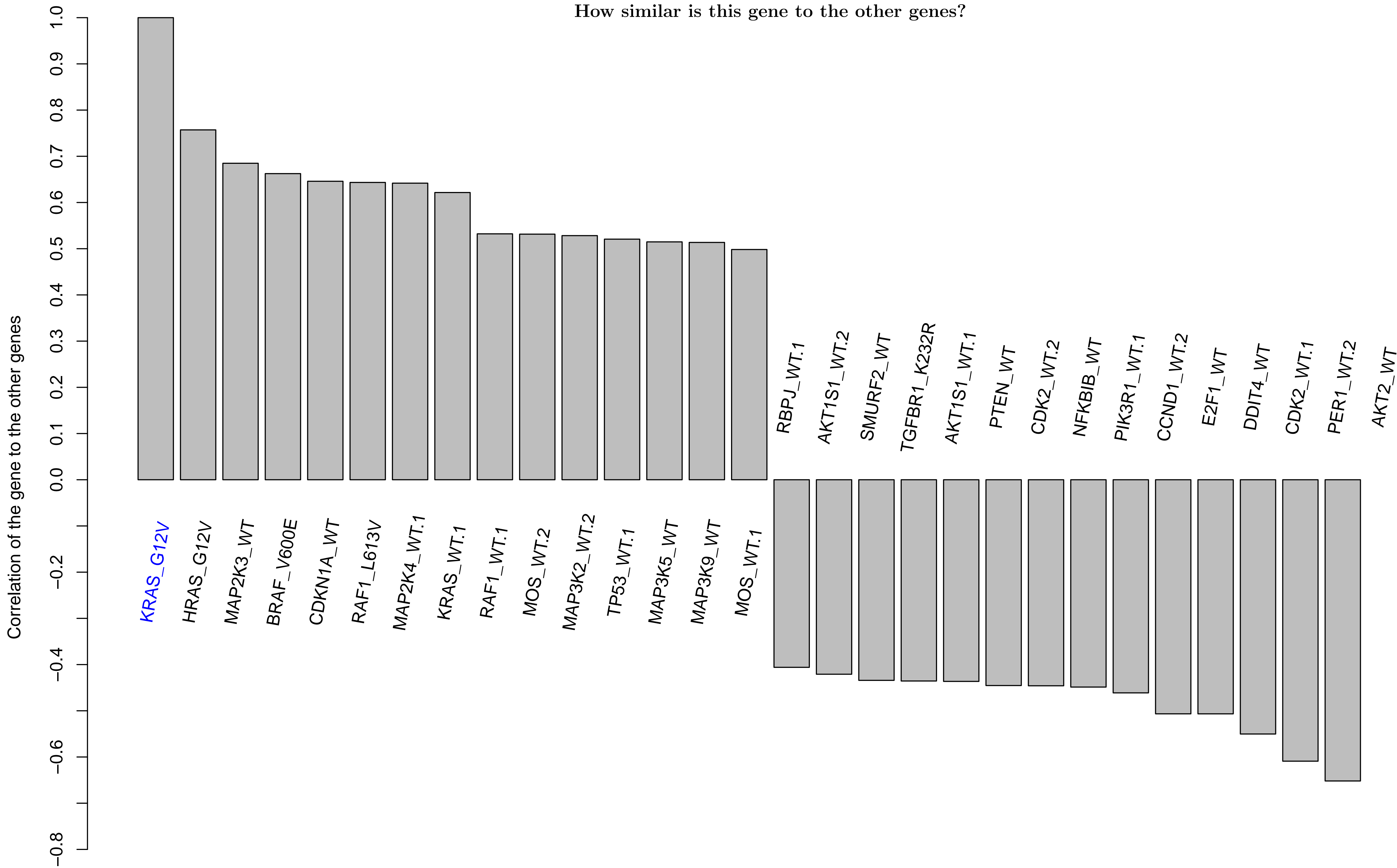
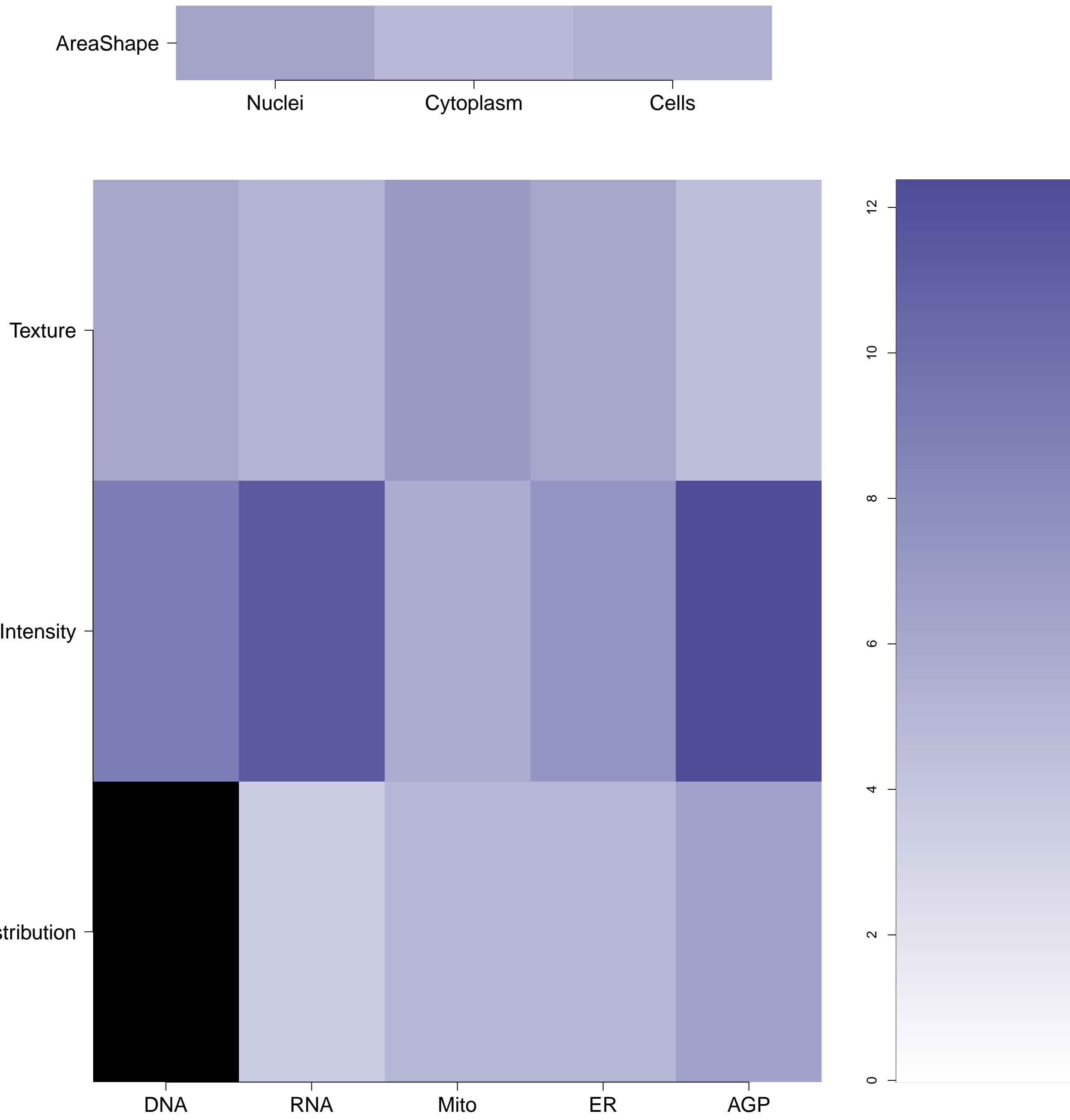


KRAS.G12V - in RTK

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)

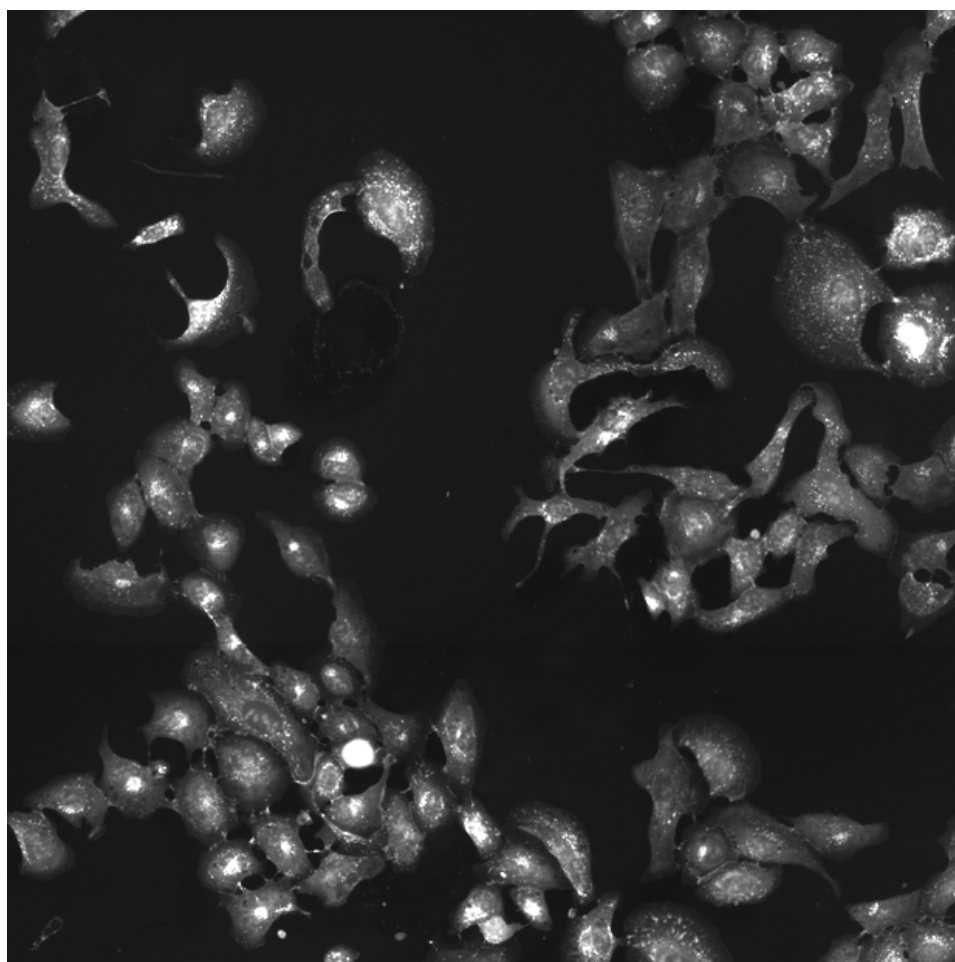
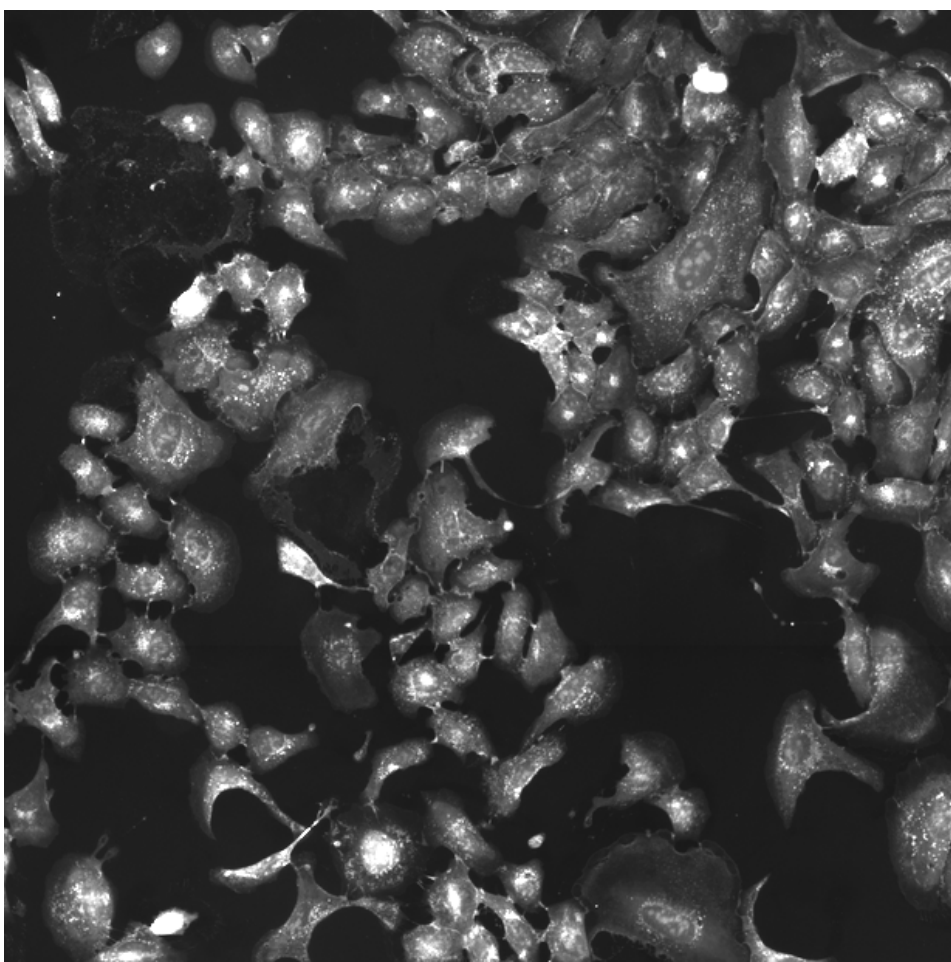
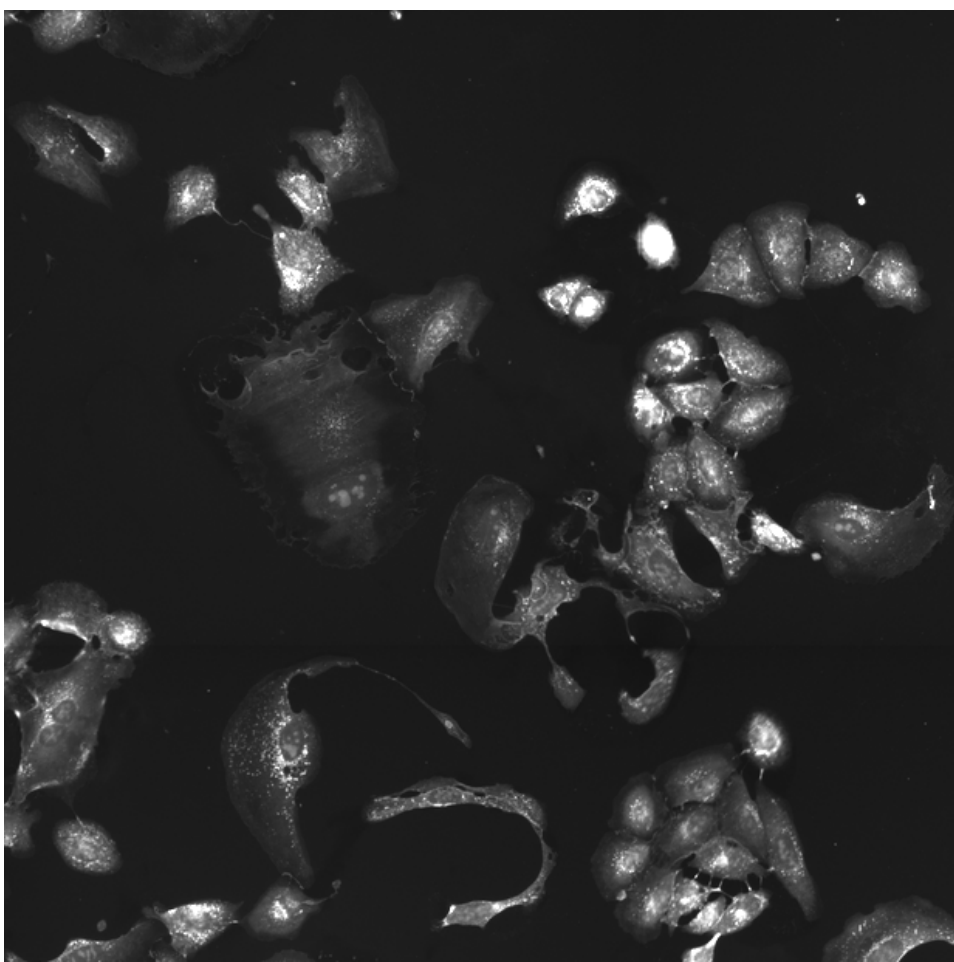
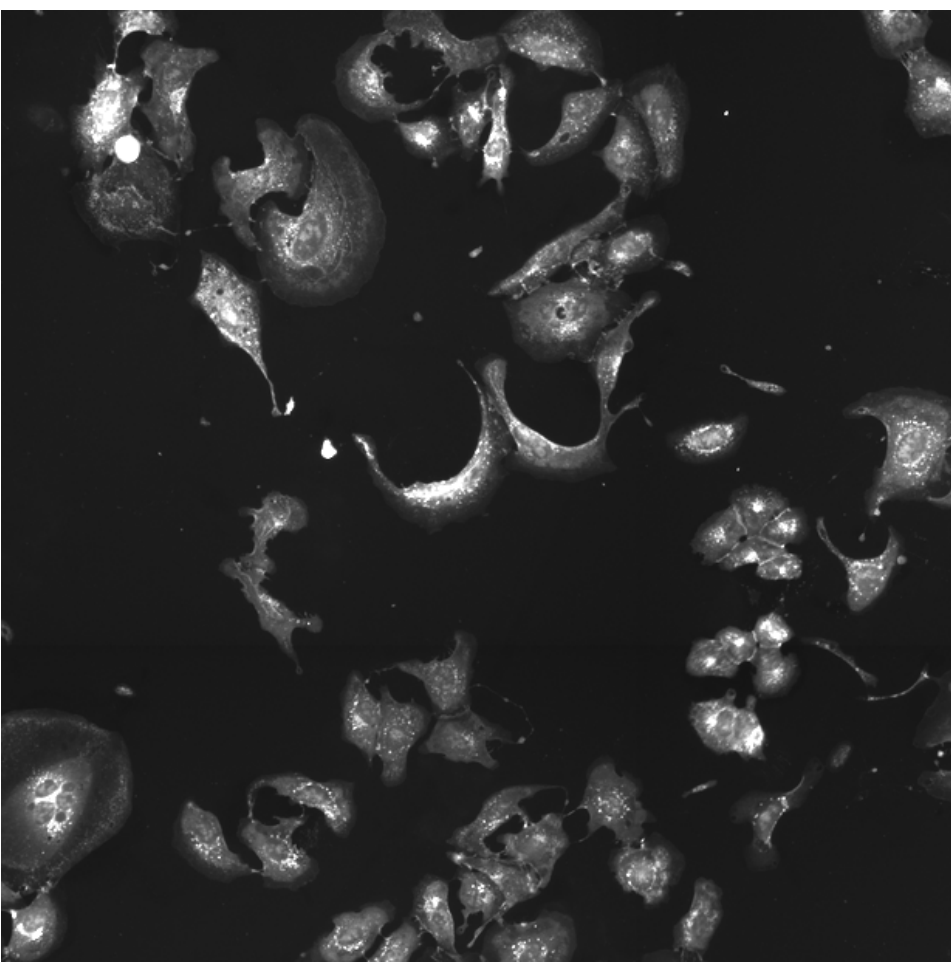
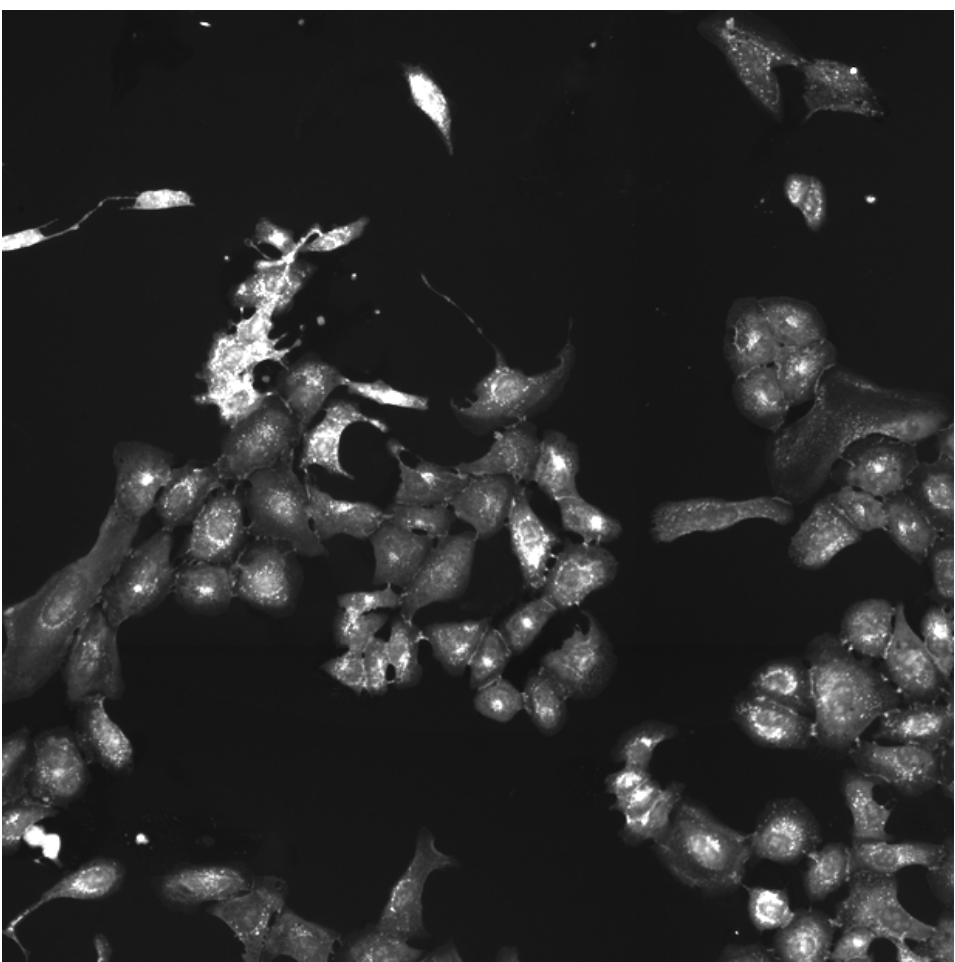
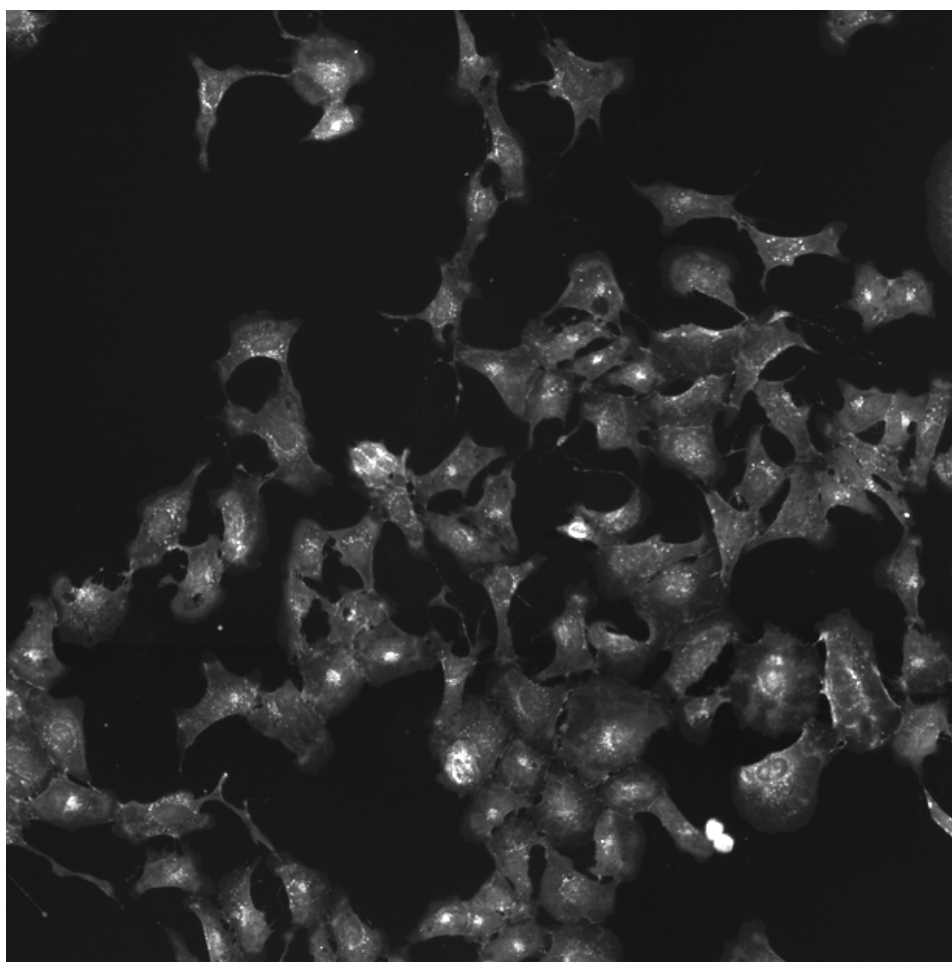
KRAS.G12V (41755)

KRAS.G12V (41756)

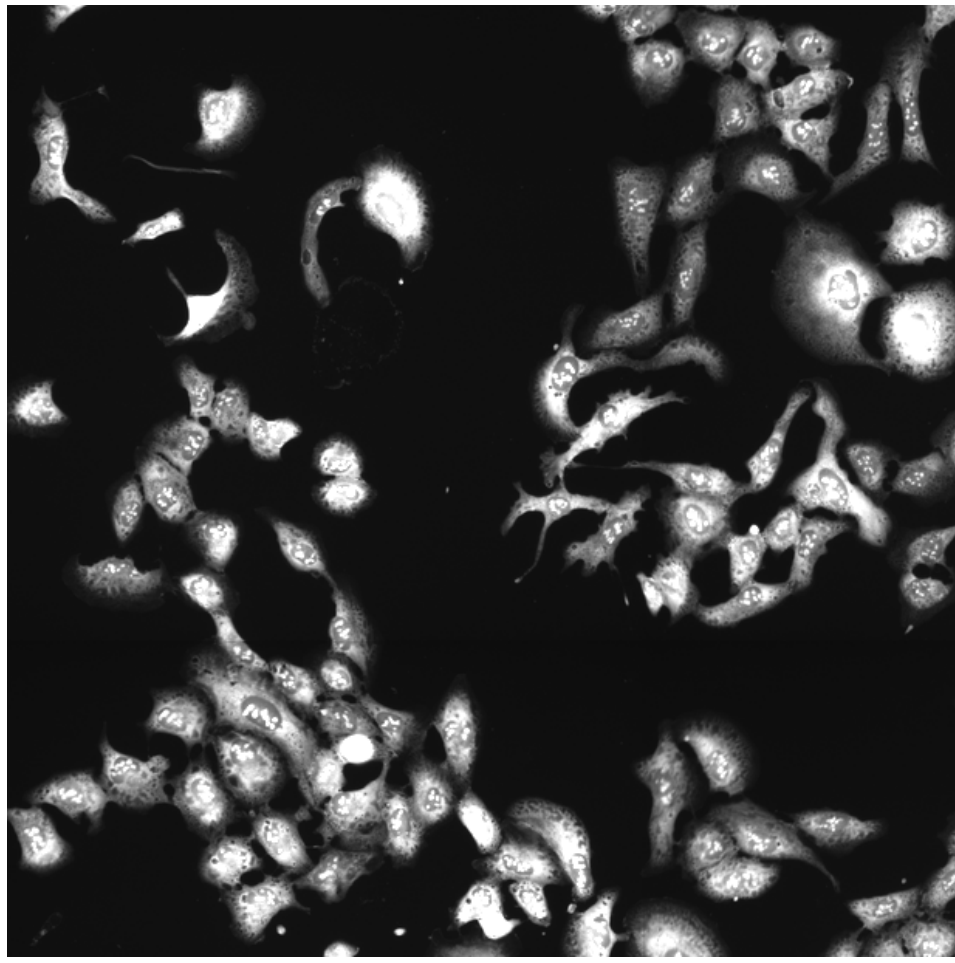
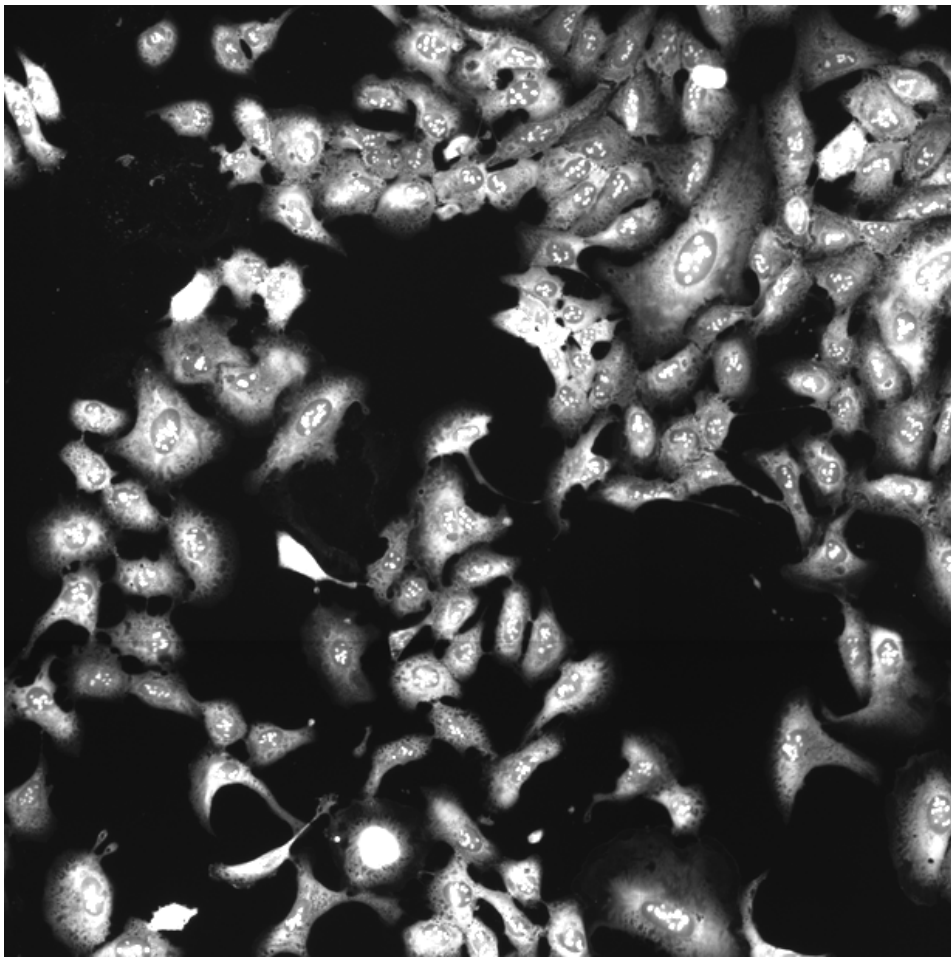
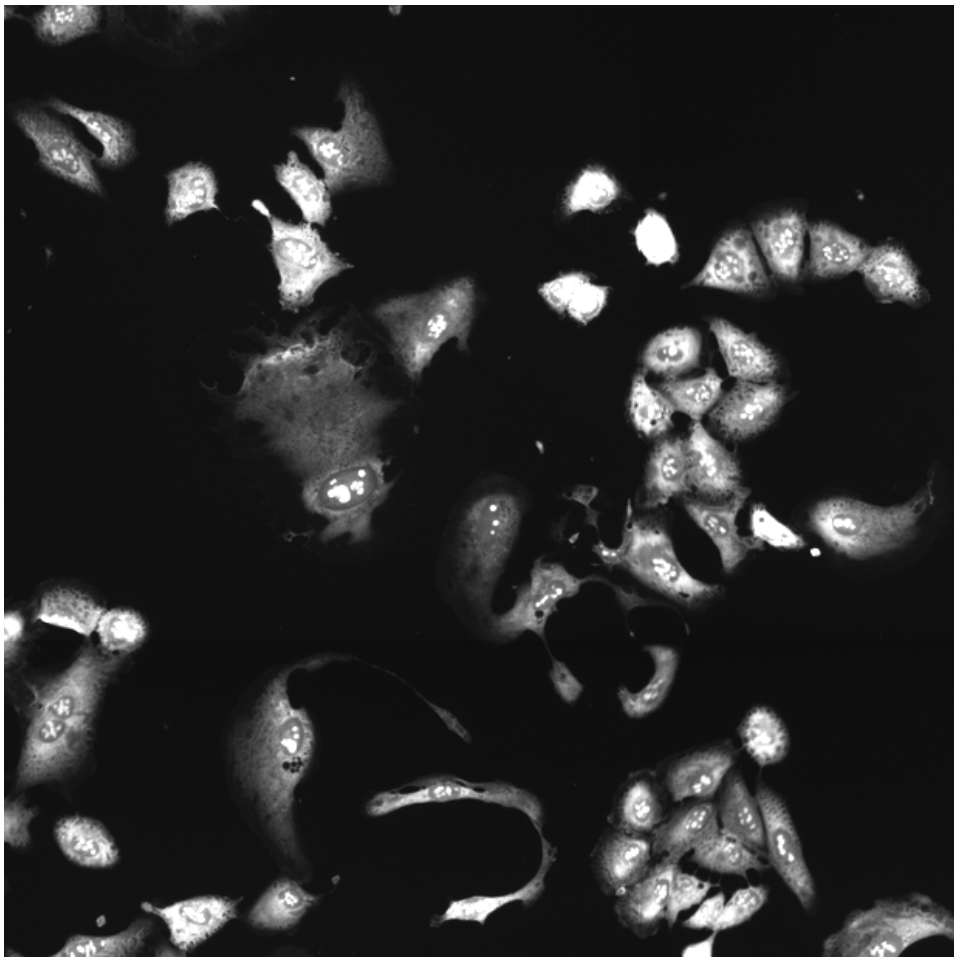
