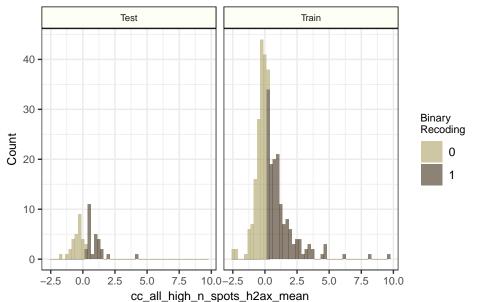
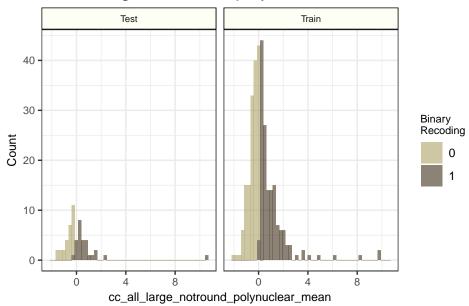
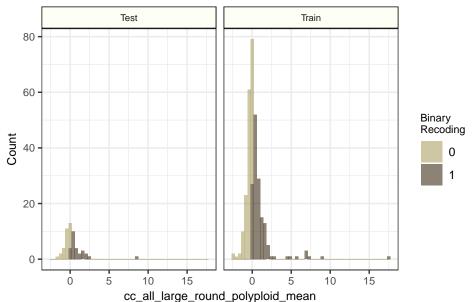
### cc\_all\_high\_n\_spots\_h2ax\_mean



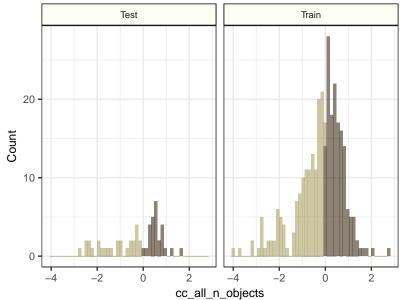
### cc\_all\_large\_notround\_polynuclear\_mean



### cc\_all\_large\_round\_polyploid\_mean

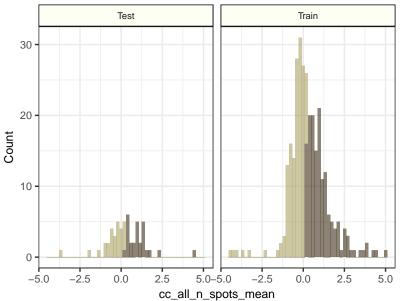


# cc\_all\_n\_objects



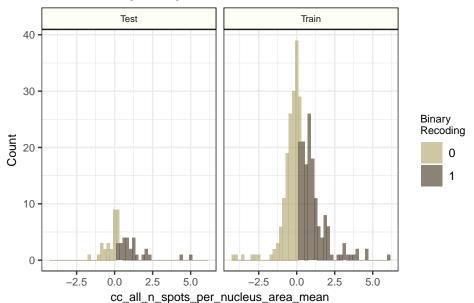


#### cc\_all\_n\_spots\_mean

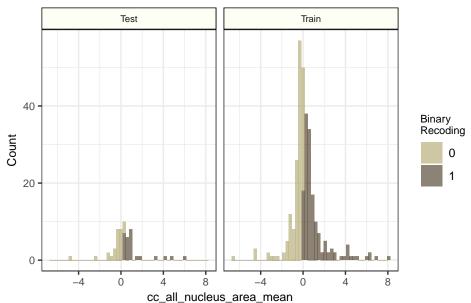




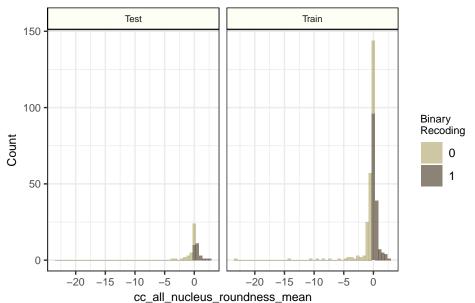
#### cc\_all\_n\_spots\_per\_nucleus\_area\_mean



