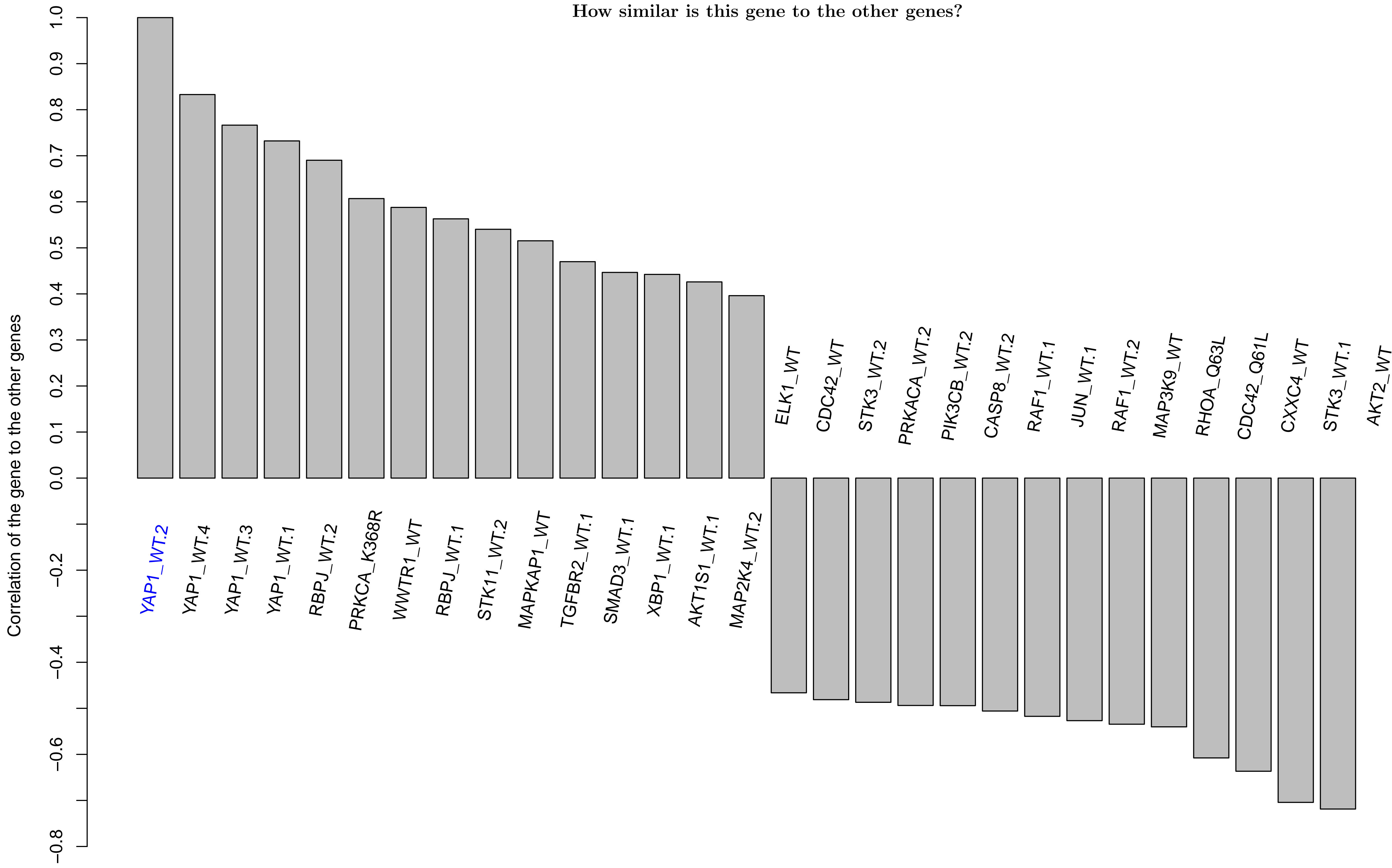
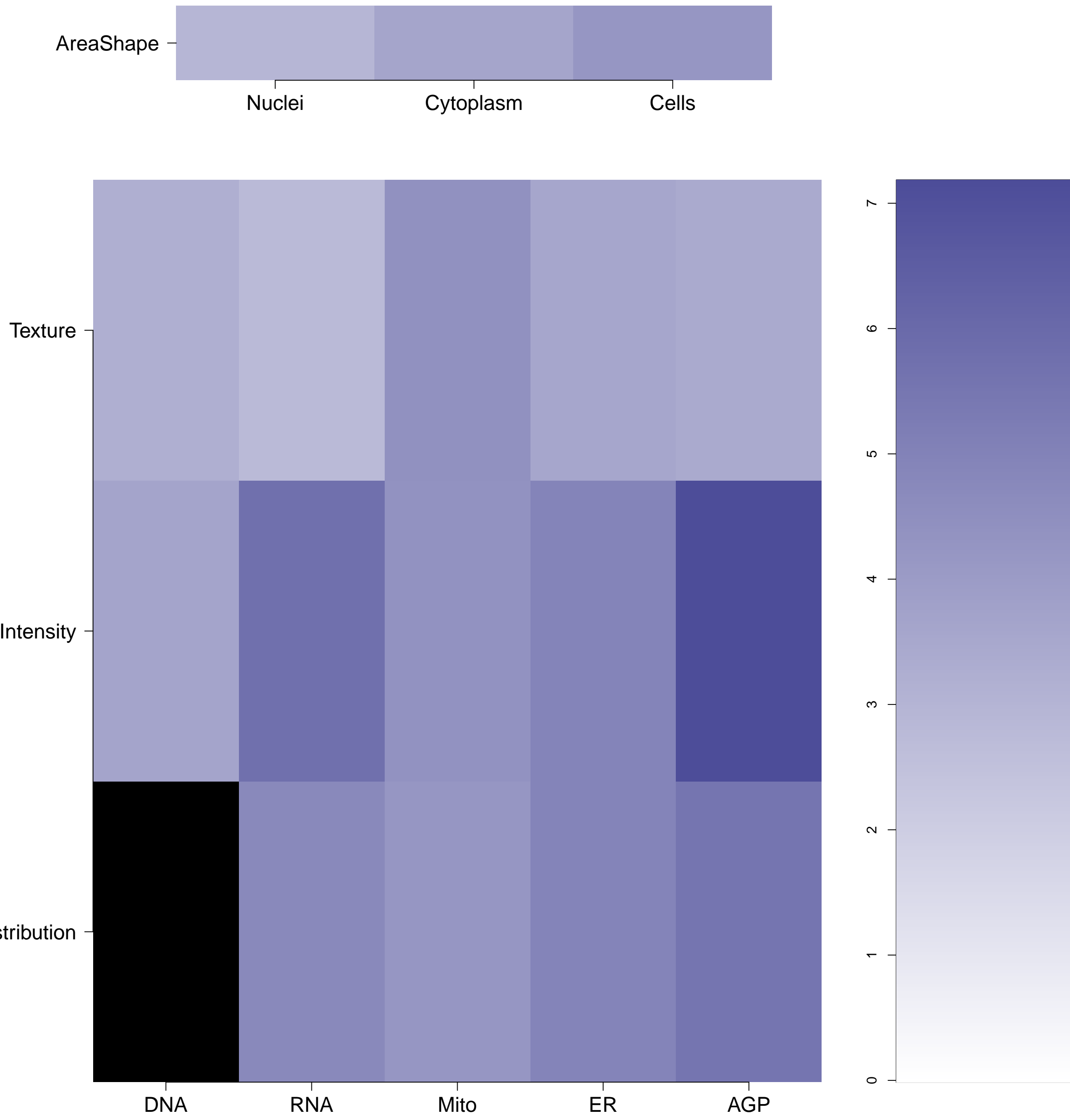


YAP1.WT.2 - in Canonical Hippo

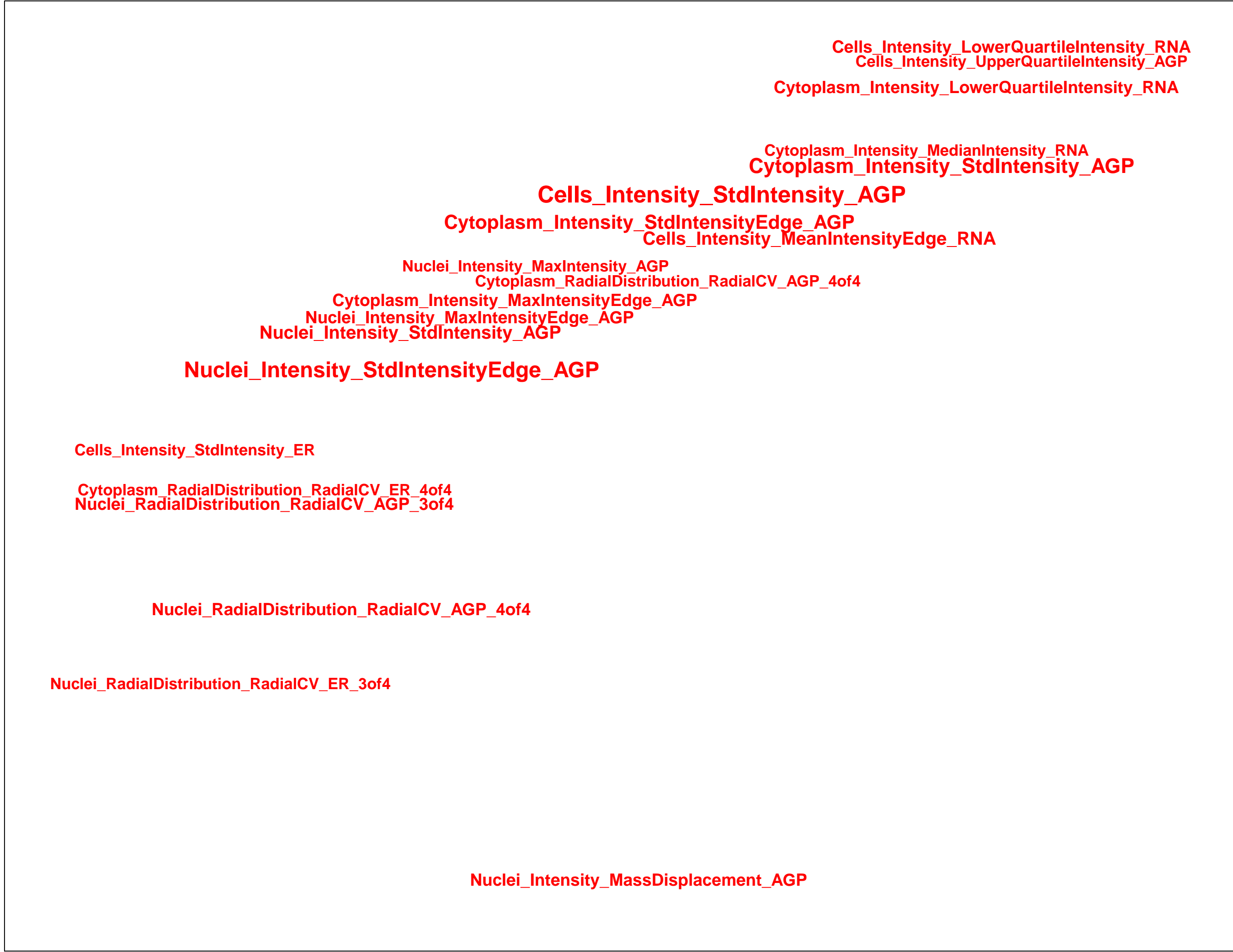
How similar is this gene to the other genes?



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



Empty

YAP1.WT.2 (41744)

