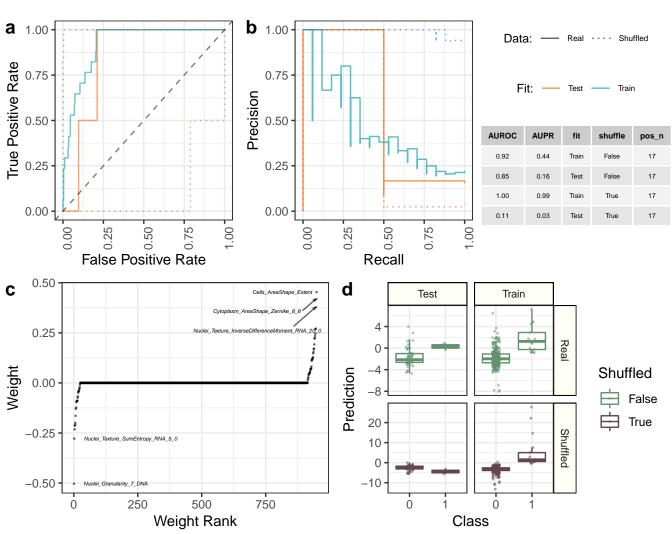
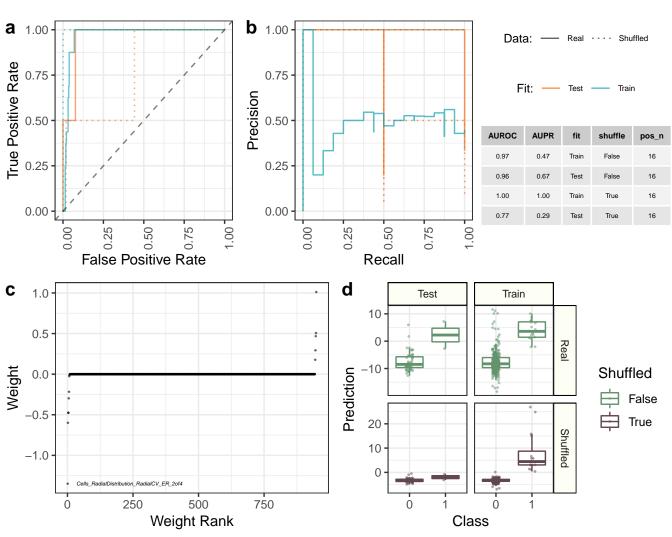
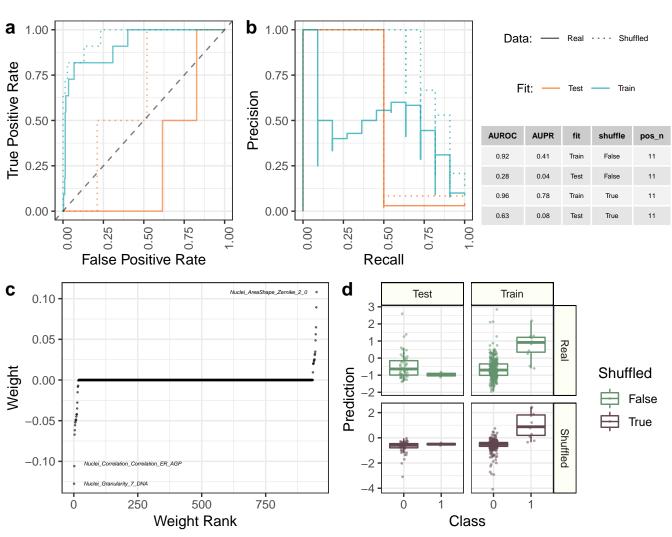
Performance: cc_early_mitosis_high_h2ax



