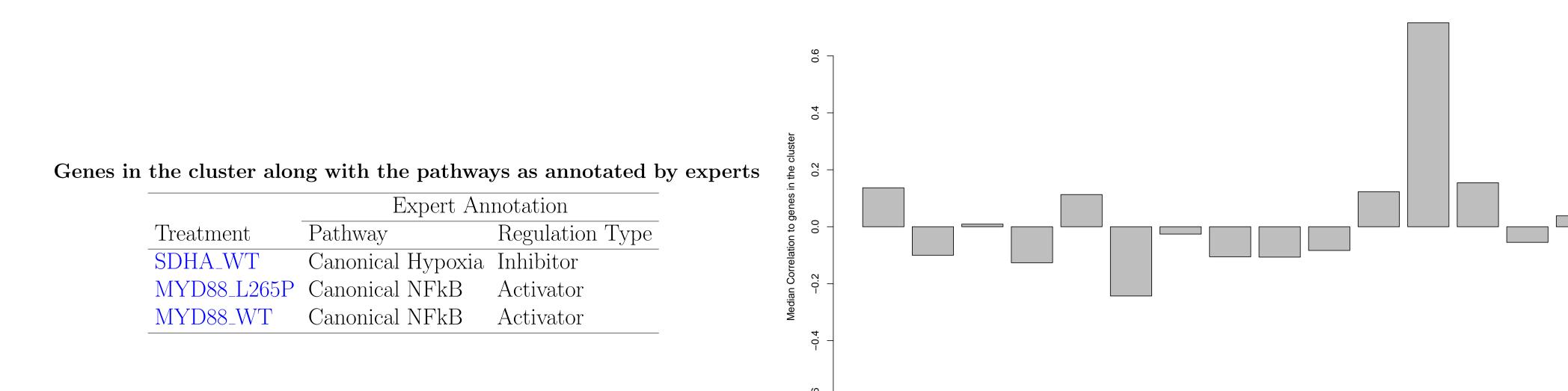
How similar is this cluster to the other clusters?



| Top 5 genes negatively correlated to the cluster |                       |                 |                  |                    |  |  |  |  |  |  |  |
|--|-----------------------|-----------------|------------------|--------------------|--|--|--|--|--|--|--|
|  | Expert Annota         |                 |                  |                    |  |  |  |  |  |  |  |
| Treatment  | Pathway               | Regulation Type | Mean Correlation | Standard Deviation |  |  |  |  |  |  |  |
| PRKACG_WT.3                                      | PKA                   | Activator       | -0.35            | 0.1                |  |  |  |  |  |  |  |
| TGFB1_WT   | Canonical TGFbeta     | Activator       | -0.29            | 0.1                |  |  |  |  |  |  |  |
| CEBPA_WT.2                                       | Transcription Factors | Activator       | -0.27            | 0.0                |  |  |  |  |  |  |  |
| CEBPA_WT.1                                       | Transcription Factors | Activator       | -0.25            | 0.0                |  |  |  |  |  |  |  |

Canonical ER Stress/UPR Activator

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 ATF4\_WT.2 MOS\_WT.1 E2F1\_WT KRAS\_G12V JUN\_WT.1 SGK3\_WT.2 STK3\_WT.2 TGFBR1\_WT.2 PRKACA\_WT.2 TRAF5\_WT SDHA\_WT PRKCZ\_WT.2 SMAD3\_WT.1 YAP1\_WT.2 MAP2K4\_WT.2 MAP2K4\_WT.2 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP2K4\_WT.1 MAP3K5\_WT WAP3K5\_WT MAP3K5\_WT MAP3K5\_WT MAP3K5\_WT

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.

ATF4\_WT.2

How strongly are genes within the cluster correlated?

