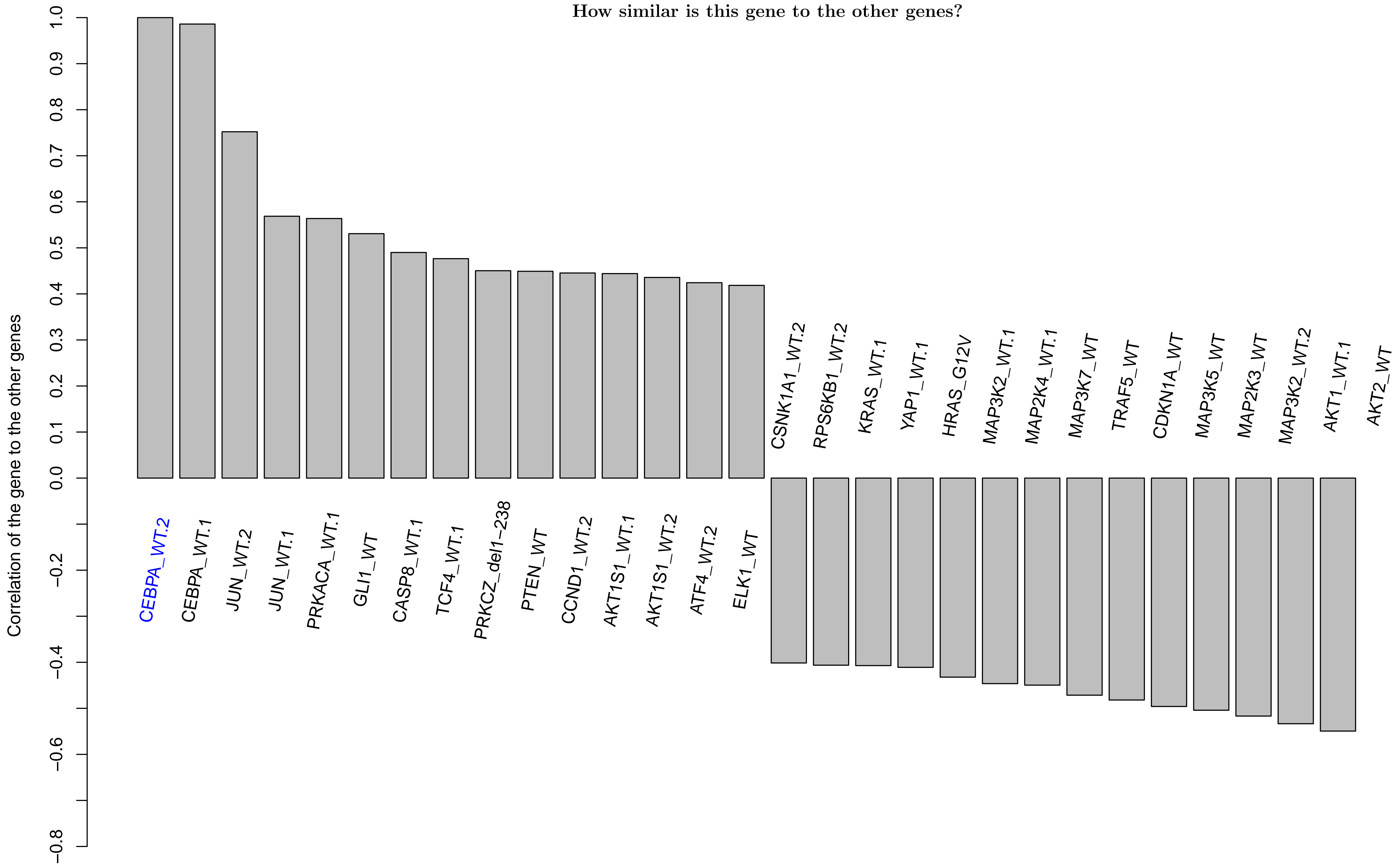
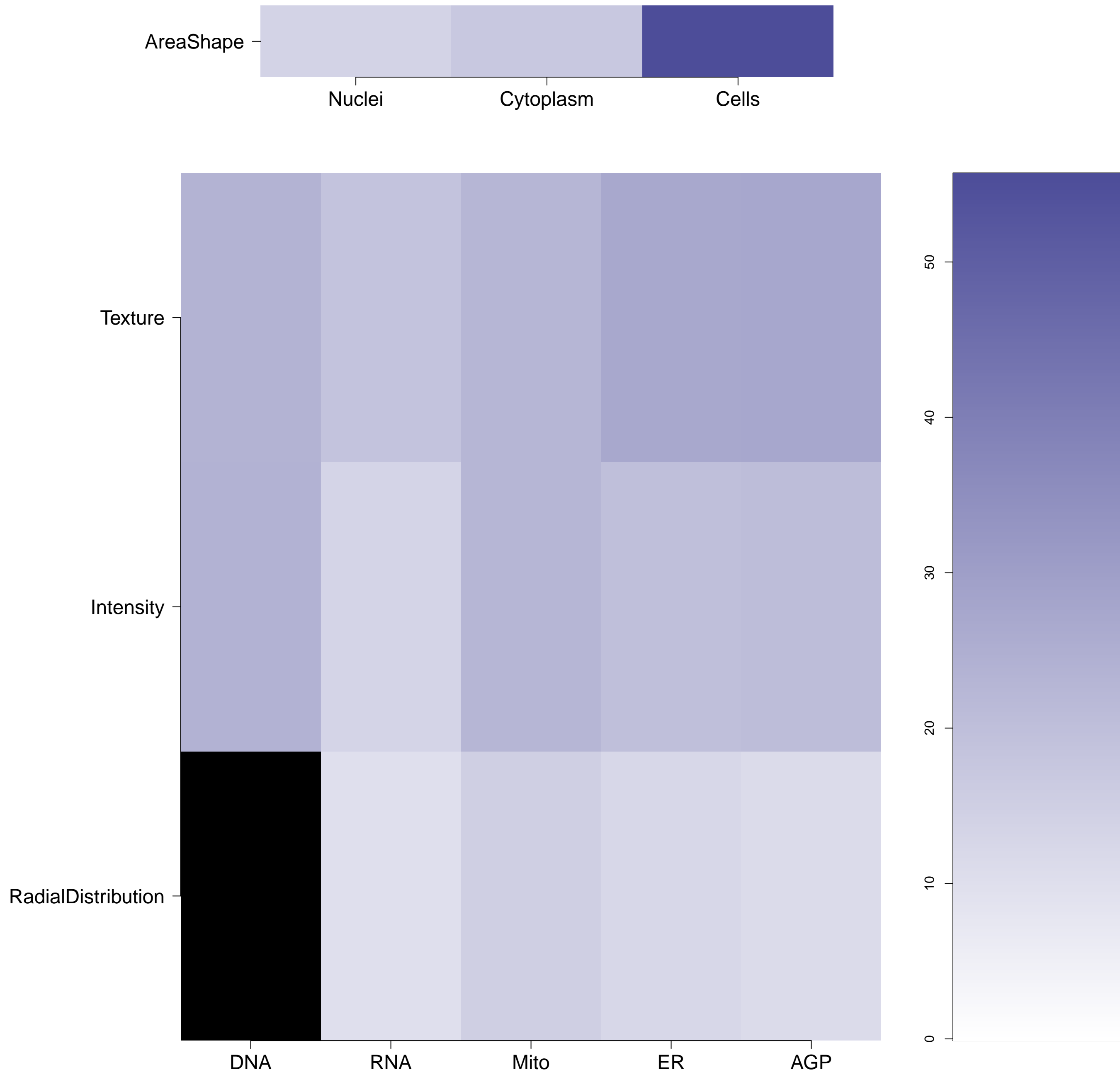


CEBPA.WT.2 - in Transcription Factors

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

CEBPA.WT.2 (41744)

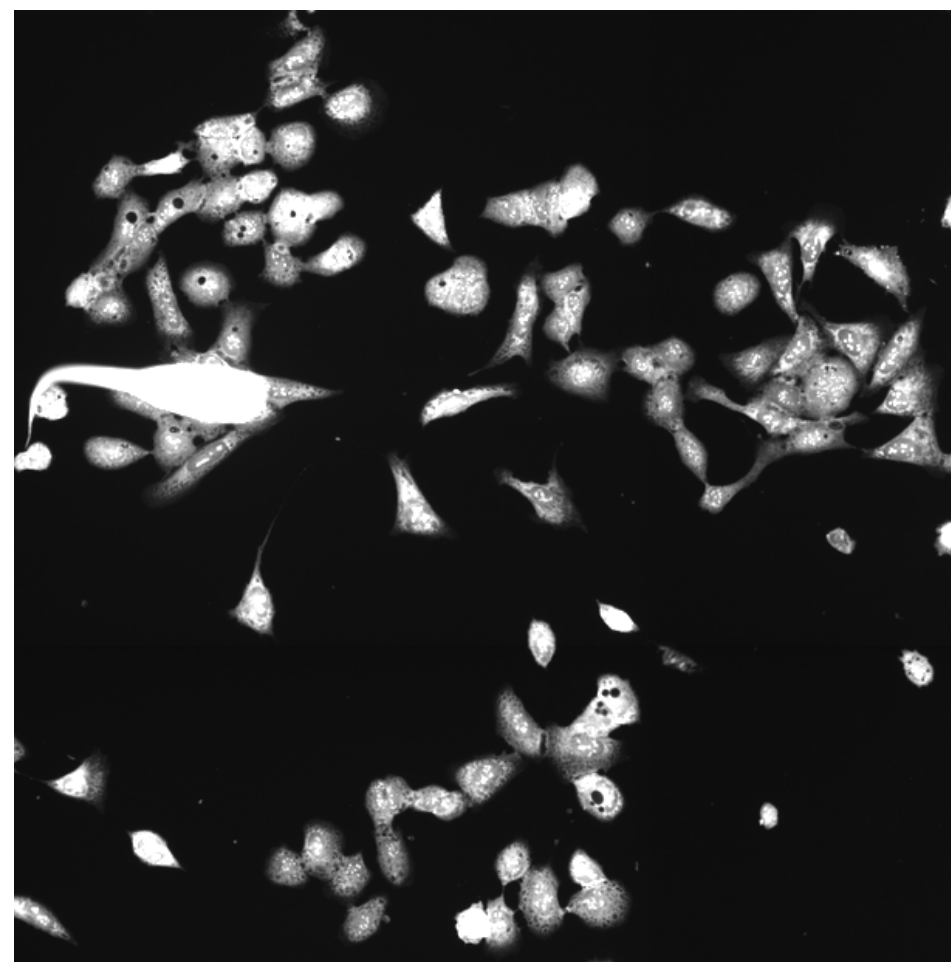
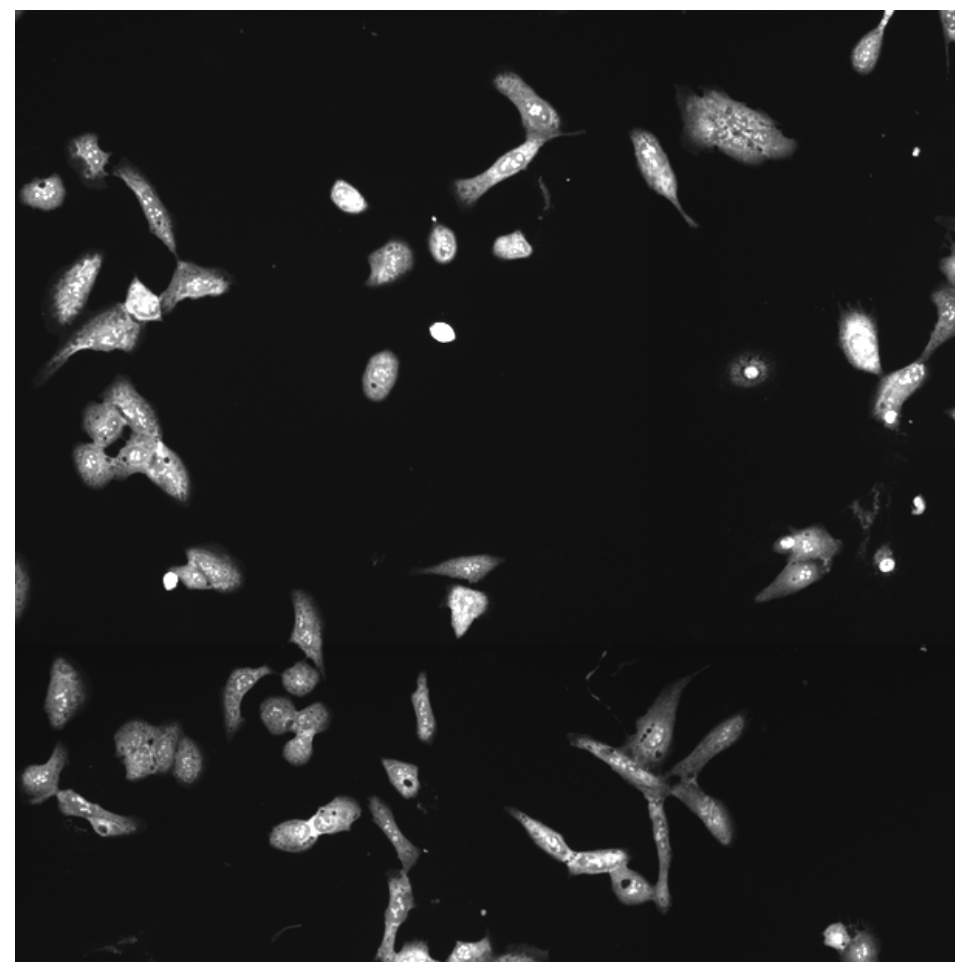
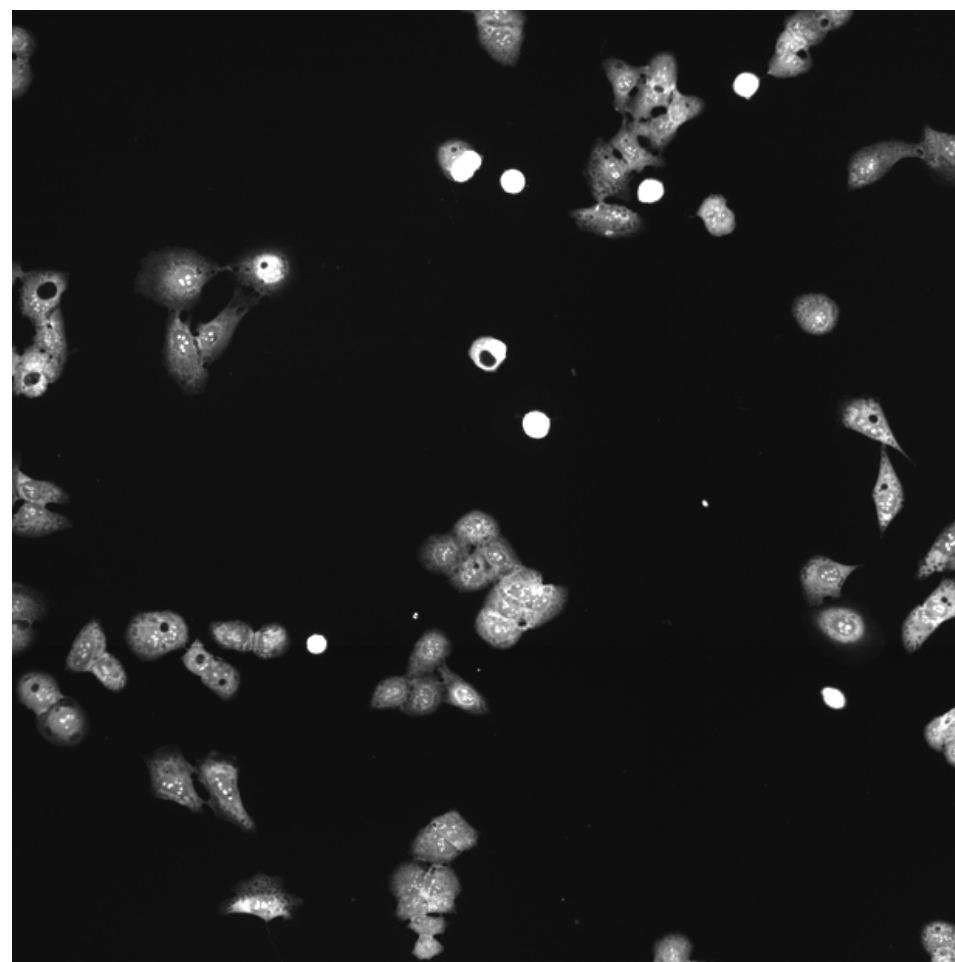
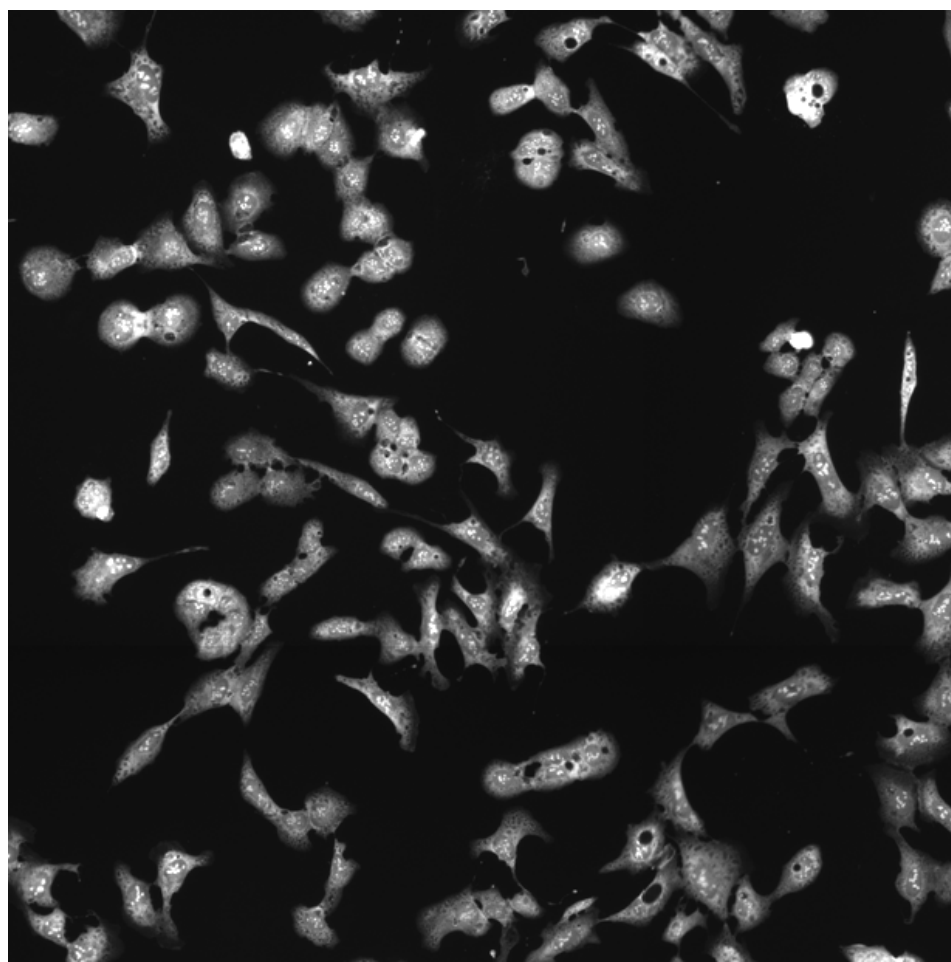
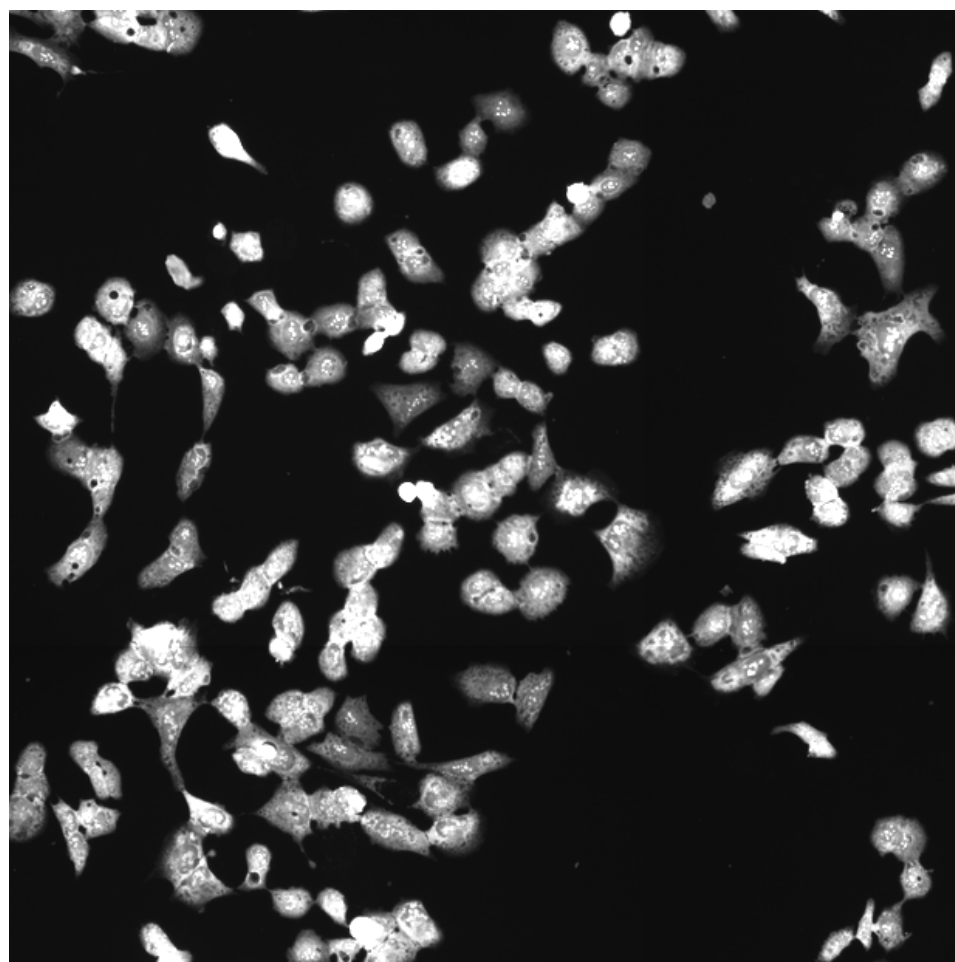
CEBPA.WT.2 (41755)

CEBPA.WT.2 (41756)

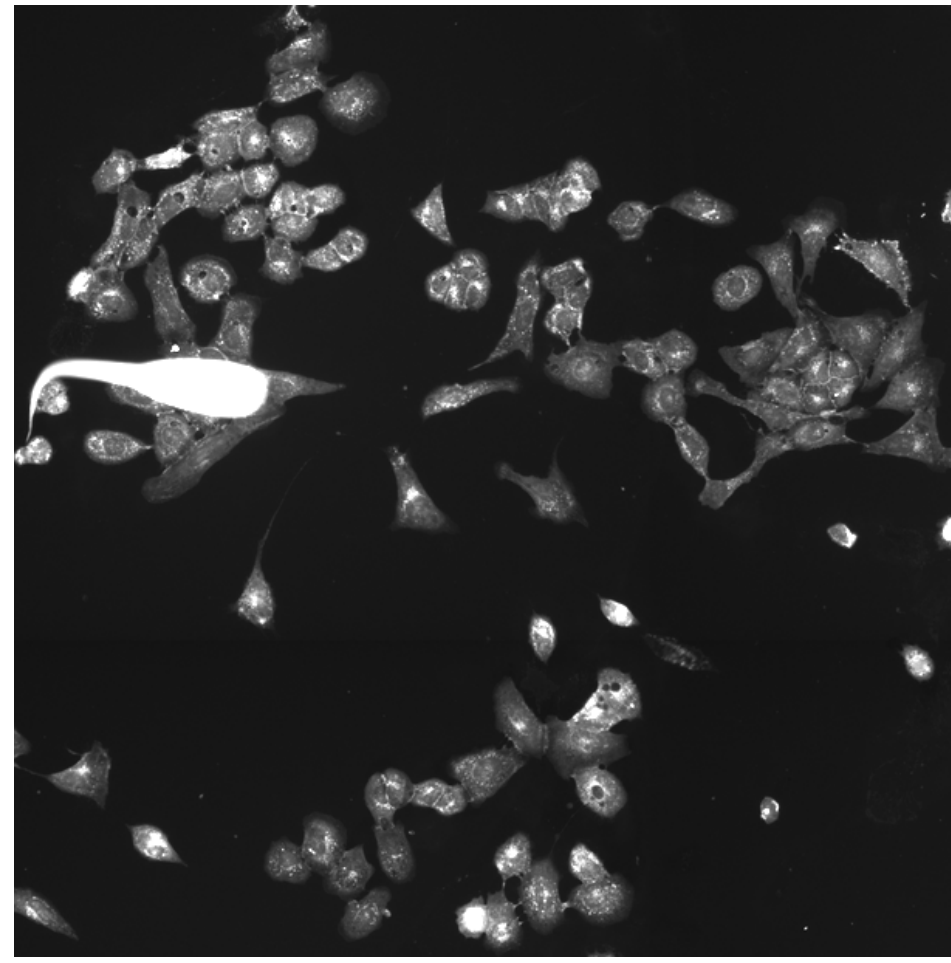
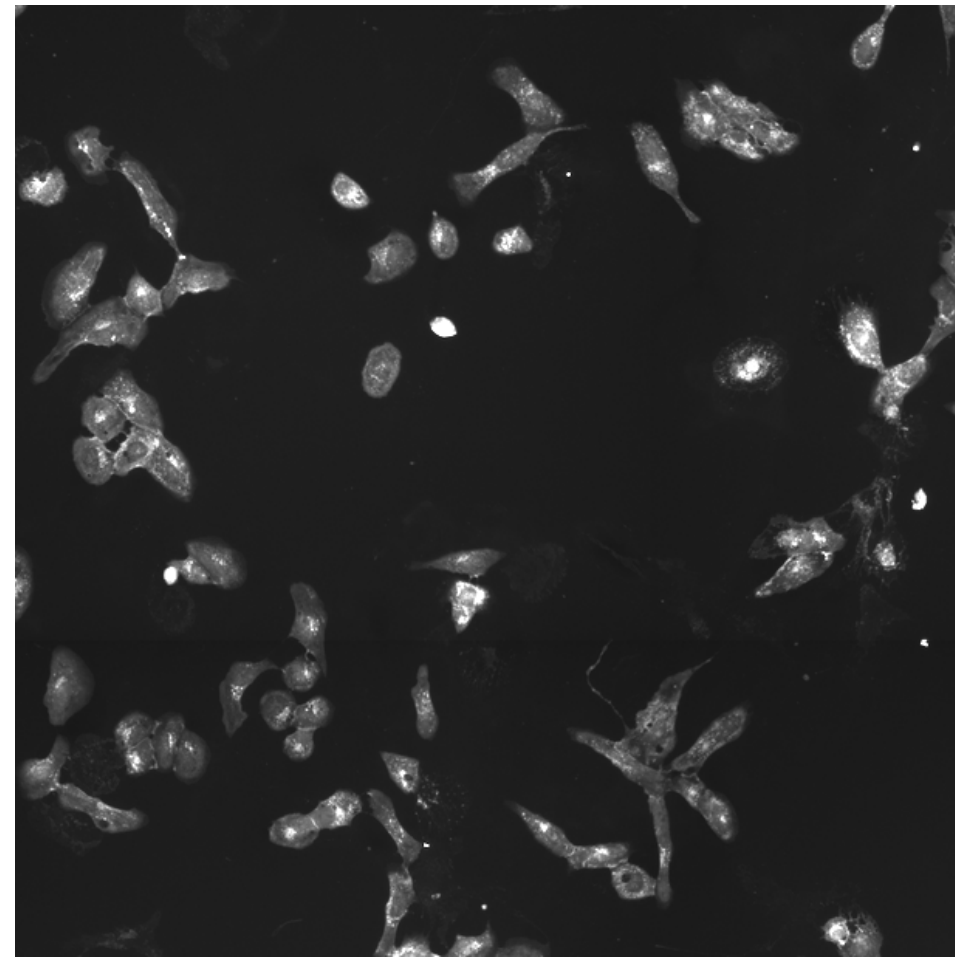
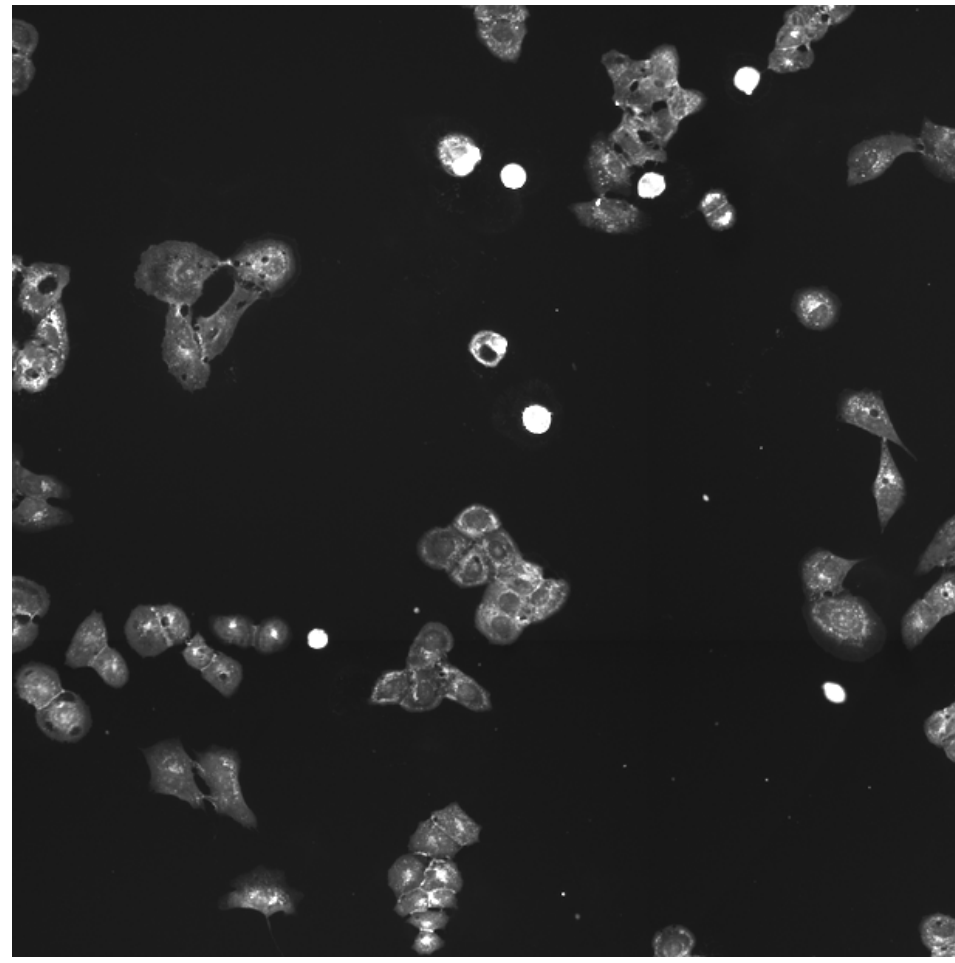
