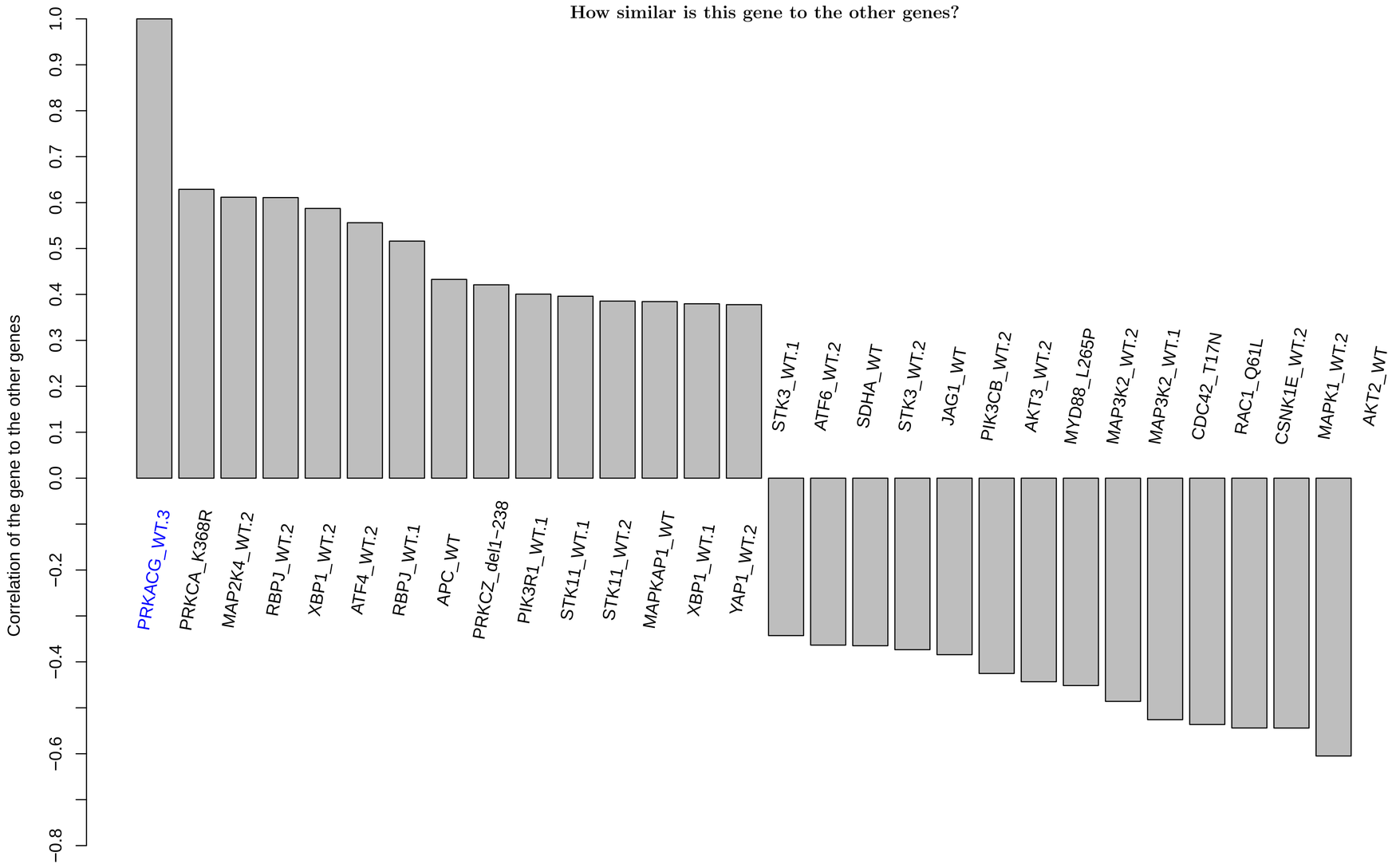
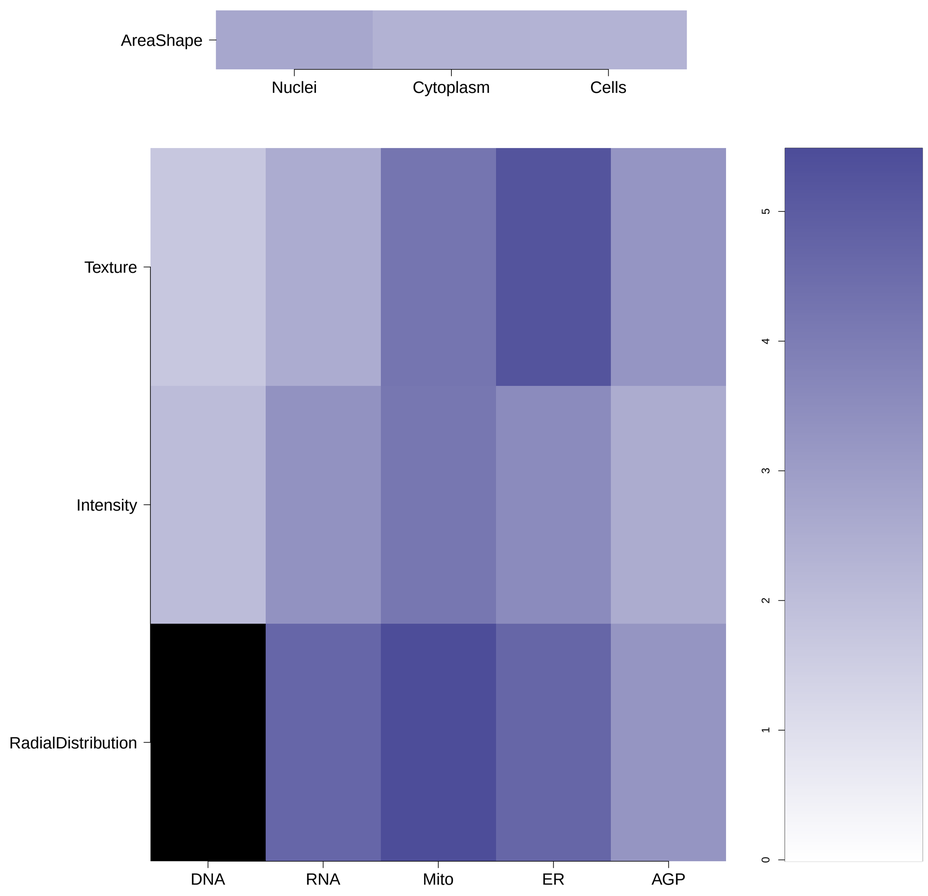
PRKACG_WT.3 - in PKA

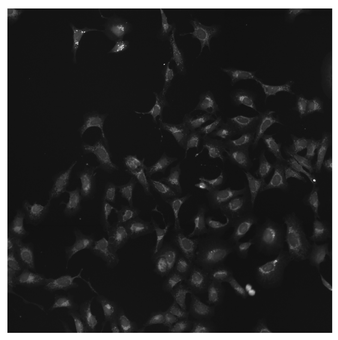
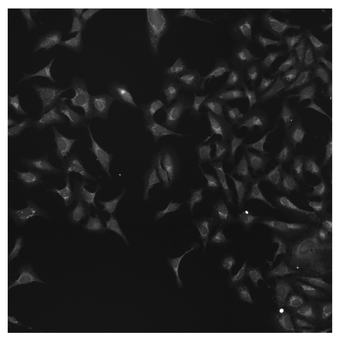
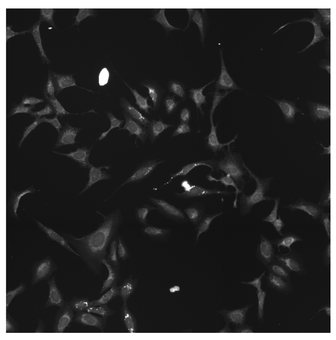
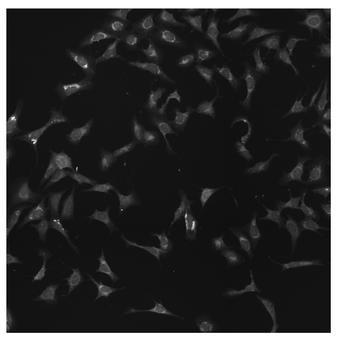
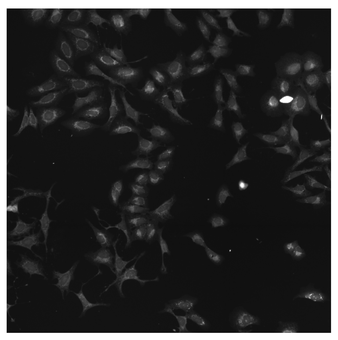
