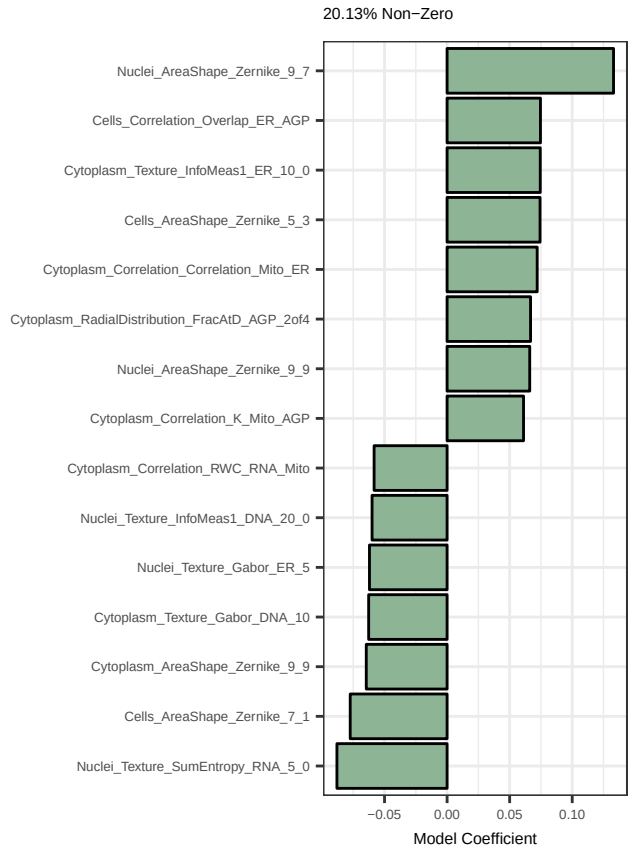
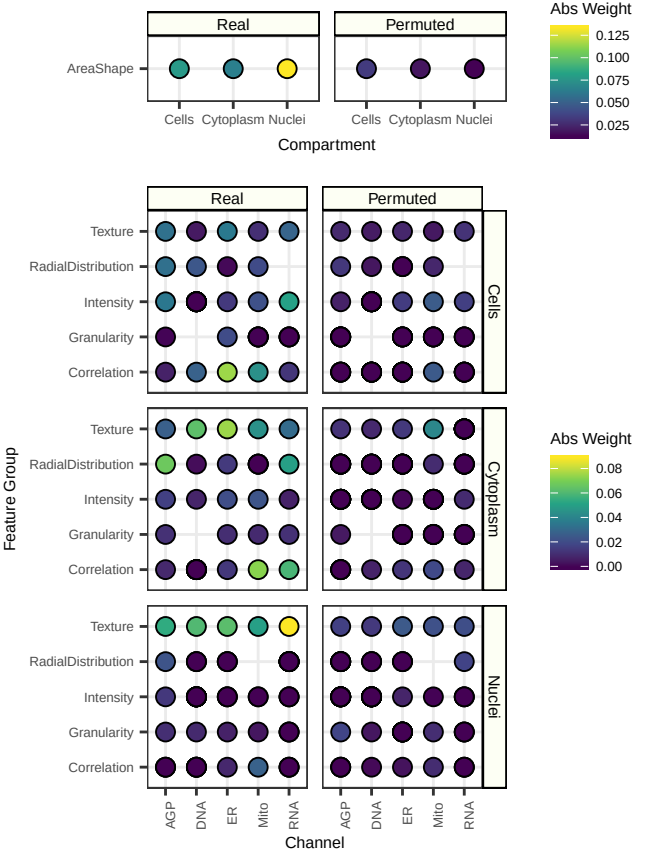
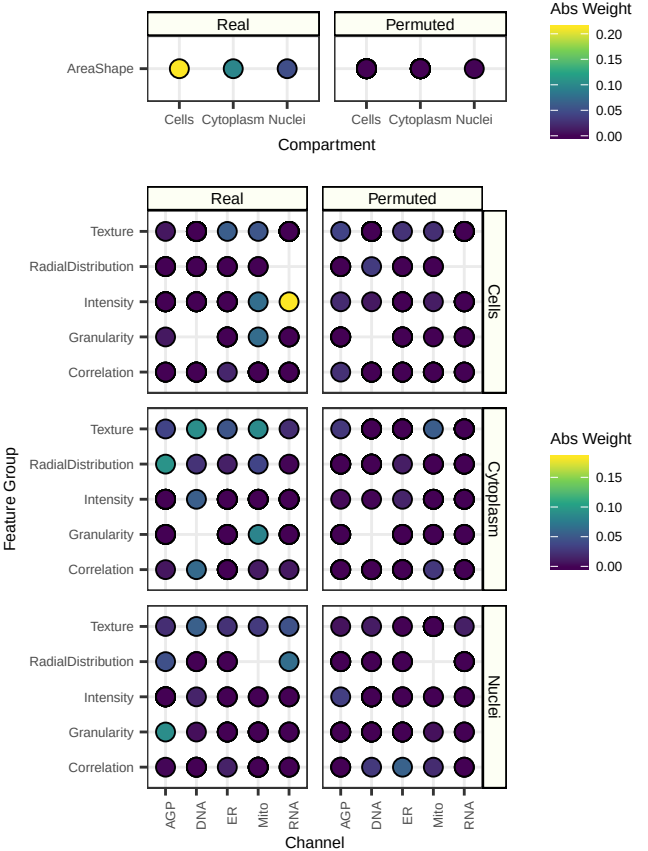
cc_all_high_h2ax

