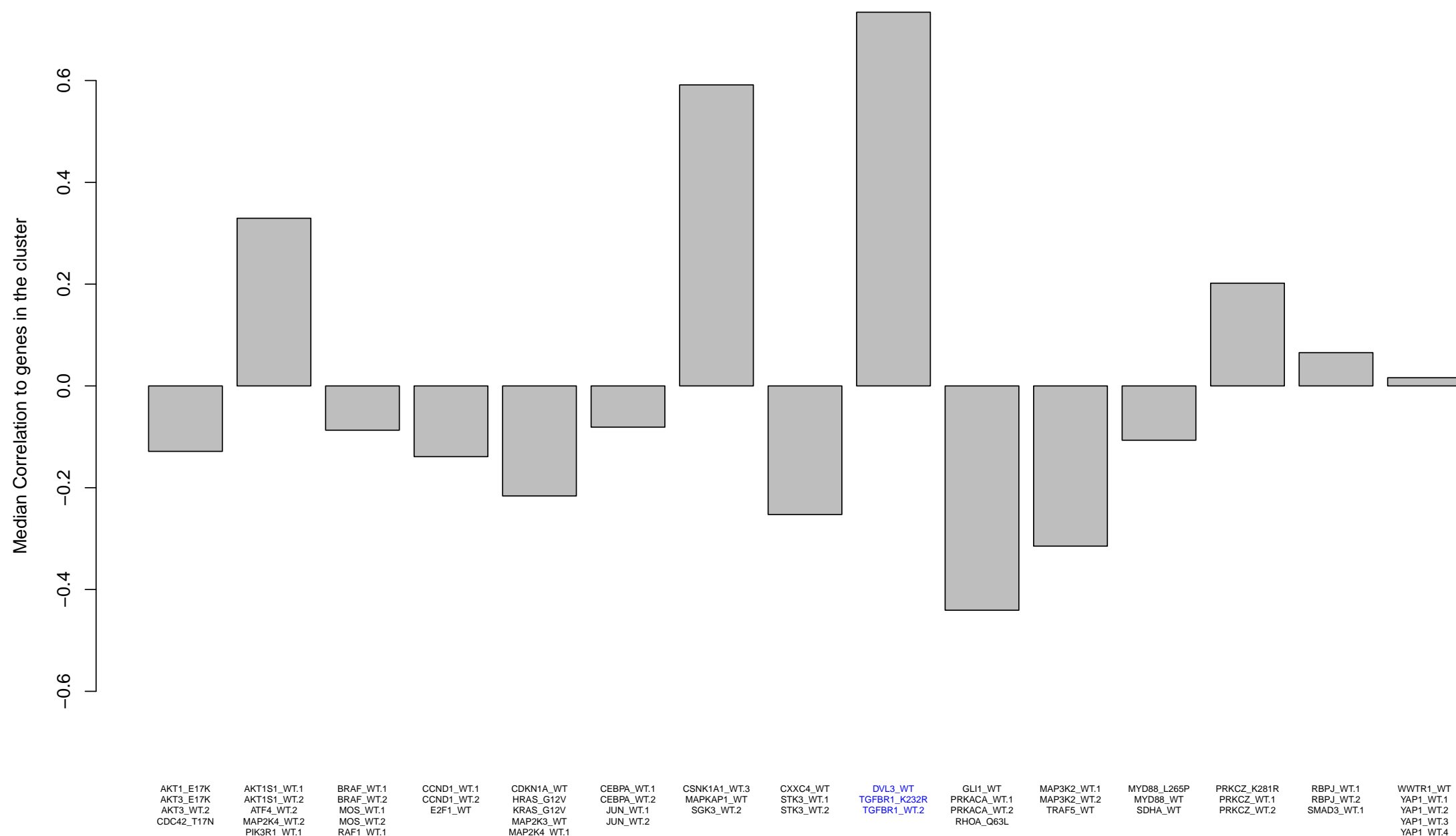


How similar is this cluster to the other clusters?

Genes in the cluster along with the pathways as annotated by experts

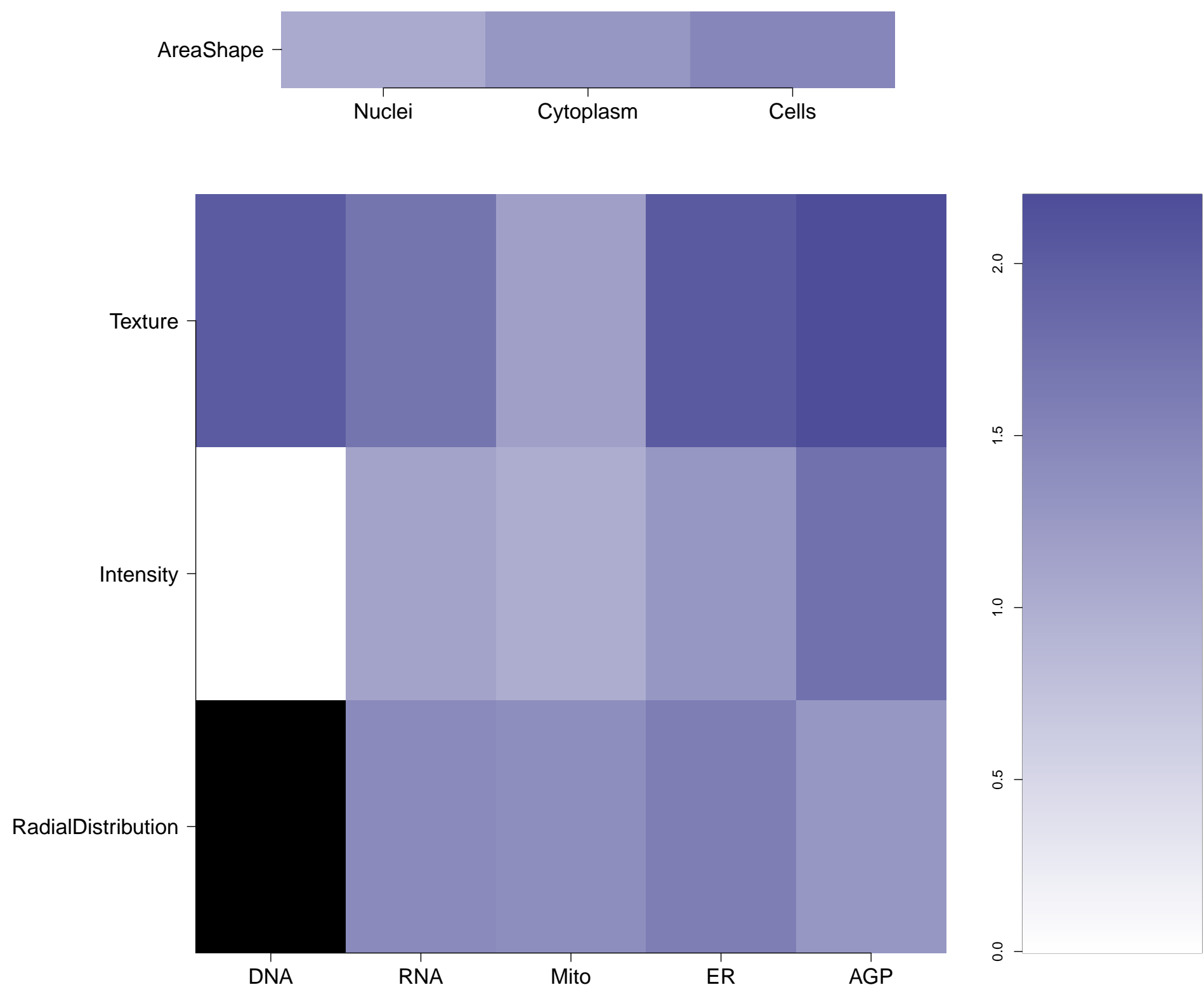
Expert Annotation		
Treatment	Pathway	Regulation Type
TGFBRI.K232R	Canonical TGFbeta	Inhibitor
TGFBRI.WT.2	Canonical TGFbeta	Activator
DVL3.WT	Canonical WNT	Activator



