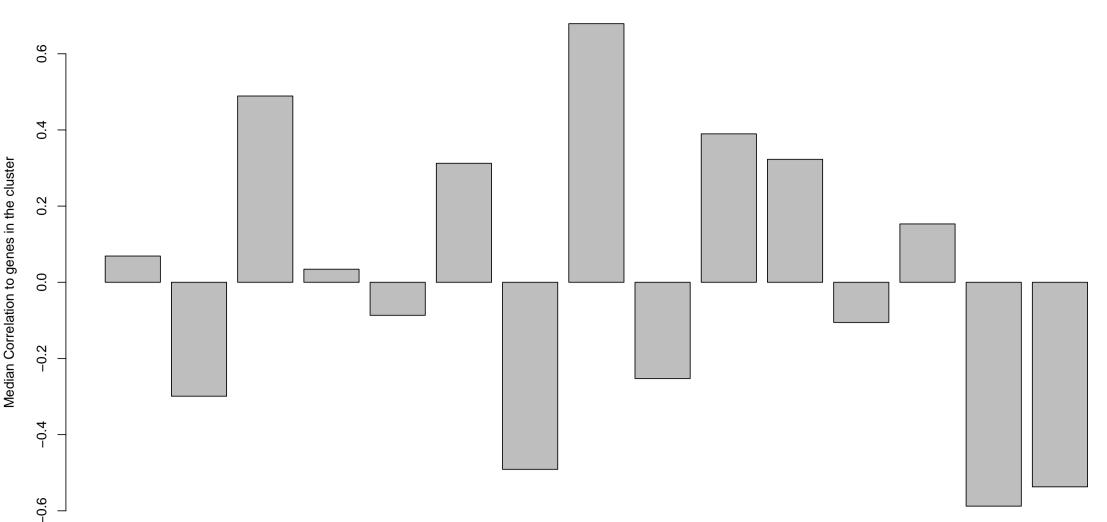
How similar is this cluster to the other clusters?

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

	Expert Annotation					
Treatment	Pathway	Regulation Type				
STK3_WT.1	Canonical Hippo	Activator				
STK3_WT.2	Canonical Hippo	Activator				
CXXC4_WT	WNT	Inhibitor				

