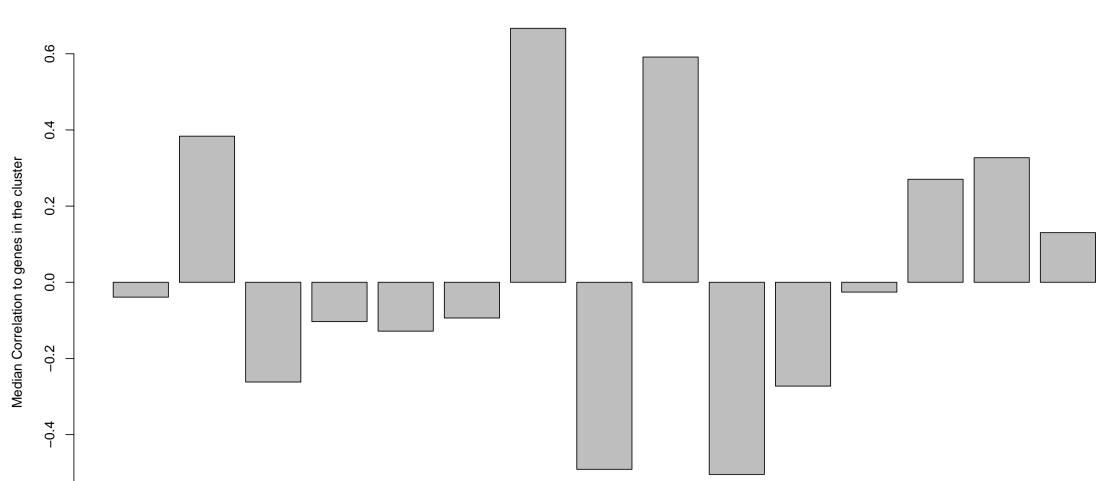
How similar is this cluster to the other clusters?

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

	Expert Annotation	
Treatment	Pathway	Regulation Type
MAPKAP1_WT	Canonical TOR	Activator
$SGK3_WT.2$	Canonical TOR	Activator
CSNK1A1_WT.3	Canonical WNT	Inhibitor



				_	_
Top 5 genes	negatively	correlated	to	the	cluster
<b>-</b> op			•	U	0101001

	Expert Anno	otation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PRKACA_WT.2	Canonical PKA	Activator	-0.60	0.02
PRKACA_WT.1	Canonical PKA	Activator	-0.51	0.05
CXXC4_WT	WNT	Inhibitor	-0.50	0.12
STK3_WT.2	Canonical Hippo	Activator	-0.49	0.26
PIK3CB_WT.2	Canonical PI3K/AKT	Activator	-0.46	0.09

AKT1\_E17K AKT1S1\_WT.1 BRAF\_WT.1 CCND1\_WT.1 CDKN1A\_WT CEBPA\_WT.1 CSNK1A1\_WT.3 CXC4\_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 PRKCA\_K368R RAF1\_WT.2 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K4\_WT.1 MAP3K6\_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?