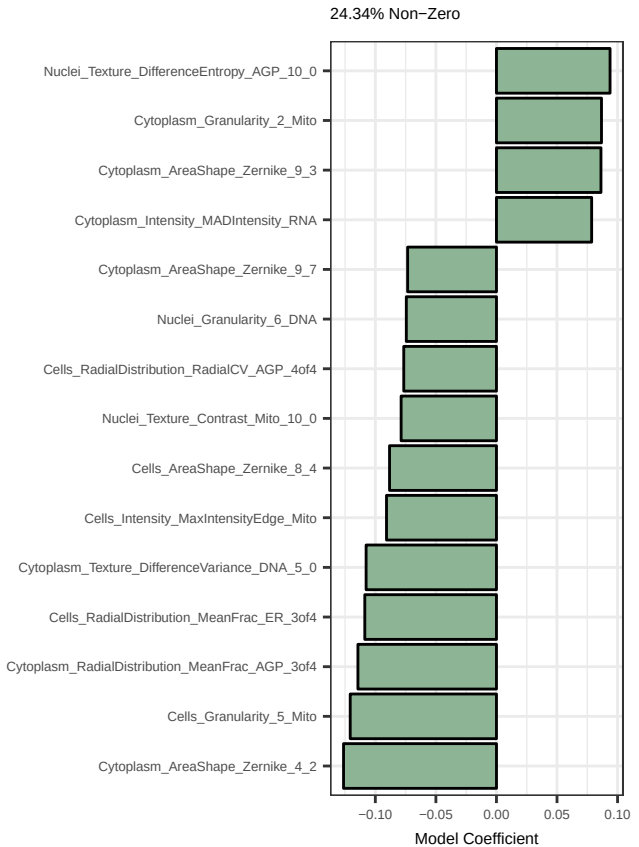


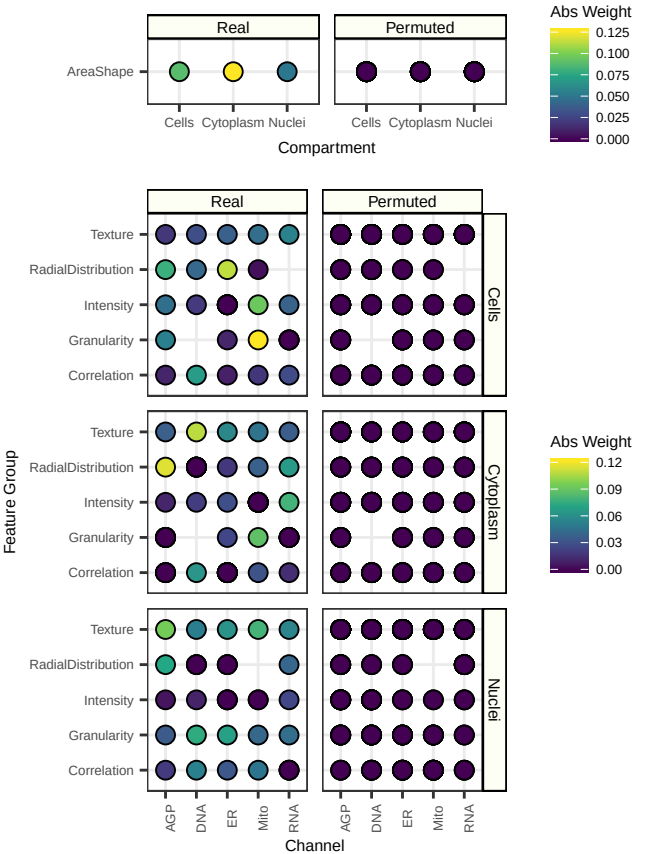


cc_all_large_notround_polynuclear_mean

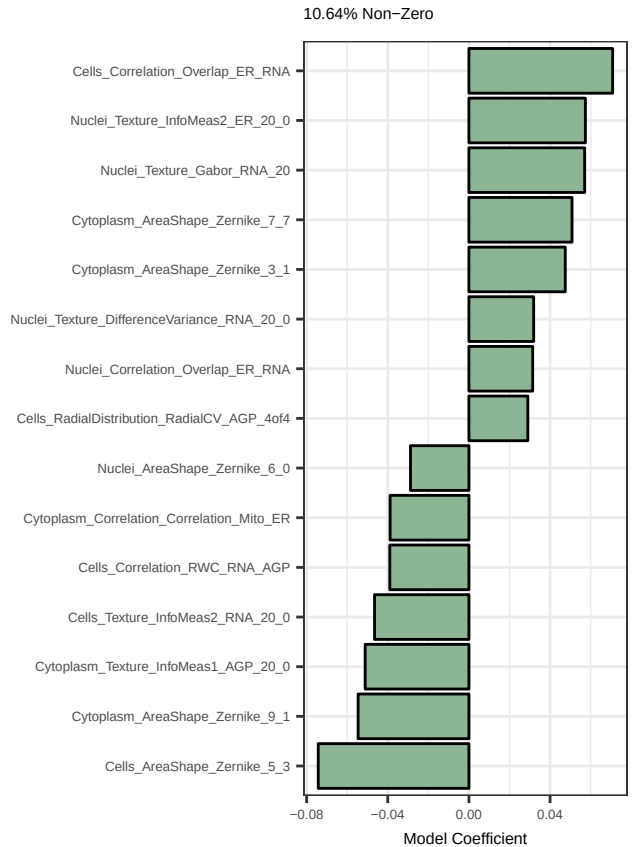


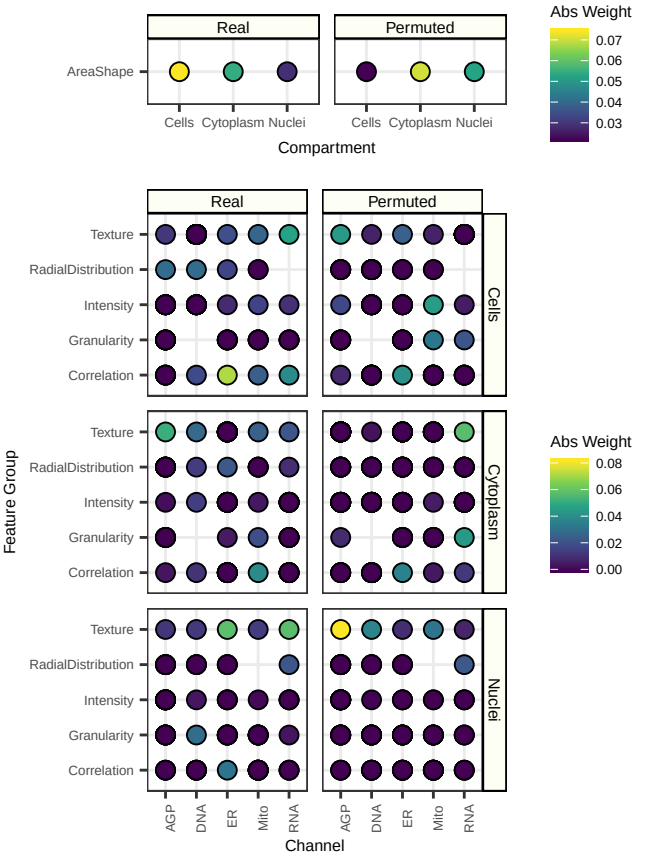
cc_all_large_round_polyploid_mean



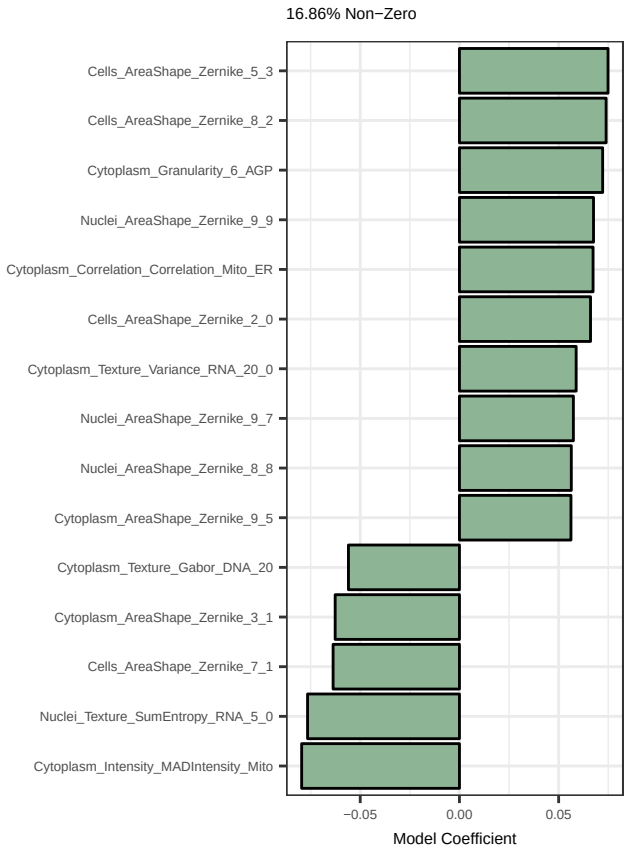


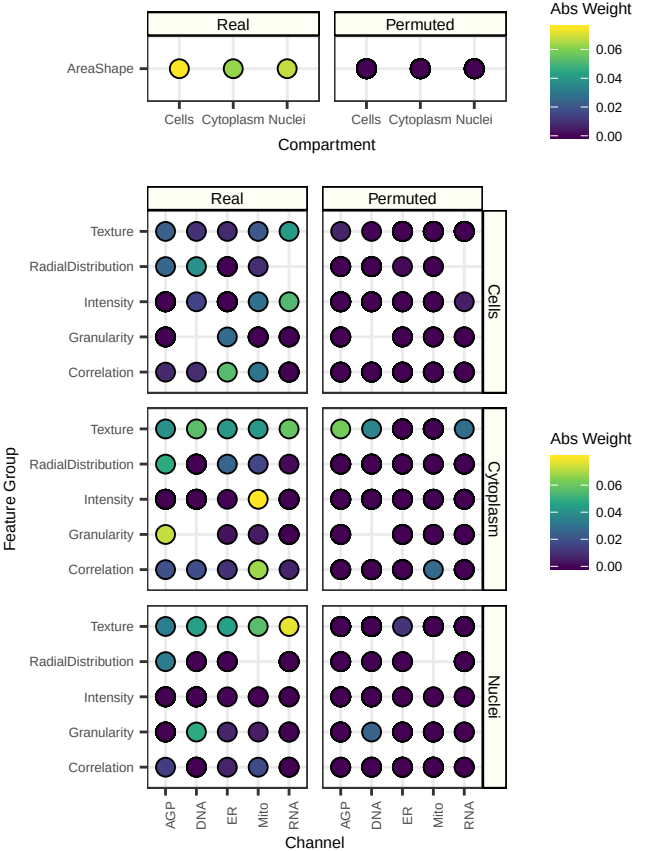
cc_all_n_objects



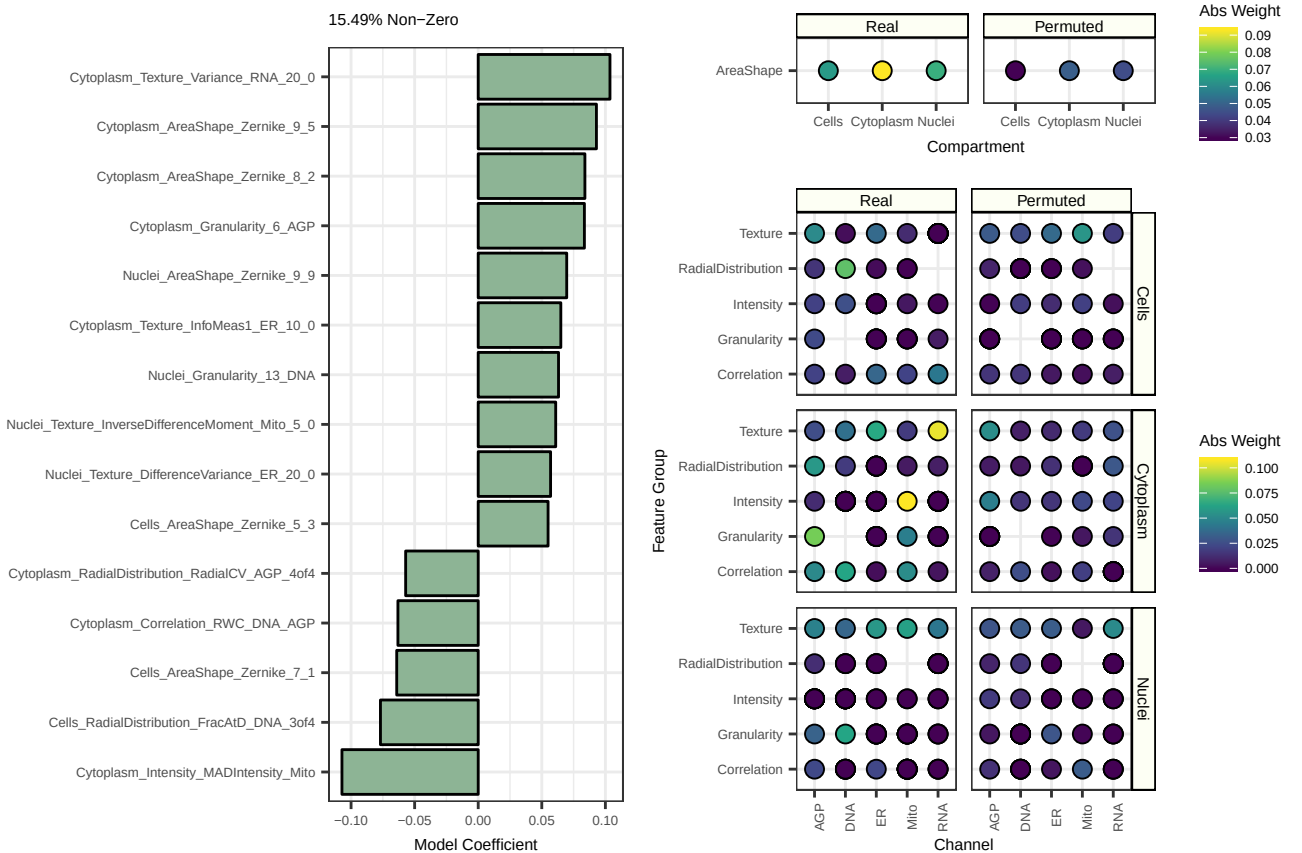


cc_all_n_spots_h2ax_mean

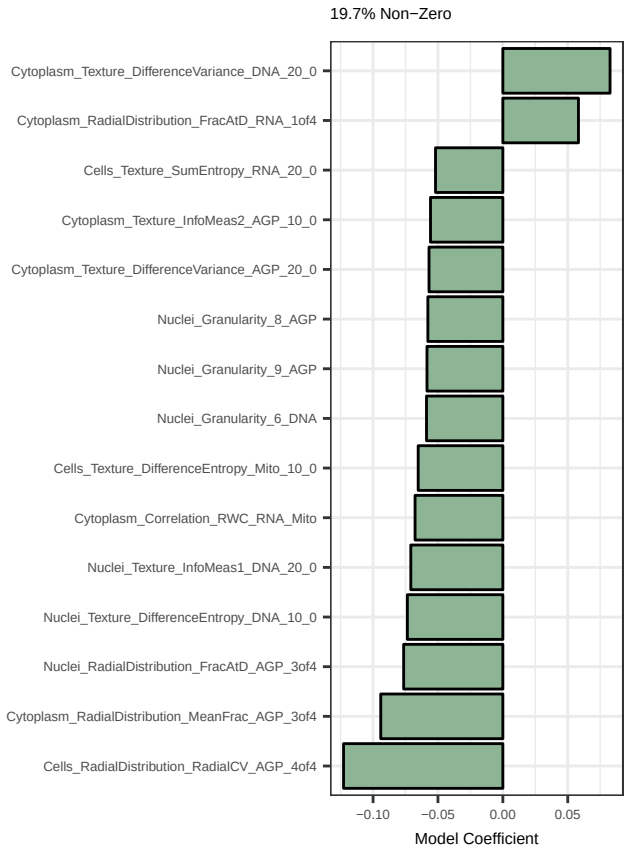


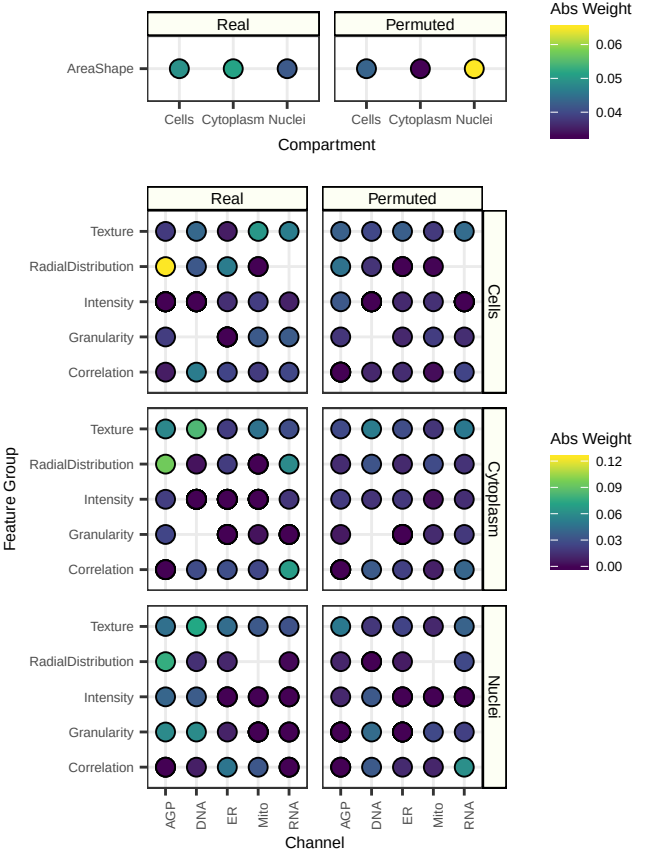


cc_all_n_spots_h2ax_per_nucleus_area_mean

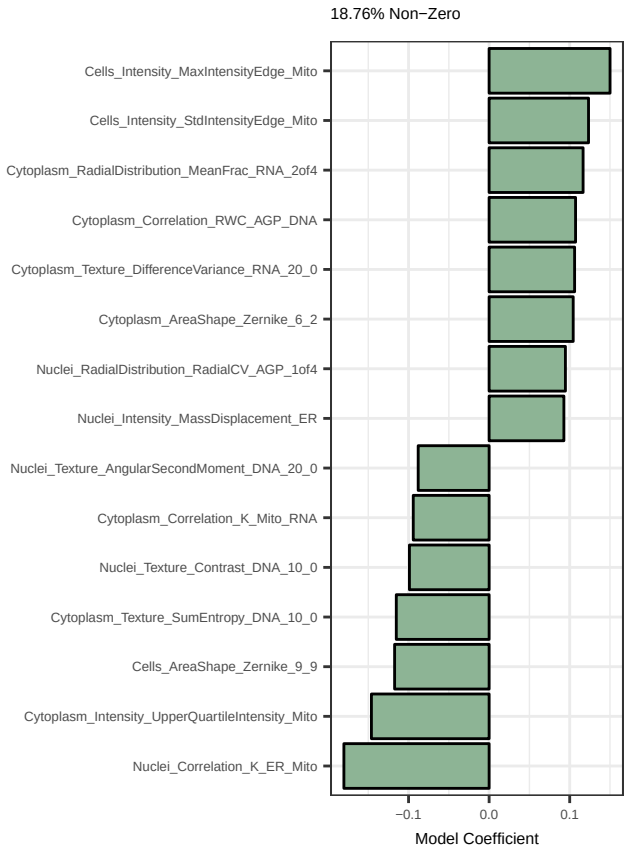


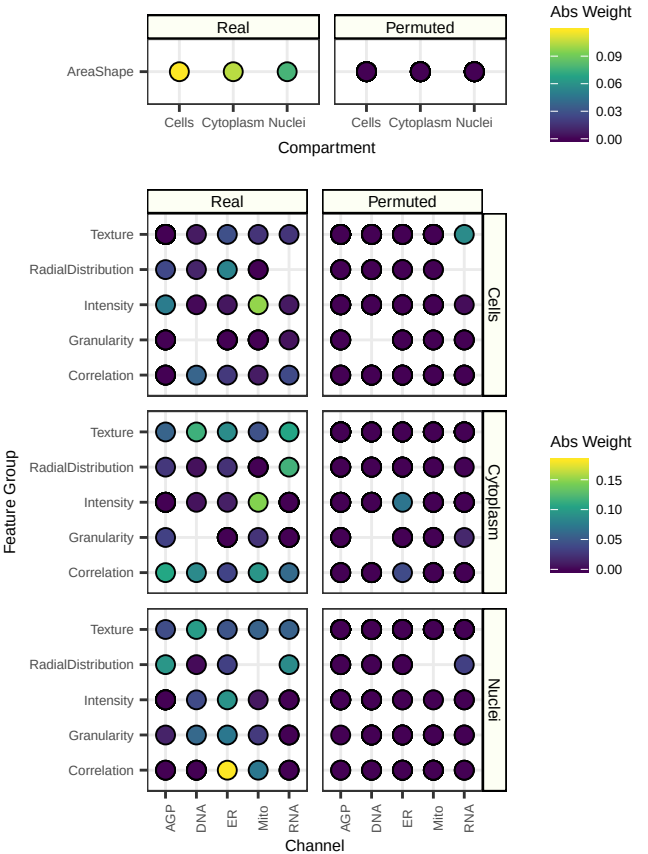
cc_all_nucleus_area_mean



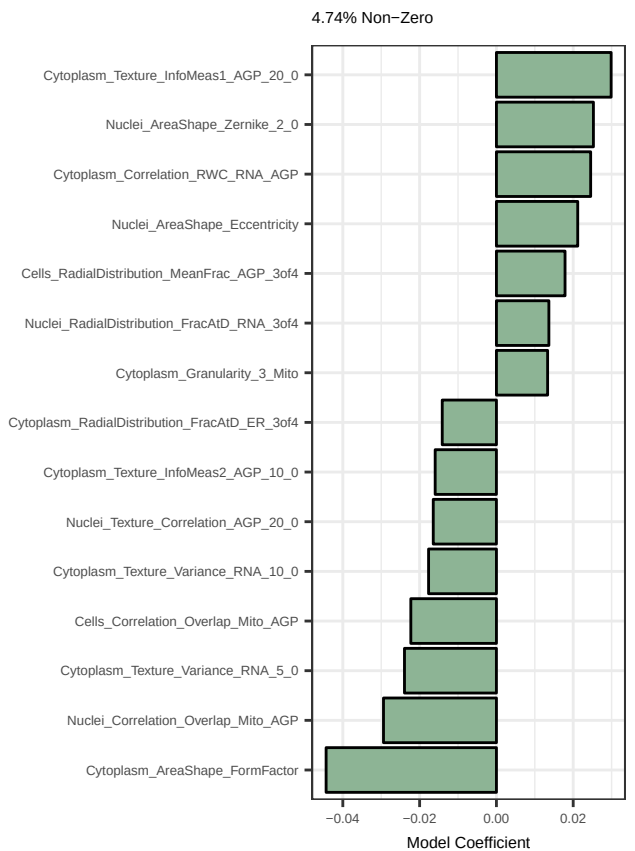


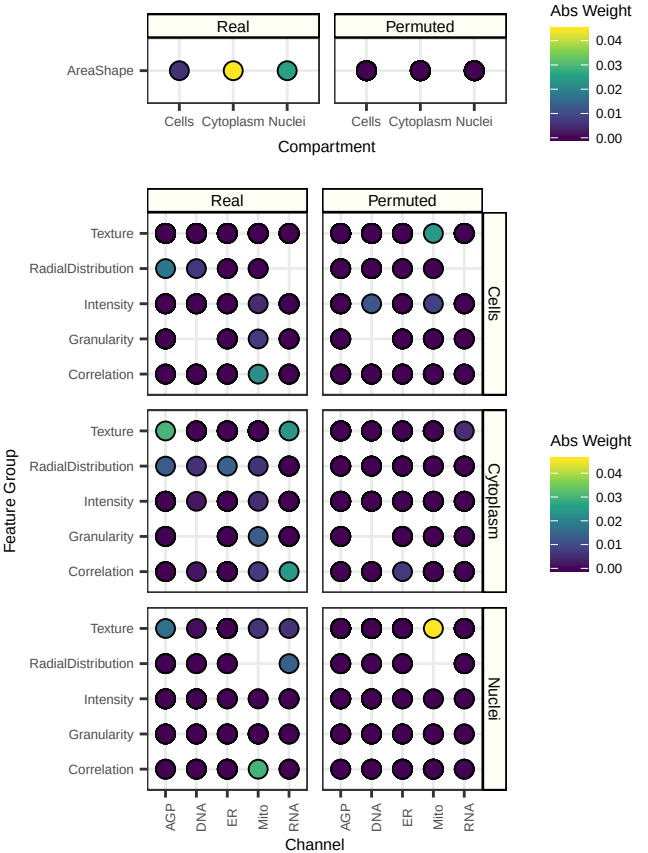
cc_all_nucleus_roundness_mean



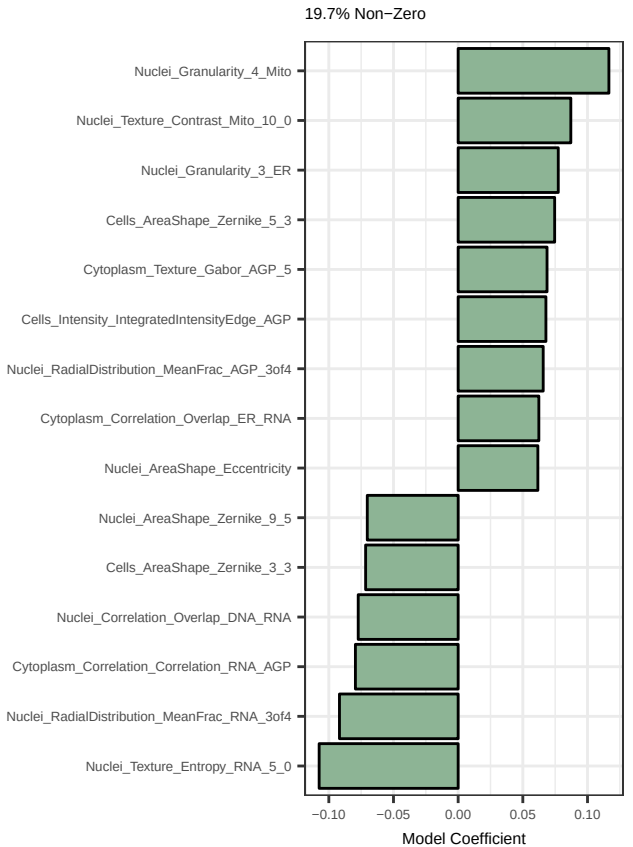


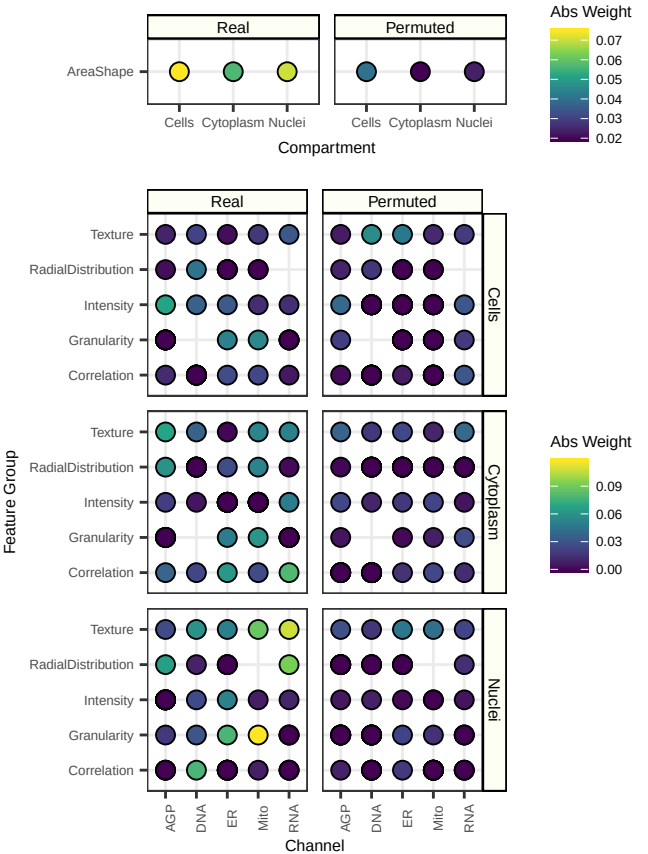
cc_cc_early_mitosis



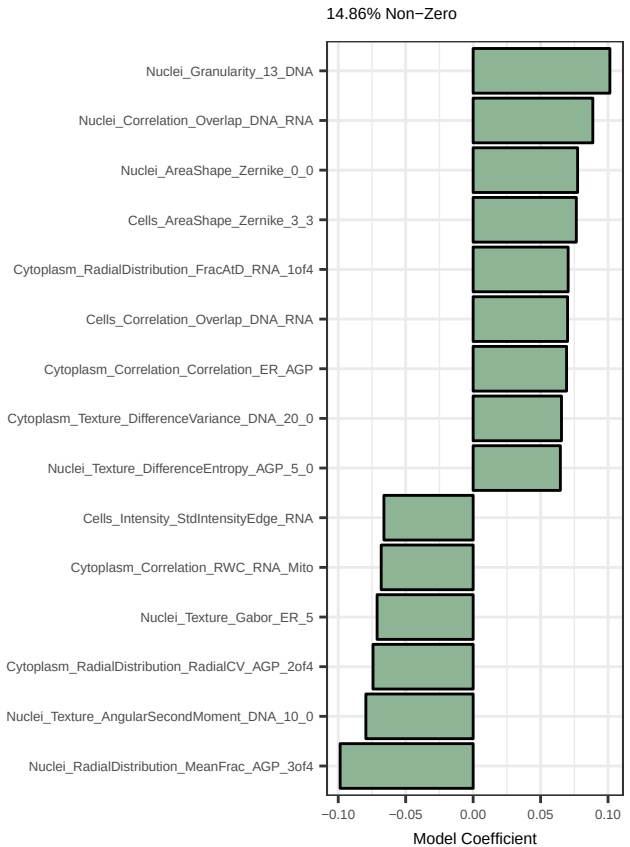


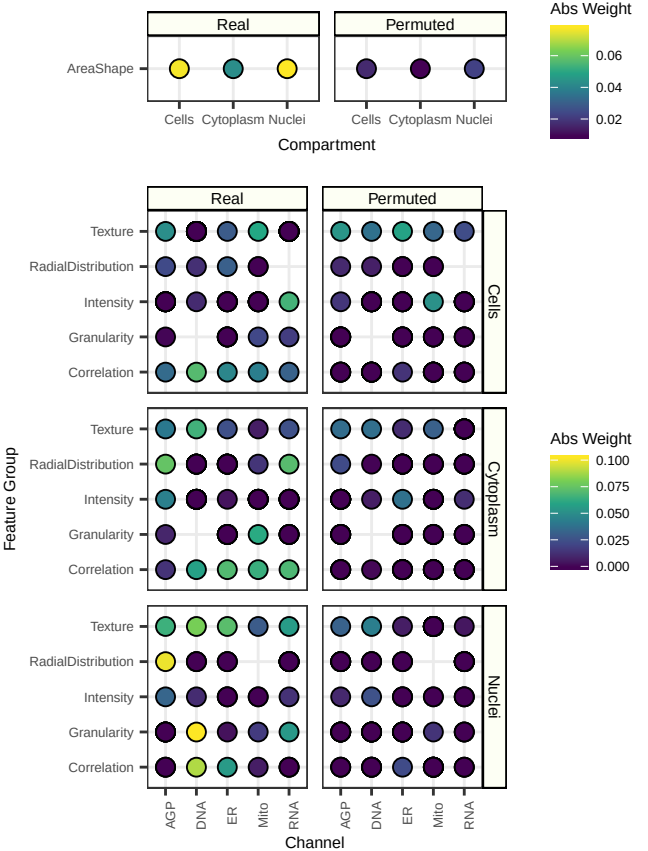
cc_cc_g1


19.7% Non−Zero
Nuclei_Granularity_4_Mito
Nuclei_Texture_Contrast_Mito_10_0
Nuclei_Granularity_3_ER
Cells_AreaShape_Zernike_5_3
Cytoplasm_Texture_Gabor_AGP_5
Cells_Intensity_IntegratedIntensityEdge_AGP
Nuclei_RadialDistribution_MeanFrac_AGP_3of4
Cytoplasm_Correlation_Overlap_ER_RNA
Nuclei_AreaShape_Eccentricity
Nuclei_AreaShape_Zernike_9_5
Cells_AreaShape_Zernike_3_3
Nuclei_Correlation_Overlap_DNA_RNA
Cytoplasm_Correlation_Correlation_RNA_AGP
Nuclei_RadialDistribution_MeanFrac_RNA_3of4
Nuclei_Texture_Entropy_RNA_5_0
−0.10
−0.05
0.00
0.05
0.10
Model Coefficient

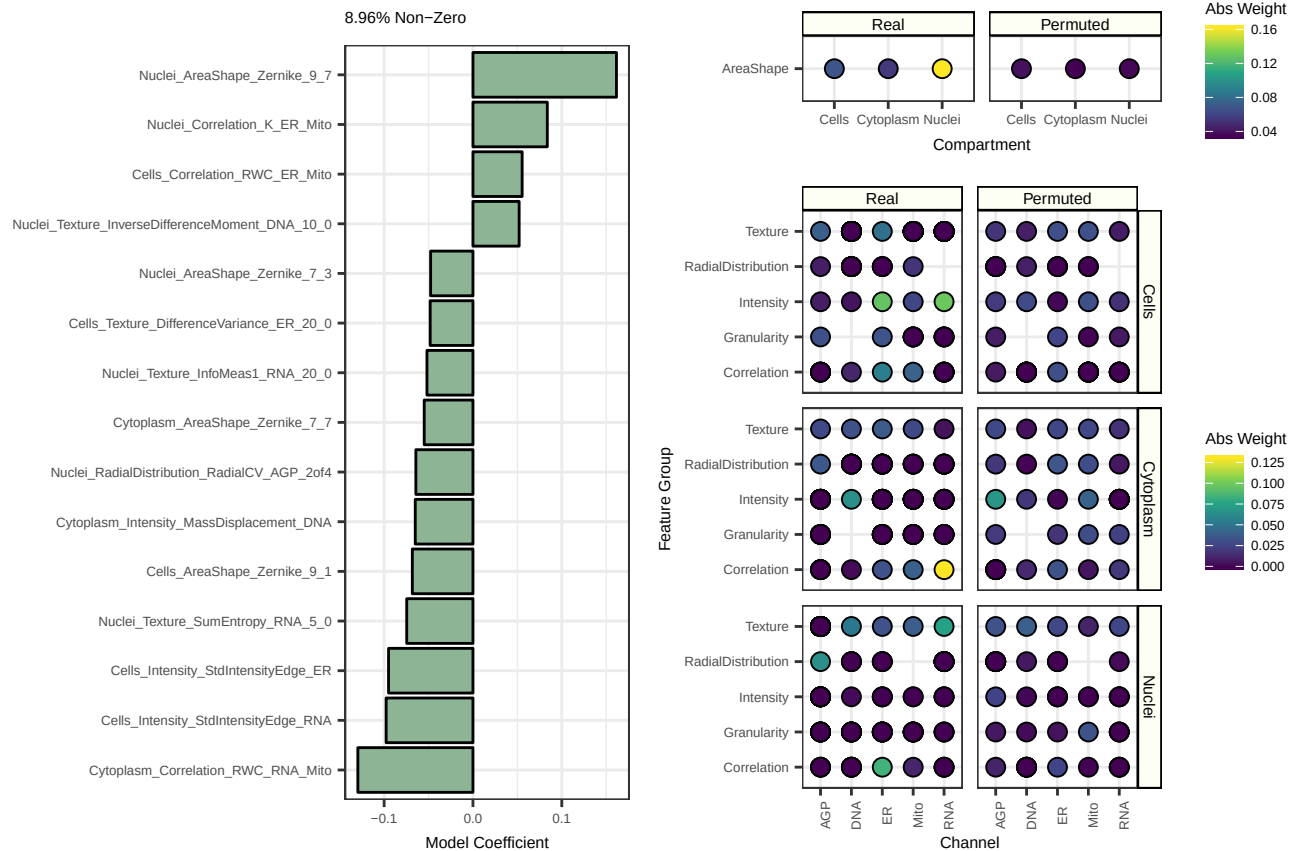

Real
Permuted
AreaShape
Cells
Cytoplasm
Nuclei
Compartment
Abs Weight
0.07
0.06
0.05
0.04
0.03
0.02
Feature Group
Texture
RadialDistribution
Intensity
Granularity
Correlation
Cells
Cytoplasm
Nuclei
Abs Weight
0.09
0.06
0.03
0.00
AGP
DNA
ER
Mito
RNA
Channel

cc_cc_g2

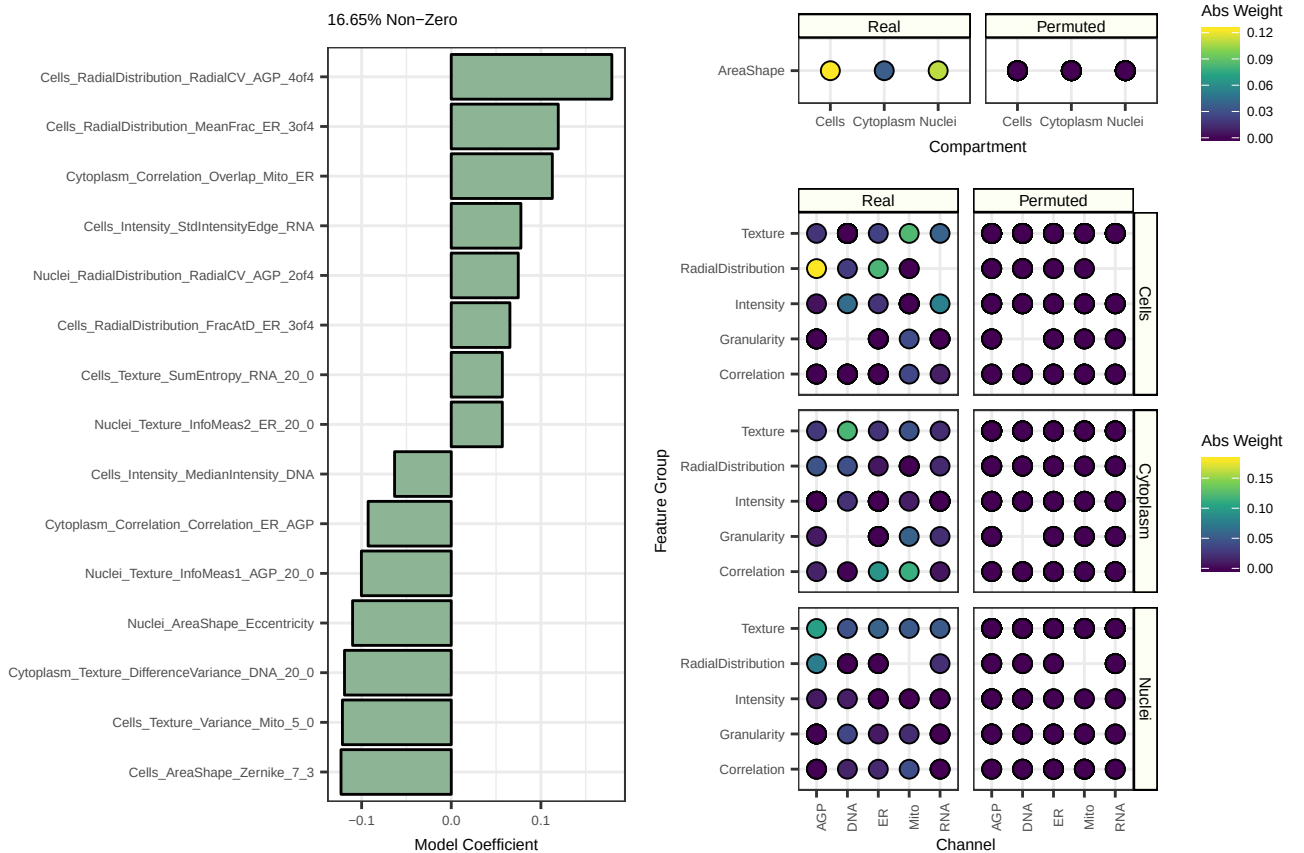

14.86% Non−Zero
Nuclei_Granularity_13_DNA
Nuclei_Correlation_Overlap_DNA_RNA
Nuclei_AreaShape_Zernike_0_0
Cells_AreaShape_Zernike_3_3
Cytoplasm_RadialDistribution_FracAtD_RNA_1of4
Cells_Correlation_Overlap_DNA_RNA
Cytoplasm_Correlation_Correlation_ER_AGP
Cytoplasm_Texture_DifferenceVariance_DNA_20_0
Nuclei_Texture_DifferenceEntropy_AGP_5_0
Cells_Intensity_StdIntensityEdge_RNA
Cytoplasm_Correlation_RWC_RNA_Mito
Nuclei_Texture_Gabor_ER_5
Cytoplasm_RadialDistribution_RadialCV_AGP_2of4
Nuclei_Texture_AngularSecondMoment_DNA_10_0
Nuclei_RadialDistribution_MeanFrac_AGP_3of4
−0.10
−0.05
0.00
0.05
0.10
Model Coefficient


Real
Permuted
AreaShape
Cells
Cytoplasm
Nuclei
Compartment
Abs Weight
0.06
0.04
0.02
Feature Group
Texture
RadialDistribution
Intensity
Granularity
Correlation
Cells
Cytoplasm
Nuclei
Abs Weight
0.100
0.075
0.050
0.025
0.000
AGP
DNA
ER
Mito
RNA
Channel

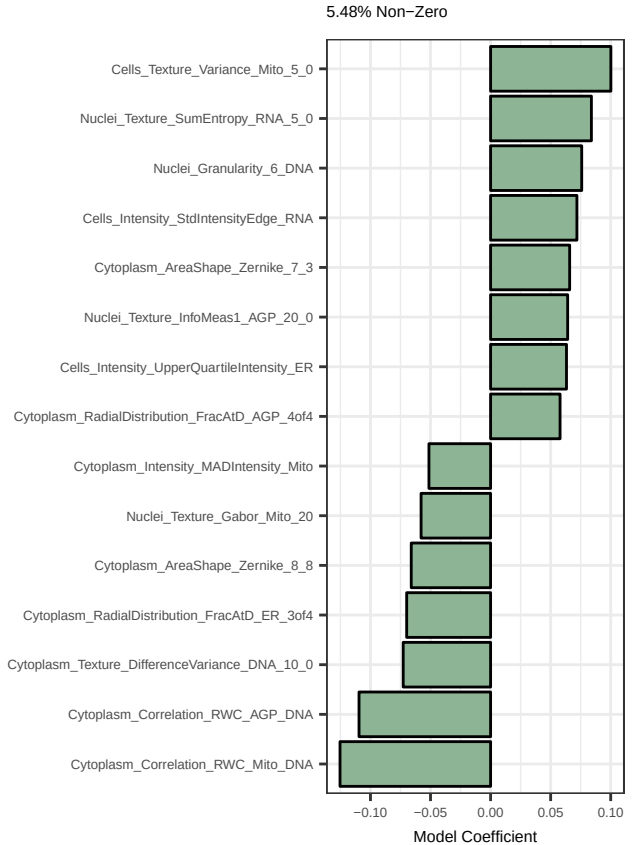
cc_cc_high_h2ax

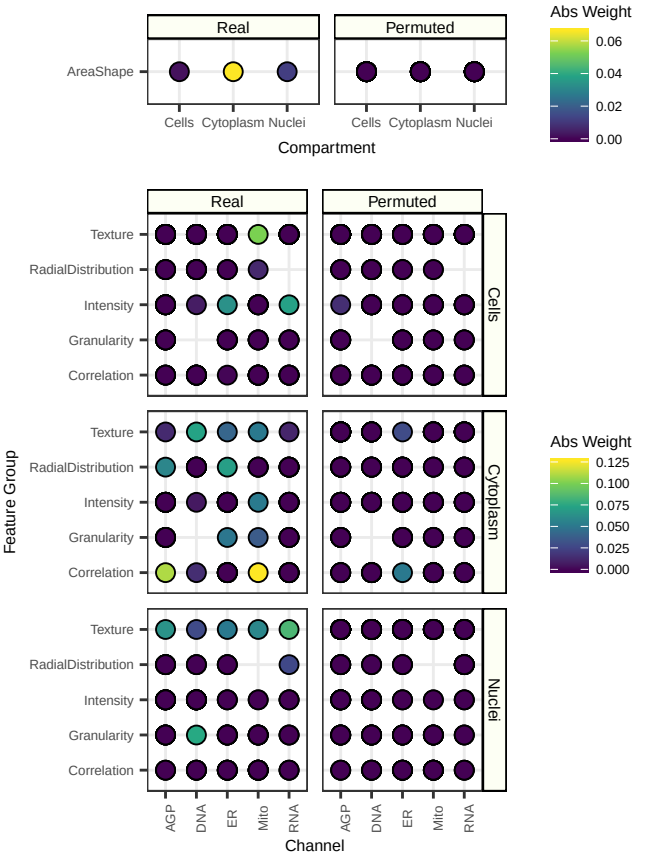


cc_cc_late_mitosis

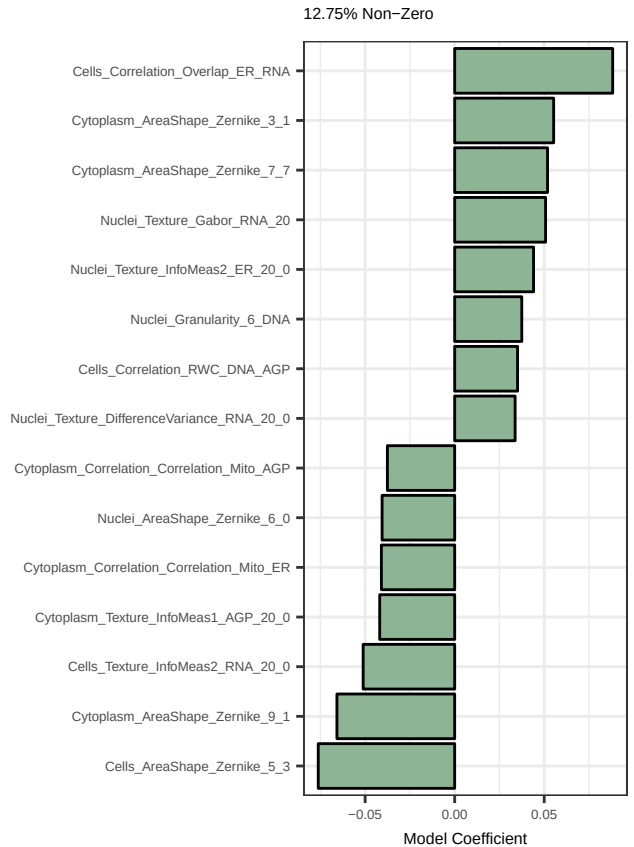


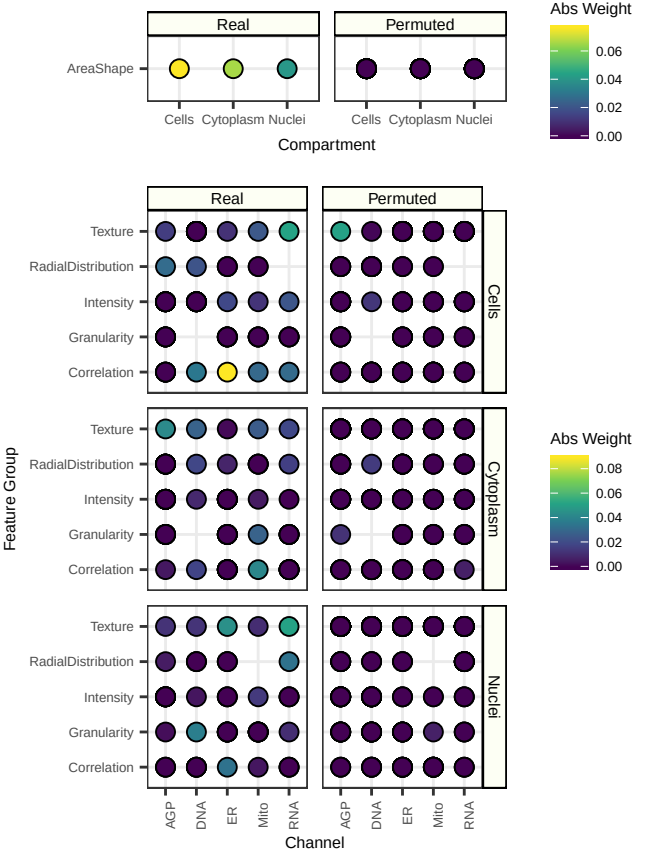
cc_cc_mitosis



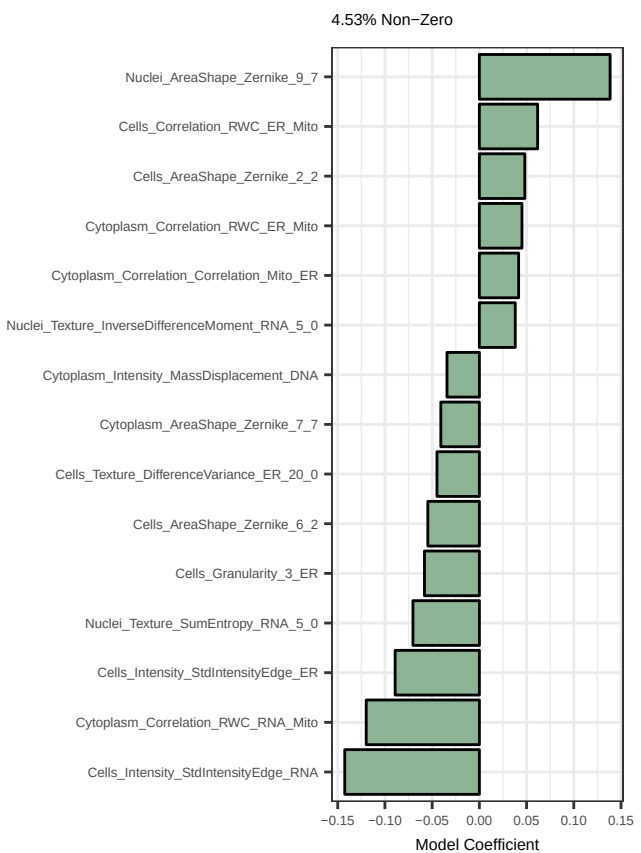


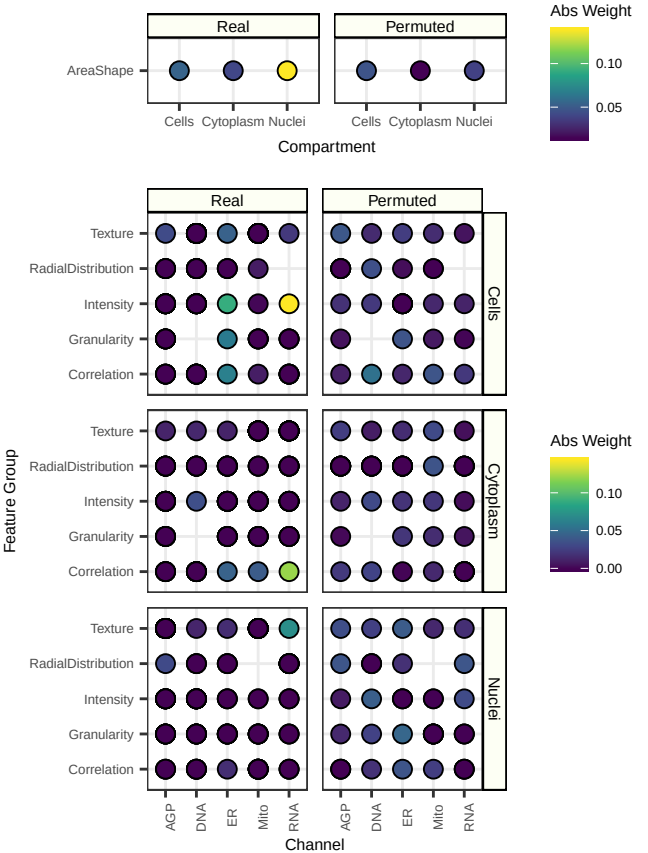
cc_cc_n_objects



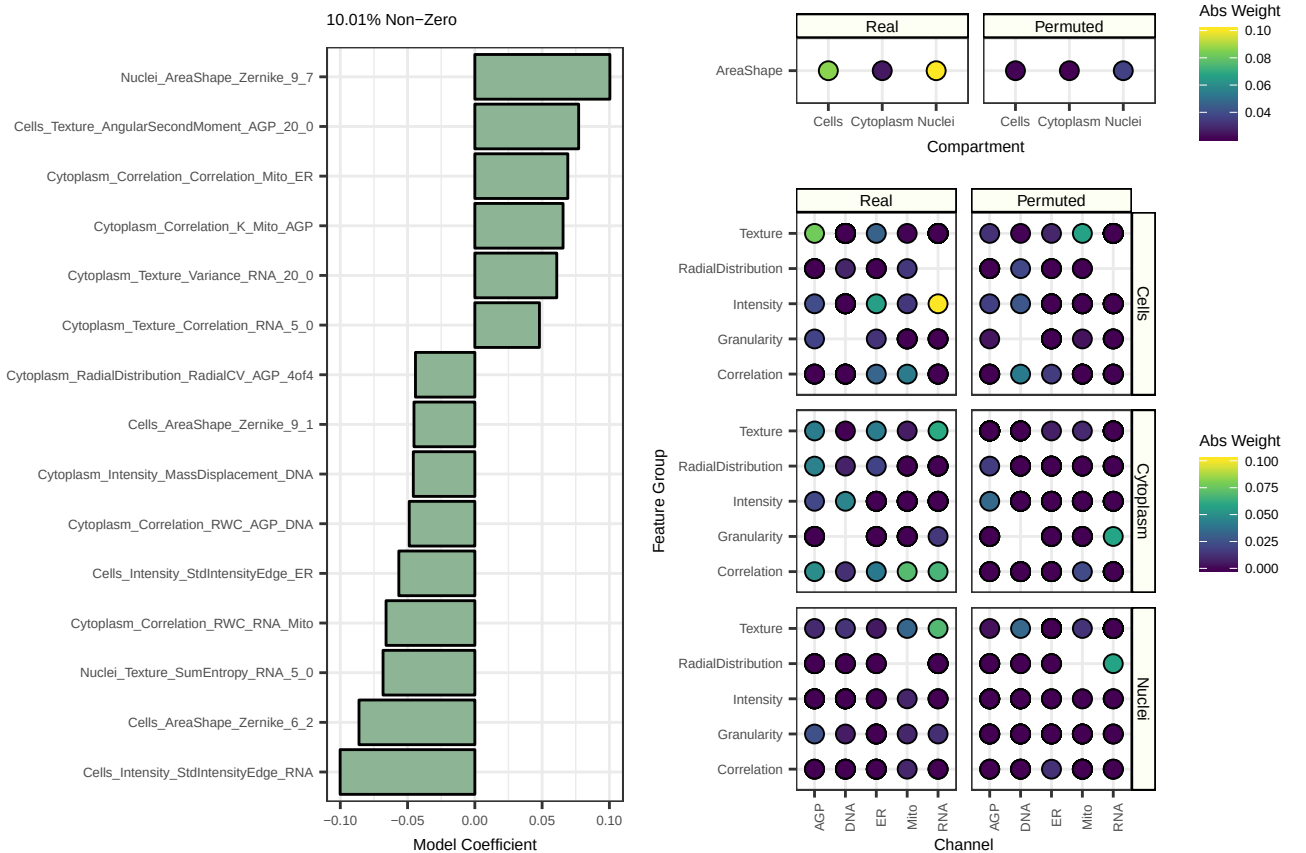


cc_cc_n_spots_h2ax_mean

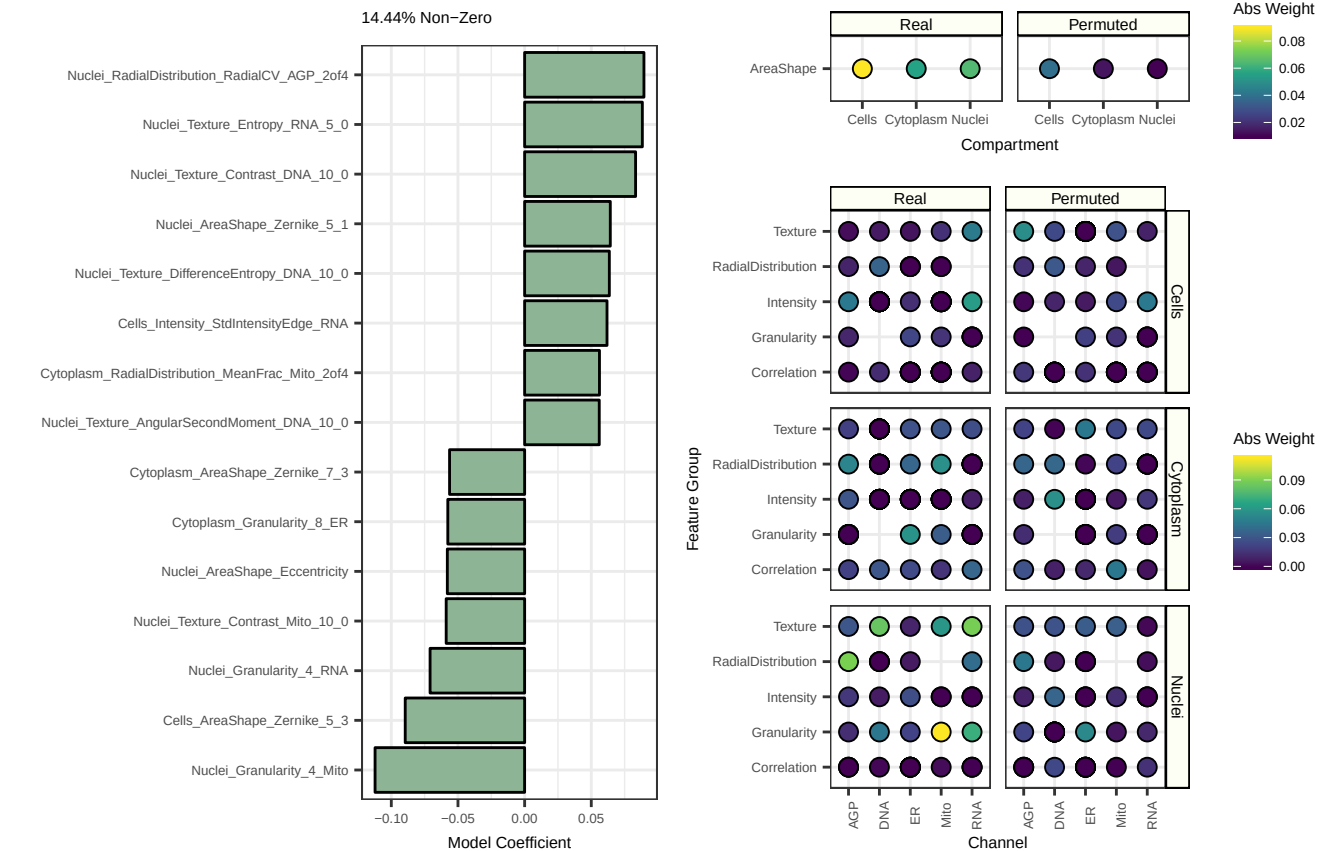




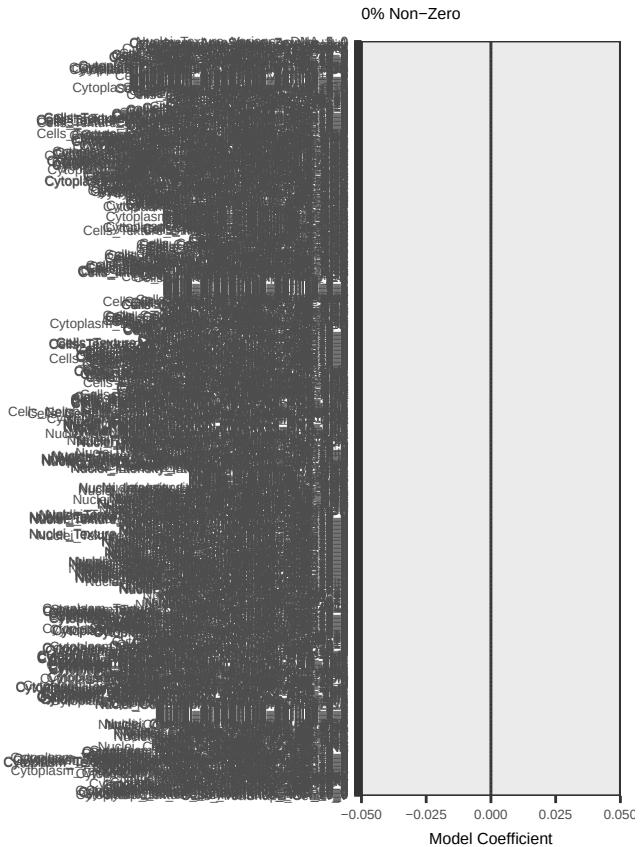
cc_cc_n_spots_h2ax_per_nucleus_area_mean

