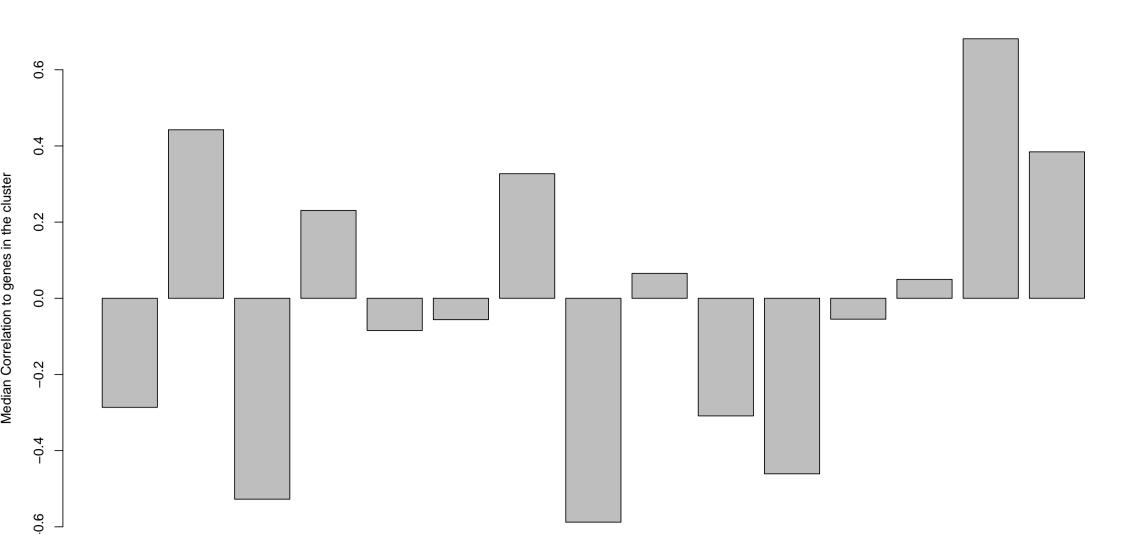
Genes in the cluster along with the pathways as annotated by experts

	Expert Annotation		
Treatment	Pathway	Regulation Type	
SMAD3_WT.1	Canonical SMAD	Activator	
RBPJ_WT.1	NOTCH	Activator	
RBPJ_WT.2	NOTCH	Activator	

