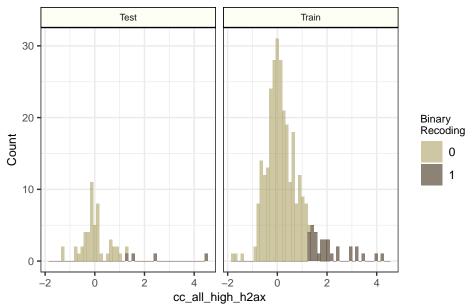
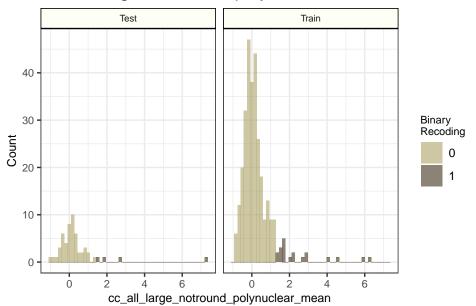
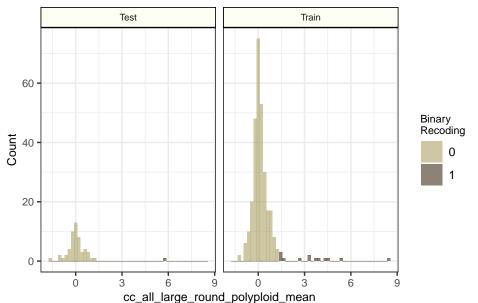
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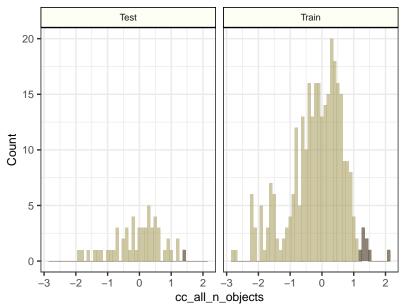
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cc_all_large_round_polyploid_mean

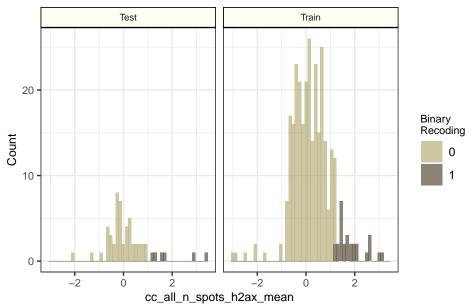


cc_all_n_objects

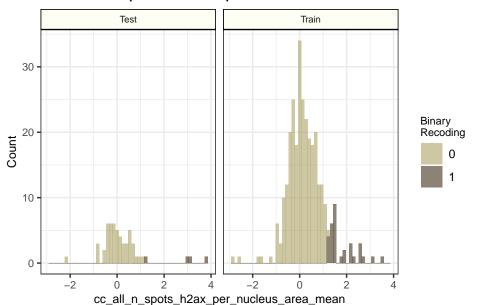




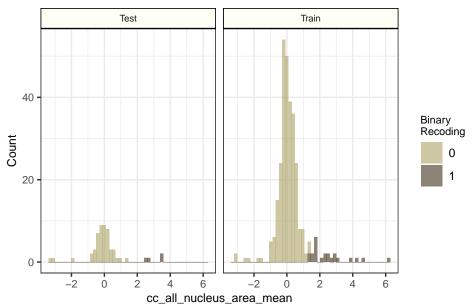
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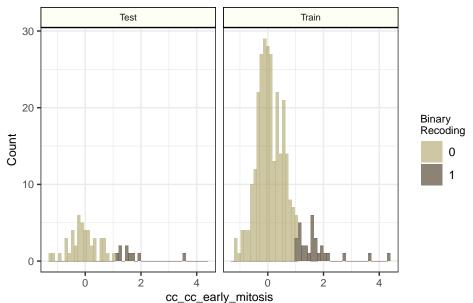
cc_all_n_spots_h2ax_per_nucleus_area_mean



cc_all_nucleus_area_mean



cc_cc_early_mitosis



cc_cc_g1 Test Train 40 -30 -Binary Recoding Count 0 10 -0

-2.5

cc_cc_g1

0.0

2.5

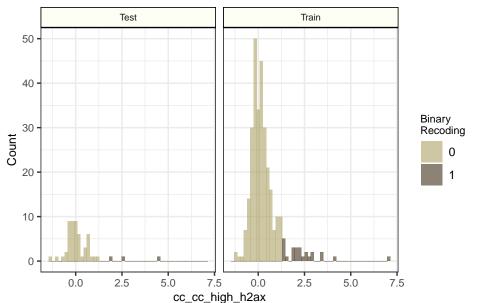
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-2.5

