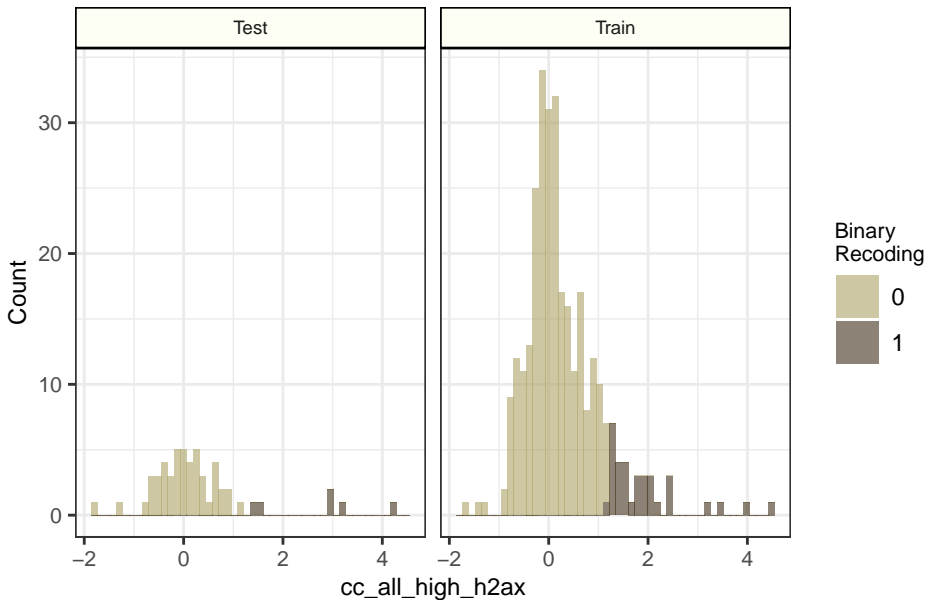
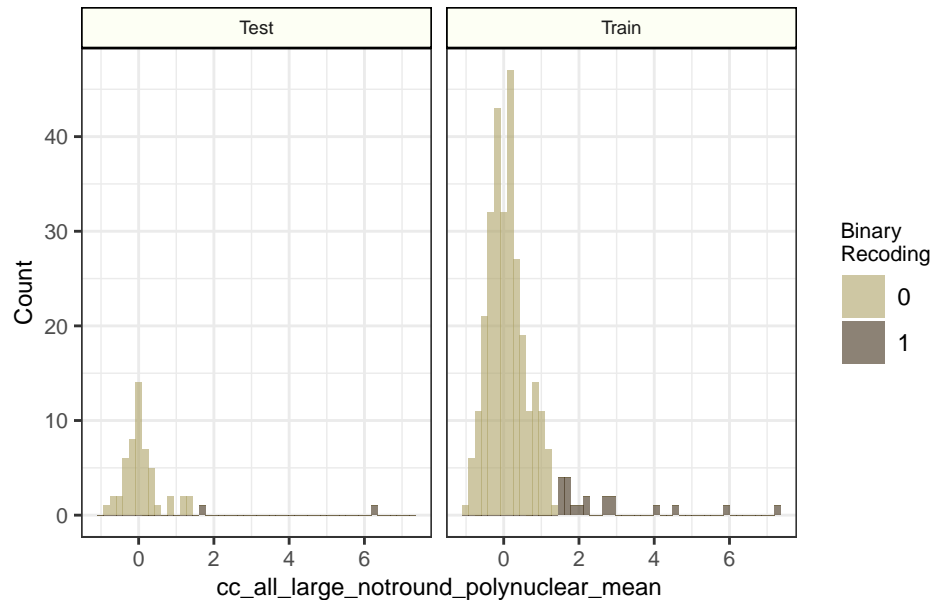


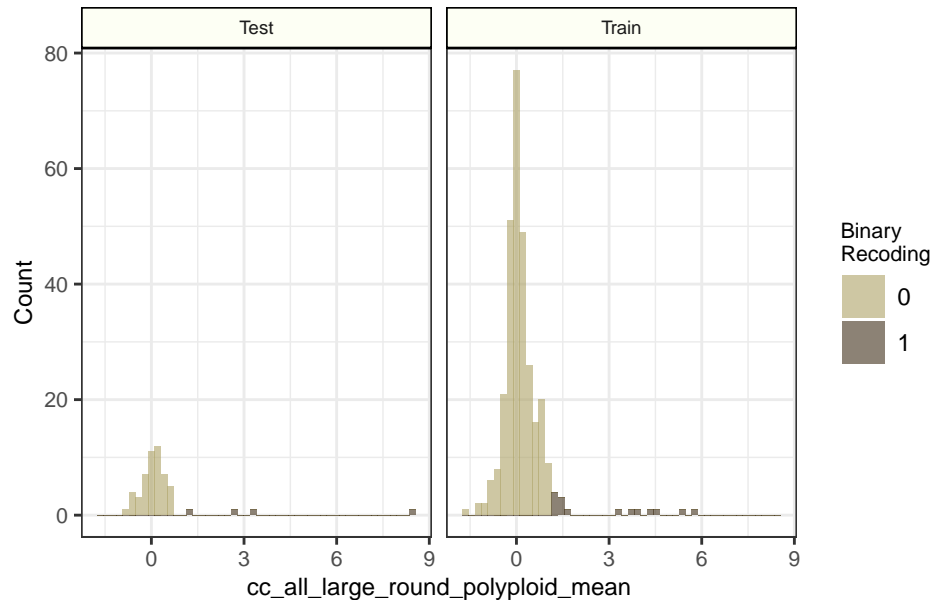
cc_all_high_h2ax



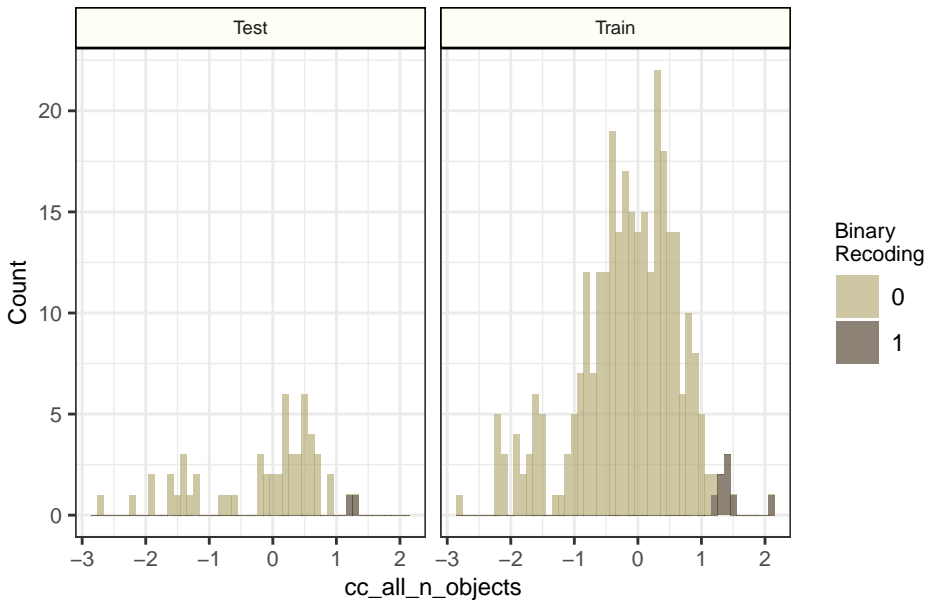
cc_all_large_notround_polynuclear_mean



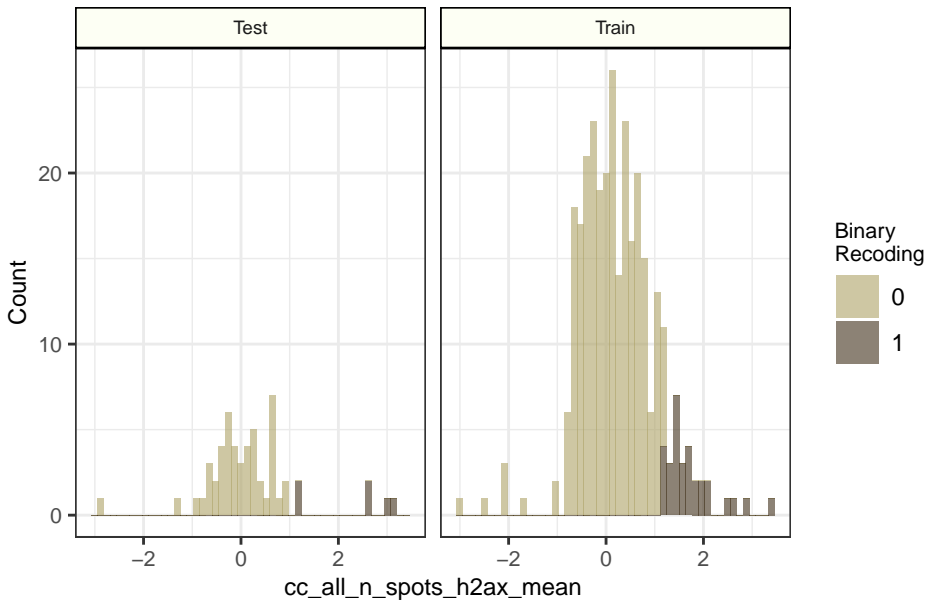
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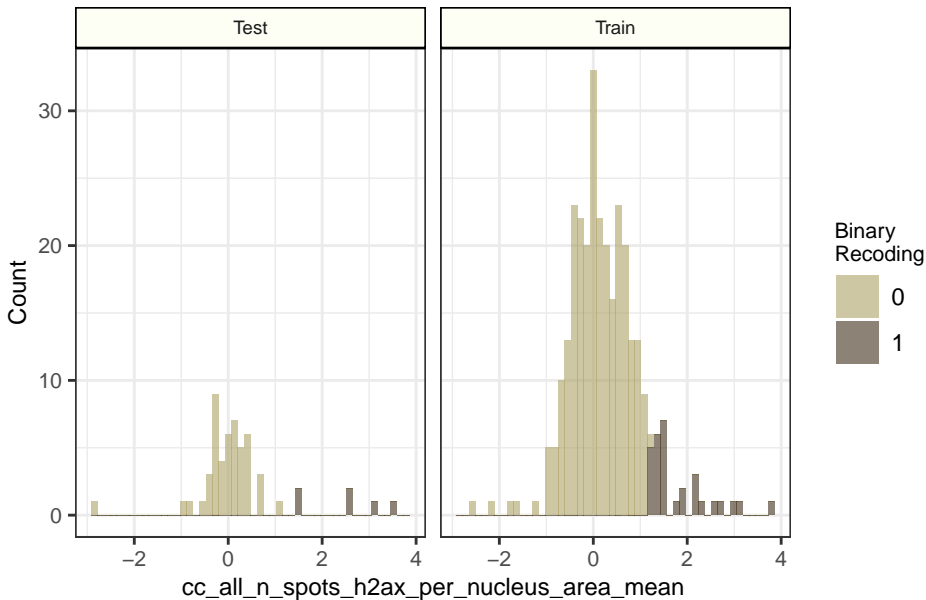
cc_all_n_objects



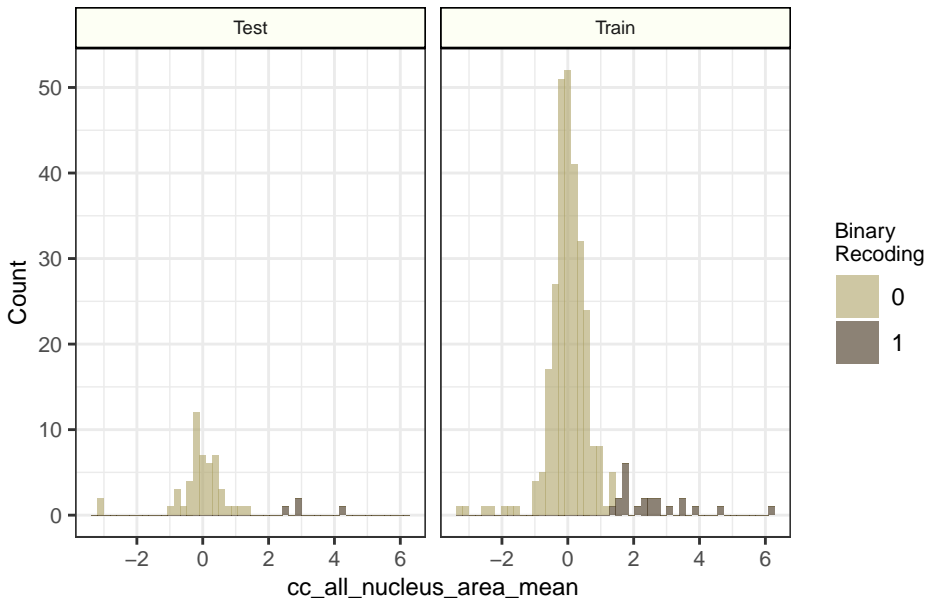
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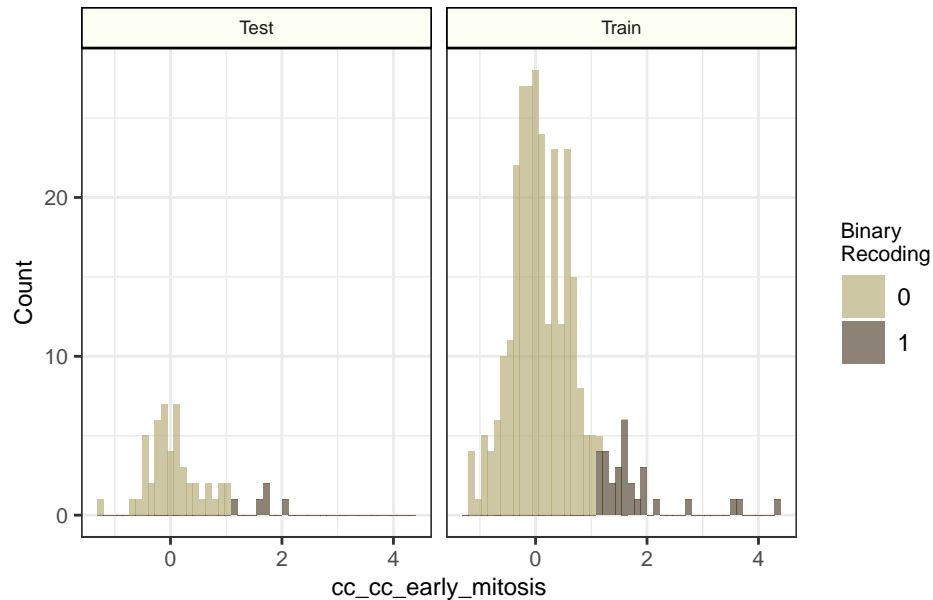
cc_all_n_spots_h2ax_per_nucleus_area_mean