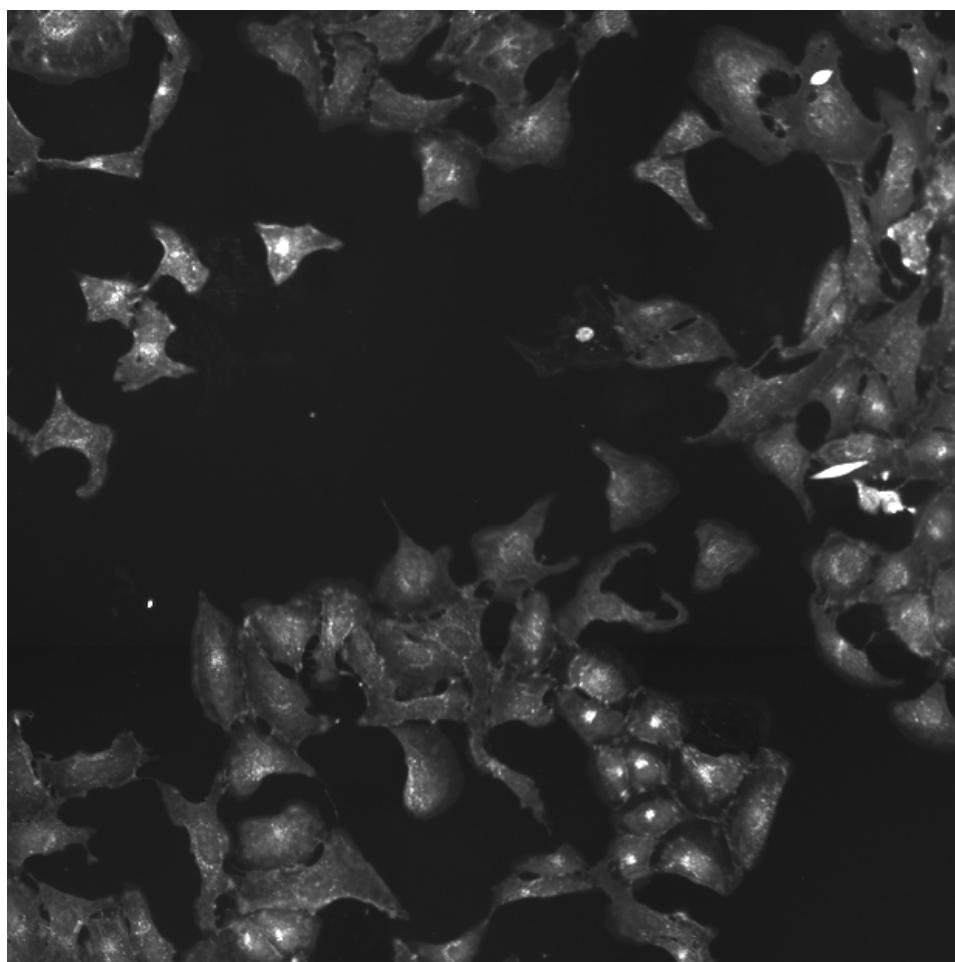
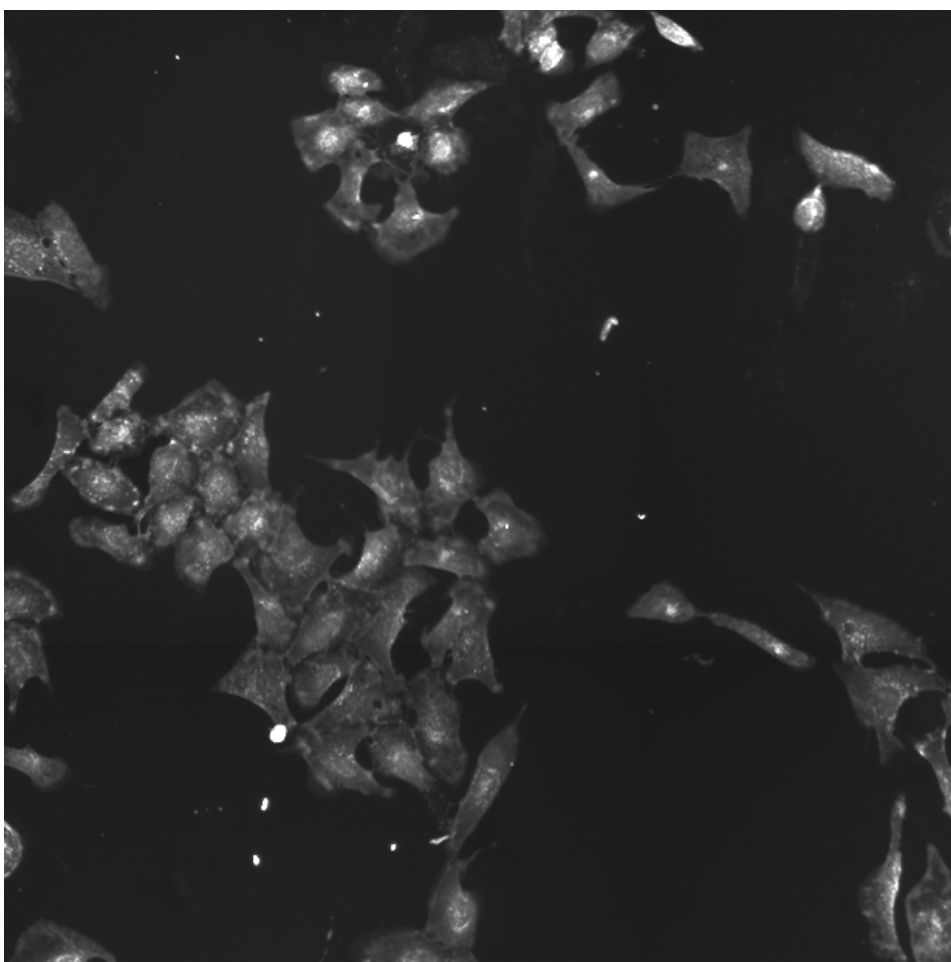
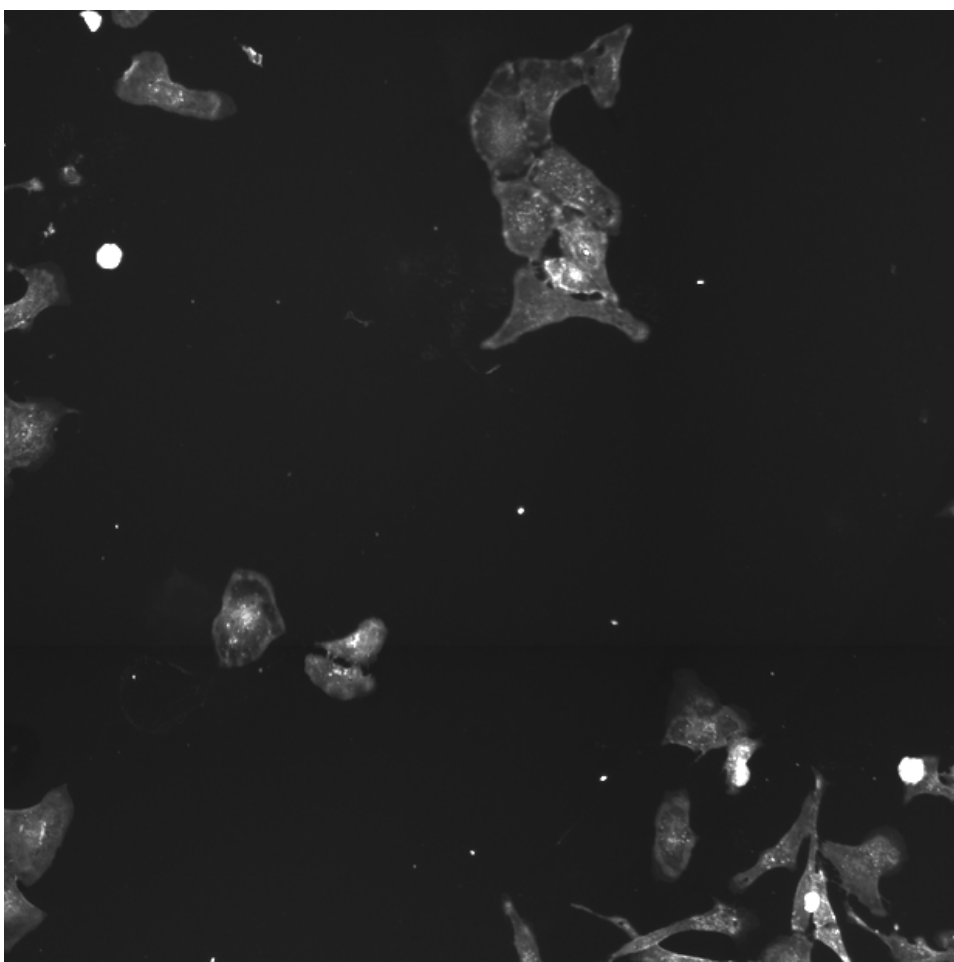
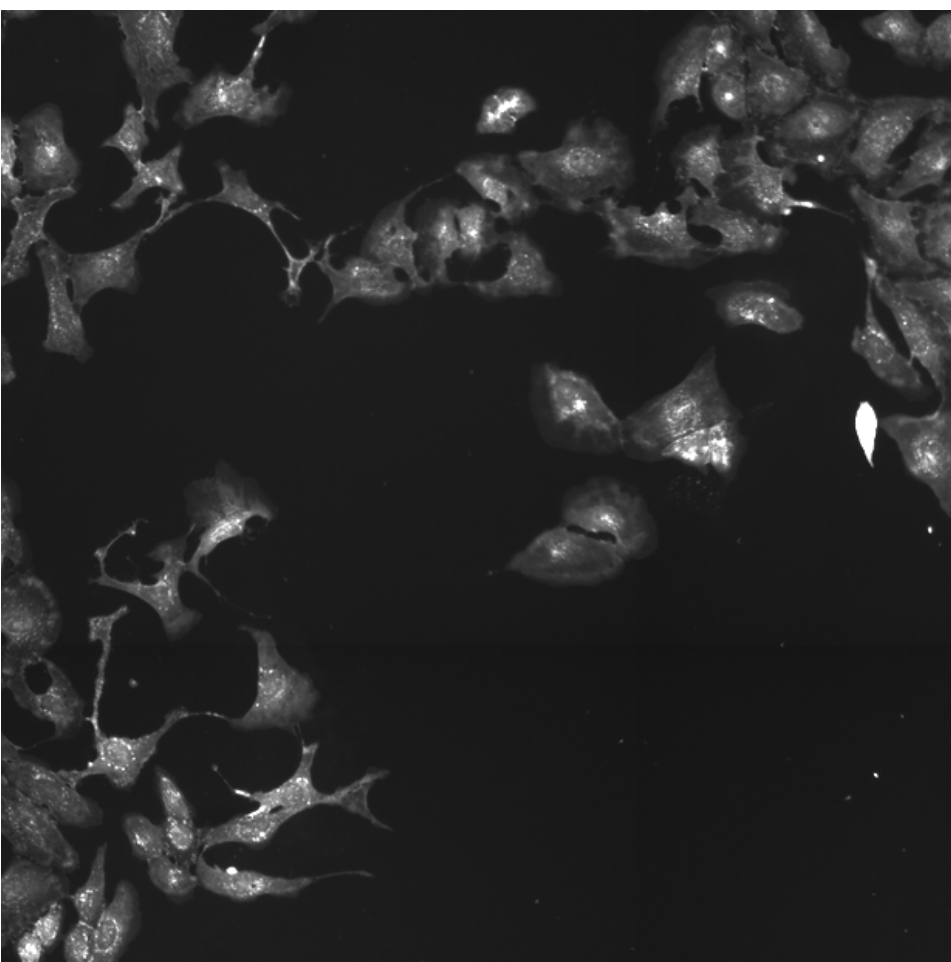
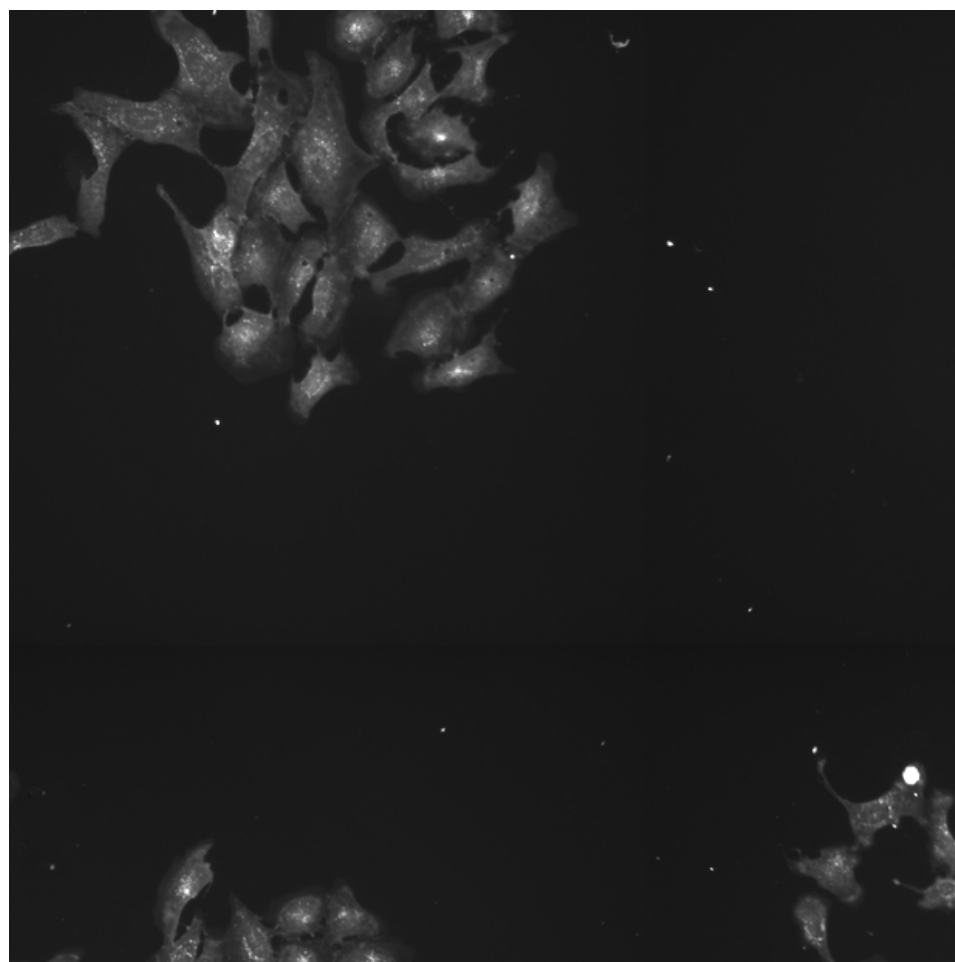
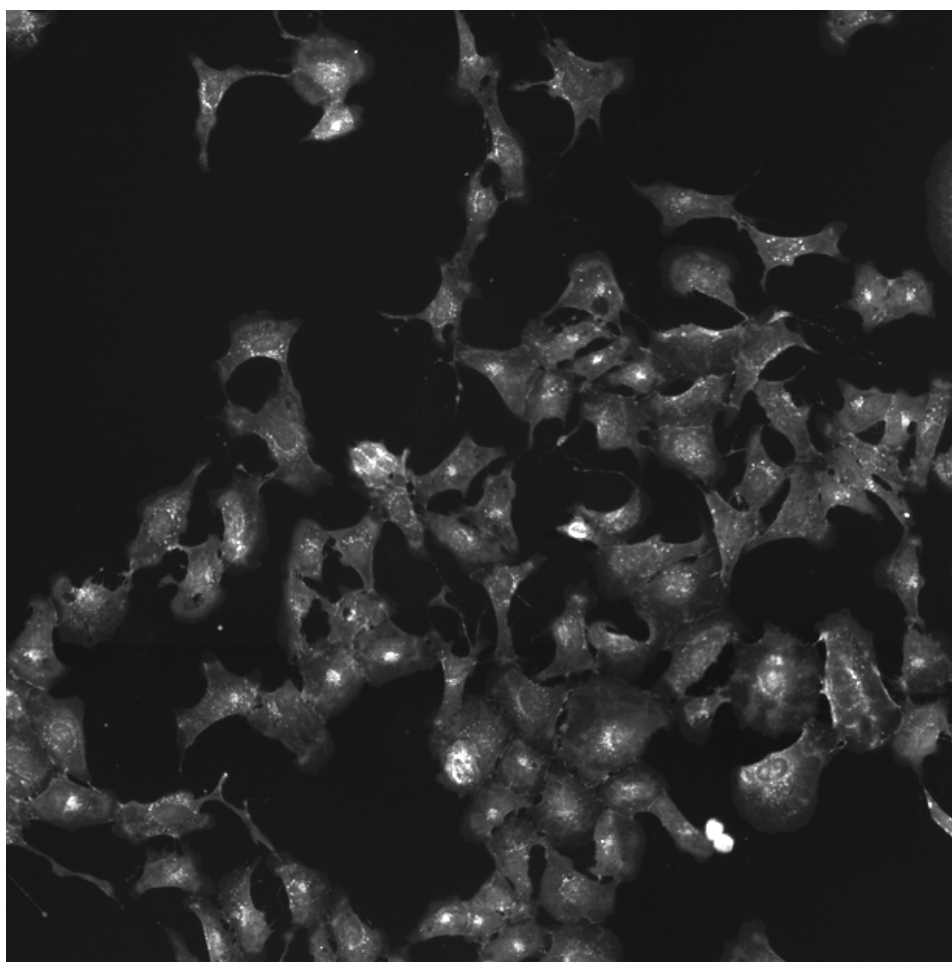
YAP1.WT.2 (41755)