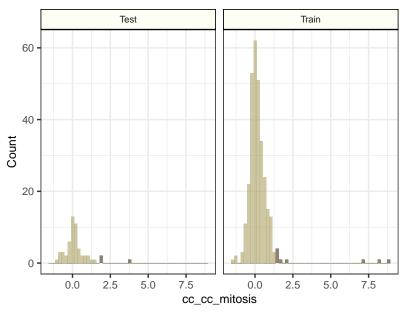
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cc_cc_high_h2ax

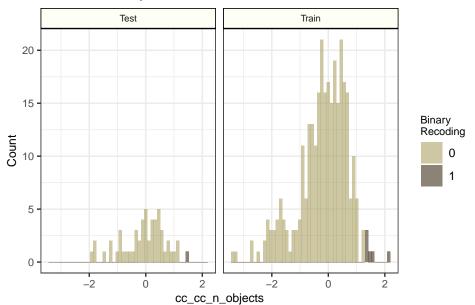


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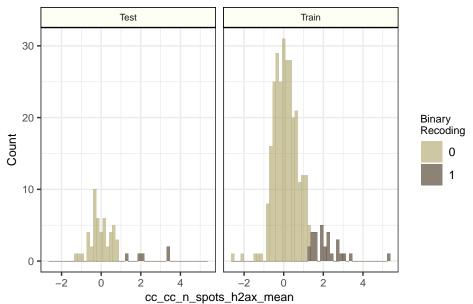


Binary Recoding 0 1

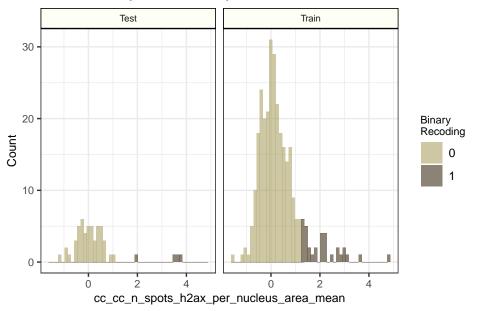
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cc_cc_n_spots_h2ax_mean



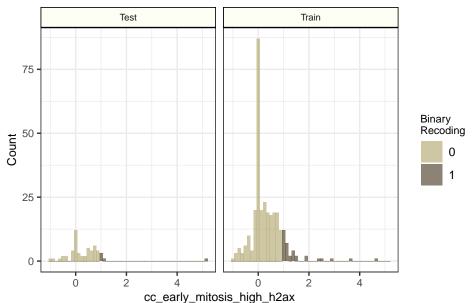
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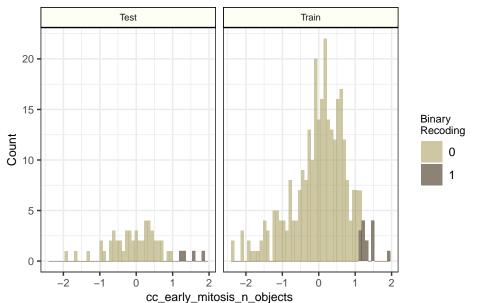
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cc_cc_s