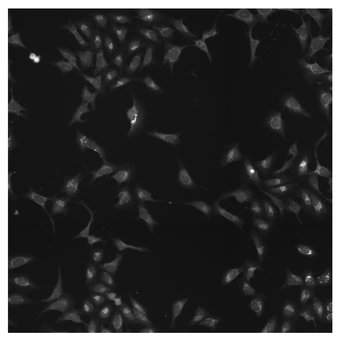
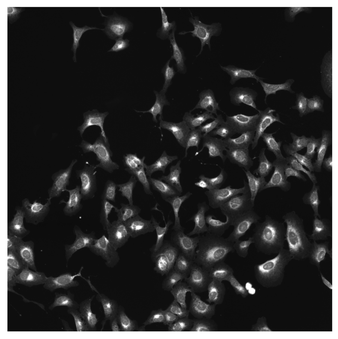
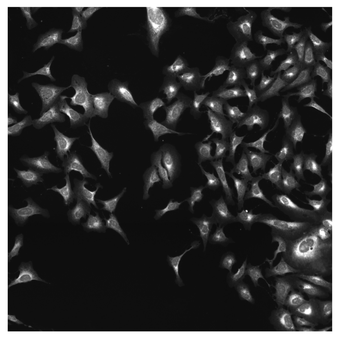
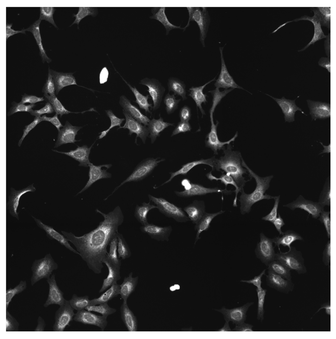
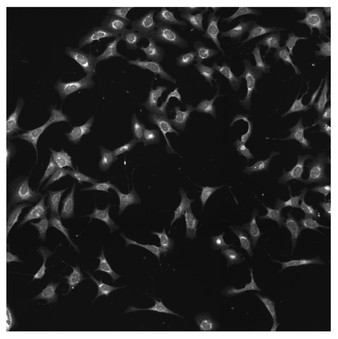
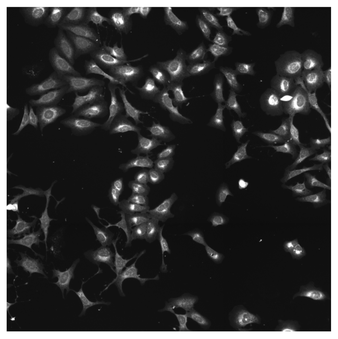
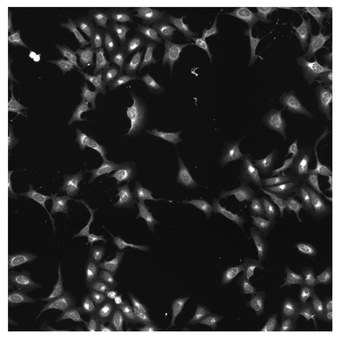
How similar is this gene to the other genes?