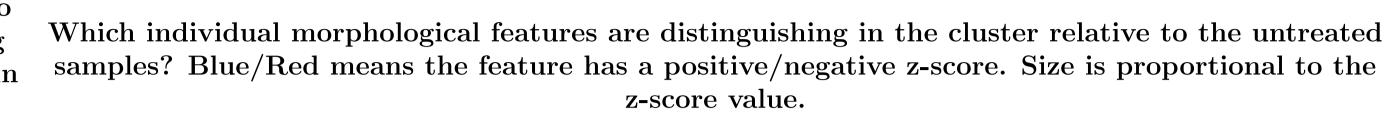


Top	5	genes	negatively	correlated	\mathbf{to}	the	cluster

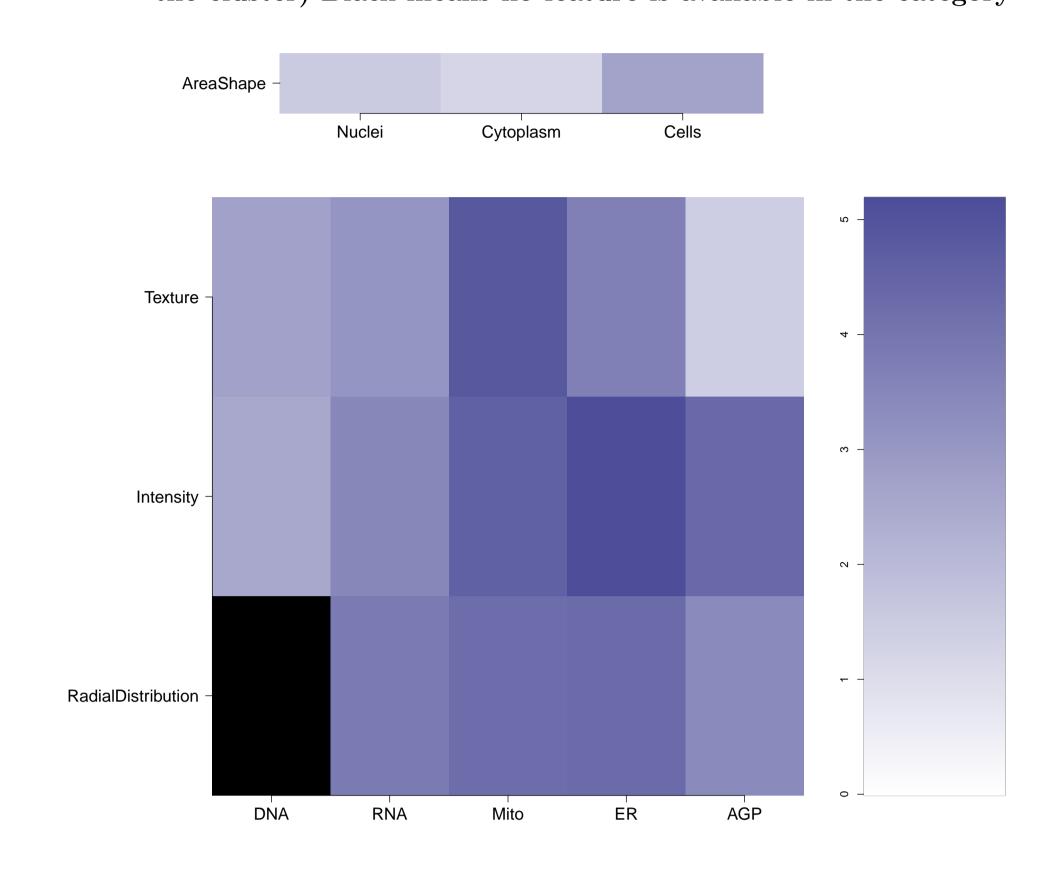
Treatment Pathway Regulation Type Mean Correlation Standard Deviation RAF1_WT.2 Canonical MAPK Activator -0.62 0.06
RAF1_WT.2 Canonical MAPK Activator -0.62 0.06
CXXC4_WT WNT Inhibitor -0.60 0.01
STK3_WT.1 Canonical Hippo Activator -0.60 0.09
MAP3K2_WT.1 Canonical MAPK Activator -0.58 0.16
PIK3CB_WT.2 Canonical PI3K/AKT Activator -0.55 0.13

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 WAP2K4_WT.2 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP3K6_WT WAP3K5_WT MAP3K6_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



How strongly are genes within the cluster correlated?