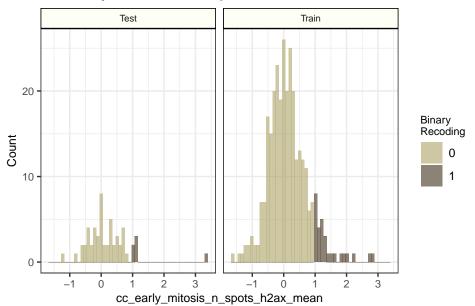
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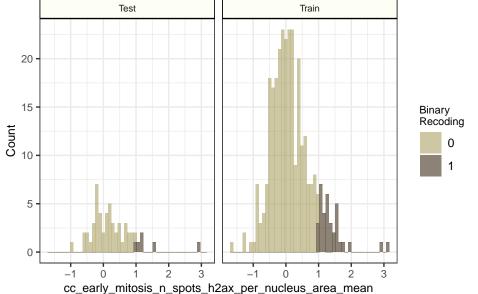
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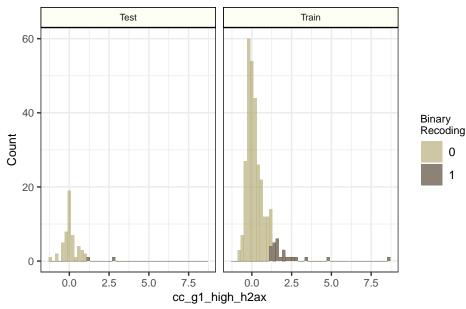
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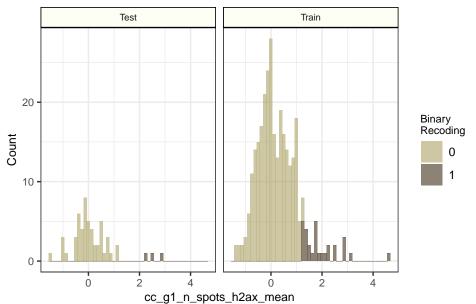


cc_g1_high_h2ax

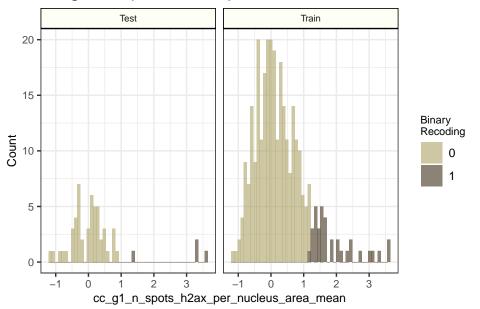


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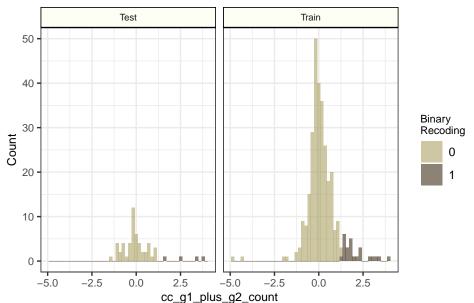
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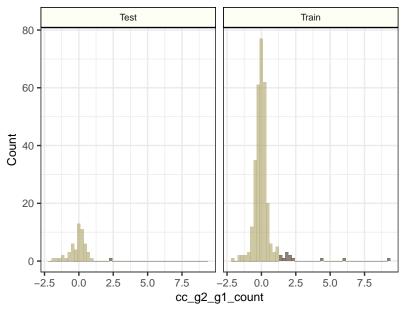
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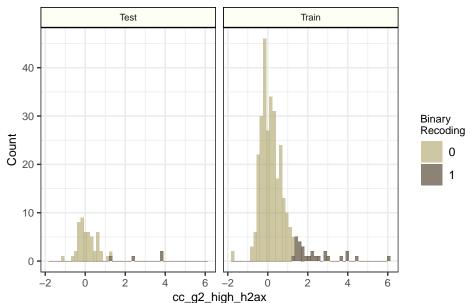
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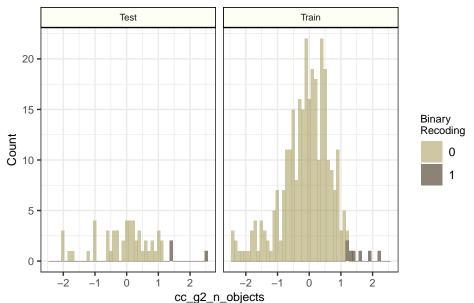
Binary Recoding

