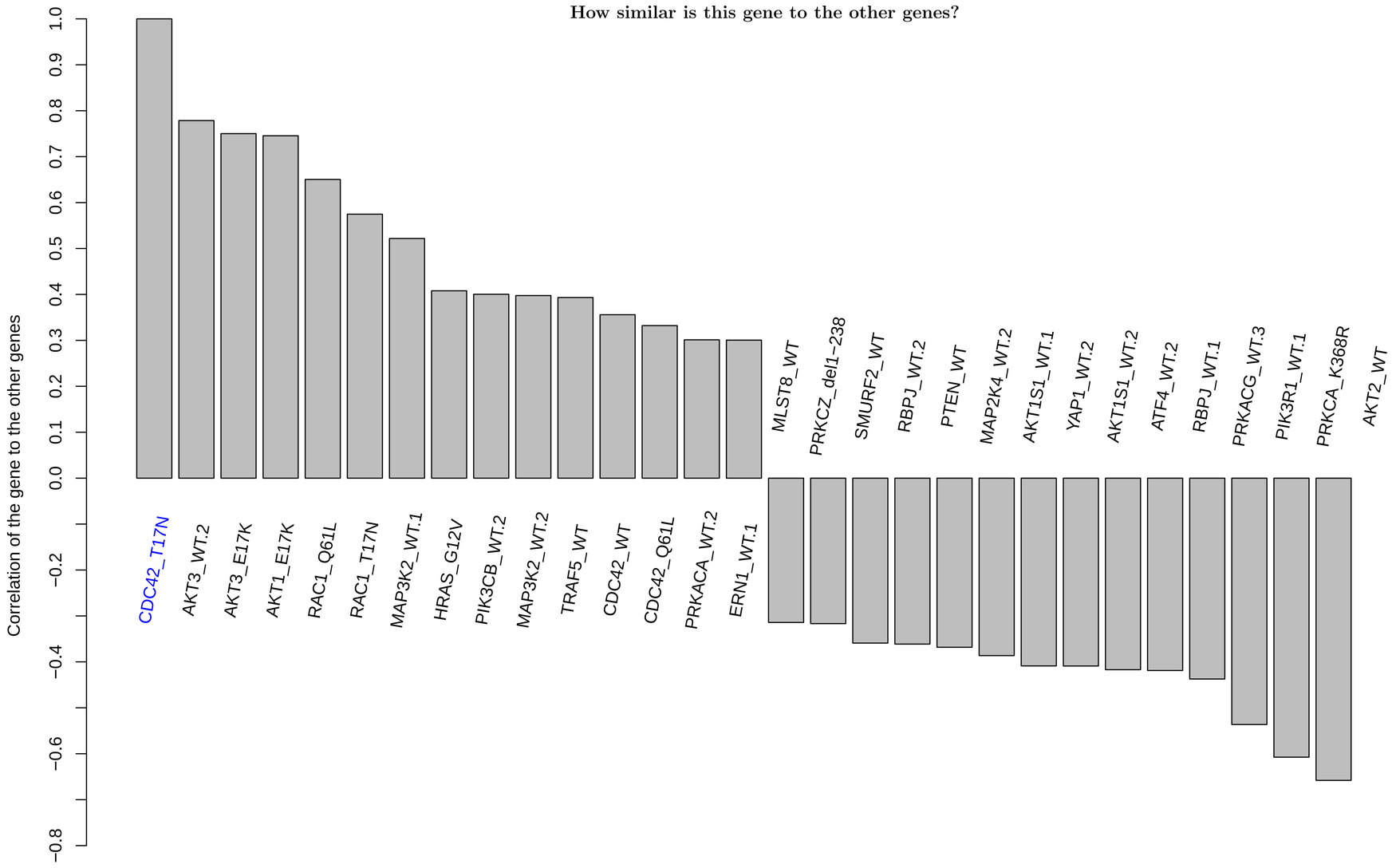
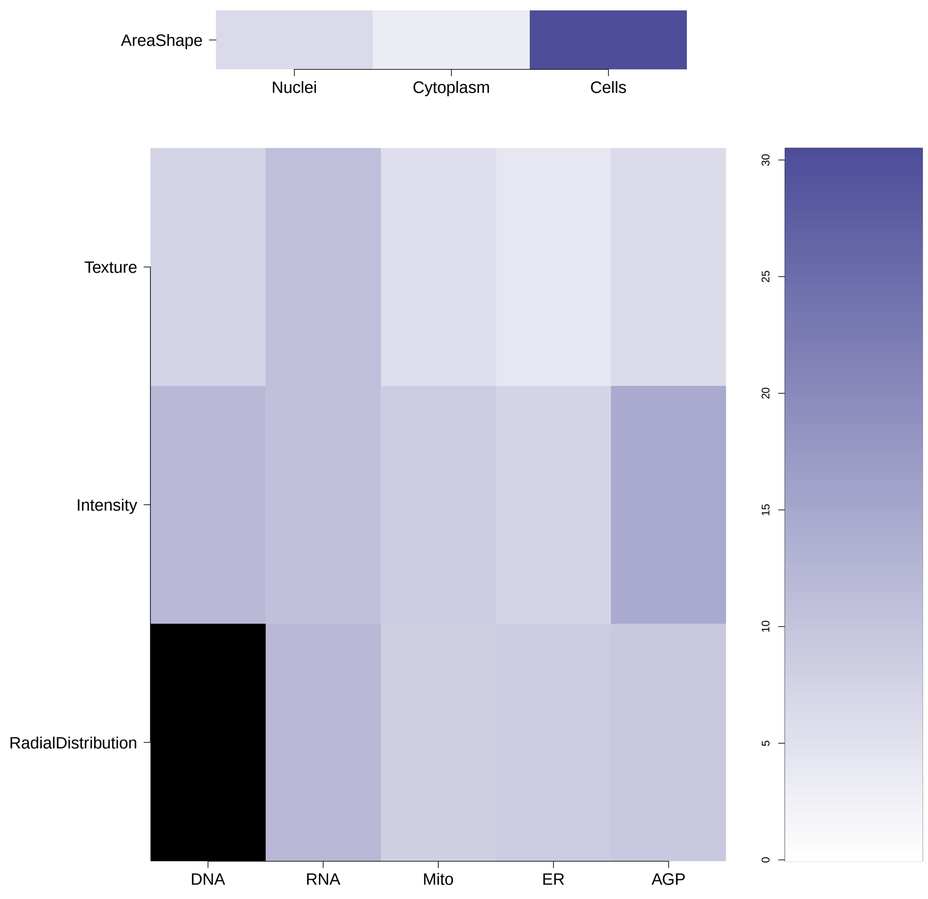
CDC42_T17N - in Canonical Cytoskeletal Re-org

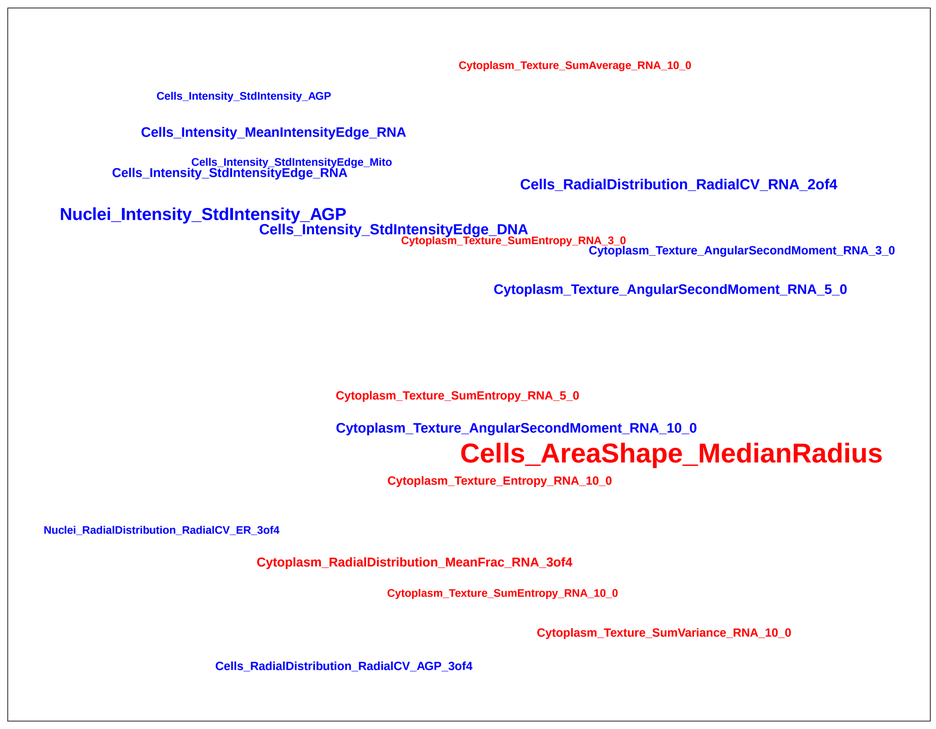
How similar is this gene to the other genes?

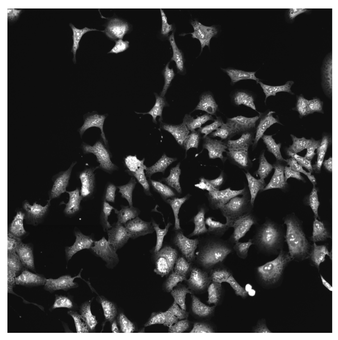
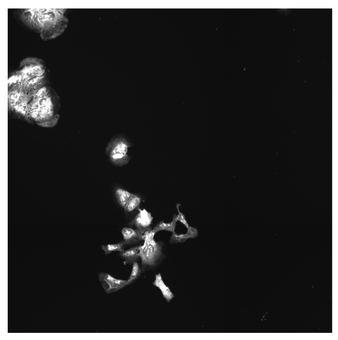
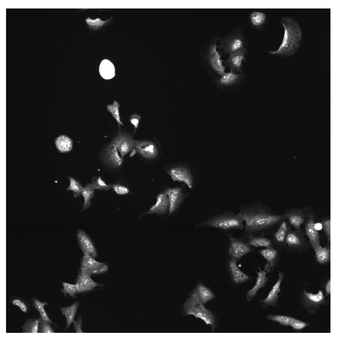
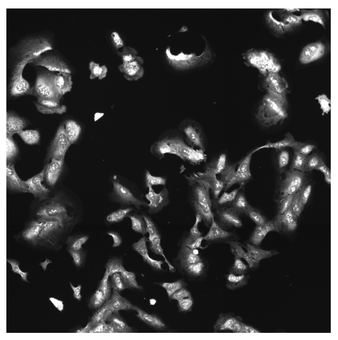
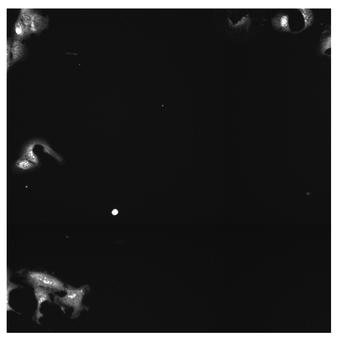
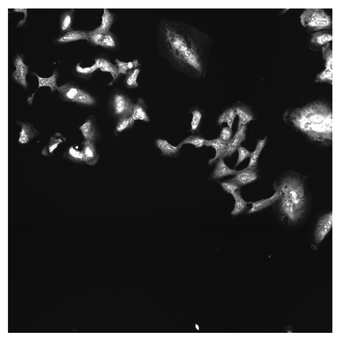
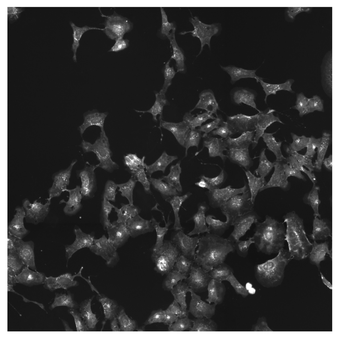
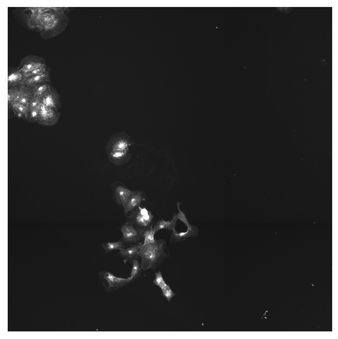
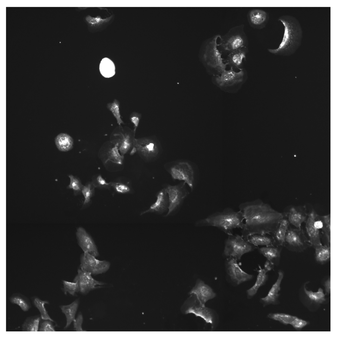
