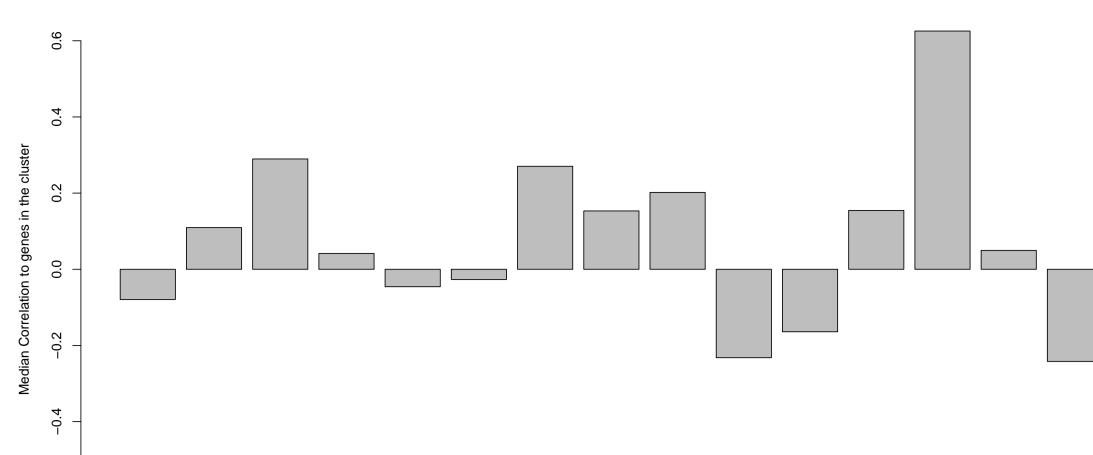
	Expert Annotation			
Treatment	Pathway	Regulation Type		
PRKCZ_WT.1	Canonical PKC	Activator		
PRKCZ_WT.2	Canonical PKC	Activator		
PRKCZ_K281R	Canonical PKC	Inhibitor		



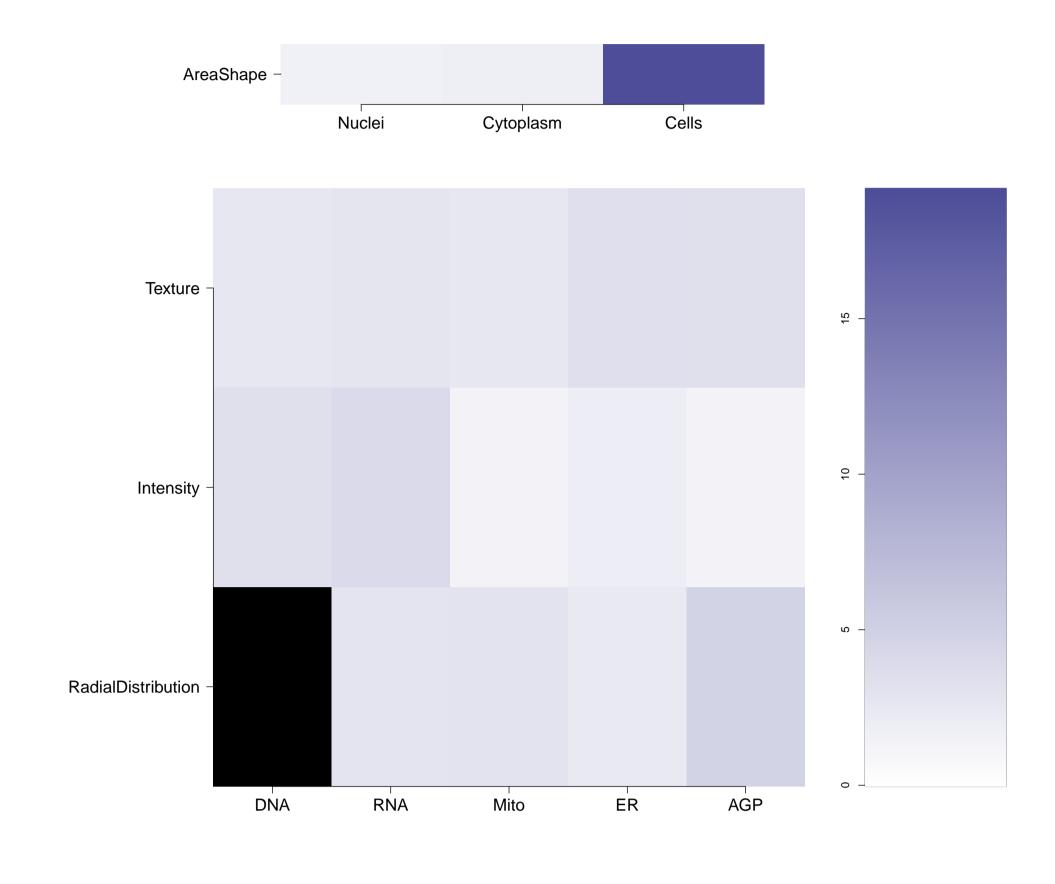
Top 5 genes negatively correlated to the cluster

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
WWTR1_WT	Canonical Hippo	Inhibitor	-0.50	0.10
STK11_WT.1	Canonical TOR	Inhibitor	-0.43	0.06
NFKBIB_WT	Canonical NFkB	Inhibitor	-0.40	0.14
TGFB1_WT	Canonical TGFbeta	Activator	-0.35	0.11
DIABLO_WT	Canonical Apoptosis	Inhibitor	-0.33	0.04

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?