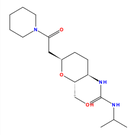
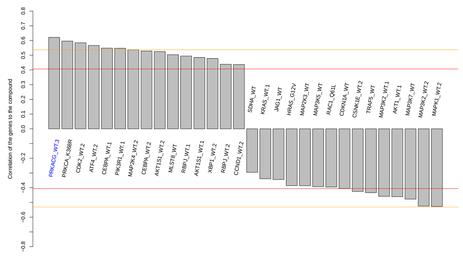
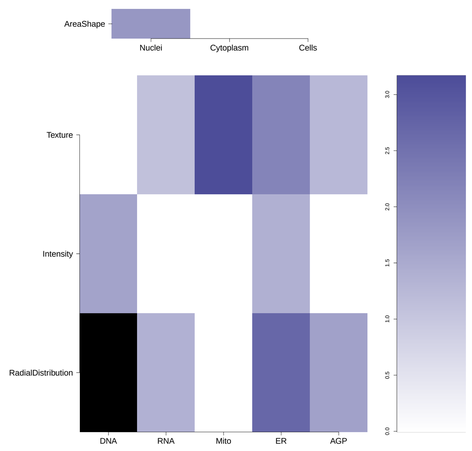
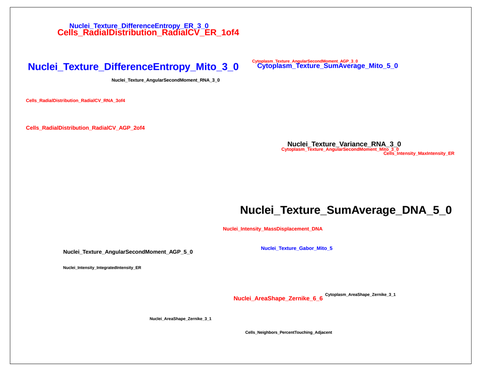
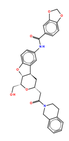
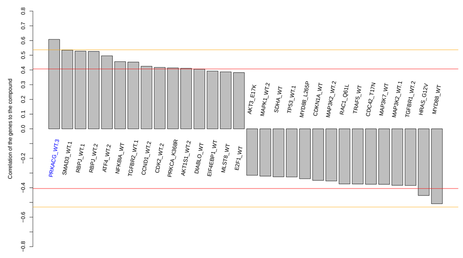
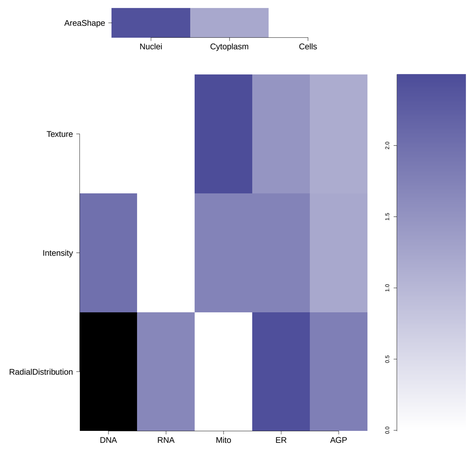
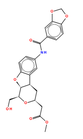
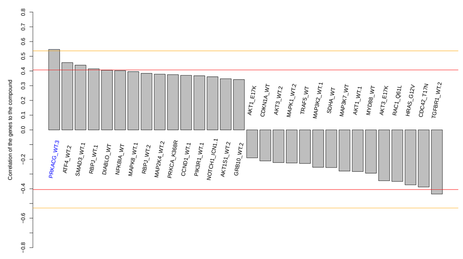
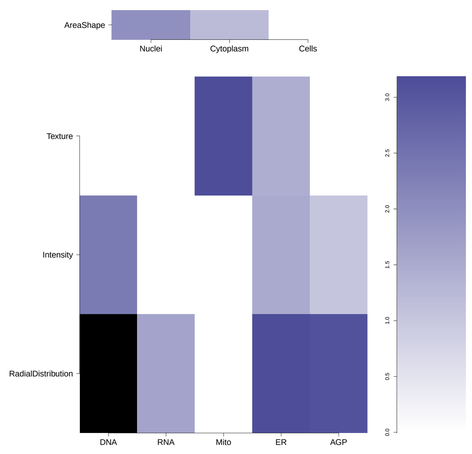
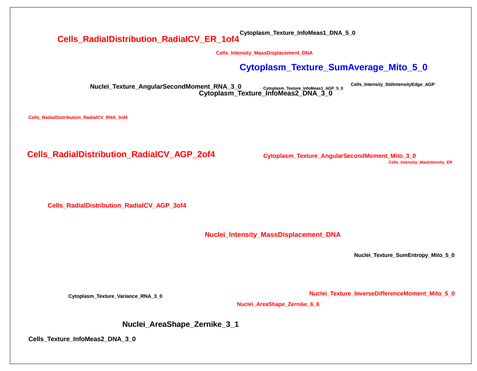
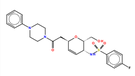
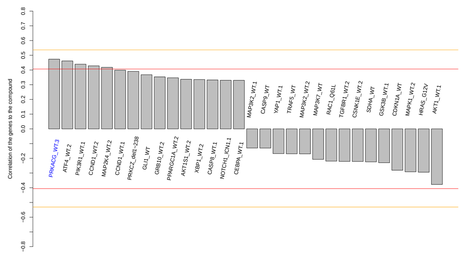
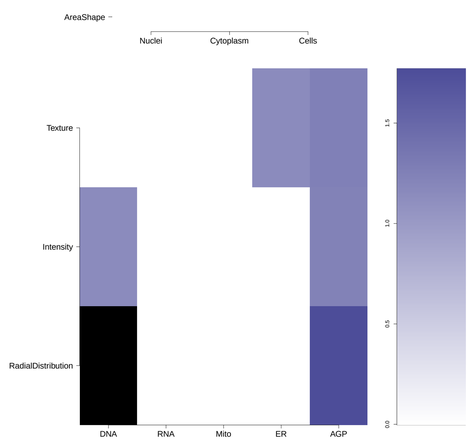
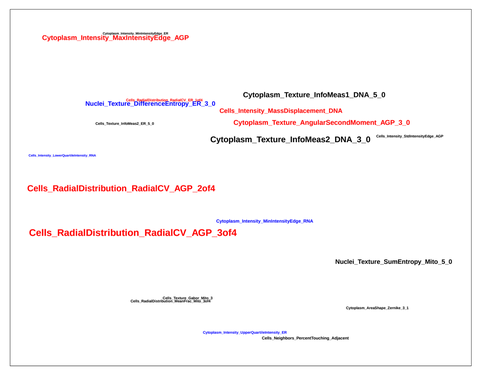
