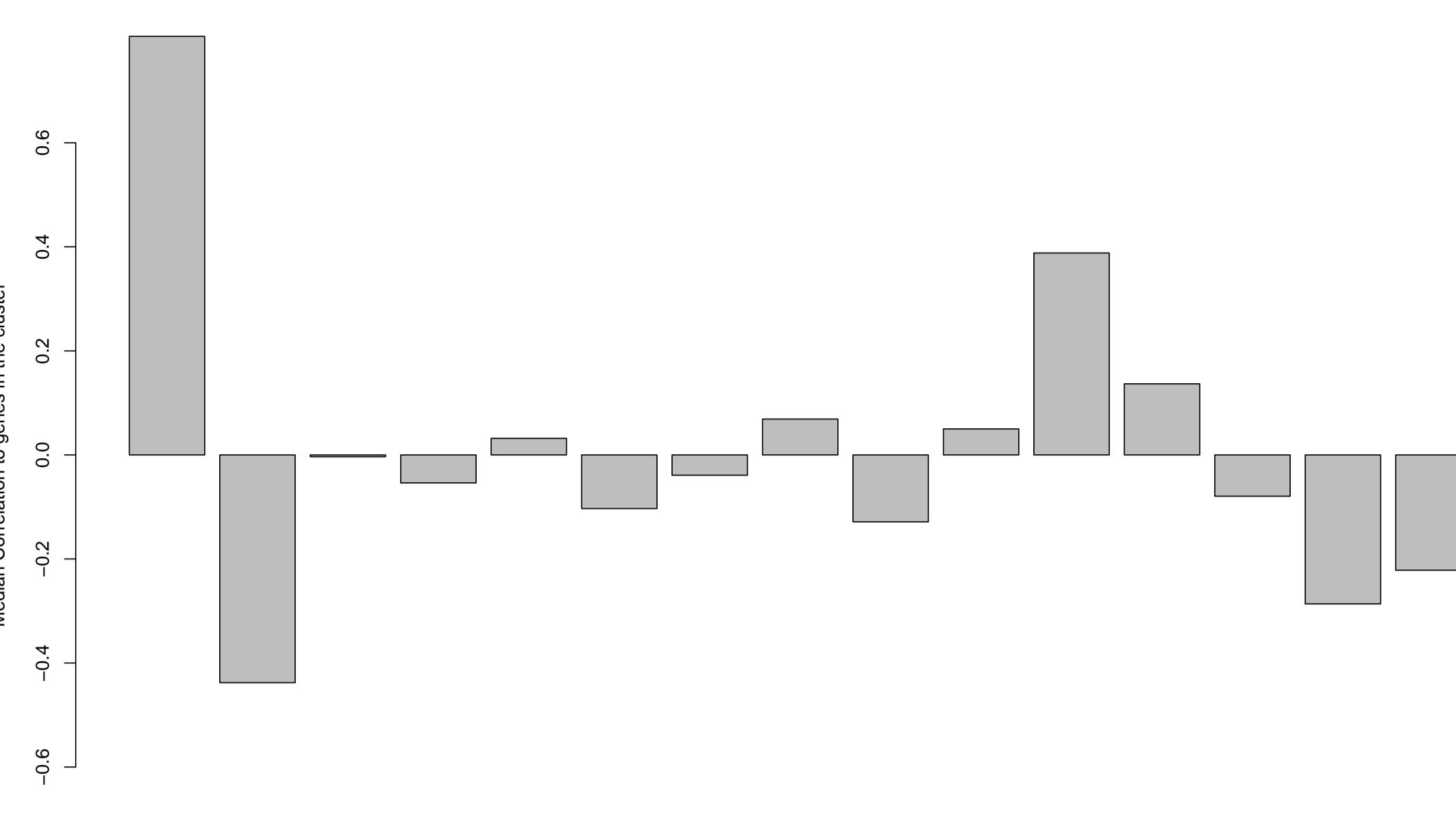


Genes in the cluster along with the pathways as annotated by experts

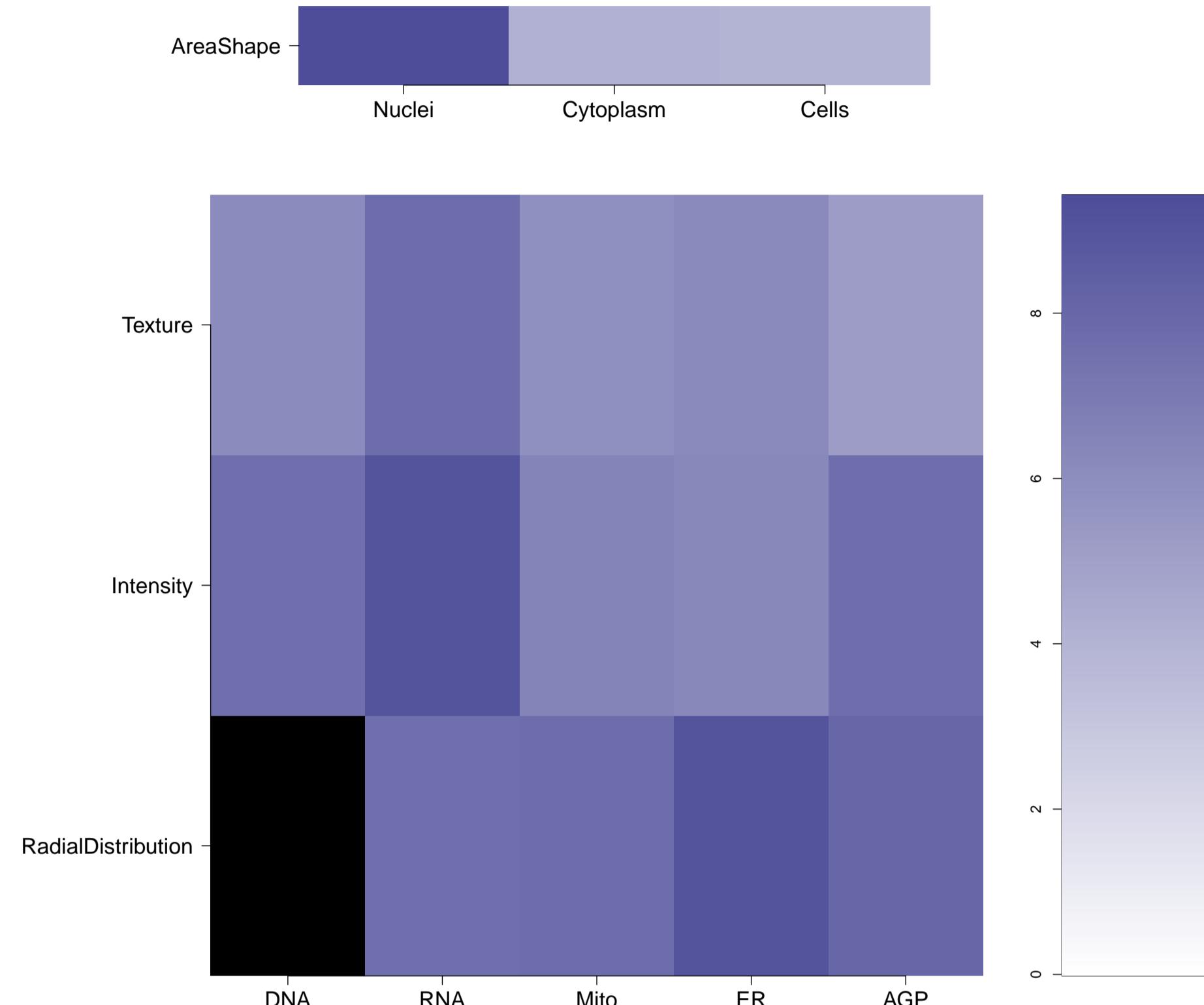
Treatment	Pathway	Regulation Type
CDC42.T17N	Canonical Cytoskeletal Re-org	Inhibitor
AKT1.E17K	Canonical PI3K/AKT	Activator
AKT3.WT.2	Canonical PI3K/AKT	Activator
AKT3.E17K	Canonical PI3K/AKT	Activator



Top 5 genes negatively correlated to the cluster

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PIK3RI.WT.1	Canonical PI3K/AKT	Activator	-0.48	0.14
AKT1S1.WT.2	TOR	Inhibitor	-0.47	0.04
AKT1S1.WT.1	TOR	Inhibitor	-0.43	0.05
PRKACG.WT.3	PKA	Activator	-0.42	0.09
ATF4.WT.2	Canonical ER Stress/UPR	Activator	-0.40	0.06

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?

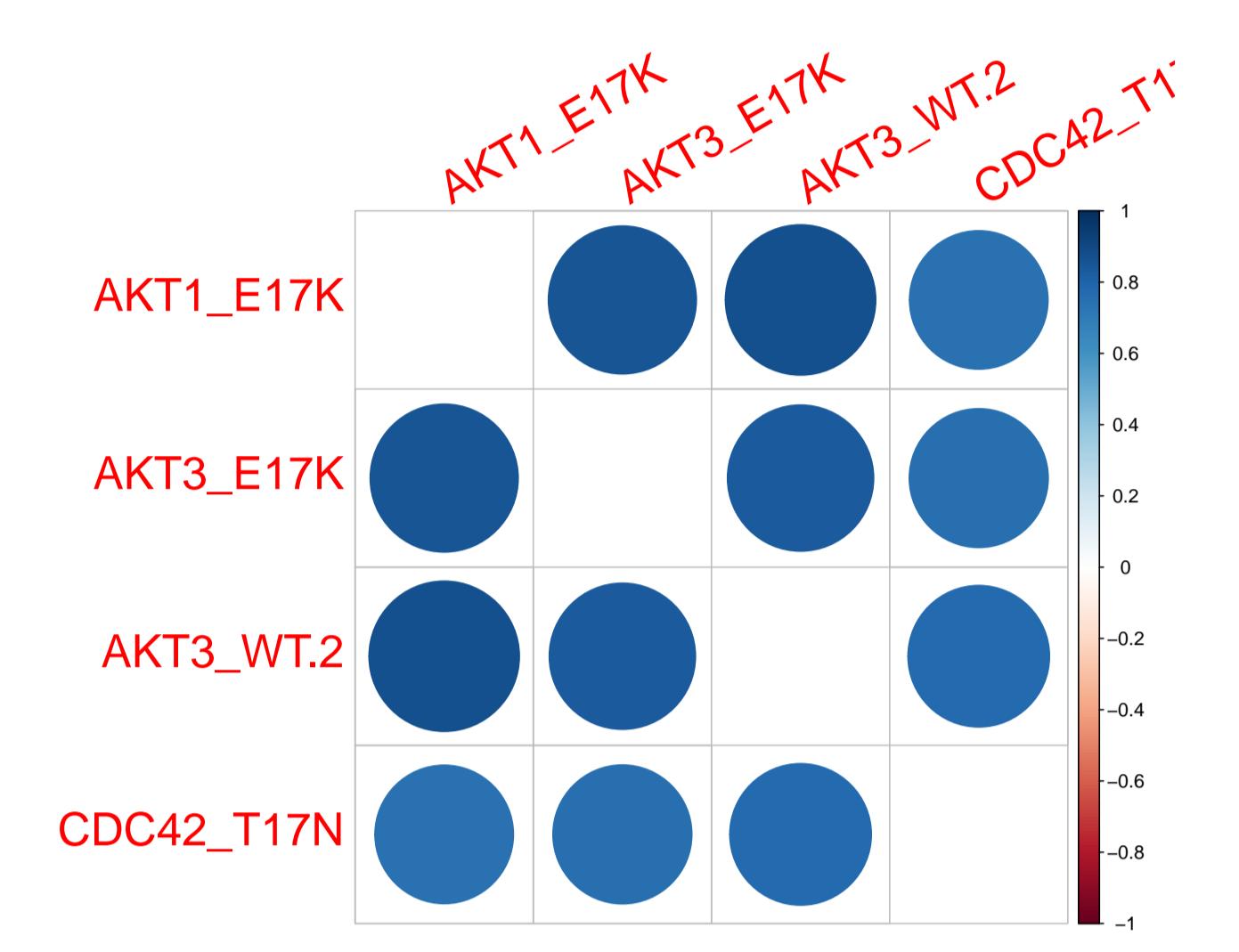


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

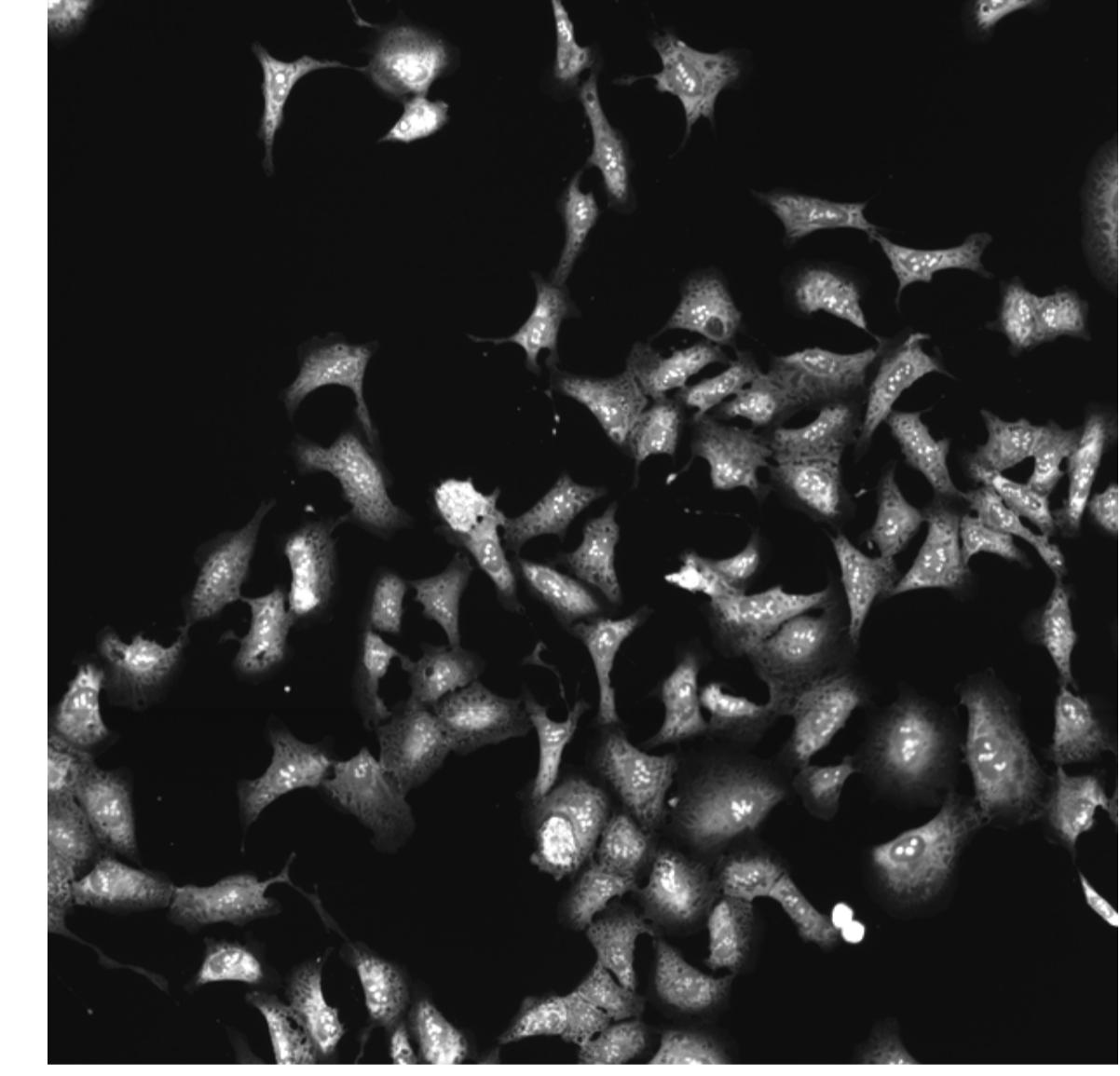
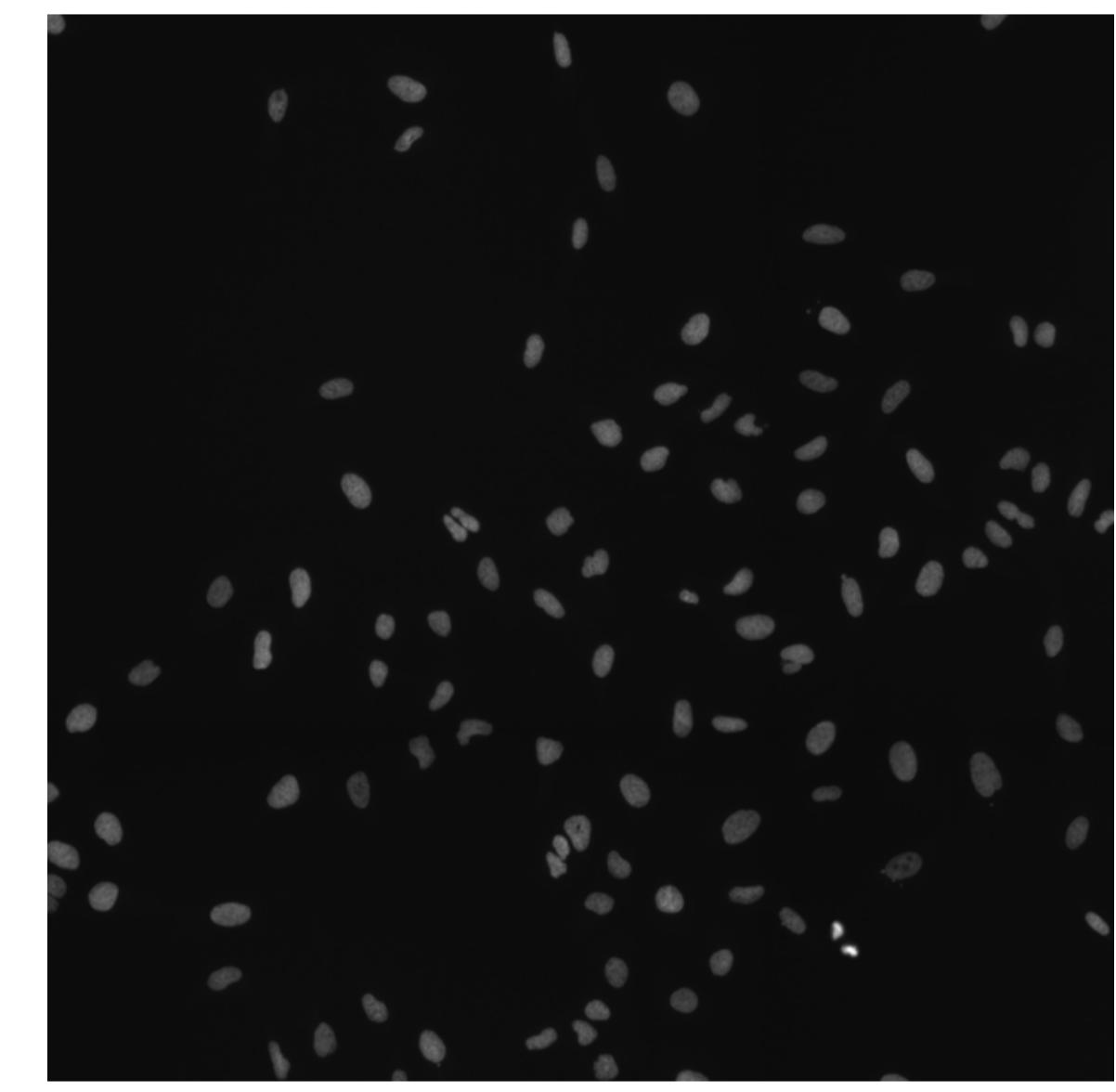
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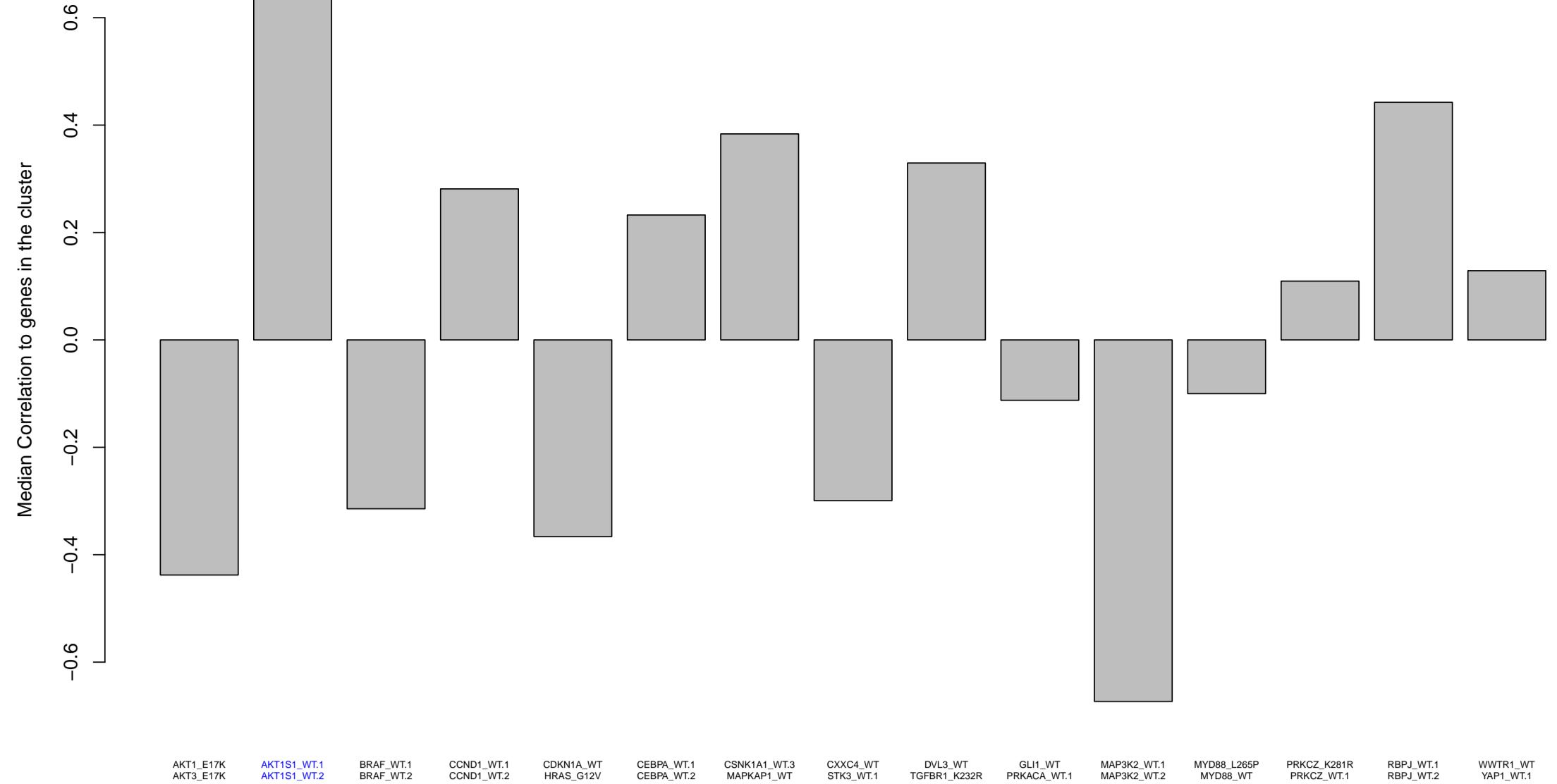
AKT1.E17K

AKT3.E17K

AKT3.WT.2

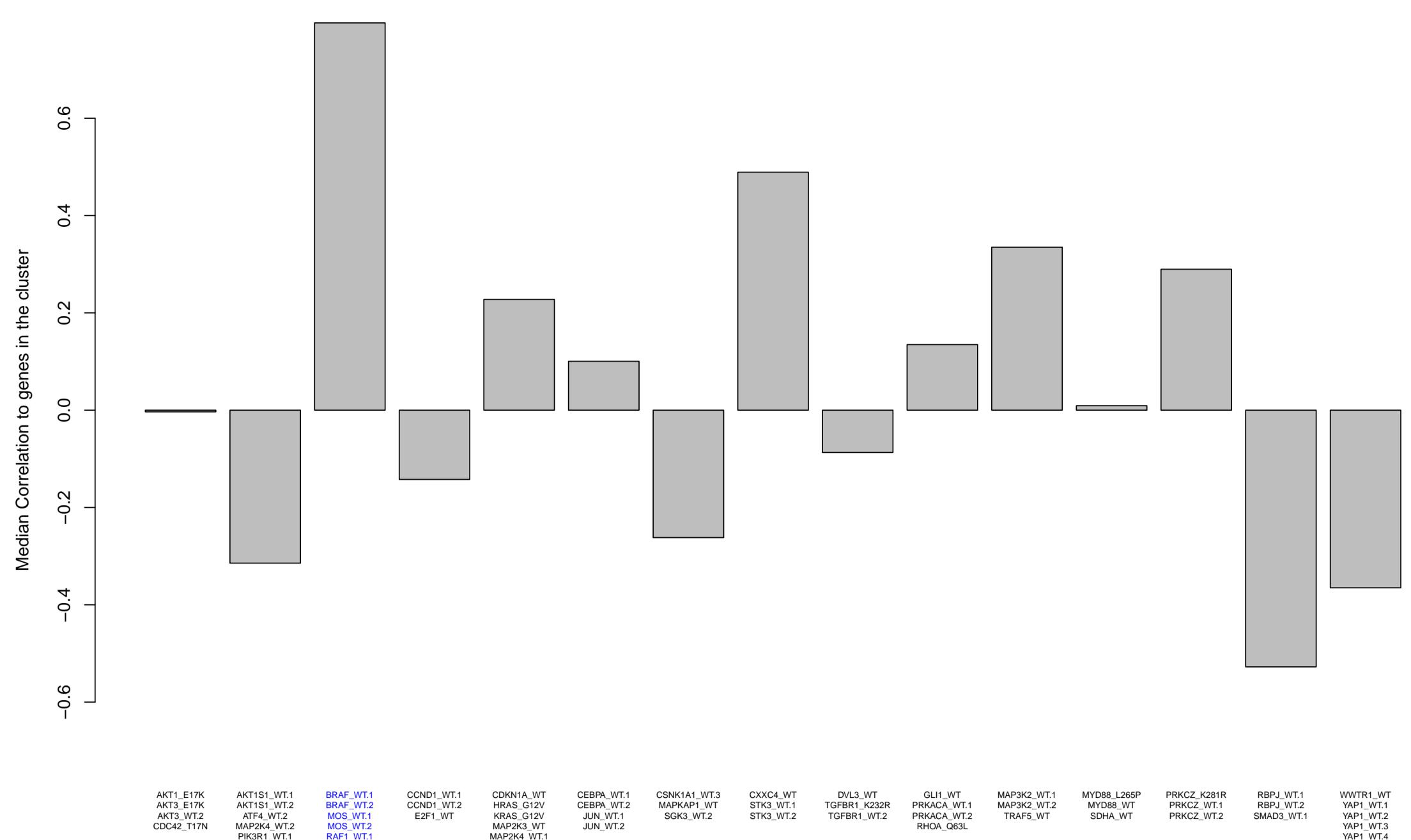
CDC42.T17N





Cluster 3

Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
RAF1_WT.1	Canonical MAPK	Activator	
BRAF_WT.1	Canonical MAPK	Activator	
BRAF_WT.2	Canonical MAPK	Activator	
RAF1_WT.2	Canonical MAPK	Activator	
MOS_WT.1	MAPK	Activator	
MOS_WT.2	MAPK	Activator	



Top 5 genes negatively correlated to the cluster						
Expert Annotation						
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation		
RBPJ_WT.1	NOTCH	Activator	-0.60	0.07		
ERN1_WT.1	Canonical ER Stress/UPR	Activator	-0.55	0.06		
XBP1_WT.1	Canonical ER Stress/UPR	Activator	-0.51	0.09		
RBPJ_WT.2	NOTCH	Activator	-0.49	0.10		
YAP1_WT.3	Canonical Hippo	Inhibitor	-0.48	0.11		

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?

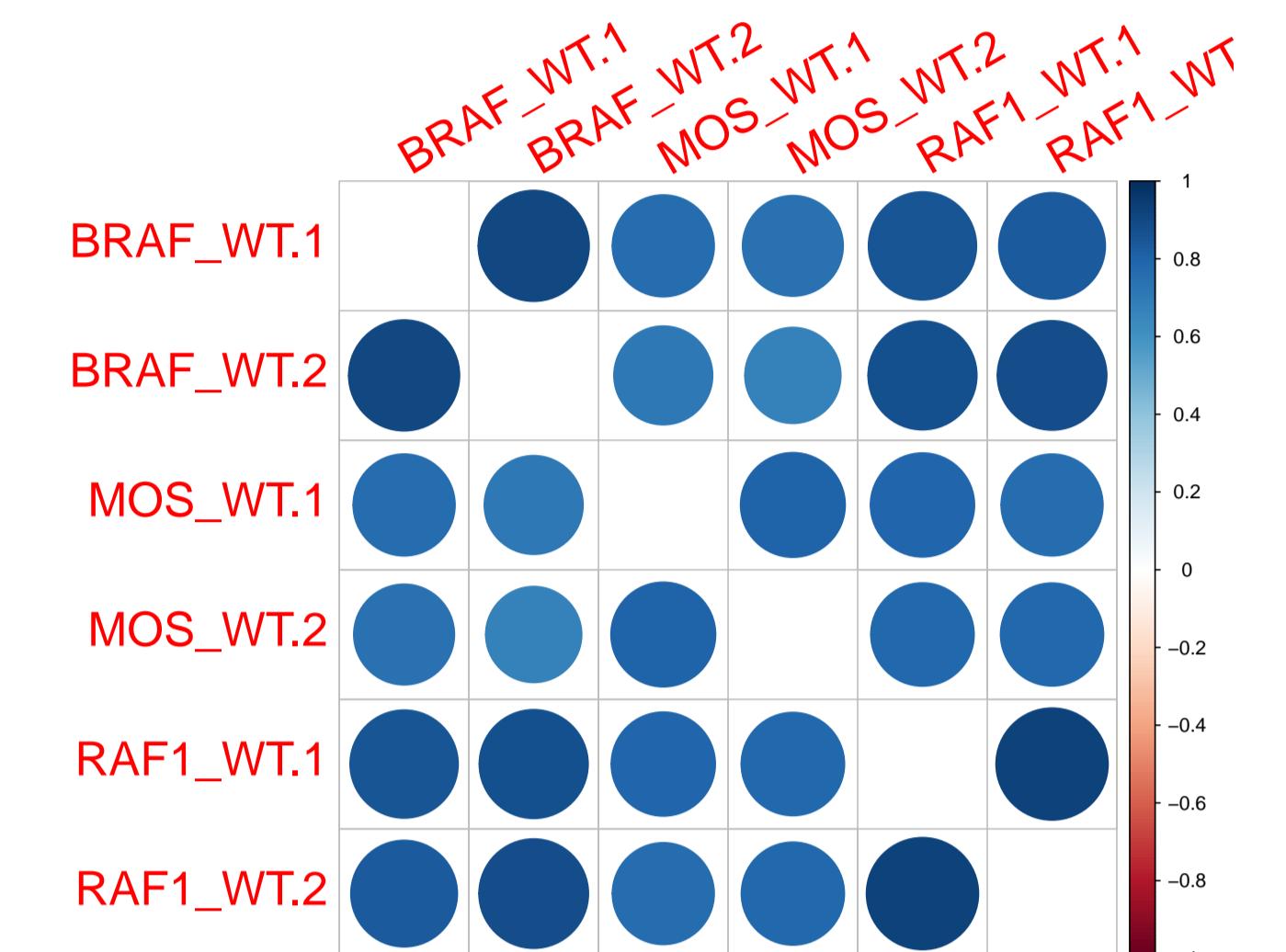
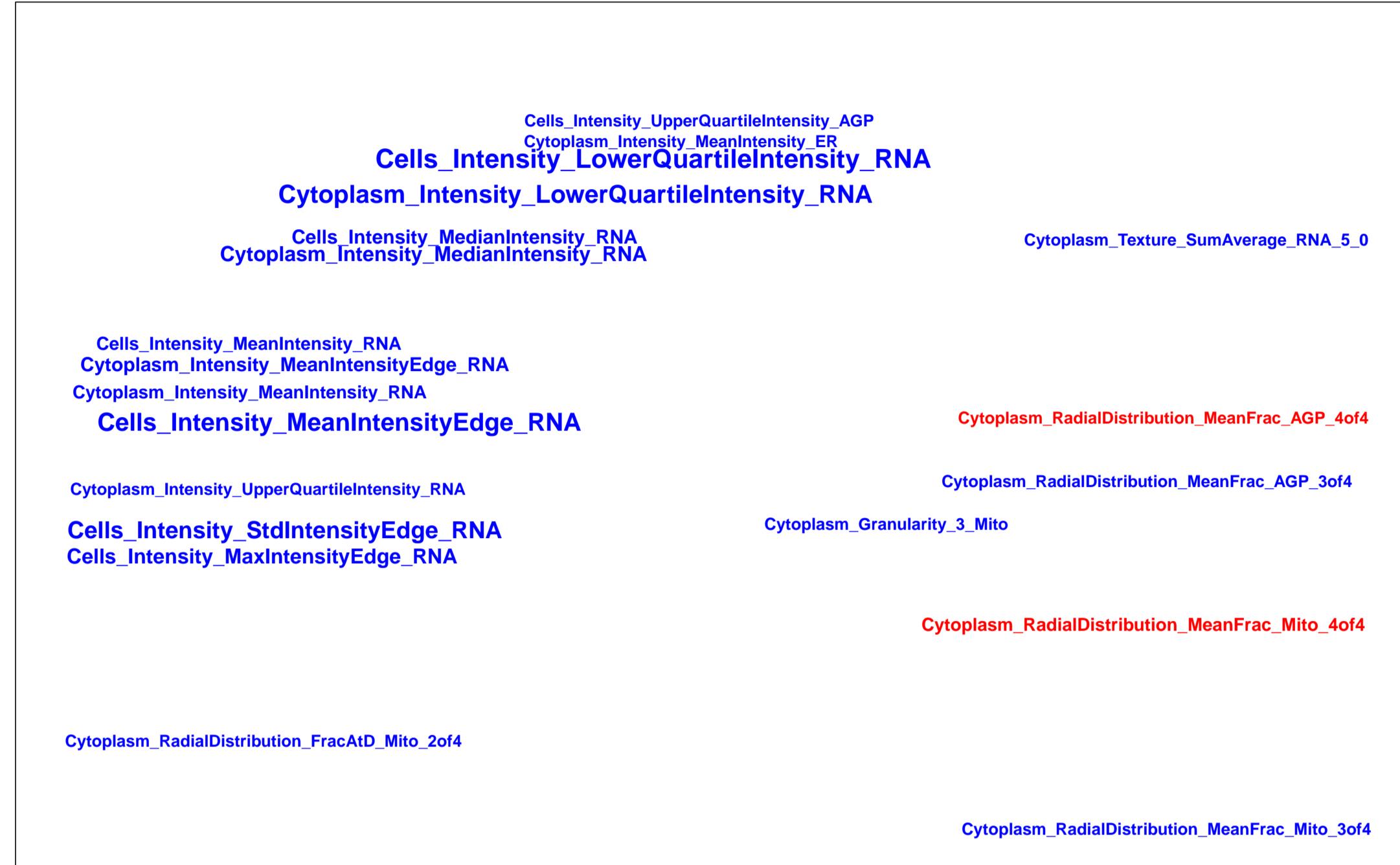
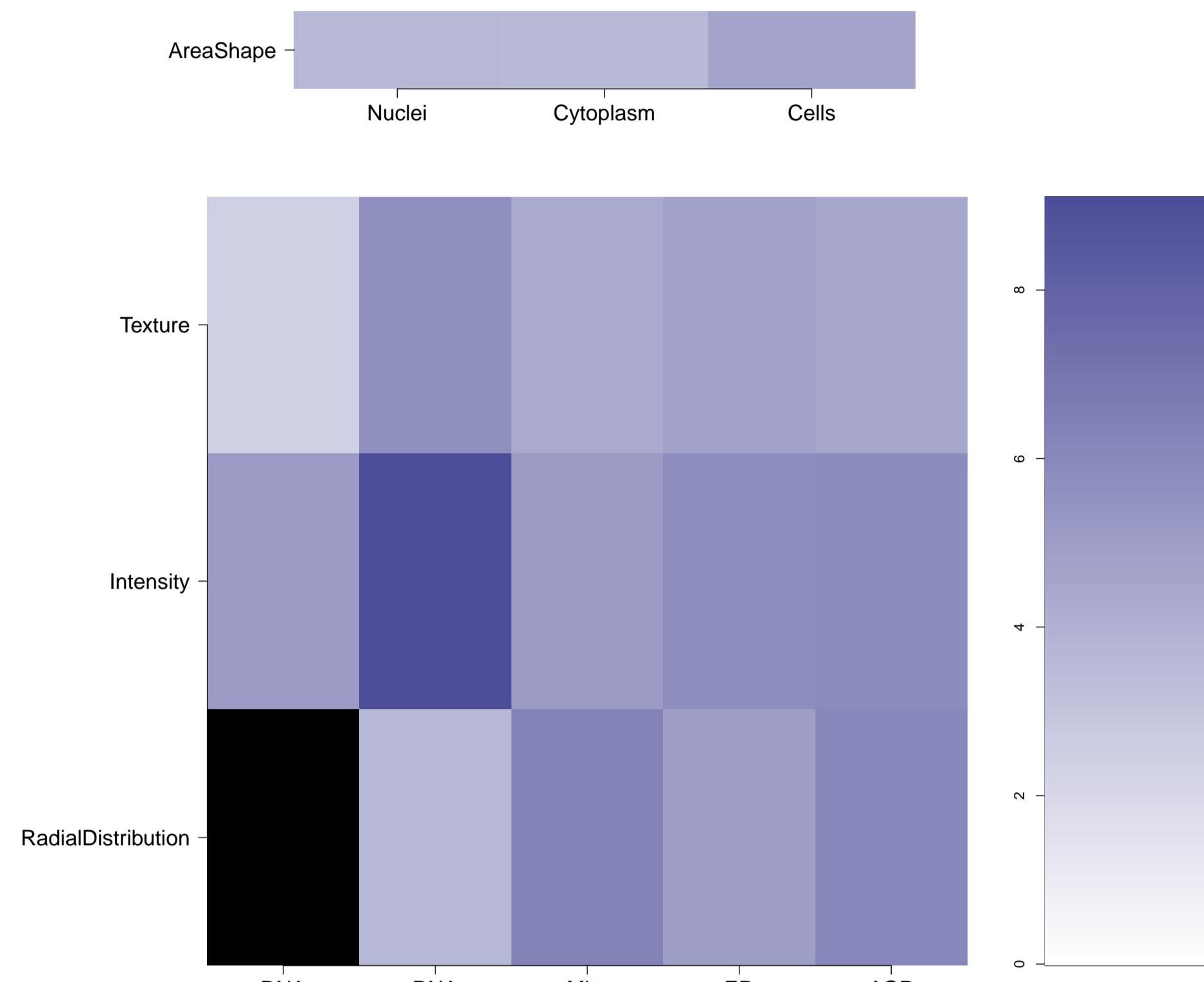


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

BRAF_WT.2

MOS_WT.1

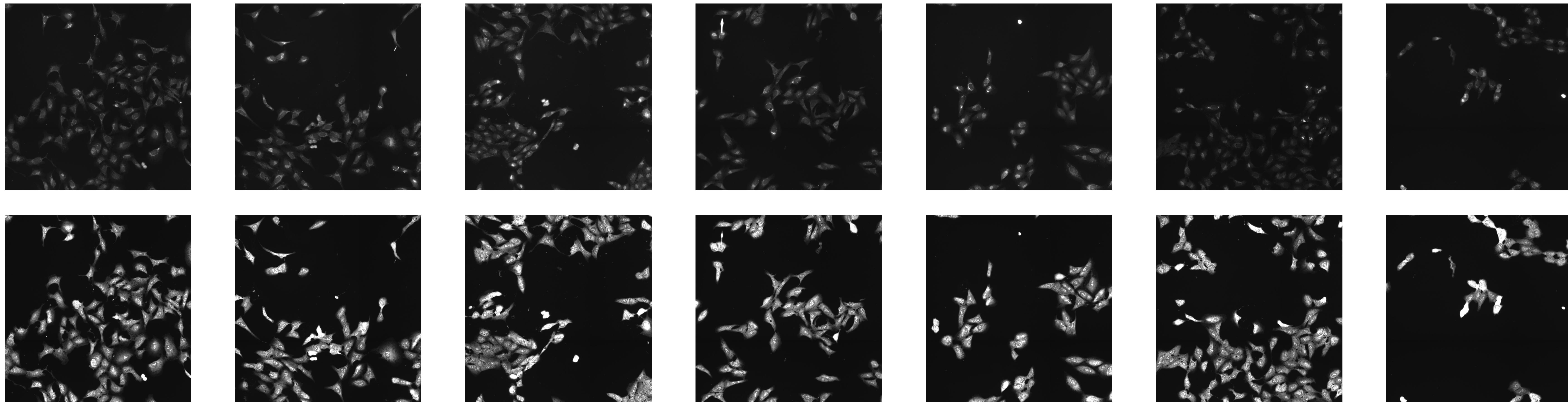
MOS_WT.2

RAF1_WT.1

RAF1_WT.2

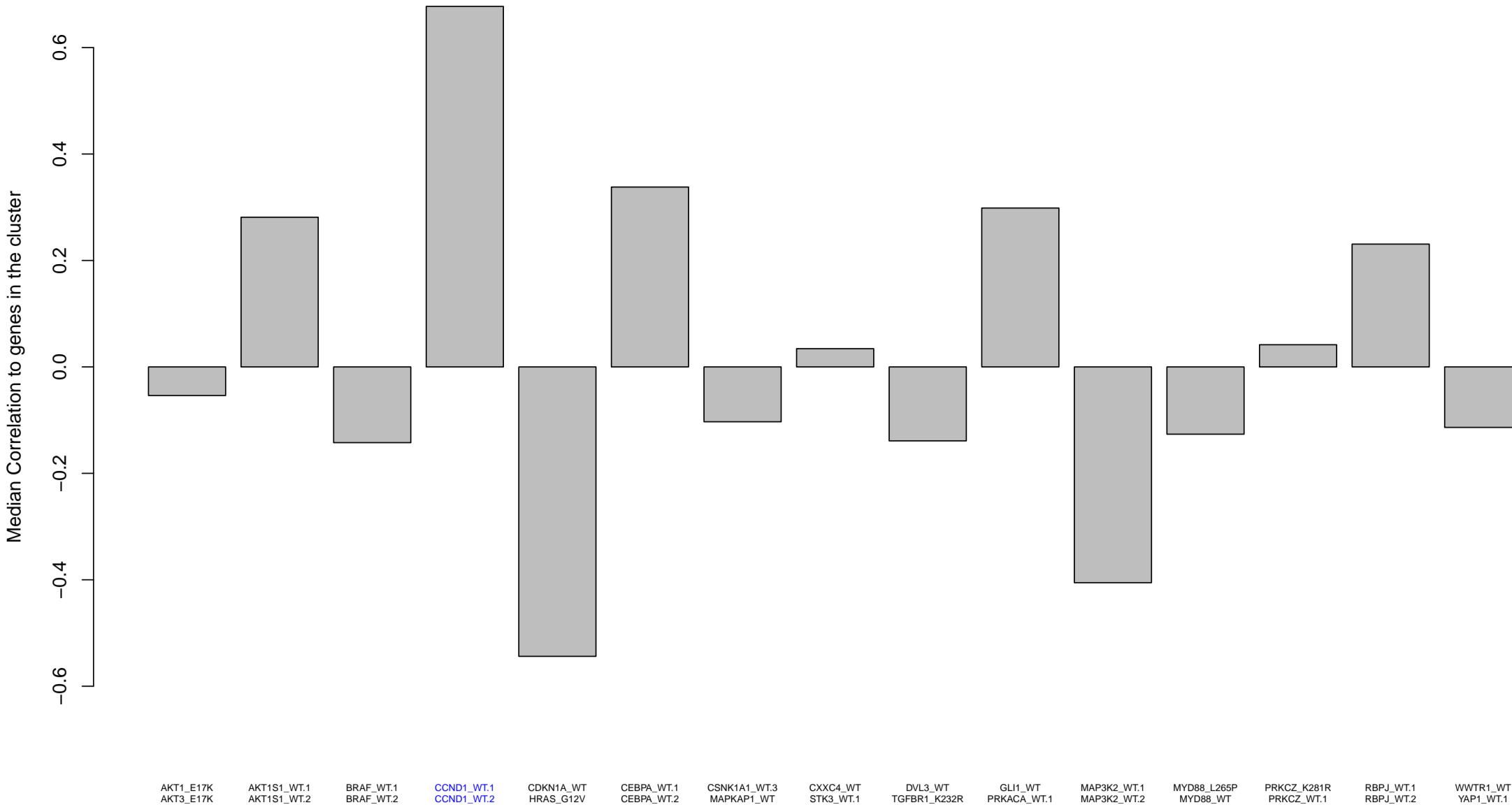
Empty

BRAF_WT.1



Cluster 4

Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
CCND1_WT.1	Canonical Cell Cycle	Activator	
E2F1_WT	Canonical Cell Cycle	Activator	
CCND1_WT.2	Canonical Cell Cycle	Activator	



Top 5 genes negatively correlated to the cluster					
Treatment	Expert Annotation		Regulation Type	Mean Correlation	Standard Deviation
	Pathway				
CDKN1A_WT	Canonical Cell Cycle		Inhibitor	-0.67	0.11
MAP3K5_WT	Canonical MAPK		Activator	-0.61	0.03
MAP2K4_WT.1	Canonical MAPK		Activator	-0.51	0.06
TP53_WT.1	Canonical DNA Damage		Activator	-0.50	0.22
MAP2K3_WT	Canonical MAPK		Activator	-0.49	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?

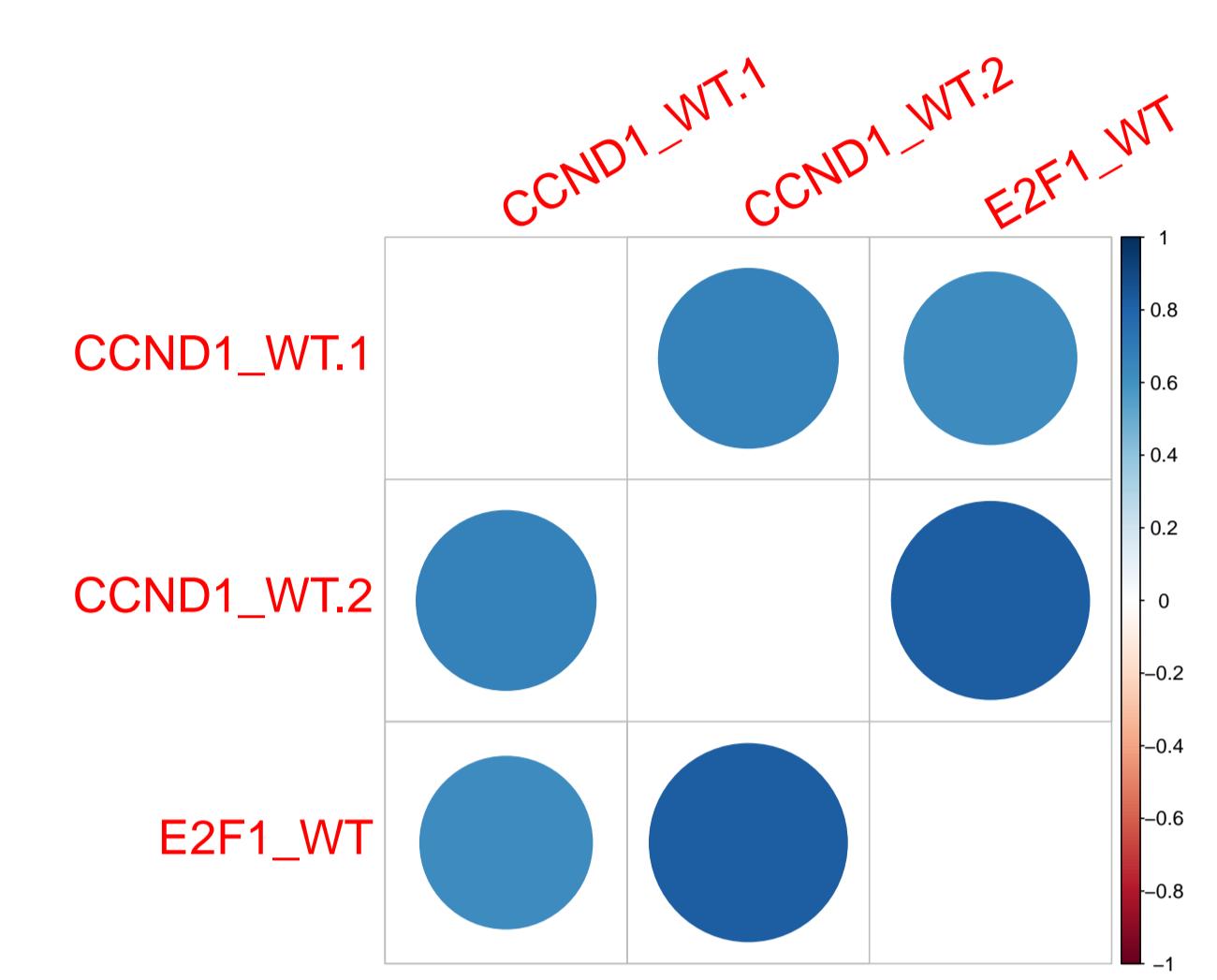
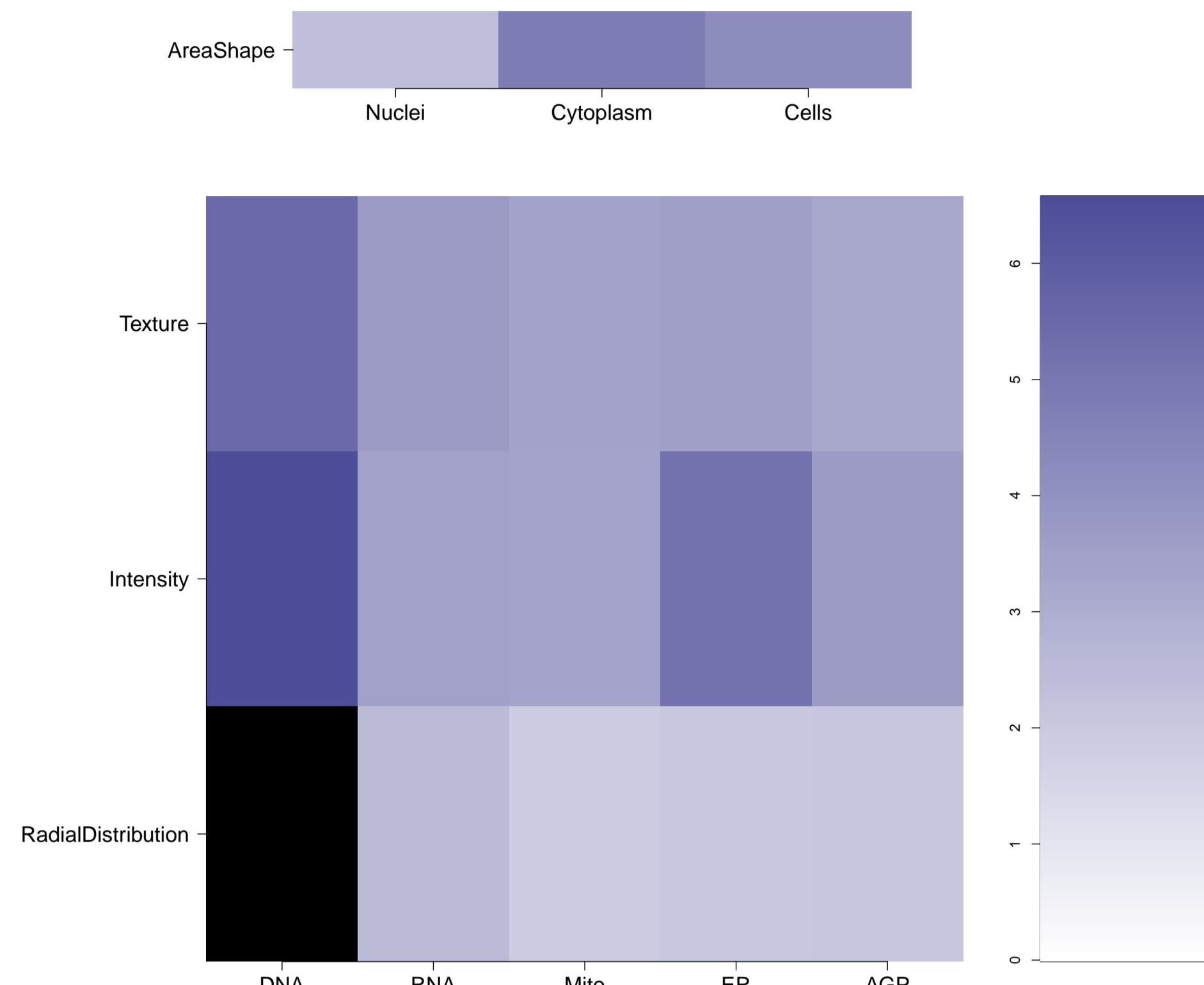


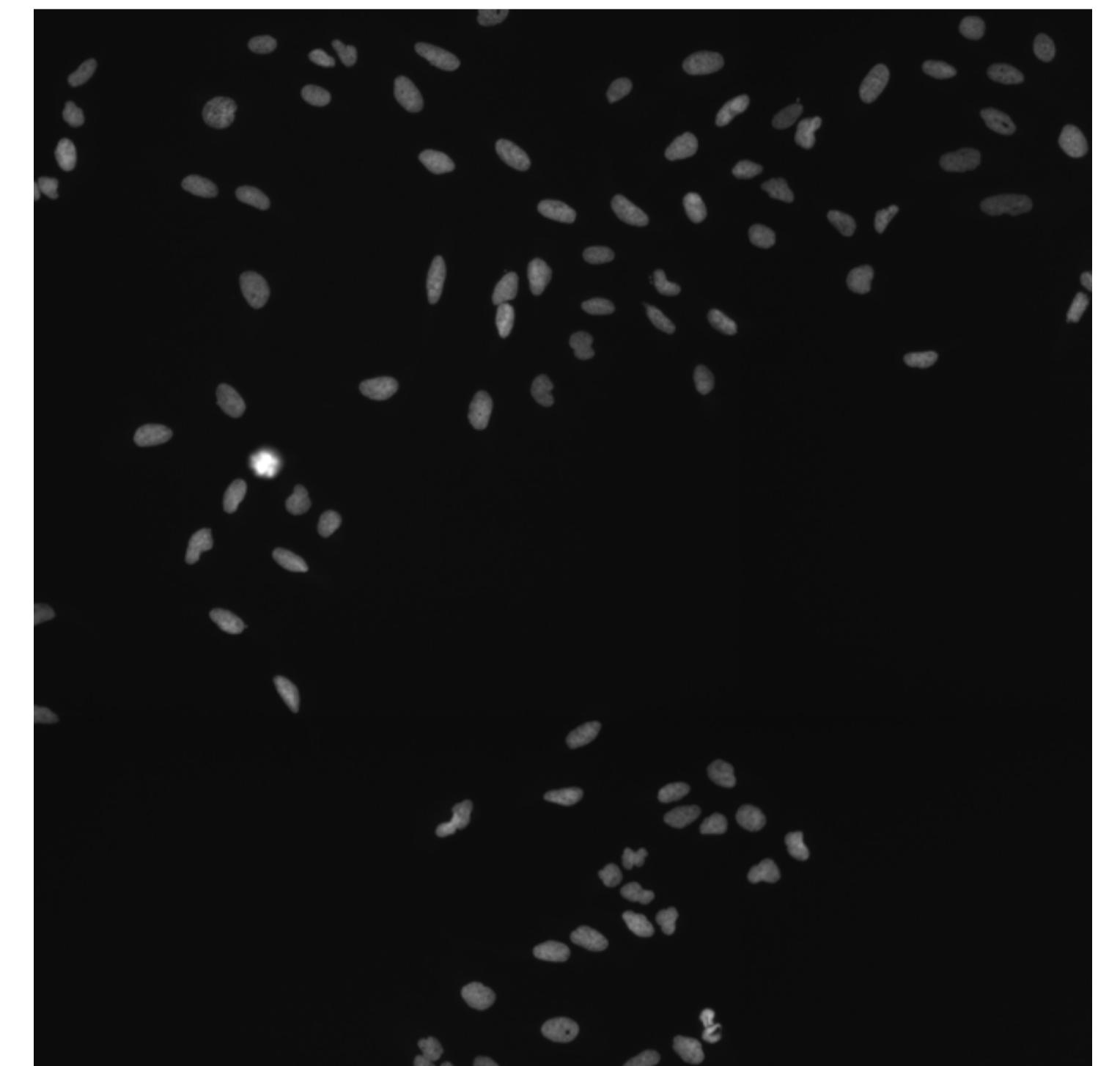
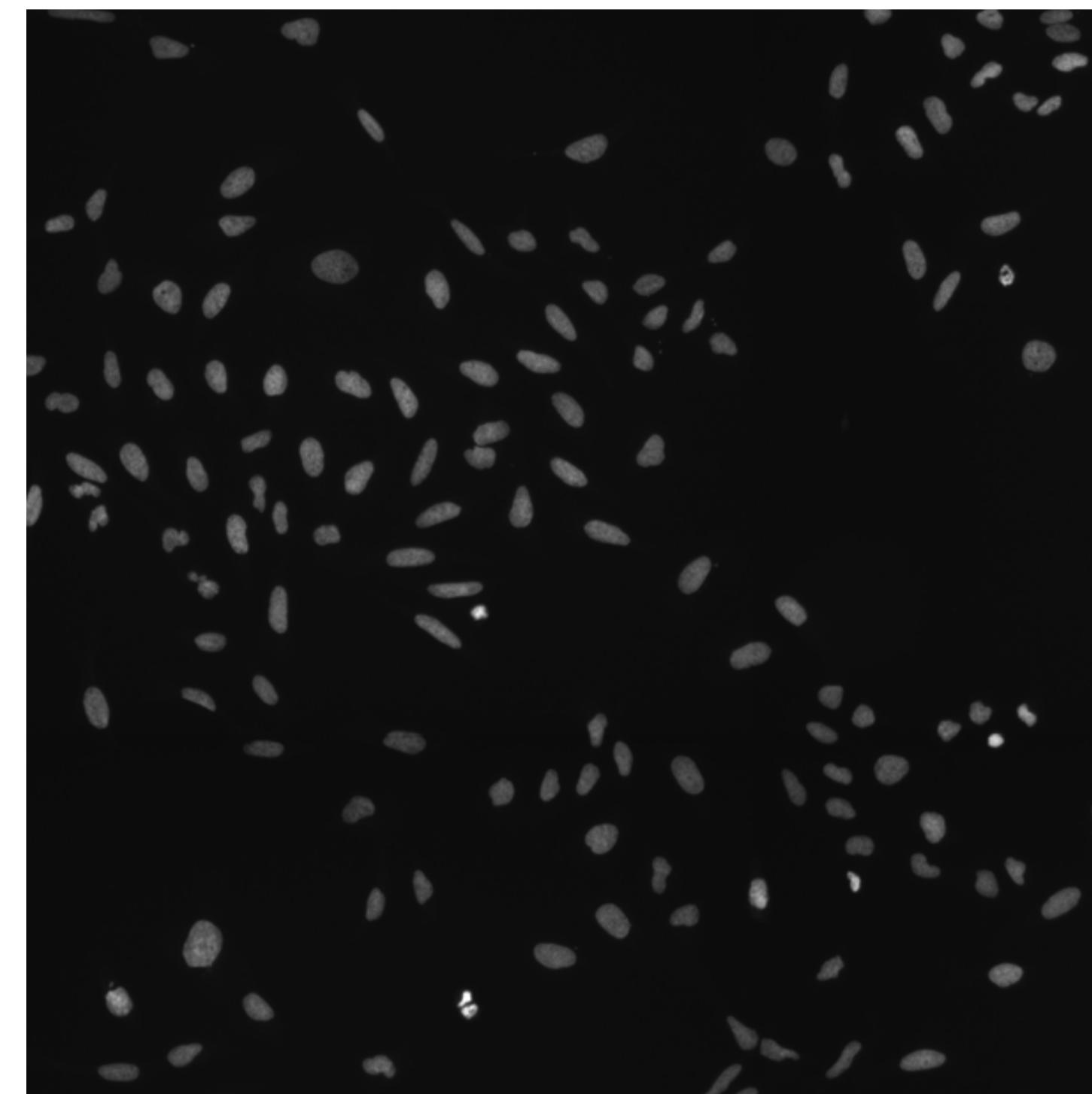
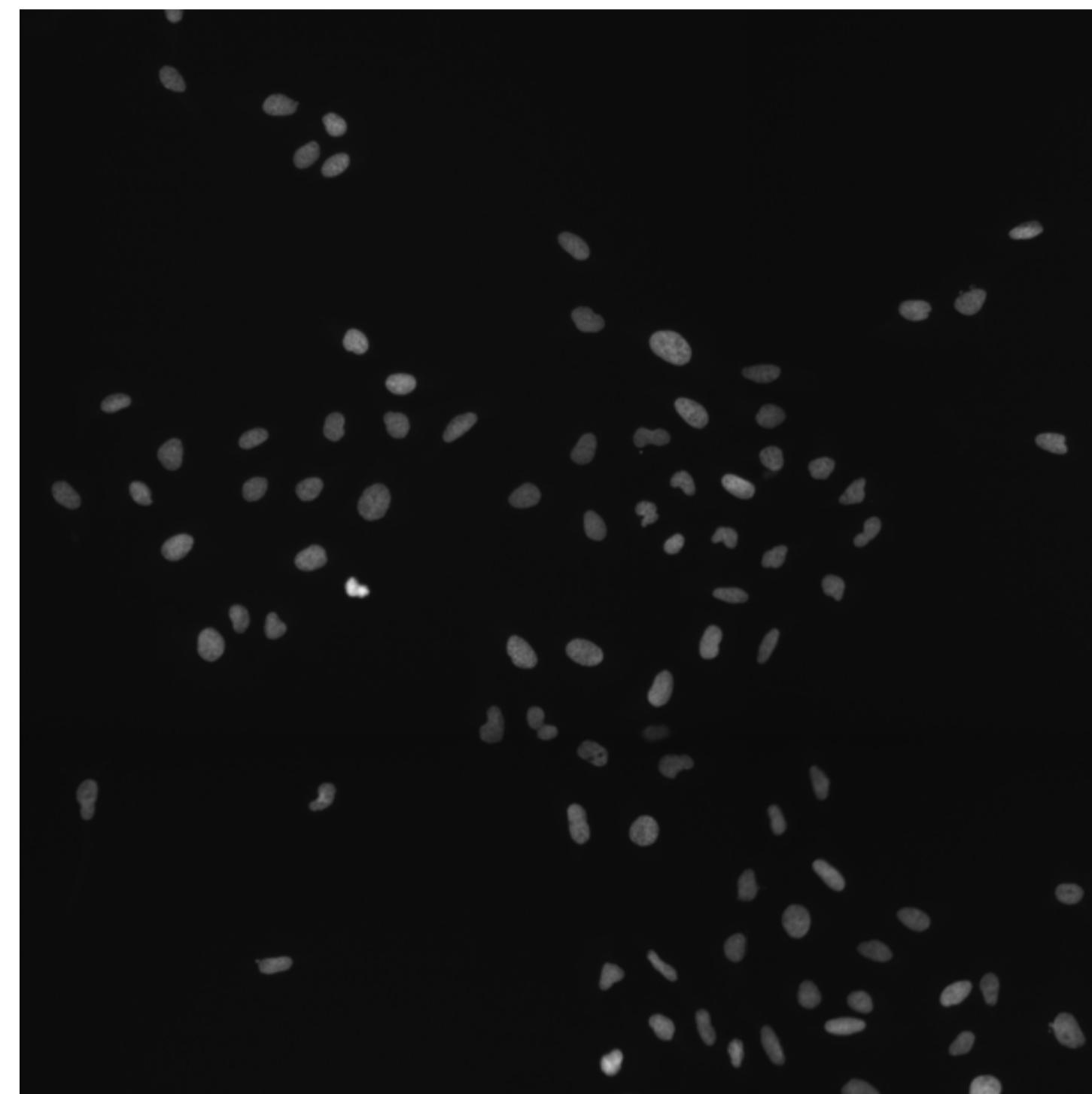
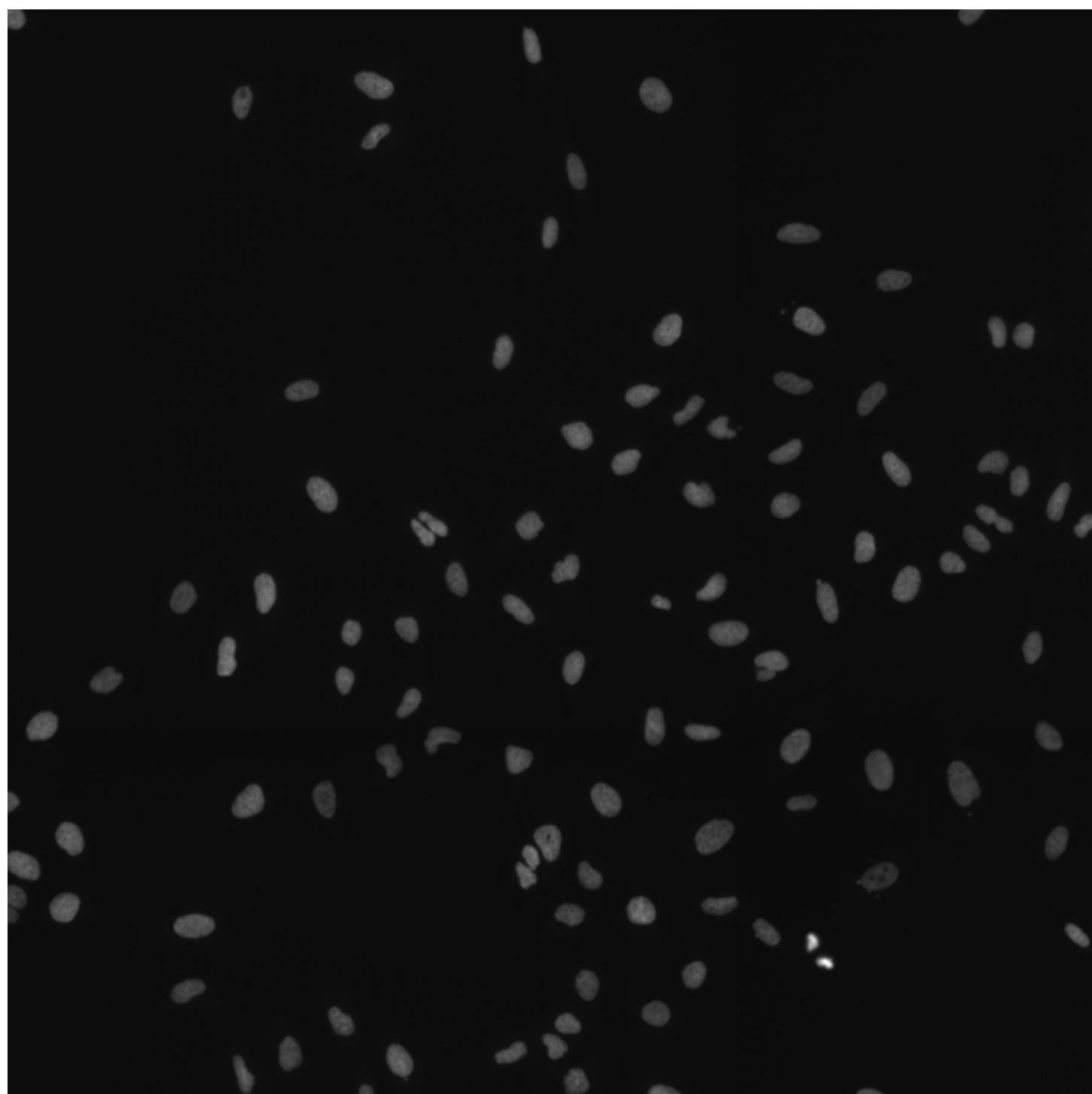
Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