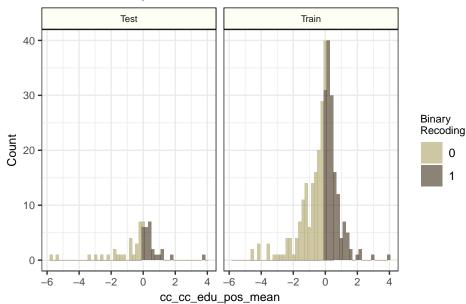
### cc\_all\_nucleus\_area\_mean



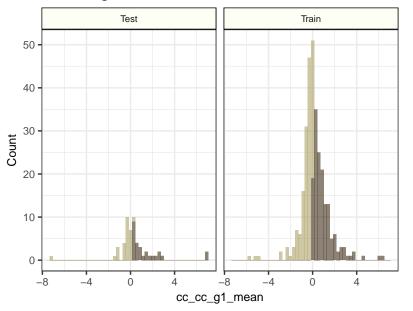
### cc\_all\_nucleus\_roundness\_mean



#### cc\_cc\_edu\_pos\_mean

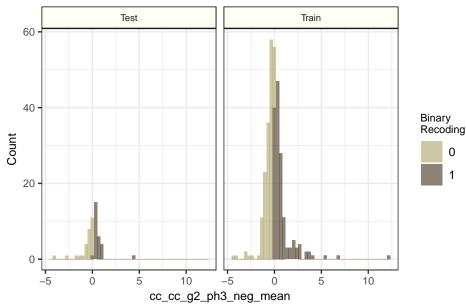


# cc\_cc\_g1\_mean



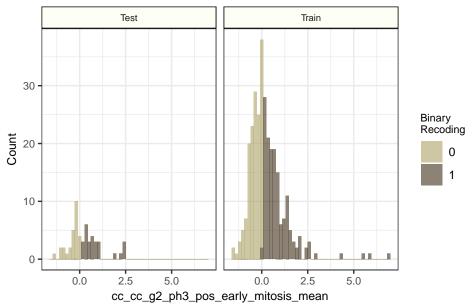


# cc\_cc\_g2\_ph3\_neg\_mean

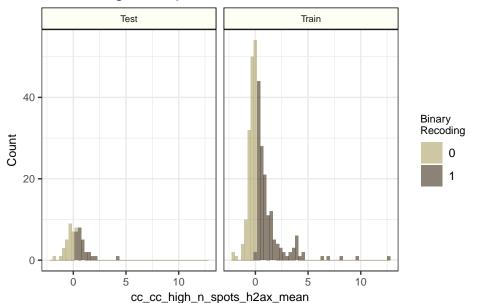


0

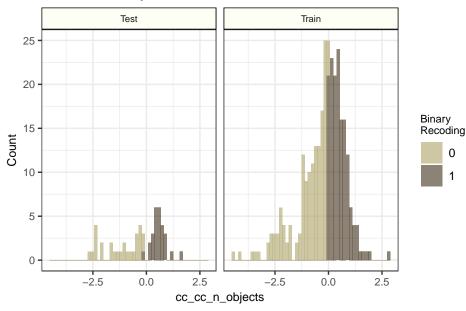
#### cc\_cc\_g2\_ph3\_pos\_early\_mitosis\_mean



