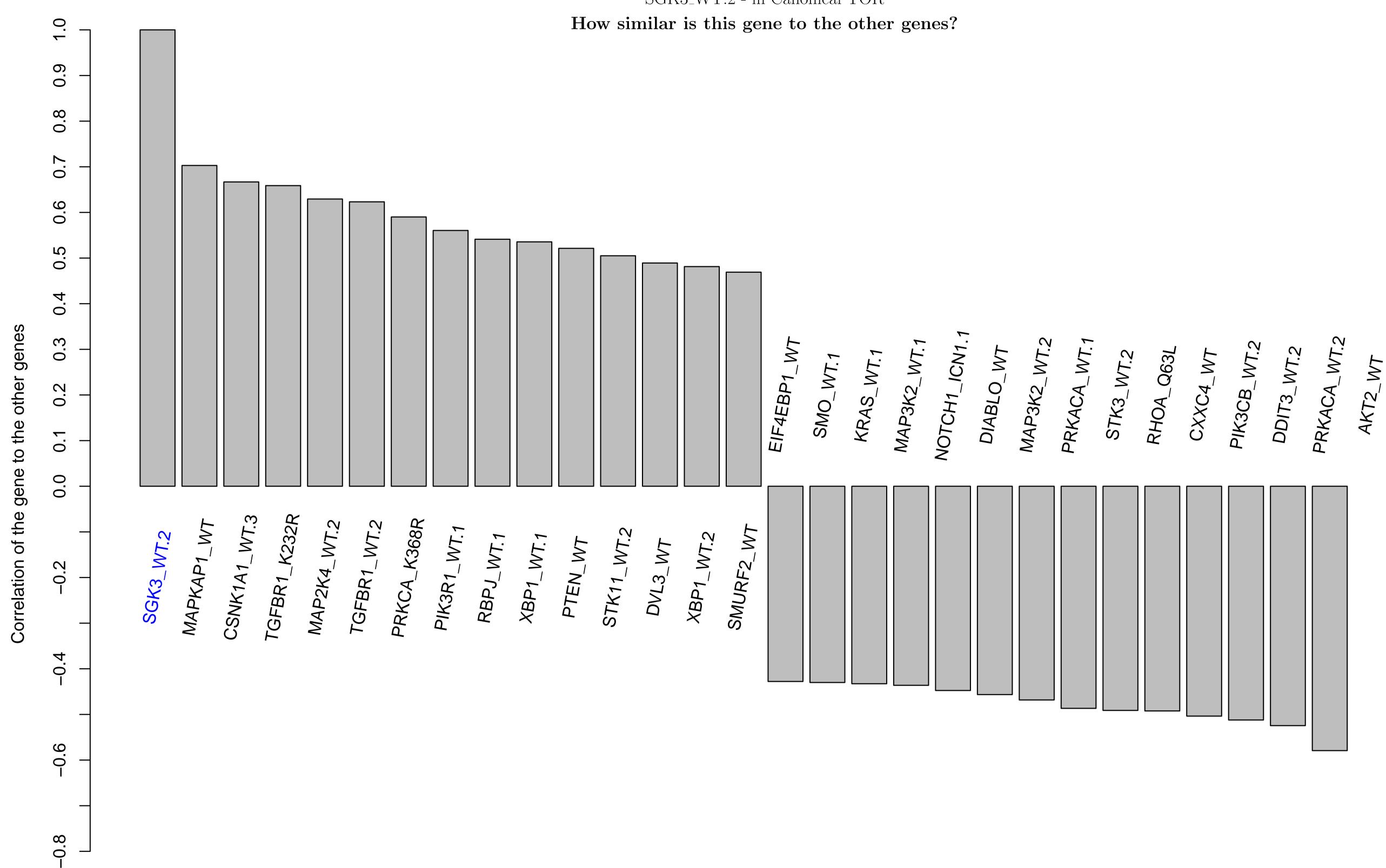
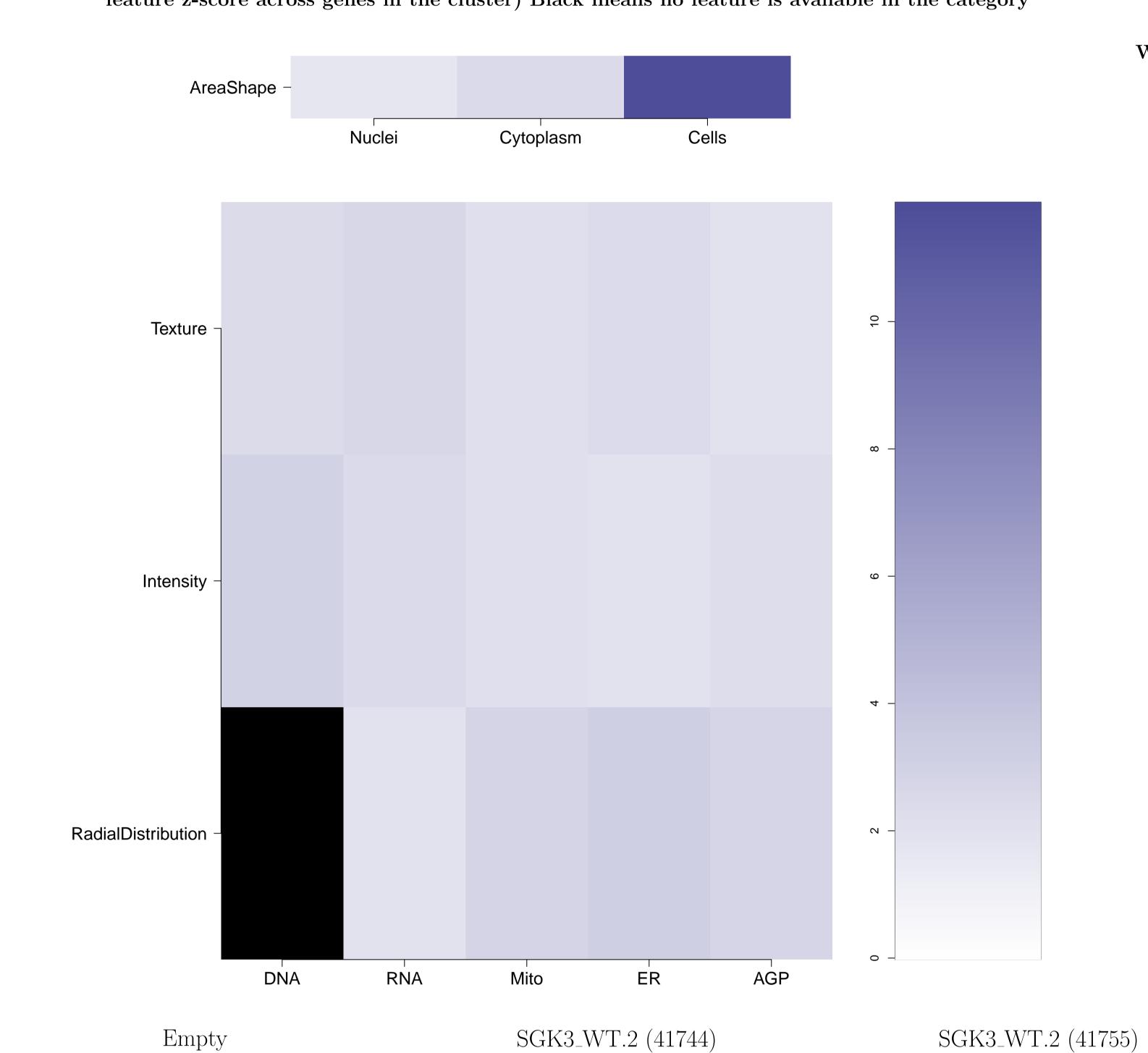
CONFIDENTIAL, contact the Imaging Platform to collaborate on the findings herein SGK3\_WT.2 - in Canonical TOR



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



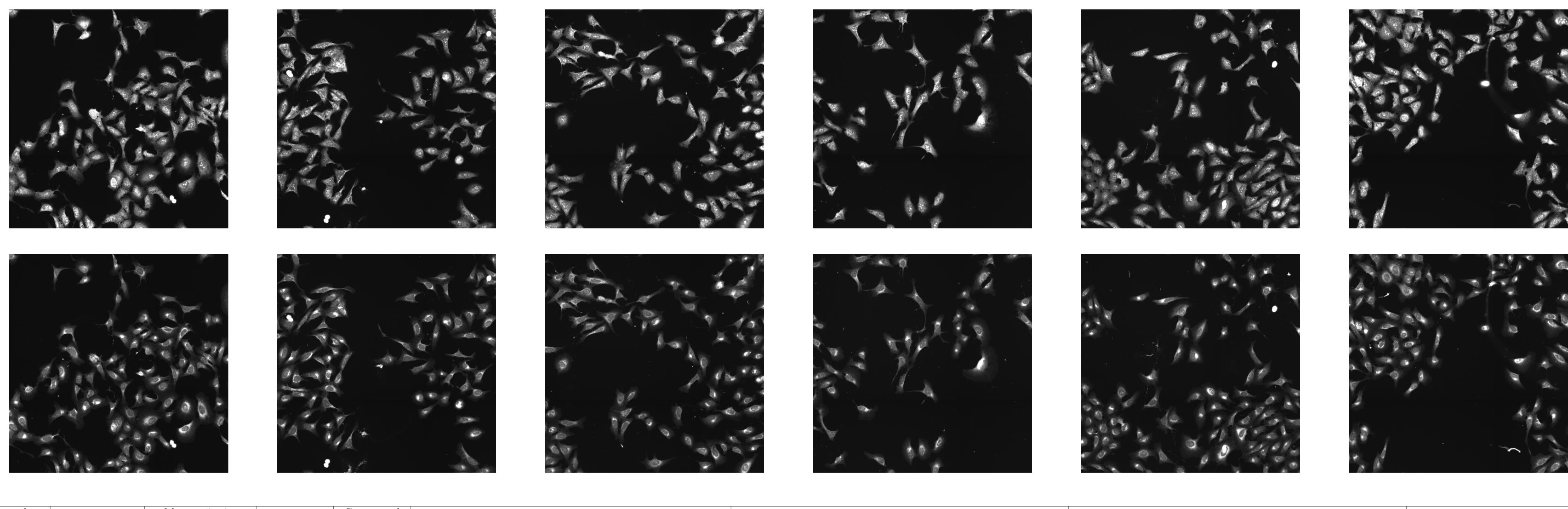
Which individual morphological features are distinguishing in the gene relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