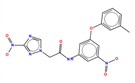
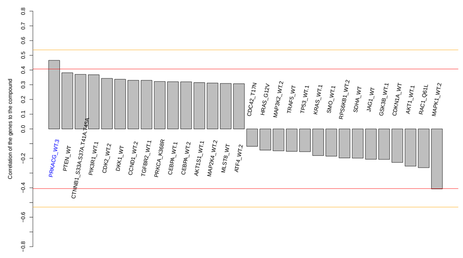
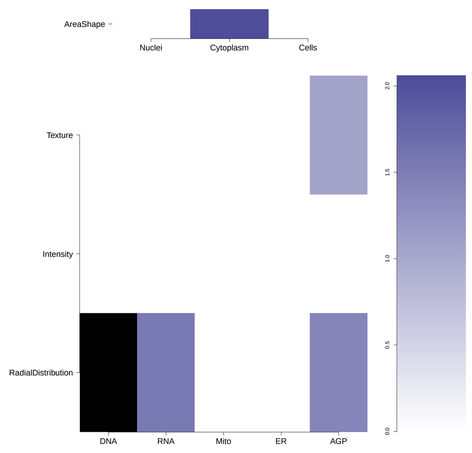
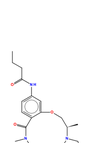
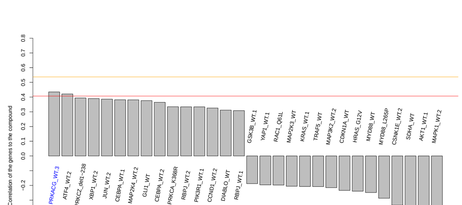
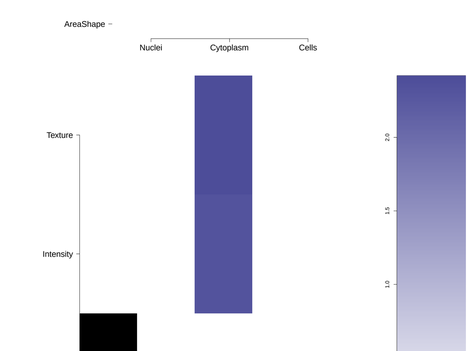
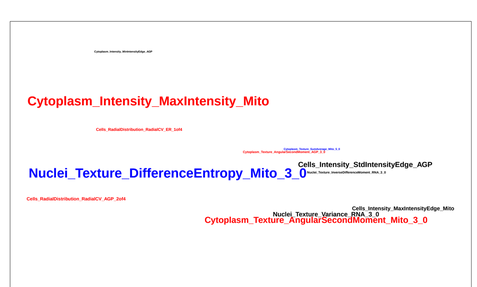
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the category

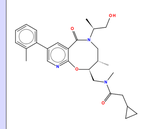
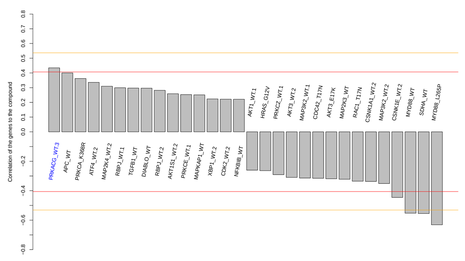
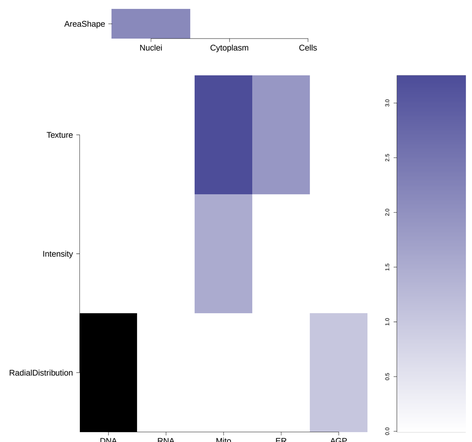
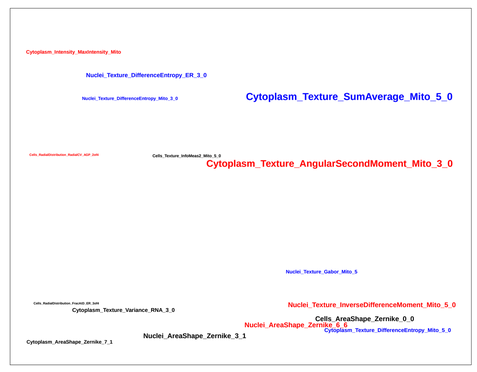
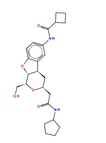
