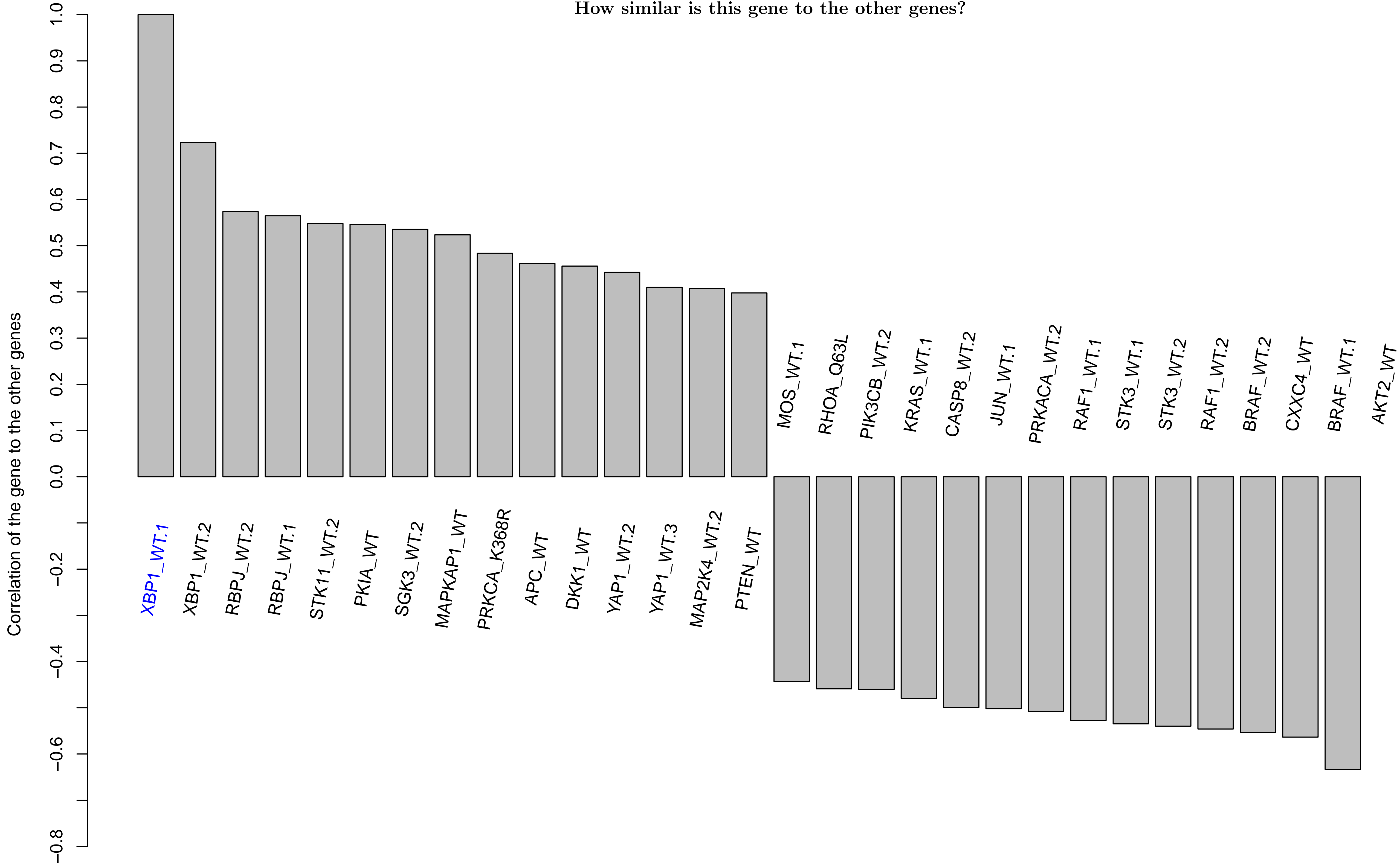
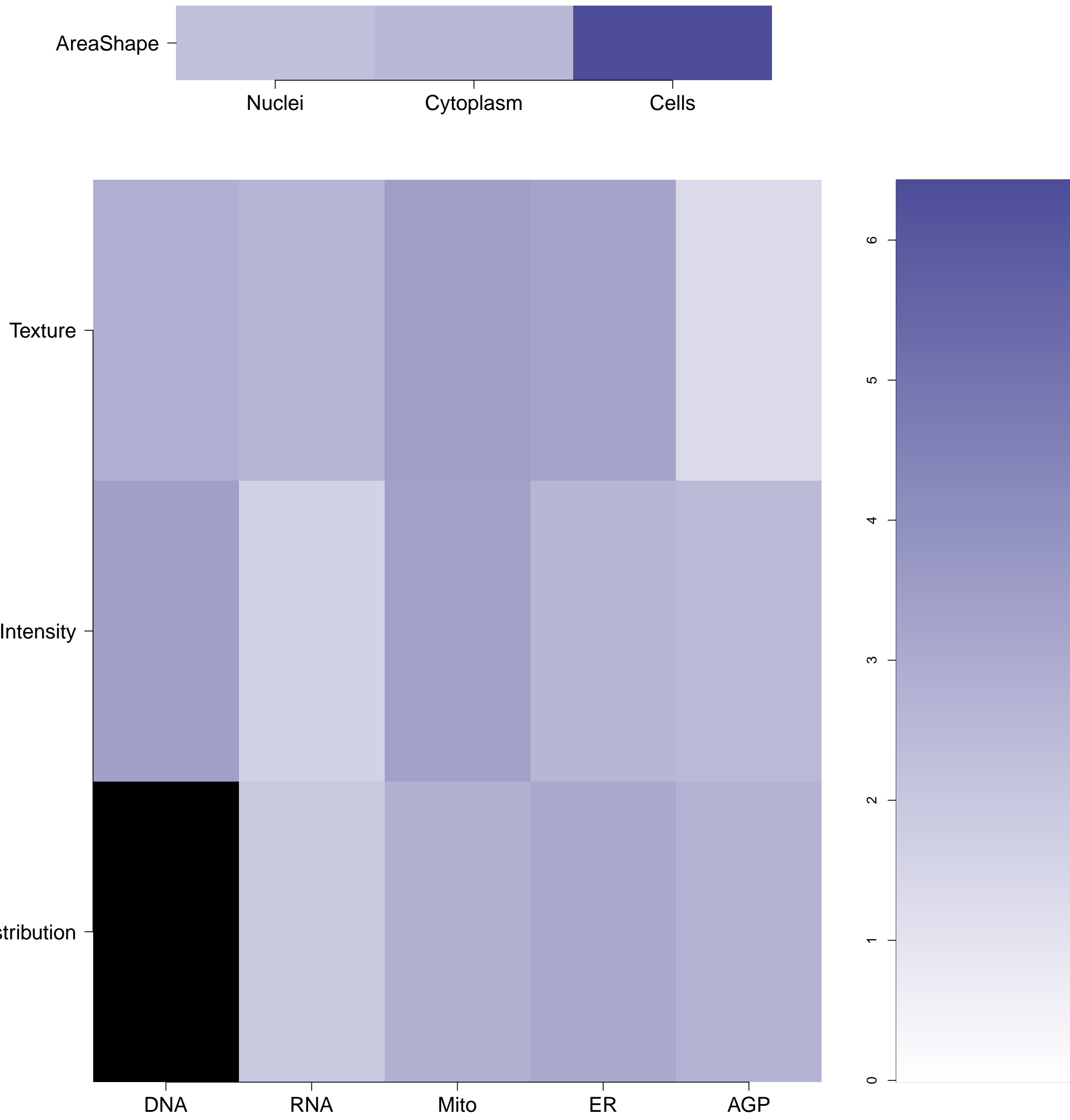


XBP1.WT.1 - in Canonical ER Stress/UPR

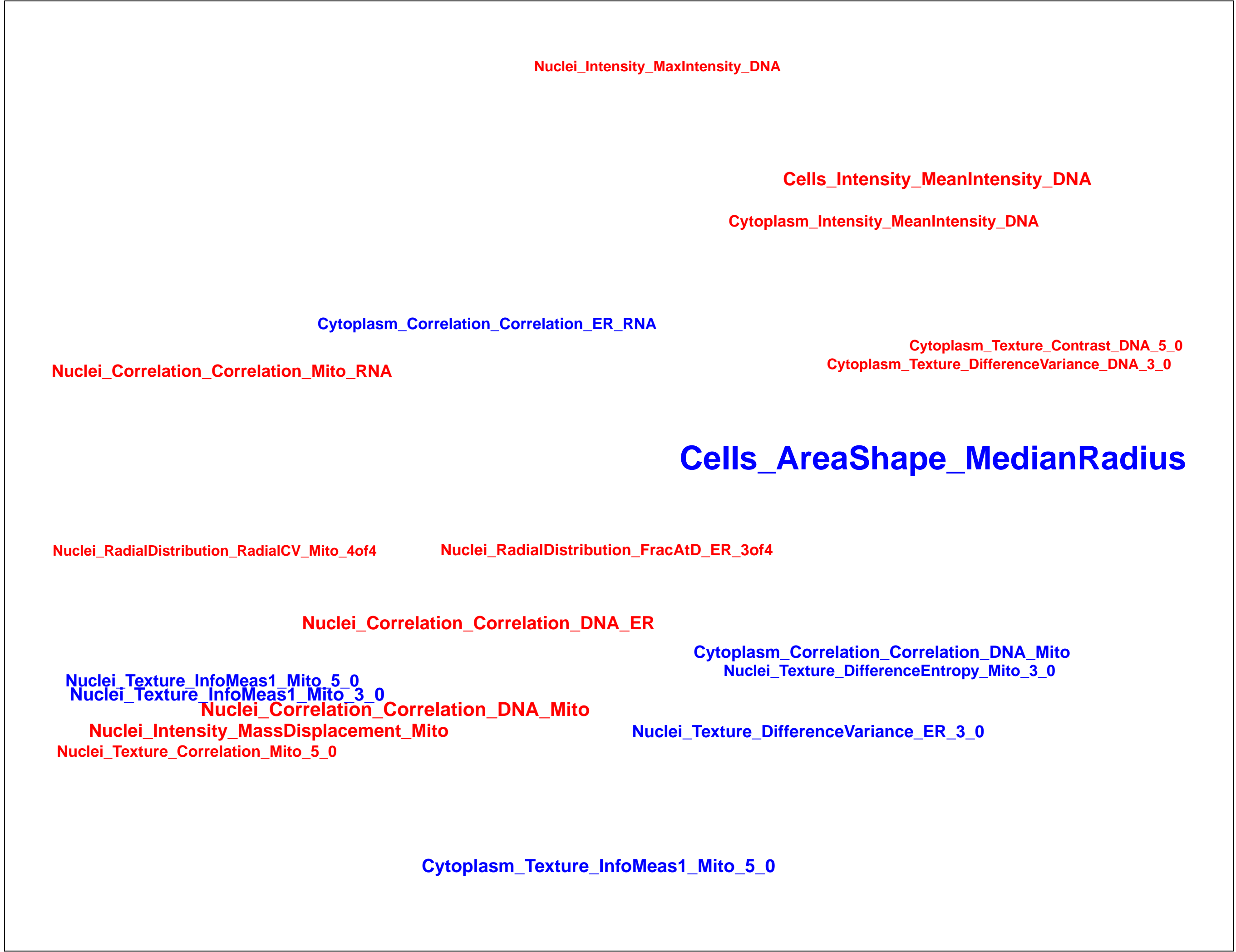
How similar is this gene to the other genes?



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.



