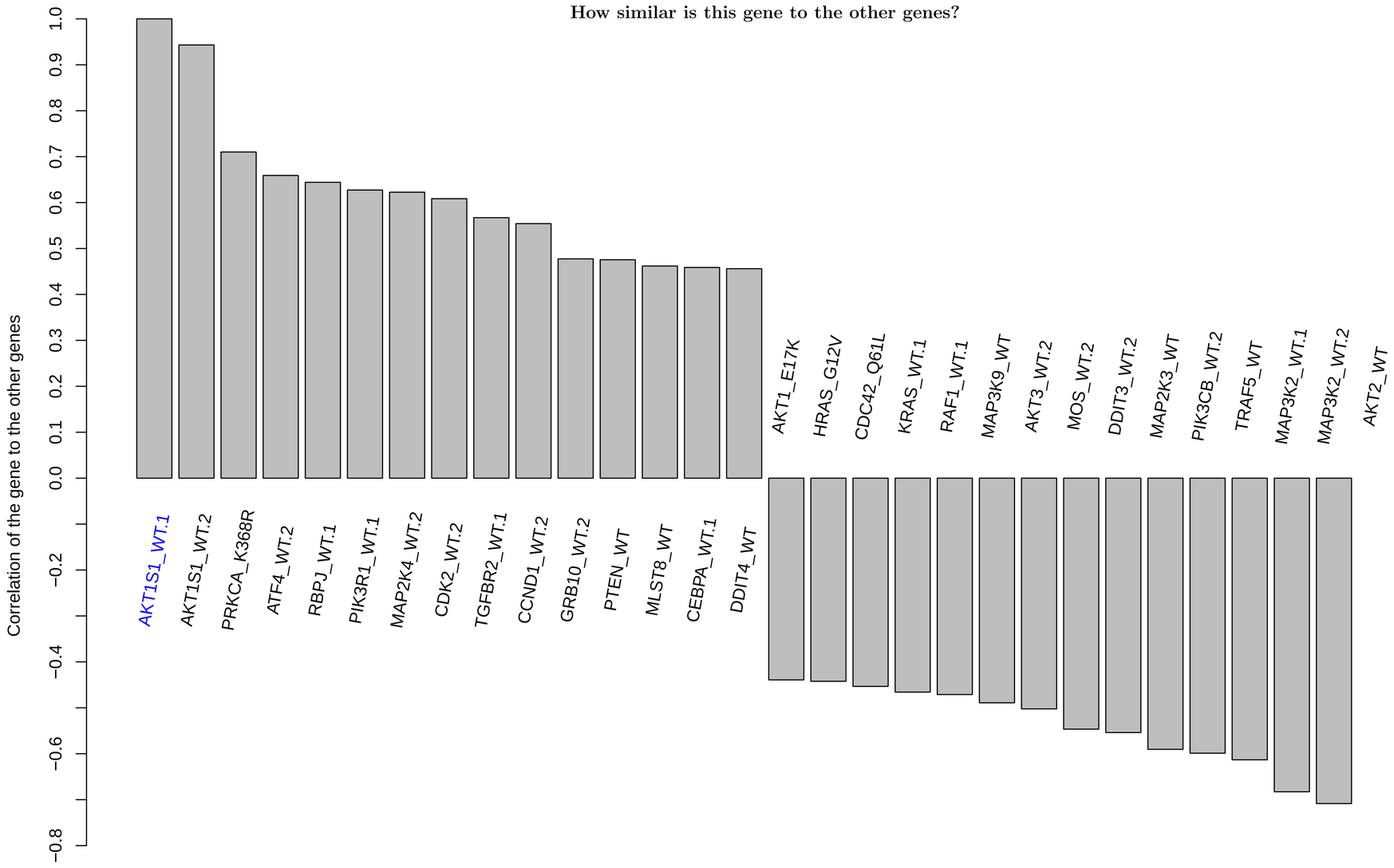
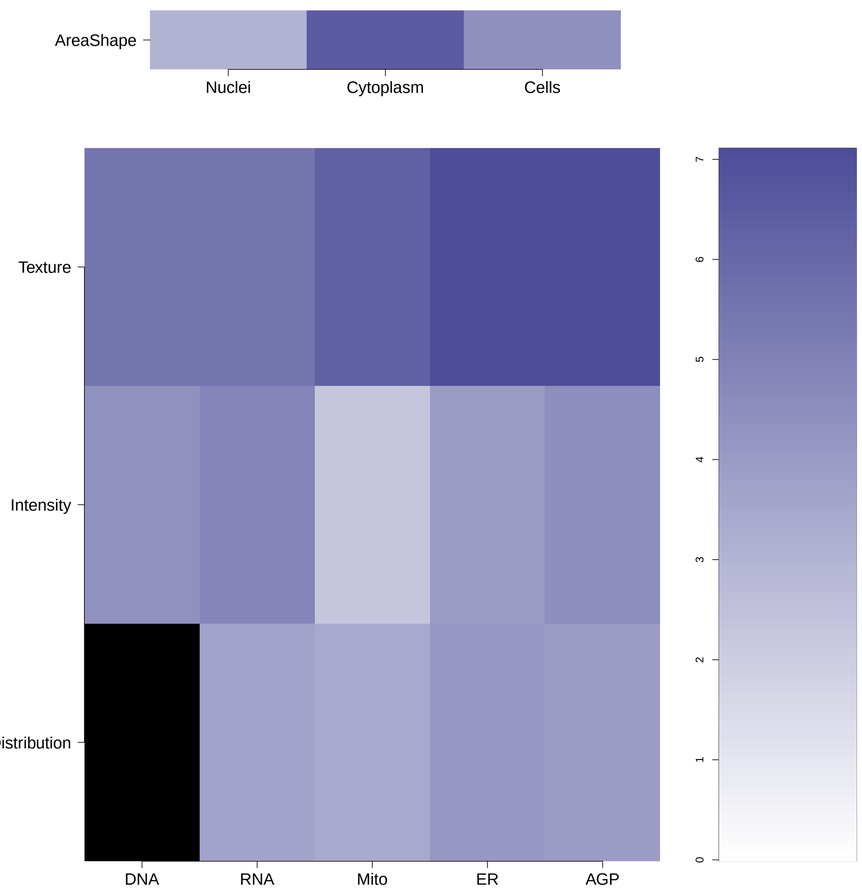
AKT1S1_WT.1 - in TOR

How similar is this gene to the other genes?



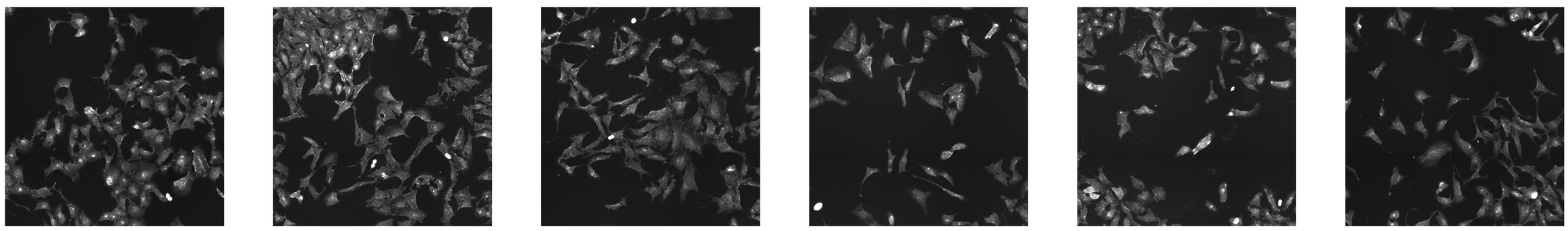
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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



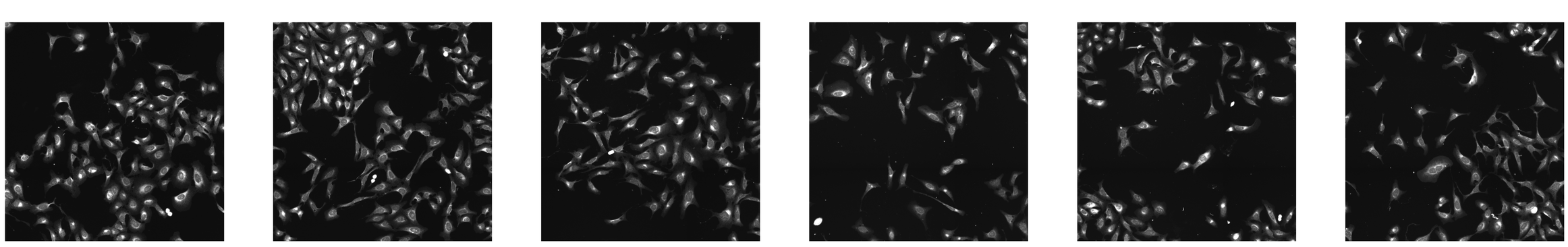
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

Empty | AKT1S1_WT.1 (41744) | AKT1S1_WT.1 (41755) | AKT1S1_WT.1 (41756) | AKT1S1_WT.1 (41757) | AKT1S1_WT.1 (41754)

