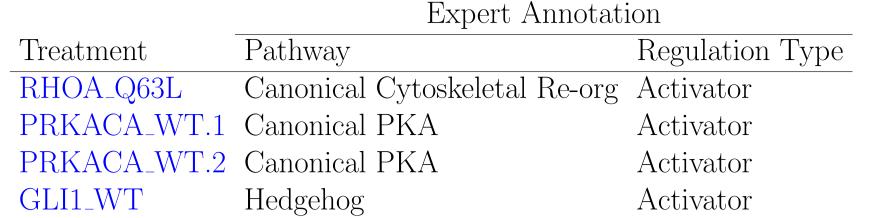
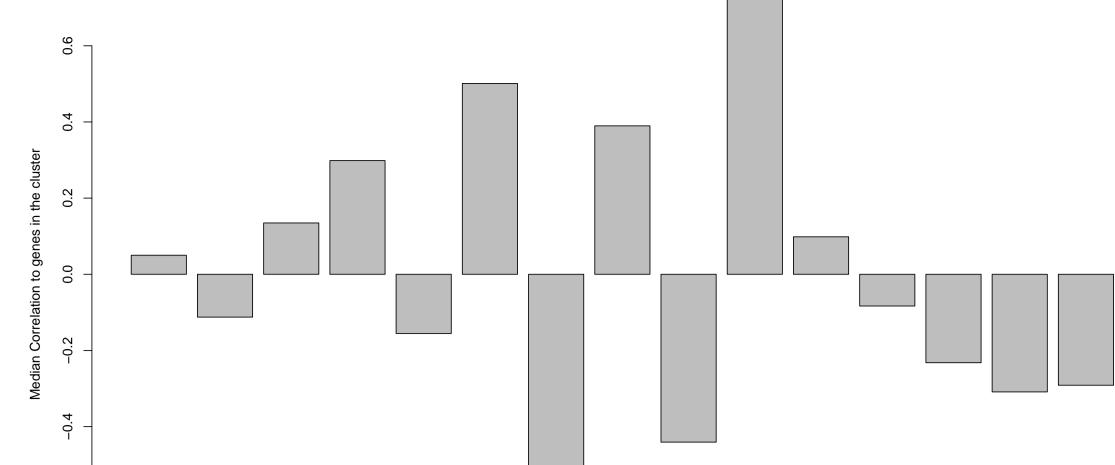
How similar is this cluster to the other clusters?

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





Top 5 genes negatively correlated to the cluster

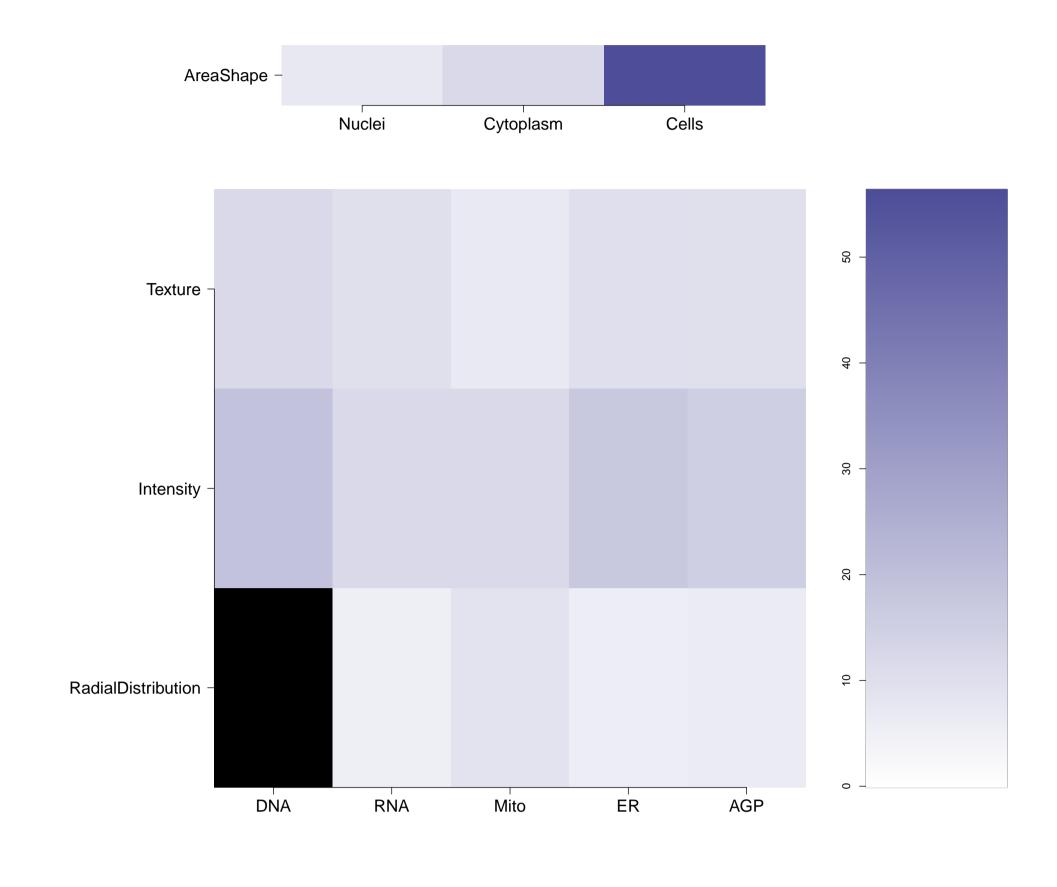
	Expert Ann	otation		
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
CSNK1A1_WT.3	Canonical WNT	Inhibitor	-0.54	0.0
RPS6KB1_WT.1	Canonical TOR	Activator	-0.54	0.1
$AKT1_WT.1$	Canonical PI3K/AKT	Activator	-0.50	0.0
$STK11_WT.2$	Canonical TOR	Inhibitor	-0.49	0.0
MAPKAP1_WT	Canonical TOR	Activator	-0.49	0.1