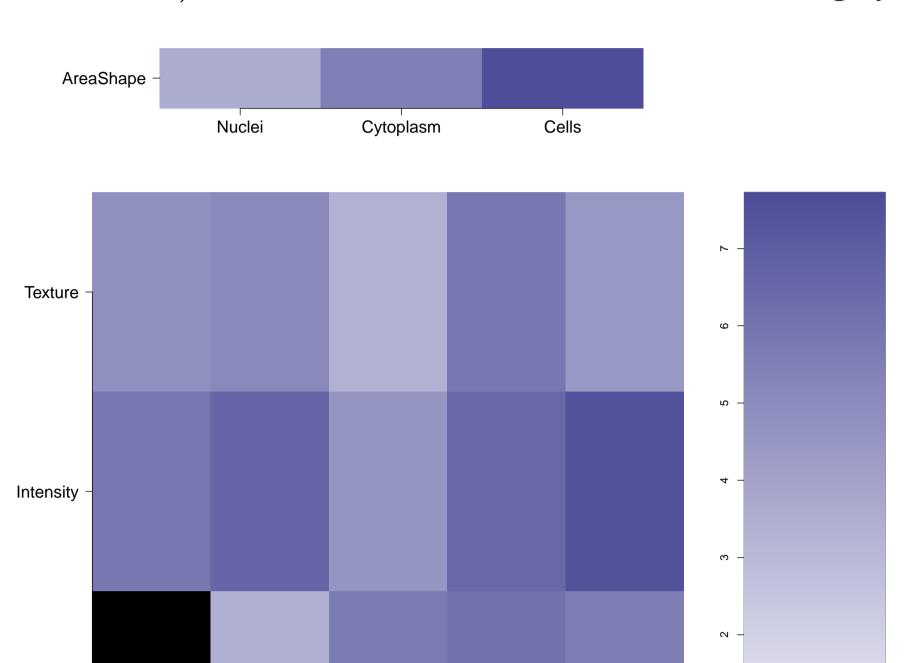


AKT1_E17K AKT1S1_WT.1 BRAF_WT.1 CCND1_WT.1 CDKN1A_WT CEBPA_WT.1 CSNK1A1_WT.3 CXXC4_WT DVL3_WT GLI1_WT MAP3K2_WT.1 MYD88_L265P PRKCZ_K281R RBPJ_WT.1 WWTR1_WT STK3_WT.1 TGFBR1_K232R PRKACA_WT.1 MAP3K2_WT.2 MYD88_WT PRKCZ_WT.1 RBPJ_WT.2 YAP1_WT.1 AKT3_WT.2 ATF4_WT.2 MOS_WT.1 E2F1_WT KRAS_G12V JUN_WT.1 SGK3_WT.2 STK3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 YAP1_WT.2 PRKACA_WT.1 MAP3K4_WT.1 NAP3K2_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 YAP1_WT.3 PIKSR1_WT.1 RAF1_WT.1 MAP3K4_WT.1 MAP3K4_WT.1 MAP3K5_WT MAP3K5_WT MAP3K5_WT MAP3K5_WT MAP3K5_WT MAP3K5_WT MAP3K5_WT MAP3K5_WT.2 STK3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 YAP1_WT.3 YAP1_WT.3 YAP1_WT.4 PRKCA_K368R RAF1_WT.2 MAP3K5_WT

Expert Annotation								
	Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation			
	STK11_WT.2	Canonical TOR	Inhibitor	-0.68	0.04			
	MAPKAP1_WT	Canonical TOR	Activator	-0.64	0.11			
	$YAP1_WT.2$	Canonical Hippo	Inhibitor	-0.64	0.13			
	$RBPJ_WT.2$	NOTCH	Activator	-0.60	0.09			
	$YAP1_WT.4$	Canonical Hippo	Inhibitor	-0.59	0.08			