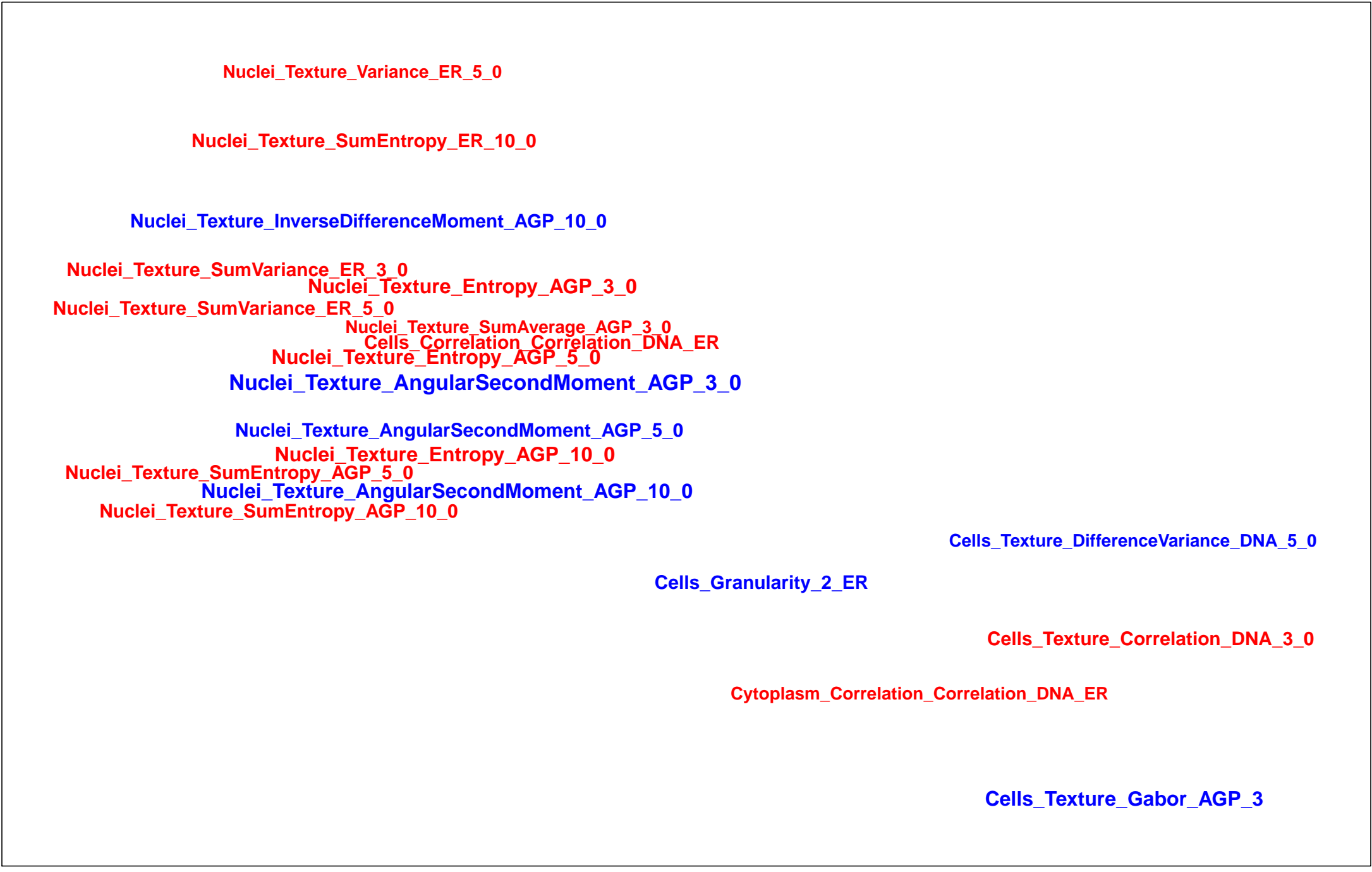
Top 5 genes negatively correlated to the cluster

Expert Annotation			Mean Correlation	Standard Deviation
Treatment	Pathway	Regulation Type		
SMO.WT.1	Hedgehog	Activator	-0.58	0.06
DDIT3.WT.2	Canonical ER Stress/UPR	Activator	-0.51	0.04
PRKACA.WT.2	Canonical PKA	Activator	-0.47	0.16
NFKBIA.WT	Canonical NFkB	Inhibitor	-0.47	0.21
DIABLO.WT	Canonical Apoptosis	Inhibitor	-0.43	0.10

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.



How strongly are genes within the cluster correlated?

