How similar is this cluster to the other clusters?

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

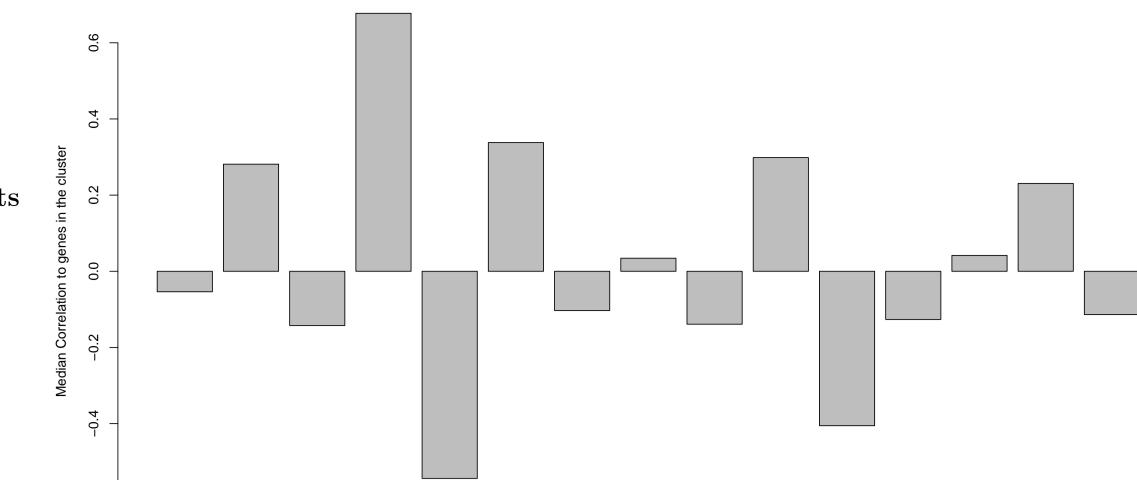
Expert Annotation

Treatment Pathway Regulation Type

CCND1\_WT.1 Canonical Cell Cycle Activator

Canonical Cell Cycle Activator

CCND1\_WT.2 Canonical Cell Cycle Activator



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

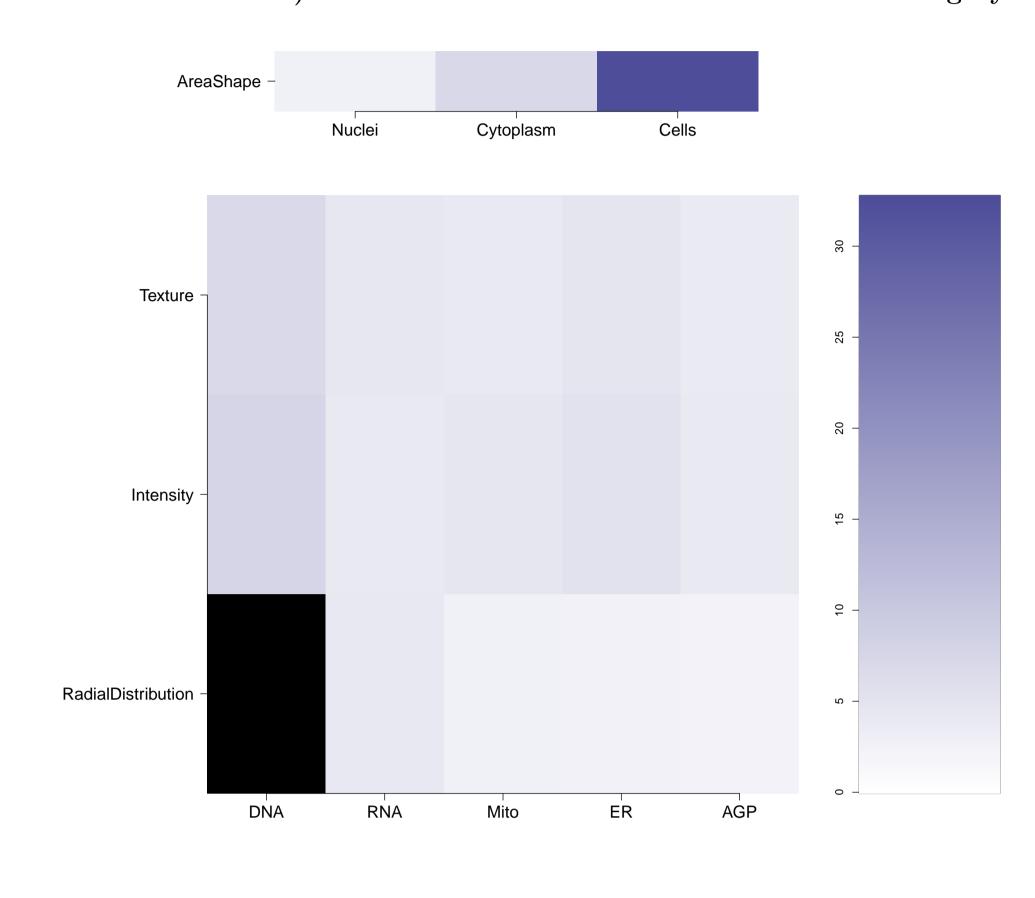
	Expert Annot			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
CDKN1A_WT	Canonical Cell Cycle	Inhibitor	-0.67	0.11
