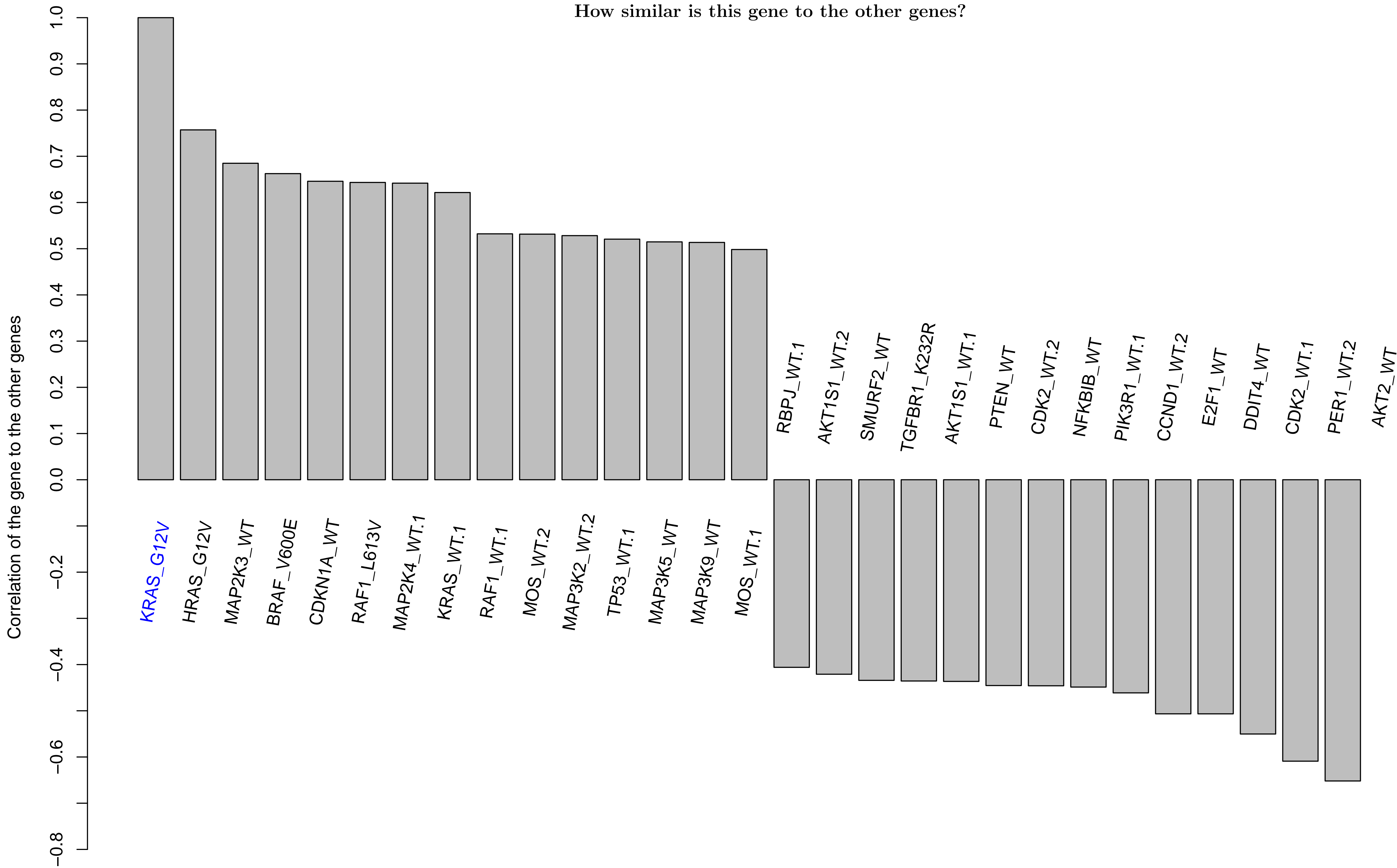
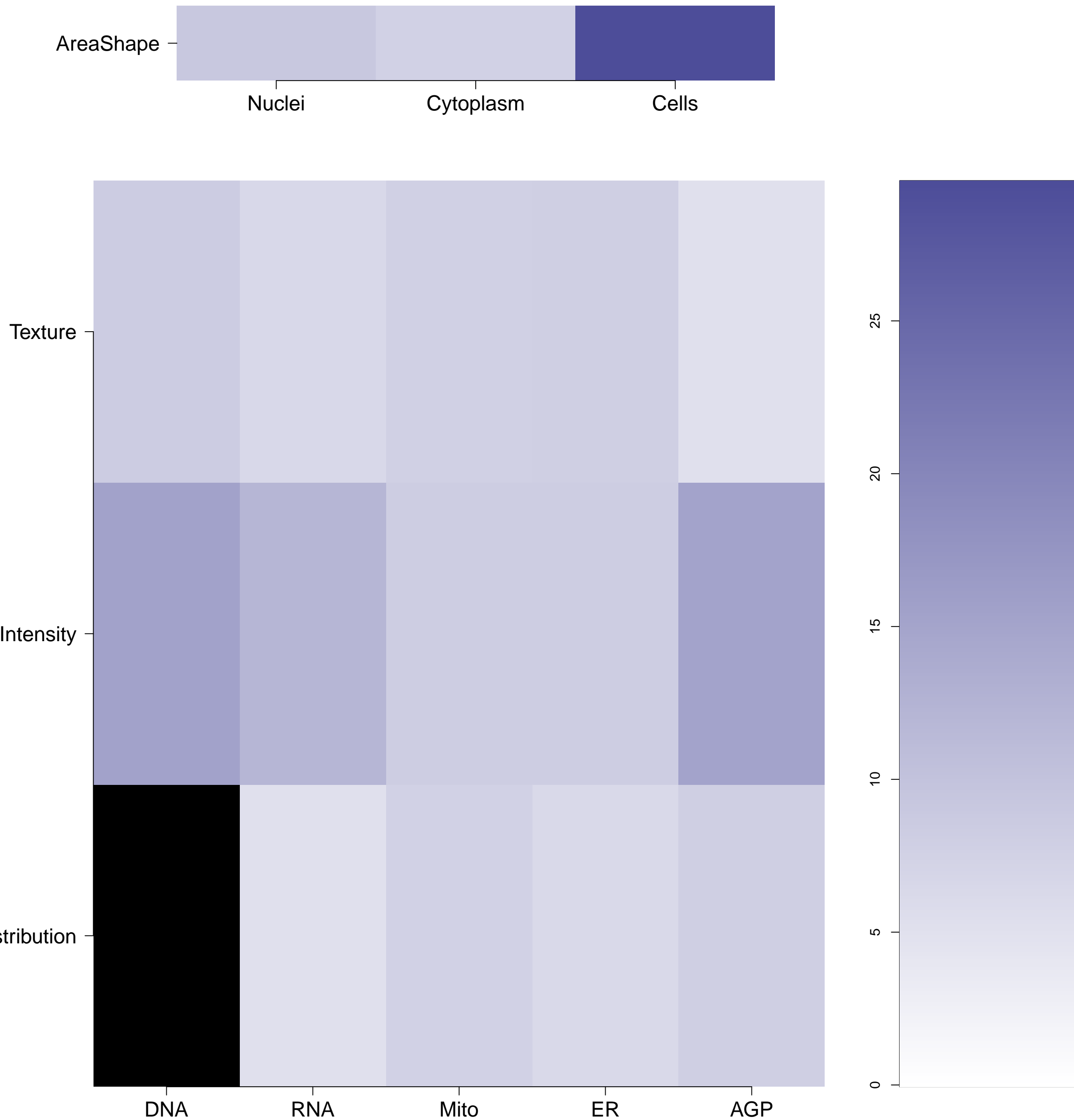


KRAS.G12V - in RTK

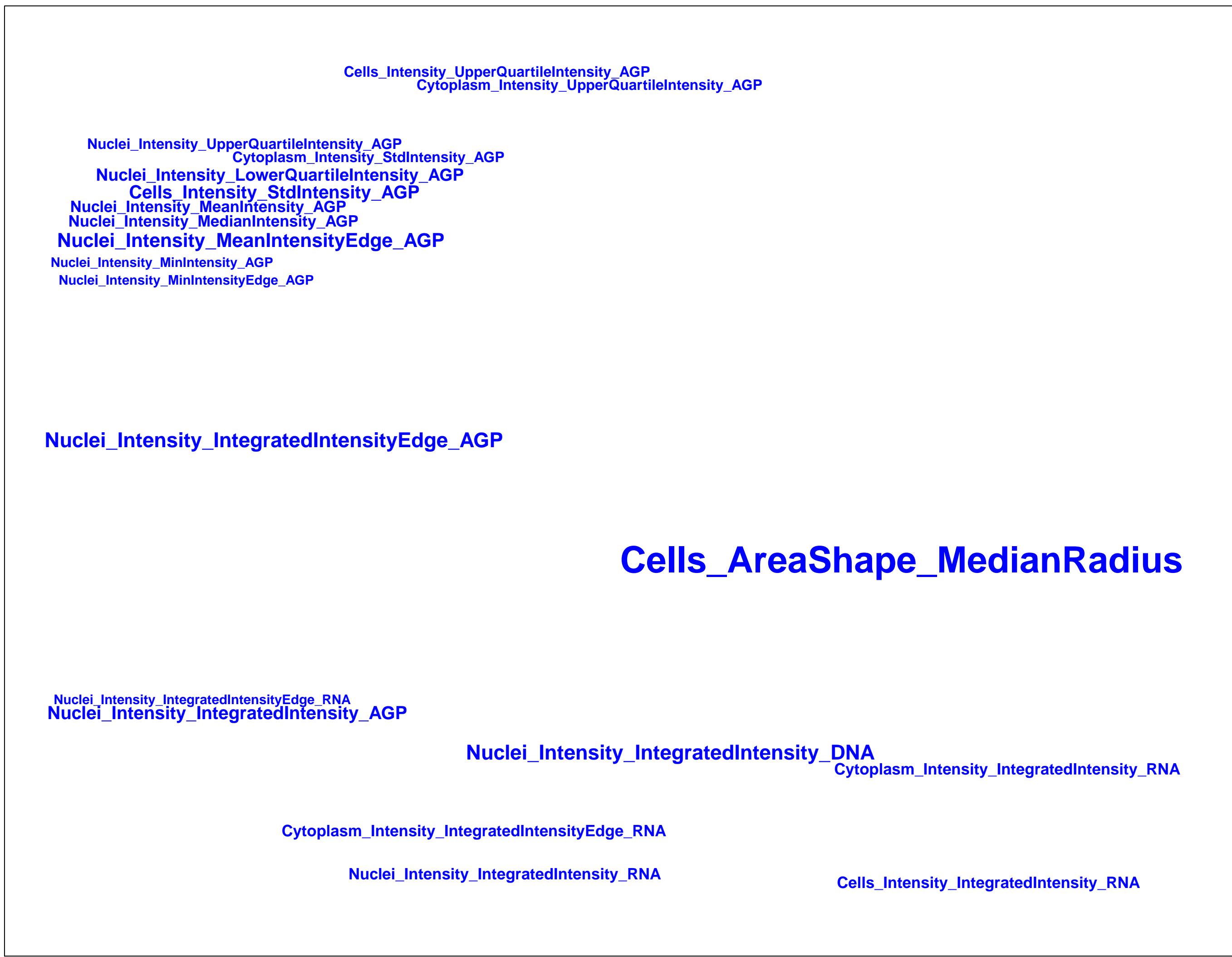
How similar is this gene to the other genes?



