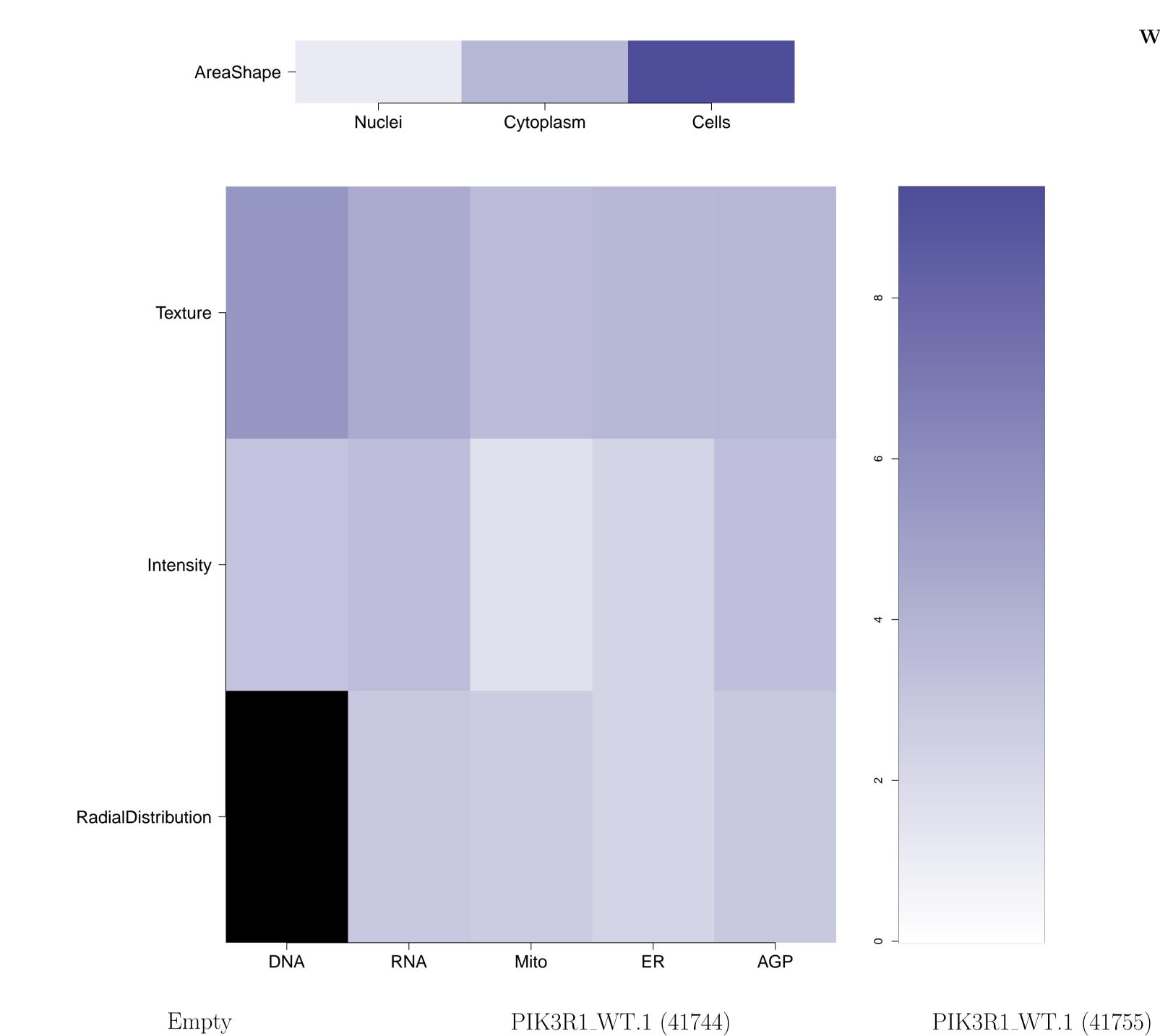
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein PIK3R1\_WT.1 - in Canonical PI3K/AKT How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes 0.3 PIK3CB\_WT.2 CDC42\_T17N CDKN1A\_WT MAP3K2\_WT. MAP2K3\_WT -G12V SMO\_WT.1 TRAF5\_WT JAG1\_WT 0.0 RBPJ\_WT.1 TGFBR1\_K232R CSNK1A1\_WT.3 SMURF2\_WT
ATF4\_WT.2
AKT1S1\_WT.1
PRKCZ\_del1-23 AKT1S1\_WT.2 SGK3\_WT.2 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