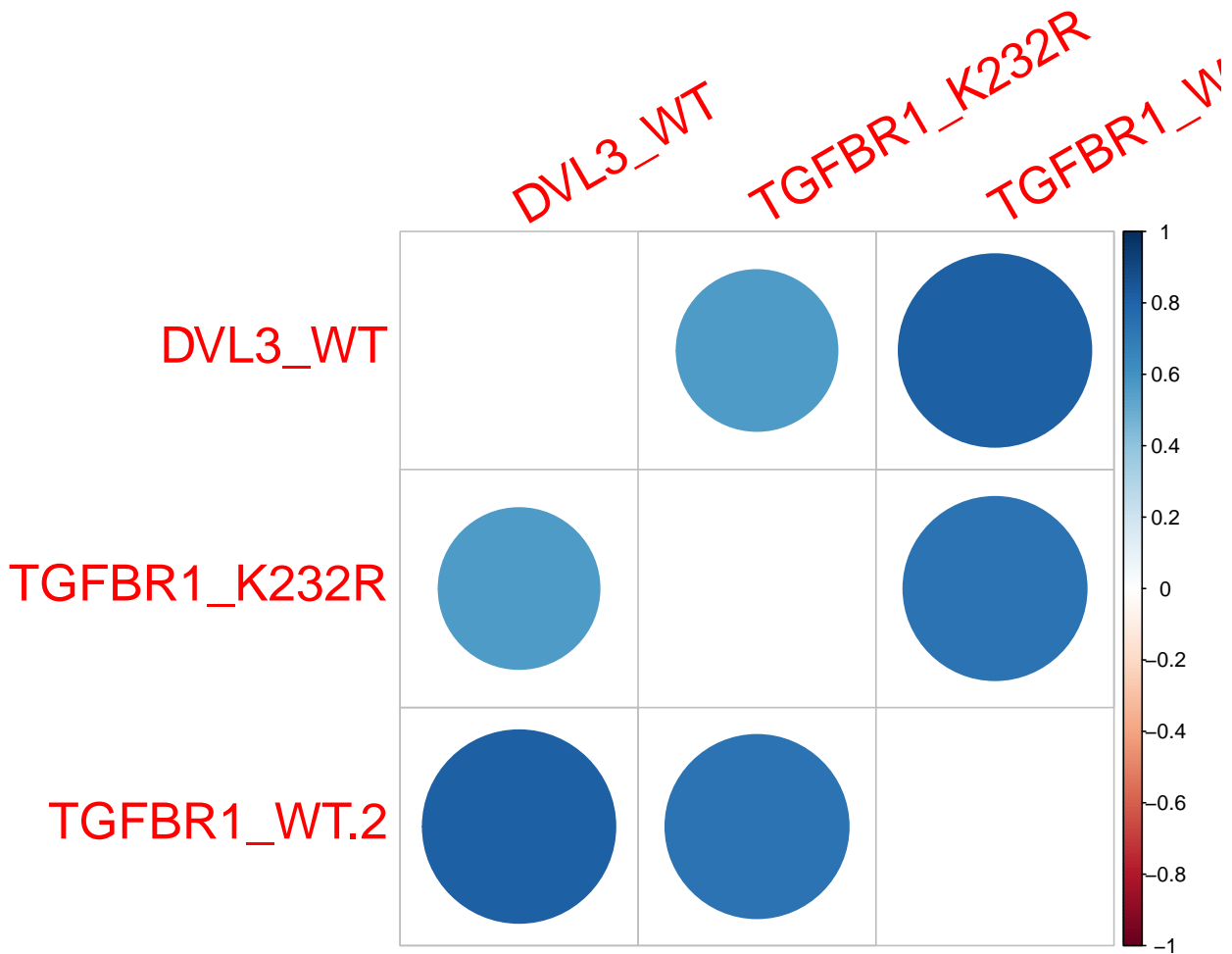


Plate : 41744 - Genes in the Cluster (Channels are sorted based on their dominance in the grid plot)

