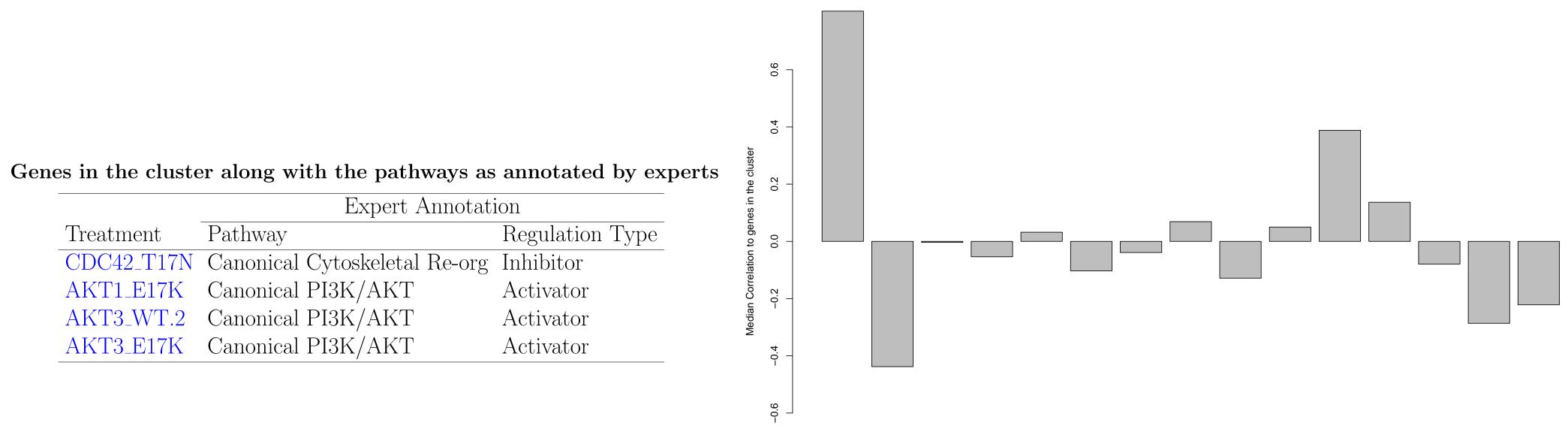
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein

How similar is this cluster to the other clusters?



	Expert Annot			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PIK3R1_WT.1	Canonical PI3K/AKT	Activator	-0.48	0.14
AKT1S1_WT.2	TOR	Inhibitor	-0.47	0.04
AKT1S1_WT.1	TOR	Inhibitor	-0.43	0.05

Activator

Canonical ER Stress/UPR Activator

Top 5 genes negatively correlated to the cluster

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.