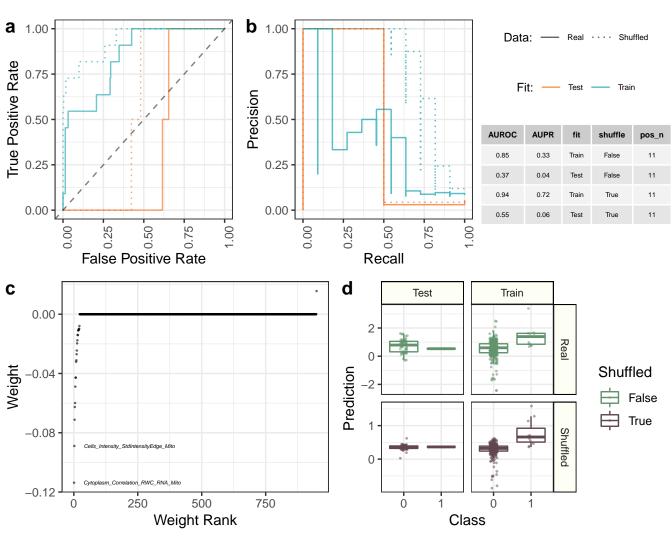
Performance: cc_g2_plus_all_m_count



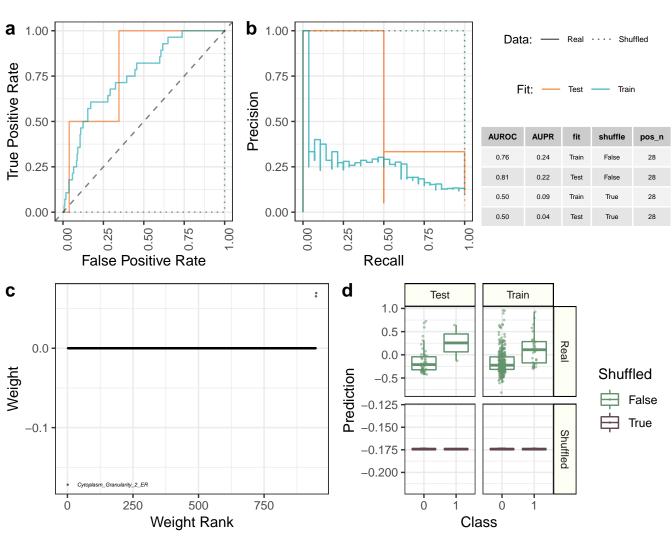
Performance: cc_infection_percentage



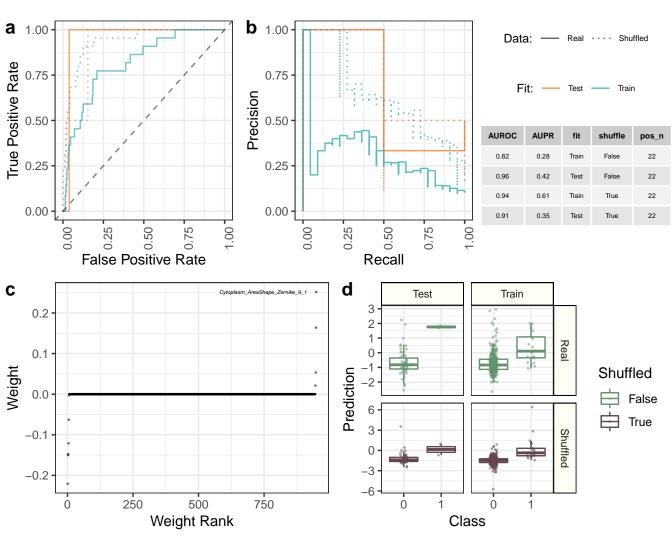
Performance: cc_late_mitosis_n_spots_h2ax_per_nucleus_area_mean



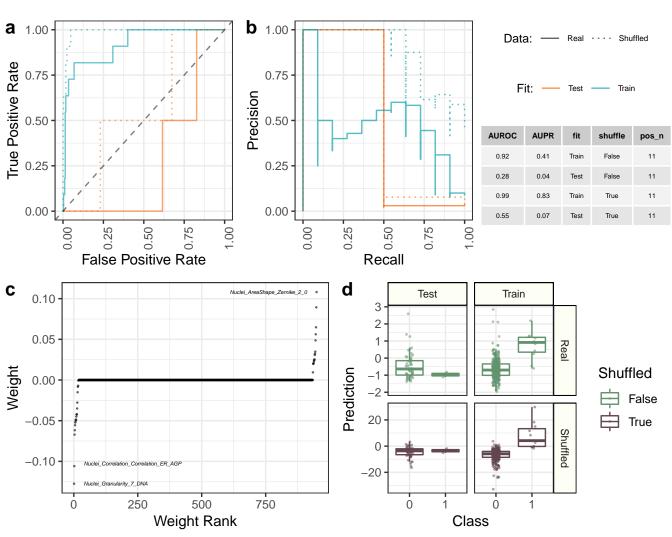
Performance: cc_mitosis_n_spots_h2ax_per_nucleus_area_mean



