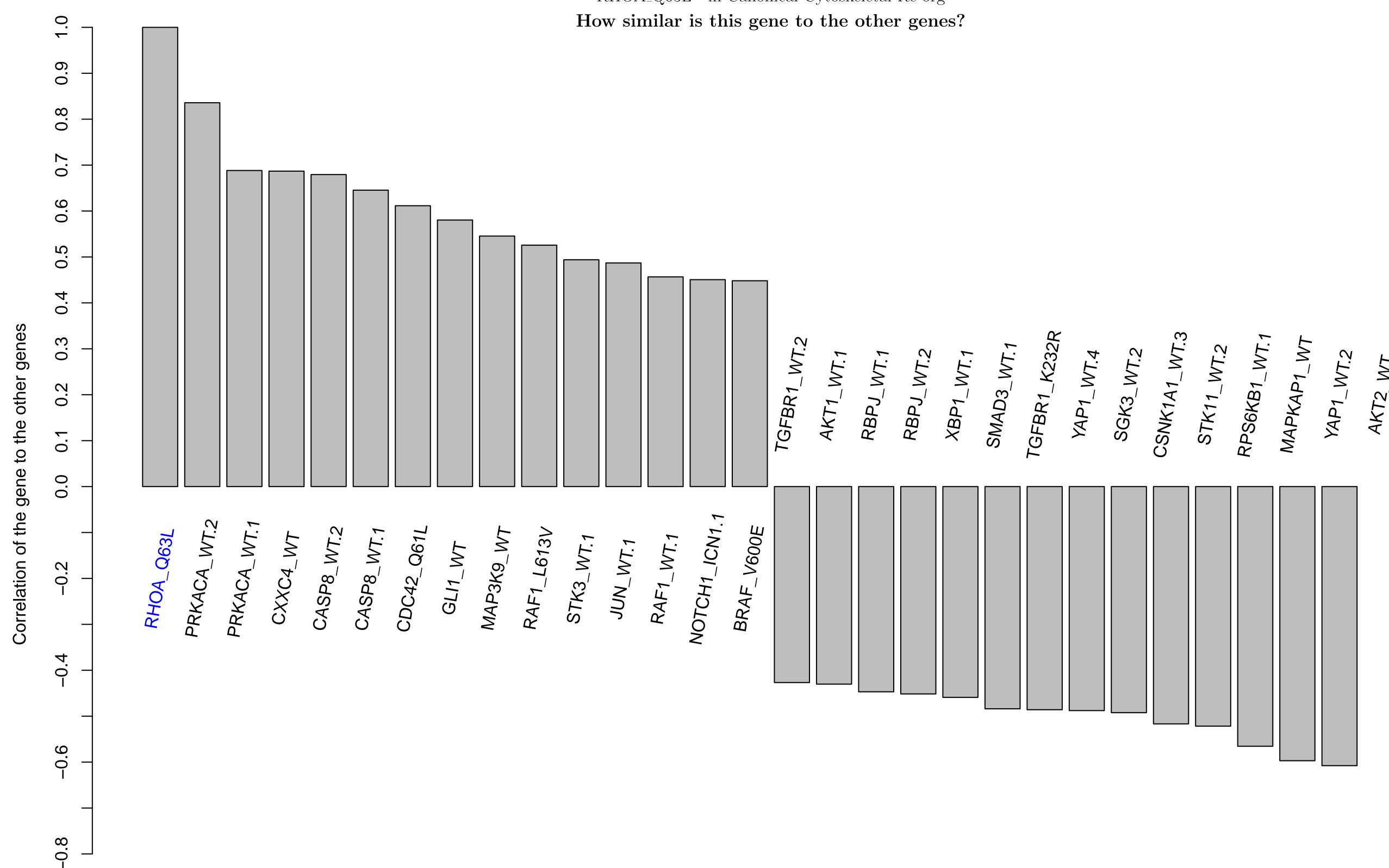
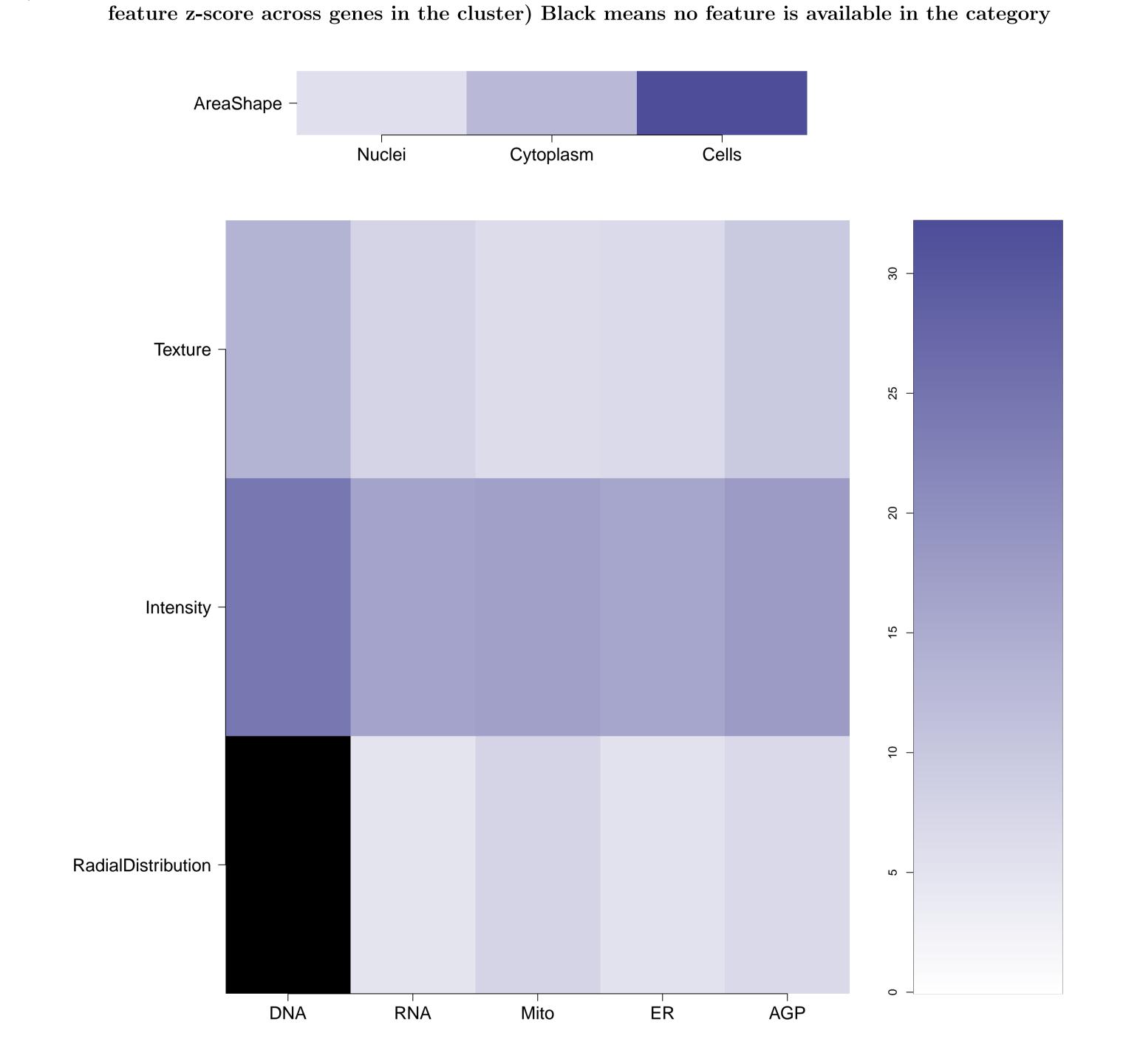
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein RHOA_Q63L - in Canonical Cytoskeletal Re-org

