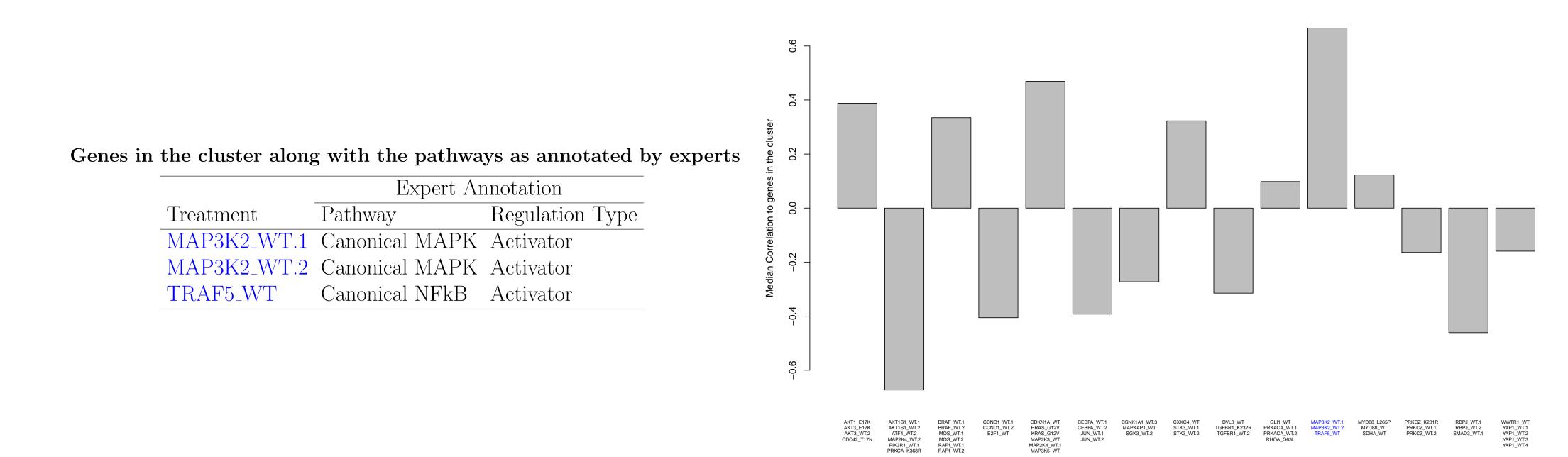
How similar is this cluster to the other clusters?



