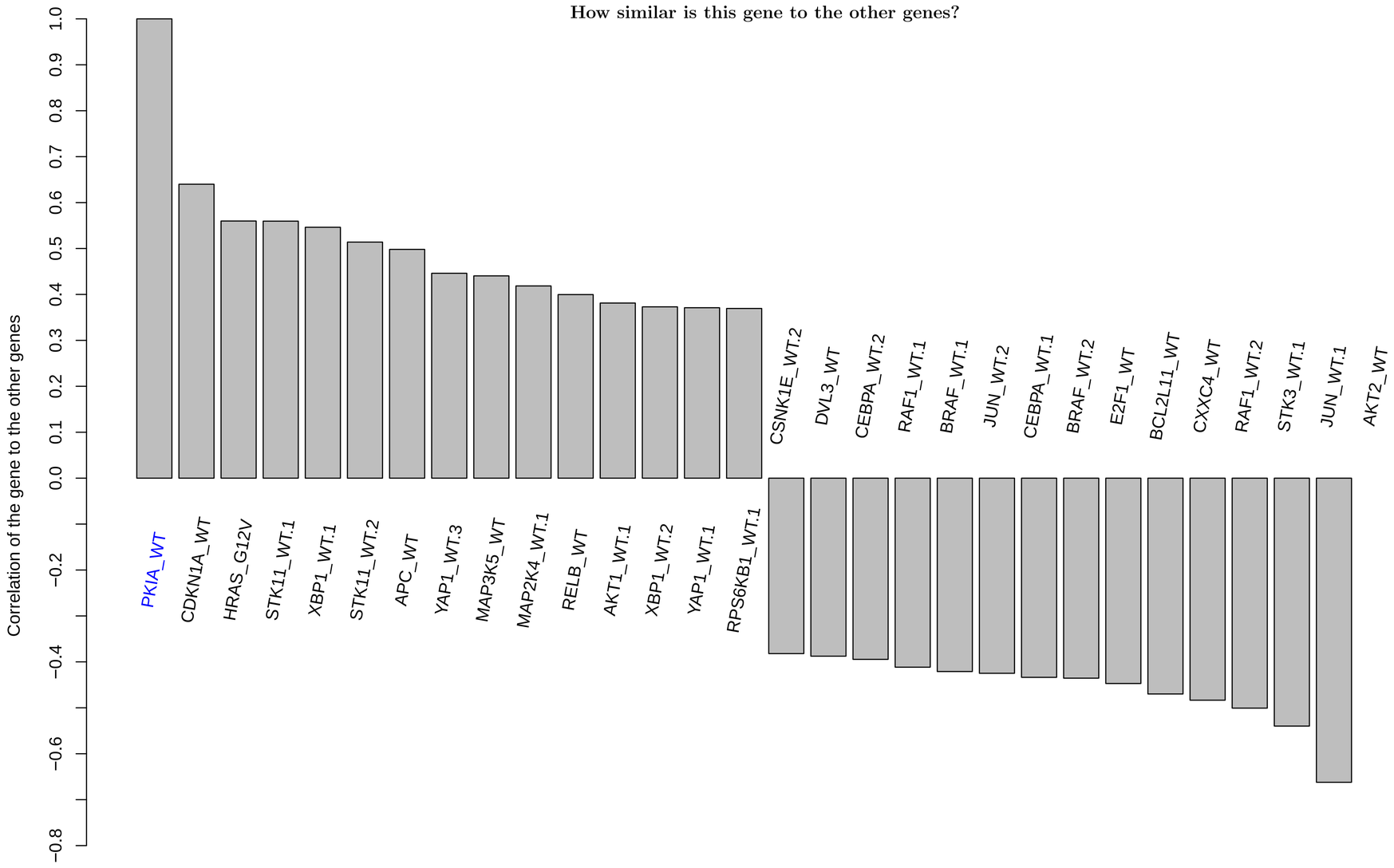
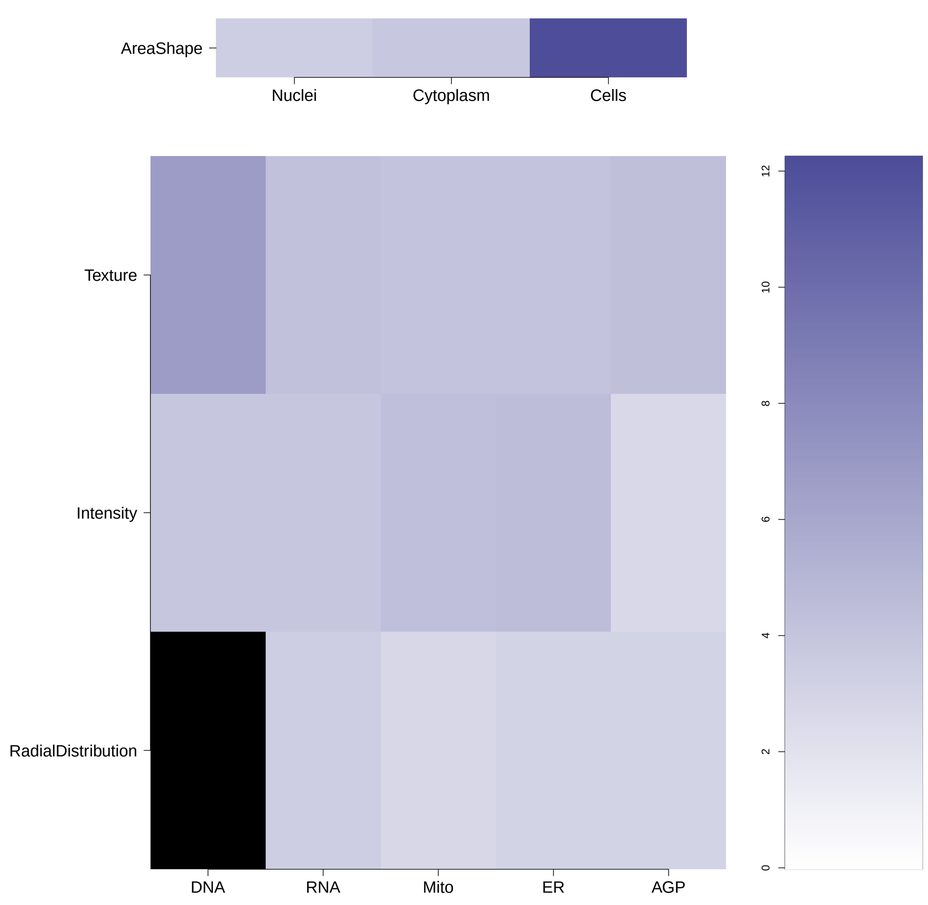
PKIA_WT - in PKA

