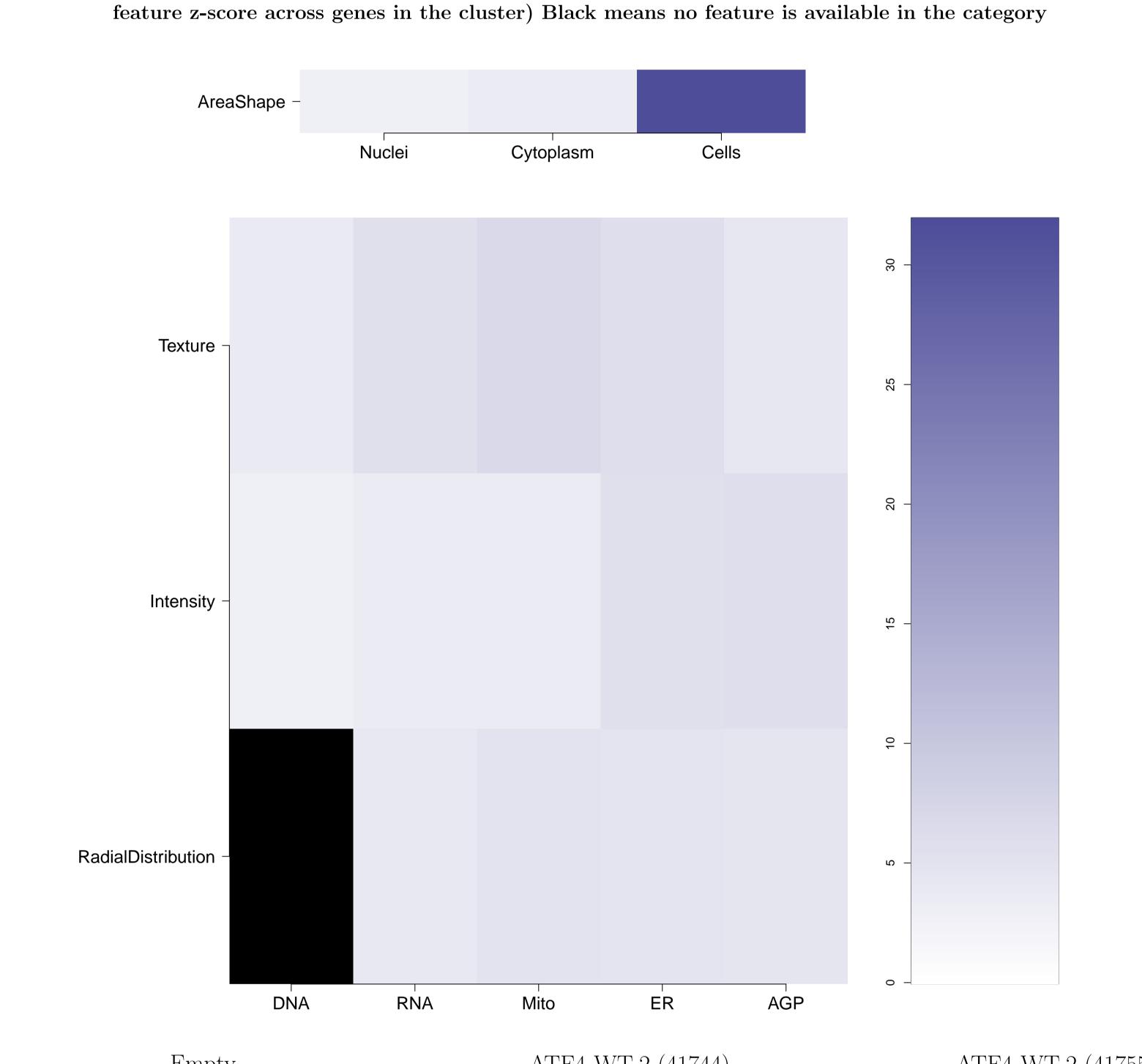
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein ATF4_WT.2 - in Canonical ER Stress/UPR How similar is this gene to the other genes? 0.9 0.4 Correlation of the gene to the other genes CSNK1E_WT.2 0.3 MAP3K2_WT.2 PIK3CB_WT.2 CDC42_T17N MAP3K7_WT RAC1_Q61L KRAS_WT.1 AKT3_WT.2 TRAF5_WT JAG1_WT 0.0 AKT1S1_WT.2
AKT1S1_WT.1
PIK3R1_WT.1
PRKACG_WT.3
PRKCZ_del1-238
CCND1_WT.2 -del1-238 PRKCA_K368R CEBPA_WT.2 RBPJ_WT.2 MLST8_WT T8_WT PTEN_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



