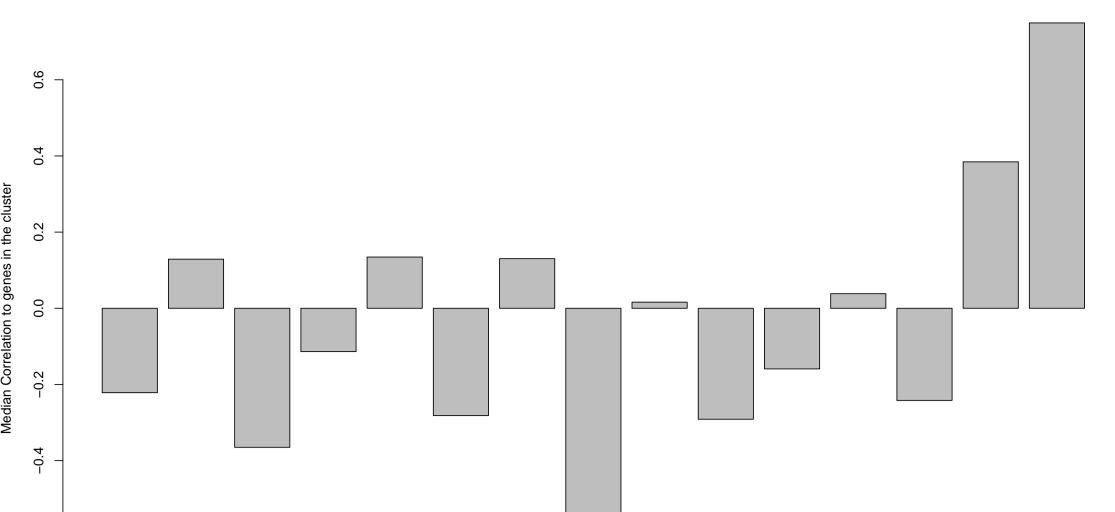
How similar is this cluster to the other clusters?

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

Export Appotation				
	Expert Annotation			
Treatment	Pathway	Regulation Type		
YAP1_WT.1	Canonical Hippo	Inhibitor		
YAP1_WT.2	Canonical Hippo	Inhibitor		
YAP1_WT.3	Canonical Hippo	Inhibitor		
YAP1_WT.4	Canonical Hippo	Inhibitor		
WWTR1_WT	Canonical Hippo	Inhibitor		



Top 5 genes negatively correlated to the cluster

Expert Annotation				
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
STK3_WT.1	Canonical Hippo	Activator	-0.63	0.08
TRAF2_WT	Canonical NFkB	Activator	-0.57	0.08
$ELK1_WT$	Canonical MAPK	Activator	-0.55	0.07
$CXXC4_WT$	WNT	Inhibitor	-0.54	0.15
CDC42 WT	Canonical Cytoskeletal Re-org	Activator	-0.52	0.05

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.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.3 PRKACA_WT.2 PRKACA_WT.2 TRAF5_WT SDHA_WT PRKCZ_WT.2 SMAD3_WT.1 YAP1_WT.4 PRKCA_K368R RAF1_WT.1 MAP3K6_WT.1 MAP3K6_WT.1 WATR1_WT.4 PRKCA_K368R RAF1_WT.2 MAP3K6_WT.1 MAP3K6_WT.1 WATR1_WT.4 PRKCA_K368R RAF1_WT.2 MAP3K6_WT.1 MAP3K6_

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?