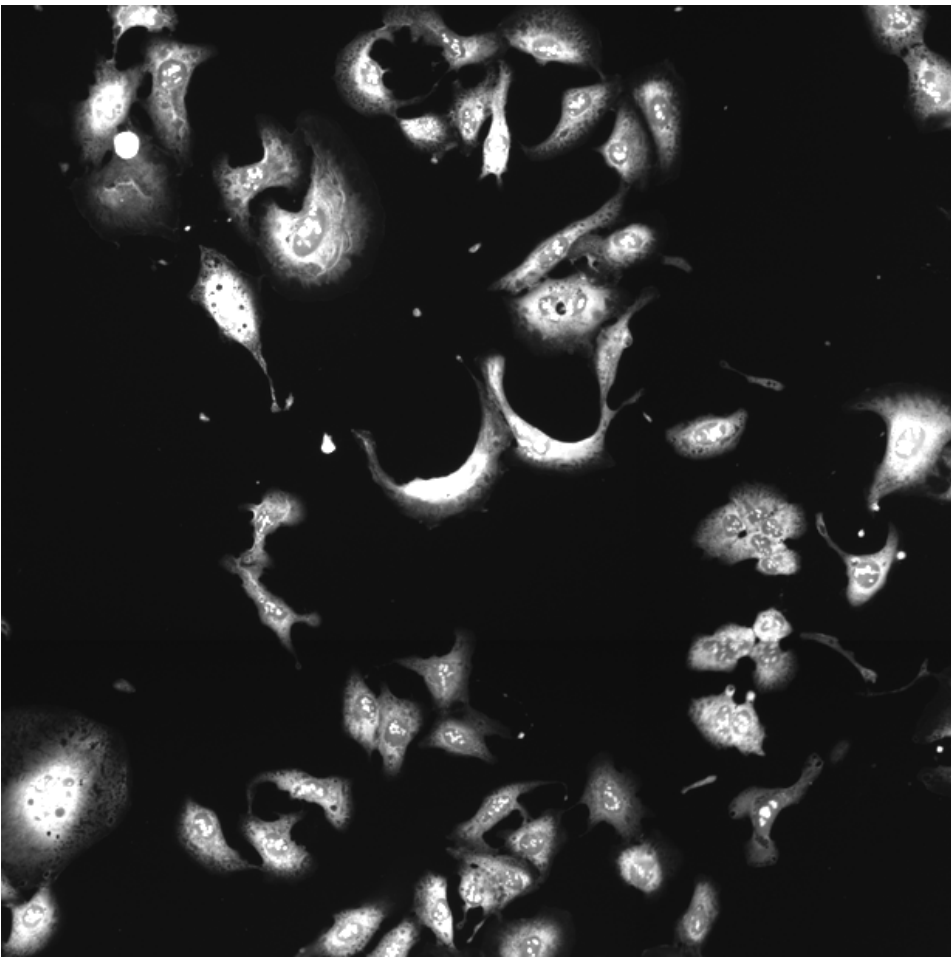
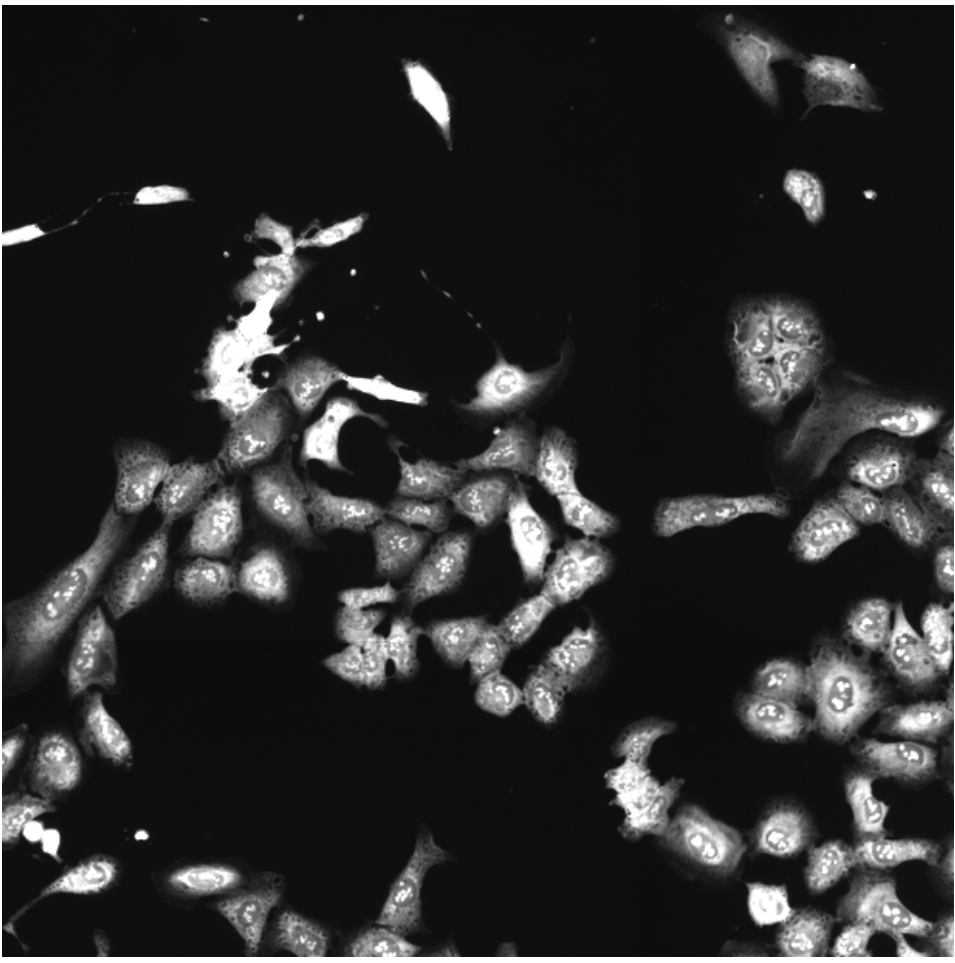
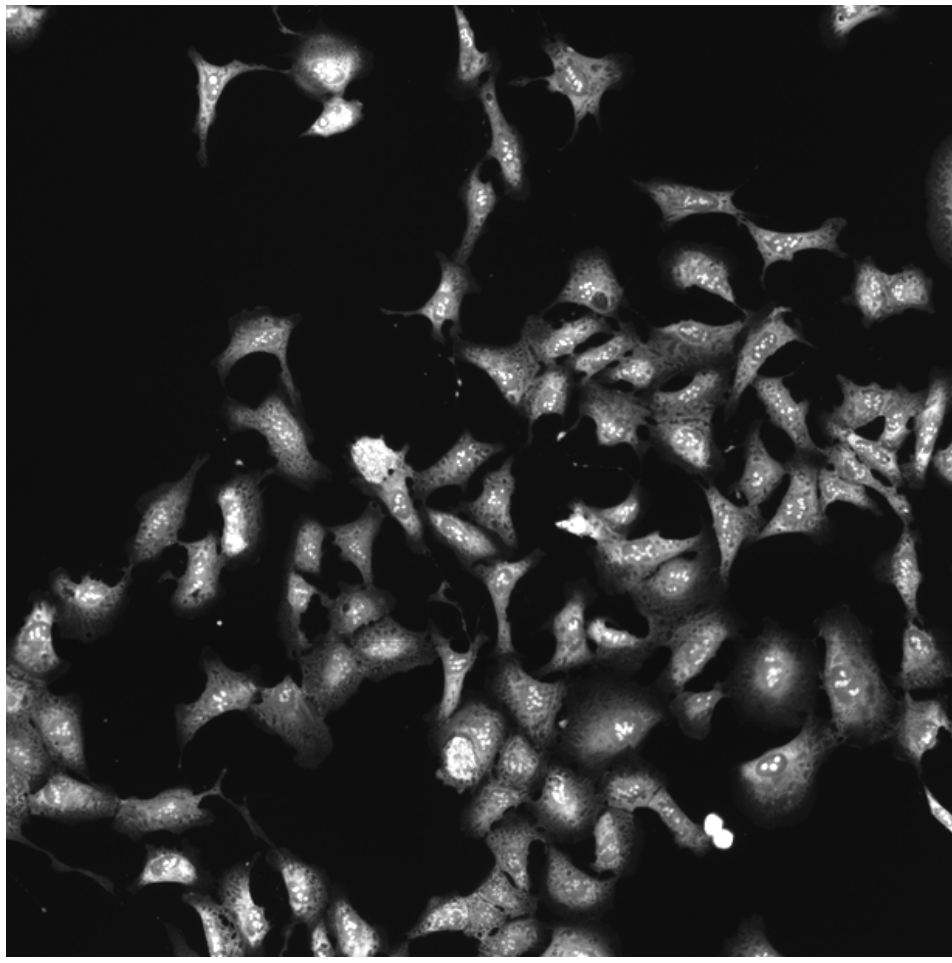
KRAS.G12V (41757)

KRAS.G12V (41754)

AGP

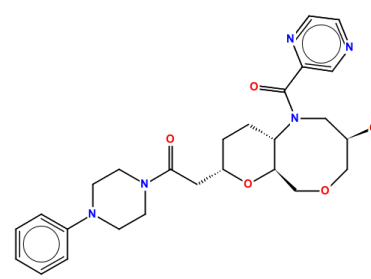
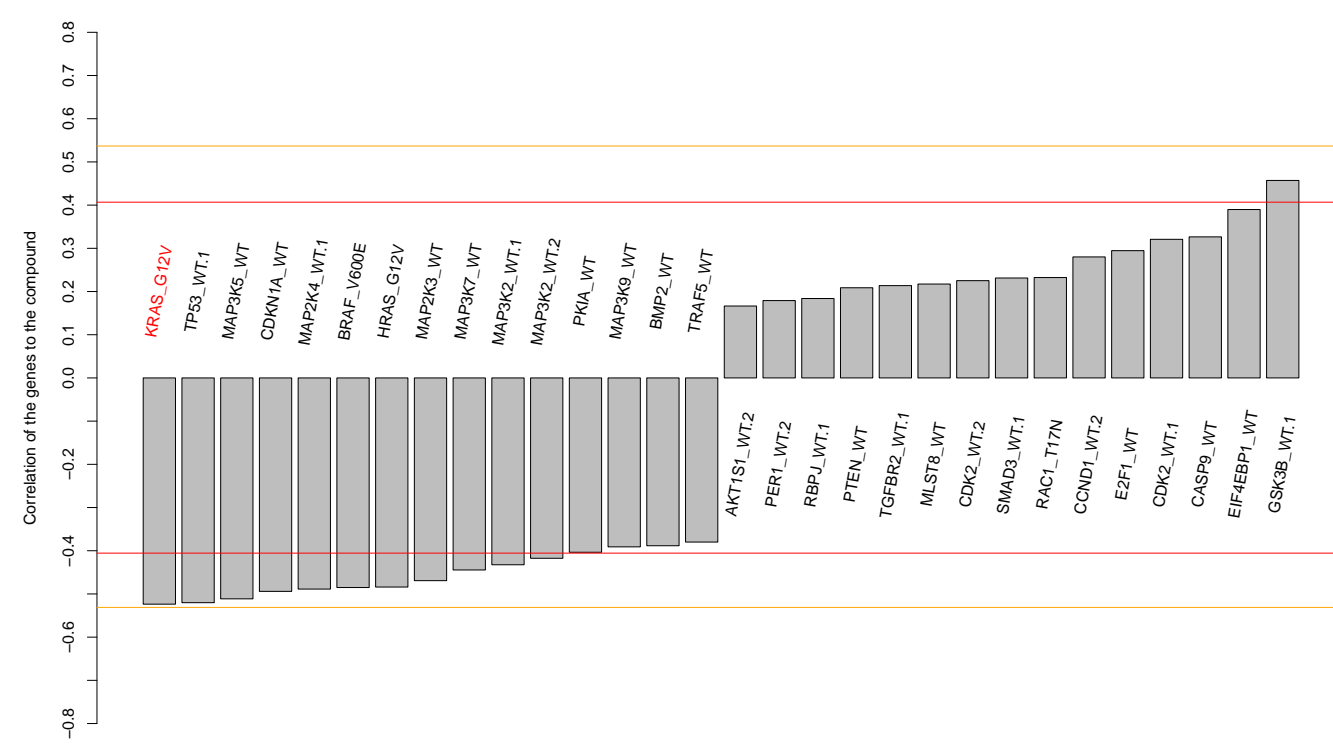
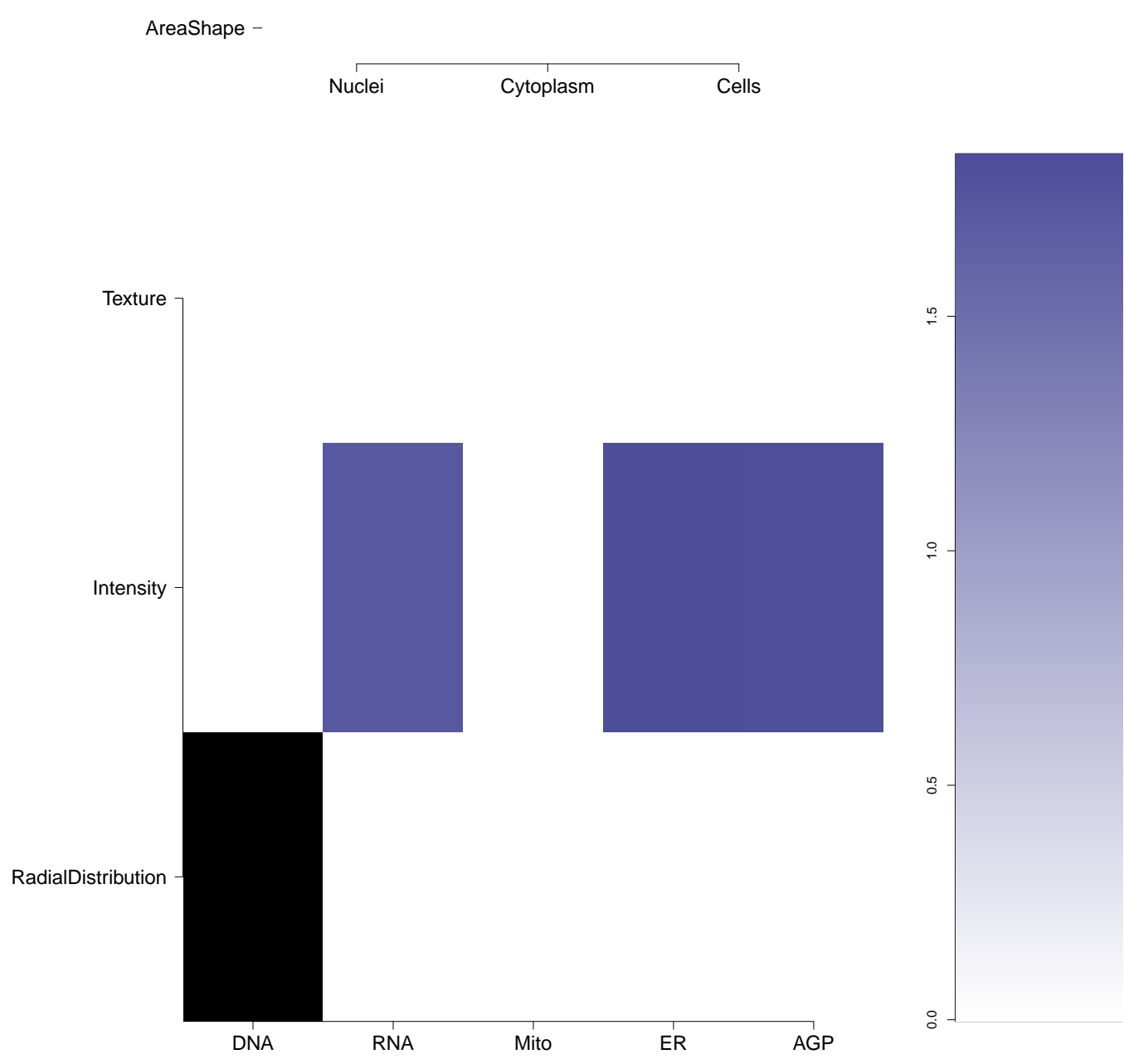

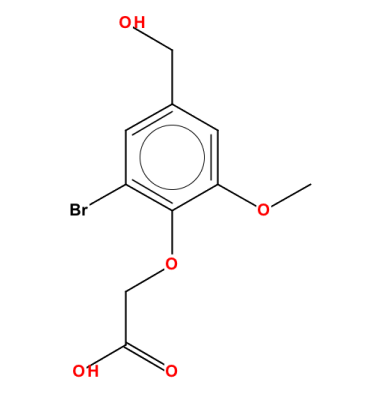
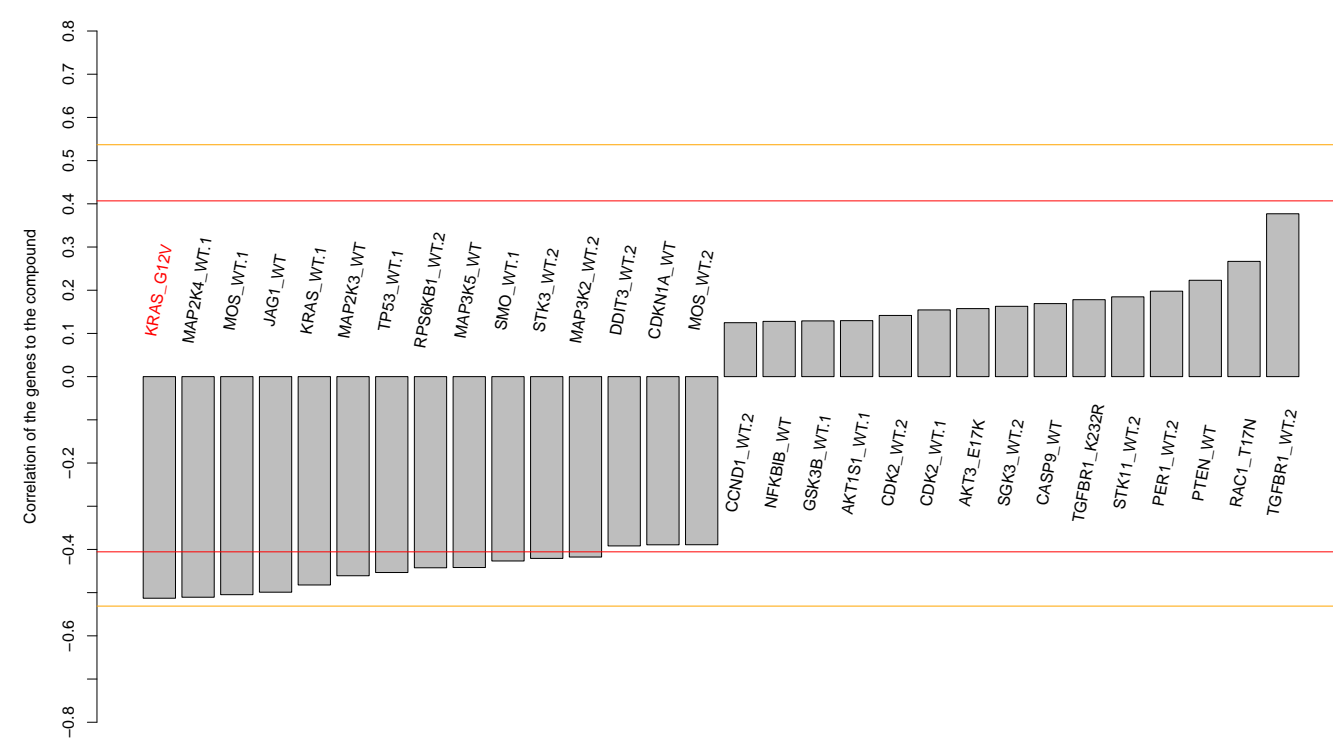
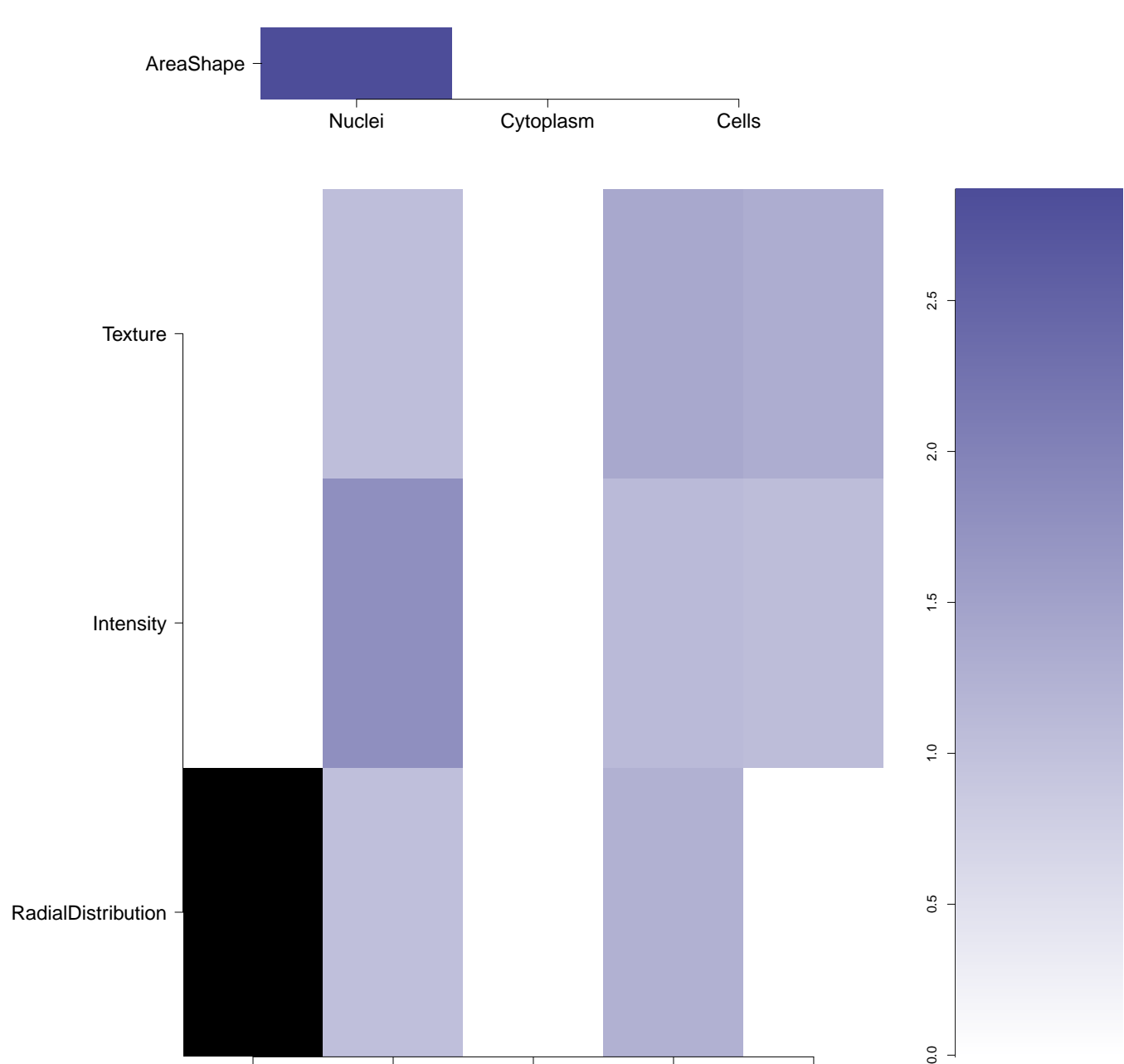

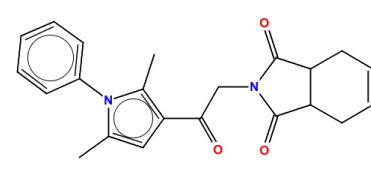
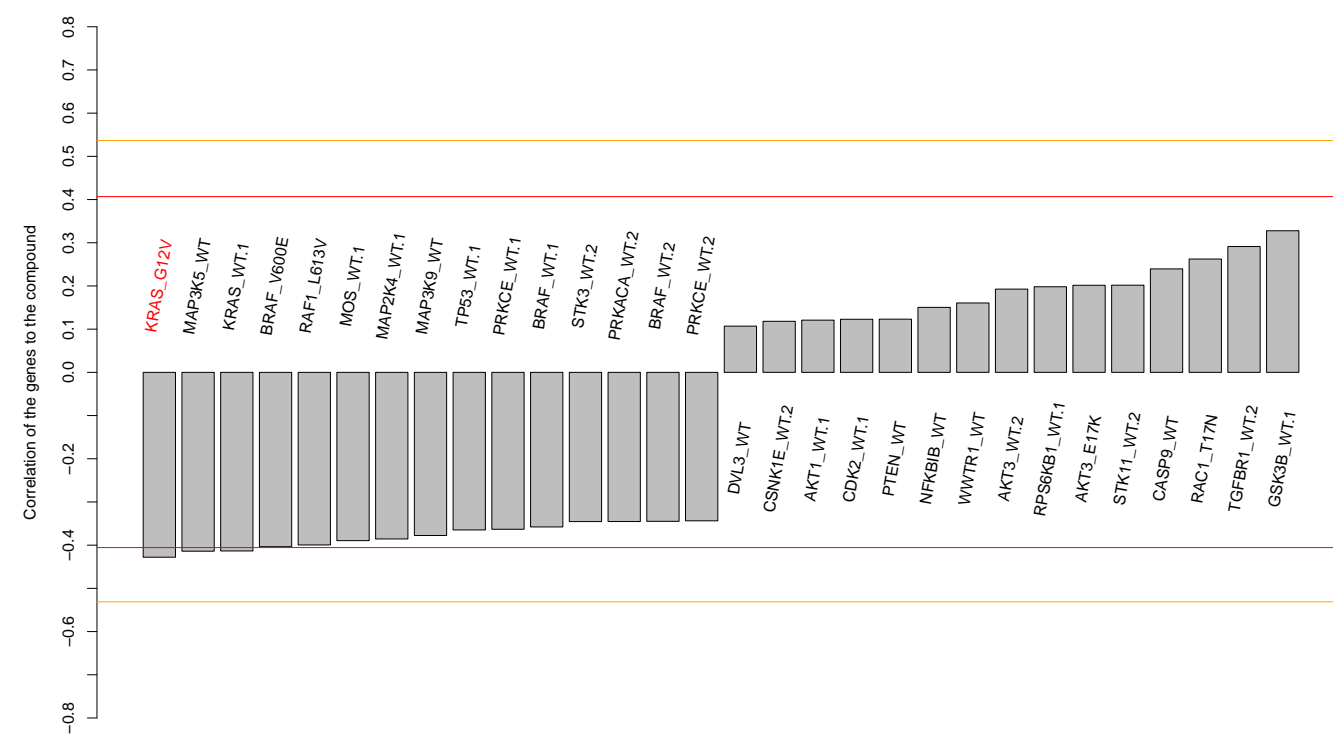
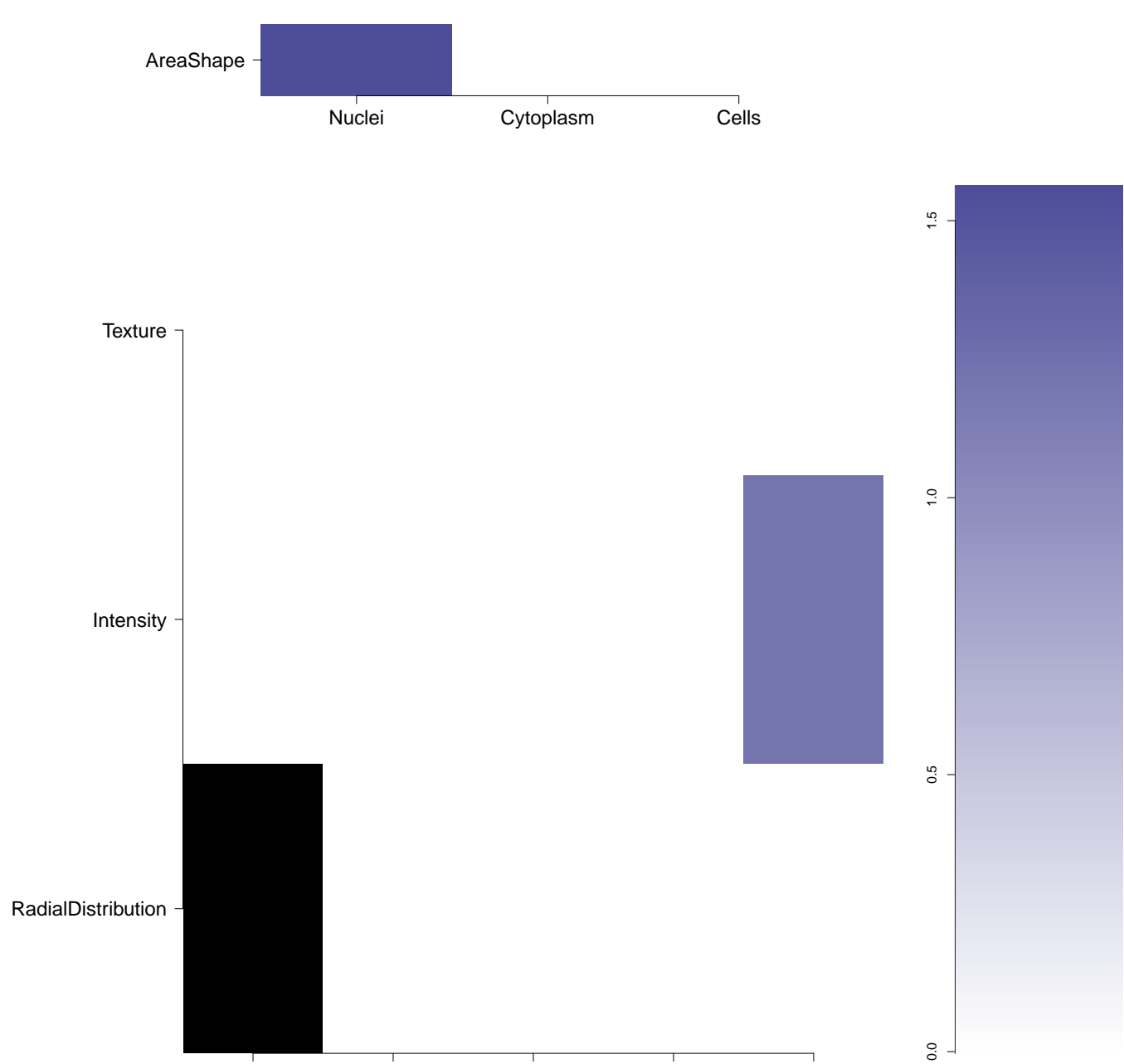
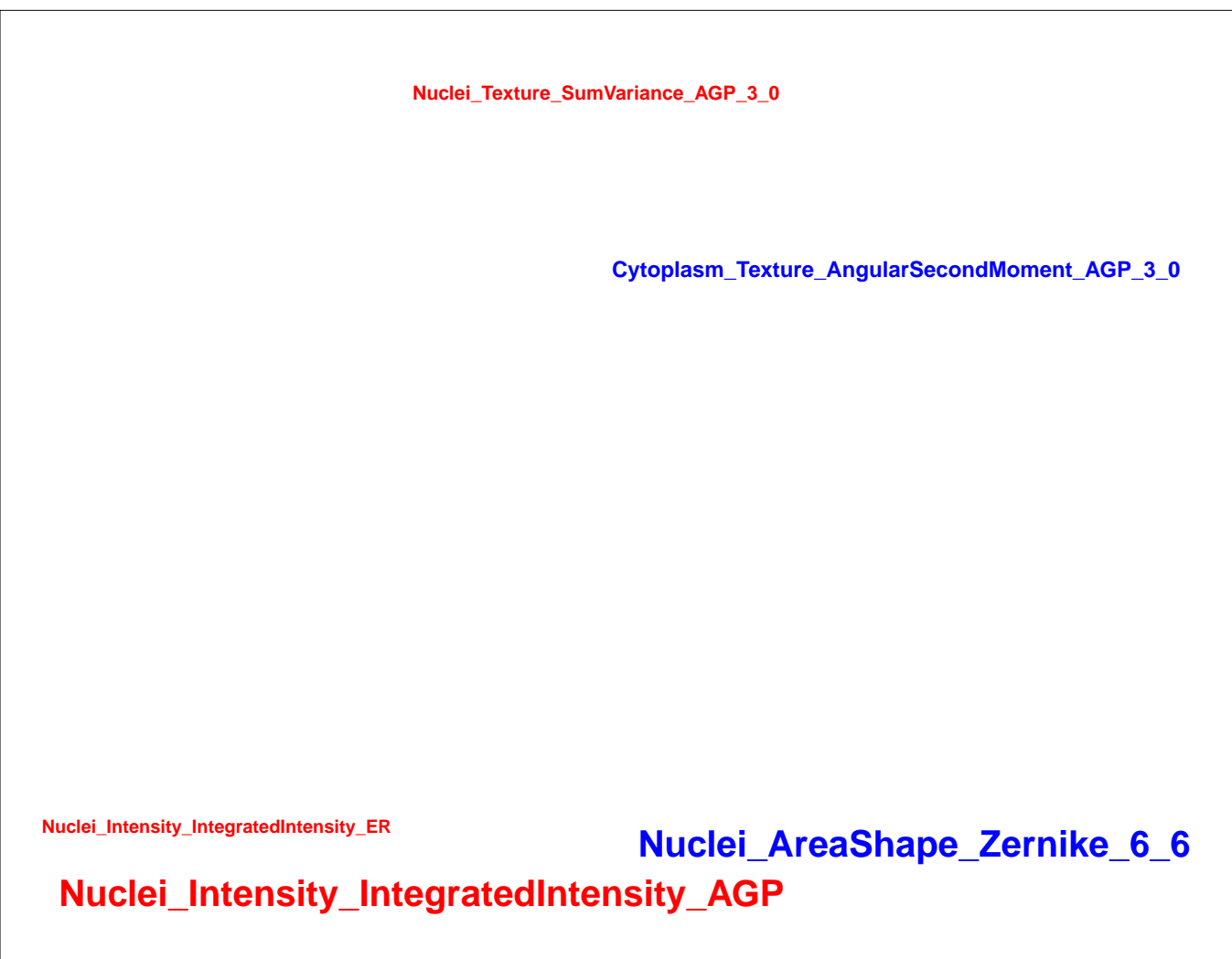
