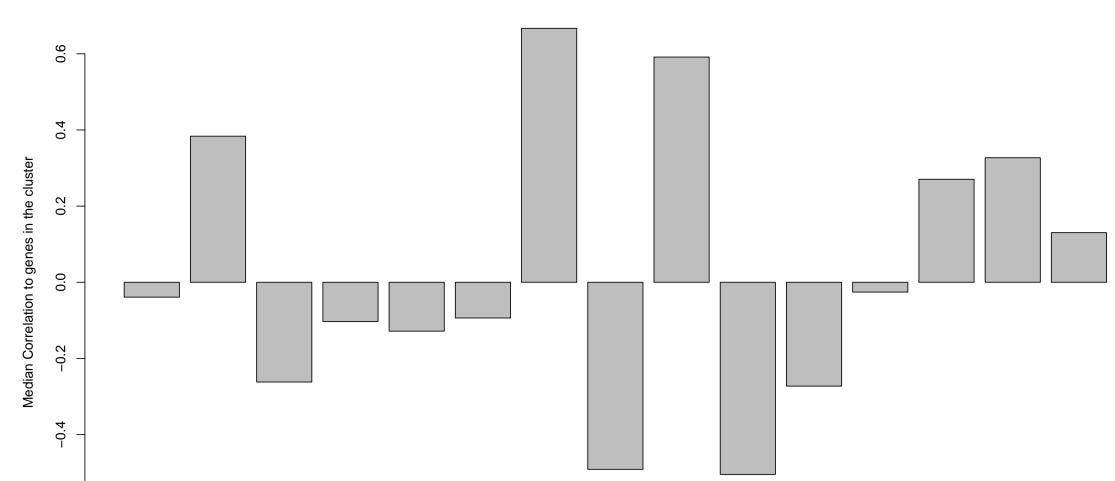
How similar is this cluster to the other clusters?



	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
	0	0				

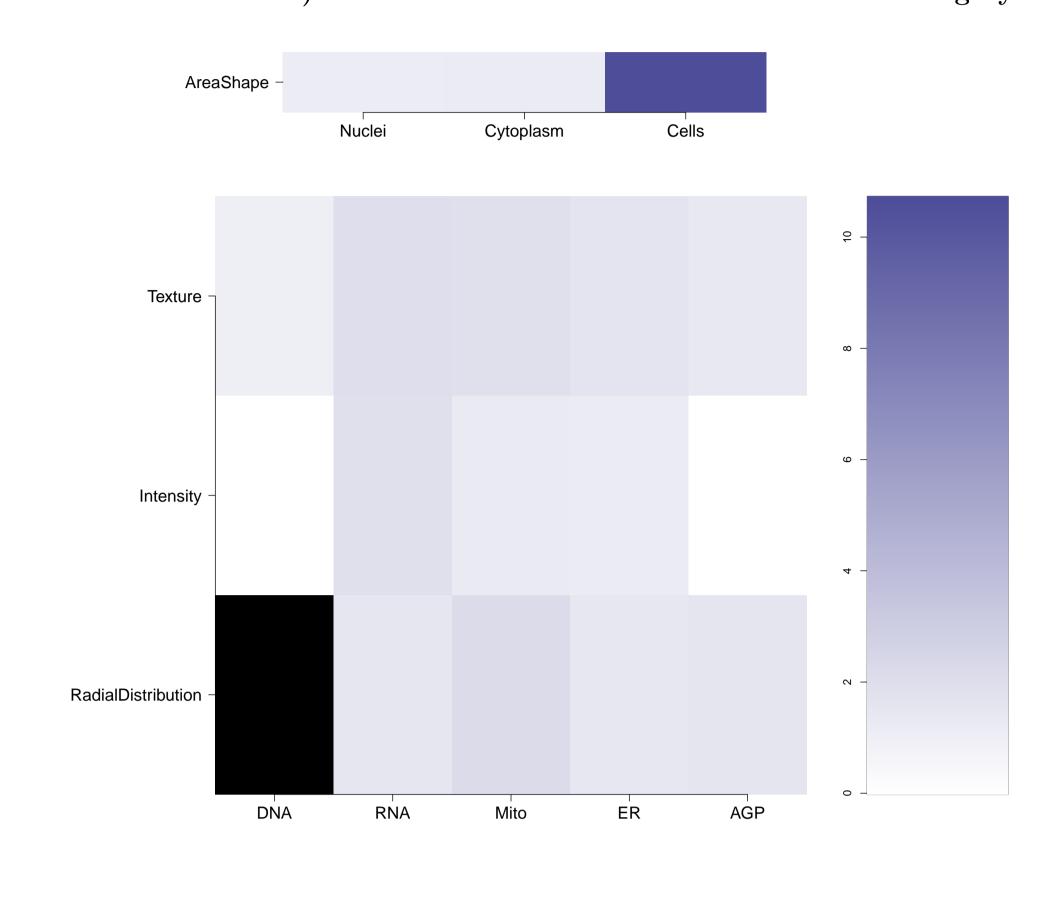
	Expert Anno			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PRKACA_WT.2	Canonical PKA	Activator	-0.60	0.02
PRKACA_WT.1	Canonical PKA	Activator	-0.51	0.05
$CXXC4_WT$	WNT	Inhibitor	-0.50	0.12
$STK3_WT.2$	Canonical Hippo	Activator	-0.49	0.26
PIK3CB_WT.2	Canonical PI3K/AKT	Activator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

