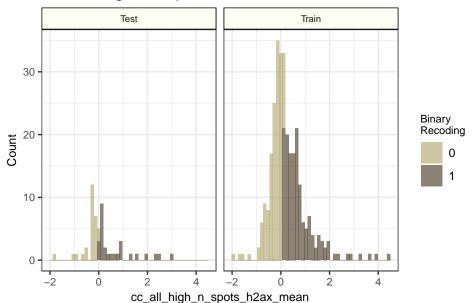
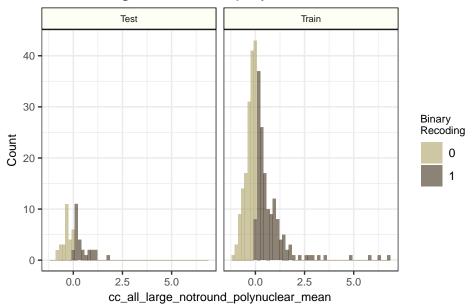
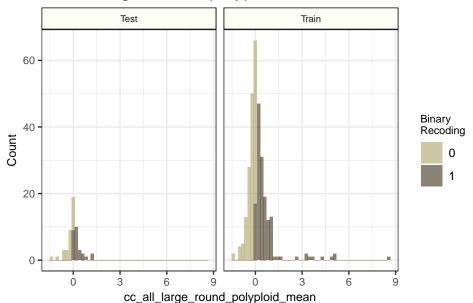
#### cc\_all\_high\_n\_spots\_h2ax\_mean



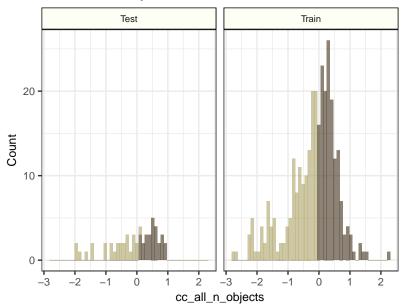
#### cc\_all\_large\_notround\_polynuclear\_mean



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

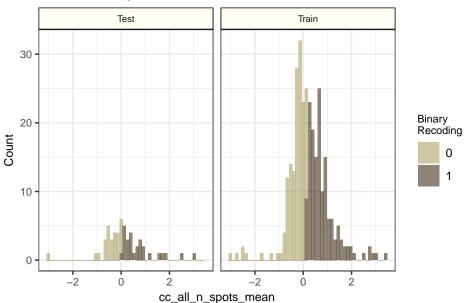


# cc\_all\_n\_objects

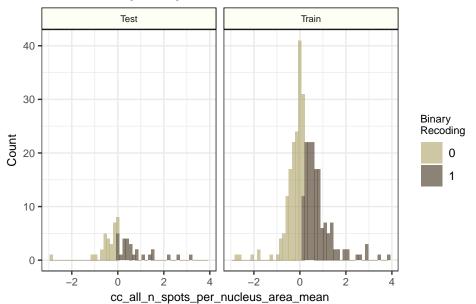




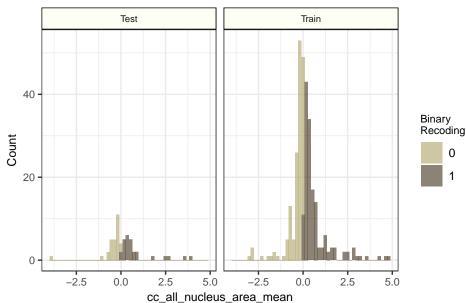
# cc\_all\_n\_spots\_mean



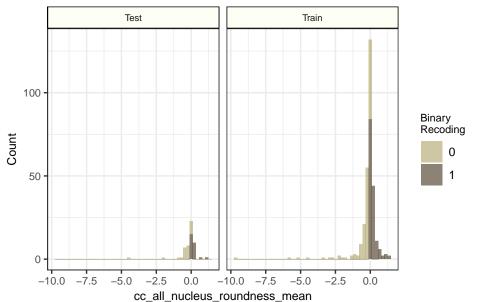
#### cc\_all\_n\_spots\_per\_nucleus\_area\_mean