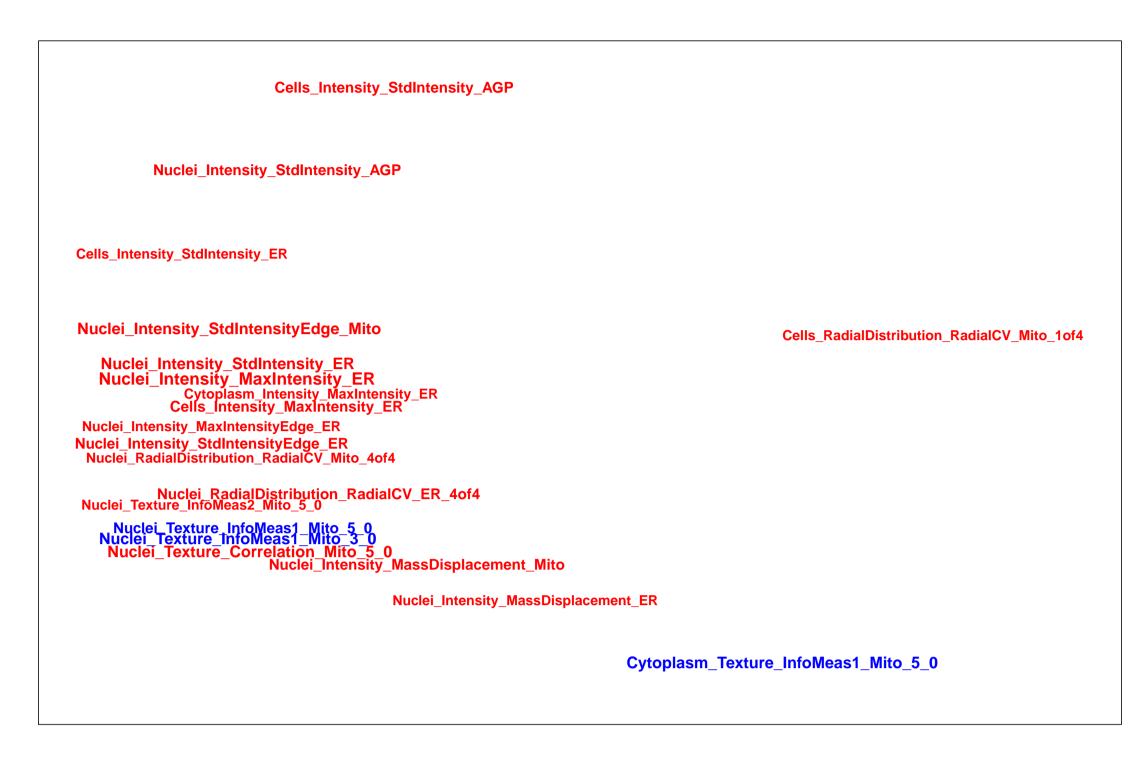
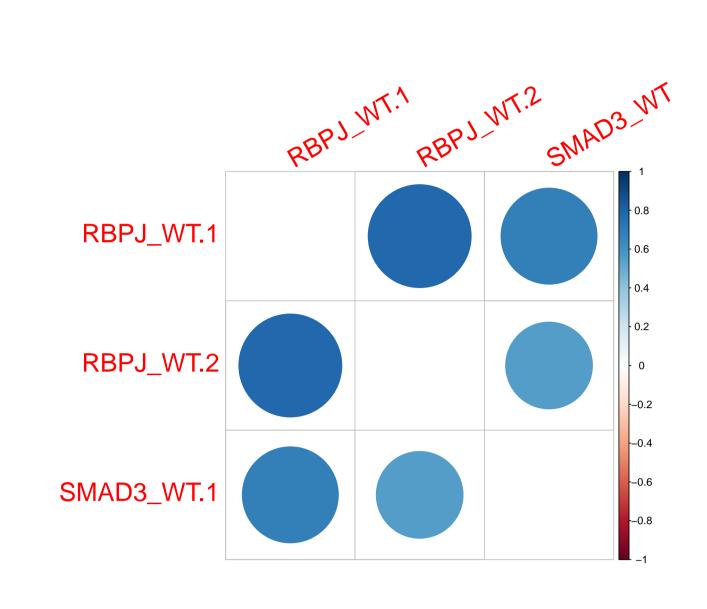
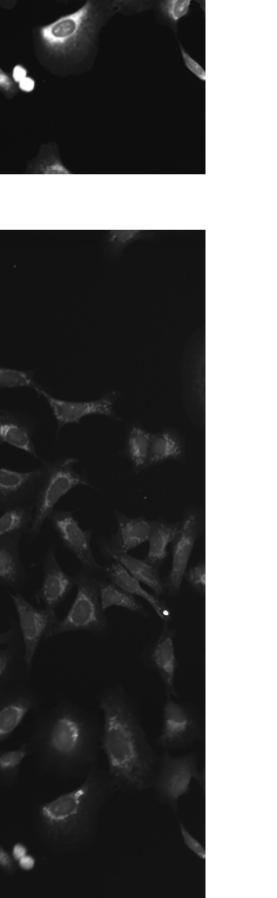