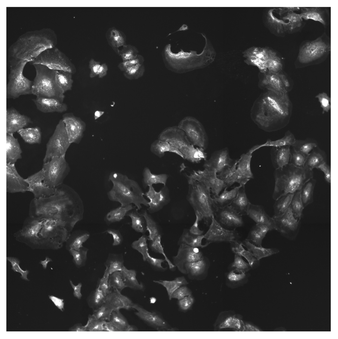
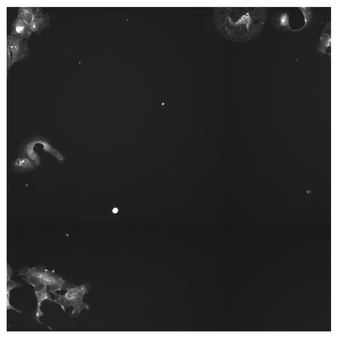
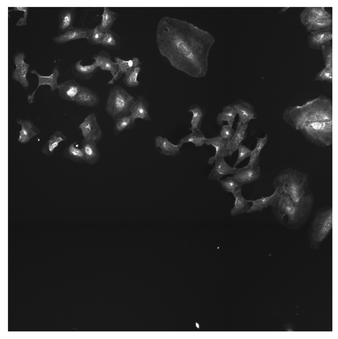


What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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

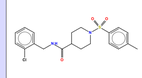
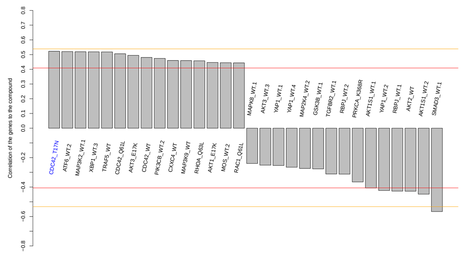
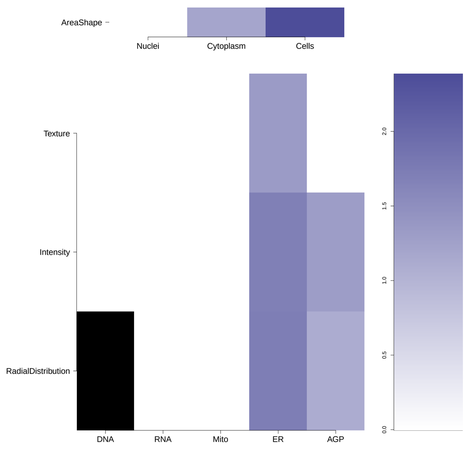
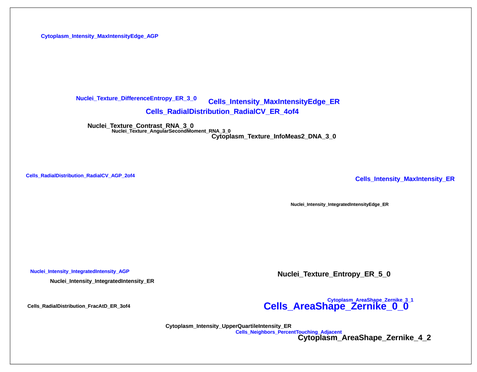
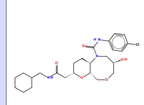
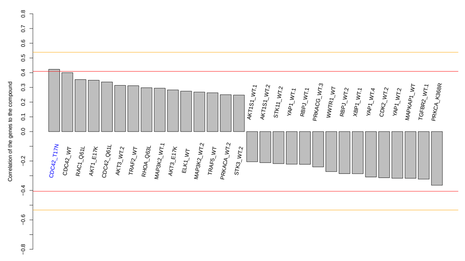
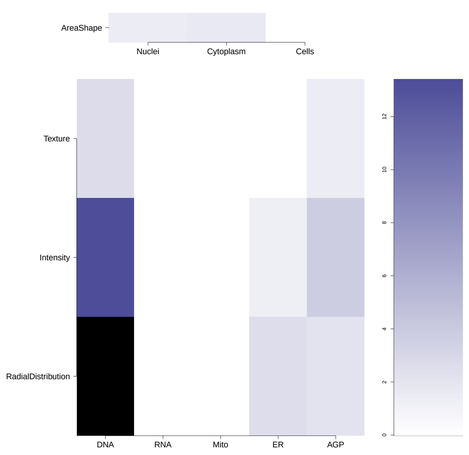
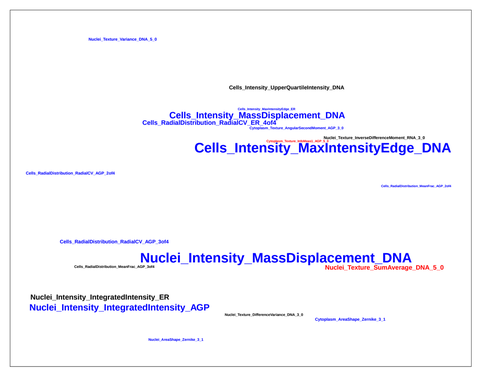
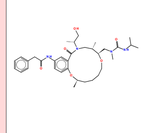