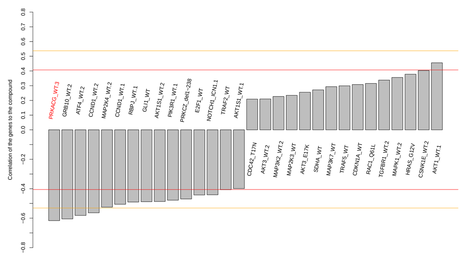
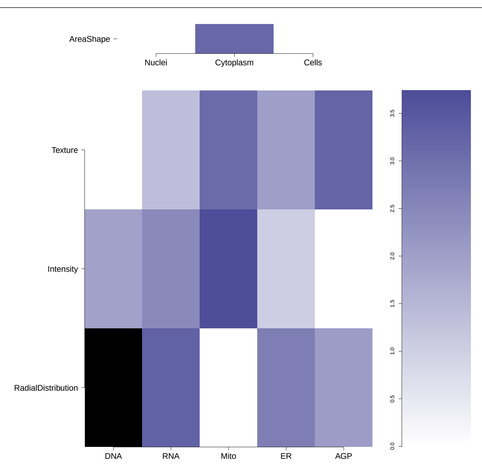
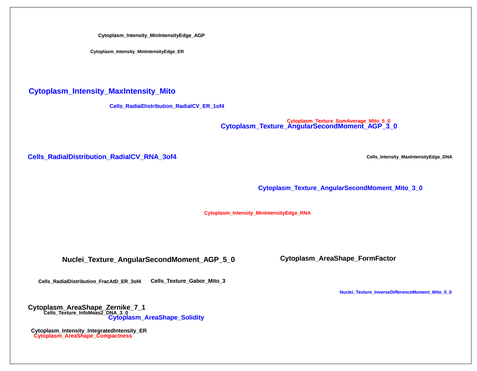
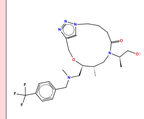
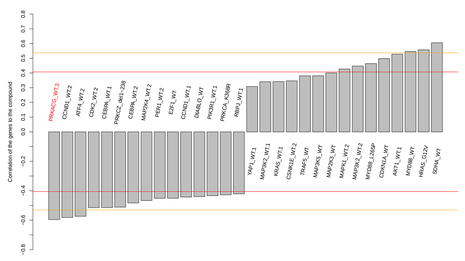
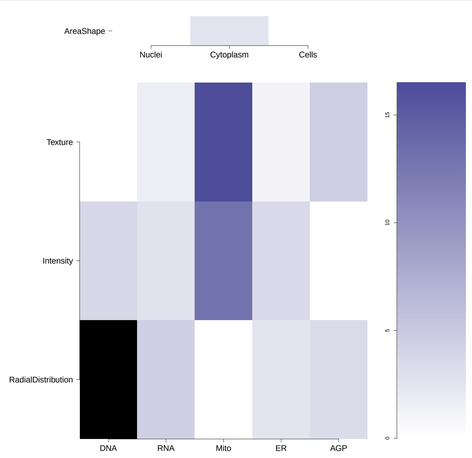
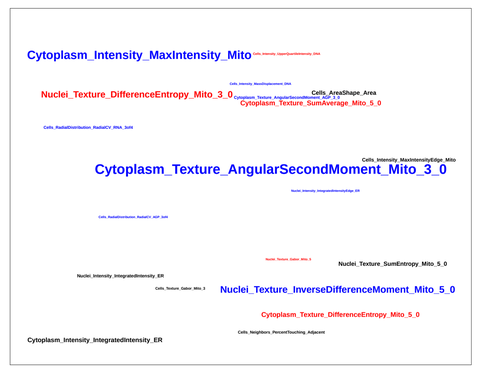
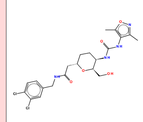
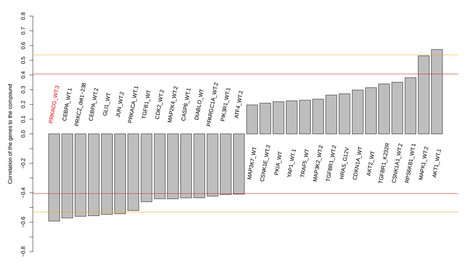
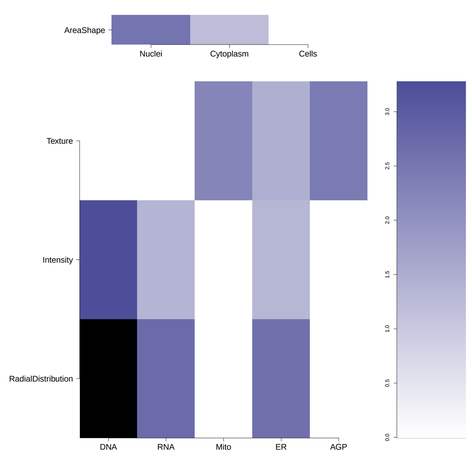
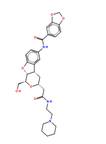
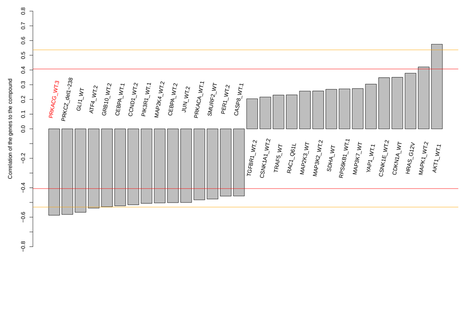
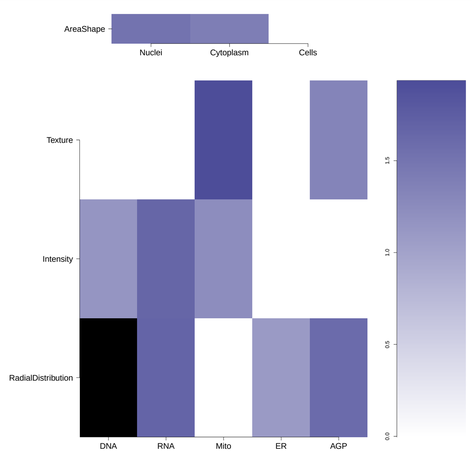
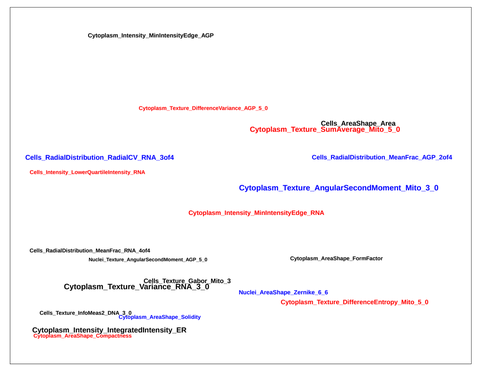
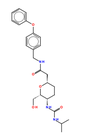
