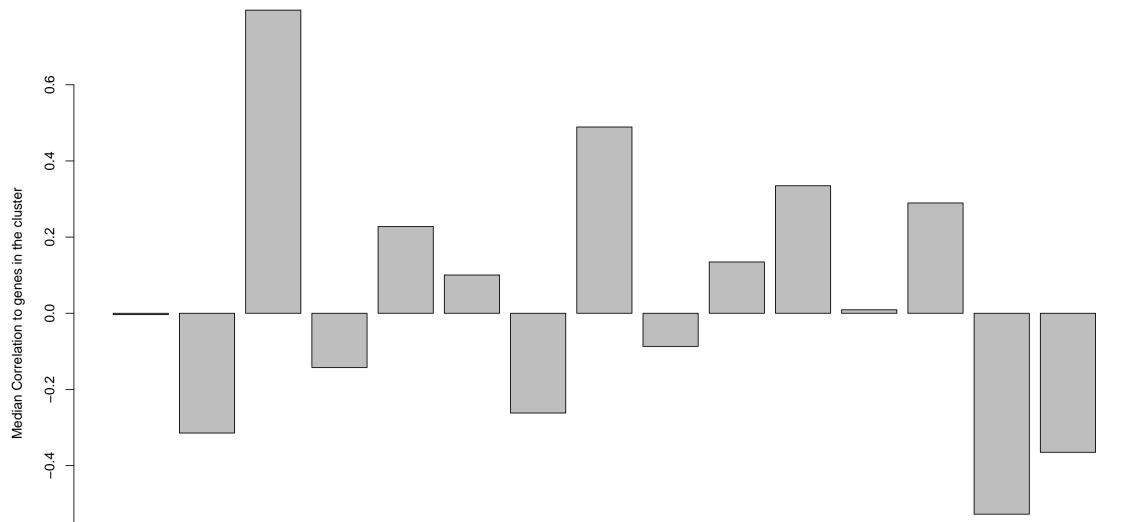
## CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein

How similar is this cluster to the other clusters?

## Genes in the cluster along with the pathways as annotated by experts | Expert Annotation | Pathway | Regulation Type | RAF1\_WT.1 | Canonical MAPK | Activator | RAFL\_WT.1 | Canonical MAPK | Activator |

Activator

Activator



Top 5 genes negatively correlated to the cluster	
Expert Annotation	

	Expert Annota			
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
RBPJ_WT.1	NOTCH	Activator	-0.60	0.07
ERN1_WT.1	Canonical ER Stress/UPR	Activator	-0.55	0.06
XBP1_WT.1	Canonical ER Stress/UPR	Activator	-0.51	0.09
RBPJ_WT.2	NOTCH	Activator	-0.49	0.10
YAP1_WT.3	Canonical Hippo	Inhibitor	-0.48	0.11

AKT1\_E17K AKT1S1\_WT.1 BRAF\_WT.1 CCND1\_WT.1 CDKN1A\_WT CEBPA\_WT.1 CSNK1A1\_WT.3 CXXC4\_WT DVL3\_WT GLI1\_WT MAP3K2\_WT.1 MYD88\_L265P PRKCZ\_K281R RBPJ\_WT.1 WWTR1\_WT AKT3\_E17K AKT1S1\_WT.2 BRAF\_WT.2 CCND1\_WT.2 HRAS\_G12V CEBPA\_WT.2 MAPKAP1\_WT STK3\_WT.1 TGFBR1\_K232R PRKACA\_WT.1 MAP3K2\_WT.2 MYD88\_WT PRKCZ\_WT.1 RBPJ\_WT.2 YAP1\_WT.1 AKT3\_WT.2 ATS4\_WT.2 MOS\_WT.1 E2F1\_WT KRAS\_G12V JUN\_WT.1 SGK3\_WT.2 STK3\_WT.2 STK3\_WT.2 TGFBR1\_WT.2 PRKACA\_WT.2 TRAF5\_WT SDHA\_WT PRKCZ\_WT.2 SMAD3\_WT.1 YAP1\_WT.3 PRKC2\_WT.2 MAP2K4\_WT.2 MAP2K4\_WT.1 MAP2K4\_WT.1 PRKC2\_WT.2 SMAD3\_WT.1 YAP1\_WT.3 PRKCA\_K368R RAF1\_WT.2 MAP2K5\_WT MAP2K5\_WT.1 MAP2K5\_WT MAP2K5\_WT.1 MAP2K5\_WT.1 MAP2K5\_WT.1 MAP2K5\_WT.1 MAP2K5\_WT.1 MAP2K5\_WT.2 MAP2K5\_