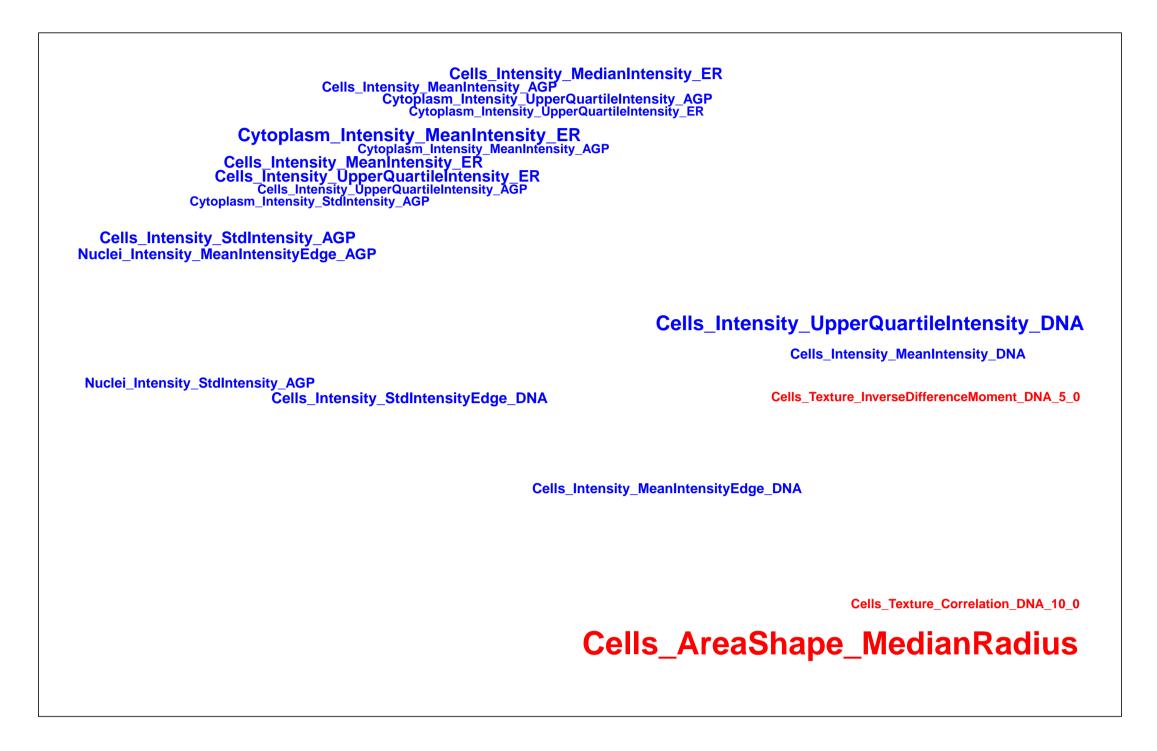
AKT1_E17K AKT1S1_WT.1 BRAF_WT.1 CCND1_WT.1 CDKN1A_WT CEBPA_WT.1 CSNK1A1_WT.3 CXXC4_WT DVL3_WT GLI1_WT MAP3K2_WT.1 MYD88_L265P PRKCZ_K281R RBPJ_WT.1 WWTR1_WT AKT3_E17K AKT1S1_WT.2 BRAF_WT.2 CCND1_WT.2 HRAS_G12V CEBPA_WT.2 MAPKAP1_WT STK3_WT.1 TGFBR1_K232R PRKACA_WT.1 MAP3K2_WT.2 MYD88_WT PRKCZ_WT.1 RBPJ_WT.2 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.2 PRKACA_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PRKACA_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PRKACA_WT.2 PRKACA_WT.2