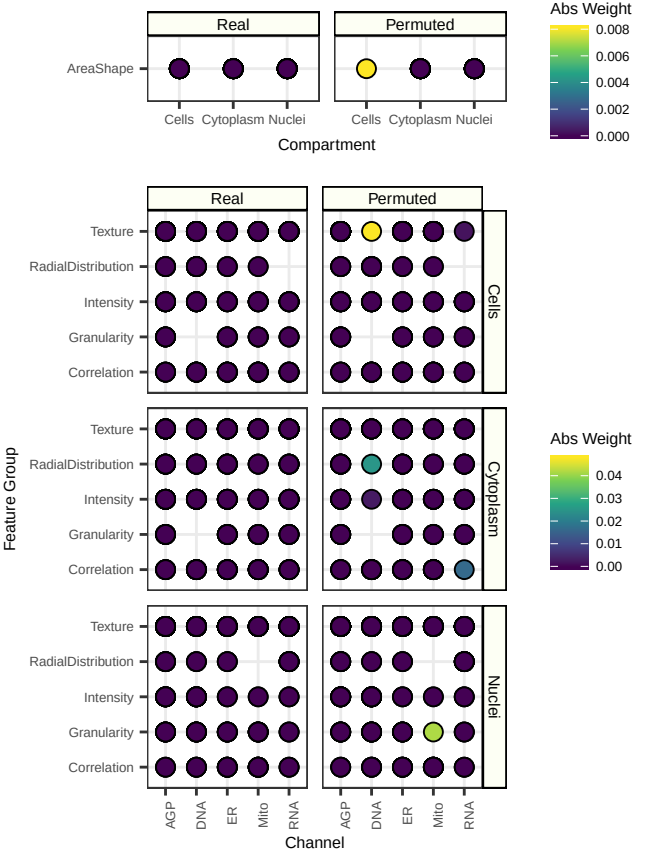


cc_cc_s

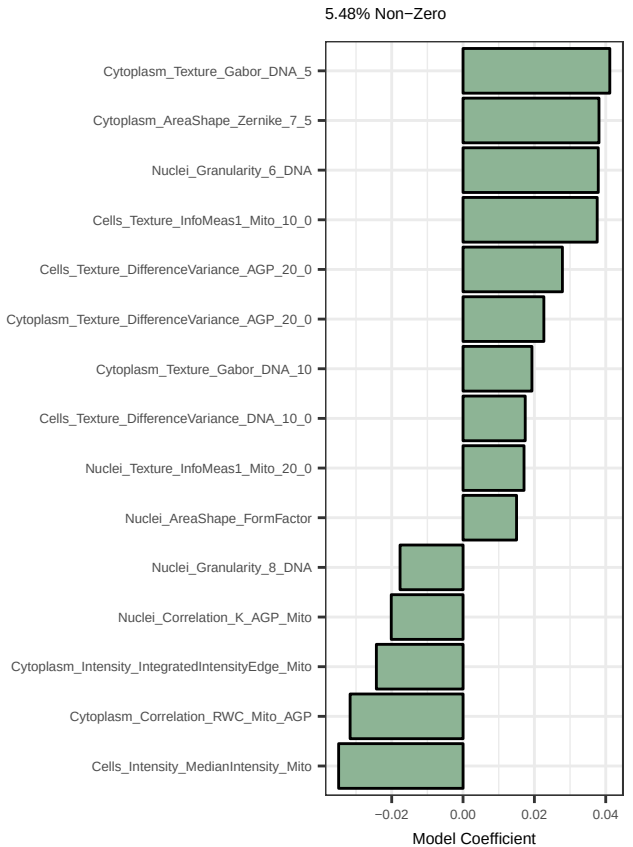

14.44% Non−Zero
Nuclei_RadialDistribution_RadialCV_AGP_2of4
Nuclei_Texture_Entropy_RNA_5_0
Nuclei_Texture_Contrast_DNA_10_0
Nuclei_AreaShape_Zernike_5_1
Nuclei_Texture_DifferenceEntropy_DNA_10_0
Cells_Intensity_StdIntensityEdge_RNA
Cytoplasm_RadialDistribution_MeanFrac_Mito_2of4
Nuclei_Texture_AngularSecondMoment_DNA_10_0
Cytoplasm_AreaShape_Zernike_7_3
Cytoplasm_Granularity_8_ER
Nuclei_AreaShape_Eccentricity
Nuclei_Texture_Contrast_Mito_10_0
Nuclei_Granularity_4_RNA
Cells_AreaShape_Zernike_5_3
Nuclei_Granularity_4_Mito
−0.10
−0.05
0.00
0.05
Model Coefficient
Real
Permuted
AreaShape
Cells
Cytoplasm
Nuclei
Compartment
Abs Weight
0.08
0.06
0.04
0.02
Feature Group
Texture
RadialDistribution
Intensity
Granularity
Correlation
Cells
Cytoplasm
Nuclei
Abs Weight
0.09
0.06
0.03
0.00
AGP
DNA
ER
Mito
RNA
Channel