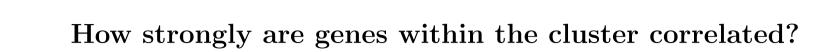
What groups of morphological features are distinguishing in the cluster relative to the untreated samples? (maximum of absolute m-score for the features belonging to the same category; m-score defined as median of a feature z-score across genes in the cluster) Black means no feature is available in the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

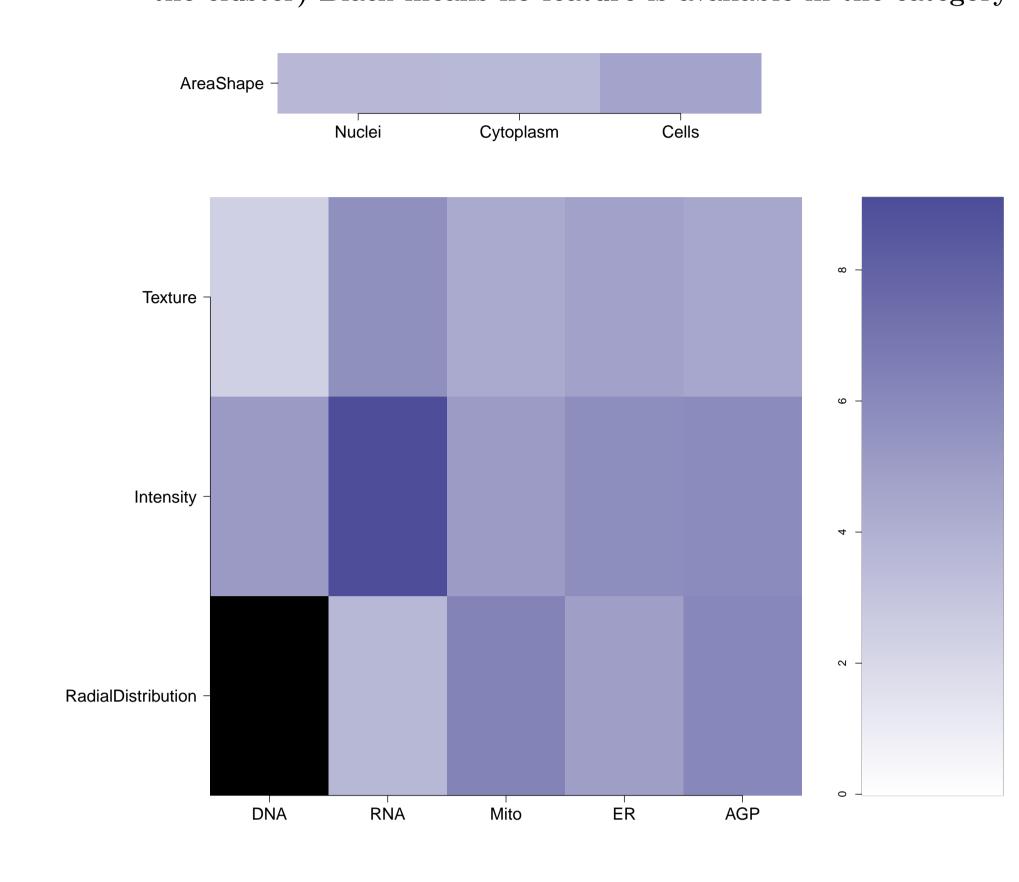
BRAF\_WT.2 Canonical MAPK Activator

RAF1\_WT.2 Canonical MAPK Activator

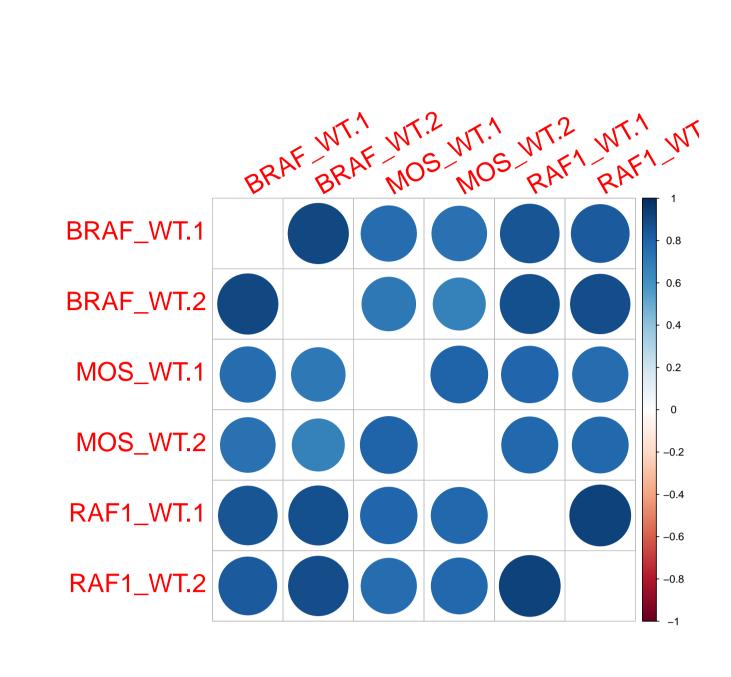
MOS\_WT.2 MAPK

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.