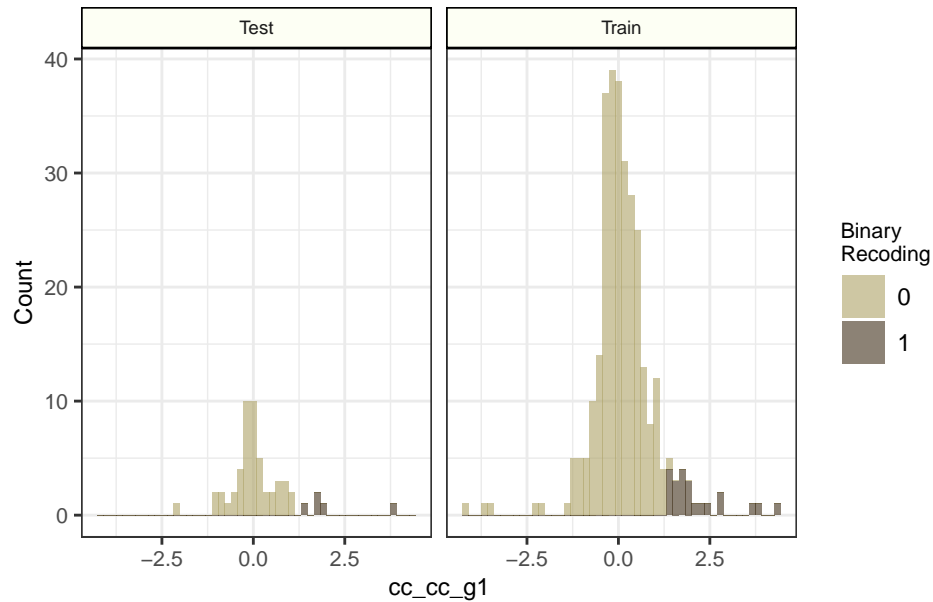
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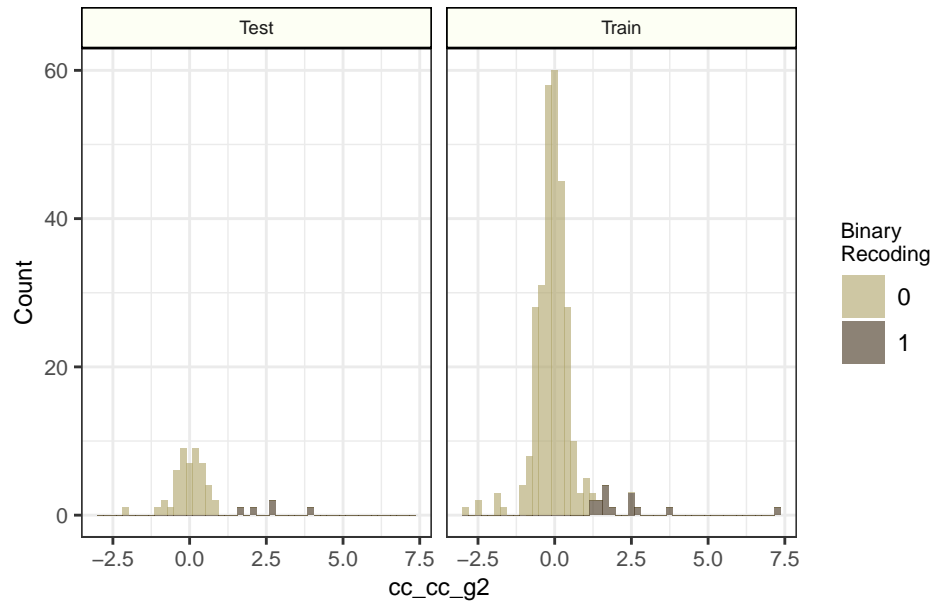
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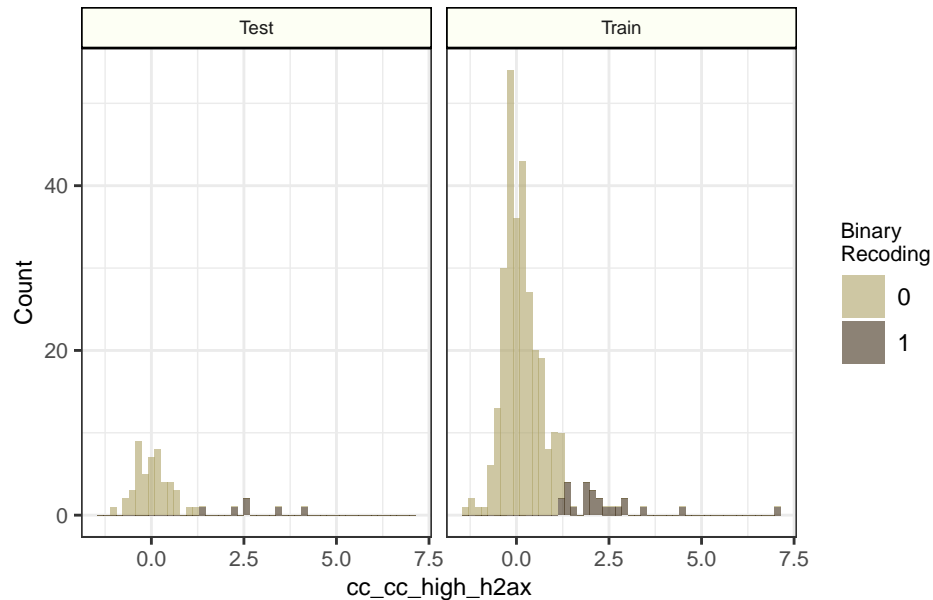
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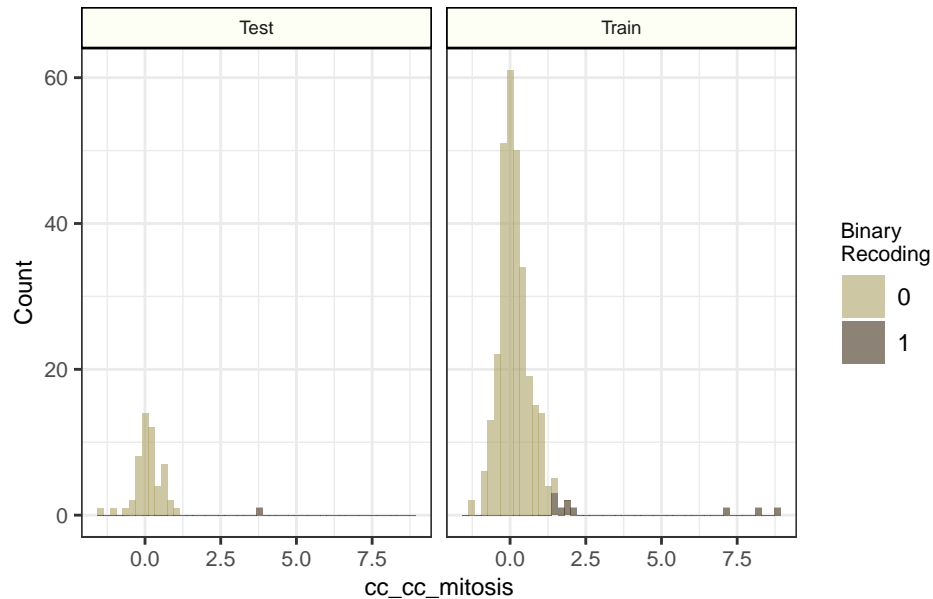
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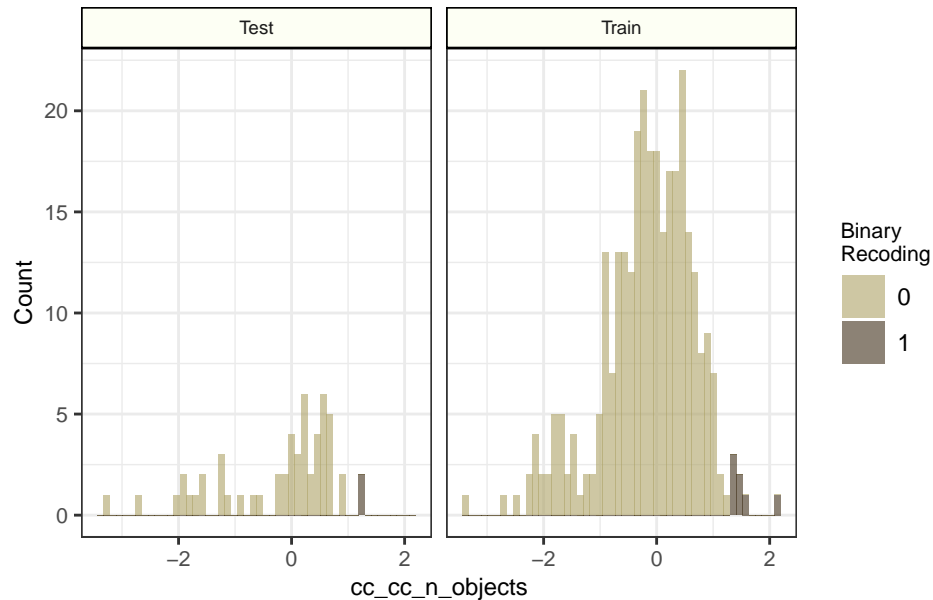
cc_cc_high_h2ax



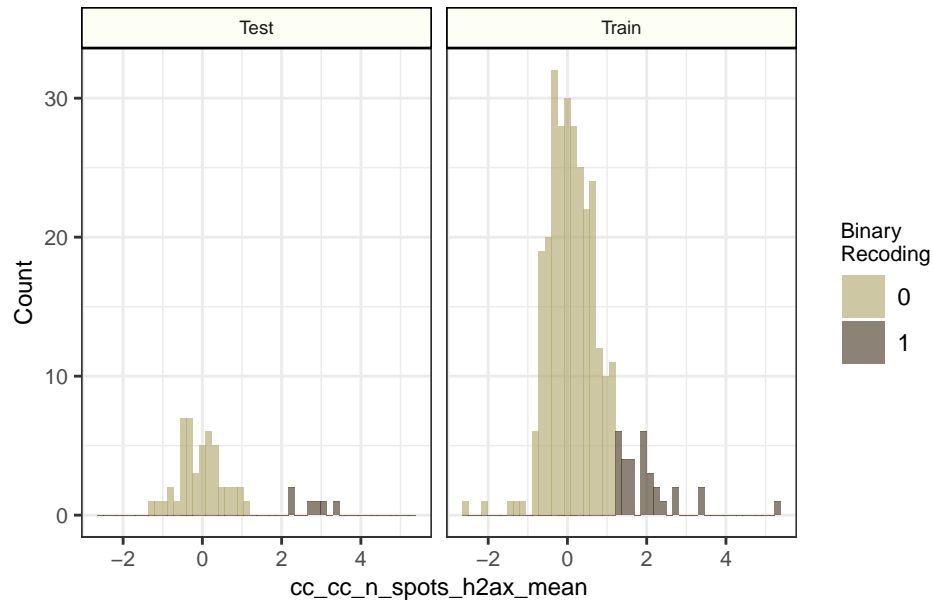
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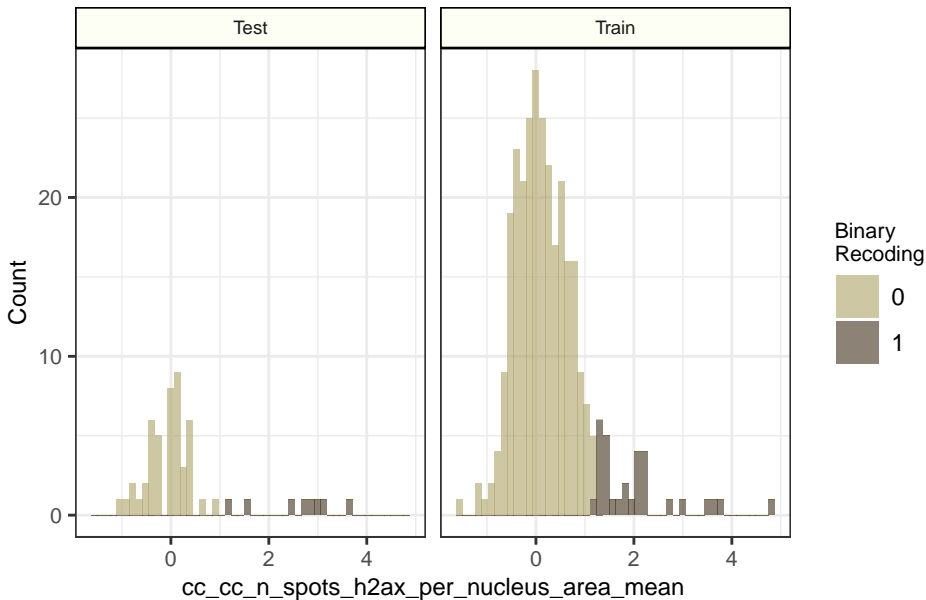
cc_cc_n_objects