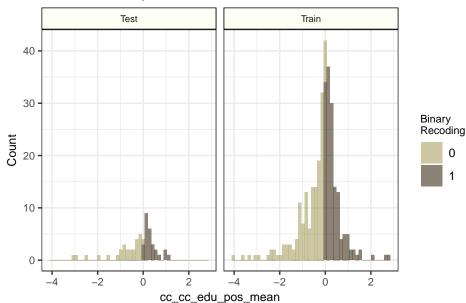
#### cc\_all\_nucleus\_area\_mean



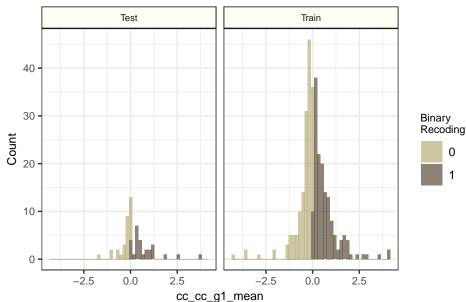
#### cc\_all\_nucleus\_roundness\_mean



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

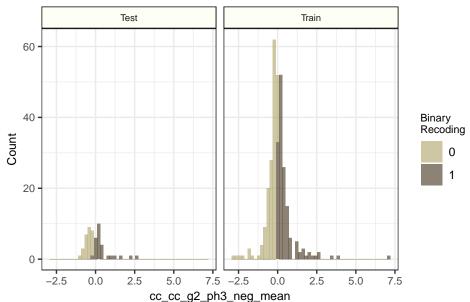


### cc\_cc\_g1\_mean

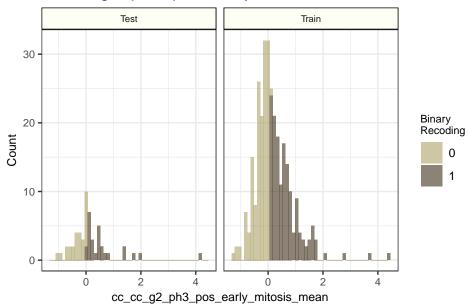


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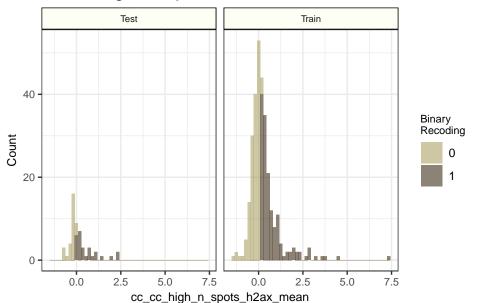
# cc\_cc\_g2\_ph3\_neg\_mean



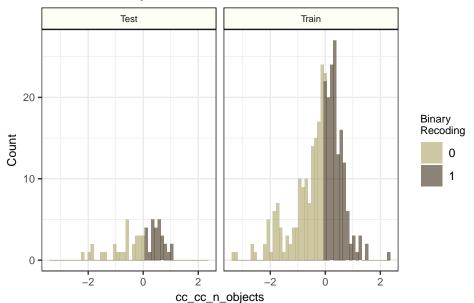
#### cc\_cc\_g2\_ph3\_pos\_early\_mitosis\_mean



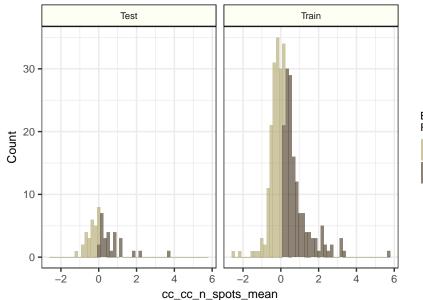
#### cc\_cc\_high\_n\_spots\_h2ax\_mean



# cc\_cc\_n\_objects

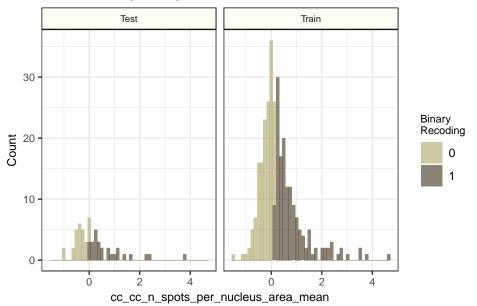


#### cc\_cc\_n\_spots\_mean

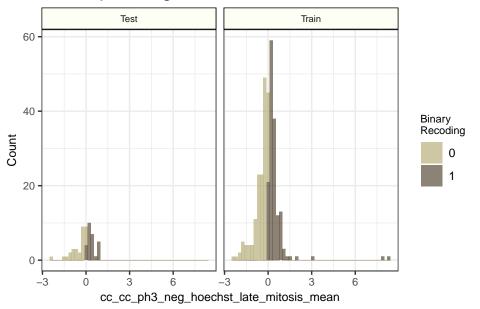




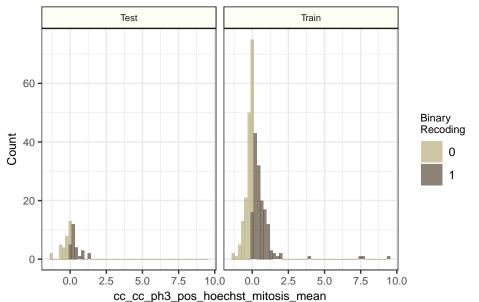
#### cc\_cc\_n\_spots\_per\_nucleus\_area\_mean