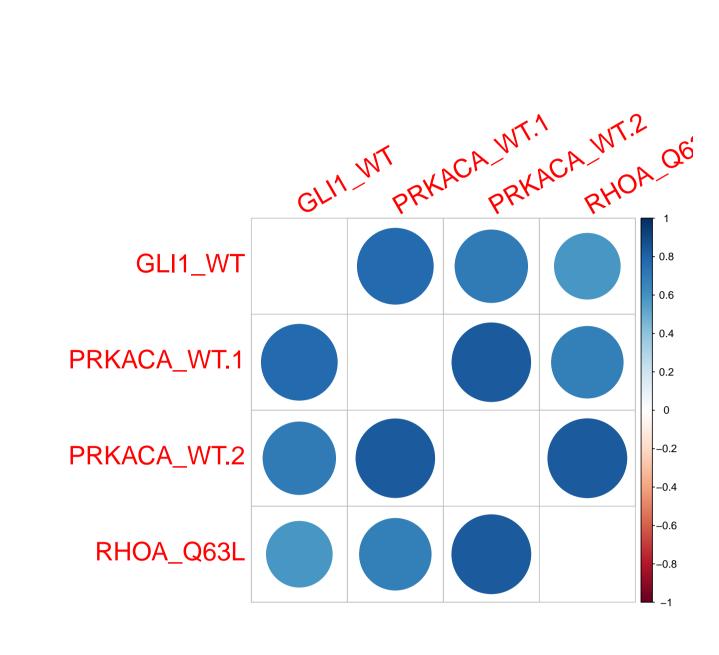
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the category

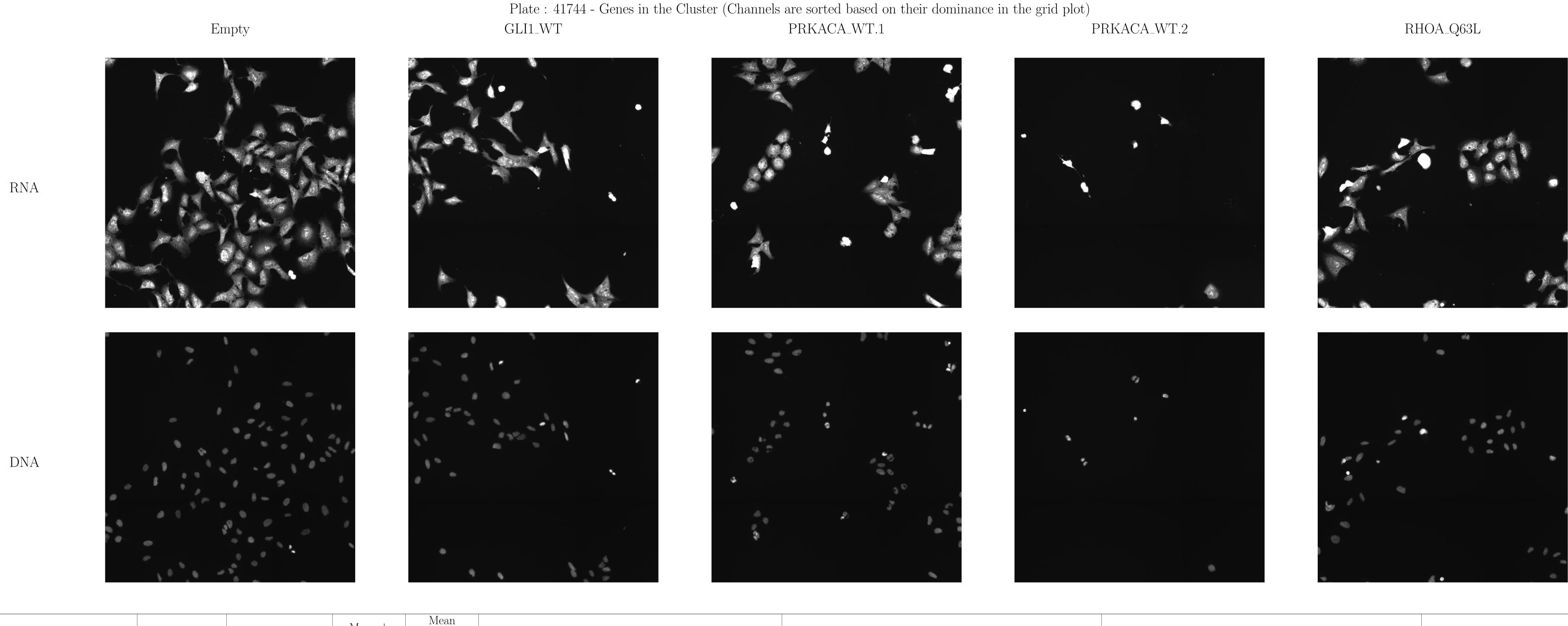
Which individual morphological features are distinguishing in the cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