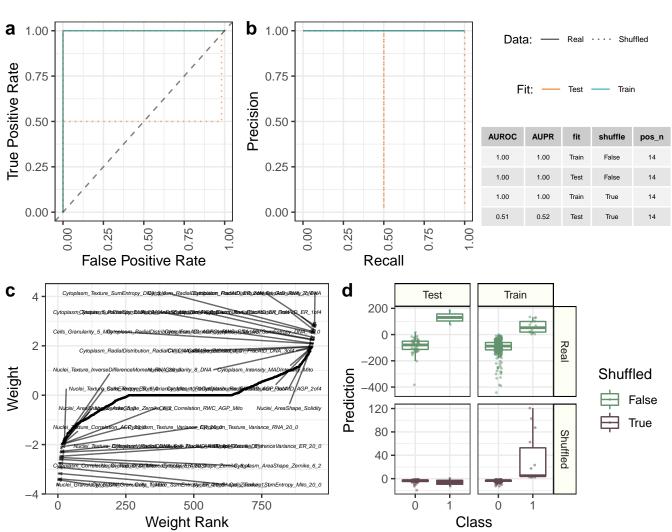
Performance: cc_polynuclear_high_h2ax



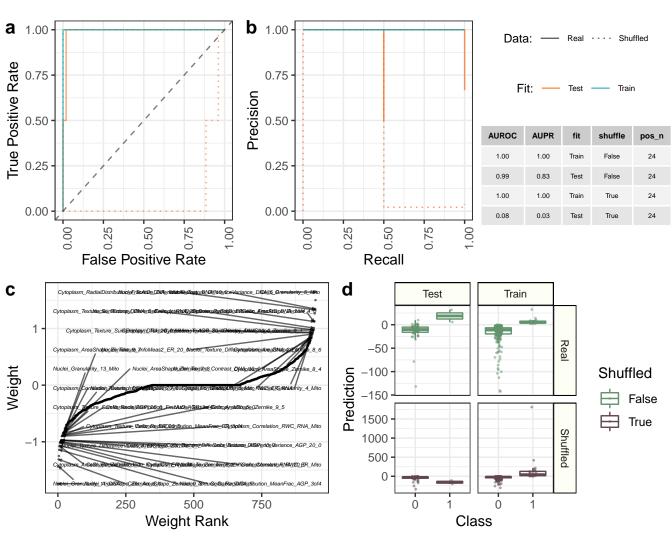
Performance: vb_infection_percentage



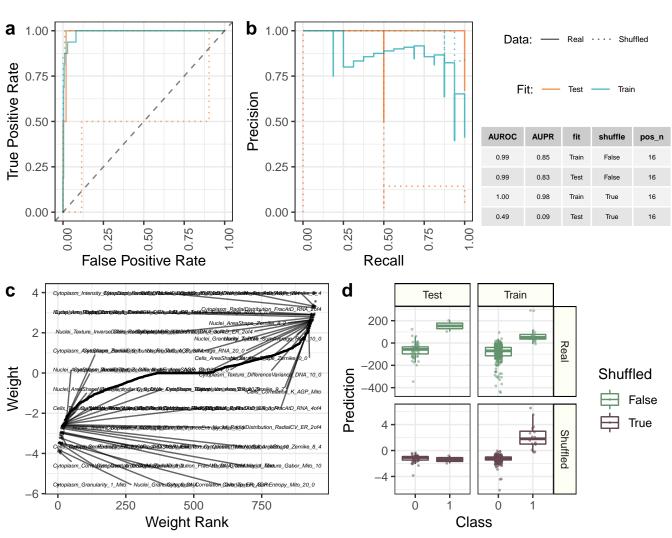
Performance: vb_percent_all_apoptosis



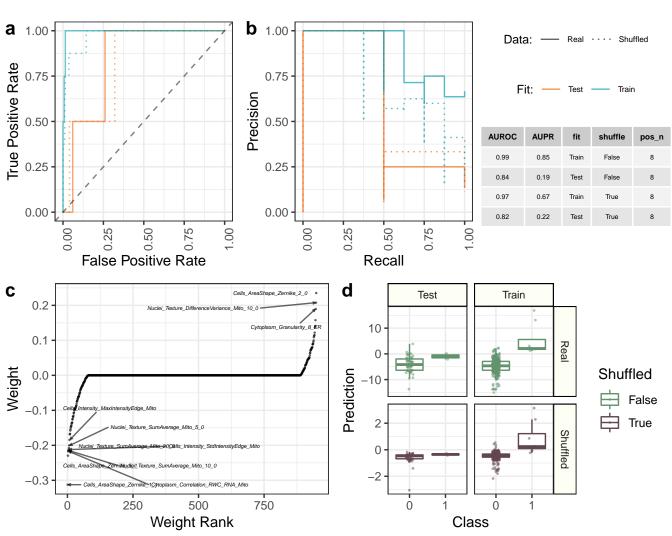
Performance: vb_percent_caspase_dead_only



