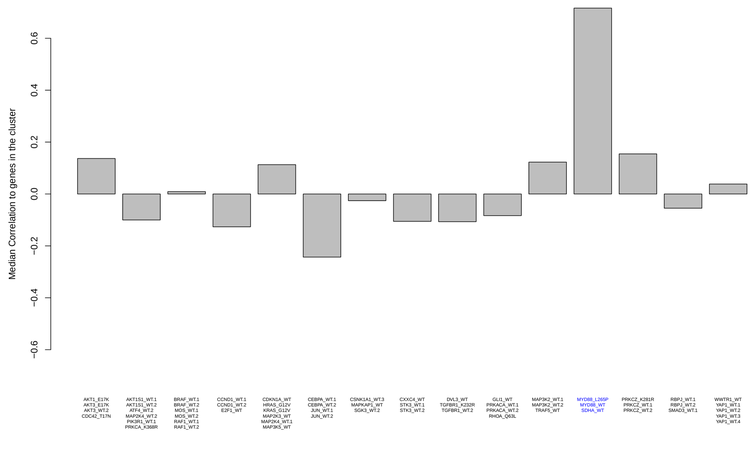
Genes in the cluster along with the pathways as annotated by experts

	Expert Annotation	
Treatment	Pathway	Regulation Type
SDHA_WT	Canonical Hypoxia	Inhibitor
MYD88_L265P	Canonical NFkB	Activator
MYD88_WT	Canonical NFkB	Activator

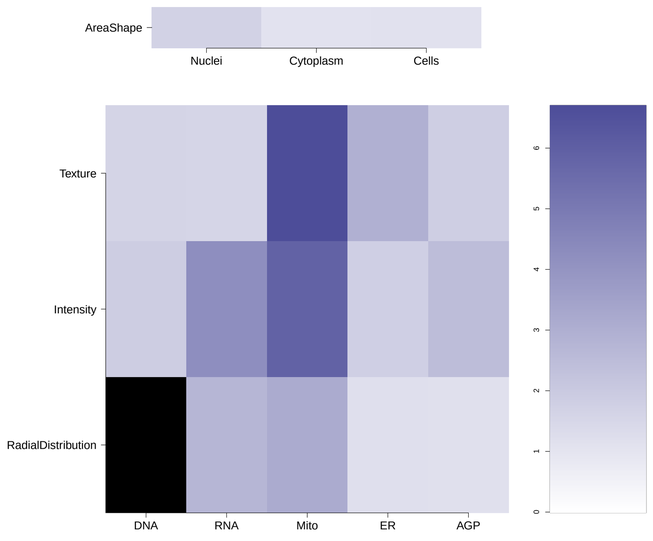
How similar is this cluster to the other clusters?



Top 5 genes negatively correlated to the cluster

	Expert Annotation			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PRKACG_WT.3	PKA	Activator	-0.35	0.11
TGFB1_WT	Canonical TGFbeta	Activator	-0.29	0.10
CEBPA_WT.2	Transcription Factors	Activator	-0.27	0.03
CEBPA_WT.1	Transcription Factors	Activator	-0.25	0.03
ATF4_WT.2	Canonical ER Stress/UPR	Activator	-0.25	0.11

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 cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