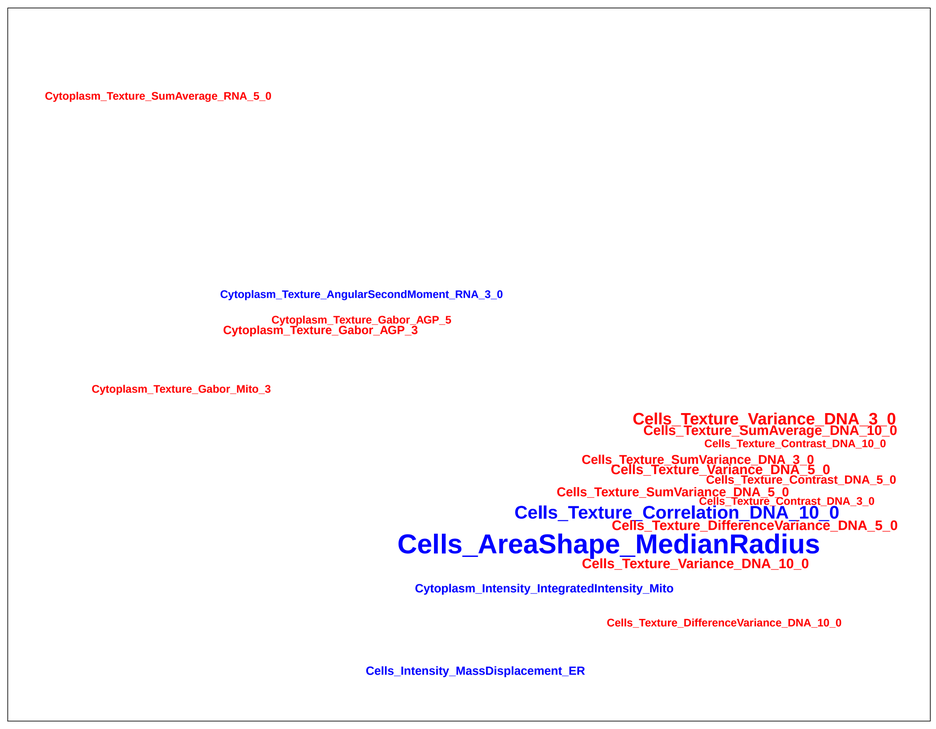
How similar is this gene to the other genes?