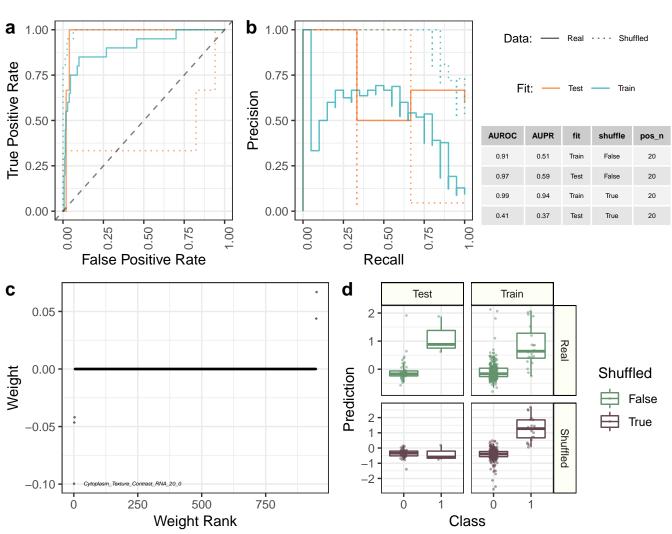
Performance: vb_percent_early_apoptosis



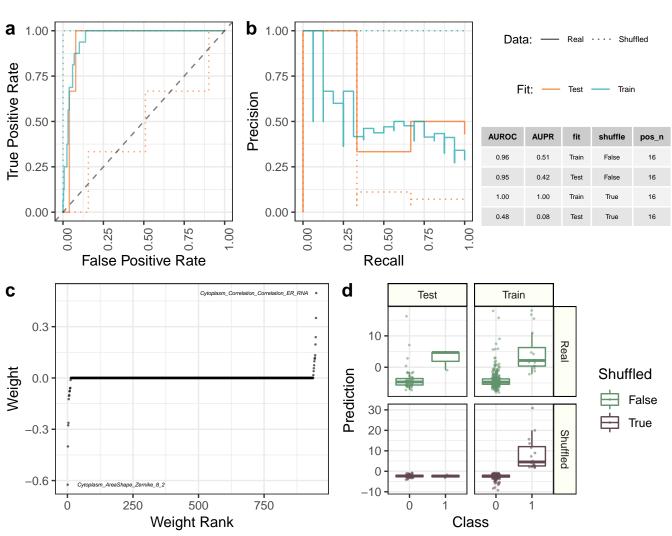
Performance: vb_ros_mean



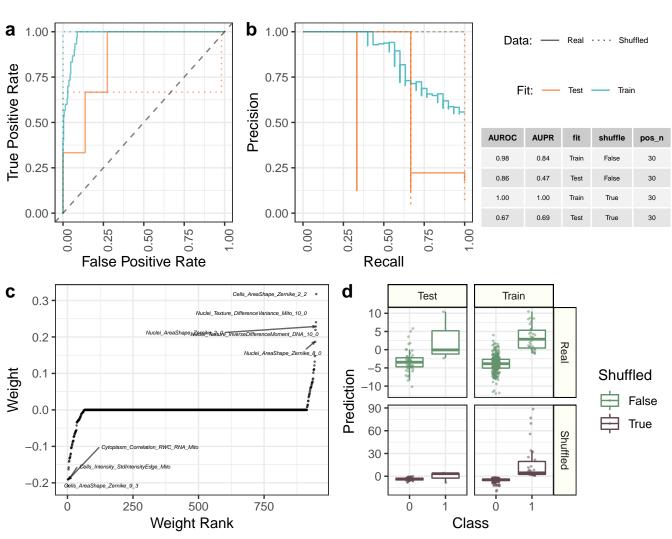
Performance: cc_cc_g1



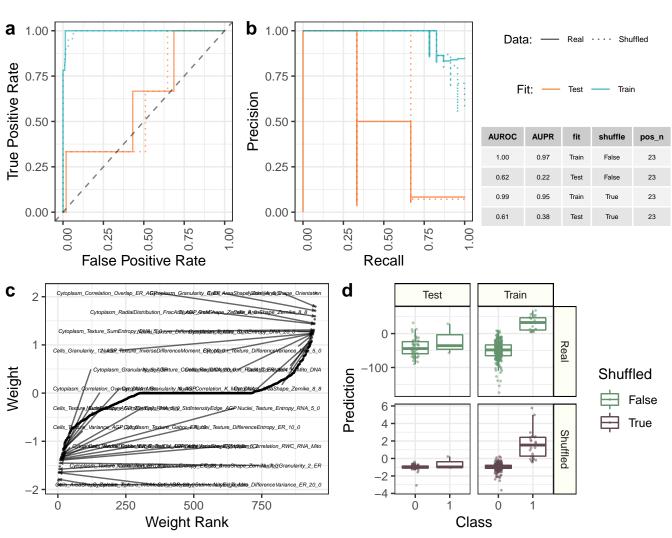
Performance: cc_cc_g2



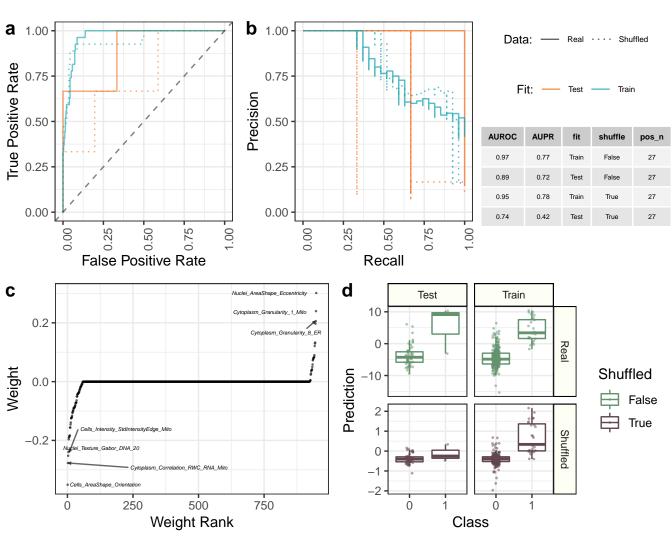
Performance: cc_cc_n_spots_h2ax_mean



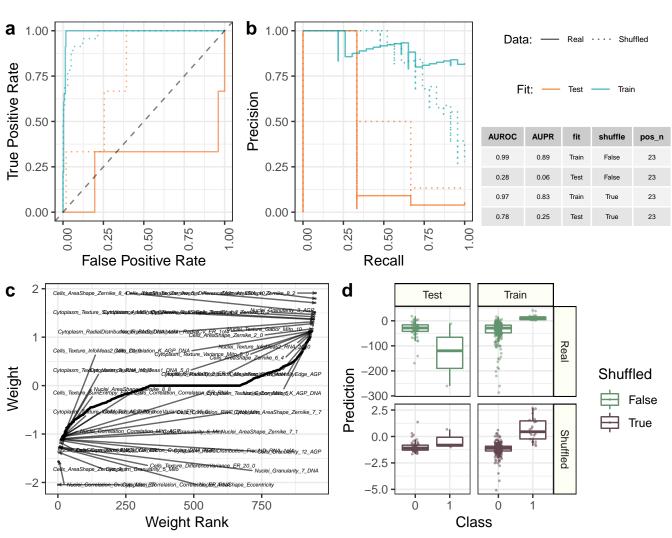
Performance: cc_g2_high_h2ax



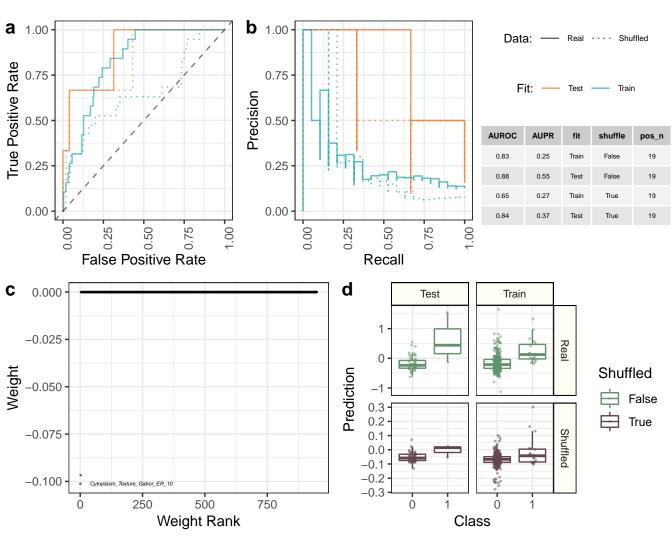
Performance: cc_g2_n_spots_h2ax_per_nucleus_area_mean



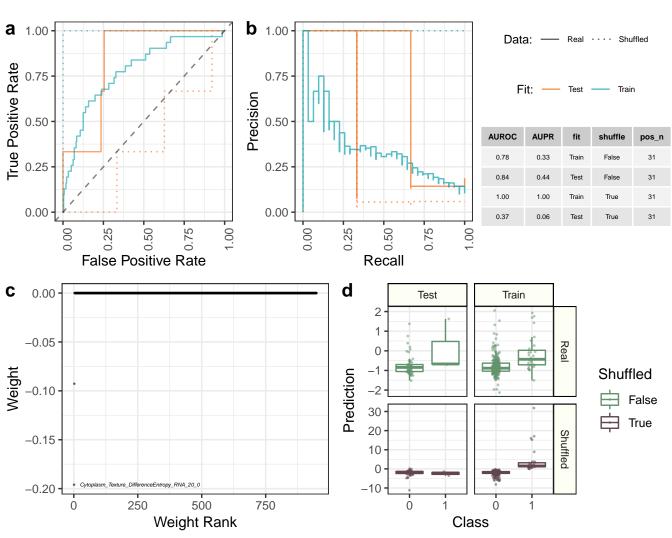
Performance: cc_mitosis_n_spots_h2ax_mean



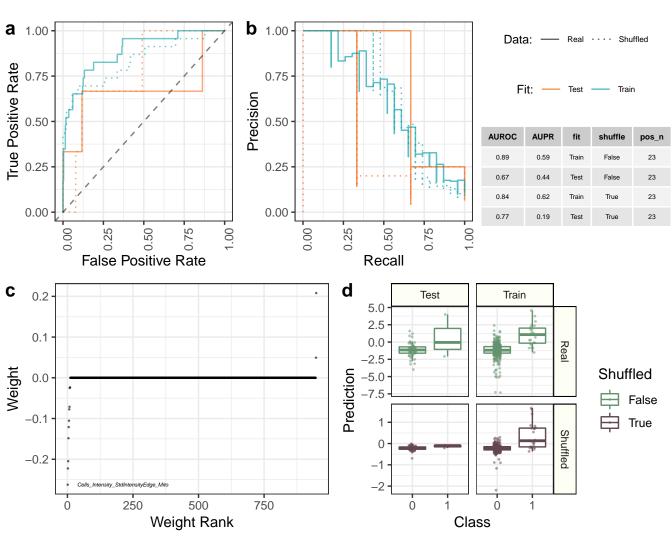
Performance: cc_polynuclear_n_spots_h2ax_per_nucleus_area_mean