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

KRAS.G12V (41744)

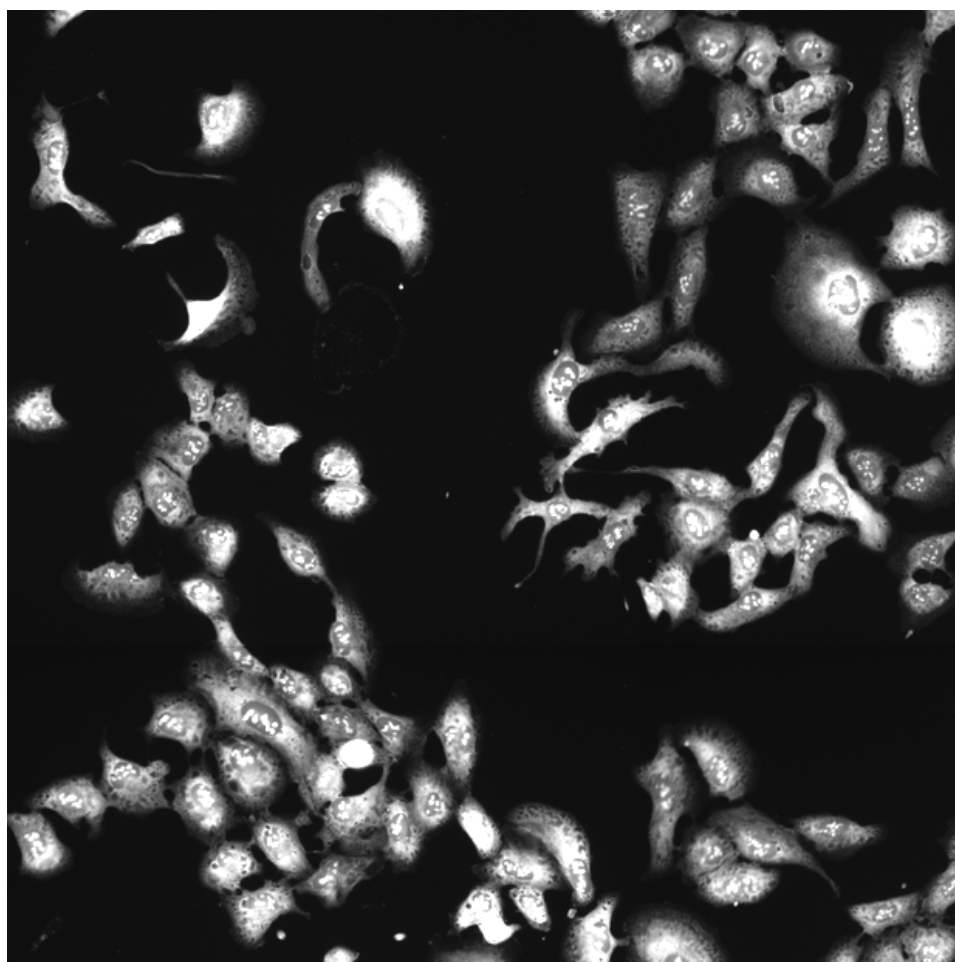
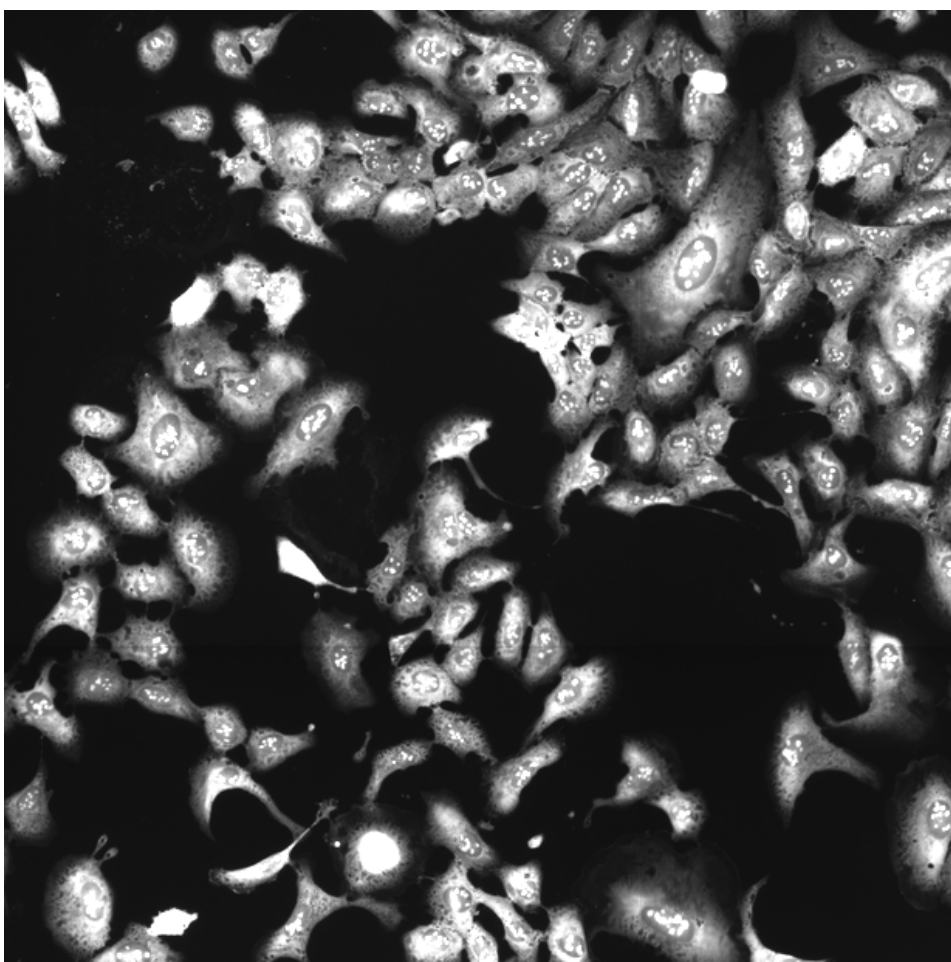
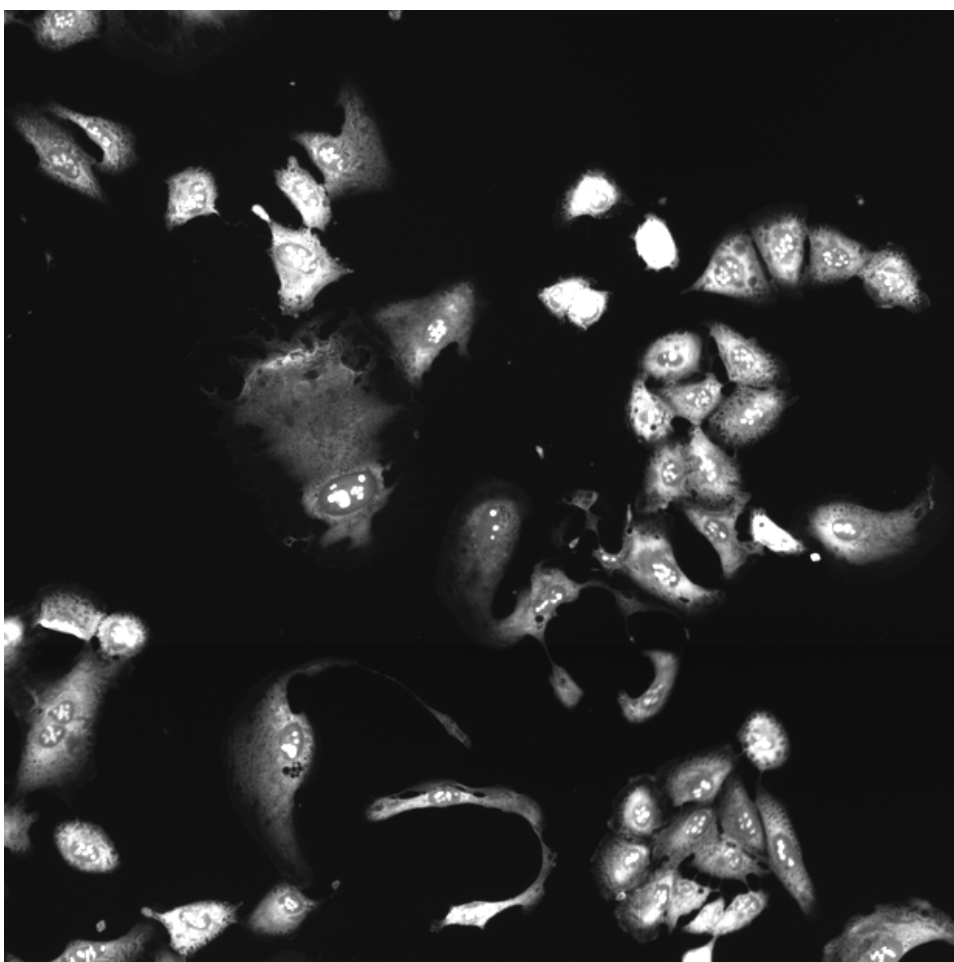
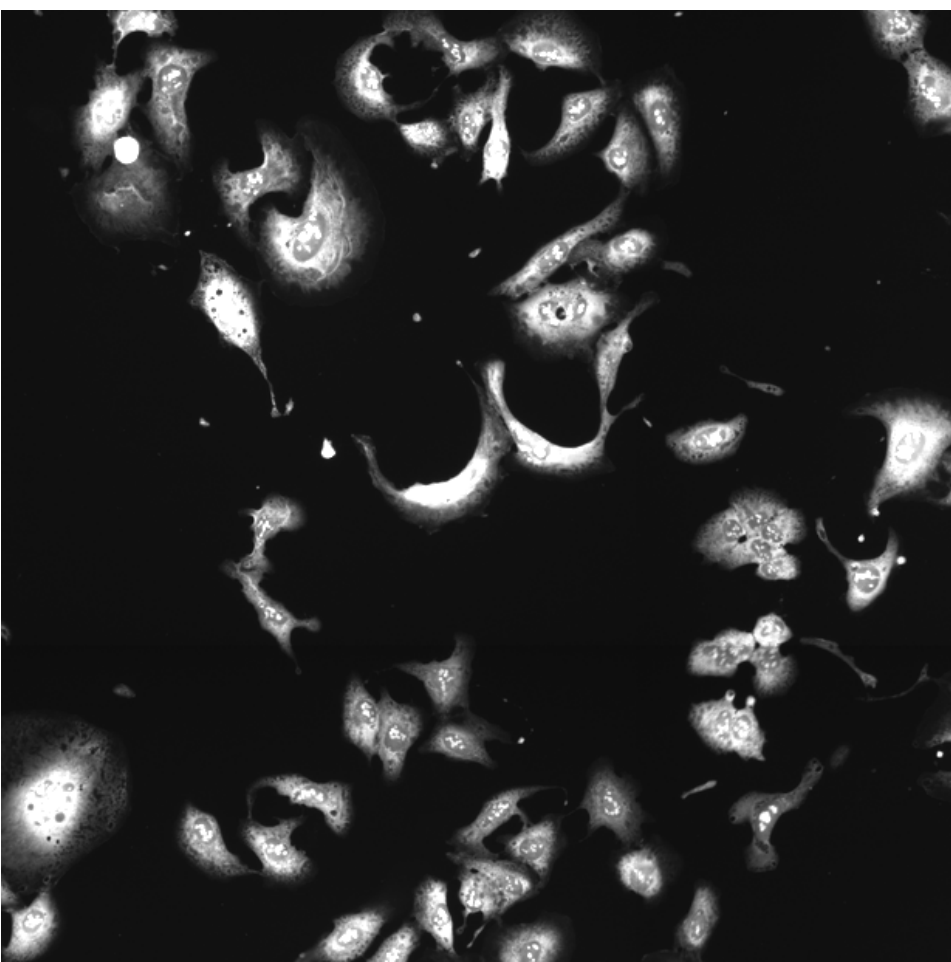
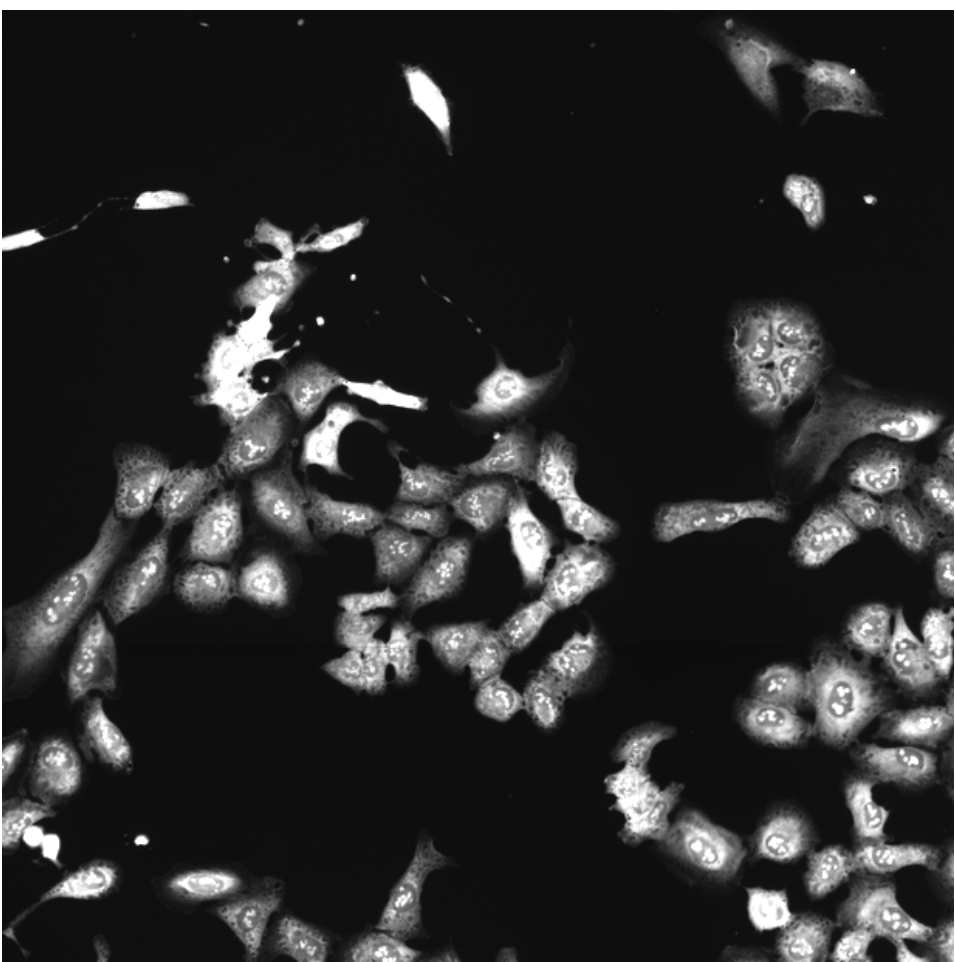
KRAS.G12V (41755)