DVL3.WT

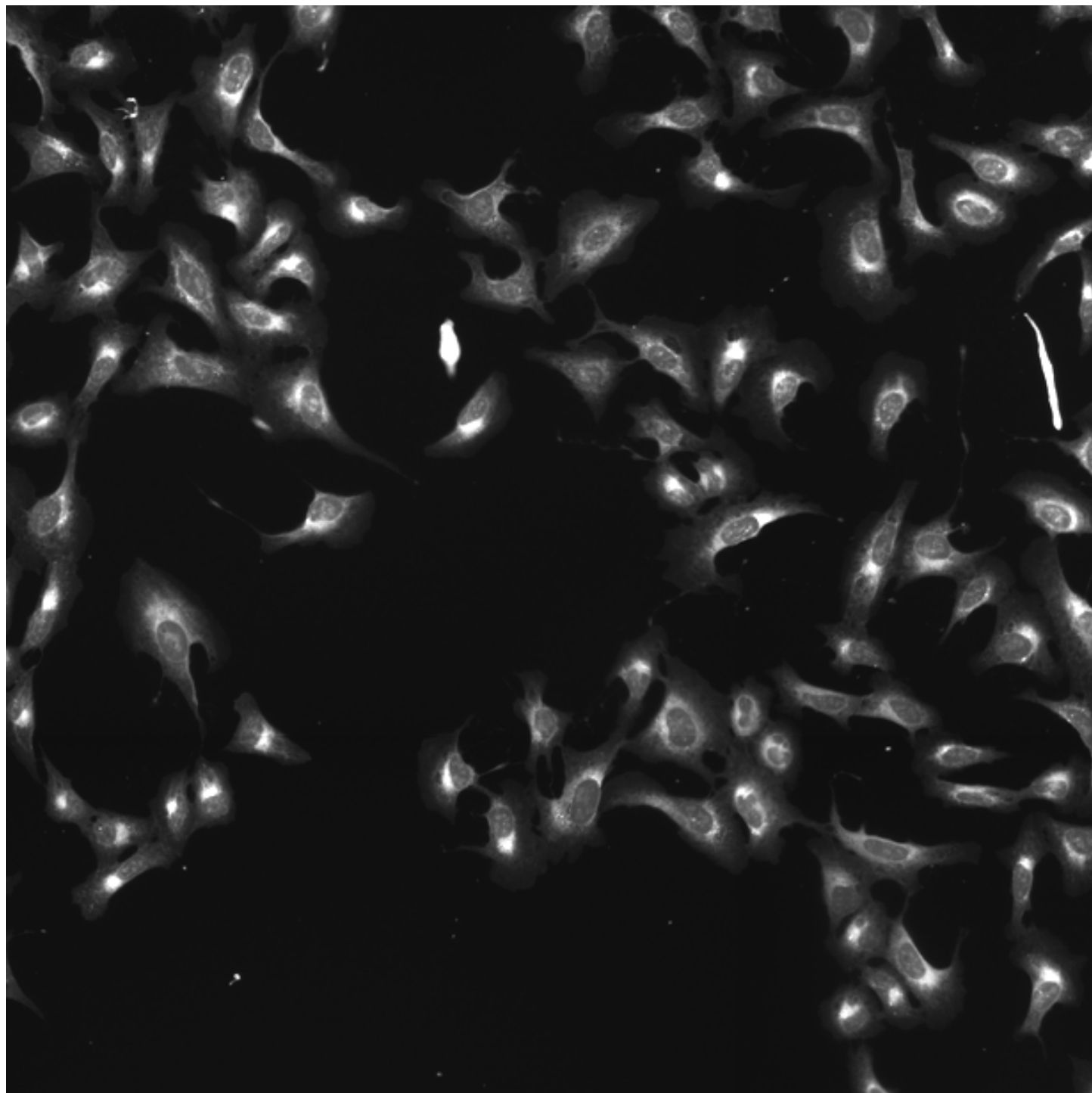
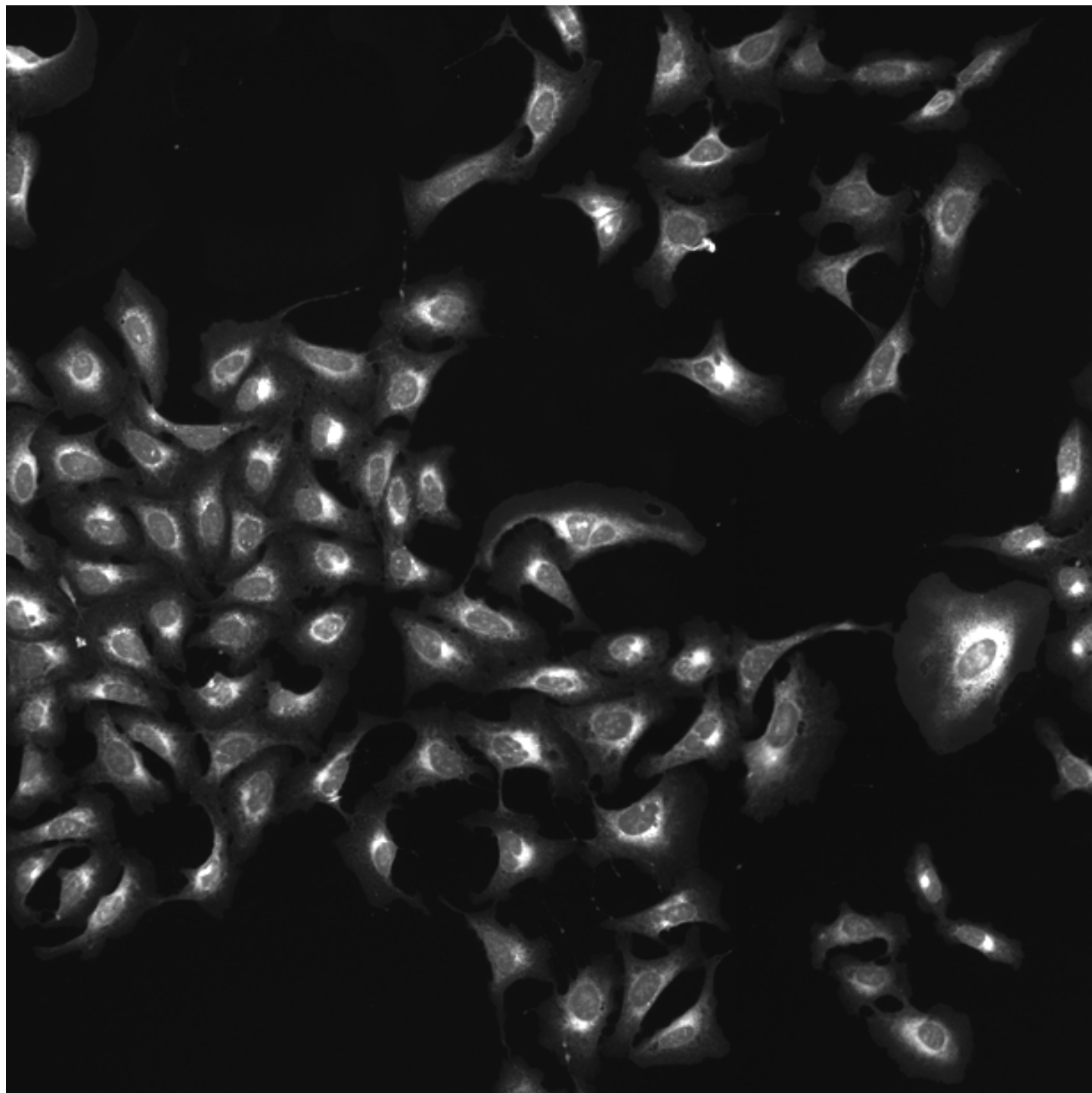
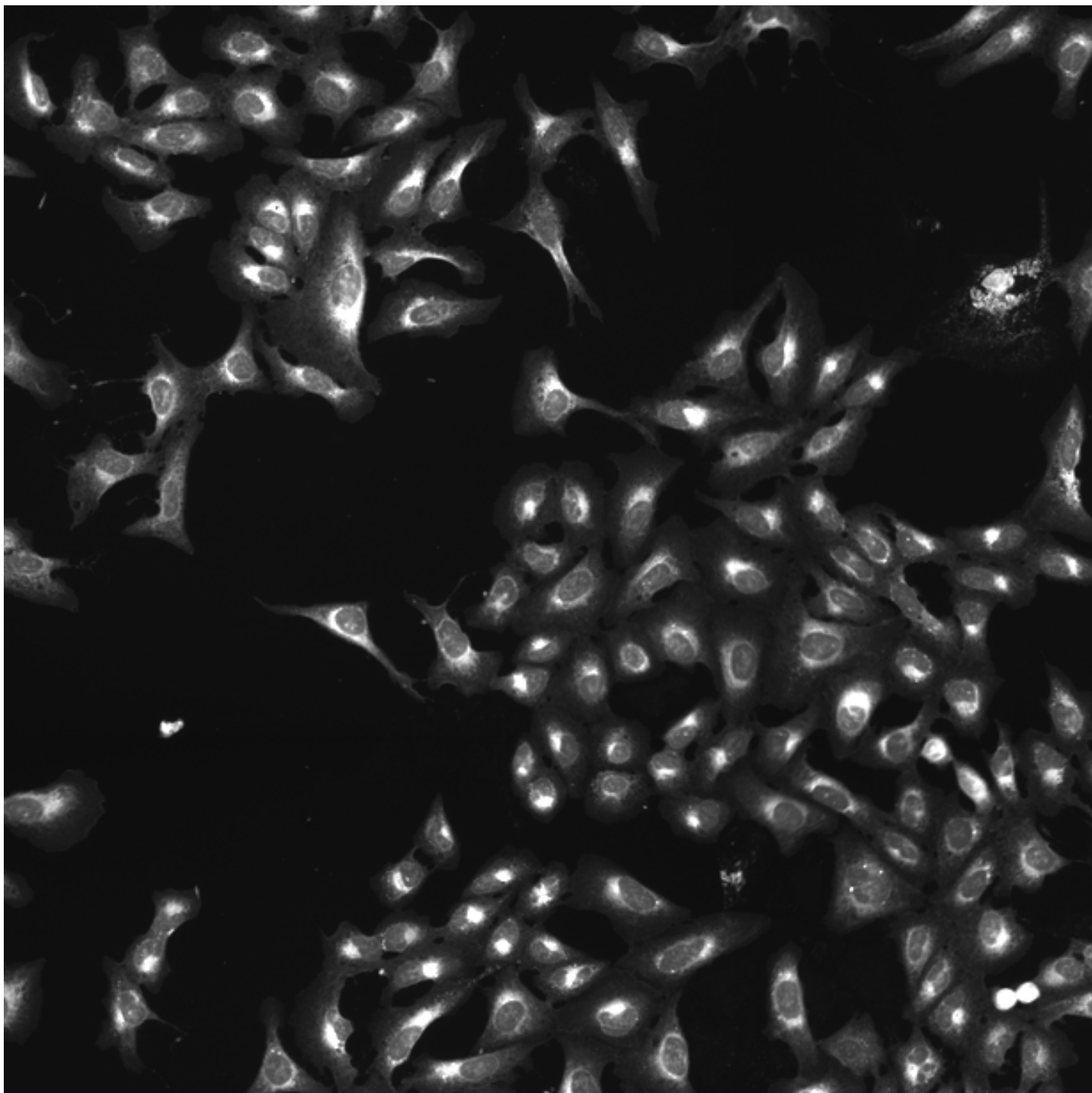
