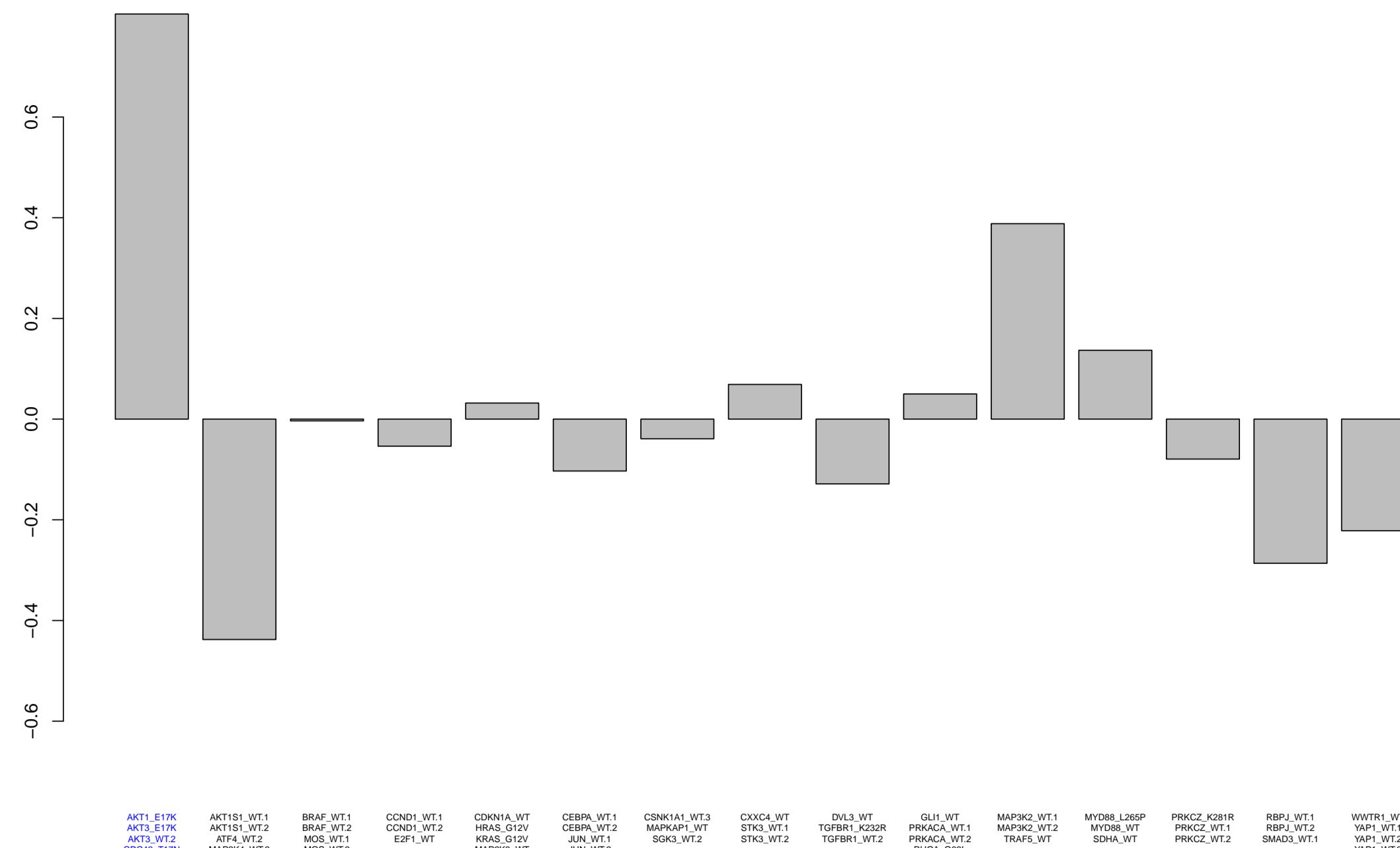


Cluster 1

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

Expert Annotation			
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	Expert Annotation			Mean Correlation	Standard Deviation	
	Pathway	Regulation	Type			
K3R1_WT.1	Canonical PI3K/AKT	Activator		-0.48	0.14	
KT1S1_WT.2	TOR	Inhibitor		-0.47	0.04	
KT1S1_WT.1	TOR	Inhibitor		-0.43	0.05	
RKACG_WT.3	PKA	Activator		-0.42	0.09	
TF4_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

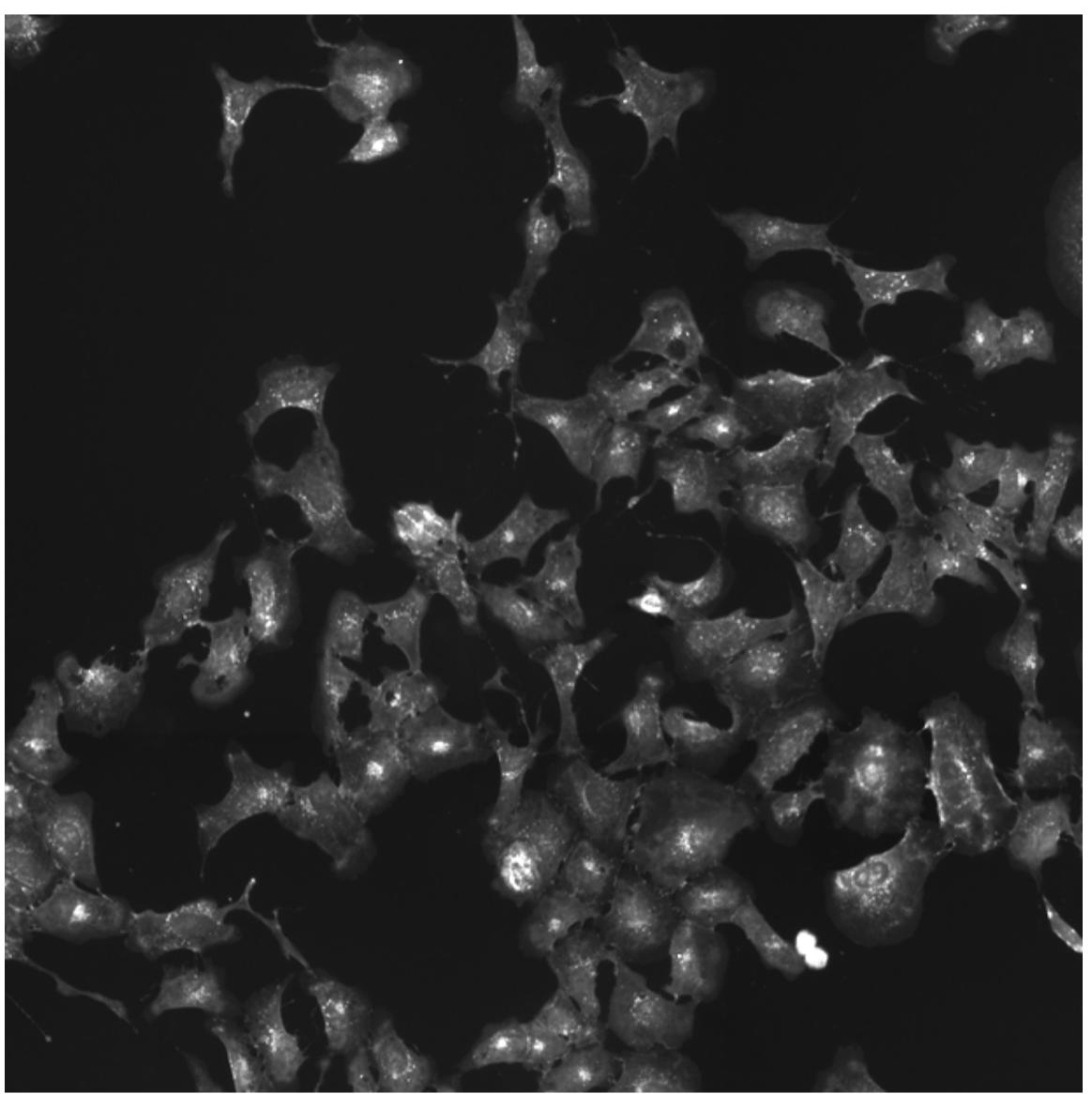
Which individual morphological features are distinguishing in the cluster relative to the untreated samples? Blue/Red means the feature has a positive/negative z-score. Size is proportional to the z-score value.

How strongly are genes within the cluster correlated?

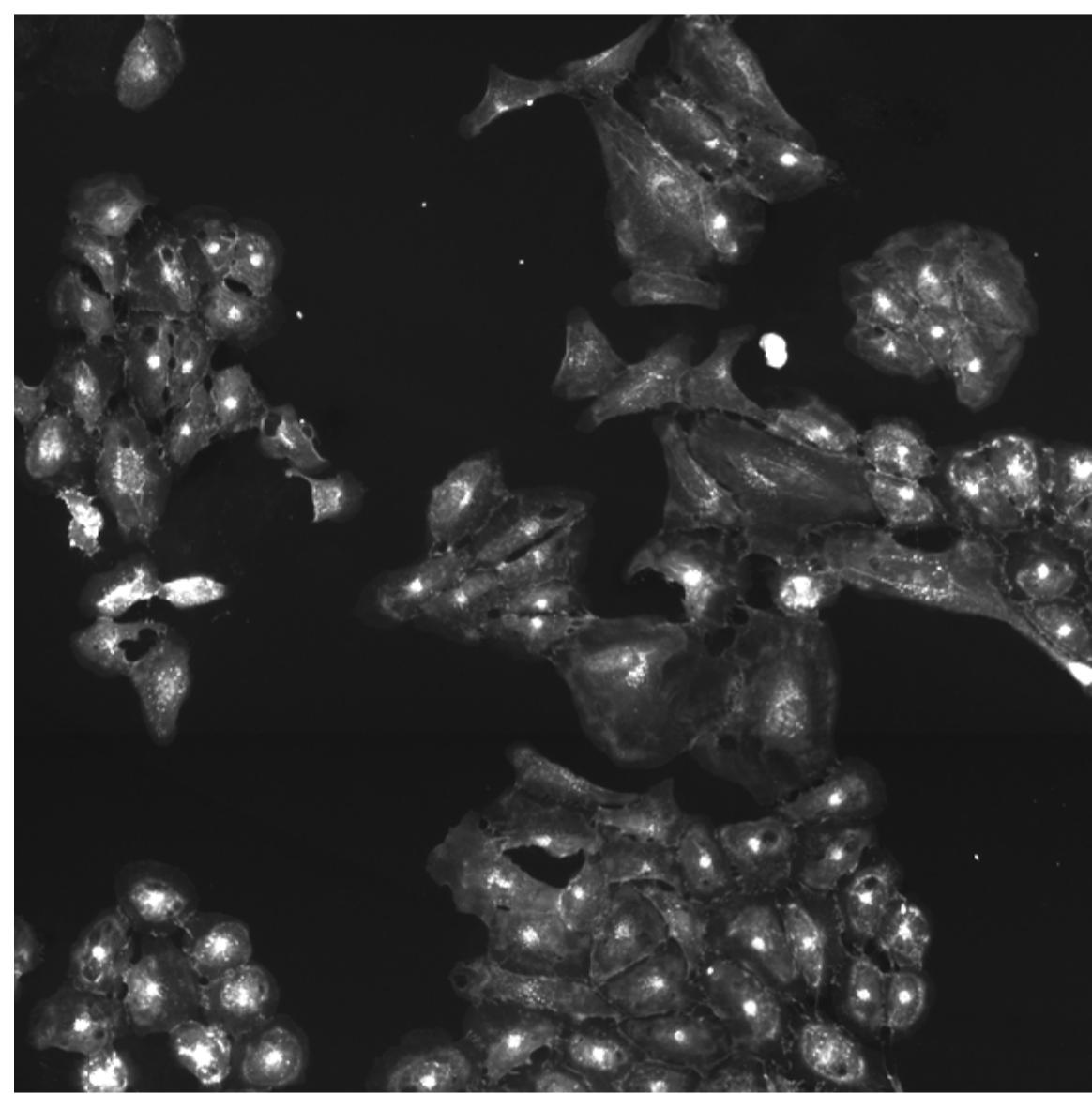


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

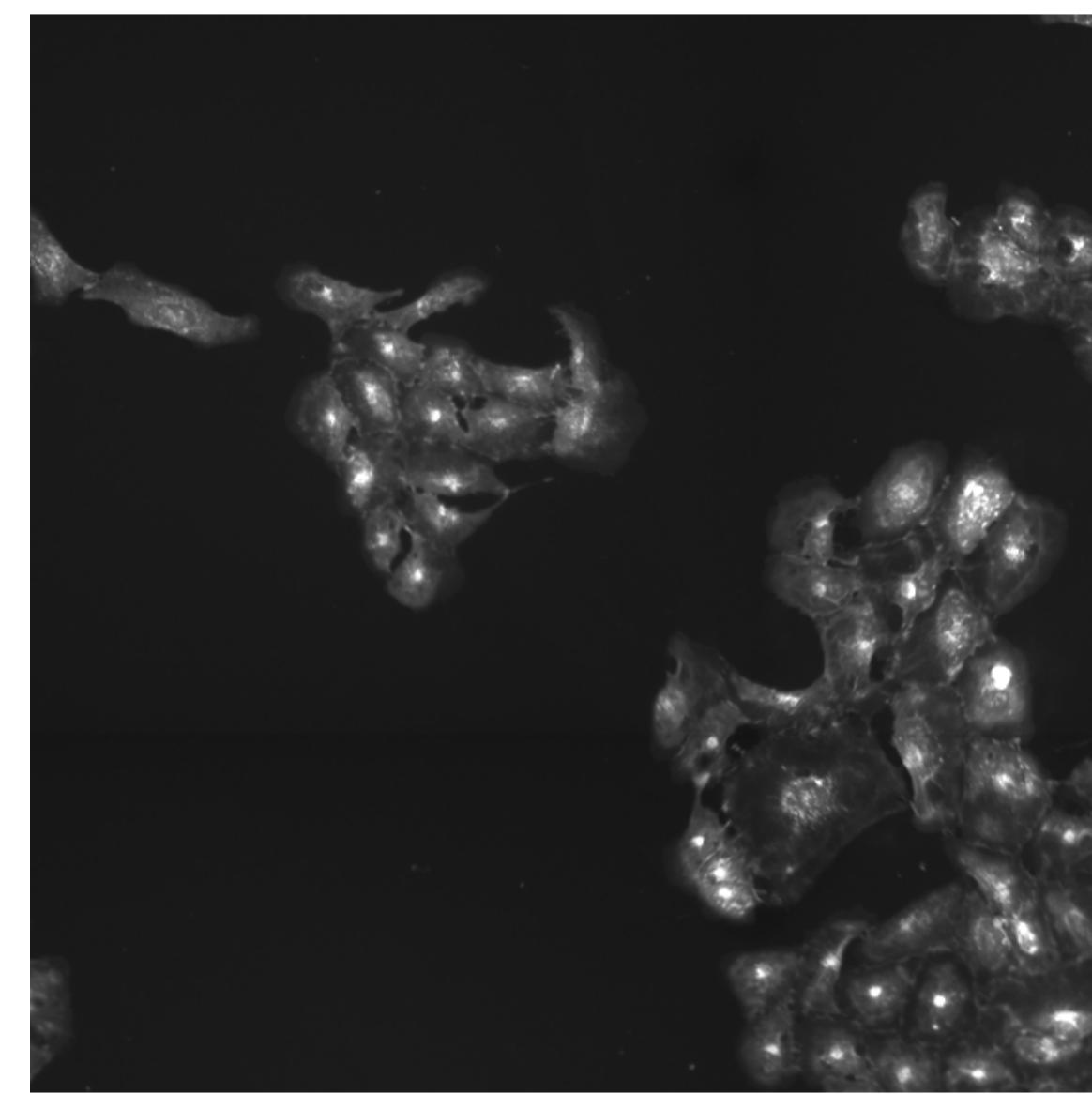
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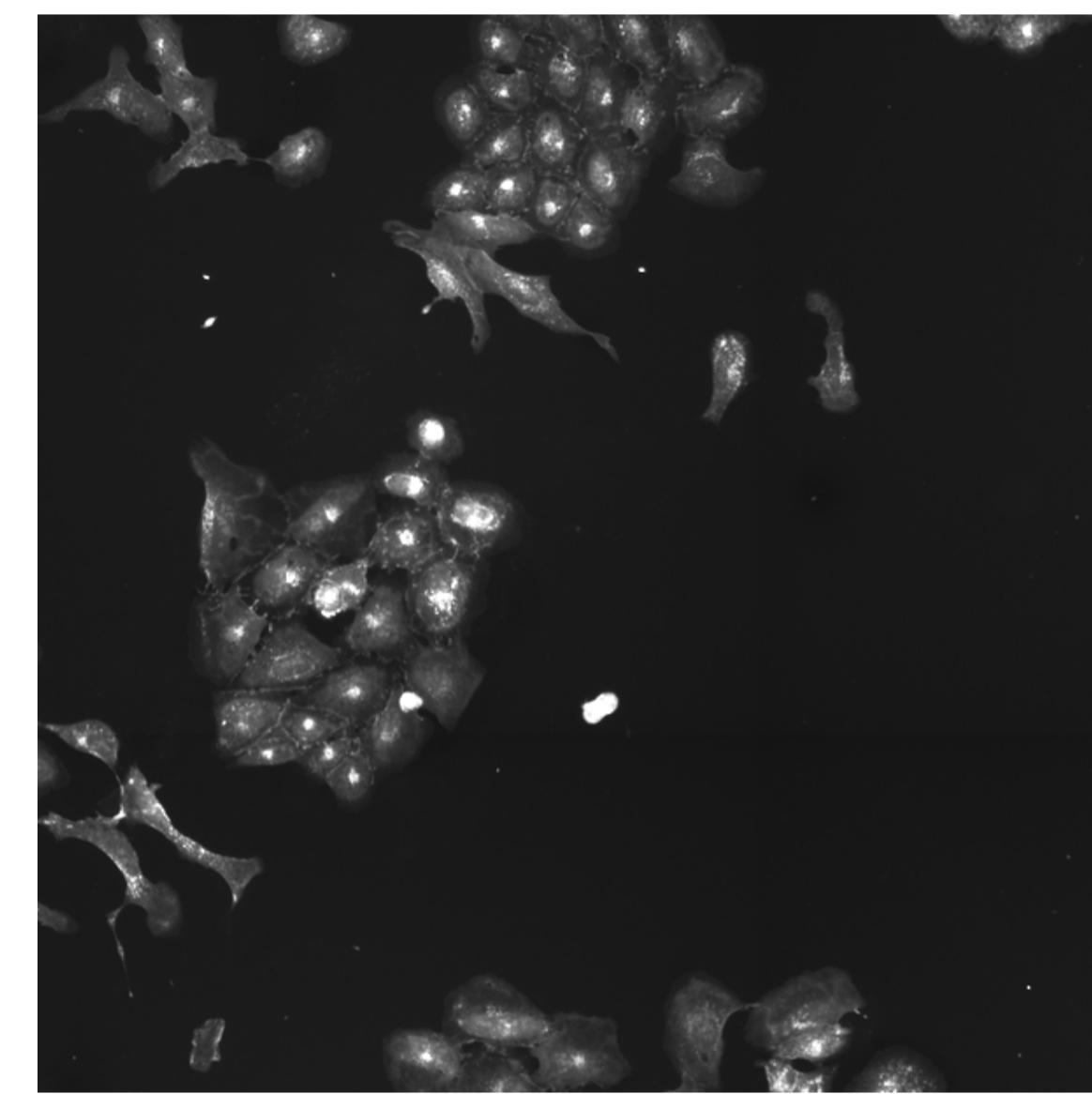
AKT1_E17K



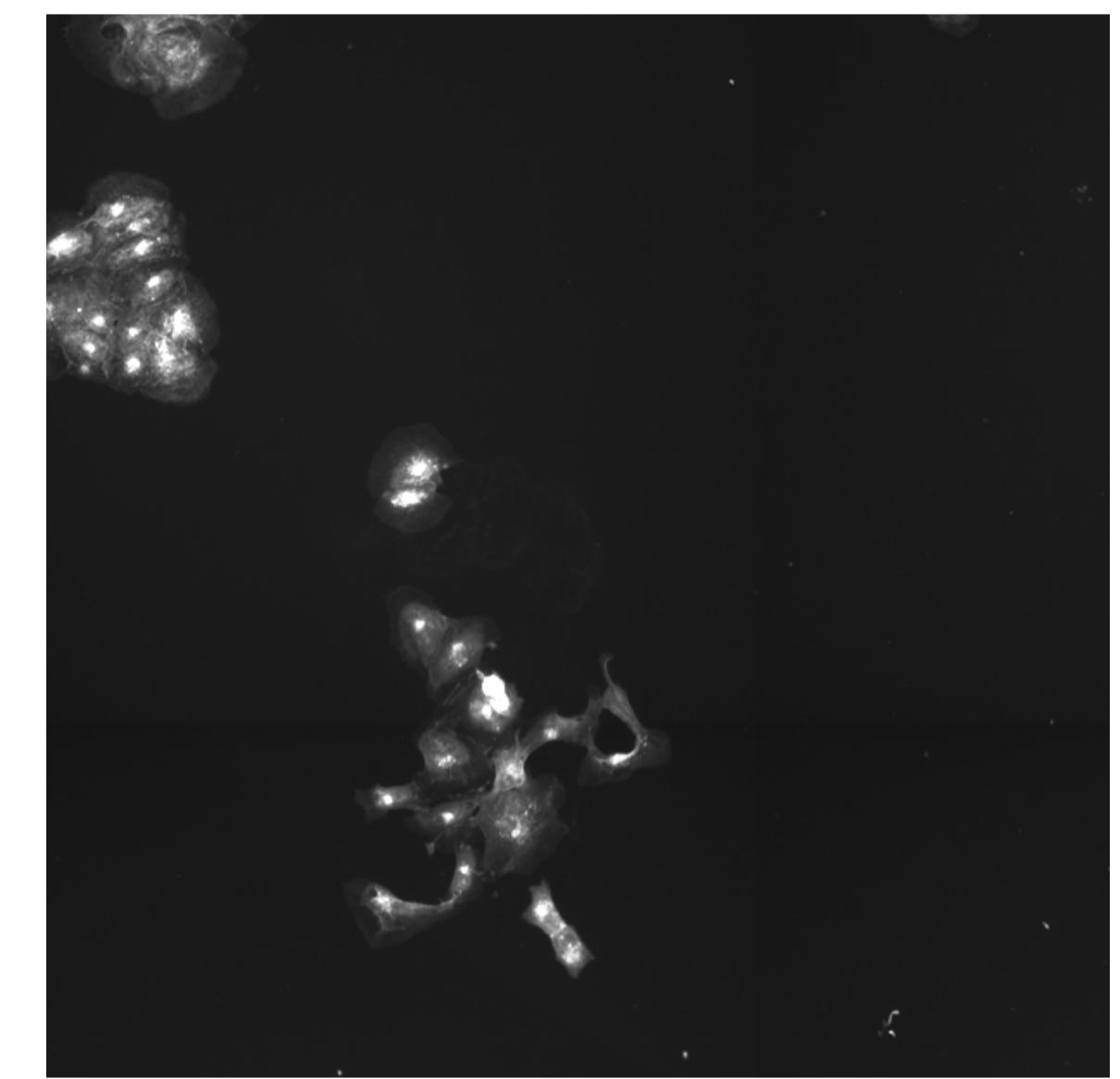
AKT3_E17K



AKT3_WT.2



CDC42_T17N

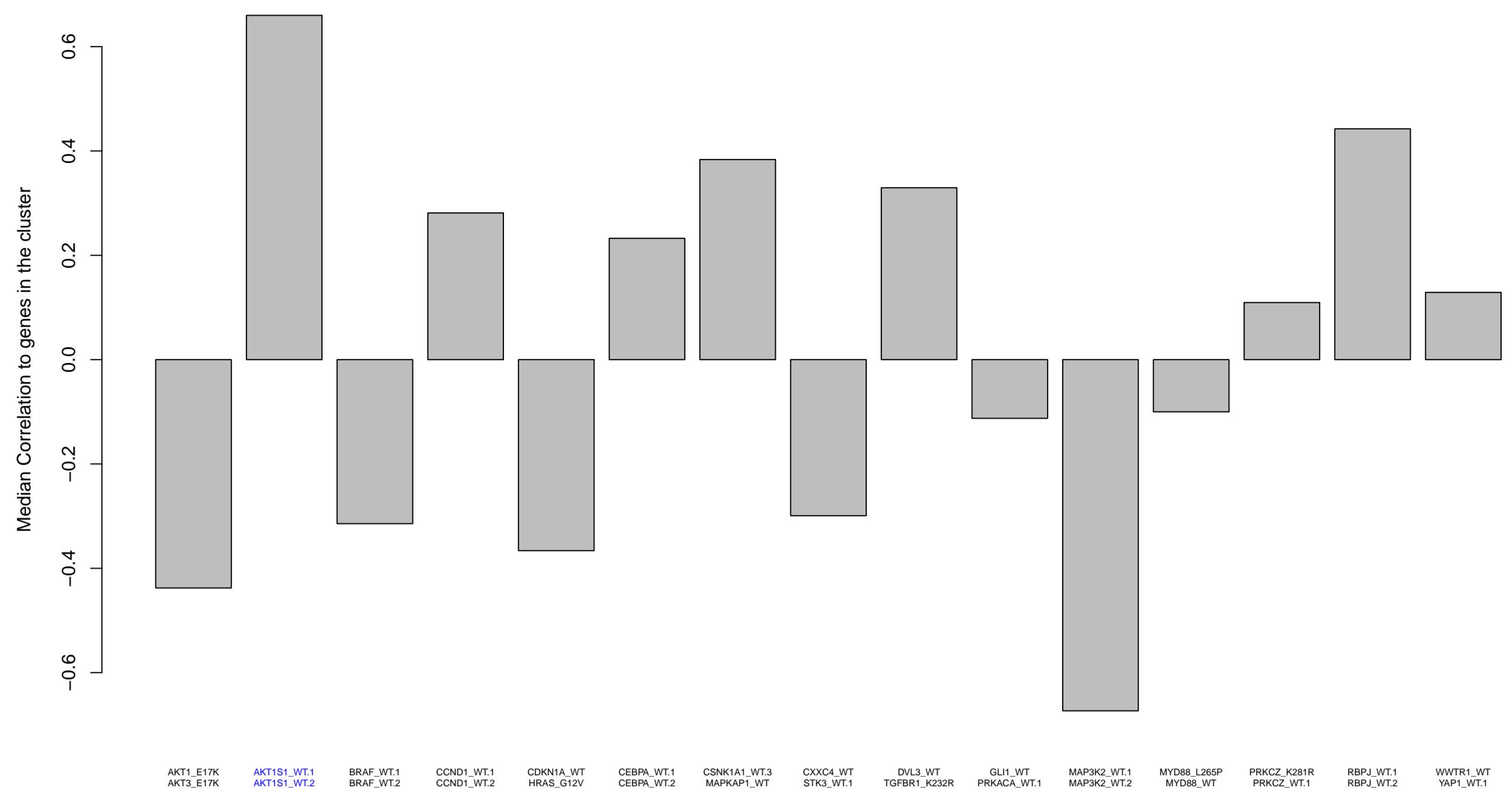


AGF

RNA

Cluster 2

Genes in the cluster along with the pathways as annotated by experts		
Treatment	Expert Annotation	
	Pathway	Regulation Type
ATF4_WT.2	Canonical ER Stress/UPR	Activator
MAP2K4_WT.2	Canonical MAPK	Activator
PIK3R1_WT.1	Canonical PI3K/AKT	Activator
PRKCA_K368R	Canonical PKC	Inhibitor
AKT1S1_WT.1	TOR	Inhibitor
AKT1S1_WT.2	TOR	Inhibitor



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?

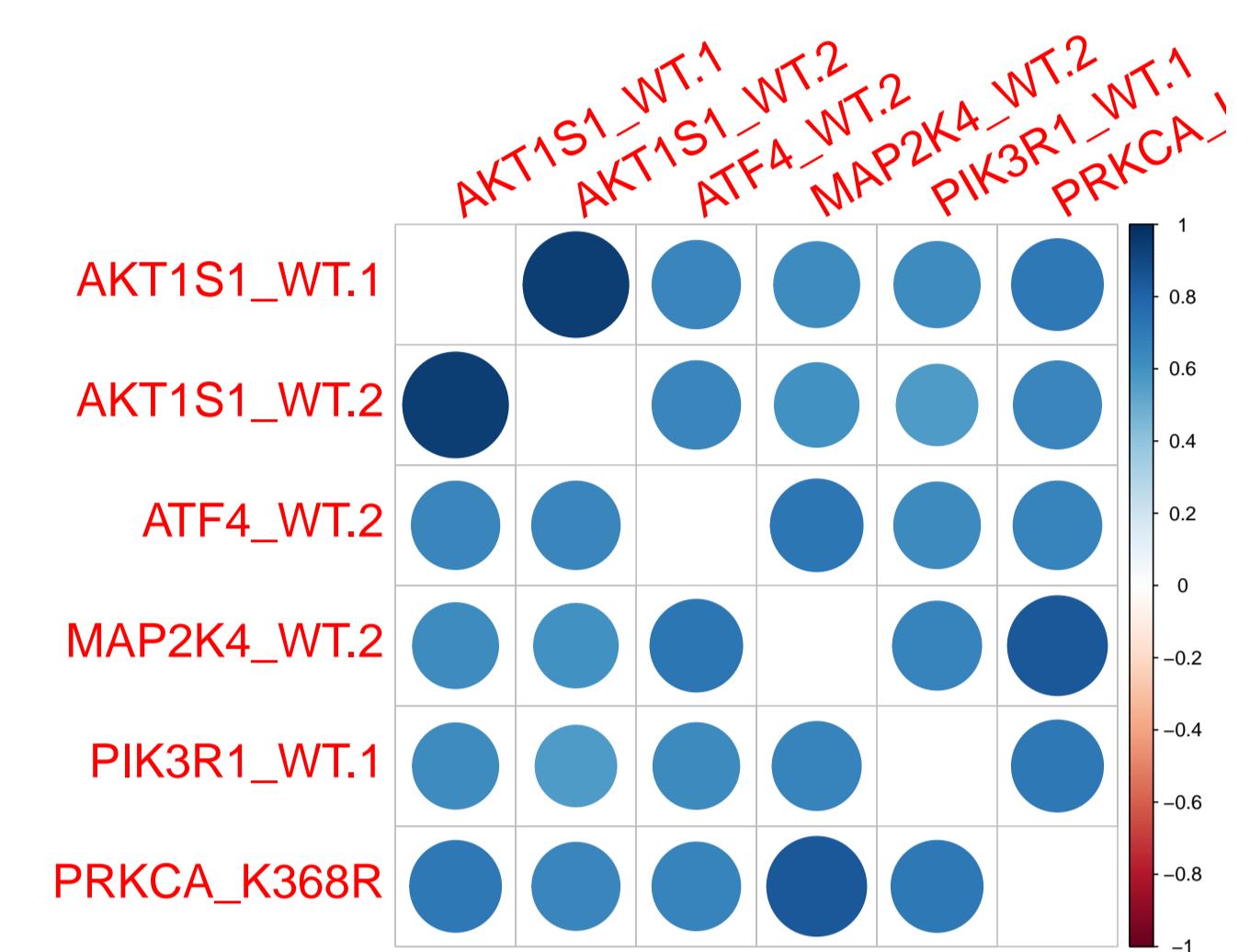
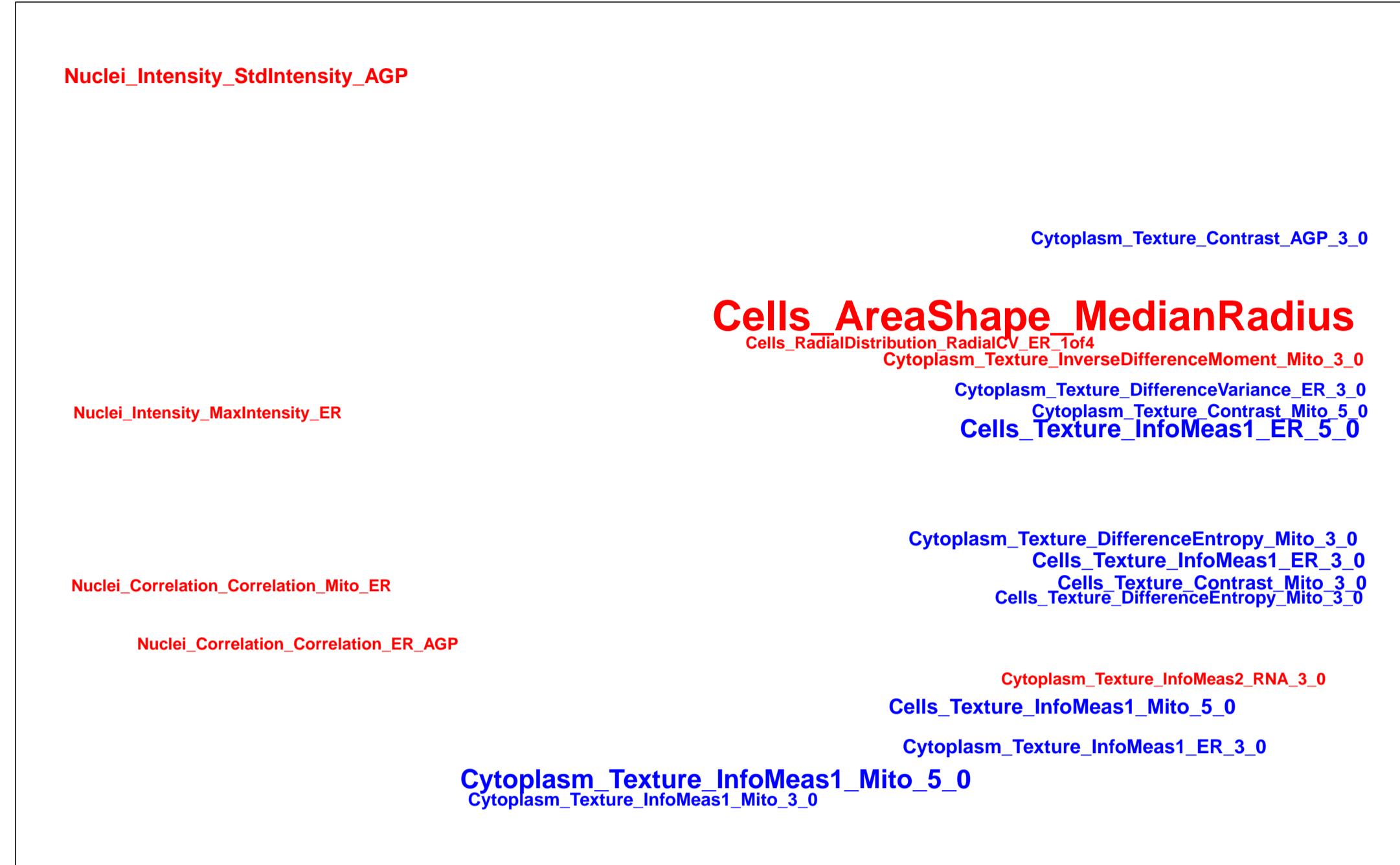
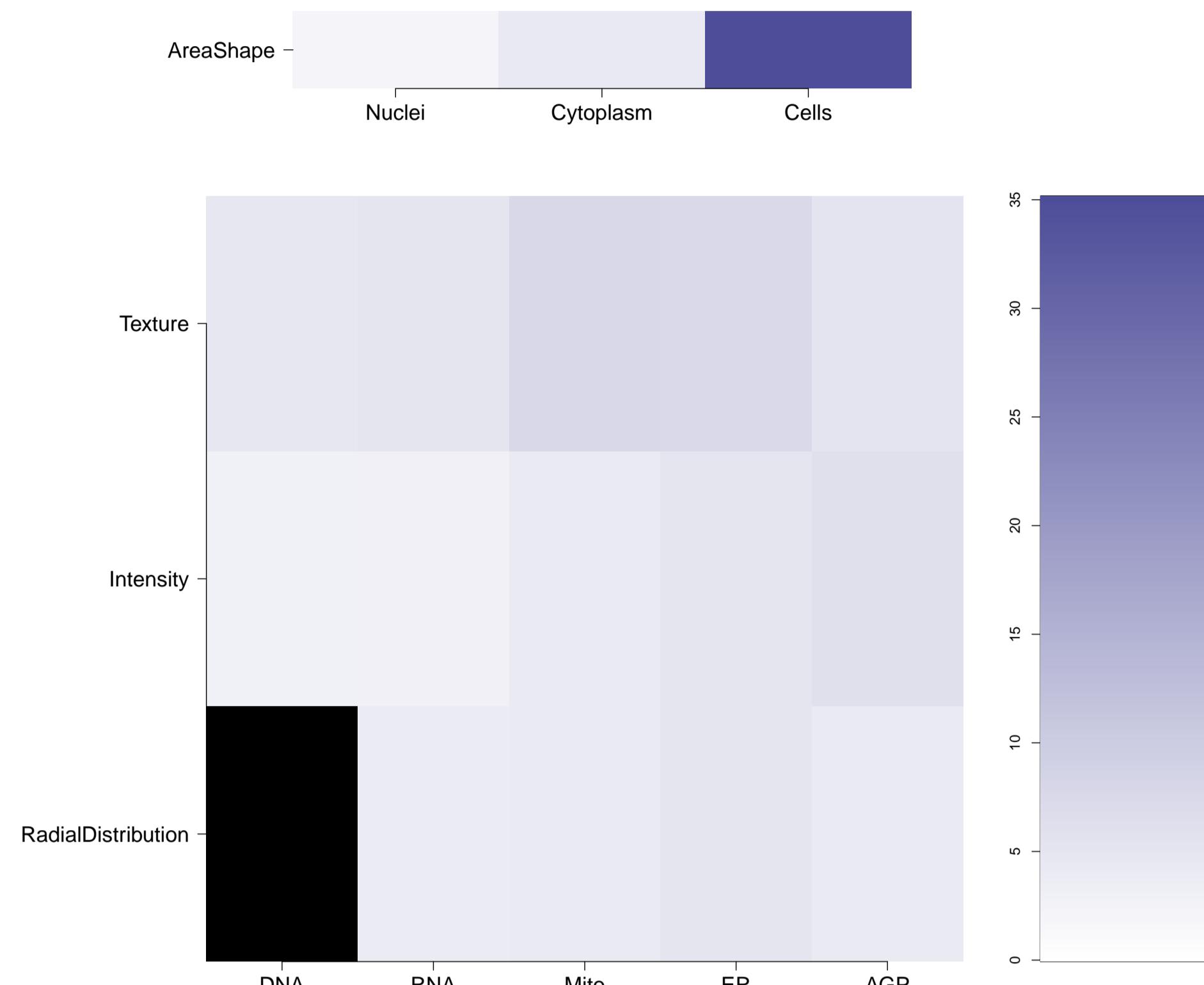


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

AKT1S1_WT.2

ATF4_WT.2

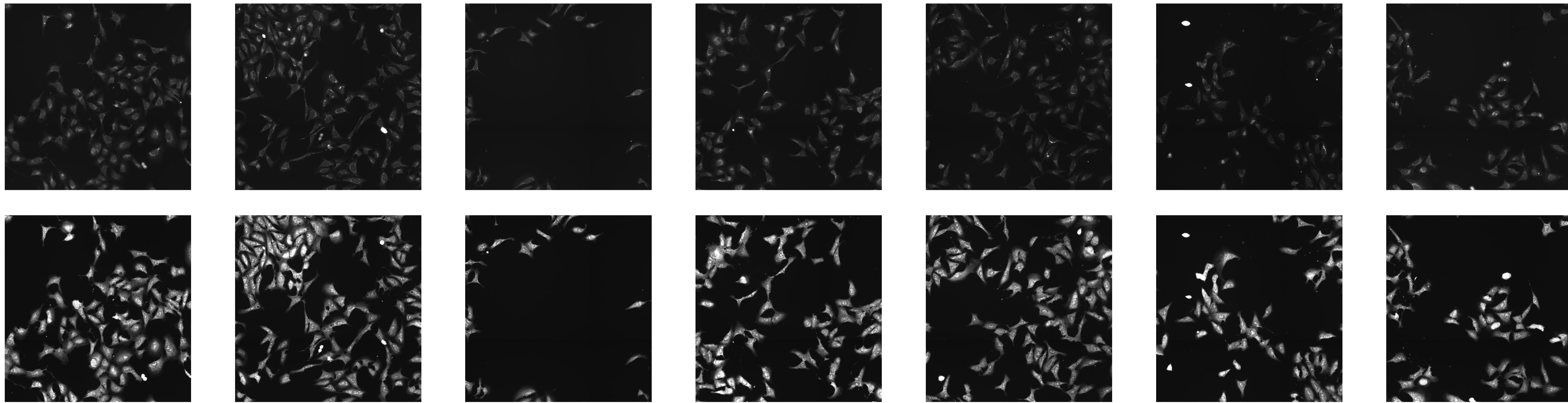
MAP2K4_WT.2

PIK3R1_WT.1

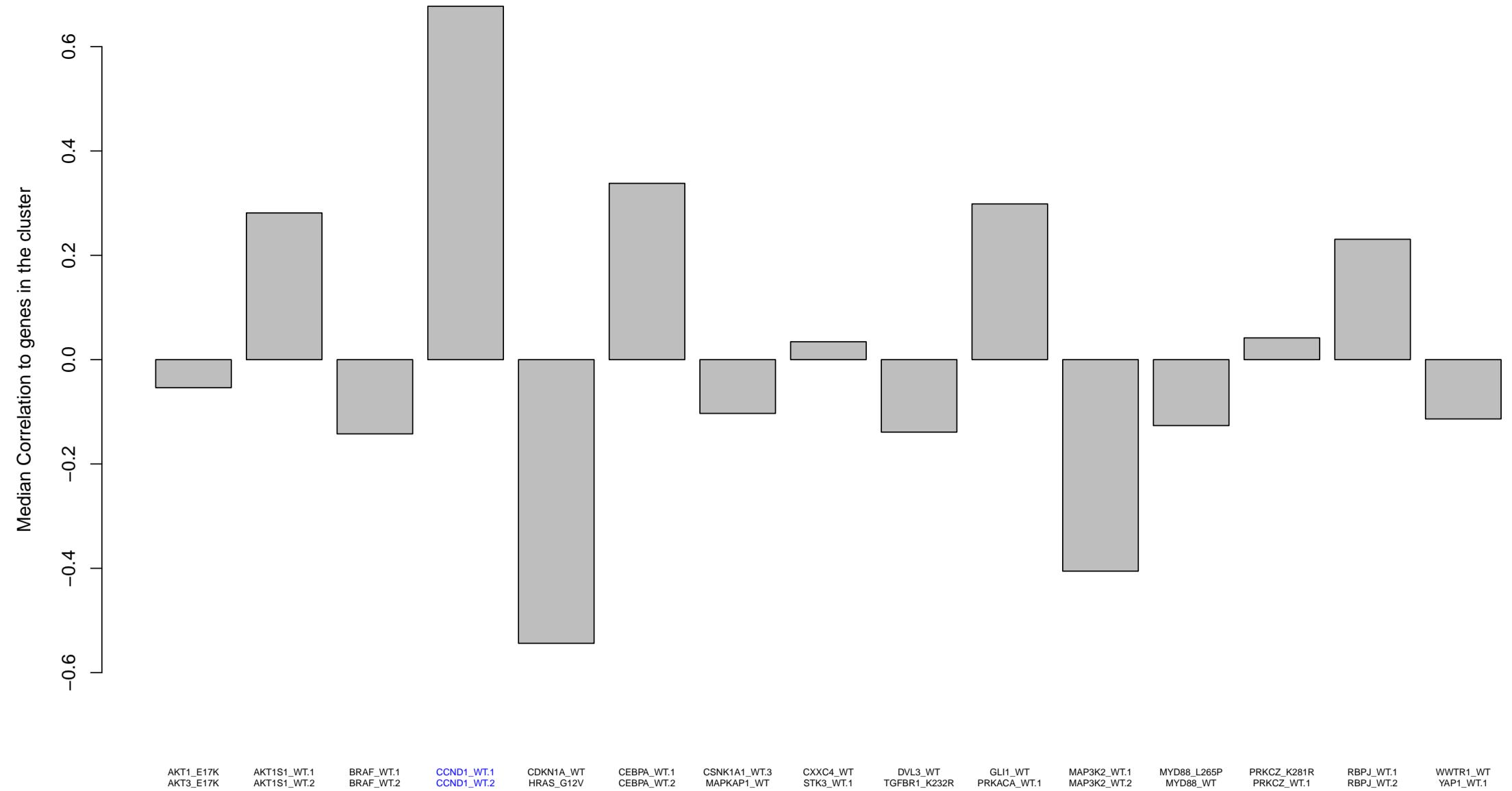
PRKCA_K368R

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AKT1S1_WT.1



Genes in the cluster along with the pathways as annotated by experts			
Expert Annotation			
Treatment	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					
Expert Annotation					
Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation	
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?

