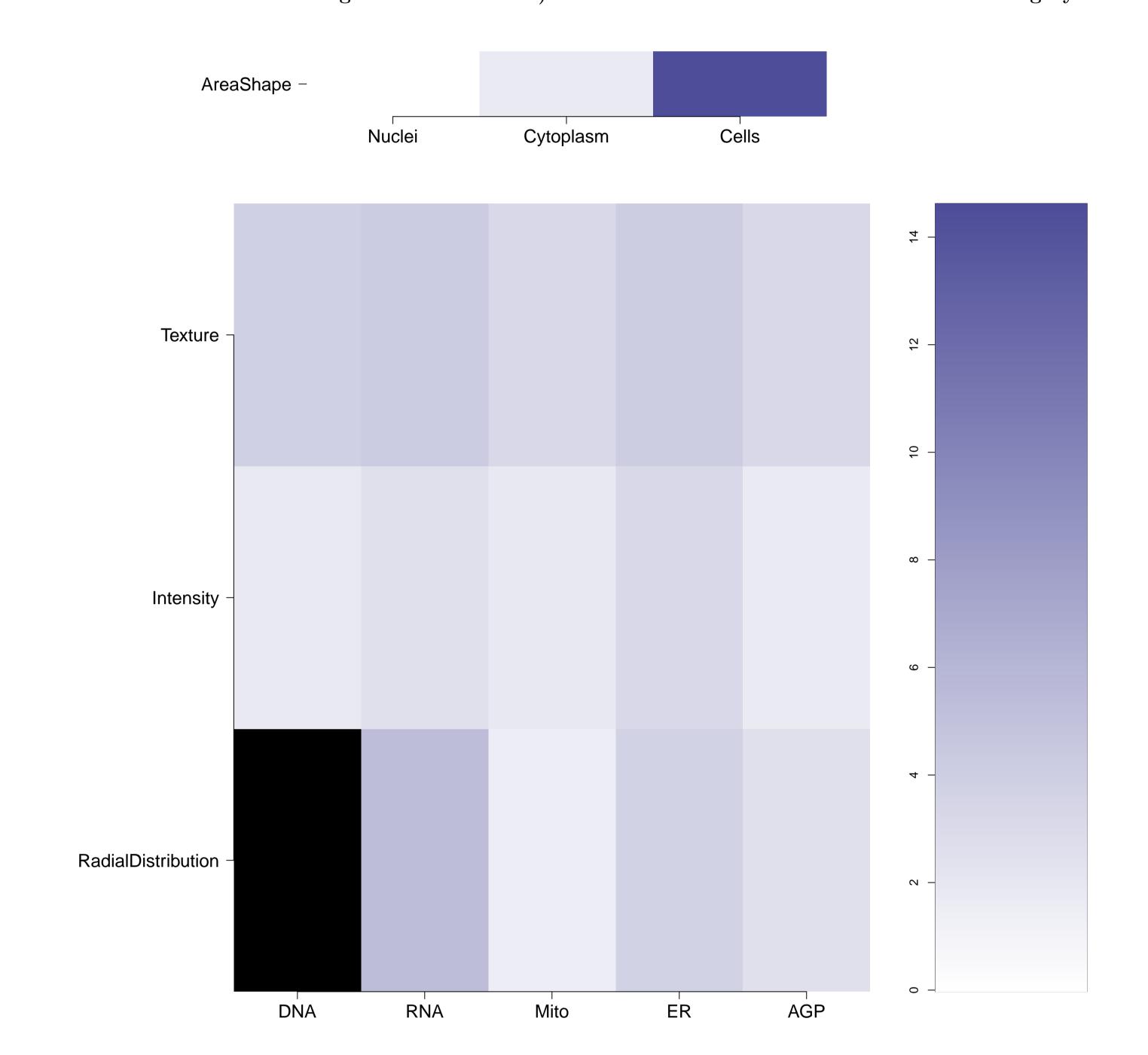
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein MAPK8_WT.1 - in Canonical MAPK How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes TGFBR1_WT.2 0.3 MAP3K2_WT.1 CSNK1A1_WT.3 CSNK1A1_WT. SGK3_WT.2 TRAF5_WT MLST8_WT MAP3K5_ CASP9_ 0.0 E2F1_WT
CCND1_WT.2
RBPJ_WT.1
AKT1S1_WT.2
NFKBIA_WT
DLL1_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

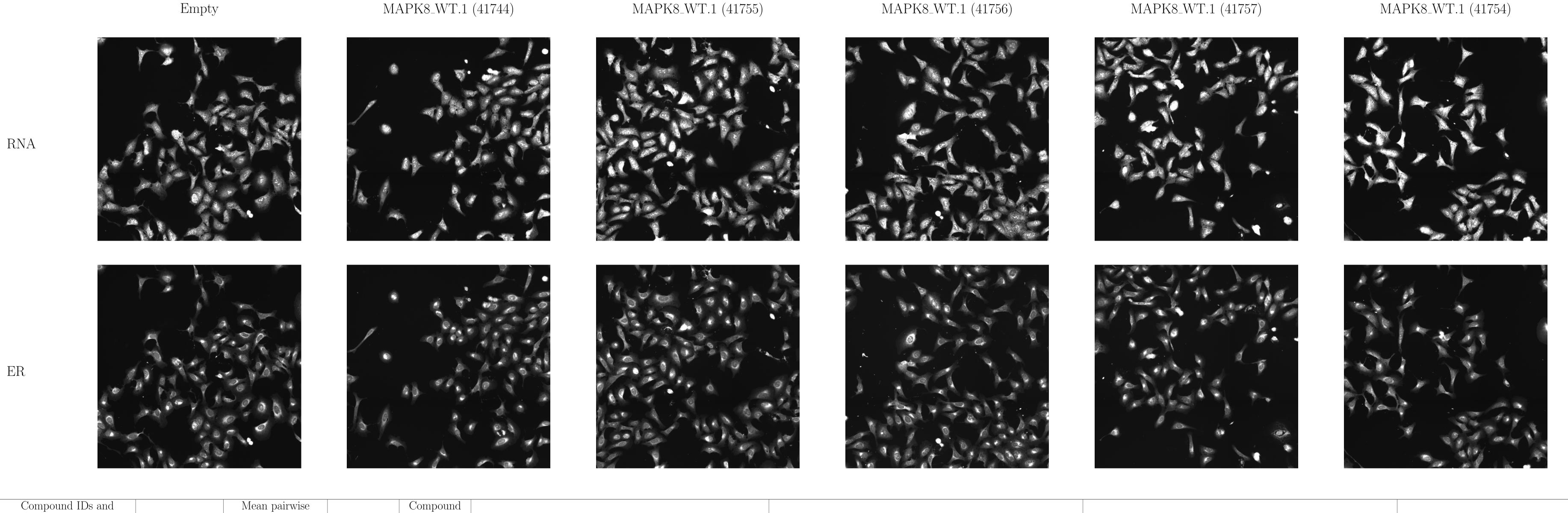


RNA

ER

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.





available); blue/red colored between between between between between between correspond to top/bottom compound signature. Scored between between between between correspond to top/bottom compound signature.	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
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