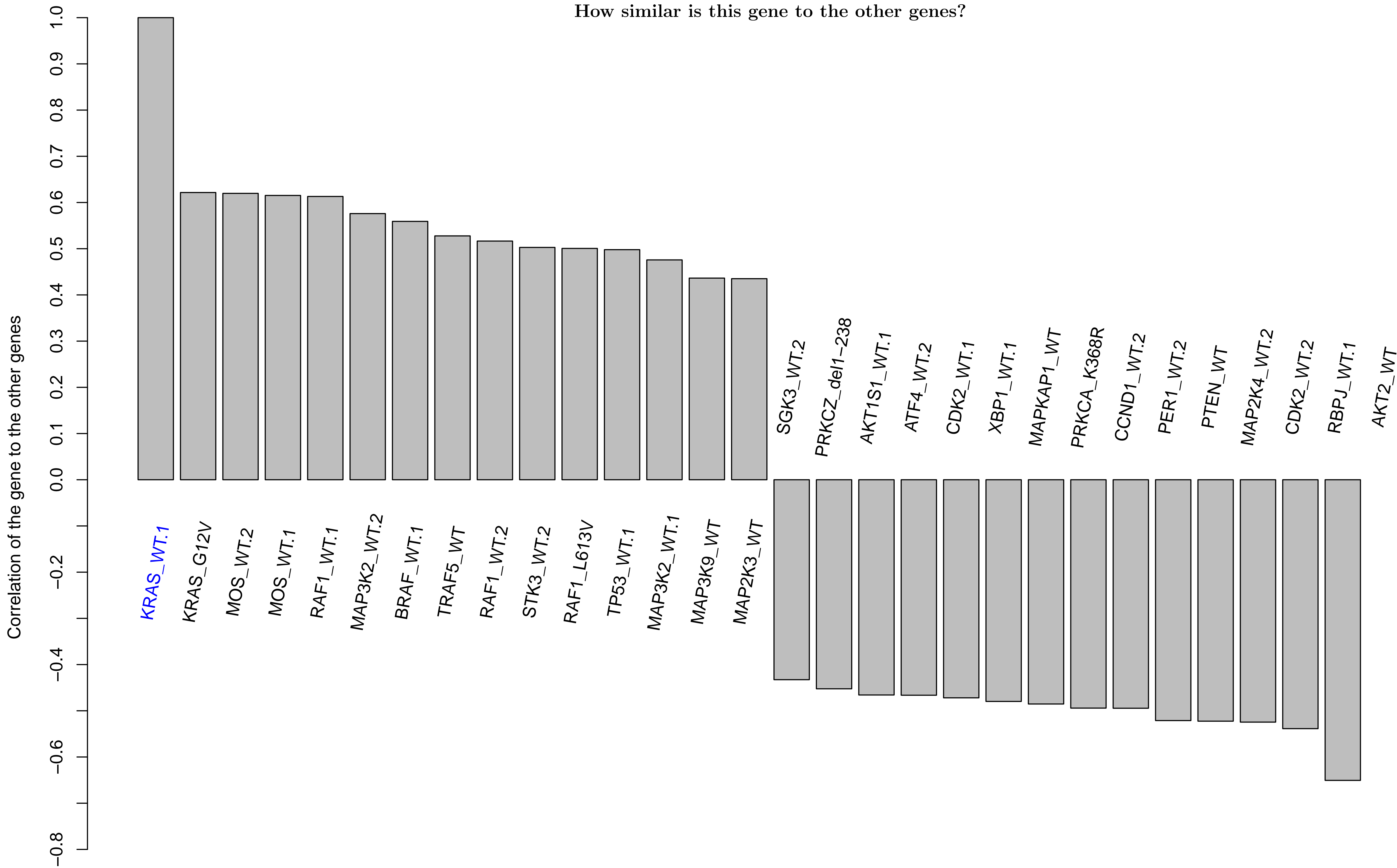
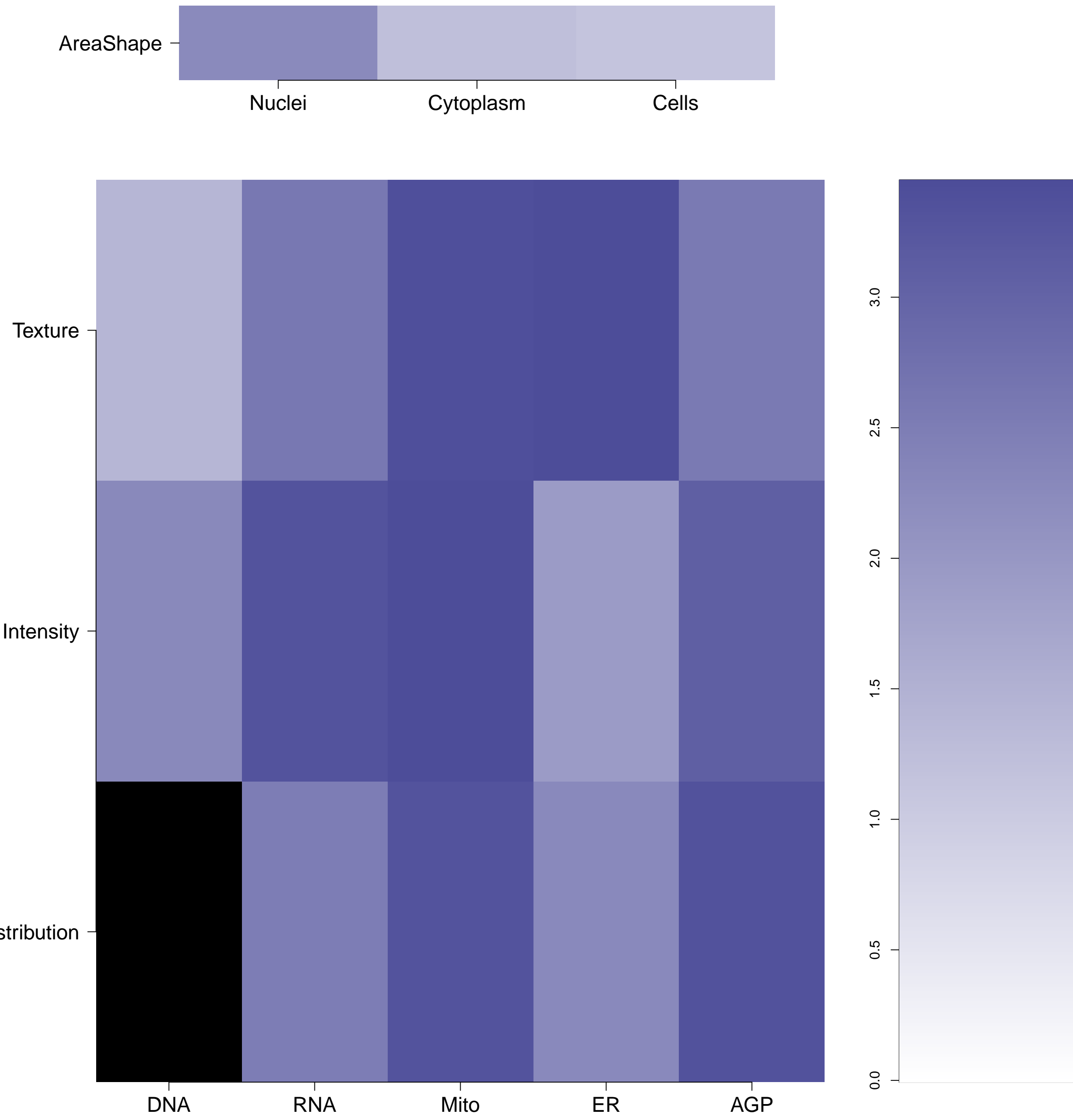


KRAS.WT.1 - in RTK

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.WT.1 (41744)

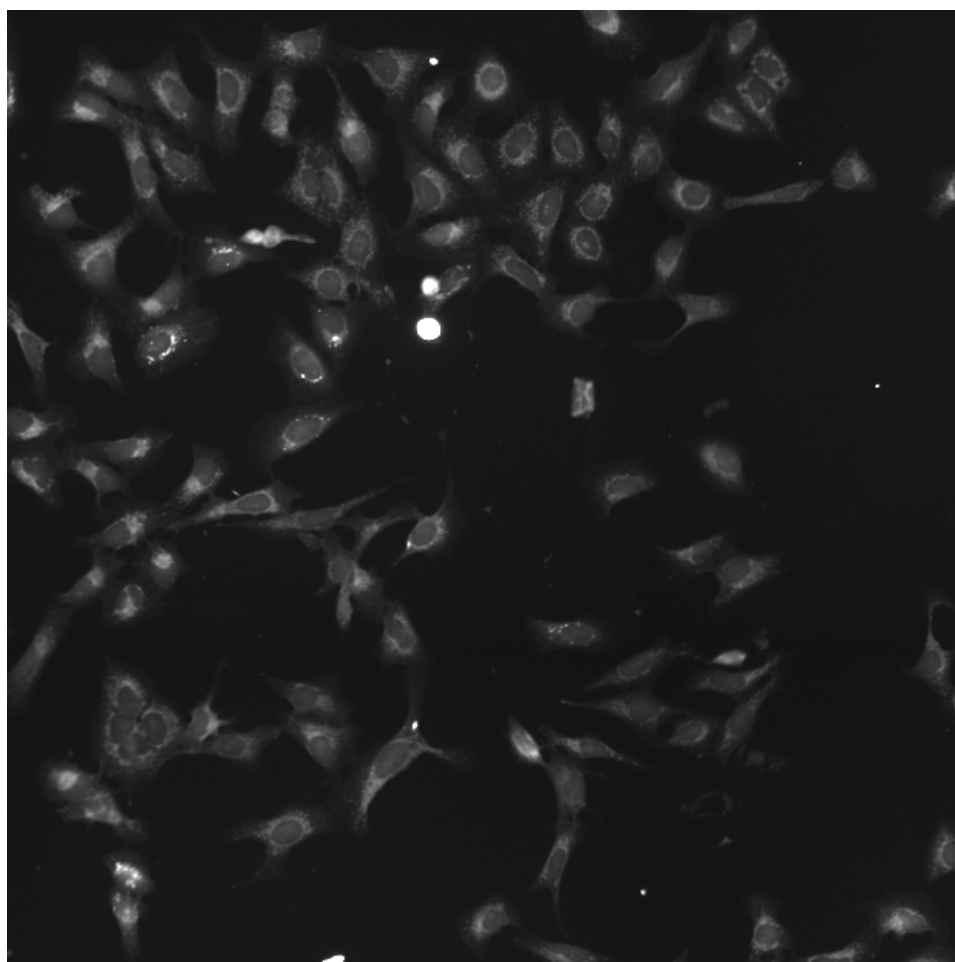
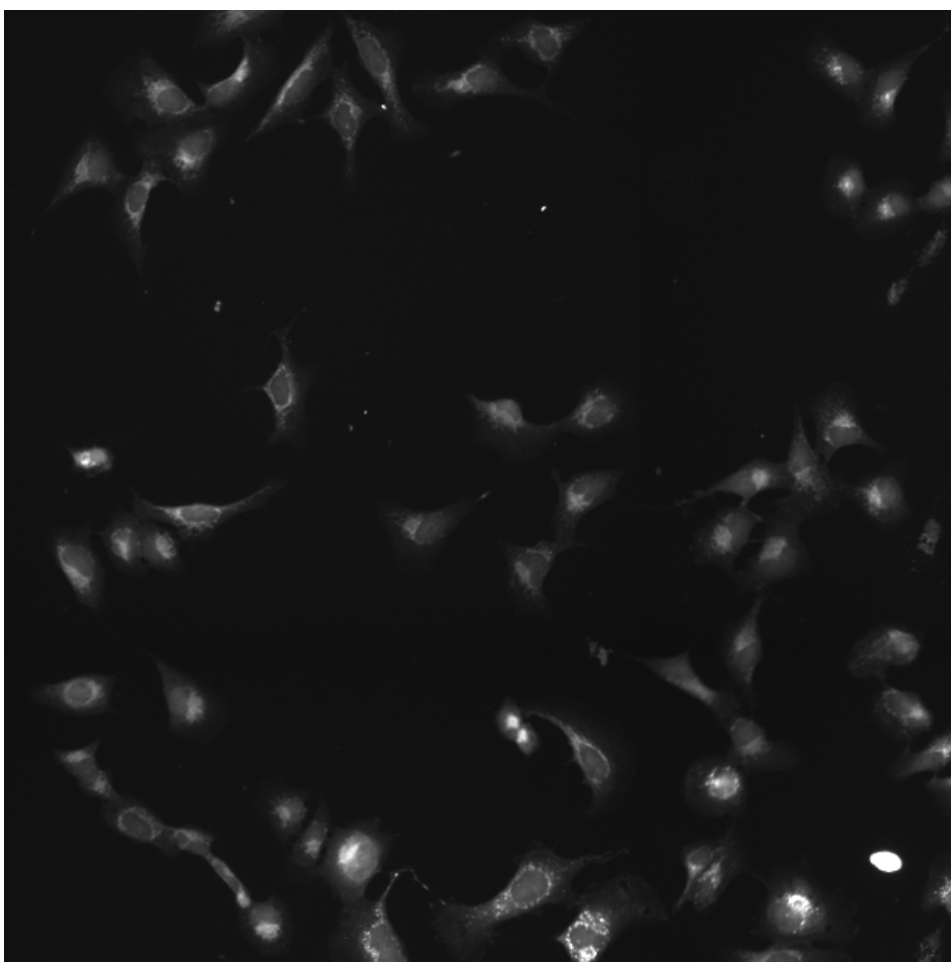
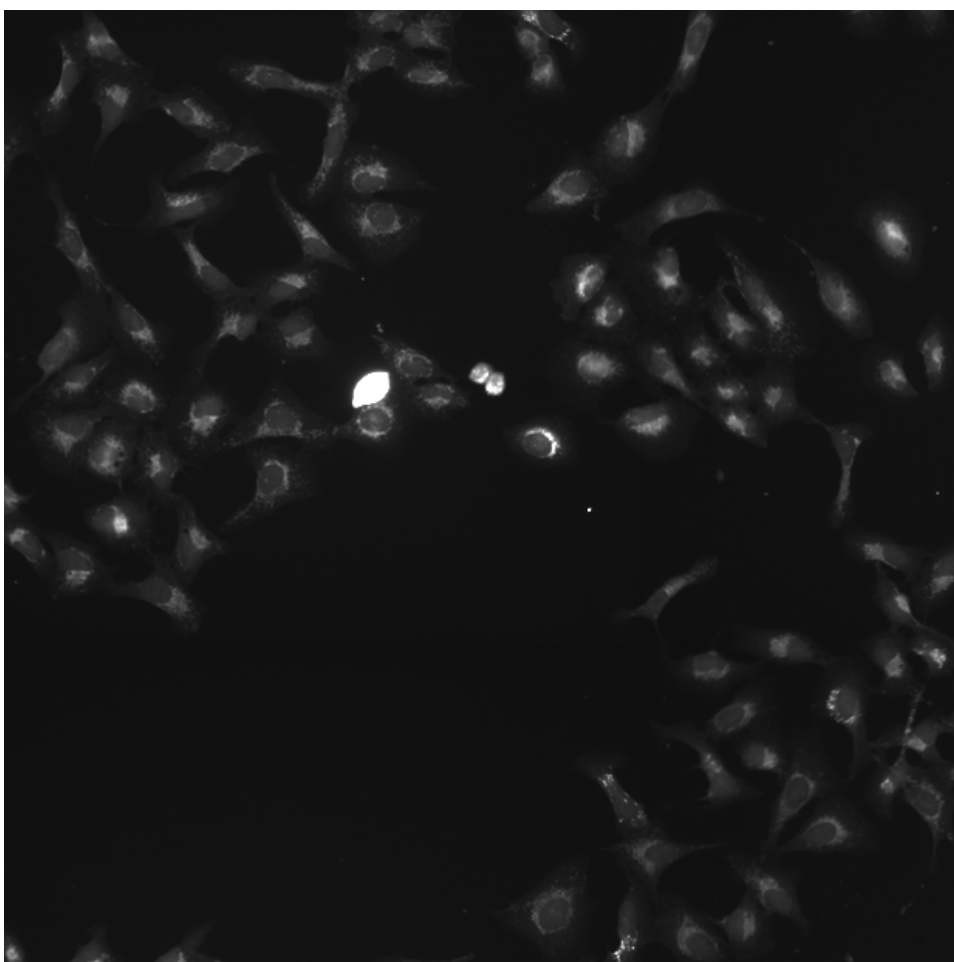
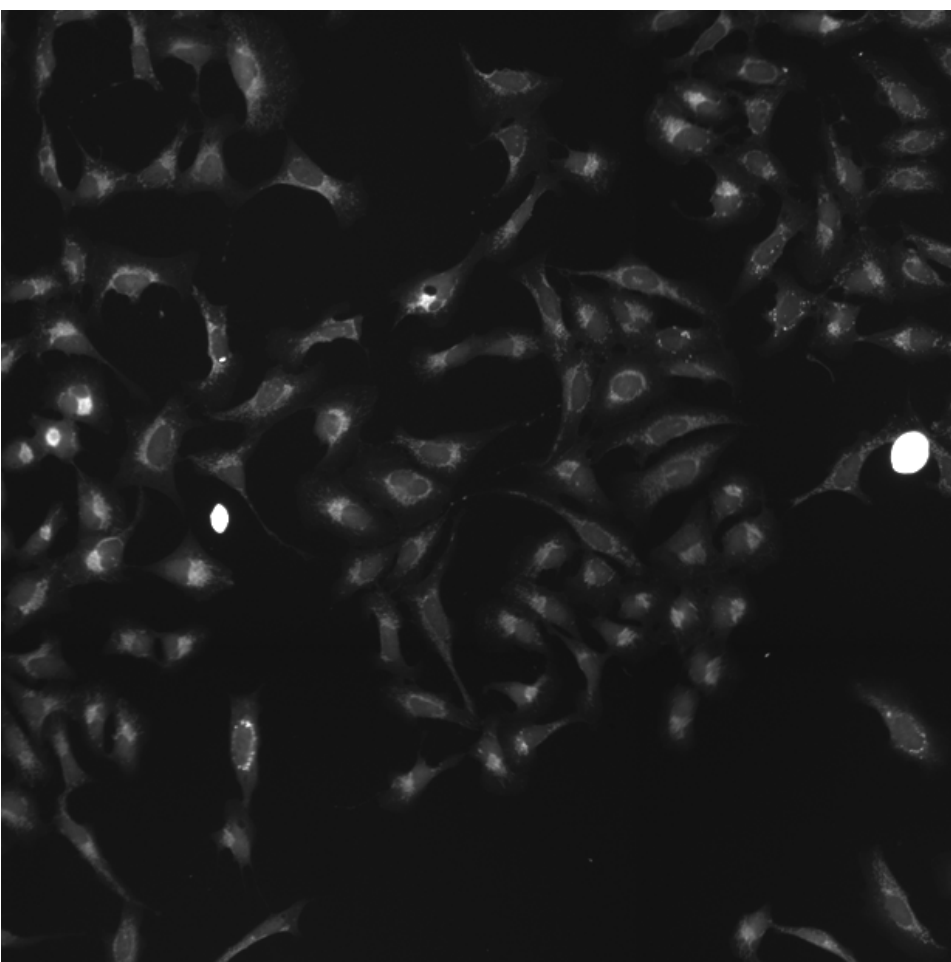
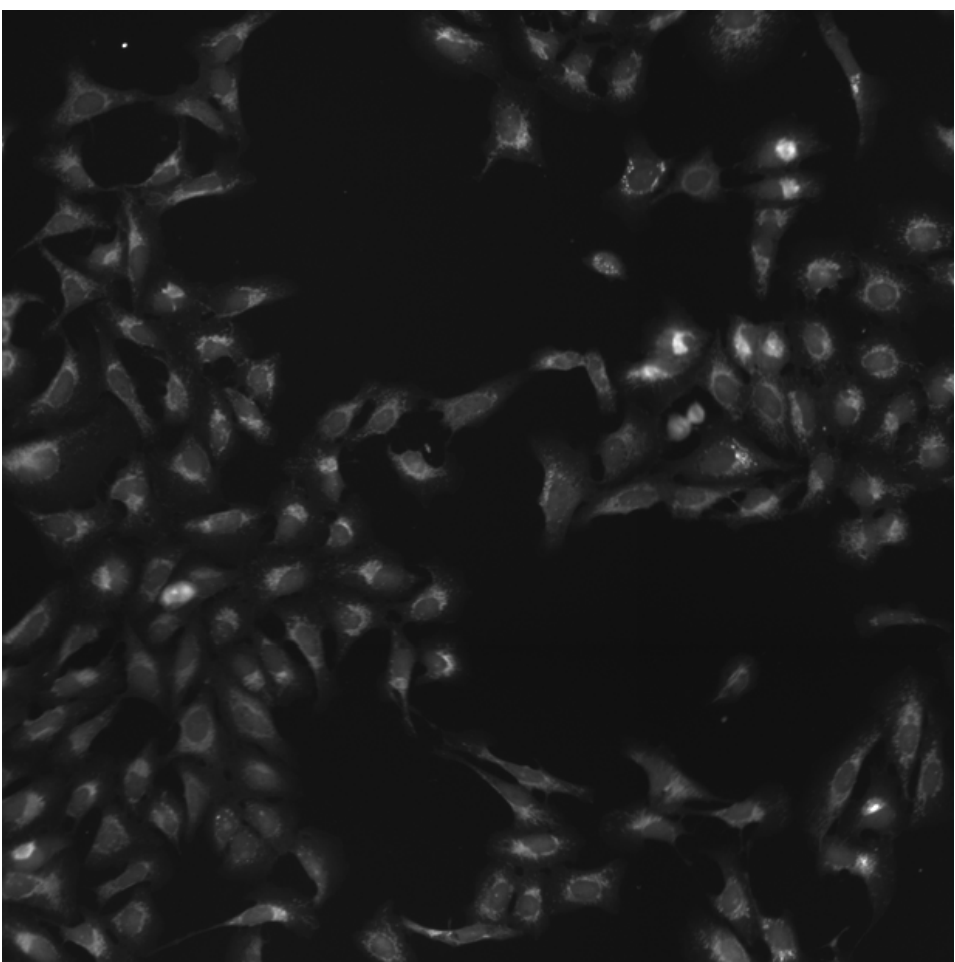
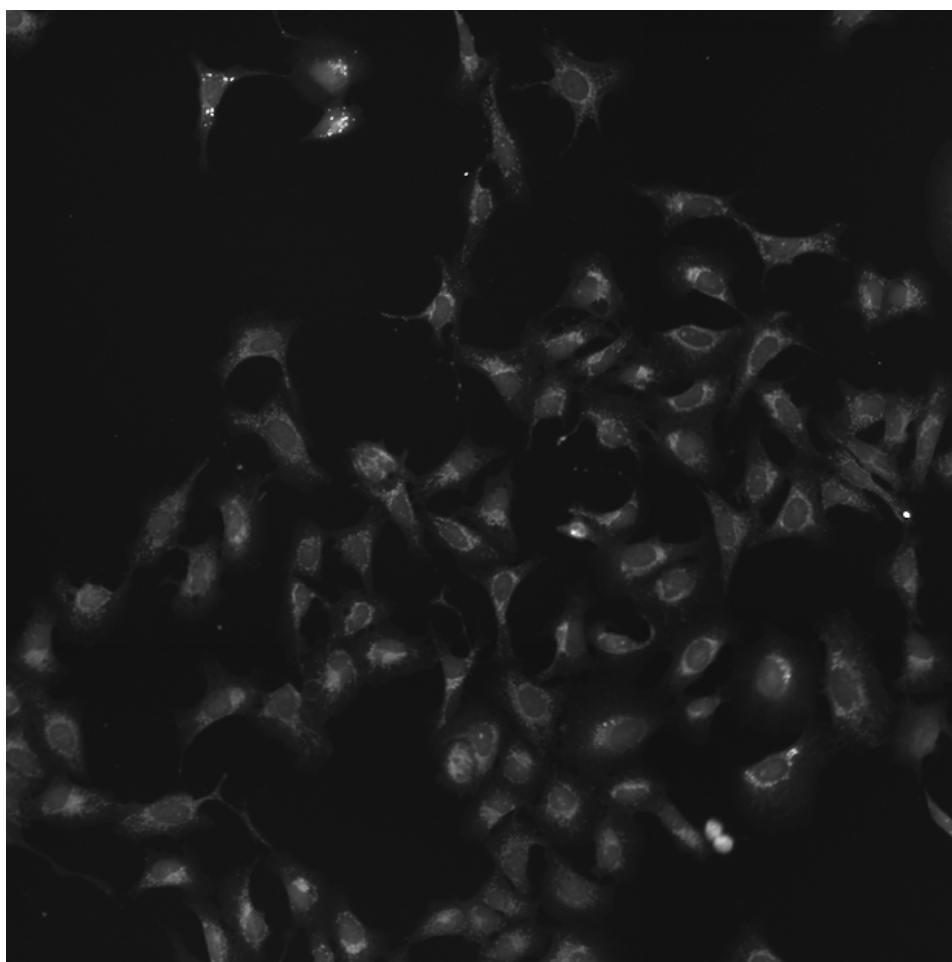
KRAS.WT.1 (41755)