KRAS.G12V (41756)

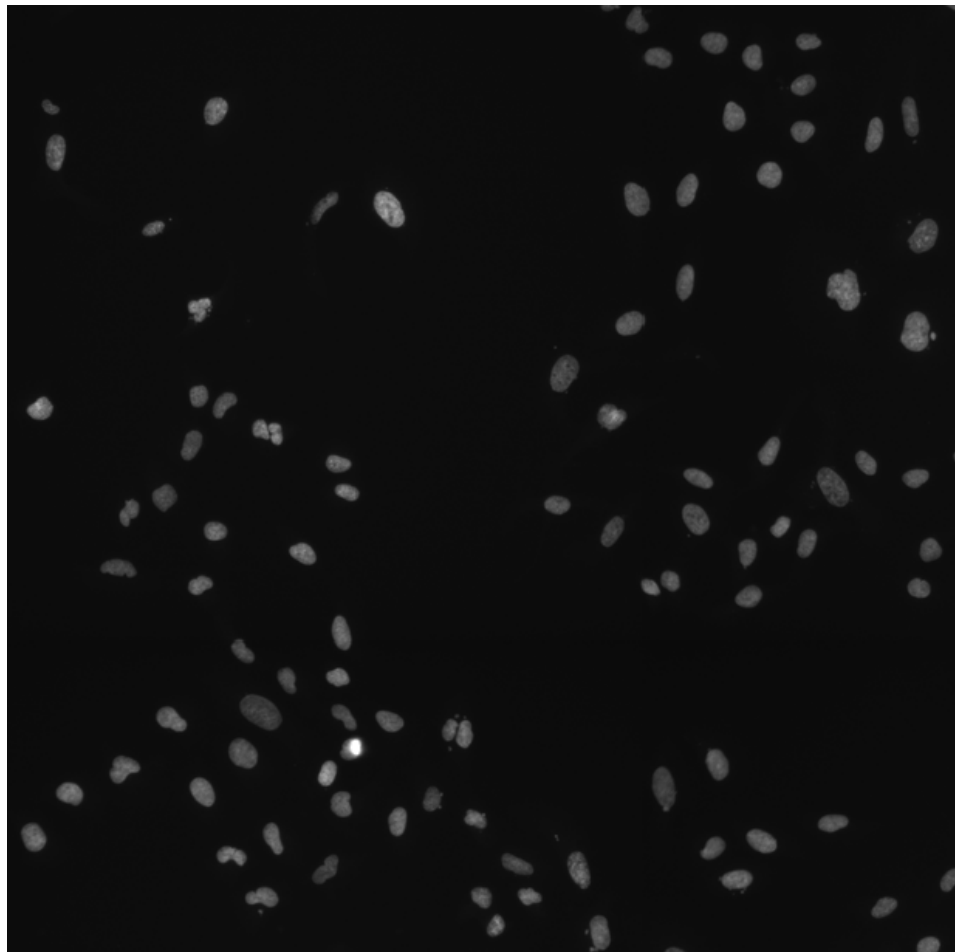
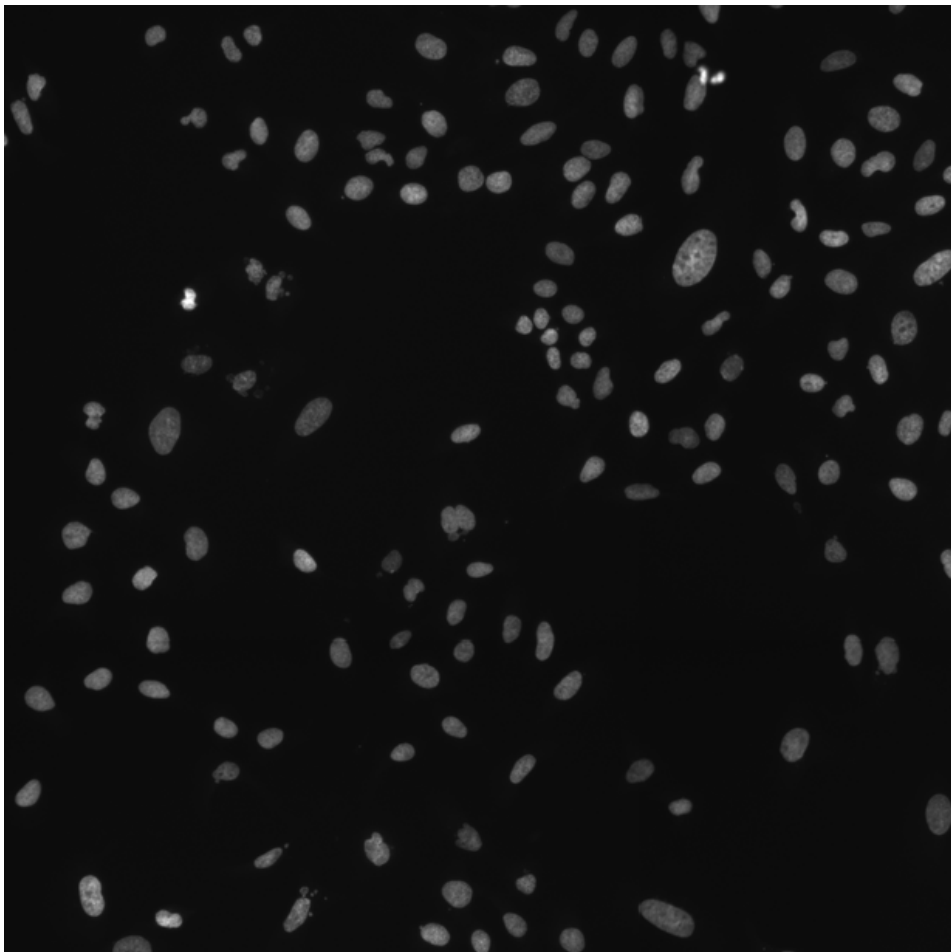
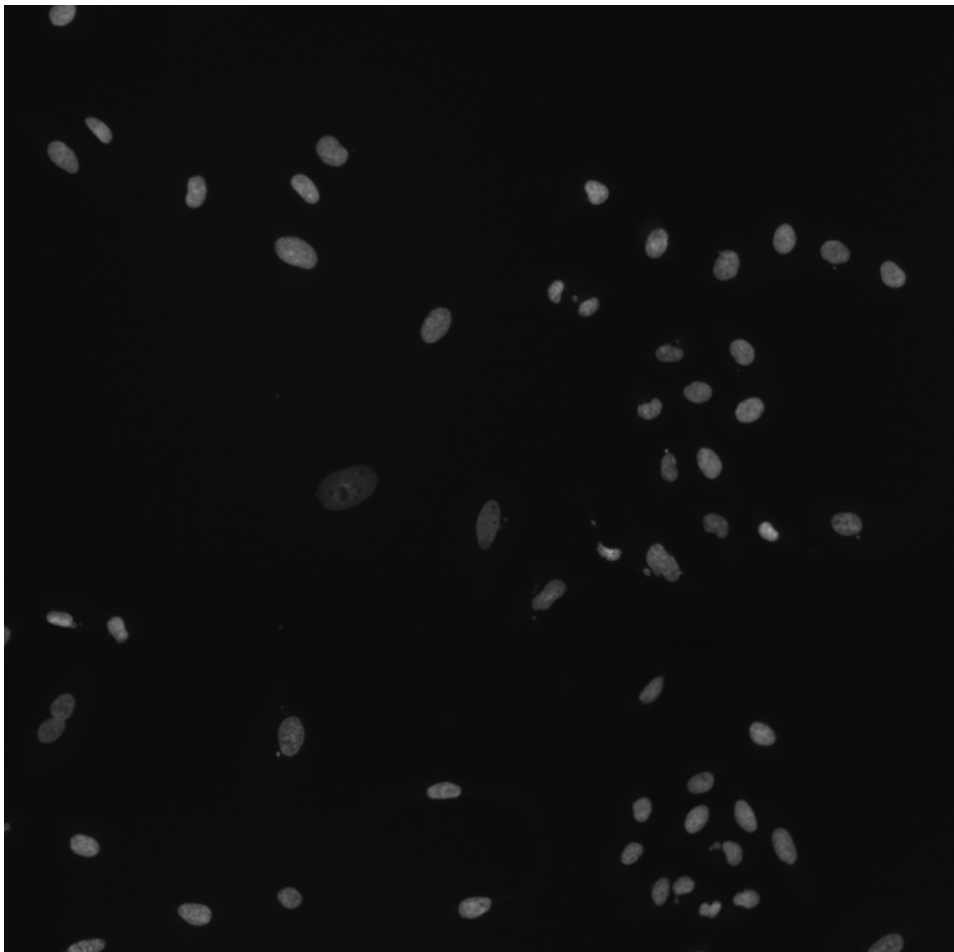