### cc\_cc\_high\_n\_spots\_h2ax\_mean

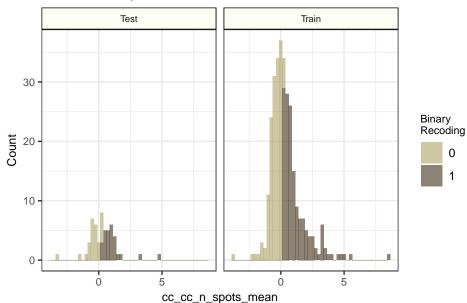


# cc\_cc\_n\_objects

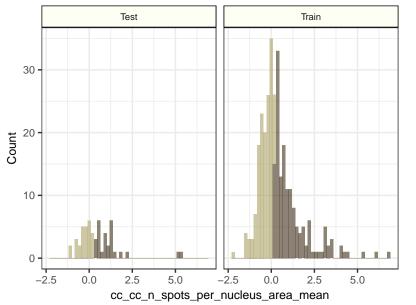


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# cc\_cc\_n\_spots\_mean

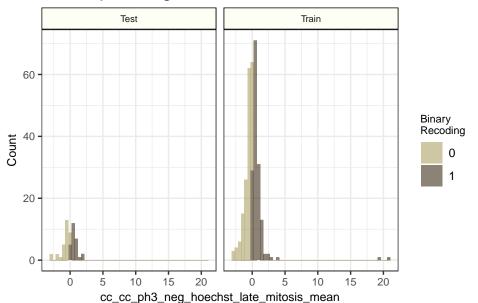


#### cc\_cc\_n\_spots\_per\_nucleus\_area\_mean

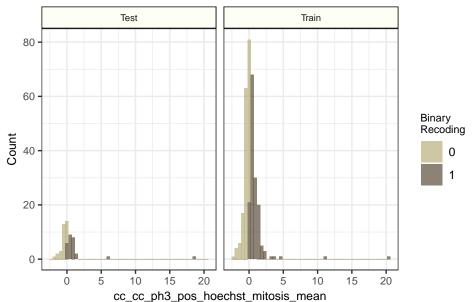




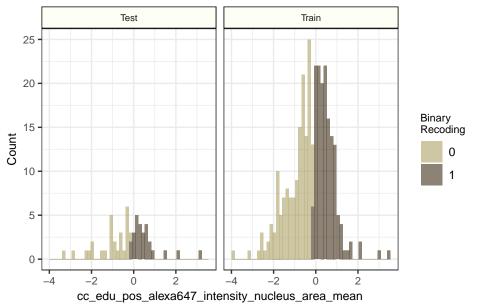
#### cc\_cc\_ph3\_neg\_hoechst\_late\_mitosis\_mean



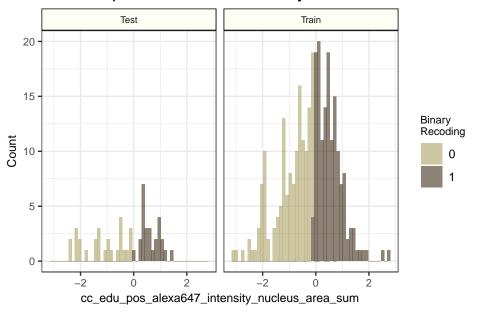
#### cc\_cc\_ph3\_pos\_hoechst\_mitosis\_mean



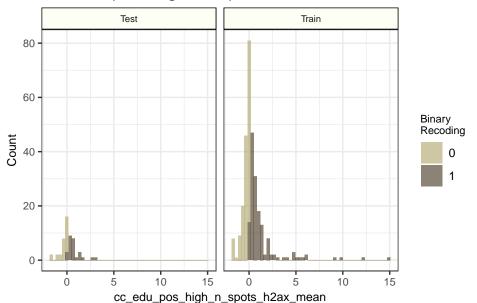
cc\_edu\_pos\_alexa647\_intensity\_nucleus\_area\_mear



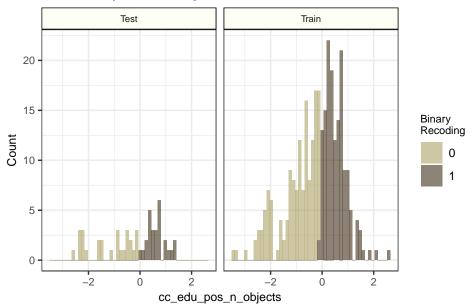
#### cc\_edu\_pos\_alexa647\_intensity\_nucleus\_area\_sum



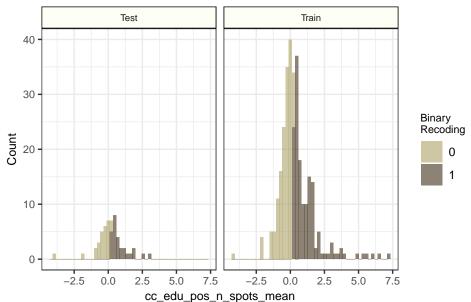
### cc\_edu\_pos\_high\_n\_spots\_h2ax\_mean



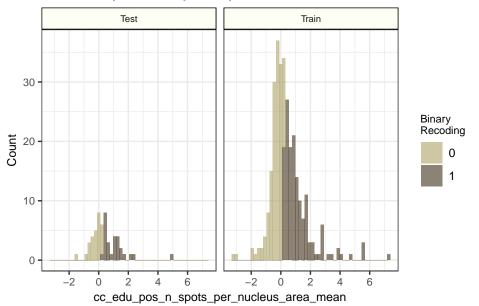
# cc\_edu\_pos\_n\_objects



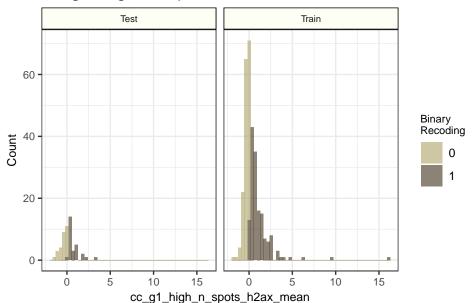
# cc\_edu\_pos\_n\_spots\_mean



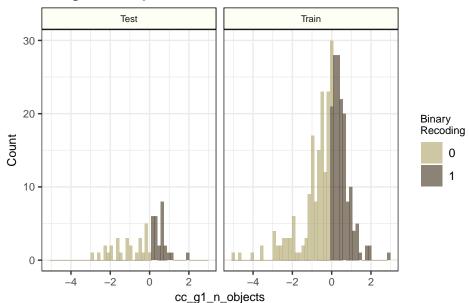
#### cc\_edu\_pos\_n\_spots\_per\_nucleus\_area\_mean



