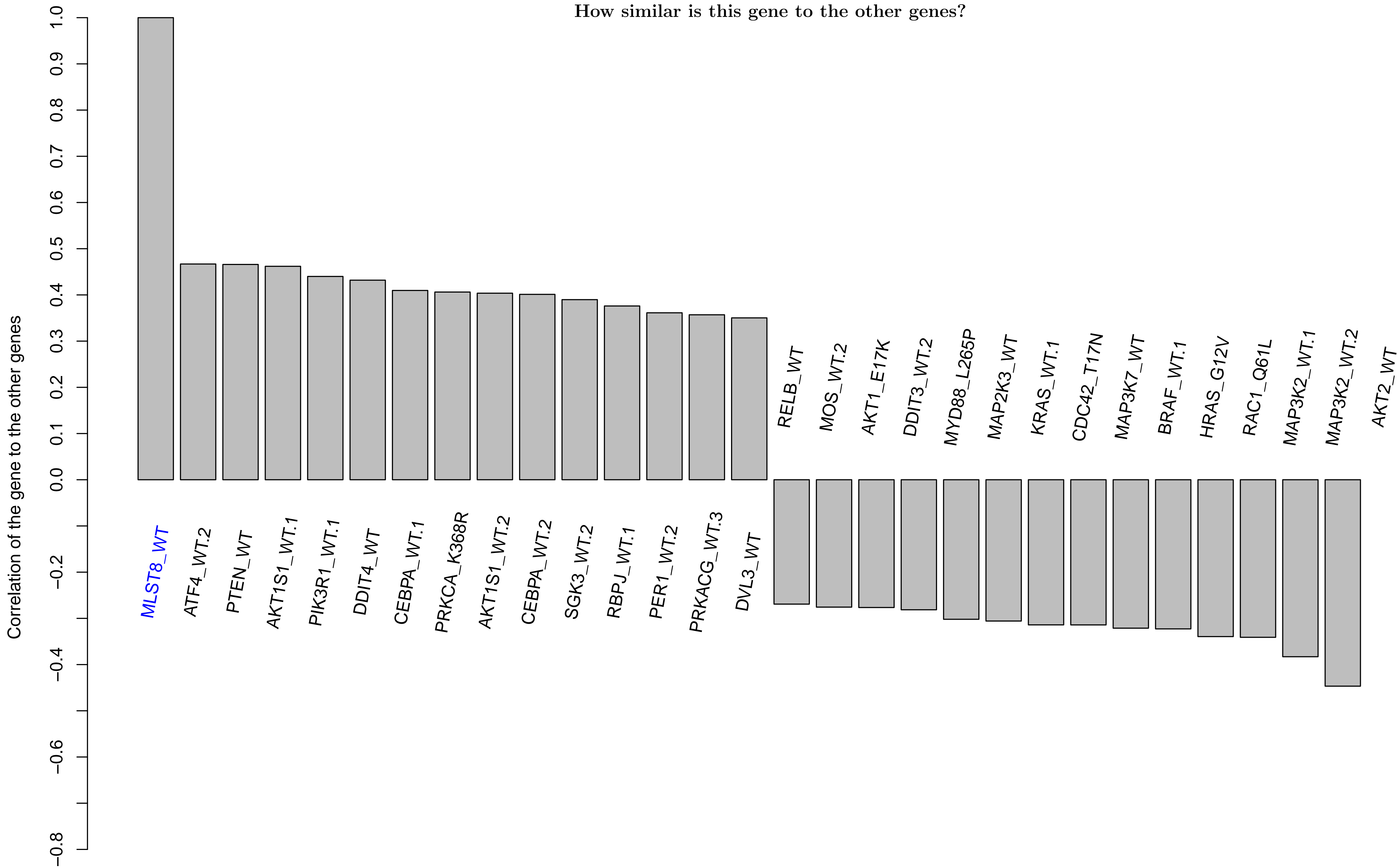
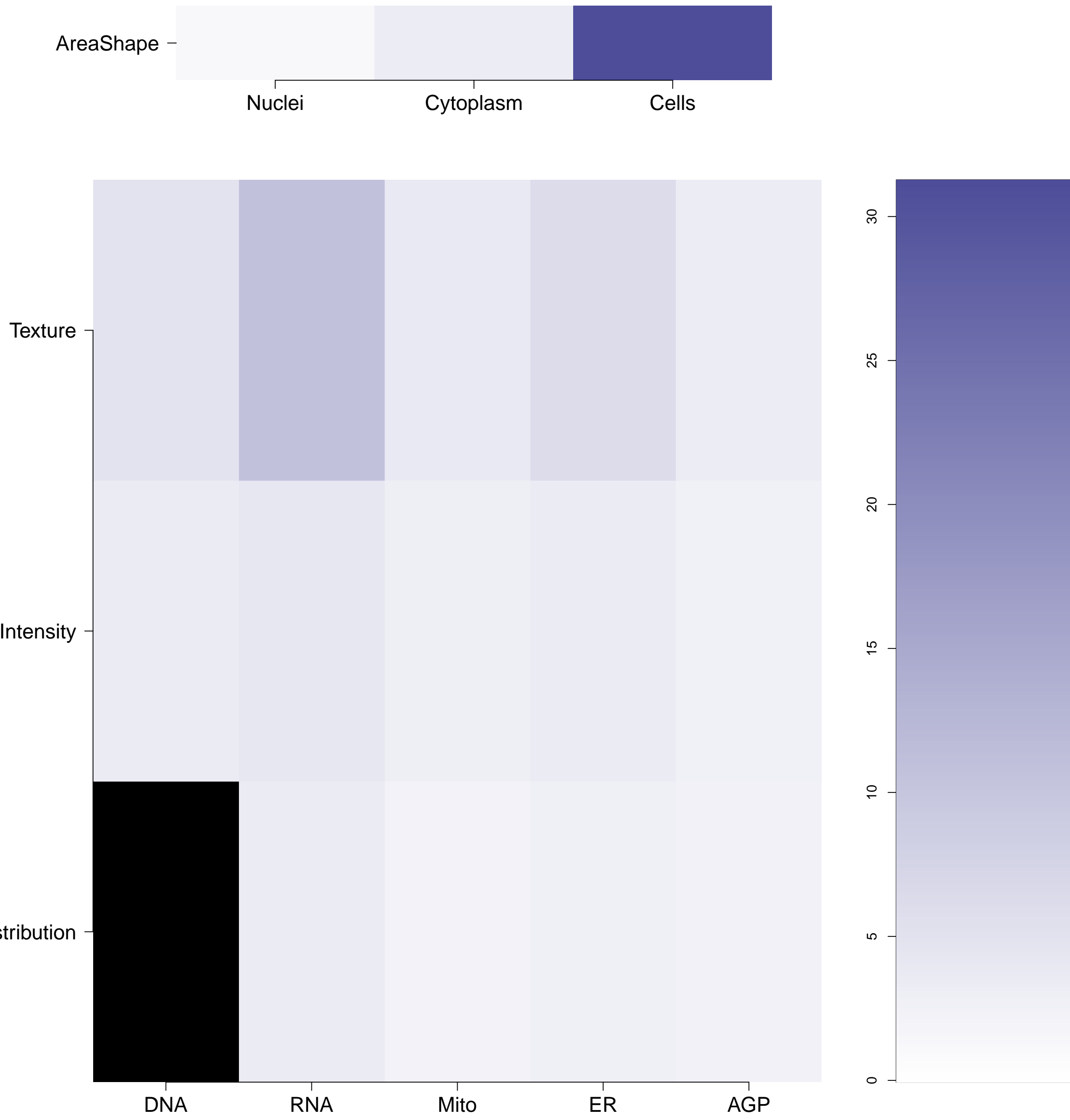


MLST8.WT - in Canonical TOR

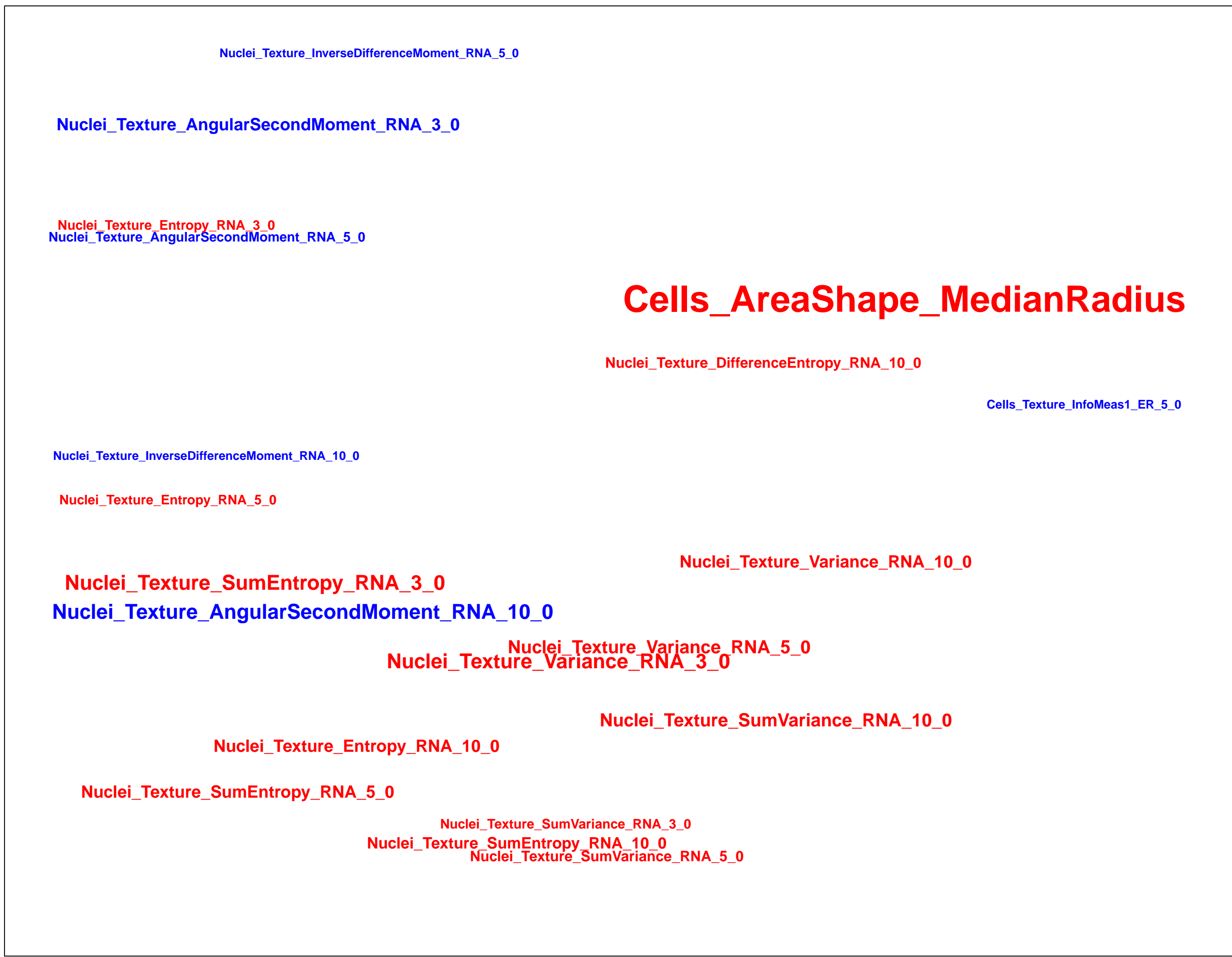
How similar is this gene to the other genes?



