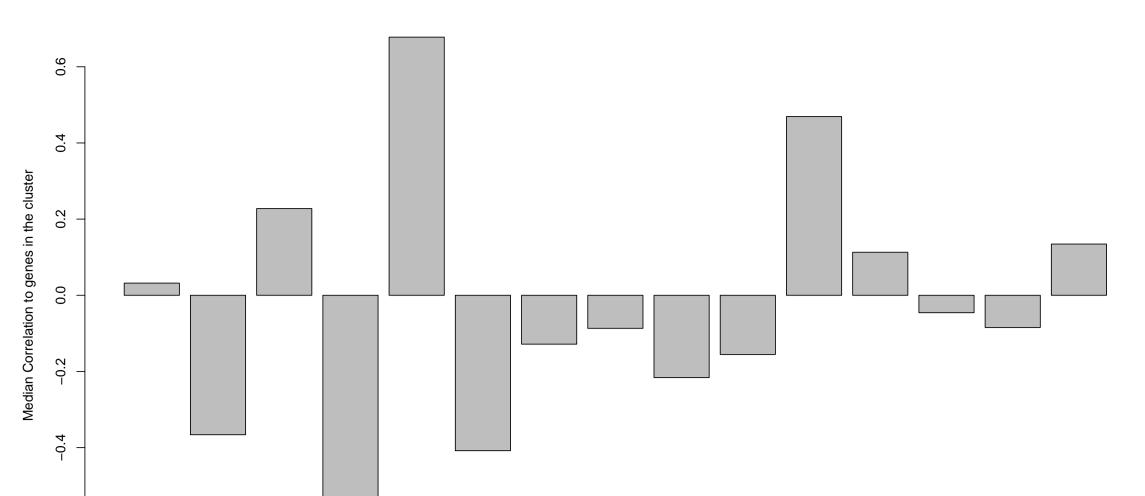
How similar is this cluster to the other clusters?

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

	Expert Annotation		
Treatment	Pathway	Regulation Type	
CDKN1A_WT	Canonical Cell Cycle	Inhibitor	
MAP3K5_WT	Canonical MAPK	Activator	
MAP2K4_WT.1	Canonical MAPK	Activator	
MAP2K3_WT	Canonical MAPK	Activator	
KRAS_G12V	RTK	Activator	
HRAS_G12V	RTK	Activator	



		Top 5	genes	negatively	correlated	to	the cluster
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	•	0 0	•	
	Expert Ann	notation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
E2F1_WT	Canonical Cell Cycle	Activator	-0.59	0.09
CCND1_WT.2	Canonical Cell Cycle	Activator	-0.58	0.08
$CDK2_WT.1$	Canonical Cell Cycle	Activator	-0.49	0.11
$DDIT4_WT$	Canonical TOR	Inhibitor	-0.49	0.07
PER1_WT.2	Circadian Rhythm	Activator	-0.49	0.09

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 ATS4_WT.2 MOS_WT.2 MAP2K4_WT.2 MOS_WT.2 STK3_WT.2 STK3_WT.2 STK3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PRKCA_K368R RAF1_WT.2 MAP2K4_WT.1 MAP2K6_WT.1 MAP2K4_WT.1 MAP2K6_WT.1 MAP2

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?