KRAS.WT.1 (41756)

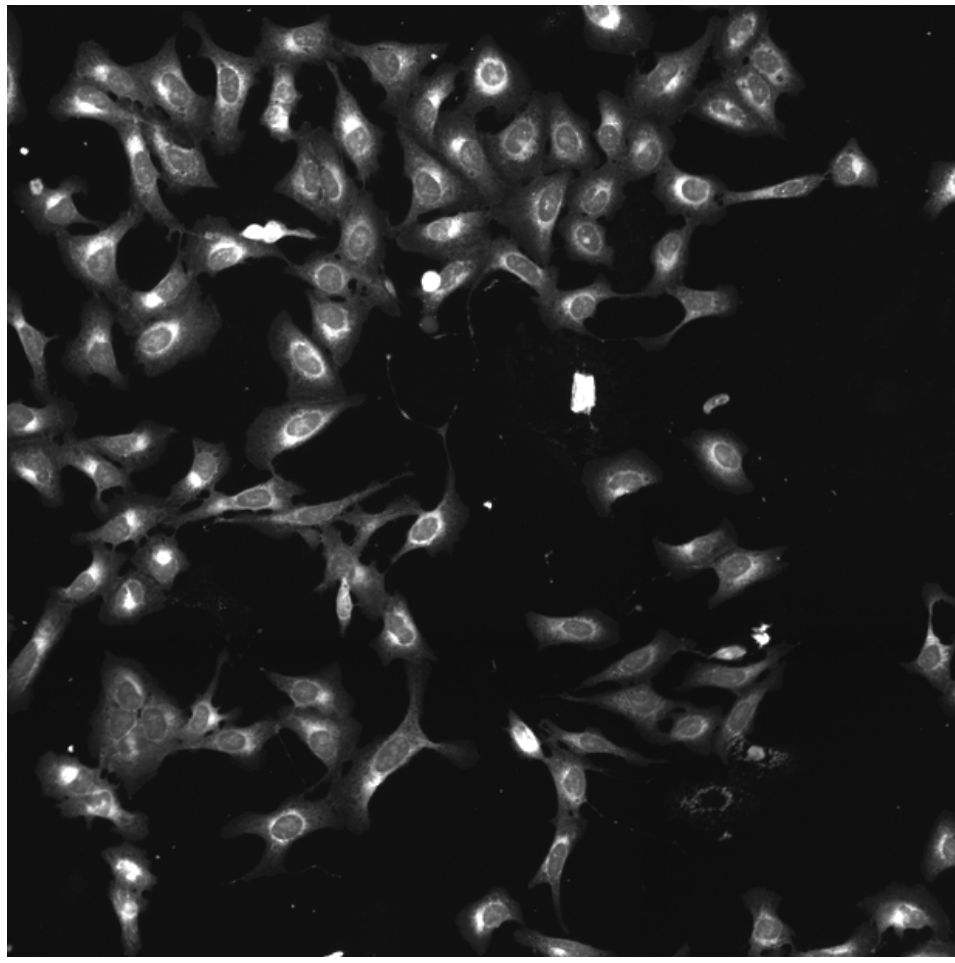
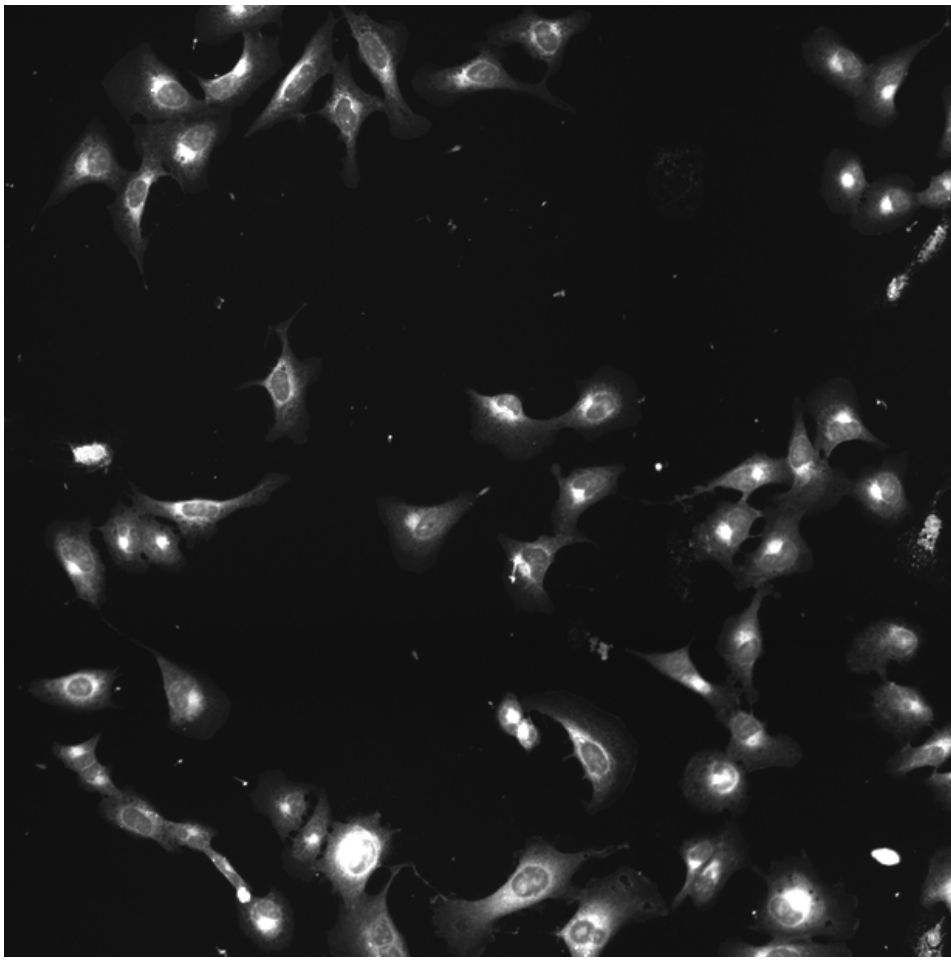
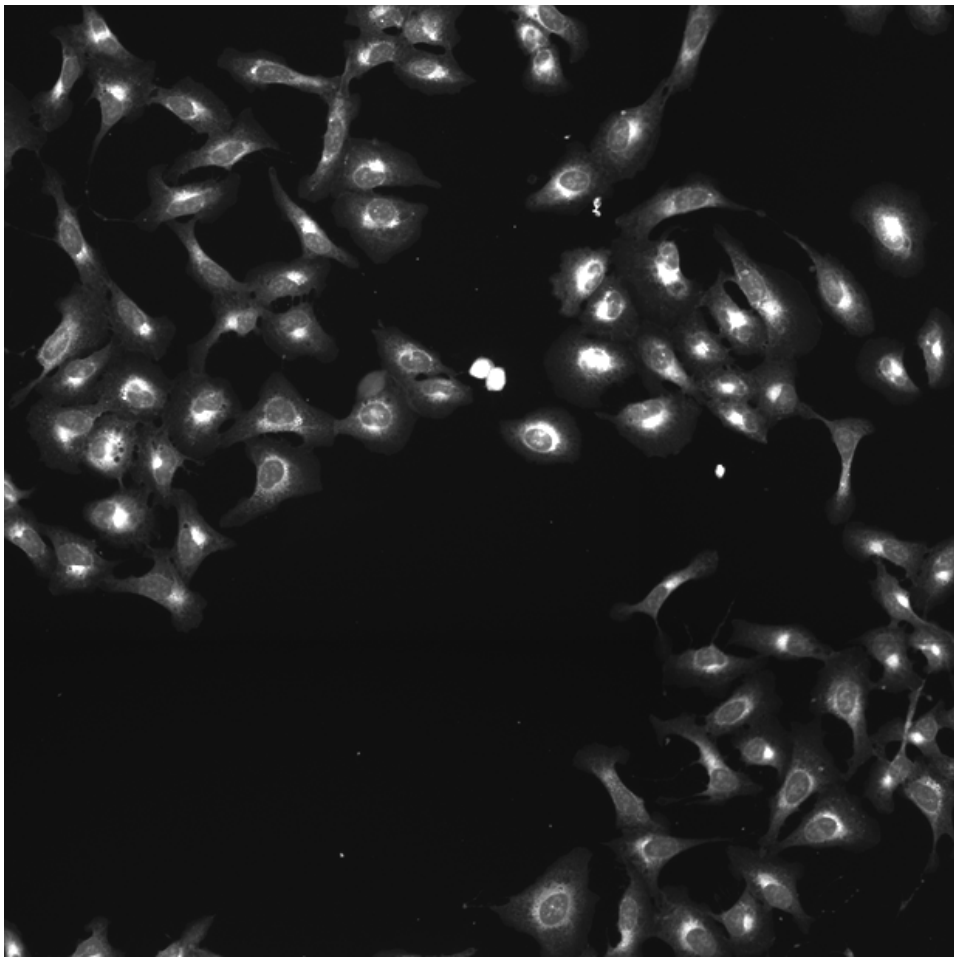
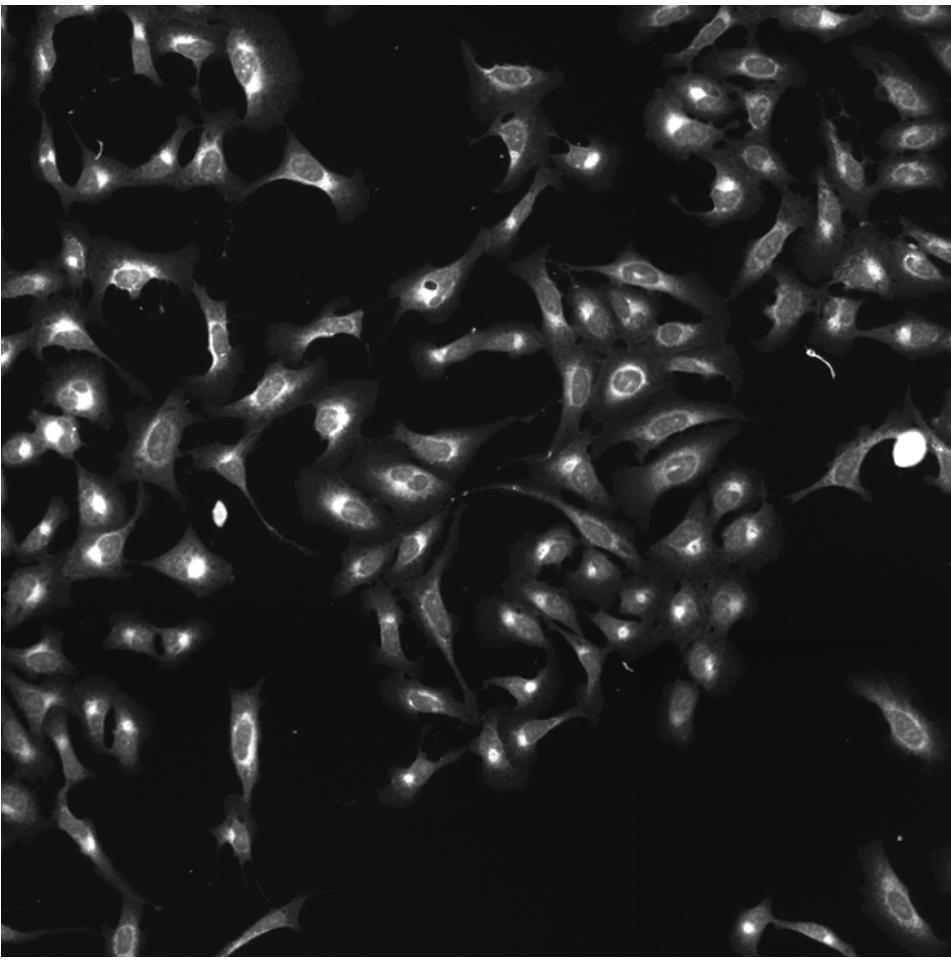
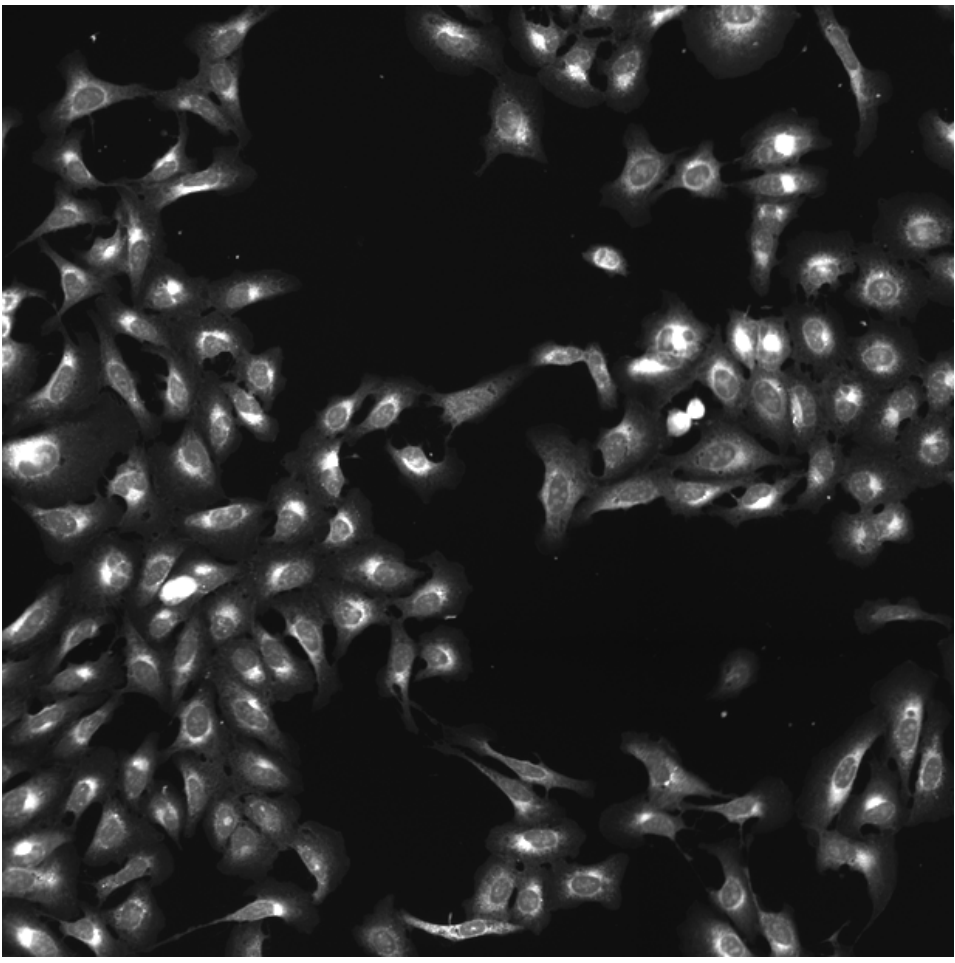
KRAS.WT.1 (41757)