Top 5 genes negatively correlated to the cluster

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



AĠP

ER

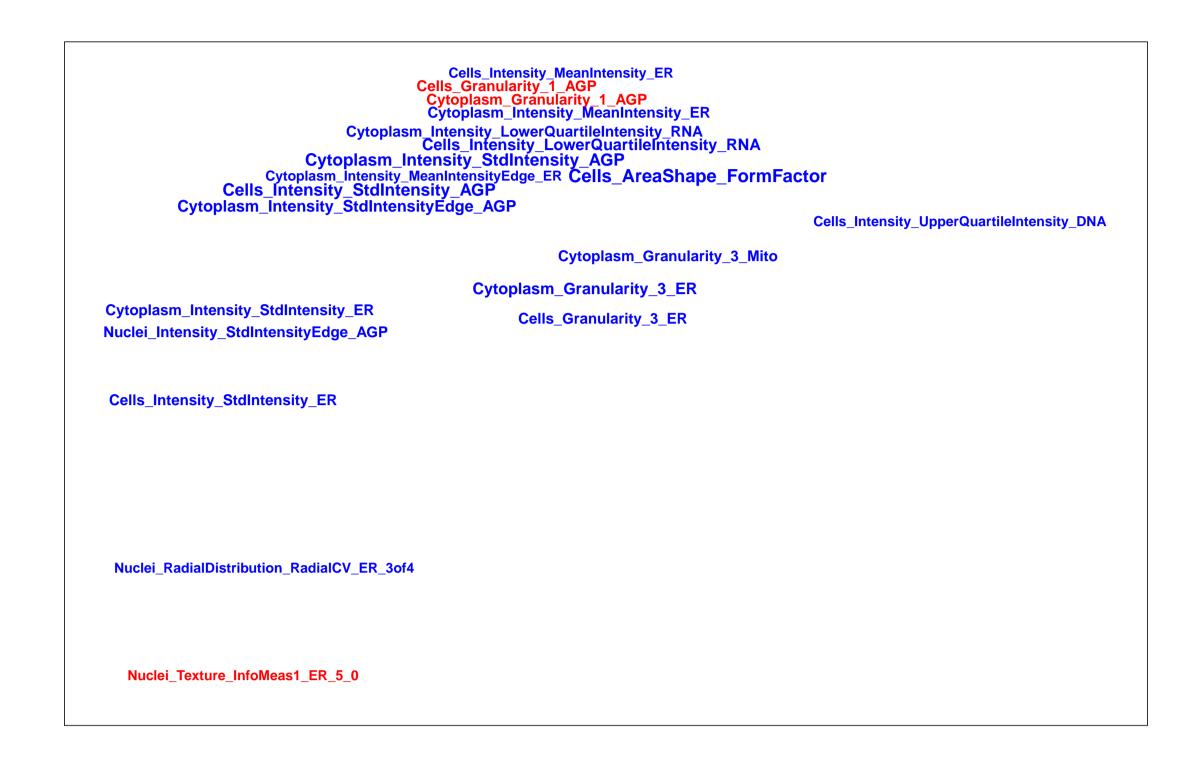
RadialDistribution -

AGP

RNA