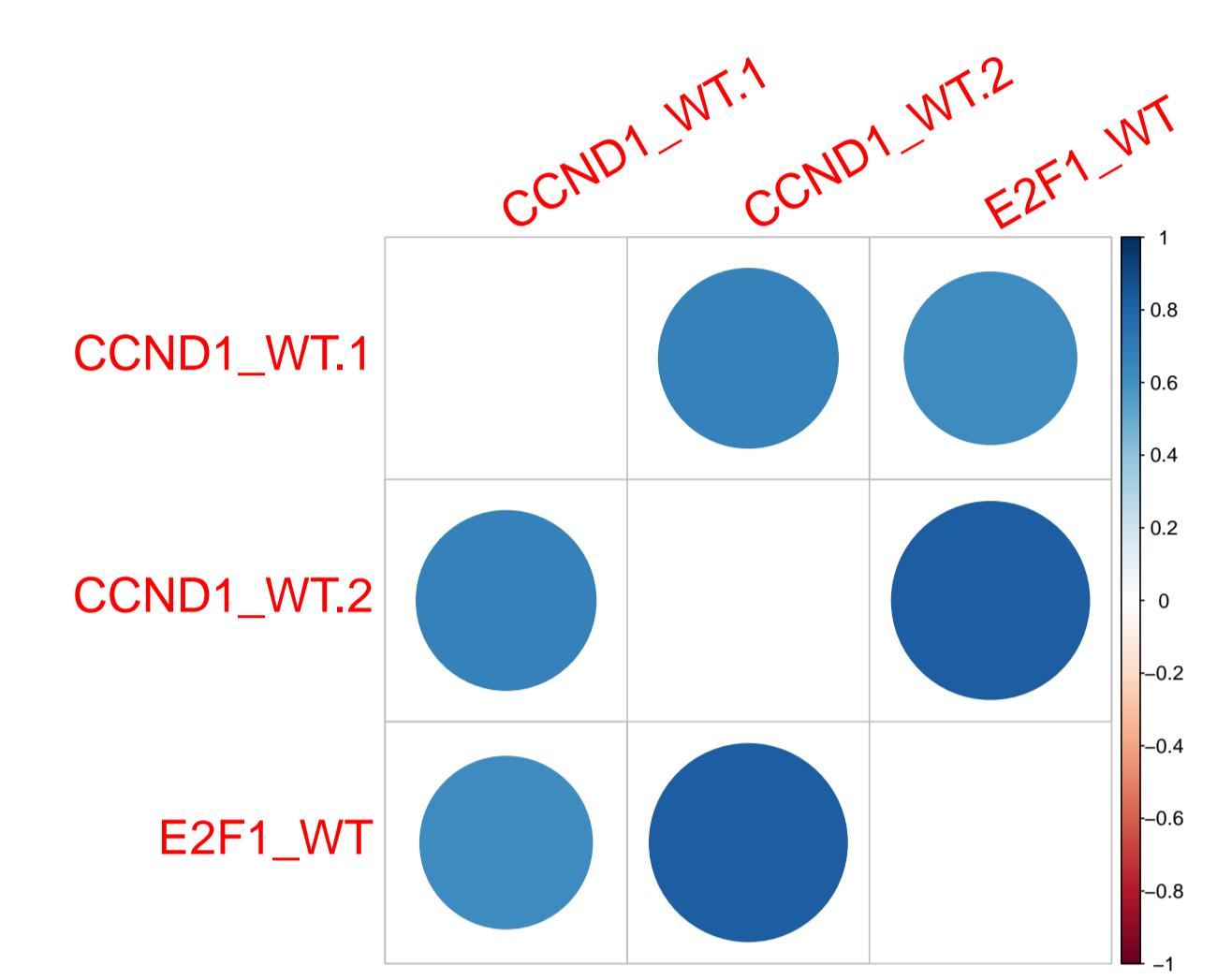
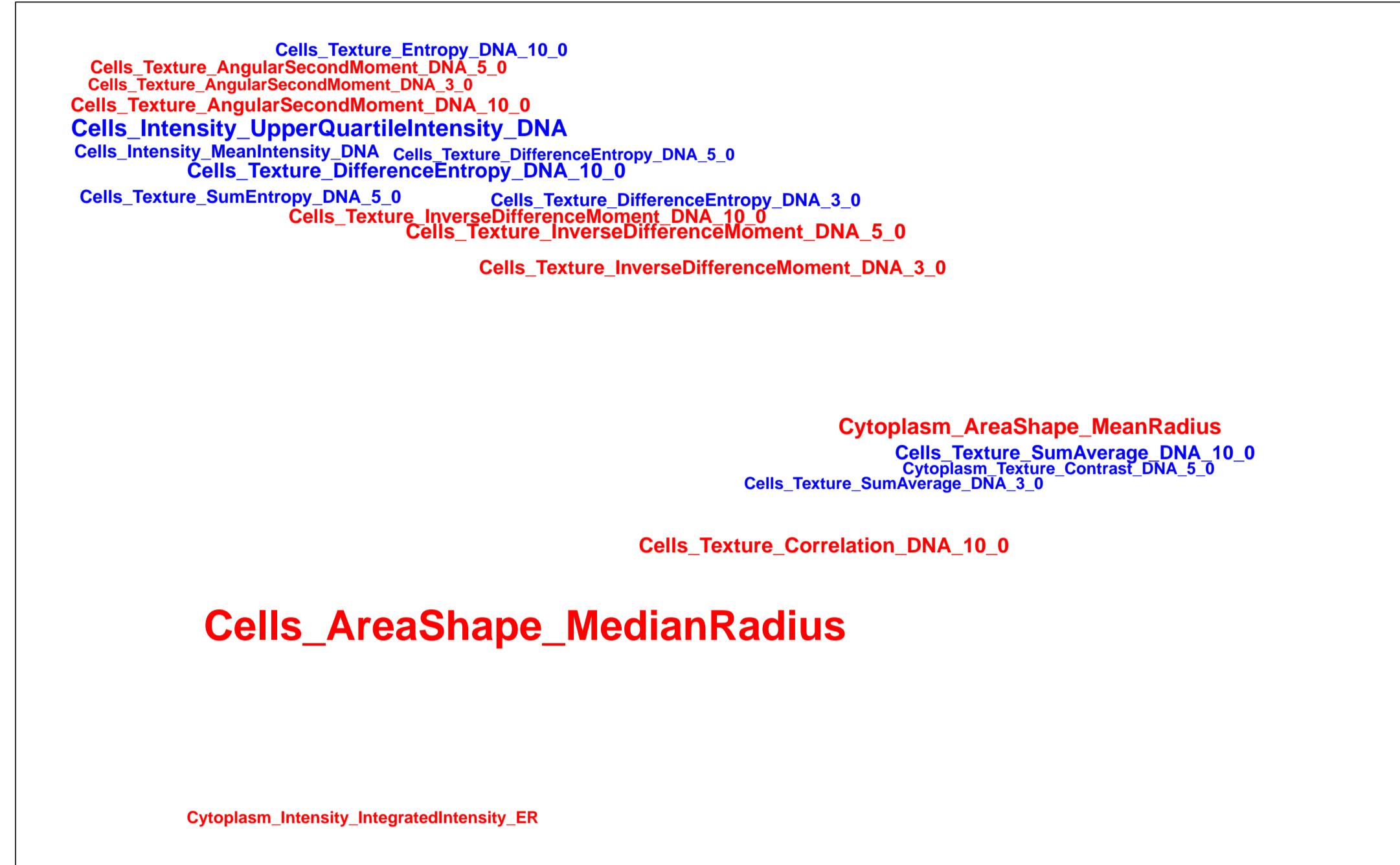
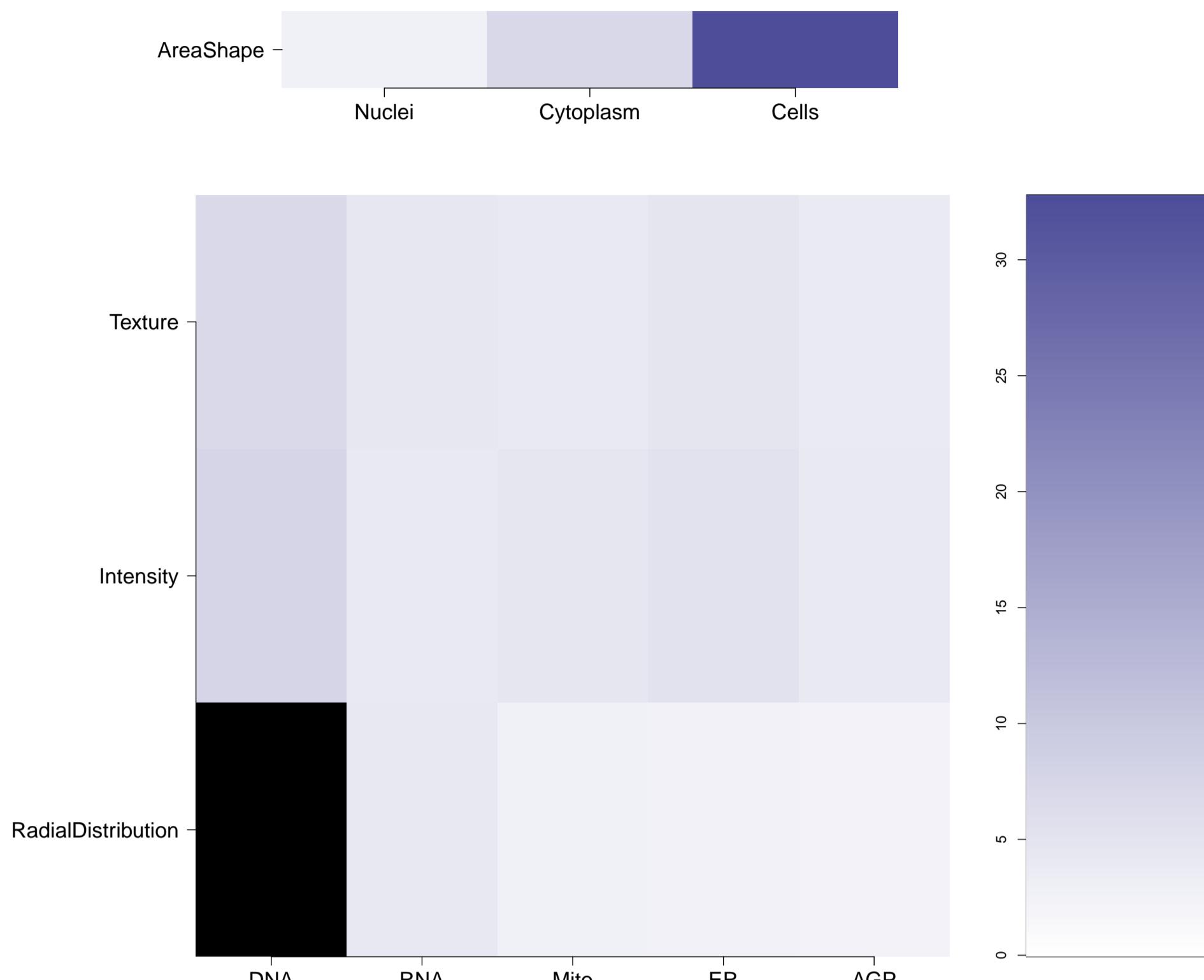


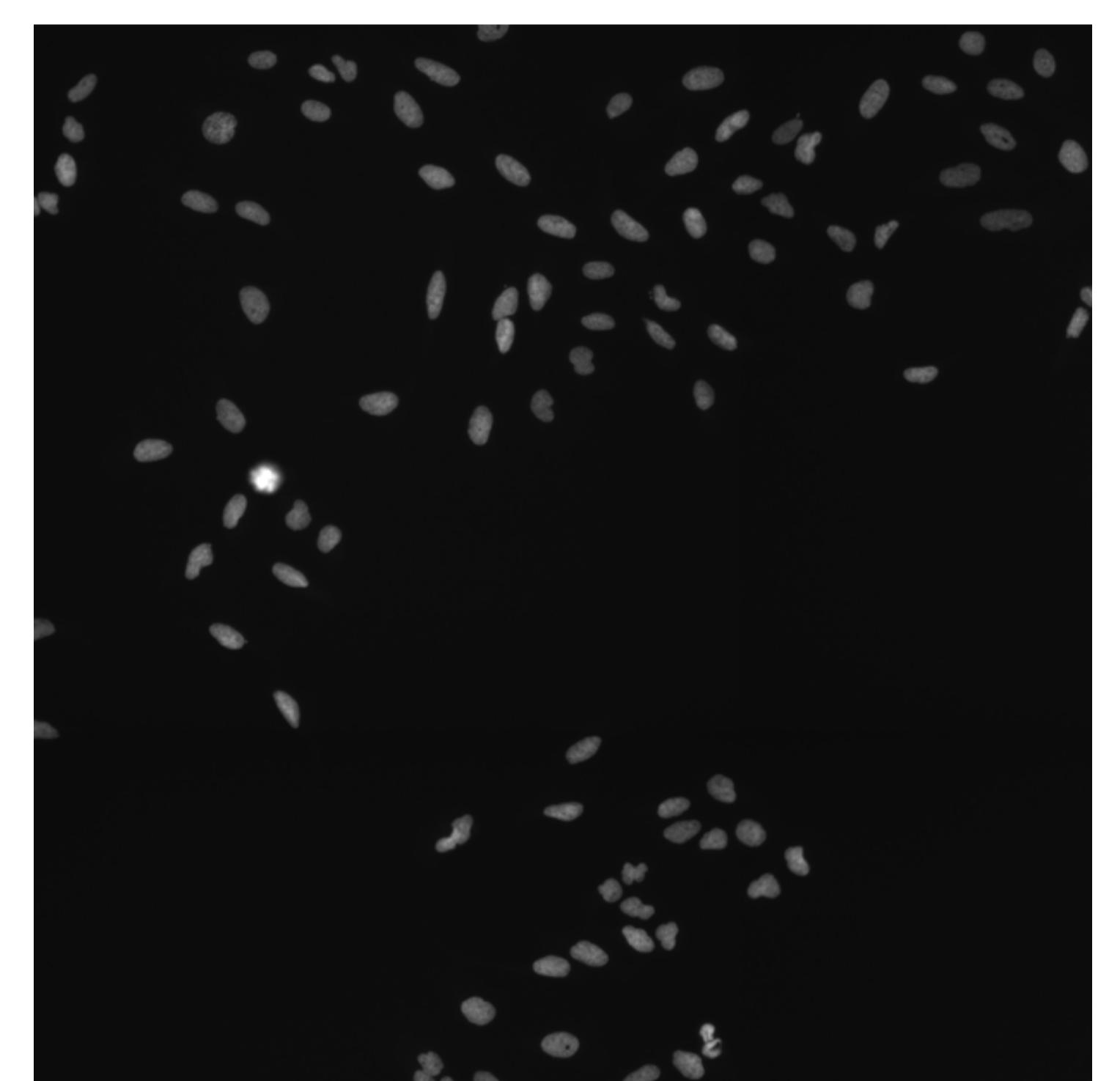
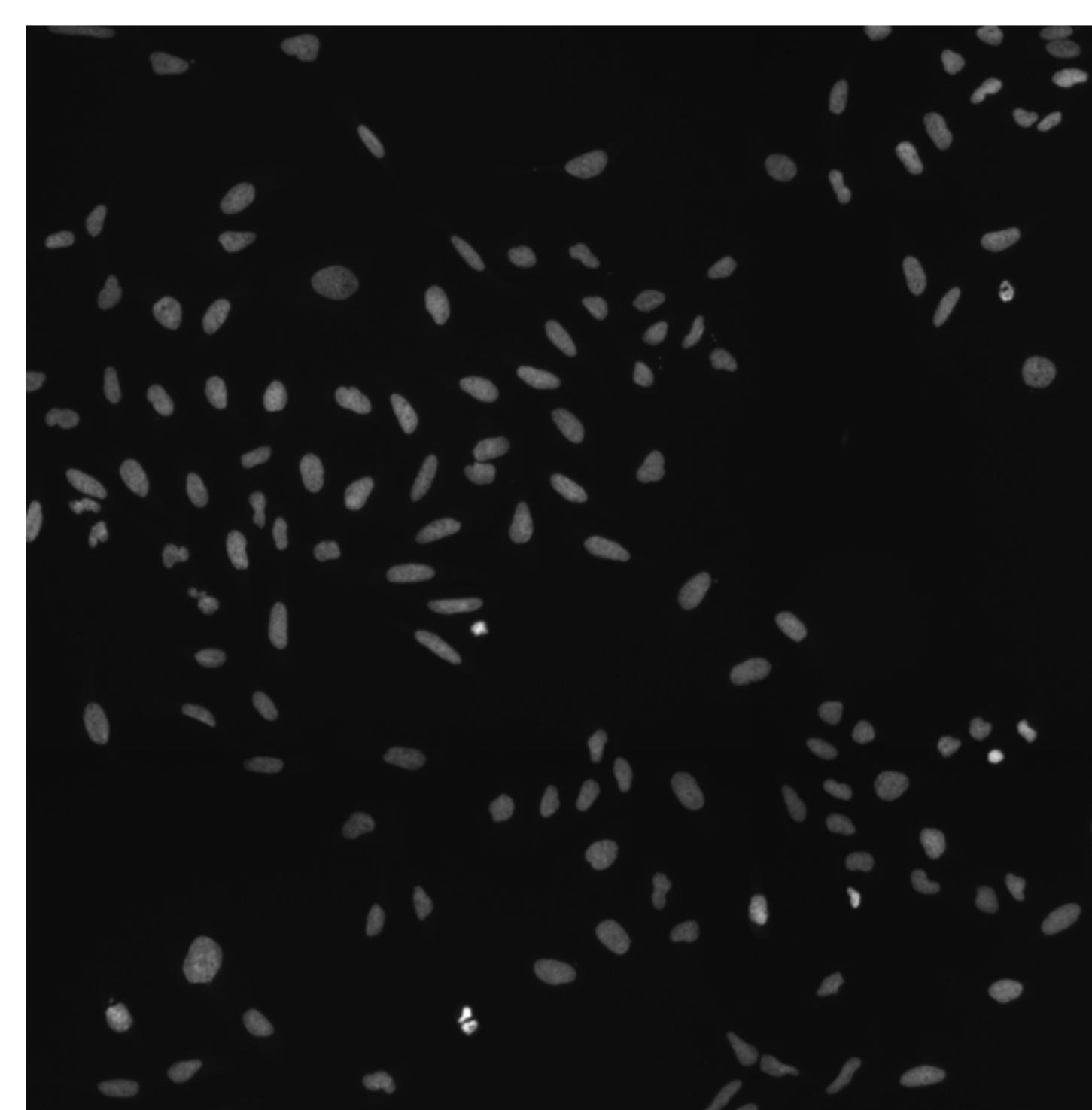
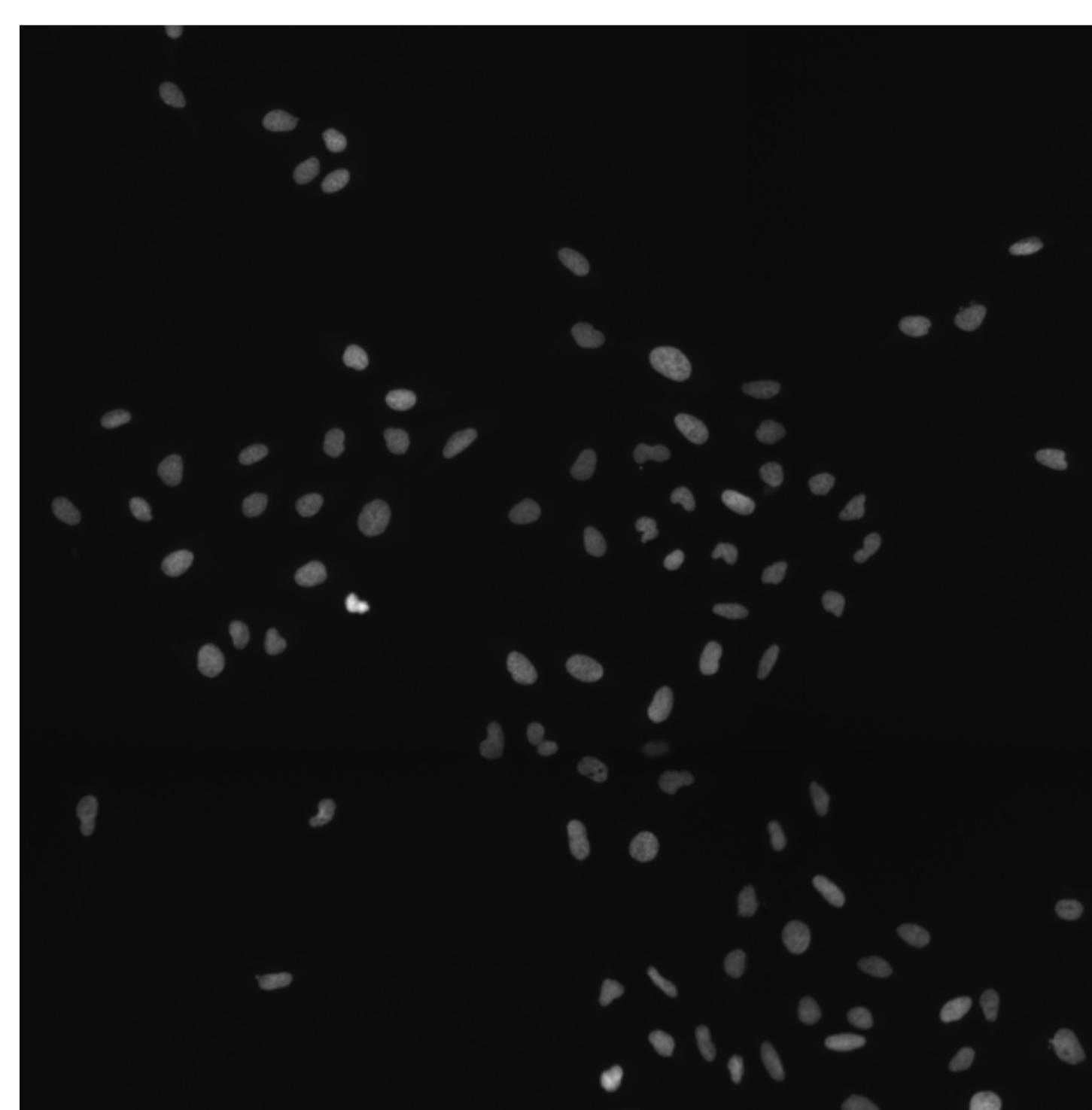
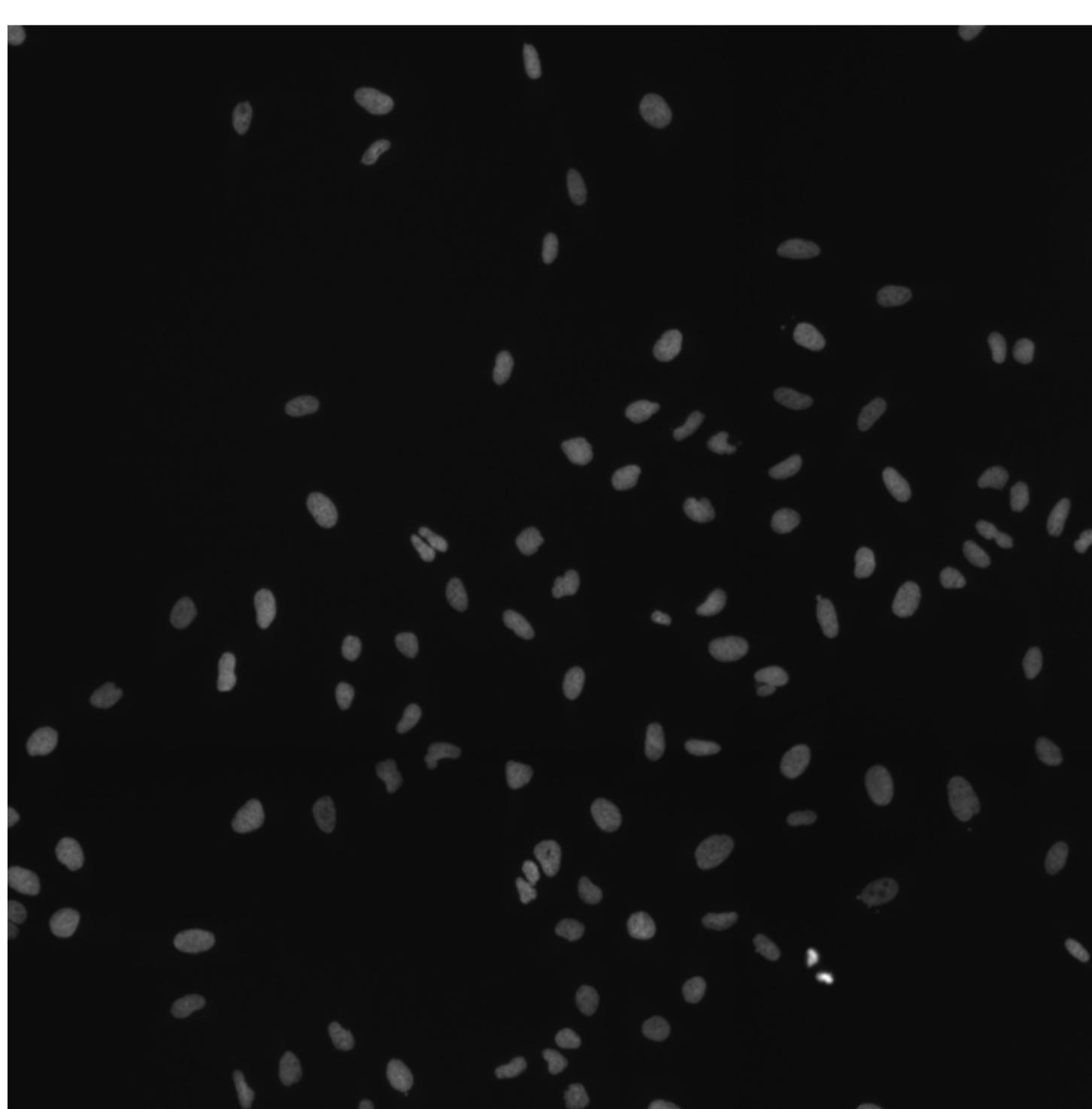
Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

CCND1_WT.1

CCND1_WT.2

E2F1_WT

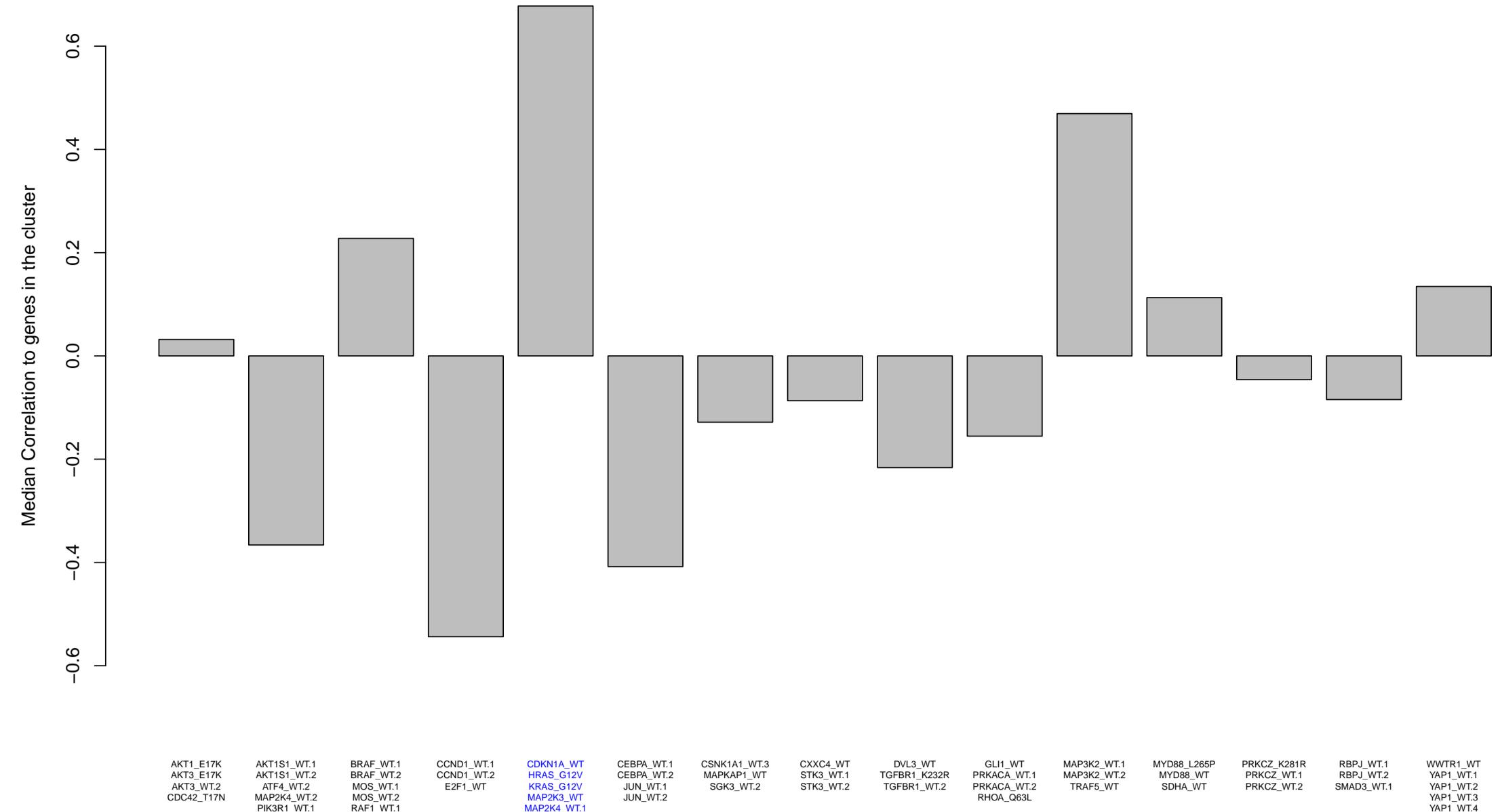
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DNA

RNA

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	



Top 5 genes negatively correlated to the cluster					
Treatment	Expert Annotation		Mean Correlation	Standard Deviation	
	Pathway	Regulation Type			
E2F1_WT	Canonical Cell Cycle	Activator	-0.59	0.09	
CCND1_WT.2	Canonical Cell Cycle	Activator	-0.58	0.08	
CDK2_WT.1	Canonical Cell Cycle	Activator	-0.49	0.11	
DDIT4_WT	Canonical TOR	Inhibitor	-0.49	0.07	
PER1_WT.2	Circadian Rhythm	Activator	-0.49	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?

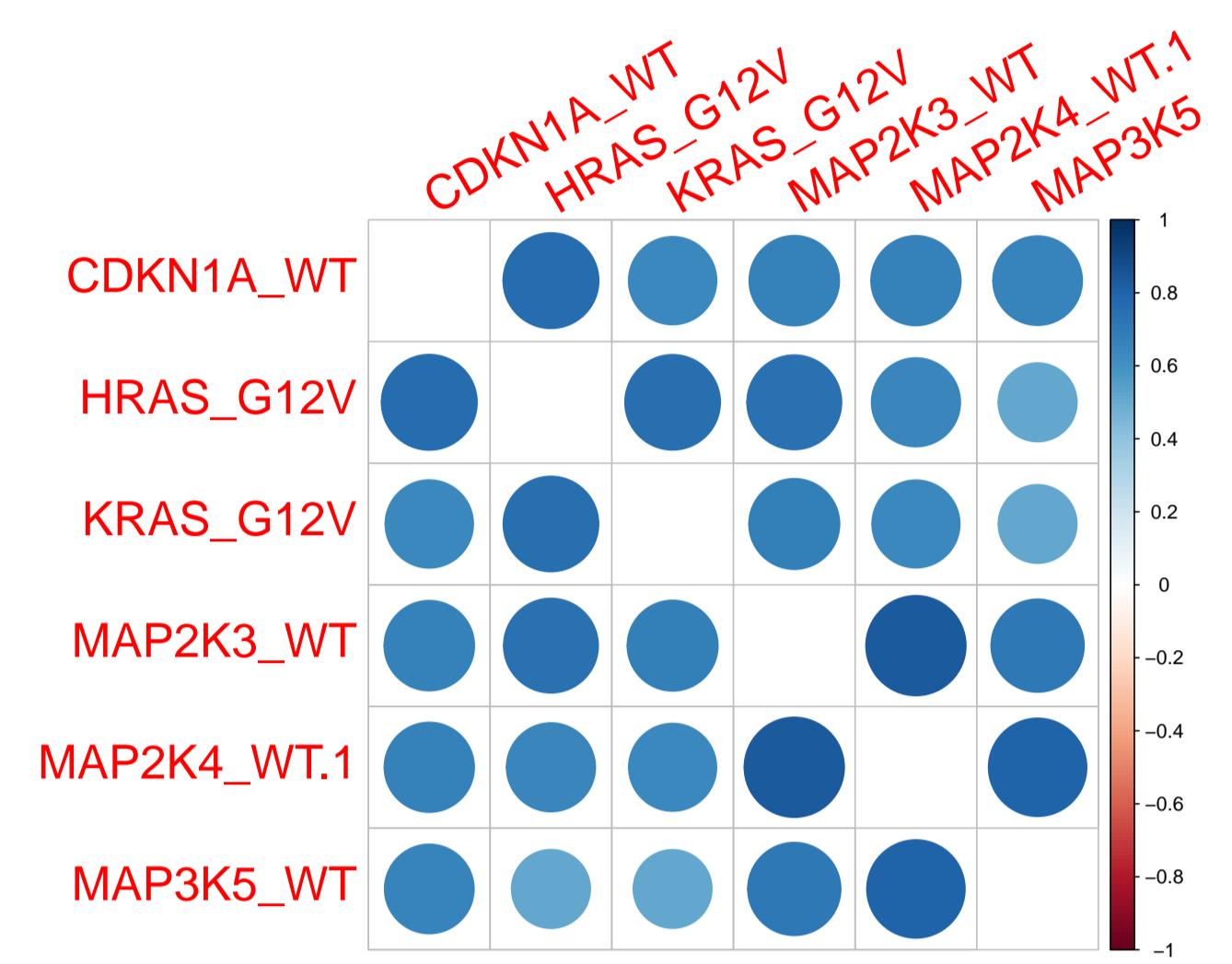
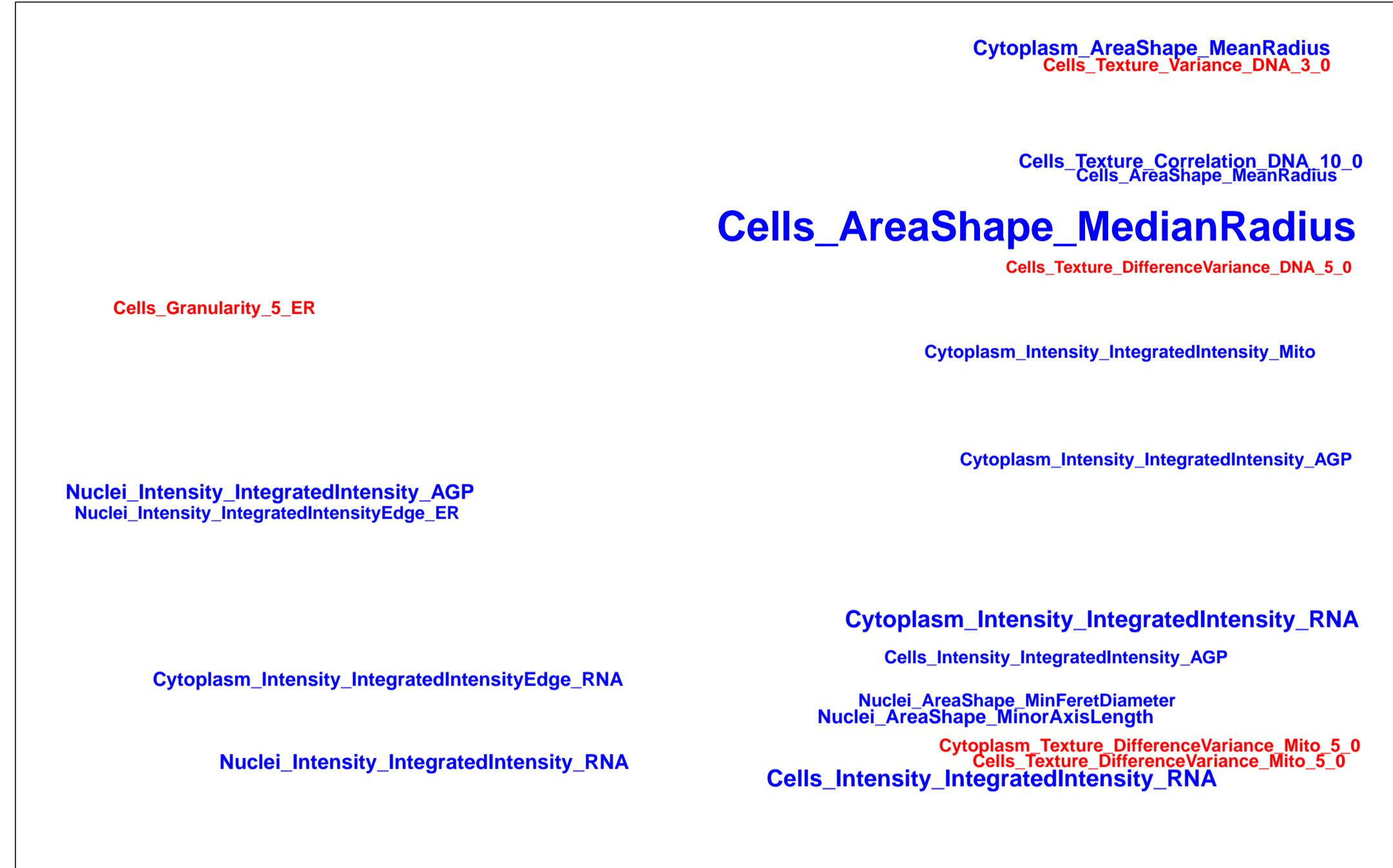
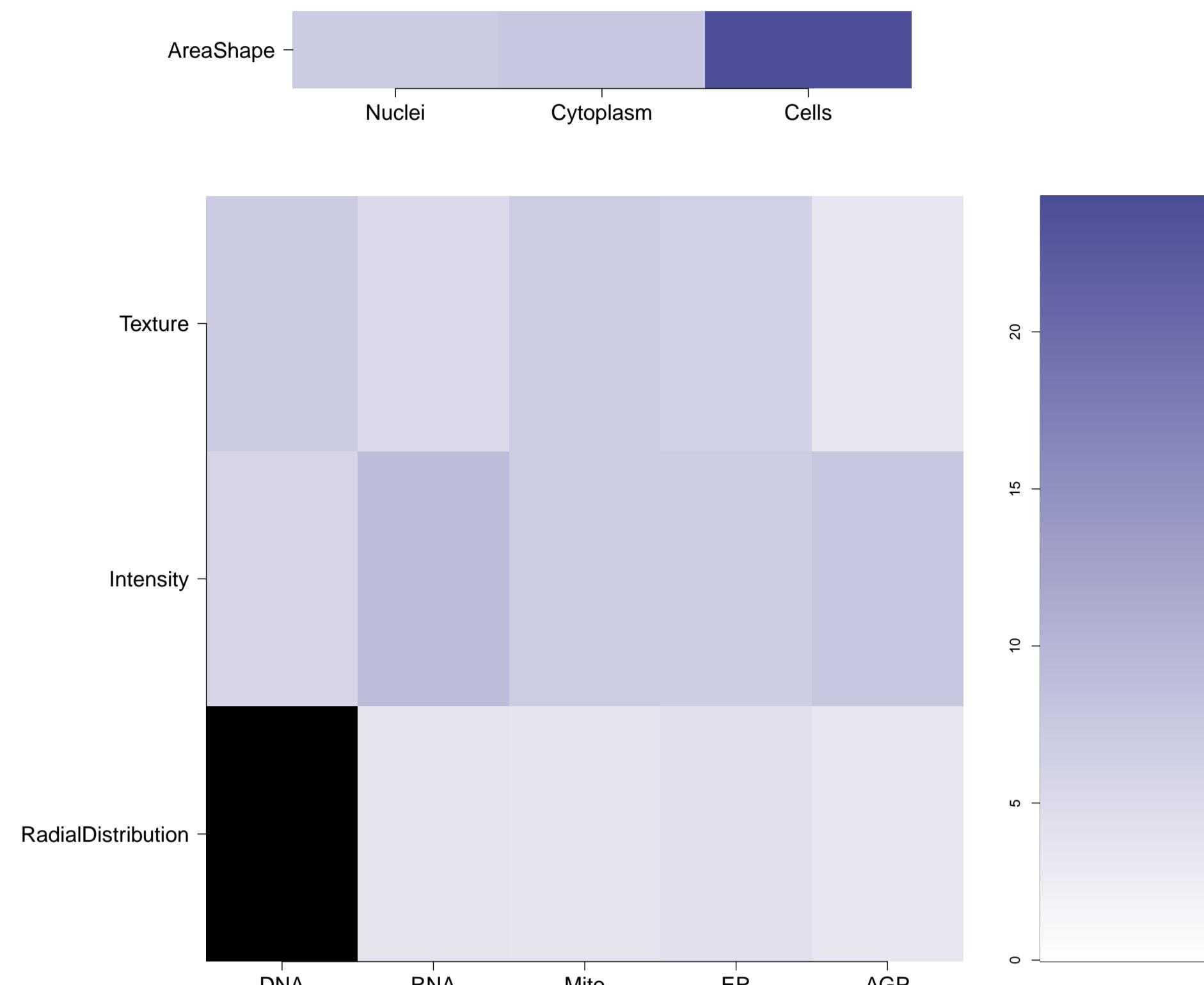


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

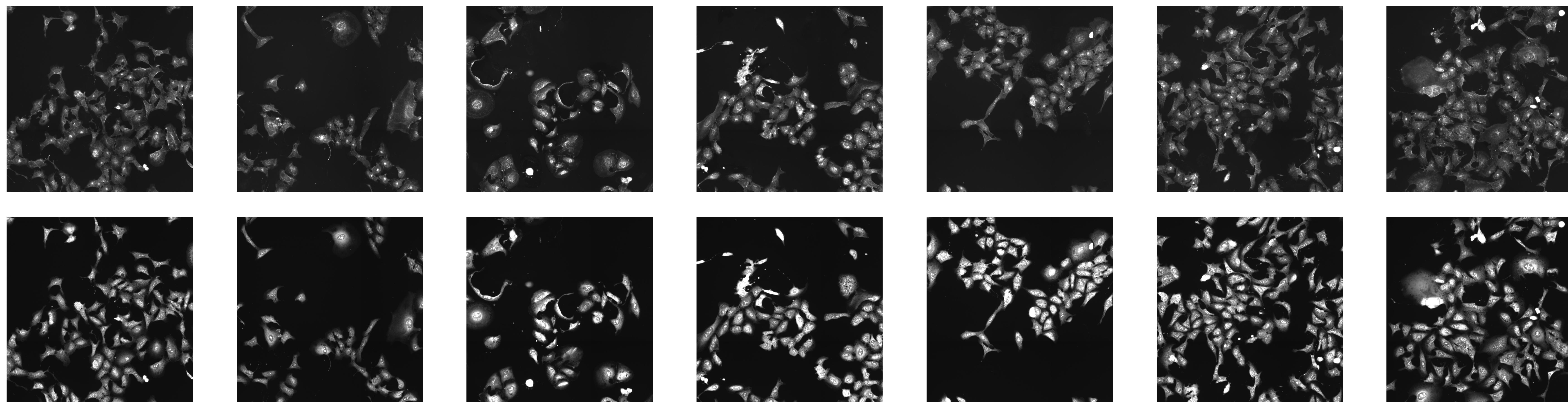
HRAS_G12V

KRAS_G12V

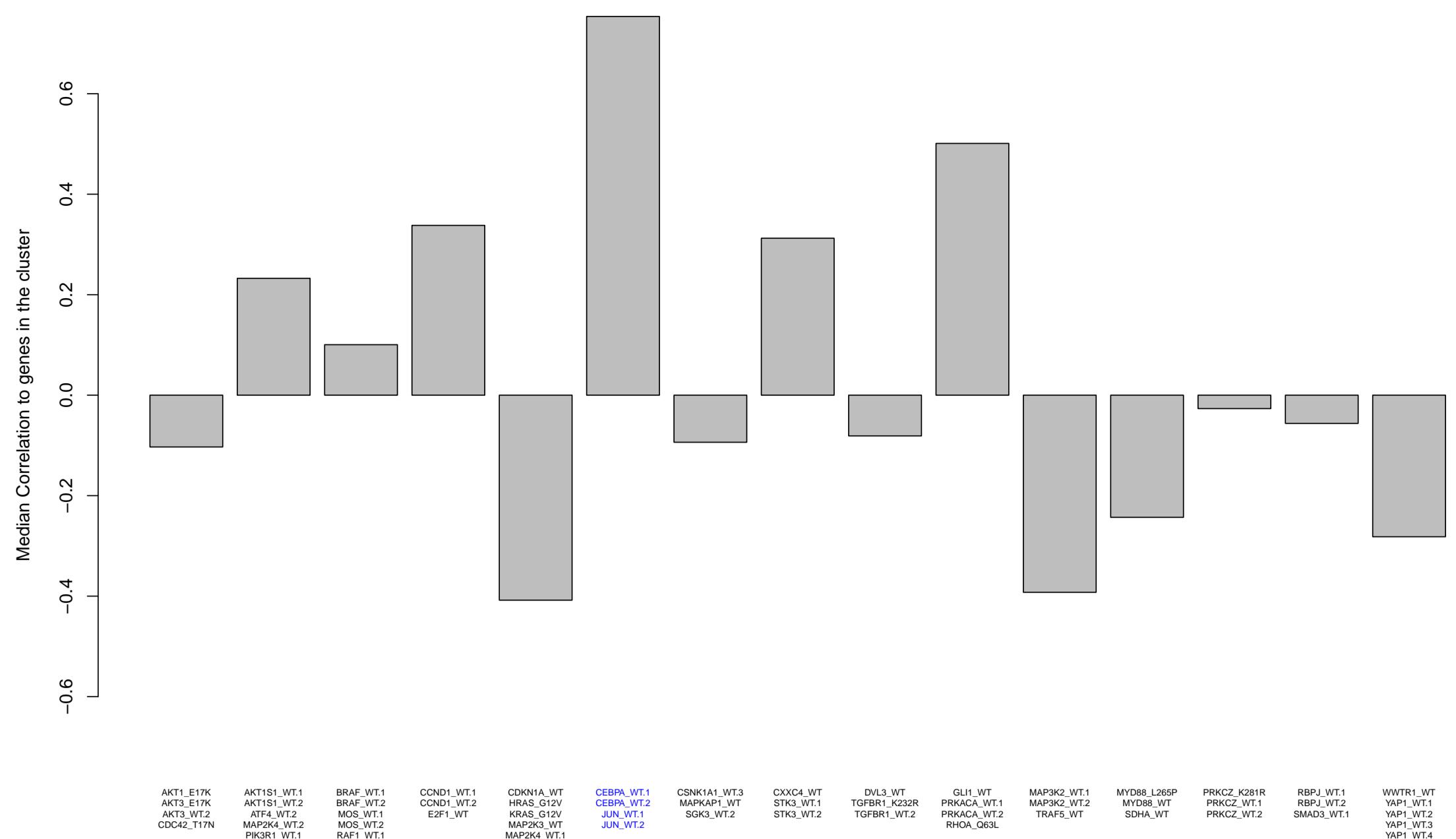
MAP2K3_WT

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	
PKA_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?

