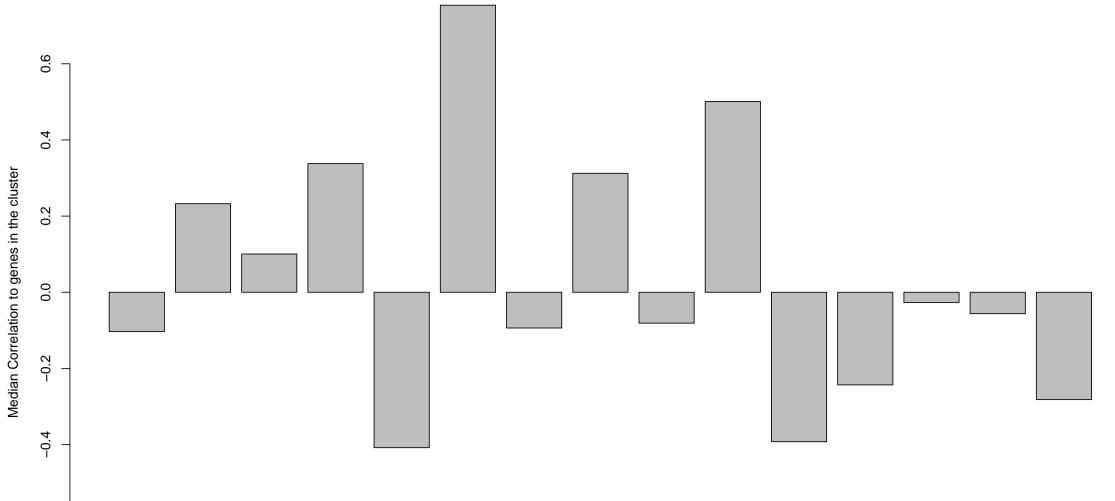
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein

How similar is this cluster to the other clusters?

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

	S i	v			
	Expert Annotation				
Treatment	Pathway	Regulation Type			
JUN_WT.1	Canonical MAPK	Activator			
$JUN_{-}WT.2$	Canonical MAPK	Activator			
CEBPA_WT.1	Transcription Factors	Activator			
CEBPA_WT.2	Transcription Factors	Activator			



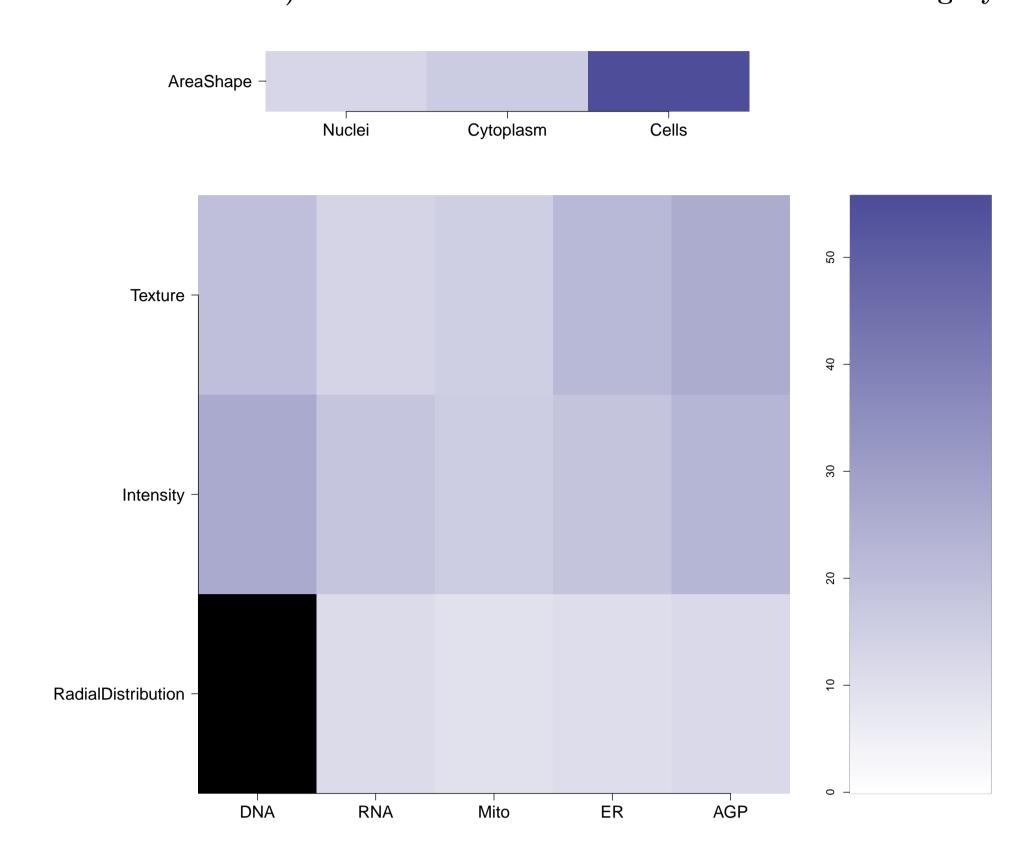
Top 5 genes negatively correlated to the cluster

