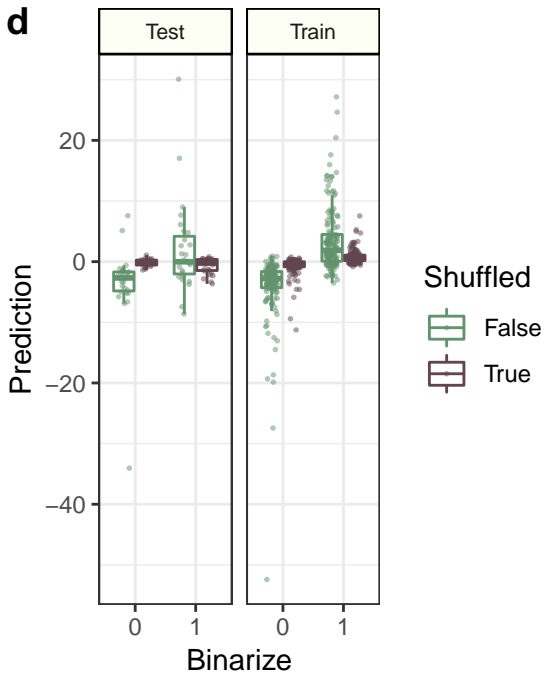
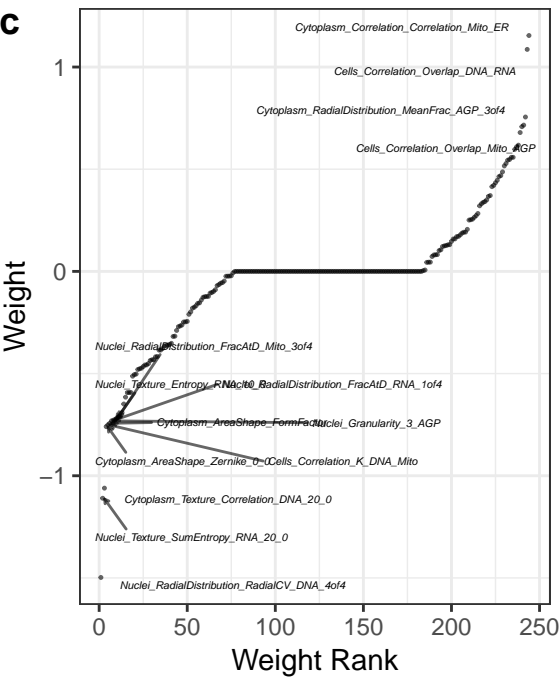
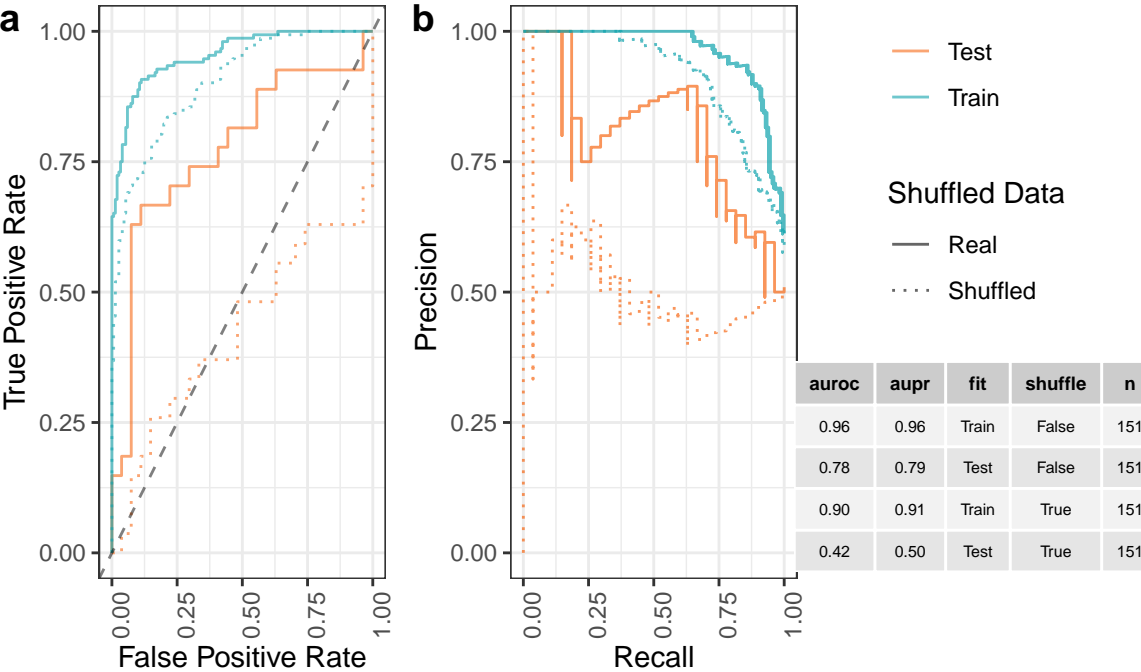
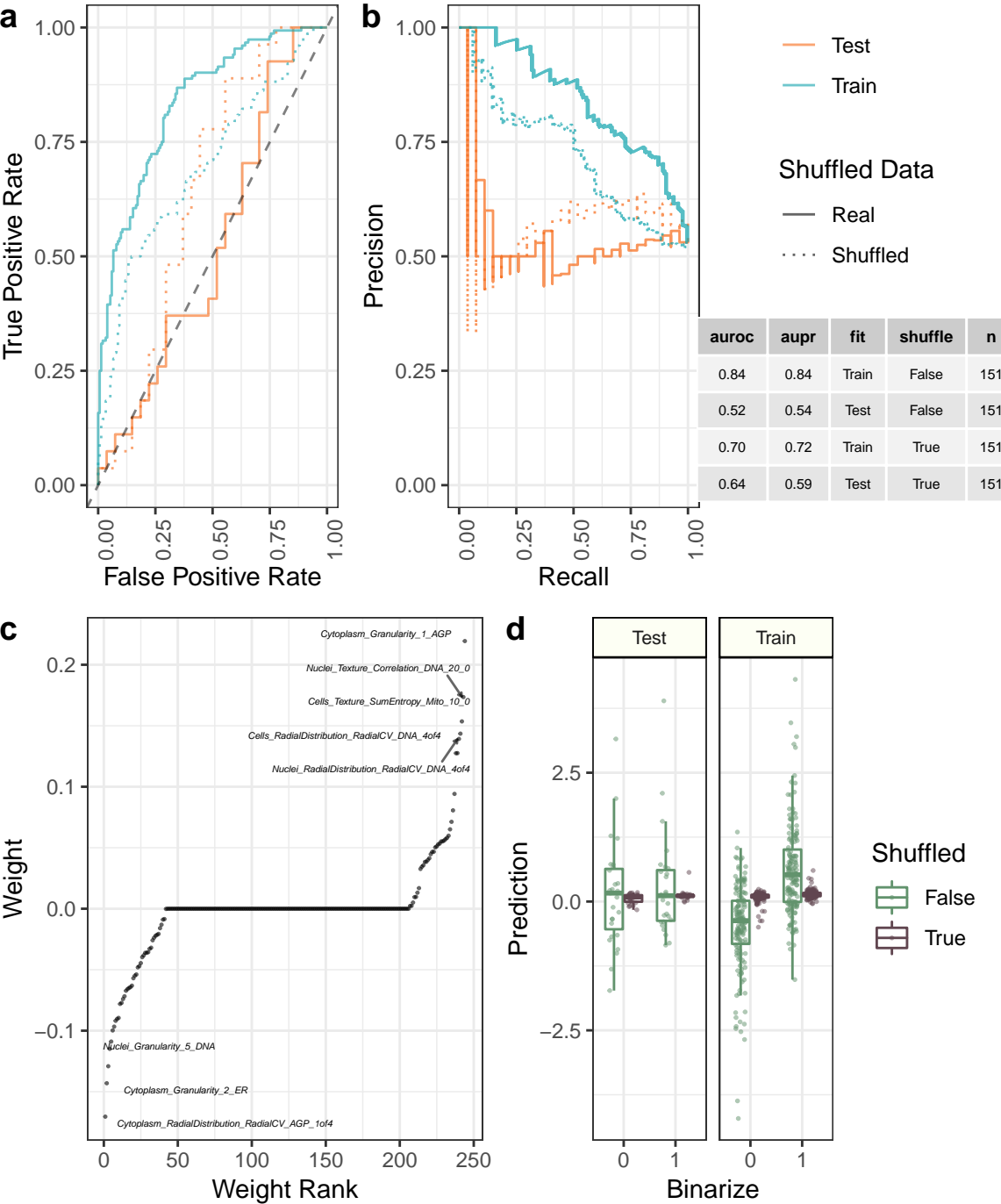


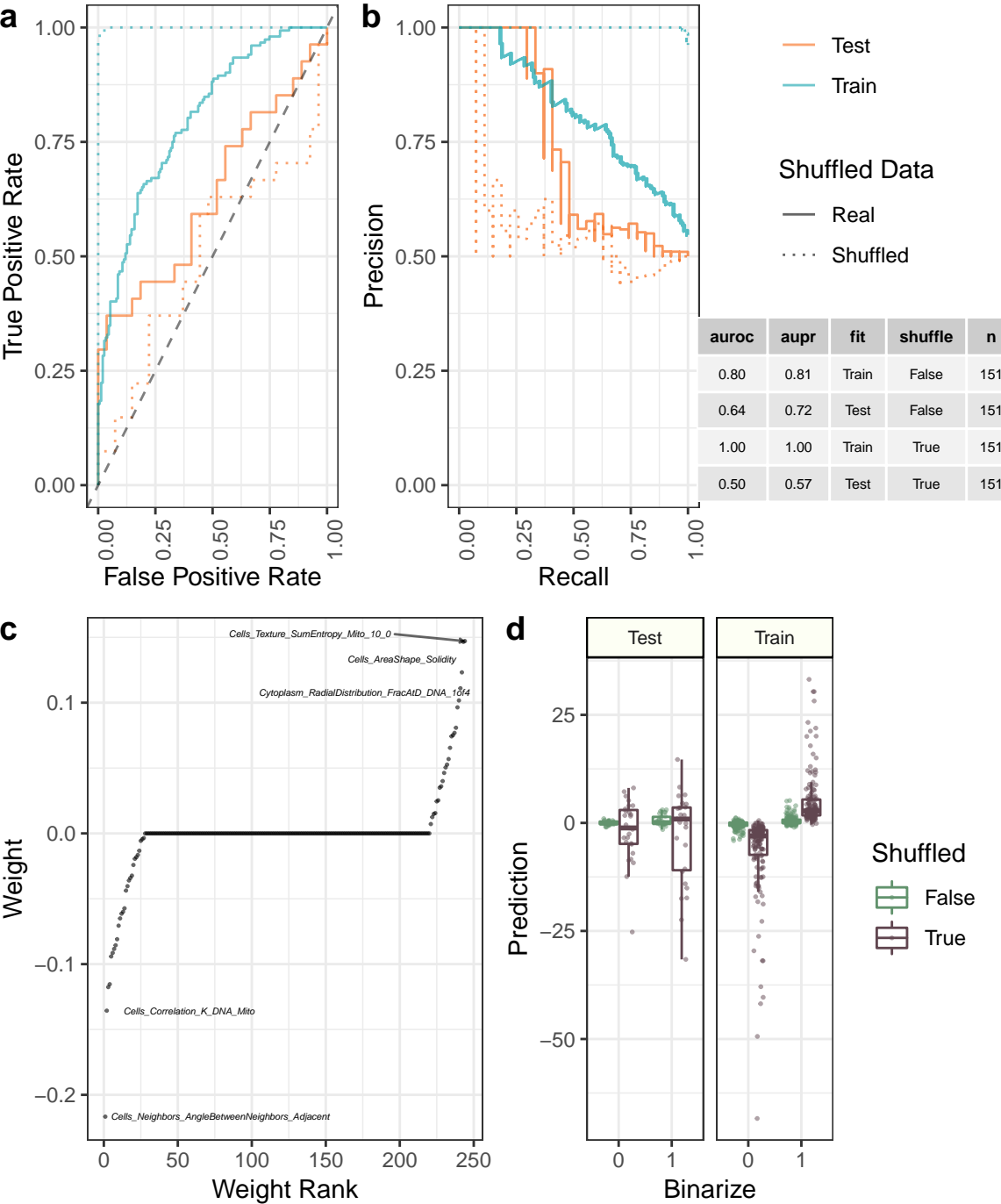
Performance: cc_all_high_n_spots_h2ax_mean



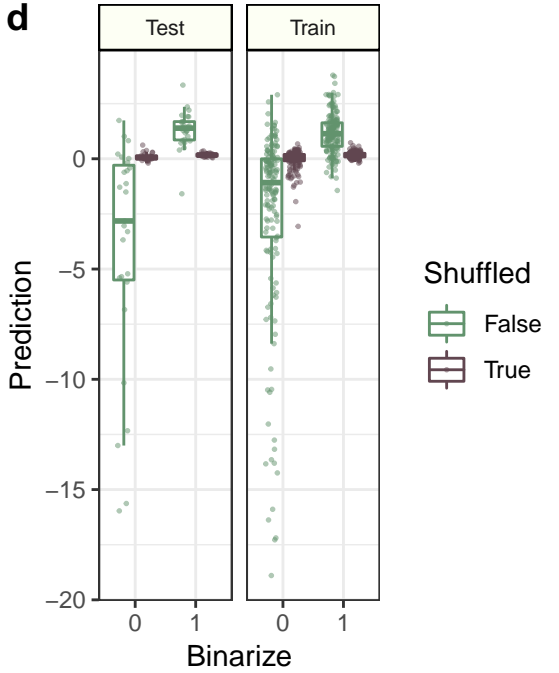
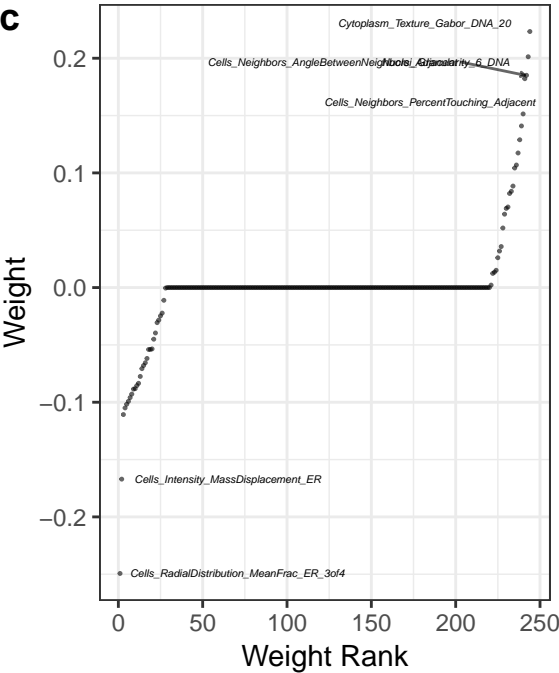
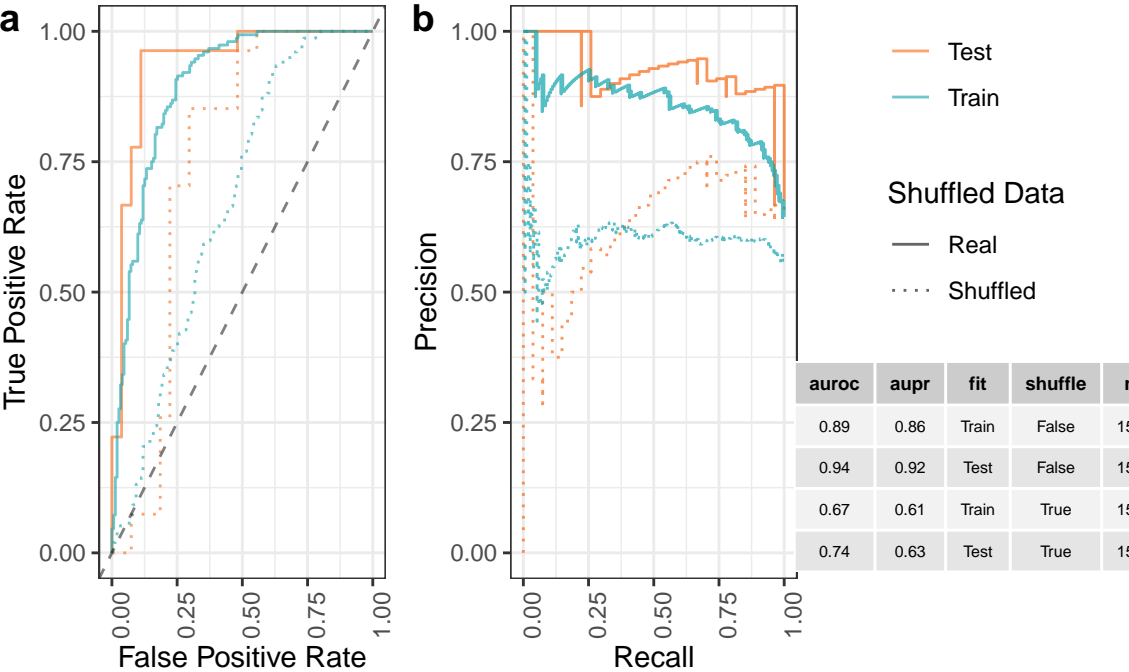
Performance: cc_all_large_notround_polynuclear_mean



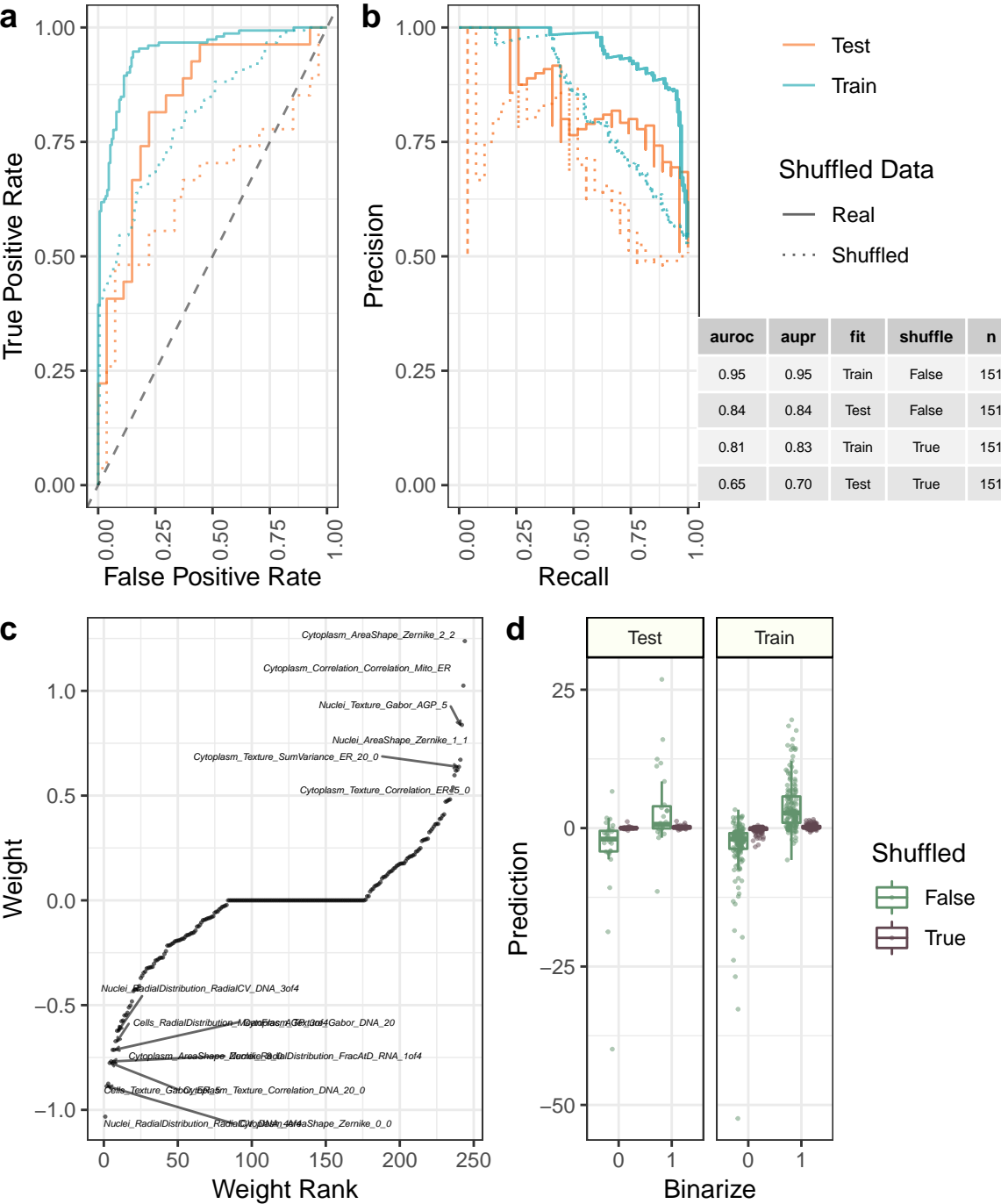
Performance: cc_all_large_round_polyloid_mean



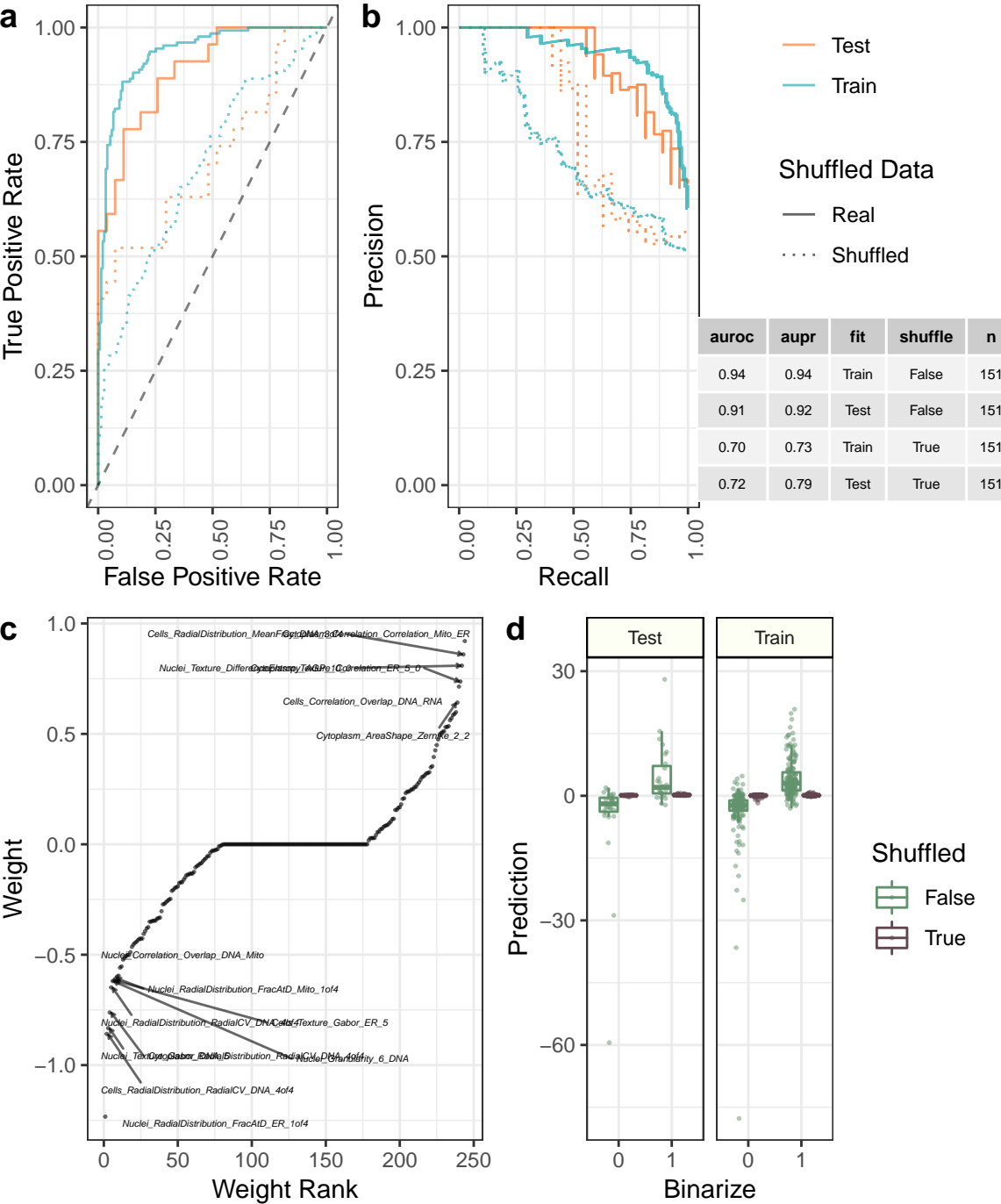
Performance: cc_all_n_objects



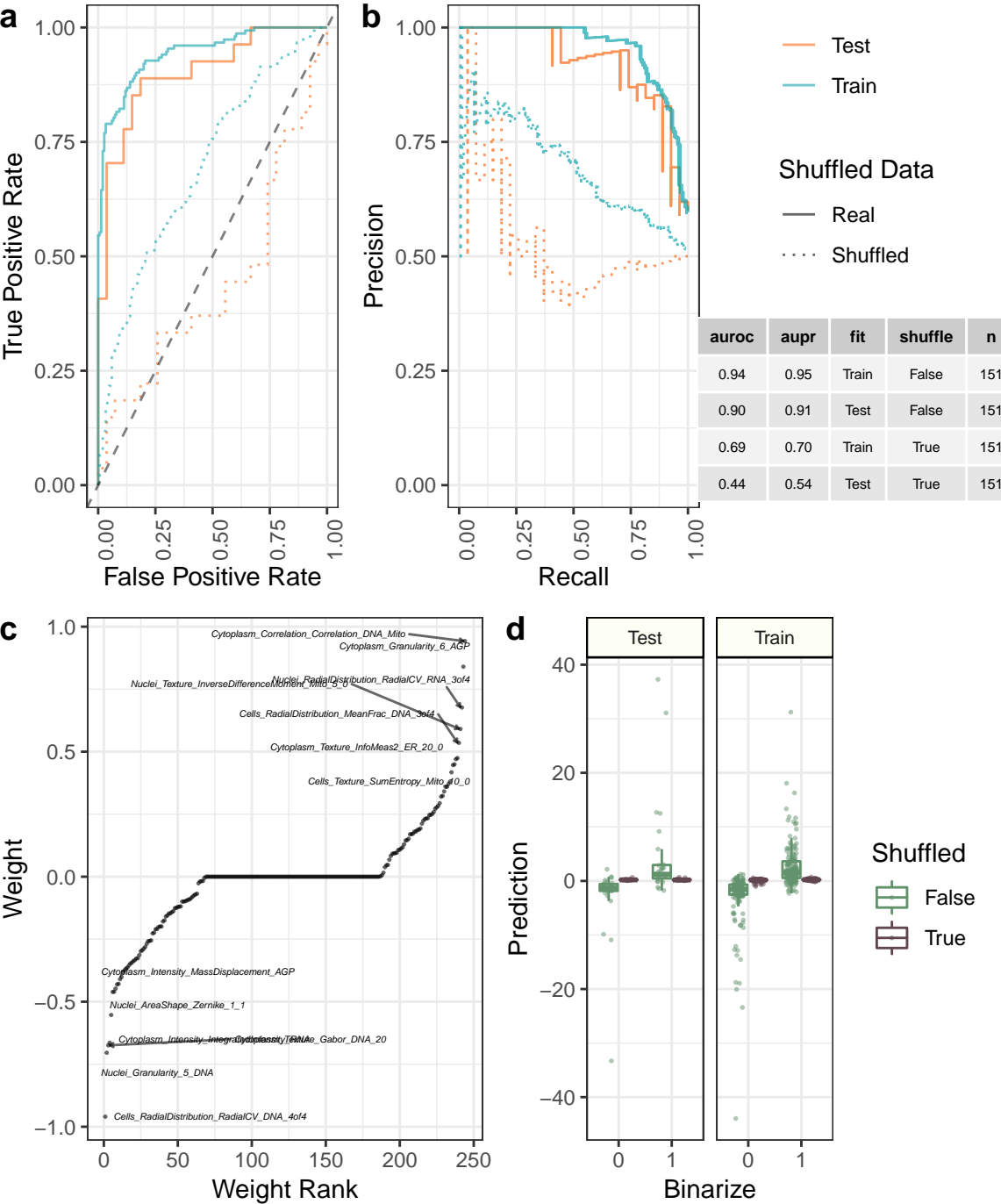
Performance: cc_all_n_spots_mean



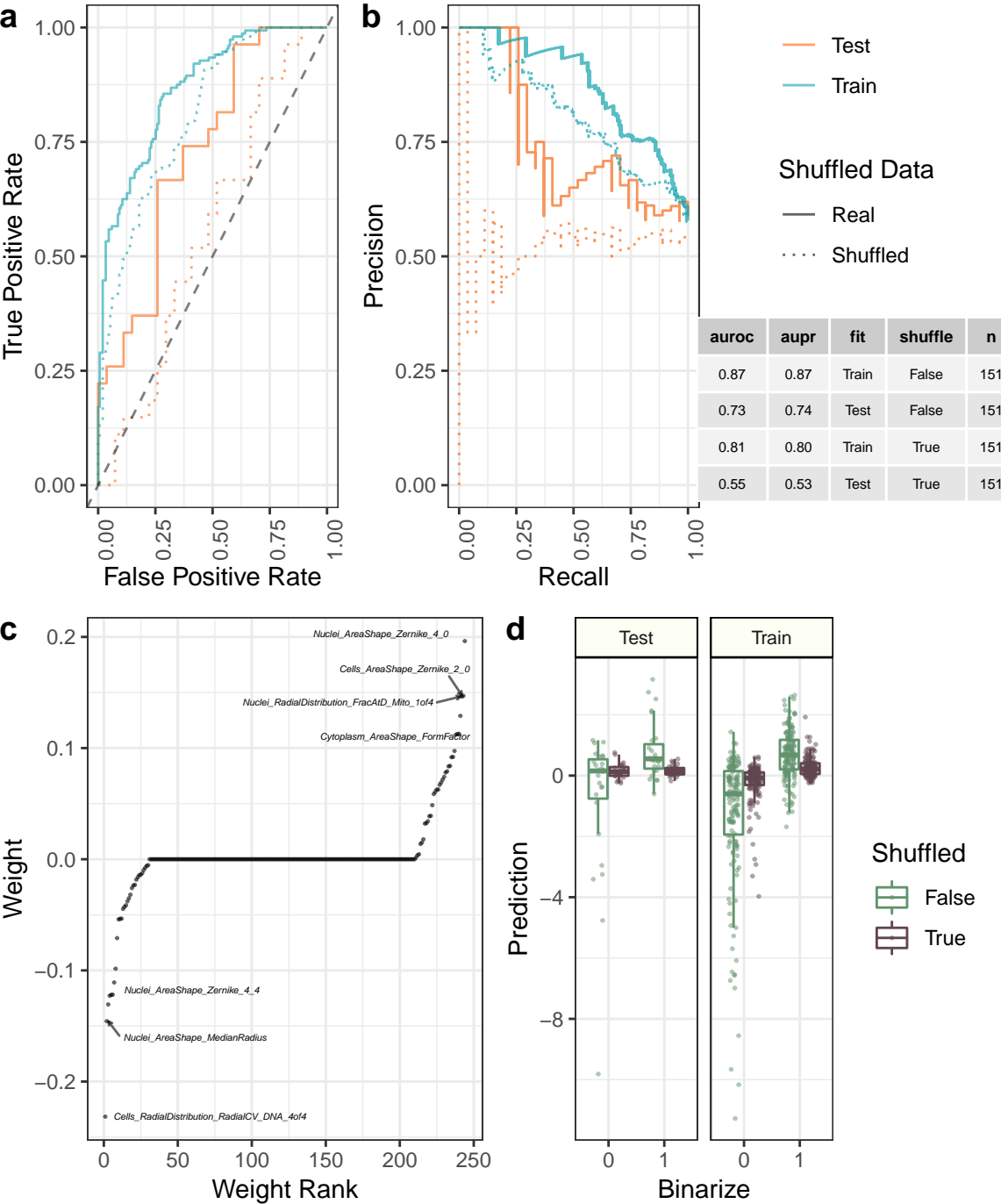
Performance: cc_all_n_spots_per_nucleus_area_mean



