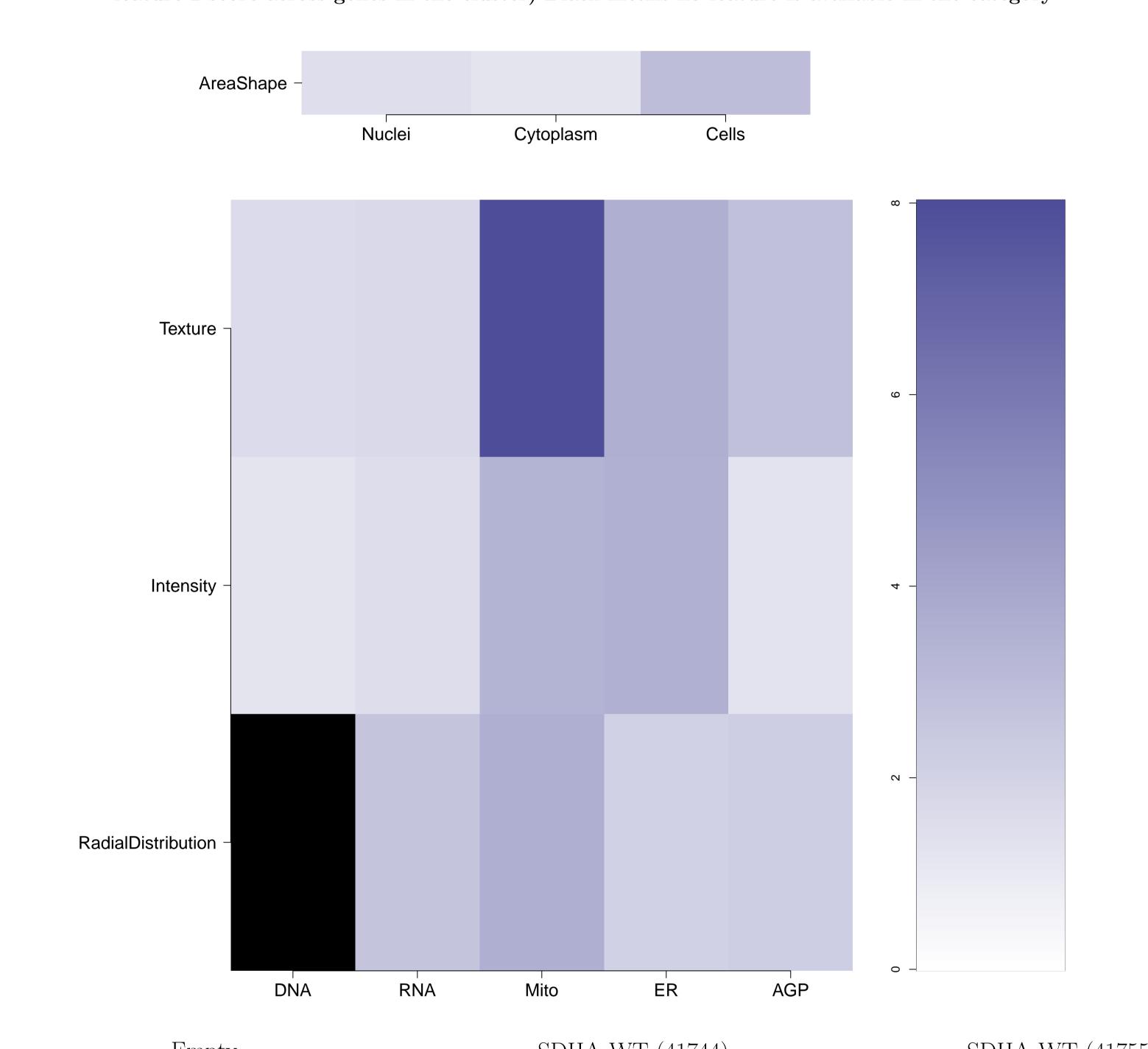
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein SDHA\_WT - in Canonical Hypoxia How similar is this gene to the other genes? 0.9 0.5 0.4 TGFBR1\_K232R 0.3 CEBPA\_WT.2 MAP3K9\_WT NFKB1\_WT.1 SGK3\_WT.2 SMURF2\_WT TRAF2\_WT CDC42 0.0 MYD88\_L265P
MYD88\_WT
YAP1\_WT.1
FRN1\_WT.1
YAP1\_WT.3
EIF4EBP1\_WT
NFKBIA\_WT
NFKBIA\_WT
NFKBIA\_WT
TCF4\_WT.1
AKT1\_WT.1
PRKCZ\_WT.1
PRKCZ\_WT.1