AKT1_E17K AKT1S1_WT.1 BRAF_WT.1 CCND1_WT.1 CDKN1A_WT CEBPA_WT.1 CSNK1A1_WT.3 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 CDC42_T17N MAP2K4_WT.2 MOS_WT.2 MAP2K4_WT.2 MAP2K4_WT.1 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 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?



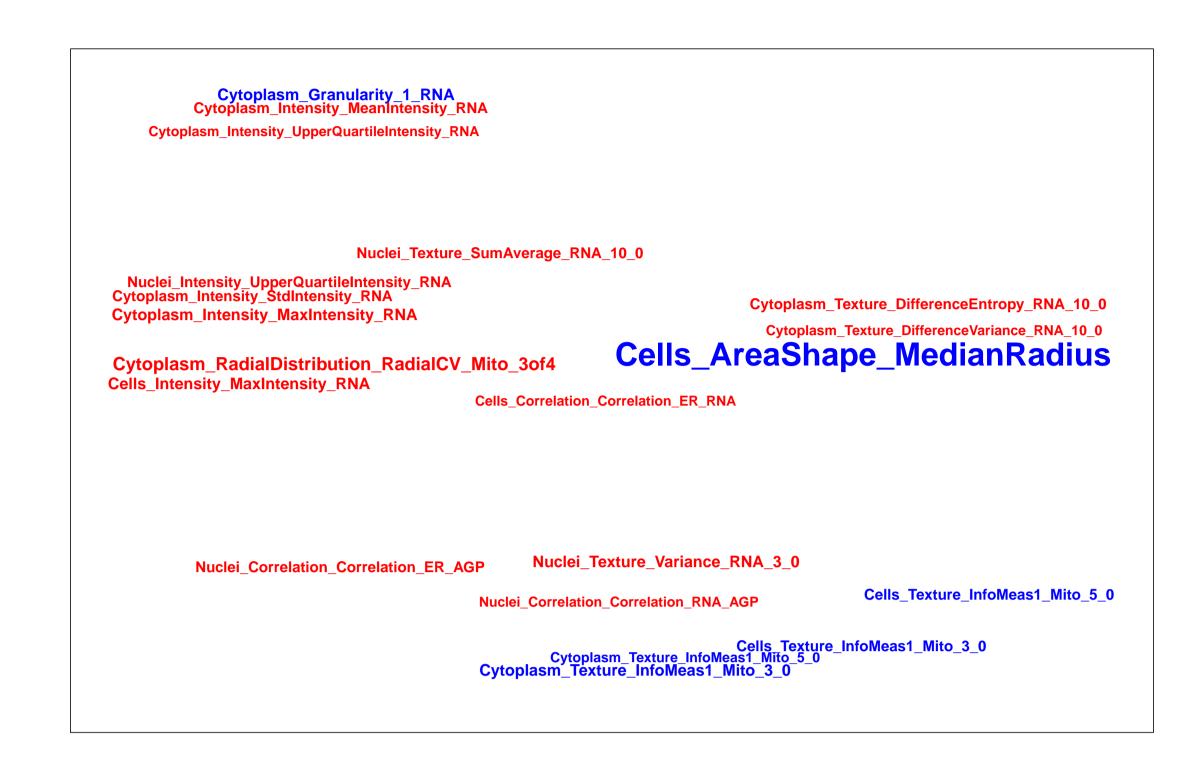
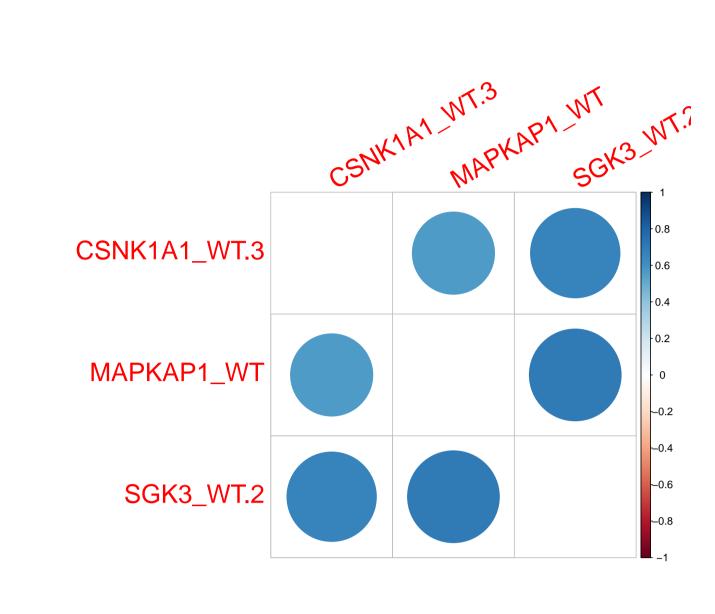
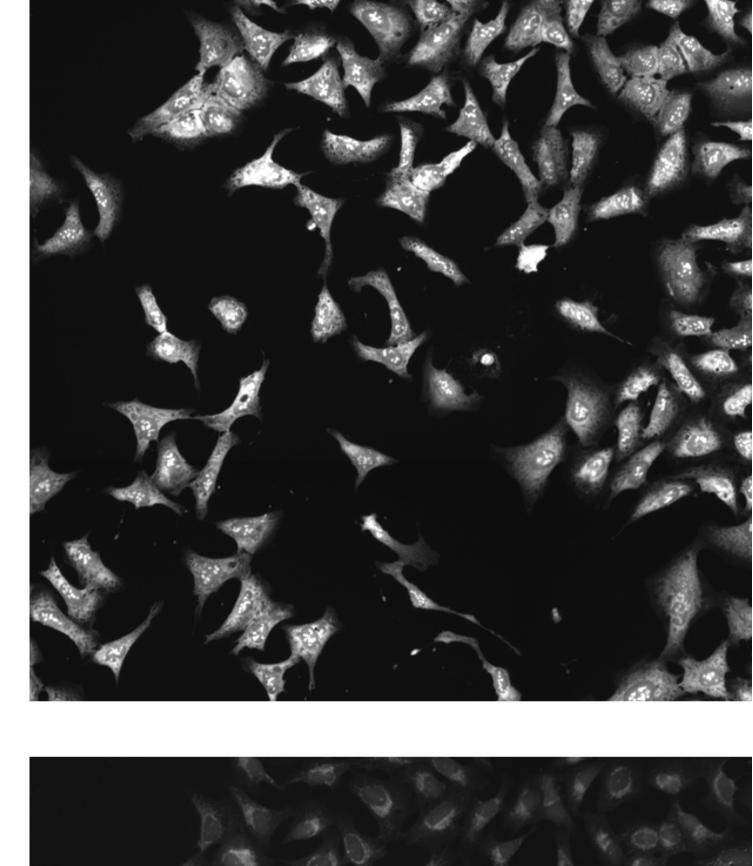