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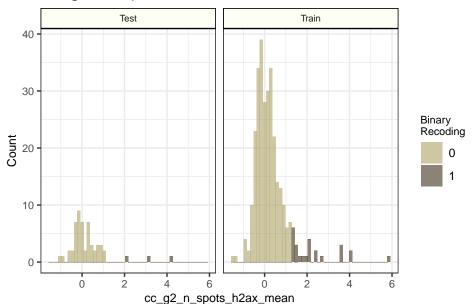
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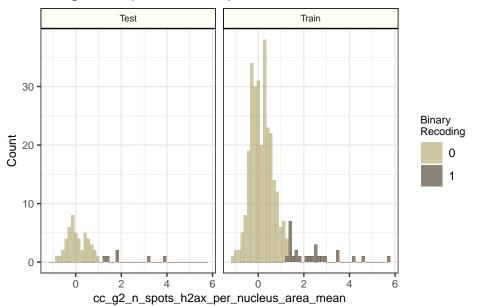
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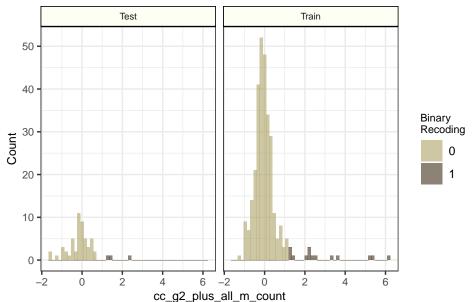
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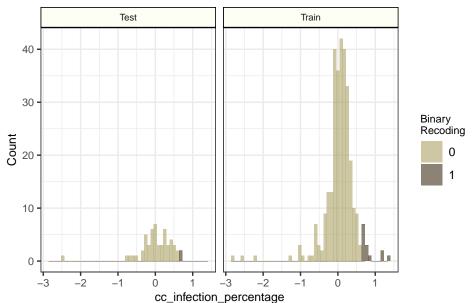
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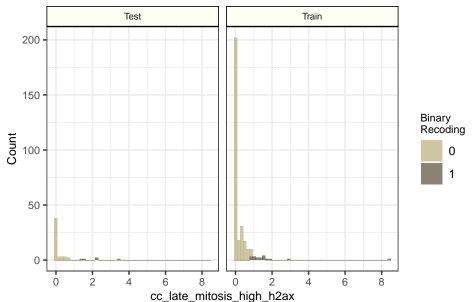
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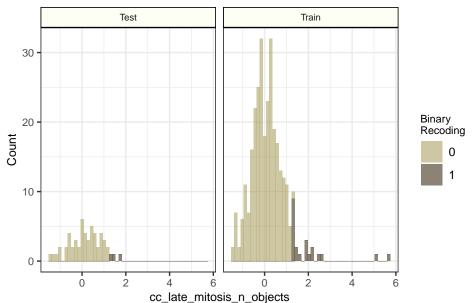
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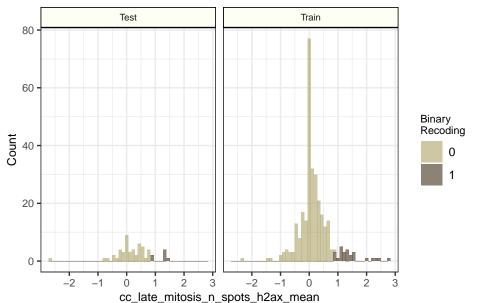
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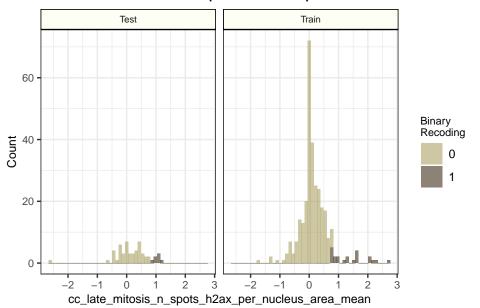