PRKACG_WT.3 PKA

 $ATF4_WT.2$

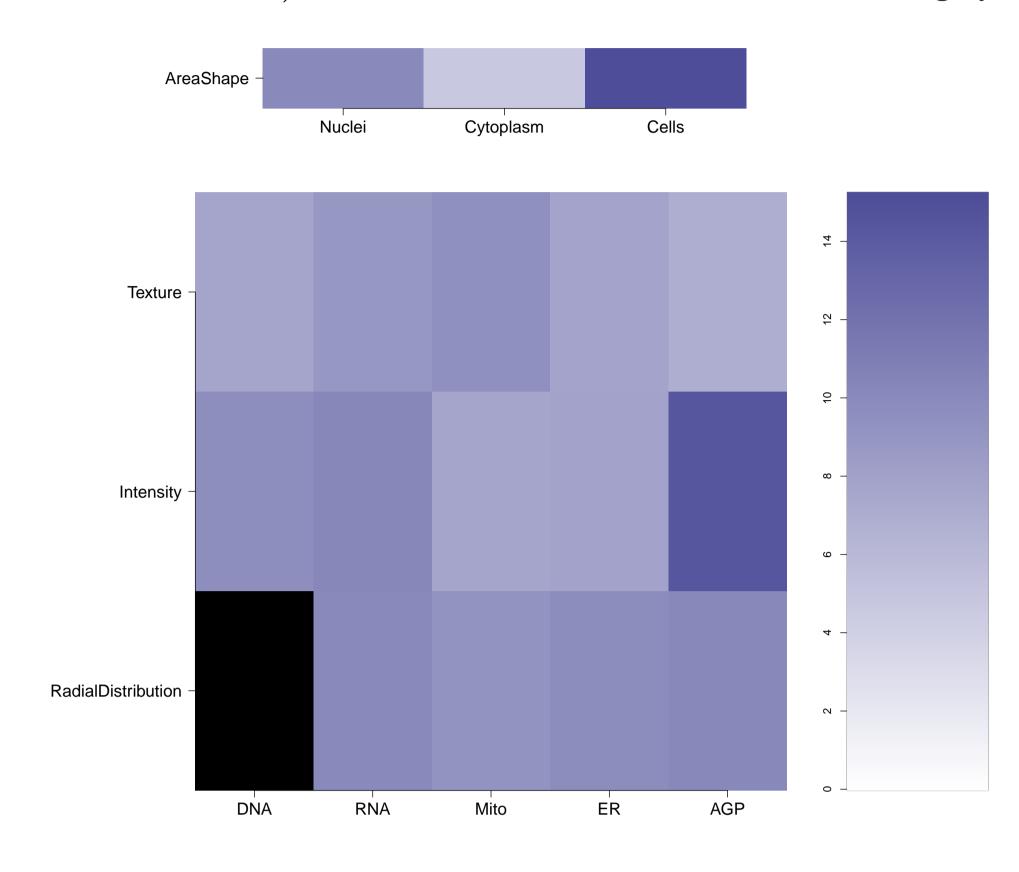
How strongly are genes within the cluster correlated?