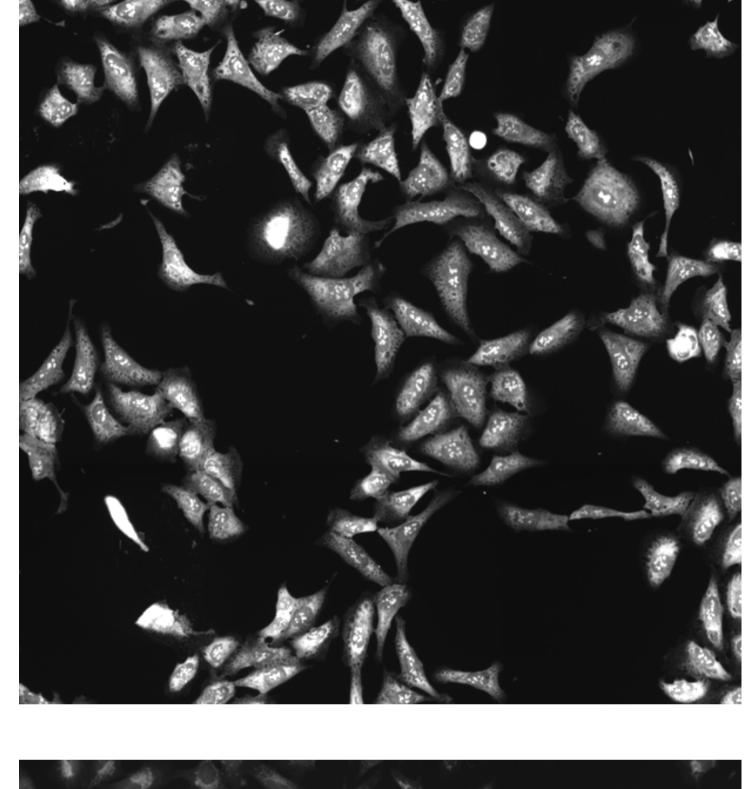
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