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

MLST8.WT (41744)

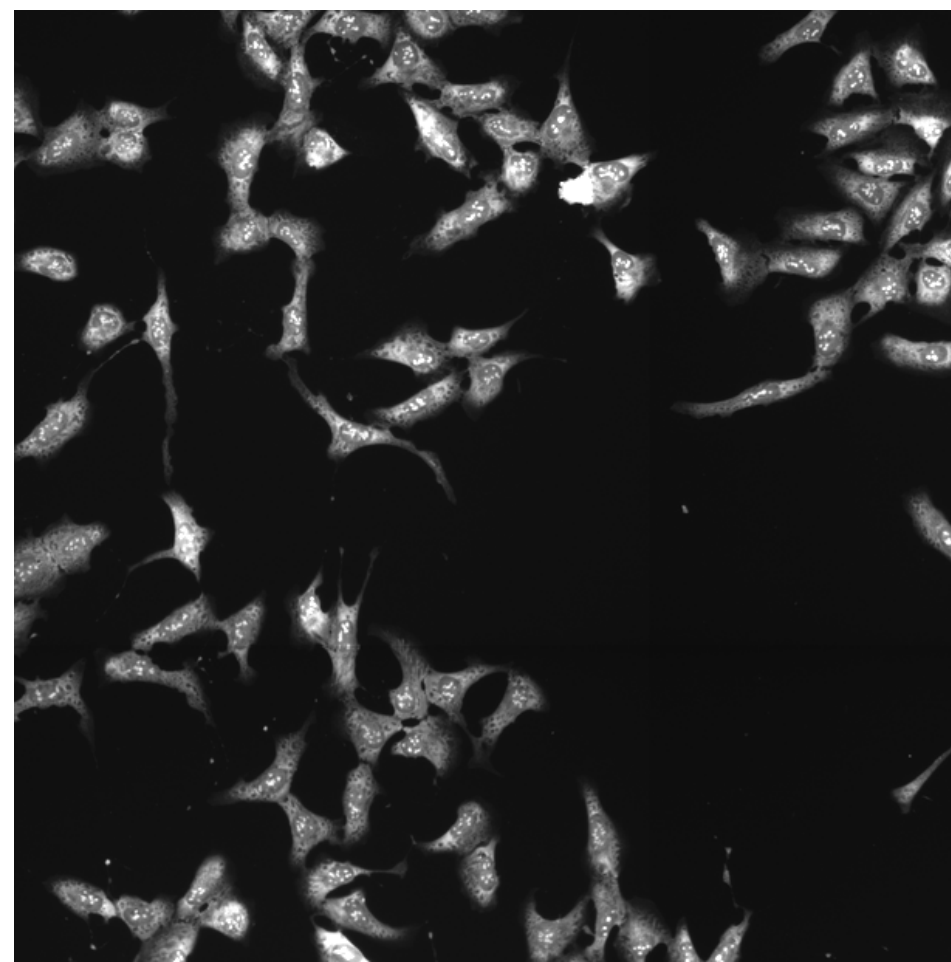
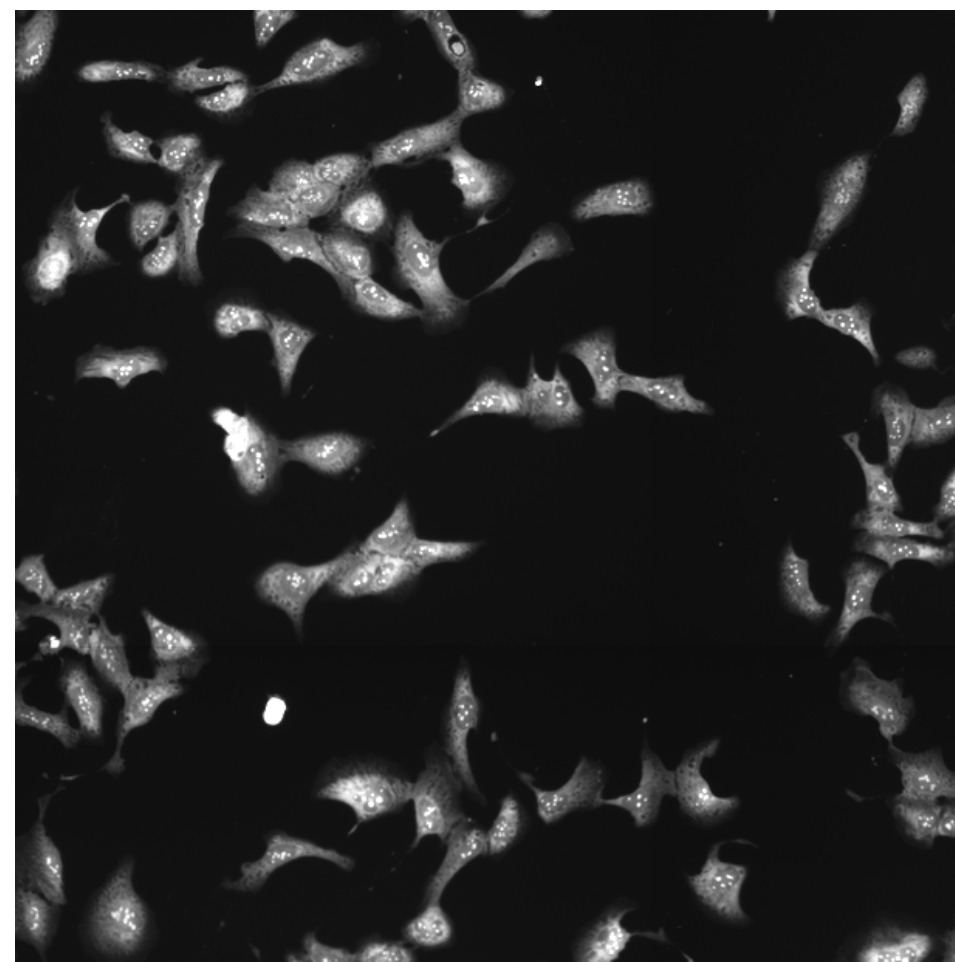
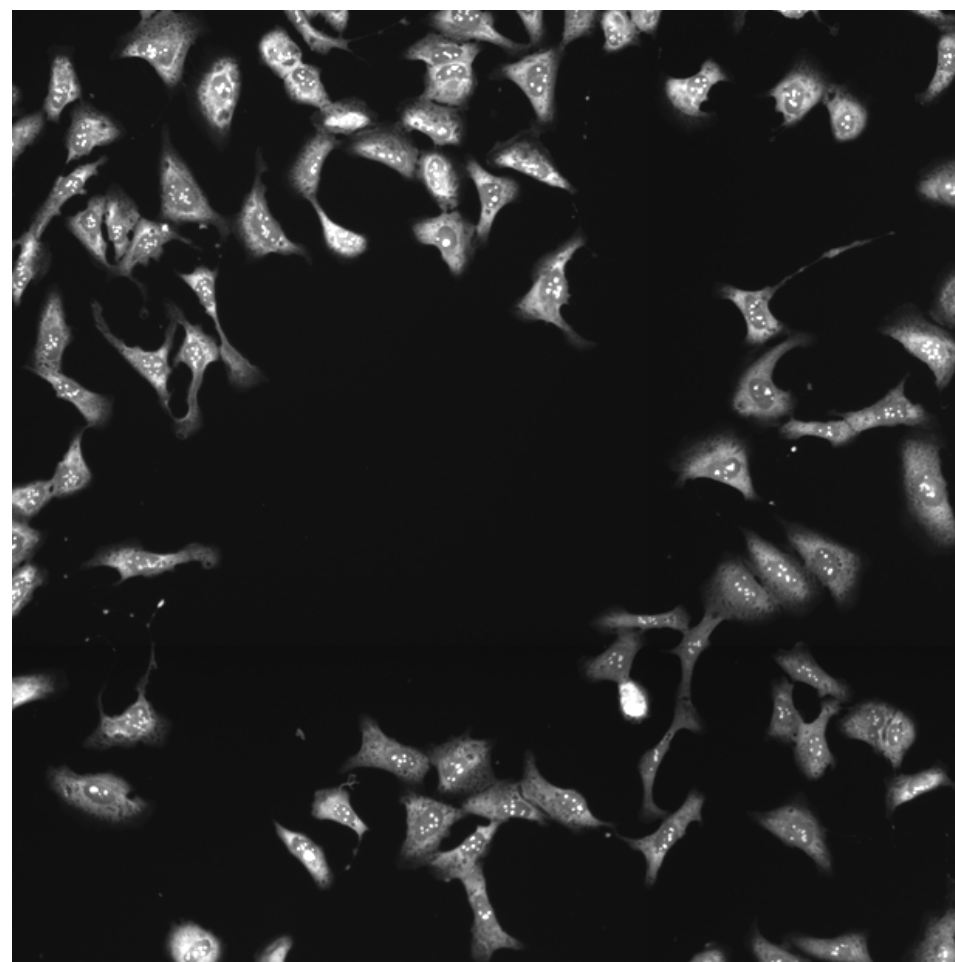
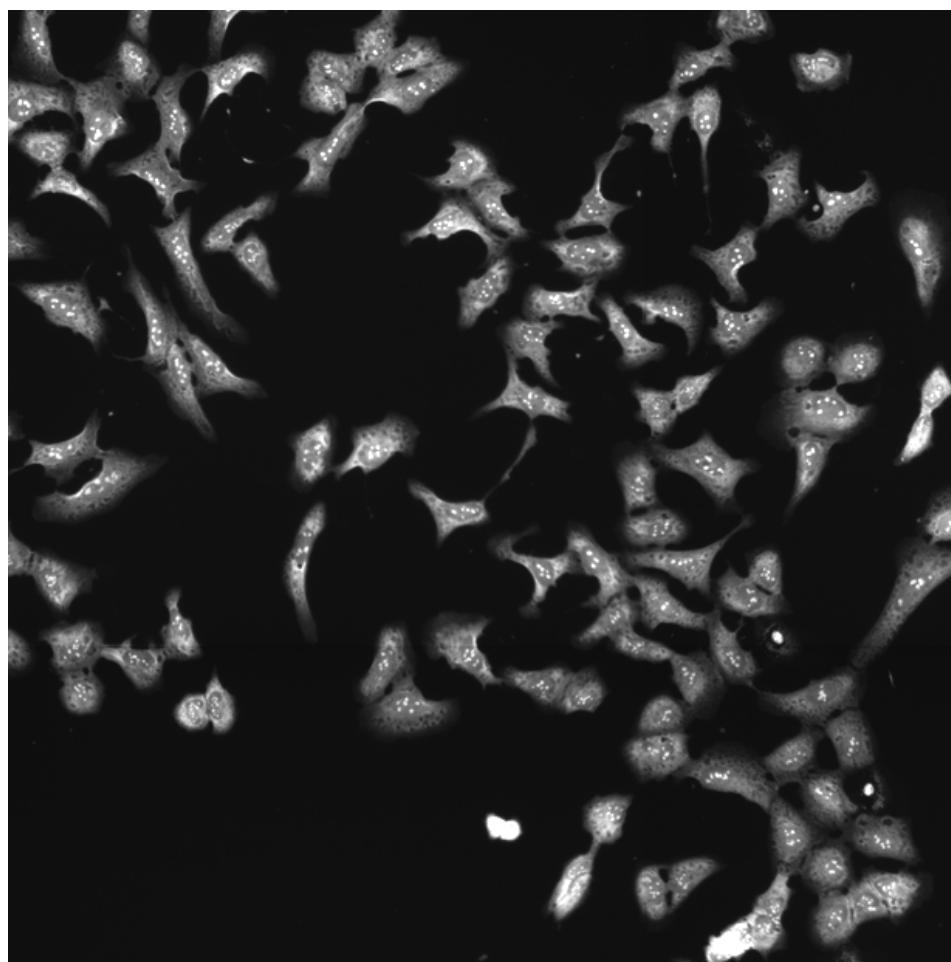
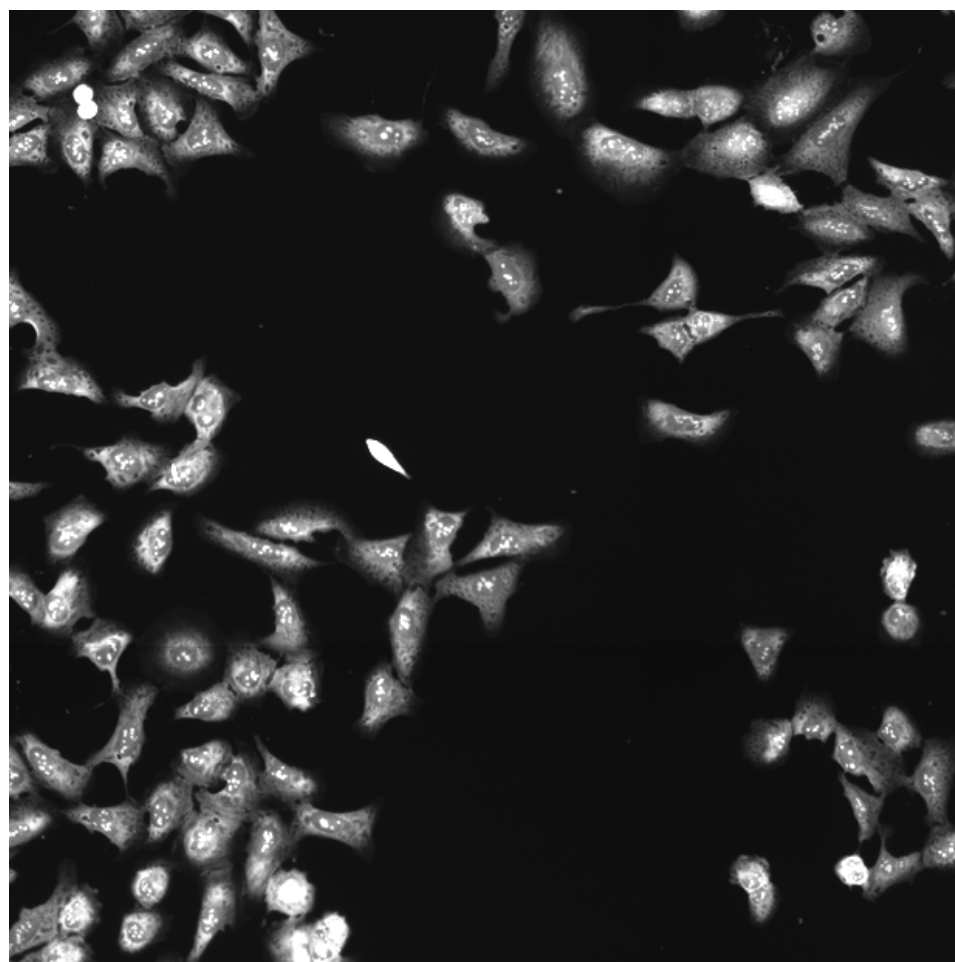
MLST8.WT (41755)

