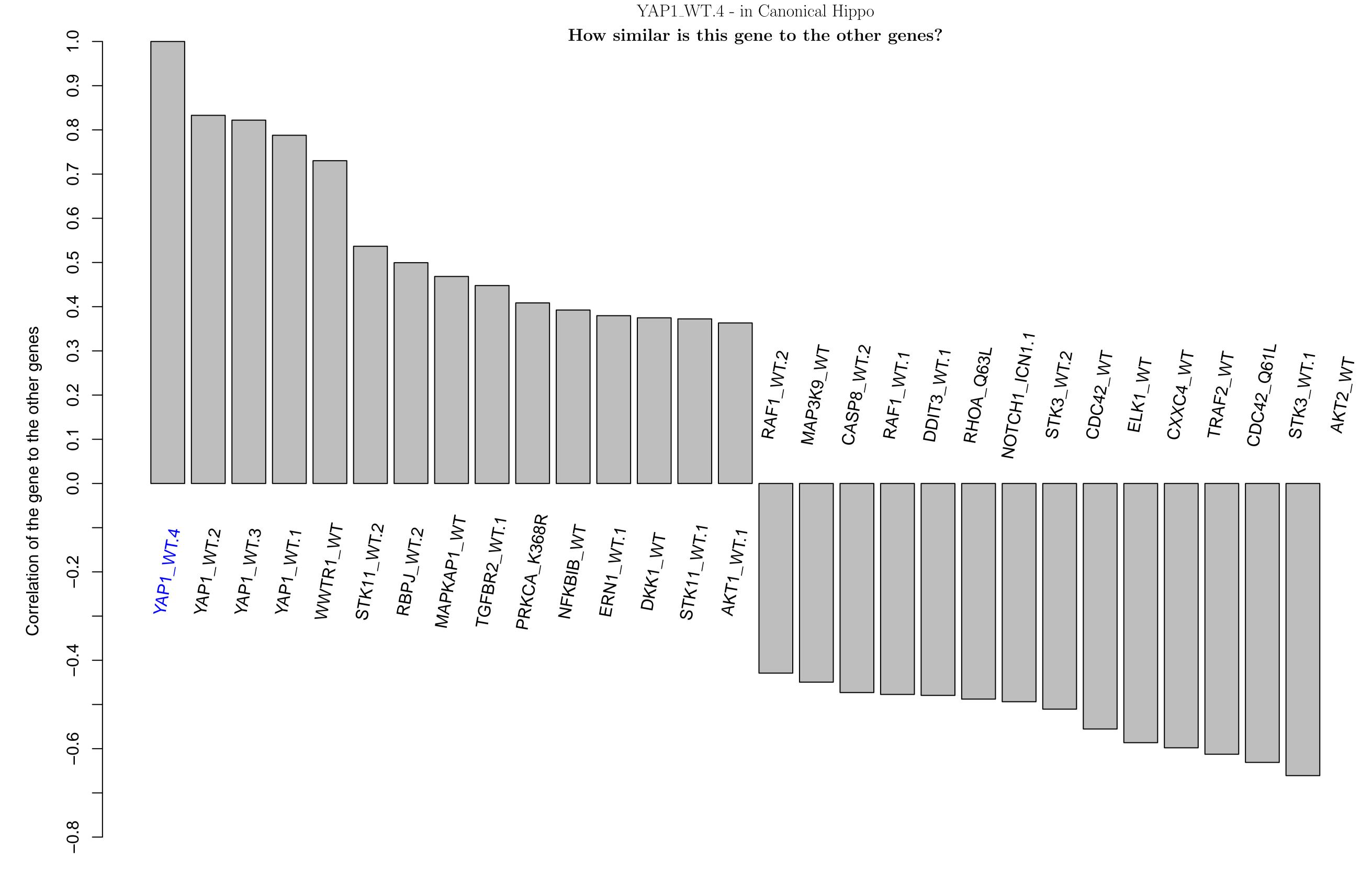
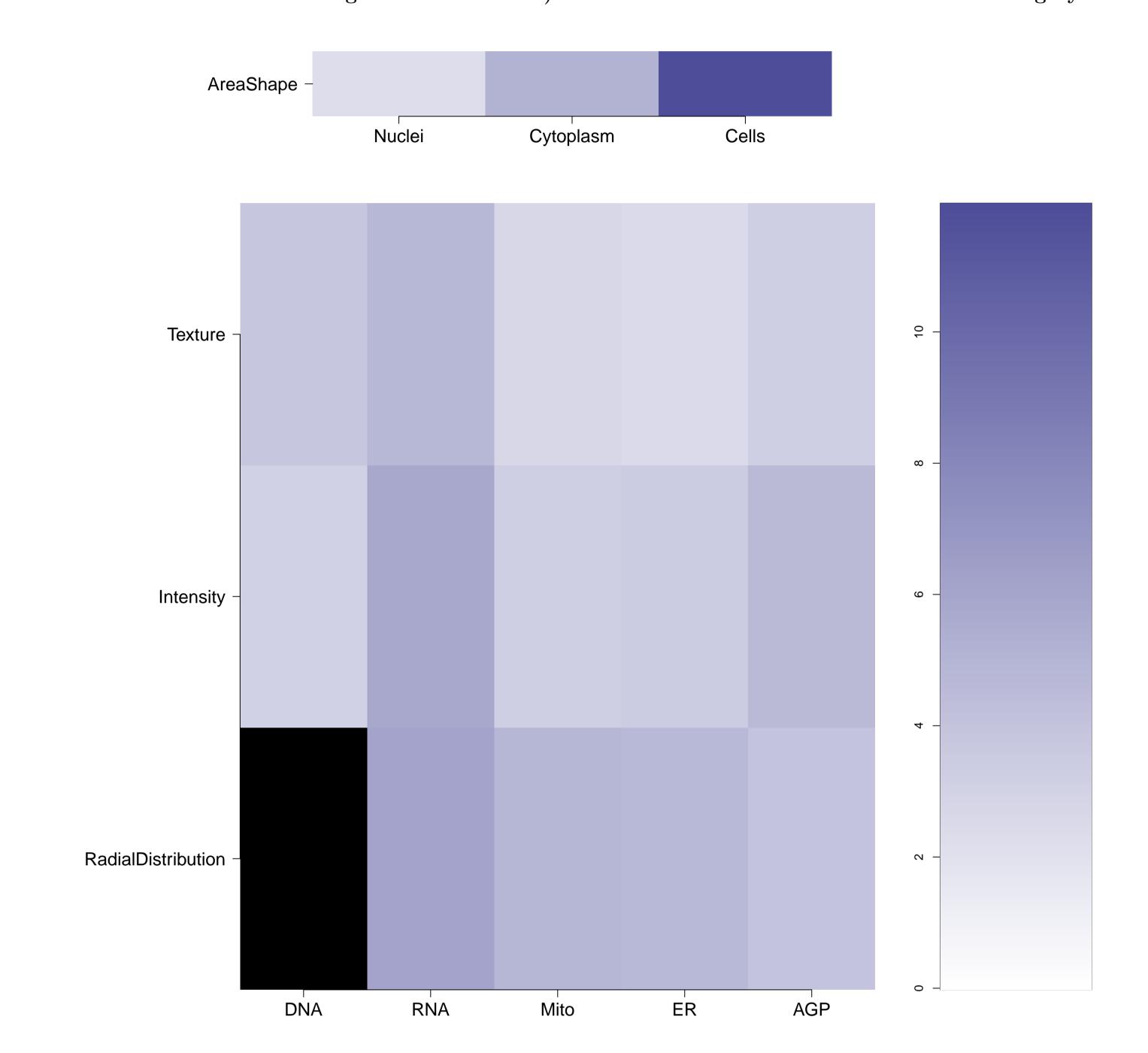
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein