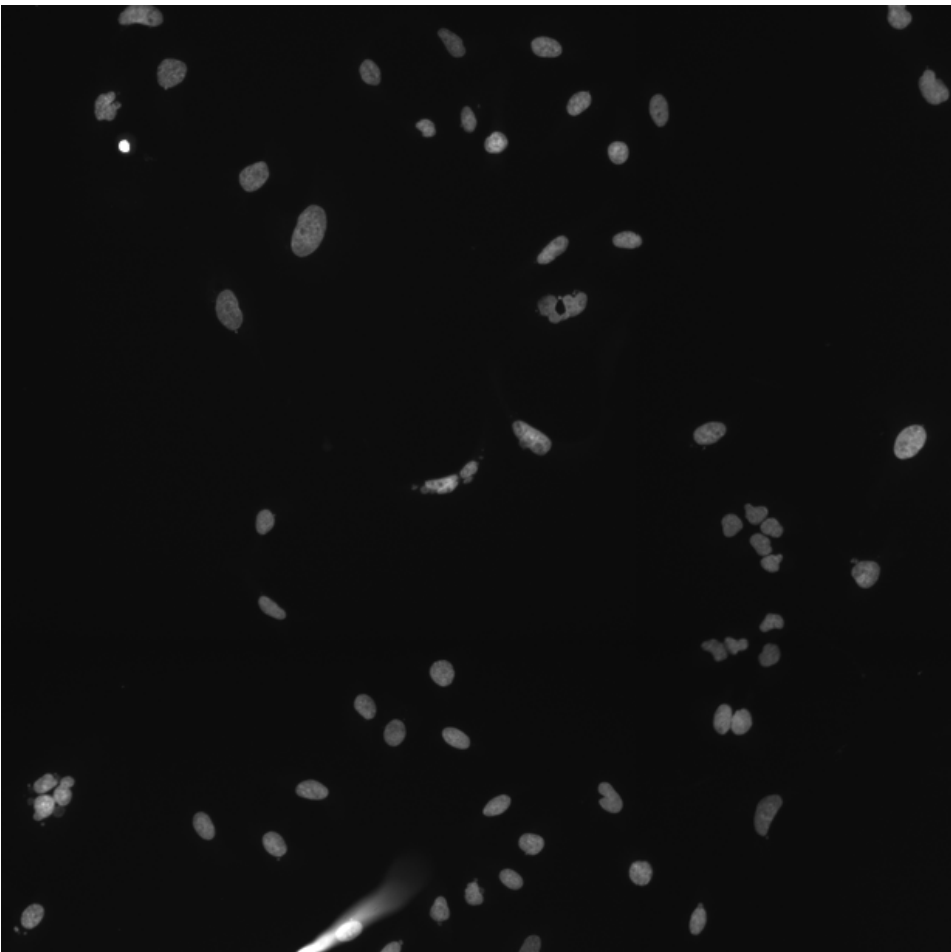
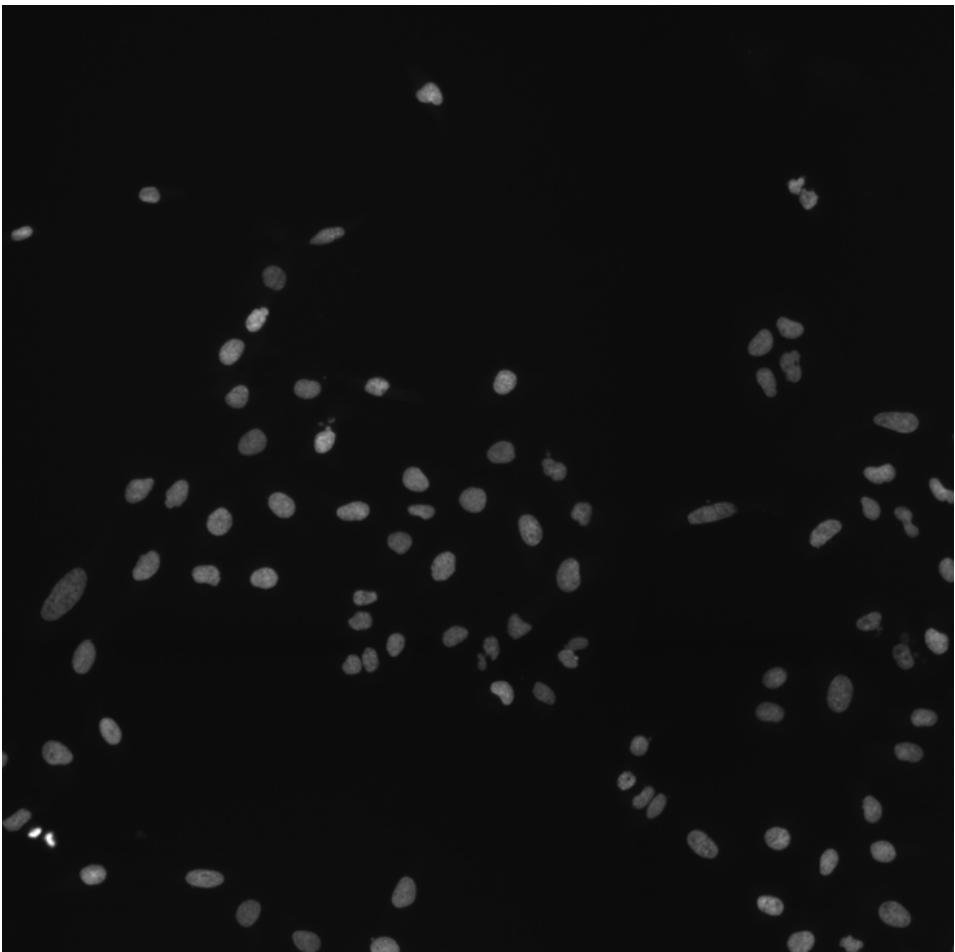
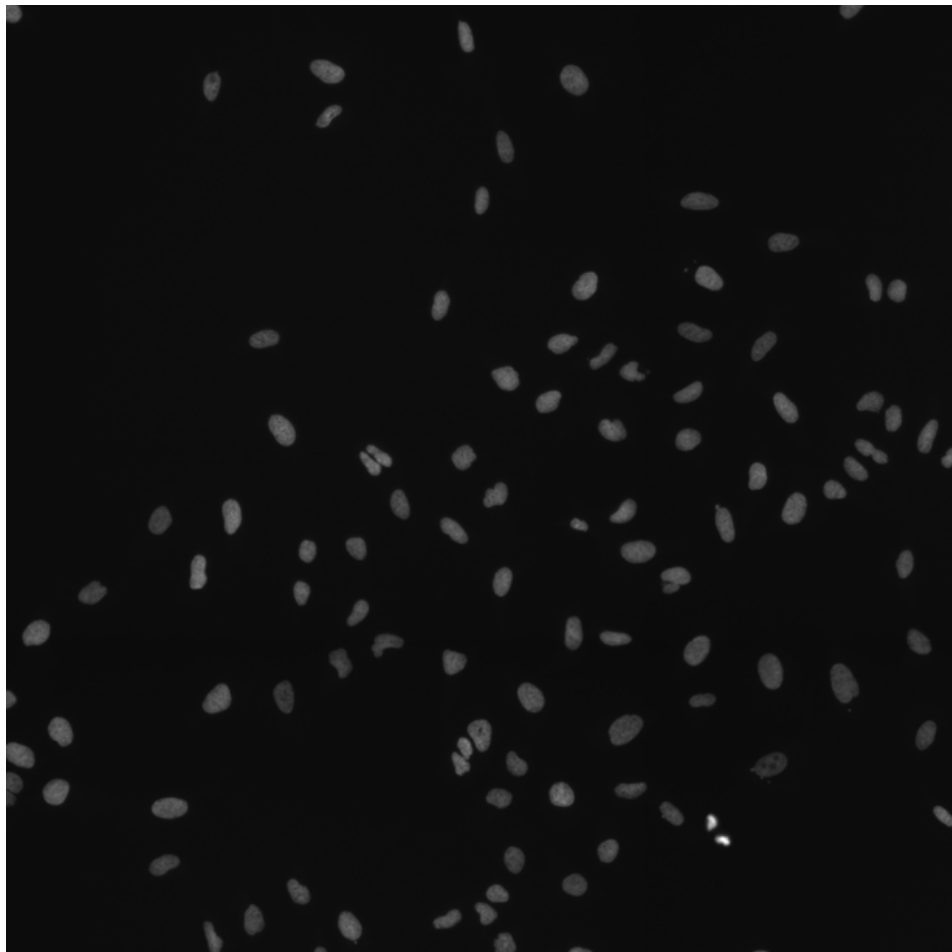
KRAS.G12V (41757)

