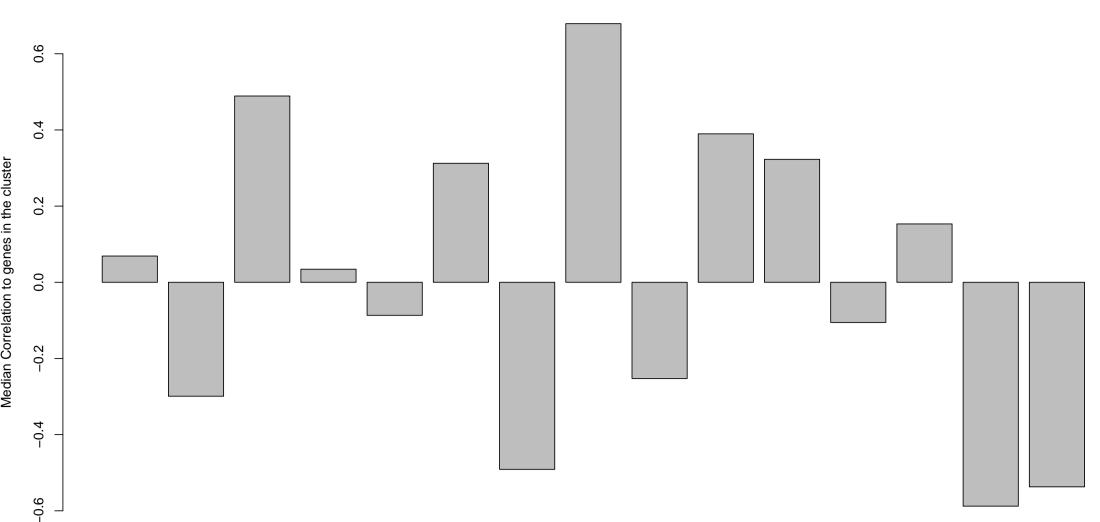
How similar is this cluster to the other clusters?

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		



	Expert A	Annotation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Devia
	Canonical TOD	Inhihitan	0.69	

Top 5 genes negatively correlated to the cluster

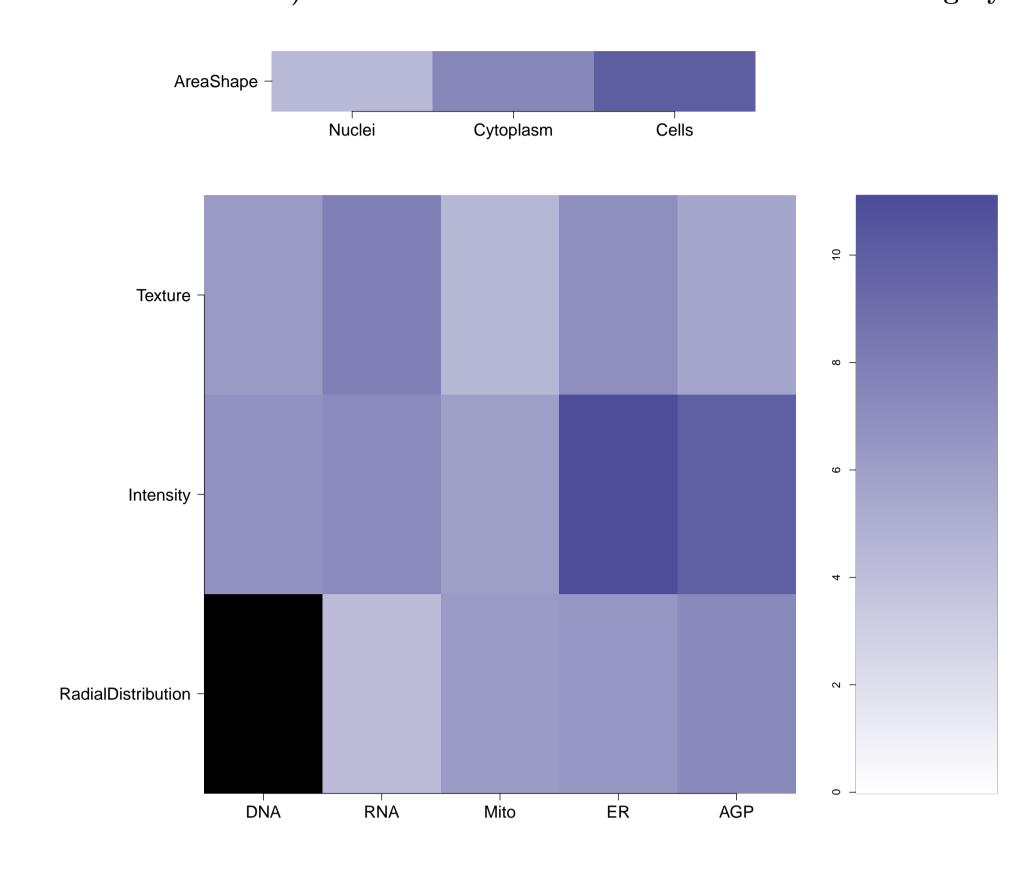
	Expert A			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
STK11_WT.2	Canonical TOR	Inhibitor	-0.68	0.04
MAPKAP1_WT	Canonical TOR	Activator	-0.64	0.11
YAP1_WT.2	Canonical Hippo	Inhibitor	-0.64	0.13
RBPJ_WT.2	NOTCH	Activator	-0.60	0.09
YAP1_WT.4	Canonical Hippo	Inhibitor	-0.59	0.08

