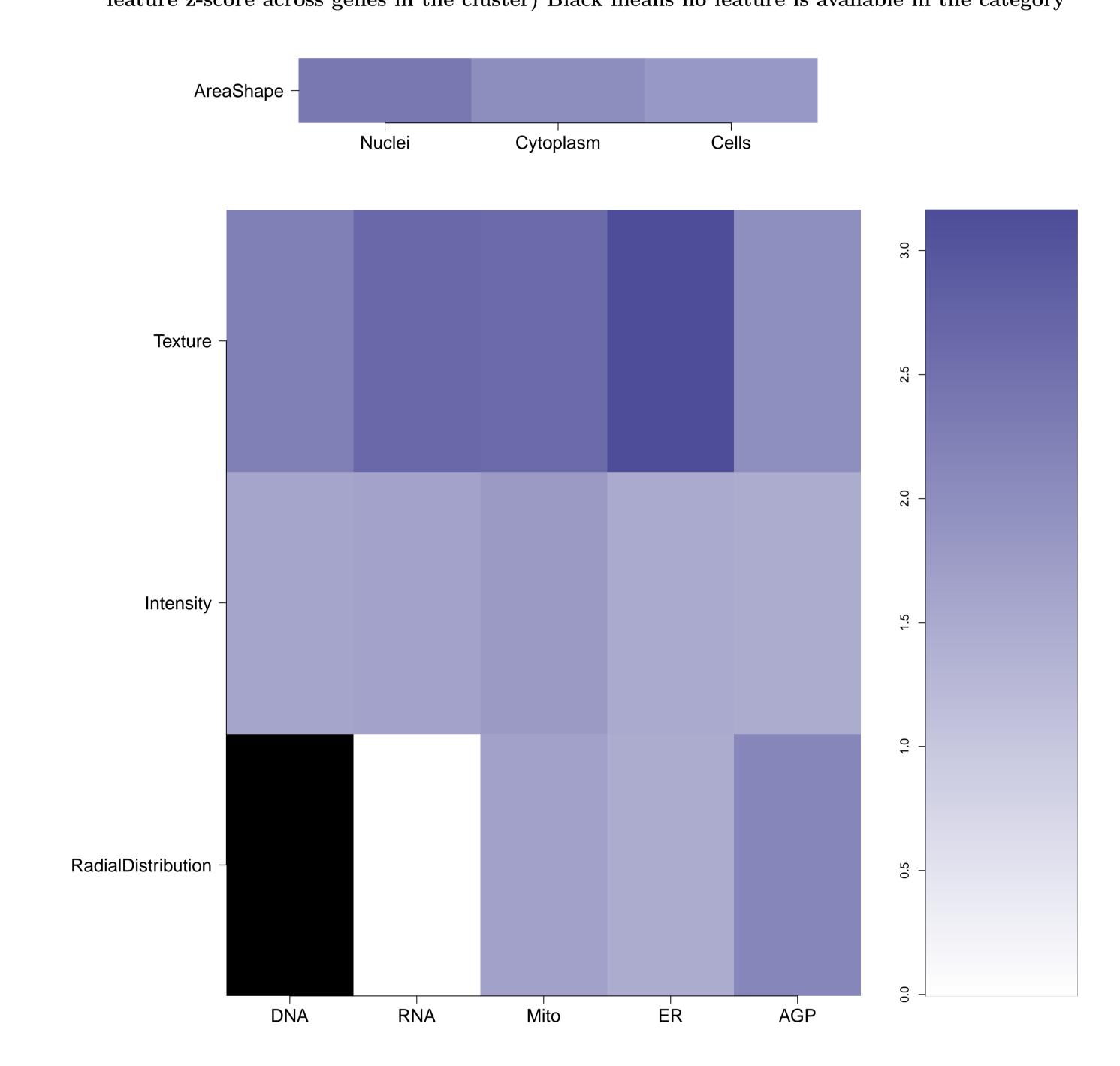
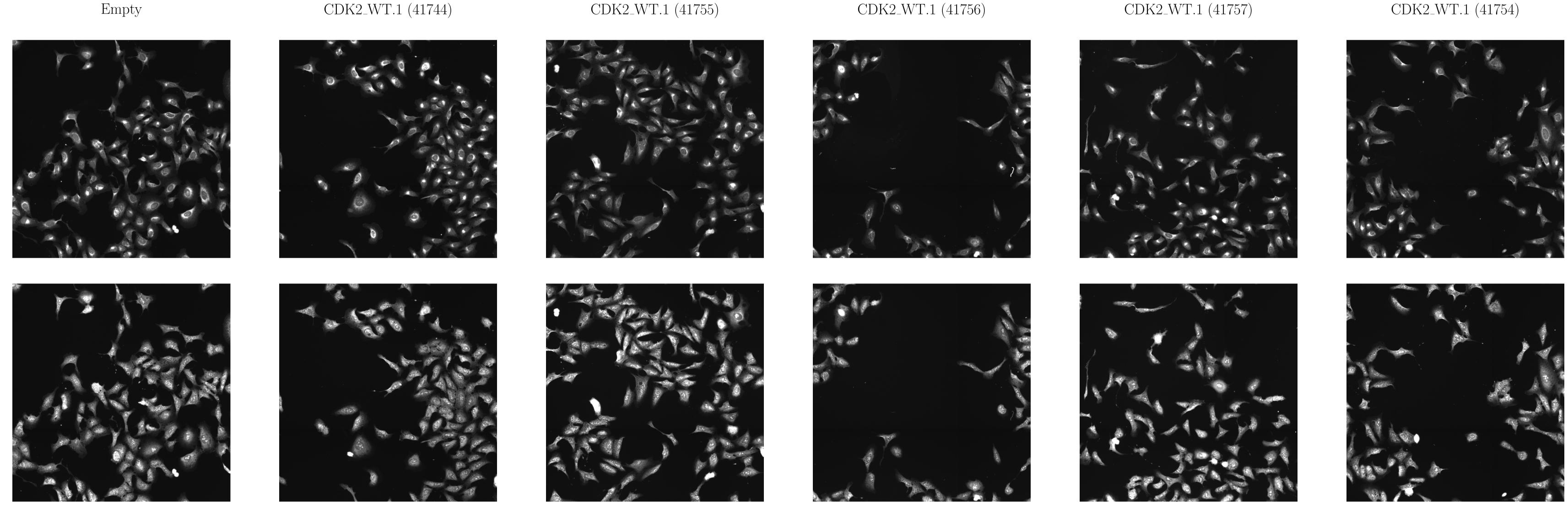


What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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



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 | d IDs and | | Mean pairwise | | Compound | | | | |
|----------------|----------------|--------------------|-----------------------|-------------------------|---------------------------------|---|--|---|------------------------------------|
| | mes (where | Chemical structure | replicates | the Correlation between | rank when | 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 | 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 (= which the compound was test and z-score in magnitude) or oppositely active in the gene | Number of PubChem assays in which |
| / / | ie/red colored | | correlation of the | | | | | | the compound was tested; assays in |
| | he matching | | compound signature | 1 | compound against the gene using | | | | |
| compo | ound is | | (95th DMSO | the gene | | | | | |
| positively/ | 'negatively | | replicate correlation | elation L1000 | | | sman z-score in magnitude, or oppositely active in the gene | Tocimized | |
| correlated wit | th the cluster | | is 0.52) | | profiling | | | | |