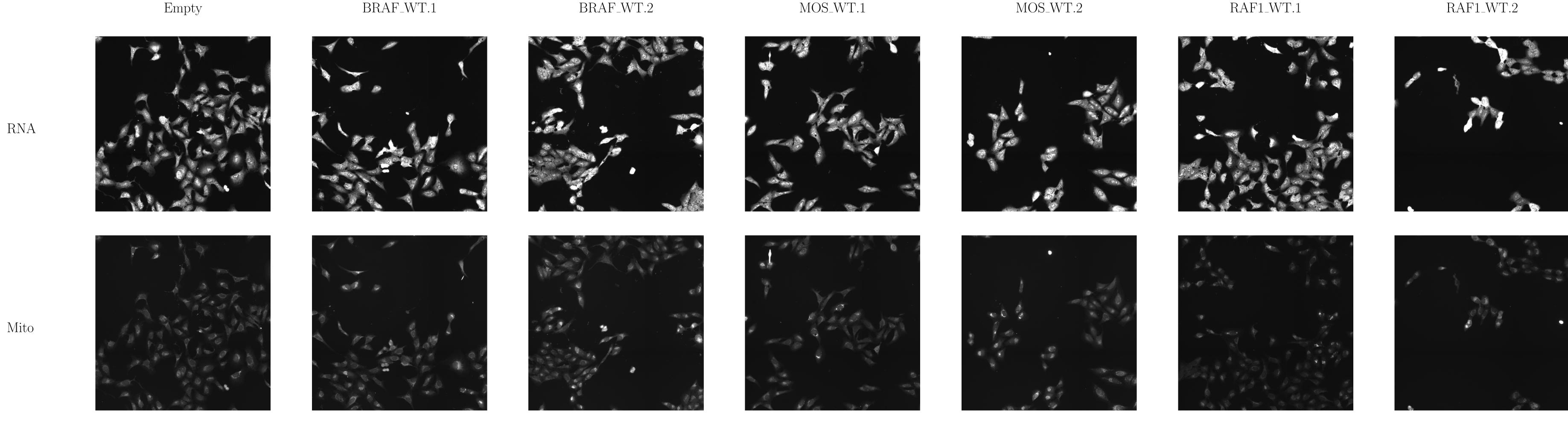