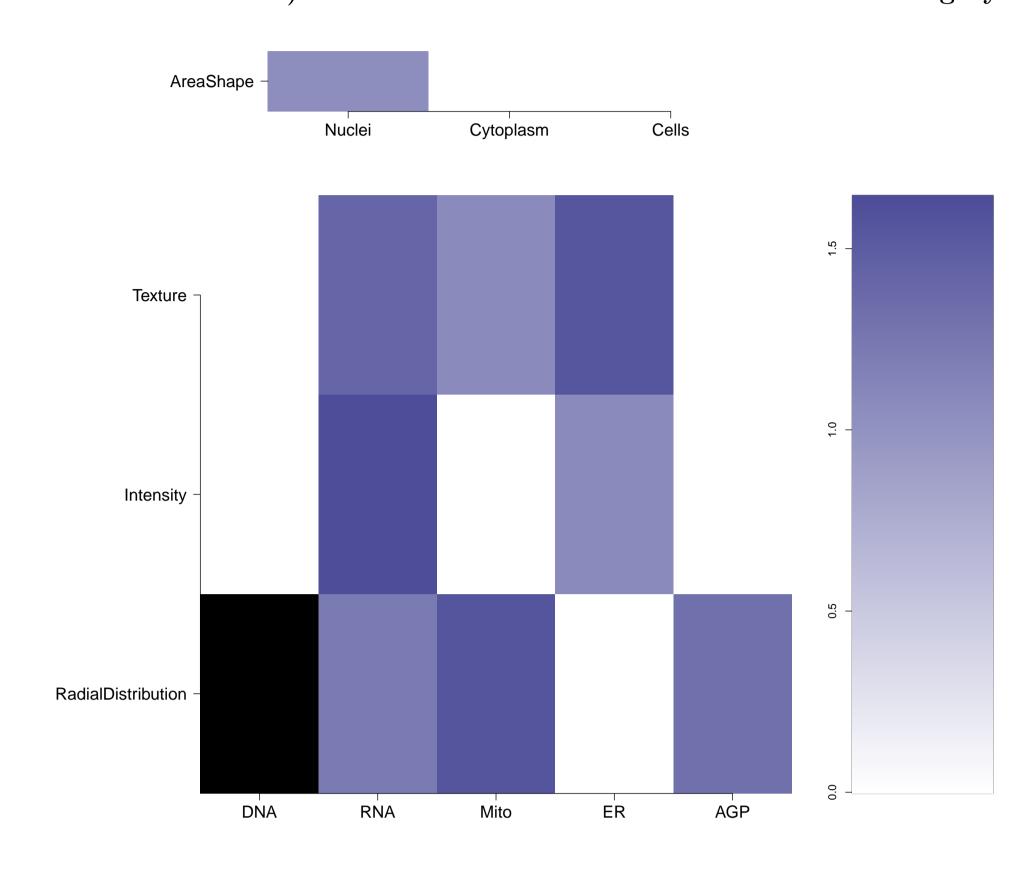
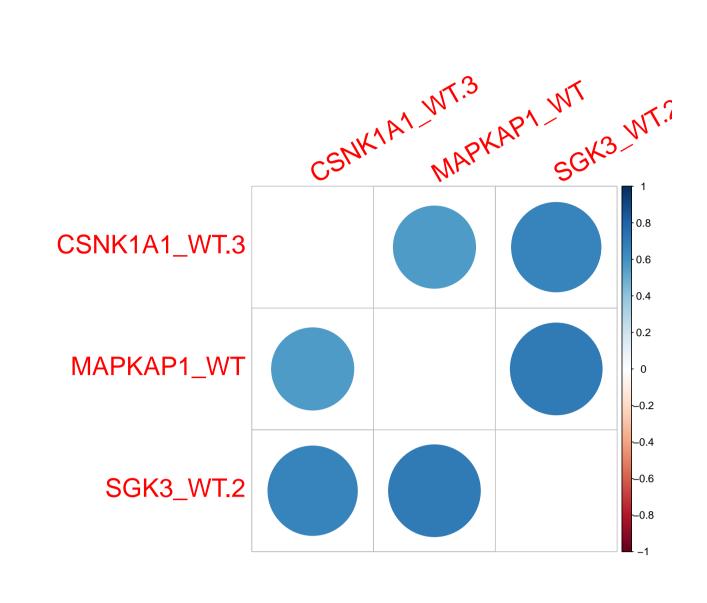
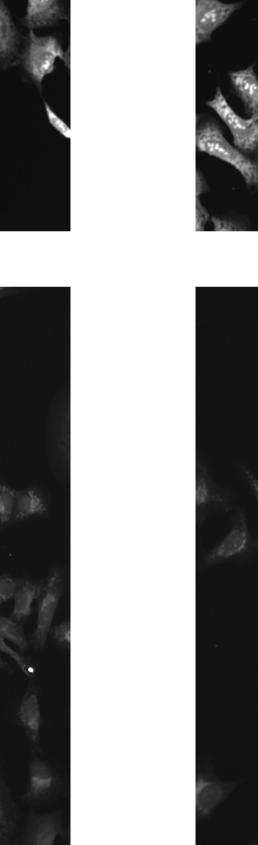