Empty

XBP1.WT.1 (41744)

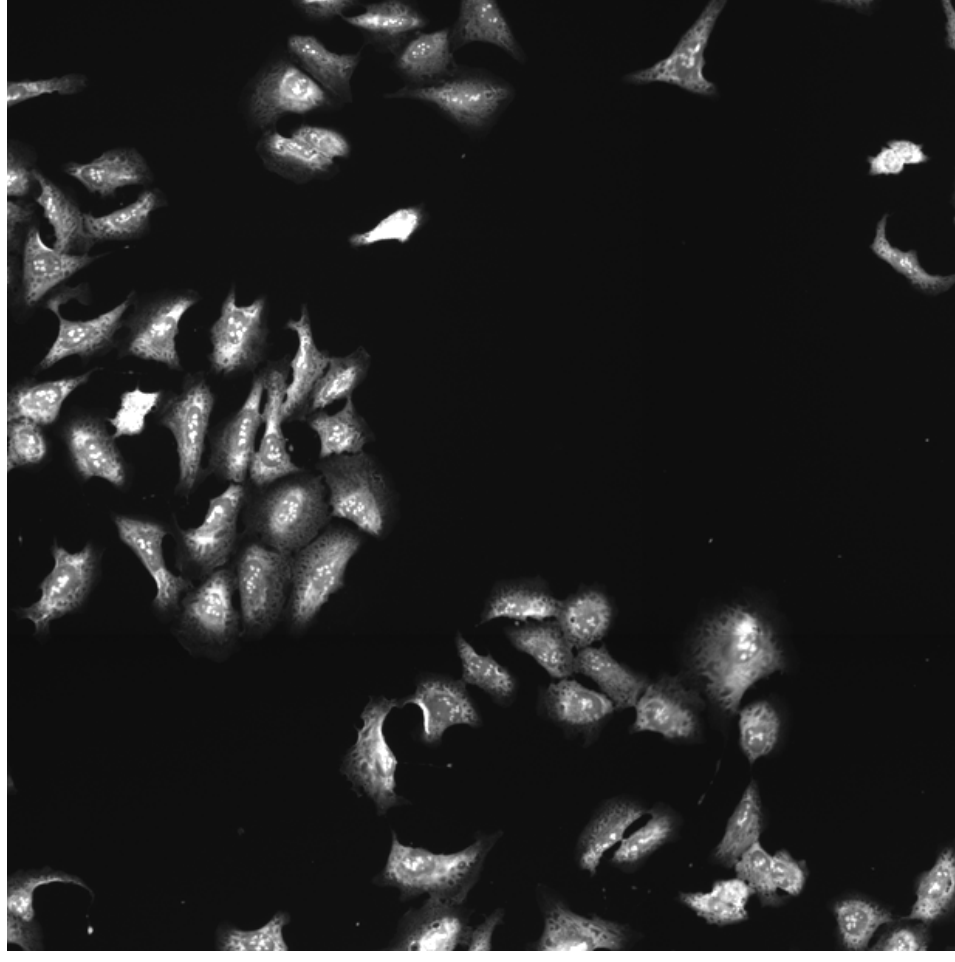
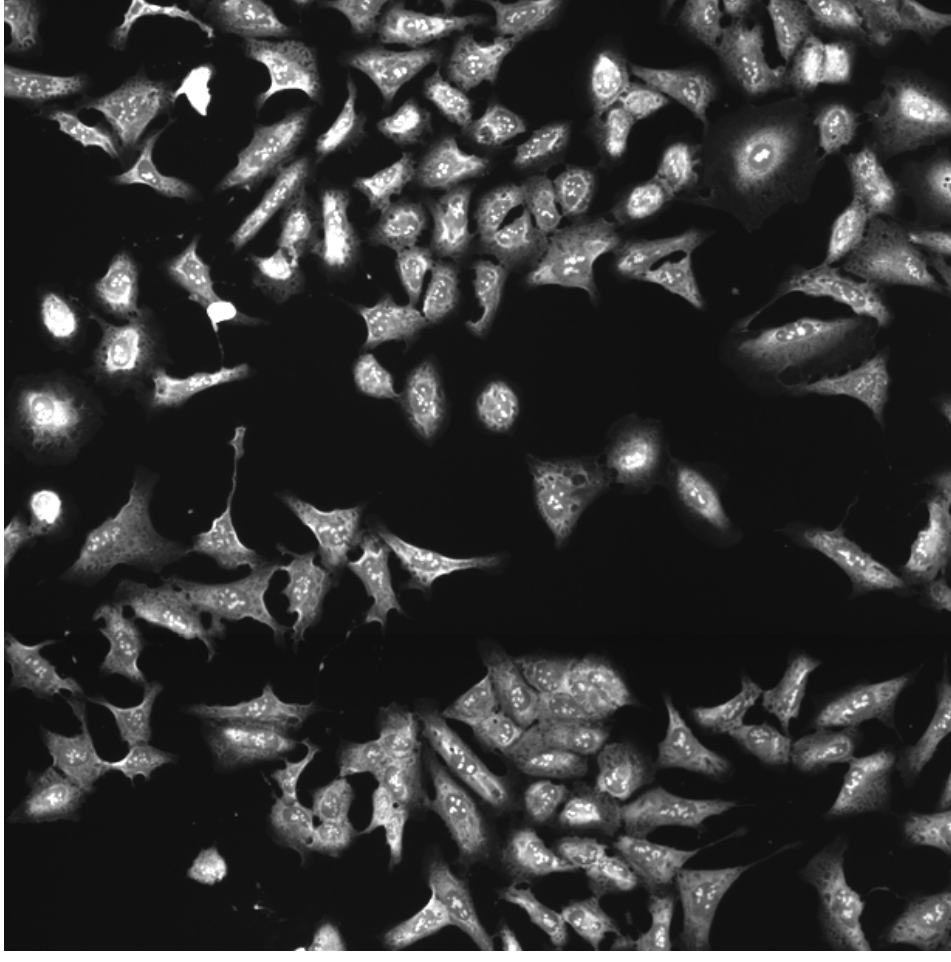
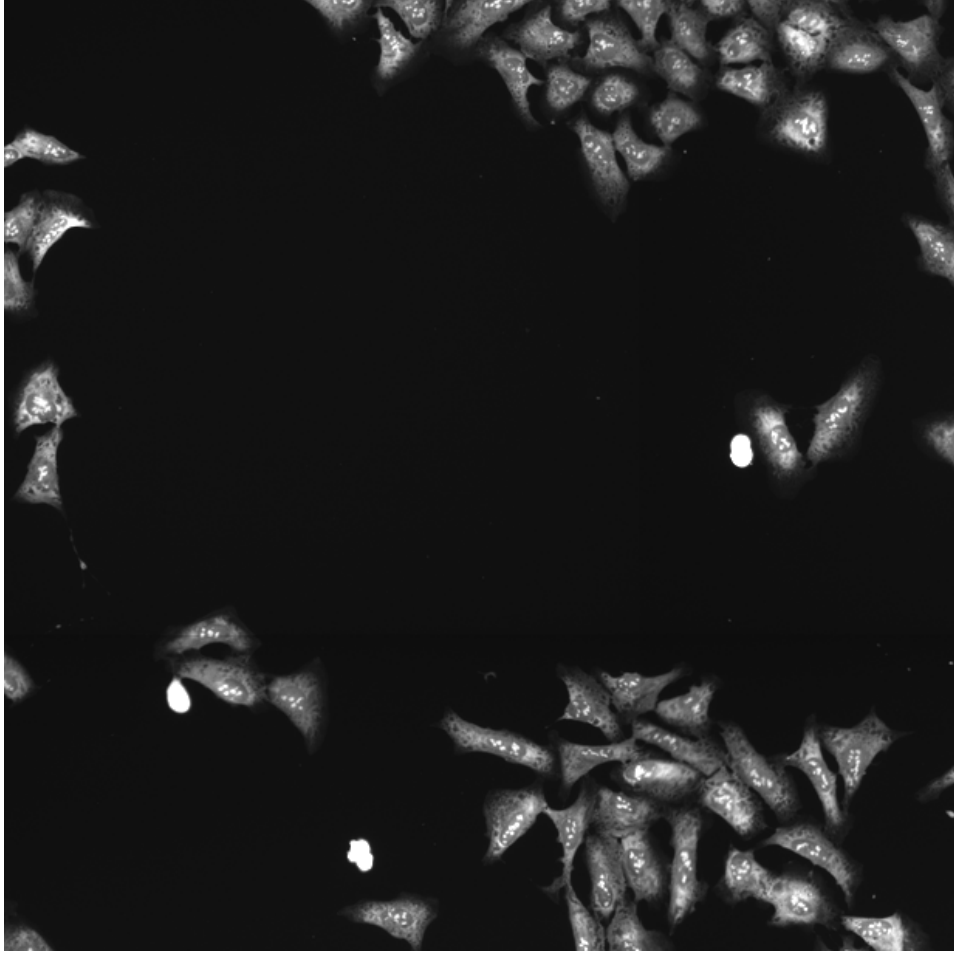
