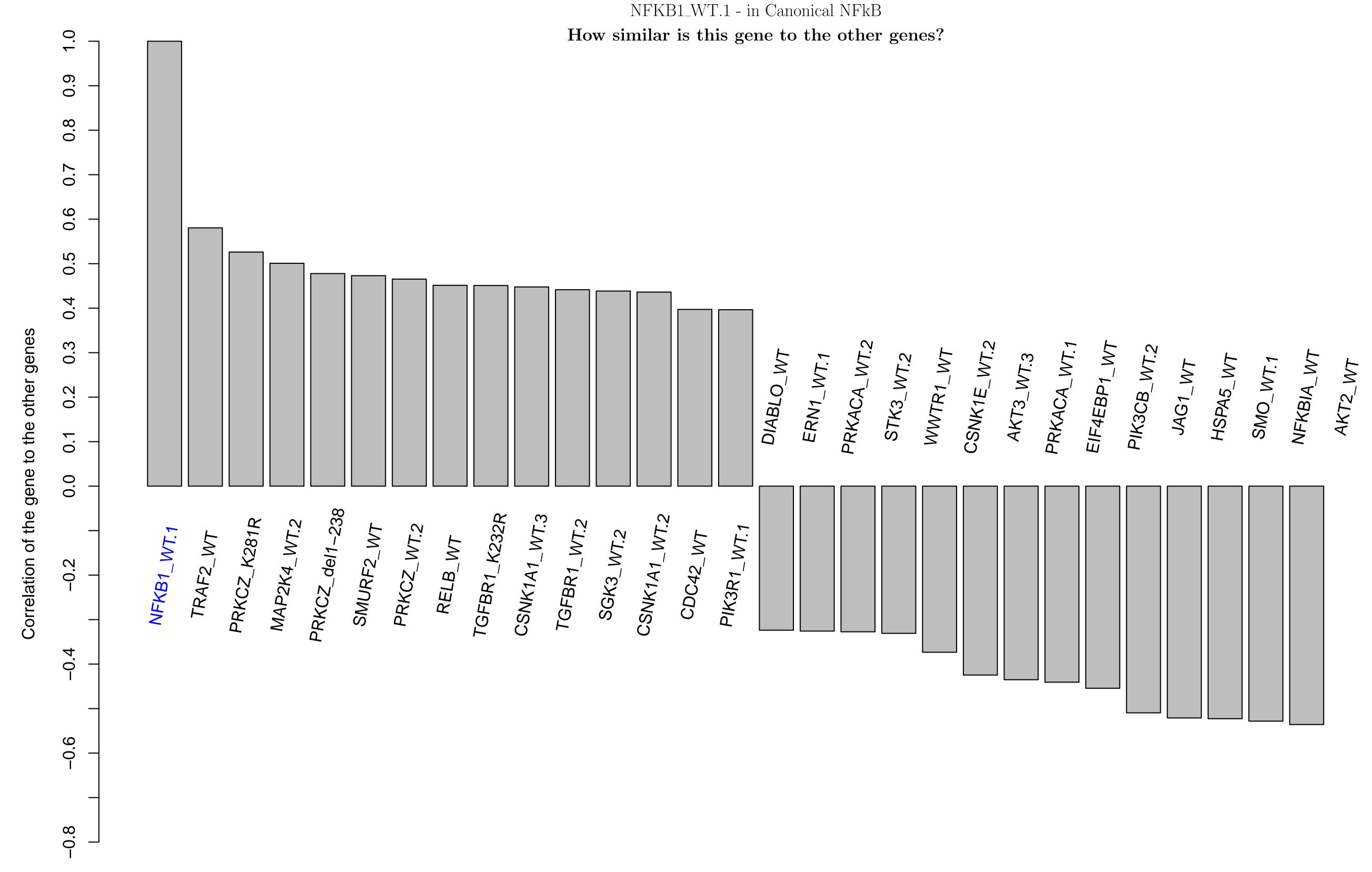
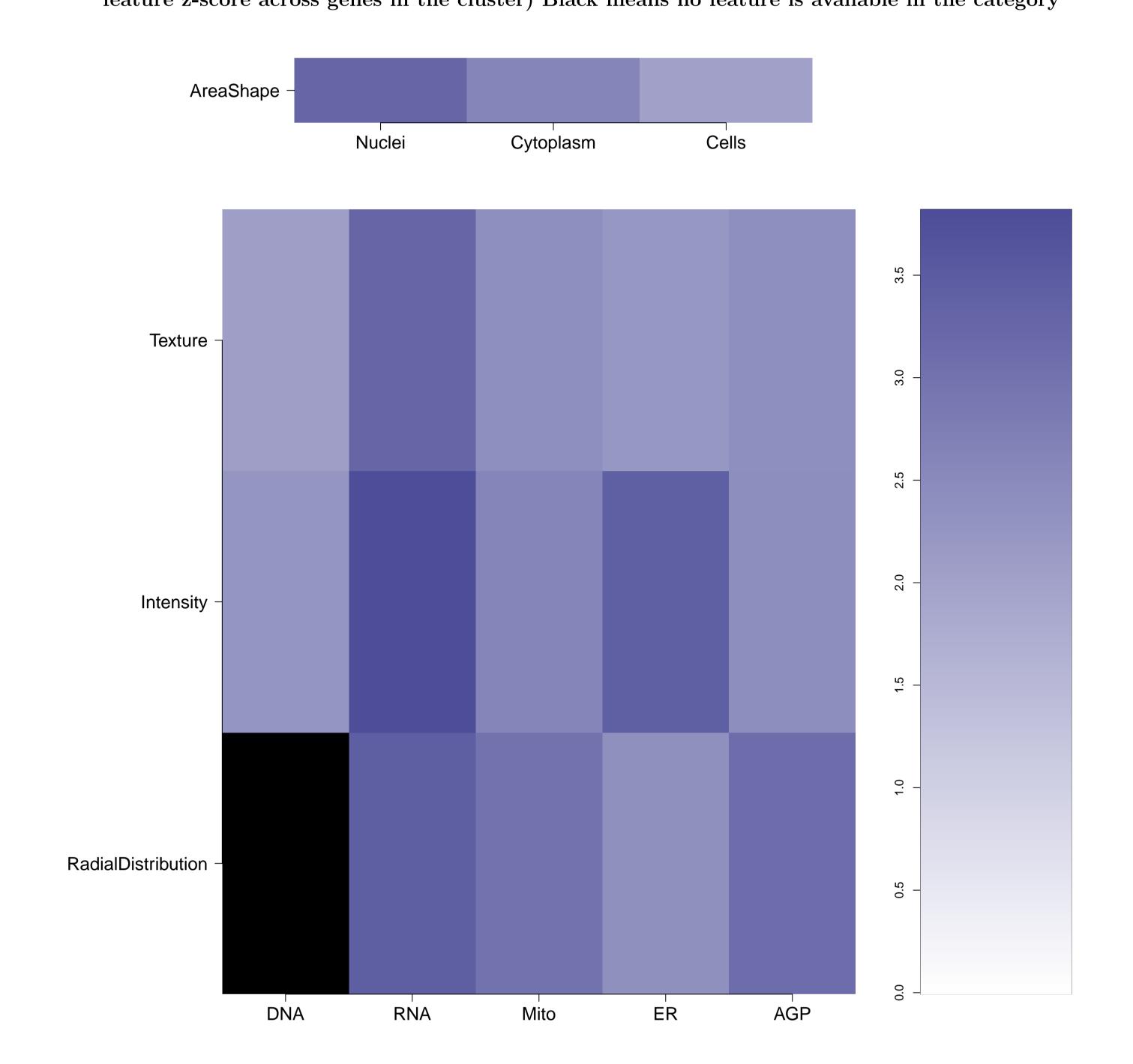
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein