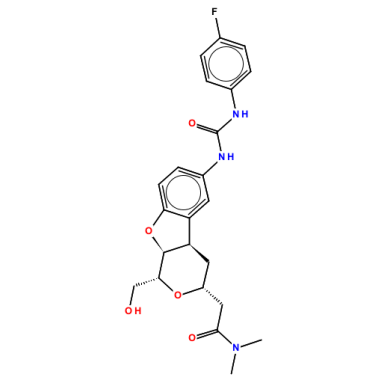
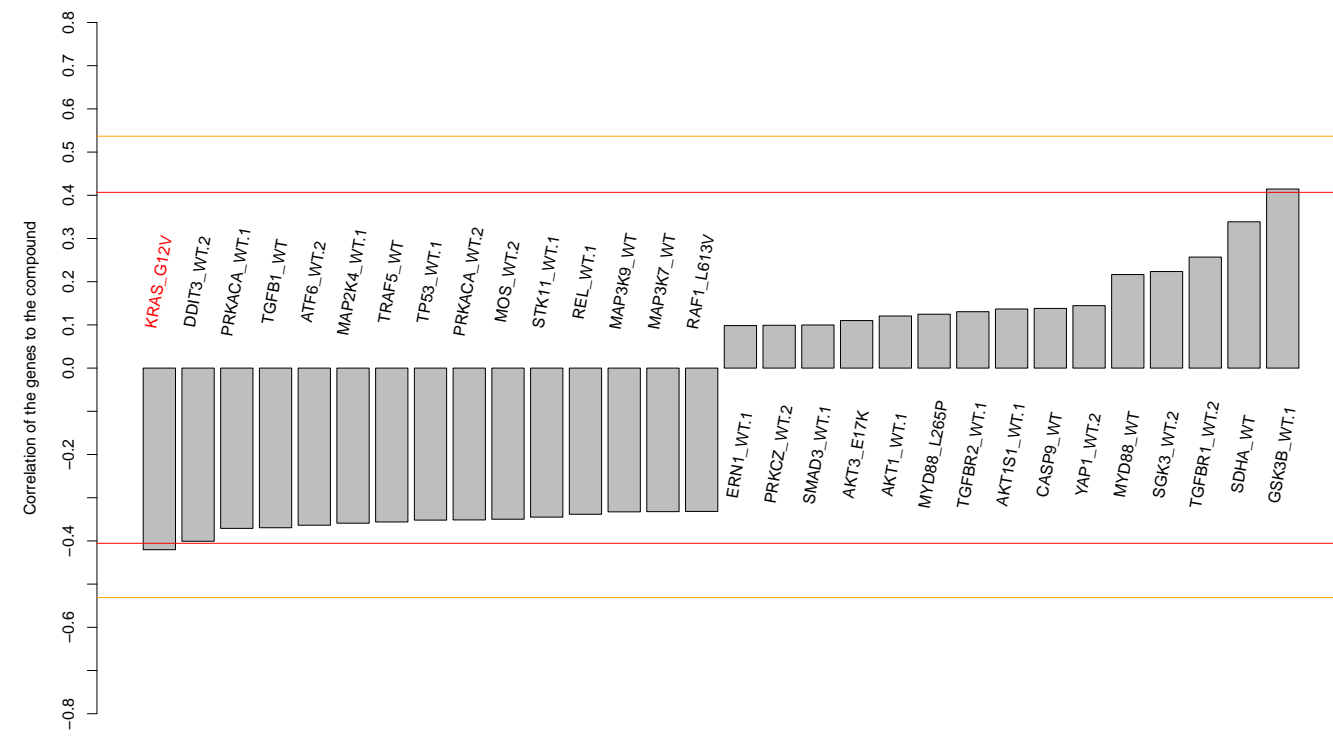
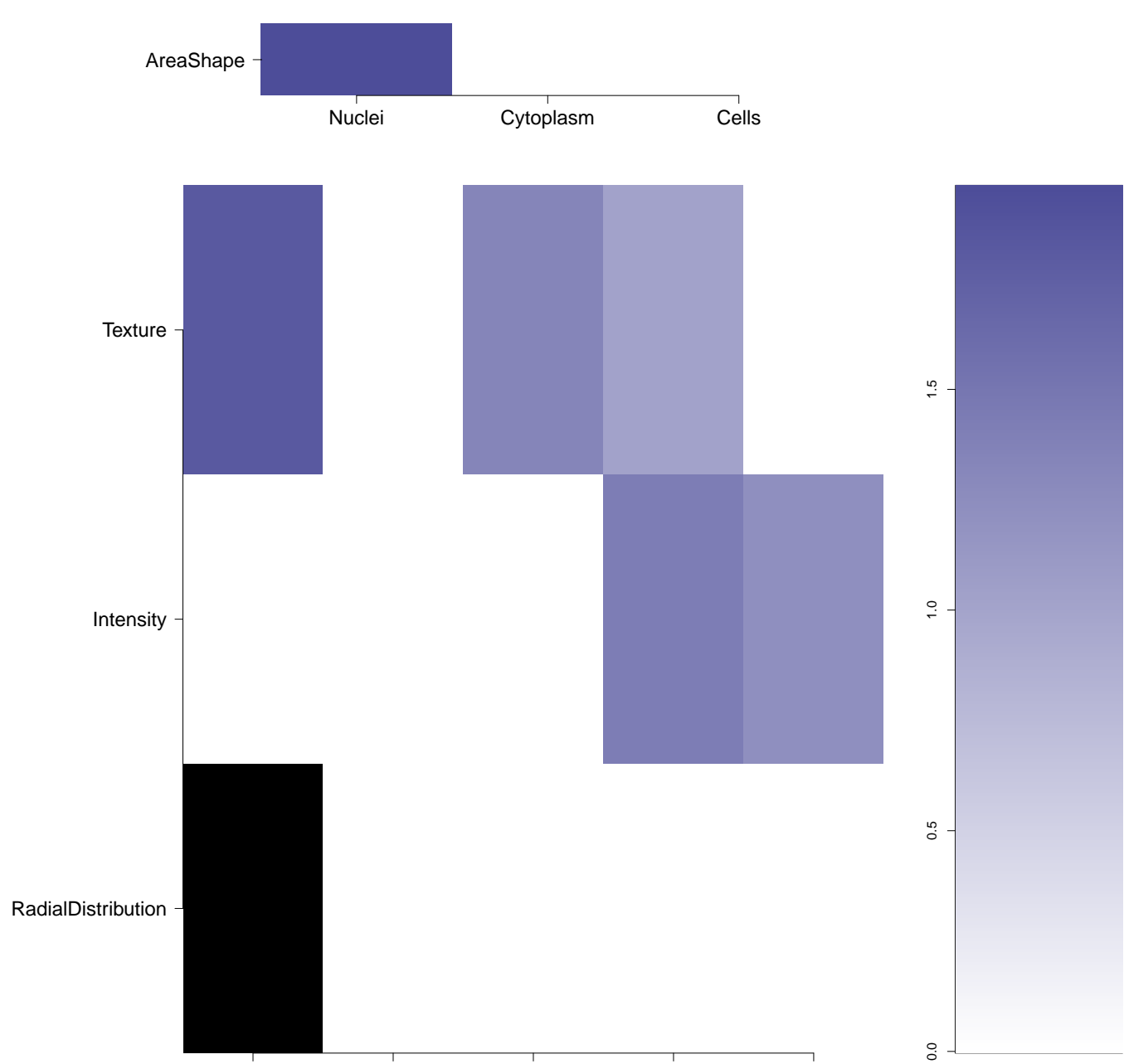
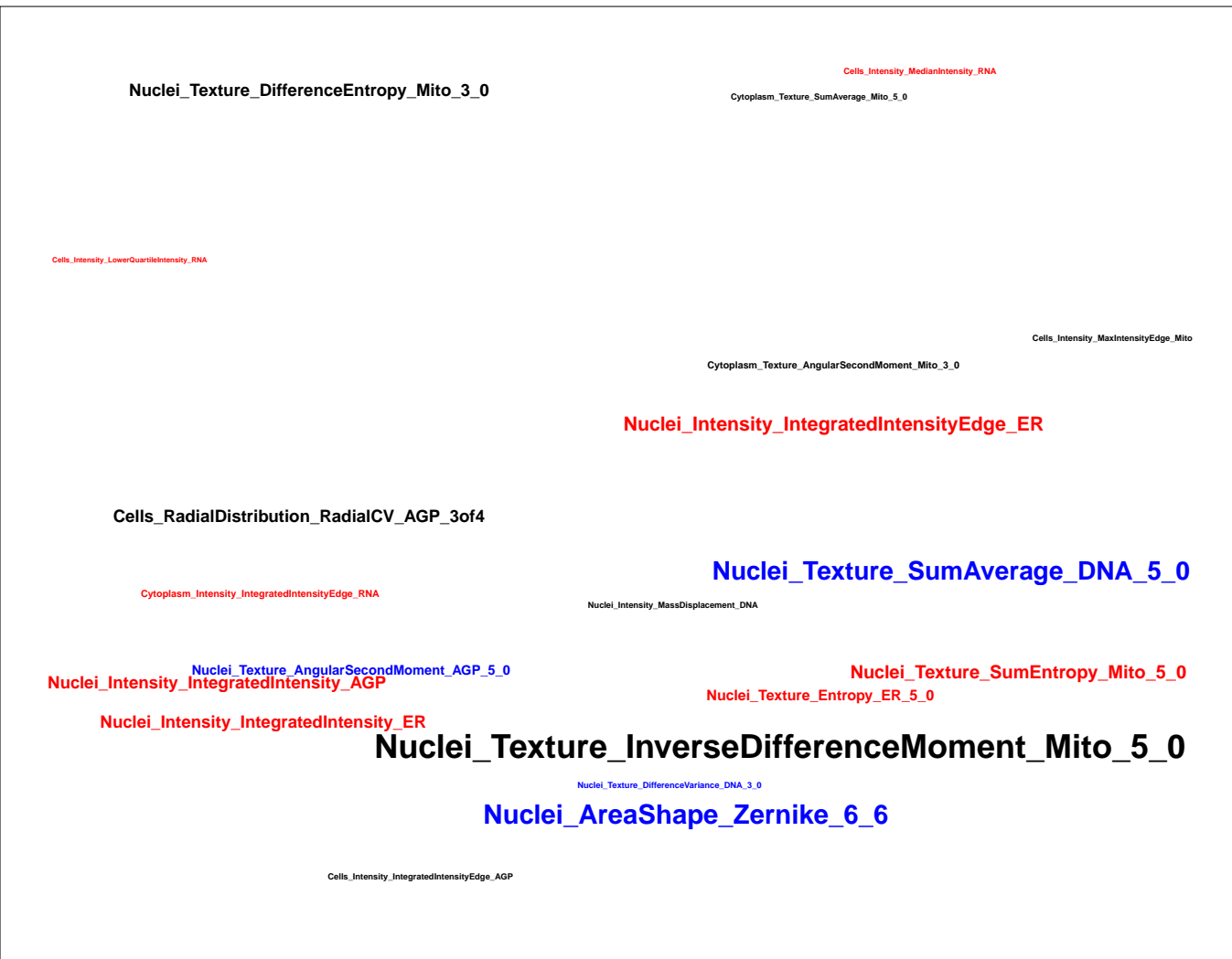


RNA



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 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
--	--------------------	--	---------------------------------------	--	---	---	---	---



<div>BRD-K83390709-001-01-2</div> <div>PubChem CID : 54657529</div>		0.58 (in 4 replicates)	-0.52	0.305				Total number of assays tested in: 39.