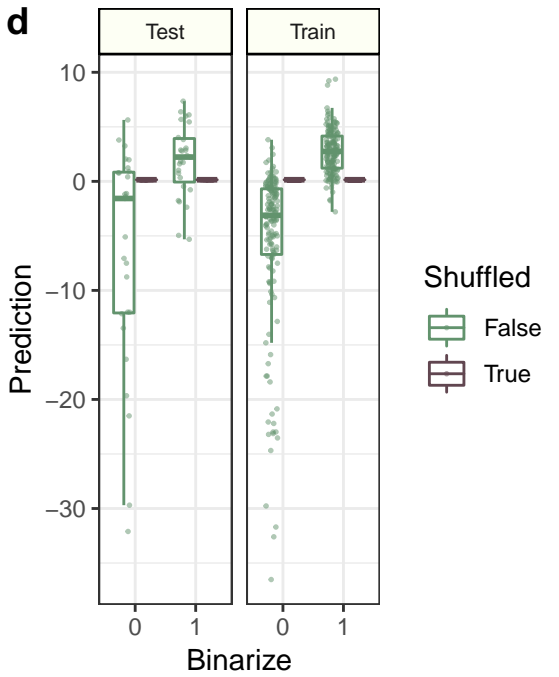
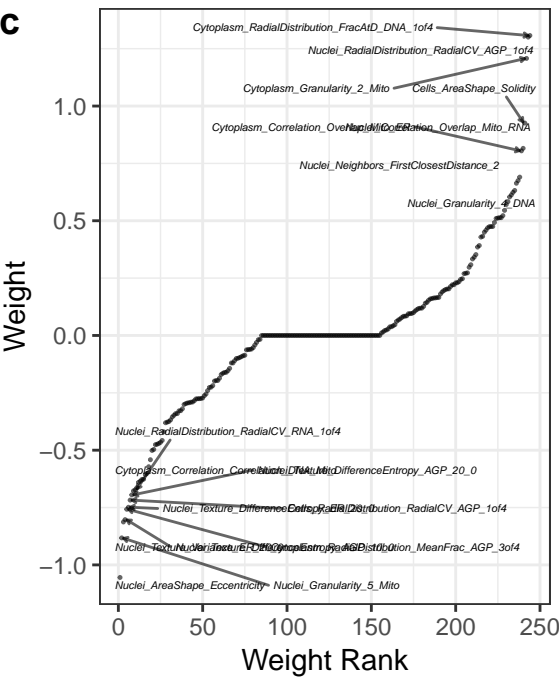
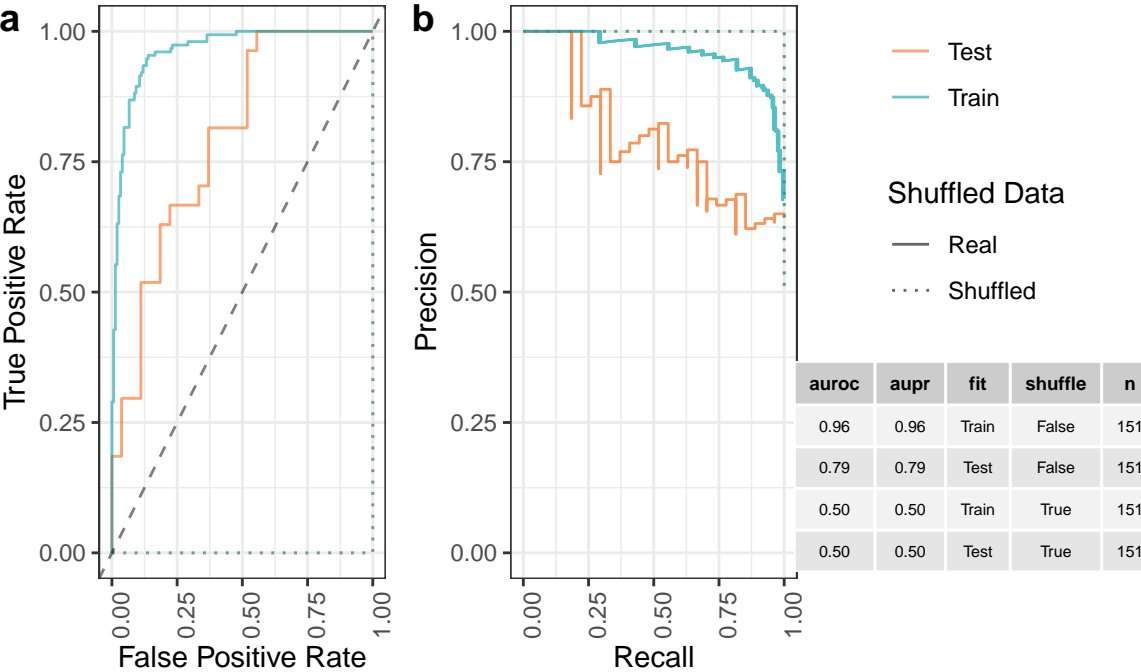
Performance: cc_all_nucleus_area_mean



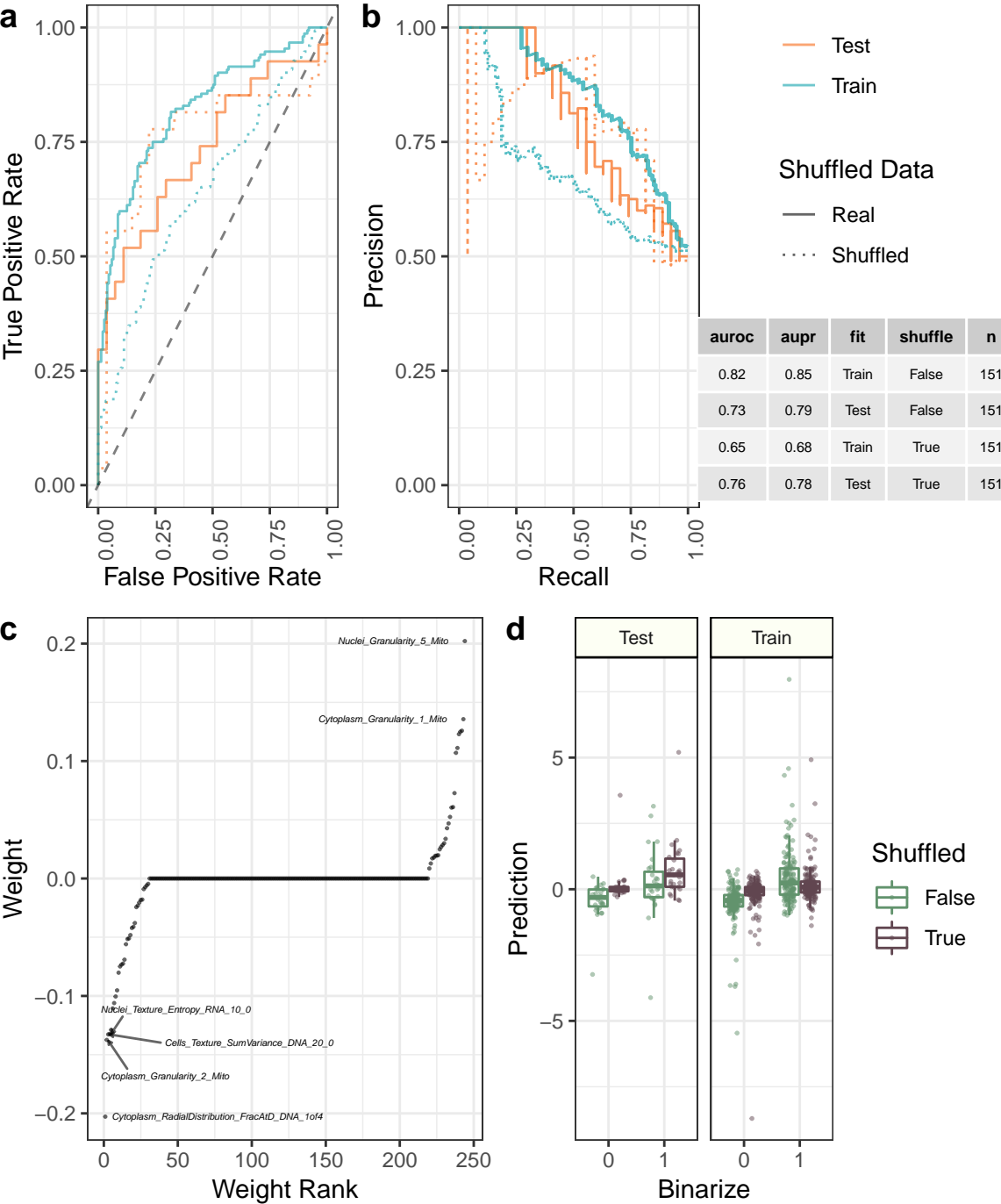
Performance: cc_all_nucleus_roundness_mean



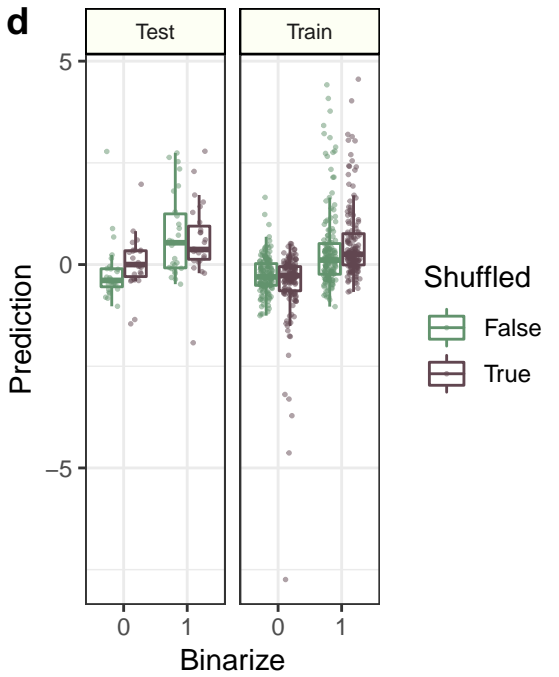
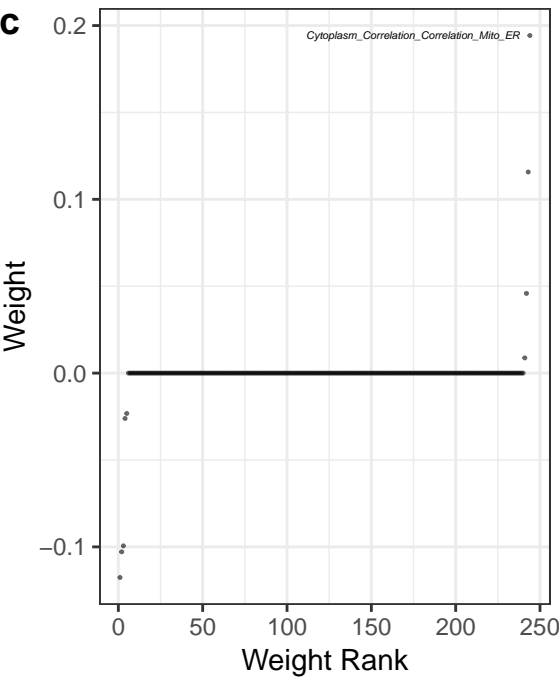
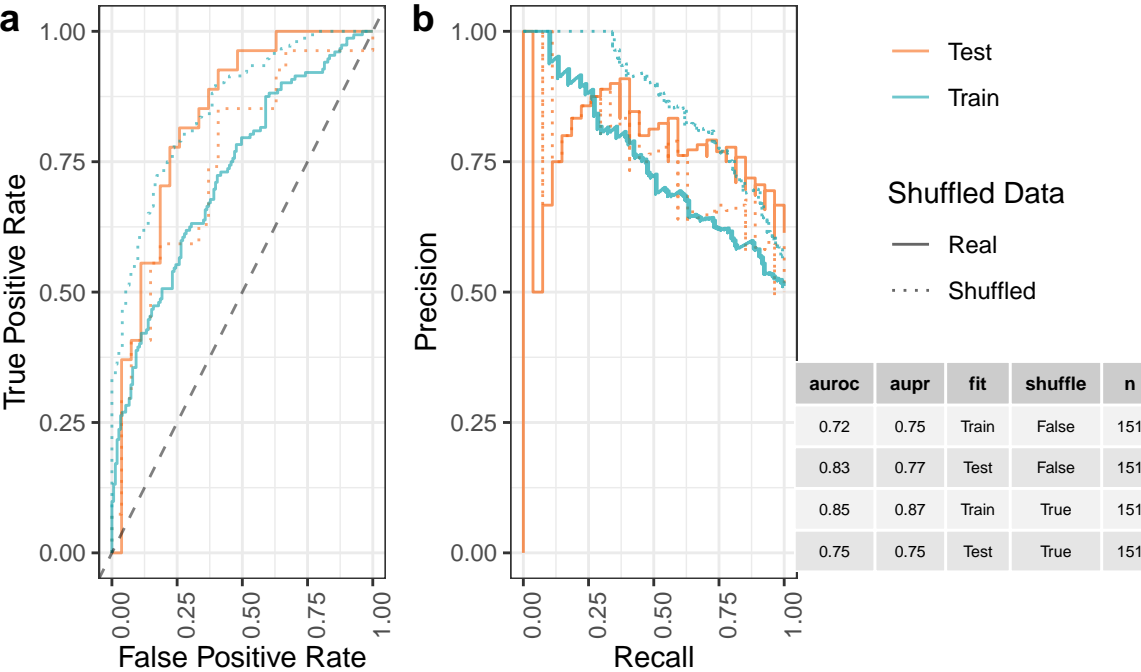
Performance: cc_cc_edu_pos_mean



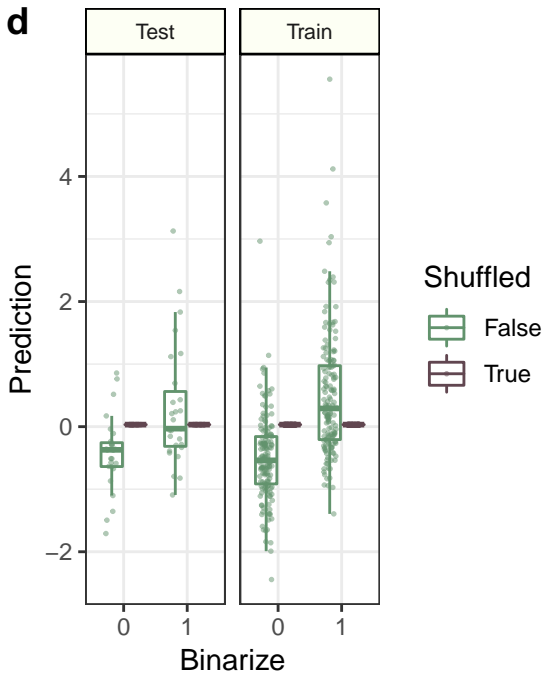
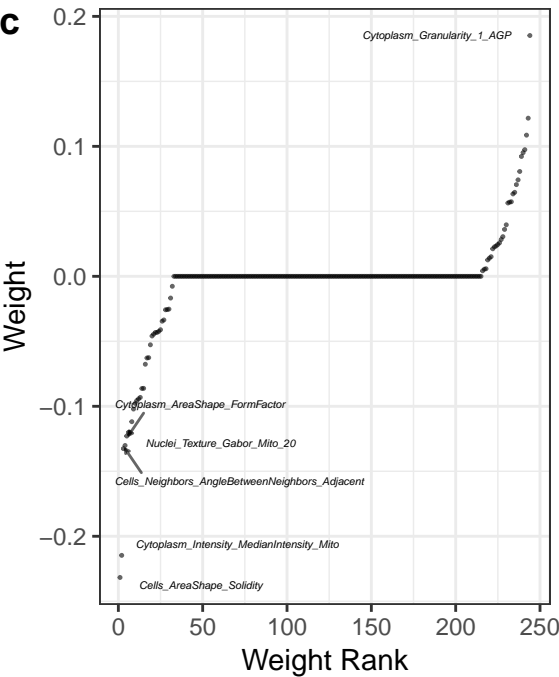
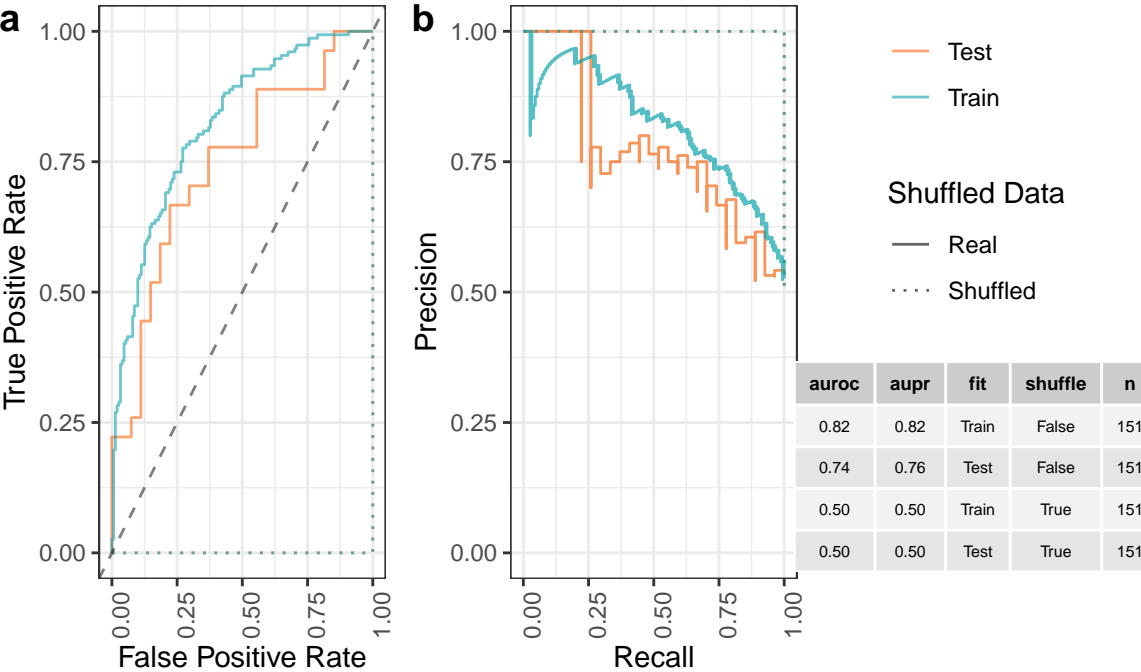
Performance: cc_cc_g1_mean



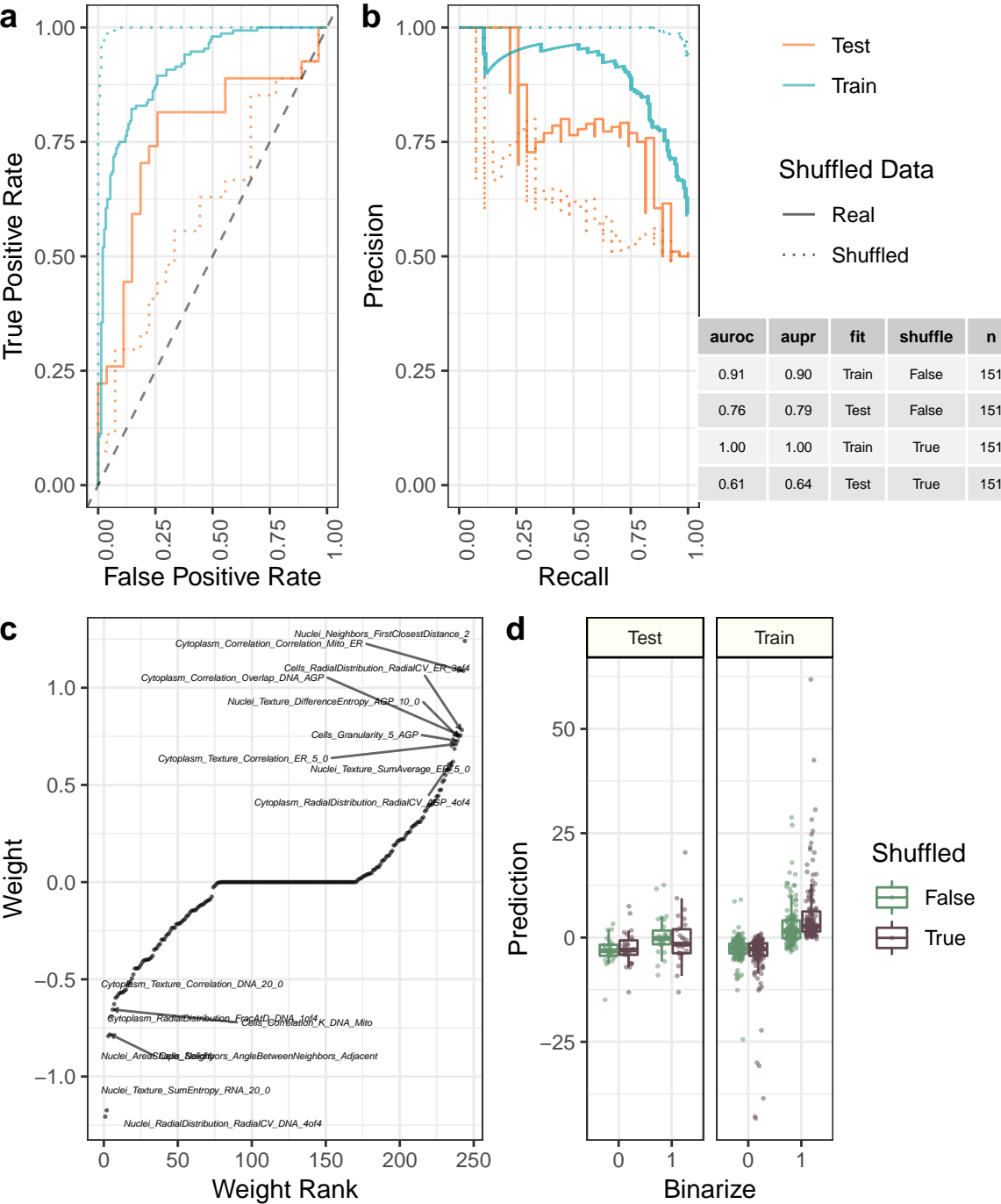
Performance: cc_cc_g2_ph3_neg_mean



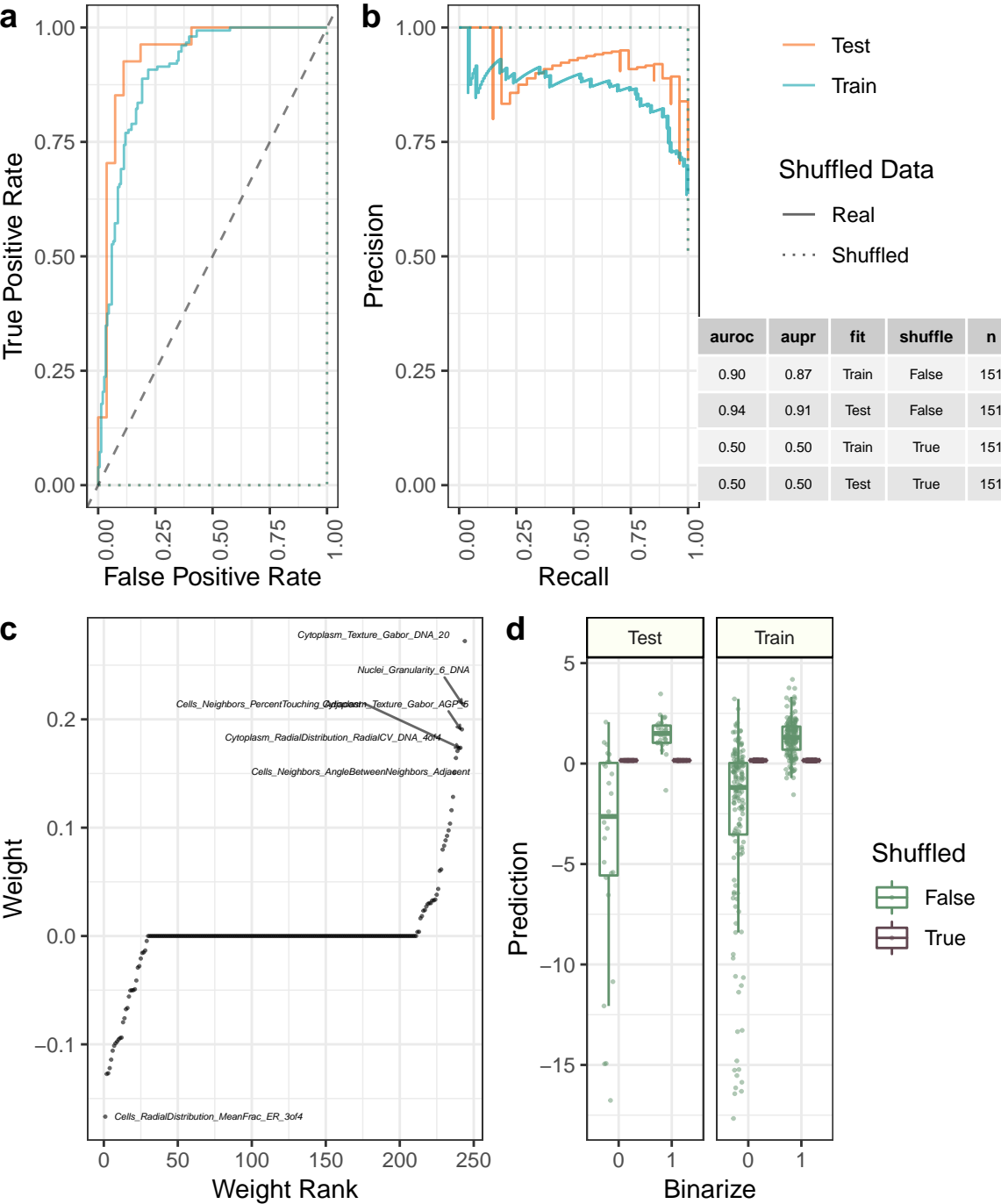
Performance: cc_cc_g2_ph3_pos_early_mitosis_mean



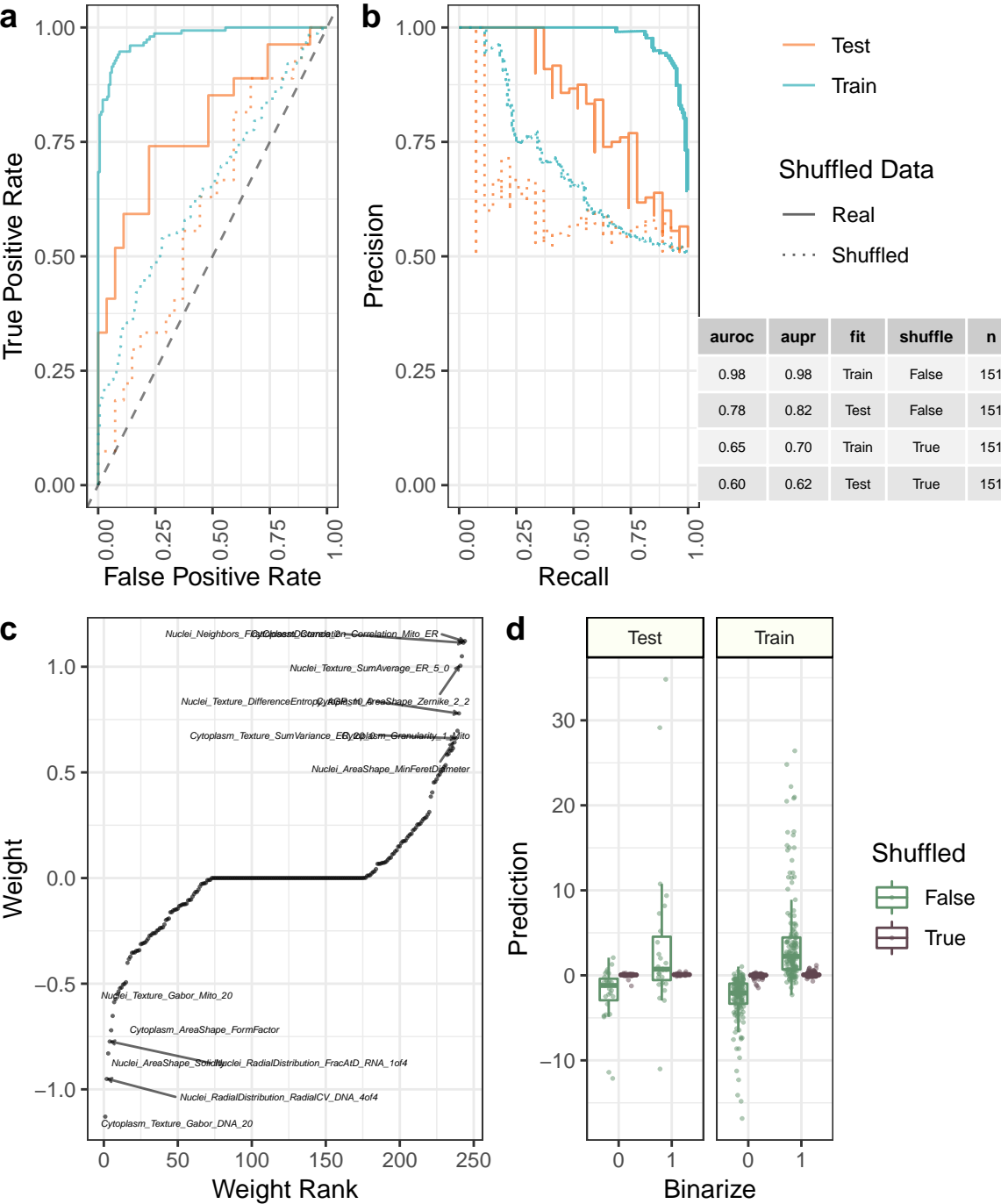
Performance: cc_cc_high_n_spots_h2ax_mean