How strongly are genes within the cluster correlated?

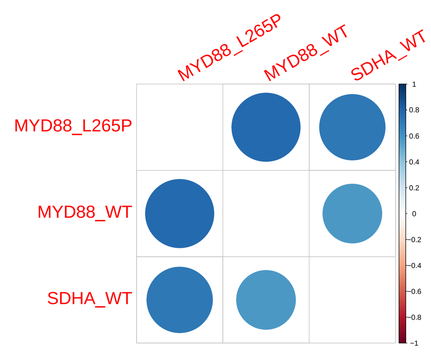
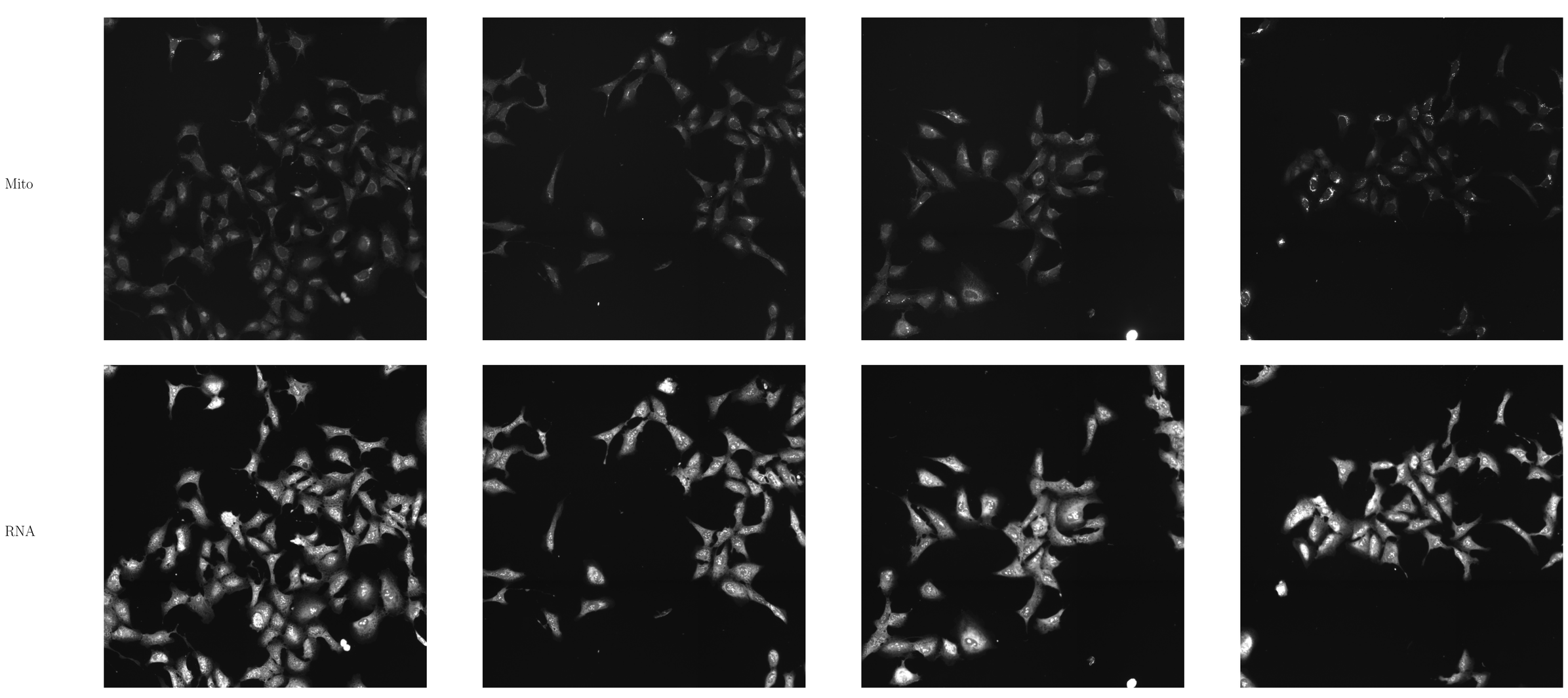
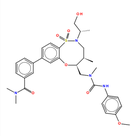
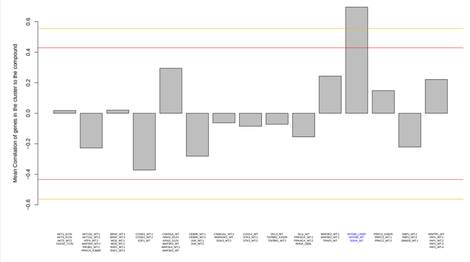
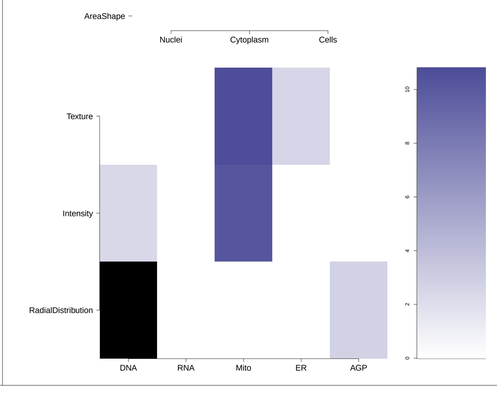
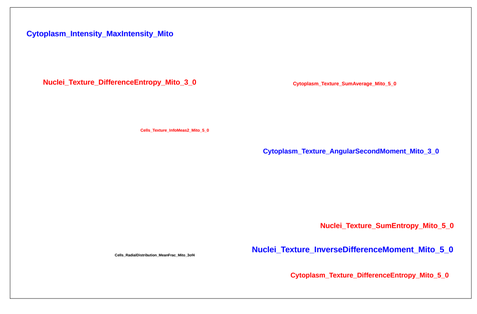
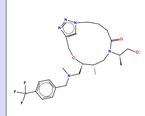
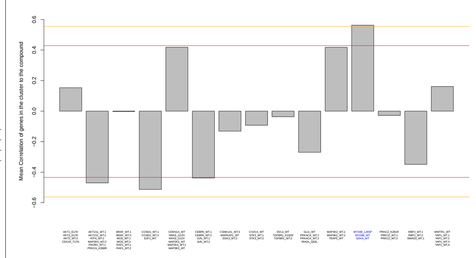
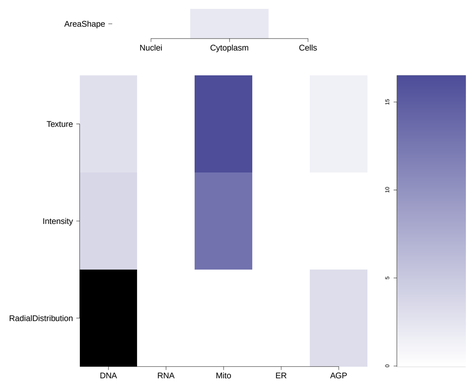
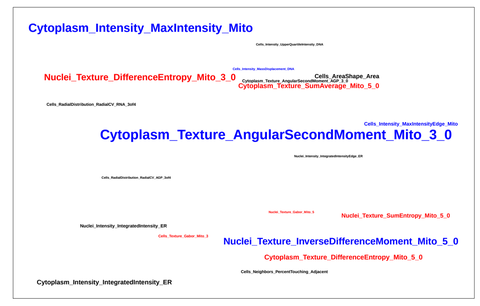
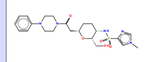
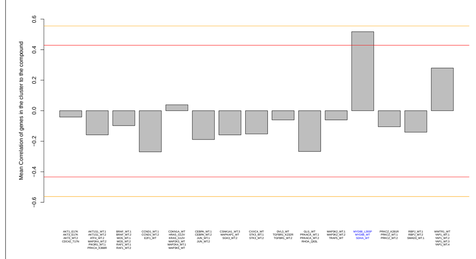
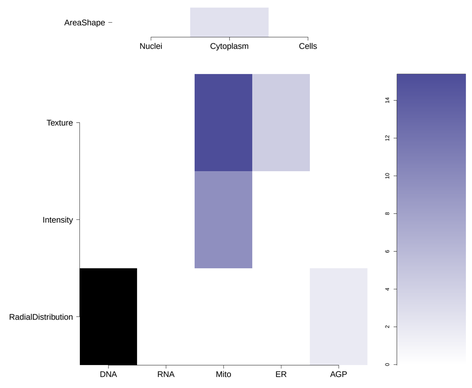
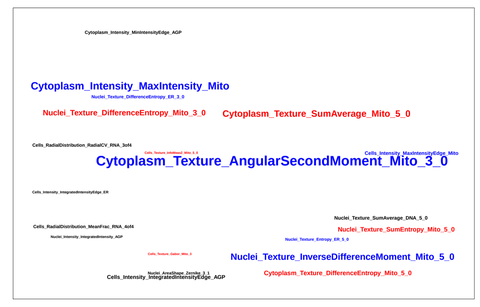
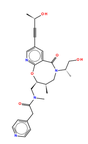
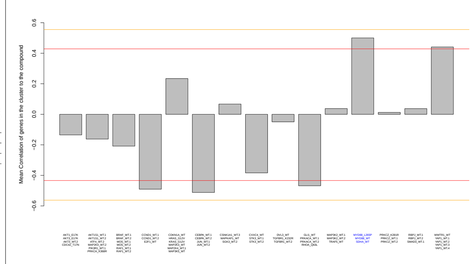
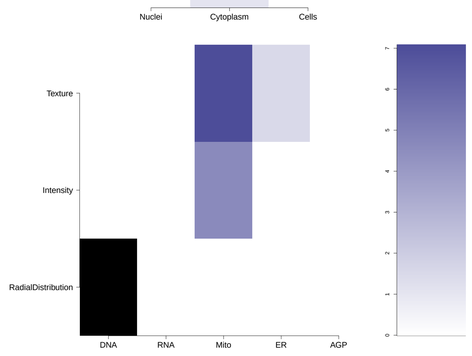
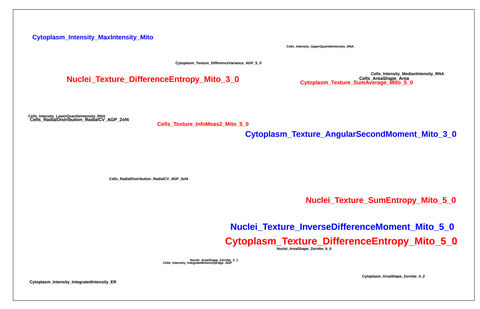
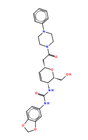
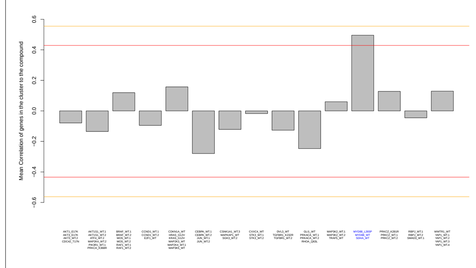