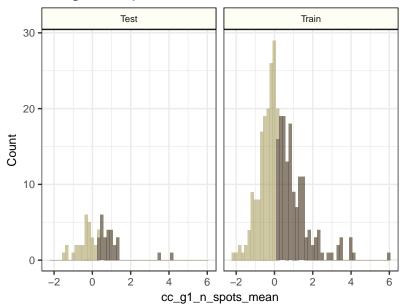
# cc\_g1\_high\_n\_spots\_h2ax\_mean



# cc\_g1\_n\_objects



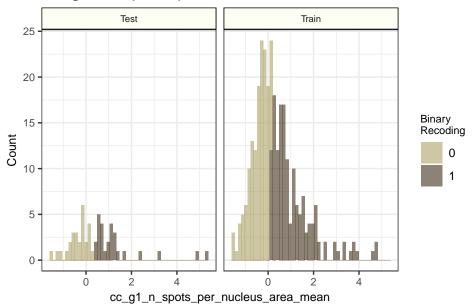
### cc\_g1\_n\_spots\_mean



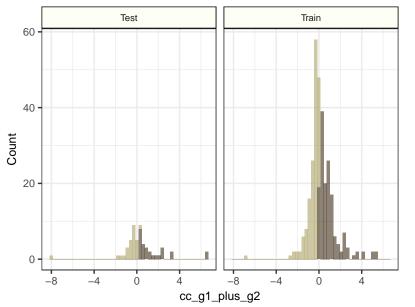
Binary Recoding

0

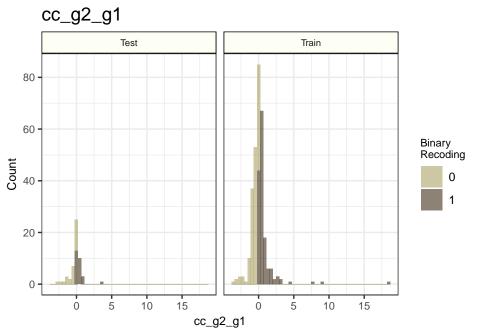
#### cc\_g1\_n\_spots\_per\_nucleus\_area\_mean



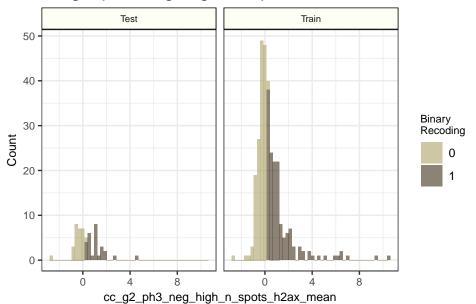
# cc\_g1\_plus\_g2



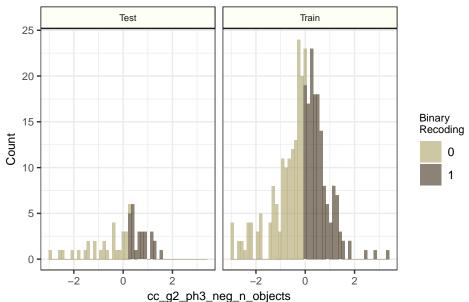




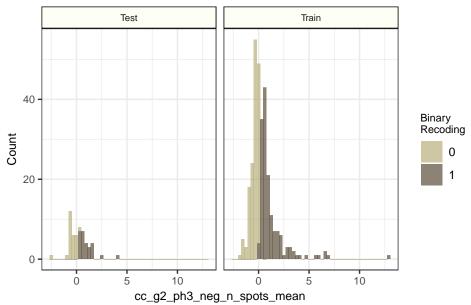
cc\_g2\_ph3\_neg\_high\_n\_spots\_h2ax\_mean