MLST8.WT (41756)

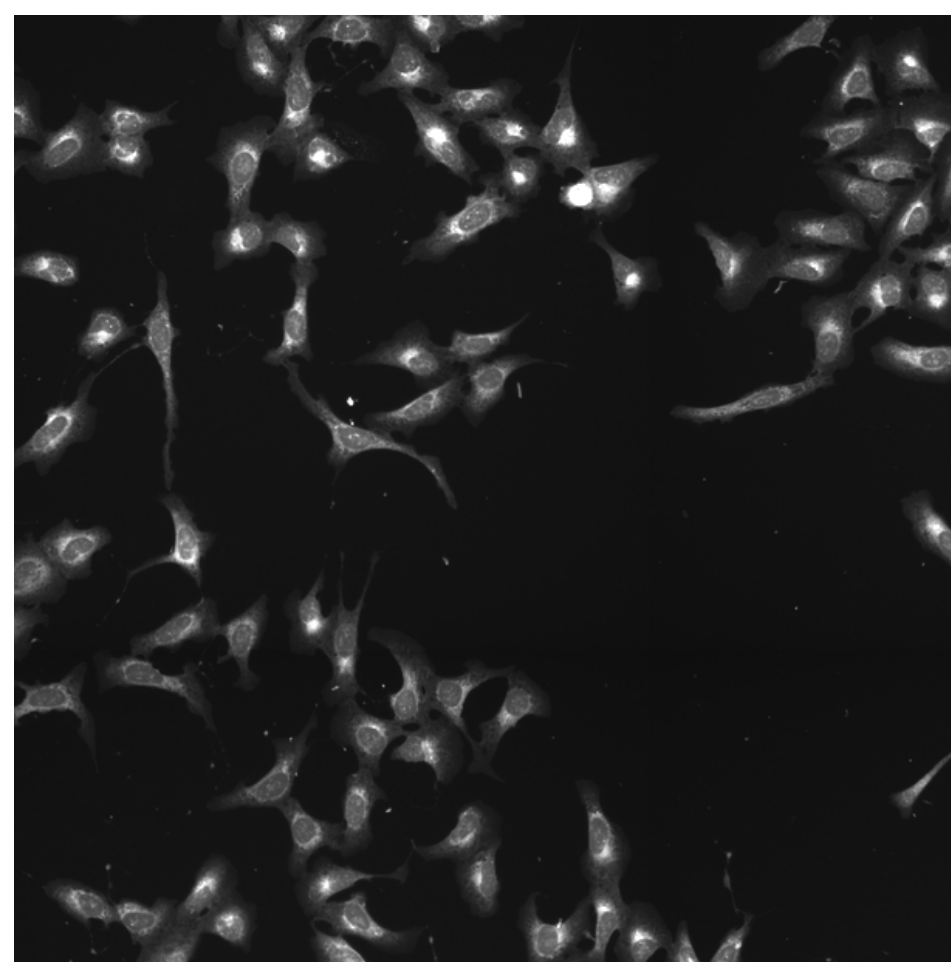
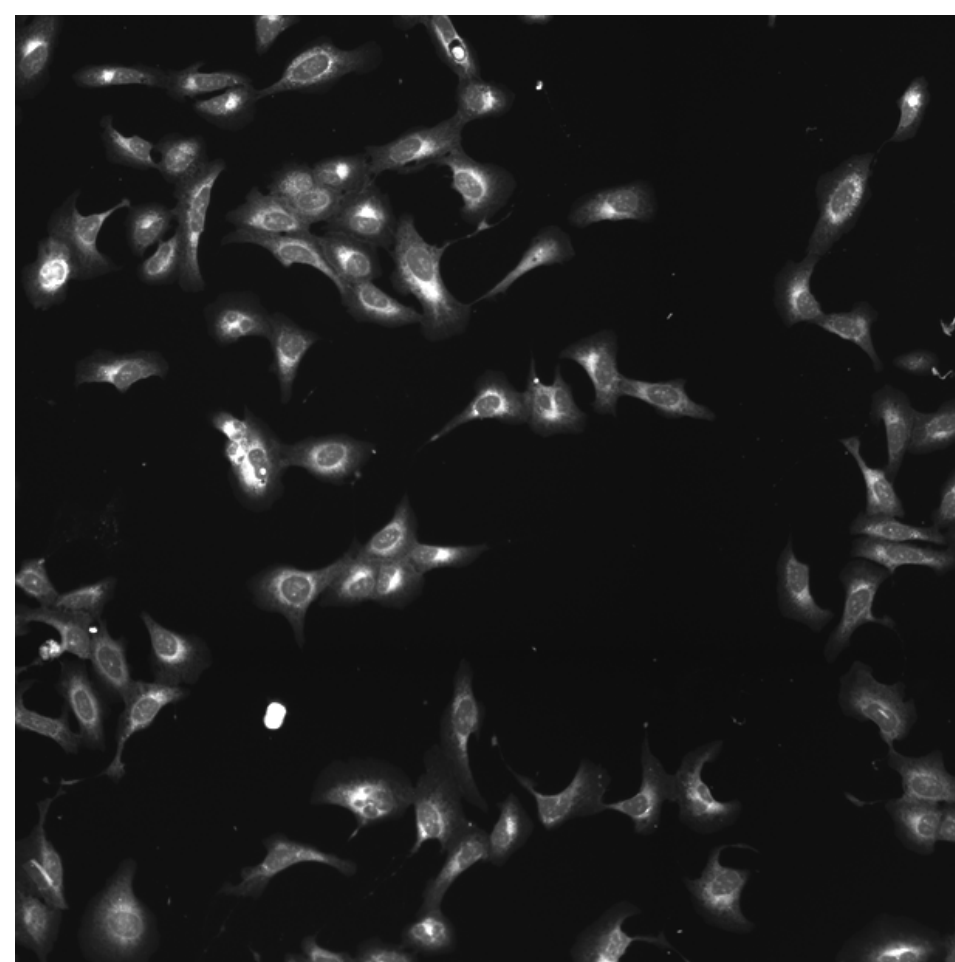
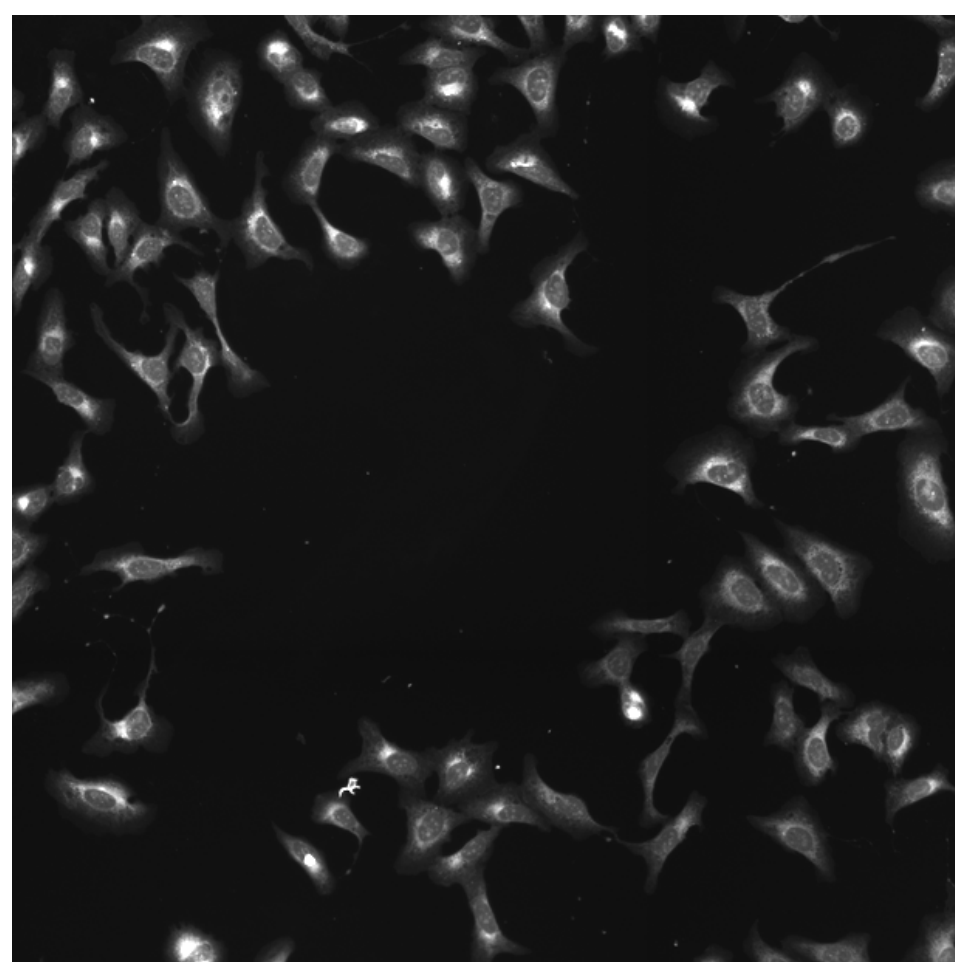
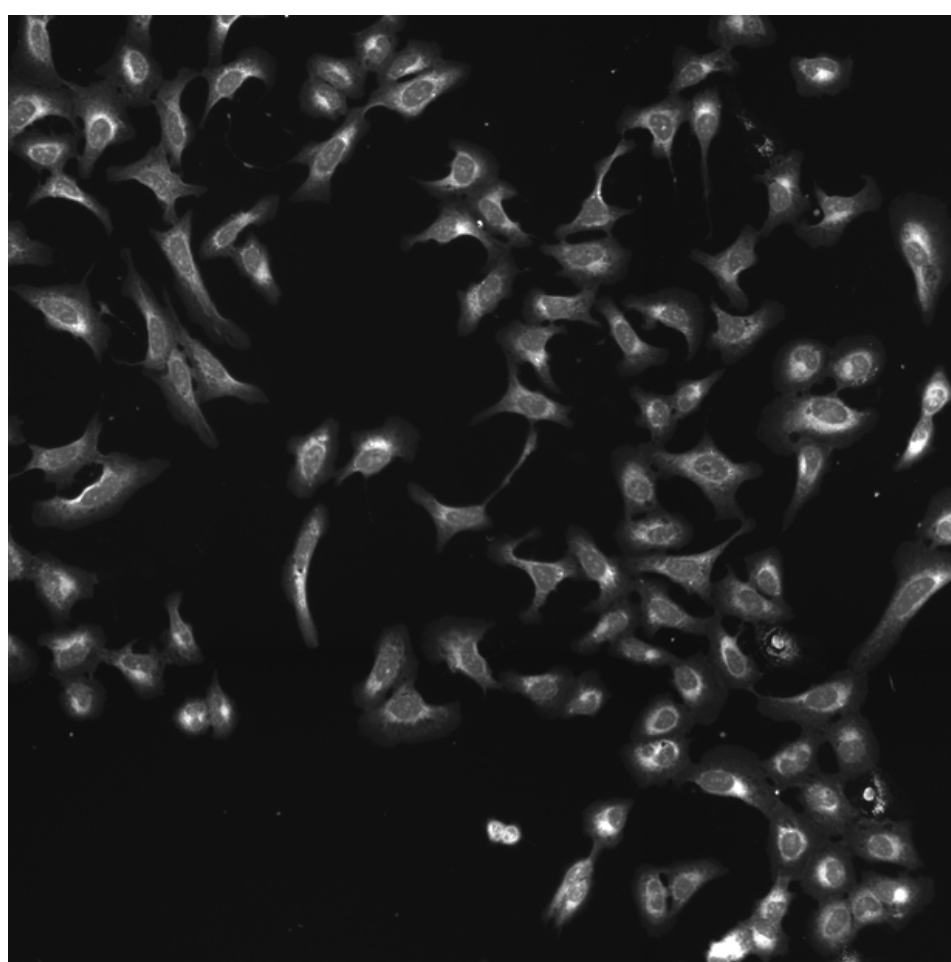
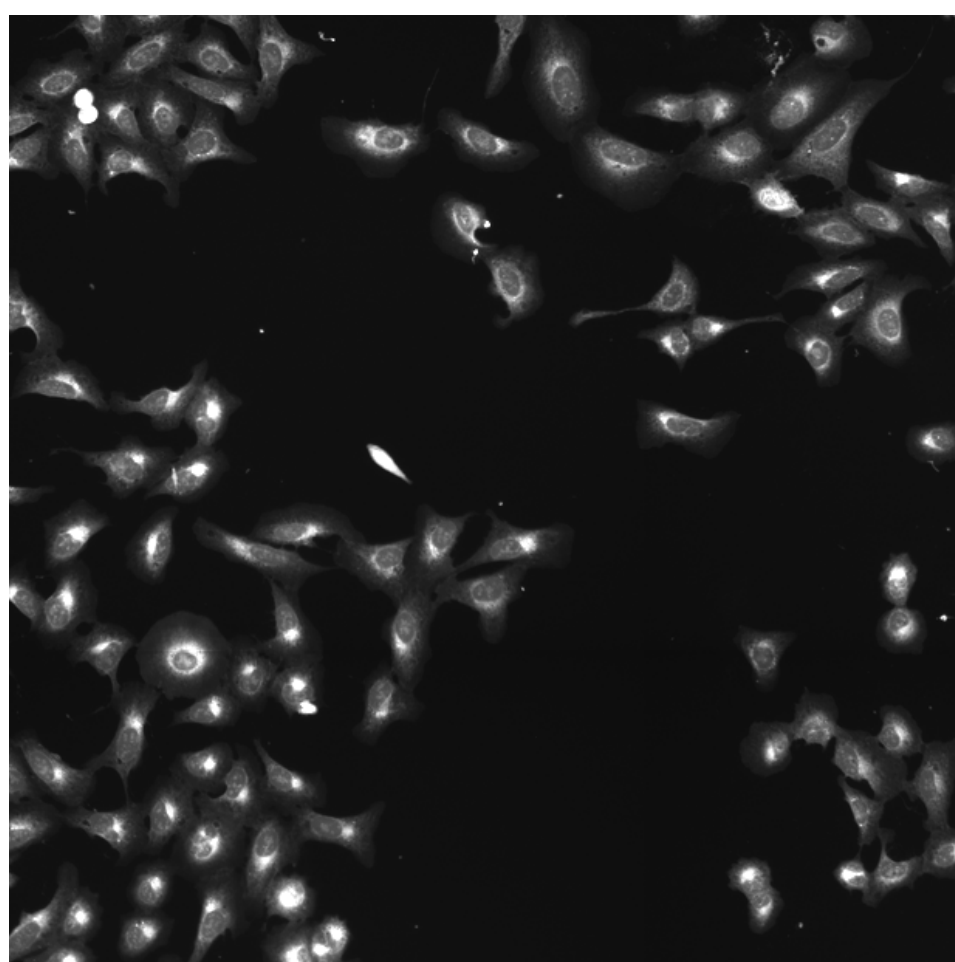
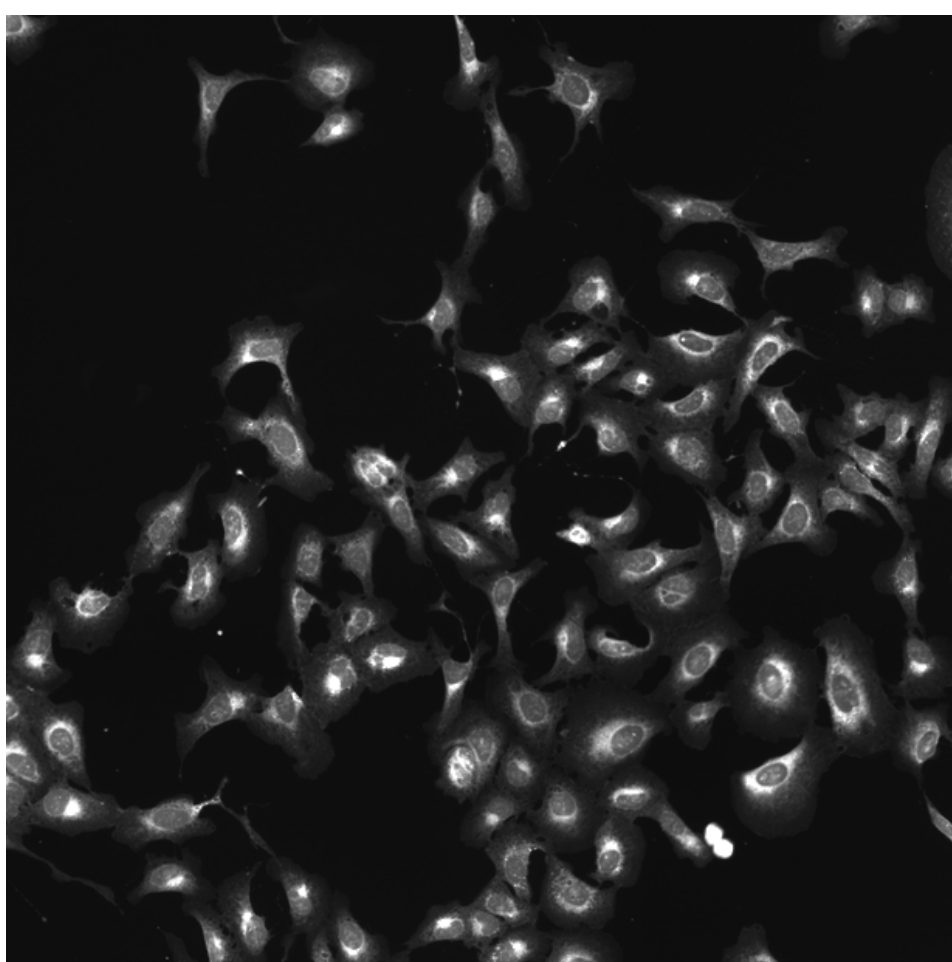
MLST8.WT (41757)

