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

	Expert Annotation			
Treatment	Pathway	Regulation Type		
PRKCZ_WT.1	Canonical PKC	Activator		
PRKCZ_WT.2	Canonical PKC	Activator		
PRKCZ_K281R	Canonical PKC	Inhibitor		

AreaShape

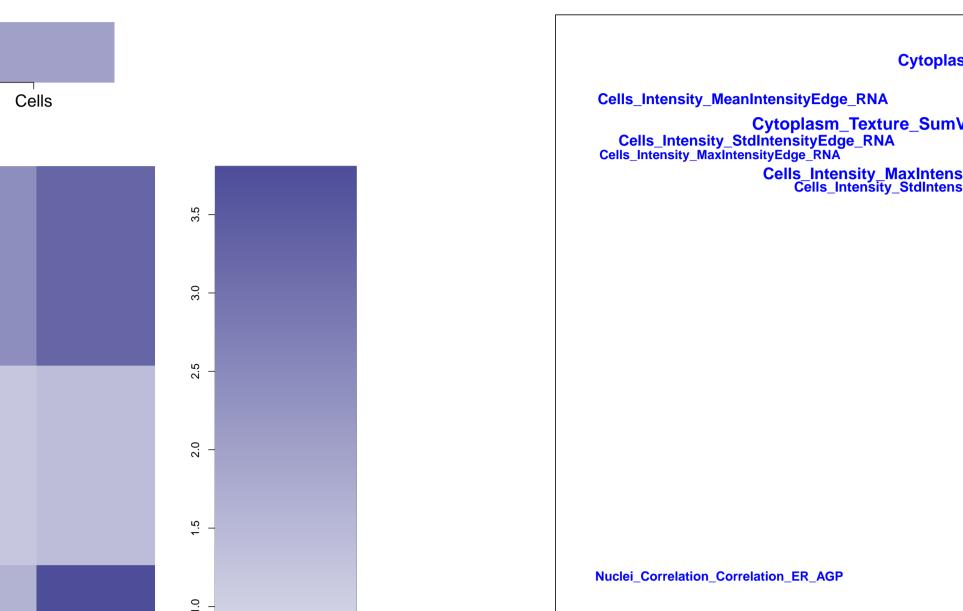
Top 5 genes negatively correlated to the cluster

	Expert Anr	notation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
WWTR1_WT	Canonical Hippo	Inhibitor	-0.50	0.10
STK11_WT.1	Canonical TOR	Inhibitor	-0.43	0.06
NFKBIB_WT	Canonical NFkB	Inhibitor	-0.40	0.14
TGFB1_WT	Canonical TGFbeta	Activator	-0.35	0.11
DIABLO_WT	Canonical Apoptosis	Inhibitor	-0.33	0.04

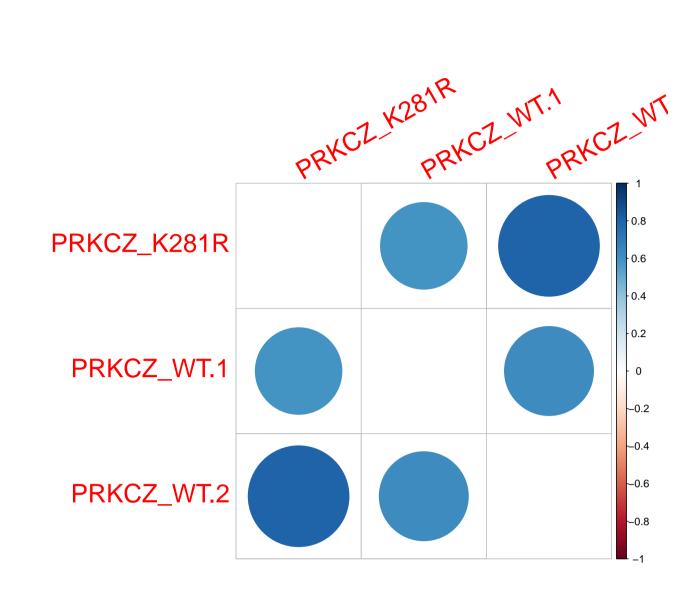
AKT1_E17K AKT1S1_WT.1 BRAF_WT.1 CCND1_WT.1 CDKN1A_WT CEBPA_WT.1 CSNK1A1_WT.3 CXXC4_WT DVL3_WT GLI1_WT MAP3K2_WT.1 MYD88_L265P PRKCZ_K281R RBPJ_WT.1 WWTR1_WT AKT3_E17K AKT1S1_WT.2 BRAF_WT.2 CCND1_WT.2 HRAS_G12V CEBPA_WT.2 MAPKAP1_WT STK3_WT.1 TGFBR1_K232R PRKACA_WT.1 MAP3K2_WT.2 MYD88_WT PRKCZ_WT.1 RBPJ_WT.2 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.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 MAP3K4_WT.1 MAP3K5_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