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 PRKACA\_WT.1 RAF1\_WT.1 RAF1\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP3K5\_WT.1 MAP3K5\_W

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?



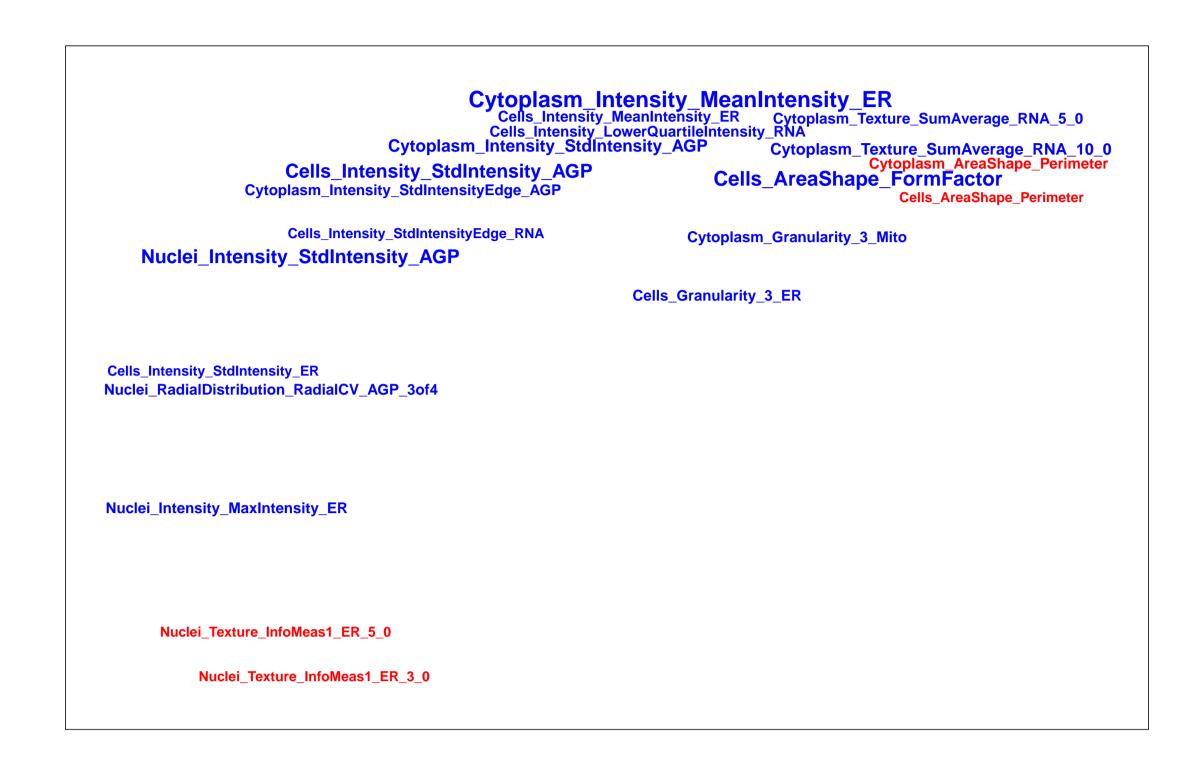
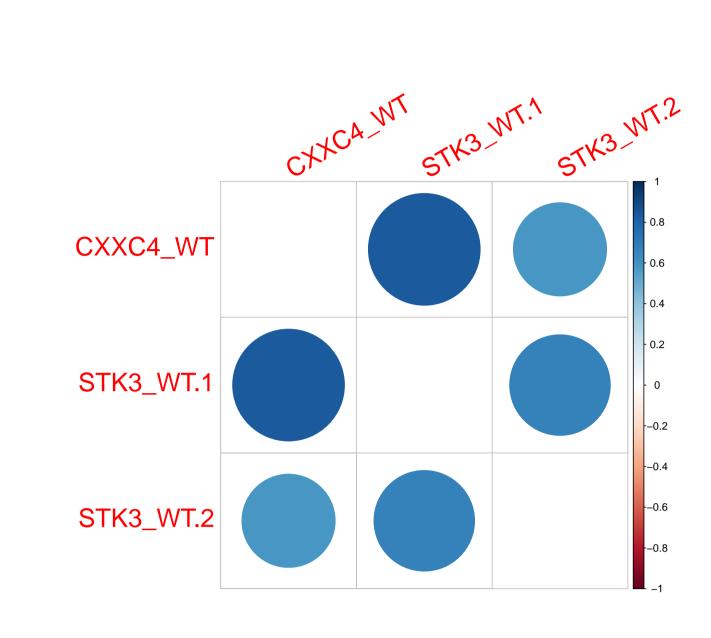
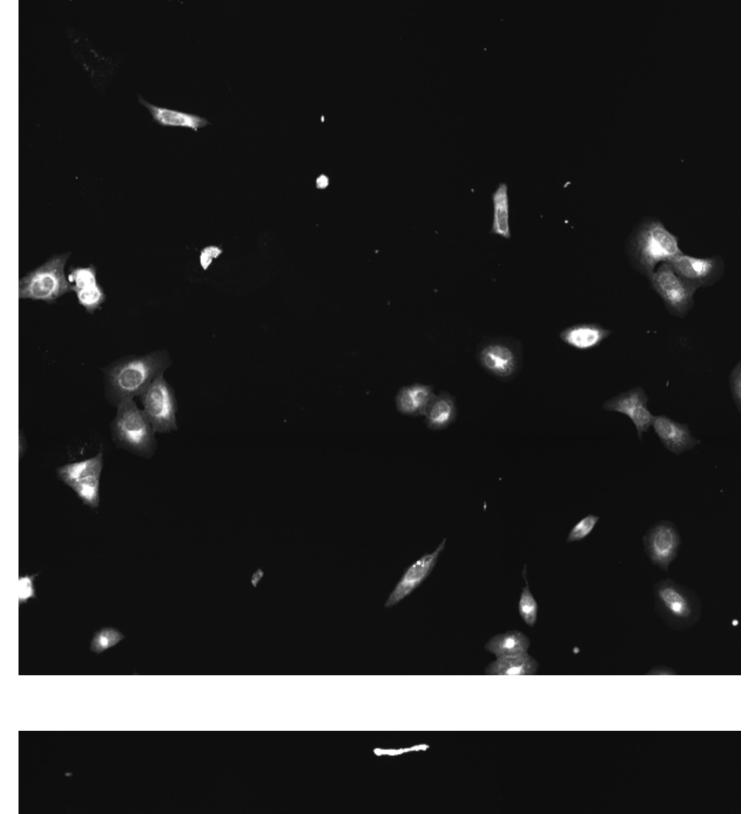


