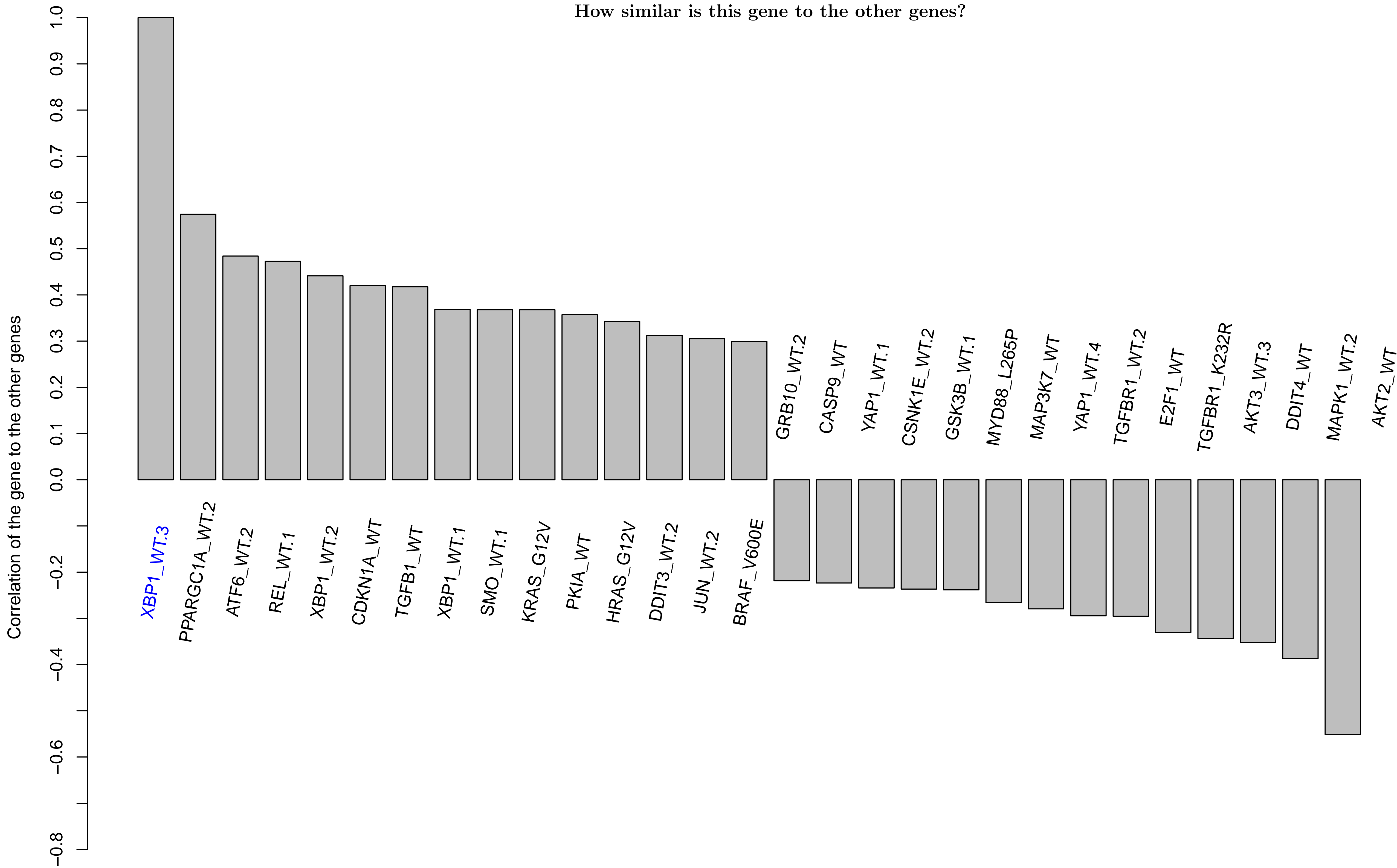
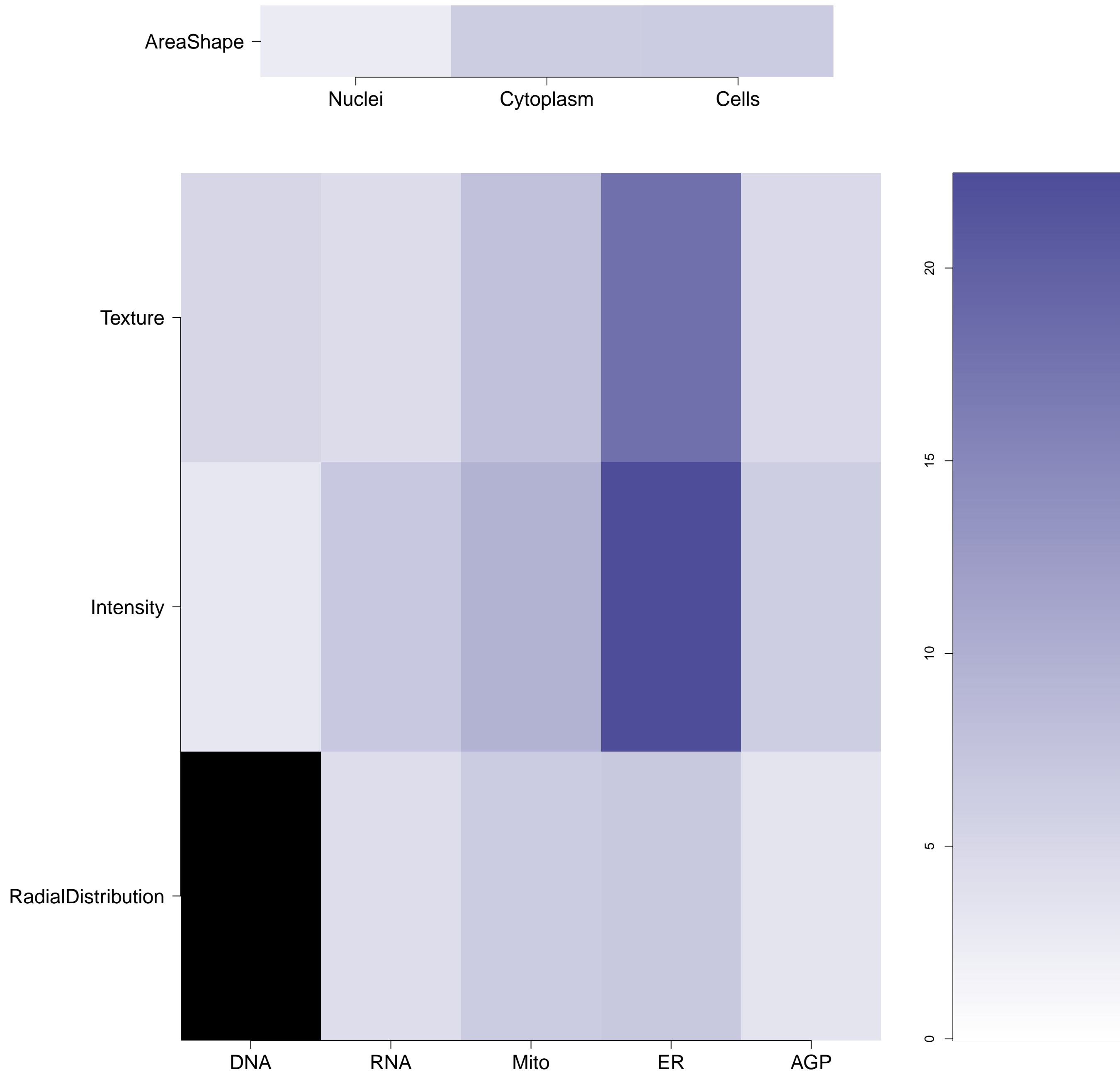


XBP1.WT.3 - in Canonical