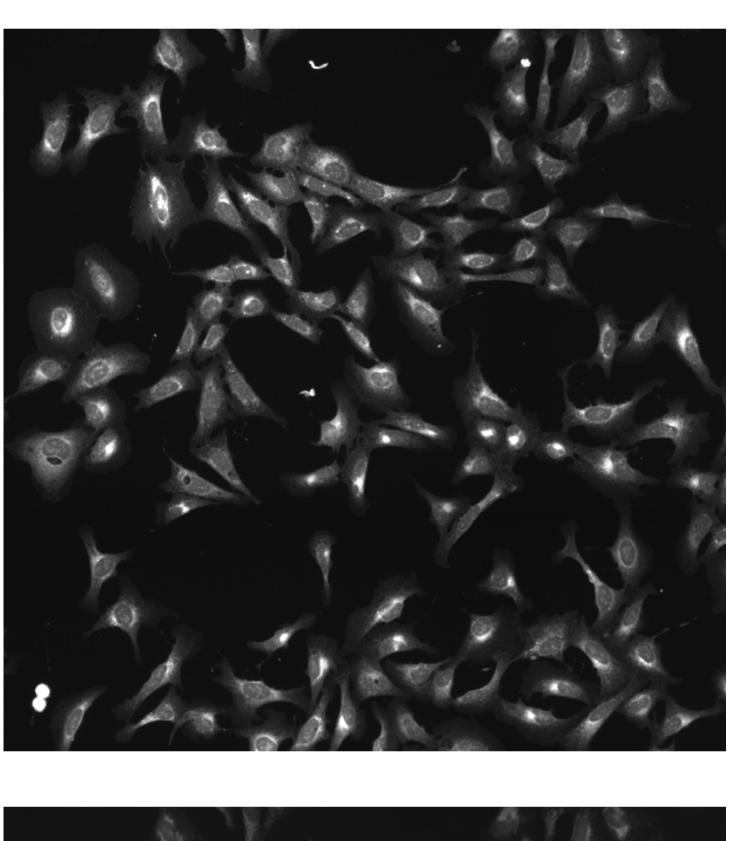
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