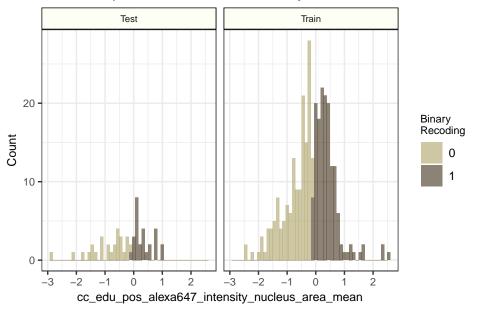
#### cc\_cc\_ph3\_neg\_hoechst\_late\_mitosis\_mean



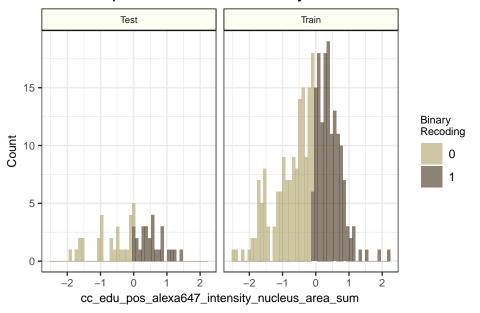
#### cc\_cc\_ph3\_pos\_hoechst\_mitosis\_mean



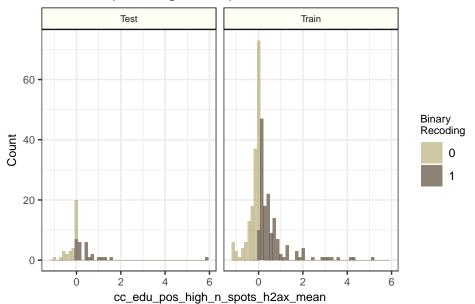
cc\_edu\_pos\_alexa647\_intensity\_nucleus\_area\_meai



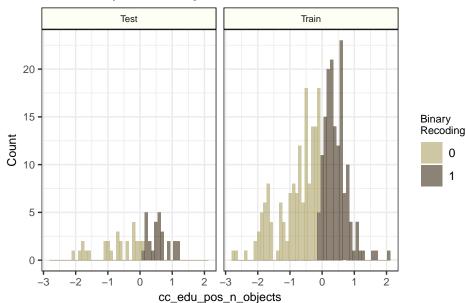
#### cc\_edu\_pos\_alexa647\_intensity\_nucleus\_area\_sum



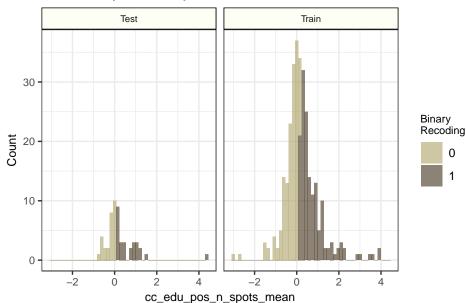
# cc\_edu\_pos\_high\_n\_spots\_h2ax\_mean



