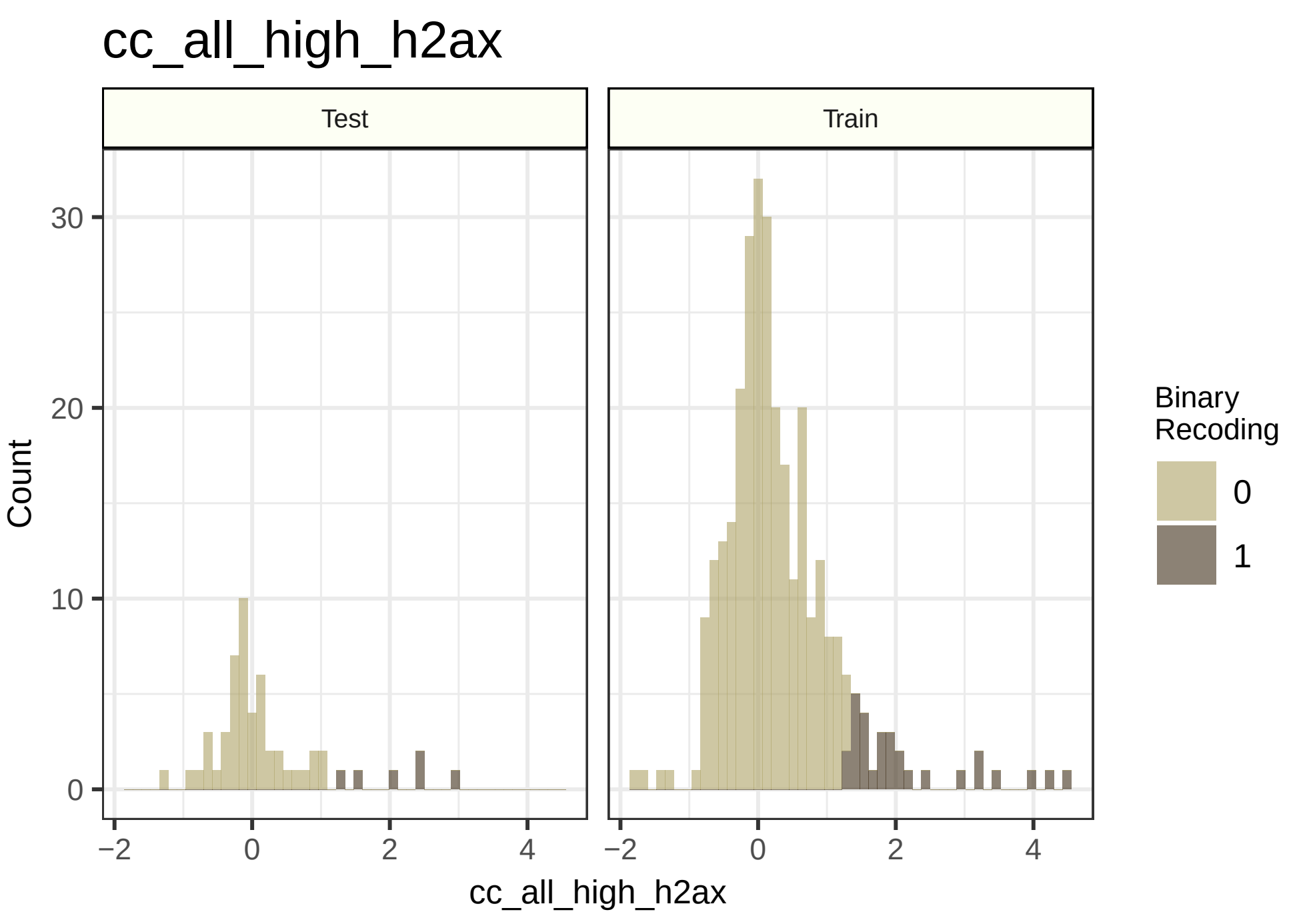
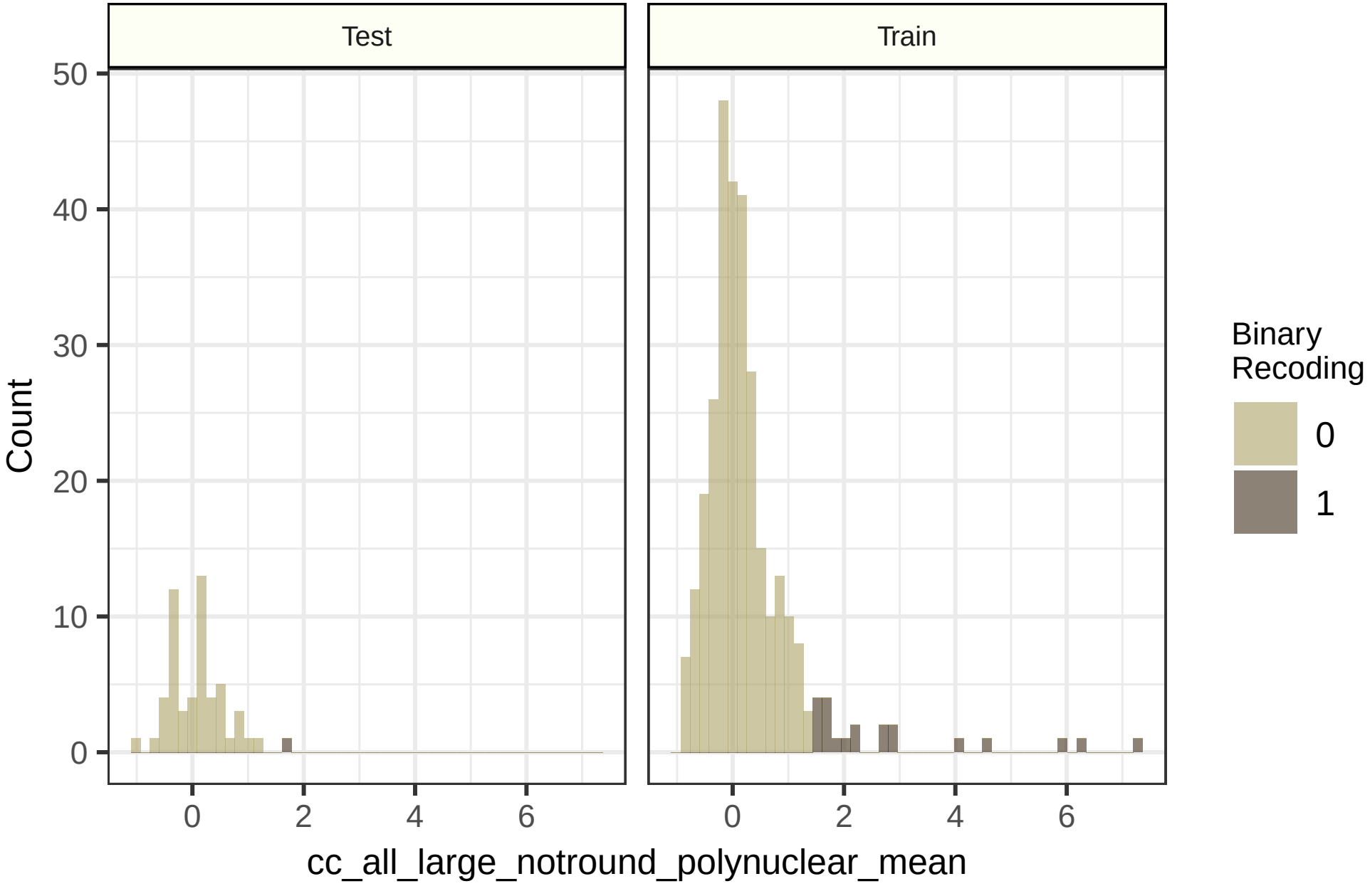
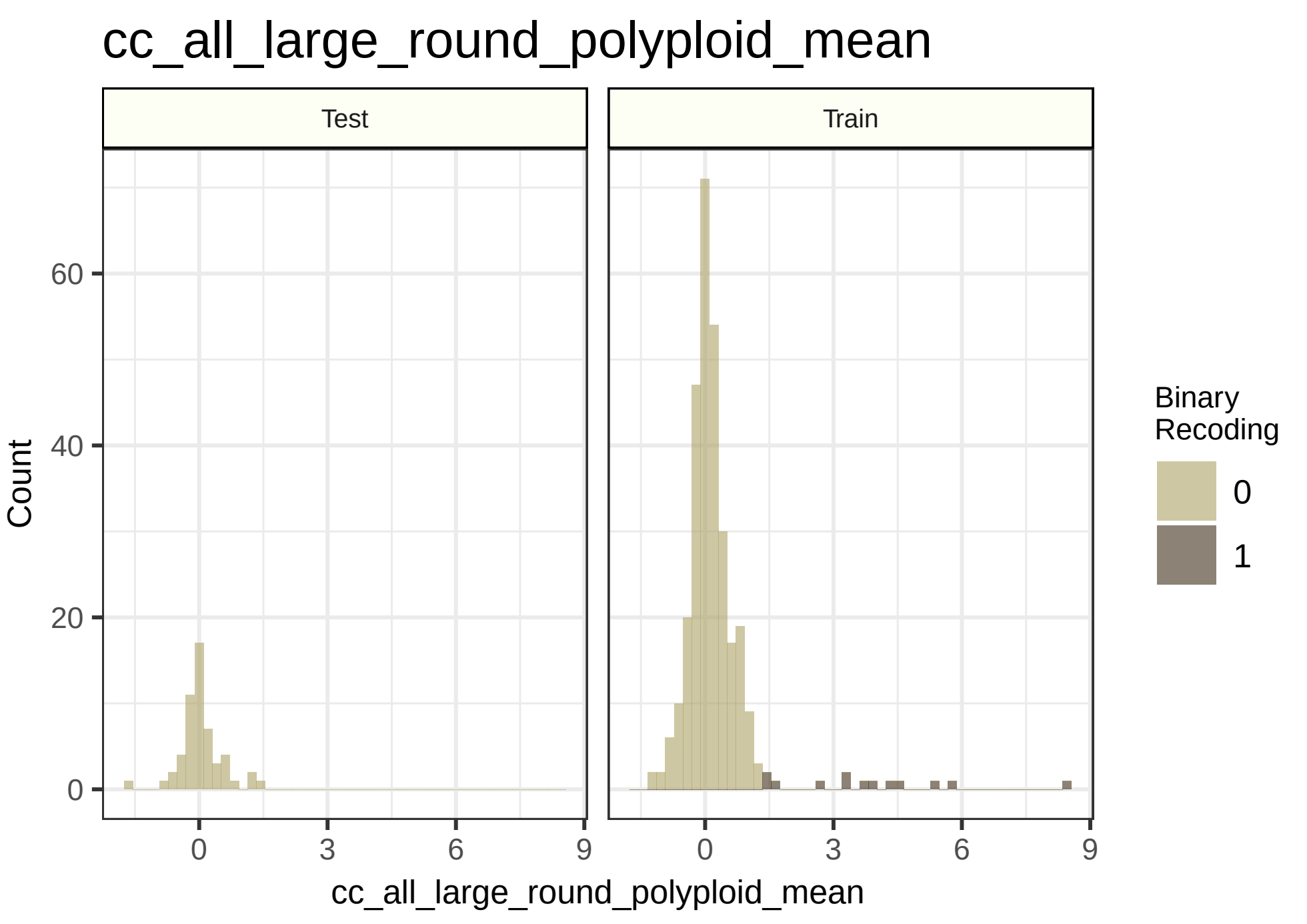
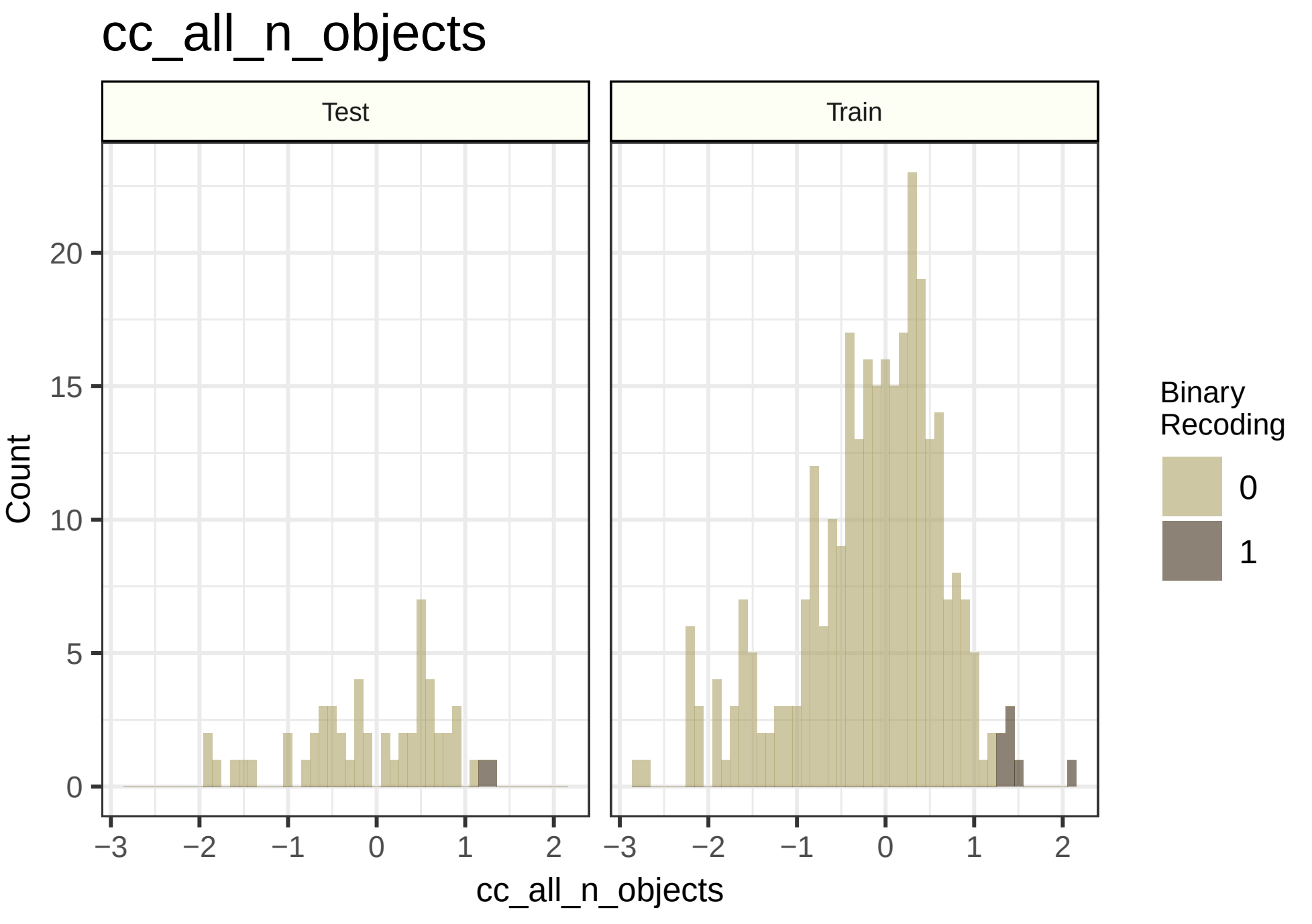
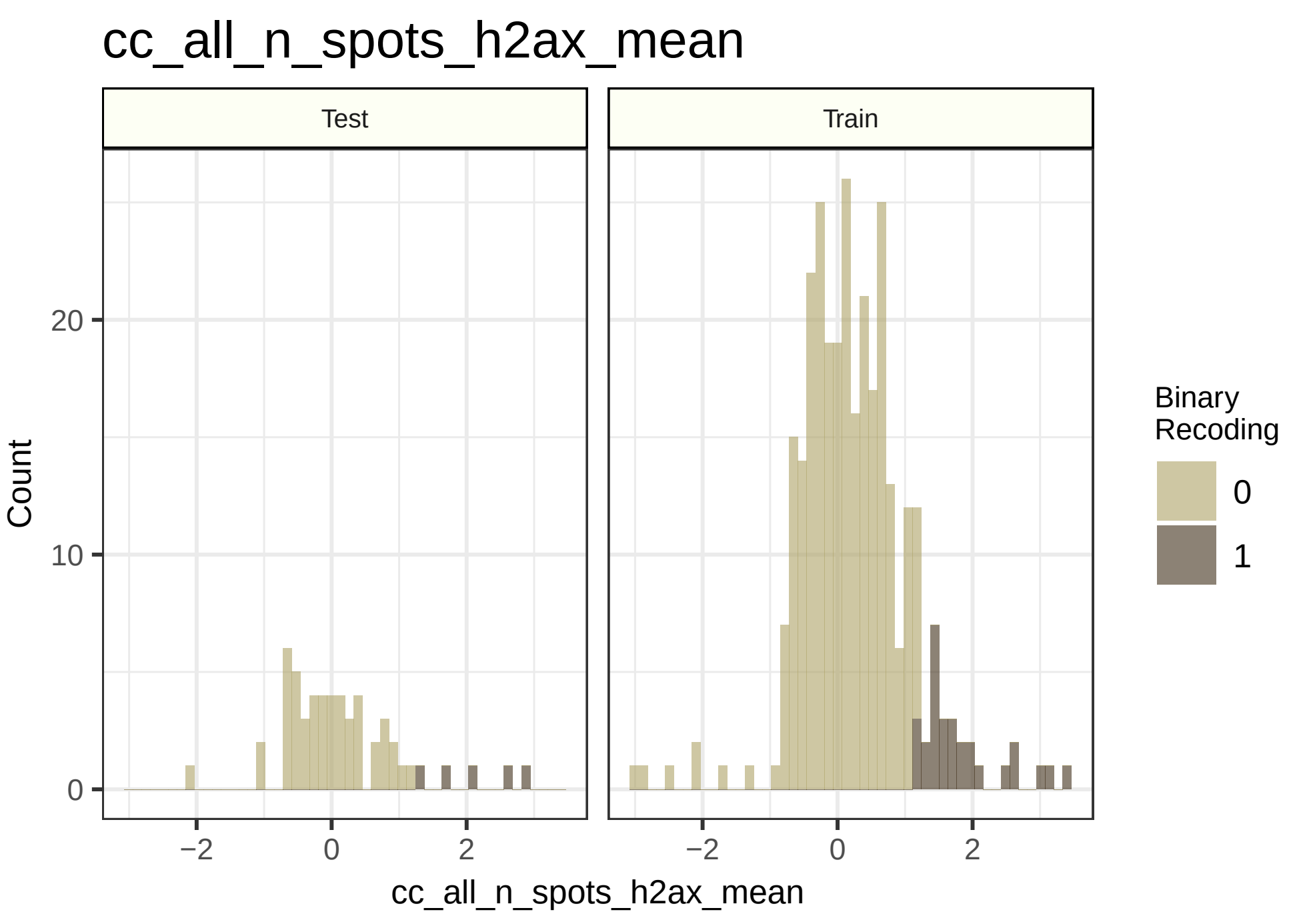
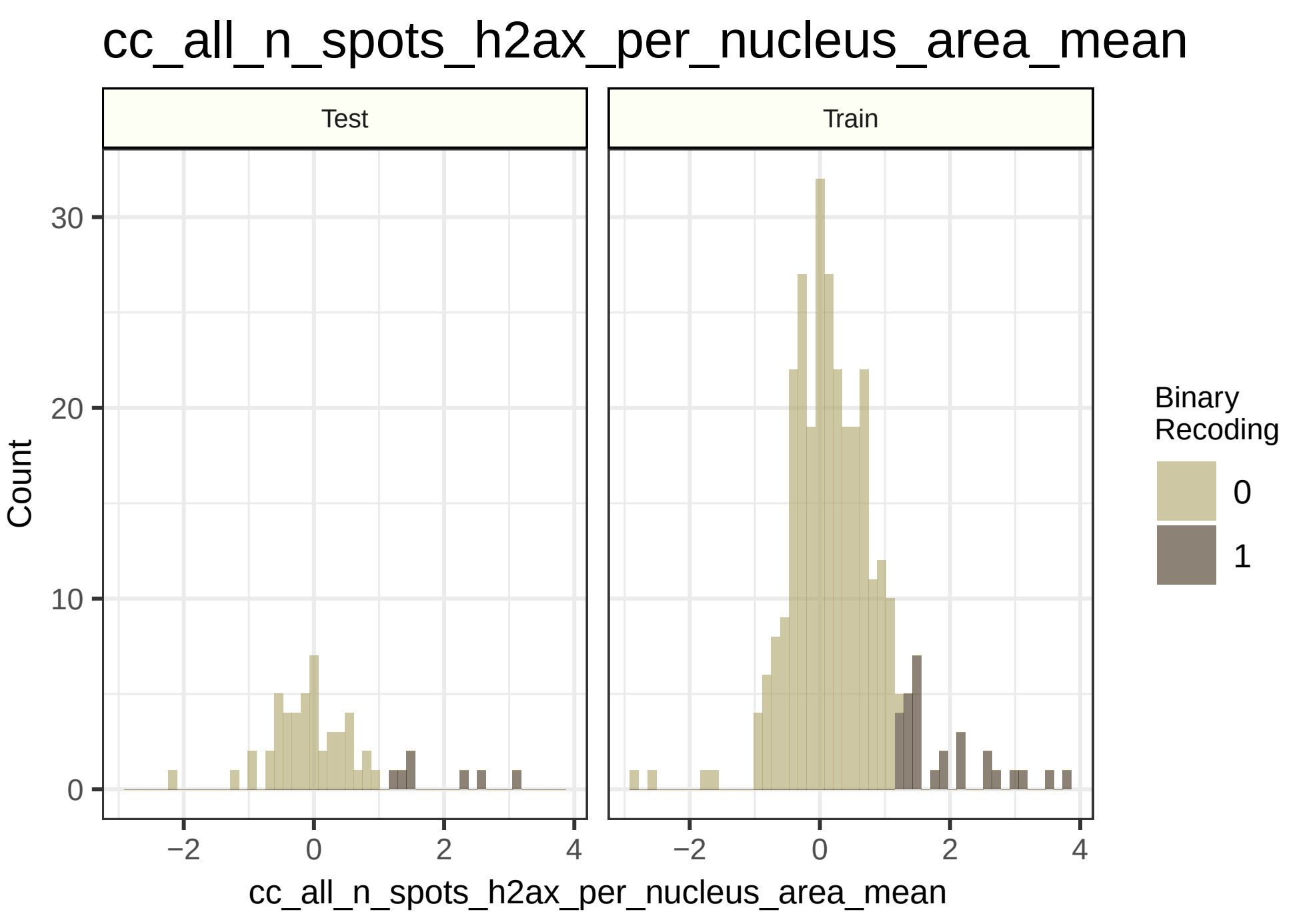

cc_all_high_h2ax
Test
Train
30
20
10
0
Count
−2
0
2
4
cc_all_high_h2ax
Binary Recoding
0
1

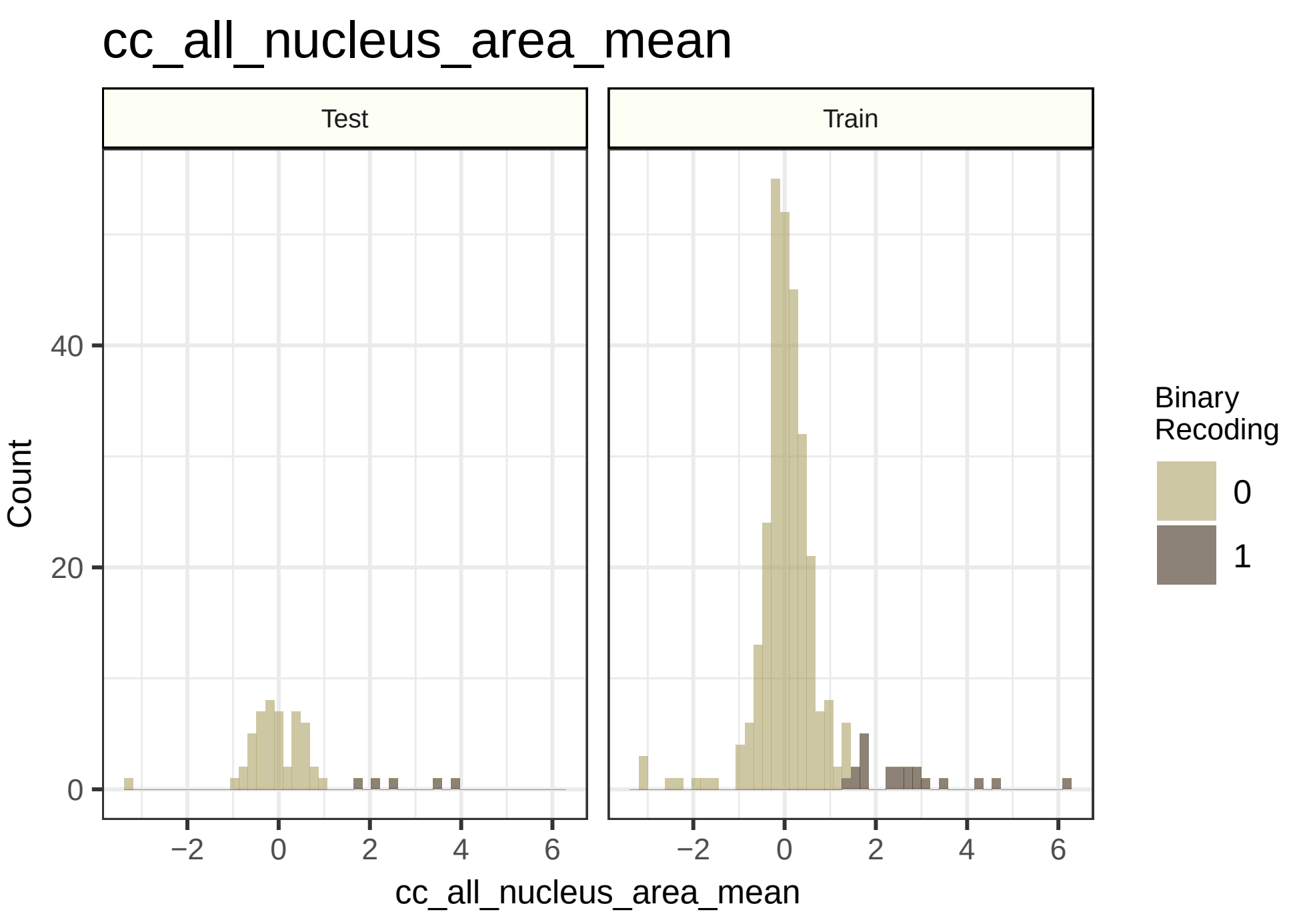

cc_all_large_notround_polynuclear_mean
Test
Train
Count
50
40
30
20
10
0
0
2
4
6
cc_all_large_notround_polynuclear_mean
Binary Recoding
0
1

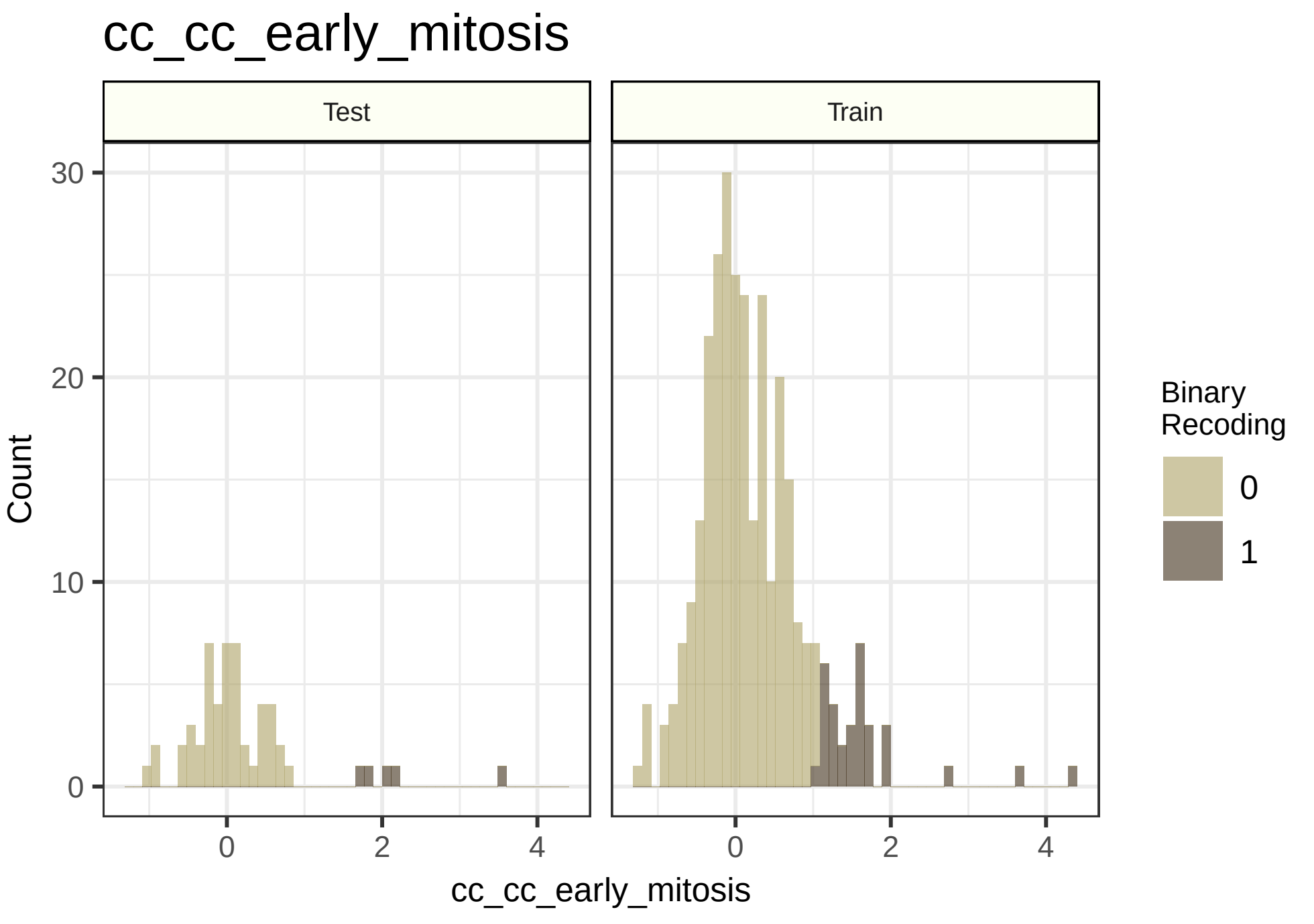

cc_all_large_round_polyploid_mean
Test
Train
Count
60
40
20
0
0
3
6
9
0
3
6
9
cc_all_large_round_polyploid_mean
Binary Recoding
0
1