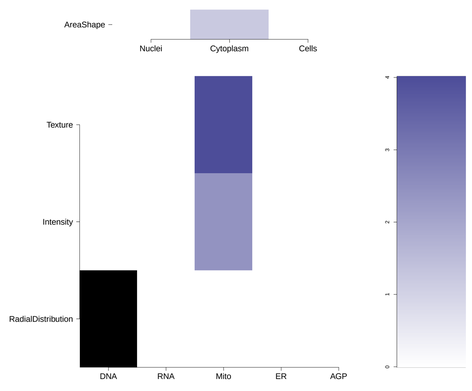
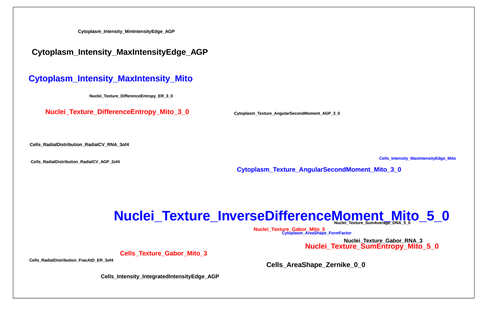
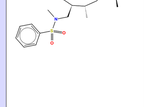
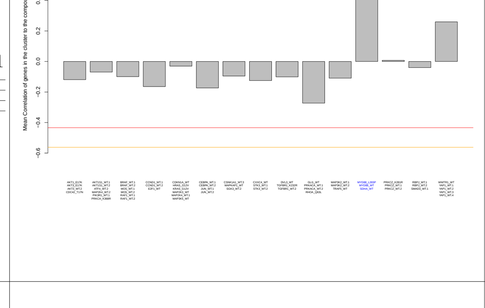
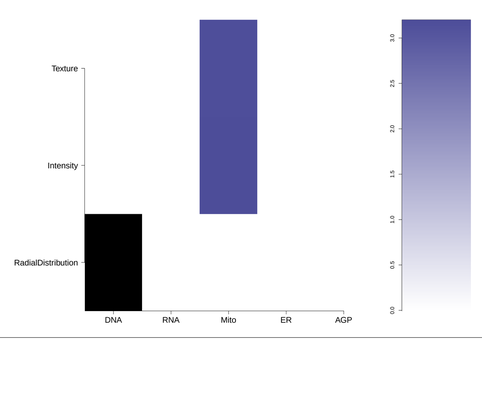
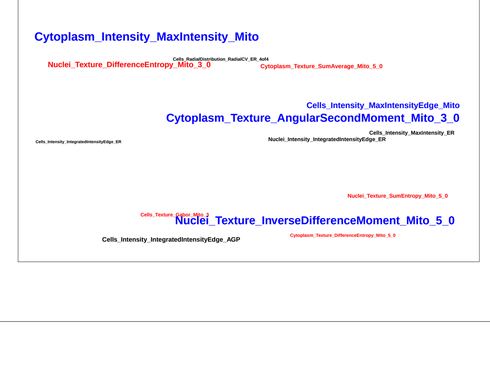
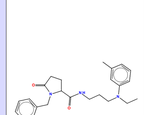
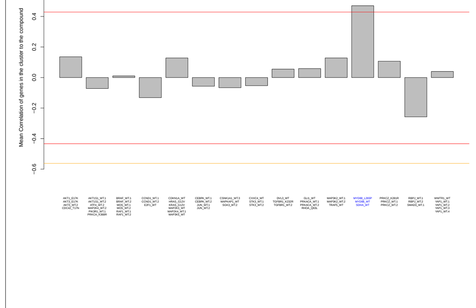
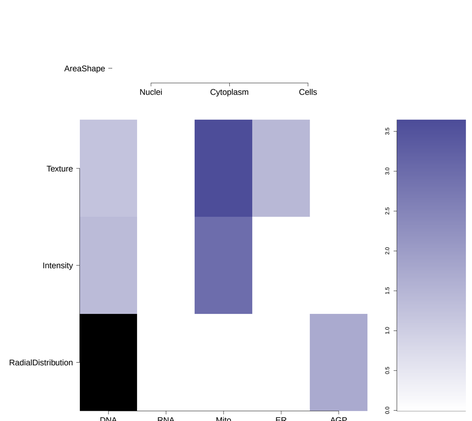
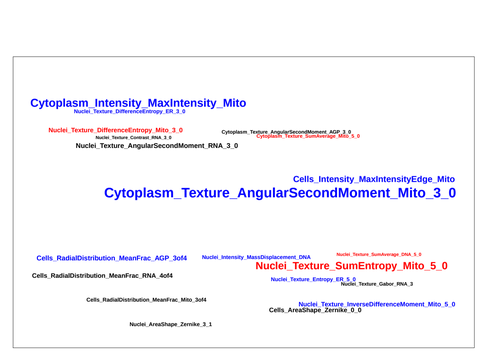
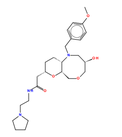
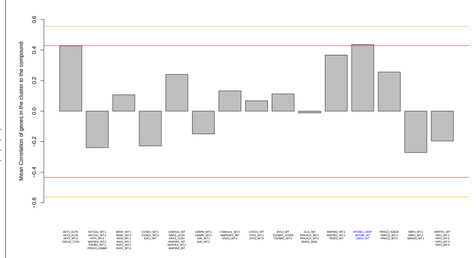
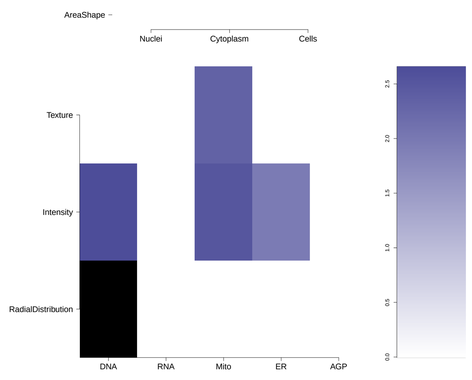
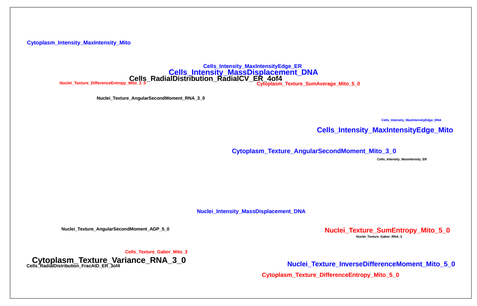
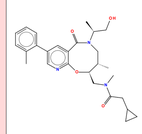
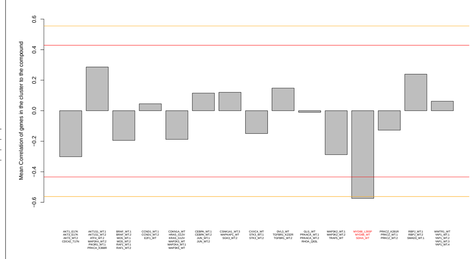
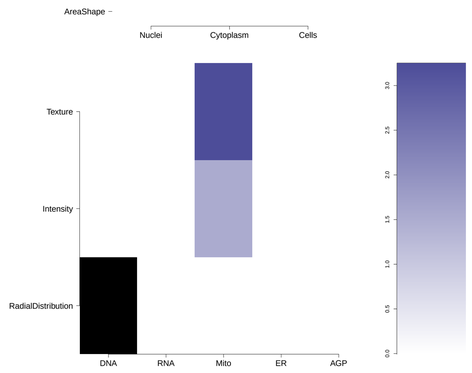
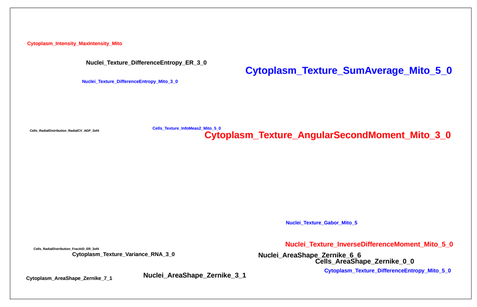
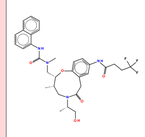
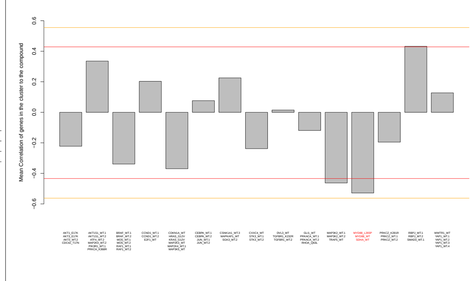
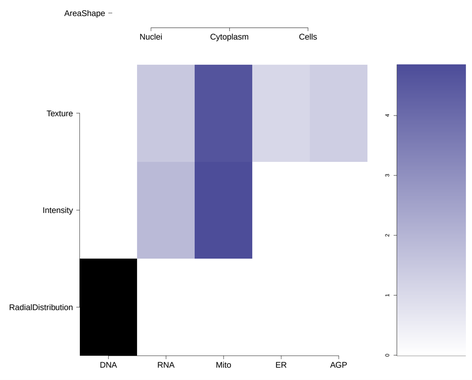