YAP1.WT.2 (41756)

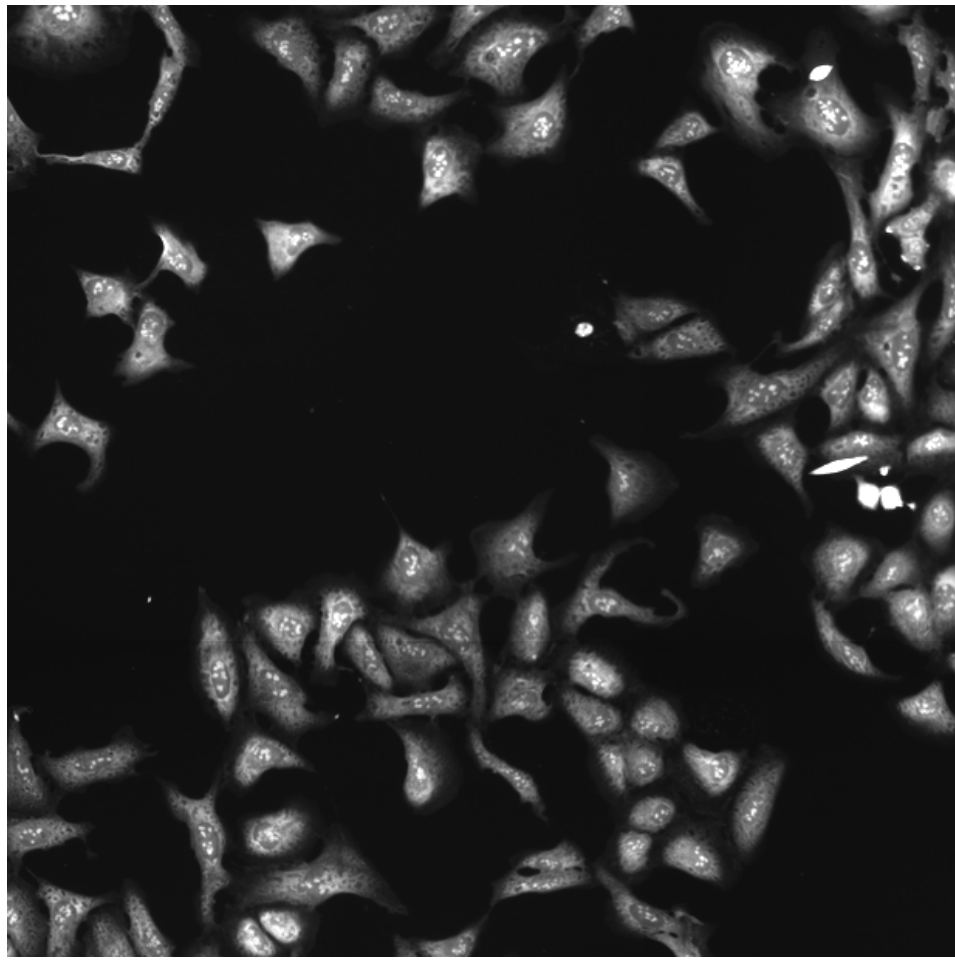
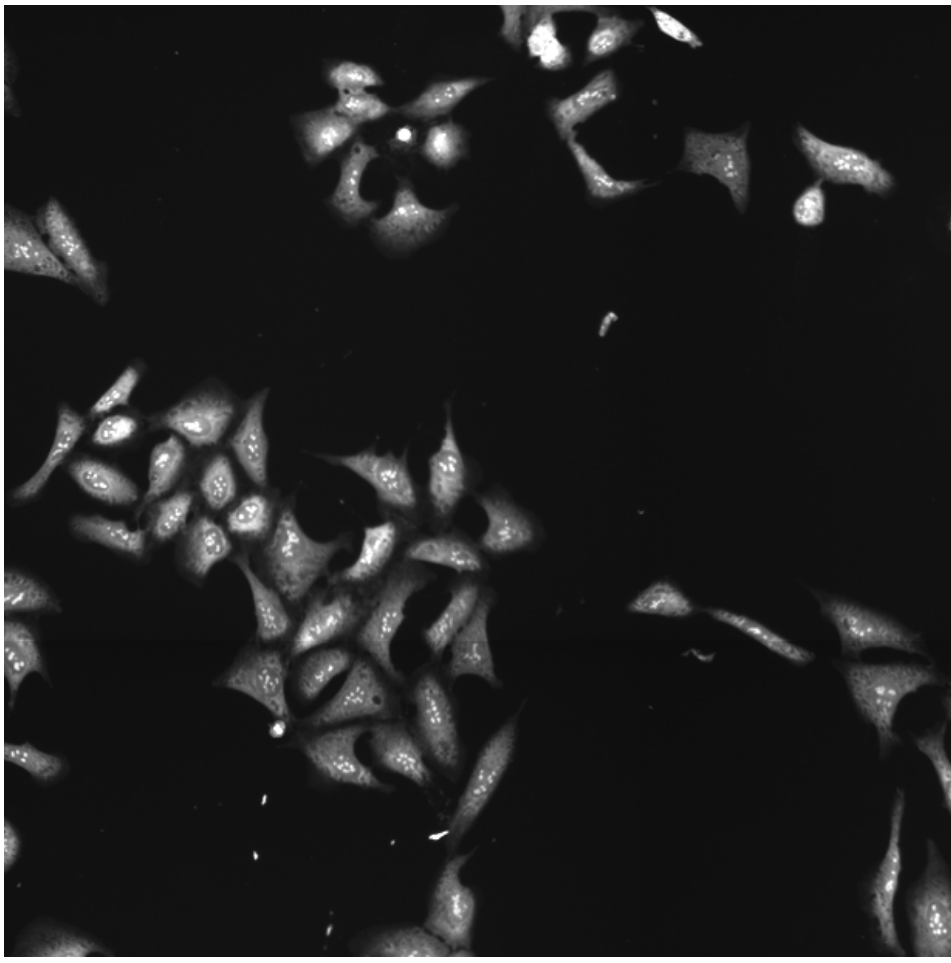
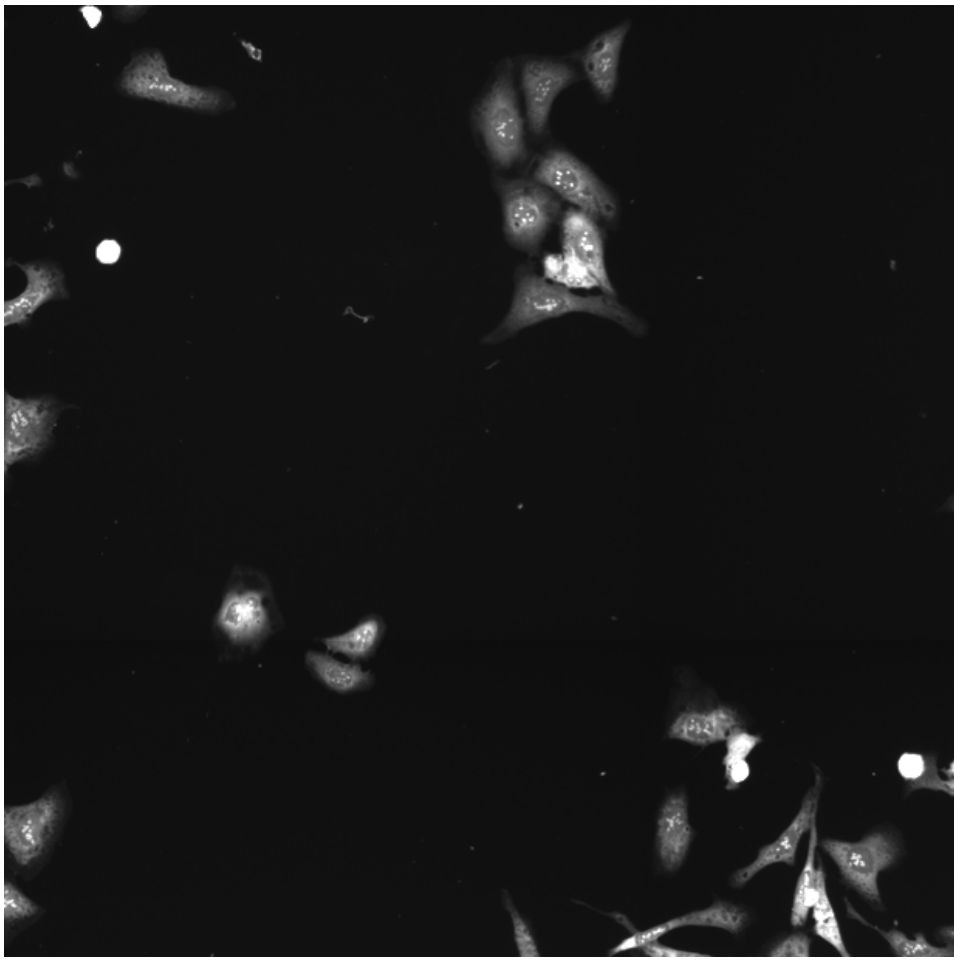
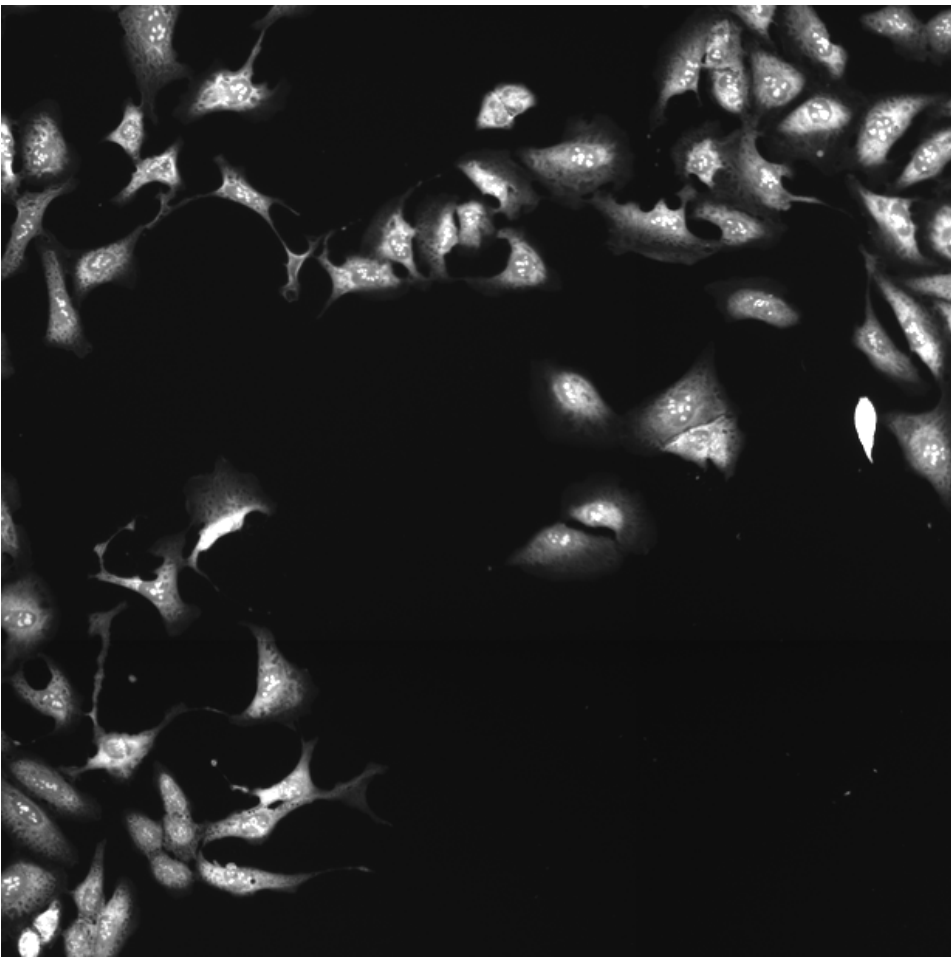
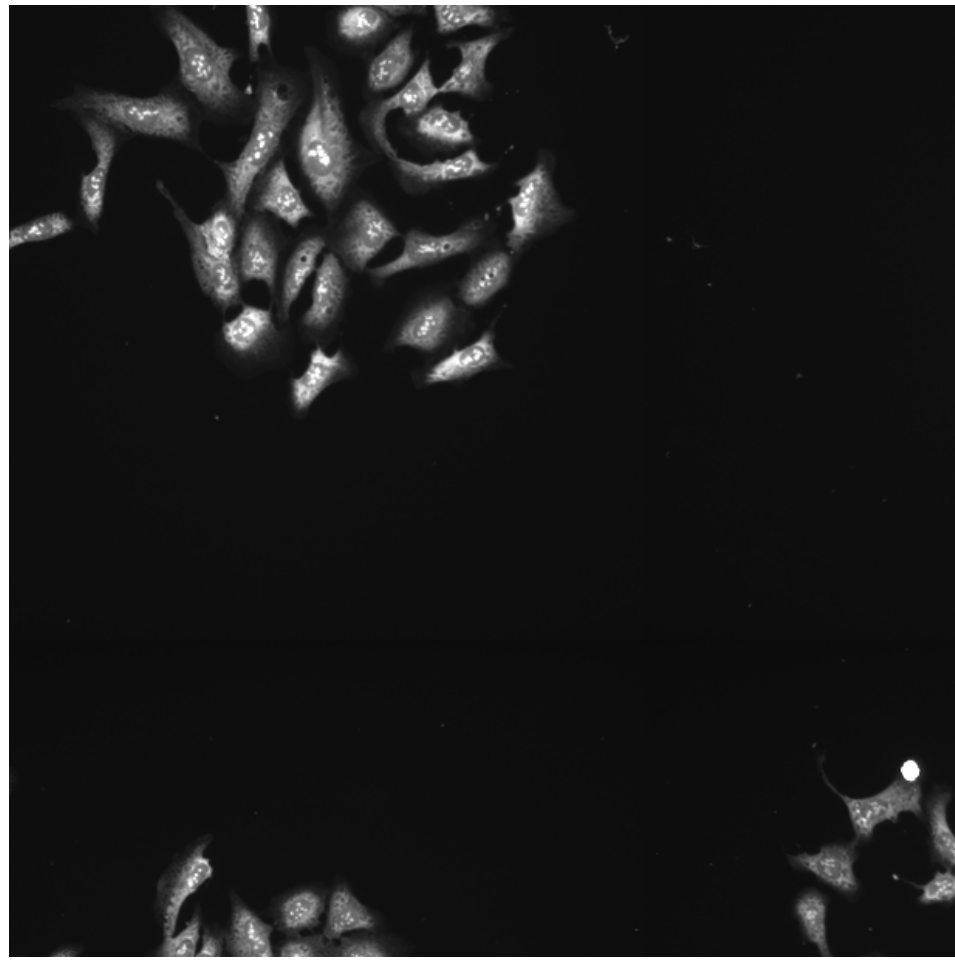
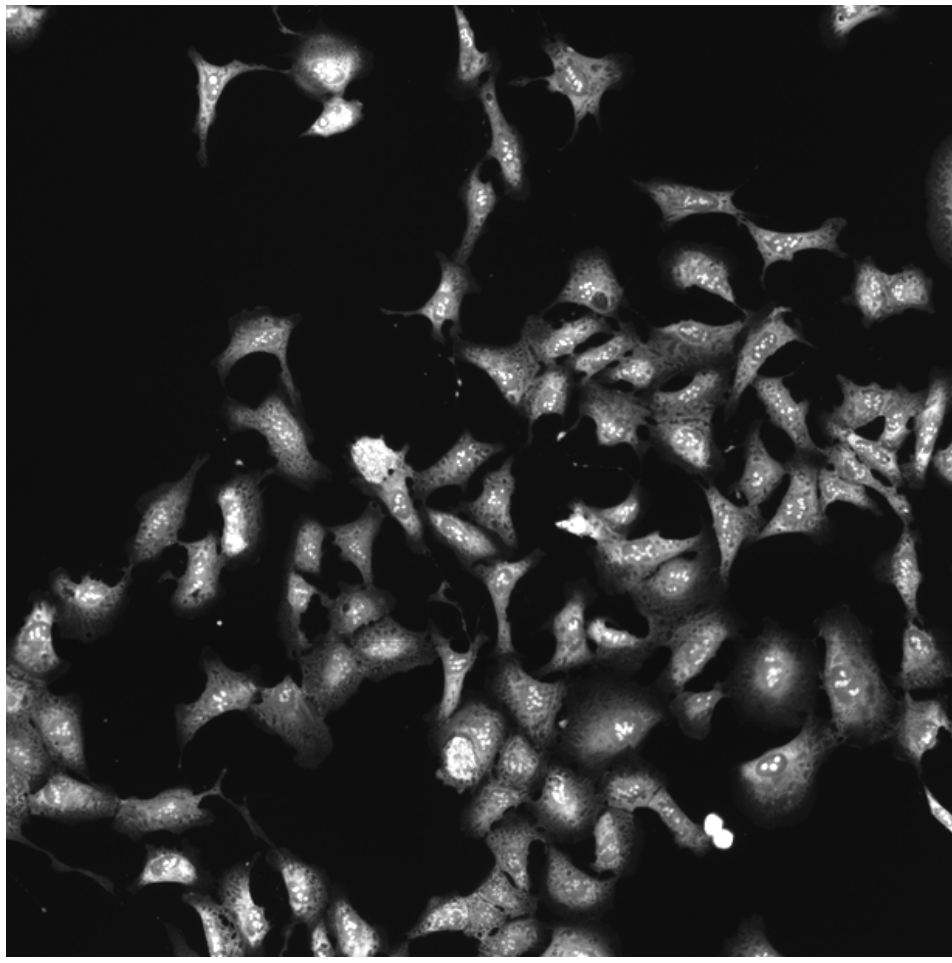
YAP1.WT.2 (41757)