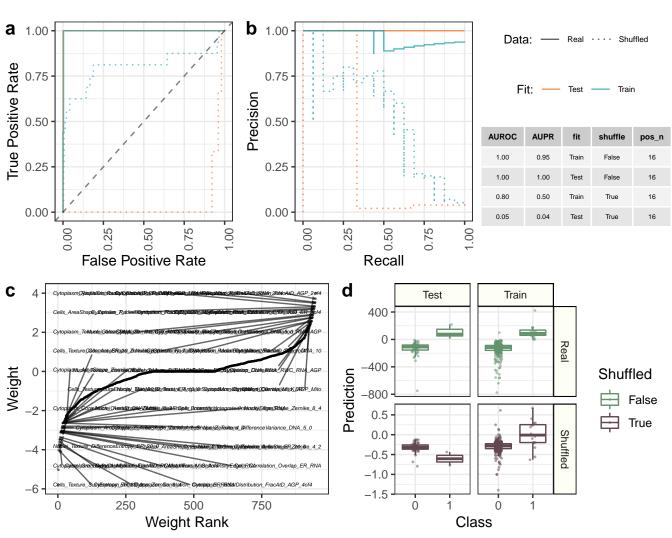
Performance: cc_polyploid_n_spots_h2ax_mean



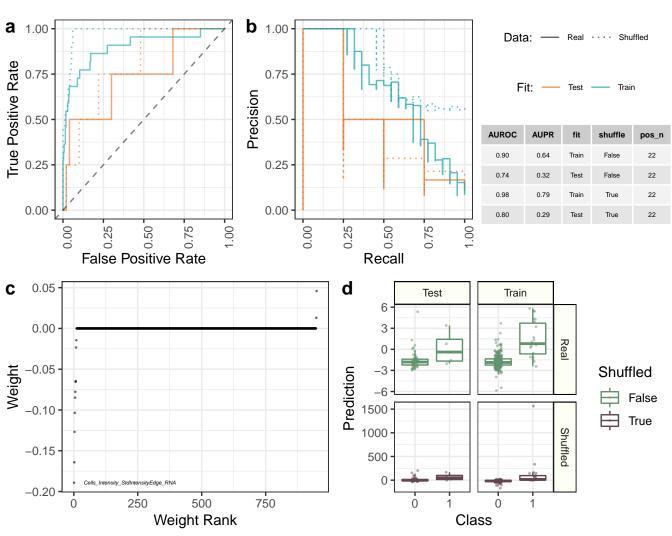
Performance: cc_s_n_spots_h2ax_mean



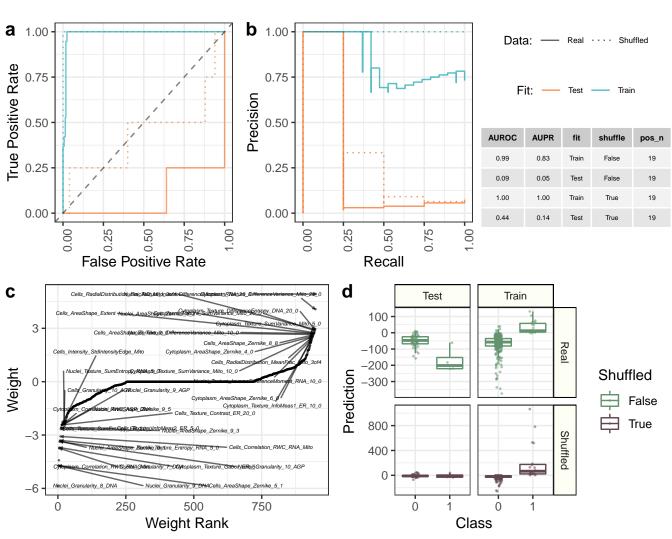
Performance: vb_percent_dead



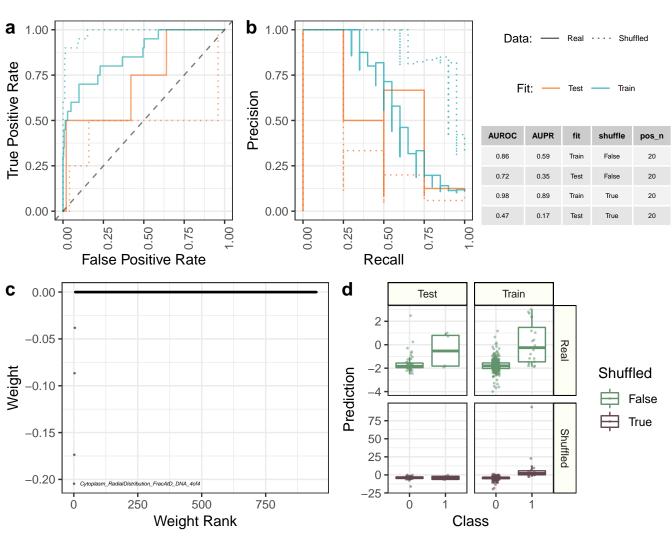
Performance: cc_cc_high_h2ax



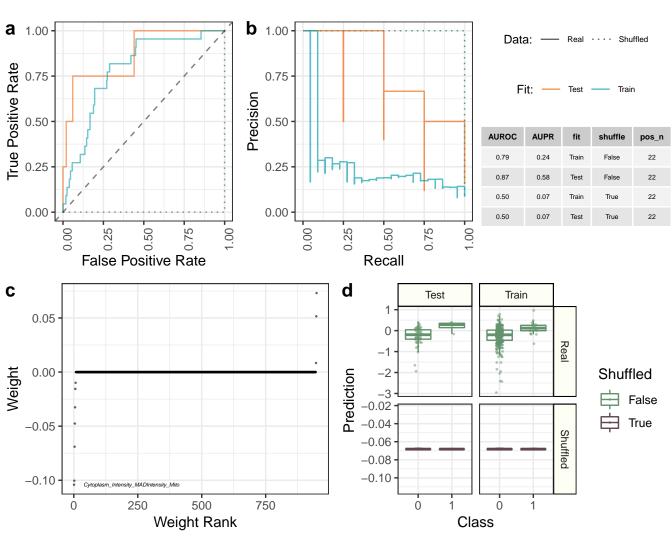
Performance: cc_early_mitosis_n_spots_h2ax_mean