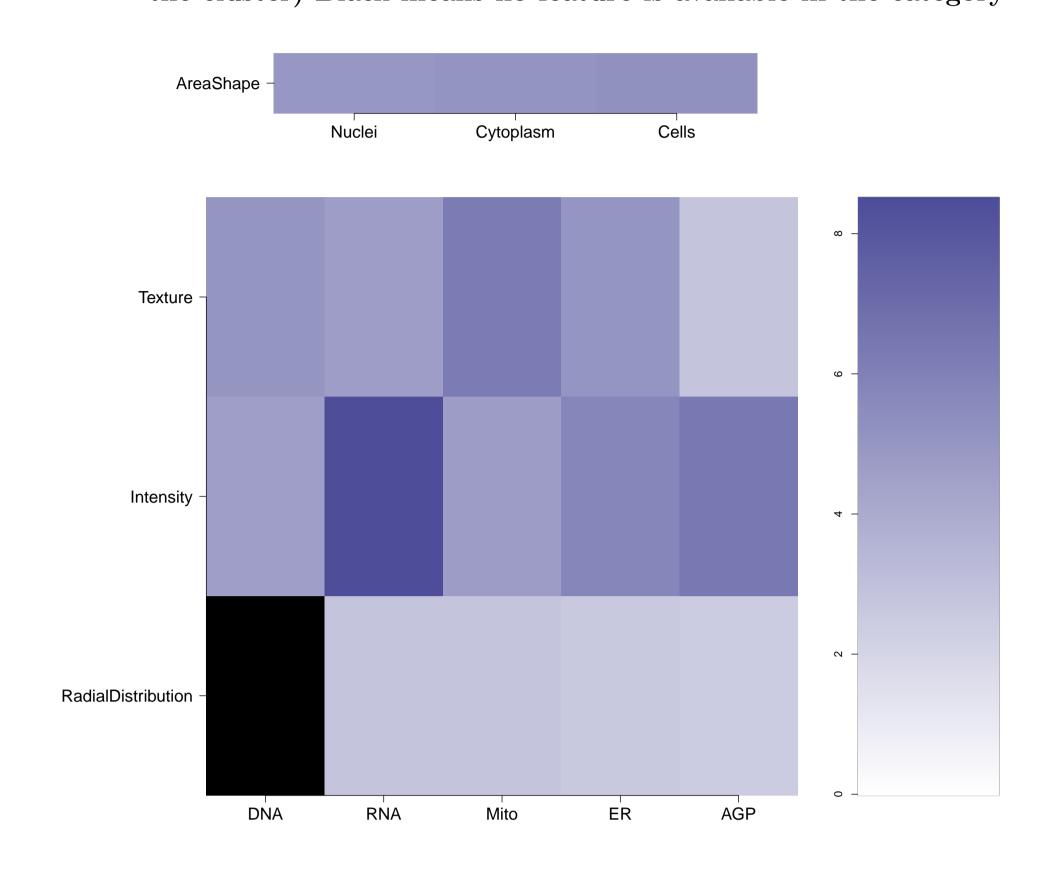
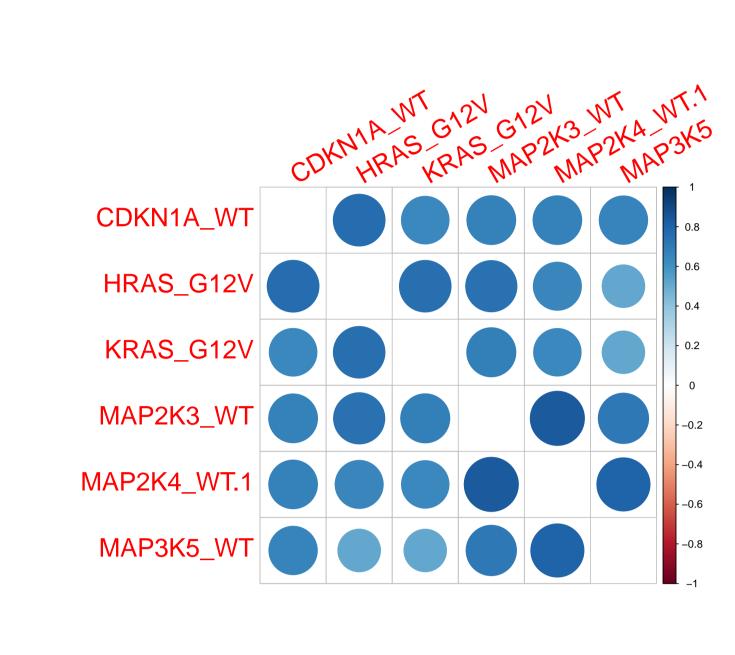
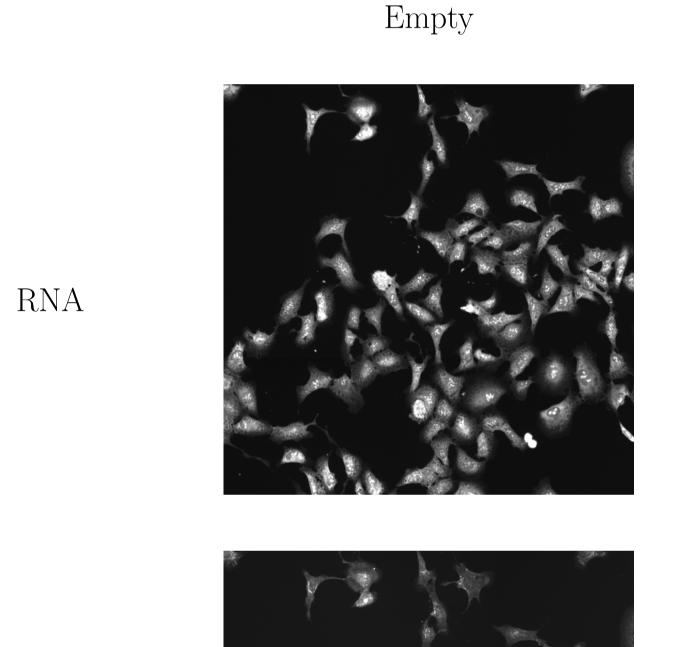
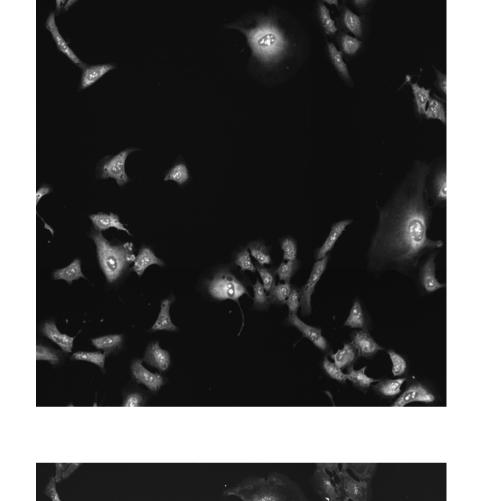