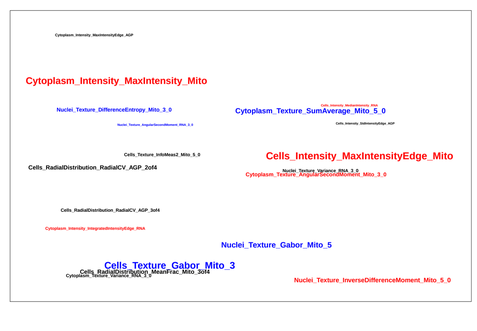
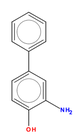
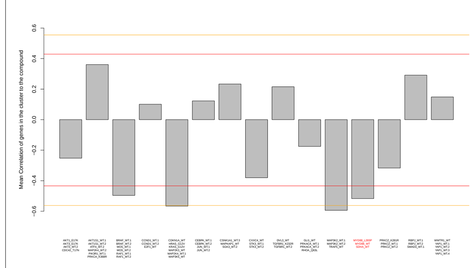
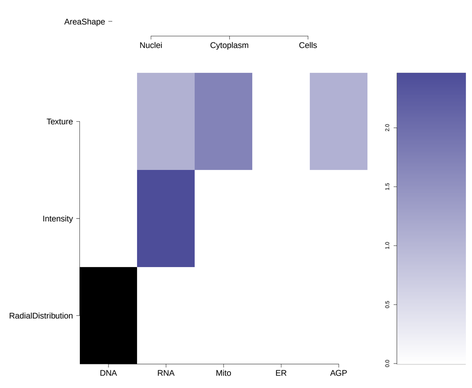
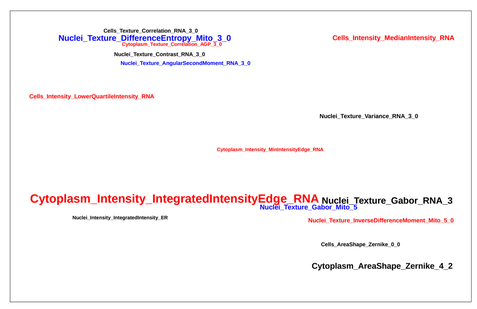
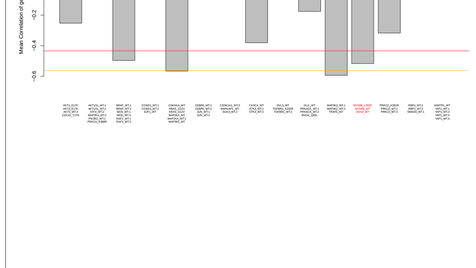


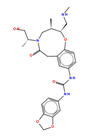
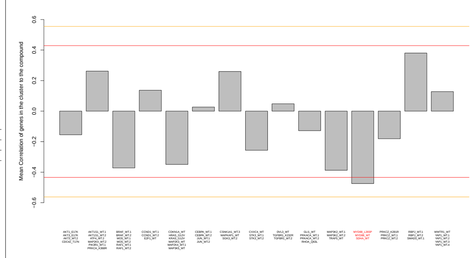
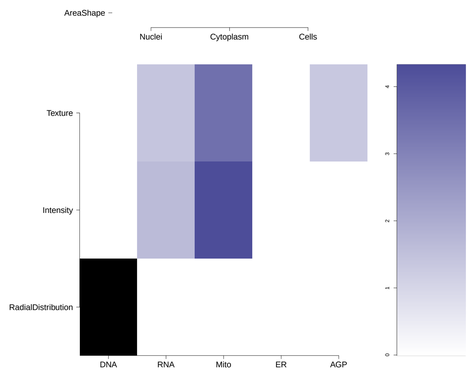
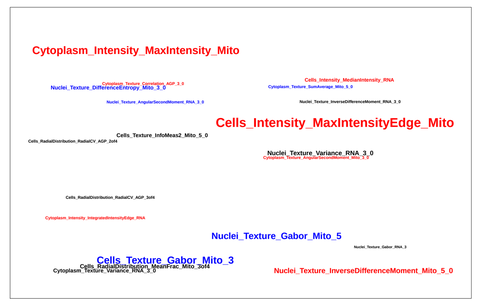
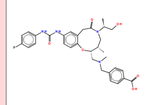
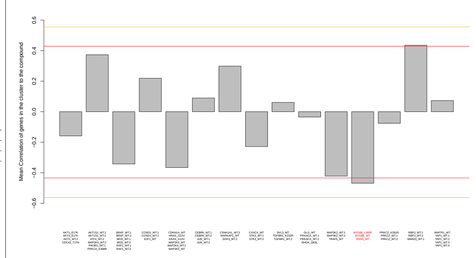
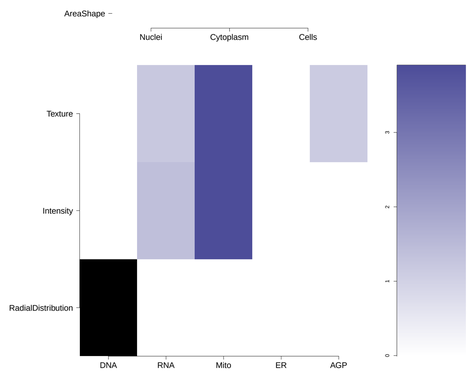
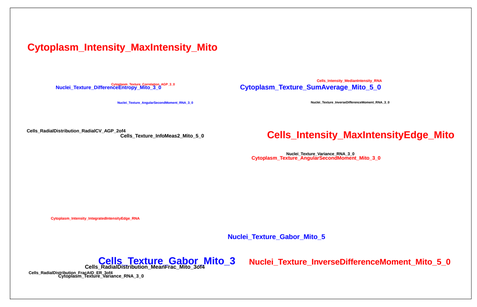
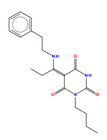
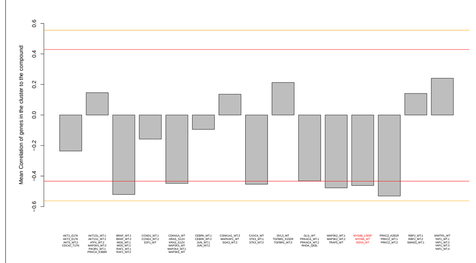
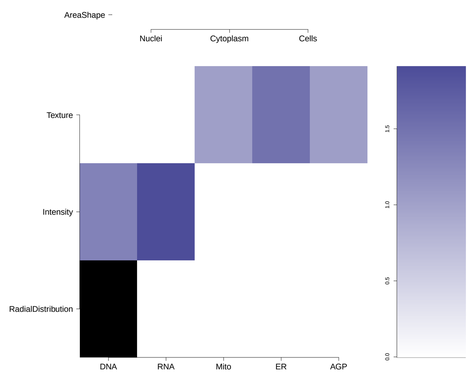
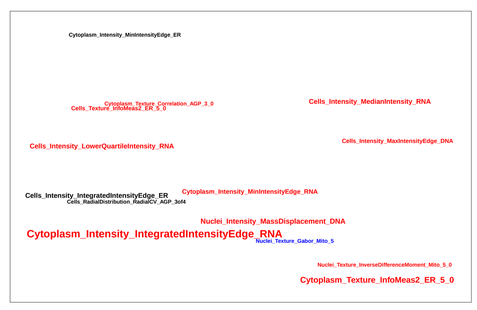
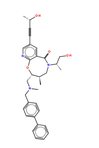
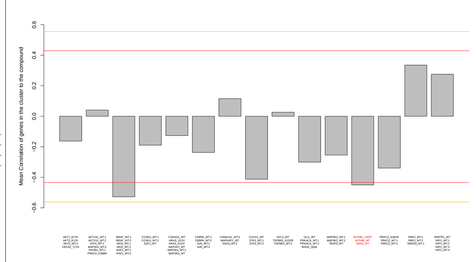
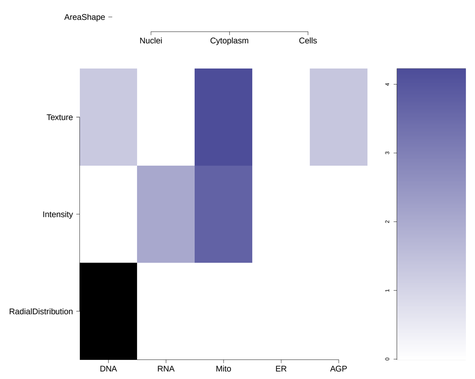
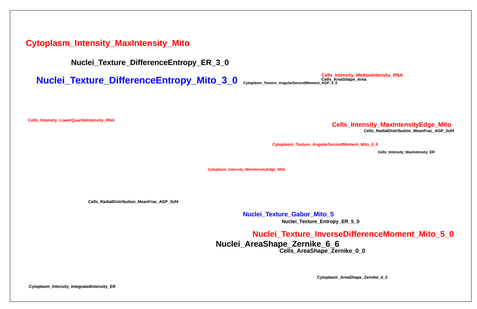