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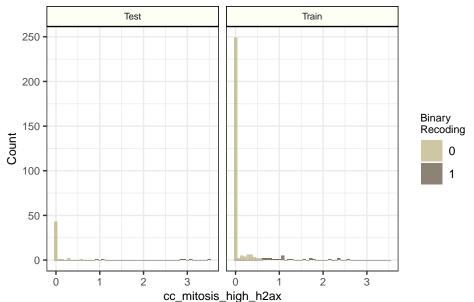
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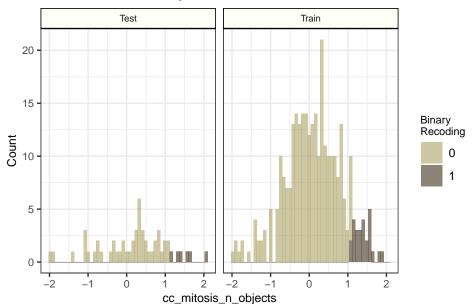
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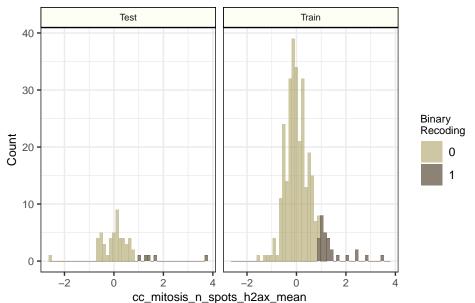
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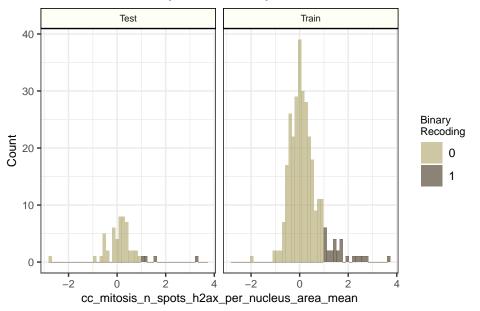
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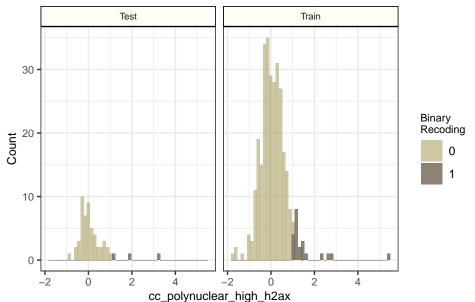
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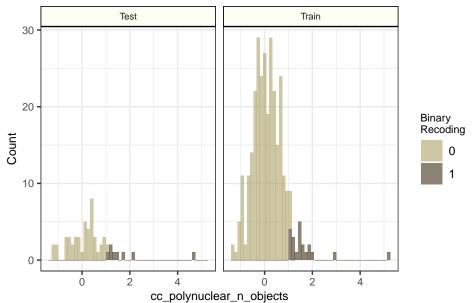
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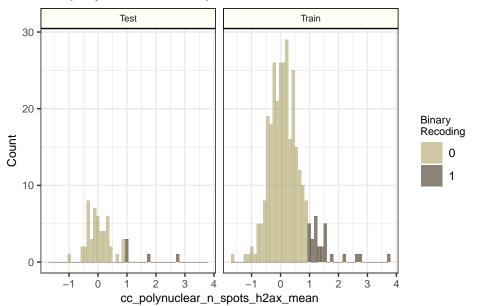
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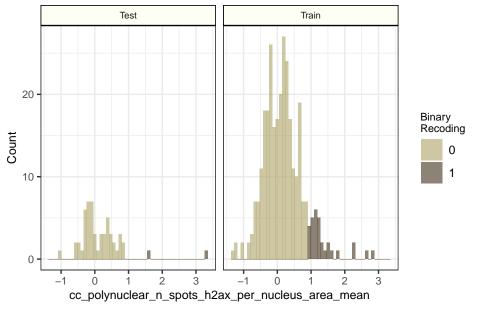
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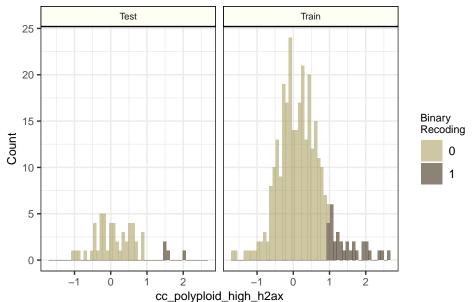