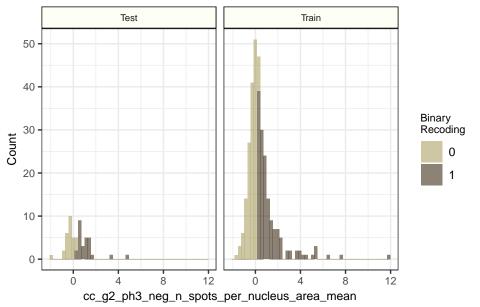
# cc\_g2\_ph3\_neg\_n\_objects



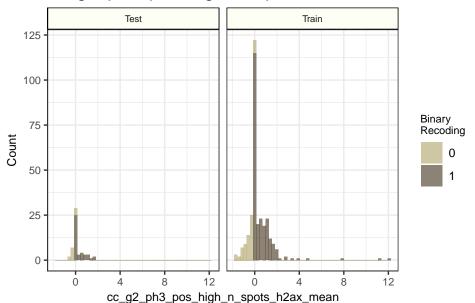
### cc\_g2\_ph3\_neg\_n\_spots\_mean



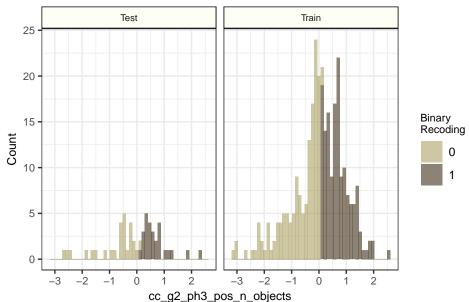
cc\_g2\_ph3\_neg\_n\_spots\_per\_nucleus\_area\_mean



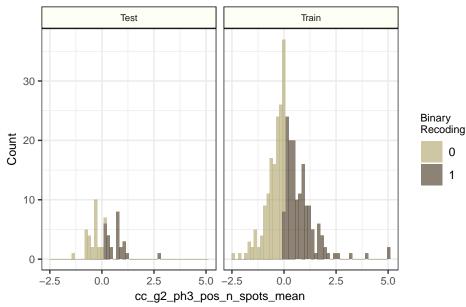
cc\_g2\_ph3\_pos\_high\_n\_spots\_h2ax\_mean