CCND1_WT.1

CCND1_WT.2

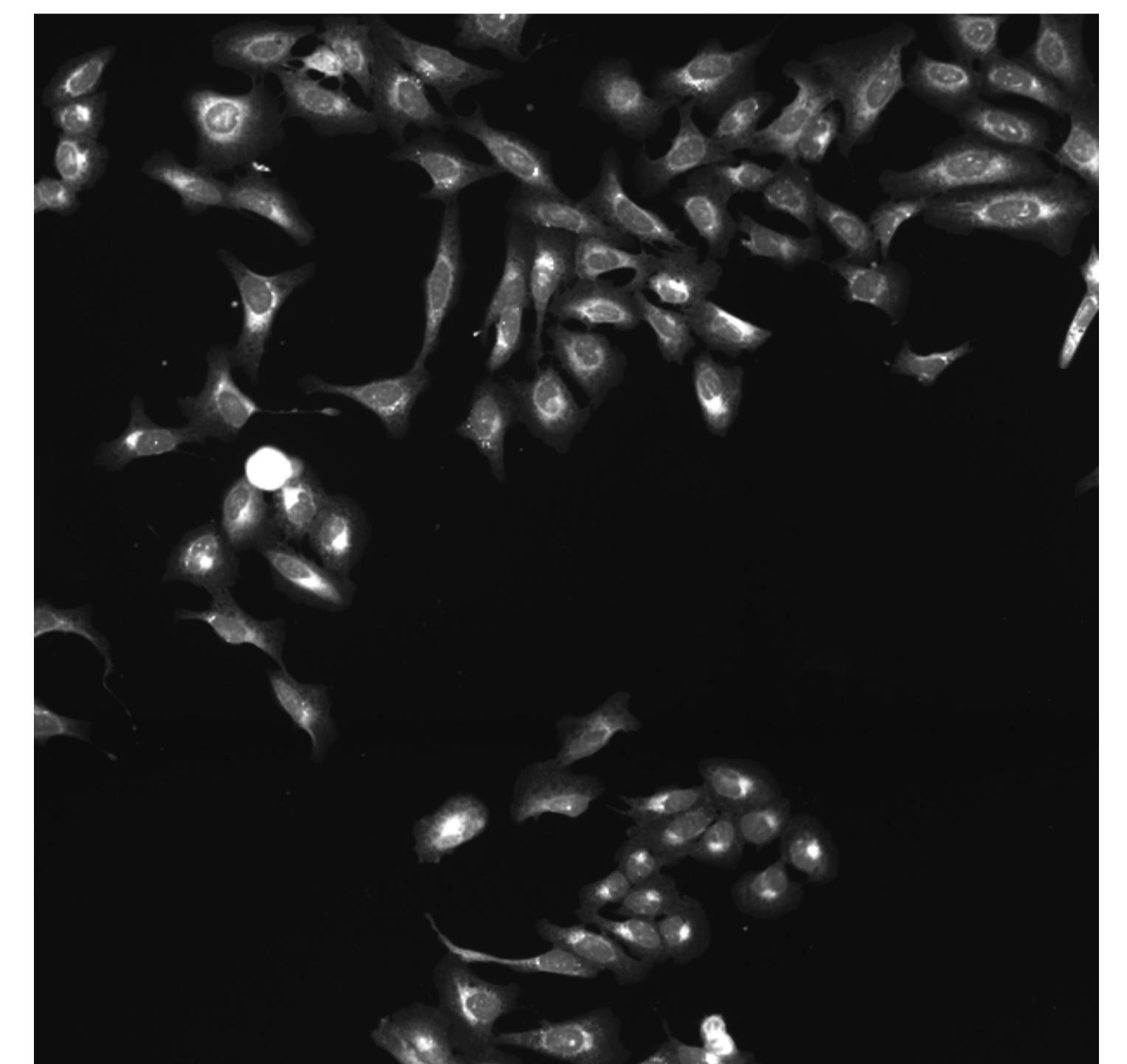
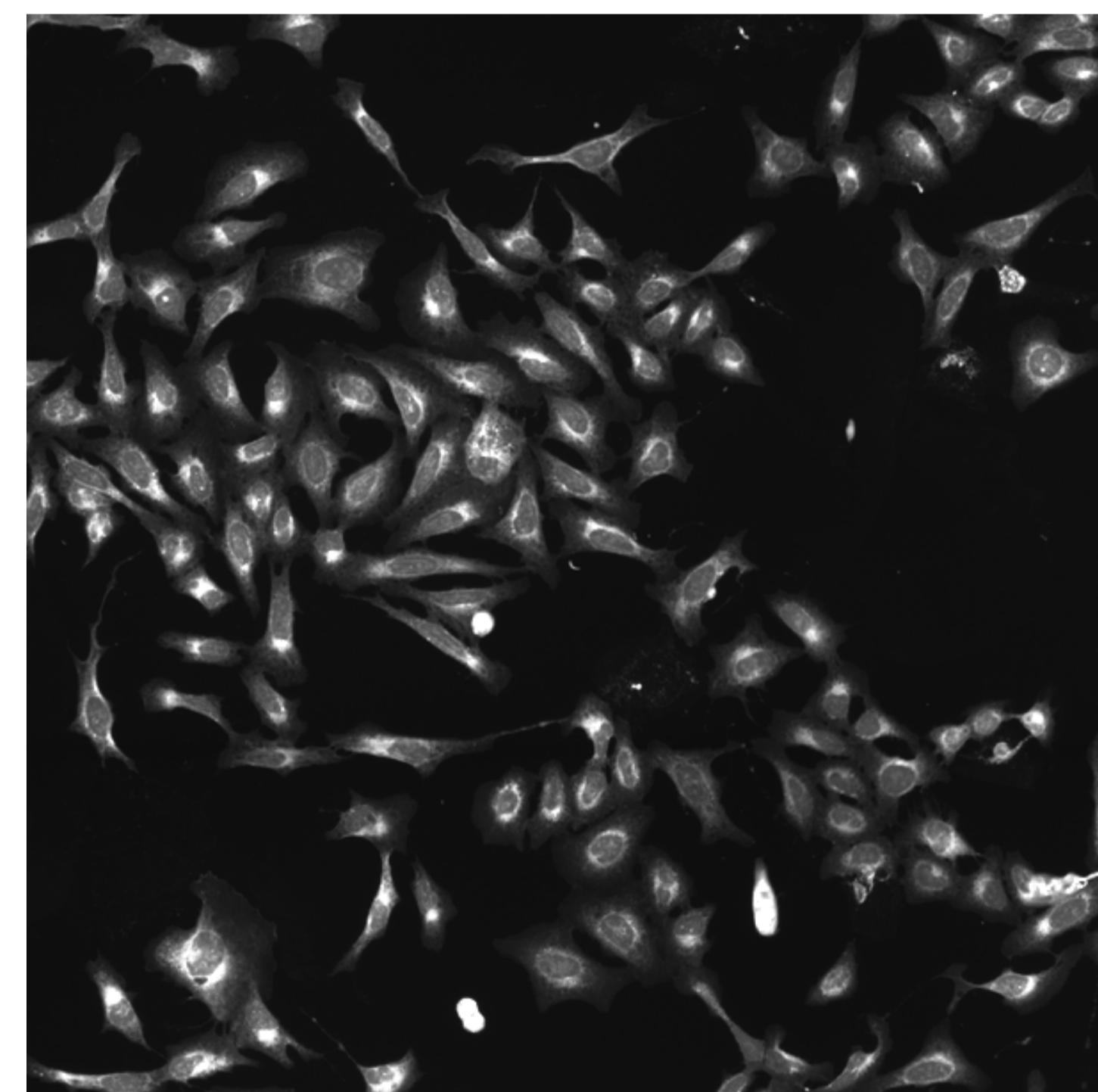
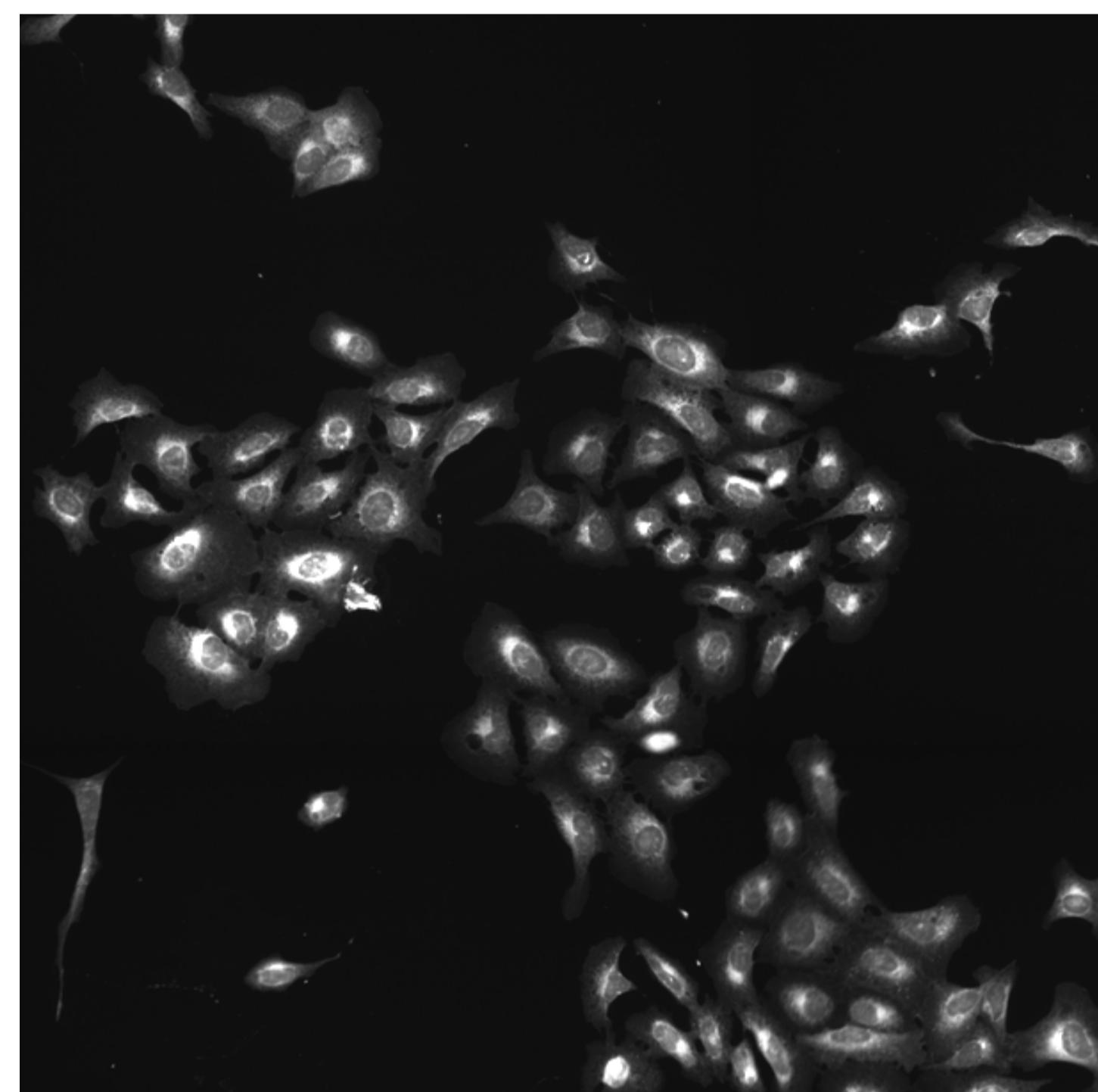
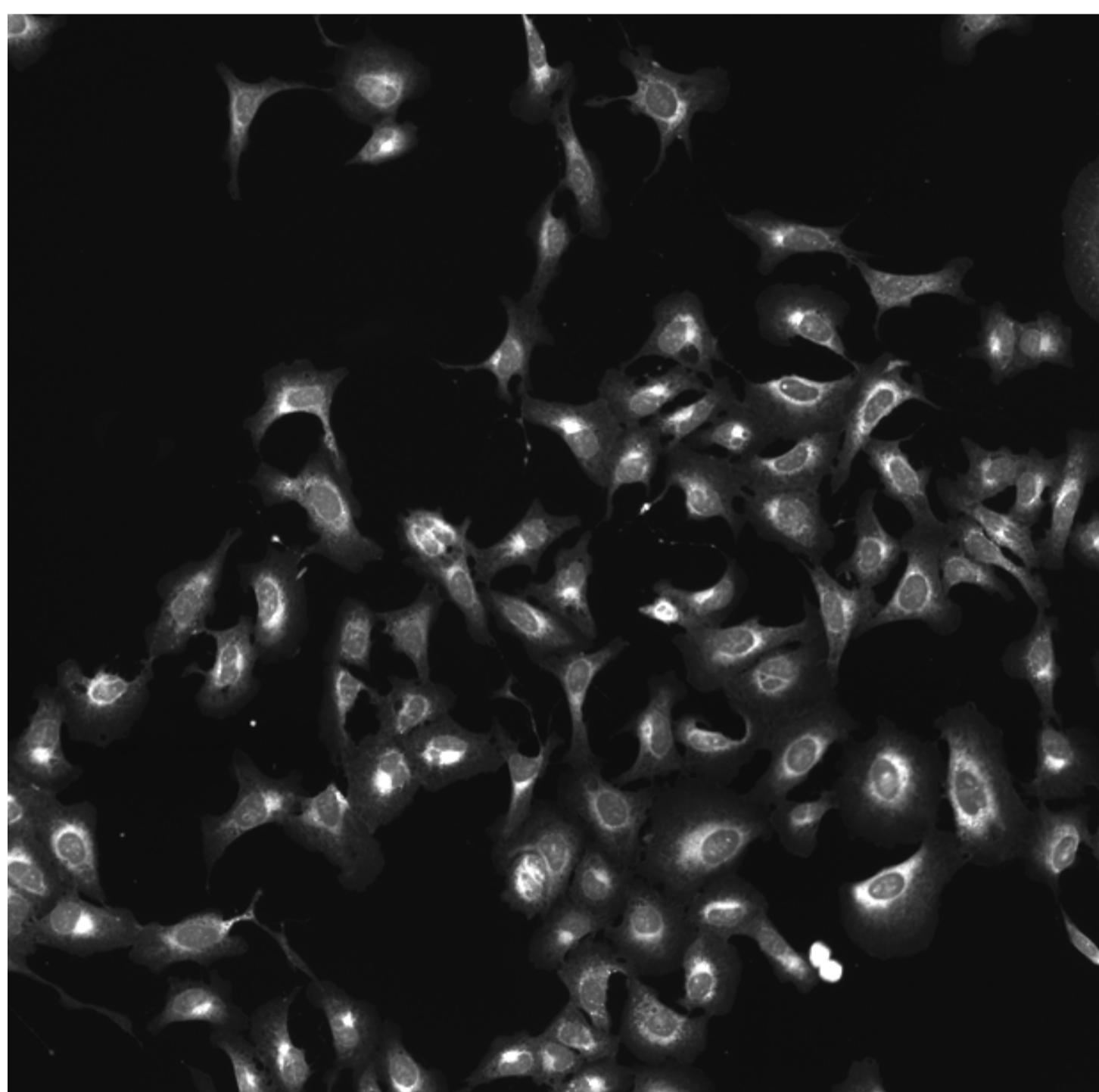
E2F1_WT

Empty

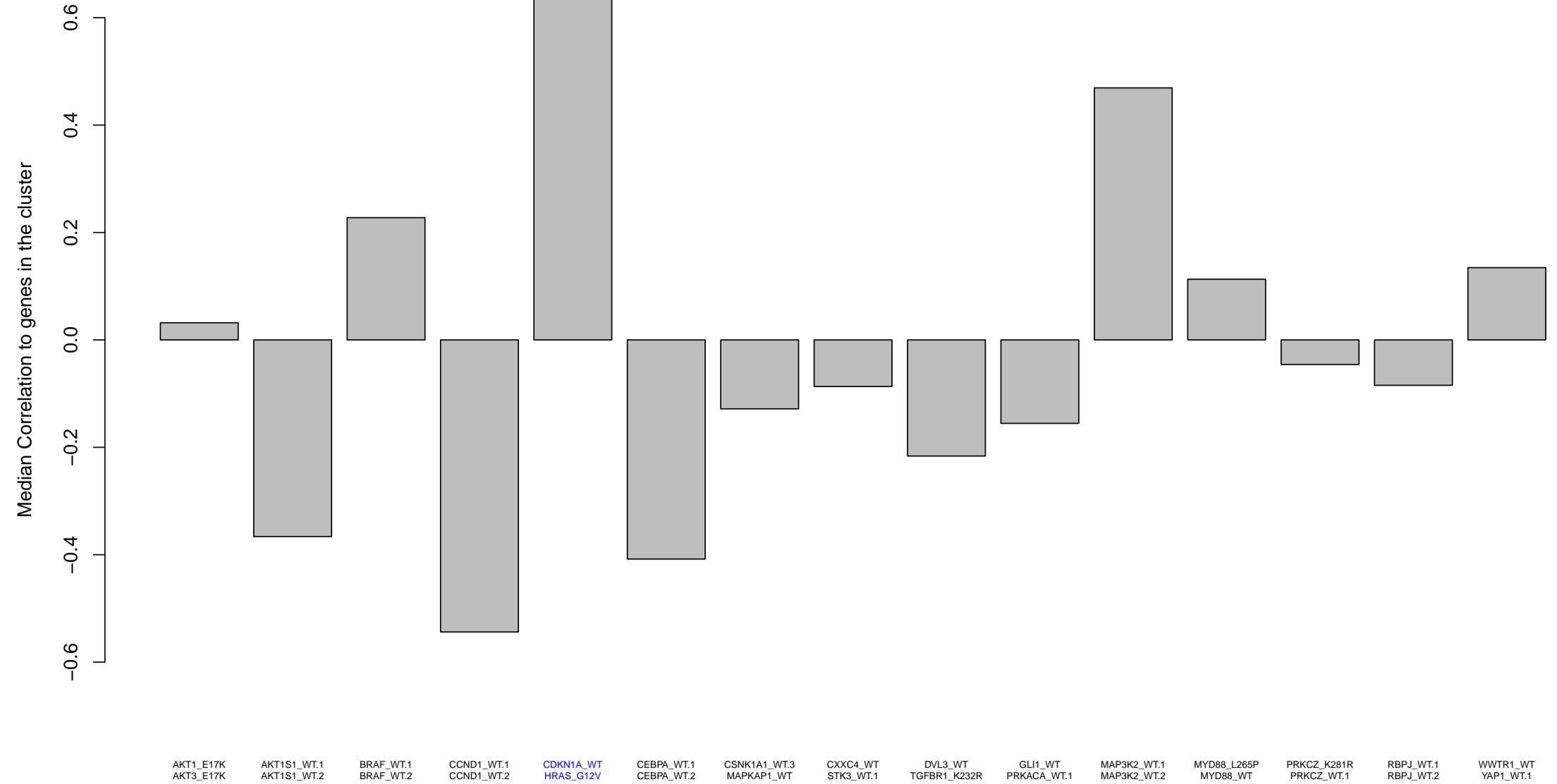


DNA

ER

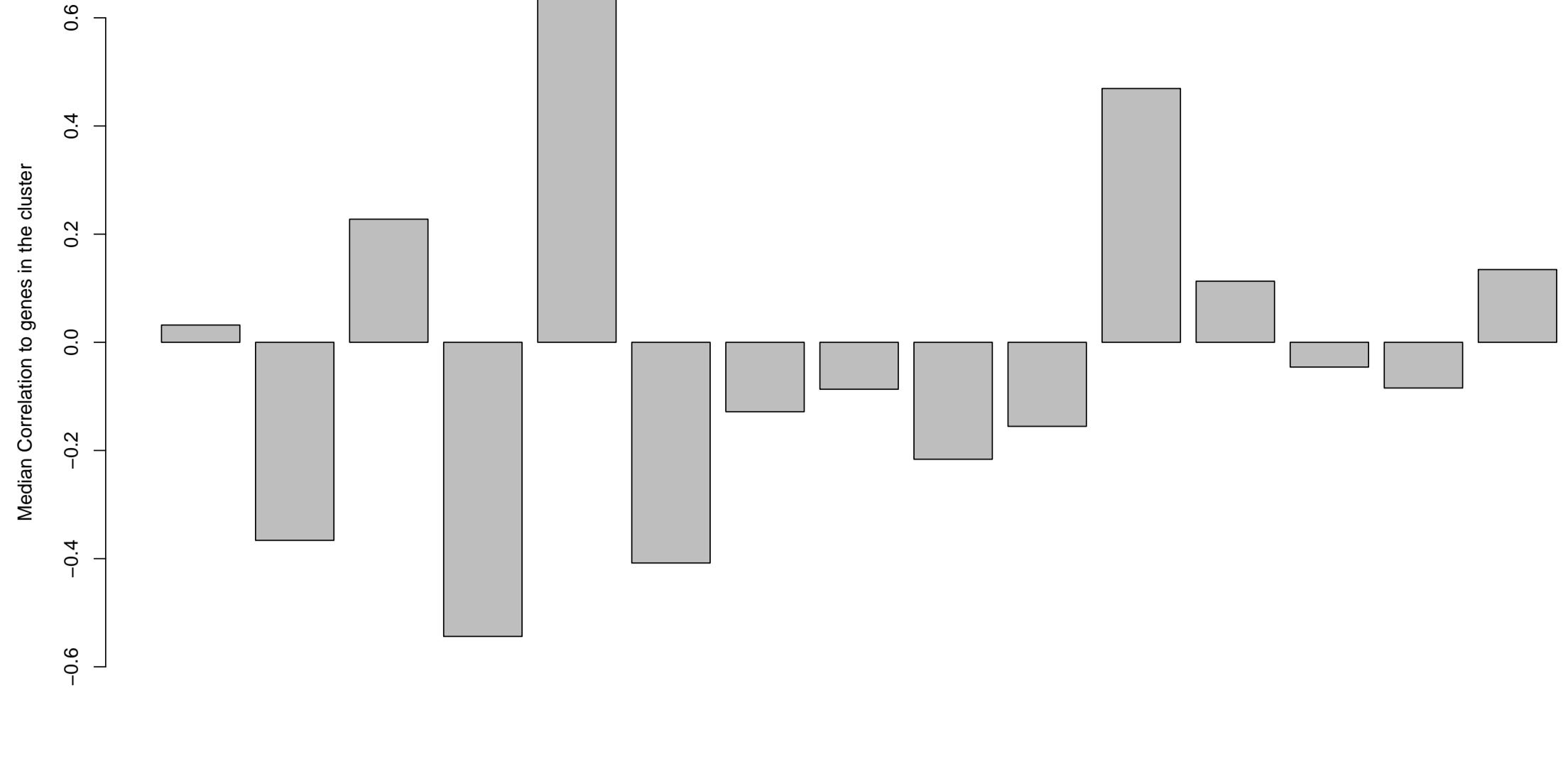


Cluster 5
How similar is this cluster to the other clusters?

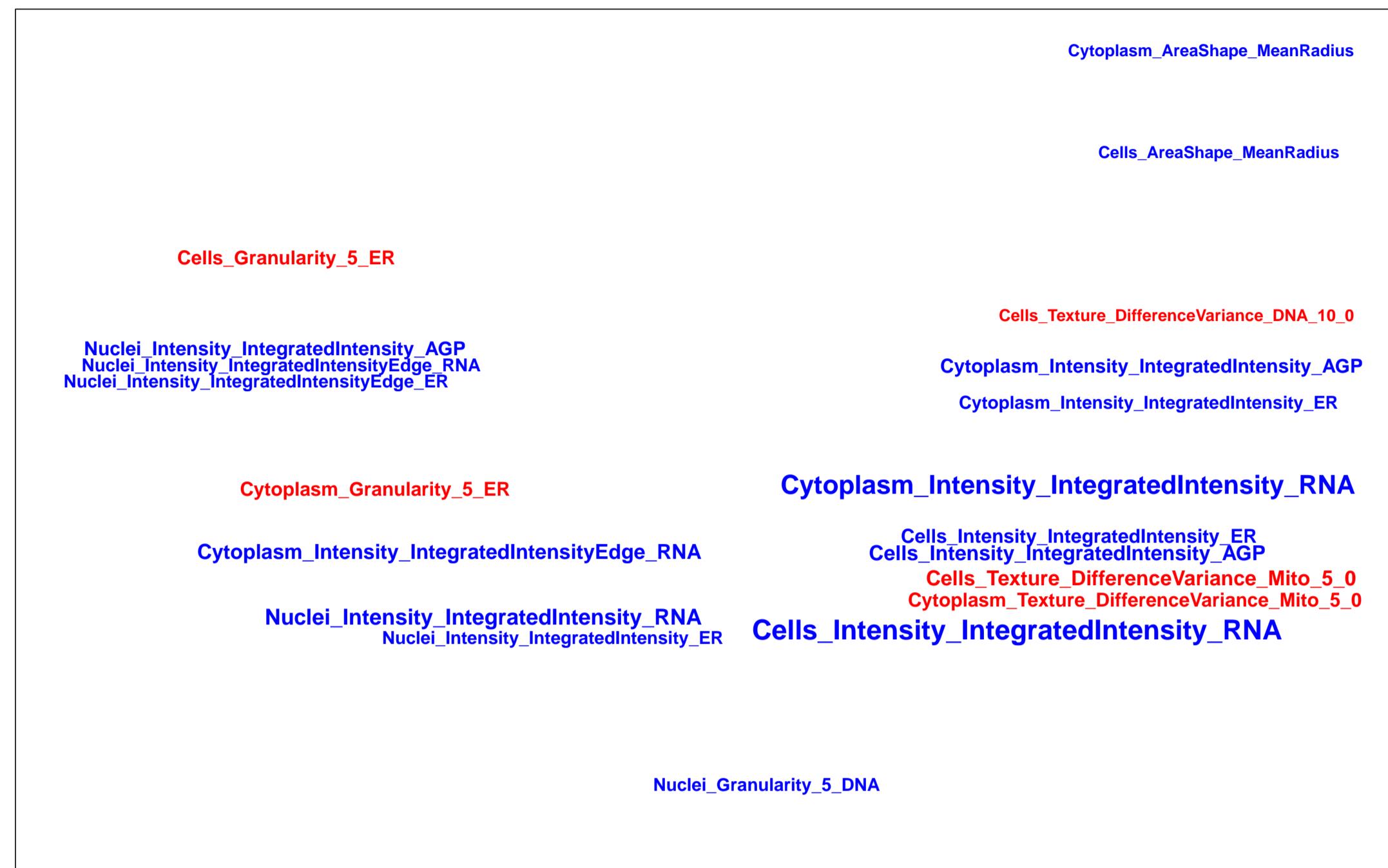
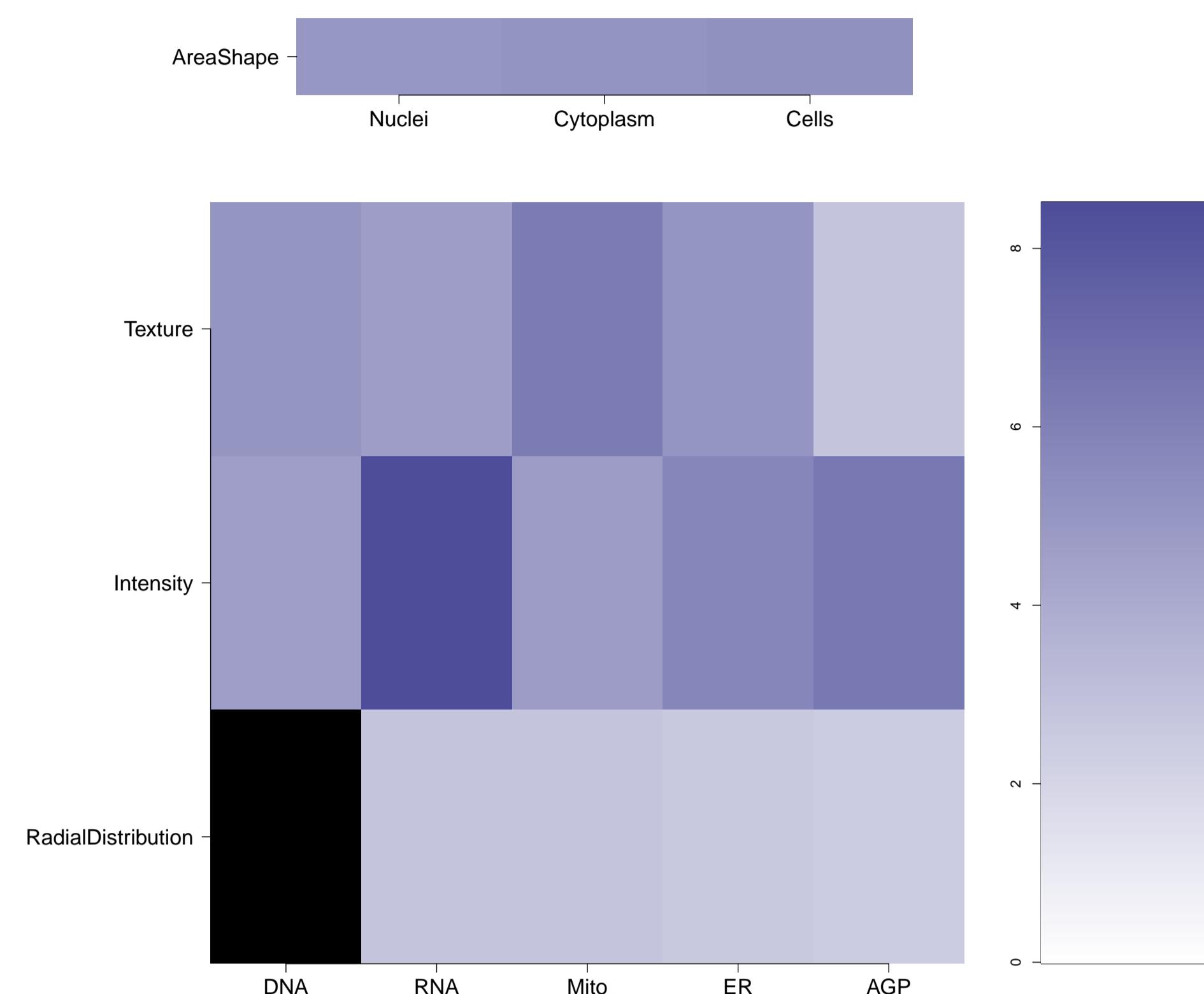


Genes in the cluster along with the pathways as annotated by experts

Treatment	Expert Annotation	
	Pathway	Regulation Type
CDKN1A_WT	Canonical Cell Cycle	Inhibitor
MAP3K5_WT	Canonical MAPK	Activator
MAP2K4_WT_1	Canonical MAPK	Activator
MAP2K3_WT	Canonical MAPK	Activator
KRAS_G12V	RTK	Activator
HRAS_G12V	RTK	Activator



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



How strongly are genes within the cluster correlated?

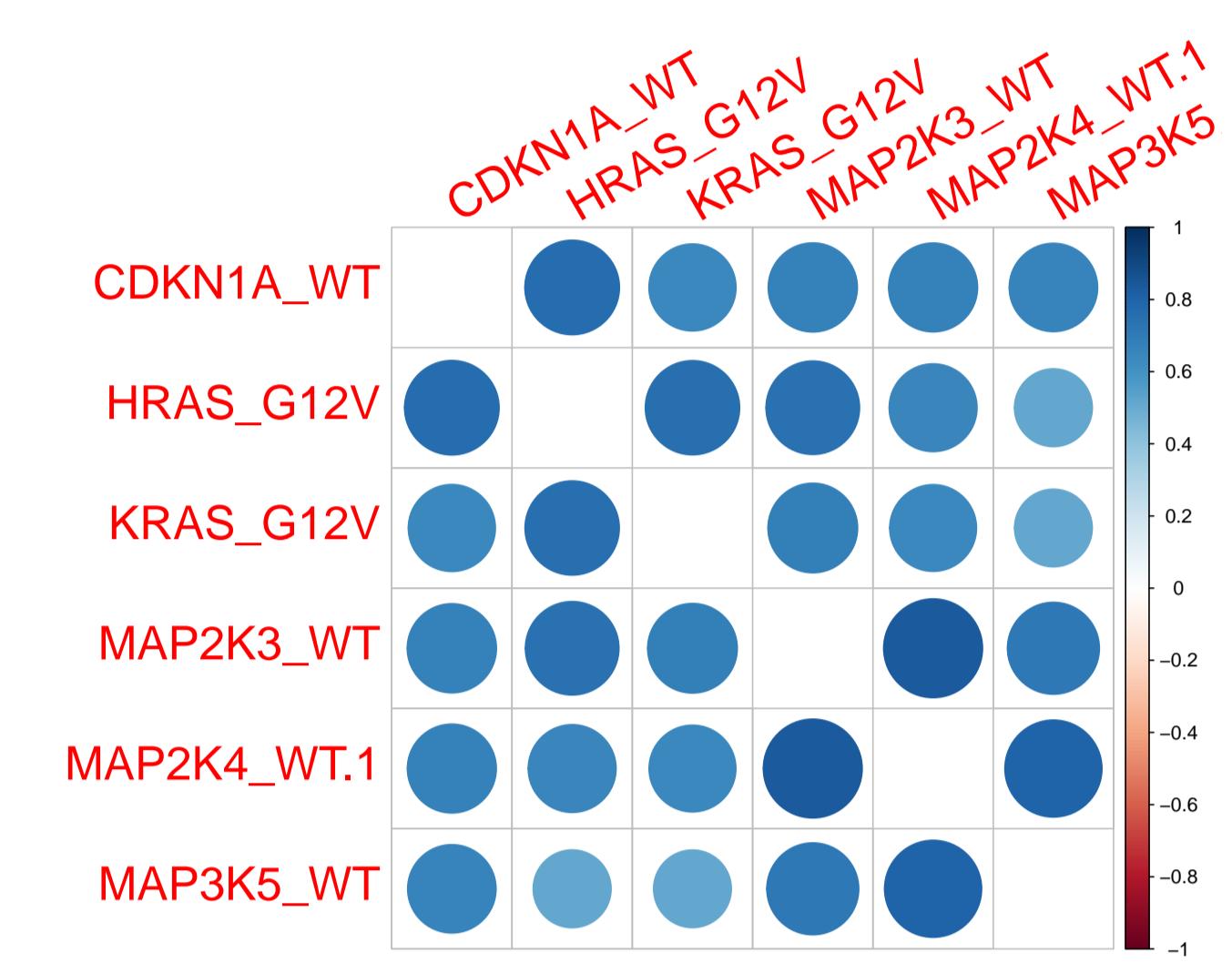


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

Empty CDKN1A_WT

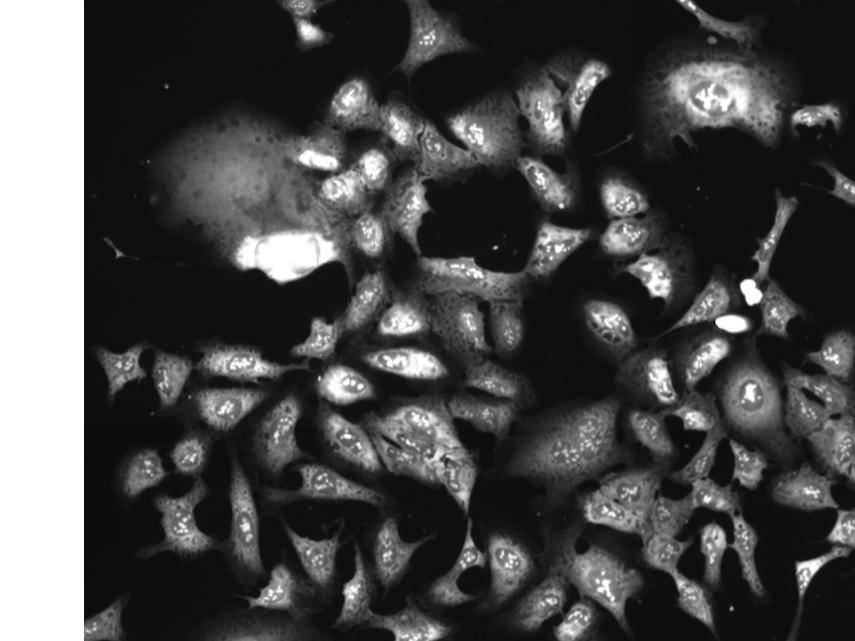
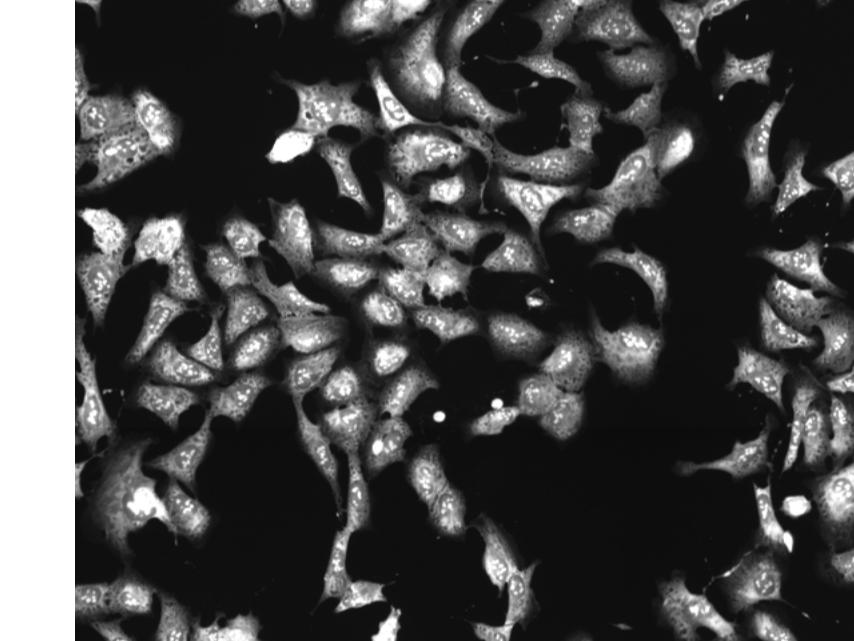
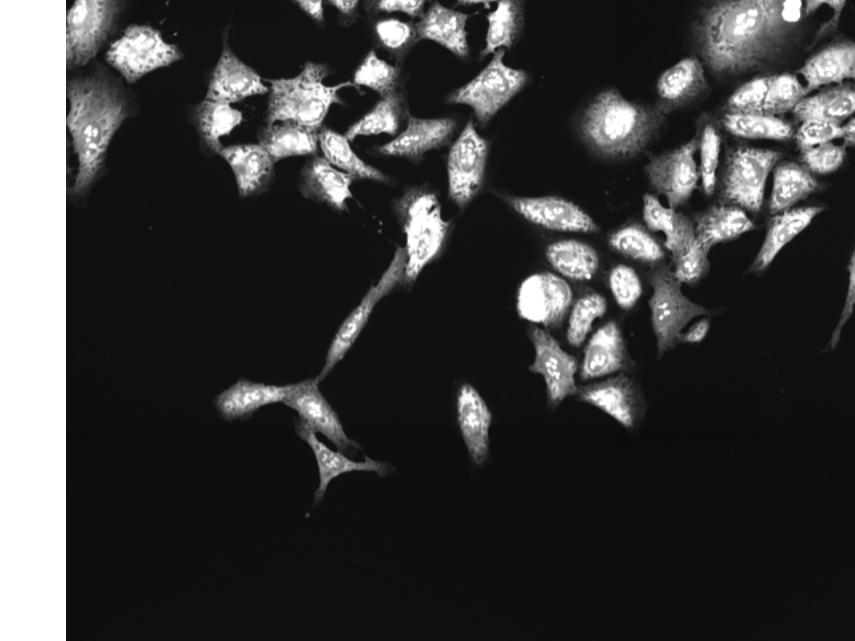
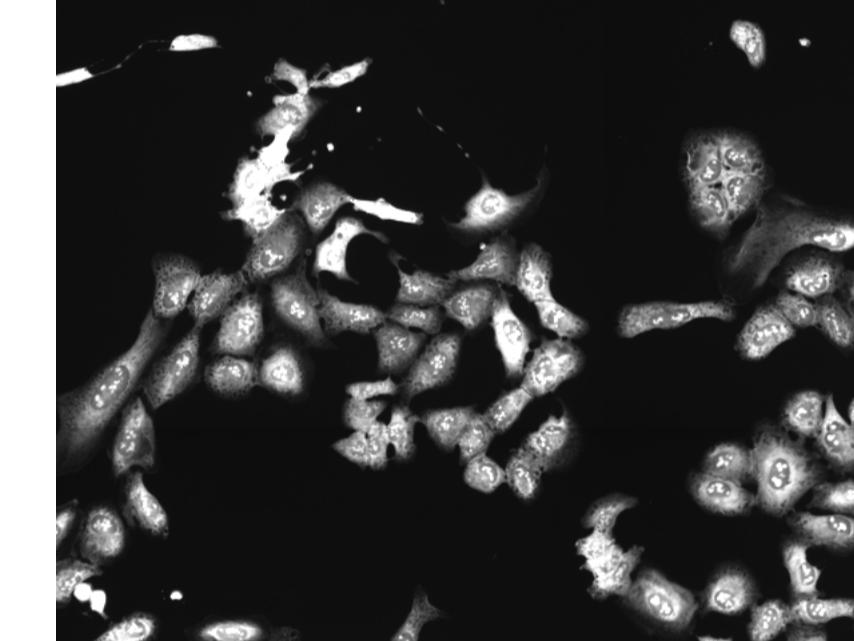
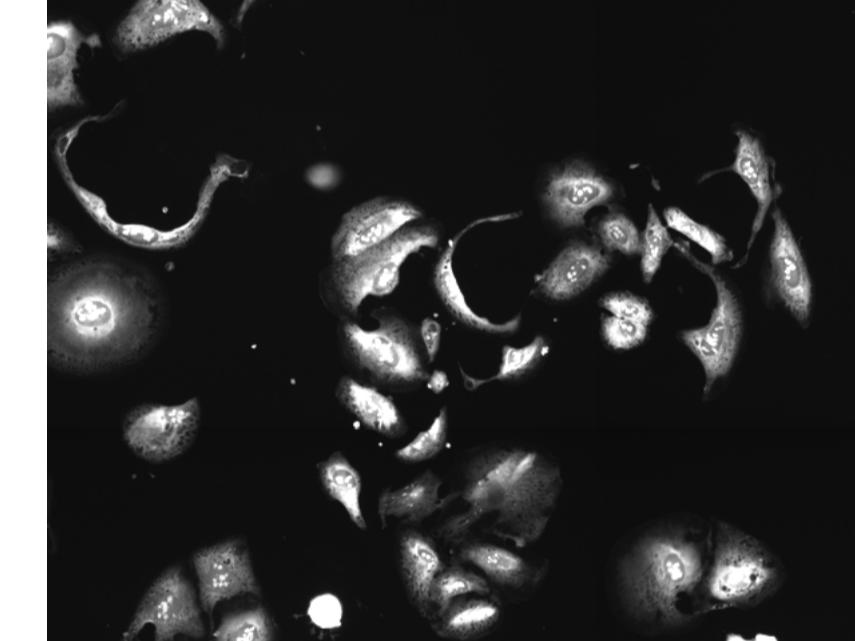
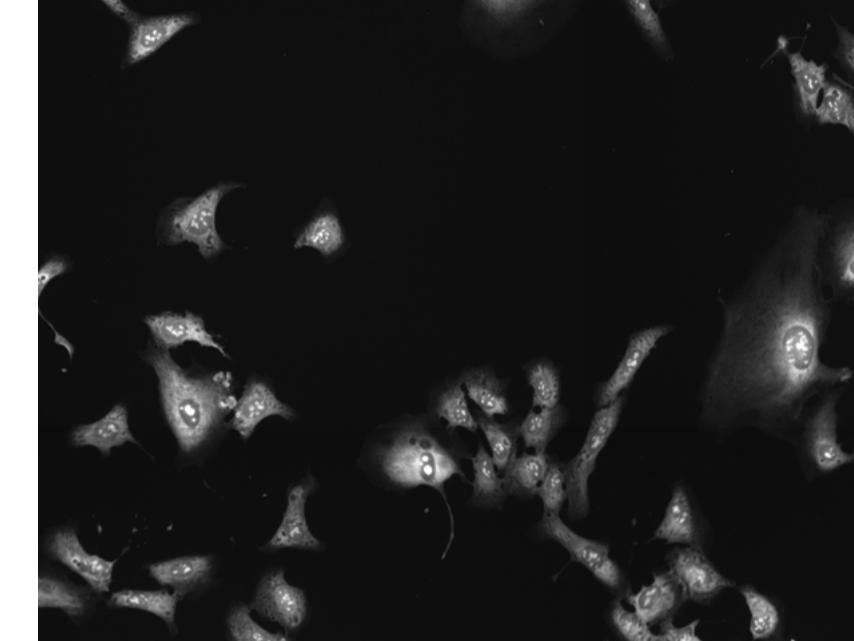
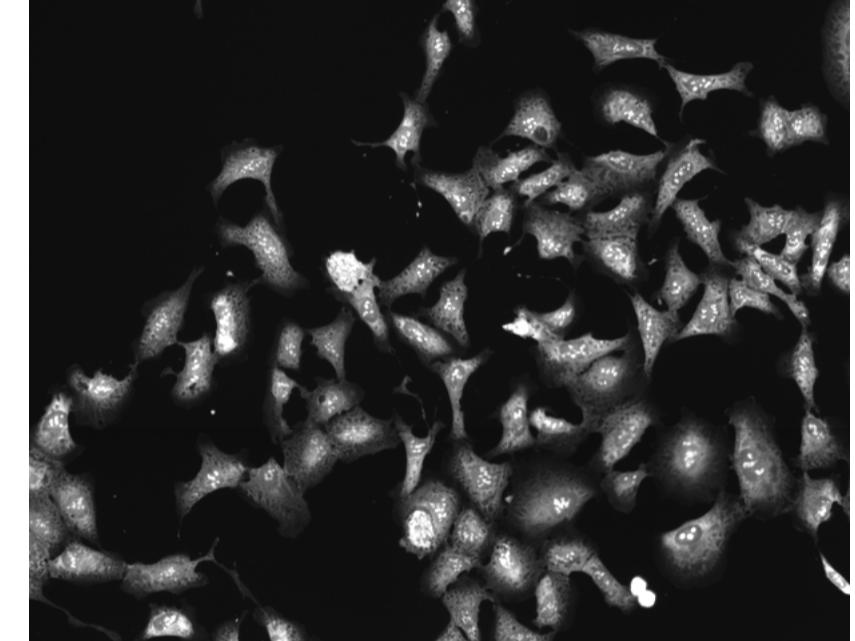
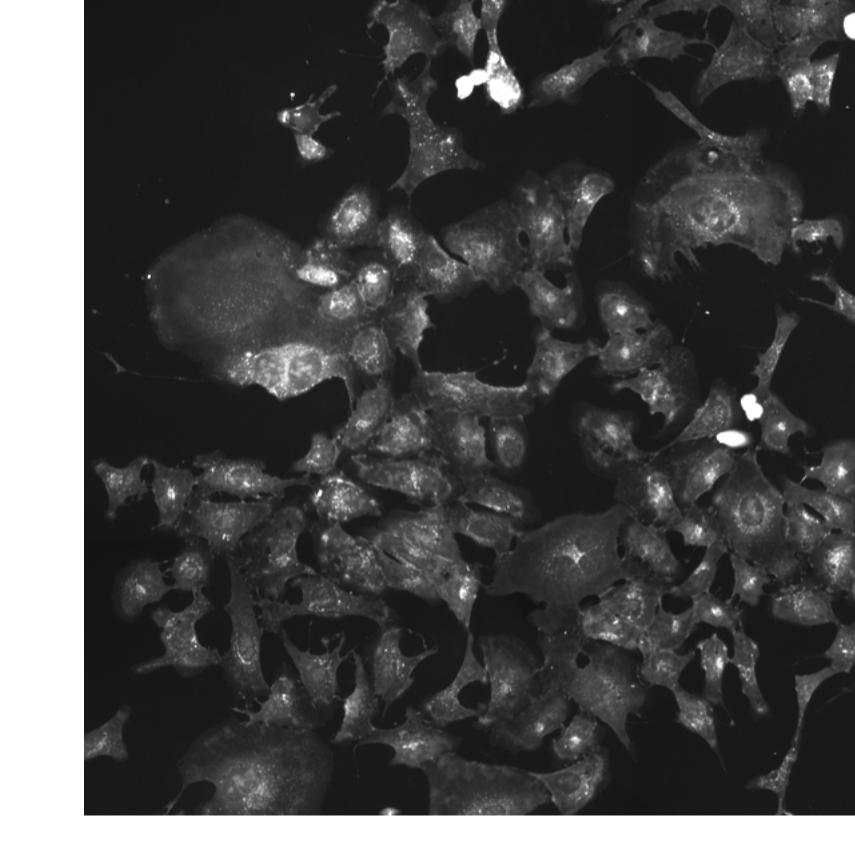
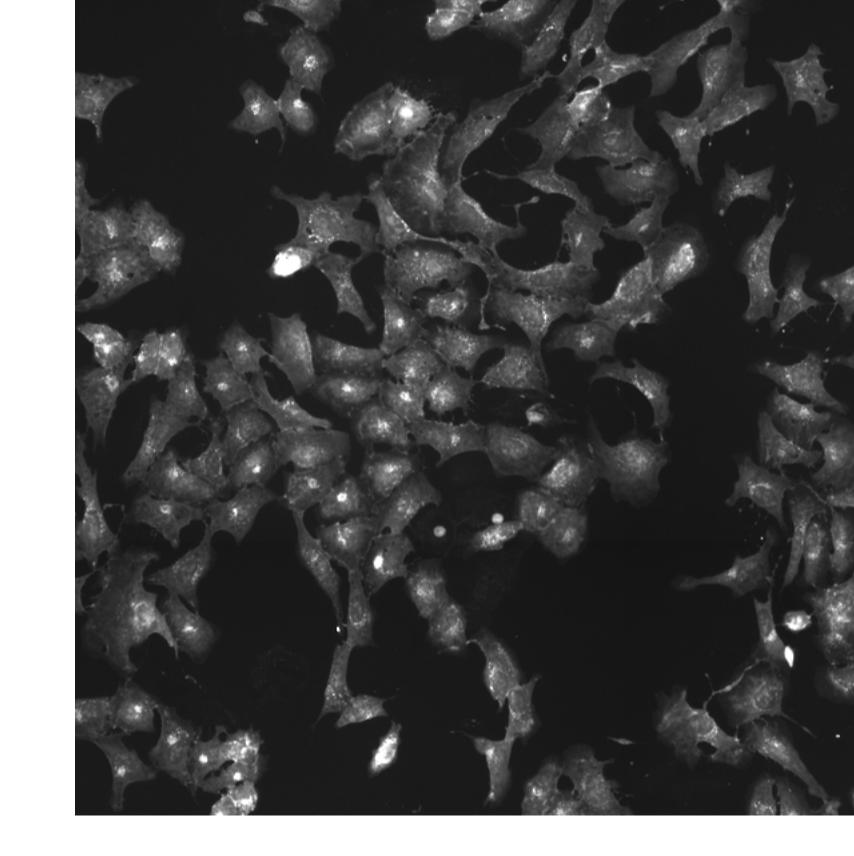
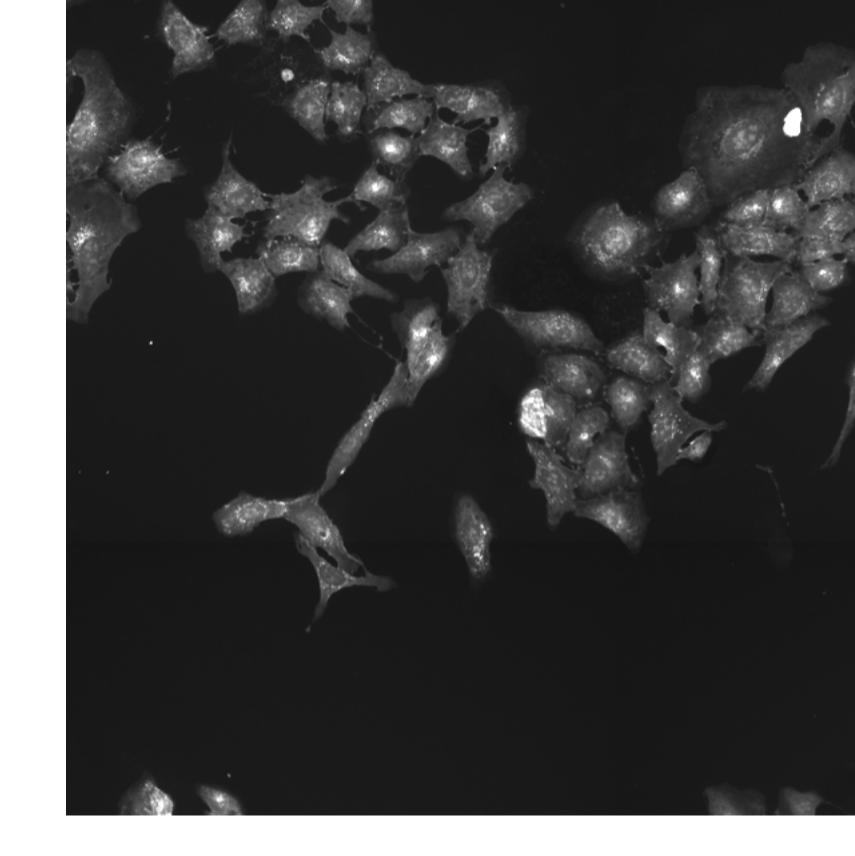
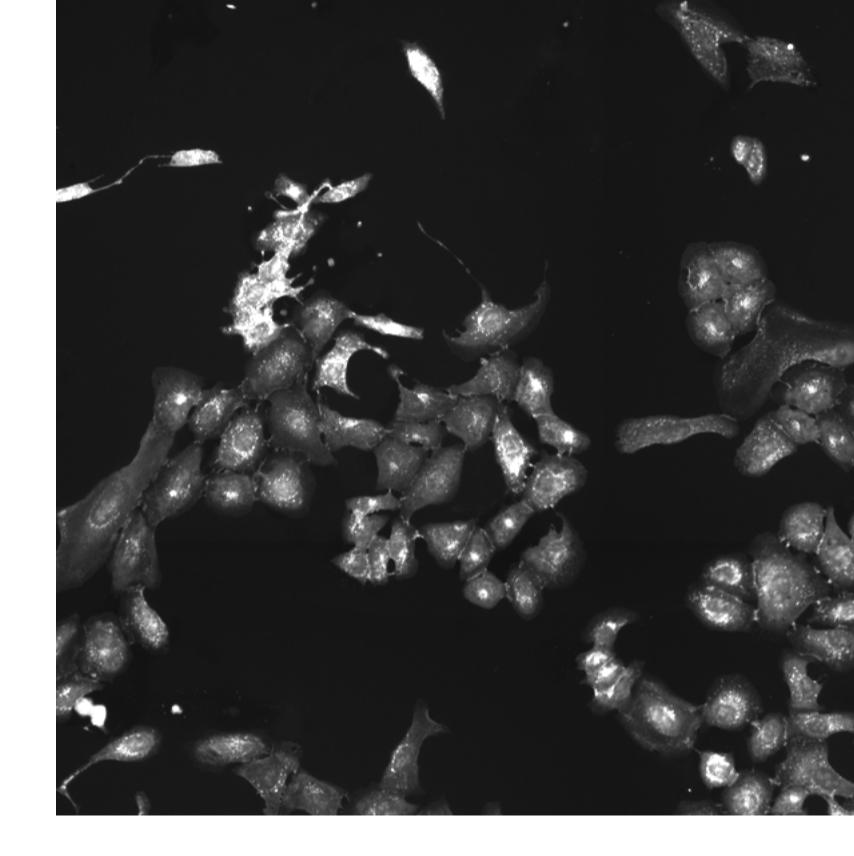
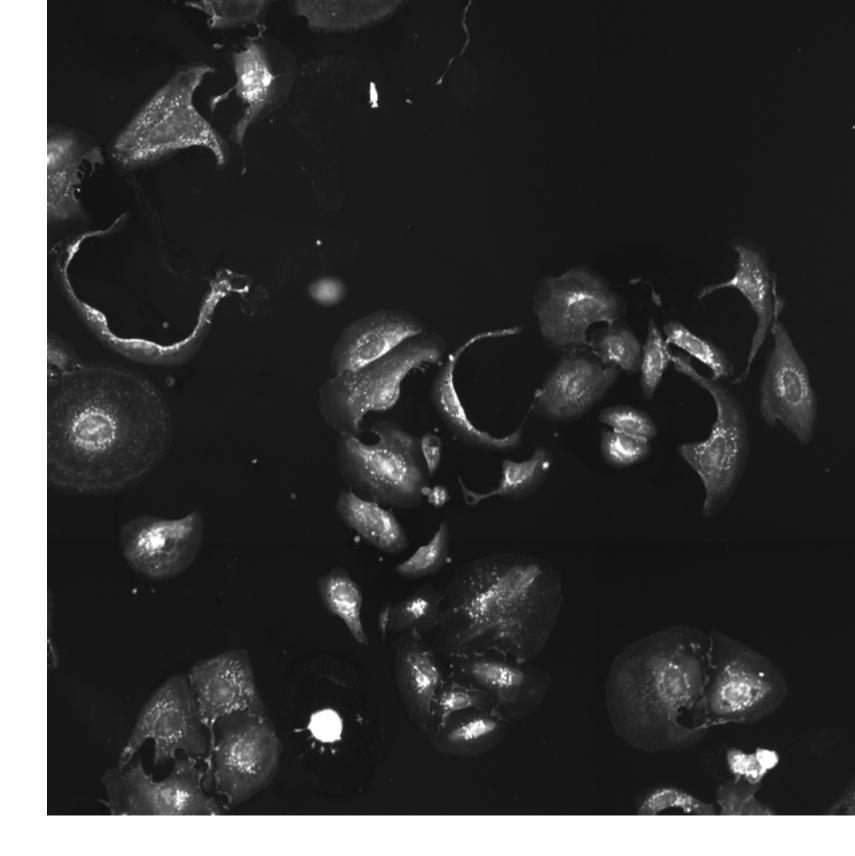
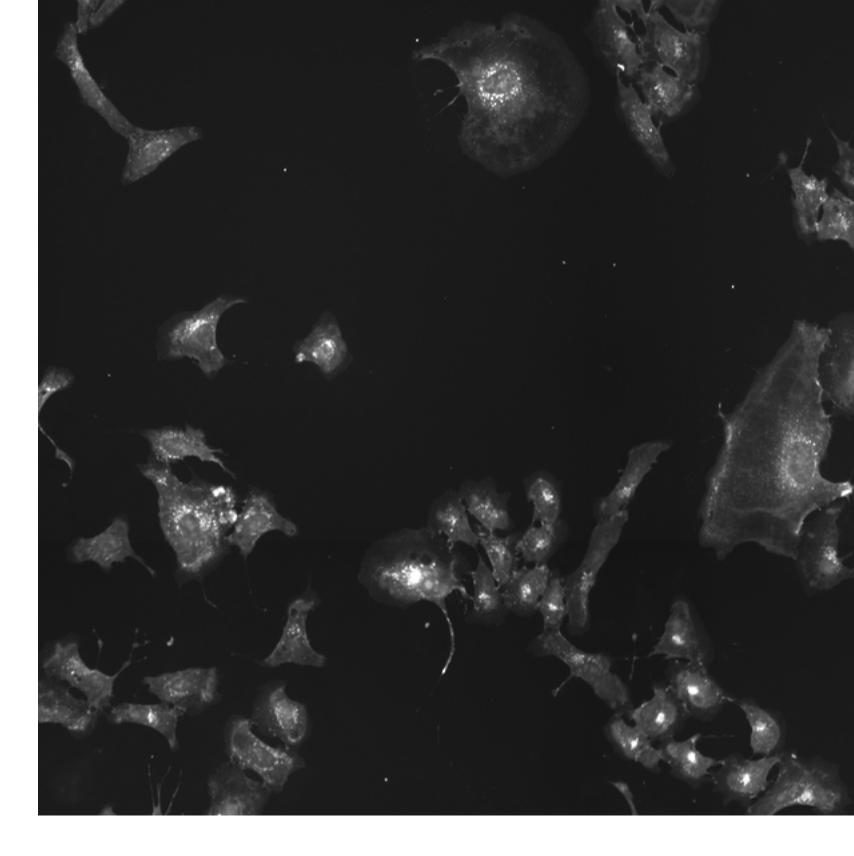
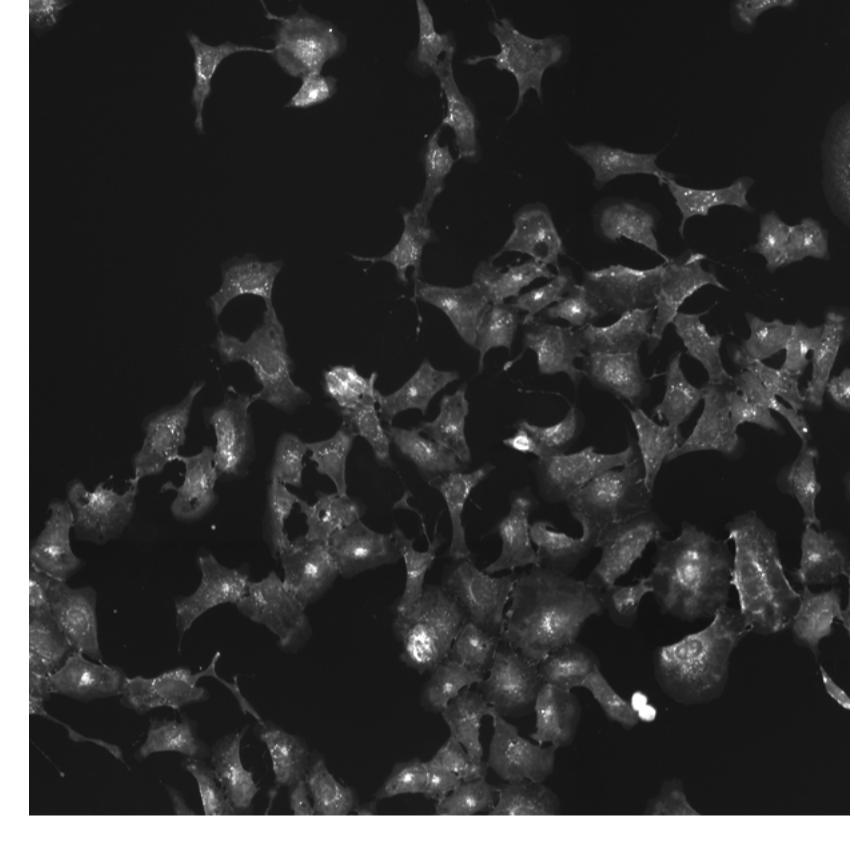
HRAS_G12V

KRAS_G12V

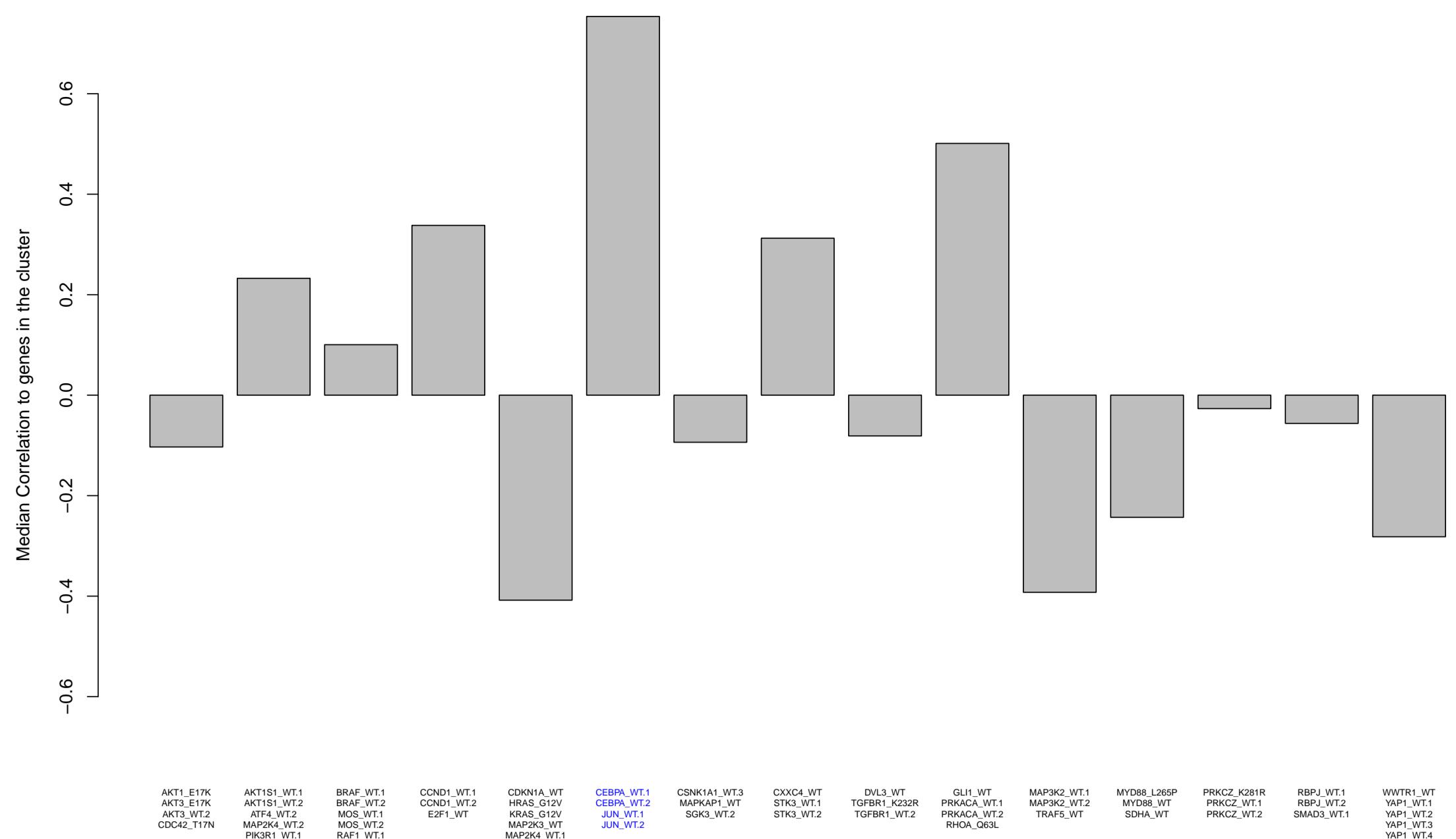
MAP2K3_WT

MAP2K4_WT_1

MAP3K5_WT



Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
JUN_WT.1	Canonical MAPK	Activator	
JUN_WT.2	Canonical MAPK	Activator	
CEBPA_WT.1	Transcription Factors	Activator	
CEBPA_WT.2	Transcription Factors	Activator	



Top 5 genes negatively correlated to the cluster						
Treatment	Expert Annotation			Mean Correlation	Standard Deviation	
	Pathway	Regulation	Type			
AKT1_WT.1	Canonical PI3K/AKT	Activator		-0.59	0.03	
PKIA_WT	PKA	Inhibitor		-0.48	0.12	
CDKN1A_WT	Canonical Cell Cycle	Inhibitor		-0.46	0.07	
RPS6KB1_WT.1	Canonical TOR	Activator		-0.46	0.09	
YAP1_WT.1	Canonical Hippo	Inhibitor		-0.44	0.05	

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?