YAP1.WT.2 (41754)

AGP

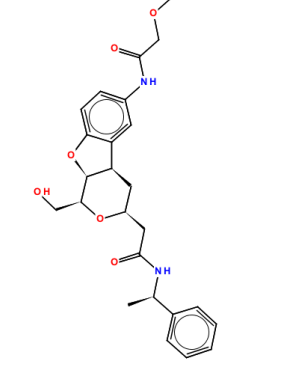
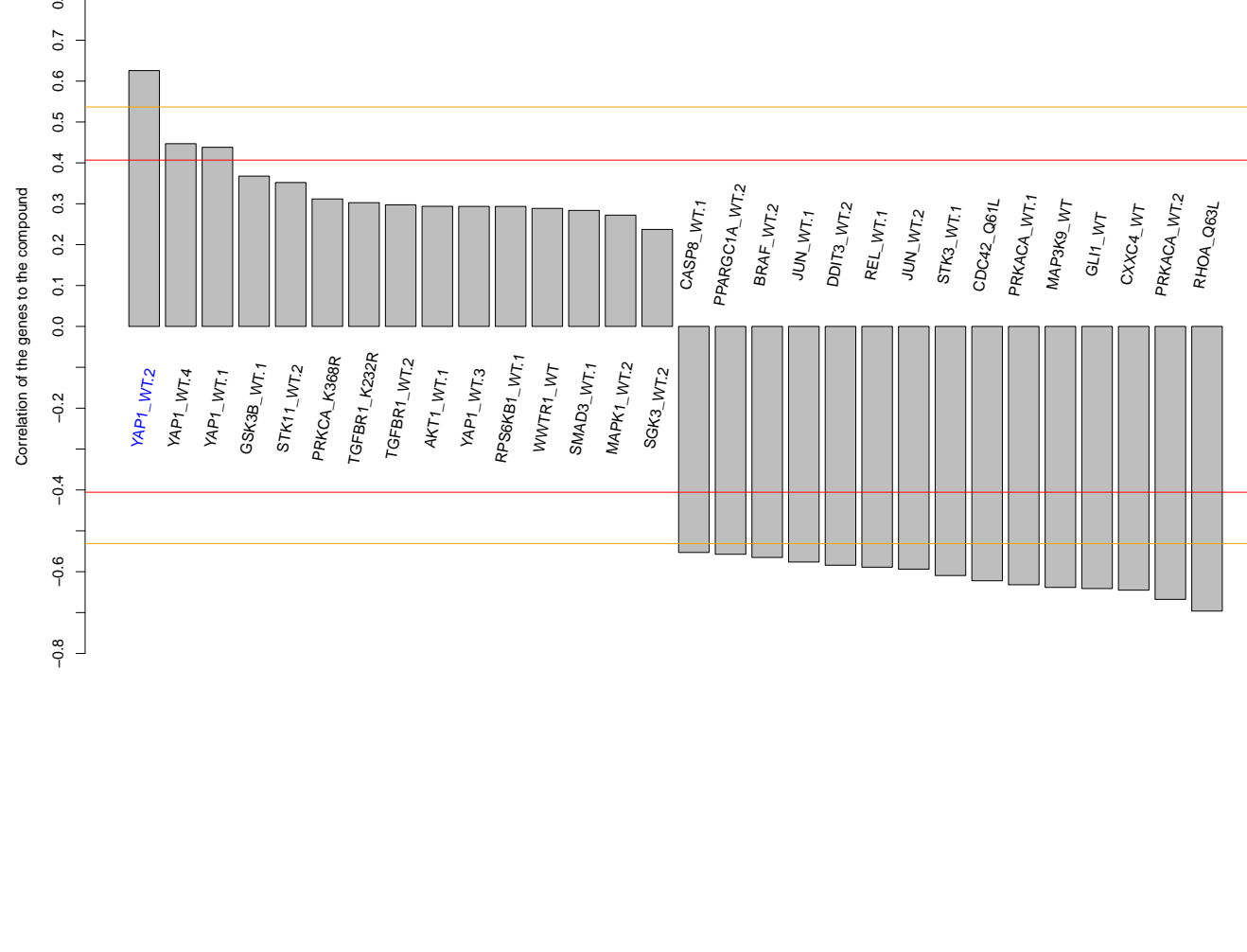
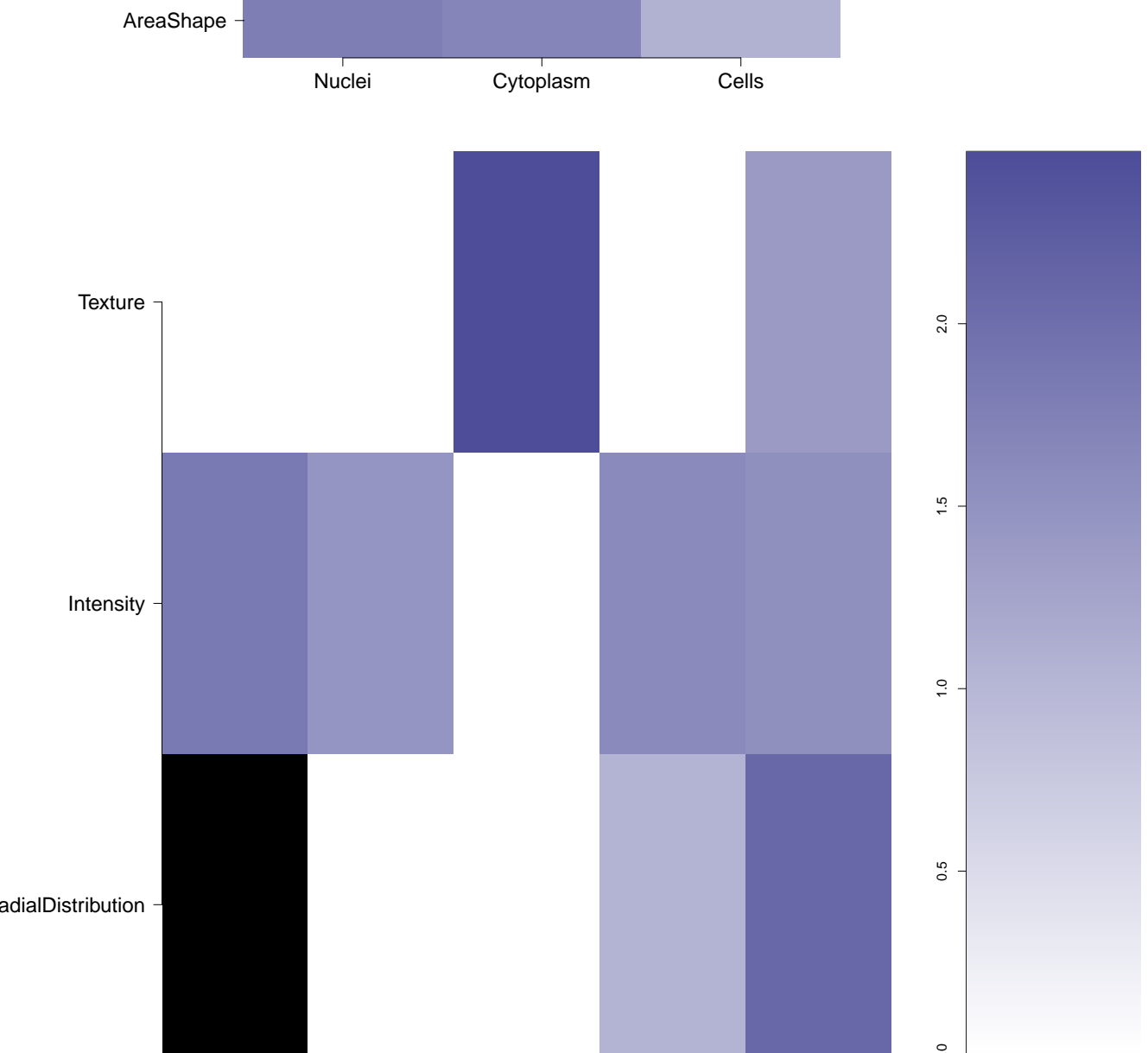

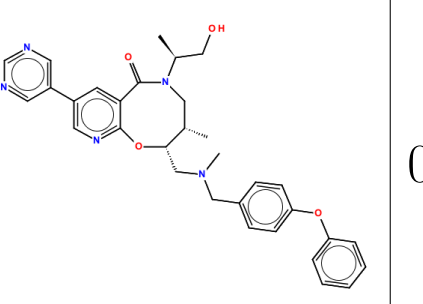
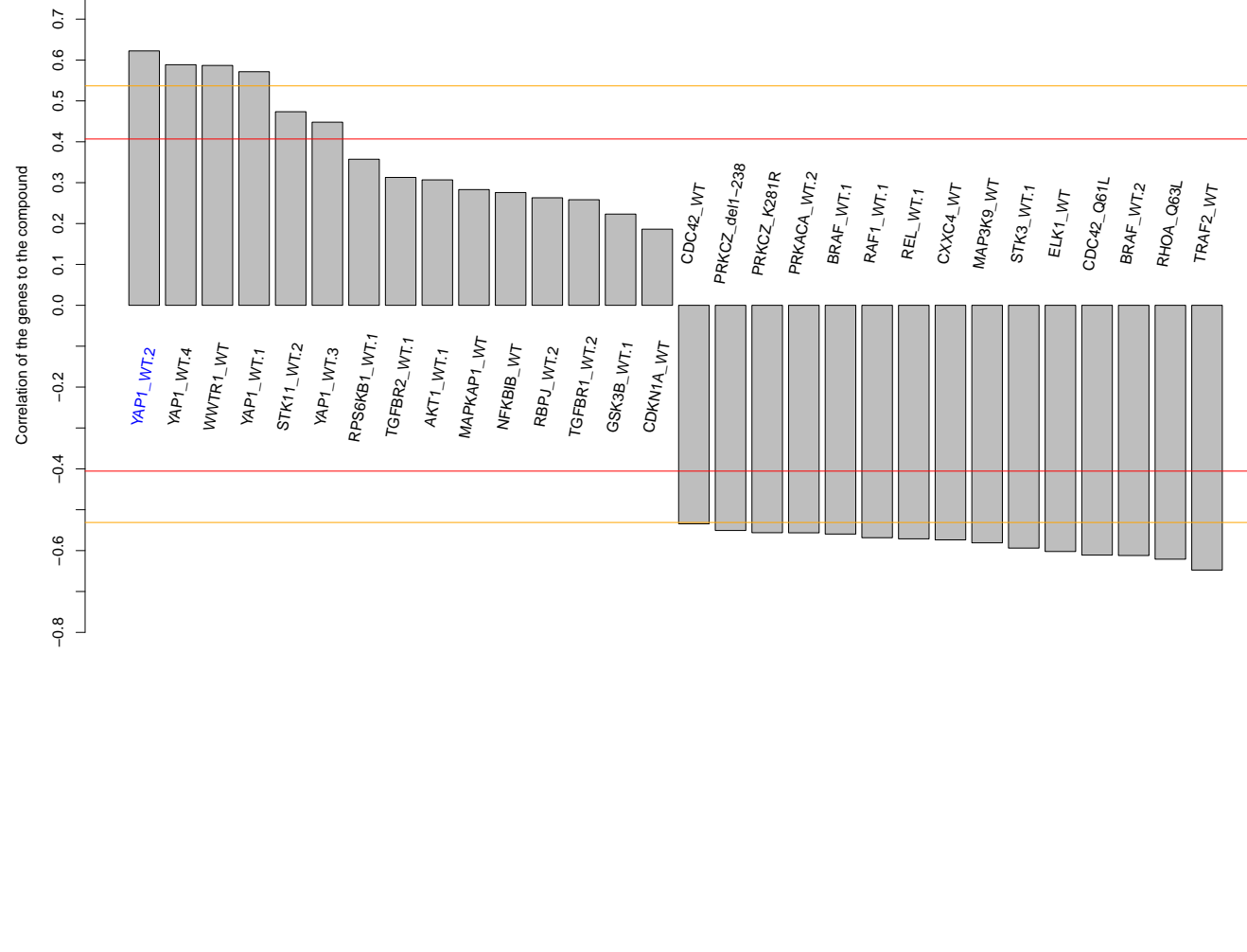
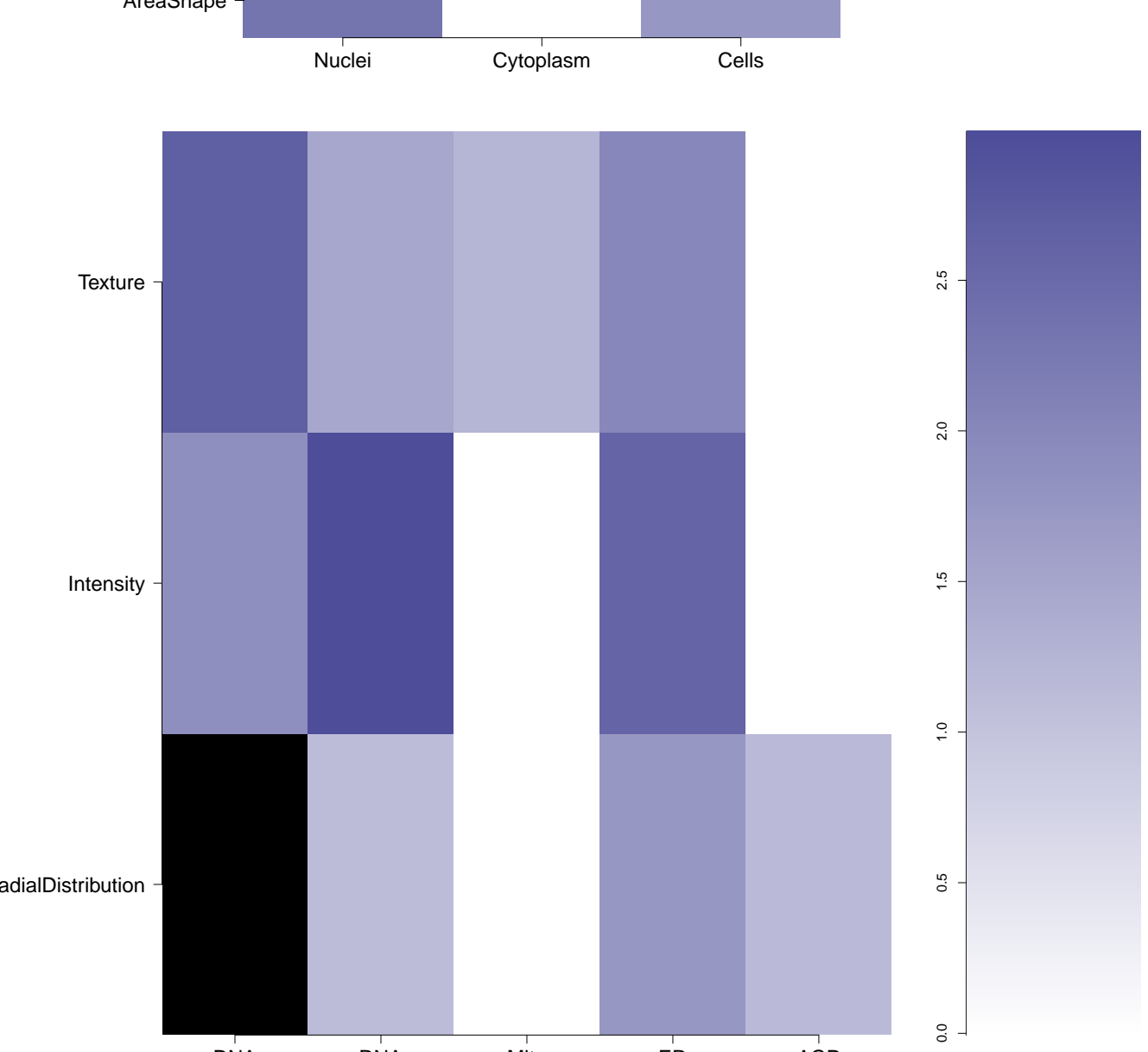

