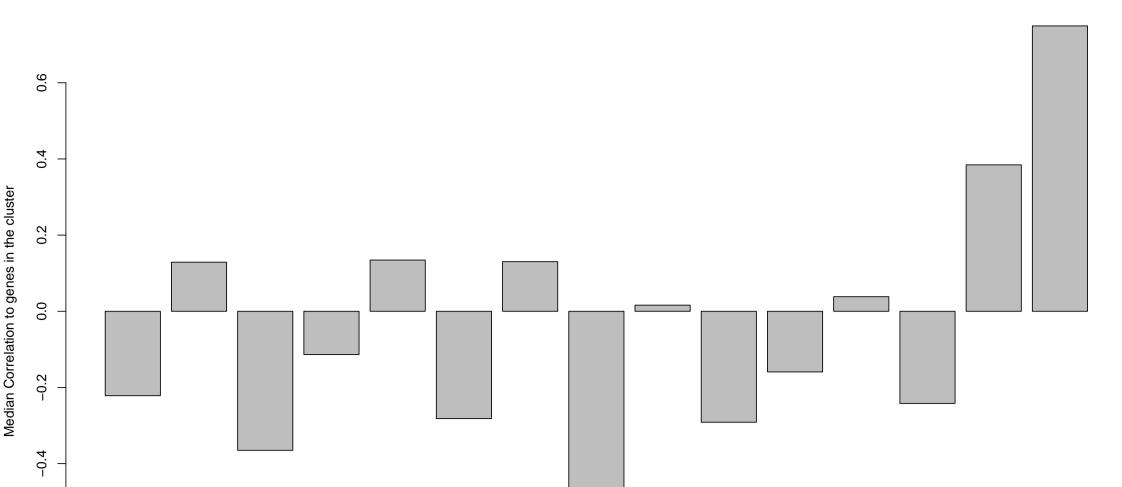
How similar is this cluster to the other clusters?

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

	Expert Annotation				
Treatment	Pathway	Regulation Type			
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

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?