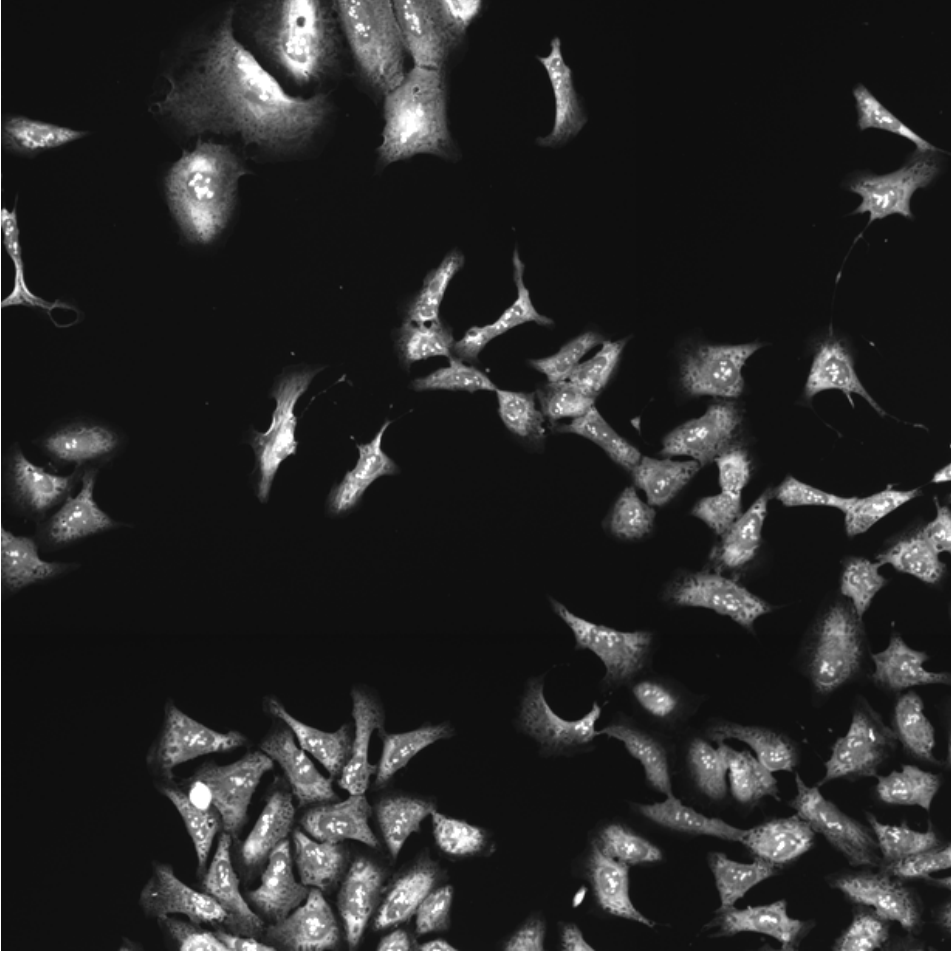
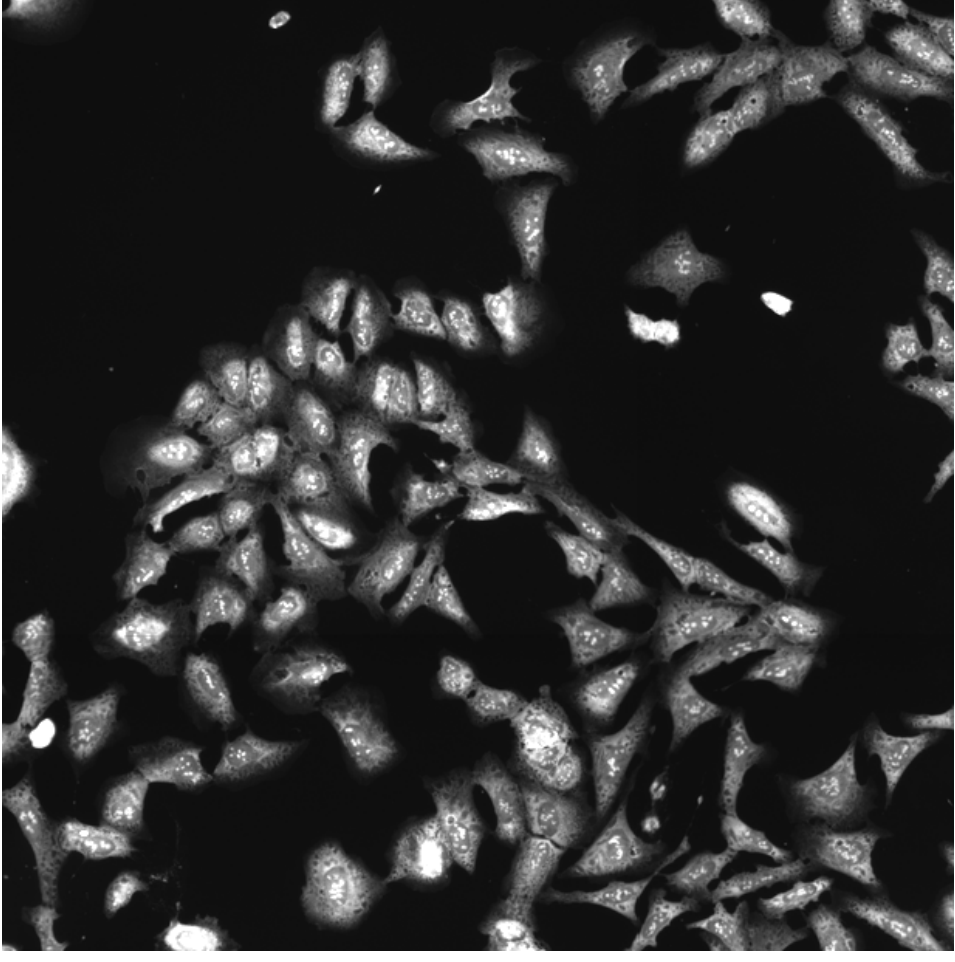
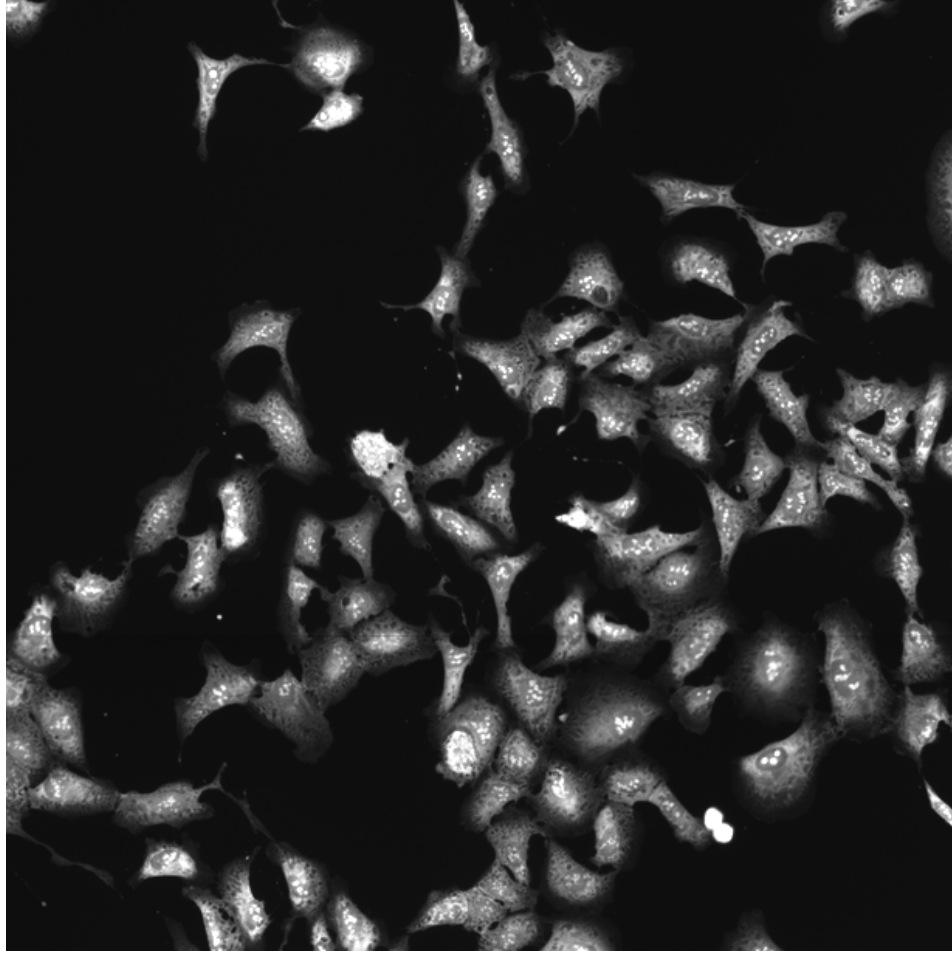
XBP1.WT.1 (41755)