Cytoplasm



How strongly are genes within the cluster correlated?



Nuclei Texture -Intensity -RadialDistribution -DNA AGP

Empty

Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot) PRKCZ_K281R PRKCZ_WT.1

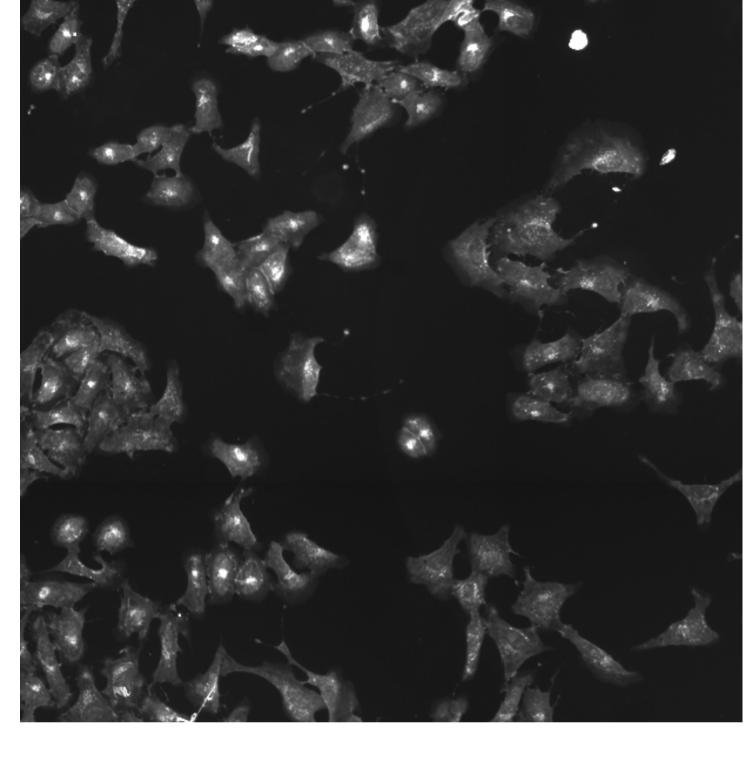
Cytoplasm_Texture_InfoMeas1_ER_10_0

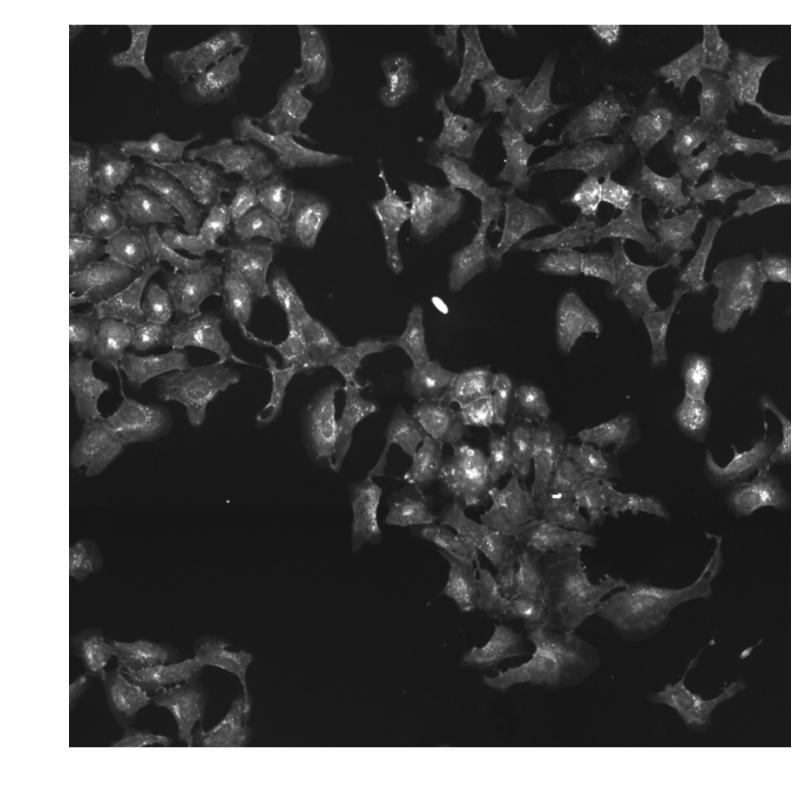
Which individual morphological features are distinguishing in the cluster relative to the untreated

samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the

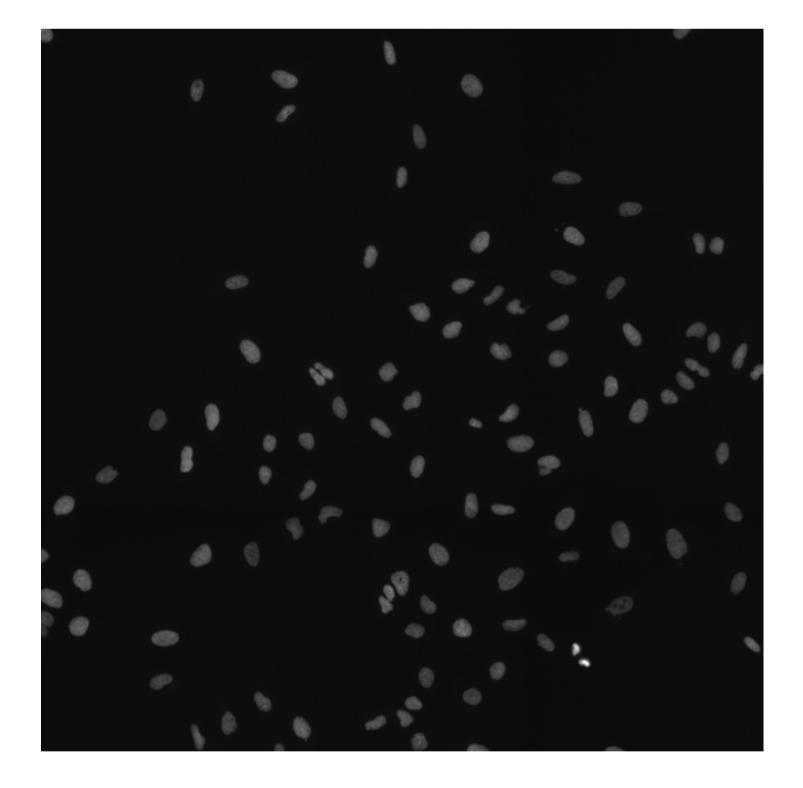
z-score value.