MLST8.WT (41754)

RNA

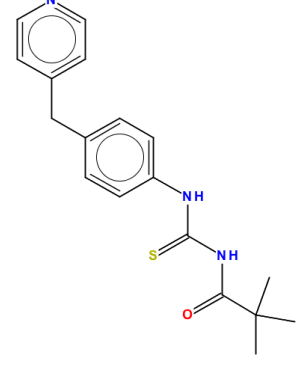
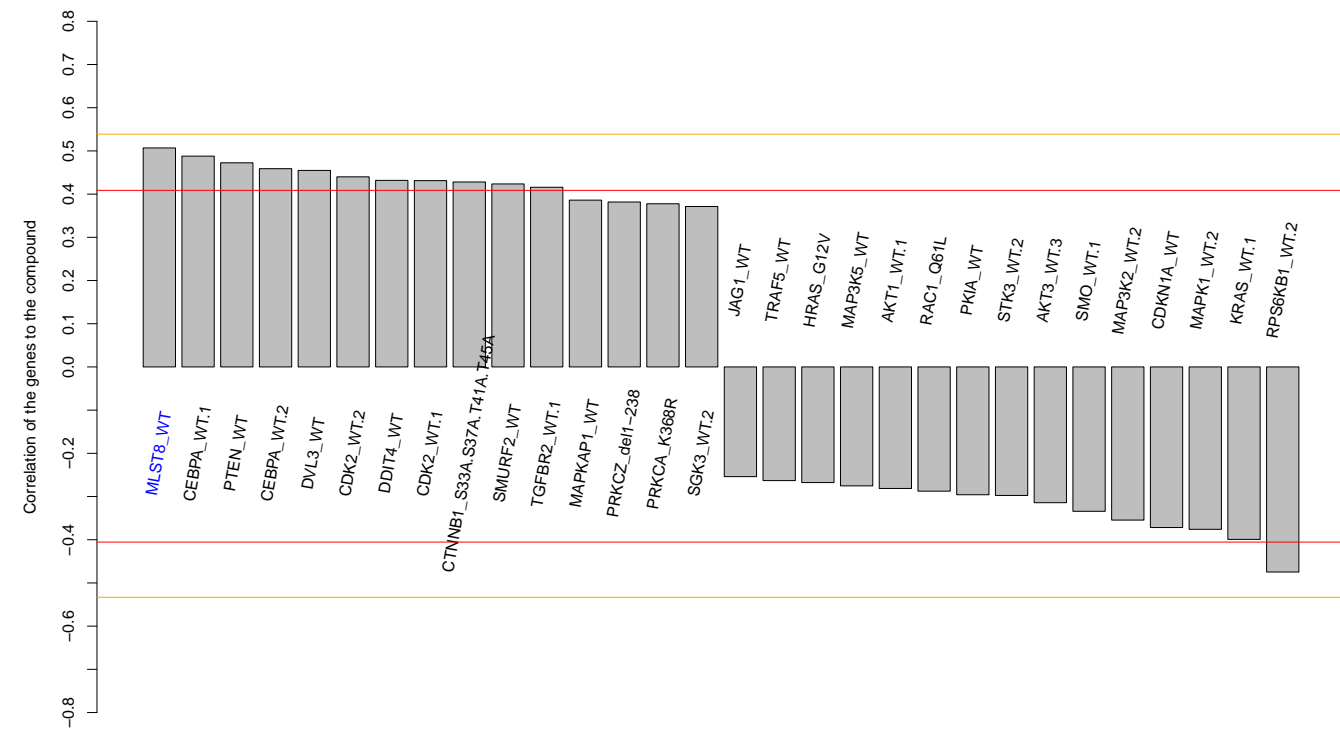
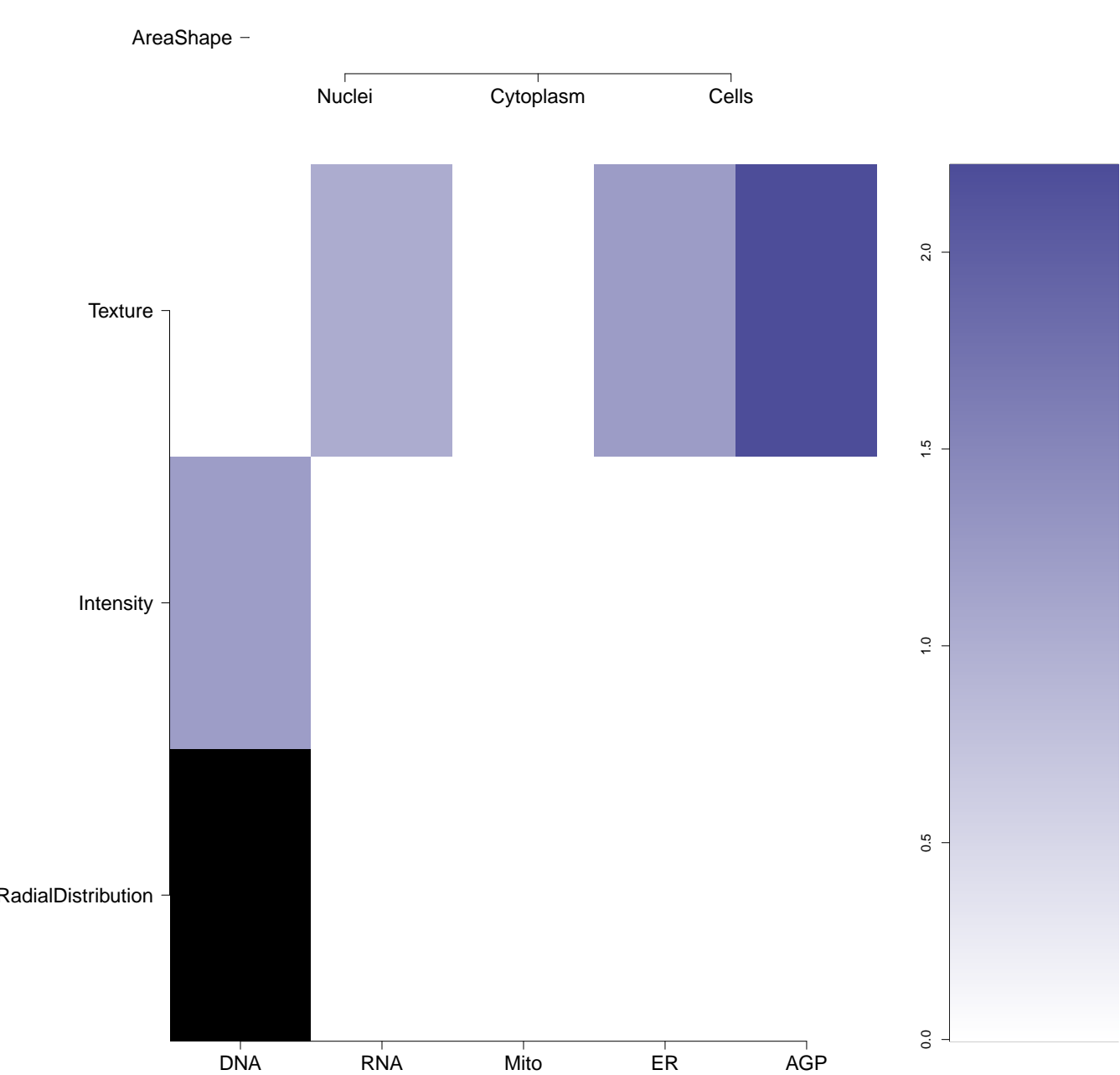

