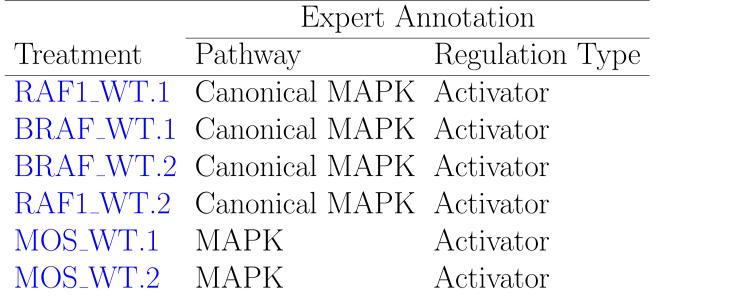
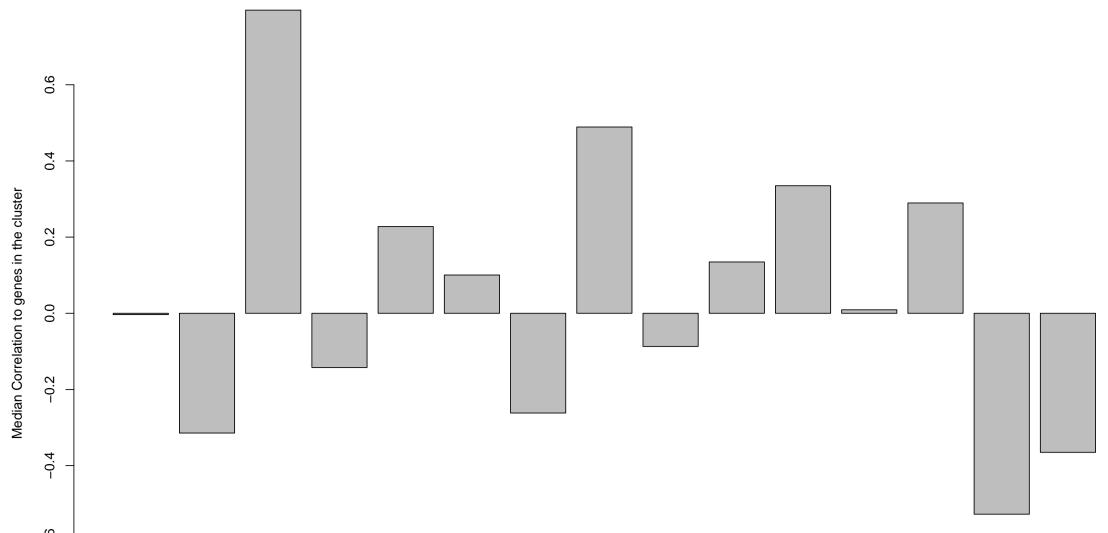
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein

How similar is this cluster to the other clusters?