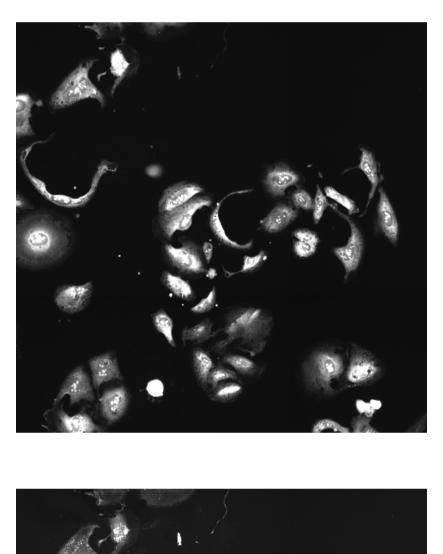
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



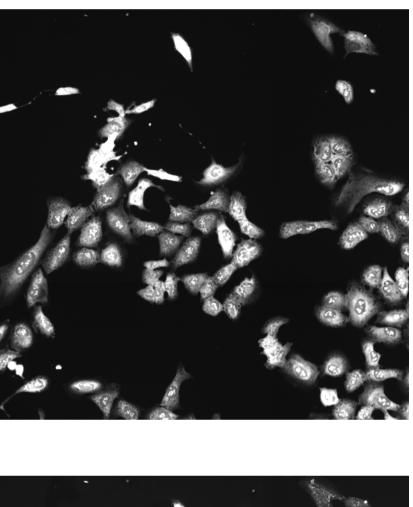




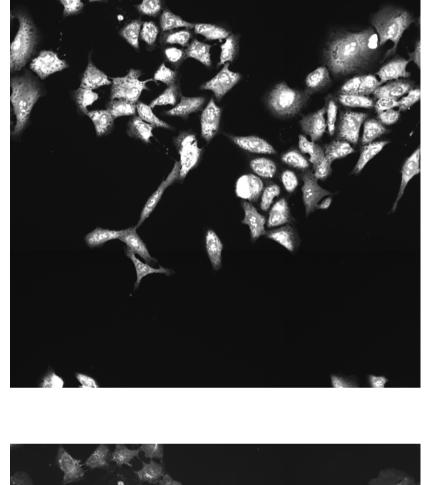
CDKN1A_WT



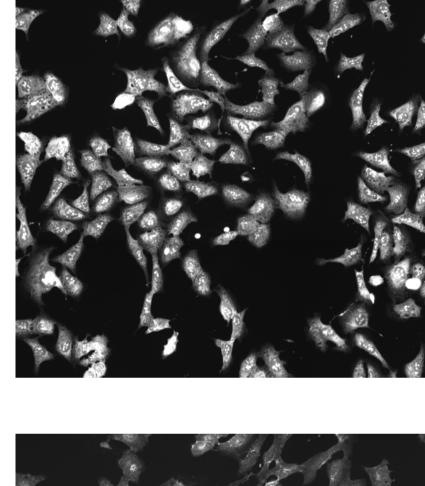
 $HRAS_{-}G12V$



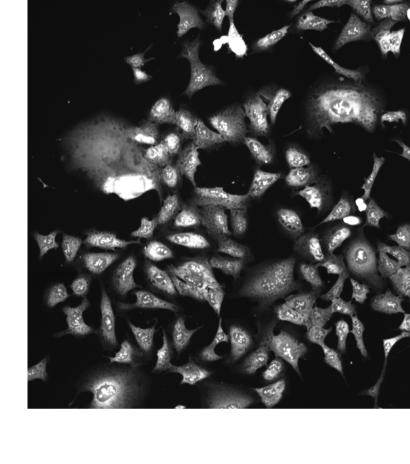
 $KRAS_{-}G12V$



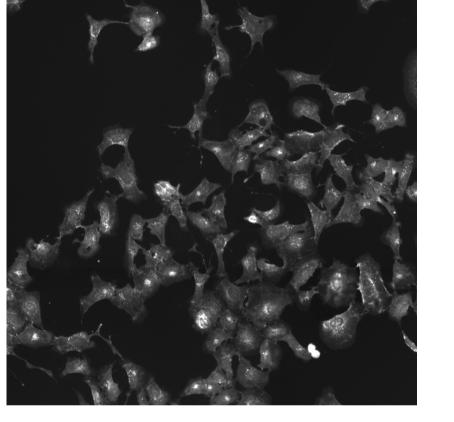
 $MAP2K3_WT$

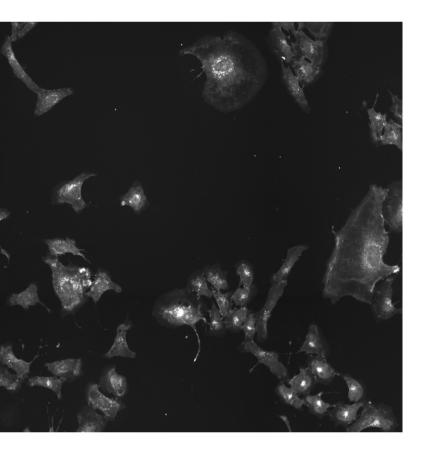


 $MAP2K4_WT.1$



 $MAP3K5_WT$





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;