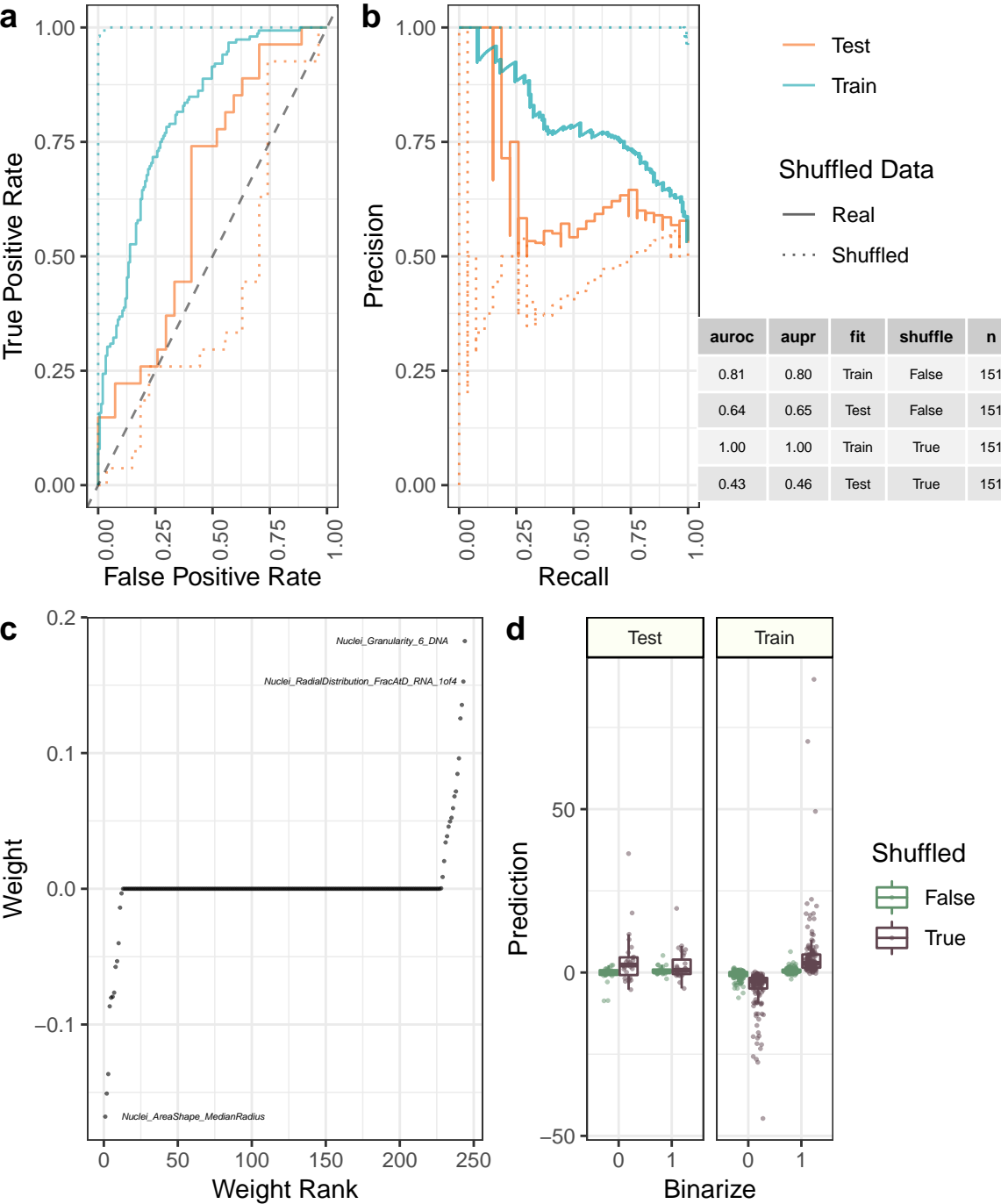
Performance: cc_cc_n_objects



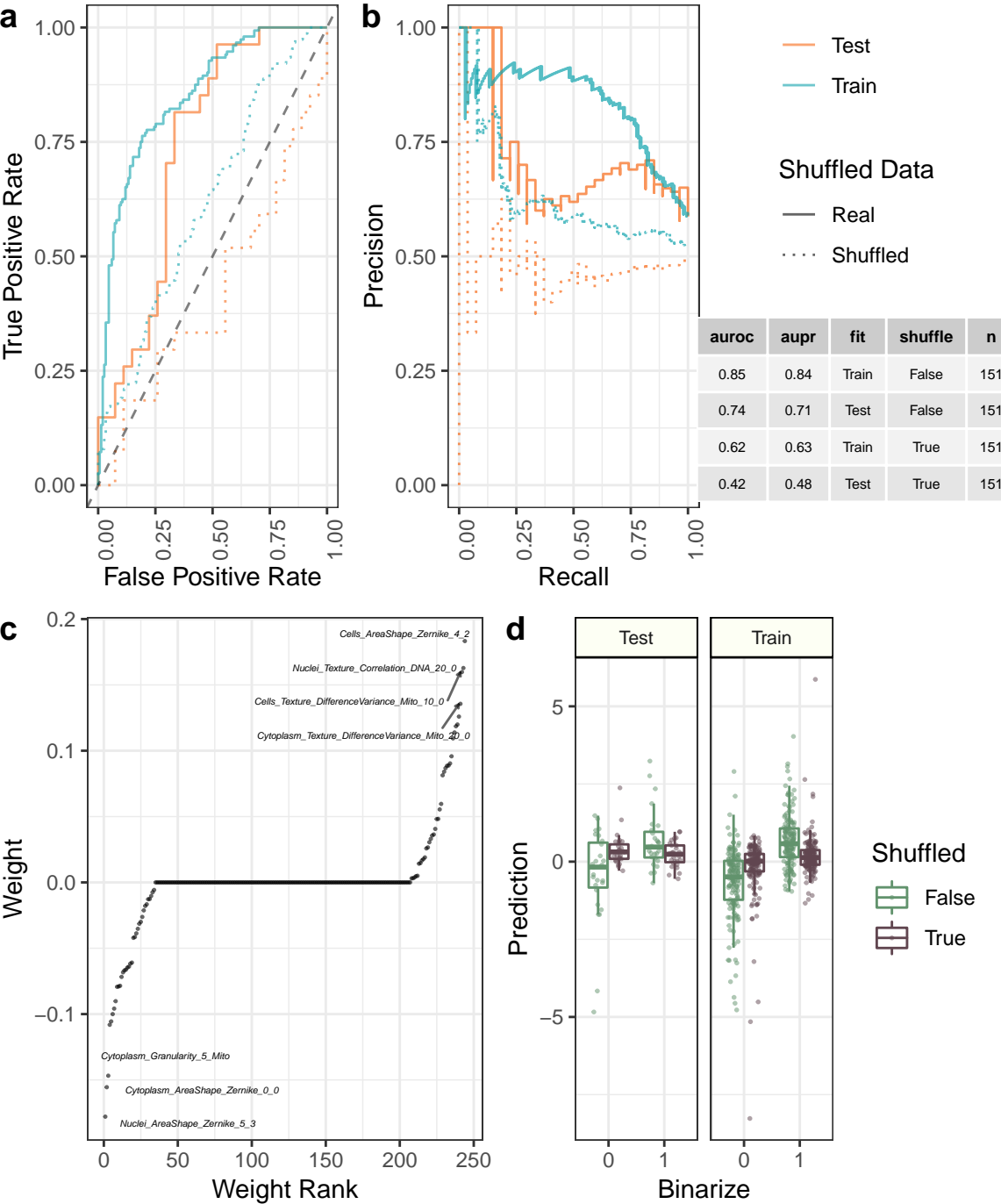
Performance: cc_cc_n_spots_mean



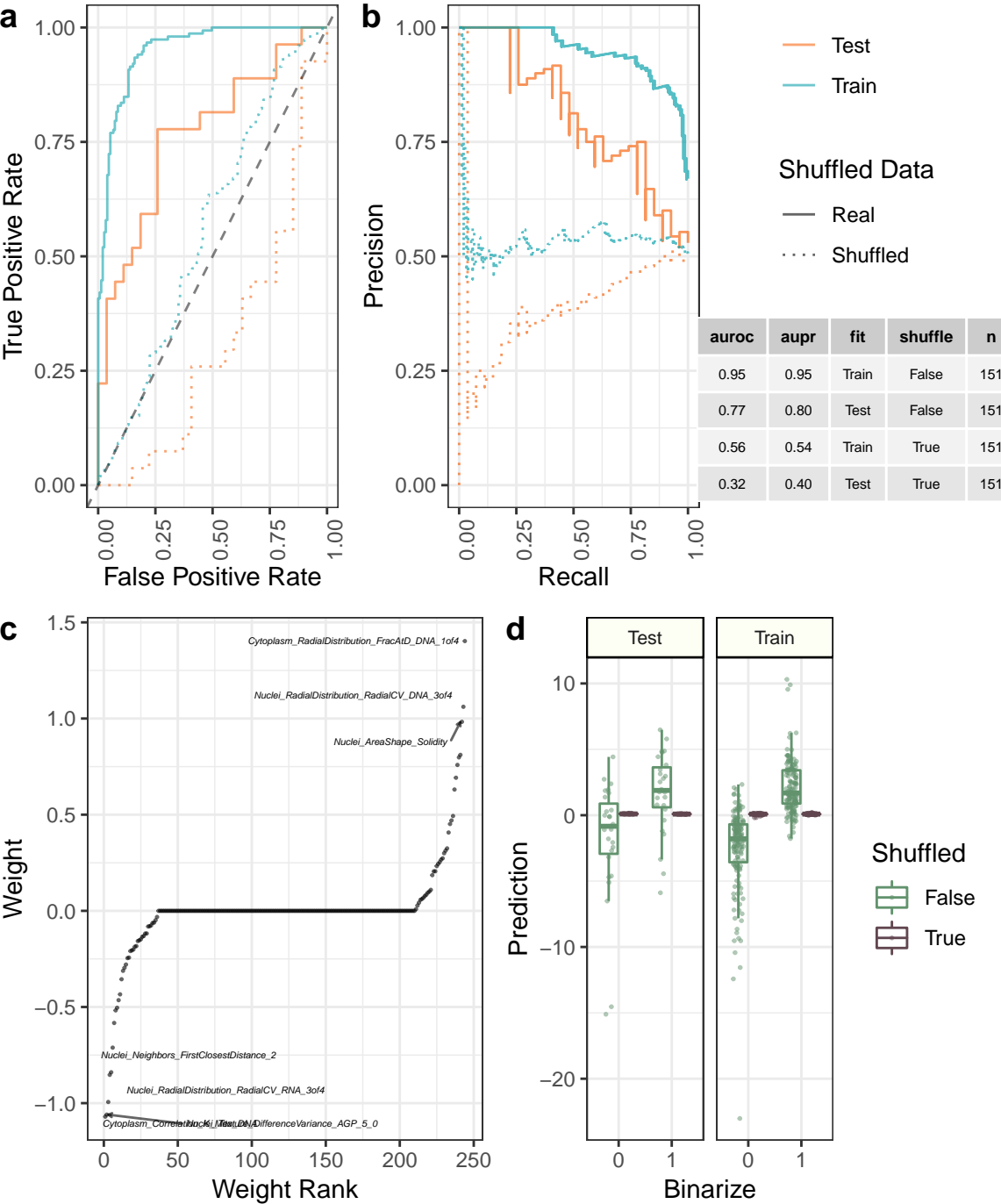
Performance: cc_cc_ph3_neg_hoechst_late_mitosis_mean



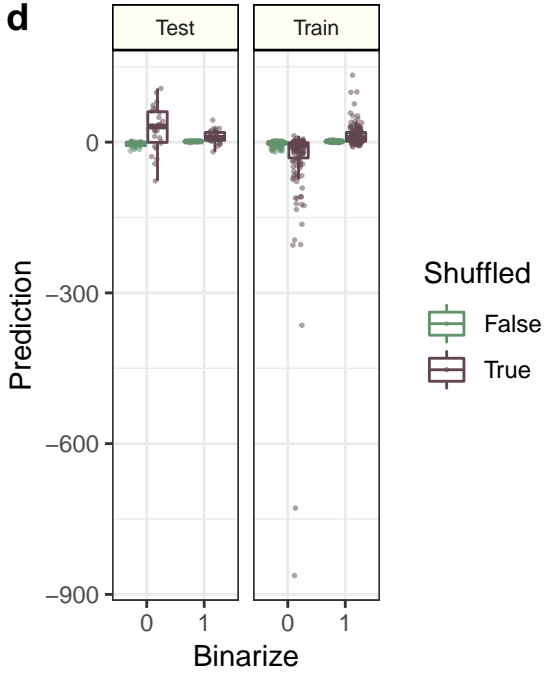
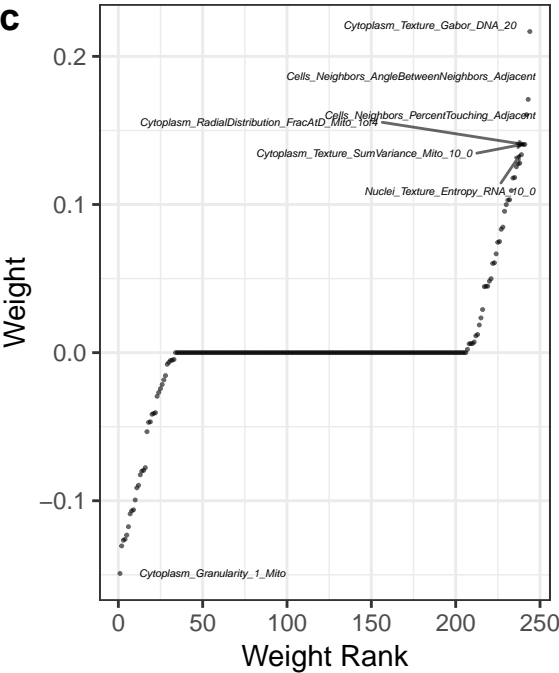
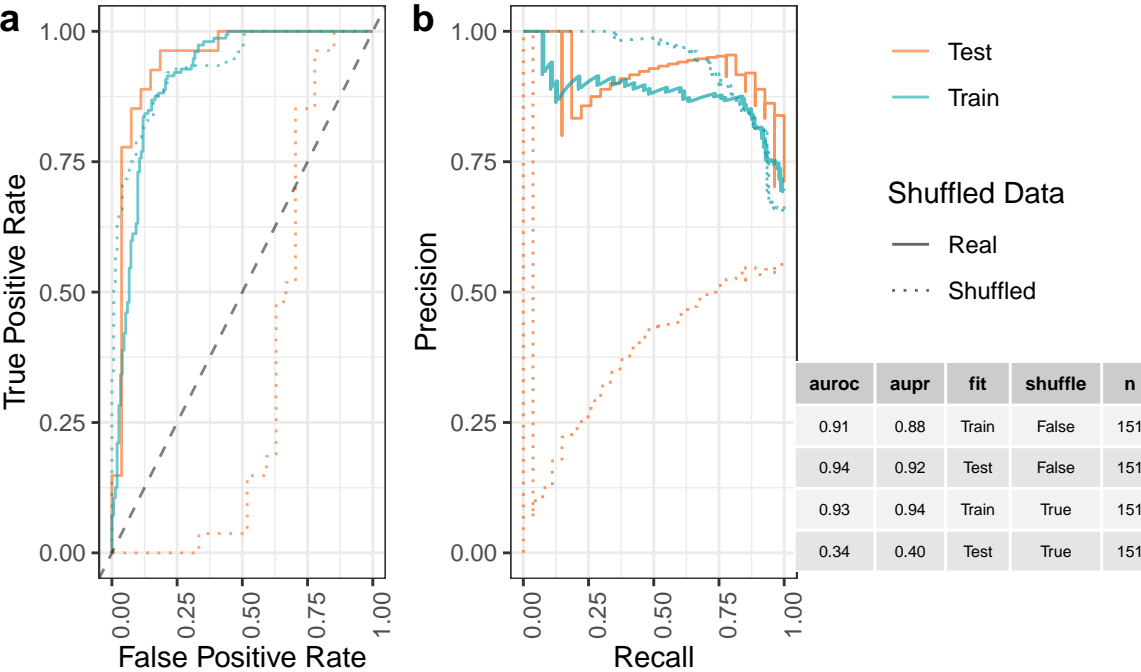
Performance: cc_cc_ph3_pos_hoechst_mitosis_mean



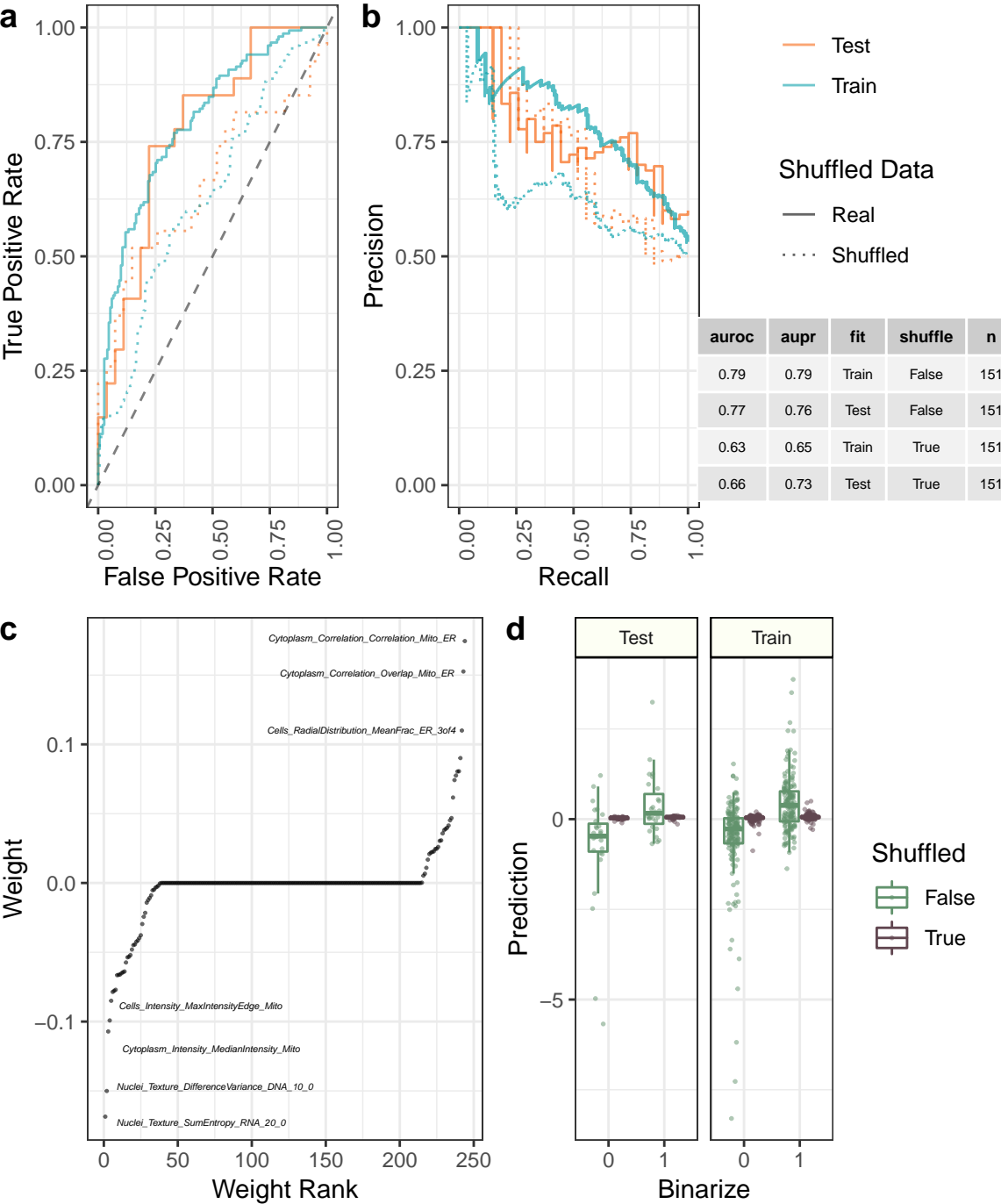
Performance: cc_edu_pos_alexa647_intensity_nucleus_area_m



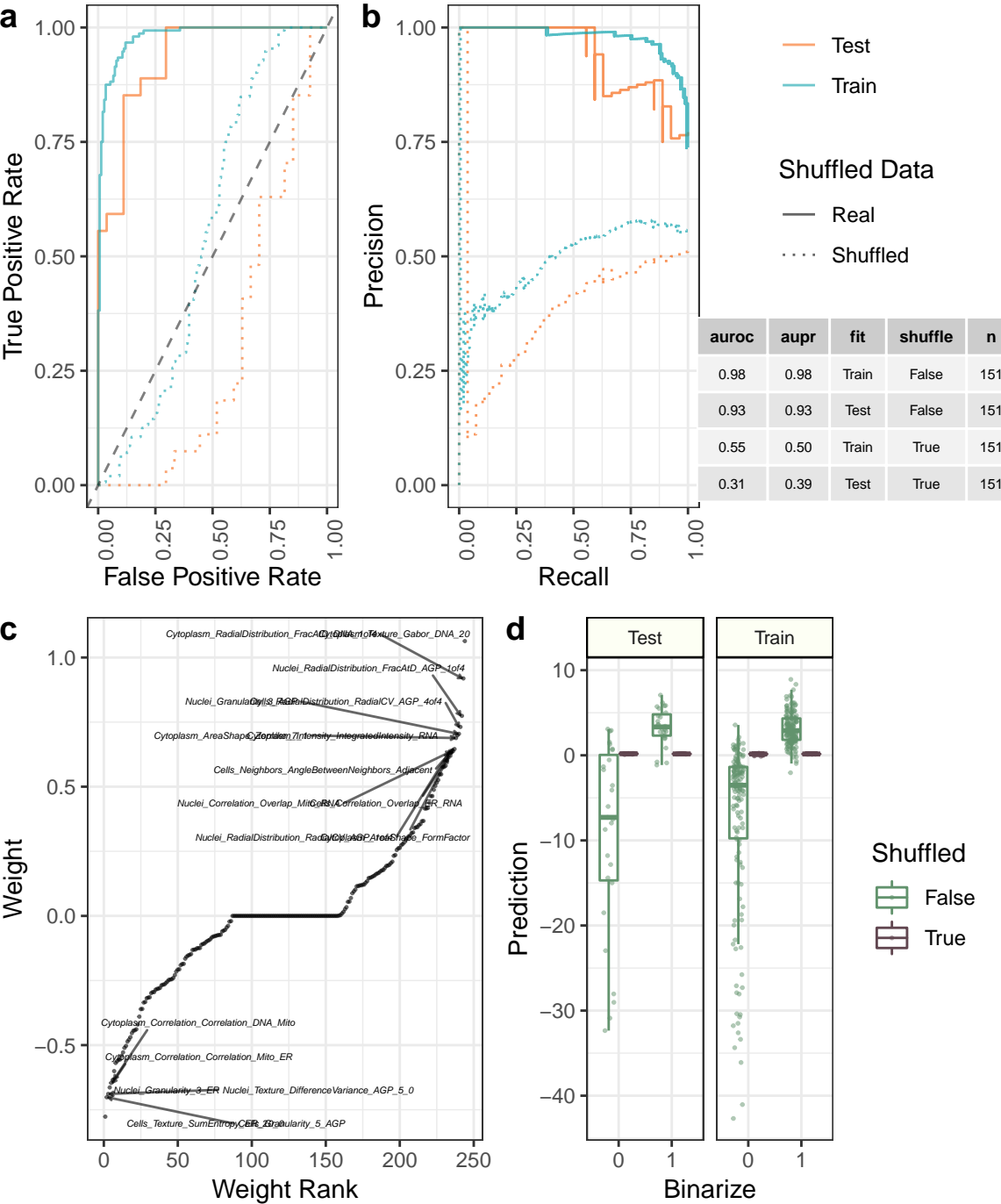
Performance: cc_edu_pos_alexa647_intensity_nucleus_area_su



Performance: cc_edu_pos_high_n_spots_h2ax_mean



Performance: cc_edu_pos_n_objects



c

Weight

Weight Rank

d

Prediction

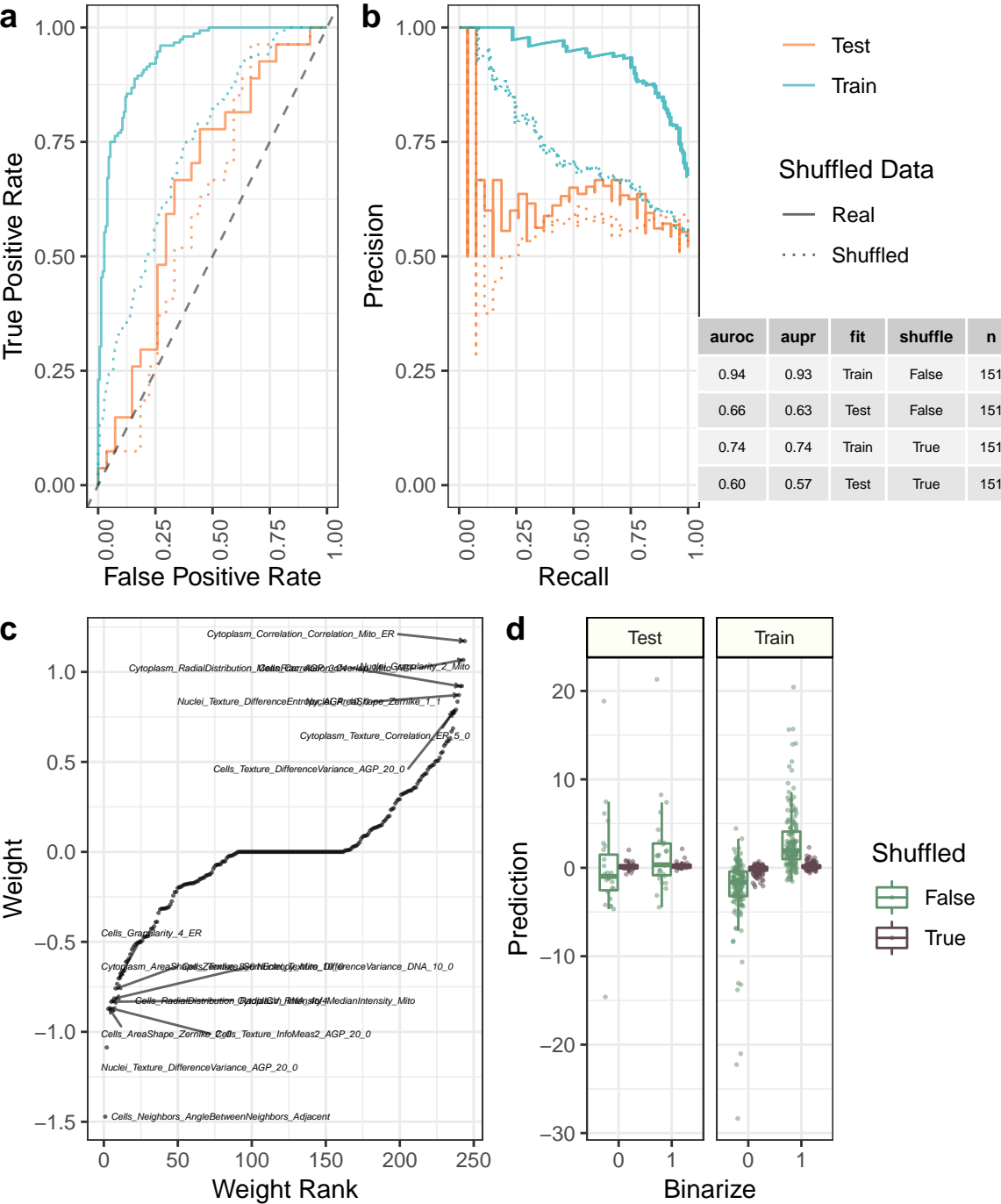
Binarize

Shuffled

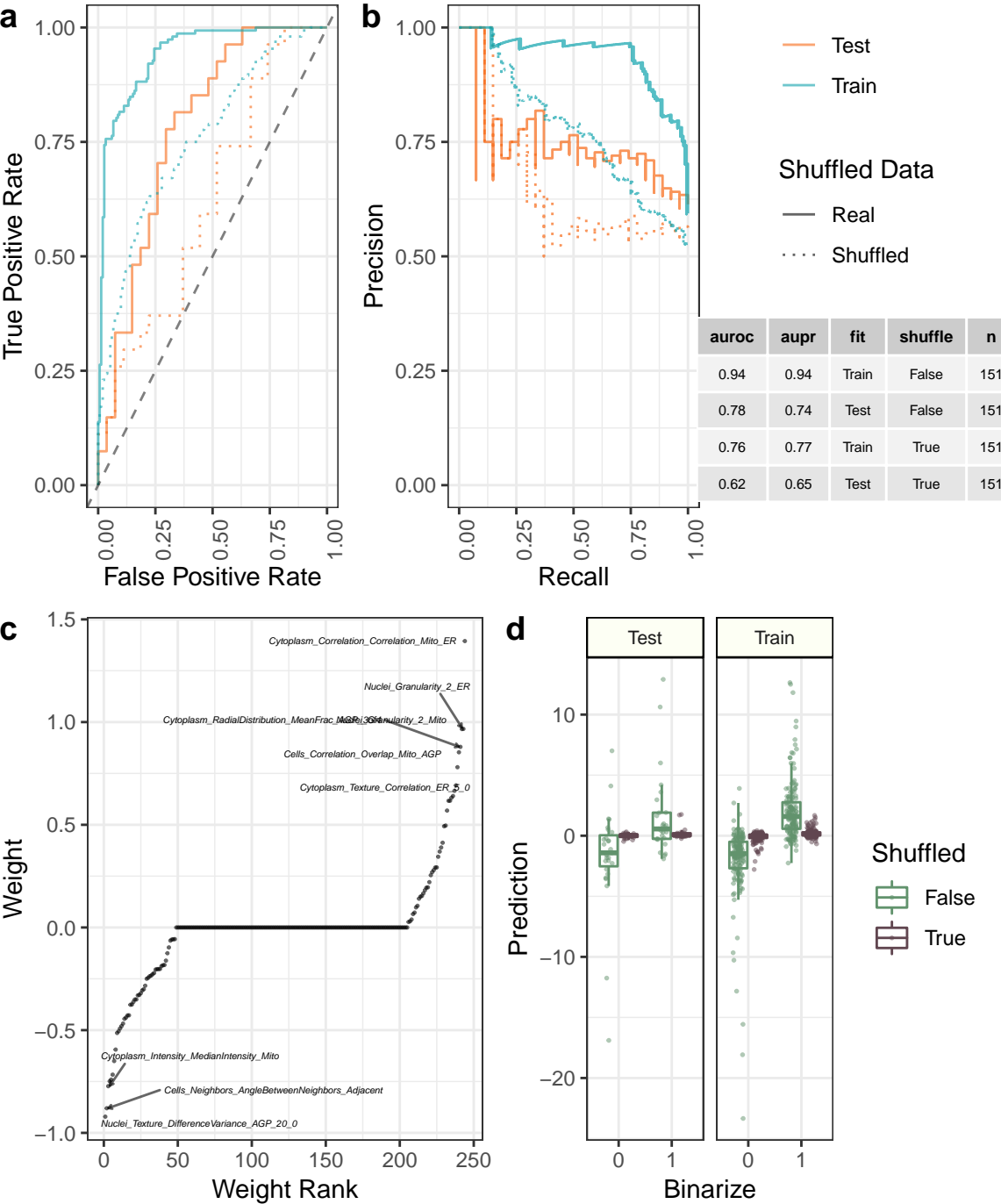
False

True

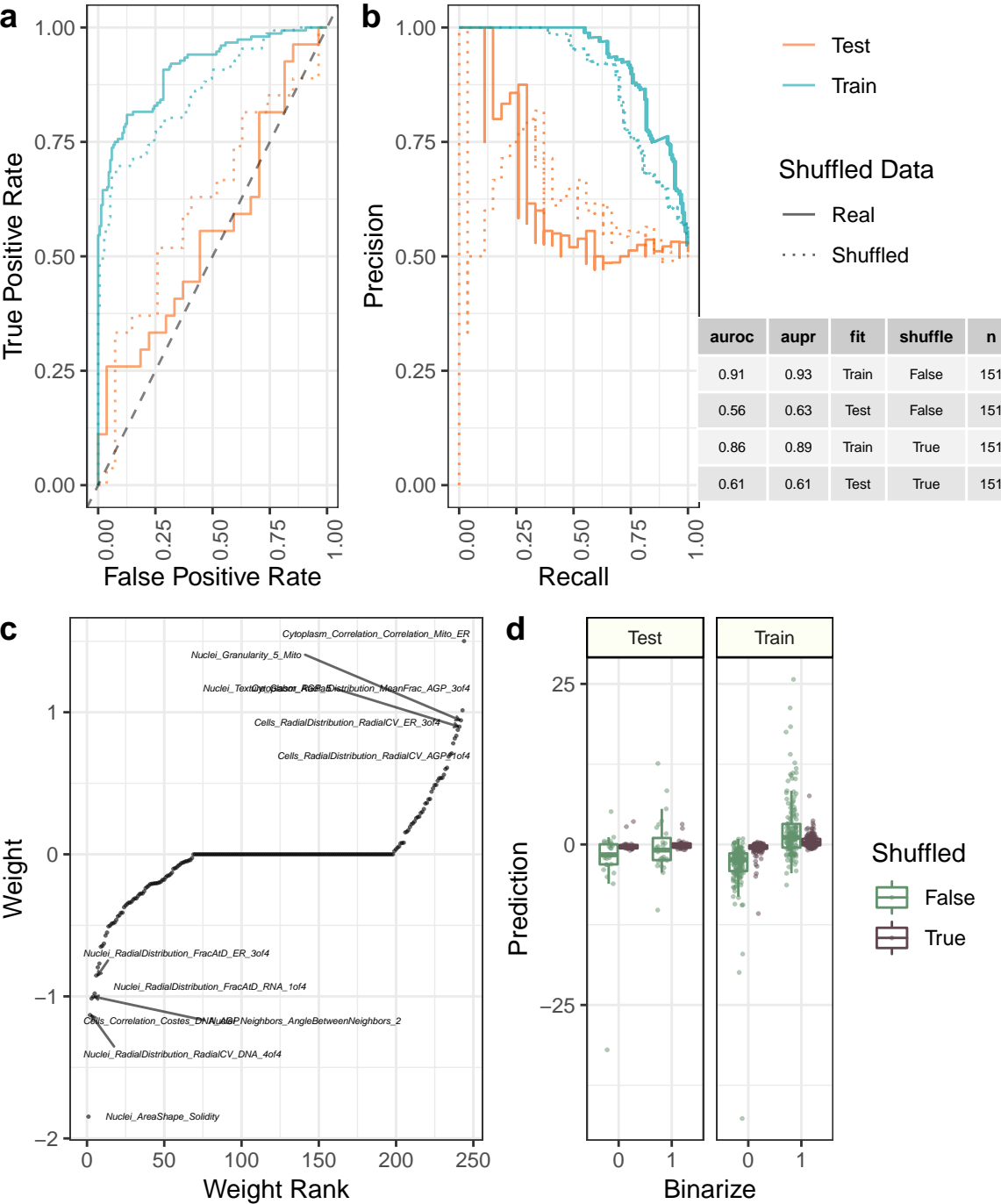
Performance: cc_edu_pos_n_spots_mean



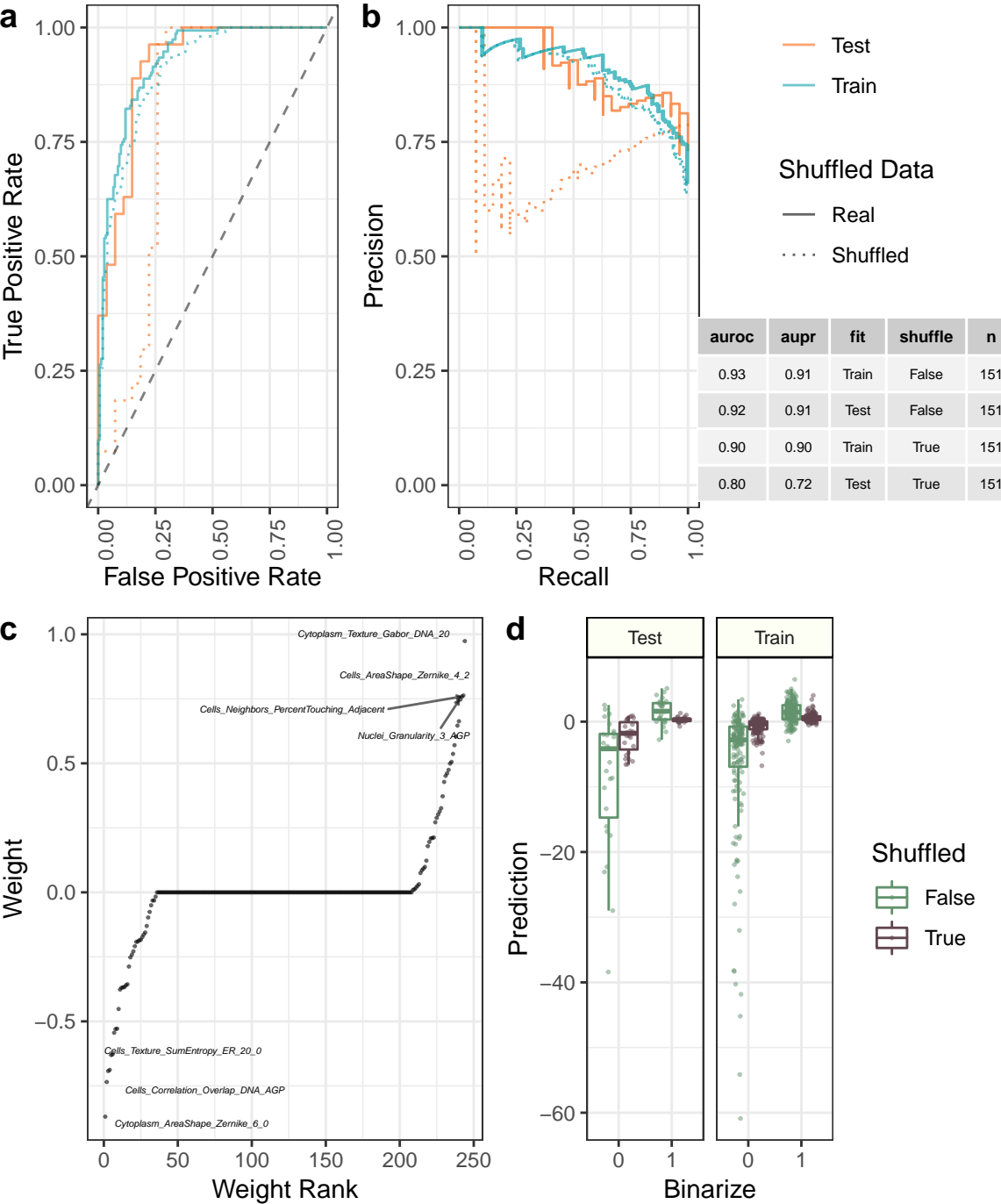
Performance: cc_edu_pos_n_spots_per_nucleus_area_mean