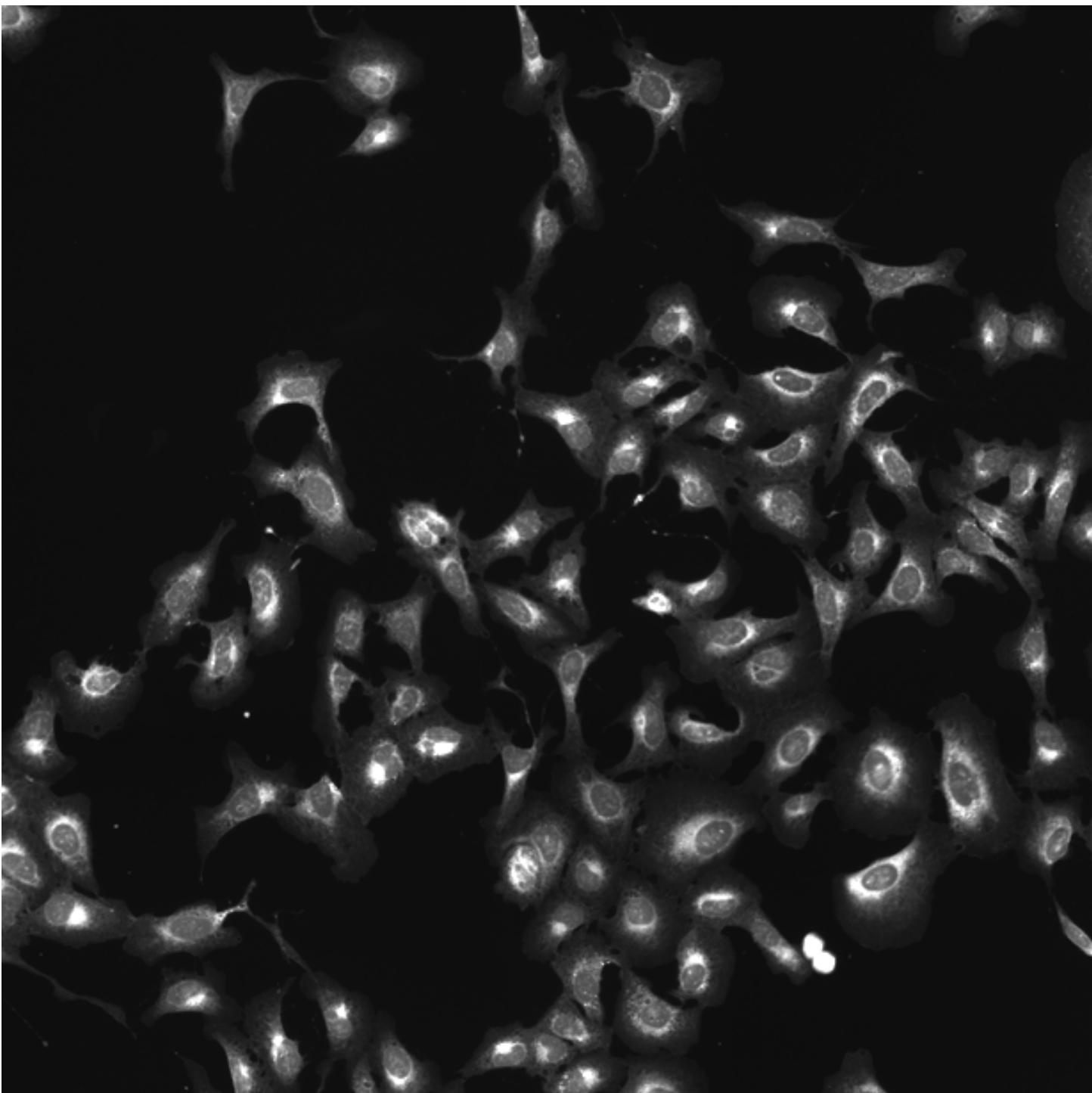
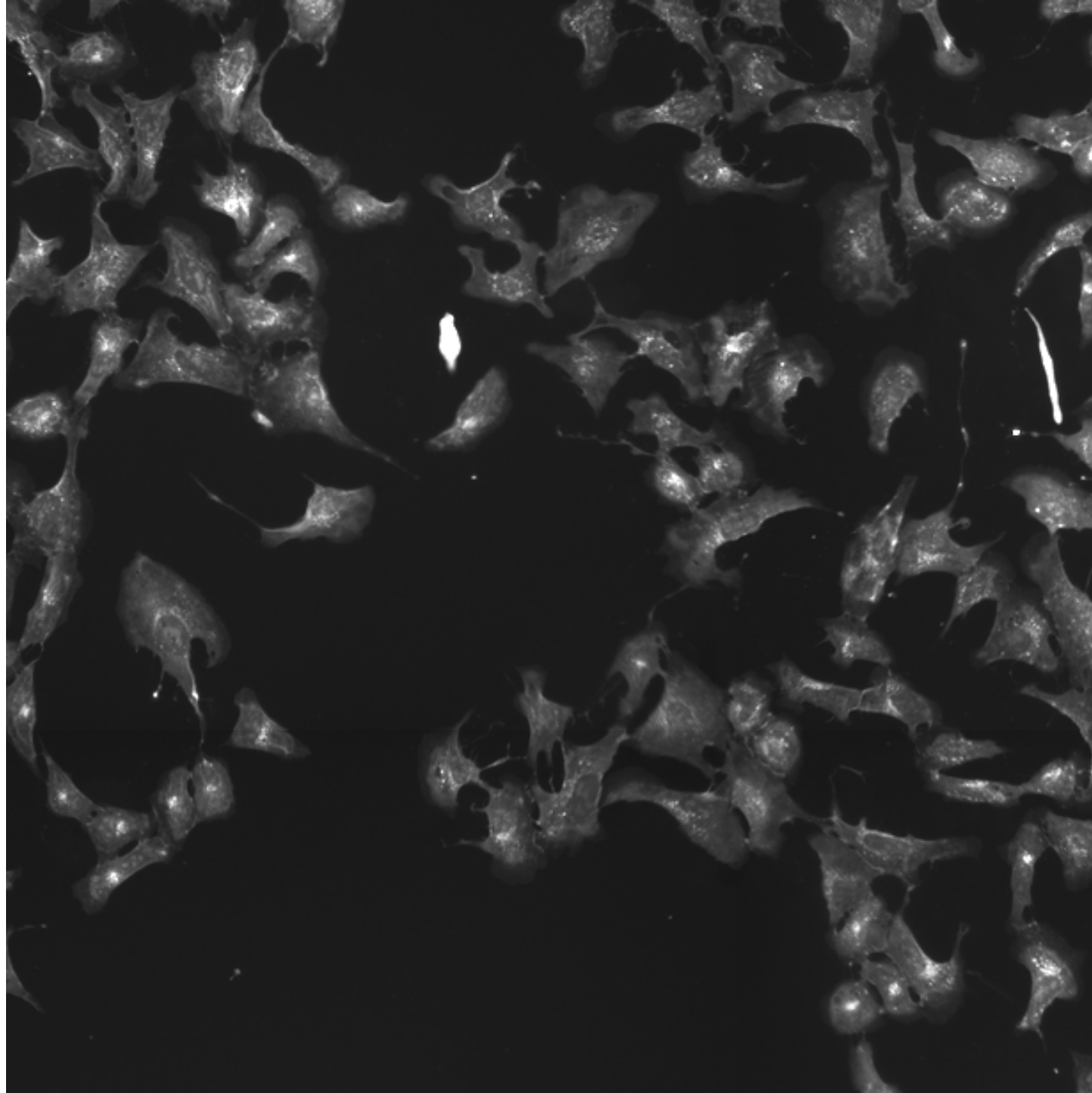