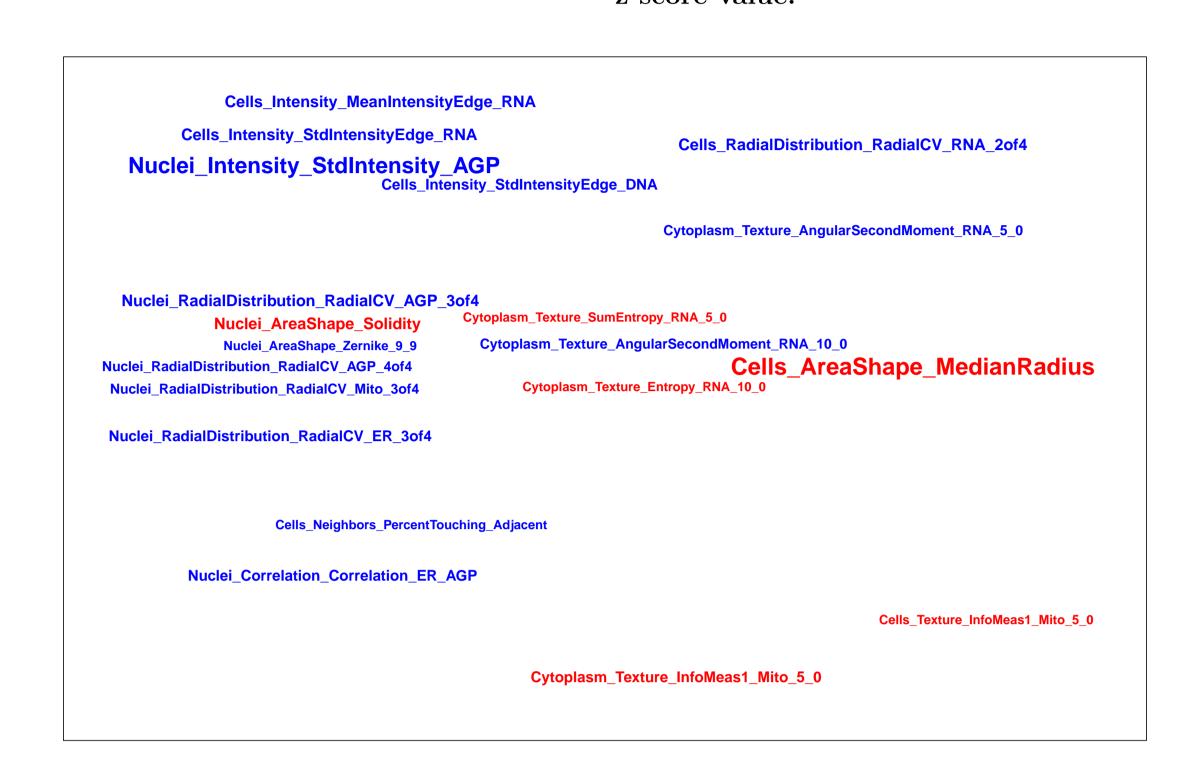
-0.42

-0.40

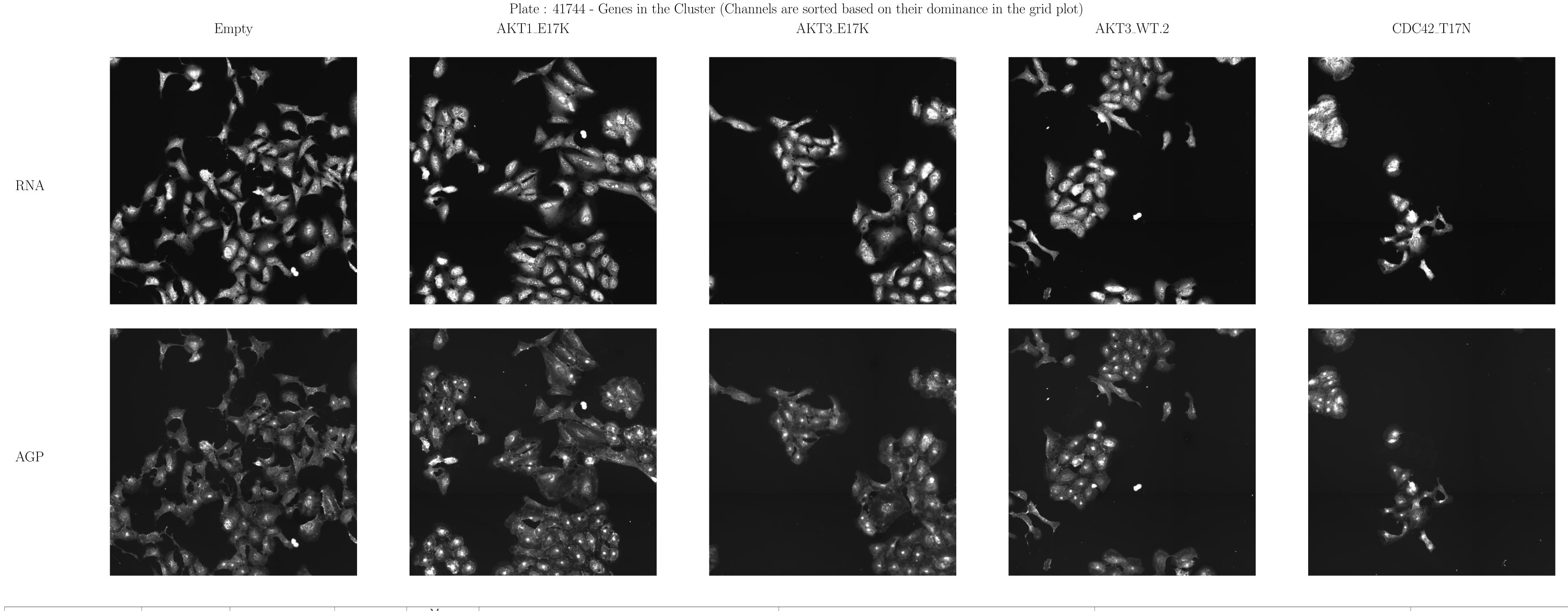