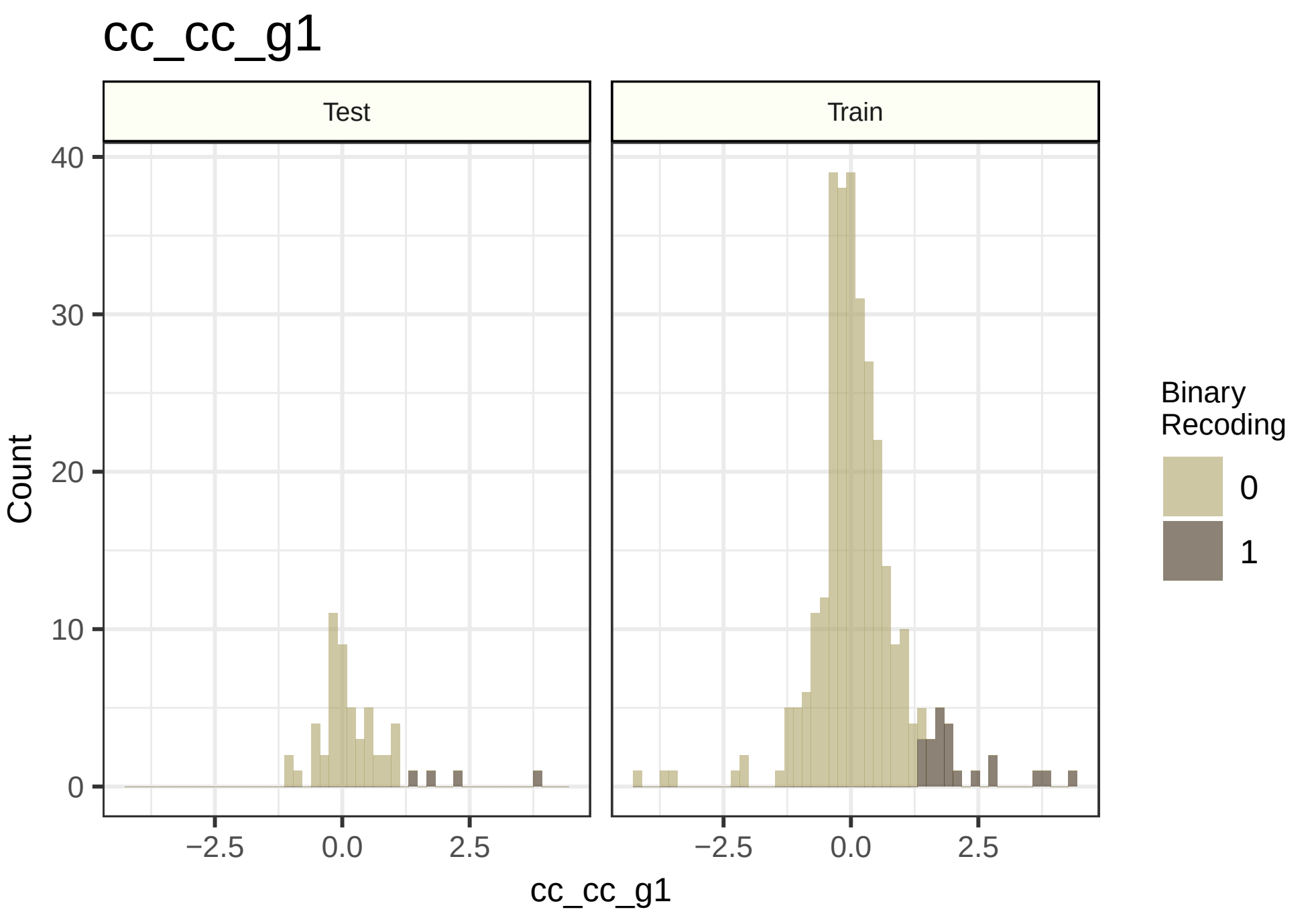

cc_all_n_objects
Test
Train
Count
20
15
10
5
0
−3
−2
−1
0
1
2
cc_all_n_objects
Binary Recoding
0
1

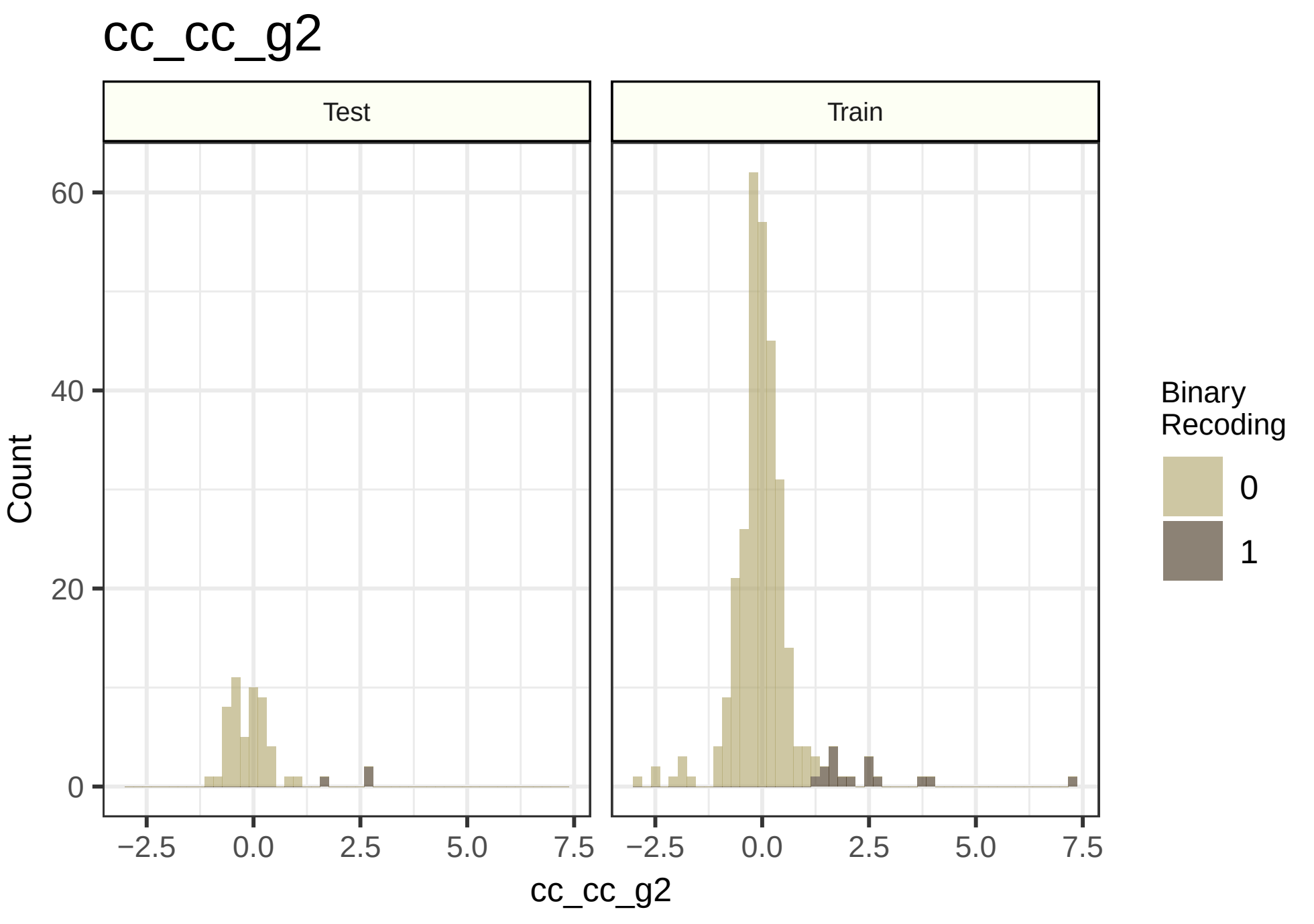

cc_all_n_spots_h2ax_mean
Test
Train
Count
20
10
0
−2
0
2
cc_all_n_spots_h2ax_mean
Binary Recoding
0
1

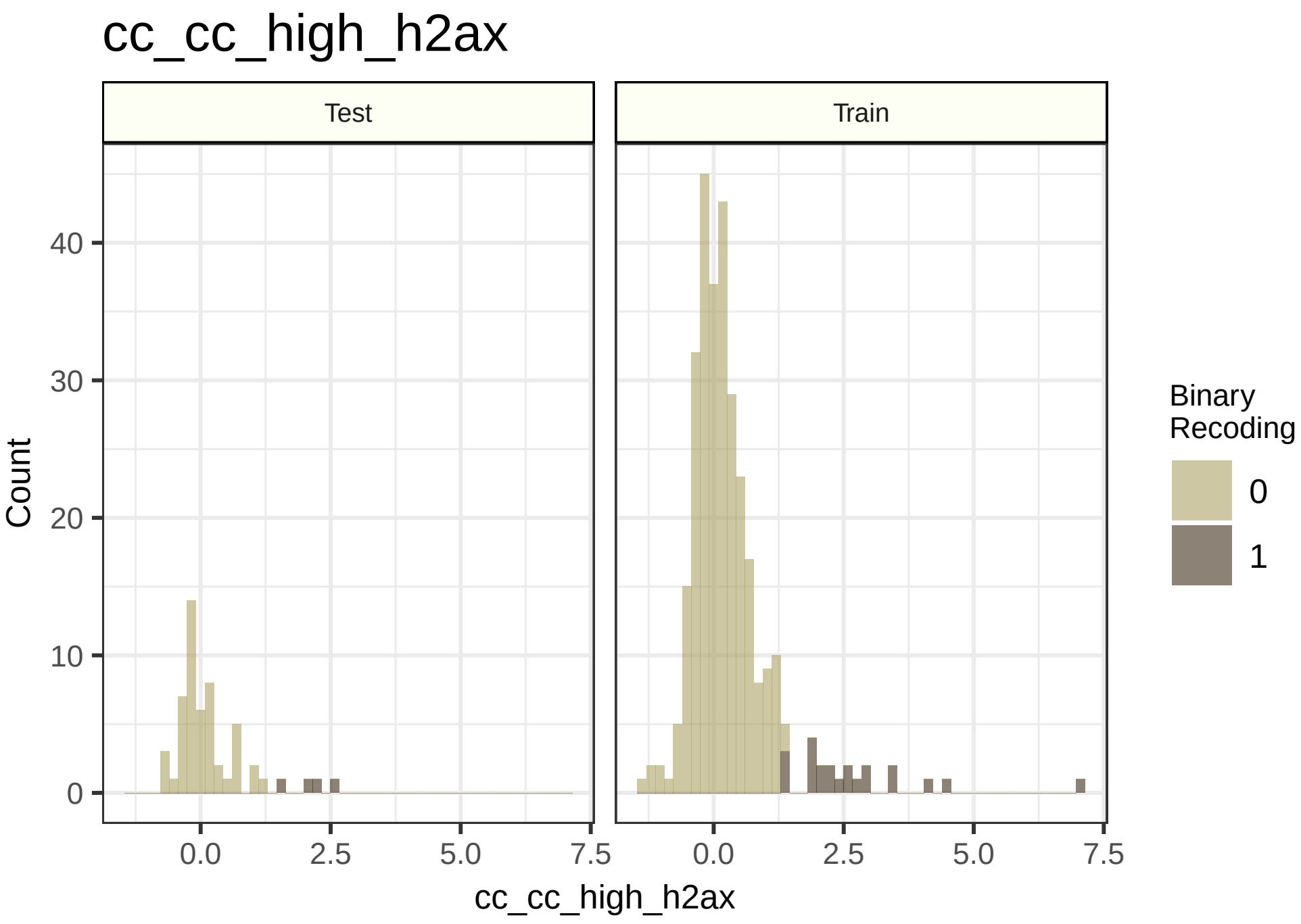

cc_all_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_all_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

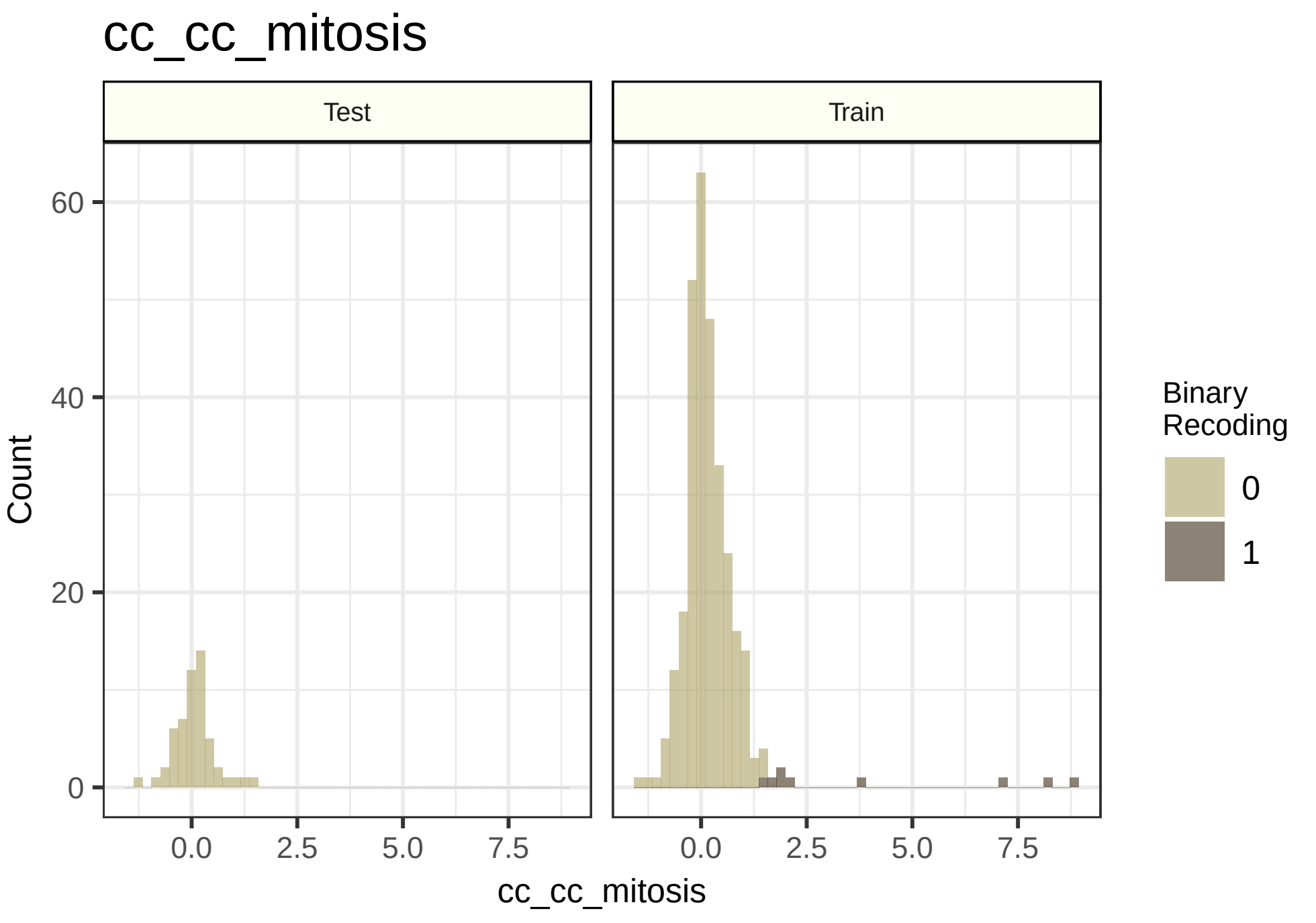

cc_all_nucleus_area_mean
Test
Train
Count
40
20
0
−2
0
2
4
6
cc_all_nucleus_area_mean
Binary Recoding
0
1

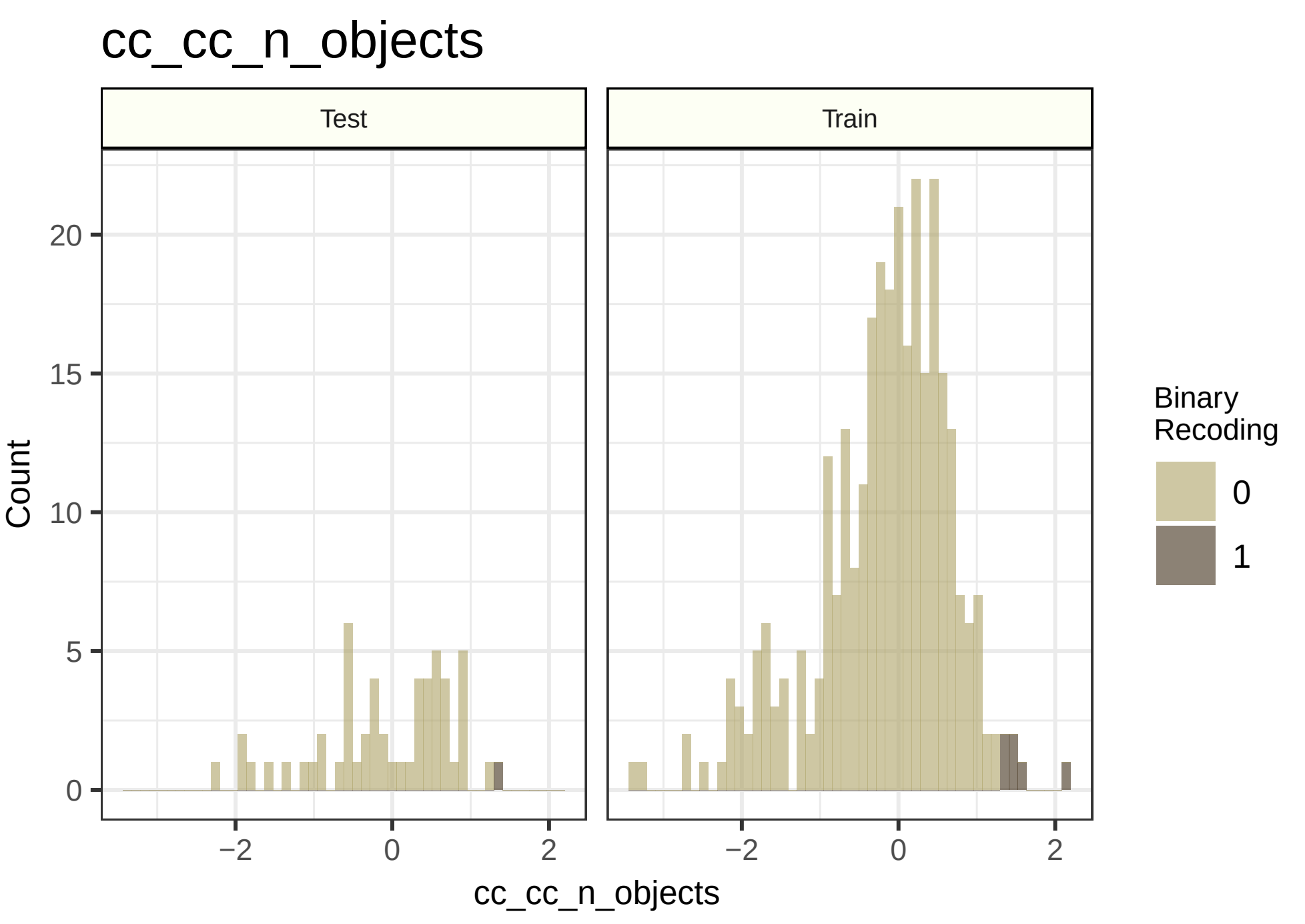

cc_cc_early_mitosis
Test
Train
30
20
10
0
Count
0
2
4
cc_cc_early_mitosis
Binary Recoding
0
1

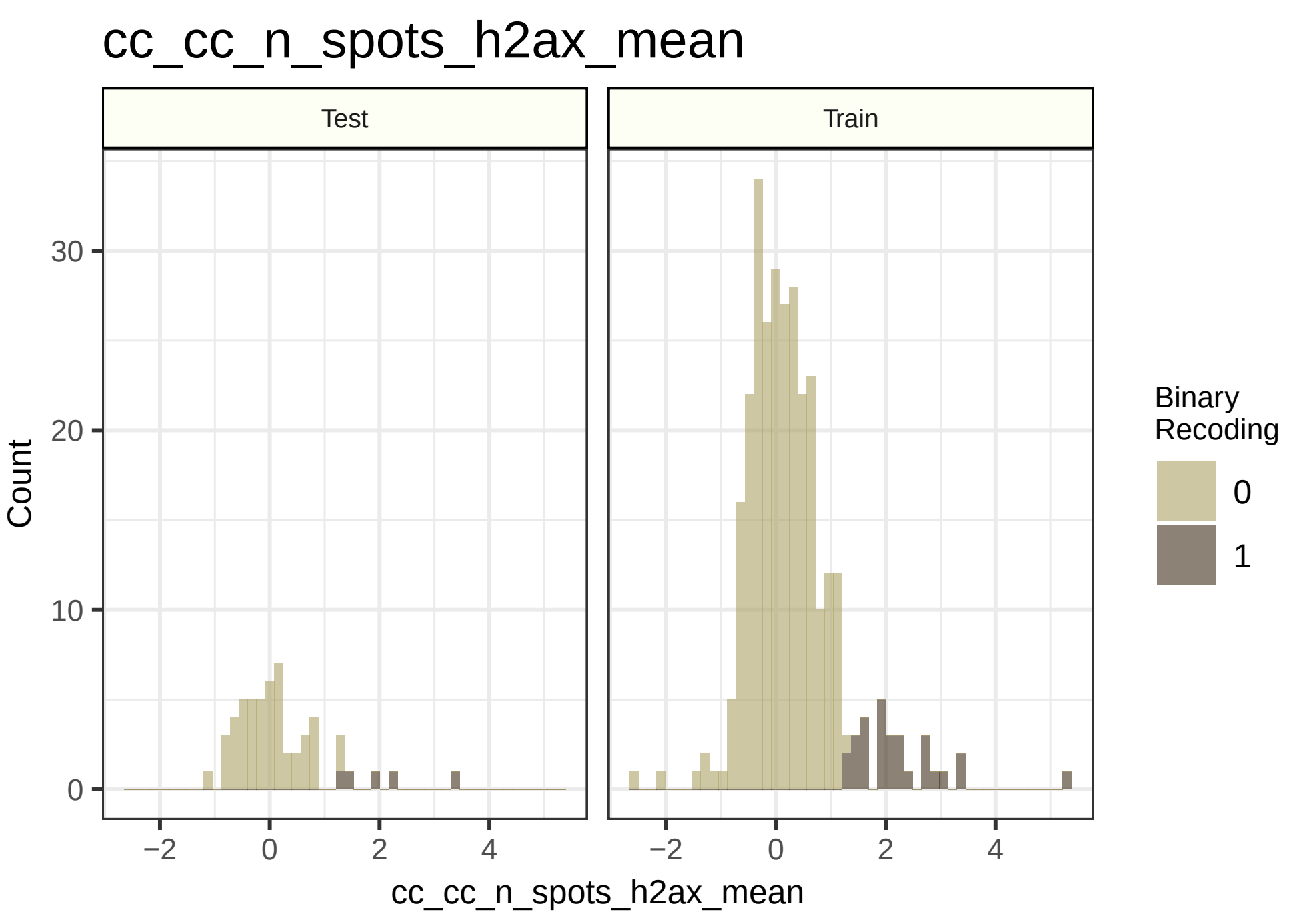

cc_cc_g1
Test
Train
40
30
20
10
0
Count
−2.5
0.0
2.5
cc_cc_g1
Binary Recoding
0
1

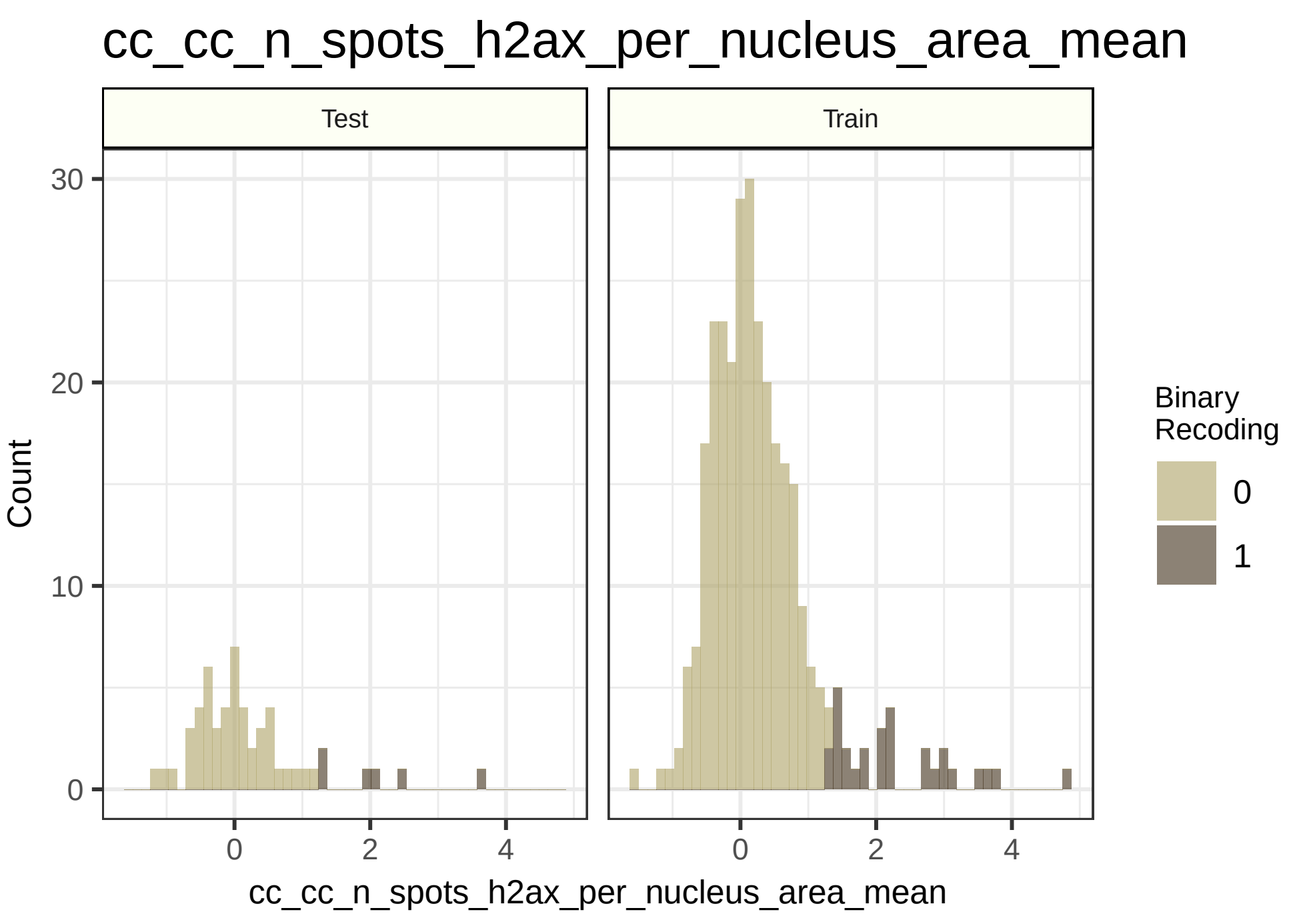

cc_cc_g2
Test
Train
60
40
20
0
Count
−2.5
0.0
2.5
5.0
7.5
cc_cc_g2
Binary Recoding
0
1

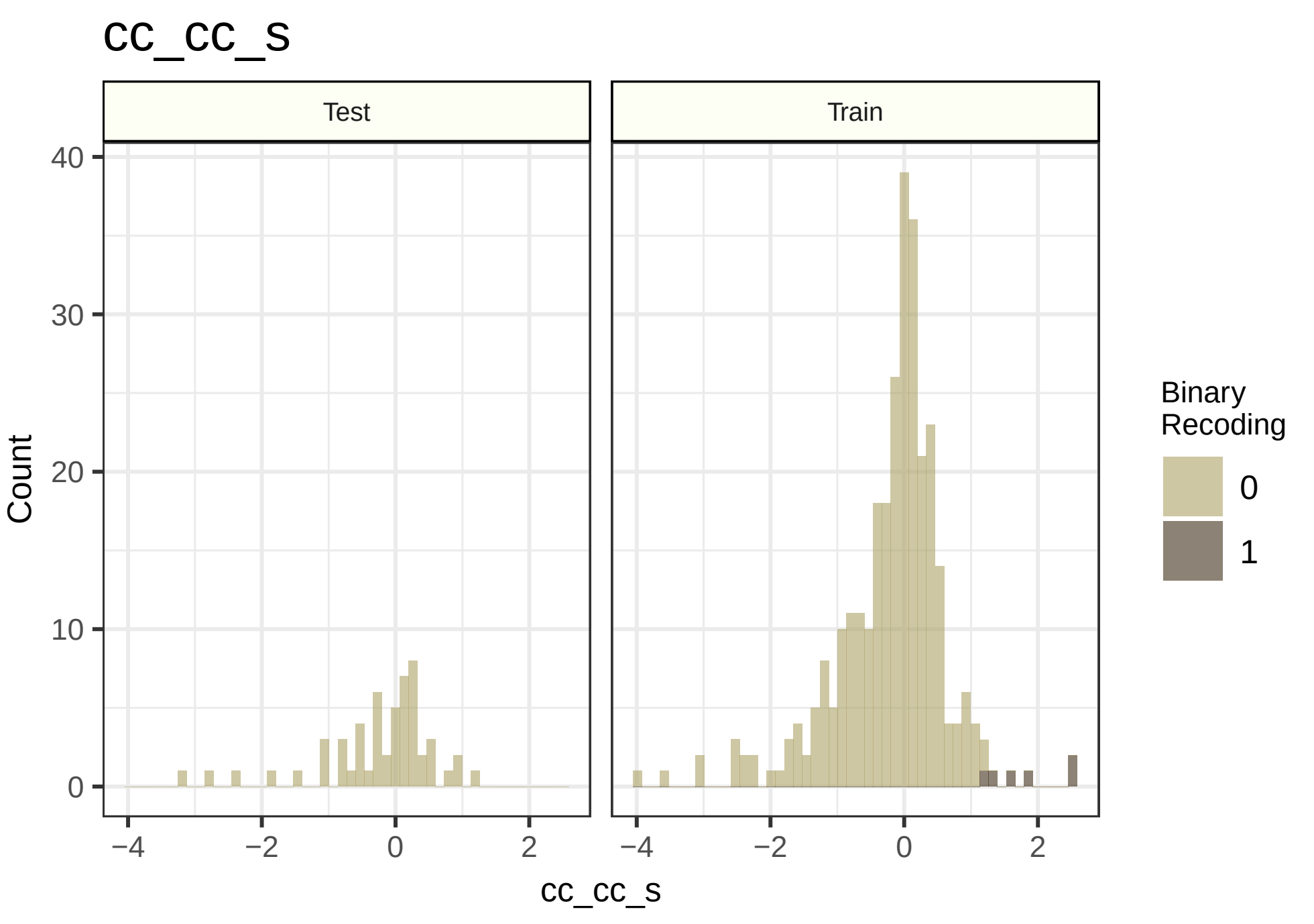

cc_cc_high_h2ax
Test
Train
Count
40
30
20
10
0
0.0
2.5
5.0
7.5
cc_cc_high_h2ax
Binary Recoding
0
1