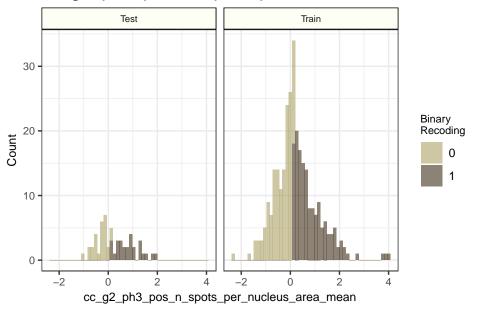
# cc\_g2\_ph3\_pos\_n\_objects



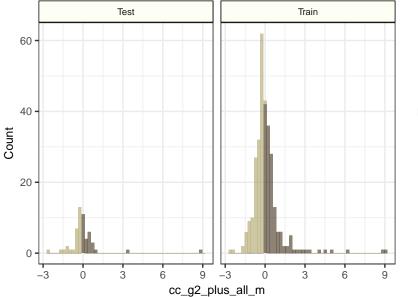
### cc\_g2\_ph3\_pos\_n\_spots\_mean



cc\_g2\_ph3\_pos\_n\_spots\_per\_nucleus\_area\_mean

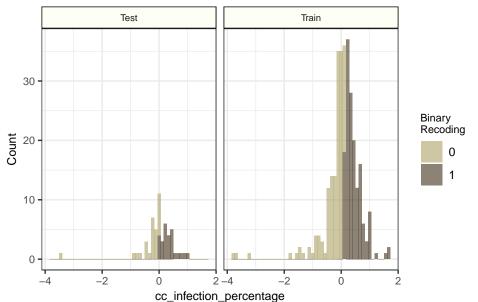


## cc\_g2\_plus\_all\_m

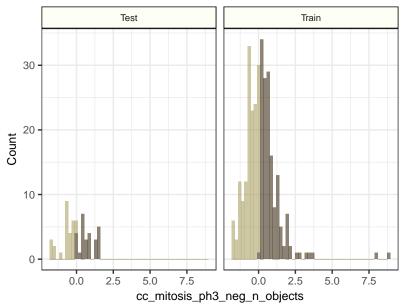




## cc\_infection\_percentage

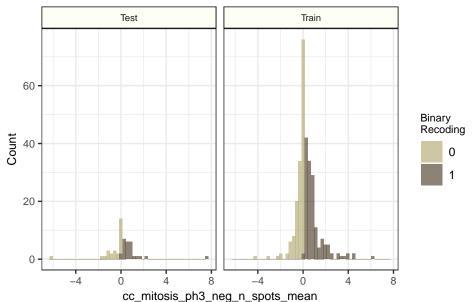


## cc\_mitosis\_ph3\_neg\_n\_objects

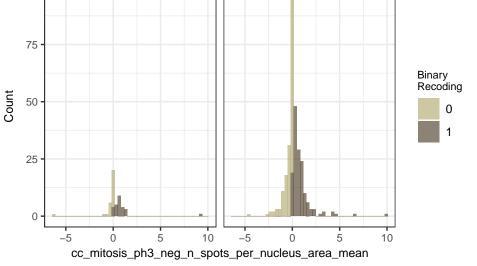




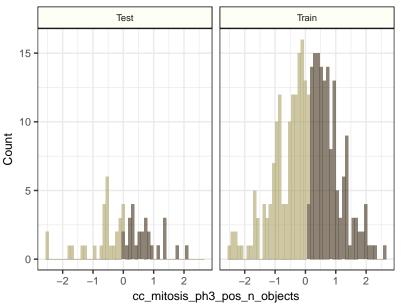
# cc\_mitosis\_ph3\_neg\_n\_spots\_mean



cc\_mitosis\_ph3\_neg\_n\_spots\_per\_nucleus\_area\_m Test Train 100 75 Binary Recoding 50 0 25



## cc\_mitosis\_ph3\_pos\_n\_objects

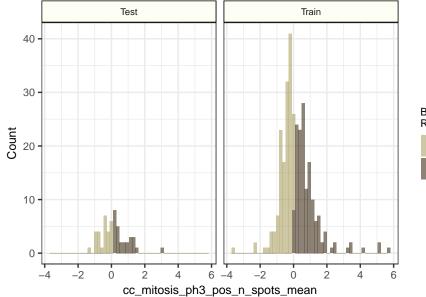


Binary

Recoding

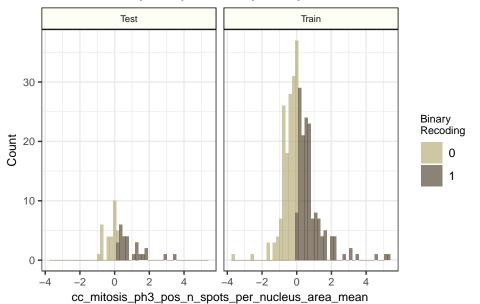
0

# cc\_mitosis\_ph3\_pos\_n\_spots\_mean

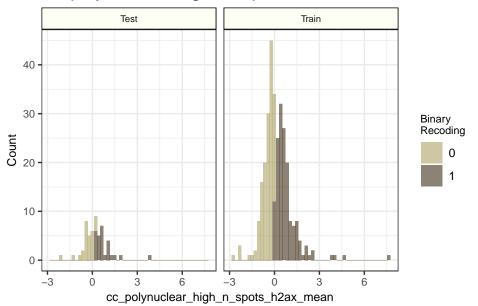




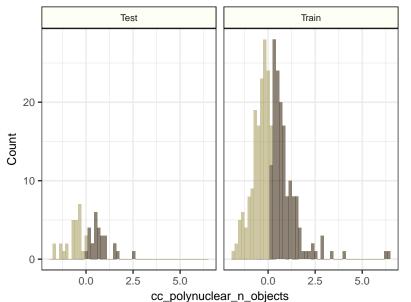
cc\_mitosis\_ph3\_pos\_n\_spots\_per\_nucleus\_area\_me