ER Stress/UPR

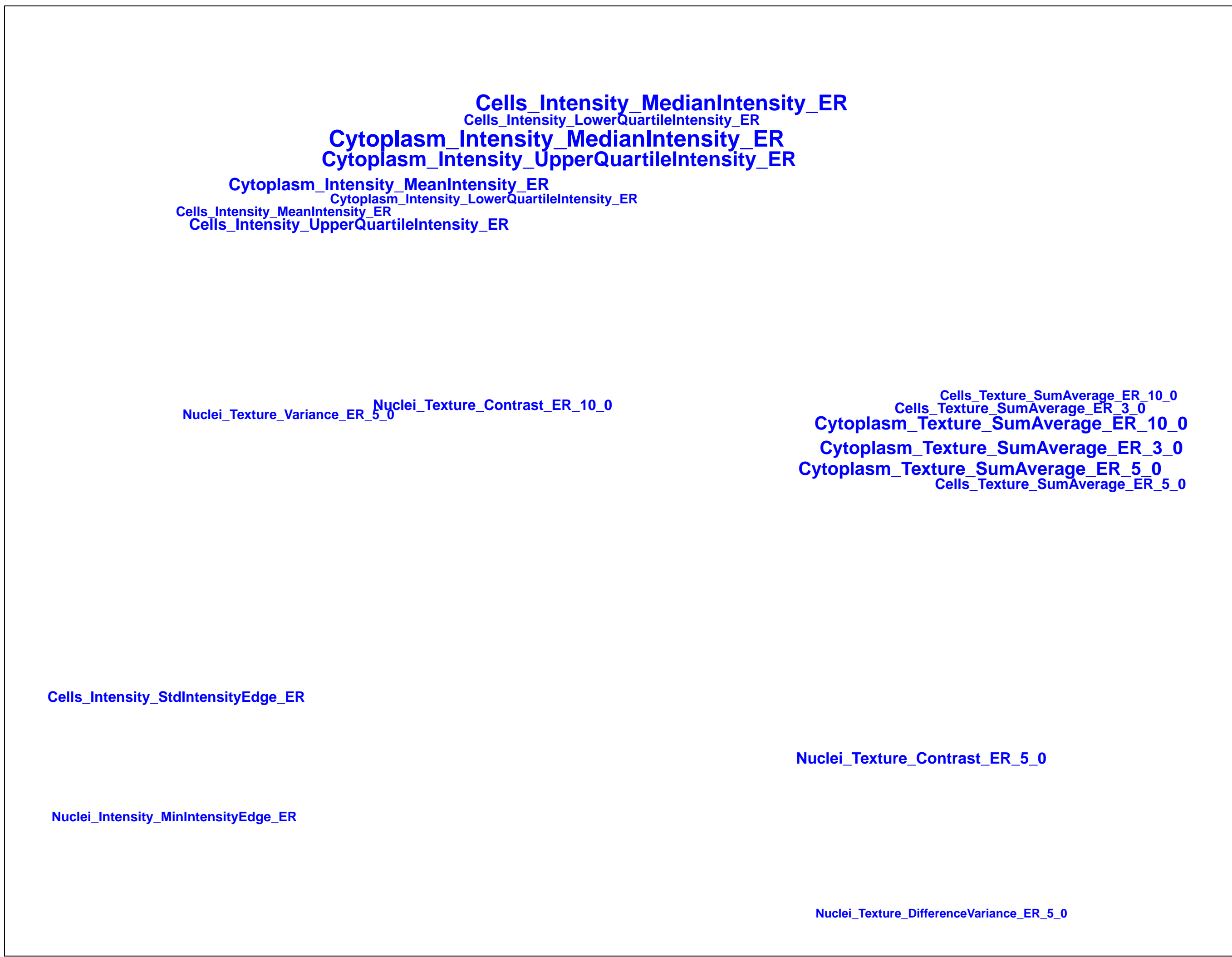
How similar is this gene to the other genes?