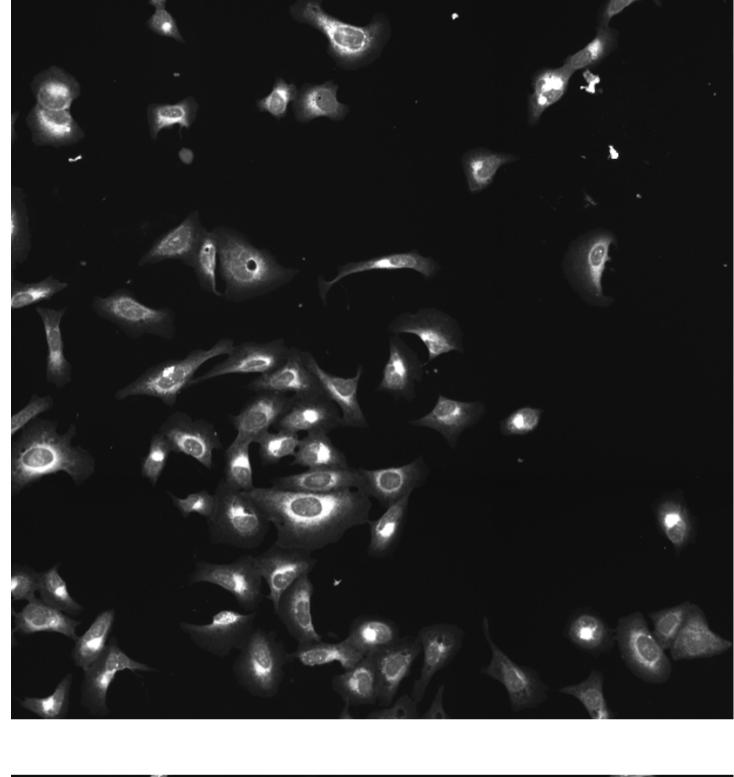
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