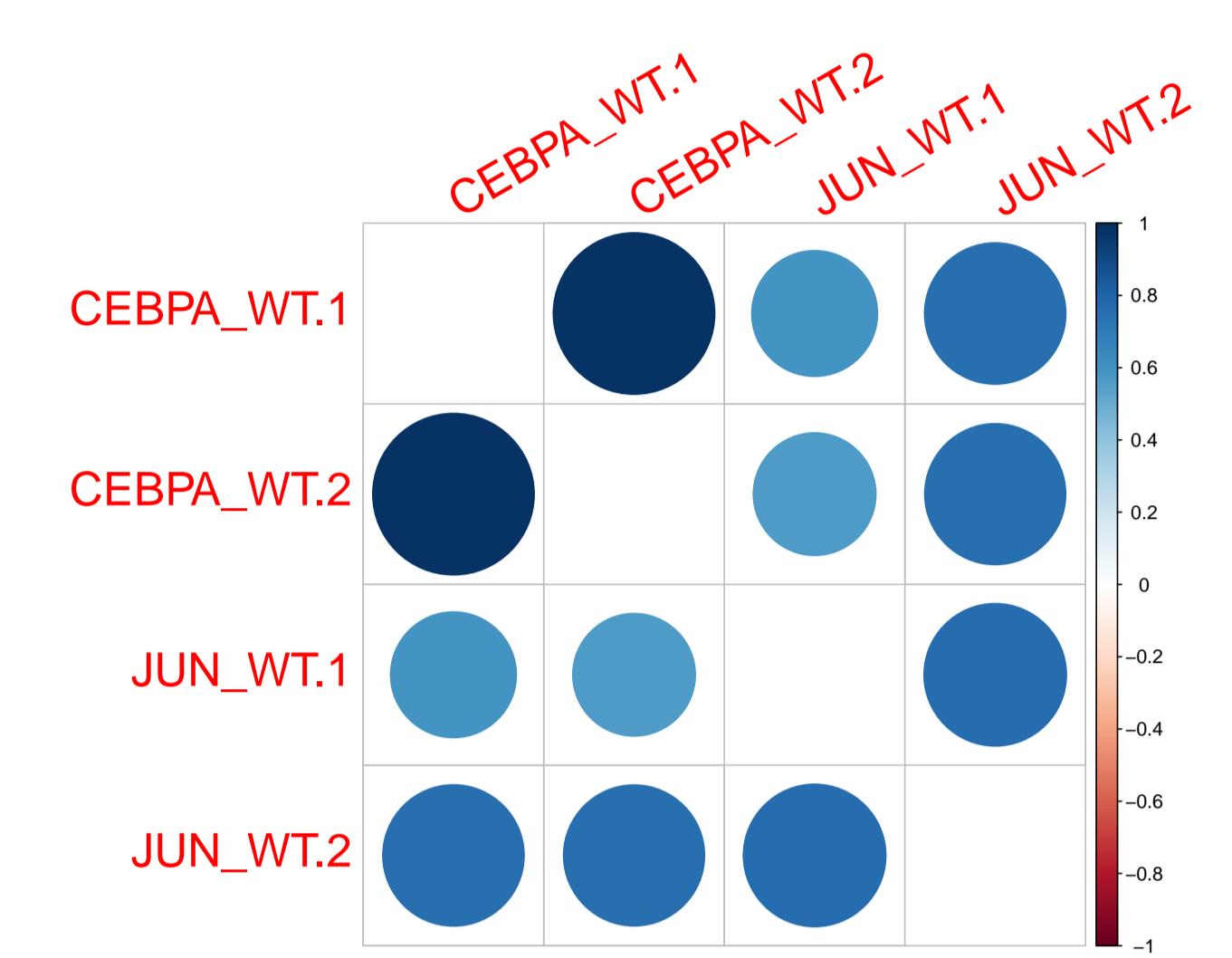
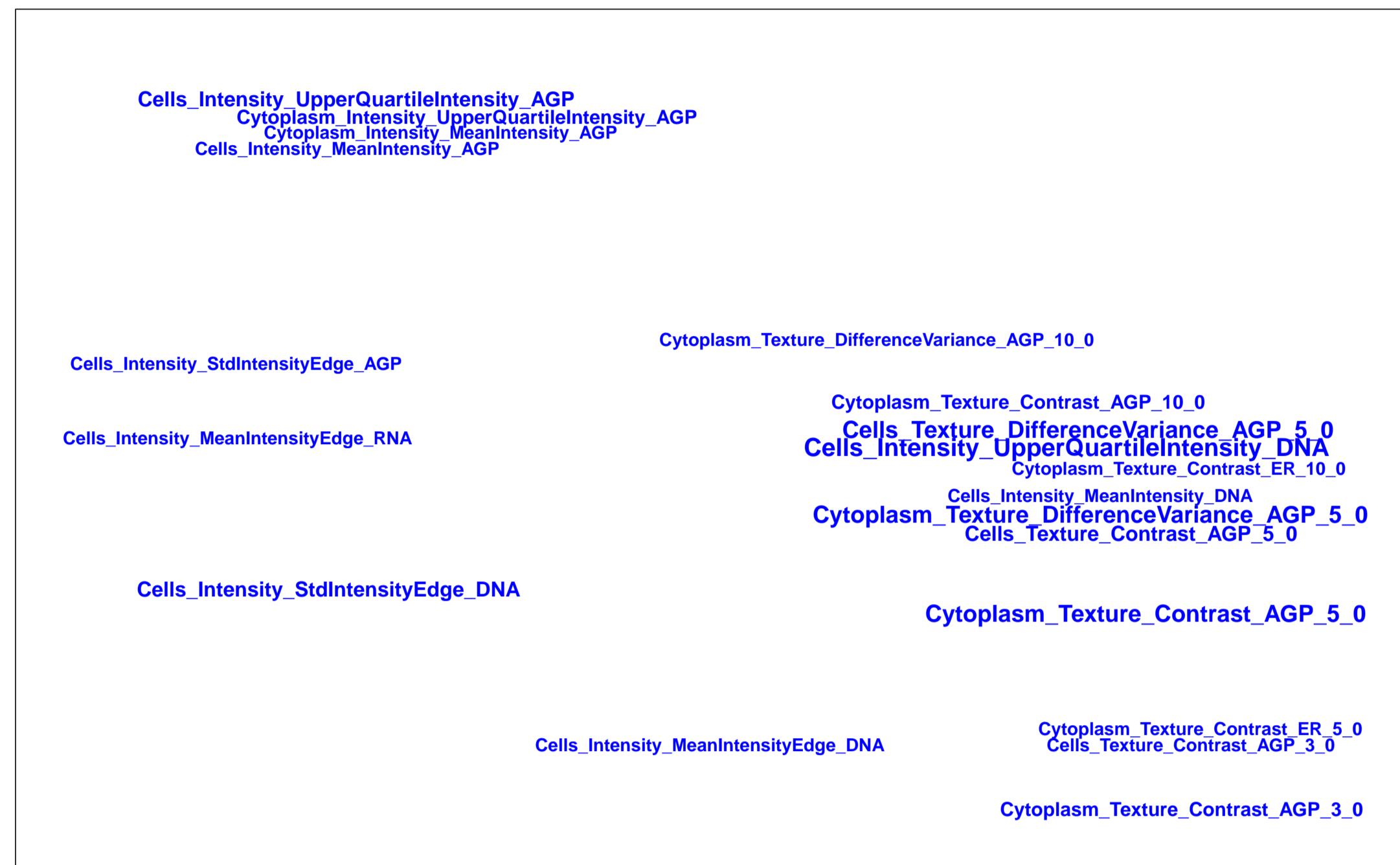
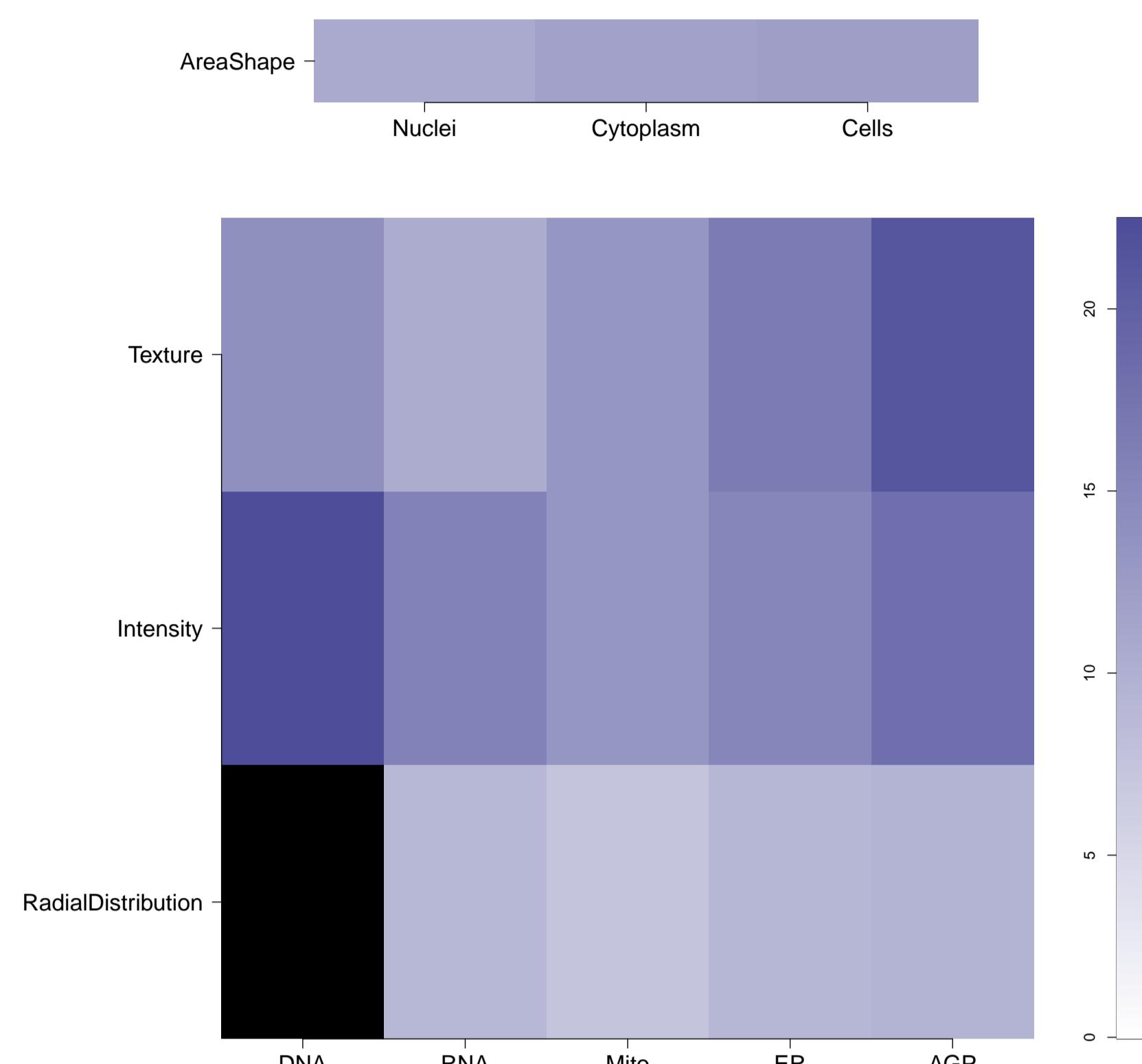


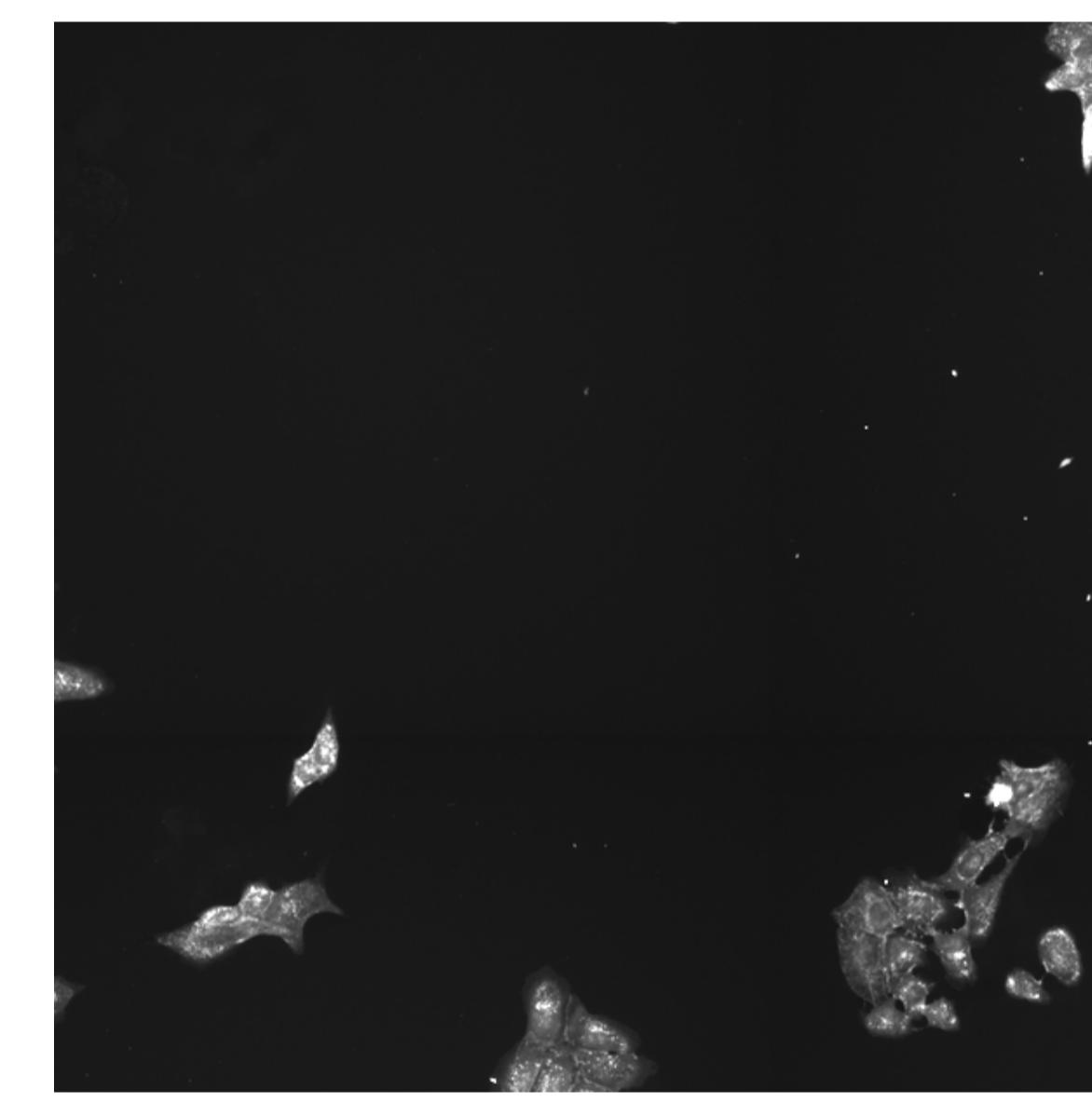
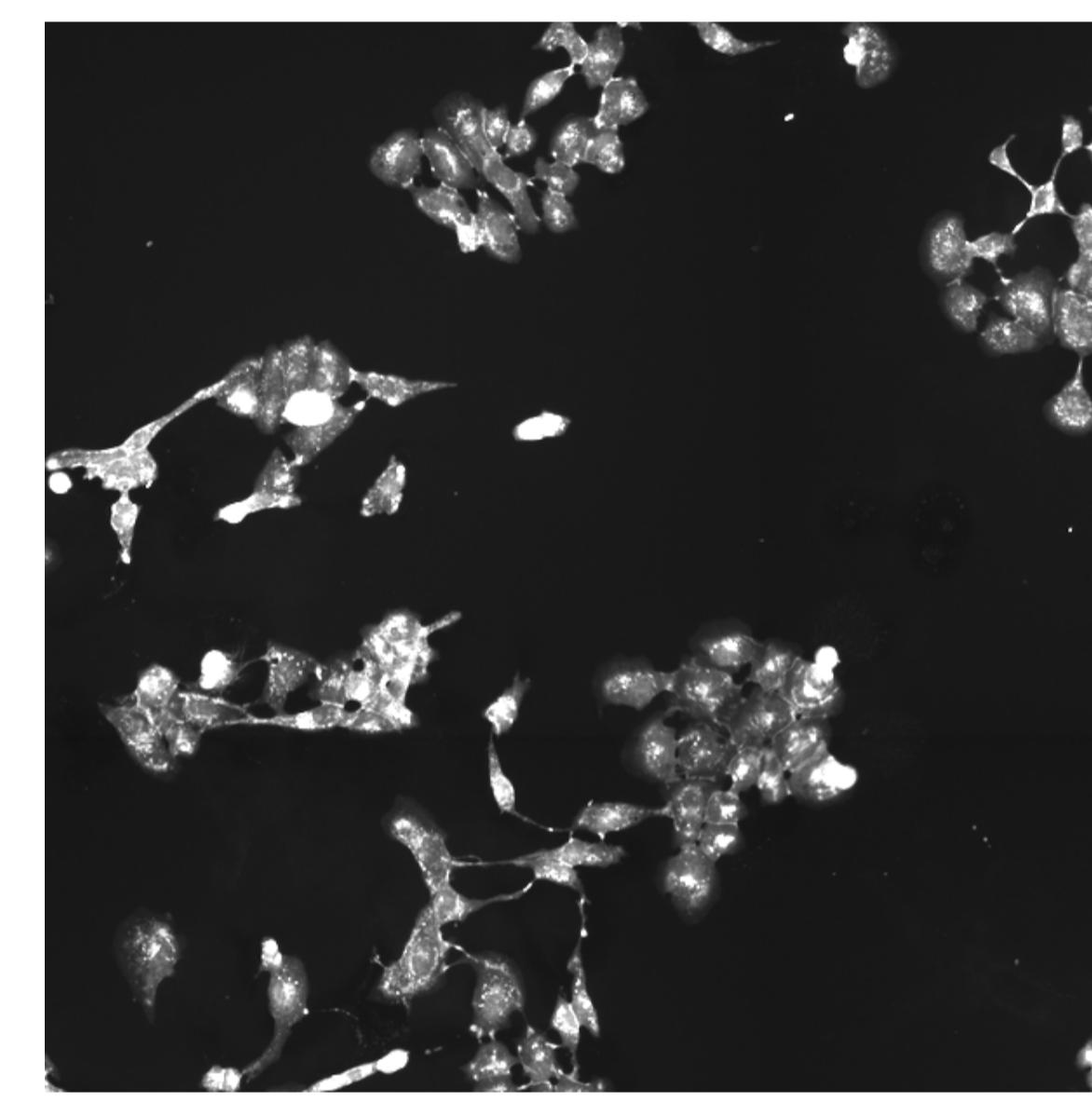
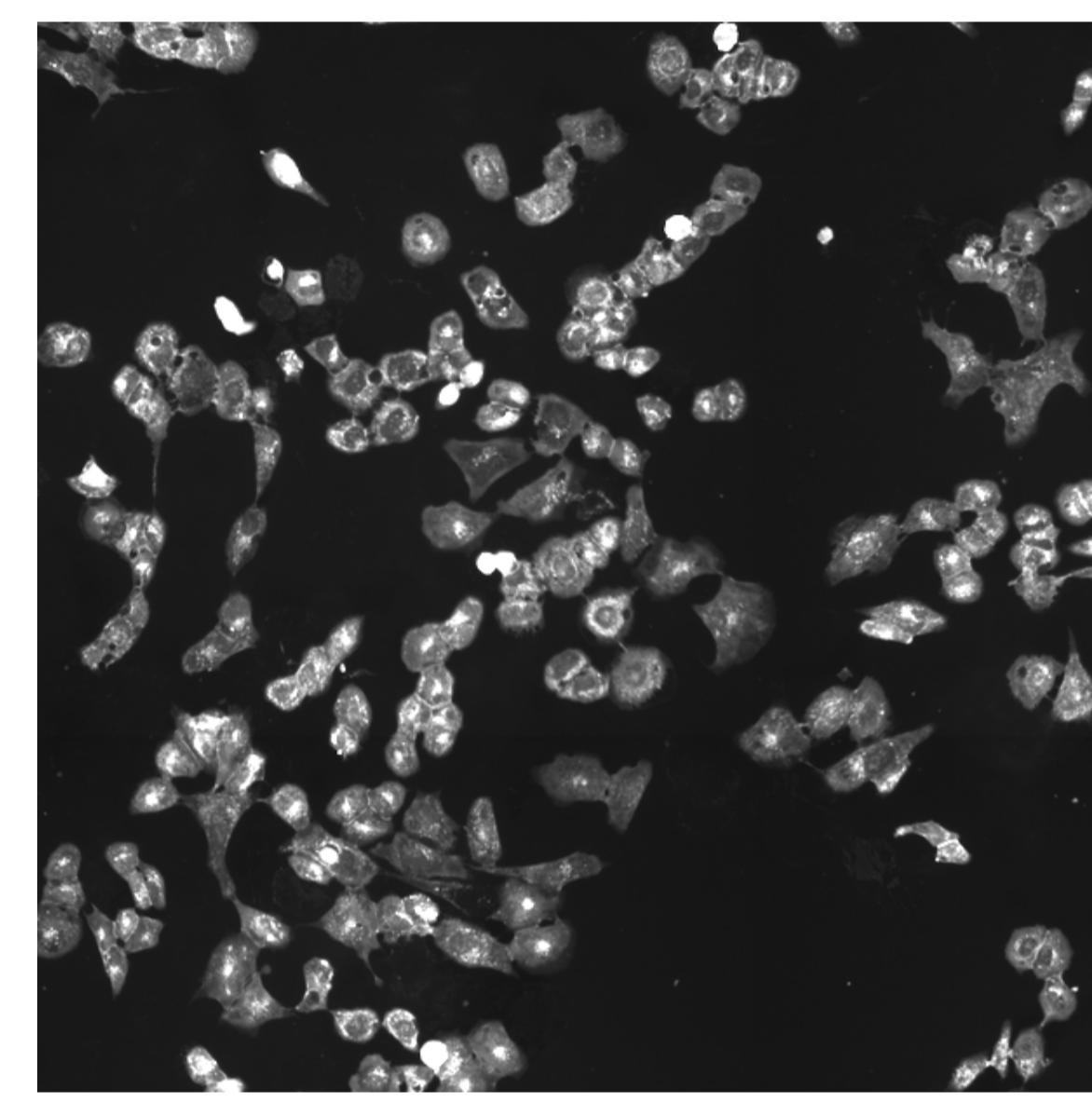
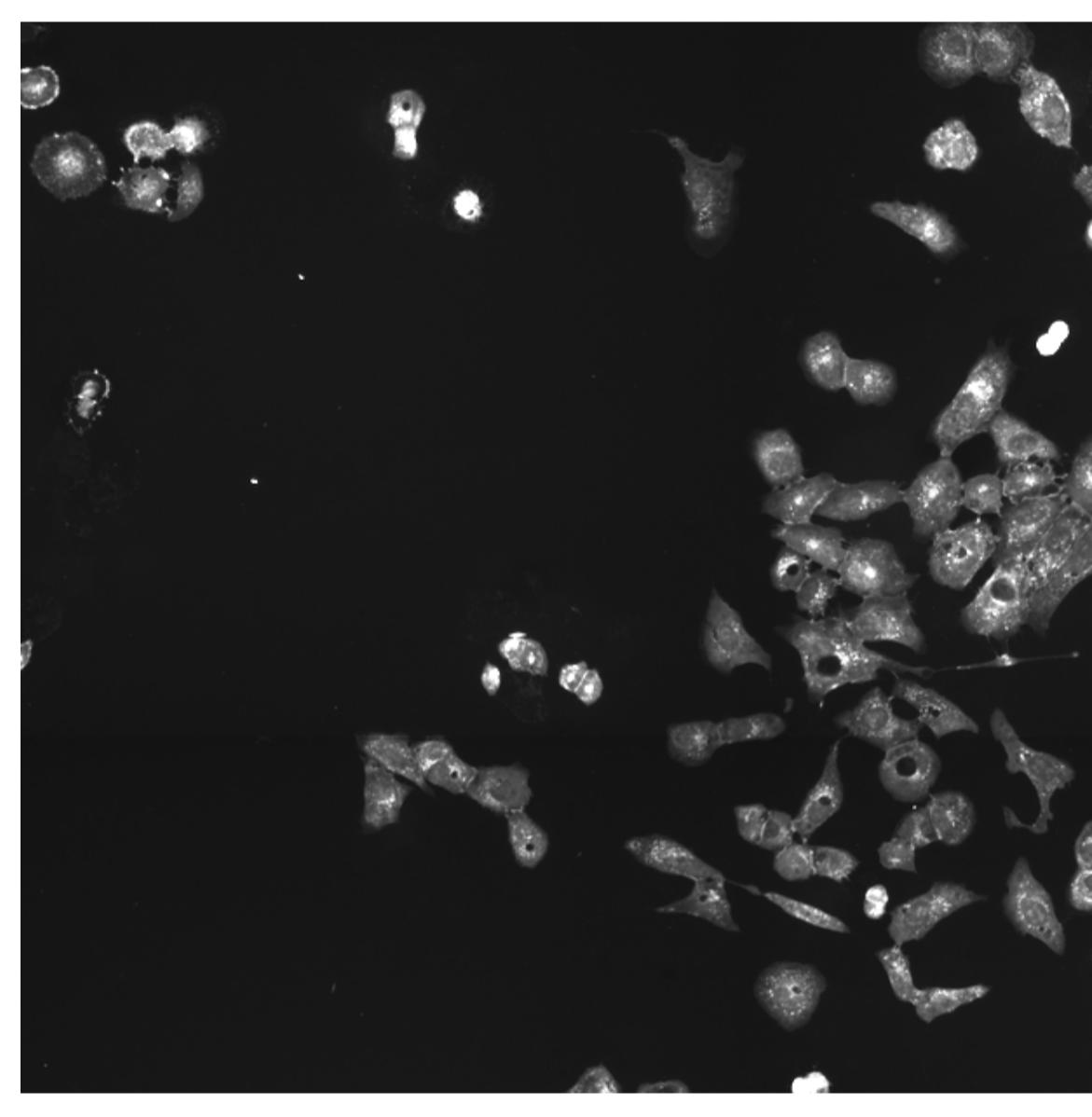
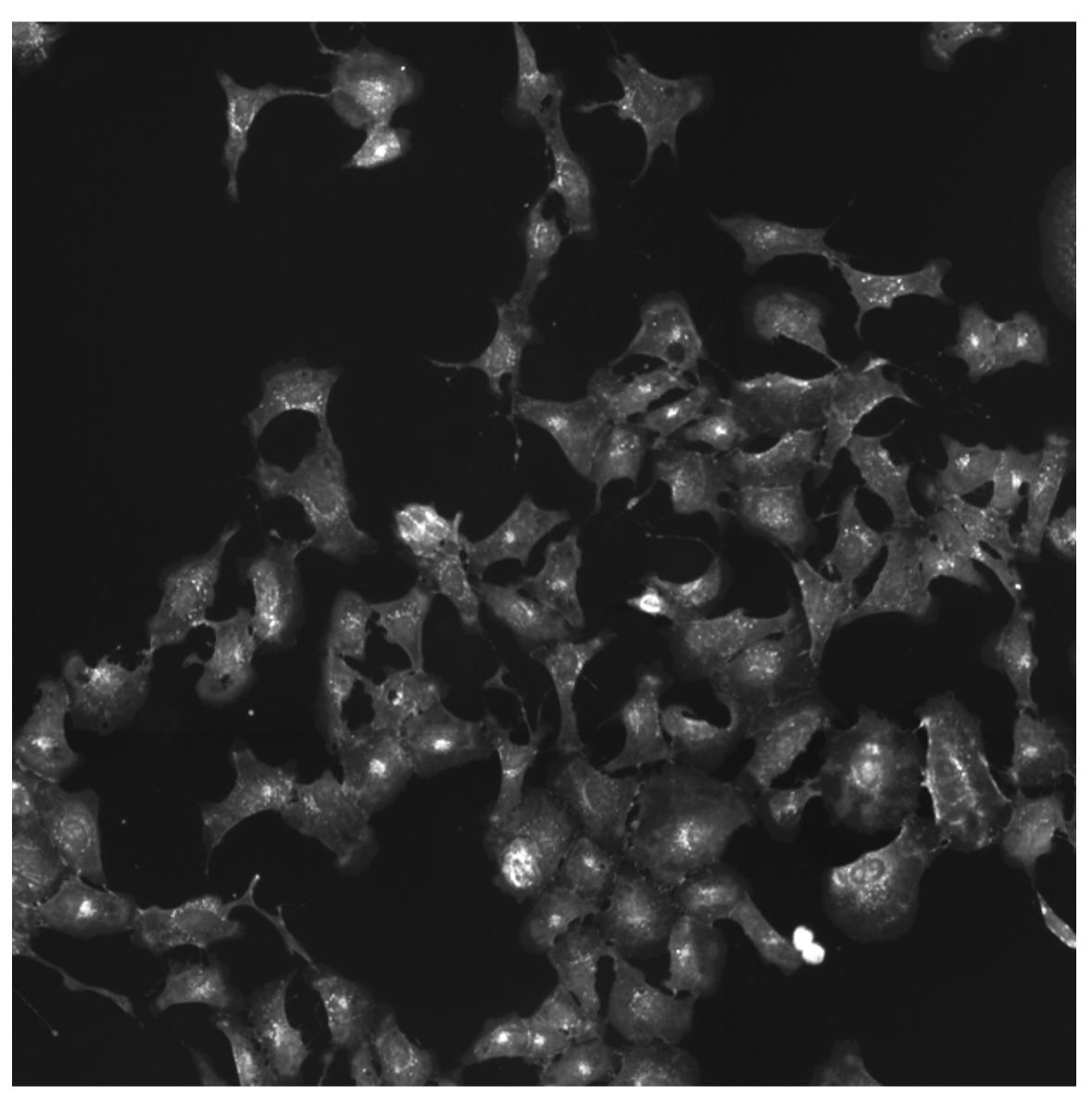
Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

CEBPA_WT.1

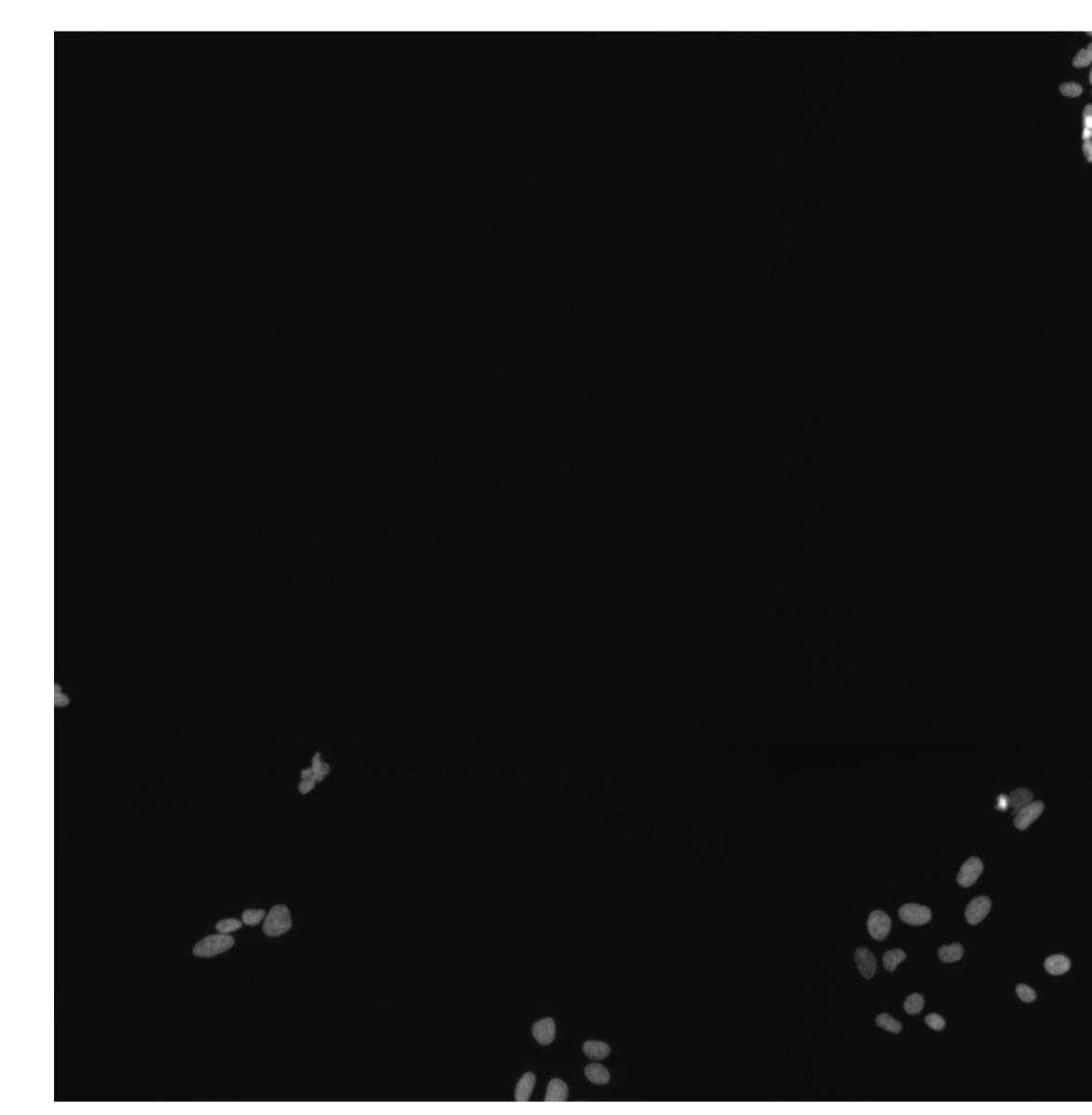
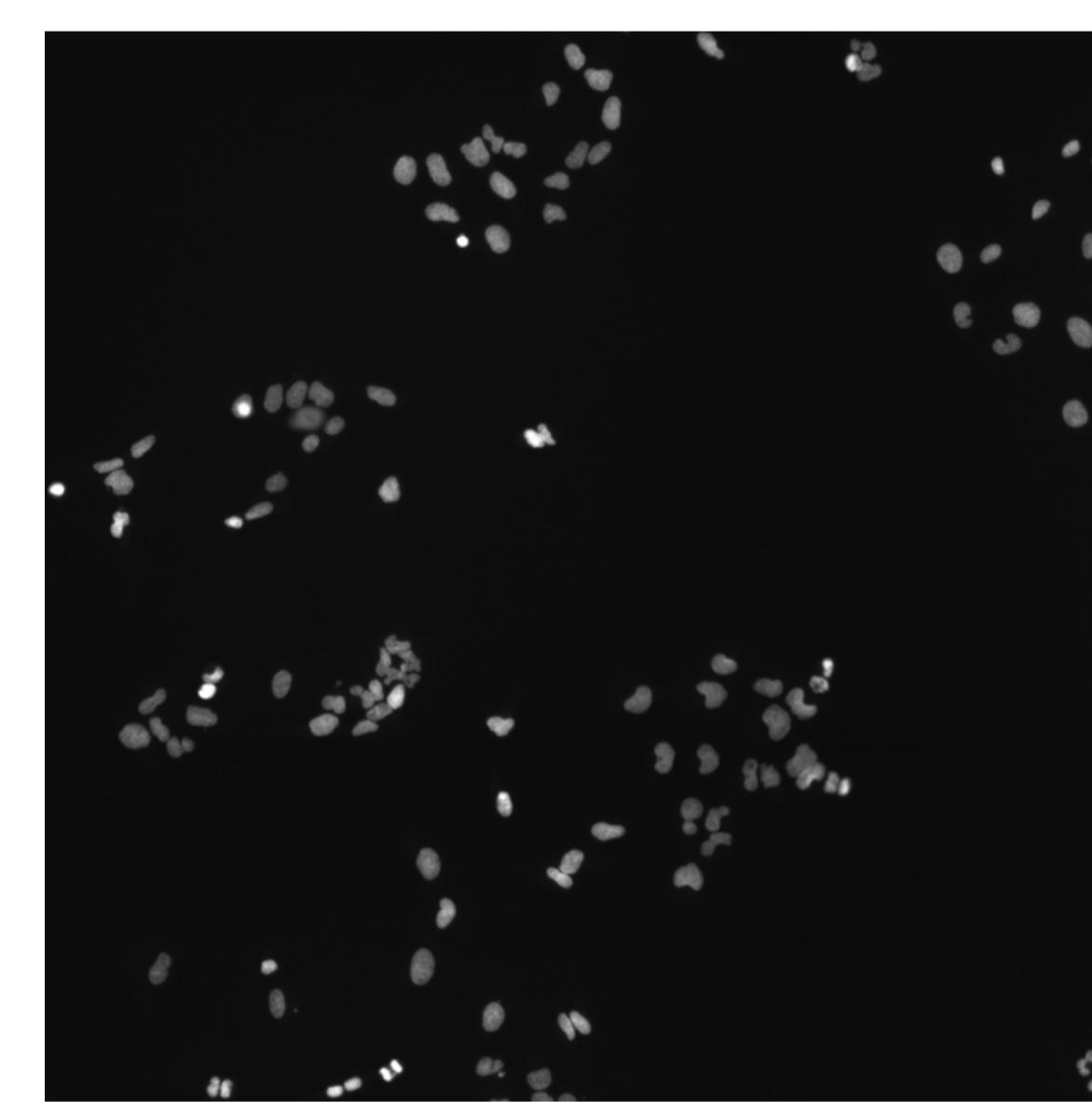
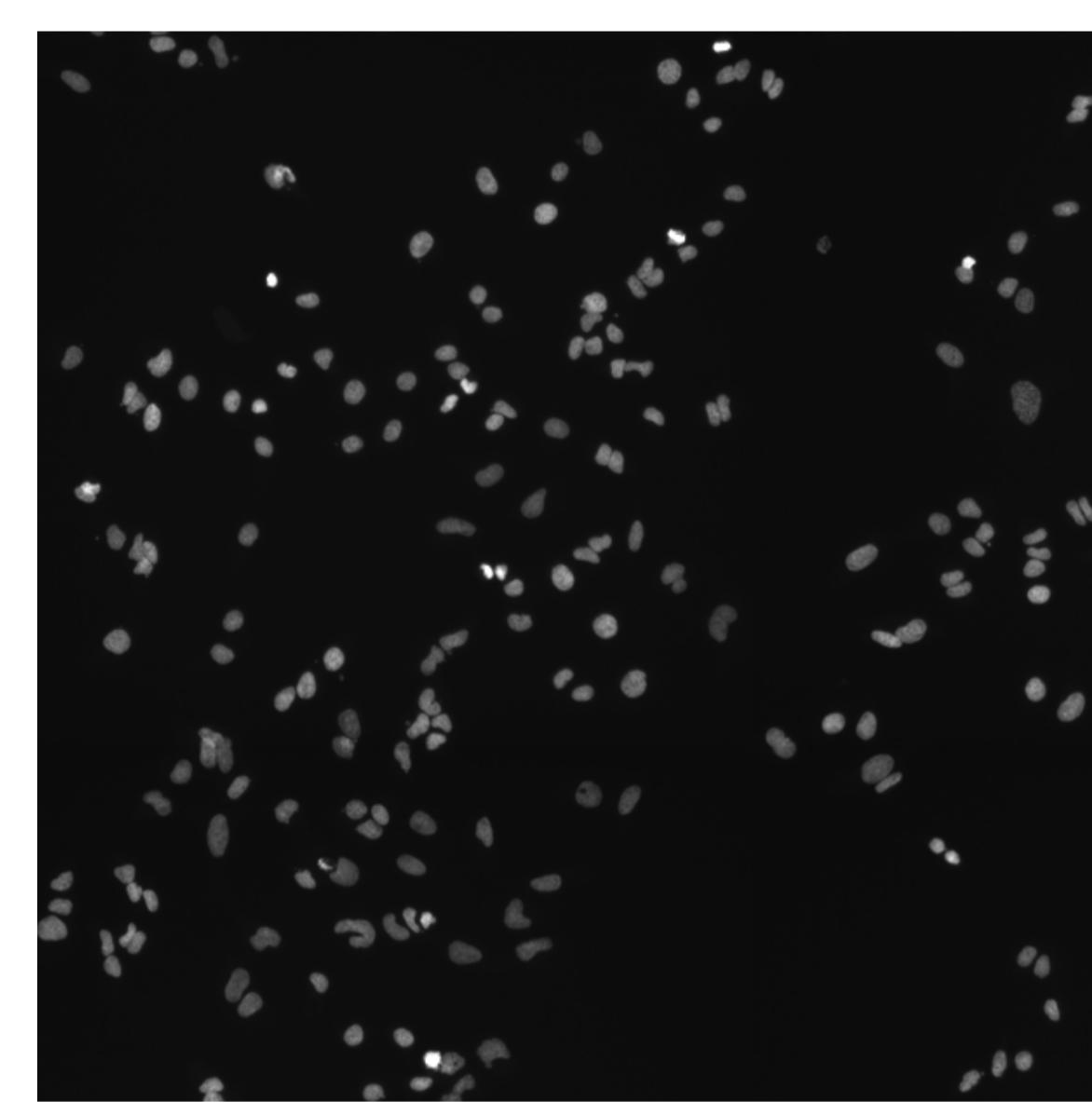
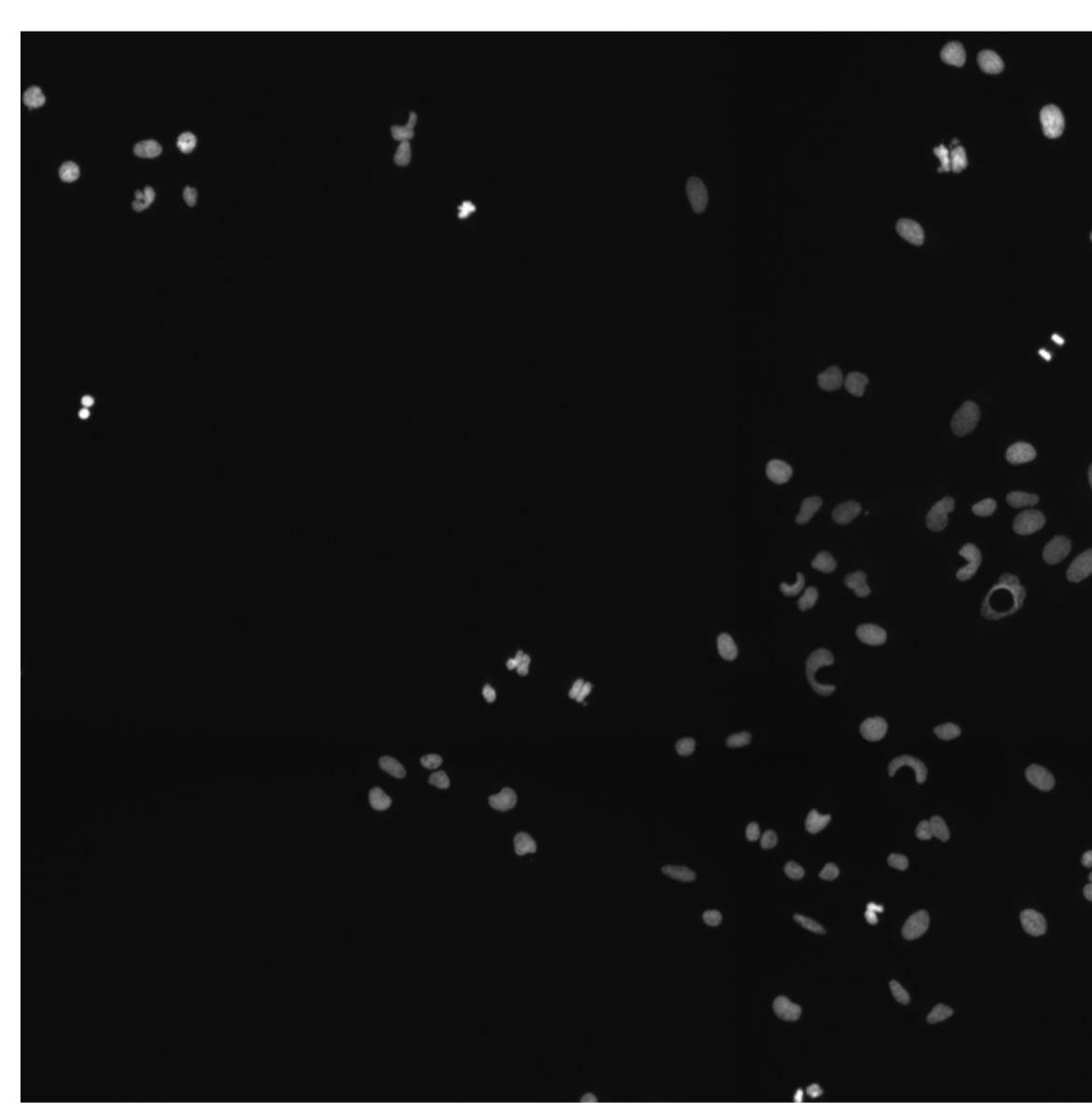
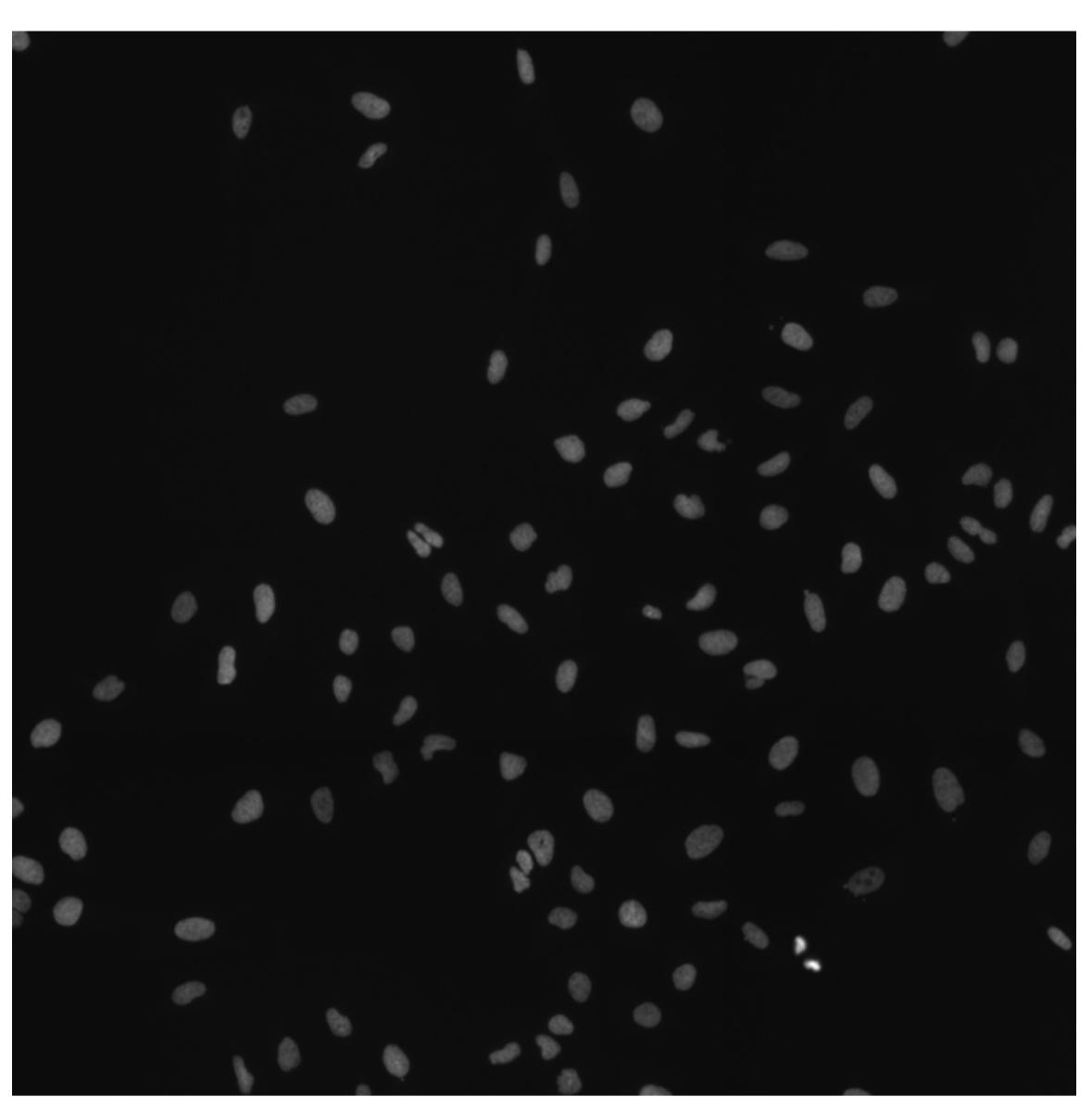
CEBPA_WT.2

JUN_WT.1

JUN_WT.2



DNA



Cluster 7
How similar is this cluster to the other clusters?

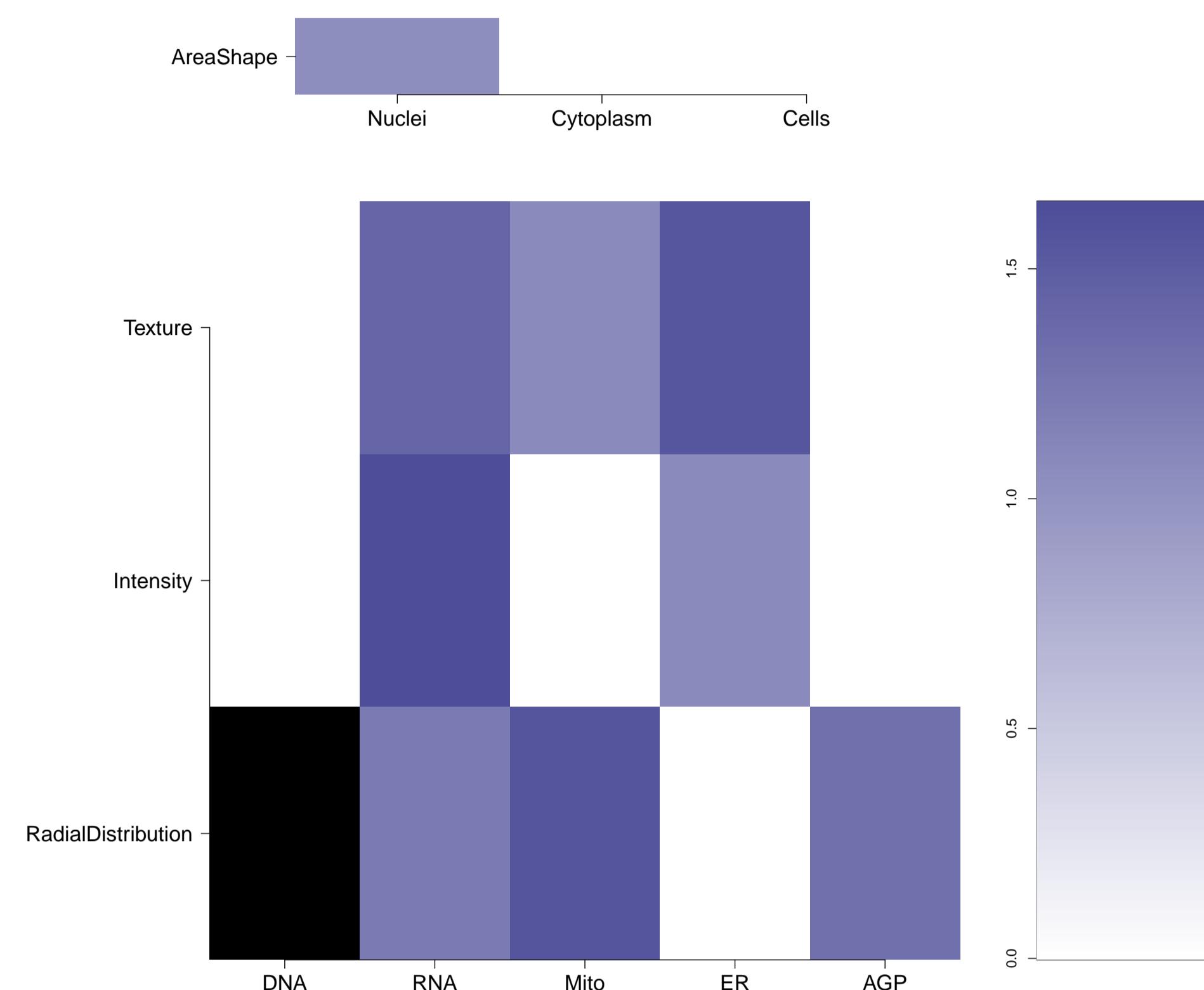


Genes in the cluster along with the pathways as annotated by experts

Treatment	Expert Annotation	
	Pathway	Regulation Type
MAPKAP1_WT	Canonical TOR	Activator
SGK3_WT_2	Canonical TOR	Activator
CSNK1A1_WT_3	Canonical WNT	Inhibitor

Treatment	Pathway	Regulation Type	Top 5 genes negatively correlated to the cluster	
			Expert Annotation	Mean Correlation
PRKACA_WT_2	Canonical PKA	Activator	-0.60	0.02
PRKACA_WT_1	Canonical PKA	Activator	-0.51	0.05
CXXC4_WT	WNT	Inhibitor	-0.50	0.12
STK3_WT_2	Canonical Hippo	Activator	-0.49	0.26
PIK3CB_WT_2	Canonical PI3K/AKT	Activator	-0.46	0.09

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?

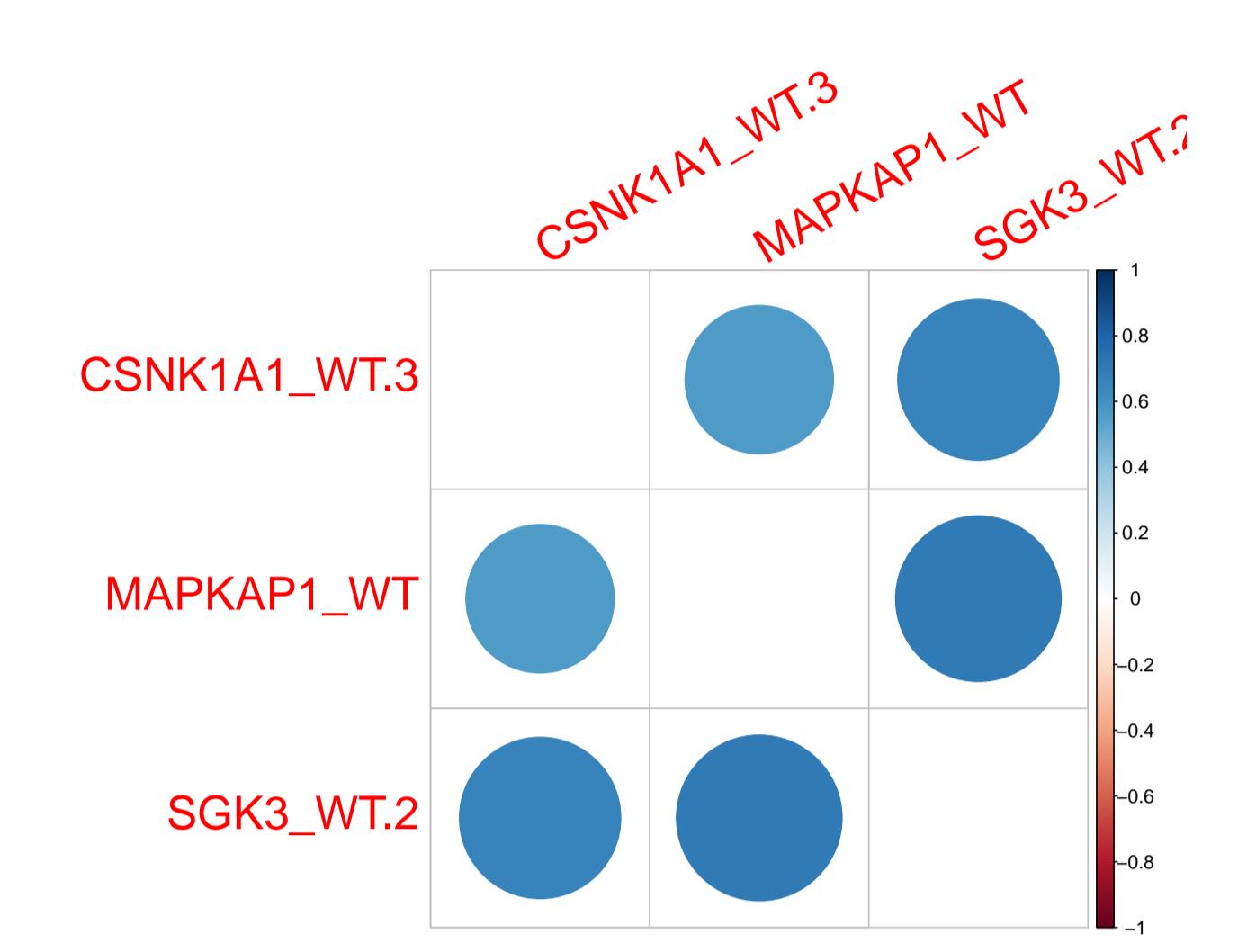


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

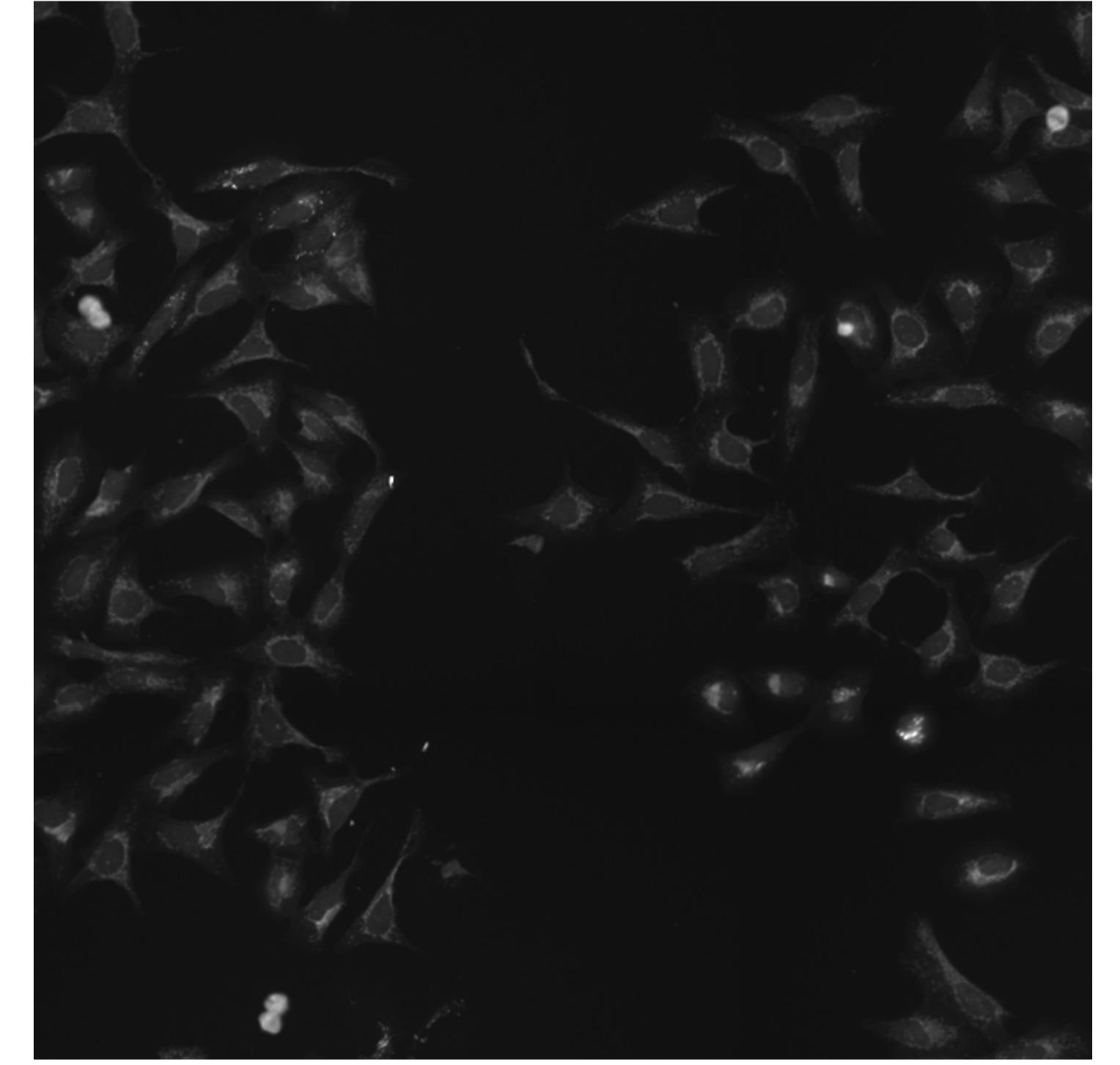
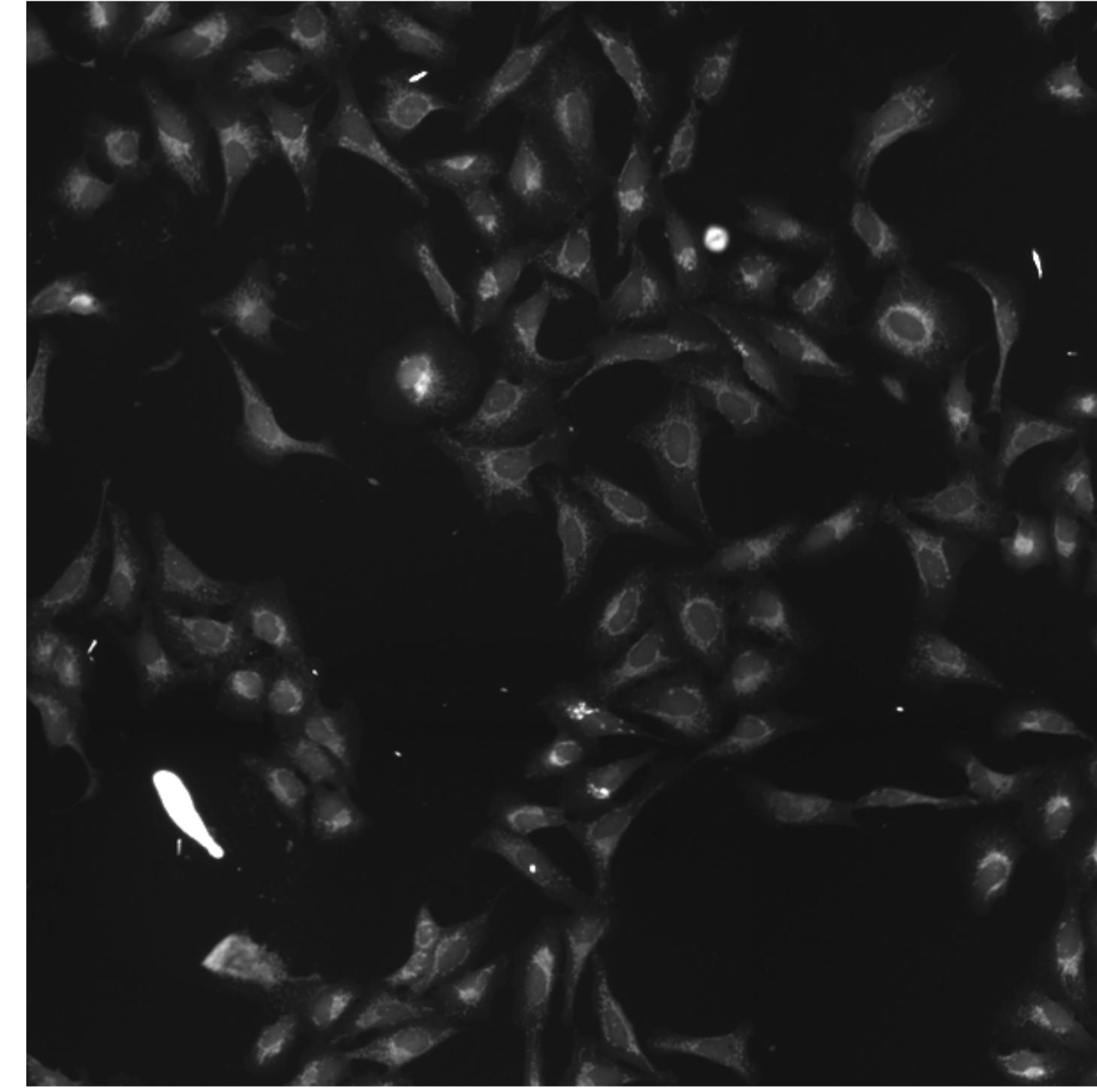
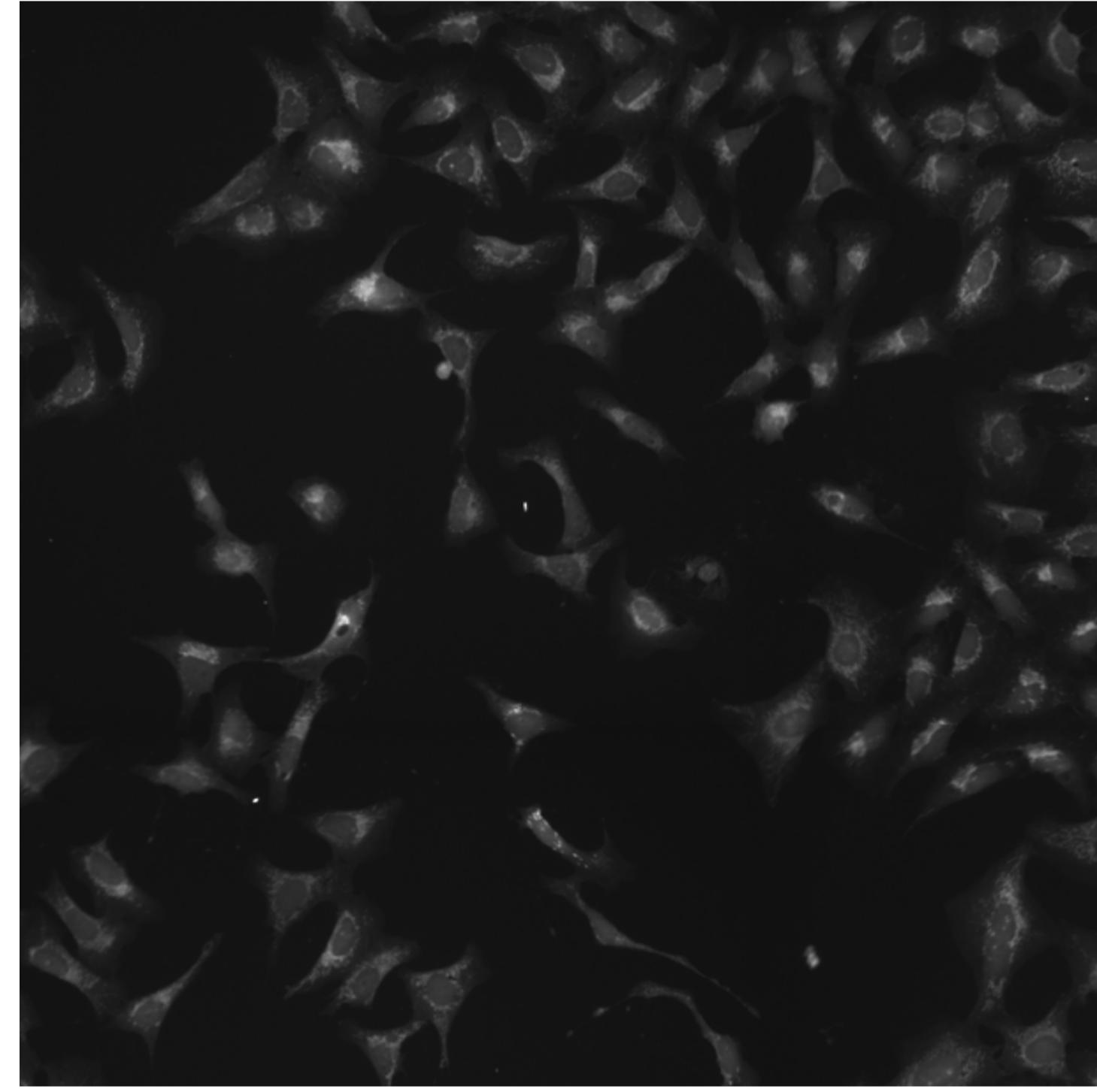
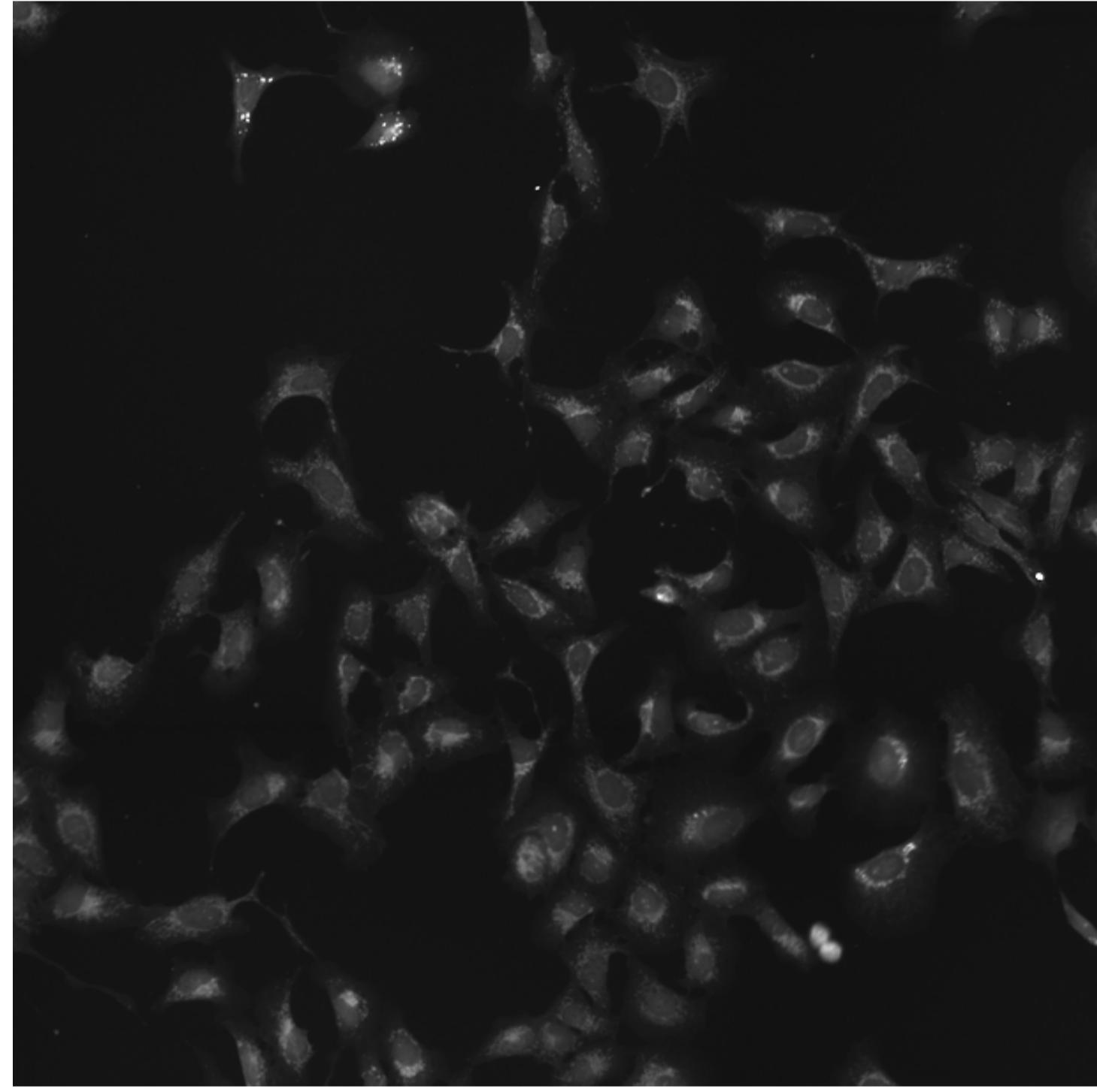
Empty