-0.25

0.11

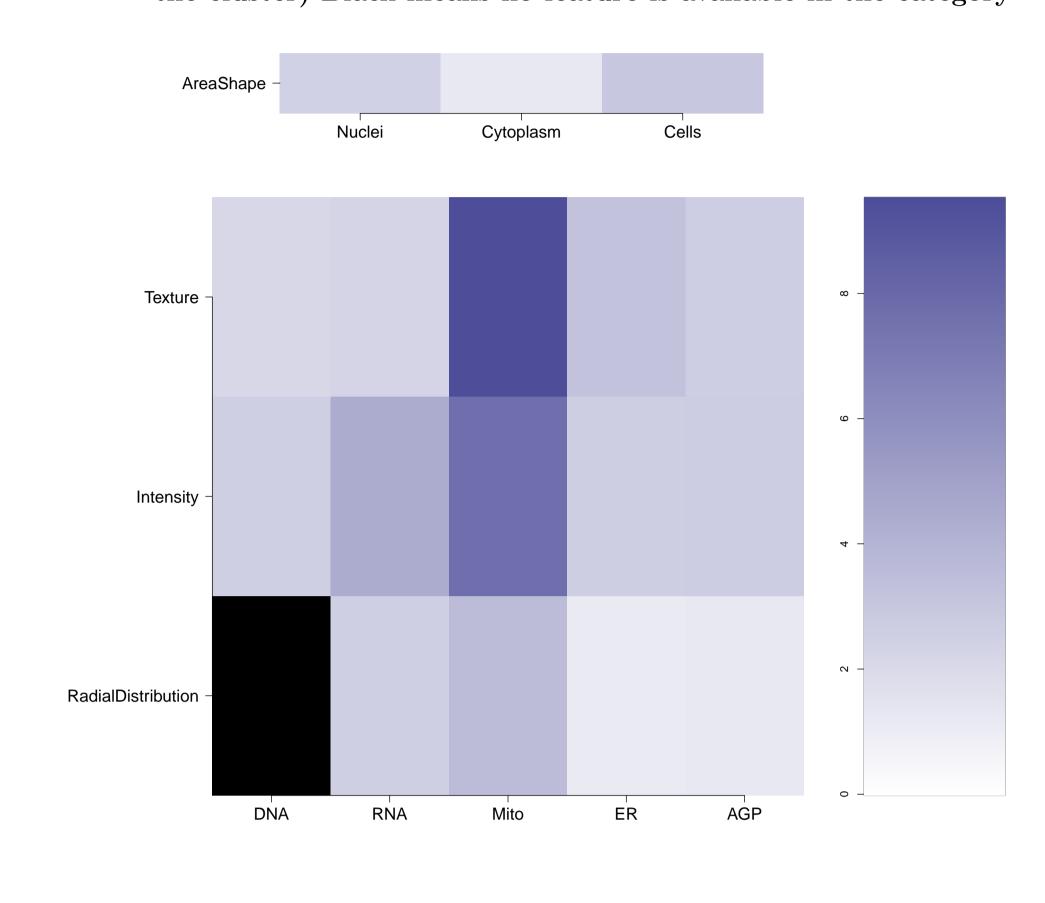
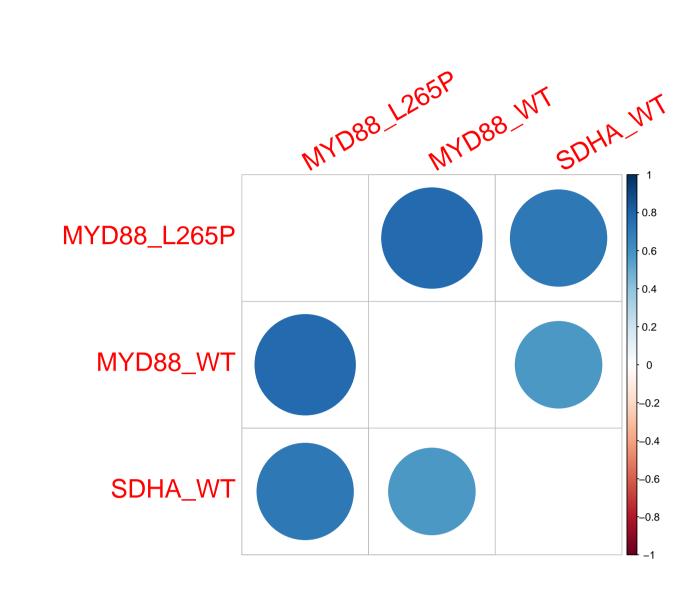
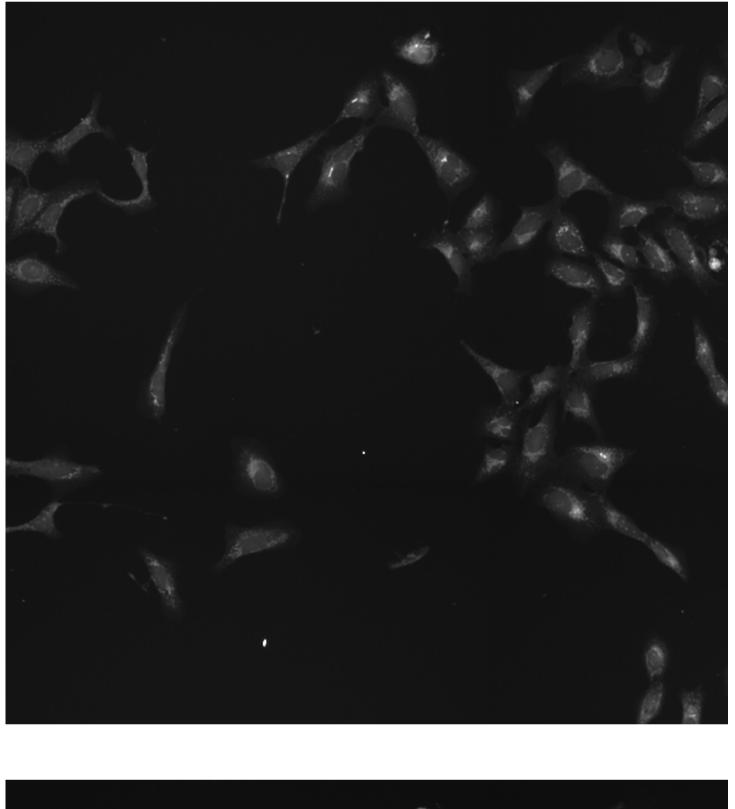