KRAS.WT.1 (41754)

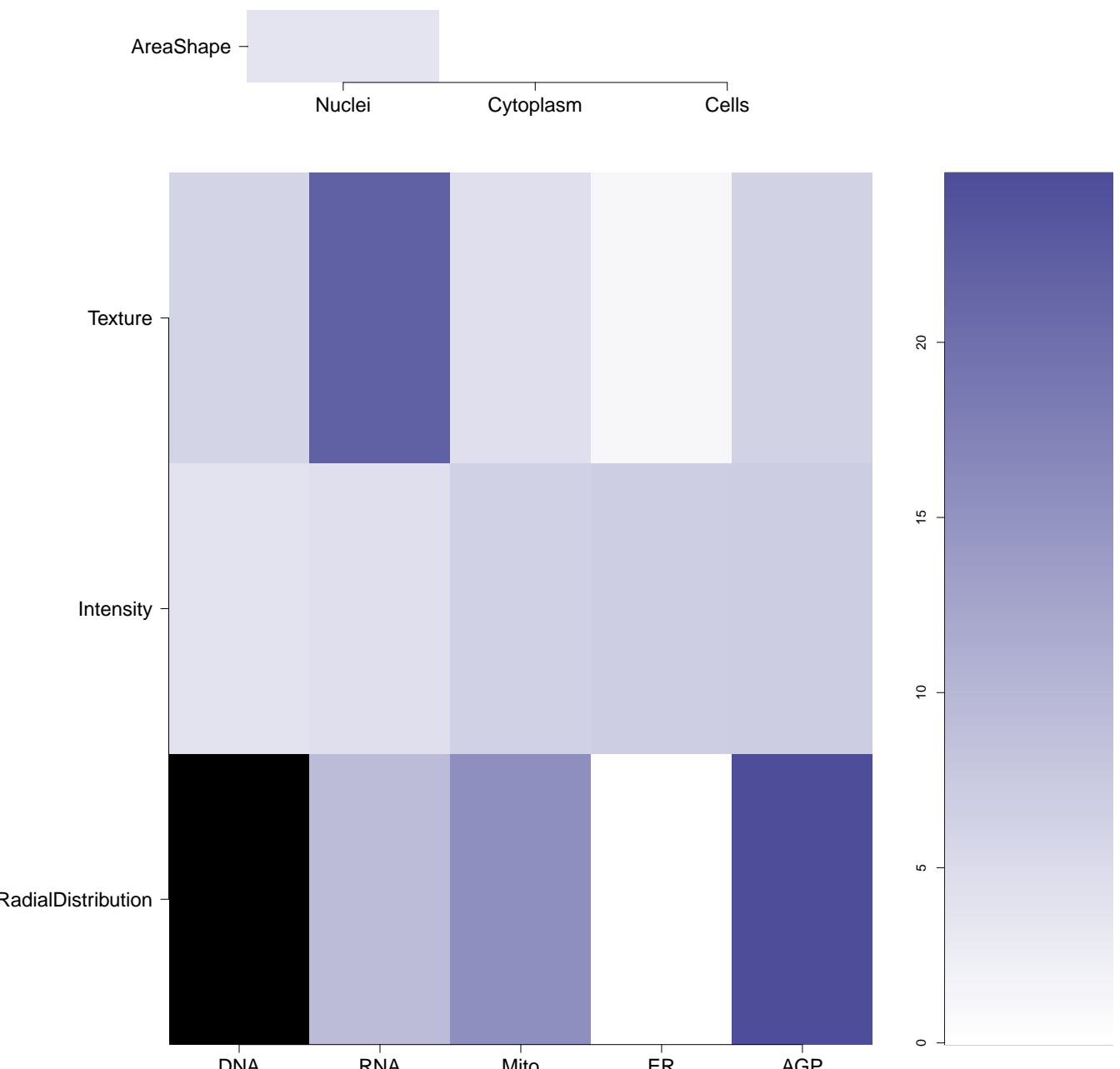
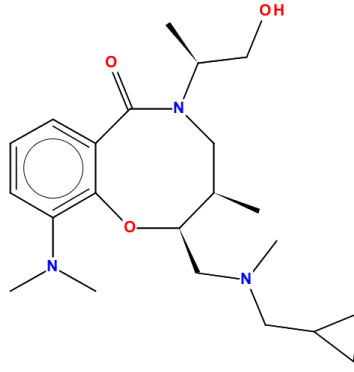
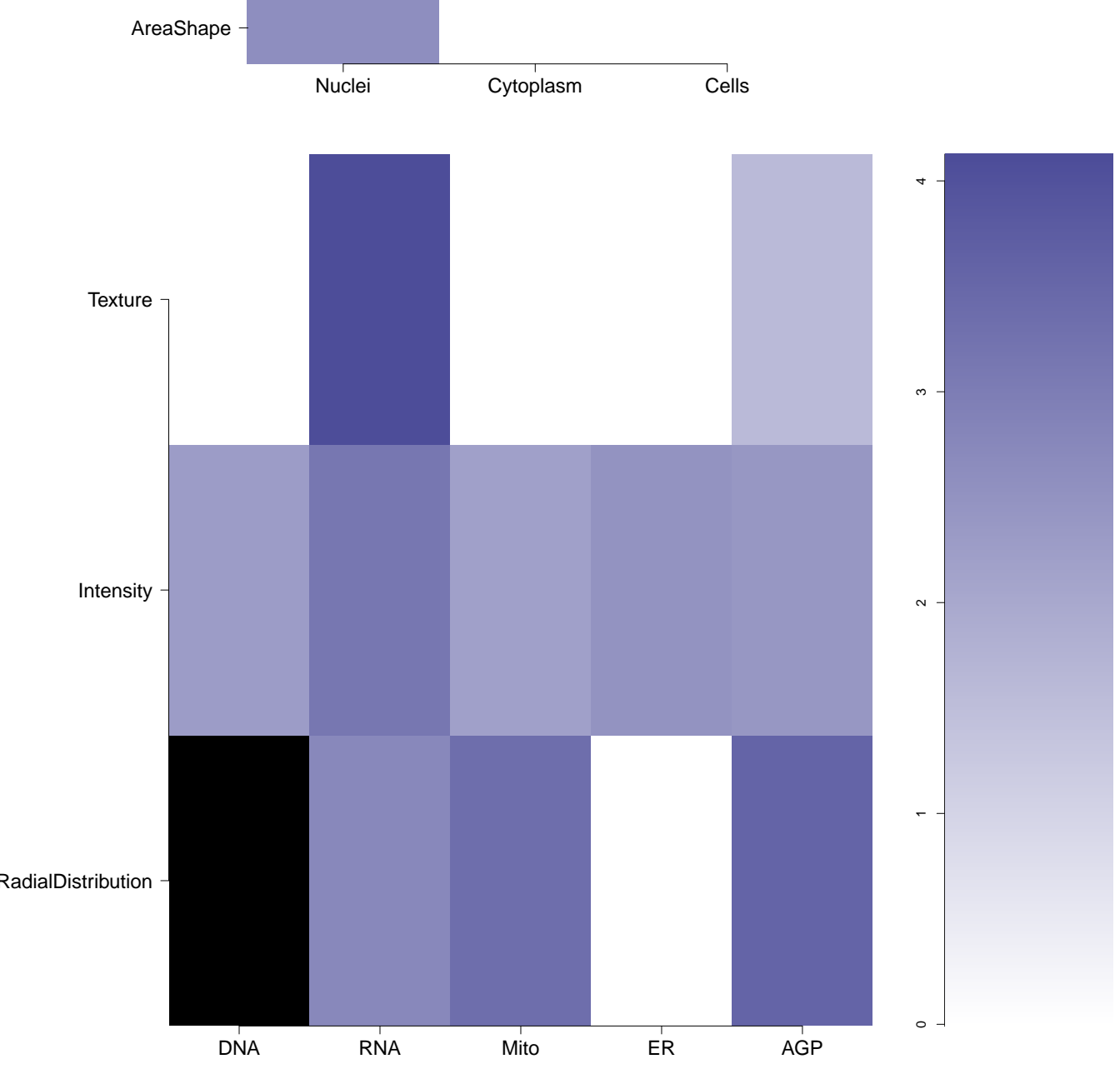