CSNK1A1_WT_3

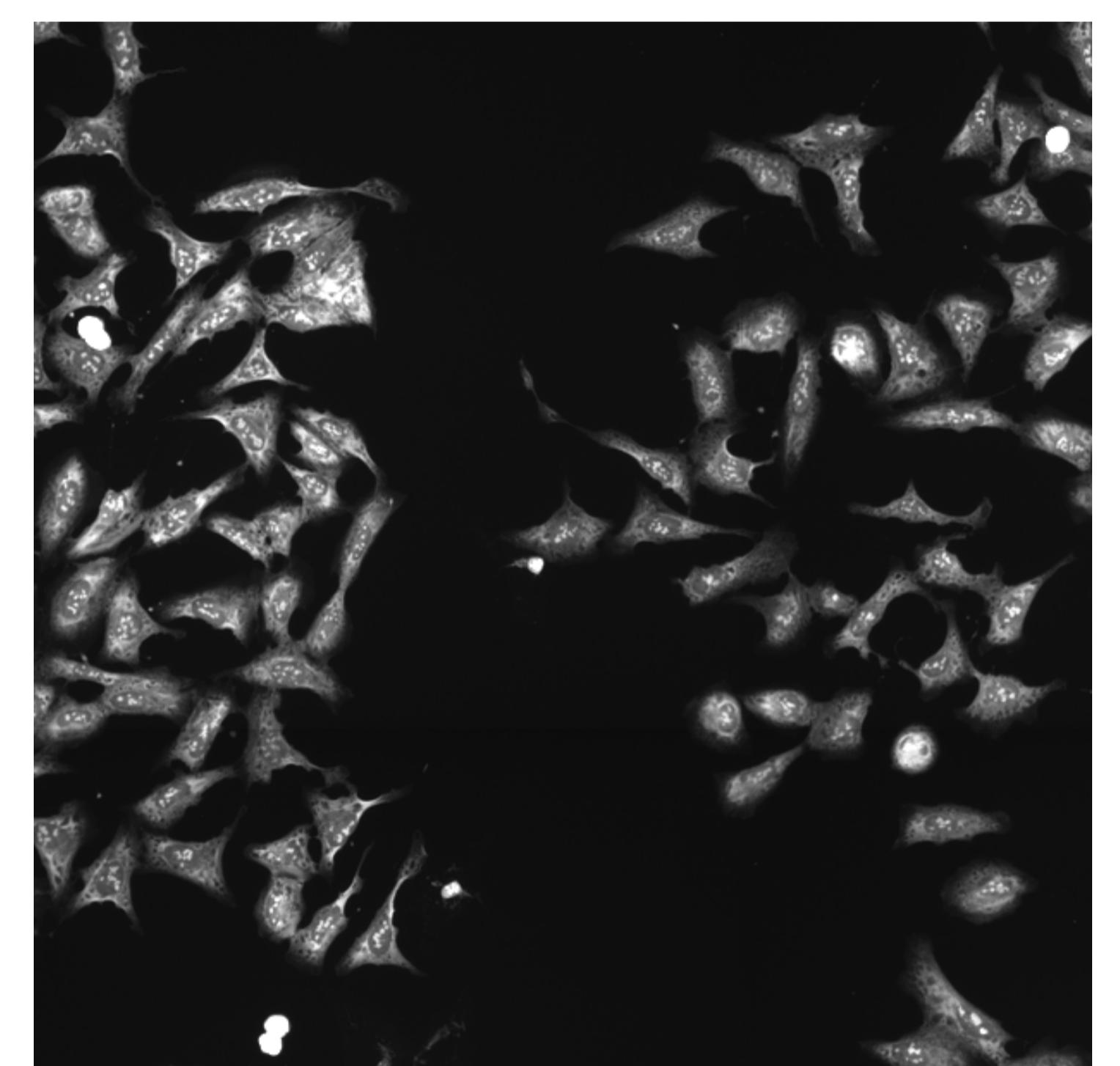
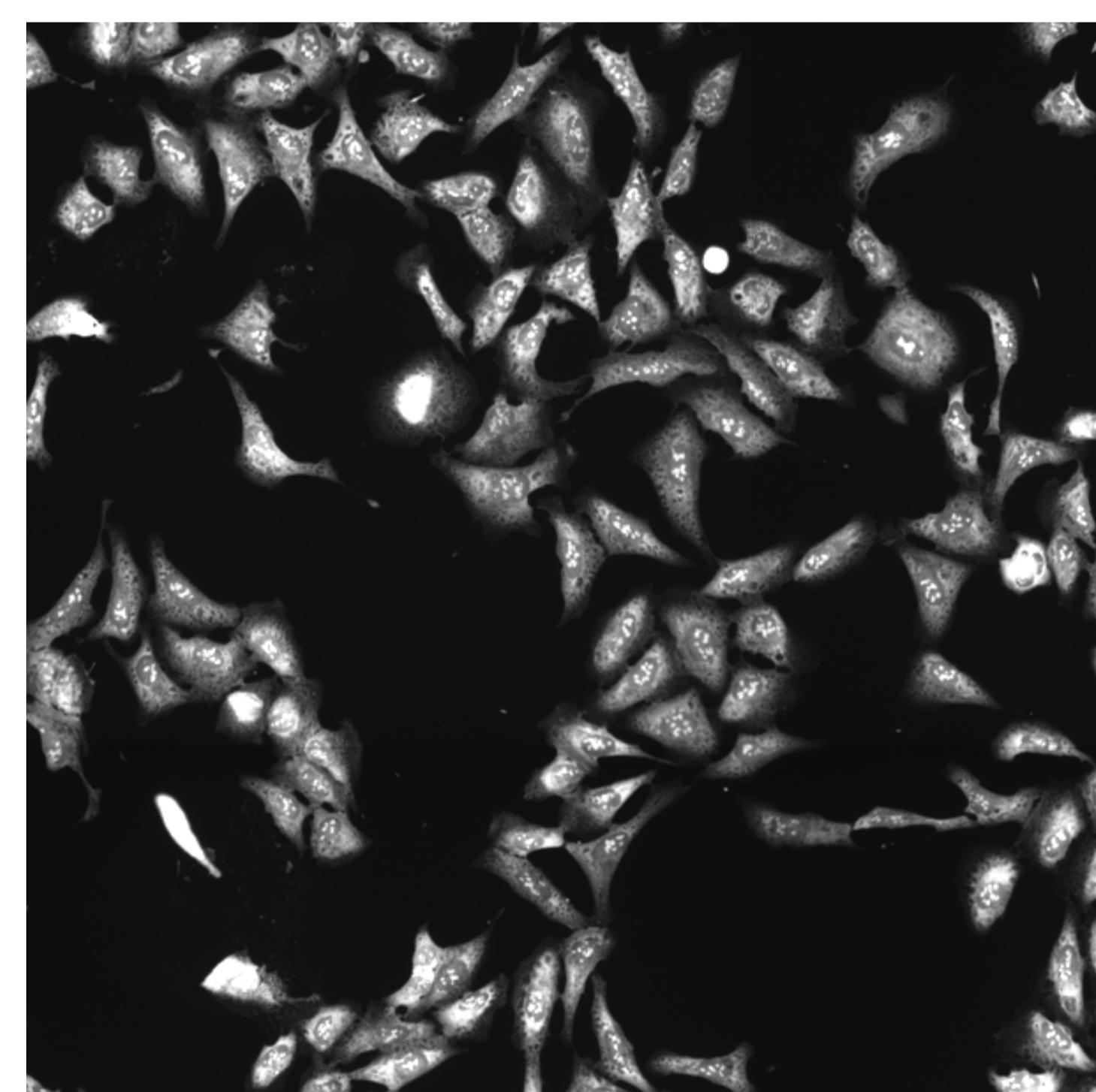
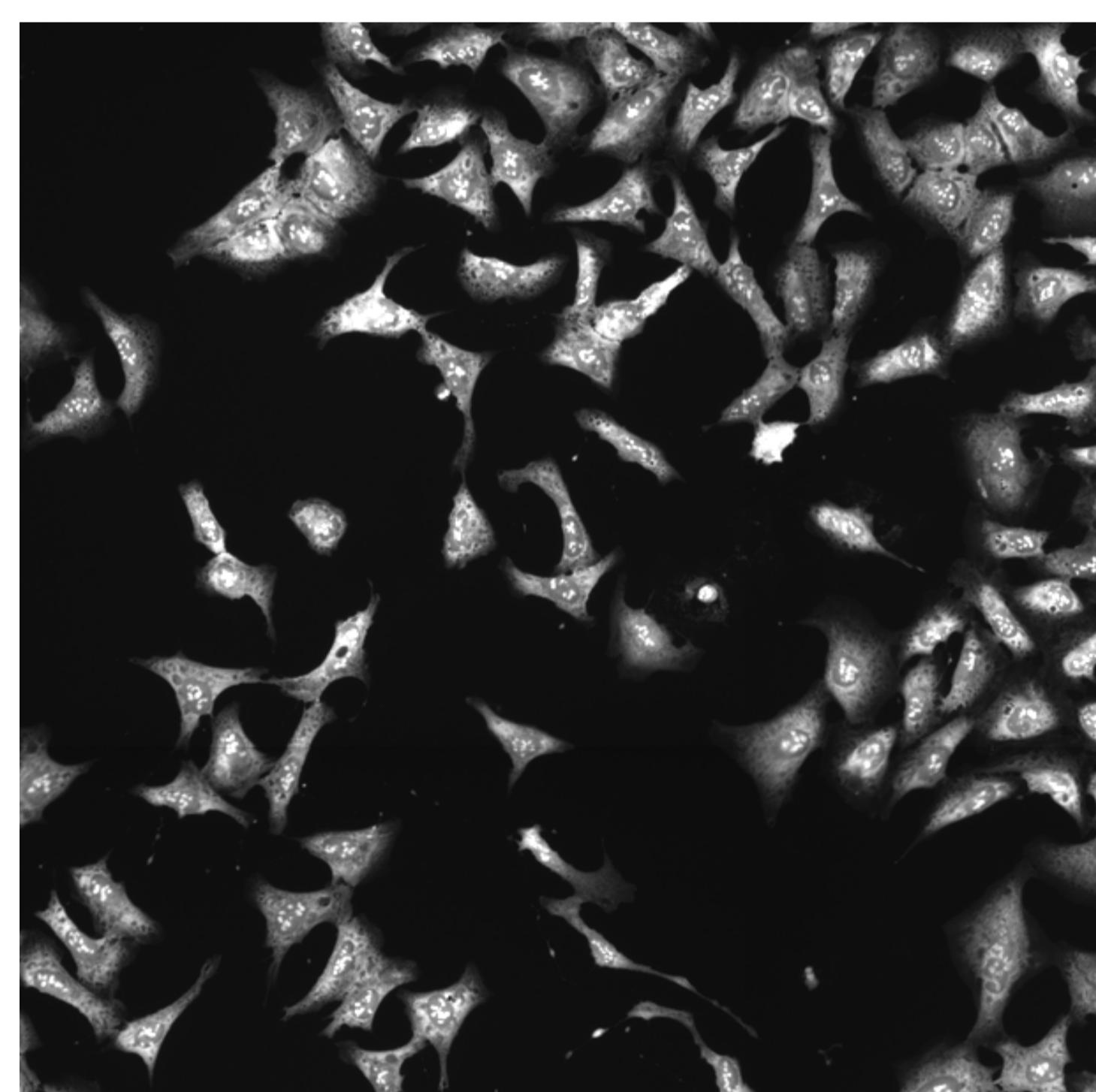
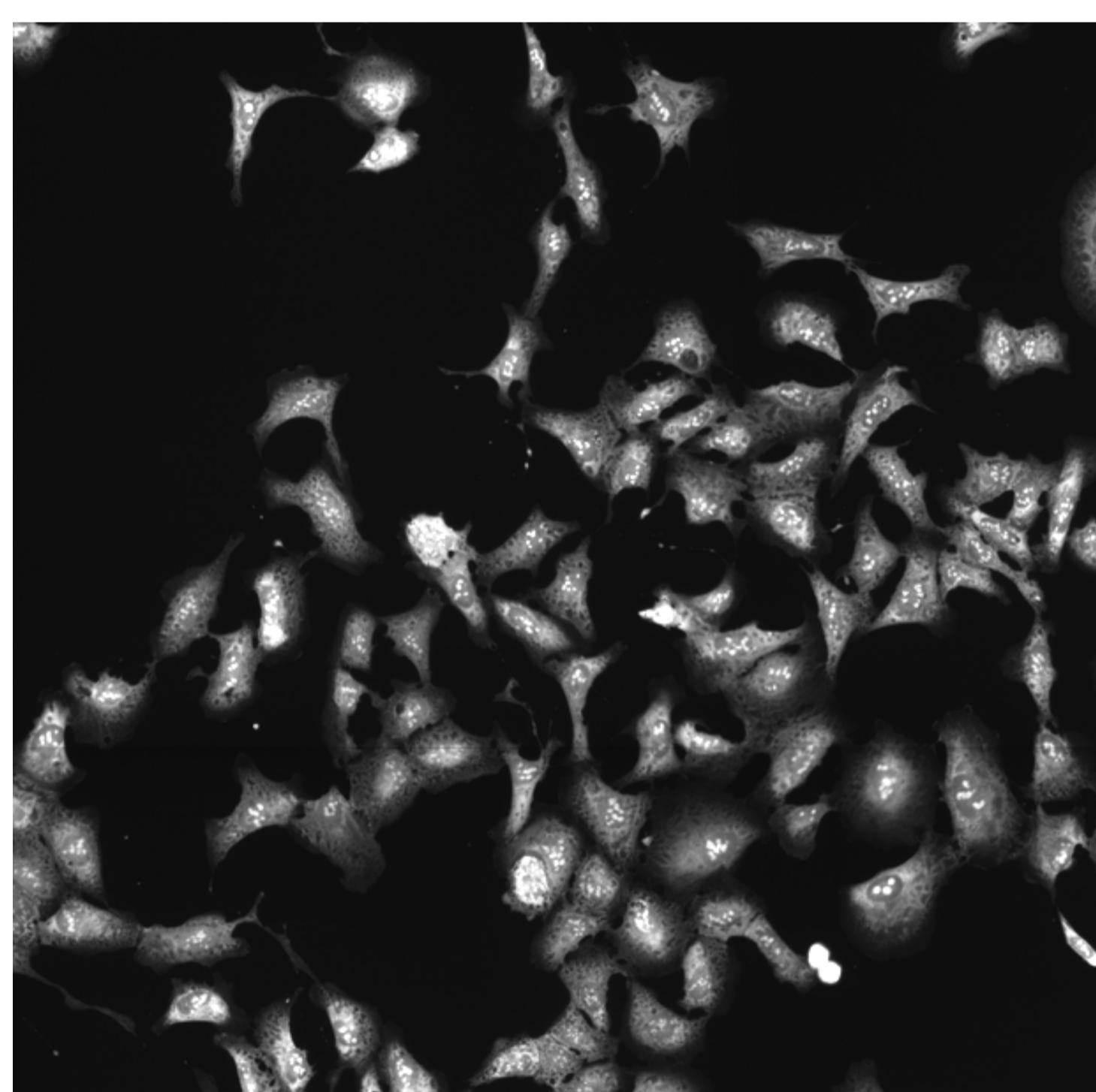
MAPKAP1_WT

SGK3_WT_2

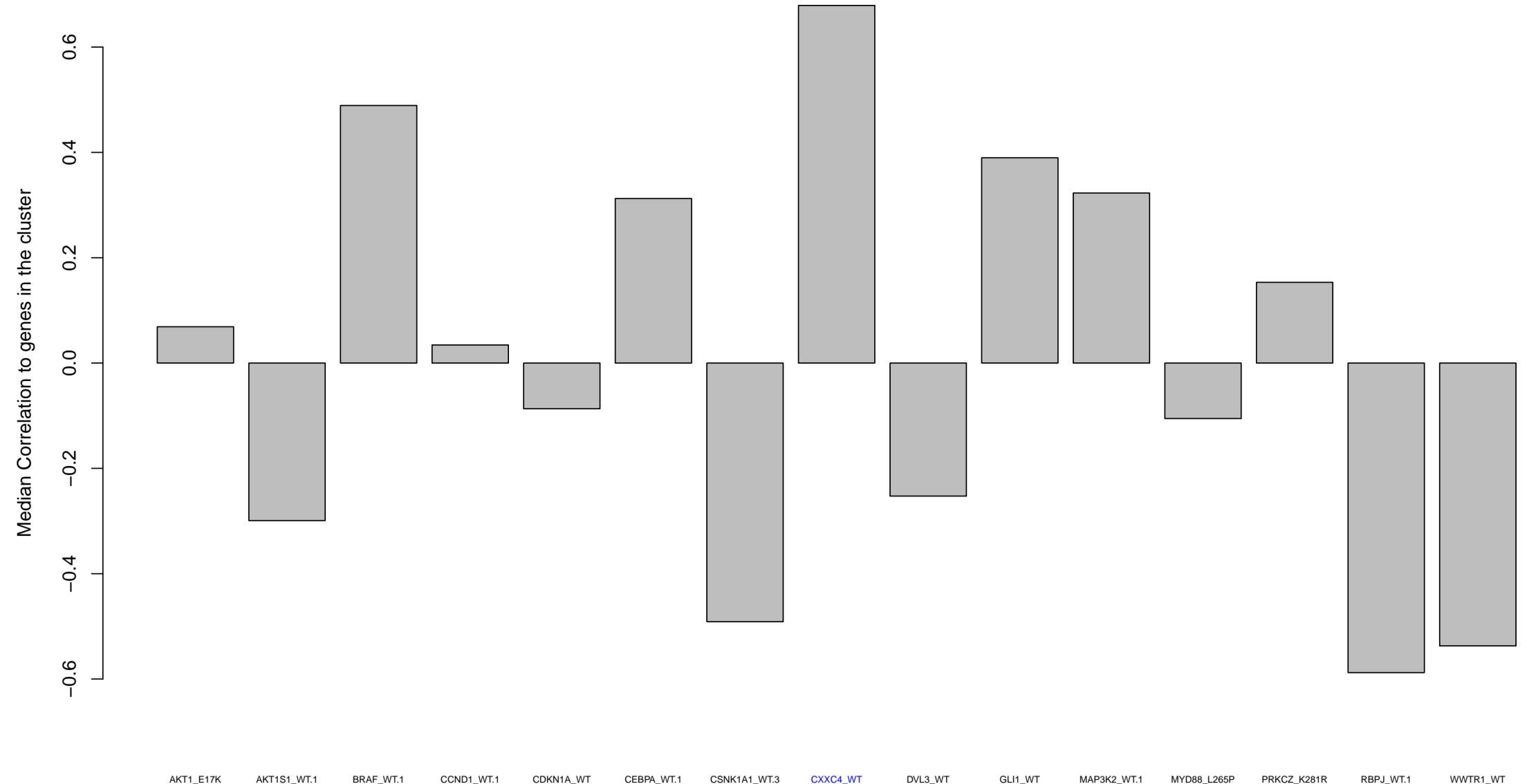
Mito



RNA



Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
STK3_WT.1	Canonical Hippo	Activator	
STK3_WT.2	Canonical Hippo	Activator	
CXXC4_WT	WNT		Inhibitor



Top 5 genes negatively correlated to the cluster						
Treatment	Expert Annotation			Mean Correlation	Standard Deviation	
	Pathway	Regulation Type				
STK11_WT.2	Canonical TOR	Inhibitor		-0.68	0.04	
MAPKAP1_WT	Canonical TOR	Activator		-0.64	0.11	
YAP1_WT.2	Canonical Hippo	Inhibitor		-0.64	0.13	
RBPJ_WT.2	NOTCH	Activator		-0.60	0.09	
YAP1_WT.4	Canonical Hippo	Inhibitor		-0.59	0.08	

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?

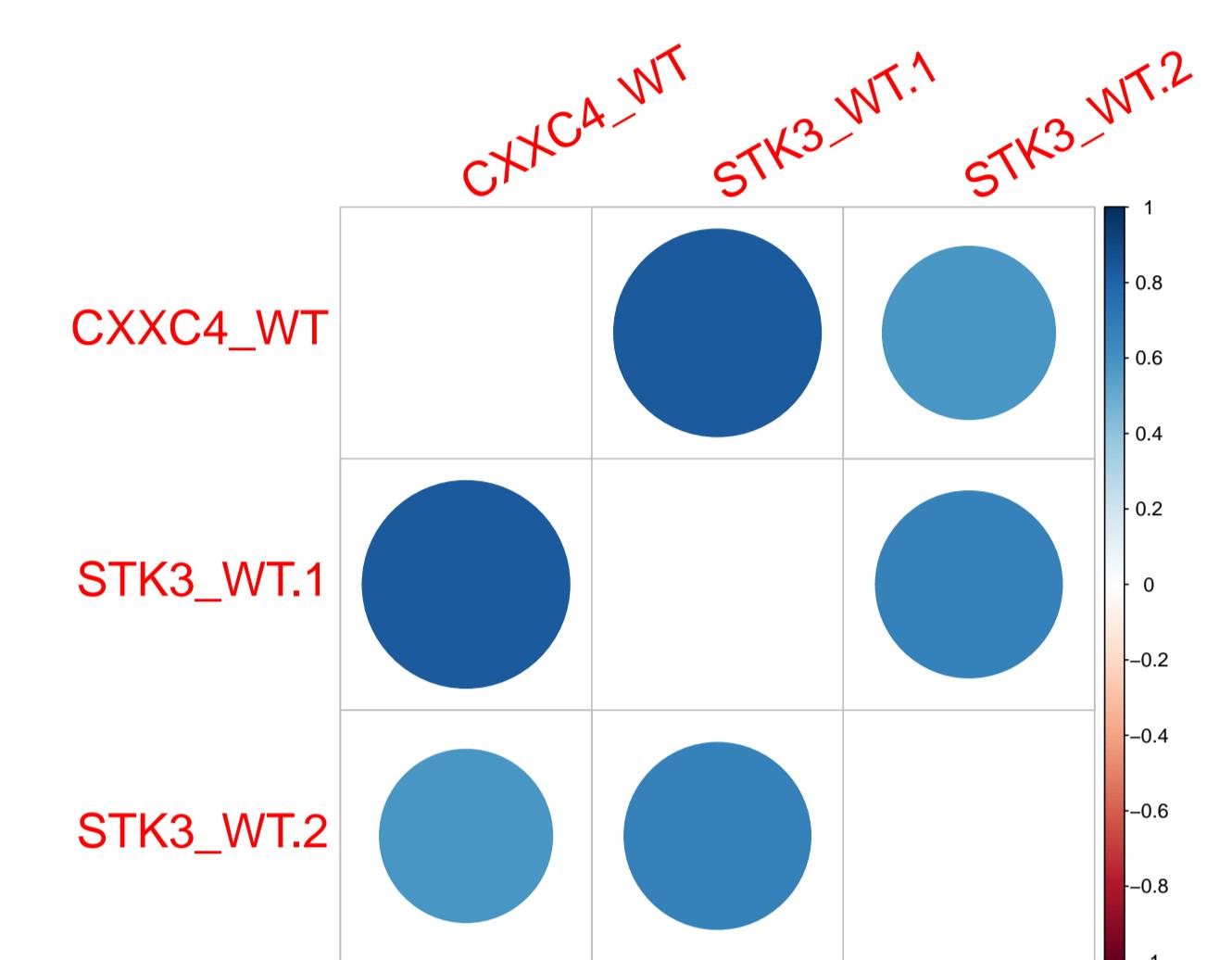
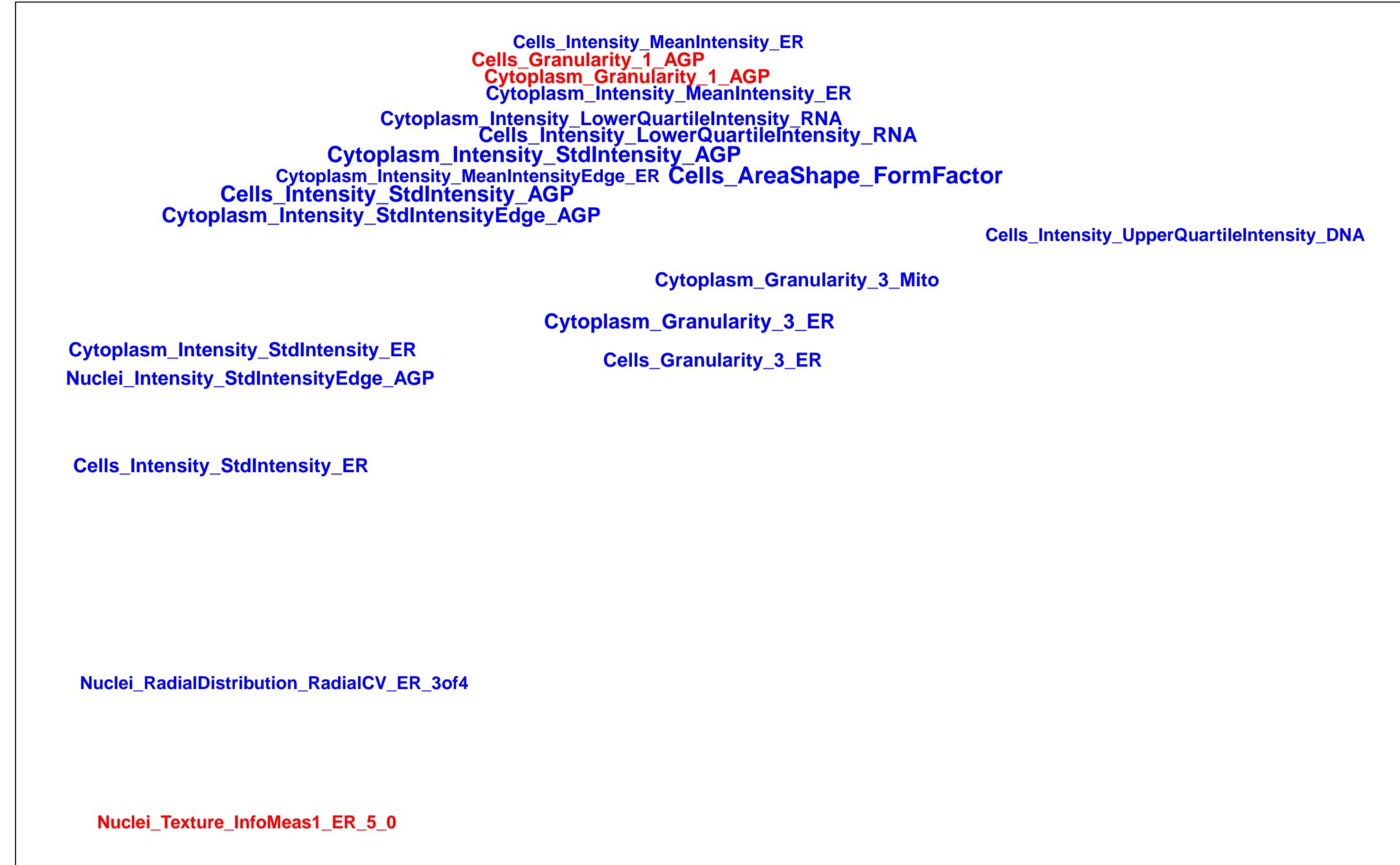
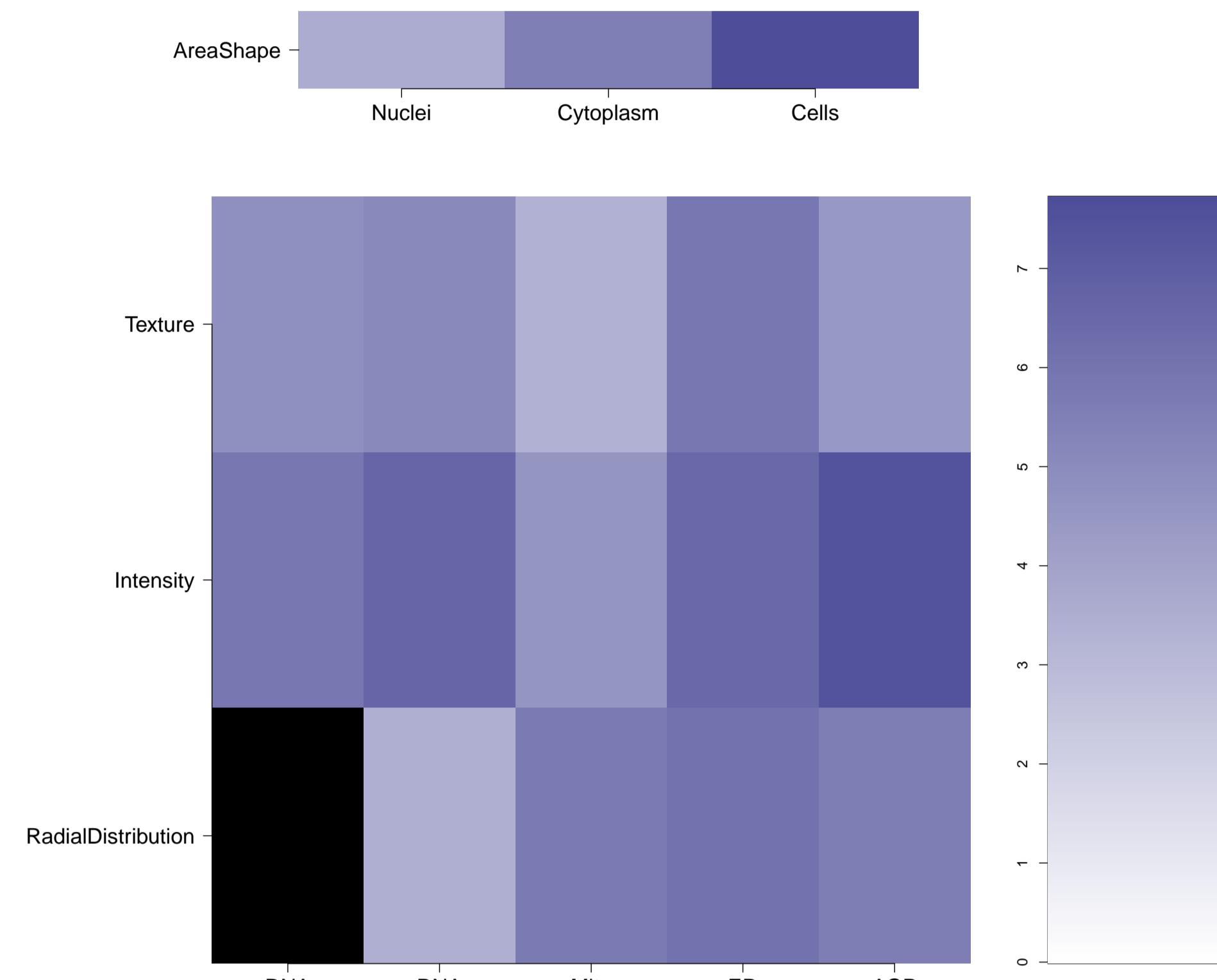


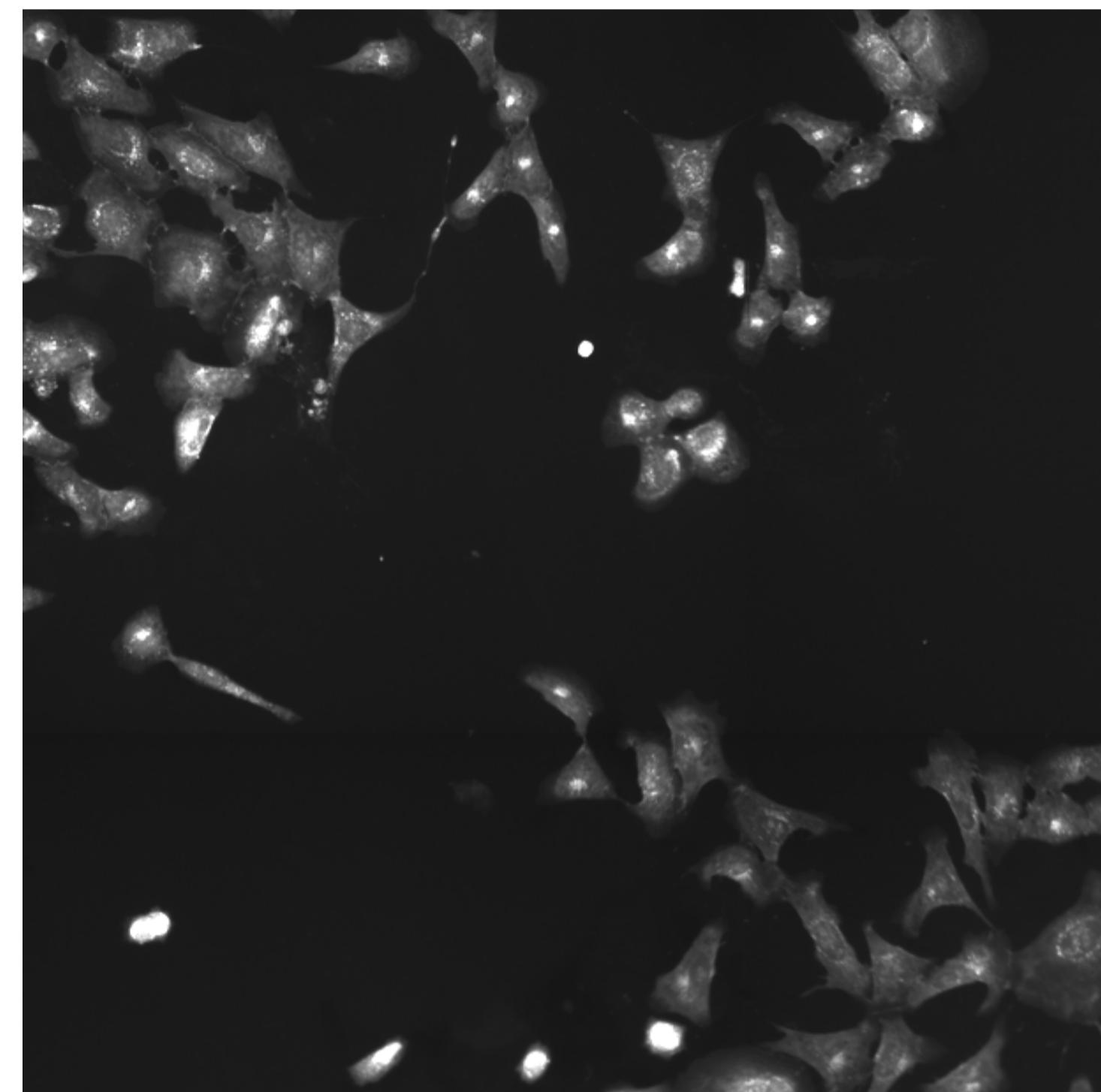
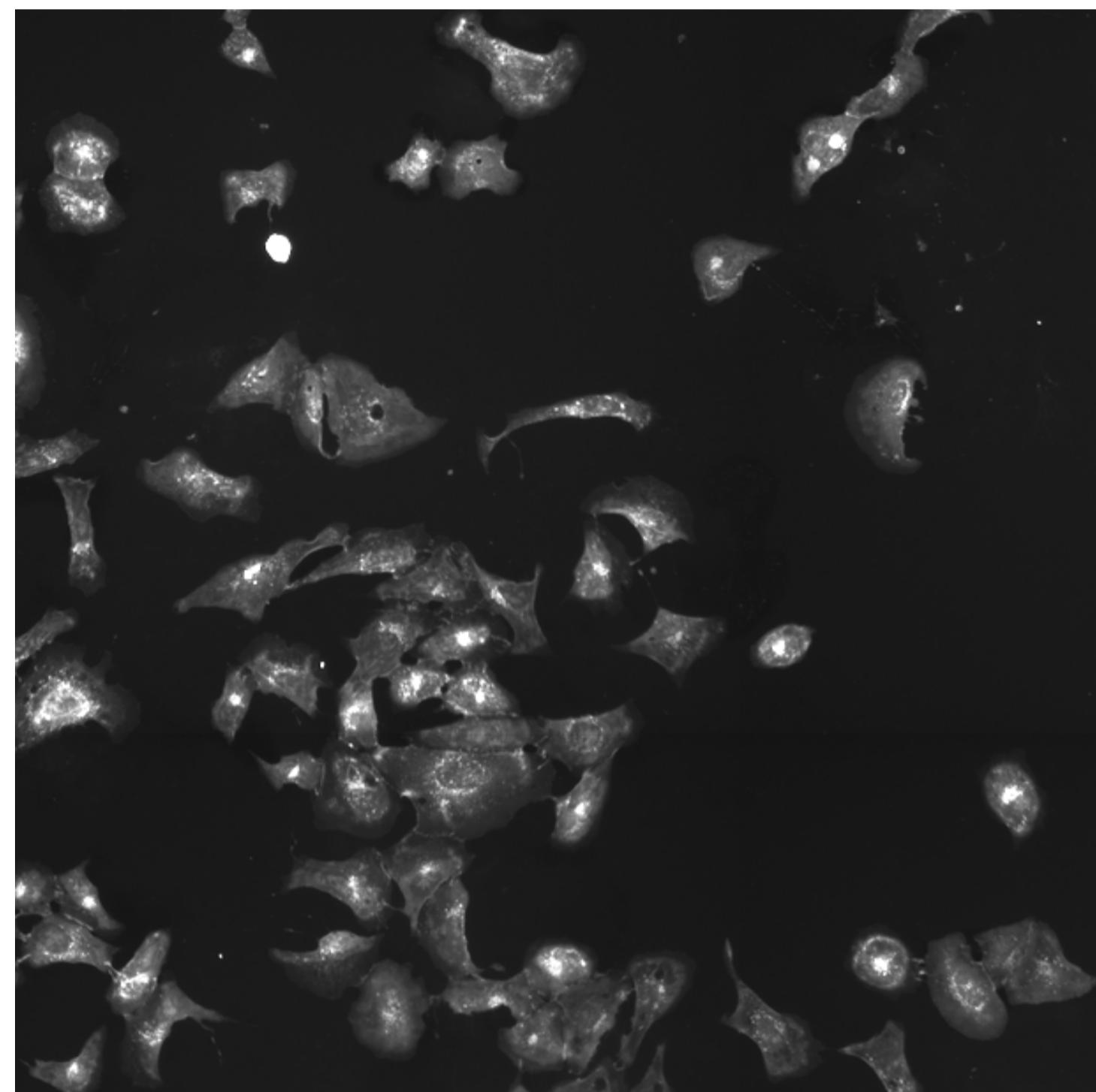
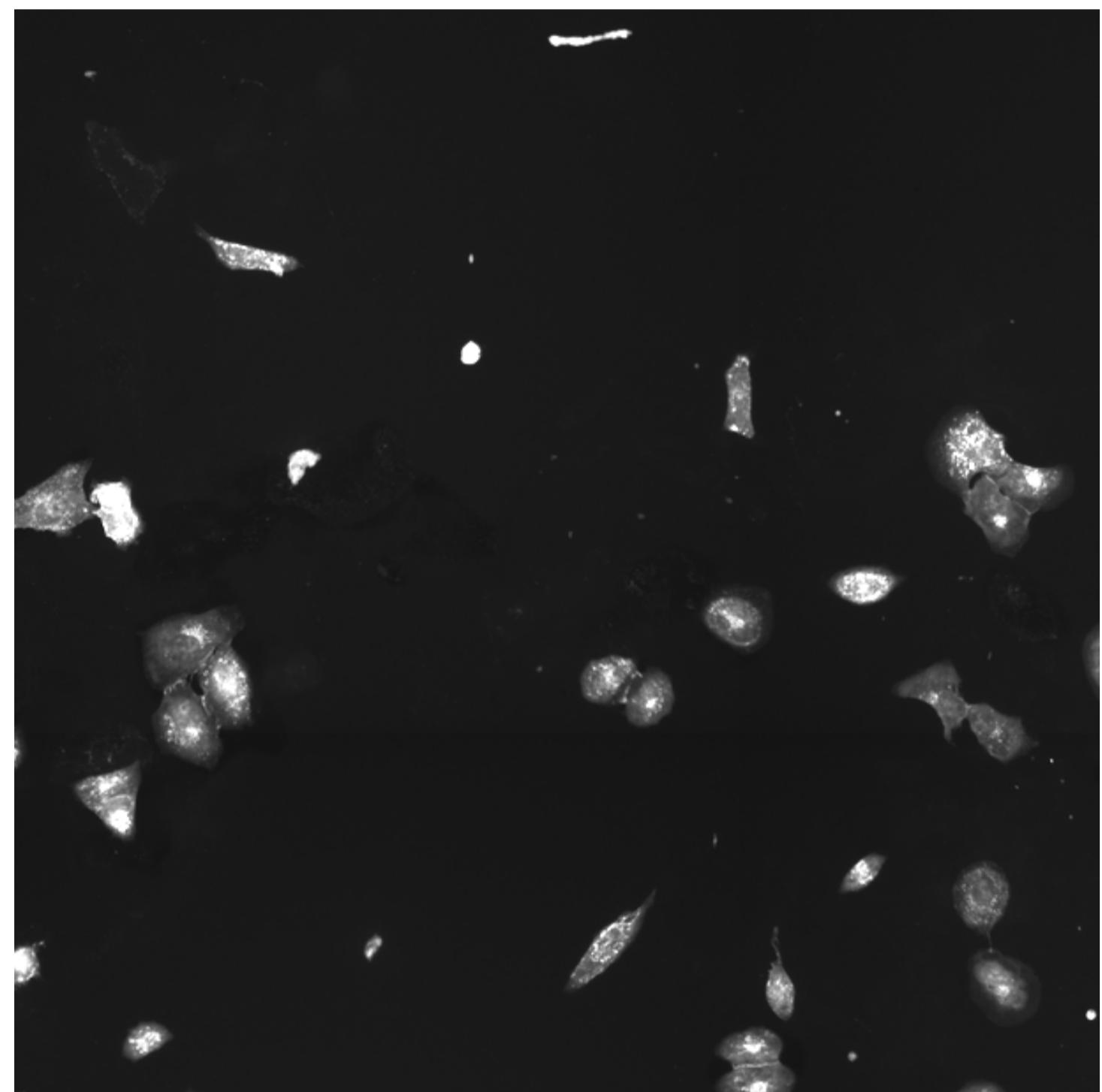
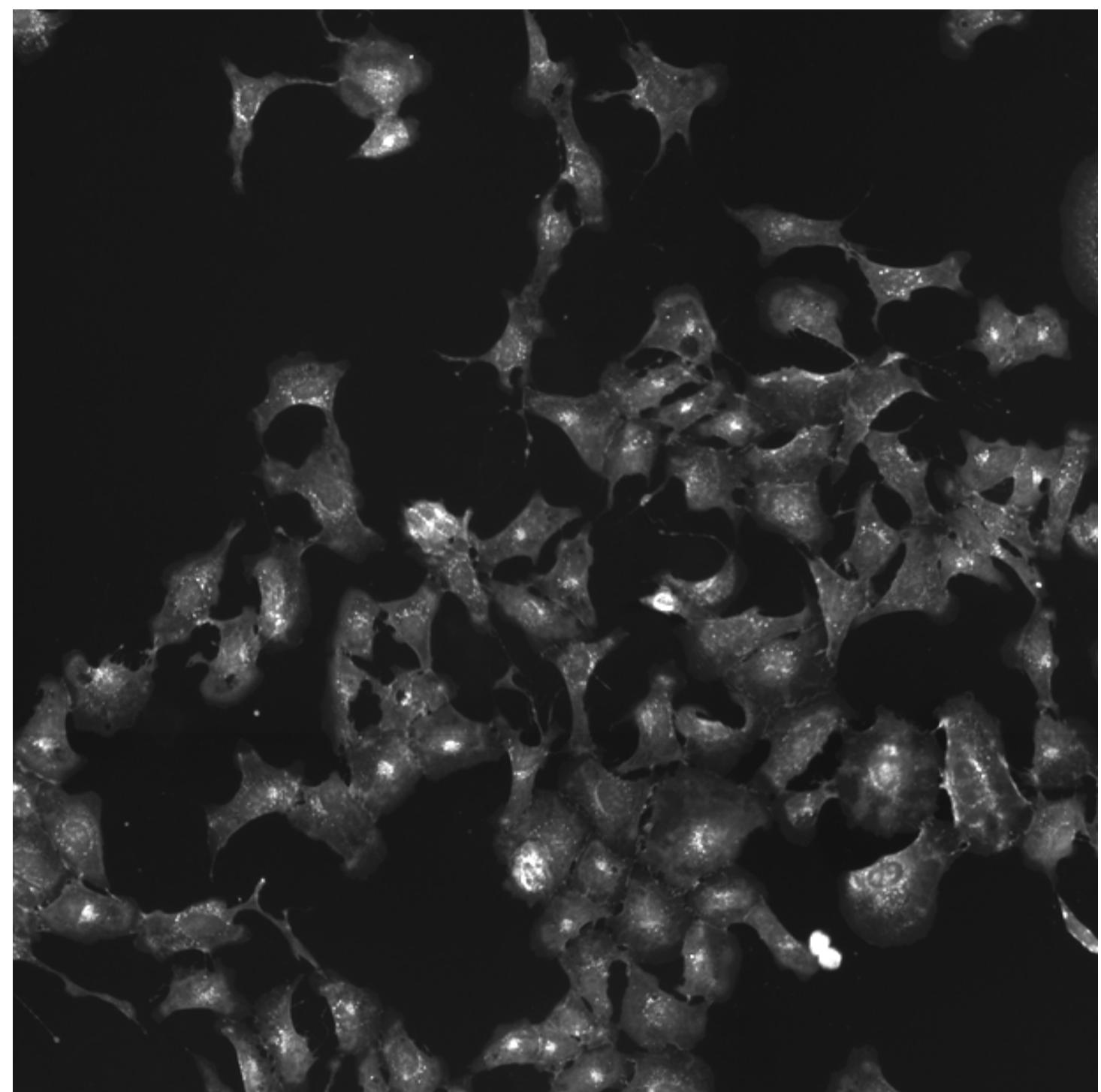
Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

CXXC4_WT

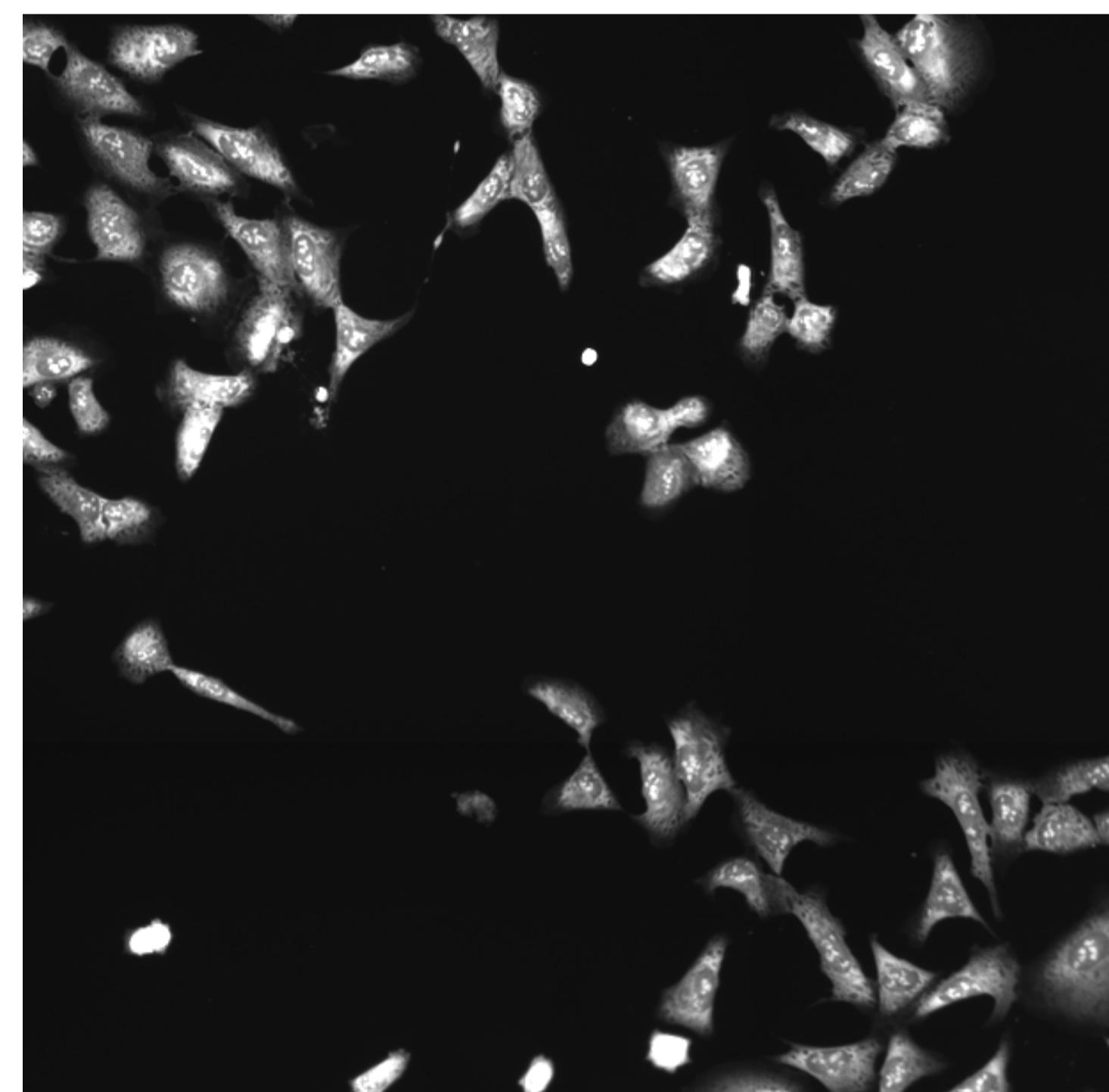
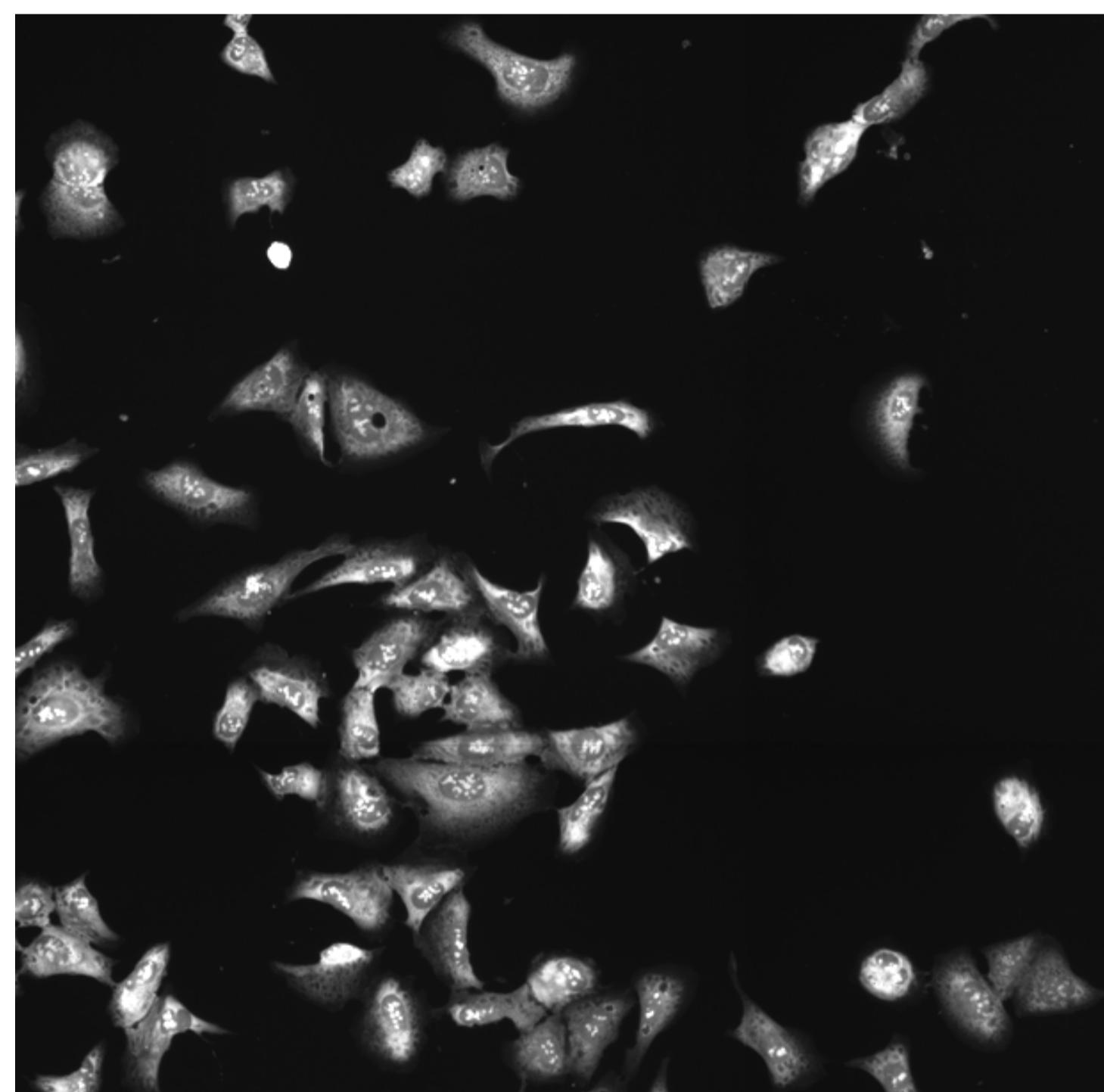
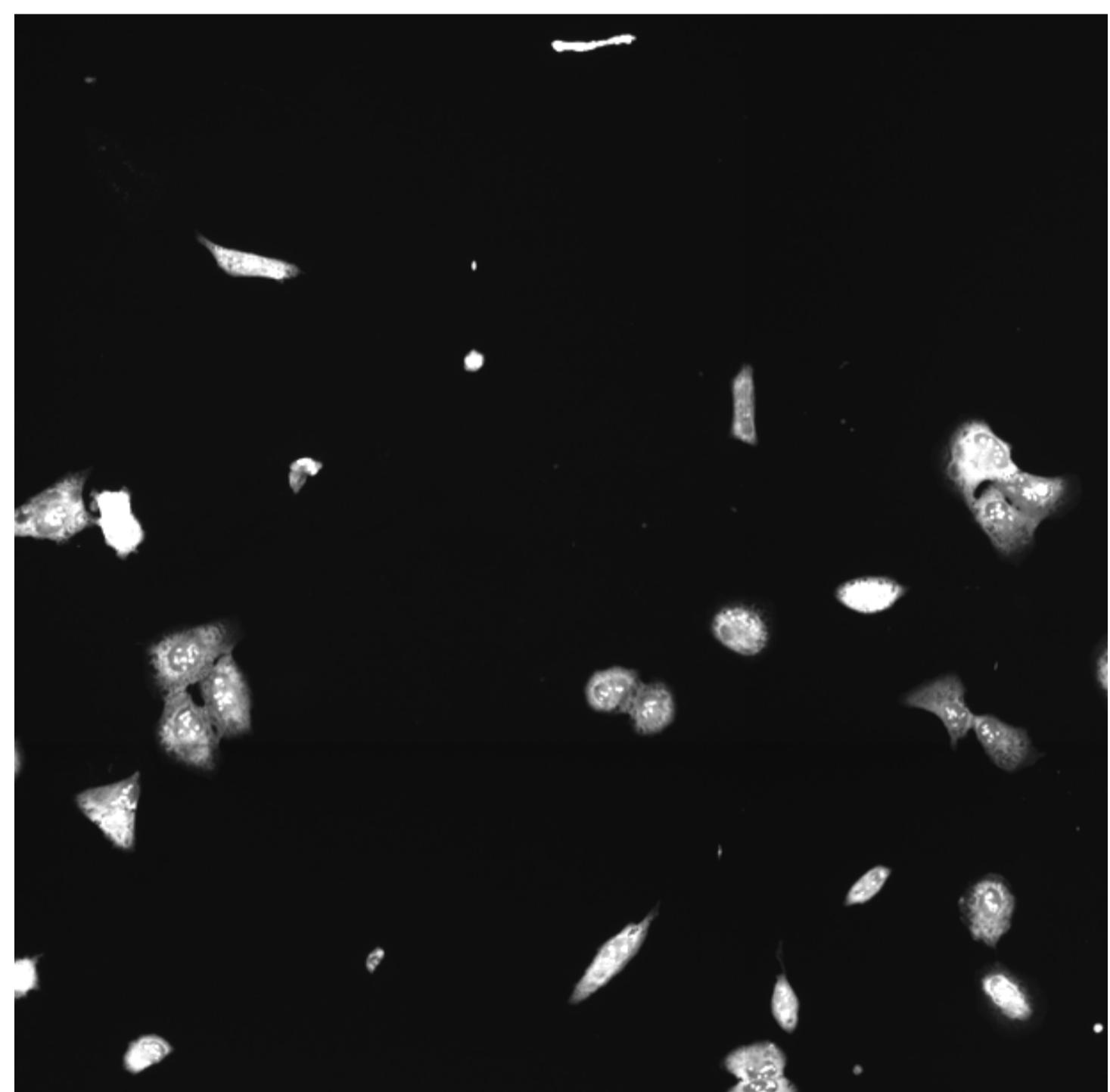
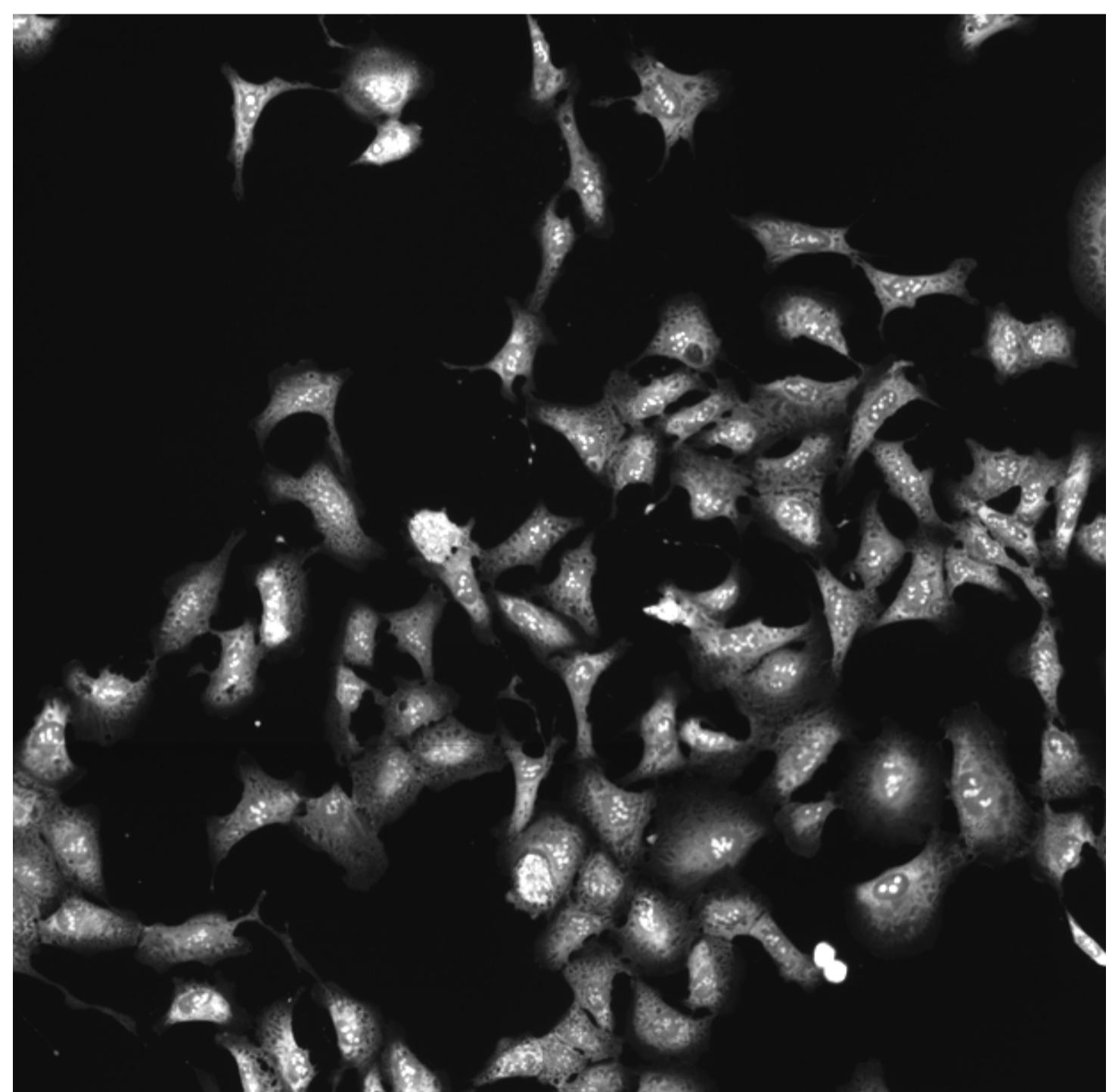
STK3_WT.1

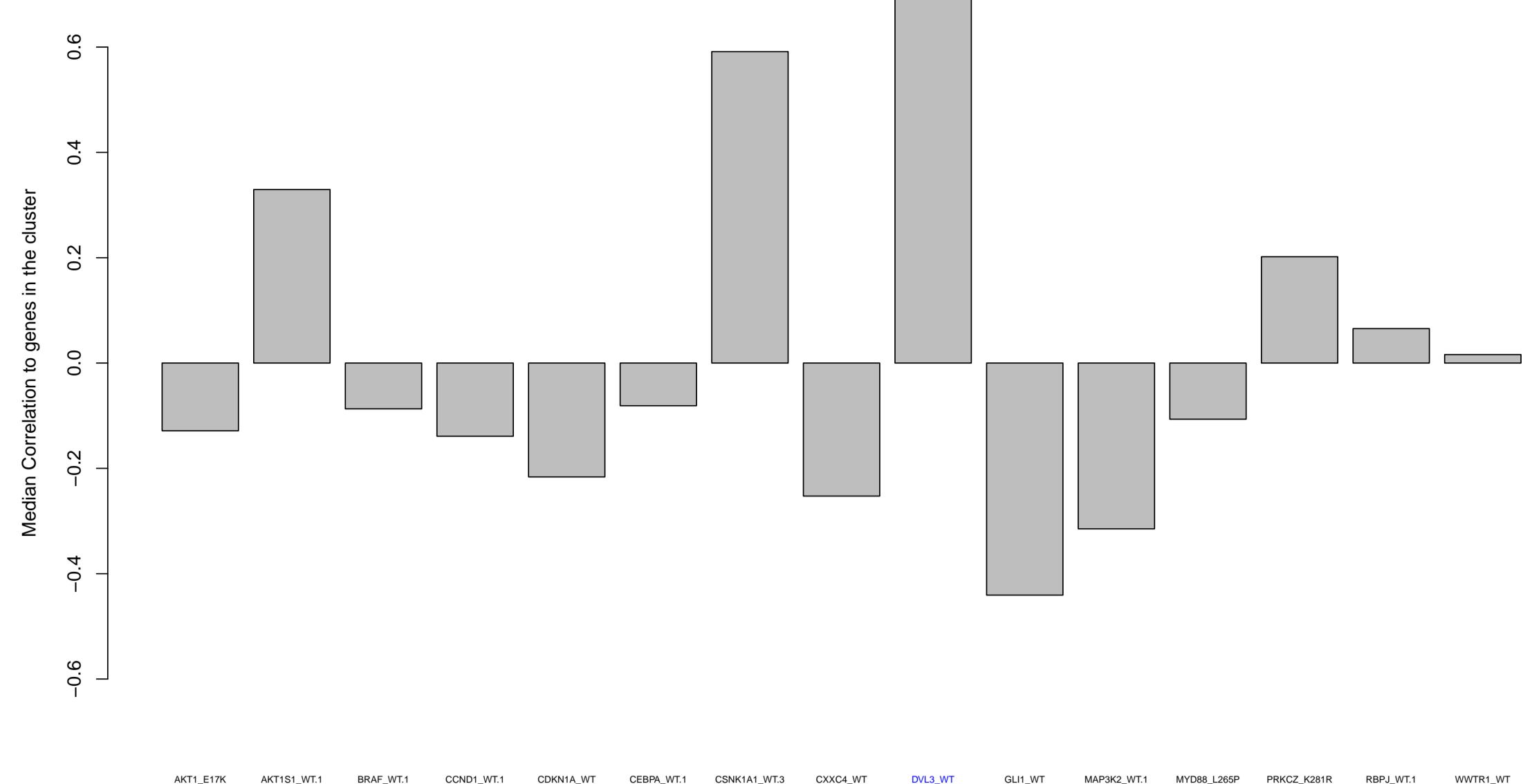
STK3_WT.2

AGP



RNA





Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
TGFBR1_K232R	Canonical TGFbeta	Inhibitor	
TGFBR1_WT.2	Canonical TGFbeta	Activator	
DVL3_WT	Canonical WNT	Activator	

Top 5 genes negatively correlated to the cluster						
Treatment	Expert Annotation			Mean Correlation	Standard Deviation	
	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?