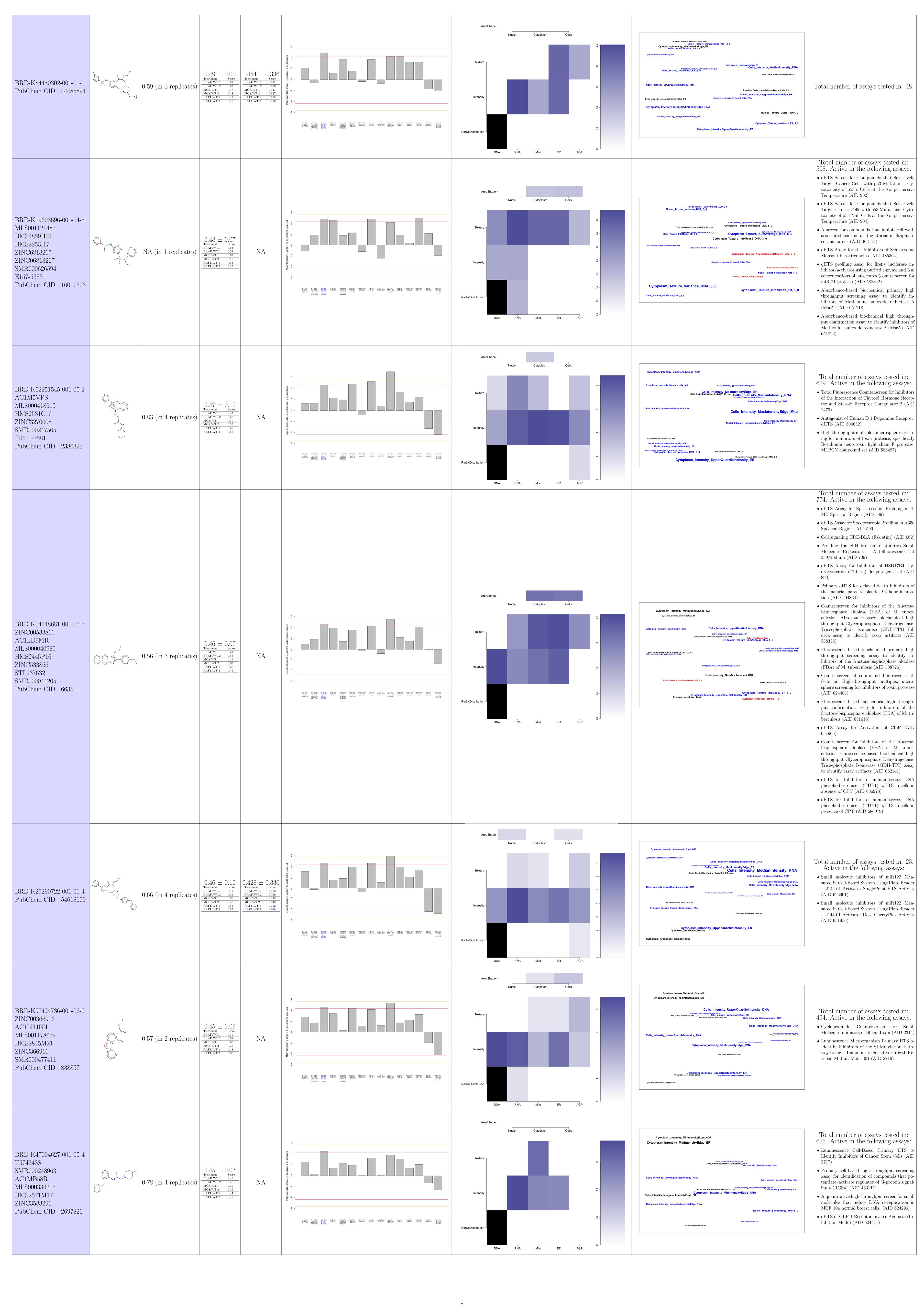