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



YAP1_WT.4 (41744)

Empty

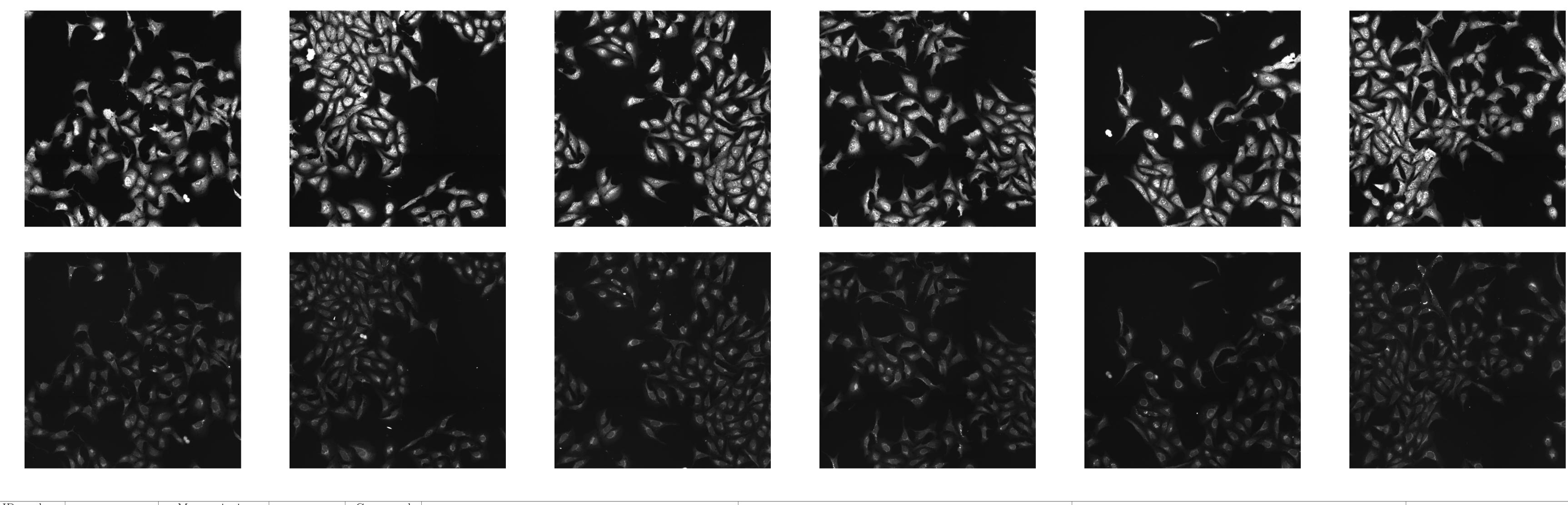
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

YAP1_WT.4 (41757)

YAP1_WT.4 (41754)



 $YAP1_WT.4 (41756)$



YAP1_WT.4 (41755)

Compound IDs and common names (where available); blue/red colored box means the matching	Chemical structure	Mean pairwise replicates correlation of the compound signature	Correlation between	etween scored against the	experiment: (Yellow and red lines correspond to top/bottom	L Common distingilishing teatilre categories in the compoling 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 Number of PubChem assays the compound was tested; a which the compound was a itemized	the compound was tested; assays in
compound is positively/negatively correlated with the cluster		(95th DMSO replicate correlation is 0.51)	the gene	gene using L1000 profiling				