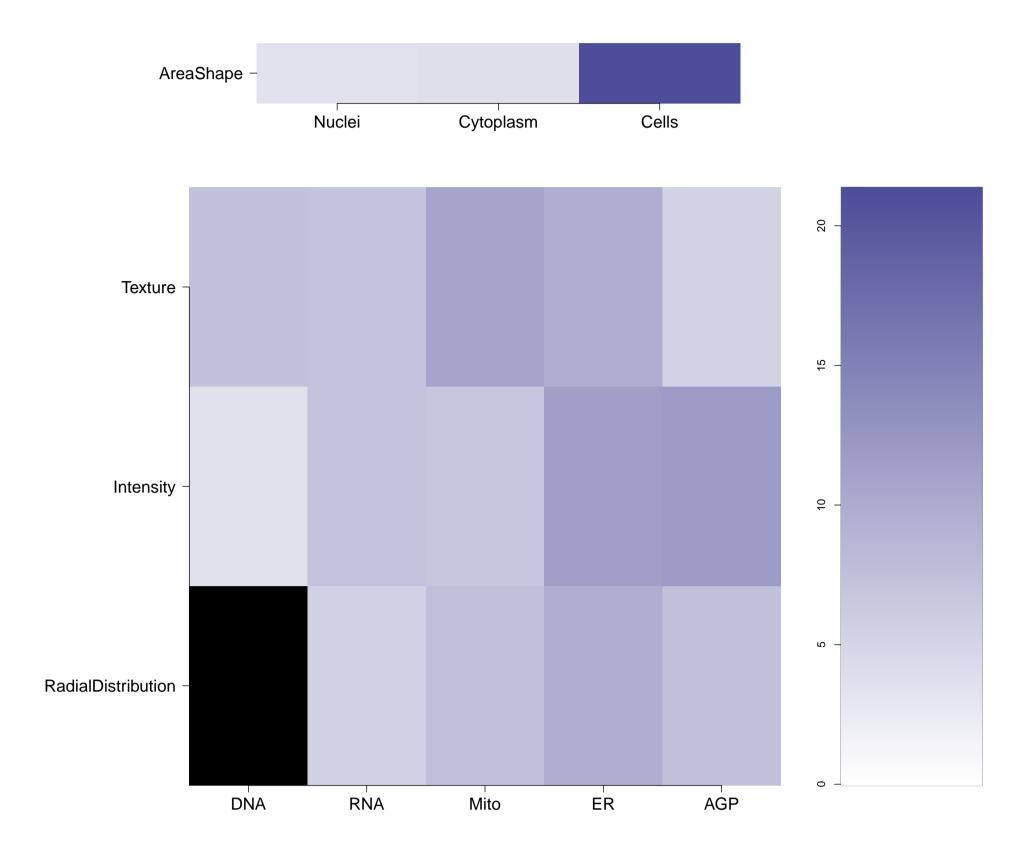
Top 5 genes negatively correlated to the cluster
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Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
MAP2K4_WT.2	Canonical MAPK	Activator	-0.68	0.13
AKT1S1_WT.1	TOR	Inhibitor	-0.67	0.05
PIK3R1_WT.1	Canonical PI3K/AKT	Activator	-0.65	0.07
RBPJ_WT.1	NOTCH	Activator	-0.64	0.10
AKT1S1_WT.2	TOR	Inhibitor	-0.64	0.06

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?