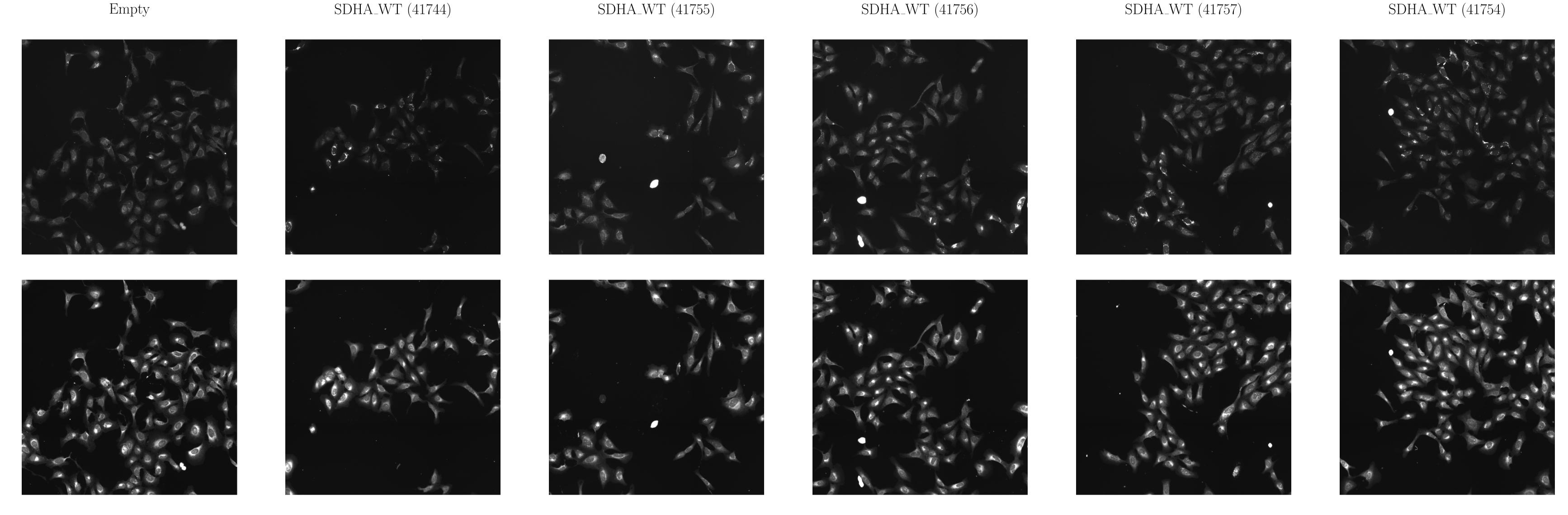
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the category

Correlation of the gene to the other genes



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 compound is positively/negatively correlated with the cluster  Chemical structure  Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.51)  Mean pairwise replicates correlation between compound the gene using L1000 profiling  Compound TDs and Compound rank when scored against the gene using L1000 profiling	$\perp$ Common distinguishing teature categories in the compound and $\perp$ intreated samples. Black means a mismatch, i.e. active $l=$ high $\perp$	the compound was tested; assays in
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