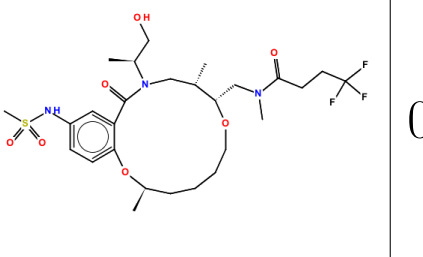
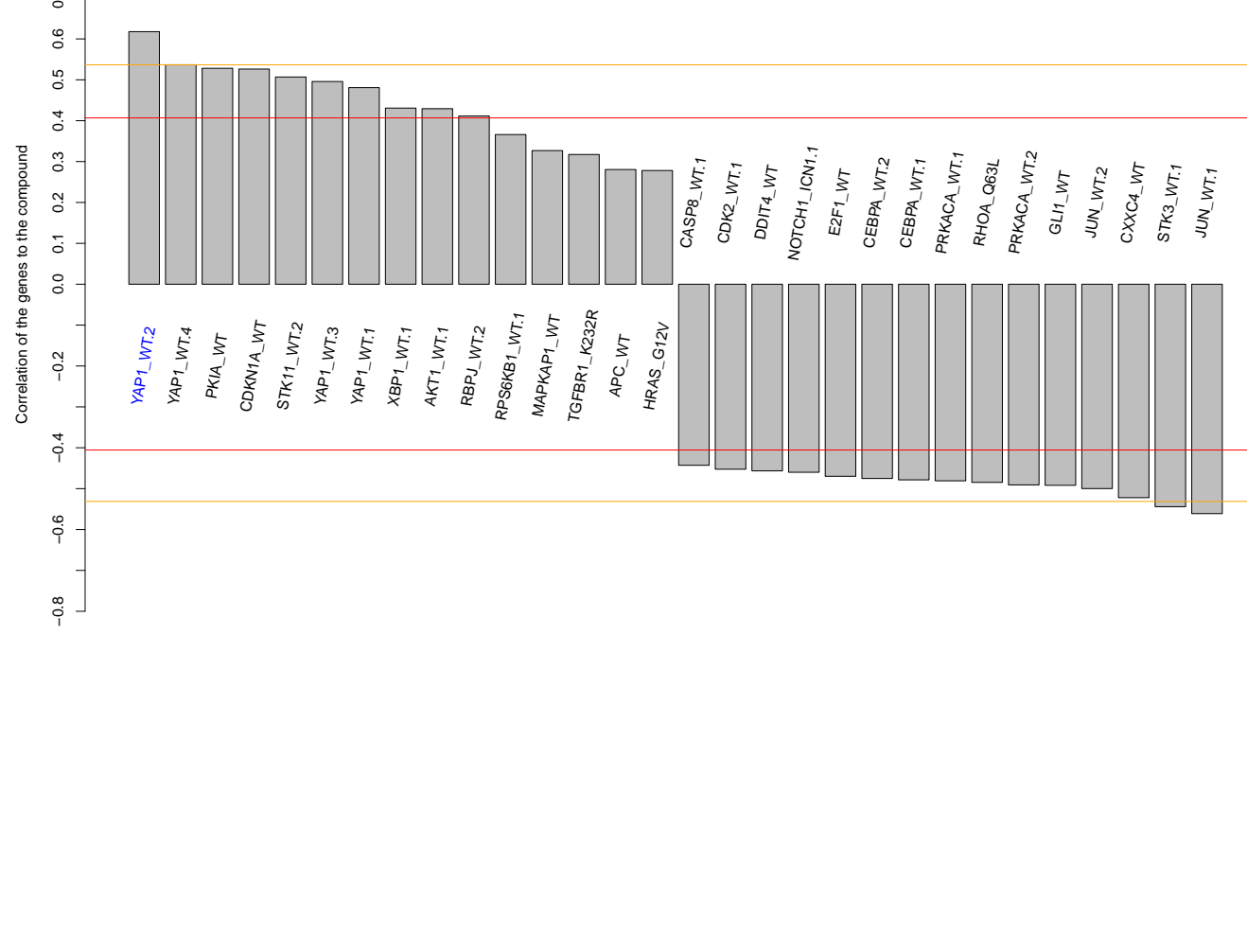
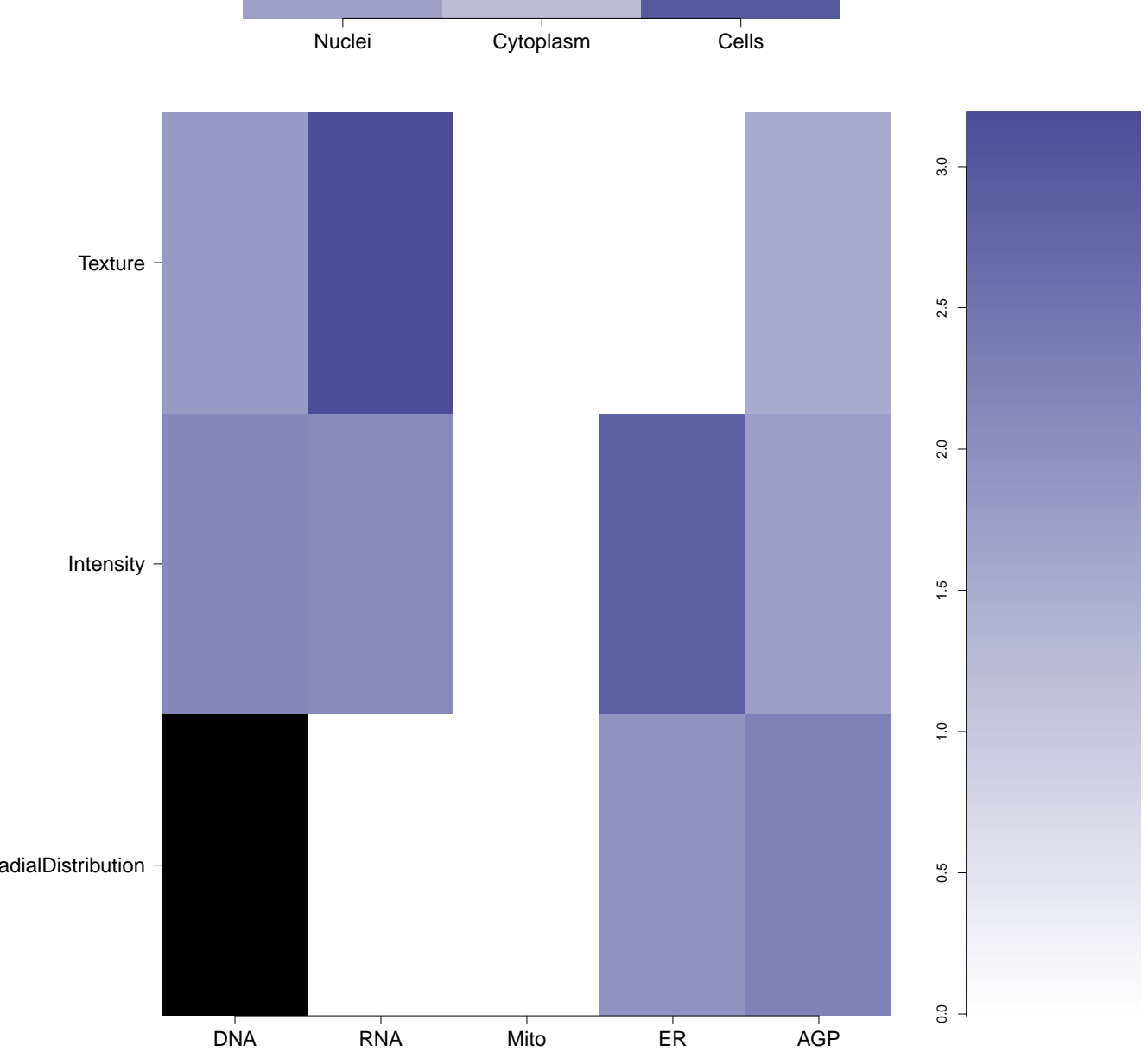

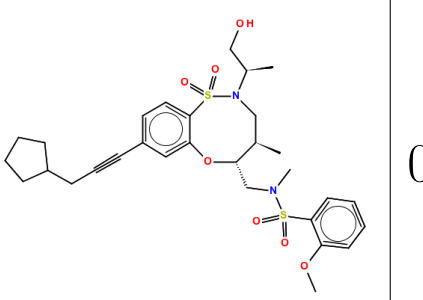
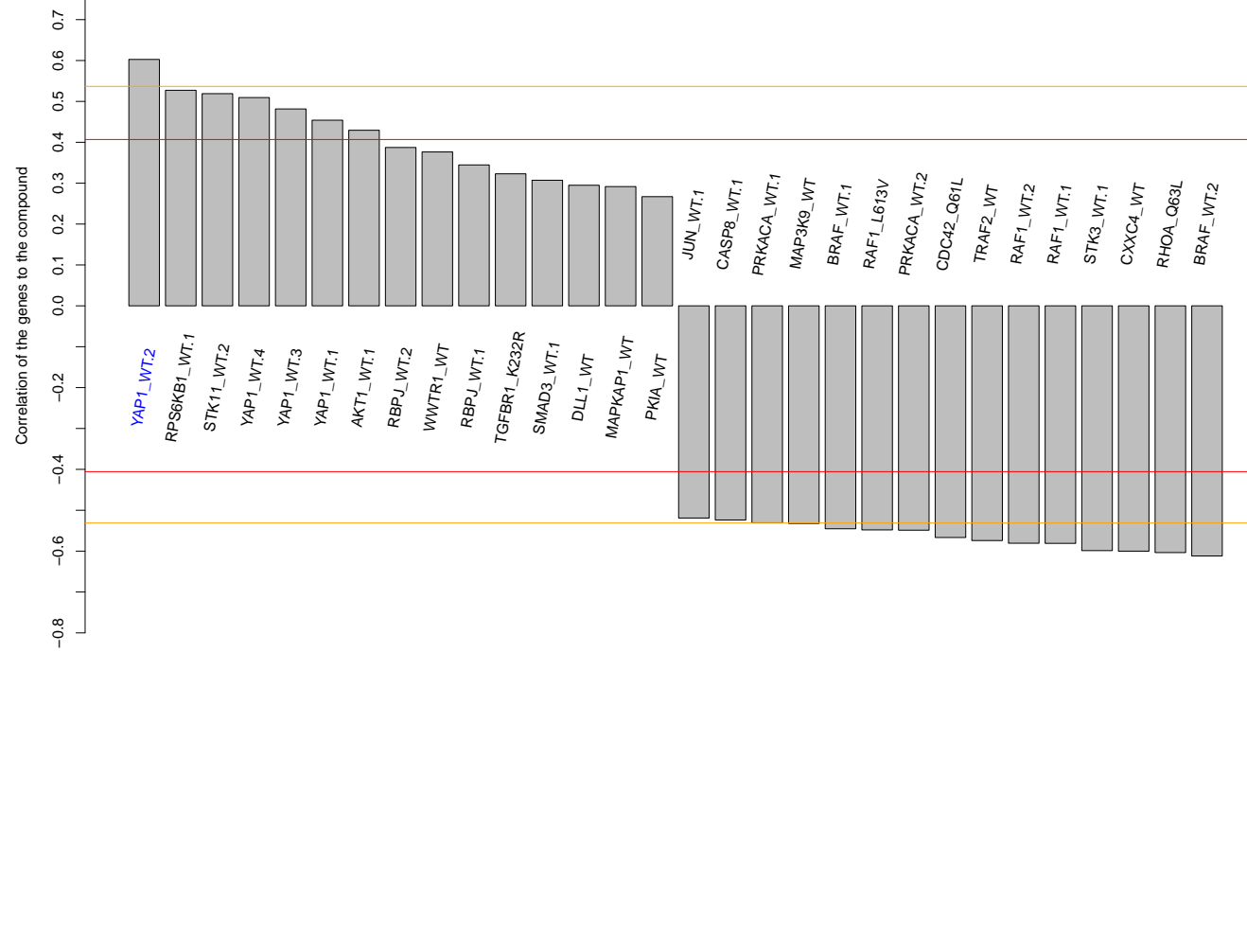
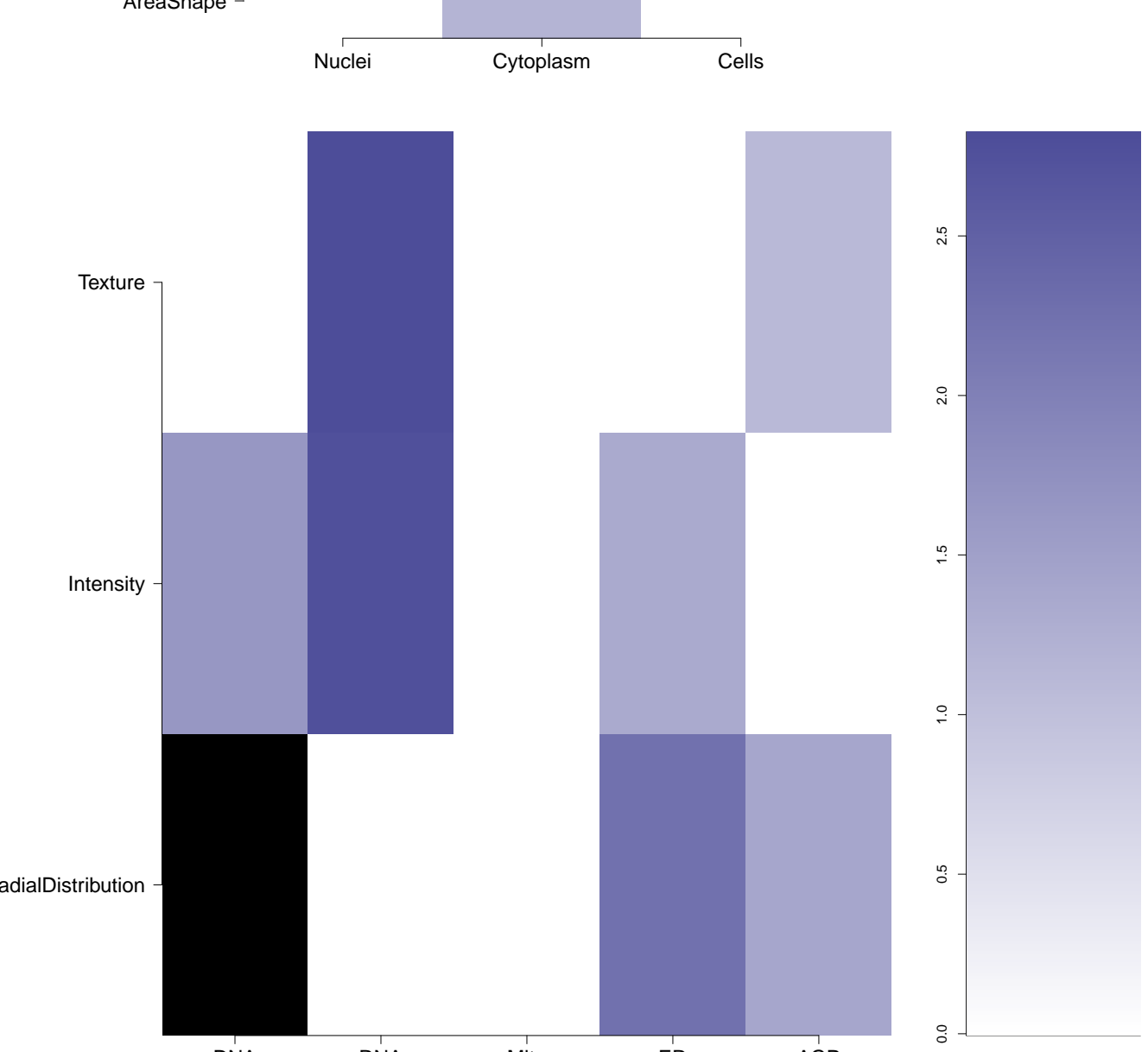