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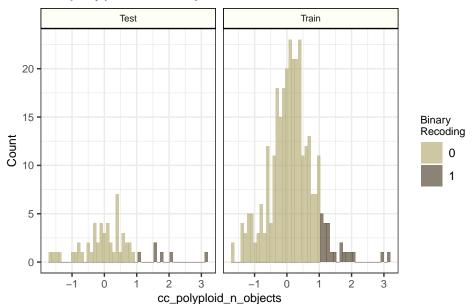
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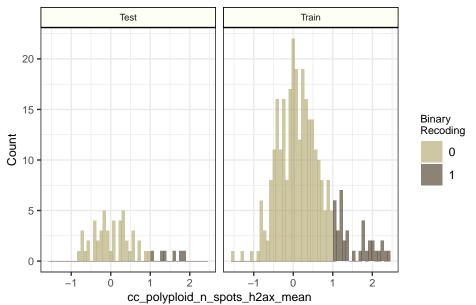
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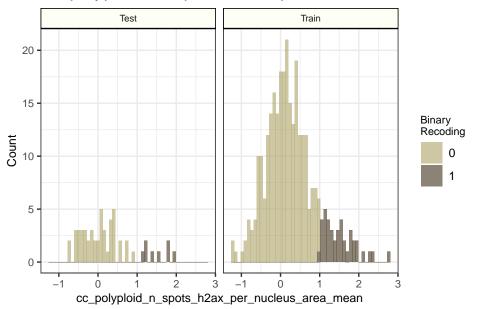
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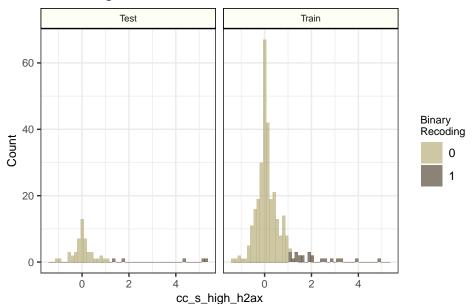
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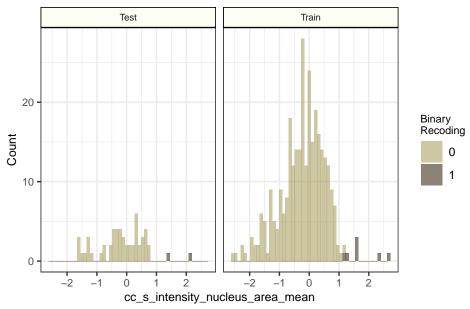
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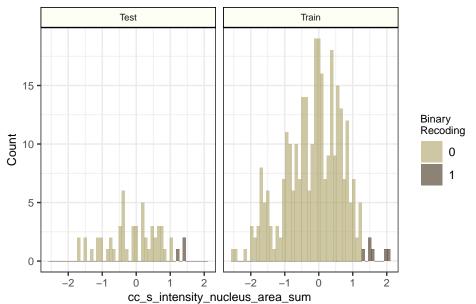
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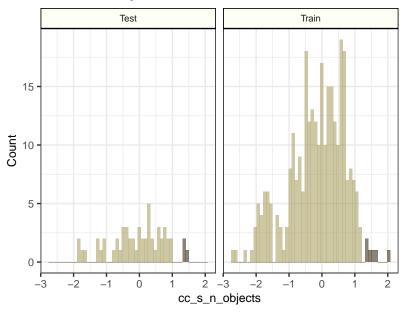
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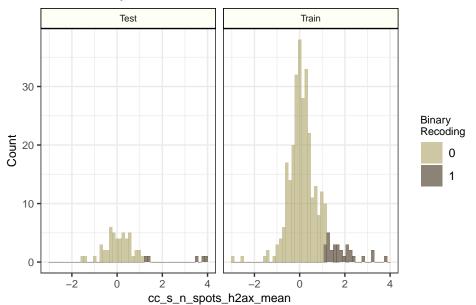