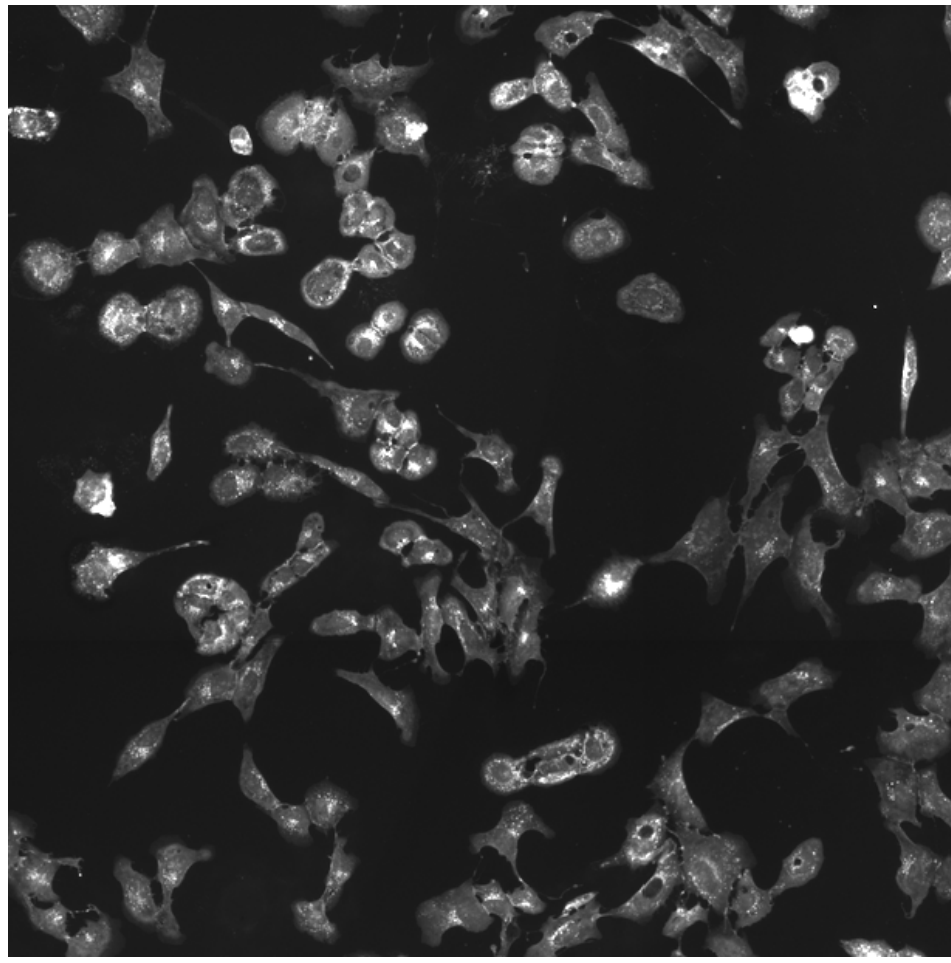
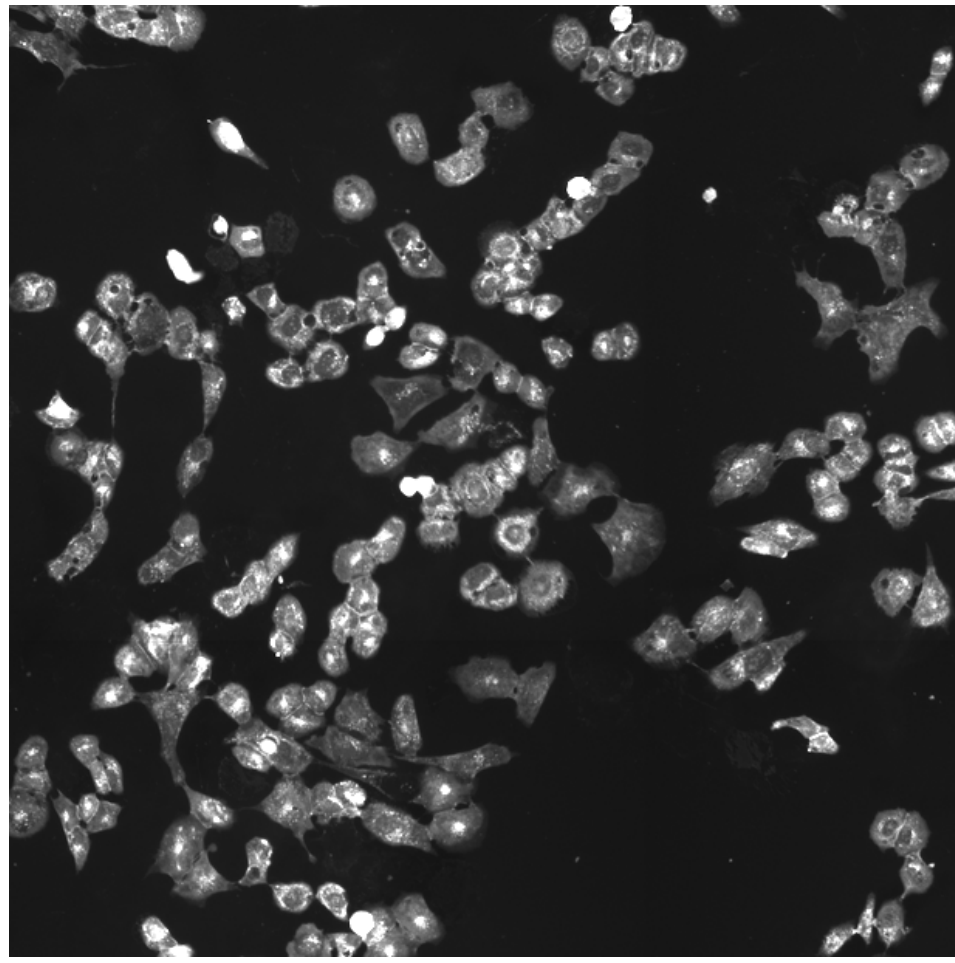
CEBPA.WT.2 (41757)

CEBPA.WT.2 (41754)

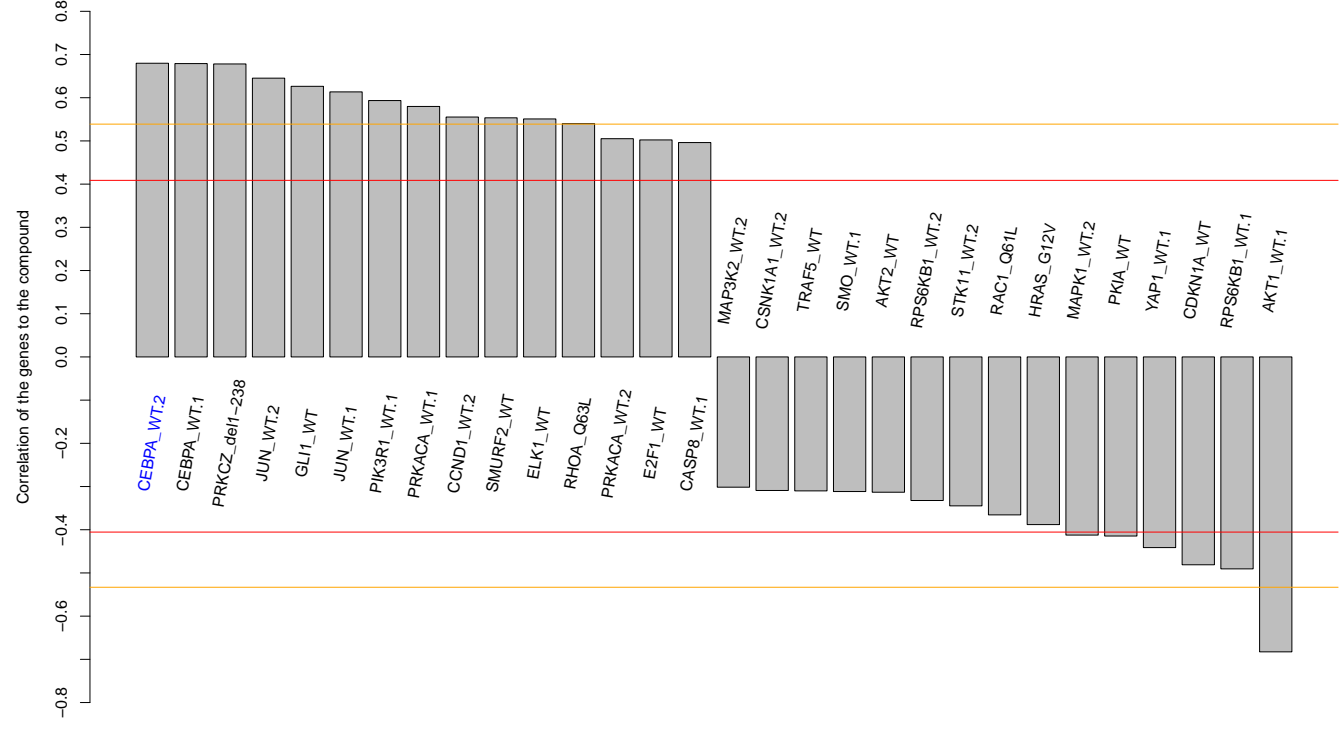
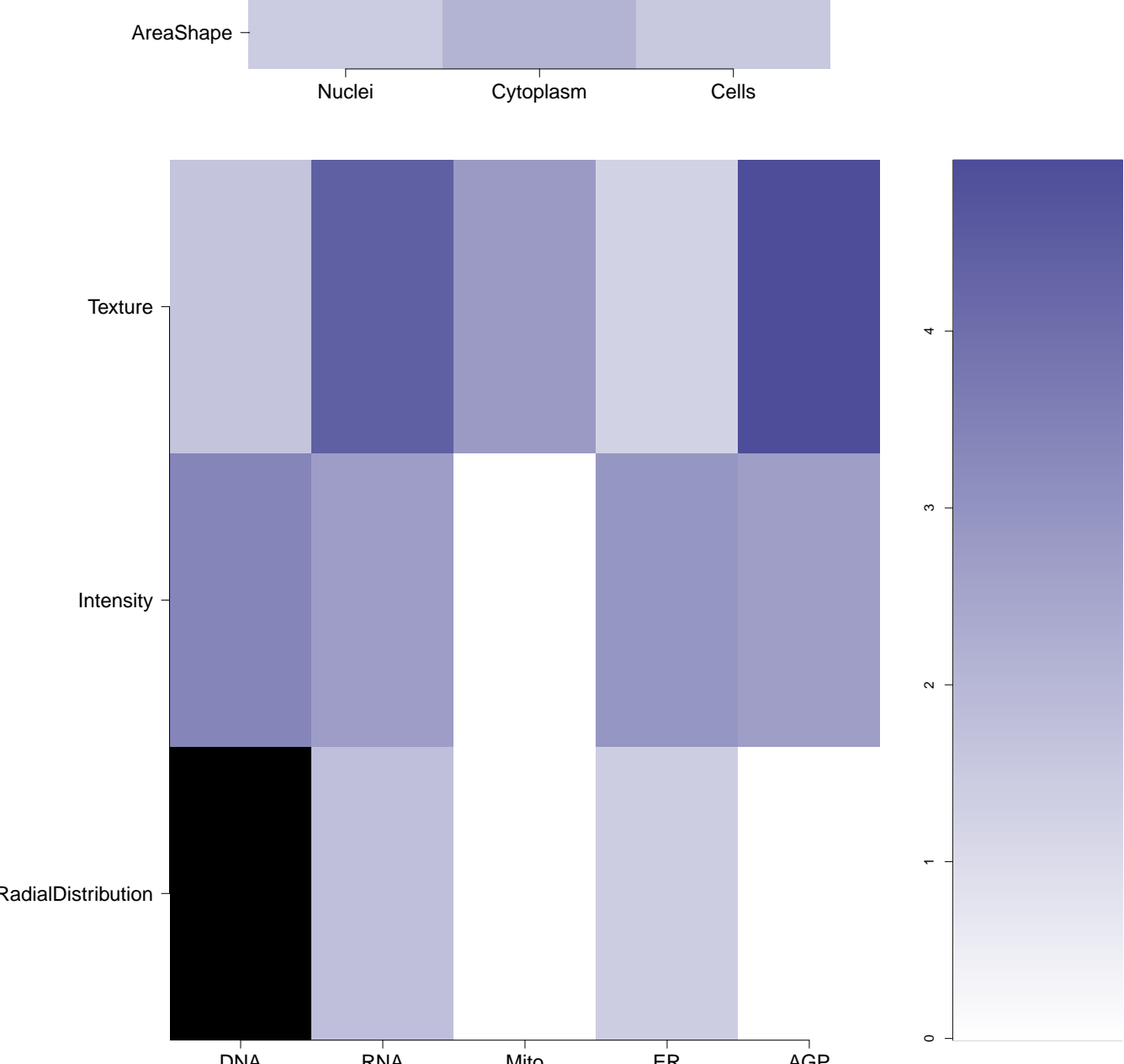
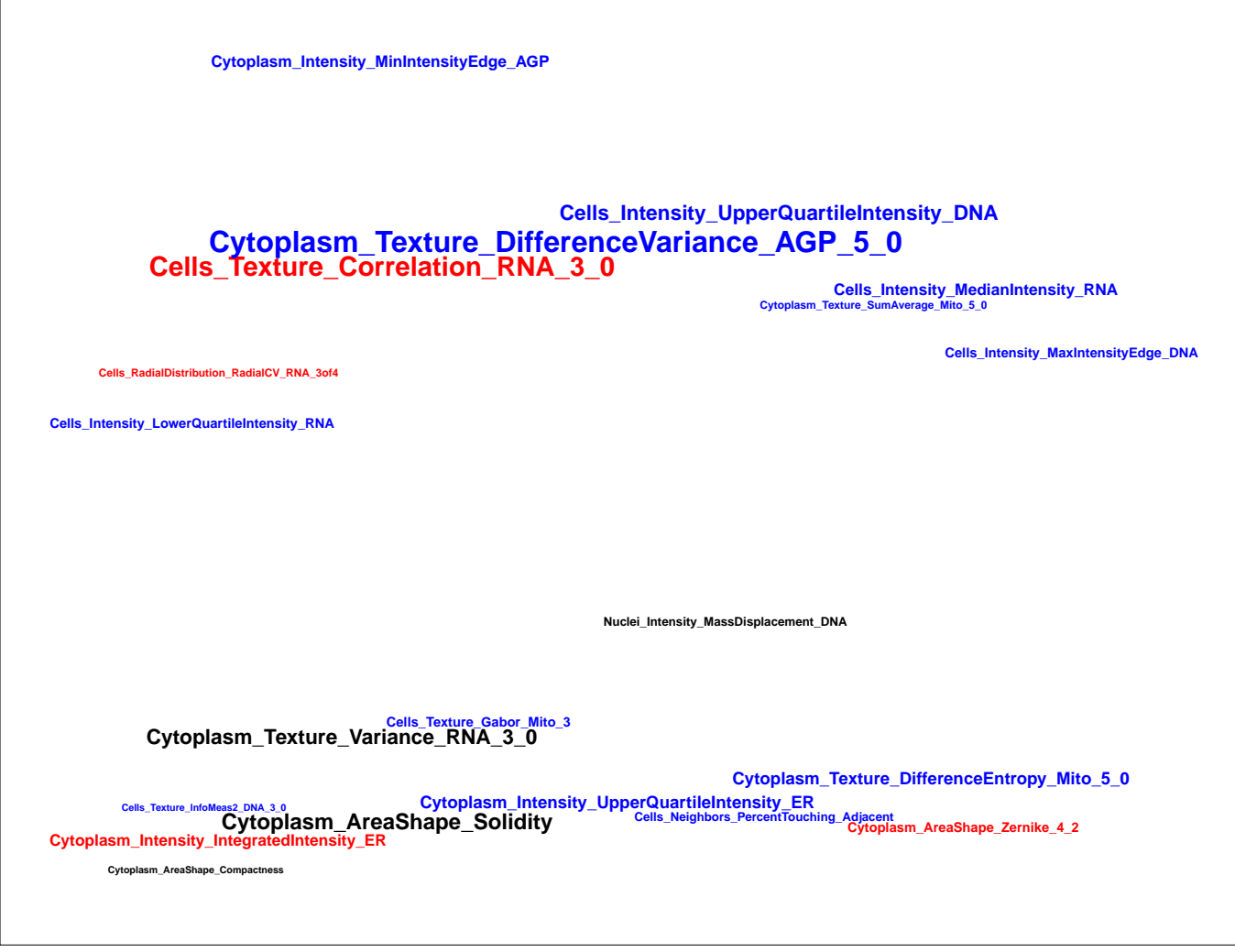
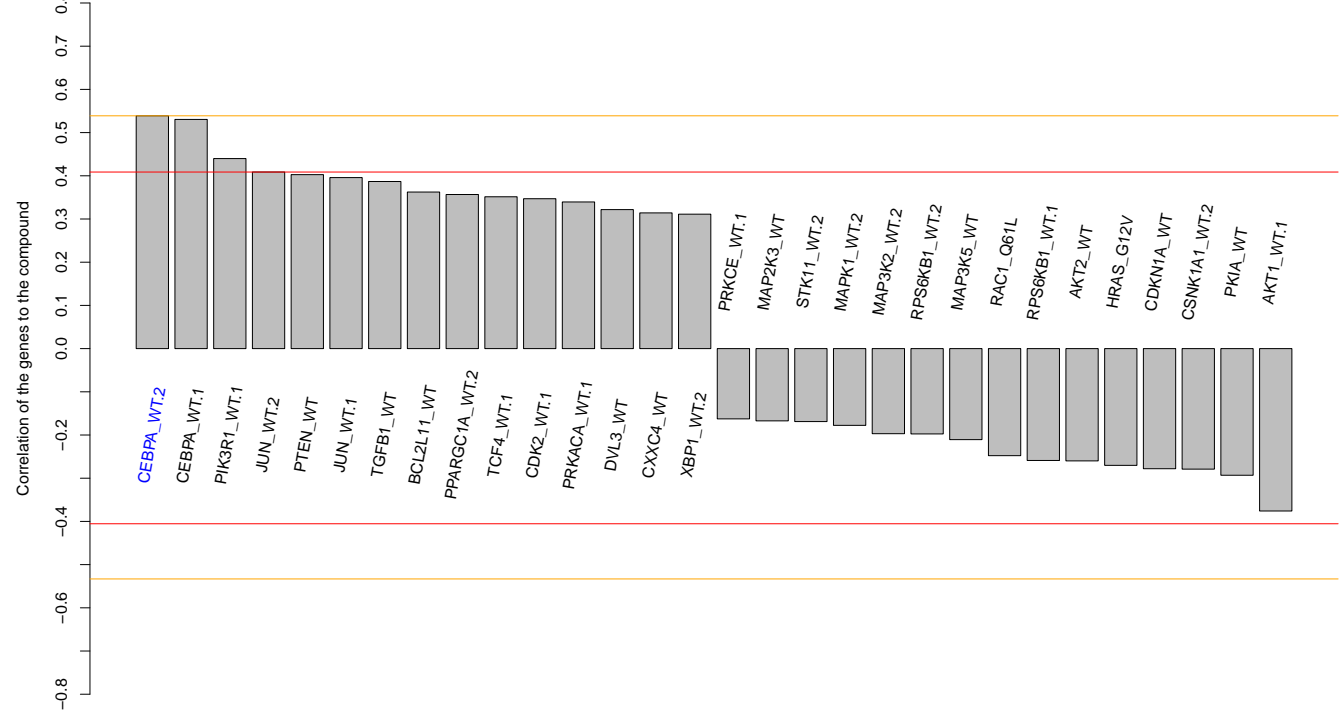
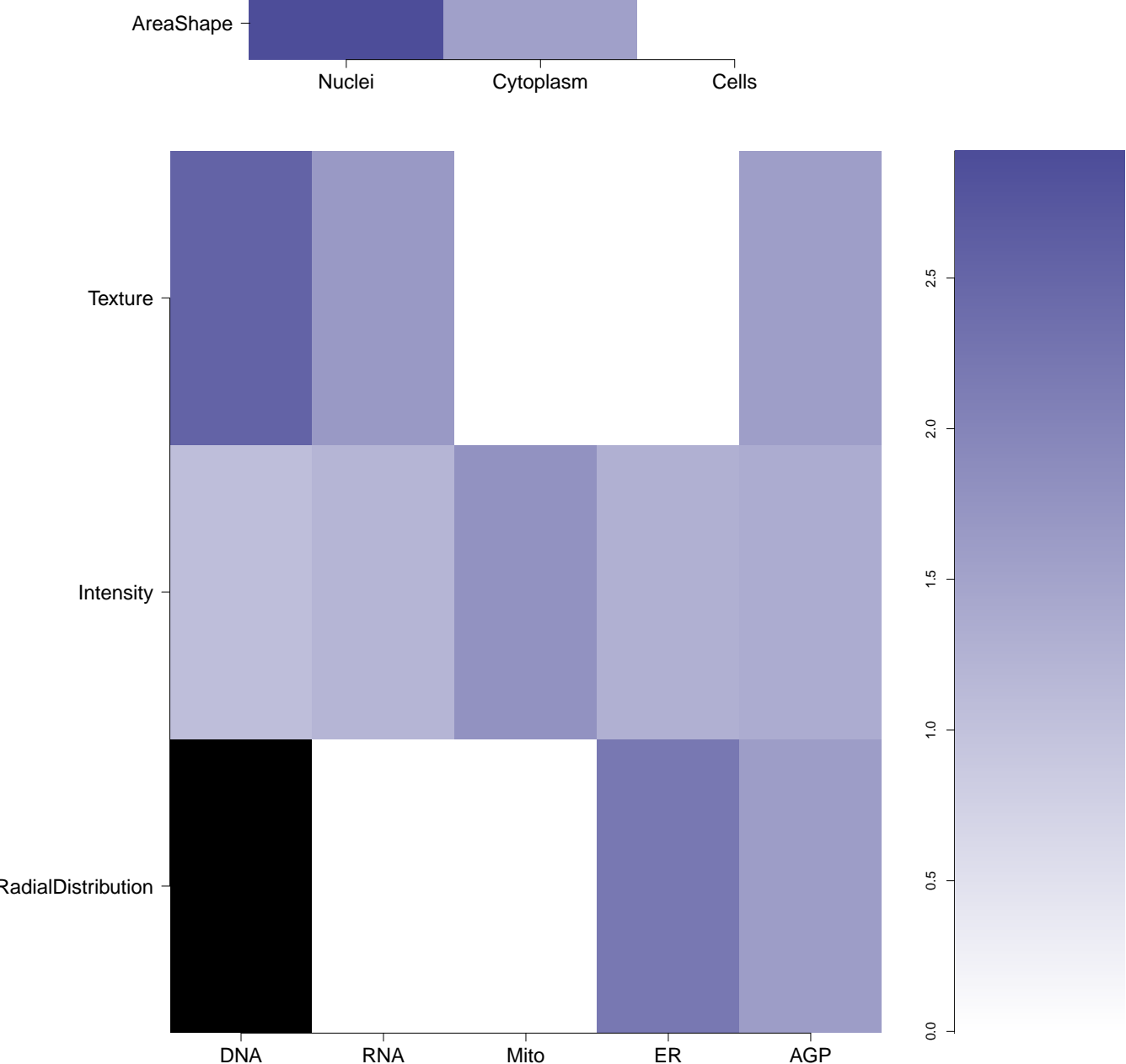

RNA



AGP



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 0.51)	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
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<div>BRD-K06736360-001-05-1</div> <div>ZINC03416368</div> <div>AC1M8DOD</div> <div>MLS000760967</div> <div>HMS2708G03</div> <div>ZINC3416368</div> <div>SMR000372267</div> <div>T5315952</div> <div>PubChem CID : 2535434</div>	<chem>O=C1C(=C(C=C1)C(=O)C2=CC=CC=C2)C(=O)C3=CC=CC=C3</chem>	NA (in 1 replicates)	0.68	NA			
<div>BRD-K83241810-001-01-3</div> <div>PubChem CID : 54618429</div>	<chem>O=C1C(=C(C=C1)C(=O)C2=CC=CC=C2)C(=O)C3=CC=CC=C3</chem>	0.68 (in 4 replicates)	0.54	0.663			

- Total number of assays tested in: 624. Active in the following assays:
- Primary screen for compounds that activate Alzheimer's amyloid precursor (AID 1276)
 - Luminescence-based primary biochemical high throughput screening assay to identify inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1789)
 - MLPCN Alpha-Synuclein 5'UTR - 5'-UTR binding - activators (AID 1814)
 - Luminescence-based confirmation biochemical high throughput screening assay for inhibitors of the Heat Shock Protein 90 (HSP90) (AID 1846)
 - Luminescence-based counterscreen assay for HSP90 inhibitors: biochemical high throughput screening assay to identify inhibitors of native luciferase. (AID 1847)