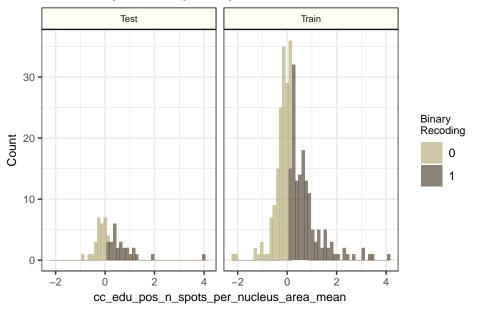
#### cc\_edu\_pos\_n\_objects



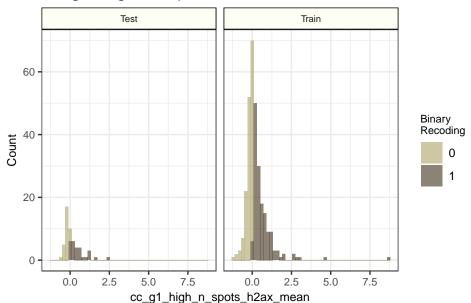
#### cc\_edu\_pos\_n\_spots\_mean



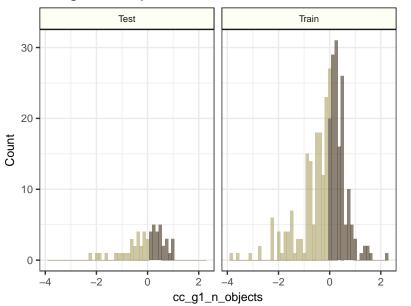
#### cc\_edu\_pos\_n\_spots\_per\_nucleus\_area\_mean



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

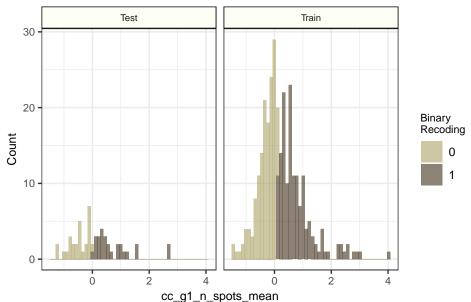


# cc\_g1\_n\_objects

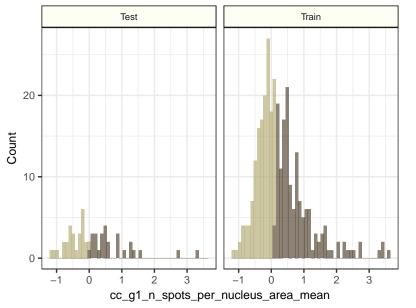




# cc\_g1\_n\_spots\_mean

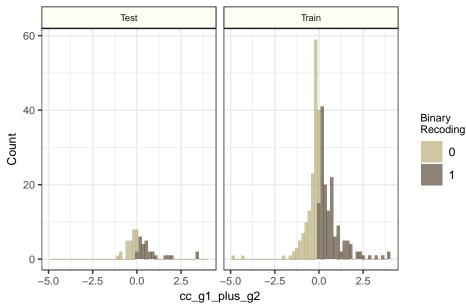


#### cc\_g1\_n\_spots\_per\_nucleus\_area\_mean





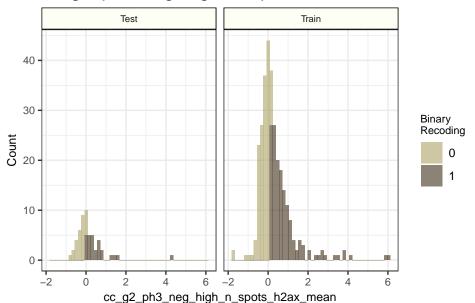
# cc\_g1\_plus\_g2



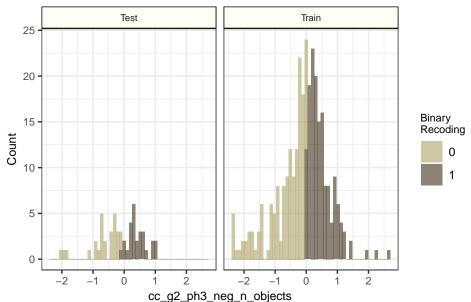
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cc\_g2\_g1 Test Train 75 **-**Binary Recoding Count 0 25 -0 2.5 5.0 7.5 10.02.5 2.5 5.0 -2.5 0.0 0.0 7.5 10.0 cc\_g2\_g1

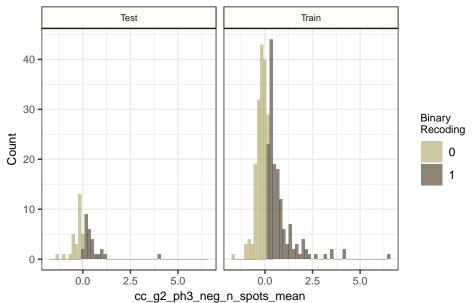
cc\_g2\_ph3\_neg\_high\_n\_spots\_h2ax\_mean