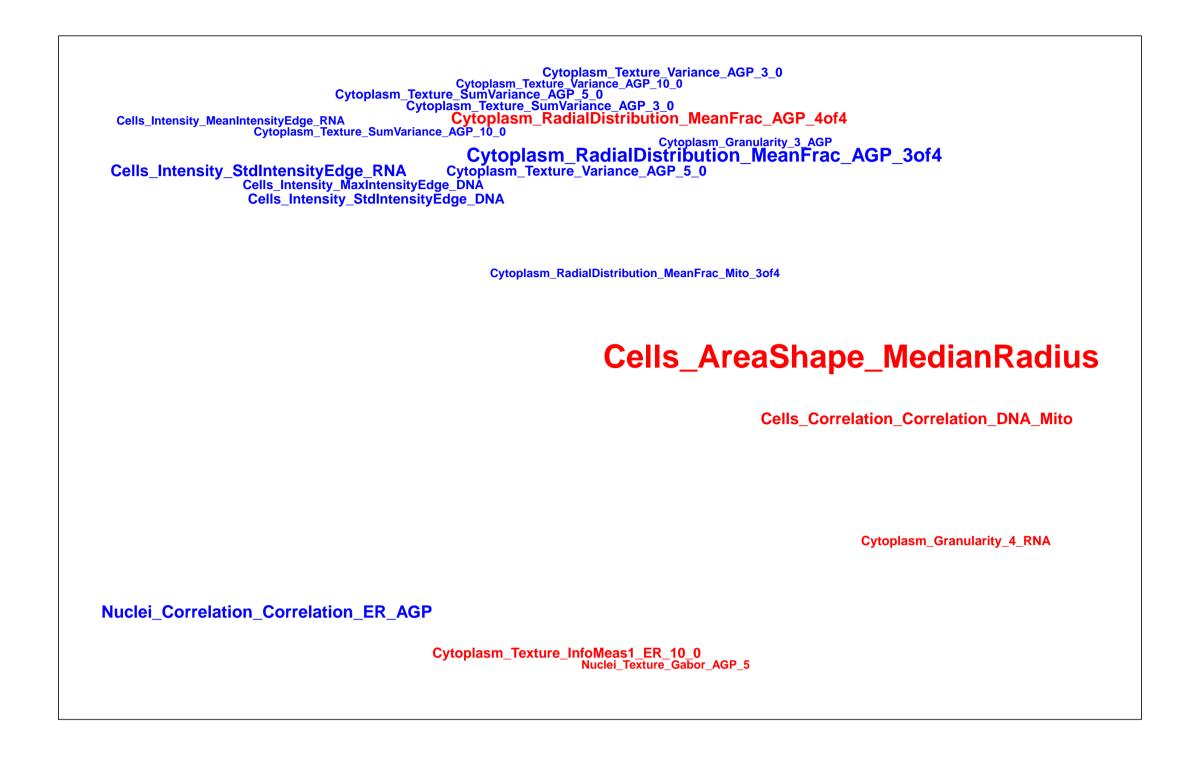
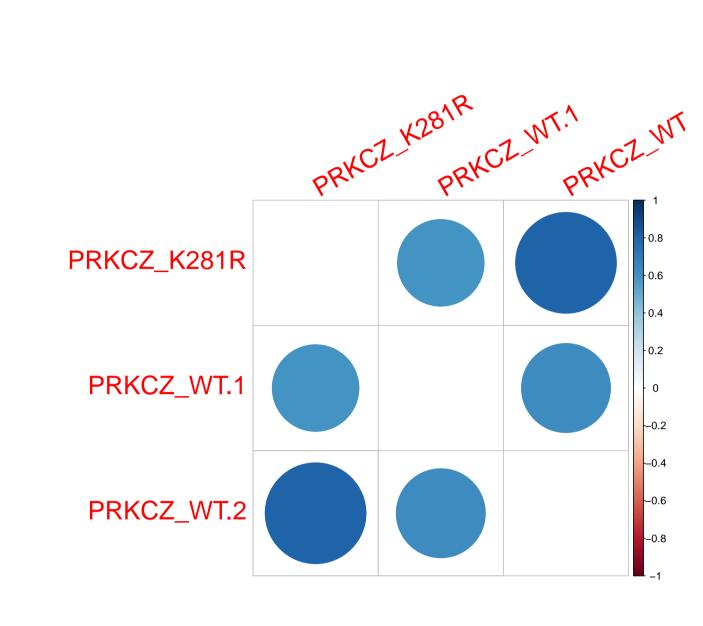
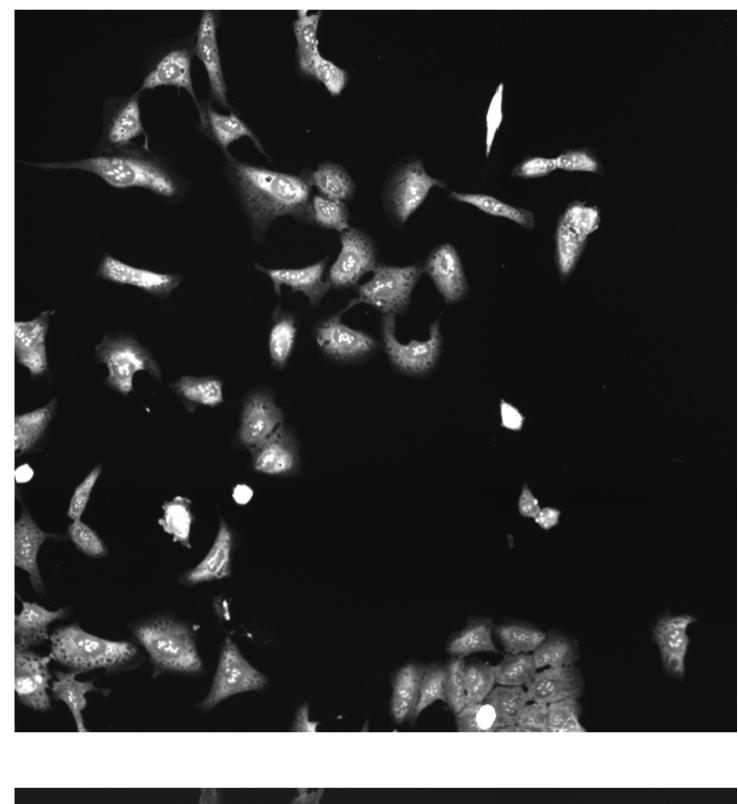