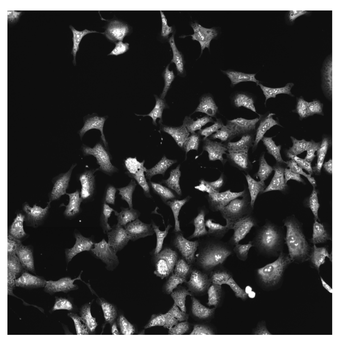
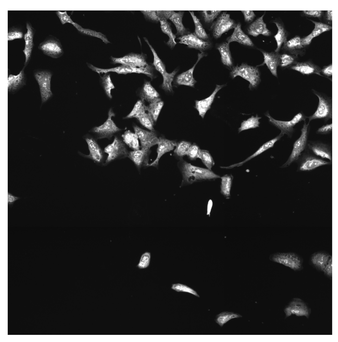
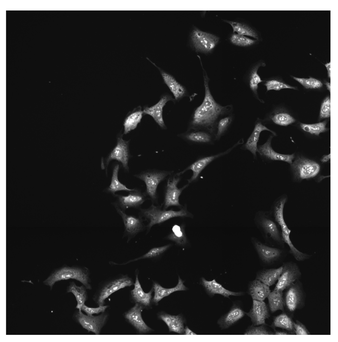
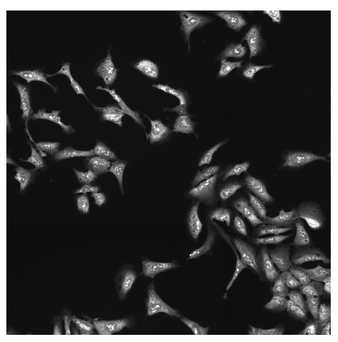
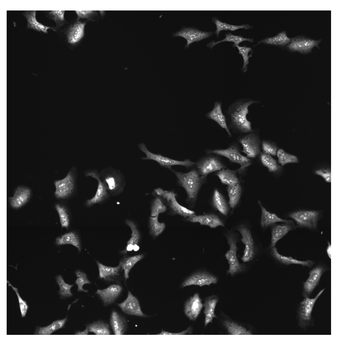
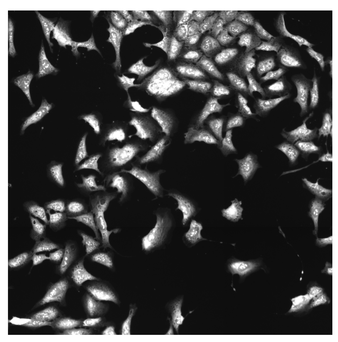
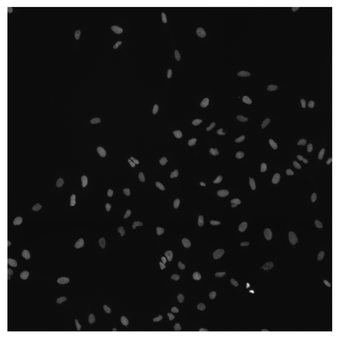
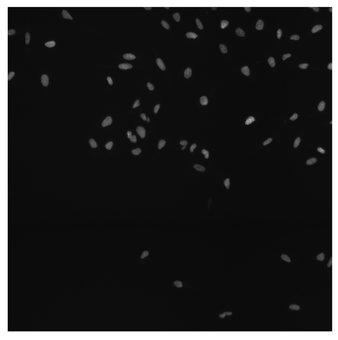
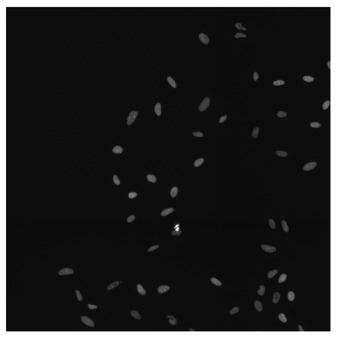
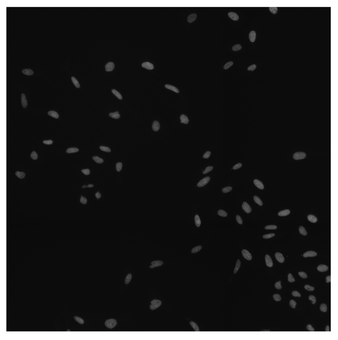
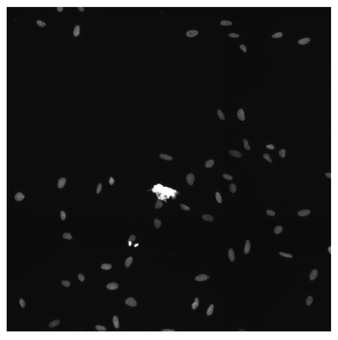
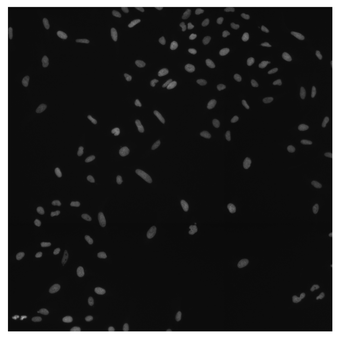


What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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

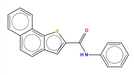
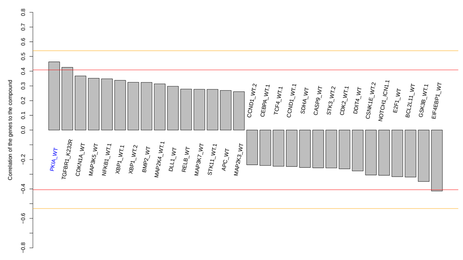
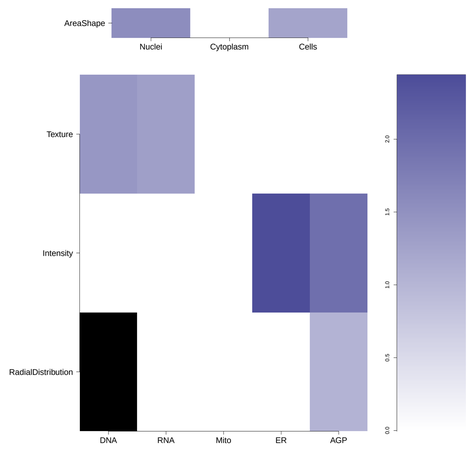
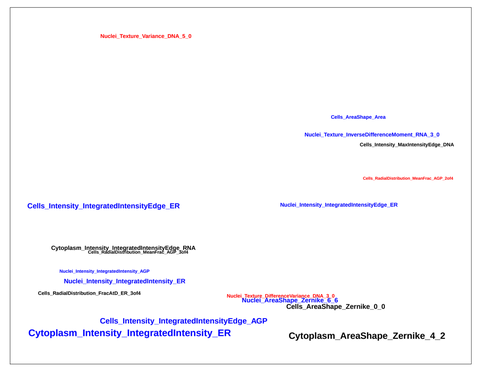
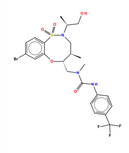
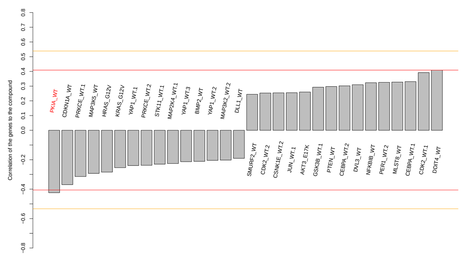
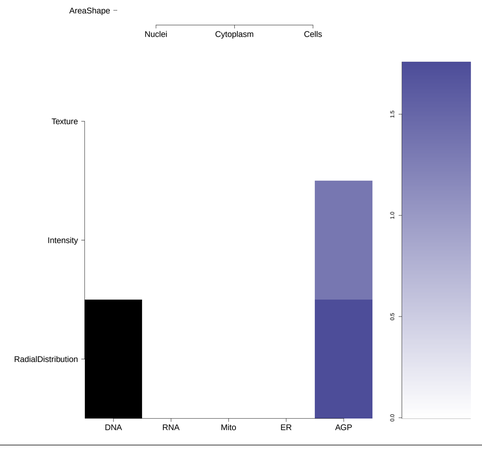
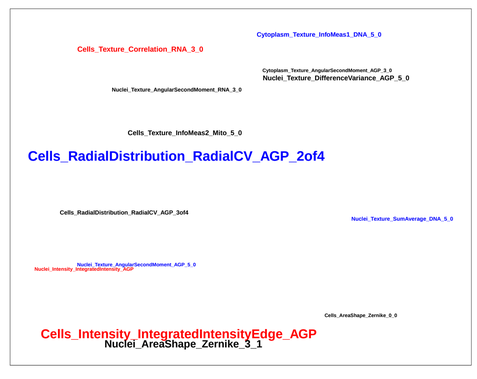


Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.



Empty	PKIA_WT (41744)	PKIA_WT (41755)	PKIA_WT (41756)	PKIA_WT (41757)	PKIA_WT (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 0.51)	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