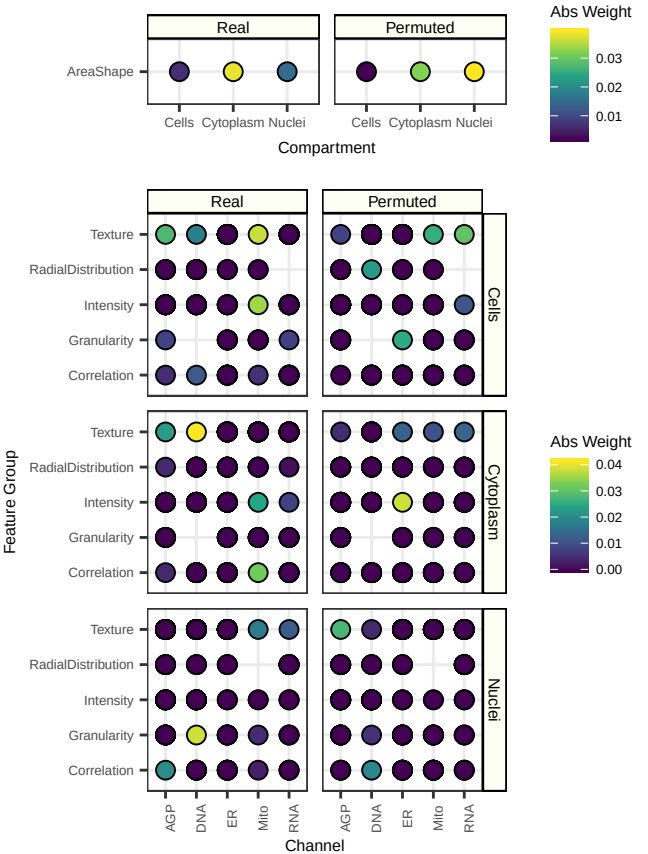
cc_early_mitosis_high_h2ax



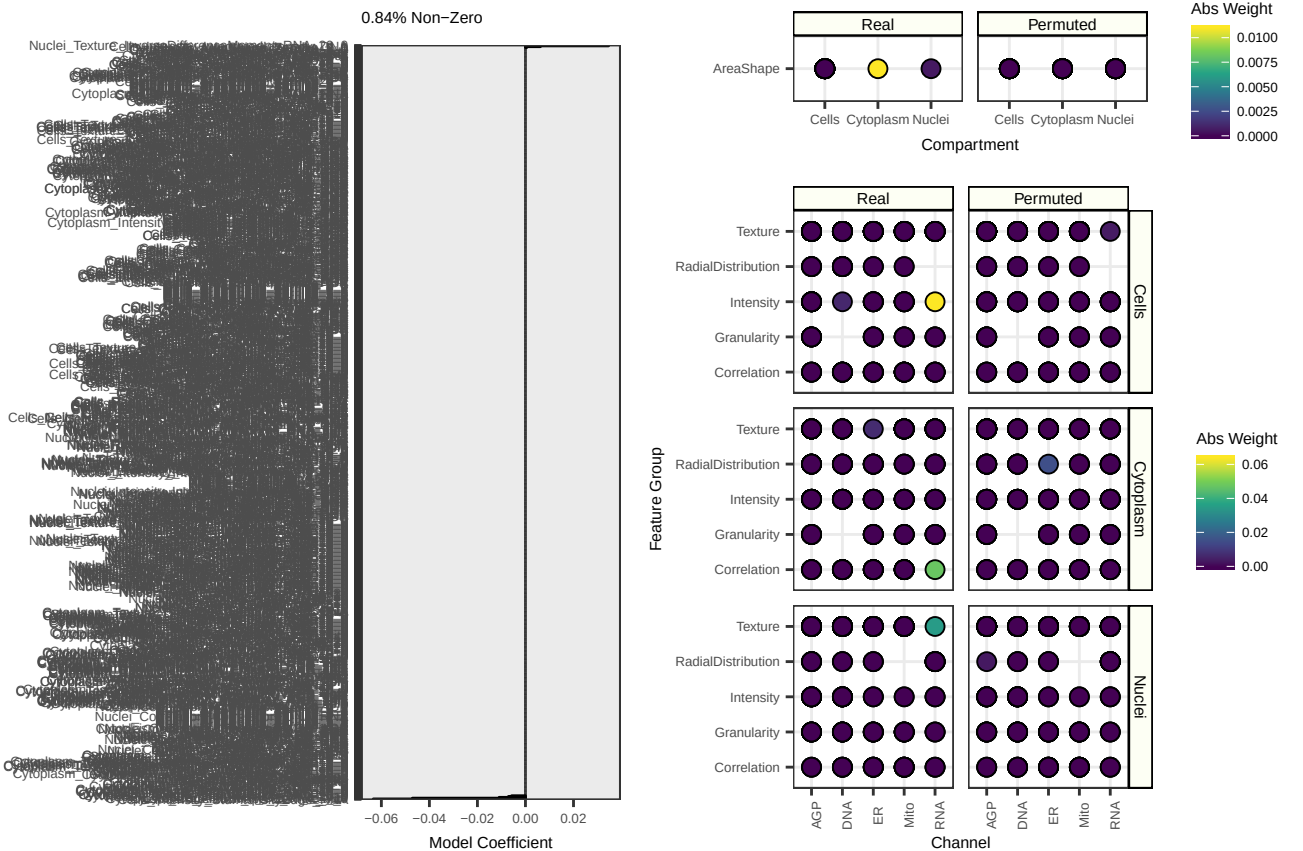


cc_early_mitosis_n_objects

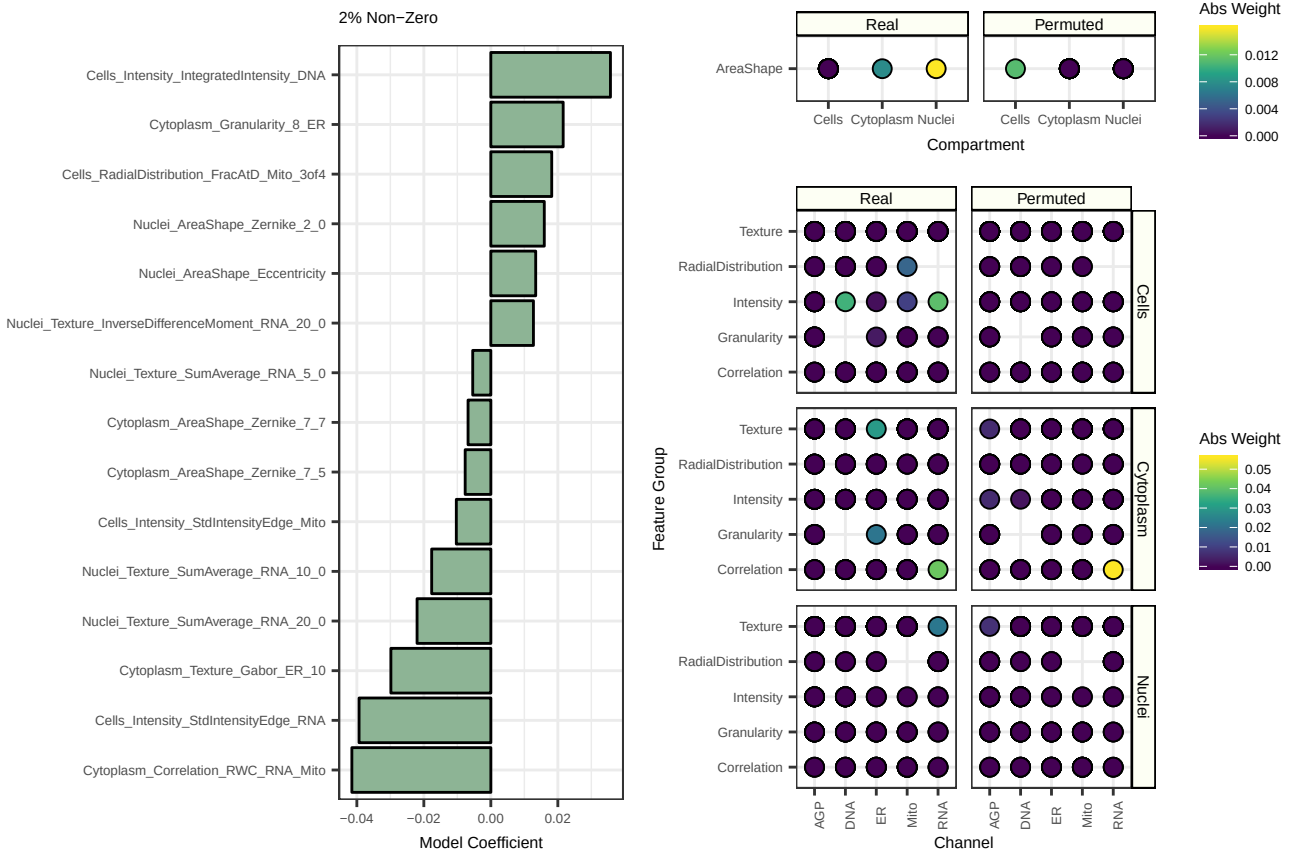




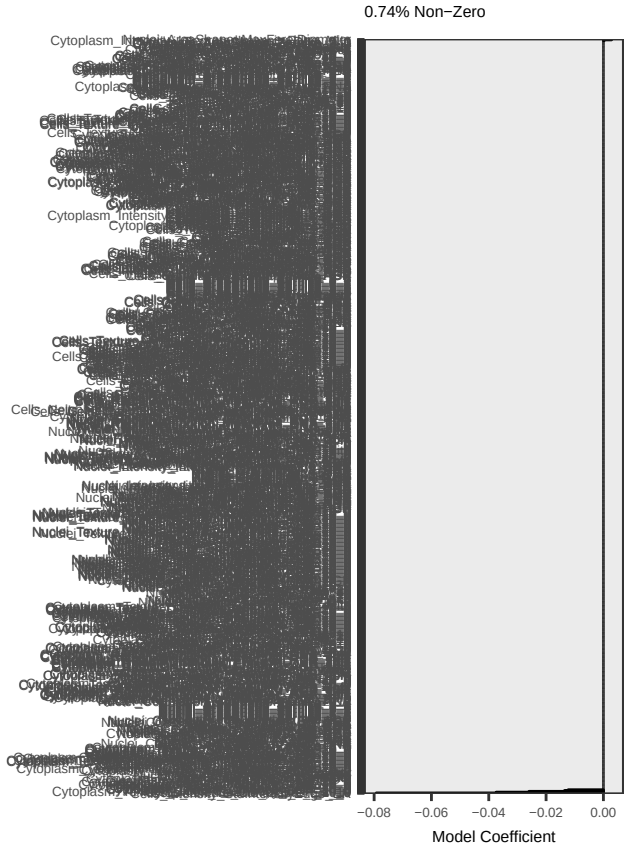
cc_early_mitosis_n_spots_h2ax_mean

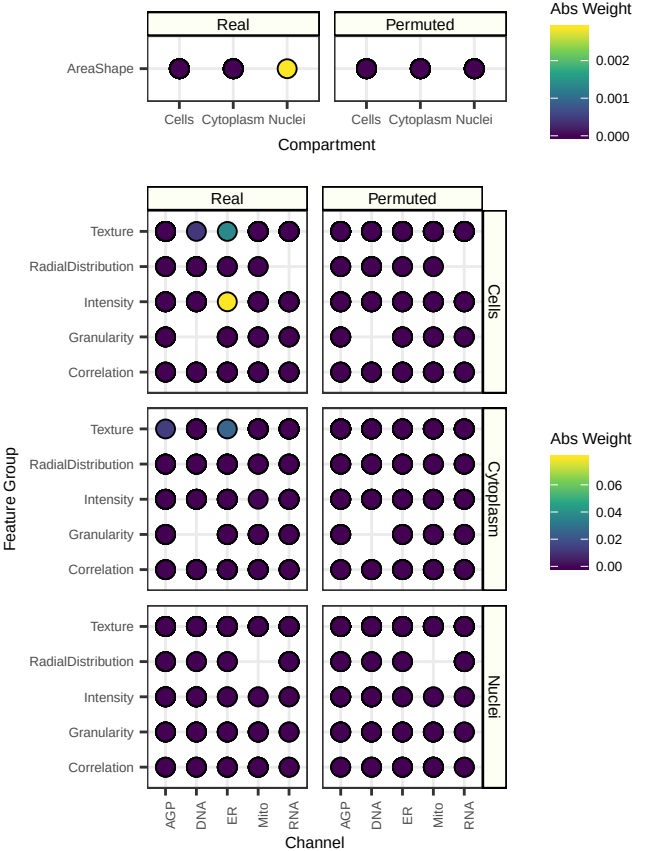


cc_early_mitosis_n_spots_h2ax_per_nucleus_area_mean

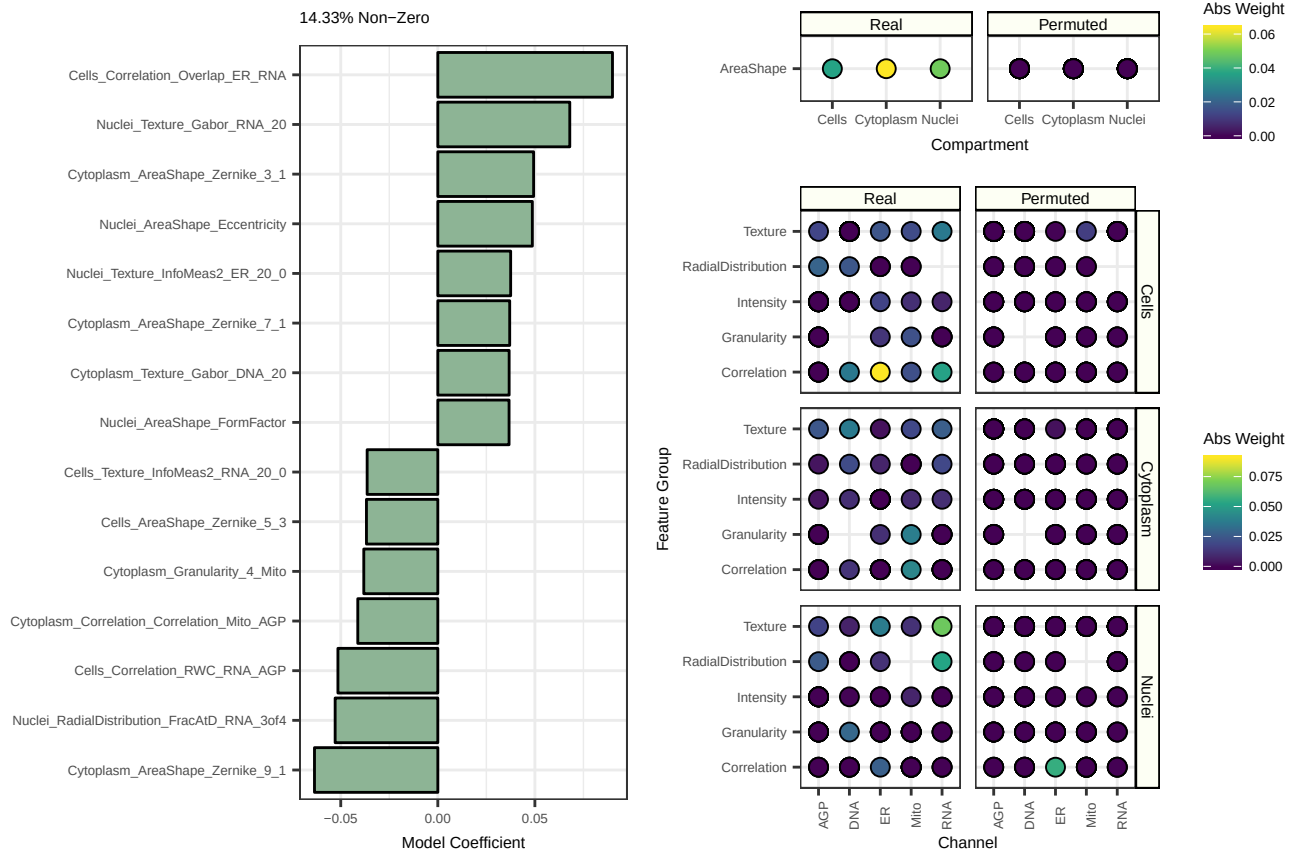


cc_g1_high_h2ax

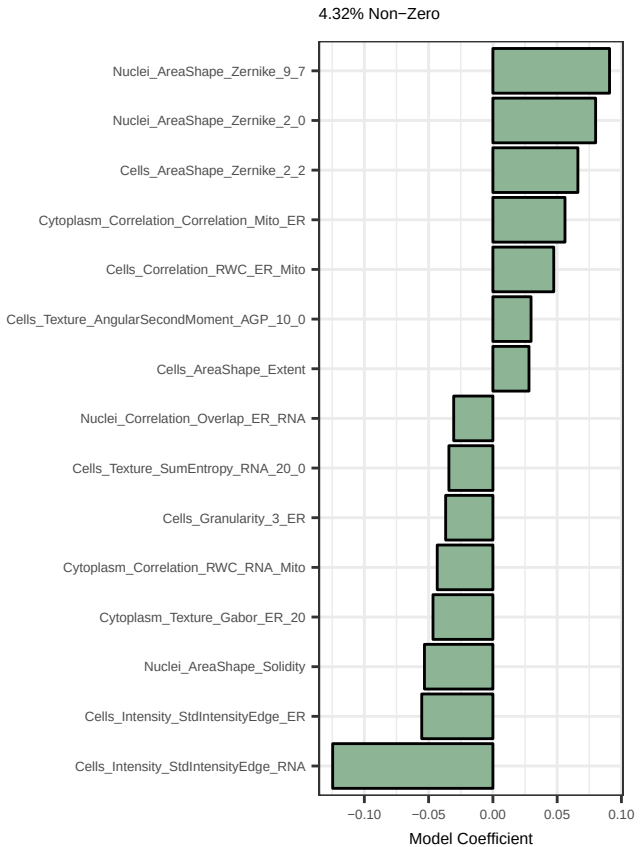


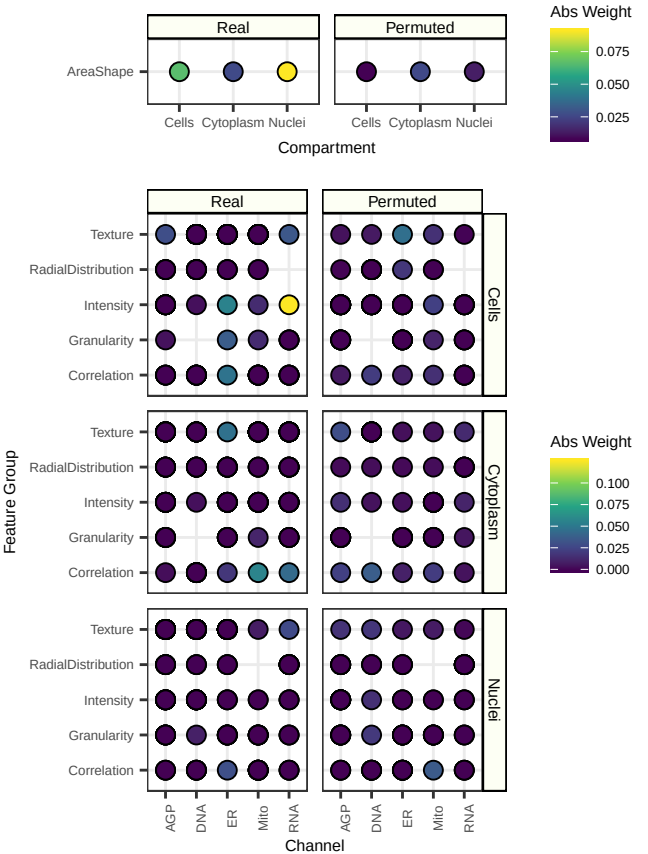


cc_g1_n_objects

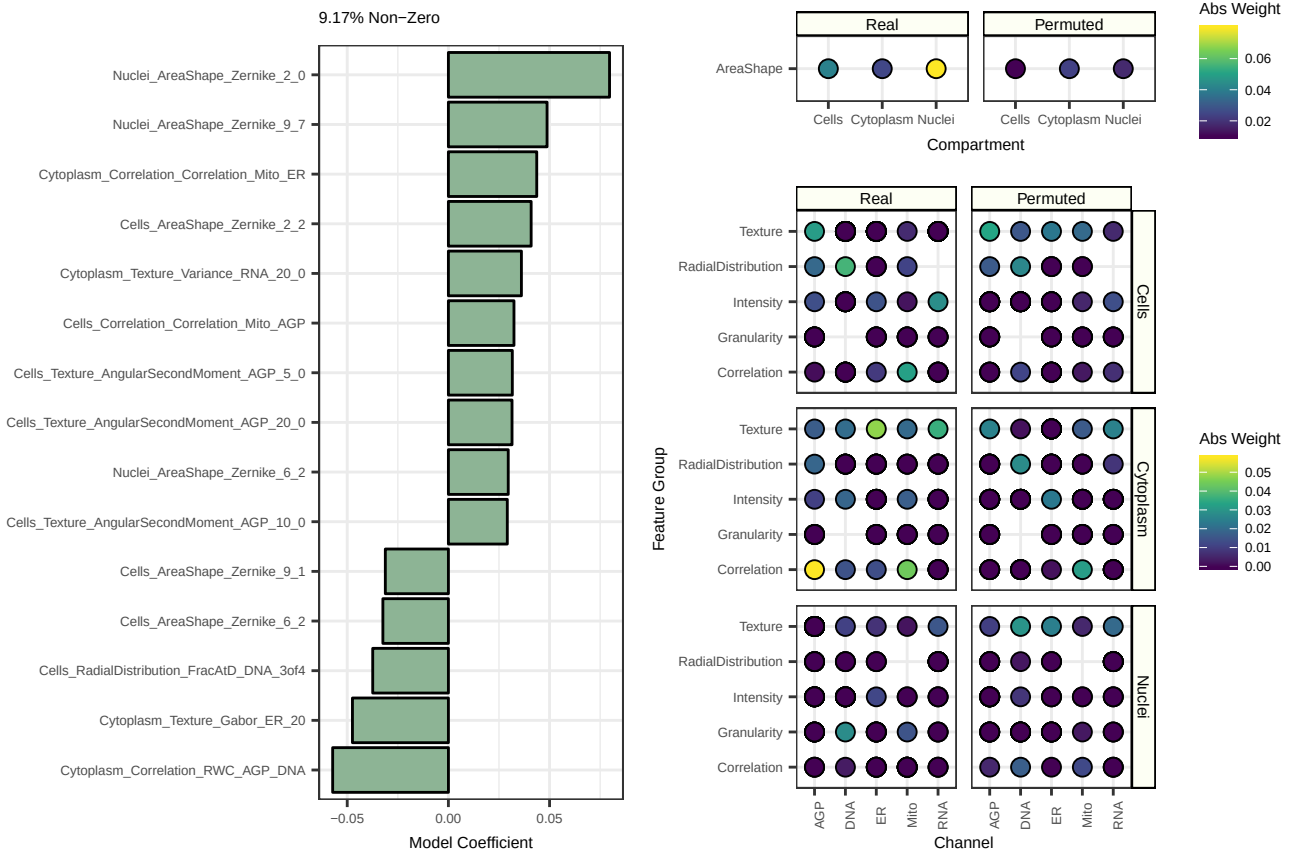


cc_g1_n_spots_h2ax_mean

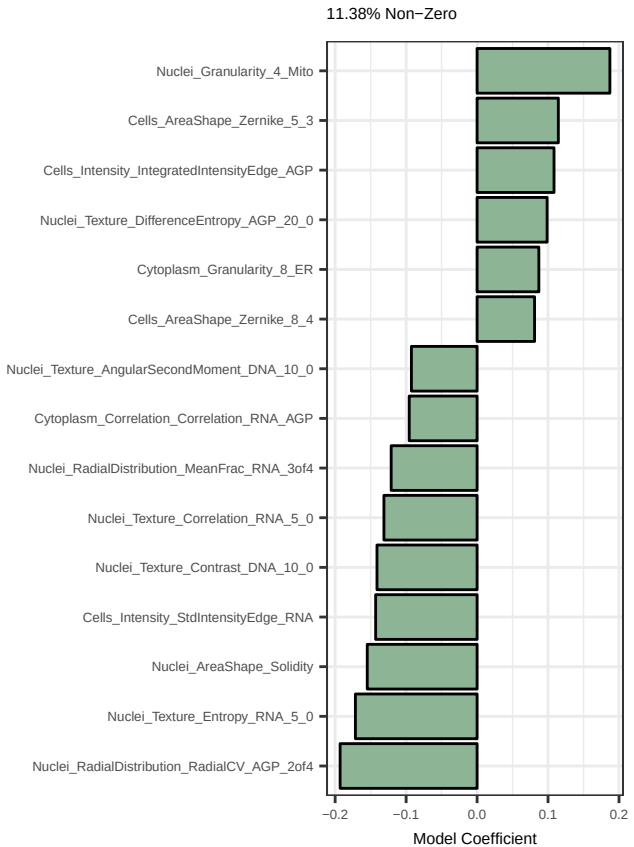


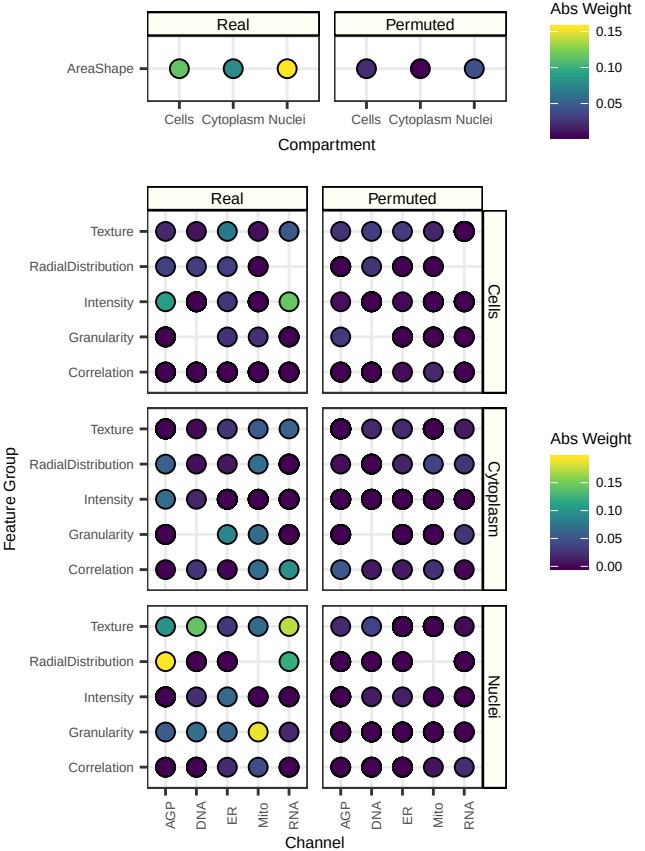


cc_g1_n_spots_h2ax_per_nucleus_area_mean

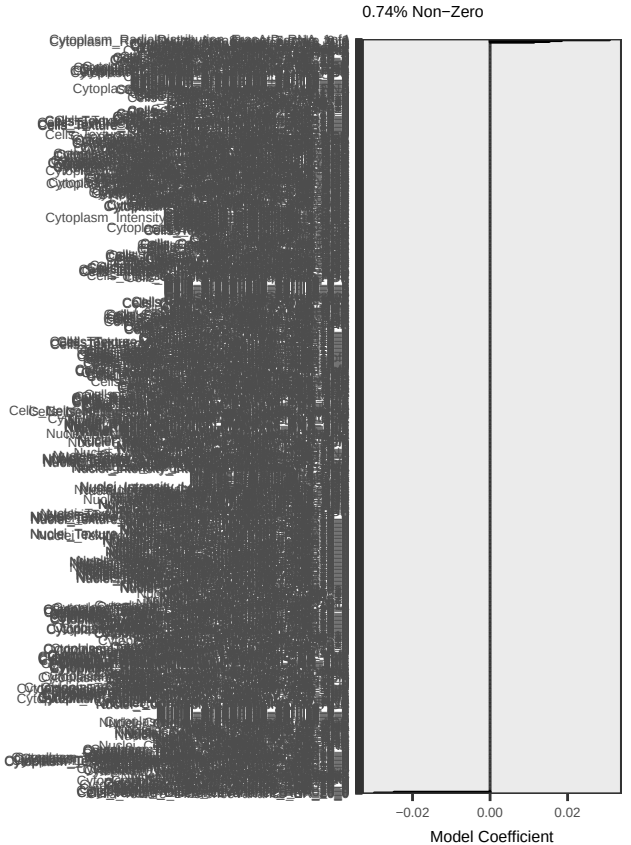


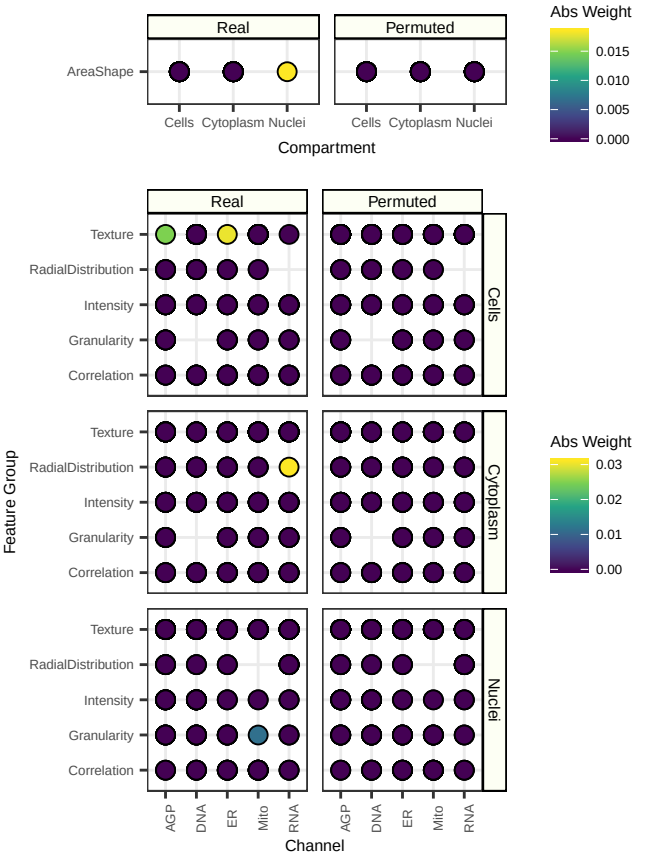
cc_g1_plus_g2_count



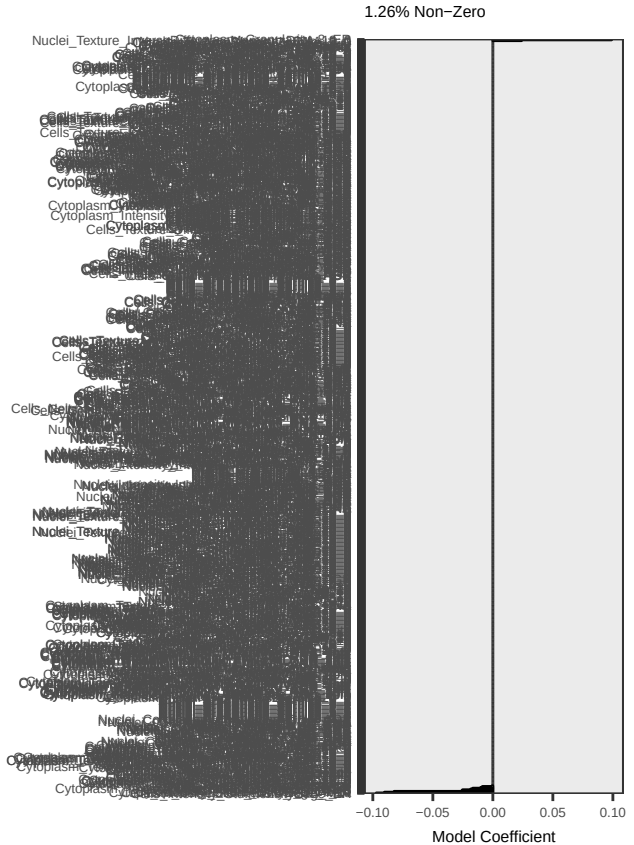


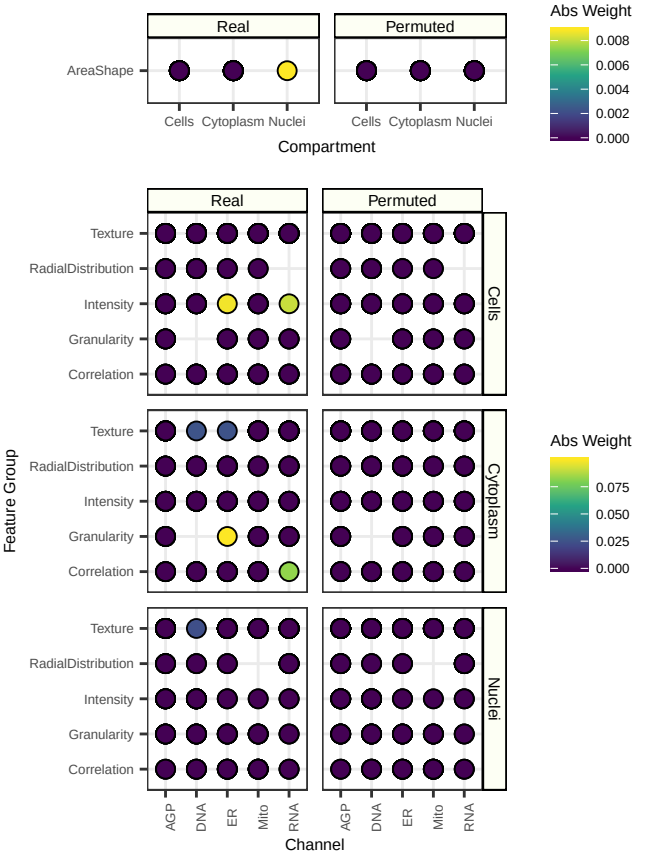
cc_g2_g1_count



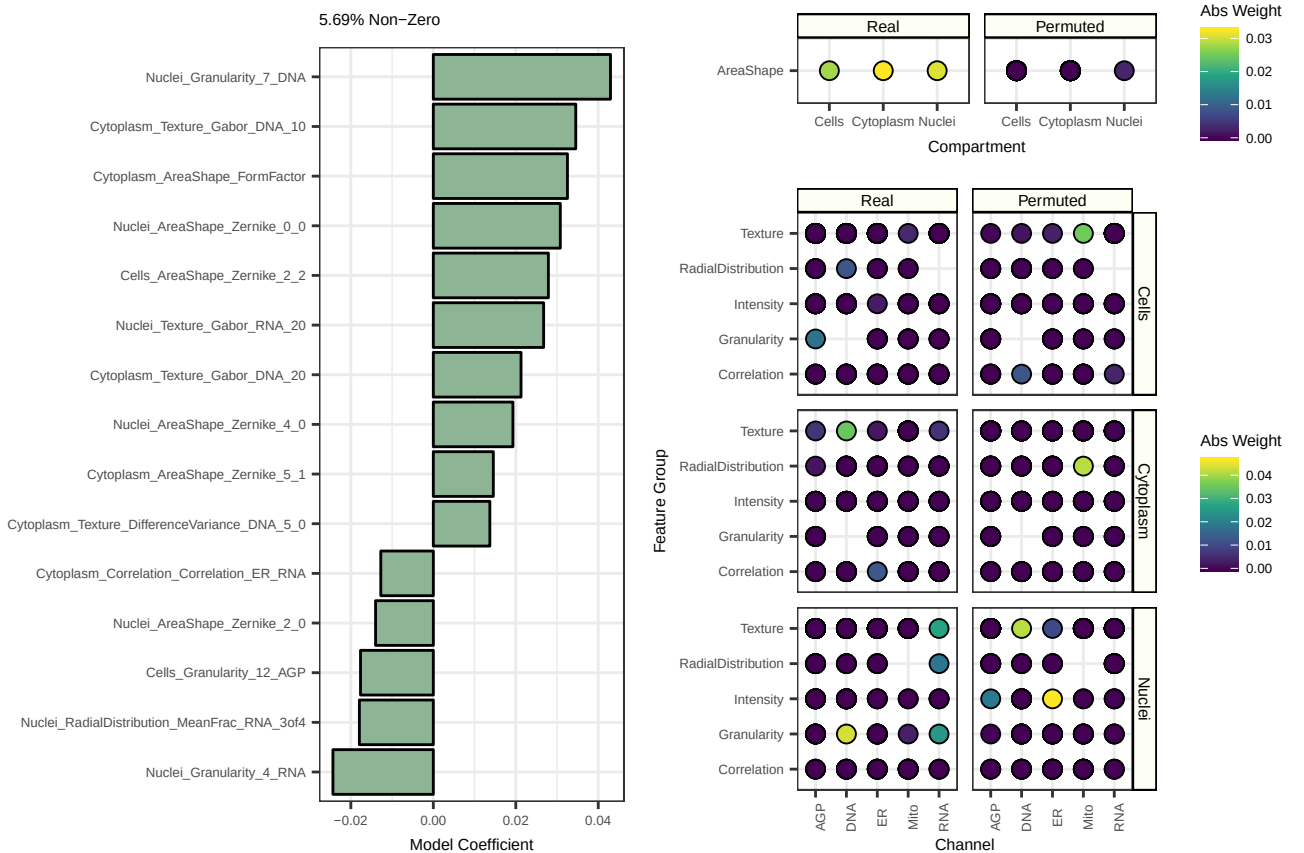


cc_g2_high_h2ax

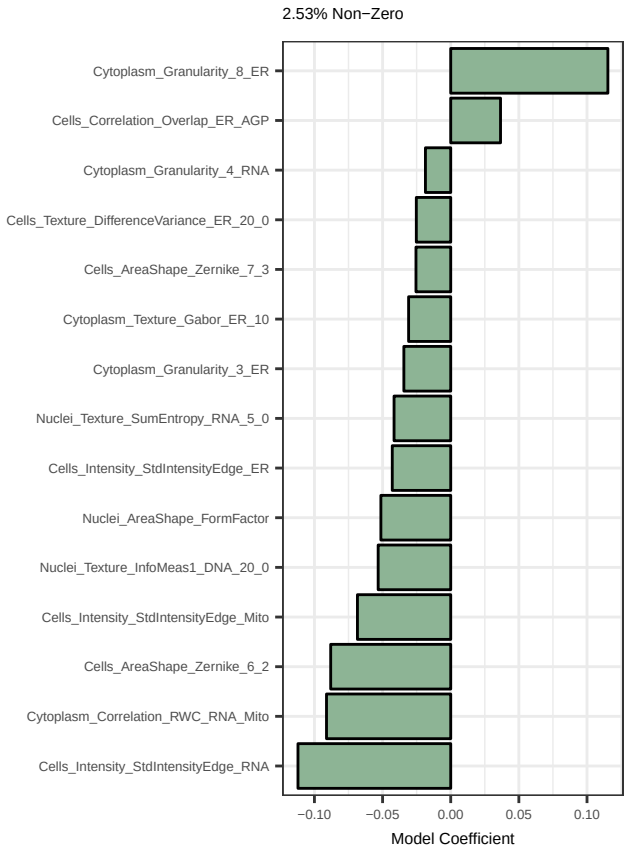


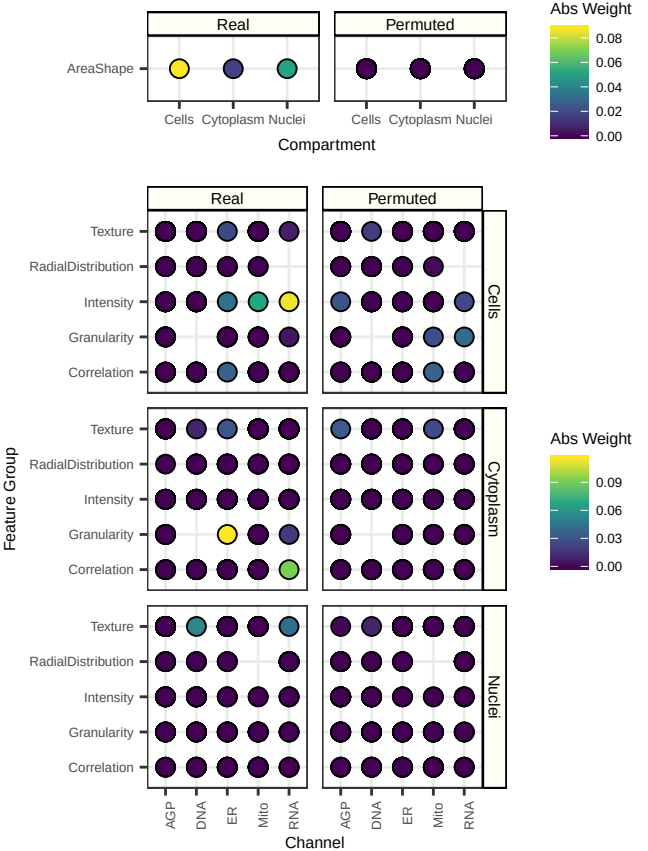


cc_g2_n_objects

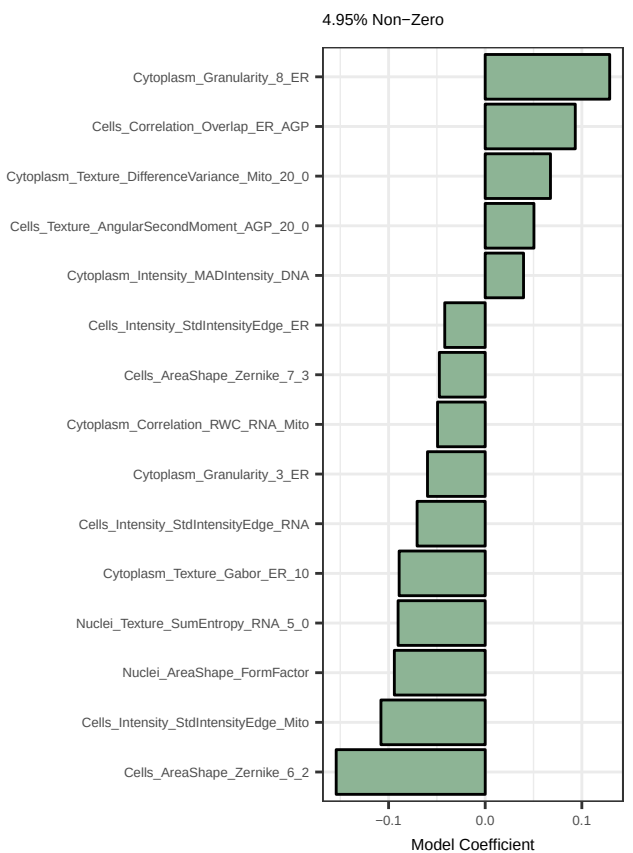


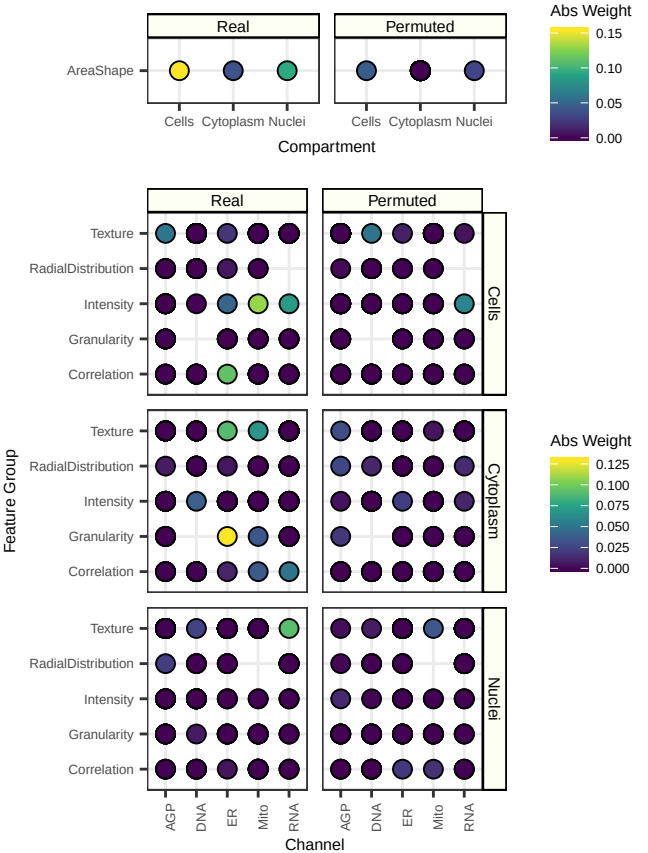
cc_g2_n_spots_h2ax_mean



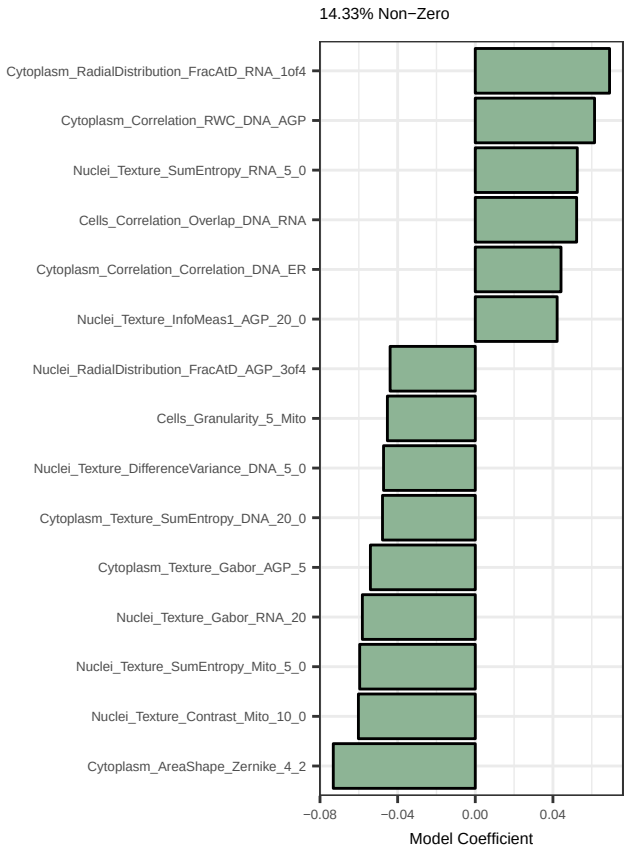


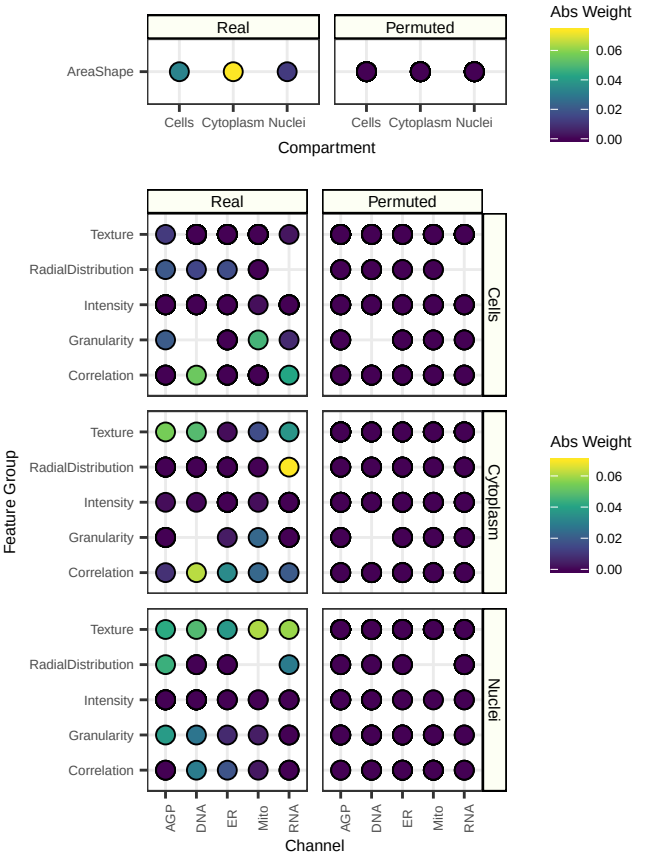
cc_g2_n_spots_h2ax_per_nucleus_area_mean