 $SGK3_WT.2 (41757)$ 

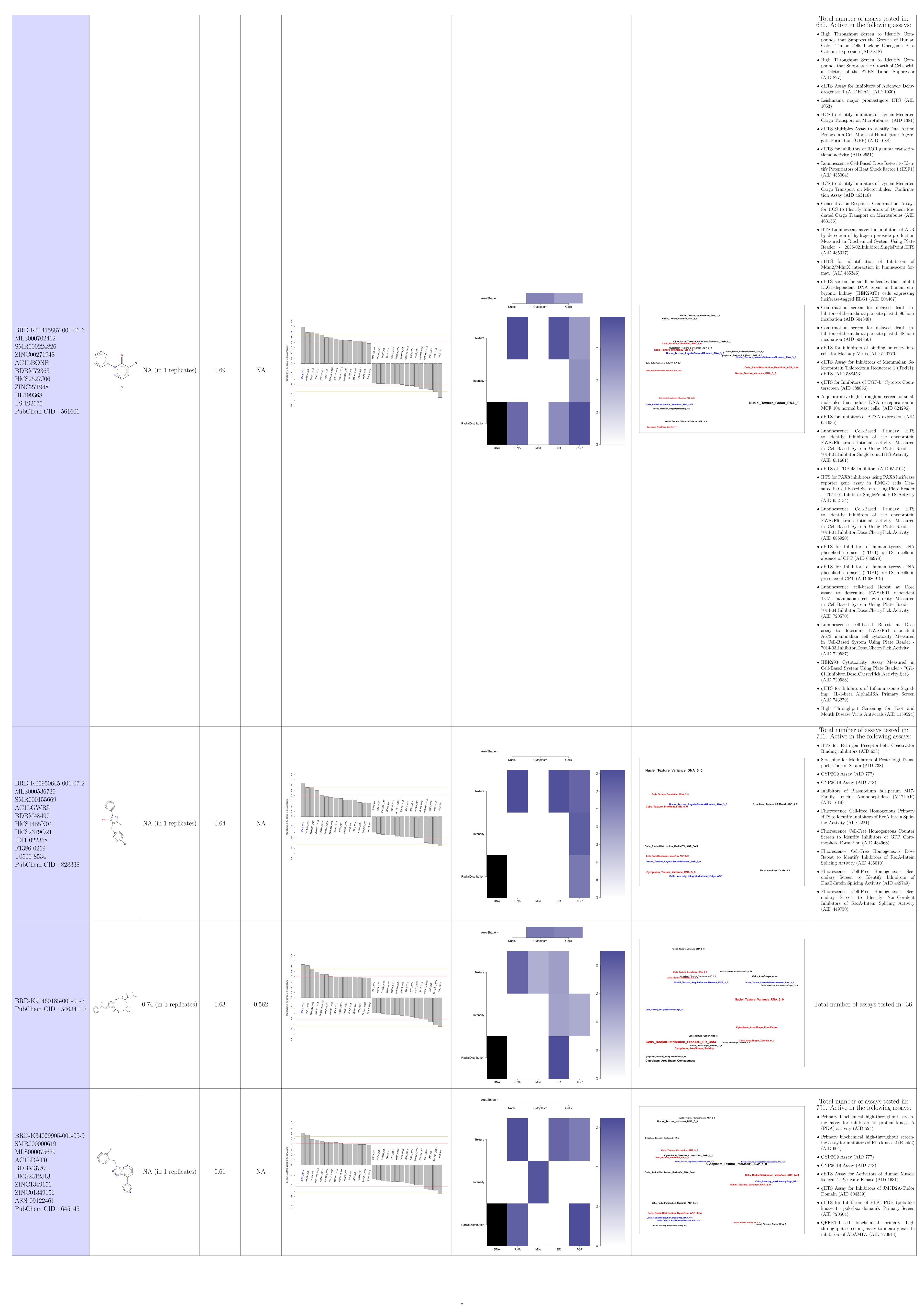
 $SGK3_WT.2 (41754)$ 

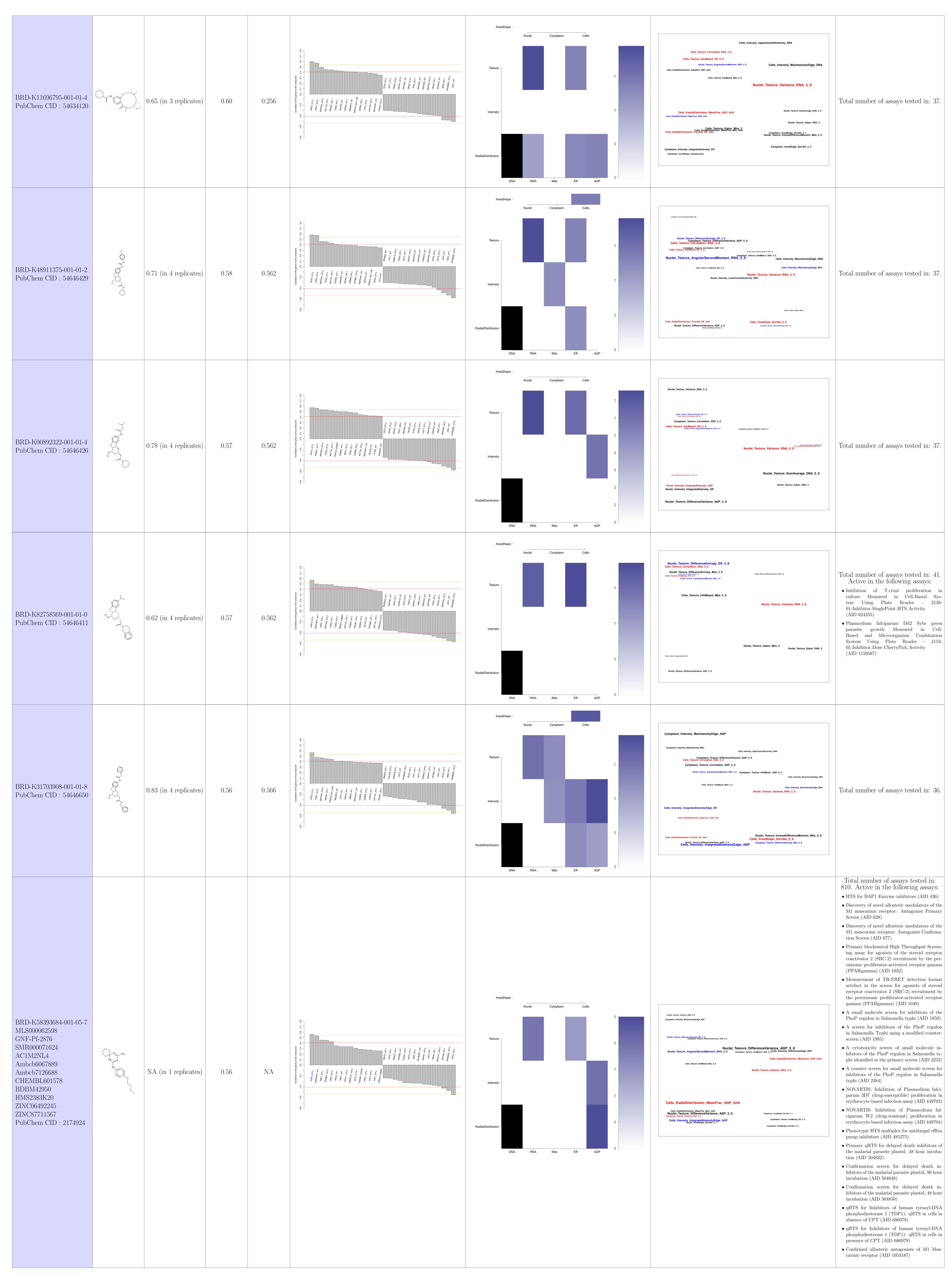


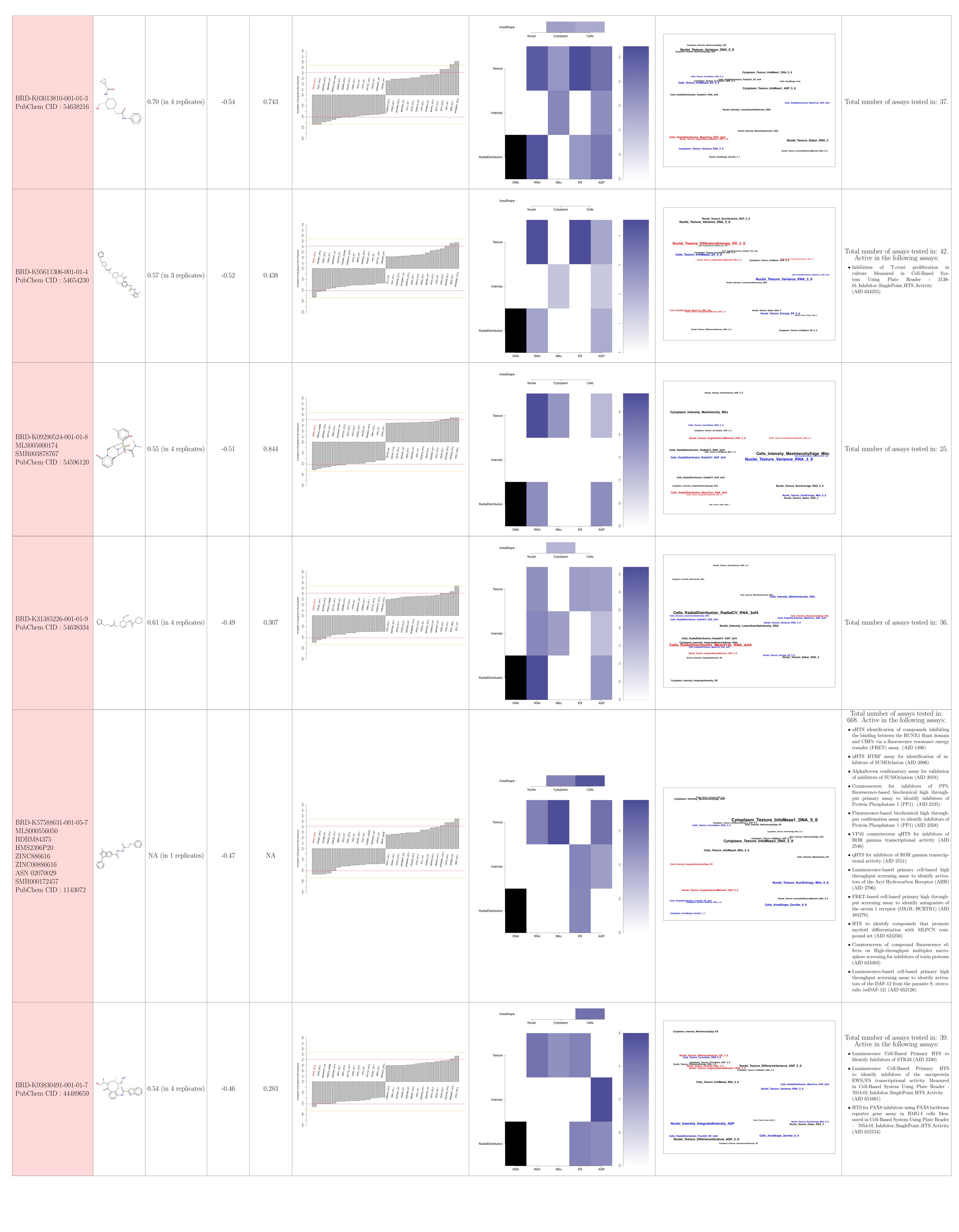
 $SGK3_WT.2 (41756)$ 



positively/negatively replicate correlation correlated with the cluster is 0.51)  the gene item of the gene correlation is 0.51)  the gene correlation