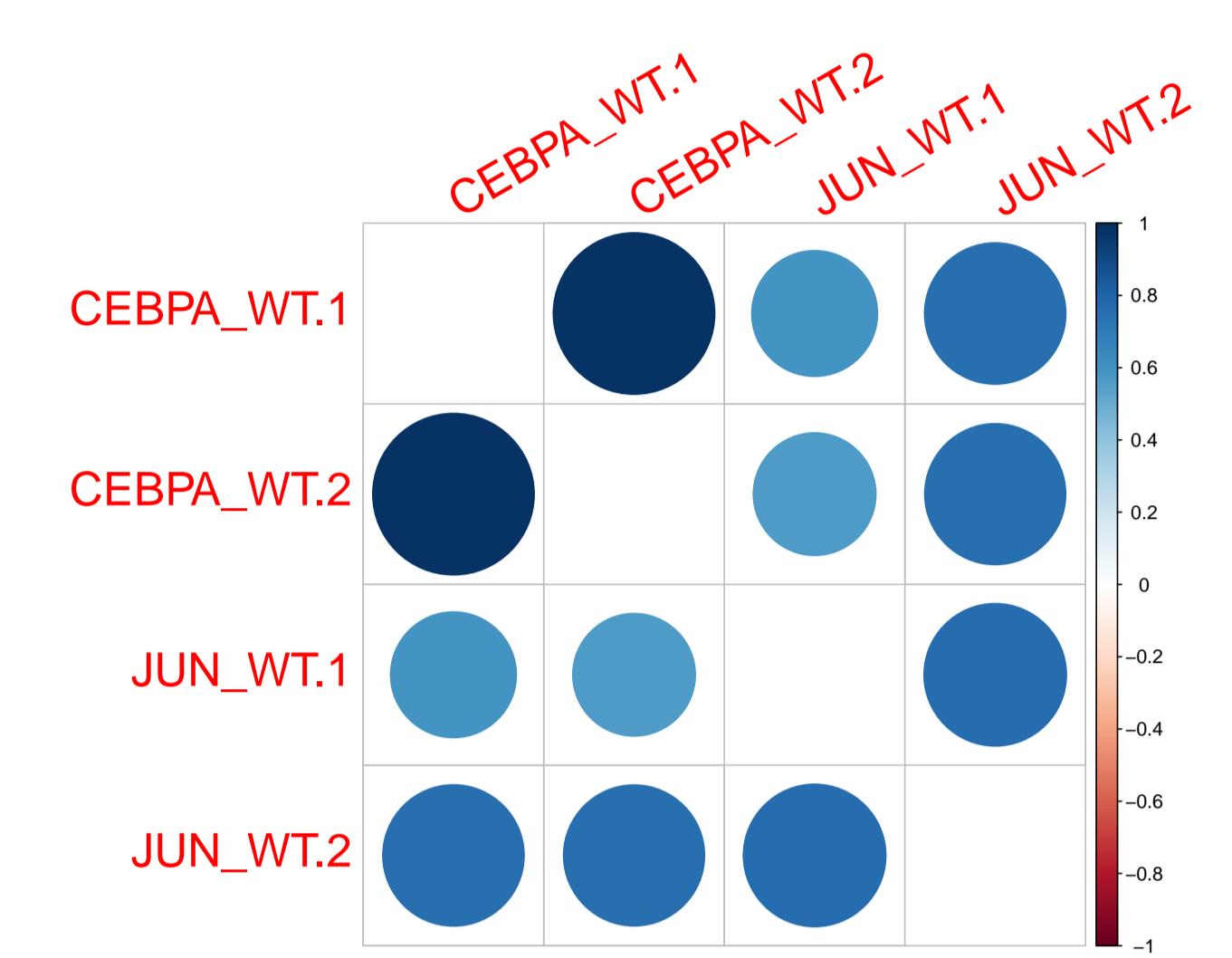
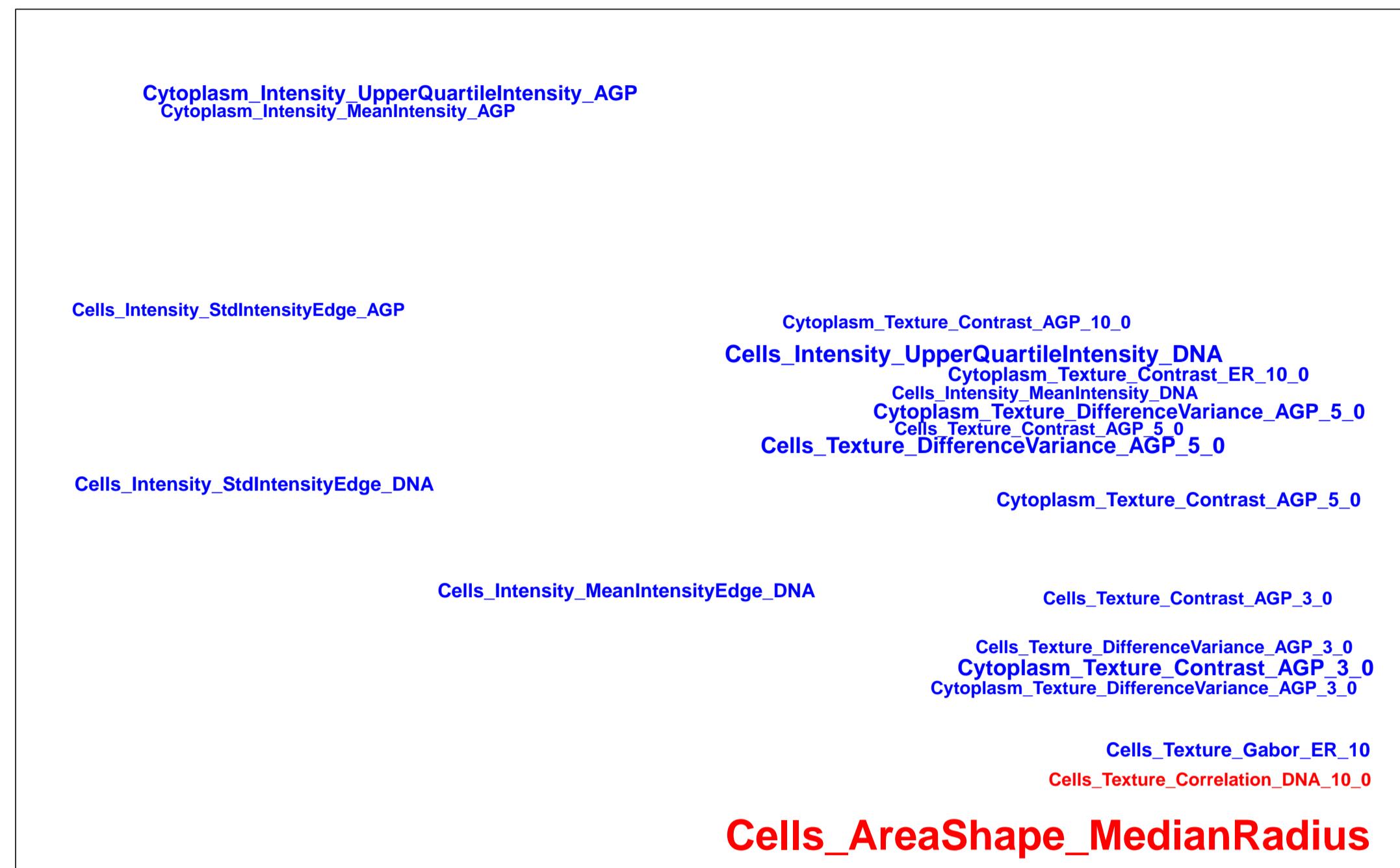
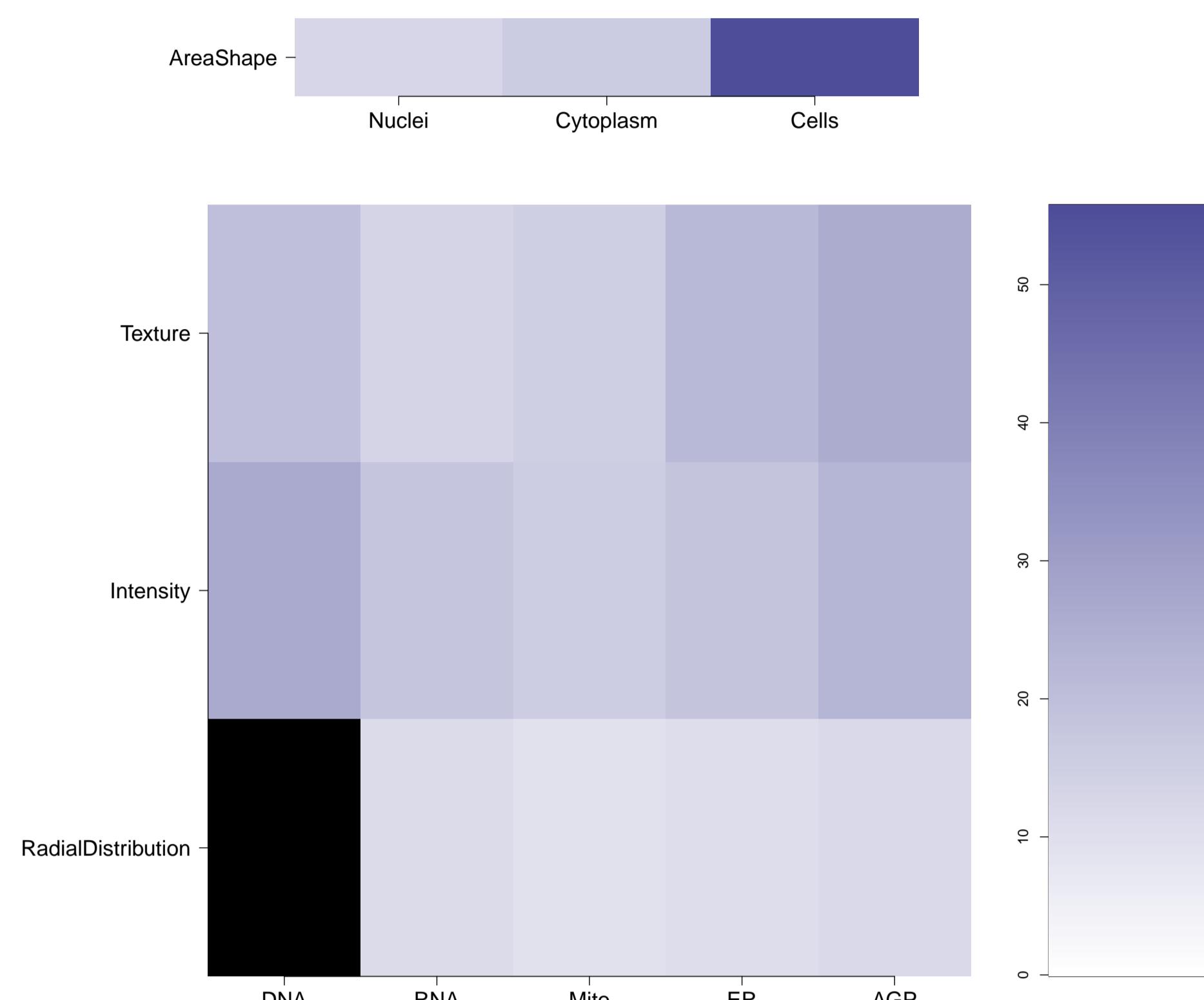


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

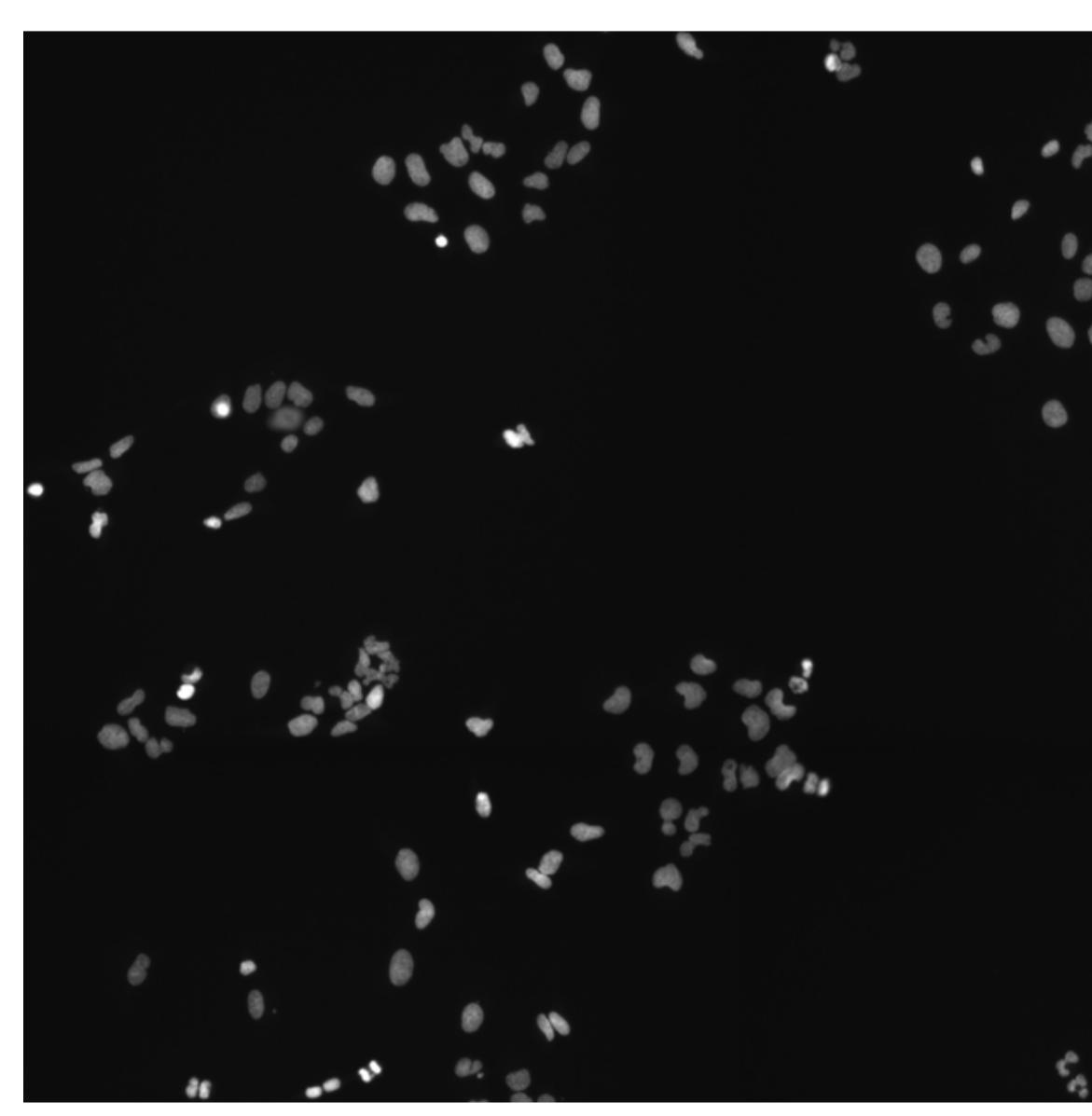
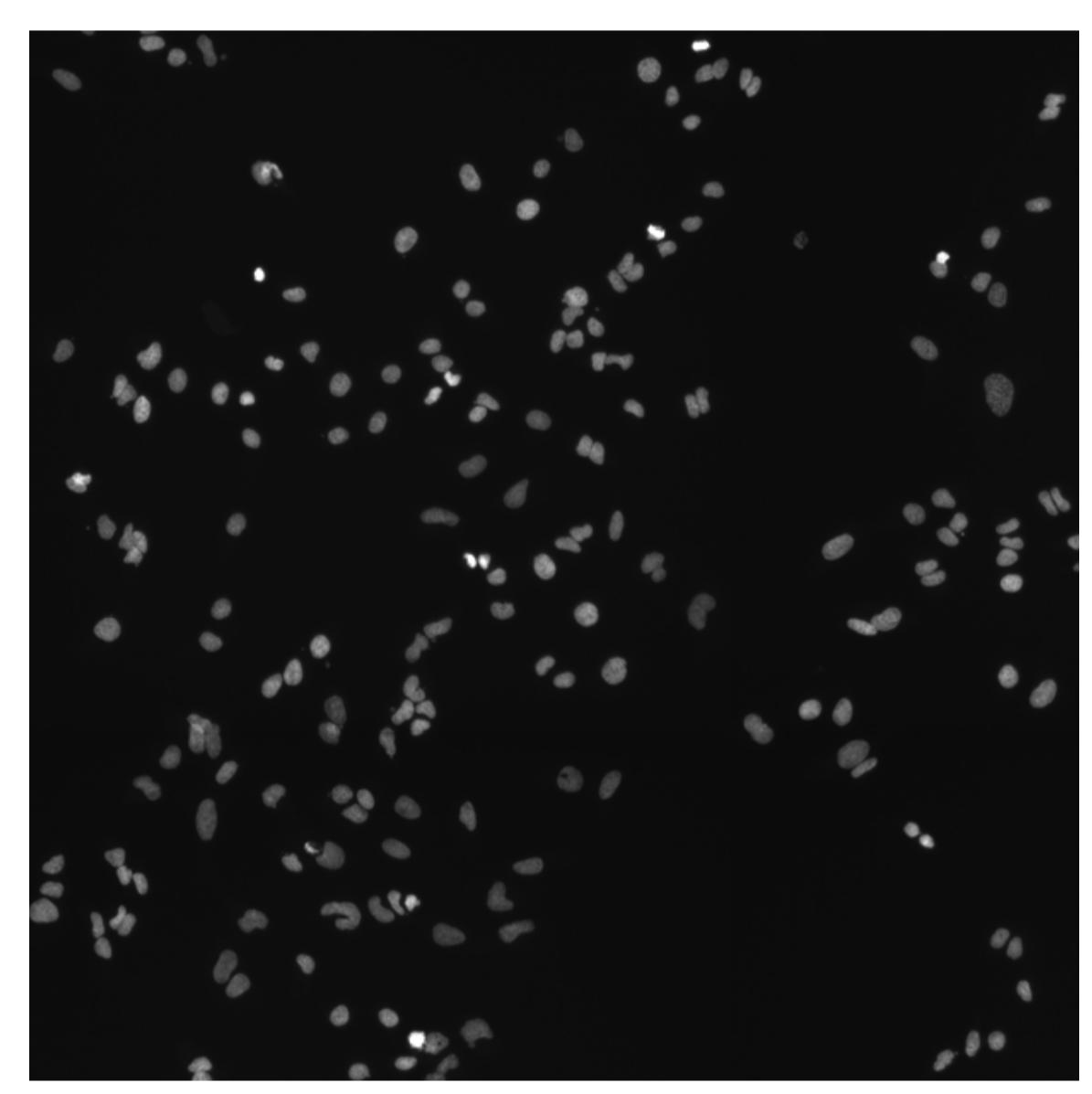
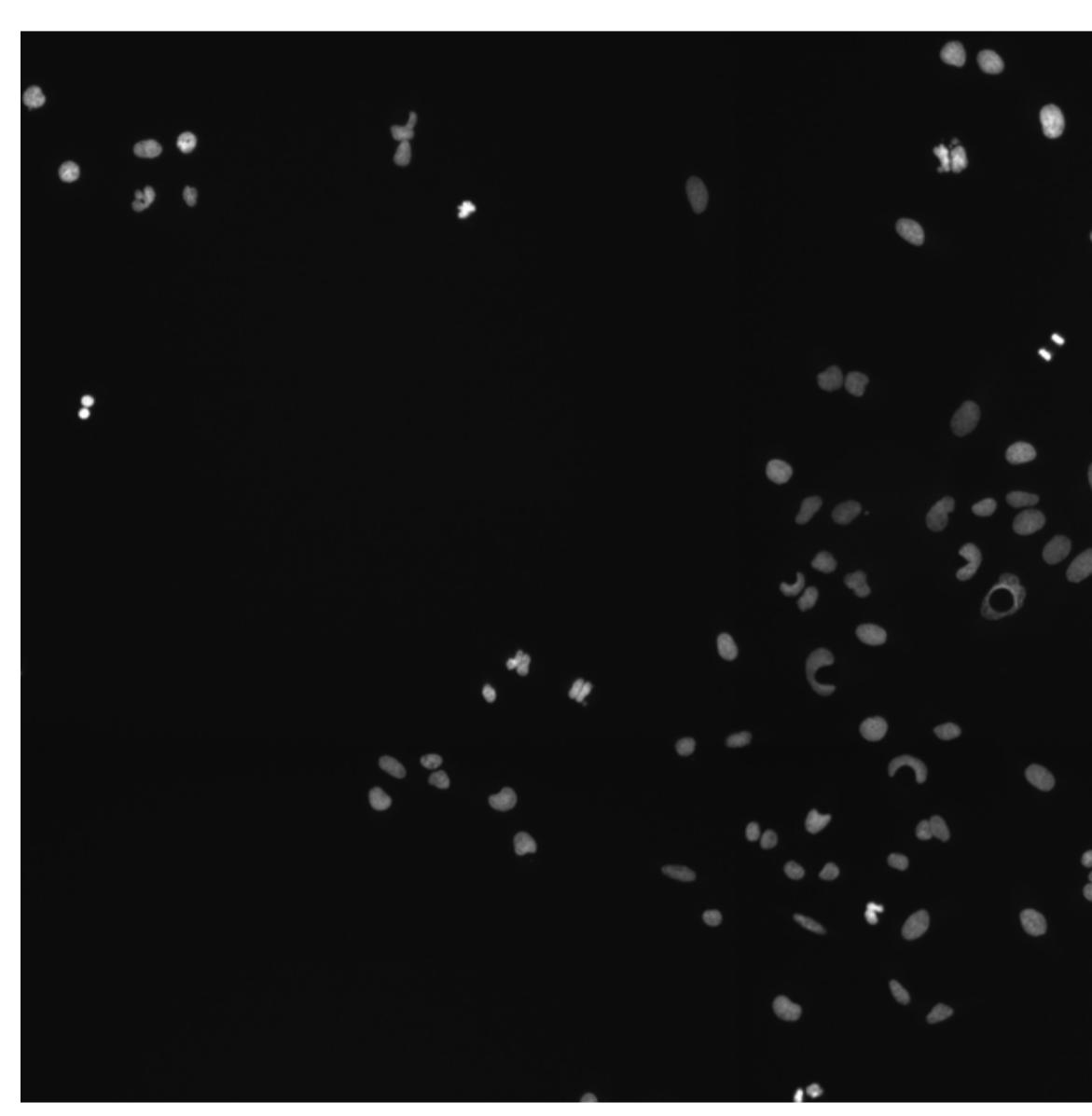
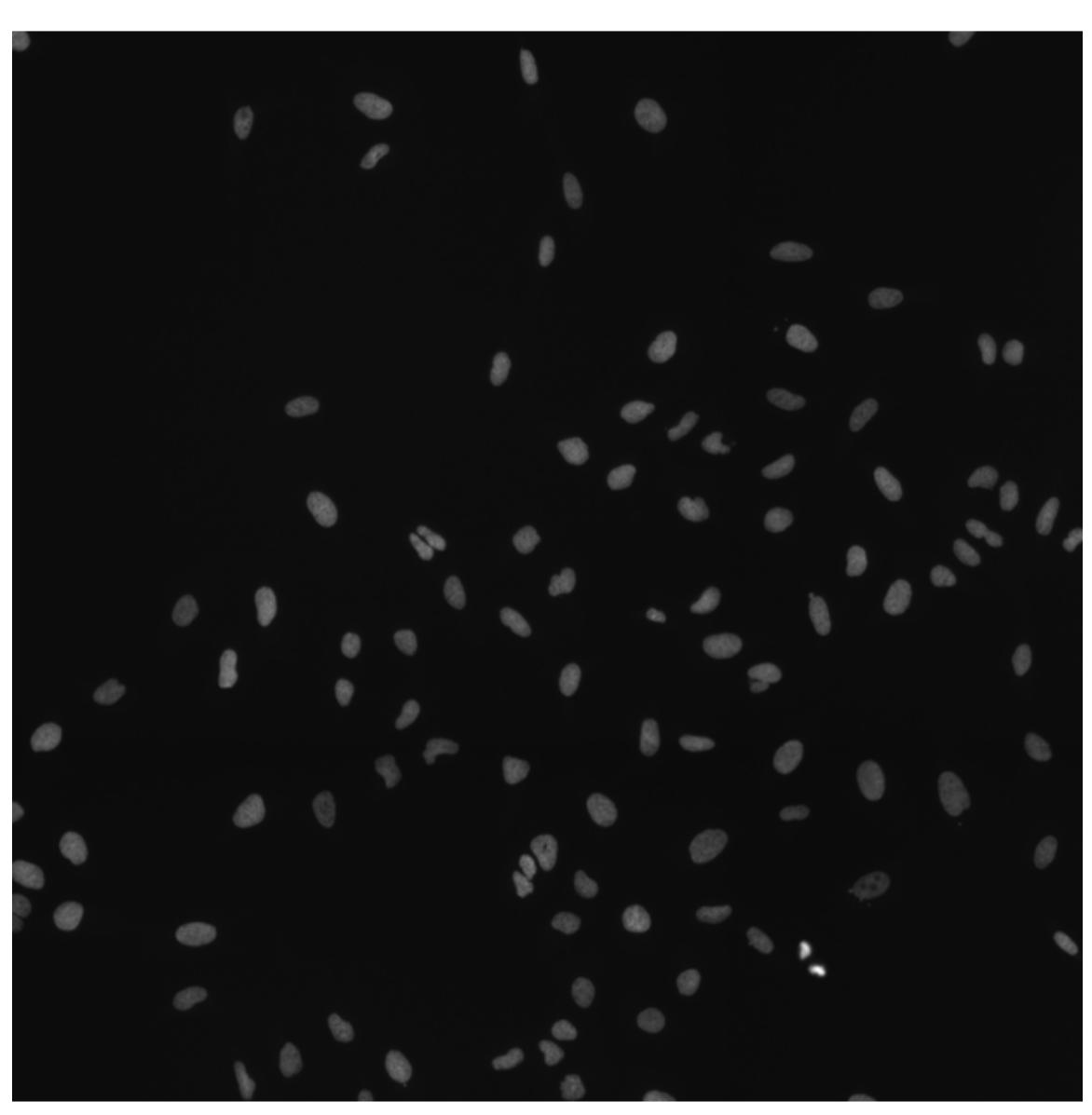
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CEBPA_WT.1

CEBPA_WT.2

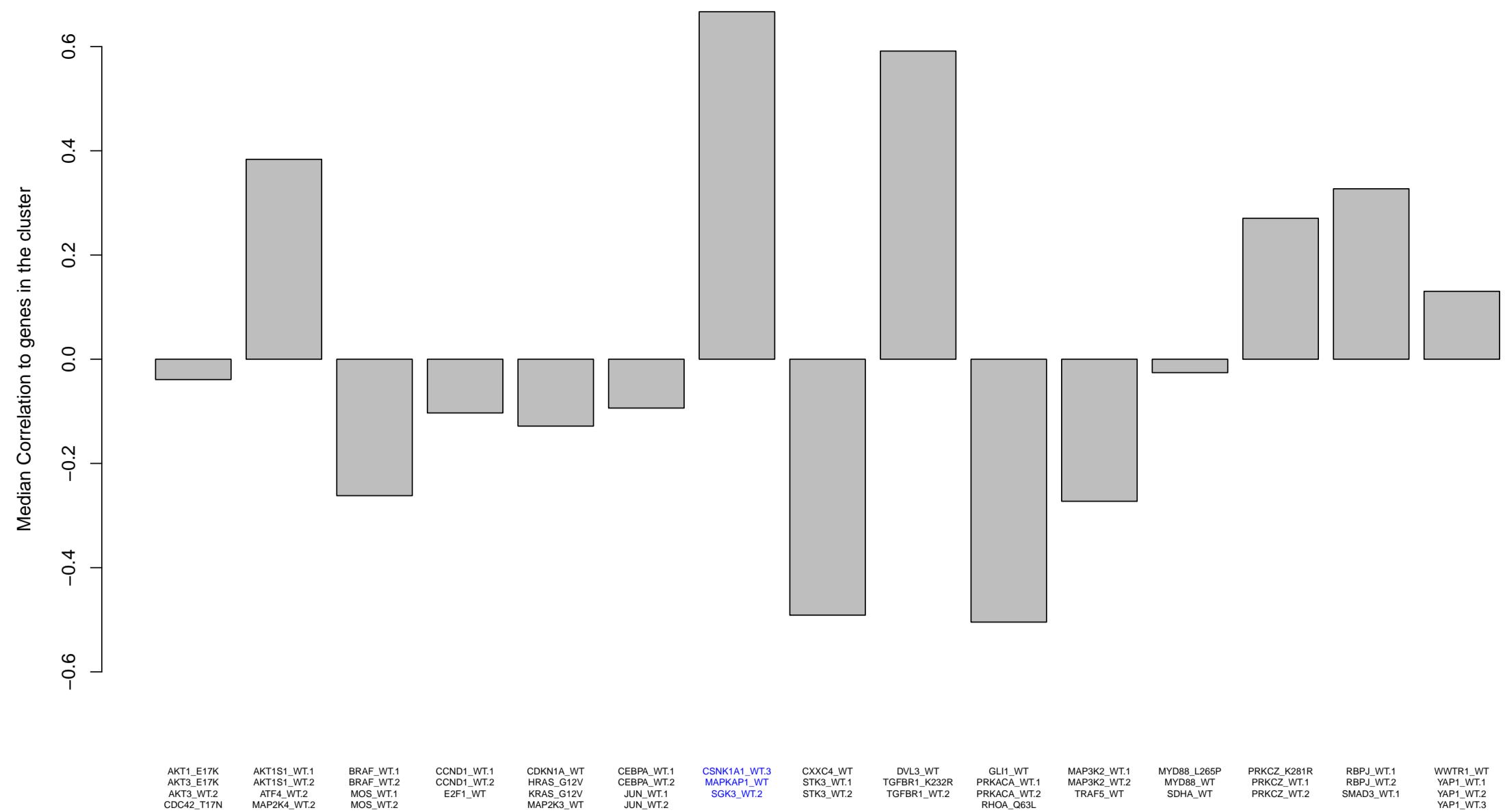
JUN_WT.1

JUN_WT.2



Cluster 7

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	



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

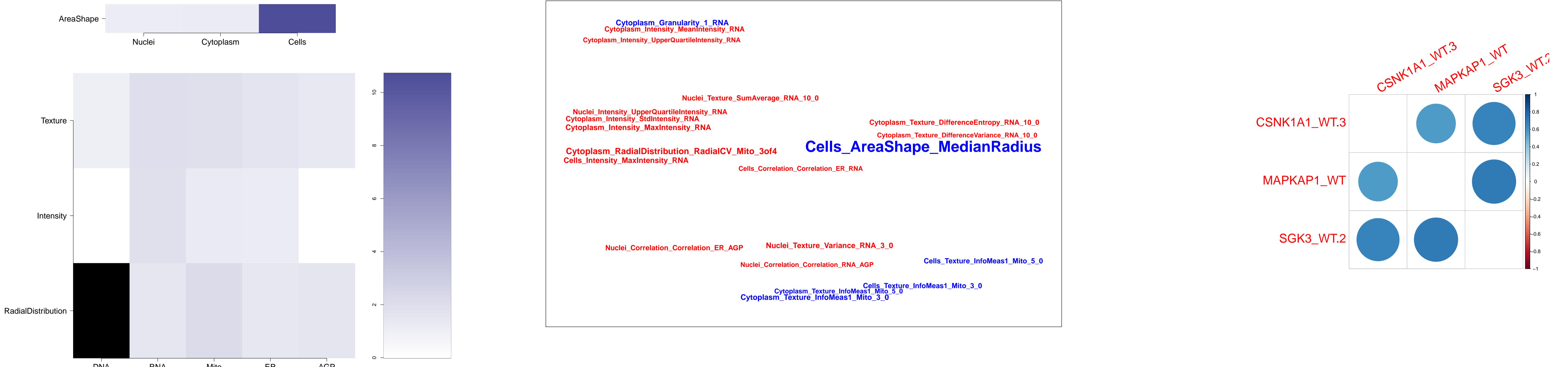
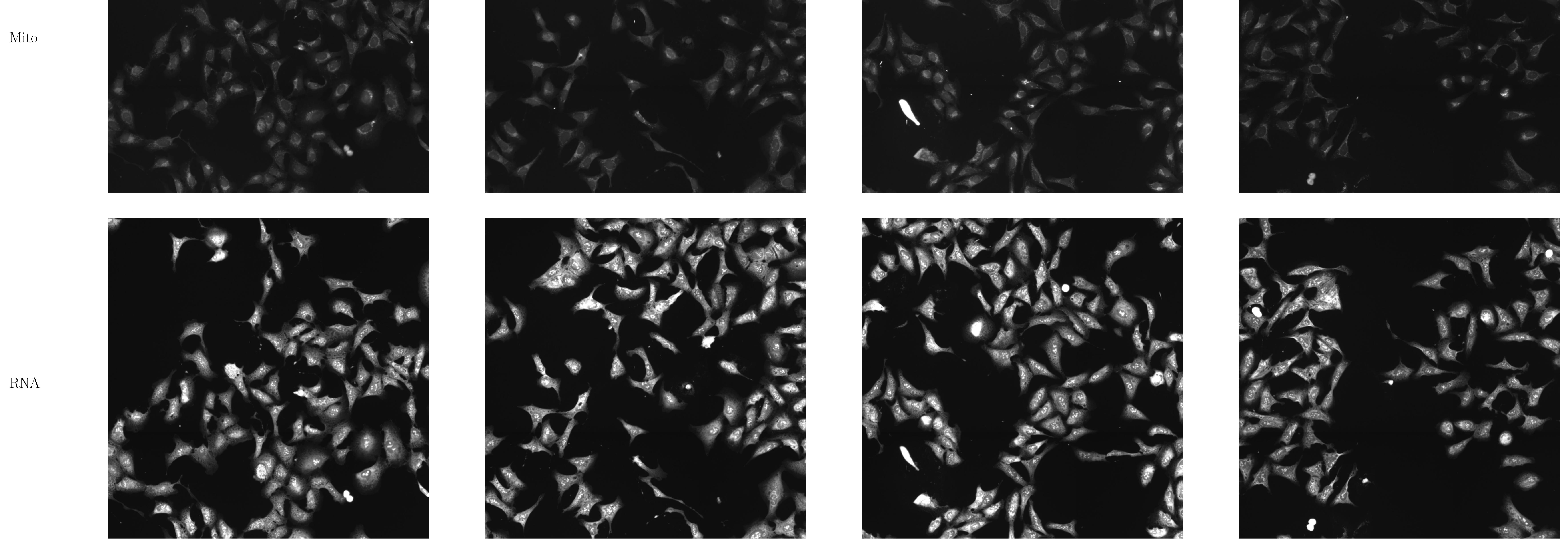


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

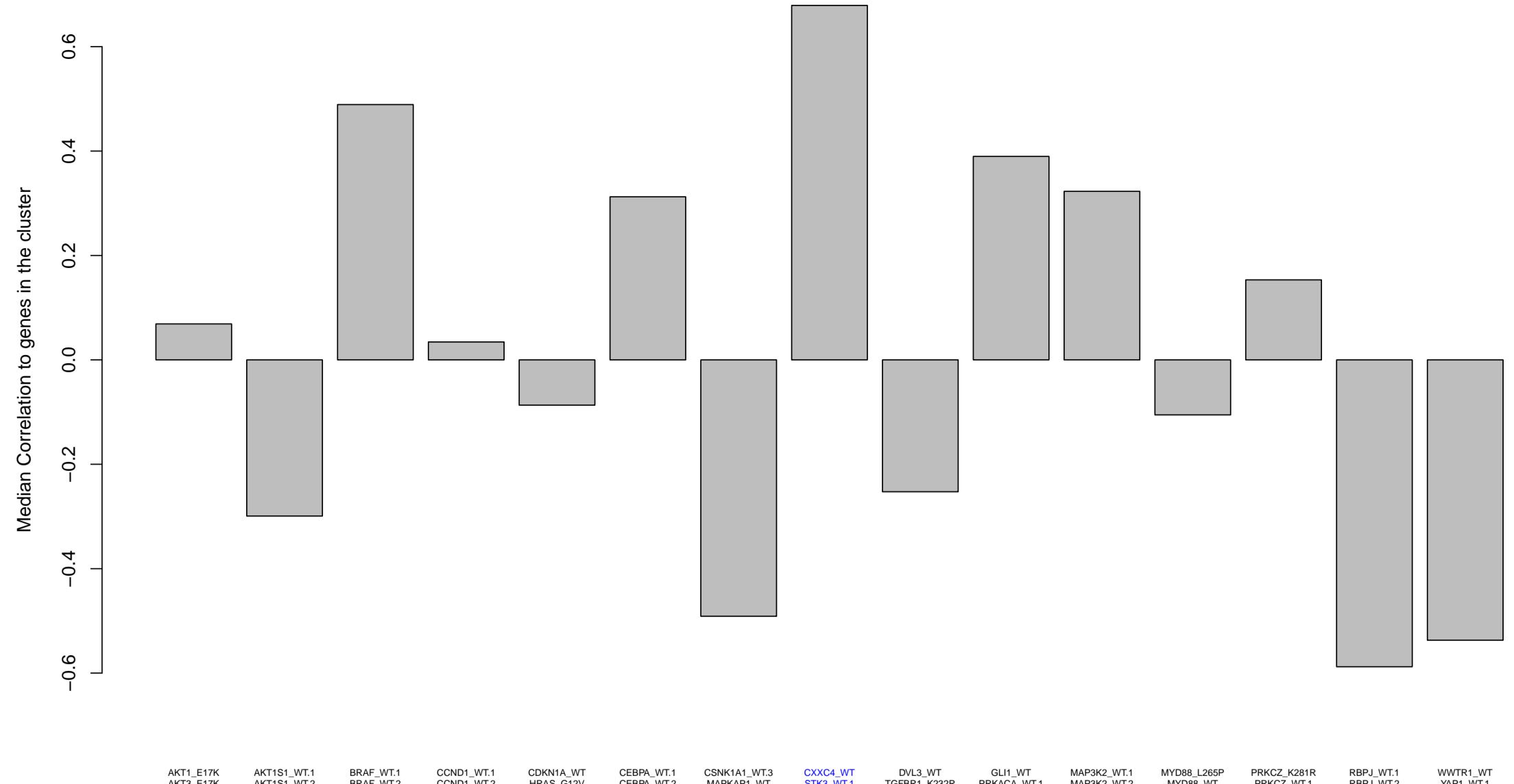
CSNK1A1_WT.3

MAPKAP1_WT

SGK3_WT.2



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?