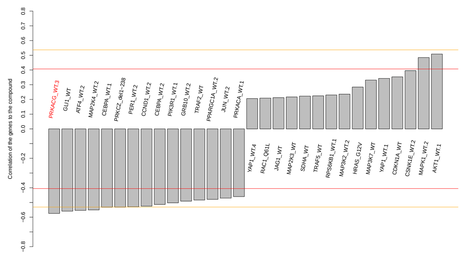
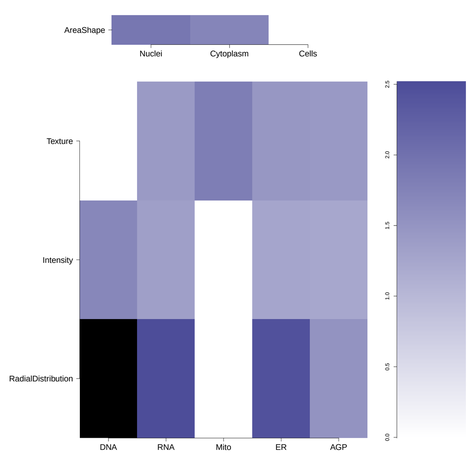
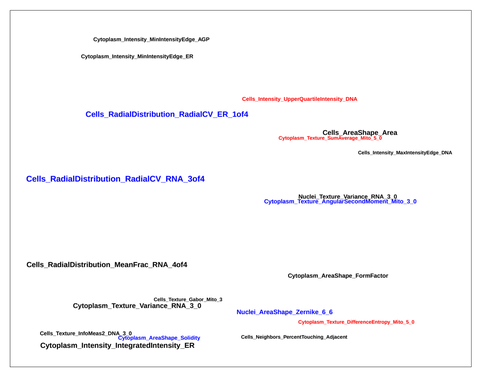
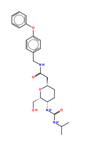
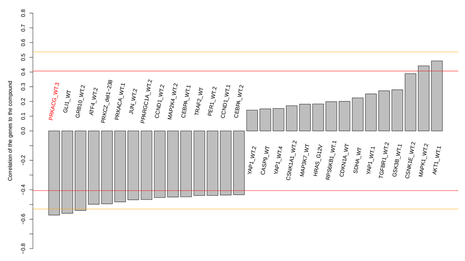
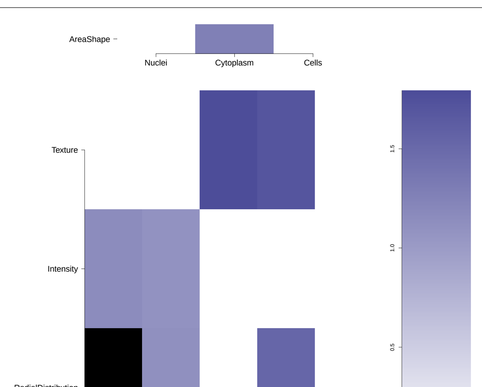


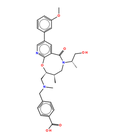
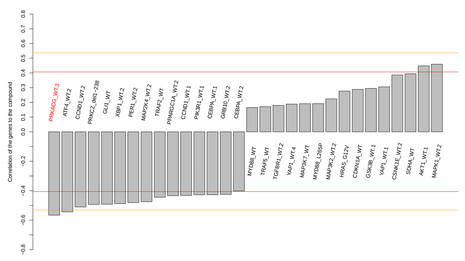
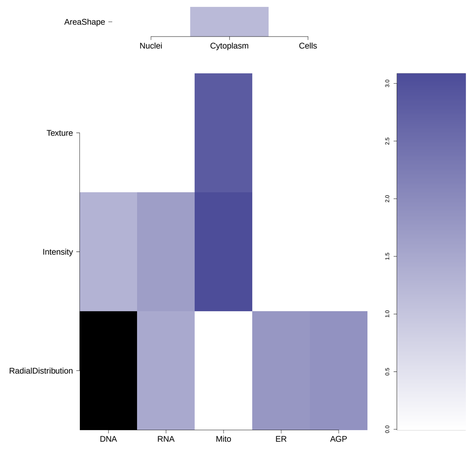
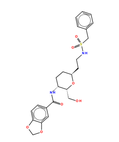
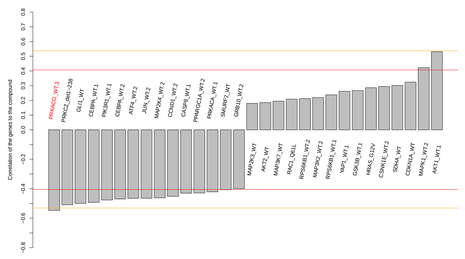
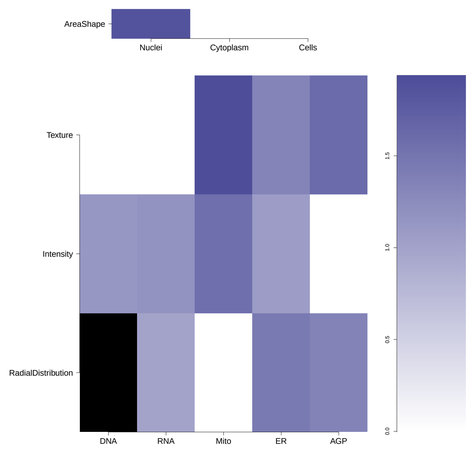
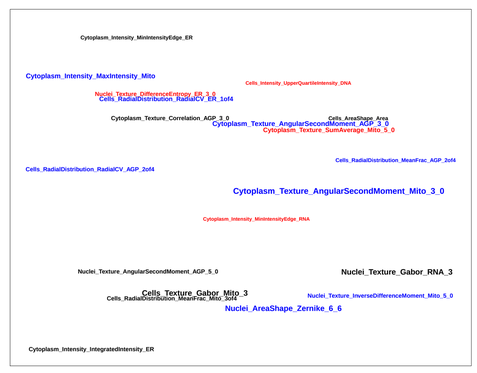
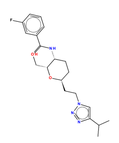
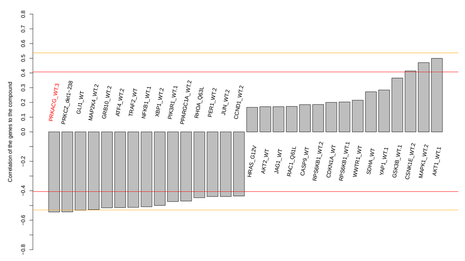