DNA

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?

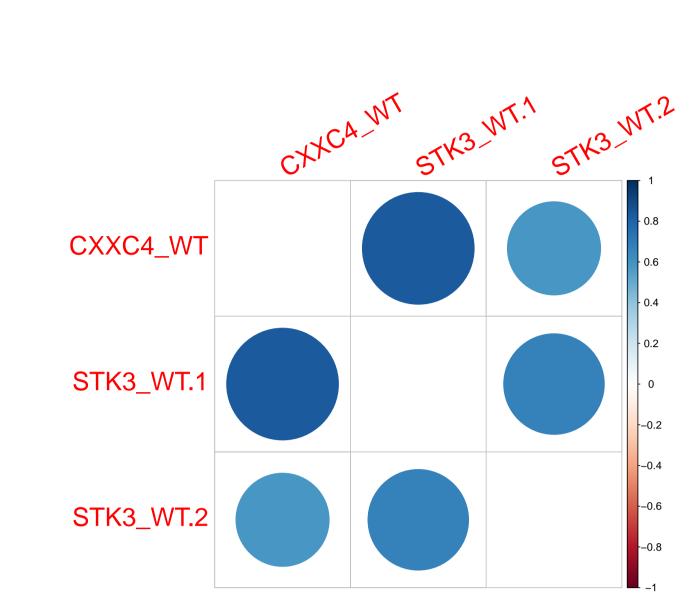
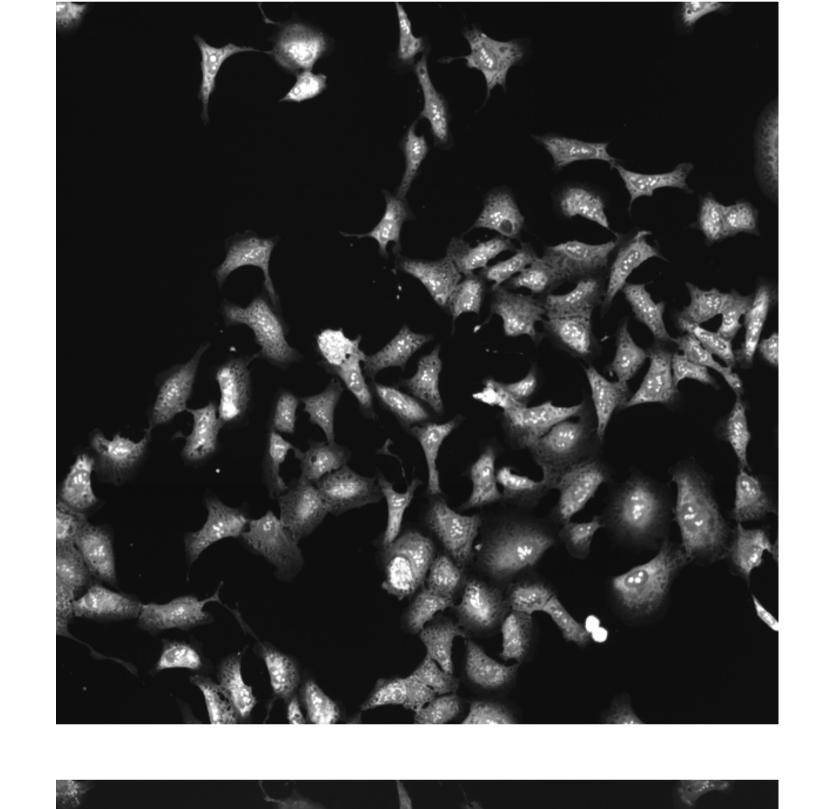
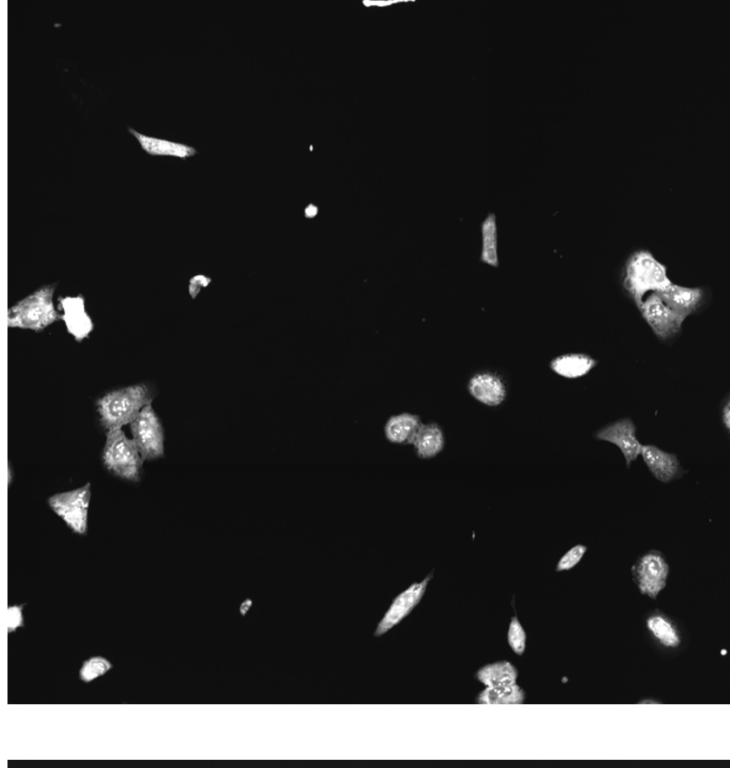