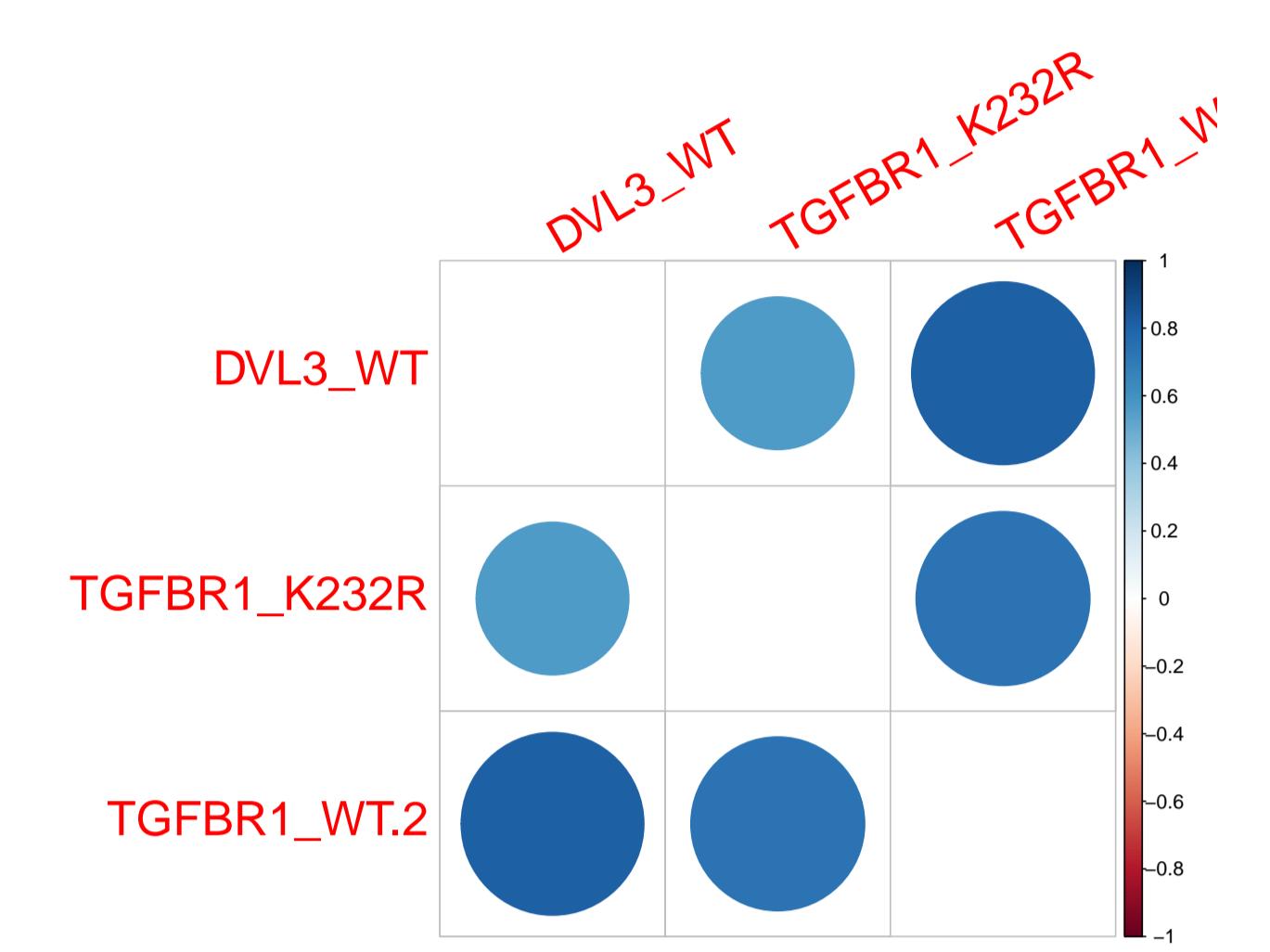
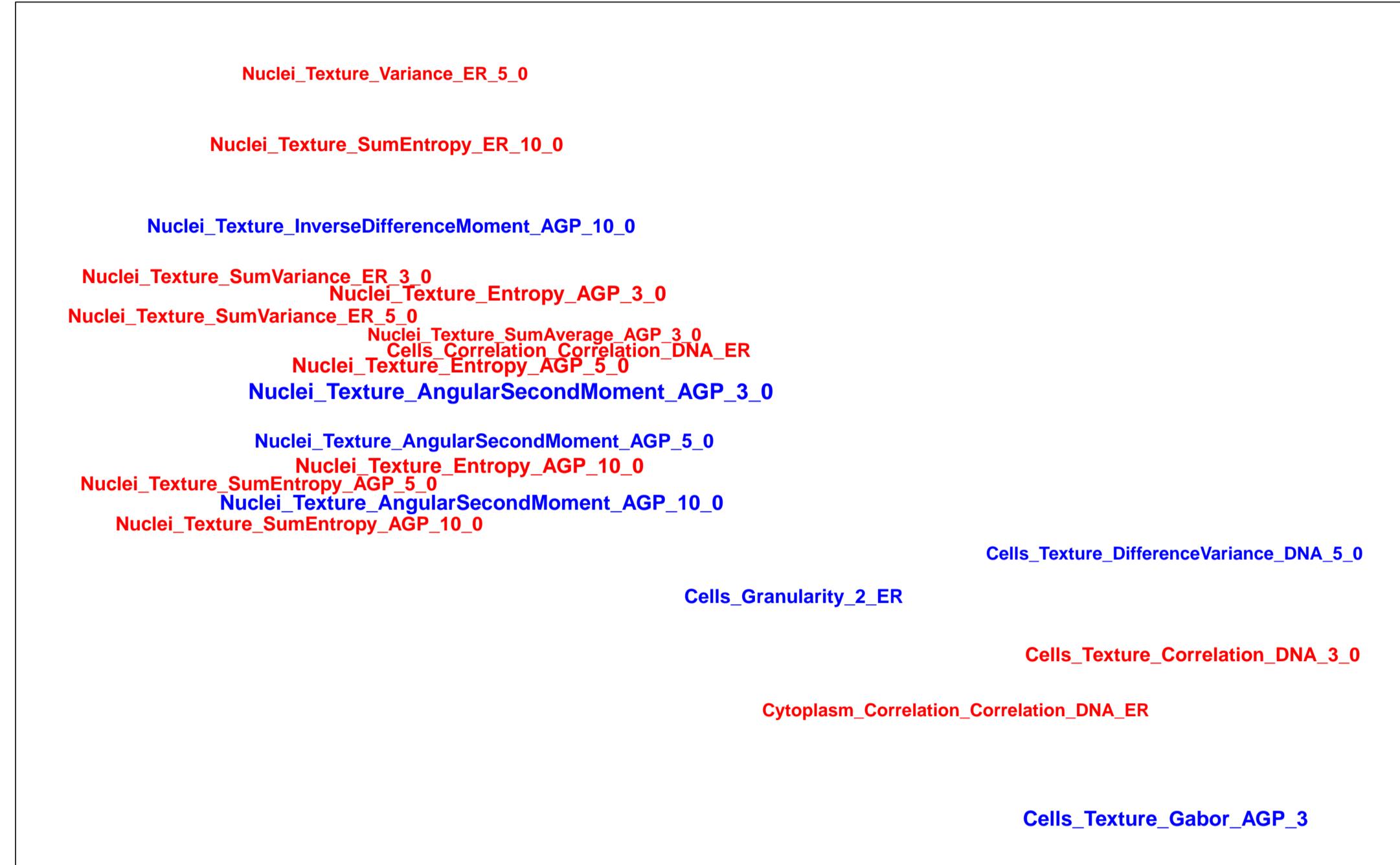
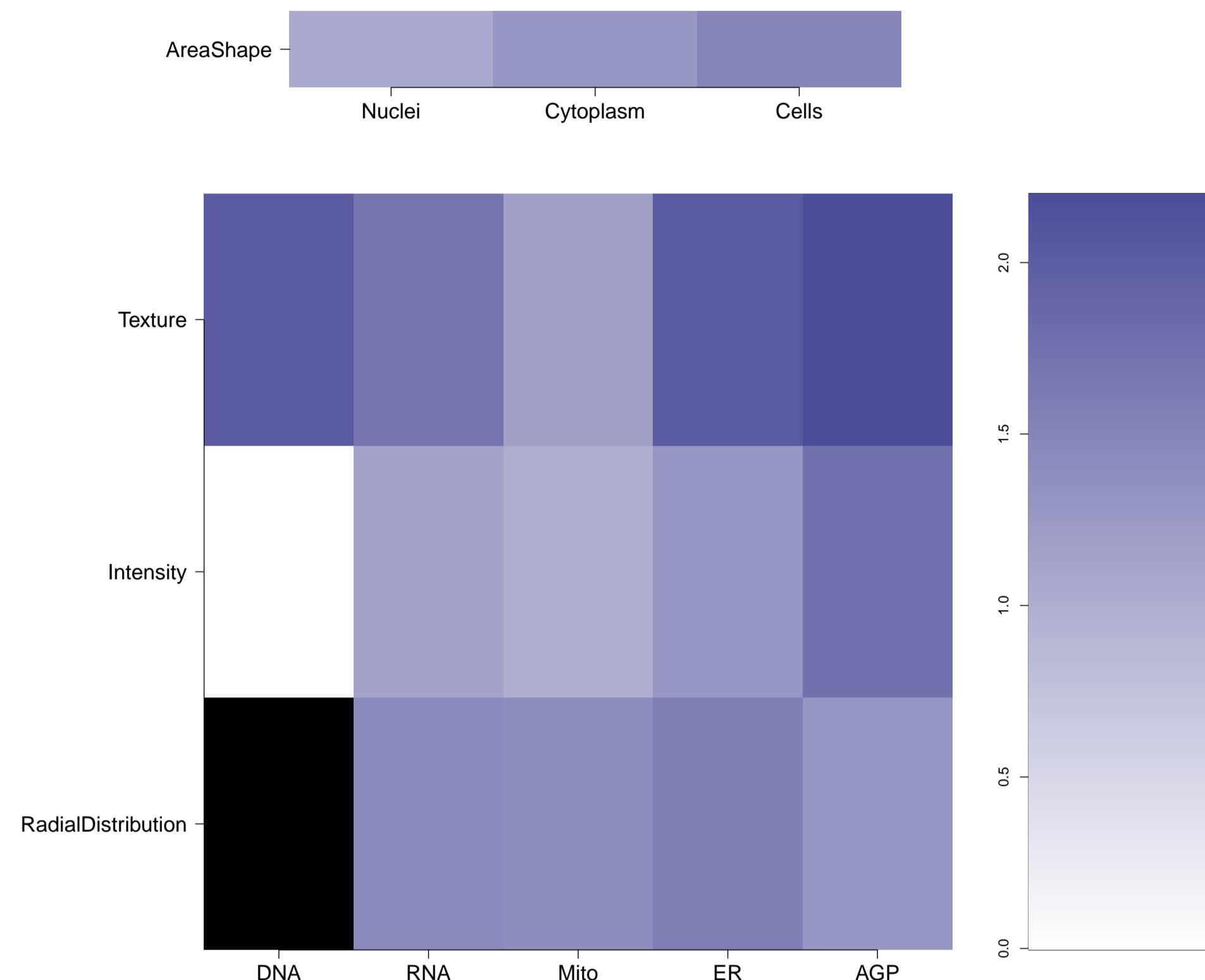
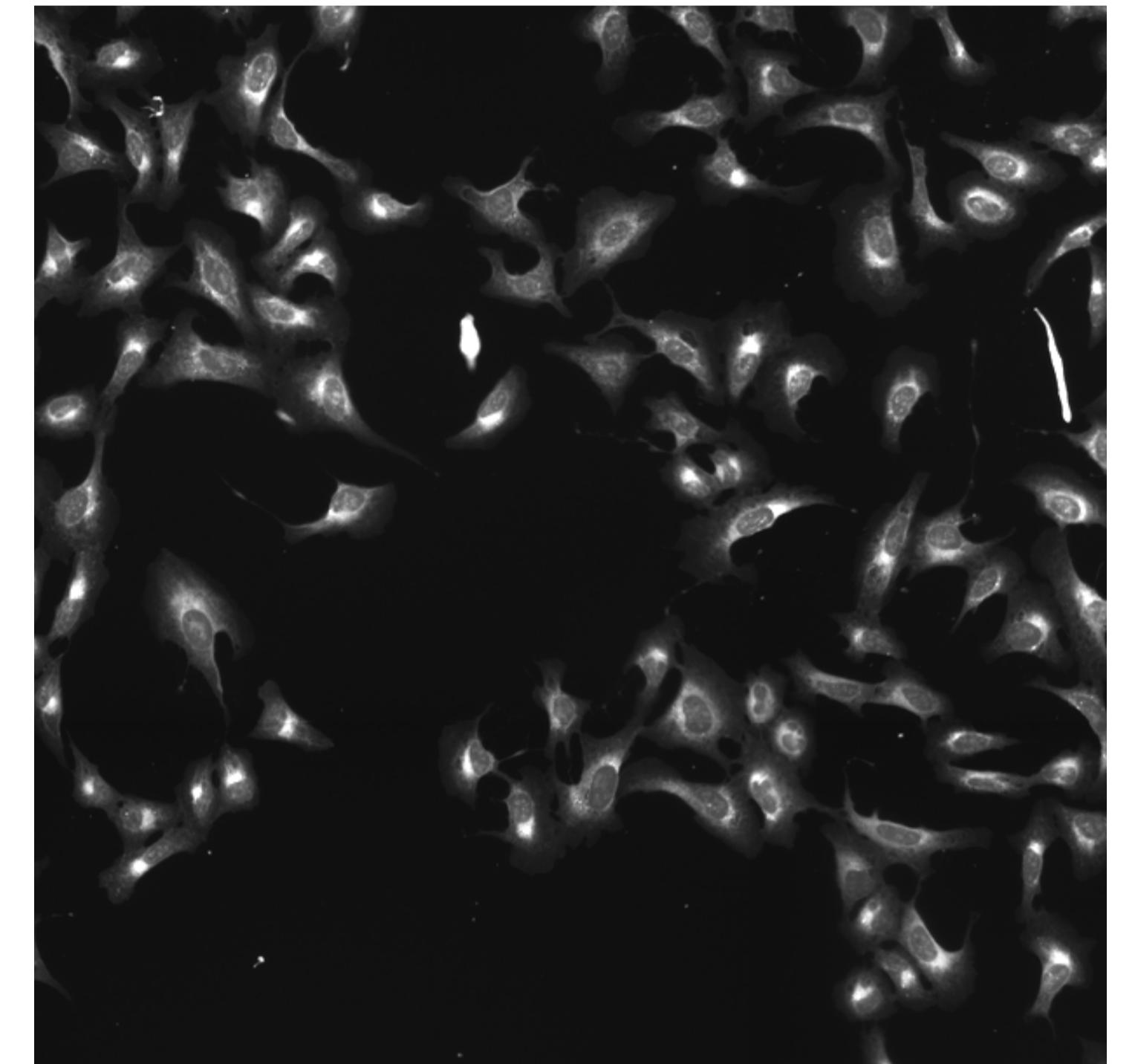
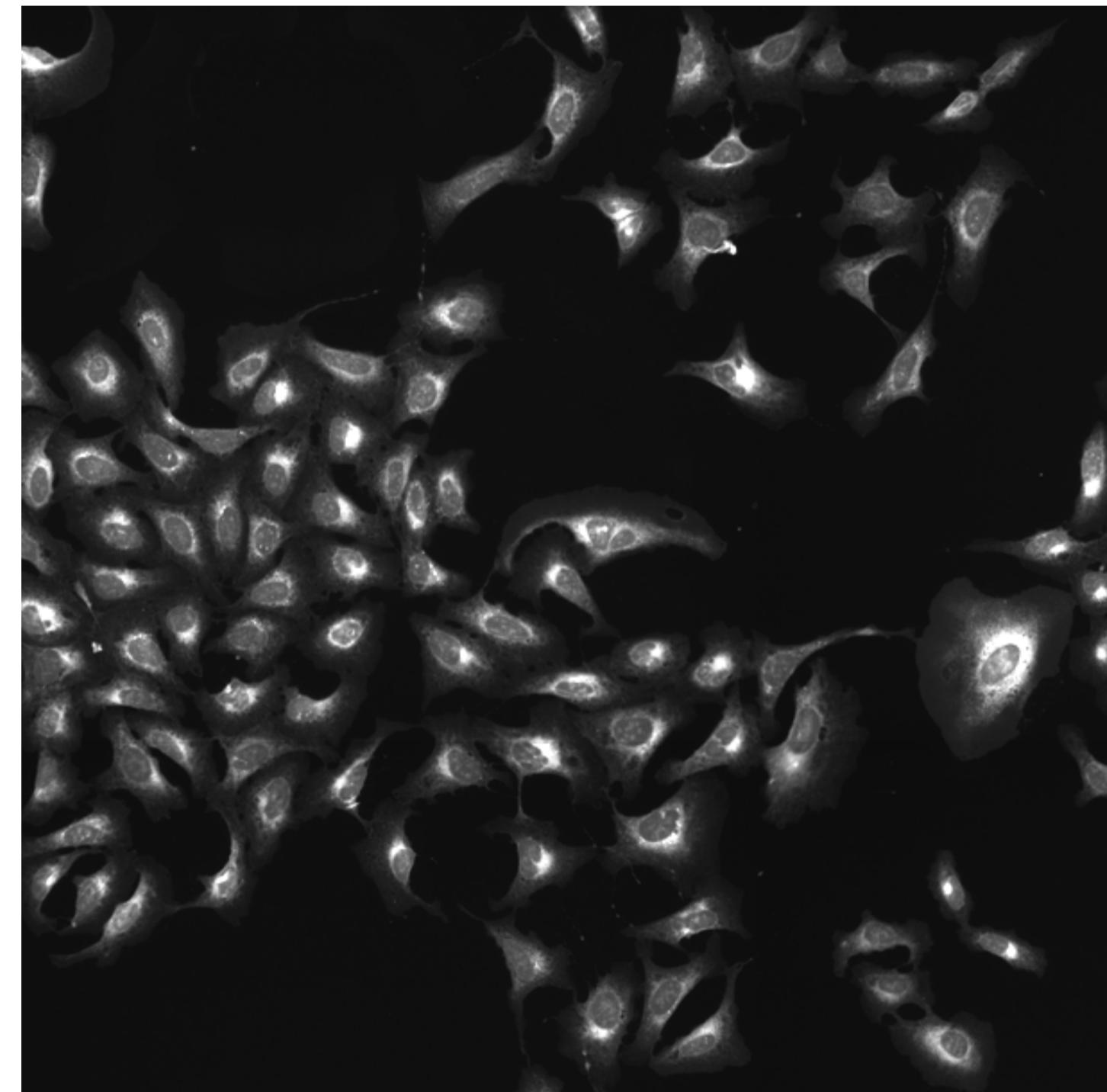
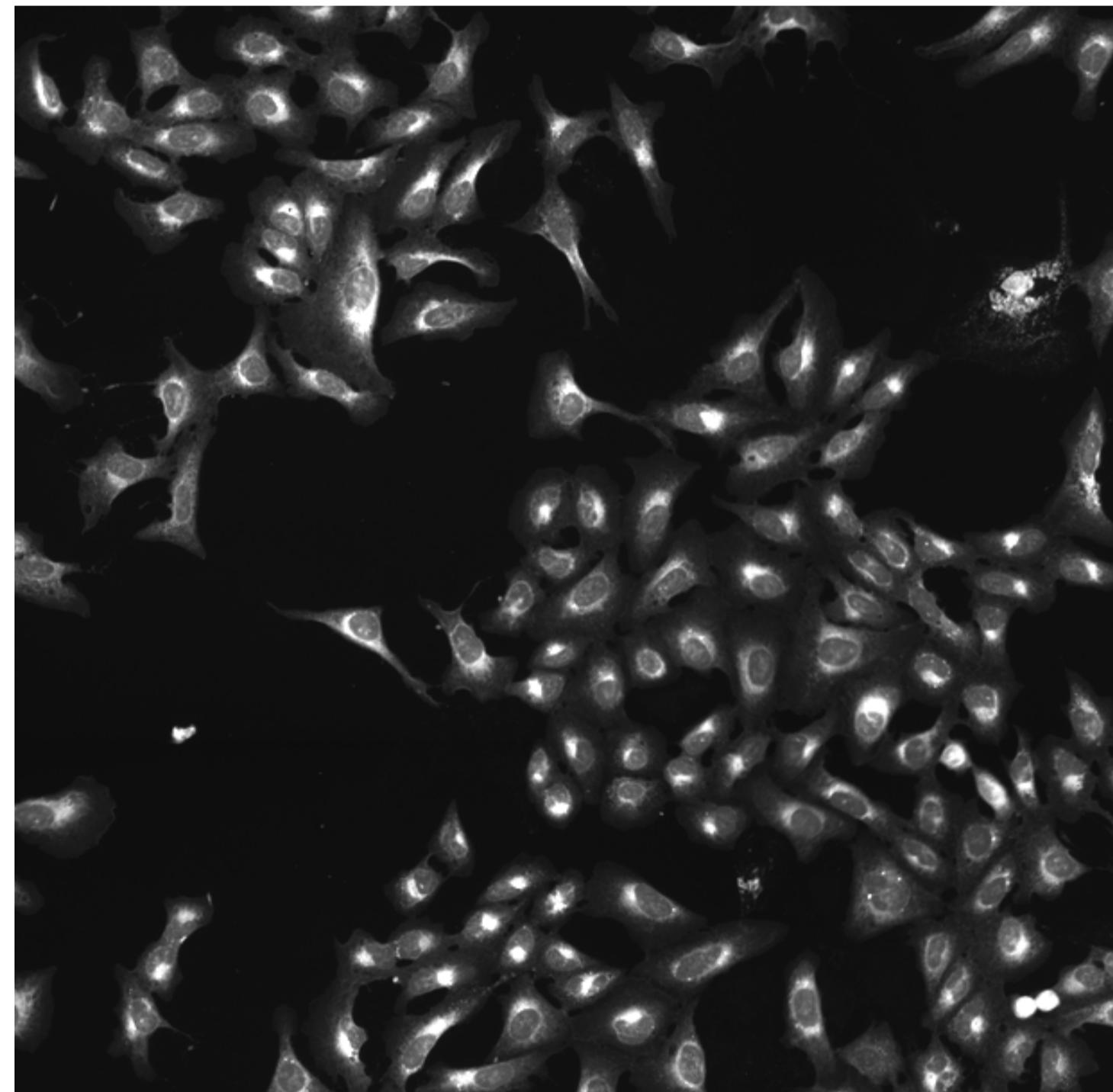
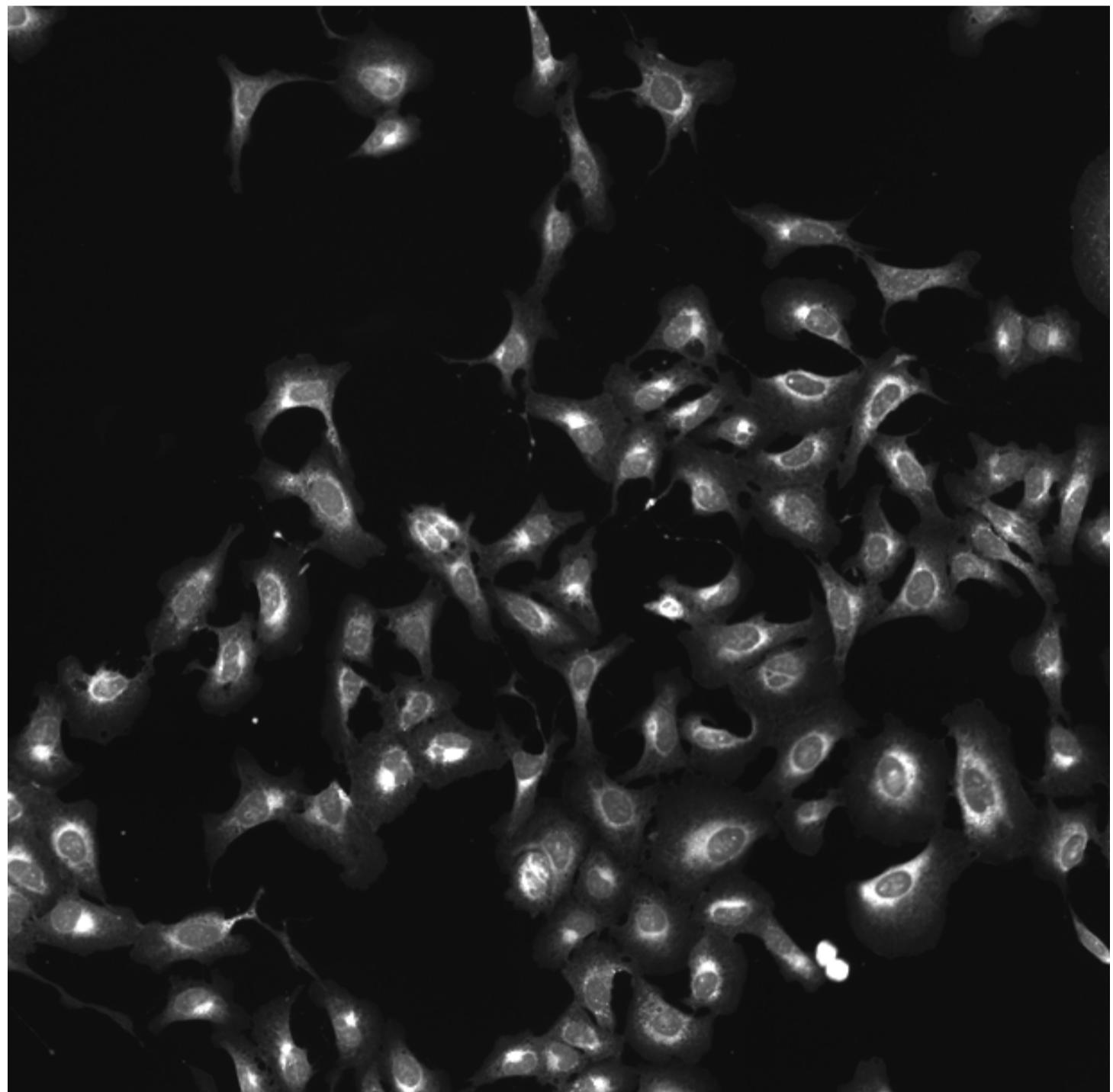
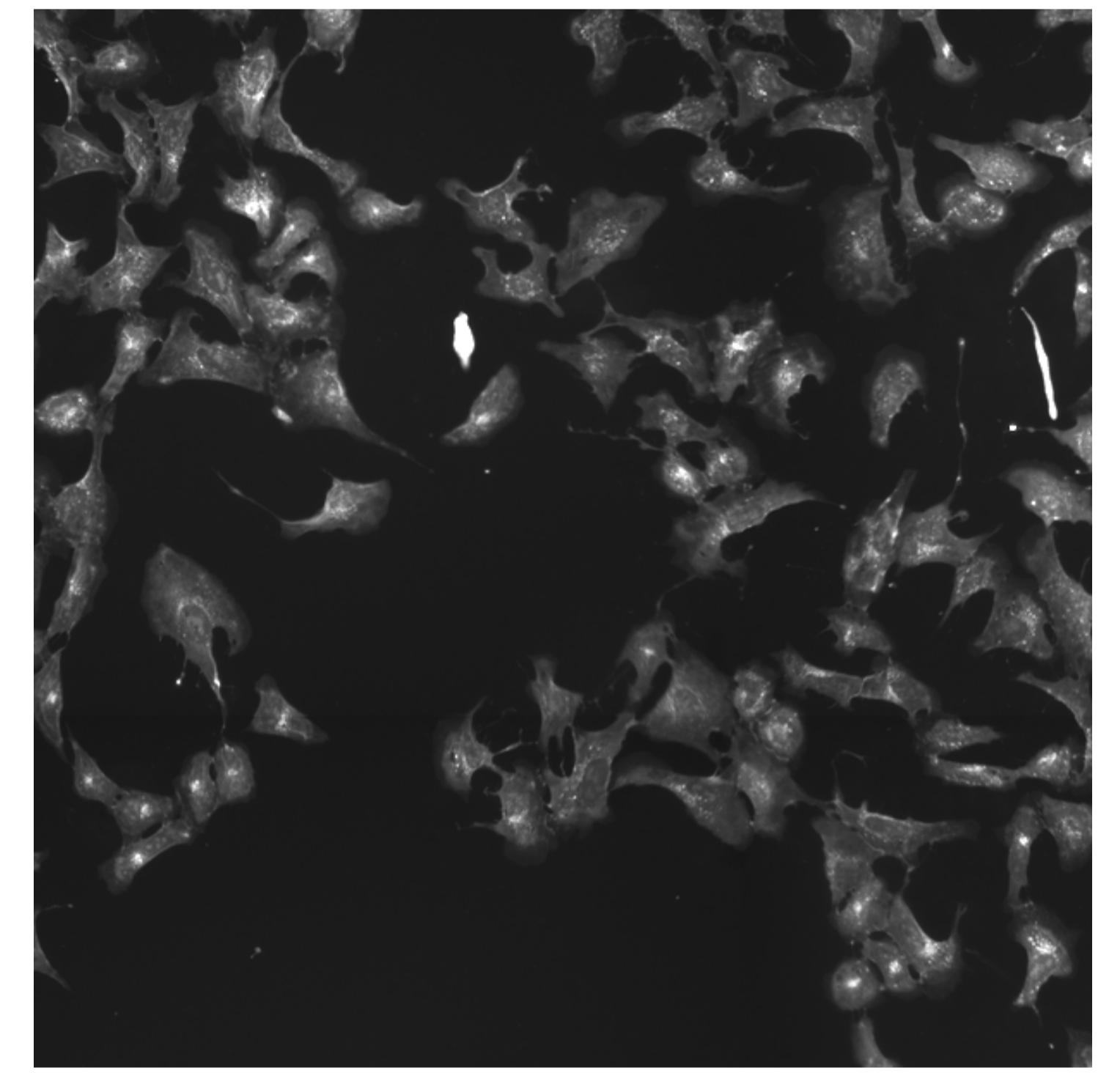
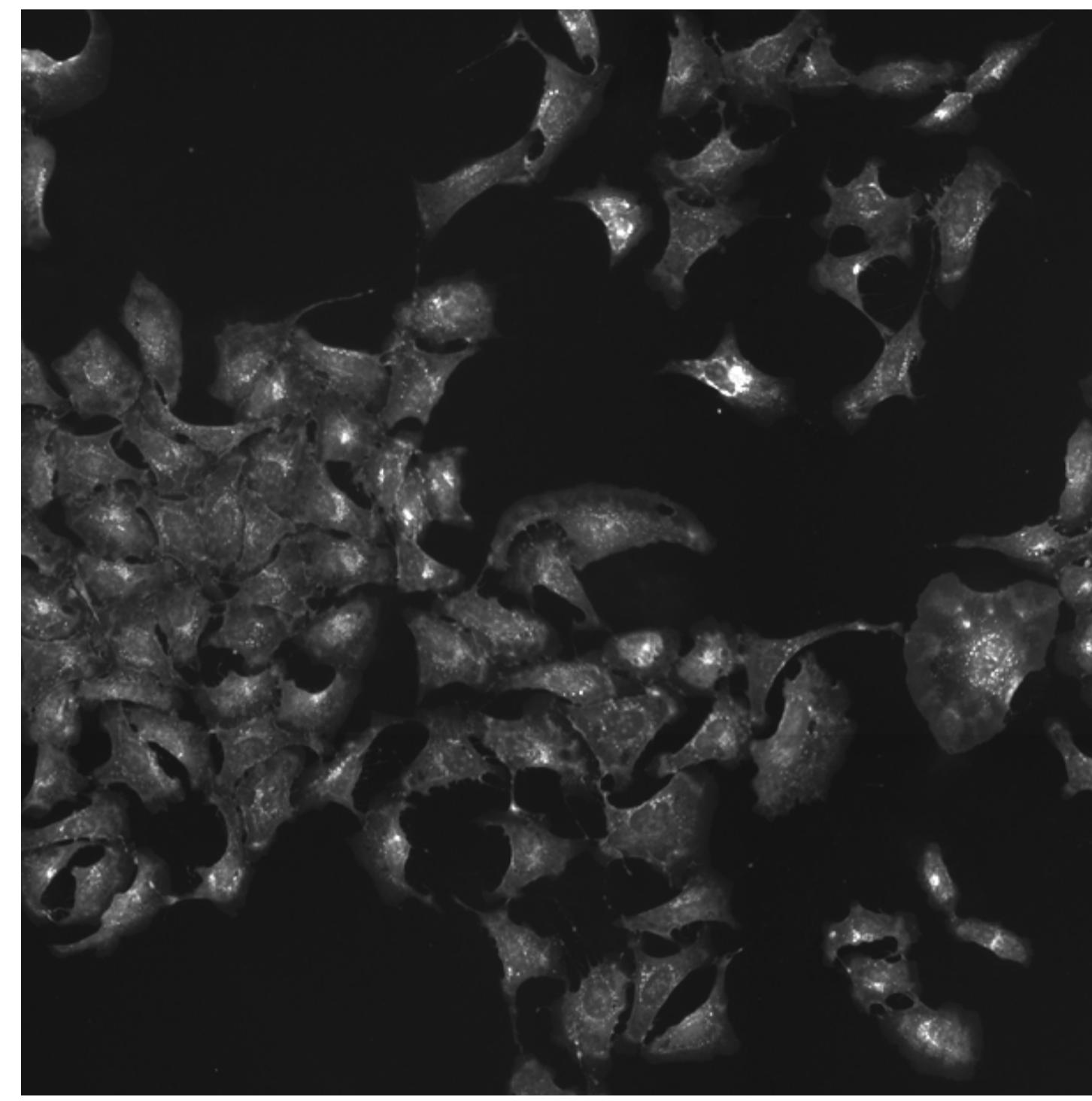
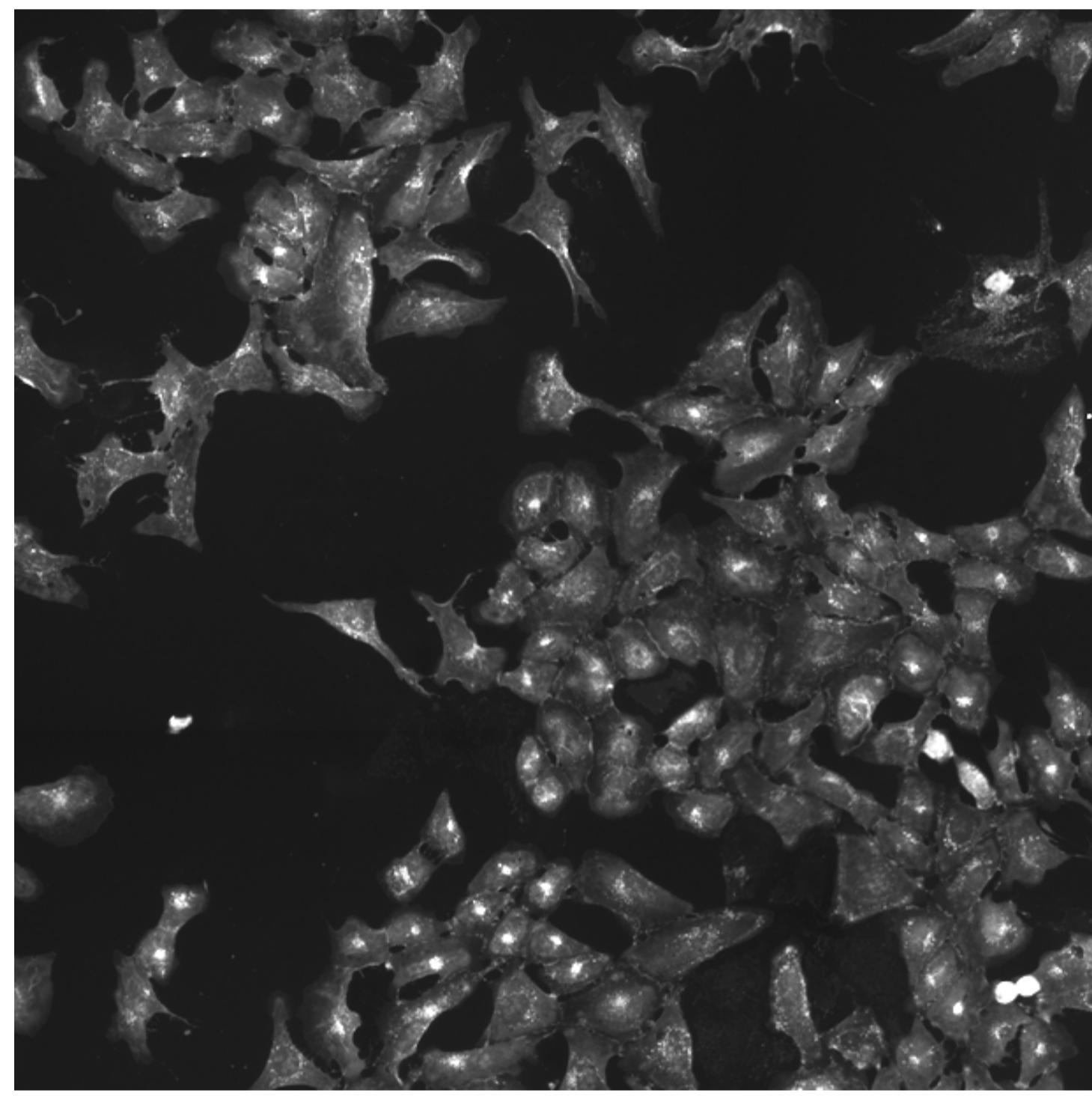
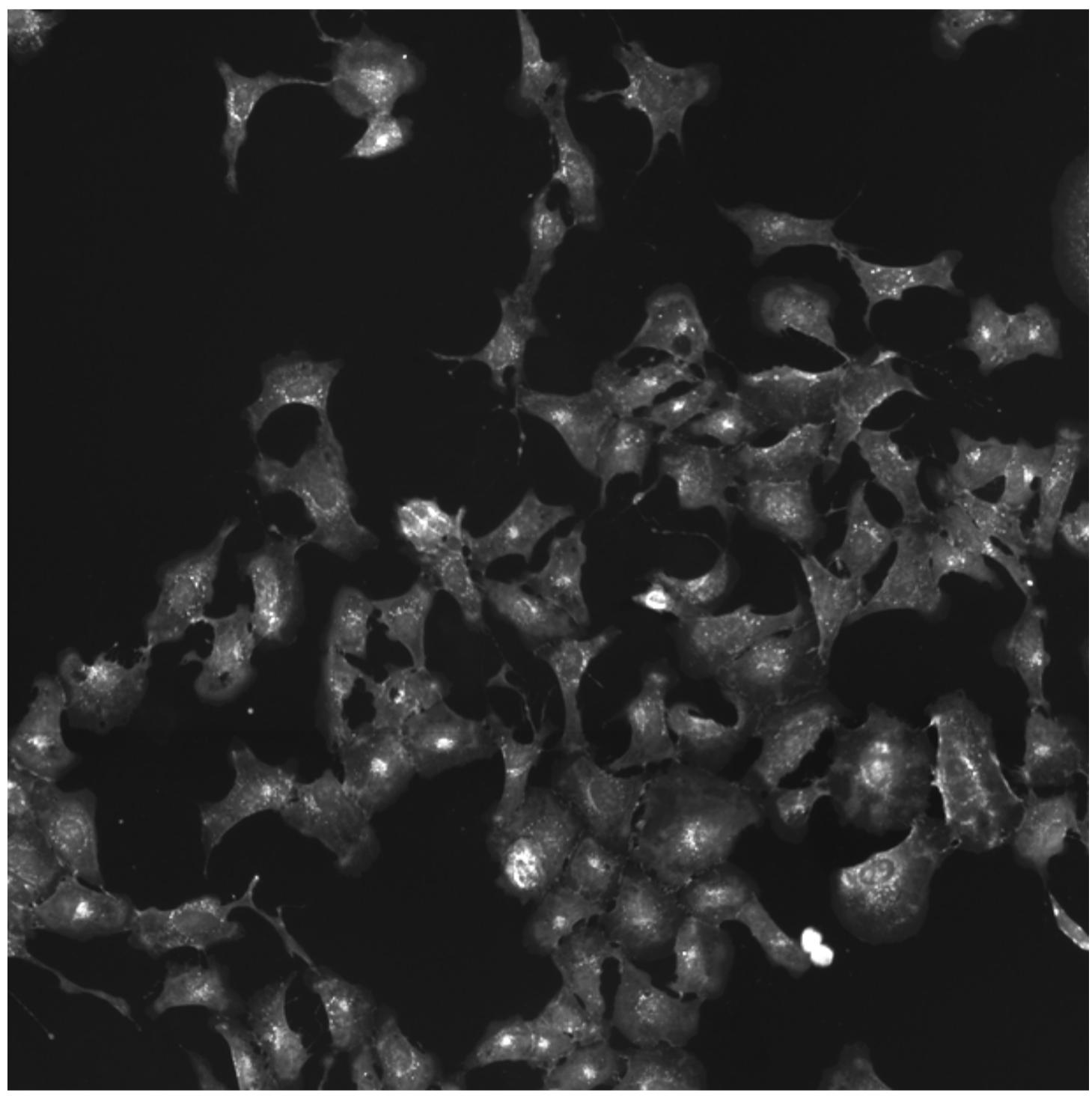


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

DVL3_WT

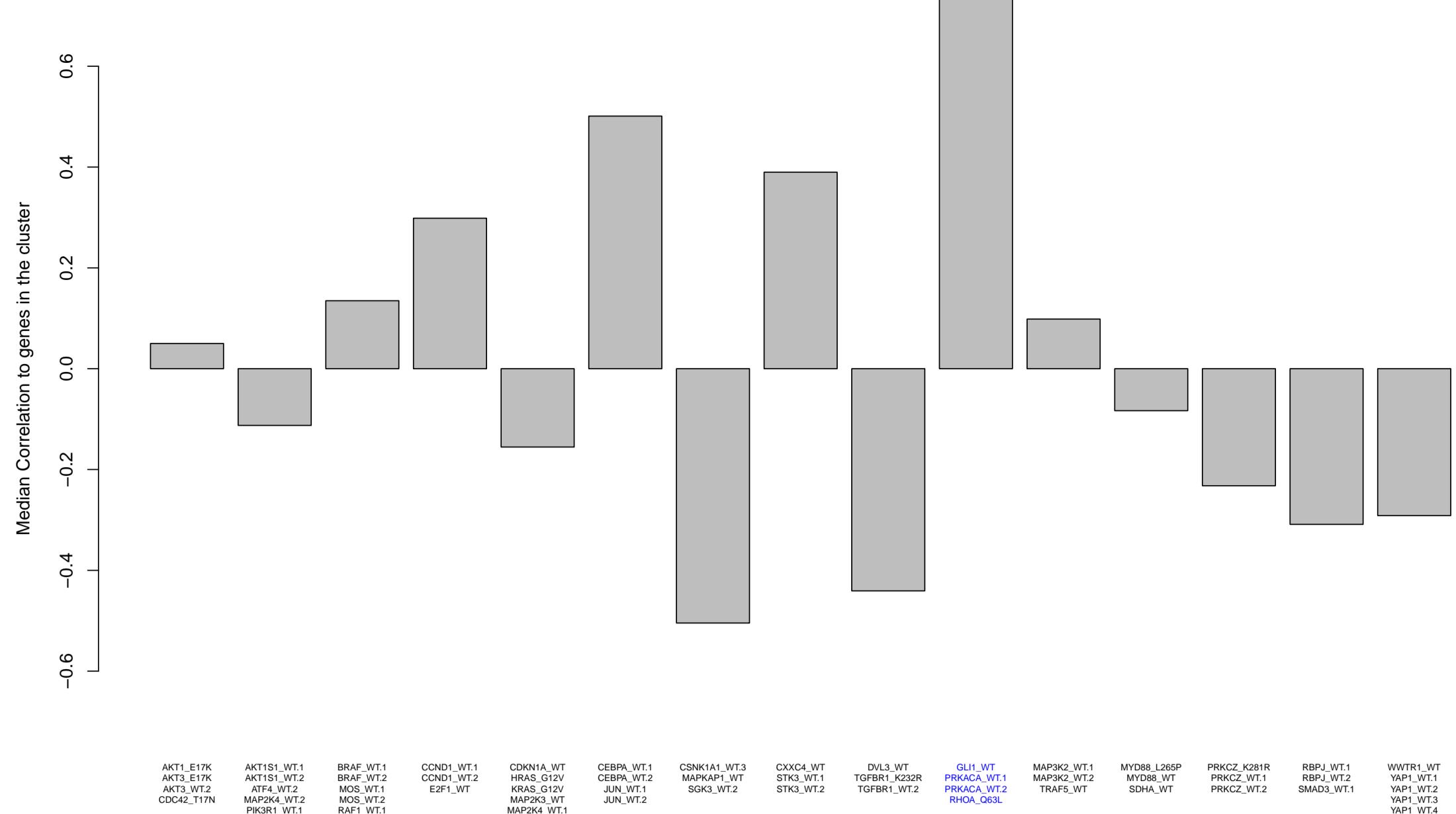
TGFBR1_K232R

TGFBR1_WT.2



Cluster 10

Genes in the cluster along with the pathways as annotated by experts			
Treatment	Pathway	Expert Annotation	
		Regulation	Type
RHOA_Q63L	Canonical Cytoskeletal Re-org	Activator	
PRKACA_WT.1	Canonical PKA	Activator	
PRKACA_WT.2	Canonical PKA	Activator	
GLI1_WT	Hedgehog	Activator	



Top 5 genes negatively correlated to the cluster					
Treatment	Expert Annotation		Mean Correlation	Standard Deviation	
	Pathway	Regulation Type			
CSNK1A1_WT.3	Canonical WNT	Inhibitor	-0.54	0.07	
RPS6KB1_WT.1	Canonical TOR	Activator	-0.54	0.10	
AKT1_WT.1	Canonical PI3K/AKT	Activator	-0.50	0.08	
STK11_WT.2	Canonical TOR	Inhibitor	-0.49	0.09	
MAPKAP1_WT	Canonical TOR	Activator	-0.49	0.15	

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?

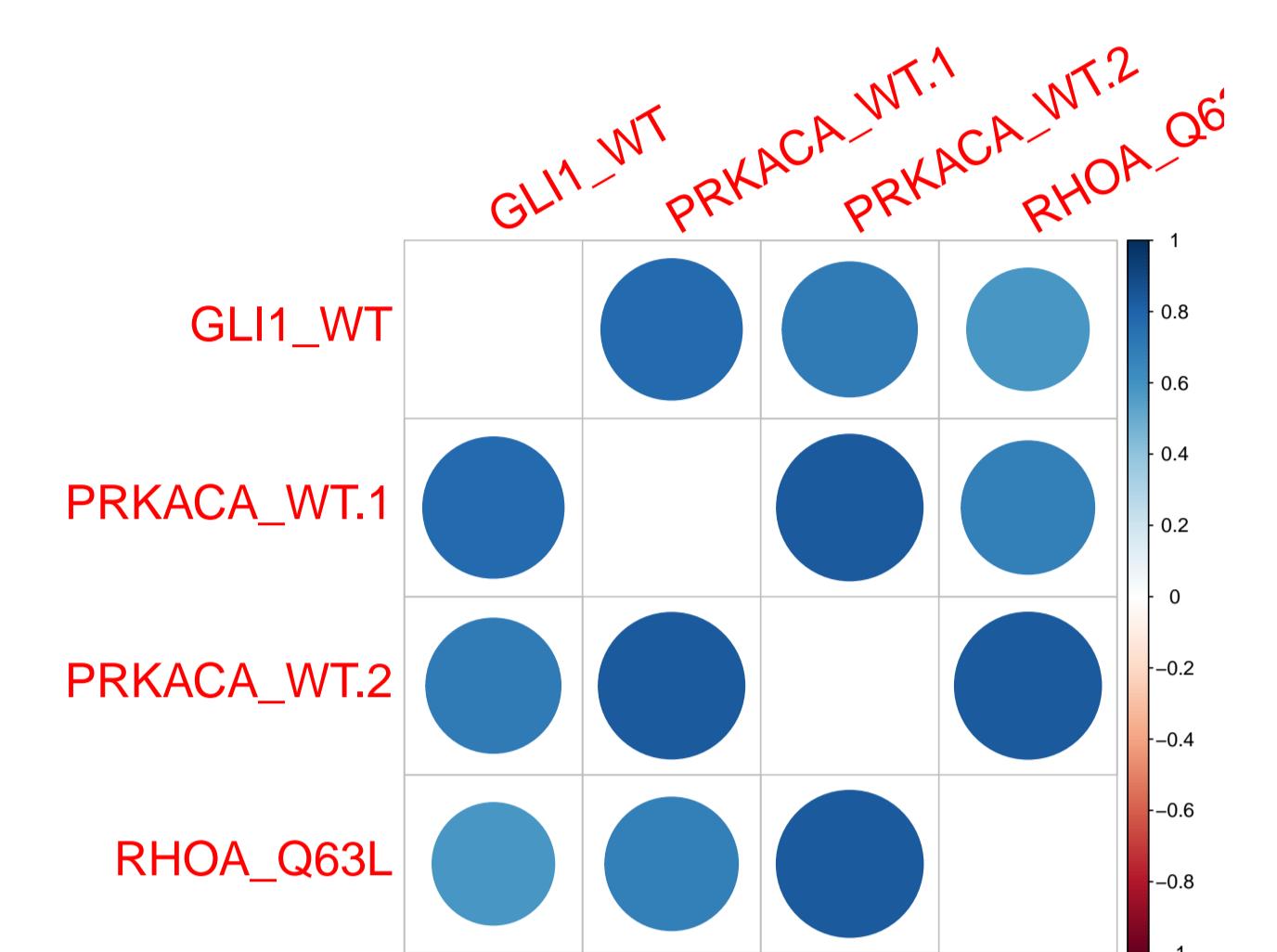
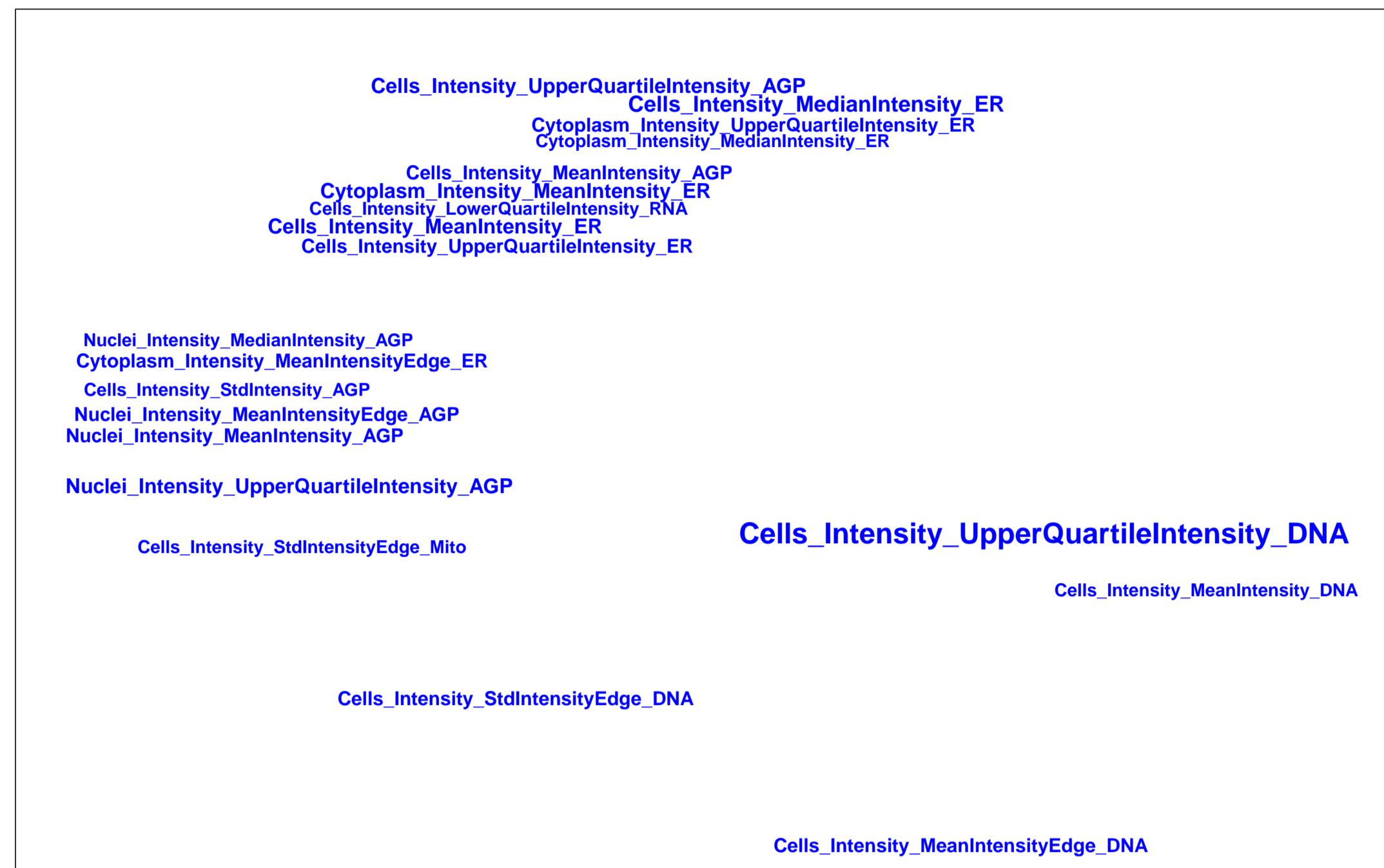
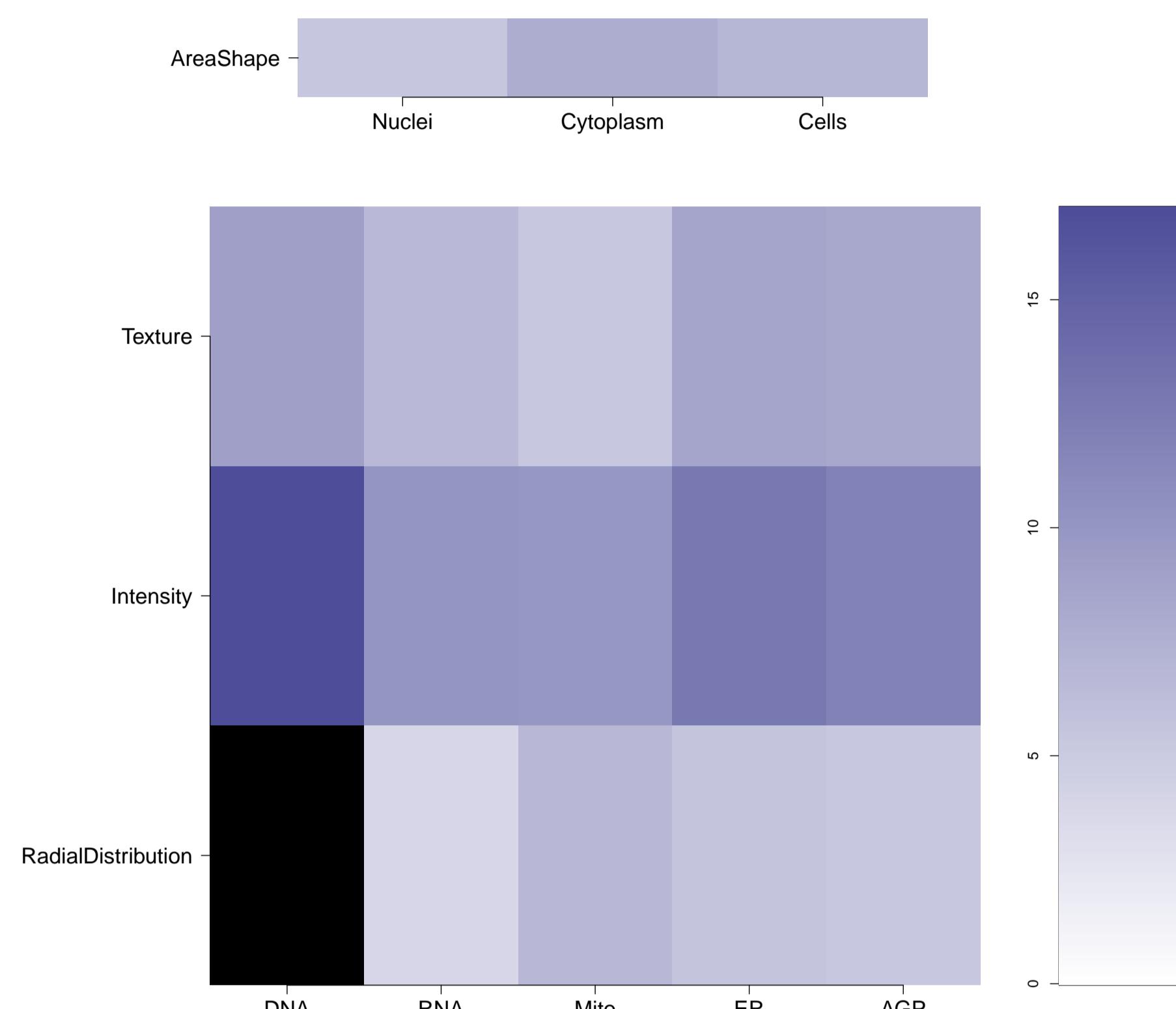


