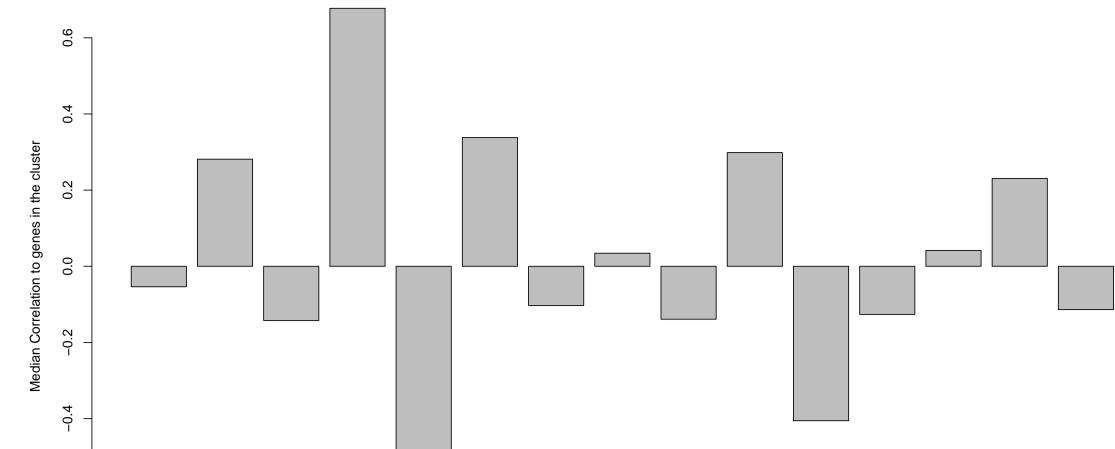
How similar is this cluster to the other clusters?

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

Expert Annotation

	Expert Annotation		
Treatment	Pathway	Regulation Type	
CCND1_WT.1	Canonical Cell Cycle	Activator	
$E2F1_WT$	Canonical Cell Cycle	Activator	
CCND1_WT.2	Canonical Cell Cycle	Activator	



Top 5 genes negatively correlated to the cluster

	Expert Annor	tation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
CDKN1A_WT	Canonical Cell Cycle	Inhibitor	-0.67	0.11
MAP3K5_WT	Canonical MAPK	Activator	-0.61	0.03
MAP2K4_WT.1	Canonical MAPK	Activator	-0.51	0.06
$TP53_WT.1$	Canonical DNA Damage	Activator	-0.50	0.22
MAP2K3_WT	Canonical MAPK	Activator	-0.49	0.10

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 MAP2K4_WT.2 MOS_WT.2 WAP2K3_WT JUN_WT.2 YAP1_WT.3 PRKCA_K368R RAF1_WT.2 MAP2K4_WT.1 MAP3K6_WT WAP3K6_WT 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?