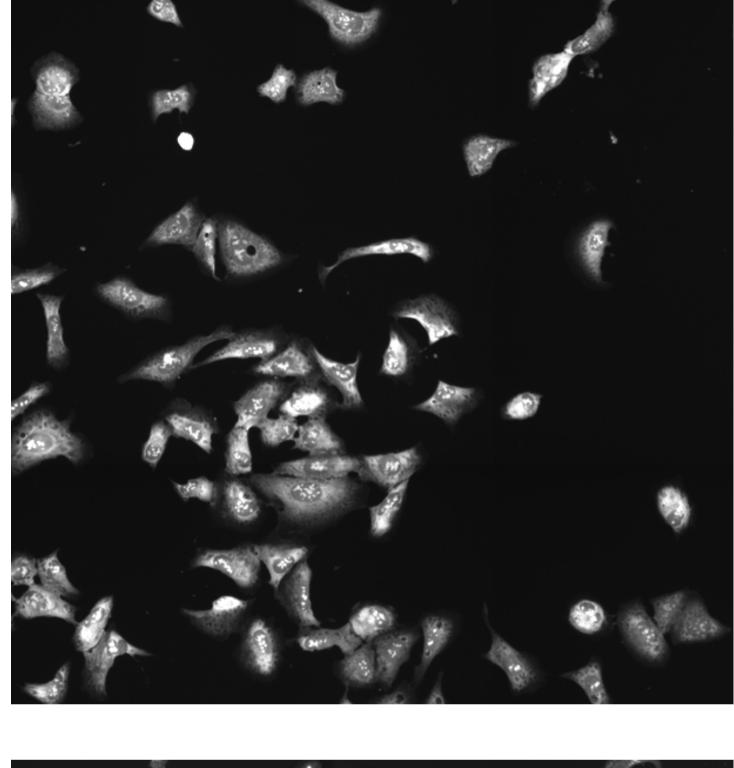
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