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

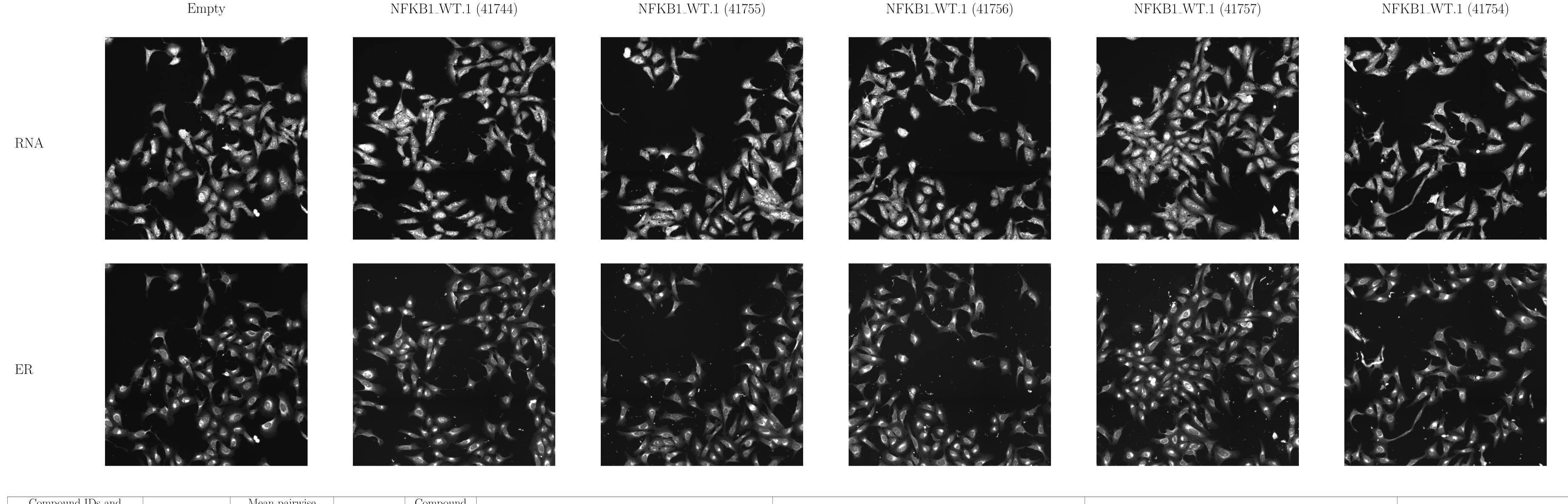


RNA

ER

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 | | Mean pairwise | | Compound | | | | |
|------------------------------|-----------------------|-----------------------|---------------------------------|-------------|---|---|--|-----|
| common names (where | Chemical structure | replicates | the gene against the gene using | | | Distinguishing individual features for the compound relative to Number of PubChem assays in wh | | |
| available); blue/red colored | | correlation of the | | scored | 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) | Common distinguishing feature categories in the compound and the gene relative to the untreated samples | untreated samples. Black means a mismatch; i.e. active (= high the compound was tested; assays z-score in magnitude) in the compound, and either inactive (= which the compound was active a | · · |
| box means the matching | | compound signature | | against the | | | | |
| compound is | | (95th DMSO | | gene using | | | | |
| positively/negatively | | replicate correlation | | | | sman z-score in magnitude) of oppositely active in the gene | itemized | |
| correlated with the cluster | | is 0.51) | | profiling | | | | |