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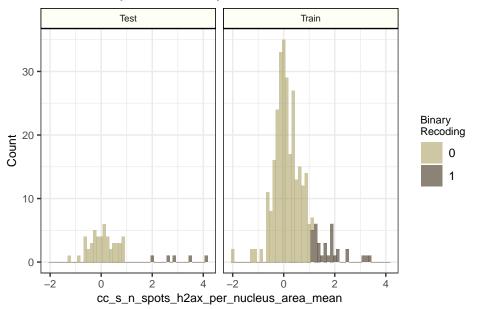




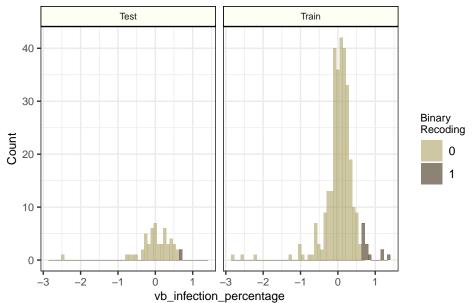
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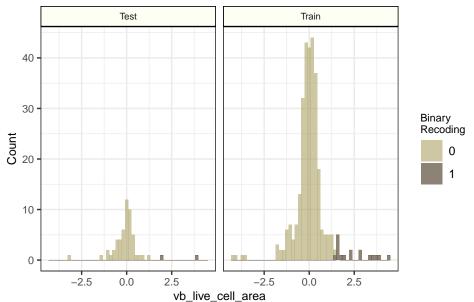
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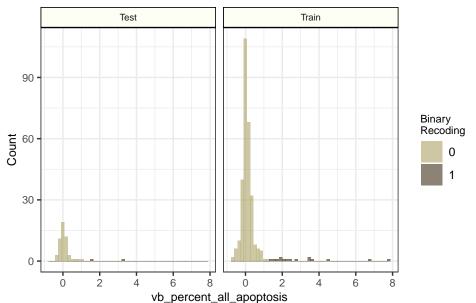
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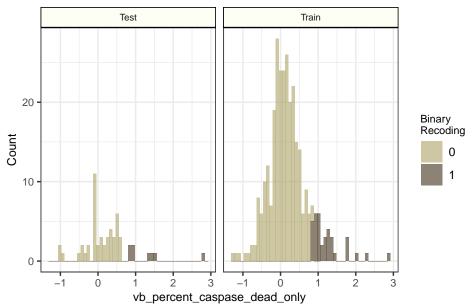
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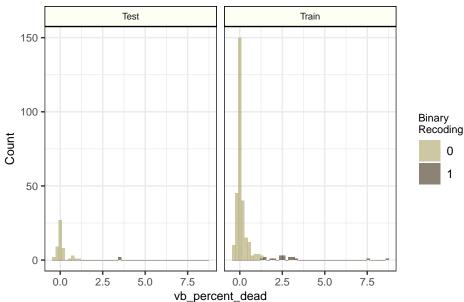
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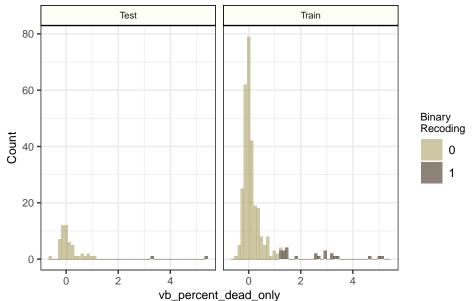
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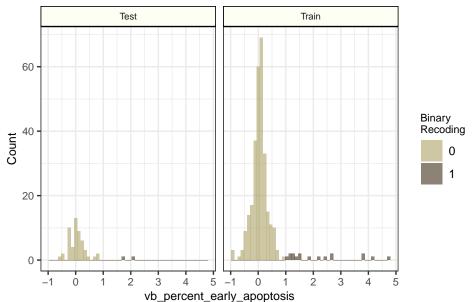
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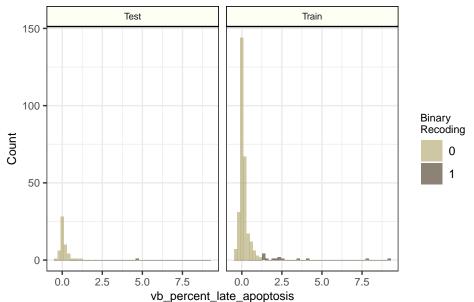
vb_percent_dead_only



vb_percent_early_apoptosis



vb_percent_late_apoptosis



vb_ros_mean