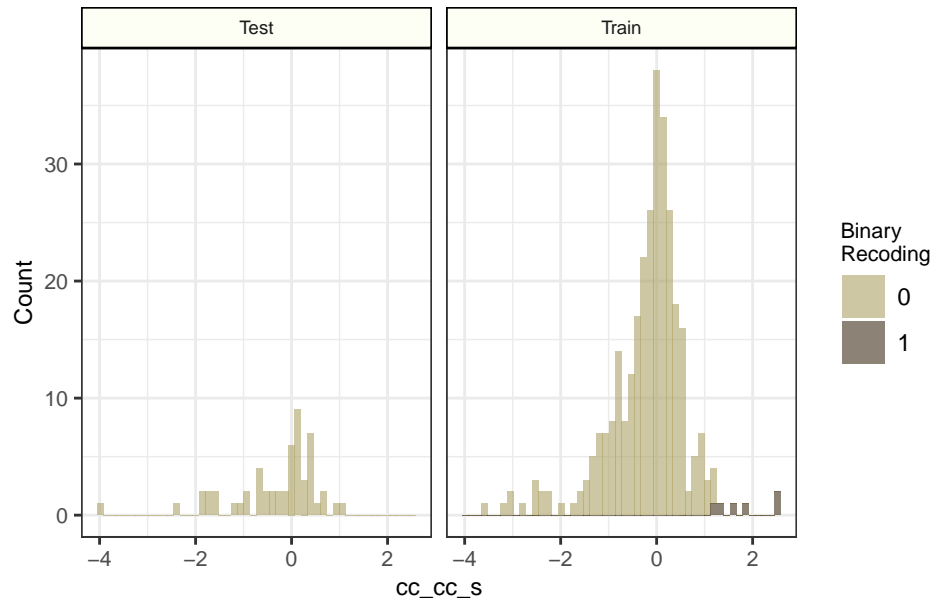
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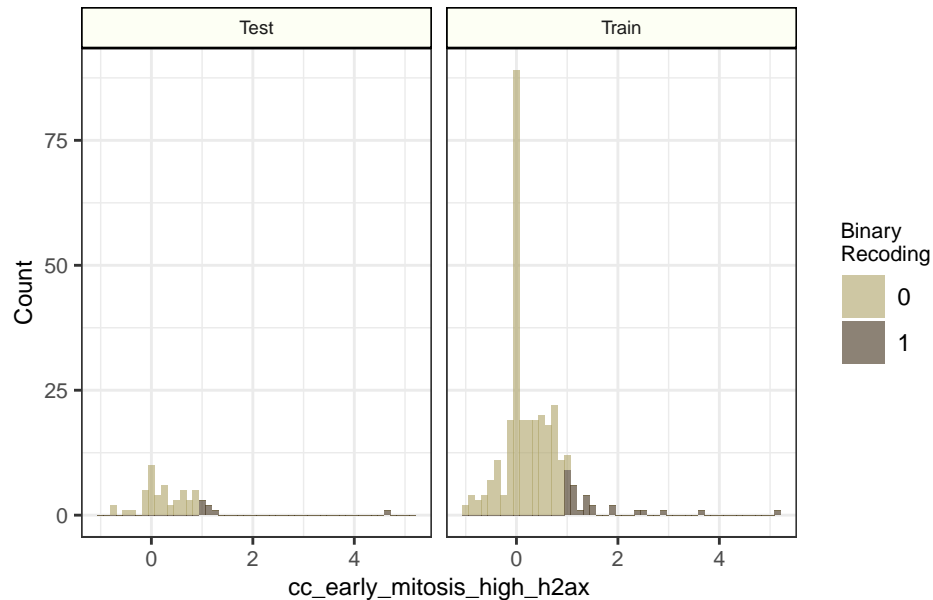
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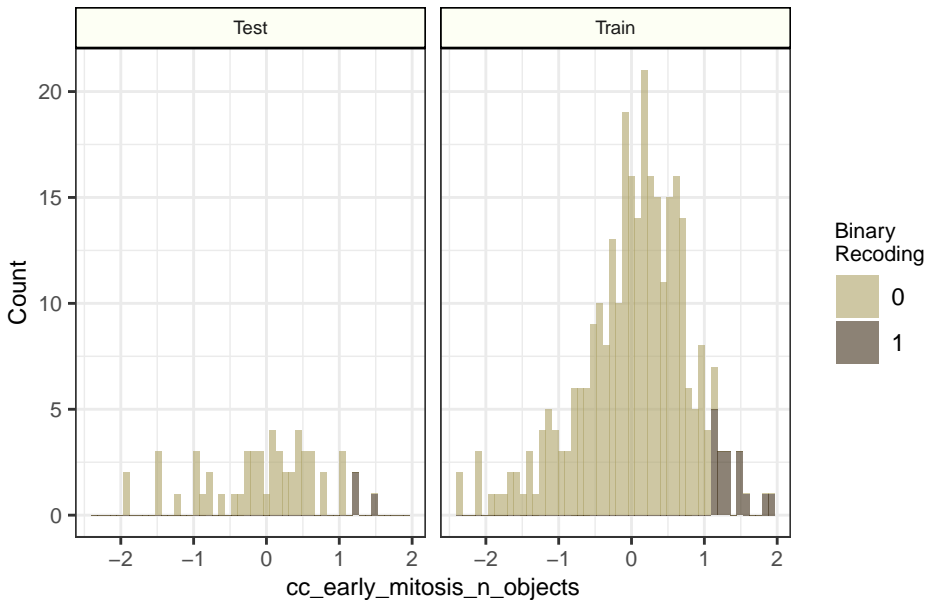
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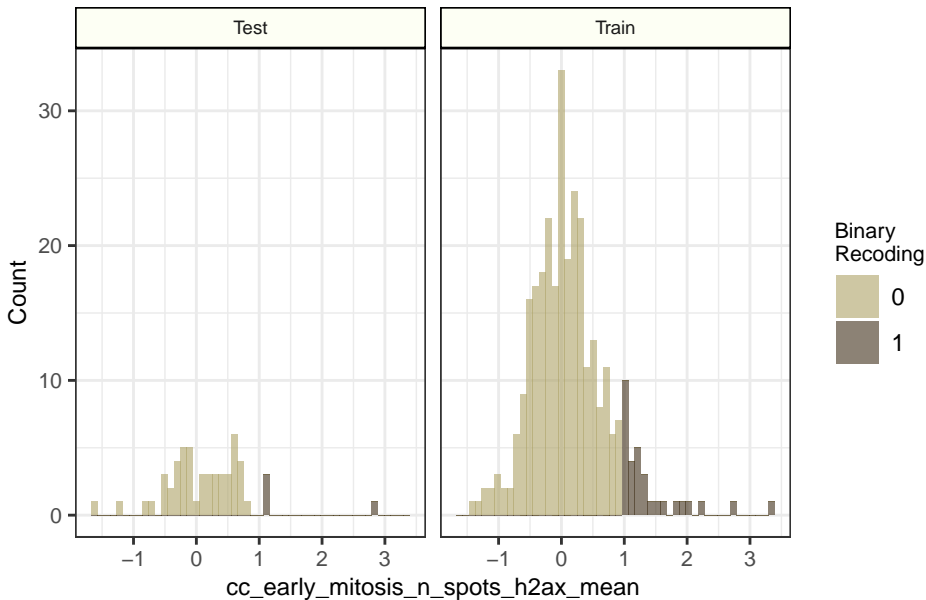
cc_early_mitosis_high_h2ax



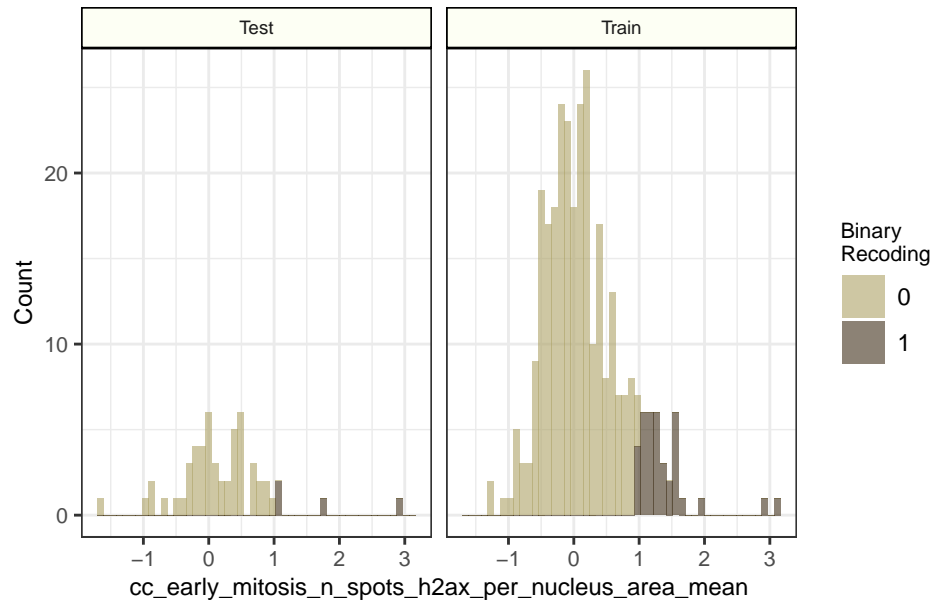
cc_early_mitosis_n_objects



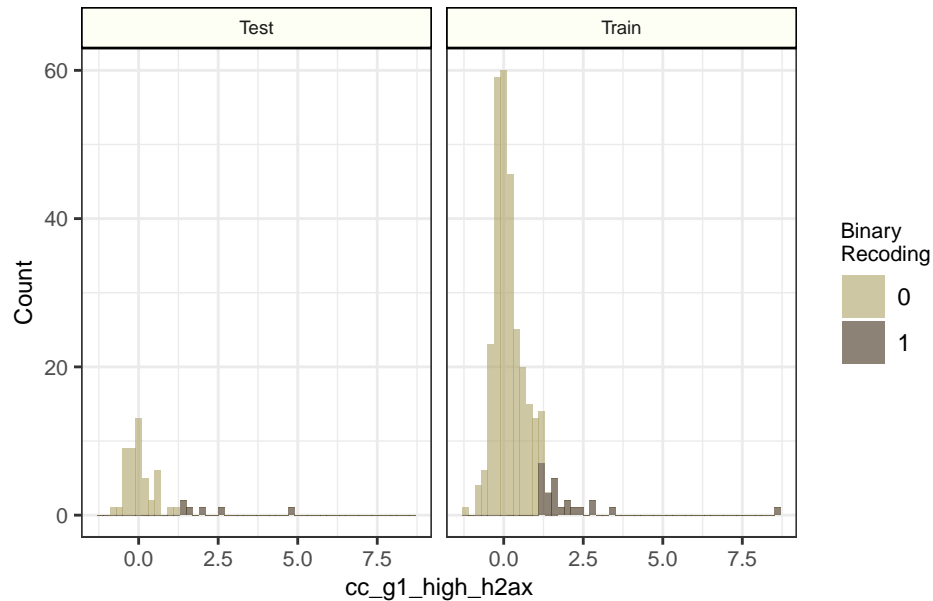
cc_early_mitosis_n_spots_h2ax_mean



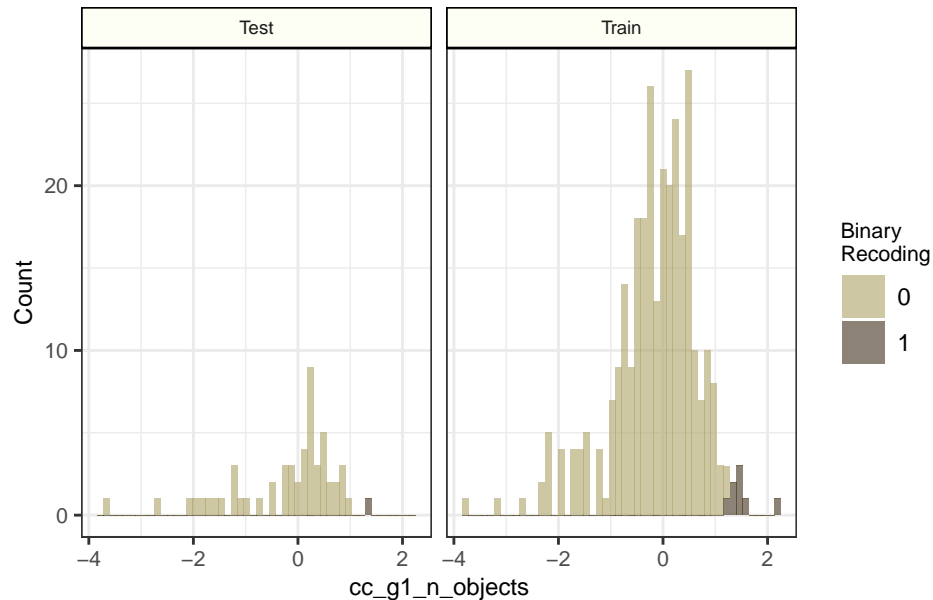
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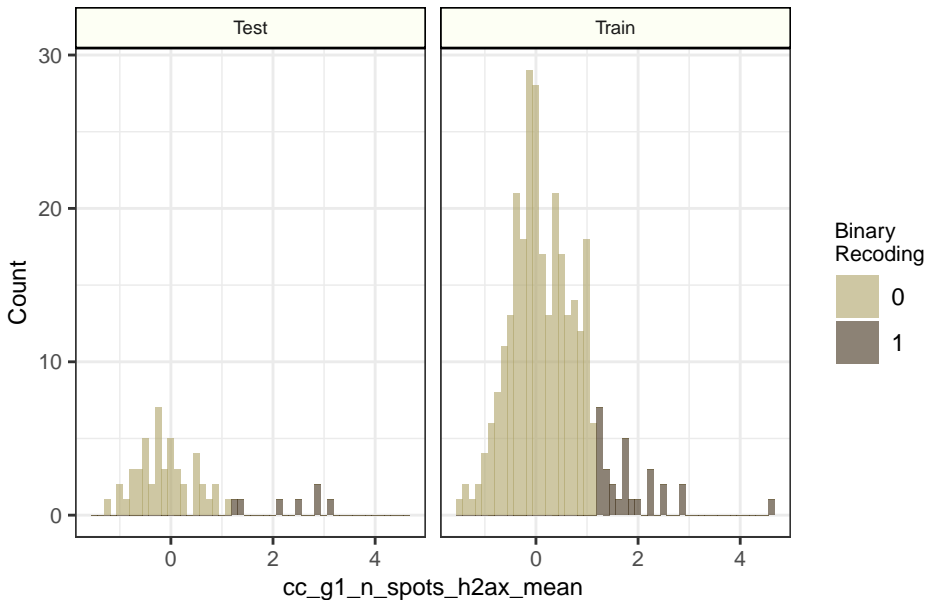
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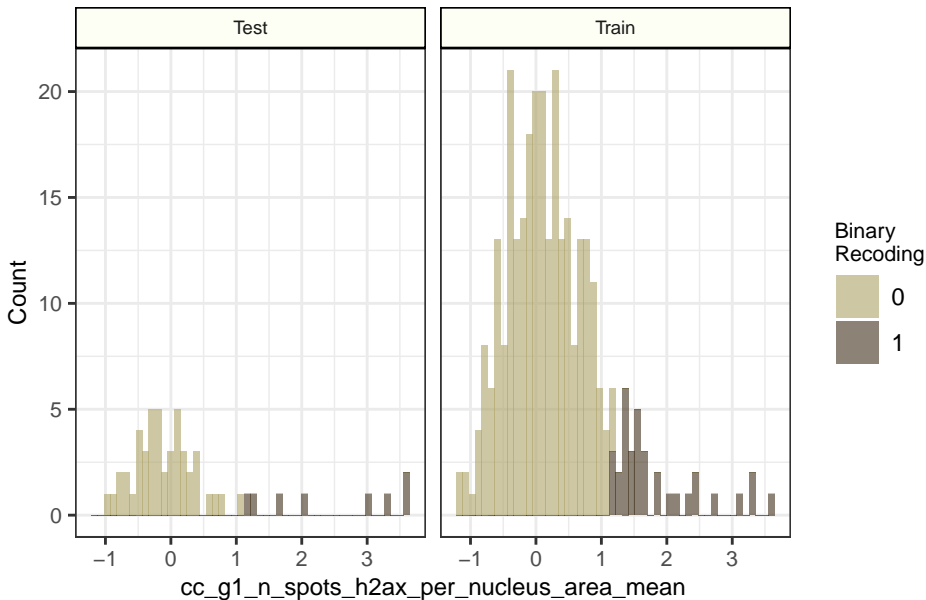
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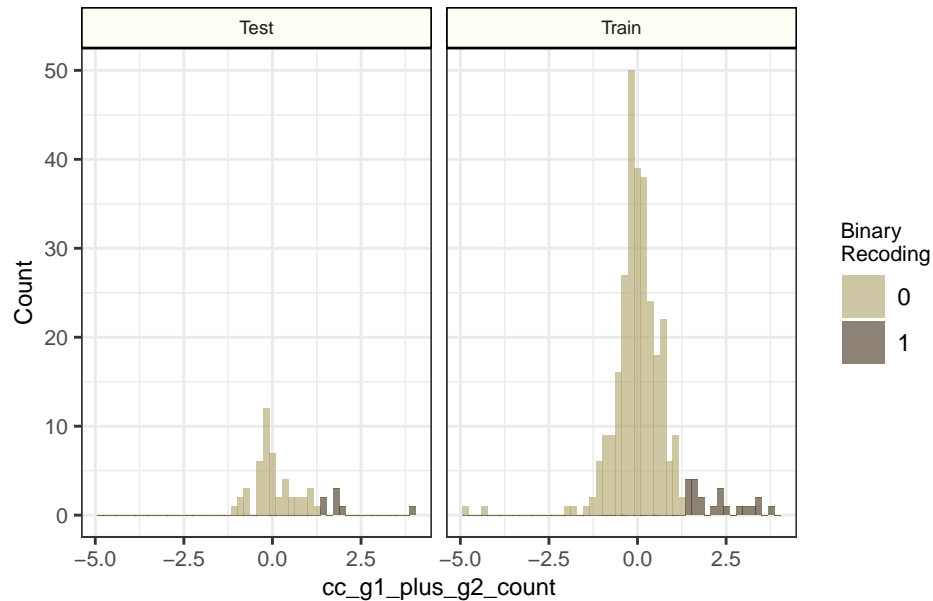
cc_g1_n_spots_h2ax_mean