 - Luminescence Cell-Based Primary HTS to Identify Inhibitors of Heat Shock Factor 1 (HSF1). (AID 2098)
 - Cycloheximide Counterscreen for Small Molecule Inhibitors of Shiga Toxin (AID 2314)
 - A qHTS for Small Molecule Inhibitors of Shiga Toxin (AID 2315)
 - uHTS for identification of Inhibitors of Mdm2/MdmX interaction in luminescent format. (AID 485346)
 - Single concentration confirmation of uHTS for Inhibitors of Mdm2/MdmX interaction in luminescent format. (AID 489028)
 - Fluorescence polarization-based primary biochemical high throughput screening assay to identify inhibitors of human platelet activating factor acetylhydrolase 2 (PAFAH2) (AID 492956)
 - Single concentration confirmation of inhibitors of Mdm2/MdmX interaction using a Full-Length Luciferase Counterscreen assay (AID 504607)
 - Antagonist of Human D 1 Dopamine Receptor: qHTS (AID 504652)
 - Single concentration confirmation of inhibitors of Mdm2/MdmX interaction using a Brcal/Bard1 BiLC Counterscreen assay. (AID 504668)
 - qHTS profiling assay for firefly luciferase inhibitor/activator using purified enzyme and Km concentrations of substrates (counterscreen for miR-21 project) (AID 588342)
 - Primary cell-based high-throughput screening for identification of compounds that activate/potenate calcium-activated chloride channels (TMEM16A) (AID 628377)
 - qHTS of GLP-1 Receptor Inverse Agonists (Inhibition Mode) (AID 624417)
 - Counterscreen for inhibitors of 5-meCpG-binding domain protein 2 (MBD2): TRFRET-based biochemical primary high throughput screening assay to identify inhibitors of binding of ubiquitin-like with PHD and ring finger domains 1 (UHRF1) to methylated oligonucleotide (AID 687016)
 - HTS for Bacterial rRNA inhibitors Measured in Microorganism-Based System Using Plate Reader - 7056-01.Inhibitor.SinglePoint.HTS.Activity (AID 720706)

- Total number of assays tested in: 32. Active in the following assays:
- EZH2/PRC2 methyltransferase inhibitors - Measured in Biochemical System Using Plate Reader - 2125-01.Inhibitor.SinglePoint.HTS.Activity (AID 651548)
 - MLPCN Sirt5 Measured in Biochemical System Using Imaging - 7044-01.Inhibitor.SinglePoint.HTS.Activity.Set5 (AID 652115)