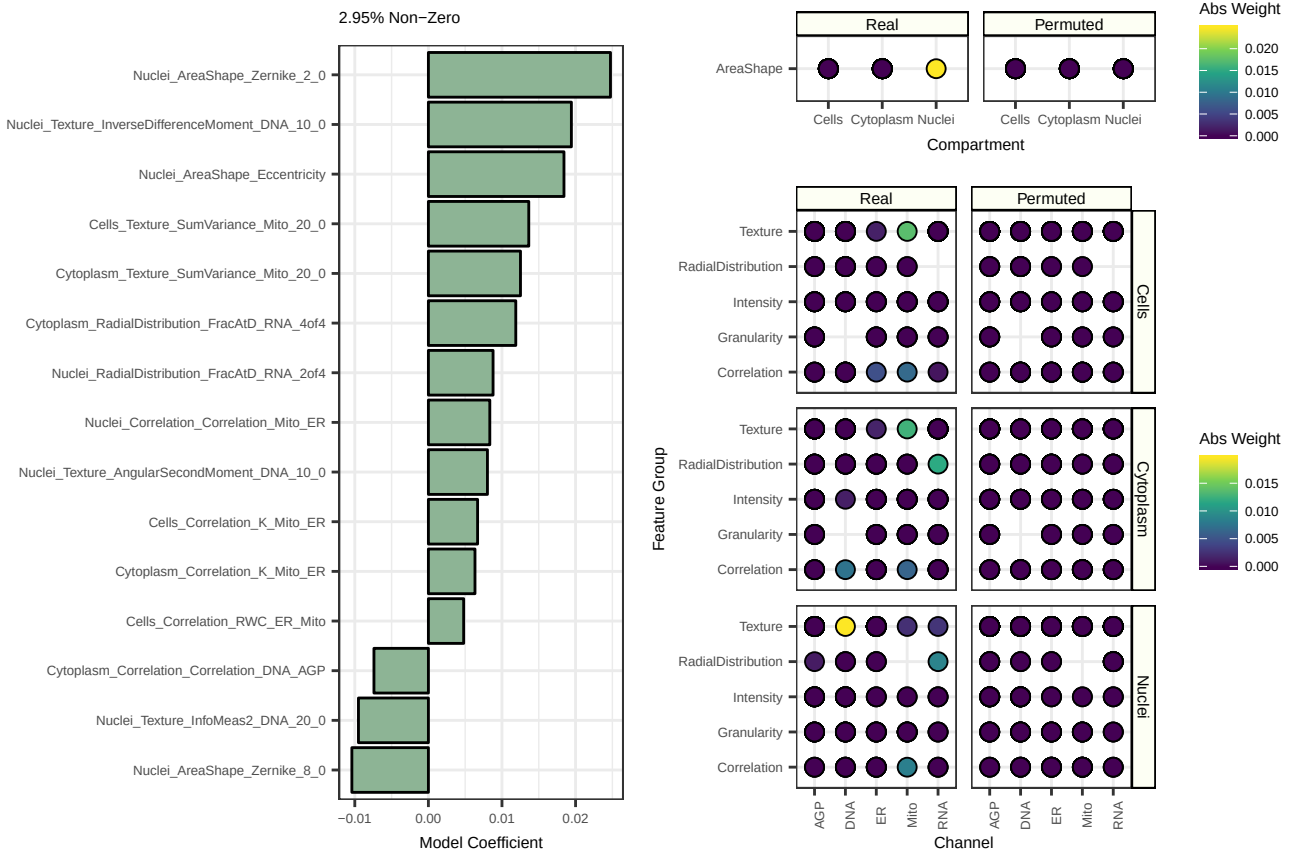


cc_g2_plus_all_m_count

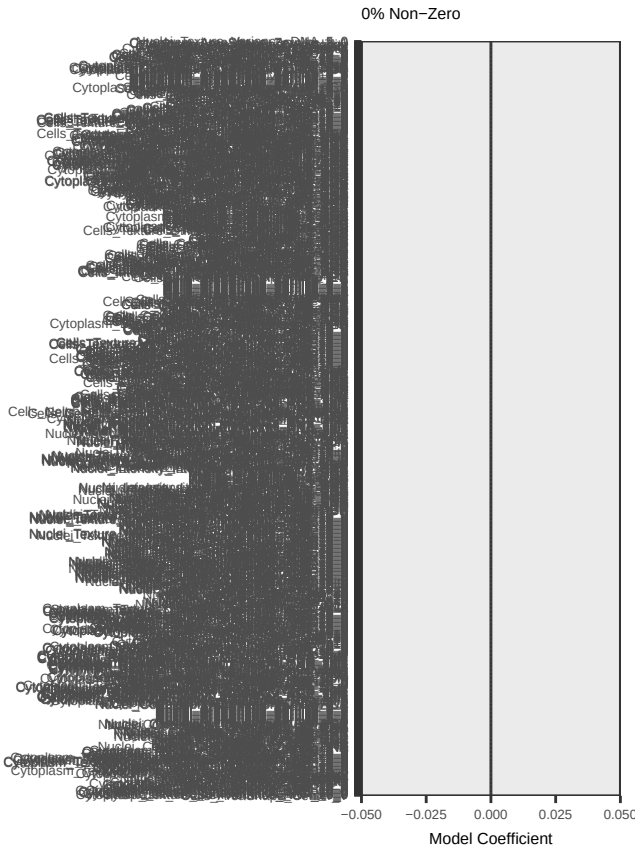


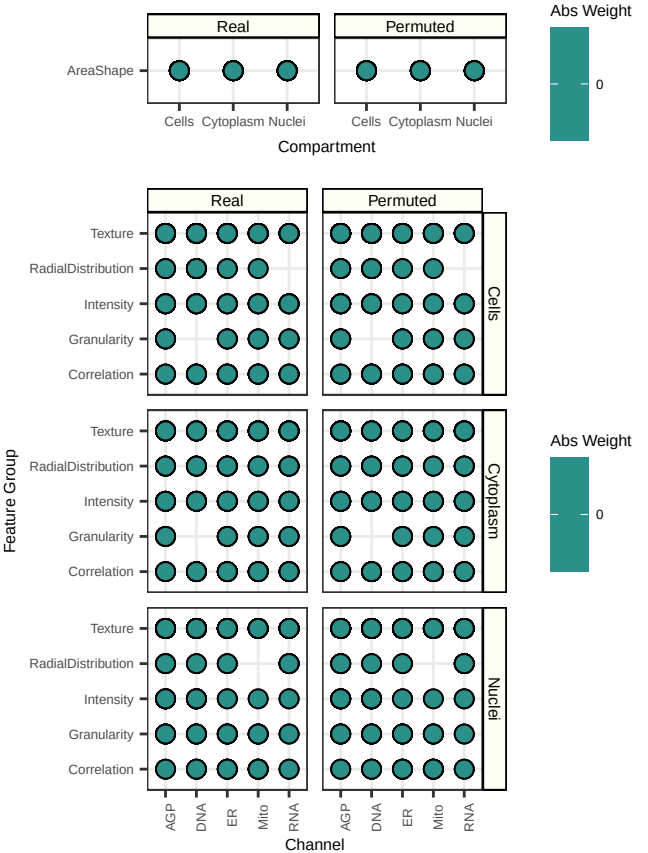


cc_infection_percentage

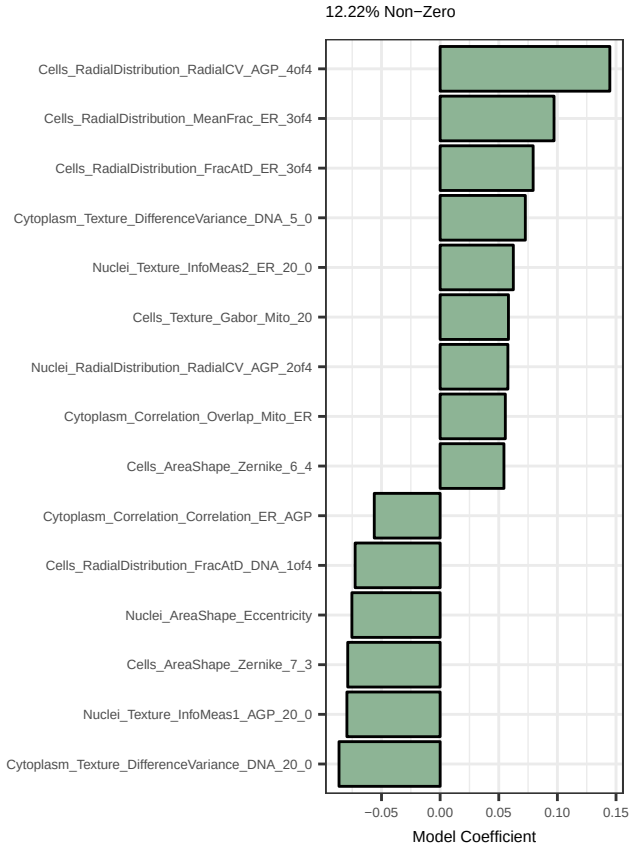


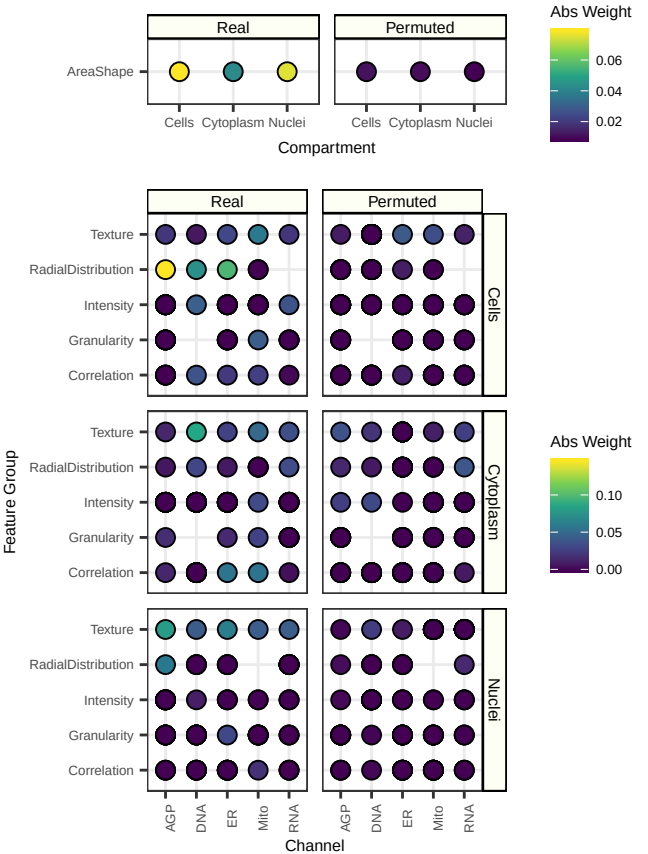
cc_late_mitosis_high_h2ax



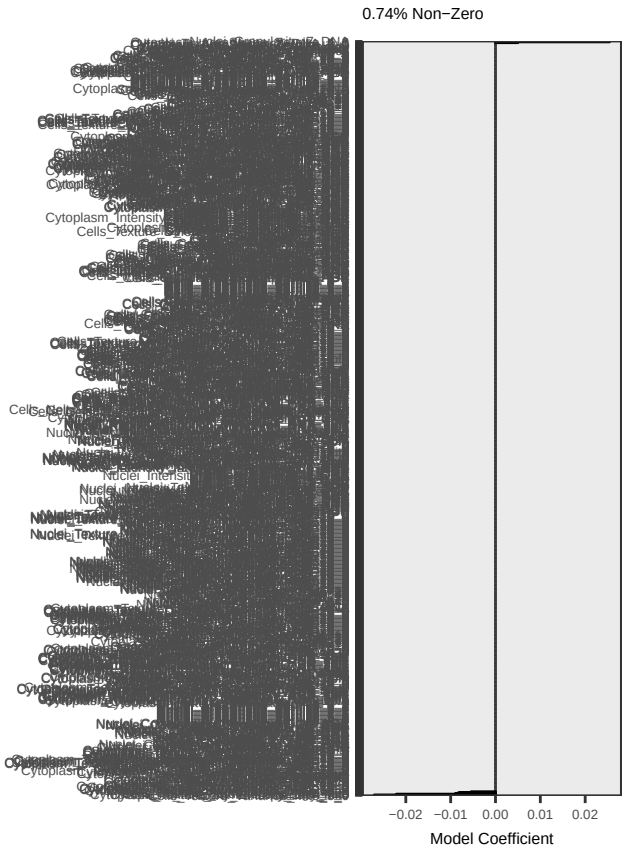


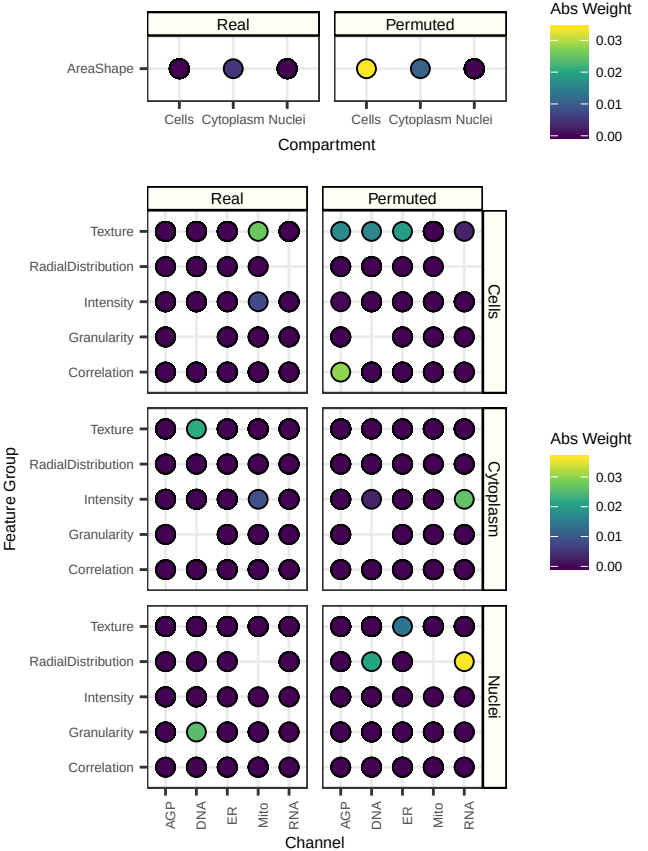
cc_late_mitosis_n_objects



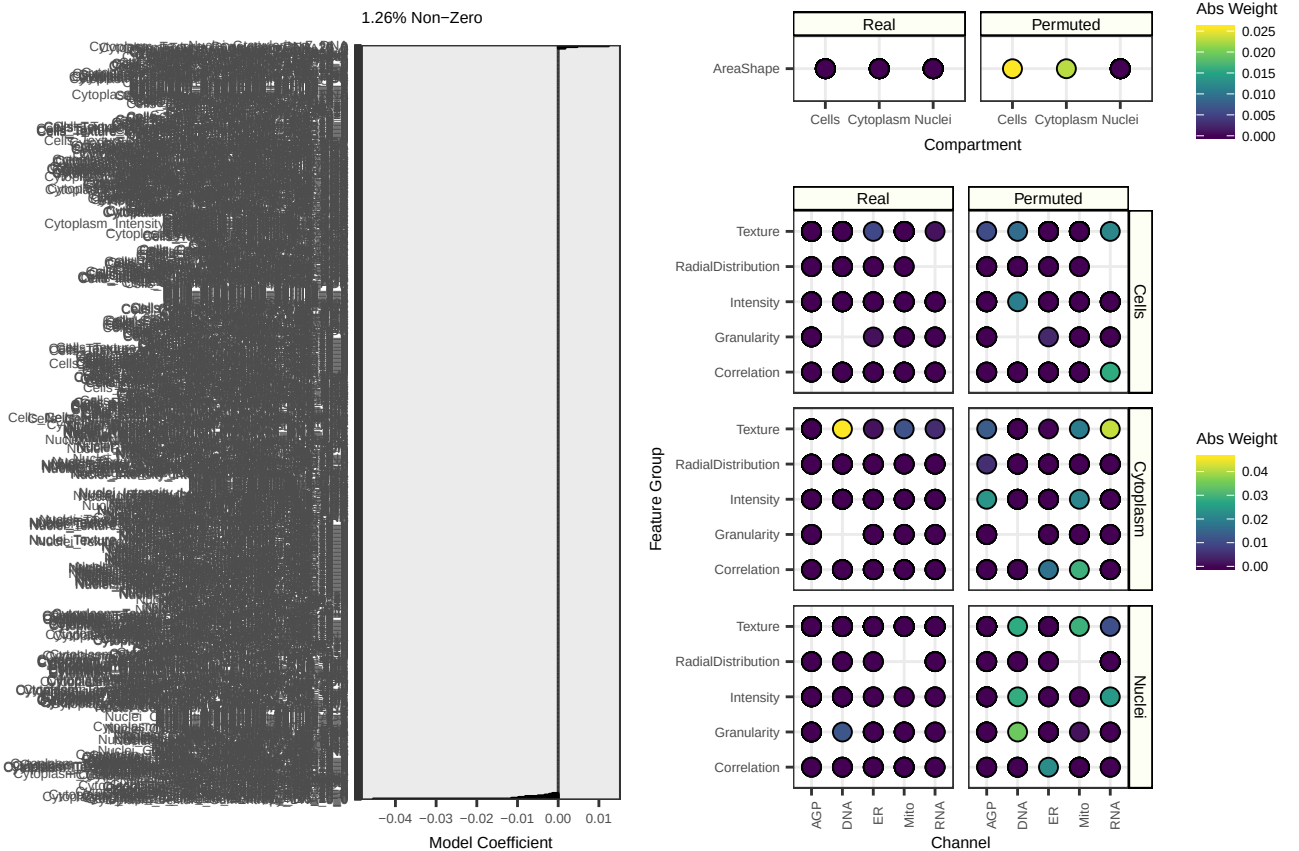


cc_late_mitosis_n_spots_h2ax_mean

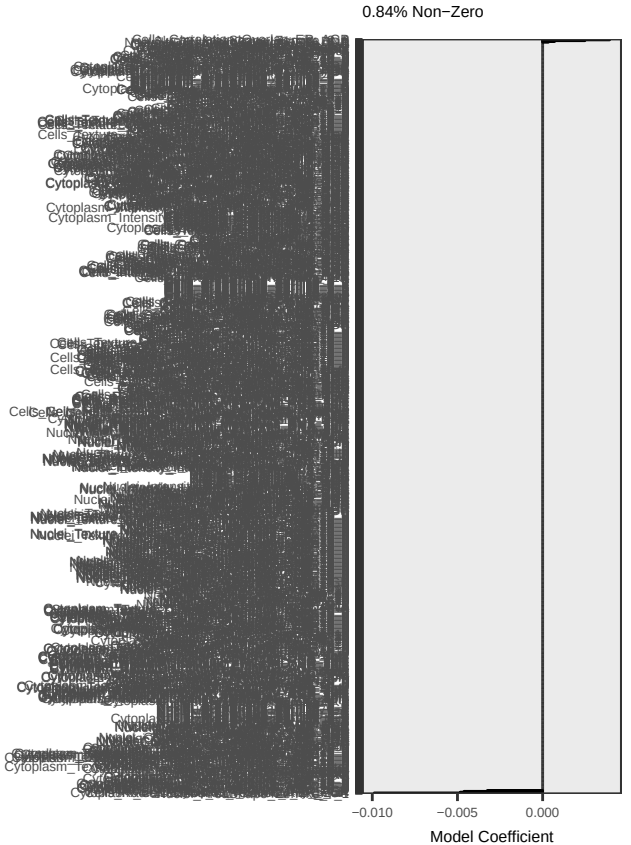


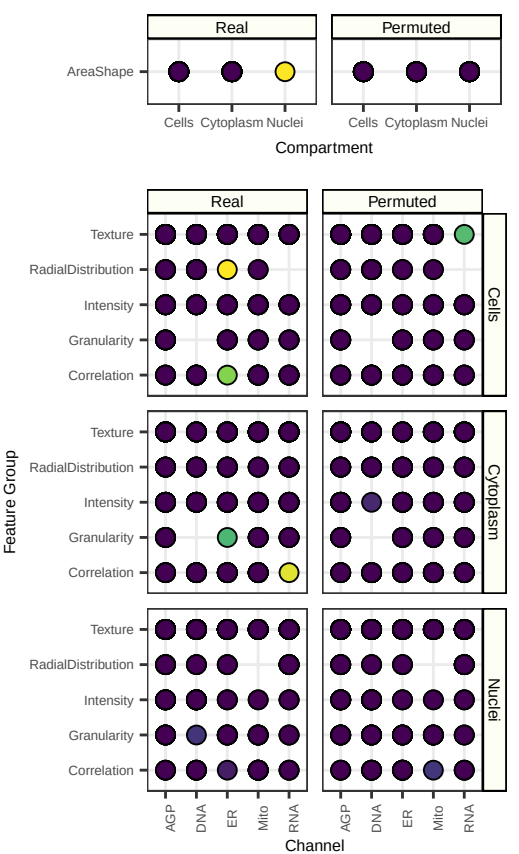


cc_late_mitosis_n_spots_h2ax_per_nucleus_area_mean

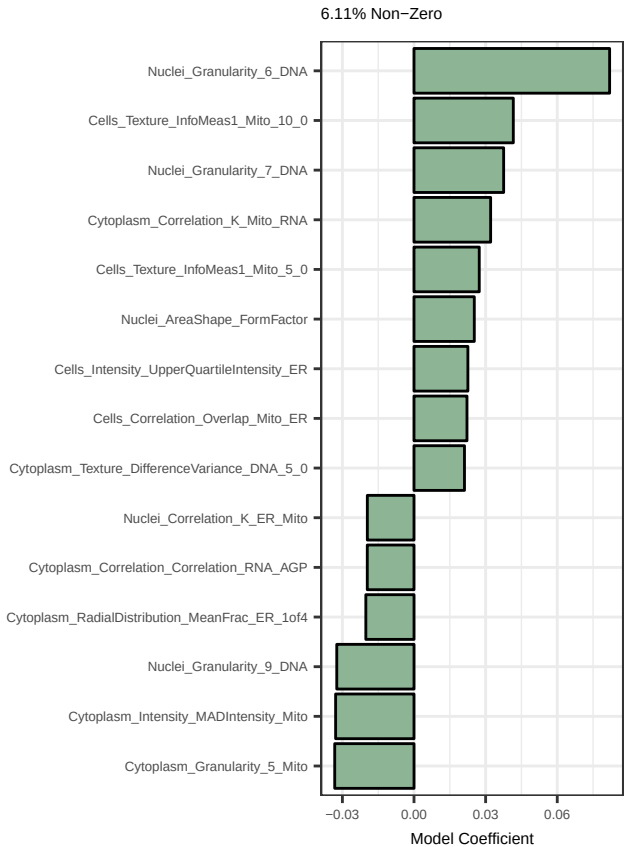


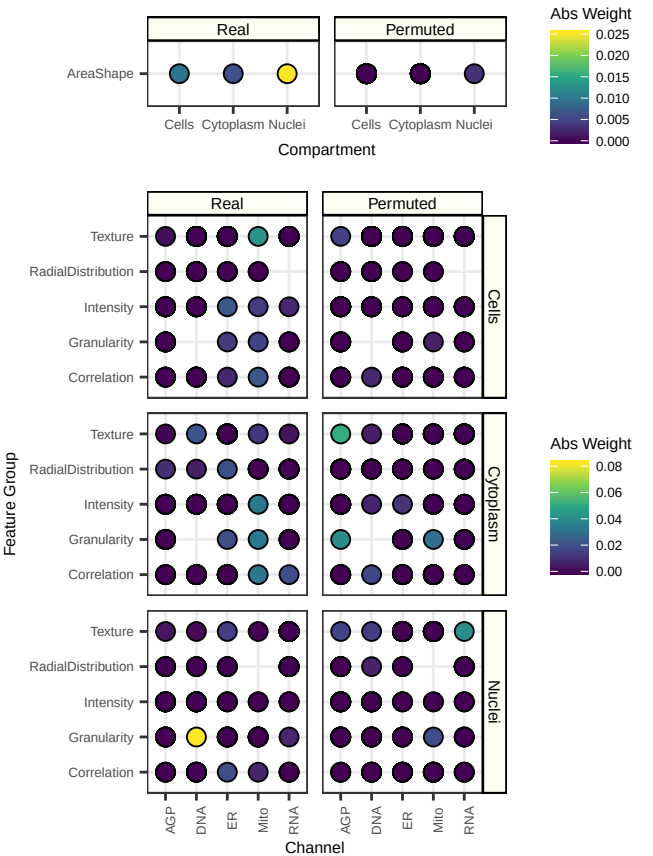
cc_mitosis_high_h2ax



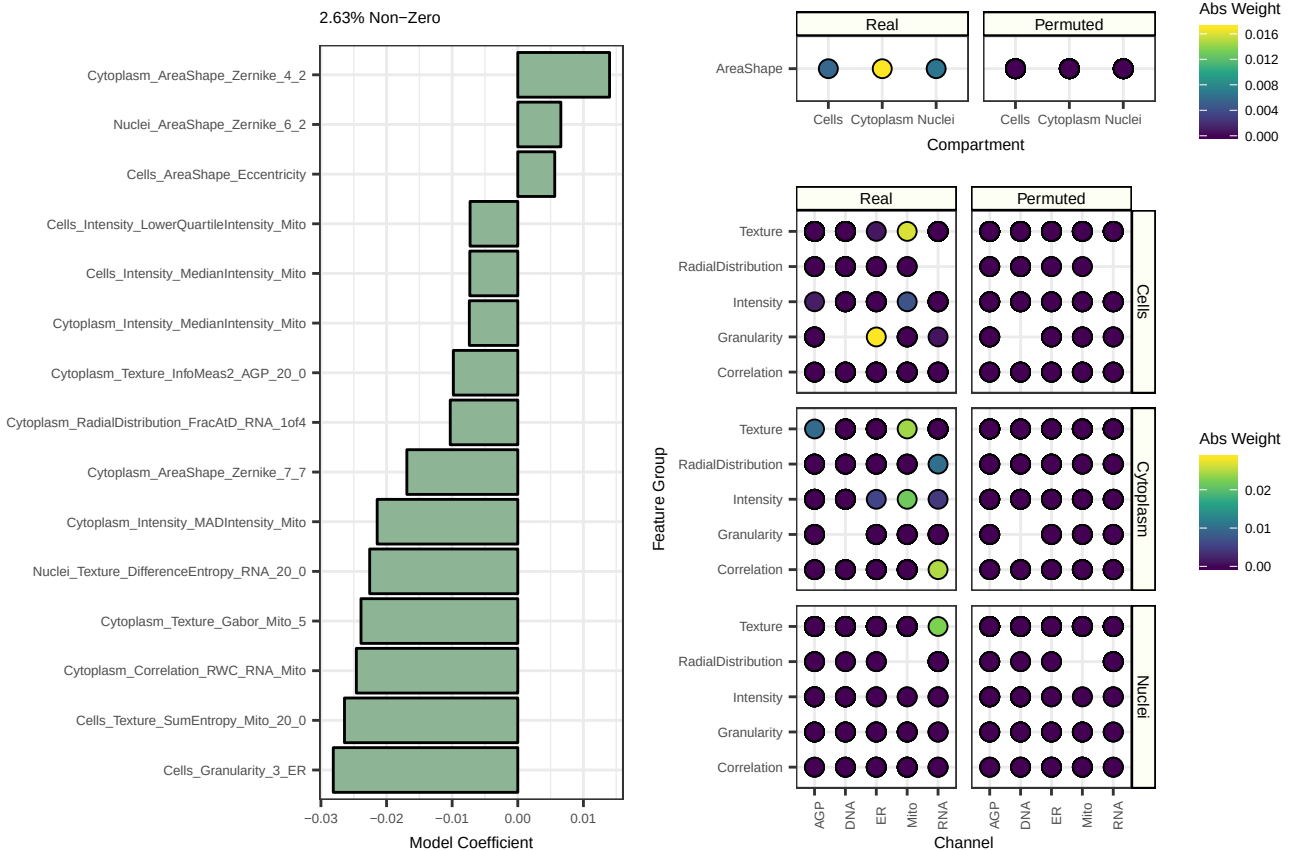


cc_mitosis_n_objects

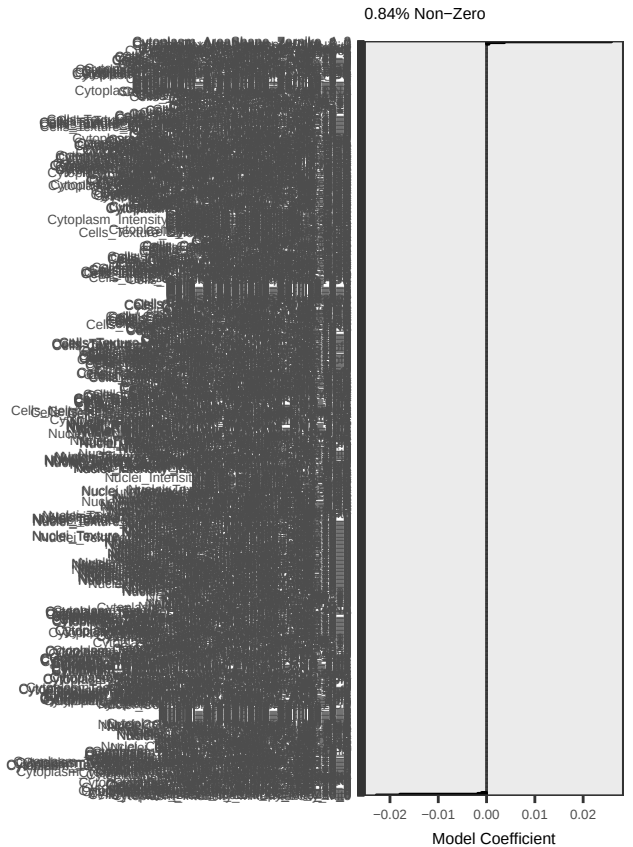


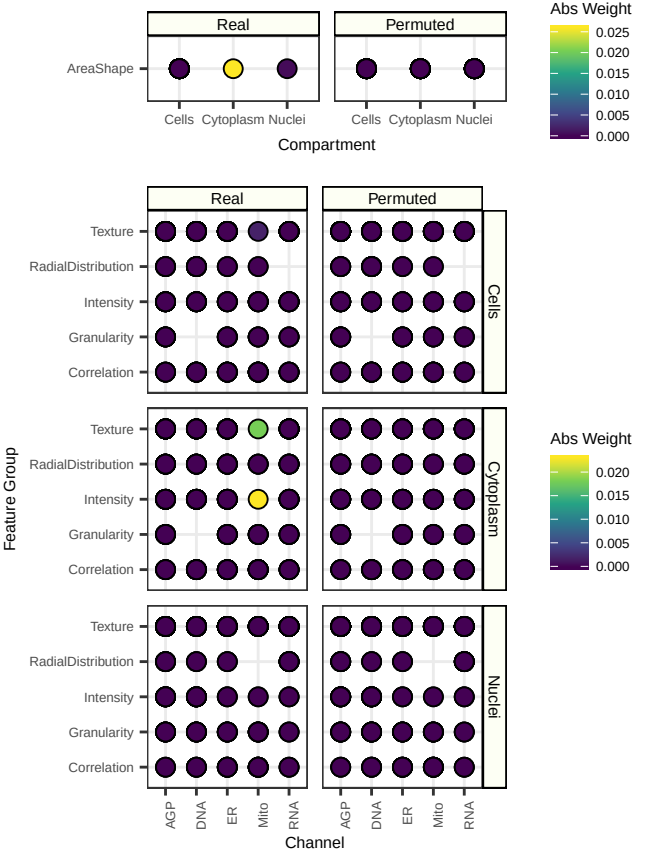


cc_mitosis_n_spots_h2ax_mean

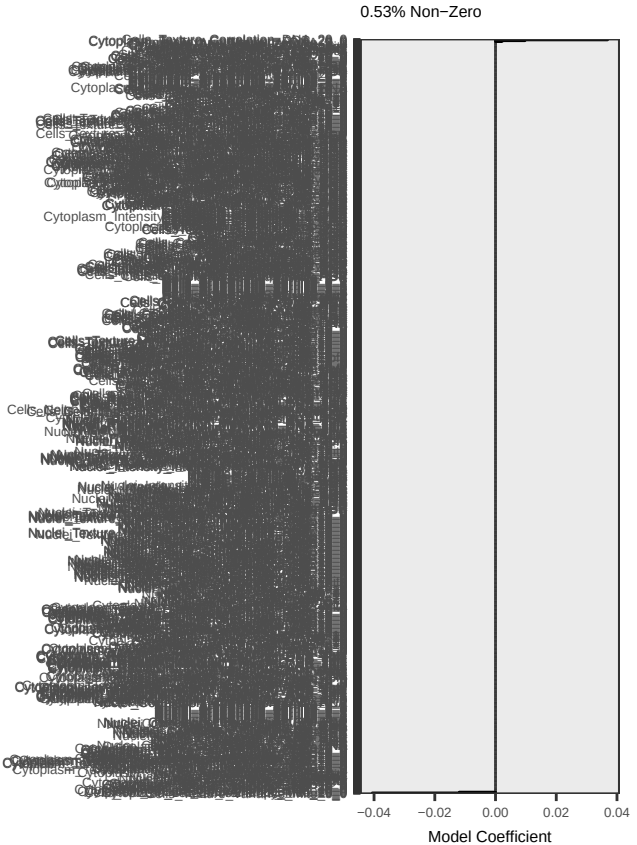


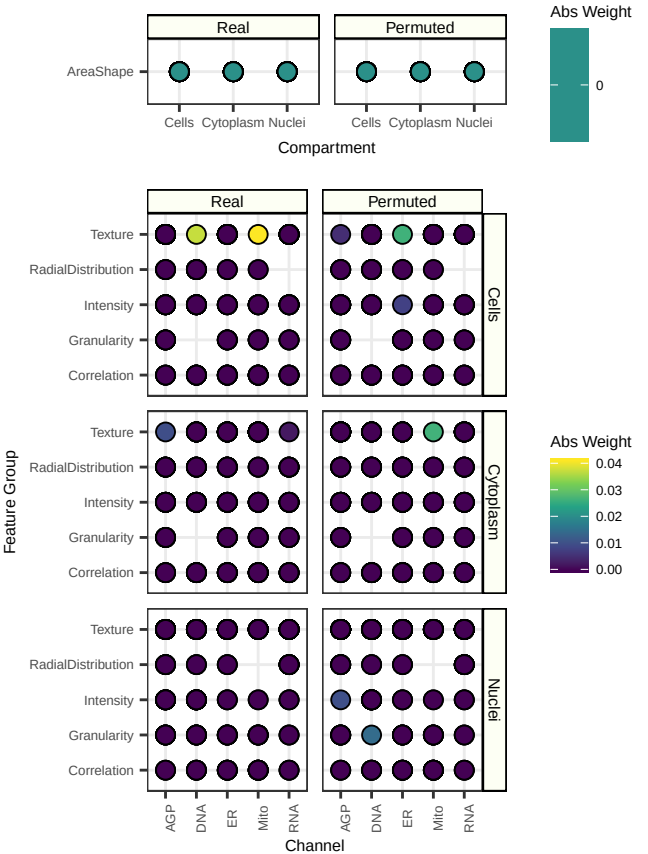
cc_mitosis_n_spots_h2ax_per_nucleus_area_mean