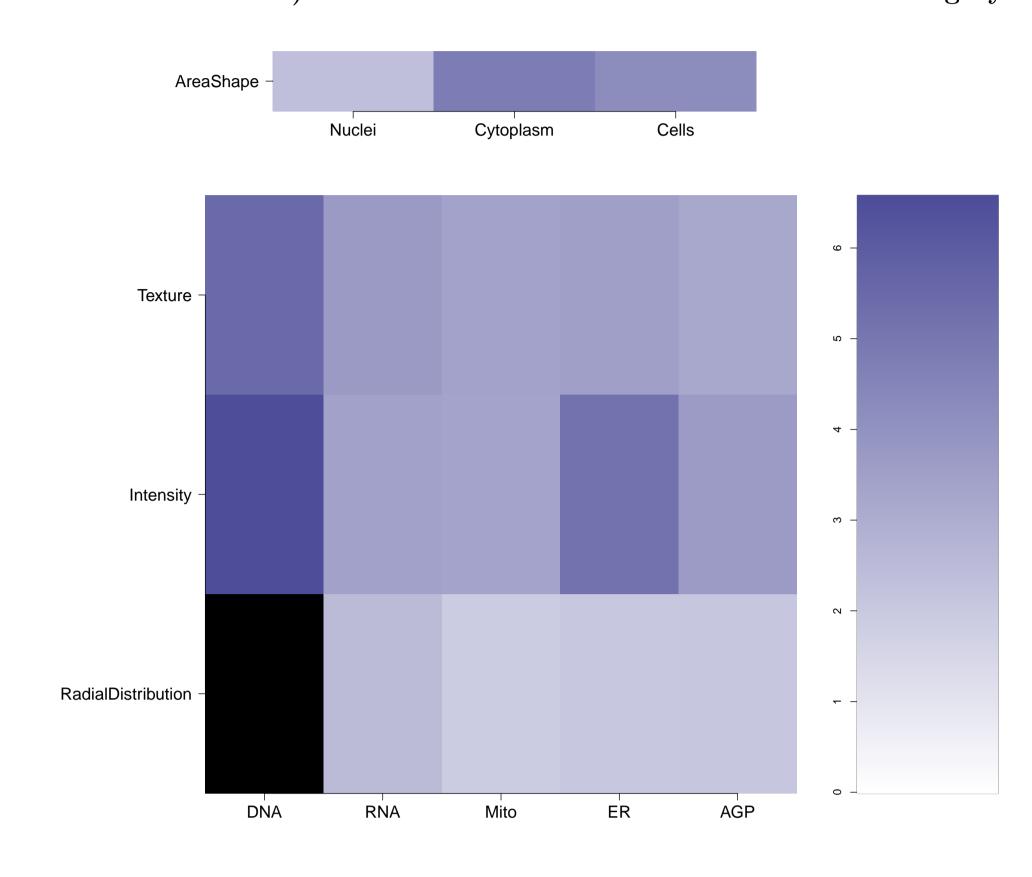
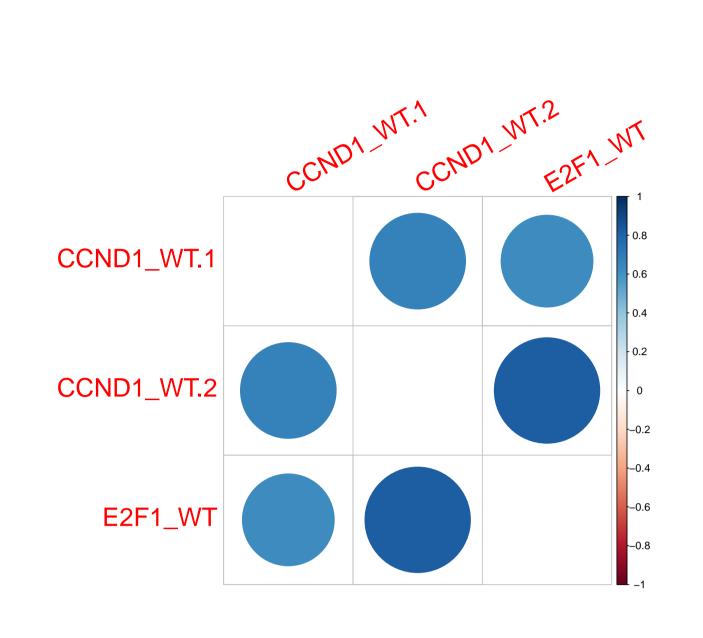
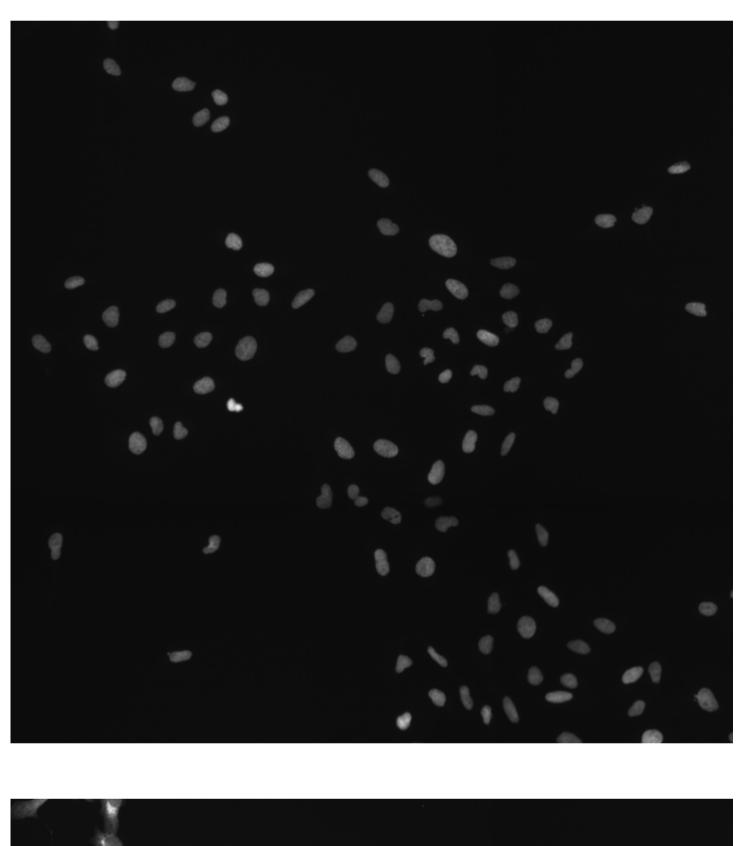