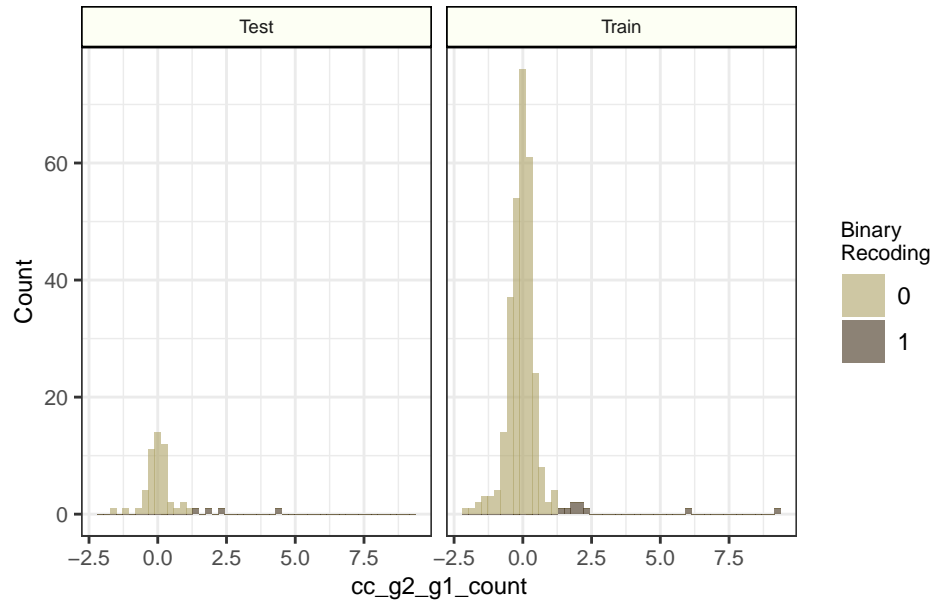
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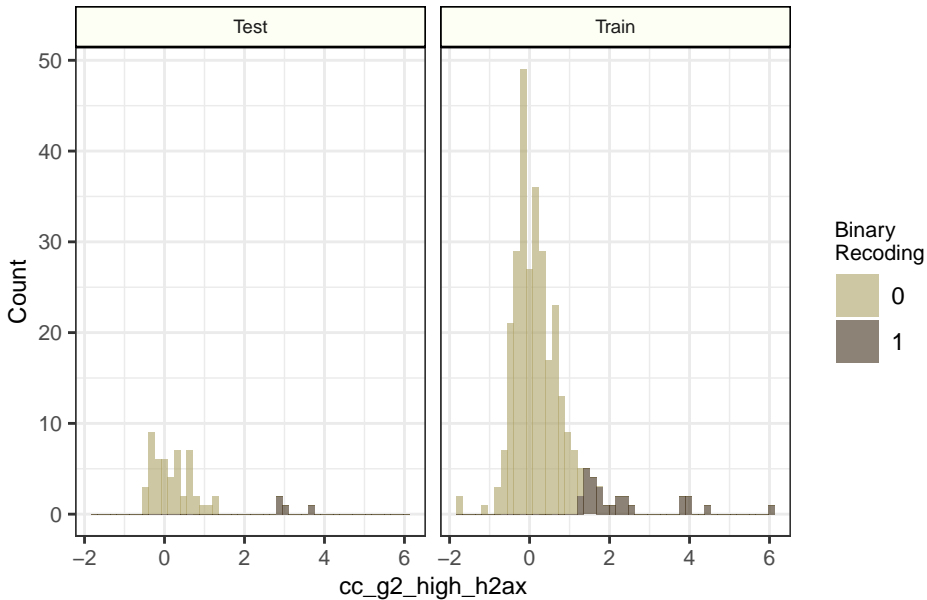
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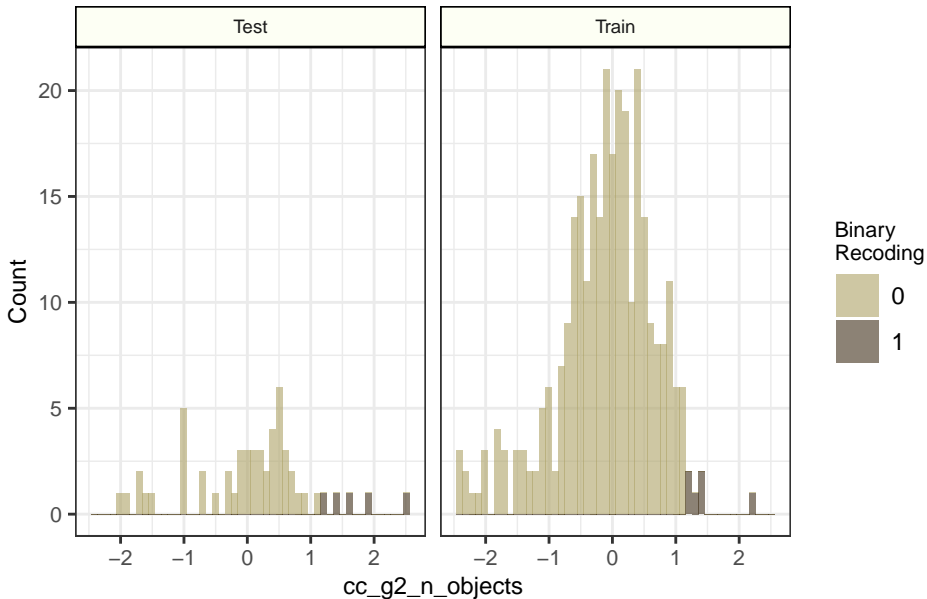
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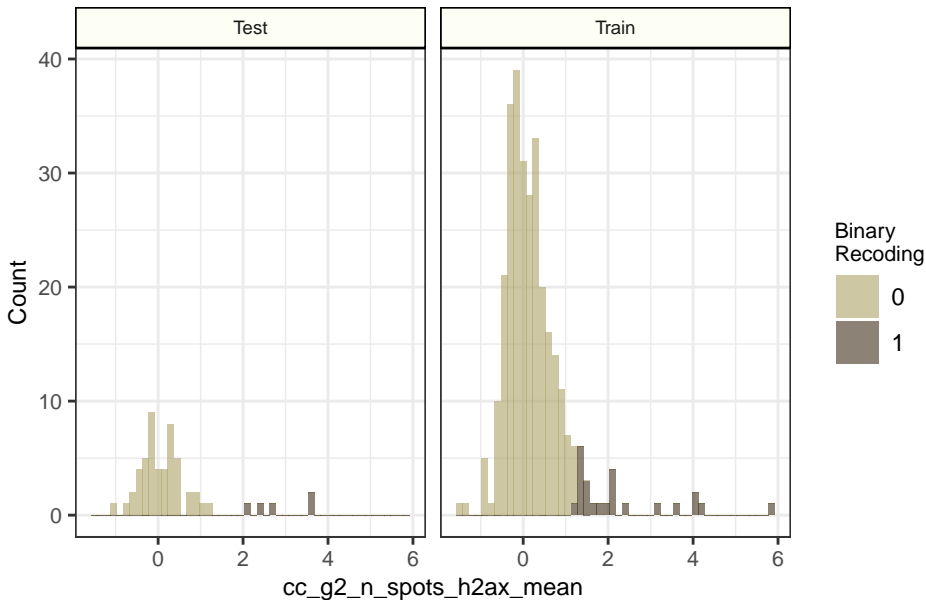
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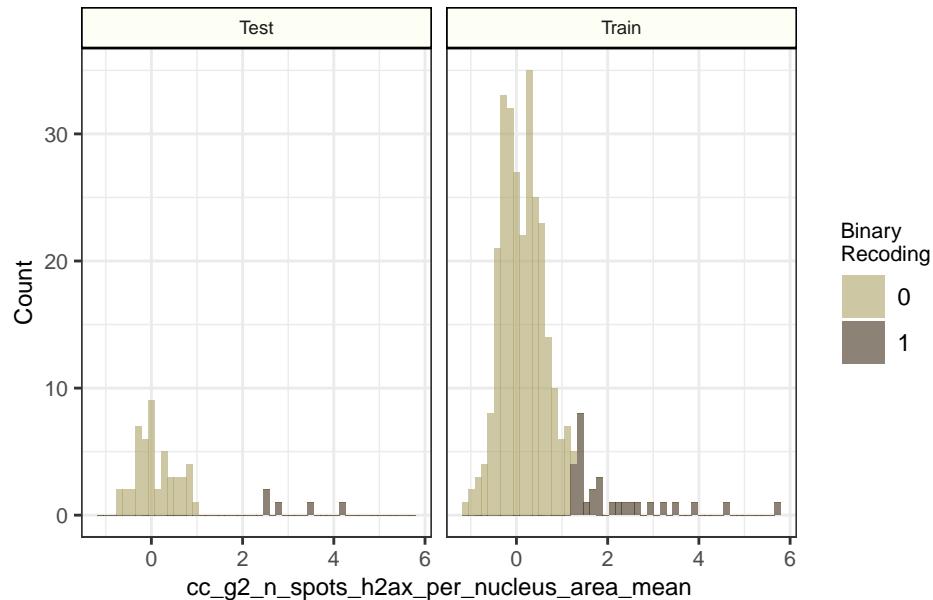
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cc_g2_n_spots_h2ax_mean



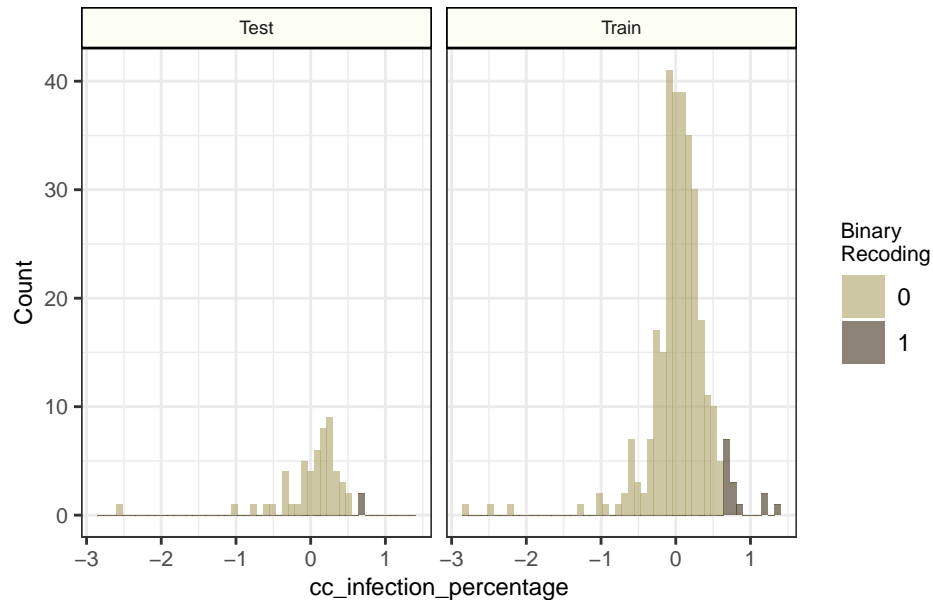
cc_g2_n_spots_h2ax_per_nucleus_area_mean



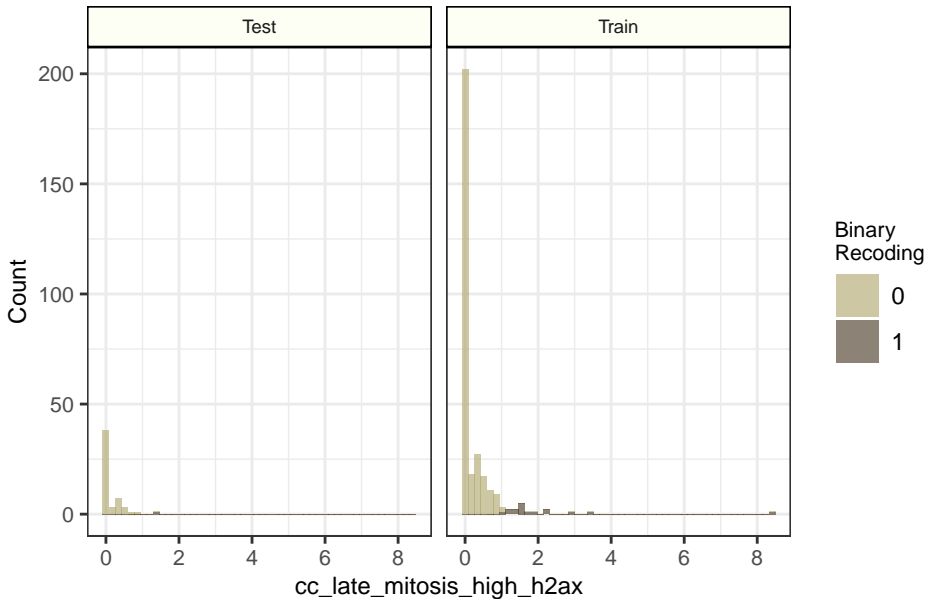
The figure consists of two side-by-side histograms. The left histogram is titled 'Test' and the right is titled 'Train'. Both share the same x-axis, labeled 'cc_g2_plus_all_m_count', with a range from -2 to 6. The 'Train' histogram shows a distribution centered near 0, with a peak frequency of approximately 100. The 'Test' histogram shows a distribution shifted to the right, centered near 1, with a peak frequency of approximately 20. Both distributions are right-skewed, with long tails extending towards higher values.