KRAS.G12V (41754)

RNA

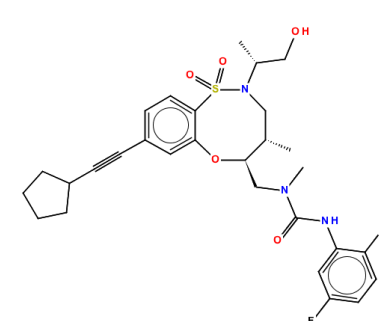
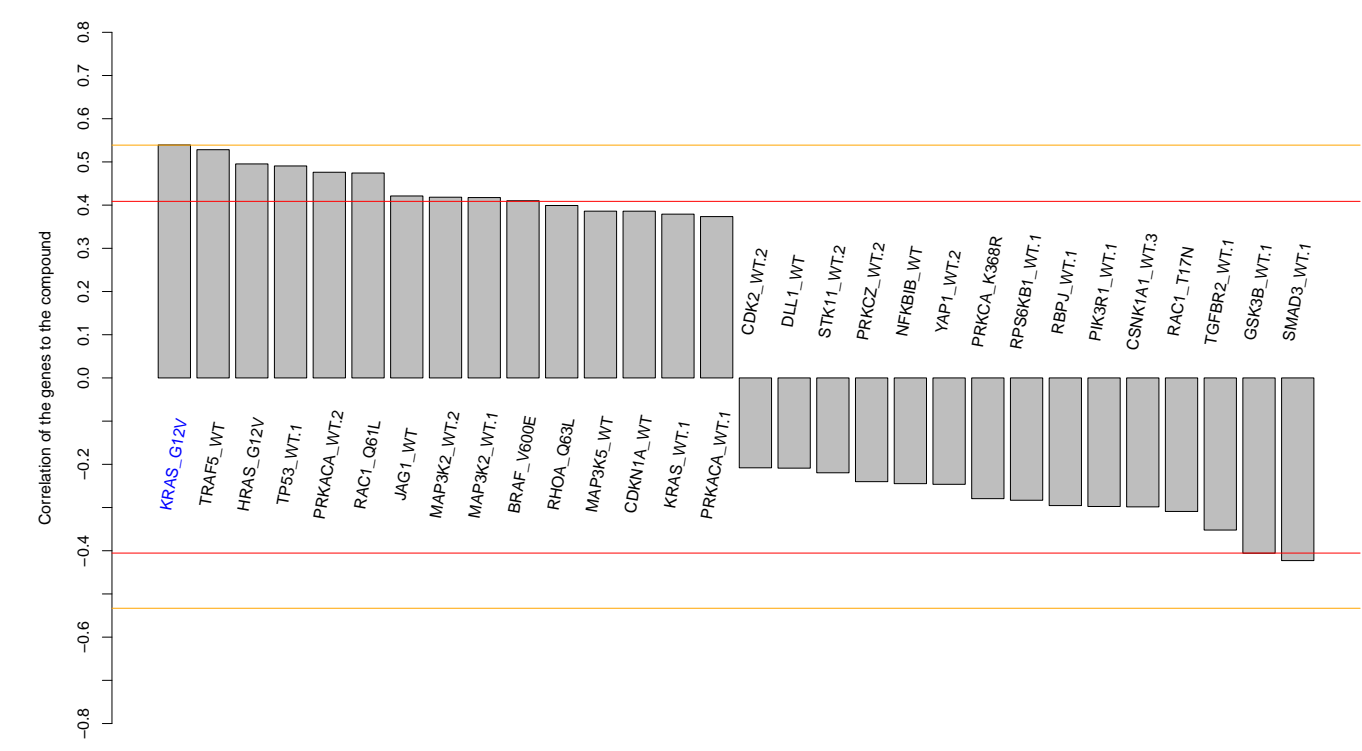
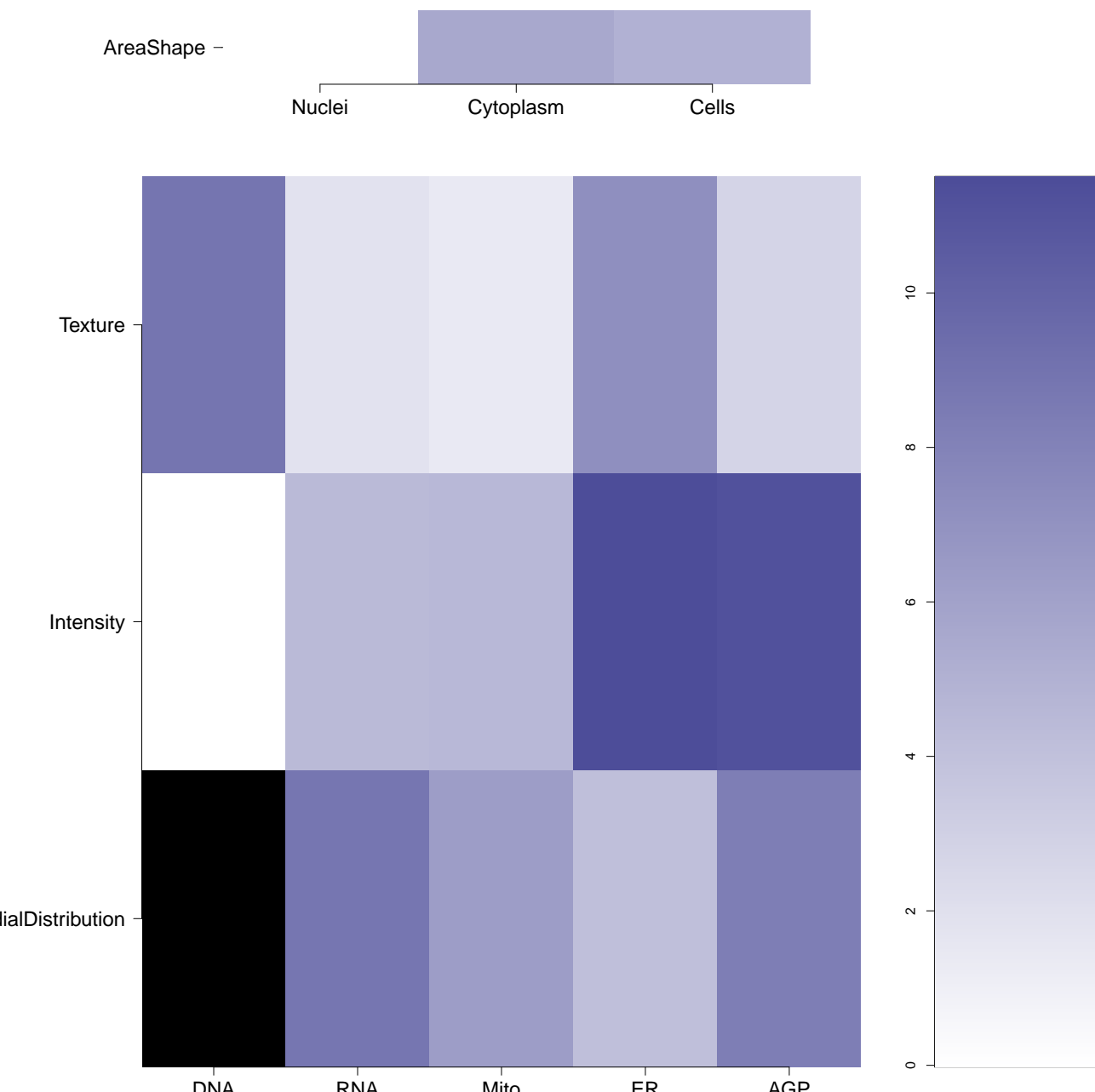

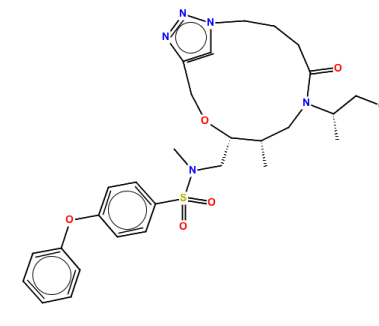
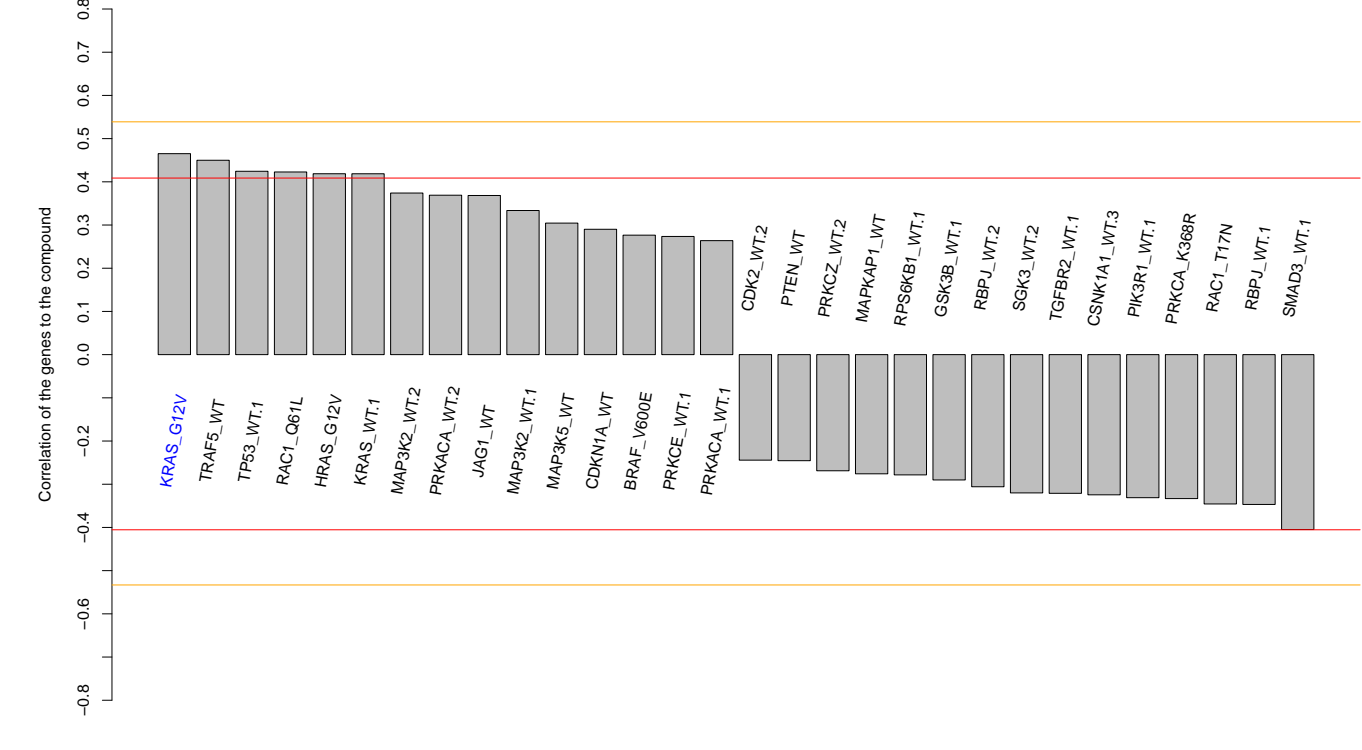
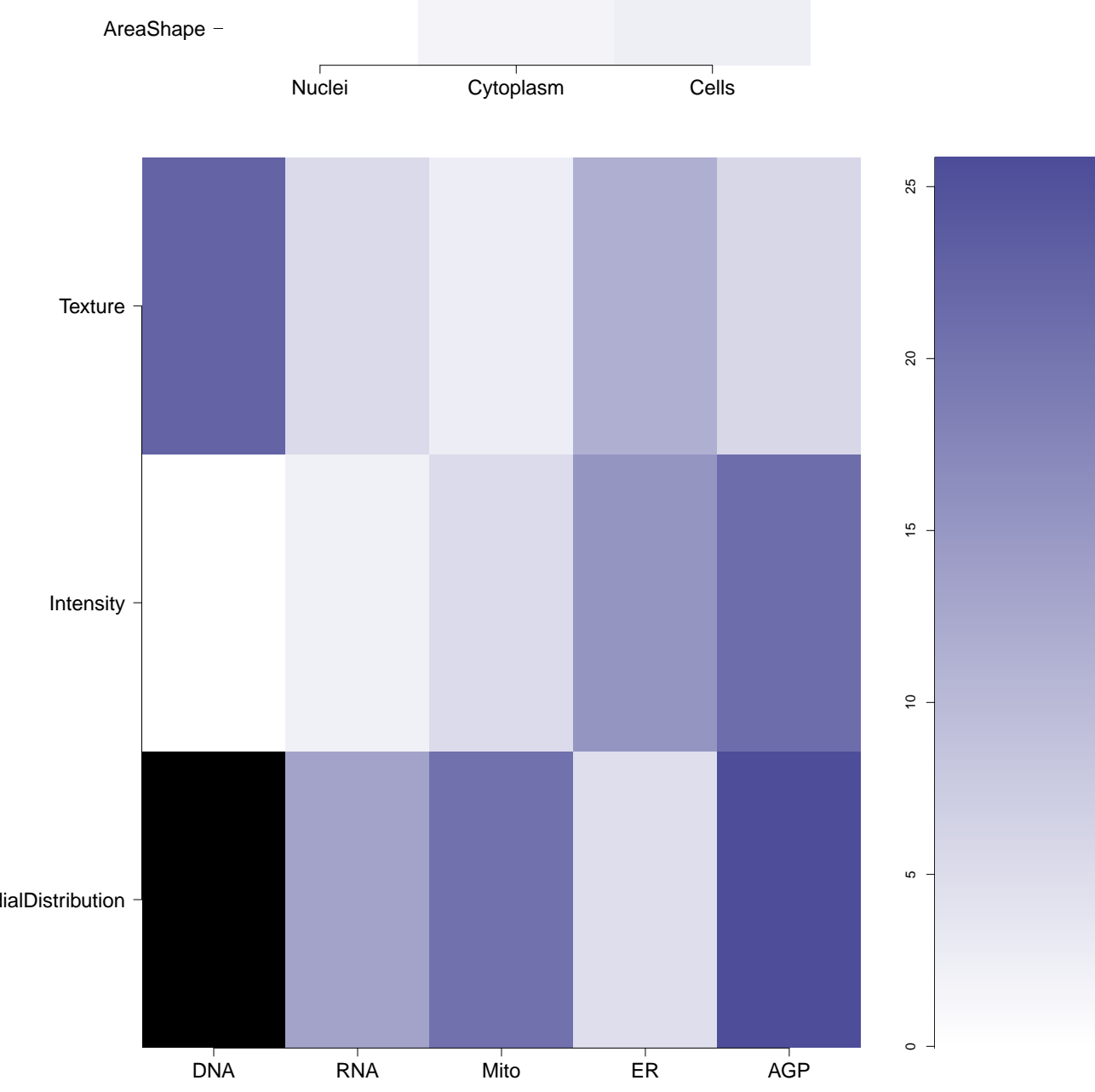