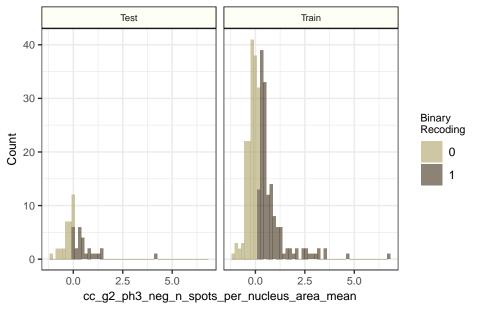
# cc\_g2\_ph3\_neg\_n\_objects



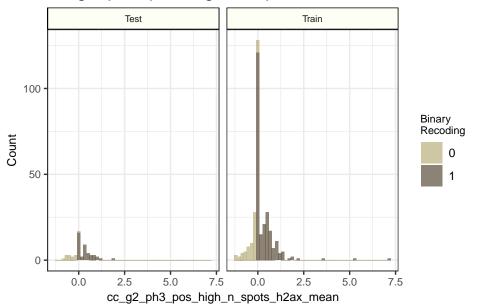
# cc\_g2\_ph3\_neg\_n\_spots\_mean



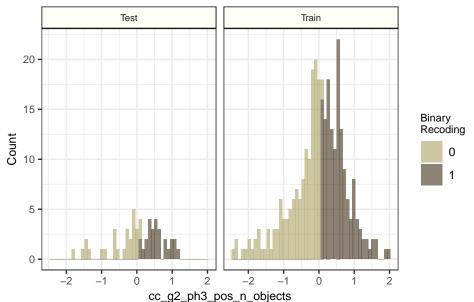
cc\_g2\_ph3\_neg\_n\_spots\_per\_nucleus\_area\_mean



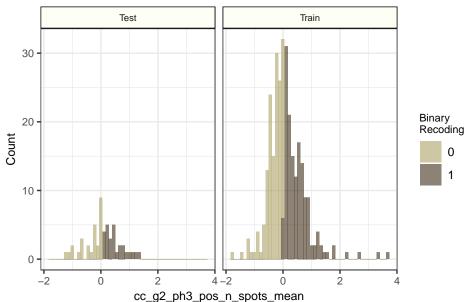
cc\_g2\_ph3\_pos\_high\_n\_spots\_h2ax\_mean