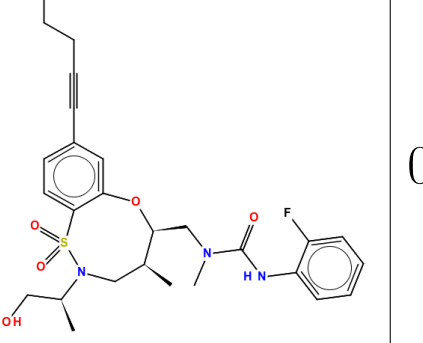
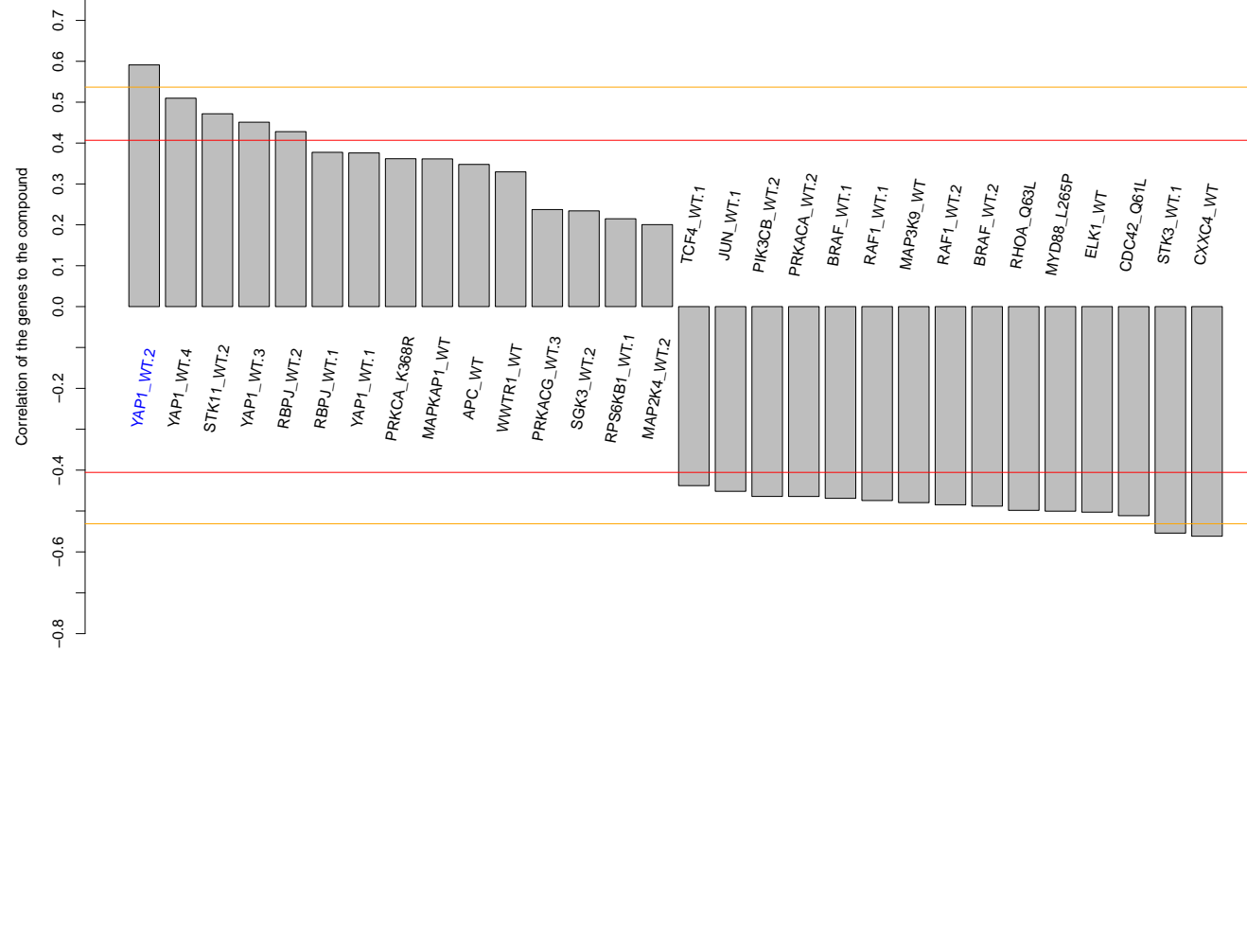
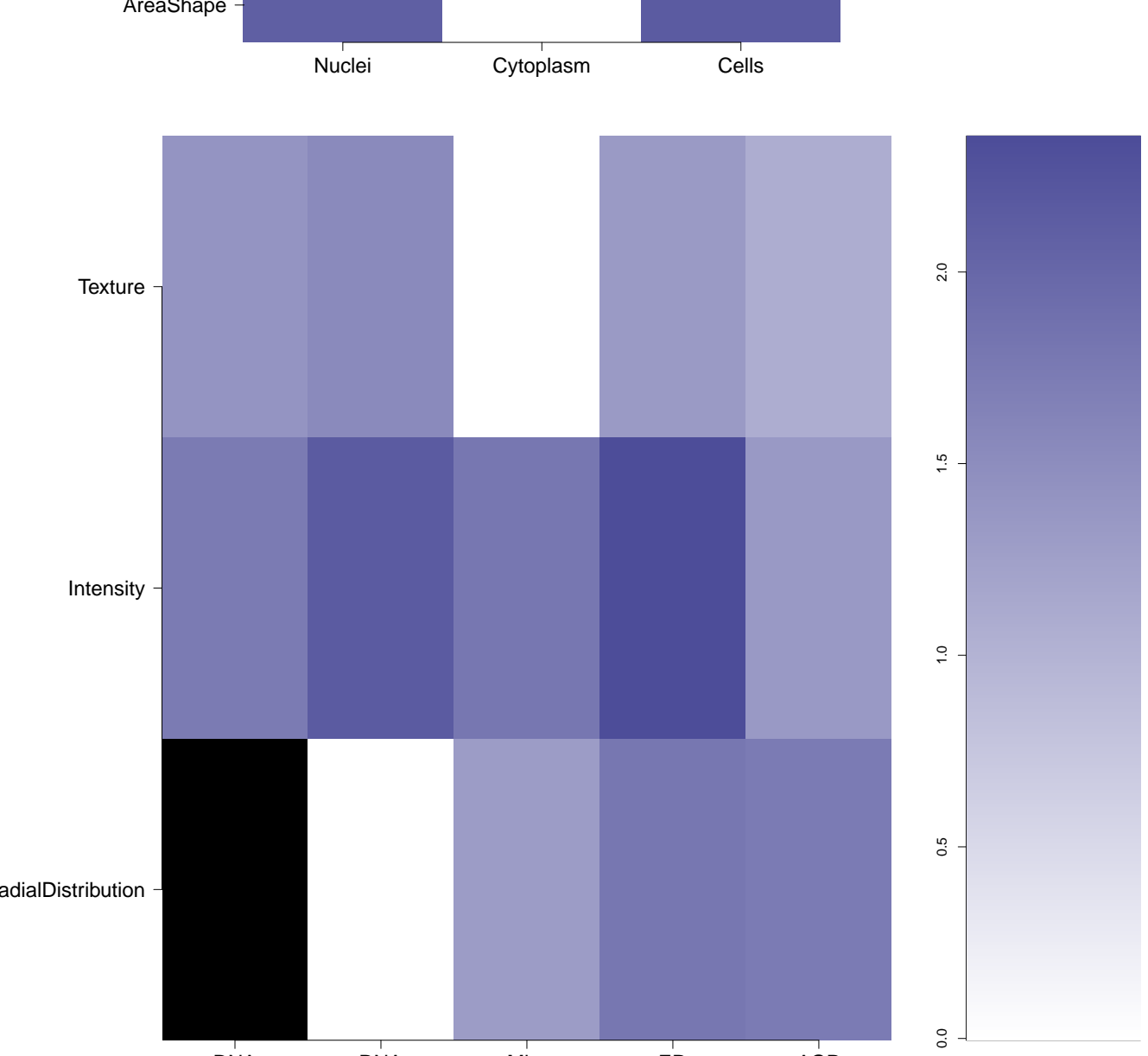
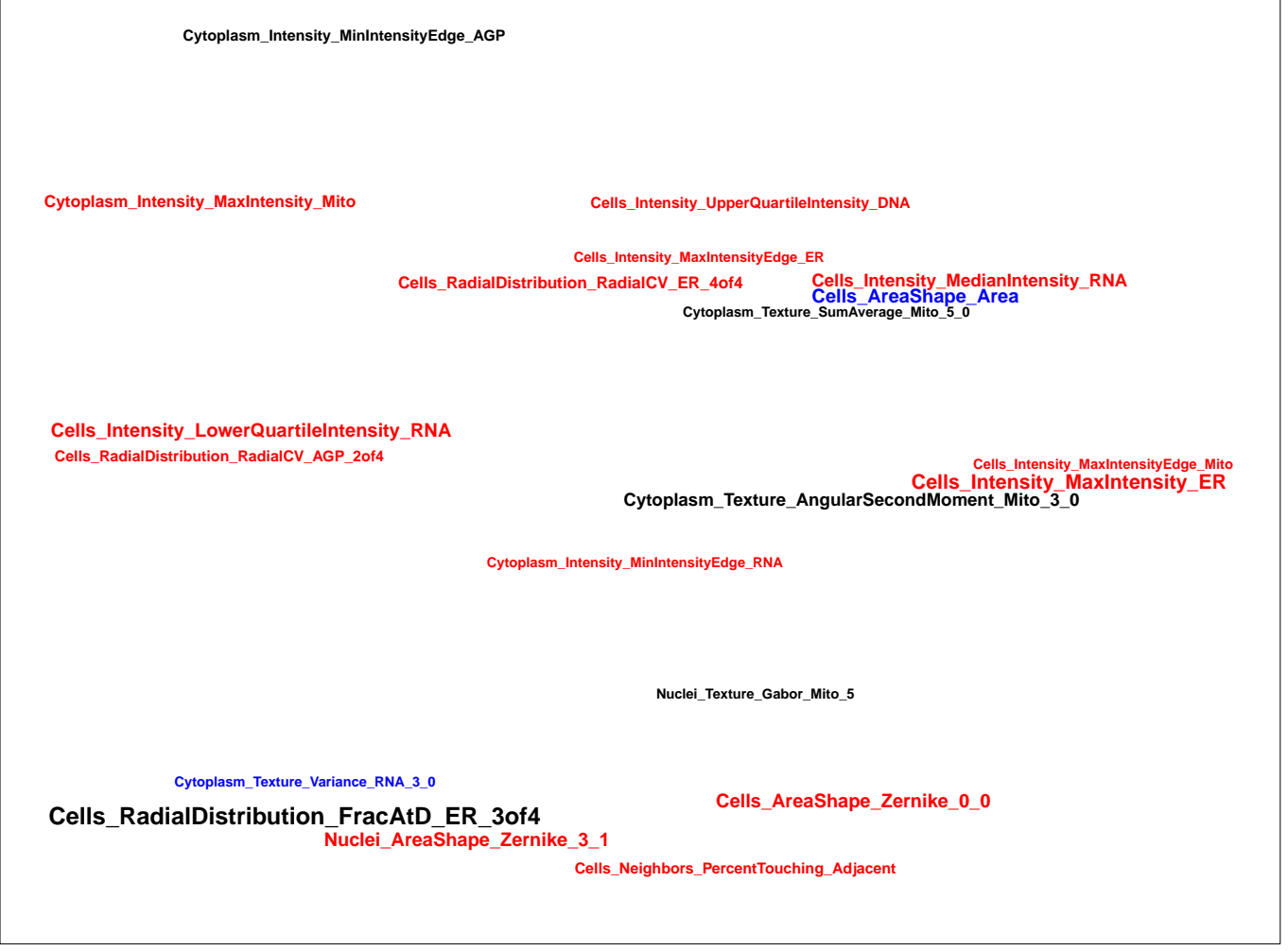
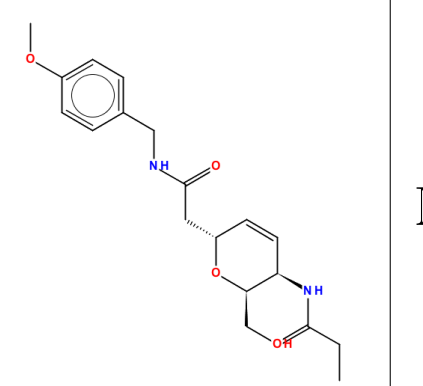
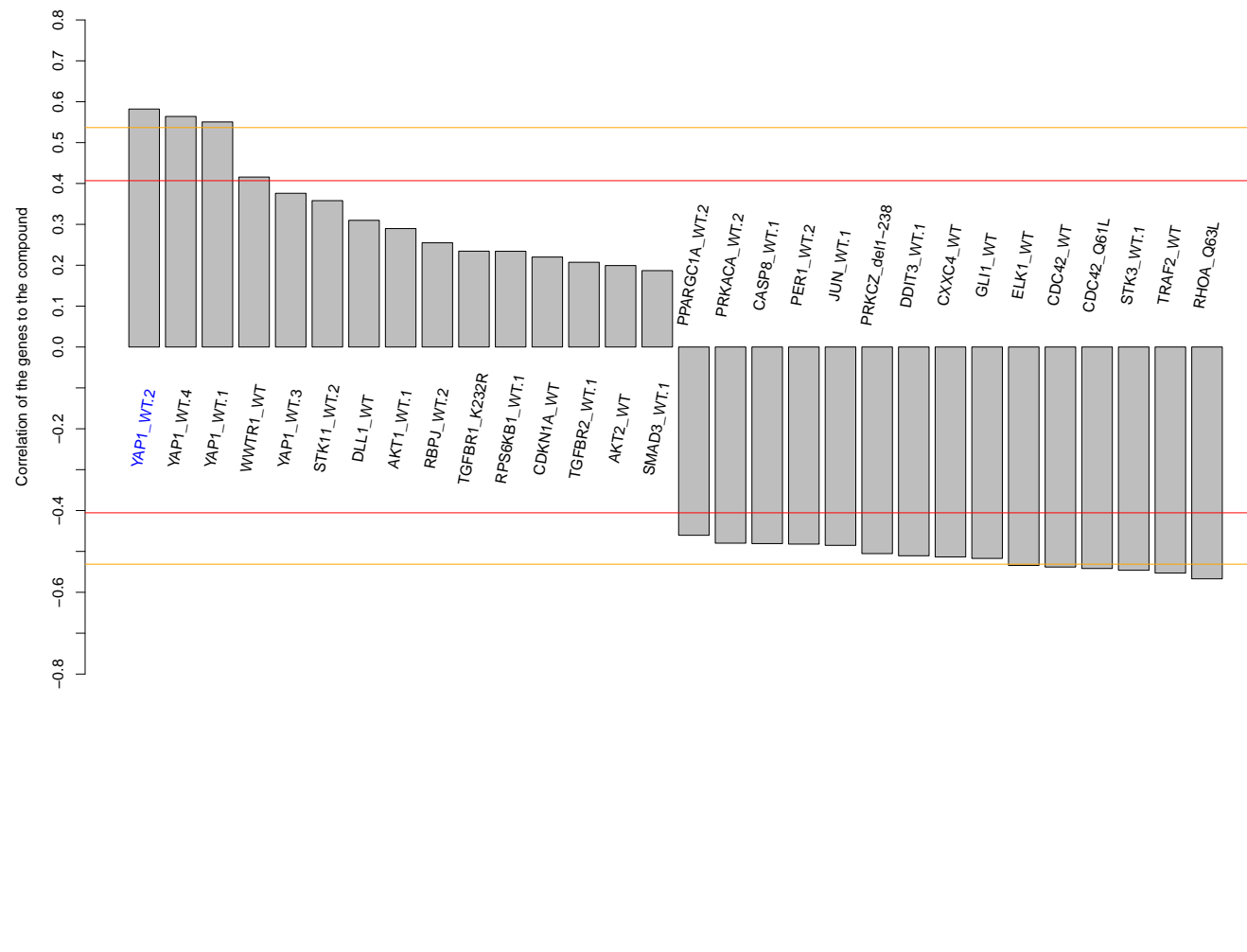
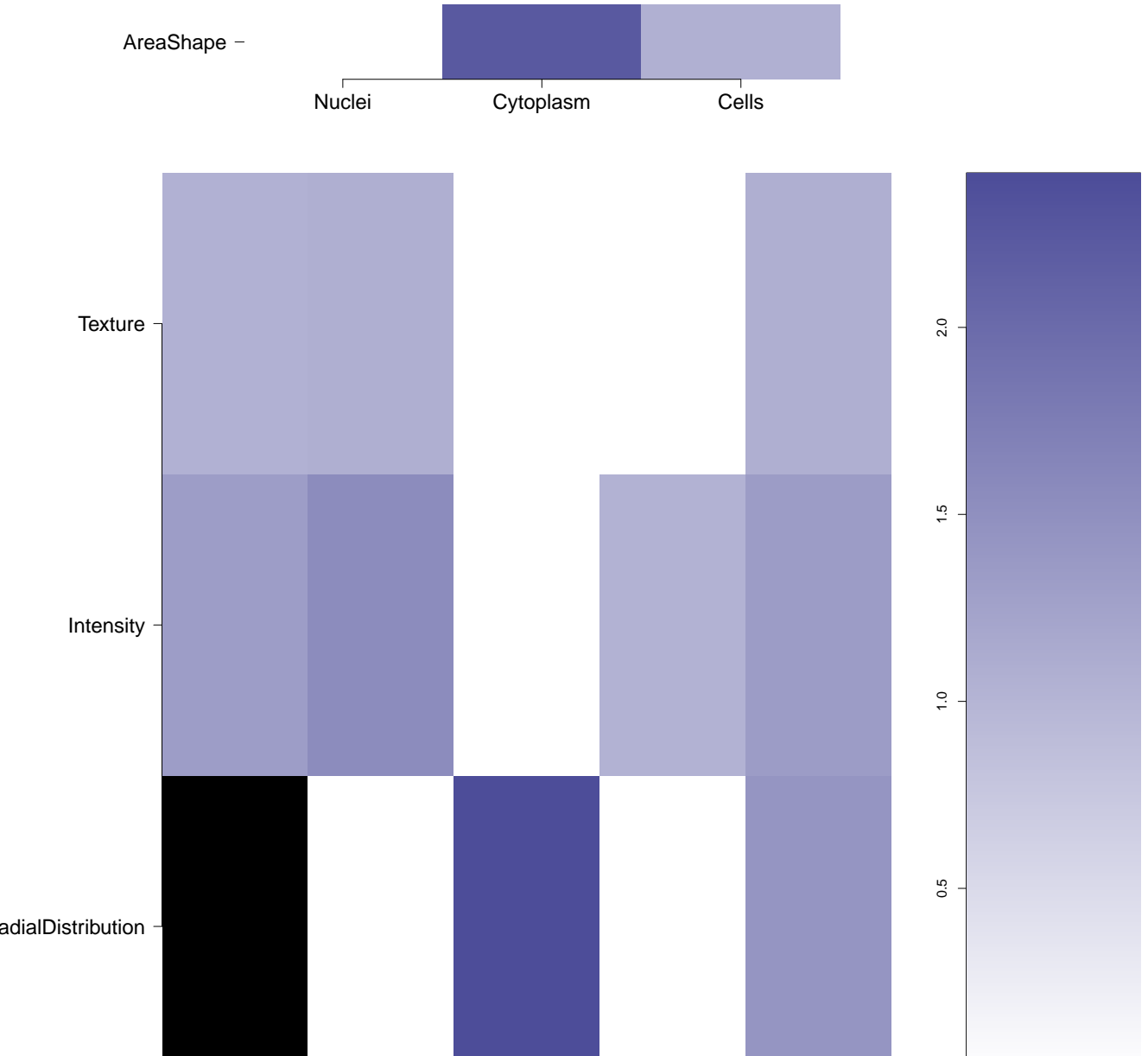
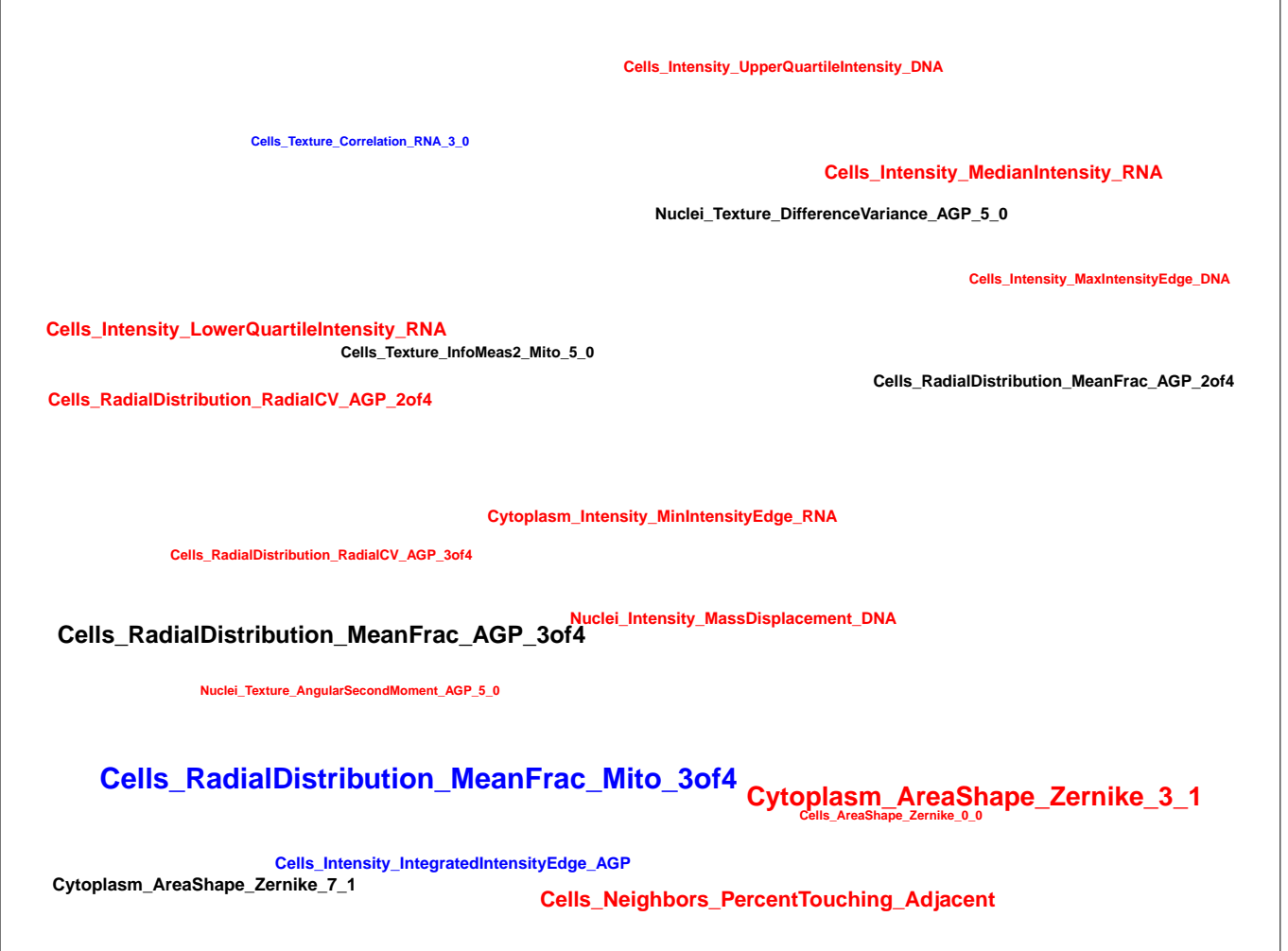
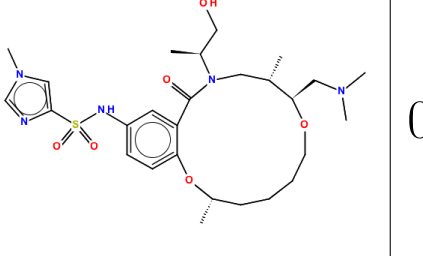
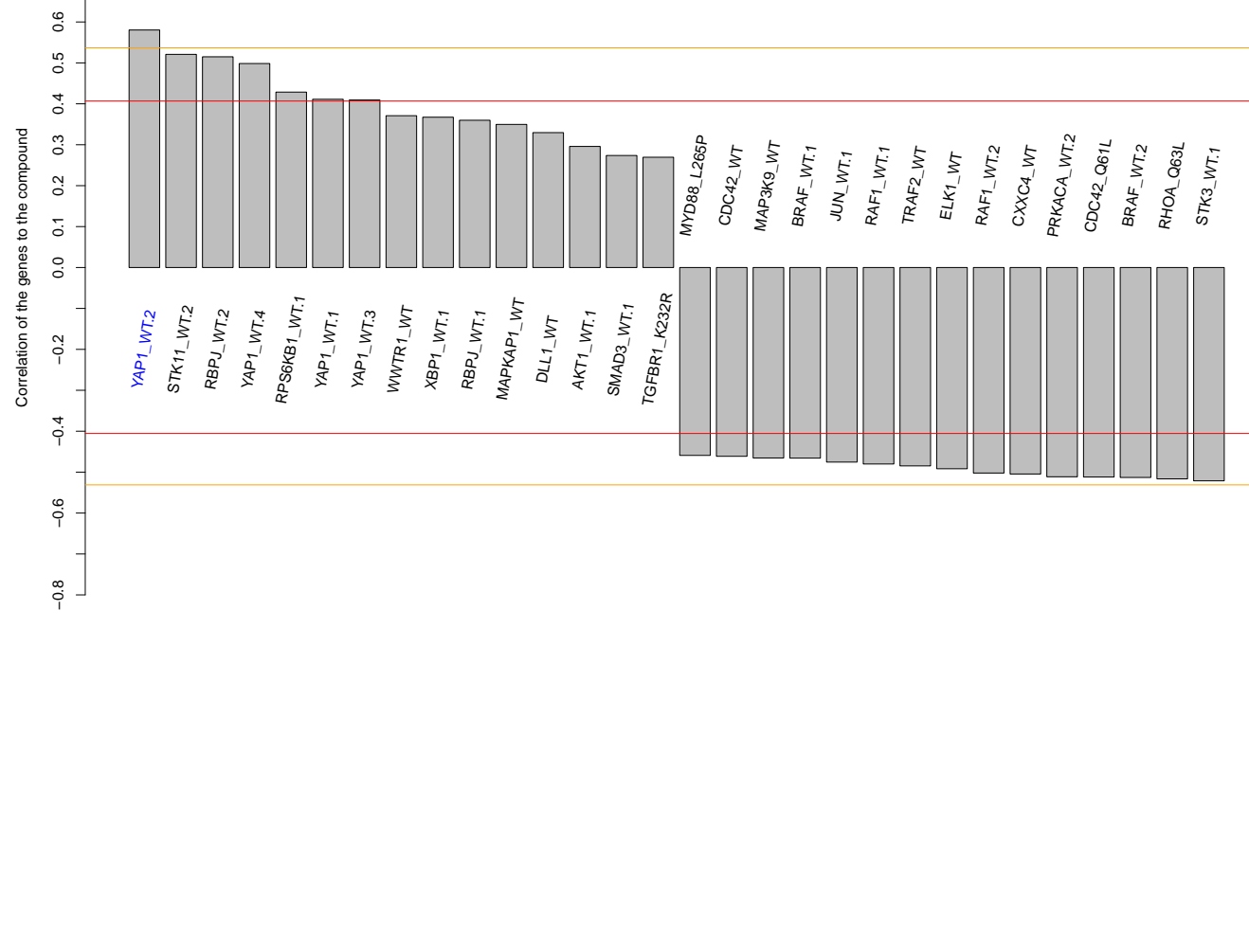
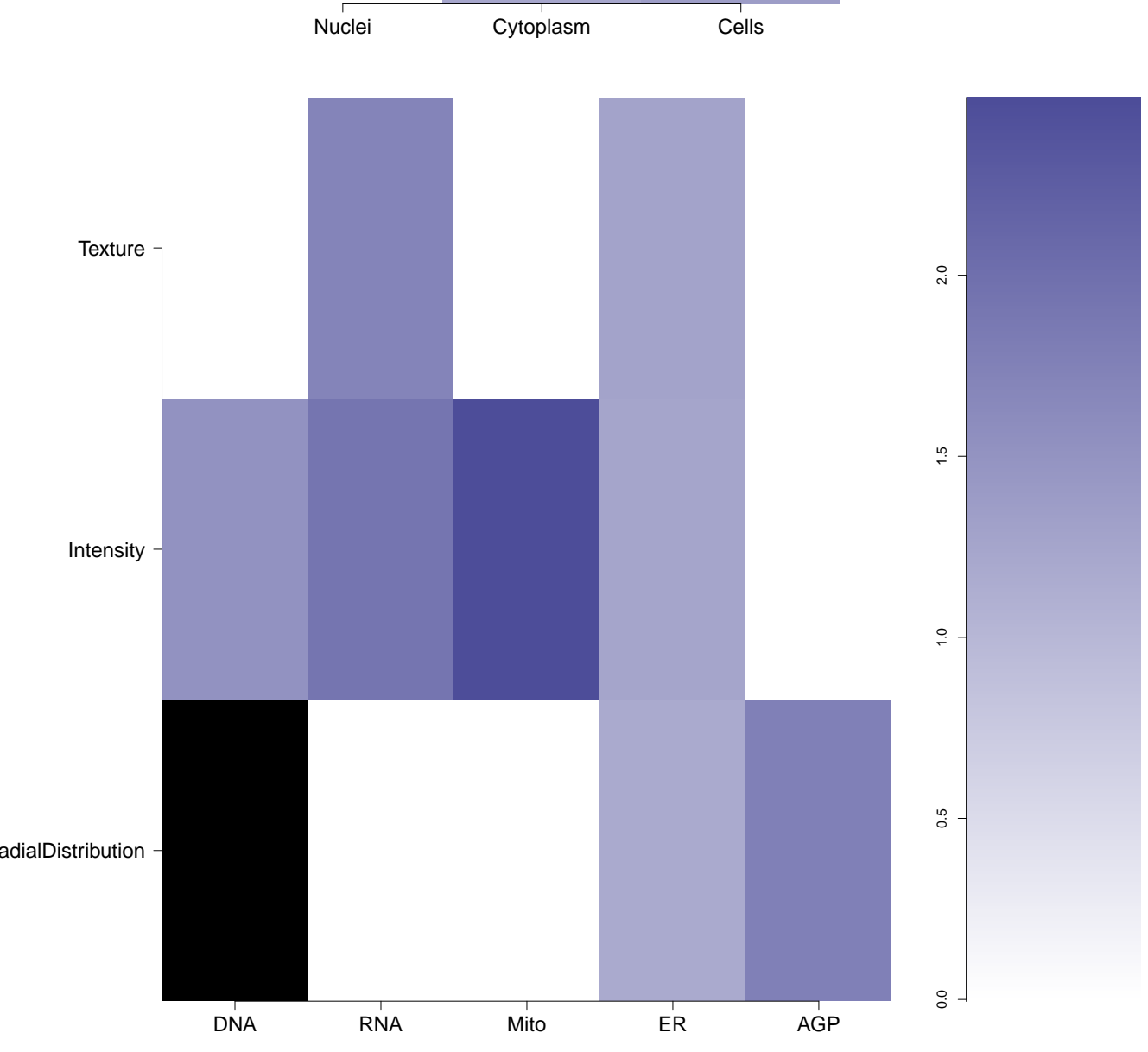