<div>BRD-K96773131-001-04-6</div> <div>MLS000120577</div> <div>AC1L9CF</div> <div>HMS1374I04</div> <div>HMS2266L11</div> <div>ZINC4124879</div> <div>CCG-117315</div> <div>SMR000097430</div> <div>PubChem CID : 900384</div>		NA (in 1 replicates)	-0.51	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>
<div>BRD-A23679683-001-06-2</div> <div>SMR000064586</div> <div>MLS000048358</div> <div>AC1MHCZO</div> <div>MLS002634818</div> <div>HMS1764A13</div> <div>HMS2404I22</div> <div>T5334992</div> <div>PubChem CID : 3000139</div>		0.57 (in 4 replicates)	-0.43	NA				Total number of assays tested in: 771. Active in the following assays: <ul style="list-style-type: none"><li>• Pyruvate Kinase (AID 361)</li><li>• qHTS Assay for Inhibitors of Firefly Luciferase (AID 411)</li><li>• Allosteric Modulators of D1 Receptors: Primary Screen (AID 641)</li><li>• qHTS Screen for Compounds that Selectively Target Cancer Cells with p53 Mutations: Cytotoxicity of p53ts Cells at the Nonpermissive Temperature (AID 902)</li><li>• qHTS Screen for Compounds that Selectively Target Cancer Cells with p53 Mutations: Cytotoxicity of p53ts Cells at the Permissive Temperature (AID 