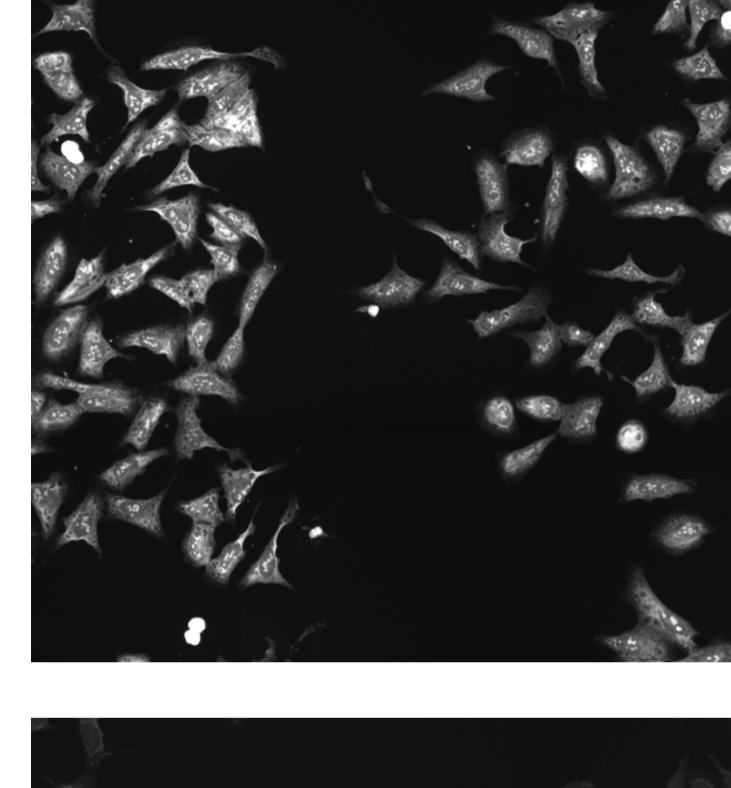
Empty



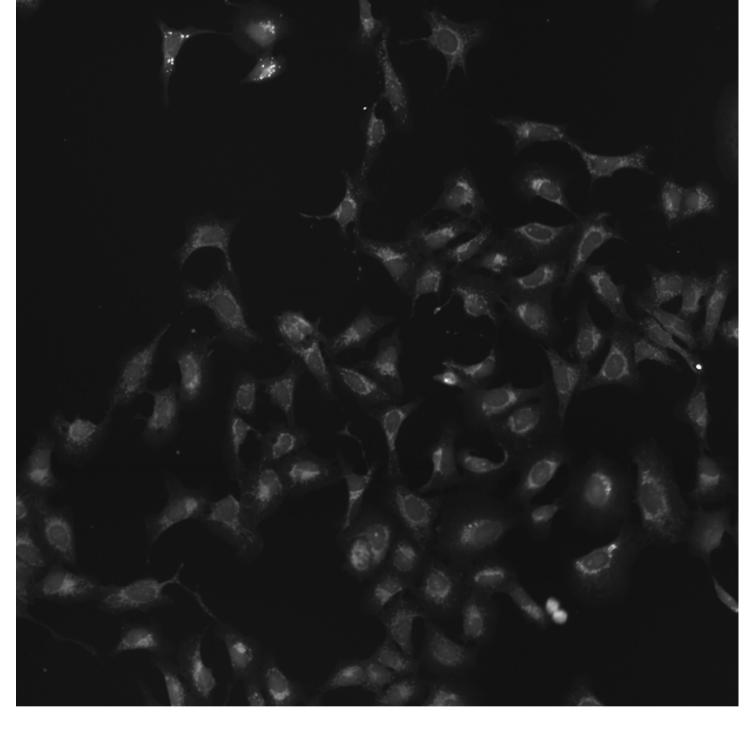
CSNK1A1_WT.3

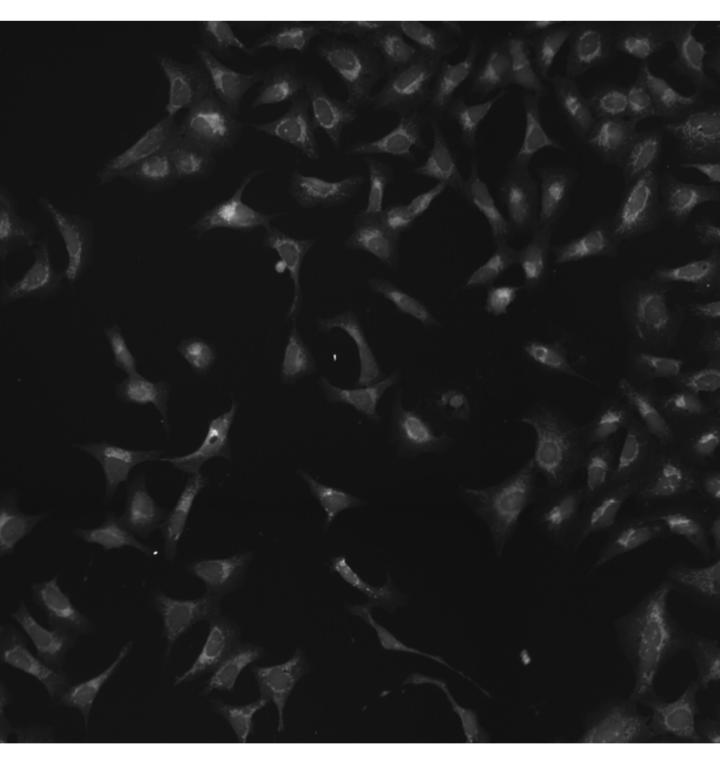


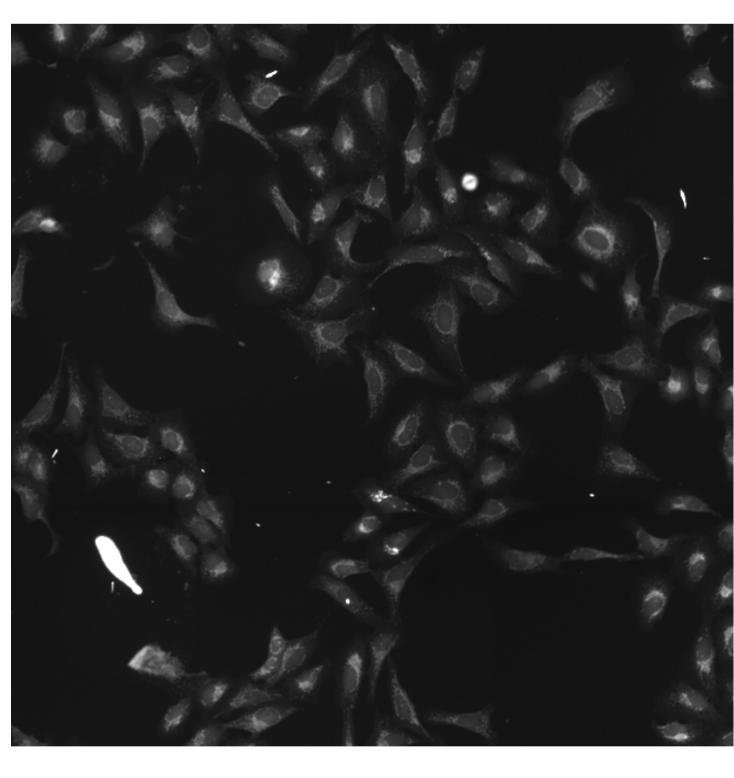
