ALL – % High gH2AX Spots

ALL – Polynuclear
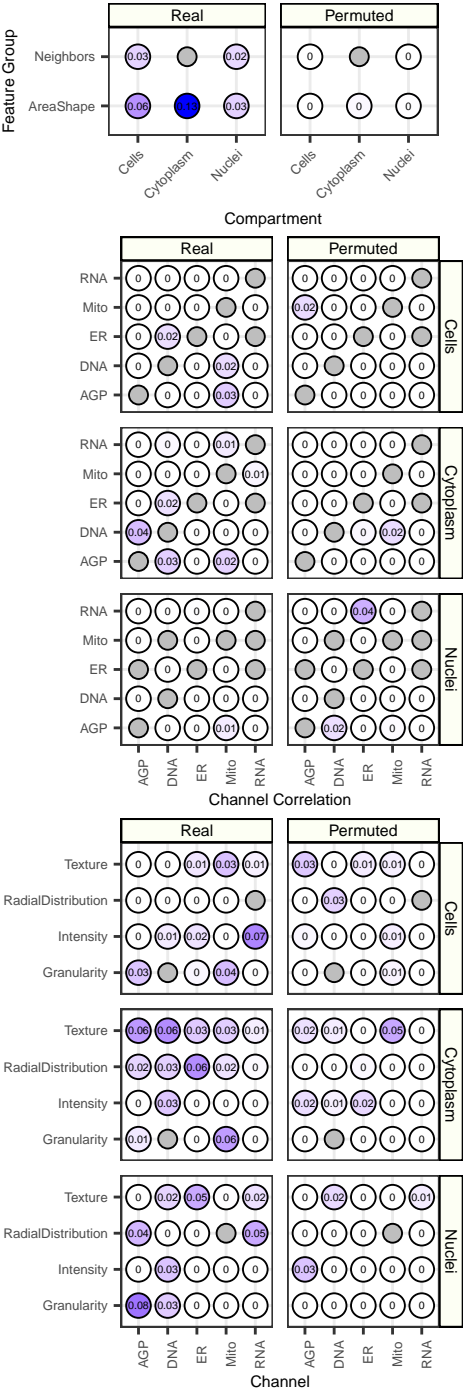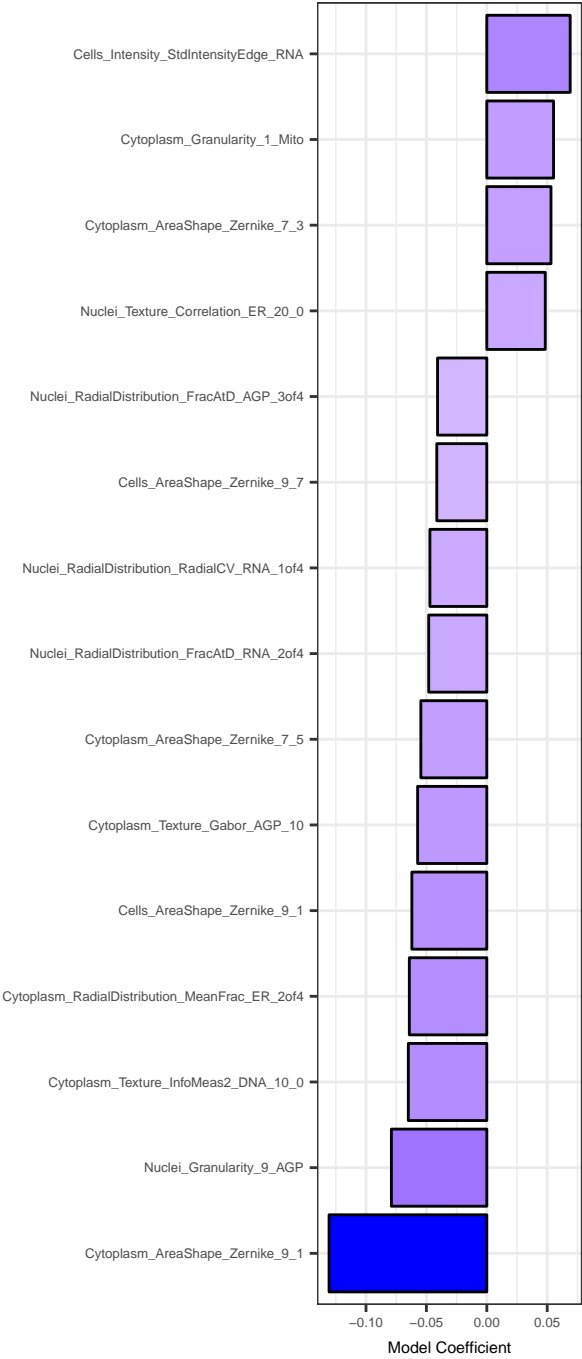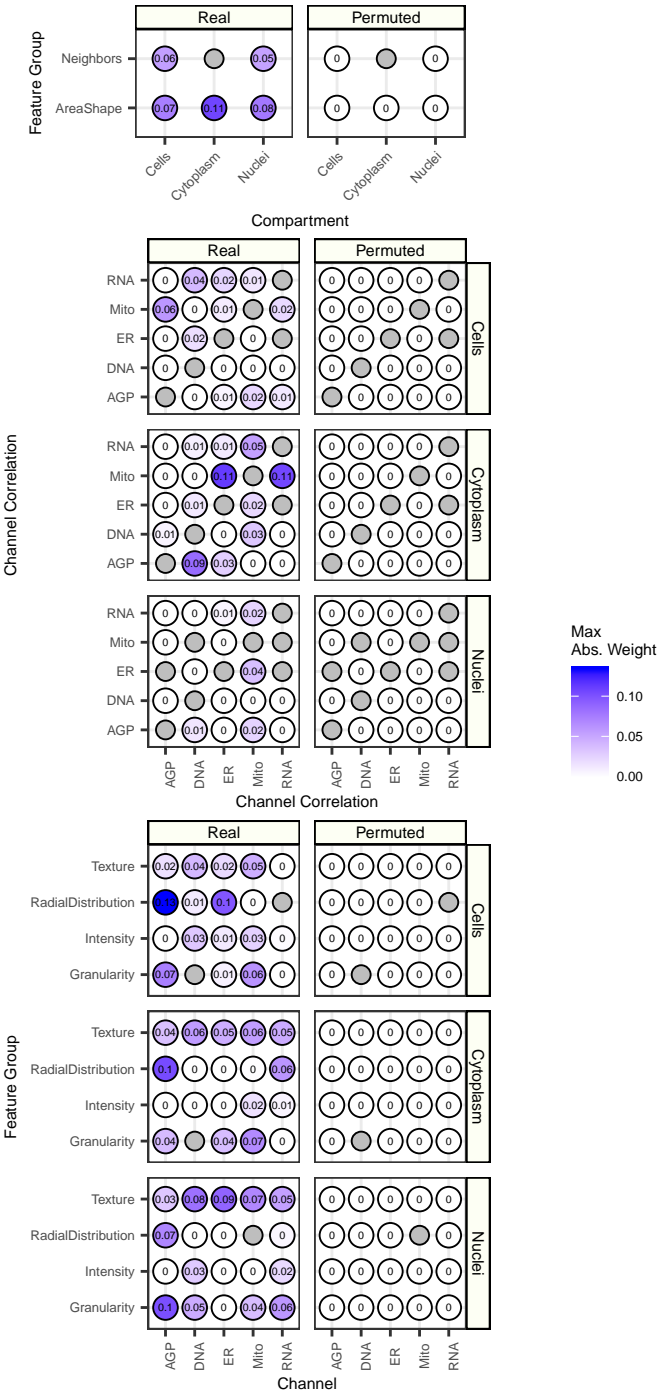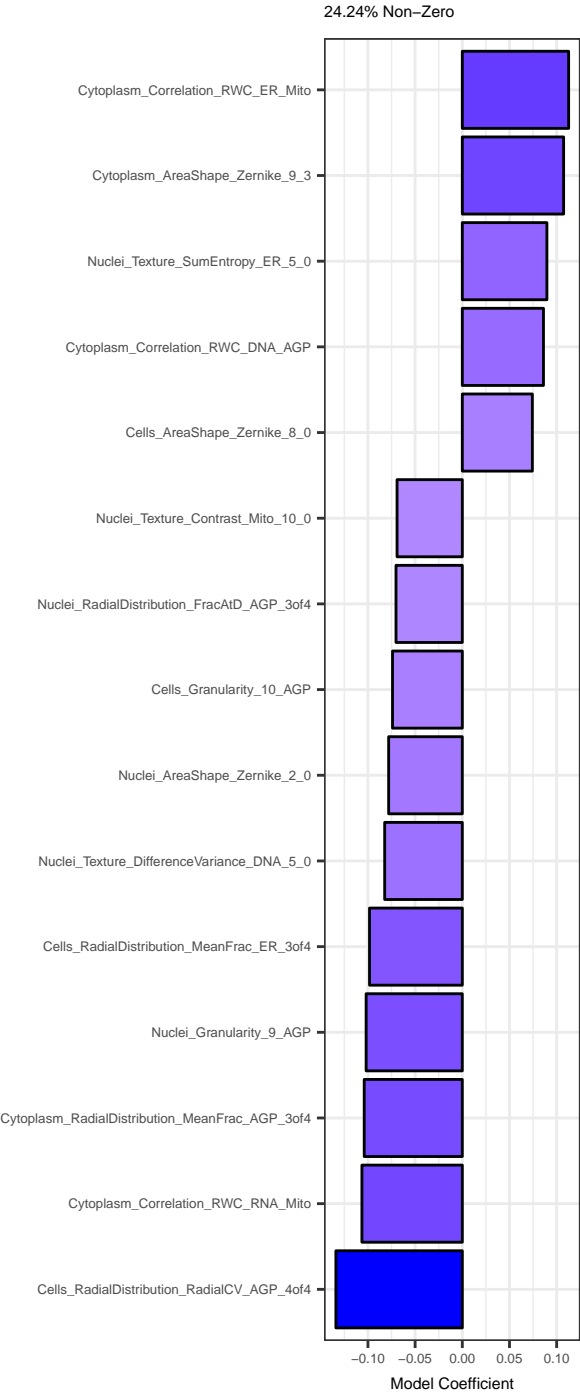