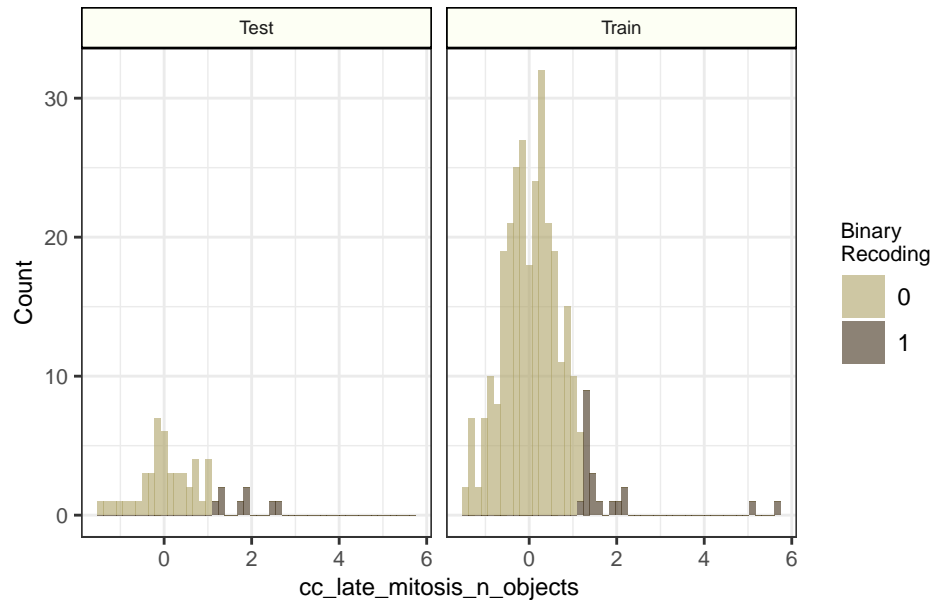
cc_infection_percentage



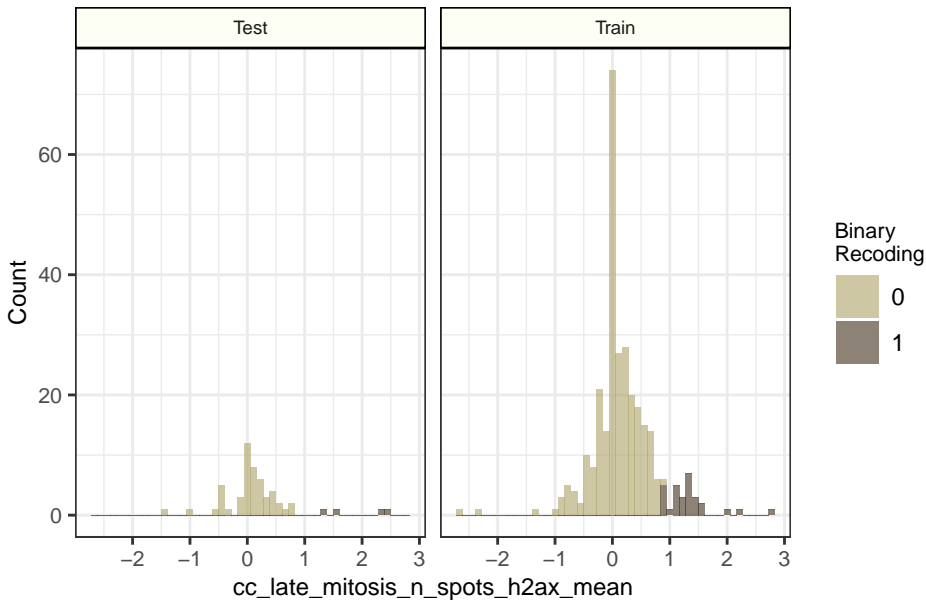
cc_late_mitosis_high_h2ax



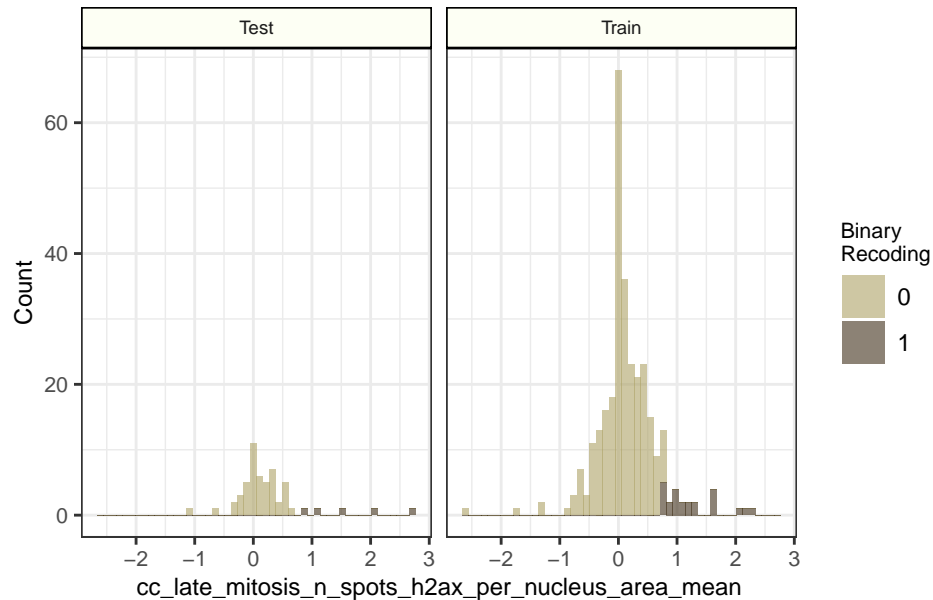
cc_late_mitosis_n_objects



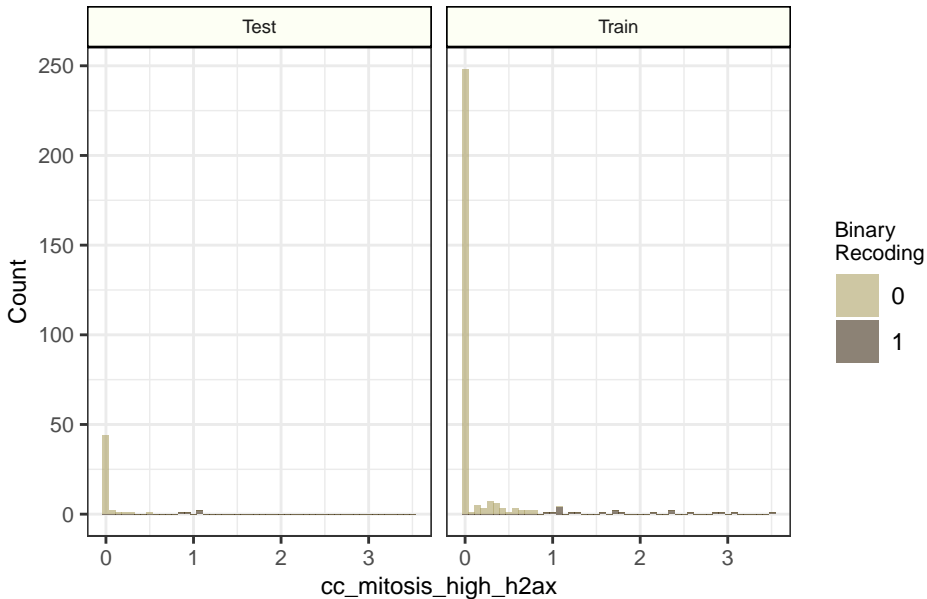
cc_late_mitosis_n_spots_h2ax_mean



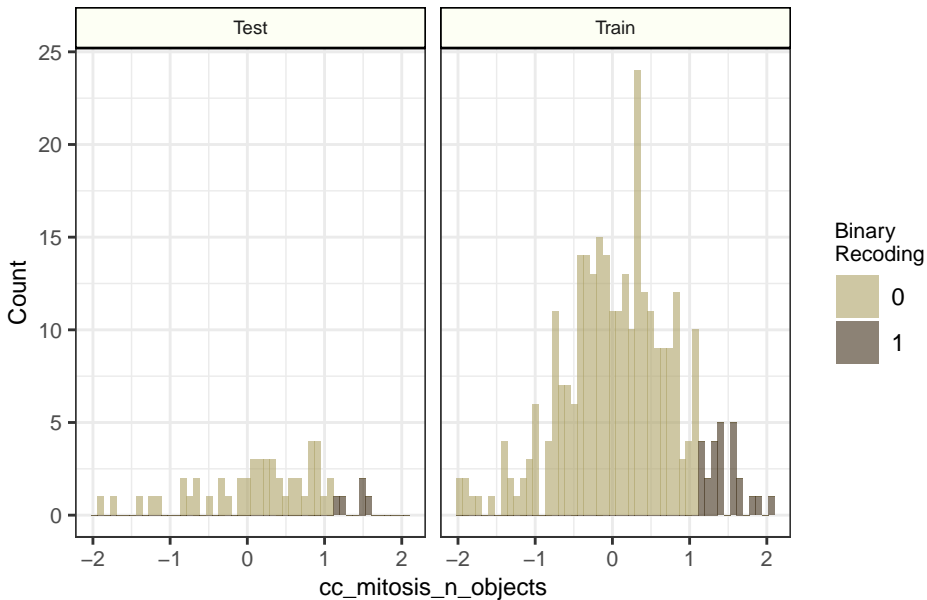
cc_late_mitosis_n_spots_h2ax_per_nucleus_area_m



