CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein GRB10_WT.2 - in Canonical Insulin Receptor Signaling How similar is this gene to the other genes? 0.9 0.5 0.4 Correlation of the gene to the other genes 0.3 PIK3CB_WT.2 MAP2K4_WT.1 CDKN1A_WT HRAS_G12V AKT3_E17K MAP2K3_WT AKT3_WT.2 TRAF5_WT MAP3K7_I CSNK1E_ 0.0 AKT1S1_WT2
AKT1S1_WT1

PRKCE_WT2
CCND1_WT2

CCND1_WT1

E2F1_WT

CCND1_WT1

FRKCZ_K281R

PRKCZ_K281R

PRKCZ_K281R

PRKCZ_WT1

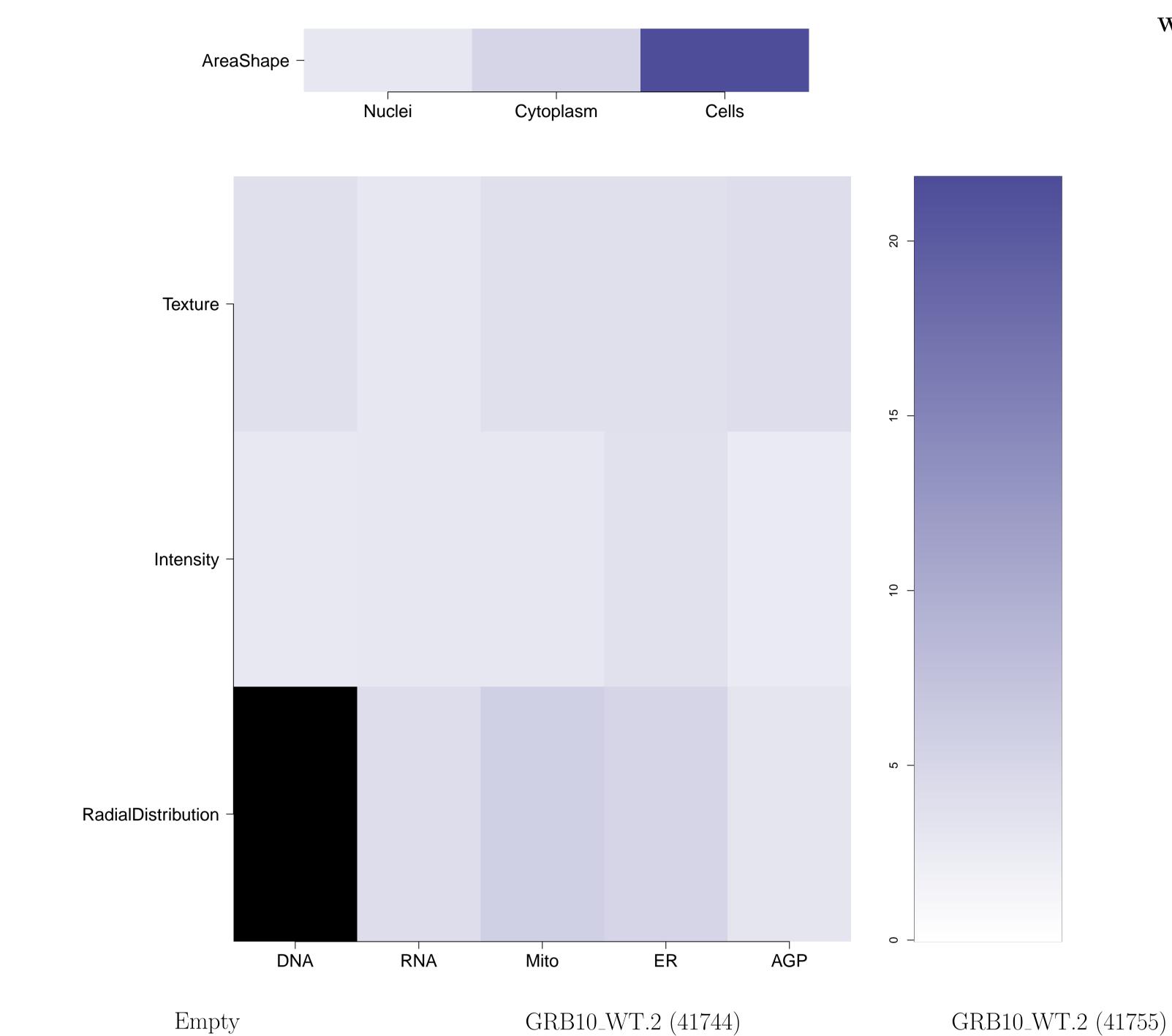
PRKCZ_WT1

NFKB1_WT1

NFKB1_WT1

NFKB1_WT1

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



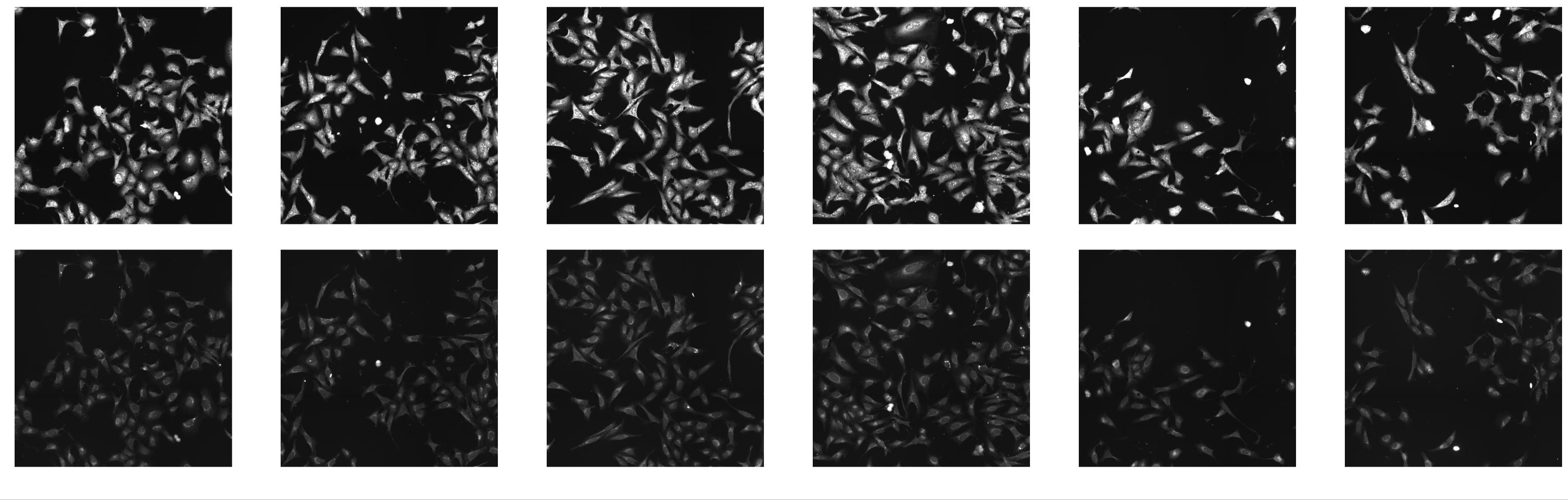
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

 $GRB10_{-}WT.2 (41757)$

GRB10_WT.2 (41754)



 $GRB10_{-}WT.2 (41756)$



Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	d Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.51)	the gene	Compound rank when scored against the gene using L1000 profiling		the gene relative to the untreated samples	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
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