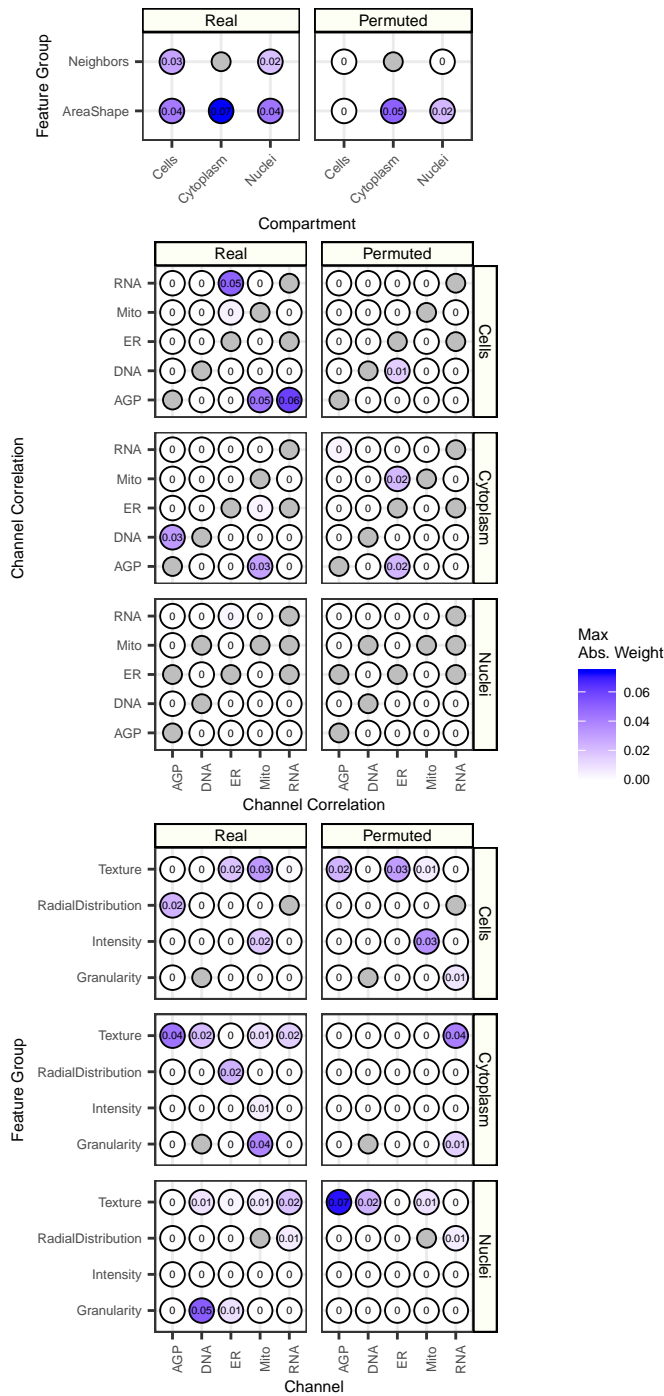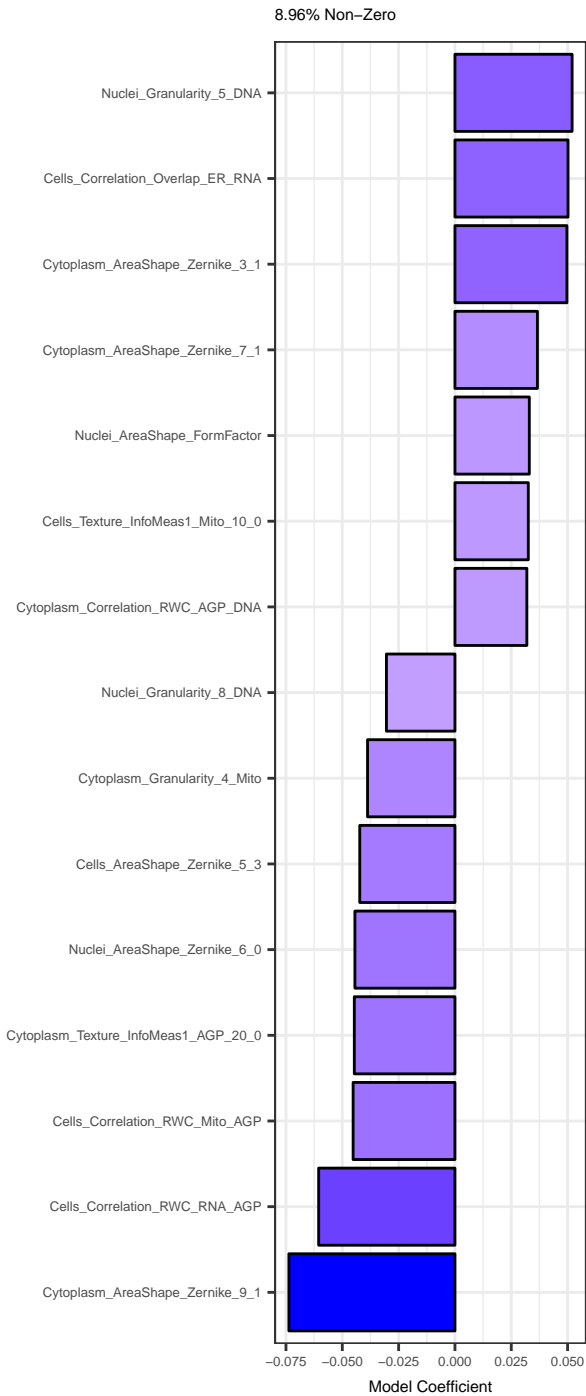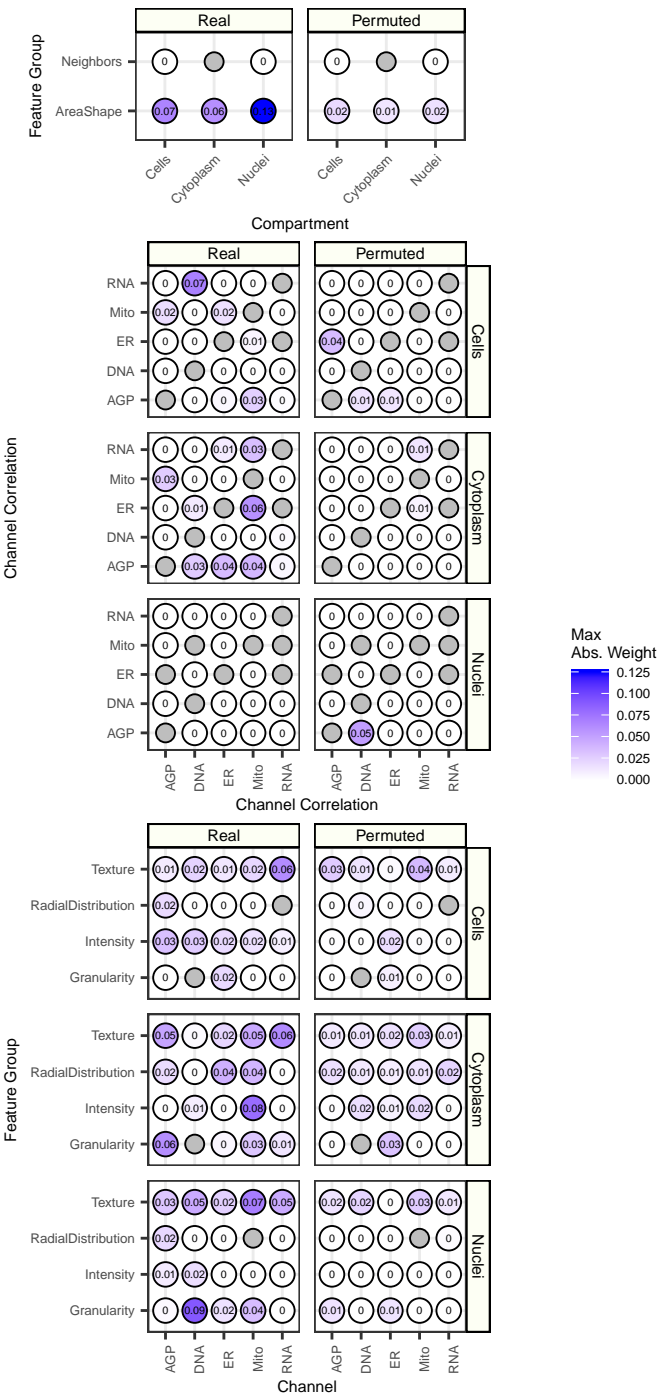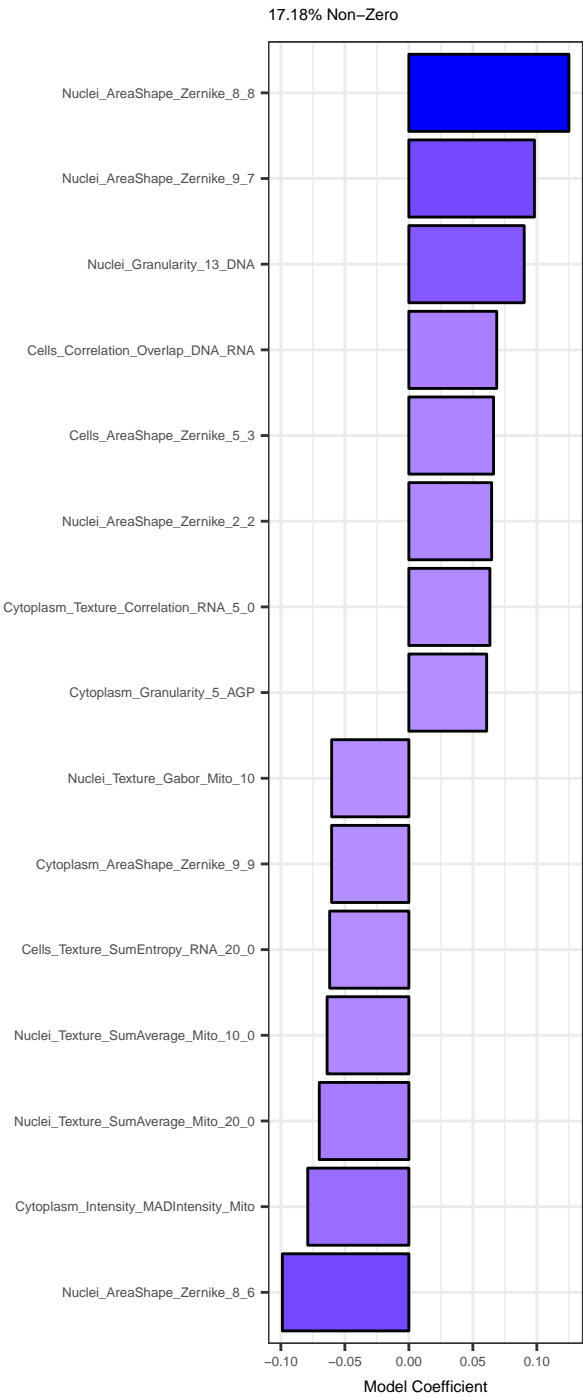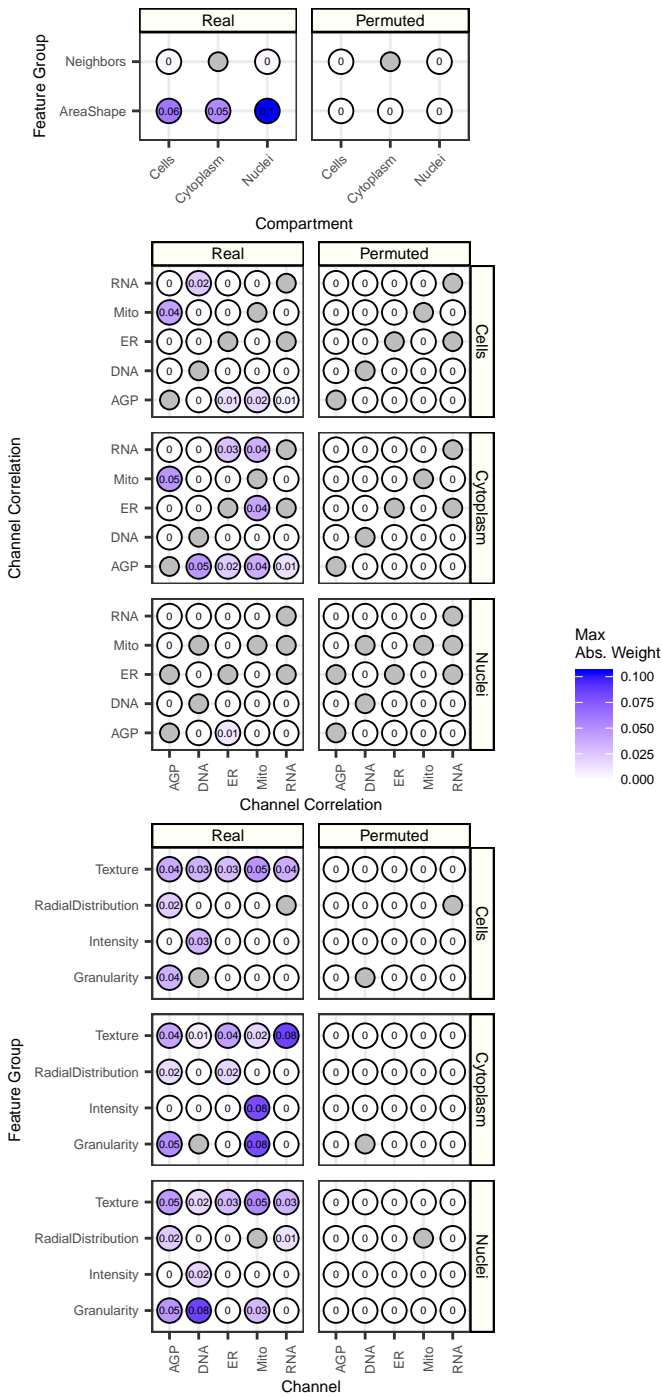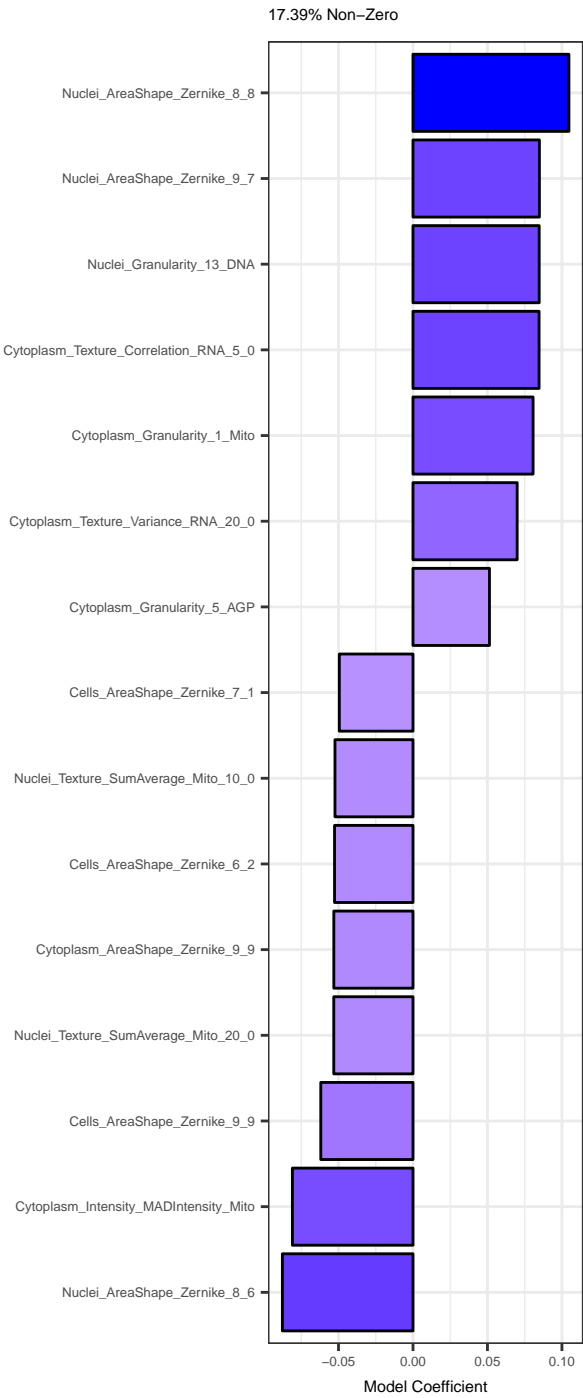

