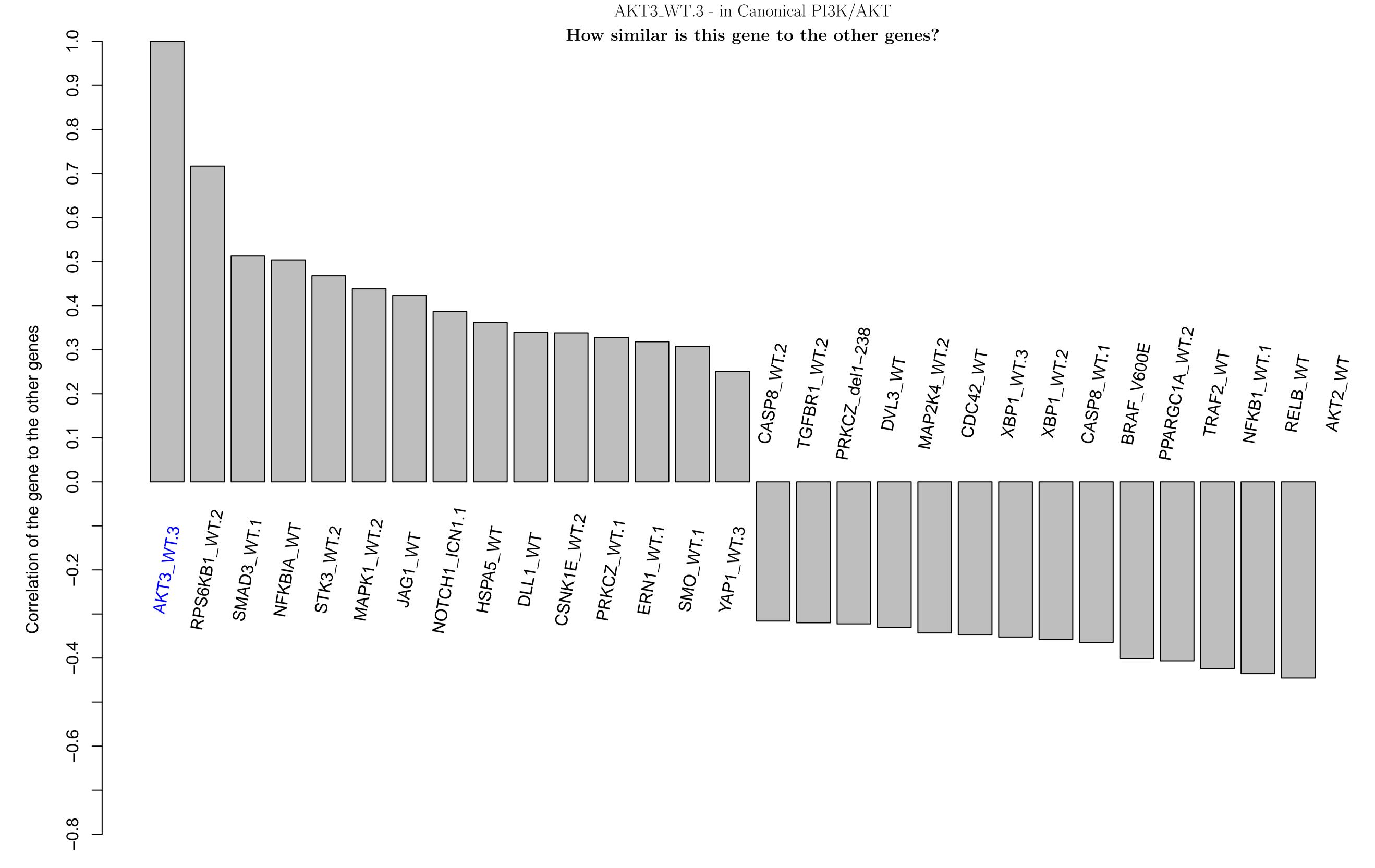
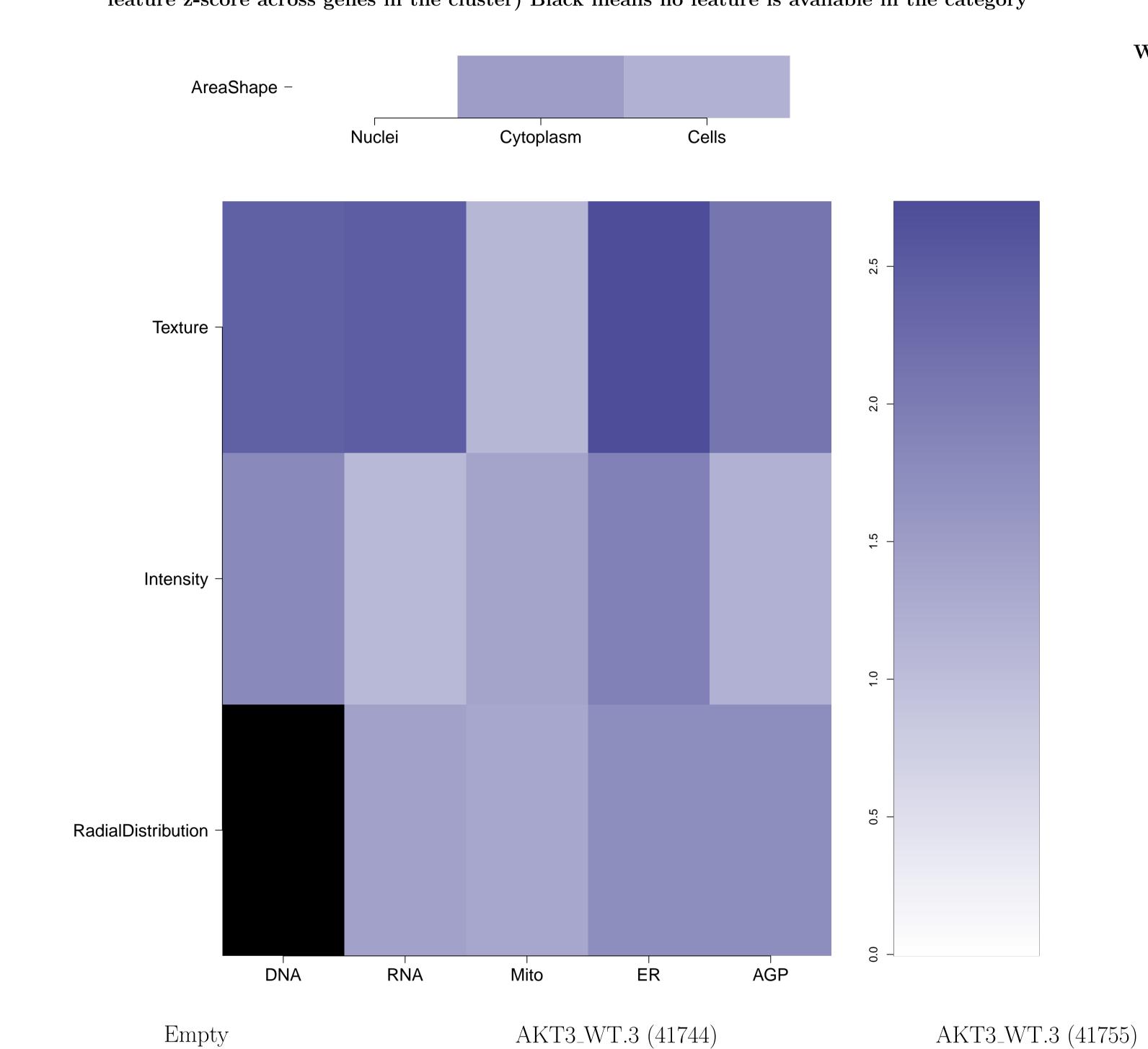
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein