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





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

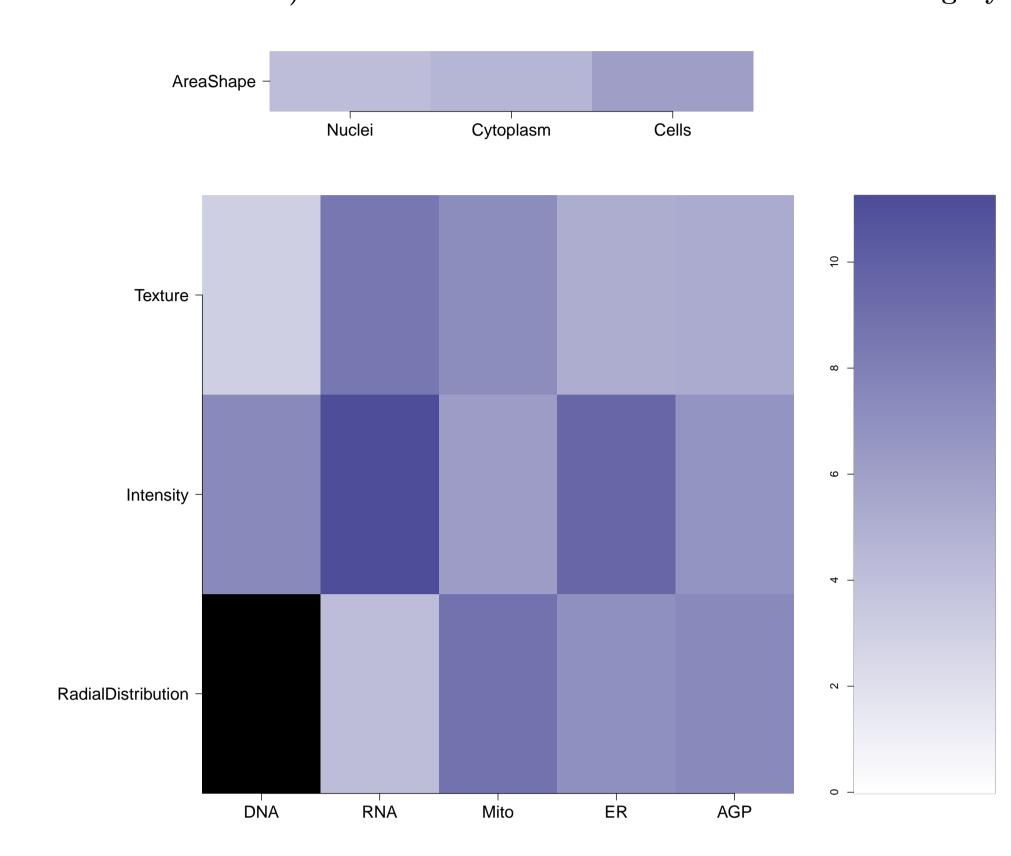
	Expert Annota						
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation			
RBPJ_WT.1	NOTCH	Activator	-0.60	0.07			
ERN1_WT.1	Canonical ER Stress/UPR	Activator	-0.55	0.06			
XBP1_WT.1	Canonical ER Stress/UPR	Activator	-0.51	0.09			
RBPJ_WT.2	NOTCH	Activator	-0.49	0.10			
YAP1_WT.3	Canonical Hippo	Inhibitor	-0.48	0.11			

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 STK3_WT.2 TGFBR1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.3 PRKACA_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP2K4_WT.1 MAP3K4_WT.1 MAP3K4_WT.1 MAP3K4_WT.1 MAP3K4_WT.1 MAP3K4_WT.1 MAP3K6_WT WAP3K6_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?