14.54% Non−Zero

ALL – Polyploid

ALL − # cells

ALL – # of gH2AX Spots

17.18% Non−Zero

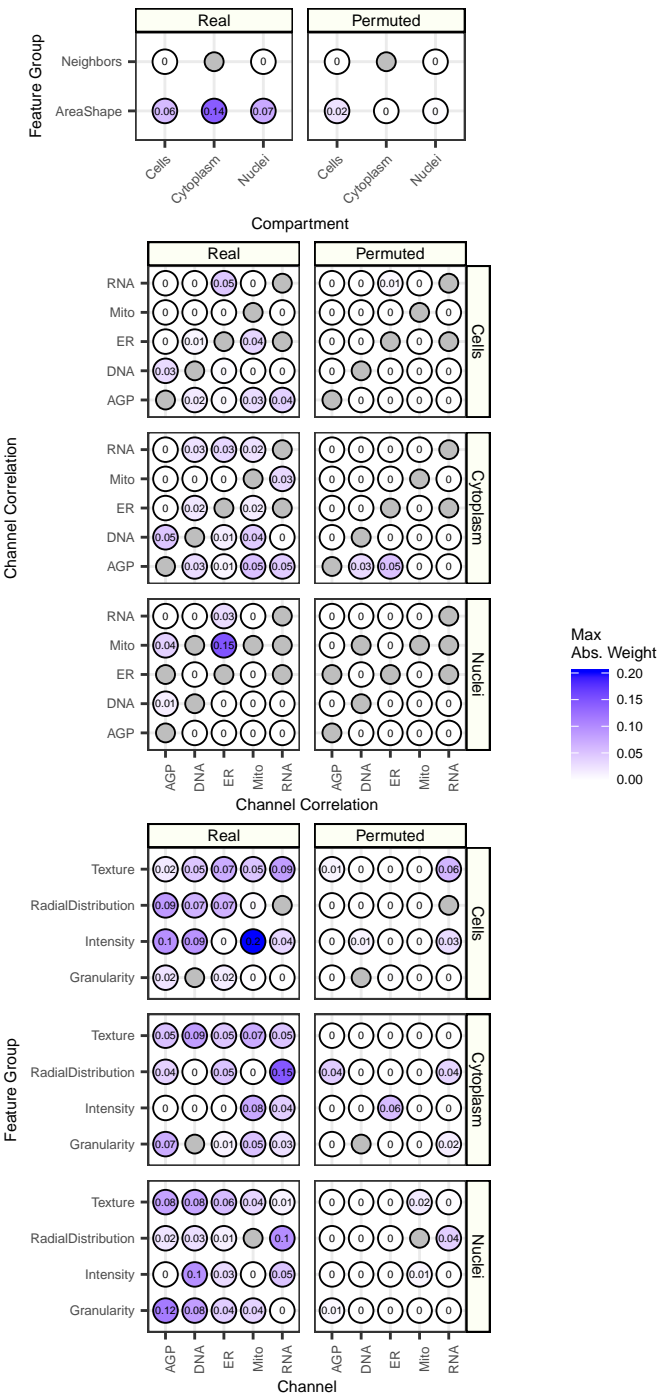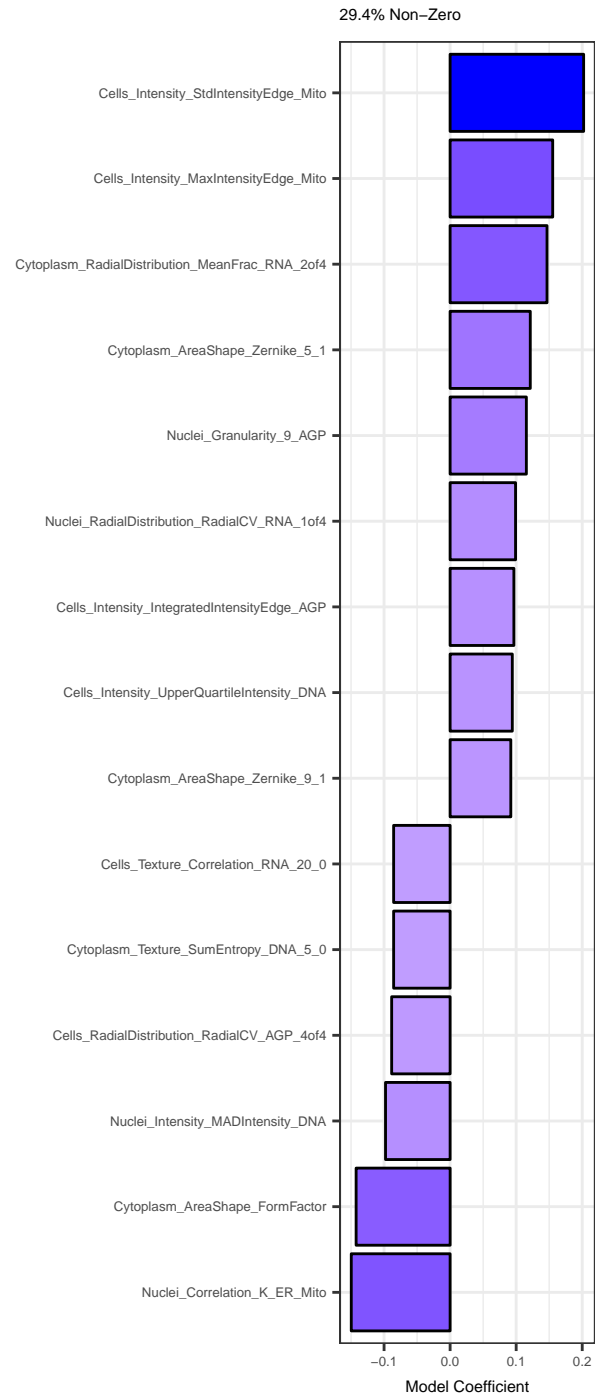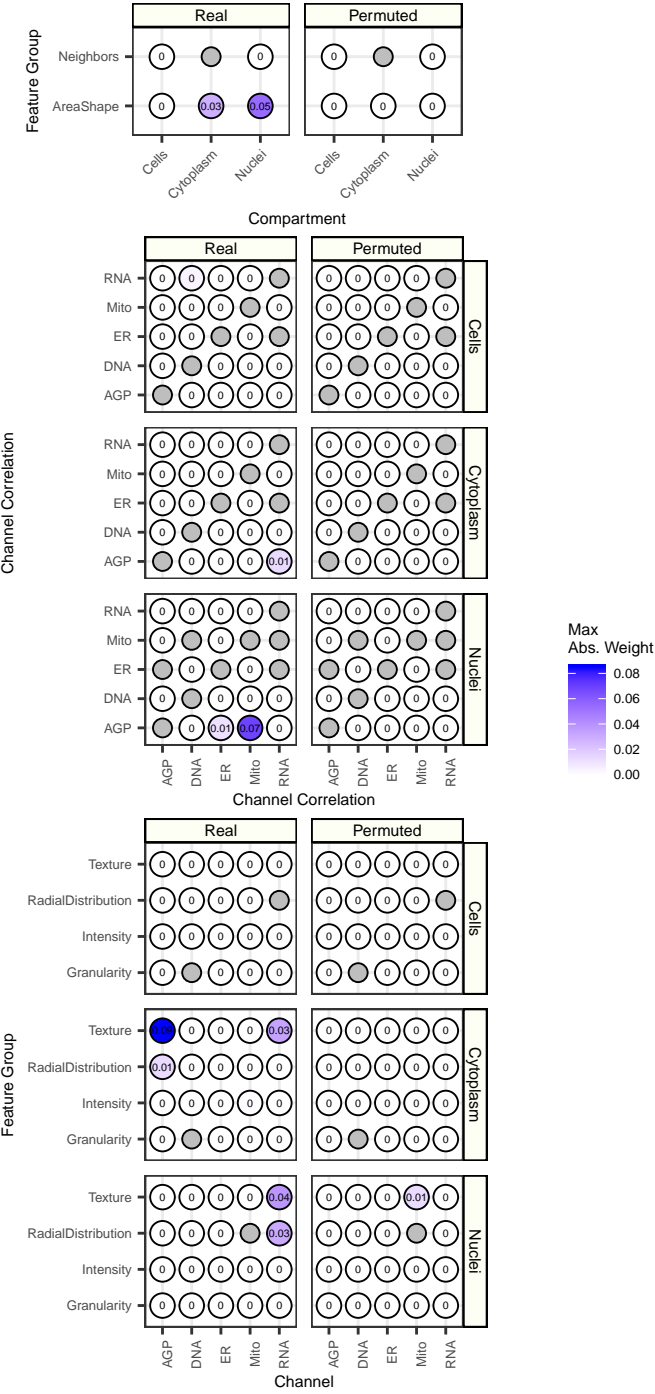# ALL – # of gH2AX Spots per Area of Nucleus
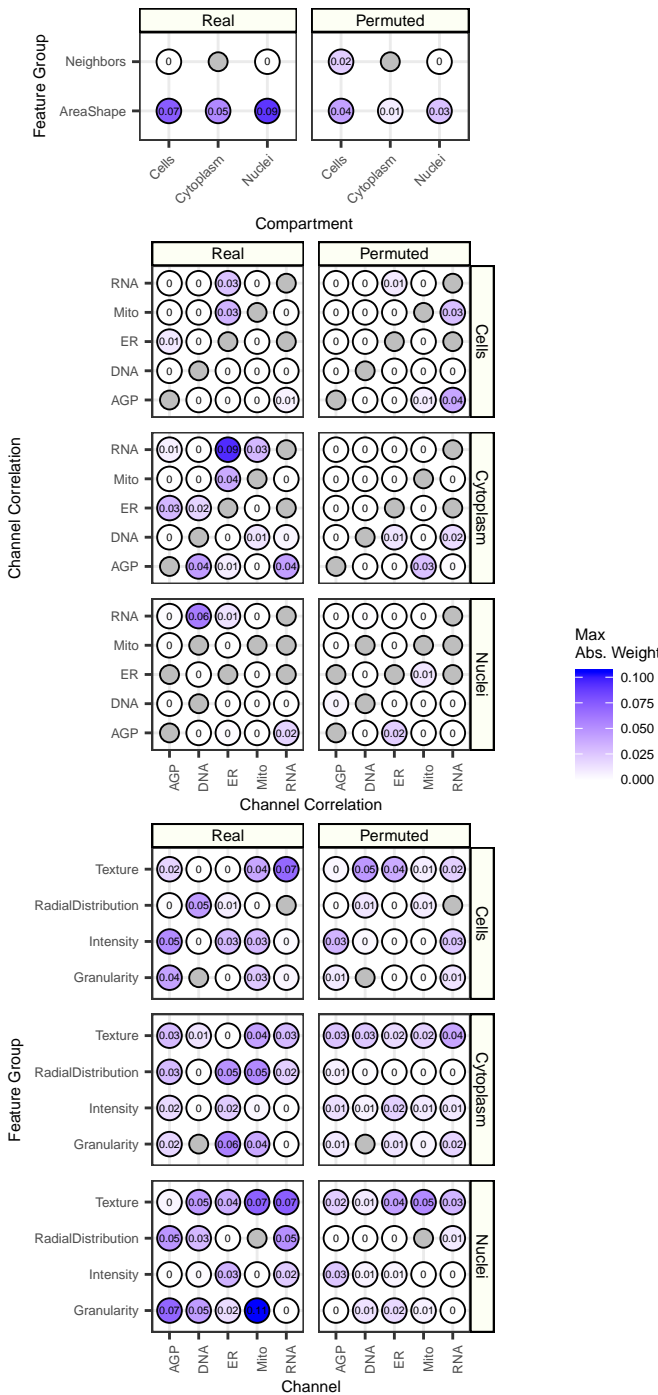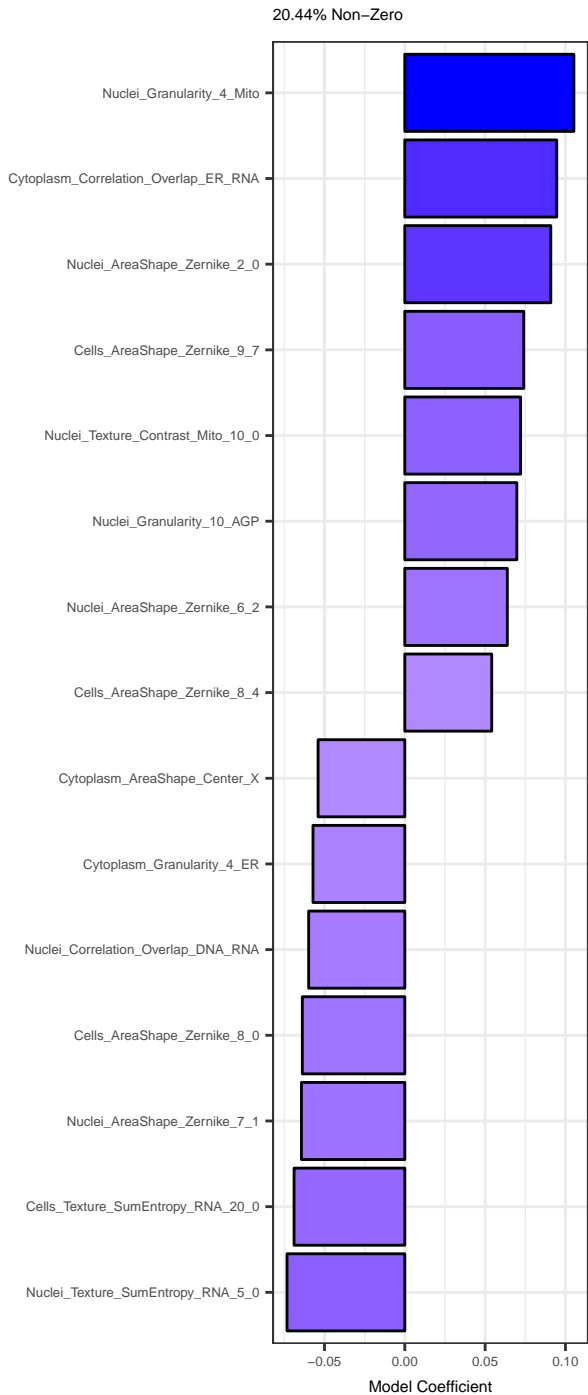
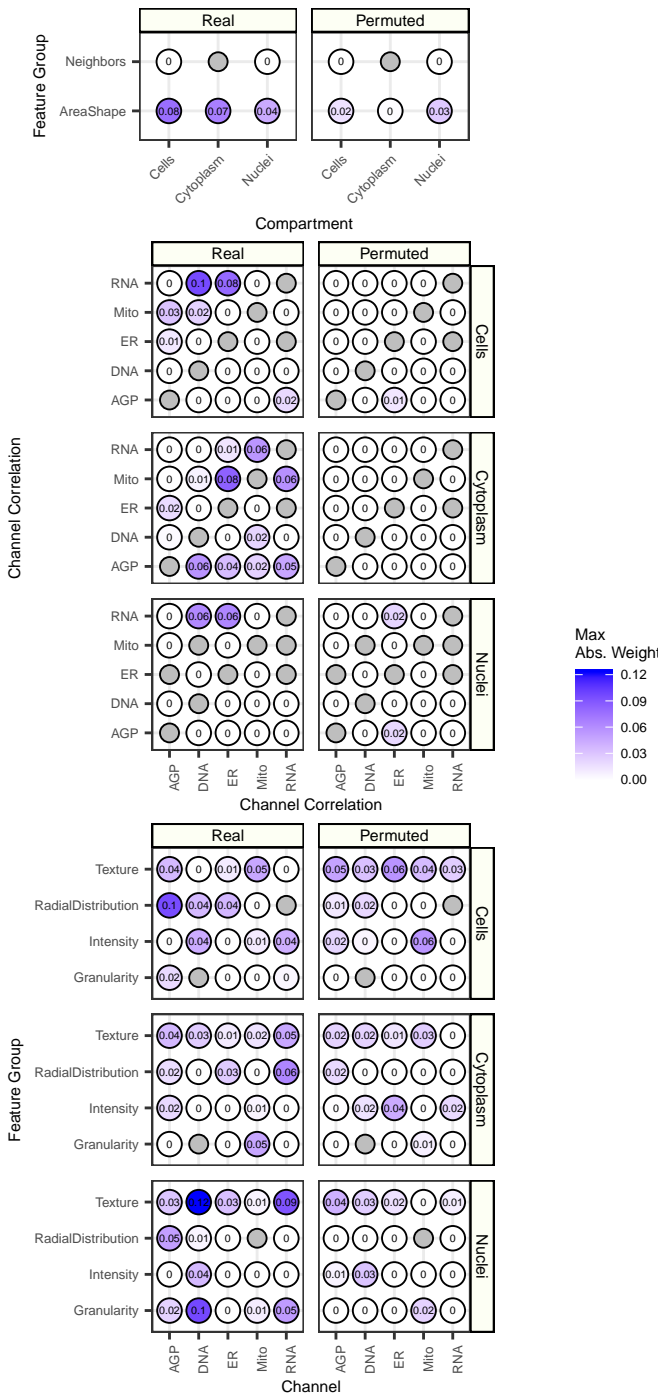# ALL – Nucleus Area