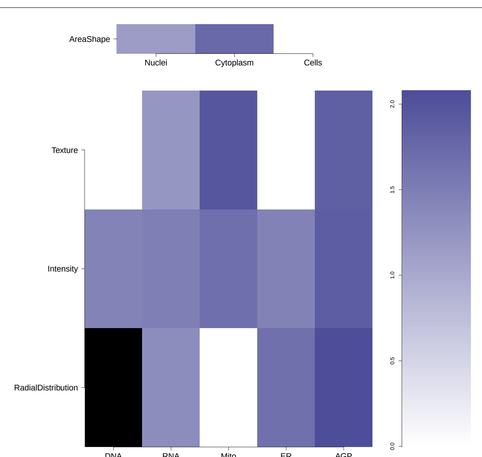
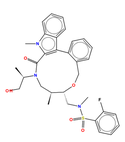
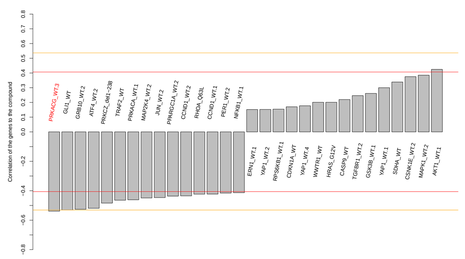
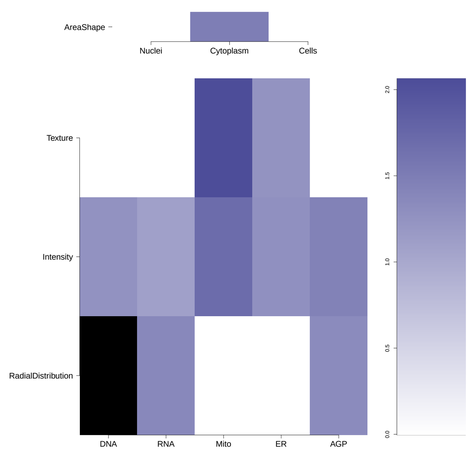
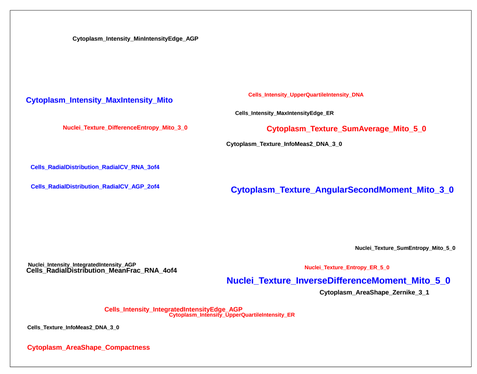
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

Empty	PRKACG_WT.3 (41744)	PRKACG_WT.3 (41755)	PRKACG_WT.3 (41756)	PRKACG_WT.3 (41757)	PRKACG_WT.3 (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 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-K43695862-001-01-6 PubChem CID : 54641228		NA (in 1 replicates)	0.62	NA				Total number of assays tested in: 35.
