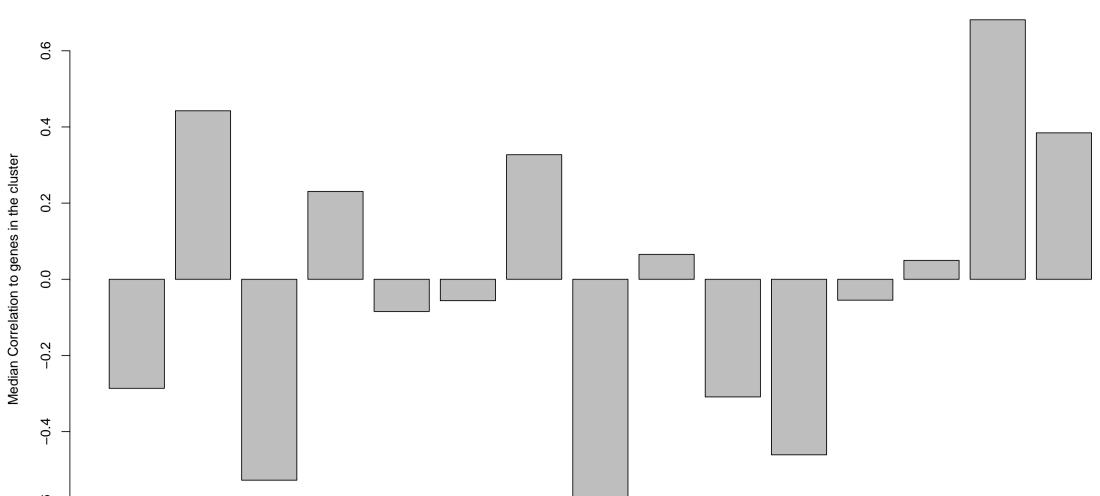
How similar is this cluster to the other clusters?

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

	Expert Annotation		
Treatment	Pathway	Regulation Type	
SMAD3_WT.1	Canonical SMAD	Activator	
RBPJ_WT.1	NOTCH	Activator	
RBPJ_WT.2	NOTCH	Activator	



Top 5 genes negatively	correlated t	o the cluster
------------------------	--------------	---------------

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
RAF1_WT.2	Canonical MAPK	Activator	-0.62	0.06
$CXXC4_WT$	WNT	Inhibitor	-0.60	0.01
$STK3_WT.1$	Canonical Hippo	Activator	-0.60	0.09
MAP3K2_WT.1	Canonical MAPK	Activator	-0.58	0.16
PIK3CB_WT.2	Canonical PI3K/AKT	Activator	-0.55	0.13

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 ATF4_WT.2 MOS_WT.1 E2F1_WT KRAS_G12V JUN_WT.1 SGK3_WT.2 STK3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PRKCA_WT.1 RAF1_WT.1 RAF1_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP3K5_WT.1 MAP3K5_WT

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?