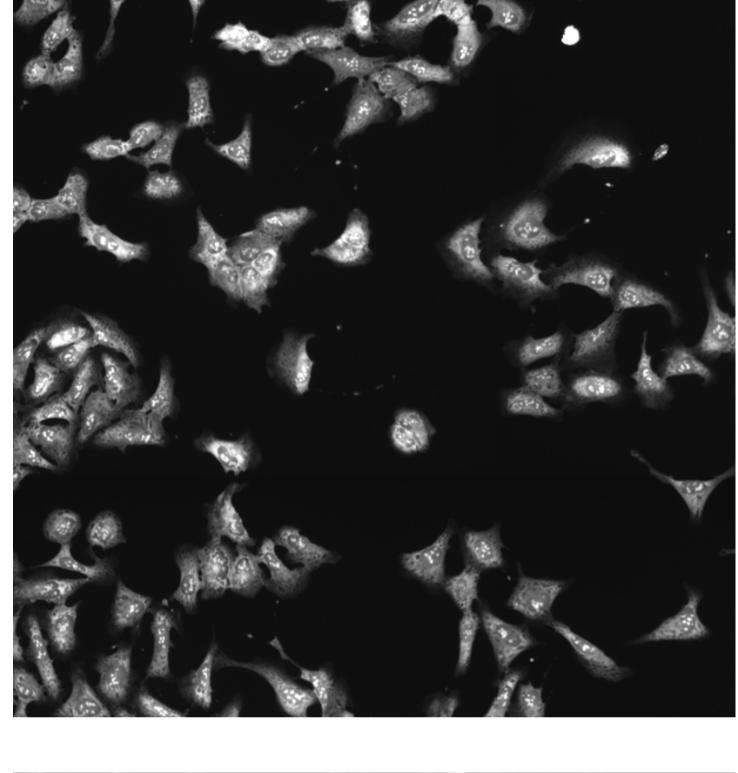
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