XBP1.WT.1 (41756)

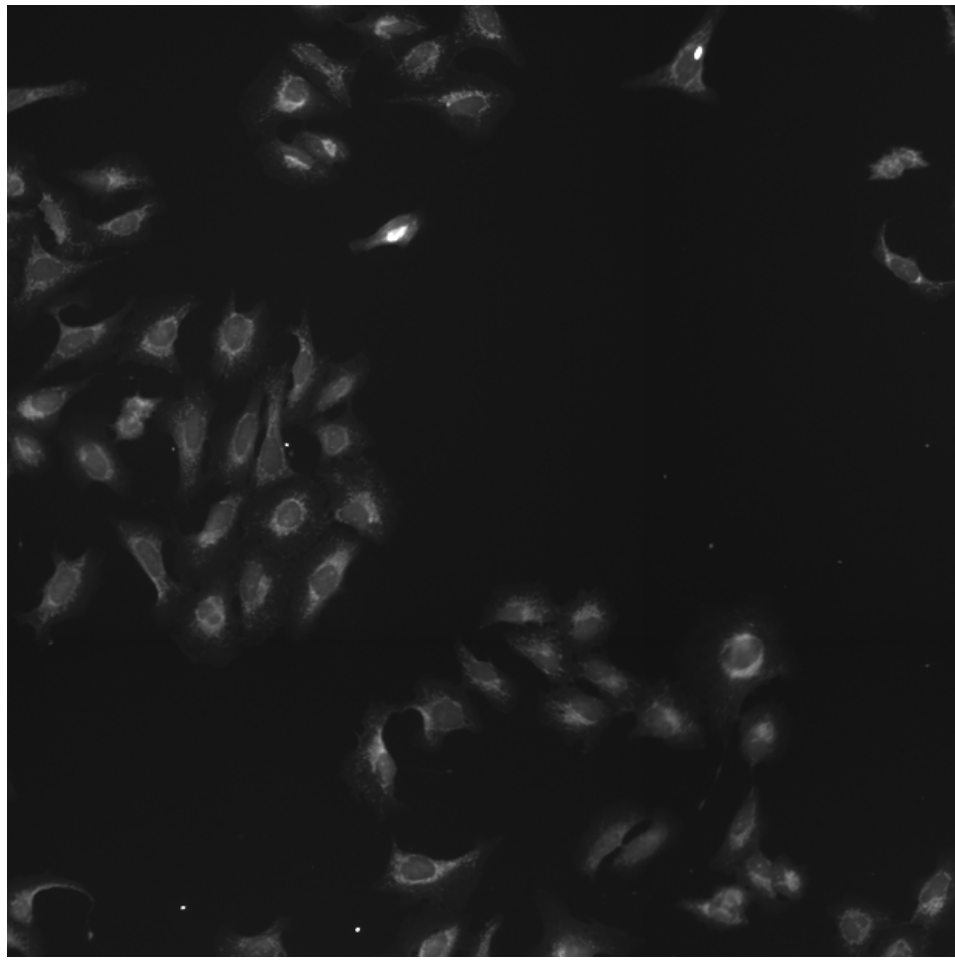
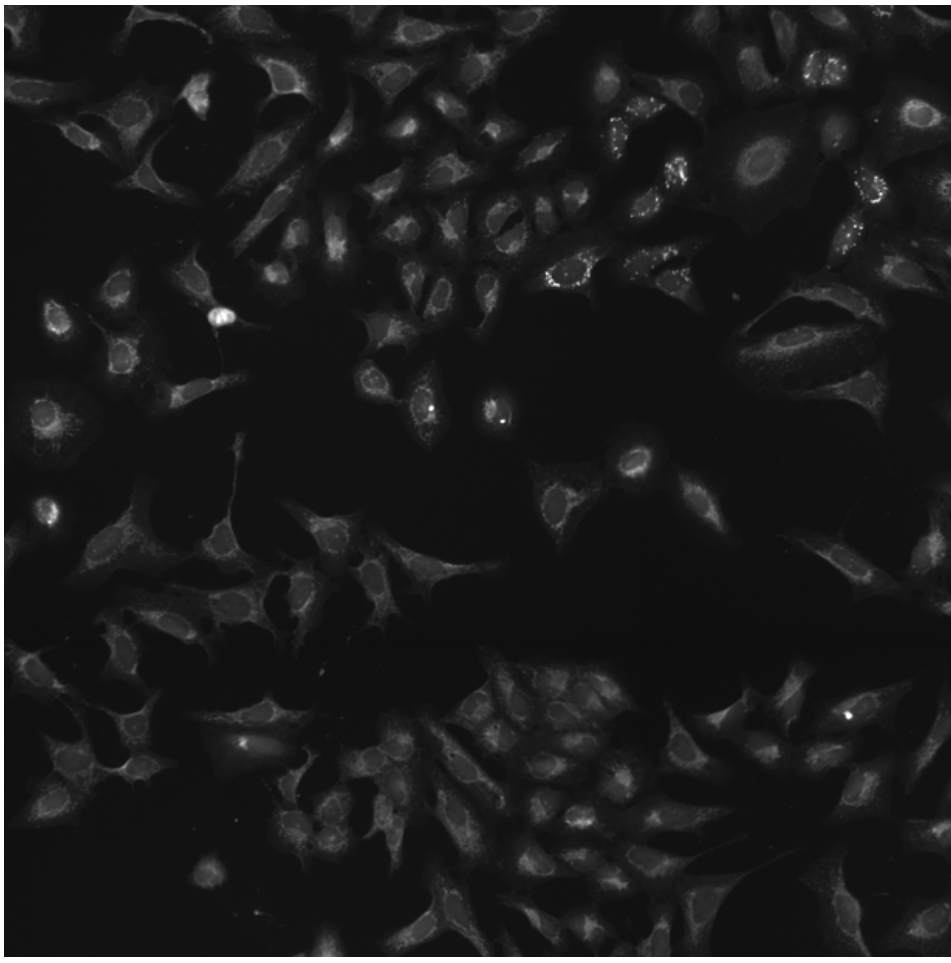
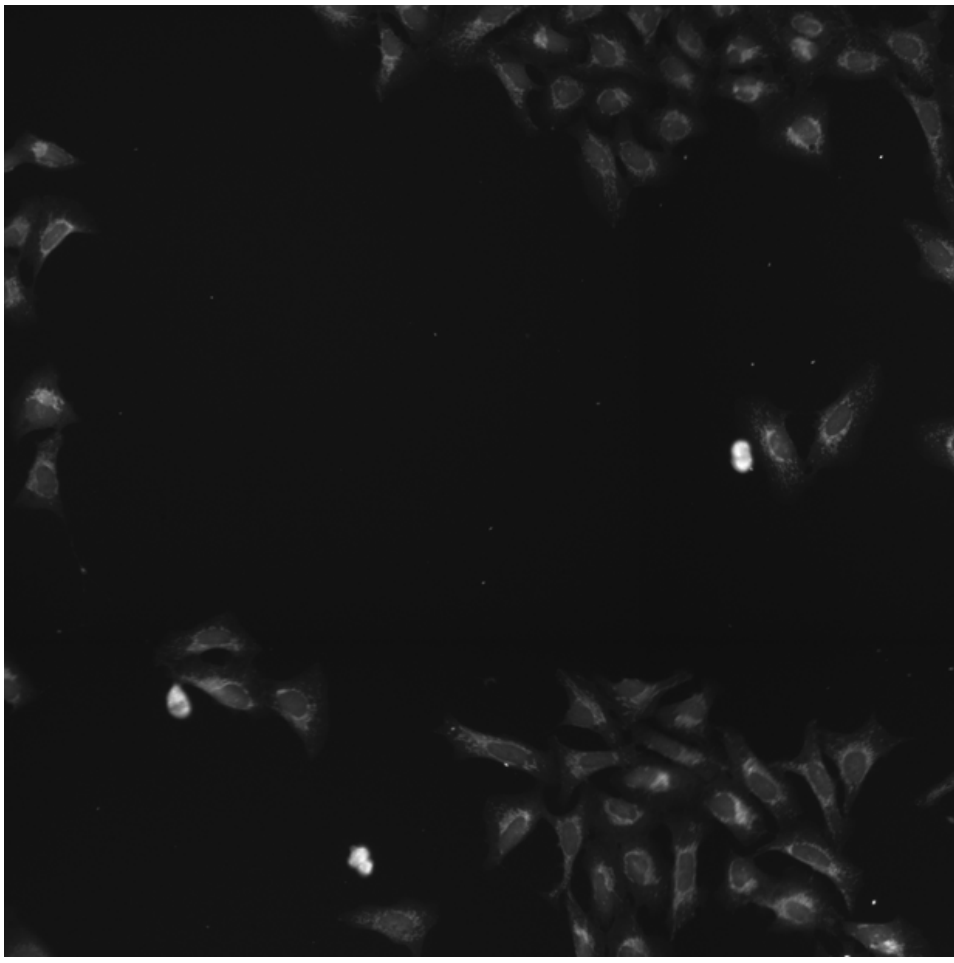
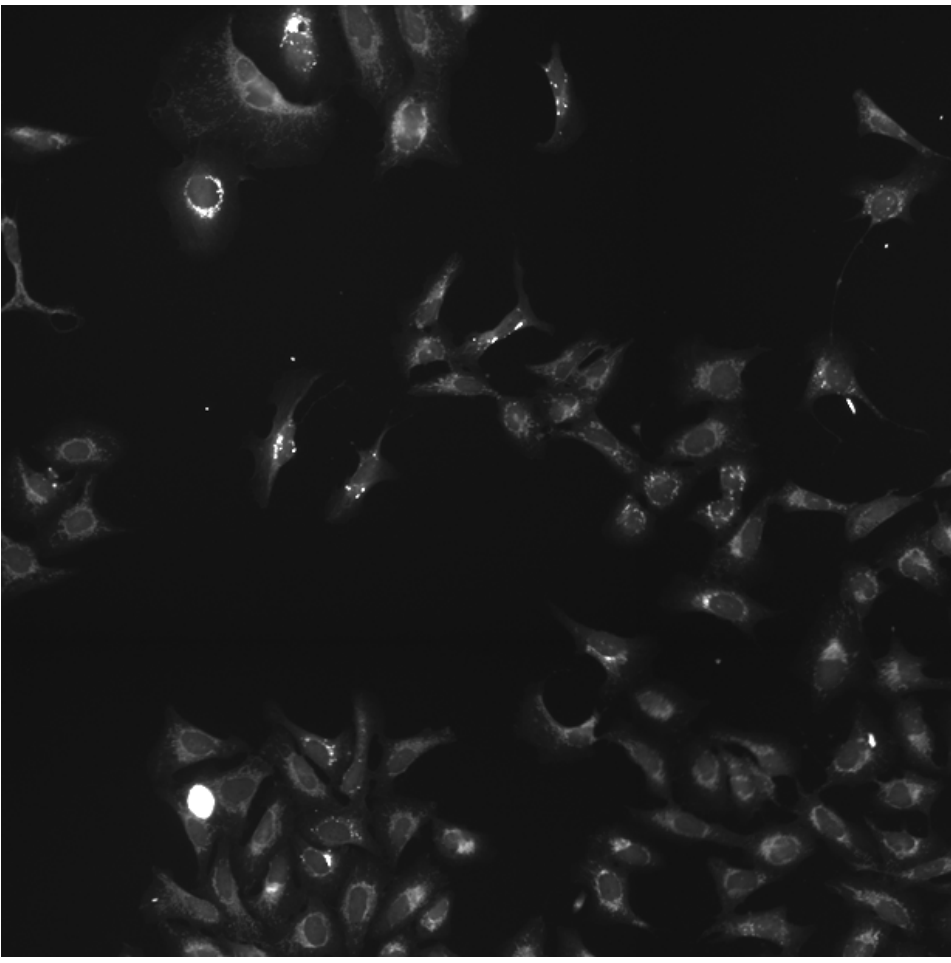
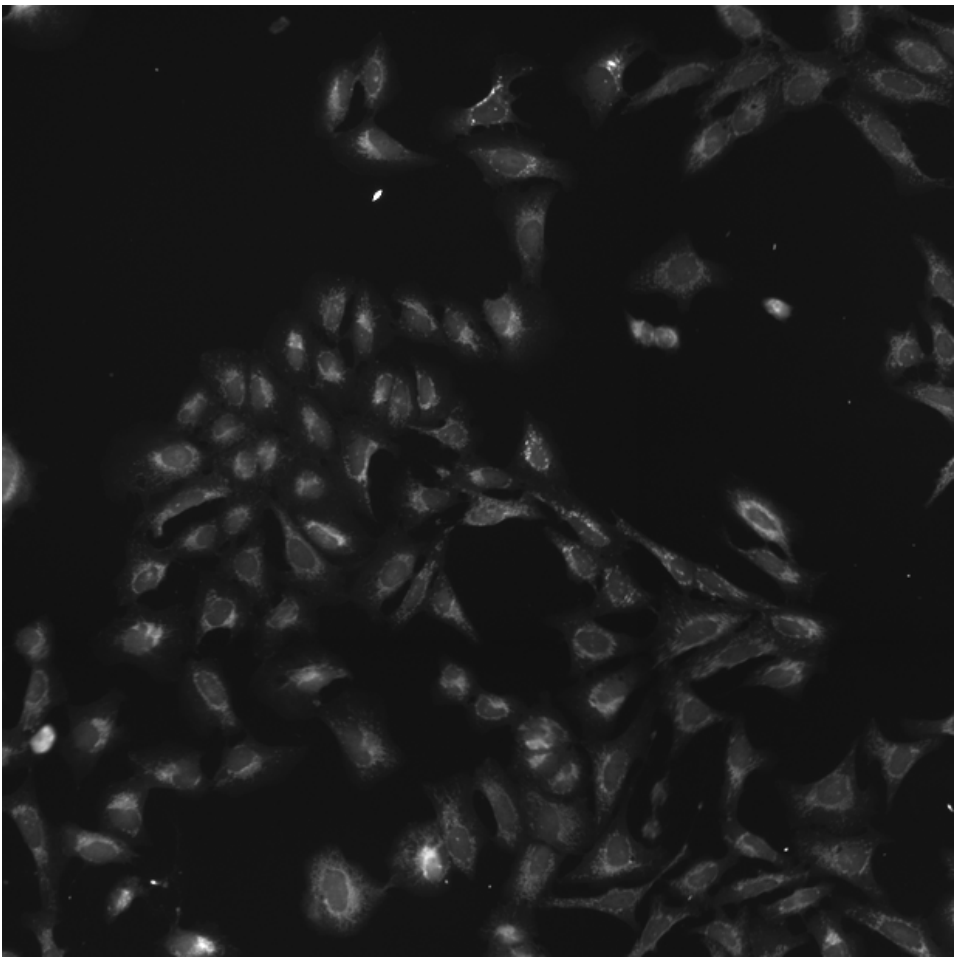
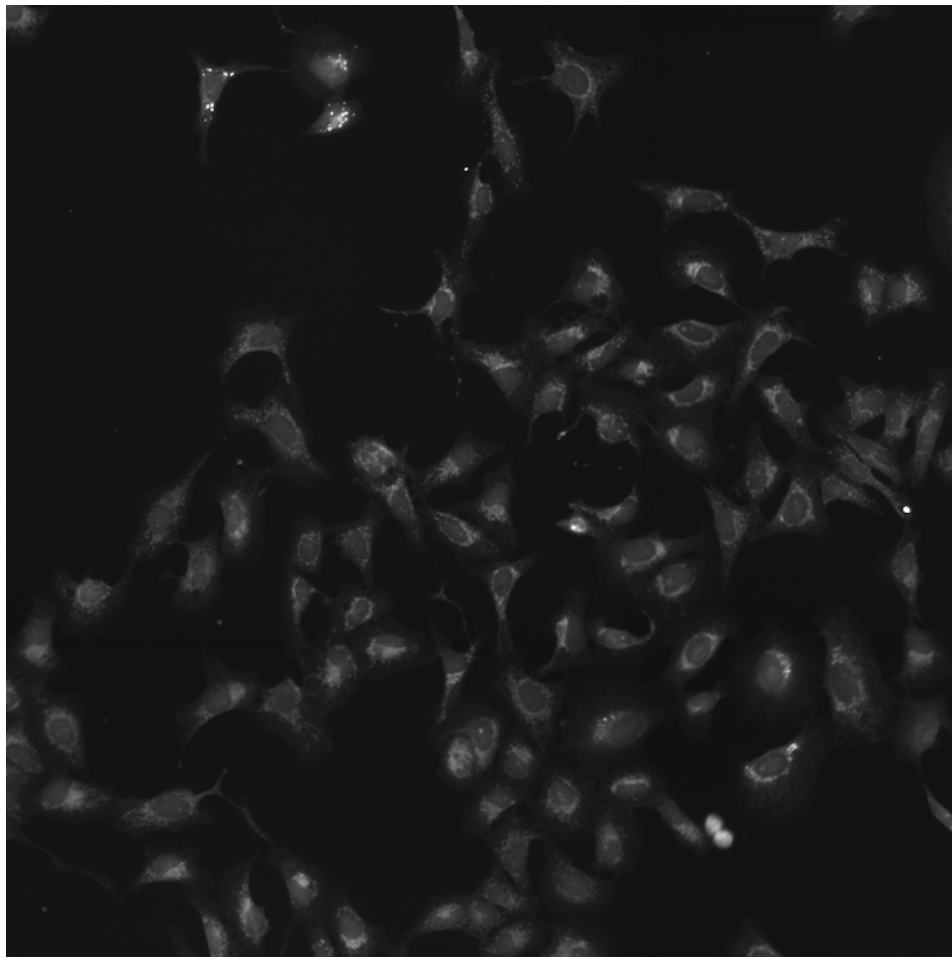
XBP1.WT.1 (41757)