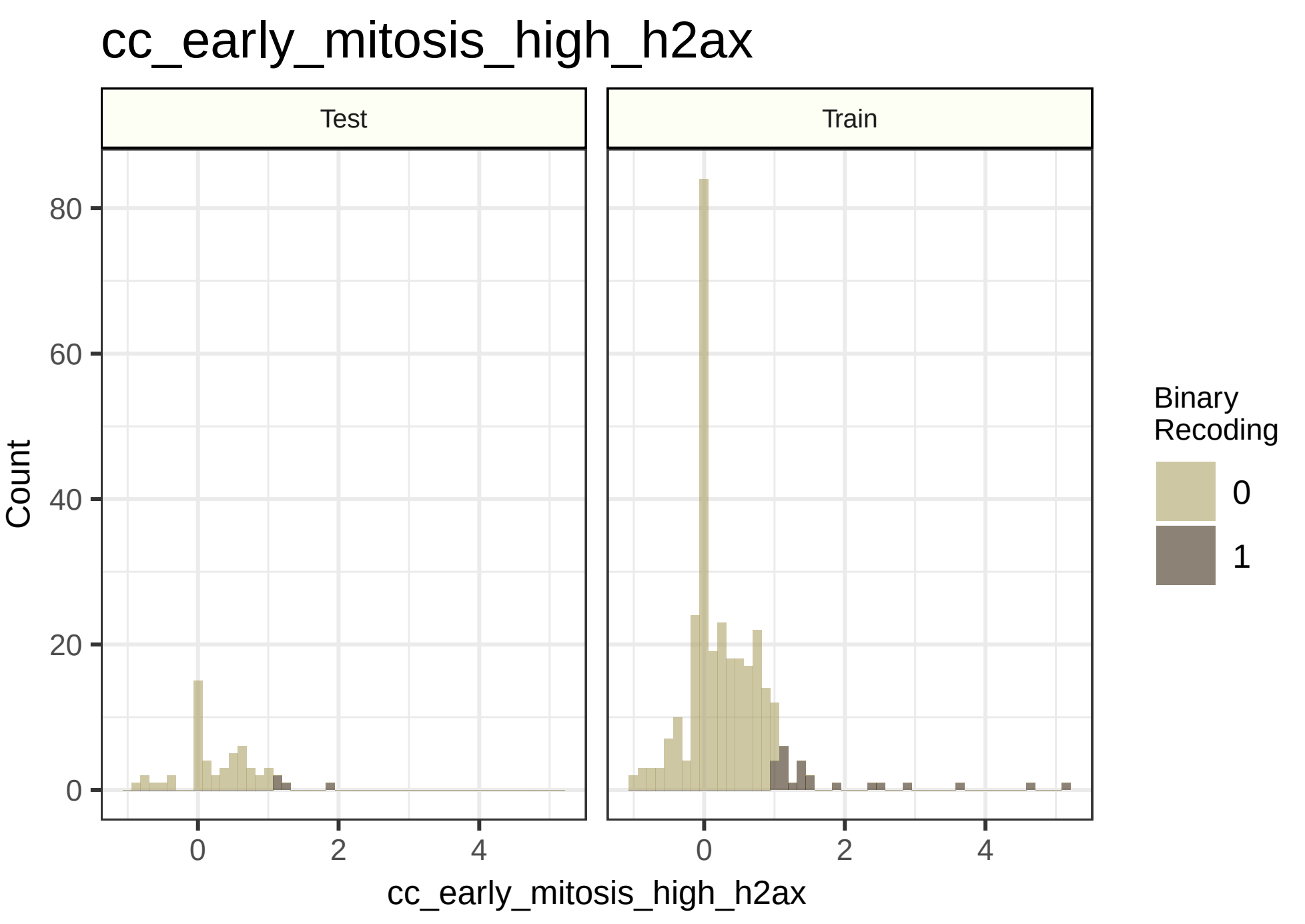

cc_cc_mitosis
Test
Train
60
40
20
0
Count
0.0
2.5
5.0
7.5
cc_cc_mitosis
Binary Recoding
0
1

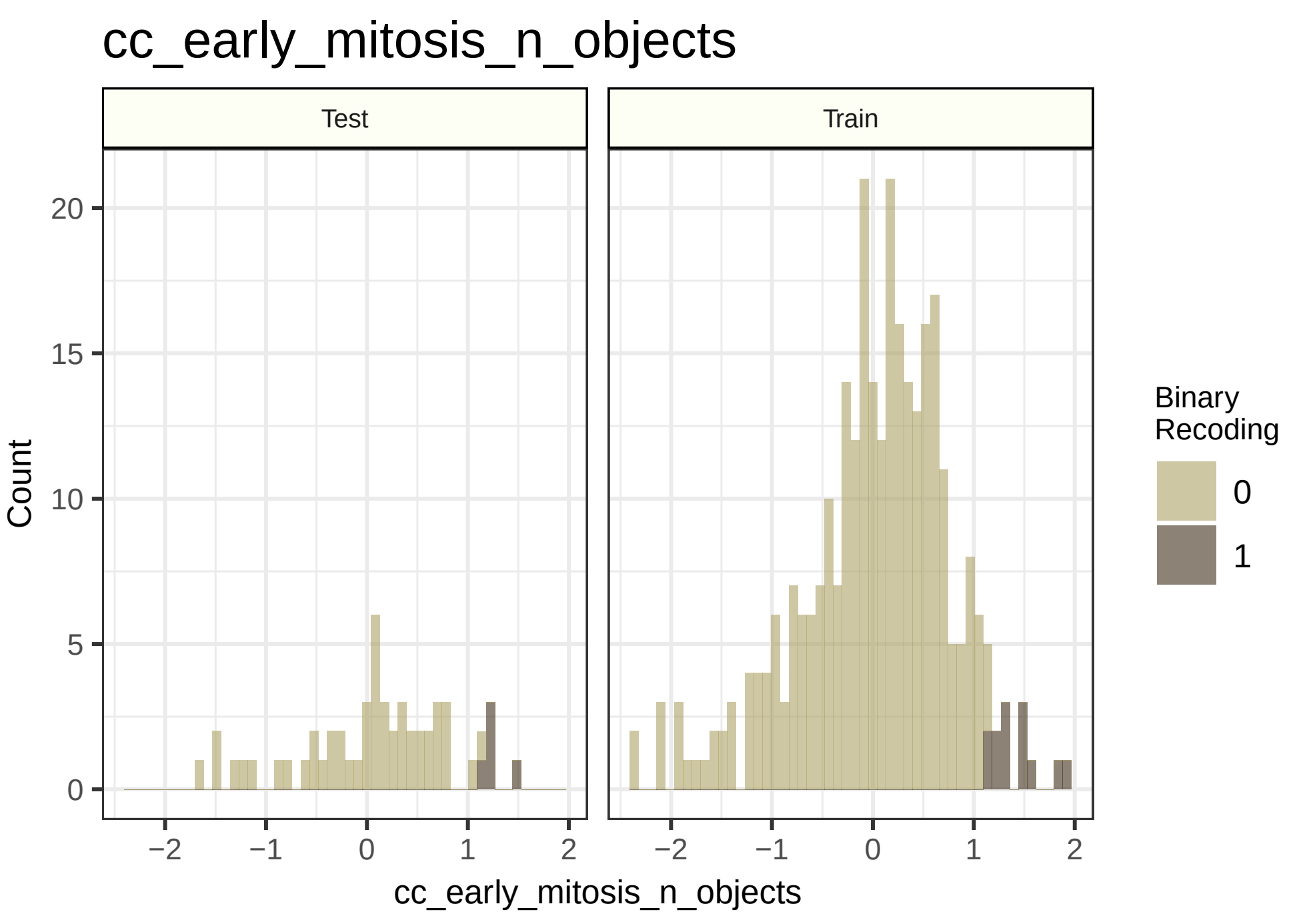

cc_cc_n_objects
Test
Train
20
15
10
5
0
Count
−2
0
2
cc_cc_n_objects
Binary Recoding
0
1

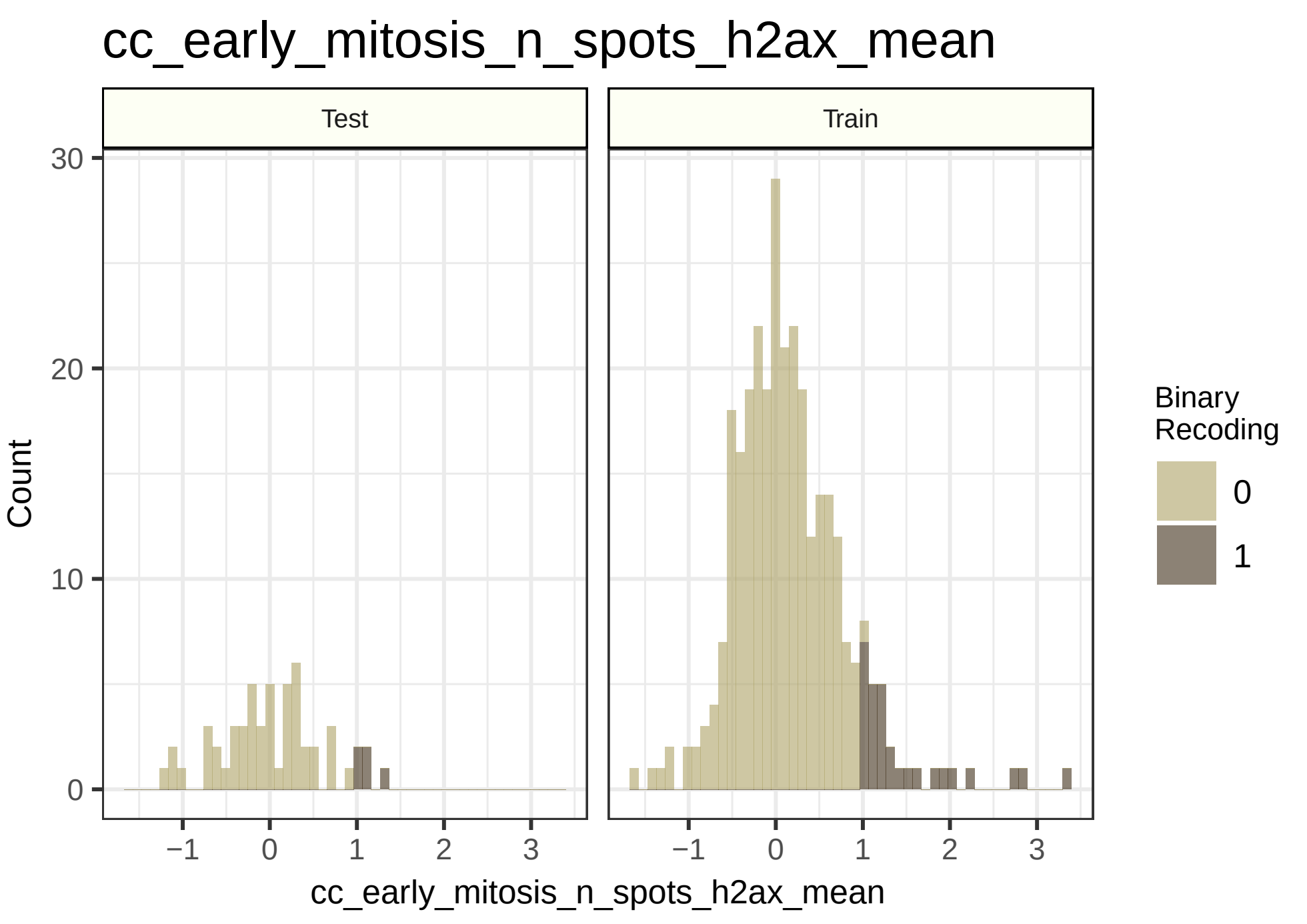

cc_cc_n_spots_h2ax_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_cc_n_spots_h2ax_mean
Binary Recoding
0
1

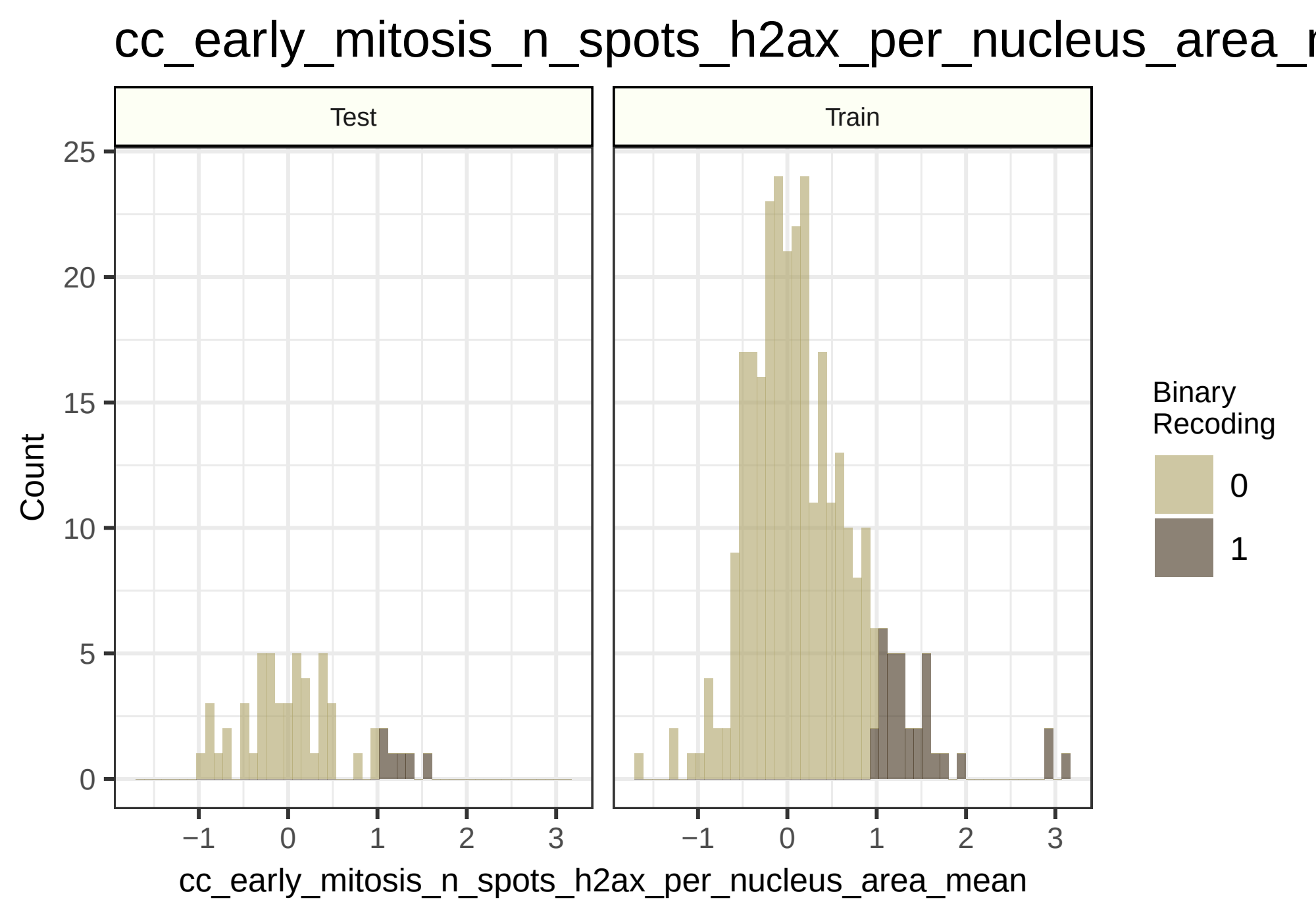

cc_cc_n_spots_h2ax_per_nucleus_area_mean
Test
Train
30
20
10
0
Count
0
2
4
0
2
4
cc_cc_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

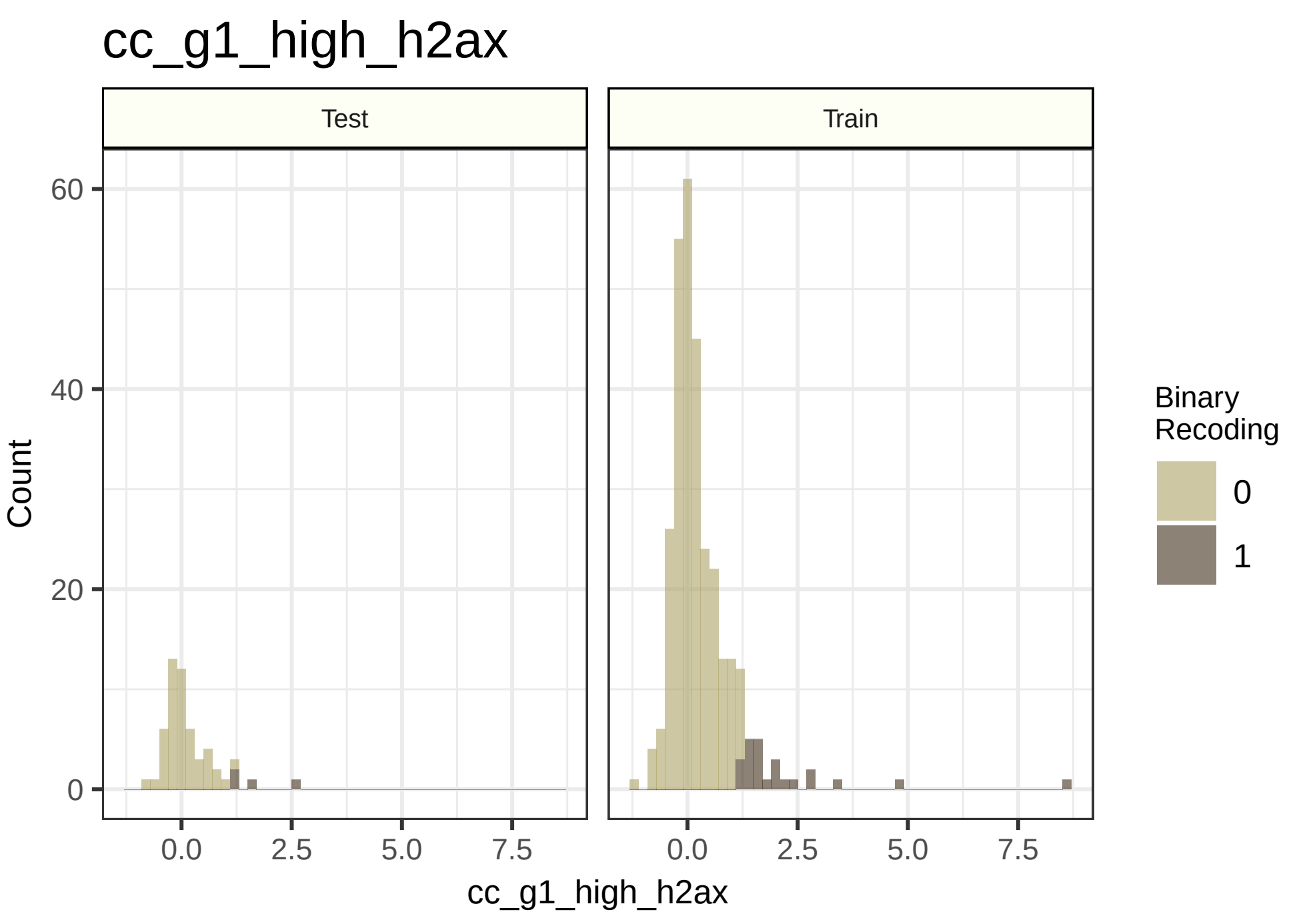

cc_cc_s
Test
Train
40
30
20
10
0
Count
−4
−2
0
2
cc_cc_s
Binary
Recoding
0
1

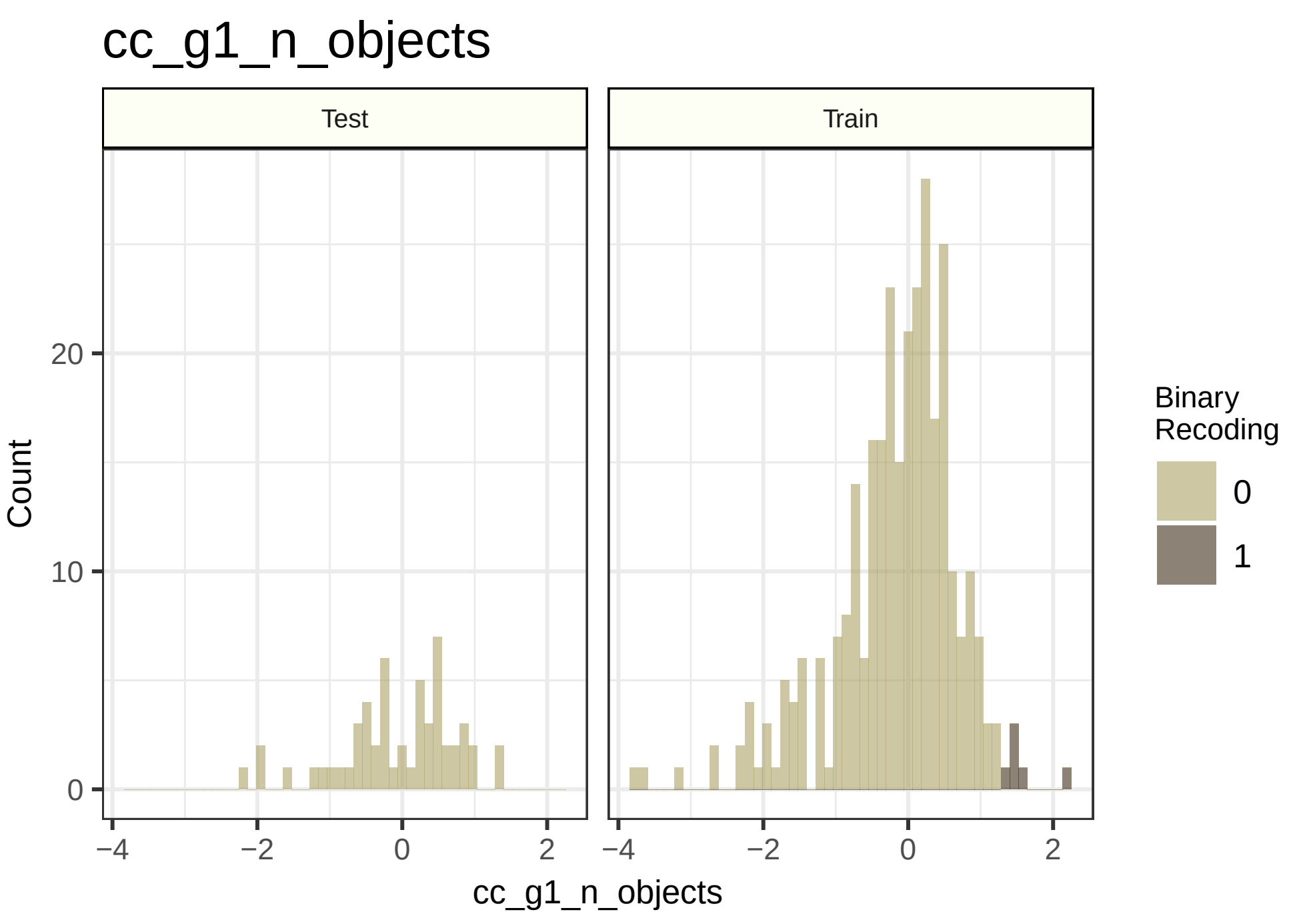

cc_early_mitosis_high_h2ax
Test
Train
Count
80
60
40
20
0
0
2
4
0
2
4
cc_early_mitosis_high_h2ax
Binary Recoding
0
1

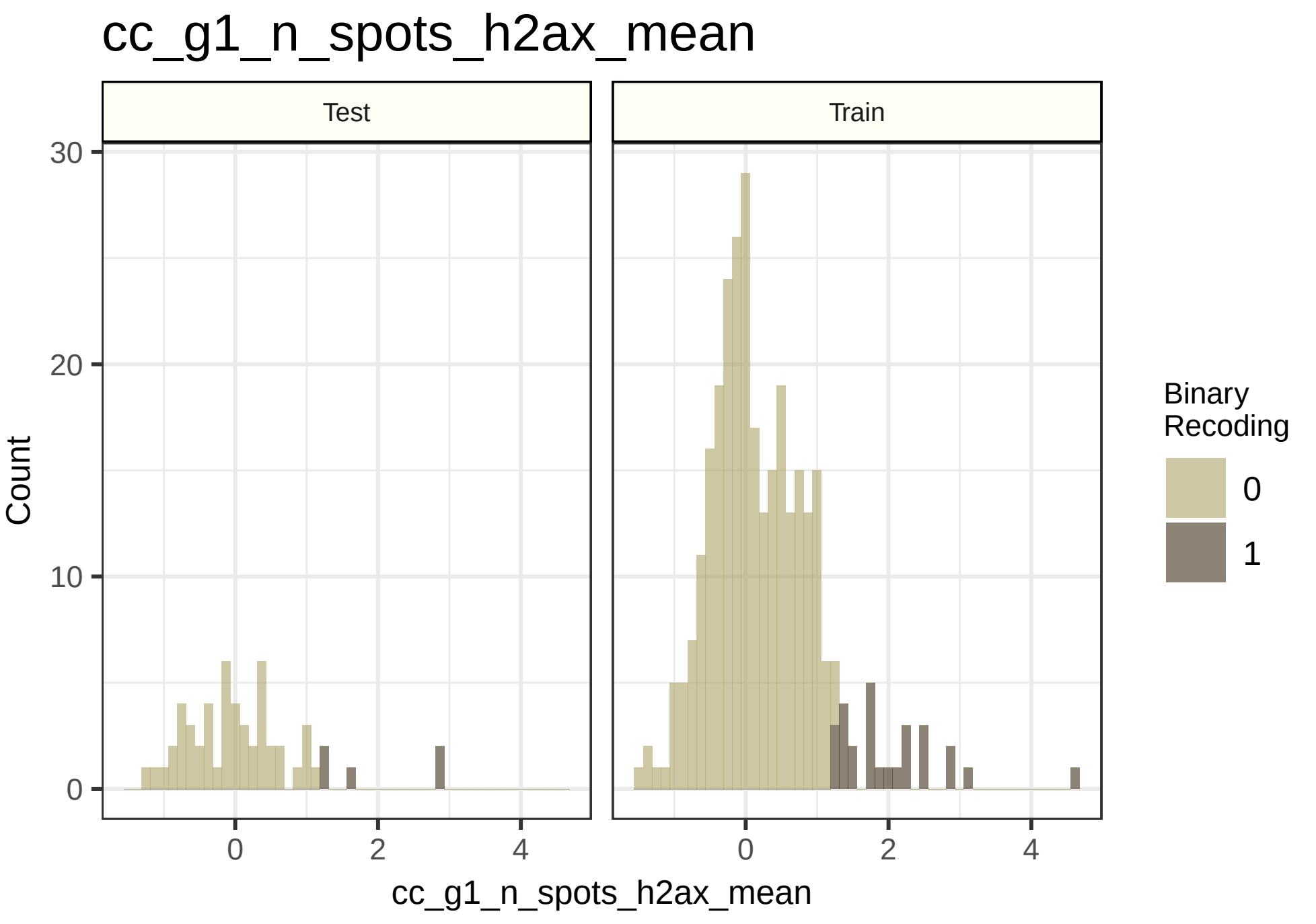

cc_early_mitosis_n_objects
Test
Train
Count
20
15
10
5
0
−2
−1
0
1
2
cc_early_mitosis_n_objects
Binary Recoding
0
1

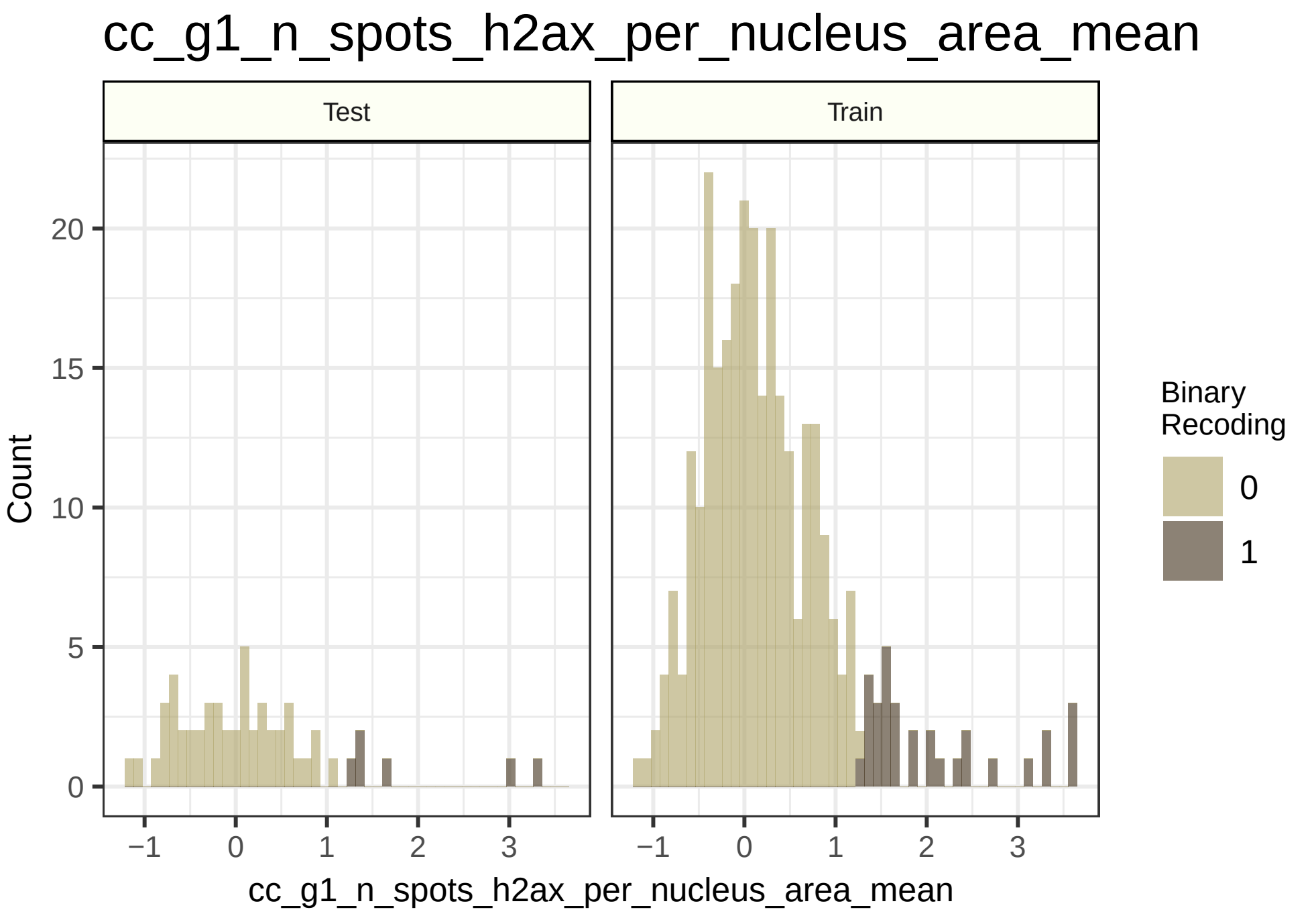

cc_early_mitosis_n_spots_h2ax_mean
Test
Train
30
20
10
0
Count
−1
0
1
2
3
cc_early_mitosis_n_spots_h2ax_mean
Binary Recoding
0
1