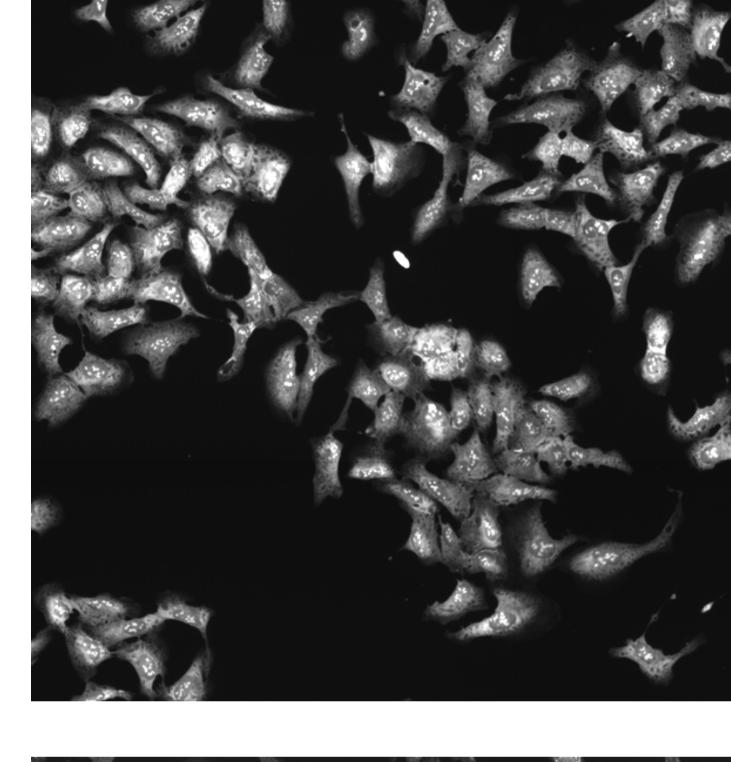
Empty



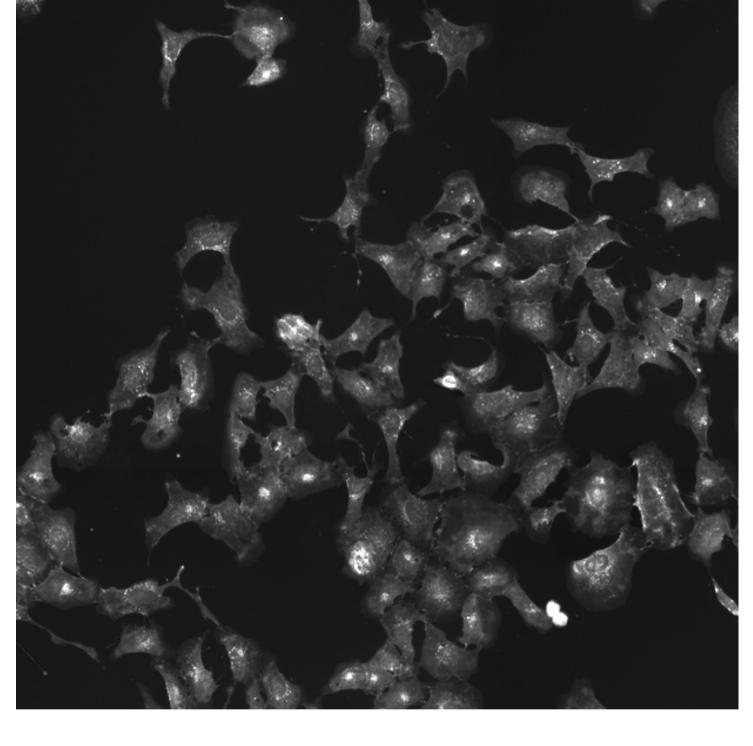
PRKCZ_K281R

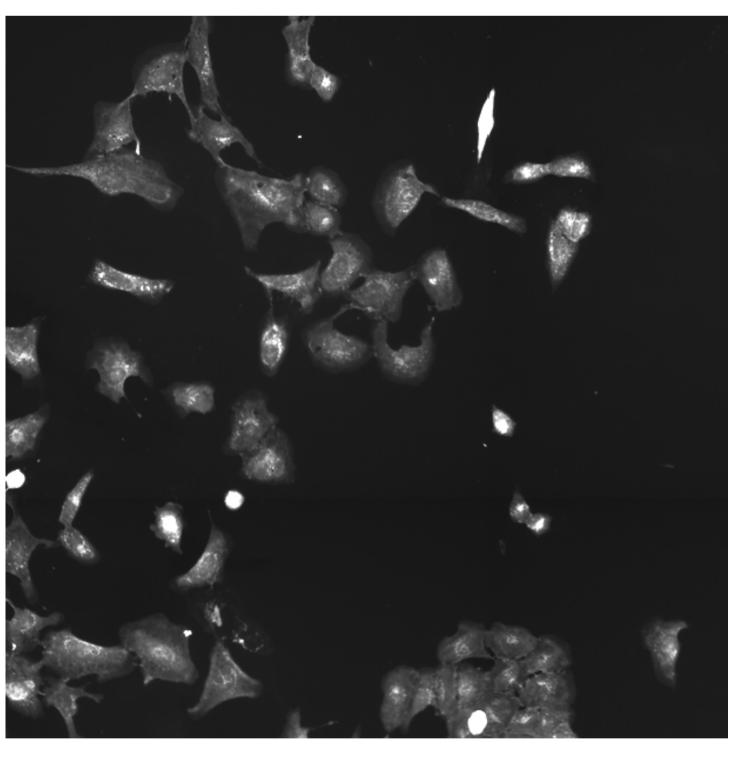


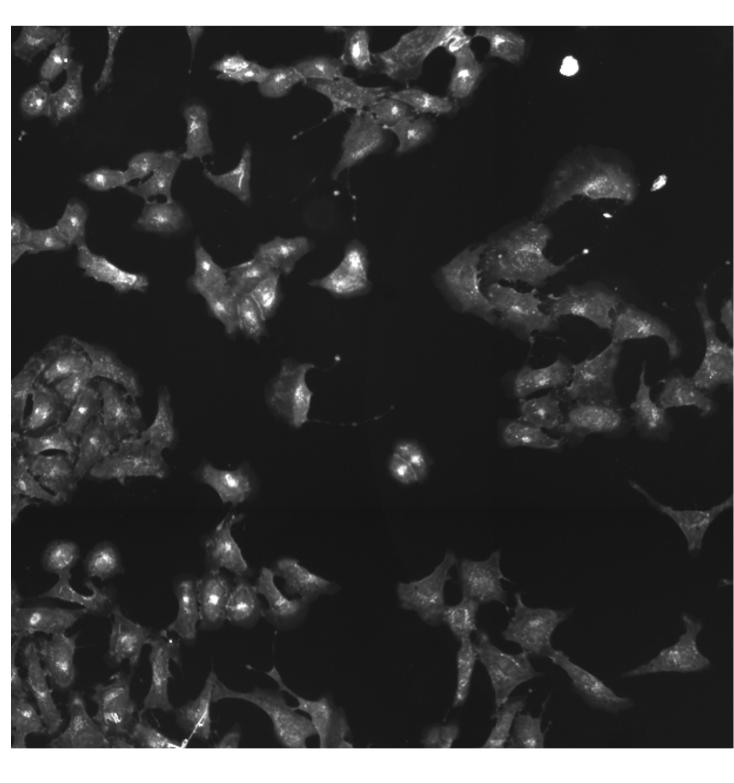
PRKCZ_WT.1

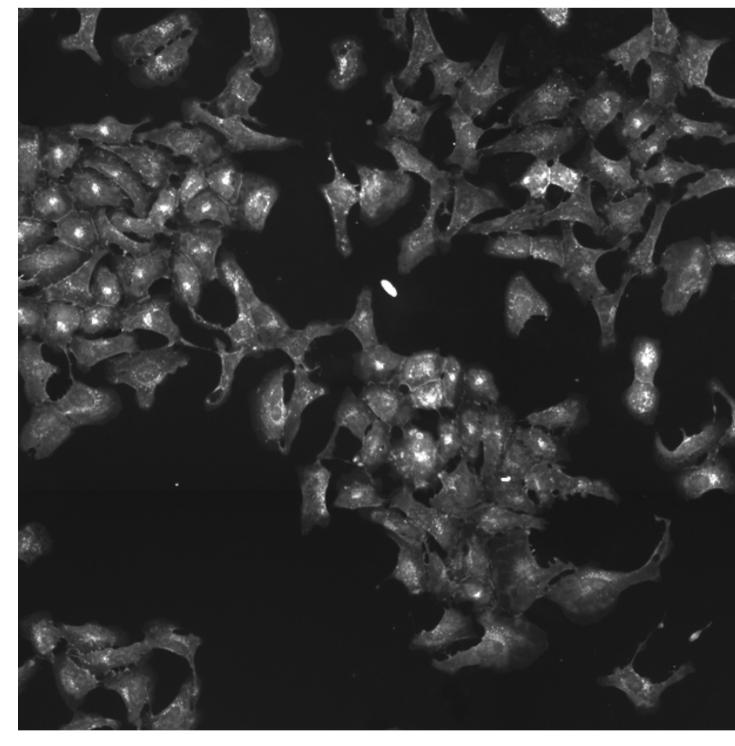


PRKCZ_WT.2









Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chem struct
BRD-K28901743-001-05-3 ZINC01748812 AC1LTAWC MLS000552933 ZINC1748812	