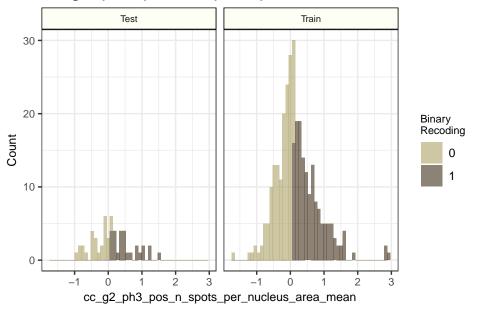
# cc\_g2\_ph3\_pos\_n\_objects



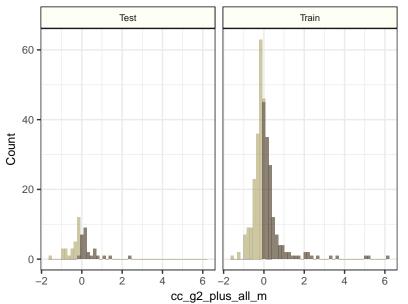
#### cc\_g2\_ph3\_pos\_n\_spots\_mean



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

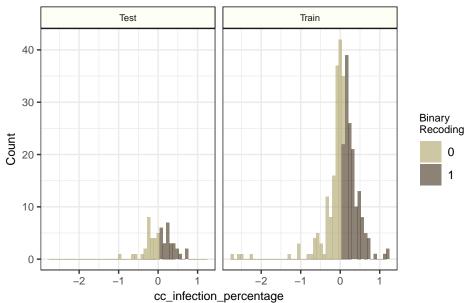


### cc\_g2\_plus\_all\_m

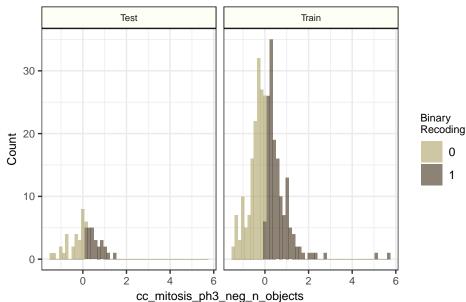




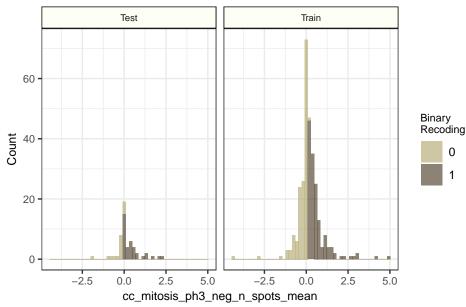
# cc\_infection\_percentage



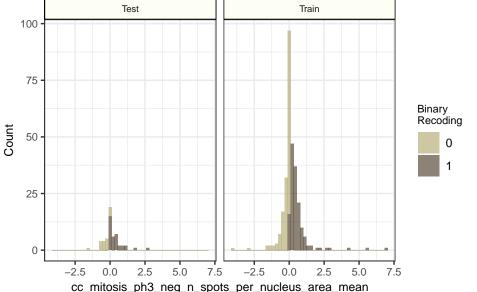
# cc\_mitosis\_ph3\_neg\_n\_objects



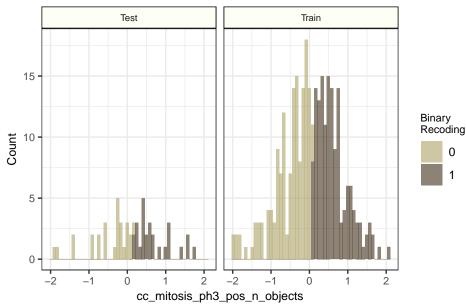
# cc\_mitosis\_ph3\_neg\_n\_spots\_mean



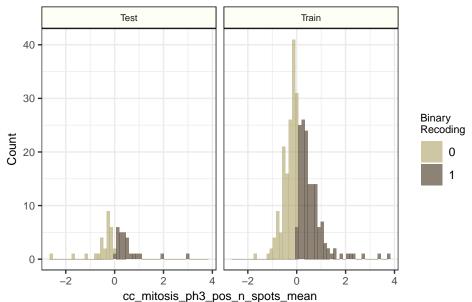
cc\_mitosis\_ph3\_neg\_n\_spots\_per\_nucleus\_area\_m Test Train 100



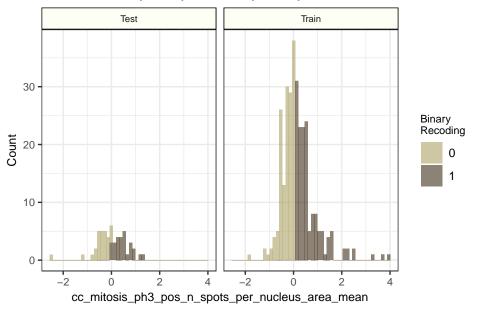
# cc\_mitosis\_ph3\_pos\_n\_objects



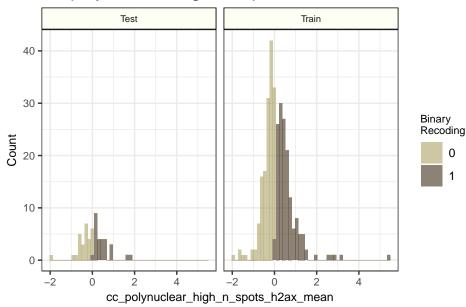
### cc\_mitosis\_ph3\_pos\_n\_spots\_mean



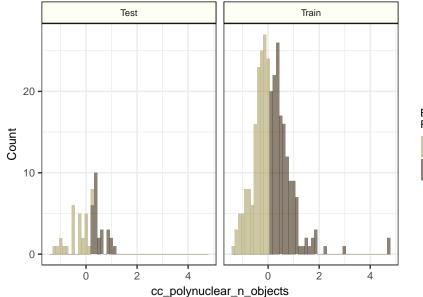
cc\_mitosis\_ph3\_pos\_n\_spots\_per\_nucleus\_area\_me