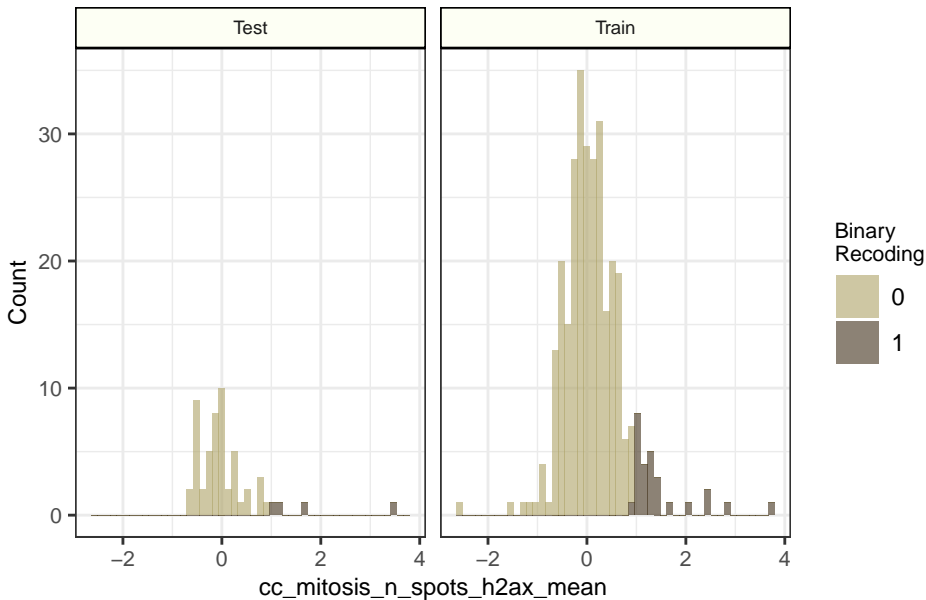
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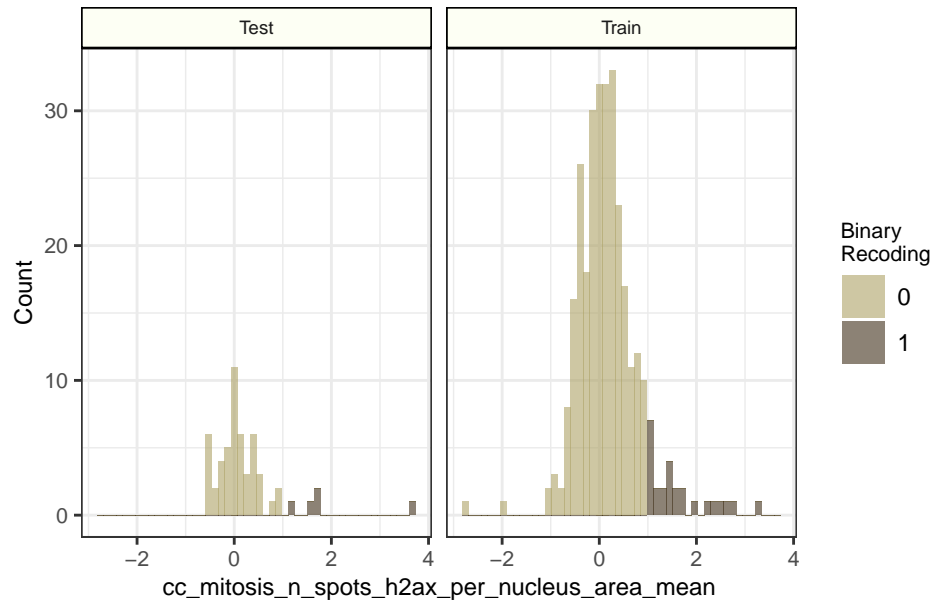
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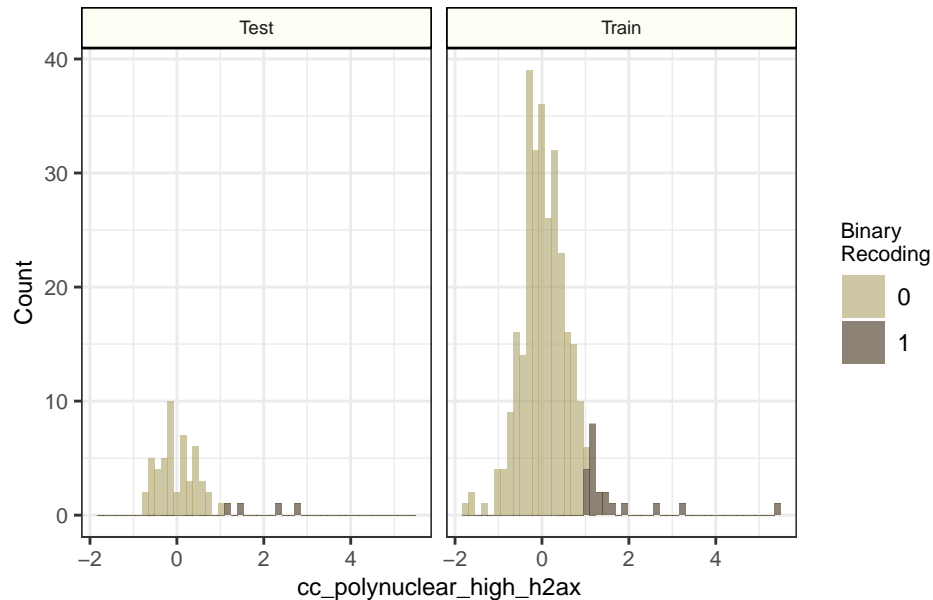
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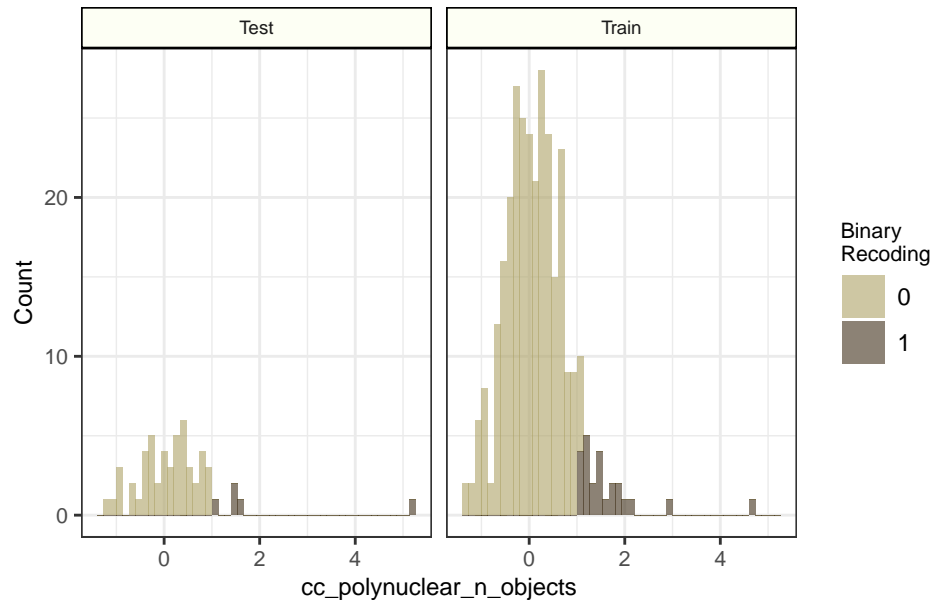
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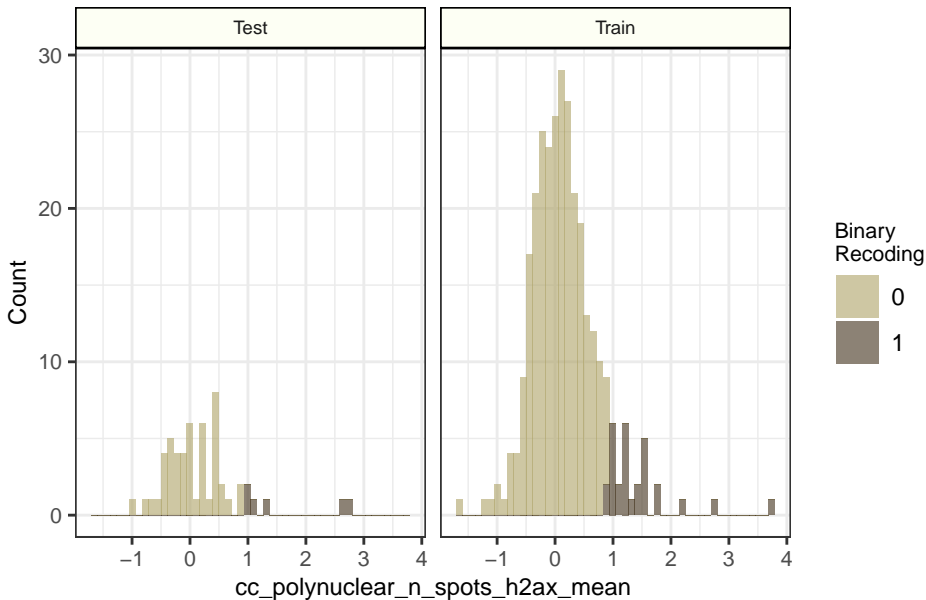
cc_polynuclear_high_h2ax



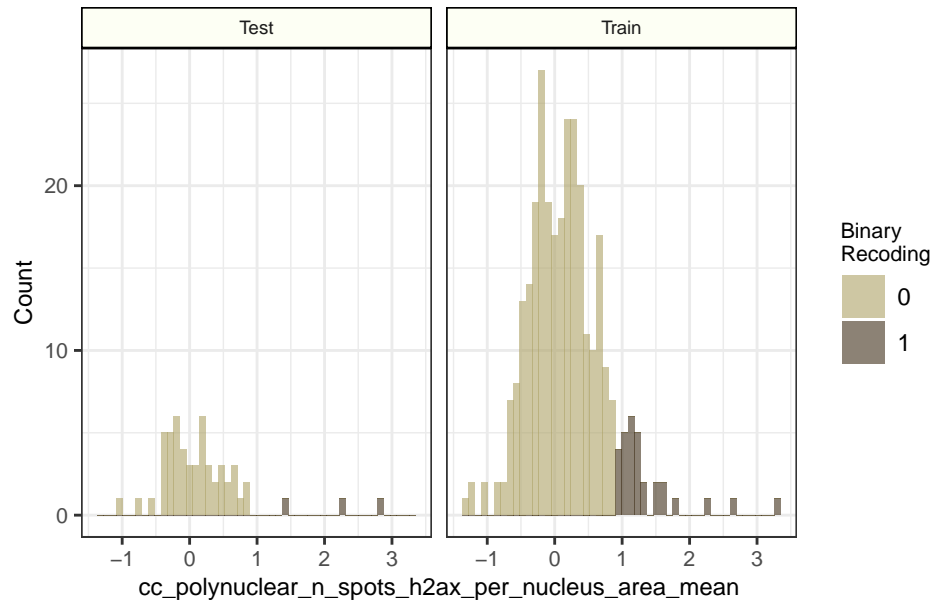
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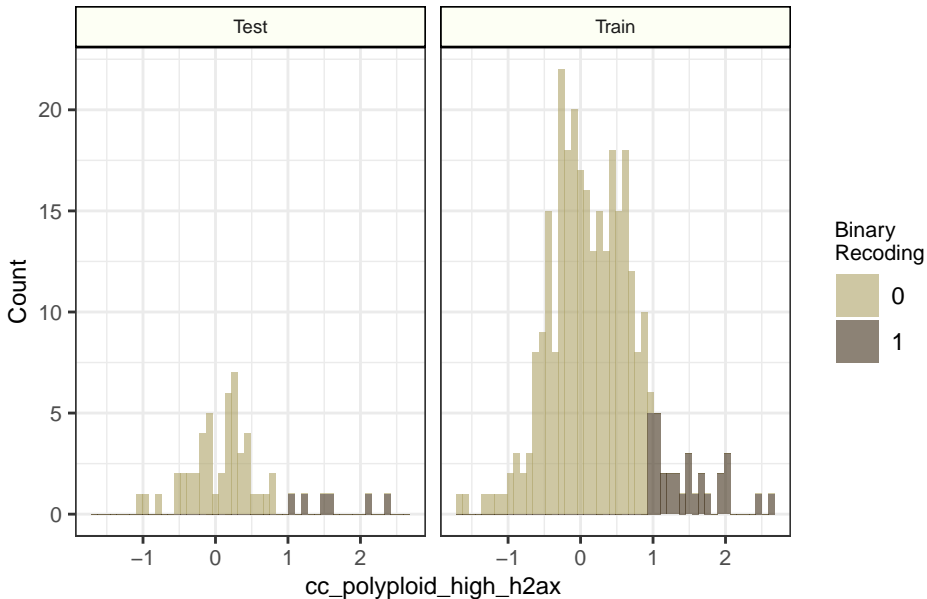
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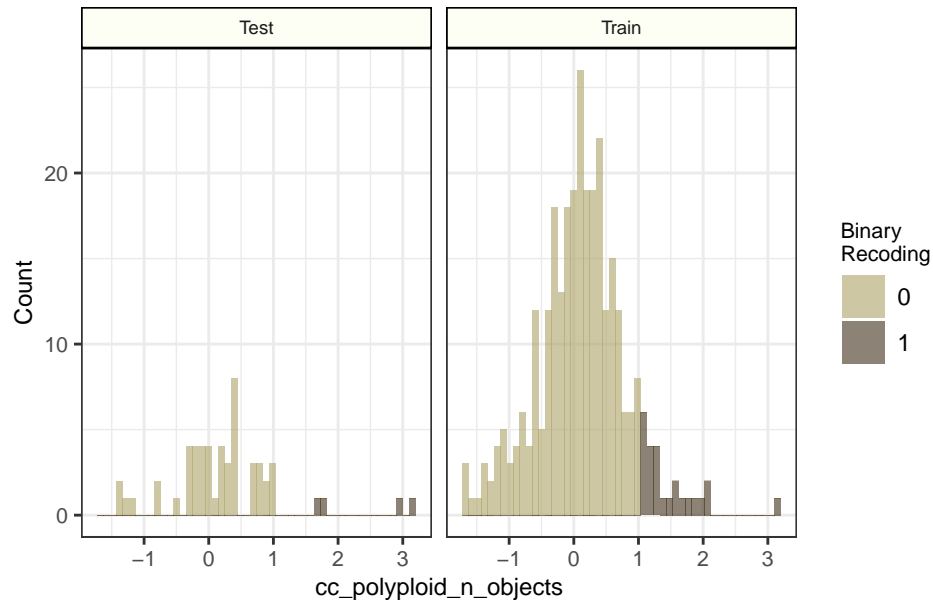
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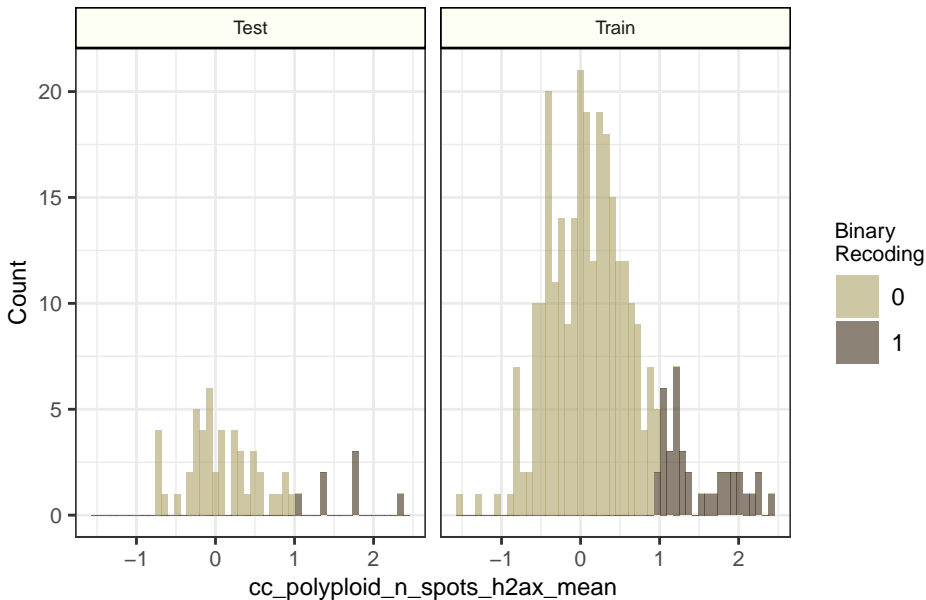
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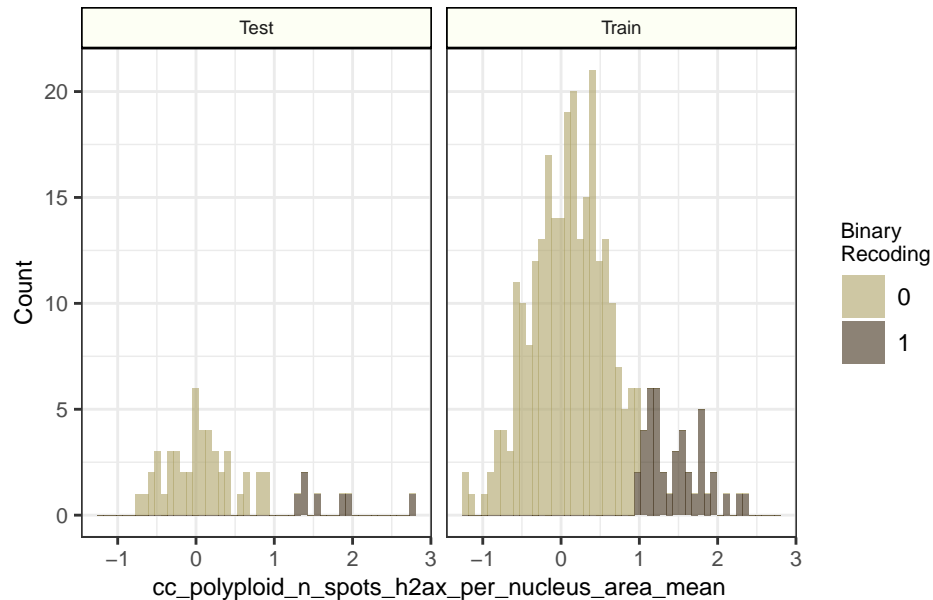
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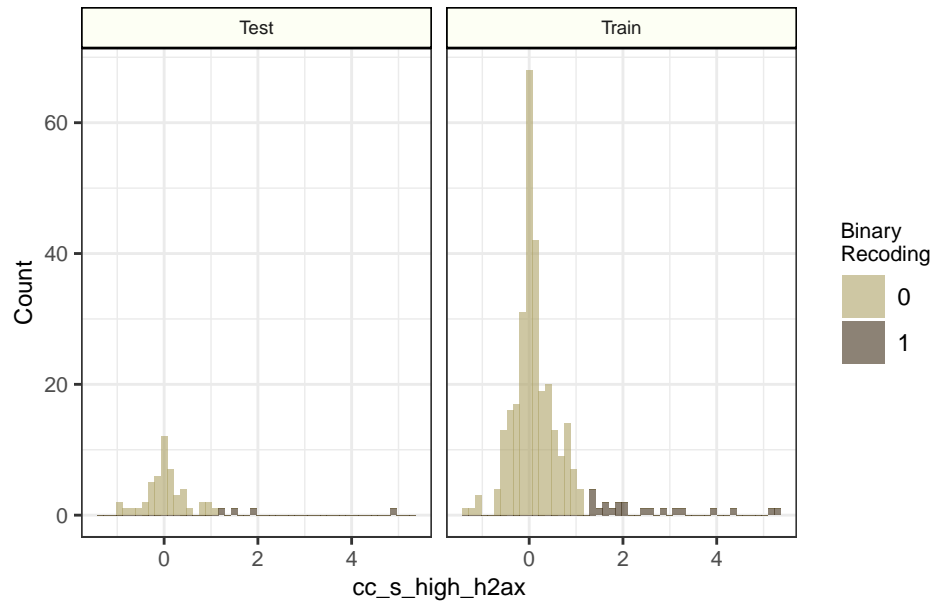
cc_polyploid_n_spots_h2ax_mean