XBP1.WT.1 (41754)

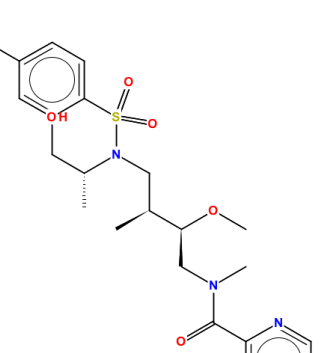
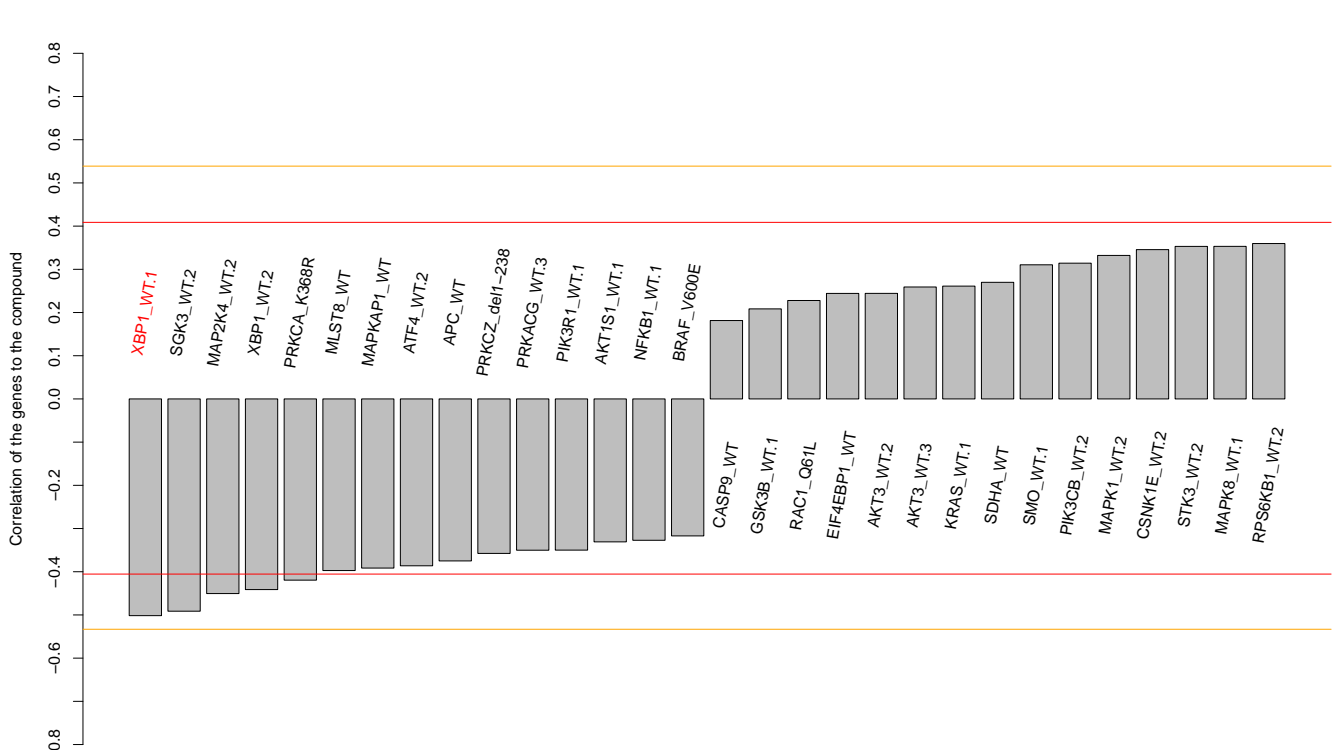
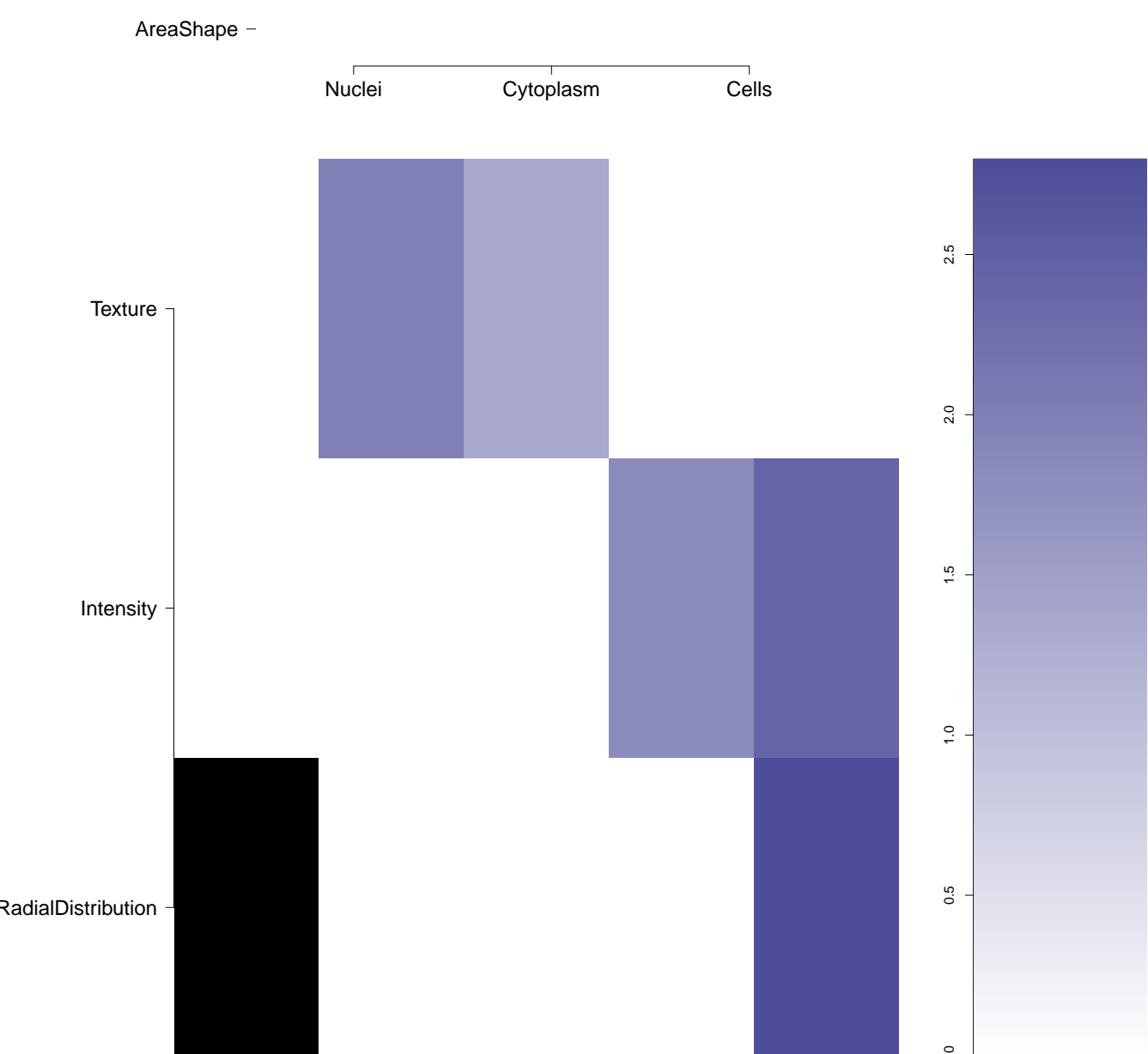