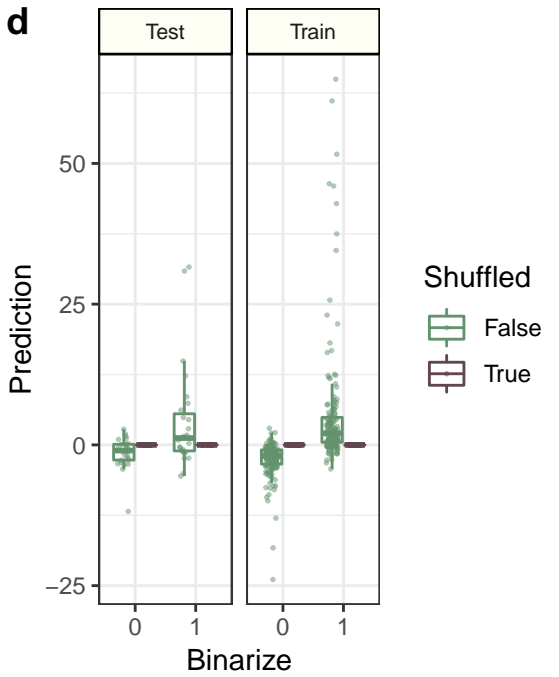
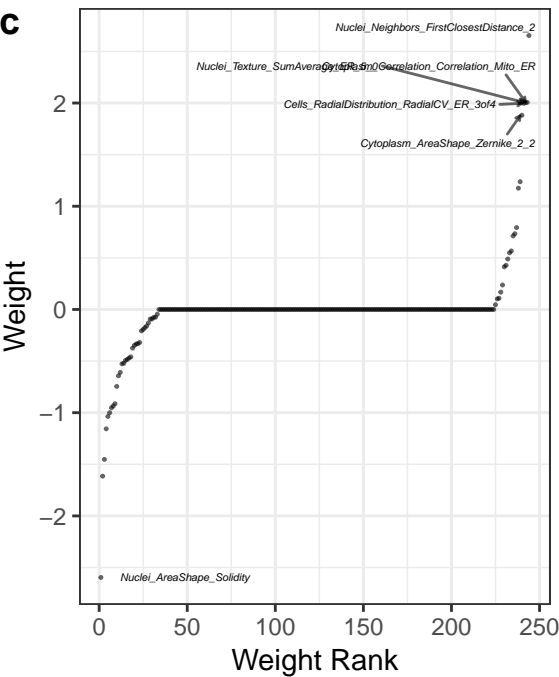
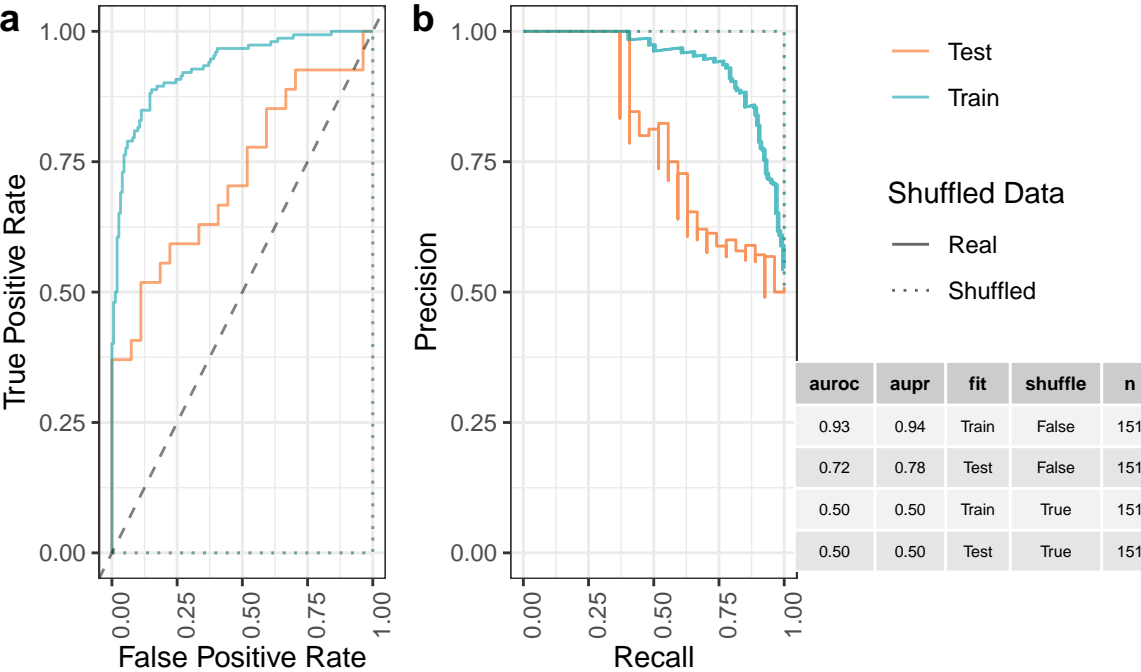
Performance: cc_g1_high_n_spots_h2ax_mean



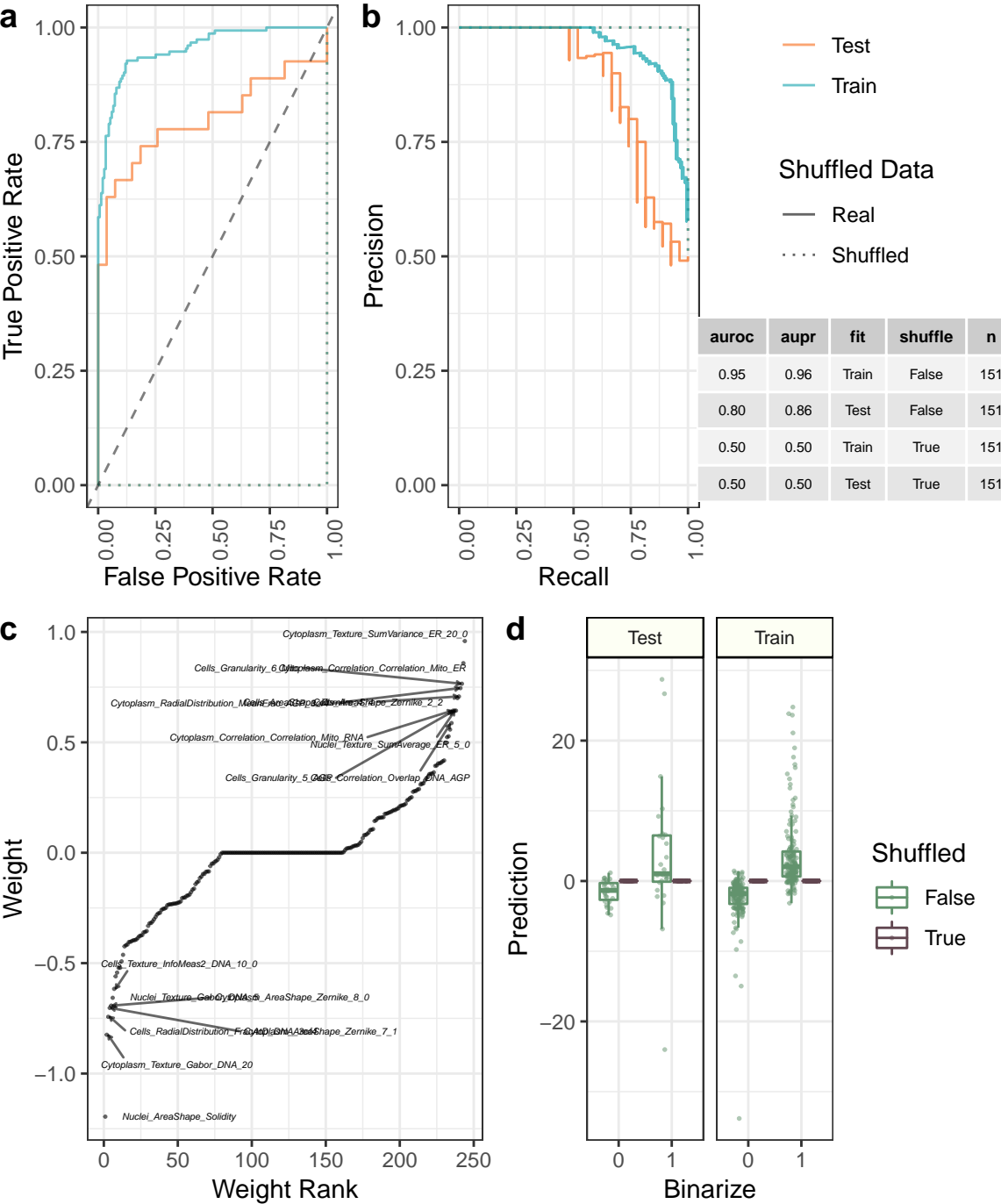
Performance: cc_g1_n_objects



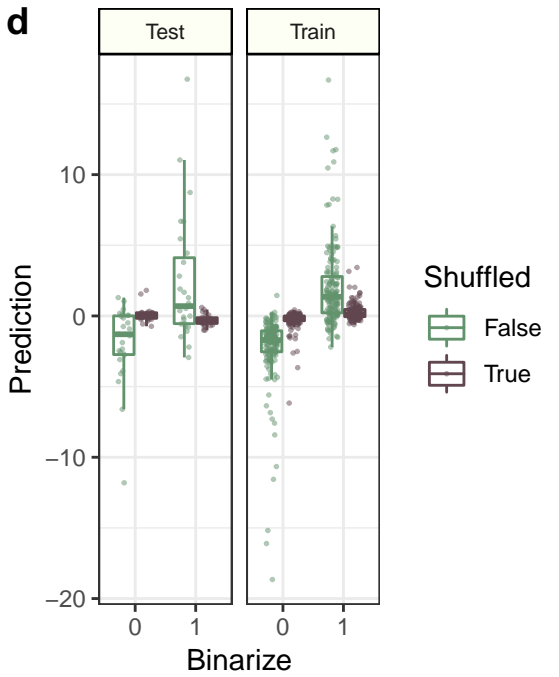
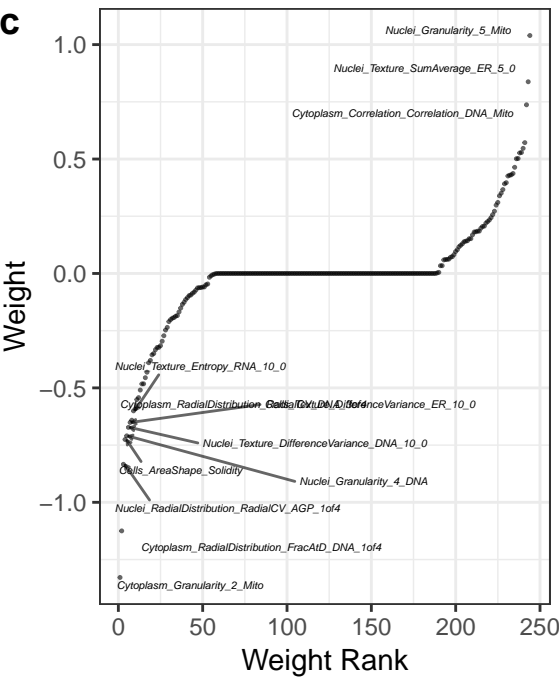
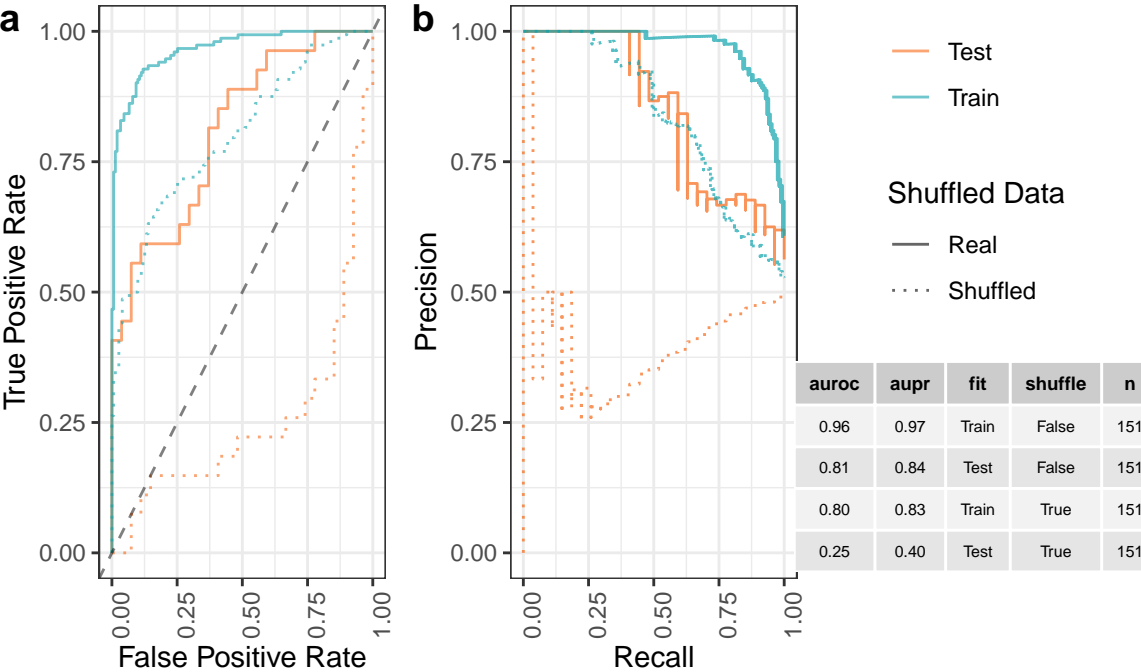
Performance: cc_g1_n_spots_mean



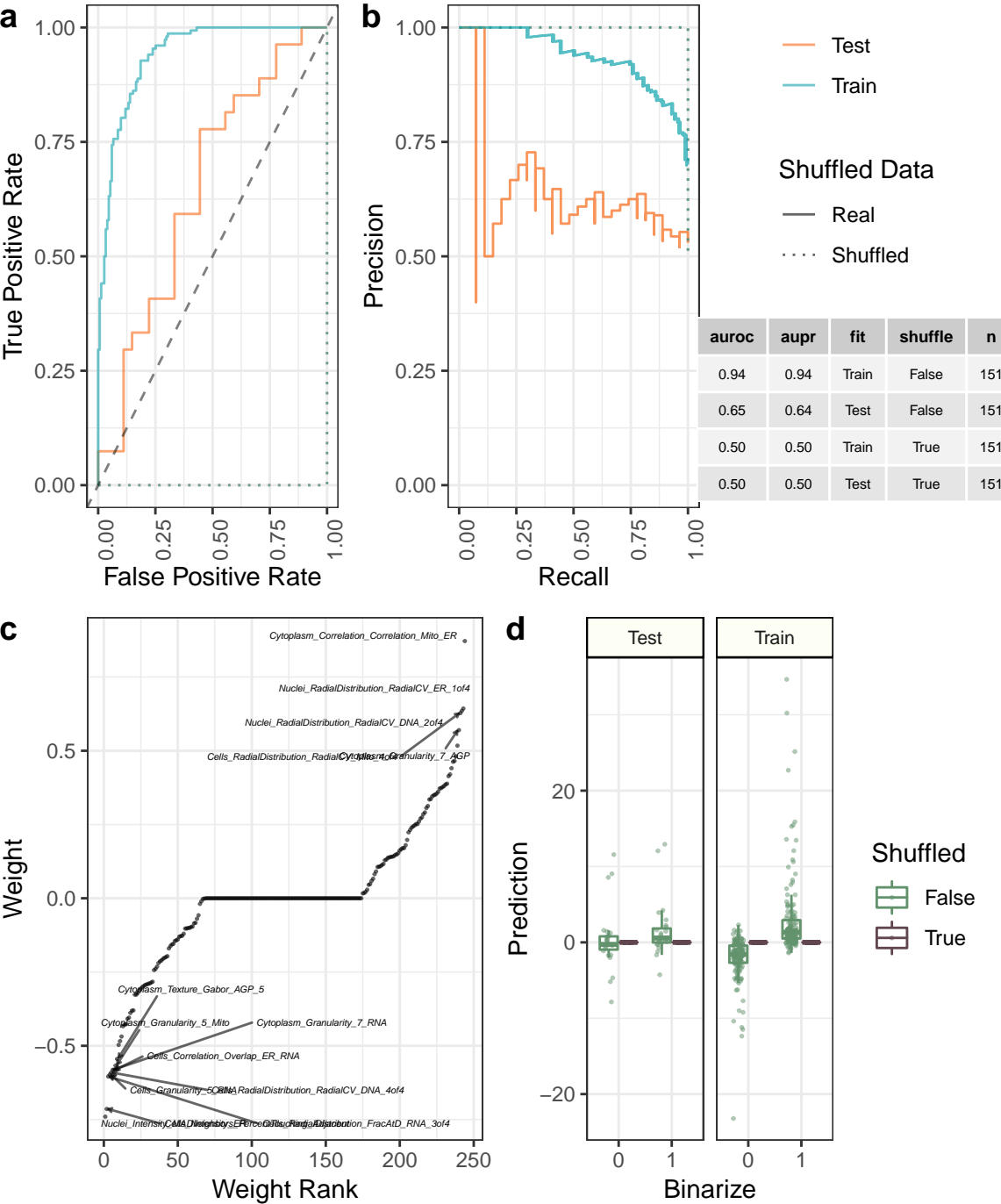
Performance: cc_g1_n_spots_per_nucleus_area_mean



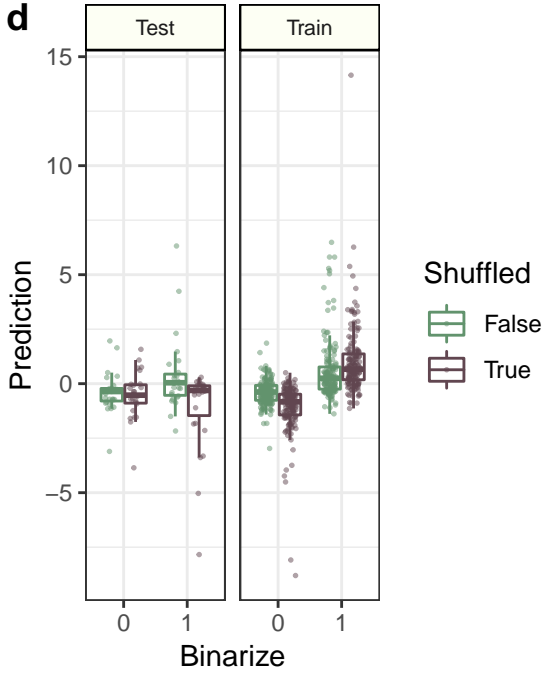
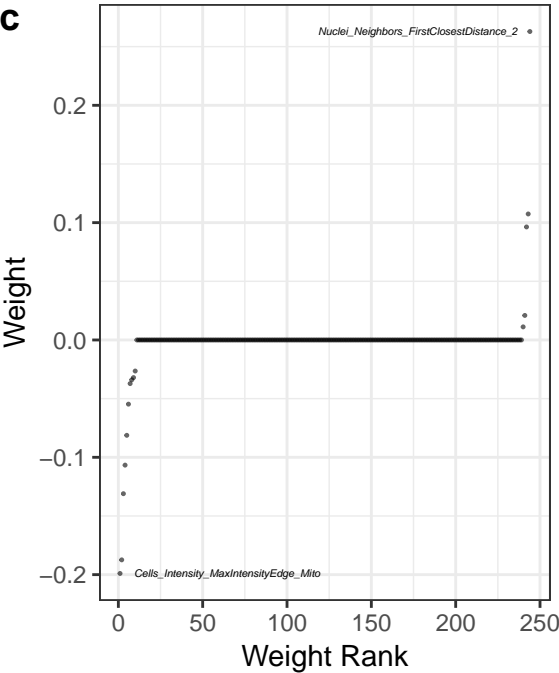
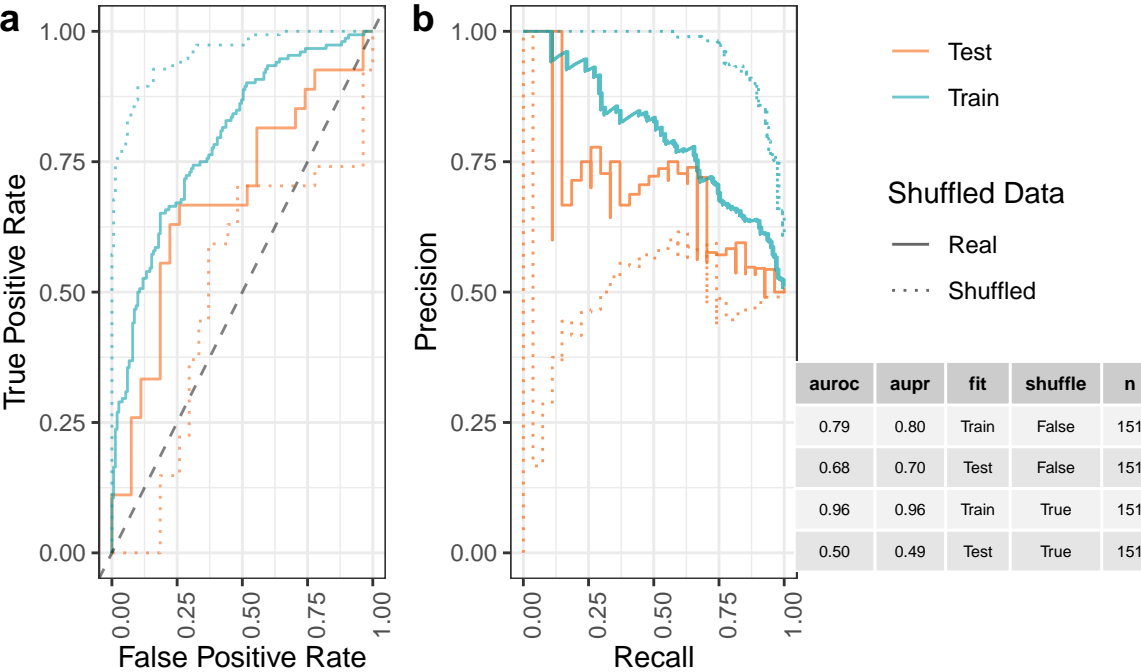
Performance: cc_g1_plus_g2



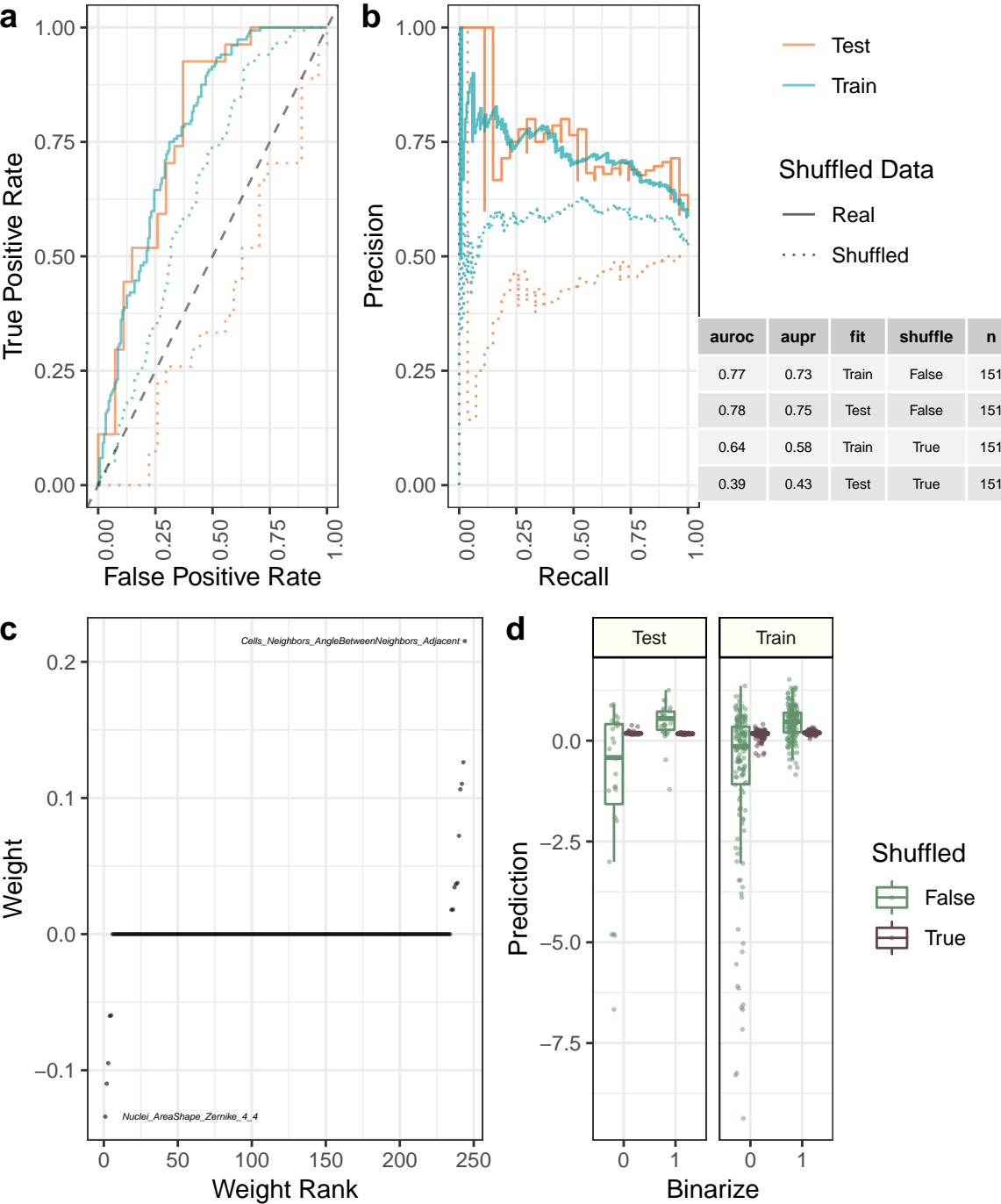
Performance: cc_g2_g1



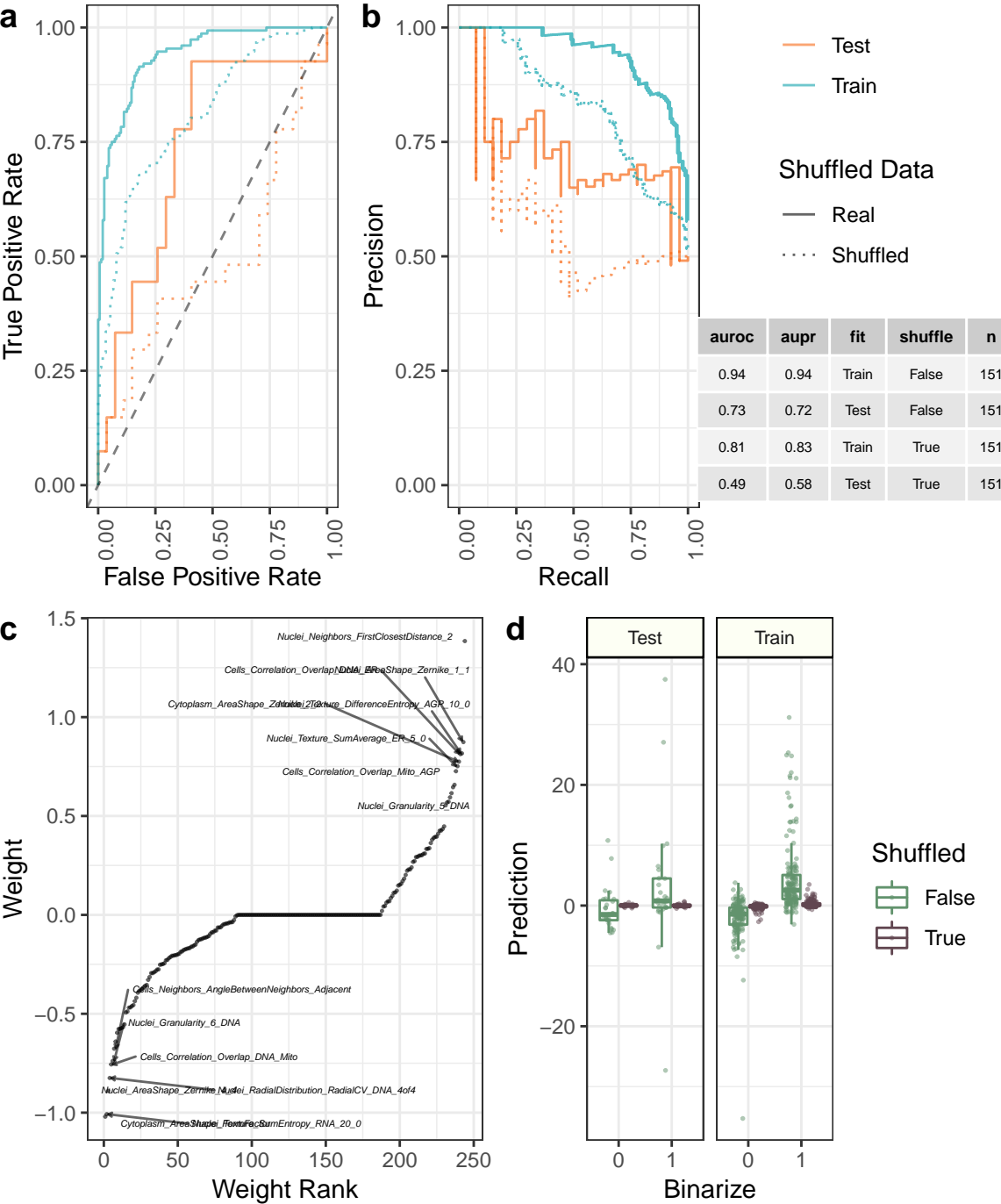
Performance: cc_g2_ph3_neg_high_n_spots_h2ax_mean



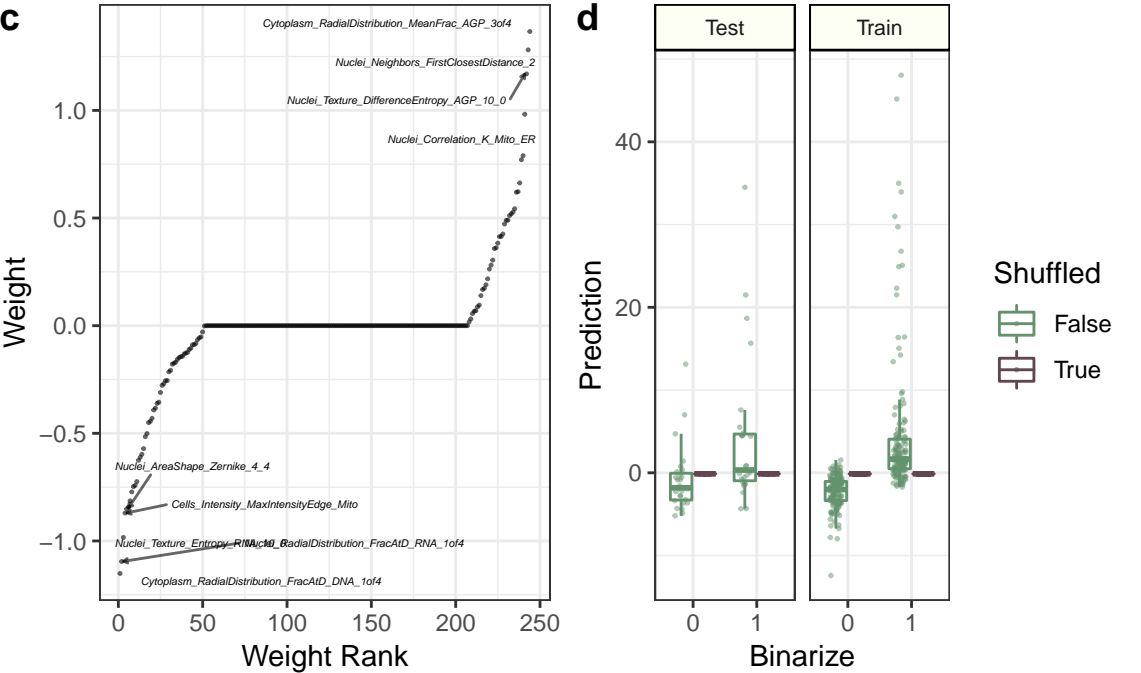
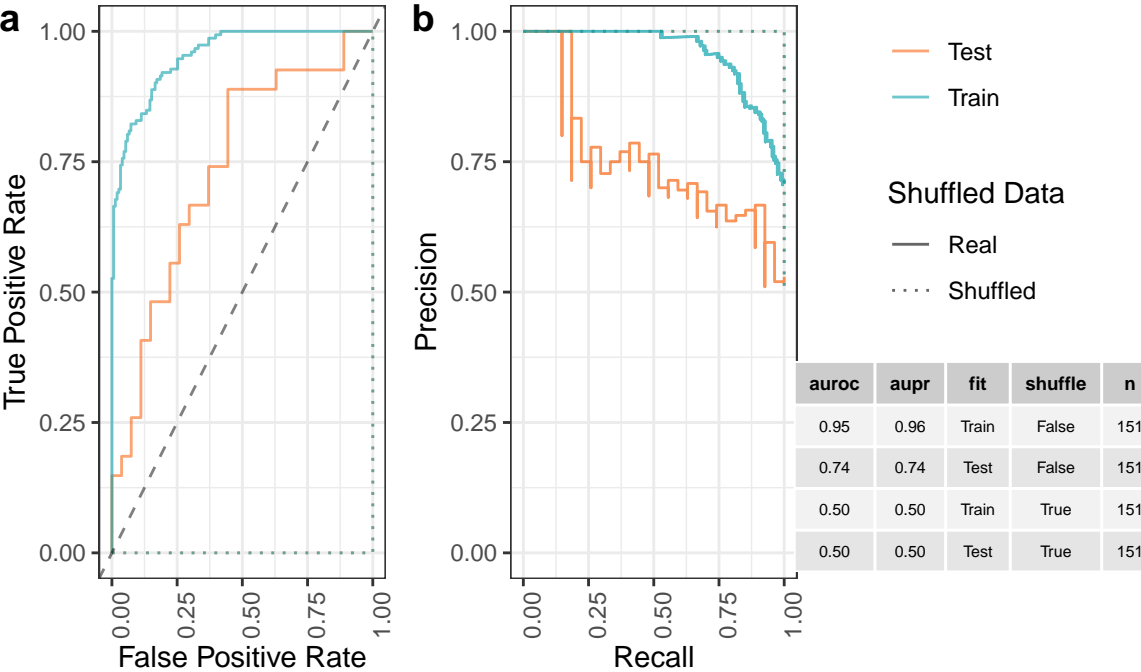
Performance: cc_g2_ph3_neg_n_objects