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

XBP1.WT.3 (41744)

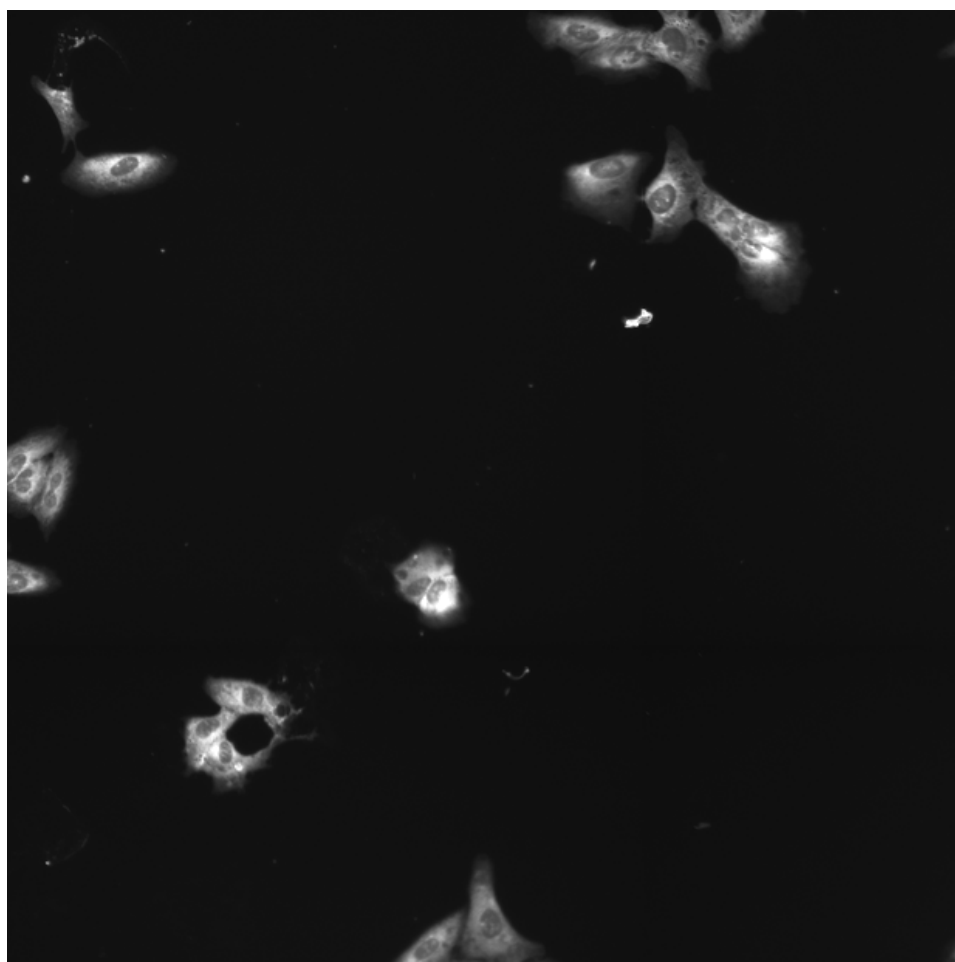
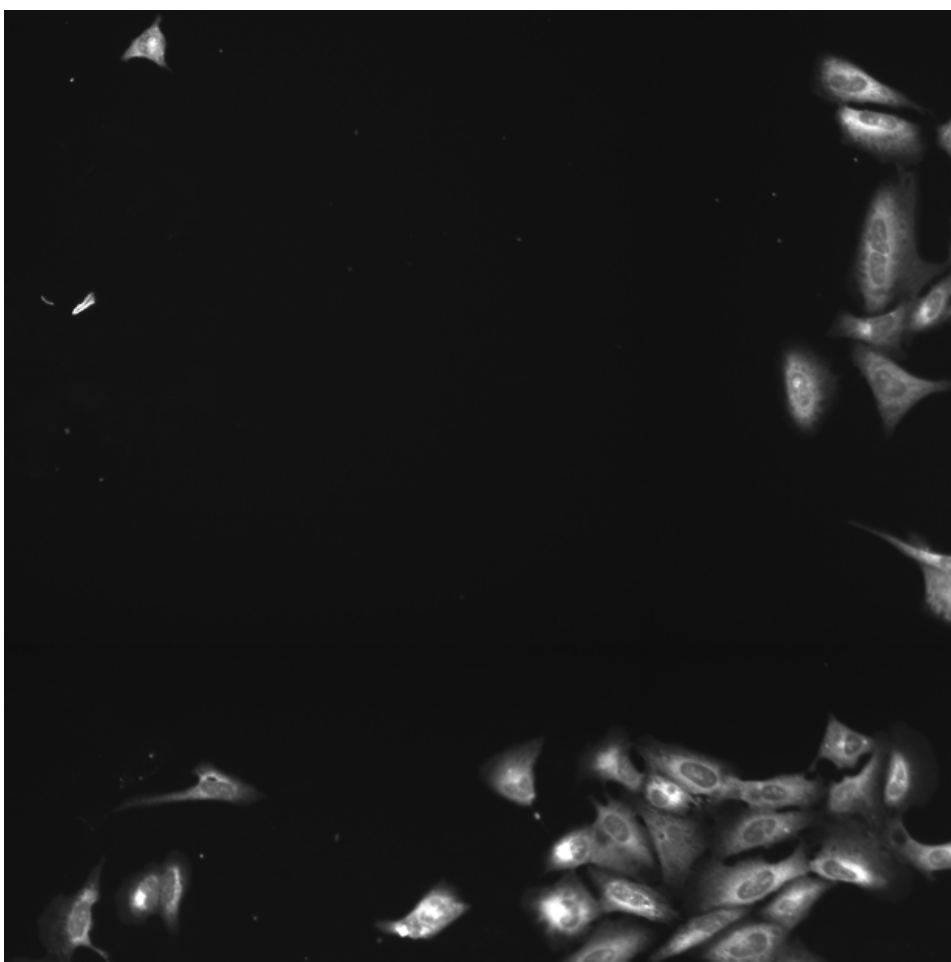
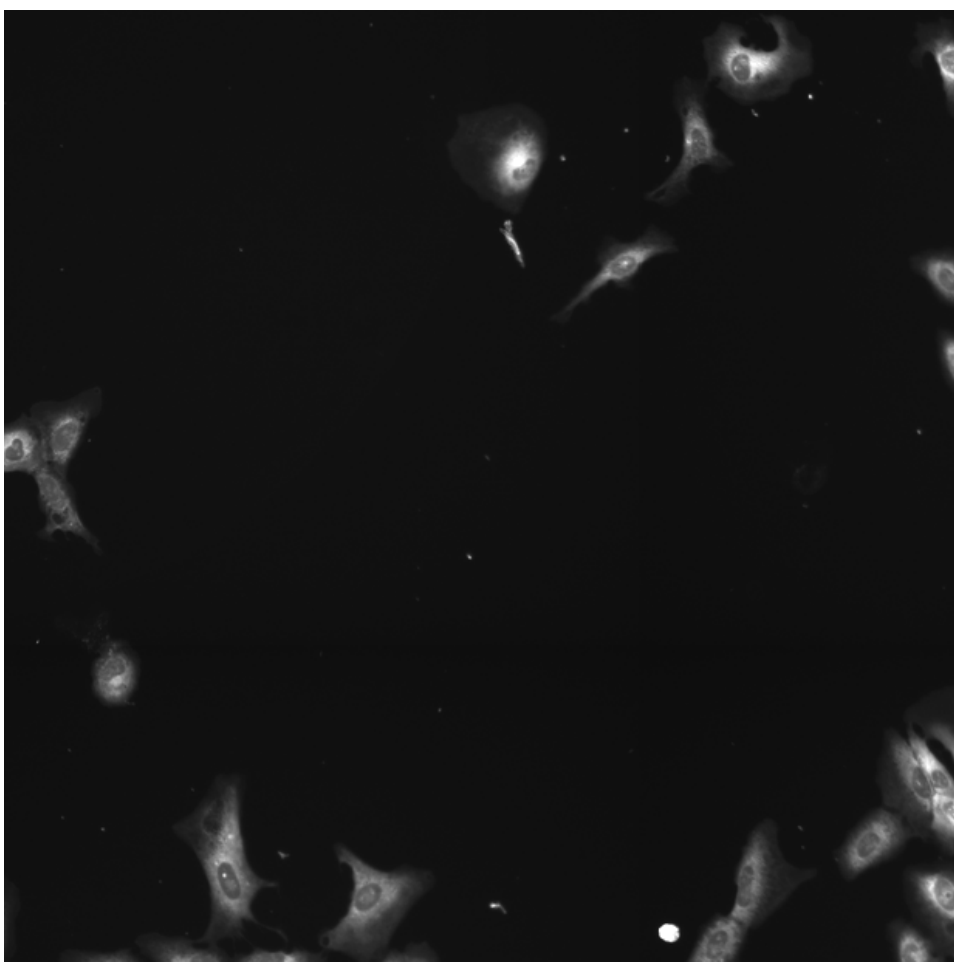
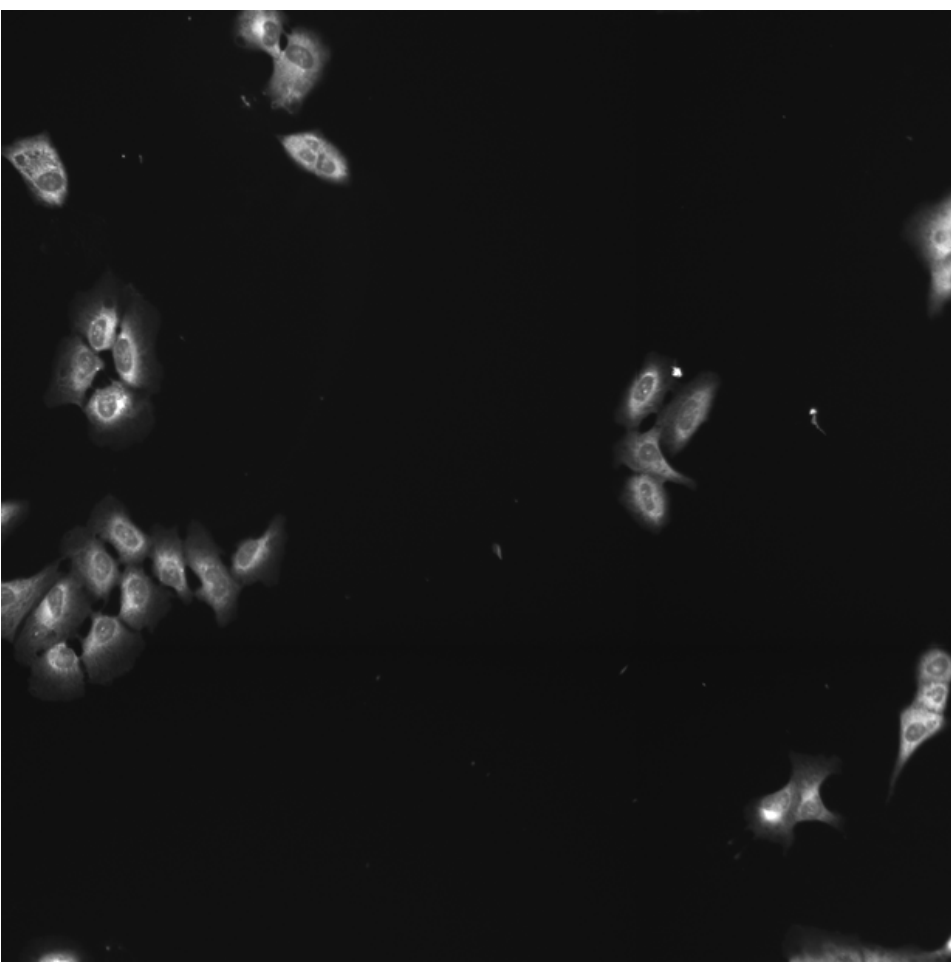
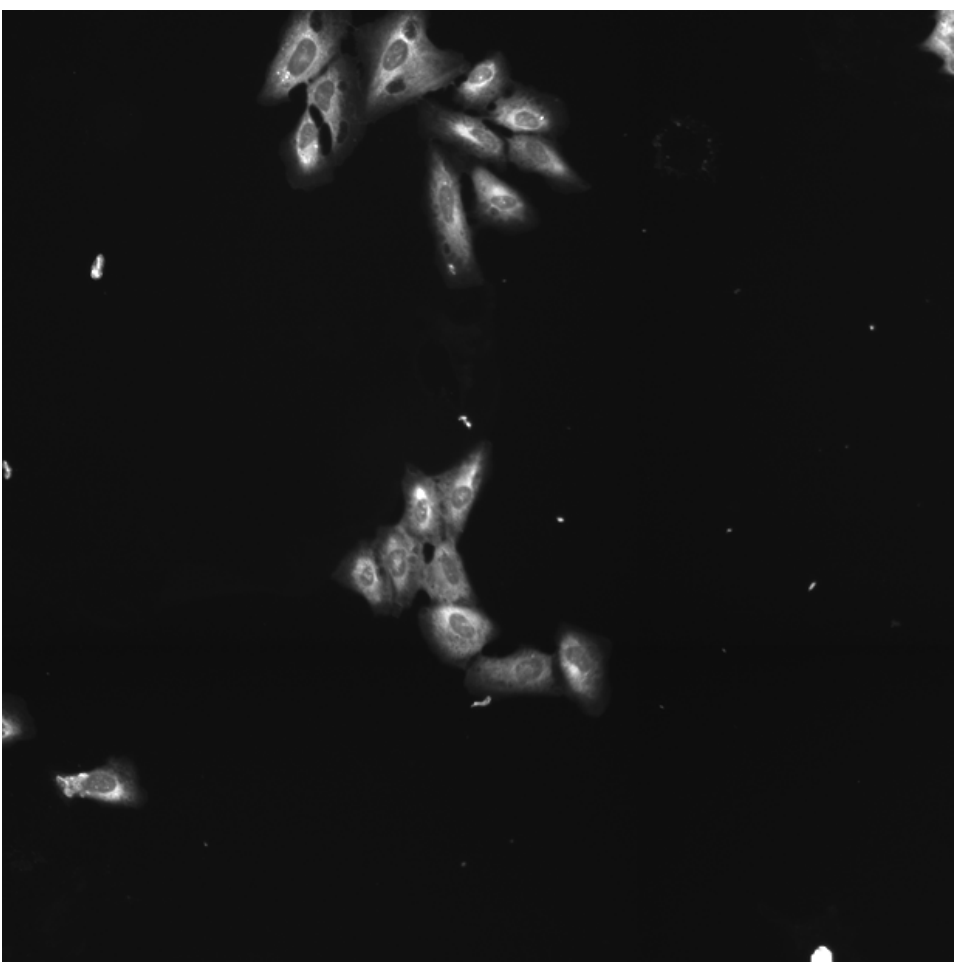
XBP1.WT.3 (41755)

XBP1.WT.3 (41756)

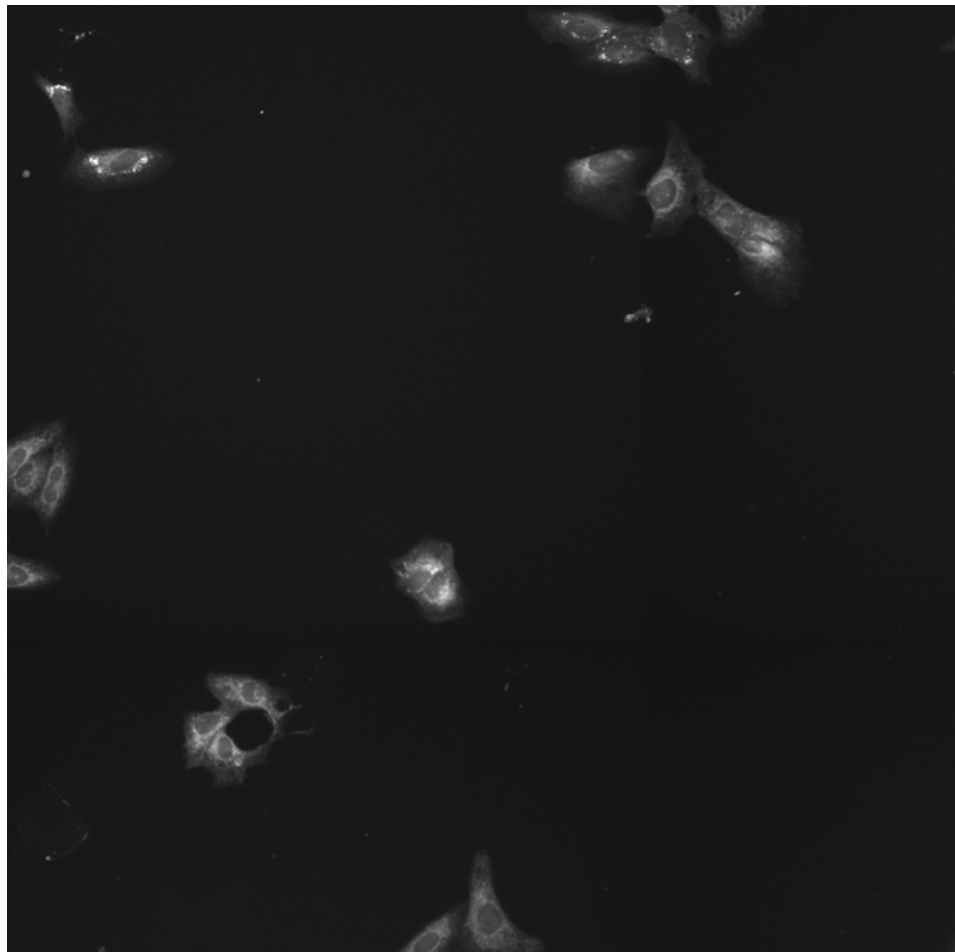
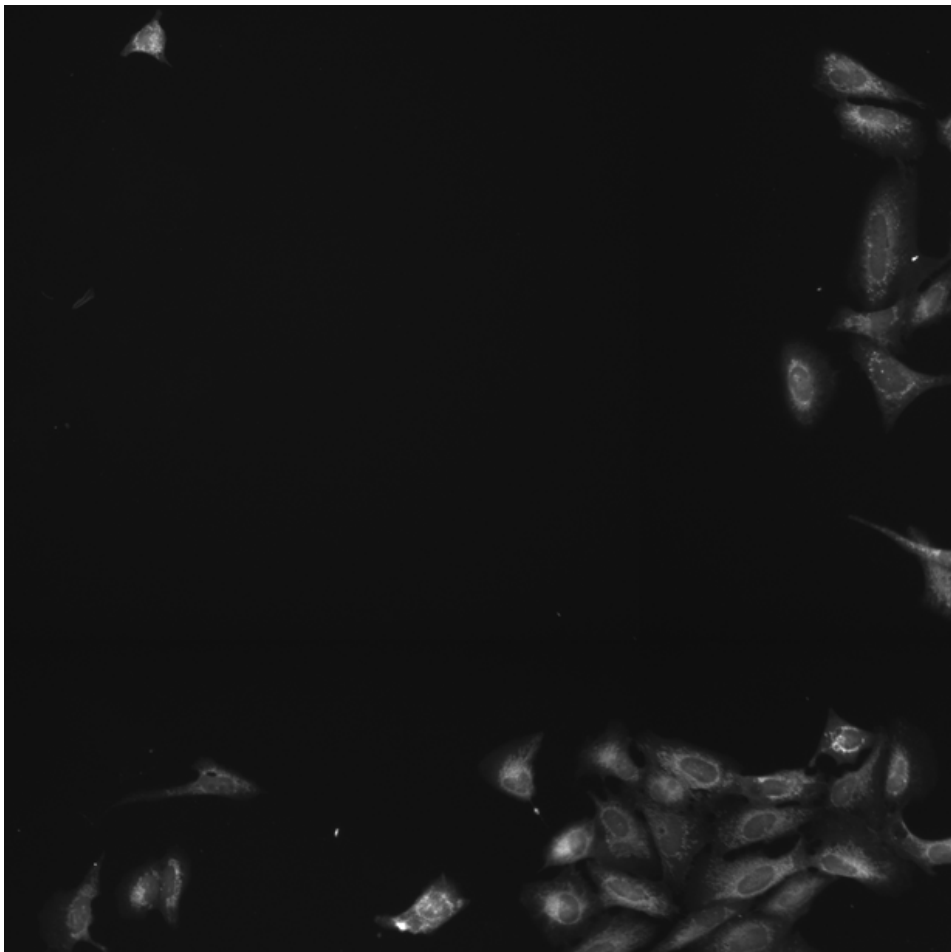