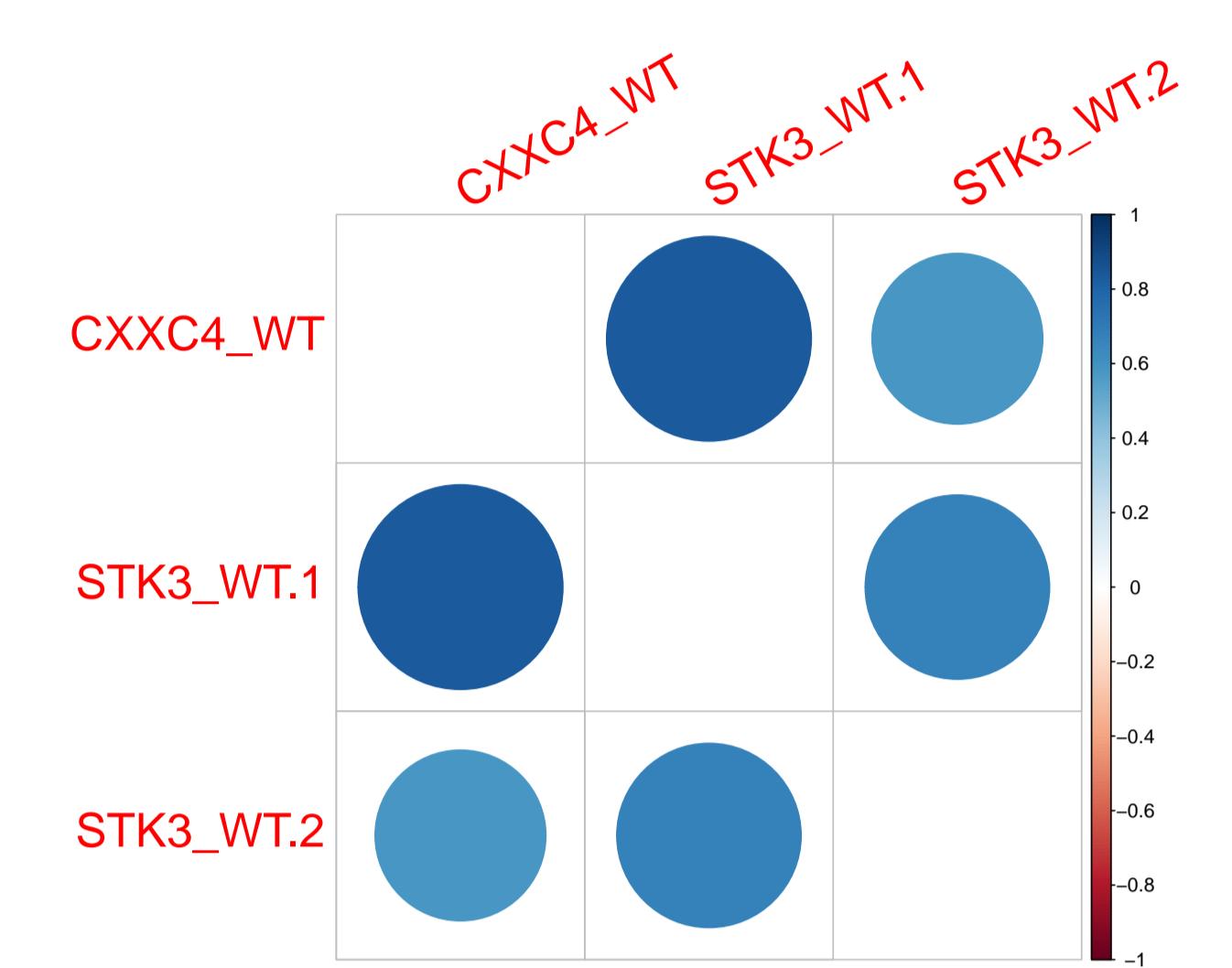
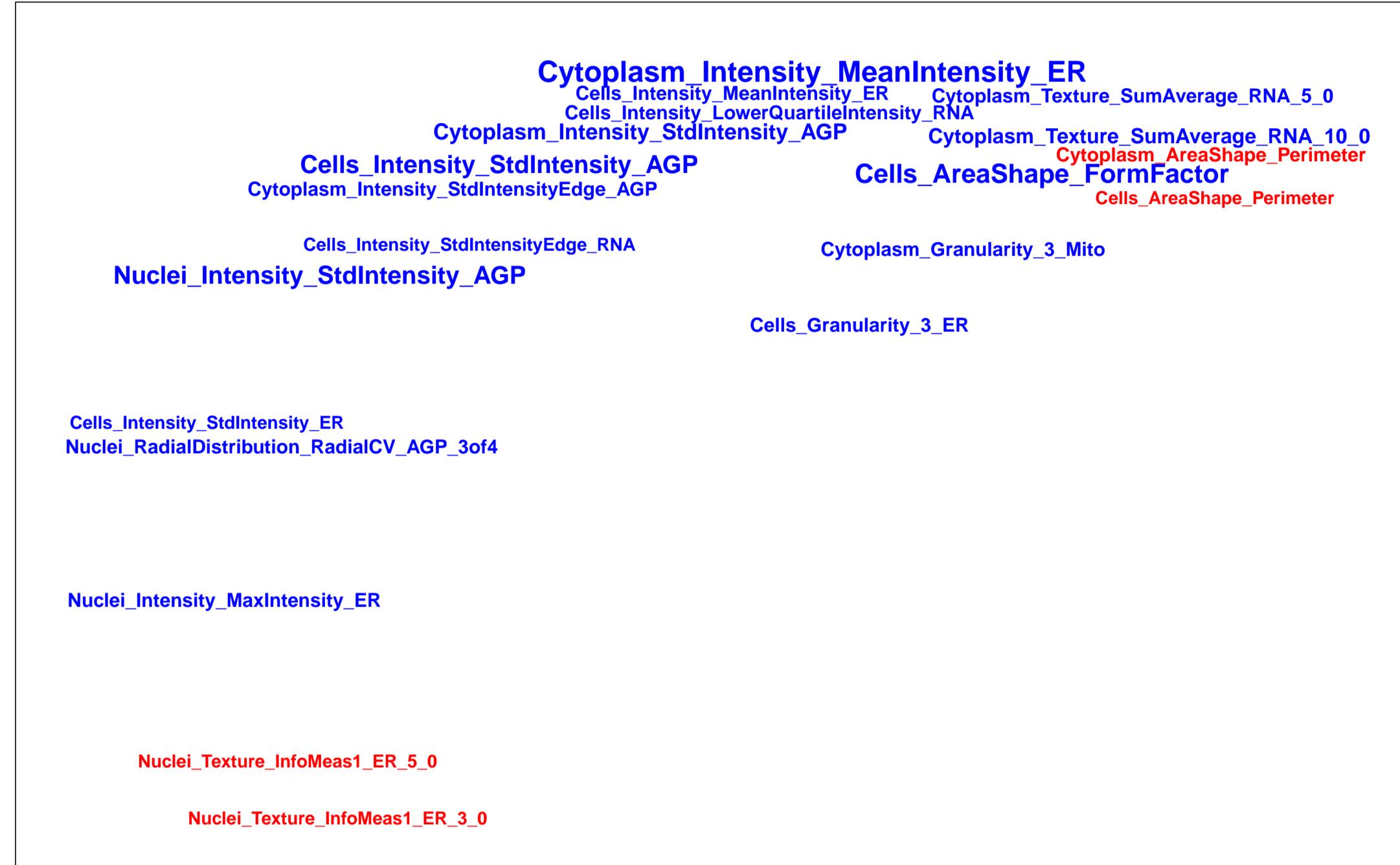
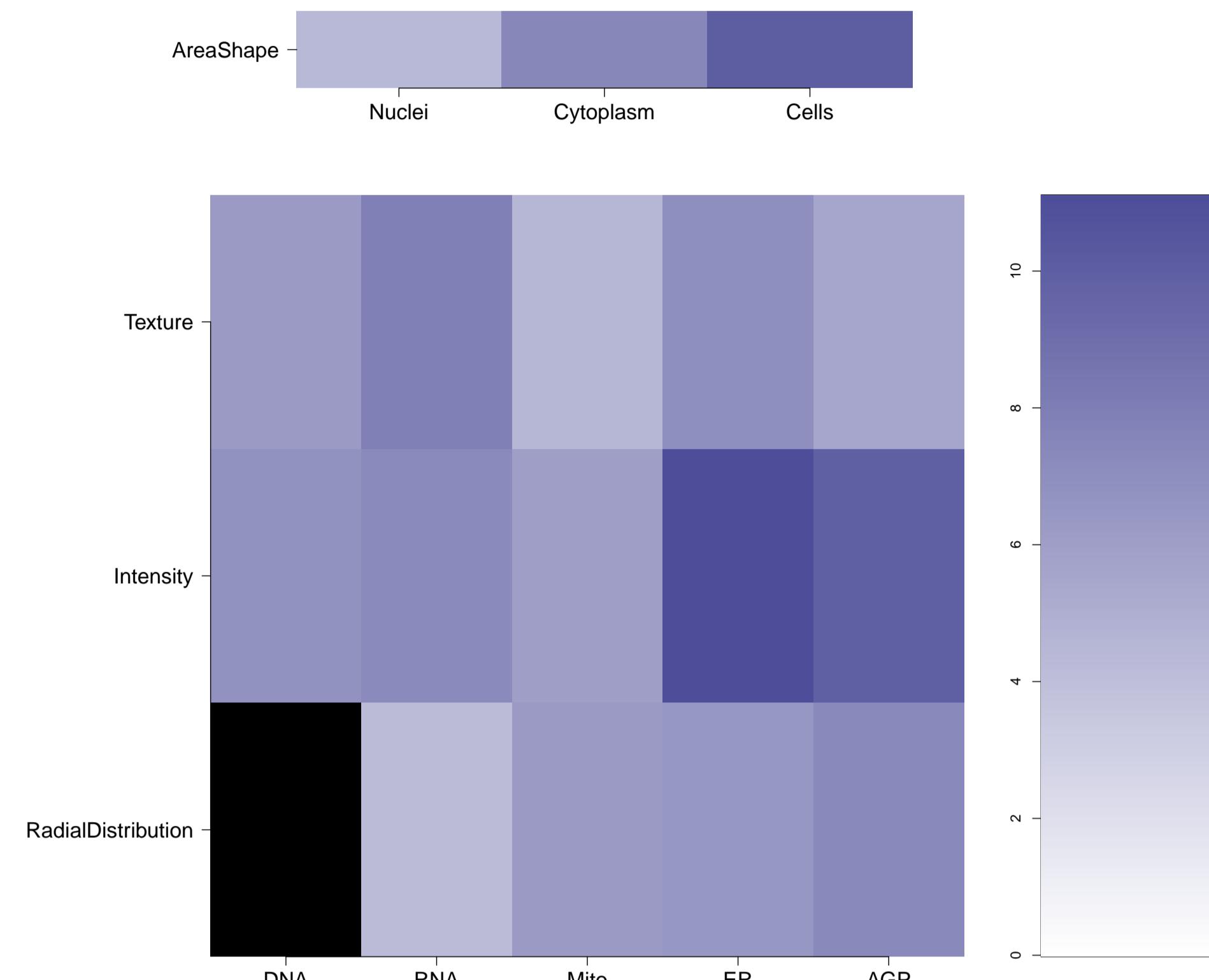
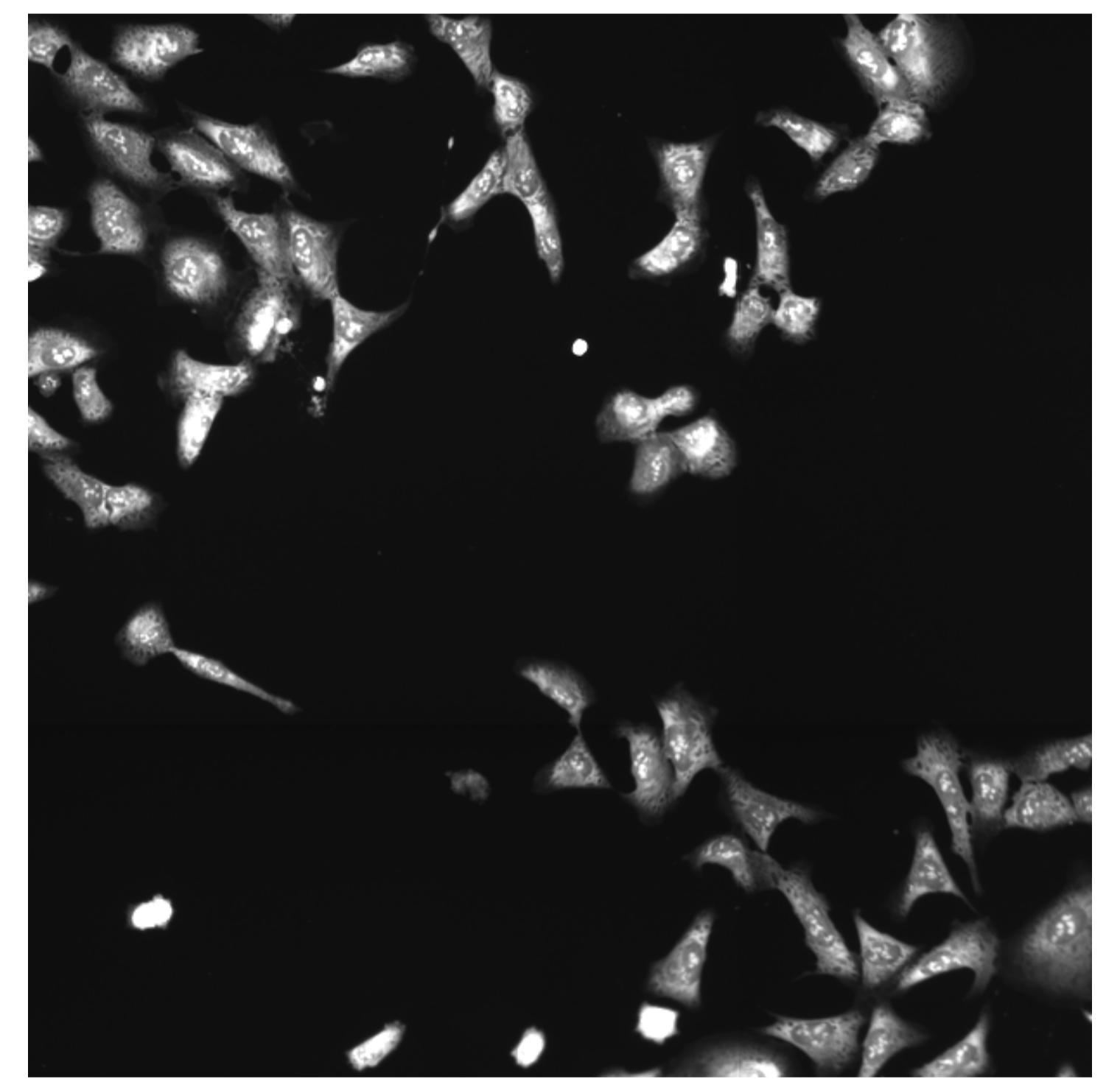
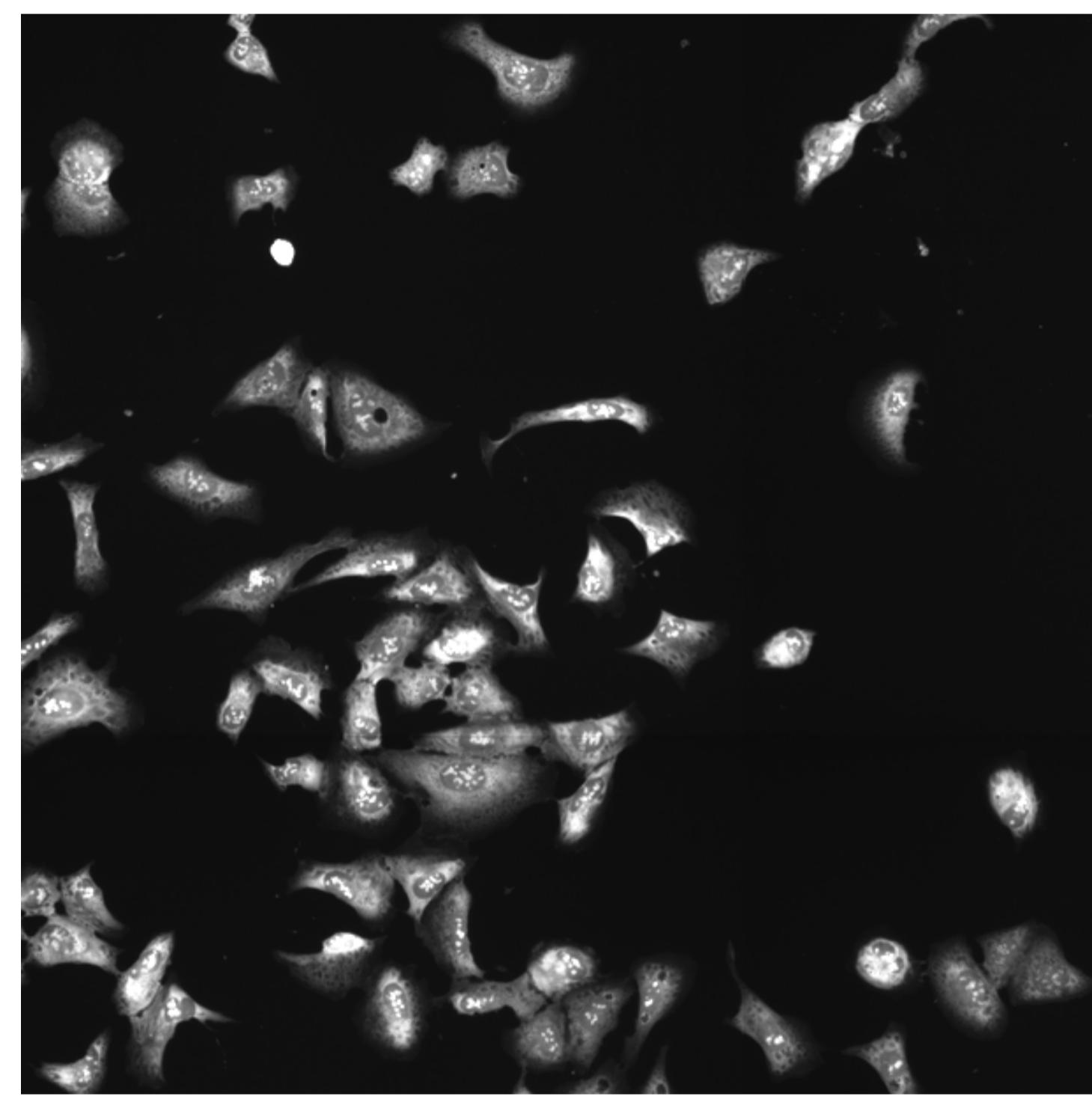
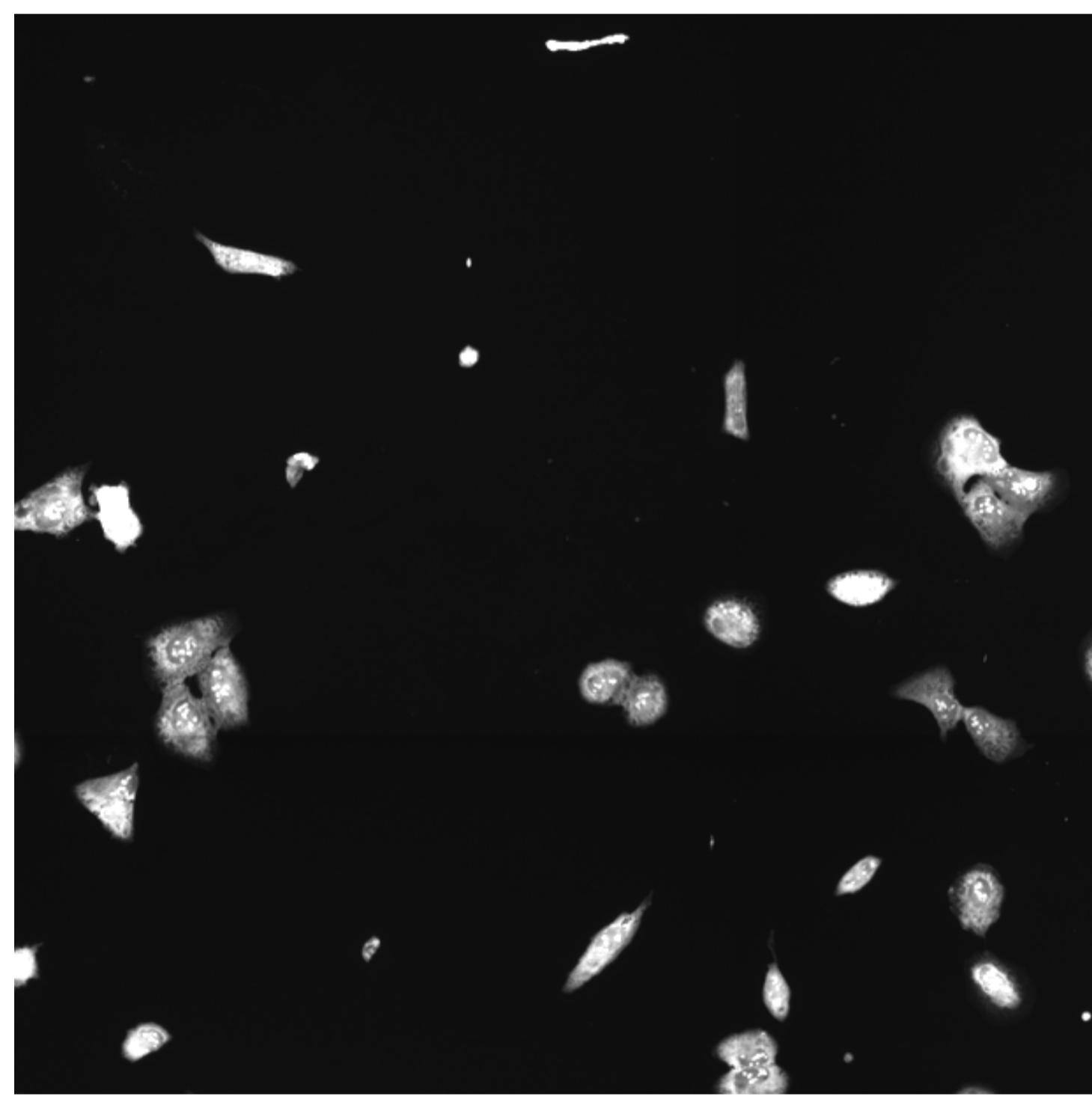
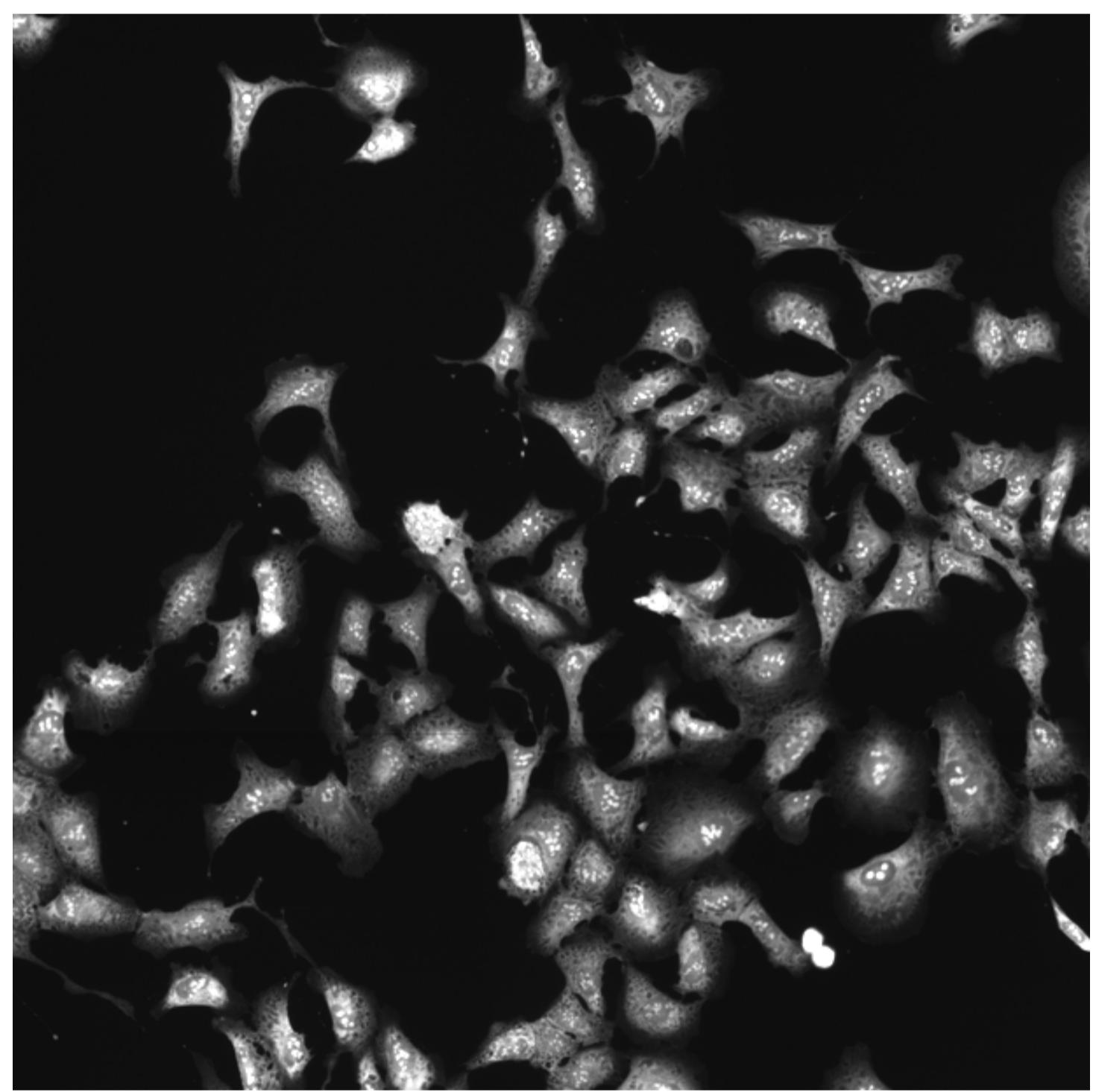
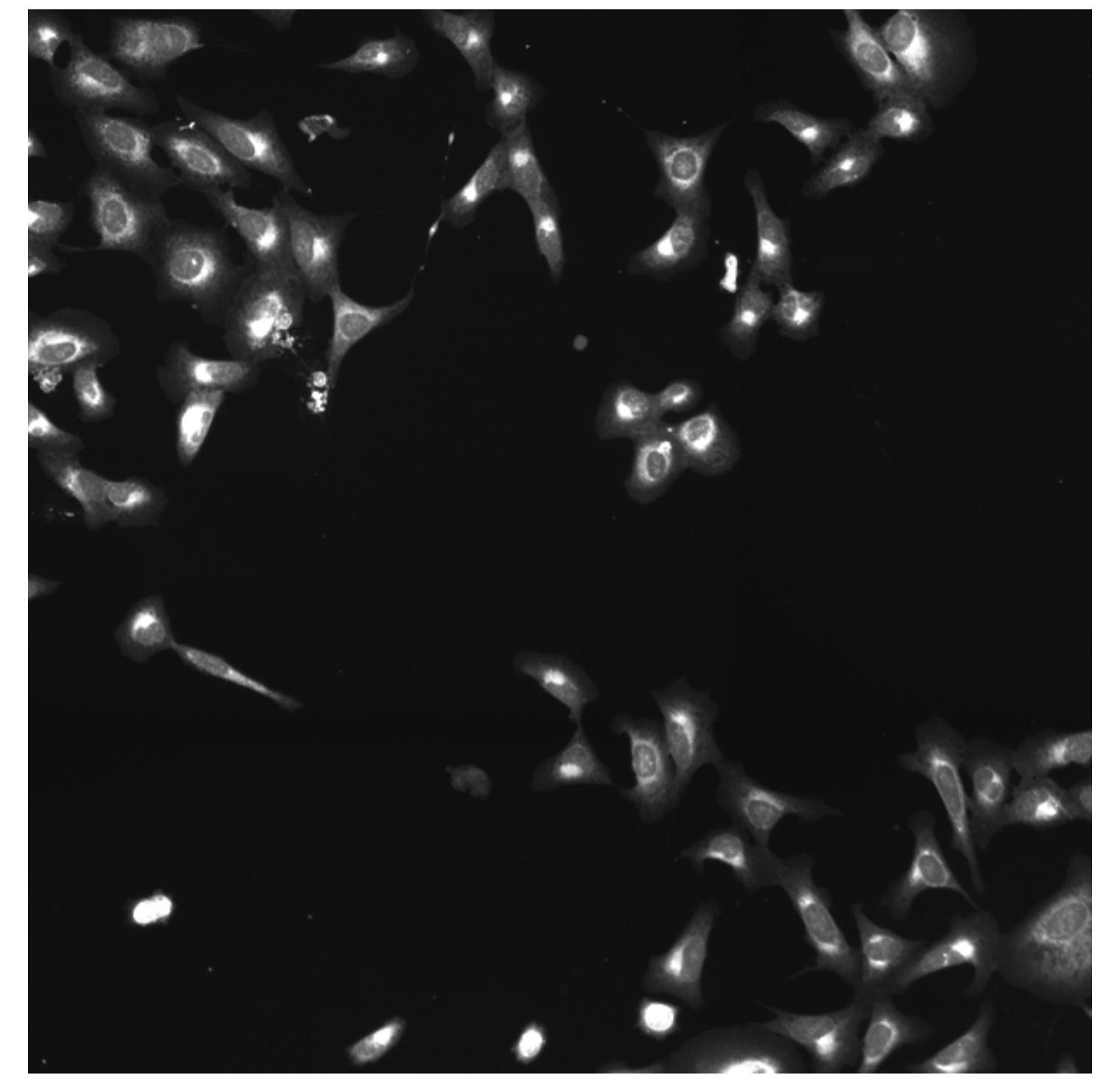
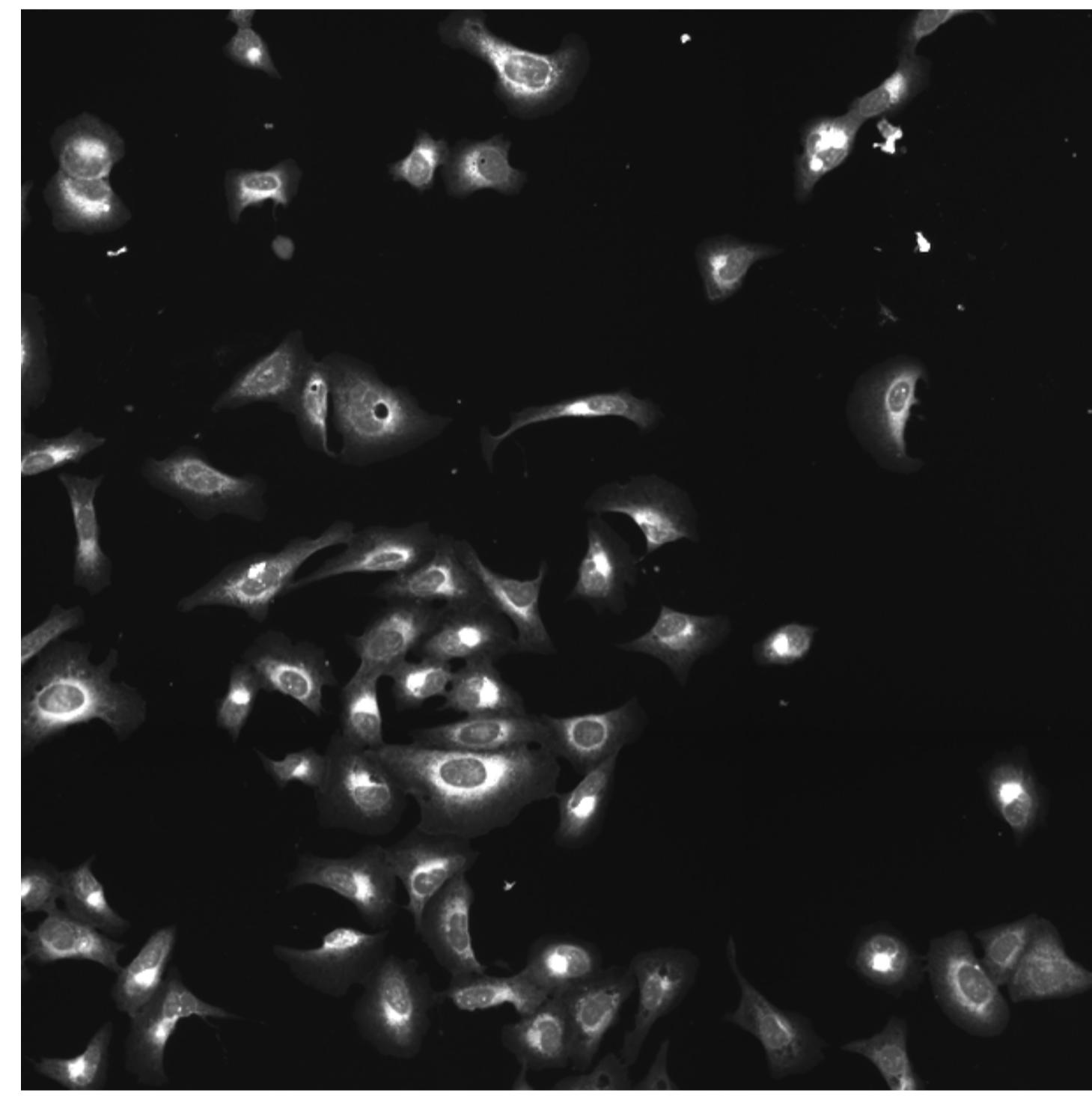
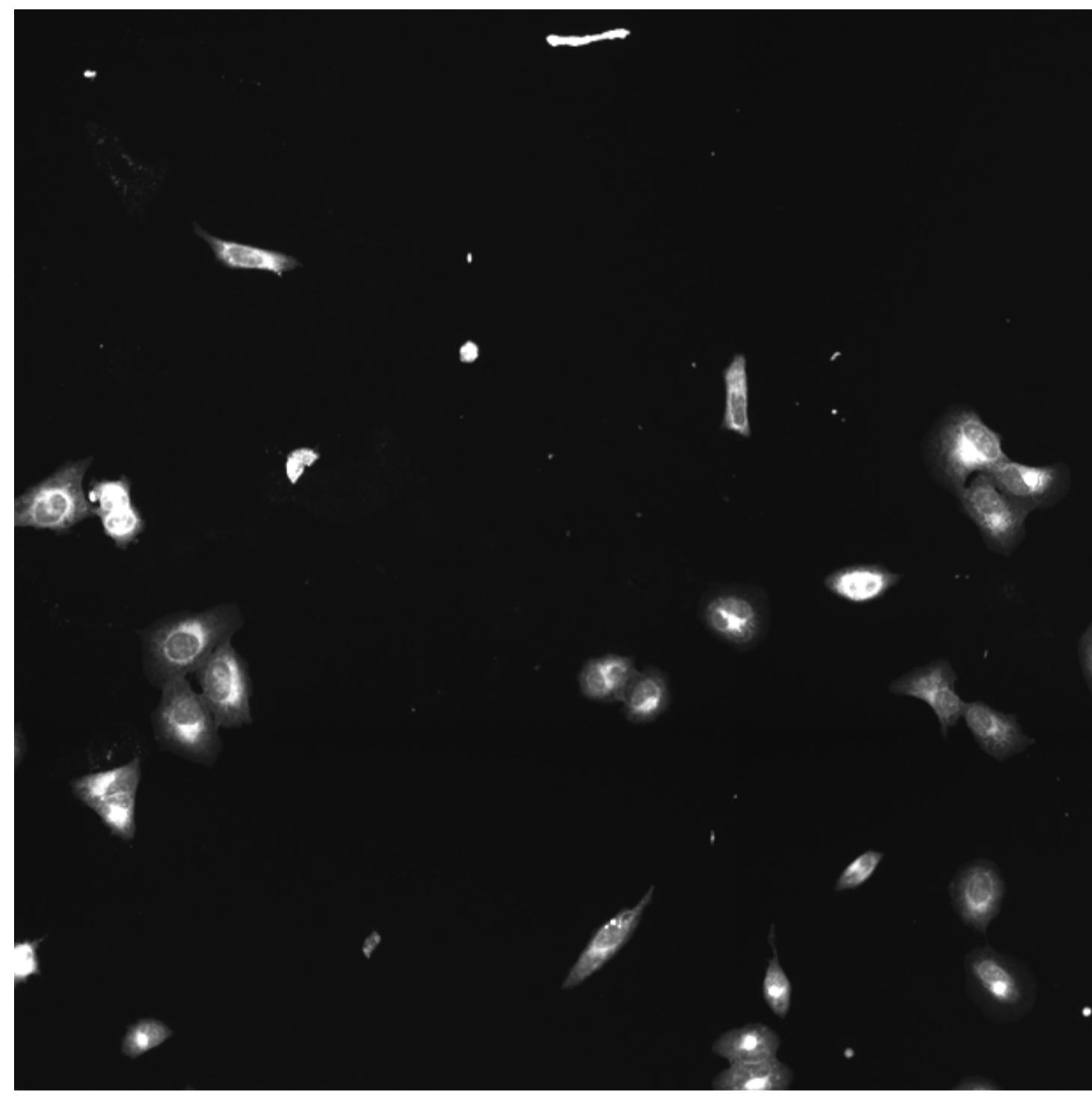
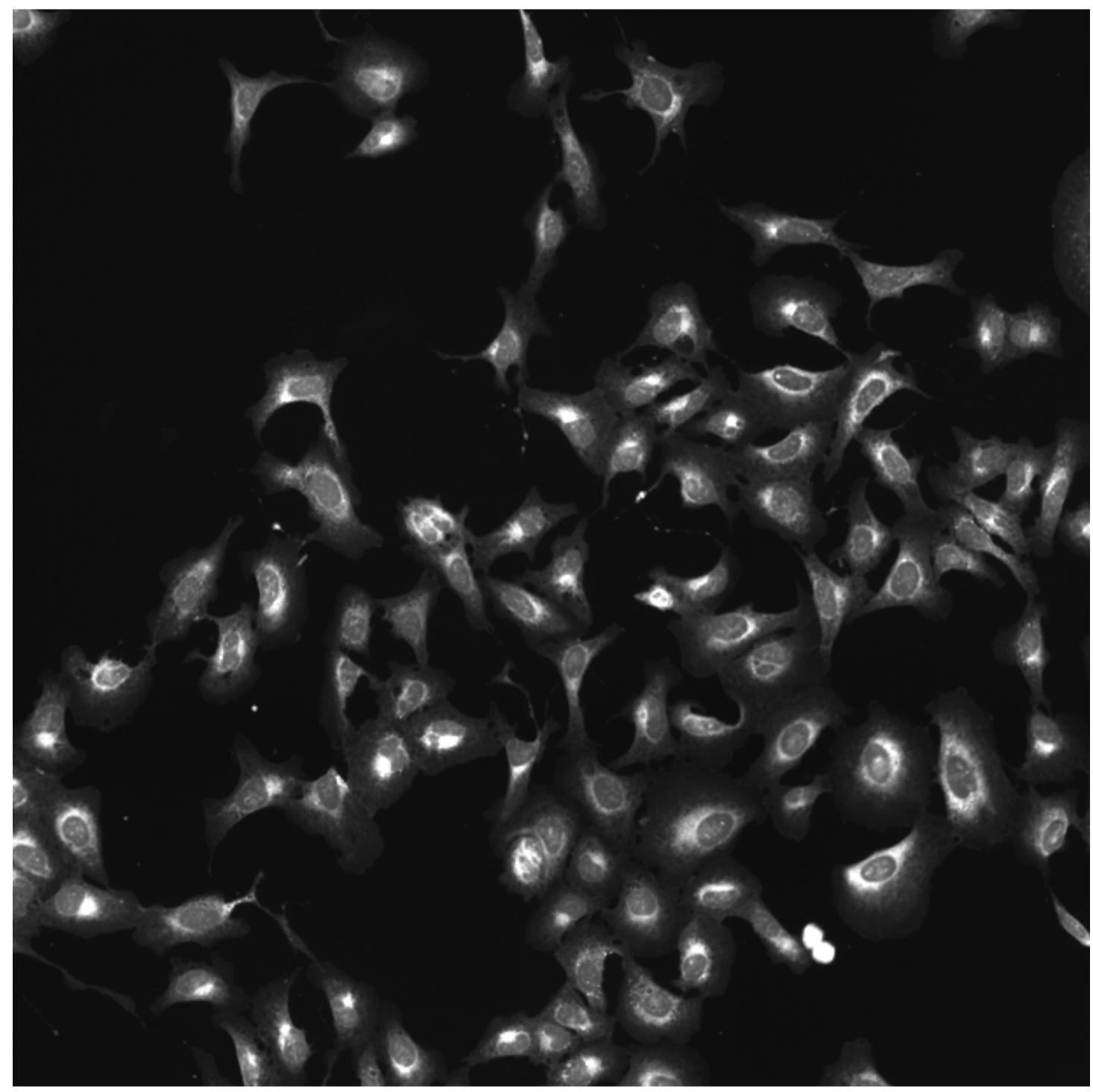


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

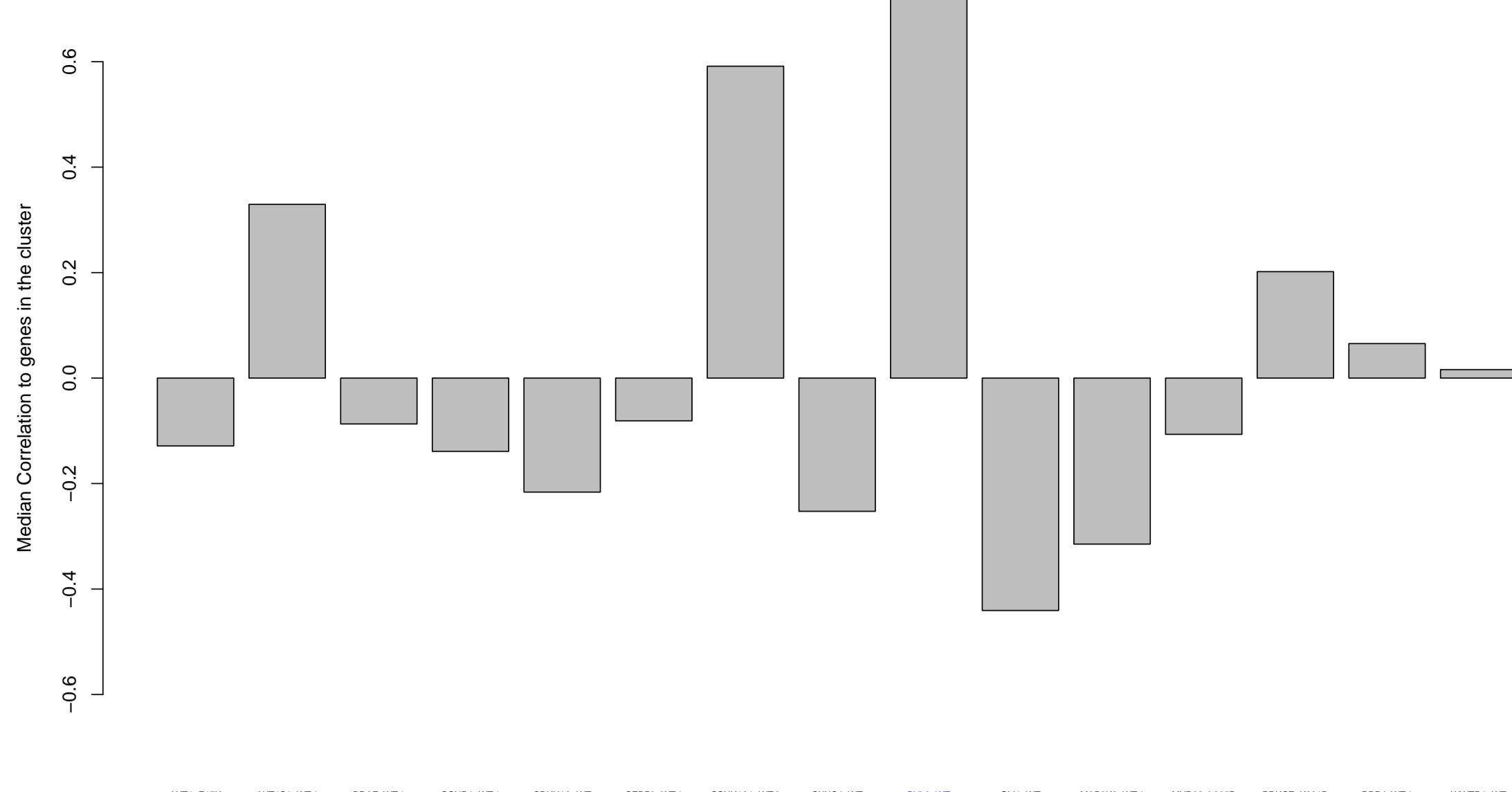
CXXC4_WT

STK3_WT.1

STK3_WT.2



Cluster 9
How similar is this cluster to the other clusters?