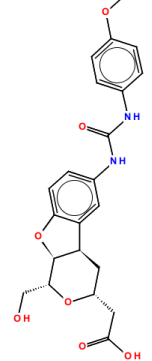
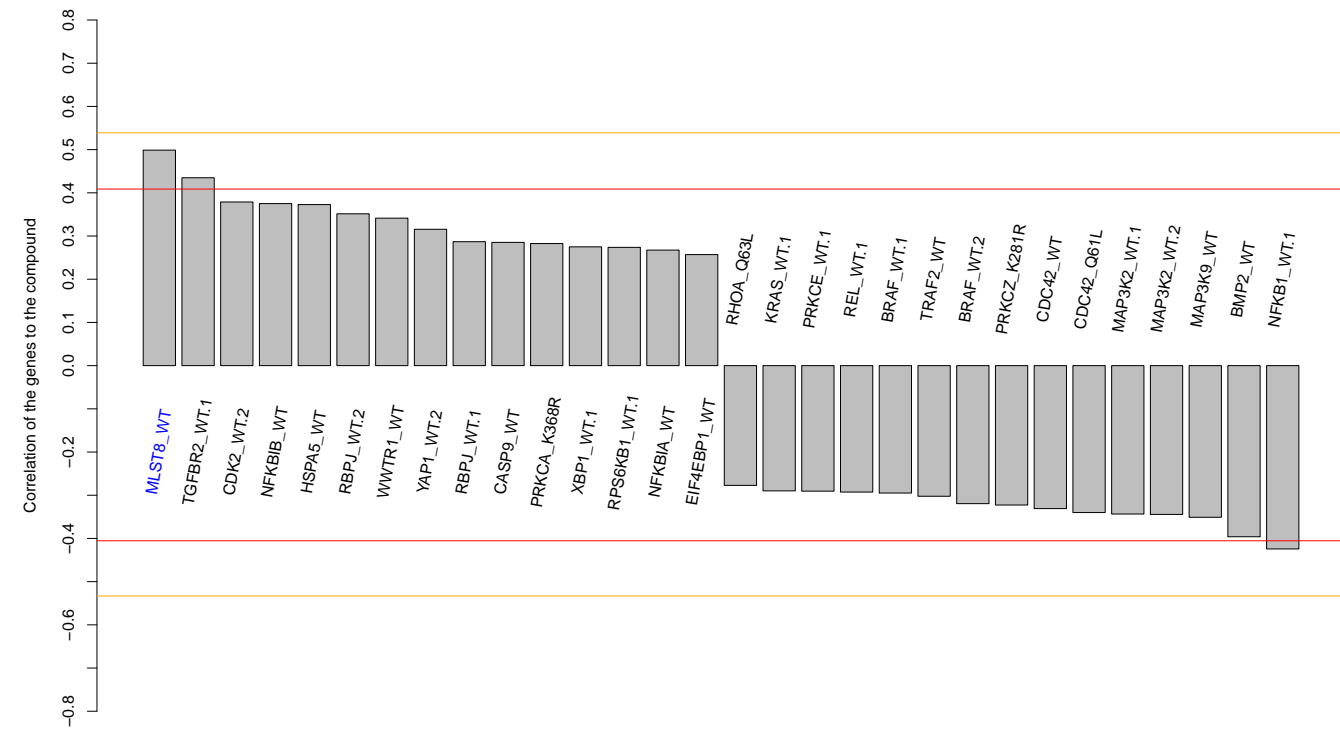
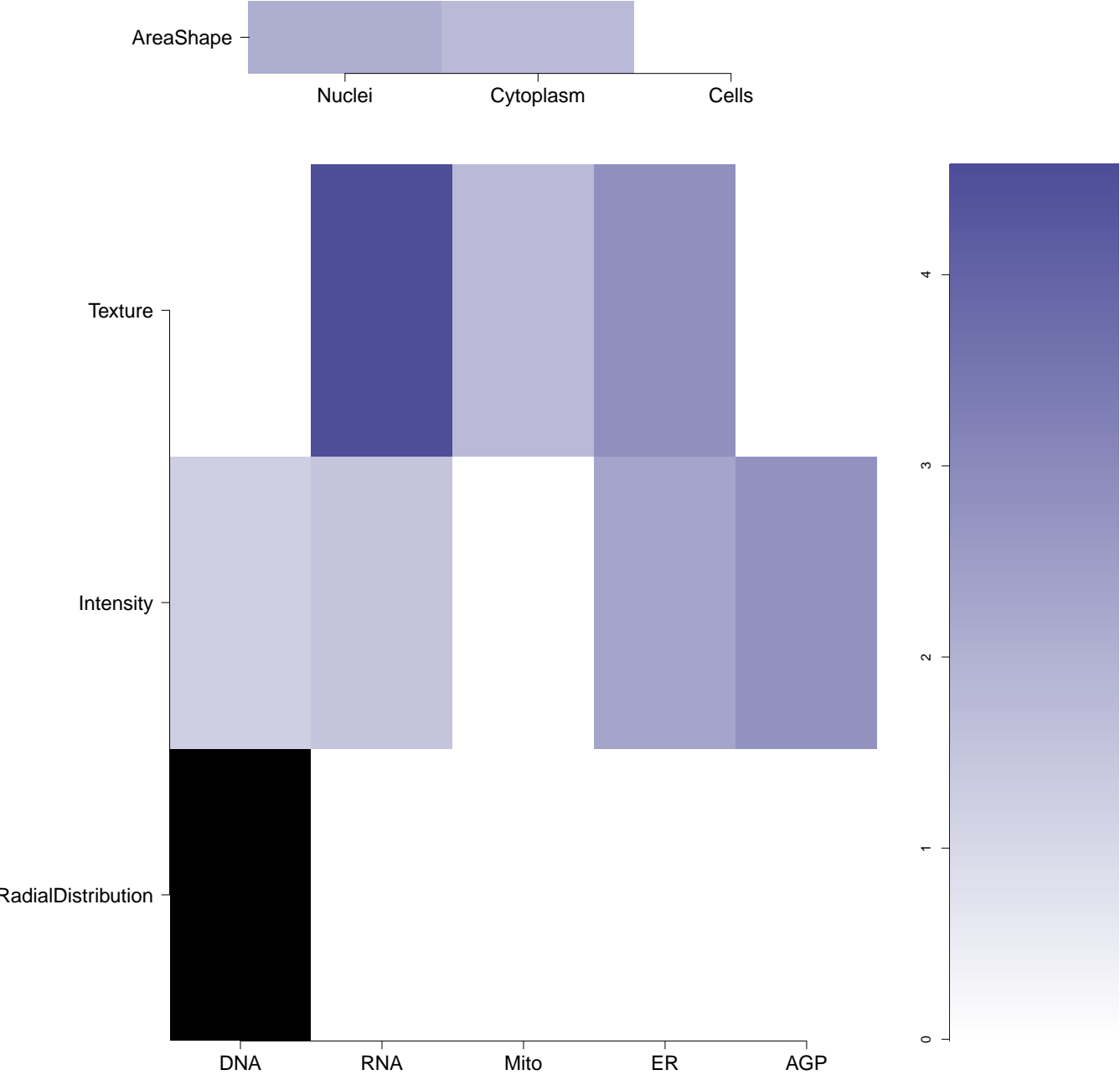
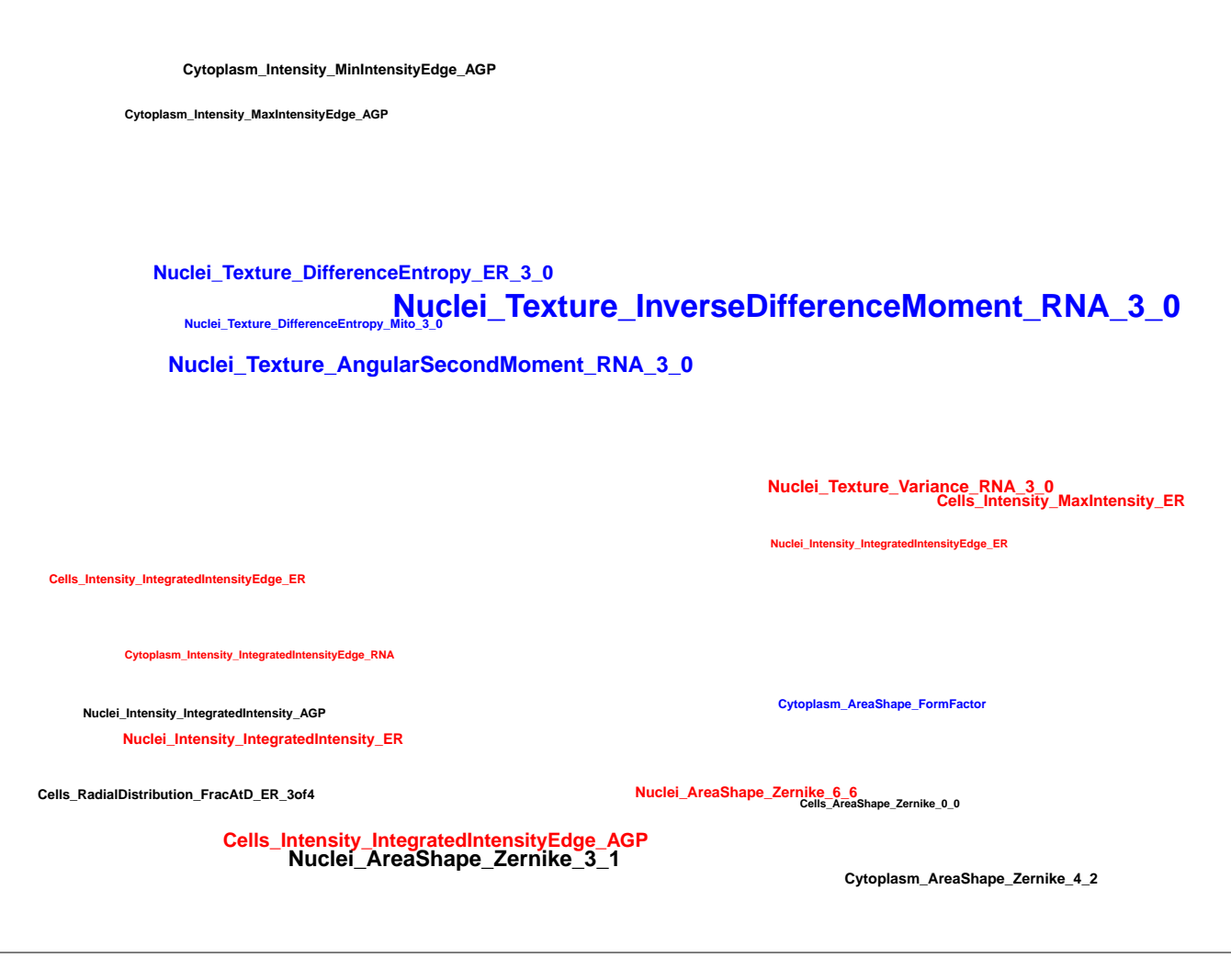
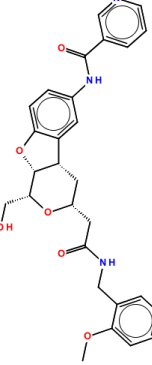
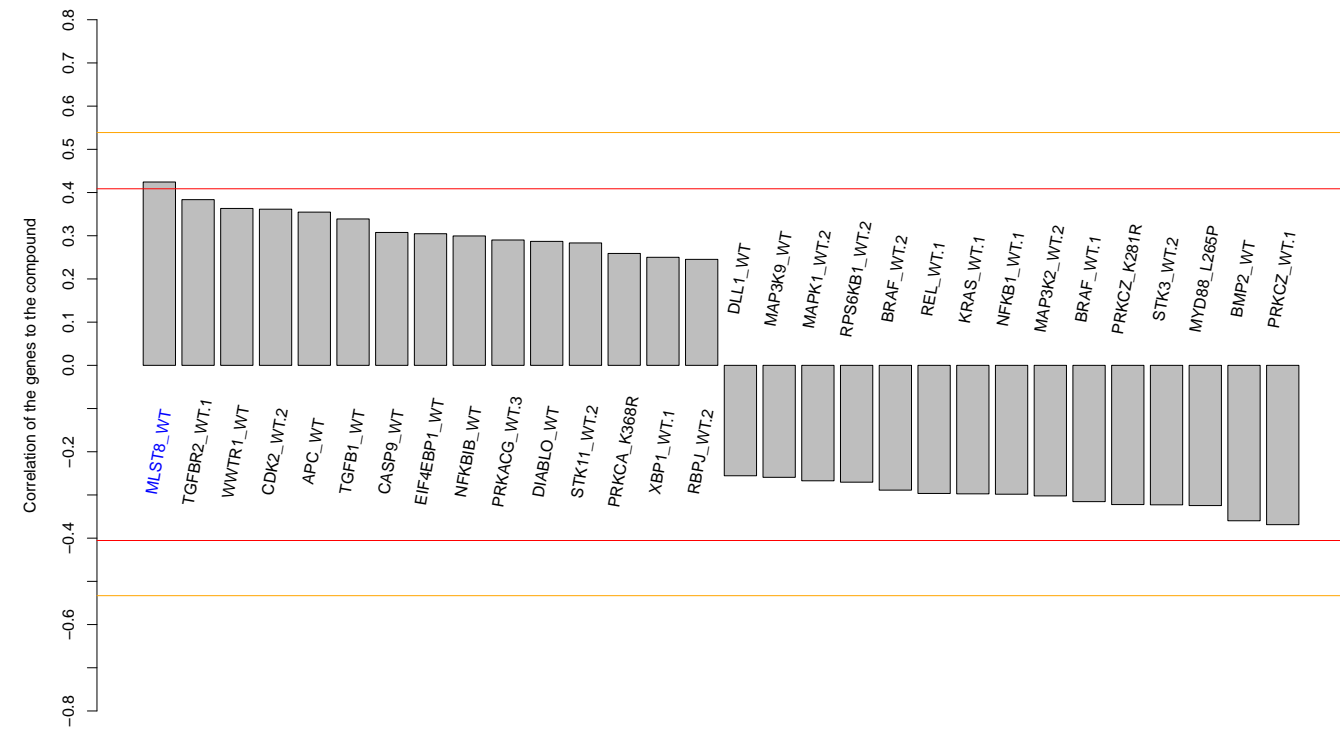
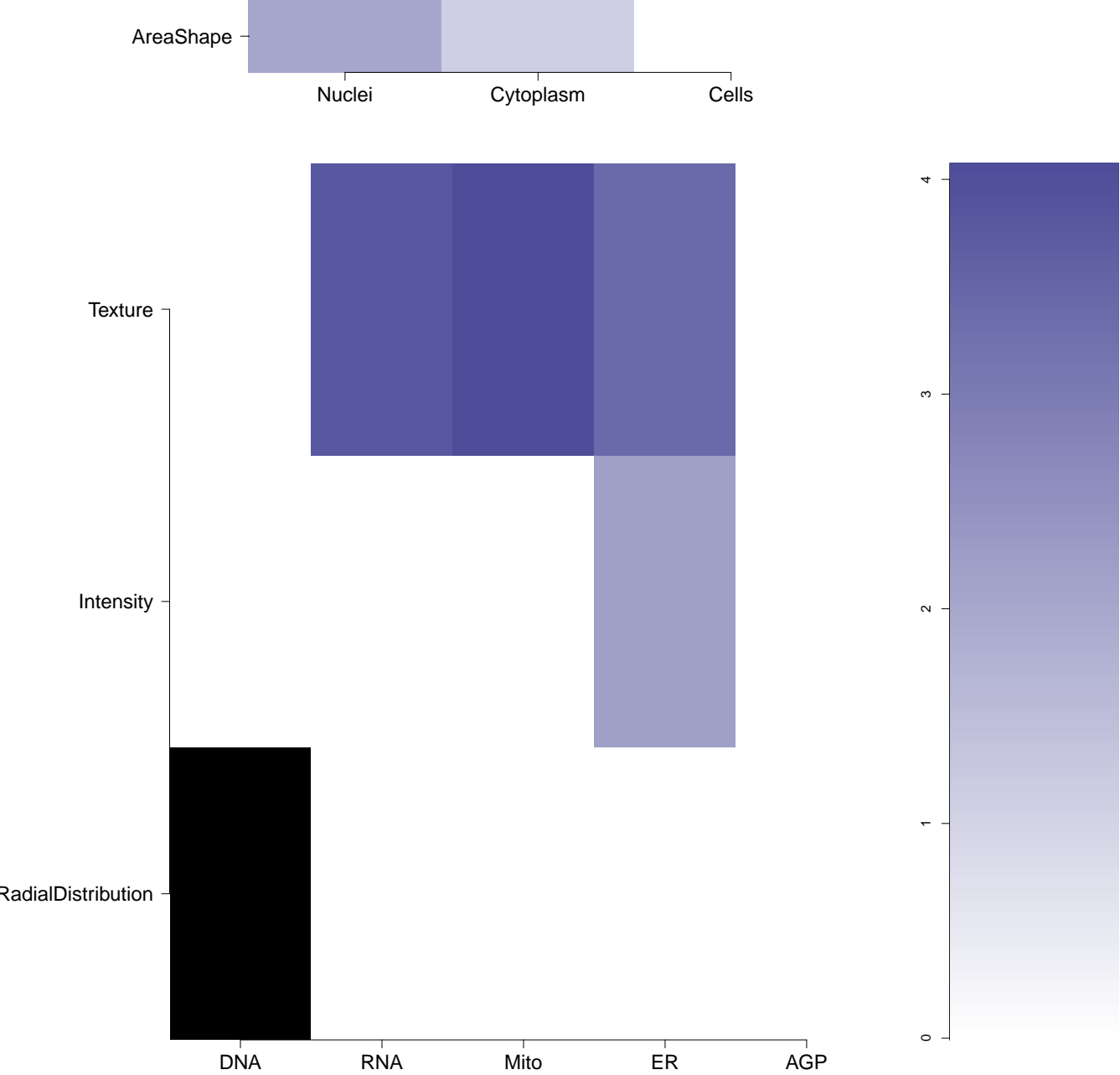
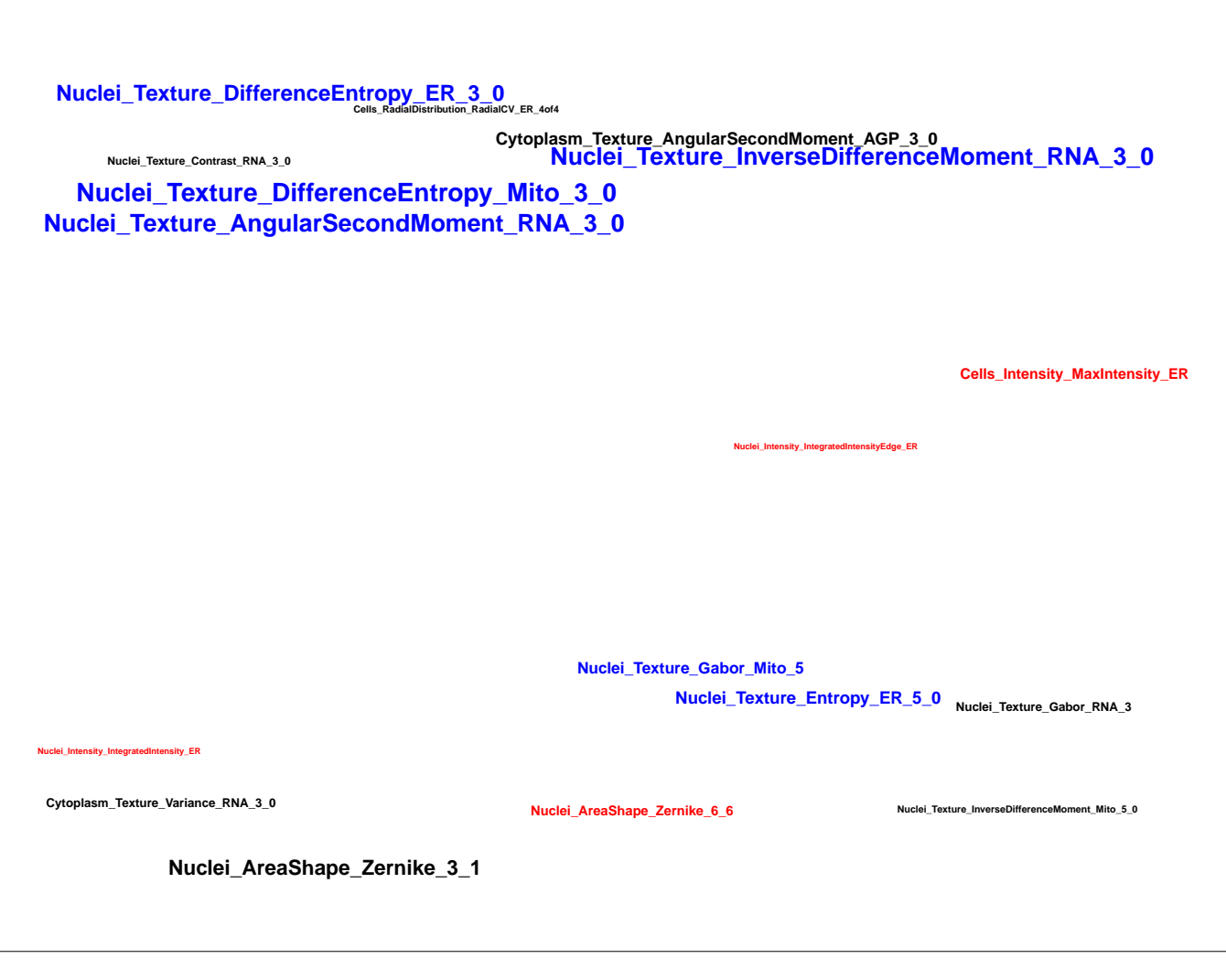
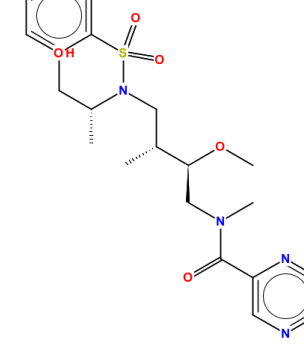
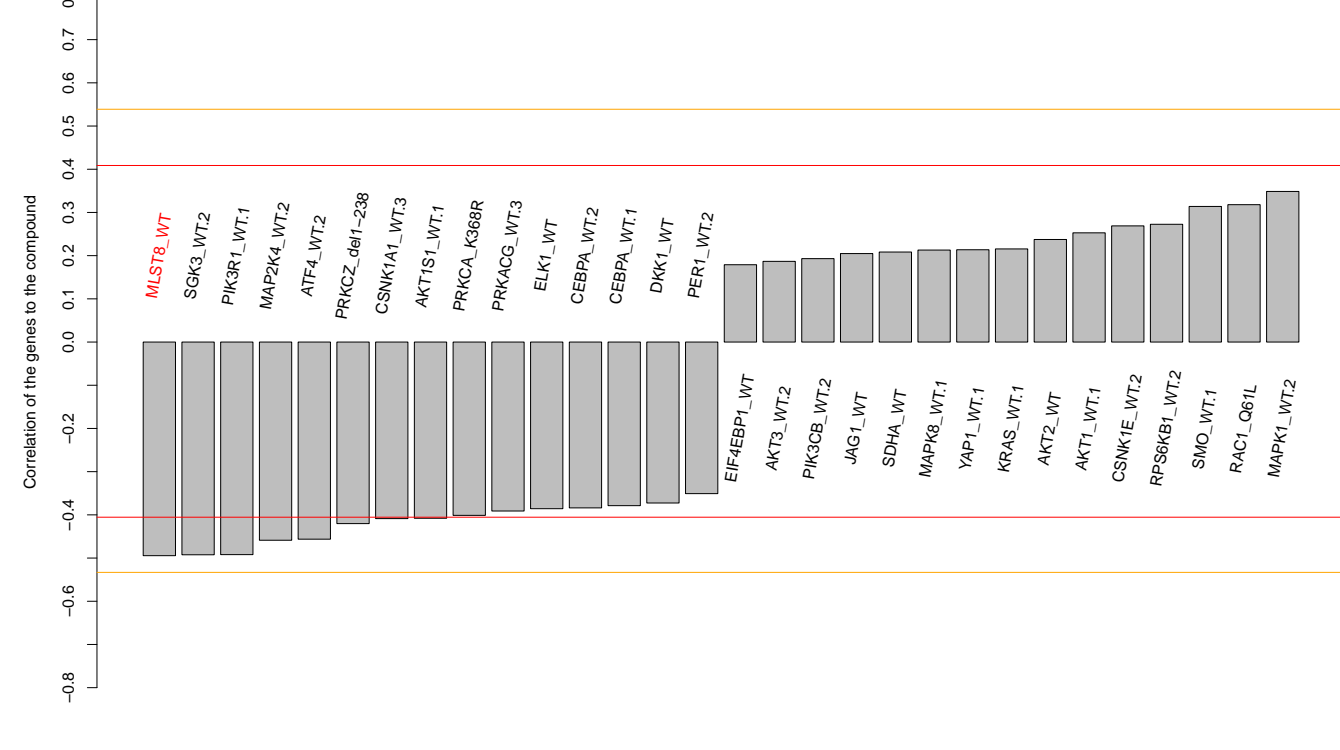
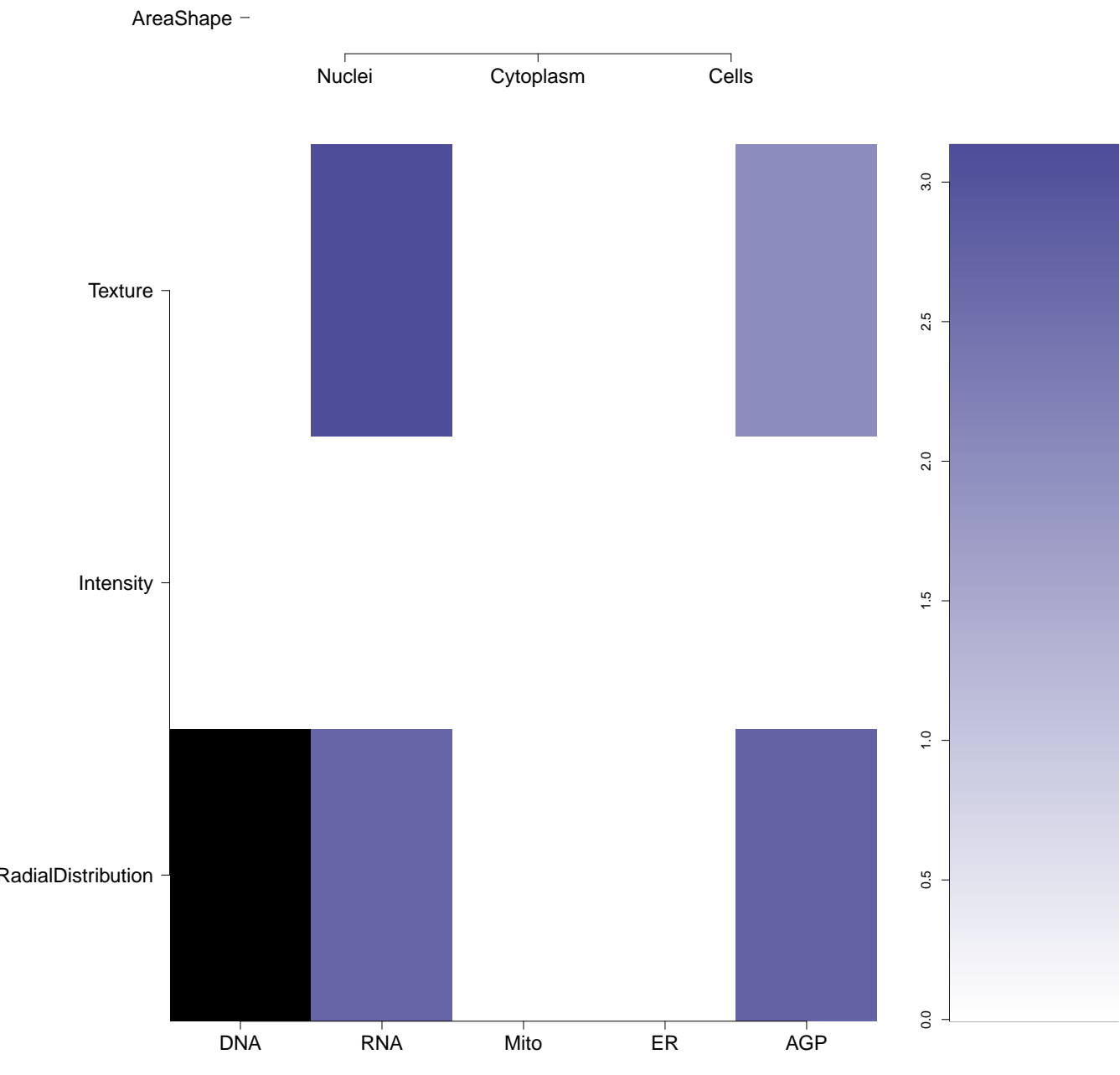