 $MAPKAP1_WT$

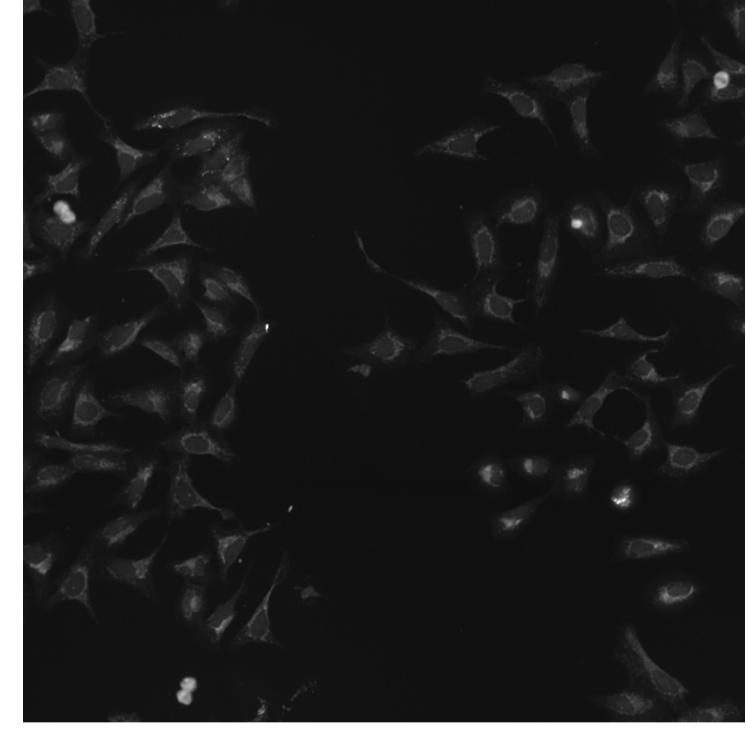


 $SGK3_WT.2$









ondary Screen to Identify Non-Covalent Inhibitors of RecA-Intein Splicing Activity