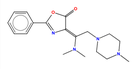
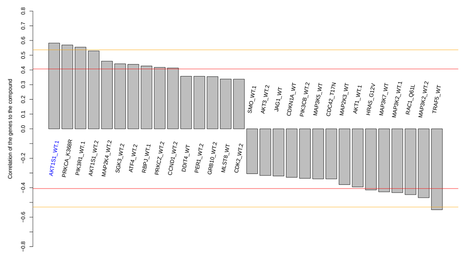
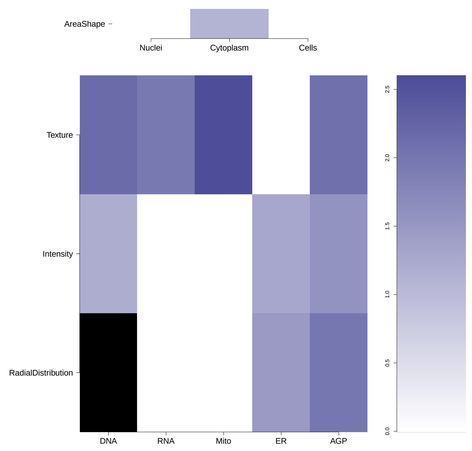
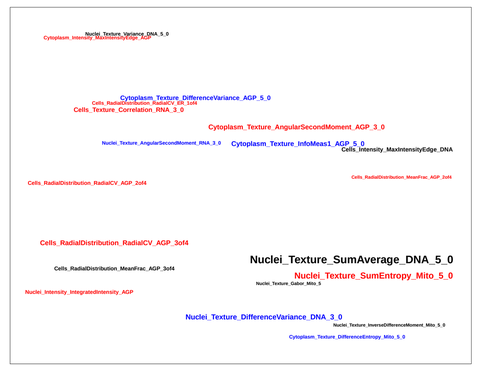
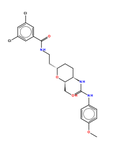
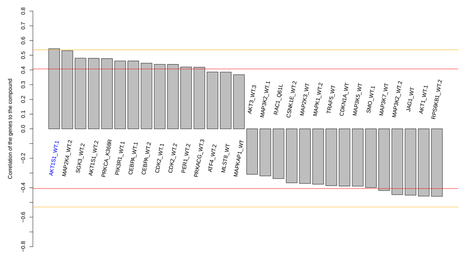
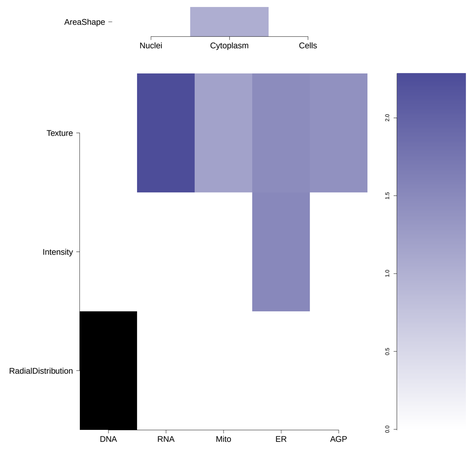
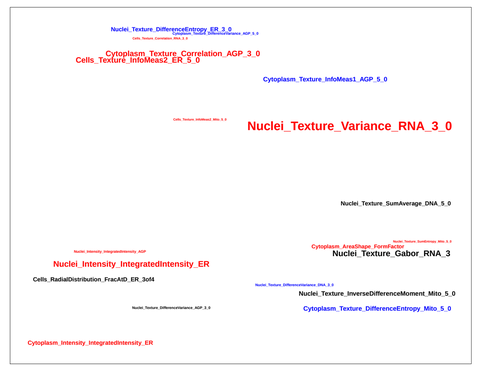
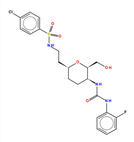
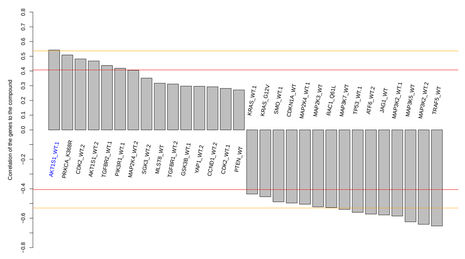