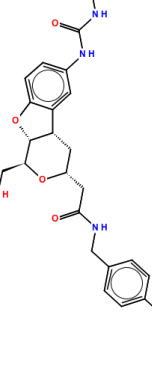
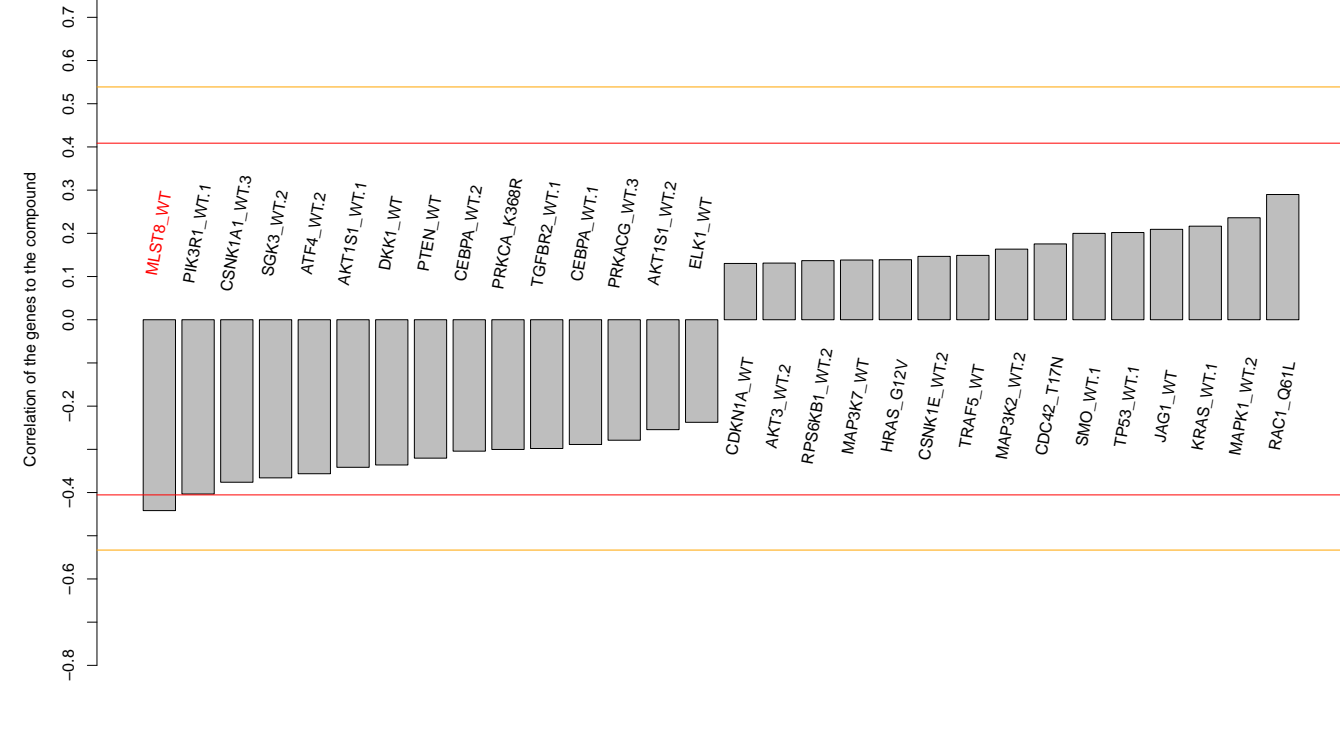
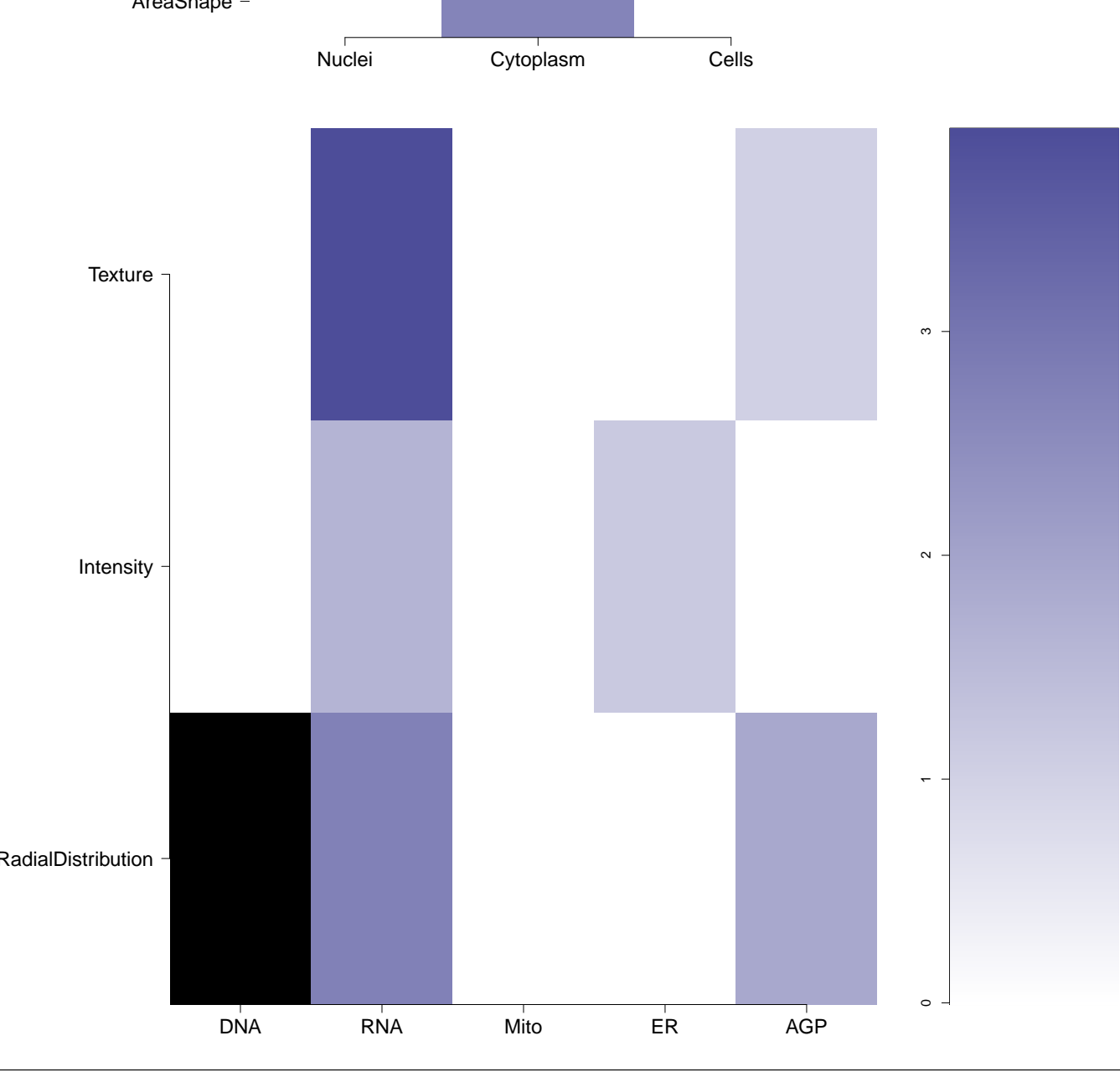