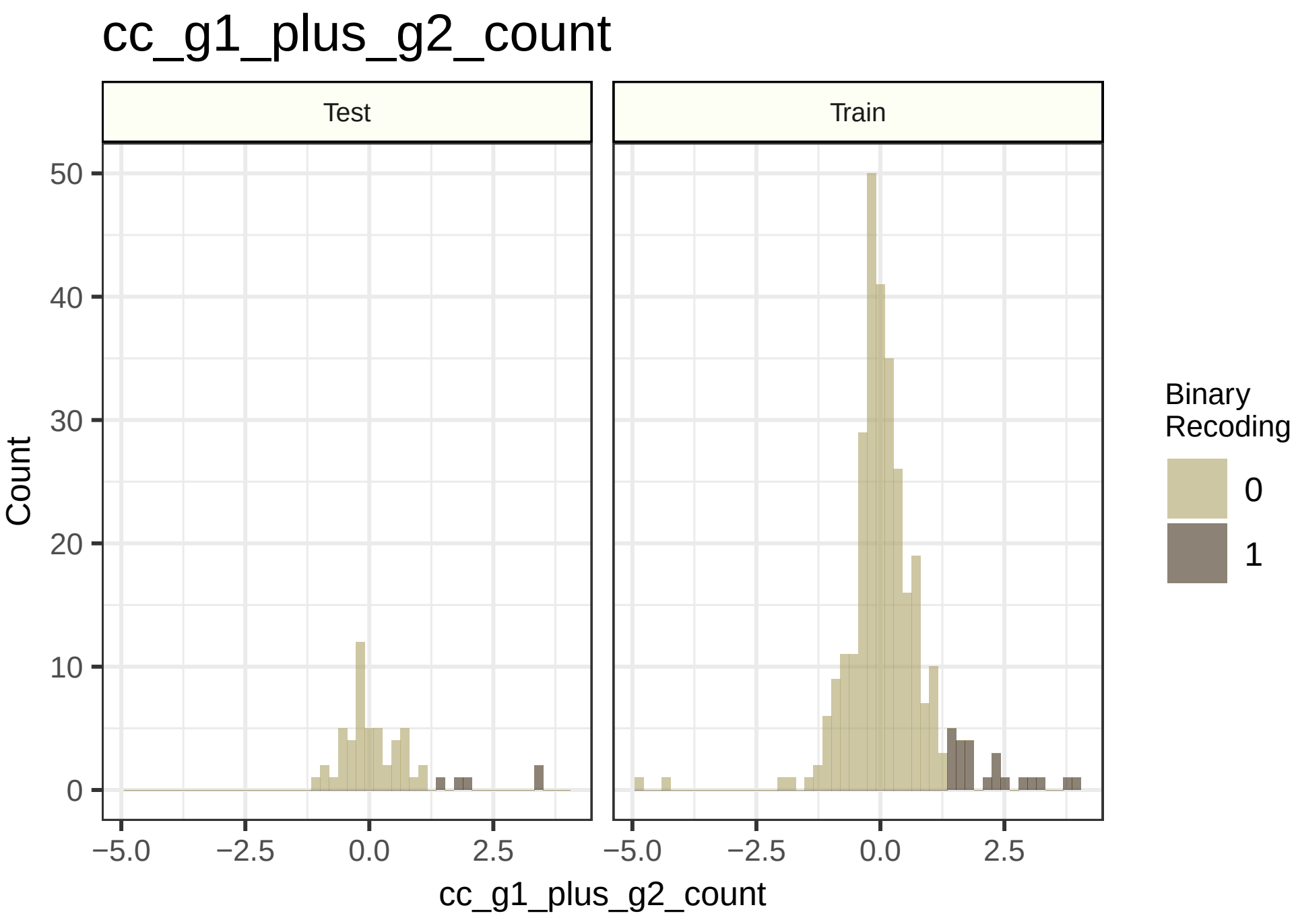

cc_early_mitosis_n_spots_h2ax_per_nucleus_area_
Test
Train
Count
25
20
15
10
5
0
−1
0
1
2
3
cc_early_mitosis_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

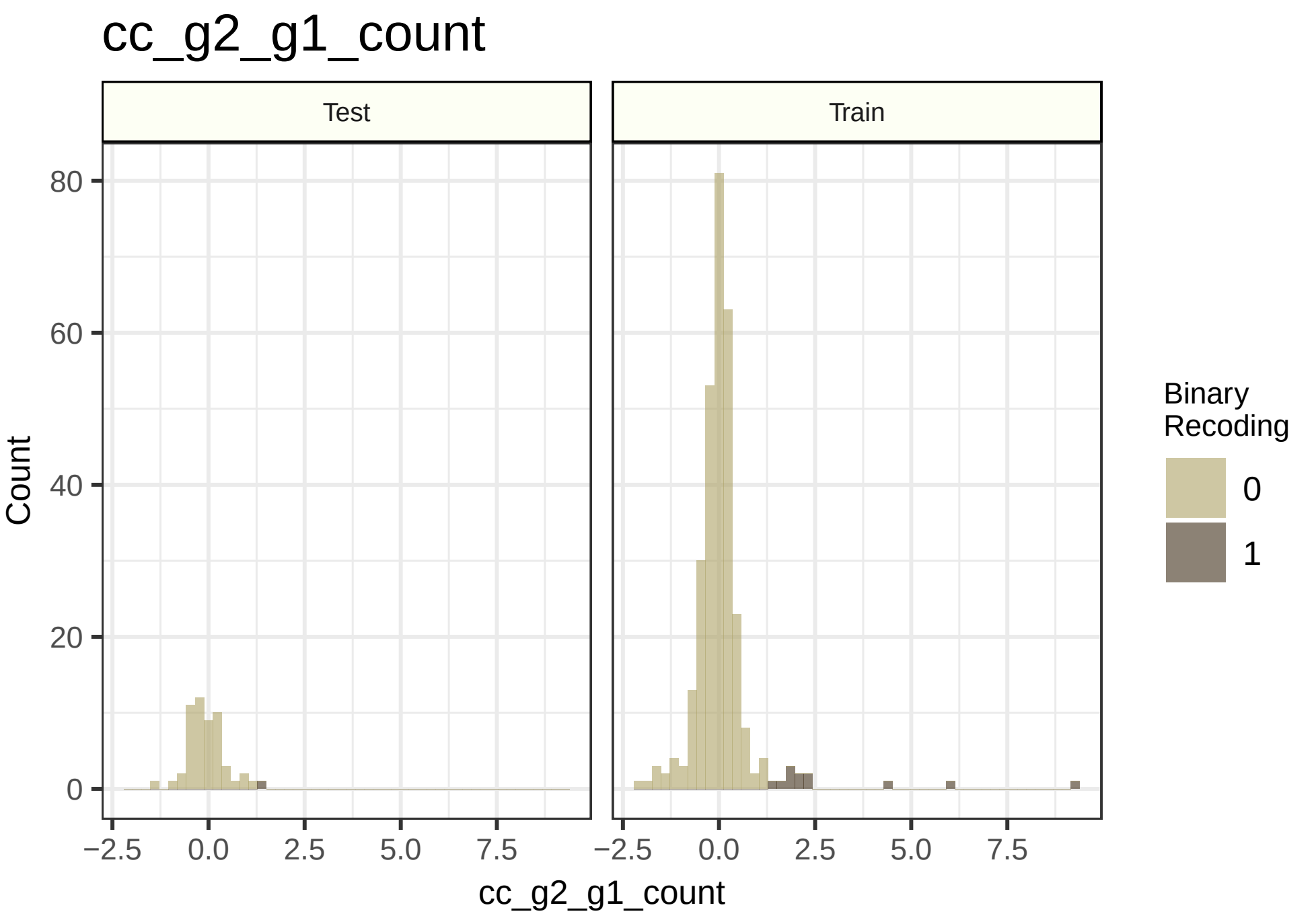

cc_g1_high_h2ax
Test
Train
60
40
20
0
Count
0.0
2.5
5.0
7.5
cc_g1_high_h2ax
Binary Recoding
0
1

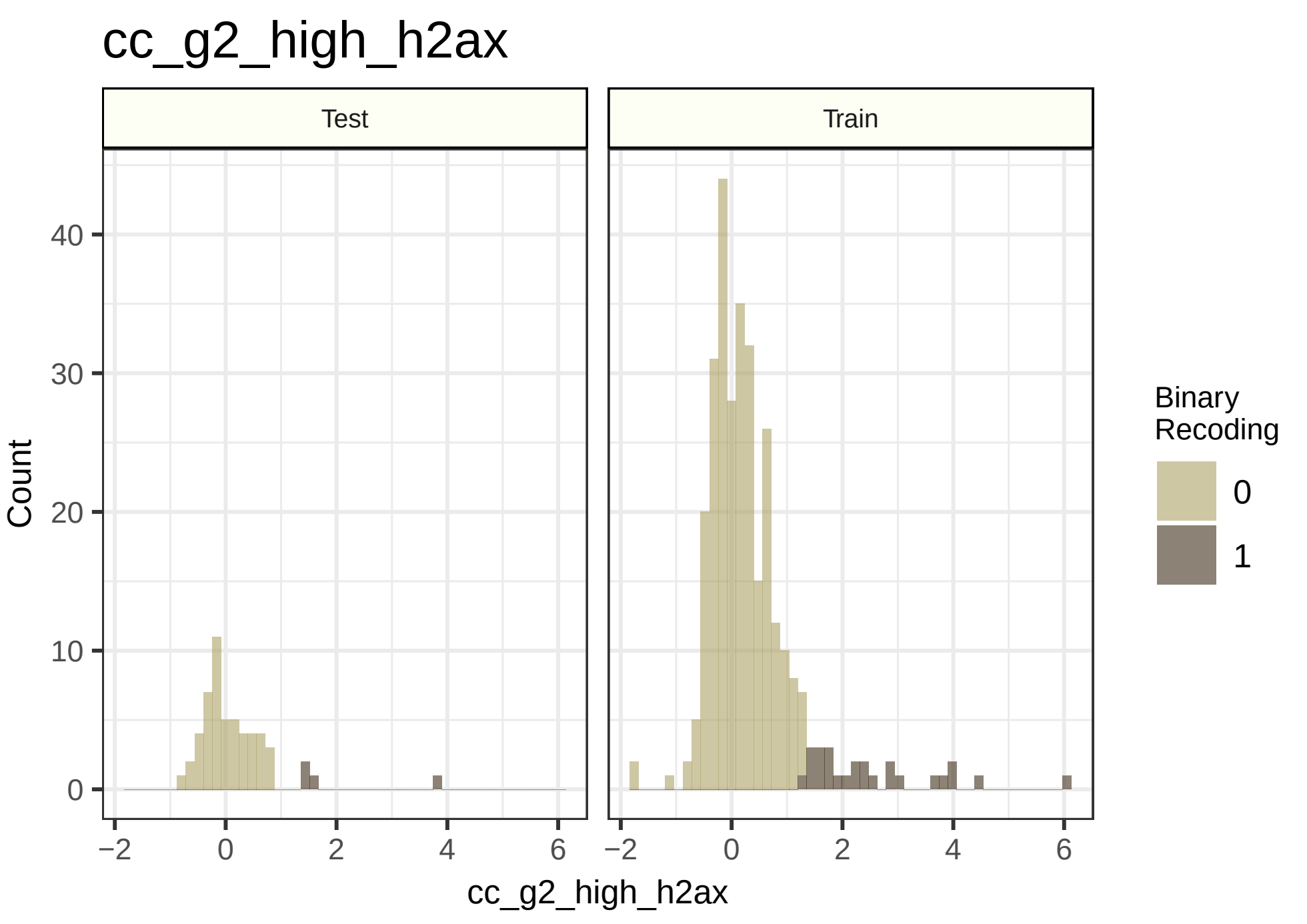

cc_g1_n_objects
Test
Train
Count
20
10
0
−4
−2
0
2
cc_g1_n_objects
Binary Recoding
0
1

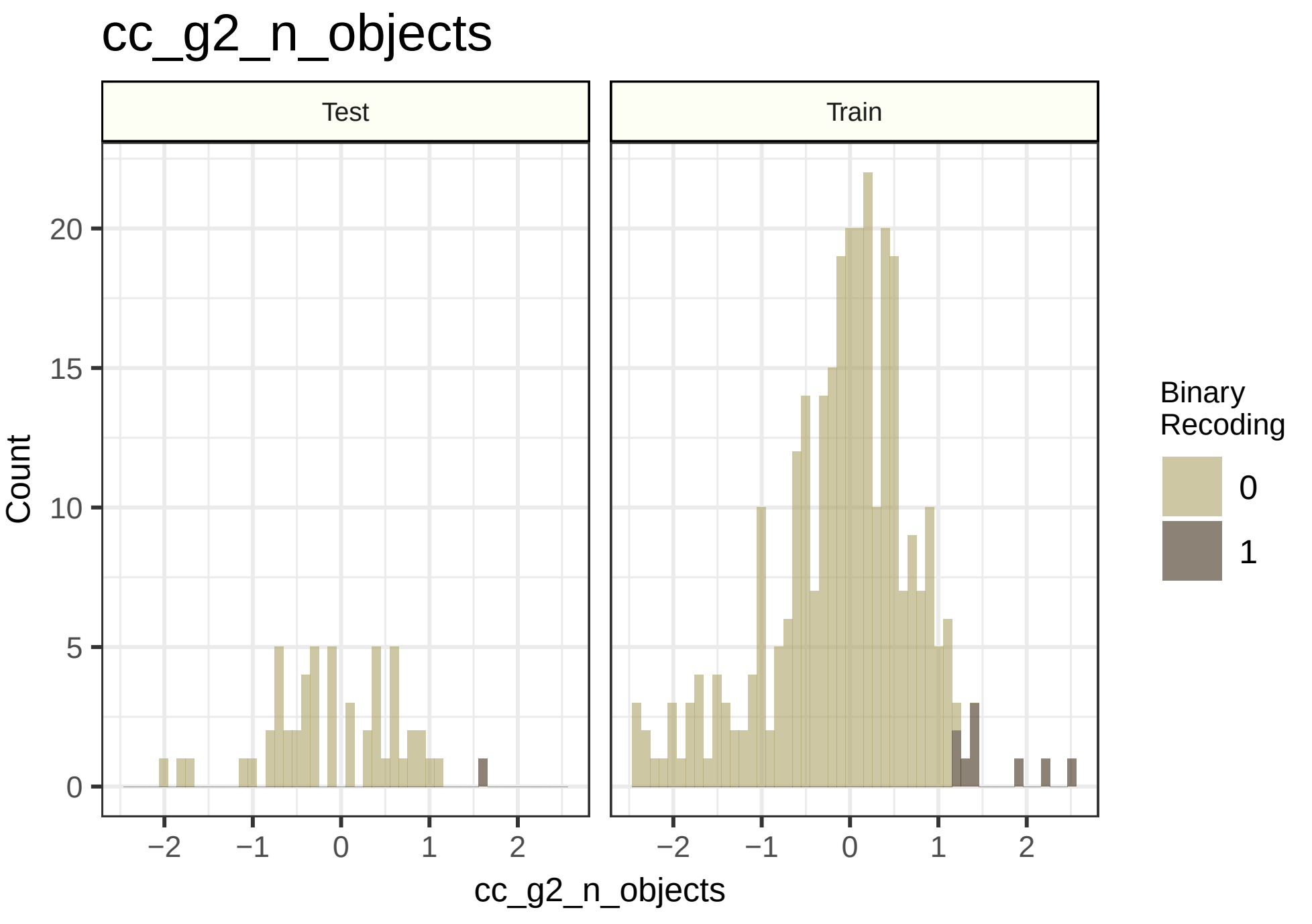

cc_g1_n_spots_h2ax_mean
Test
Train
30
20
10
0
Count
0
2
4
0
2
4
cc_g1_n_spots_h2ax_mean
Binary Recoding
0
1

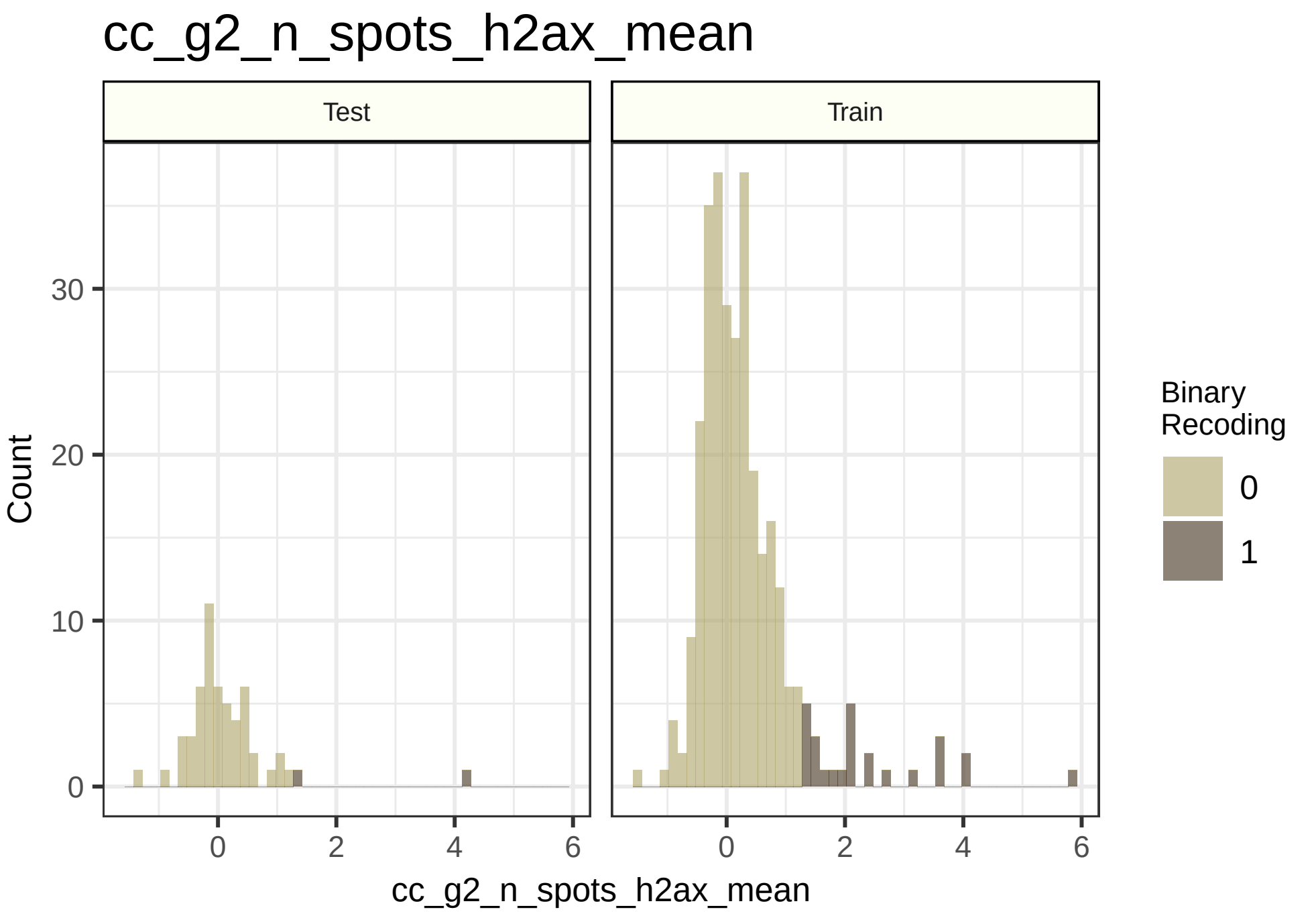

cc_g1_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
20
15
10
5
0
−1
0
1
2
3
cc_g1_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

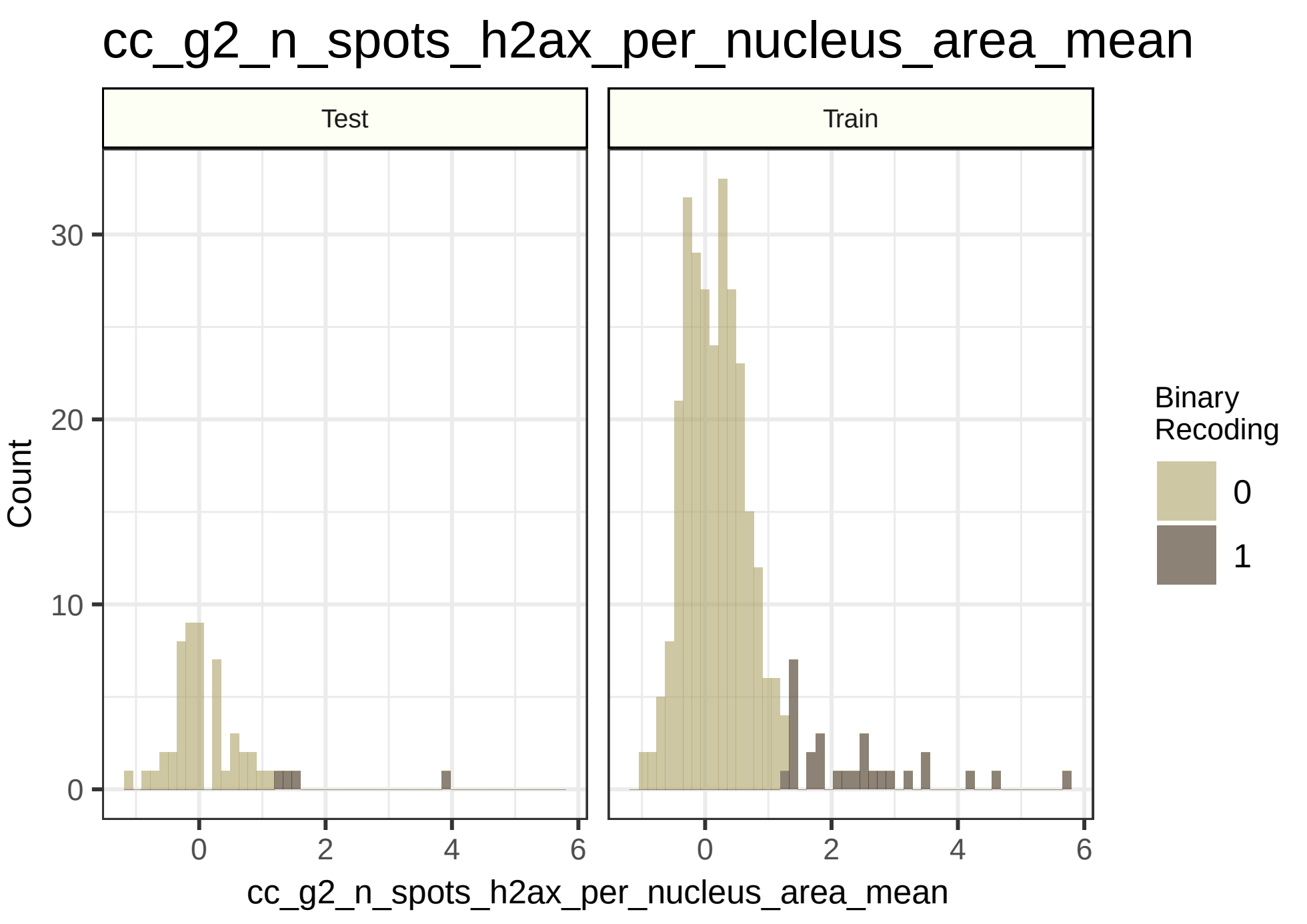

cc_g1_plus_g2_count
Test
Train
Count
50
40
30
20
10
0
−5.0
−2.5
0.0
2.5
cc_g1_plus_g2_count
Binary Recoding
0
1

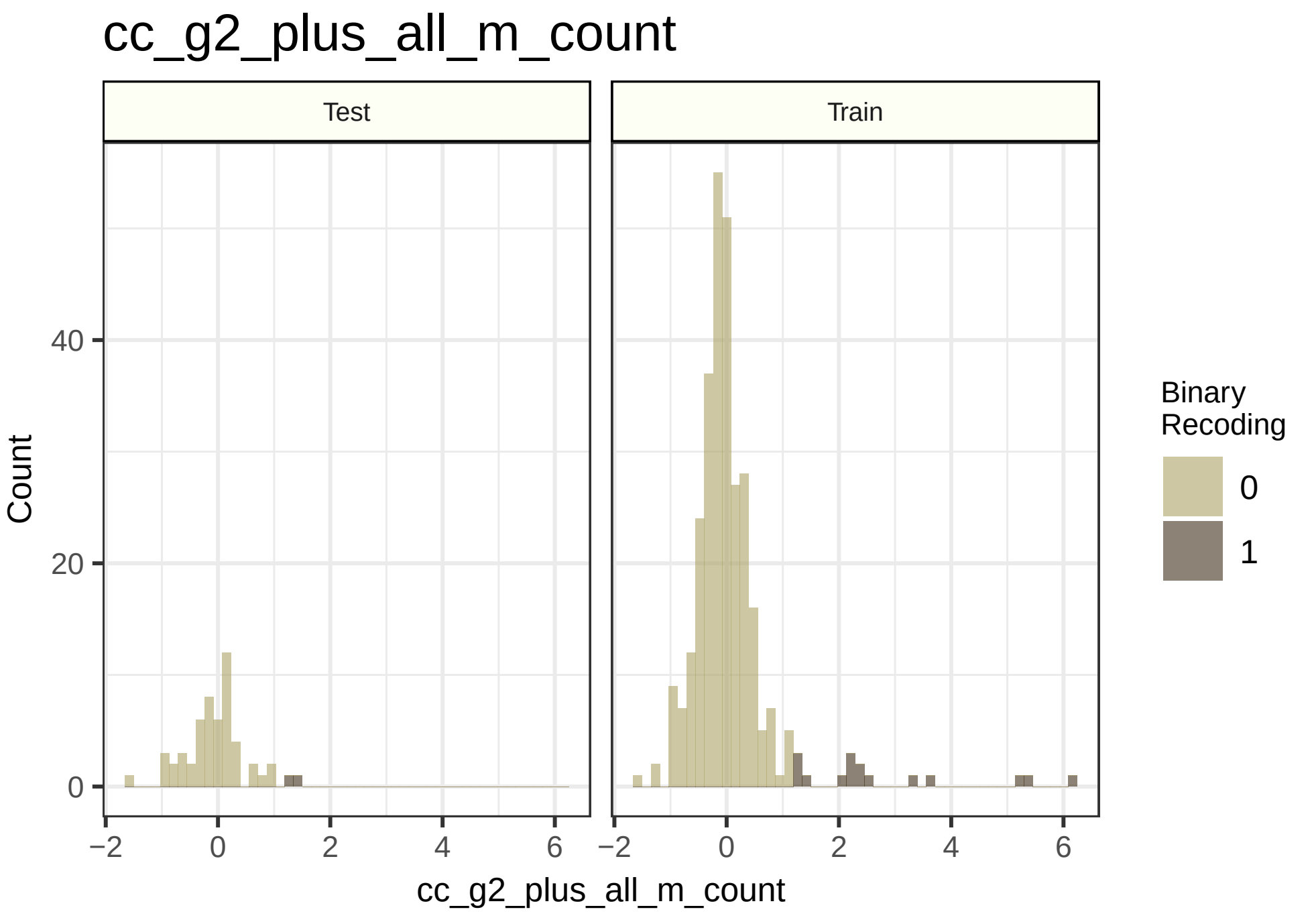

cc_g2_g1_count
Test
Train
Count
80
60
40
20
0
−2.5
0.0
2.5
5.0
7.5
cc_g2_g1_count
Binary Recoding
0
1

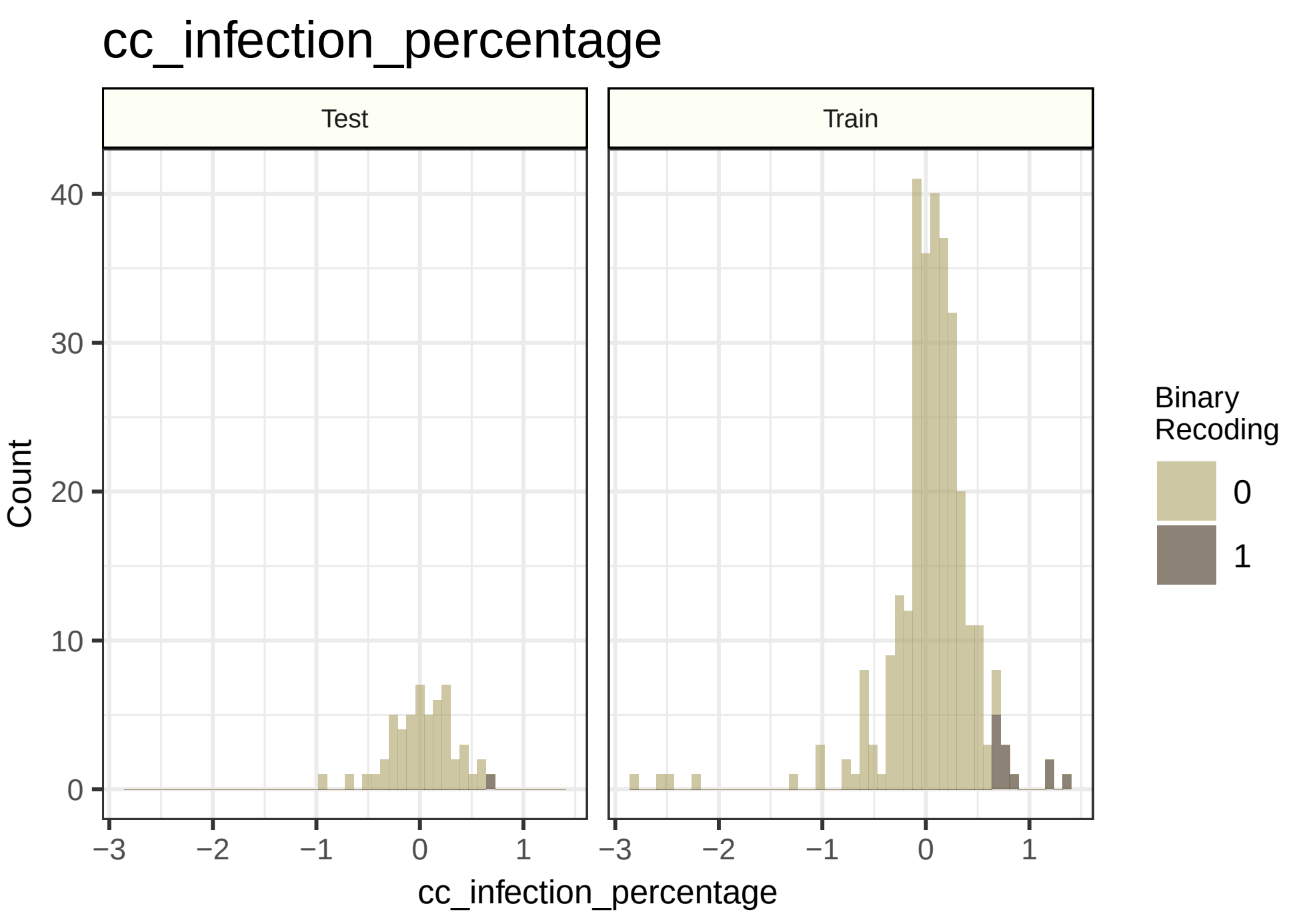

cc_g2_high_h2ax
Test
Train
Count
40
30
20
10
0
−2
0
2
4
6
cc_g2_high_h2ax
Binary Recoding
0
1