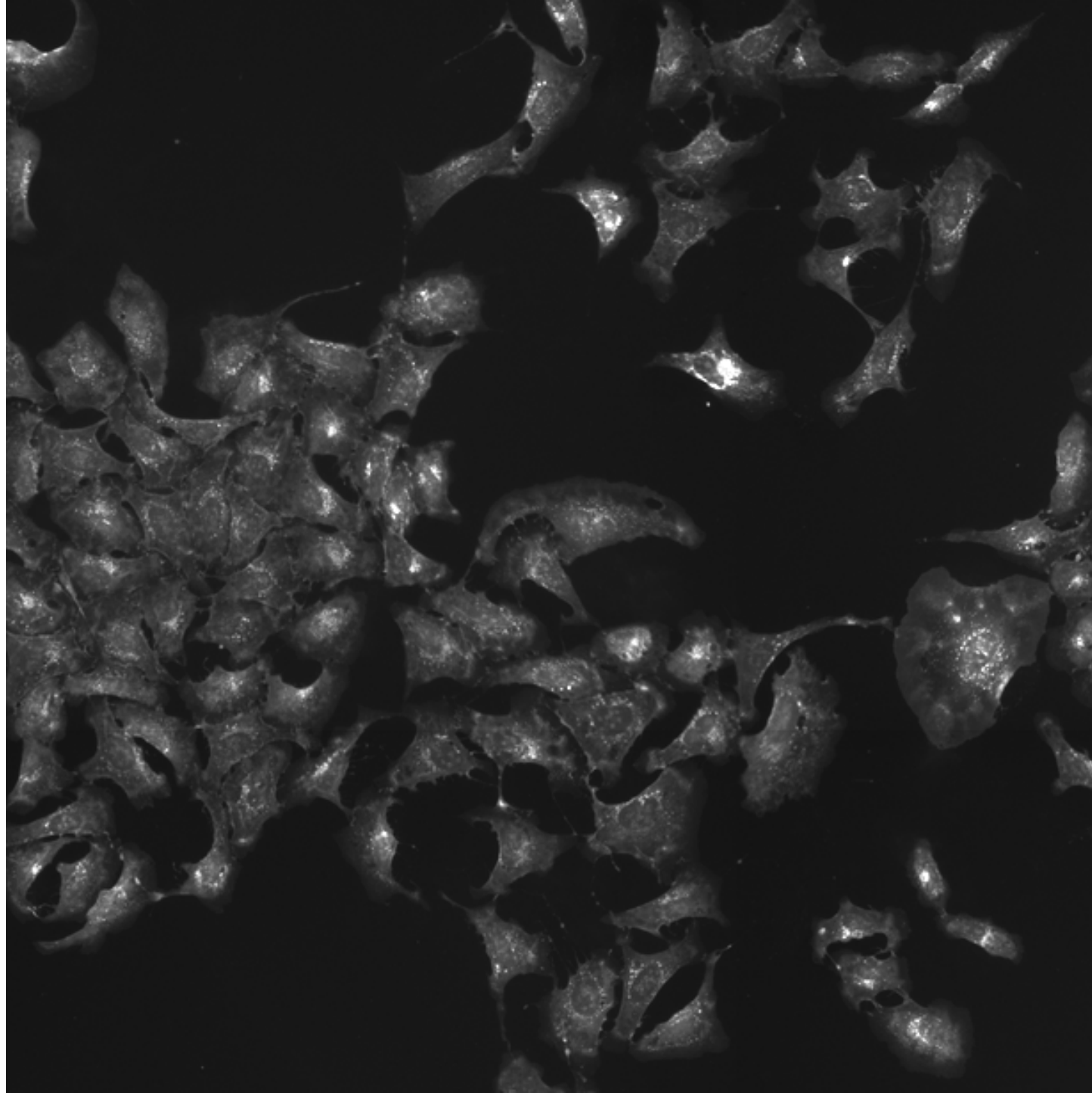
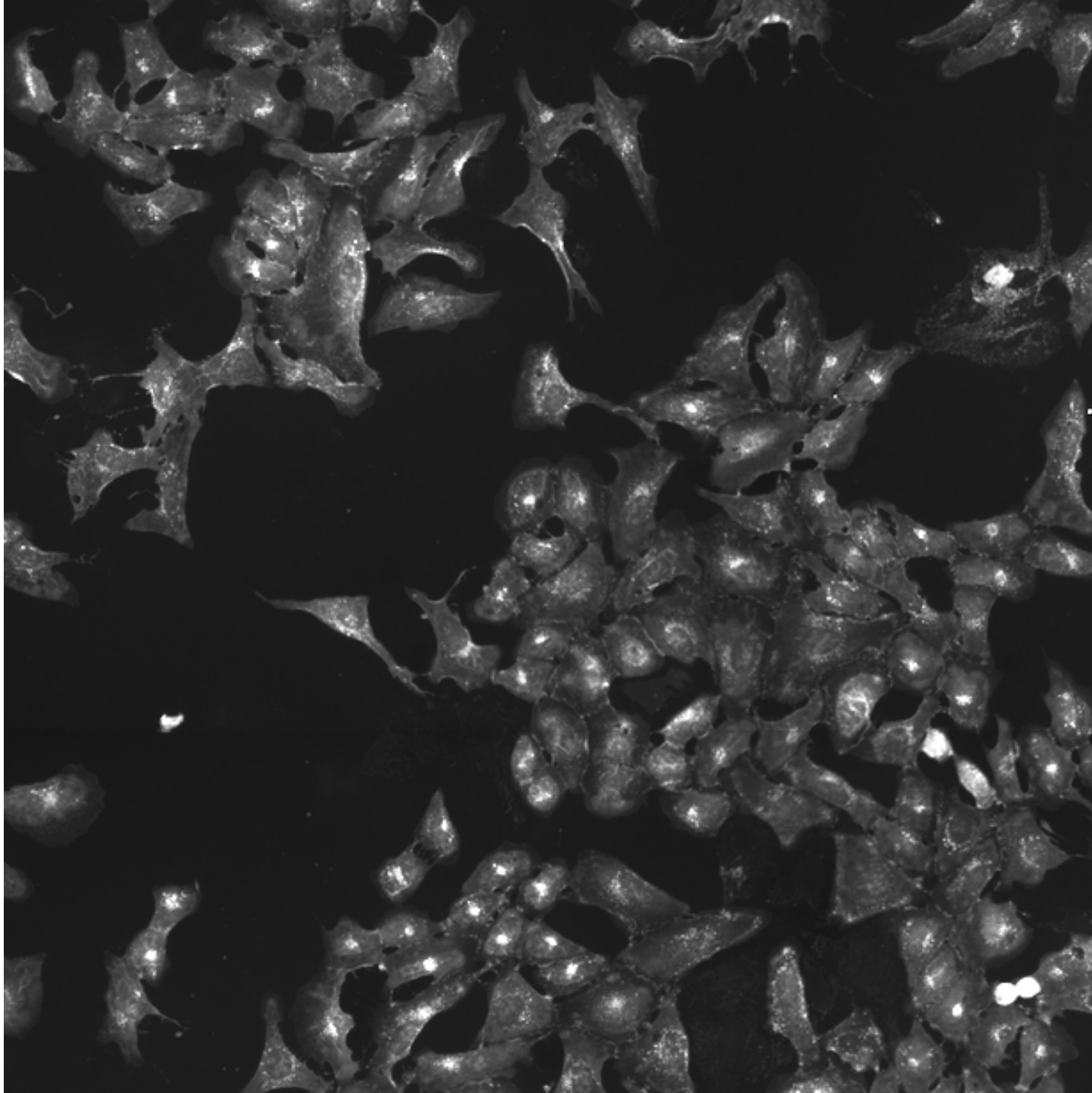
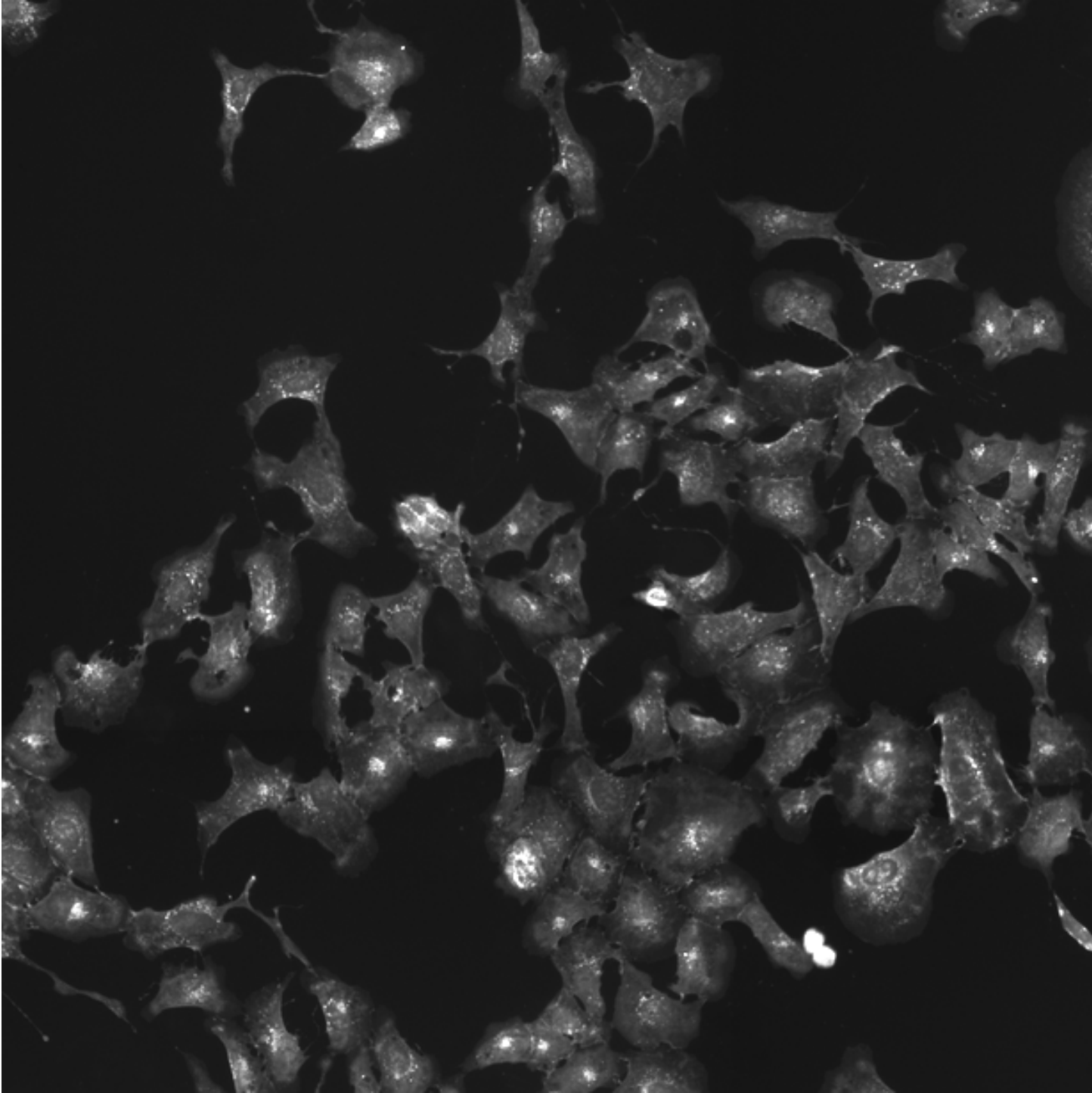
TGFBRI.K232R