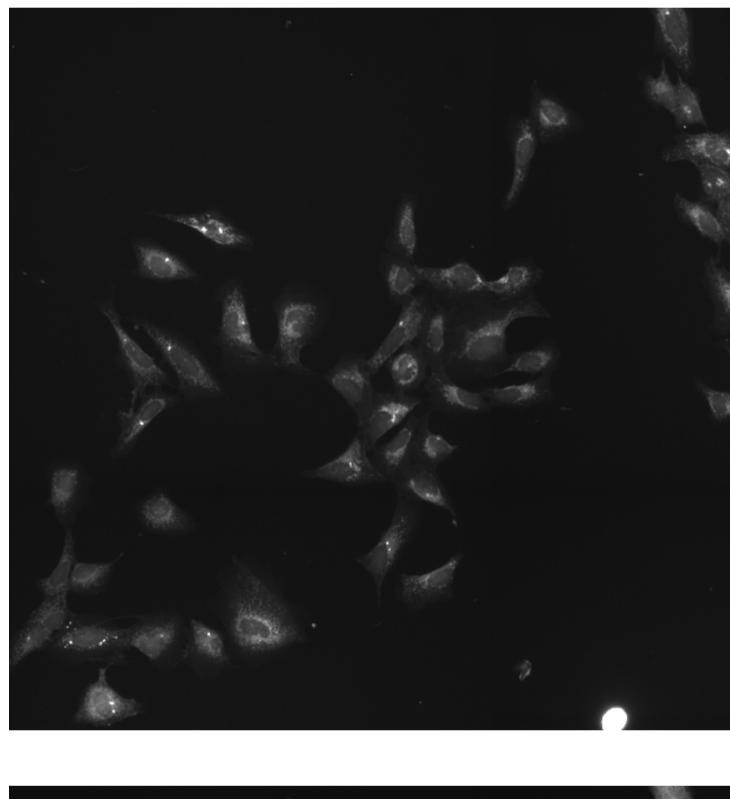
Plate: 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)