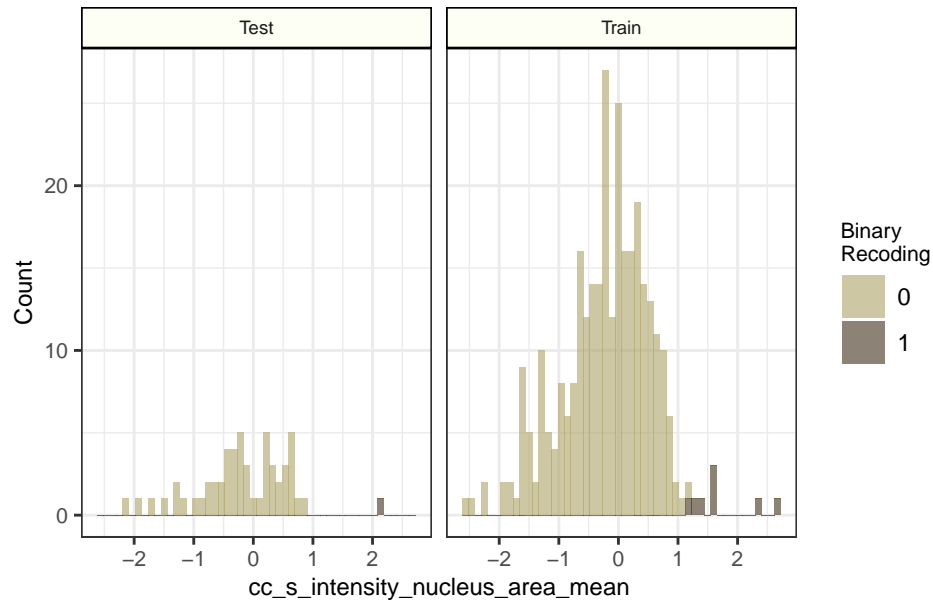
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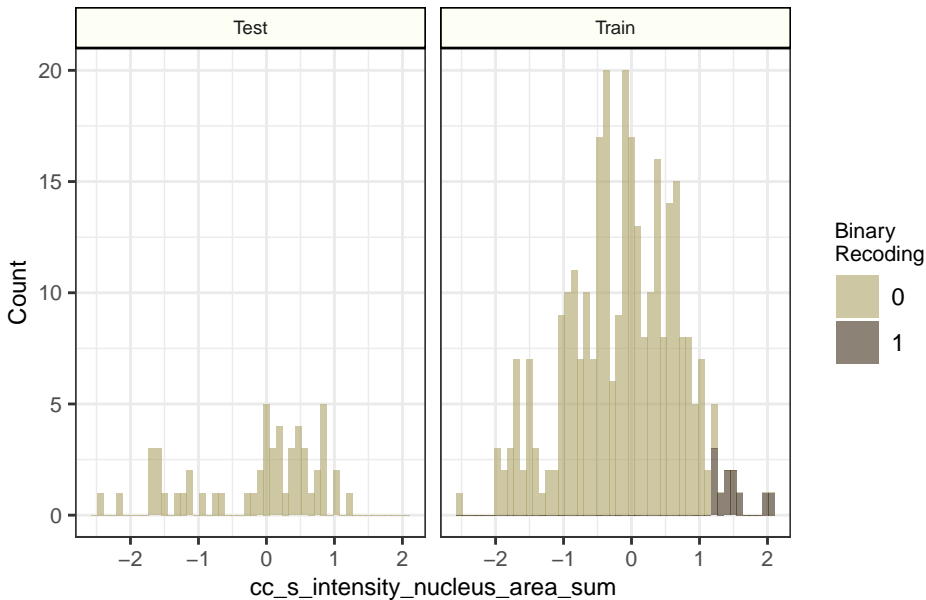
cc_s_high_h2ax