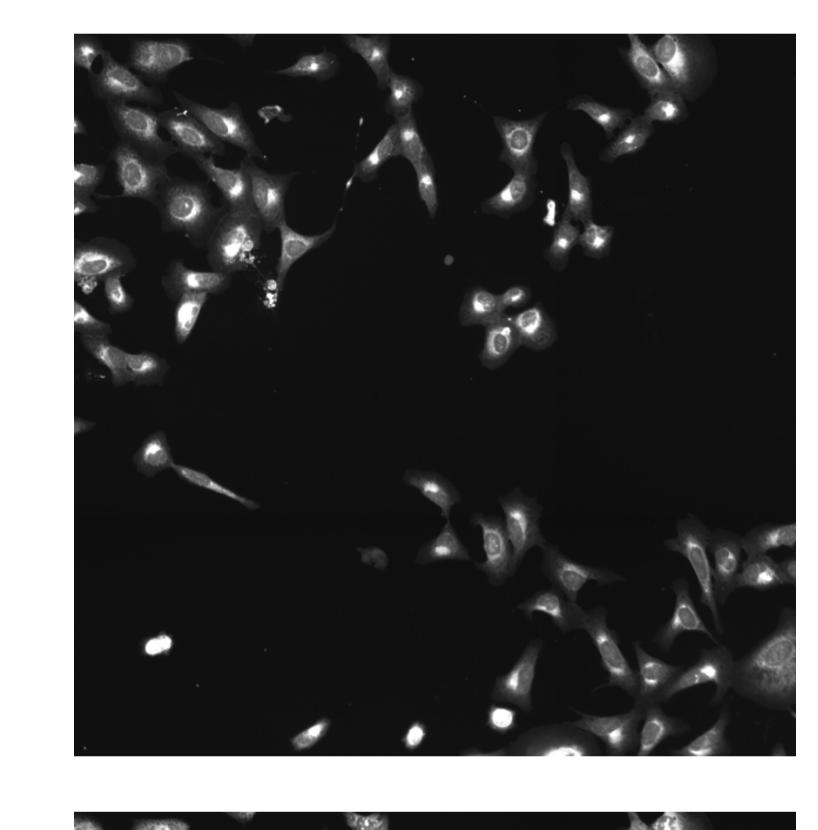
Empty ER



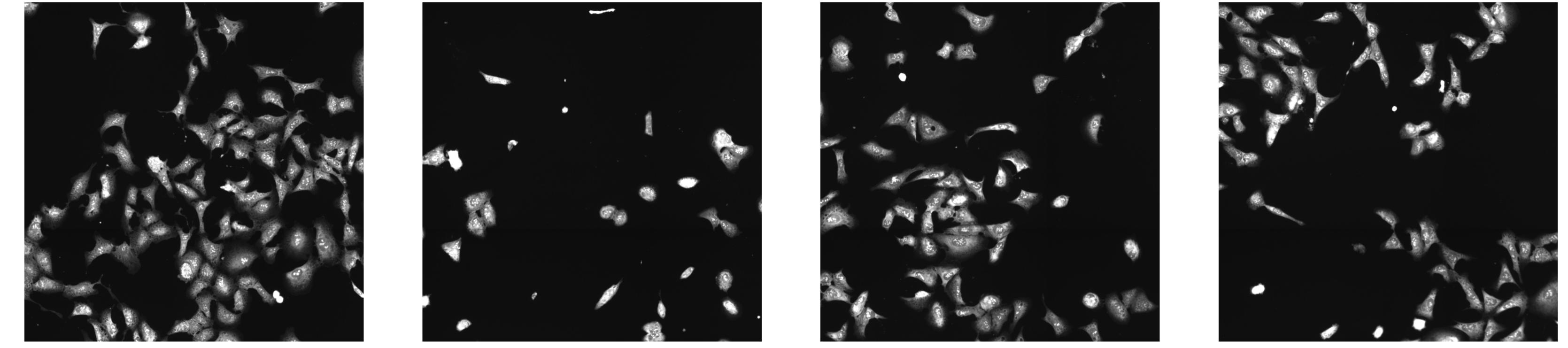
 $CXXC4_{-}WT$ 

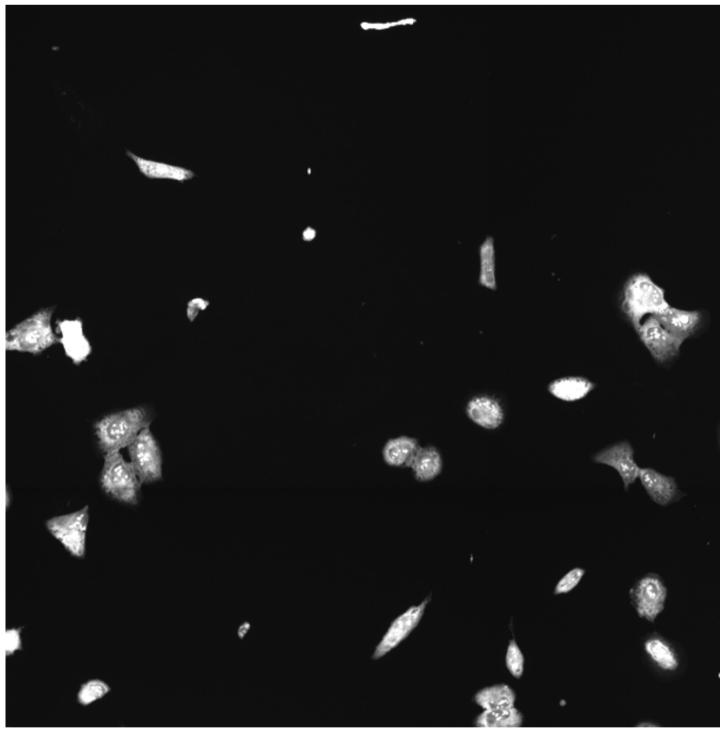


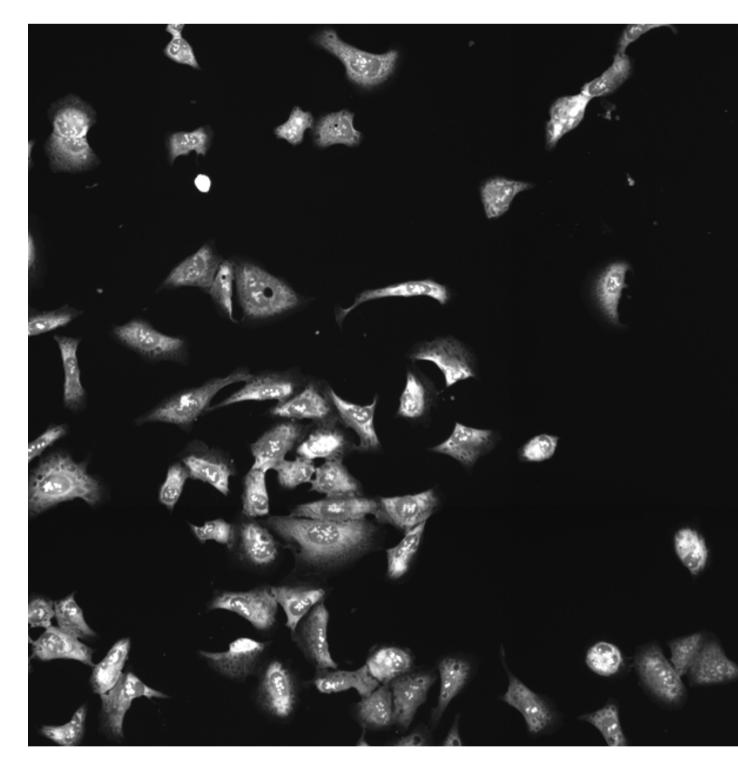
 $STK3_WT.1$ 

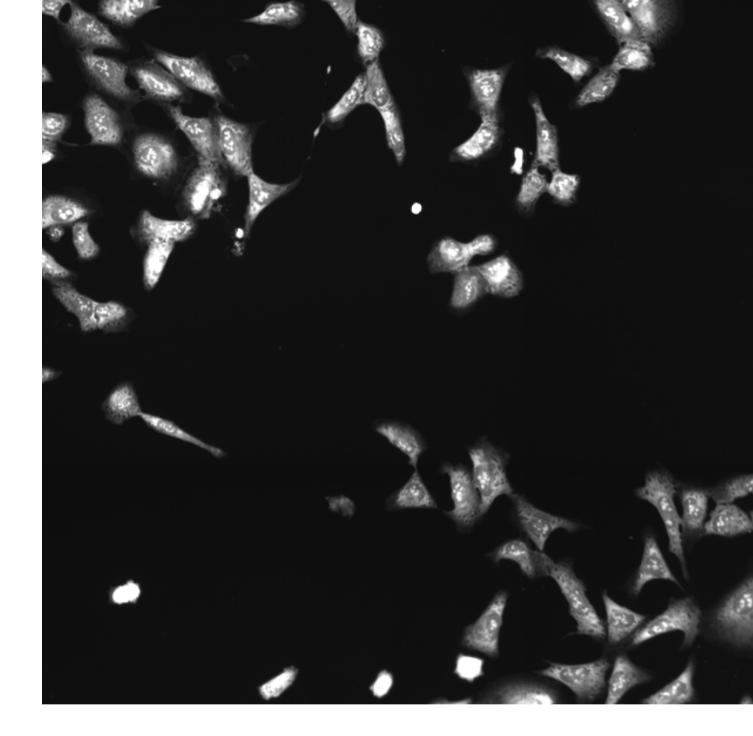


 $STK3_WT.2$ 









Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	and each gene in	using L1000 profiling ± standard deviation; Tables	How similar is the compound signature to the gene clusters in this experiment? (Yellow and red lines correspond to	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