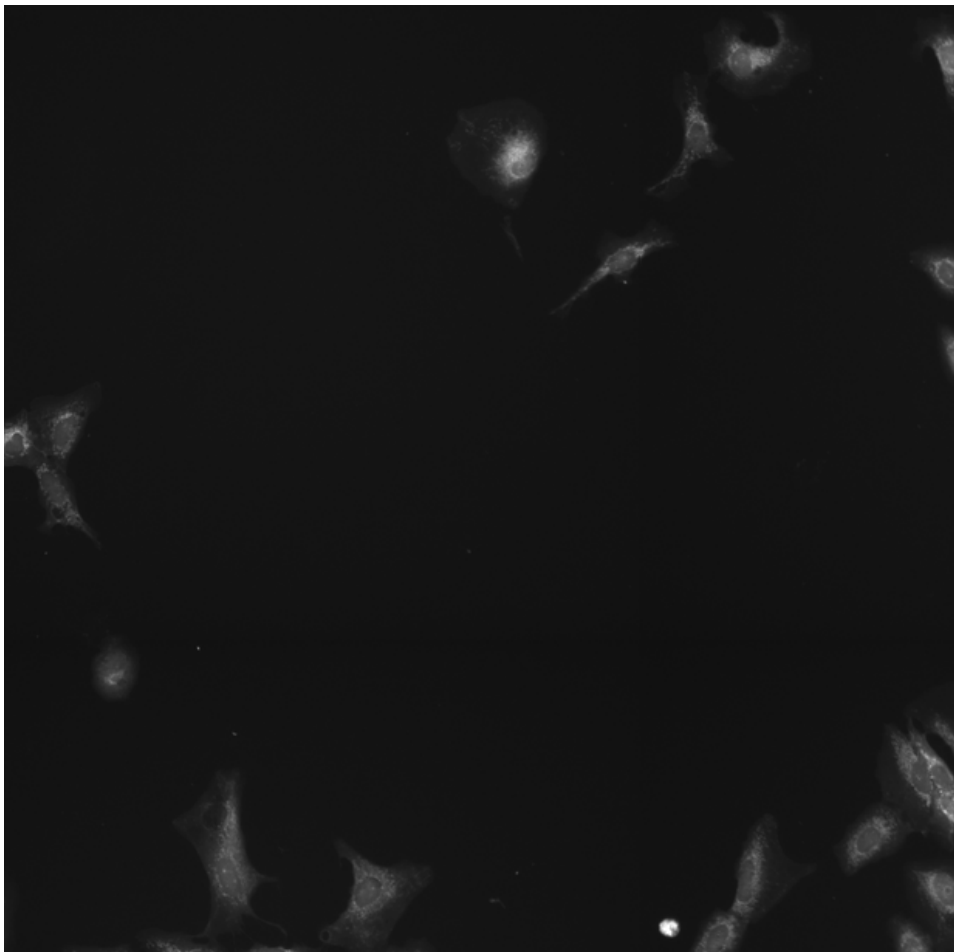
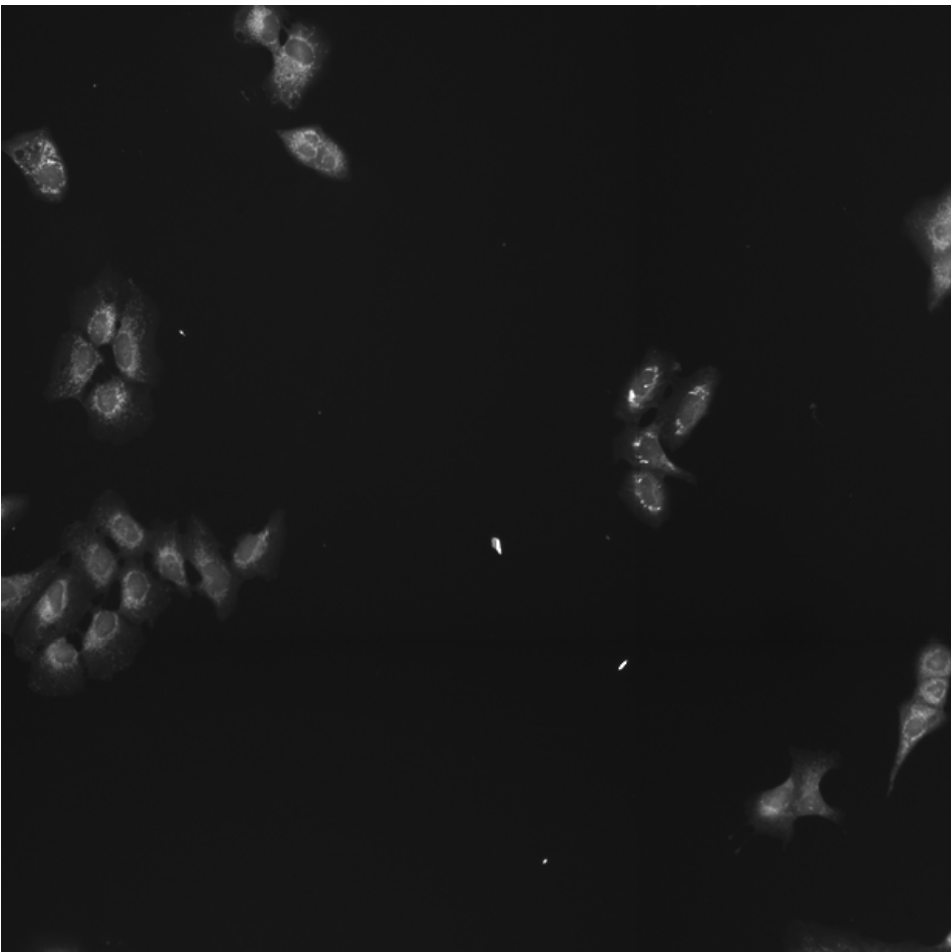
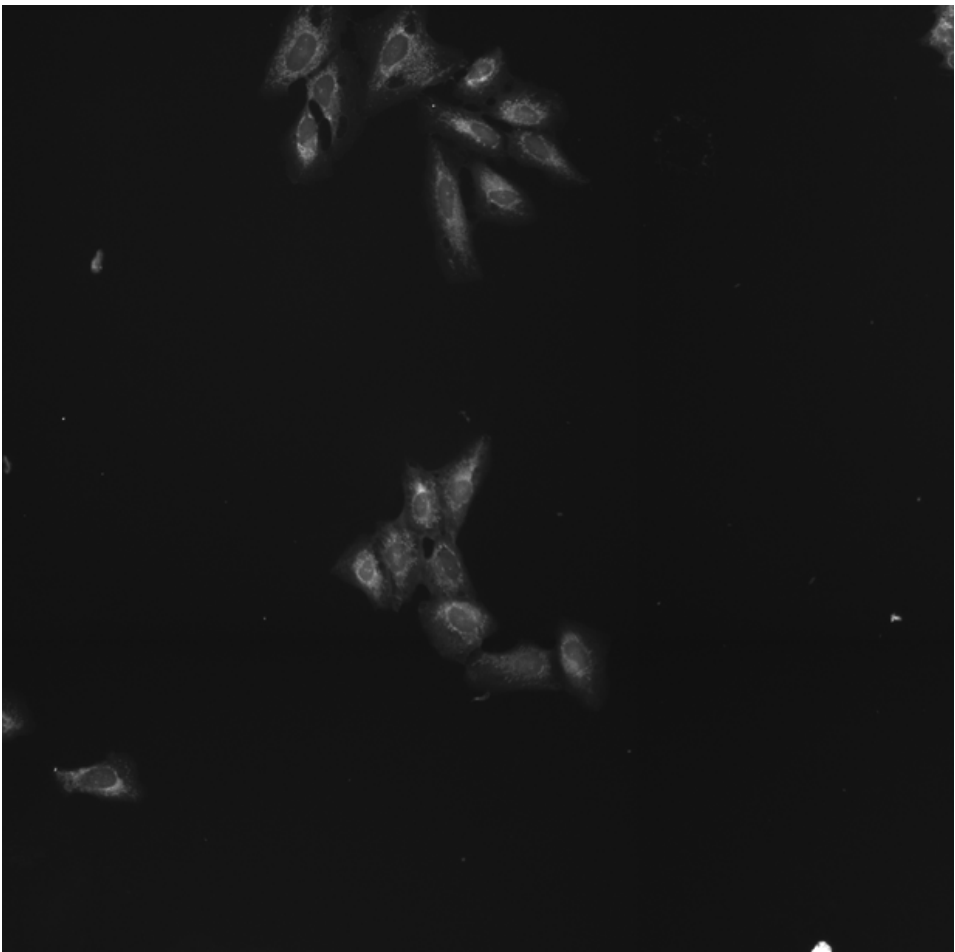
XBP1.WT.3 (41757)

XBP1.WT.3 (41754)

ER



Mito



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)	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-K48929882-001-05-1</div> <div>ASN 03067318</div> <div>AC1ML71R</div> <div>MLS000715091</div> <div>HMS2711E13</div> <div>ZINC12496877</div> <div>SMR000275070</div> <div>PubChem