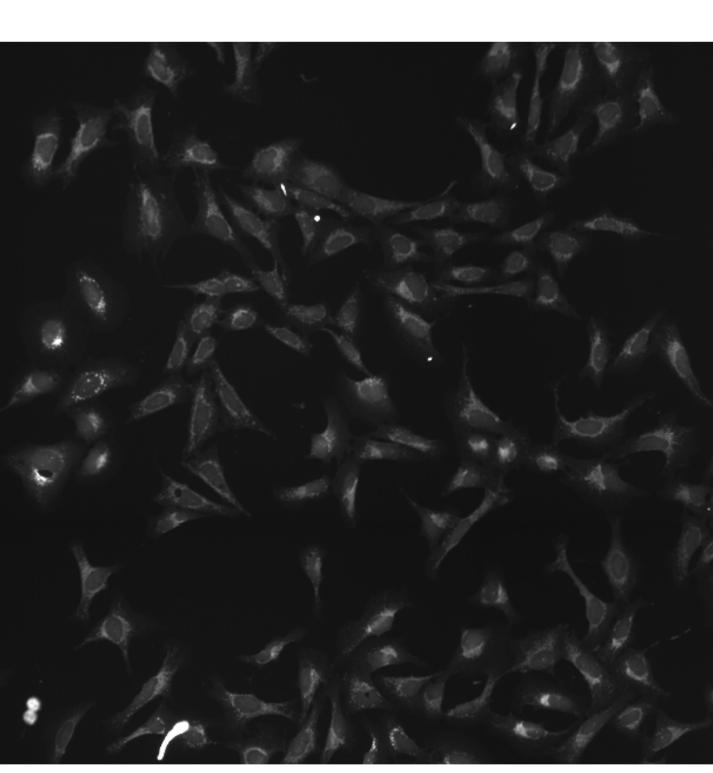
Empty

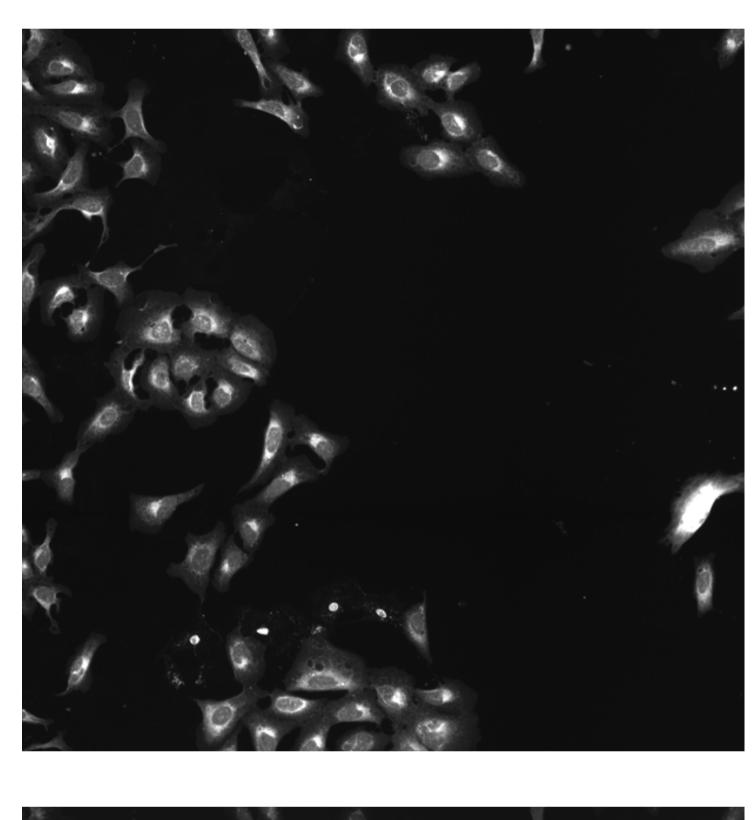
ER



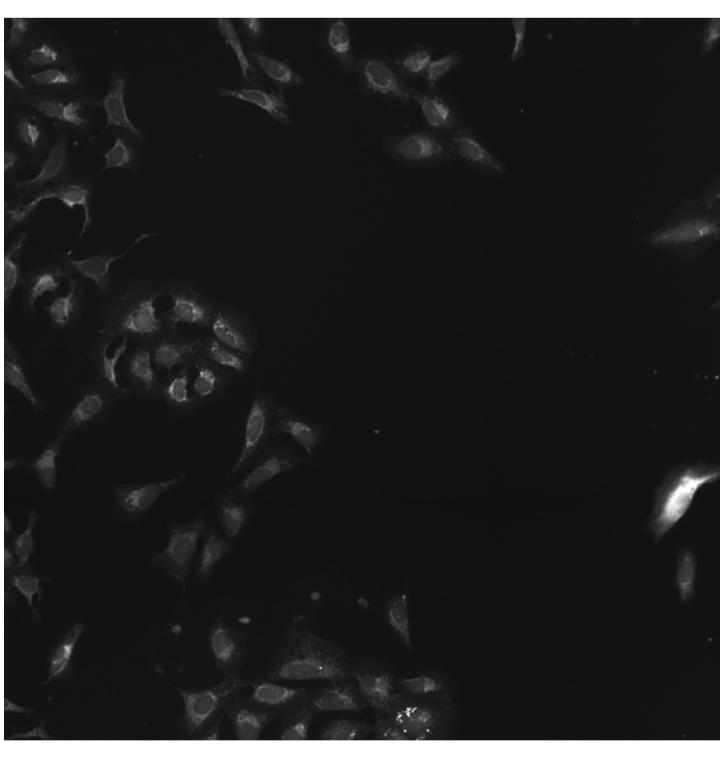


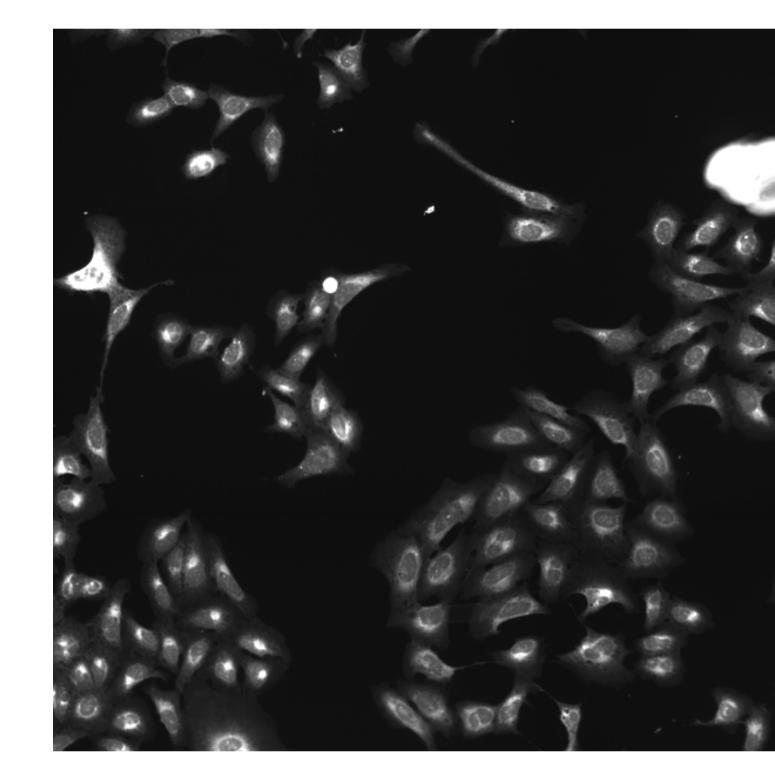
 $RBPJ_WT.1$



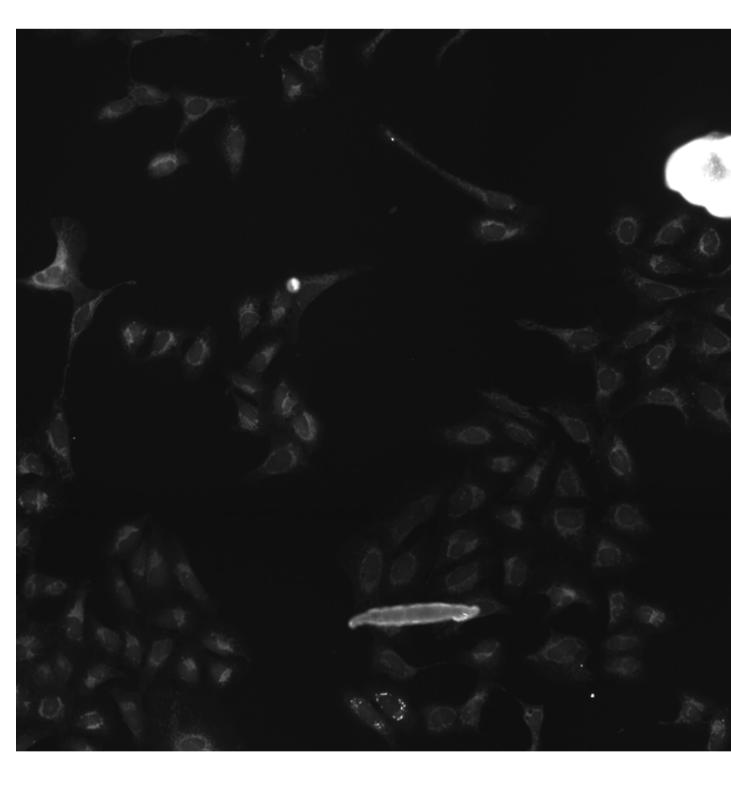


 $RBPJ_WT.2$





 $SMAD3_WT.1$



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 signatur (95th DMSO replicate correlation is 0.52)	and each gene in cluster; Tables contain data for individual genes 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	the compound was tested: assays in
BRD-K62943397-001-01-0 PubChem CID: 54646065	OH NH	NA (in 1 replicates	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Mean Company of the C	AreaShape - Nuclei Cytoplasm Cells Texture -	Cytoplasm_Intensity_MaxintensityEdge_AGP Cytoplasm_Intensity_MaxintensityEdge_AGP Cells_RadialDistribution_RadialCV_ER_1of4 Cells_RadialDistribution_RadialCV_ER_4of4 Cytoplasm_Texture_Derrelation_AGP_3_Tribution_RadialCV_ER_4of4 Cytoplasm_Texture_Derrelation_AGP_3_Tribution_RadialCV_ER_4of4 Cells_RadialDistribution_Macnfrac_AGP_2of4 Cells_RadialDistribution_RadialCV_AGP_2of4 Nuclei_Texture_Variance_RNA_3_0 Nuclei_Texture_Variance_RNA_3_0 Nuclei_Intensity_IntegratedintensityEdge_ER Cells_RadialDistribution_RadialCV_AGP_3of4 Nuclei_Texture_InverseDifferenceMoment_Mito_5_0 Nuclei_Texture_InverseDifferenceMoment_Mito_5_0 Nuclei_AreaShape_Zernike_6_6 Cytoplasm_AreaShape_Zernike_7_1 Cells_Neighbors_PercentTouching_Adjacent	Total number of assays tested in: 39.