BRD-K78761249-001-01-8 PubChem CID : 54645870		NA (in 1 replicates)	0.61	0.036				Total number of assays tested in: 42.
BRD-K74287511-001-01-9 PubChem CID : 54645804		NA (in 1 replicates)	0.55	0.048				Total number of assays tested in: 40.
BRD-K08514109-001-01-5 PubChem CID : 54640866		0.64 (in 4 replicates)	0.47	0.695				Total number of assays tested in: 37.
BRD-K23860736-001-04-8 BAS 00535158 AC1LYXQ4 MLS000566921 HMS2574L15 ZINC2287951 STK342654 ZINC02287951 SMR000175371 ST50686648 PubChem CID : 1910052		NA (in 1 replicates)	0.47	NA				Total number of assays tested in: 586. Active in the following assays: • High Throughput Screen to Identify Compounds that Suppress the Growth of Human Colon Tumor Cells Lacking Oncogenic Beta Catenin Expression - Dose Response (AID 1045) • High Throughput Screen to Identify Compounds that Suppress the Growth of Cells with a Deletion of the PTEN Tumor Suppressor - Dose Response (AID 1047) • Leishmania major promastigote HTS (AID 1063) • Counterscreen for PME1 inhibitors: fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of lysophospholipase 2 (LYPLA2). (AID 2177) • HTS for small molecule inhibitors of CHOP to regulate the unfolded protein response to ER stress (AID 2732) • Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of the plasma platelet activating factor acetylhydrolase (pPAFAH) (AID 463082) • qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332) • uHTS identification of small molecule inhibitors of the thioesterase domain of fatty acid synthase via a fluorescence intensity assay (AID 602261) • uHTS identification of small molecule inhibitors of the mitochondrial permeability transition pore via an absorbance assay (AID 602449) • Single concentration confirmation of uHTS inhibitor hits of the mitochondrial permeability transition pore via a fluorescent based assay (AID 624504) • Fluorescence-based biochemical high throughput screening primary assay to identify inhibitors of Crimean-Congo Hemorrhagic Fever (CCHF) viral ovarian tumor domain protease (vOTU): Pep-AMC substrate (AID 651958) • QFRET-based biochemical primary high throughput screening assay to identify exosite inhibitors of ADAM10. (AID 720582) • Fluorescence-based biochemical high throughput primary assay to identify inhibitors of phospholipase C isozymes (PLC-gamma1). (AID 720700)
BRD-K82073510-001-01-4 PubChem CID : 54632730		0.58 (in 4 replicates)	0.43	NA				Total number of assays tested in: 40.

BRD-K40321450-001-01-0 PubChem CID : 54618404		0.74 (in 4 replicates)	0.43	0.693				Total number of assays tested in: 23.
BRD-K25994126-001-01-7 PubChem CID : 54645954		NA (in 1 replicates)	-0.62	0.281				Total number of assays tested in: 40.
BRD-K54647996-001-01-2 PubChem CID : 44495442		0.92 (in 3 replicates)	-0.60	0.734				Total number of assays tested in: 33.
BRD-K20546229-001-01-6 PubChem CID : 54641131		NA (in 1 replicates)	-0.59	NA				Total number of assays tested in: 38.
BRD-K56719502-001-01-4 PubChem CID : 54646017		0.64 (in 2 replicates)	-0.59	0.209				Total number of assays tested in: 42.
BRD-K72934042-001-01-6 PubChem CID : 54640569		0.77 (in 4 replicates)	-0.57	0.312				Total number of assays tested in: 36. Active in the following assays: • ARNT-TAC3: AlphaScreen HTS to detect disruption of ARNT/TAC3 interactions Measured in Biochemical System Using Plate Reader - 2158-01_Inhibitor_SinglePoint_HTS_Activity (AID 623870)
BRD-K84990603-001-01-5 PubChem CID : 54640565		0.61 (in 4 replicates)	-0.57	0.174				Total number of assays tested in: 36.

BRD-K72694472-001-01-5 PubChem CID : 54619548		0.75 (in 4 replicates)	-0.57	0.312				Total number of assays tested in: 32.
BRD-K08899466-001-01-7 PubChem CID : 54639932		0.64 (in 4 replicates)	-0.55	0.160				Total number of assays tested in: 36.
BRD-K96218803-001-01-5 PubChem CID : 54640781		0.77 (in 4 replicates)	-0.54	0.268				Total number of assays tested in: 39.
BRD-K43980524-001-01-2 PubChem CID : 56835389		0.57 (in 3 replicates)	-0.54	0.201				Total number of assays tested in: 34.