contain data

for individual

 0.70 ± 0.10 Treatment | Score
CDKN1A_WT | 0.81

HRAS_G12V 0.79 KRAS_G12V 0.54 MAP2K3_WT 0.66 MAP2K4_WT.1 0.65 MAP3K5_WT 0.72

Mean pairwise

replicates

correlation of the

compound signature

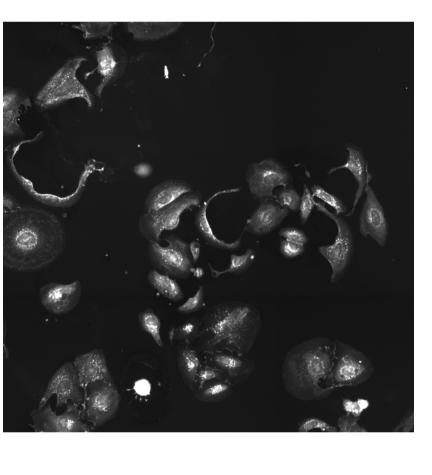
(95th DMSO

replicate correlation

is 0.54)

0.95 (in 4 replicates)

0.93 (in 3 replicates)



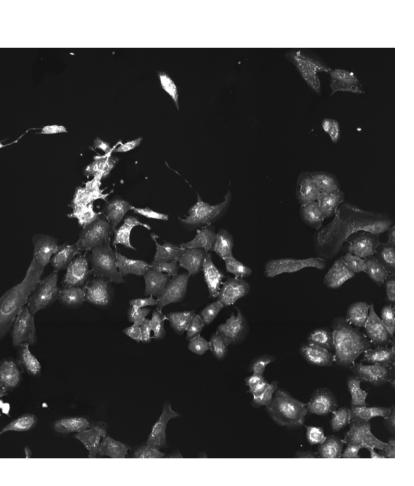
How similar is the compound signature to the gene clusters in