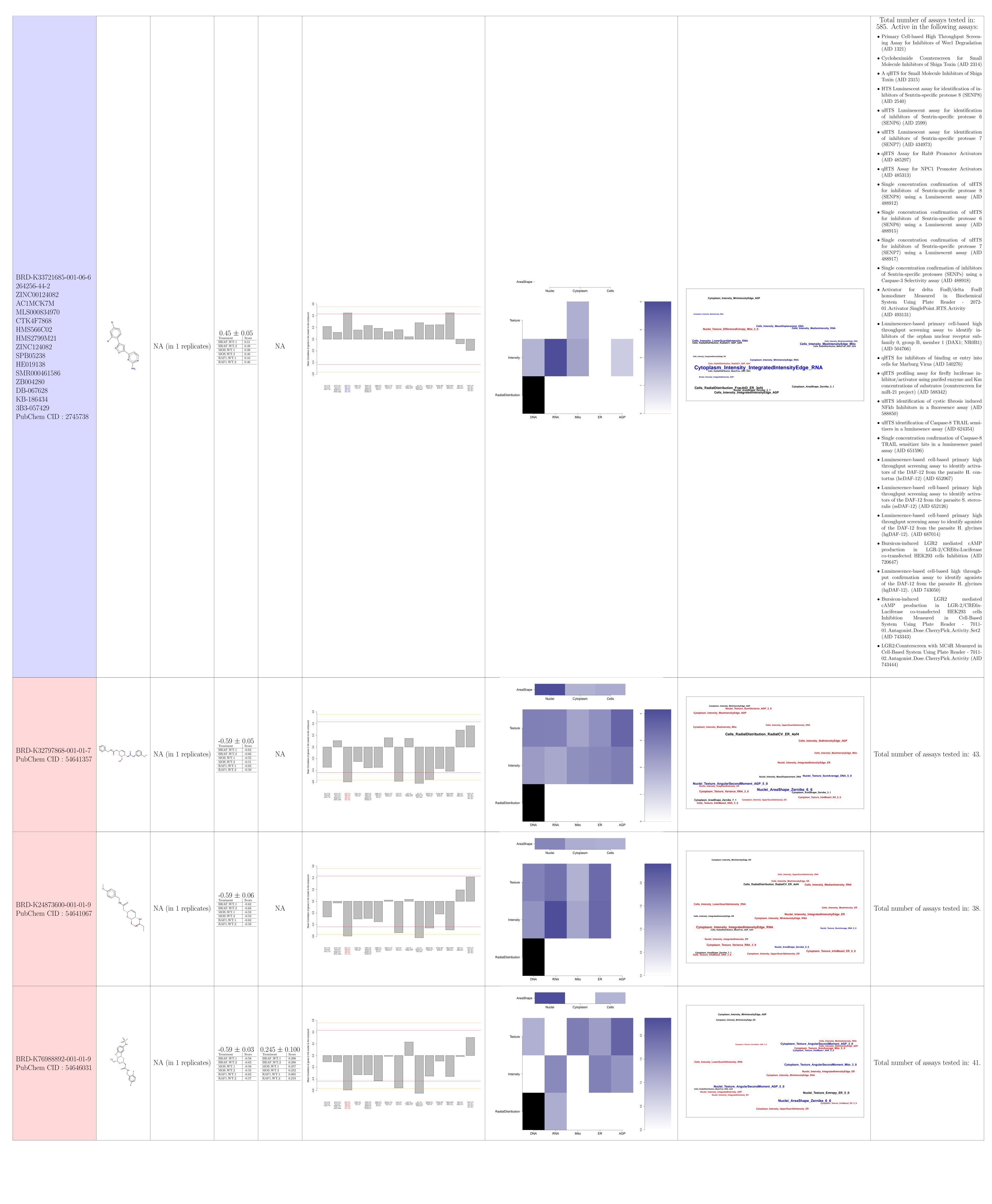