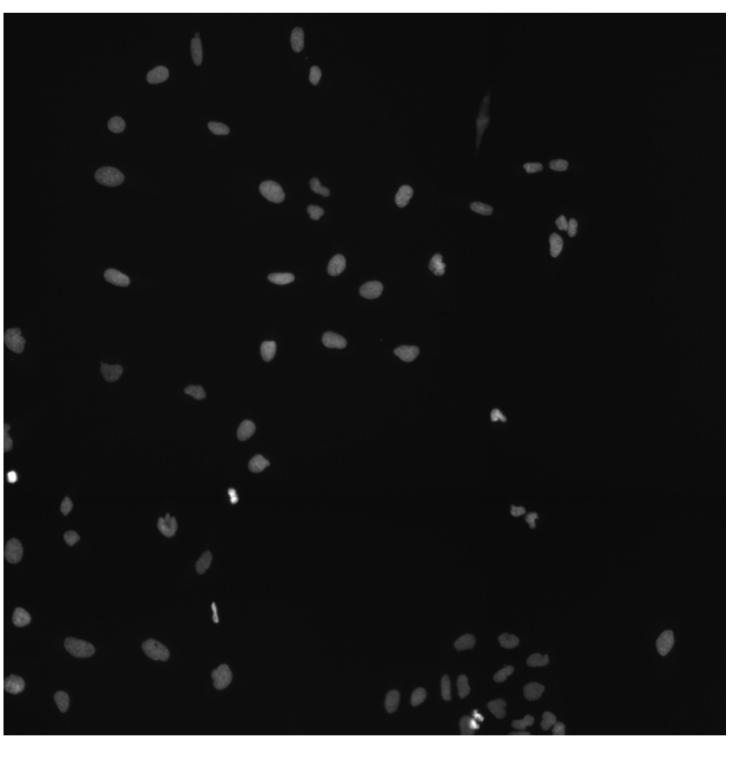
Cells_Correlation_Correlation_DNA_Mito

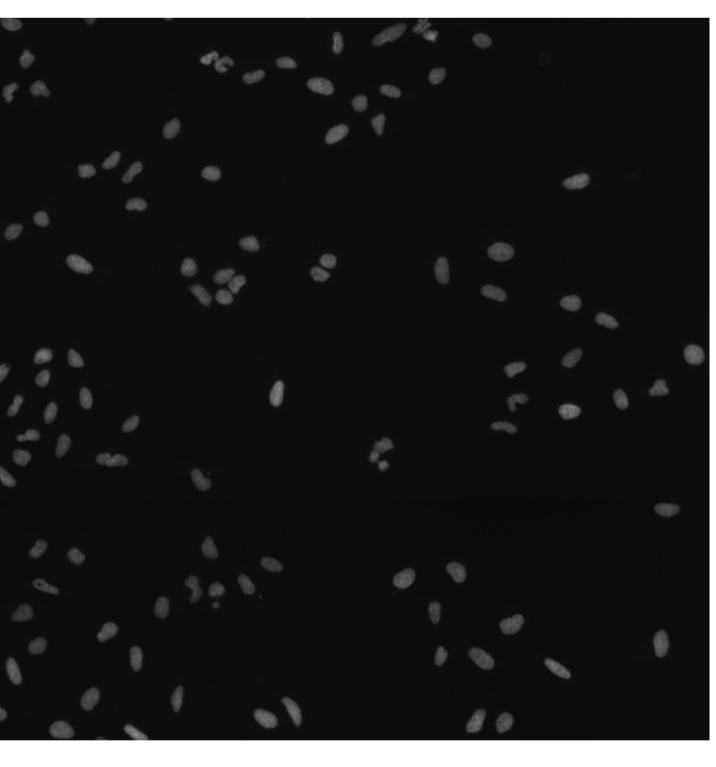


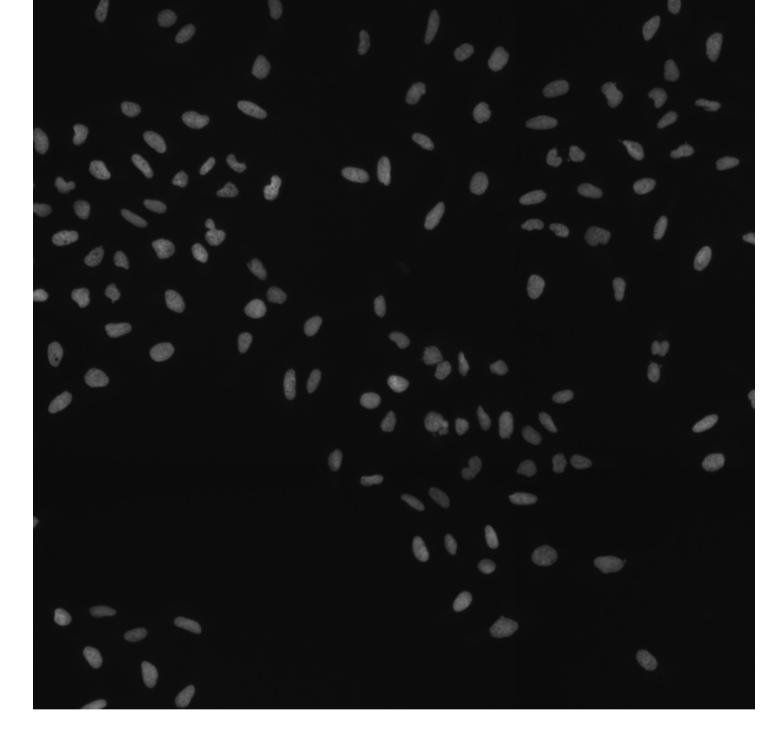


PRKCZ_WT.2









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 0.54)	gene in	against genes in cluster 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 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	1 Number of PubChem assays in which the compound was tested; assays in
								Total number of assays tested in: 626. Active in the following assays:
								• Screen for Chemicals that Extend Yeast Lifespan (AID 775)
						AreaShape -		• uHTS identification of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463190)
BRD-K28901743-001-05-3 ZINC01748812 AC1LTAWC					0.6 O.6	Texture -	Cytoplasm_Intensity_MinIntensityEdge_AGP Cytoplasm_Intensity_MinIntensityEdge_ER Cells_Intensity_UpperQuartileIntensity_DNA Cells_Texture_Correlation_RNA_3_0 Cells_Intensity_MaxIntensityEdge_ER Cells_Intensity_MedianIntensity_RNA Cells_Intensity_Intensity_MedianIntensity_RNA Cells_Intensity_MedianIntensity_RNA	 Single concentration confirmation of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463213) Fluorescence-based biochemical primary high

say (AID 463190) Single concentration confirmation of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463213) • Fluorescence-based biochemical primary high Cells_Texture_Correlation_RNA_3_0 Cells_Texture_InfoMeas2_ER_5_0

Cells_RadialDistribution_MeanFrac_RNA_4of4

Cytoplasm_Texture_Variance_RNA_3_0

throughput screening assay to identify inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 588726) • Fluorescence Intensity-based biochemical pri-