ALL – Nucleus Roundness

CC – % early M

CC − % G1

20.44% Non−Zero

Model Coefficient axis with bars for:

- Nuclei_Granularity_4_Mito
- Cytoplasm_Correlation_Overlap_ER_RNA
- Nuclei_AreaShape_Zernike_2_0
- Cells_AreaShape_Zernike_9_7
- Nuclei_Texture_Contrast_Mito_10_0
- Nuclei_Granularity_10_AGP
- Nuclei_AreaShape_Zernike_6_2
- Cells_AreaShape_Zernike_8_4
- Cytoplasm_AreaShape_Center_X
- Cytoplasm_Granularity_4_ER
- Nuclei_Correlation_Overlap_DNA_RNA
- Cells_AreaShape_Zernike_8_0
- Nuclei_AreaShape_Zernike_7_1
- Cells_Texture_SumEntropy_RNA_20_0
- Nuclei_Texture_SumEntropy_RNA_5_0

−0.05   0.00   0.05   0.10

Model Coefficient

Feature Group / Compartment panels (Real, Permuted):

Neighbors: Real — Cells 0, Cytoplasm (gray), Nuclei 0; Permuted — Cells 0.02, Cytoplasm (gray), Nuclei 0
AreaShape: Real — Cells 0.07, Cytoplasm 0.05, Nuclei 0.09; Permuted — Cells 0.04, Cytoplasm 0.01, Nuclei 0.03

Compartment

Channel Correlation panels (Real, Permuted):

Cells:
- RNA: 0, 0, 0.03, 0, (gray) | 0, 0, 0.01, 0, (gray)
- Mito: 0, 0, 0.03, (gray), 0 | 0, 0, 0, (gray), 0.01
- ER: 0.01, 0, 0, 0, 0 | 0, 0, 0, 0, 0
- DNA: 0, (gray), (gray), 0, 0 | 0, 0, 0, 0, 0
- AGP: (gray), 0, 0, 0, 0.01 | (gray), 0, 0, 0.01, 0.04

Cytoplasm:
- RNA: 0.01, 0, 0.09, 0.03, (gray) | 0, 0, 0, 0, 0
- Mito: 0, 0, 0.04, 0, 0 | 0, 0, 0, 0, 0
- ER: 0.03, 0.02, 0, 0, 0 | 0, 0, 0, 0, 0
- DNA: 0, 0, 0, 0.01, 0 | 0, 0.01, 0, 0, 0.02
- AGP: 0, 0.04, 0.01, 0, 0.04 | 0, 0, 0, 0.03, 0

Nuclei:
- RNA: 0, 0.06, 0.01, 0, (gray) | 0, 0, 0, 0, (gray)
- Mito: 0, 0, 0, (gray), (gray) | 0, 0, 0, (gray), (gray)
- ER: 0, (gray), 0, 0, 0 | 0, 0, 0, 0.01, 0
- DNA: 0, 0, (gray), 0, 0 | 0, 0, 0, 0, 0
- AGP: (gray), 0, 0, 0, 0.02 | (gray), 0, 0.02, 0, 0

AGP DNA ER Mito RNA

Channel Correlation

Feature Group / Channel panels (Real, Permuted):

Cells:
- Texture: 0.02, 0, 0, 0.04, 0.07 | 0, 0.05, 0.04, 0.01, 0.02
- RadialDistribution: 0, 0.05, 0.01, 0, (gray) | 0, 0, 0, 0.01, 0
- Intensity: 0.05, 0, 0.03, 0.03, 0 | 0.03, 0, 0, 0, 0.03
- Granularity: 0.04, (gray), 0, 0.03, 0 | 0.01, (gray), 0, 0, 0.01

Cytoplasm:
- Texture: 0.03, 0.01, 0, 0.04, 0.03 | 0.03, 0.03, 0.02, 0.02, 0.04
- RadialDistribution: 0.05, 0, 0.05, 0.05, 0.02 | 0.01, 0, 0, 0, 0
- Intensity: 0.02, 0, 0.02, 0, 0 | 0.01, 0.01, 0.02, 0.01, 0.01
- Granularity: 0.02, (gray), 0, 0.06, 0.04 | 0.01, (gray), 0, 0.01, 0.02