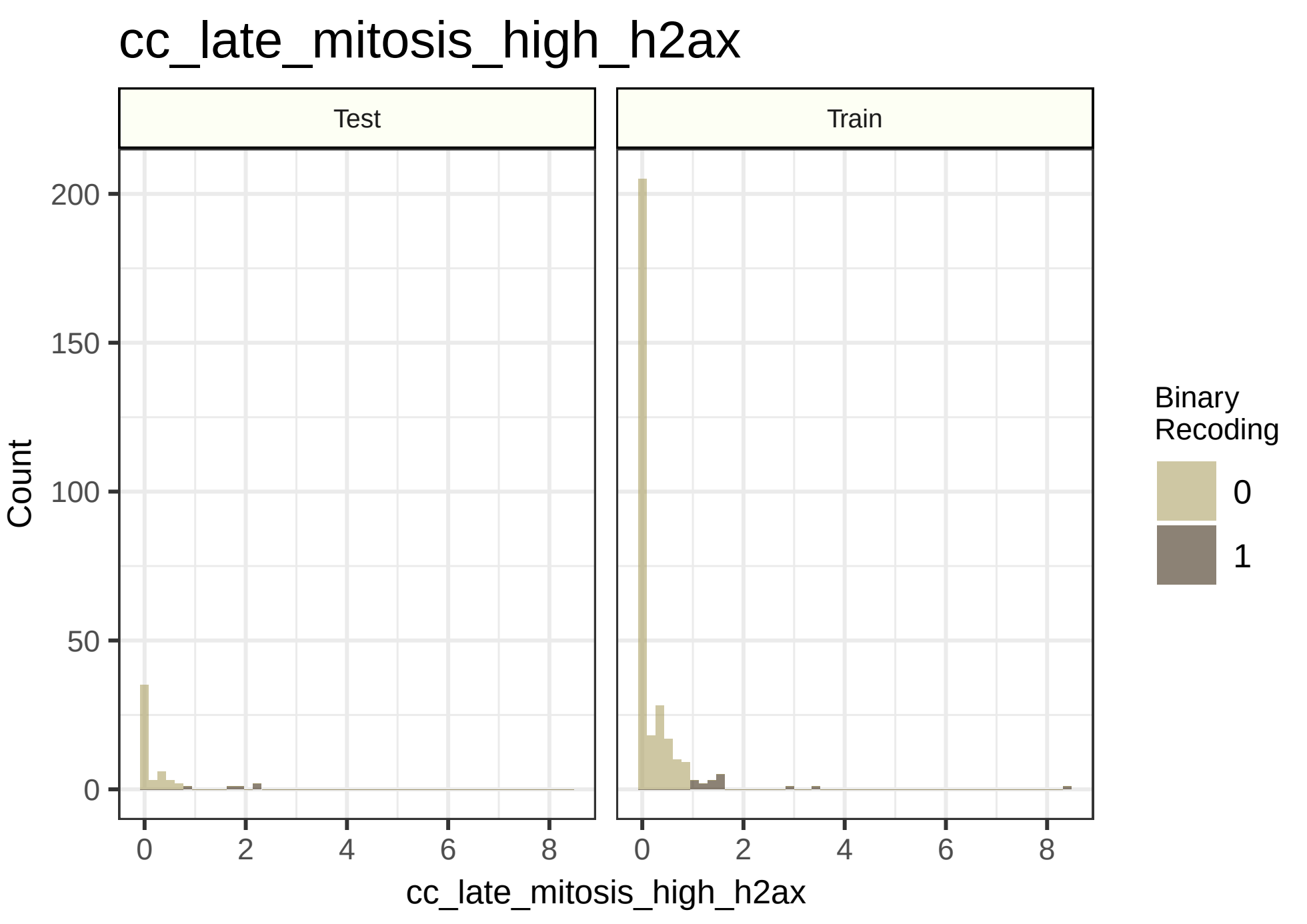

cc_g2_n_objects
Test
Train
Count
20
15
10
5
0
−2
−1
0
1
2
cc_g2_n_objects
Binary Recoding
0
1

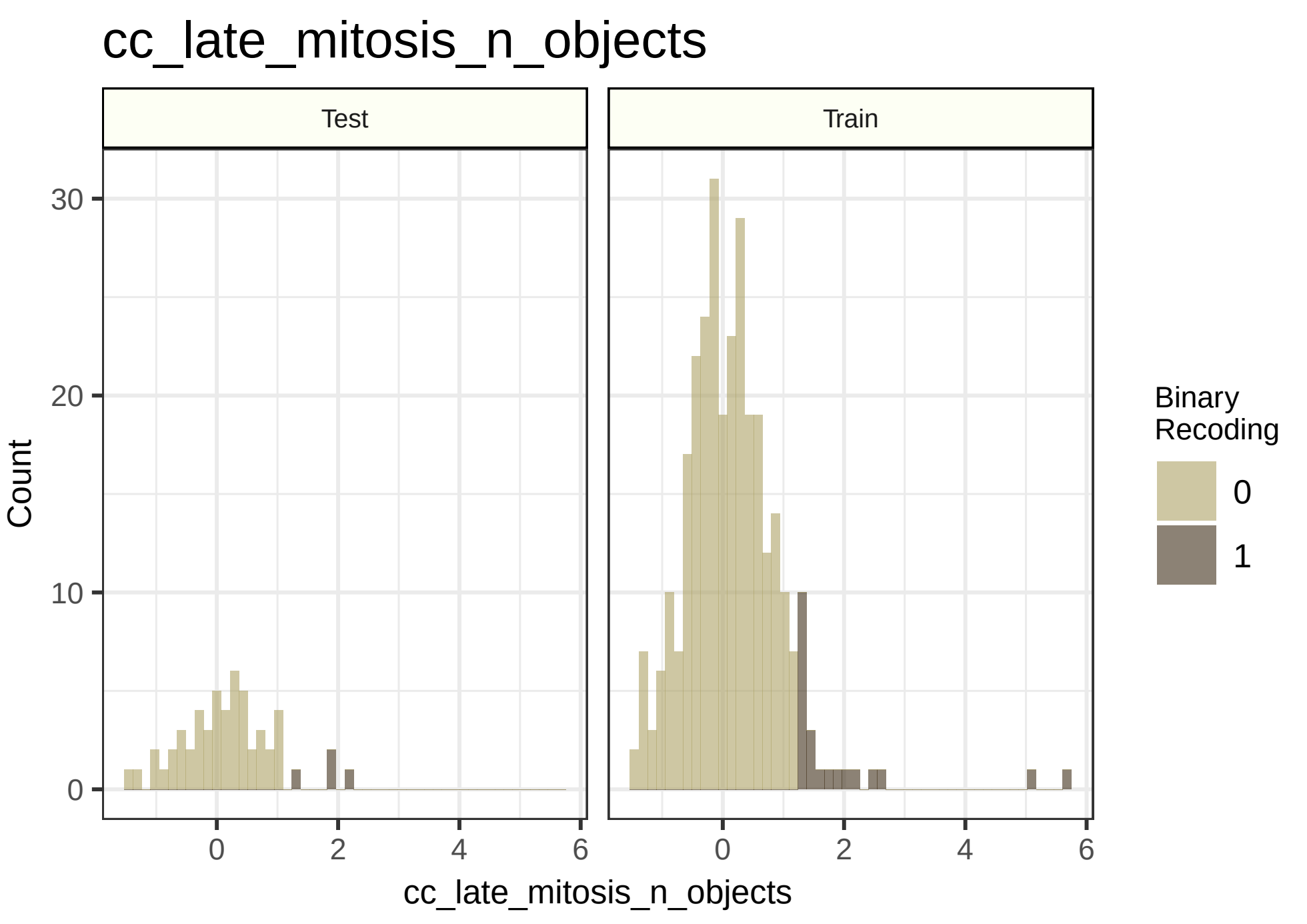

cc_g2_n_spots_h2ax_mean
Test
Train
Count
30
20
10
0
0
2
4
6
0
2
4
6
cc_g2_n_spots_h2ax_mean
Binary Recoding
0
1

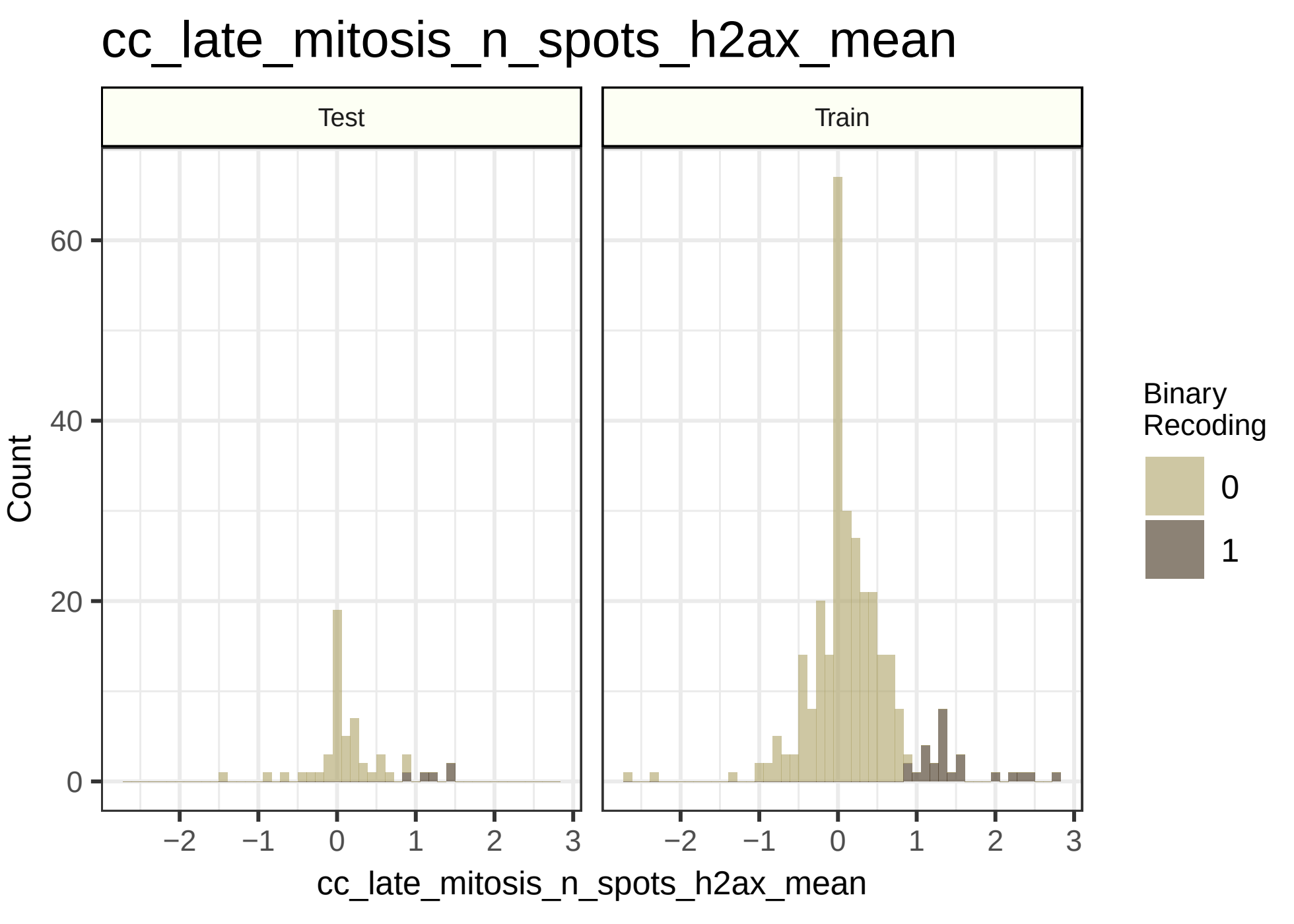

cc_g2_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
30
20
10
0
0
2
4
6
0
2
4
6
cc_g2_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

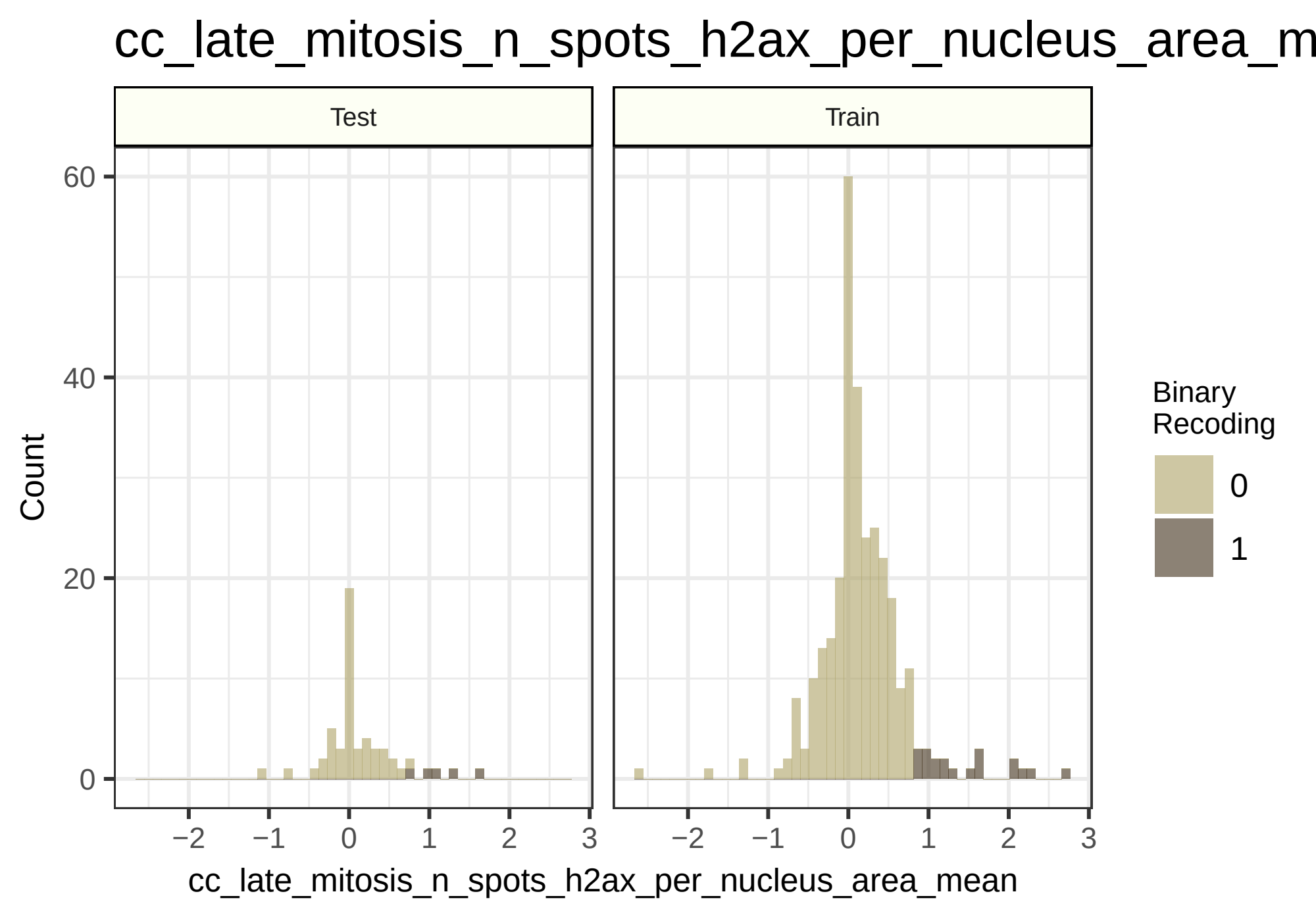

cc_g2_plus_all_m_count
Test
Train
Count
40
20
0
−2
0
2
4
6
cc_g2_plus_all_m_count
Binary Recoding
0
1

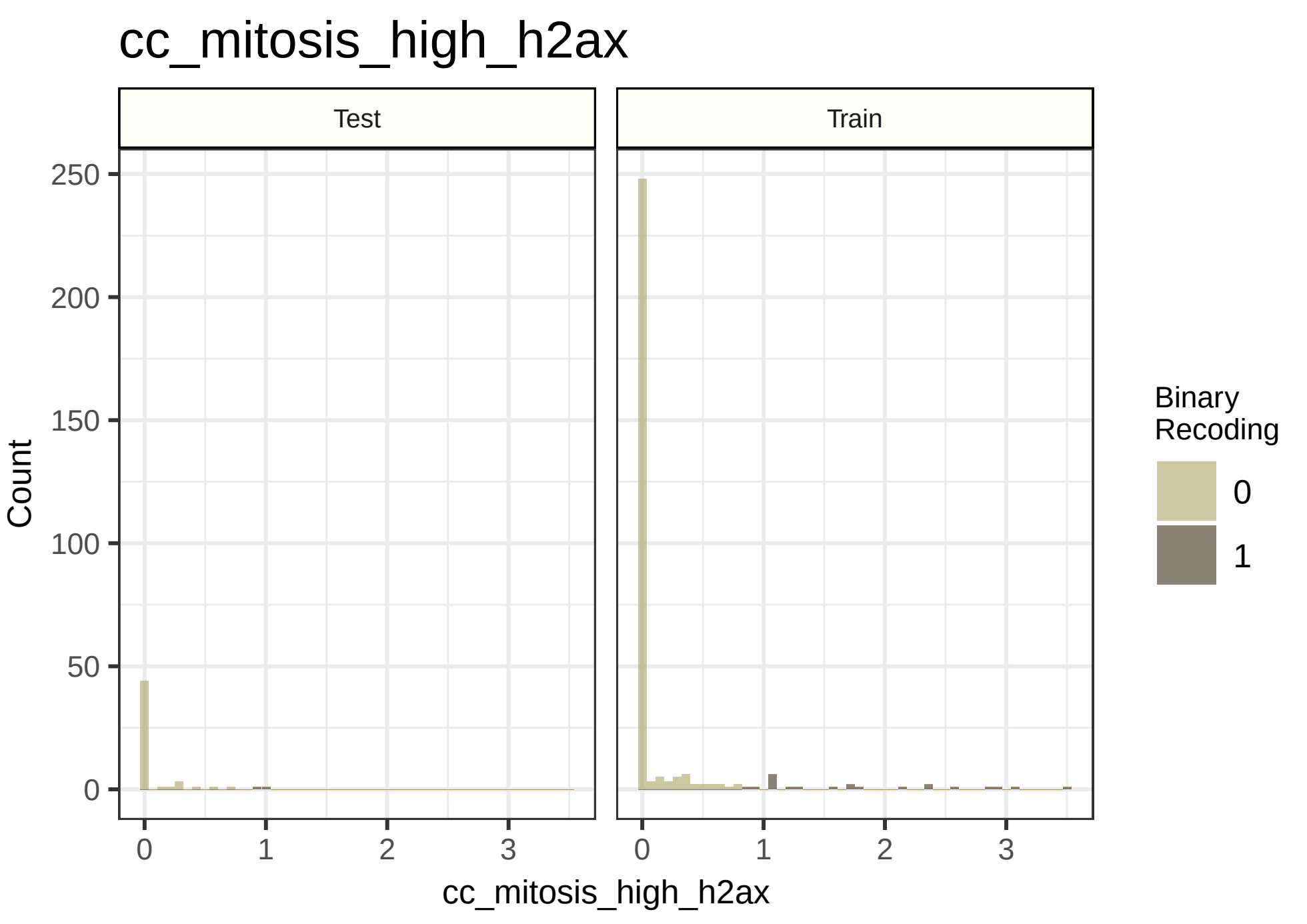

cc_infection_percentage
Test
Train
Count
40
30
20
10
0
−3
−2
−1
0
1
cc_infection_percentage
Binary Recoding
0
1

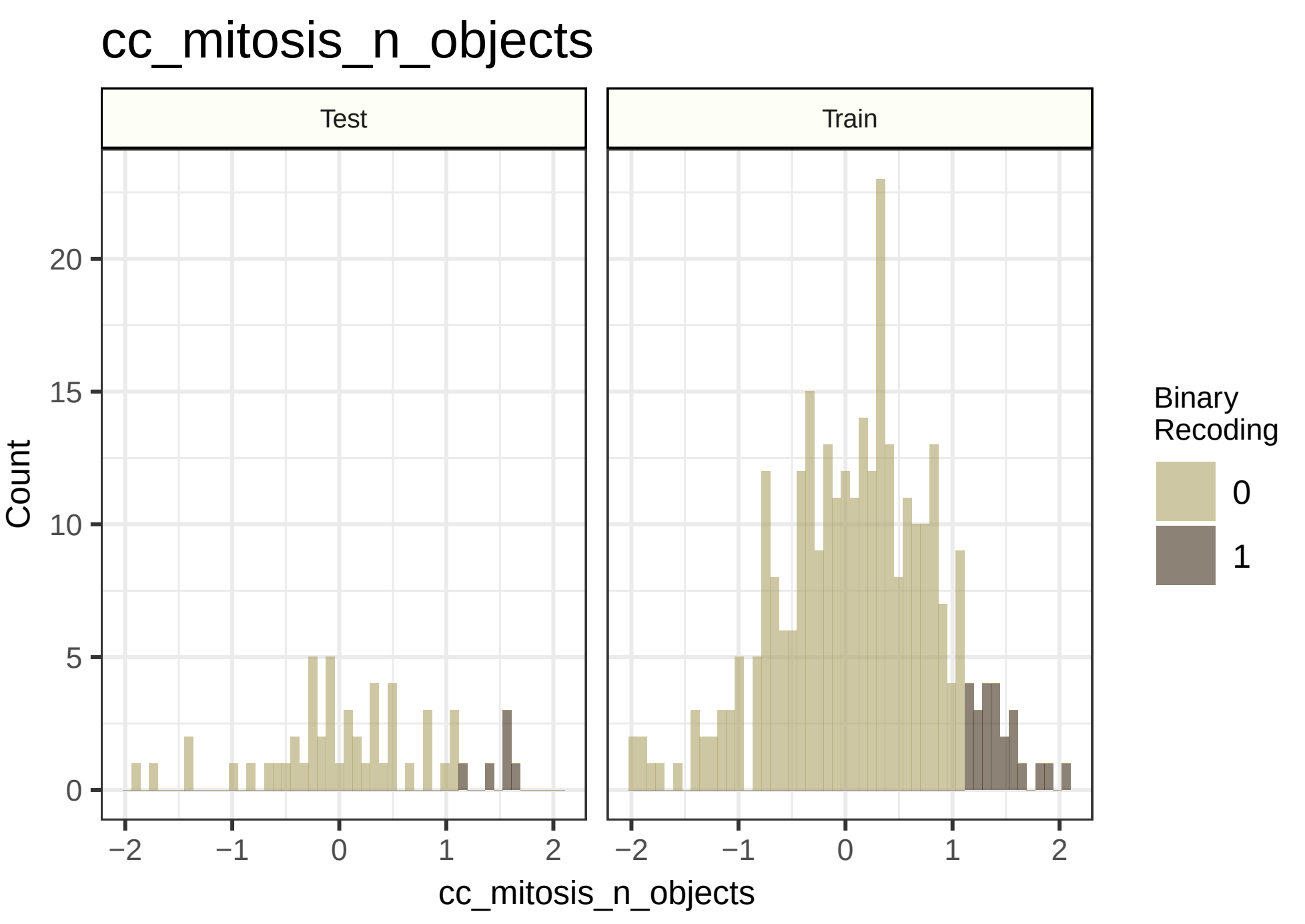

cc_late_mitosis_high_h2ax
Test
Train
Count
200
150
100
50
0
0
2
4
6
8
cc_late_mitosis_high_h2ax
Binary Recoding
0
1

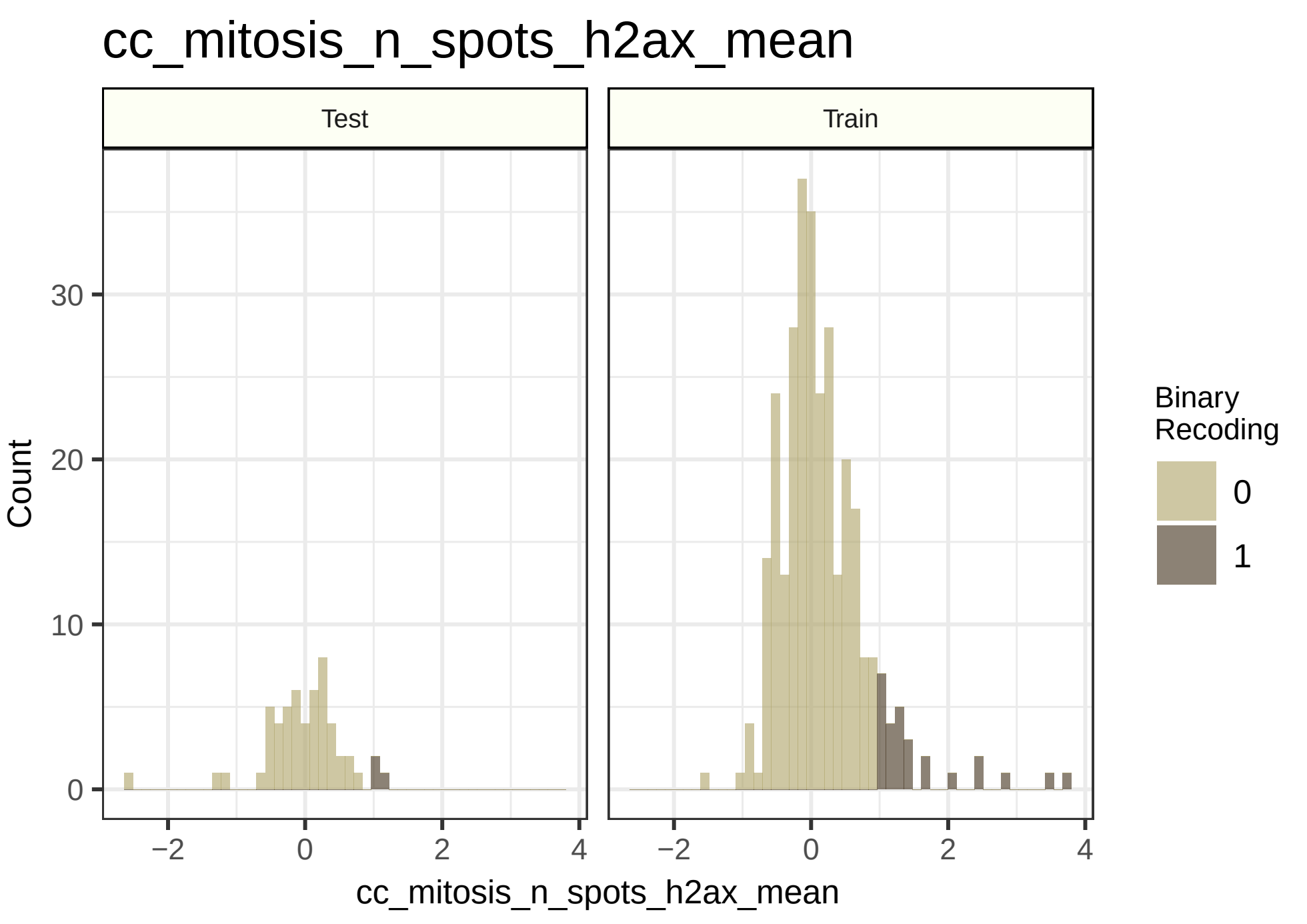

cc_late_mitosis_n_objects
Test
Train
Count
30
20
10
0
0
2
4
6
0
2
4
6
cc_late_mitosis_n_objects
Binary Recoding
0
1

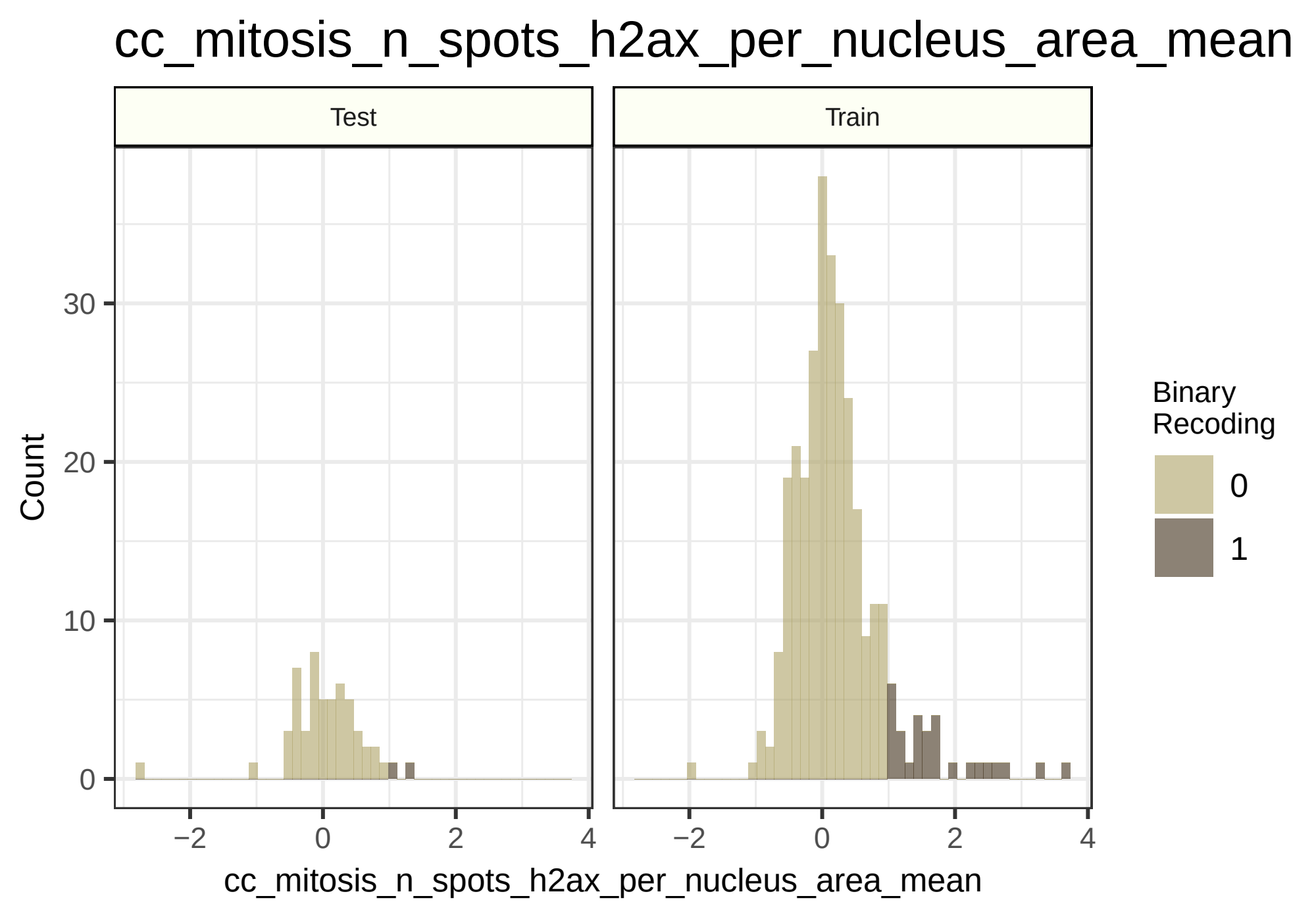

cc_late_mitosis_n_spots_h2ax_mean
Test
Train
Count
60
40
20
0
−2
−1
0
1
2
3
cc_late_mitosis_n_spots_h2ax_mean
Binary Recoding
0
1