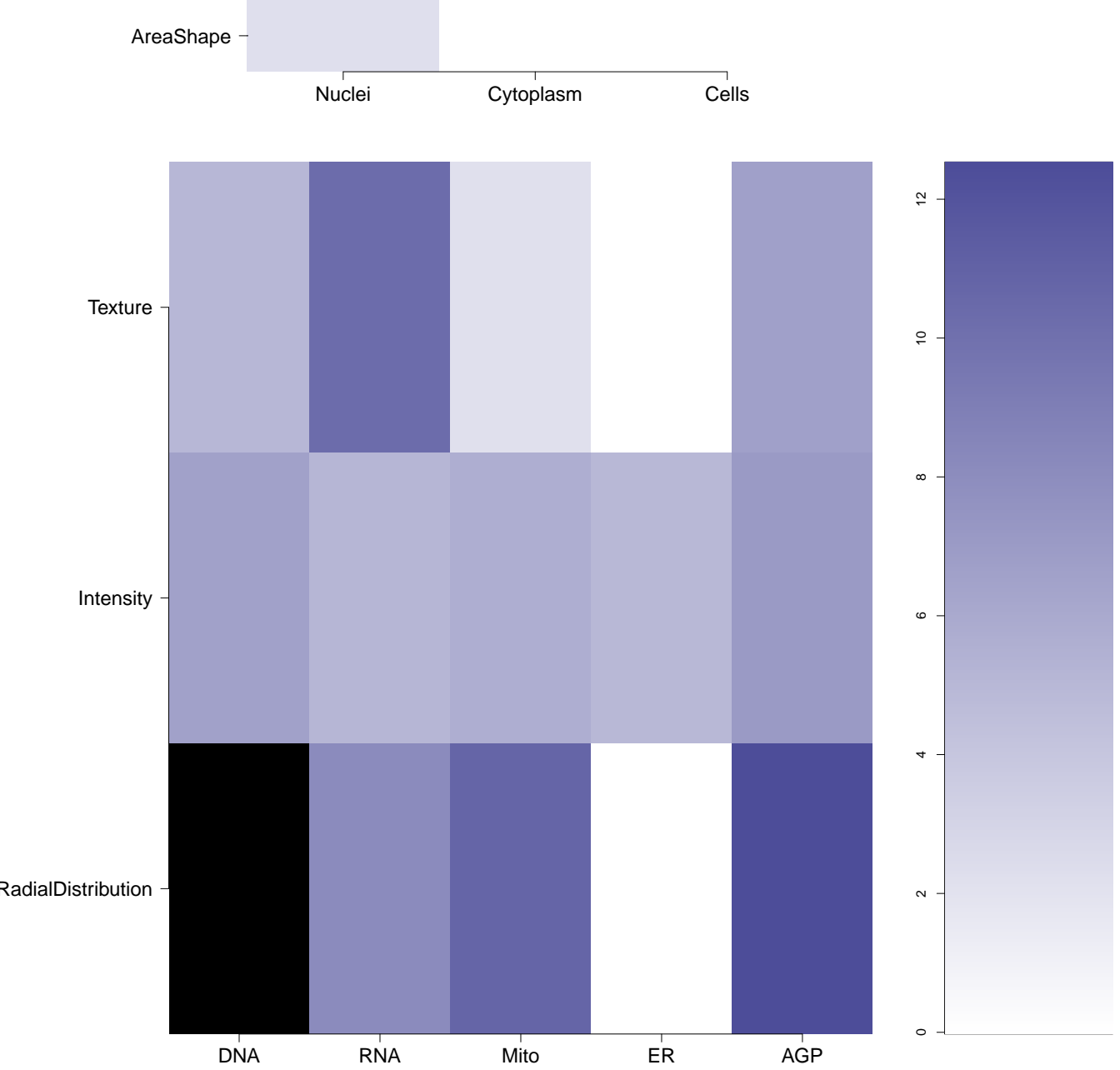
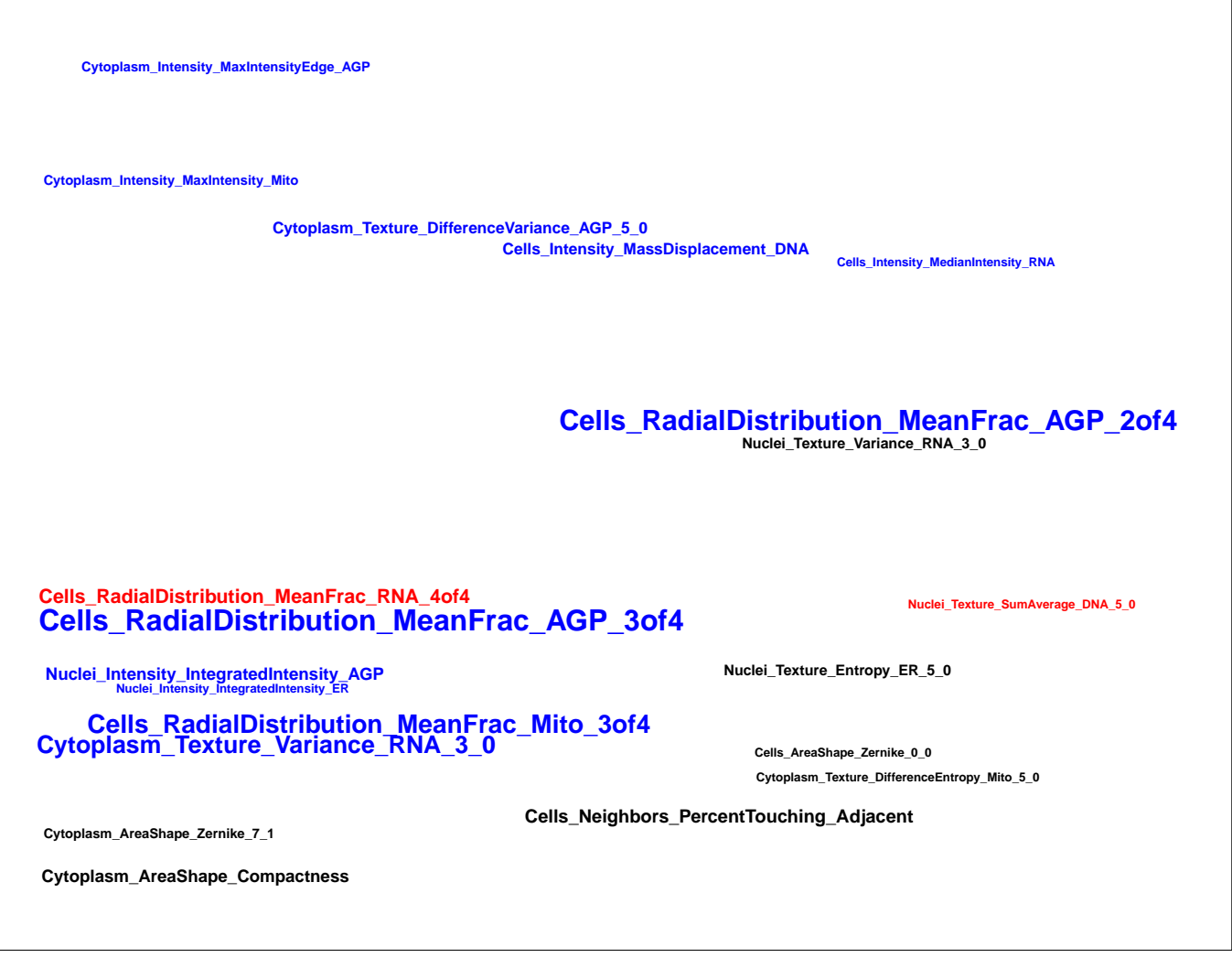
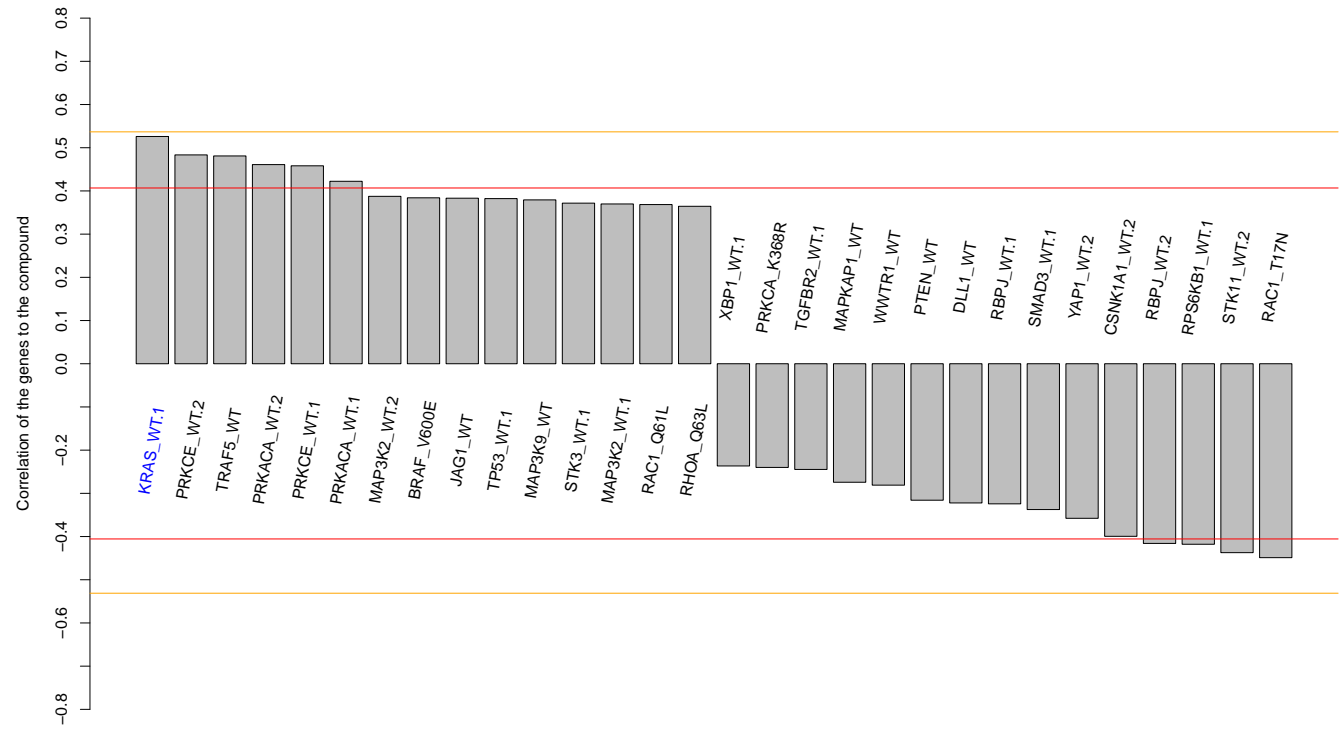