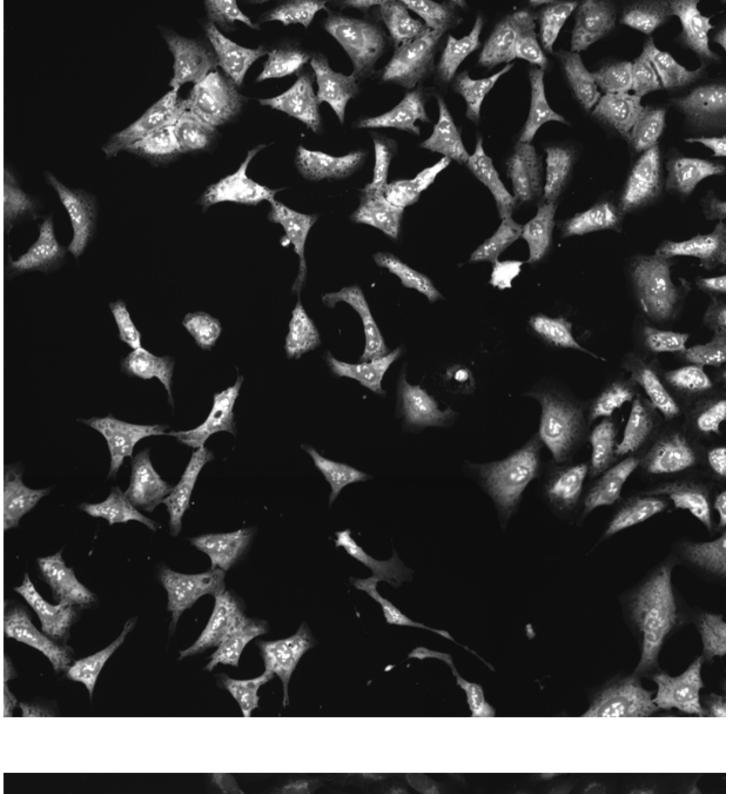


Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

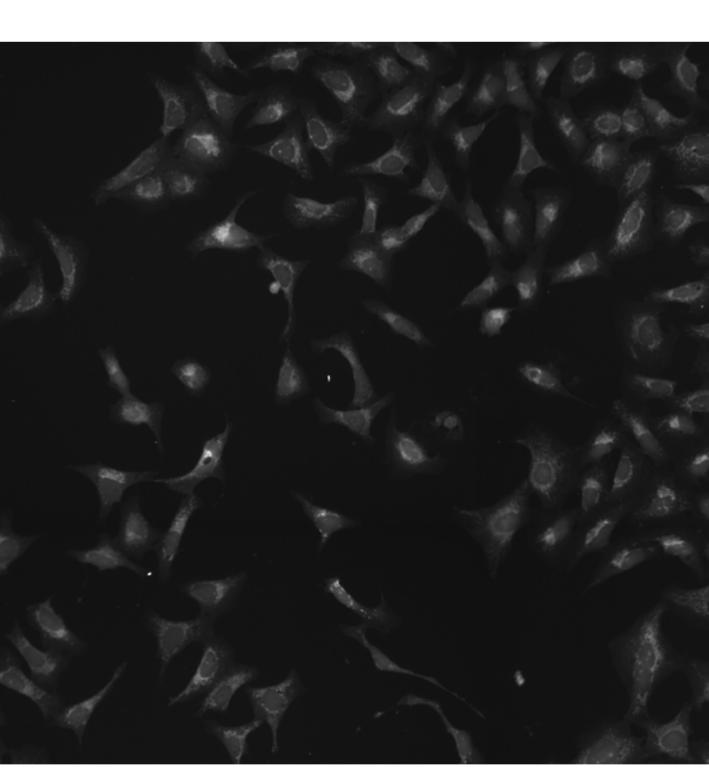


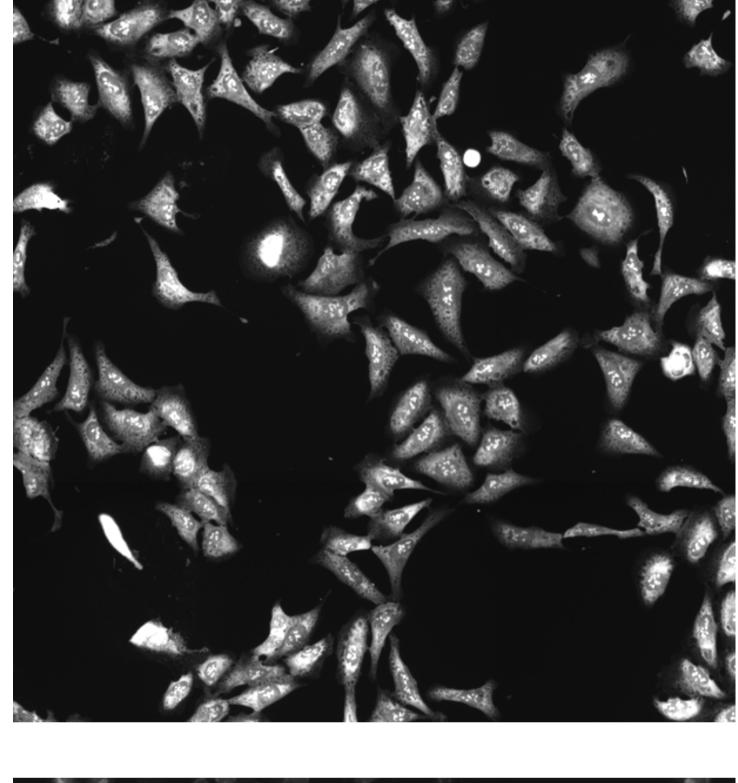
Empty



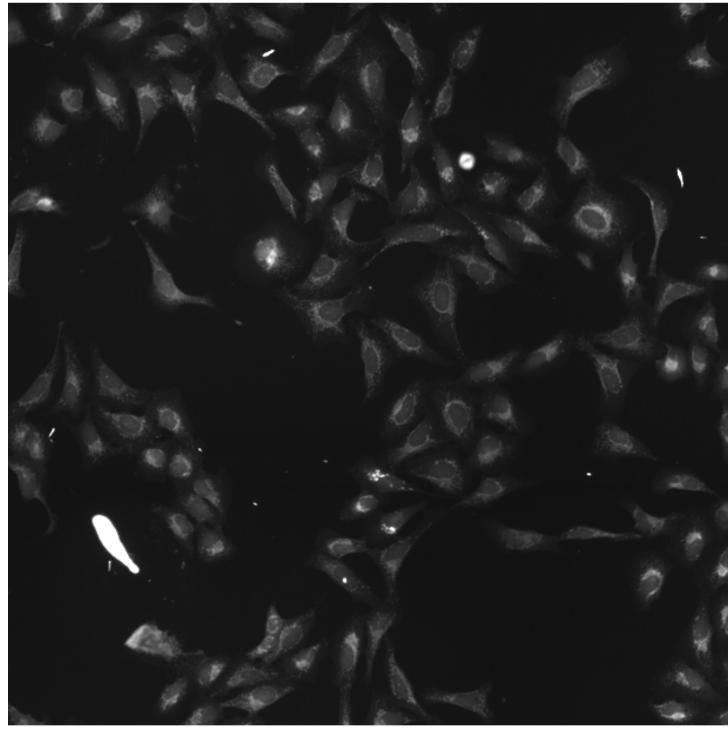


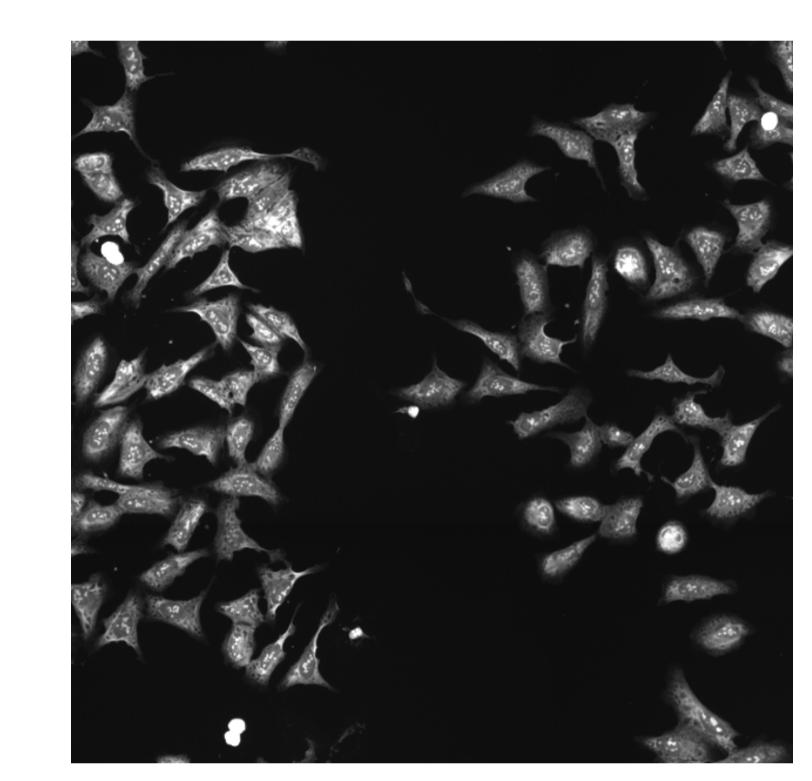
CSNK1A1\_WT.3



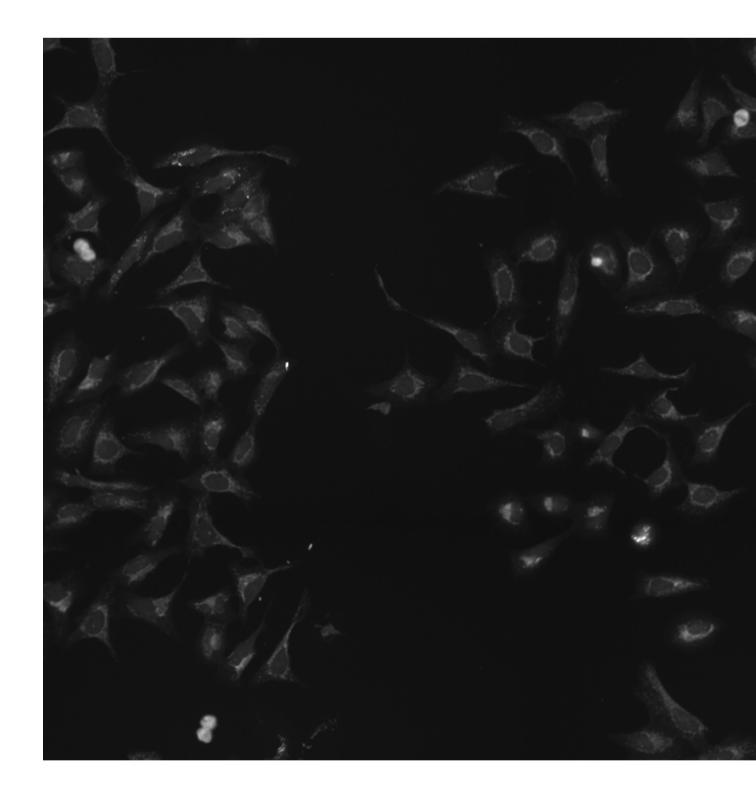


 $MAPKAP1_WT$ 





 $SGK3_WT.2$ 



	5
	(
Mean pairwise	C
replicates	
correlation of the	C
compound signature	6
(95th DMSO	
replicate correlation	
is $0.54$ )	
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	for

Mean ±	Mean
standard	compound
deviation	rank when
correlation	scored
between	against genes
compound	in cluster
and each	using L1000
gene in	profiling ±
cluster;	standard
Tables	deviation; Tables
ontain data	contain data
or individual	for individual
genes	genes
	801100

How similar is the compound signature to the gene clusters
this experiment? (Yellow and red lines correspond to
top/bottom 1st and 5th percentile DMSO correlation to a
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