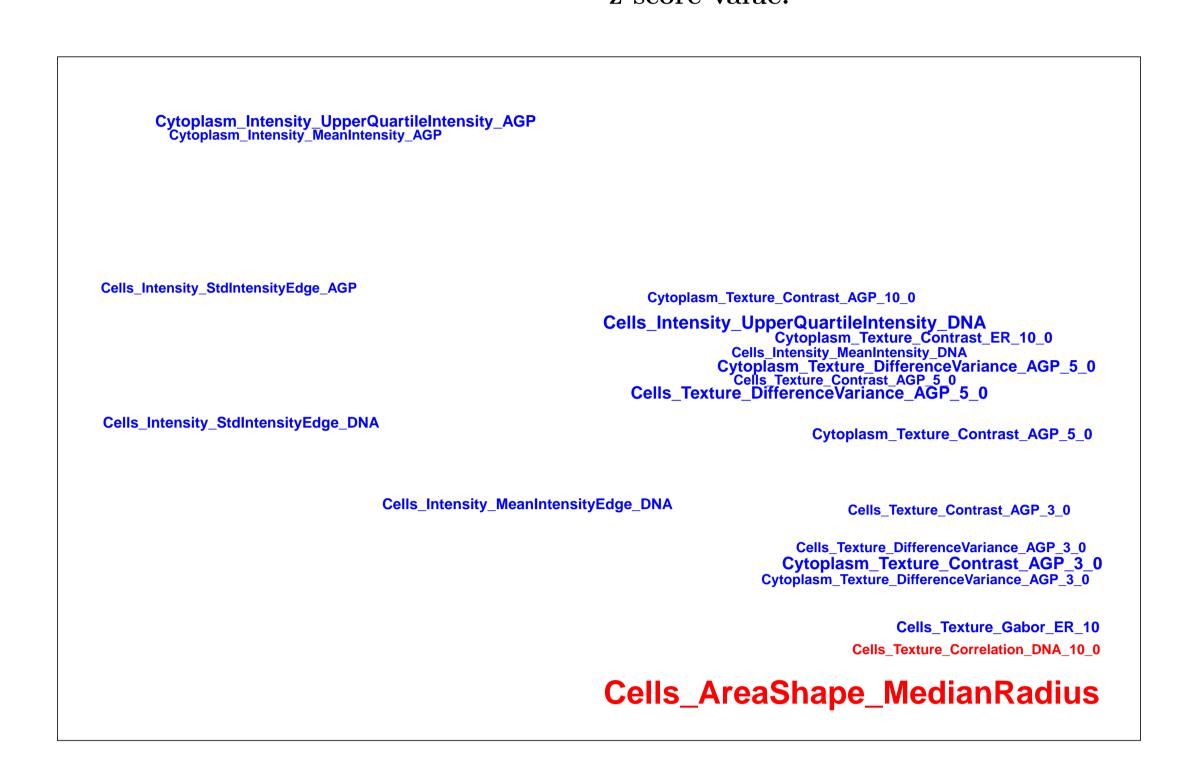
	1 0	8					
Expert Annotation							
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation			
AKT1_WT.1	Canonical PI3K/AKT	Activator	-0.59	0.03			
PKIA_WT	PKA	Inhibitor	-0.48	0.12			
CDKN1A_WT	Canonical Cell Cycle	Inhibitor	-0.46	0.07			
RPS6KB1_WT.1	Canonical TOR	Activator	-0.46	0.09			
YAP1_WT.1	Canonical Hippo	Inhibitor	-0.44	0.05			