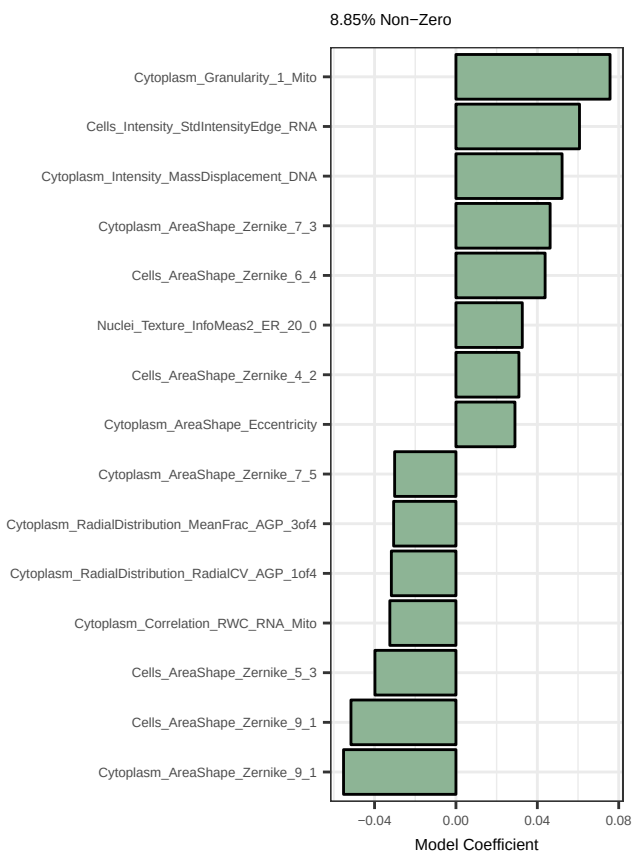


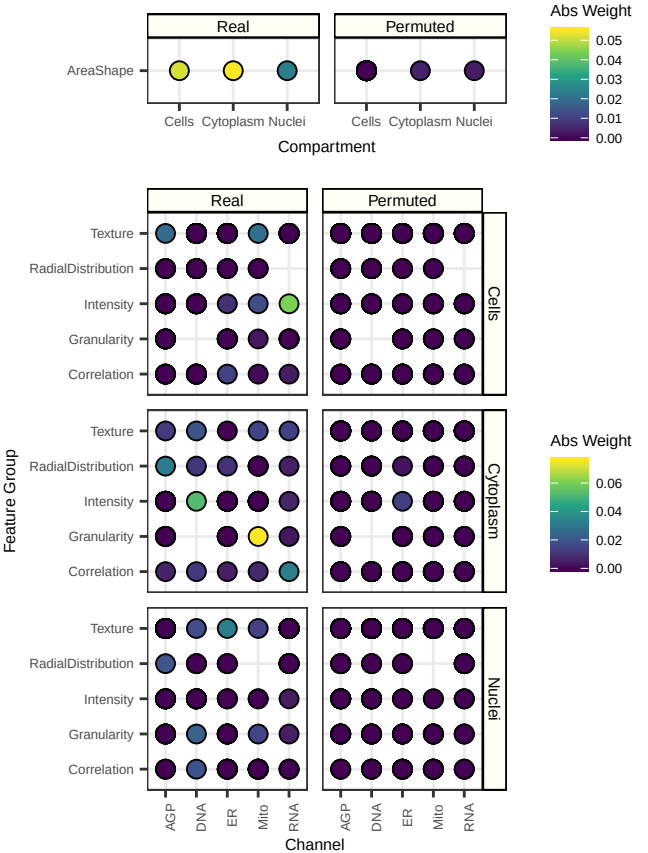
cc_polynuclear_high_h2ax



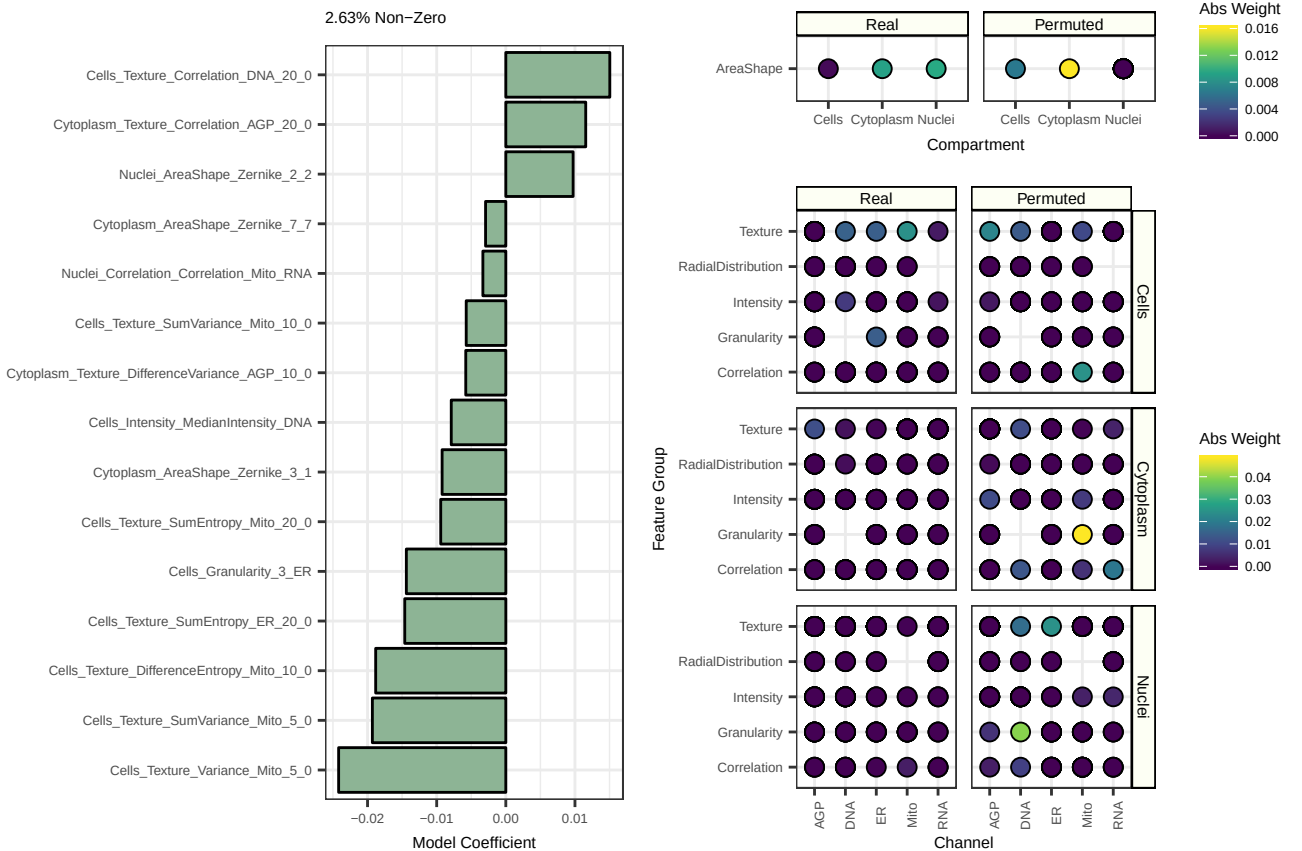


cc_polynuclear_n_objects

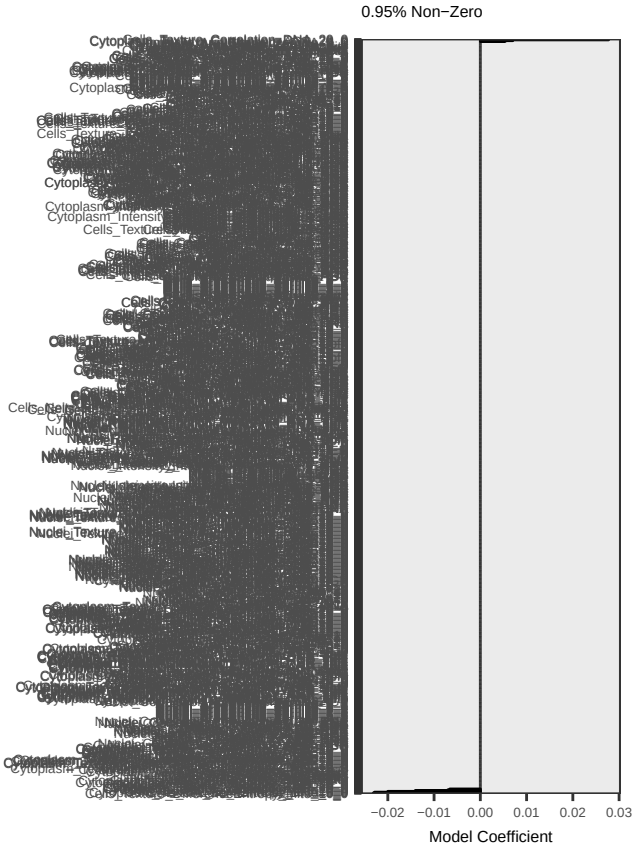


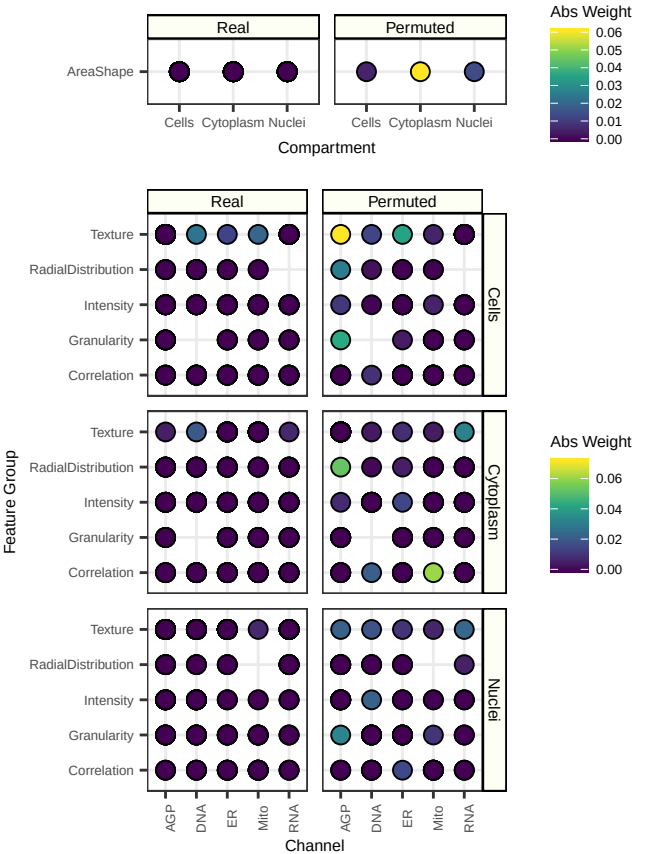


cc_polynuclear_n_spots_h2ax_mean

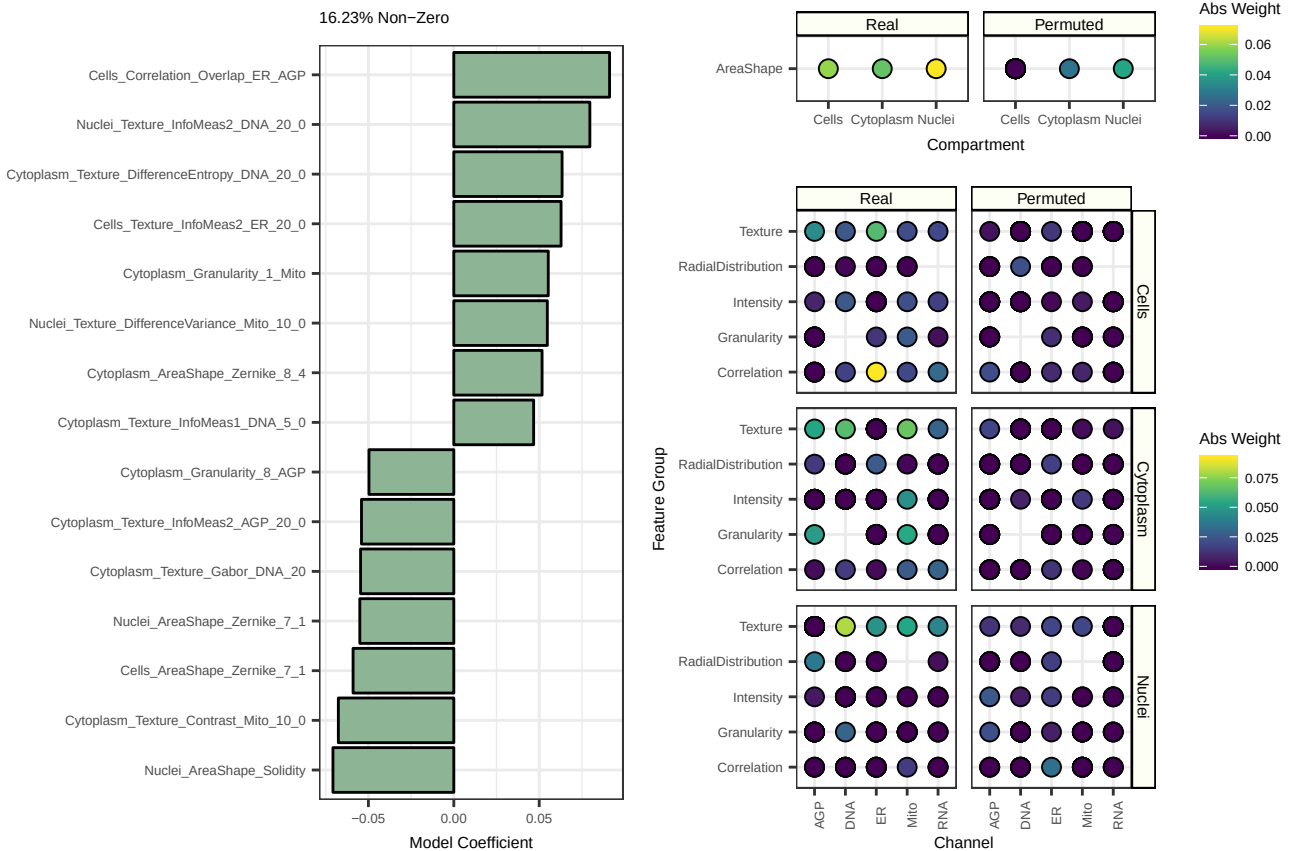


cc_polynuclear_n_spots_h2ax_per_nucleus_area_mean

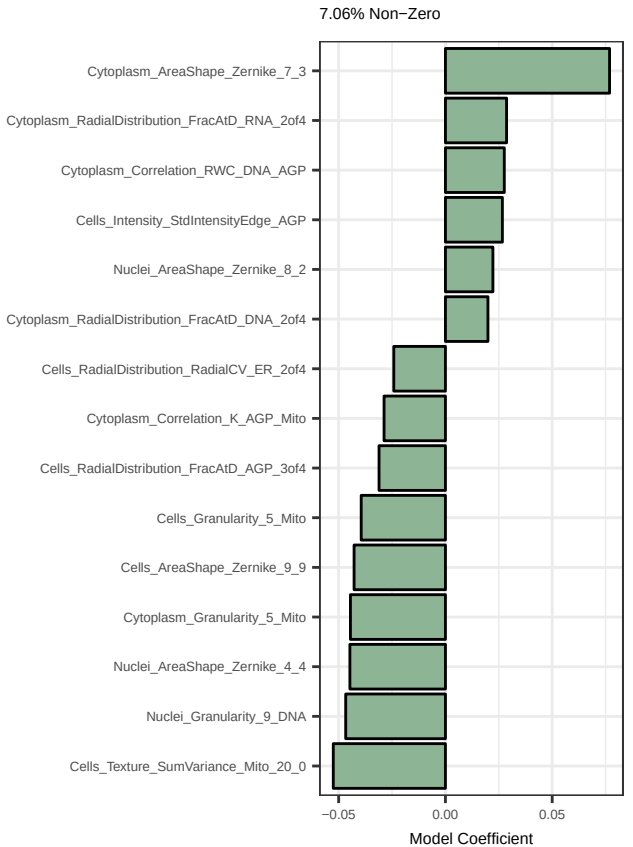


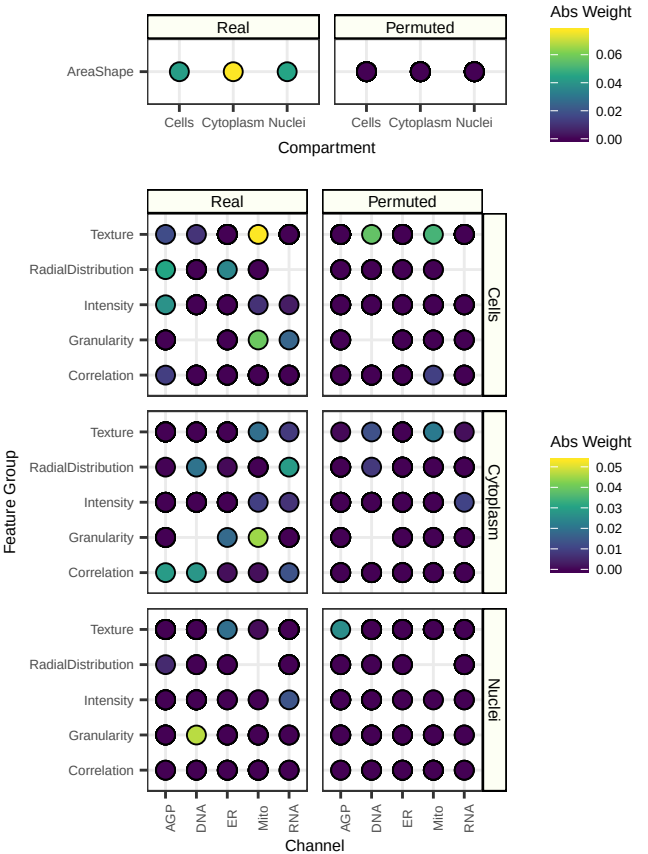


cc_polyploid_high_h2ax

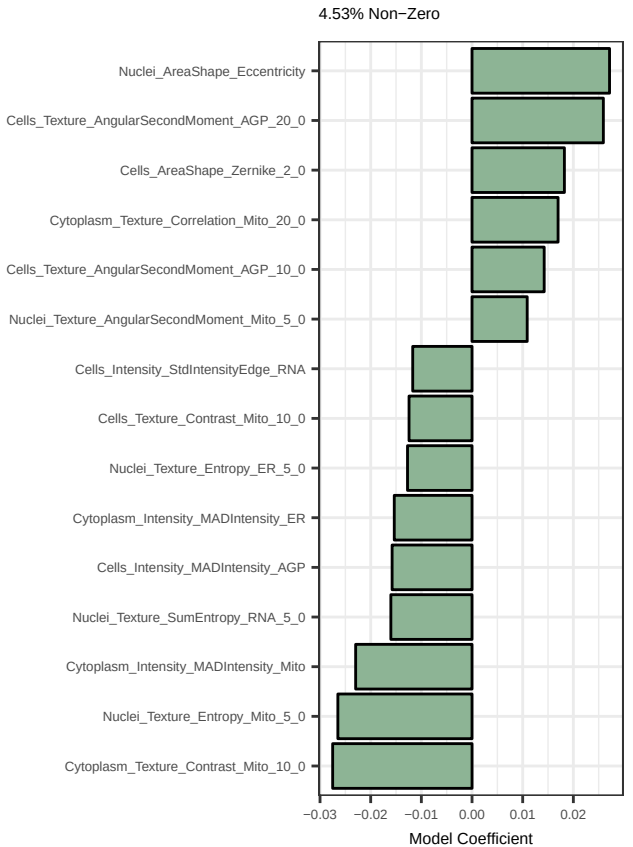


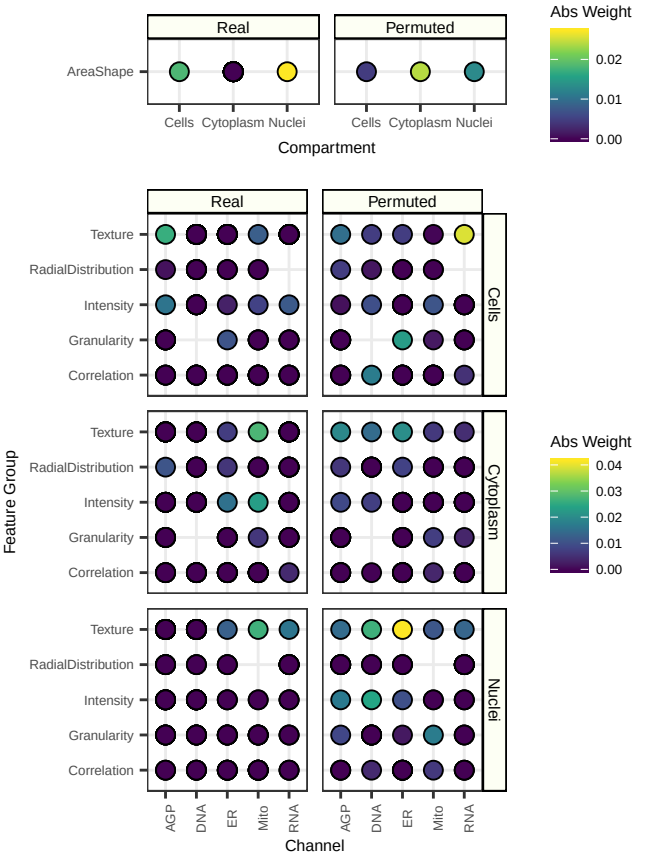
cc_polyploid_n_objects



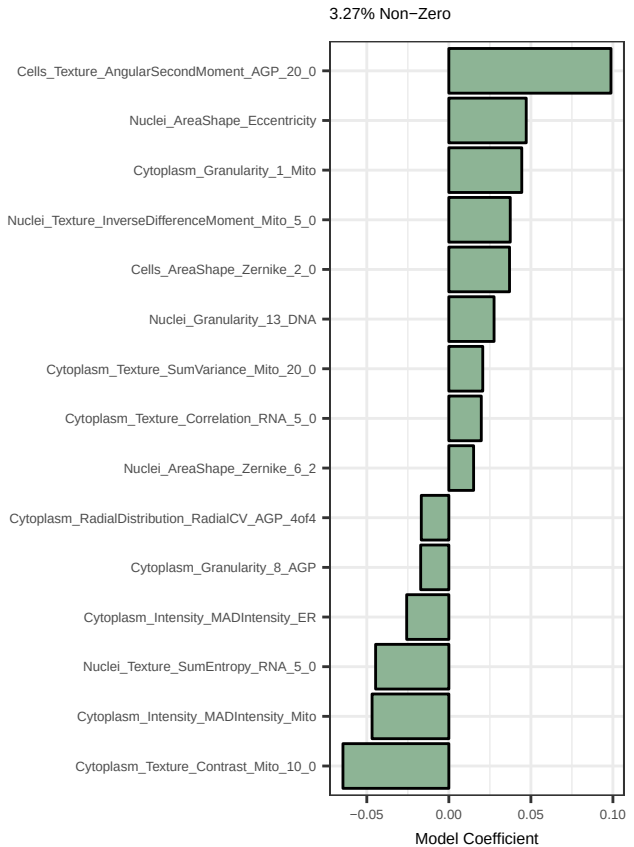


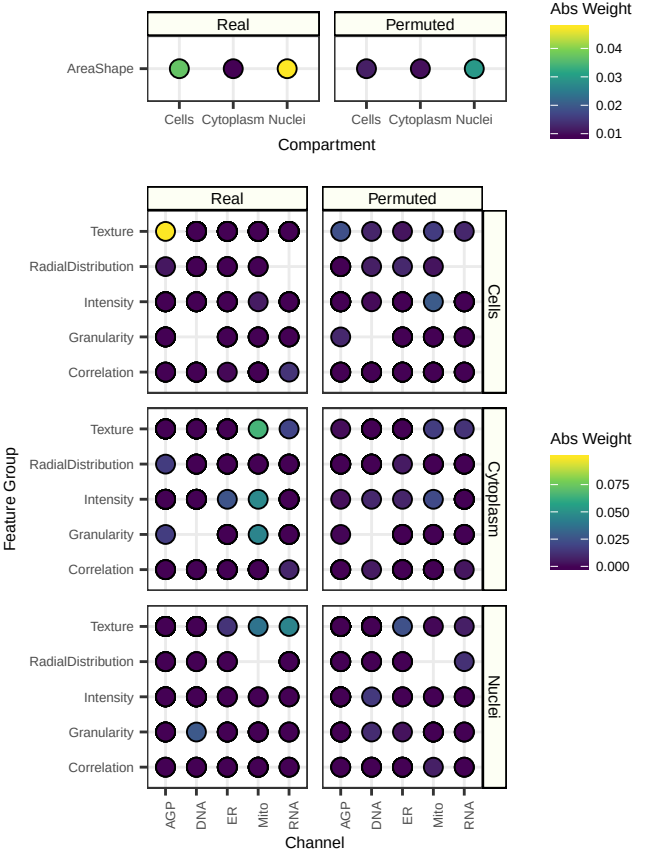
cc_polyploid_n_spots_h2ax_mean



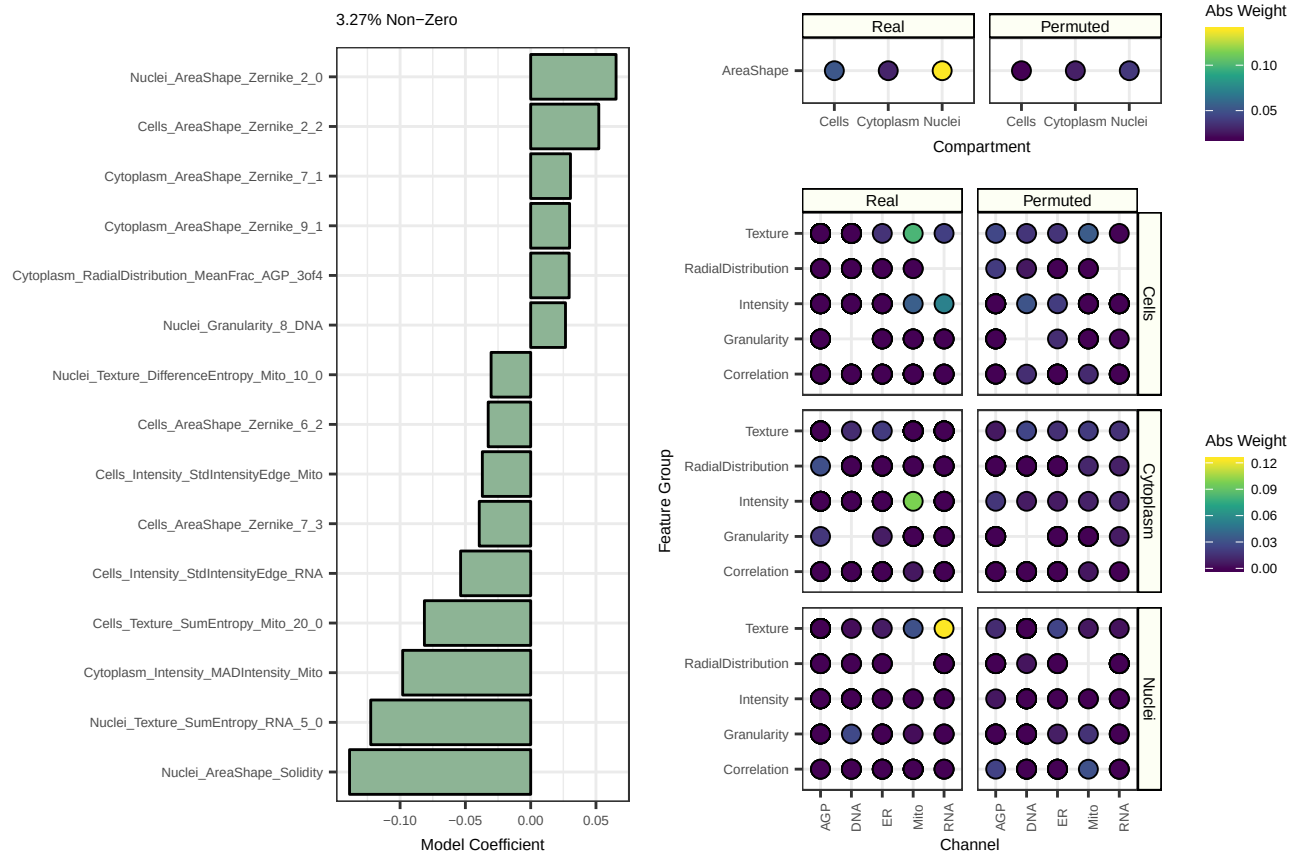


cc_polyploid_n_spots_h2ax_per_nucleus_area_mean

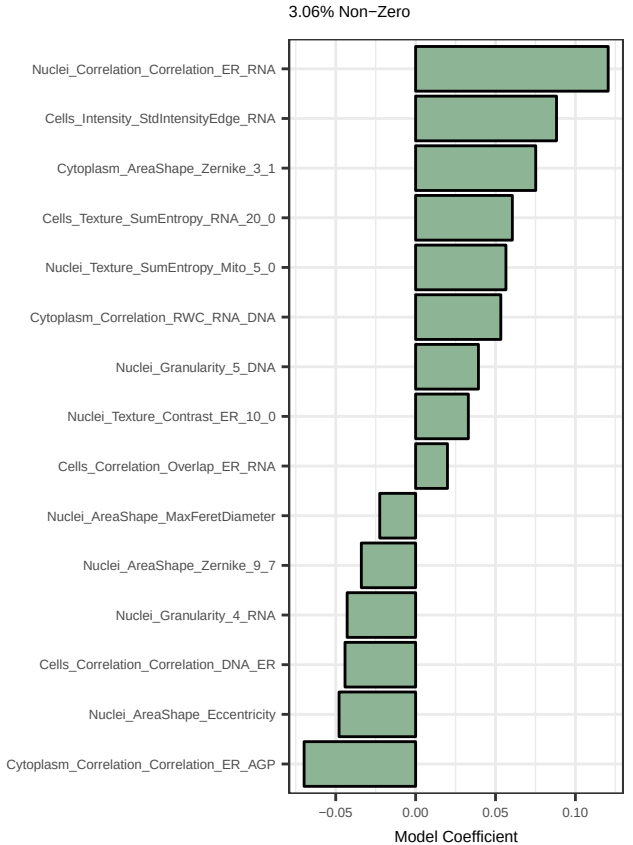


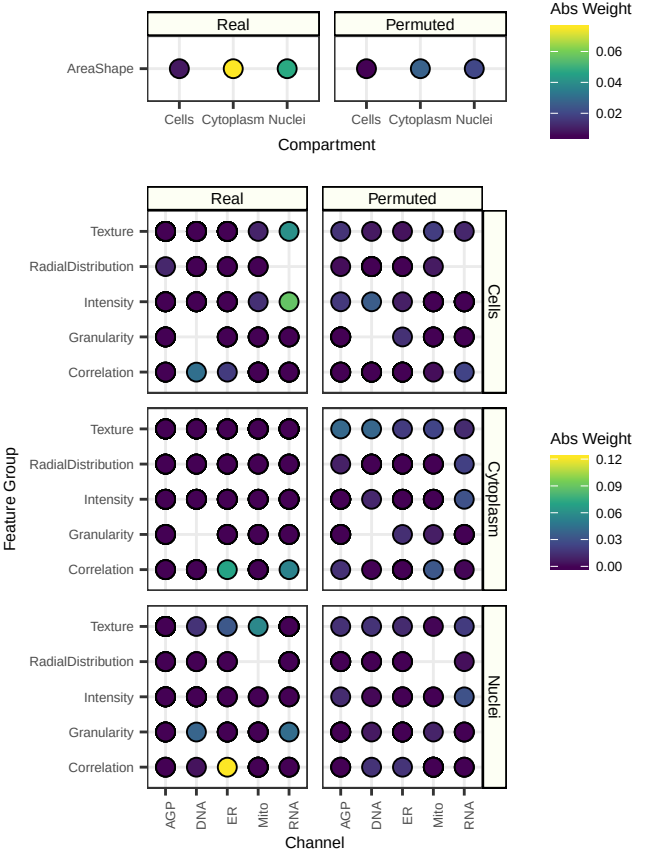


cc_s_high_h2ax

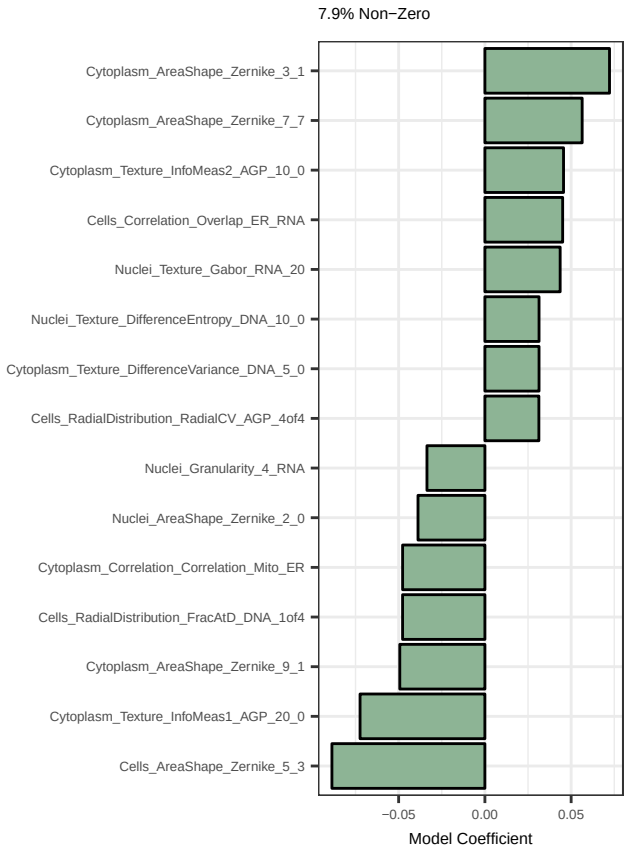


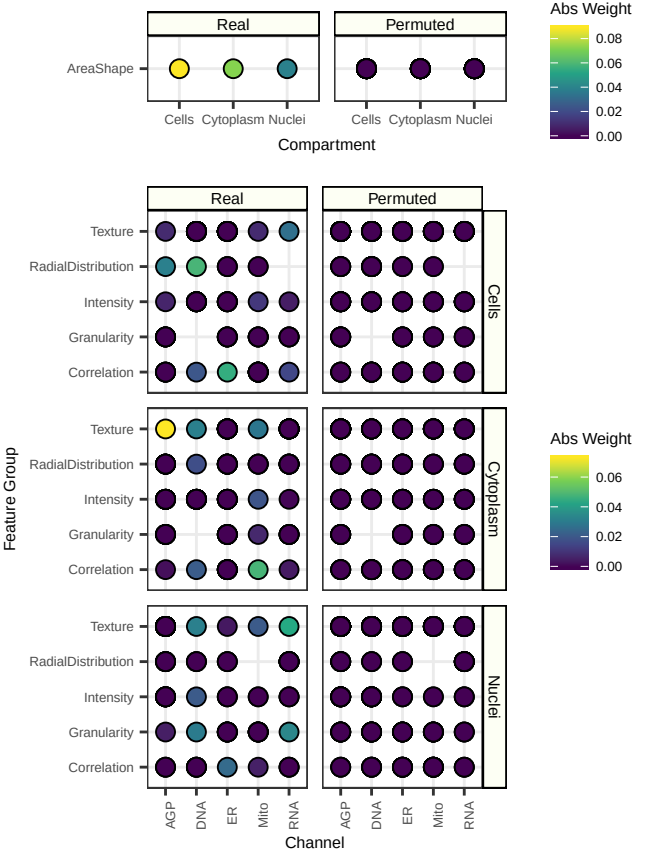
cc_s_intensity_nucleus_area_mean



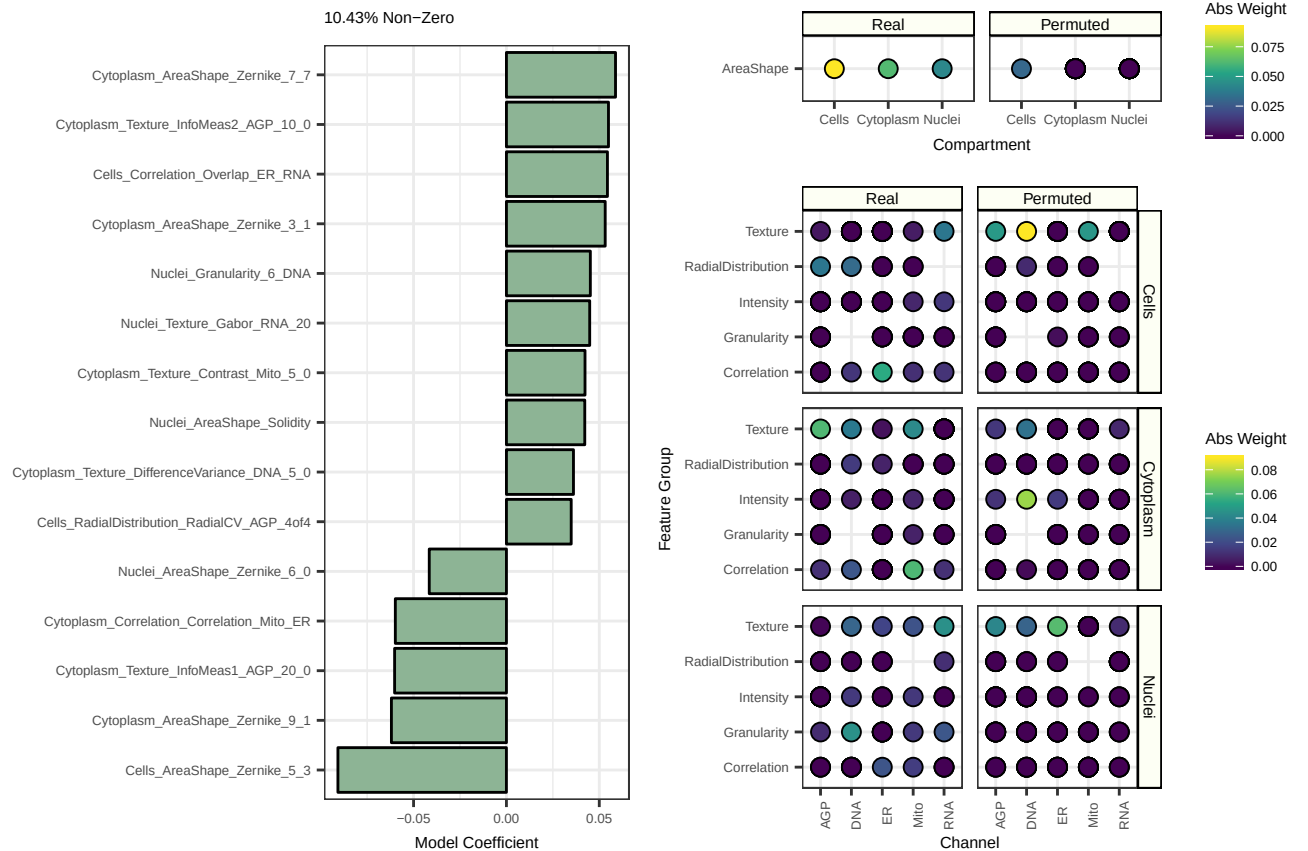


cc_s_intensity_nucleus_area_sum