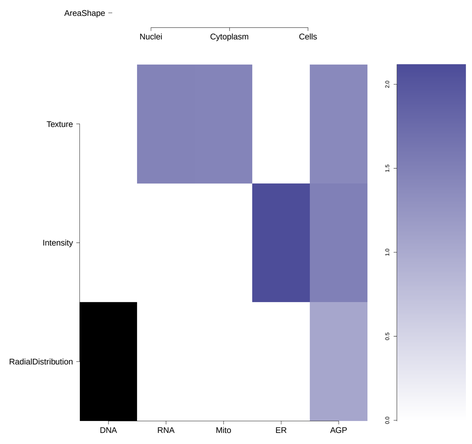
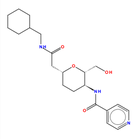
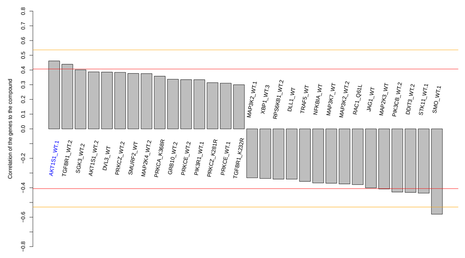
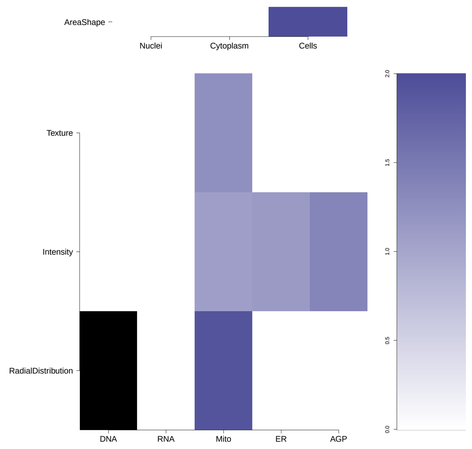
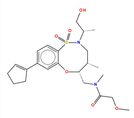
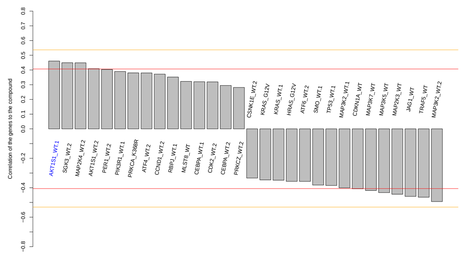
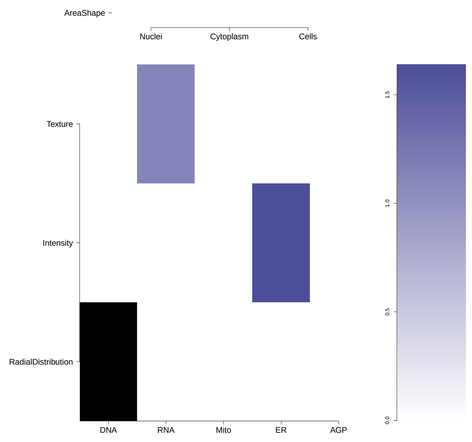
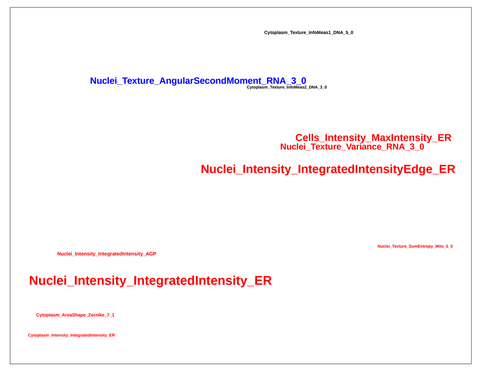
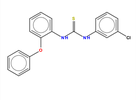
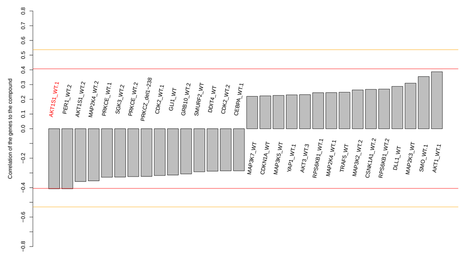
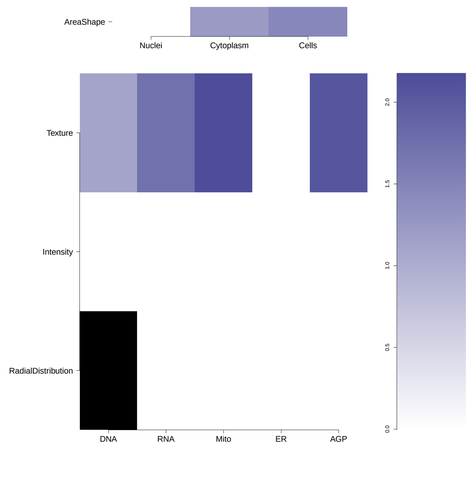
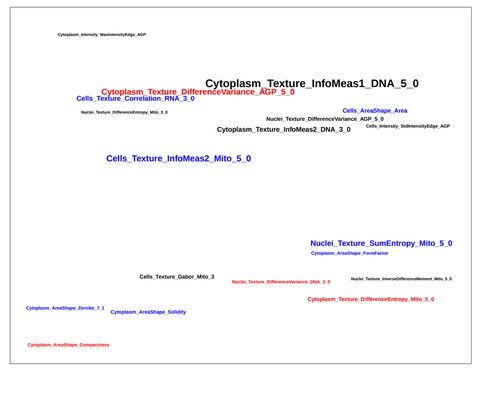
AGP



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-K64231918-001-05-9 MS-3063 MLS000327824 AC1NXO4W HMS2444N09 ZINC20445571 SMR000180808 PubChem CID : 5786980		NA (in 1 replicates)	0.58	NA				Total number of assays tested in: 660. Active in the following assays: • Primary cell-based high-throughput screening assay for identification of compounds that allosterically potentiate transient receptor potential cation channel C4 (TRPC4) (AID 2227) • HTS-Luminescent assay for inhibitors of ALR by detection of hydrogen peroxide production Measured in Biochemical System Using Plate Reader - 2036-02_Inhibitor_SinglePoint_HTS (AID 485317) • Absorbance-based biochemical primary high throughput screening assay to identify inhibitors of Methionine sulfoxide reductase A (MsrA) (AID 651718)
BRD-K82056353-001-01-9 PubChem CID : 54640693		0.72 (in 4 replicates)	0.54	0.946				Total number of assays tested in: 35.