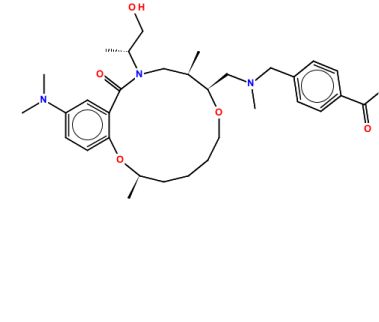
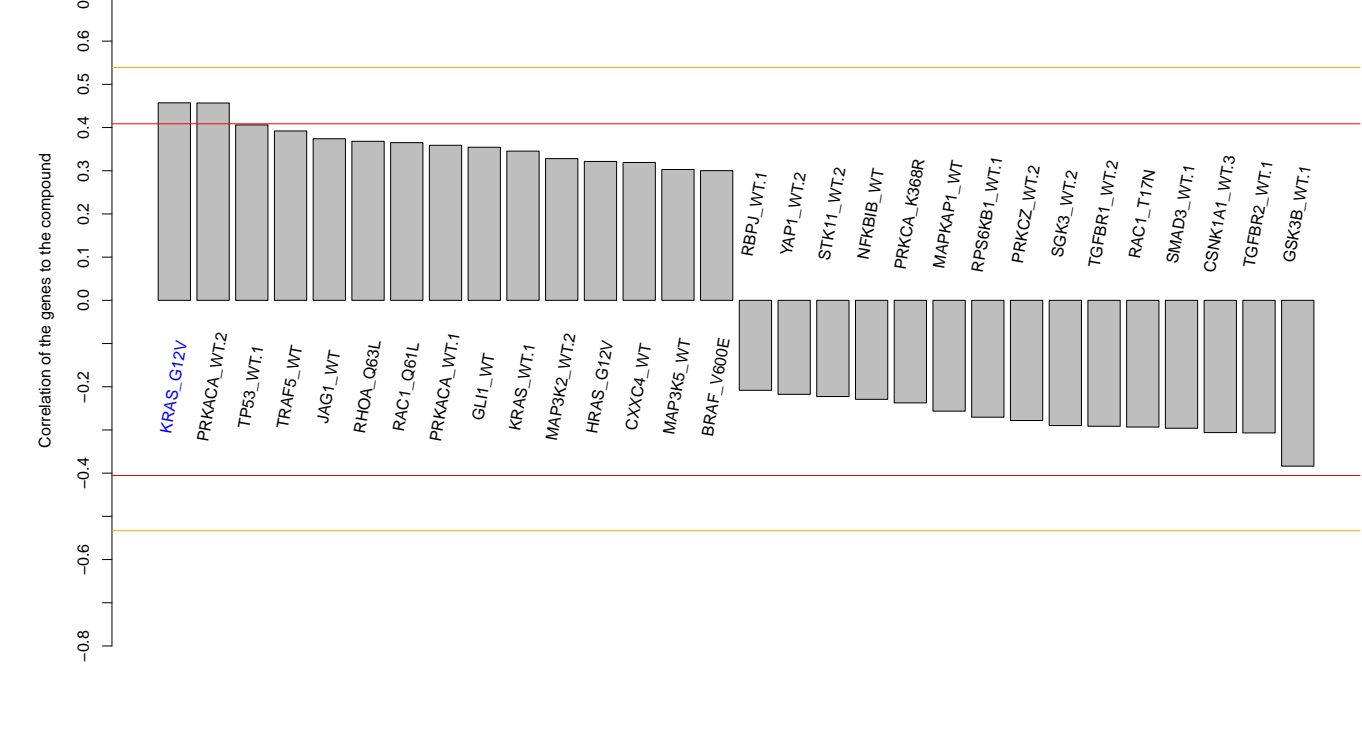
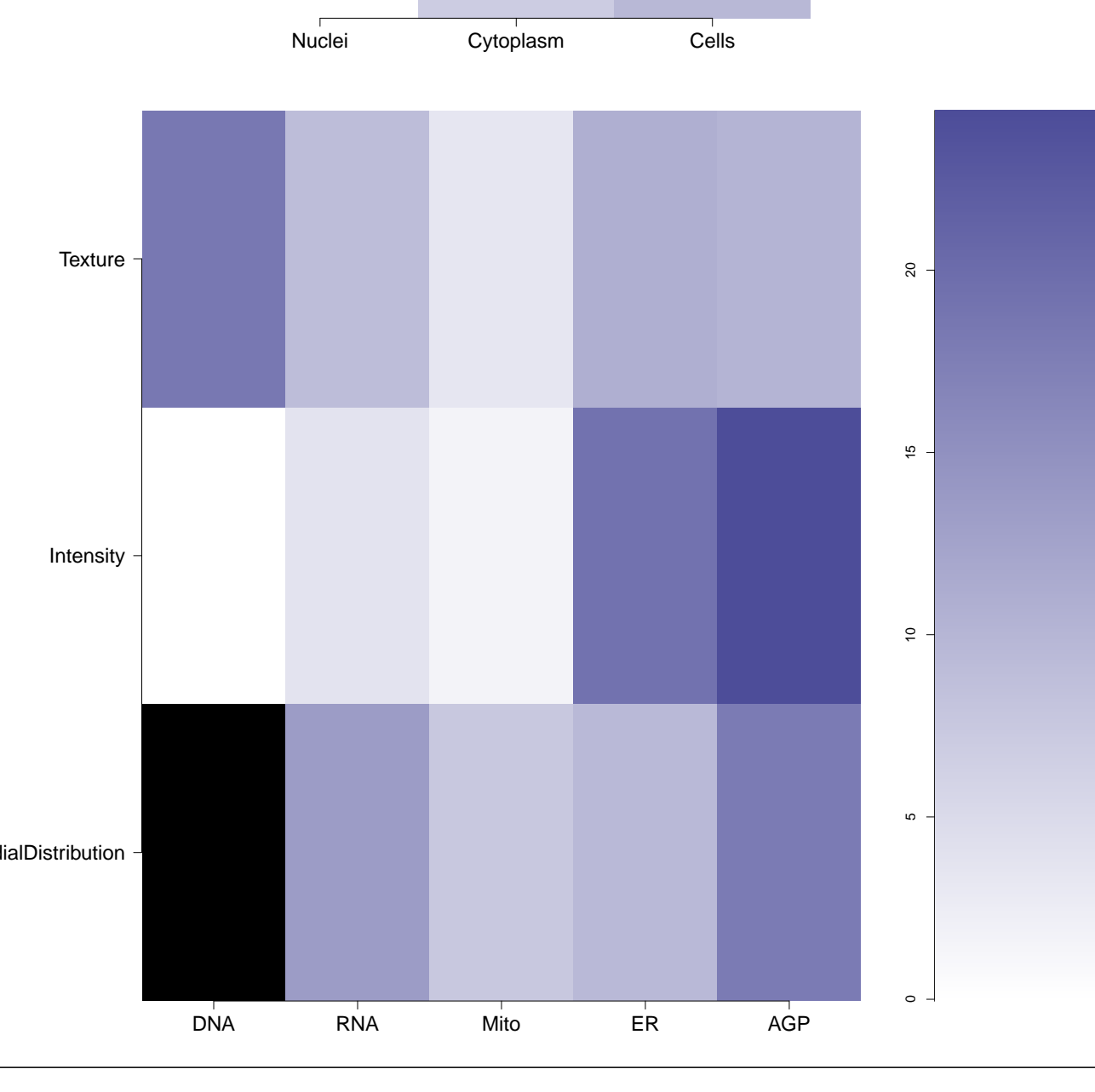

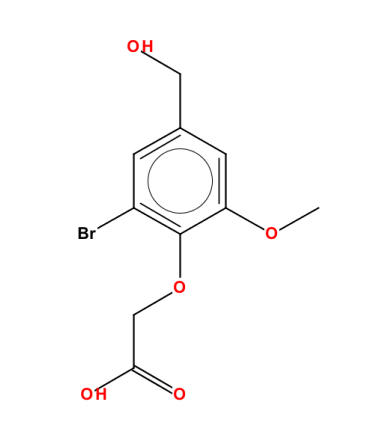
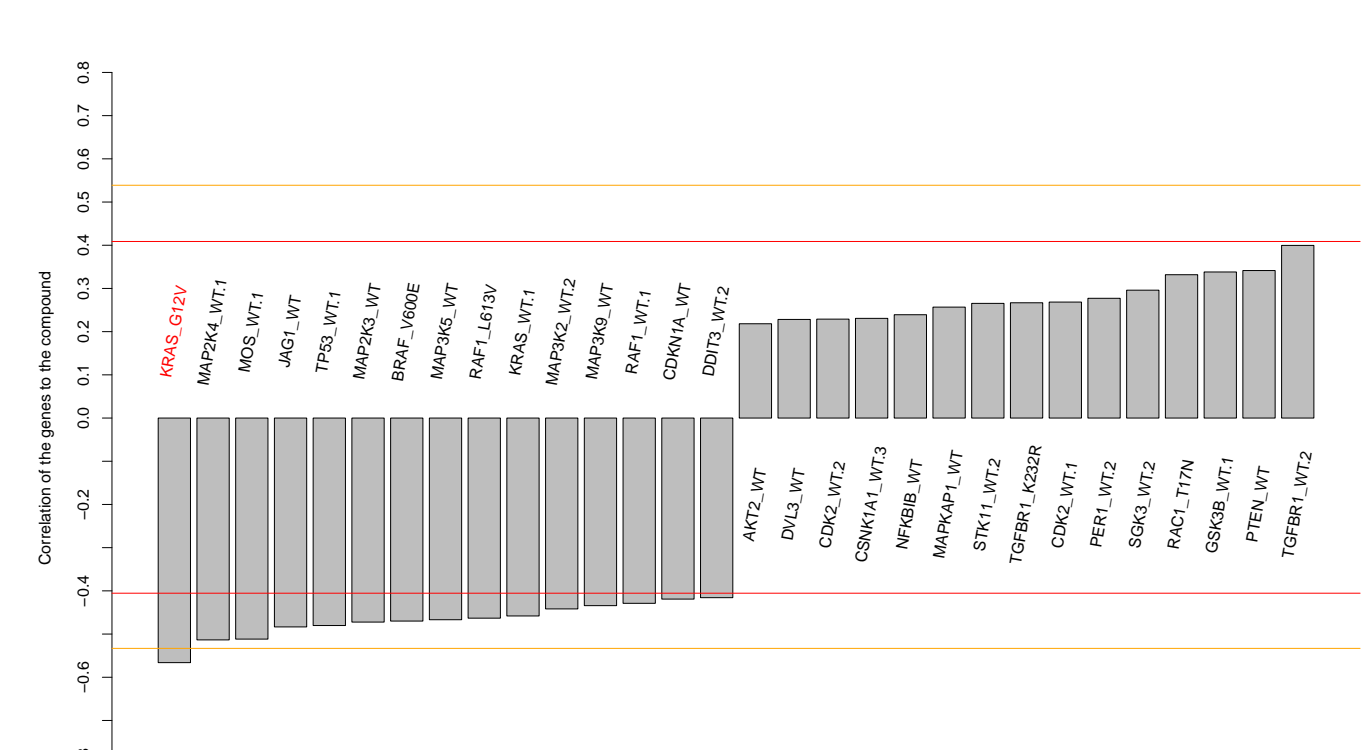
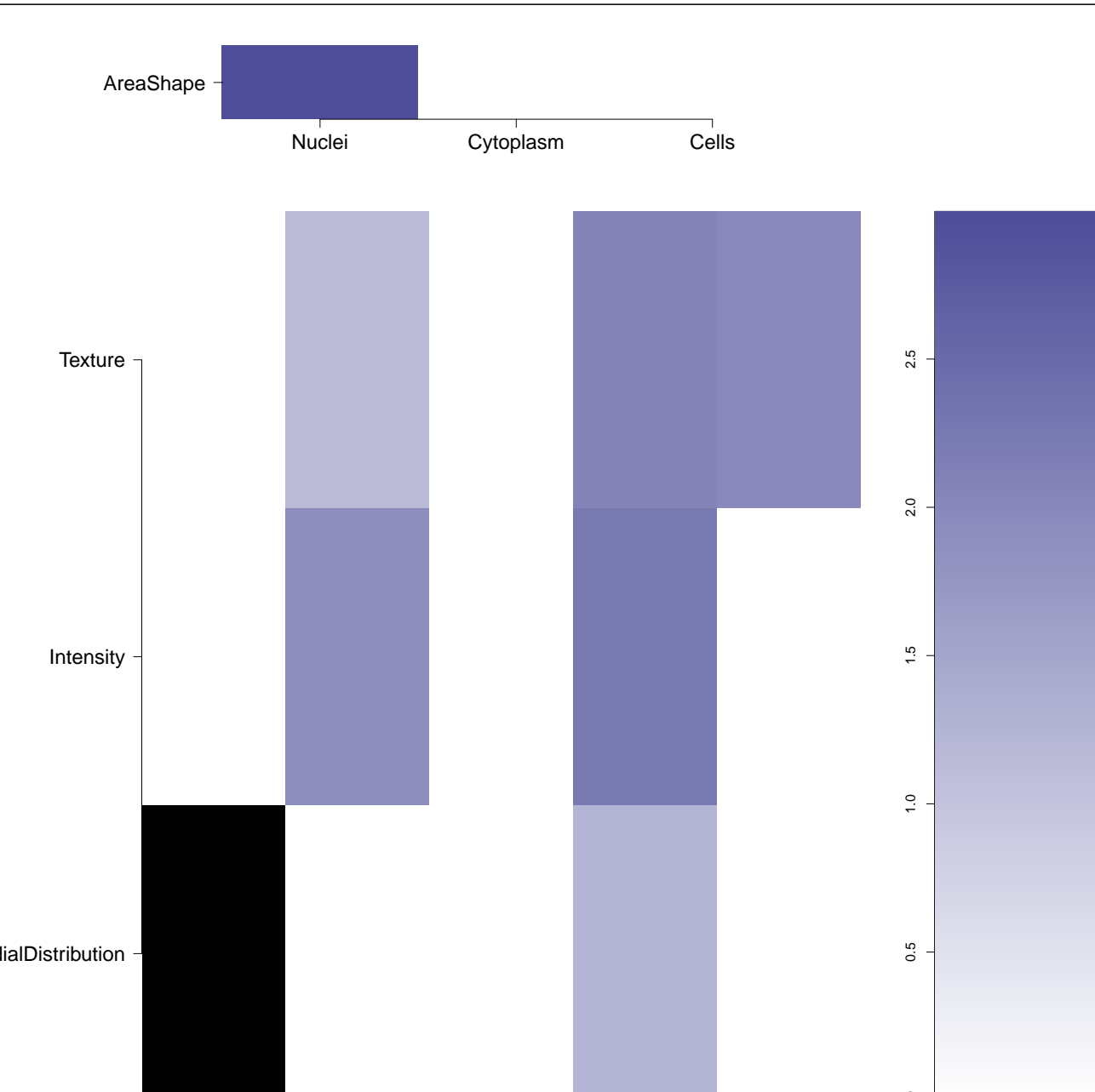