924)</li><li>• Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932)</li><li>• Counter Screen for Luciferase-based Primary Inhibition Assays (AID 1006)</li><li>• qHTS Assay for Inhibitors of Aldehyde Dehydrogenase 1 (ALDH1A1) (AID 1030)</li><li>• Primary screen for compounds that activate Alzheimer's amyloid precursor (AID 1276)</li><li>• Identification of compounds which are cytotoxic to PPC-1 cells. (AID 1447)</li><li>• Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)</li><li>• A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)</li><li>• VP166 counterscreen qHTS for inhibitors of ROR gamma transcriptional activity (AID 2546)</li><li>• uHTS identification of small molecule inhibitors of tin10 yeast via a luminescent assay (AID 463195)</li><li>• qHTS Assay for Rab9 Promoter Activators (AID 485297)</li><li>• qHTS Assay for NPC1 Promoter Activators (AID 485313)</li><li>• qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342)</li><li>• uHTS identification of modulators of interaction between CendR and NRP-1 using Fluorescence Polarization assay (AID 602438)</li><li>• uHTS identification of Caspase-8 TRAIL sensitizers in a luminescence assay (AID 624354)</li><li>• qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 686978)</li><li>• qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in presence of CPT (AID 686979)</li><li>• Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glycines (tgDAF-12). (AID 687014)</li><li>• Wnt/Beta-catenin HTS Measured in Cell-Based System Using Plate Reader - 2161-01 Activator SinglePoint HTS Activity (AID 743398)</li></ul>
<div>BRD-K16792691-001-01-1</div> <div>PubChem CID : 54645889</div>		0.52 (in 2 replicates)	-0.42	0.305				Total number of assays tested in: 41.