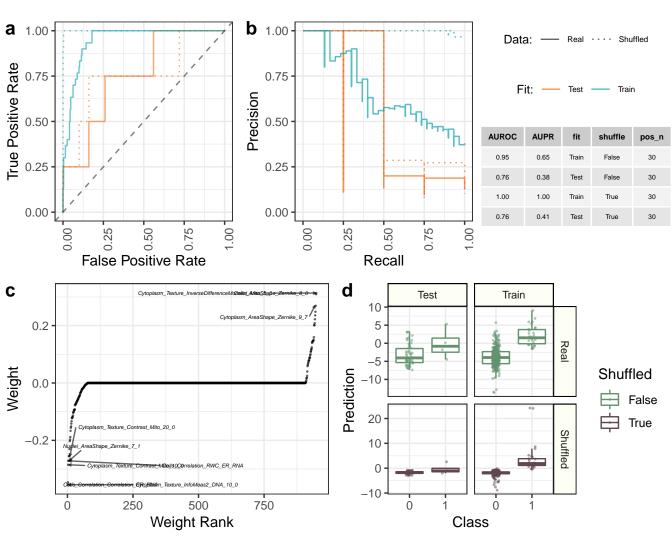
Performance: cc_g1_high_h2ax



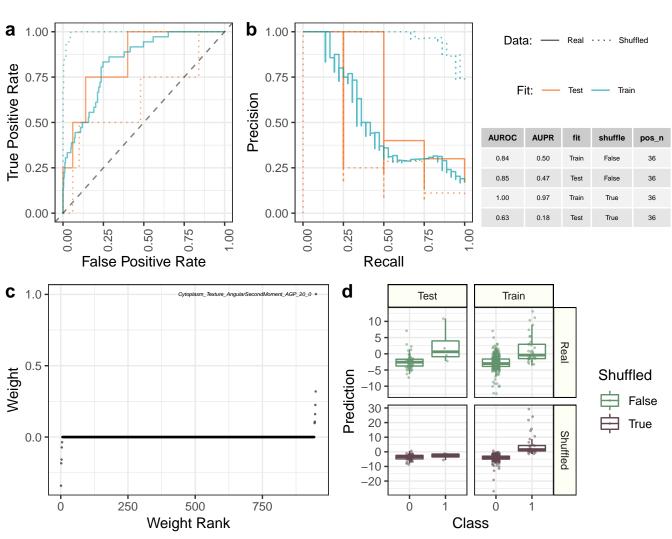
Performance: cc_mitosis_n_objects



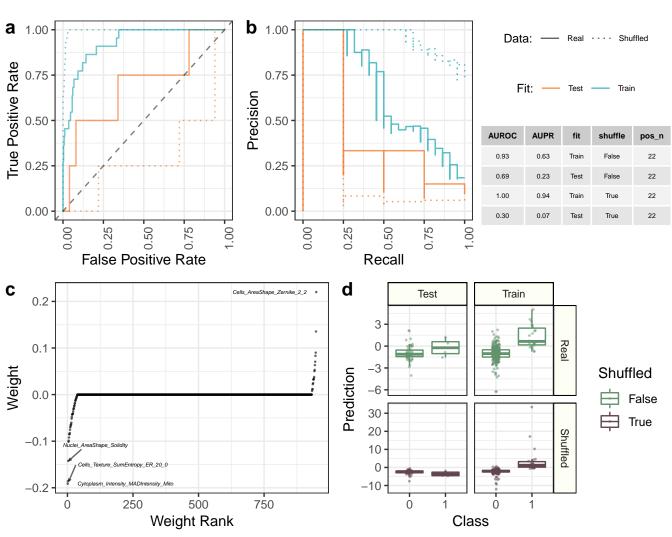
Performance: cc_polyploid_high_h2ax



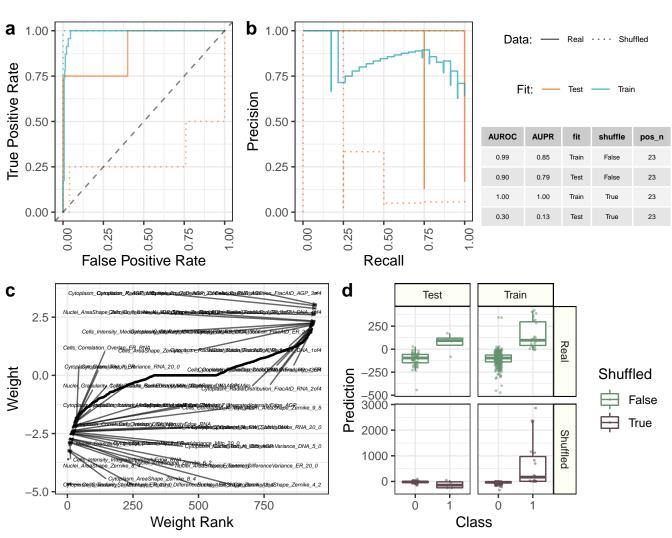
Performance: cc_polyploid_n_spots_h2ax_per_nucleus_area_mean