rank when

scored

against the

gene using

L1000

profiling

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)

Correlation

between

compound

the gene

replicates

correlation of the

compound signature

(95th DMSO

replicate correlation

is 0.52)

Chemical

structure

common names (where

available); blue/red colored

box means the matching

compound is

positively/negatively

correlated with the cluster

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.

Distinguishing individual features for the compound relative to Number of PubChem assays in which

untreated samples. Black means a mismatch; i.e. active (= high

z-score in magnitude) in the compound, and either inactive (=

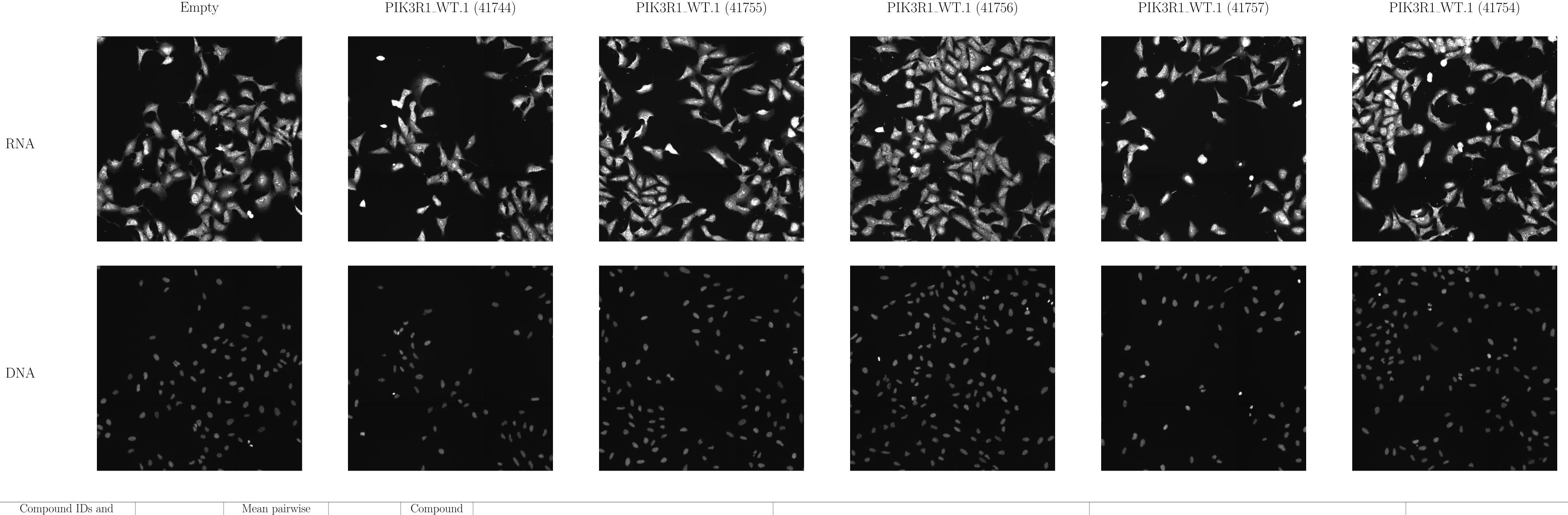
small z-score in magnitude) or oppositely active in the gene

the compound was tested; assays in

which the compound was active are

itemized





Common distinguishing feature categories in the compound and

the gene relative to the untreated samples