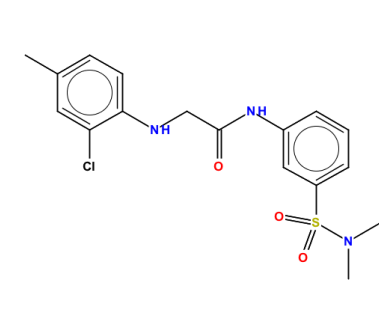
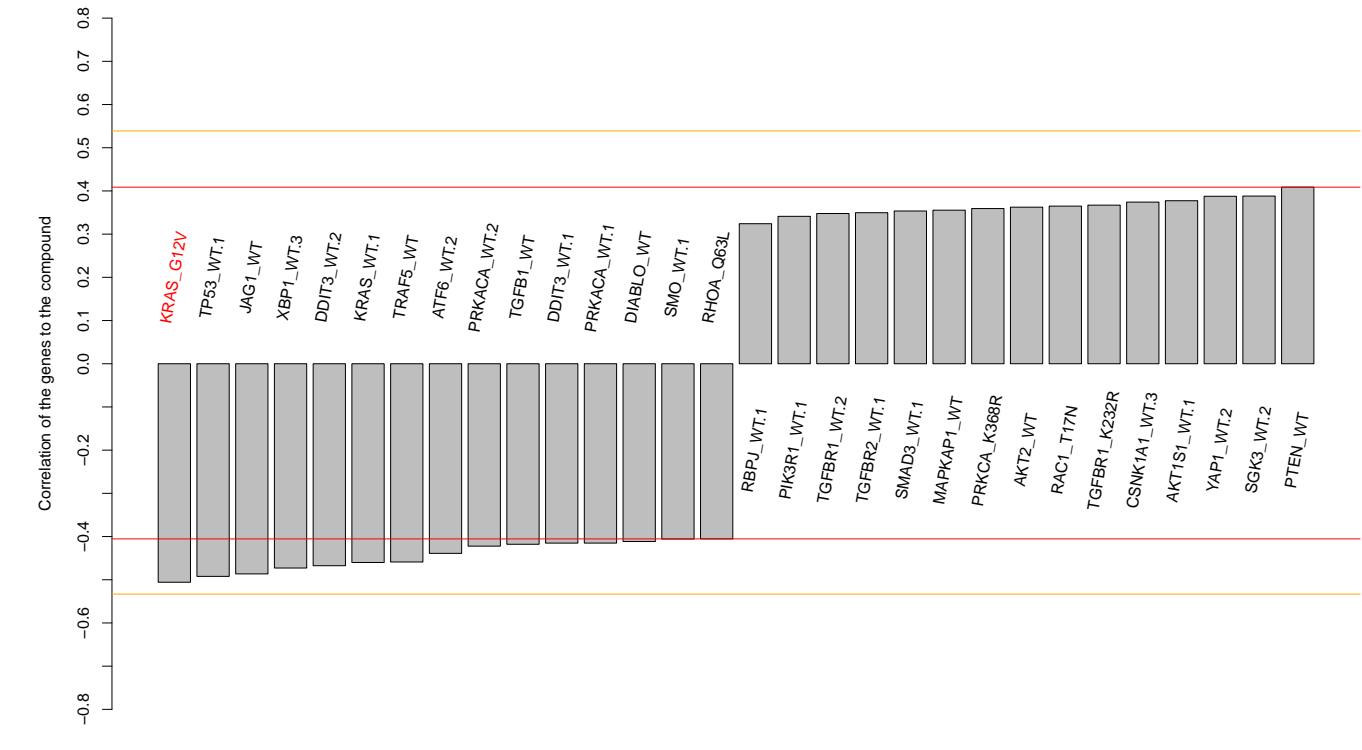
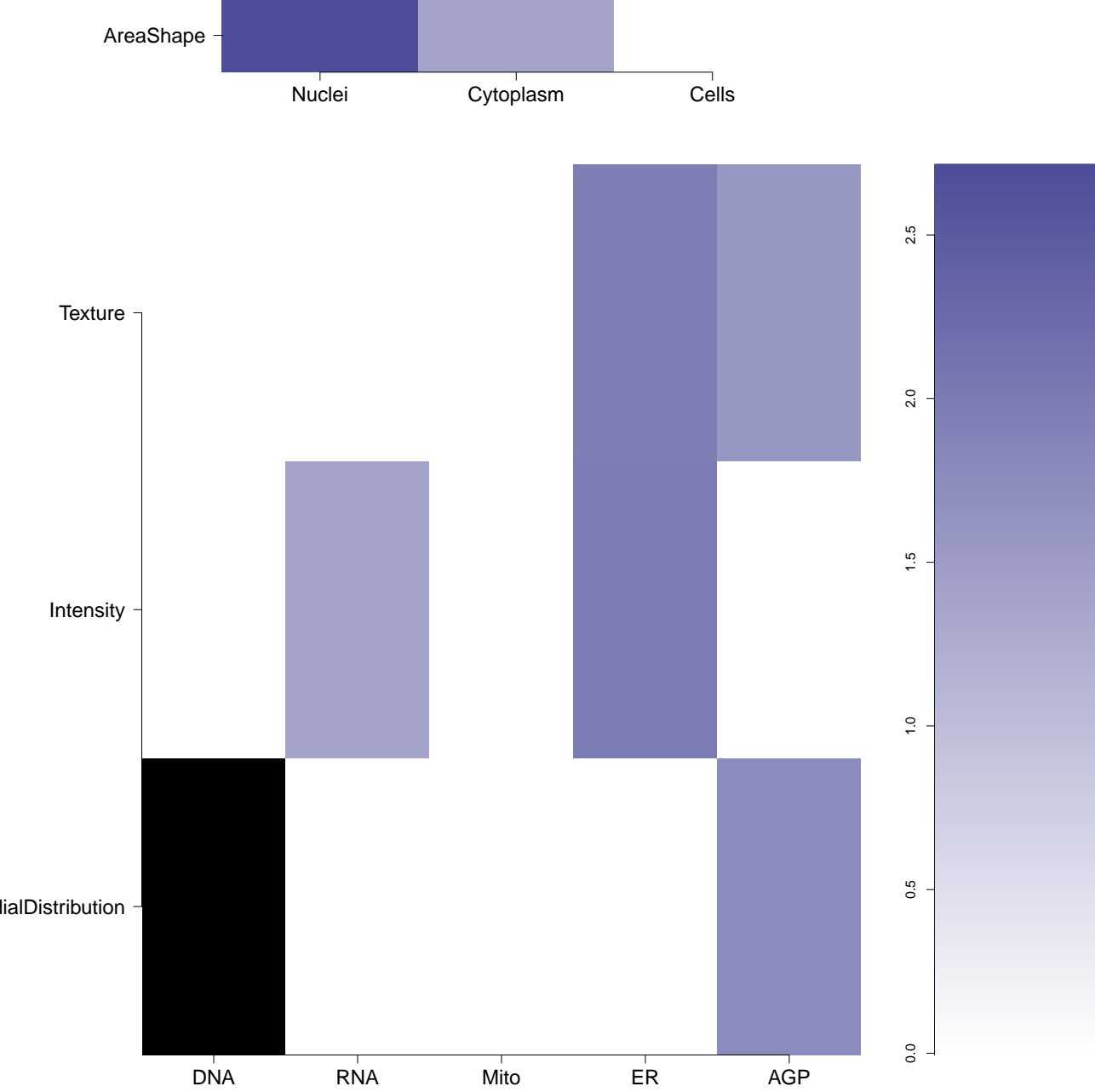