RNA



|  |                    |  |                                       |  |   |   |   |   |
|--|--------------------|--|---------------------------------------|--|---|---|---|---|
| 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 0.53) | Correlation between compound the gene | Compound rank when scored against the gene using L1000 profiling | How similar is the compound signature to the genes 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 the gene 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 | Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized |
|--|--------------------|--|---------------------------------------|--|---|---|---|---|

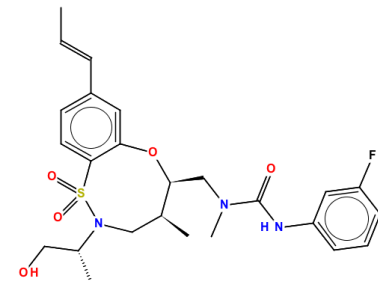
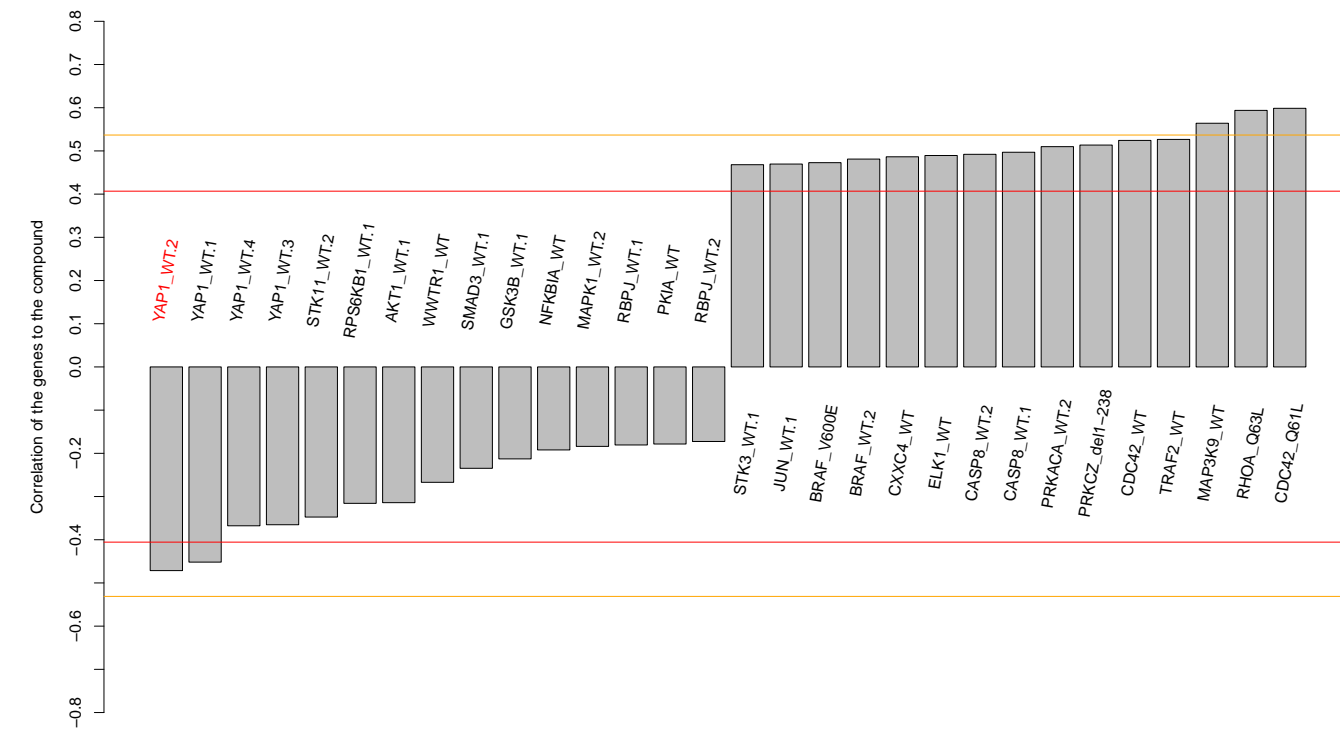
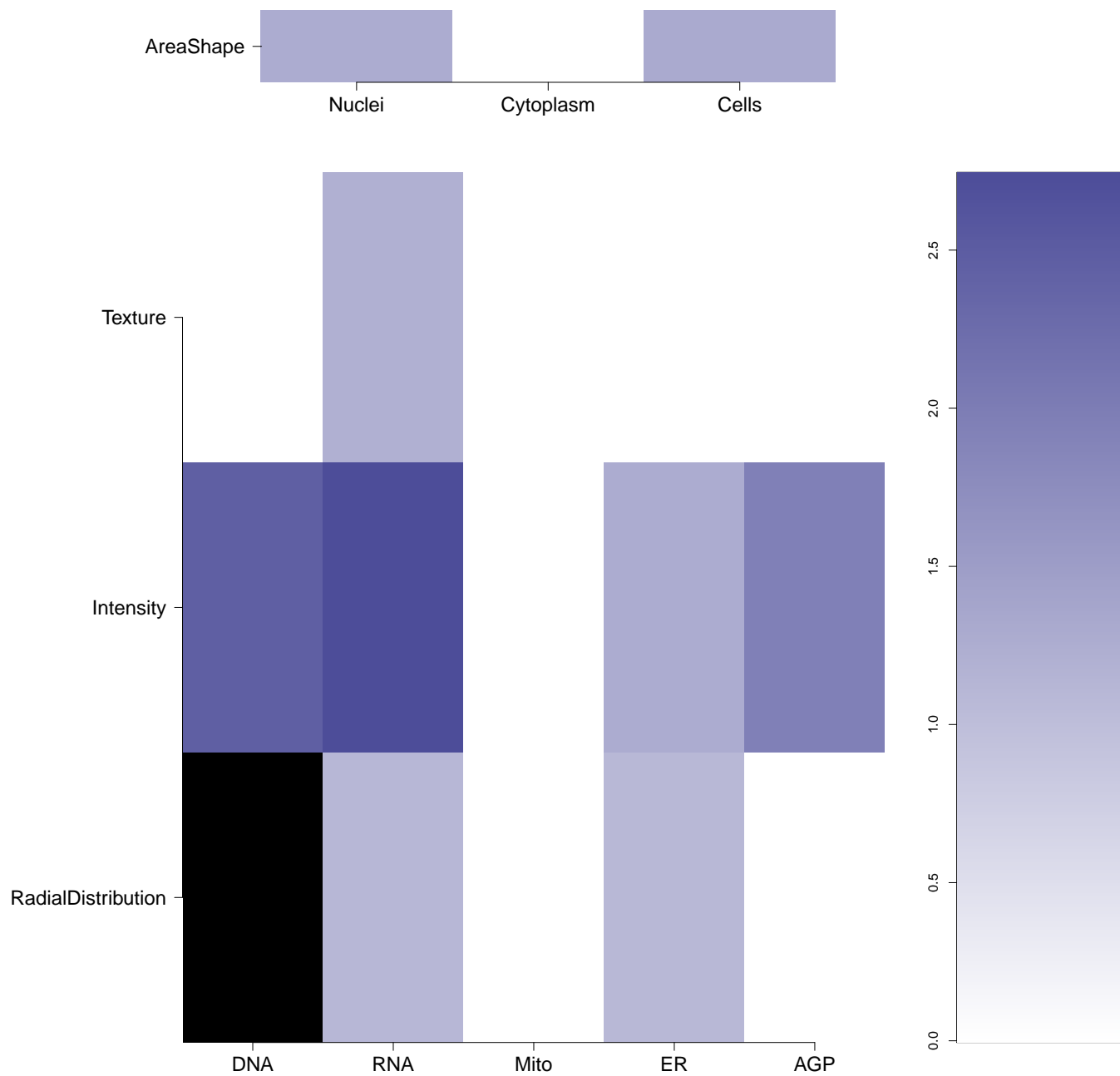
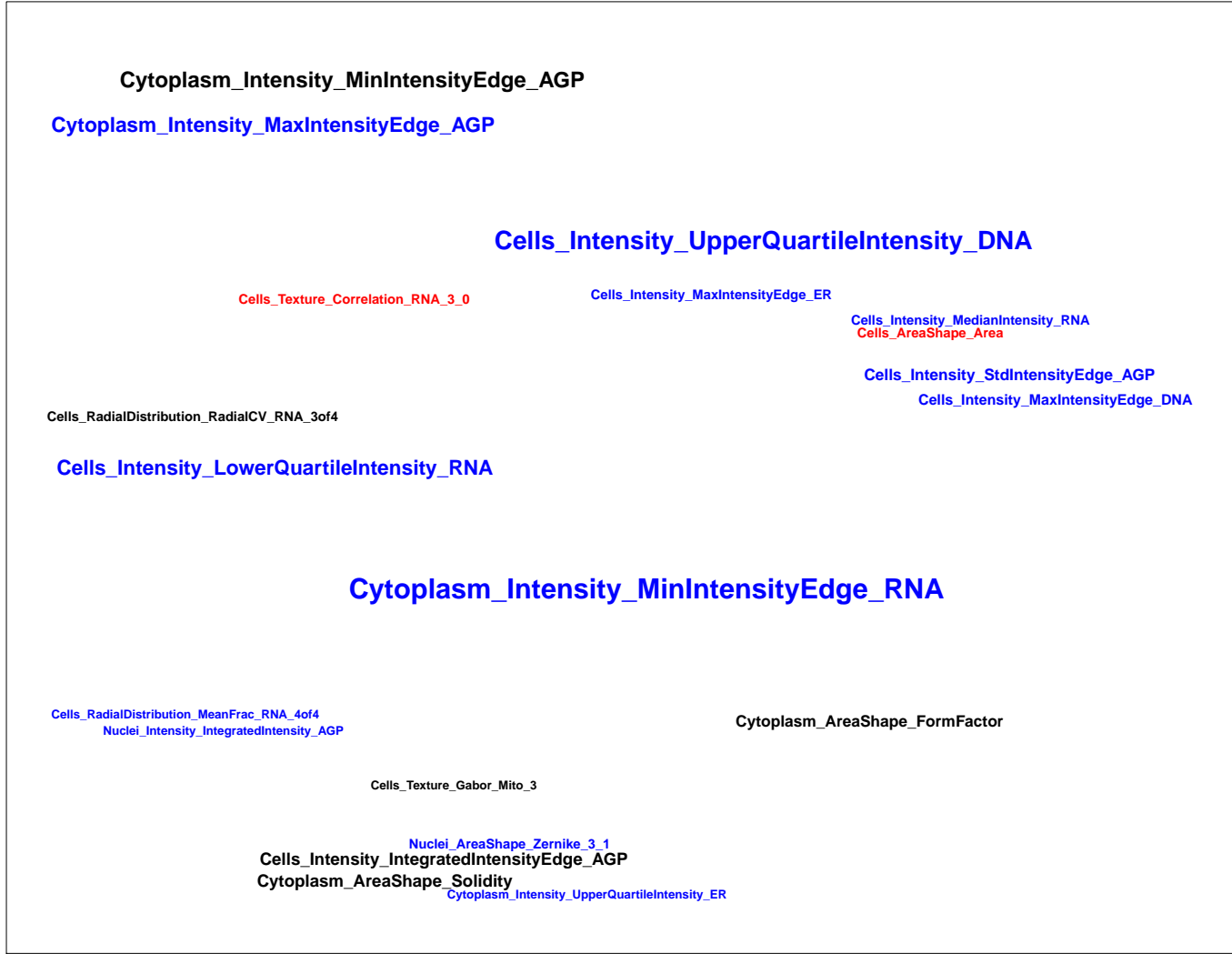
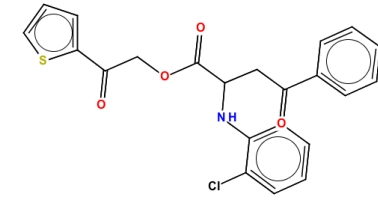
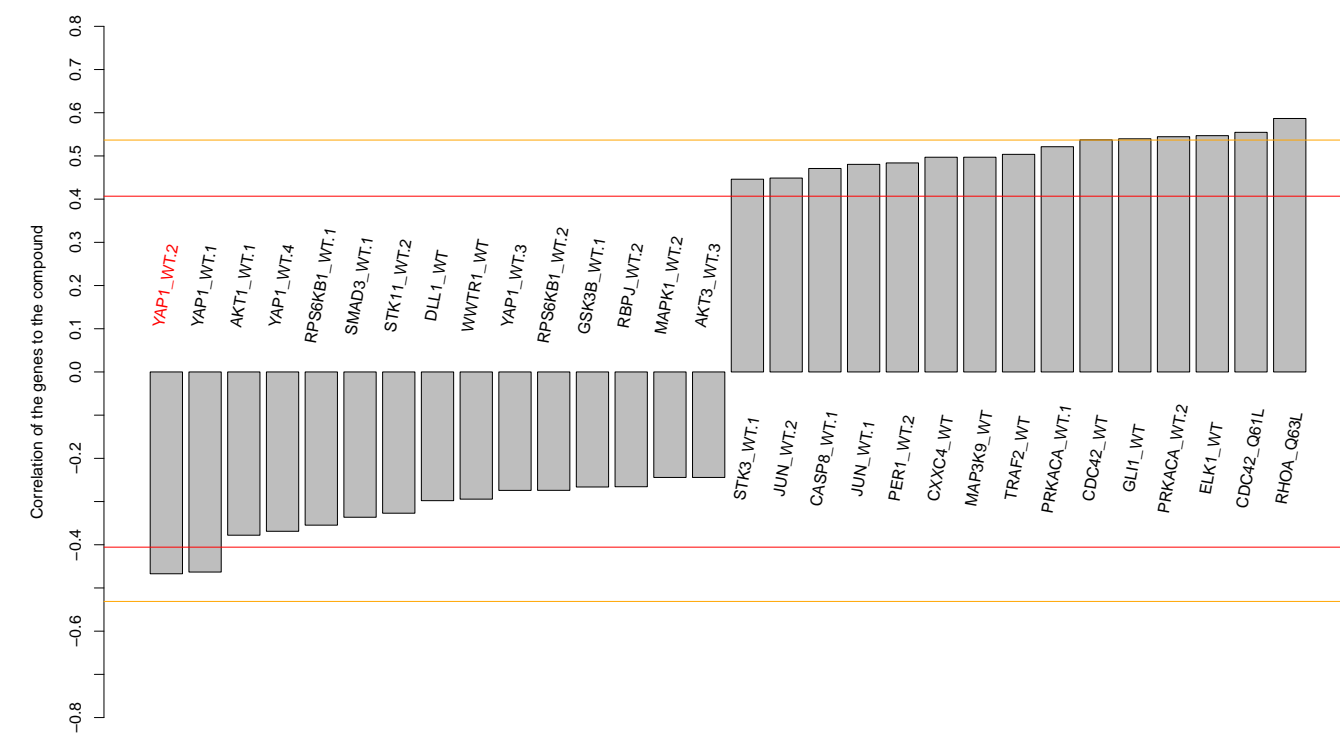
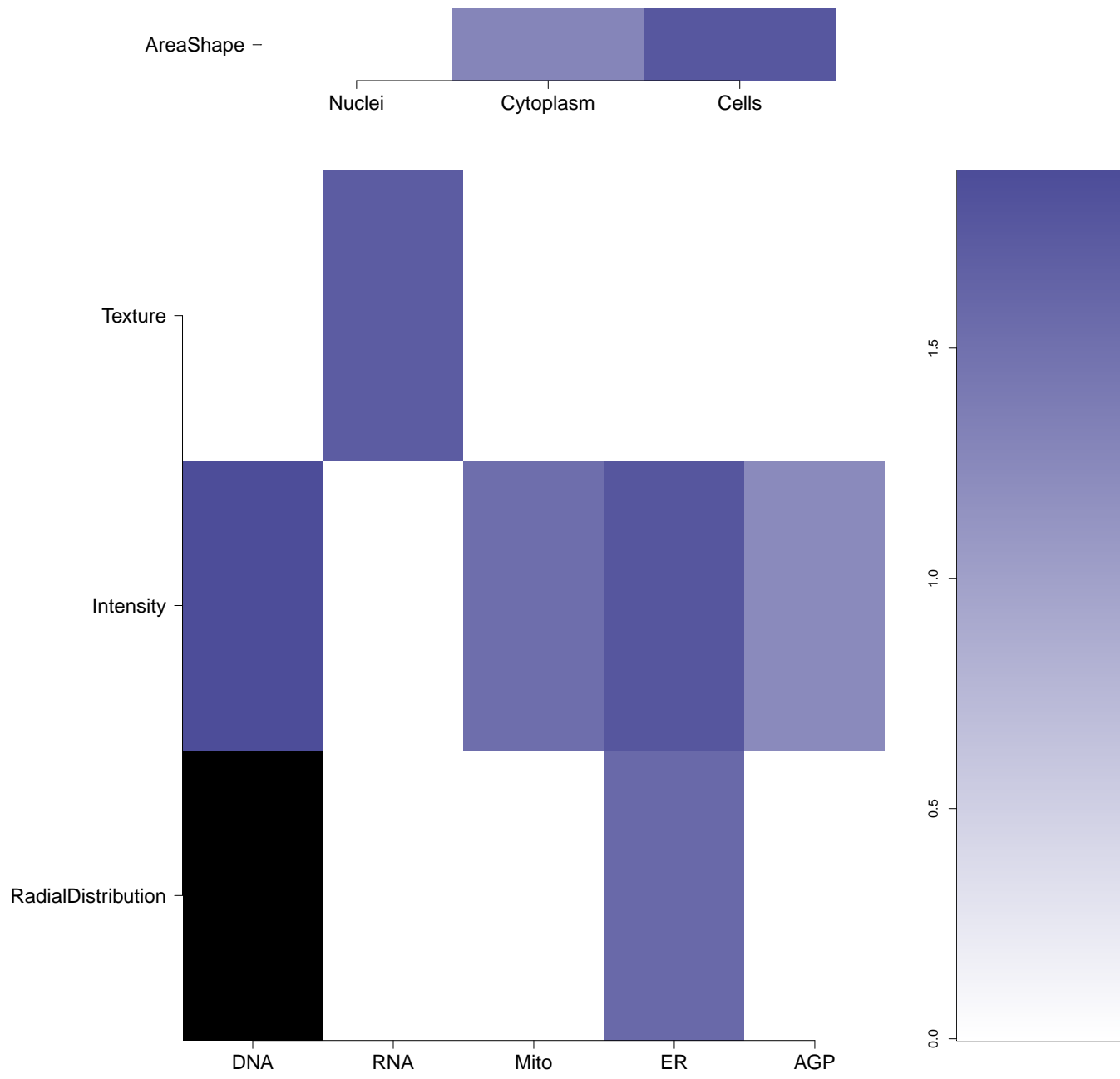

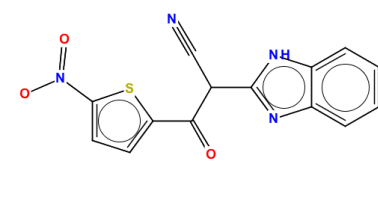
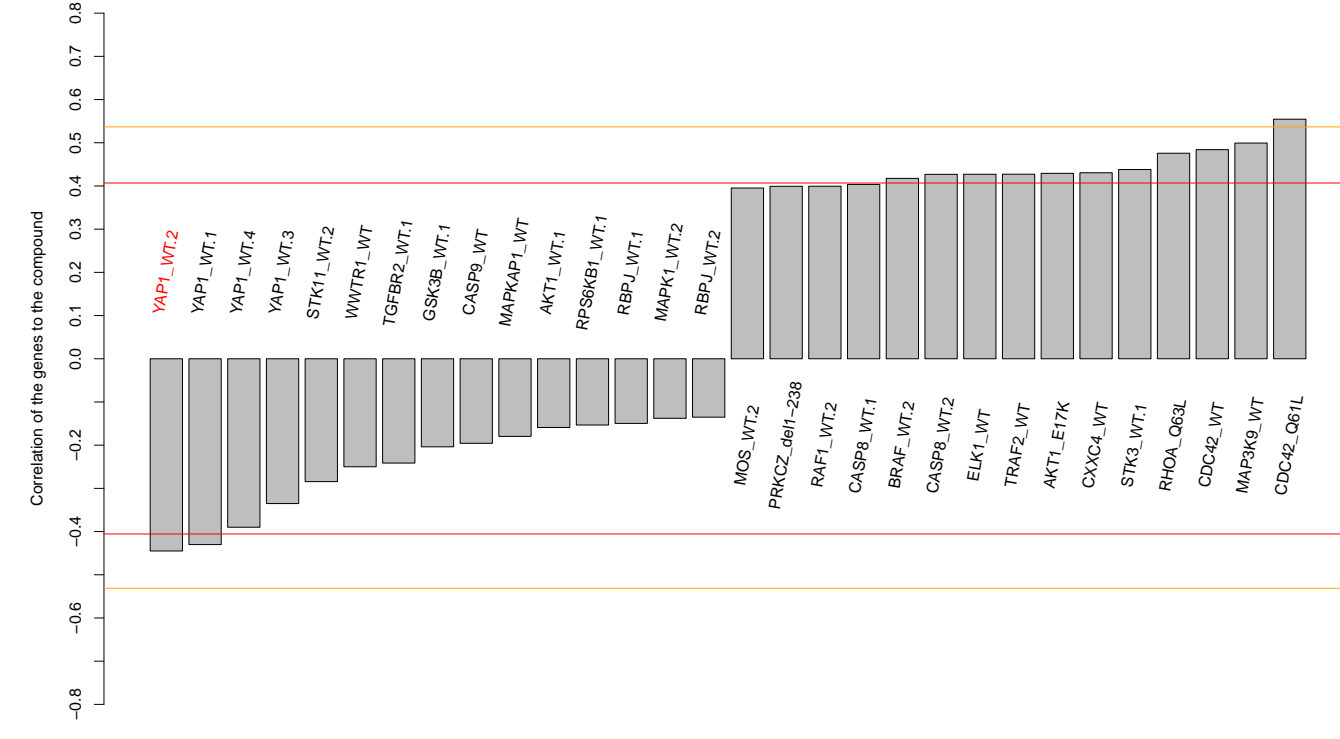
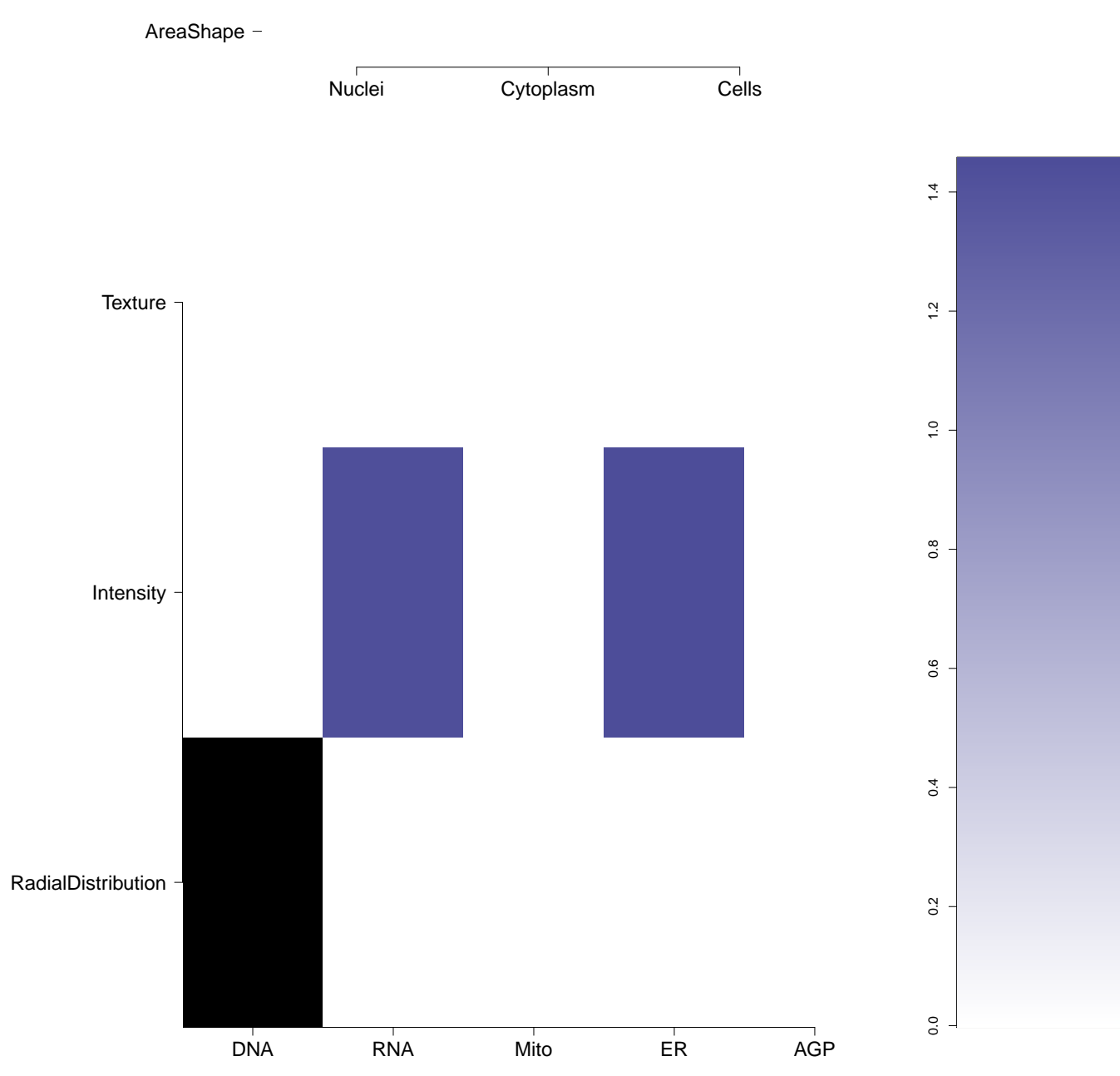



|  |   |                        |      |       |  |   |   |  |
|--|---|------------------------|------|-------|--|---|---|--|
| BRD-K58469266-001-01-0<br>PubChem CID : 54646063 |    | NA (in 1 replicates)   | 0.63 | 0.767 |    |     |     | Total number of assays tested in: 39.  |
| BRD-K88597074-001-01-4<br>PubChem CID : 54618422 |    | 0.82 (in 4 replicates) | 0.62 | 0.767 |    |    |    | Total number of assays tested in: 36.  |
| BRD-K43729445-001-01-9<br>PubChem CID : 44484576 |   | 0.80 (in 4 replicates) | 0.62 | 0.767 |   |   |   | Total number of assays tested in: 45.  |
| BRD-K17923226-001-01-5<br>PubChem CID : 54619100 |  | 0.77 (in 4 replicates) | 0.60 | 0.132 |  |  |  | Total number of assays tested in: 38.<br>Active in the following assays: <ul style="list-style-type: none"> <li>MLPCN SirT5 Measured in Biochemical System Using Imaging - 7044-01.Inhibitor.SinglePoint.HTS.Activity.Set5 (AID 652115)</li> <li>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)</li> <li>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)</li> <li>HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader - 2153-03.Inhibitor.Dose.DryPowder.Activity (AID 1159569)</li> <li>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)</li> <li>Plasmodium falciparum PIN1TD609-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)</li> <li>HepG2 cytotoxicity counterscreen Measured in Cell-Based System Using Plate Reader - 2153-03.Inhibitor.Dose.CherryPick.Activity (AID 1159577)</li> </ul> |
| BRD-K60245465-001-01-9<br>PubChem CID : 54618660 |  | 0.69 (in 4 replicates) | 0.59 | 0.767 |  |  |  | Total number of assays tested in: 37.  |
| BRD-K64243825-001-01-2<br>PubChem CID : 54641063 |  | NA (in 1 replicates)   | 0.58 | NA    |  |  |  | Total number of assays tested in: 38.  |
| BRD-K19764902-001-01-2<br>PubChem CID : 44490887 |  | 0.64 (in 4 replicates) | 0.58 | NA    |  |  |  | Total number of assays tested in: 43.  |