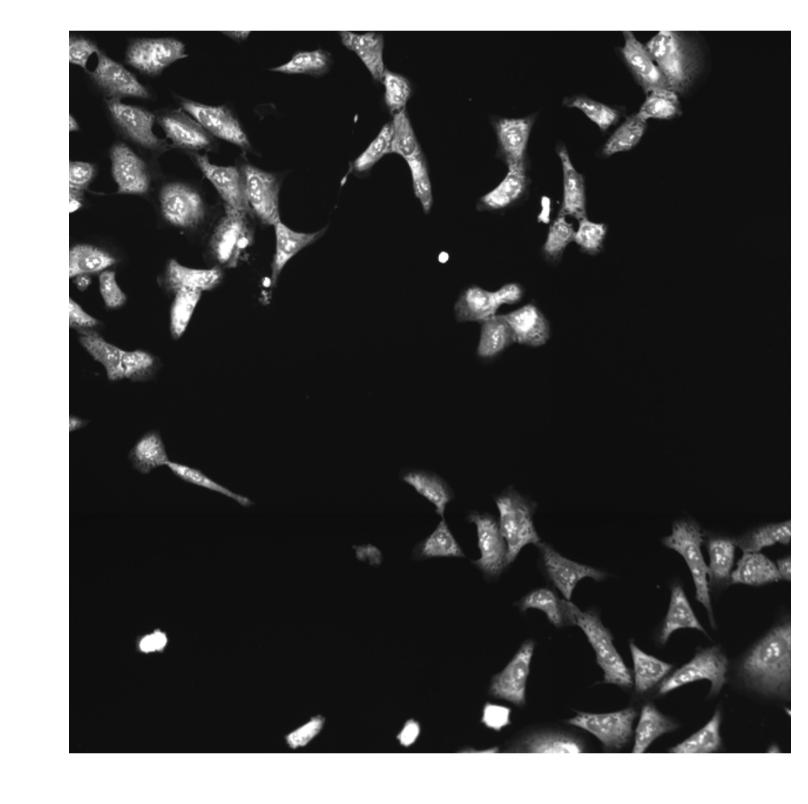
CXXC4_WT

STK3_WT.1

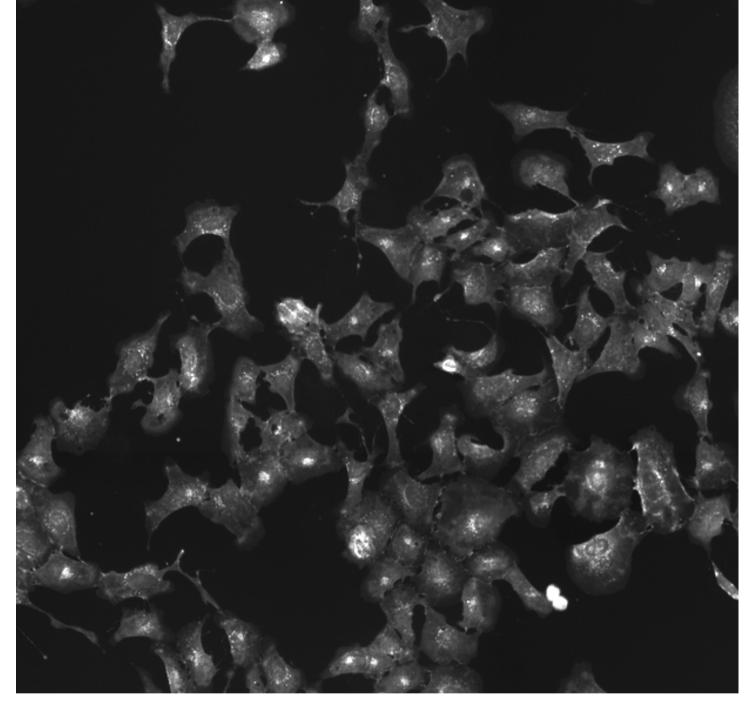


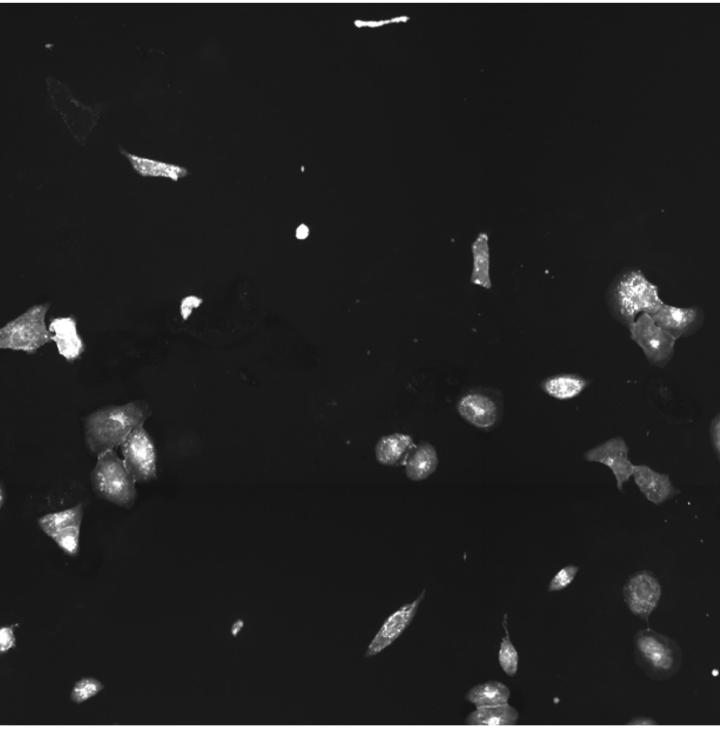


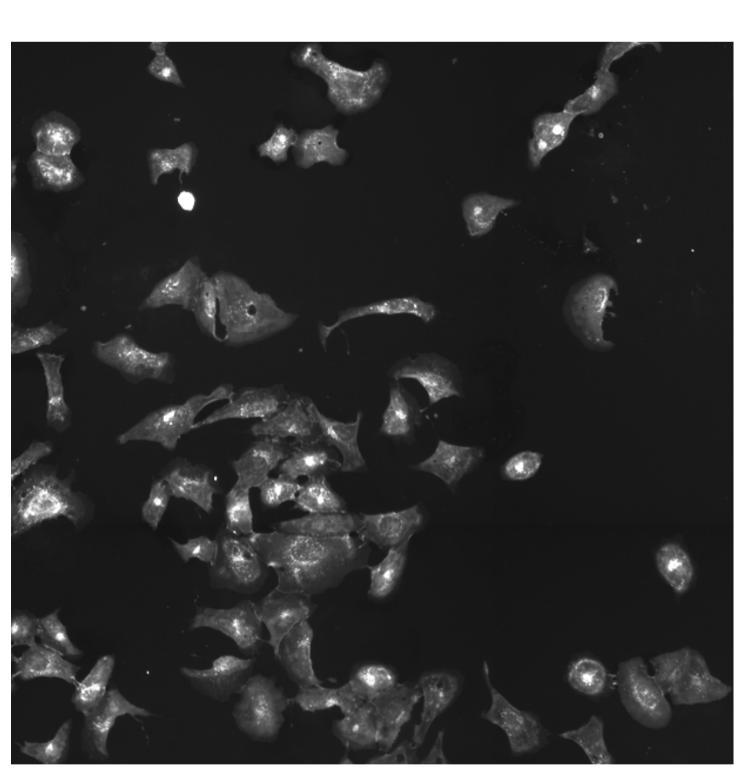


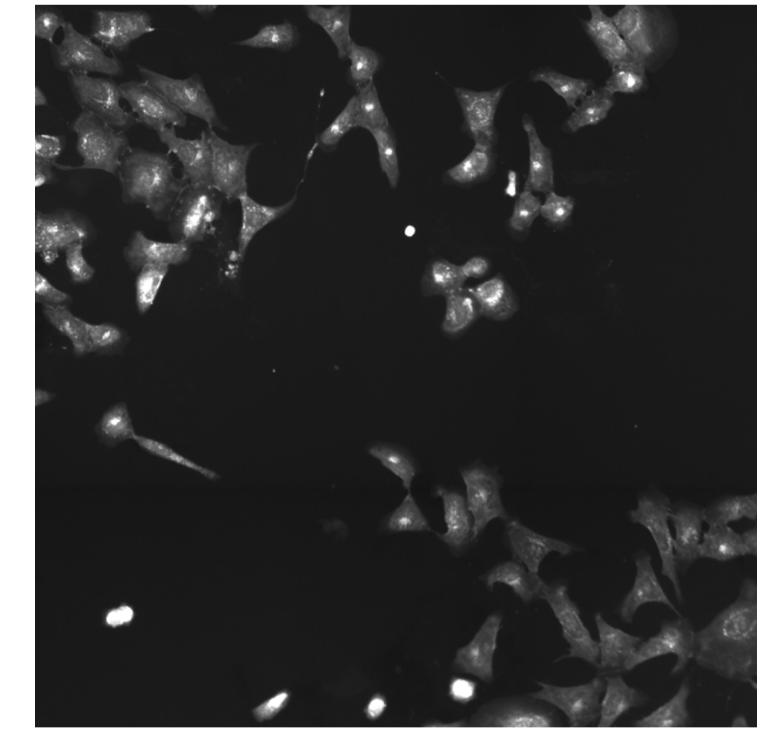


 $STK3_WT.2$









Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	structure c		correlation between compound and each gene in cluster; Tables contain data for individual	using L1000 profiling ± standard deviation; 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)	Common distinguishing feature categories in the	he compound and	untreated samples. Black m z-score in magnitude) in the	Teatures for the compound relative to neans a mismatch; i.e. active (= high ne compound, and either inactive (= de) 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
BRD-K52251545-001-05-2 AC1M5VPS MLS000418615 HMS2531C16 ZINC3270008 SMR000247565 T0510-7581 PubChem CID: 2386323	NH O O O	0.83 (in 4 replicates)	0.53 ± 0.18 Treatment Score CXXC4_WT 0.66 STK3_WT.1 0.60 STK3_WT.2 0.32	genes	Method Correlation of genes in the cluster to the compound The street of the street o	AreaShape – Nuclei Cytoplasm Cells Texture – Intensity –	60 - 80 -	Cytoplasm_Intensity_MaxIntensityEdge_AGP