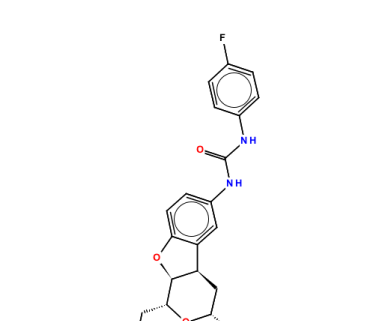
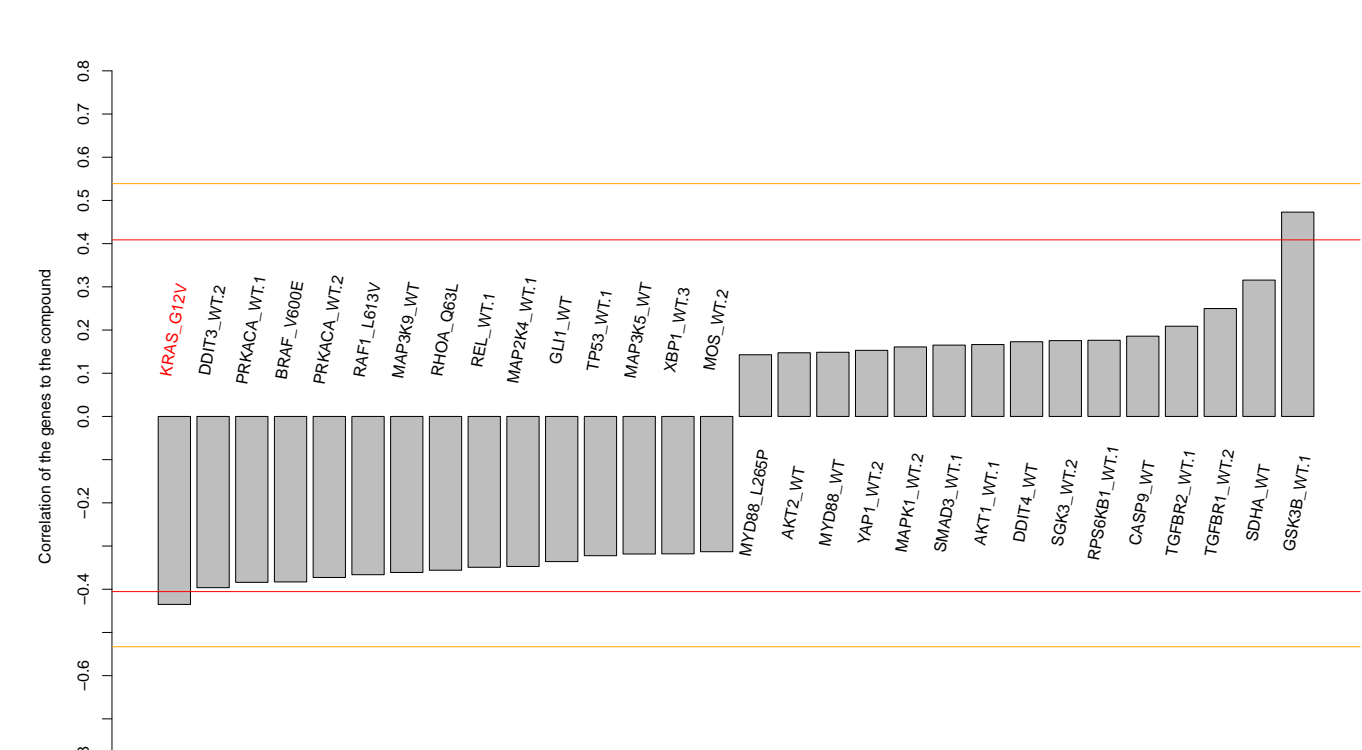
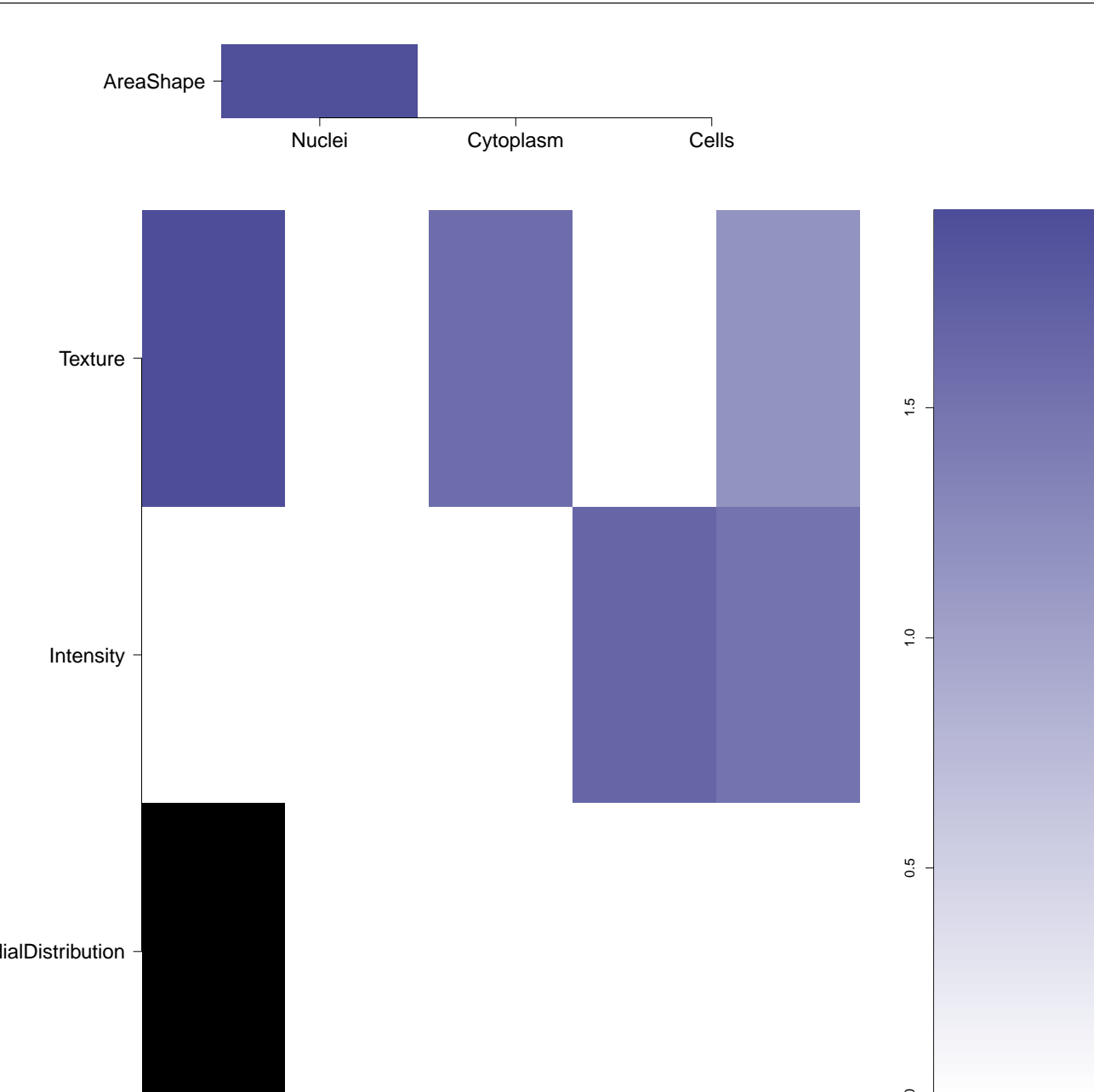
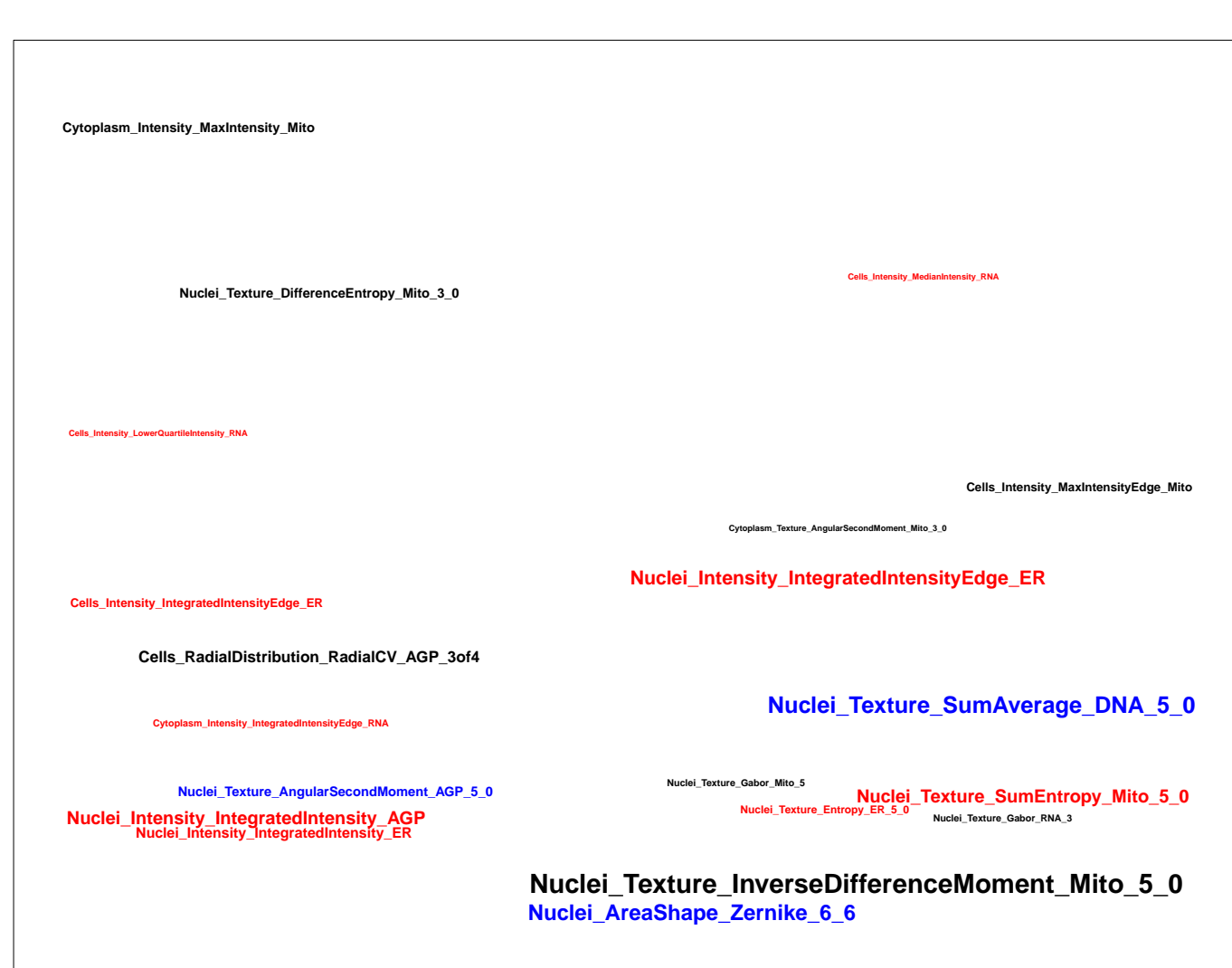


DNA



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 and 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-K63157607-001-01-2 PubChem CID : 54619030		0.88 (in 4 replicates)	0.54	0.935				Total number of assays tested in: 32.
BRD-K02063190-001-01-9 PubChem CID : 44493065		0.92 (in 2 replicates)	0.47	0.172				Total number of assays tested in: 50.
BRD-K54081441-001-01-5 PubChem CID : 44620446		0.79 (in 4 replicates)	0.46	0.876				Total number of assays tested in: 43.
BRD-K96773131-001-04-6 MLS000120577 AC1L19CF HMS1374104 ZINC4124879 CCG-117315 SMR000097430 PubChem CID : 900384		NA (in 1 replicates)	-0.57	NA				Total number of assays tested in: 788. Active in the following assays: <ul style="list-style-type: none"> <li>qHTS Assay for Inhibitors of RGS12 GoLoco Motif Activity (Red Fluorophore) (AID 880)</li> <li>qHTS Assay for Agonists of the Thyroid Stimulating Hormone Receptor (AID 926)</li> <li>qHTS Assay for Lipid Storage Modulators in Drosophila S3 Cells (AID 2685)</li> <li>qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)</li> </ul>
BRD-K29367859-001-05-6 T5324502 ZINC05262205 AC1NK3FS MLS000416581 HMS2515D15 HMS3376B17 ZINC5262205 SMR000243435 PubChem CID : 4881794		NA (in 1 replicates)	-0.51	NA				Total number of assays tested in: 635. Active in the following assays: <ul style="list-style-type: none"> <li>Leishmania - major promastigote HTS (AID 1063)</li> <li>Assay for HTS of Gi/Go-linked GPCRs using mGluR8: Primary Screening (AID 488969)</li> </ul>
BRD-K16792691-001-01-1 PubChem CID : 54645889		0.53 (in 2 replicates)	-0.44	0.305				Total number of assays tested in: 41.