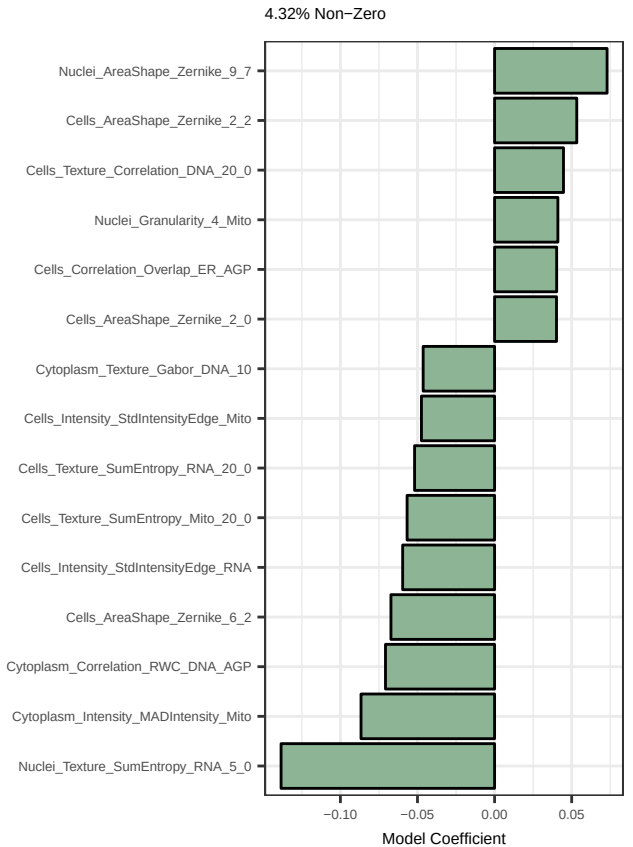


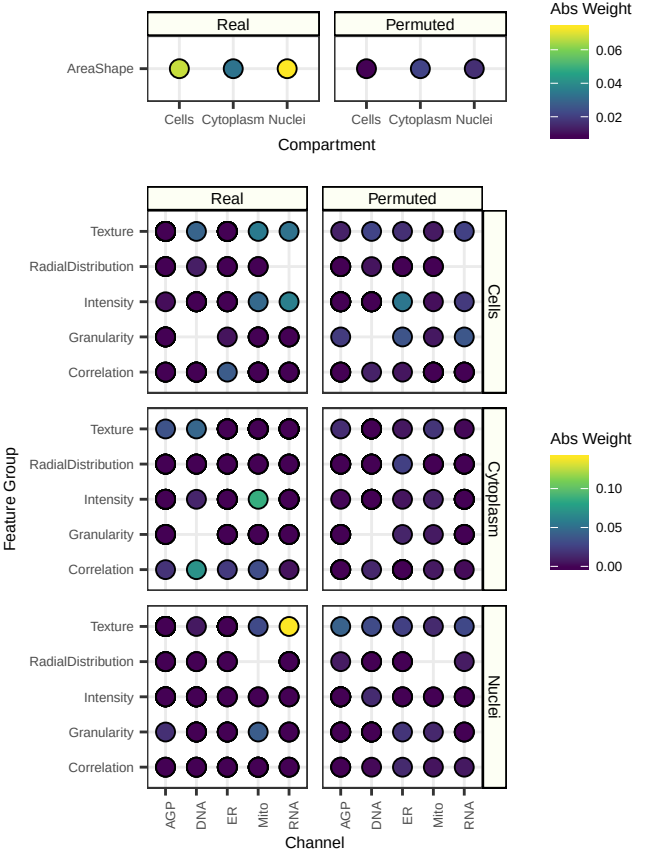


cc_s_n_objects

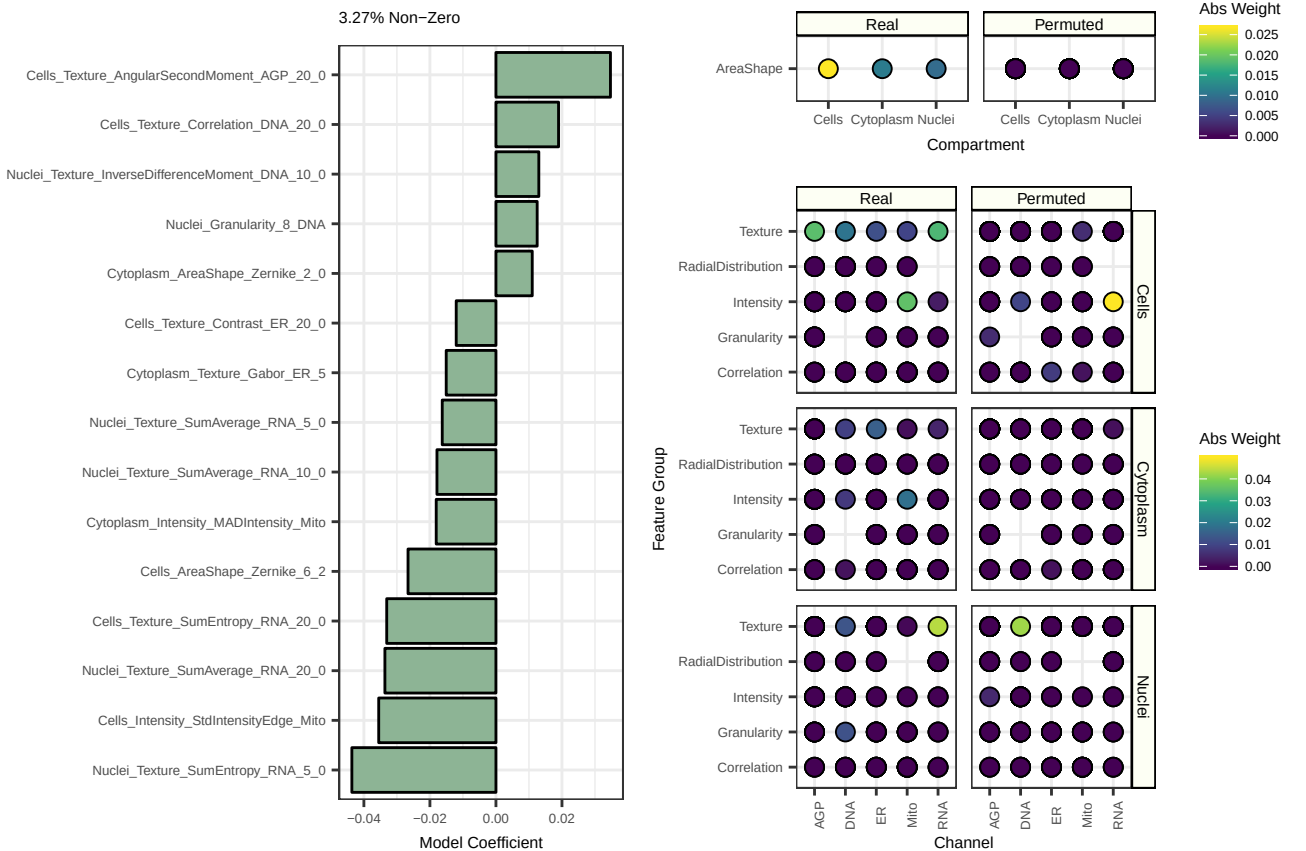


cc_s_n_spots_h2ax_mean

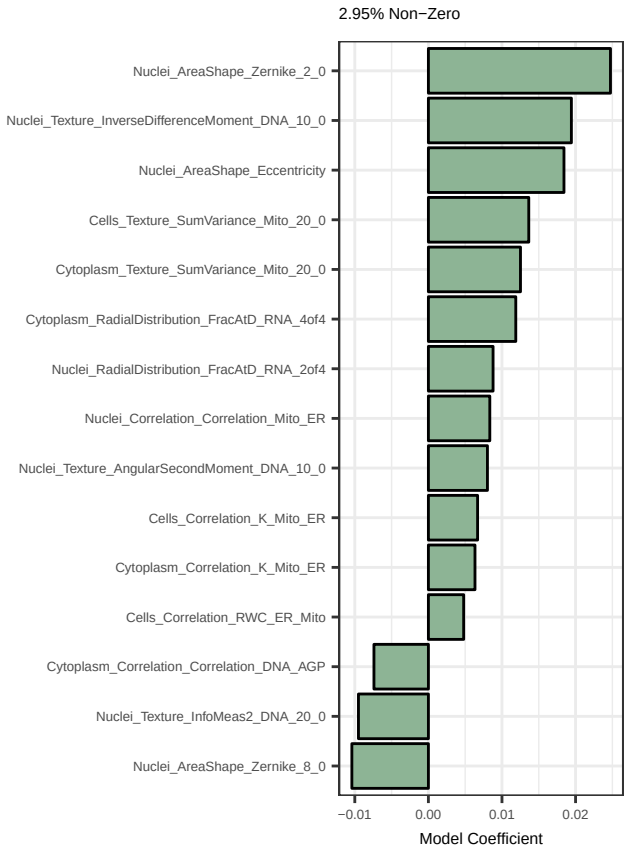


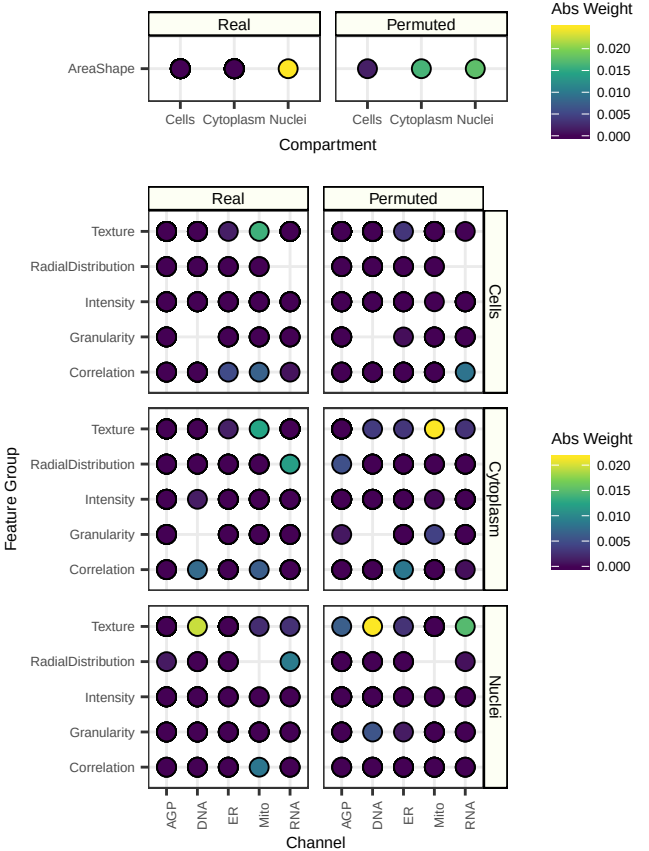


cc_s_n_spots_h2ax_per_nucleus_area_mean

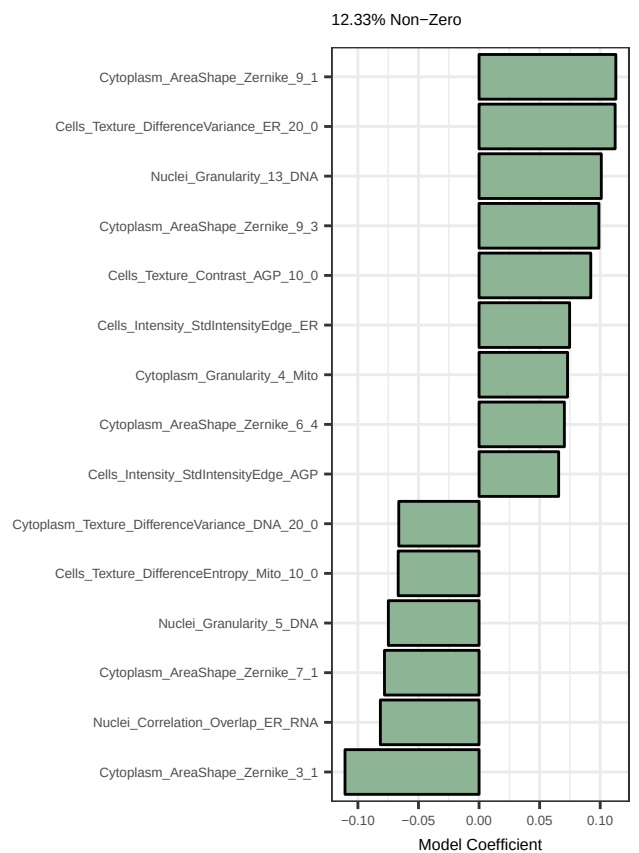


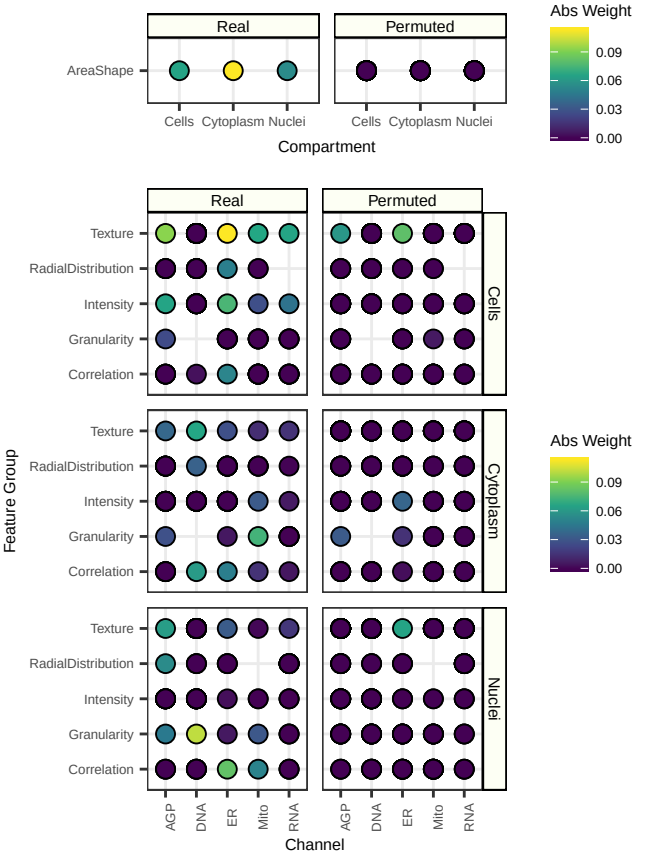
vb_infection_percentage



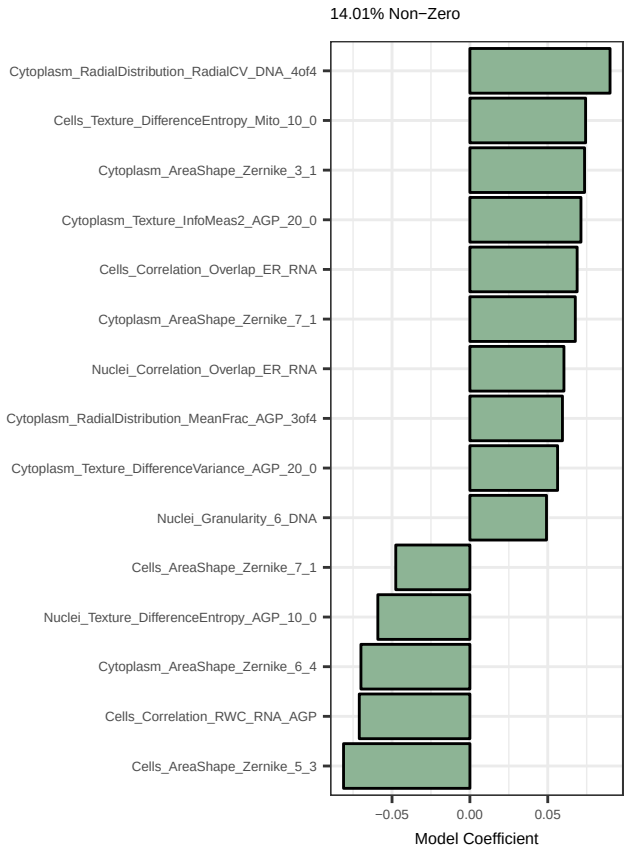


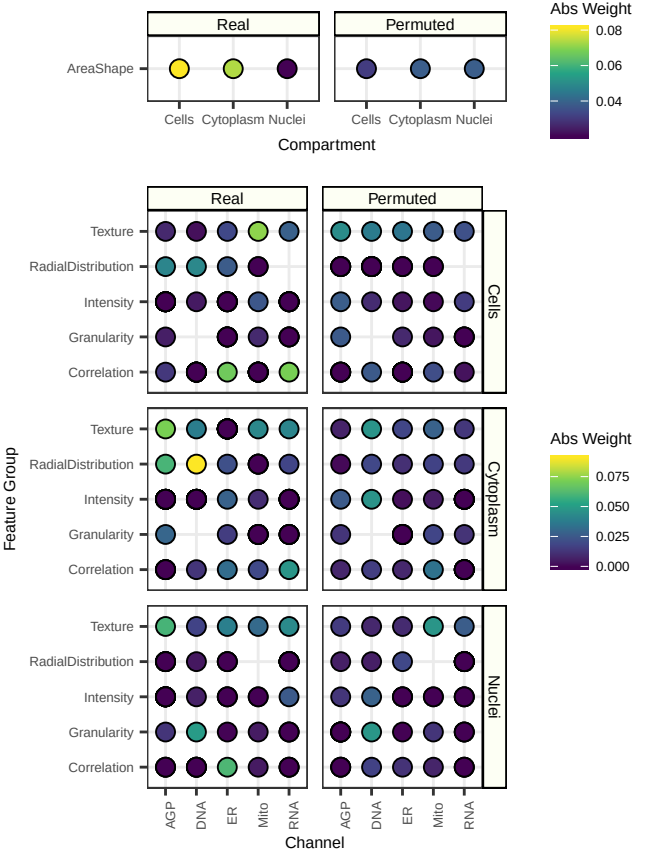
vb_live_cell_area



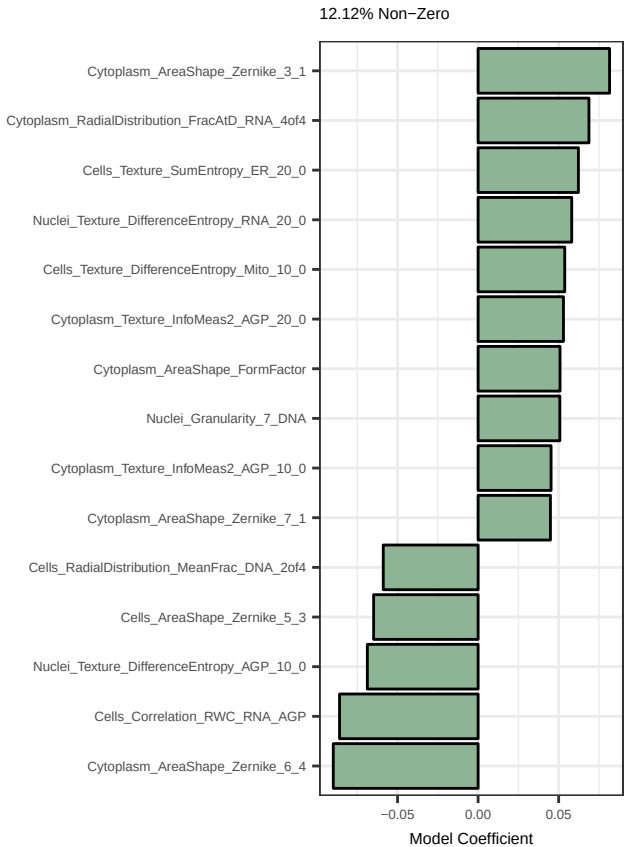


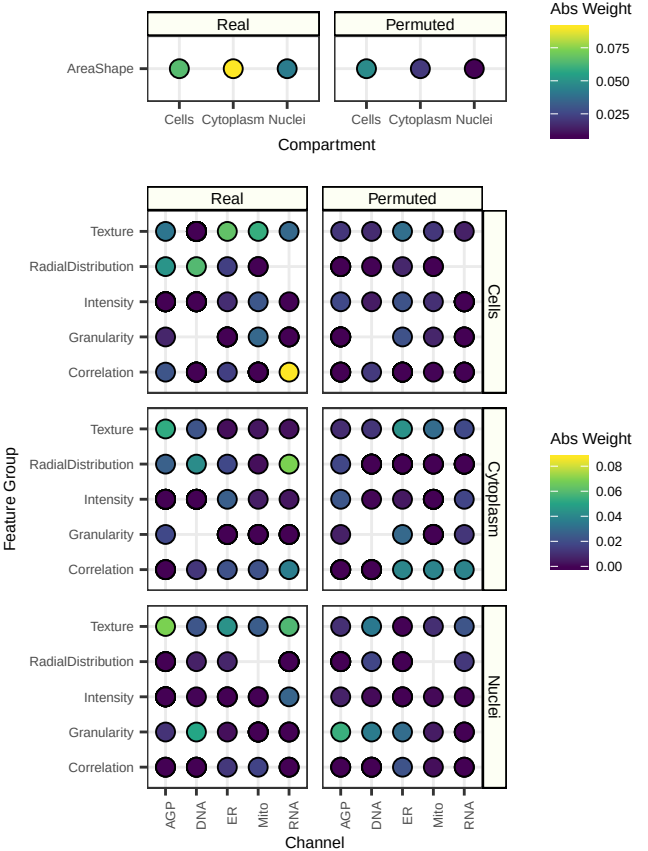
vb_live_cell_roundness



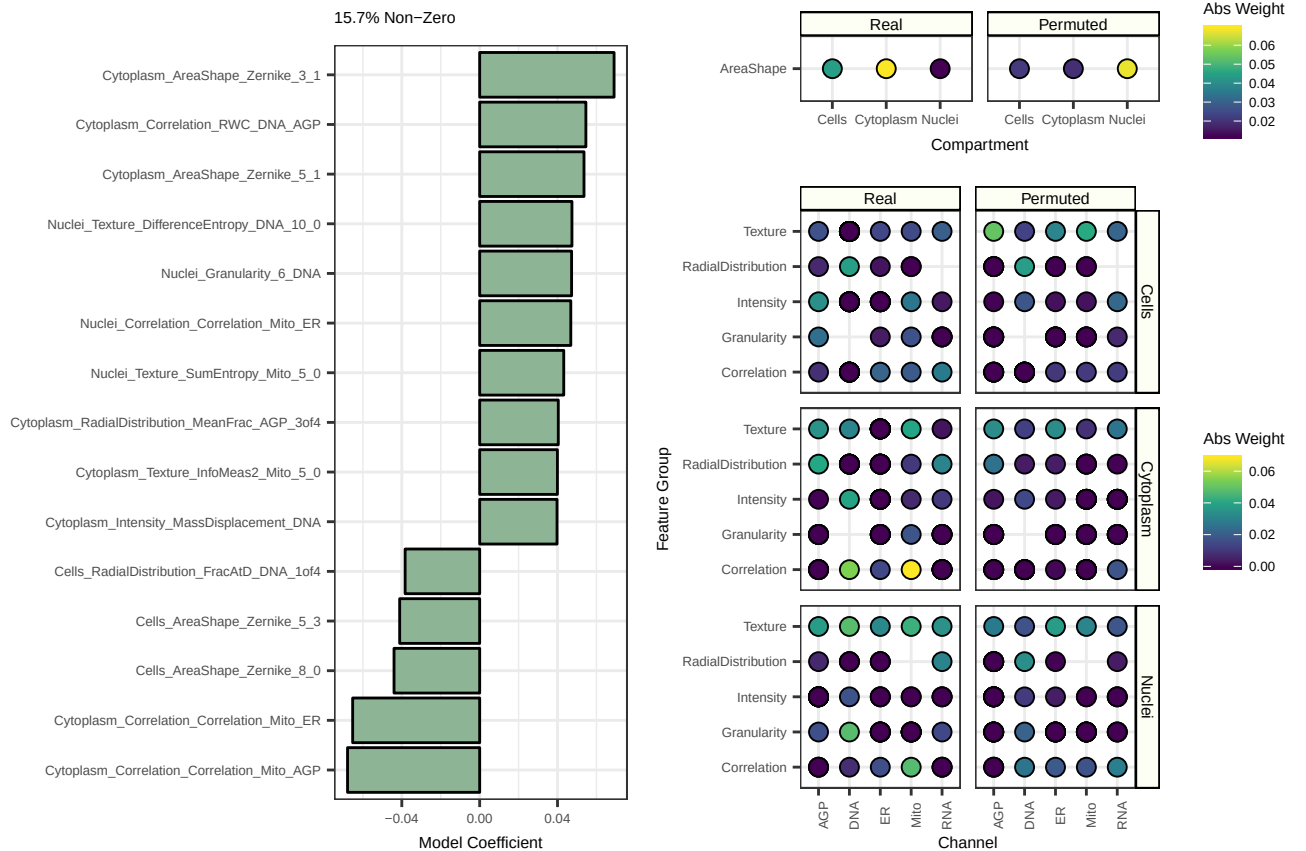


vb_live_cell_width_length

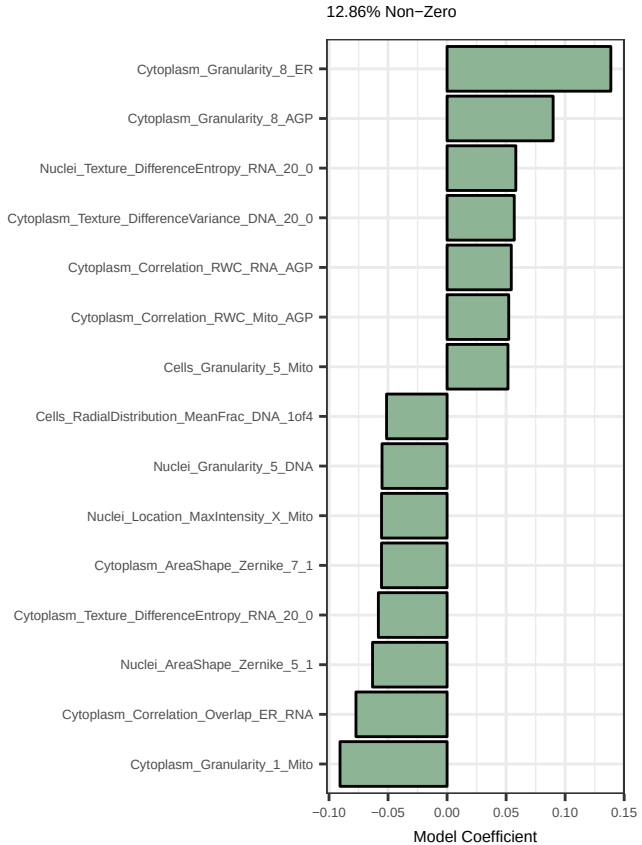


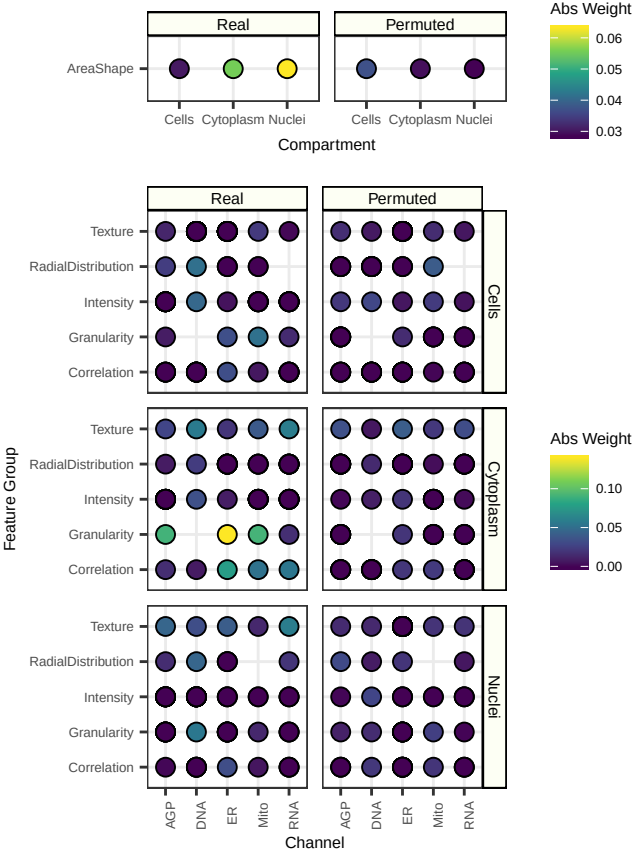


vb_num_live_cells

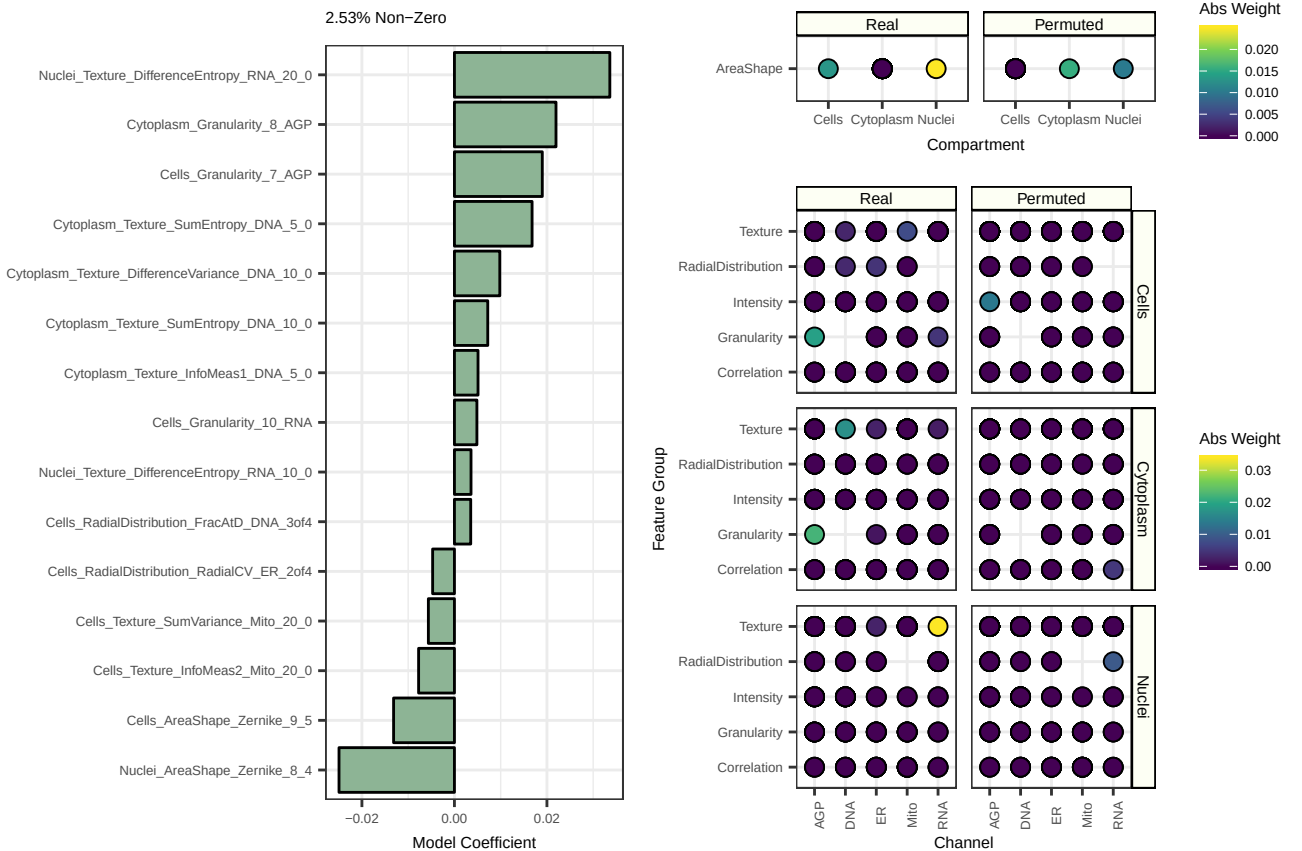


vb_percent_all_apoptosis

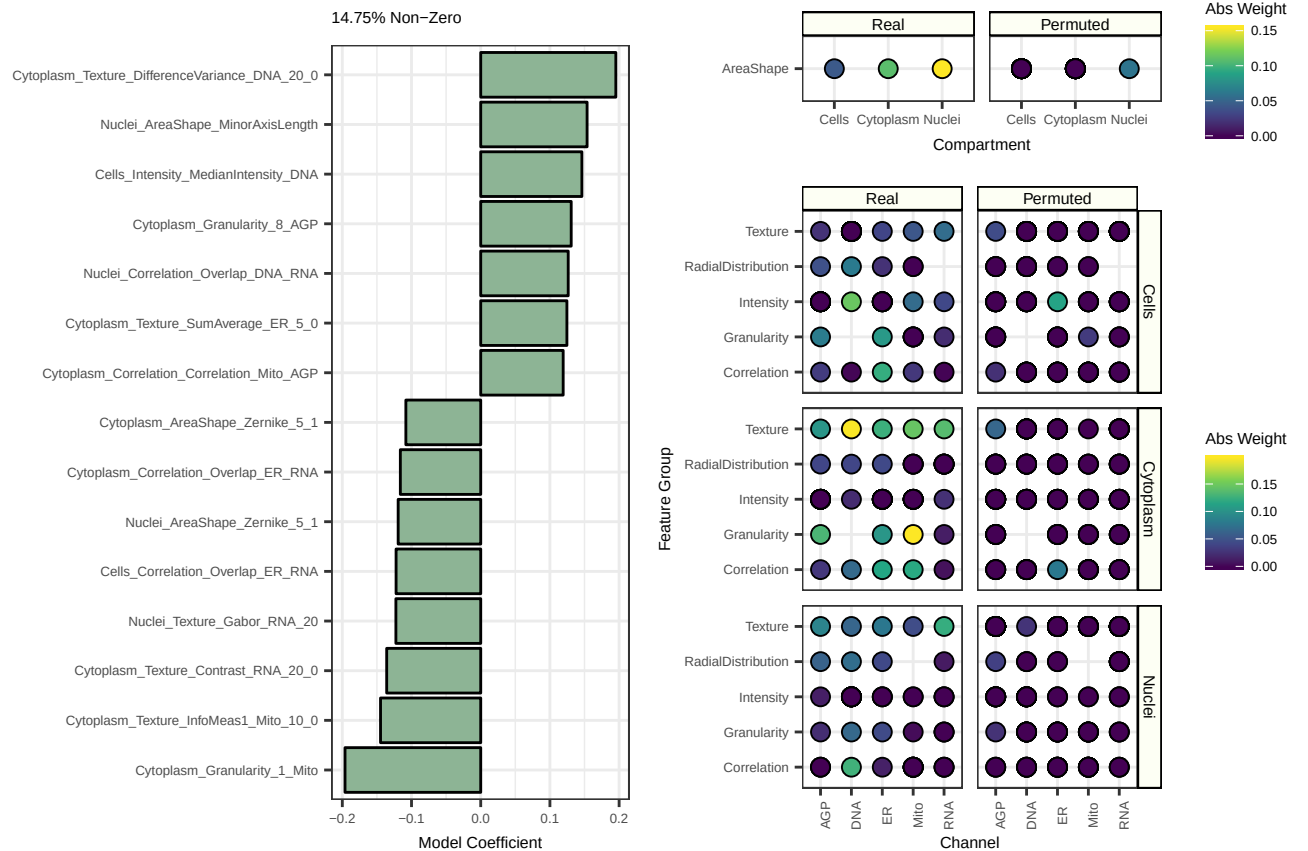




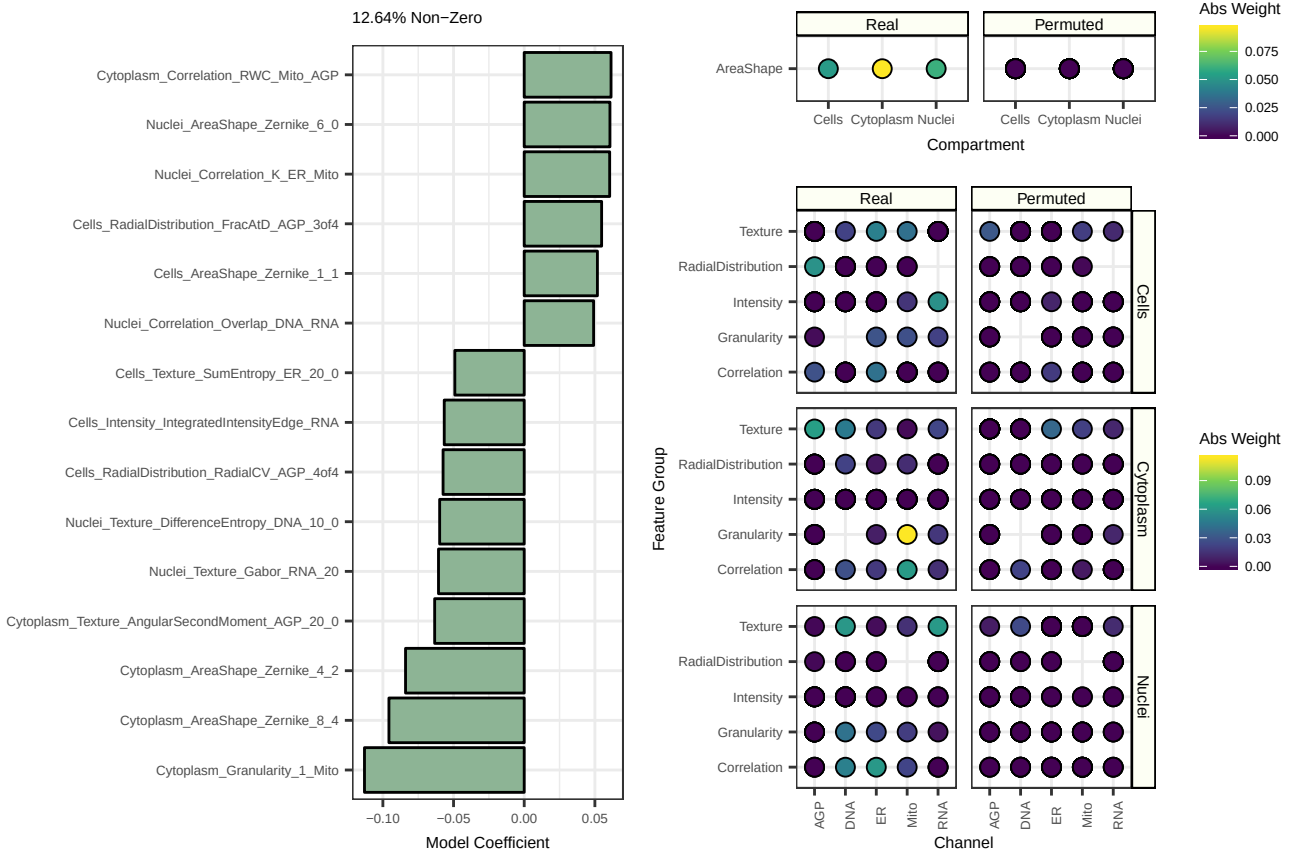
vb_percent_caspase_dead_only



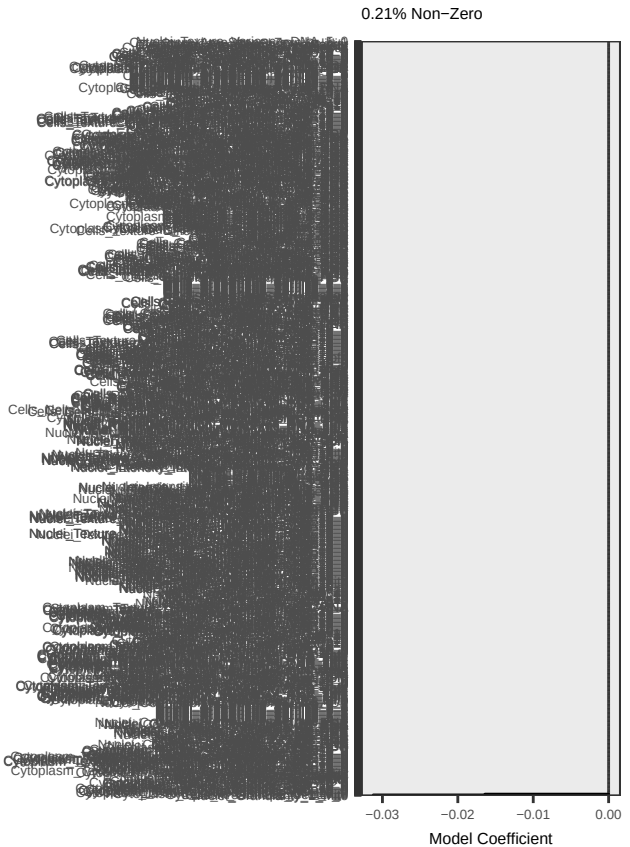
vb_percent_dead

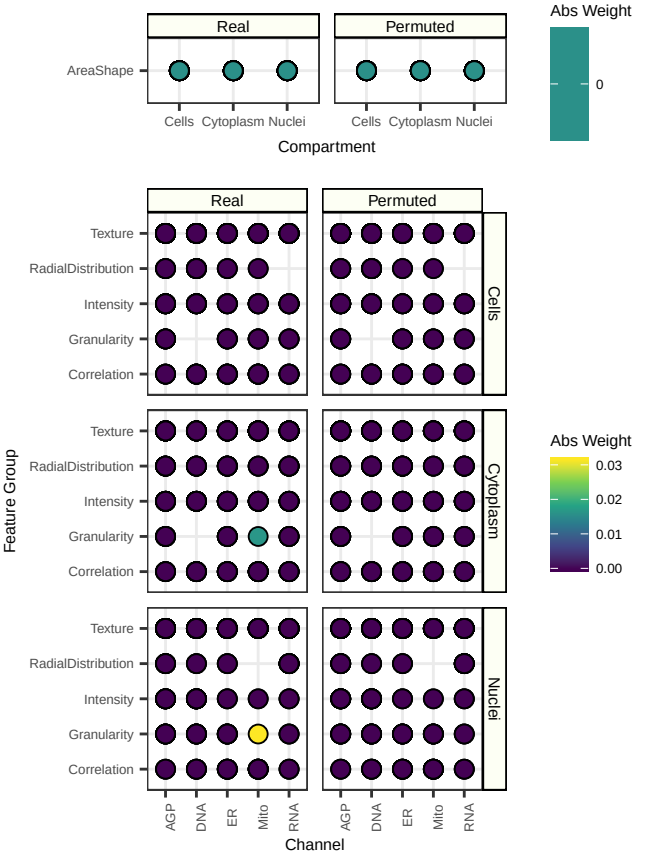