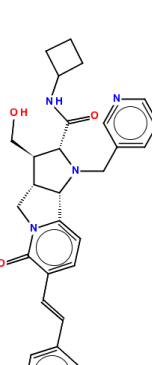
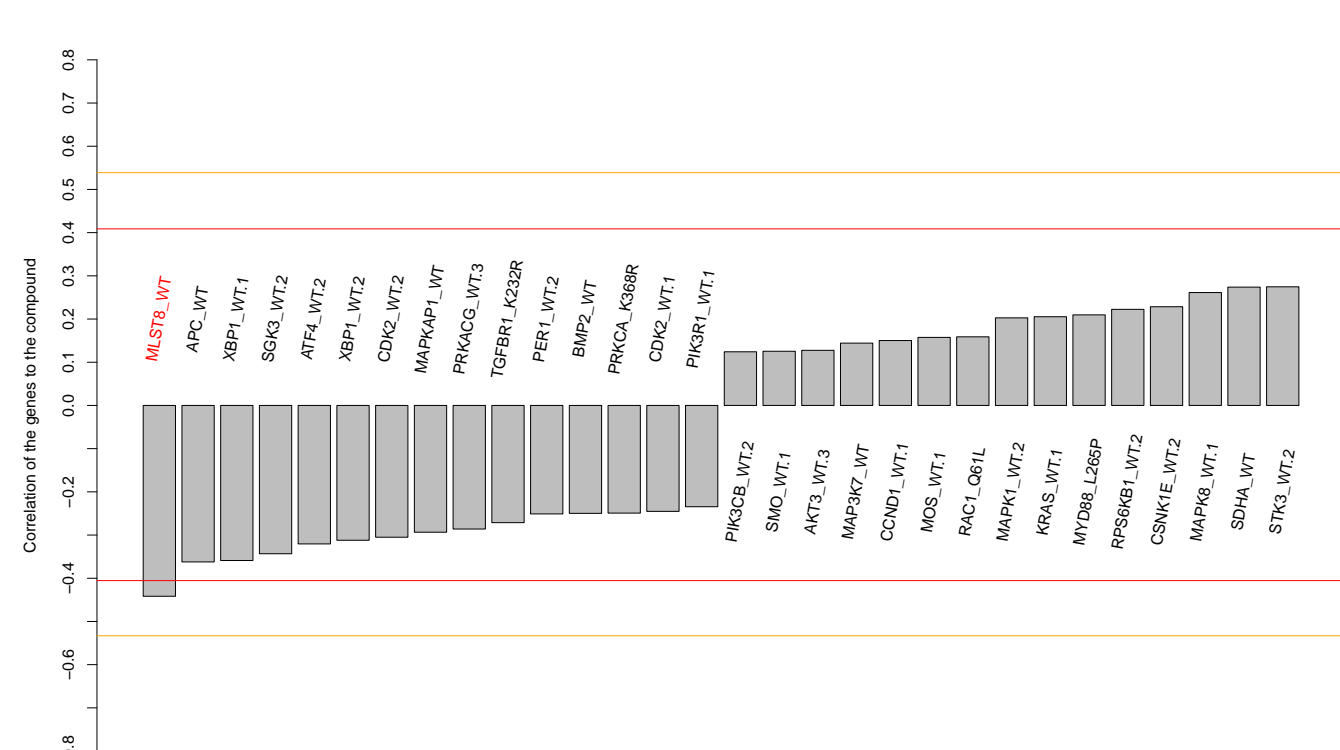
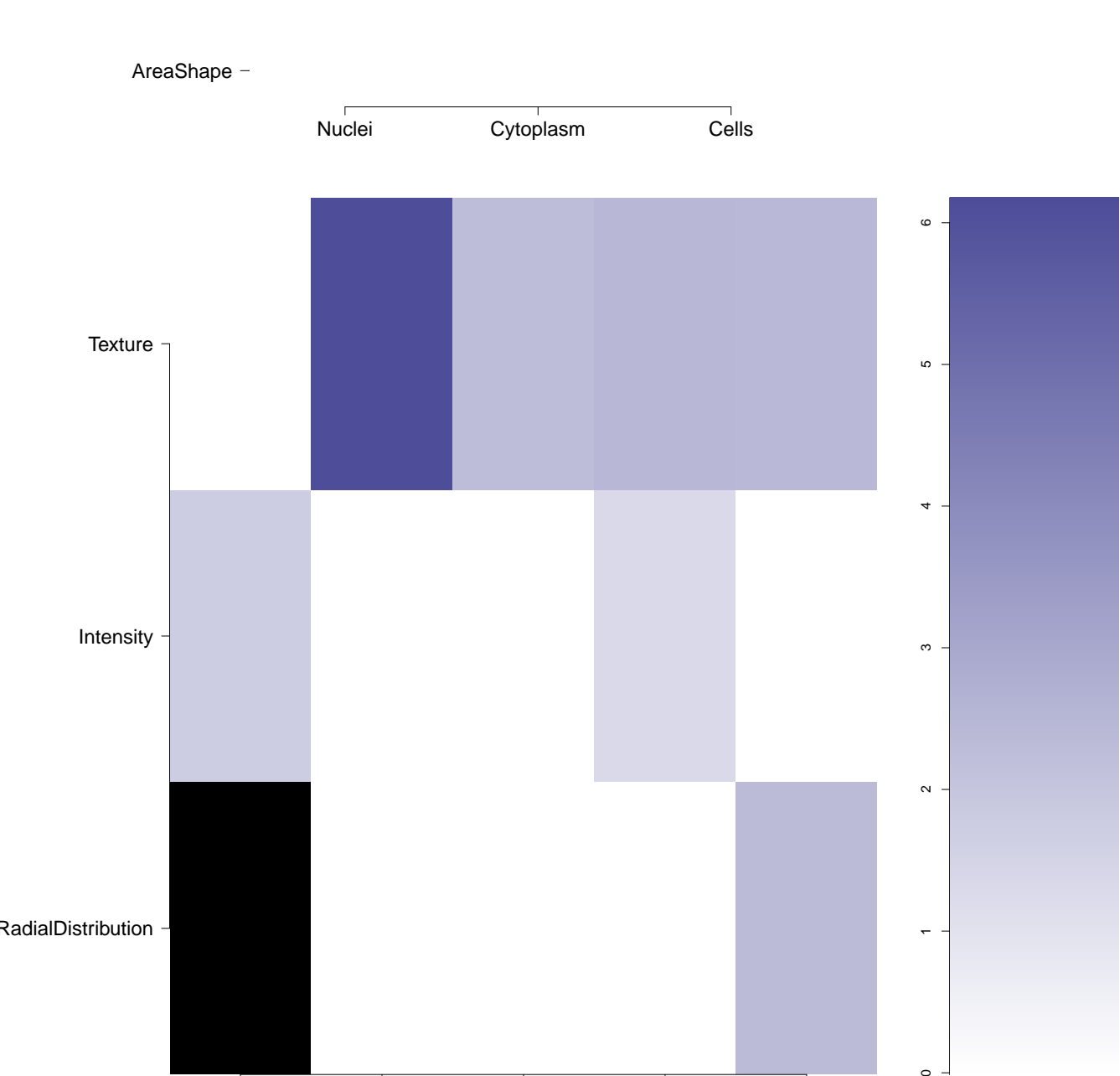
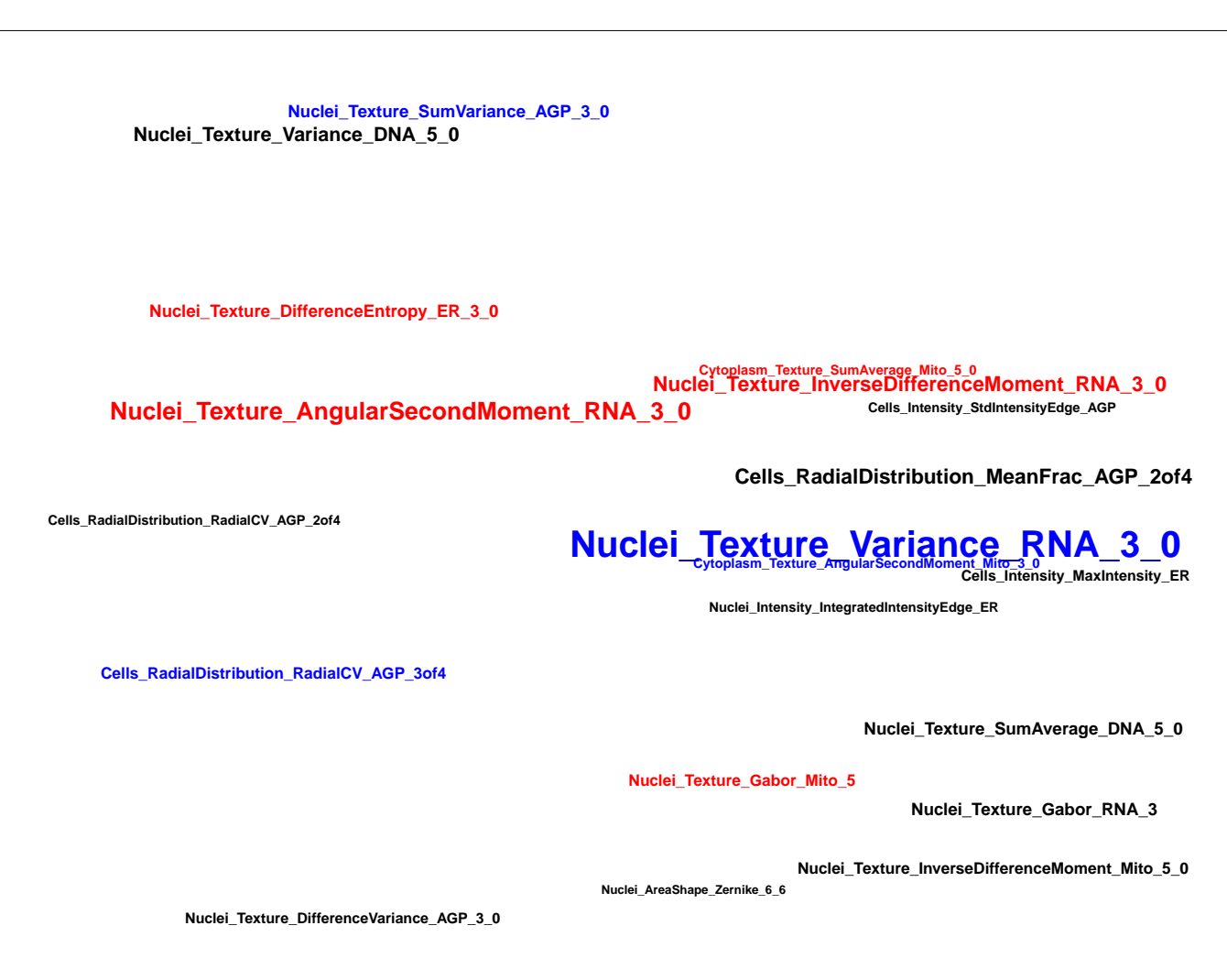