$MAP3K5\_WT$	Canonical MAPK	Activator	-0.61	0.03
MAP2K4_WT.1	Canonical MAPK	Activator	-0.51	0.06
$TP53\_WT.1$	Canonical DNA Damage	Activator	-0.50	0.22
MAP2K3_WT	Canonical MAPK	Activator	-0.49	0.10

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.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP3K5\_WT MAP3K5\_WT MAP3K5\_WT MAP3K5\_WT MAP3K5\_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

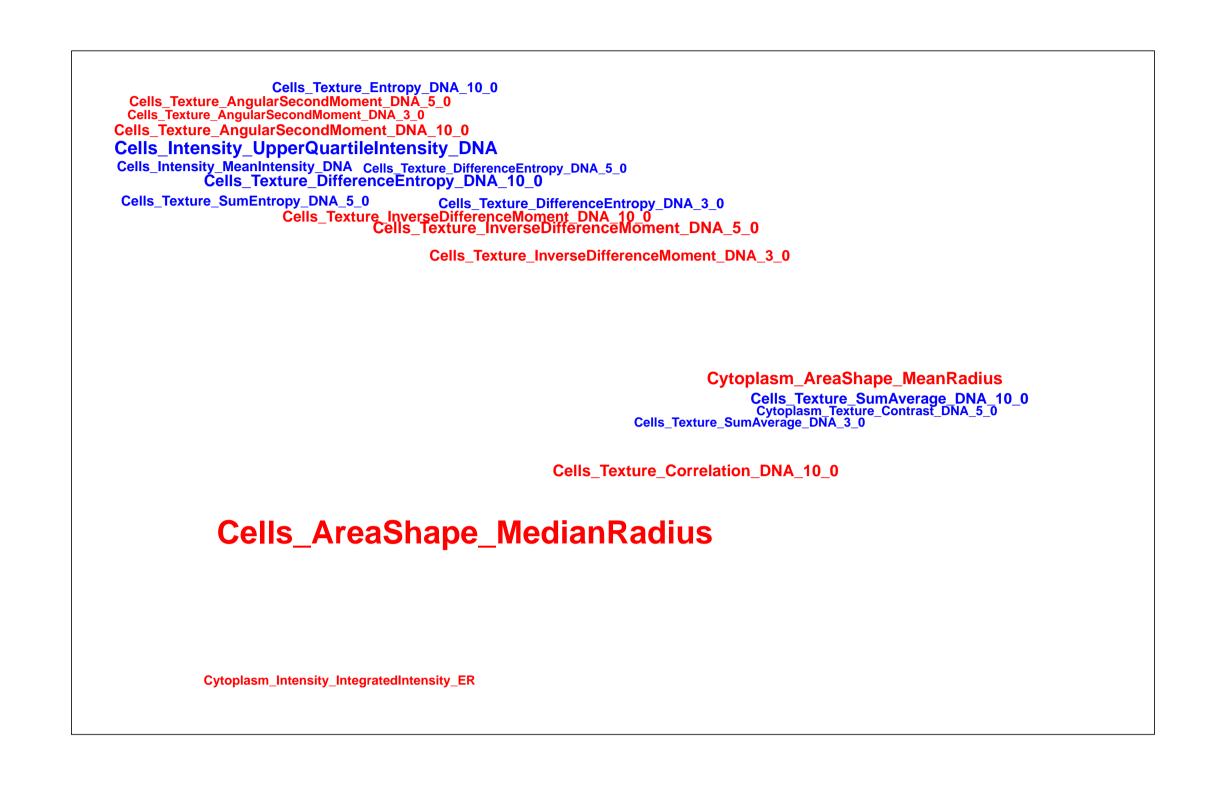
Which individual morphological features are distinguishing in the cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