RNA

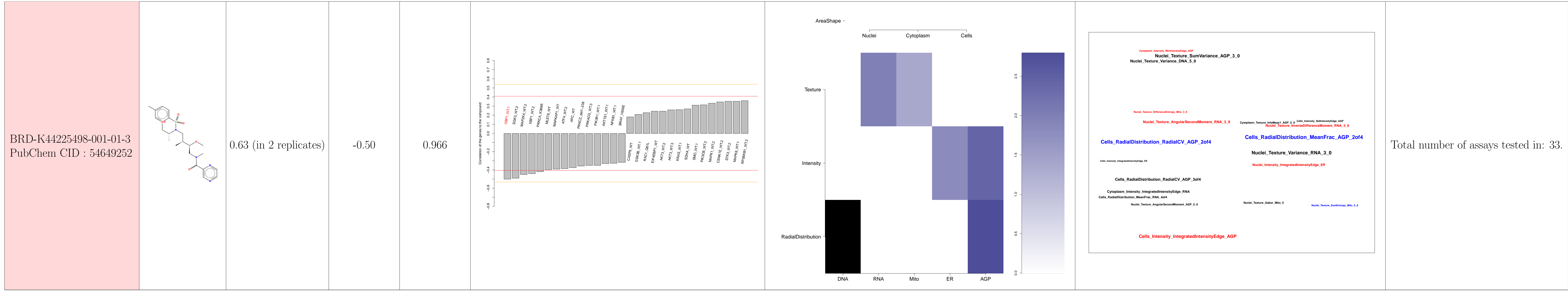


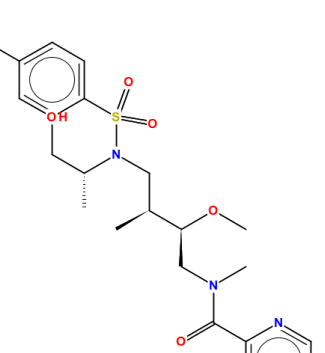
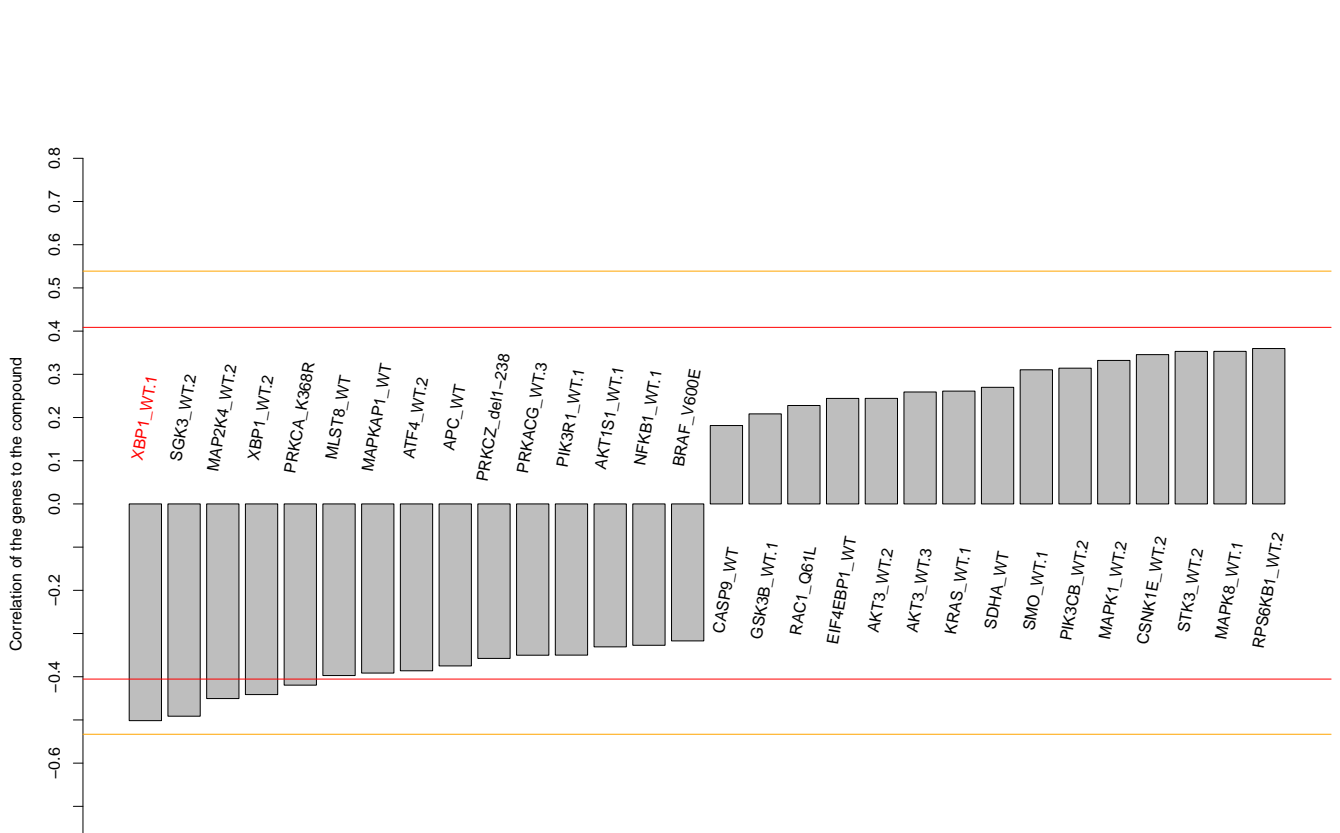
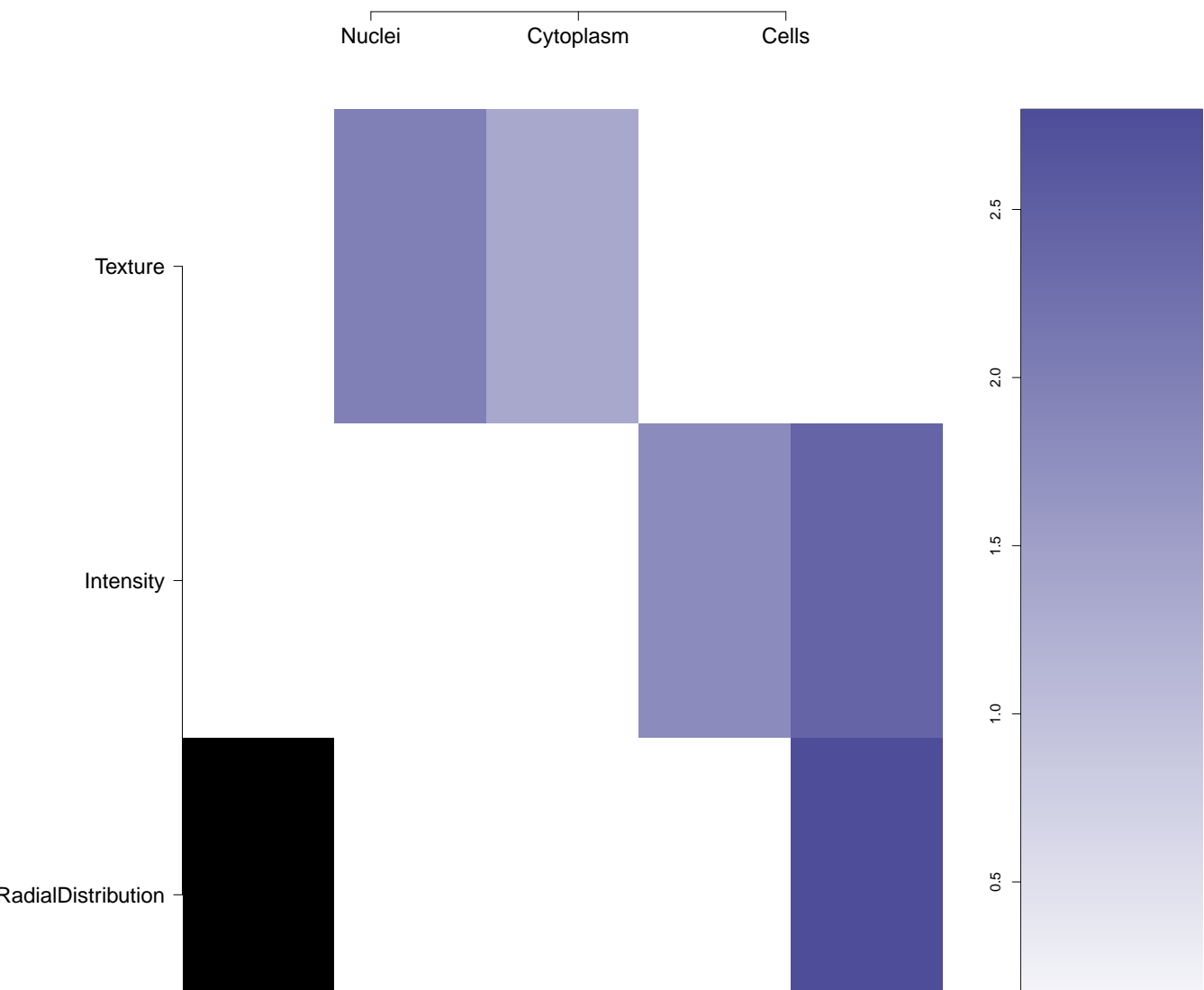

Mito

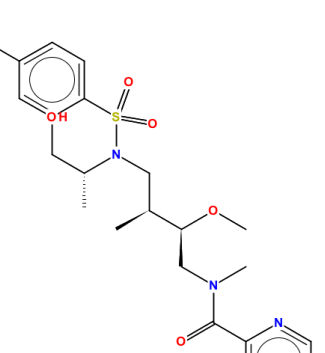
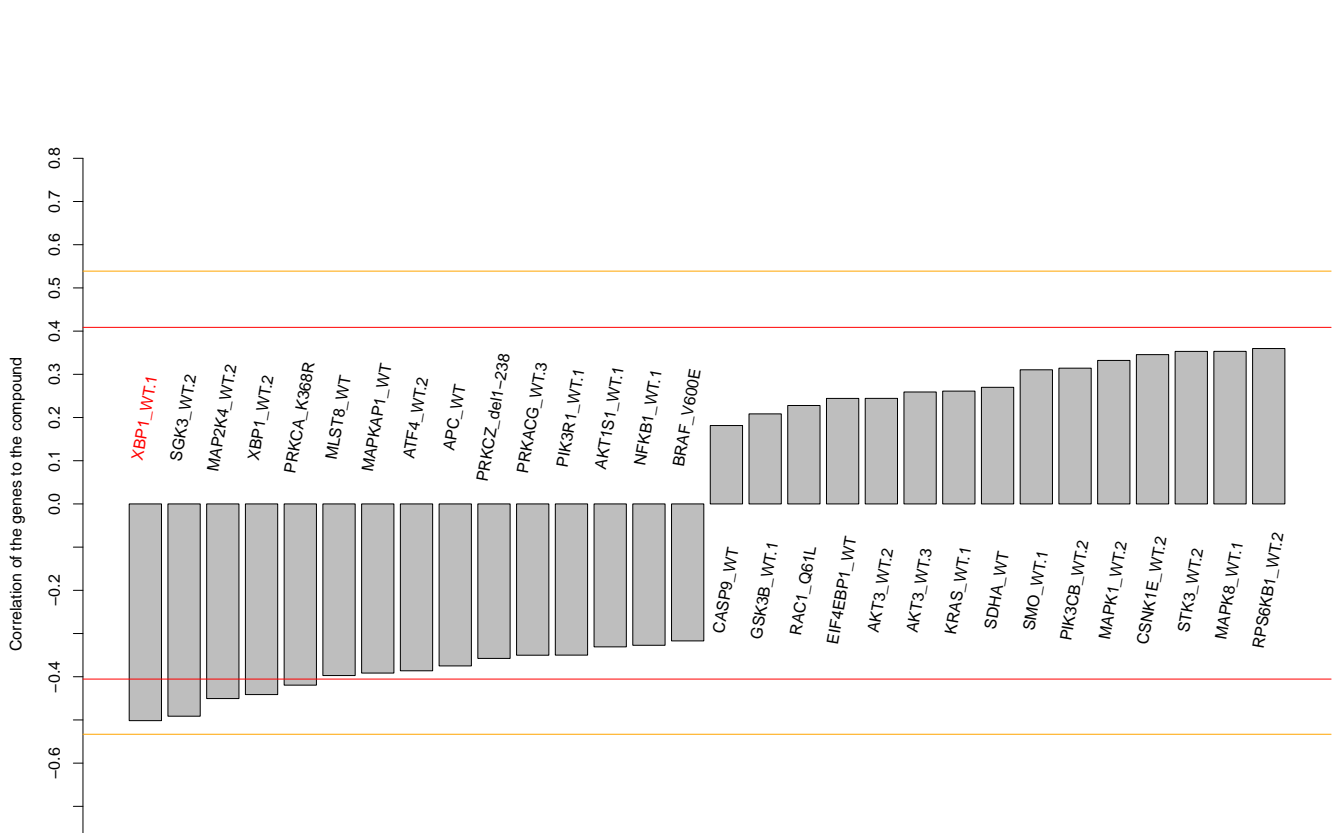
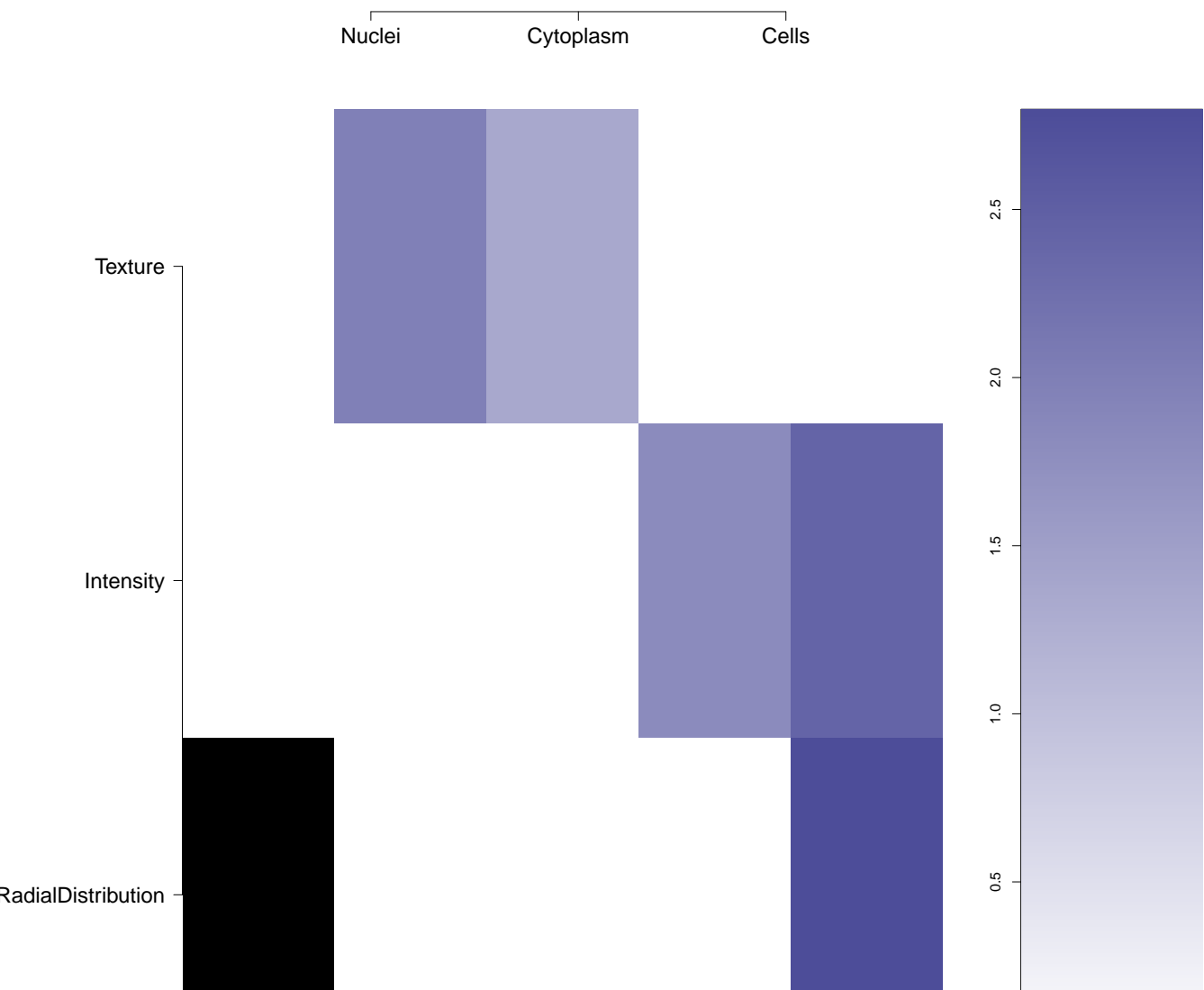