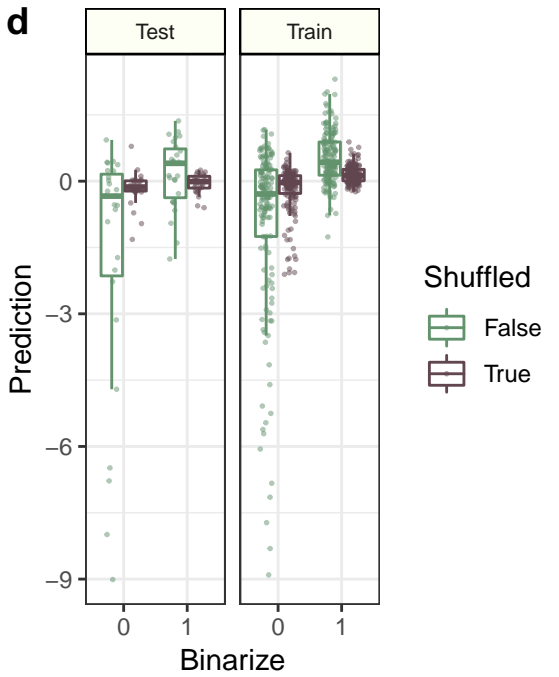
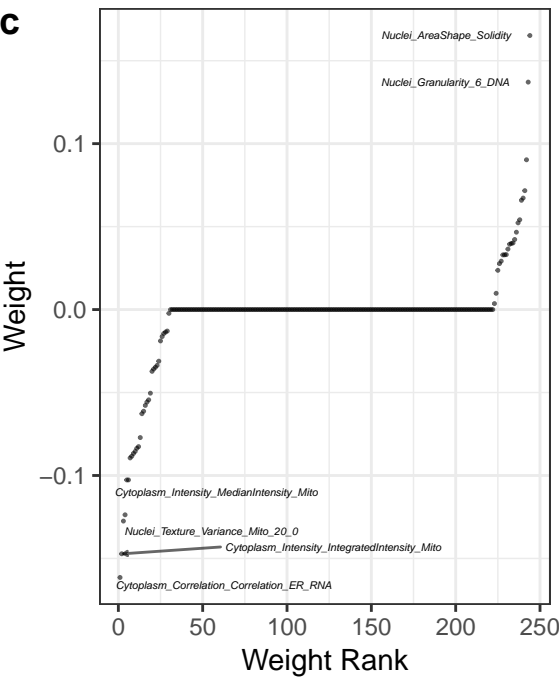
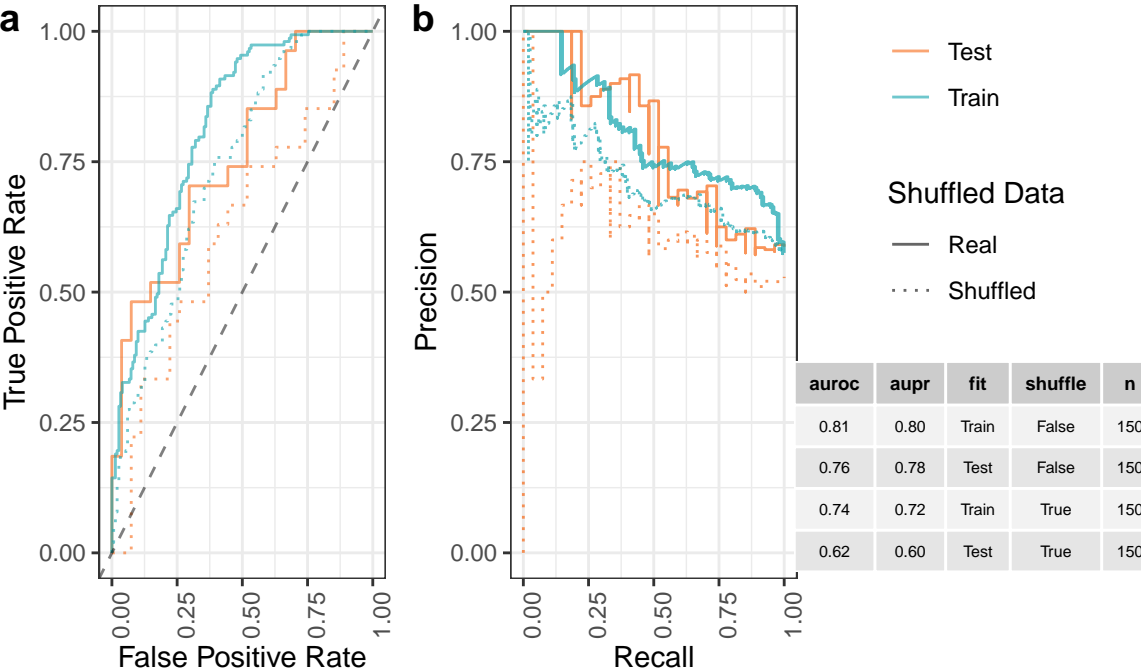
Performance: cc_g2_ph3_neg_n_spots_mean



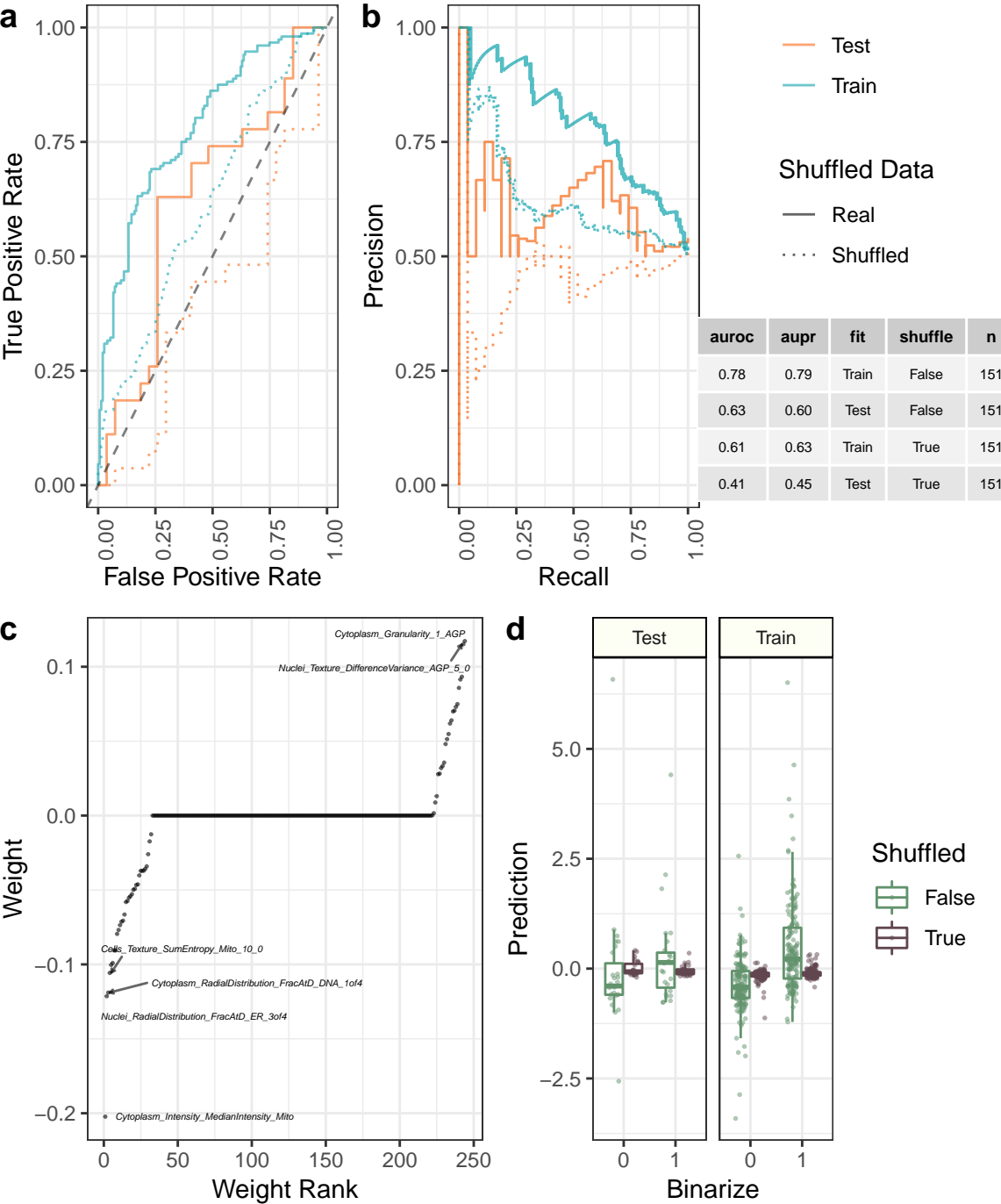
Performance: cc_g2_ph3_neg_n_spots_per_nucleus_area_mean



Performance: cc_g2_ph3_pos_n_objects



Performance: cc_g2_ph3_pos_n_spots_mean



c

Weight

Weight Rank

Cytoplasm_Granularity_1_AGP

Nuclei_Texture_DifferenceVariance_AGP_5_0

Cytoplasm_RadialDistribution_FracAID_DNA_1of4

Nuclei_RadialDistribution_FracAID_ER_3of4

Cytoplasm_Intensity_MedianIntensity_Mito

Cells_Texture_SumEntropy_Mito_10_0

d

Prediction

Binarize

Test

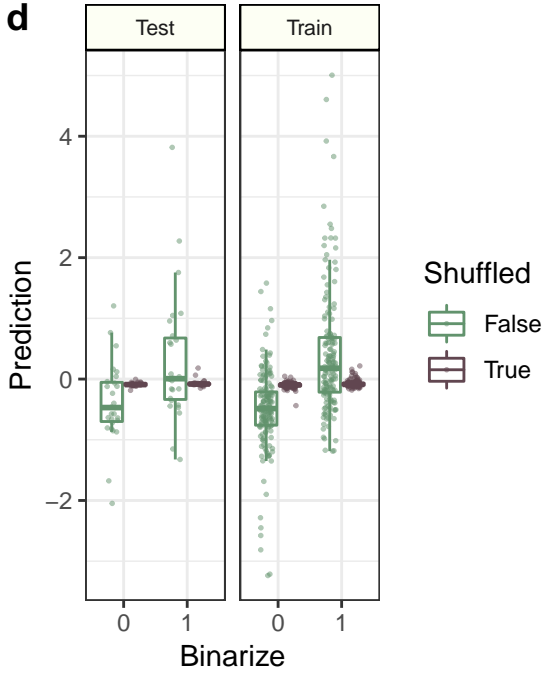
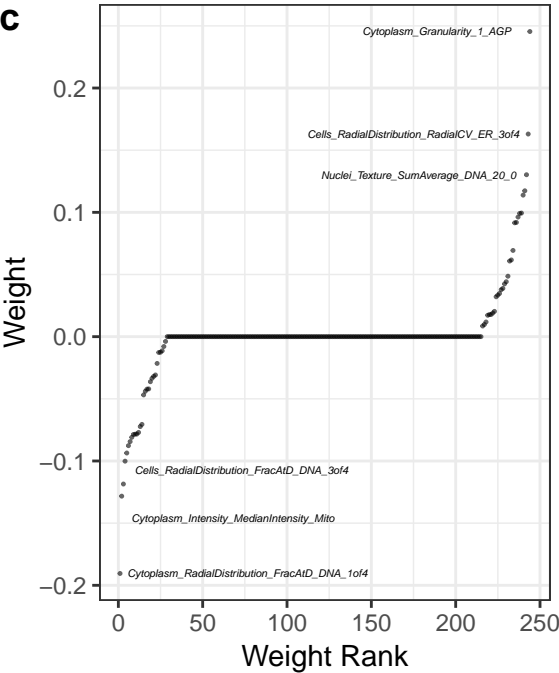
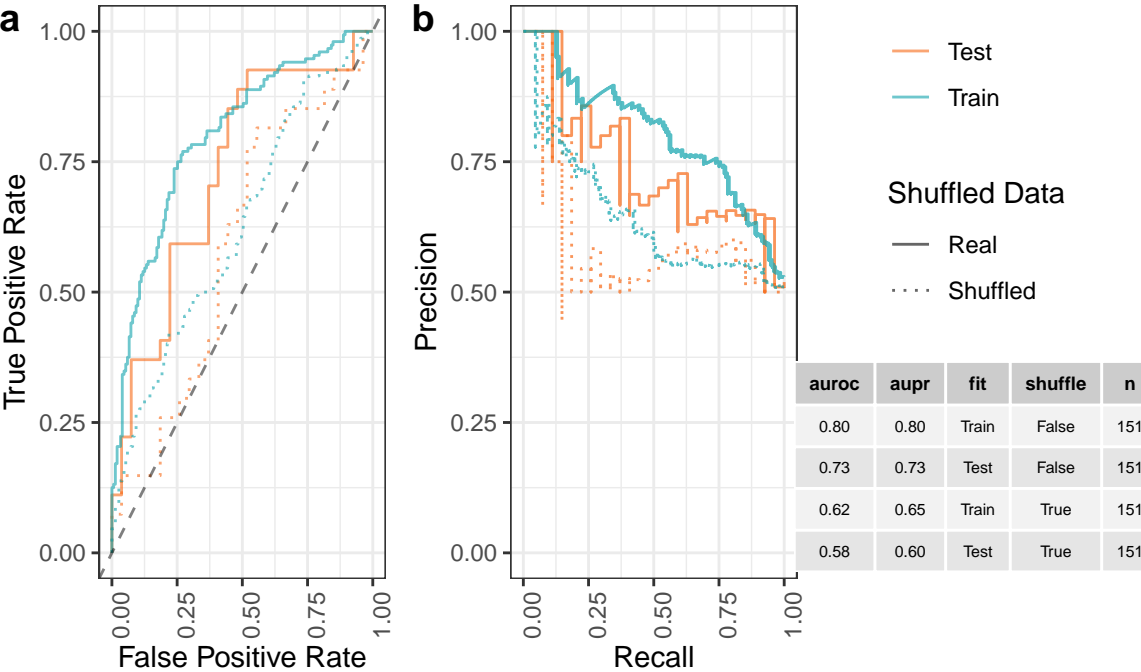
Train

Shuffled

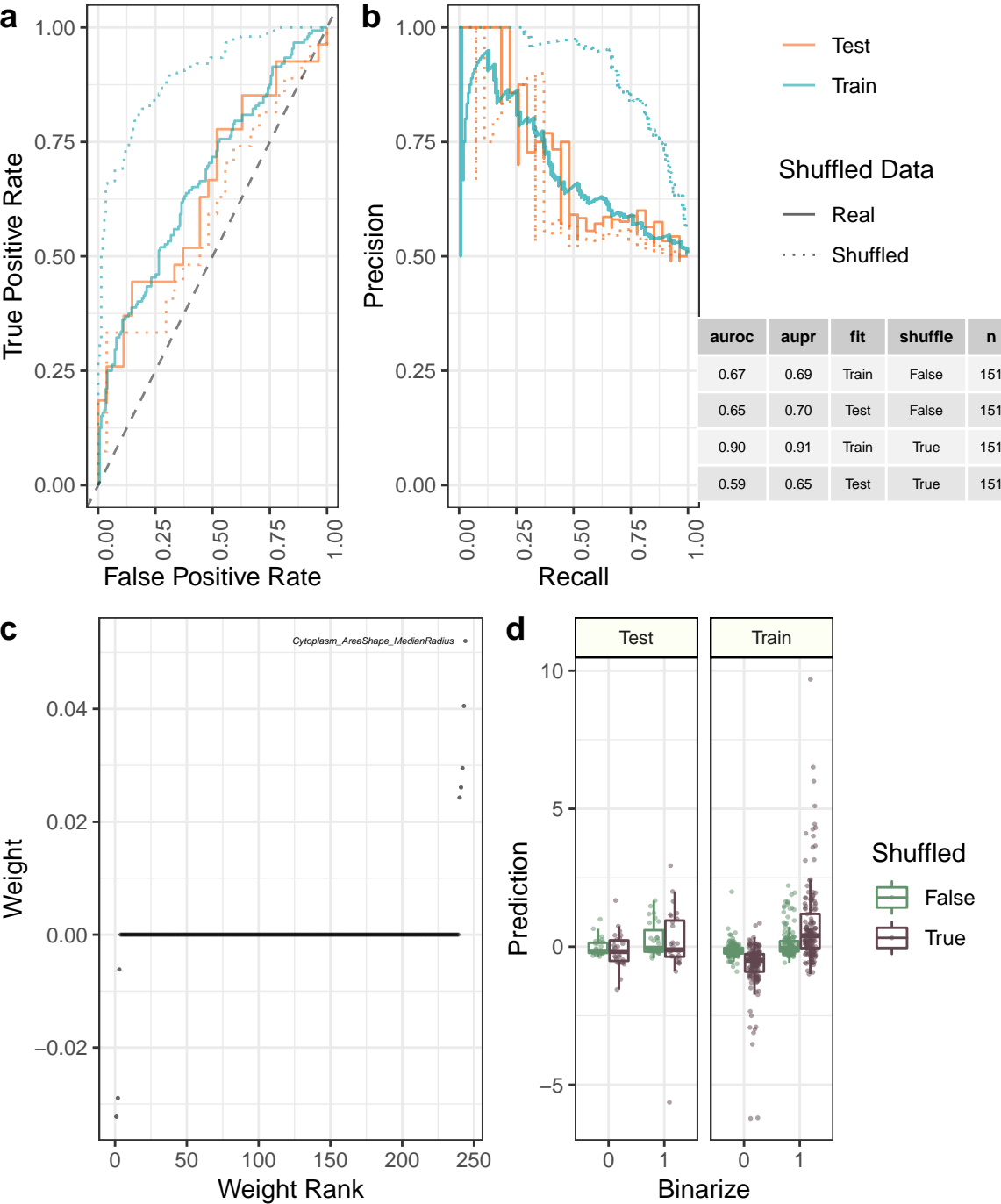
False

True

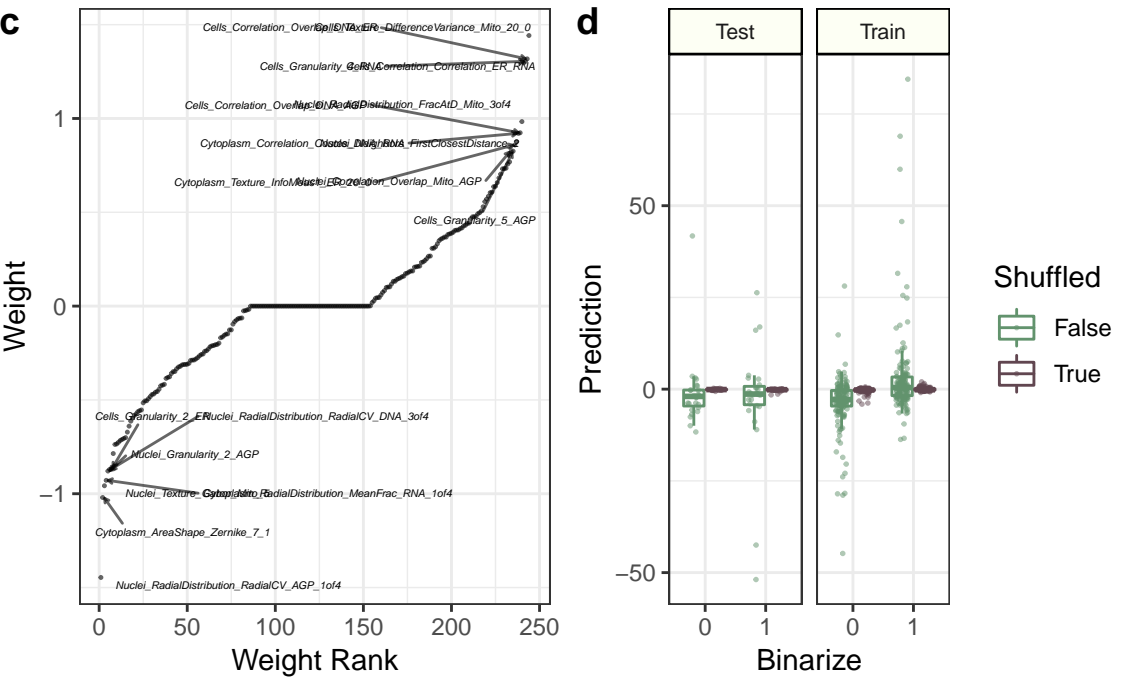
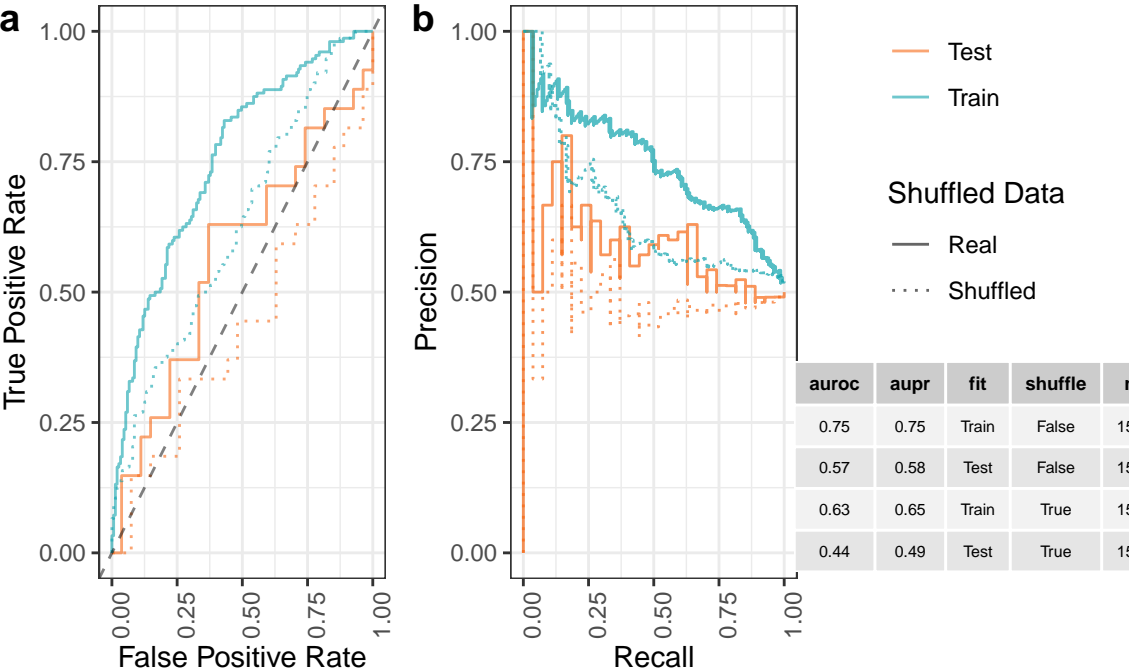
Performance: cc_g2_ph3_pos_n_spots_per_nucleus_area_mean



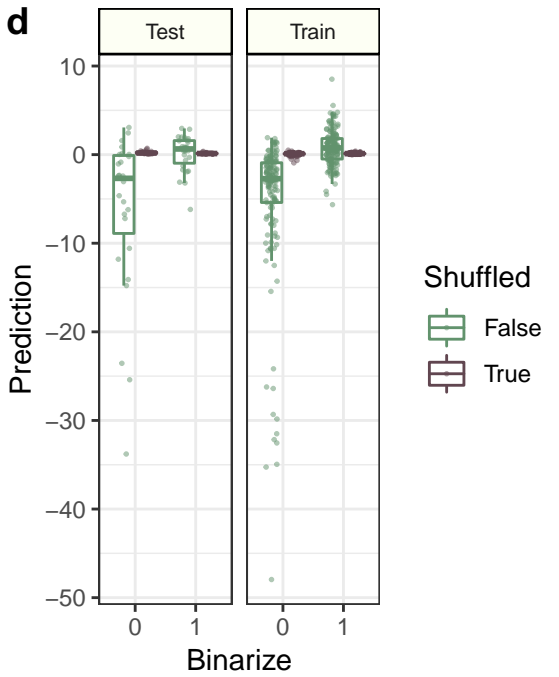
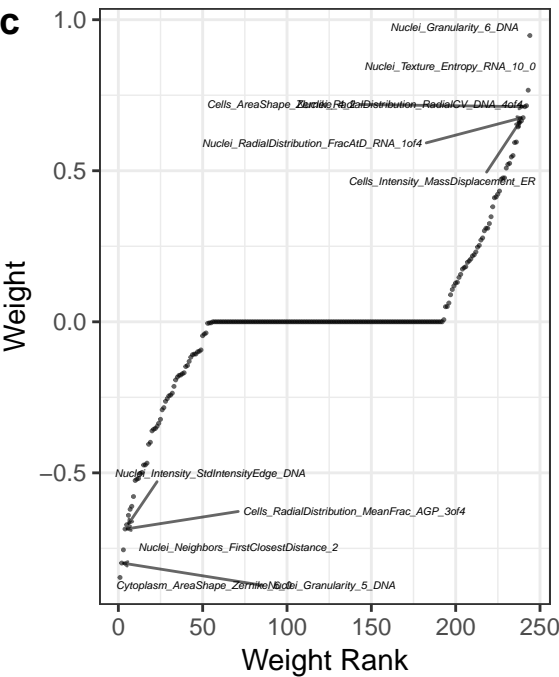
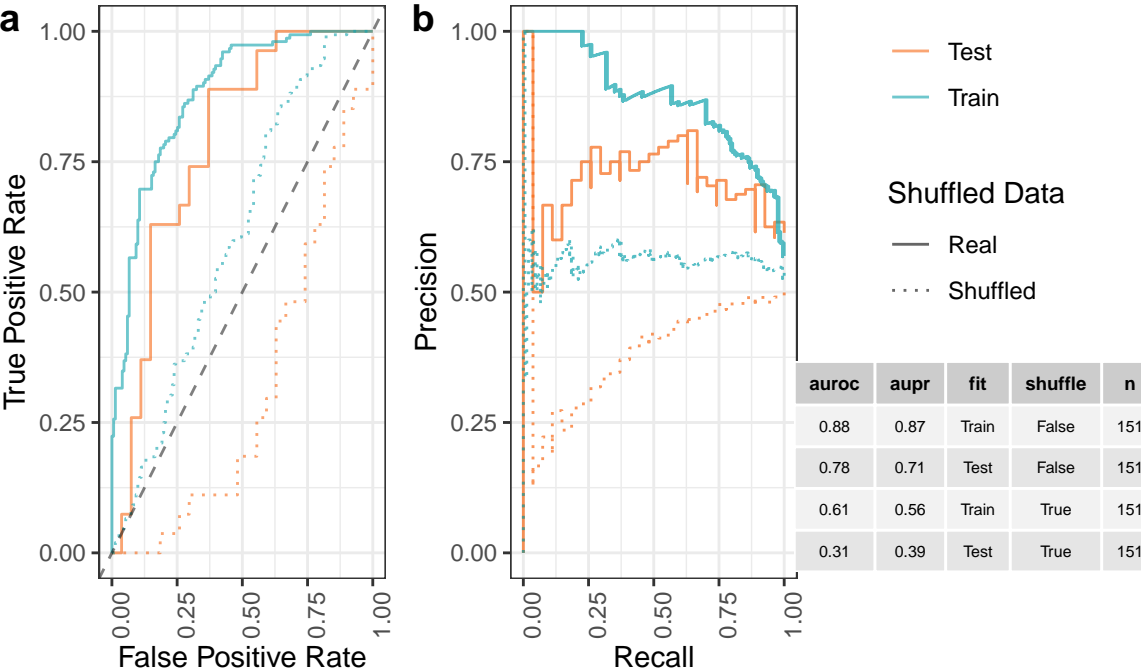
Performance: cc_g2_plus_all_m



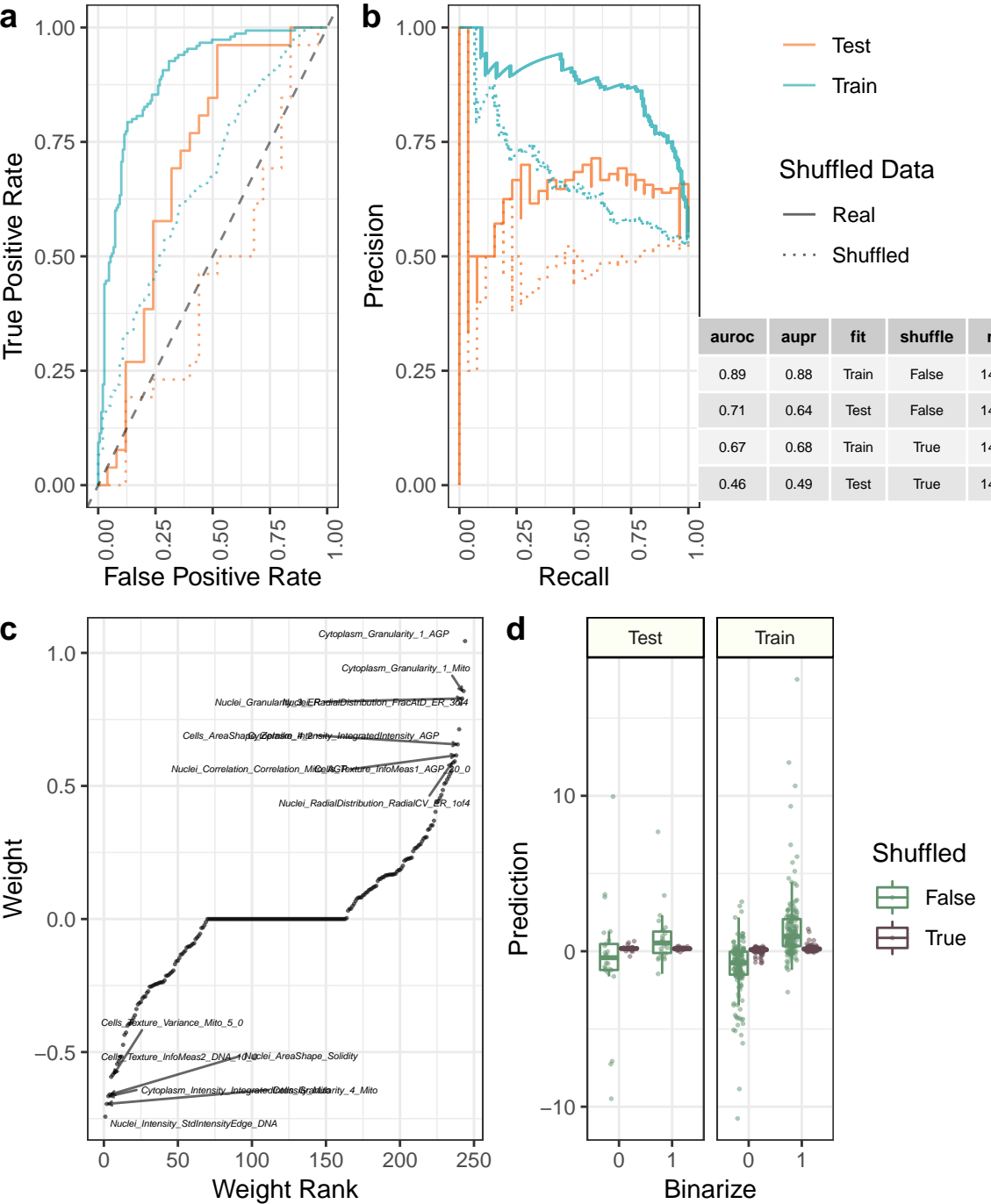
Performance: cc_infection_percentage



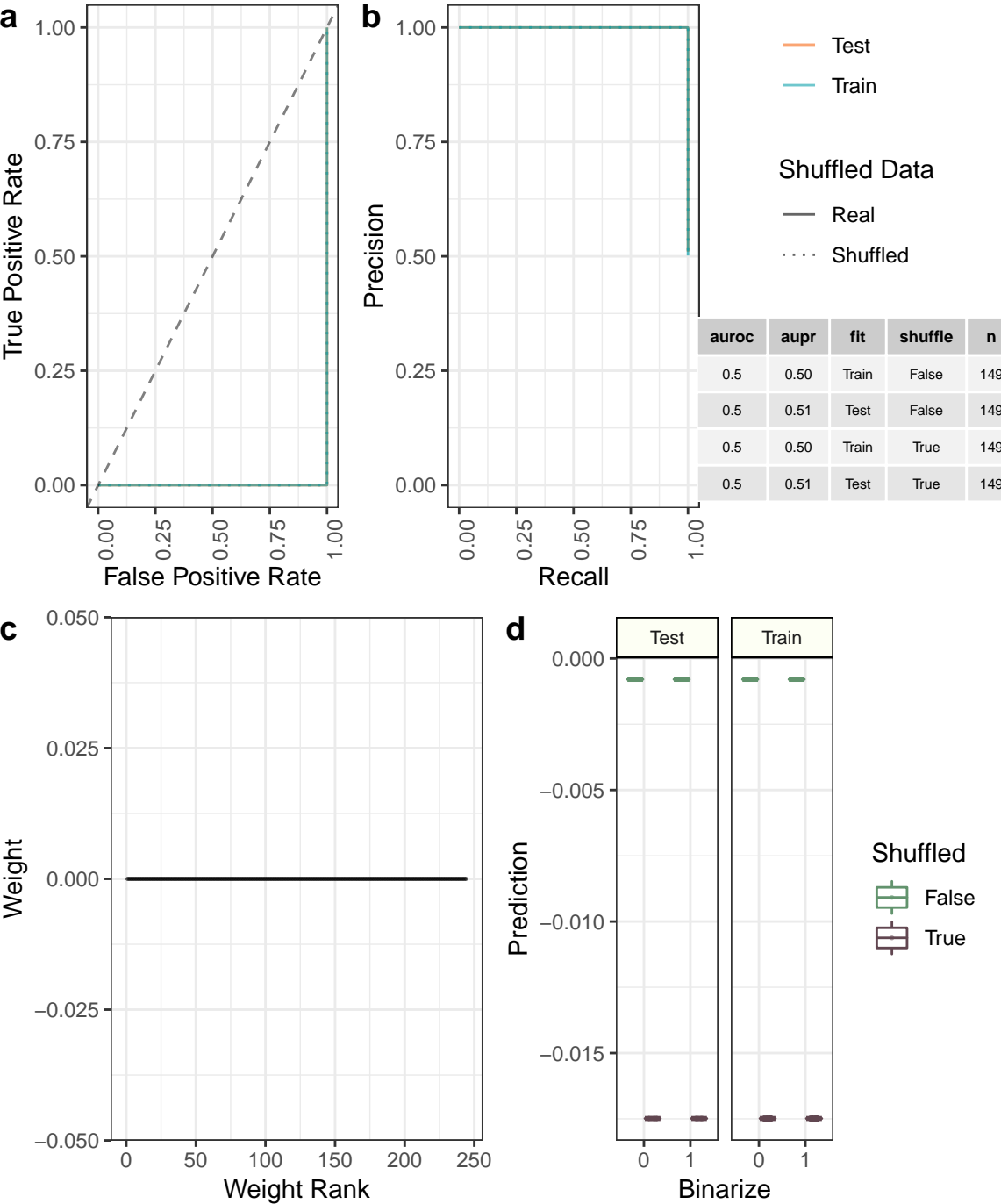
Performance: cc_mitosis_ph3_neg_n_objects