RNA

Mito

Compound IDs and

common names (where

available); blue/red colored

box means the matching

compound is

positively/negatively

correlated with the cluster

Mean pairwise

replicates

correlation of the

compound signature

(95th DMSO

replicate correlation

is 0.52)

Chemical

structure

Compound

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

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

the compound was tested; assays in

which the compound was active are

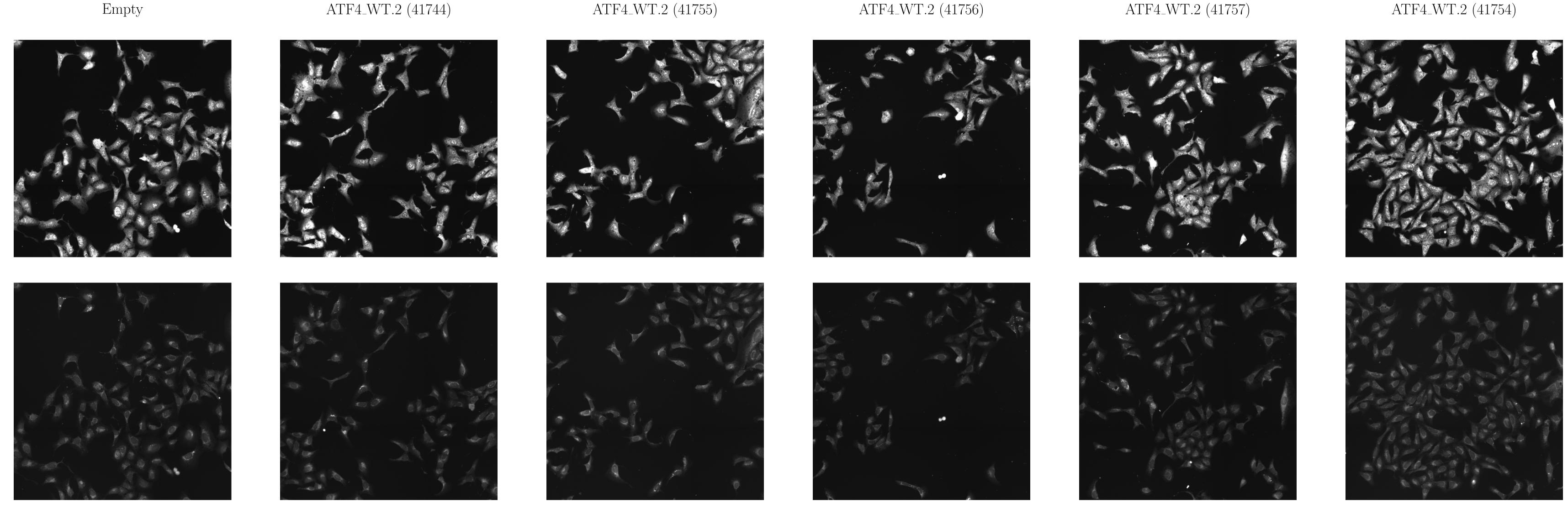
itemized

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





Common distinguishing feature categories in the compound and

the gene relative to the untreated samples