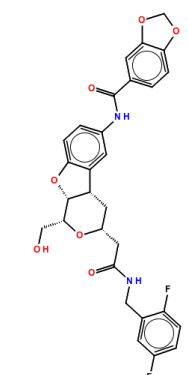
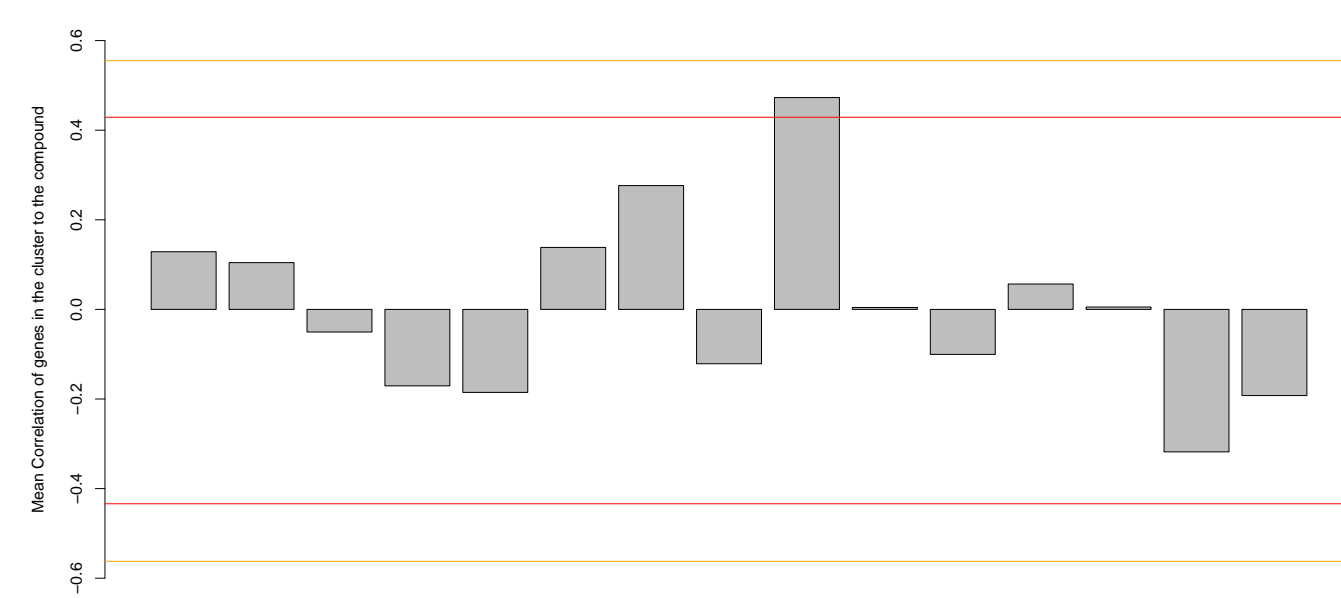
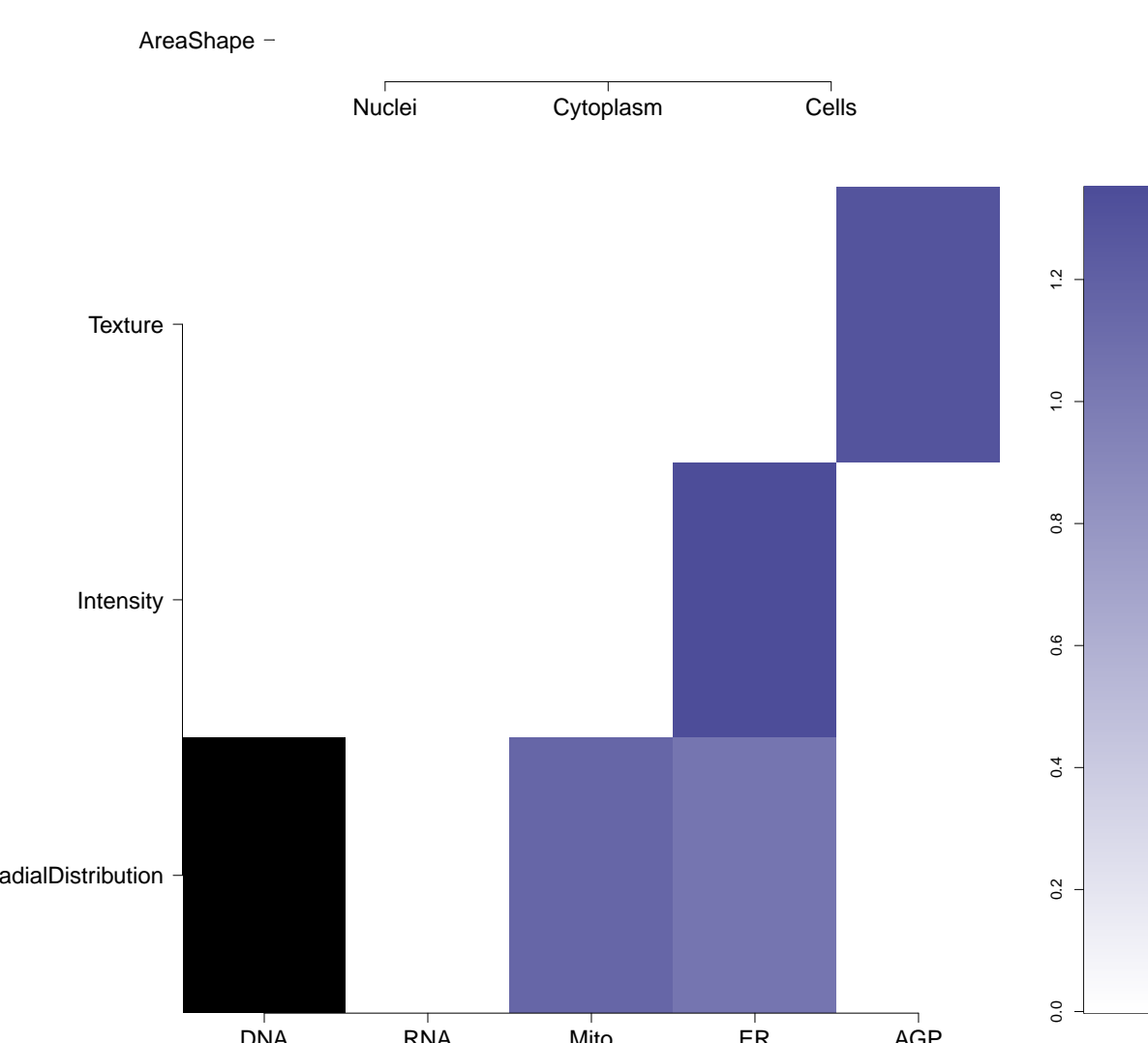
TGFBRI.WT.2

