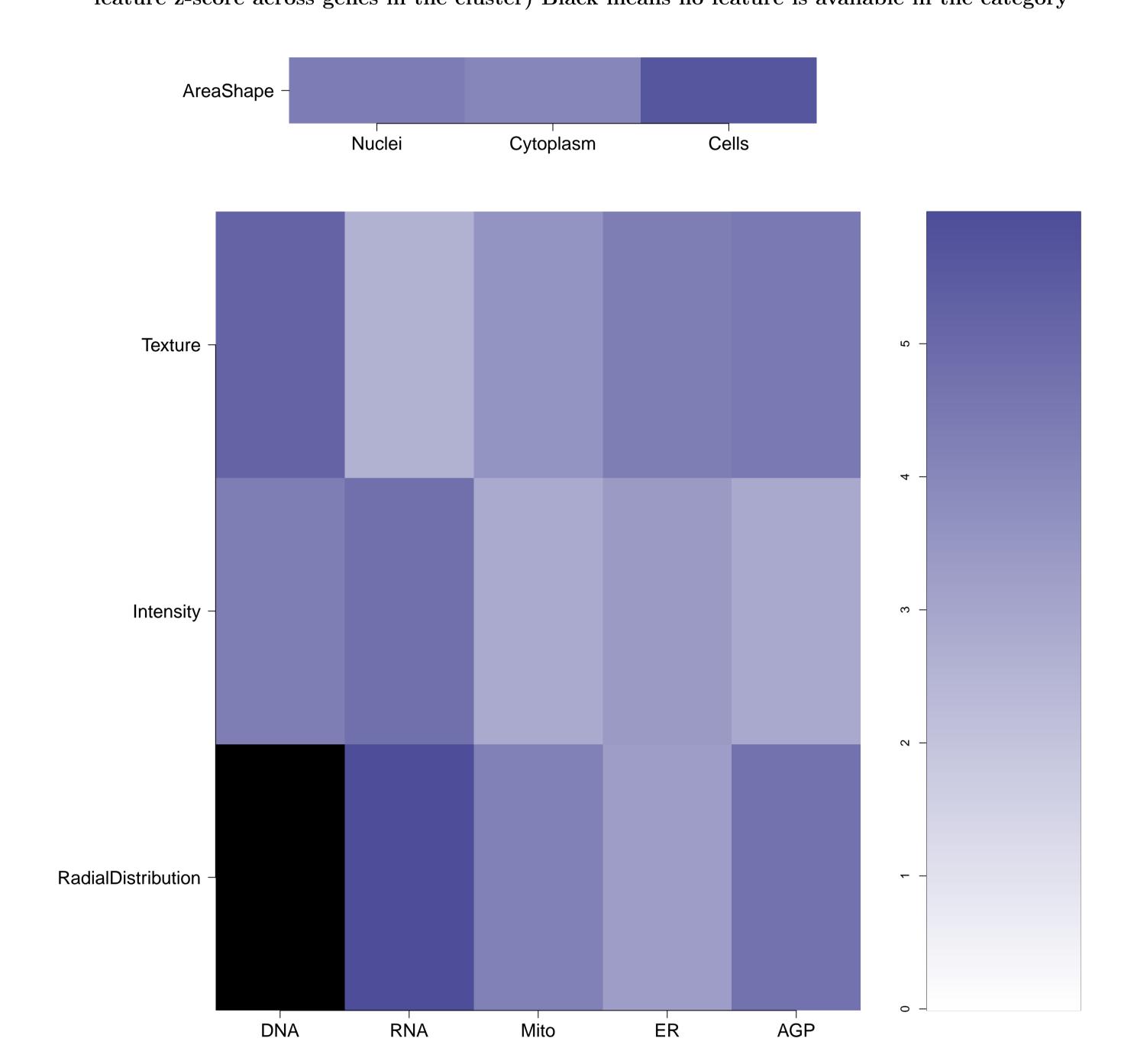
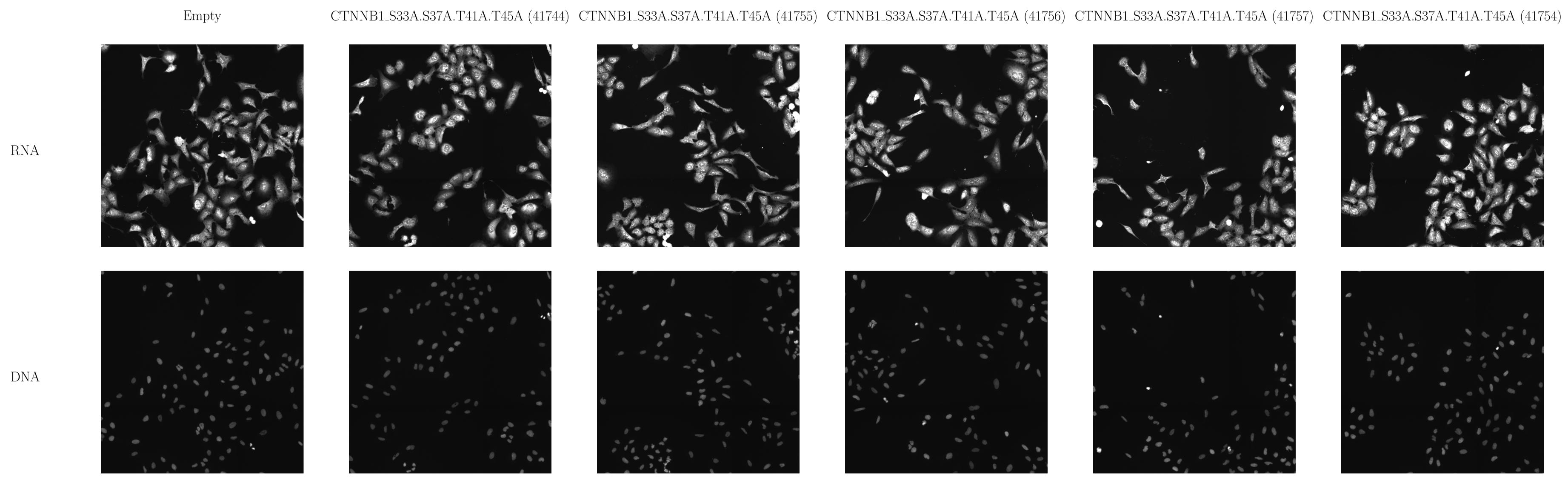
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein CTNNB1_S33A.S37A.T41A.T45A - in Canonical WNT How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes 0.3 RPS6KB1_WT.2 CDKN1A_WT MAP2K4_WT.1 HRAS_G12V DIABLO_WT SMO_WT.1 MOS_WT.1 TRAF5_WT KRAS_WT.1 0.0 CEBPA_WT.1 CCND1_WT.2 PER1_WT.2 CEBPA_WT.2 CDK2_WT.2 DDIT4_WT .S37A.

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 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 features for the compound relative to	Number of PubChem aggreg in which	
available); blue/red colored	Unemical	correlation of the	ompound signature compound compound	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)	Common distinguishing feature categories in the compound and	Distinguishing individual features for the compound relative to Number of PubChem assays in which untreated samples. Black means a mismatch: i.e. active (— bigh the compound was tested; assays in		
box means the matching		compound signature		against the			z-score in magnitude) in the compound, and either inactive (= which the compound was active ar		
compound is		(95th DMSO		gene using					
positively/negatively		replicate correlation	the gene	L1000			small z-score in magnitude) or oppositely active in the gene	itemized	
correlated with the cluster		is 0.52)		profiling					