ER



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)	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
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BRD-K66770982-001-05-5 ZINC04842737 AC1MH4LZ Amcb9013812 MLS000999655 HMS2841F18 ZINC4842737 SMR000498760 PubChem CID : 2996252		NA (in 1 replicates)	0.51	NA				Total number of assays tested in: 495. Active in the following assays: <ul style="list-style-type: none"> <li>Epi-absorbance primary biochemical high throughput screening assay to identify inhibitors of IMP-1 metallo-beta-lactamase (AID 1556)</li> <li>VP16 countercreen qHTS for inhibitors of ROR gamma transcriptional activity (AID 2546)</li> <li>qHTS for inhibitors of ROR gamma transcriptional activity (AID 2551)</li> <li>qHTS identification of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463190)</li> <li>qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)</li> <li>qHTS for Inhibitors of Inflammasome Signaling: IL-1-beta AlphaLISA Primary Screen (AID 743279)</li> </ul>
BRD-K09864793-001-01-4 PubChem CID : 54646581		0.85 (in 4 replicates)	0.50	0.976				Total number of assays tested in: 37.
BRD-K70899691-001-01-7 PubChem CID : 54646657		0.80 (in 4 replicates)	0.42	0.285				Total number of assays tested in: 37.
BRD-K47885451-001-01-6 PubChem CID : 54649254		0.74 (in 2 replicates)	-0.49	0.219				Total number of assays tested in: 33.
BRD-K28936732-001-01-1 PubChem CID : 54647741		0.55 (in 3 replicates)	-0.44	NA				Total number of assays tested in: 37.
BRD-K82779934-001-01-4 PubChem CID : 54661036		0.57 (in 4 replicates)	-0.44	NA				Total number of assays tested in: 27.