Nuclei:
- Texture: 0, 0.05, 0.04, 0.07, 0.07 | 0.02, 0.01, 0.04, 0.05, 0.03
- RadialDistribution: 0.05, 0.03, 0, (gray), 0.05 | 0, 0, 0, (gray), 0.01
- Intensity: 0, 0, 0, 0, 0 | 0.03, 0.01, 0, 0, 0
- Granularity: 0.07, 0.05, 0.02, 0.100, 0 | 0, 0.01, 0.02, 0.01, 0
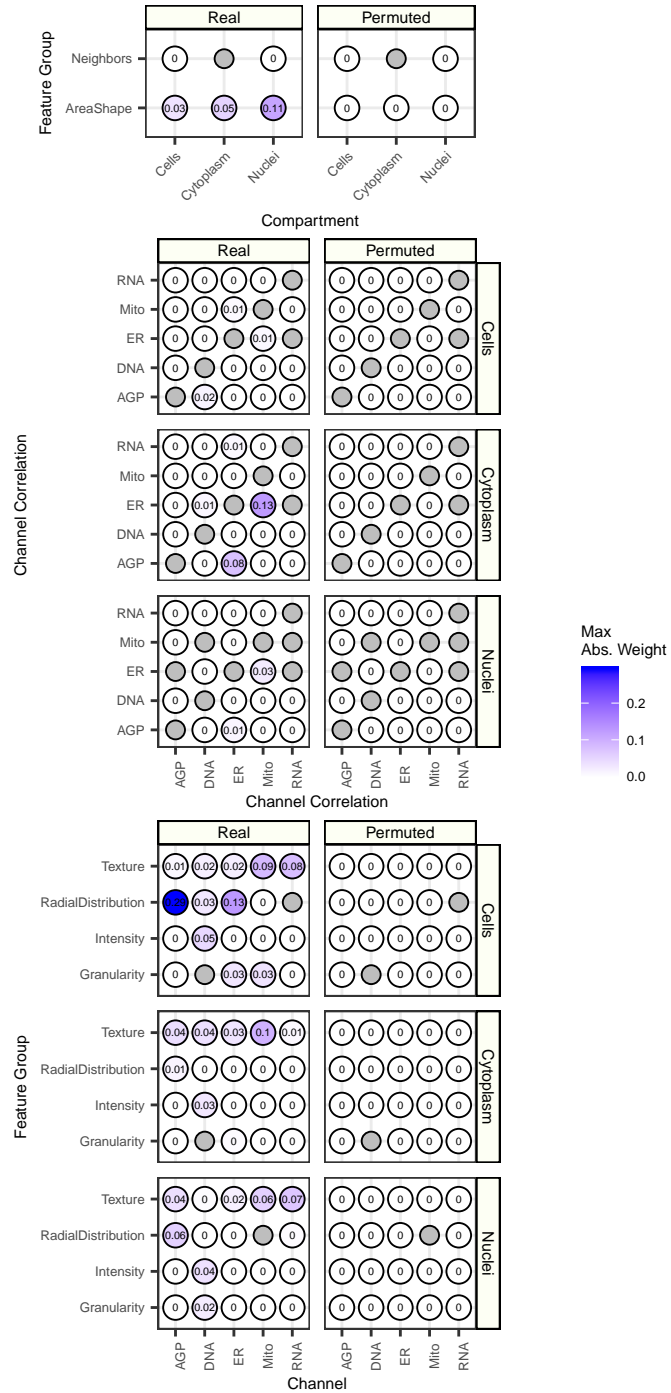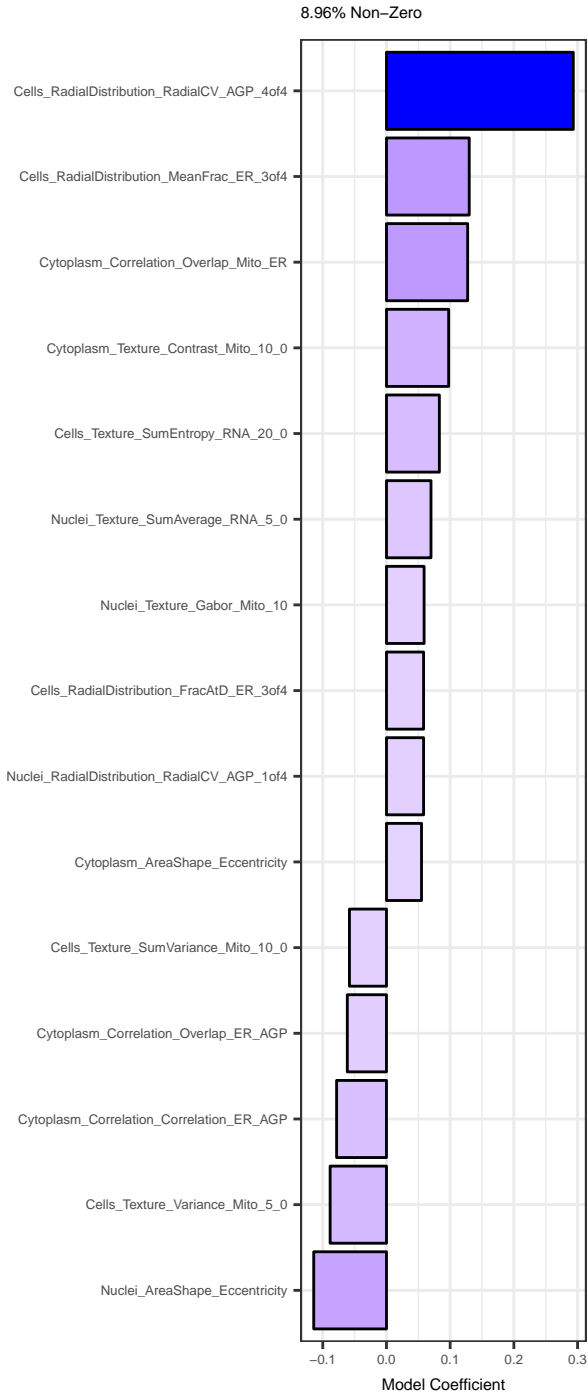
AGP DNA ER Mito RNA
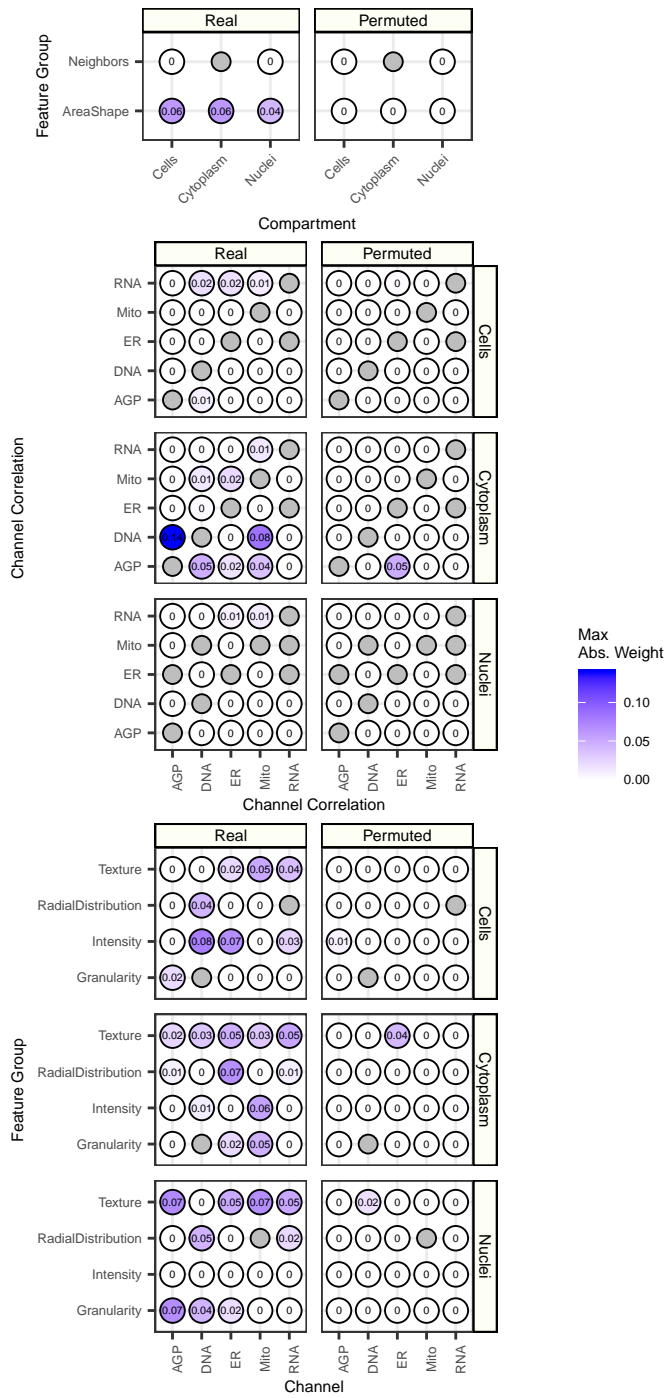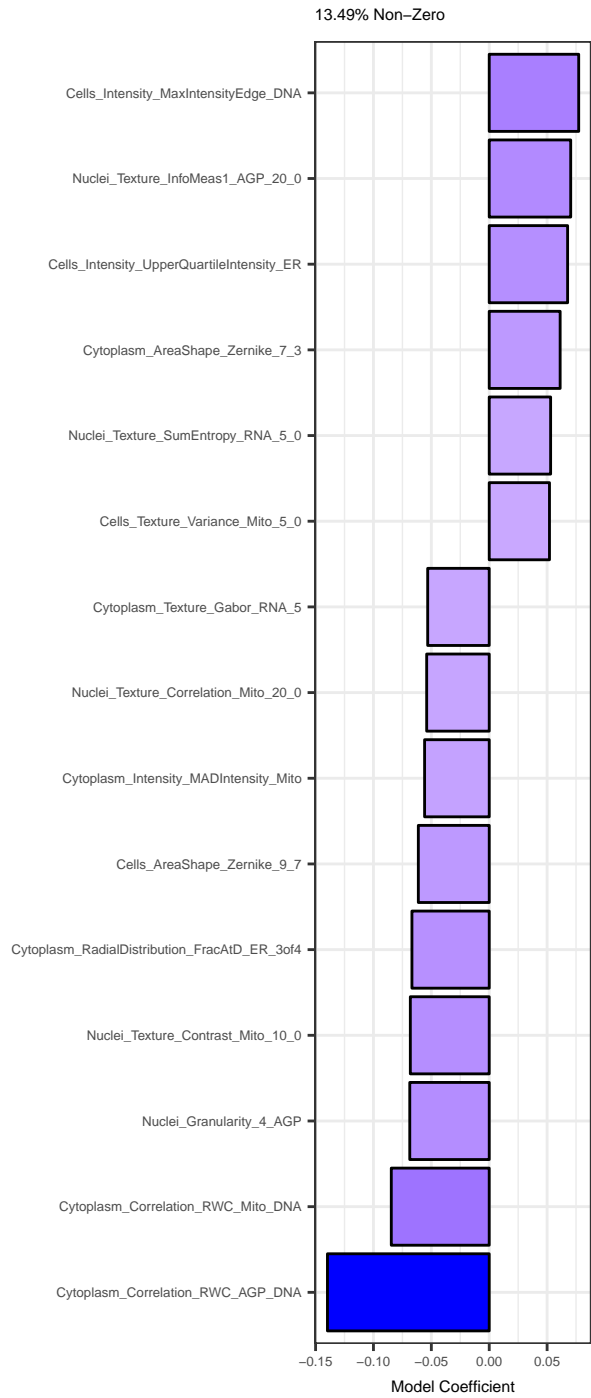
Channel