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

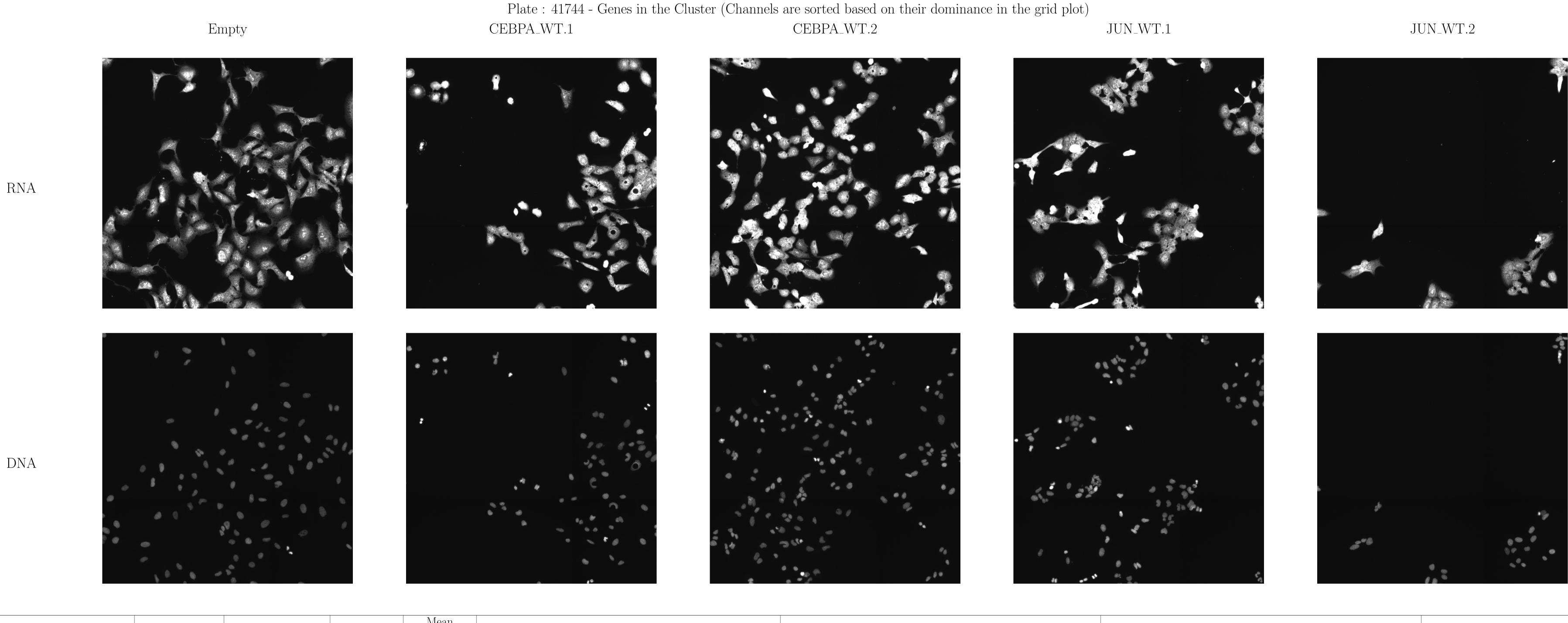
Which individual morphological features are distinguishing in the cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

How strongly are genes within the cluster correlated?





	-cB	PA_WT.1	PAWT?	W.1	W.
	CE	CE	30.	20,	1
CEBPA_WT.1					- 0.8
					- 0.4
CEBPA_WT.2					- 0.2
					- 0
JUN_WT.1					-0.2
					0.6
JUN_WT.2					0.8



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster		Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	and each gene in	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 i 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	- $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$
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