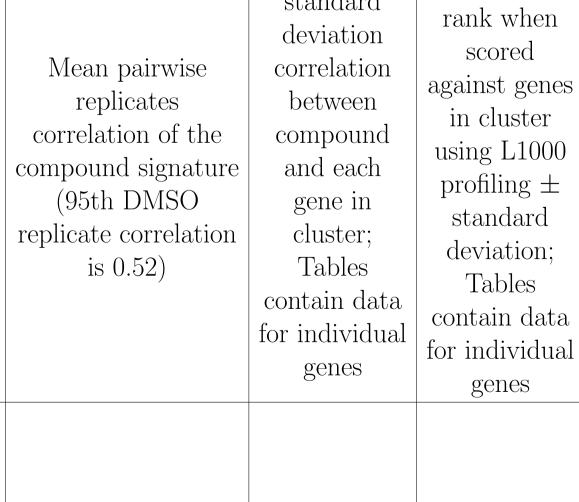
CCG-15676

STL331422

ST50181975

BAS 00558059

SMR000175471



Mean \pm

standard

compound

scored

standard

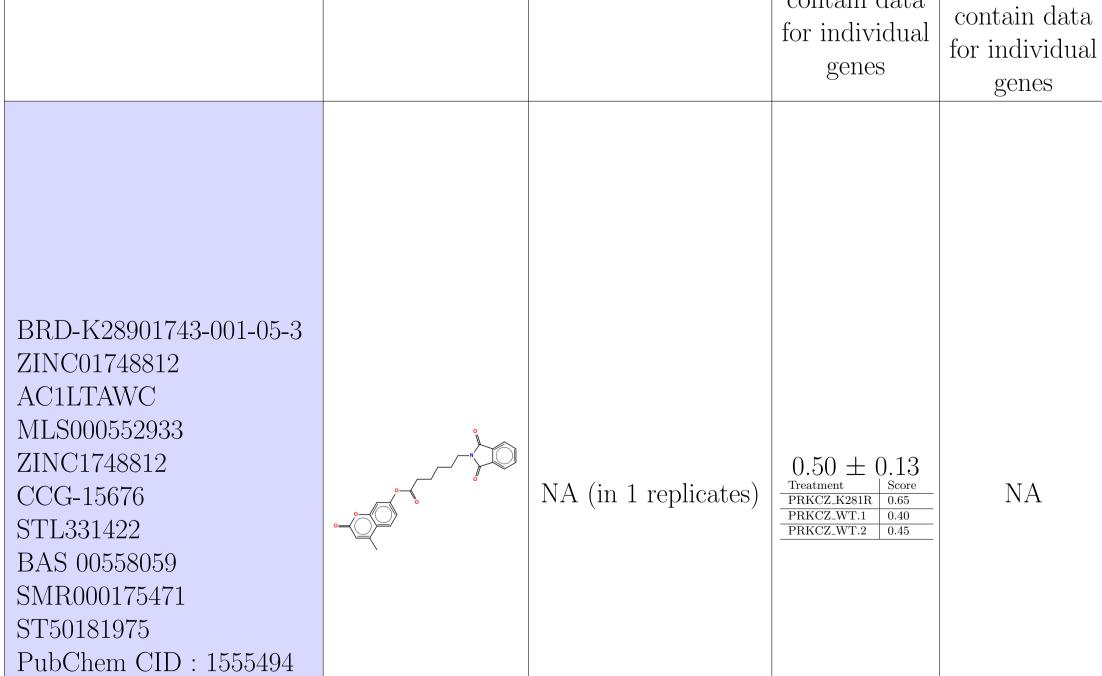
Tables

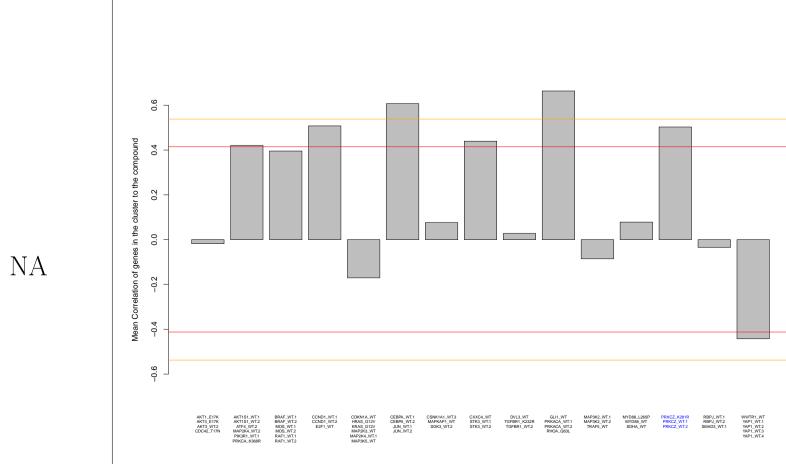
How similar is the compound signature to the gene clusters in this experiment? (Yellow and red lines correspond to top/bottom 1st and 5th percentile DMSO correlation to all the genes)

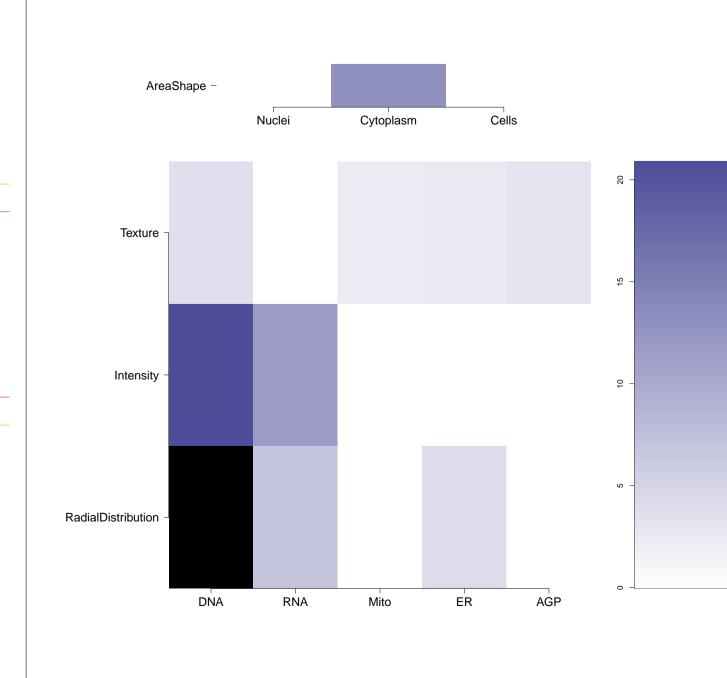
Common distinguishing feature categories in the compound and genes in the cluster relative to the untreated samples