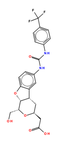
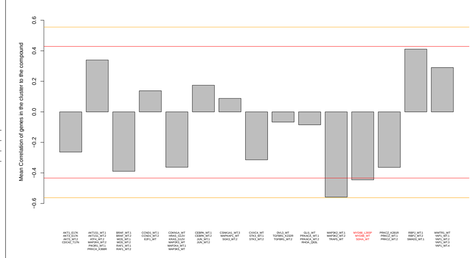
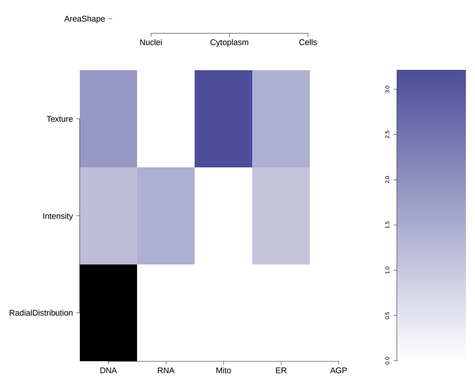
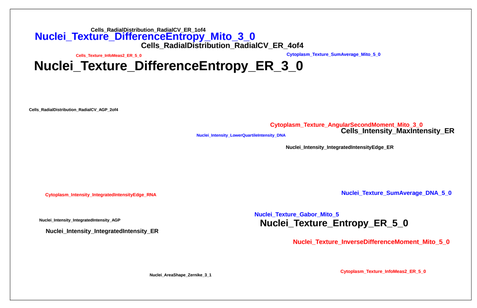
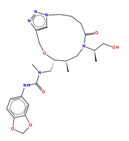
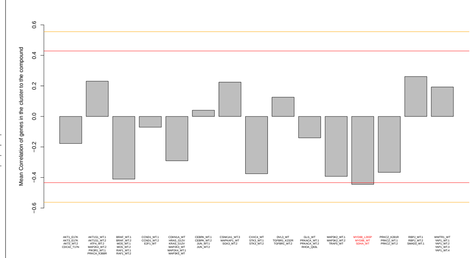
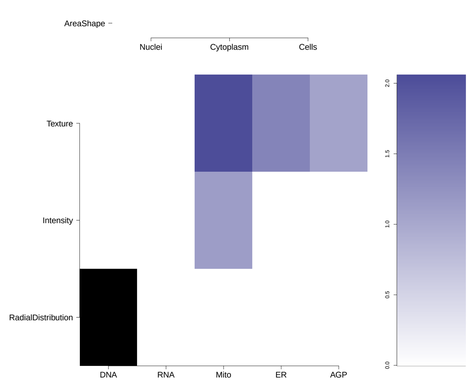
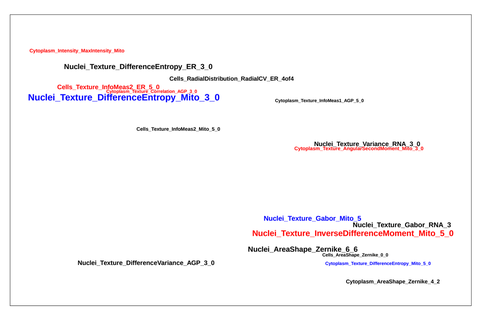
Plate : 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



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 0.54)	Mean ± standard deviation correlation between compound and each gene in cluster; Tables contain data for individual genes	Mean compound rank when scored against genes in cluster using L1000 profiling ± standard deviation; Tables contain data for individual genes	How similar is the compound signature to the gene clusters 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 genes in the cluster 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 cluster	Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized
BRD-K54419202-001-01-6 PubChem CID : 54618507		0.96 (in 4 replicates)	0.70 ± 0.09 Treatment | Score MYD88_L265P | 0.61 MYD88_WT | 0.70 SDHA_WT | 0.78	0.265 ± 0.132 Treatment | Score MYD88_L265P | 0.379 MYD88_WT | 0.295 SDHA_WT | 0.121				Total number of assays tested in: 25.

BRD-K54647996-001-01-2 PubChem CID : 44495442		0.92 (in 3 replicates)	0.56 ± 0.07 Treatment | Score MYD88_L265P | 0.49 MYD88_WT | 0.57 SDHA_WT | 0.63	0.645 ± 0.045 Treatment | Score MYD88_L265P | 0.681 MYD88_WT | 0.594 SDHA_WT | 0.659				Total number of assays tested in: 33.
BRD-K89838866-001-01-3 PubChem CID : 54641283		0.87 (in 3 replicates)	0.52 ± 0.15 Treatment | Score MYD88_L265P | 0.44 MYD88_WT | 0.42 SDHA_WT | 0.69	NA				Total number of assays tested in: 40.