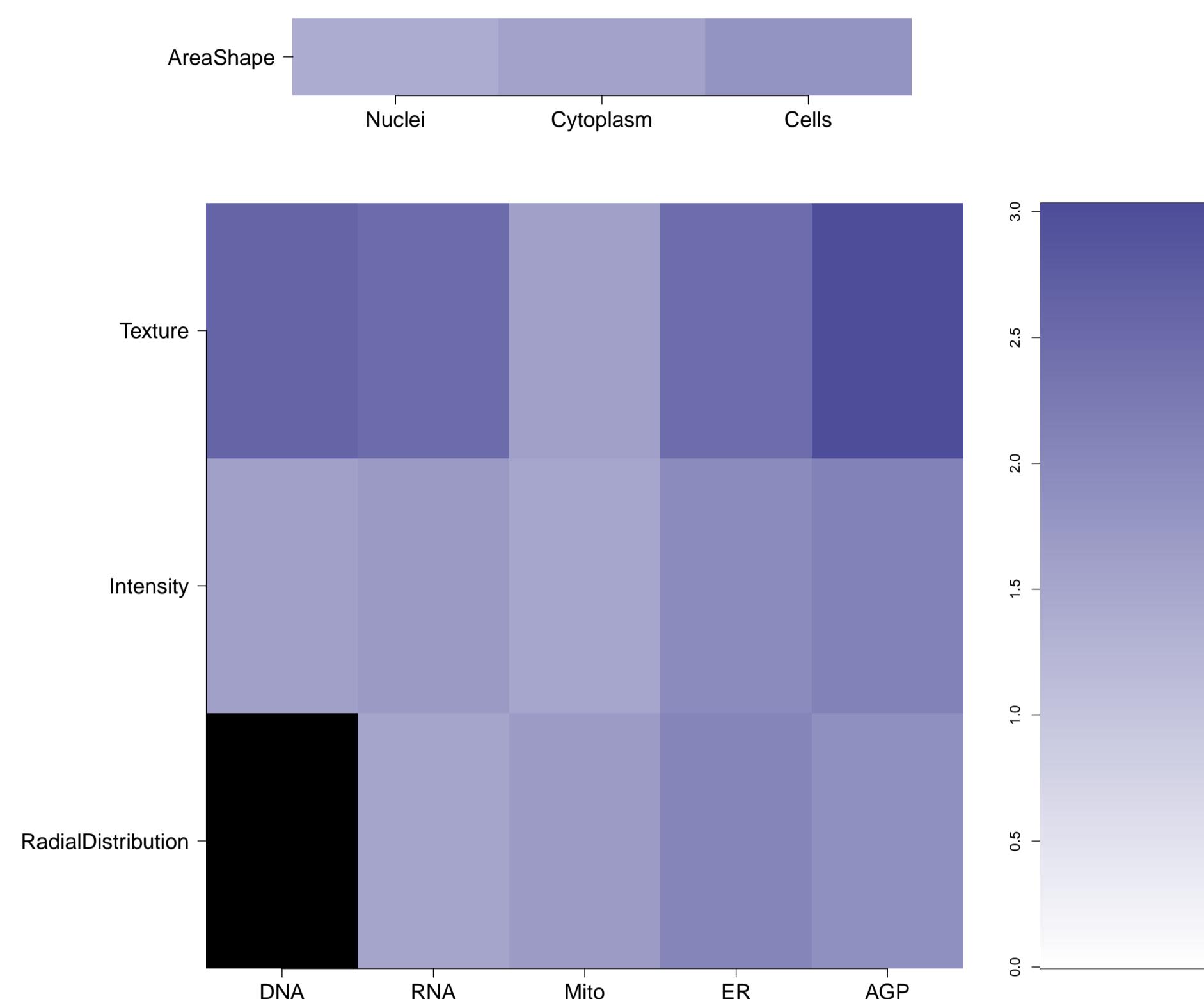
Genes in the cluster along with the pathways as annotated by experts

Treatment	Pathway	Regulation Type
TGFBR1_K232R	Canonical TGFbeta	Inhibitor
TGFBR1_WT_2	Canonical TGFbeta	Activator
DVL3_WT	Canonical WNT	Activator

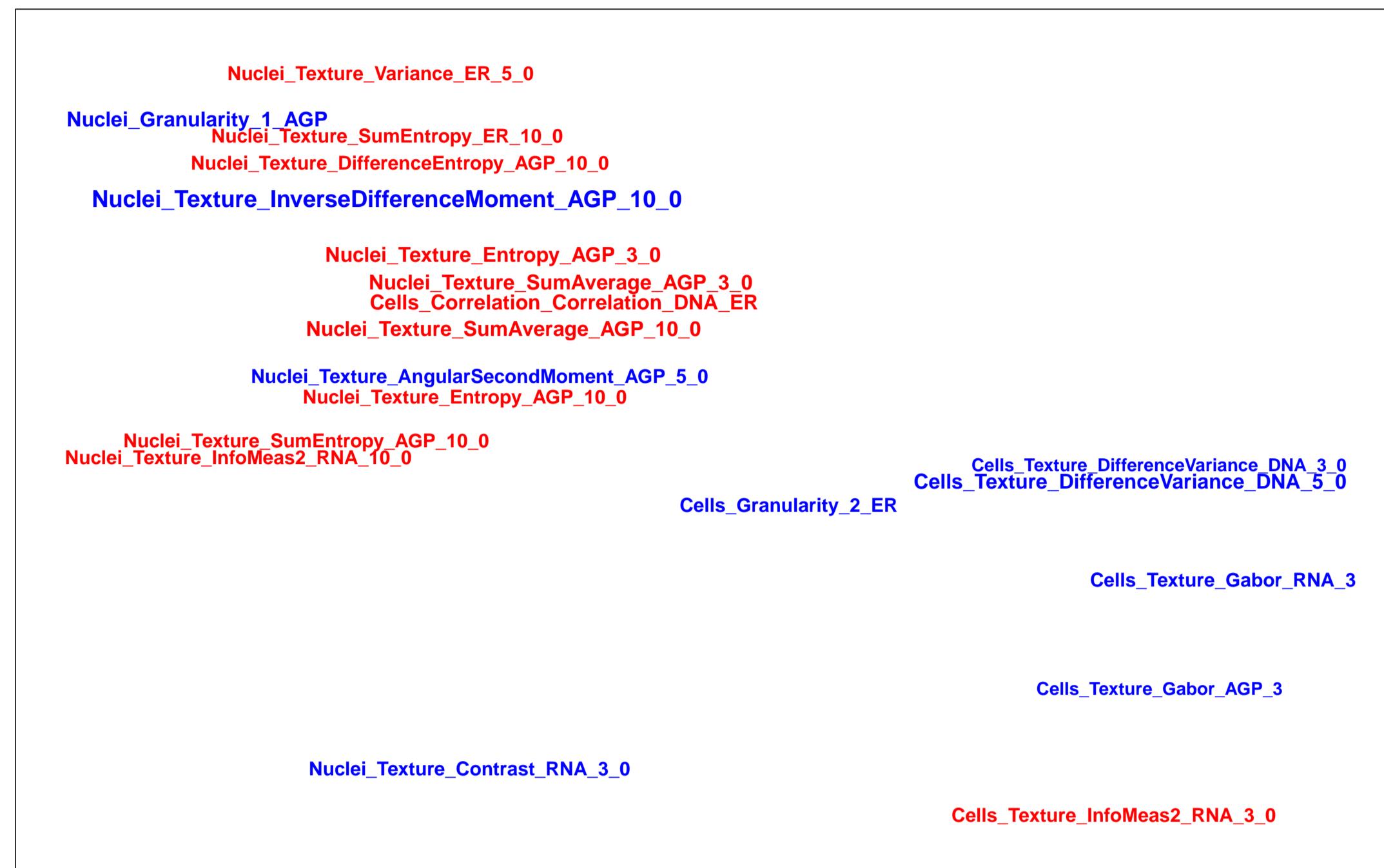
Top 5 genes negatively correlated to the cluster

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
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 PIKA	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?

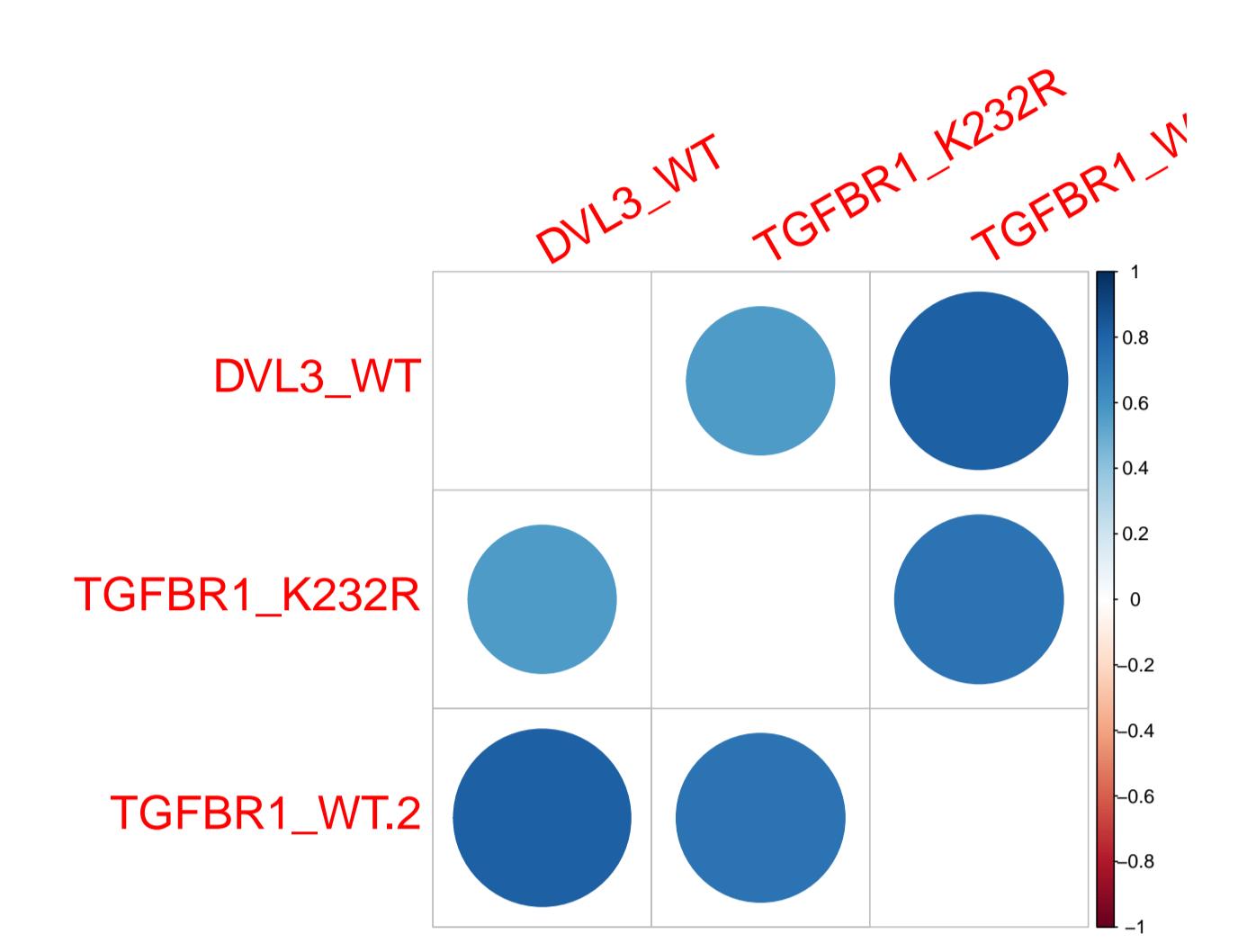


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

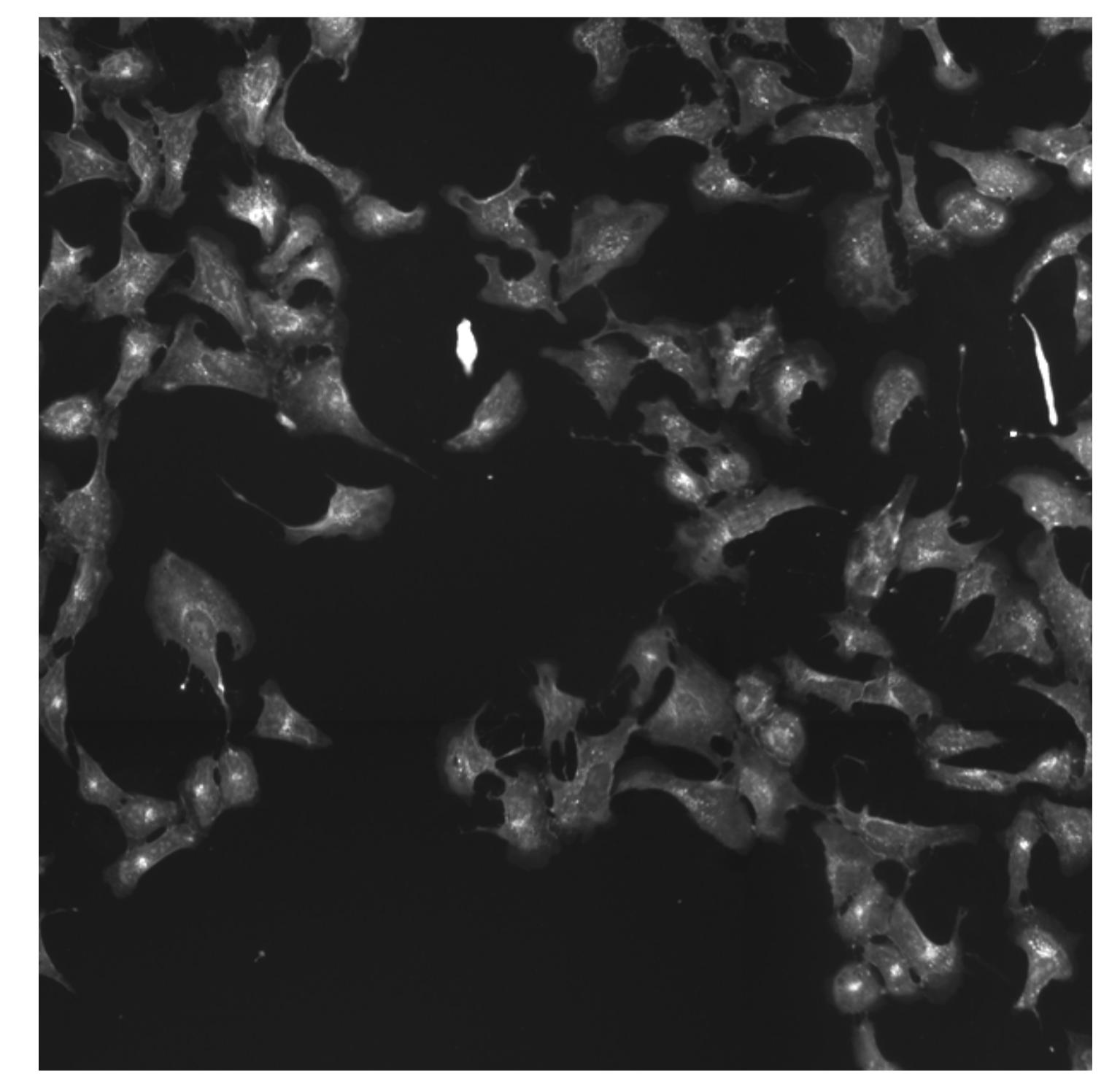
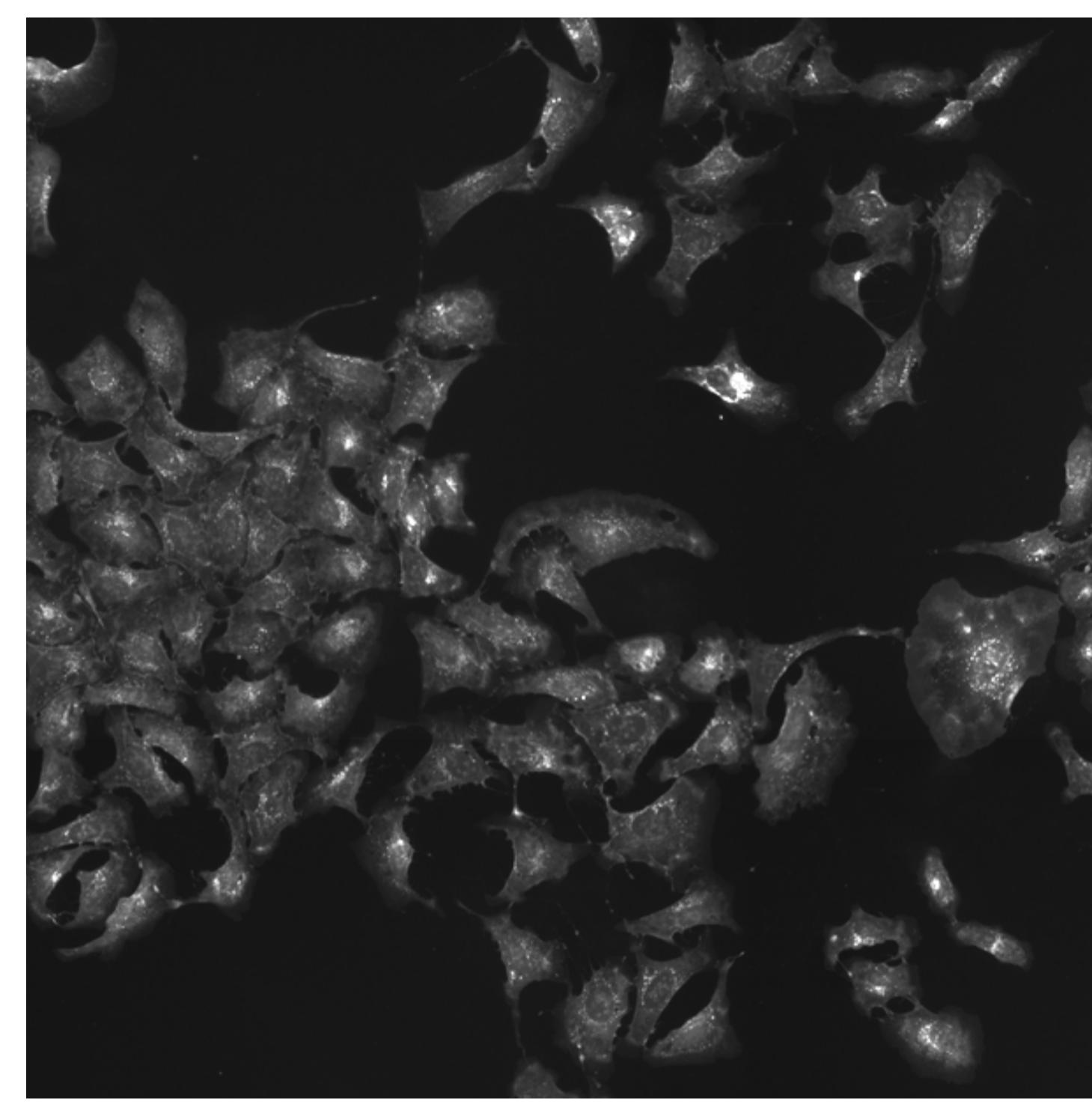
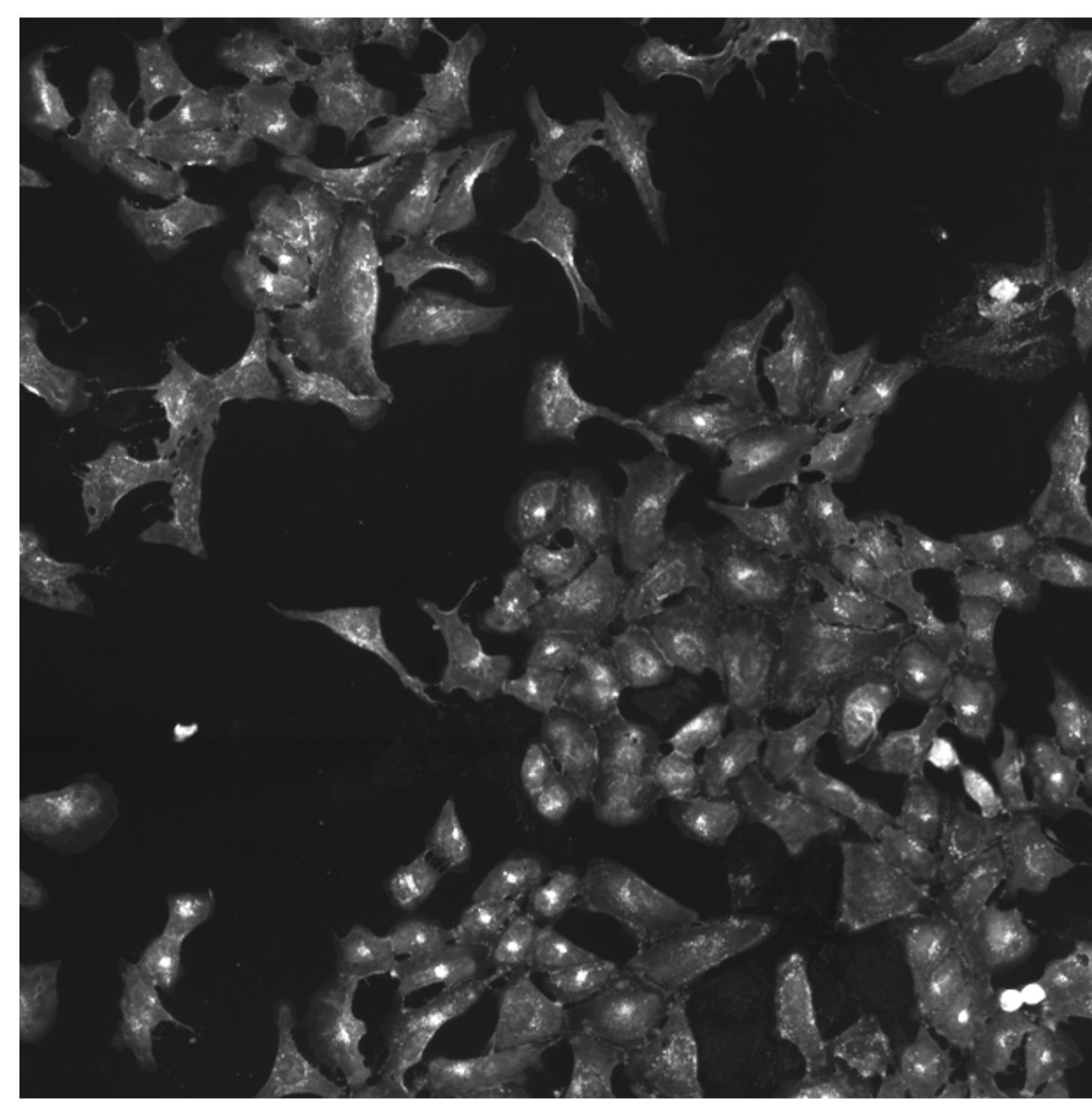
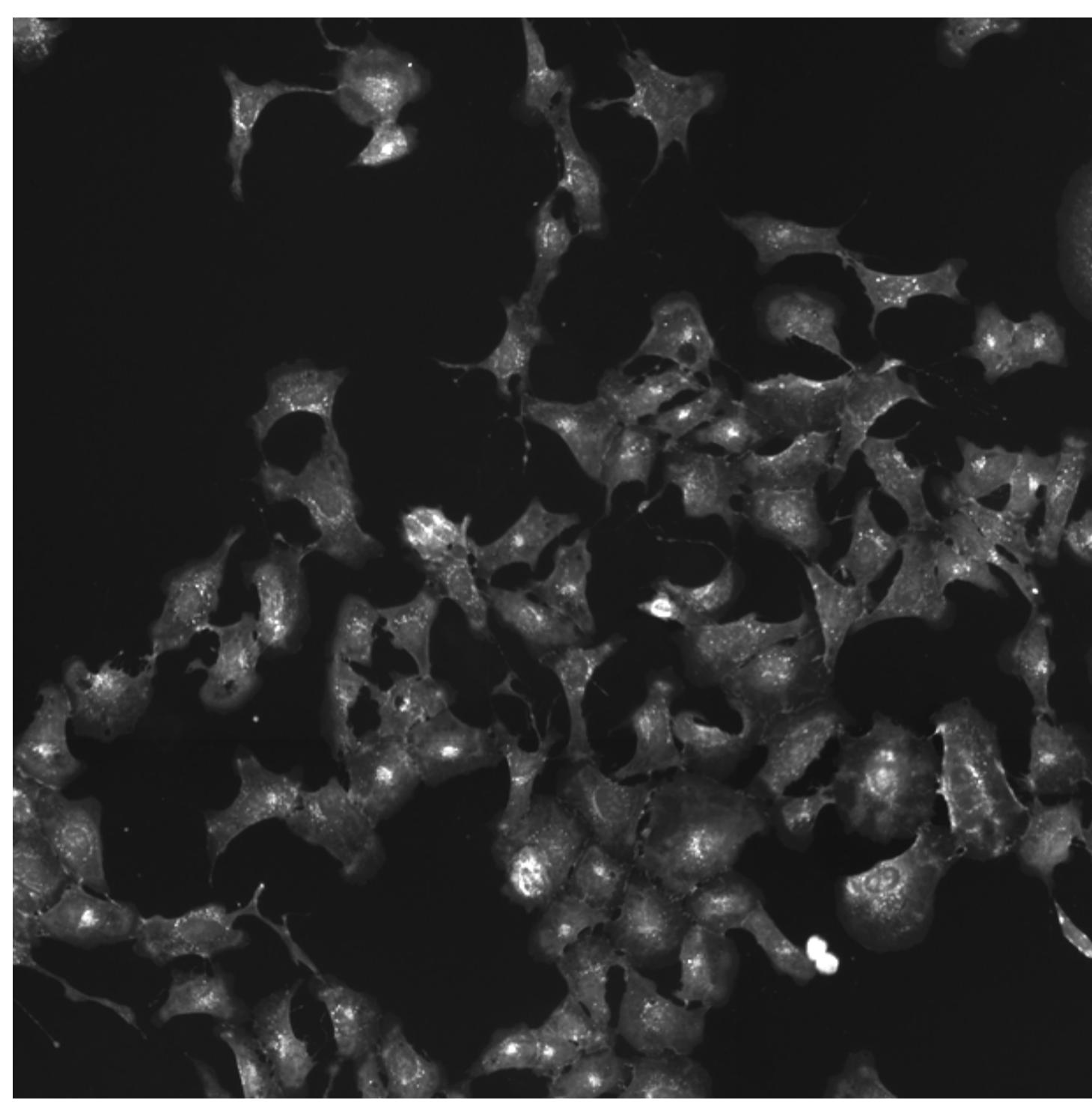
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DVL3_WT

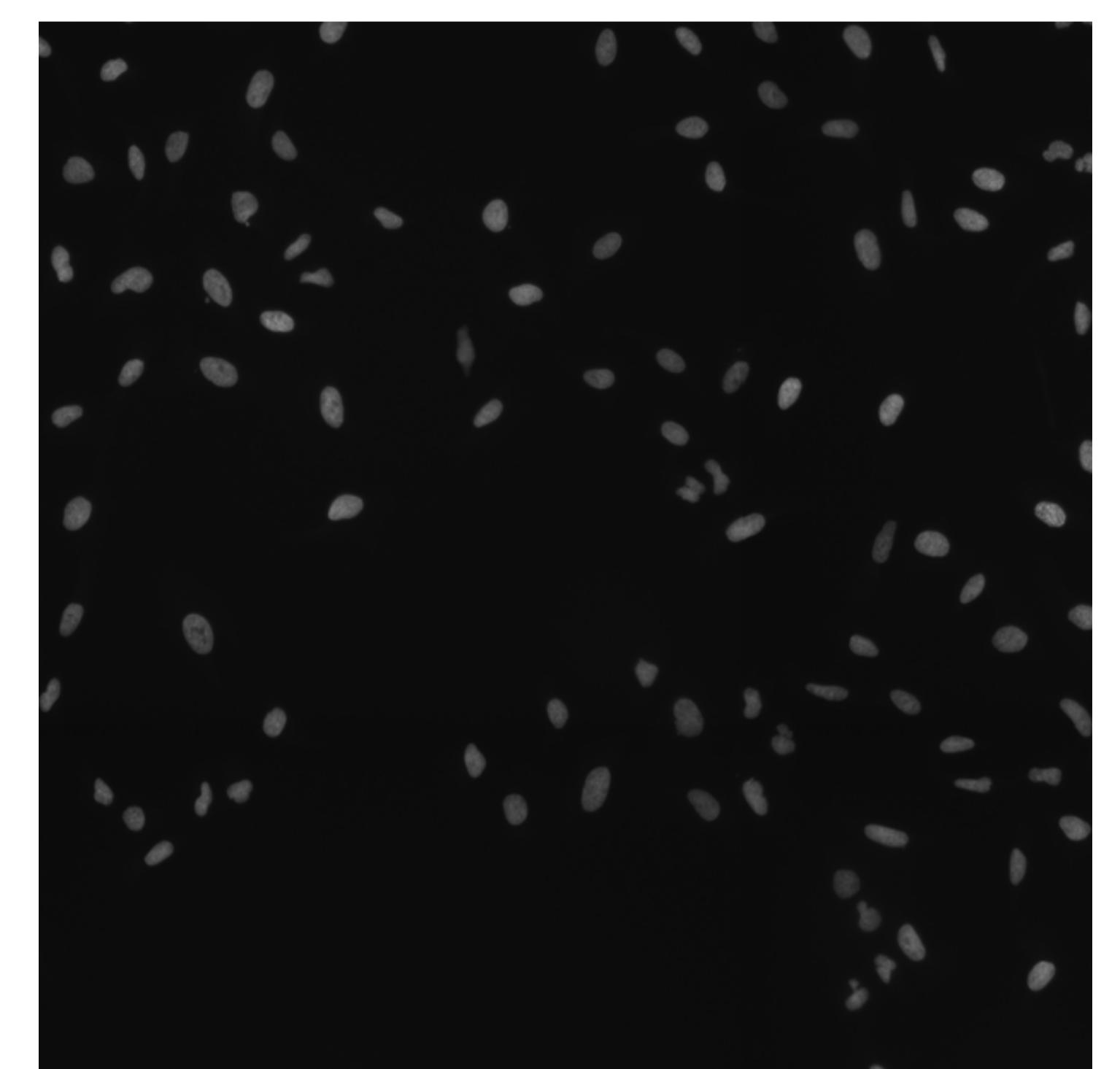
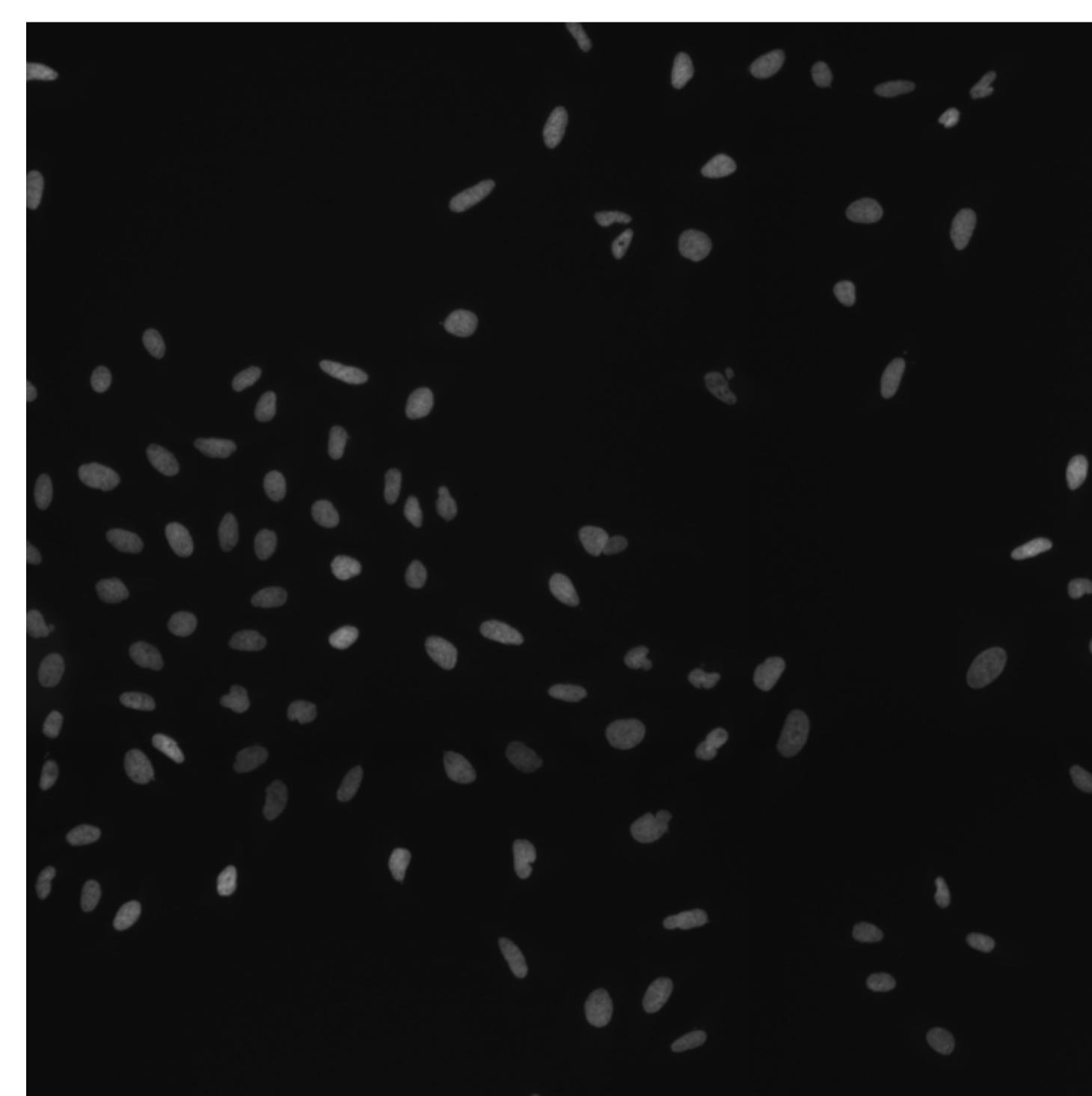
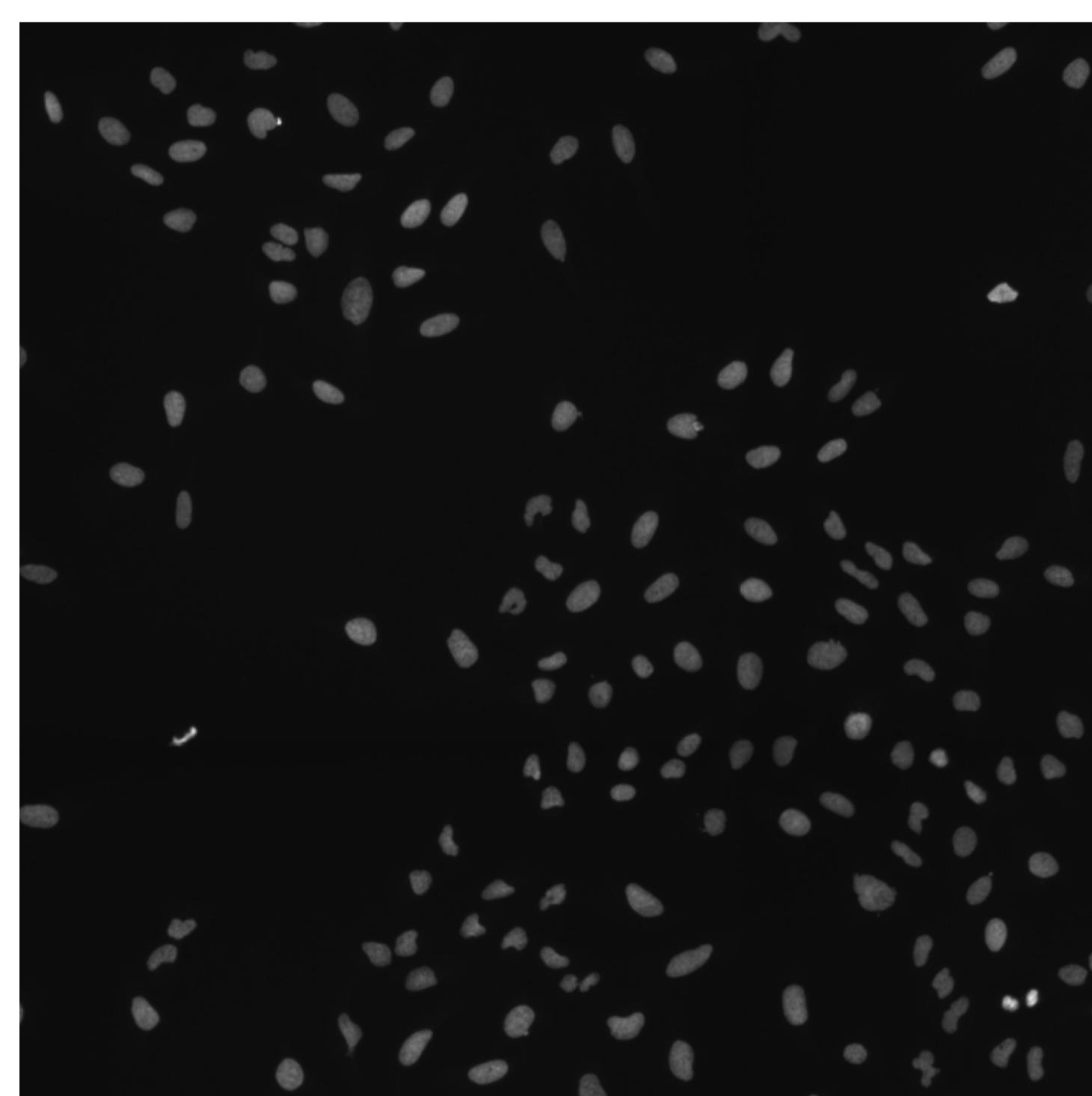
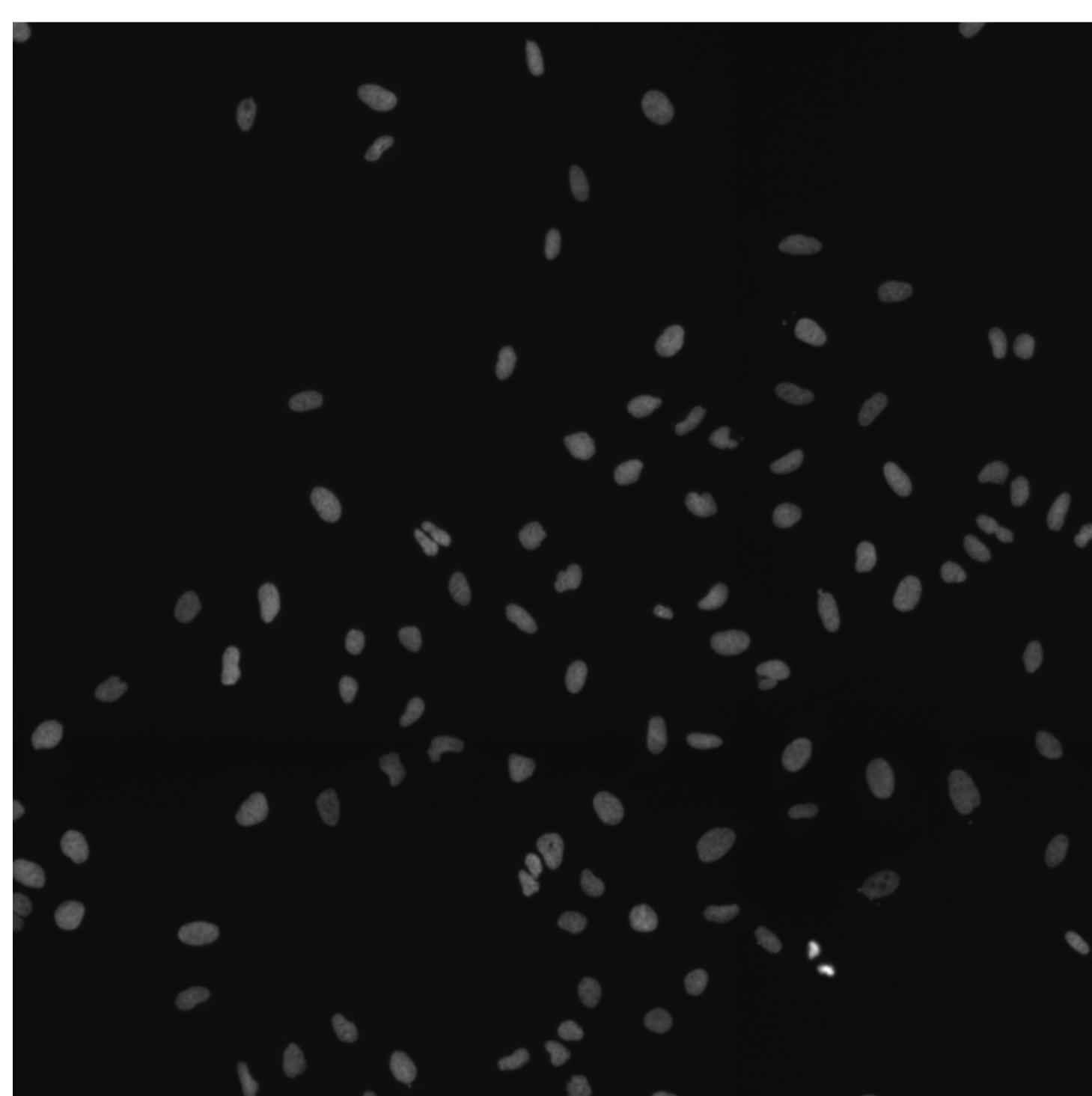
TGFBR1_K232R

TGFBR1_WT_2

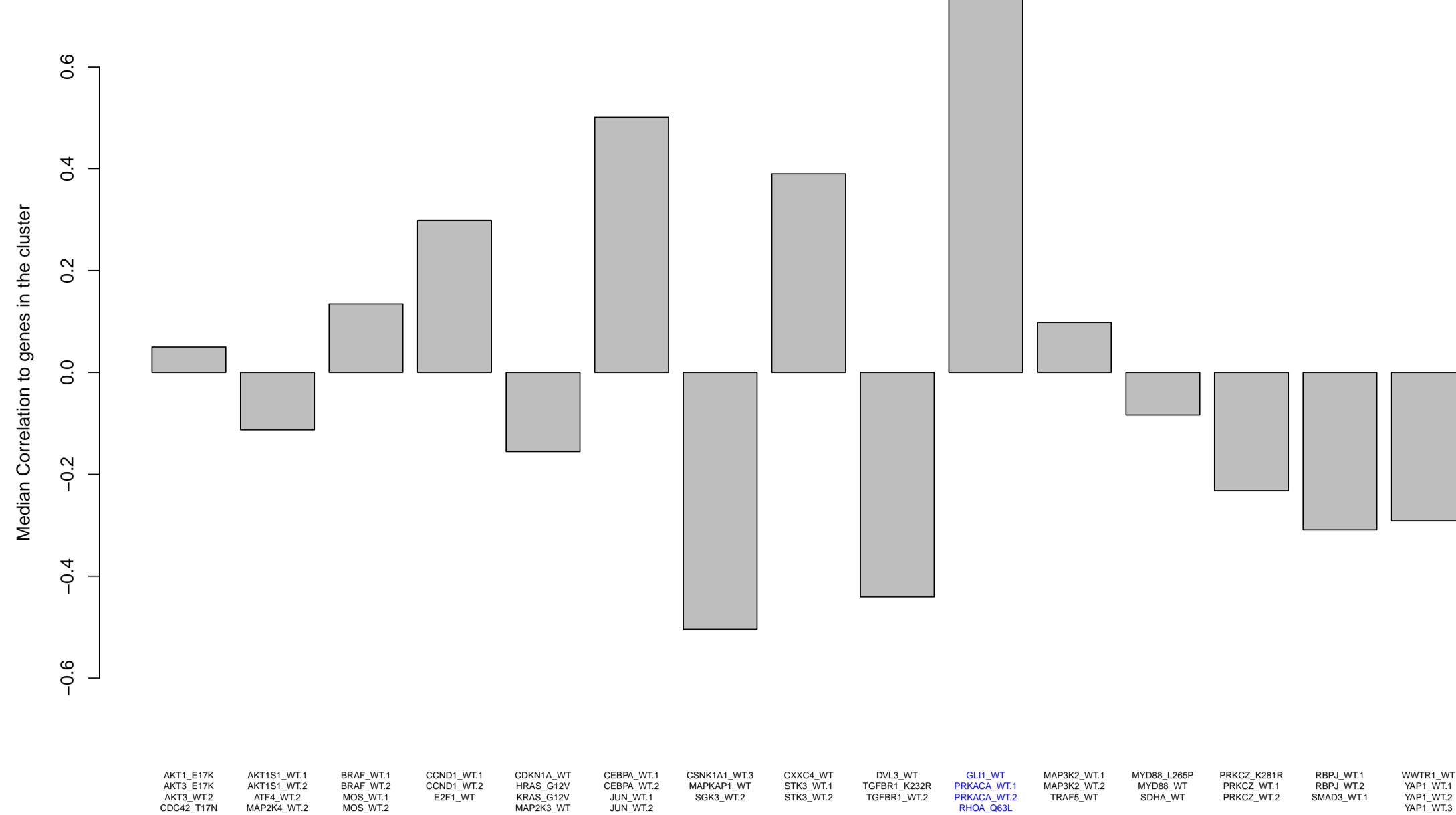
AGP



DNA



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?