BRD-K19209439-001-05-1 ZINC00068797 AC1MCU2K MLS000861032 ZINC68797 HMS2802H10 PD00015 SMR000459816 PubChem CID : 2825931		0.56 (in 3 replicates)	0.46	NA				Total number of assays tested in: 576. Active in the following assays: • MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814) • Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314) • A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315) • Luminescence-based primary cell-based high throughput screening assay to identify activators of the Aryl Hydrocarbon Receptor (AHR) (AID 2796) • uHTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 7 (SENP7) (AID 434973) • FRET-based cell-based primary high throughput screening assay to identify antagonists of the orexin 1 receptor (OX1R; HCRTR1) (AID 485270) • 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 purifed enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342) • Screen for inhibitors of the SWI/SNF chromatin remodeling complex (esBAF) in mouse embryonic stem cells with Luciferase reporter assay Measured in Cell-Based System Using Plate Reader - 2141-01_Inhibitor_SinglePoint_HTS_Activity (AID 602393) • qHTS Assay for Inhibitors of Hepatitis C Virus (HCV) (AID 651820) • Luminescence-based cell-based primary high throughput screening assay to identify activators of the DAF-12 from the parasite H. contortus (hcDAF-12) (AID 652067) • Luminescence-based cell-based primary high throughput screening assay to identify activators of the DAF-12 from the parasite S. stercoralis (ssDAF-12) (AID 652126) • 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) • Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. contortus (hcDAF-12) (AID 743032) • Luminescence-based cell-based high throughput confirmation assay to identify agonists of the DAF-12 from the parasite H. glycines (hgDAF-12). (AID 743050) • Wnt/Beta-catenin HTS Measured in Cell-Based System Using Plate Reader - 2161-01_Activator_SinglePoint_HTS_Activity (AID 743398)
BRD-K32099399-001-01-6 MLS003129983 SMR001834429 PubChem CID : 46903353		0.54 (in 4 replicates)	-0.42	0.862				Total number of assays tested in: 215. Active in the following assays: • HTS Assay for Peg3 Promoter Inhibitors (AID 588405) • qHTS of GLP-1 Receptor Inverse Agonists (Inhibition Mode) (AID 624417) • qHTS for Inhibitors of ATXN expression (AID 651635) • QFRET-based biochemical primary high throughput screening assay to identify exosite inhibitors of ADAM10. (AID 720582)