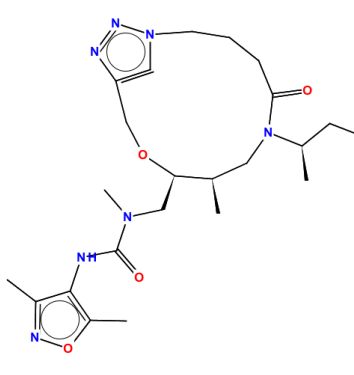
Mito

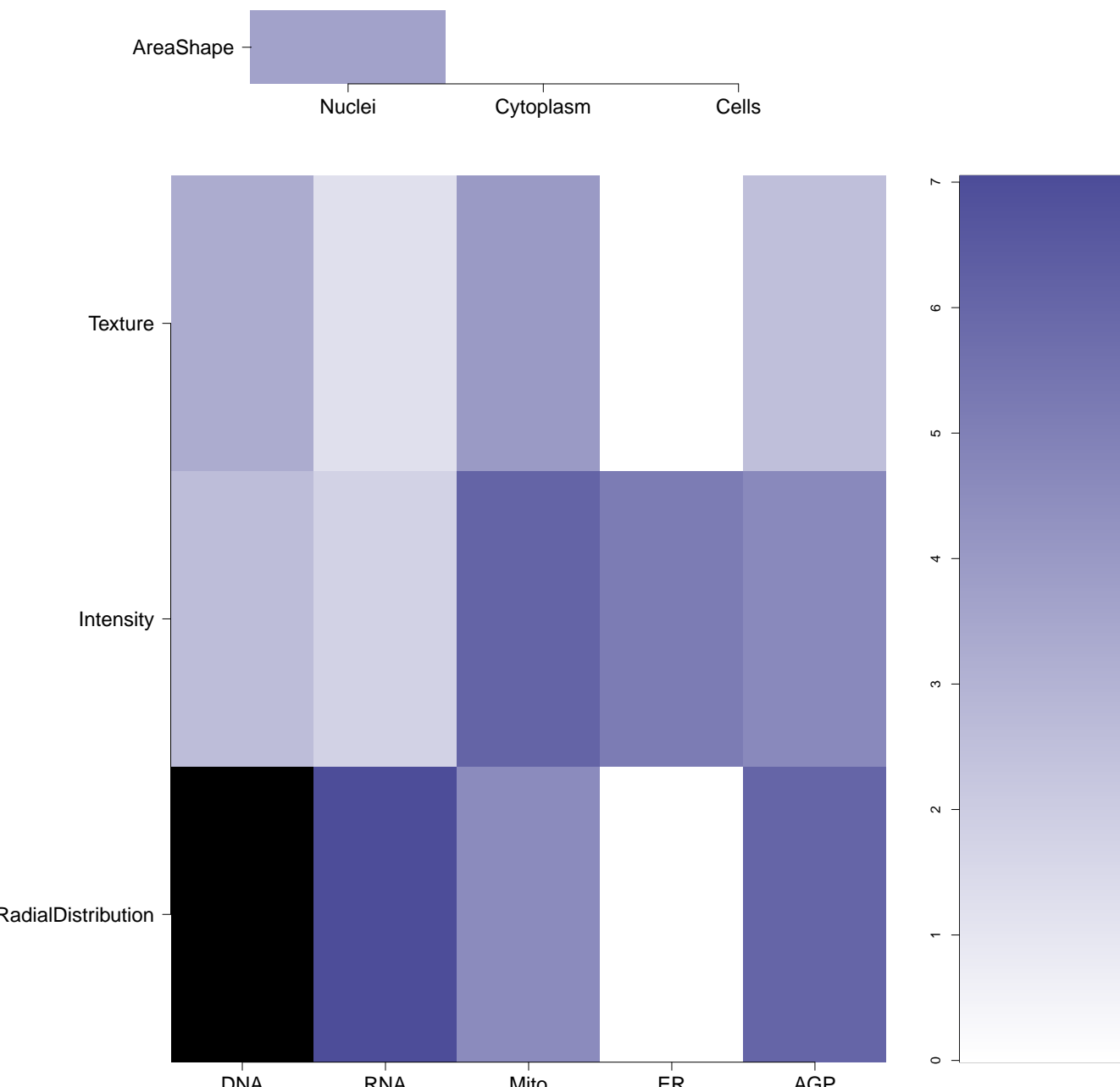
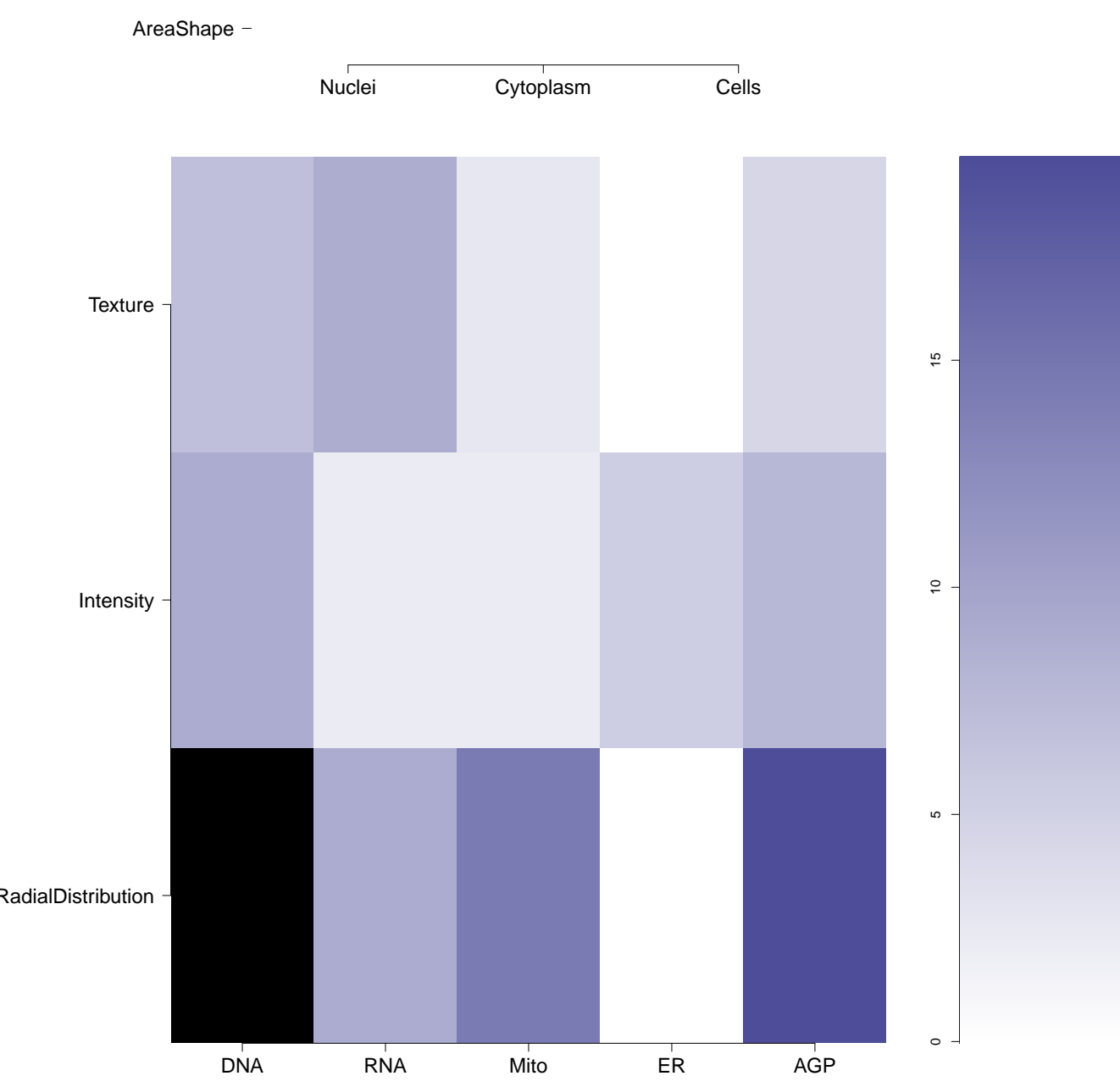
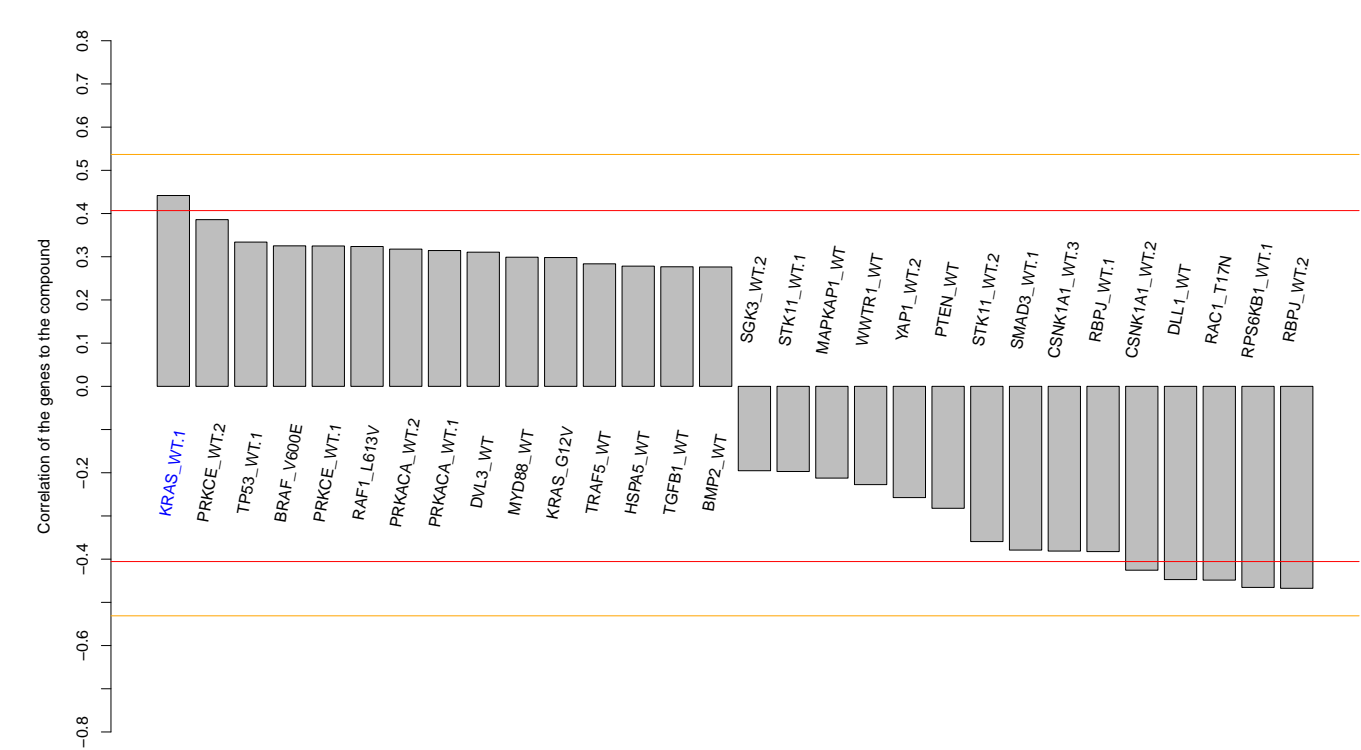
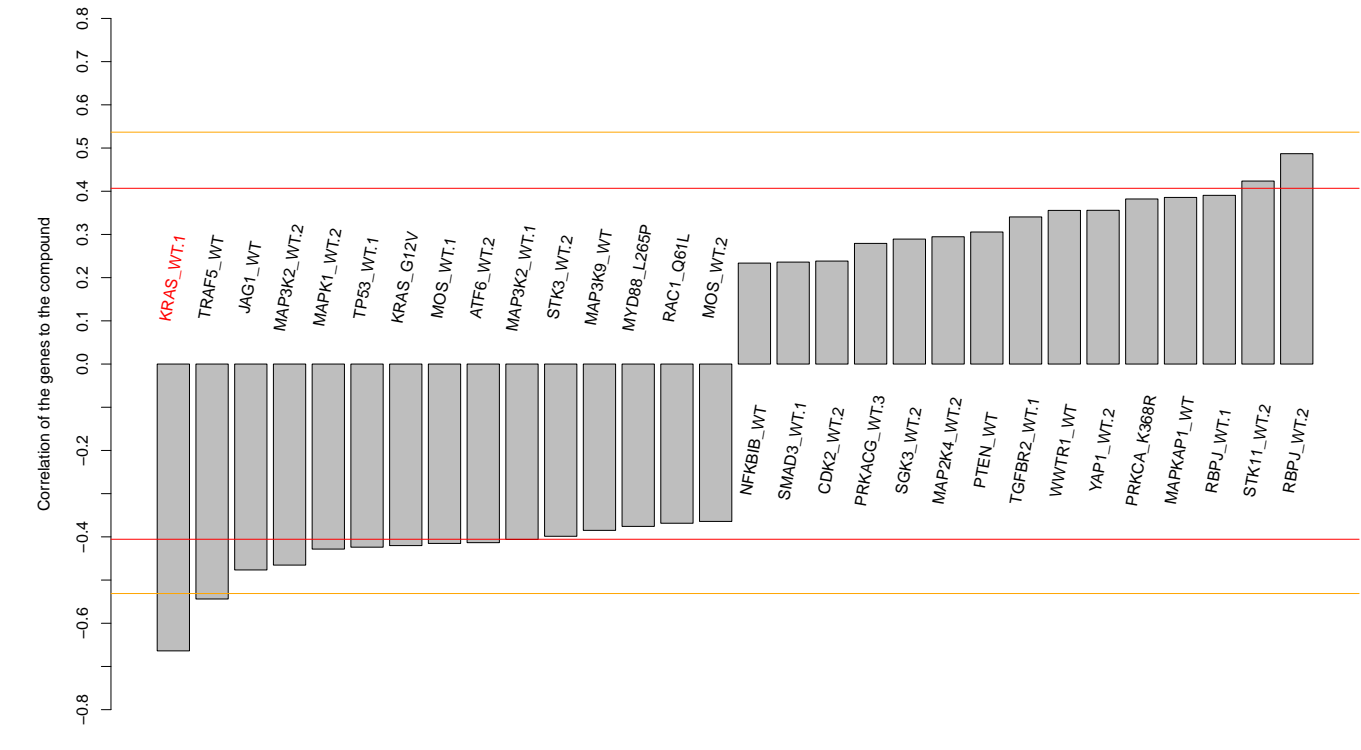

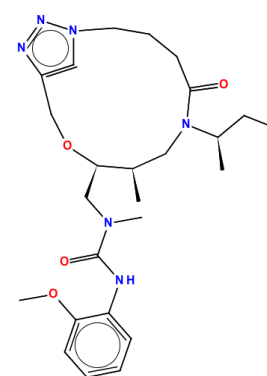


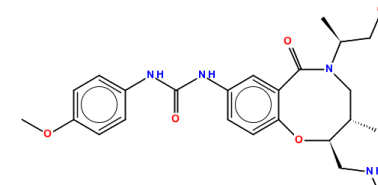
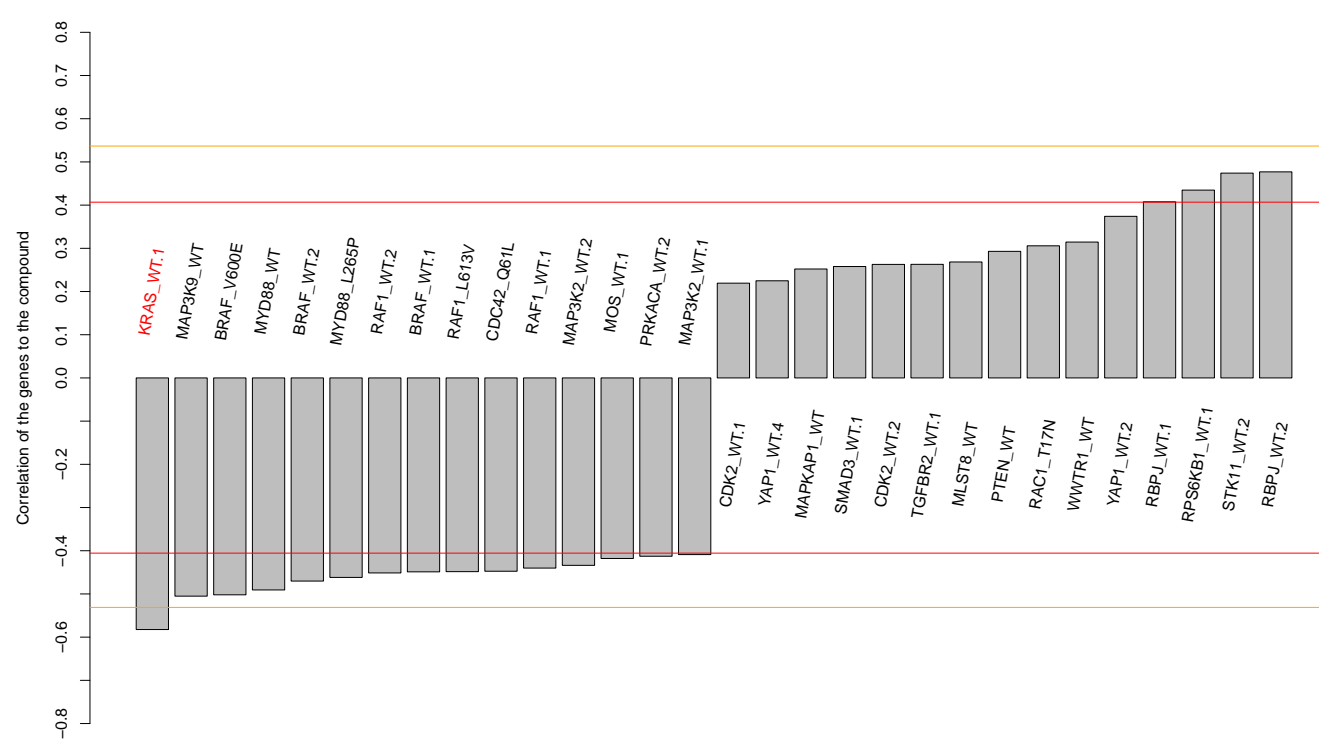
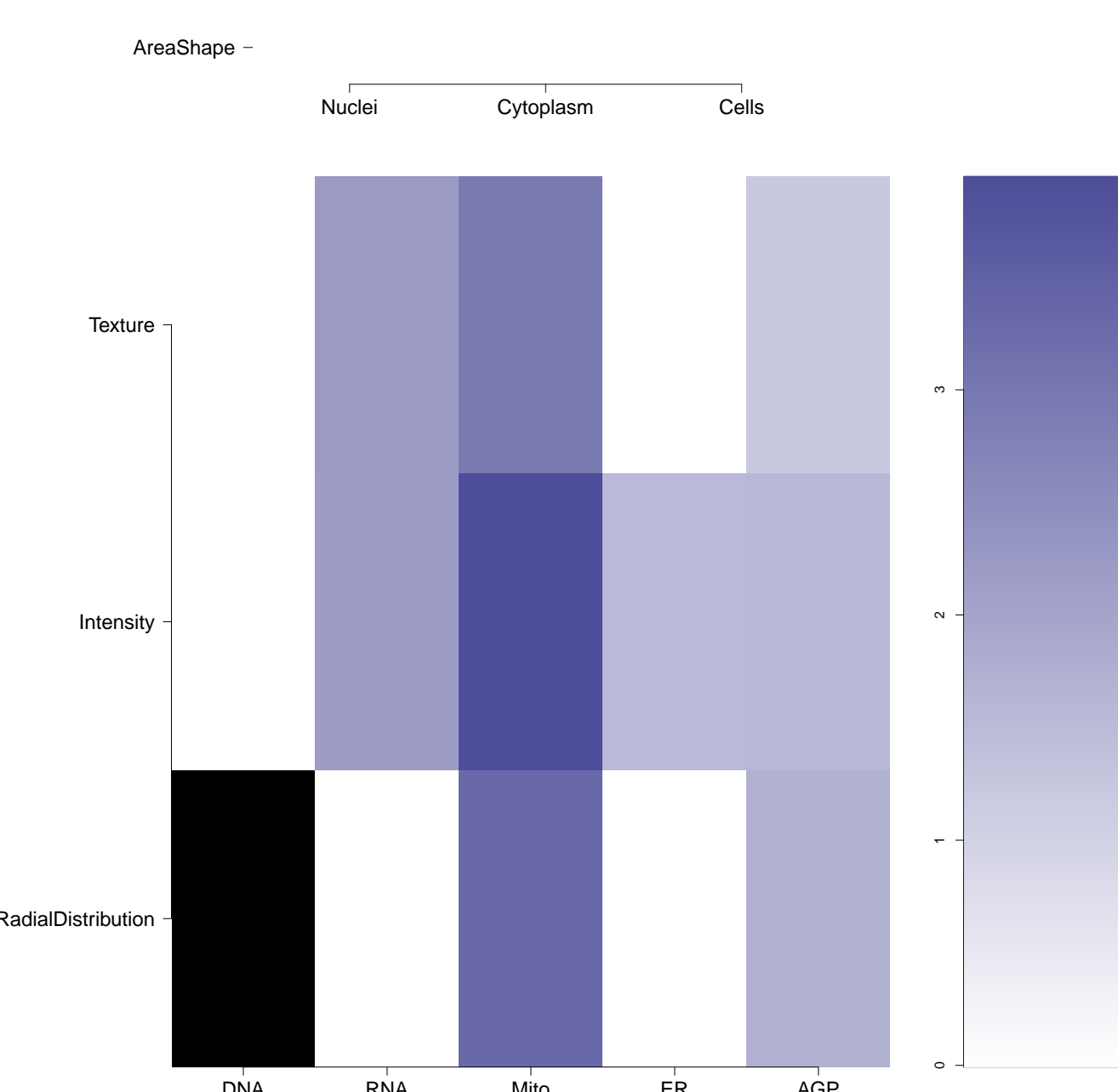