How strongly are genes within the cluster correlated?









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	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	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)	0.73 ± 0.04 Treatment Score GLI1_WT 0.70 PRKACA_WT.1 0.76 PRKACA_WT.2 0.77 RHOA_Q63L 0.70	0.910 ± 0.038 Treatment Score GLI1_WT 0.936 PRKACA_WT.1 0.885 PRKACA_WT.2 0.950 RHOA_Q63L 0.870	Mean Controlled to the Control	AreaShape - Nuclei Cytoplasm Cells Texture - Intensity - RadialDistribution - DNA RNA Mito ER AGP	Cells_Intensity_UpperQuartileIntensity_DNA Cytoplasm_Texture_DifferenceVariance_AGP_5_0 Cells_Intensity_MaintensityGeg_ER Cells_Intensity_MaintensityGeg_ER Cells_Intensity_MaintensityGeg_ER Cells_Intensity_MaintensityGeg_DNA Cells_Intensity_MaintensityGeg_DNA Cells_Intensity_LowerQuartileIntensity_RNA Cells_Intensity_IntegratedIntensity_RNA Cells_Intensity_IntegratedIntensity_Geg_ER Nuclei_Intensity_IntegratedIntensityGeg_ER Cells_RadiaDistribution_MeanFrae_AGP_3of4 Nuclei_Intensity_IntegratedIntensity_ER Cytoplasm_Texture_Variance_RNA_3_0 Cytoplasm_Texture_DifferenceEntropy_Mito_5_0 Cytoplasm_Texture_DifferenceEntropy_Mito_5_0 Cytoplasm_AreaShape_Compactness	Total number of assays tested in: 19.
BRD-K86981519-001-01-5 PubChem CID : 44496872		0.91 (in 4 replicates)	Treatment Score GLI1 WT 0.64	0.656 ± 0.339 Treatment Score GLI1_WT 0.152 PRKACA_WT.1 0.874 PRKACA_WT.2 0.763 RHOA_Q63L 0.837		AreaShape - Nuclei Cytoplasm Cells Texture - Intensity - RadialDistribution - DNA RNA Mito ER AGP	Cells Intensity UpperQuartileintensity DNA Cytoplasm_Texture_DifferenceVariance_AGP_5_0 Nuclei_Tenure_DifferenceCurryy_Min_3.3 Cells_Intensity_MedianIntensity_RNA Cells_Intensity_MedianIntensity_RNA Cells_Intensity_Sidninensity_Edge_AGP Cells_Relationstruction_MeanFrac_AGP_2of4 Nuclei_Texture_Variance_RNA_3.0 Nuclei_Intensity_IntegratedIntensity_ER Cells_Relationstruction_MeanFrac_AGP_3of4 Cells_Relationstruction_MeanFrac_AGP_3of4 Nuclei_Intensity_IntegratedIntensity_AGP Nuclei_Intensity_IntegratedIntensity_AGP Nuclei_Intensity_IntegratedIntensity_ER Cytoplasm_Texture_SimplexedCorrepy_Min_5_5 Cytoplasm_AreaShape_Solidity Cytoplasm_AreaShape_Compactness	Total number of assays tested in: 29.