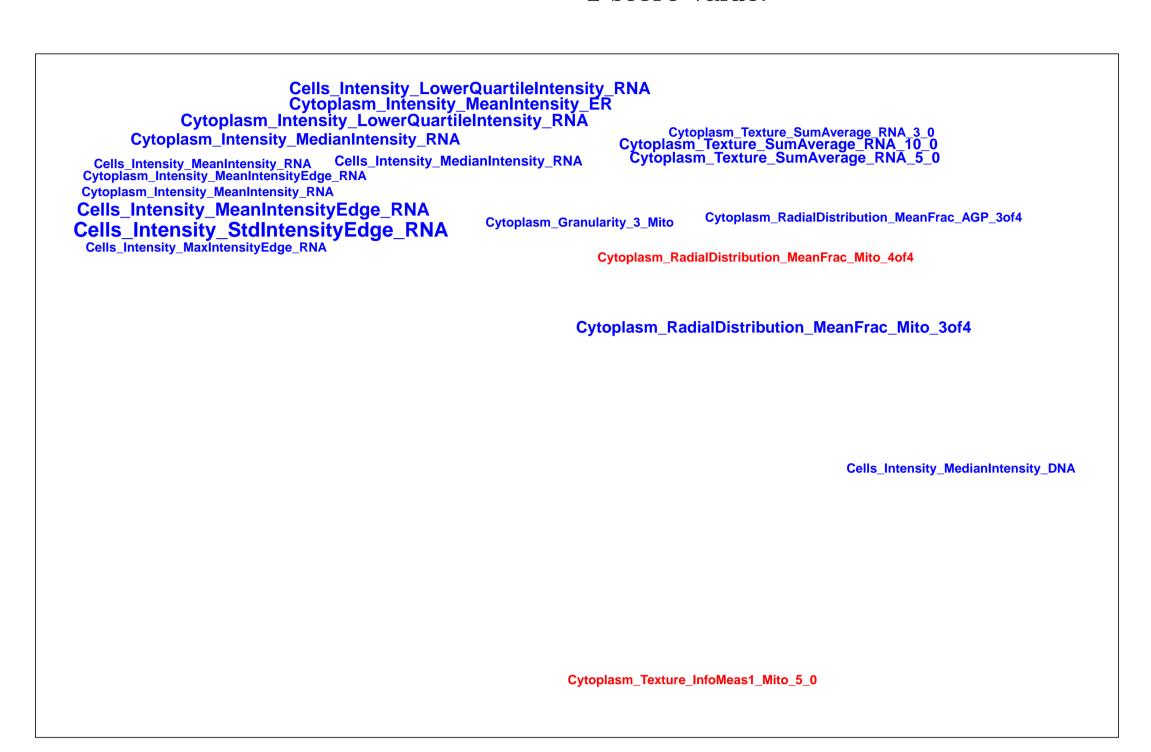
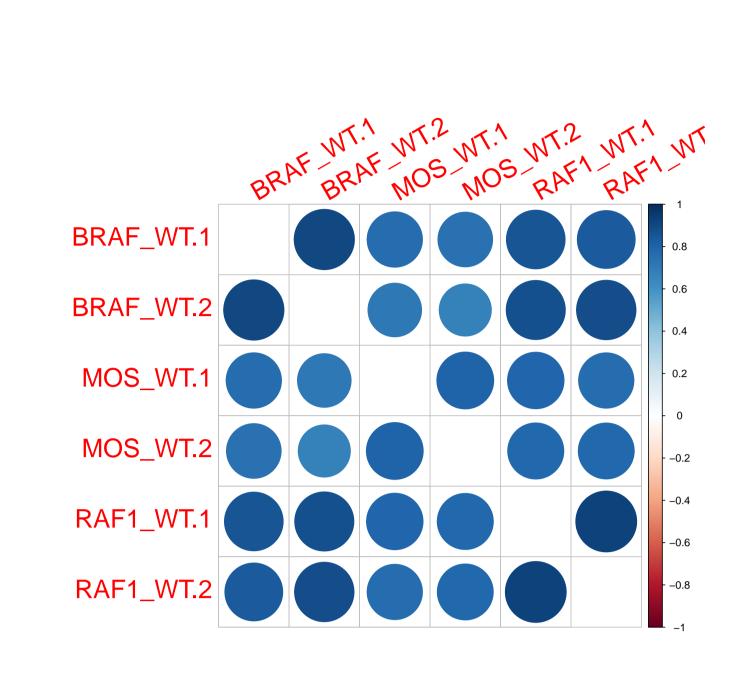
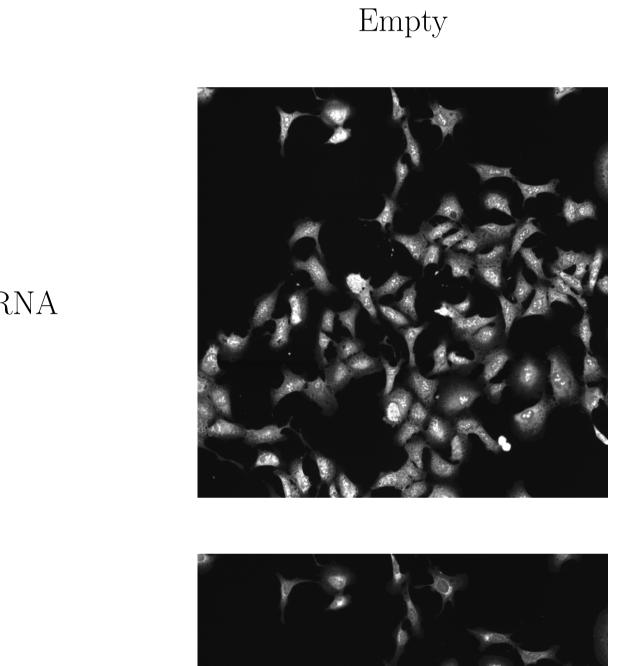
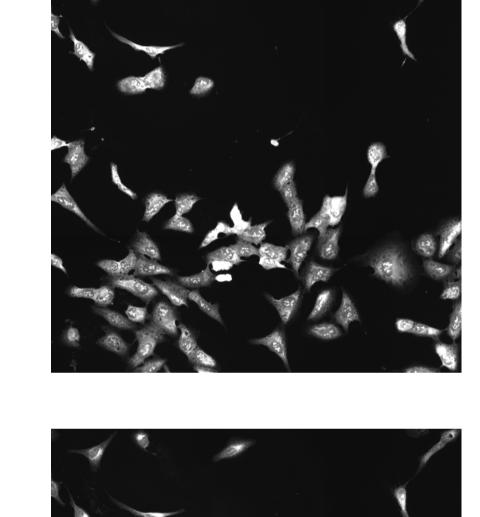


