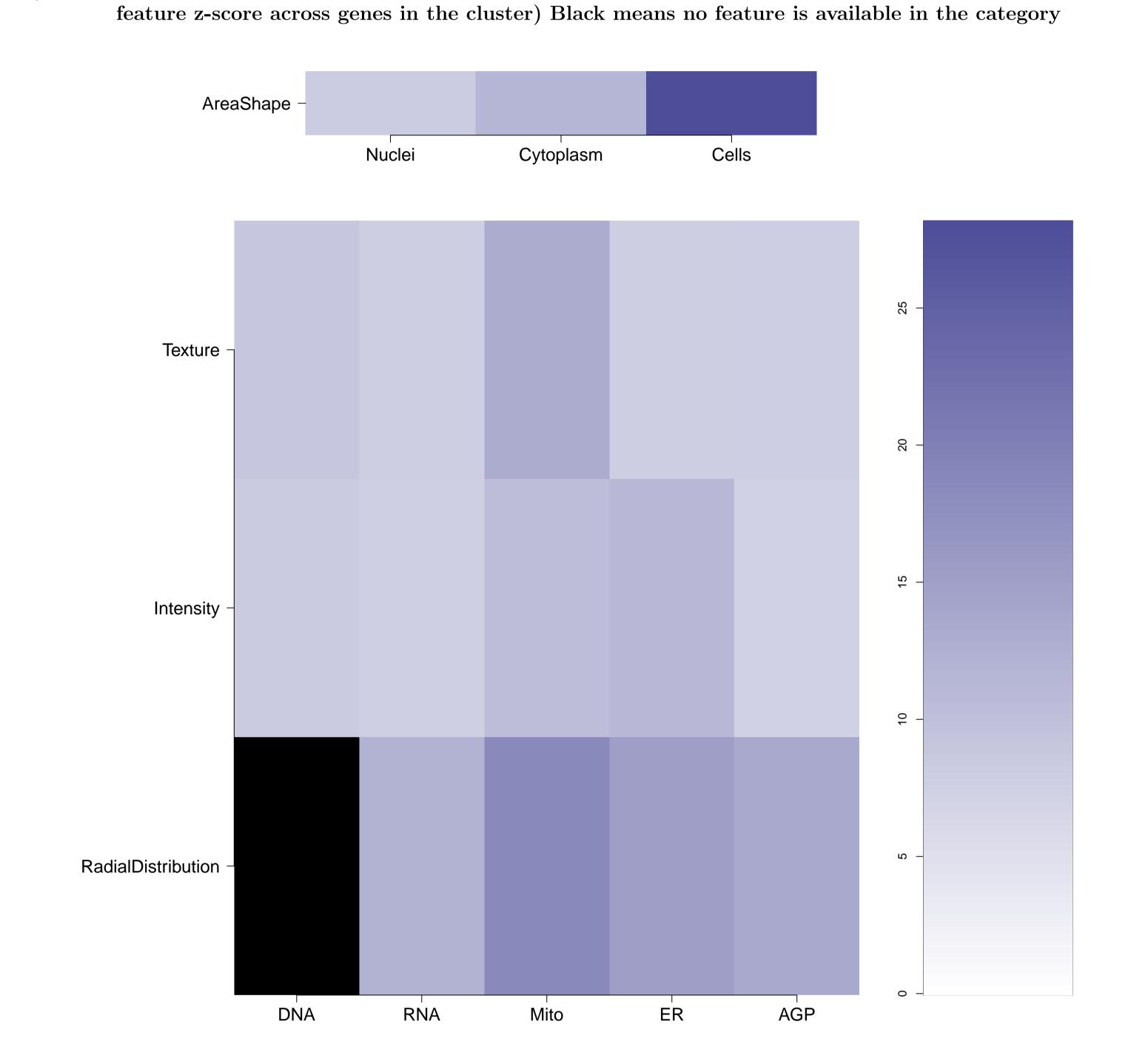
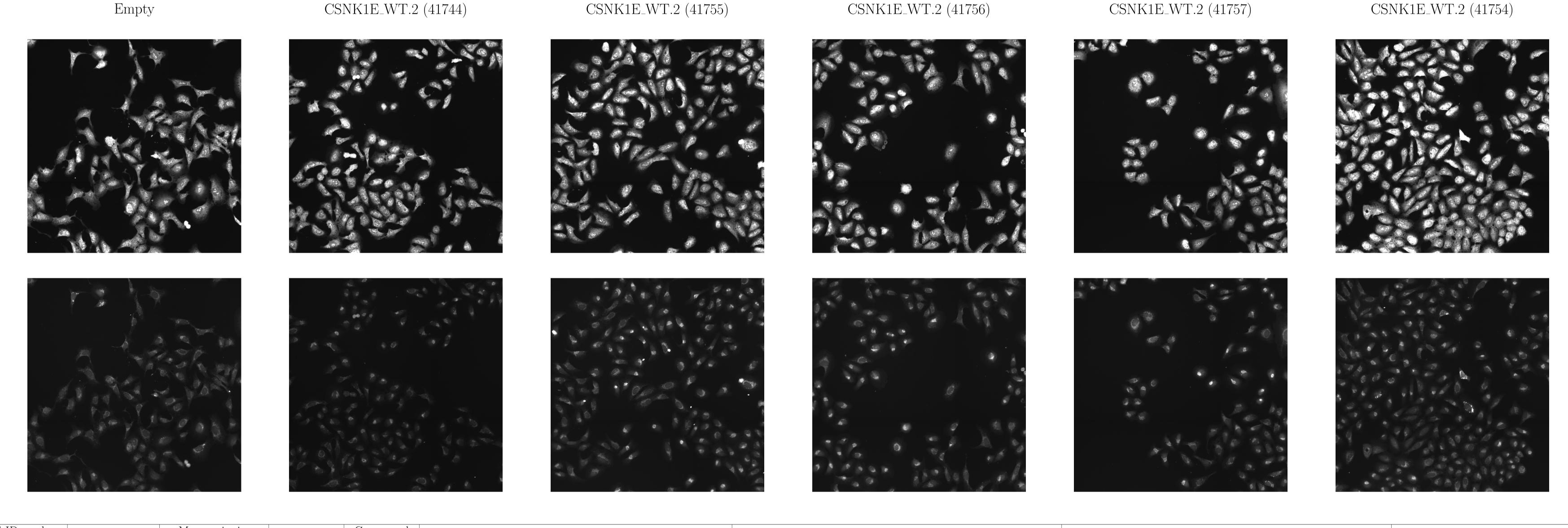
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein CSNK1E_WT.2 - in Canonical Circadian Rhythm How similar is this gene to the other genes? 0.9 0.5 0.4 Correlation of the gene to the other genes PRKCA_K368R PRKACG_WT.3 0.3 PRKCE_WT.1 NFKB1_WT.1 RBPJ_WT.2 RBPJ_WT.1 TRAF2_WT RELB_WT PRKCZ_del1_ 0.0 CSNK1E_WT.2
PIK3CB_WT.2
STK3_WT.1
MAPK1_WT.2
CXXC4_WT
STK3_WT.2
TCF4_WT.1
MAP3K2_WT.1
JUN_WT.1
JAG1_WT. MAP3K7_WT BCL2L11_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



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	Chemical structure	Mean pairwise replicates correlation of the compound signature	Correlation between	scored	experiment: (Yellow and red lines correspond to top/bottom	Common distinguishing feature categories in the compound 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 assay, the compound was tested; which the compound was a standard property of the compound was tested; which the compound was a standard property of the compound was tested; which the compound was a standard property of the compound was tested; which the compound was tested; which the compound was a standard property of the compound was tested; which the compound was a standard property of the compound was tested; which the compound was a standard property of the compound was a standard prope	the compound was tested; assays in
compound is positively/negatively correlated with the cluster		(95th DMSO replicate correlation is 0.52)	the gene	gene using L1000 profiling				