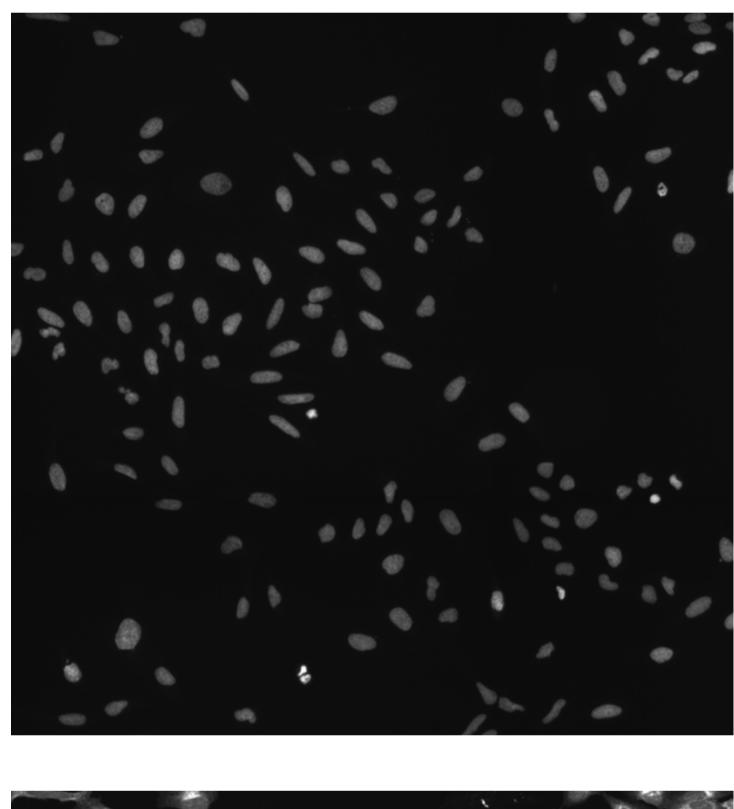
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