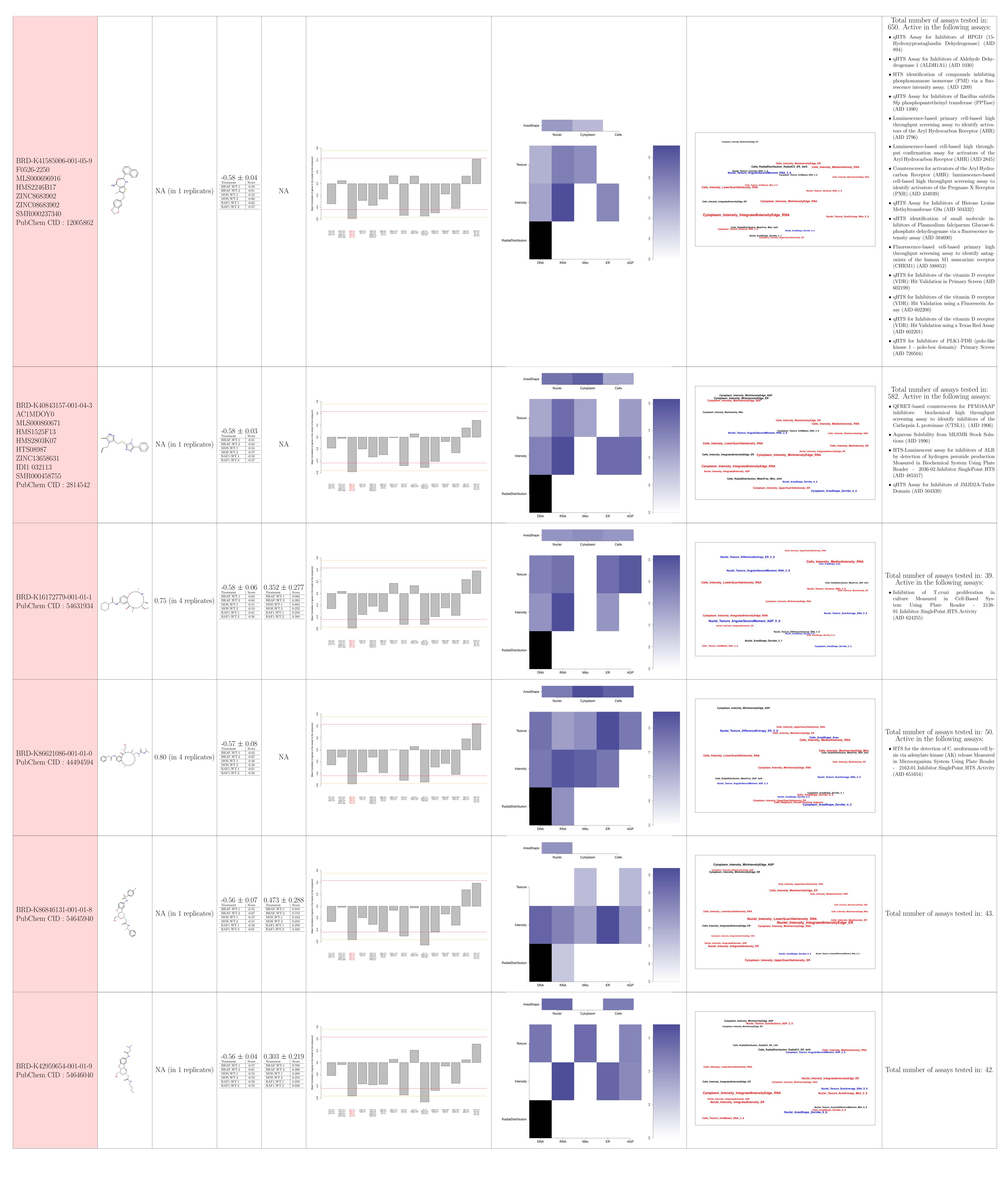