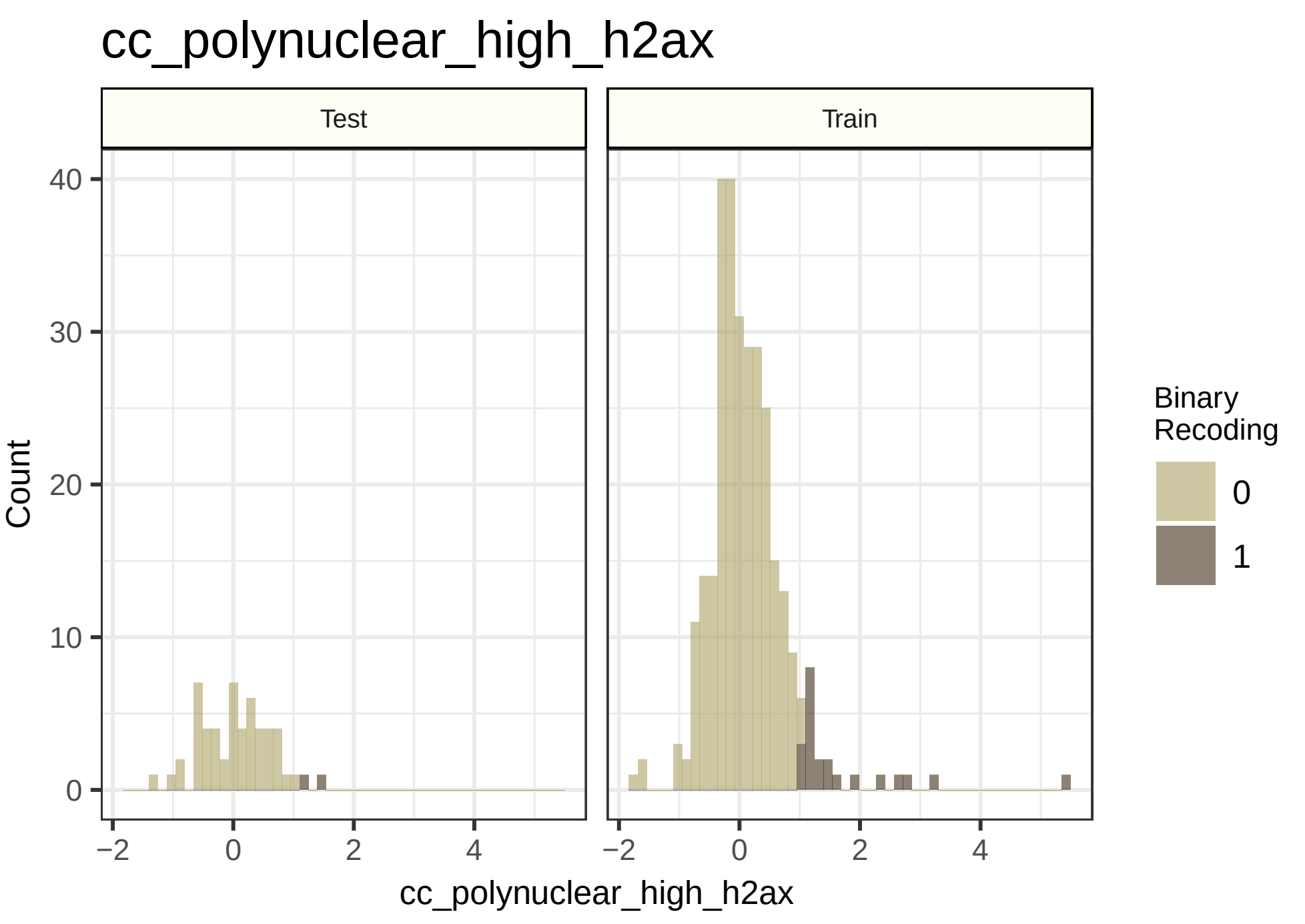

cc_late_mitosis_n_spots_h2ax_per_nucleus_area_m
Test
Train
60
40
20
0
Count
−2
−1
0
1
2
3
cc_late_mitosis_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

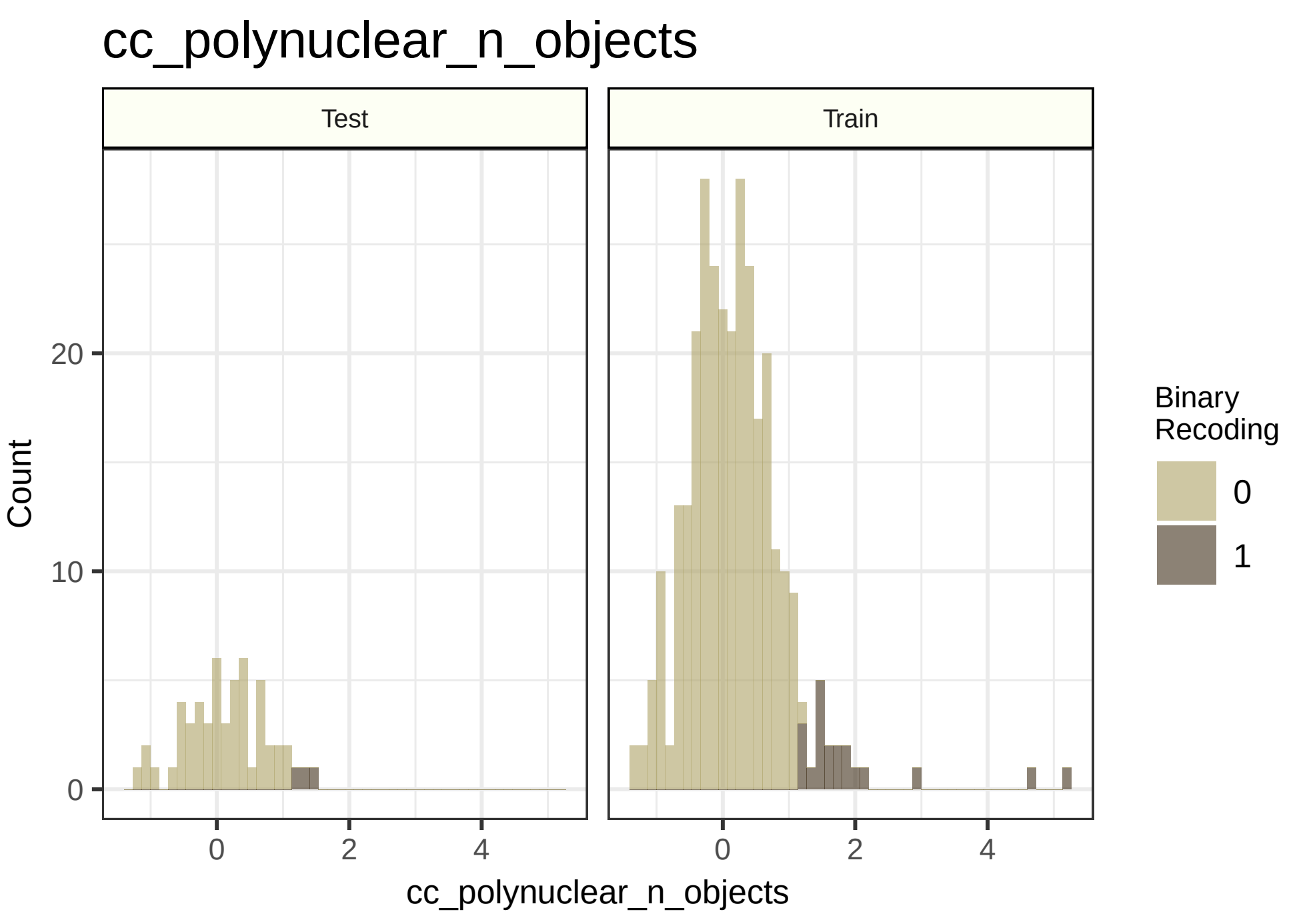

cc_mitosis_high_h2ax
Test
Train
250
200
150
100
50
0
Count
0
1
2
3
cc_mitosis_high_h2ax
Binary Recoding
0
1

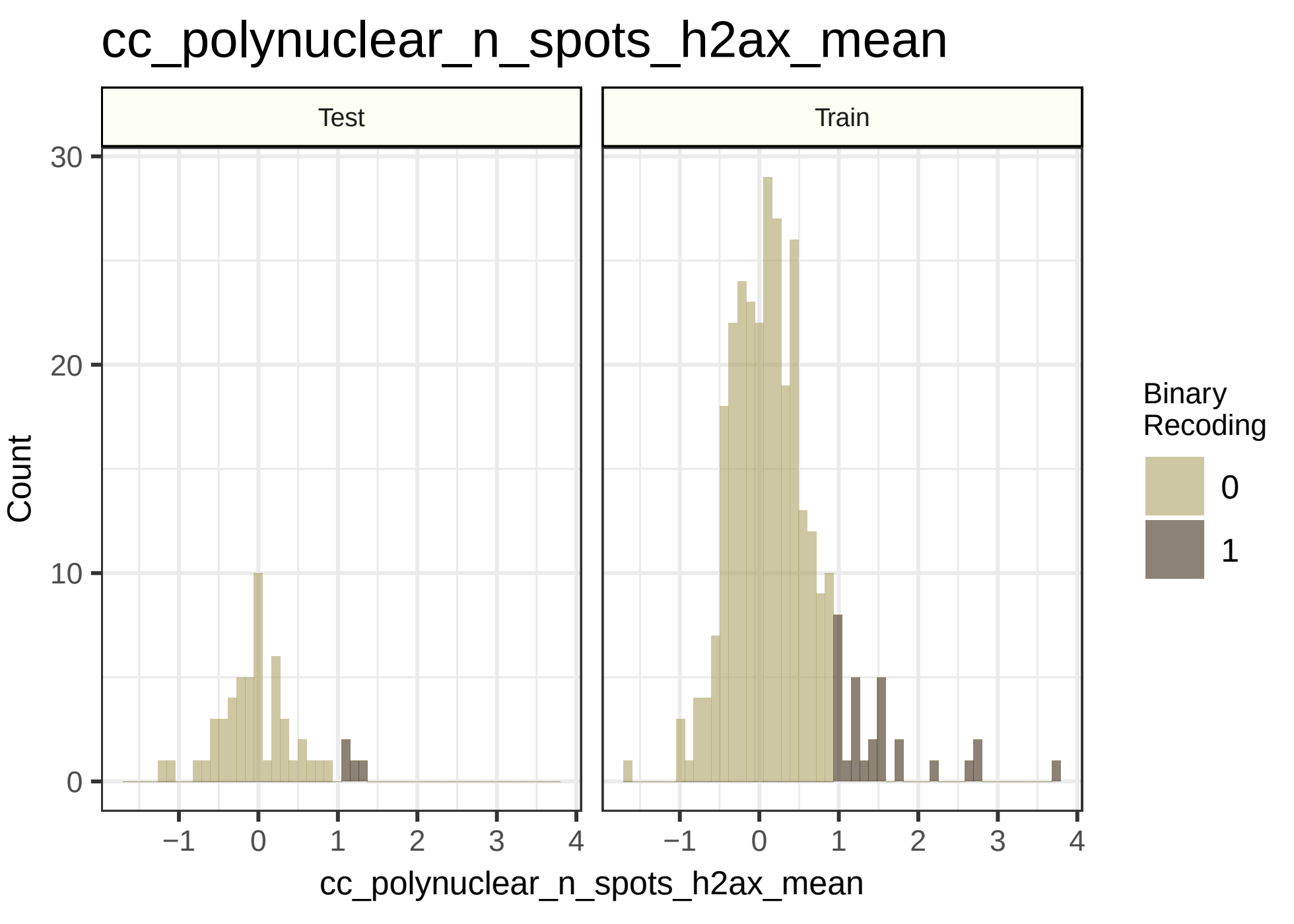

cc_mitosis_n_objects
Test
Train
Count
20
15
10
5
0
−2
−1
0
1
2
cc_mitosis_n_objects
Binary Recoding
0
1

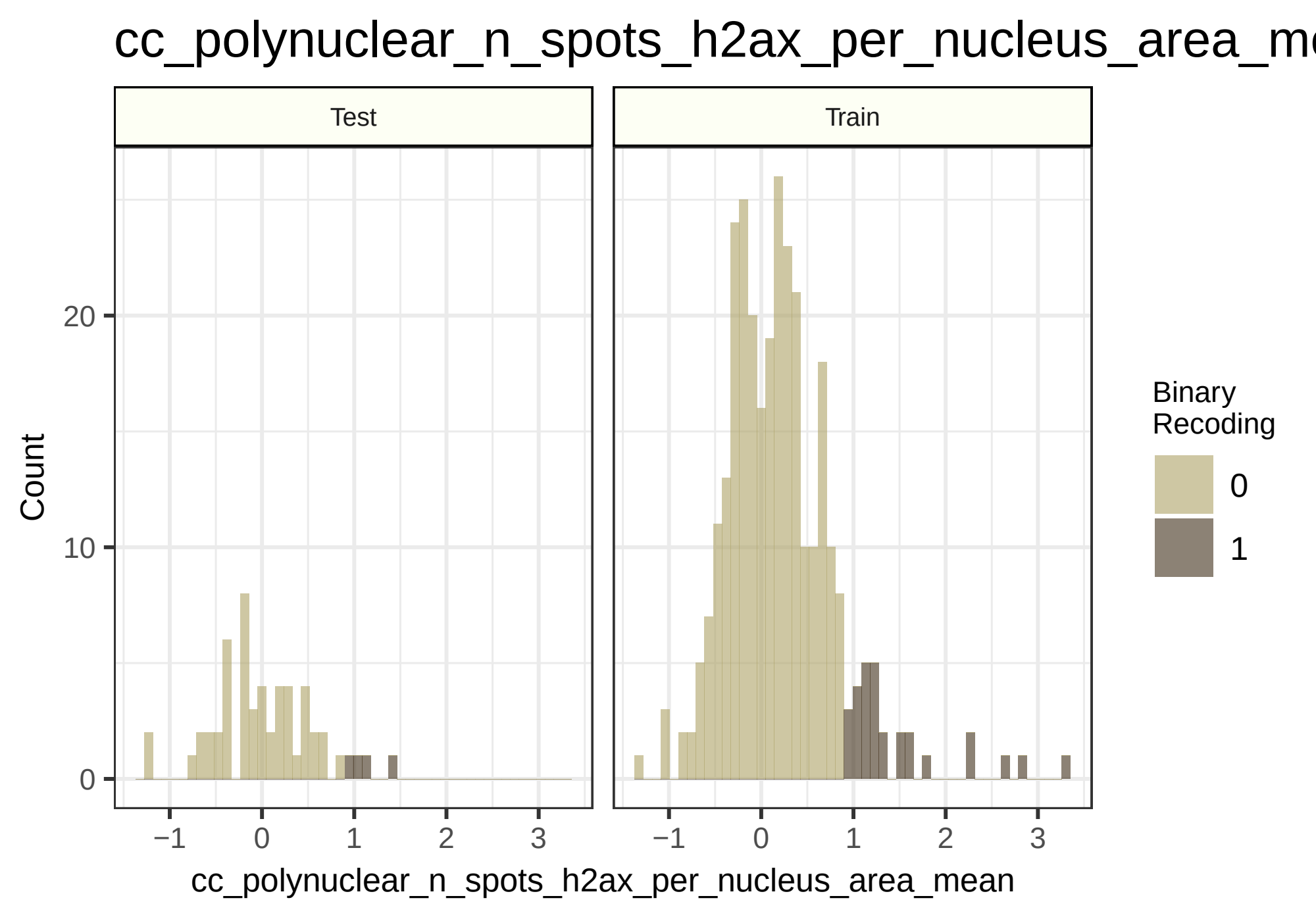

cc_mitosis_n_spots_h2ax_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_mitosis_n_spots_h2ax_mean
Binary Recoding
0
1

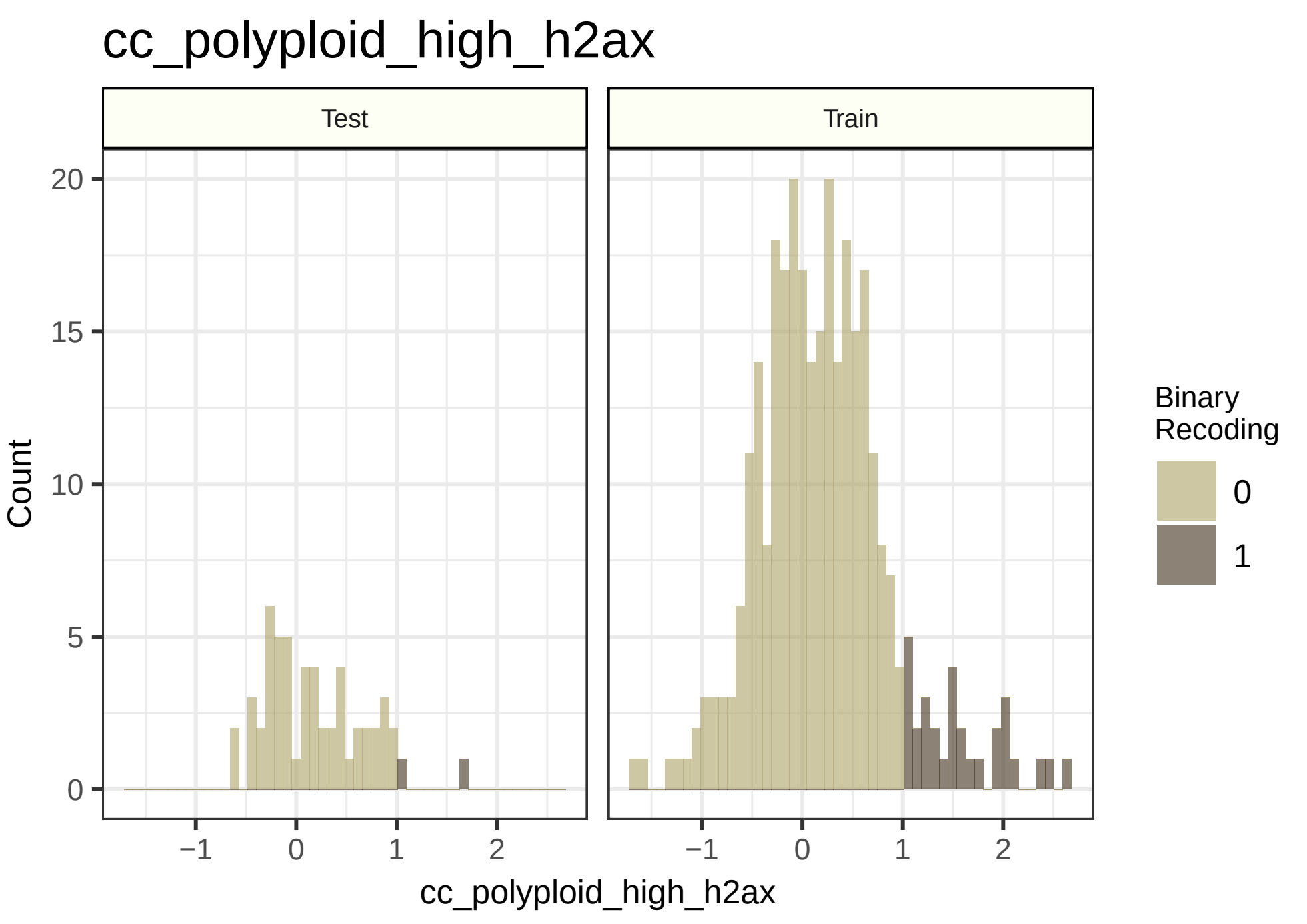

cc_mitosis_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_mitosis_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

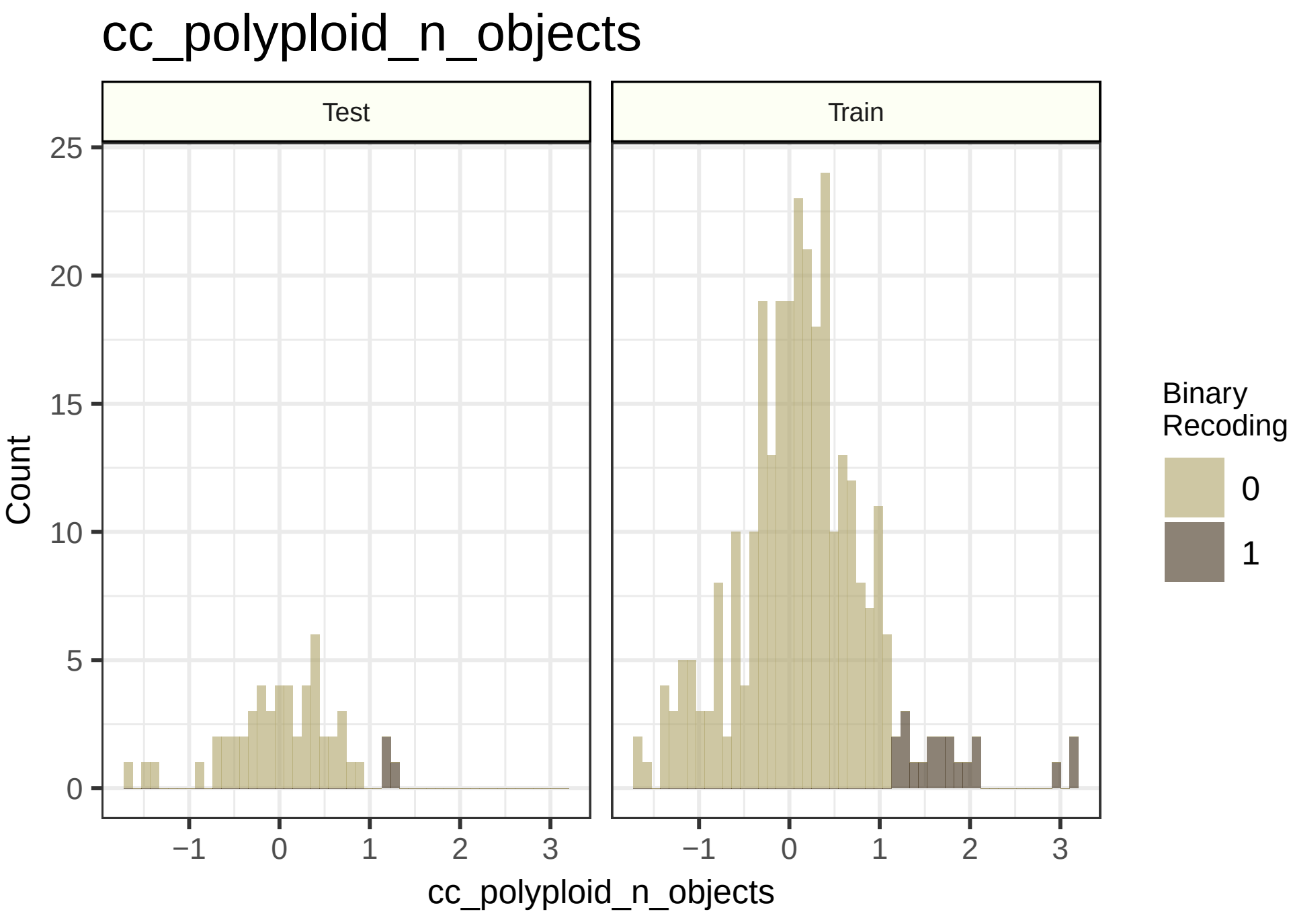

cc_polynuclear_high_h2ax
Test
Train
Count
40
30
20
10
0
−2
0
2
4
cc_polynuclear_high_h2ax
Binary Recoding
0
1

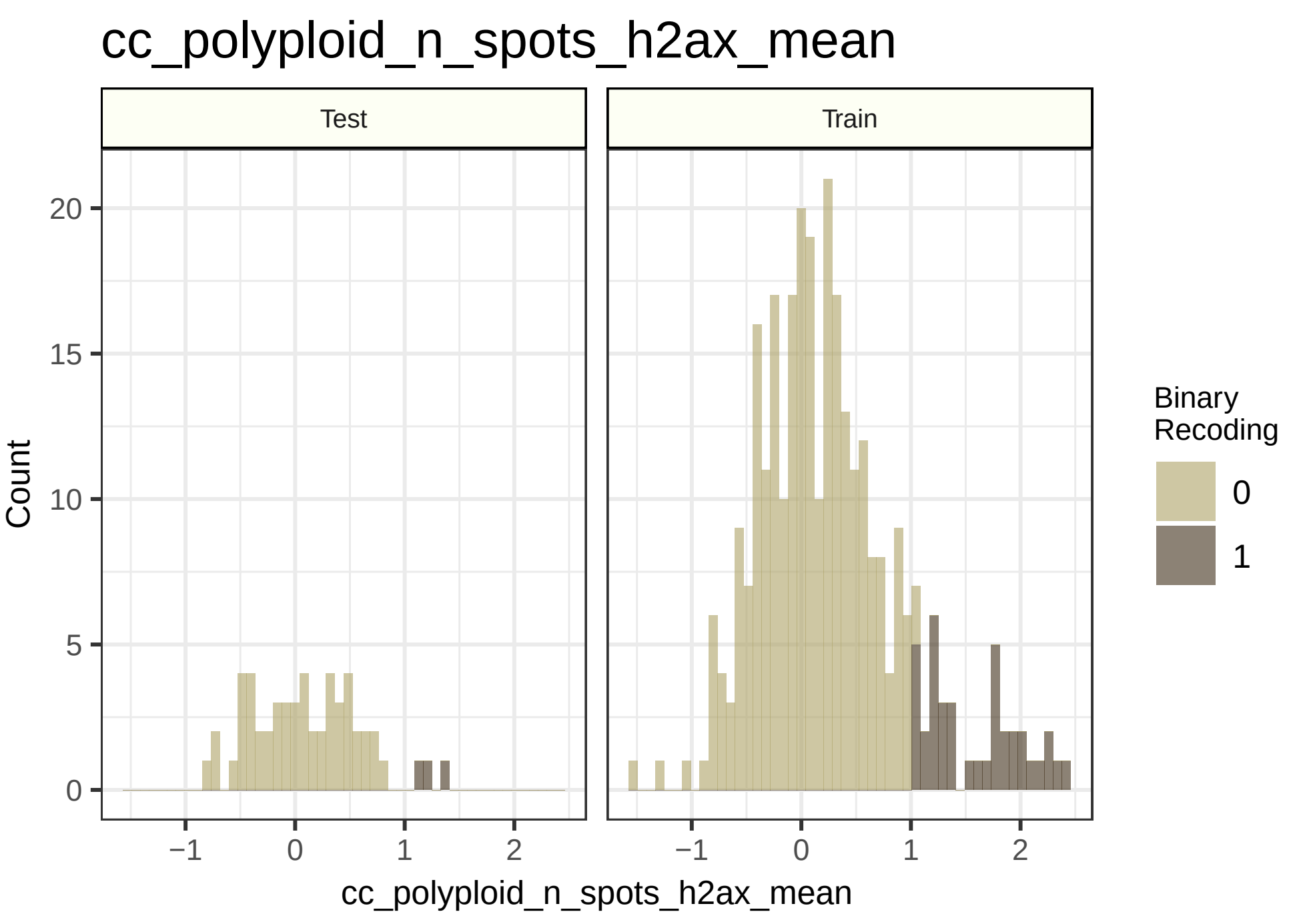

cc_polynuclear_n_objects
Test
Train
Count
20
10
0
0
2
4
0
2
4
cc_polynuclear_n_objects
Binary Recoding
0
1