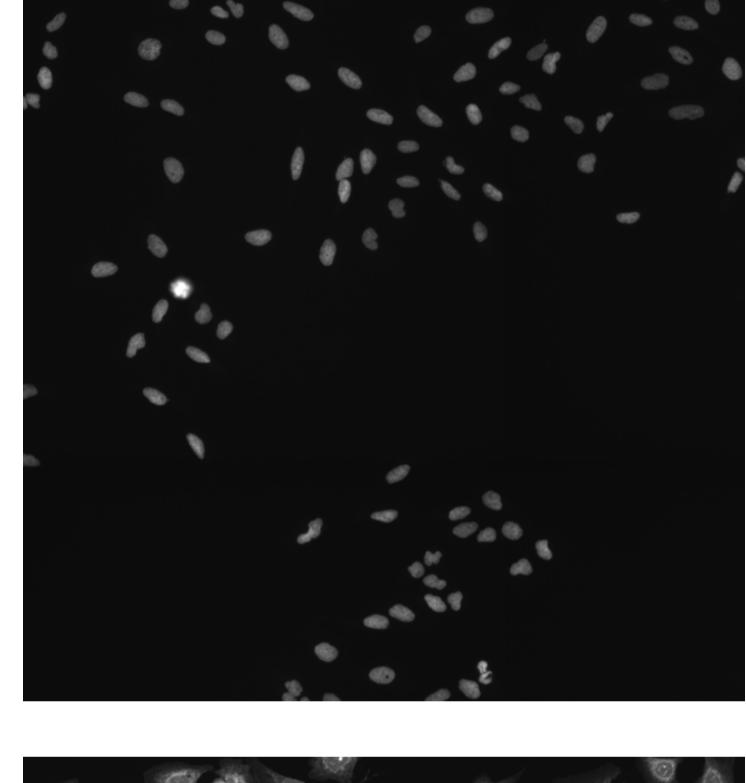
DNA



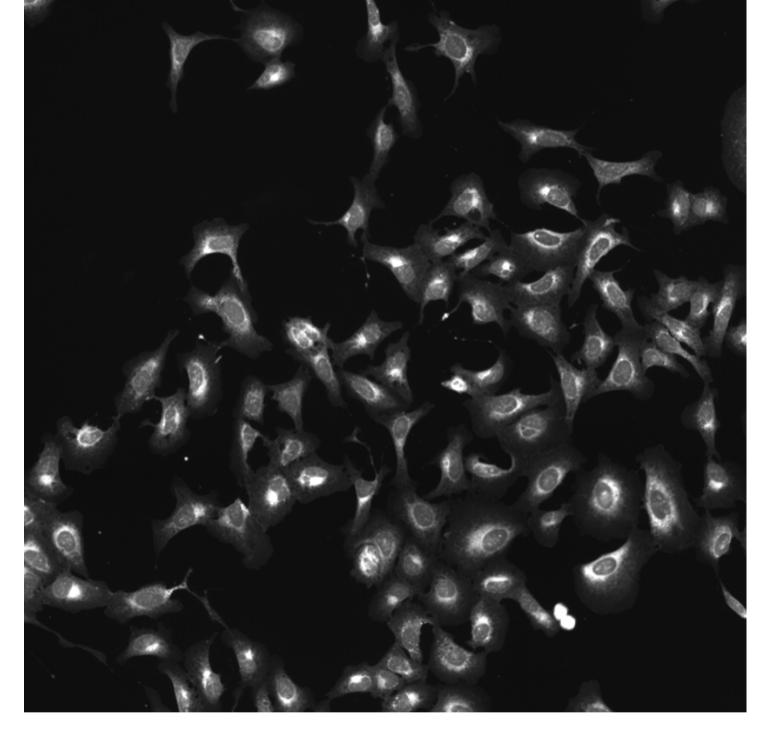
 $CCND1_WT.1$



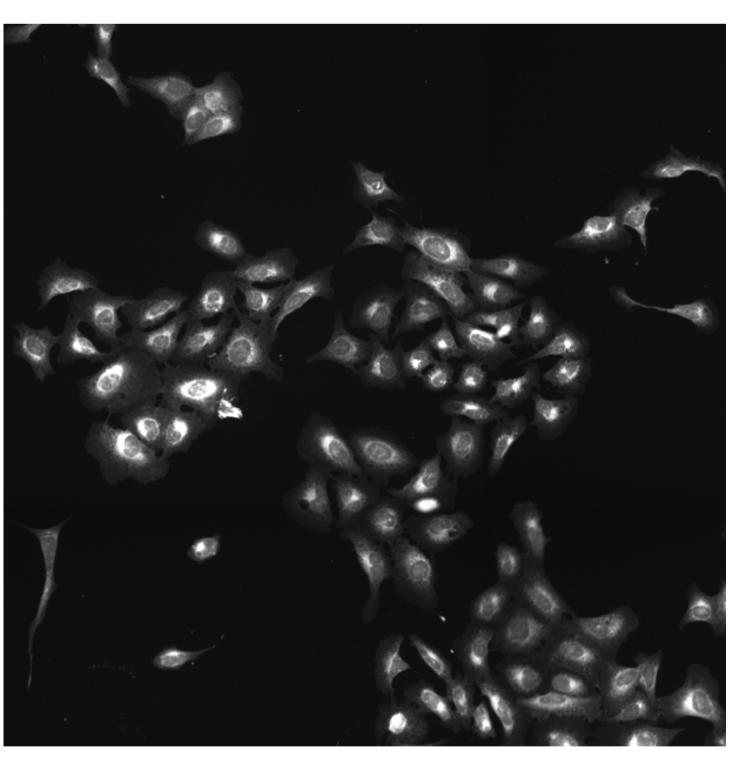
 $CCND1_WT.2$

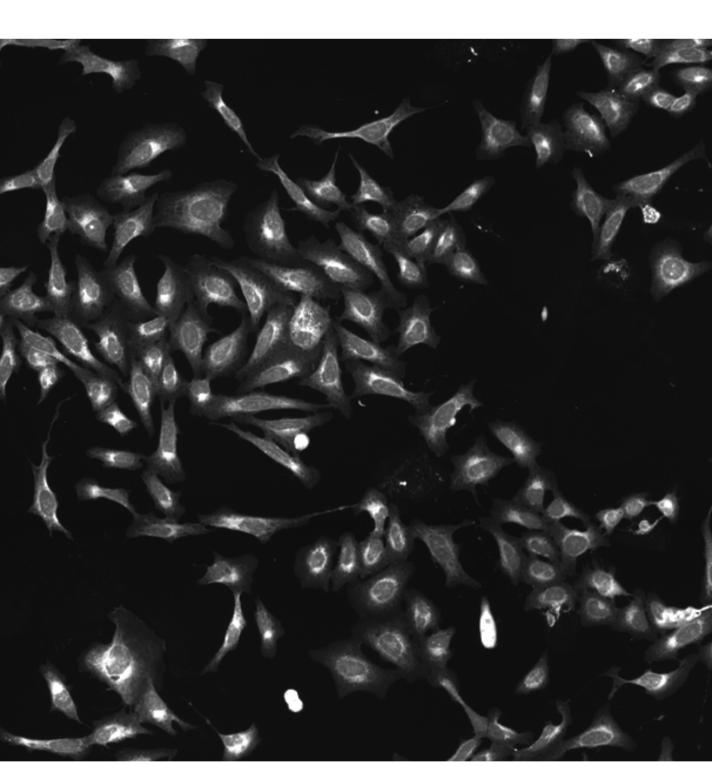


 $E2F1_WT$



genes





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3		

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 0.54)	Mean ± standard deviation correlation between compound and each gene in cluster; Tables contain data for individual genes	Mean compound rank when scored against genes in cluster 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 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

