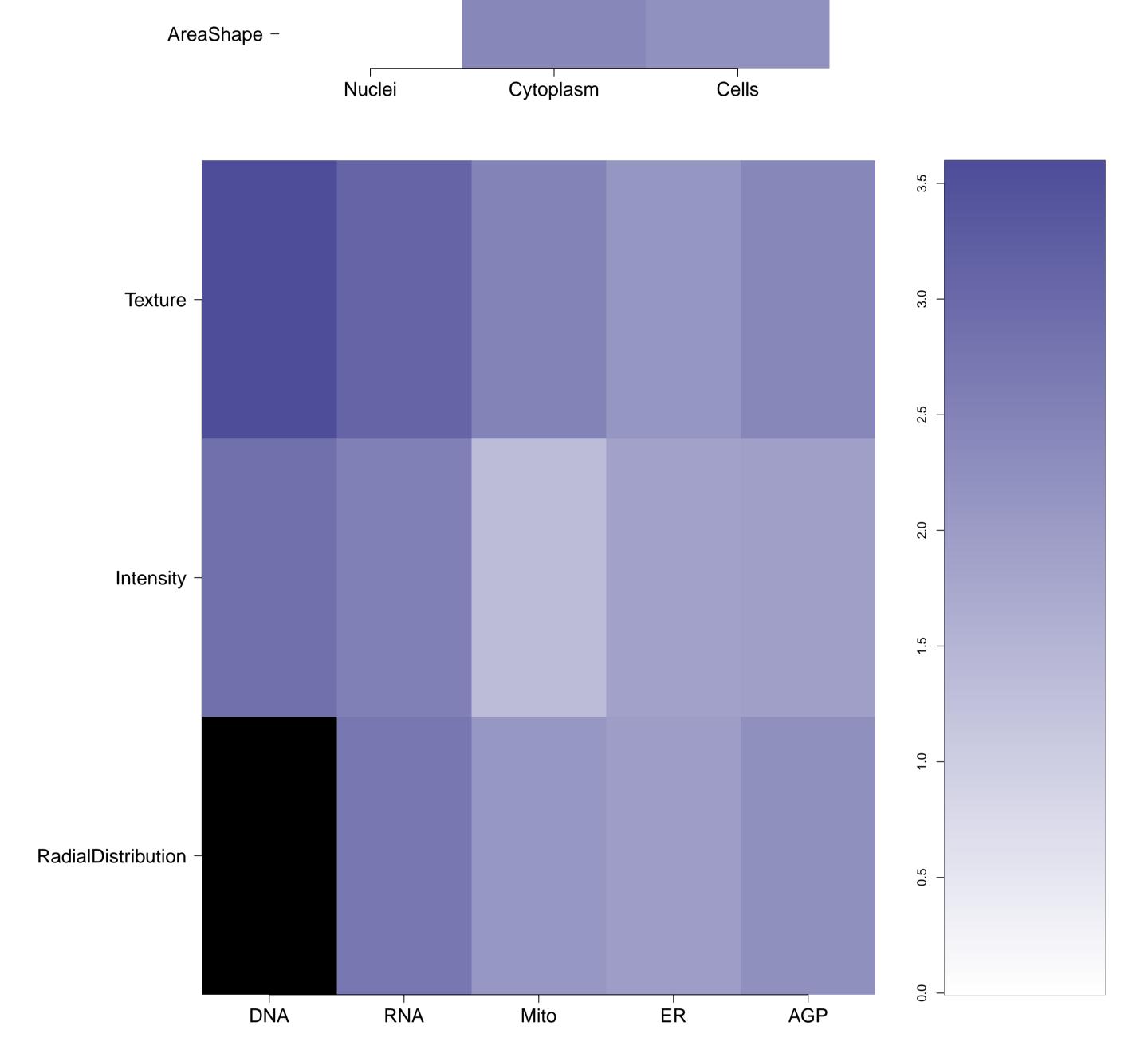
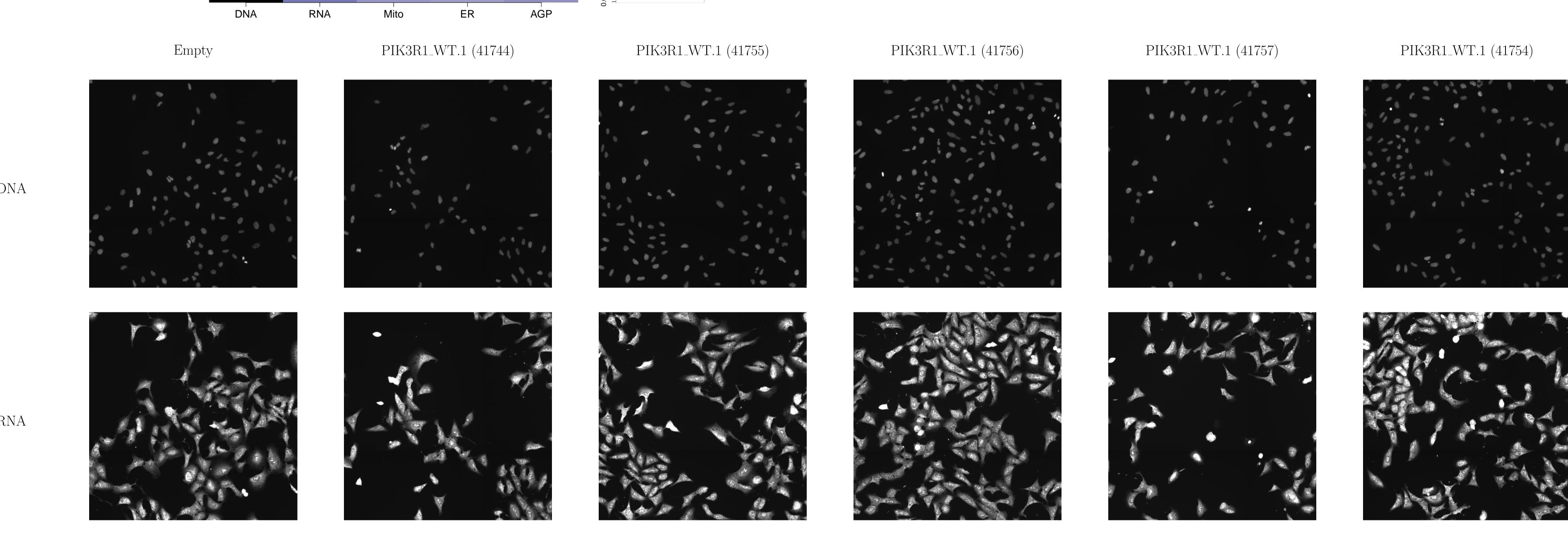
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein PIK3R1\_WT.1 - in Canonical PI3K/AKT How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes 0.3 PIK3CB\_WT.2 CDC42\_T17N HRAS\_G12V CDKN1A\_WT MAP3K2\_WT.1 MAP2K3\_WT AKT3\_WT.2 SMO\_WT.1 TRAF5\_WT JAG1\_WT 0.0 \_del1-238 MAP2K4\_WT.2
SMURF2\_WT
ATF4\_WT.2
AKT1S1\_WT.1
PRKCZ\_del1-238
AKT1S1\_WT.2
SGK3\_WT.2
SGK3\_WT.2
SGK3\_WT.2
SGK3\_WT.1
TGFBR1\_K232R
CSNK1A1\_WT.3 MLST8\_WT -3\_WT

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 common names (where available); blue/red colored box means the matching compound is positively/negatively	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation	compound the gene		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)	$\perp$ Common distinctiishing teatiire categories in the composing 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	the compound was tested; assays in
positively/negatively correlated with the cluster		replicate correlation is 0.52)		profiling				