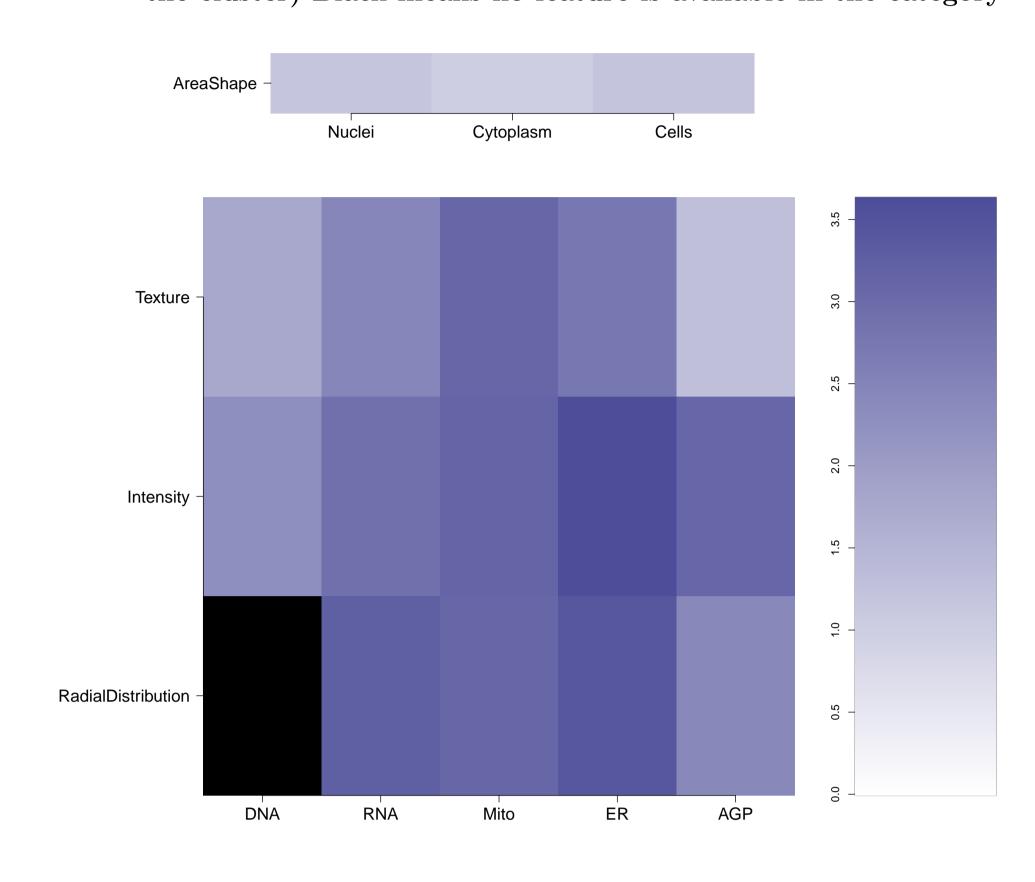
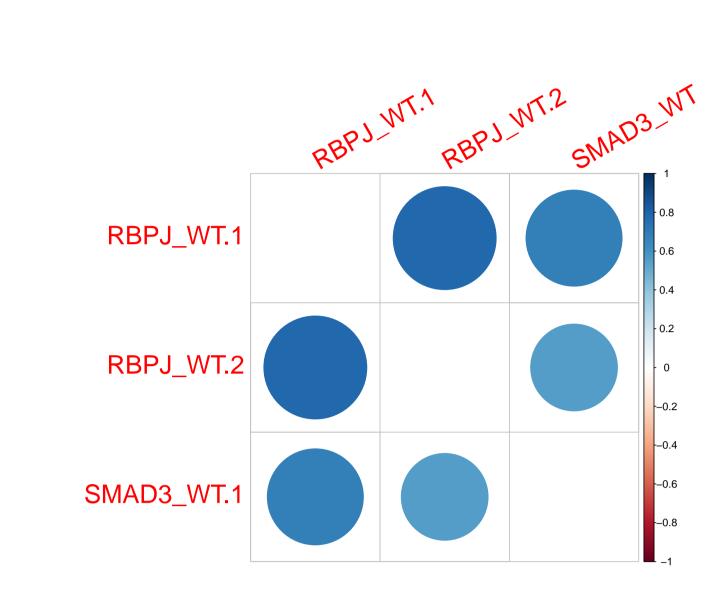
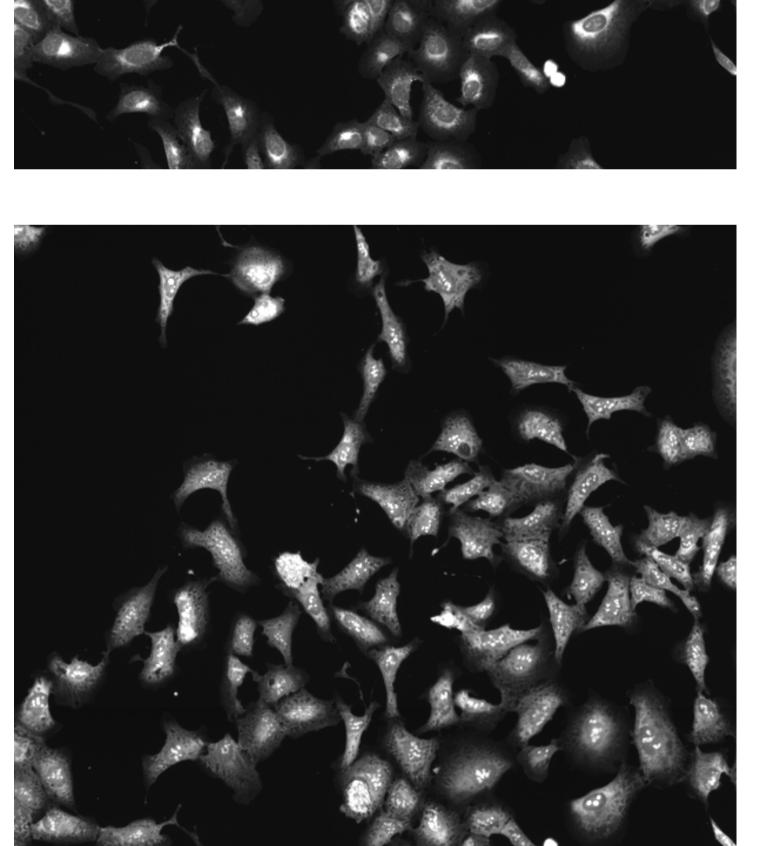




Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



Empty



Mean \pm

standard

deviation

correlation

between

compound

and each

gene in

cluster;

Tables

contain data

for individual

genes

compound

rank when

scored

against genes

in cluster

using L1000

profiling \pm

standard

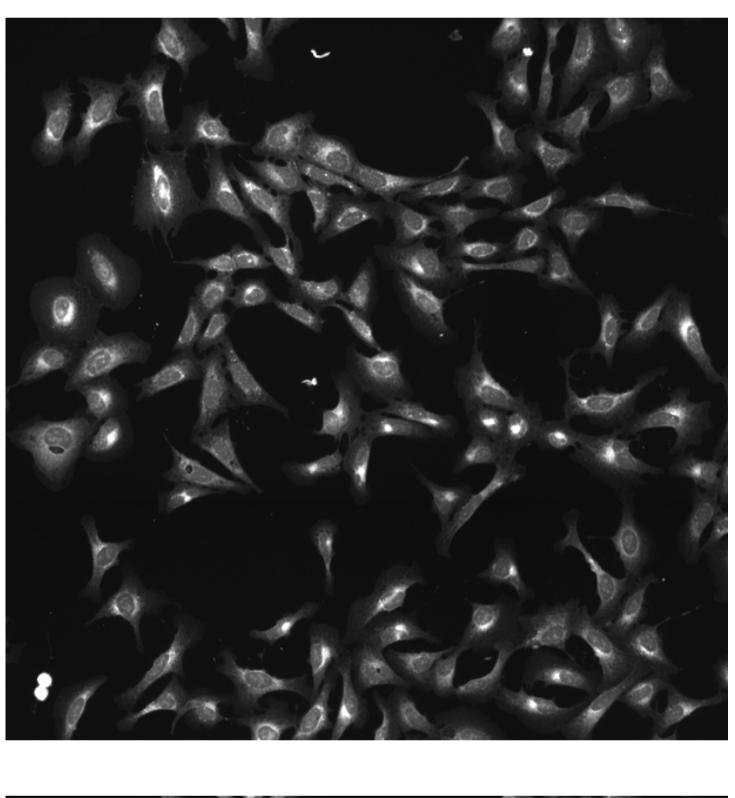
deviation;