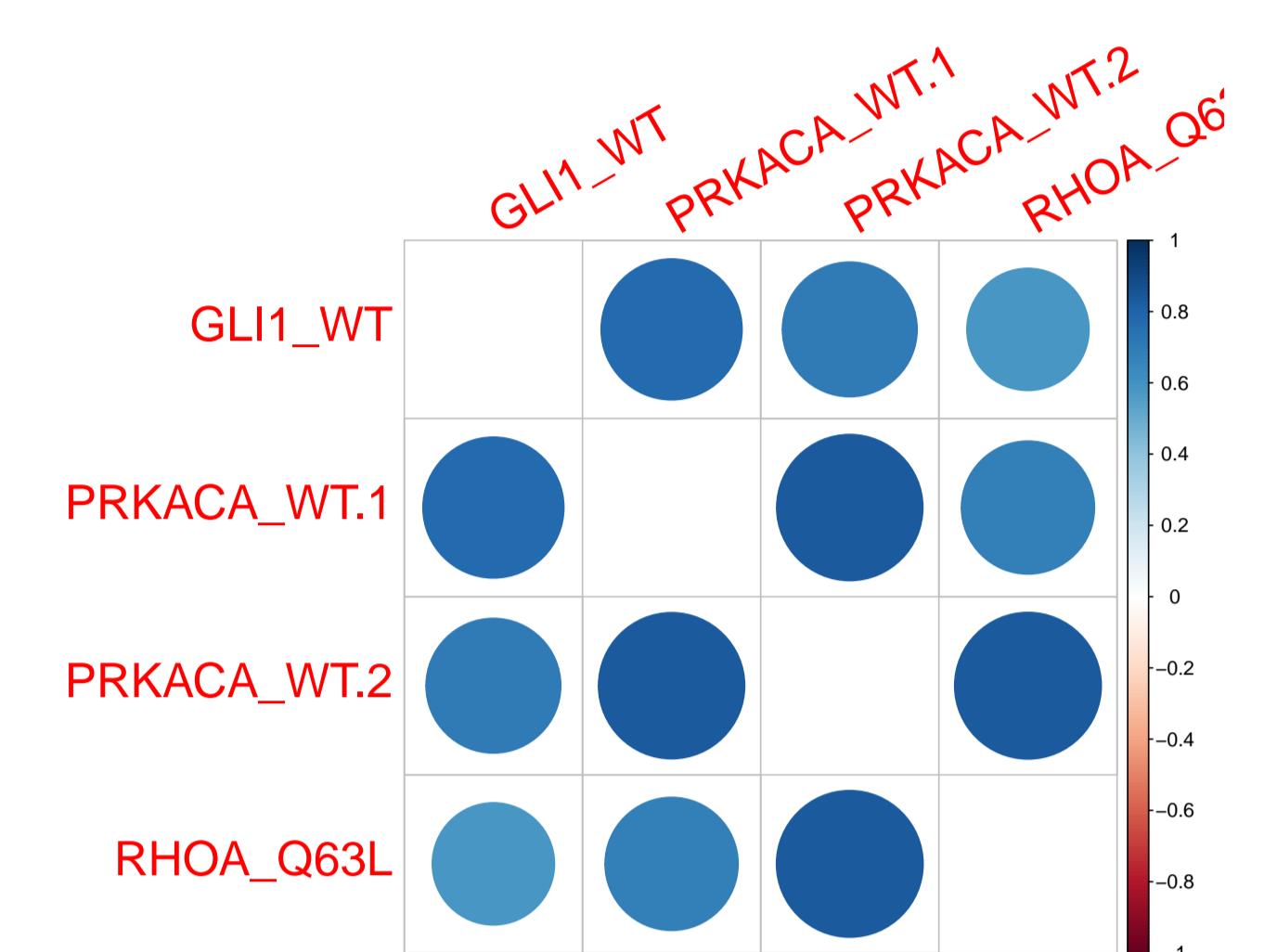
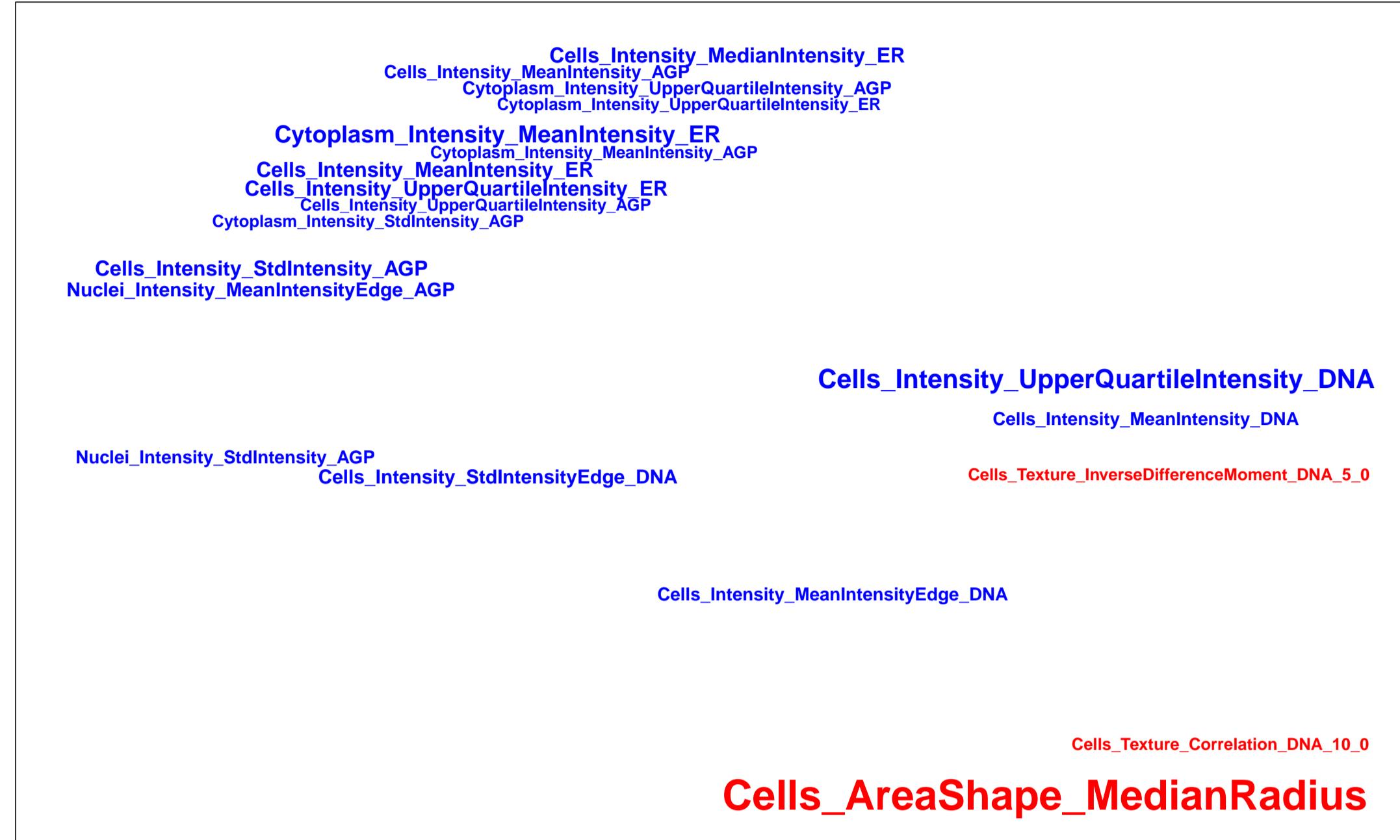
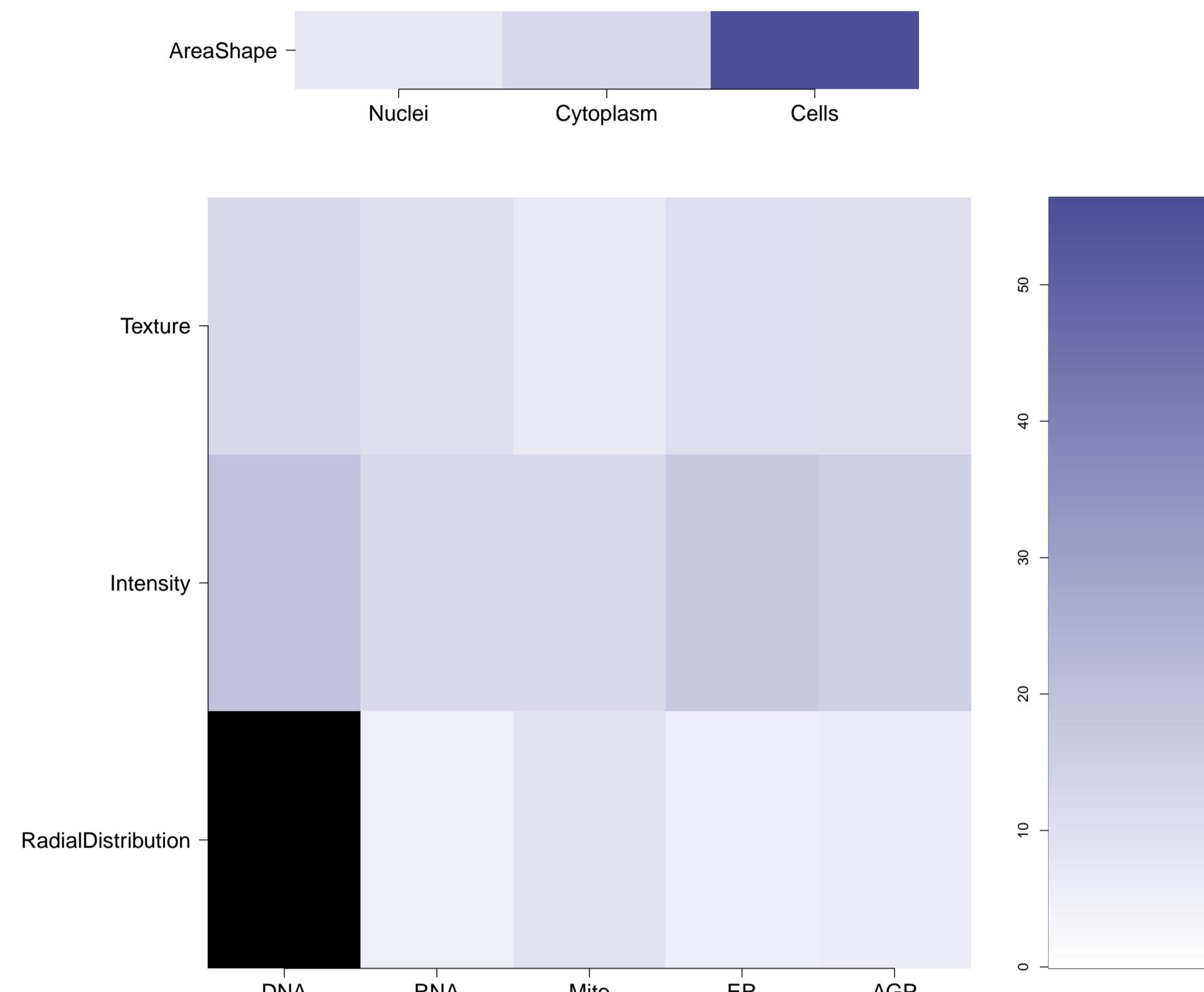


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

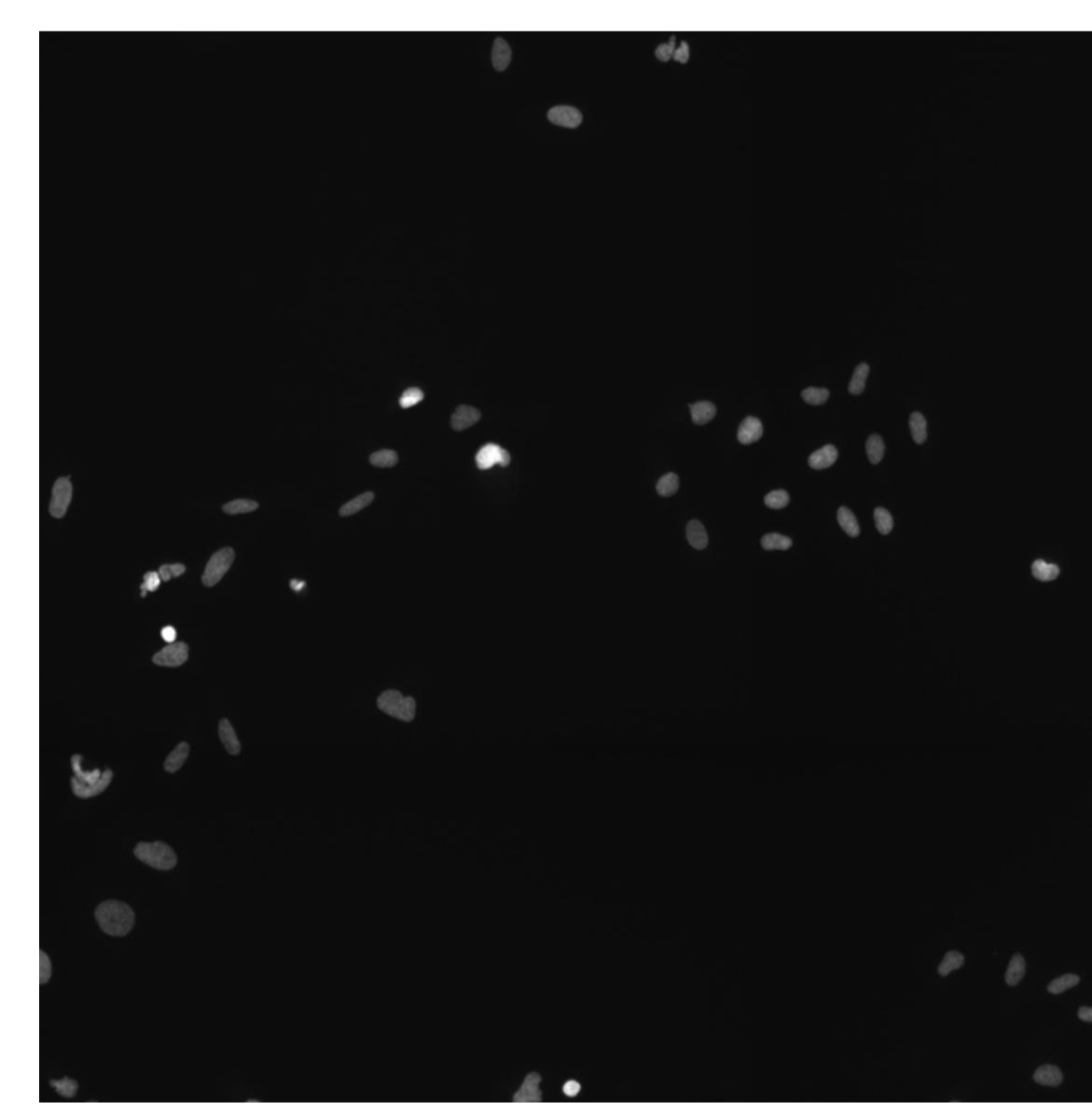
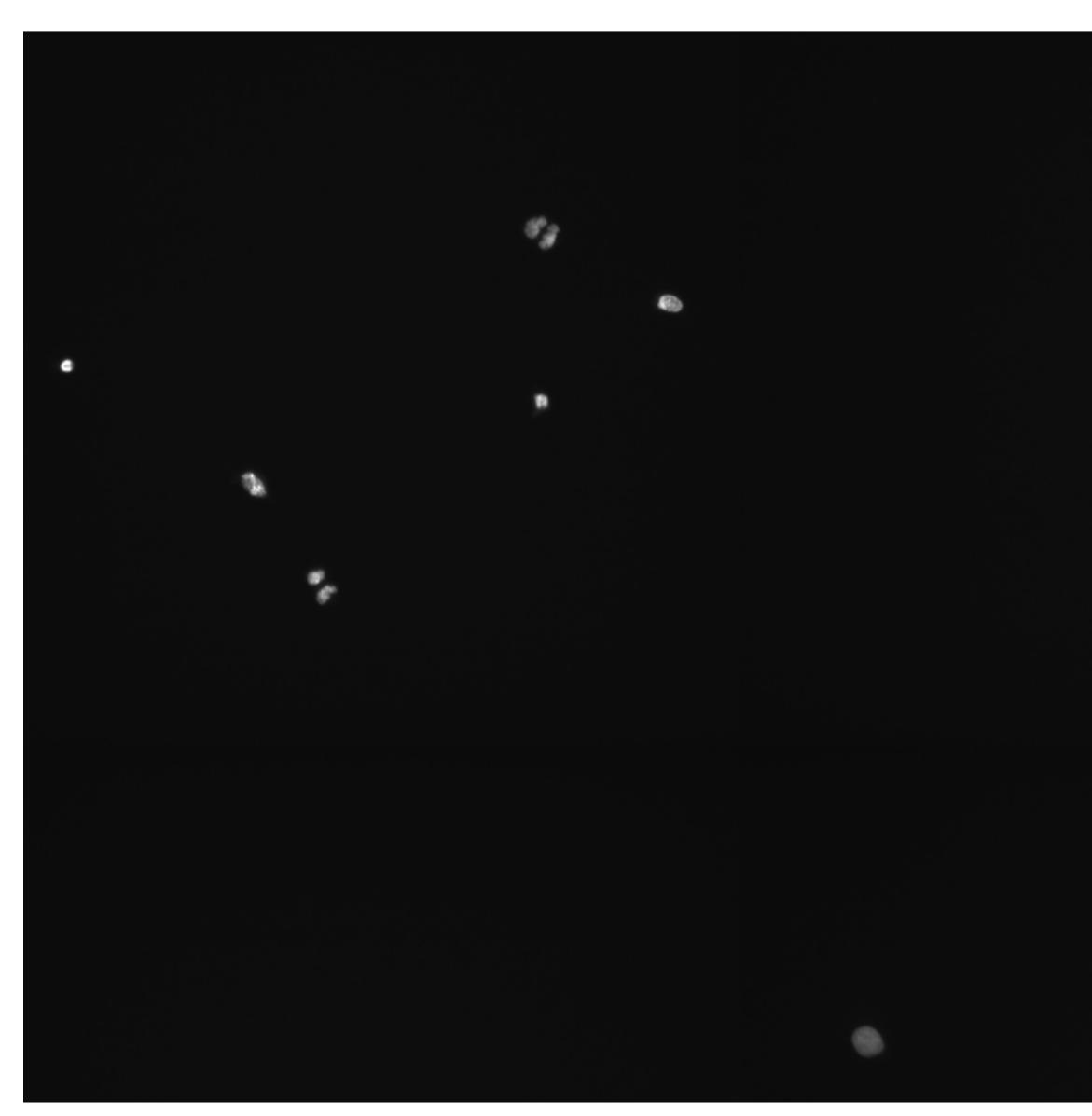
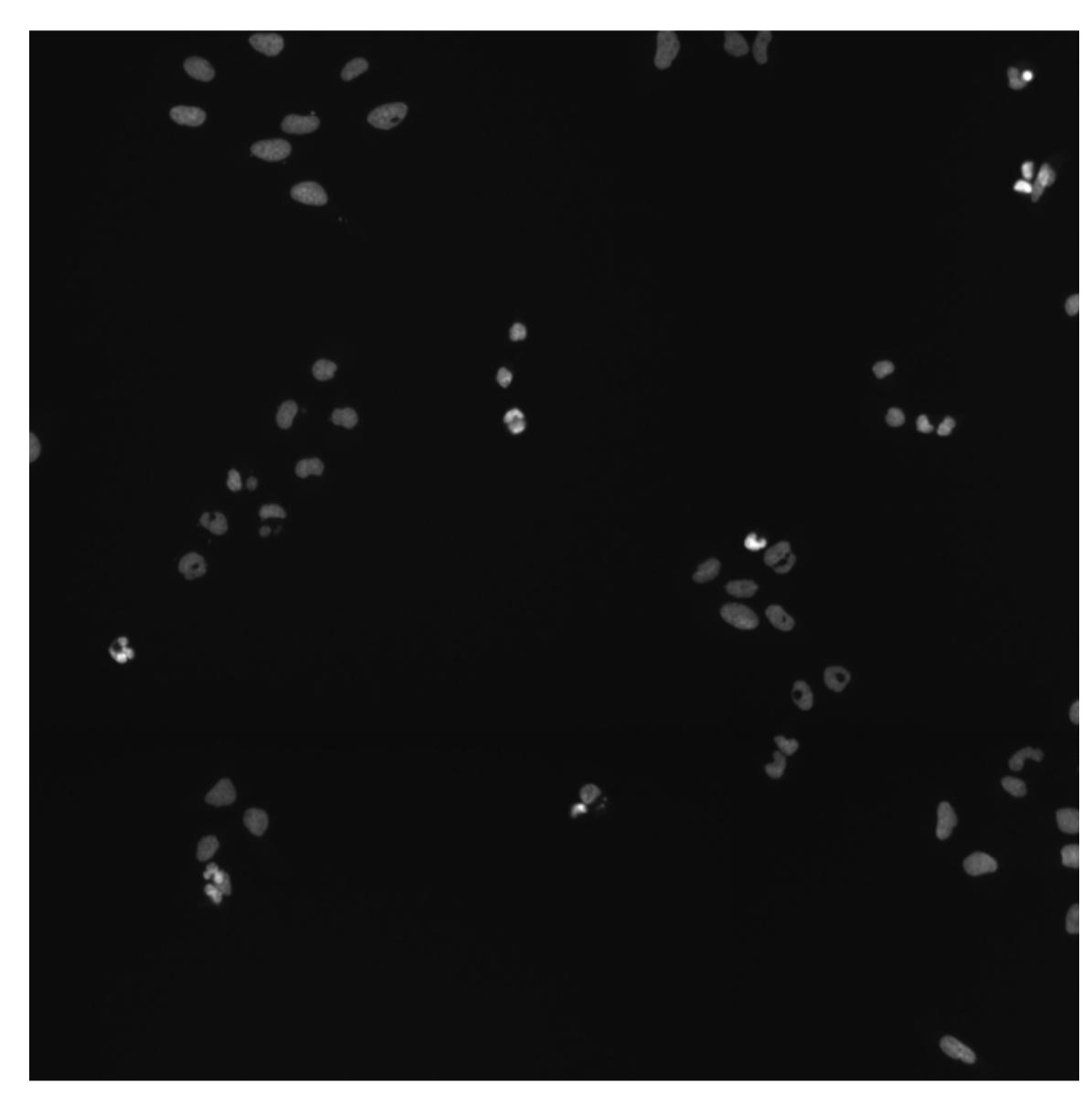
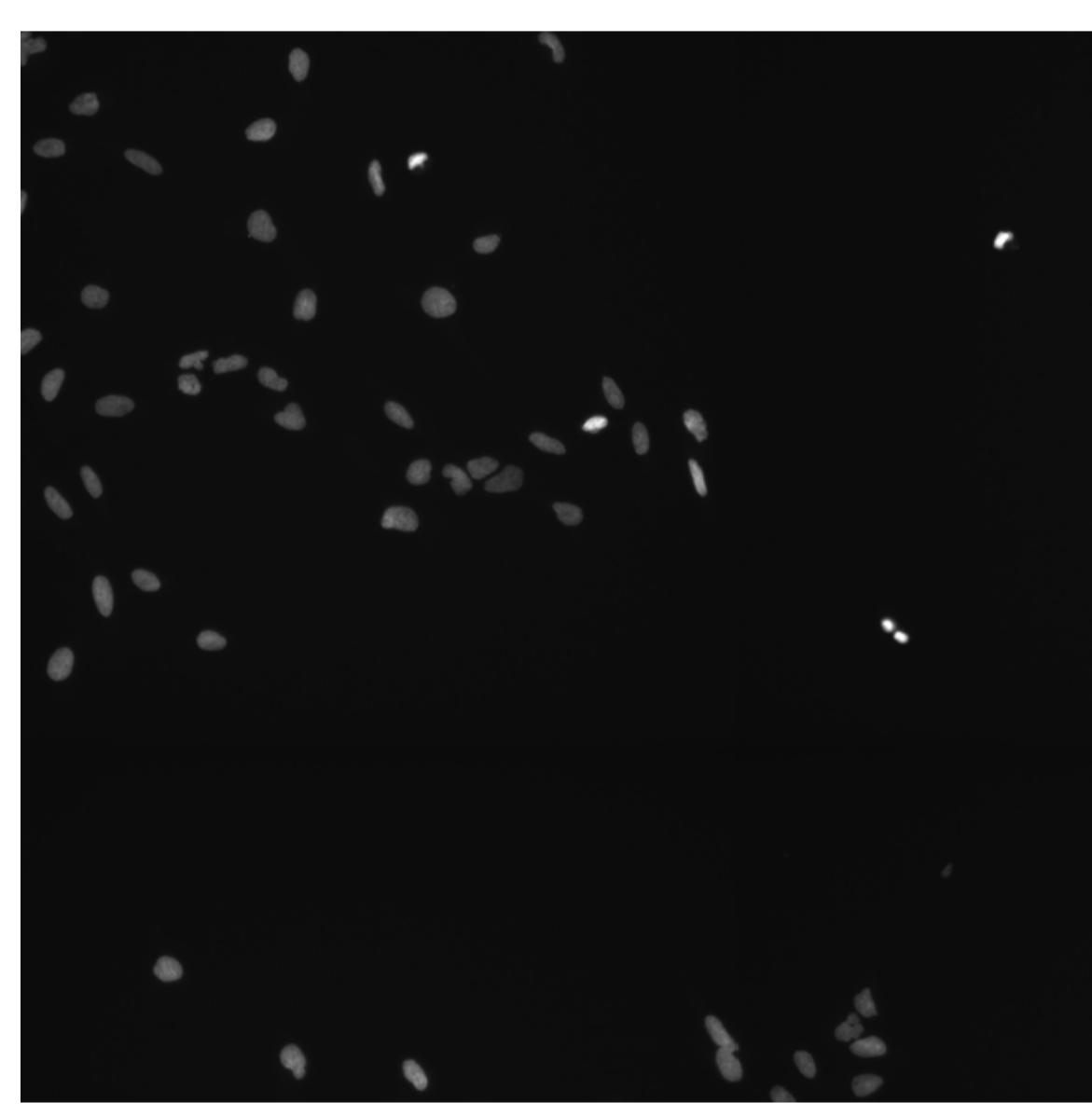
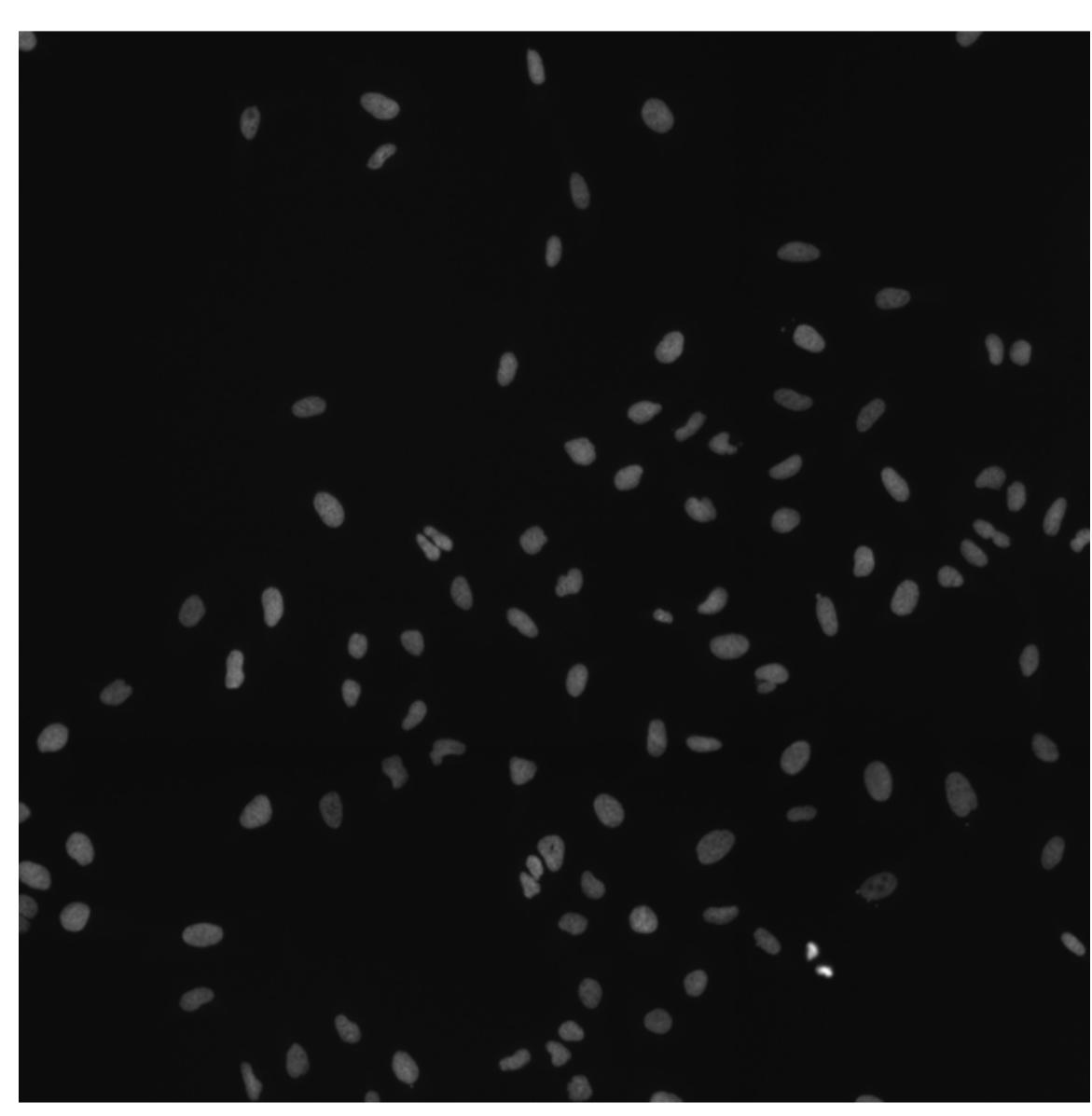
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GLI1_WT

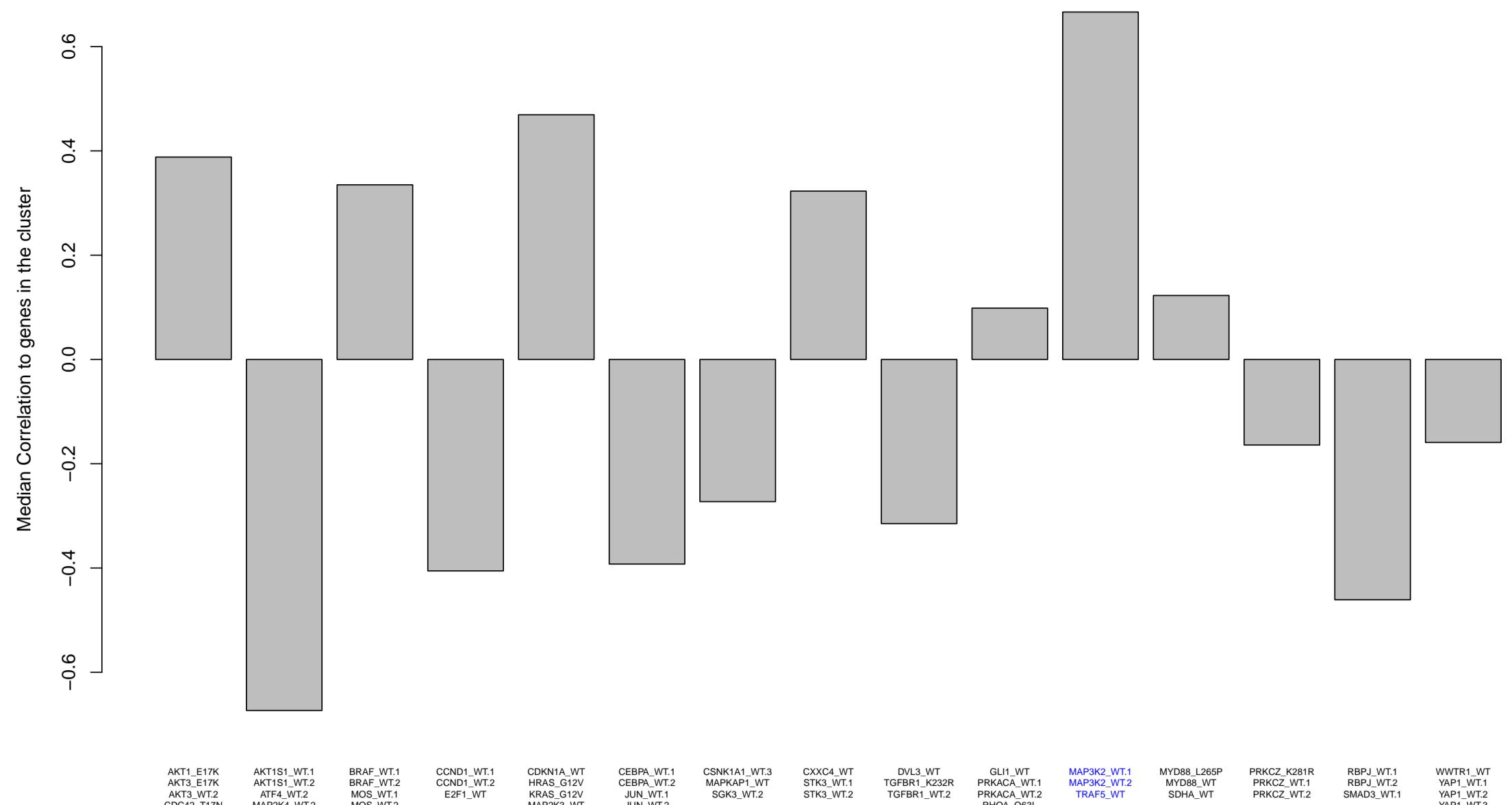
PRKACA_WT.1

PRKACA_WT.2

RHOA_Q63L



Genes in the cluster along with the pathways as annotated by experts			
Treatment	Expert Annotation		
	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	Expert Annotation			Mean Correlation	Standard Deviation	
	Pathway	Regulation Type				
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

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How strongly are genes within the cluster correlated?