# cc\_polynuclear\_high\_n\_spots\_h2ax\_mean

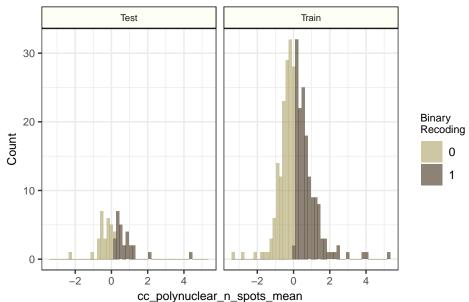


## cc\_polynuclear\_n\_objects

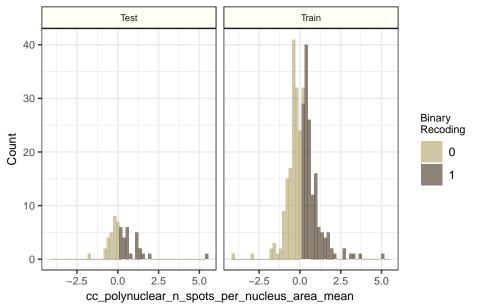




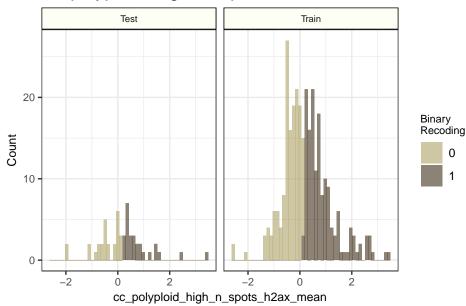
# cc\_polynuclear\_n\_spots\_mean



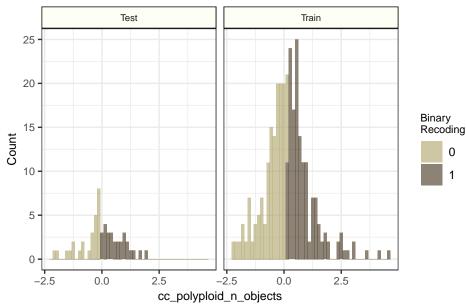
#### cc\_polynuclear\_n\_spots\_per\_nucleus\_area\_mean



# cc\_polyploid\_high\_n\_spots\_h2ax\_mean

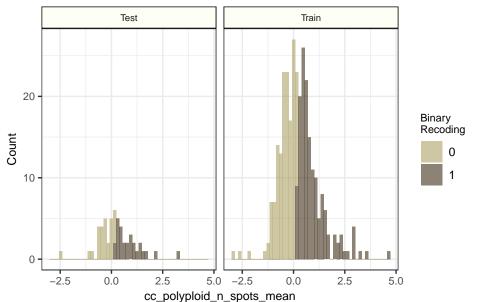


# cc\_polyploid\_n\_objects

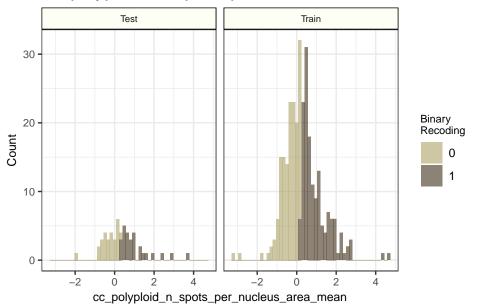


0

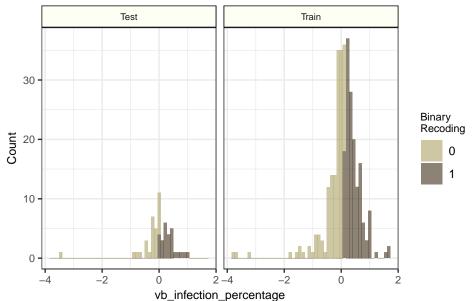
## cc\_polyploid\_n\_spots\_mean



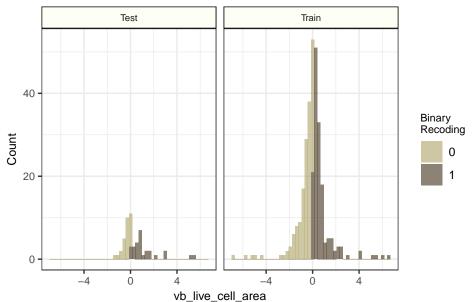
#### cc\_polyploid\_n\_spots\_per\_nucleus\_area\_mean