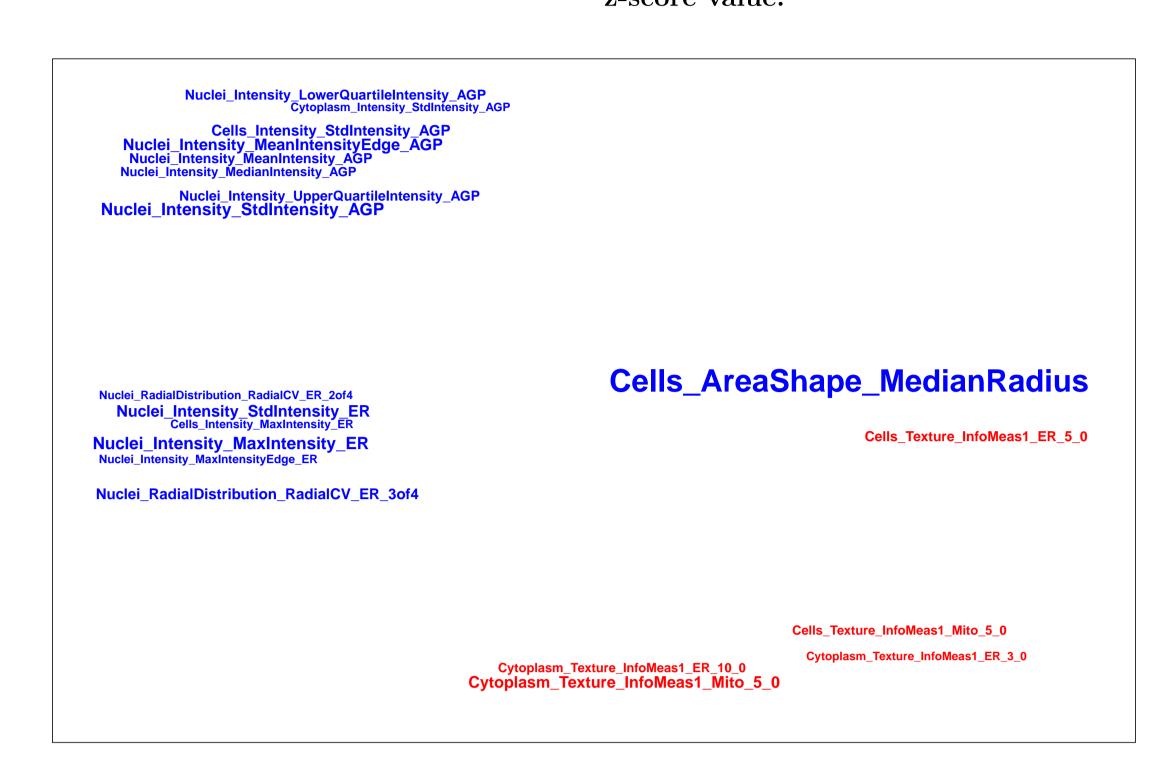
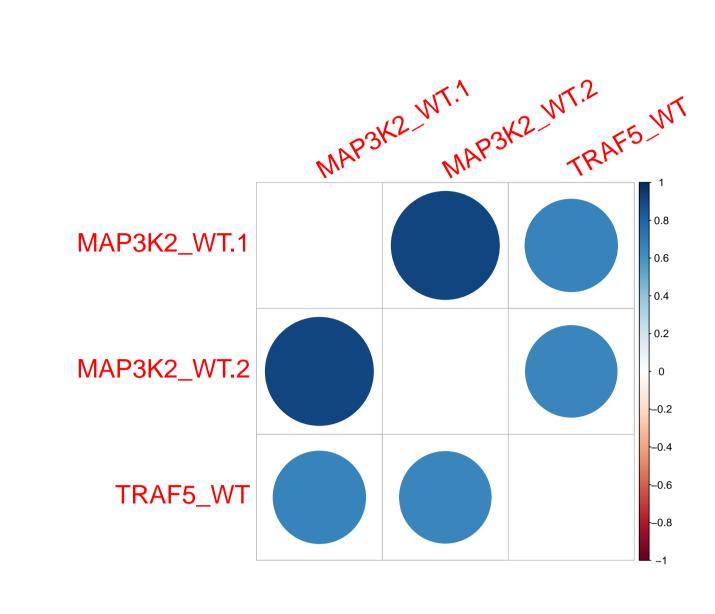