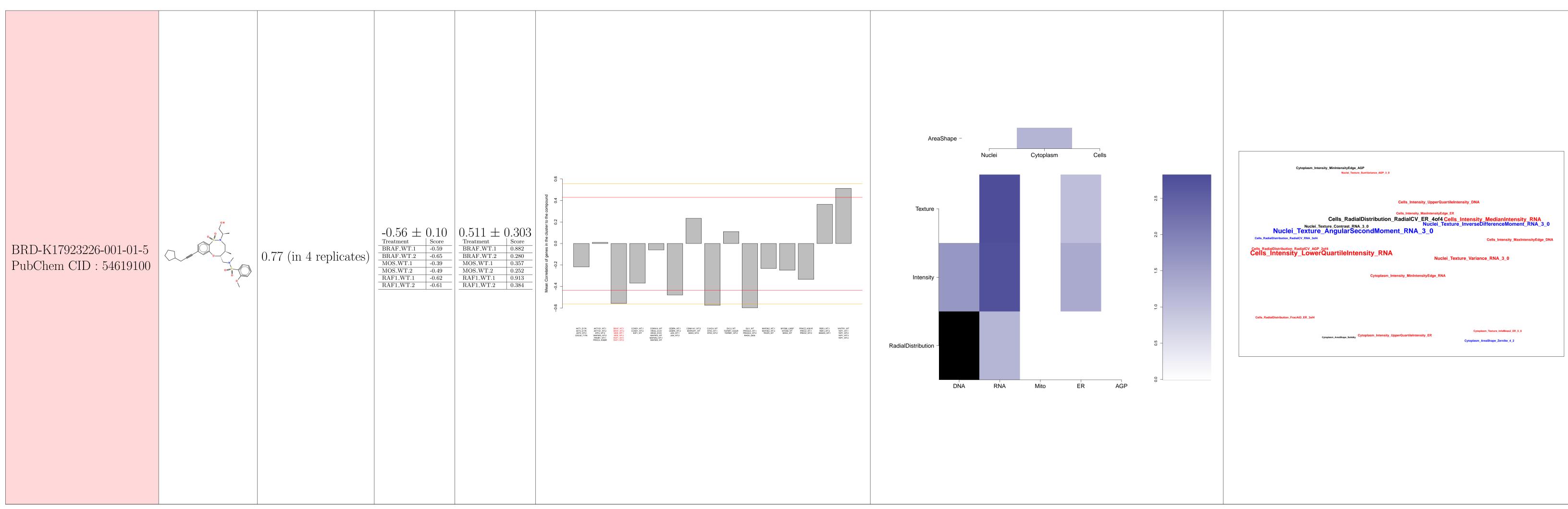
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)











- Total number of assays tested in: 38. Active in the following assays:
  - MLPCN SirT-5 Measured in Biochemical System Using Imaging 7044-01\_Inhibitor\_SinglePoint\_HTS\_Activity\_Set5 (AID 652115)
- Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader 2153-01\_Inhibitor\_Dose\_DryPowder\_Activity (AID 1159566)
- Plasmodium falciparum Dd2 Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader 2153-05\_Inhibitor\_Dose\_CherryPick\_Activity (AID 1159567)
- HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader
   2153-03\_Inhibitor\_Dose\_DryPowder\_Activity (AID 1159569)
   Plasmodium falciparum 3D7-ScDHODH
- Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader 2153-02\_Inhibitor\_Dose\_DryPowder\_Activity (AID 1159570)

   Plasmodium falciparum PfNITD609-resistant
- ATP4 D1247Y Sybr green parasite growth Measured in Cell-Based and Microorganism Combination System Using Plate Reader 2153-11\_Inhibitor\_Dose\_DryPowder\_Activity (AID 1159571)
- HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader
   2153-03\_Inhibitor\_Dose\_CherryPick\_Activity (AID 1159577)