0.09

0.06

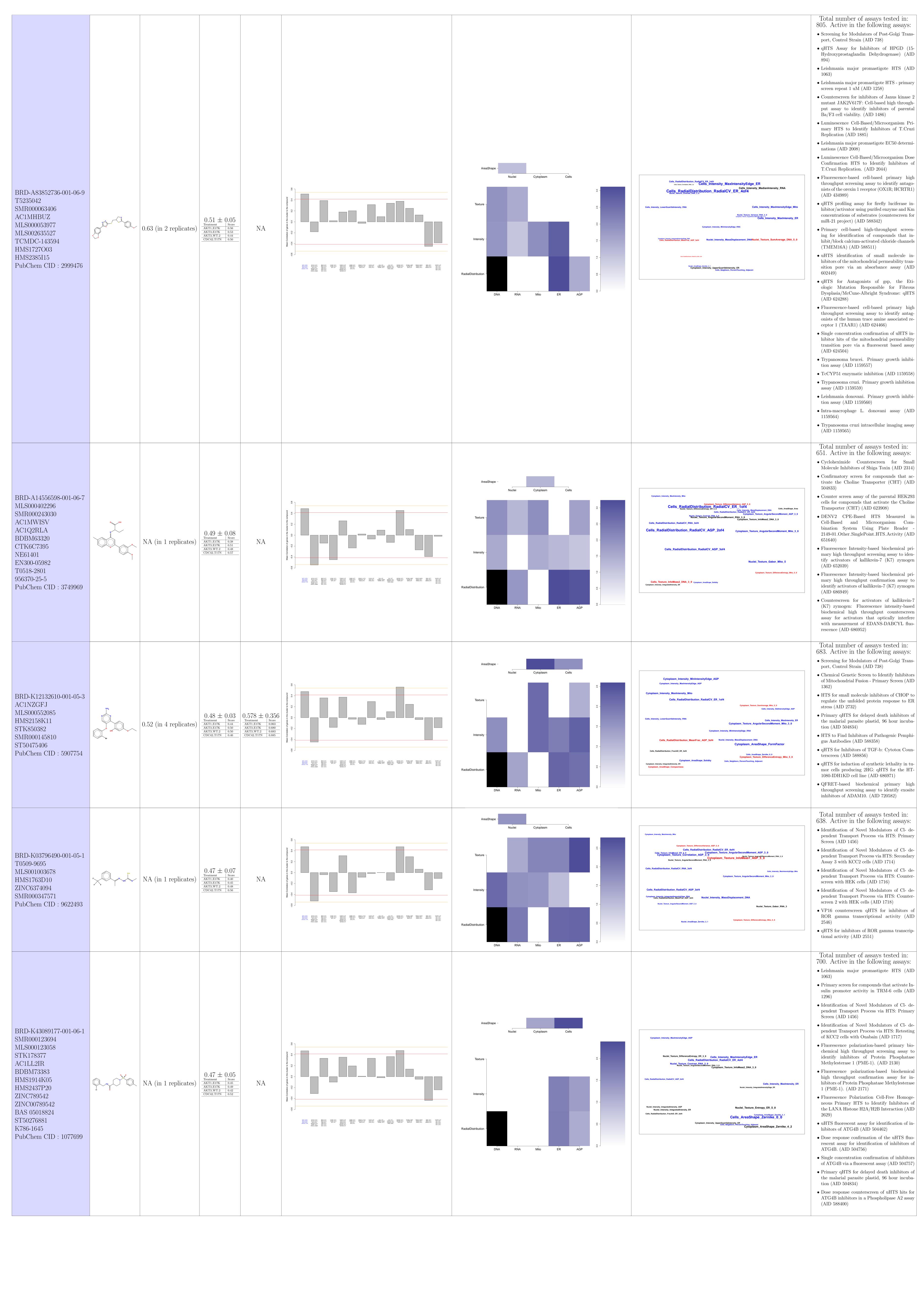


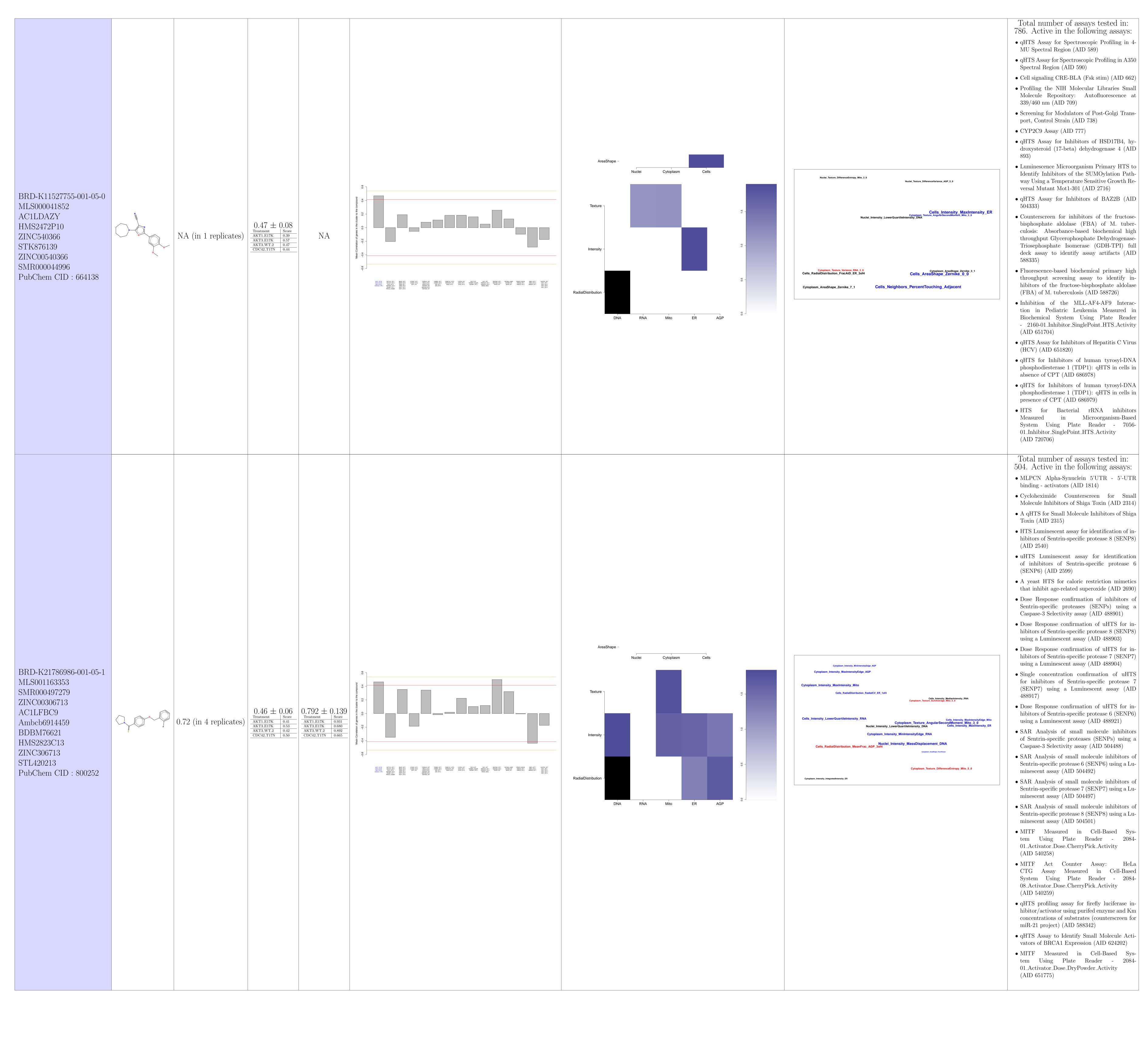