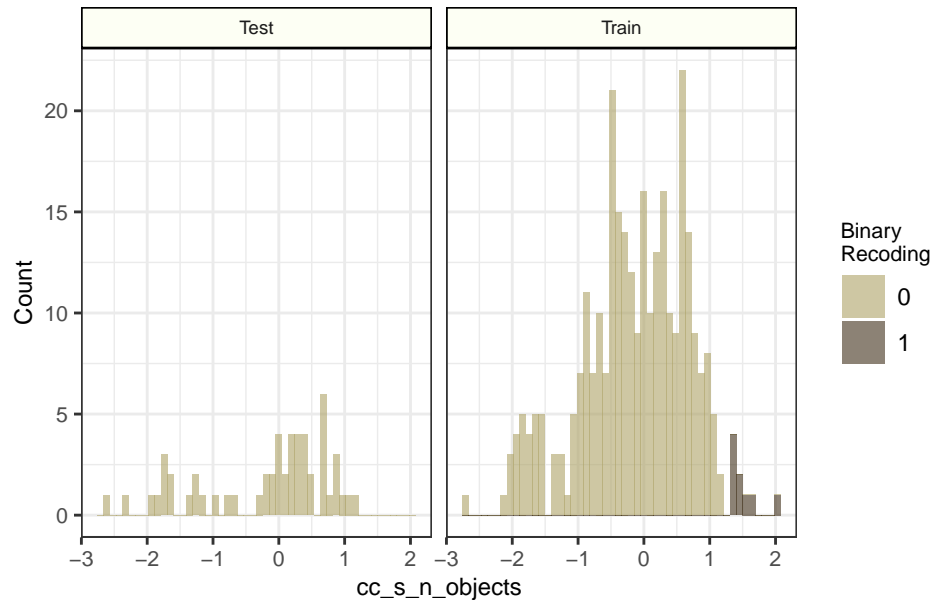
cc_s_intensity_nucleus_area_mean



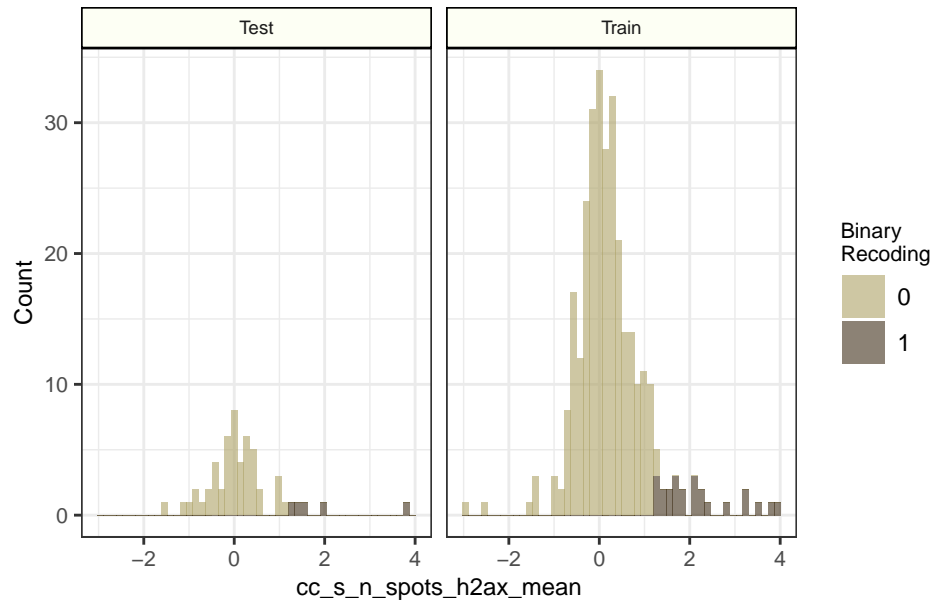
cc_s_intensity_nucleus_area_sum



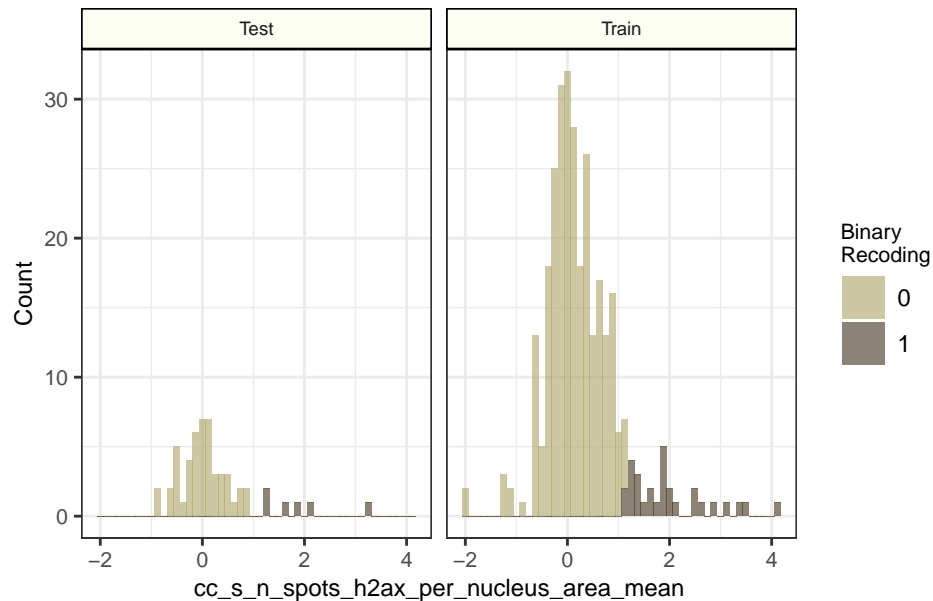
cc_s_n_objects



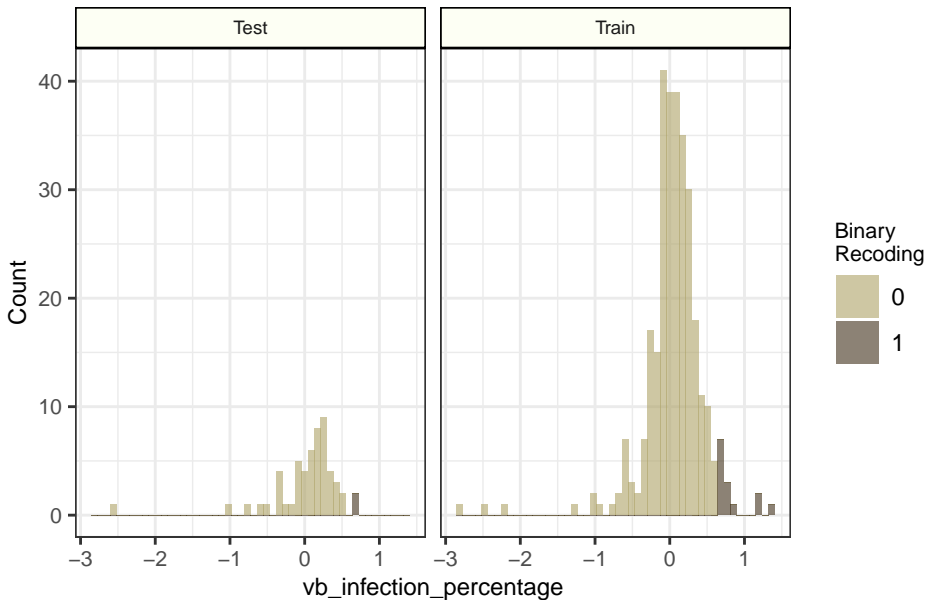
cc_s_n_spots_h2ax_mean



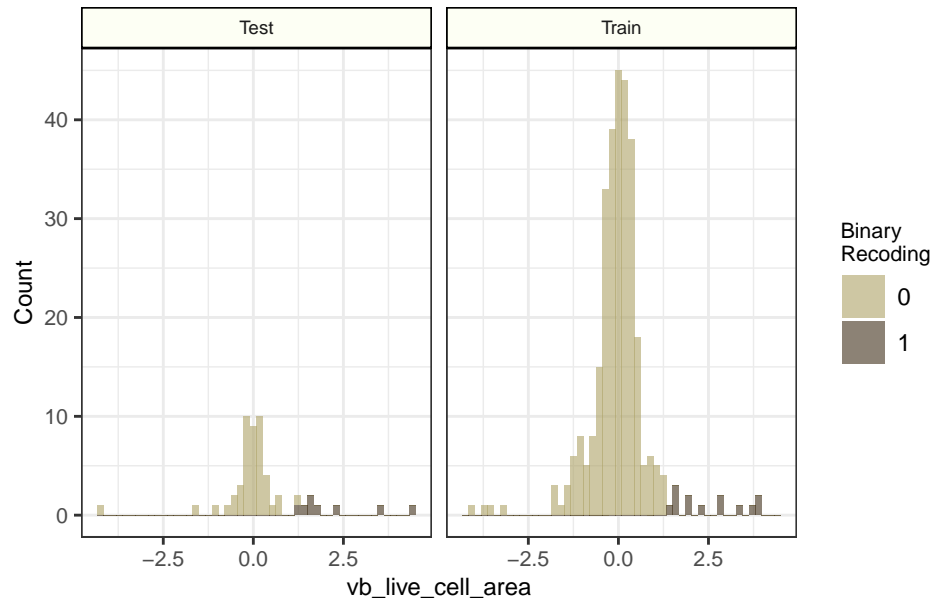
cc_s_n_spots_h2ax_per_nucleus_area_mean



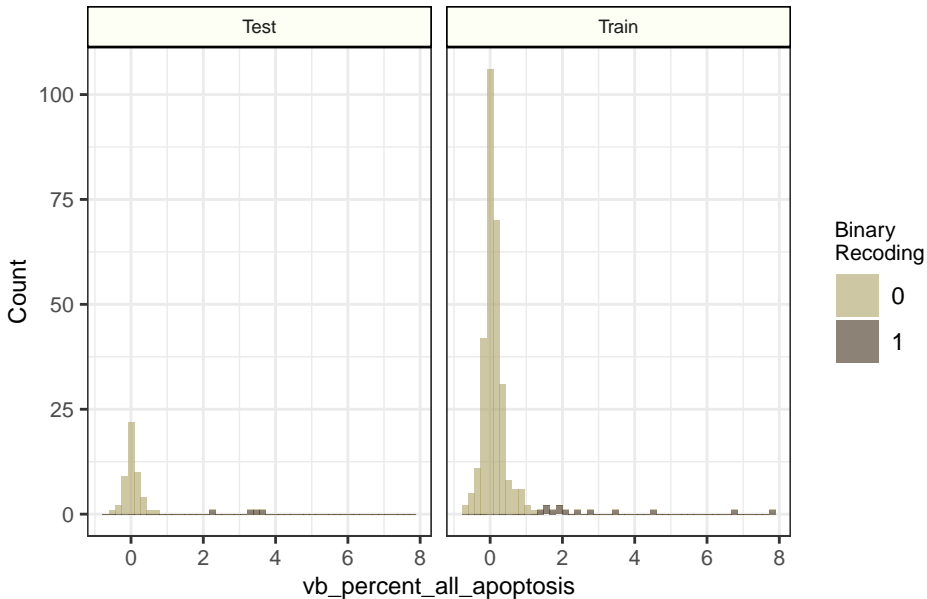
vb_infection_percentage



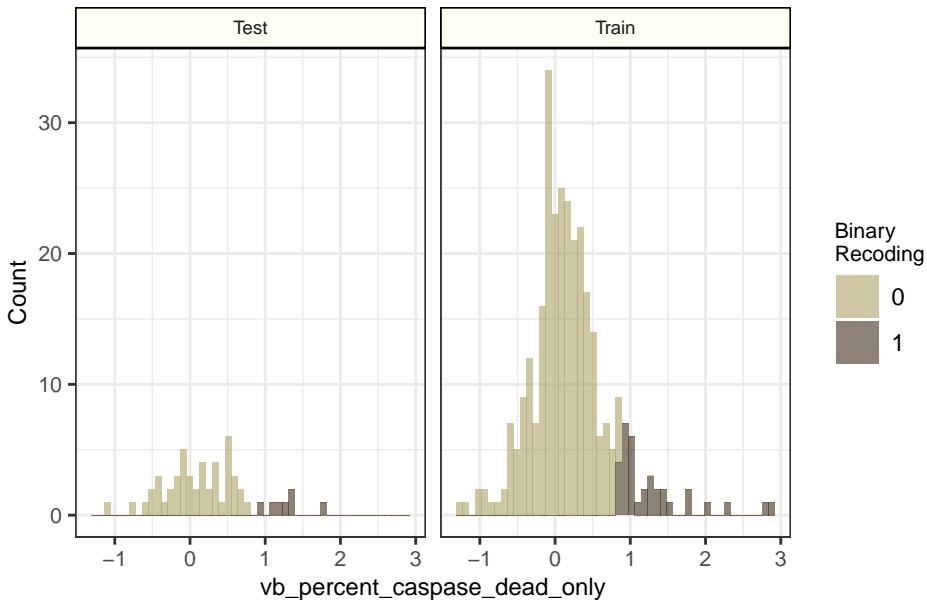
vb_live_cell_area



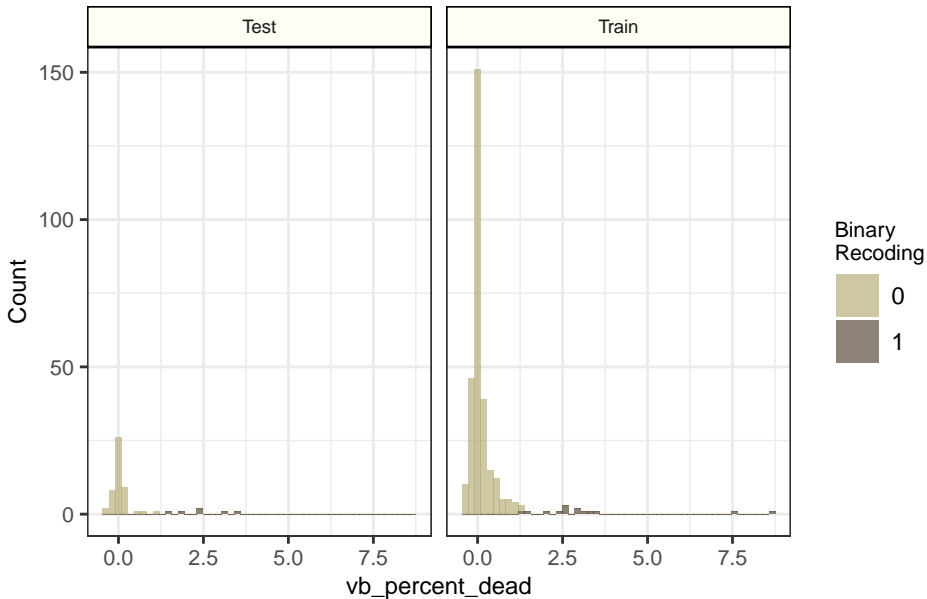
vb_percent_all_apoptosis



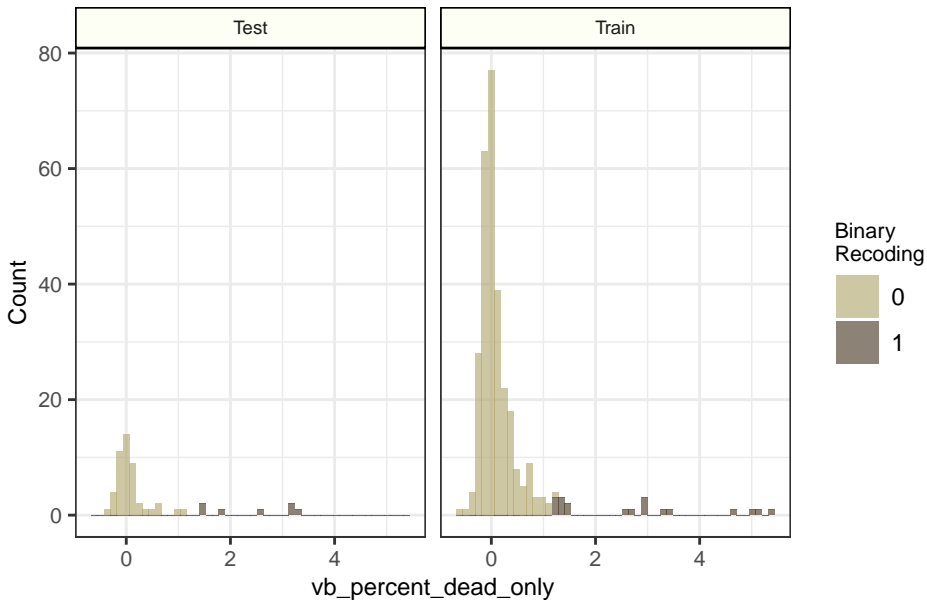
vb_percent_caspase_dead_only



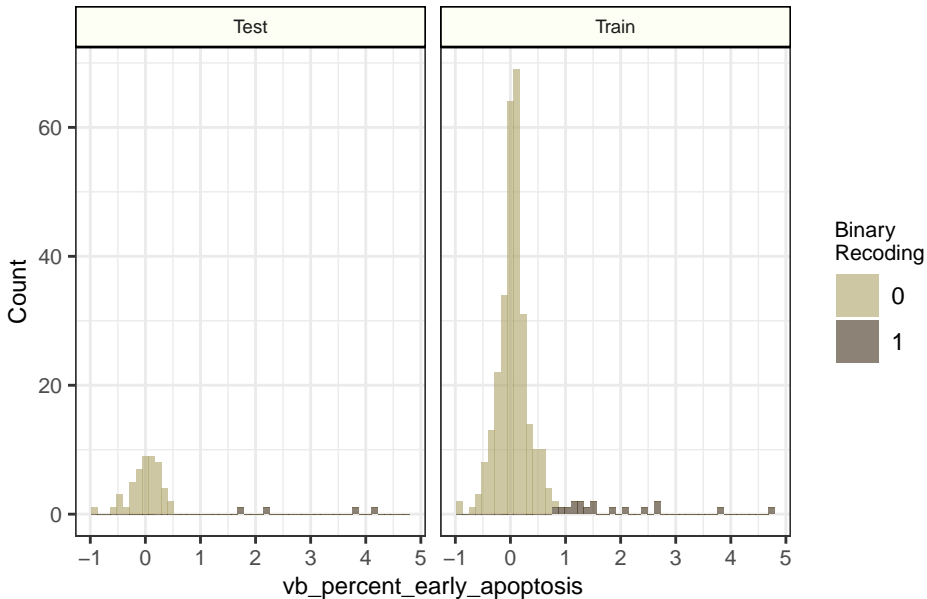
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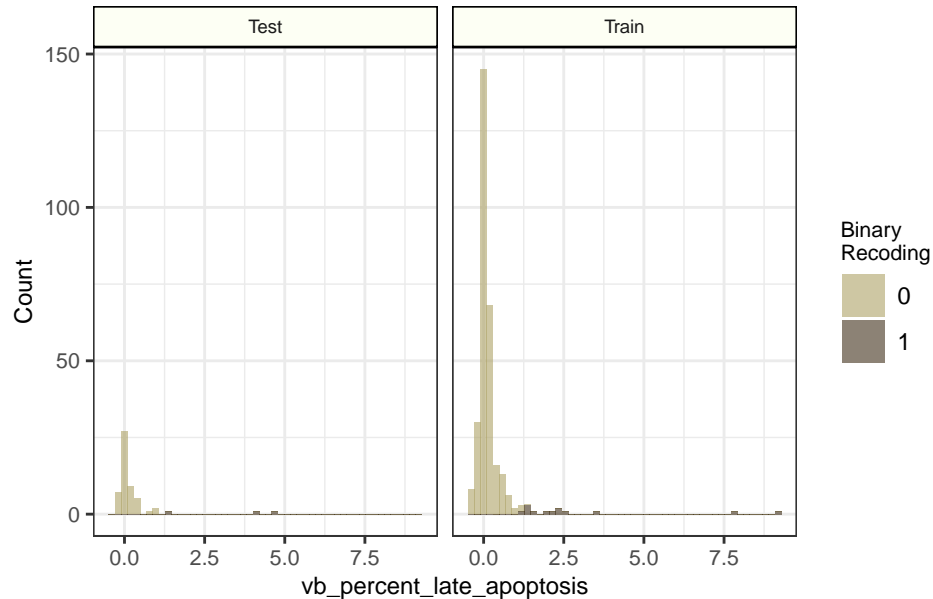
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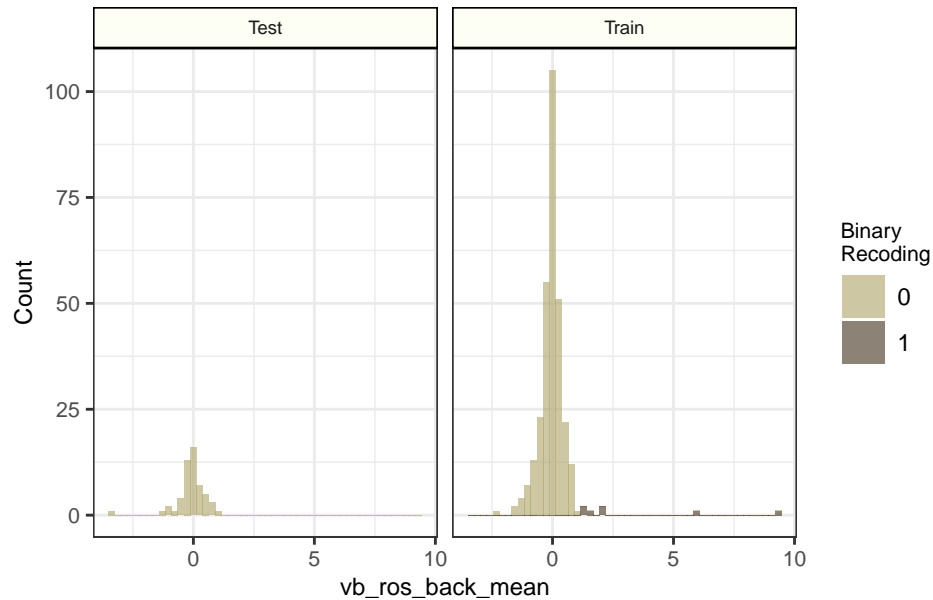
vb_percent_early_apoptosis



vb_percent_late_apoptosis



vb_ros_back_mean



vb_ros_mean