BRD-K90201499-001-01-6 PubChem CID : 54641127		NA (in 1 replicates)	0.54	NA				Total number of assays tested in: 37.
BRD-K56300782-001-01-4 PubChem CID : 54641200		NA (in 1 replicates)	0.46	NA				Total number of assays tested in: 37.
BRD-K61313778-001-01-6 PubChem CID : 54619959		0.53 (in 4 replicates)	0.46	NA				Total number of assays tested in: 32.
BRD-K27093637-001-05-9 STK133805 AC1LPITF SMR000199376 MLS000580489 HMS2156O04 HMS3315M17 ZINC1109443 ZINC01109443 PubChem CID : 1288168		0.64 (in 3 replicates)	-0.41	NA				Total number of assays tested in: 672. Active in the following assays: • CYP2C9 Assay (AID 777) • Identification of Novel Modulators of Cl- dependent Transport Process via HTS: Primary Screen (AID 1456) • qHTS for inhibitors of ROR gamma transcriptional activity (AID 2551) • Primary cell-based high-throughput screening assay for identification of compounds that inhibit KCNQ1 potassium channels (AID 2642) • HTS for small molecule inhibitors of CHOP to regulate the unfolded protein response to ER stress (AID 2732) • Inhibitors of Cav3 T-type Calcium Channels: Primary Screen (AID 449739) • Assay for HTS of Gi/Go-linked GPCRs using mGluR8: Primary Screening (AID 488969) • uHTS fluorescent assay for identification of inhibitors of ATG4B (AID 504462) • Primary qHTS for delayed death inhibitors of the malarial parasite plastid, 96 hour incubation (AID 504834) • Single concentration counterscreen of uHTS hits for ATG4B inhibitors in a Phospholipase A2 assay (AID 588402) • Primary cell-based high-throughput screening for identification of compounds that inhibit/block calcium-activated chloride channels (TMEM16A) (AID 588511) • Primary cell-based high-throughput screening for identification of compounds that antagonize MrgX1 receptor signaling (AID 588676) • uHTS identification of small molecule inhibitors of the mitochondrial permeability transition pore via an absorbance assay (AID 602449) • Activators of the GIRK family of Potassium Channels (GIRK_Confirmatory_CRC) (AID 623909) • Activators of the GIRK family of Potassium Channels (GIRK1/2_Confirmatory) (AID 623911) • Single concentration confirmation of uHTS inhibitor hits of the mitochondrial permeability transition pore via a fluorescent based assay (AID 624504) • qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 686978) • IC50 with Alamar Blue Measured in Microorganism System Using Plate Reader - 2162-02_Inhibitor_Dose_CherryPick_Activity (AID 686998) • HEK293 Cytotoxicity Assay Measured in Cell-Based System Using Plate Reader - 7071-01_Inhibitor_Dose_CherryPick_Activity (AID 687005) • HEK293 Cytotoxicity Assay Measured in Cell-Based System Using Plate Reader - 7071-01_Inhibitor_Dose_CherryPick_Activity_Set2 (AID 720491)