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

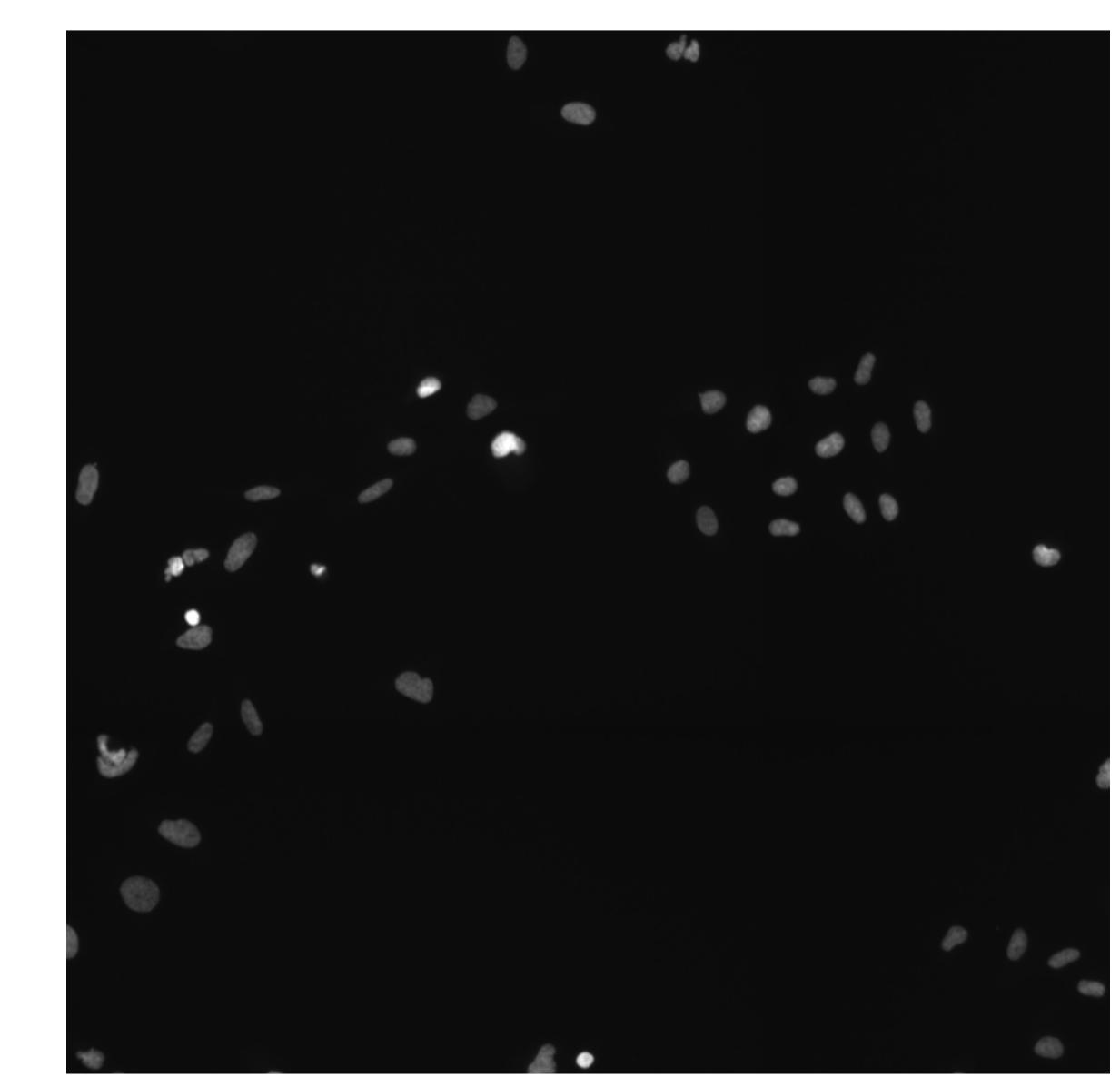
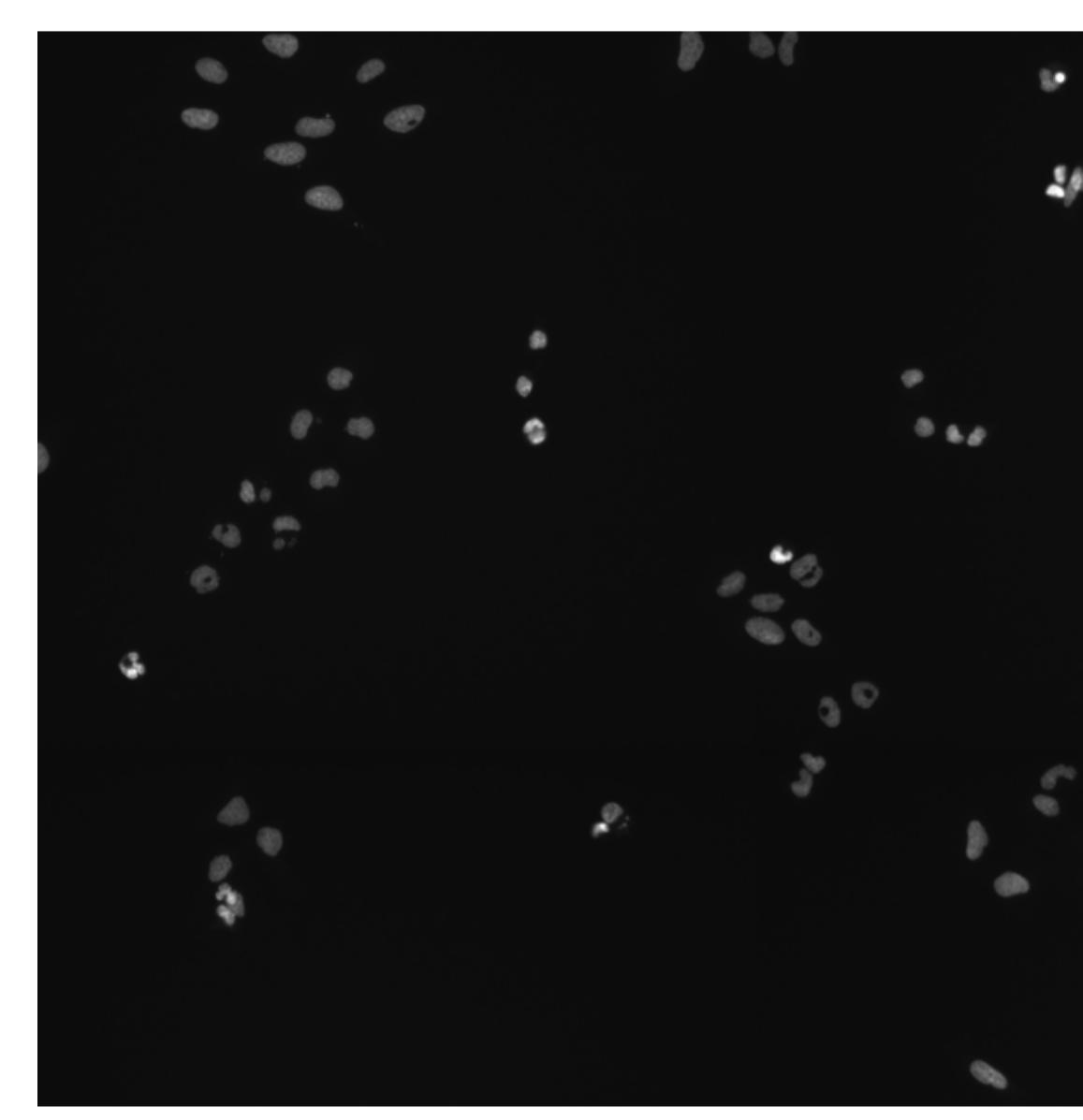
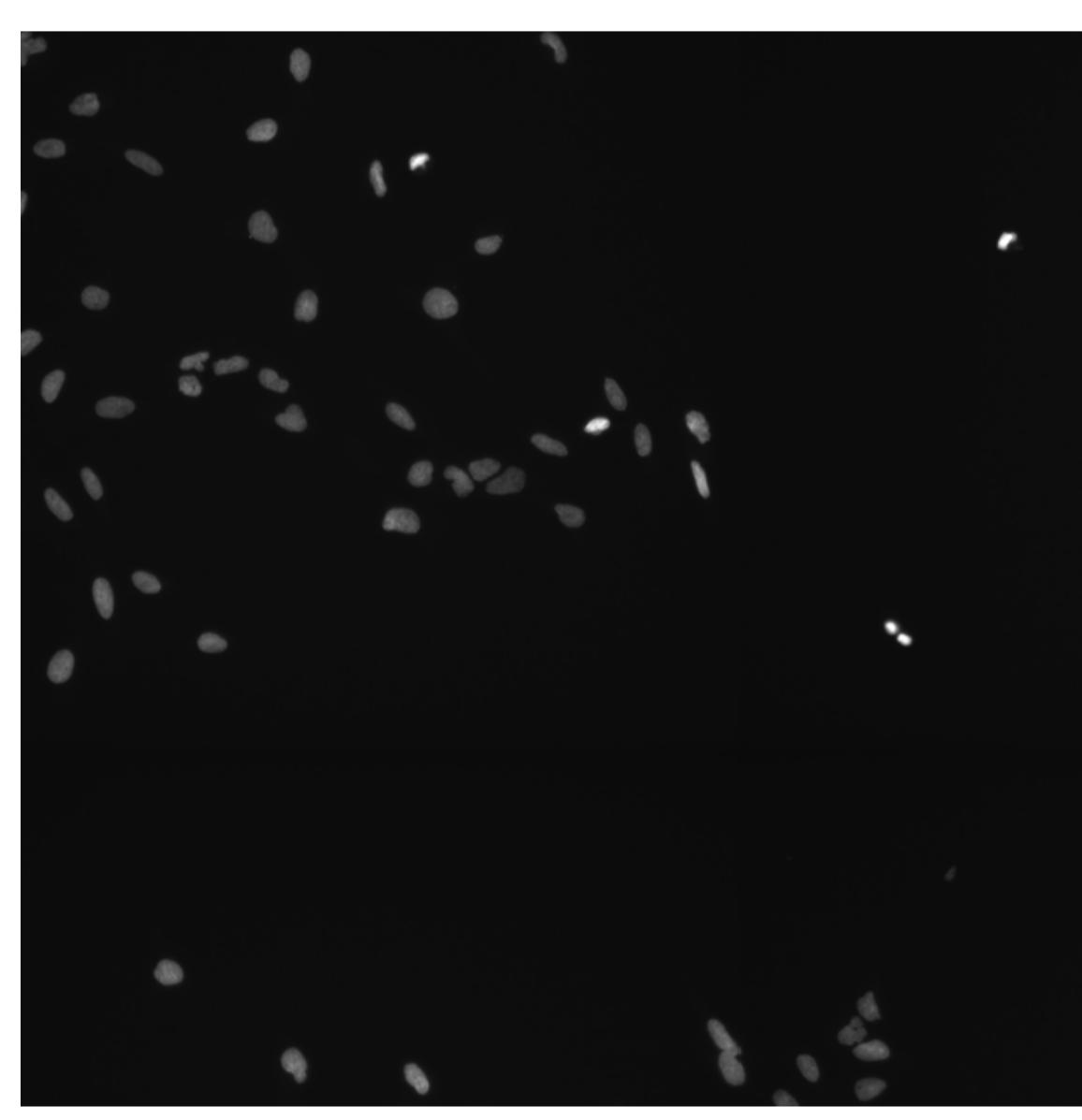
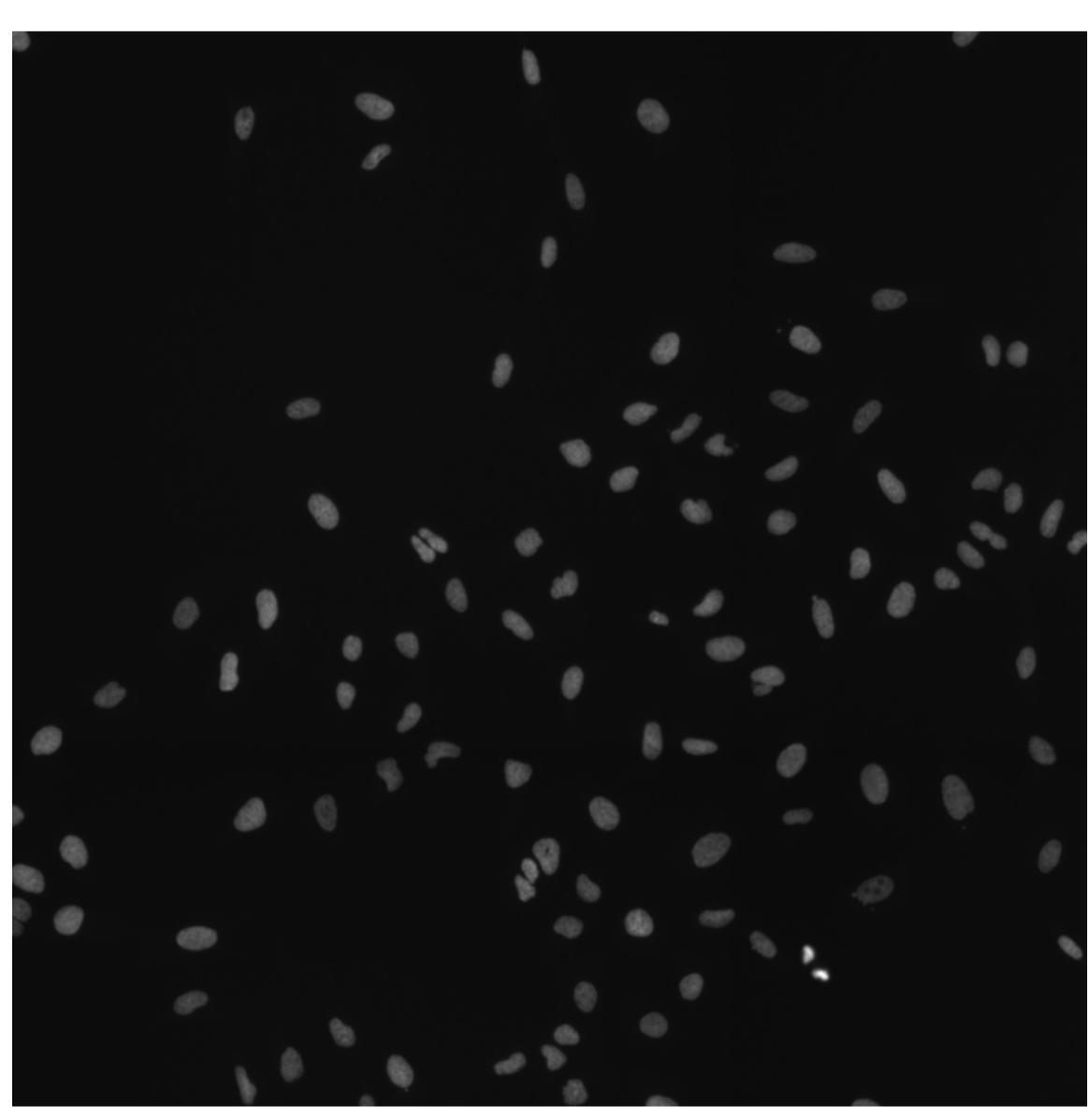
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GLI1_WT

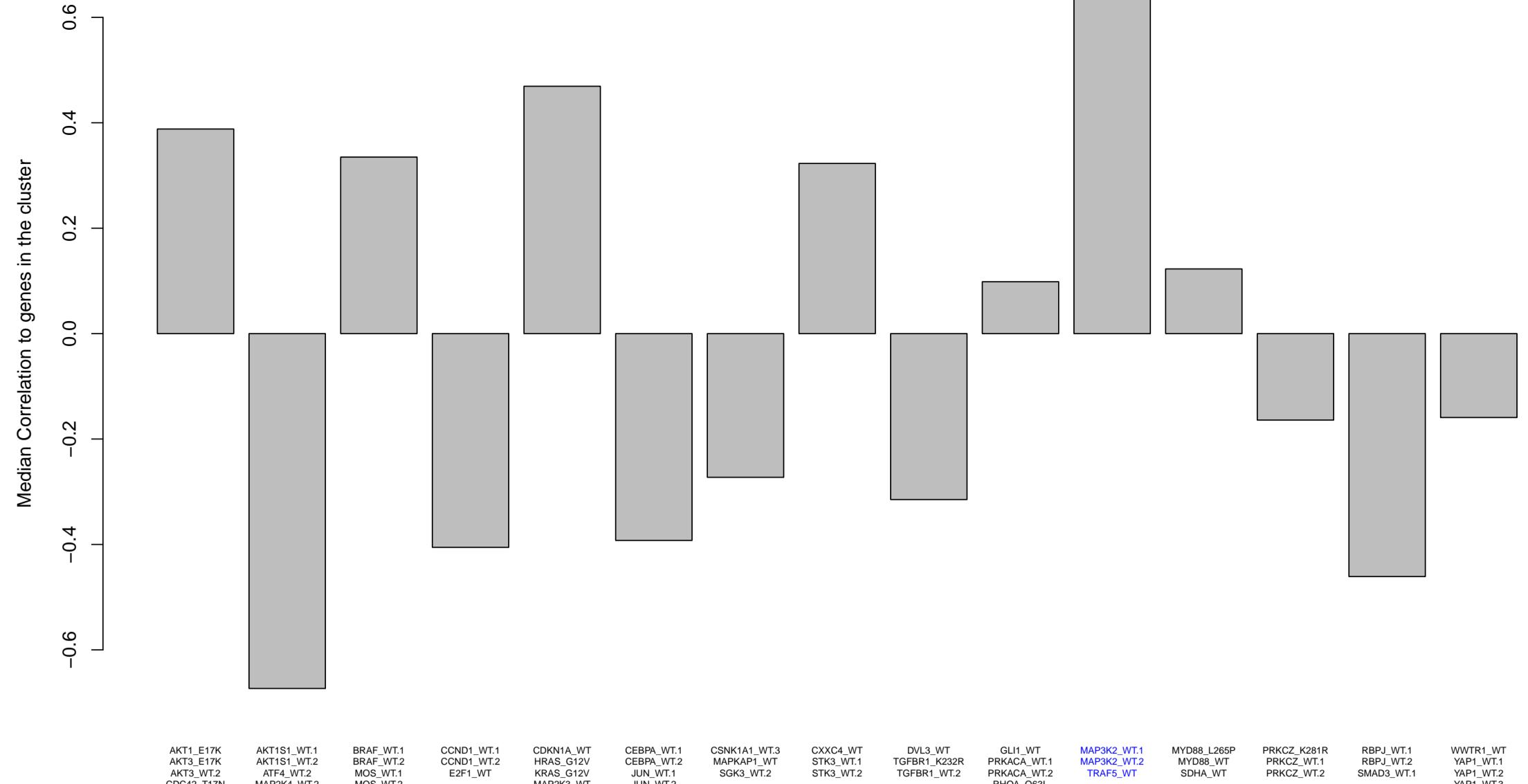
PRKACA_WT.1

PRKACA_WT.2

RHOA_Q63L



ER



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

Treatment	Pathway	Regulation Type
MAP3K2_WT_1	Canonical MAPK	Activator
MAP3K2_WT_2	Canonical MAPK	Activator
TRAF5_WT	Canonical NFkB	Activator

Top 5 genes negatively correlated to the cluster

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
MAP2K4_WT_2	Canonical MAPK	Activator	-0.68	0.13
AKT1S1_WT_1	TOR	Inhibitor	-0.67	0.05
PIK3R1_WT_1	Canonical PI3K/AKT	Activator	-0.65	0.07
RBPJ_WT_1	NOTCH	Activator	-0.64	0.10
AKT1S1_WT_2	TOR	Inhibitor	-0.64	0.06

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?

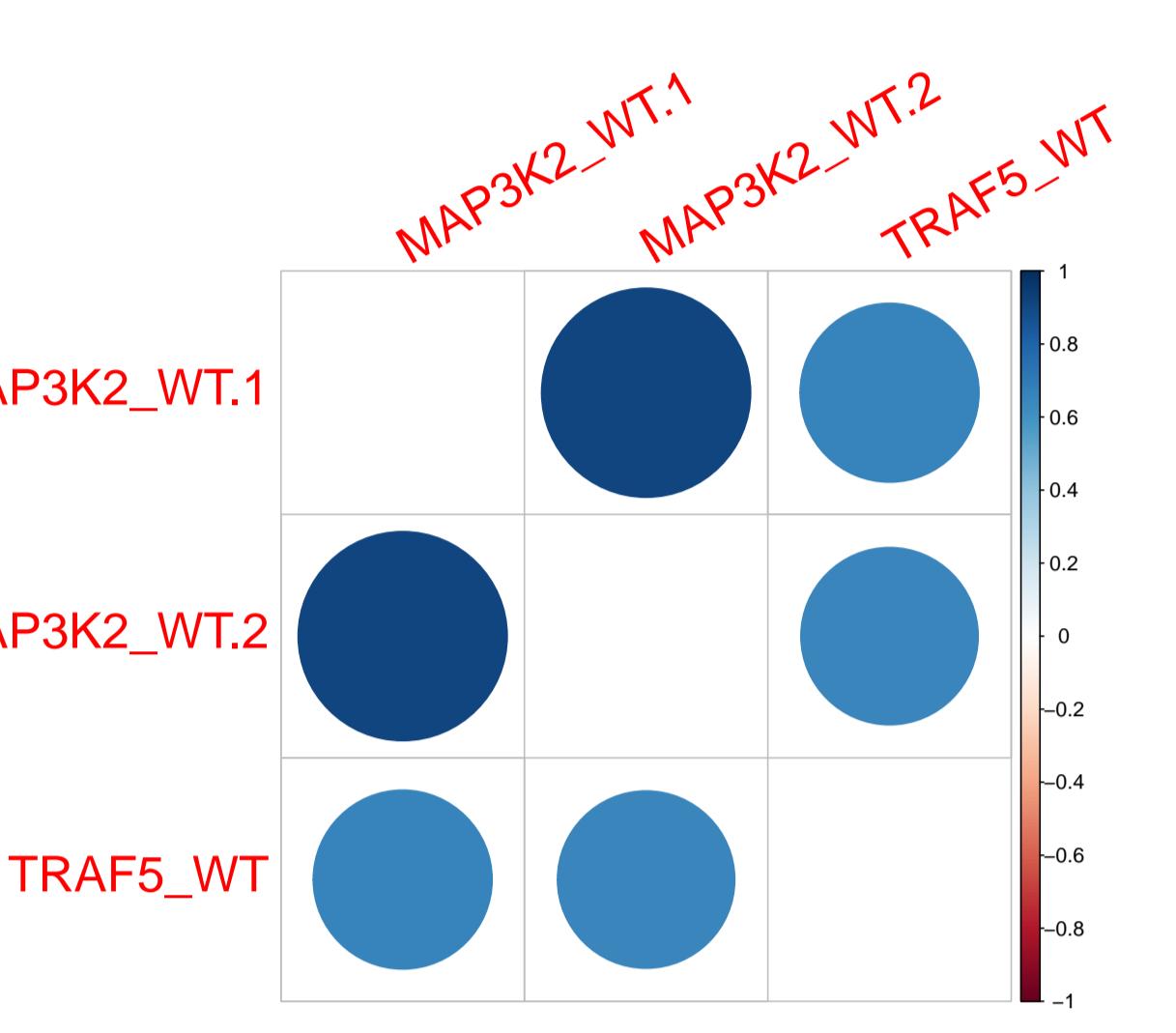
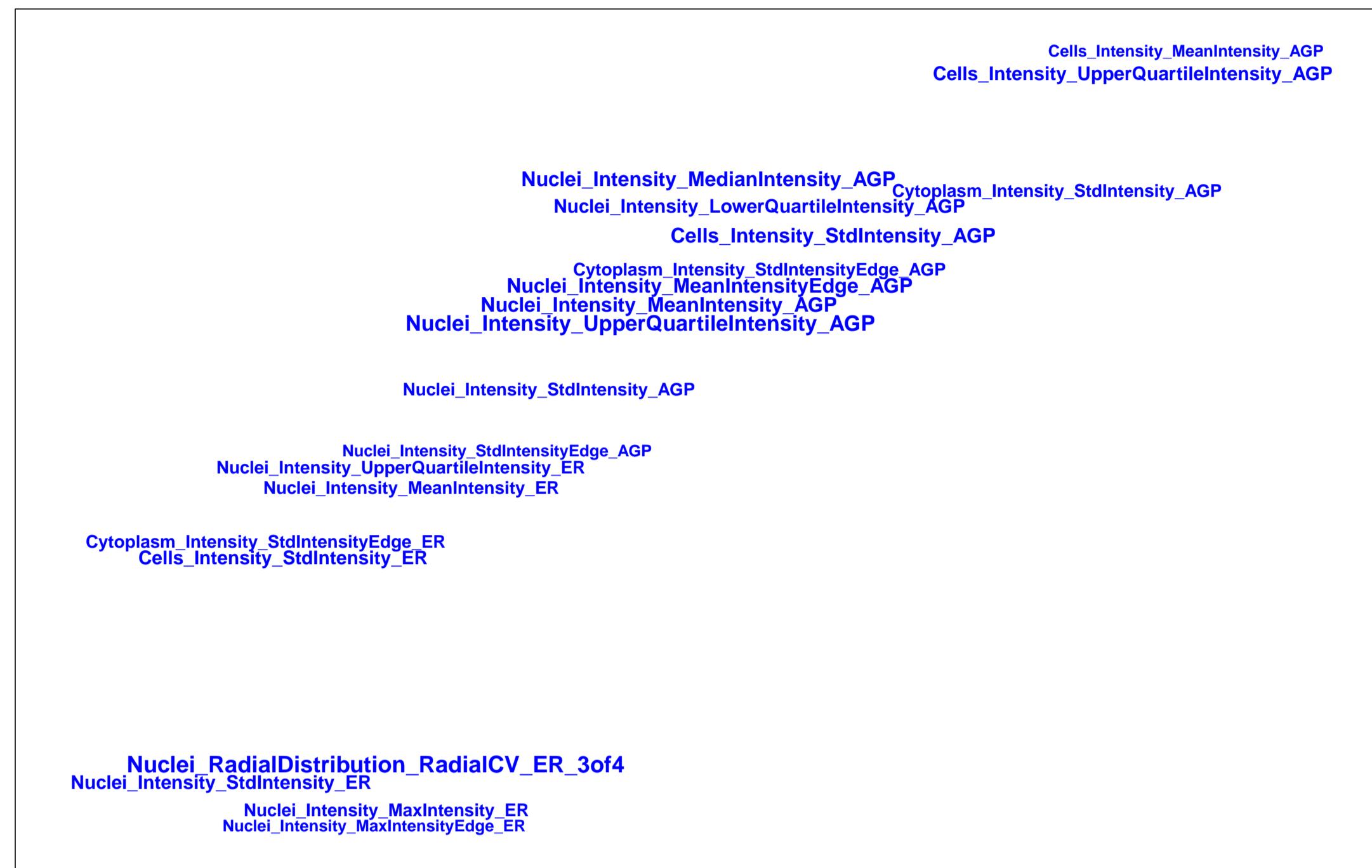
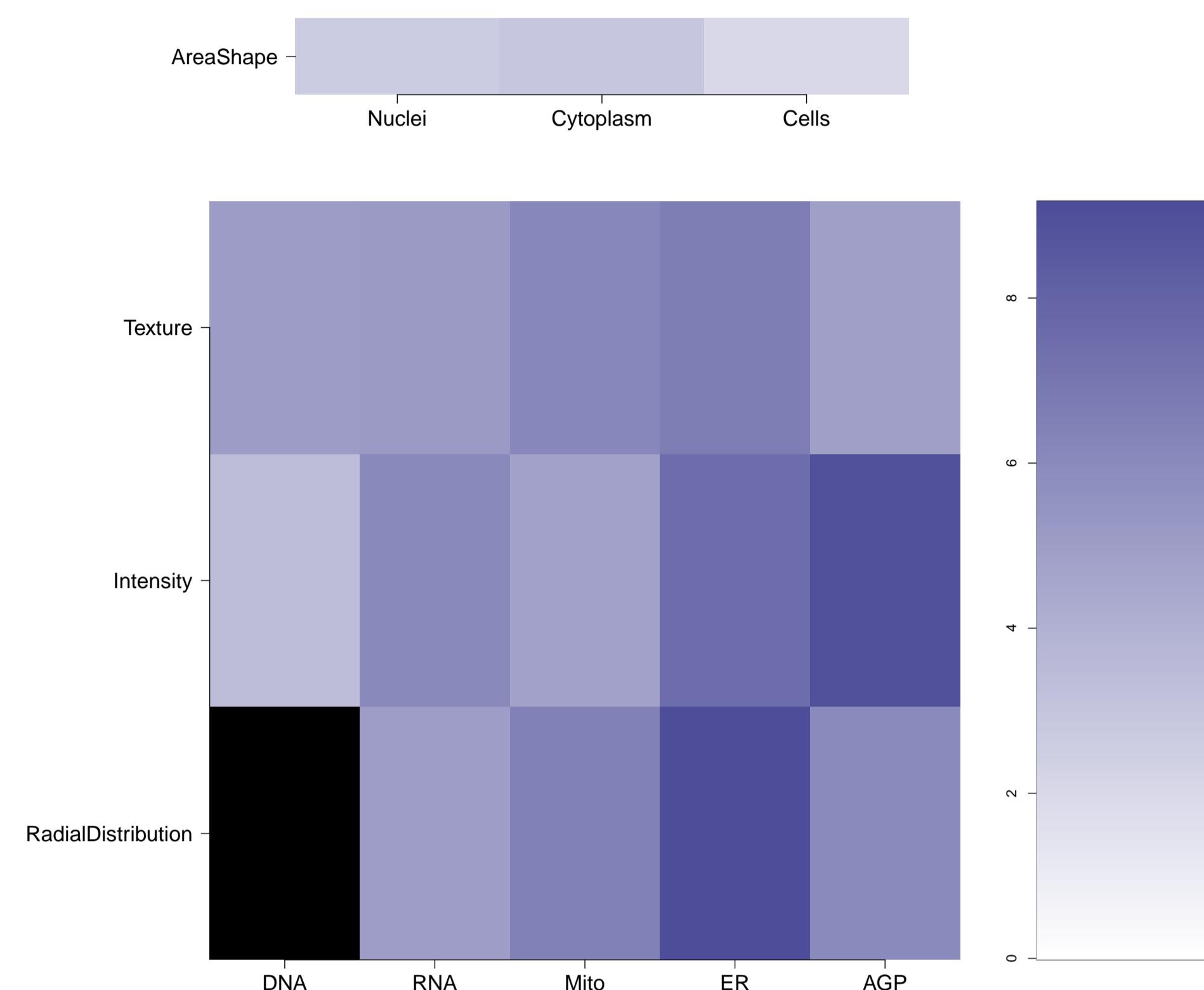


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

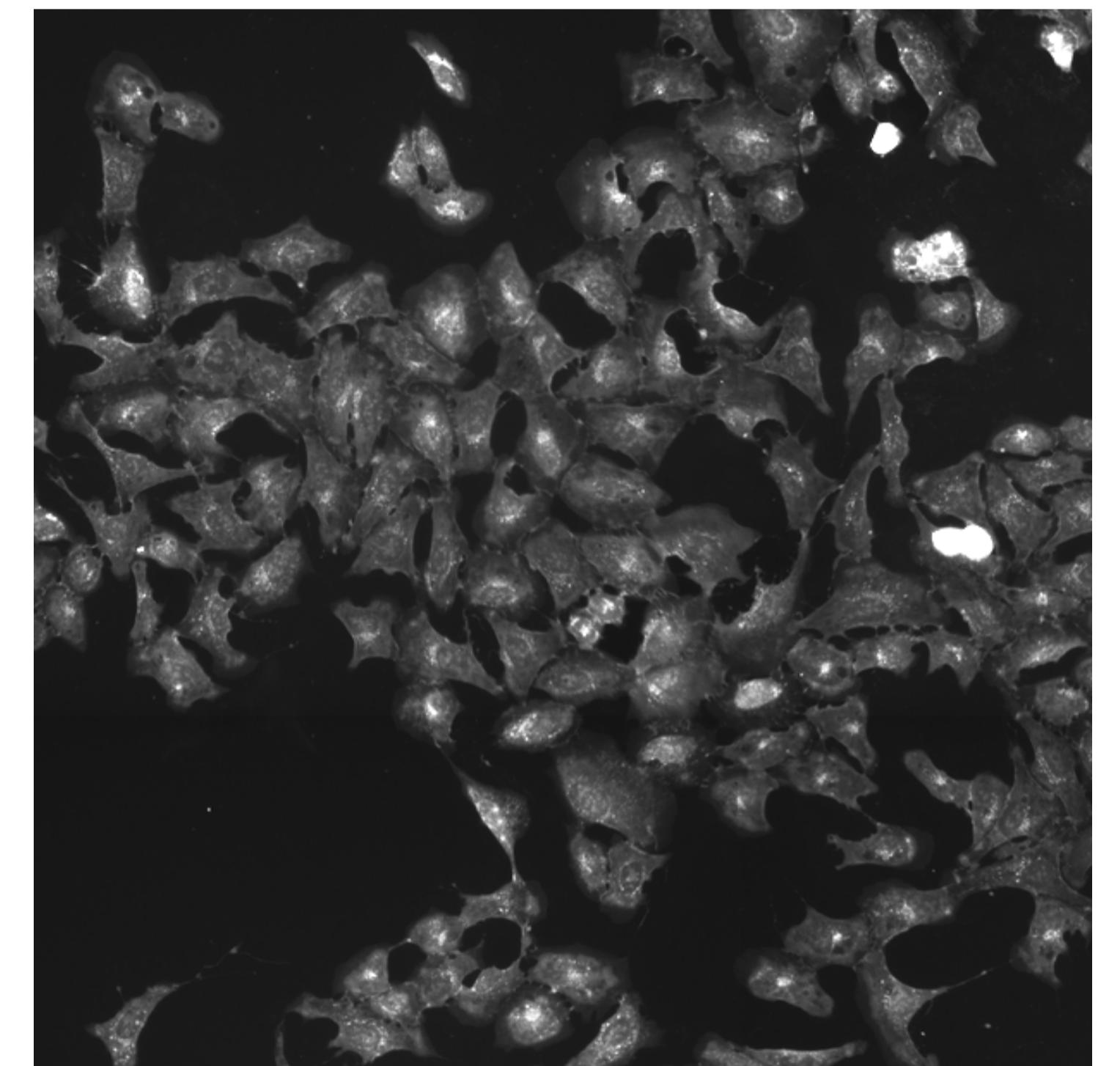
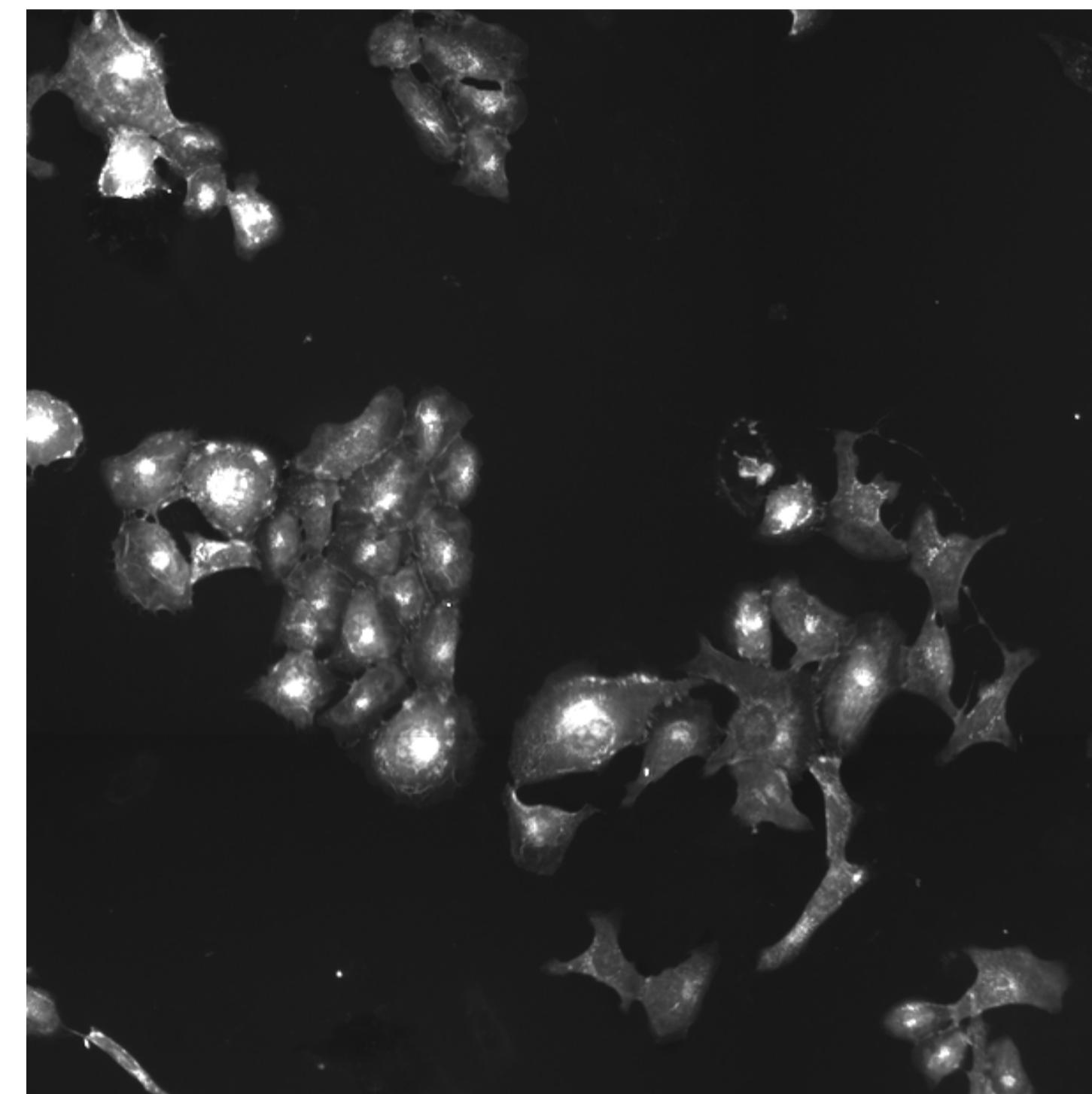
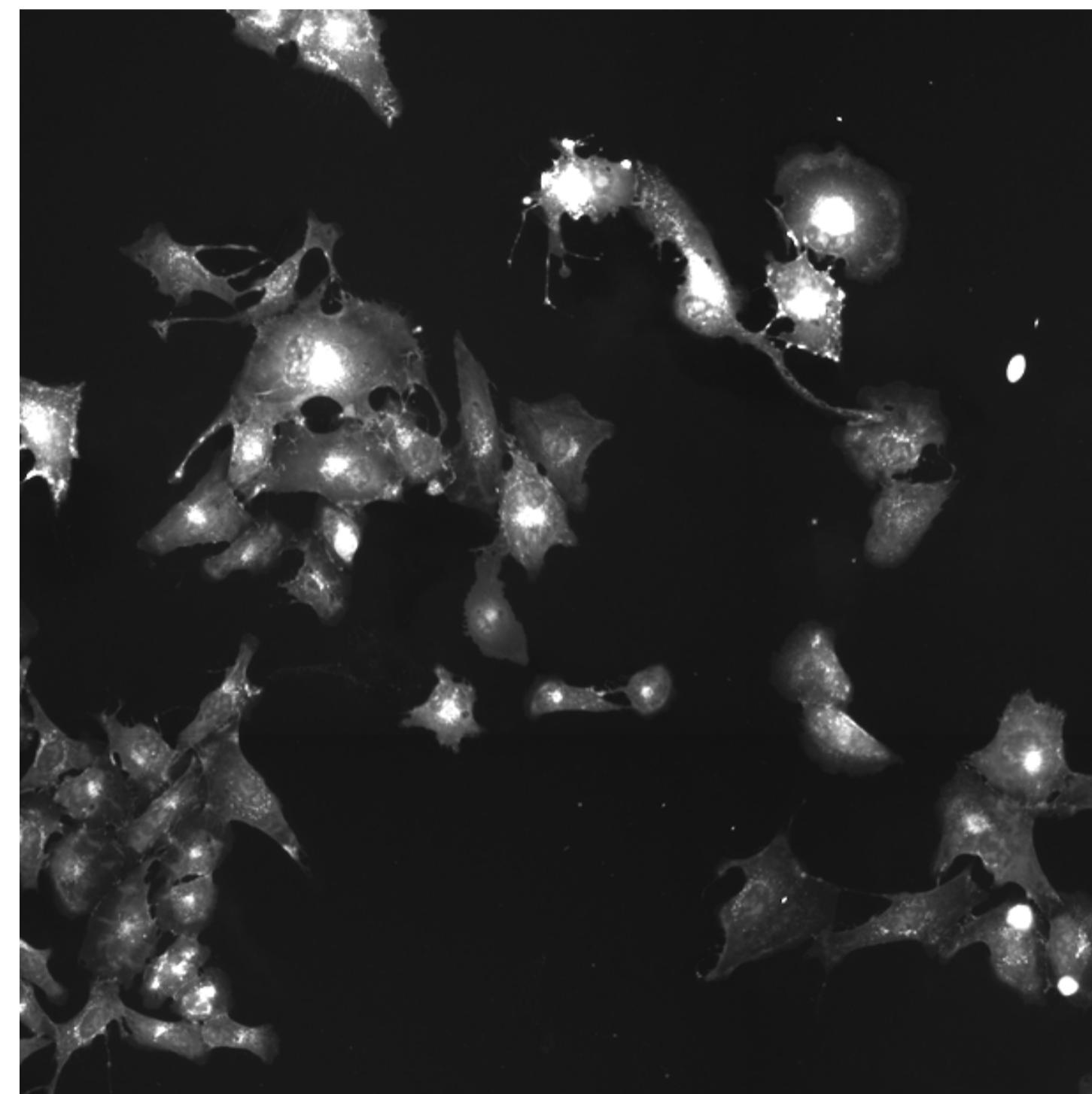
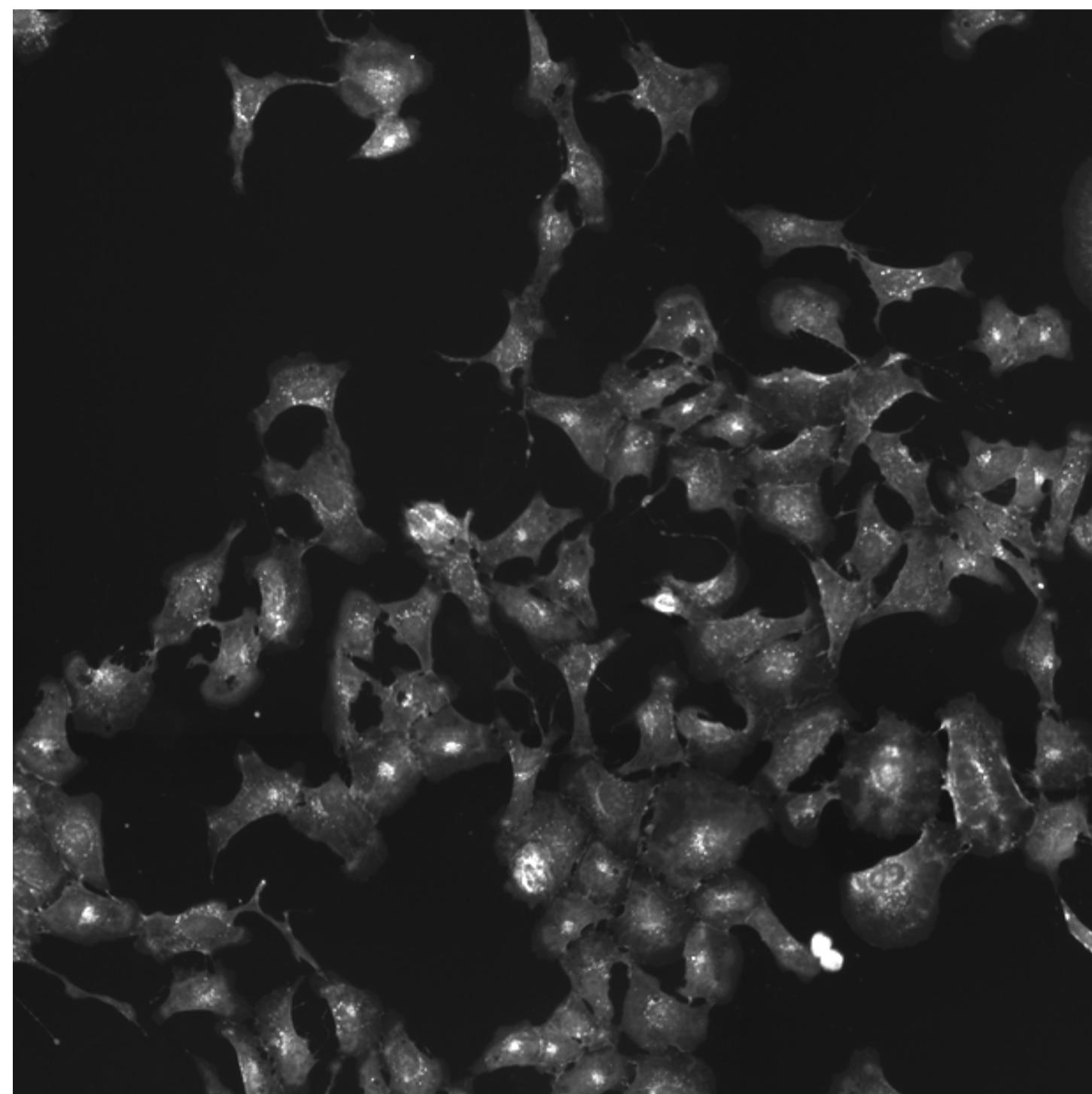
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MAP3K2_WT_1

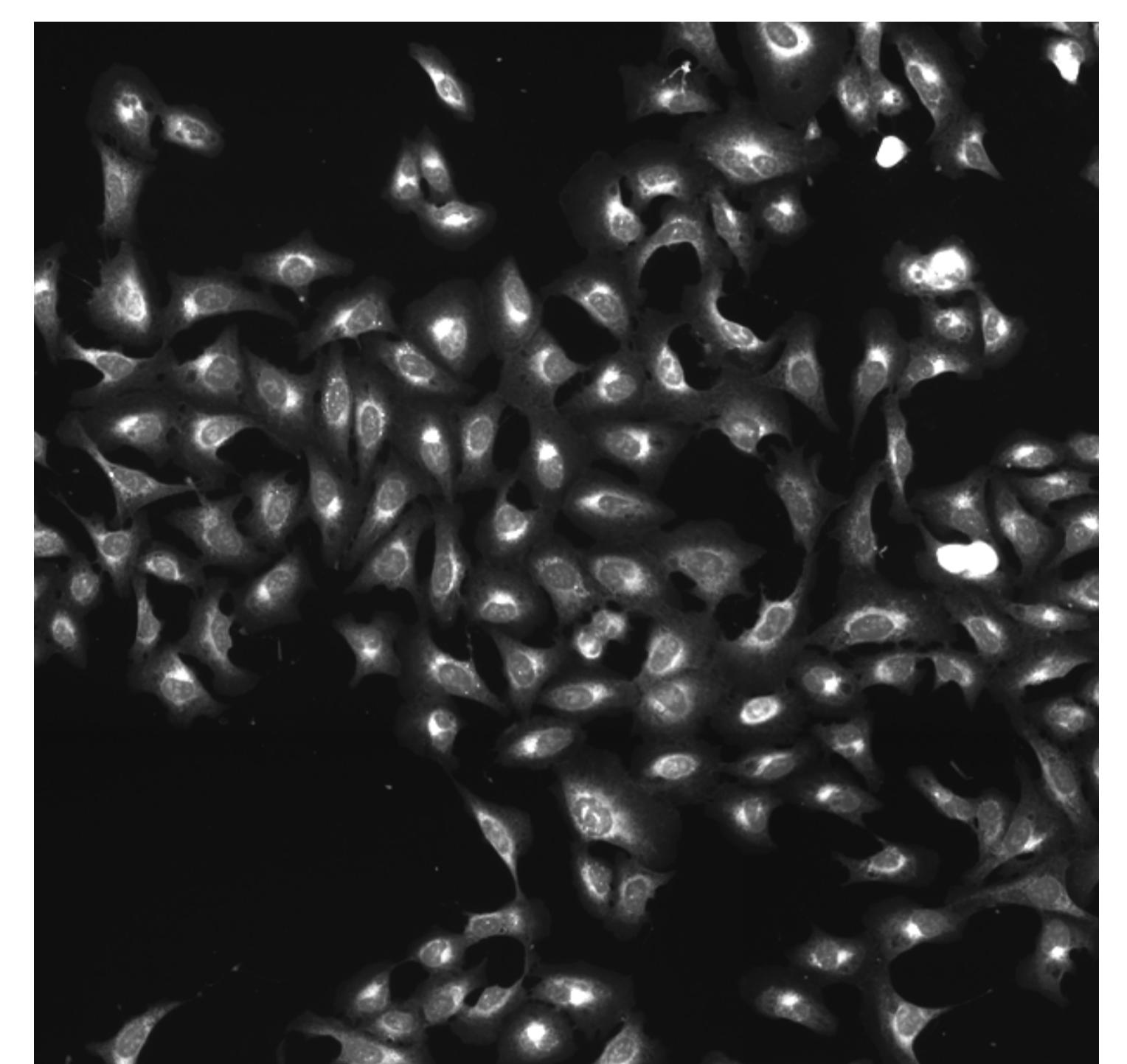
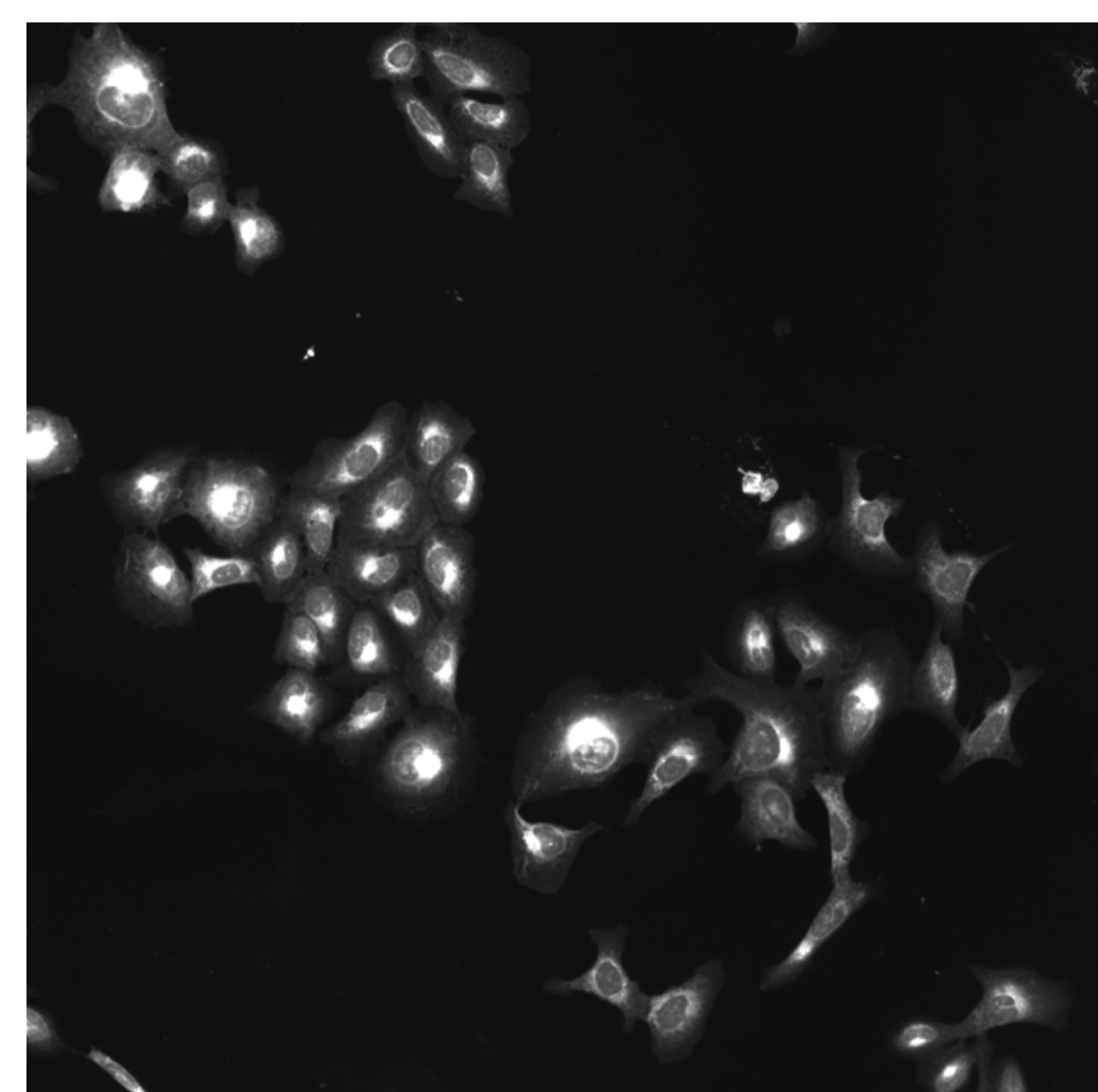
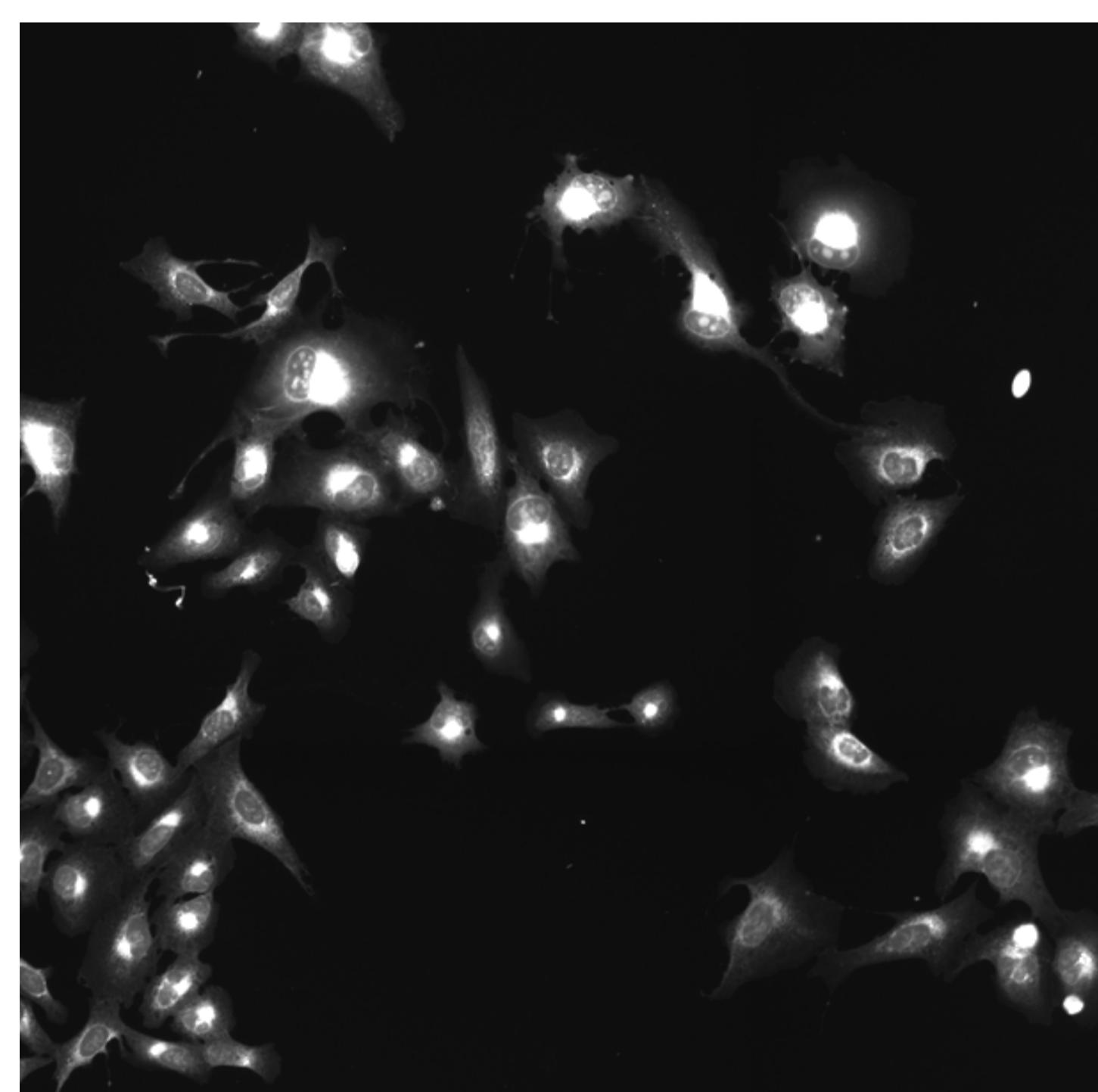
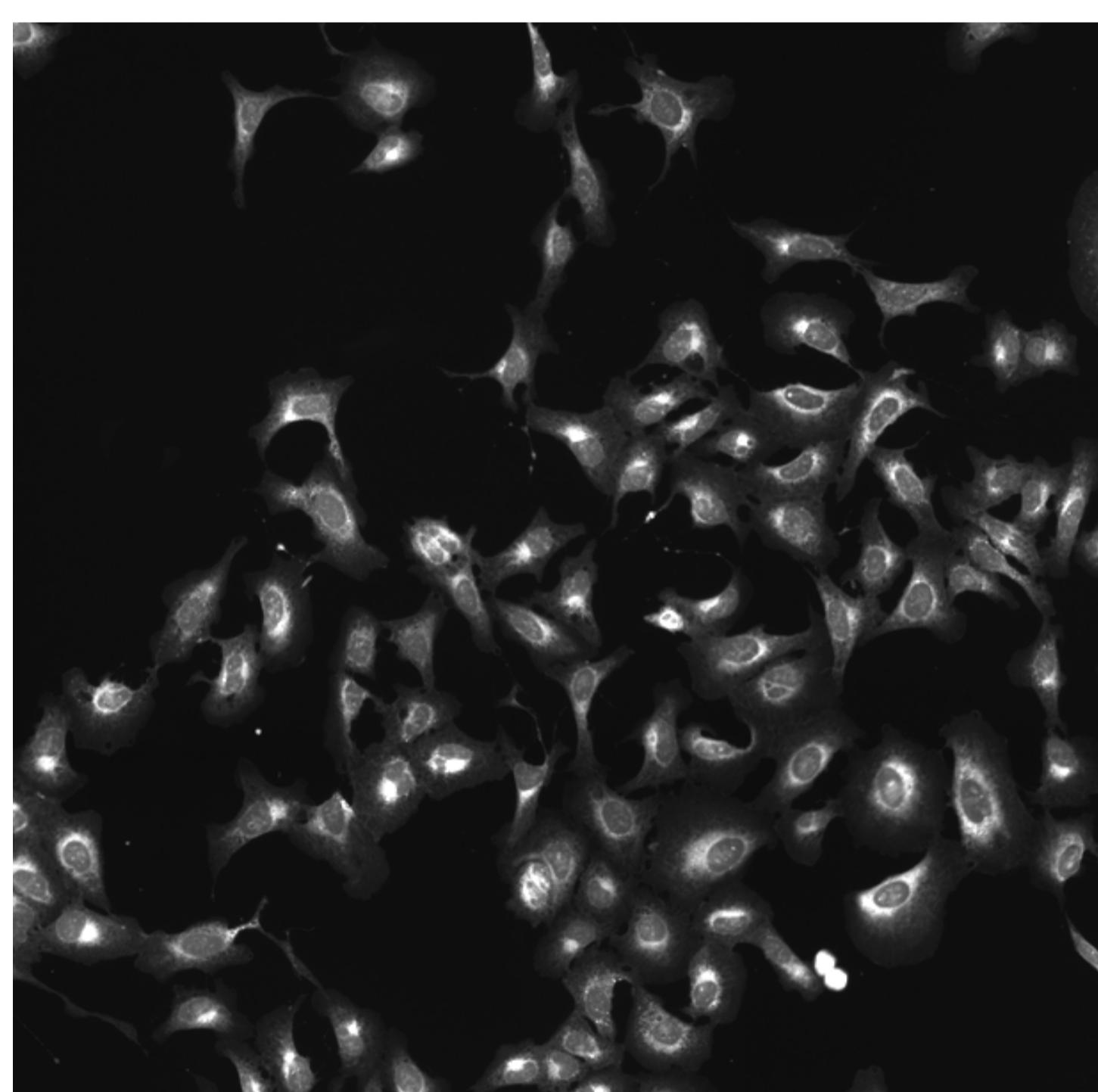
MAP3K2_WT_2

TRAF5_WT

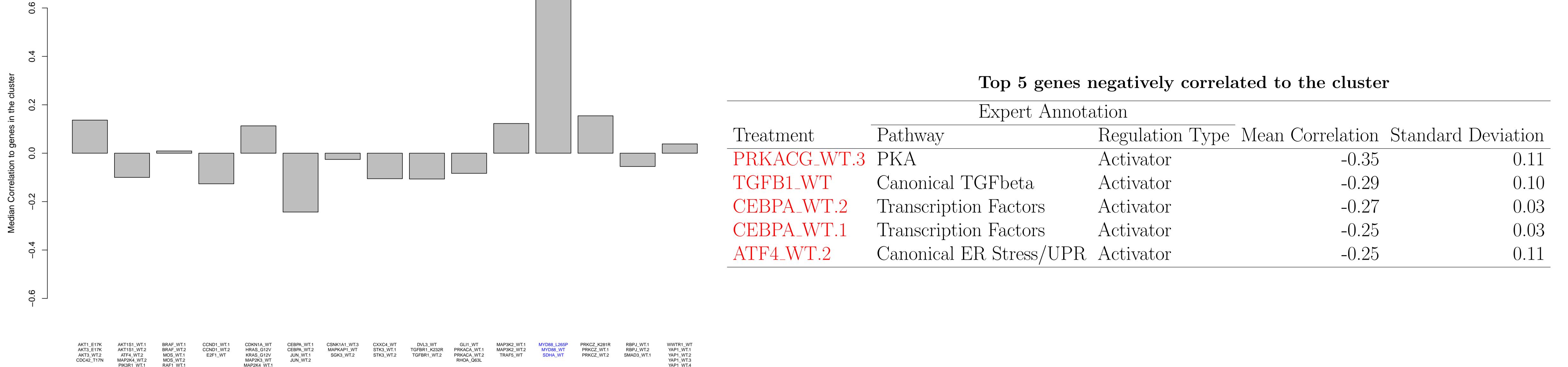
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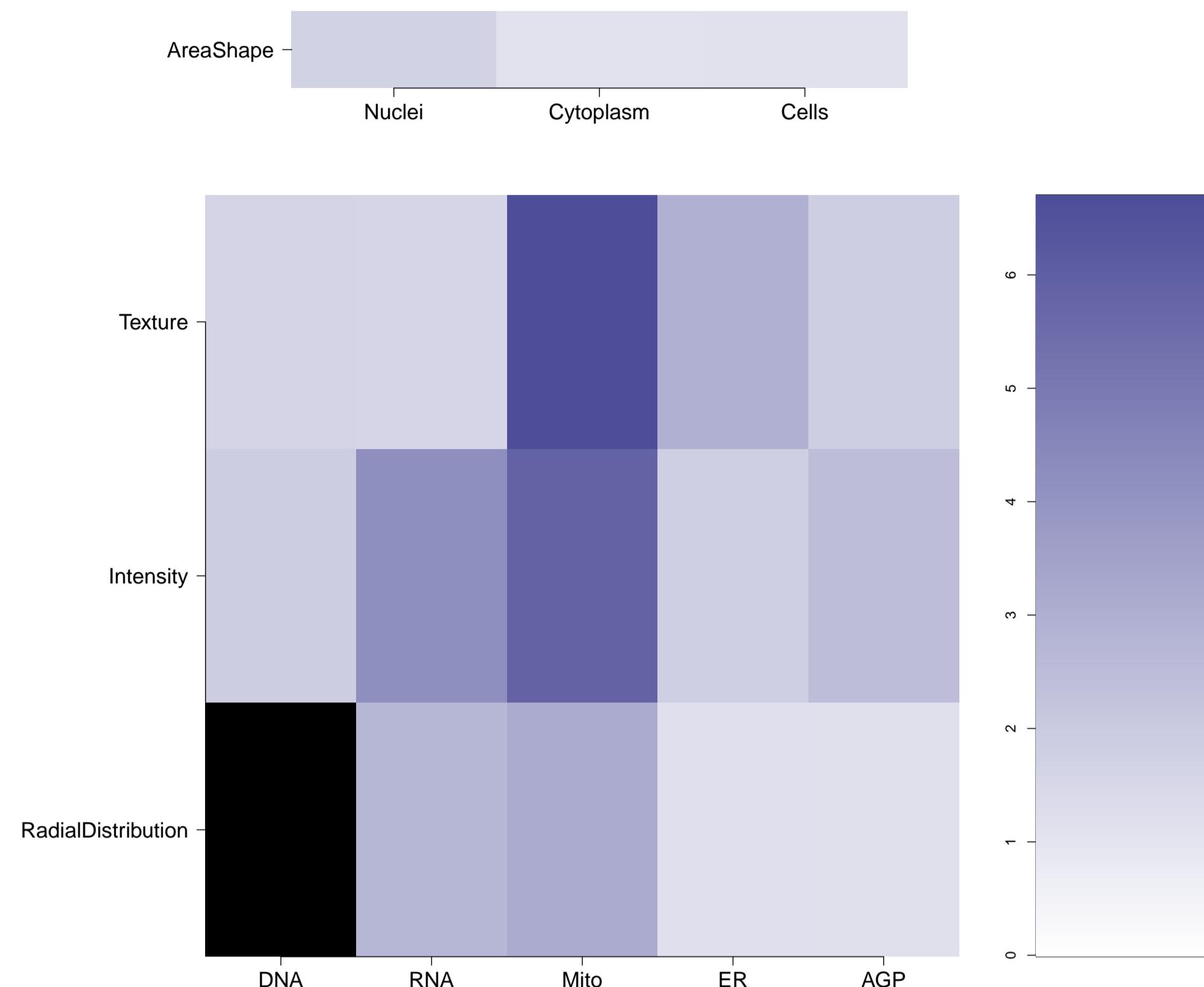
ER



Cluster 12
How similar is this cluster to the other clusters?



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?