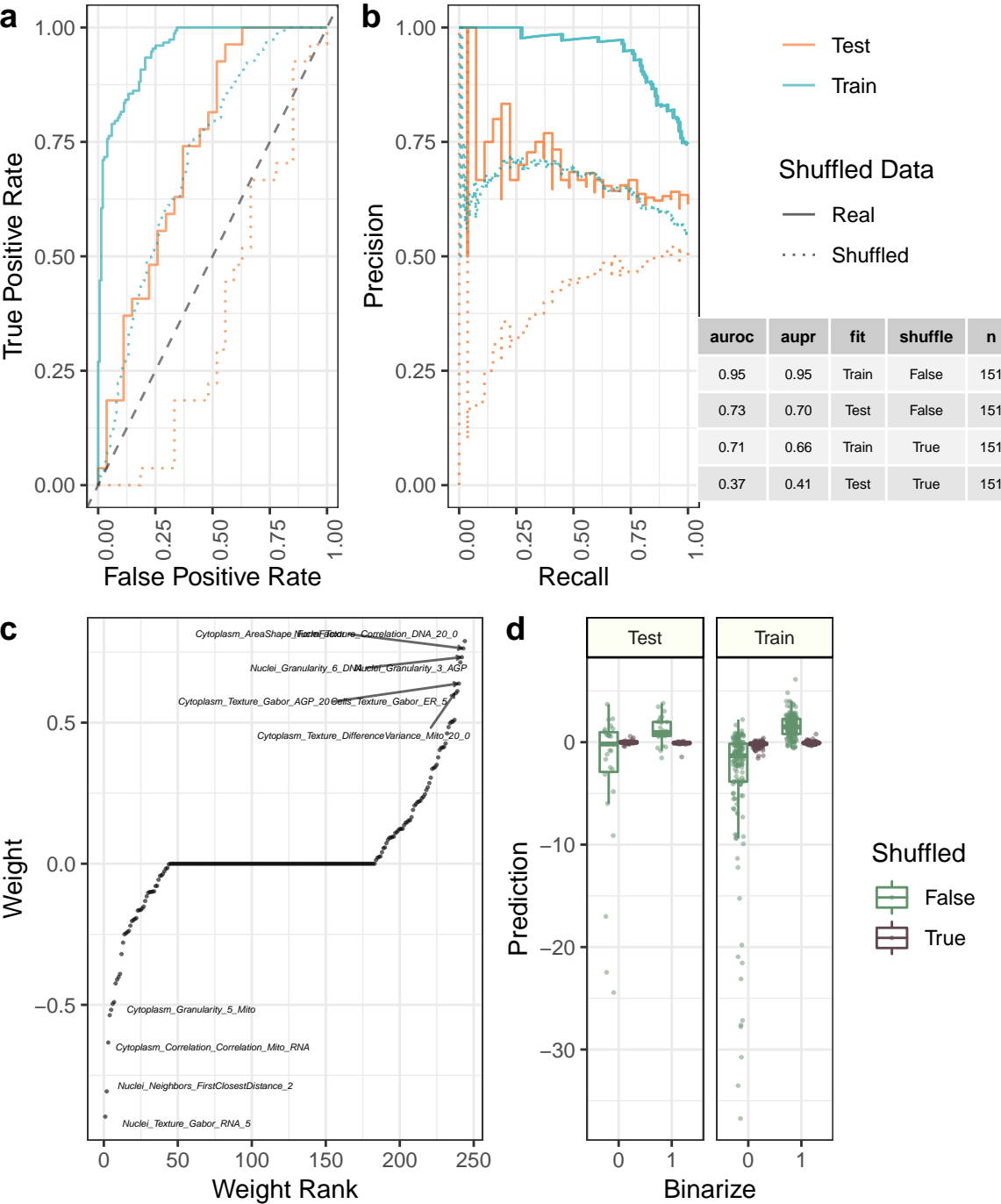
Performance: cc_mitosis_ph3_neg_n_spots_mean



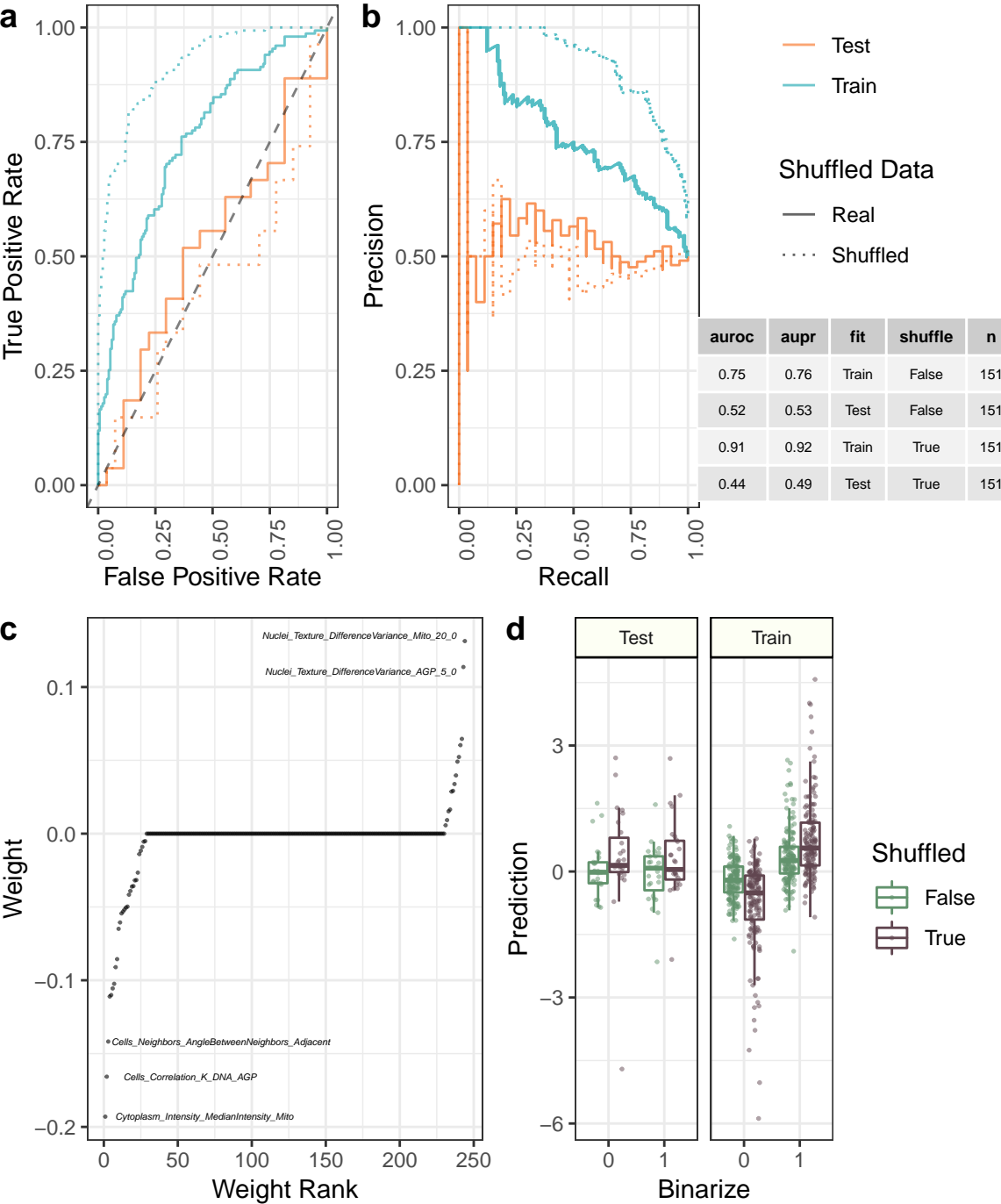
Performance: cc_mitosis_ph3_neg_n_spots_per_nucleus_area



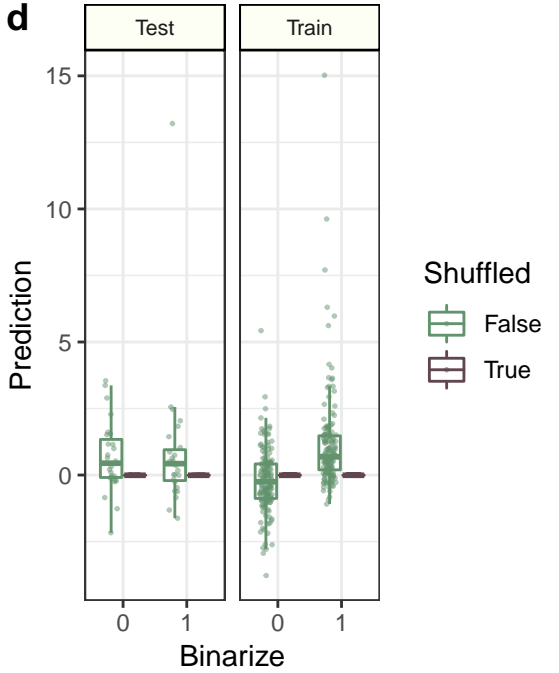
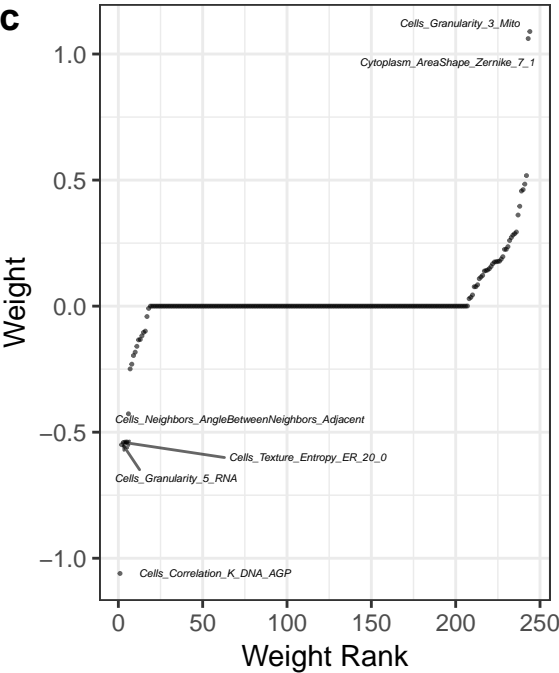
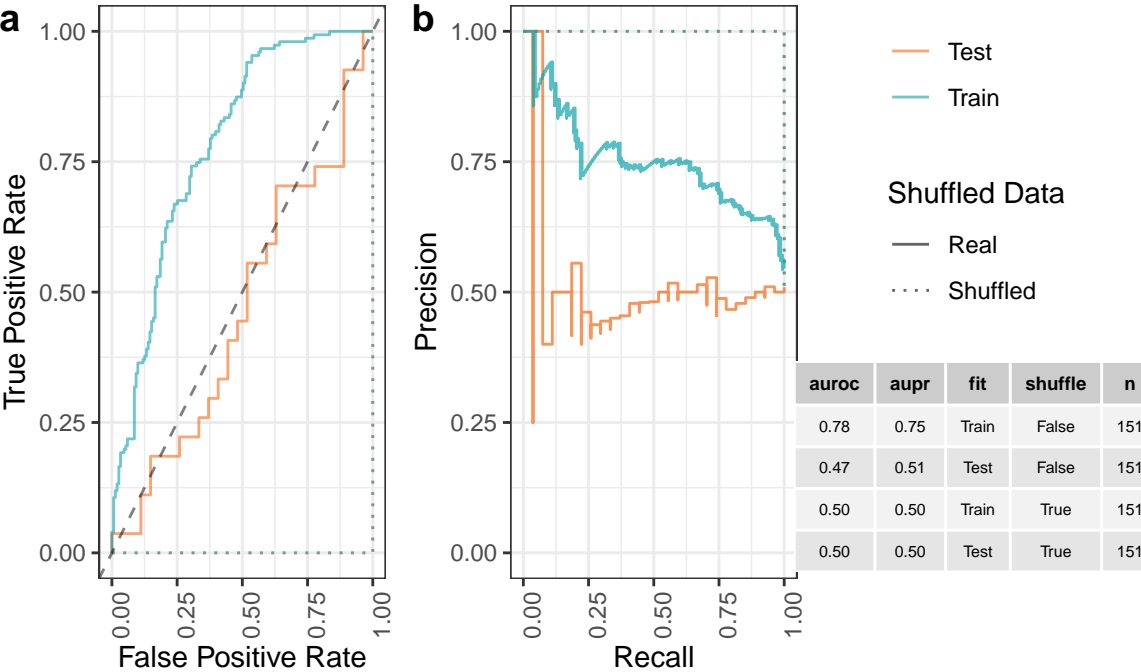
Performance: cc_mitosis_ph3_pos_n_objects



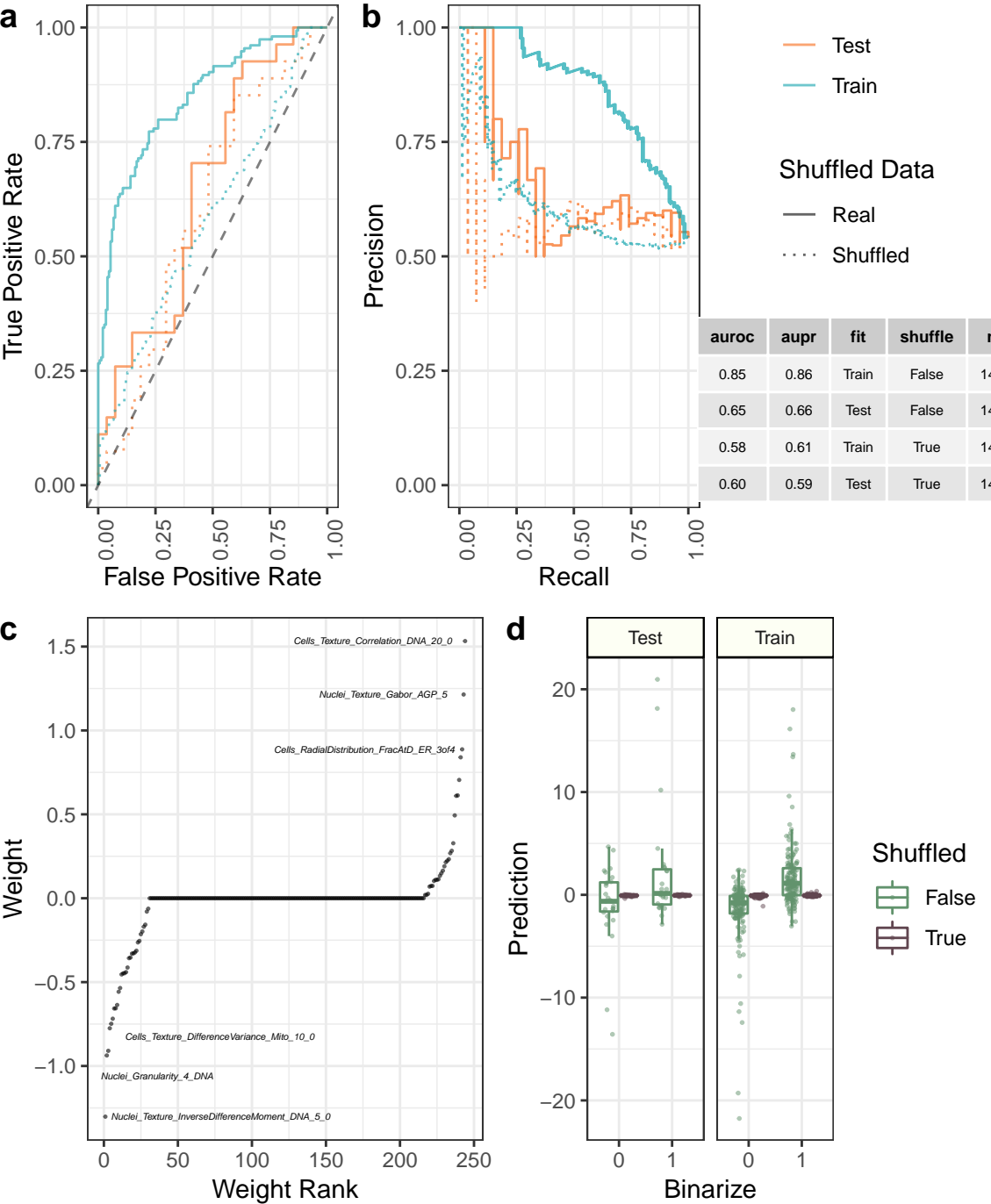
Performance: cc_mitosis_ph3_pos_n_spots_mean



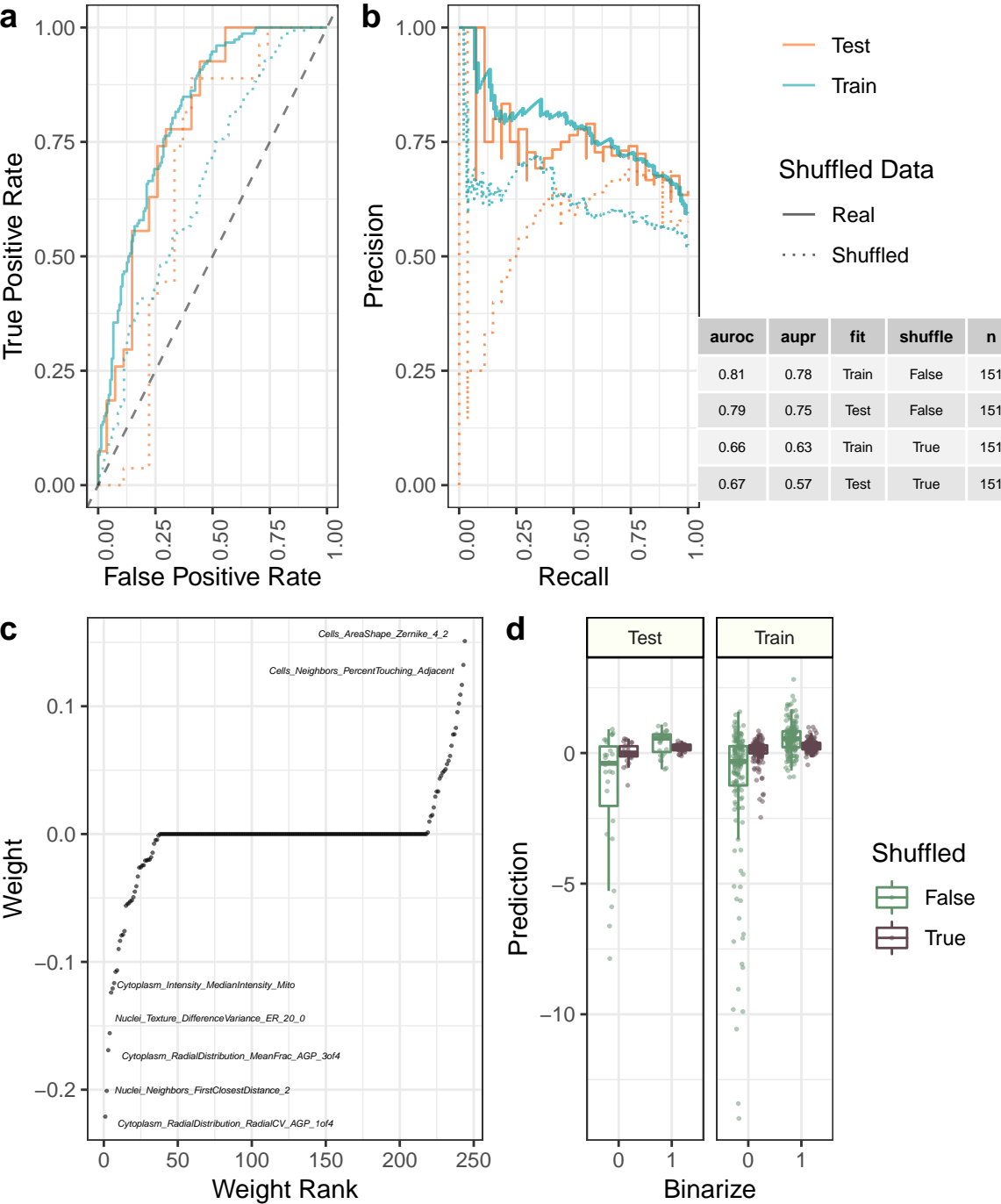
Performance: cc_mitosis_ph3_pos_n_spots_per_nucleus_area



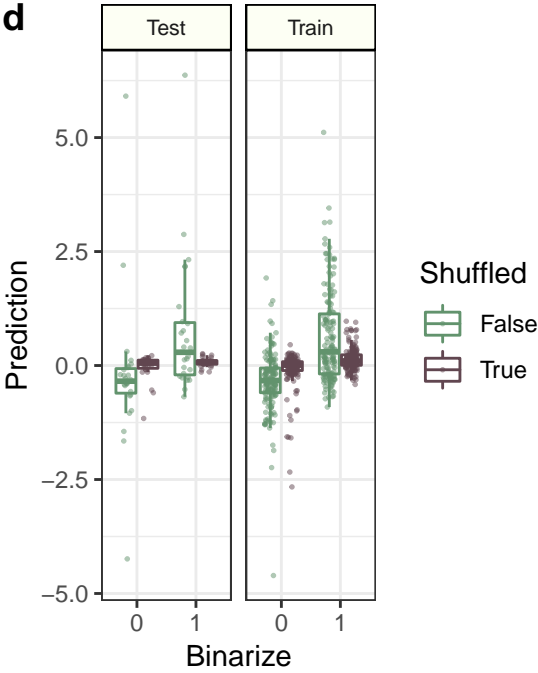
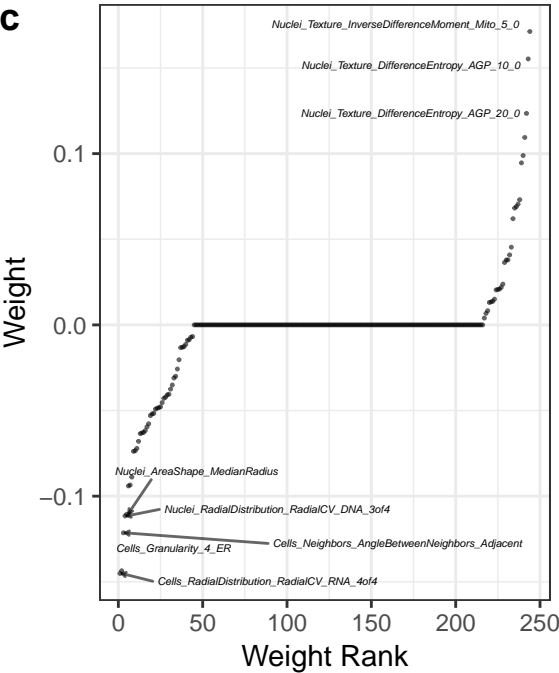
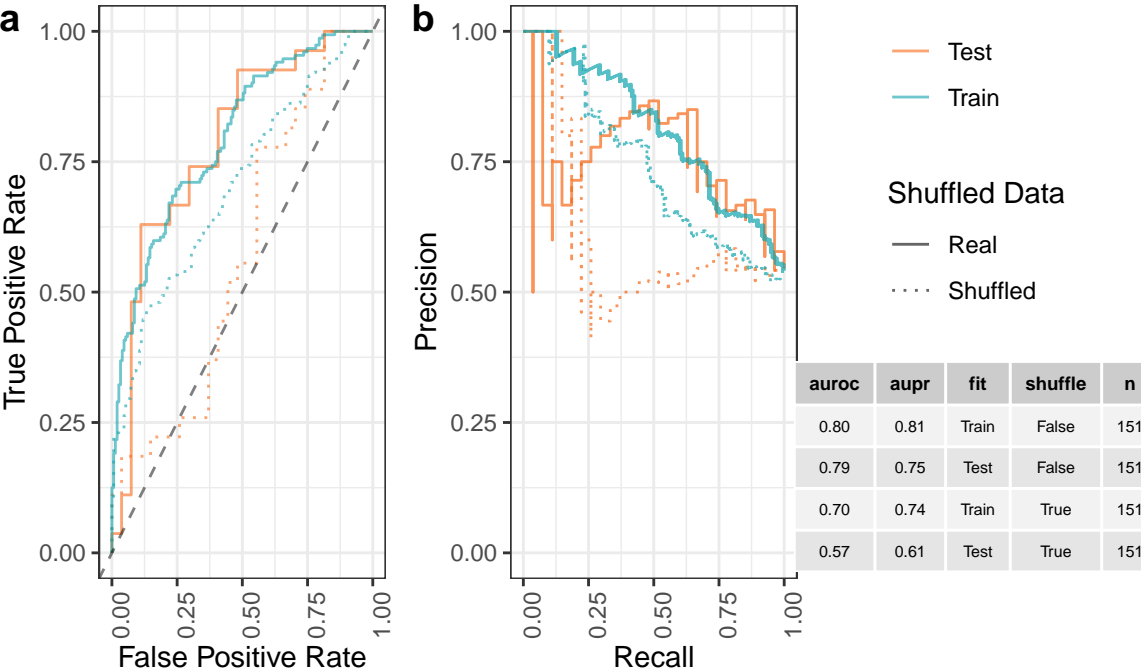
Performance: cc_polynuclear_high_n_spots_h2ax_mean



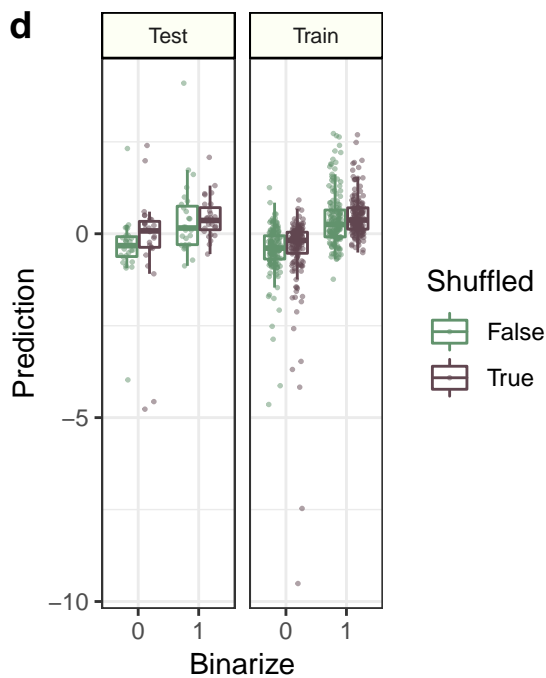
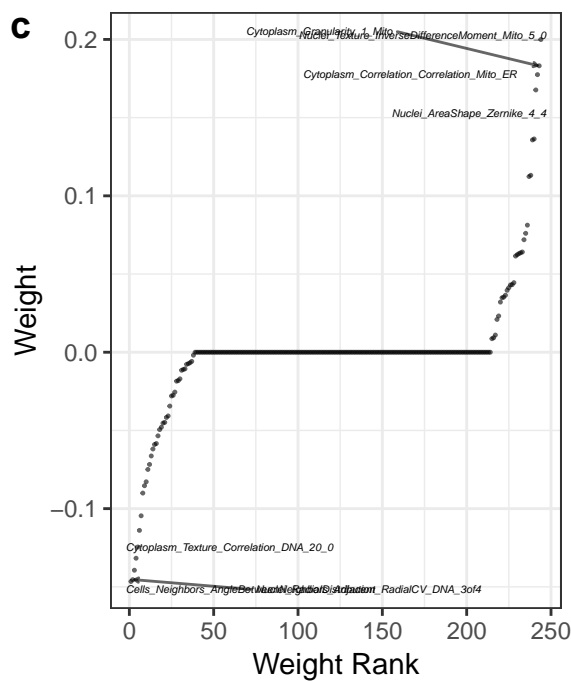
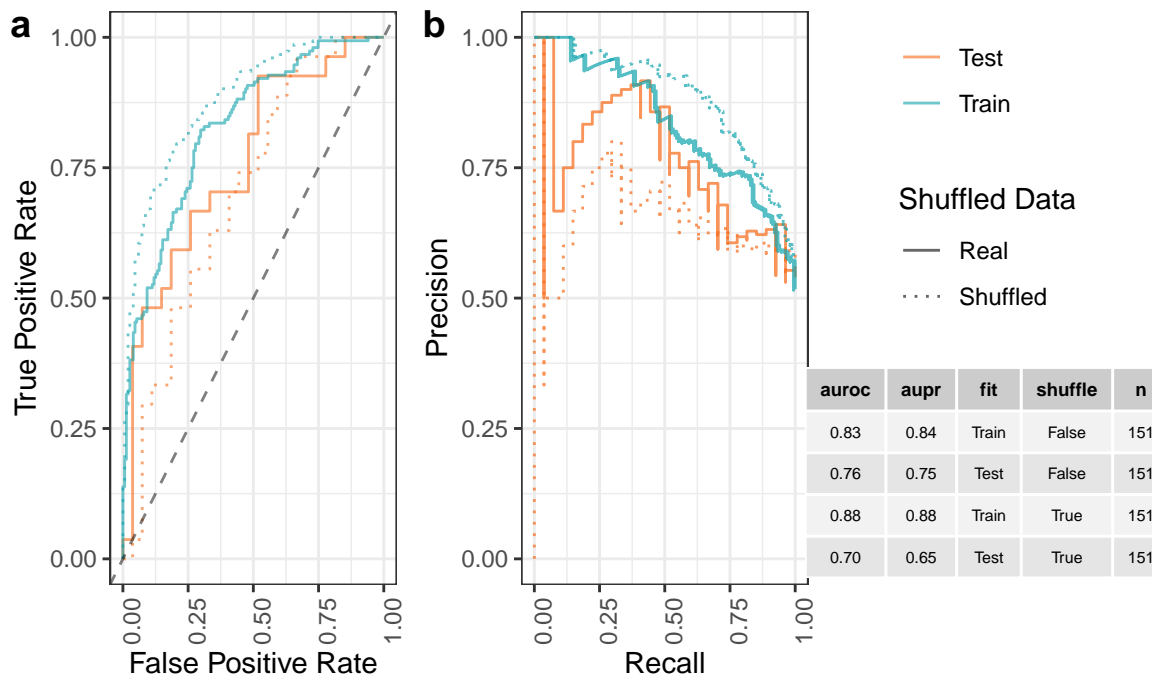
Performance: cc_polynuclear_n_objects



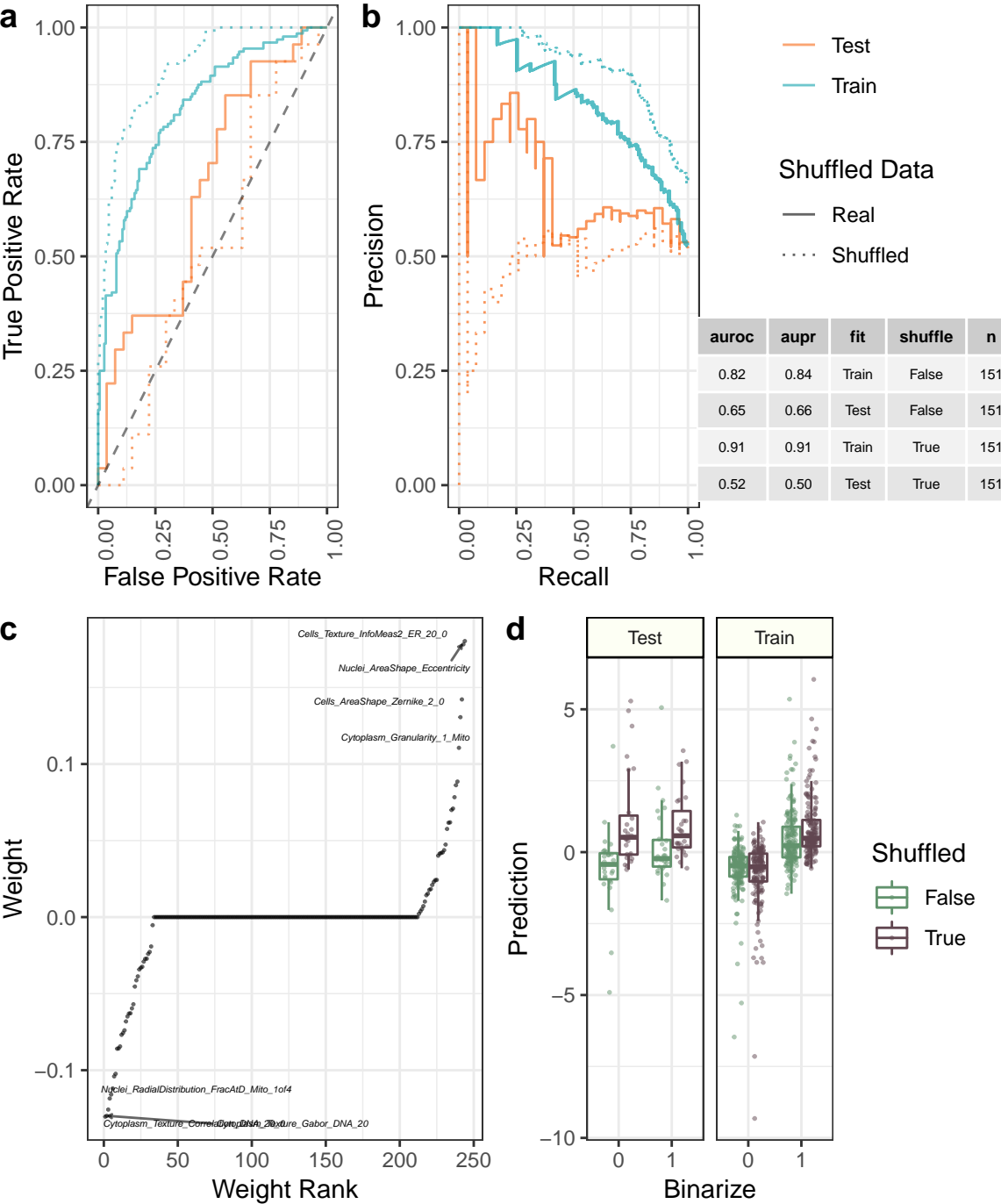
Performance: cc_polynuclear_n_spots_mean