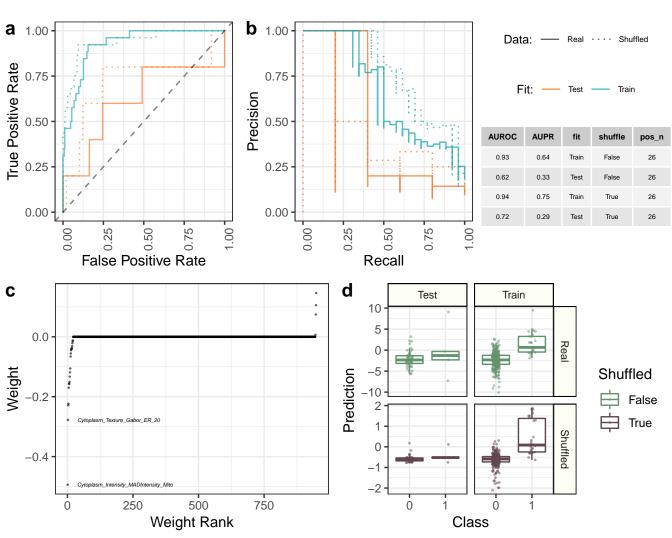
Performance: cc_s_high_h2ax



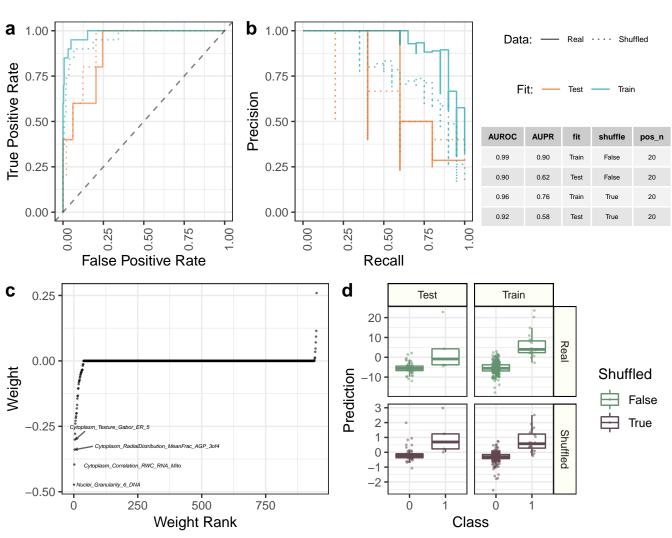
Performance: vb_percent_dead_only



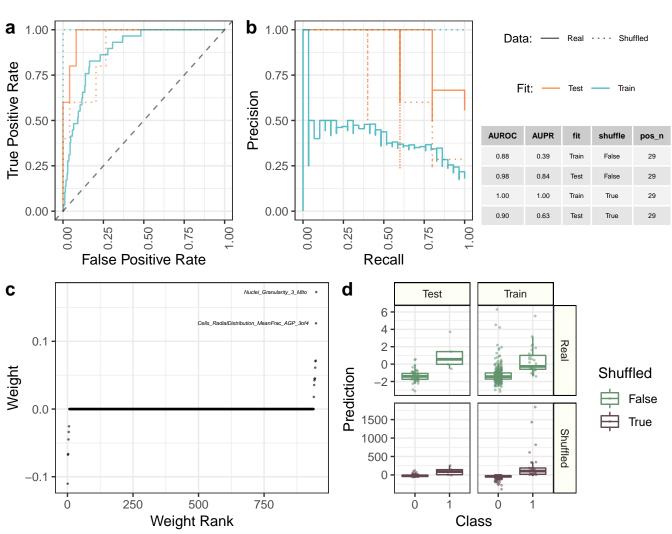
Performance: cc_all_n_spots_h2ax_mean



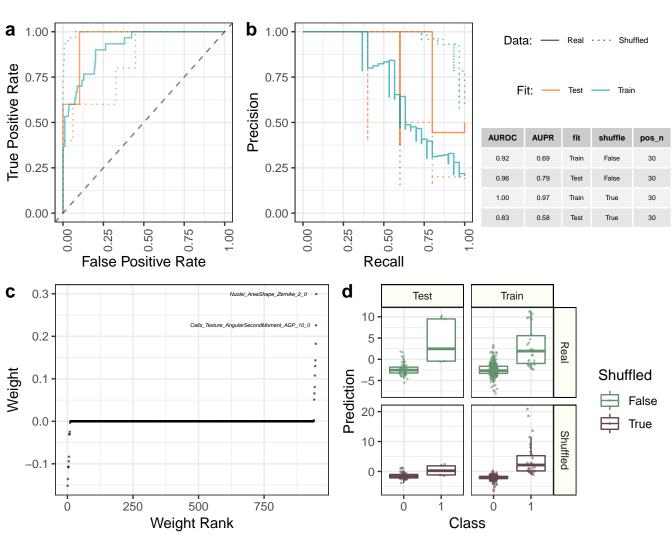
Performance: cc_all_nucleus_area_mean



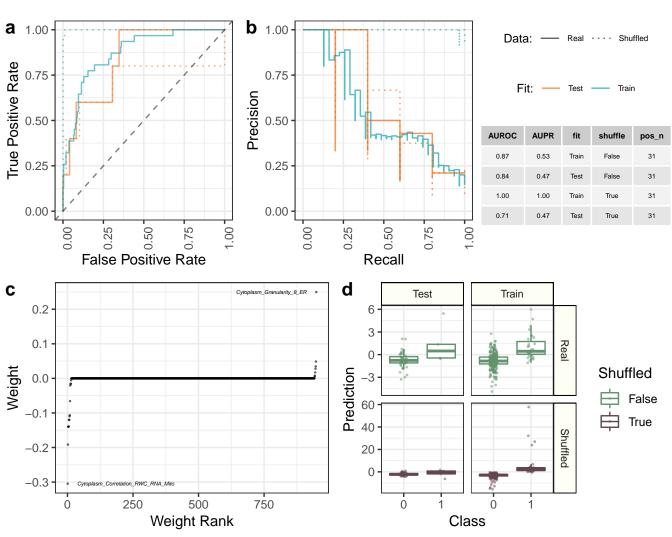
Performance: cc_cc_early_mitosis



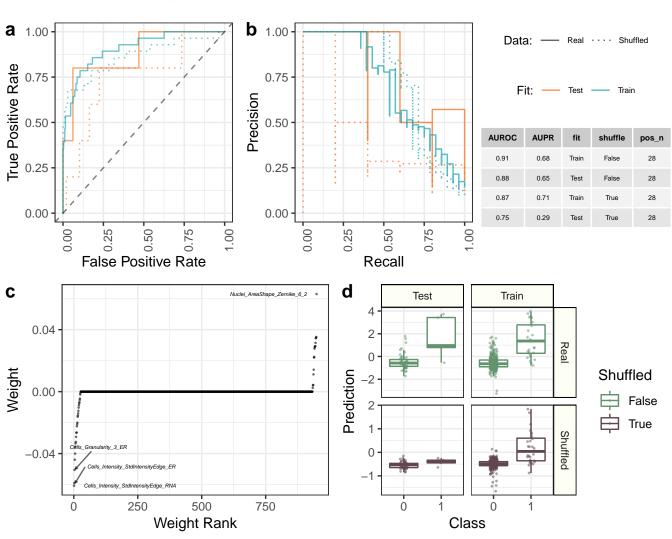
Performance: cc_cc_n_spots_h2ax_per_nucleus_area_mean