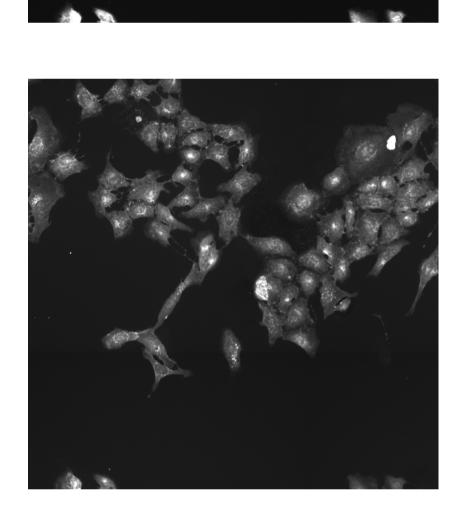
this experiment? (Yellow and red lines correspond to

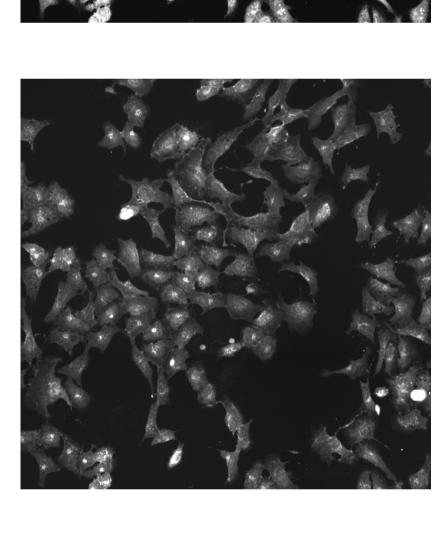
top/bottom 1st and 5th percentile DMSO correlation to all

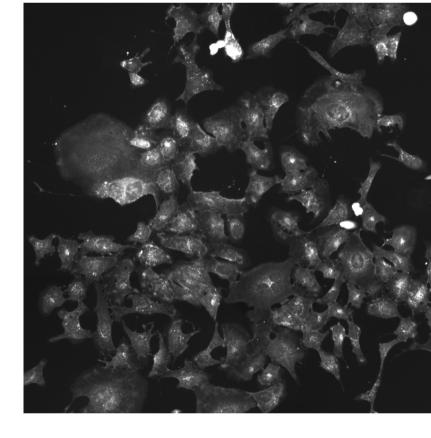
the genes)

AKT1_E17K AKT1S1_WT1 BRAF_WT1 COND1_WT1 CDNH_A_WT CEBPA_WT1 CSNK1A1_WT3 CXXC4_WT D/L3_WT GLIT_WT MAP3K2_WT1 MYD88_LBSP PRXC2_XG81R RBPJ_WT1 WWTR1_WT AKT3_E17K AKT1S1_WT2 BRAF_WT2 CXXD1_WT2 LPAN_A_WT2 LPAN_A_WT2 LPAN_A_WT2 LPAN_A_WT3_LPAN_A_WT









Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemi
BRD-A81850691-001-05-0 F1734-0091 AC1NJT6B MLS000697333 HMS2580B04 SMR000238009 ST50110788 PubChem CID: 4902407	