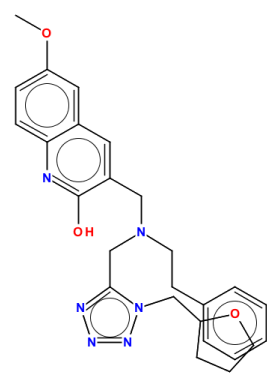




|   |   |                        |       |       |  |   |   |  |
|---|---|------------------------|-------|-------|--|---|---|--|
| <div>BRD-K43419088-001-01-9</div> <div>PubChem CID : 54618842</div>   |    | 0.55 (in 3 replicates) | -0.47 | 0.887 |    |     |     | Total number of assays tested in: 37.  |
| <div>BRD-A96875824-001-06-8</div> <div>MLS000576285<br/>STK286148<br/>SMR000197925<br/>AC1MGC3Z<br/>BDBM63137<br/>HMS2419L03<br/>PubChem CID : 2933627</div>  |    | 0.66 (in 4 replicates) | -0.47 | NA    |    |   |    | Total number of assays tested in: 661. Active in the following assays: <ul style="list-style-type: none"><li>• CYP2C9 Assay (AID 777)</li><li>• CYP2C19 Assay (AID 778)</li><li>• Screen for Chemicals that Inhibit the RAM Network (AID 868)</li><li>• qHTS Assay for Inhibitors of Aldolhyde Dehydrogenase 1 (ALDH1A1) (AID 1030)</li><li>• qHTS Assay for Inhibitors of Bacillus subtilis Stp phosphopantetheinyl transferase (PTase) (AID 1490)</li><li>• Luminescence-based primary biochemical high throughput screening assay to identify inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1789)</li><li>• MLPCN Alpha-Synuclein 5'UTR - 5'UTR binding - activators (AID 1814)</li><li>• Luminescence-based confirmation biochemical high throughput screening assay for inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1846)</li><li>• Luminescence-based counterscreen assay for HSP90 inhibitors: biochemical high throughput screening assay to identify inhibitors of native luciferase. (AID 1847)</li><li>• Luminescence Cell-Based Primary HTS to Identify Inhibitors of Heat Shock Factor 1 (HSF1). (AID 2098)</li><li>• Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)</li><li>• A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)</li><li>• Luminescence Cell-Based Dose Confirmation HTS to Identify Inhibitors of Heat Shock Factor 1 (HSF1) (AID 2382)</li><li>• Primary cell-based screen for identification of compounds that inhibit the two-pore domain potassium channel KCNK9 (AID 488922)</li><li>• Confirmatory screen for identification of compounds that inhibit the two-pore domain potassium channel (KCNK9) (AID 492992)</li><li>• Second counter screen for compounds that modulate the two-pore domain potassium channel (KCNK9) (AID 492997)</li><li>• qHTS Assay for Inhibitors of Histone Lysine Methyltransferase G9a (AID 504332)</li><li>• qHTS Assay for Inhibitors of Mammalian Selenoprotein Thioredoxin Reductase 1 (Txr1): qHTS (AID 588453)</li><li>• Primary biochemical fluorescence polarization-based high throughput screening assay to identify inhibitors of protein arginine methyltransferase 1 (PRMT1) (AID 652257)</li></ul>   |
| <div>BRD-A03579949-001-06-8</div> <div>ST51021638<br/>SMR000354156<br/>ZINC00381341<br/>AC1NTVTU<br/>MLS001017934<br/>MLS001167404<br/>HMS2745L03<br/>ZINC381341<br/>T0506-5460<br/>PubChem CID : 5412646</div> |  | 0.58 (in 4 replicates) | -0.44 | NA    |  |  |  | Total number of assays tested in: 593. Active in the following assays: <ul style="list-style-type: none"><li>• Primary cell-based high-throughput screening assay for potentiators or agonists of NPY-Y1 (AID 1304)</li><li>• uHTS luminescence assay for the identification of compounds that inhibit NOD1 (AID 1578)</li><li>• Fluorescence counterscreen assay for potentiators or agonists of NPY-Y1: cell-based high-throughput screening assay to identify agonists of NPY-Y2. (AID 1698)</li><li>• Luminescence Cell-Based/Microorganism Primary HTS to Identify Inhibitors of T.Cruzi Replication (AID 1885)</li><li>• Luminescence Cell-Based Dose Response HTS Screen to Identify Cytotoxic Compounds of NIH3T3 cells. (AID 2010)</li><li>• Luminescence Cell-Based/Microorganism Dose Confirmation HTS to Identify Inhibitors of T.Cruzi Replication. (AID 2044)</li><li>• uHTS Luminescent assay for identification of inhibitors of Sentrin-specific protease 7 (SENPT7) (AID 434973)</li><li>• uHTS for identification of Inhibitors of Mdm2/MdmX interaction in luminescent format. (AID 485346)</li><li>• Single concentration confirmation of uHTS for Inhibitors of Mdm2/MdmX interaction in luminescent format. (AID 489028)</li><li>• uHTS identification of small molecule antagonists of the CCR6 receptor via a luminescent beta-arrestin assay (AID 493998)</li><li>• qHTS screen for small molecules that inhibit ELG1-dependent DNA repair in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1: Hit Confirmation using Full-Length Luciferase Counterscreen assay (AID 504607)</li><li>• Single concentration confirmation of inhibitors of Mdm2/MdmX interaction using a Breal/Bard1 BILC Counterscreen assay. (AID 504668)</li><li>• qHTS of small molecules that selectively kill Giardia lamblia: Hit Validation. (AID 588397)</li><li>• Single concentration confirmation of uHTS antagonist hits from Gli-SUFU in a luminescent reporter assay (AID 602428)</li><li>• uHTS identification of small molecule inhibitors of the mitochondrial permeability transition pore via an absorbance assay (AID 602449)</li><li>• qHTS screen for small molecules that inhibit ELG1-dependent DNA repair in human embryonic kidney (HEK293T) cells expressing luciferase-tagged ELG1: Hit Confirmation using MMS Stimulated ELG1 (AID 624249)</li><li>• qHTS screen for small molecules that inhibit ELG1-dependent DNA repair: Hit Confirmation with MMS Viability (AID 624251)</li><li>• uHTS identification of Caspase-8 TRAIL sensitizers in a luminescence assay (AID 624354)</li><li>• Single concentration confirmation of uHTS inhibitor hits of the mitochondrial permeability transition pore via a fluorescent based assay (AID 624504)</li><li>• Single concentration confirmation of Caspase-8 TRAIL sensitizer hits in a luminescence panel assay (AID 651596)</li><li>• Single concentration confirmation of uHTS Gli-SUFU antagonist hits in a Wnt3a luminescent reporter assay (AID 651995)</li><li>• qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDPI): qHTS in cells in absence of CPT (AID 686978)</li></ul> |



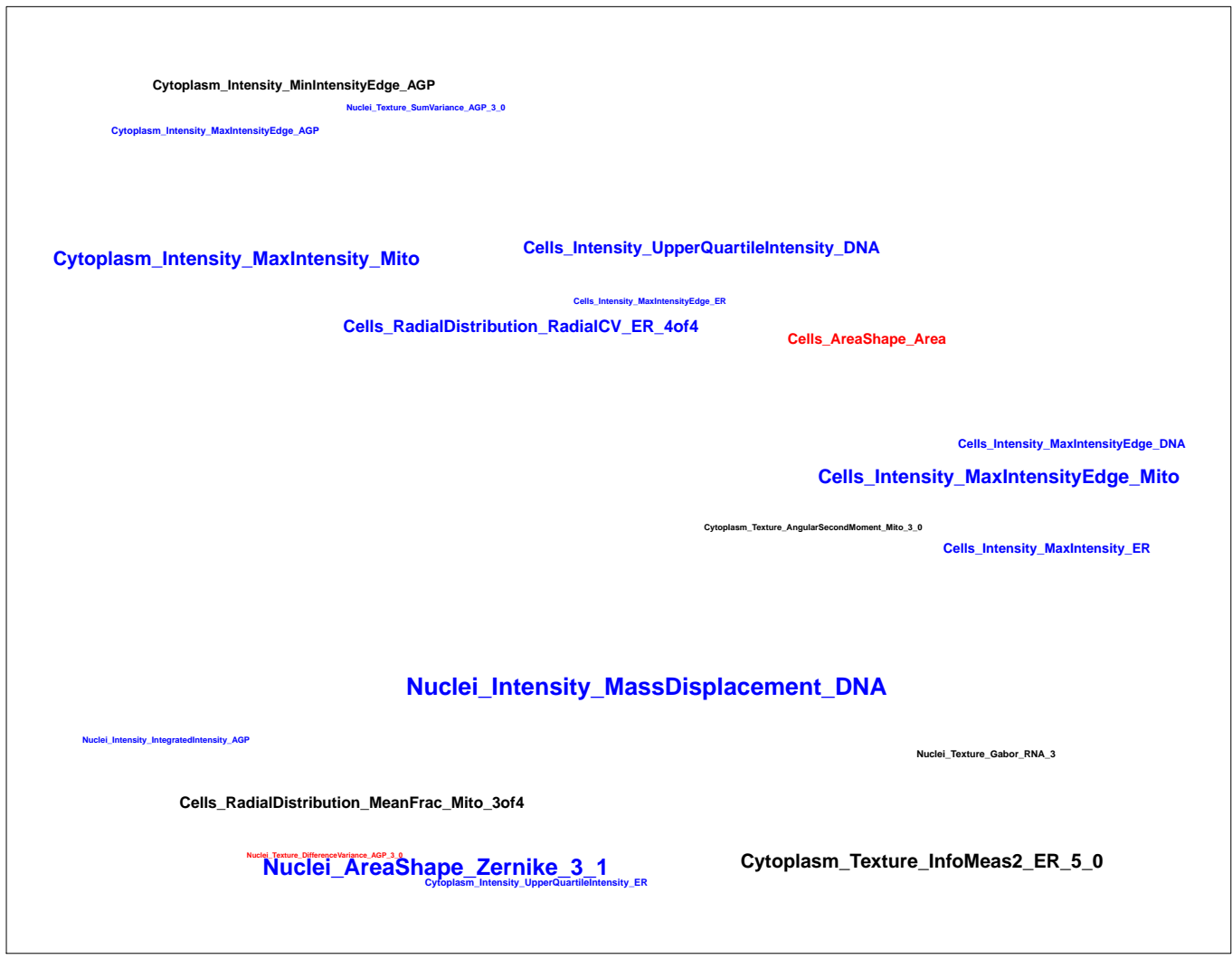
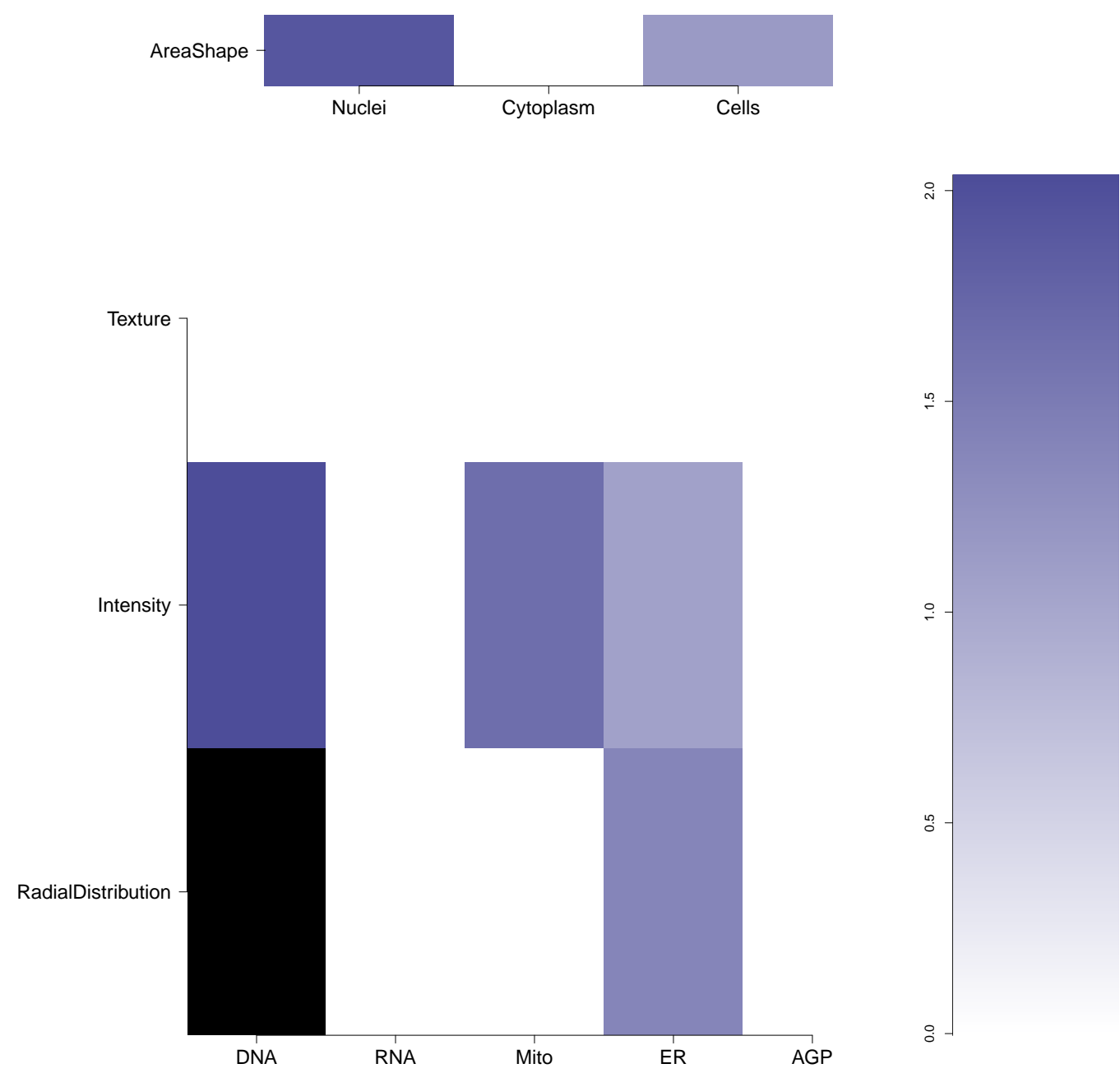
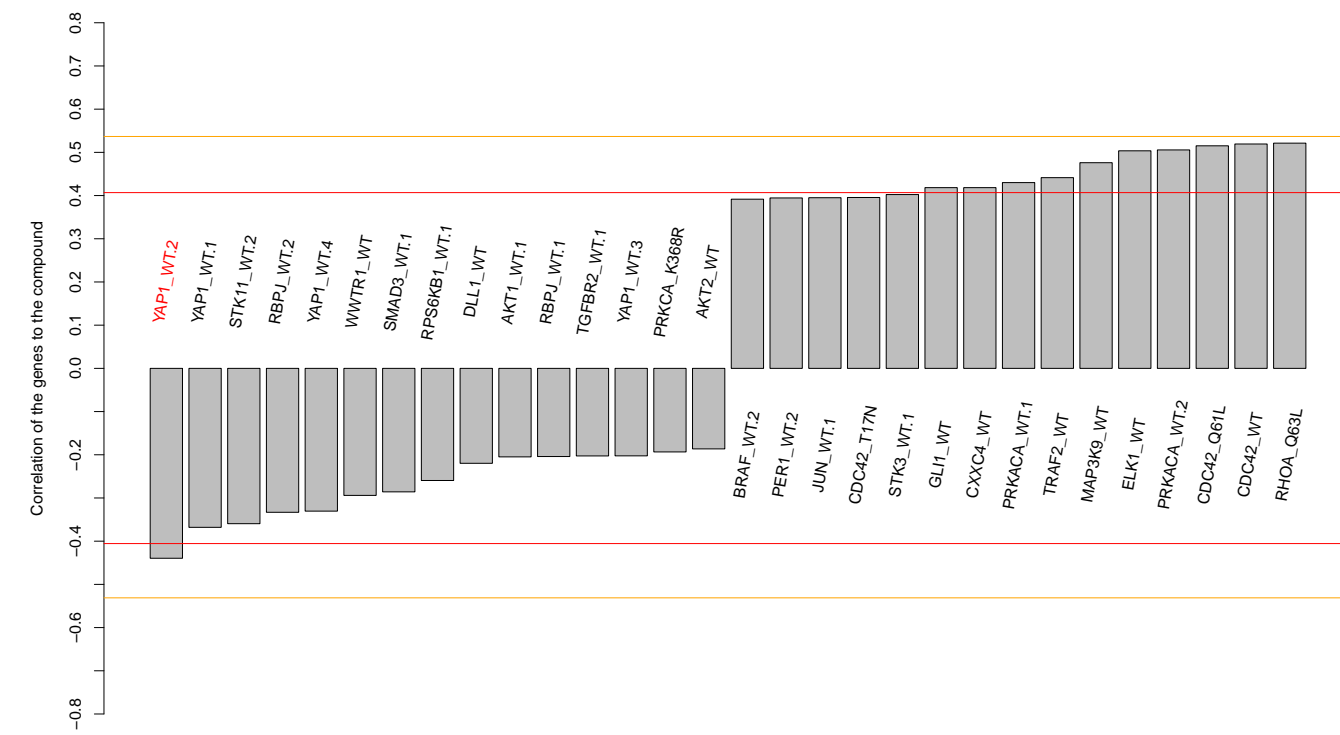
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HMS2496A23  
PubChem CID : 655253



0.62 (in 4 replicates)

-0.44

NA



- Total number of assays tested in: 775. Active in the following assays:
- qHTS Assay for Spectroscopic Profiling in 4-MU Spectral Region (AID 589)
  - qHTS Assay for Spectroscopic Profiling in A350 Spectral Region (AID 590)
  - Human H69AR Lung Tumor Cell Growth Inhibition Assay - 86K Screen (AID 598)
  - Profiling the NIH Molecular Libraries Small Molecule Repository: Autofluorescence at 339/460 nm (AID 709)
  - CYP2C19 Assay (AID 778)
  - qHTS Assay for Inhibitors of Bacillus subtilis Sp phosphopantetheinyl transferase (PPTase) (AID 1490)
  - qHTS Assay for Inhibitors of Fructose-1,6-bisphosphate Aldolase from Giardia Lamblia: Coupling assay counterscreen (AID 2472)
  - qHTS Assay for Inhibitors of Histone Lysine Methyltransferase C9a (AID 504332)
  - uHTS identification of small molecule modulators of myocardial damage (AID 588492)
  - Dose response confirmation of uHTS hits for small molecule modulators of myocardial damage (AID 588779)
  - 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 hTAAR1 agonists that also desensitize TAAR1 receptor response. (AID 651951)
  - 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)
  - qHTS Assay for Activators of ClpP (AID 651965)
  - qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDPI): qHTS in cells in absence of CPT (AID 686978)
  - qHTS for Inhibitors of human tyrosyl-DNA phosphodiesterase 1 (TDPI): qHTS in cells in presence of CPT (AID 686979)