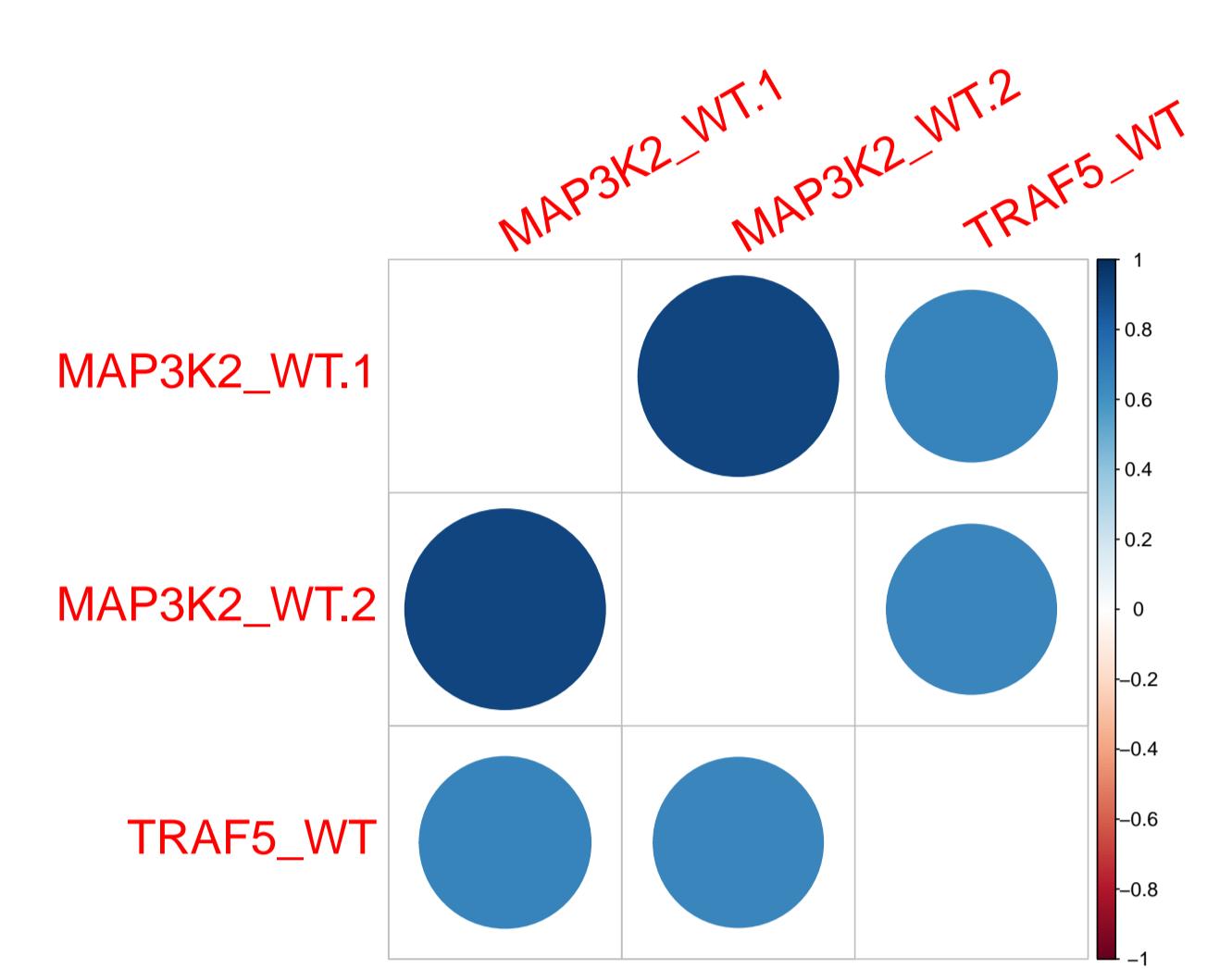
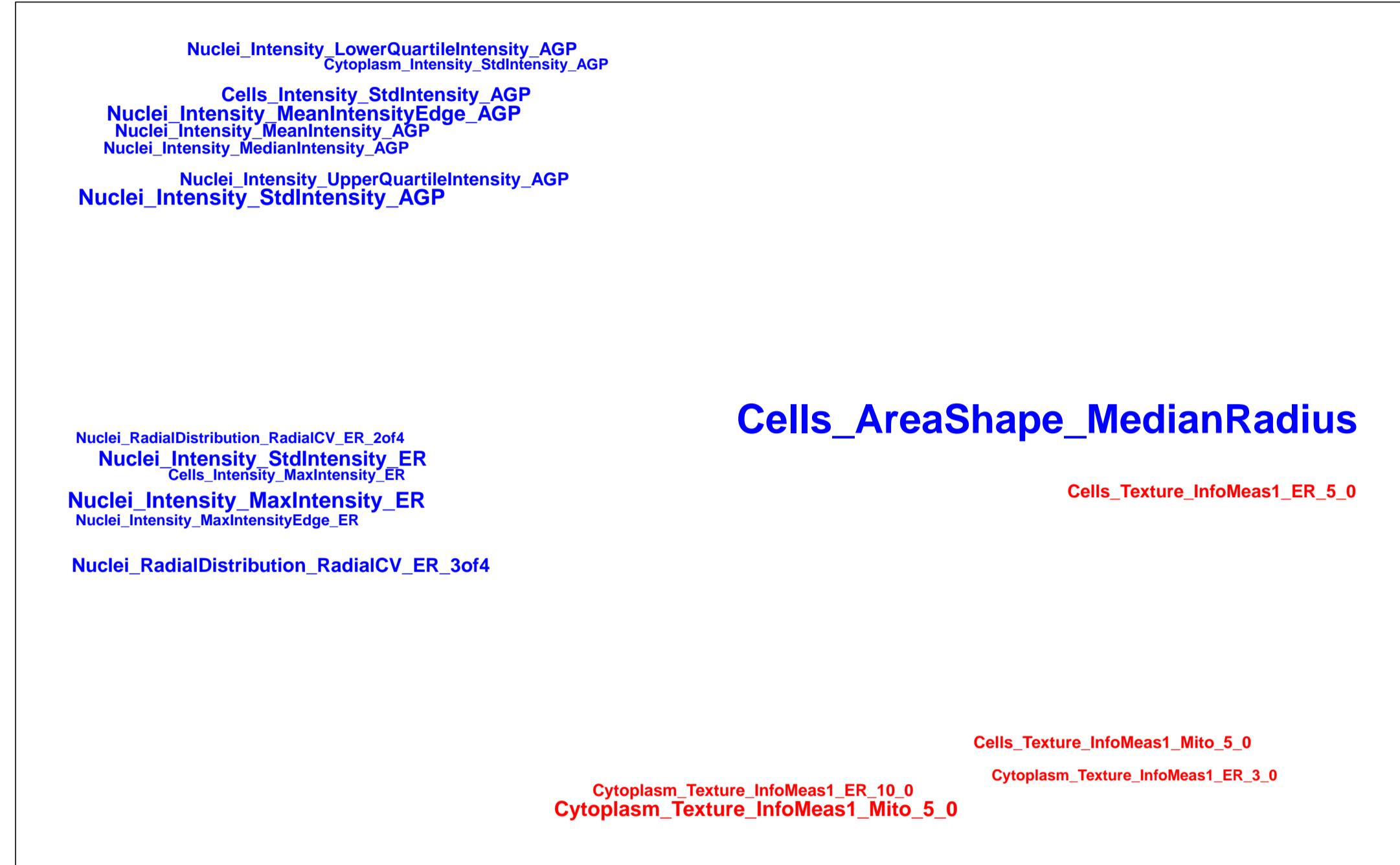
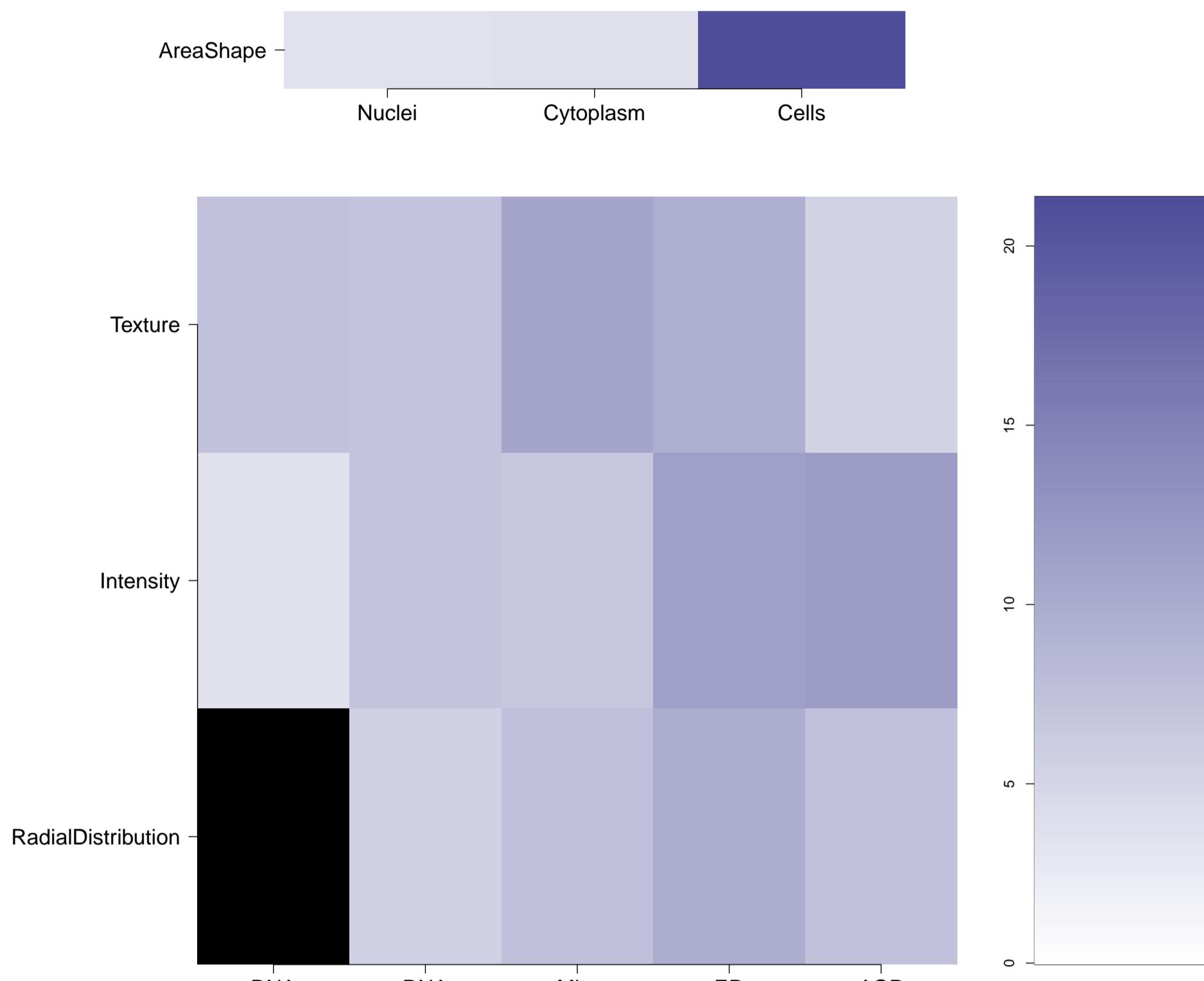
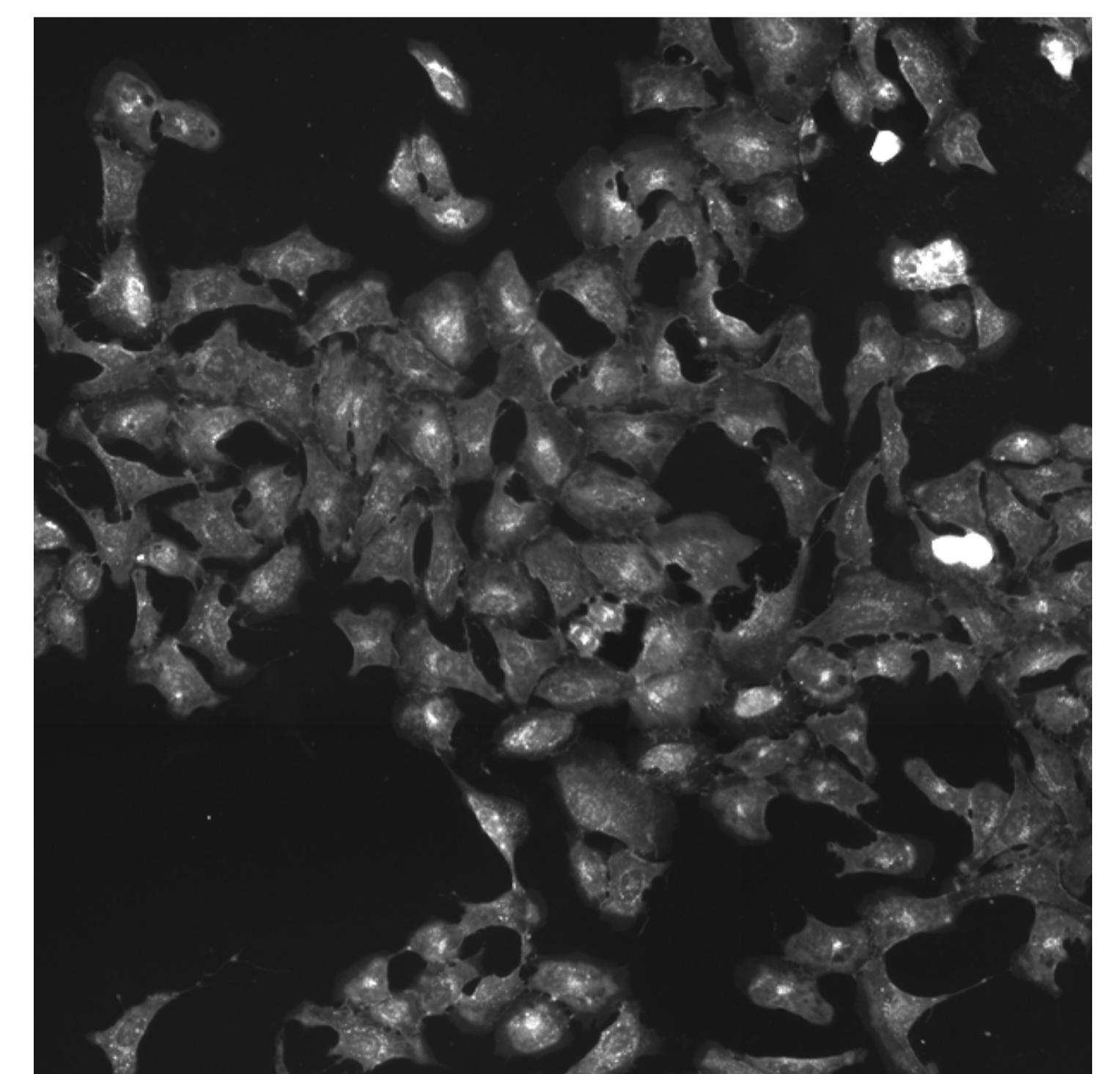
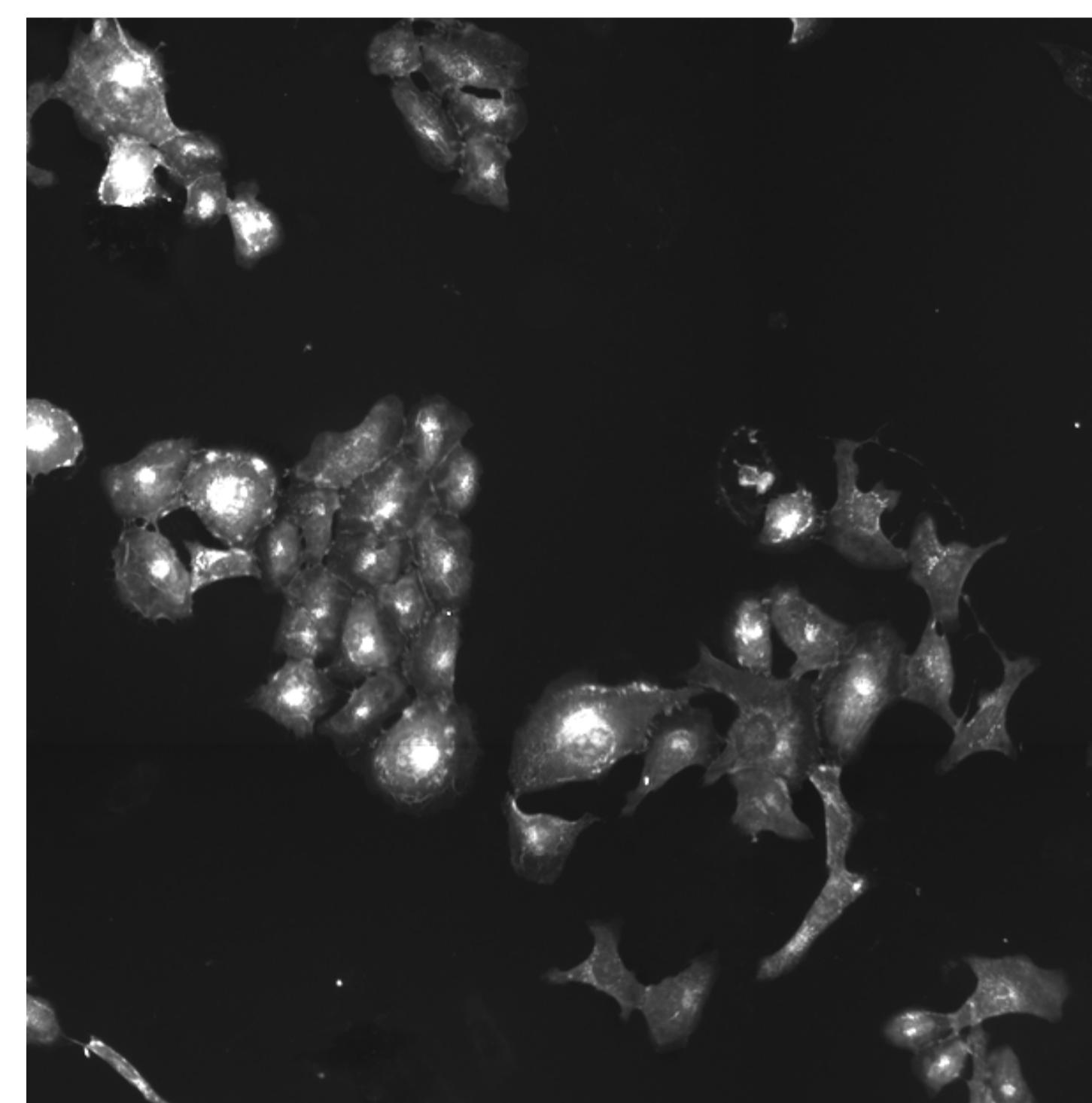
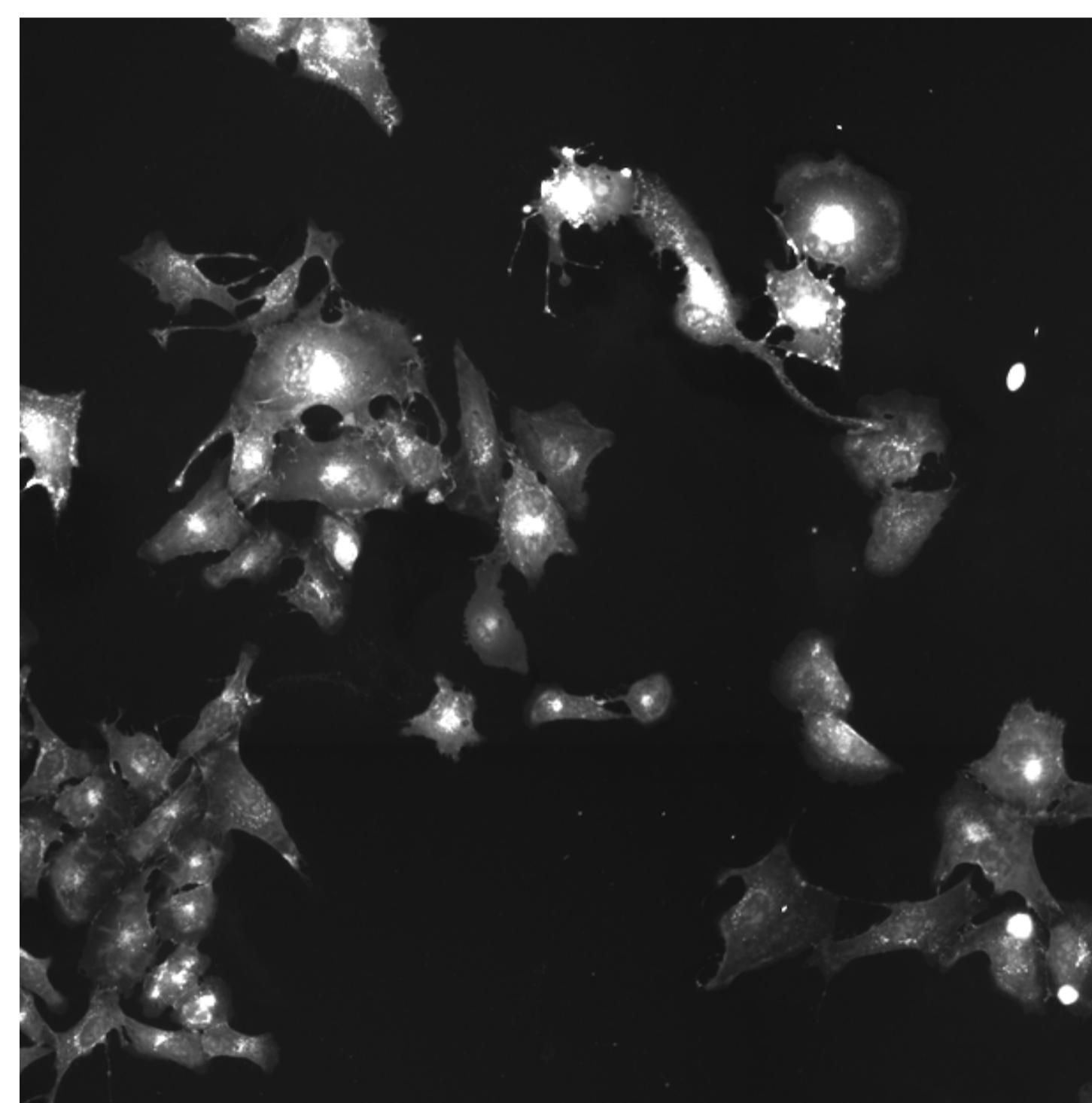
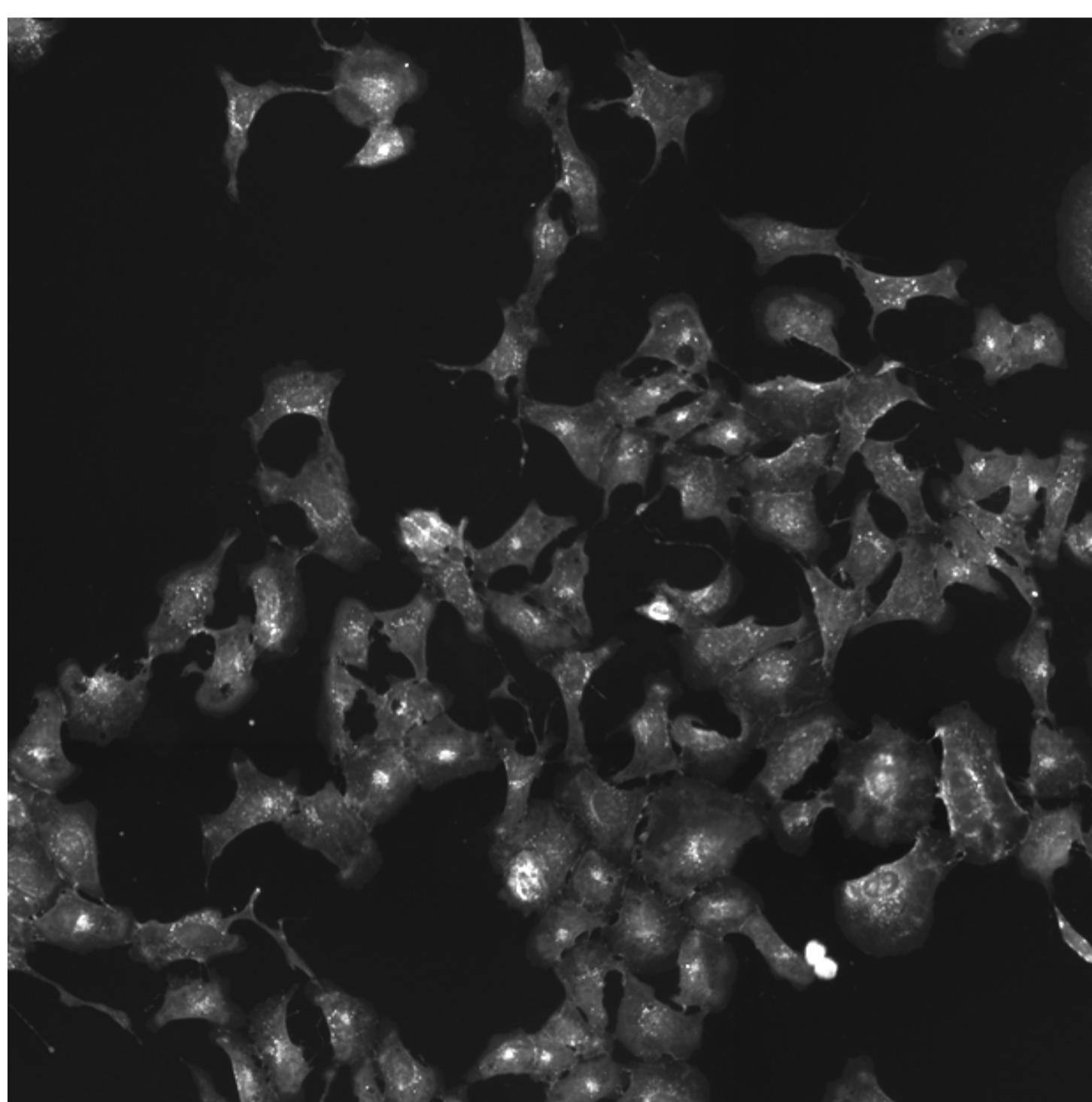


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

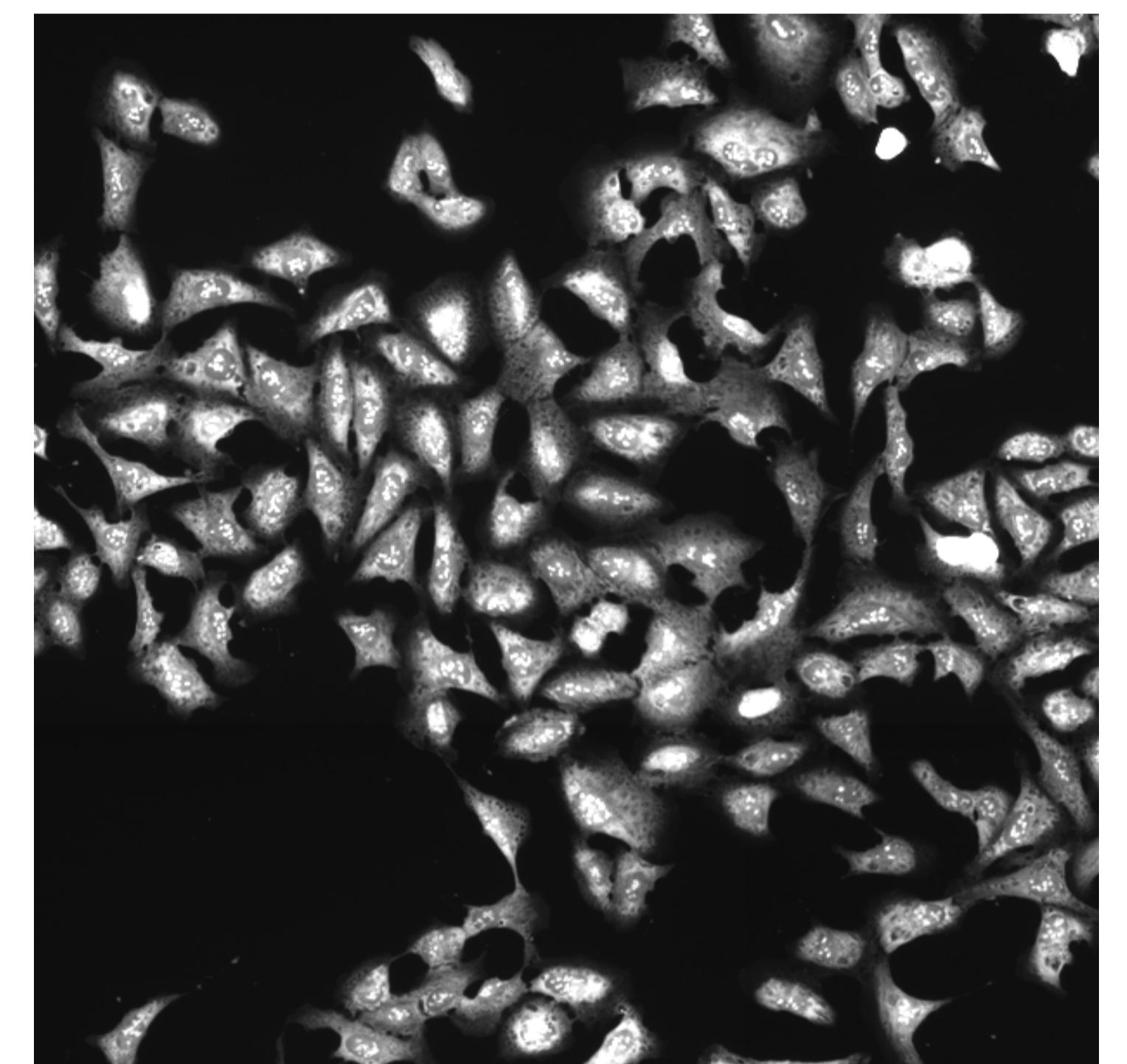
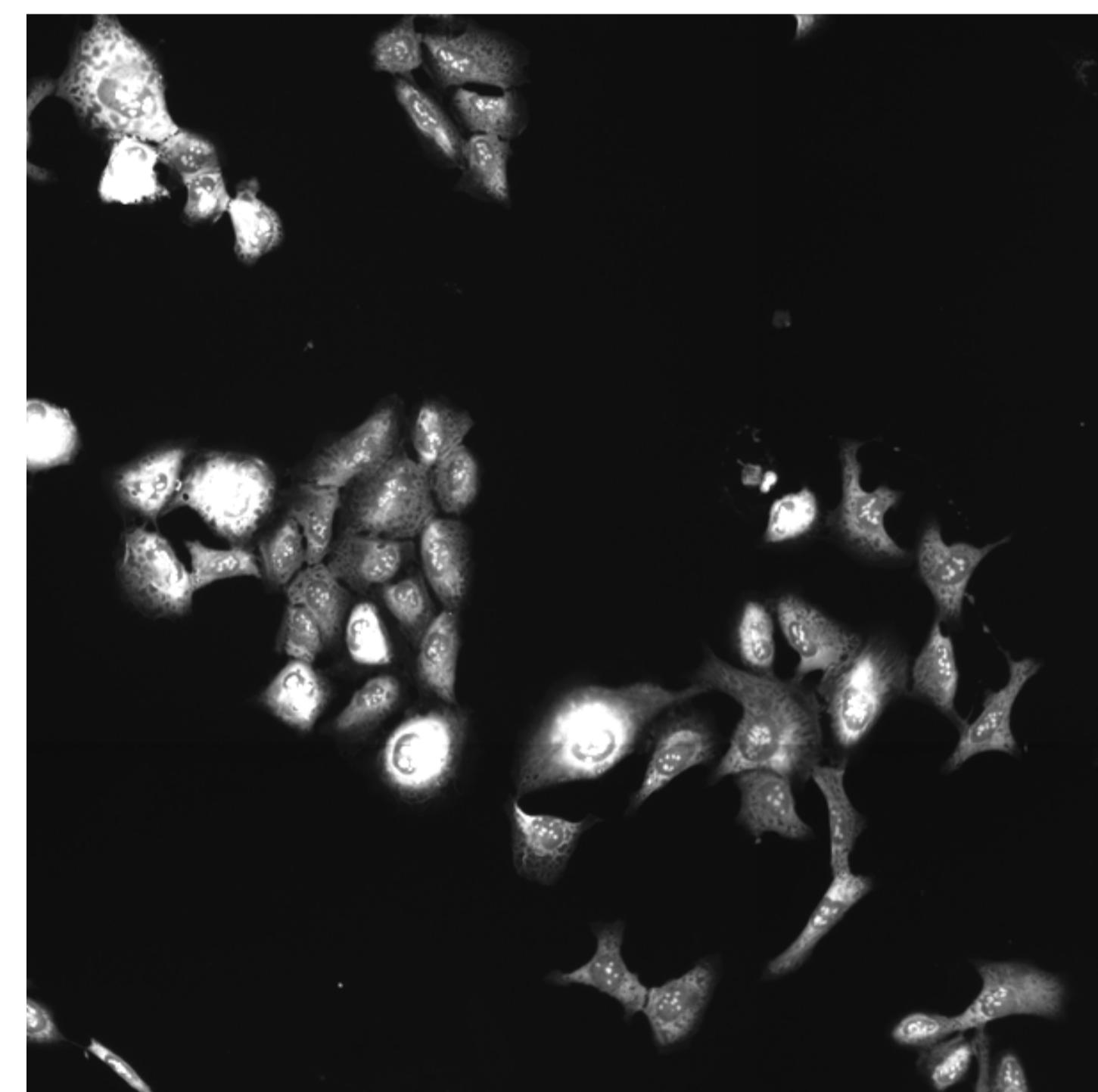
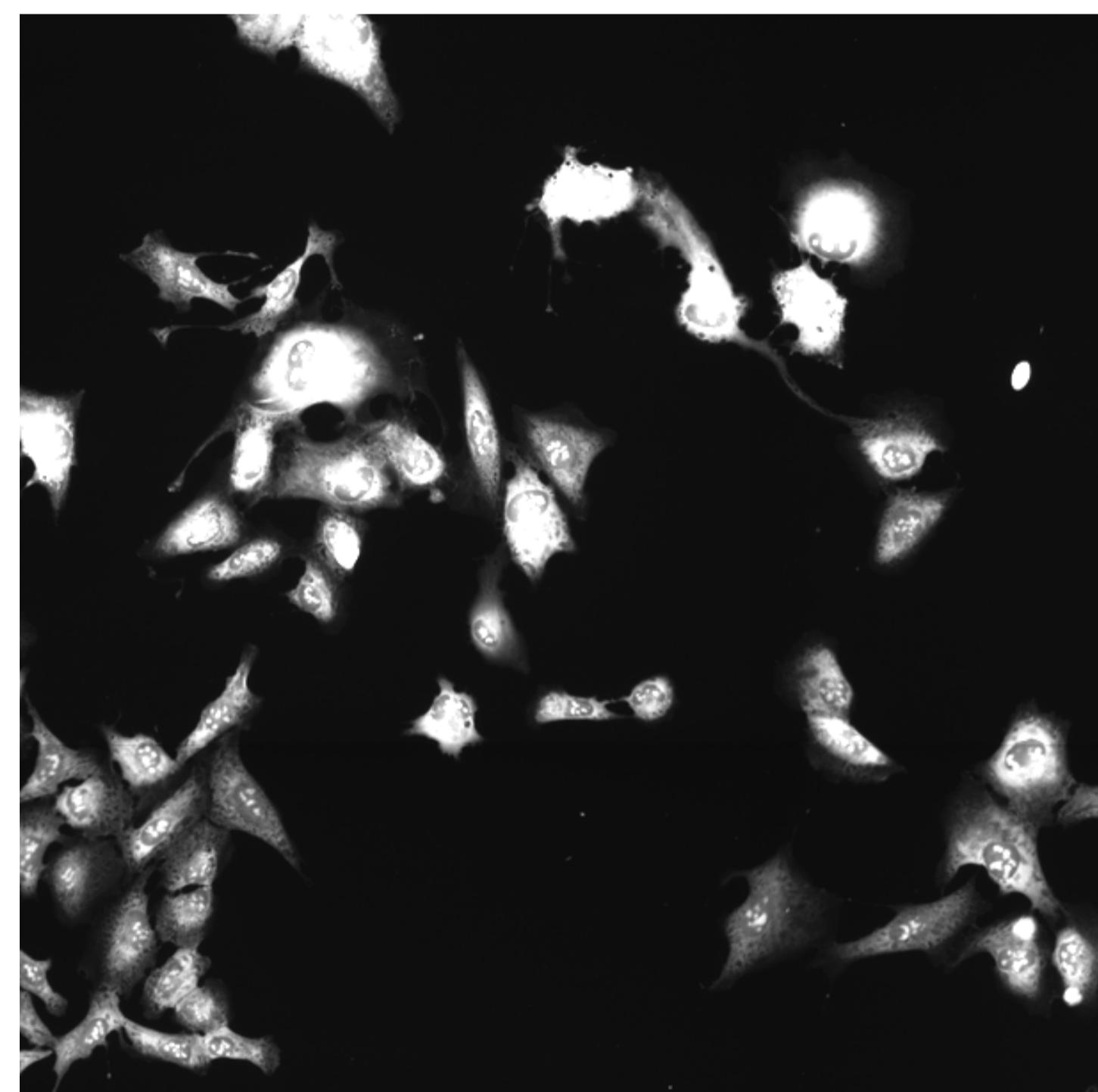
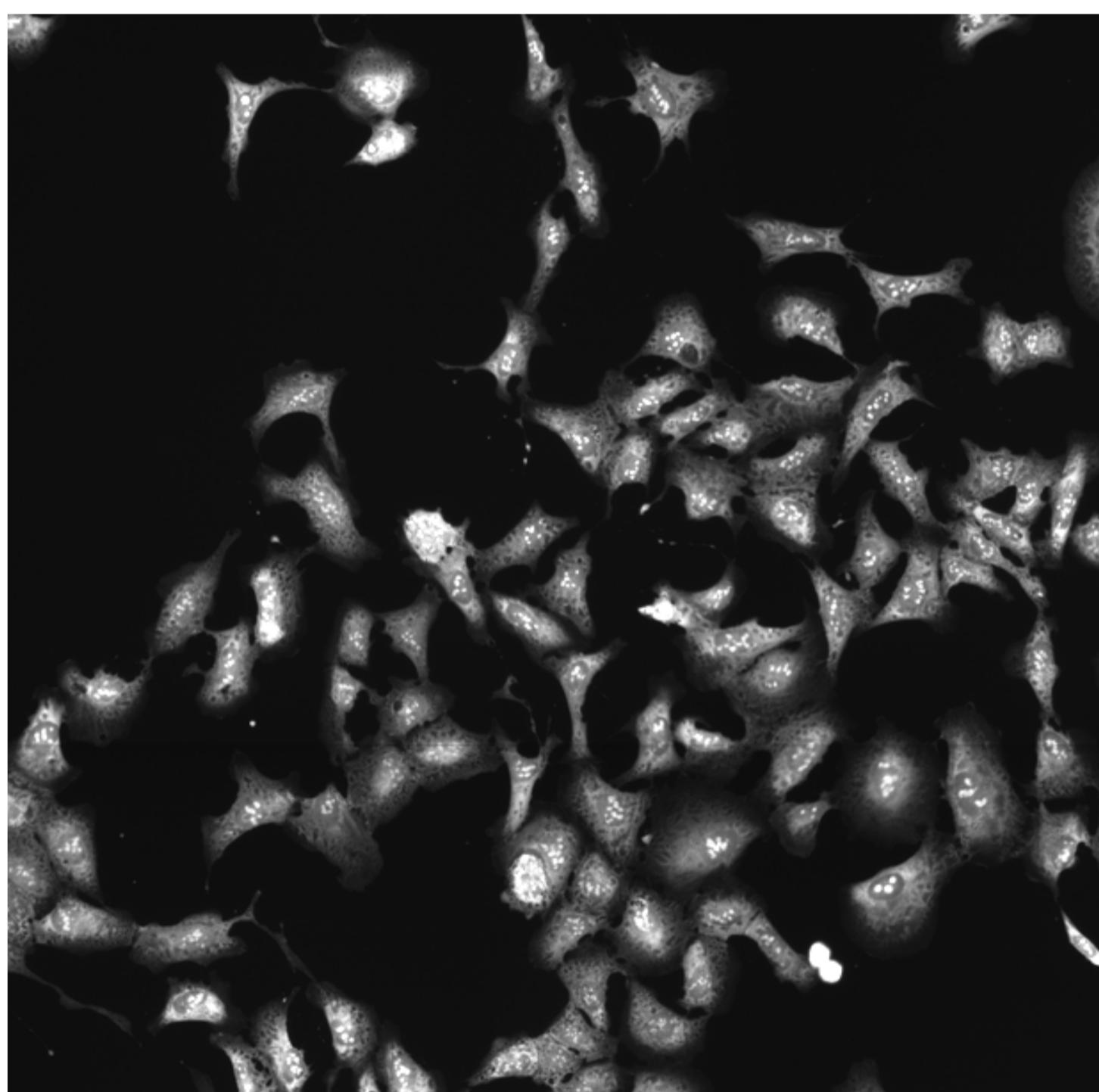
MAP3K2_WT.1

MAP3K2_WT.2

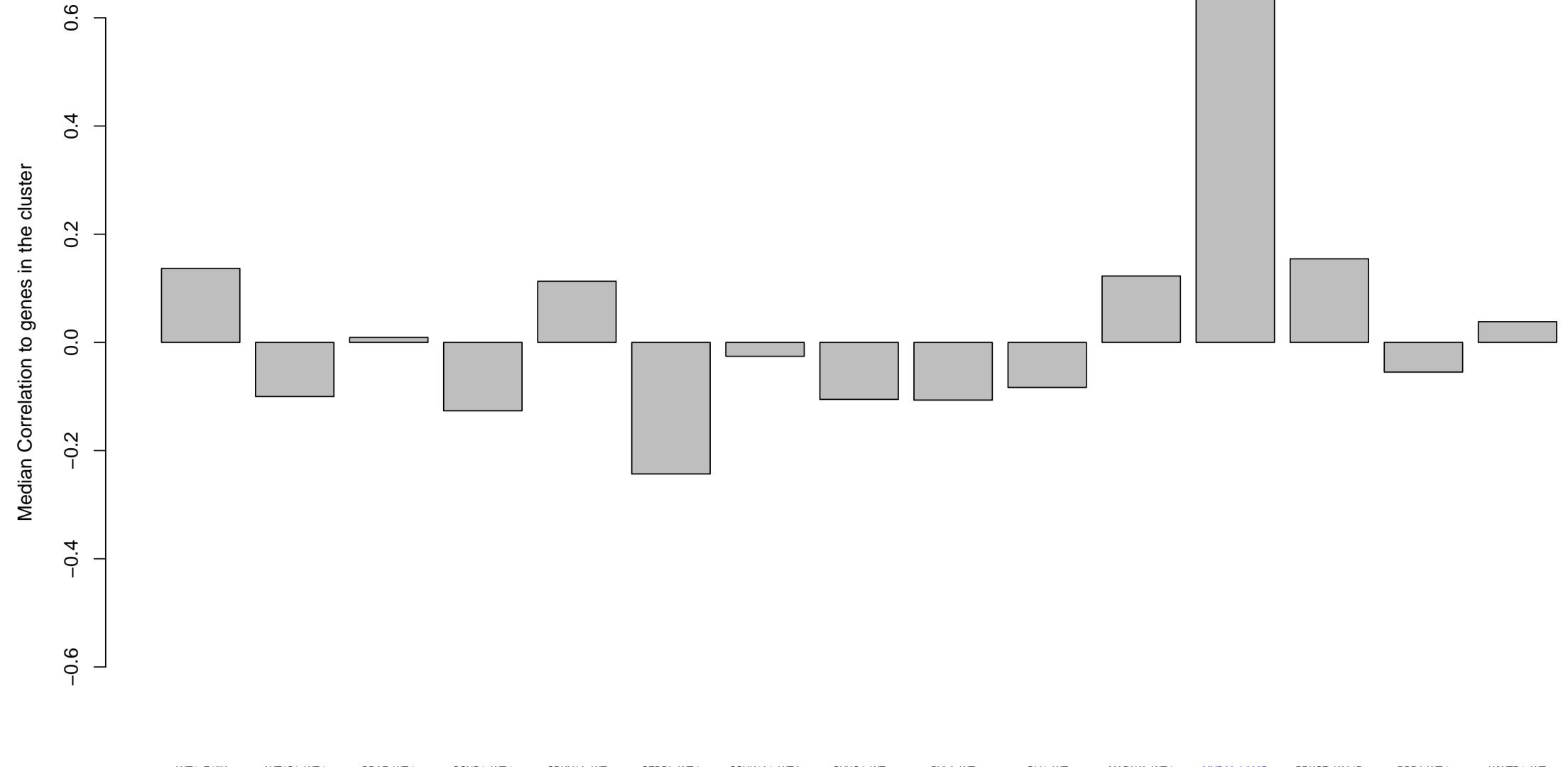
TRAF5_WT



RNA



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



Top 5 genes negatively correlated to the cluster

Treatment	Pathway	Regulation Type	Mean Correlation	Standard Deviation
PRKACG_WT 3	PKA	Activator	-0.35	0.11
TGFB1_WT	Canonical TGFbeta	Activator	-0.29	0.10
CEBPA_WT 2	Transcription Factors	Activator	-0.27	0.03
CEBPA_WT 1	Transcription Factors	Activator	-0.25	0.03
ATF4_WT 2	Canonical ER Stress/UPR	Activator	-0.25	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)

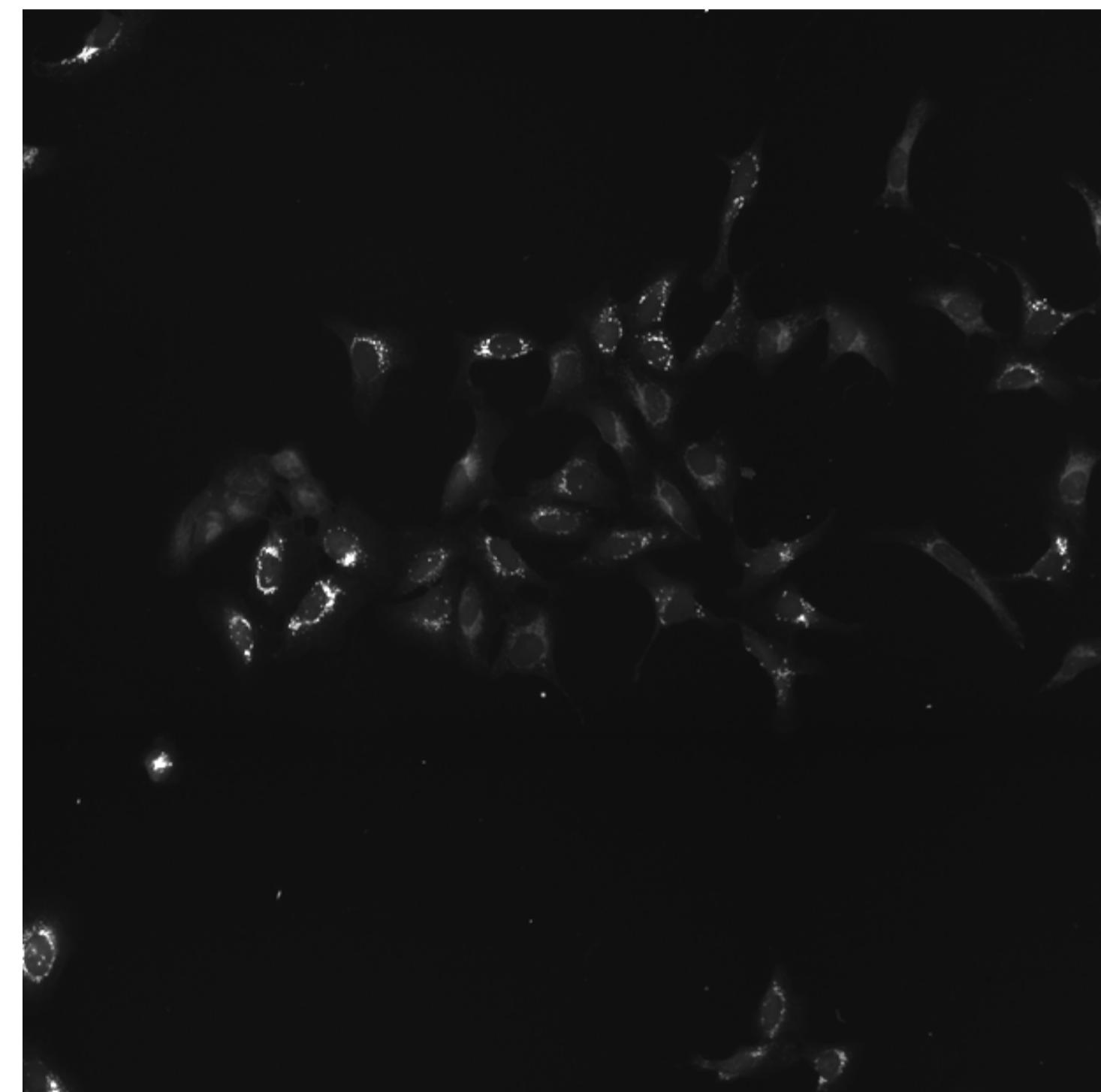
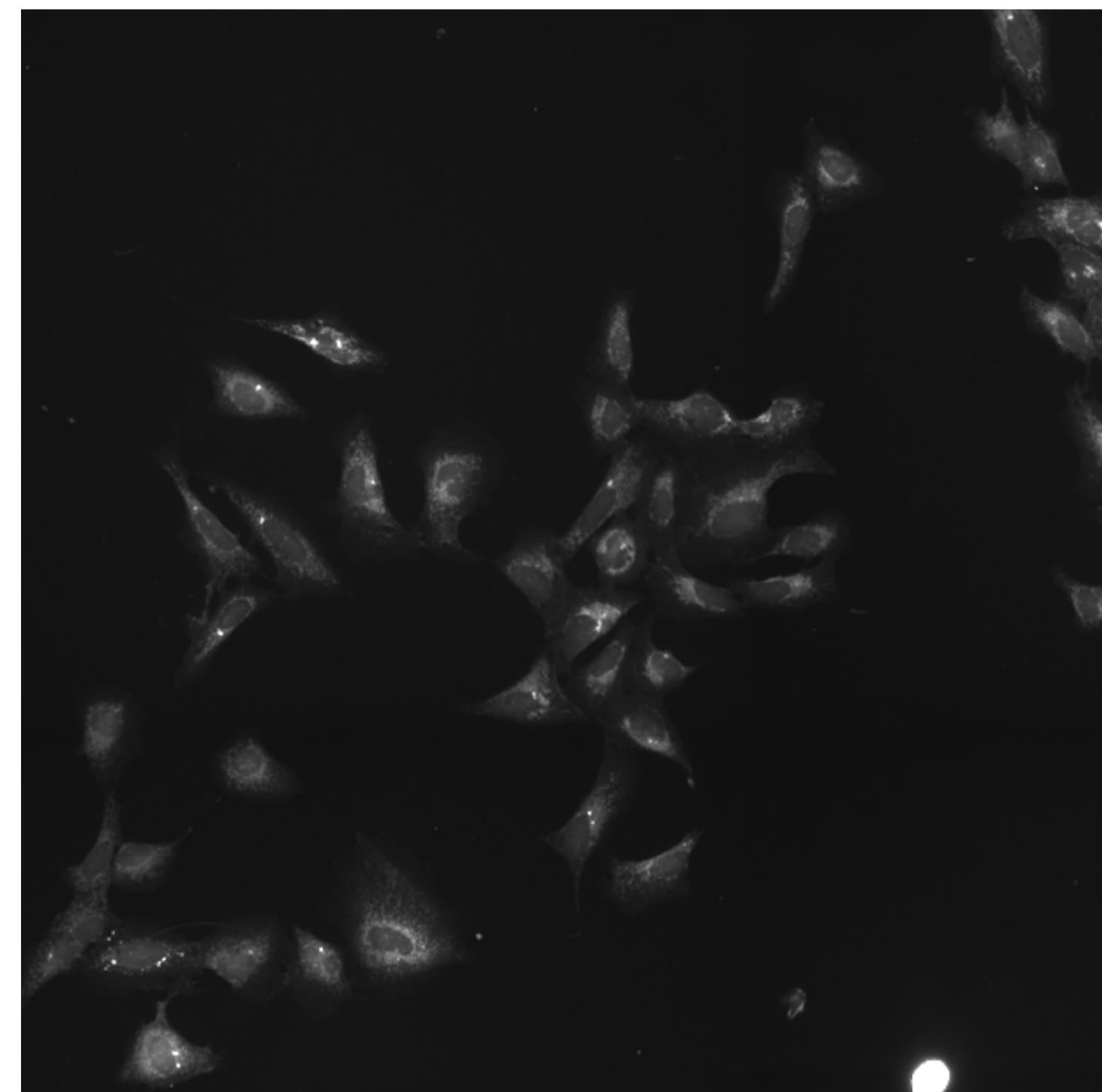
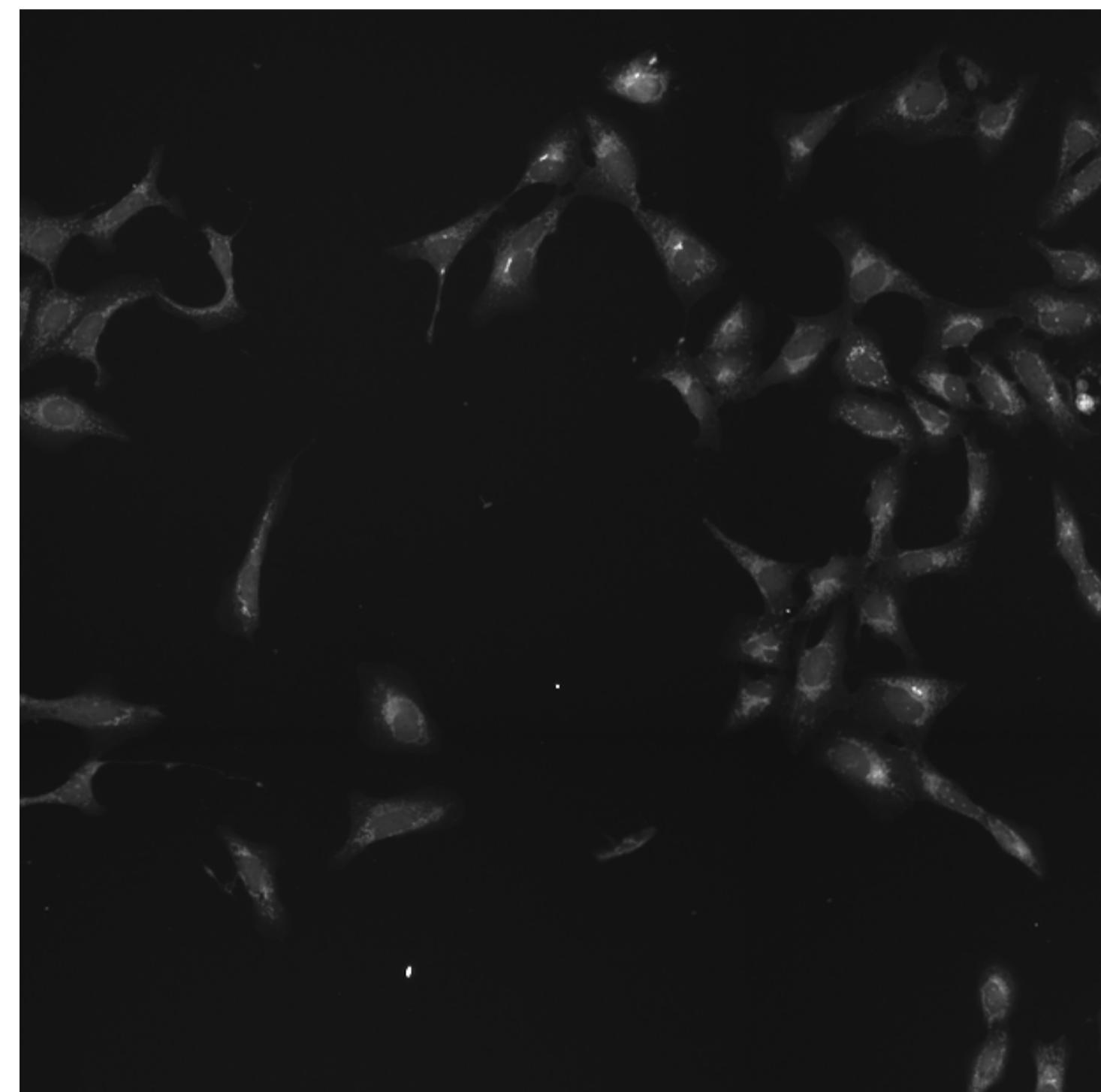
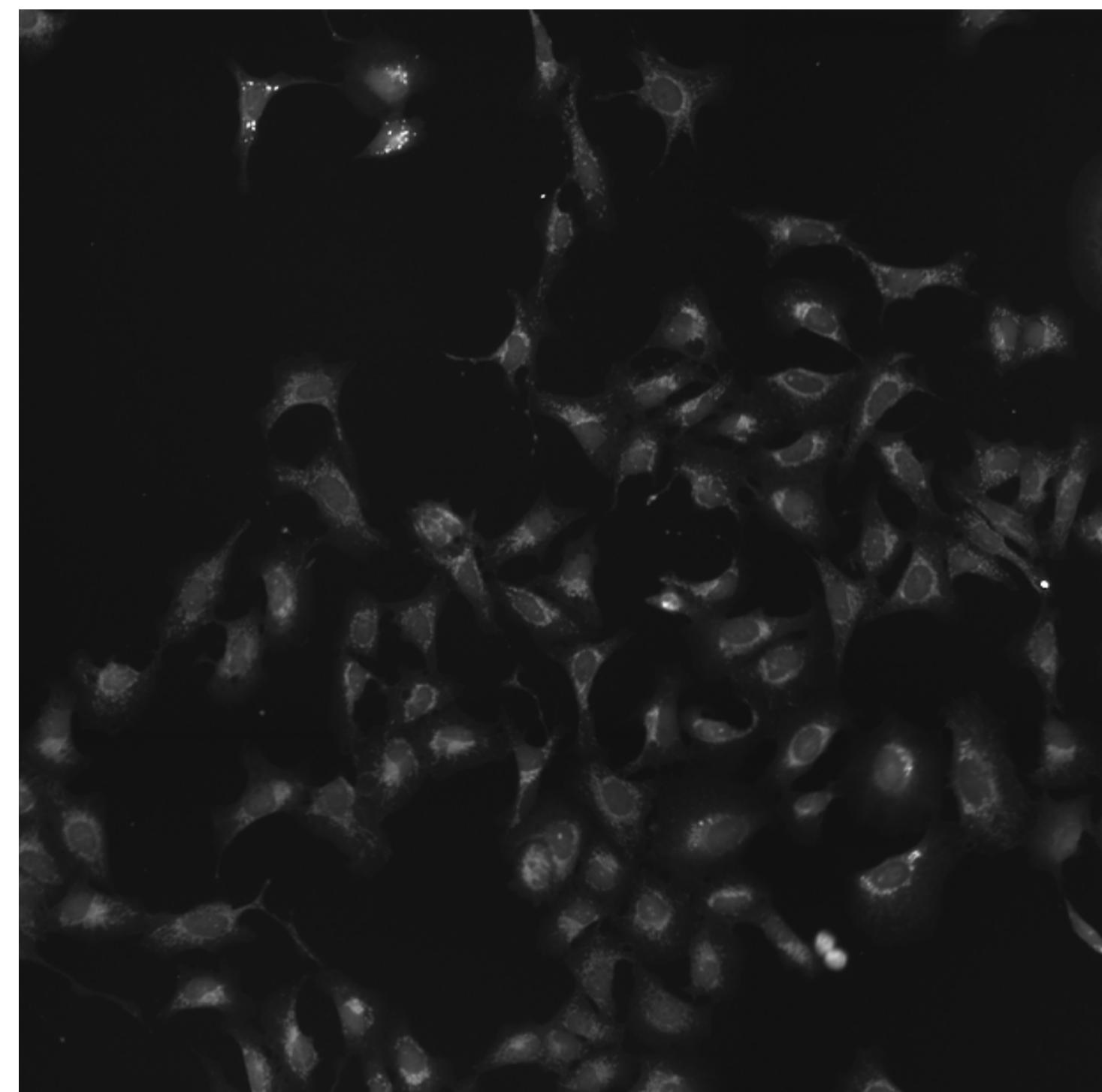
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MYD88_L265P