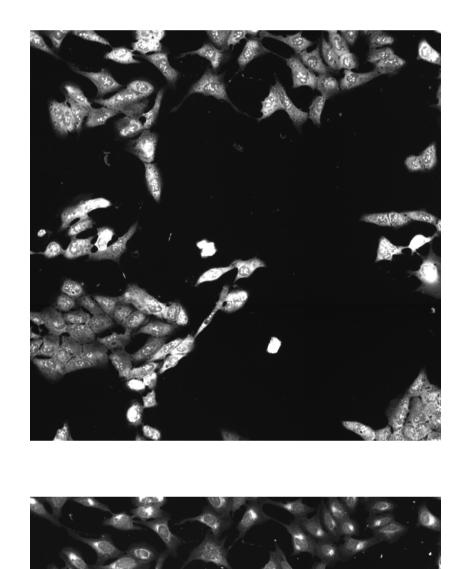
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



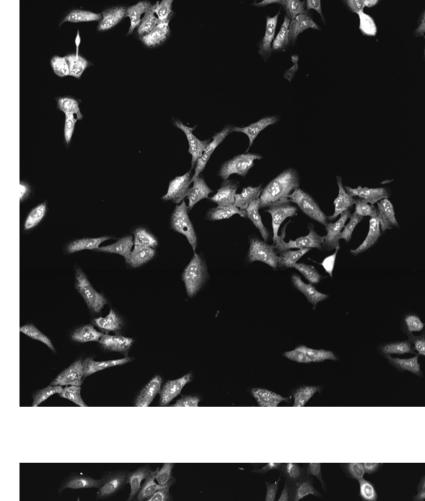




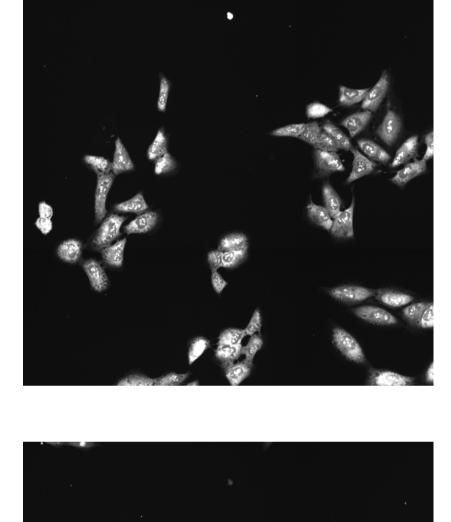
 $BRAF_WT.1$



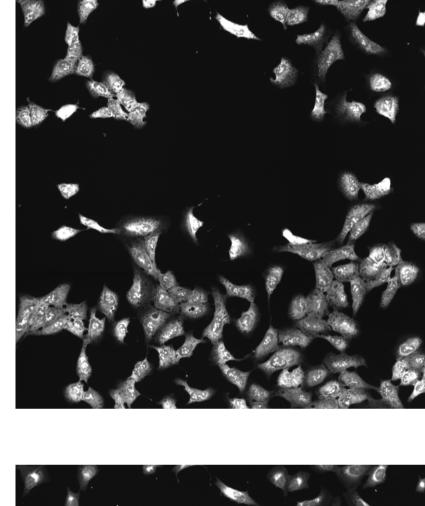
 $BRAF_WT.2$



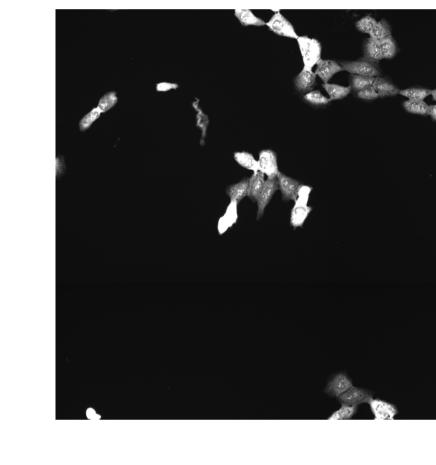
 $MOS_WT.1$



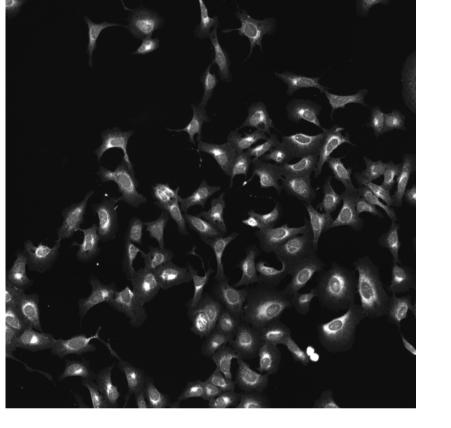
 $MOS_WT.2$

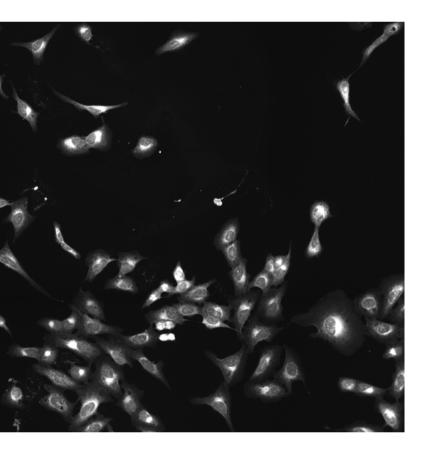


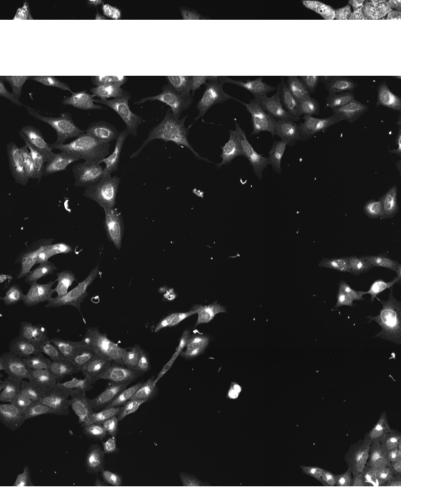
 $RAF1_WT.1$

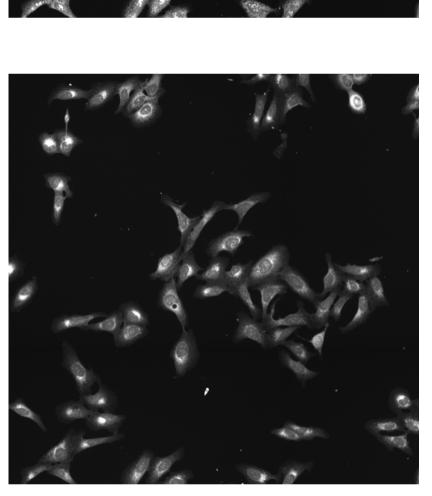


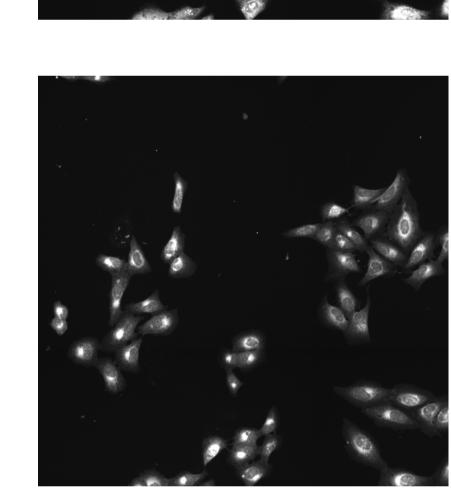
 $RAF1_WT.2$

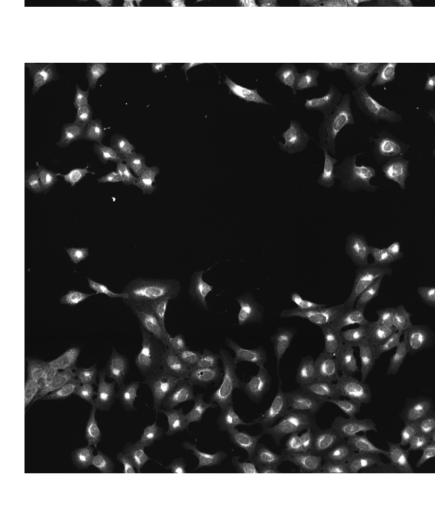


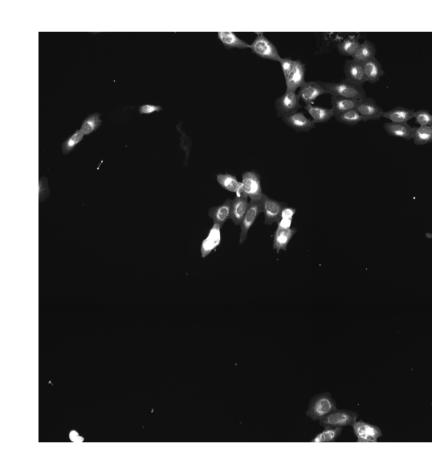












Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	gene in	using L1000 profiling ± standard deviation; Tables	How similar is the compound signature to the gene clusters in this experiment? (Yellow and red lines correspond to top/bottom 1st and 5th percentile DMSO correlation to all the genes)	Common distinguishing feature categories in the compound	\perp 7 coord in magnified in the composine and office inactive $l-$	the compound was tested: assays in