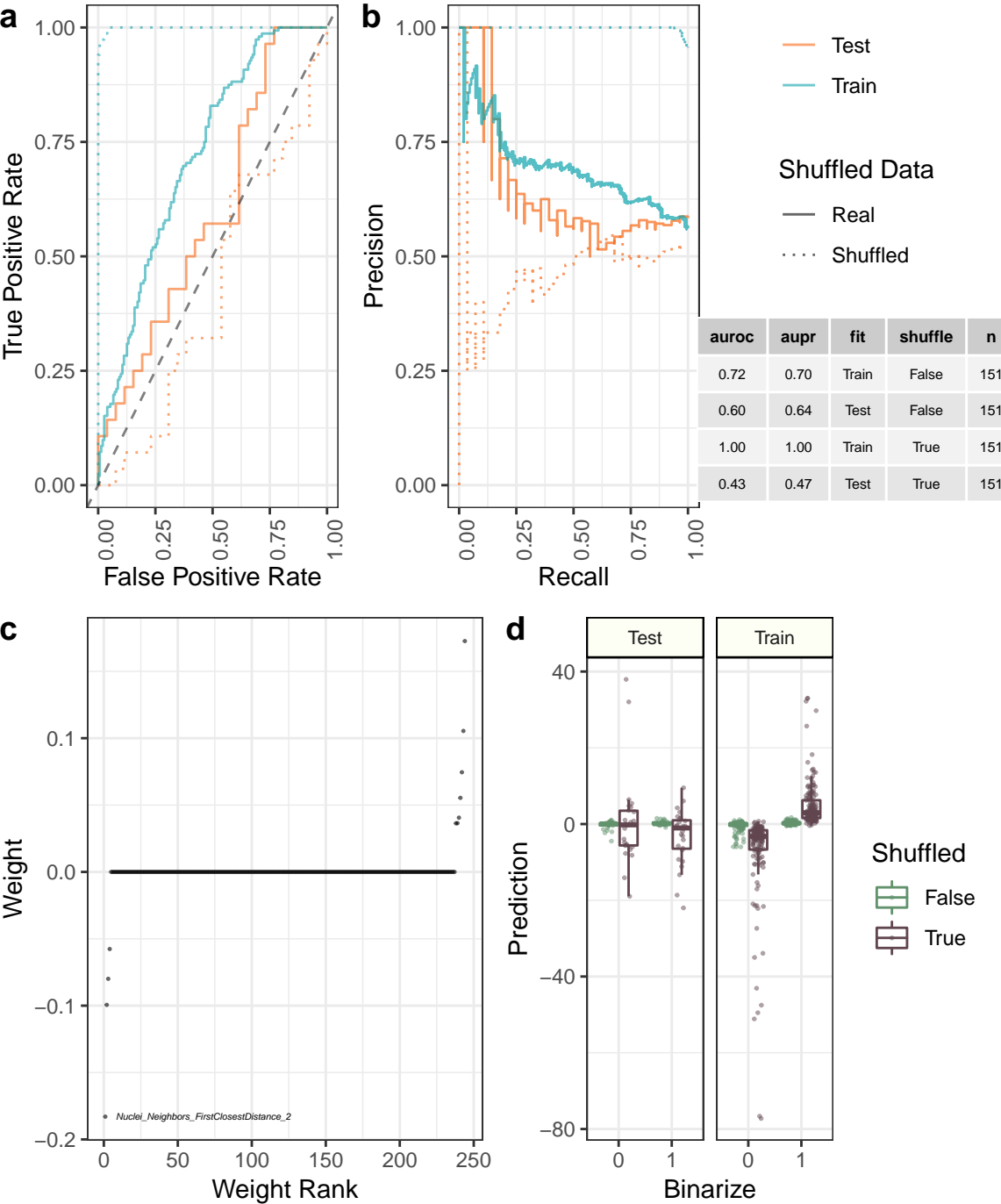
Performance: cc_polynuclear_n_spots_per_nucleus_area_mean



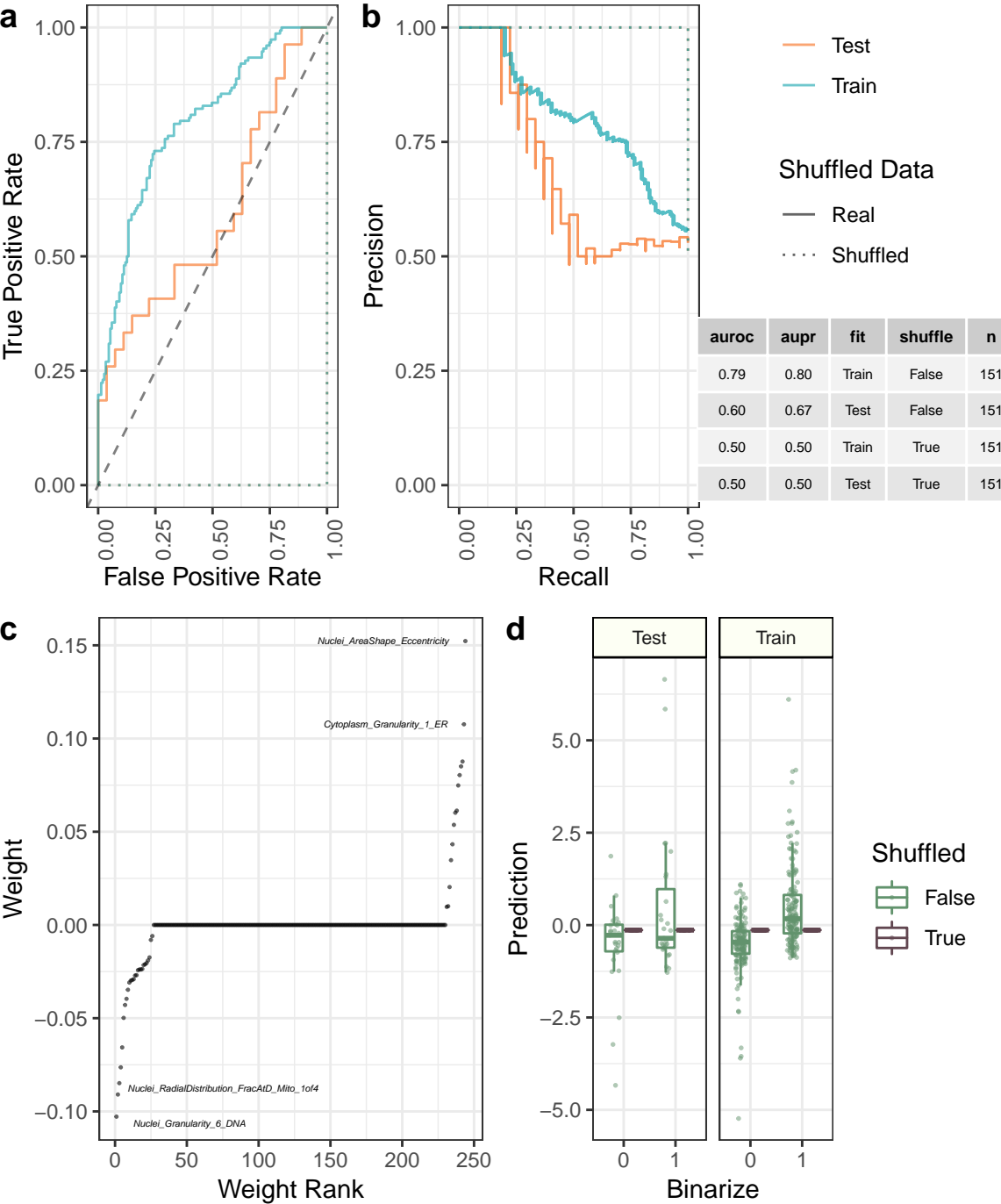
Performance: cc_polyloid_high_n_spots_h2ax_mean



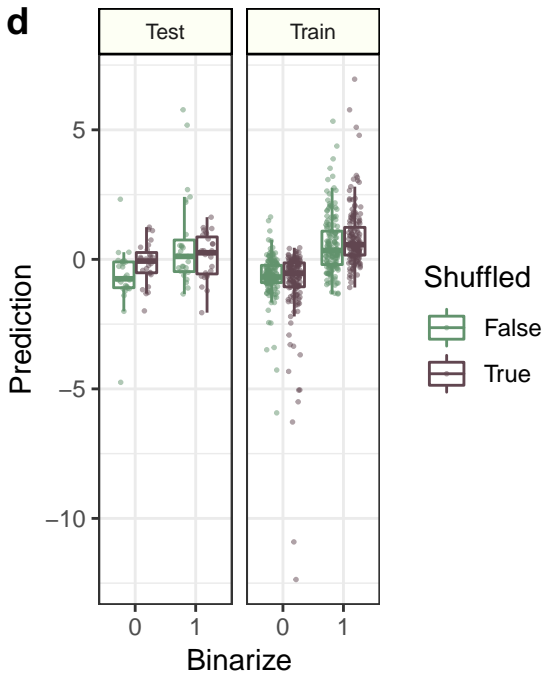
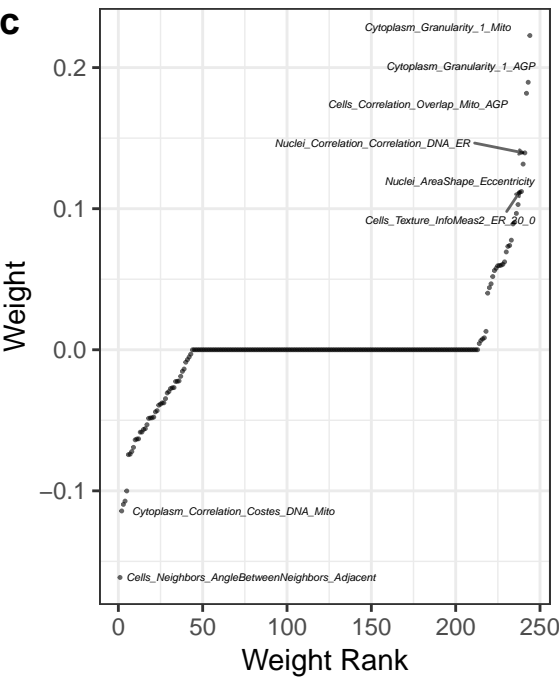
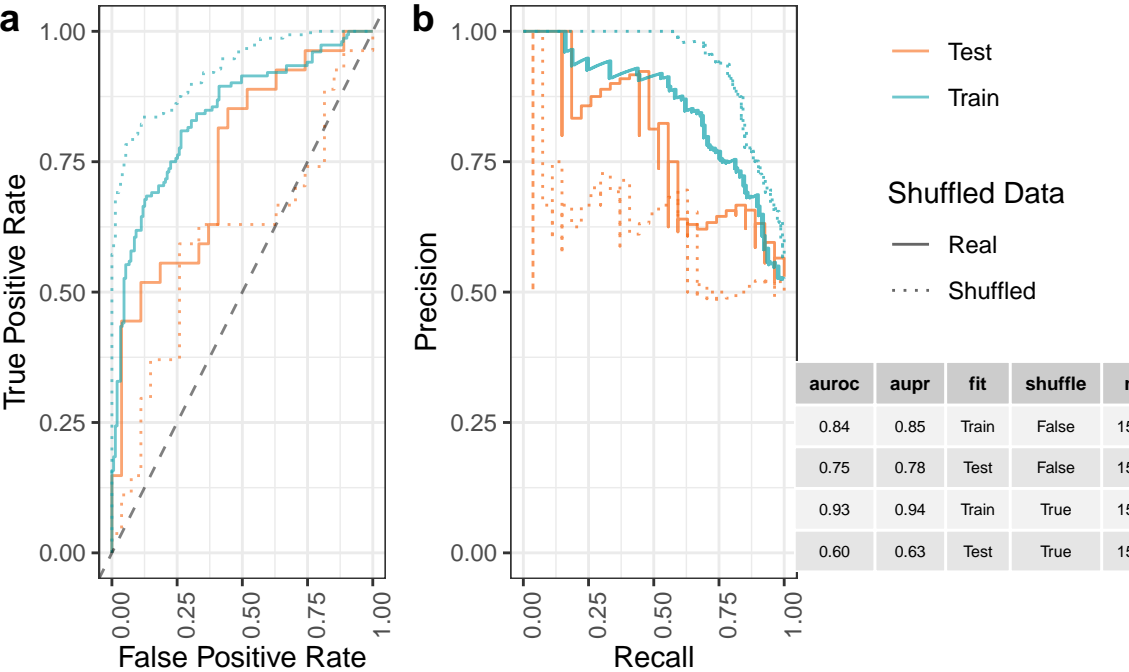
Performance: cc_polyloid_n_objects



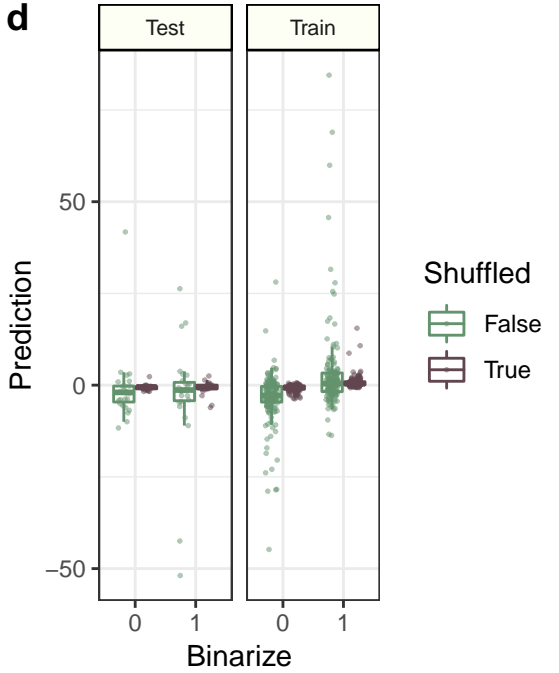
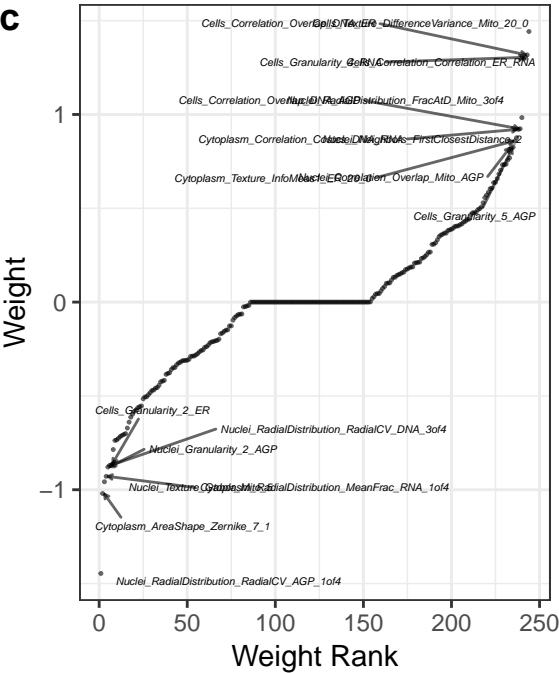
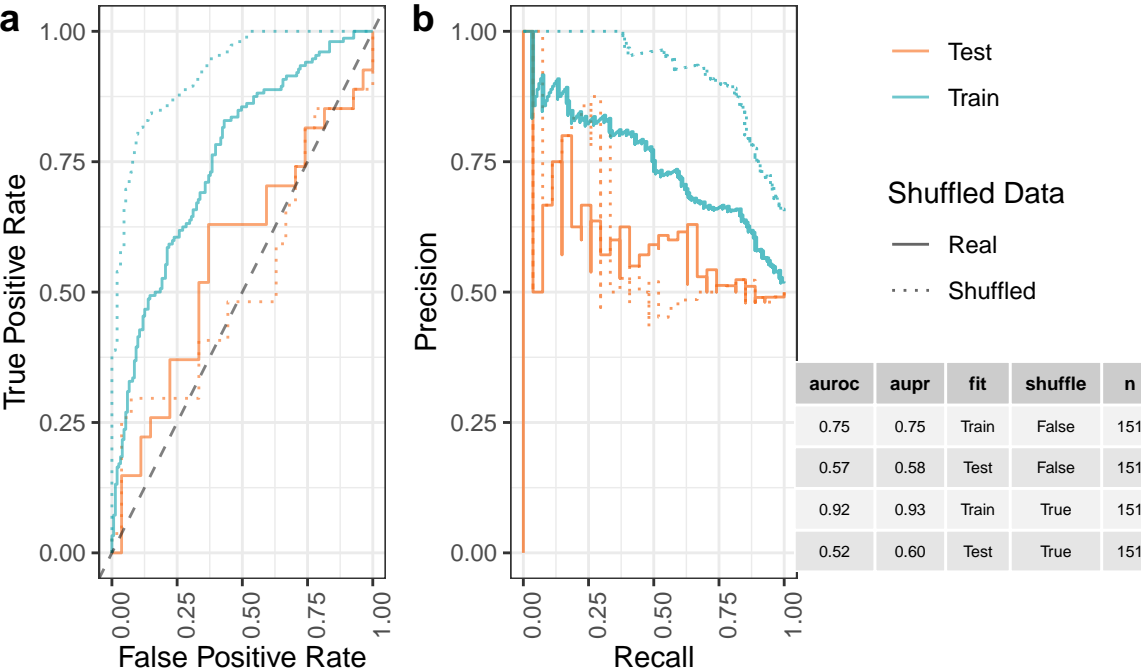
Performance: cc_polyloid_n_spots_mean



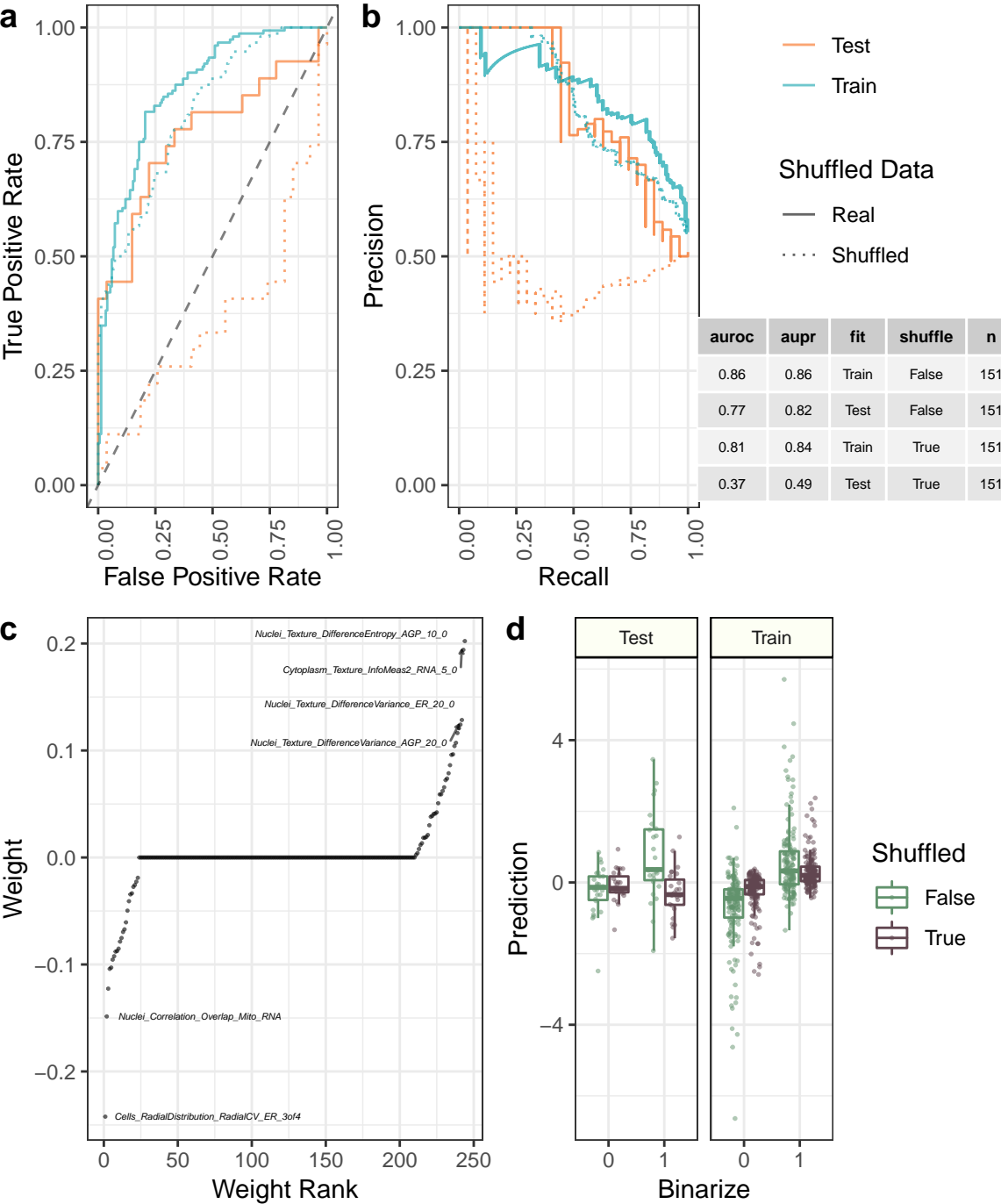
Performance: cc_polyloid_n_spots_per_nucleus_area_mean



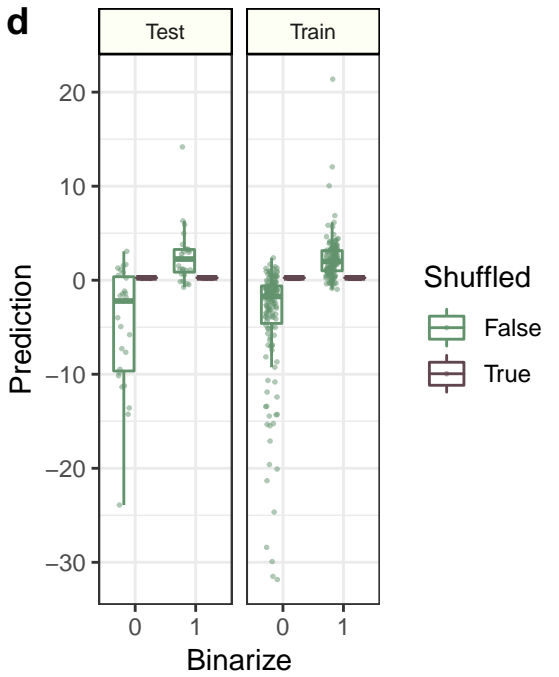
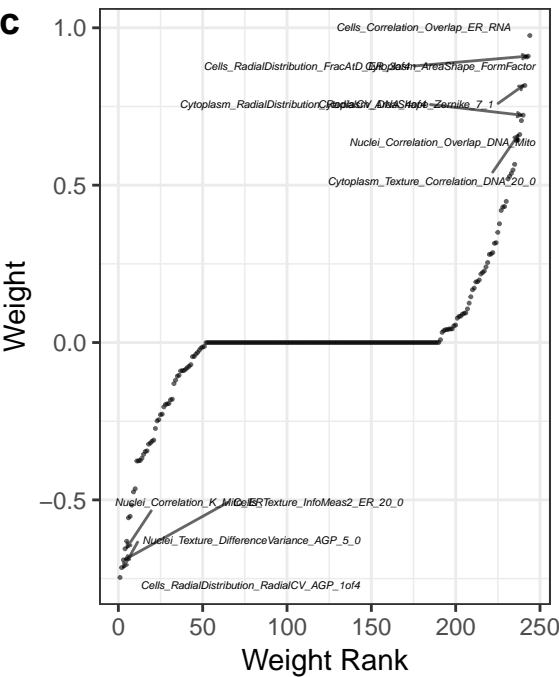
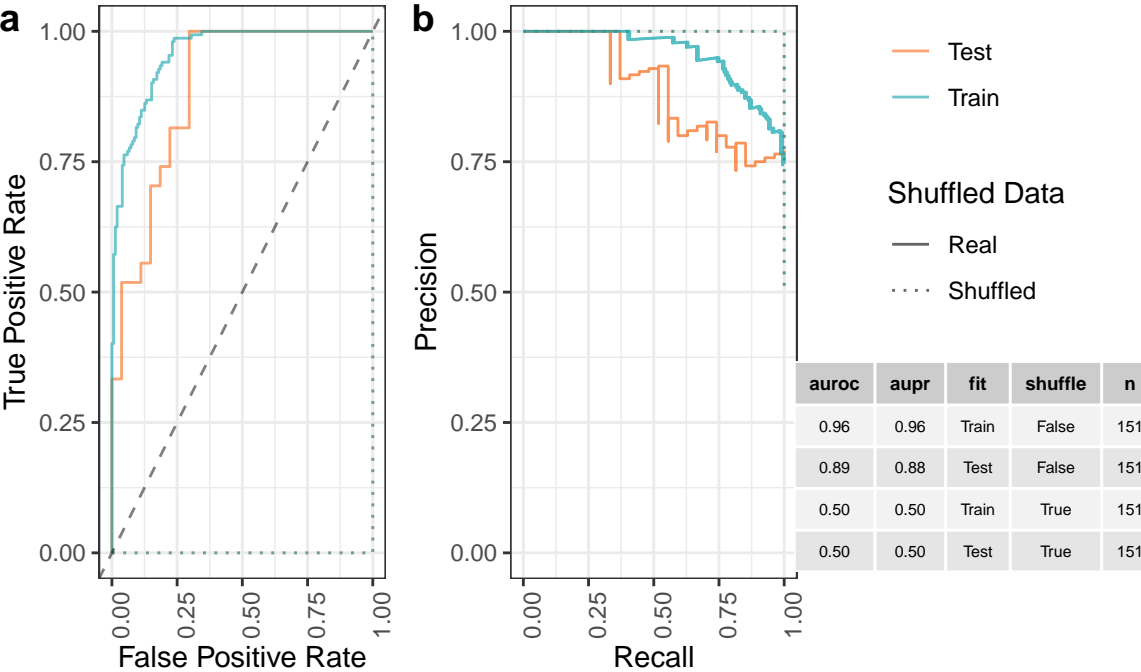
Performance: vb_infection_percentage