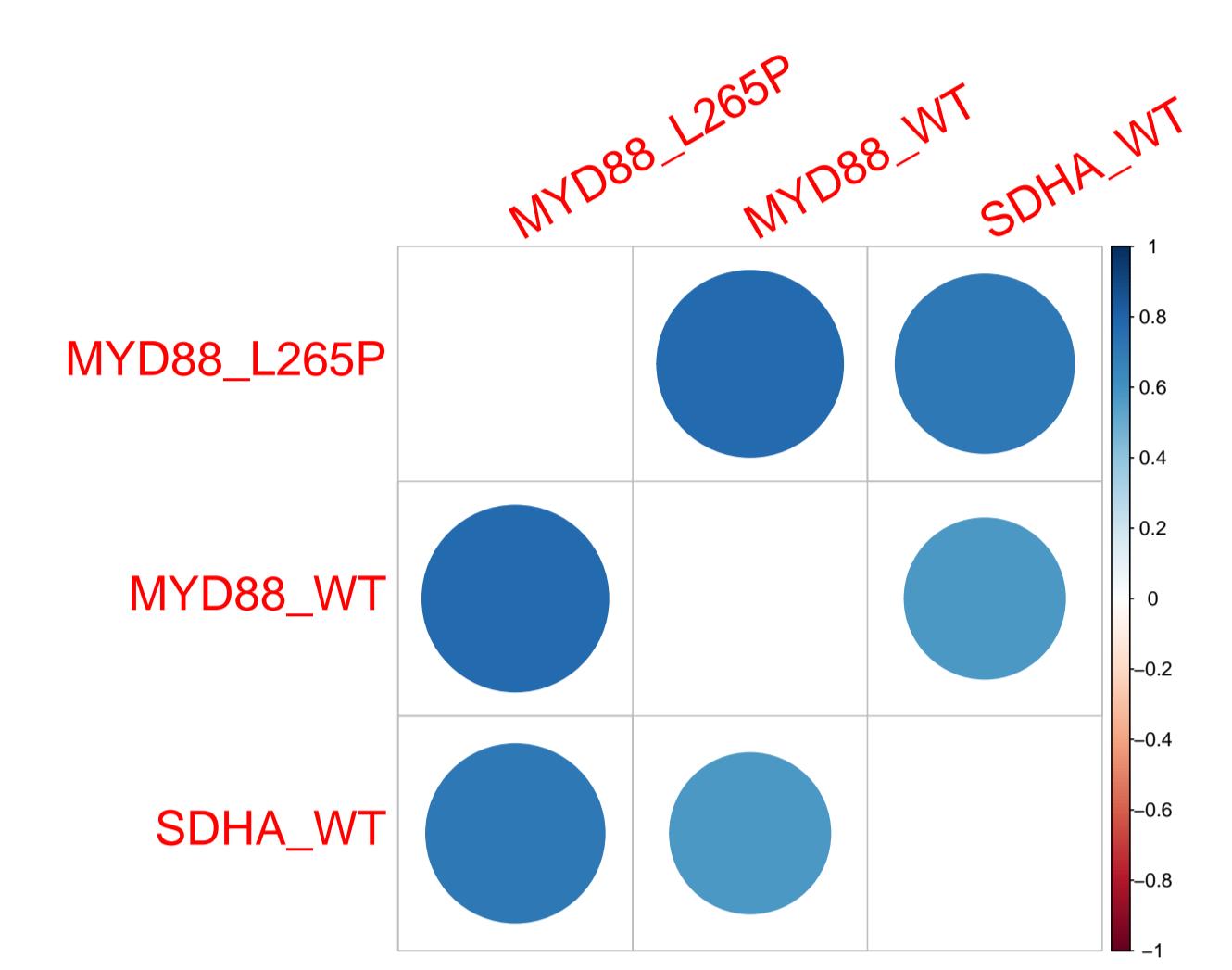


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

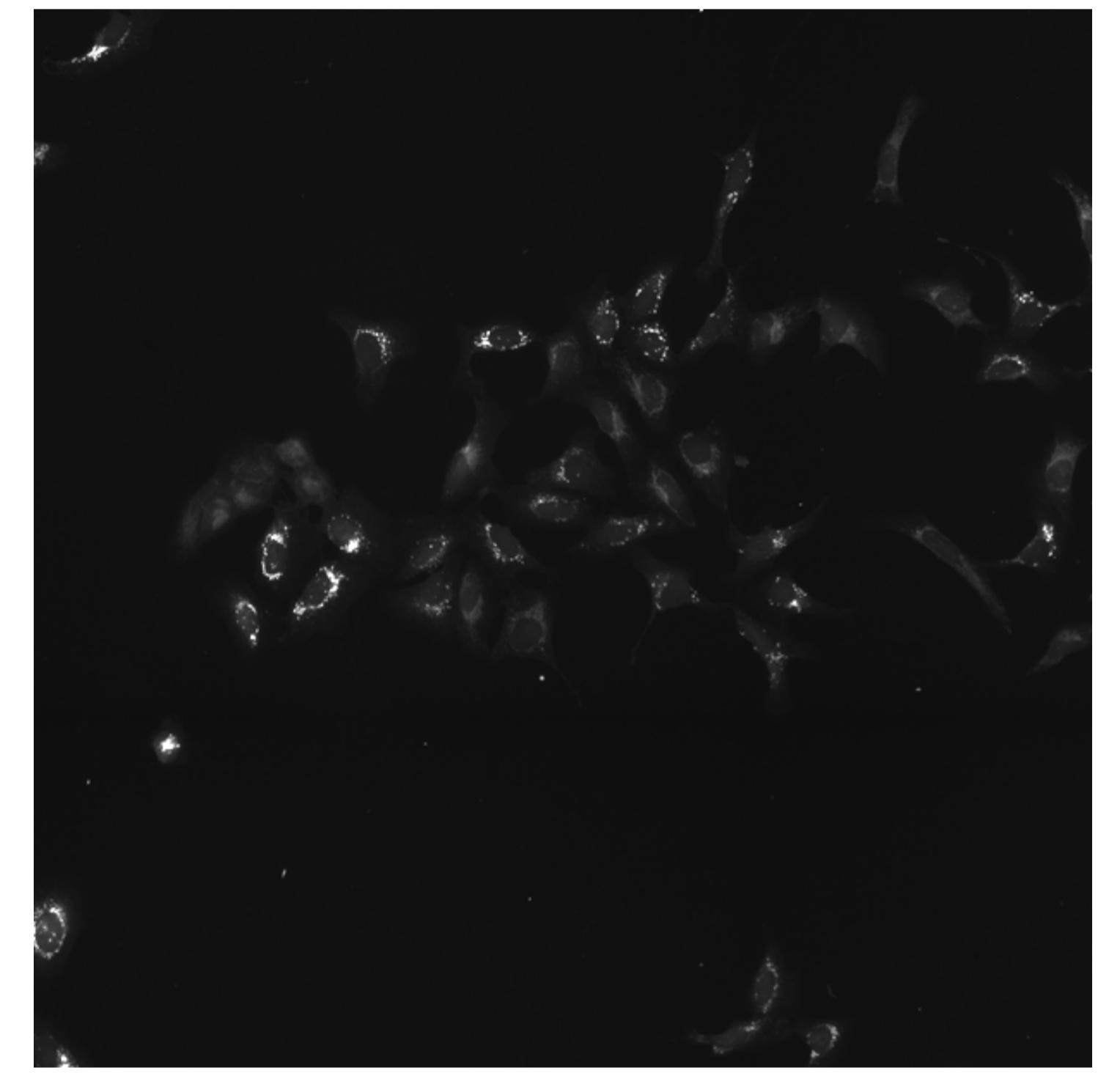
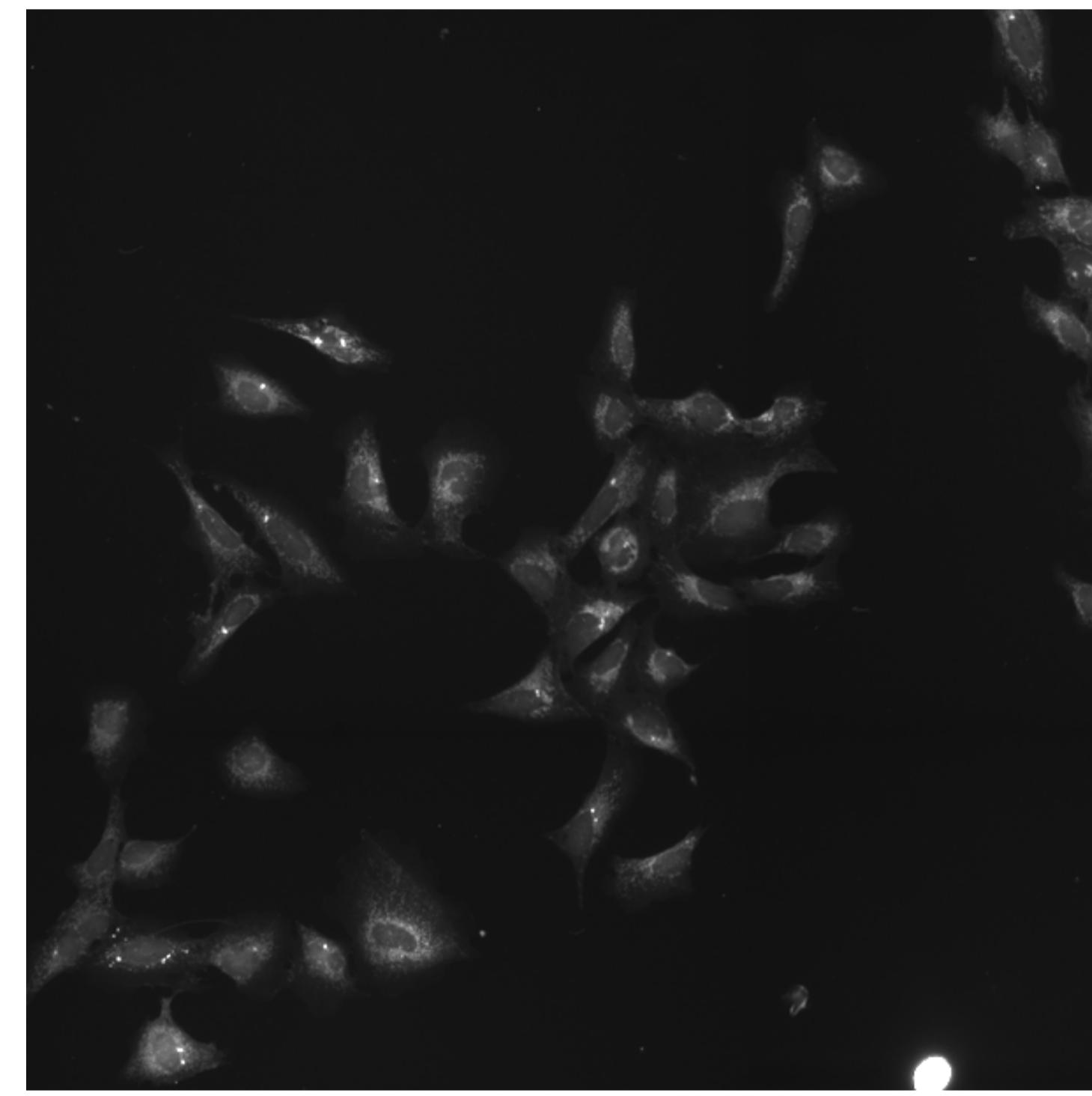
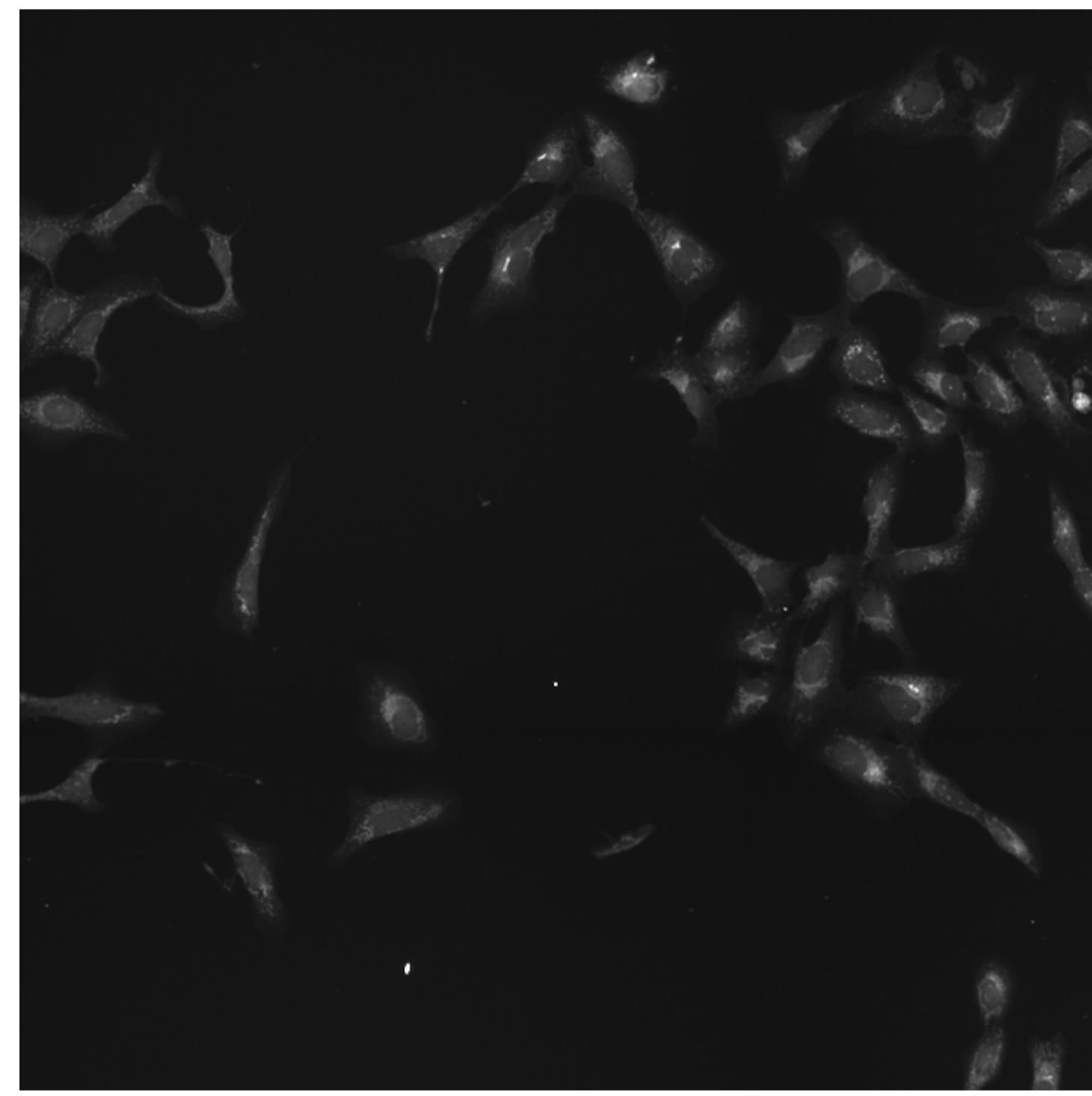
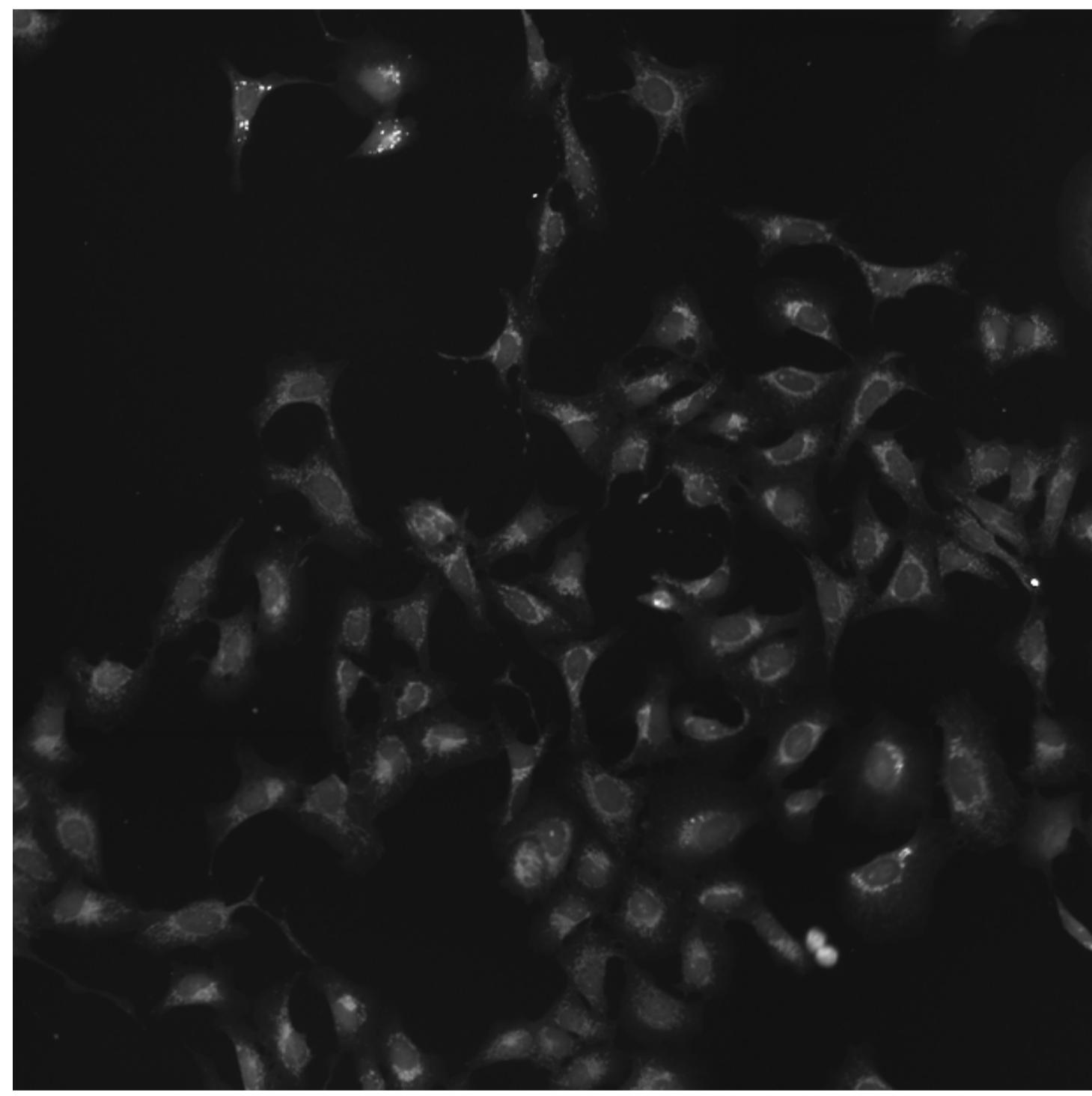
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MYD88_L265P

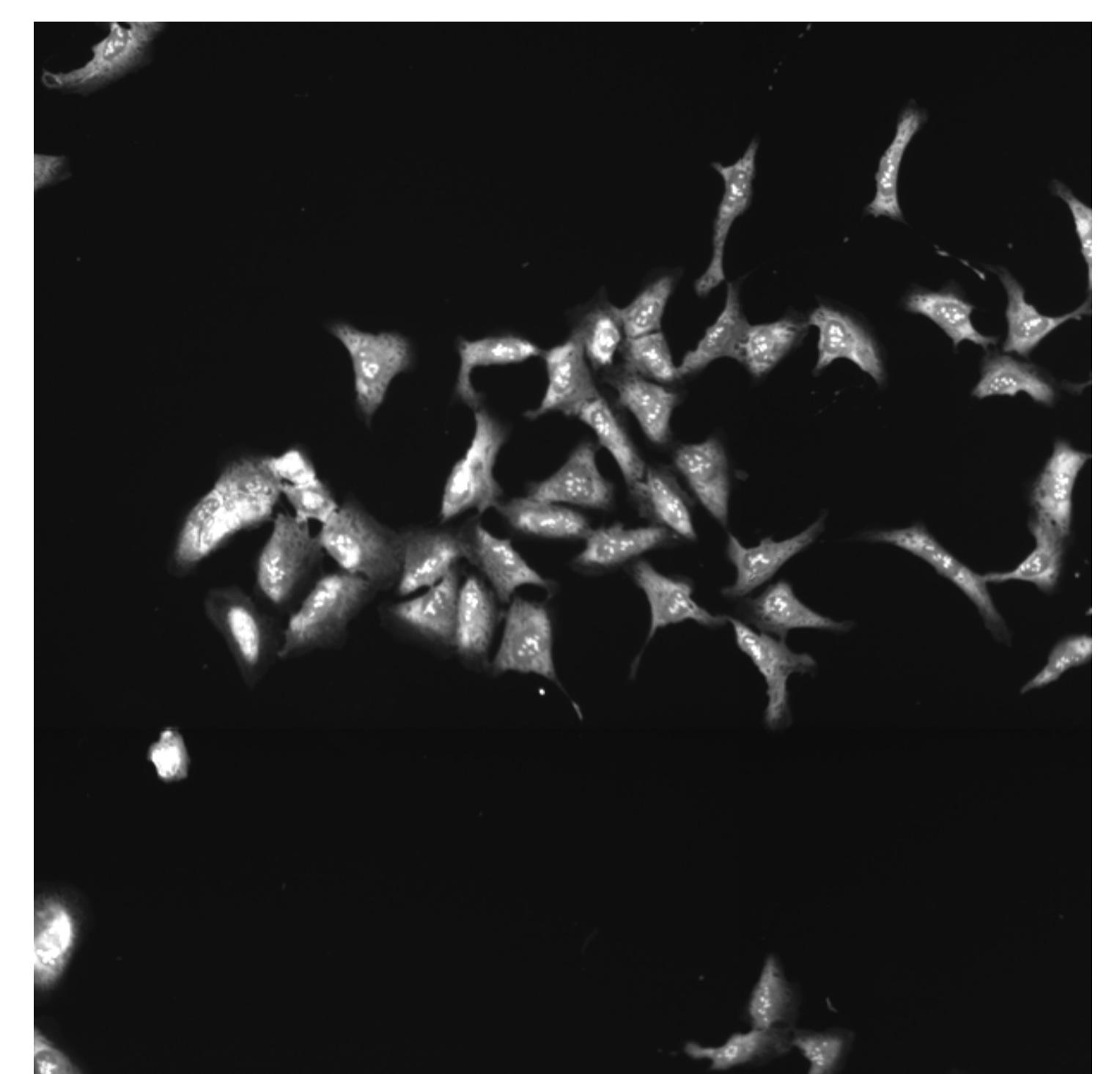
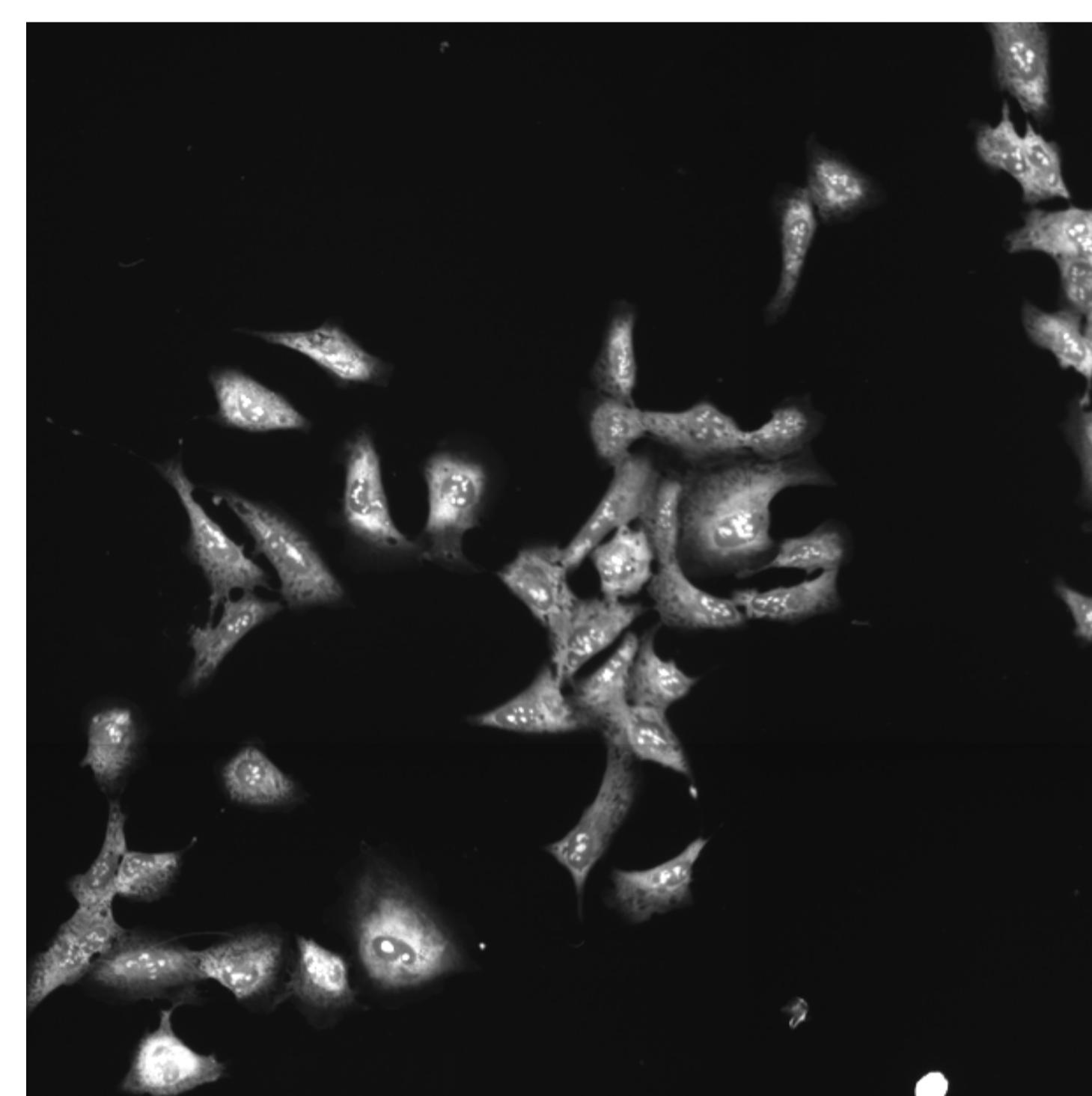
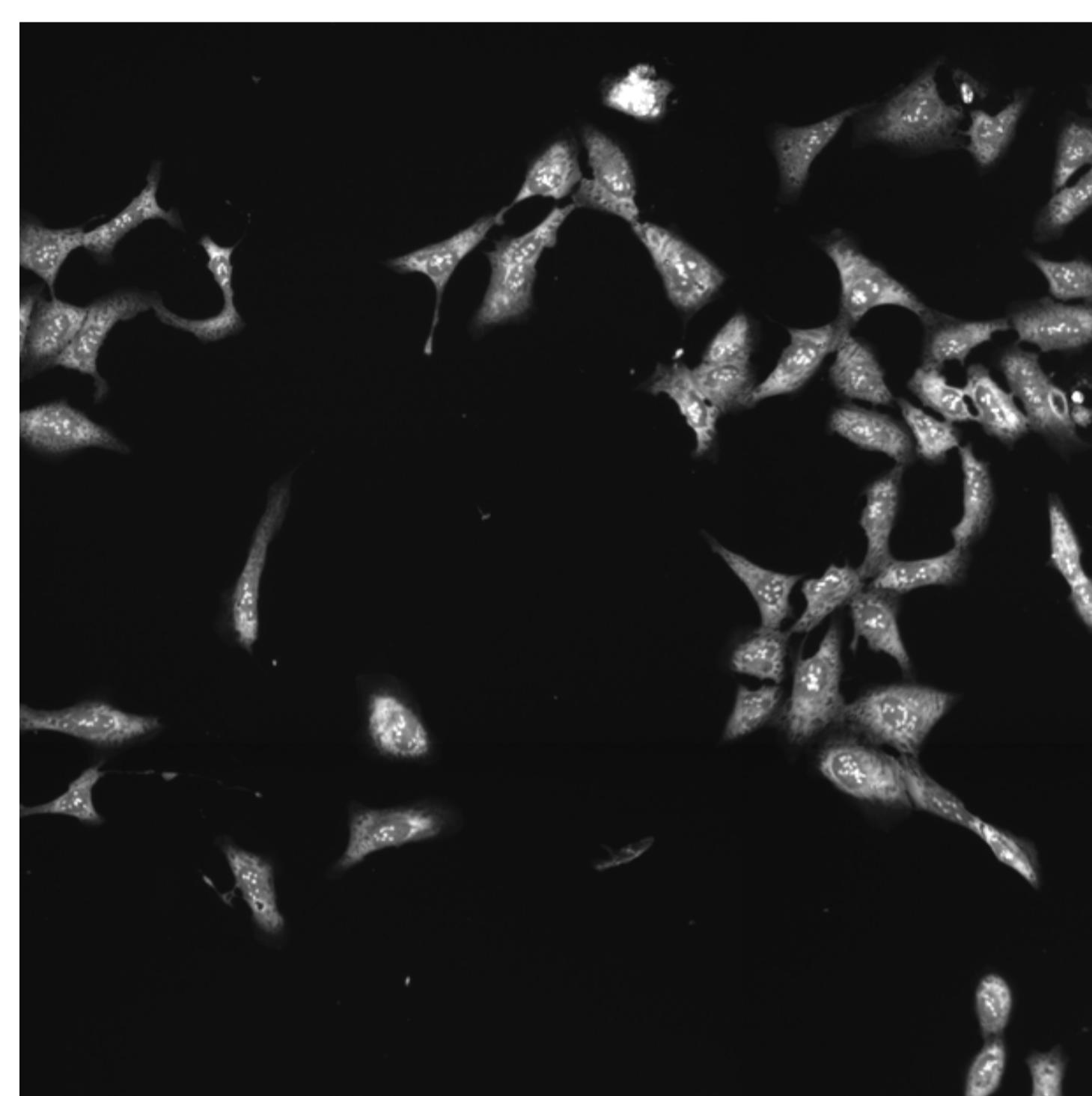
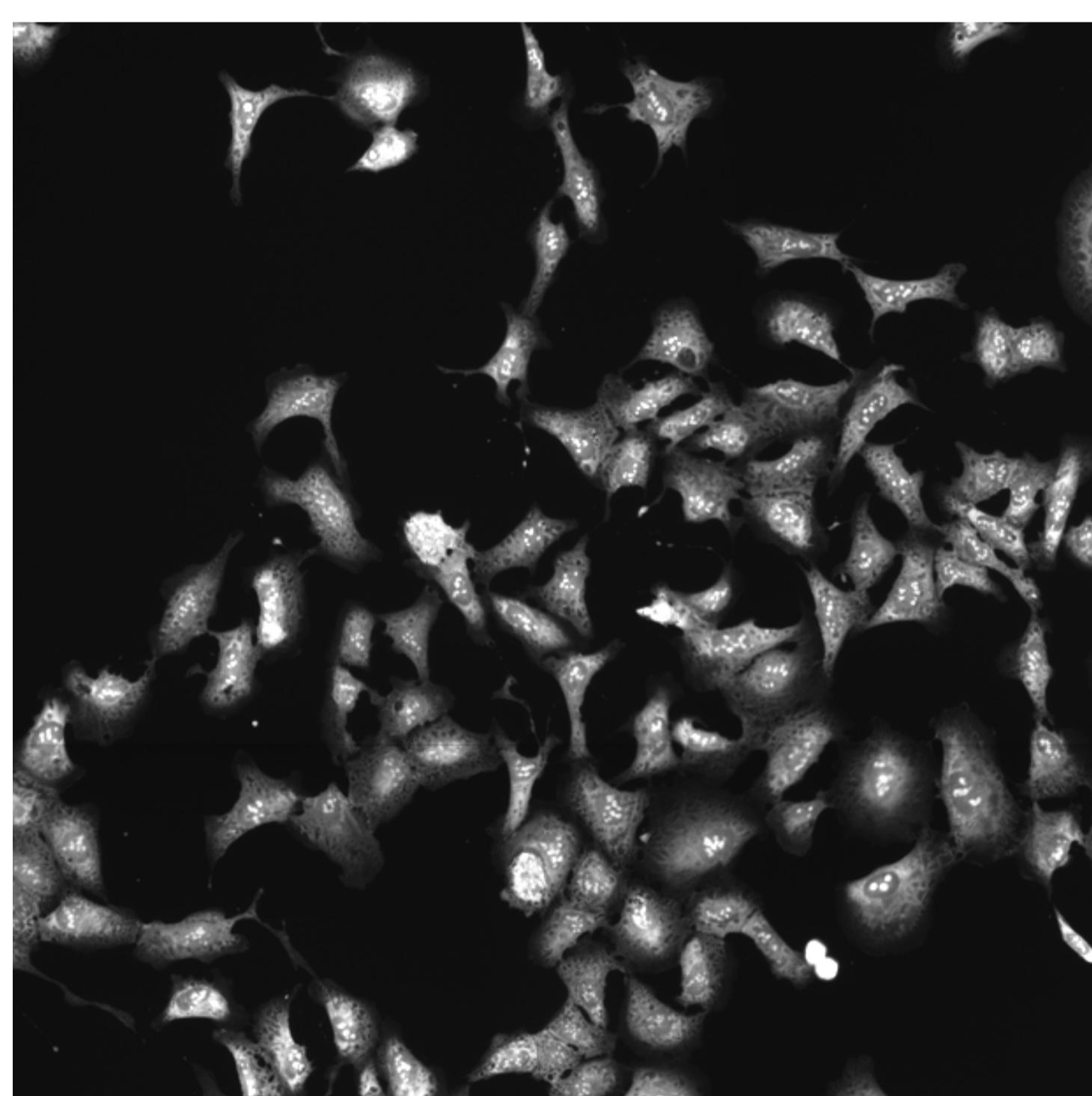
MYD88_WT

SDHA_WT

Mito

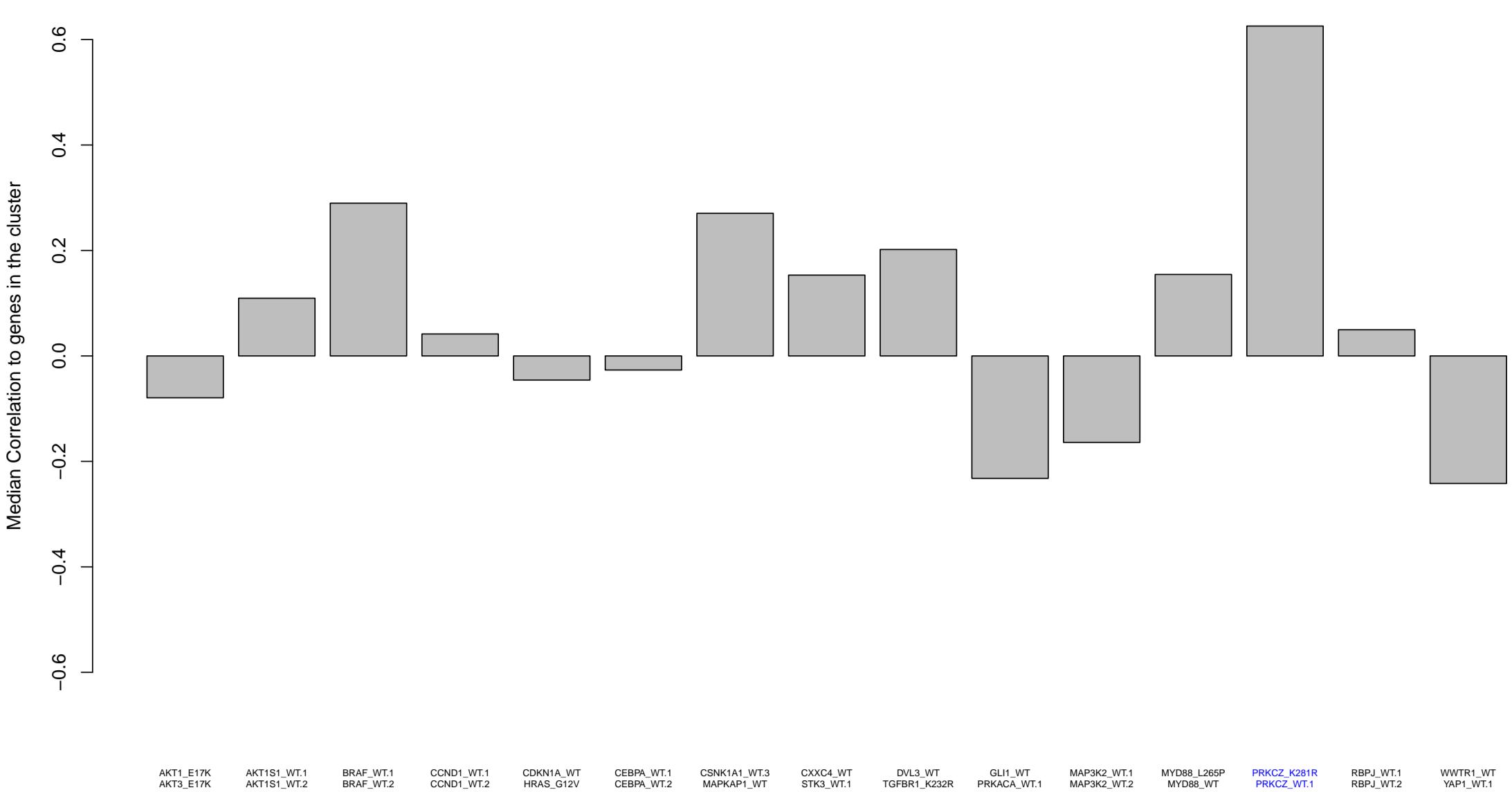


RNA



Cluster 13

Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
PRKCZ_WT.1	Canonical PKC	Activator	
PRKCZ_WT.2	Canonical PKC	Activator	
PRKCZ_K281R	Canonical PKC	Inhibitor	



Top 5 genes negatively correlated to the cluster					
Treatment	Expert Annotation		Mean Correlation	Standard Deviation	
	Pathway	Regulation Type			
WWTR1_WT	Canonical Hippo	Inhibitor	-0.50	0.10	
STK11_WT.1	Canonical TOR	Inhibitor	-0.43	0.06	
NFKBIB_WT	Canonical NFkB	Inhibitor	-0.40	0.14	
TGFB1_WT	Canonical TGFbeta	Activator	-0.35	0.11	
DIABLO_WT	Canonical Apoptosis	Inhibitor	-0.33	0.04	

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?

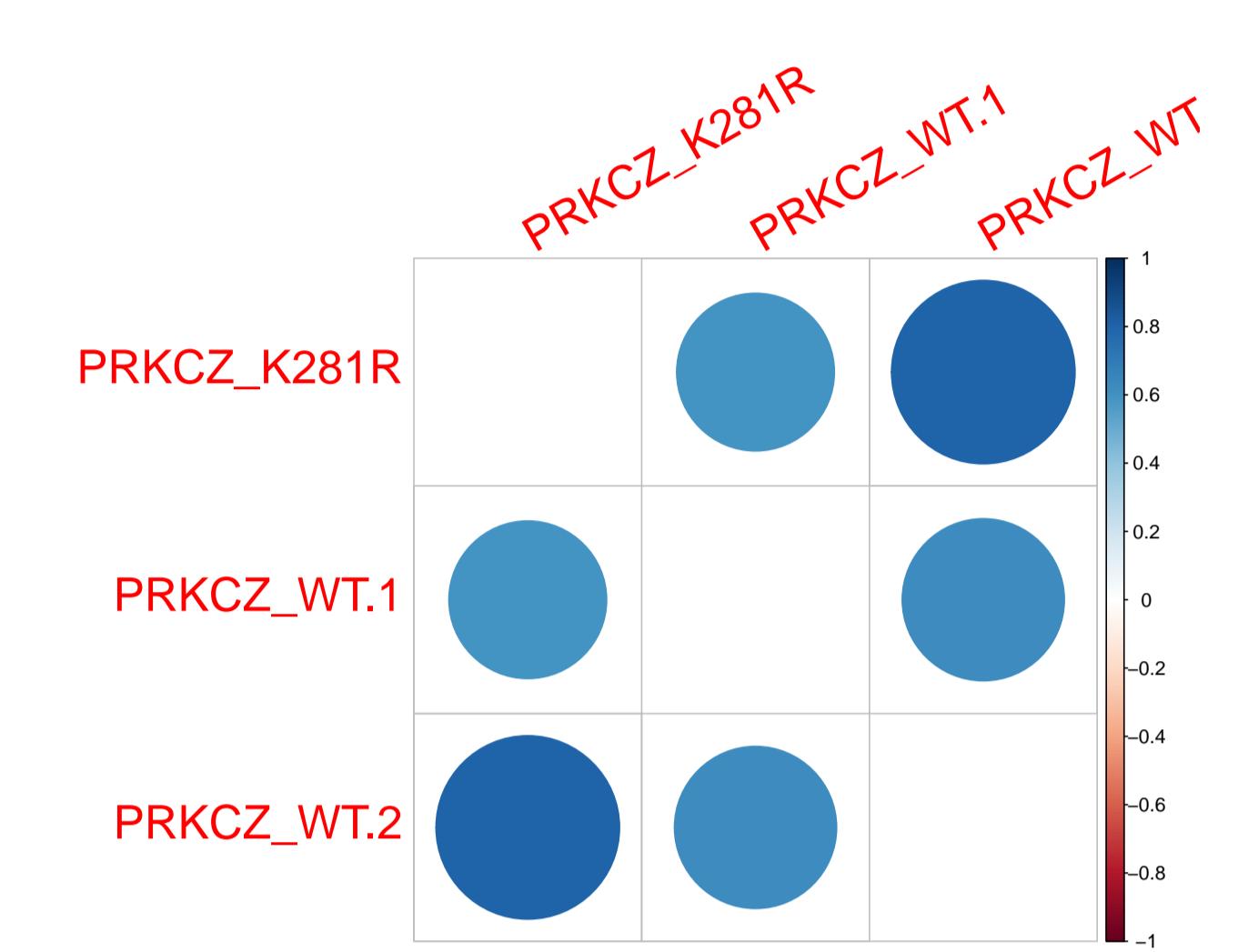
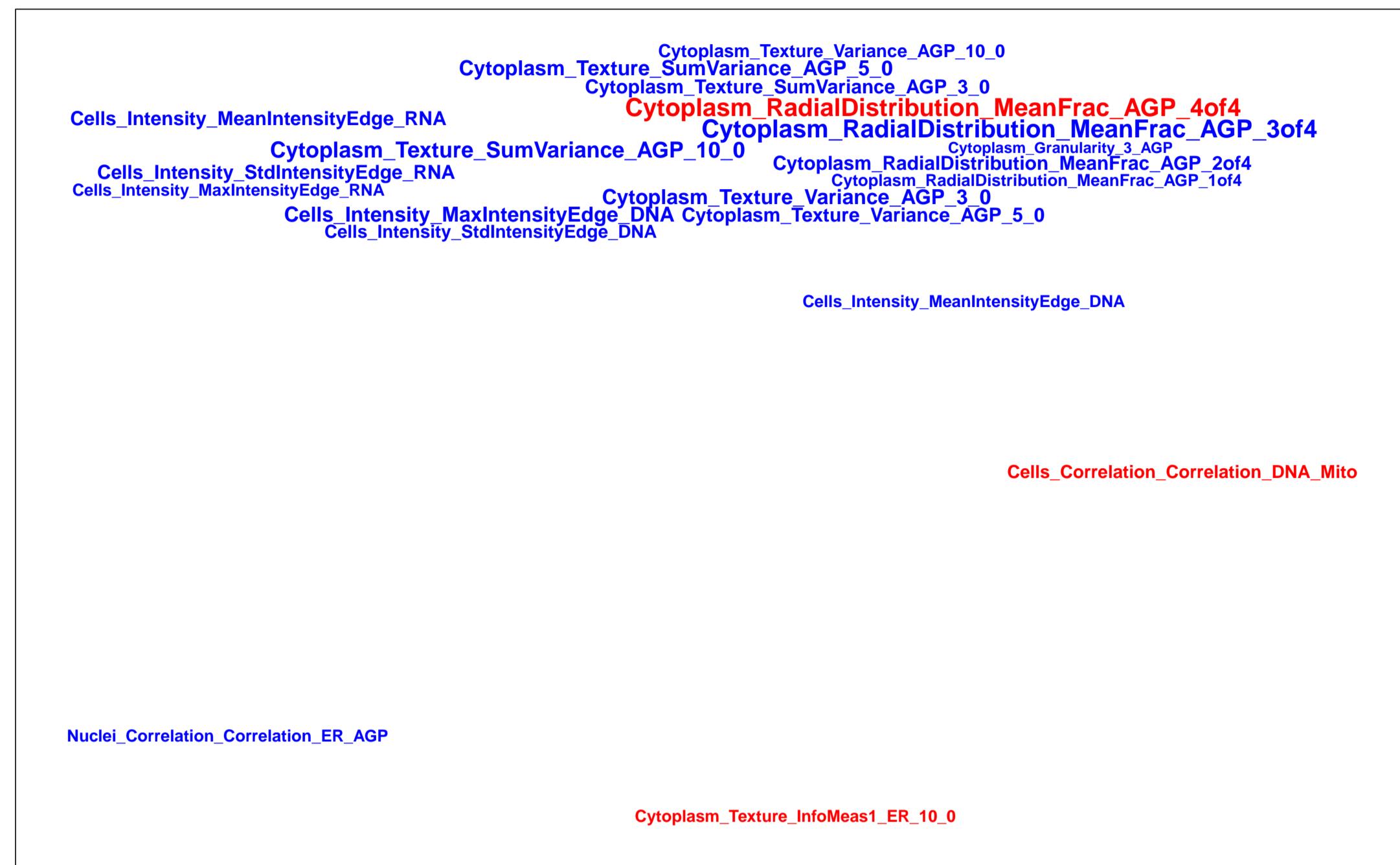
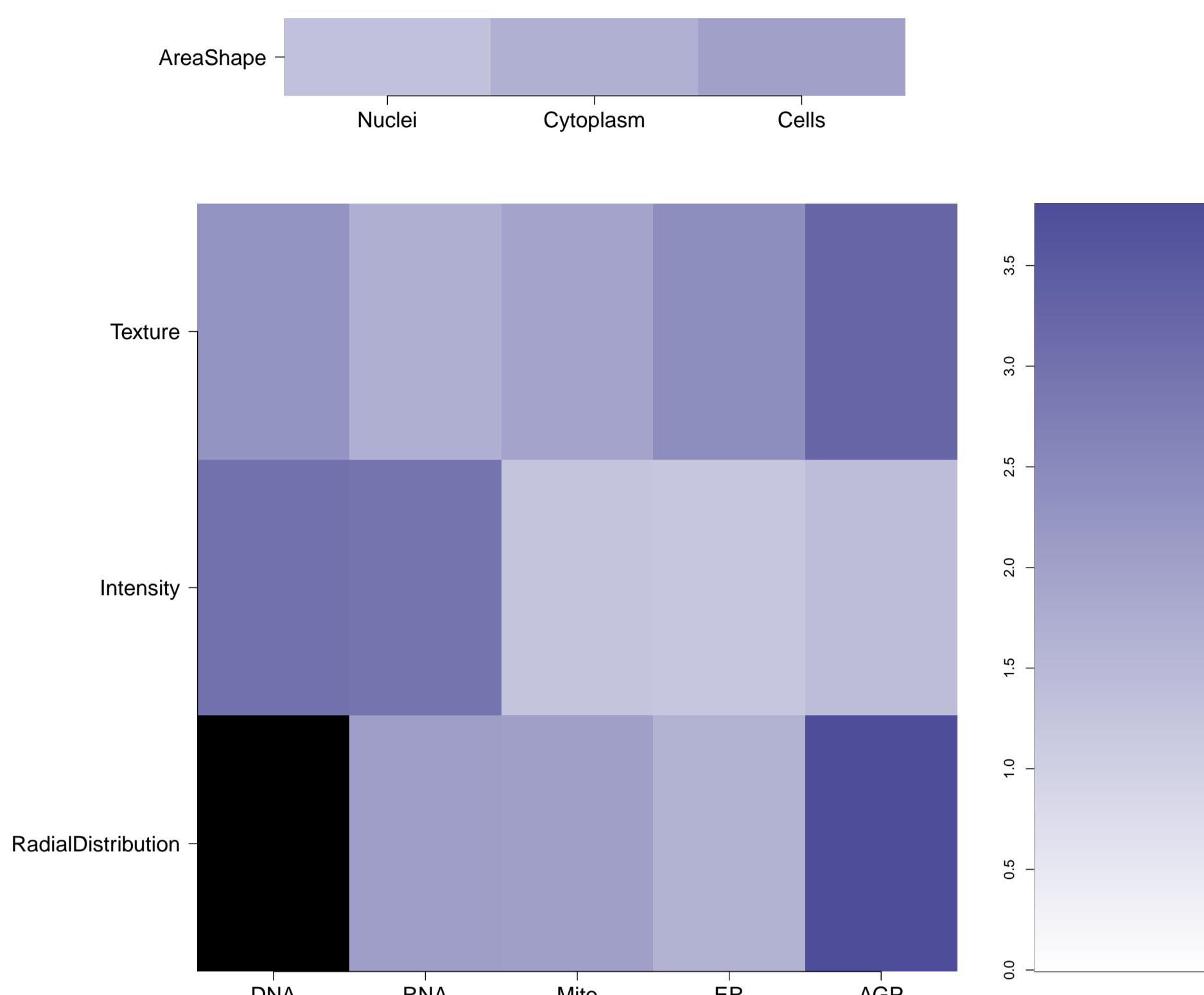
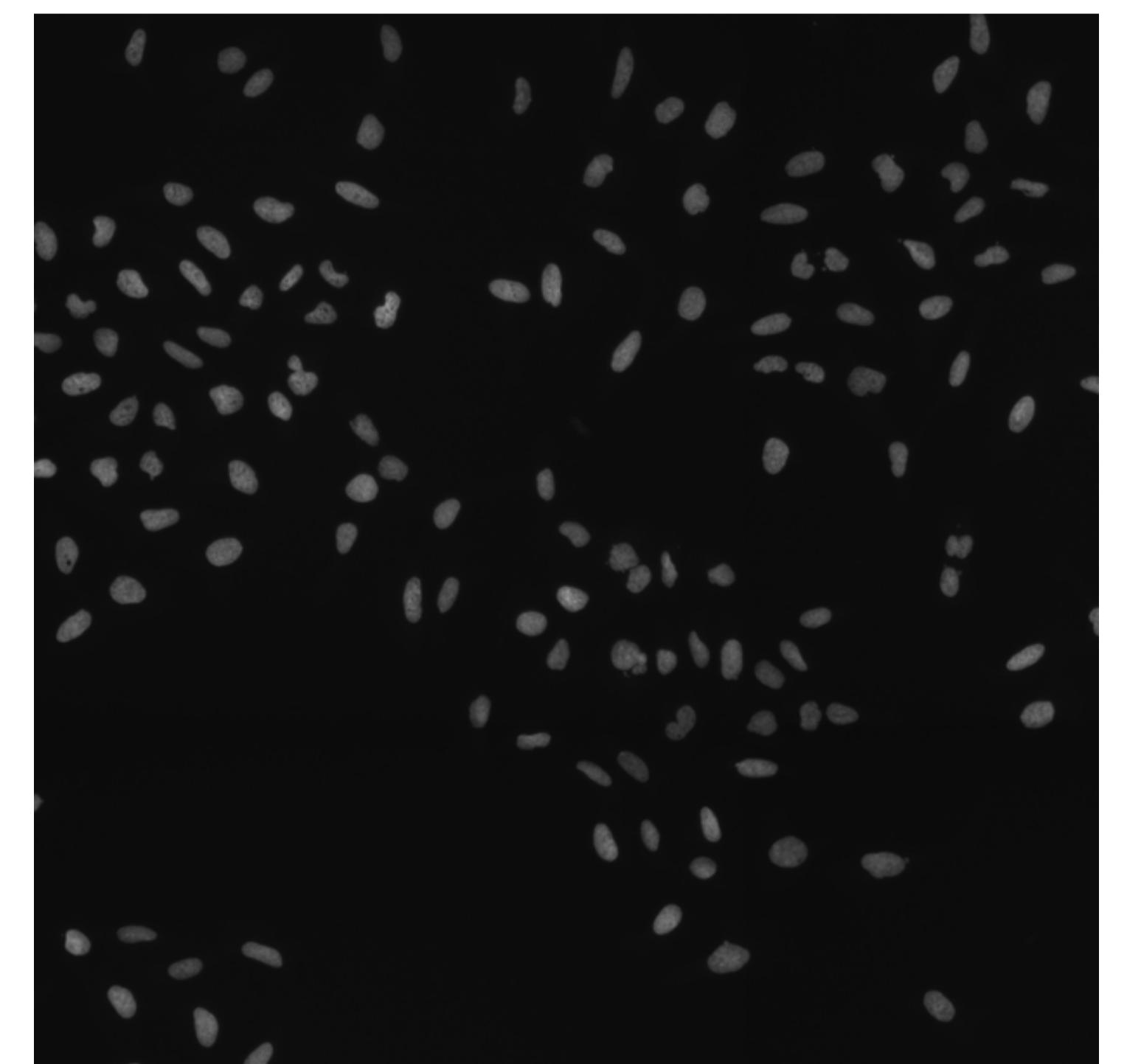
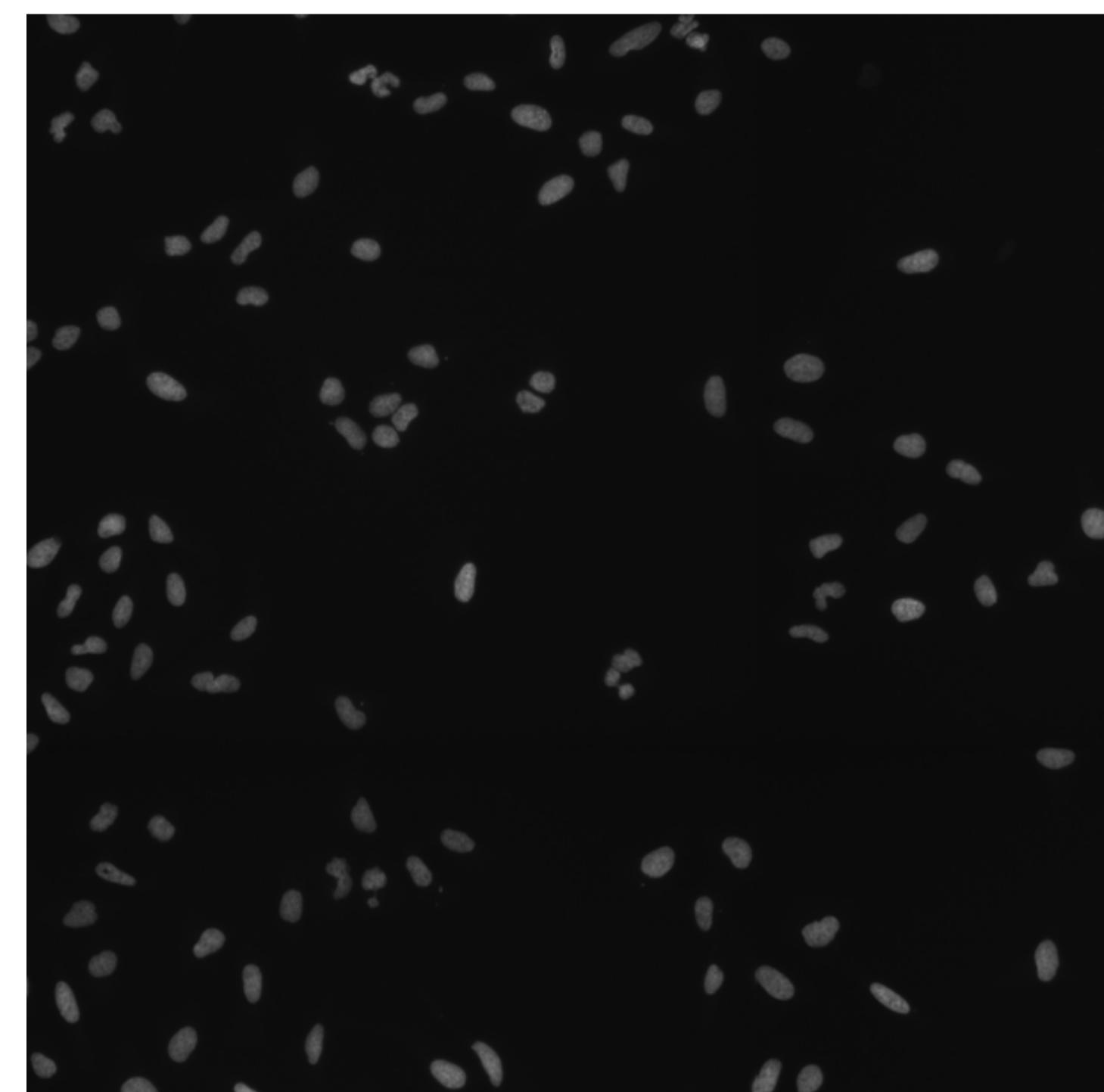
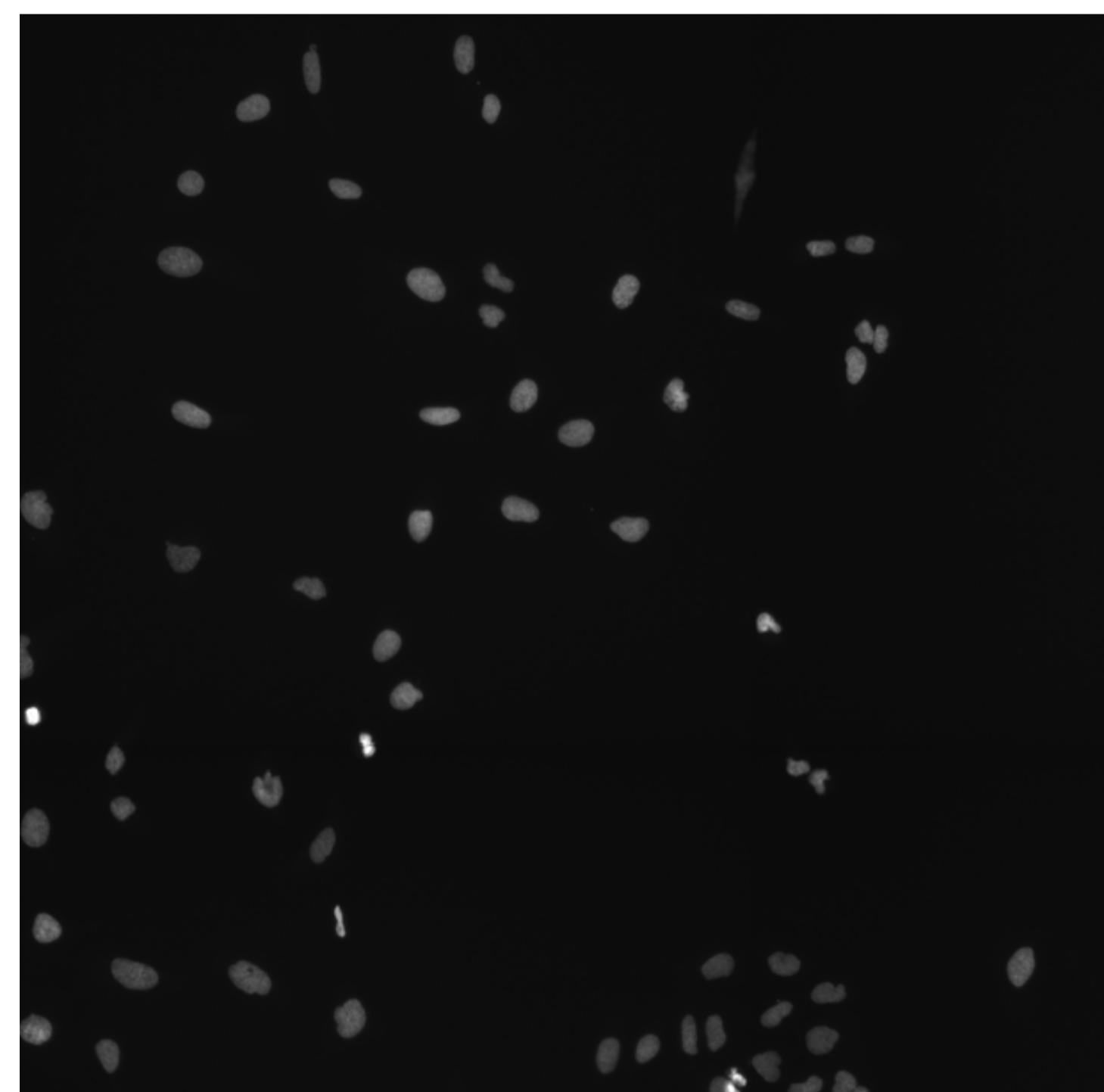
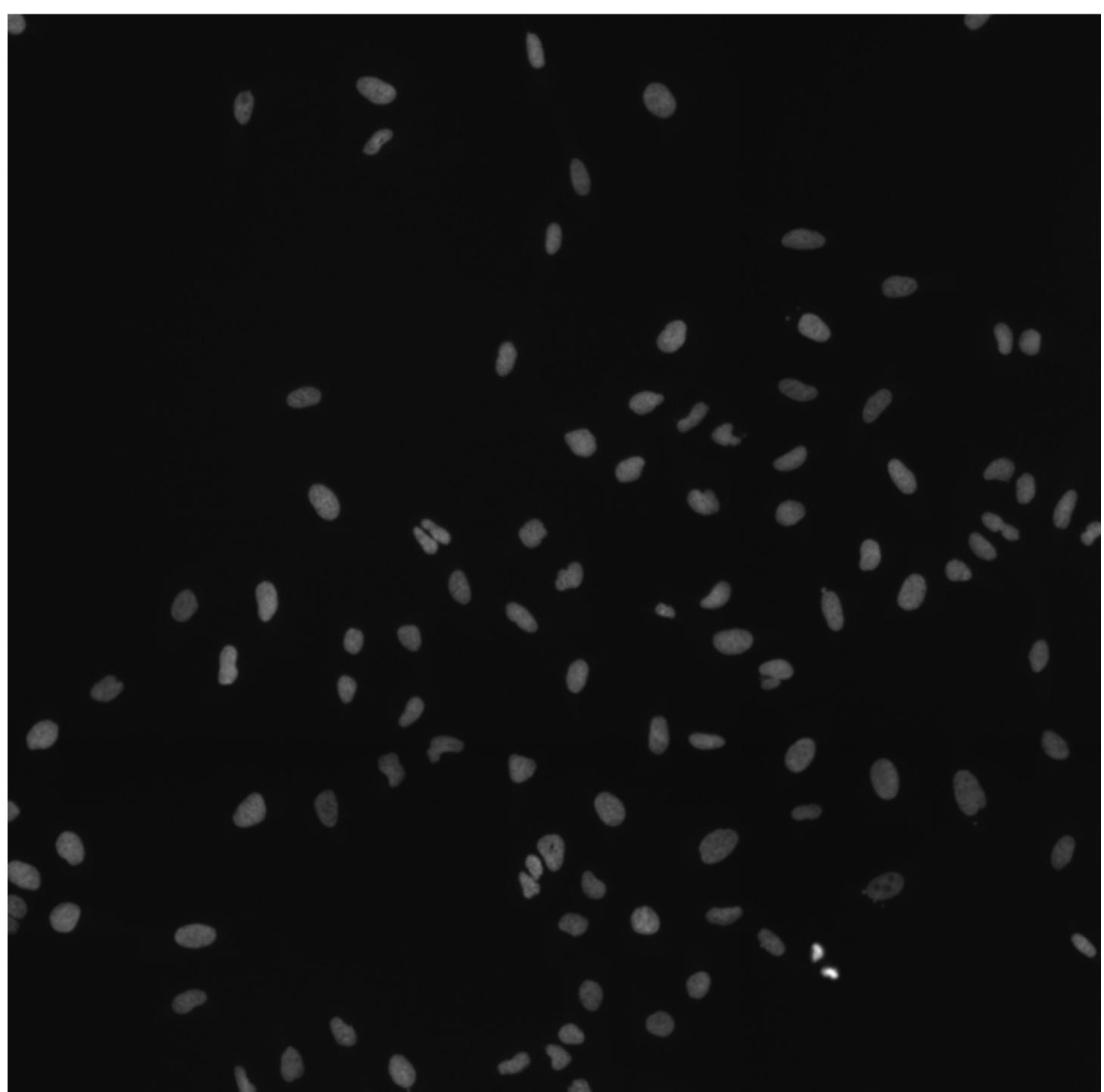
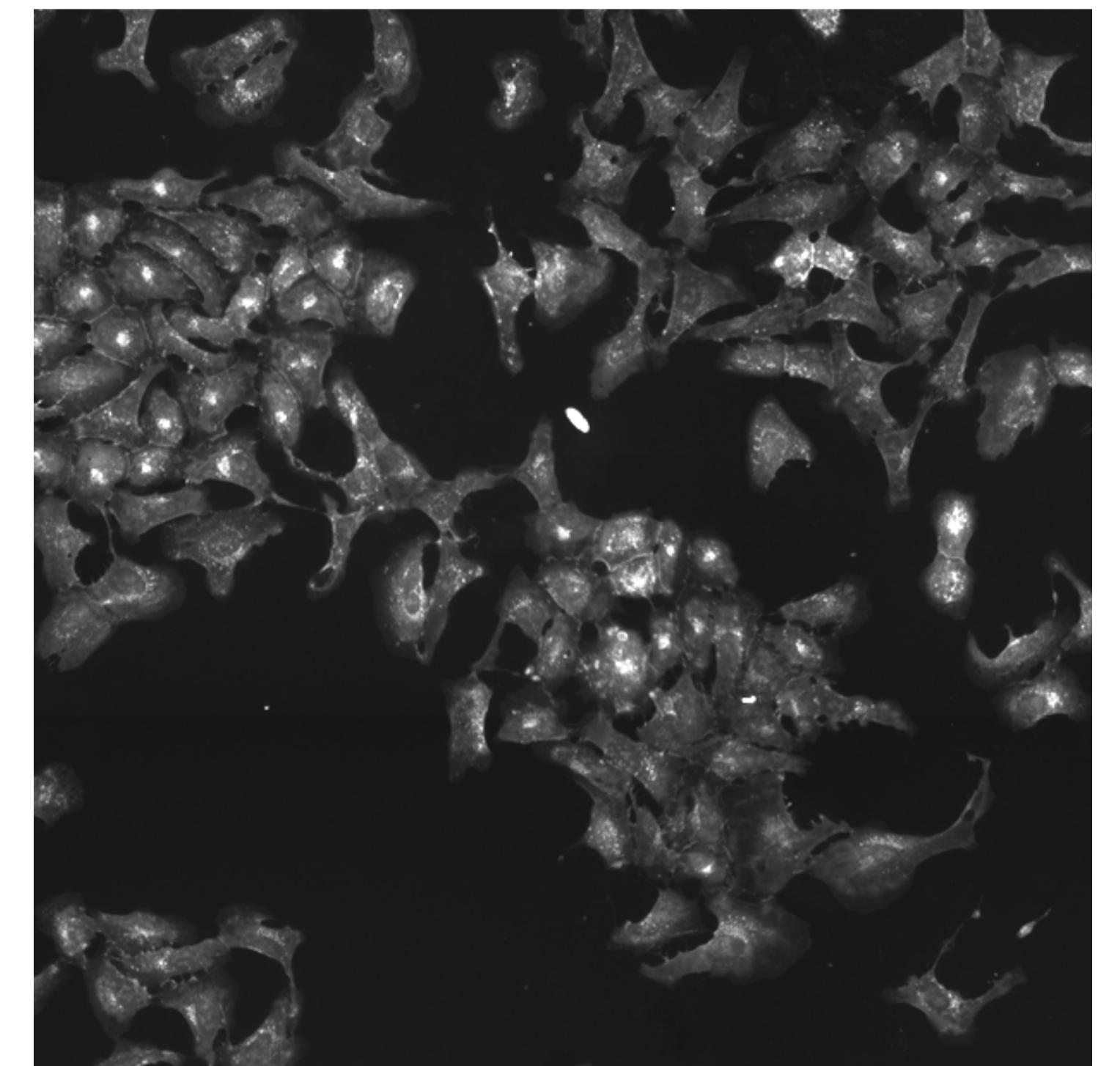
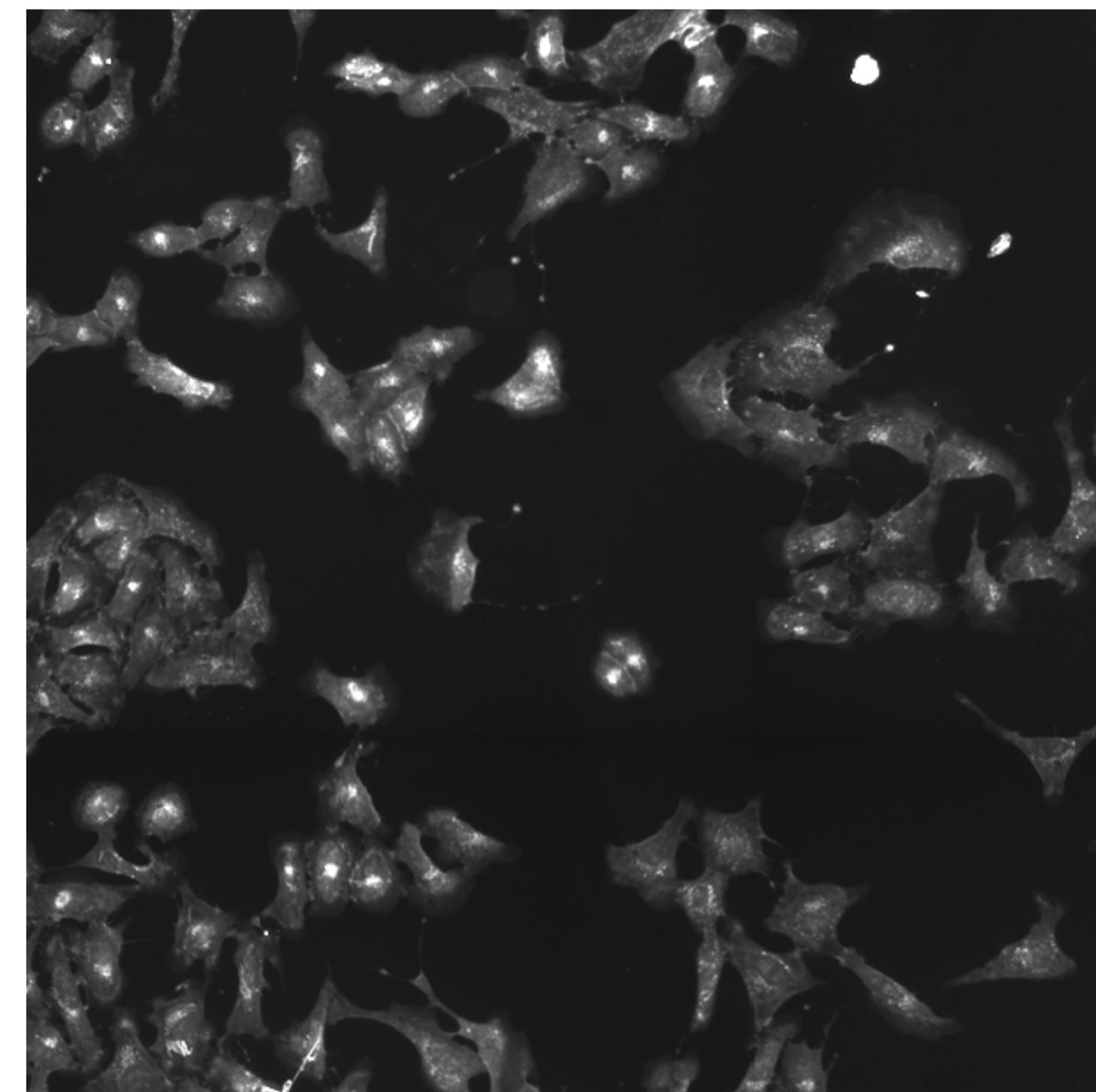
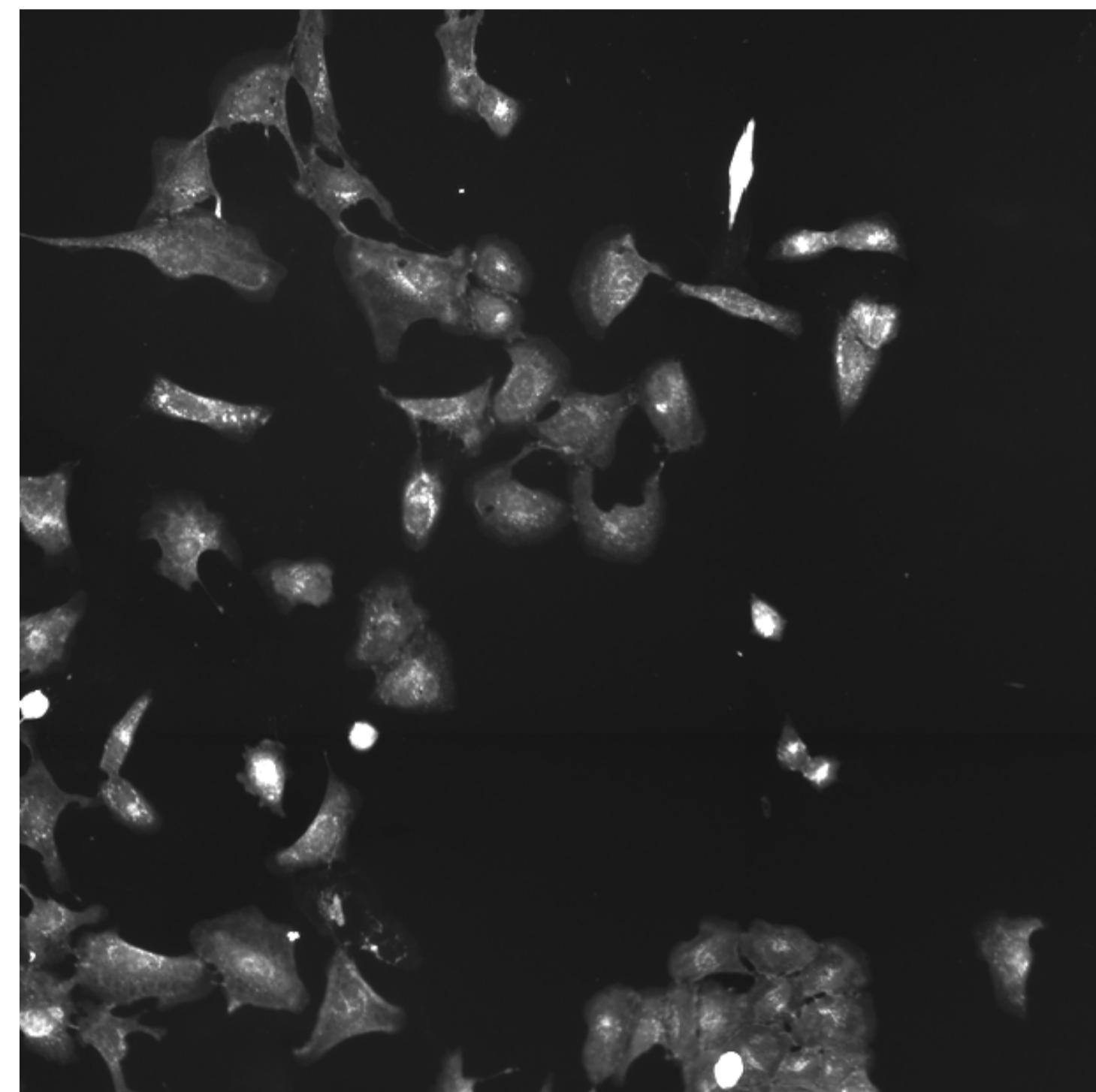
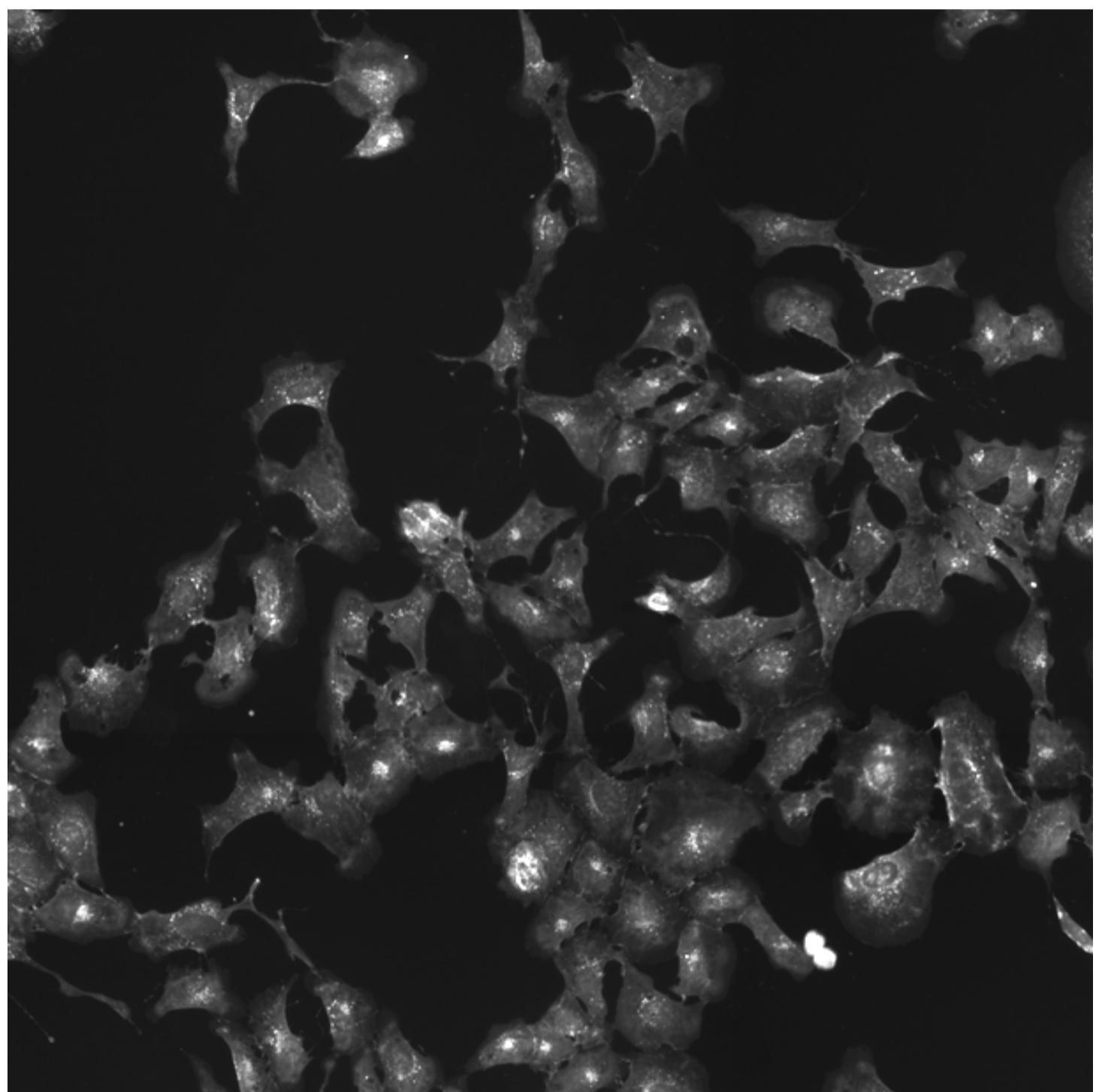