BRD-K62246028-001-05-6 T5321448 AC1M8FFC MLS000772051 HMS2744H14 ZINC12484090 SMR000376604 PubChem CID: 2485743		0.85 (in 2 replicates)	0.56 ± 0.06 Treatment Score BRAF_WT.1 0.61 BRAF_WT.2 0.57 MOS_WT.1 0.62 MOS_WT.2 0.53 RAF1_WT.1 0.59 RAF1_WT.2 0.47	NA	West Consistent of the compound of the state of the compound o	AreaShape - Nuclei Cytoplasm Cells Texture - 97 - 97 - 97 - 97 - 97 - 97 - 97 - 9	Cytoplasm_Intensity_MinintensityEdge_AGP Nuclei_Texture_SumVariance_AGP_3_0 Cytoplasm_Intensity_MinintensityEdge_ER Cells_Intensity_UpperQuartileIntensity_DNA Nuclei_Texture_DifferenceEntropy_ER_3_0 Cells_Texture_InfoMeas2_ER_5_0 Cytoplasm_Texture_InfoMeas2_ER_5_0 Cytoplasm_Texture_InfoMeas2_DNA_3_0 Cells_Intensity_LowerQuartileIntensity_RNA Cells_Intensity_LowerQuartileIntensity_RNA Cytoplasm_Intensity_MinintensityEdge_ER Cytoplasm_Intensity_MinintensityEdge_RNA Cytoplasm_Intensity_IntegratedIntensityEdge_RNA Nuclei_Texture_SumEntropy_Min_5_0 Nuclei_Texture_Gabor_RNA_3 Nuclei_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_UpperQuartileIntensity_ER Cytoplasm_Texture_InfoMeas2_ER_5_0 Cytoplasm_Texture_InfoMeas2_ER_5_0 Cytoplasm_Texture_InfoMeas2_ER_5_0	 Total number of assays tested in: 554. Active in the following assays: Aqueous Solubility from MLSMR Stock Solutions (AID 1996) Counterscreen for inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis: Absorbance-based biochemical high throughput Glycerophosphate Dehydrogenase-Triosephosphate Isomerase (GDH-TPI) full deck assay to identify assay artifacts (AID 588335)
BRD-K88156935-001-01-8 PubChem CID: 44494858	OH NH	0.65 (in 4 replicates)	Treatment Score BRAF_WT.1 0.55 BRAF_WT.2 0.59 MOS_WT.1 0.43 MOS_WT.2 0.47 RAF1_WT.1 0.55	0.762 ± 0.118 Treatment Score BRAF_WT.1 0.702 BRAF_WT.2 0.720 MOS_WT.1 0.955 MOS_WT.2 0.748 RAF1_WT.1 0.833 RAF1_WT.2 0.616	Sometation of genes in the contract of the con	AreaShape - Nuclei Cytoplasm Cells Texture - Intensity - RadialDistribution -	Cults_Intensity_DoperChart/Behnensity_DNA Cells_Intensity_MaxIntensityEdge_ER Cells_Intensity_MedianIntensity_RNA Cytoplasm_Testure_Intensity_MedianIntensity_RNA Cytoplasm_Testure_Intensity_IntegratedIntensity_ER Cells_Intensity_IntegratedIntensity_ER Cells_Intensity_IntegratedIntensity_ER Cults_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_MinIntensityEdge_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_IntegratedIntensity_ER Cytoplasm_Intensity_UpperQuartileIntensity_ER Cytoplasm_ArtaShape_Zernike_4.2	Total number of assays tested in: 53.