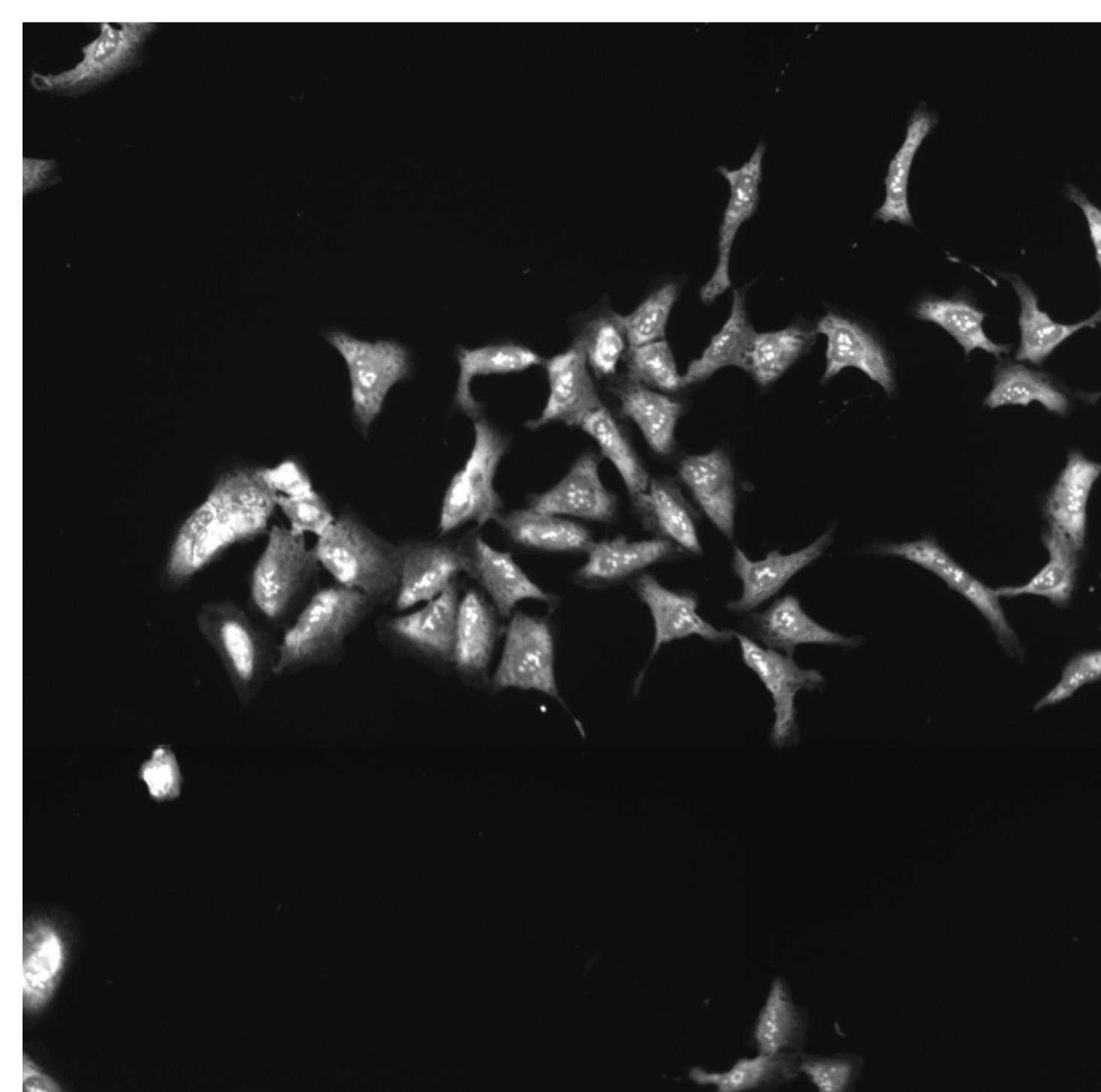
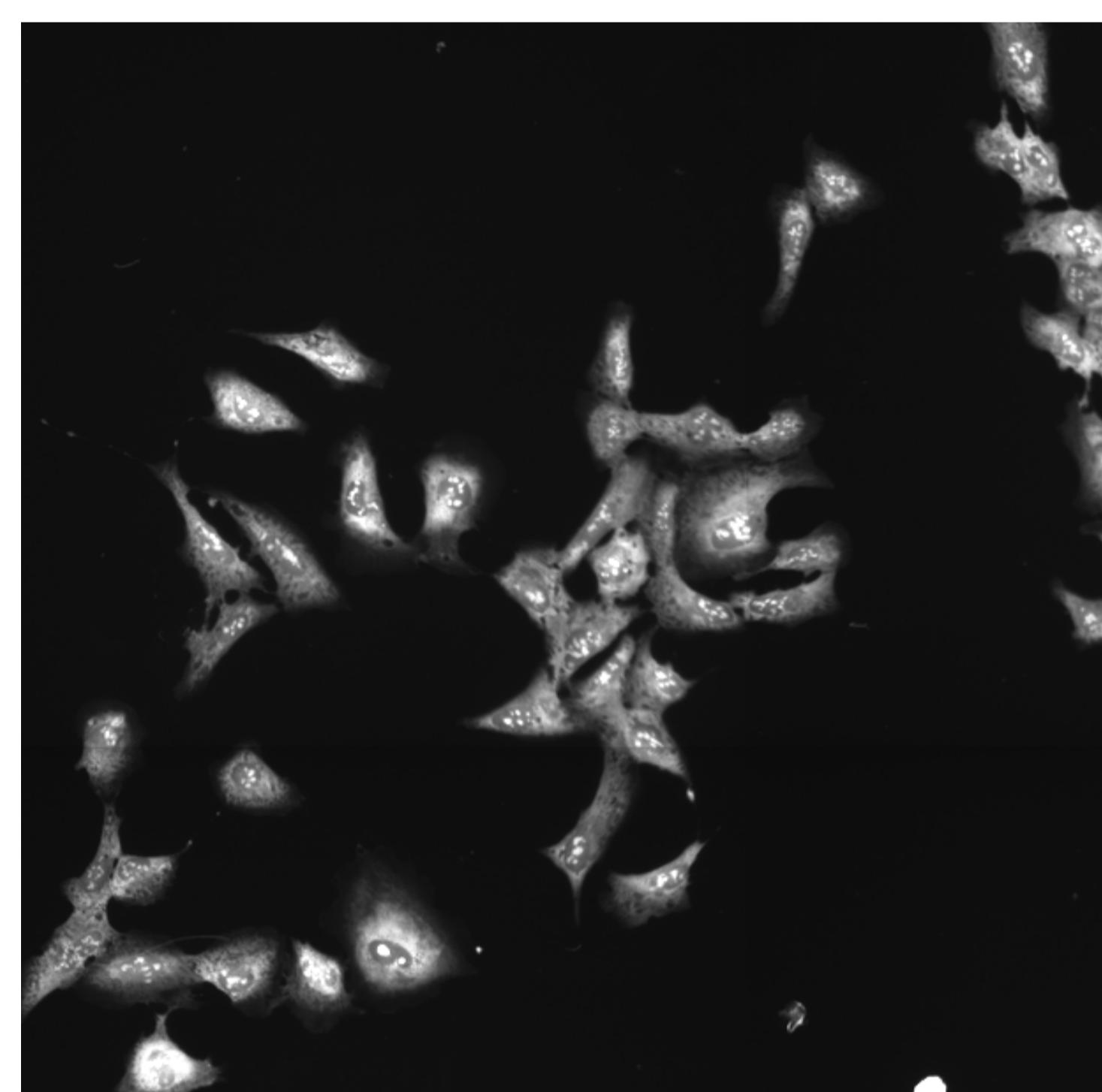
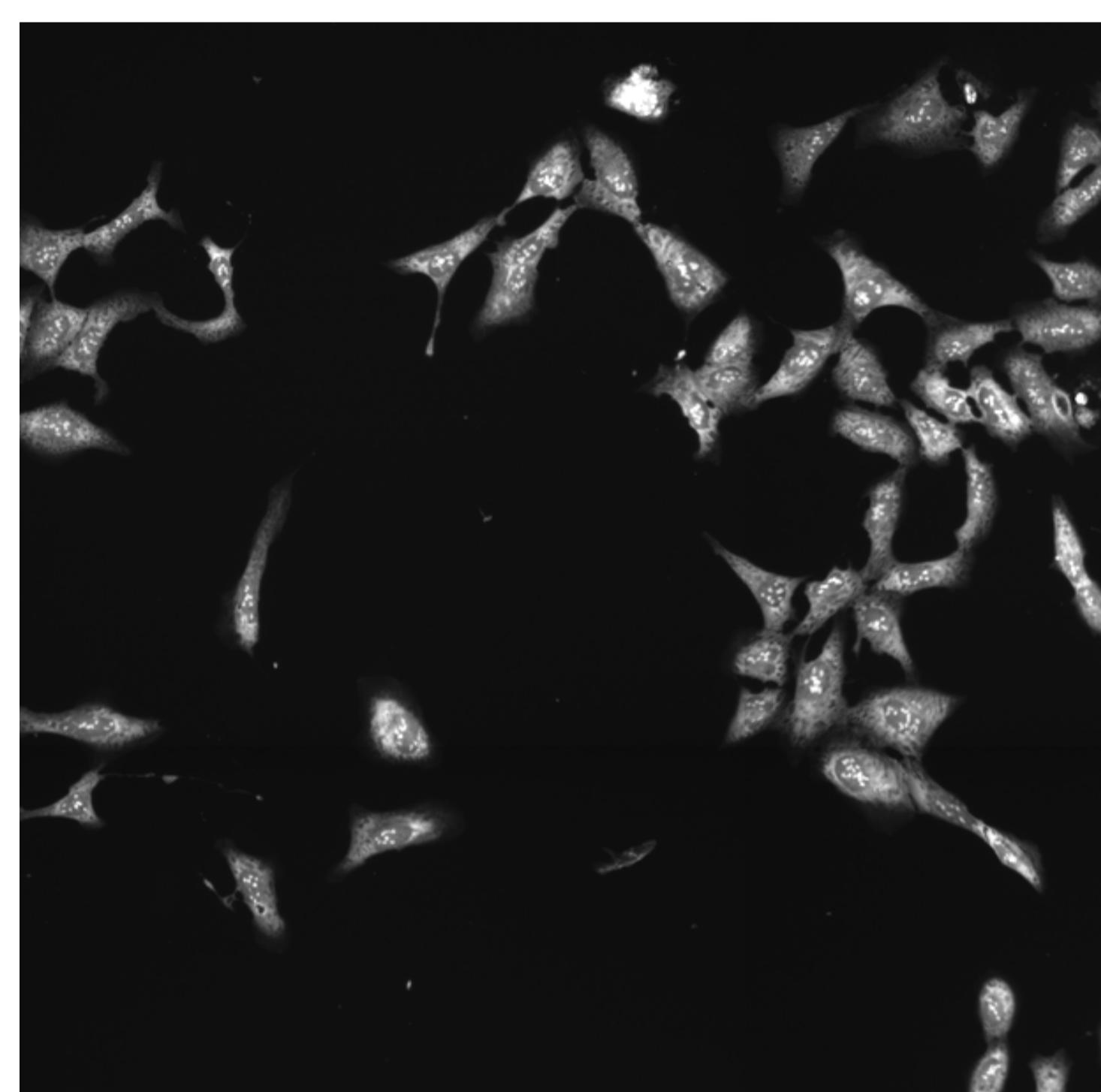
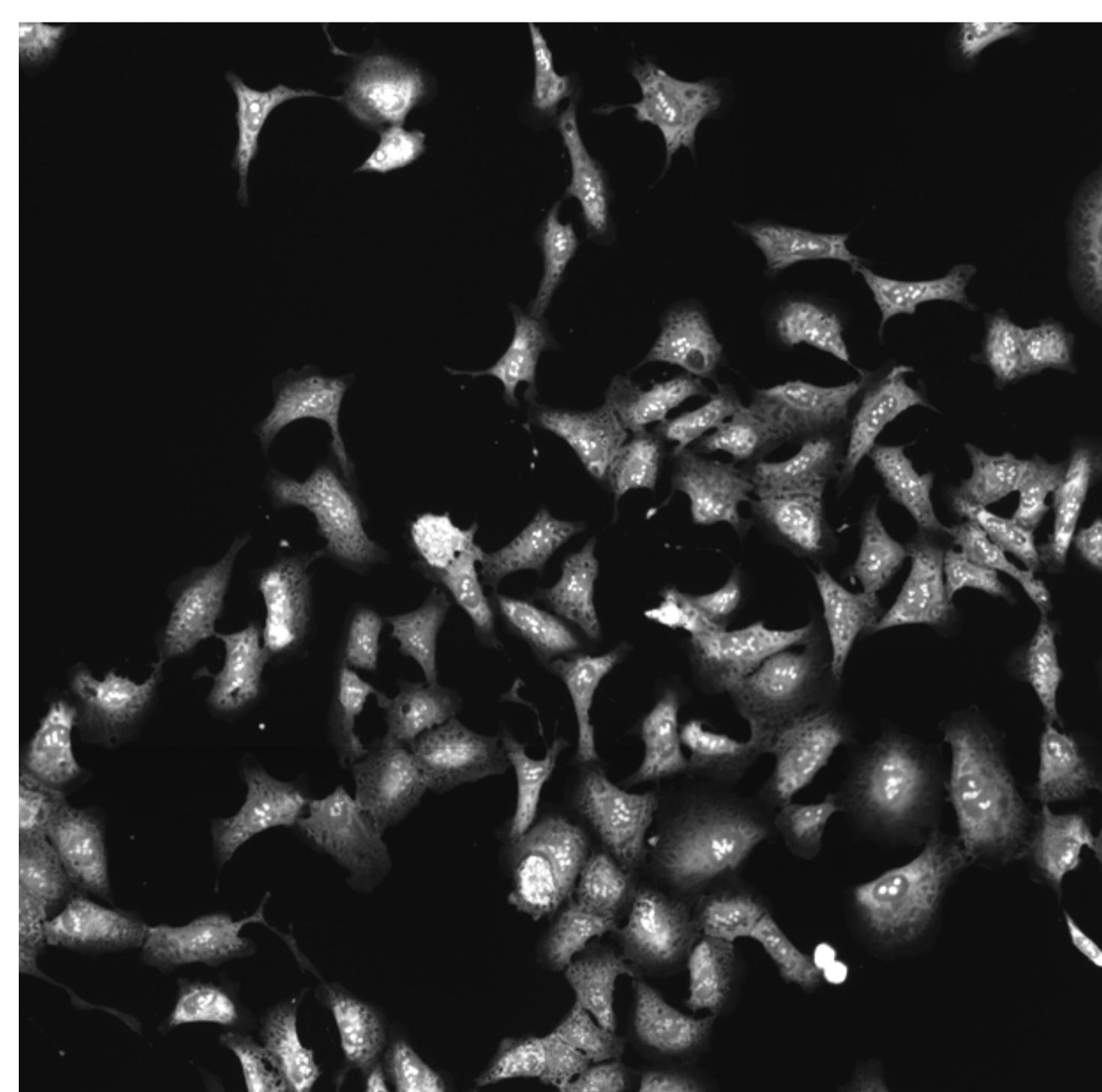
MYD88_WT

SDHA_WT

Mito

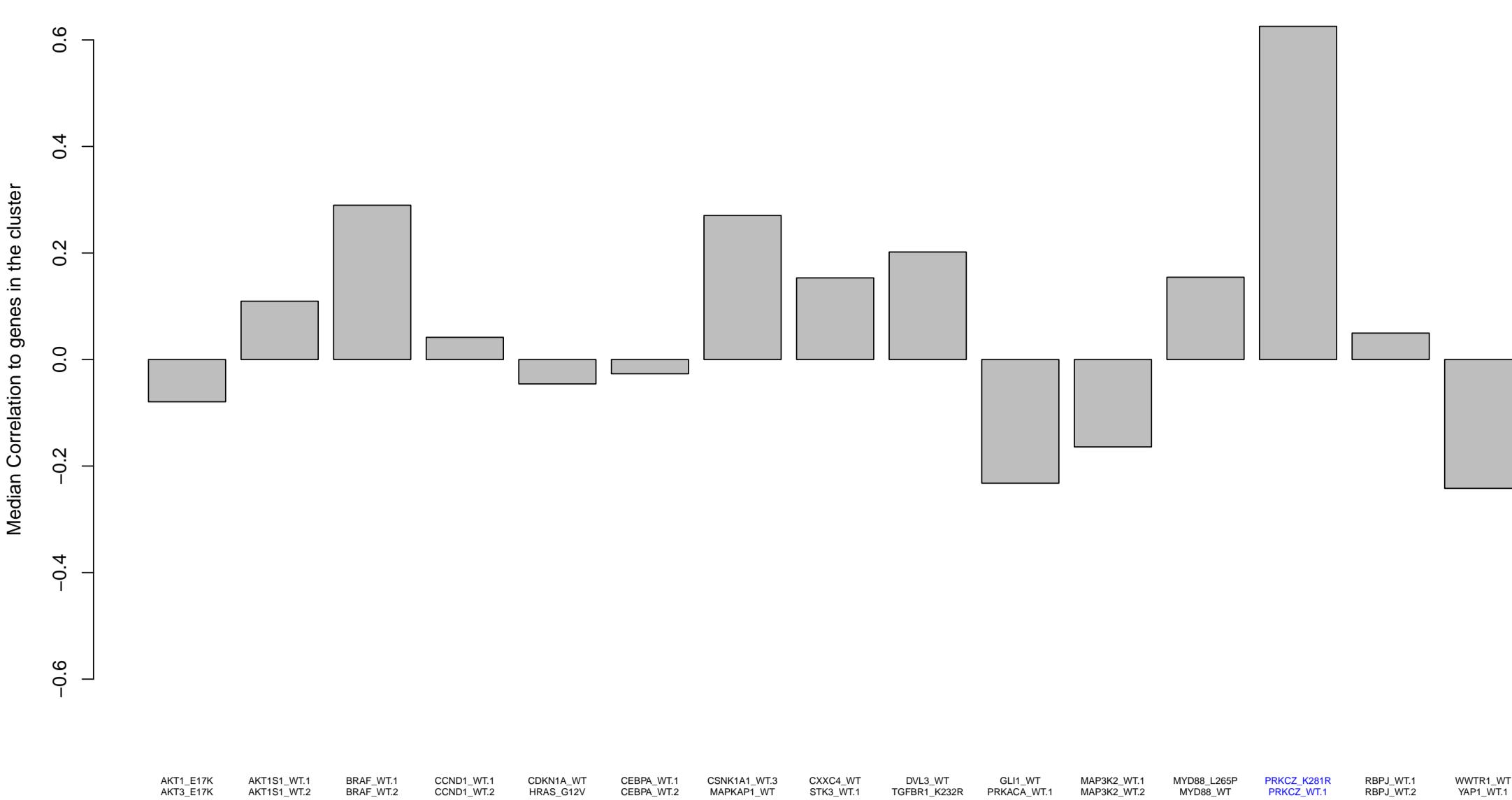


RNA



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?

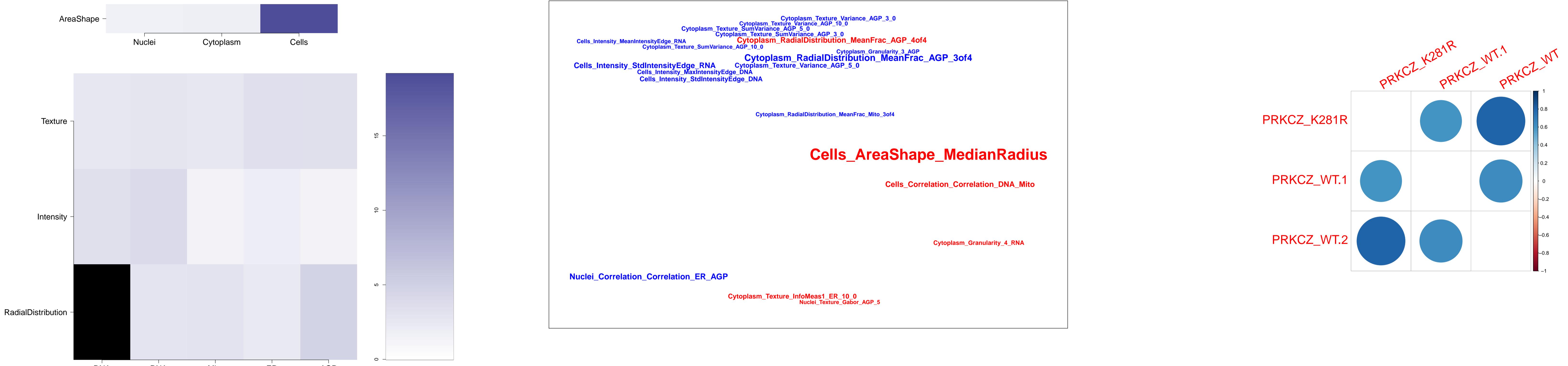
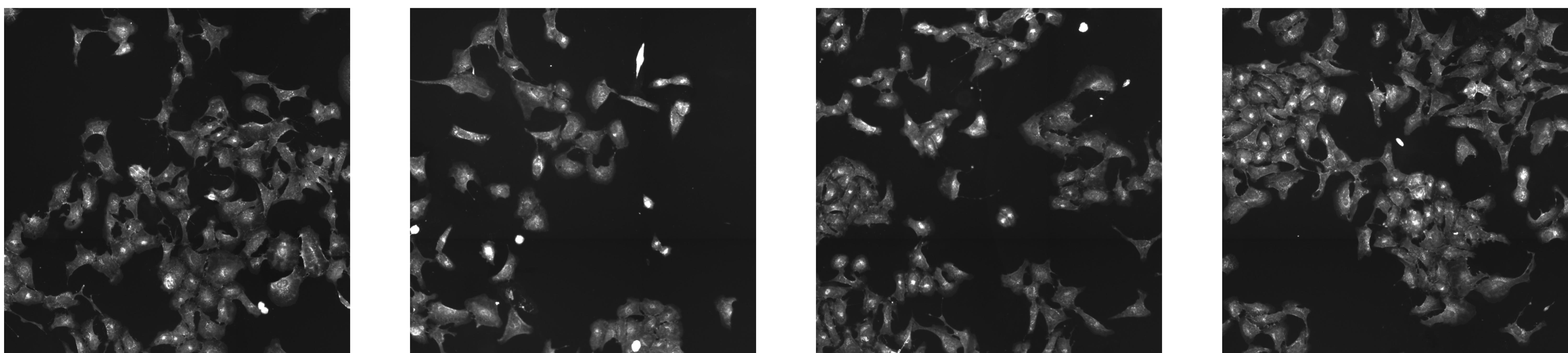


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

PRKCZ_K281R

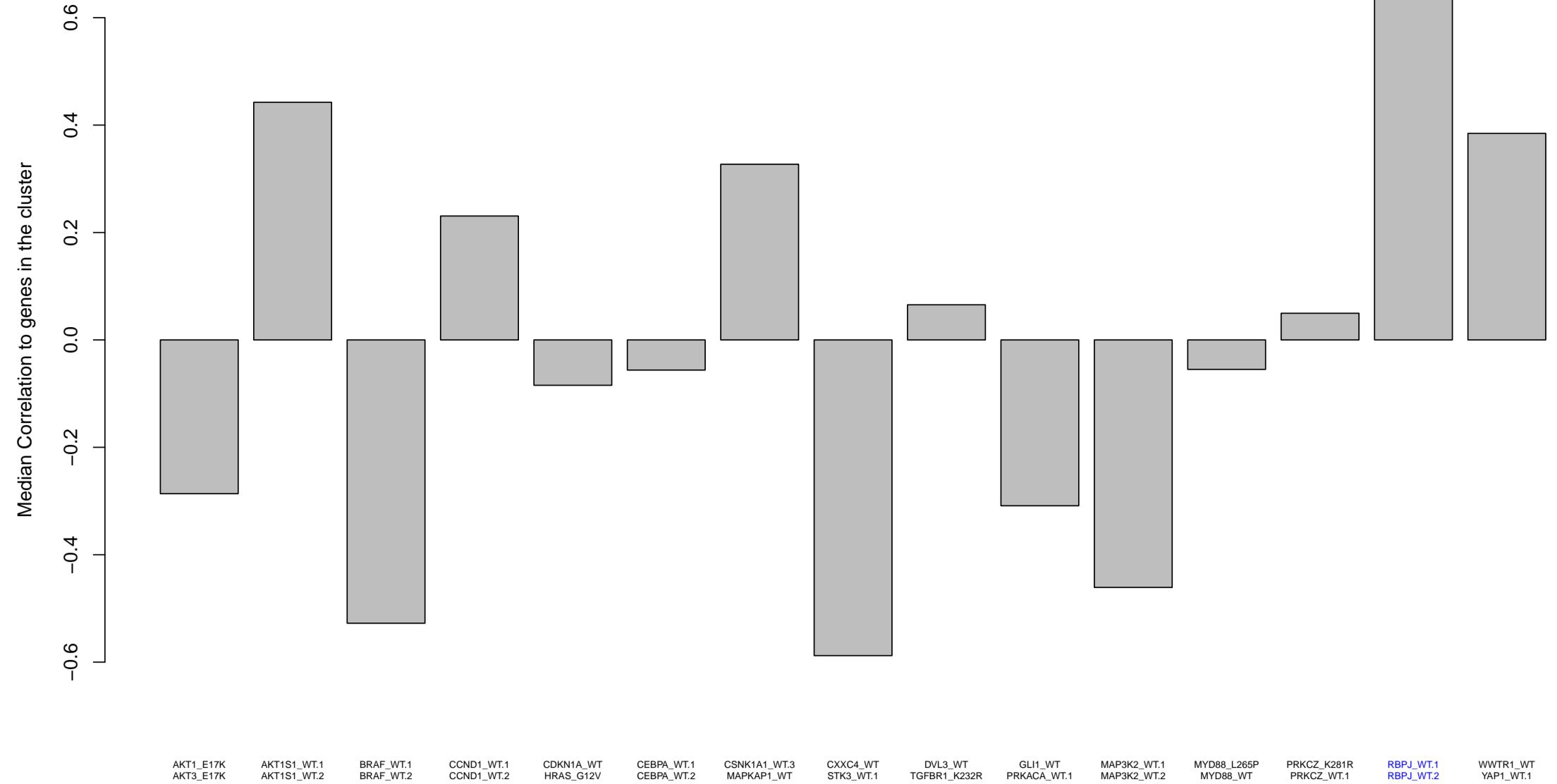
PRKCZ_WT.1

PRKCZ_WT.2



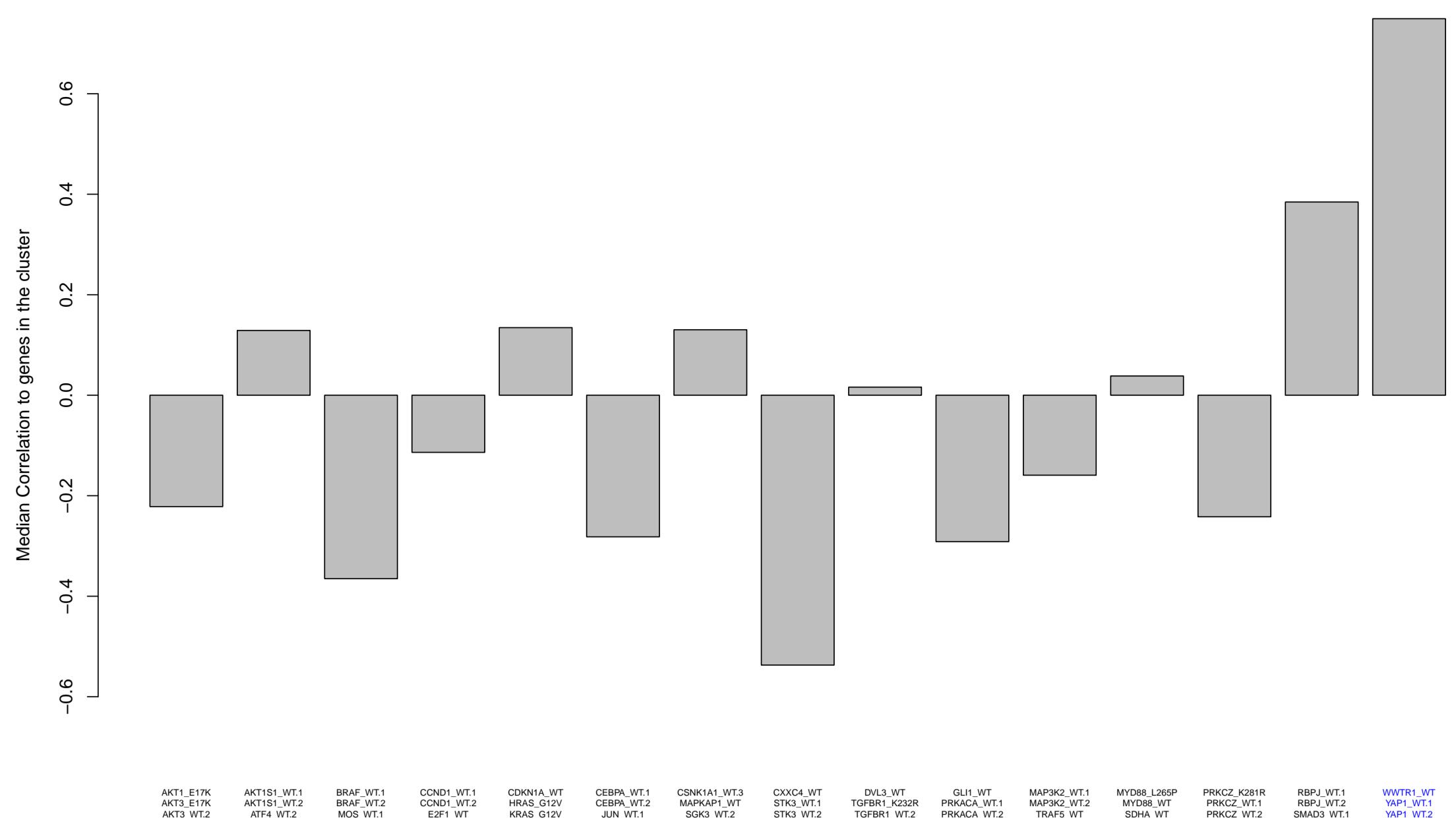
AGP

RNA



Cluster 15

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	Expert Annotation		Regulation Type	Mean Correlation	Standard Deviation	
	Pathway					
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	

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?

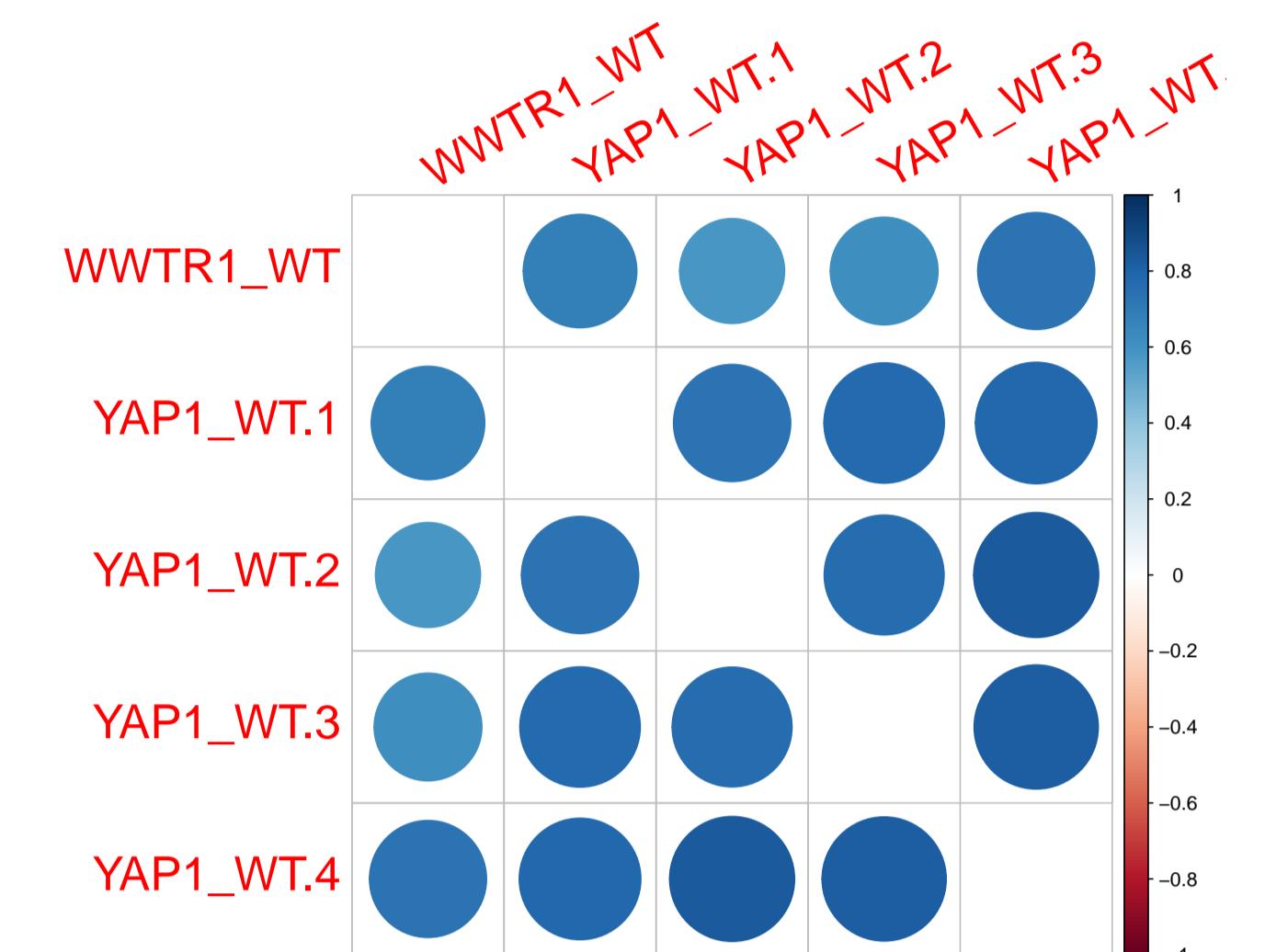
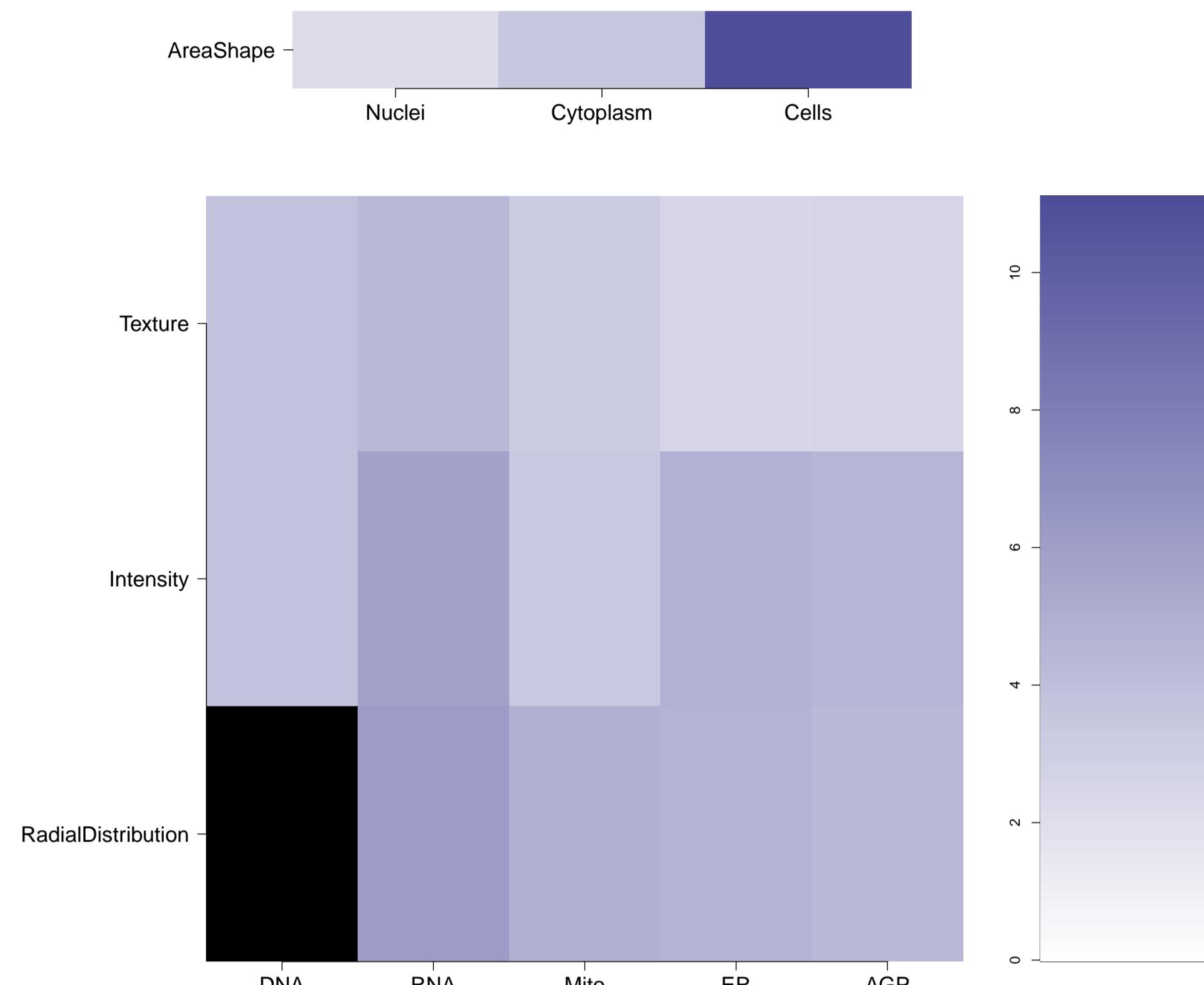


Plate : 41744 (Channels are sorted based on their dominance in the grid plot)

Empty

WWTR1_WT

YAP1_WT.1

YAP1_WT.2

YAP1_WT.3

YAP1_WT.4