BRD-K98803880-001-01-8 PubChem CID : 54618470		0.95 (in 4 replicates)	0.50 ± 0.12 Treatment | Score MYD88_L265P | 0.39 MYD88_WT | 0.49 SDHA_WT | 0.62	0.598 ± 0.378 Treatment | Score MYD88_L265P | 0.894 MYD88_WT | 0.728 SDHA_WT | 0.173				Total number of assays tested in: 35.
BRD-K80190213-001-01-8 PubChem CID : 54641277		NA (in 1 replicates)	0.50 ± 0.08 Treatment | Score MYD88_L265P | 0.51 MYD88_WT | 0.41 SDHA_WT | 0.56	NA				Total number of assays tested in: 40.
BRD-K39299017-001-02-5 MLS003129671 SMR001834117 PubChem CID : 44488152		0.66 (in 3 replicates)	0.48 ± 0.15 Treatment | Score MYD88_L265P | 0.43 MYD88_WT | 0.36 SDHA_WT | 0.65	0.510 ± 0.351 Treatment | Score MYD88_L265P | 0.692 MYD88_WT | 0.733 SDHA_WT | 0.105				Total number of assays tested in: 227. Active in the following assays: • Fluorescence-based cell-based primary high throughput screening assay to identify antagonists of the human M1 muscarinic receptor (CHRM1) (AID 588852)
BRD-A29506681-001-05-5 SMR000131579 MLS000521170 MLS002589135 HMS2467M17 PubChem CID : 9550560		0.57 (in 3 replicates)	0.47 ± 0.08 Treatment | Score MYD88_L265P | 0.41 MYD88_WT | 0.56 SDHA_WT | 0.45	NA				Total number of assays tested in: 688. Active in the following assays: • Primary screen for compounds that activate Insulin promoter activity in TRM-6 cells (AID 1296) • QFRET-based primary biochemical high throughput screening assay to identify inhibitors of the Plasmodium falciparum M18 Aspartyl Aminopeptidase (PFM18AAP). (AID 1822) • 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) • qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332) • Heat Shock Factor-1 (HSF-1) Measured in Cell-Based System Using Plate Reader - 2038-01_Activator_SinglePoint_HTS_Activity (AID 504408) • HTS to Find Inhibitors of Pathogenic Pemphigus Antibodies (AID 588358) • Counterscreen of compound fluorescence effects on High-throughput multiplex microsphere screening for inhibitors of toxin protease (AID 624483) • qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in absence of CPT (AID 686978) • qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDP1): qHTS in cells in presence of CPT (AID 686979)
BRD-K34197007-001-01-0 PubChem CID : 49850002		0.63 (in 4 replicates)	0.47 ± 0.03 Treatment | Score MYD88_L265P | 0.43 MYD88_WT | 0.49 SDHA_WT | 0.49	0.541 ± 0.313 Treatment | Score MYD88_L265P | 0.588 MYD88_WT | 0.208 SDHA_WT | 0.828				Total number of assays tested in: 19.
BRD-K67832115-001-01-1 PubChem CID : 54619033		0.79 (in 4 replicates)	0.46 ± 0.08 Treatment | Score MYD88_L265P | 0.37 MYD88_WT | 0.51 SDHA_WT | 0.51	0.735 ± 0.084 Treatment | Score MYD88_L265P | 0.832 MYD88_WT | 0.681 SDHA_WT | 0.691				Total number of assays tested in: 42. Active in the following assays: • Identification of Small Molecule Correctors of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Delta508 Mutation Function in Human Bronchial Epithelial Cells. Measured in Cell-Based System Using Plate Reader - 7017-01_Other_SinglePoint_HTS_Activity (AID 720511)

BRD-K52662613-001-01-6 PubChem CID : 54657569		0.54 (in 4 replicates)	0.44 ± 0.13 Treatment | Score MYD88_L265P | 0.42 MYD88_WT | 0.57 SDHA_WT | 0.31	0.390 ± 0.230 Treatment | Score MYD88_L265P | 0.298 MYD88_WT | 0.220 SDHA_WT | 0.653				Total number of assays tested in: 37. Active in the following assays: • MLPCN SirT-5 Measured in Biochemical System Using Imaging - 7044-01_Inhibitor_SinglePoint_HTS_Activity_Set5 (AID 652115)
BRD-K40321450-001-01-0 PubChem CID : 54618404		0.75 (in 4 replicates)	-0.57 ± 0.04 Treatment | Score MYD88_L265P | -0.62 MYD88_WT | -0.55 SDHA_WT | -0.55	0.487 ± 0.188 Treatment | Score MYD88_L265P | 0.412 MYD88_WT | 0.701 SDHA_WT | 0.347				Total number of assays tested in: 23.
BRD-K49424866-001-01-1 PubChem CID : 44488107		0.86 (in 4 replicates)	-0.53 ± 0.06 Treatment | Score MYD88_L265P | -0.55 MYD88_WT | -0.58 SDHA_WT | -0.46	0.306 ± 0.131 Treatment | Score MYD88_L265P | 0.412 MYD88_WT | 0.159 SDHA_WT | 0.347				Total number of assays tested in: 56.