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

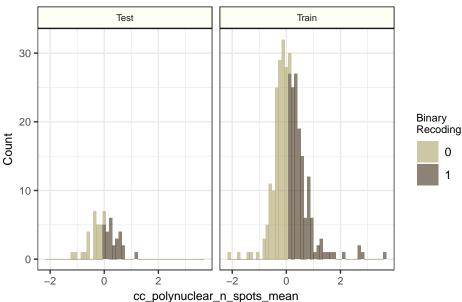


# cc\_polynuclear\_n\_objects

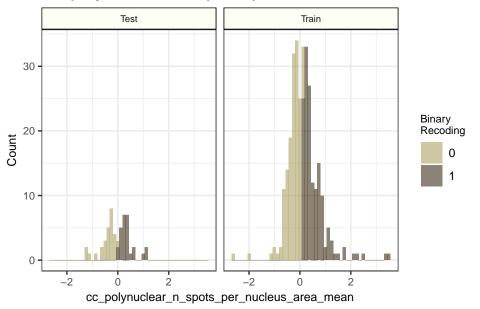




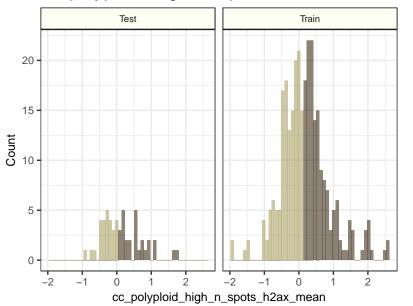
# cc\_polynuclear\_n\_spots\_mean



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

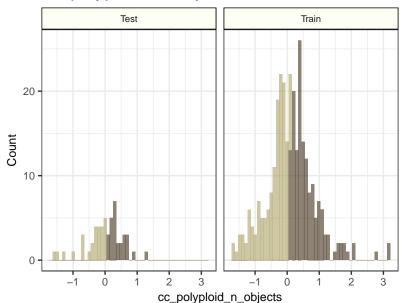


# cc\_polyploid\_high\_n\_spots\_h2ax\_mean



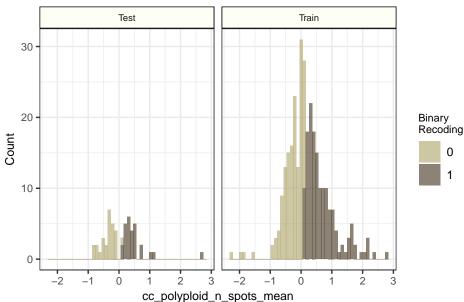
Binary Recoding

# cc\_polyploid\_n\_objects

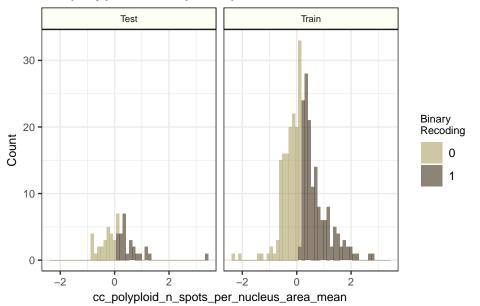




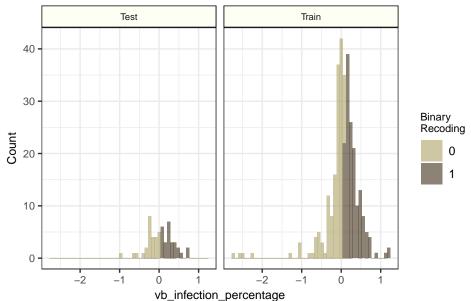
### cc\_polyploid\_n\_spots\_mean



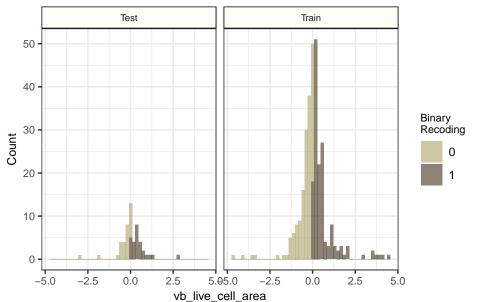
#### cc\_polyploid\_n\_spots\_per\_nucleus\_area\_mean