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

PRKCZ_K281R

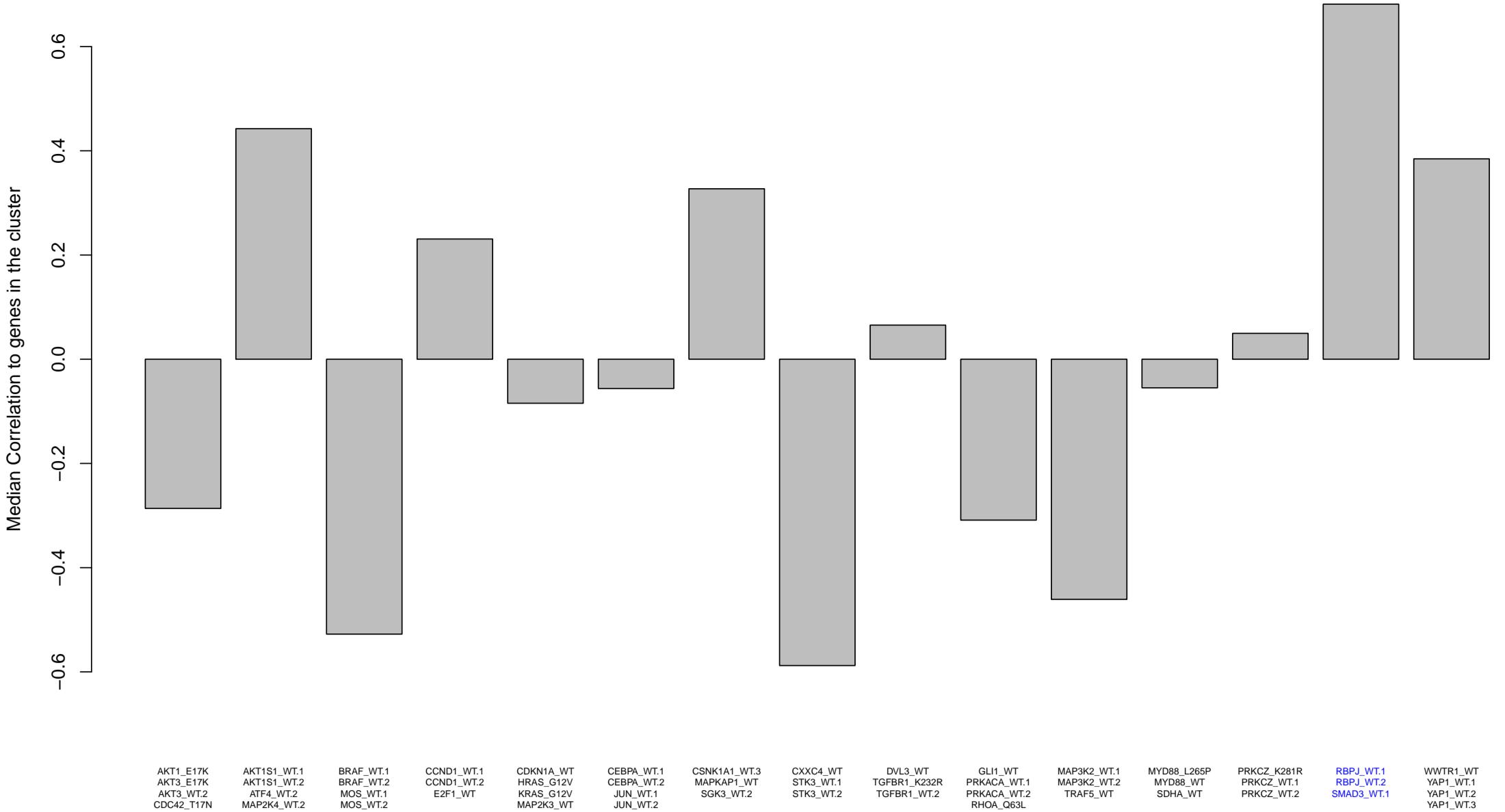
PRKCZ_WT.1

PRKCZ_WT.2



Cluster 14

Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
SMAD3_WT.1	Canonical SMAD	Activator	
RBPJ_WT.1	NOTCH	Activator	
RBPJ_WT.2	NOTCH	Activator	



Top 5 genes negatively correlated to the cluster						
Treatment	Expert Annotation		Mean Correlation	Standard Deviation	P-value	Adjusted P-value
	Pathway	Regulation Type				
RAF1_WT.2	Canonical MAPK	Activator	-0.62	0.06	0.0001	0.0001
CXXC4_WT	WNT	Inhibitor	-0.60	0.01	0.0002	0.0002
STK3_WT.1	Canonical Hippo	Activator	-0.60	0.09	0.0003	0.0003
MAP3K2_WT.1	Canonical MAPK	Activator	-0.58	0.16	0.0005	0.0005
PIK3CB_WT.2	Canonical PI3K/AKT	Activator	-0.55	0.13	0.0007	0.0007

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?

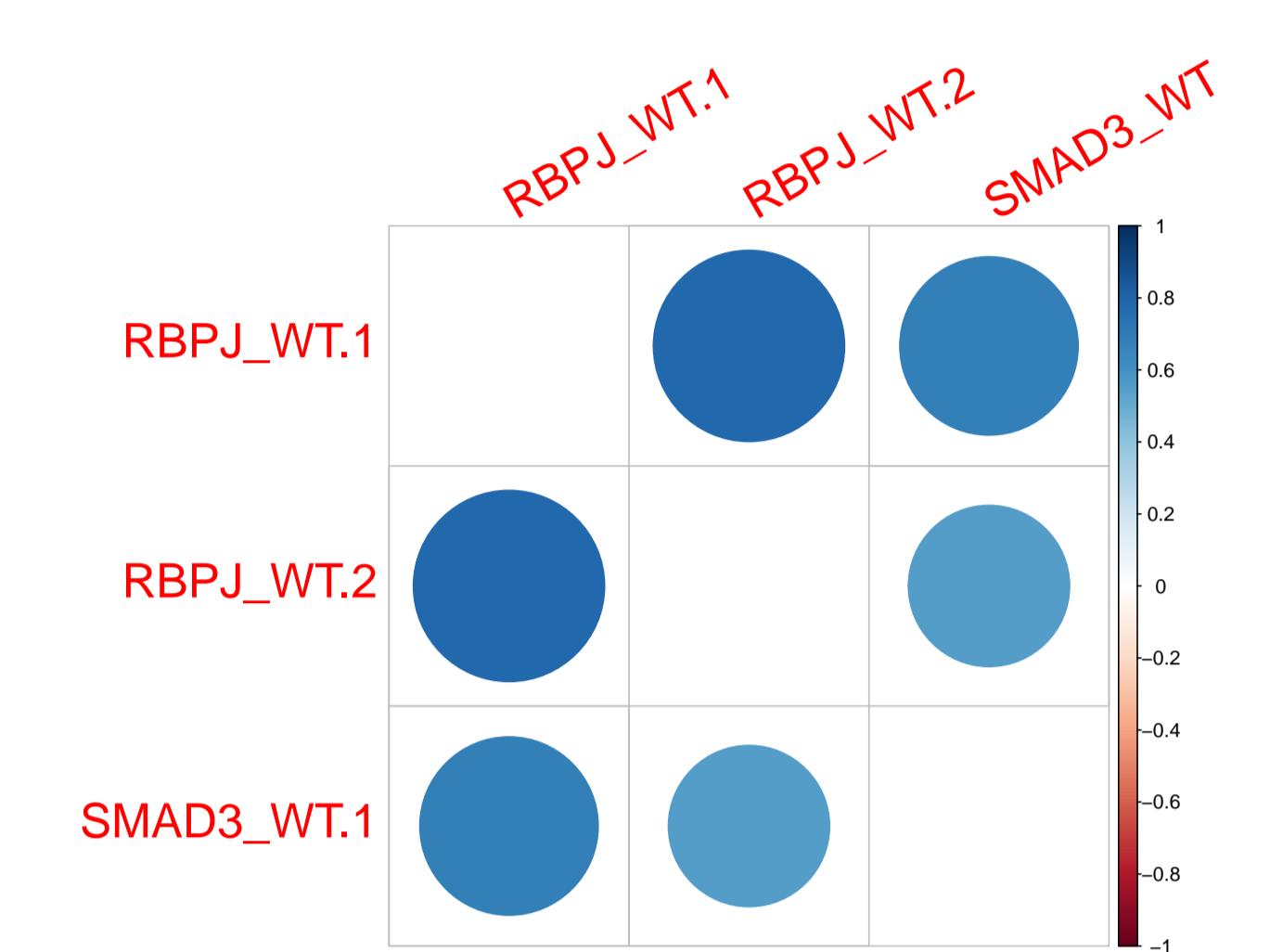
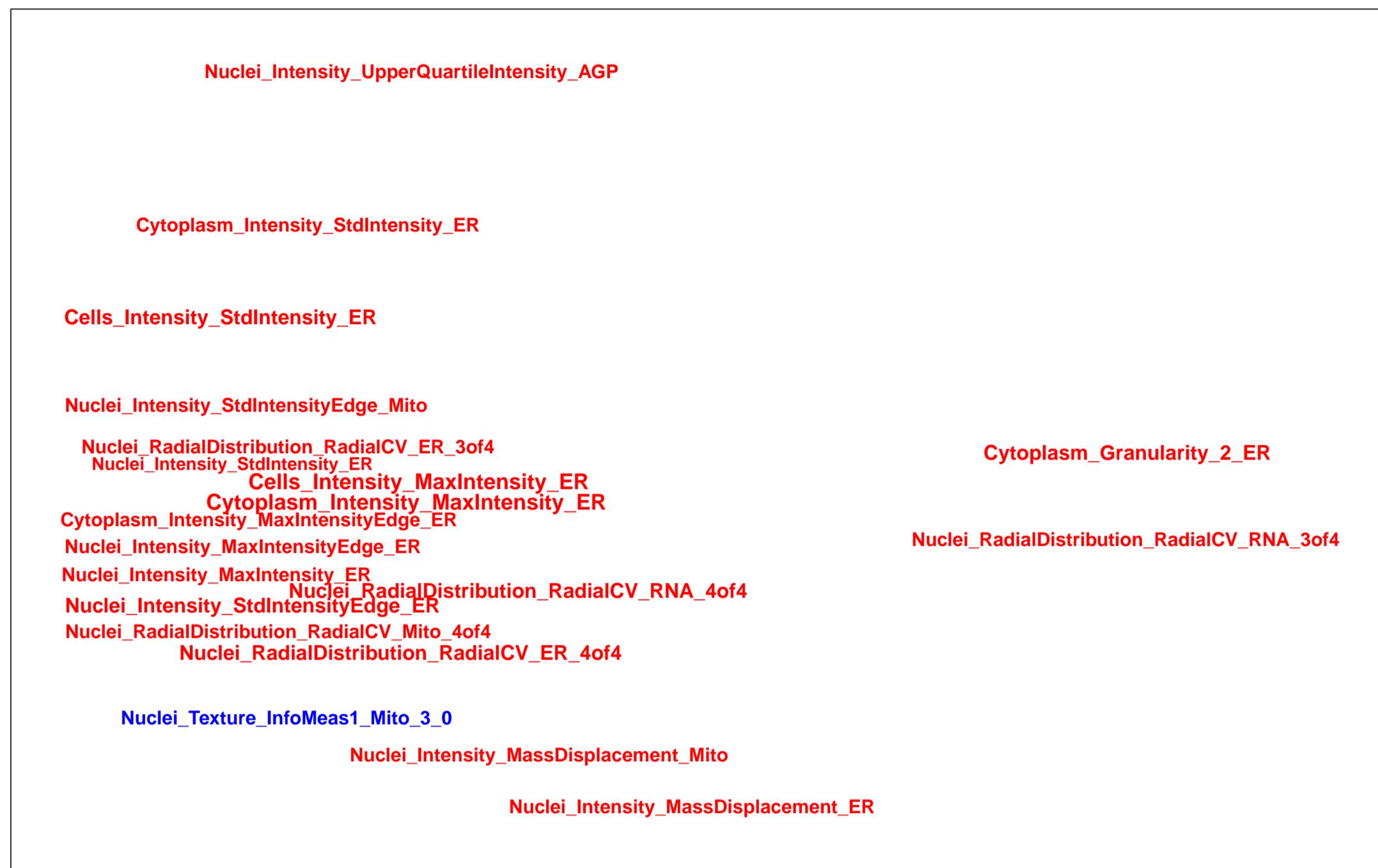
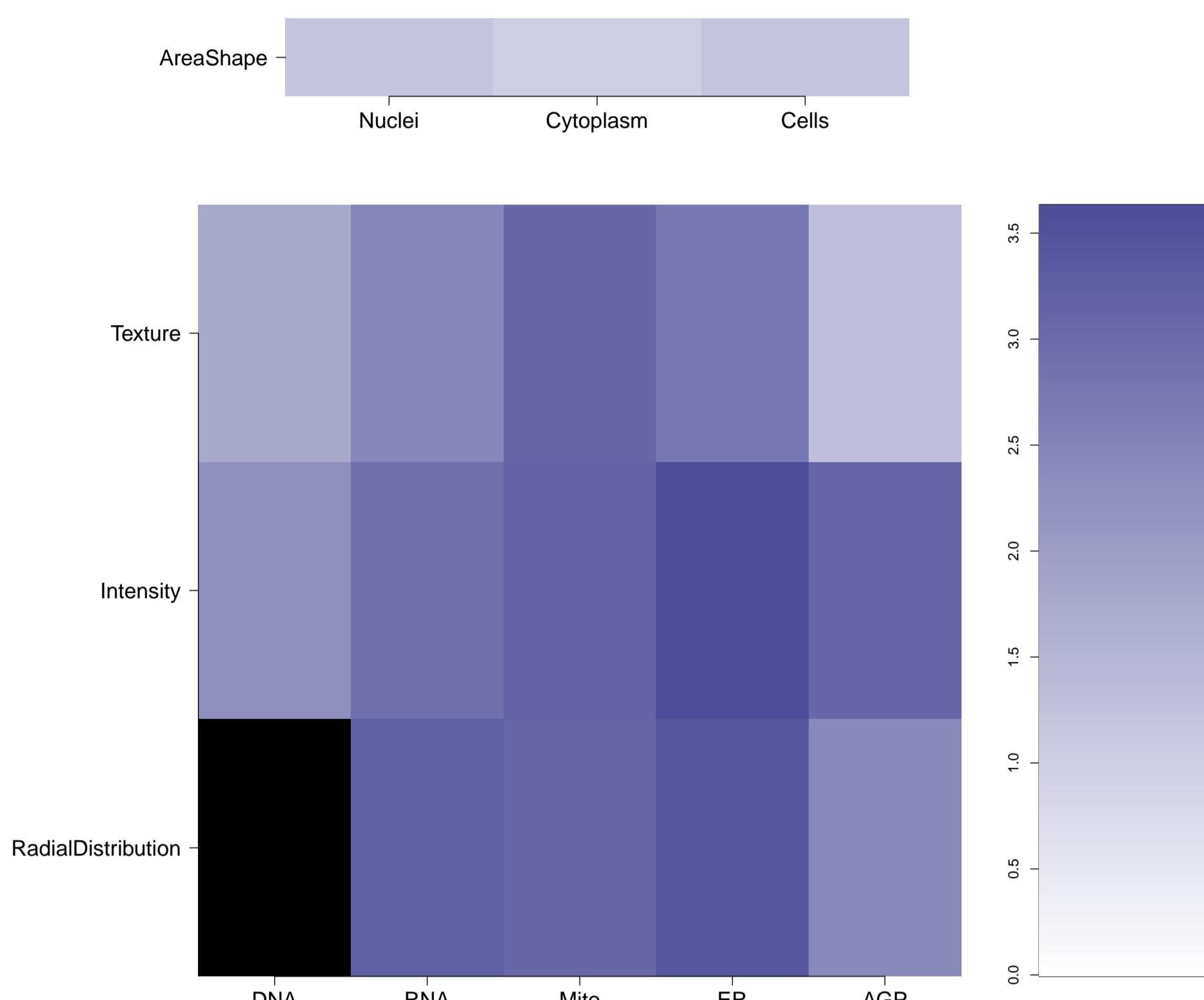
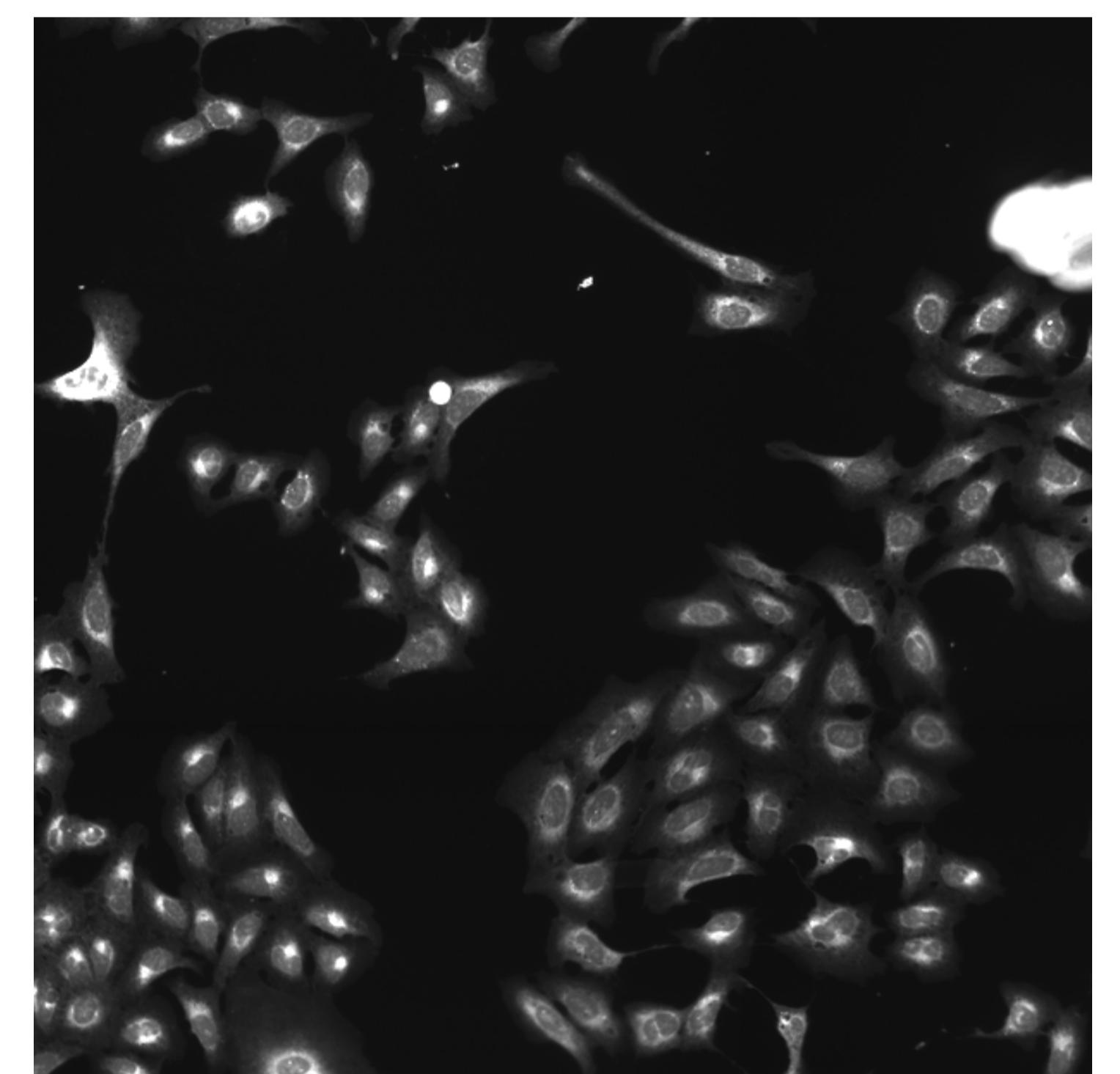
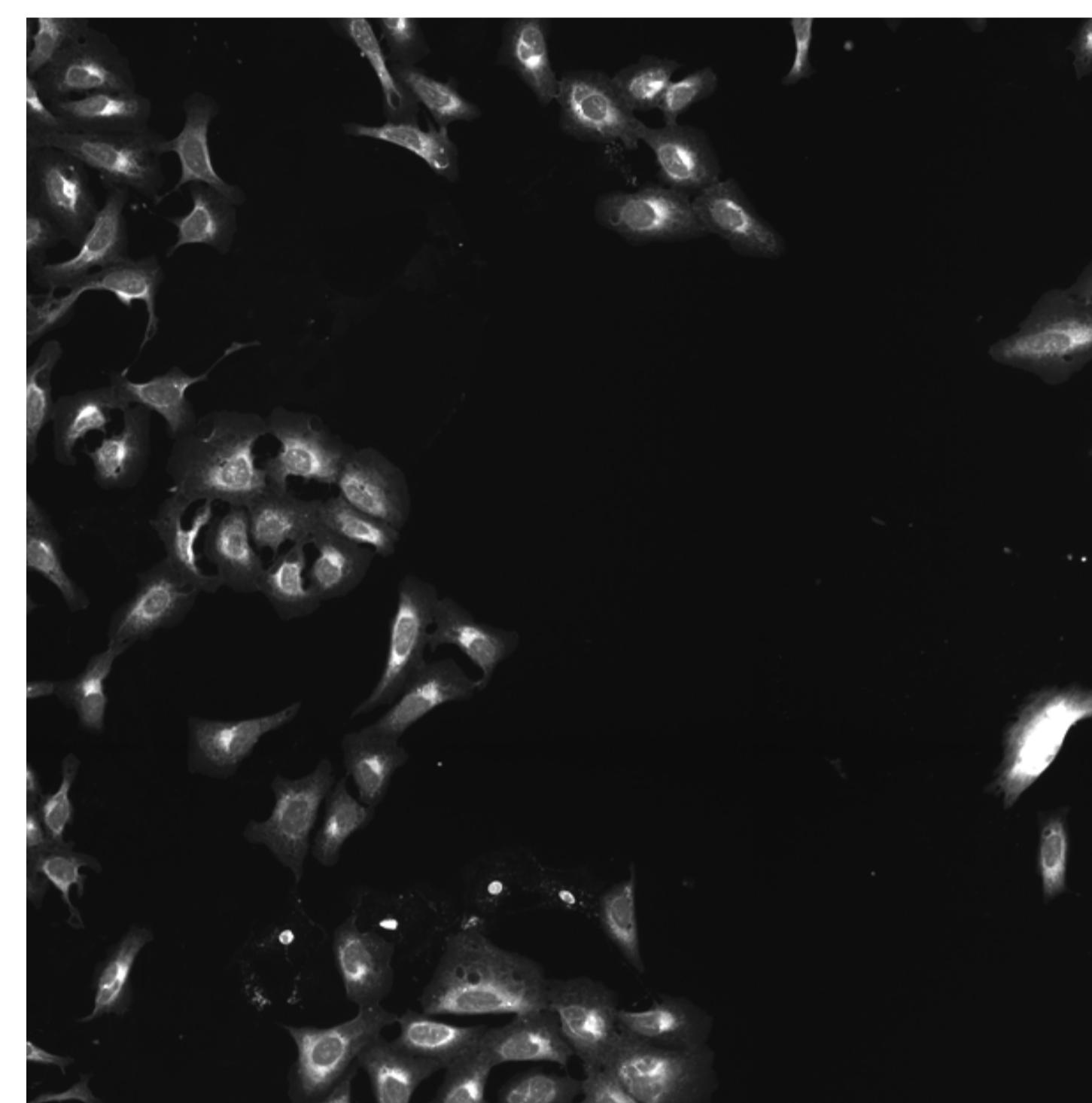
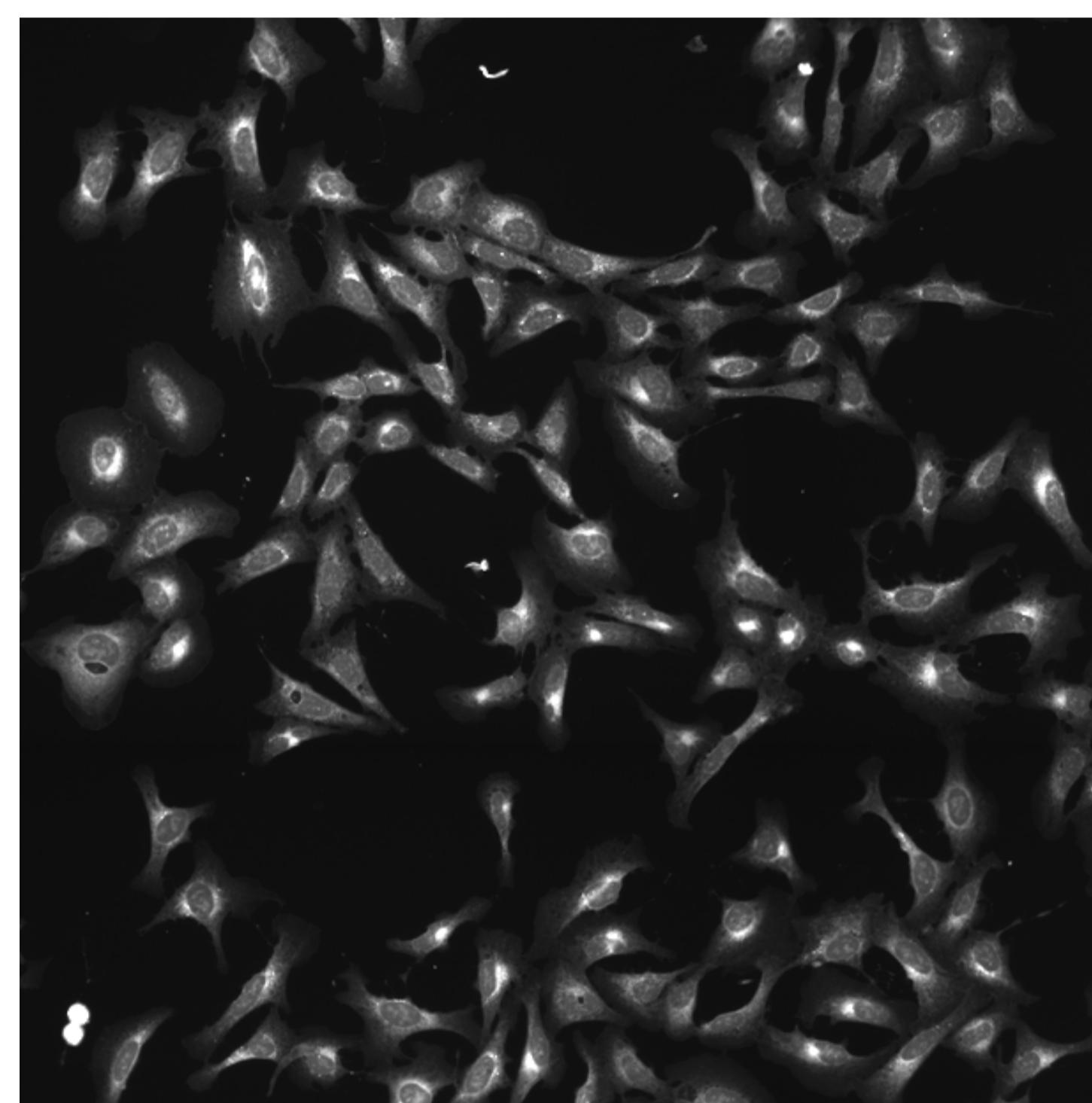
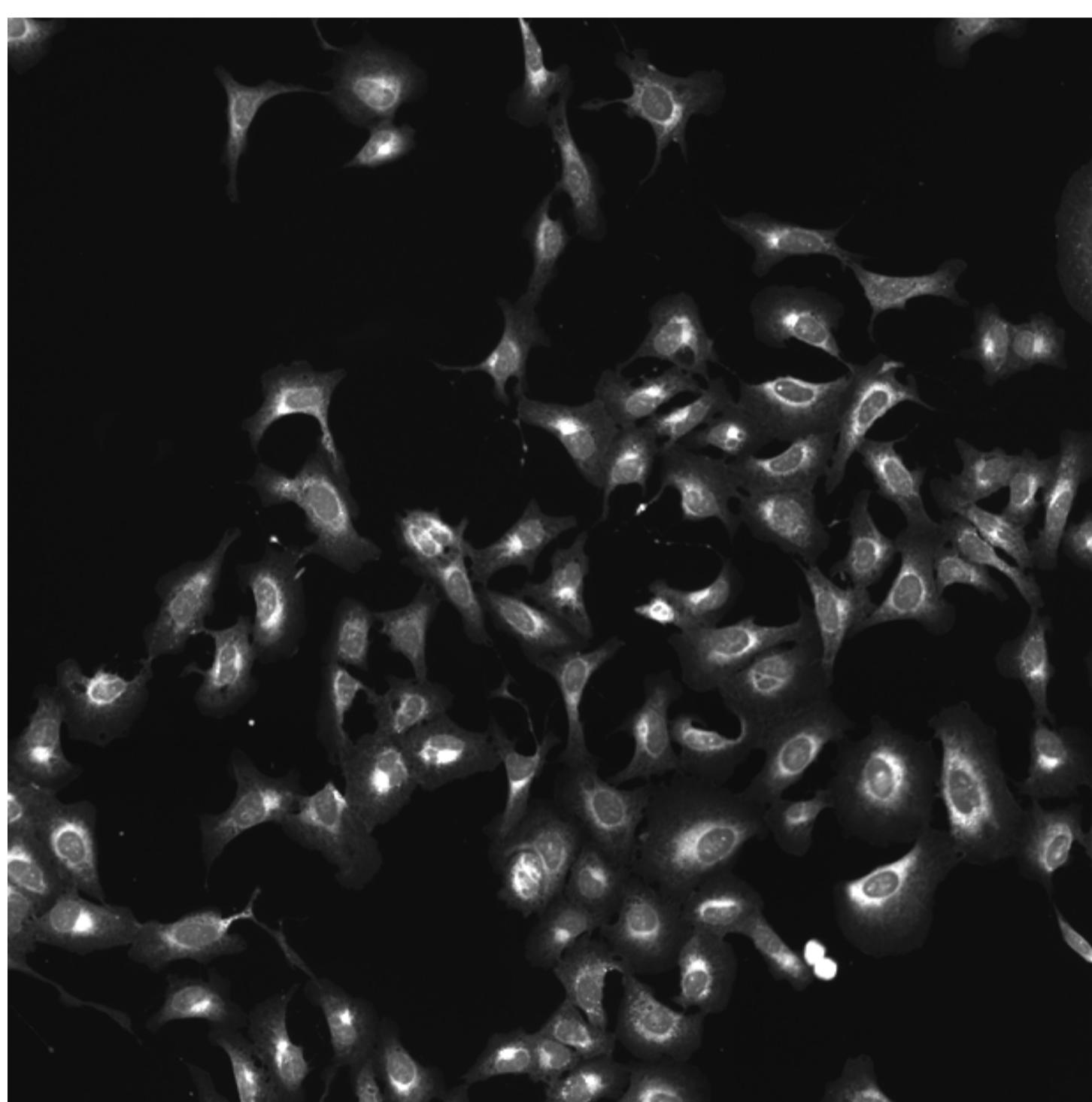


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

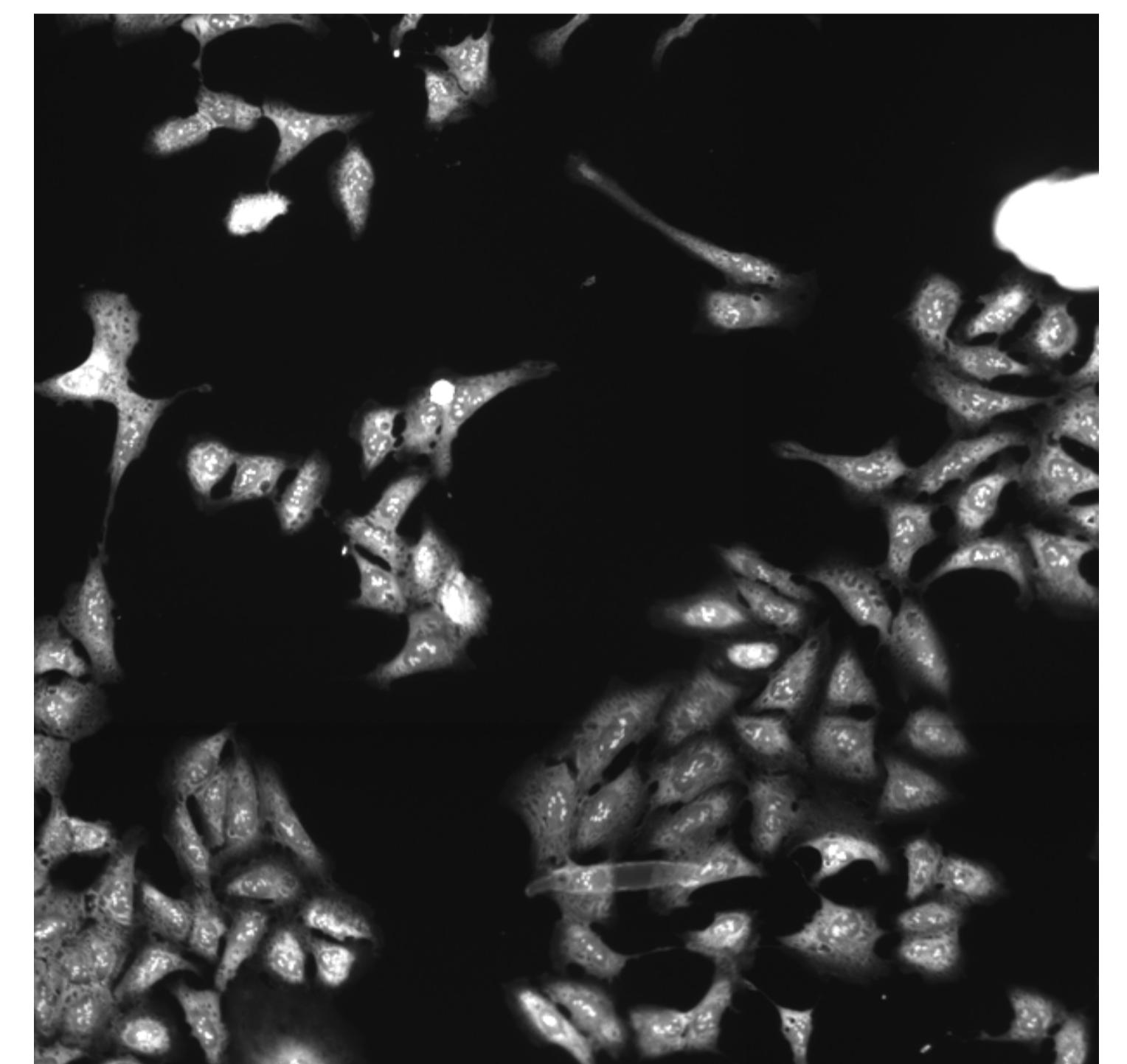
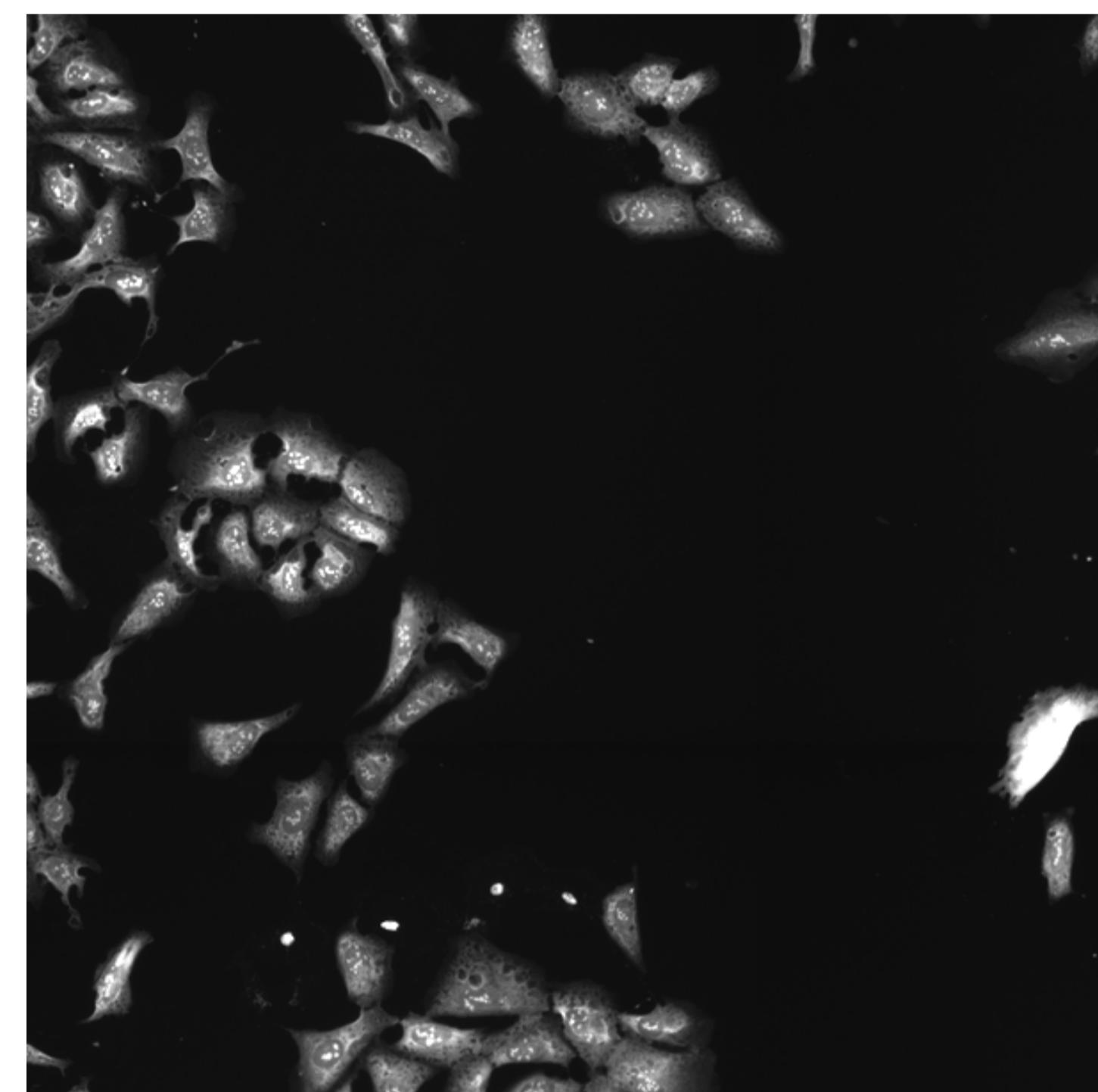
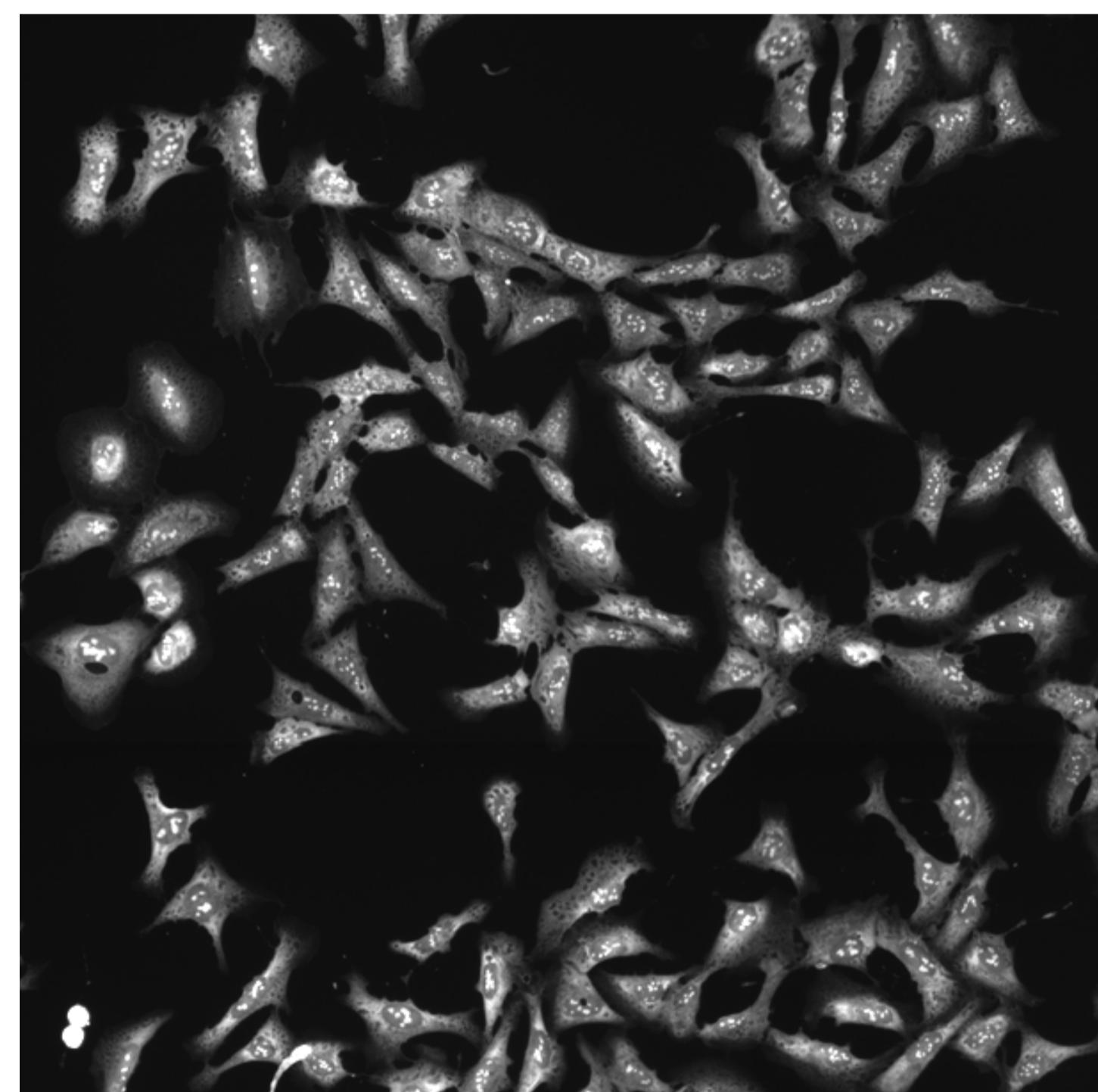
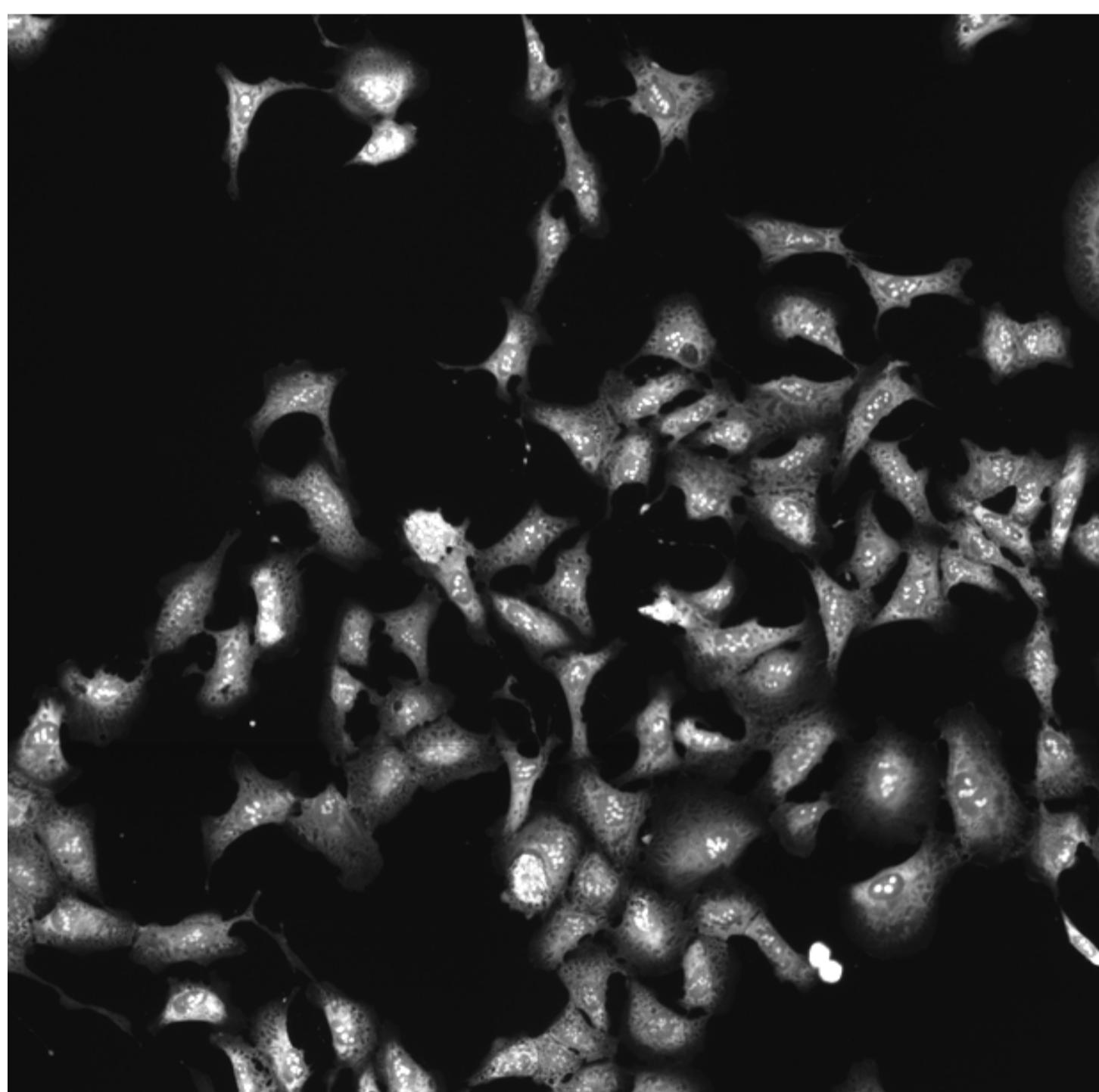
RBPJ_WT.1

RBPJ_WT.2

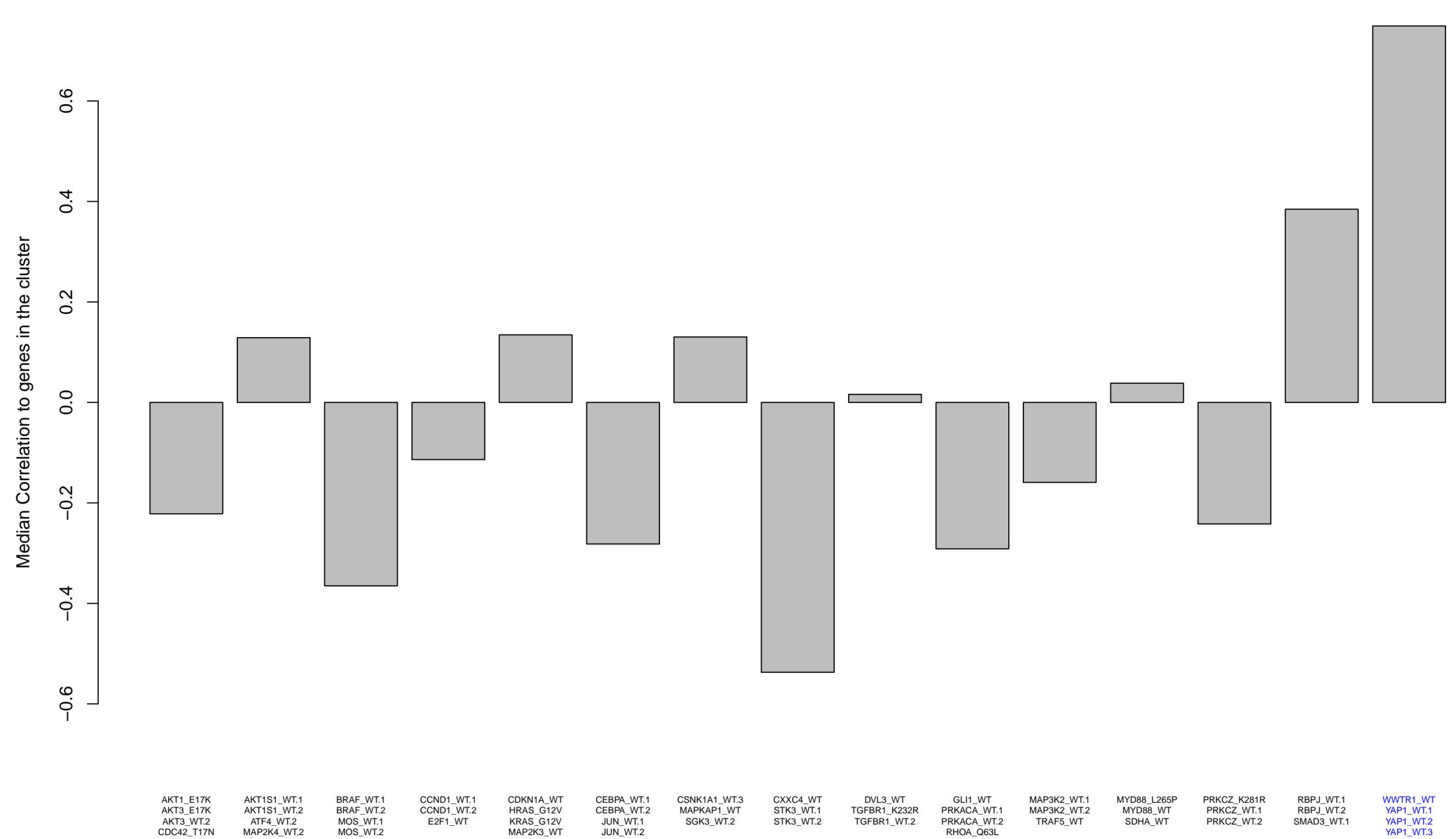
SMAD3_WT.1



RNA



Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	Pathway	Regulation	Type
YAP1_WT.1	Canonical Hippo	Inhibitor	
YAP1_WT.2	Canonical Hippo	Inhibitor	
YAP1_WT.3	Canonical Hippo	Inhibitor	
YAP1_WT.4	Canonical Hippo	Inhibitor	
WWTR1_WT	Canonical Hippo	Inhibitor	



Top 5 genes negatively correlated to the cluster						
Treatment	Pathway	Expert Annotation		Mean Correlation	Standard Deviation	
		Regulation	Type			
STK3_WT.1	Canonical Hippo	Activator		-0.63	0.08	
TRAF2_WT	Canonical NFkB	Activator		-0.57	0.08	
ELK1_WT	Canonical MAPK	Activator		-0.55	0.07	
CXXC4_WT	WNT	Inhibitor		-0.54	0.15	
CDC42_WT	Canonical Cytoskeletal Re-org	Activator		-0.52	0.05	

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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?

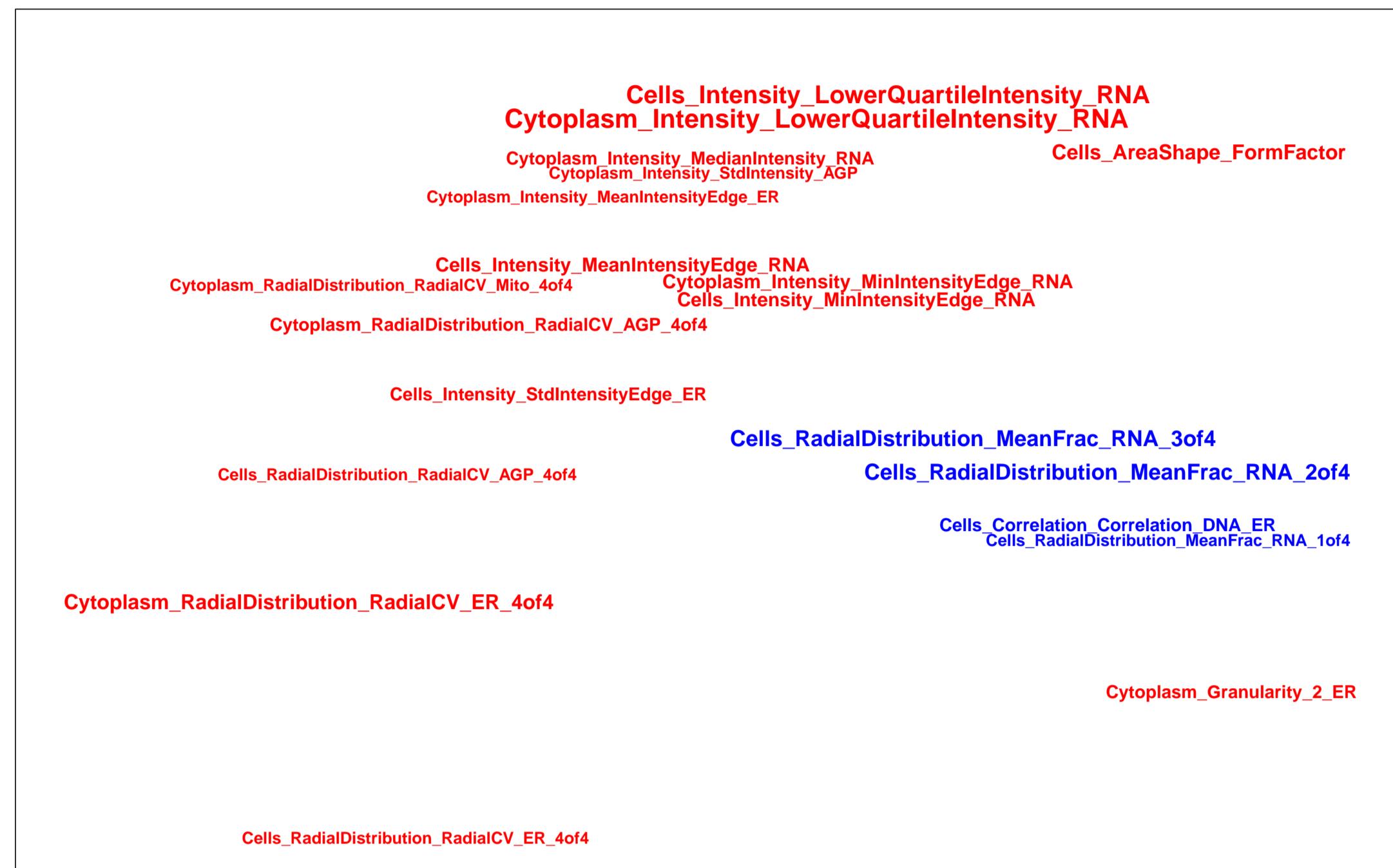
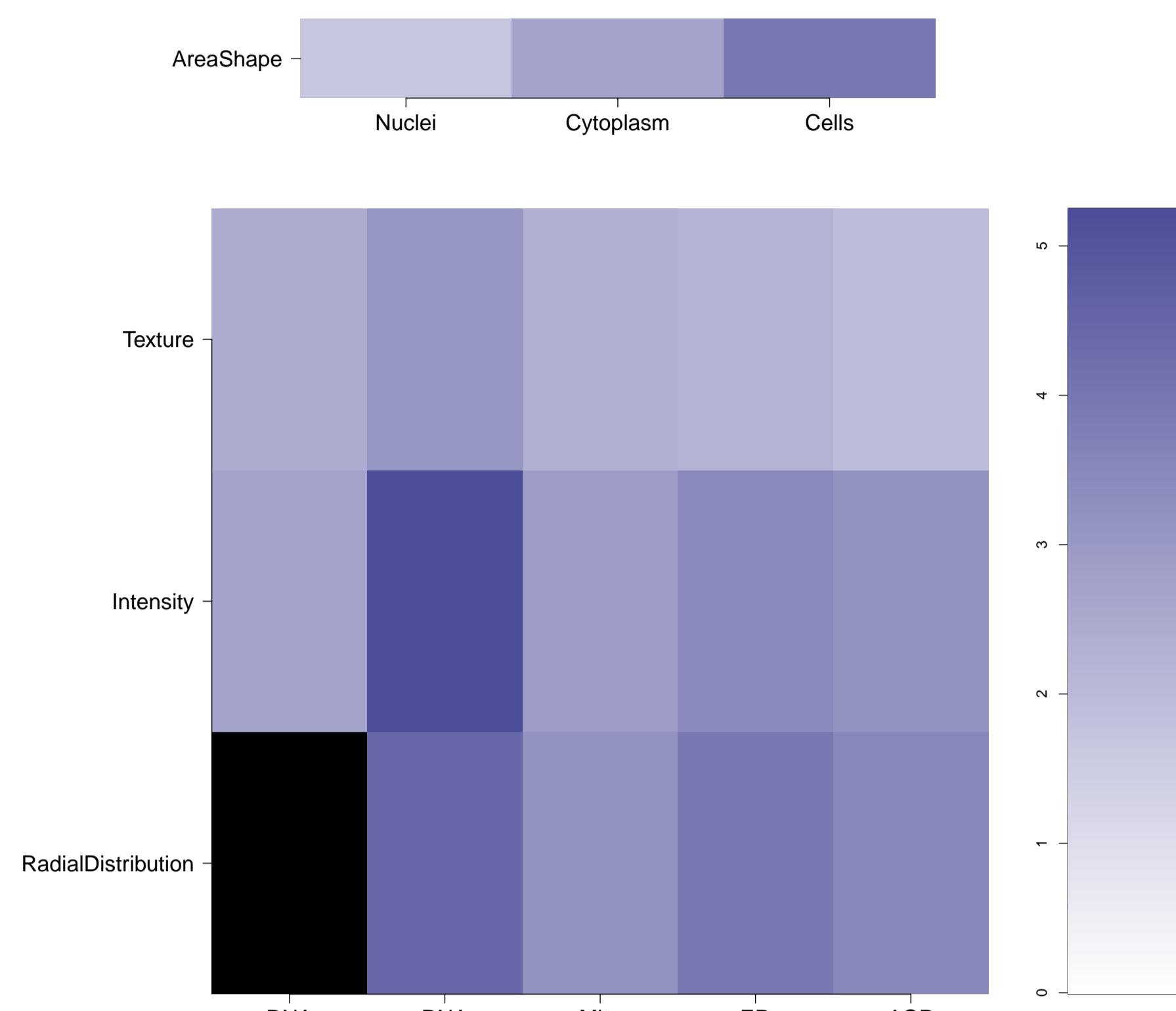


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