AGP

ER

Empty



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 0.54)	Mean \pm standard deviation correlation between compound and each gene in cluster; Tables contain data for individual genes	Mean compound rank when scored against genes in cluster using L1000 profiling \pm standard deviation; Tables contain data for individual genes	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 distinguishing feature categories in the compound and genes in the cluster 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 cluster	Number of PubChem assays in which the compound was tested; assays in which the compound was active are itemized																
BRD-K04267190-001-01-4 PubChem CID : 54646512		0.72 (in 4 replicates)	<div>0.47 \pm 0.21</div> <table><thead><tr><th>Treatment</th><th>Score</th></tr></thead><tbody><tr><td>DVL3.WT</td><td>0.25</td></tr><tr><td>TGFBRI.K232R</td><td>0.25</td></tr><tr><td>TGFBRI.WT.2</td><td>0.07</td></tr></tbody></table>	Treatment	Score	DVL3.WT	0.25	TGFBRI.K232R	0.25	TGFBRI.WT.2	0.07	<div>0.705 \pm 0.049</div> <table><thead><tr><th>Treatment</th><th>Score</th></tr></thead><tbody><tr><td>DVL3.WT</td><td>0.002</td></tr><tr><td>TGFBRI.K232R</td><td>0.001</td></tr><tr><td>TGFBRI.WT.2</td><td>0.001</td></tr></tbody></table>	Treatment	Score	DVL3.WT	0.002	TGFBRI.K232R	0.001	TGFBRI.WT.2	0.001				Total number of assays tested in: 37.
Treatment	Score																							
DVL3.WT	0.25																							
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