BRD-K40926874-001-06-3

PubChem CID: 6902822

T6051781

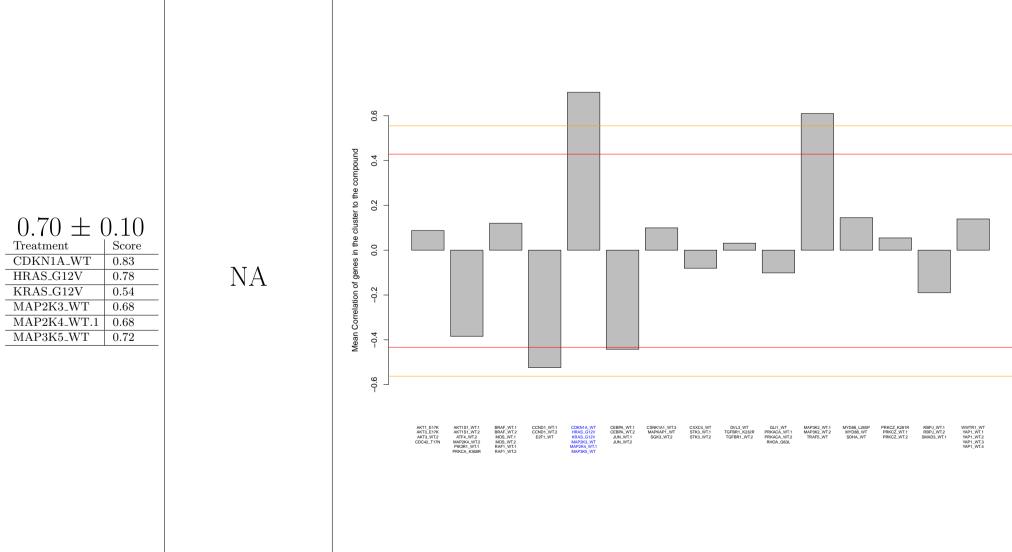
AC1OBTHD

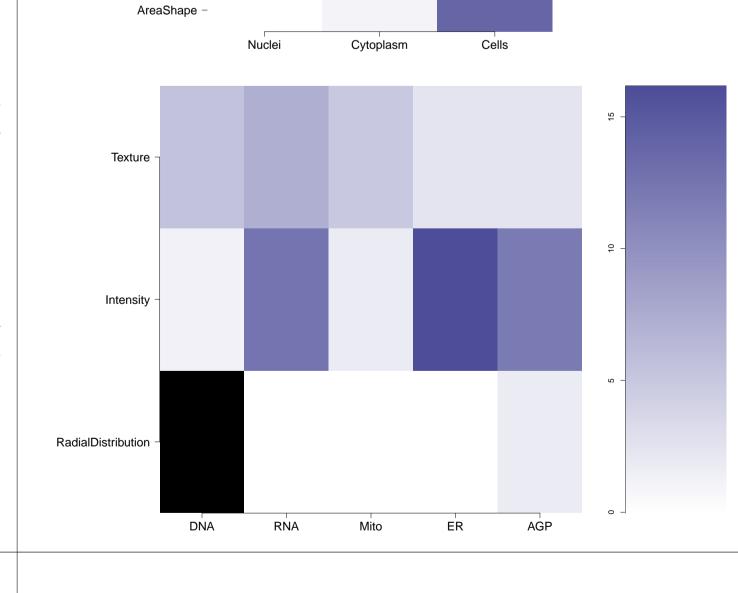
MLS000516321

ZINC12727563

SMR000372882

AGP





Cytoplasm

AreaShape -

Texture -

Intensity -

RadialDistribution -

Common distinguishing feature categories in the compound and

genes in the cluster relative to the untreated samples



Cells_RadialDistribution_RadialCV_ER_1of4

Nuclei_Intensity_IntegratedIntensity_AGP

Cytoplasm_Intensity_IntegratedIntensity_ER

Cells_AreaShape_Area

Nuclei_Texture_SumAverage_DNA_5_0

Cytoplasm_Texture_DifferenceEntropy_Mito_5_0

Nuclei_Texture_DifferenceVariance_DNA_3_0

Cells_Neighbors_PercentTouching_Adjacent

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



Total number of assays tested in: 639. Active in the following assays:

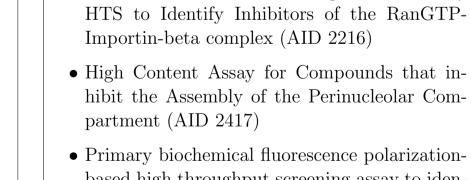
• Fluorescence Cell-Free Homogeneous Primary

Number of PubChem assays in which

the compound was tested; assays in

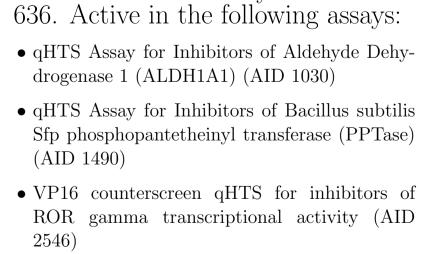
which the compound was active are

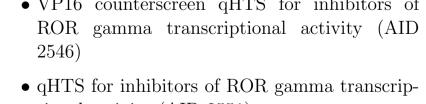
itemized



based high throughput screening assay to identify inhibitors of protein arginine methyltransferase 1 (PRMT1) (AID 652257)

Total number of assays tested in:





- tional activity (AID 2551) • uHTS identification of small molecule inhibitors of tim10-1 yeast via a luminescent as-
- say (AID 463190) • uHTS identification of small molecule inhibitors of tim23-1 yeast via a luminescent as-
- say (AID 463212) • Single concentration confirmation of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463213)
- Single concentration confirmation of small molecule inhibitors of tim23-1 yeast via a luminescent assay (AID 463218)
- HTS-Luminescent assay for inhibitors of ALR by detection of hydrogen peroxide production Measured in Biochemical System Using Plate Reader - 2036-02_Inhibitor_SinglePoint_HTS (AID 485317)
- qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)