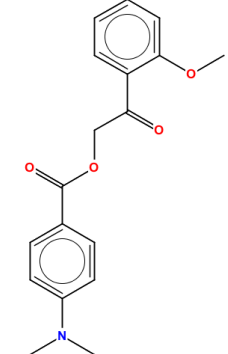
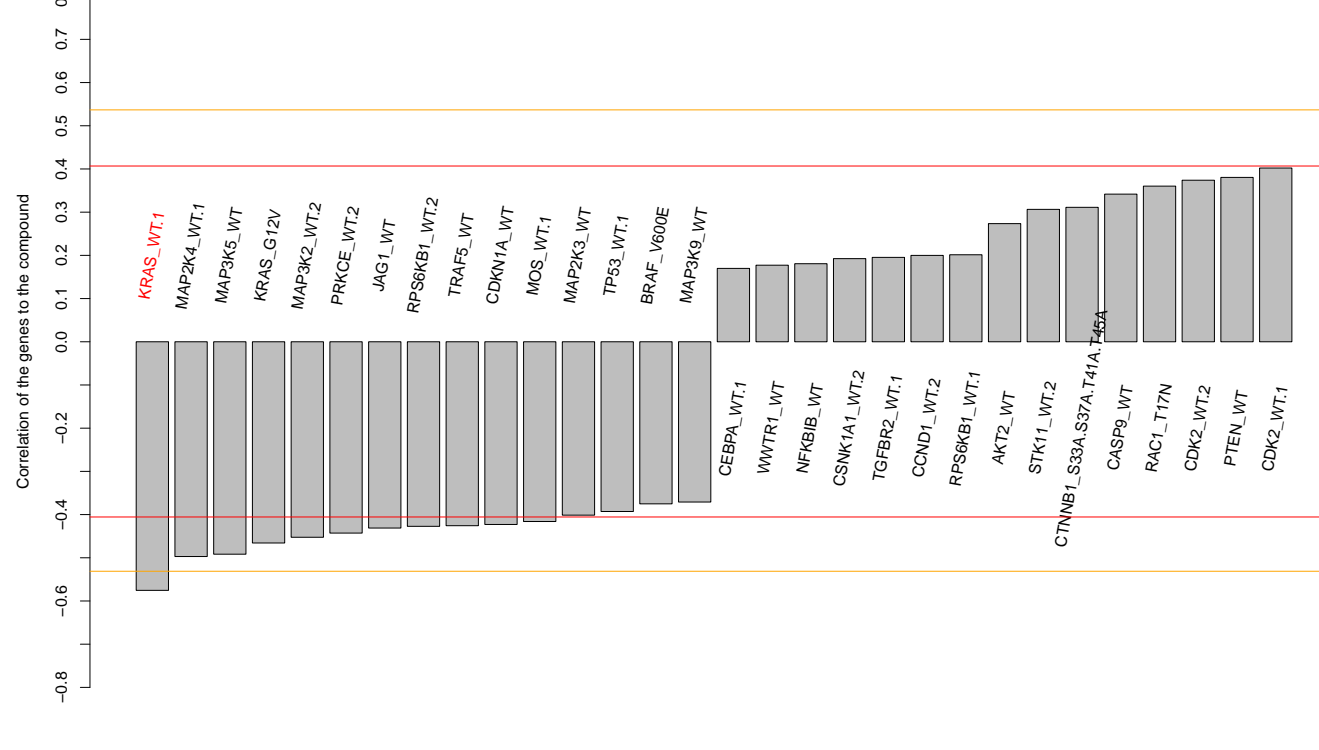
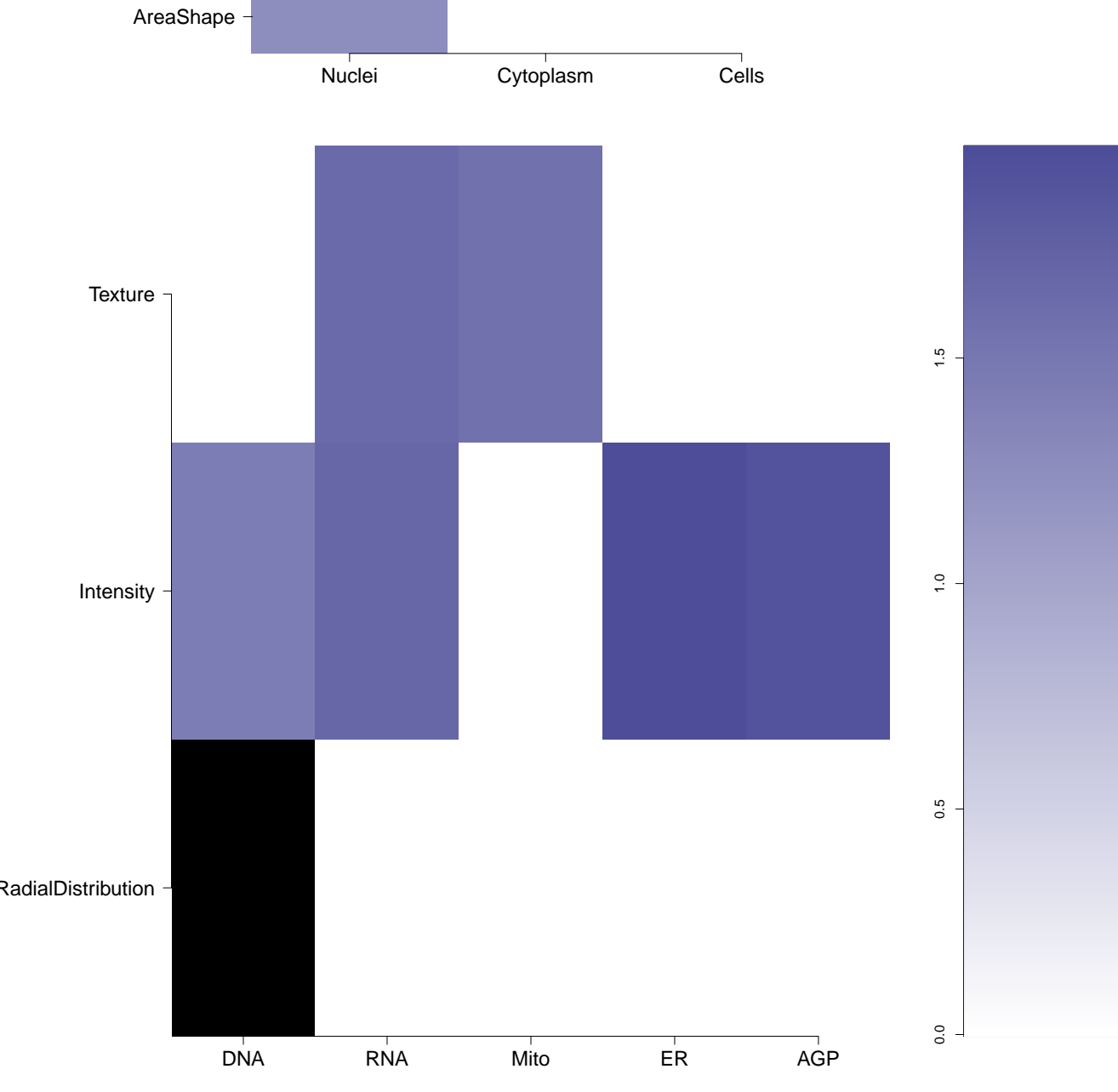
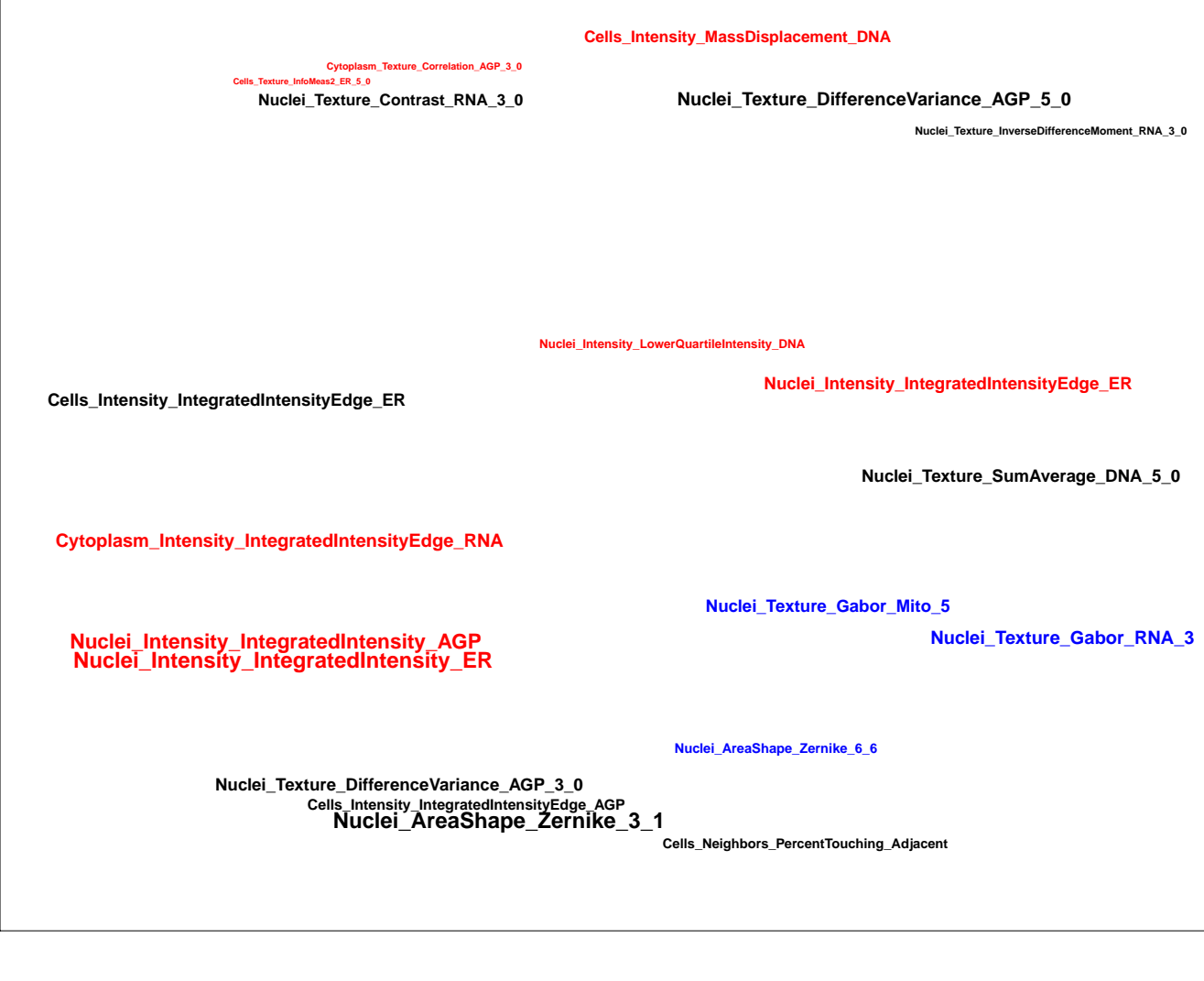
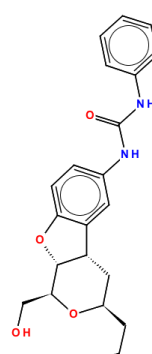
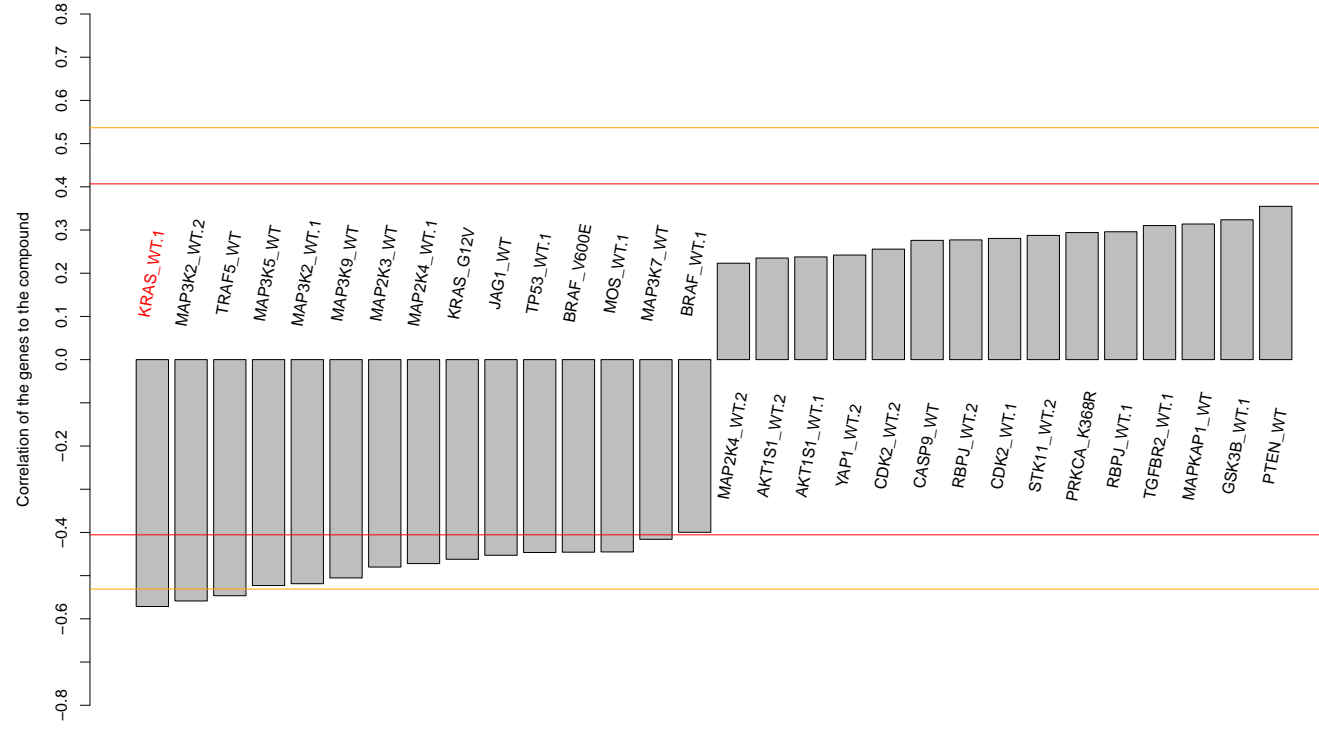
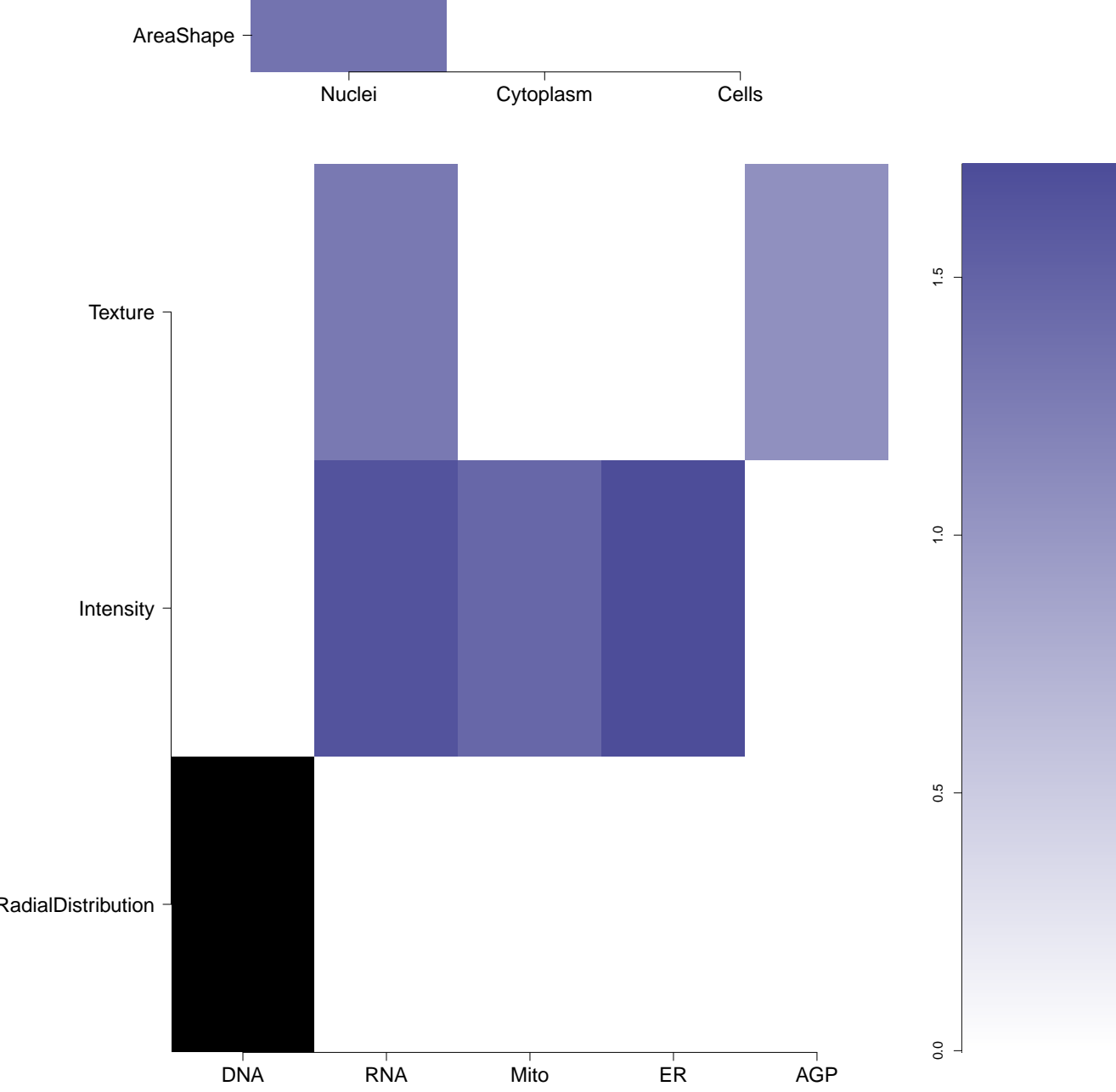