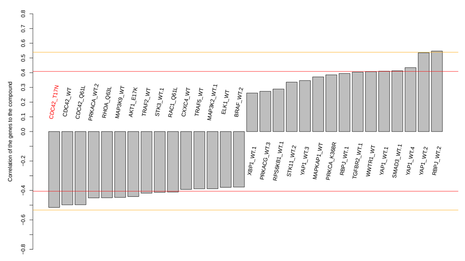
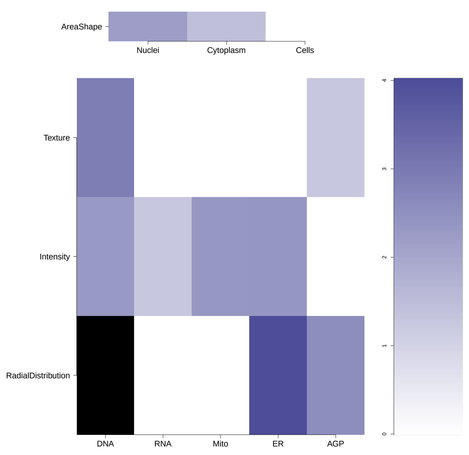
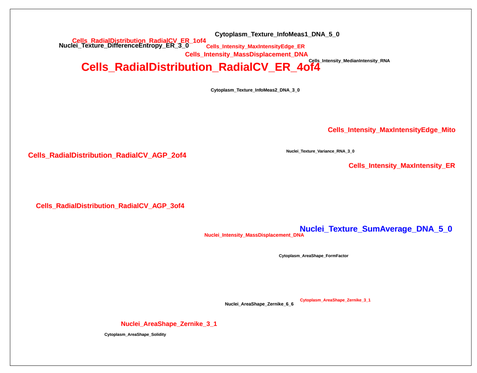
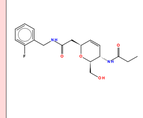
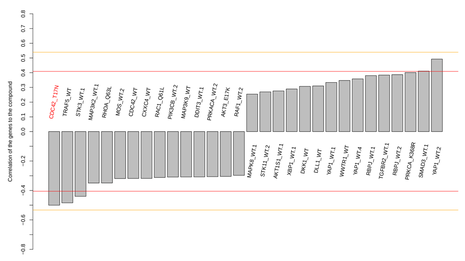
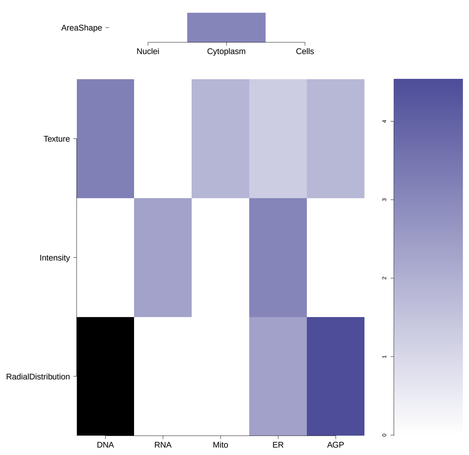
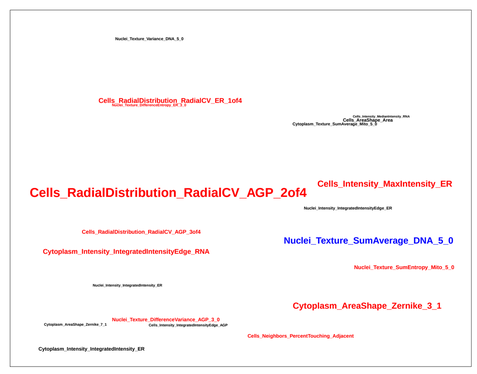
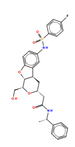
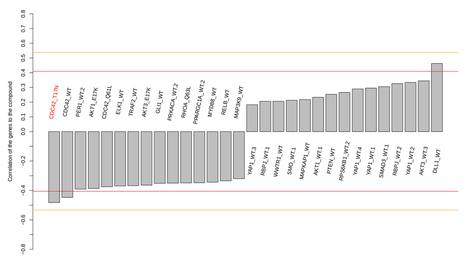
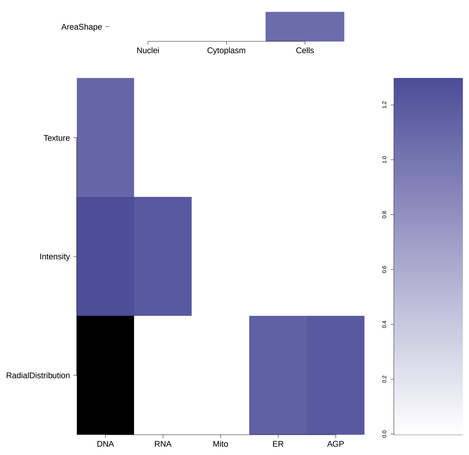
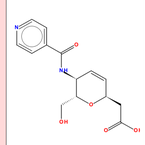
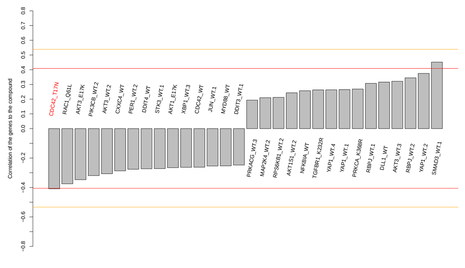
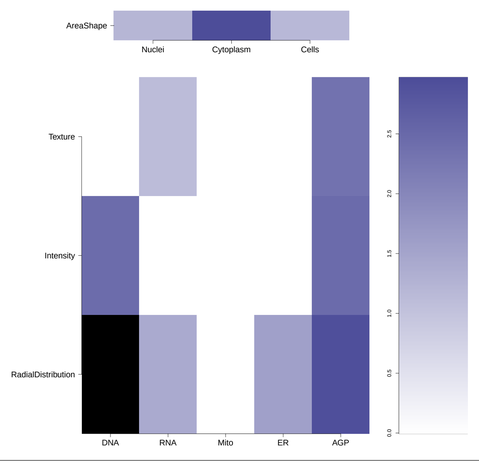
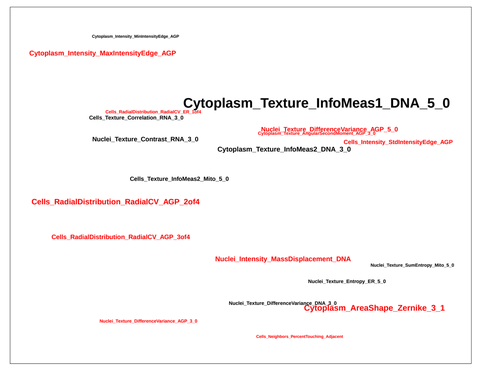


Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.