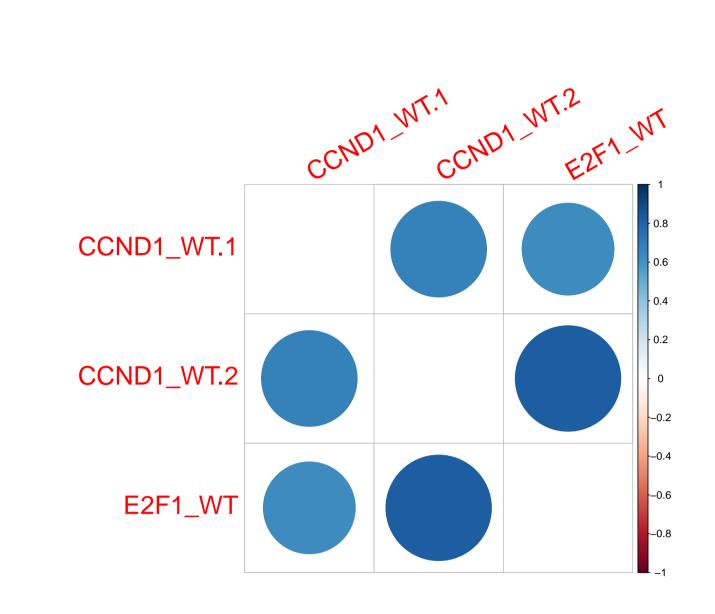
How strongly are genes within the cluster correlated?



ST50181975

PubChem CID: 1555494





• Fluorescence Intensity-based biochemical pri-

mary high throughput confirmation assay to

identify activators of kallikrein-7 (K7) zymogen

• Counterscreen for activators of kallikrein-7 (K7) zymogen: Fluorescence intensity-based biochemical high throughput counterscreen assay for activators that optically interfere with measurement of EDANS-DABCYL fluo-