to an the gene correlation item of the gene correlation is 0.51)  the gene correlation to an the gene correlation item of the gene correlation to an the gene correlation correlation to an the gene correlation correlation to an the gene correlation to an the gene correlation correlation to an the gene correlation correlation to an the gene correlation correlati		Chemical structure		Correlation between compound the gene	gene using L1000	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)	I Common distinctiisning teature categories in the compound and	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	the compound was tested;
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AreaShape -Cytoplasm Nuclei\_Texture\_SumVariance\_AGP\_3\_0
Nuclei\_Texture\_Variance\_DNA\_5\_0 Nuclei\_Texture\_AngularSecondMoment\_RNA\_3\_0
Nuclei\_Texture\_InverseDifferenceMoment\_RNA\_3\_0 BRD-K91229058-001-01-9 MLS003129166 Cells\_RadialDistribution\_MeanFrac\_AGP\_2of4 0.52 (in 7 replicates) Total number of assays tested in: 221. SMR001833612 PubChem CID : 44505433 Nuclei\_Texture\_Variance\_RNA\_3\_0 Nuclei\_Intensity\_IntegratedIntensityEdge\_ER Intensity -Cells\_RadialDistribution\_RadialCV\_AGP\_3of4 Nuclei\_Texture\_SumAverage\_DNA\_5\_0 Nuclei\_Texture\_Gabor\_Mito\_5

Nuclei\_Texture\_Entropy\_ER\_5\_0
Nuclei\_Texture\_Gabor\_RNA\_3 Nuclei\_Texture\_AngularSecondMoment\_AGP\_5\_0 Nuclei\_Texture\_InverseDifferenceMoment\_Mito\_5\_0 RadialDistribution -Cells\_Intensity\_IntegratedIntensityEdge\_AGP ER AGP Mito