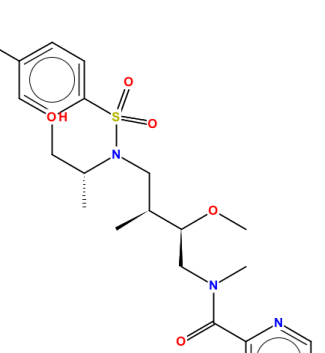
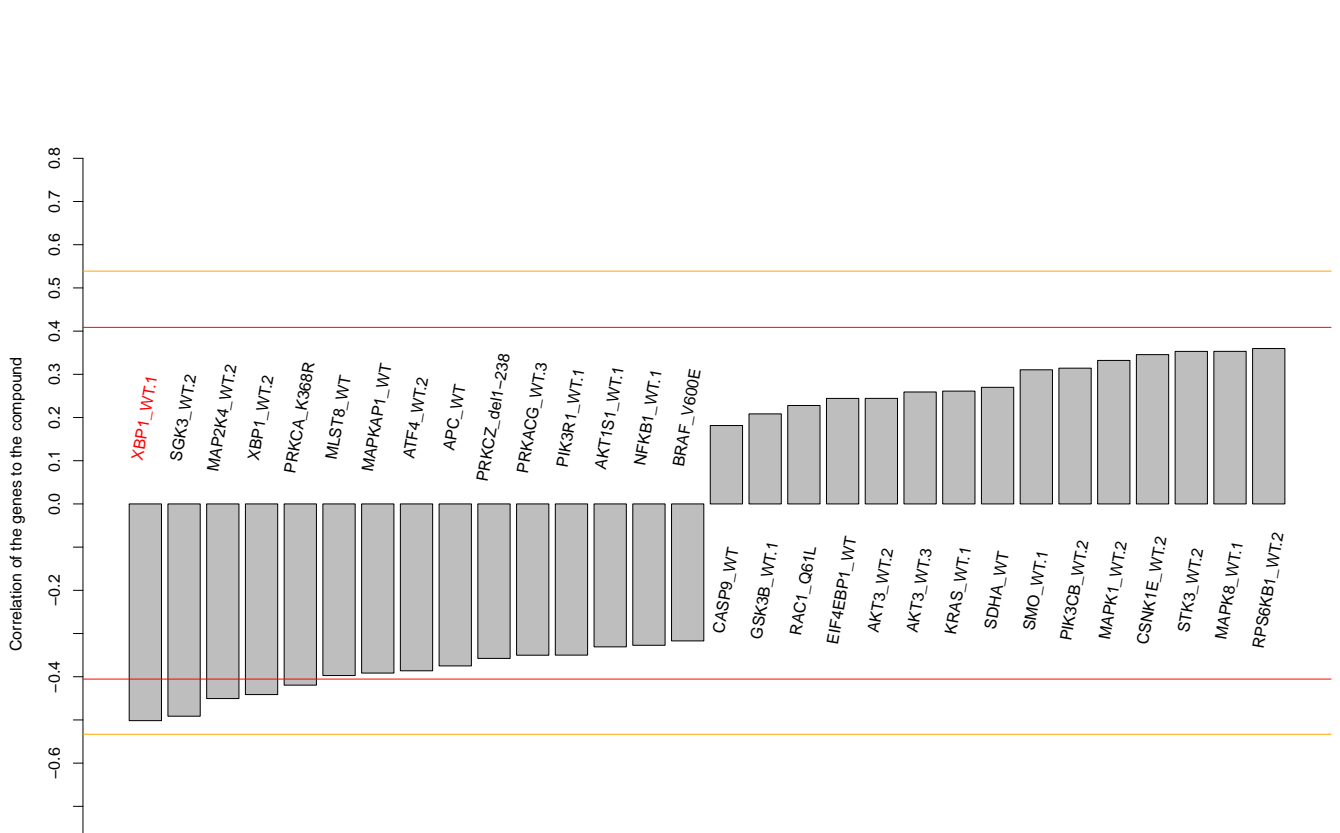
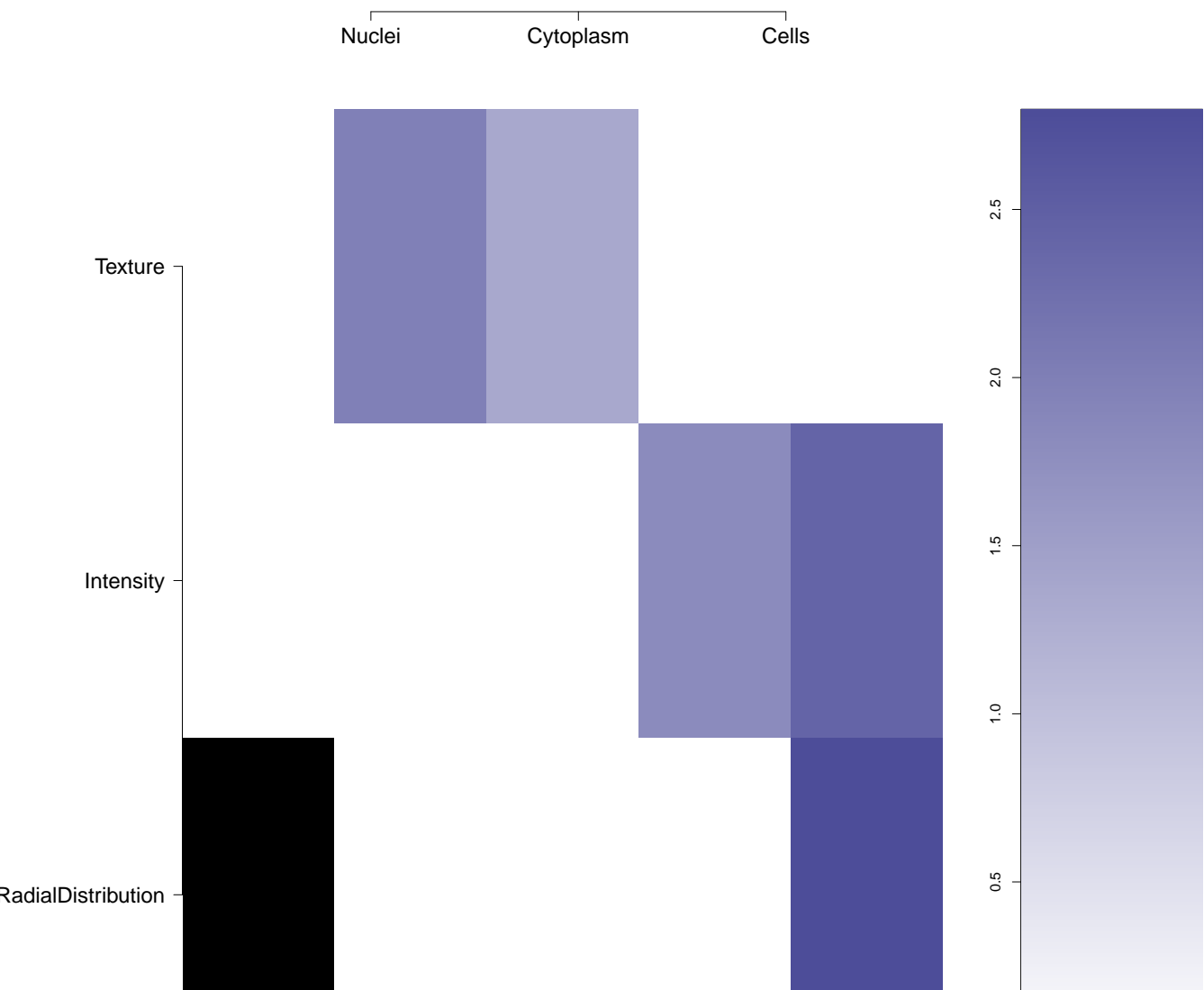

| | | | | | | | | |
|--|--------------------|--|---------------------------------------|--|---|---|---|---|
| Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster | Chemical structure | Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52) | Correlation between compound the gene | 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) | Common distinguishing feature categories in the compound and 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 |
|--|--------------------|--|---------------------------------------|--|---|---|---|---|