BRD-K92570288-001-01-7 PubChem CID : 54614939		0.91 (in 4 replicates)	CXXC4_WT 0.66	$0.827 \pm 0.133$ Treatment   Score   CXXC4_WT   0.980   STK3_WT.1   0.769   STK3_WT.2   0.733	Post Control of Dates in the C	AreaShape -  Nuclei Cytoplasm Cells  Texture -  RadialDistribution -  RadialDistribution -  RadialDistribution -  RadialDistribution -  RadialDistribution -	Cells_Intensity_UpperQuartileIntensity_DNA Cytoplasm_Texture_DifferenceVariance_AGP_5_0 Cells_Intensity_MaxinensityEdge_ER Cells_Intensity_MaxinensityEdge_ER Cells_Intensity_MaxinensityEdge_DNA Cells_Intensity_LowerQuartileIntensity_RNA  Cells_Intensity_LowerQuartileIntensity_RNA  Cells_Intensity_LowerQuartileIntensity_RNA  Cells_Intensity_LowerQuartileIntensity_RNA  Cells_Intensity_LowerQuartileIntensity_Ege_DNA  Cells_Intensity_LowerQuartileIntensity_Ege_Entensity_MaxinensityEdge_DNA  Cells_Intensity_LowerQuartileIntensity_ER  Nuclel_Intensity_IntegratedIntensity_ER  Copposition_Anadhups_FormFator  Nuclel_Intensity_IntegratedIntensity_ER  Cytoplasm_Texture_Variance_RNA_3_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Anadhups_Solidity  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_AreaShape_Compactness	Total number of assays tested in: 19.