mary high throughput screening assay to identify activators of kallikrein-7 (K7) zymogen (AID 652039) • Fluorescence Intensity-based biochemical pri-

mary high throughput confirmation assay to identify activators of kallikrein-7 (K7) zymogen (AID 686949)

• Counterscreen for activators of kallikrein-7 (K7) zymogen: Fluorescence intensity-based biochemical high throughput counterscreen assay for activators that optically interfere with measurement of EDANS-DABCYL fluorescence (AID 686952)

ZINC1748812 CCG-15676 STL331422 BAS 00558059 SMR000175471 ST50181975 PubChem CID: 1555494

MLS000552933

NA (in 1 replicates)

 $\begin{array}{c|c} 0.56 \pm 0.14 \\ \hline \text{Treatment} & \text{Score} \\ \hline \text{PRKCZ.K281R} & 0.70 \\ \hline \text{PRKCZ.WT.1} & 0.43 \\ \hline \text{PRKCZ.WT.2} & 0.55 \\ \hline \end{array}$ NA

ART1_E17K ART1S1_WT1 BRAF_WT1 CCND1_WT1 CSNN1A_WT CEBPA_WT1 CSNN1A_WT3 CXXC4_WT DVI3_WT GLI1_WT MAP9K2_WT1 MYDB8_L288P PRKC2_X3818 RBPJ_WT1 WYTR_WT ART3_WT2 ARS_GIVE CBPA_WT2 MAPKAP1_WT STK3_WT1 TOFBR1_D23R PRKAC_A_WT1 MAP9K2_WT1 MYDB8_L288P PRKC2_X3818 RBPJ_WT1 WYTR_WT ARS_GIVE WYTR_WT2 ARS_GIVE WYTR_WT2 TOFBR1_D23R PRKAC_A_WT1 MAP9K2_WT2 MYDB8_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAP9K2_WT2 MYDB8_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MYDB8_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAP9K2_WT1 SKI_WT1 TOFBR1_D23R PRKAC_A_WT1 MAPSK_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAPSK_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAPSK_WT2 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAPSK_WT1 MAPKAP1_WT1 TOFBR1_D23R PRKAC_A_WT1 MAPSK_WT1 MAPKAP1_WT1 MAPKAP1_WT

Intensity -RadialDistribution -