Max Abs. Weight
0.100
0.075
0.050
0.025
0.000

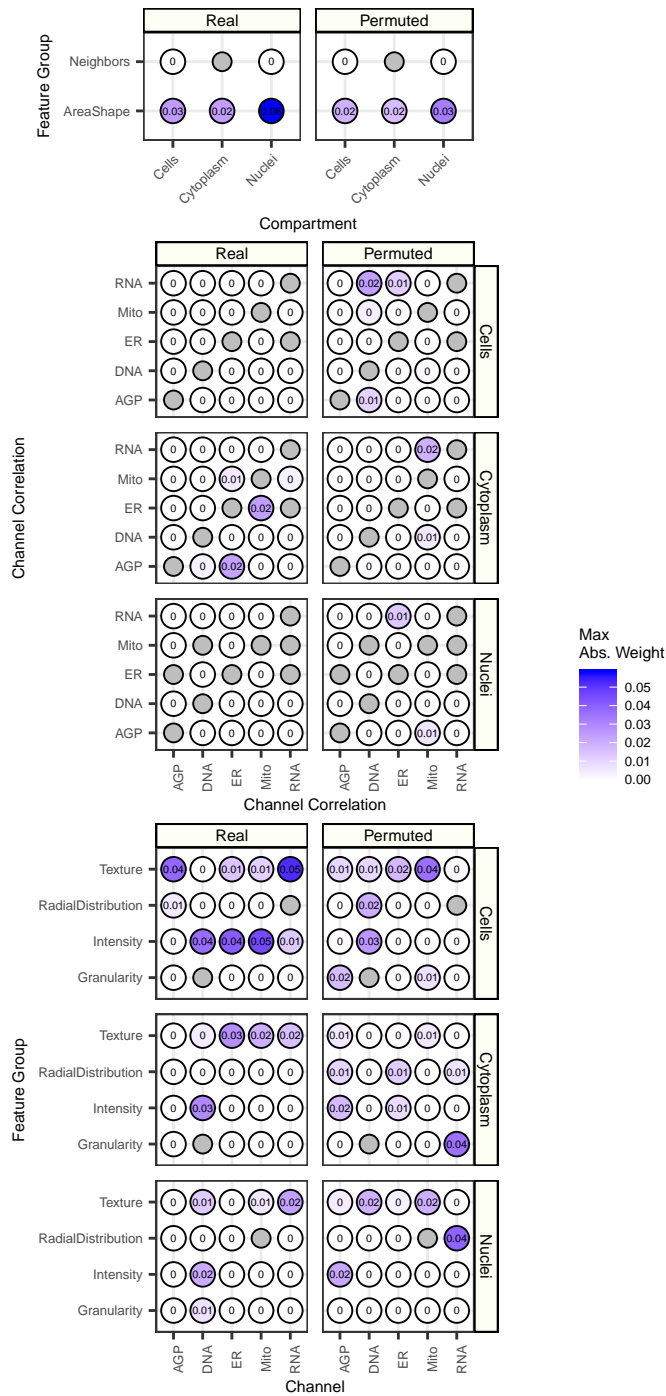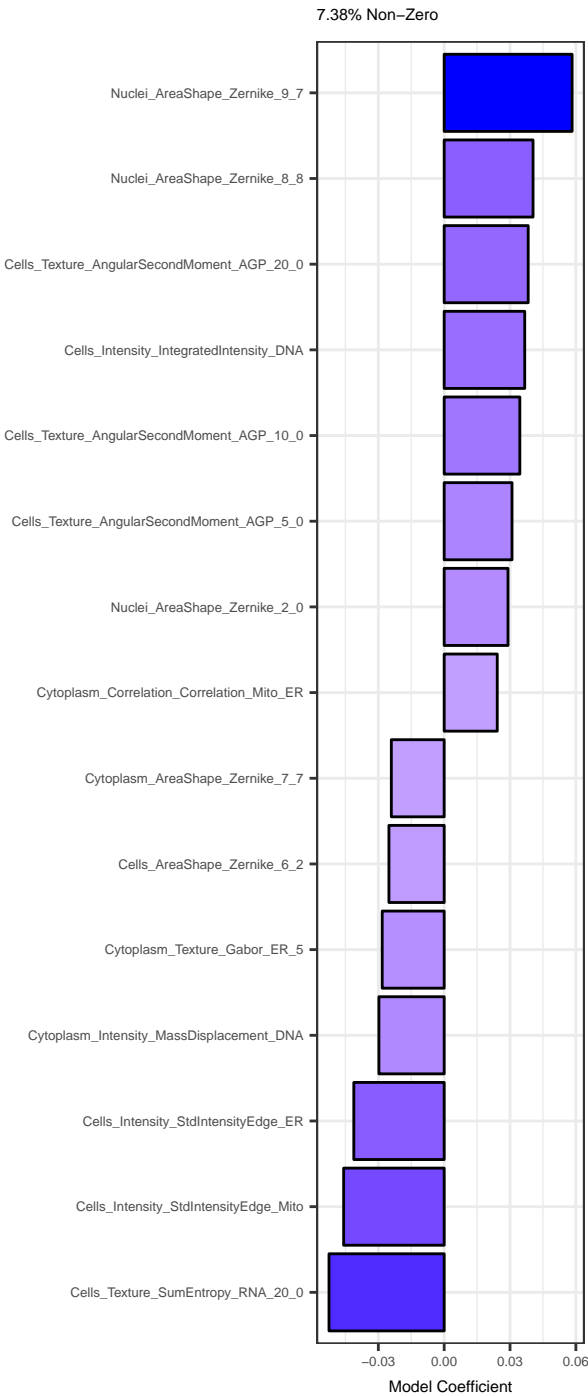# CC – % G2

CC − % High gH2AX spots

CC – % Late M

CC – % M

13.49% Non−Zero

CC − # cells

CC – # of gH2AX Spots

6.53% Non−Zero

CC – # of gH2AX Spots per Area of Nucleus

7.38% Non−Zero

CC – % S

15.28% Non−Zero

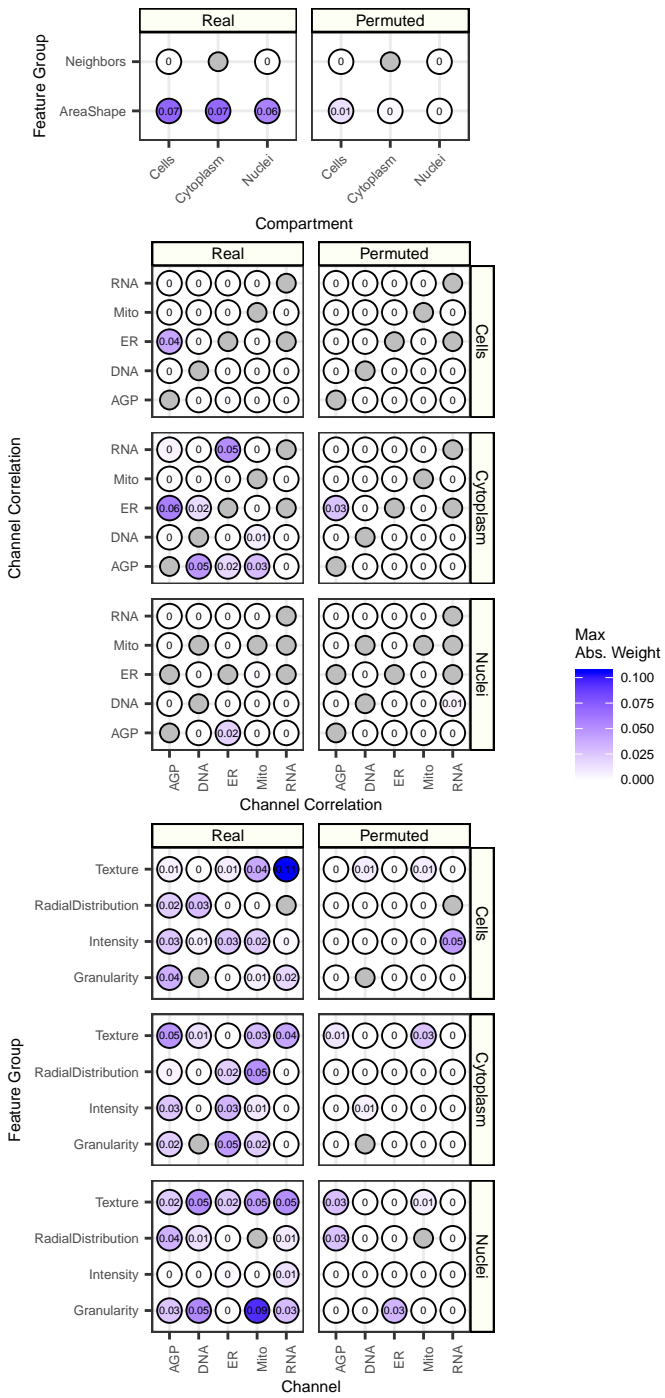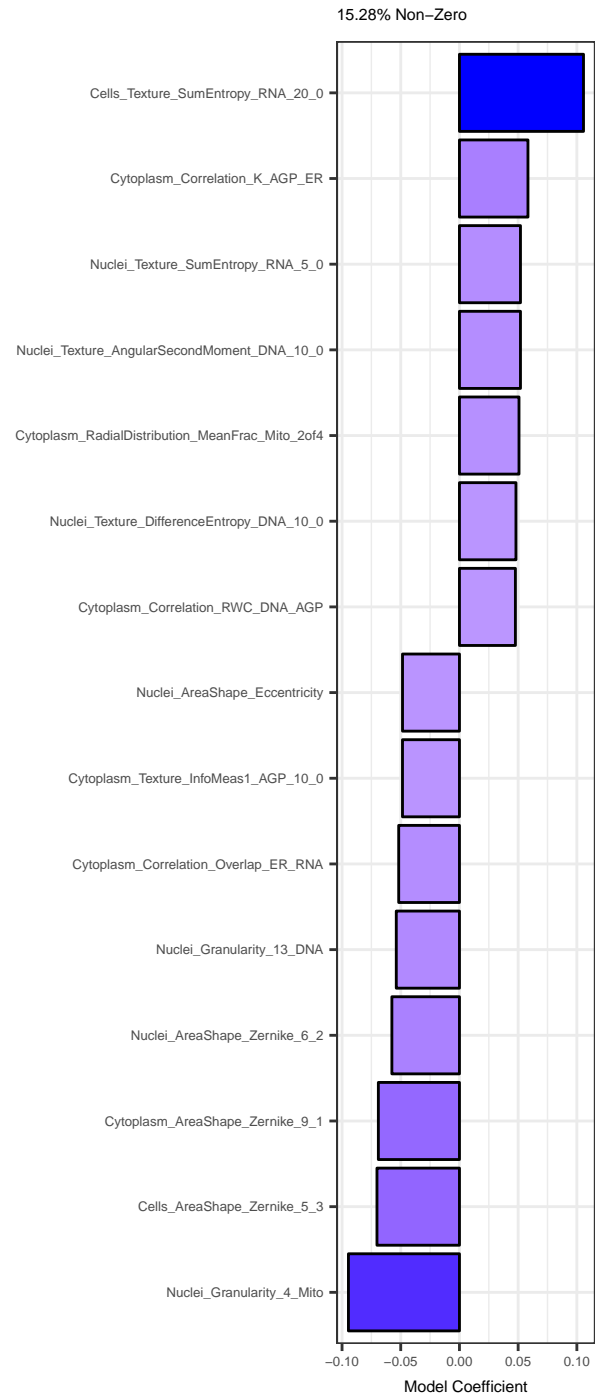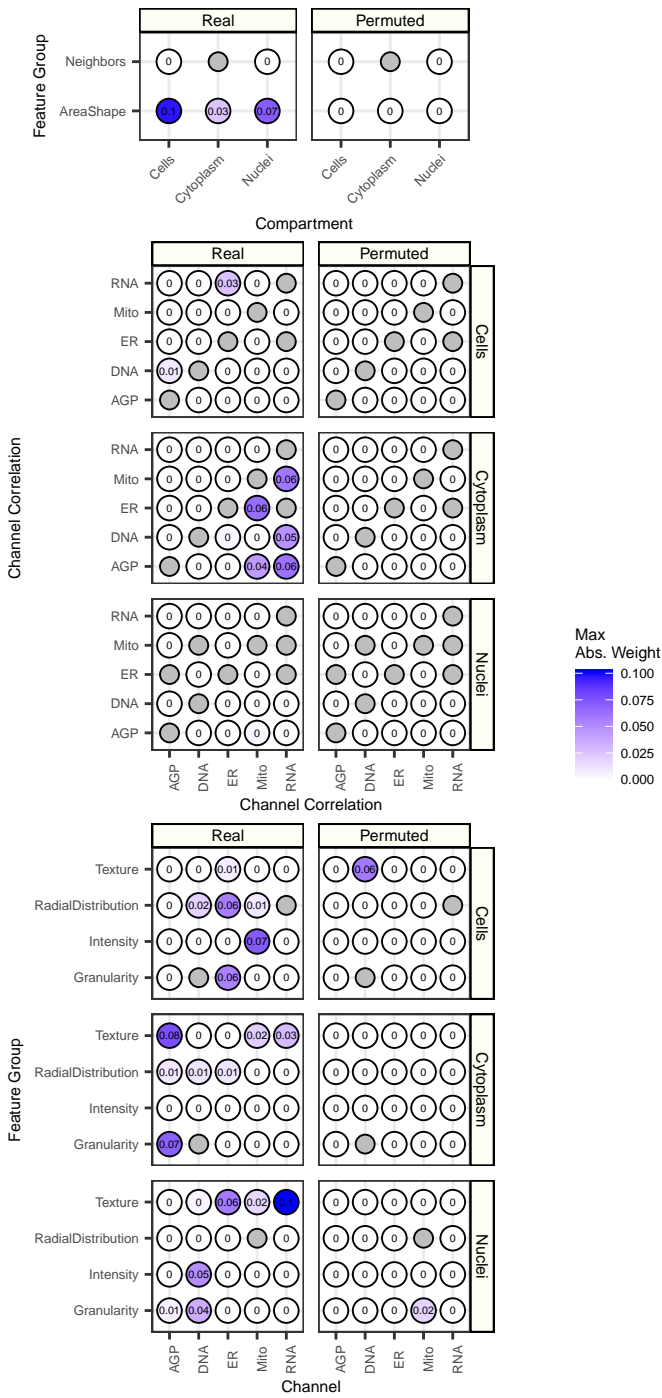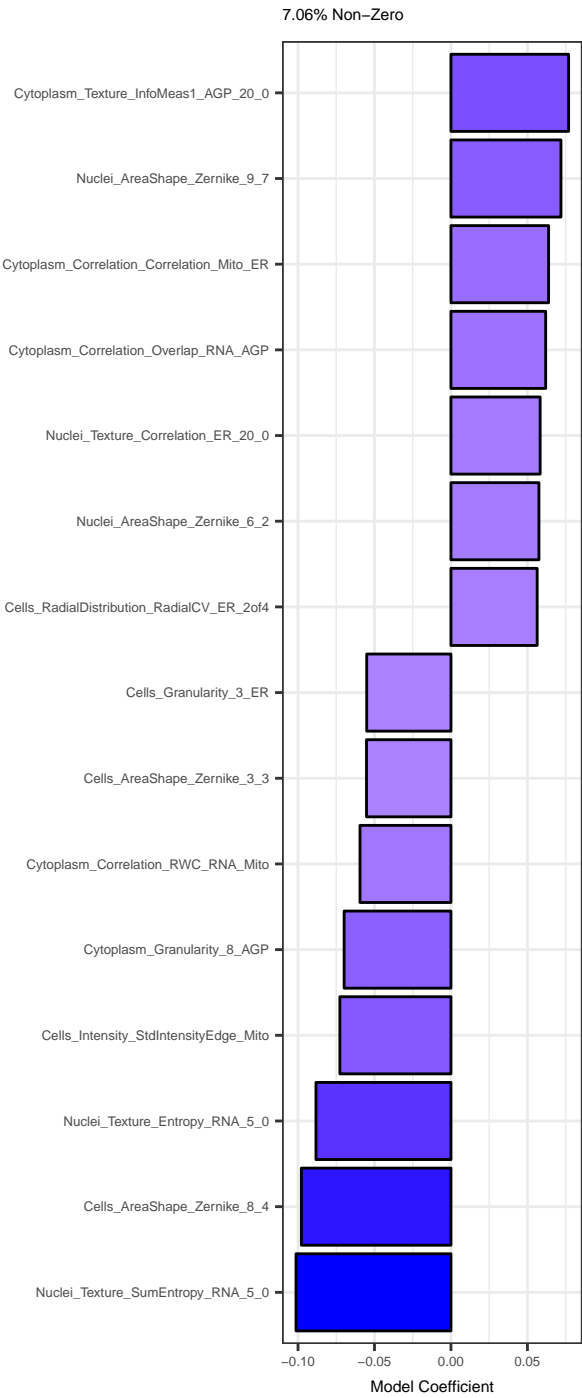**early M − % High gH2AX Spots**