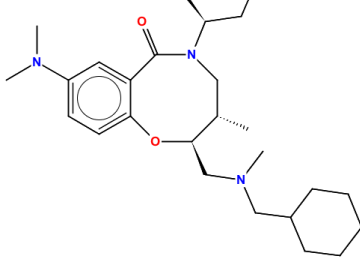
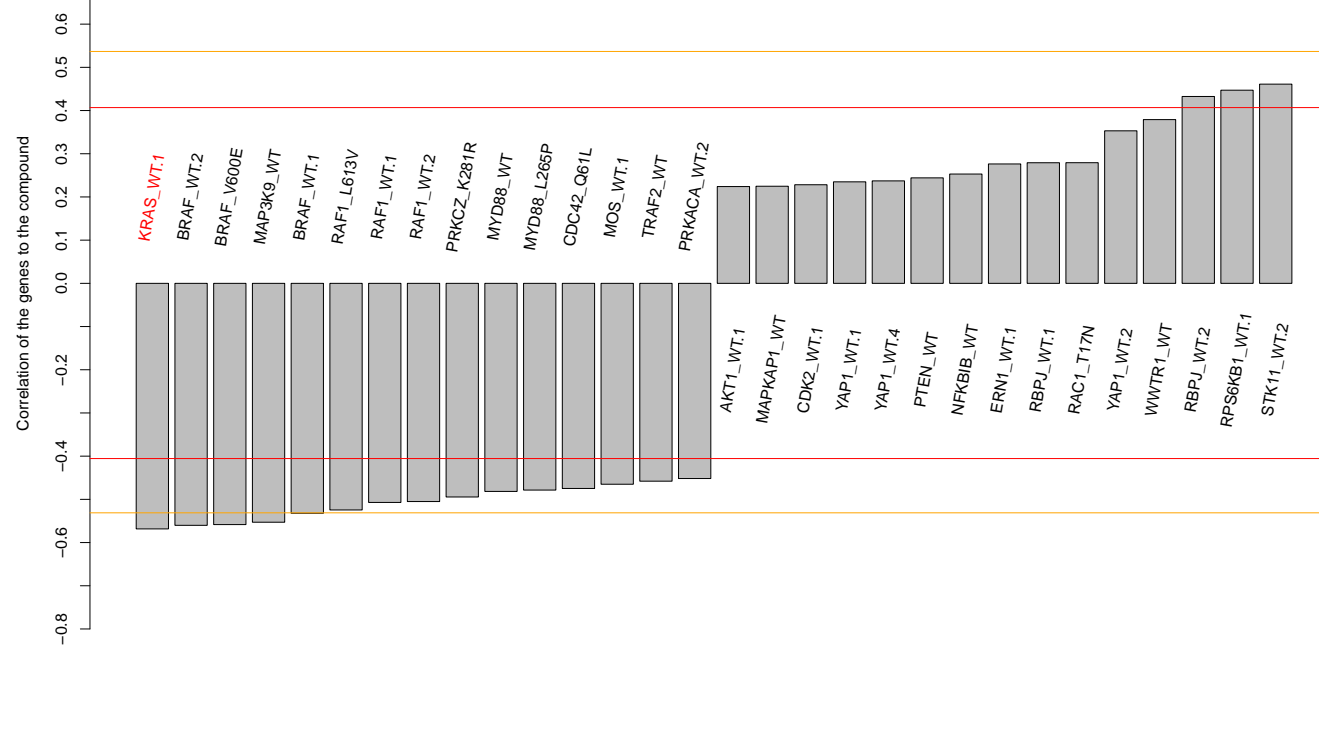
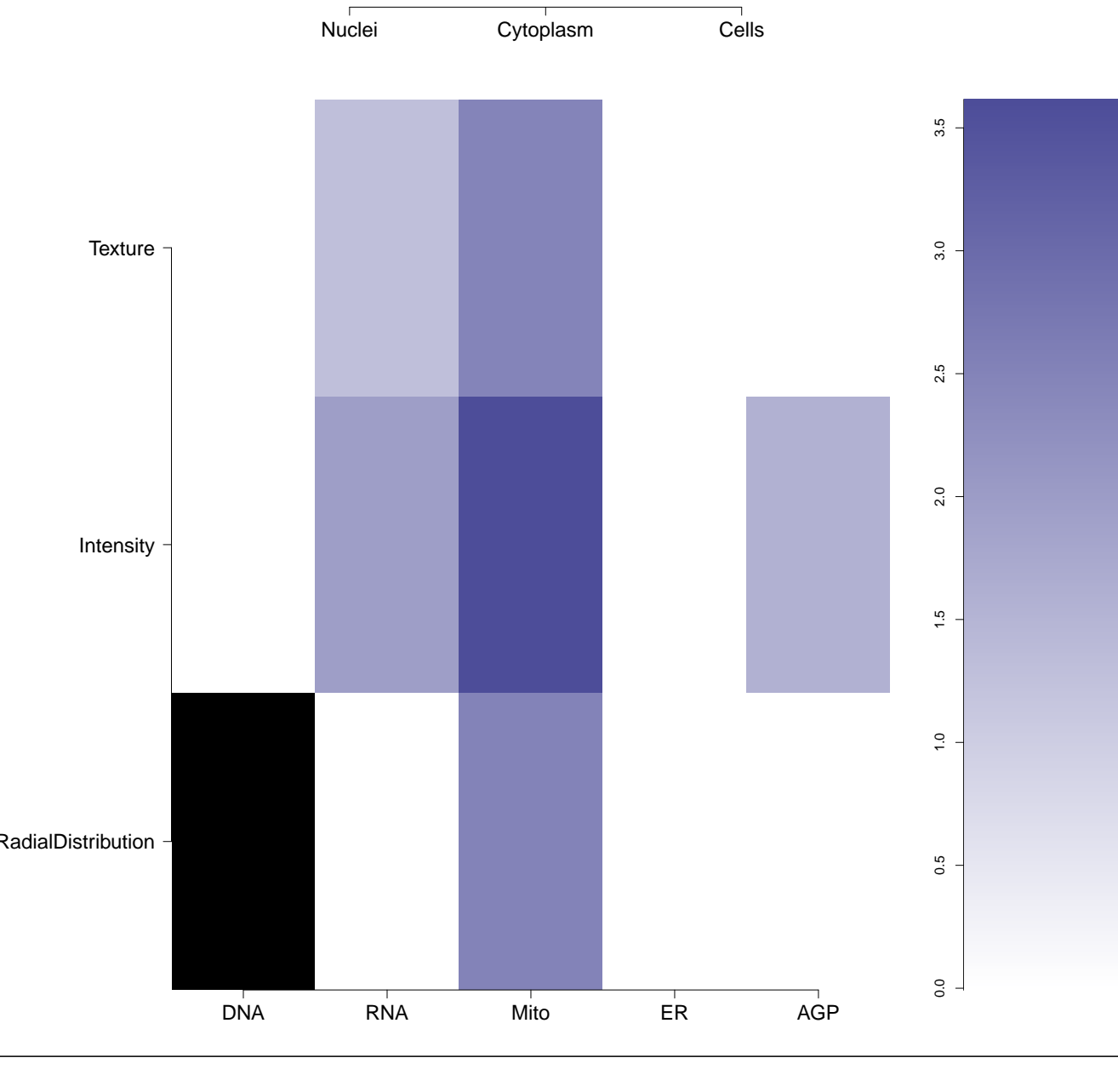