Cytoplasm_Intensity_MaxIntensity_Mito Cells_ Cells_Cells_RadialDistrib Cells_Intensity_LowerQuartileIntensity_RNA Cells_Intensity_LowerQuartileIntensity_RNA Cells_RadialDistribution_MeanFrac_RNA_4of4 Nuclei_Intensity_IntegratedIntensity_AGP Nuclei_Intensity_IntegratedIntensity_ER Cells_RadialDistribution_FracAtD_ER_3of4 Cytoplasm_Texture_Variance_RNA_3_0	Cells_Intensity_UpperQuartileIntensity_DNA S_Intensity_MaxIntensityEdge_ER ribution_RadialCV_ER_40f4Cells_Intensity_MedianIntensity_RNA Cytoplasm_Fexture_SumAverage_Mito_5_0 Cells_Intensity_StdIntensityEdge_AGP Cells_Intensity_MaxIntensityEdge_Mito Cells_Intensity_MaxIntensityEdge_Mito Cells_Intensity_IntegratedIntensityEdge_ER Nuclei_Intensity_IntegratedIntensityEdge_ER	Total number of assays tested in: 629. Active in the following assays: • Total Fluorescence Counterscreen for Inhibitors of the Interaction of Thyroid Hormone Receptor and Steroid Receptor Coregulator 2 (AID 1479) • Antagonist of Human D 1 Dopamine Receptor: qHTS (AID 504652) • High-throughput multiplex microsphere screening for inhibitors of toxin protease, specifically Botulinum neurotoxin light chain F protease, MLPCN compound set (AID 588497)