(AID 449750)

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 0.52)	e and each gene in	in cluster using L1000 profiling ± standard deviation; Tables	How similar is the competitive this experiment? (Y	ound signature to the gene clusters is Tellow and red lines correspond to h percentile DMSO correlation to all the genes)	Common distinguishing feature categories in the compoun	und and	Distinguishing individual features for the untreated samples. Black means a misma z-score in magnitude) in the compound, small z-score in magnitude) or opposite cluster	atch; i.e. active (= high and either inactive (=	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: 701. Active in the following assays: • HTS for Estrogen Receptor-beta Coactivator
											Binding inhibitors (AID 633)
							AreaShape -				• Screening for Modulators of Post-Golgi Transport, Control Strain (AID 738)
							Nuclei Cytoplasm Cells				• CYP2C9 Assay (AID 777)
BRD-K05950645-001-07-2					90 7				Nuclei_Texture_Variance_DNA_5_0		• CYP2C19 Assay (AID 778)
MLS000536739 SMR000155669					10 the compound		Texture		Cells_Texture_Correlation_RNA_3_0 Cells_Texture_InfoMeas2_FR_5_0	Cytoplasm_Texture_InfoMeas1_AGP_5_0	• Inhibitors of Plasmodium falciparum M17- Family Leucine Aminopeptidase (M17LAP) (AID 1619)
AC1LGWR5 BDBM48497 HMS1485K04	но	NA (in 1 replicates)	$\begin{array}{c c} 0.56 \pm 0.07 \\ \hline \text{Treatment} & \text{Score} \\ \hline \text{CSNK1A1_WT.3} & 0.50 \end{array}$	– NA	of genes in the cluster		89 - 100		Cells_Texture_InfoMeas2_ER_5_0 Nuclei_Texture_AngularSecondMoment_RNA_3_0		• Fluorescence Cell-Free Homogenous Primary HTS to Identify Inhibitors of RecA Intein Splic- ing Activity (AID 2221)
HMS2379O21 IDI1 022358	S		Treatment Score CSNK1A1_WT.3 0.50 MAPKAP1_WT 0.55 SGK3_WT.2 0.64		Mean Correlation -0.4 -0.7		Intensity –		Cells_RadialDistribution_RadialCV_AGP_3of4		• Fluorescence Cell-Free Homogeneous Counter Screen to Identify Inhibitors of GFP Chro- mophore Formation (AID 434968)
F1386-0259 T0500-8534 PubChem CID: 828338					COD4_T/TR MAPSK_WT1 BRAF_WT1 CCND1_WT1 CDNH_A_WT CBBAWT1 CSNH_A1_WT3 CXXC_L_WT DVI3WT GLIWT MAPSKWT1 MYDBL_1288P PRKC_Z_K381R RBBWT1 MAPSKWT1 MAPSKWT1 MAPSKWT1 MAPSKWT1 MAPSKWT1 MAPSKWT1 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT2 MAPSKWT3 MAP	4. –		Cells_RadialDistribution_MeanFrac_AGP_3of4 Nuclei_Texture_AngularSecondMoment_AGP_5_0 Nuclei_AreaShape_Zernike_6_6 Cytoplasm_Texture_Variance_RNA_3_0 Cells_Intensity_IntegratedIntensityEdge_AGP	Nuclei_AreaShape_Zernike_6_6	• Fluorescence Cell-Free Homogeneous Dose Retest to Identify Inhibitors of RecA-Intein Splicing Activity (AID 435010)	
					PRICA_JCHSRR RAF1_WT.2 MAP3KS_WT	Fritannaddt EAP1_W1.4 MAPANW1	RadialDistribution -		Gelis_intensity_integratedIntensityEdge_AGP		• Fluorescence Cell-Free Homogeneous Secondary Screen to Identify Inhibitors of DnaB-Intein Splicing Activity (AID 449749)
							DNA RNA Mito ER AGP				• Fluorescence Cell-Free Homogeneous Sec-