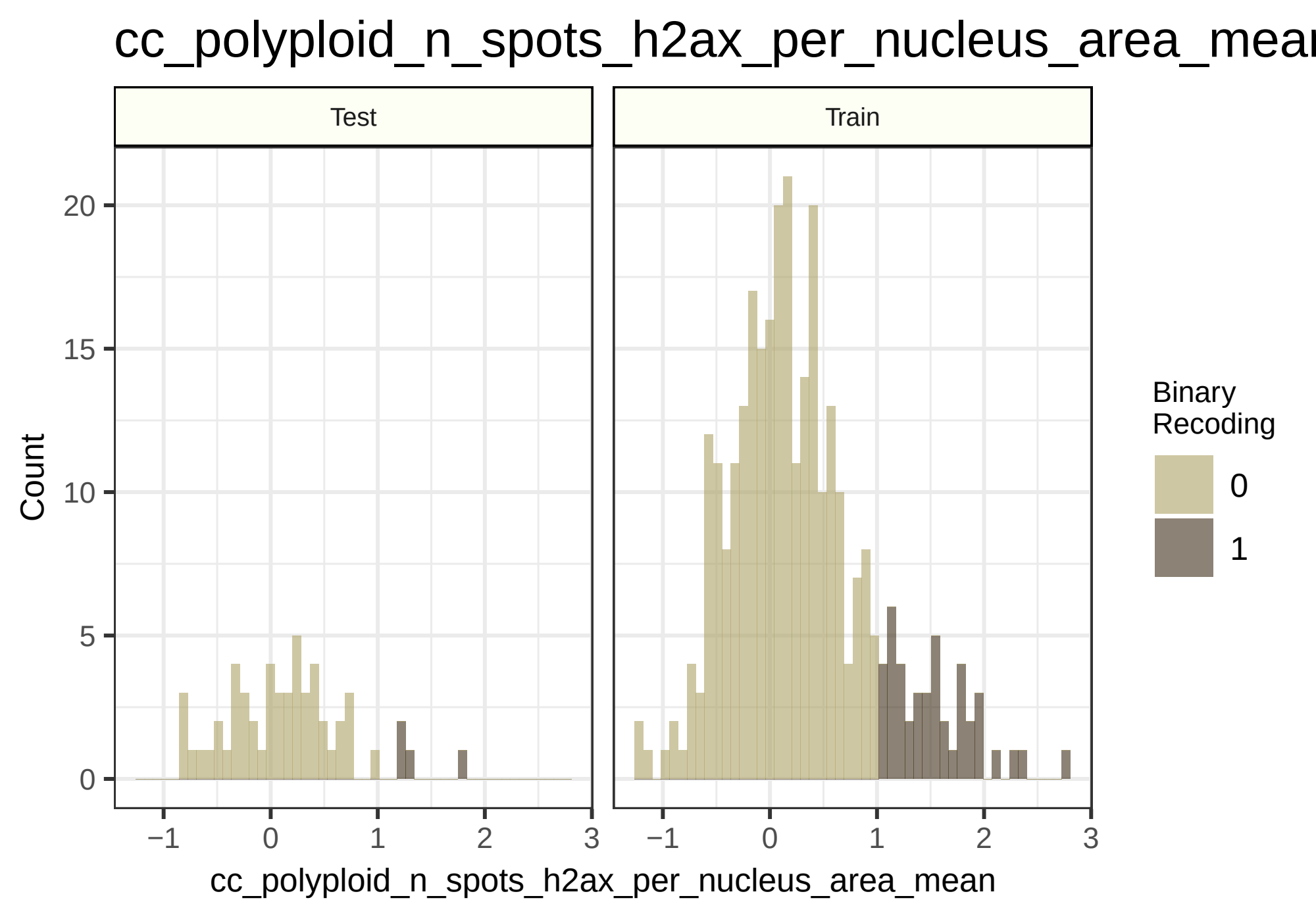

cc_polynuclear_n_spots_h2ax_mean
Test
Train
30
20
10
0
Count
−1
0
1
2
3
4
cc_polynuclear_n_spots_h2ax_mean
Binary Recoding
0
1

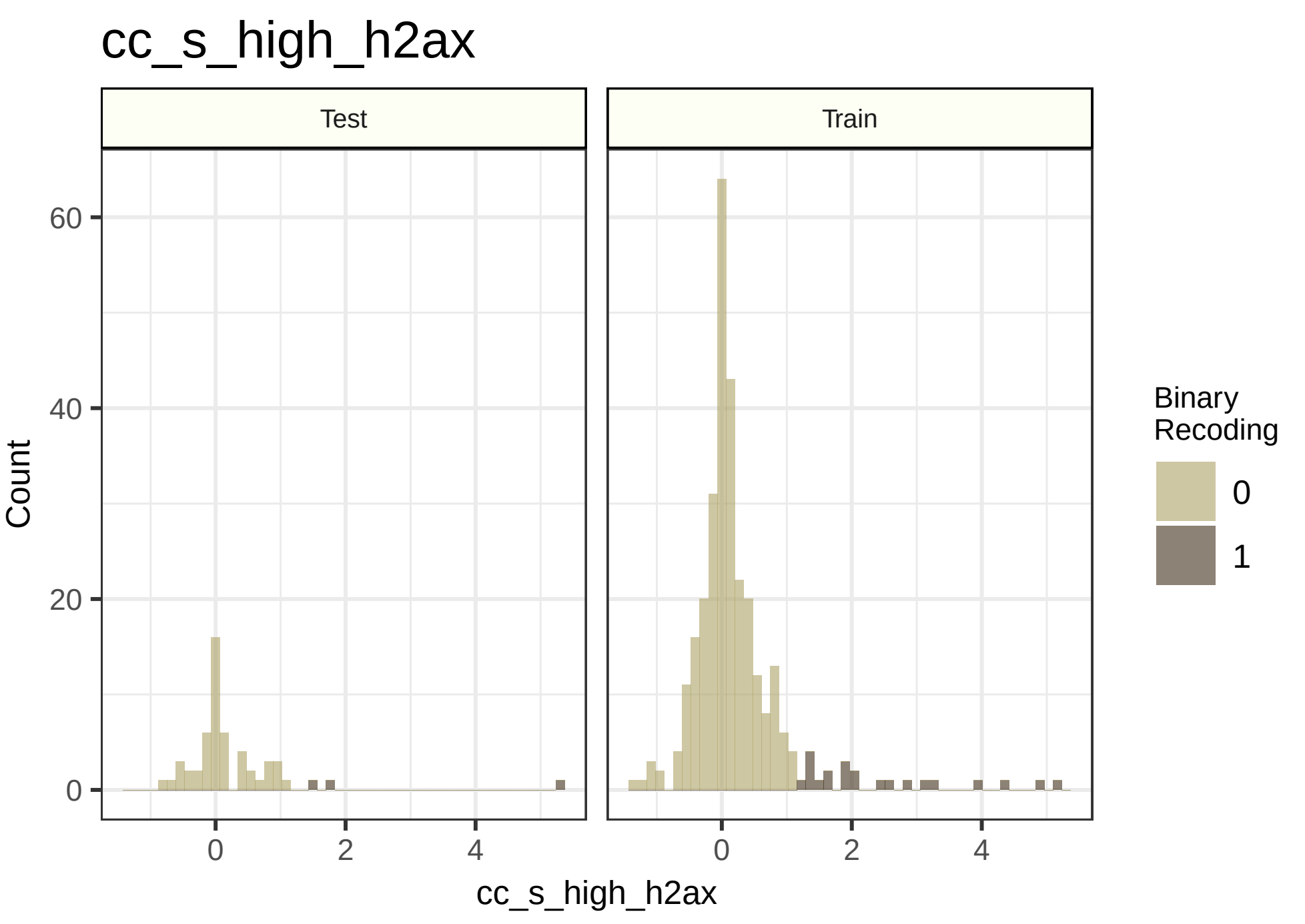

cc_polynuclear_n_spots_h2ax_per_nucleus_area_m
Test
Train
Count
20
10
0
−1
0
1
2
3
cc_polynuclear_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

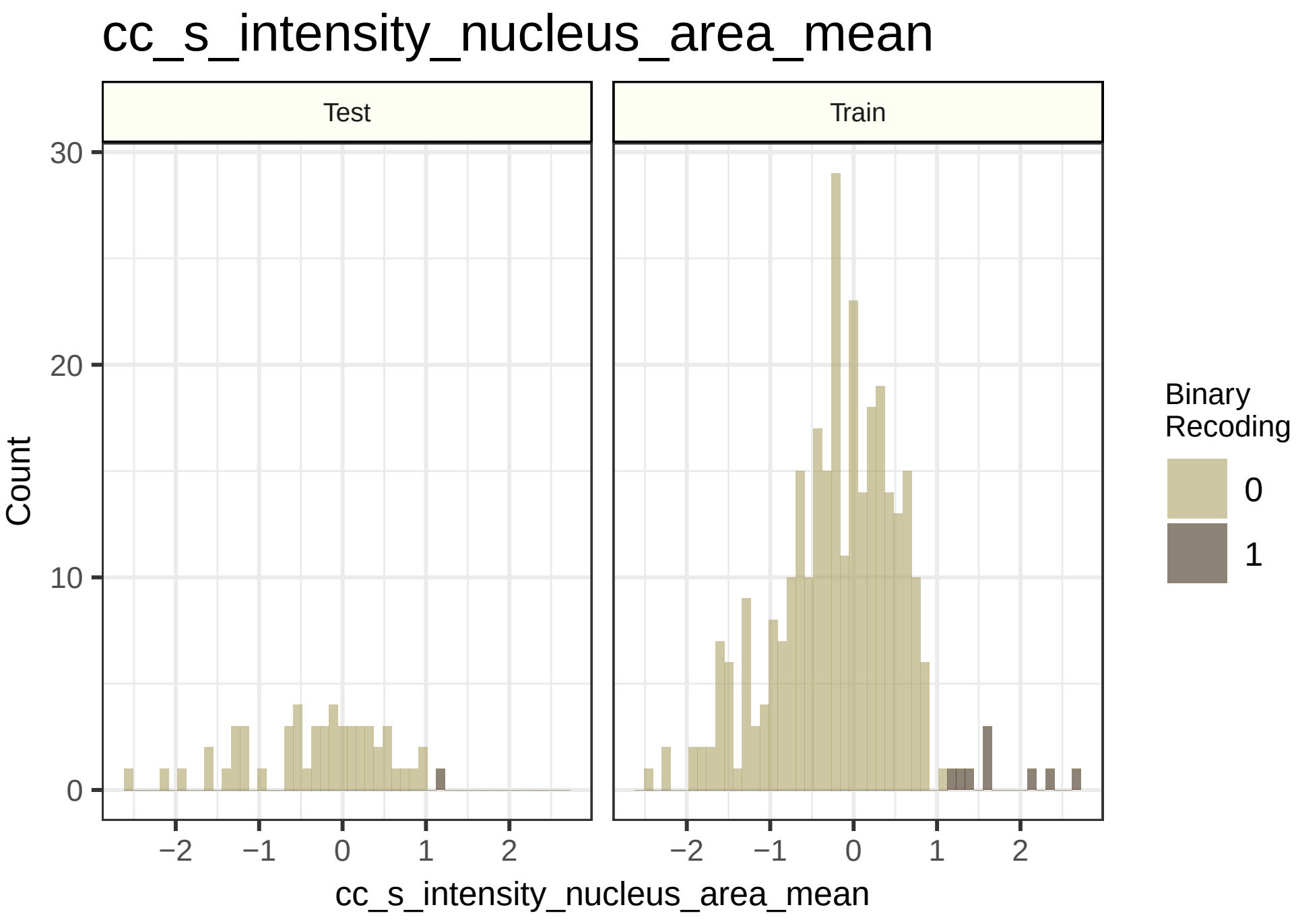

cc_polyploid_high_h2ax
Test
Train
Count
20
15
10
5
0
−1
0
1
2
cc_polyploid_high_h2ax
Binary Recoding
0
1

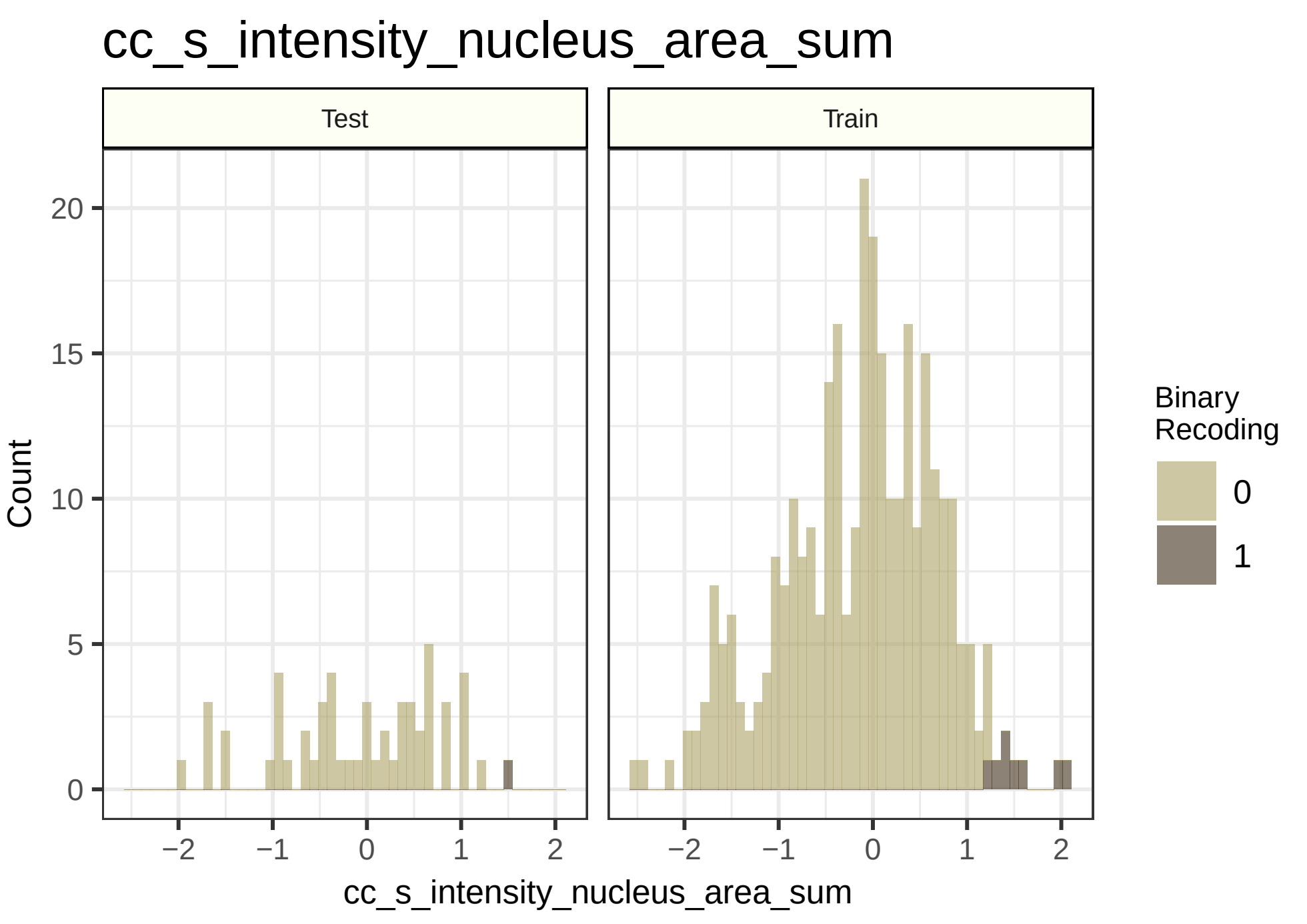

cc_polyploid_n_objects
Test
Train
Count
25
20
15
10
5
0
−1
0
1
2
3
cc_polyploid_n_objects
Binary Recoding
0
1

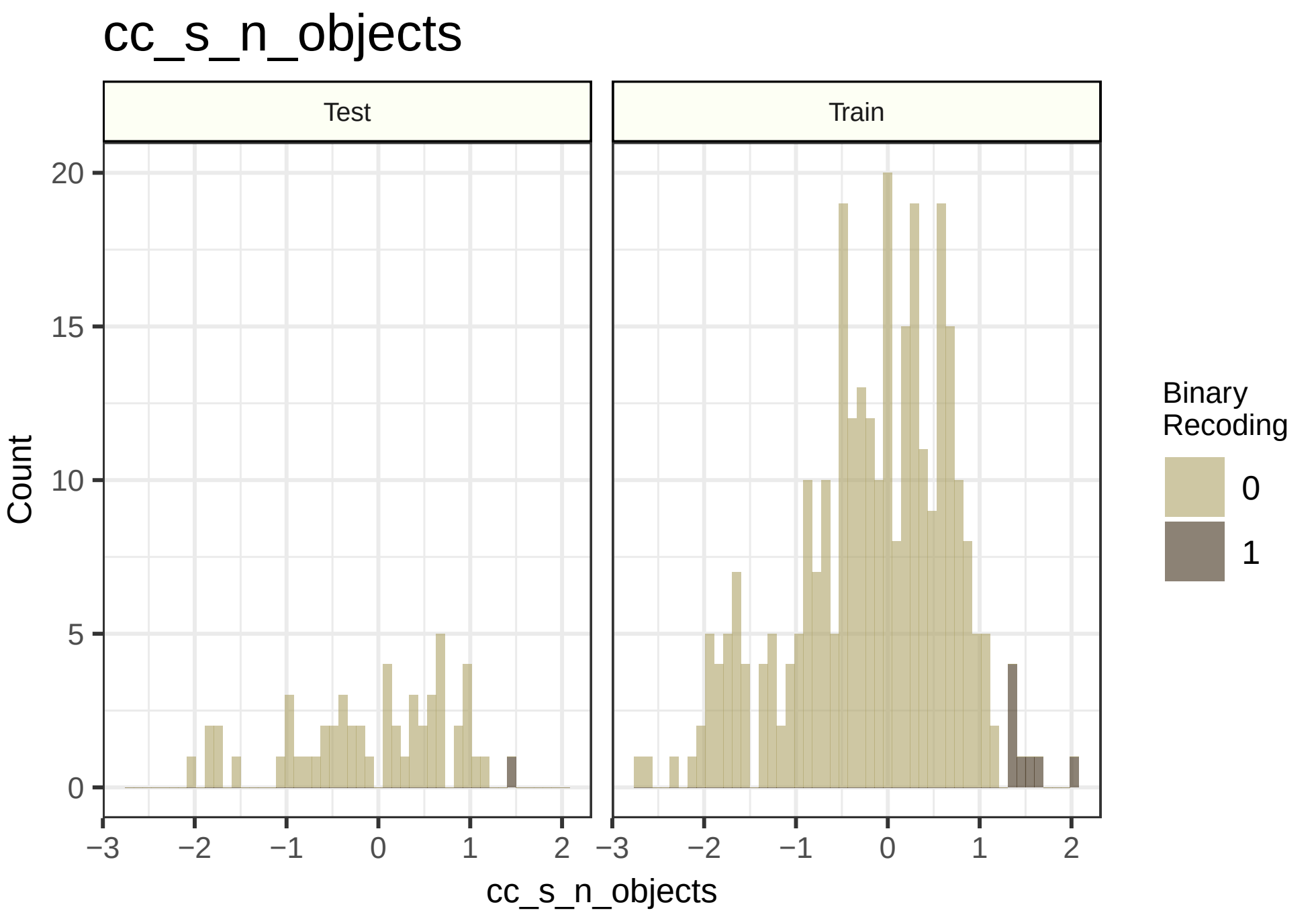

cc_polyploid_n_spots_h2ax_mean
Test
Train
Count
20
15
10
5
0
−1
0
1
2
cc_polyploid_n_spots_h2ax_mean
Binary Recoding
0
1

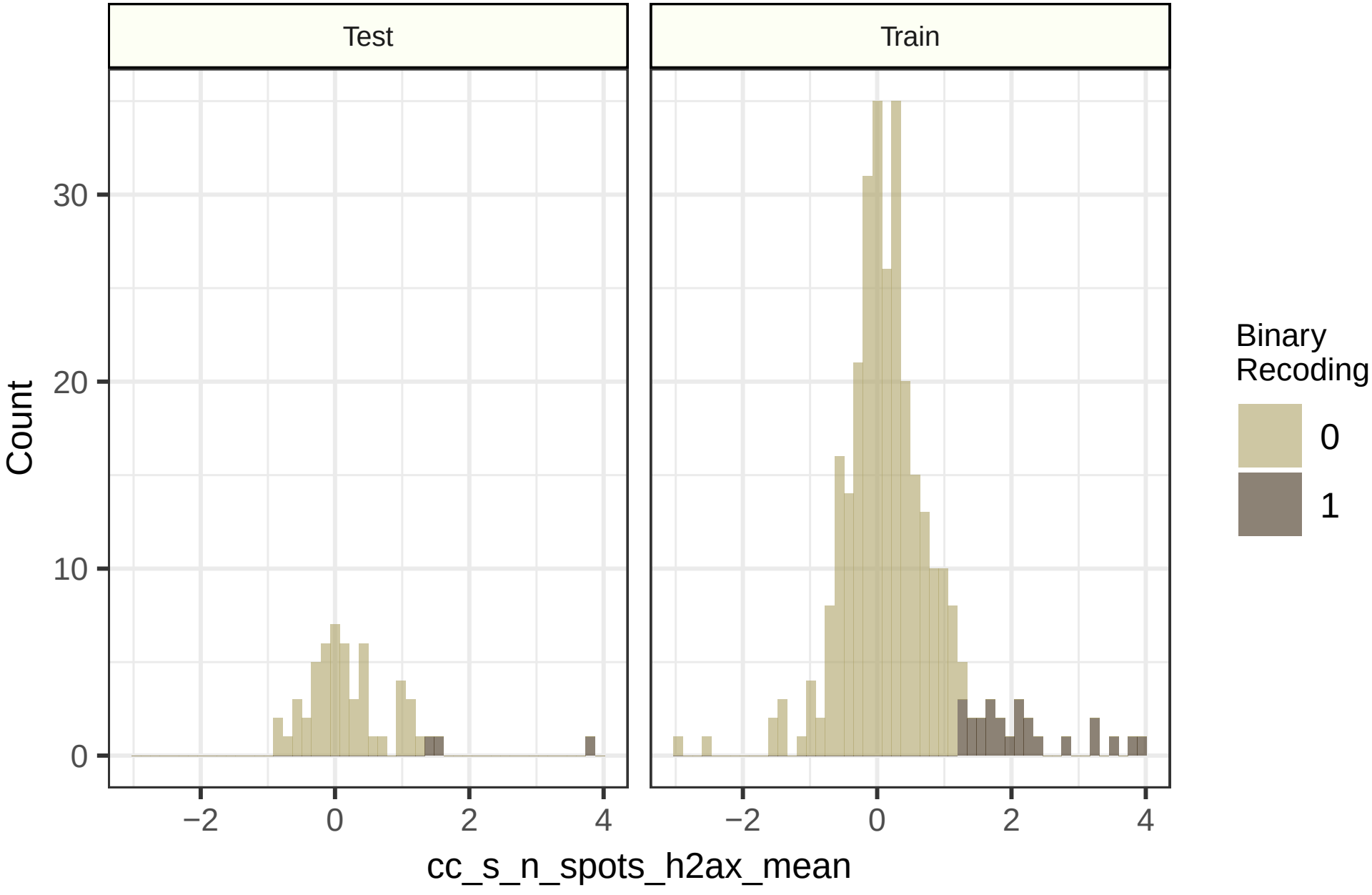

cc_polyploid_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
20
15
10
5
0
−1
0
1
2
3
cc_polyploid_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

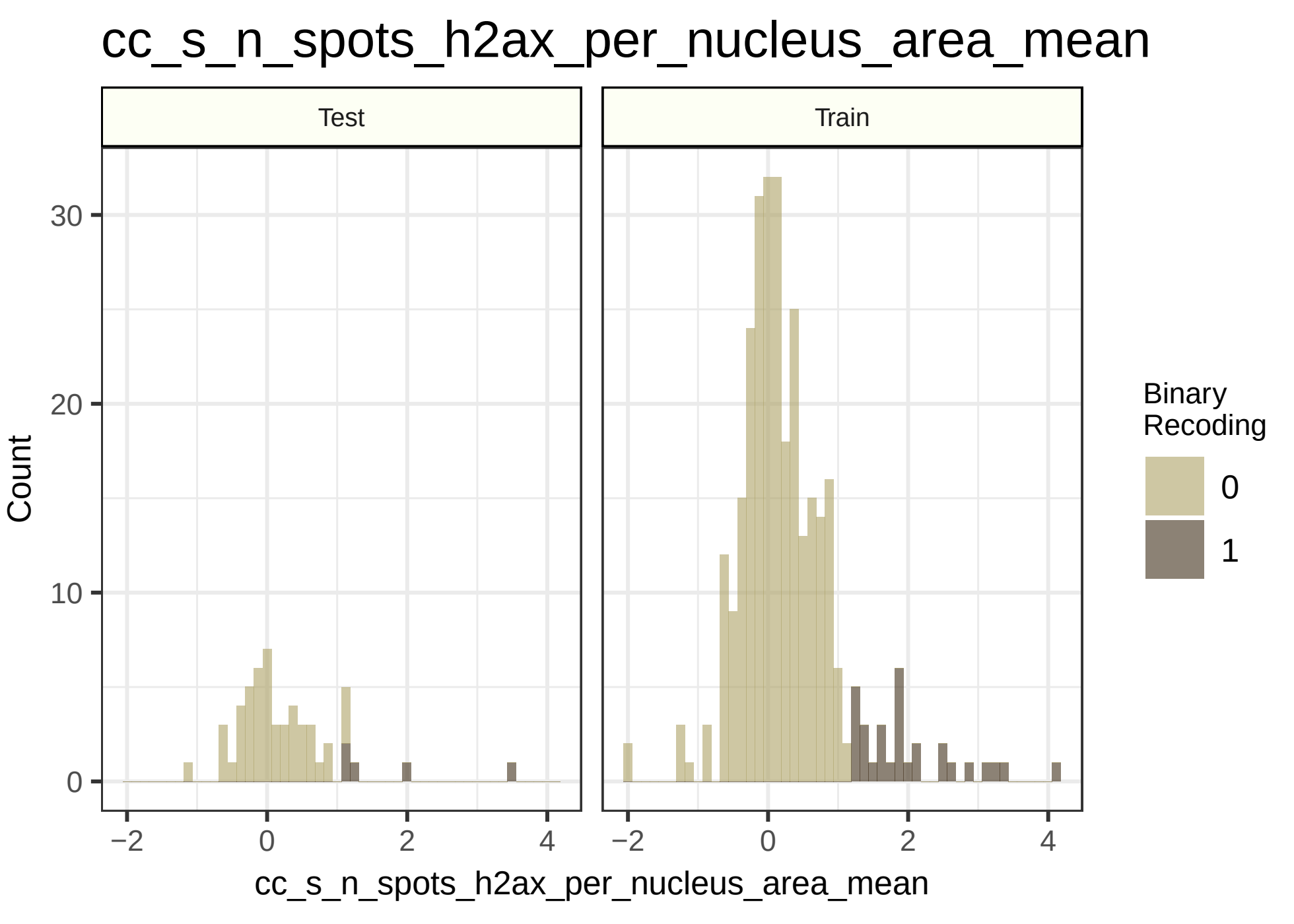

cc_s_high_h2ax
Test
Train
60
40
20
0
Count
0
2
4
0
2
4
cc_s_high_h2ax
Binary
Recoding
0
1

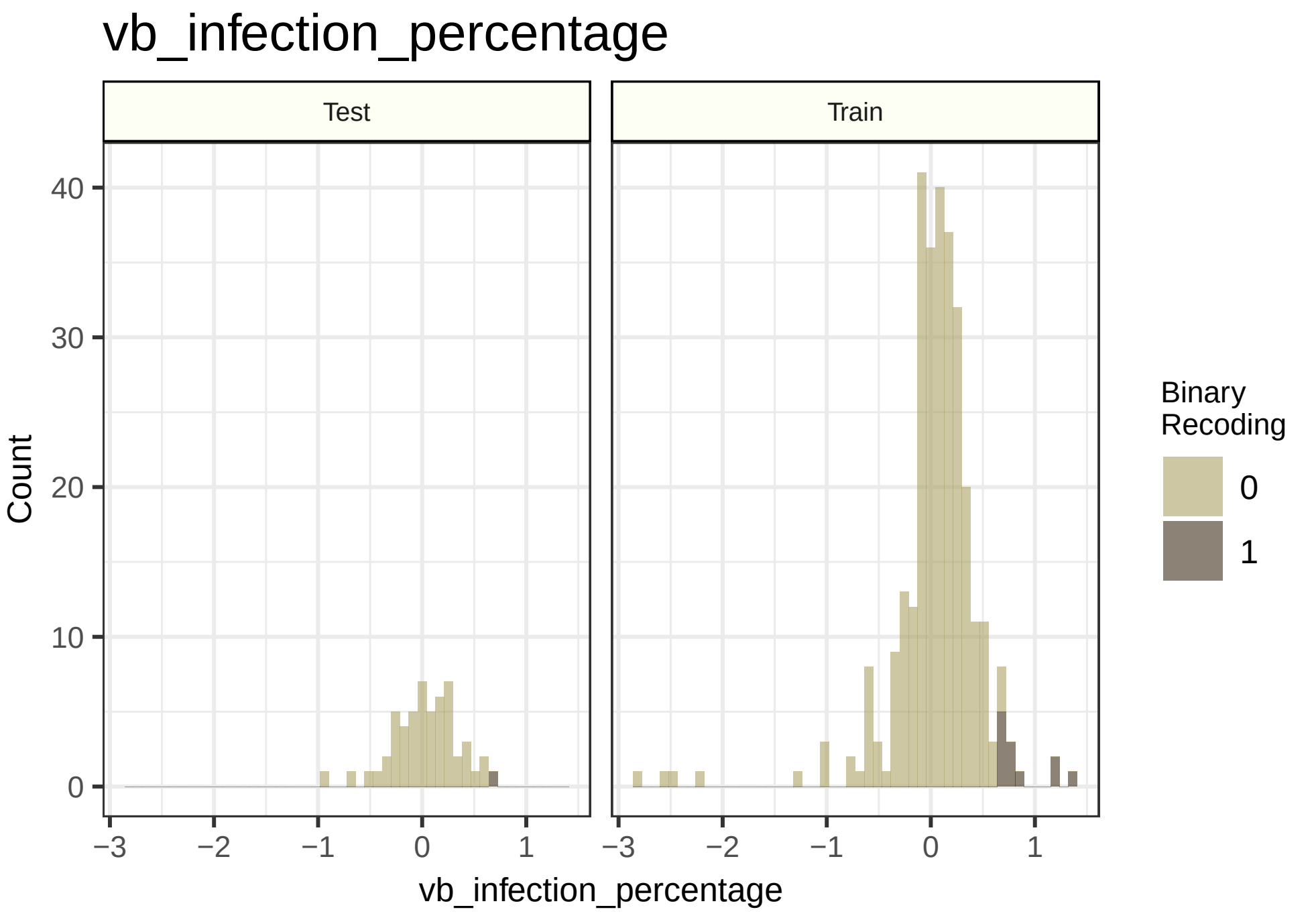

cc_s_intensity_nucleus_area_mean
Test
Train
Count
30
20
10
0
−2
−1
0
1
2
cc_s_intensity_nucleus_area_mean
Binary Recoding
0
1