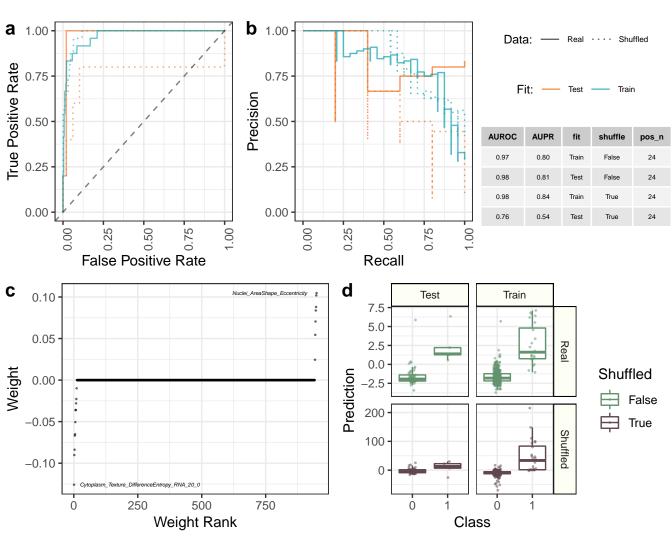
Performance: cc_early_mitosis_n_spots_h2ax_per_nucleus_area_mean



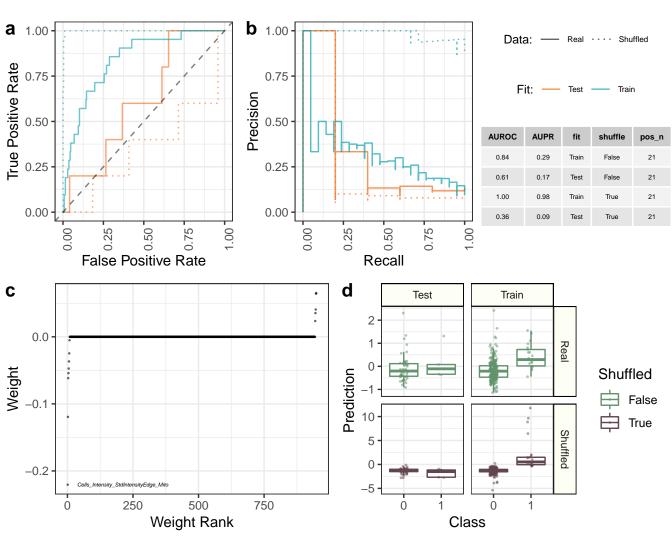
Performance: cc_g1_n_spots_h2ax_mean



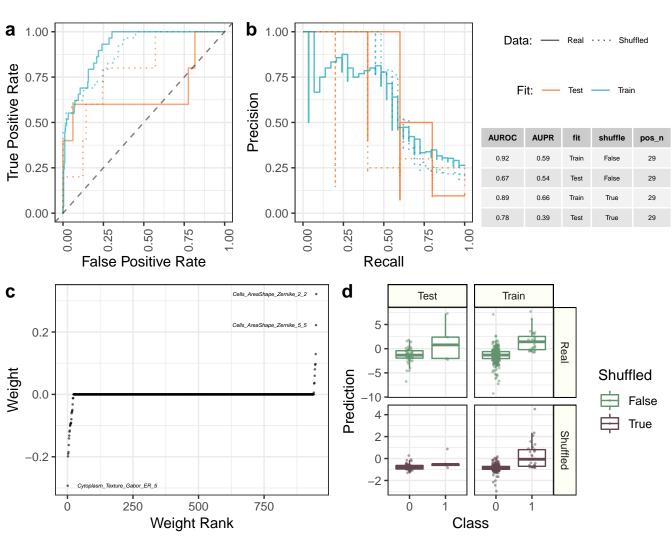
Performance: cc_g1_plus_g2_count



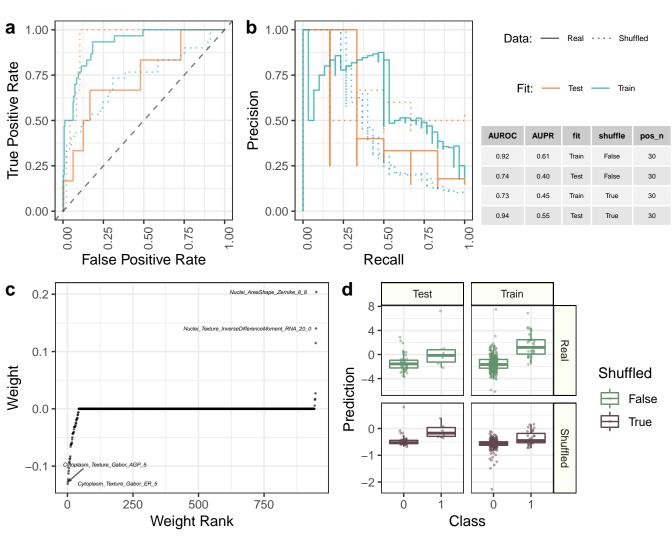
Performance: cc_late_mitosis_n_spots_h2ax_mean



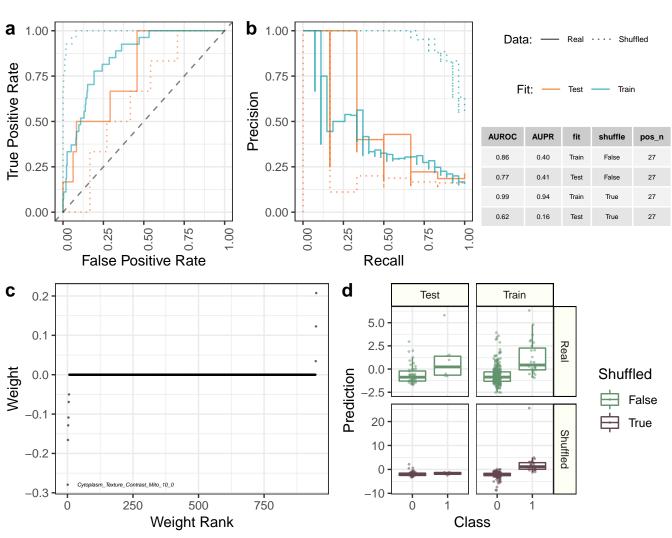
Performance: cc_s_n_spots_h2ax_per_nucleus_area_mean



Performance: cc_all_high_h2ax



Performance: cc_all_n_spots_h2ax_per_nucleus_area_mean



Performance: cc_g1_n_spots_h2ax_per_nucleus_area_mean