early M – # cells

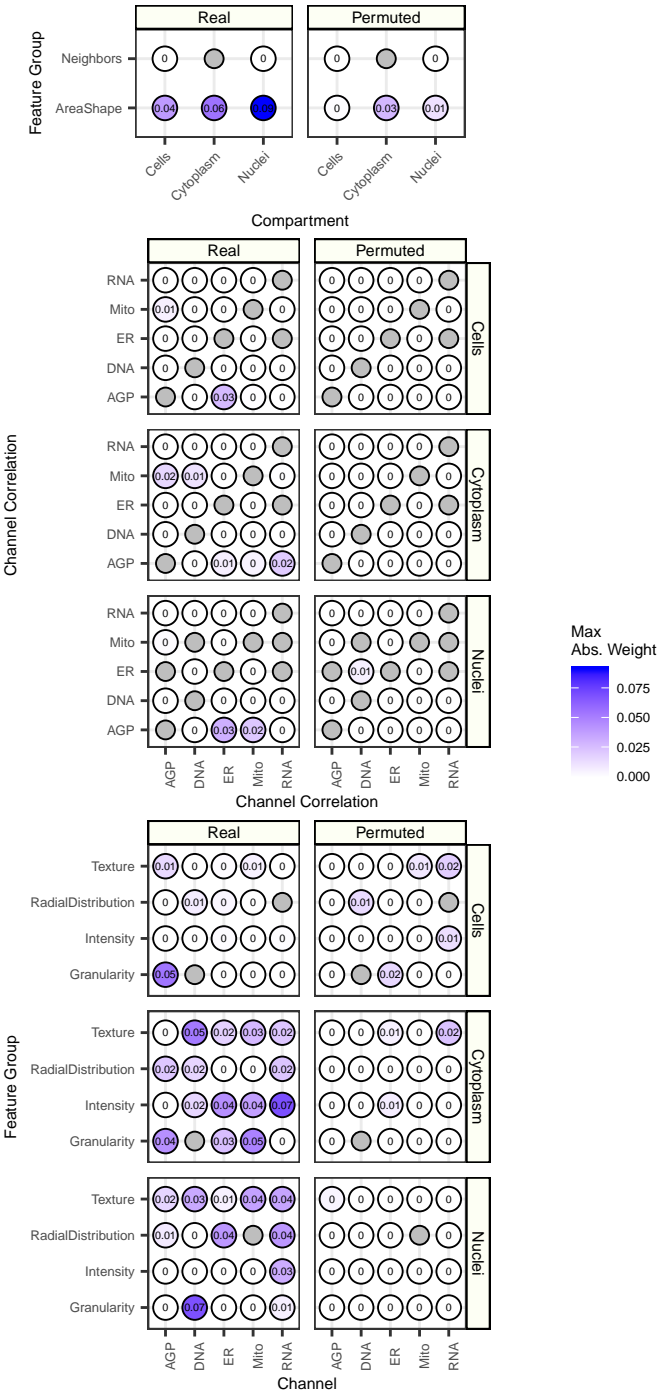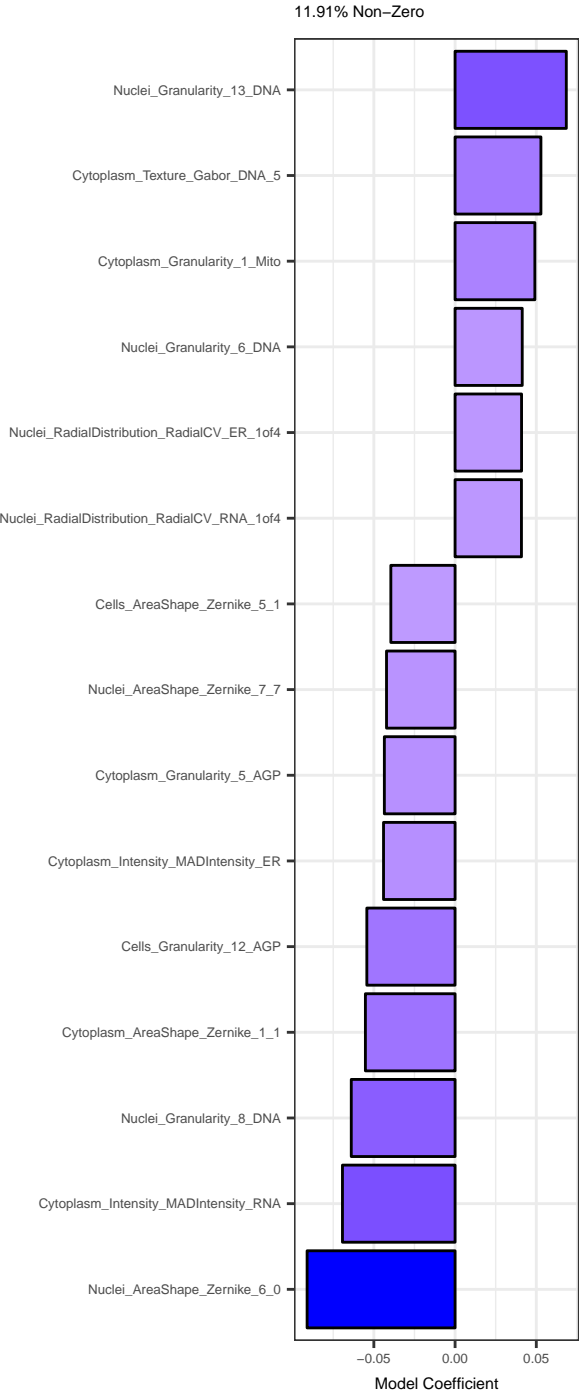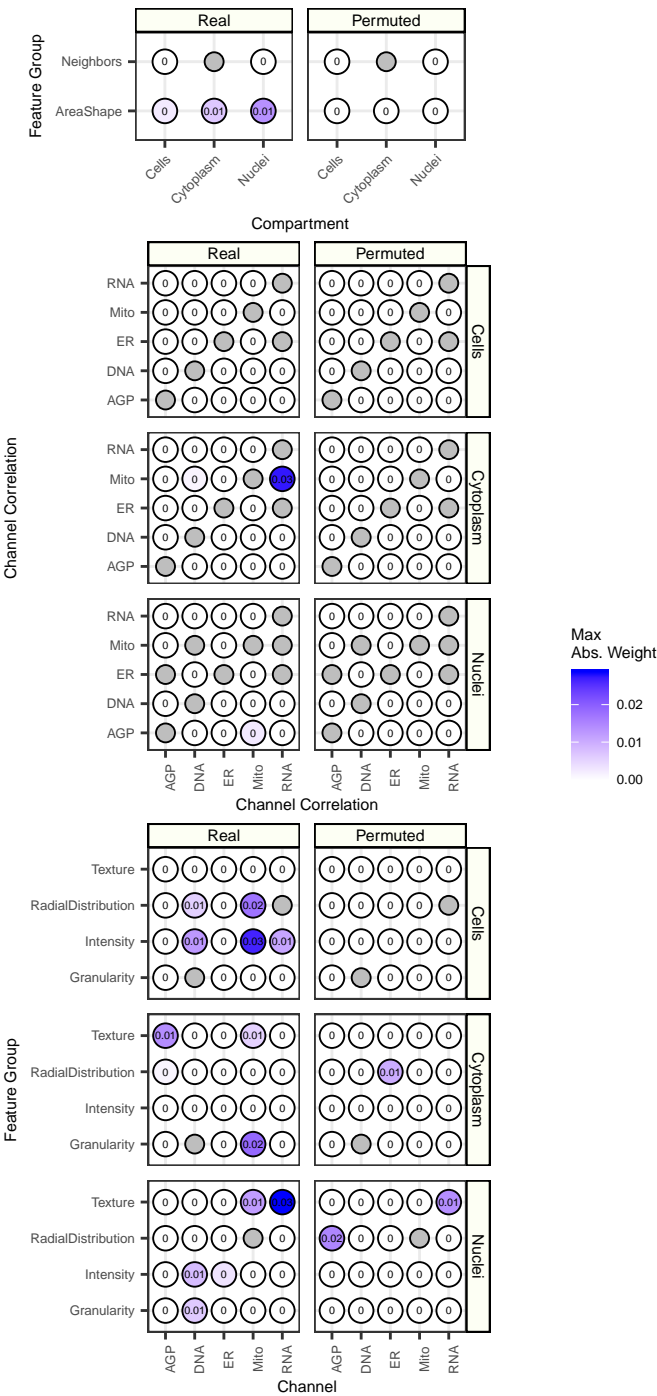