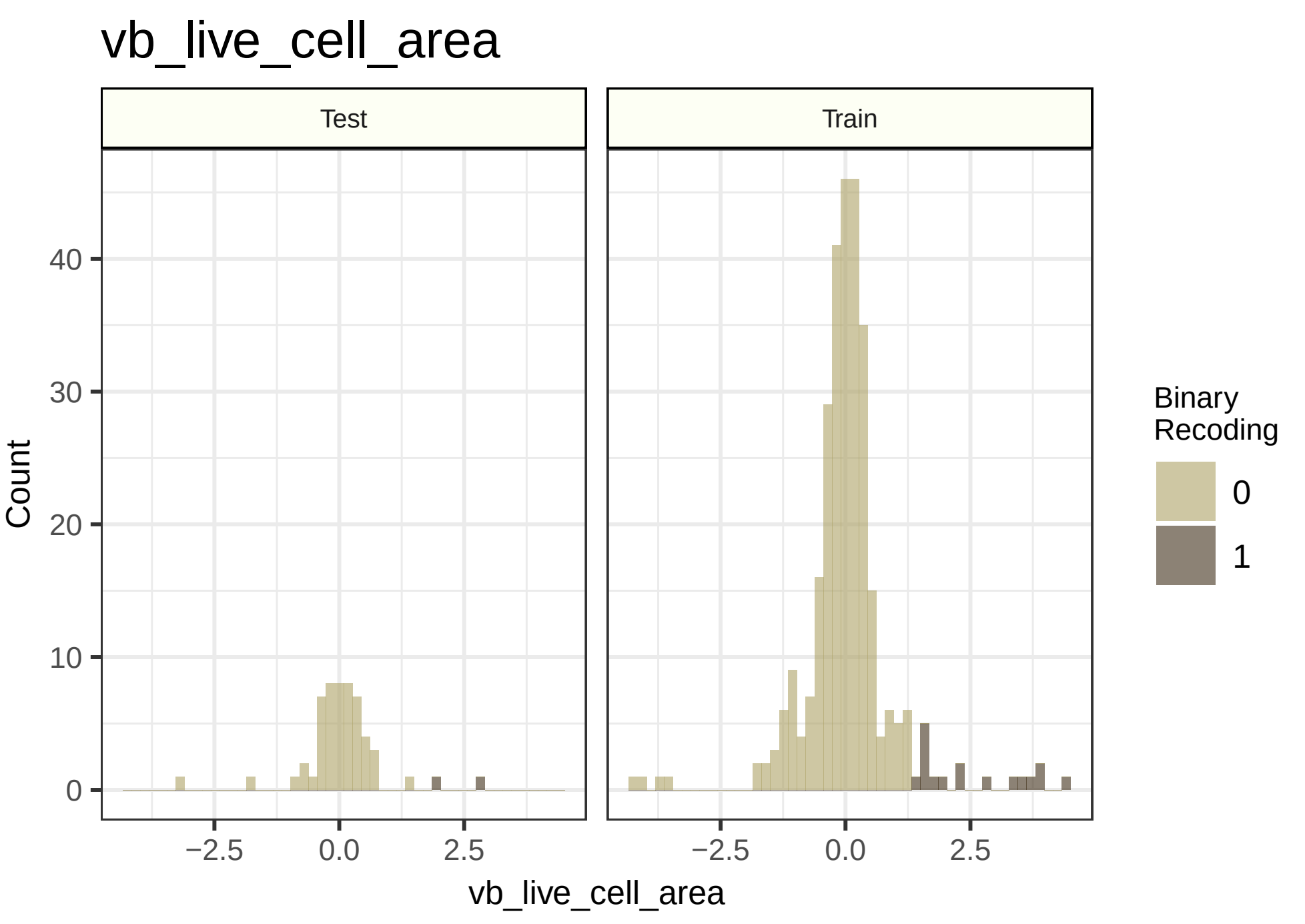

cc_s_intensity_nucleus_area_sum
Test
Train
Count
20
15
10
5
0
−2
−1
0
1
2
cc_s_intensity_nucleus_area_sum
Binary Recoding
0
1

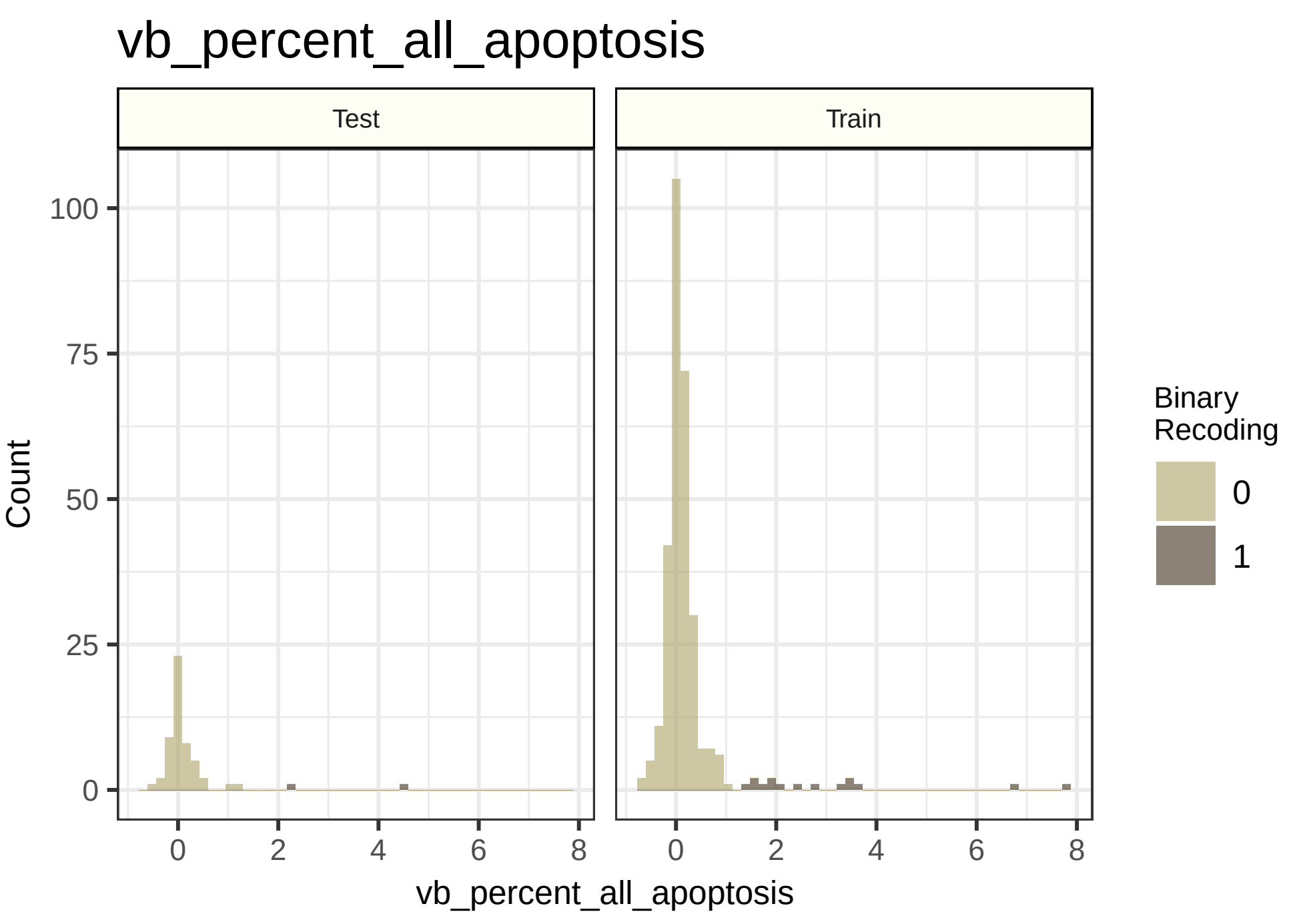

cc_s_n_objects
Test
Train
Count
20
15
10
5
0
−3
−2
−1
0
1
2
cc_s_n_objects
Binary Recoding
0
1

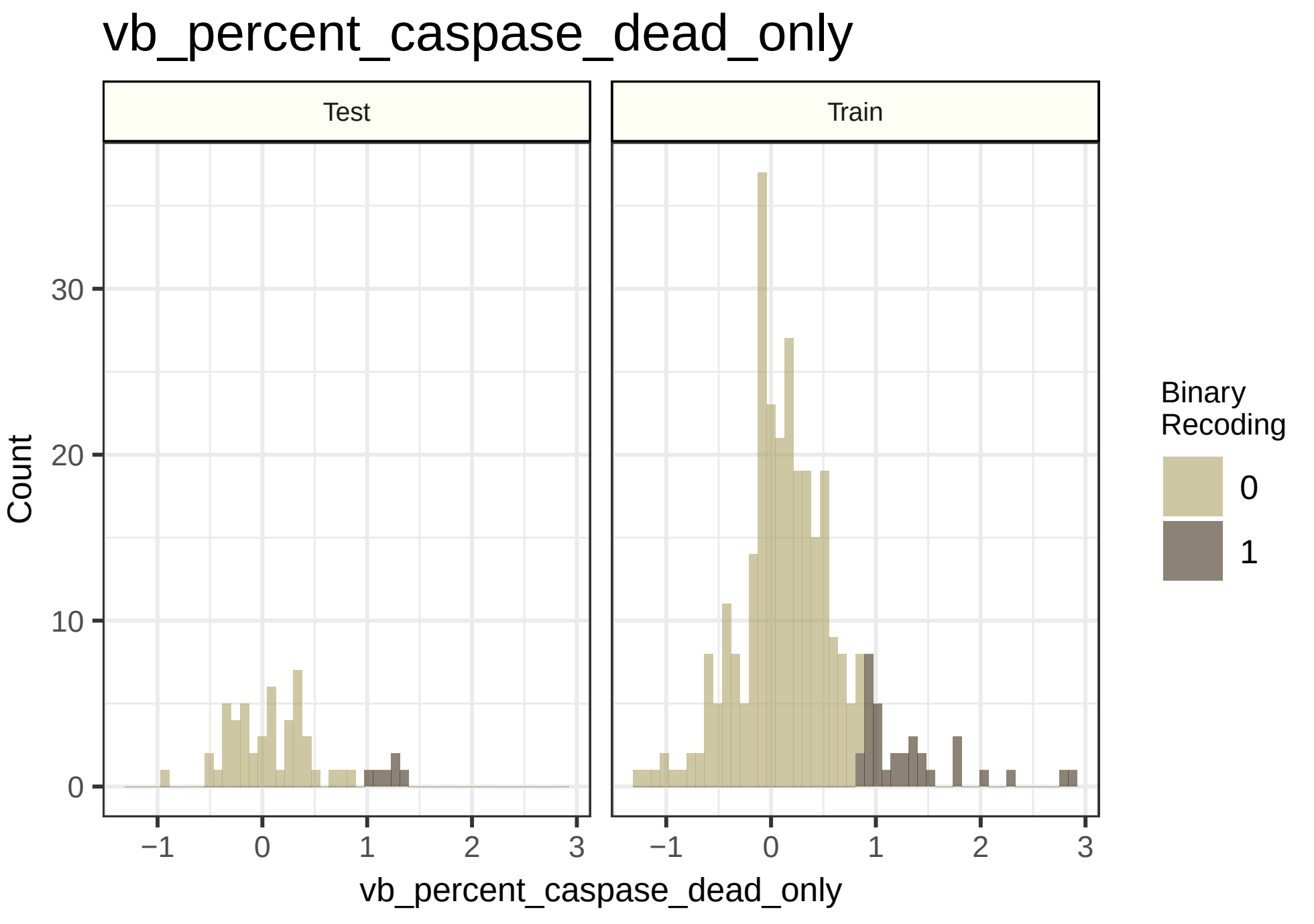

cc_s_n_spots_h2ax_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_s_n_spots_h2ax_mean
Binary Recoding
0
1

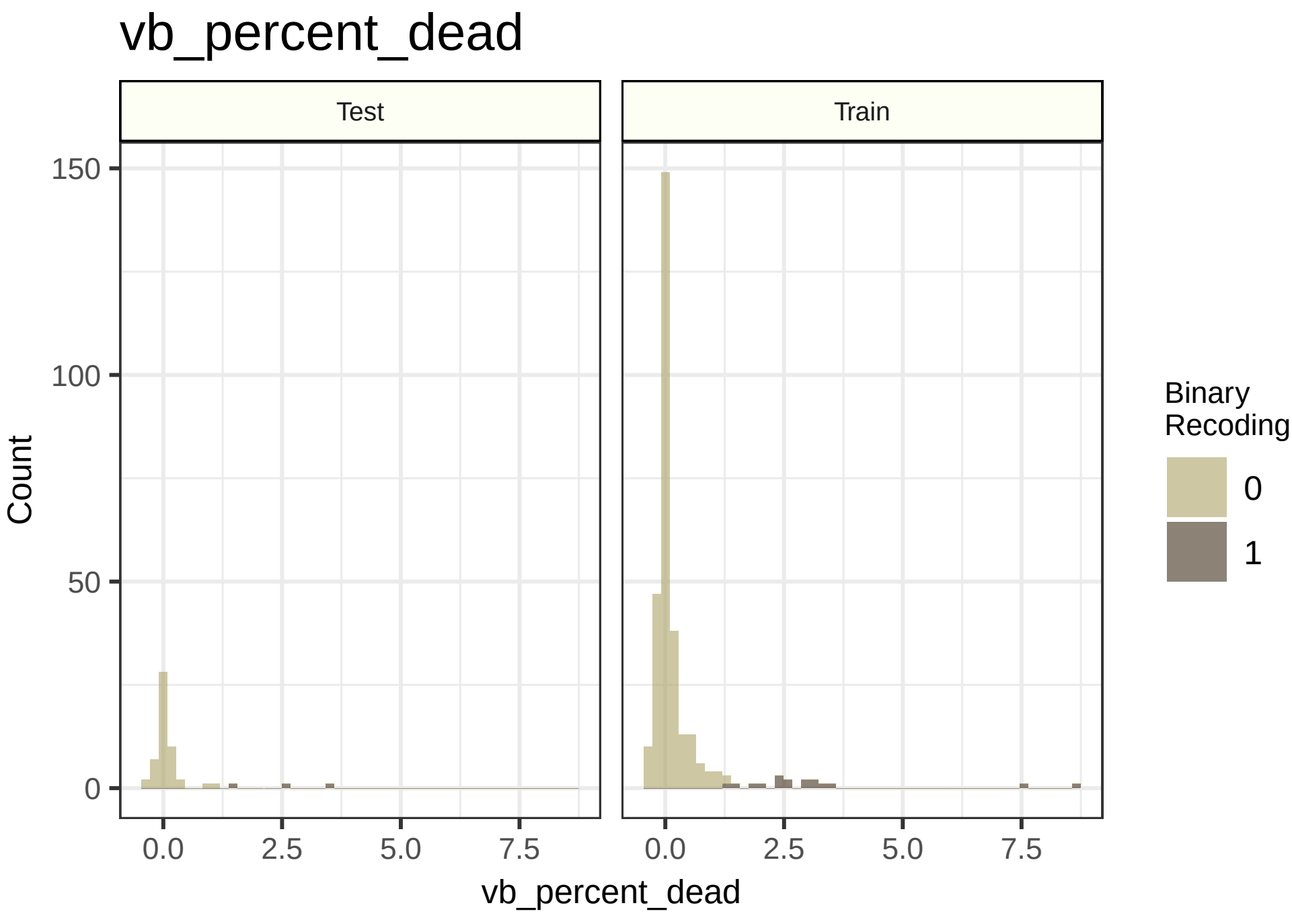

cc_s_n_spots_h2ax_per_nucleus_area_mean
Test
Train
Count
30
20
10
0
−2
0
2
4
cc_s_n_spots_h2ax_per_nucleus_area_mean
Binary Recoding
0
1

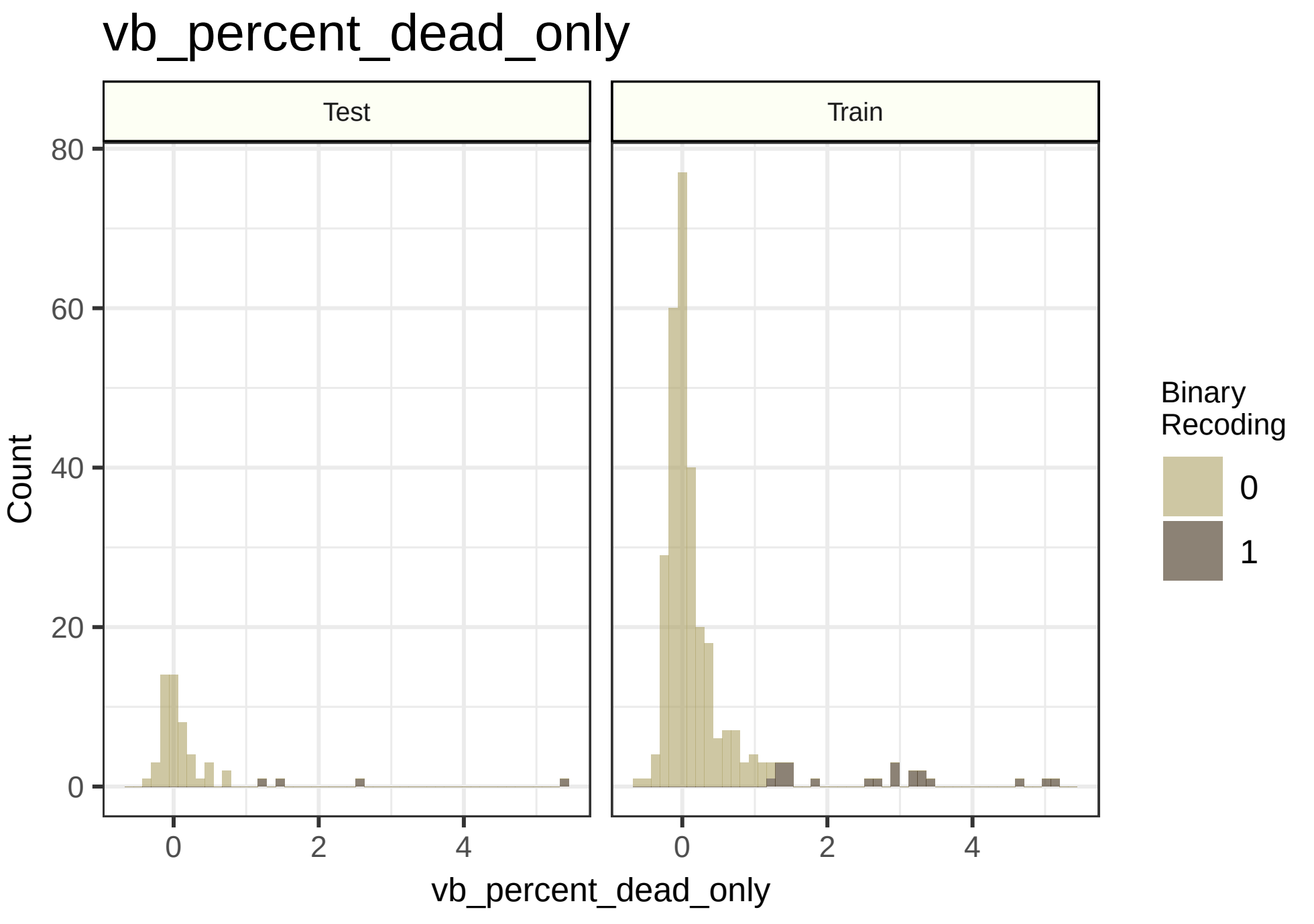

vb_infection_percentage
Test
Train
Count
40
30
20
10
0
−3
−2
−1
0
1
vb_infection_percentage
Binary Recoding
0
1

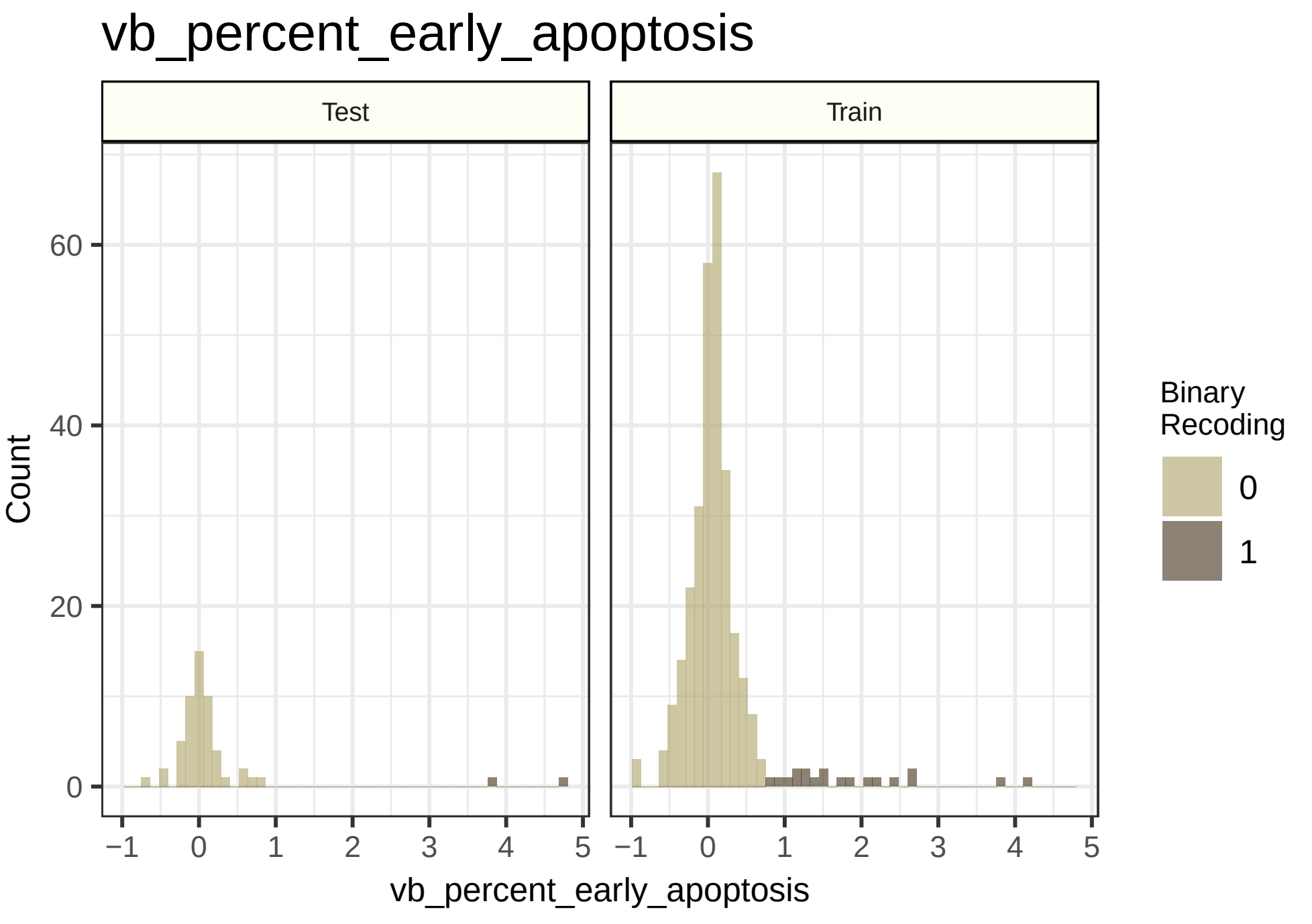

vb_live_cell_area
Test
Train
Count
40
30
20
10
0
−2.5
0.0
2.5
vb_live_cell_area
Binary Recoding
0
1

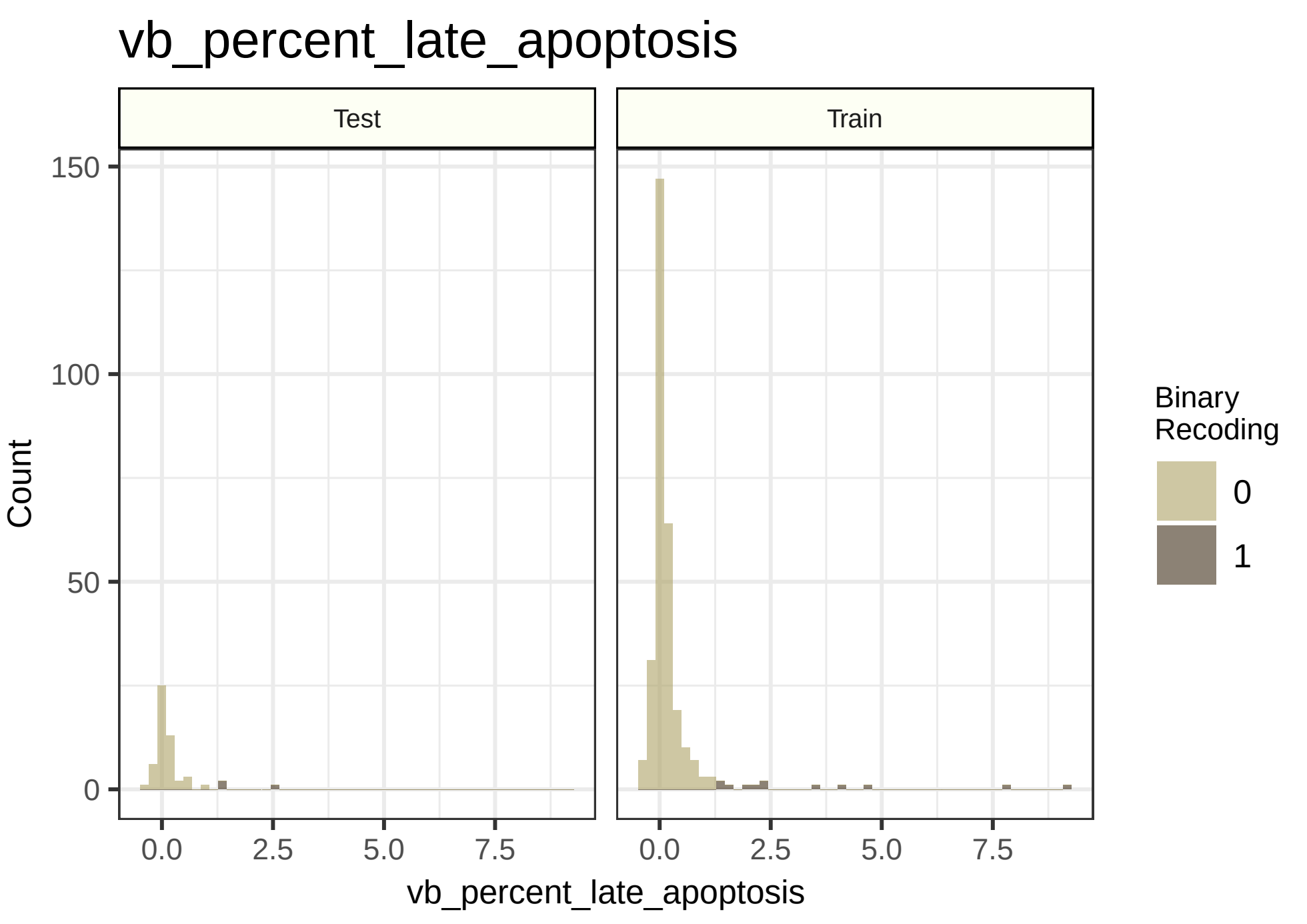

vb_percent_all_apoptosis
Test
Train
100
75
50
25
0
Count
0
2
4
6
8
vb_percent_all_apoptosis
Binary Recoding
0
1

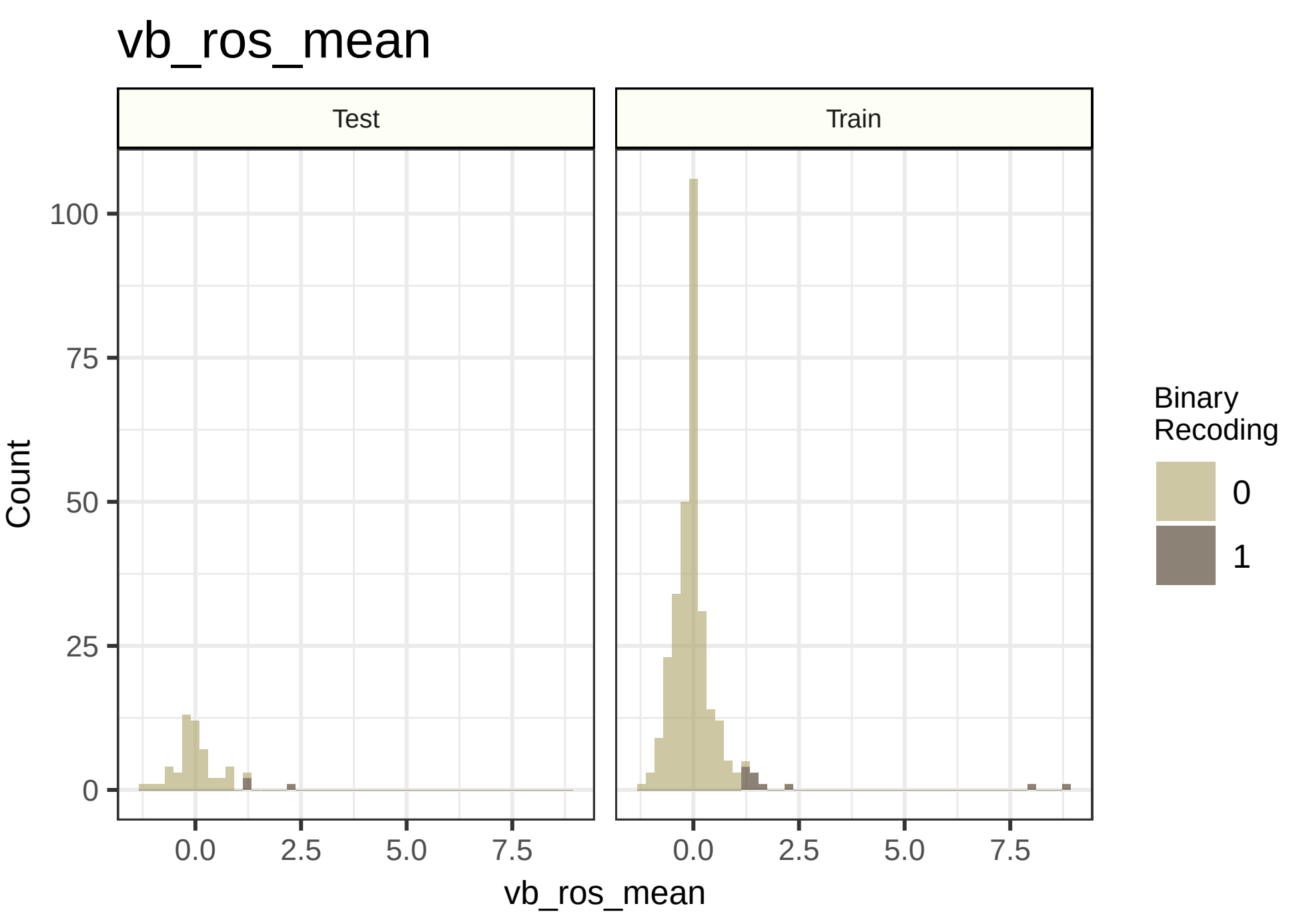

vb_percent_caspase_dead_only
Test
Train
Count
30
20
10
0
−1
0
1
2
3
vb_percent_caspase_dead_only
Binary Recoding
0
1


vb_percent_dead
Test
Train
150
100
50
0
Count
0.0
2.5
5.0
7.5
vb_percent_dead
Binary Recoding
0
1


vb_percent_dead_only
Test
Train
80
60
40
20
0
Count
0
2
4
0
2
4
vb_percent_dead_only
Binary
Recoding
0
1


vb_percent_early_apoptosis
Test
Train
Count
60
40
20
0
−1
0
1
2
3
4
5
vb_percent_early_apoptosis
Binary Recoding
0
1


vb_percent_late_apoptosis
Test
Train
150
100
50
0
Count
0.0
2.5
5.0
7.5
vb_percent_late_apoptosis
Binary Recoding
0
1


vb_ros_mean
Test
Train
100
75
50
25
0
Count
0.0
2.5
5.0
7.5
vb_ros_mean
Binary Recoding
0
1