BRD-K47707616-001-06-3 1134-36-7 MLS000084764 MLS000737887 NSC 7950 SMR000019110 NSC7950 ACMC-2099js AC1L243I AC1Q516N AC1Q516O CHEMBL574583 BDBM37561 CTK3J4347 BB SC-8440 HMS1473J22 HMS2363K13 KUC106663N ZINC154832 KSC-22-7 NSC-7950 ANW-16646 BBL008080 SBB056916 STK513465 ZINC00154832 CCG-103916 PS-8495 VZ26294 IDI1 019538 AJ-13396 AK135459 AN-48686 BP-30020 KB-19962 LS-44455 OR003129 OR174385 ZB005897 DB-022223 RT-001962 3D49P06660 A0397 AM20120625 BB 0246046 FT-0614978 R1875 ST24041772 ST45004729 EN300-88962 A803050 I14-6050 3B3-001248 PubChem CID : 14562		NA (in 1 replicates)	-0.52 ± 0.06 Treatment | Score MYD88_L265P | -0.57 MYD88_WT | -0.52 SDHA_WT | -0.46	NA				Total number of assays tested in: 835. Active in the following assays: • NCI Yeast Anticancer Drug Screen. Data for the rad50 strain (AID 155) • NCI Yeast Anticancer Drug Screen. Data for the mec2-1 strain (AID 157) • NCI Yeast Anticancer Drug Screen. Data for the sgs1 mgt1 strain (AID 161) • NCI Yeast Anticancer Drug Screen. Data for the cln2 rad14 strain (AID 165) • NCI Yeast Anticancer Drug Screen. Data for the bub3 strain (AID 167) • NCI Yeast Anticancer Drug Screen. Data for the mlh1 rad18 strain (AID 175) • Aggregation and Clearance of Mutant Huntingtin Protein (AID 483) • qHTS Assay for Tau Filament Binding (AID 596) • qHTS Assay for Inhibitors of 15-hLO-2 (15-human lipoxygenase 2) (AID 881) • qHTS Assay for Inhibitors of HADH2 (Hydroxyacyl-Coenzyme A Dehydrogenase, Type II) (AID 886) • qHTS Assay for Inhibitors of 15-hLO (15-human lipoxygenase) (AID 887) • qHTS Assay for Inhibitors of HSD17B4, hydroxysteroid (17-beta) dehydrogenase 4 (AID 893) • Primary Cell-based High Throughput Screening Assay for Inhibitors of Wee1 Degradation (AID 1321) • Luminescence-based primary biochemical high throughput screening assay to identify inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1789) • MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814) • QFRET-based primary biochemical high throughput screening assay to identify inhibitors of the Plasmodium falciparum M18 Aspartyl Aminopeptidase (PFM18AAP). (AID 1822) • Luminescence-based confirmation biochemical high throughput screening assay for inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1846) • Luminescence-based dose response biochemical high throughput screening assay for inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1913) • qHTS Assay for Inhibitors and Activators of Human alpha-Glucosidase Cleavage of Glycogen (AID 2100) • Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314) • A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315) • 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) • qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332) • qHTS screen for small molecules that inhibit ELG1-dependent DNA repair in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1 (AID 504467) • In vivo-based yeast HTS to detect compounds rescuing yeast growth/survival of Plasmodium Falciparum HSP40-mediated toxicity Measured in Whole Organism System Using Plate Reader - 2120-01_Inhibitor_SinglePoint_HTS_Activity (AID 504582) • Primary qHTS for delayed death inhibitors of the malarial parasite plastid, 96 hour incubation (AID 504834) • qHTS profiling assay for firefly luciferase inhibitor/activator using purifed enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342) • Beta-Arrestin HTS for Positive Allosteric Modulators of the Human D2 Dopamine Receptor: Potentiators (AID 624464) • qHTS Assay for Activators of ClpP (AID 651965) • qHTS for Inhibitors of PLK1-PDB (polo-like kinase 1 - polo-box domain): Primary Screen (AID 720504)
BRD-K05001008-001-01-8 PubChem CID : 44504628		0.74 (in 4 replicates)	-0.50 ± 0.04 Treatment | Score MYD88_L265P | -0.50 MYD88_WT | -0.54 SDHA_WT | -0.46	0.773 ± 0.130 Treatment | Score MYD88_L265P | 0.752 MYD88_WT | 0.654 SDHA_WT | 0.912				Total number of assays tested in: 46.

BRD-K82102697-001-01-6 PubChem CID : 44484498		0.78 (in 4 replicates)	-0.47 ± 0.06 Treatment | Score MYD88_L265P | -0.51 MYD88_WT | -0.51 SDHA_WT | -0.41	0.210 ± 0.079 Treatment | Score MYD88_L265P | 0.207 MYD88_WT | 0.133 SDHA_WT | 0.291				Total number of assays tested in: 53.
BRD-K80439500-001-01-1 PubCID : 44493522		0.83 (in 4 replicates)	-0.47 ± 0.03 Treatment | Score MYD88_L265P | -0.50 MYD88_WT | -0.47 SDHA_WT | -0.44	0.499 ± 0.230 Treatment | Score MYD88_L265P | 0.389 MYD88_WT | 0.344 SDHA_WT | 0.762				Total number of assays tested in: 54.
BRD-K07787963-001-05-4 MLS000042070 AC1NTW7G HMS2183L15 STL057077 ZINC20326393 SMR000058149 PubChem CID : 5389638		NA (in 1 replicates)	-0.46 ± 0.06 Treatment | Score MYD88_L265P | -0.50 MYD88_WT | -0.49 SDHA_WT | -0.39	NA				Total number of assays tested in: 768. Active in the following assays: • 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 (Fsk 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-K21433749-001-01-7 PubCID : 54619579		0.81 (in 4 replicates)	-0.45 ± 0.14 Treatment | Score MYD88_L265P | -0.60 MYD88_WT | -0.43 SDHA_WT | -0.32	0.415 ± 0.235 Treatment | Score MYD88_L265P | 0.677 MYD88_WT | 0.222 SDHA_WT | 0.347				Total number of assays tested in: 36. Active in the following assays: • HTS for PAX8 inhibitors using PAX8 luciferase reporter gene assay in RMG-I cells Measured in Cell-Based System Using Plate Reader - 7054-01_Inhibitor_SinglePoint_HTS_Activity (AID 652154)
BRD-K90466405-001-01-8 PubCID : 54646111		NA (in 1 replicates)	-0.45 ± 0.13 Treatment | Score MYD88_L265P | -0.55 MYD88_WT | -0.48 SDHA_WT | -0.30	0.249 ± 0.161 Treatment | Score MYD88_L265P | 0.063 MYD88_WT | 0.336 SDHA_WT | 0.347				Total number of assays tested in: 43. Active in the following assays: • Small Molecule Inhibitors of FGF22-Mediated Excitatory Synaptogenesis and Epilepsy Measured in Biochemical System Using RT-PCR - 7012-01_Inhibitor_SinglePoint_HTS_Activity (AID 651658)
BRD-K67314051-001-02-4 MLS003129211 SMR001833657 PubCID : 44484526		0.54 (in 3 replicates)	-0.44 ± 0.10 Treatment | Score MYD88_L265P | -0.55 MYD88_WT | -0.39 SDHA_WT | -0.39	0.497 ± 0.210 Treatment | Score MYD88_L265P | 0.737 MYD88_WT | 0.406 SDHA_WT | 0.347				Total number of assays tested in: 233.