vb_percent_dead_only

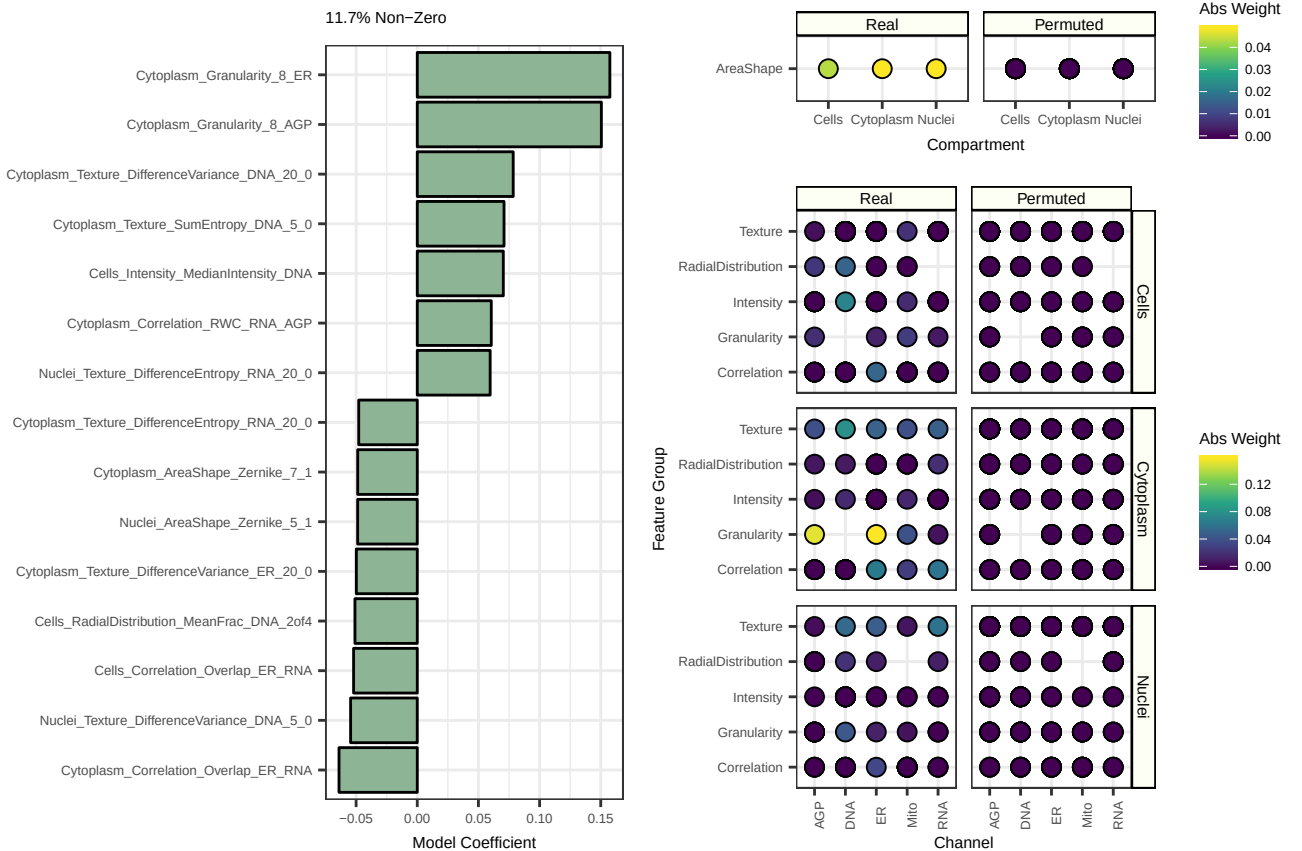


vb_percent_early_apoptosis

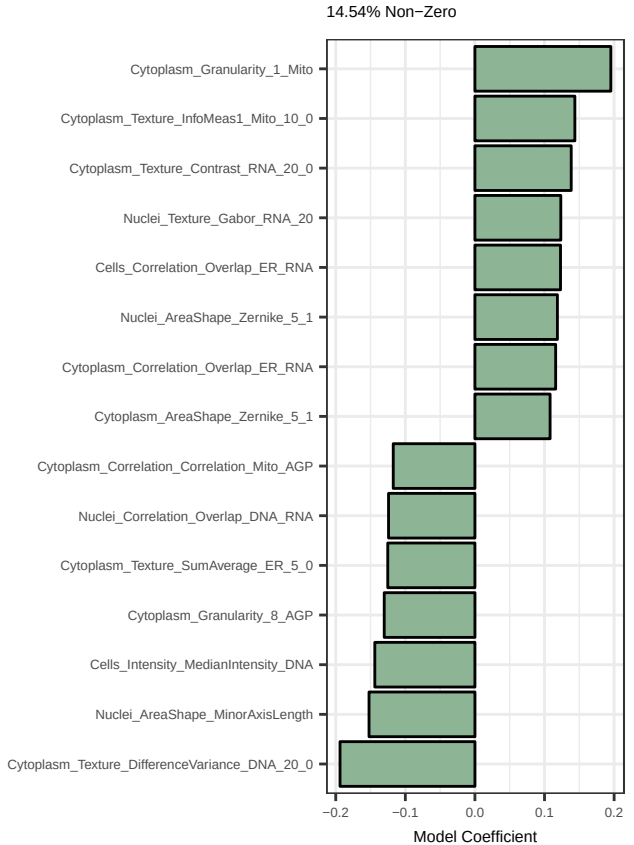


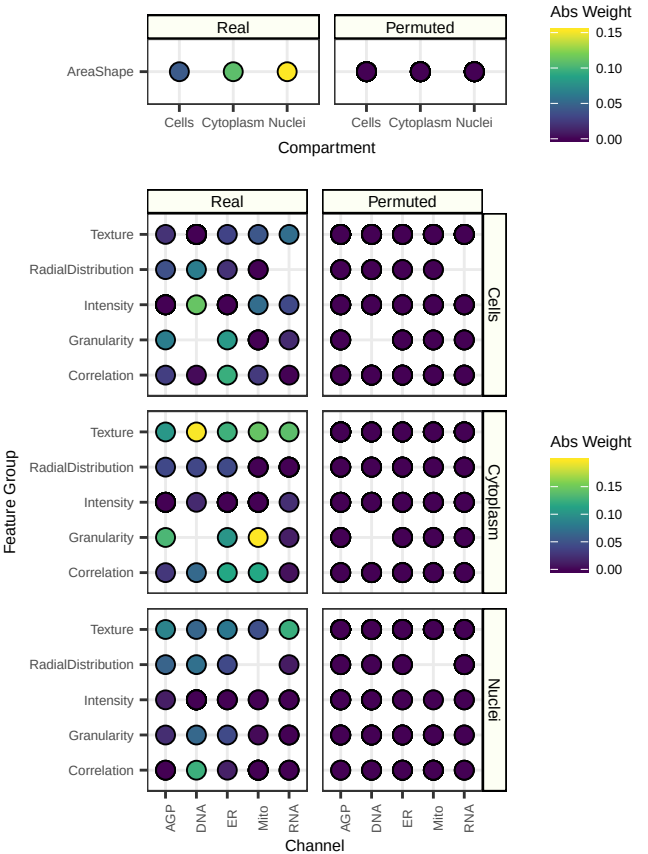


vb_percent_late_apoptosis

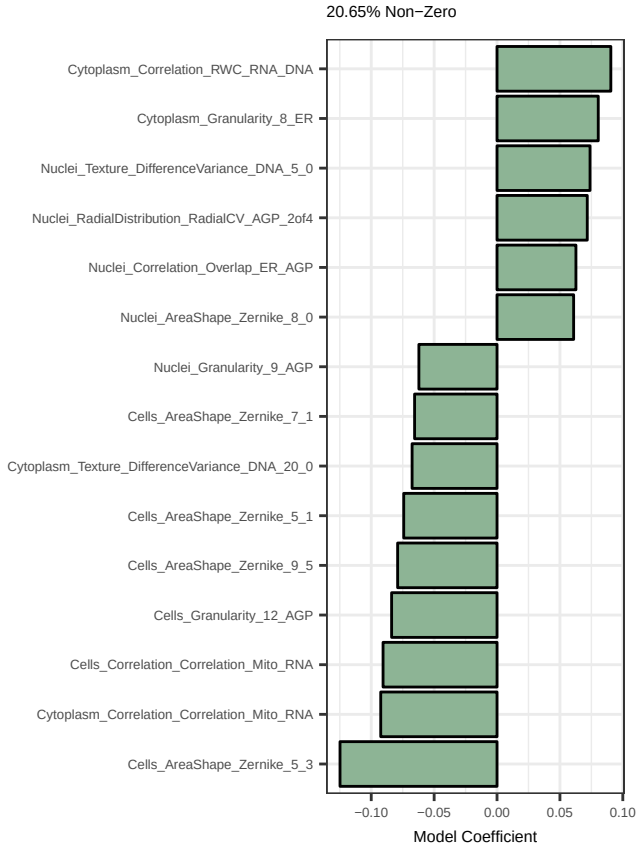


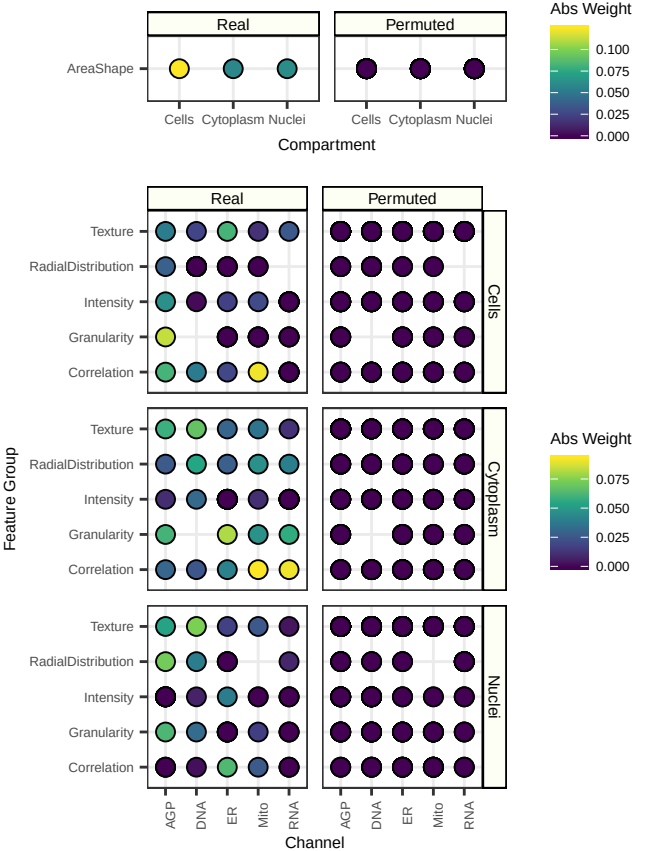
vb_percent_live



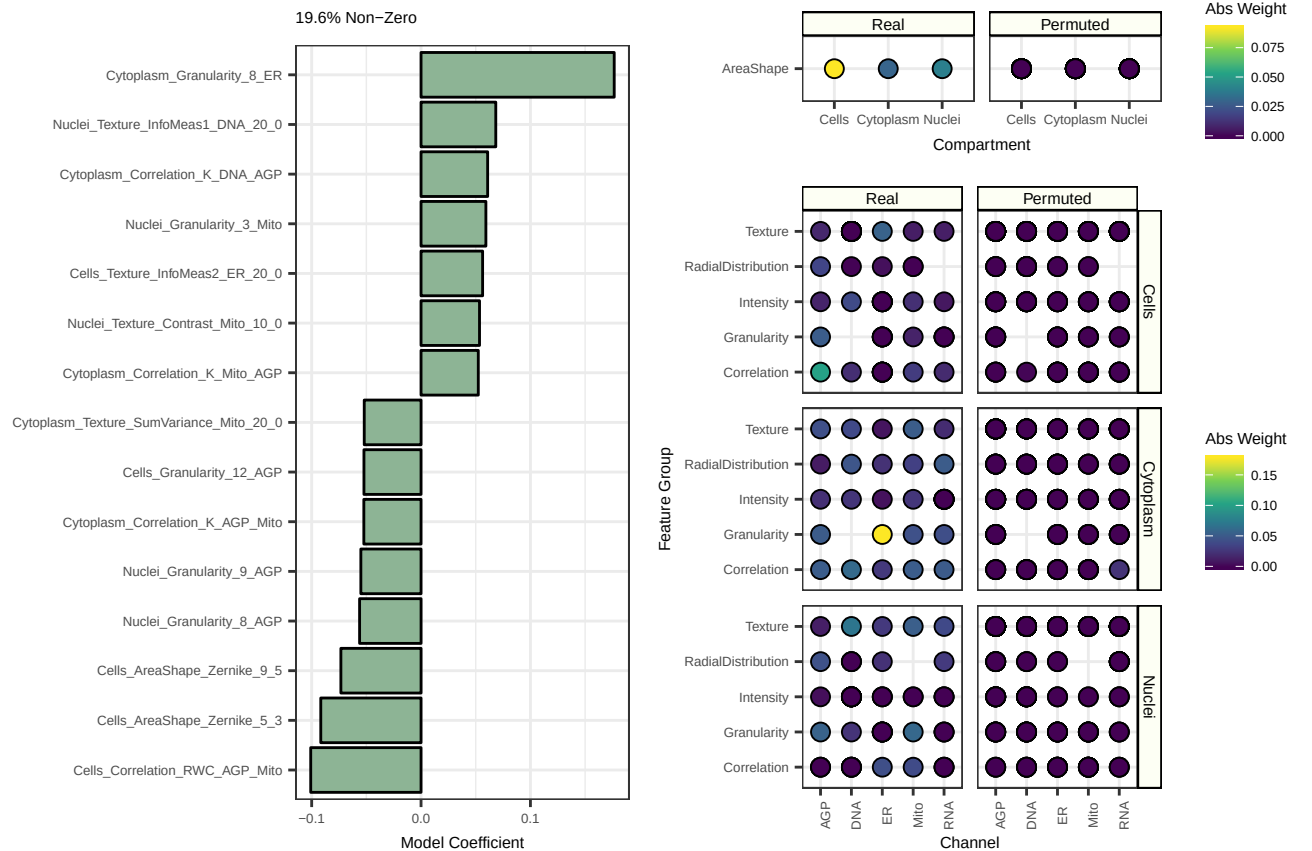


vb_ros_back_mean





vb_ros_mean


19.6% Non−Zero
Cytoplasm_Granularity_8_ER
Nuclei_Texture_InfoMeas1_DNA_20_0
Cytoplasm_Correlation_K_DNA_AGP
Nuclei_Granularity_3_Mito
Cells_Texture_InfoMeas2_ER_20_0
Nuclei_Texture_Contrast_Mito_10_0
Cytoplasm_Correlation_K_Mito_AGP
Cytoplasm_Texture_SumVariance_Mito_20_0
Cells_Granularity_12_AGP
Cytoplasm_Correlation_K_AGP_Mito
Nuclei_Granularity_9_AGP
Nuclei_Granularity_8_AGP
Cells_AreaShape_Zernike_9_5
Cells_AreaShape_Zernike_5_3
Cells_Correlation_RWC_AGP_Mito
−0.1
0.0
0.1
Model Coefficient
Real
Permuted
AreaShape
Cells
Cytoplasm
Nuclei
Compartment
Abs Weight
0.075
0.050
0.025
0.000
Feature Group
Texture
RadialDistribution
Intensity
Granularity
Correlation
Abs Weight
0.15
0.10
0.05
0.00
AGP
DNA
ER
Mito
RNA
Channel