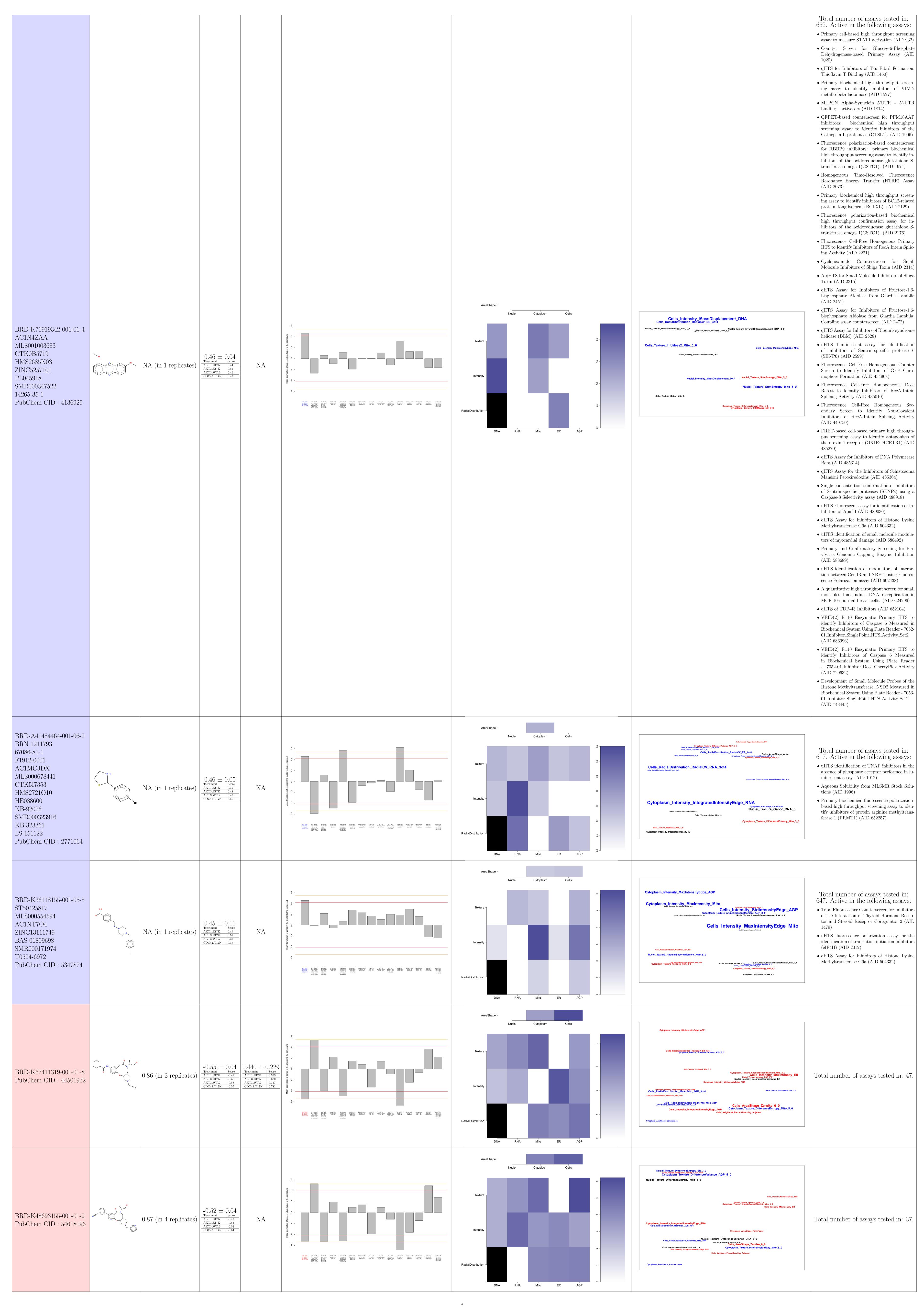
	aKT^	ENTK	SENTK AKT	S.WT.2	42-11
AKT1_E17K					- 0.8
AKT3_E17K					- 0.4
AKT3_WT.2					-0.2
CDC42_T17N					0.6 0.8