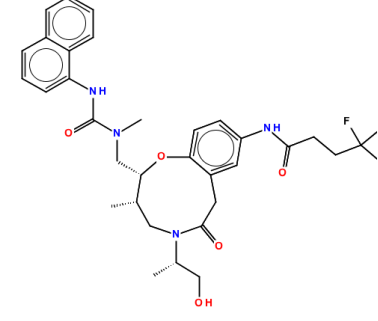
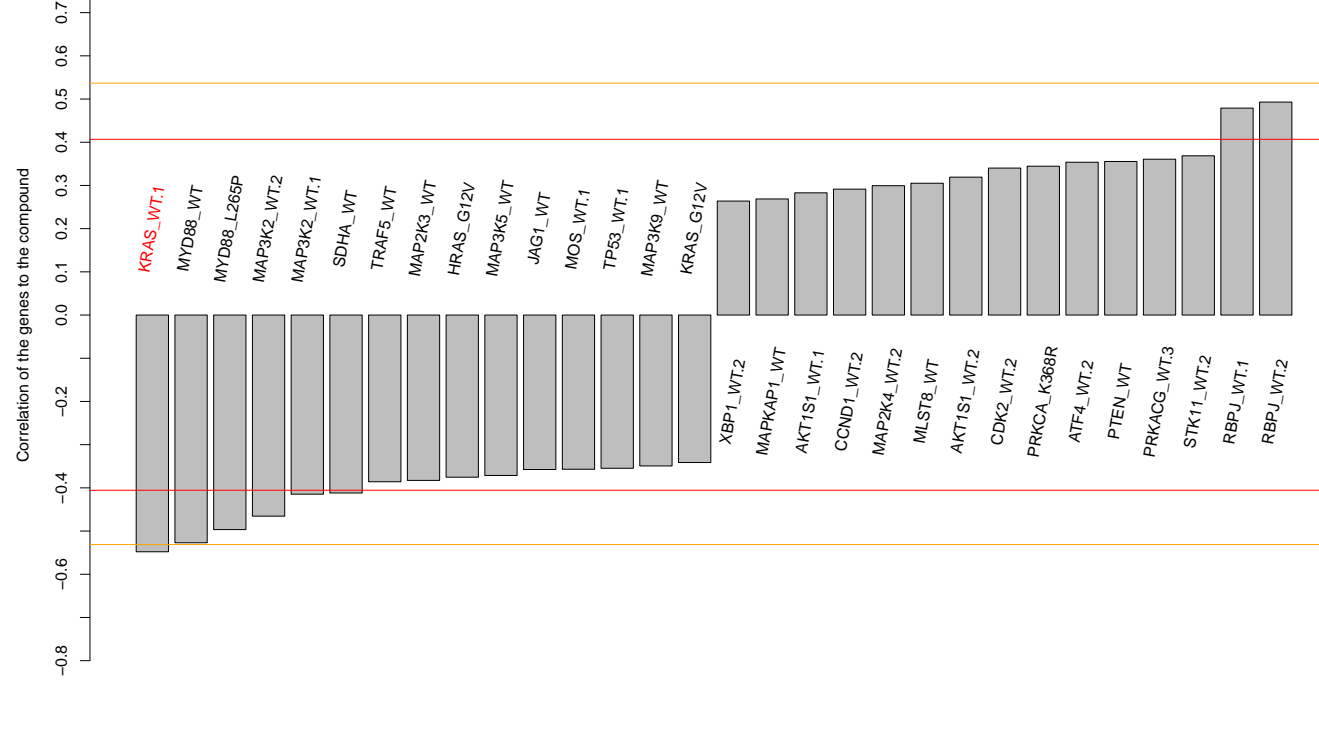
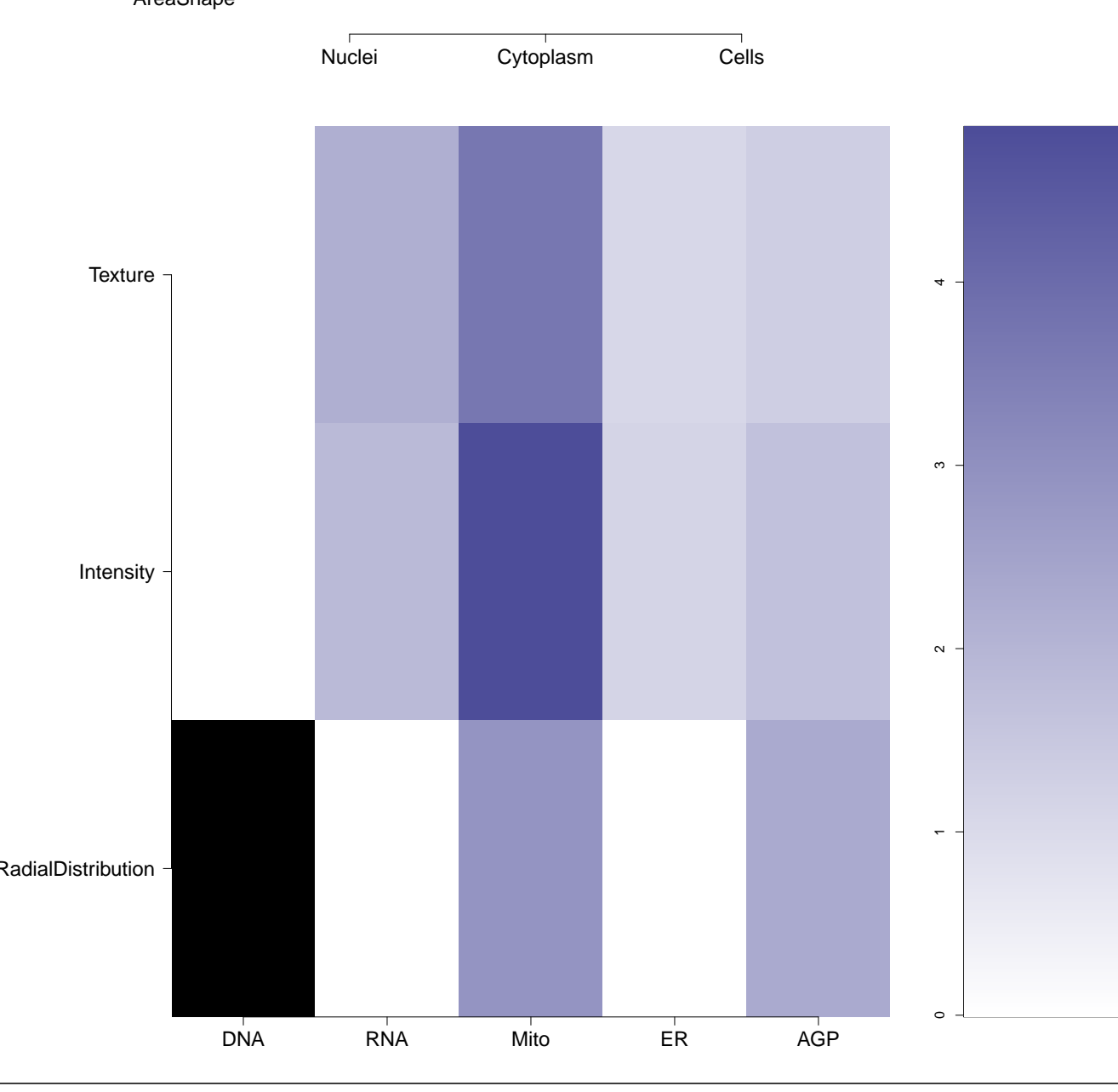
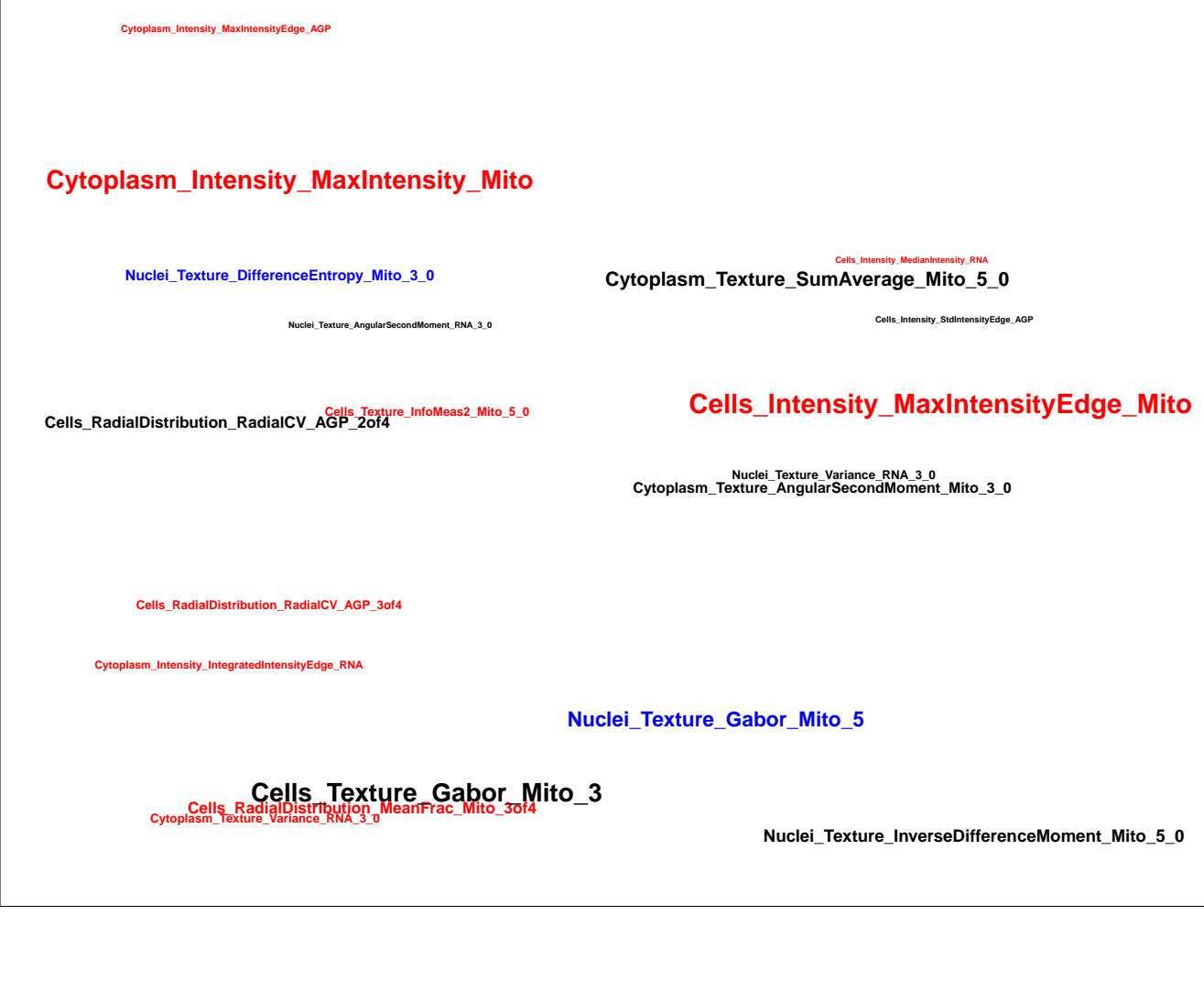
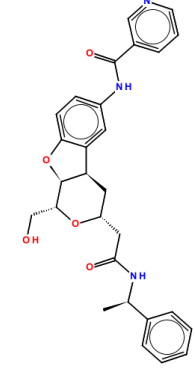
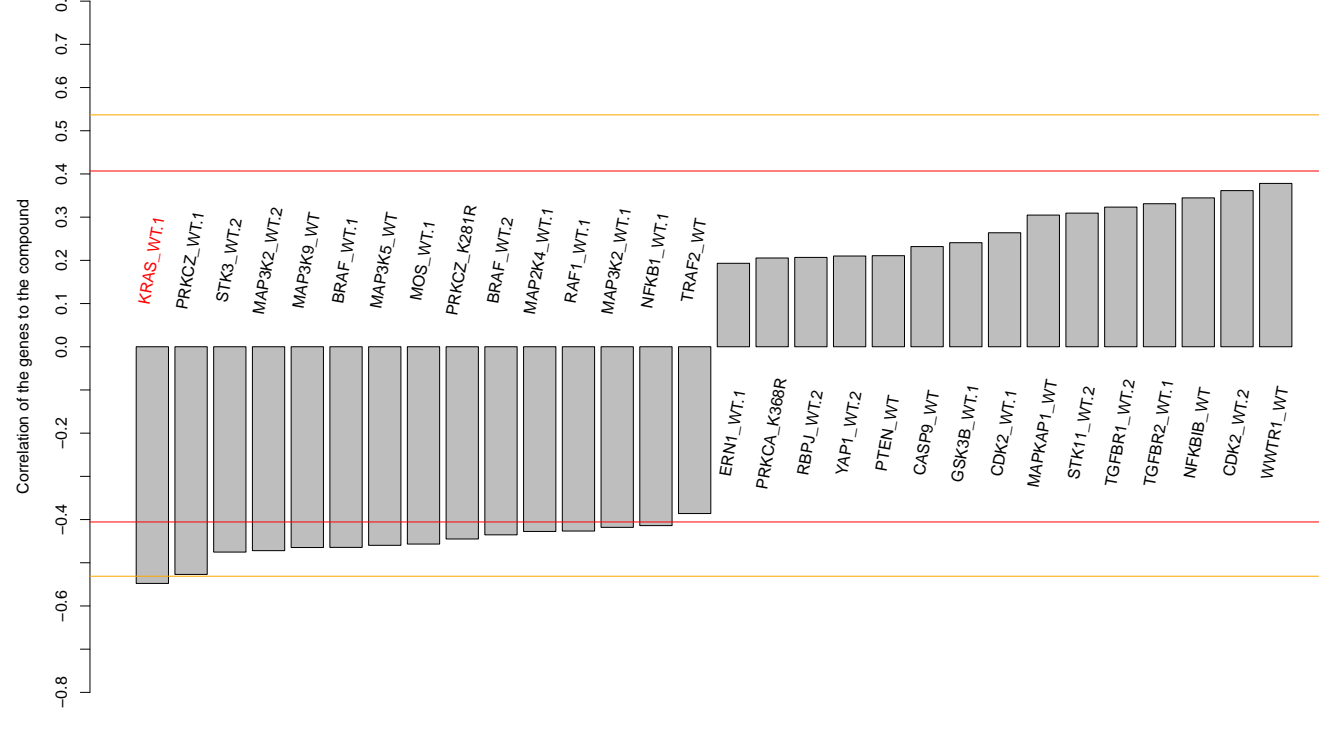
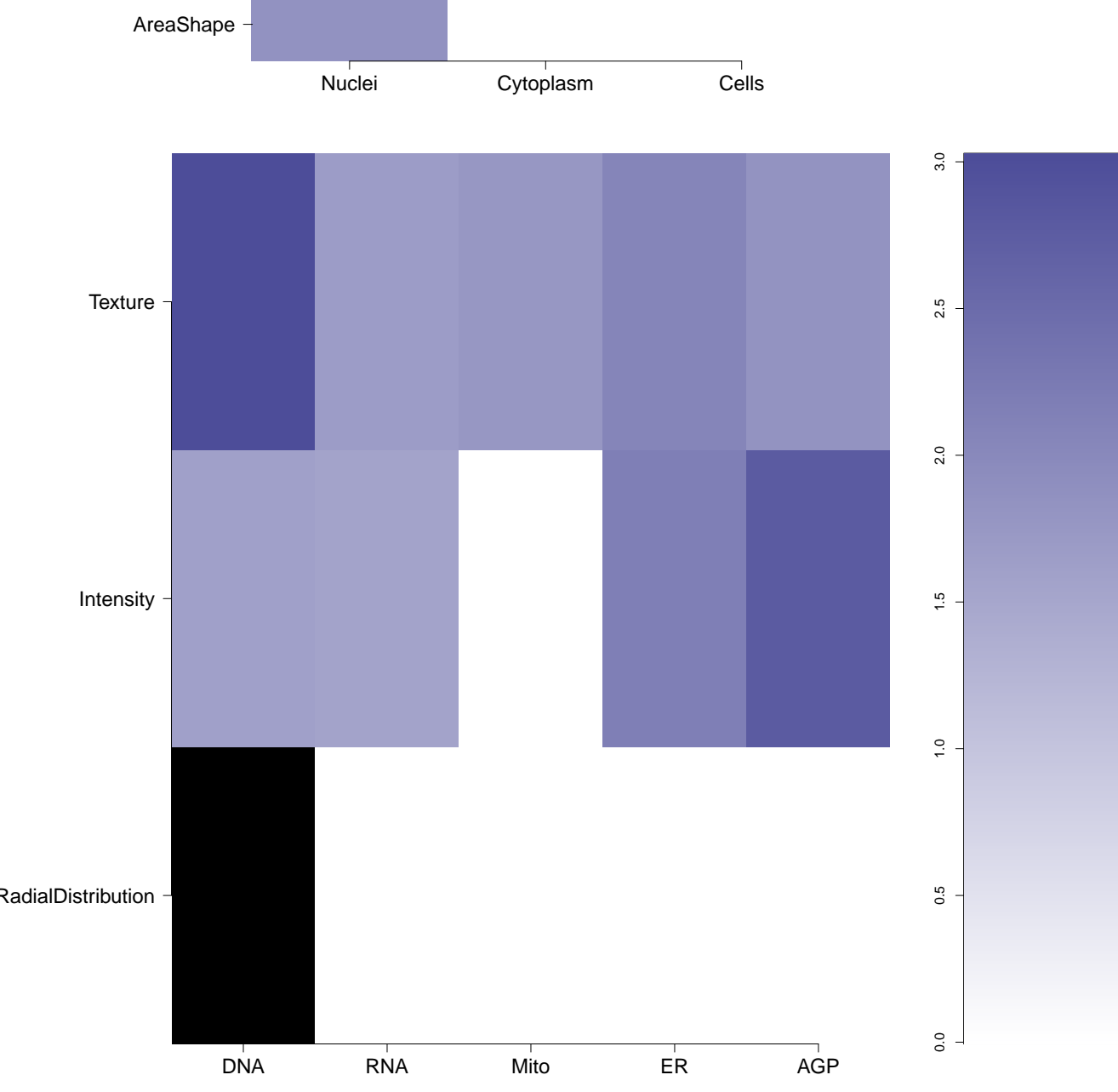

ER



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 0.52)	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-K60861723-001-01-1 PubChem CID : 54646599		0.90 (in 4 replicates)	0.57	0.662				Total number of assays tested in: 38.
BRD-K65963096-001-01-9 PubChem CID : 44486854		0.77 (in 3 replicates)	0.56	0.008				Total number of assays tested in: 54.
BRD-K12834930-001-01-6 PubChem CID : 54618605		0.91 (in 4 replicates)	0.55	0.831				Total number of assays tested in: 23.
BRD-K82157325-001-02-8 MLS002474370 SMR001398531 PubChem CID : 44202021		0.93 (in 3 replicates)	0.54	0.662				Total number of assays tested in: 372. Active in the following assays: <ul style="list-style-type: none"> HTS for Identification of VLA-4 Allosteric Modulators from MLPCN library (AID 2557) uHTS Luminescent assay for identification of activators of mouse intestinal alkaline phosphatase (AID 2805) DENV2 CPE-Based HTS Measured in Cell-Based and Microorganism Combination System Using Plate Reader - 2149-01.Other.SinglePoint.HTS.Activity (AID 651640)
BRD-K91684468-001-01-9 PubChem CID : 54618781		0.88 (in 3 replicates)	0.53	0.672				Total number of assays tested in: 39.
BRD-K40750649-001-01-2 PubChem CID : 44488168		0.64 (in 3 replicates)	0.51	0.662				Total number of assays tested in: 46.
BRD-K08043024-001-01-7 PubChem CID : 44486366		0.91 (in 3 replicates)	0.50	0.766				Total number of assays tested in: 37.

BRD-K14518681-001-01-4 PubChem CID : 54647915		0.56 (in 3 replicates)	0.48	NA				Total number of assays tested in: 37.
BRD-K29285912-001-01-4 PubChem CID : 44497256		NA (in 1 replicates)	0.45	0.662				Total number of assays tested in: 47.
BRD-K44746563-001-01-8 PubChem CID : 44505605		NA (in 1 replicates)	0.44	0.662				Total number of assays tested in: 27.
BRD-K30562320-001-01-9 PubChem CID : 54641066		NA (in 1 replicates)	-0.66	NA				Total number of assays tested in: 38.
BRD-K18341023-001-01-4 PubChem CID : 54634197		0.56 (in 4 replicates)	-0.61	NA				Total number of assays tested in: 34.
BRD-K07787963-001-05-4 MLS000042070 AC1NTW7G HMS2183L15 STL057077 ZINC20326393 SMR000058149 PubChem CID : 5389638		NA (in 1 replicates)	-0.61	NA				Total number of assays tested in: 768. Active in the following assays: <ul style="list-style-type: none"> Primary Antimicrobial Assay for E. coli BW25113 and 8710:tolC::kan Protocol for 384-well HTS (AID 573) Antimicrobial Assay for E. coli BW25113 and 8710:tolC::kan - Dose Response (AID 617) Allosteric Modulators of D1 Receptors: Primary Screen (AID 641) Allosteric Modulators of D1 Receptors: Confirmation Screen (AID 642) Allosteric Modulators of D1 Receptors: Secondary Assay 2 (AID 647) Cell signaling CRE-BLA (Fak stim) (AID 662) Screening for Modulators of Post-Golgi Transport, Control Strain (AID 738) CYP2C9 Assay (AID 777) Fluorescence-based cell-based primary high throughput screening assay to identify antagonists of the human trace amine associated receptor 1 (TAAR1) (AID 624466) Fluorescence-based cell-based primary high throughput screening assay to identify agonists of the human trace amine associated receptor 1 (TAAR1) (AID 624467) Fluorescence-based cell-based primary high throughput confirmation assay to identify agonists of the human trace amine associated receptor 1 (TAAR1) (AID 651783) Counterscreen for agonists of the human trace amine associated receptor 1 (hTAAR1): Fluorescence-based cell-based high throughput screening assay to identify nonselective Ga16 antagonists (AID 651952) Fluorescence-based biochemical high throughput primary assay to identify inhibitors of phospholipase C isozymes (PLC-gamma1). (AID 720700)
BRD-K76825413-001-01-3 PubChem CID : 44496828		0.83 (in 3 replicates)	-0.59	0.338				Total number of assays tested in: 33.

BRD-K84054400-001-01-5 PubChem CID : 44485354		0.84 (in 3 replicates)	-0.58	0.209				Total number of assays tested in: 55.
BRD-K78842668-001-06-7 T0509-3020 ZINC03240940 AC1M5Q0E MLS001004239 HMS2700G23 ZINC3240940 SMR000347877 PubChem CID : 2358432		0.82 (in 2 replicates)	-0.58	NA				Total number of assays tested in: 637. Active in the following assays: <ul style="list-style-type: none"> Primary cell-based high throughput screening assay to measure STAT1 activation (AID 932) Confirmation cell-based high throughput screening assay to measure STAT1 activation (AID 1262) Primary screen for compounds that activate Alzheimer's amyloid precursor (AID 1276) Counterscreen assay for STAT1 activators: Cell-based high throughput assay to measure NF-kappaB activation (AID 1306) Counterscreen assay for STAT1 activators: Cell-based high throughput assay to measure STAT3 activation (AID 1316) qHTS Assay for Enhancers of SMN2 Splice Variant Expression (AID 1458) MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814) Luminescence Cell-Based Dose Response HTS to Identify Activators of 5'UTR Stem-Loop Driven Prion Protein mRNA Translation in H4 Neuroglia2oma Cells (AID 1999) qHTS Assay for Modulators of miR-21 and/or Inhibitors of miR-21 (AID 2289) Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314) A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315) qHTS Assay for Rab9 Promoter Activators (AID 485297) qHTS Assay for NPC1 Promoter Activators (AID 485313) Luminescence-based primary cell-based high throughput screening assay to identify inhibitors of the orphan nuclear receptor subfamily 0, group B, member 1 (DAX1; NR0B1) (AID 504766) qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342) qHTS Assay to Identify Small Molecule Activators of BRCA1 Expression (AID 624202) qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 686978) Luminescence-based cell-based primary high throughput screening assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12). (AID 687014) Counterscreen for inhibitors of 5-mCpG-binding domain protein 2 (MBD2): TRFRET-based biochemical primary high throughput screening assay to identify inhibitors of binding of ubiquitin-like with PHD and ring finger domains 1 (UHRF1) to methylated oligonucleotide (AID 687016) Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12). (AID 743050)
BRD-K44287054-001-01-9 PubChem CID : 54647377		0.61 (in 4 replicates)	-0.57	0.241				Total number of assays tested in: 39.
BRD-K98061543-001-01-2 PubChem CID : 44485960		0.79 (in 3 replicates)	-0.57	0.141				Total number of assays tested in: 56.
BRD-K49424866-001-01-1 PubChem CID : 44488107		0.86 (in 4 replicates)	-0.55	0.131				Total number of assays tested in: 56.
BRD-K21281680-001-01-1 PubChem CID : 54646634		0.81 (in 4 replicates)	-0.55	0.338				Total number of assays tested in: 43. Active in the following assays: <ul style="list-style-type: none"> Viability counterscreen of potential LMP-1 inhibitors in HEK293 cell background Measured in Cell-Based System Using Plate Reader - 2122-02.Inhibitor.Dose.DryPowder.Activity.Set2 (AID 624374)