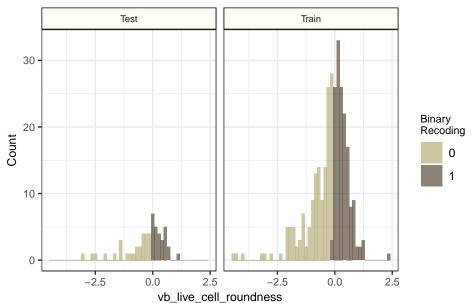
# vb\_infection\_percentage



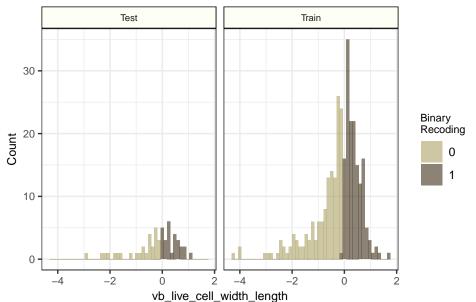
# vb\_live\_cell\_area



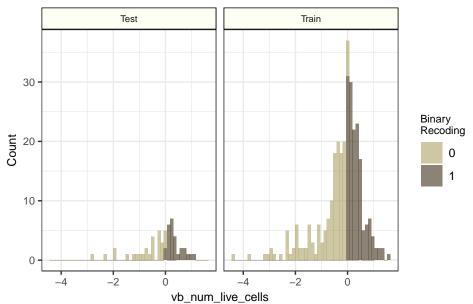
# vb\_live\_cell\_roundness



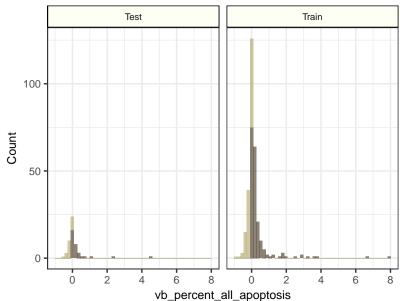
# vb\_live\_cell\_width\_length



### vb\_num\_live\_cells

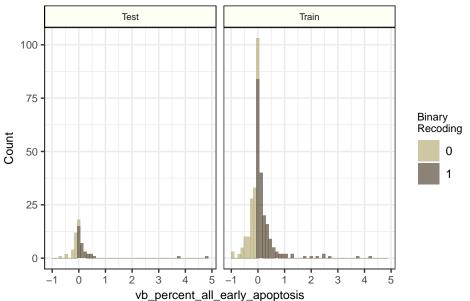


# vb\_percent\_all\_apoptosis

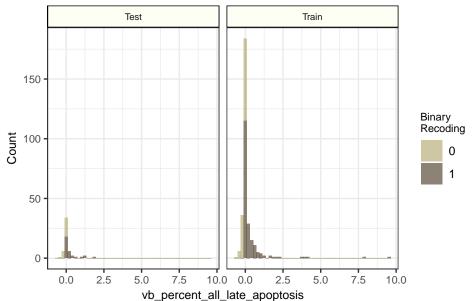


Binary Recoding

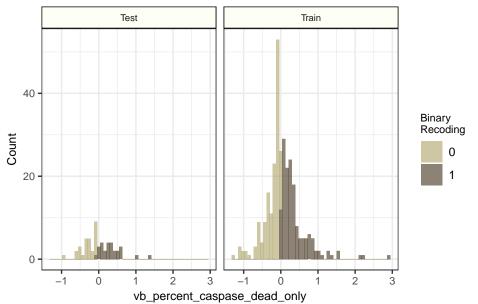
# vb\_percent\_all\_early\_apoptosis



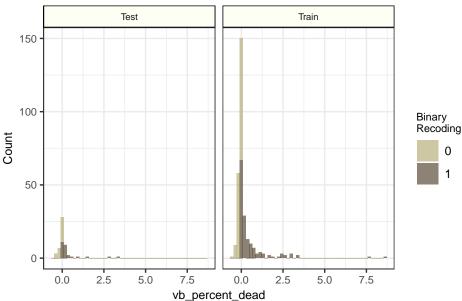
# vb\_percent\_all\_late\_apoptosis



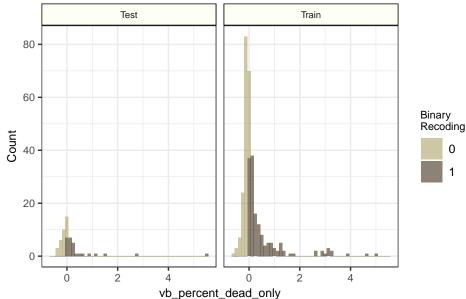
# vb\_percent\_caspase\_dead\_only



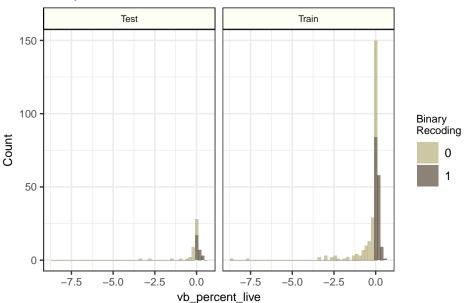
# vb\_percent\_dead



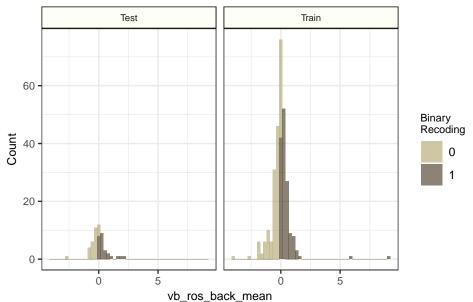
# vb\_percent\_dead\_only



vb\_percent\_live



# vb\_ros\_back\_mean



#### vb\_ros\_mean