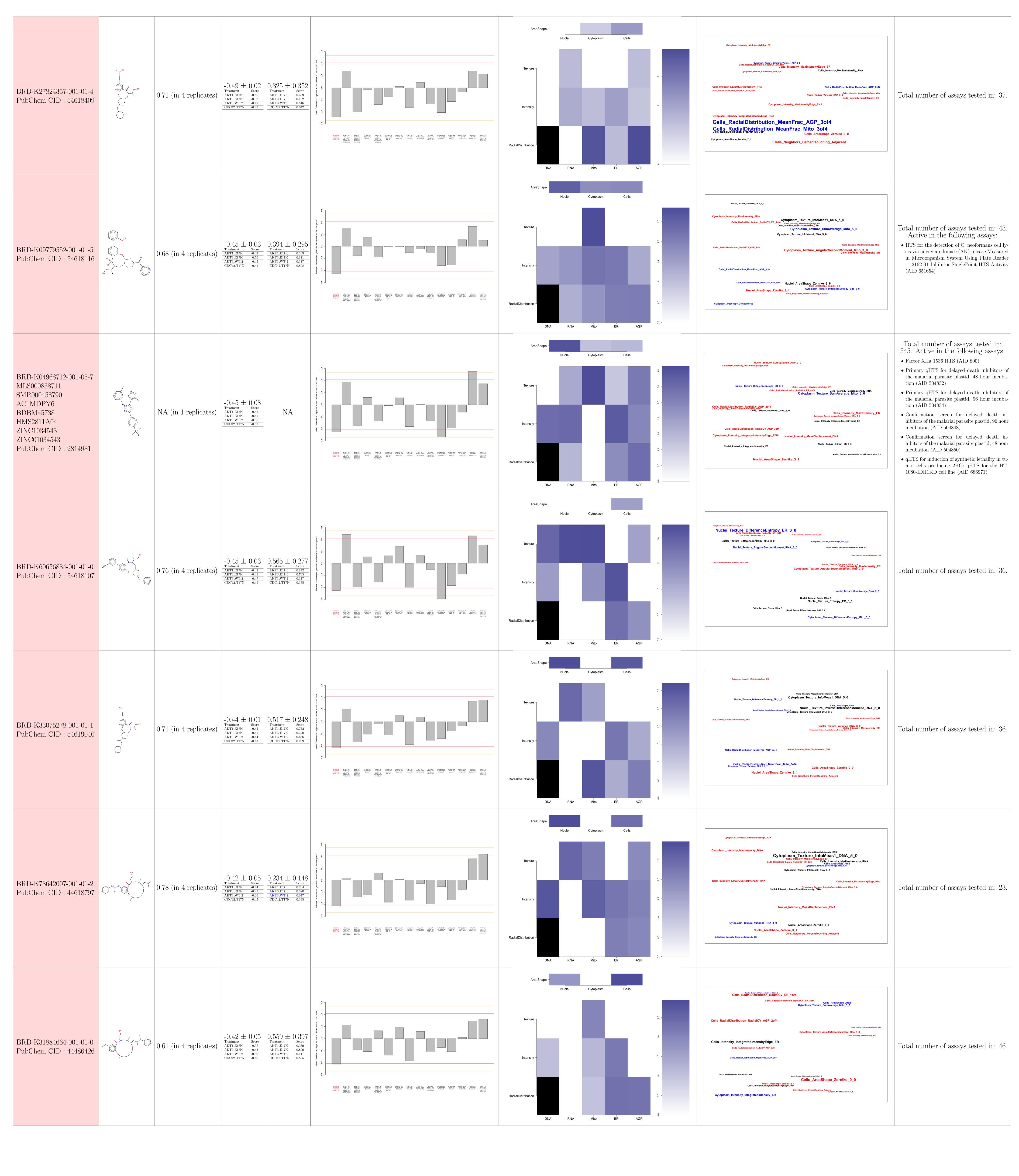


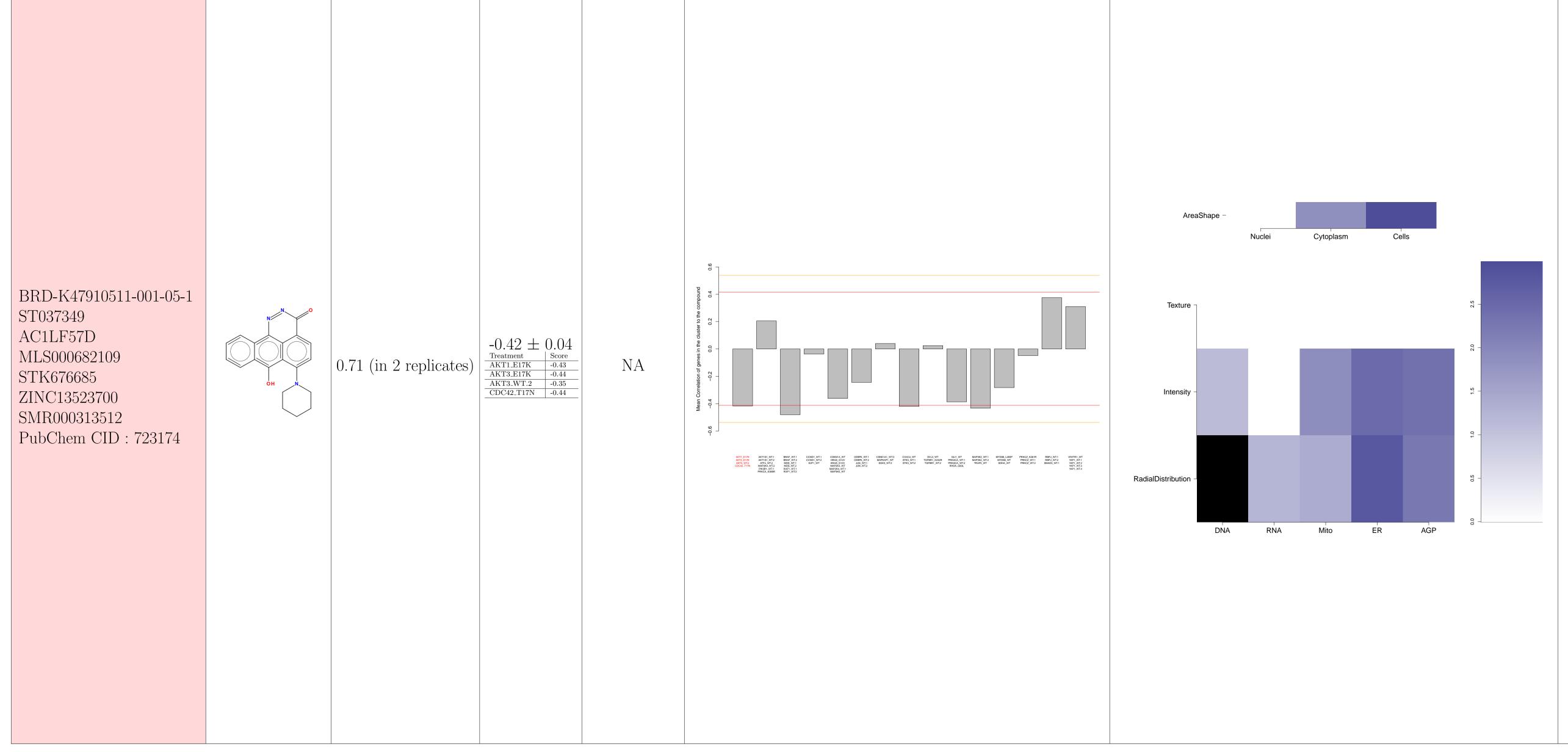
Compound IDs and common names (where available); blue/red colored box means the matching compound is positively/negatively correlated with the cluster	Chemical structure	Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52)	Mean ± standard deviation correlation between compound and each gene in cluster; Tables contain data for individual genes	using L1000 profiling ± standard deviation; 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	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	T NHIMBER OF PILOCHEM ACCAVE IN WAIRIN
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Total number of assays tested in: 642. Active in the following assays:

• Chemical Genetic Screen to Identify Inhibitors of Mitochondrial Fusion - Primary Screen (AID)

Thioflavin T Binding (AID 1460)

- 1362)

 qHTS for Inhibitors of Tau Fibril Formation,
- qHTS Multiplex Assay to Identify Dual Action Probes in a Cell Model of Huntington: Aggregate Formation (GFP) (AID 1688)
- HTS for small molecule inhibitors of CHOP to regulate the unfolded protein response to ER stress (AID 2732)
 Fluorescence polarization-based primary bio-
- chemical high throughput screening assay to identify inhibitors of the plasma platelet activating factor acetylhydrolase (pPAFAH) (AID 463082)
- uHTS for identification of Inhibitors of Mdm2/MdmX interaction in luminescent format. (AID 485346)
- qHTS for Inhibitors of mutant isocitrate dehydrogenase 1 (IDH1): Confirmation of Cherrypicks (AID 624002)
- qHTS Assay for Inhibitors of Hepatitis C Virus (HCV) (AID 651820)
 Fluorescence-based biochemical primary
- high throughput screening assay to identify molecules that bind r(CAG) RNA repeats (AID 651821)

 Counterscreen for molecules that bind rCAG
- RNA repeats: fluorescent based biochemical counterscreen assay for inhibitors of the DNA-based (5'CAG/3'GTC) TO-PRO-1 dye complex (AID 652068)

 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)
- qHTS for Inhibitors of Inflammasome Signaling: IL-1-beta AlphaLISA Primary Screen (AID 743279)