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

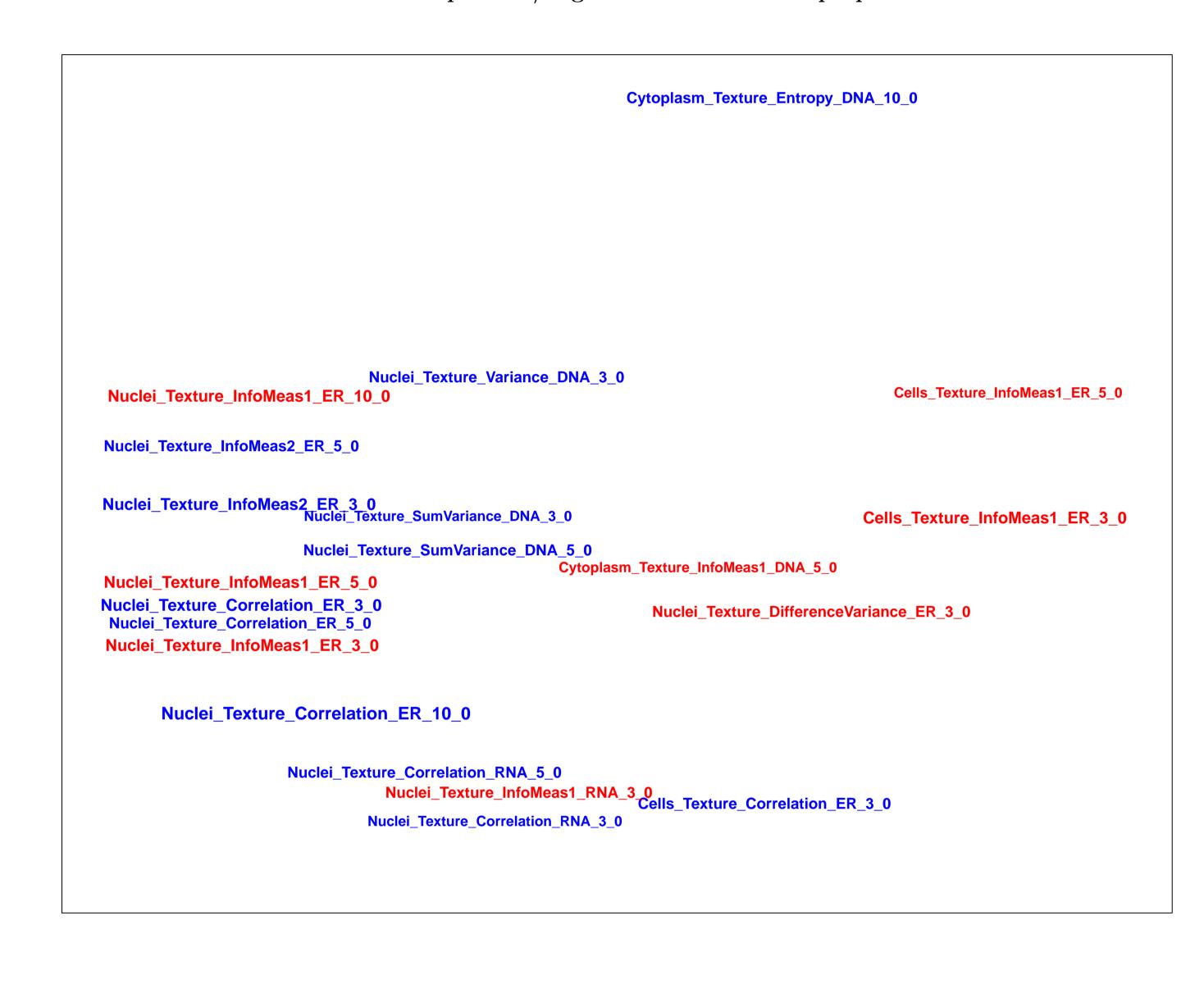


RNA

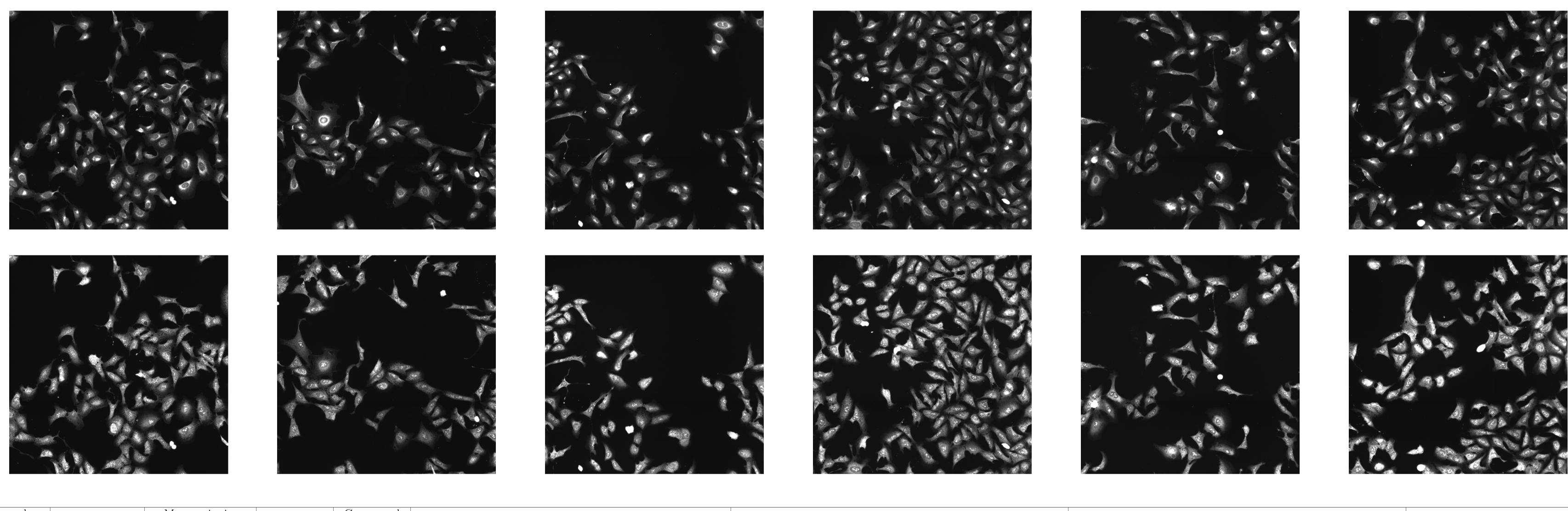
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

 $AKT3_WT.3 (41757)$

AKT3_WT.3 (41754)



AKT3_WT.3 (41756)



| Compound IDs and common names (where available); blue/red colored | Chemical | Mean pairwise replicates correlation of the | Correlation between | | How similar is the compound signature to the genes in this | 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 Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized. |
|--|-----------|--|------------------------|--|---|--|---|
| box means the matching compound is positively/negatively correlated with the cluster | structure | compound signature (95th DMSO replicate correlation is 0.52) | compound the gene | against the gene using L1000 profiling | experiment? (Yellow and red lines correspond to top/bottom 1st and 5th percentile DMSO correlation to all the genes) | | |