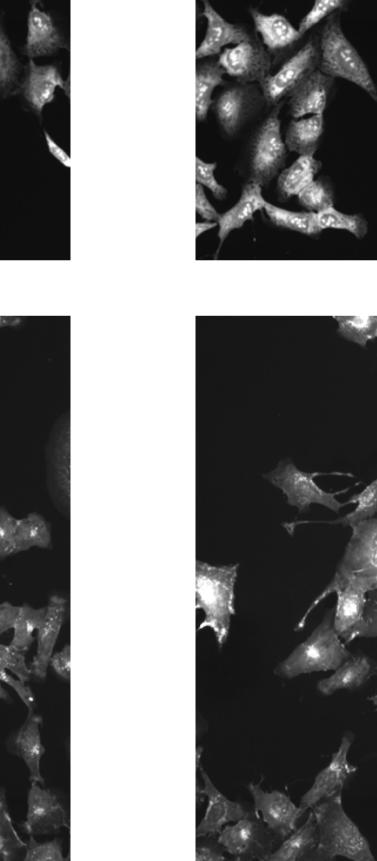
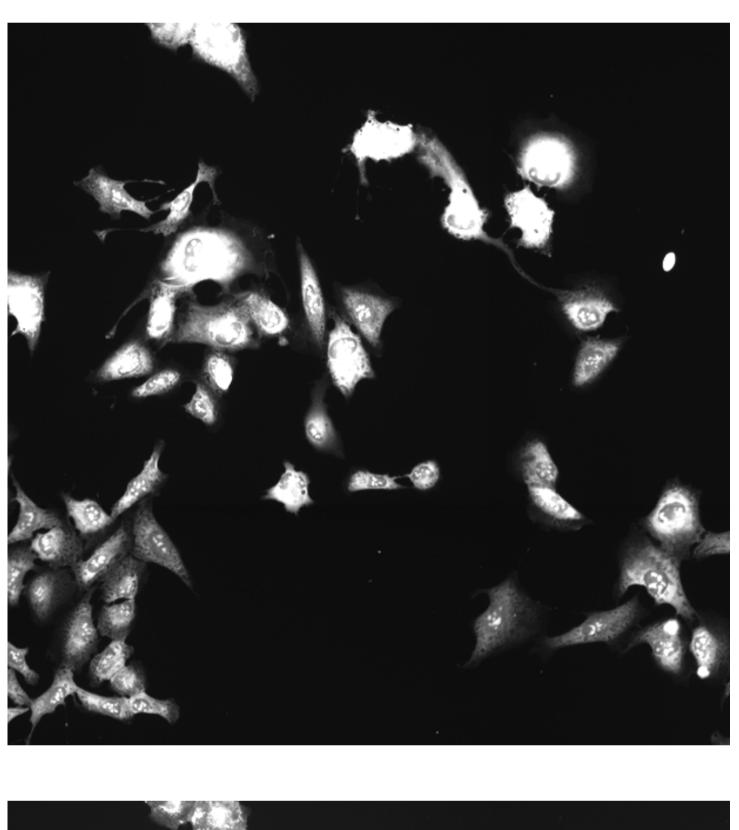


Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

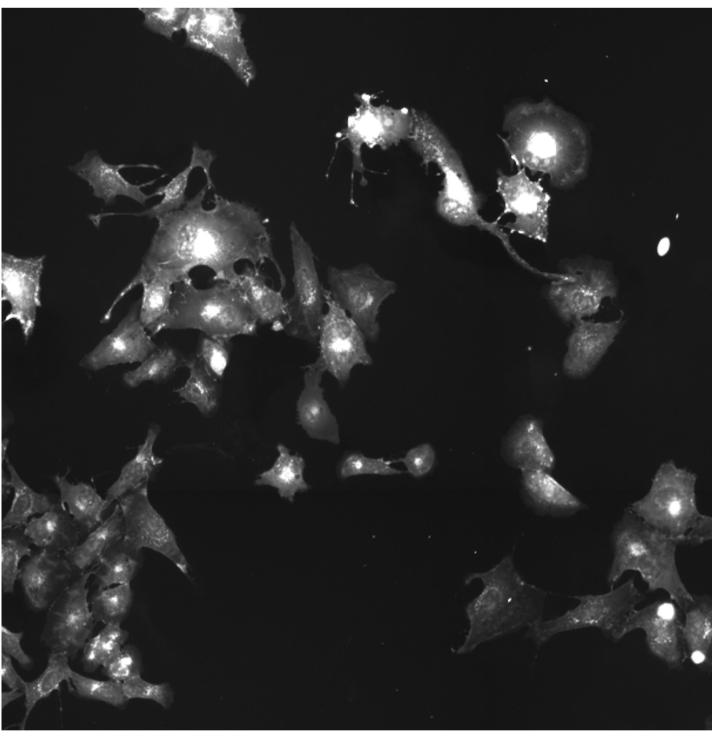


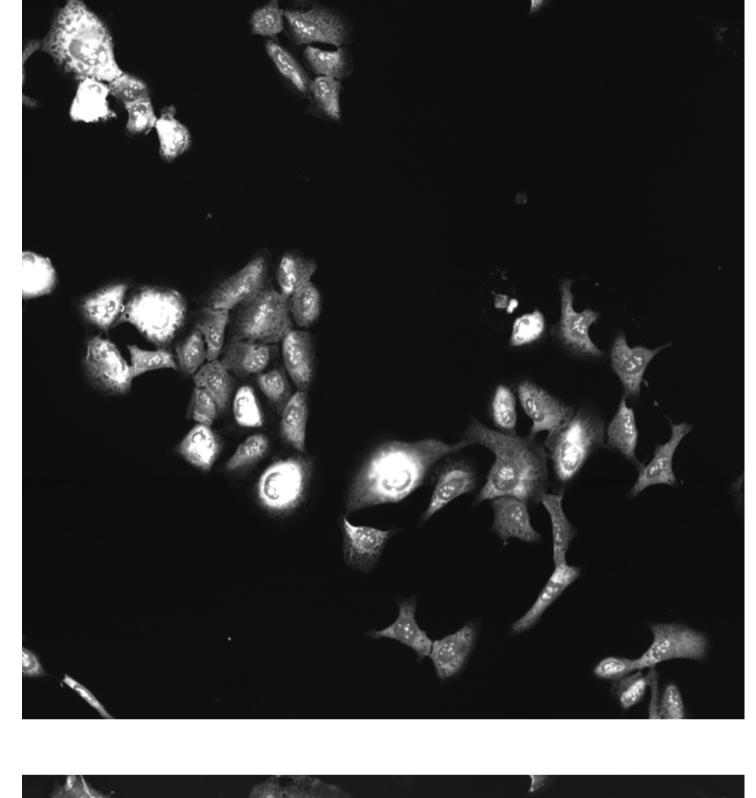
RNA Empty



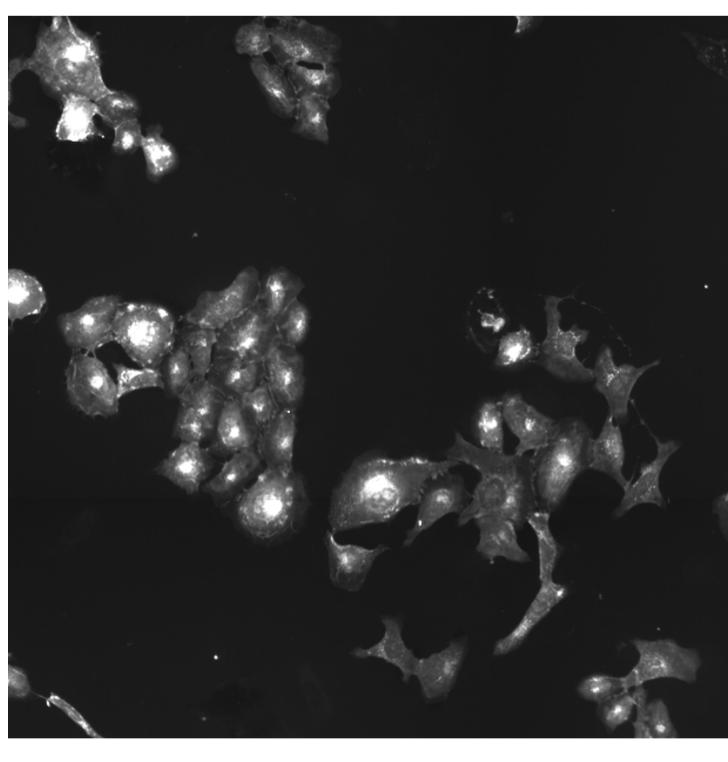


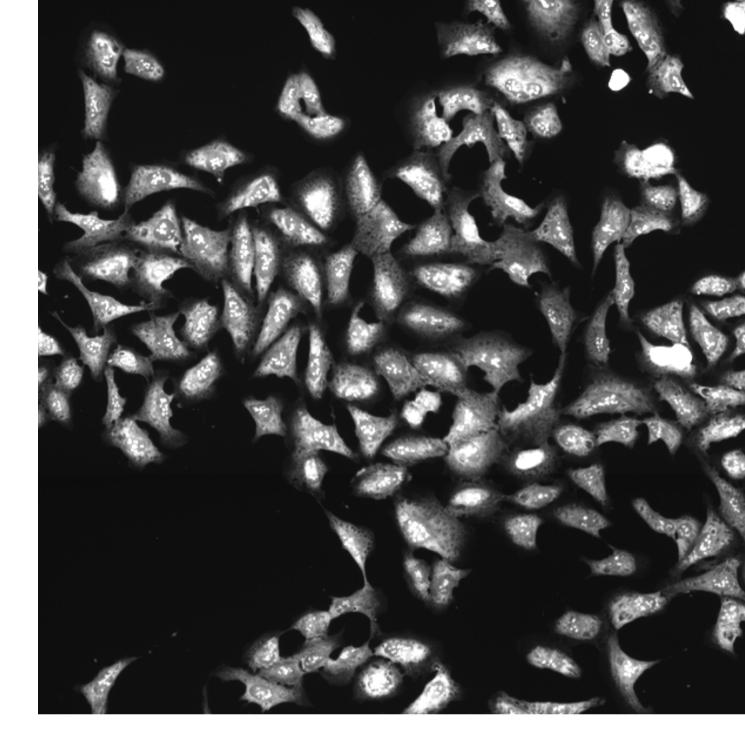
 $MAP3K2_WT.1$



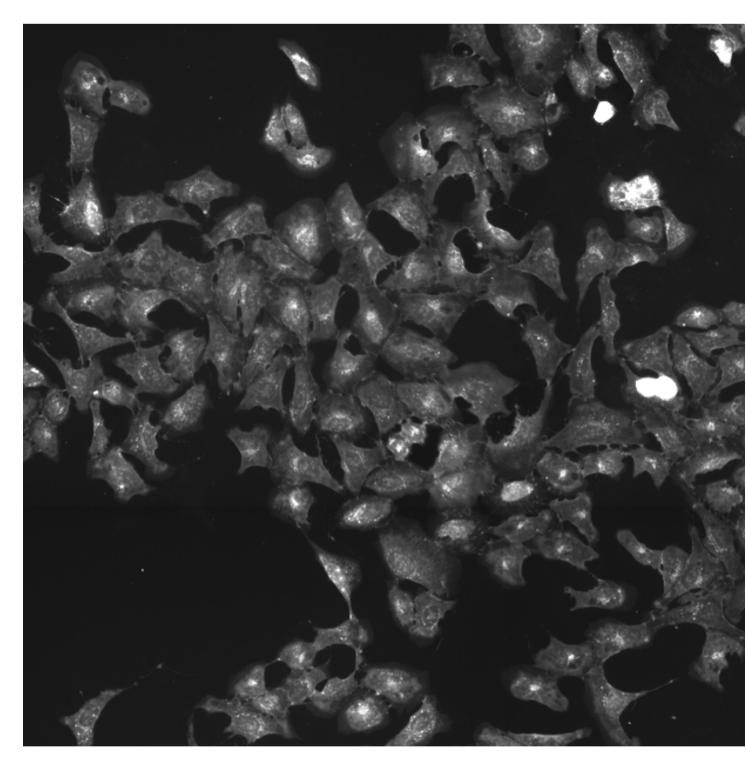


 $MAP3K2_WT.2$





 $TRAF5_WT$



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	compound and each gene in cluster; Tables contain data for individual	Mean compound rank when scored against genes in cluster using L1000 profiling ± standard deviation; Tables contain data for individual genes	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)		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-A50921700-001-05-5 ST50843211 AC1MG1XY MLS001035763 HMS2980J20 STK436533 SMR000666319 PubChem CID: 2954221	NH NH NH F	NA (in 1 replicates)	0.69 ± 0.06 Treatment Score MAP3K2_WT.1 0.65 MAP3K2_WT.2 0.65 TRAF5_WT 0.76	NA	Mean Compound of general to the compound of gene	AreaShape - Nuclei Cytoplasm Cells Texture 9 9 - Intensity - RadialDistribution - RadialDistribution -	Cotts_RadialDestribution_RadialCy_ER_1of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Cotts_RadialDestribution_RadialCy_ER_4of4 Ruclel_Texture_Destribution_RadialCy_ER_4of4	Total number of assays tested in: 491. Active in the following assays: • uHTS Luminescent assay for identification of activators of human intestinal alkaline phosphatase (AID 2524) • qHTS for inhibitors of ROR gamma transcriptional activity (AID 2551)