CID : 3169072</div>	<chem>Cc1ccc(cc1)C(=O)Nc2ccccc2</chem>	NA (in 1 replicates)	0.52	NA					<div>Cytoplasm_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_Intensity_MassWeightedEdge_Min</div> <div>Nuclei_Intensity_IntegratedIntensityEdge_ER</div> <div>Nuclei_Intensity_MassDisplacement_DNA</div> <div>Nuclei_Texture_Entropy_ER_3.0</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div> <div>Cells_AreaShape_Zernike_3.0</div> <div>Cytoplasm_Texture_InfoMean2_ER_5.0</div> <div>Cytoplasm_AreaShape_Zernike_4.2</div> <div>Cytoplasm_AreaShape_Zernike_3.1</div>	Total number of assays tested in: 622.
<div>BRD-K67502058-001-01-9</div> <div>PubChem CID : 54646068</div>	<chem>Cc1ccc(cc1)C(=O)Nc2ccccc2</chem>	NA (in 1 replicates)	-0.53	0.305					<div>Nuclei_Texture_DifferenceEntropy_ER_3.0</div> <div>Cytoplasm_Intensity_MassWeightedEdge_ER</div> <div>Nuclei_Texture_DifferenceEntropy_ER_3.0</div> <div>Nuclei_Texture_DifferenceEntropy_Min_3.0</div> <div>Nuclei_Texture_Content_Min_3.0</div> <div>Cells_Intensity_IntegratedIntensity_Min</div> <div>Cytoplasm_Intensity_MassWeightedEdge_Min</div> <div>Cells_RadiiDistribution_MeanFreq_AGP_3.0</div> <div>Nuclei_Texture_AngularSecondMoment_AGP_3.0</div> <div>Cells_RadiiDistribution_MeanFreq_Min_3.0</div> <div>Nuclei_AreaShape_Zernike_3.0</div> <div>Cytoplasm_AreaShape_ParetoFactor</div> <div>Nuclei_Texture_Entropy_ER_3.0</div> <div>Cells_RadiiDistribution_MeanFreq_Min_3.0</div> <div>Nuclei_AreaShape_Zernike_3.0</div> <div>Cells_Neighbors_PercentTouching_Adjacent</div> <div>Cytoplasm_AreaShape_Zernike_4.2</div>	Total number of assays tested in: 39.