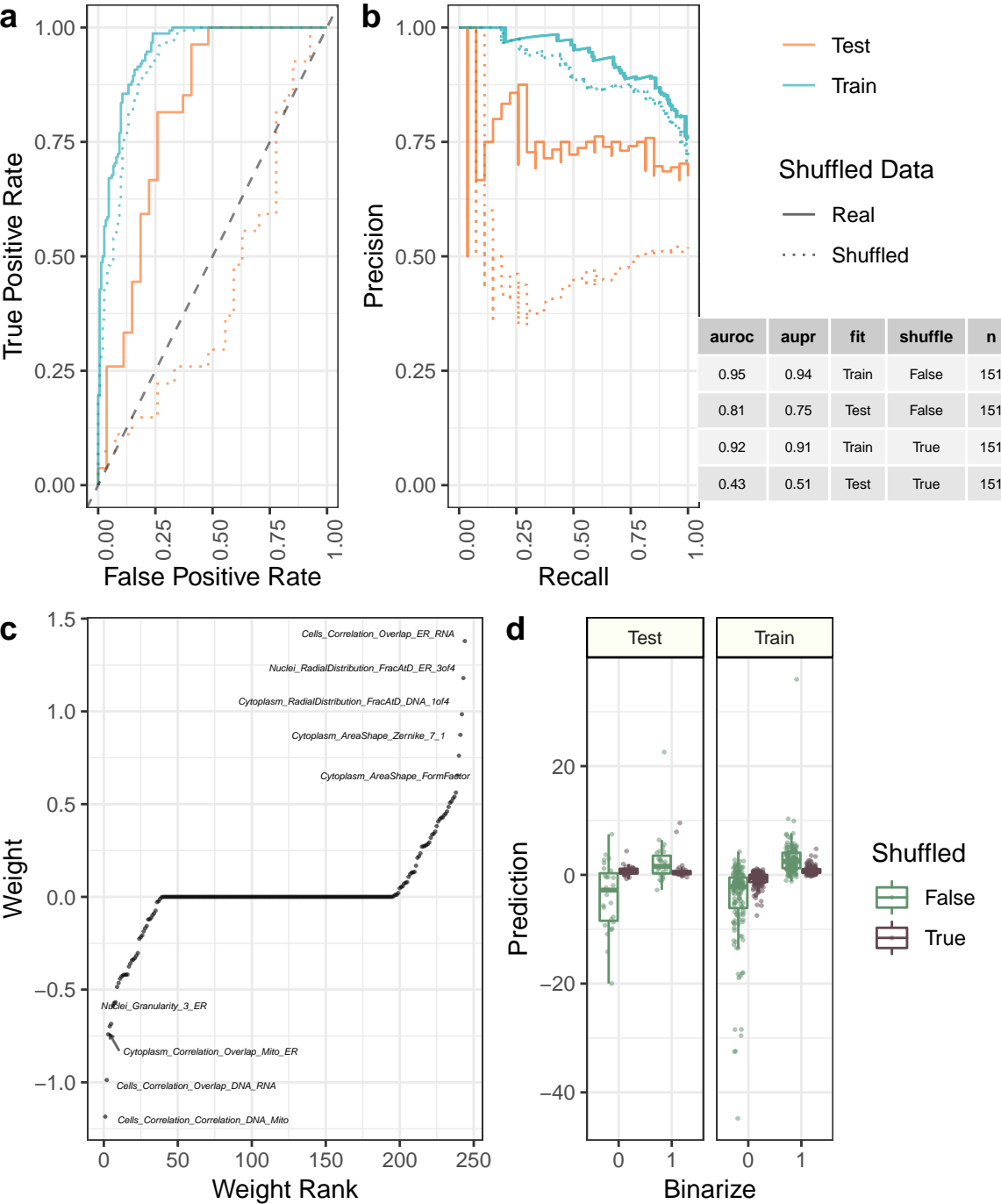
Performance: vb_live_cell_area



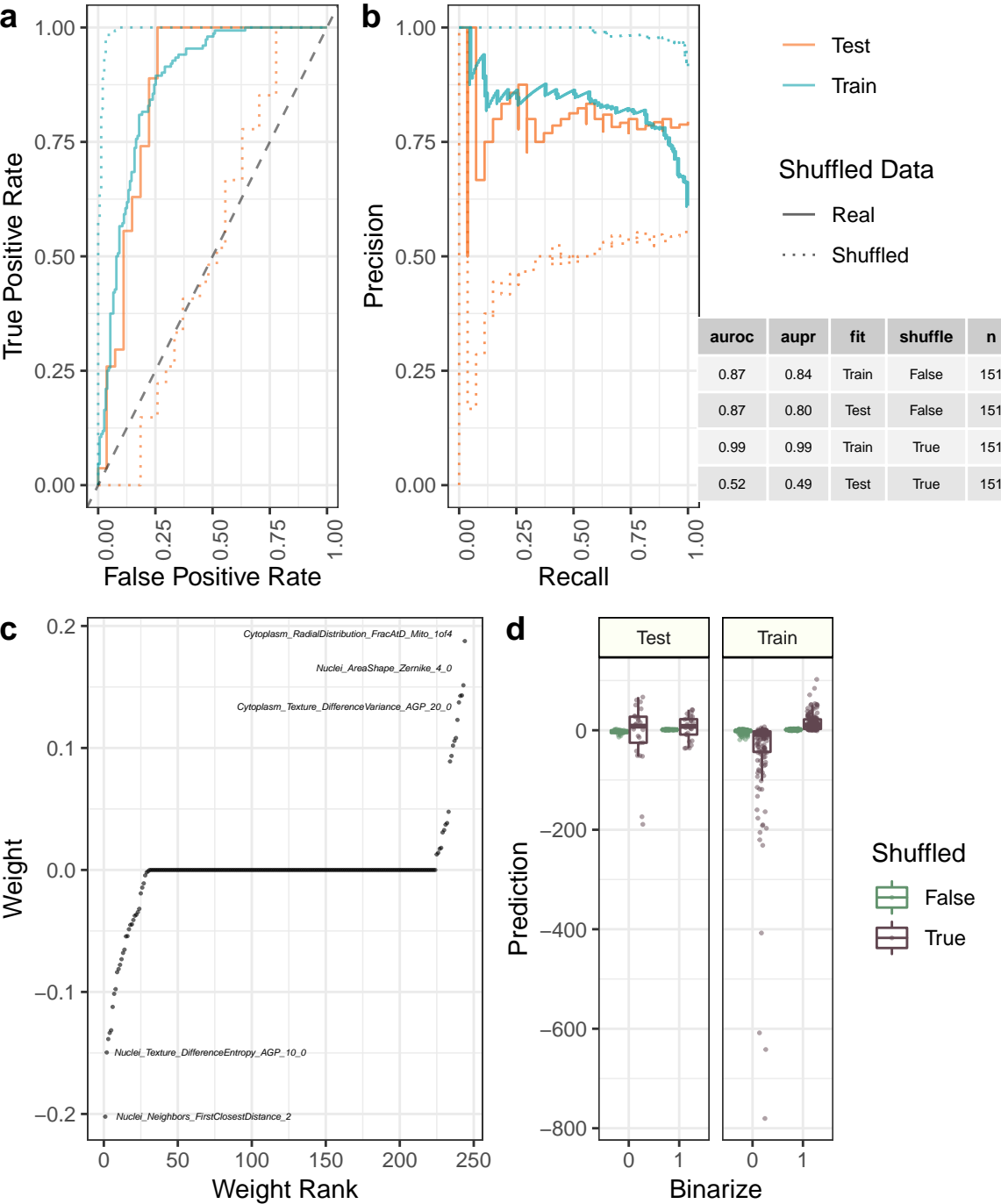
Performance: vb_live_cell_roundness



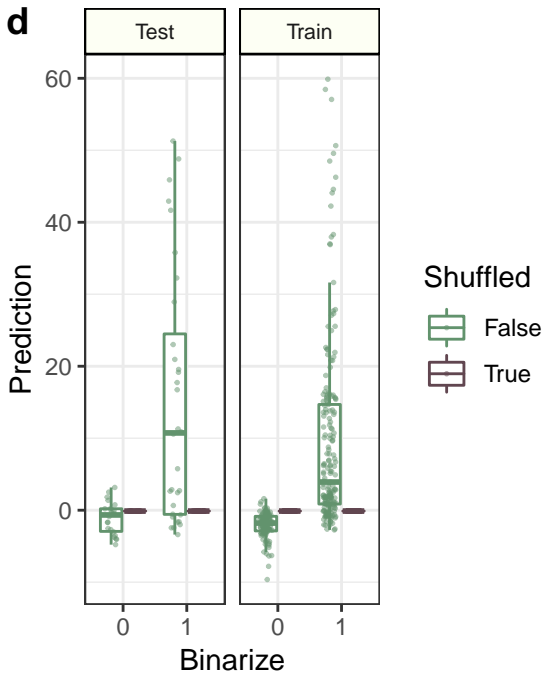
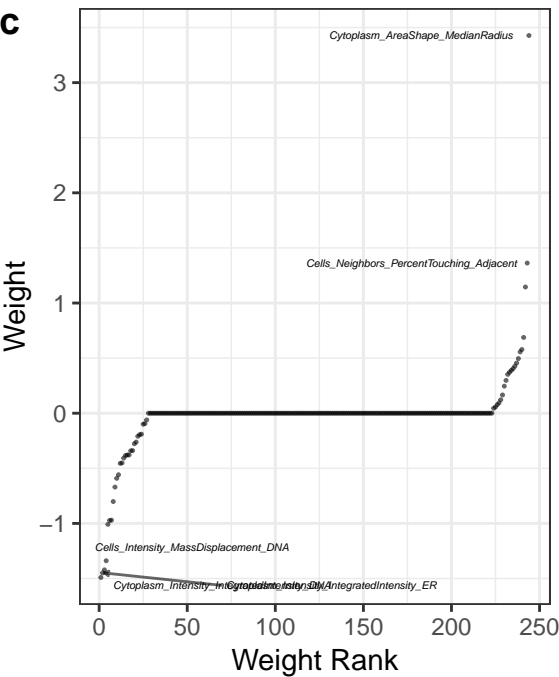
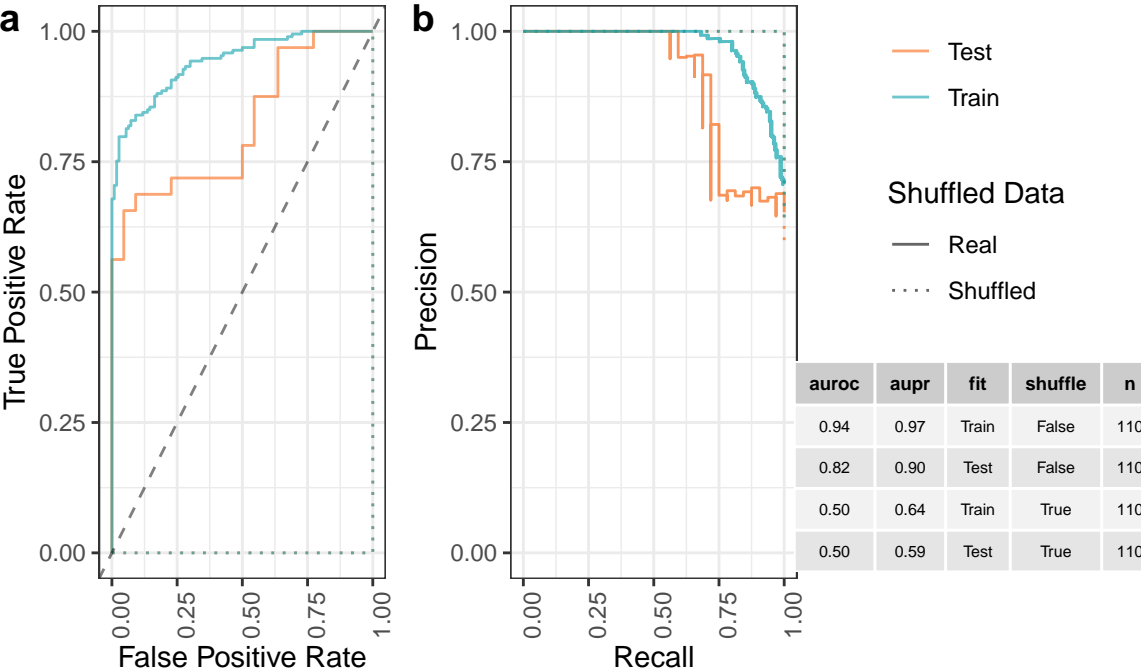
Performance: vb_live_cell_width_length



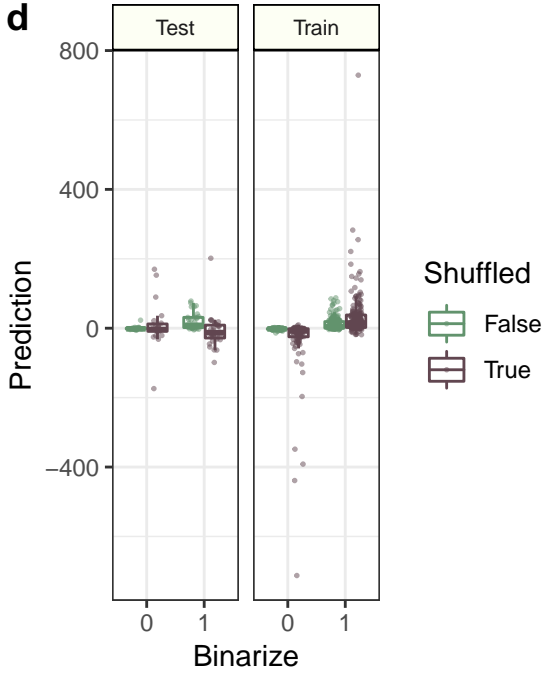
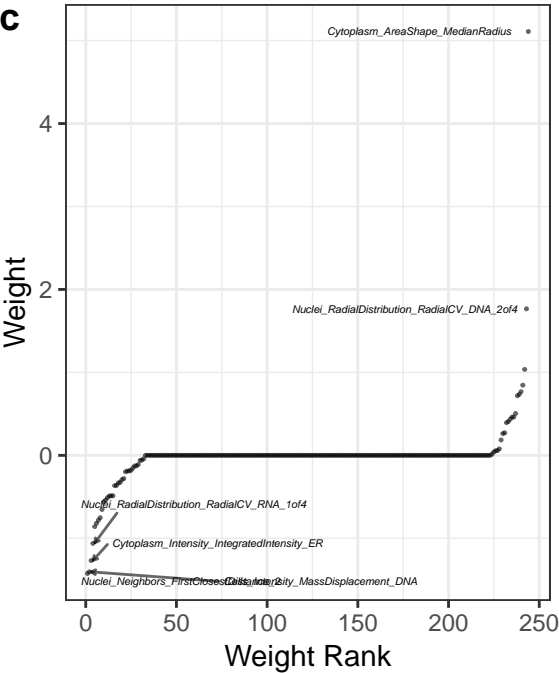
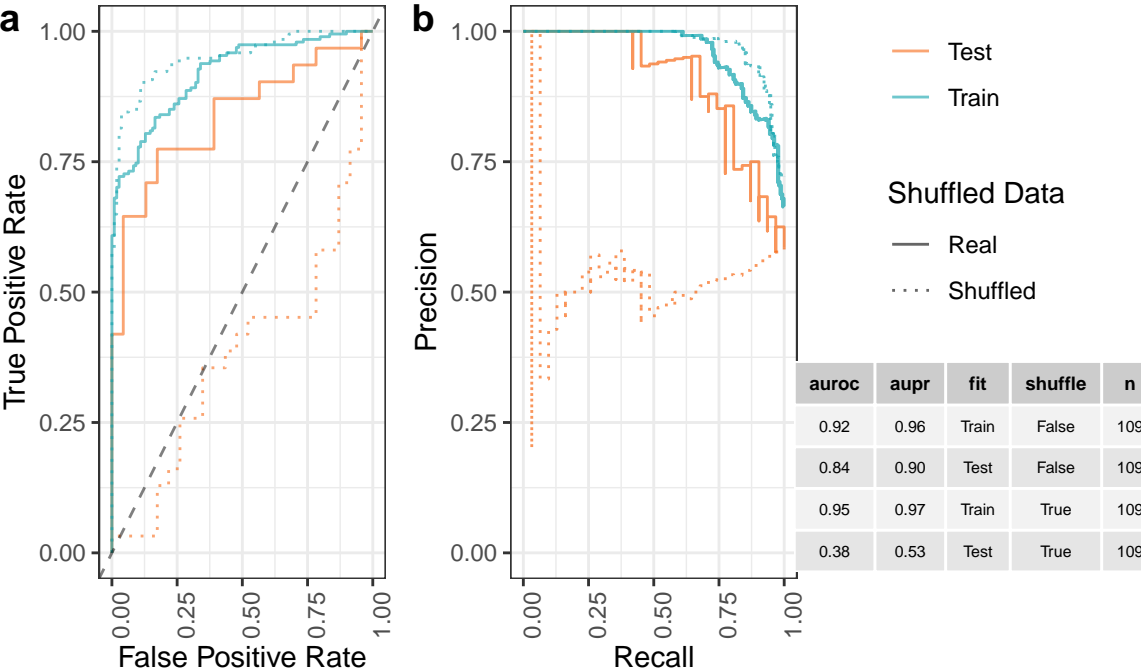
Performance: vb_num_live_cells



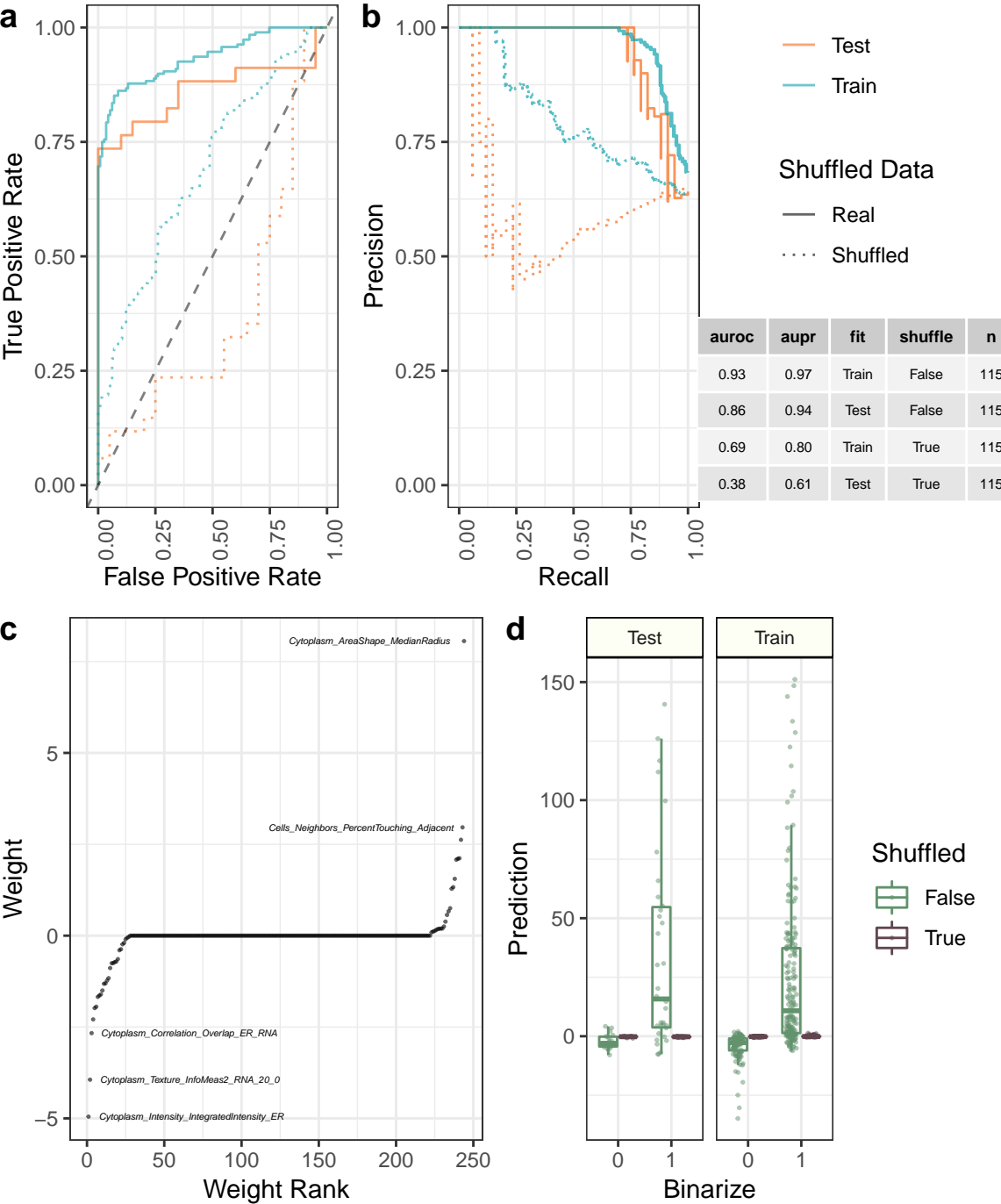
Performance: vb_percent_all_apoptosis



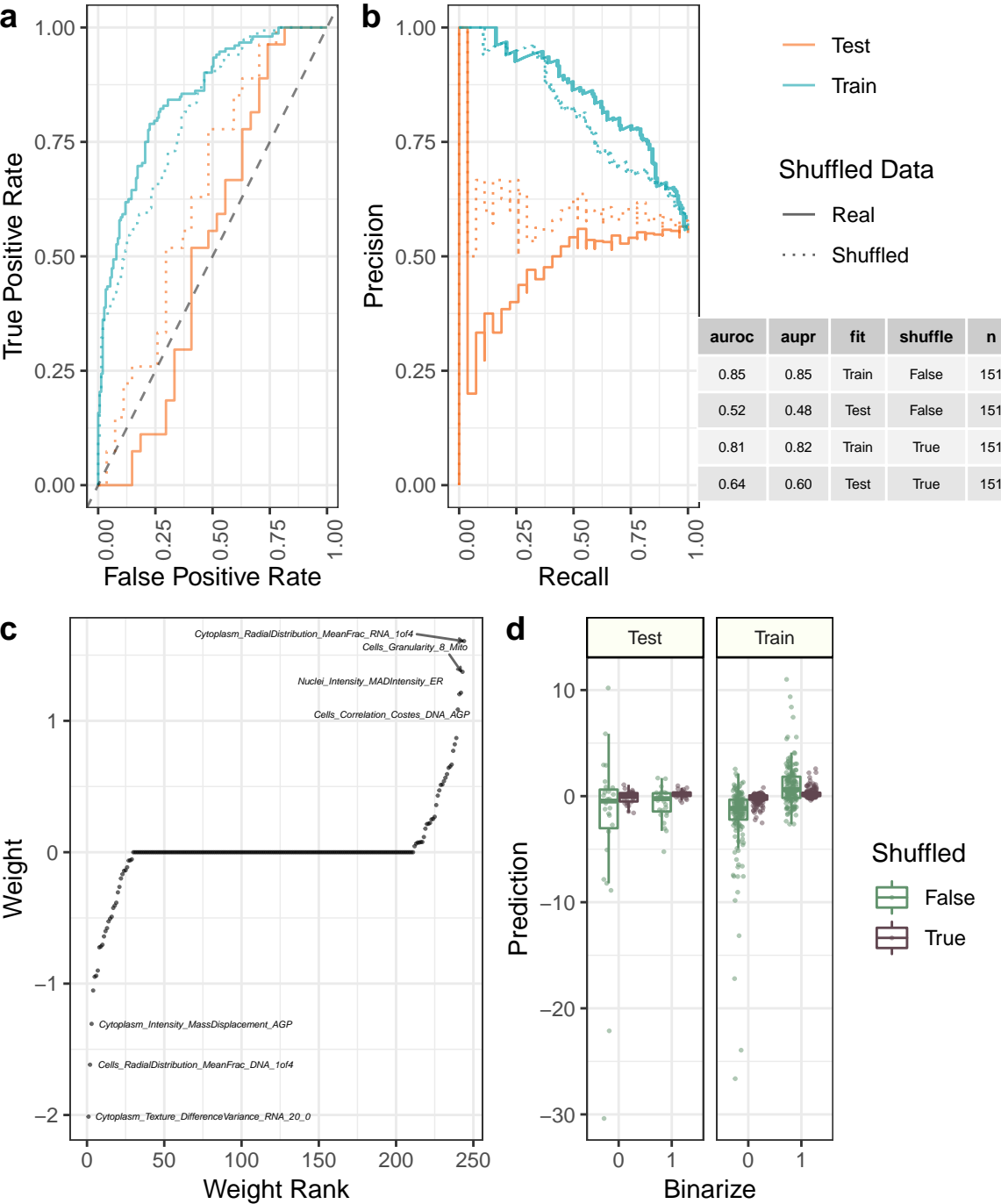
Performance: vb_percent_all_early_apoptosis



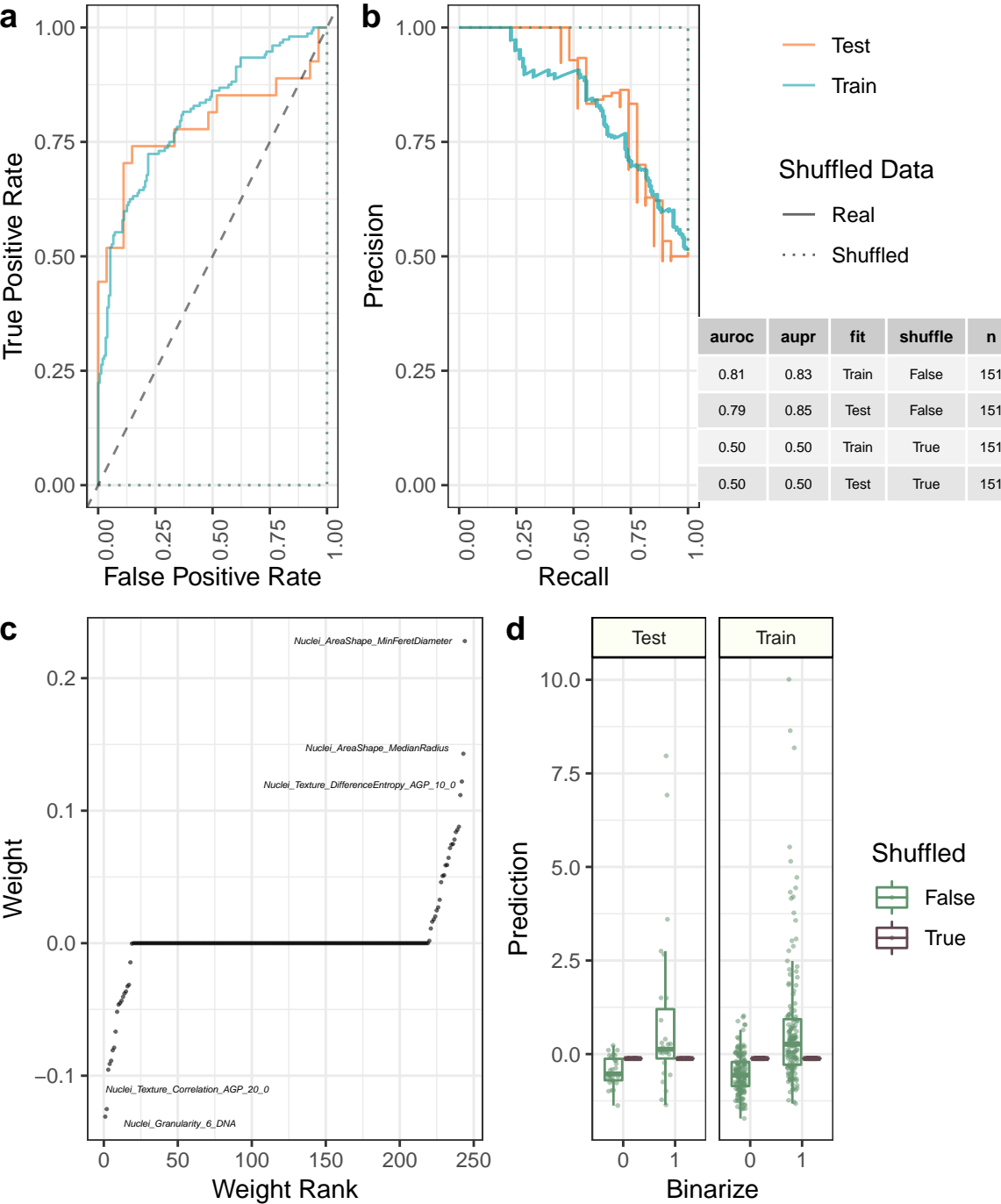
Performance: vb_percent_all_late_apoptosis



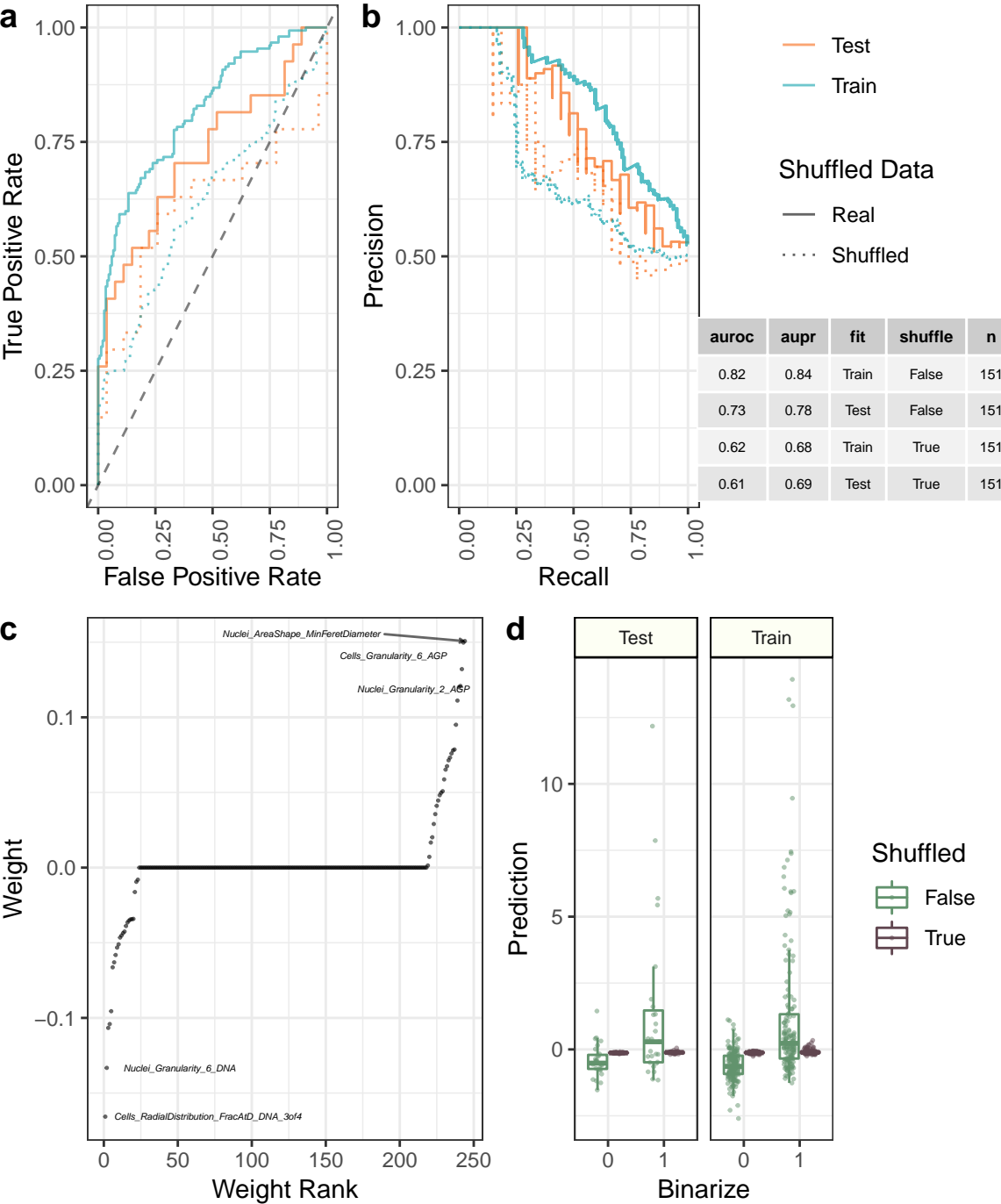
Performance: vb_percent_caspase_dead_only



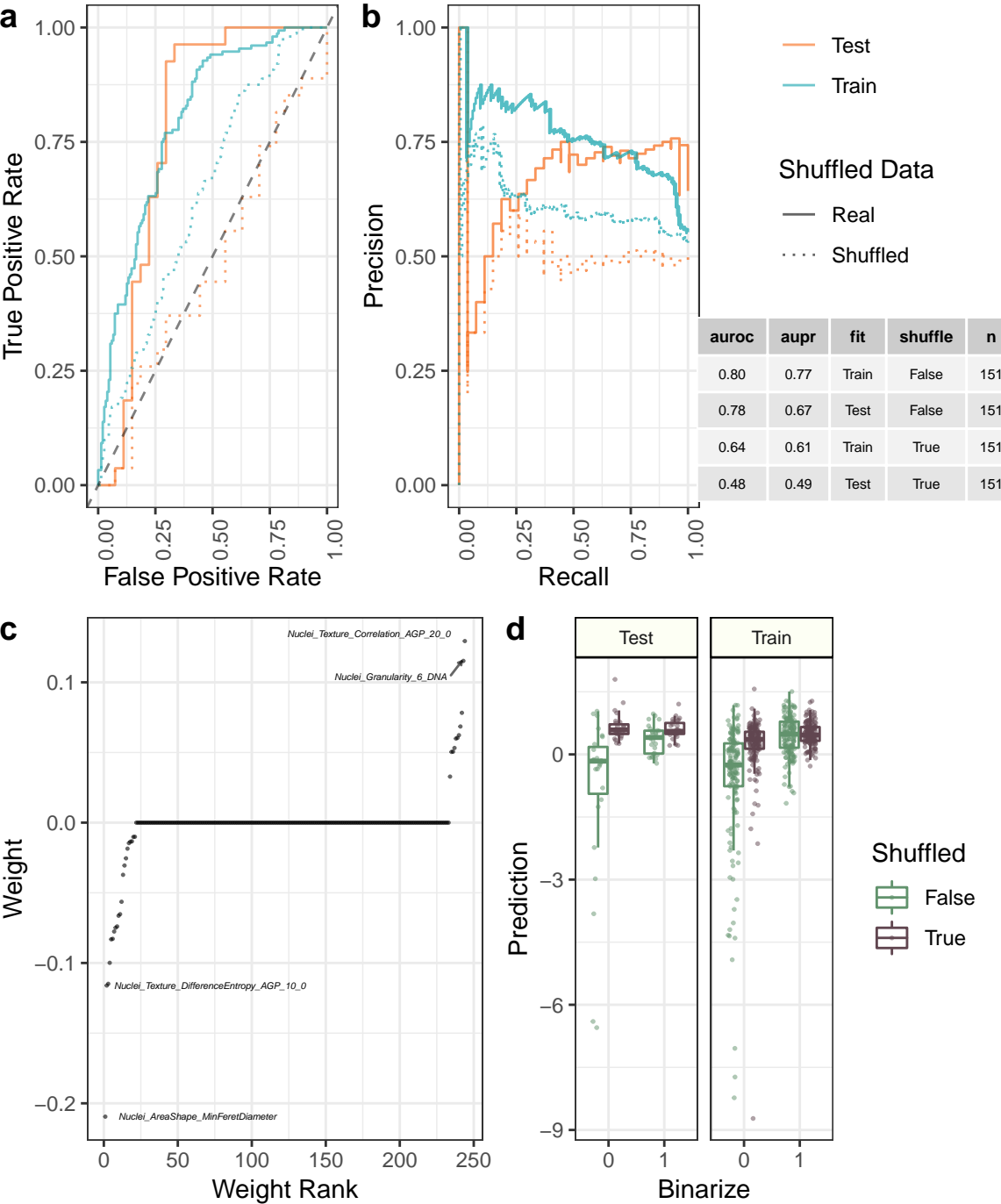
Performance: vb_percent_dead



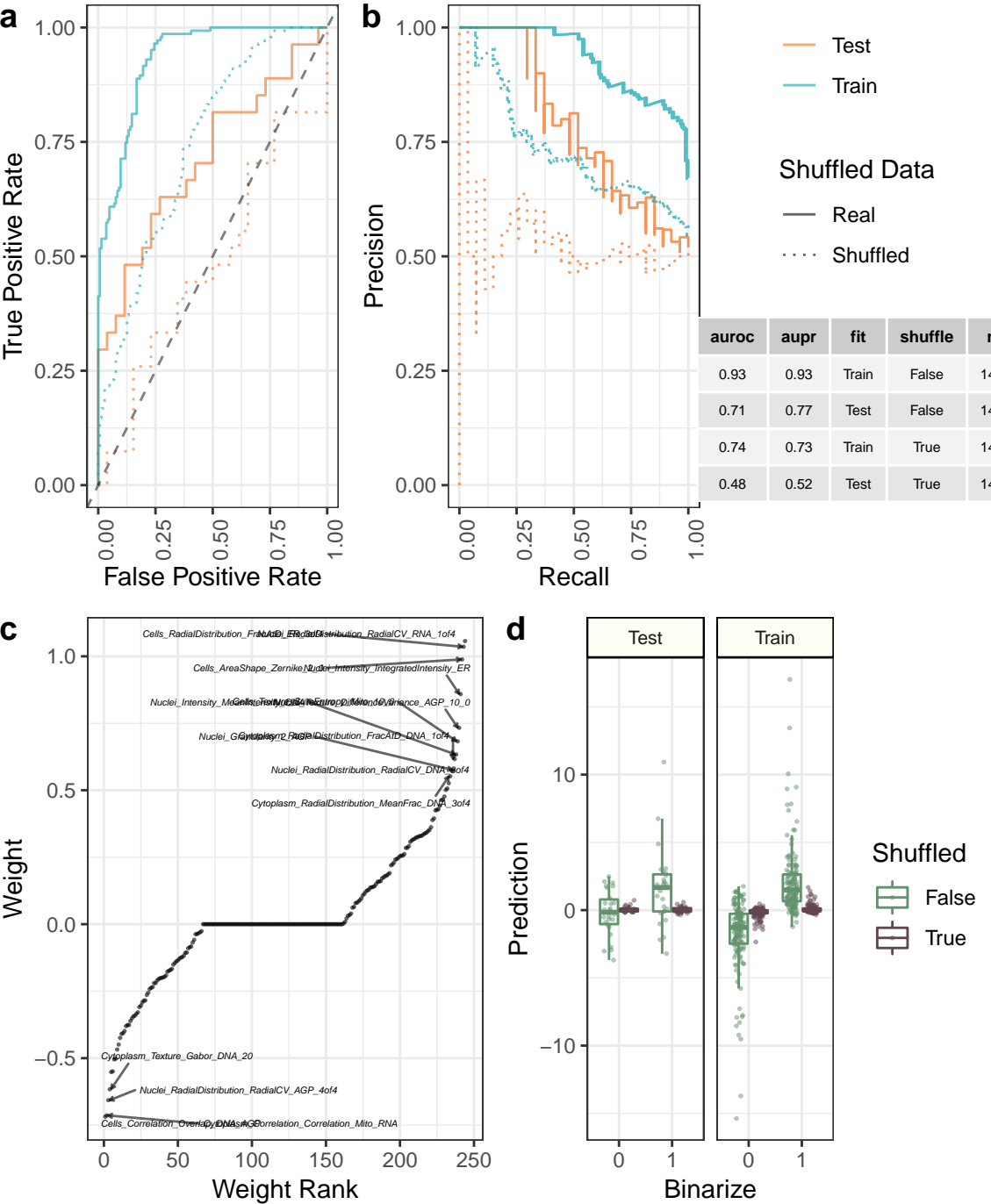
Performance: vb_percent_dead_only



Performance: vb_percent_live



Performance: vb_ros_back_mean



Performance: vb_ros_mean