Empty	CDC42_T17N (41744)	CDC42_T17N (41755)	CDC42_T17N (41756)	CDC42_T17N (41757)	CDC42_T17N (41754)
RNA						
AGP						

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-K43089177-001-06-1 SMR000123694 MLS000123058 STK178377 AC1LL2IR BDBM73383 HMS1914K05 HMS2437P20 ZINC789542 ZINC00789542 BAS 05018824 ST50276881 K786-1645 PubChem CID : 1077699		NA (in 1 replicates)	0.52	NA				Total number of assays tested in: 700. Active in the following assays: • Leishmania major promastigote HTS (AID 1063) • Primary screen for compounds that activate Insulin promoter activity in TRM-6 cells (AID 1296) • Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Primary Screen (AID 1456) • Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Retesting of KCC2 cells with Ouabain (AID 1717) • Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of Protein Phosphatase Methylesterase 1 (PME-1). (AID 2130) • Fluorescence polarization-based biochemical high throughput confirmation assay for inhibitors of Protein Phosphatase Methylesterase 1 (PME-1). (AID 2171) • Fluorescence Polarization Cell-Free Homogeneous Primary HTS to Identify Inhibitors of the LANA Histone H2A/H2B Interaction (AID 2629) • uHTS fluorescent assay for identification of inhibitors of ATG4B (AID 504462) • Dose response confirmation of the uHTS fluorescent assay for identification of inhibitors of ATG4B. (AID 504756) • Single concentration confirmation of inhibitors of ATG4B via a fluorescent assay (AID 504757) • Primary qHTS for delayed death inhibitors of the malarial parasite plastid, 96 hour incubation (AID 504834) • Dose response counterscreen of uHTS hits for ATG4B inhibitors in a Phospholipase A2 assay (AID 588400)
BRD-K36130407-001-01-5 PubChem CID : 54657759		0.62 (in 4 replicates)	0.42	0.016				Total number of assays tested in: 40. Active in the following assays: • 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_Dose_CherryPick_Activity (AID 651717)
BRD-K89505656-001-01-2 PubChem CID : 44494377		0.65 (in 4 replicates)	-0.52	NA				Total number of assays tested in: 51.
BRD-K30158311-001-01-7 PubCID : 54641076		NA (in 1 replicates)	-0.50	NA				Total number of assays tested in: 38.
BRD-K08306736-001-01-7 PubCID : 54645948		NA (in 1 replicates)	-0.48	0.335				Total number of assays tested in: 40.
BRD-K29548095-001-01-4 PubCID : 54641321		NA (in 1 replicates)	-0.41	NA				Total number of assays tested in: 38.