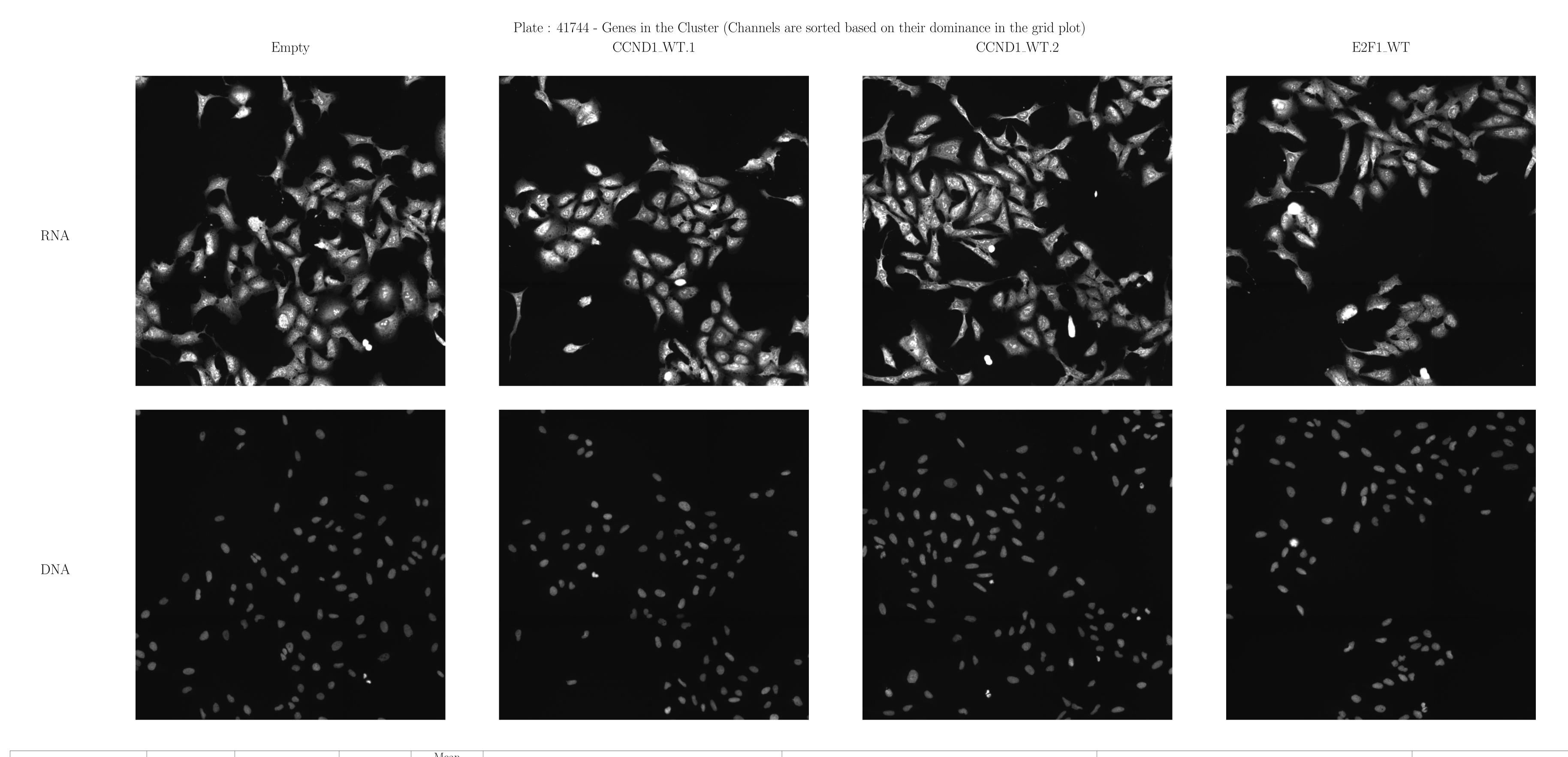
(AID 686949)

rescence (AID 686952)

Cytoplasm\_Intensity\_UpperQuartileIntensity\_ER

Cytoplasm\_AreaShape\_Solidity

Cytoplasm\_AreaShape\_Compactness





RadialDistribution -

AKT1\_E17K AKT1S1\_WT1 BRAF\_WT1 CCND1\_WT1 CDNN1A\_WT CEBPA\_WT1 CSNK1A1\_WT3 CXXC4\_WT DV13\_WT GLI1\_WT MAPRIC\_WT1 MYD88\_1289P PRICZ\_KG81R RBP\_L/WT1 WWTR1\_WT AKT1S\_ETY\_C AKT1S\_ETY\_C