Tables

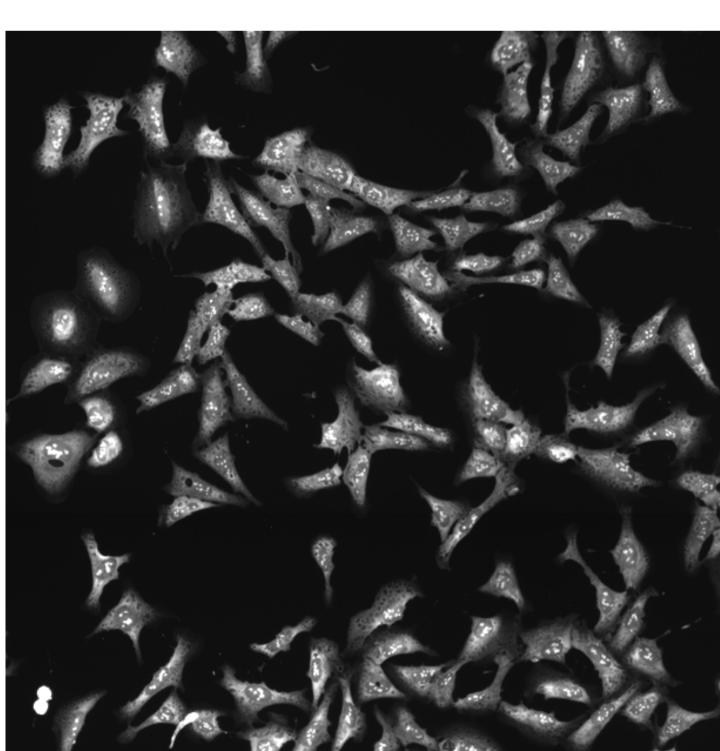
contain data

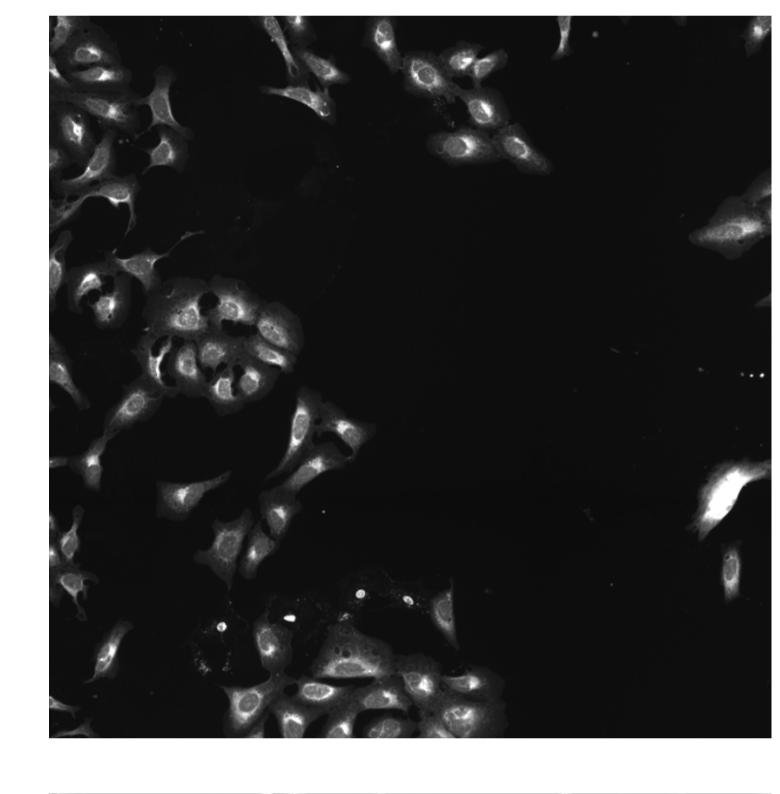
for individual

genes

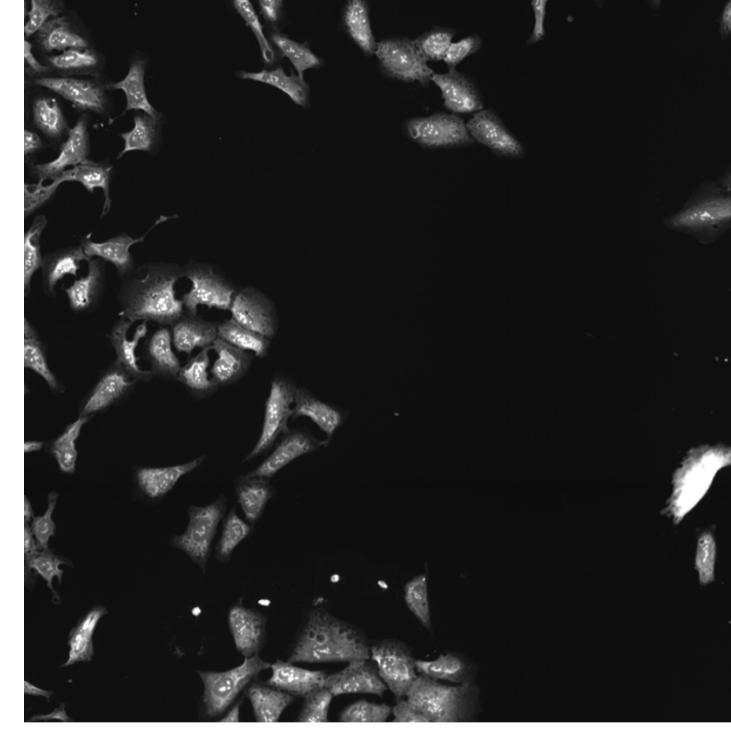


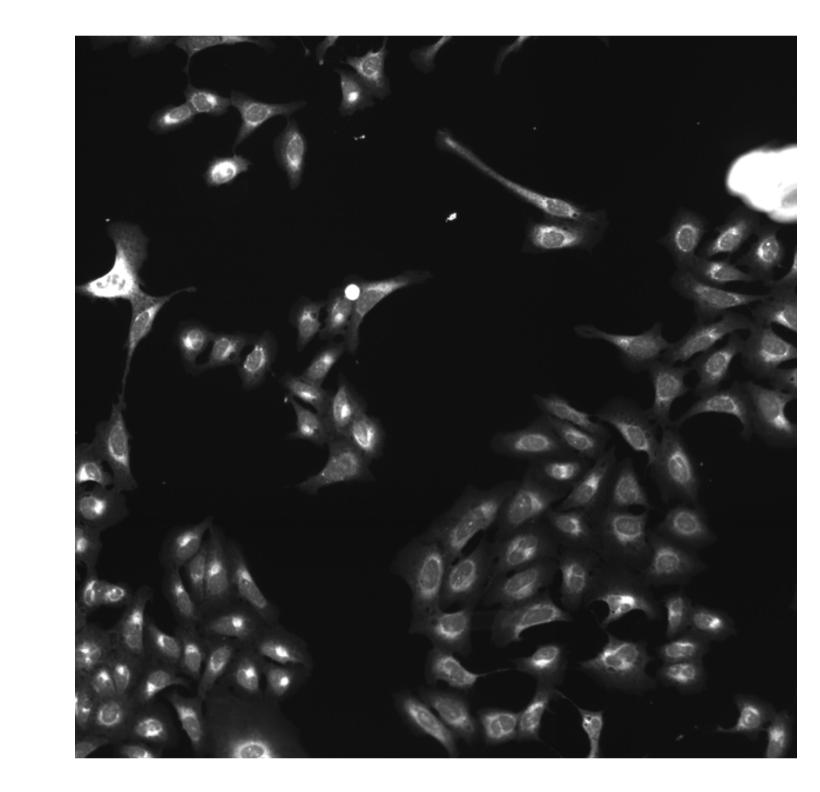
 $RBPJ_WT.1$



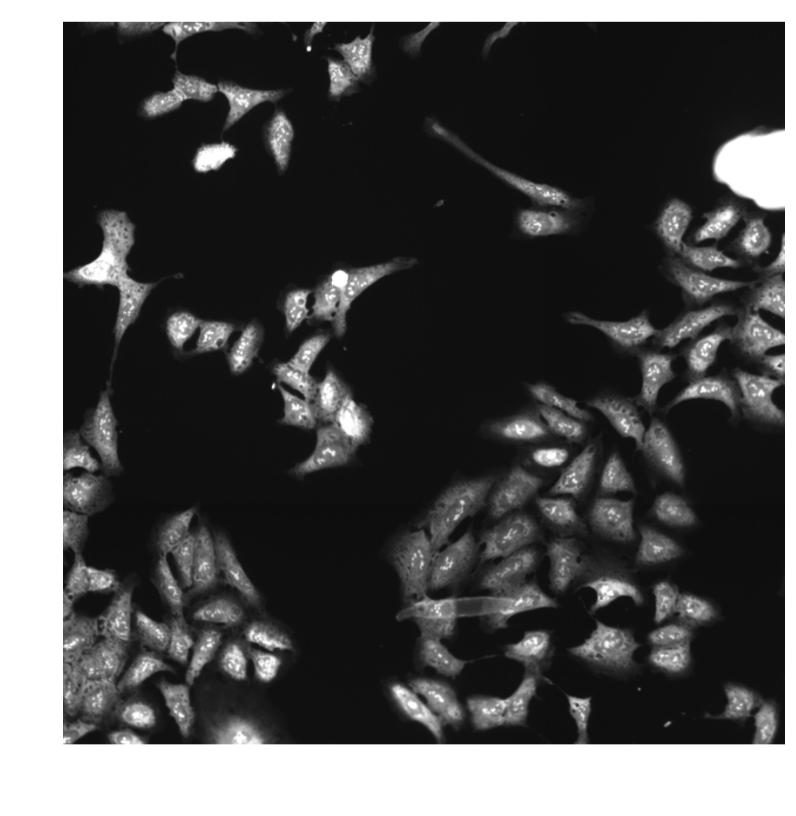


 $RBPJ_WT.2$





 $SMAD3_WT.1$



Nuclei_Texture_InverseDifferenceMoment_Mito_5_0

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-K04968712-001-05-7 MLS000858711 SMR000458790 AC1MDPY6	F N N N N N N N N N N N N N N N N N N N