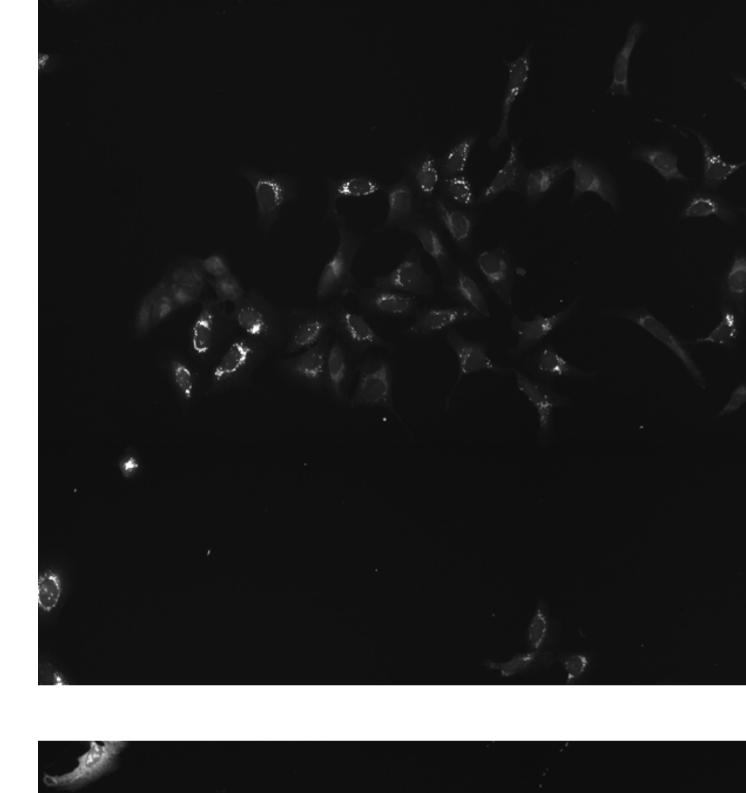
Mito



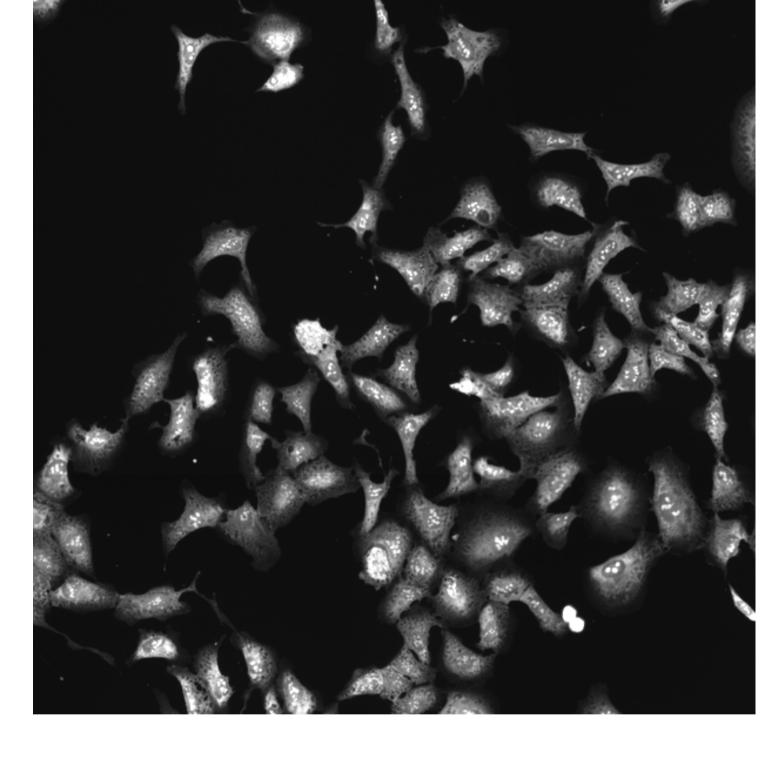
MYD88\_L265P



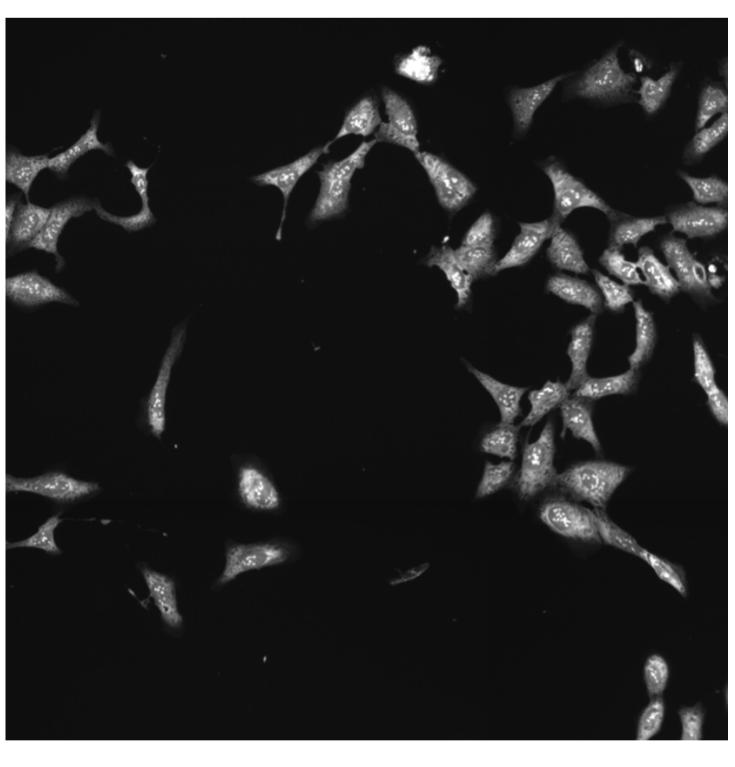
 $MYD88_WT$ 

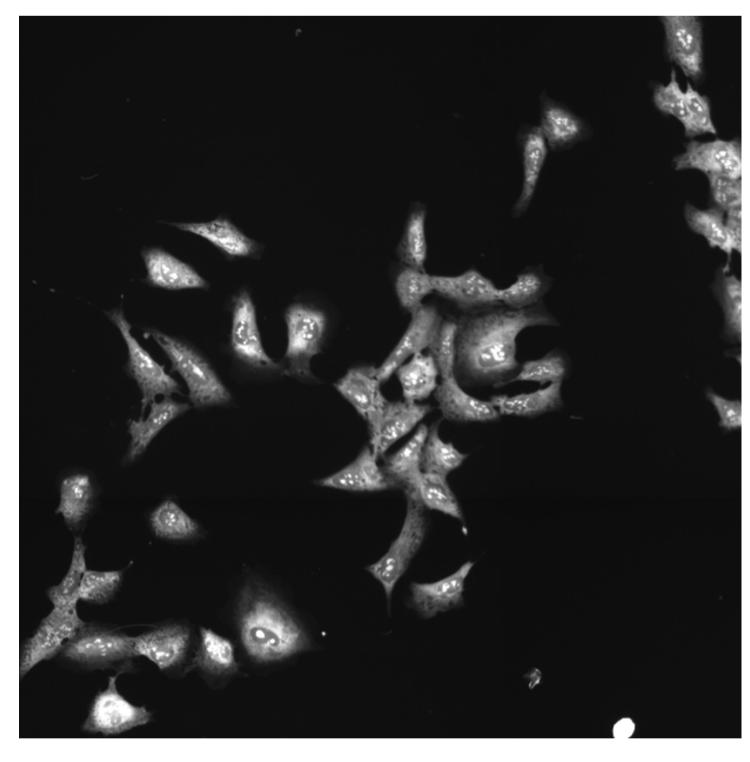


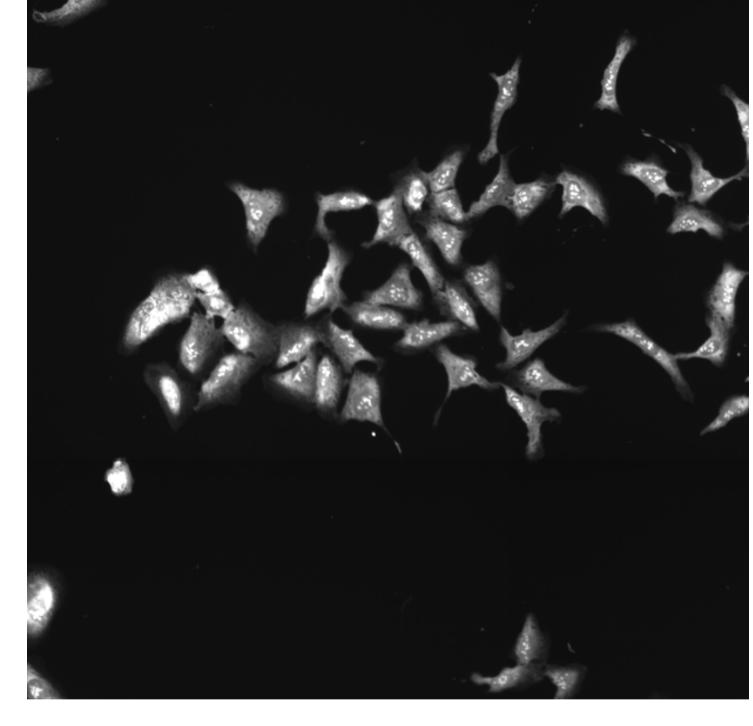
 $SDHA_WT$ 



RNA







| Compound IDs common names (available); blue/red box means the macompound is positively/negated with the | (where d colored atching is tively | structure      | Mean pairwise replicates correlation of the compound signature (95th DMSO replicate correlation is 0.52) | and each<br>gene in   | against genes in cluster 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 disti          | _                              | gories in the compound and 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  | the compound was tosted; assays in    |
|---|------------------------------------|----------------|--|---|--|--|-----------------------|--------------------------------|--|--|---------------------------------------|
| BRD-K54419202-0<br>PubChem CID : 54   |                                    | OH<br>ON<br>NH | 0.95 (in 4 replicates  | 0.67 ± 0.05 Treatment   Score MYD88_L265P   0.62 MYD88_WT   0.70 SDHA_WT   0.70 | 0.265 ± 0.132 Treatment   Score MYD88_L265P   0.379 MYD88_WT   0.295 SDHA_WT   0.121 | Metal Confidence of General Library (1997) ( | Texture - Intensity - | Nuclei Cytoplasm  DNA RNA Mito | Cells  The second of the secon | Cytoplasm_Intensity_MaxIntensity_Mito  Nuclei_Texture_DifferenceEntropy_Mito_3_0  CottTexture_DifferenceEntropy_Mito_3_0  CottTexture_DifferenceEntropy_Mito_3_0  CottTexture_DifferenceEntropy_Mito_3_0  Cytoplasm_Texture_AngularSecondMoment_Mito_3_0  Cytoplasm_Texture_AngularSecondMoment_Mito_3_0  Note Texture_DifferenceMoment_Mito_5_0  Nuclei_Texture_SumEntropy_Mito_5_0  Nuclei_Texture_SumEntropy_Mito_5_0  Nuclei_Texture_DifferenceMoment_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0  Cytoplasm_Texture_DifferenceEntropy_Mito_5_0 | Total number of assays tested in: 25. |