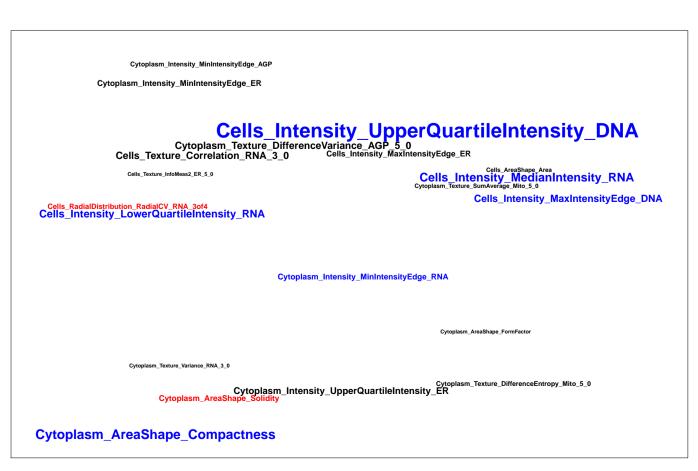
Distinguishing individual features for the compound relative to untreated samples. Black means a mismatch; i.e. active (= high z-score in magnitude) in the compound, and either inactive (= small z-score in magnitude) or oppositely active in the gene cluster

Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized

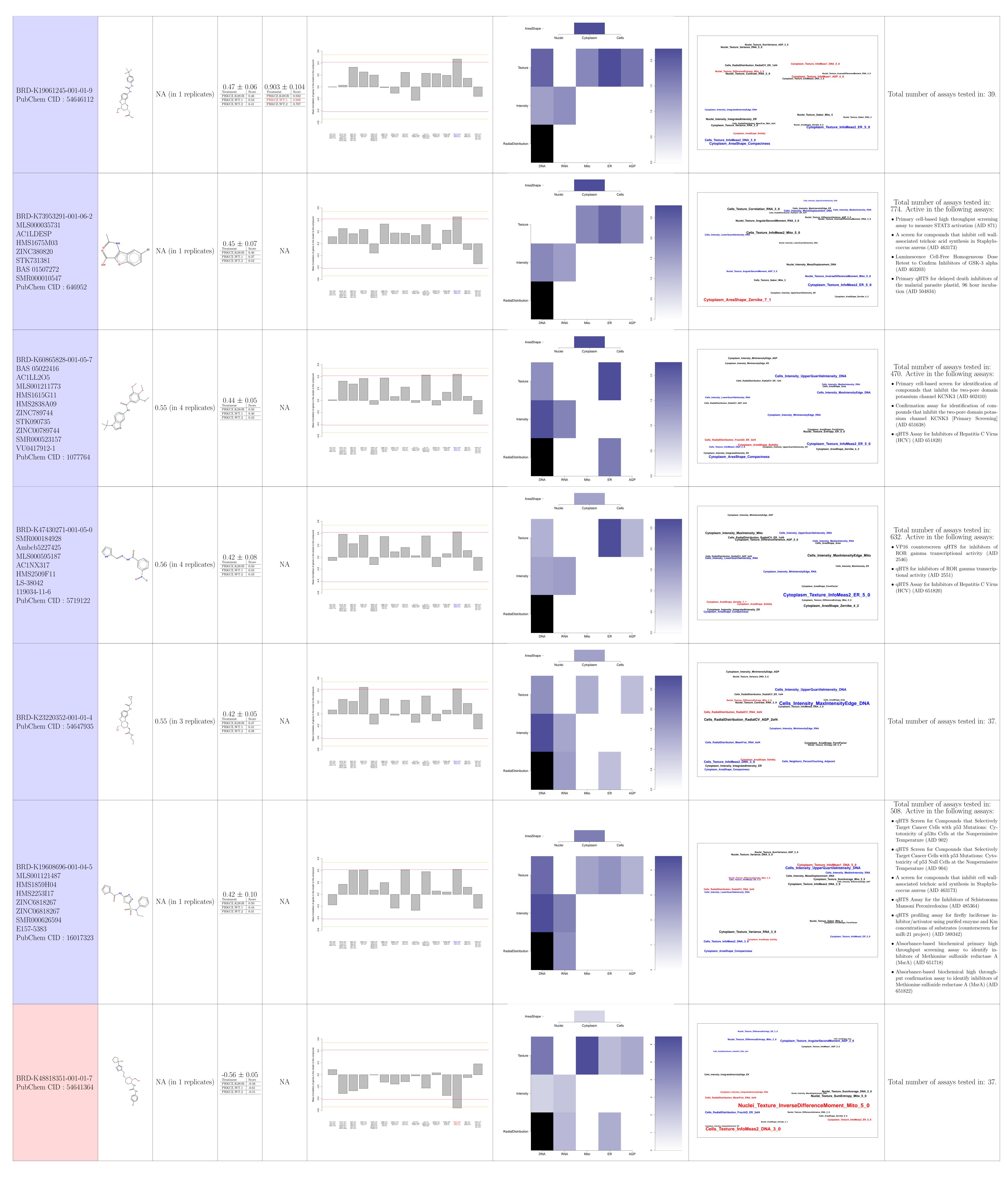


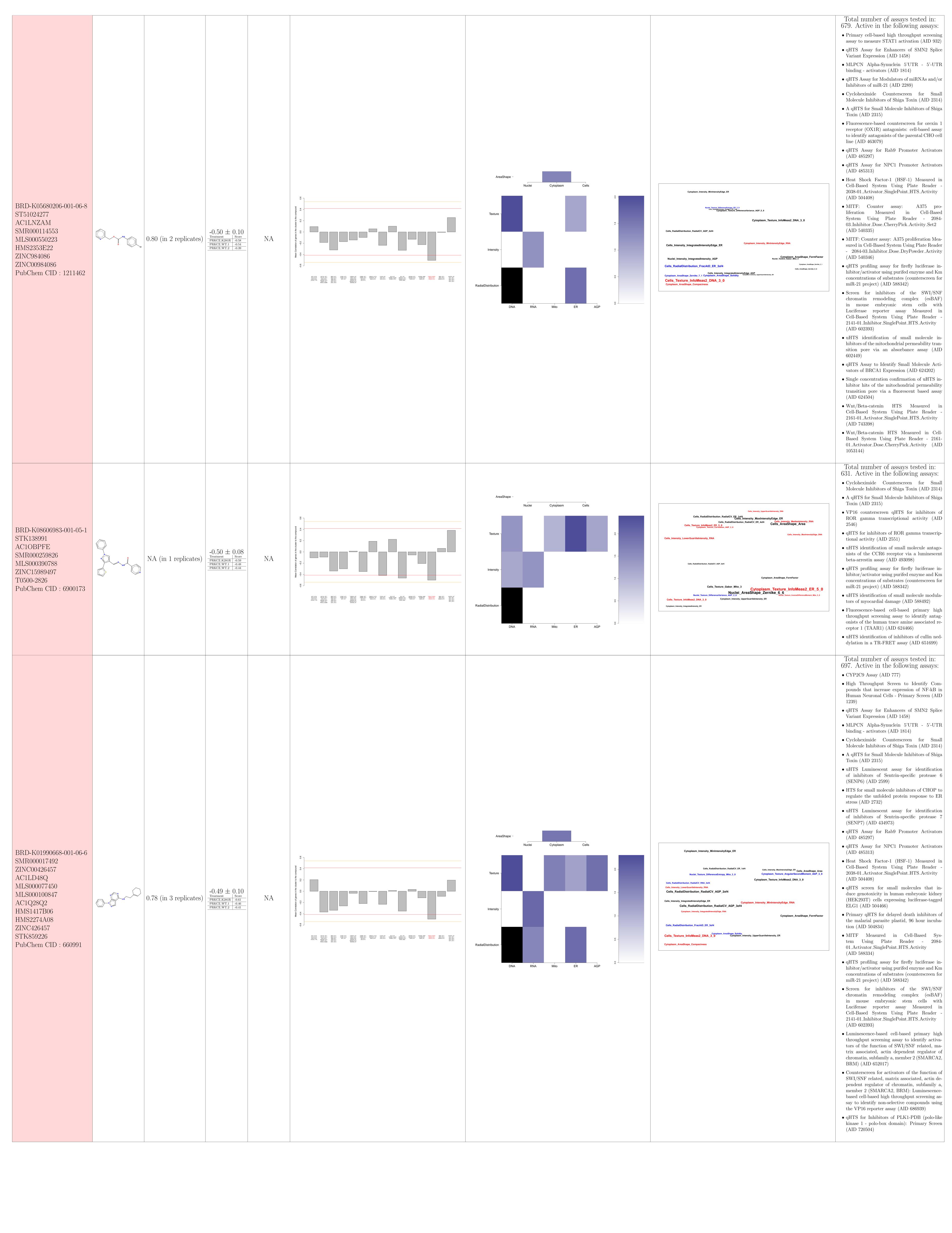


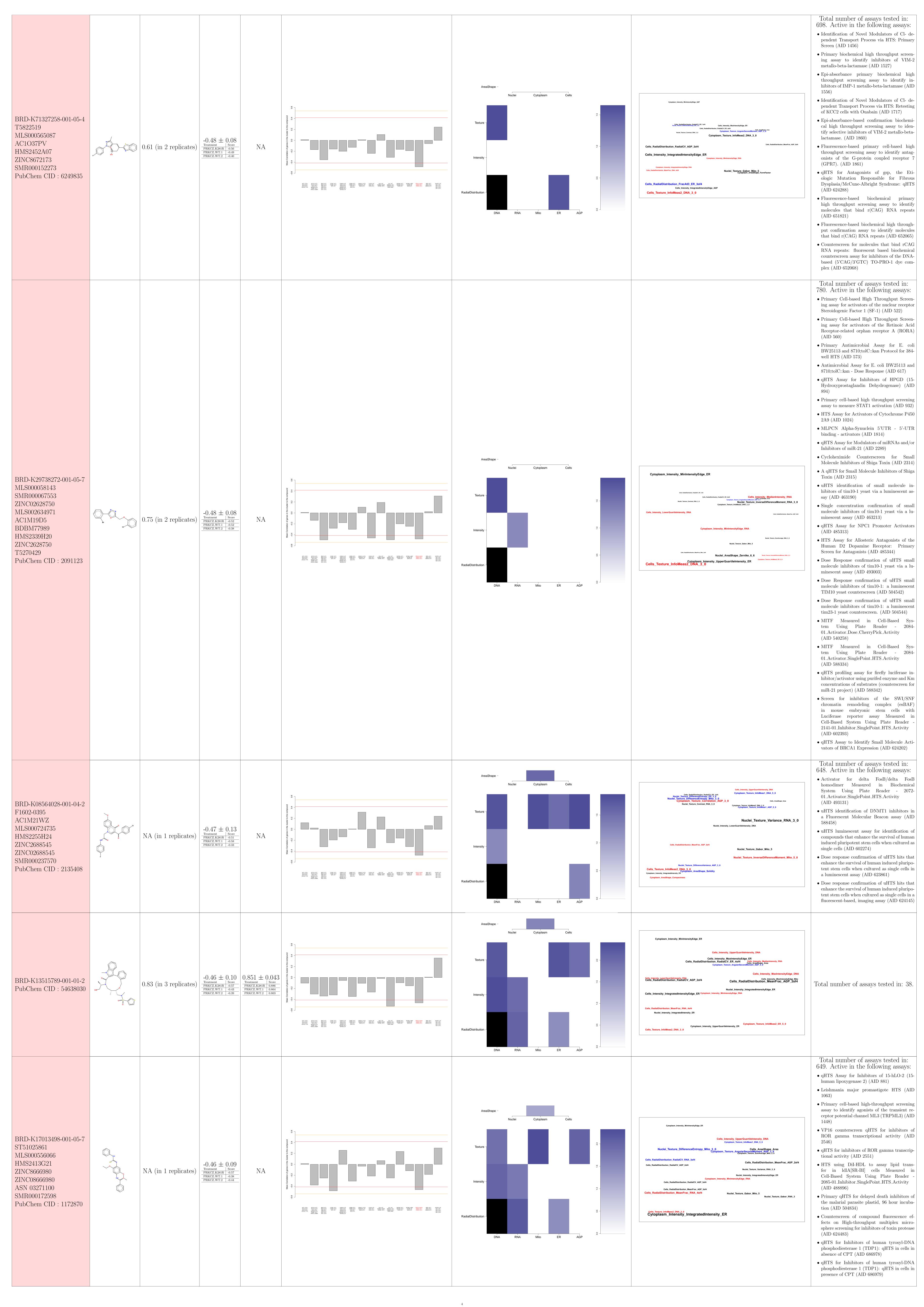


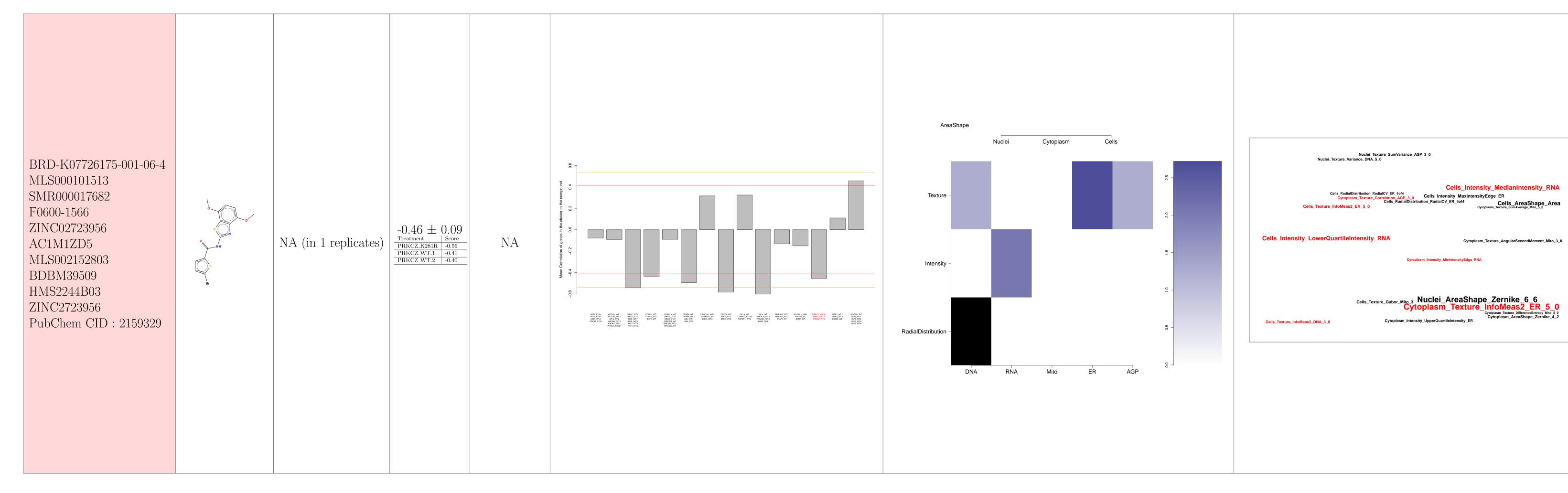


- Total number of assays tested in: 626. Active in the following assays: • Screen for Chemicals that Extend Yeast Lifespan (AID 775)
- uHTS identification of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463190)
- Single concentration confirmation of small molecule inhibitors of tim10-1 yeast via a luminescent assay (AID 463213)
- Fluorescence-based biochemical primary high throughput screening assay to identify inhibitors of the fructose-bisphosphate aldolase (FBA) of M. tuberculosis (AID 588726)
- Fluorescence Intensity-based biochemical primary high throughput screening assay to identify activators of kallikrein-7 (K7) zymogen (AID 652039)
- Fluorescence Intensity-based biochemical primary high throughput confirmation assay to identify activators of kallikrein-7 (K7) zymogen
- (AID 686949)• Counterscreen for activators of kallikrein-7 (K7) zymogen: Fluorescence intensity-based biochemical high throughput counterscreen assay for activators that optically interfere with measurement of EDANS-DABCYL fluorescence (AID 686952)