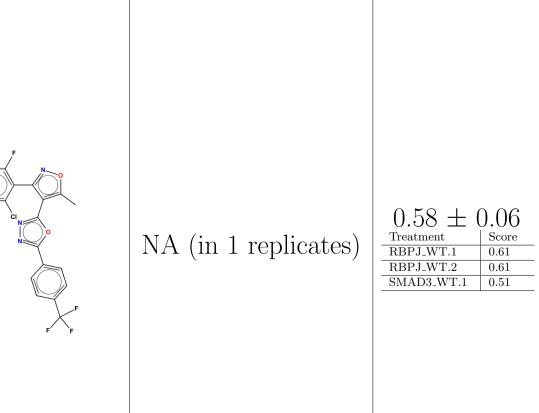
BDBM45738

HMS2811A04

ZINC1034543

ZINC01034543

PubChem CID : 2814981



Mean pairwise

replicates

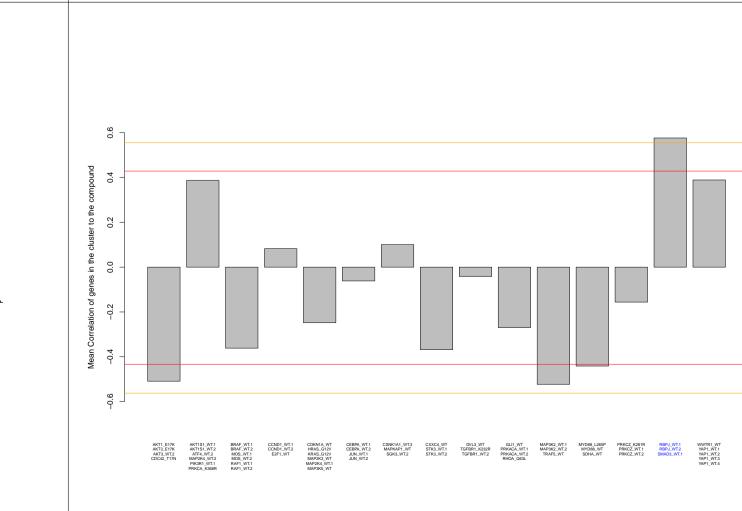
correlation of the

compound signature

(95th DMSO

replicate correlation

is 0.54)

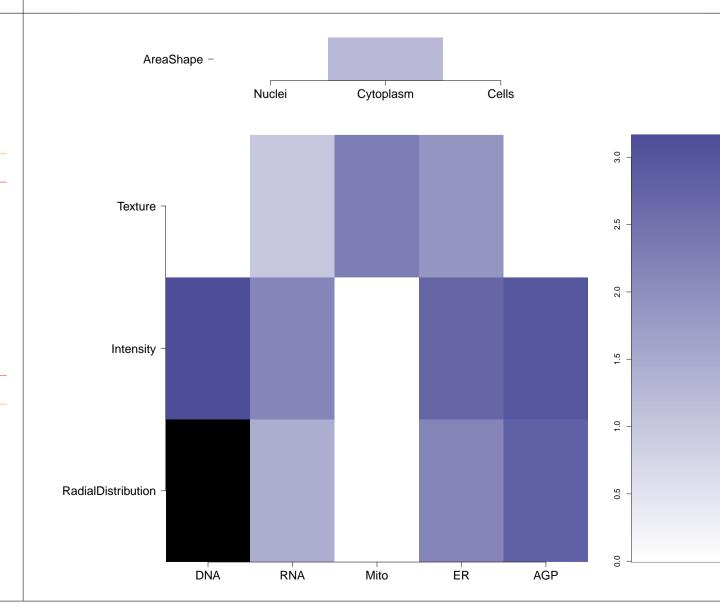


How similar is the compound signature to the gene clusters in

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

Cytoplasm_Intensity_MaxIntensityEdge_AGP

Cells_RadialDistribution_RadialCV_AGP_2of4

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: 545. Active in the following assays:
• Factor XIIa 1536 HTS (AID 800)
• Primary qHTS for delayed death inhibitors of

- the malarial parasite plastid, 48 hour incubation (AID 504832) • Primary qHTS for delayed death inhibitors of the malarial parasite plastid, 96 hour incubation (AID 504834)
- Confirmation screen for delayed death inhibitors of the malarial parasite plastid, 96 hour incubation (AID 504848)
- Confirmation screen for delayed death inhibitors of the malarial parasite plastid, 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)