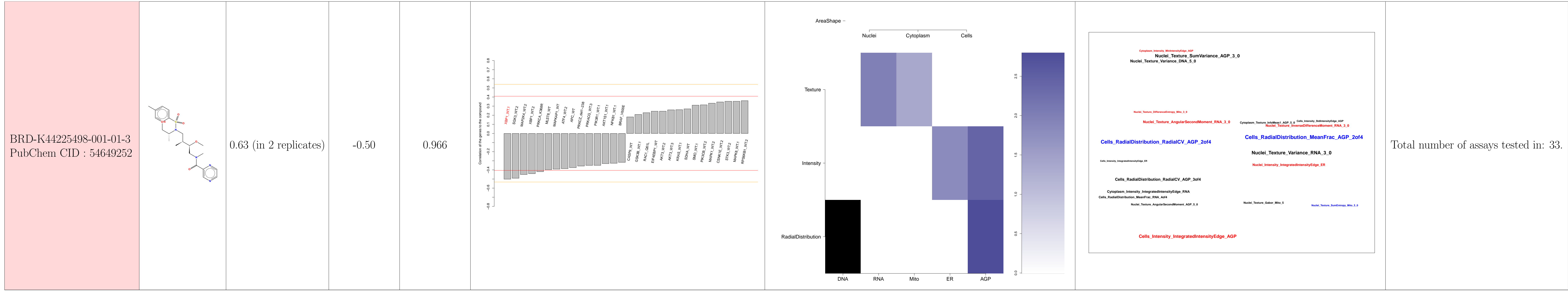
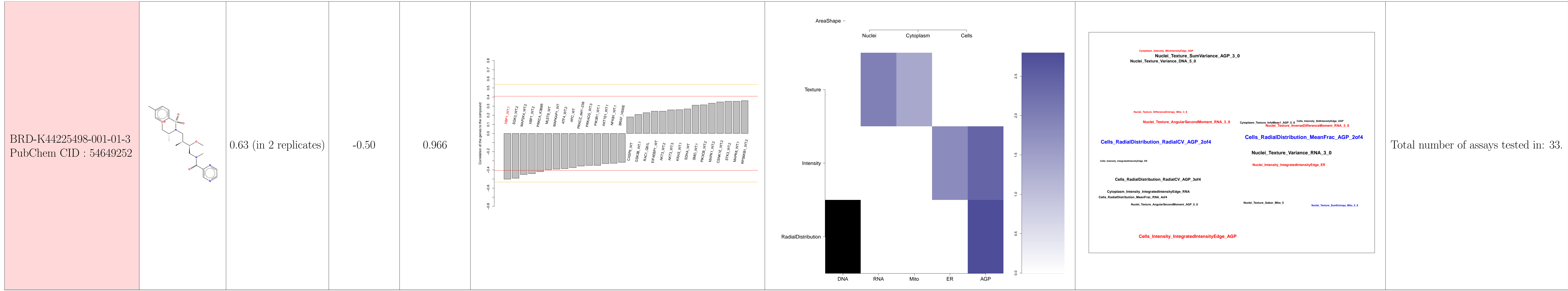
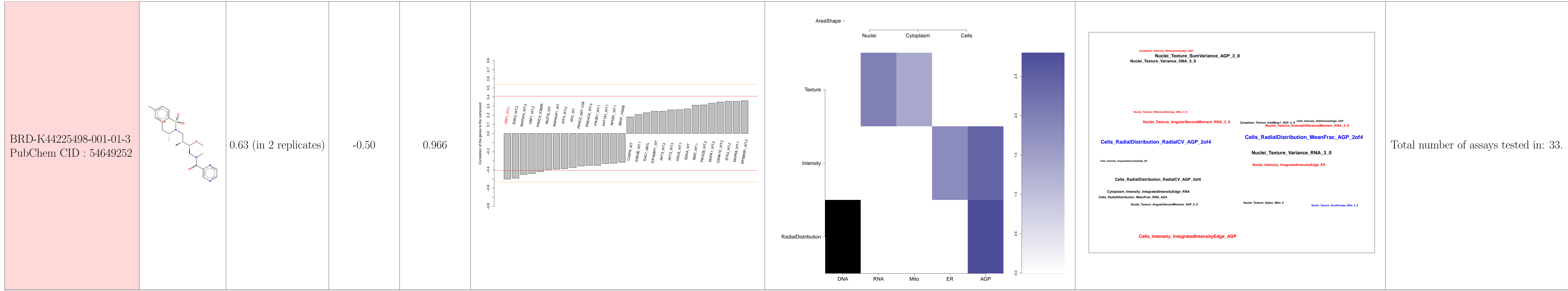
| | | | | |
|--|---|------------------------|-------|-------|
| BRD-K44225498-001-01-3 PubChem CID : 54649252 |  | 0.63 (in 2 replicates) | -0.50 | 0.966 |
|  | | | | |
|  | | | | |
|  | | | | |
| Total number of assays tested in: 33. | | | | |

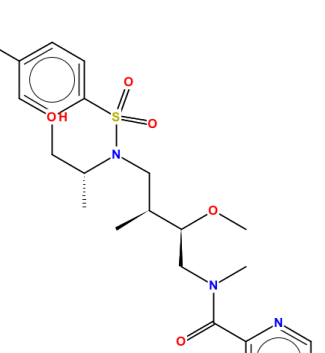
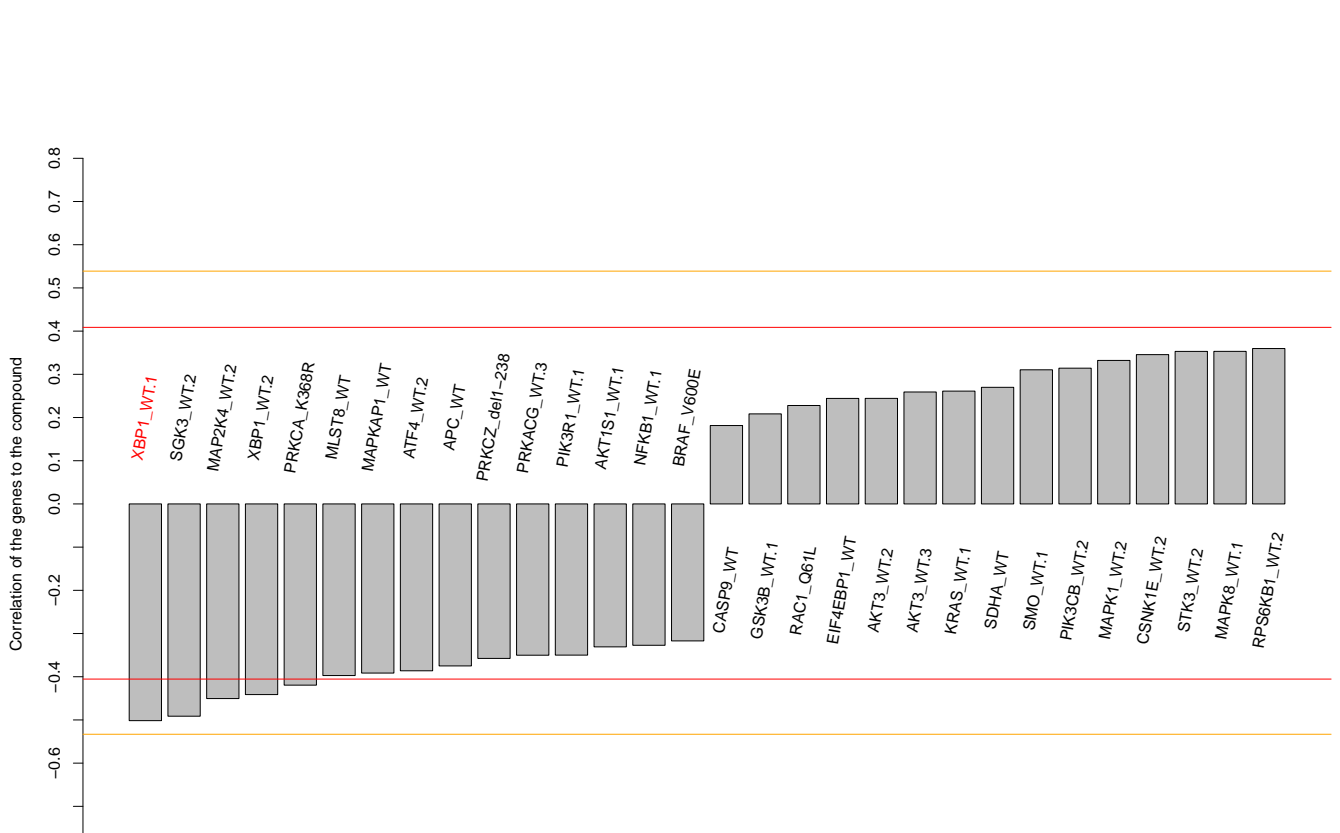
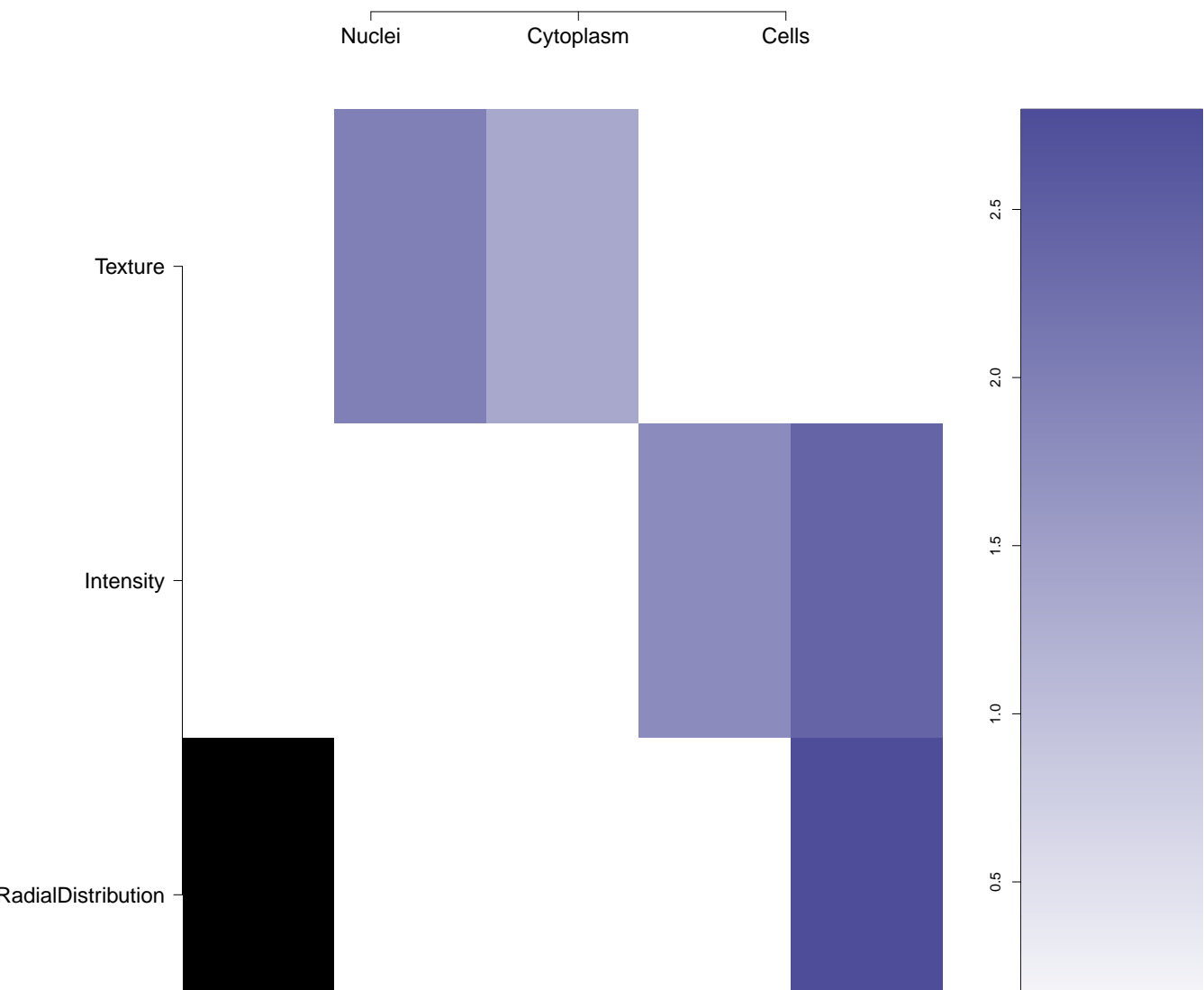



| | | | | |
|--|---|------------------------|-------|-------|
| BRD-K44225498-001-01-3 PubChem CID : 54649252 |  | 0.63 (in 2 replicates) | -0.50 | 0.966 |
|  | | | | |
|  | | | | |
|  | | | | |
| Total number of assays tested in: 33. | | | | |

| | | | | |
|--|---|------------------------|-------|-------|
| BRD-K44225498-001-01-3 PubChem CID : 54649252 |  | 0.63 (in 2 replicates) | -0.50 | 0.966 |
|  | | | | |
|  | | | | |
|  | | | | |
| Total number of assays tested in: 33. | | | | |

| | | | | |
|--|---|------------------------|-------|-------|
| BRD-K44225498-001-01-3 PubChem CID : 54649252 |  | 0.63 (in 2 replicates) | -0.50 | 0.966 |
|  | | | | |
|  | | | | |
|  | | | | |
| Total number of assays tested in: 33. | | | | |



| | | | | |
|--|---|------------------------|-------|-------|
| BRD-K44225498-001-01-3 PubChem CID : 54649252 |  | 0.63 (in 2 replicates) | -0.50 | 0.966 |
|  | | | | |
|  | | | | |
|  | | | | |
| Total number of assays tested in: 33. | | | | |