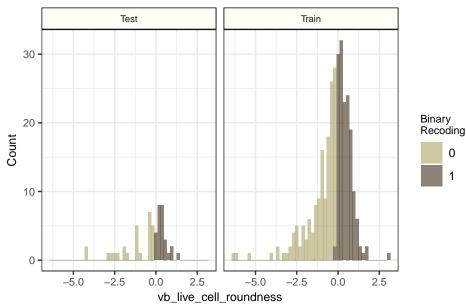
## vb\_infection\_percentage



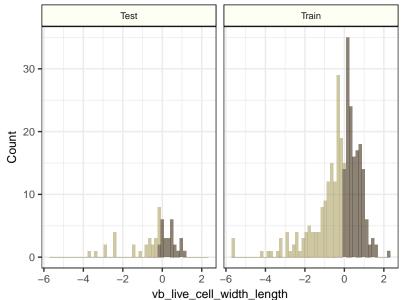
## vb\_live\_cell\_area



## vb\_live\_cell\_roundness

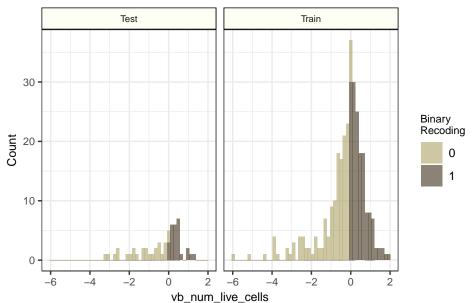


# vb\_live\_cell\_width\_length

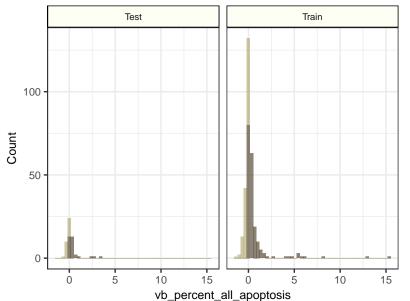




#### vb\_num\_live\_cells

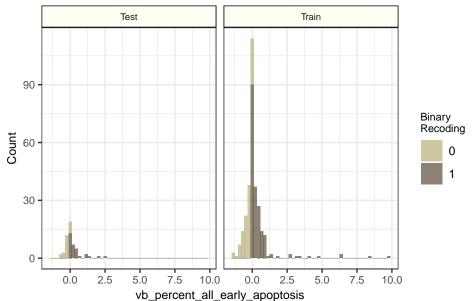


# vb\_percent\_all\_apoptosis

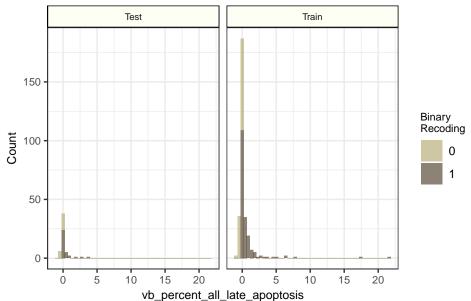




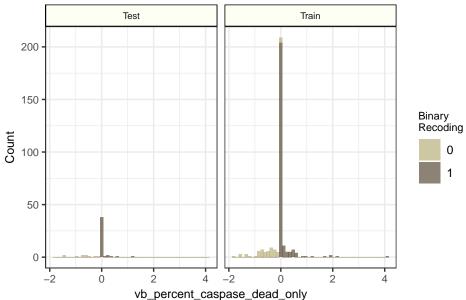
## vb\_percent\_all\_early\_apoptosis



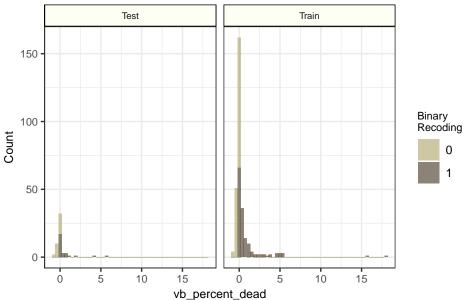
## vb\_percent\_all\_late\_apoptosis



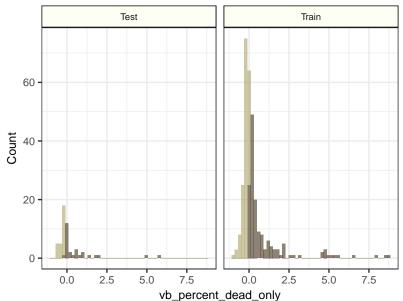
# vb\_percent\_caspase\_dead\_only



# vb\_percent\_dead



# vb\_percent\_dead\_only



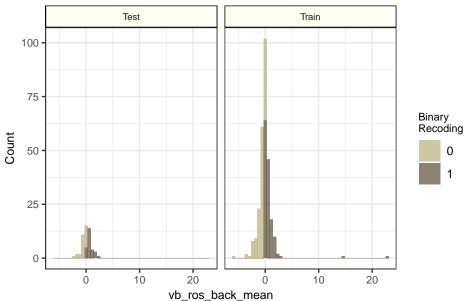
Binary Recoding

0

vb\_percent\_live Test Train 150 Binary 100 Recoding Count 0 50 0 **-**5 -10 -10 -15 -15 -5 0

vb\_percent\_live

## vb\_ros\_back\_mean



vb\_ros\_mean Test Train Binary Recoding Count 

vb\_ros\_mean