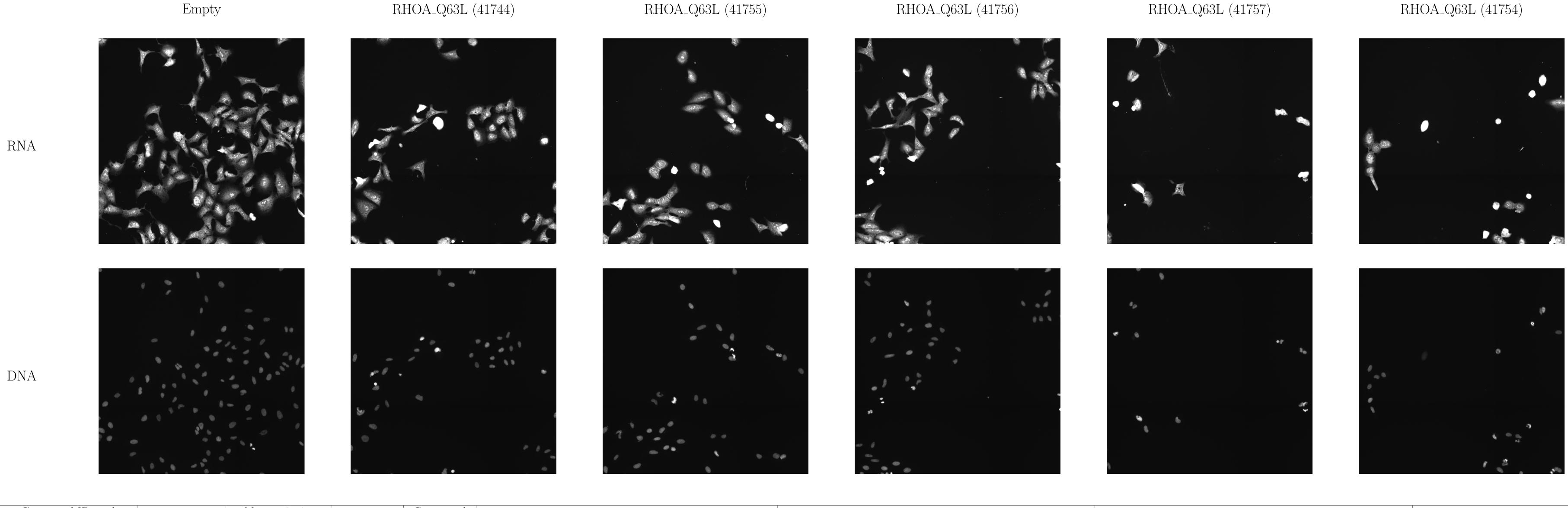


What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a



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.





Compound IDs and		Mean pairwise		Compound				
common names (where		replicates	Correlation	rank when			Distinguishing individual factures for the compound relative to	Number of Dub Cham agains in which
available); blue/red colored	L Chemical	correlation of the	re between against the gene usin	scored	How similar is the compound signature to the genes in this experiment? (Yellow and red lines correspond to top/bottom 1st and 5th percentile DMSO correlation to all the genes)	The common distinction of the common and the common	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 in which the compound was tested; assays in which the compound was active are itemized	
box means the matching		compound signature		against the				
compound is		(95th DMSO		gene using				
positively/negatively		replicate correlation		L1000				
correlated with the cluster		is 0.52)		profiling				