Total number of assays tested in: 760. Active in the following assays: • Primary Cell-based High Throughput Screen-

ing assay for activators of the nuclear receptor Steroidogenic Factor 1 (SF-1) (AID 522)

• HTS of Estrogen Receptor- alpha Coactivator Binding inhibitors (AID 629) • HTS for Estrogen Receptor-beta Coactivator Binding inhibitors (AID 633)

• Primary cell-based high-throughput screening assay to identify agonists of Galanin Receptor

2 (GALR2) (AID 803) • uHTS of Mcl-1/Bid interaction inhibitors (AID

• uHTS of Mcl-1/Noxa interaction inhibitors (AID 1022)

• Dose Response Confirmation for Mcl-1/Bid Interaction Inhibitors (AID 1418)

• Identification of Novel Modulators of Cl- de-

pendent Transport Process via HTS: Primary

Screen (AID 1456) • qHTS Assay for Promiscuous and Specific Inhibitors of Cruzain (without detergent) (AID

regulate the unfolded protein response to ER stress (AID 2732) • uHTS identification of DNMT1 inhibitors in

• HTS for small molecule inhibitors of CHOP to

a Fluorescent Molecular Beacon assay (AID 588458)

• qHTS for Stage-Specific Inhibitors of Vaccinia Orthopoxvirus: Venus Reporter Primary qHTS (AID 720580)