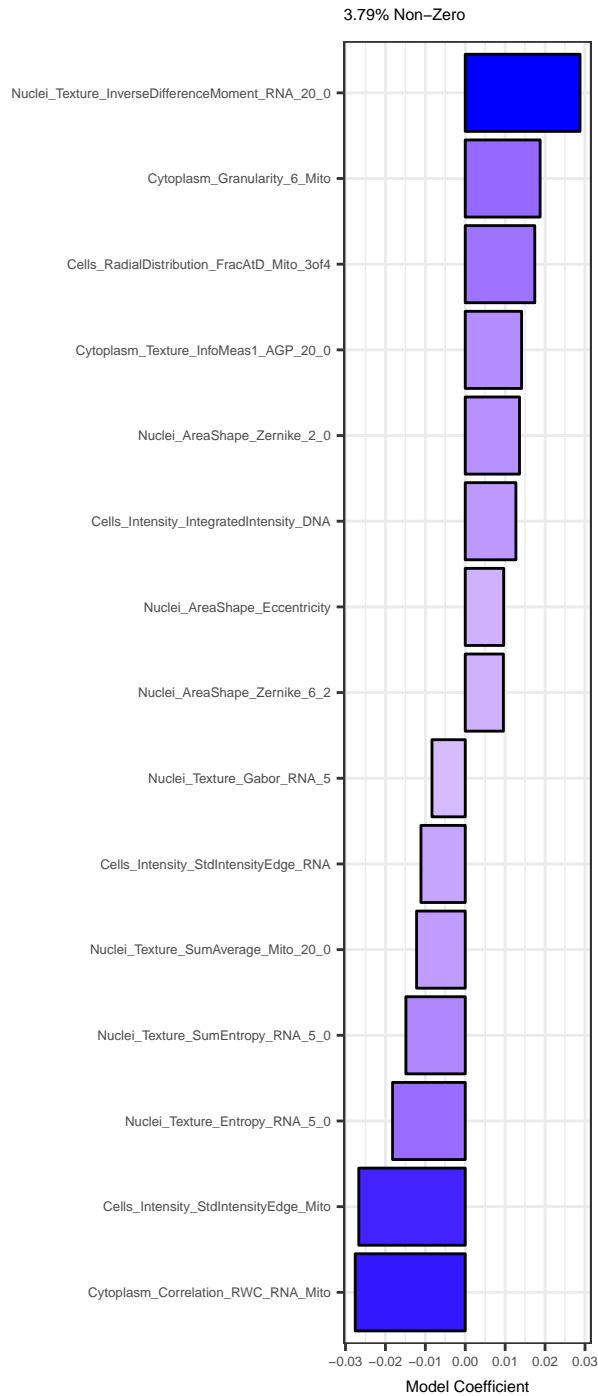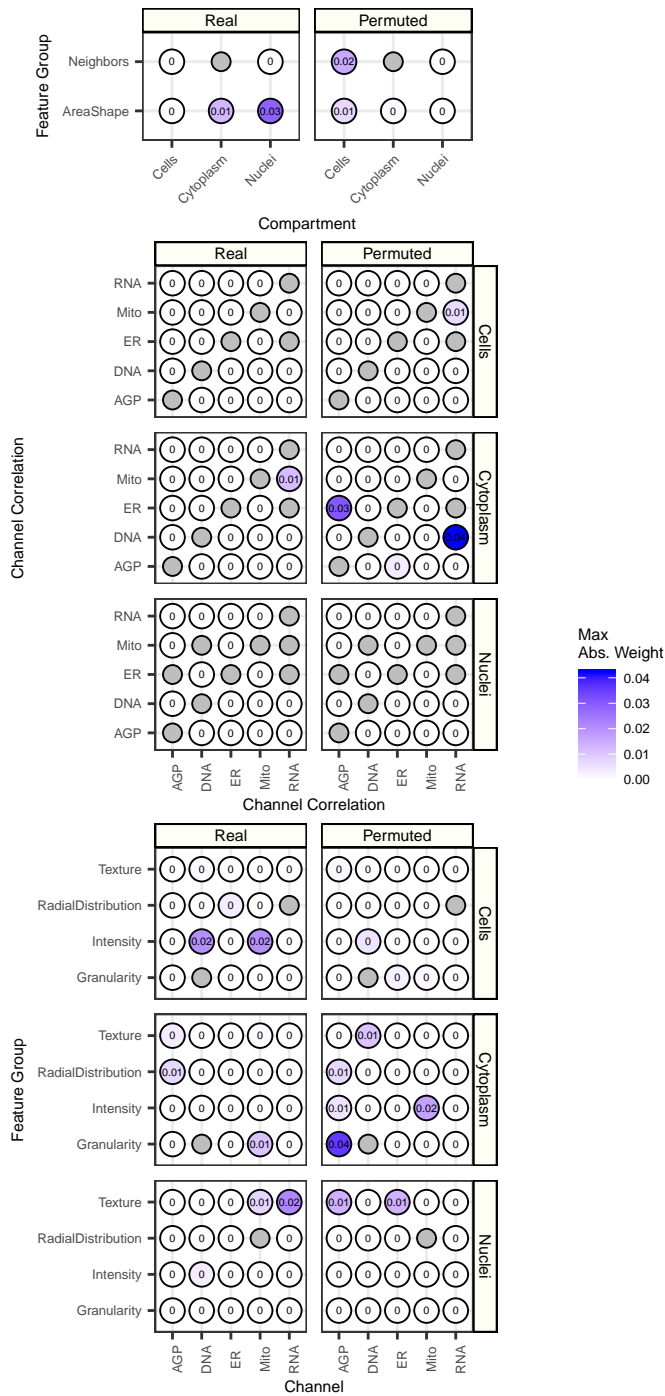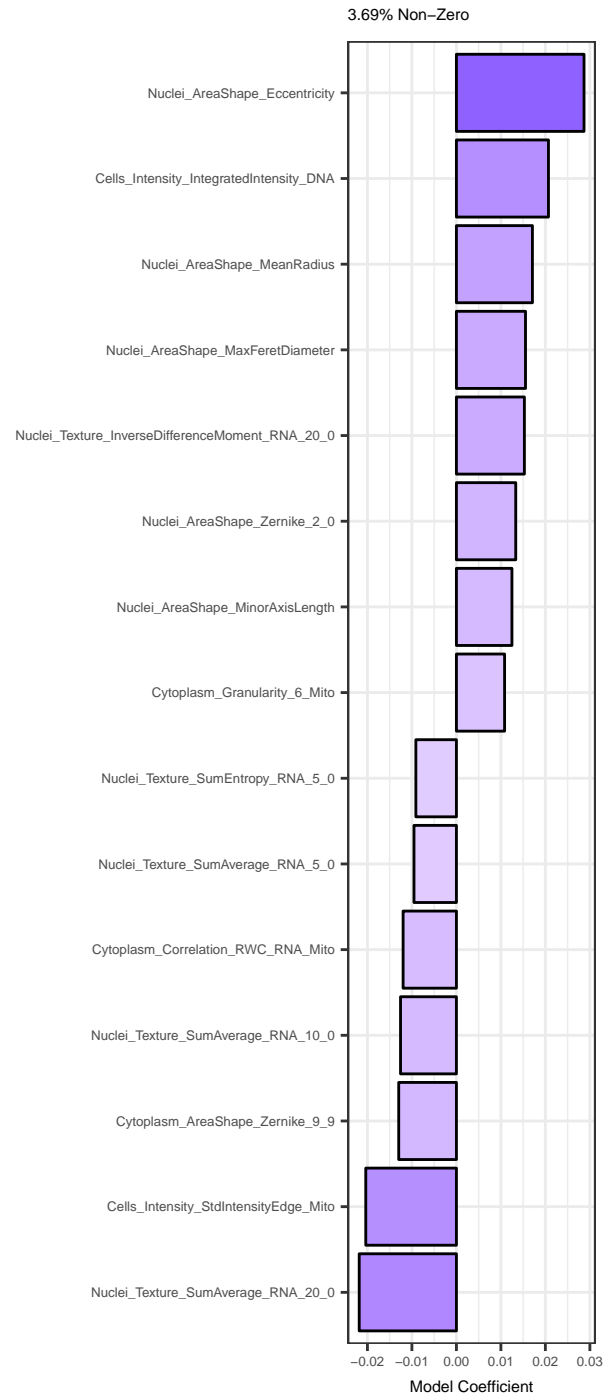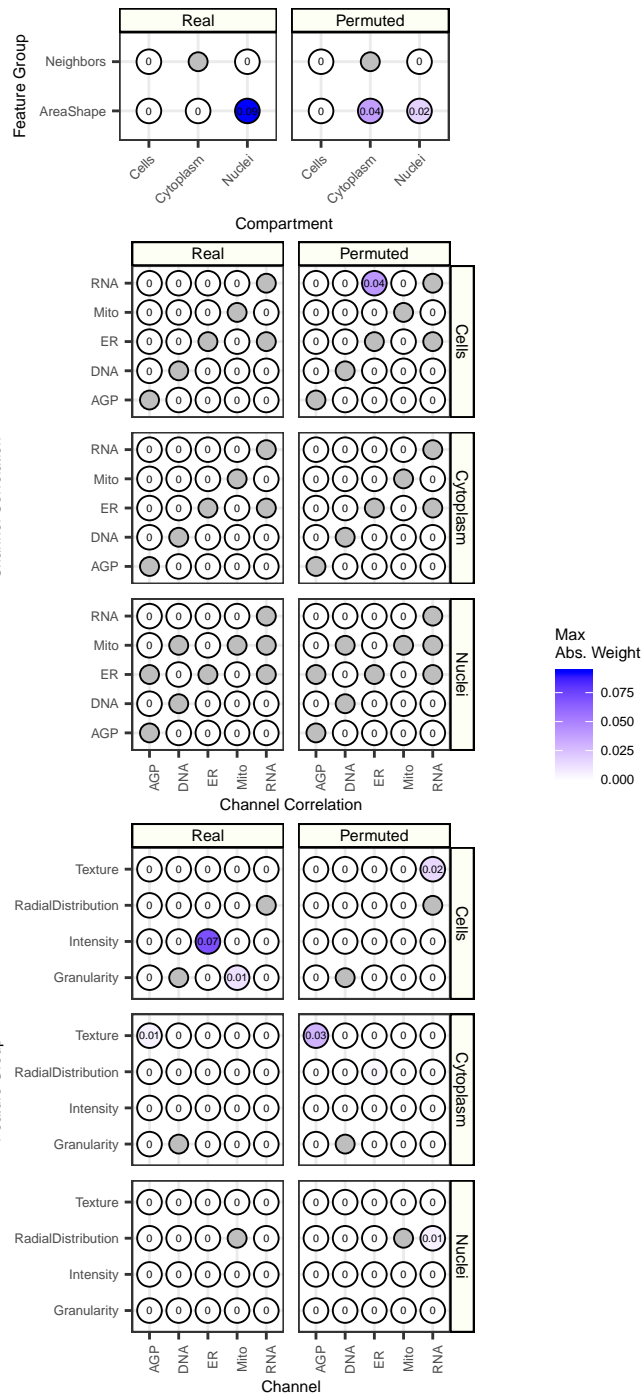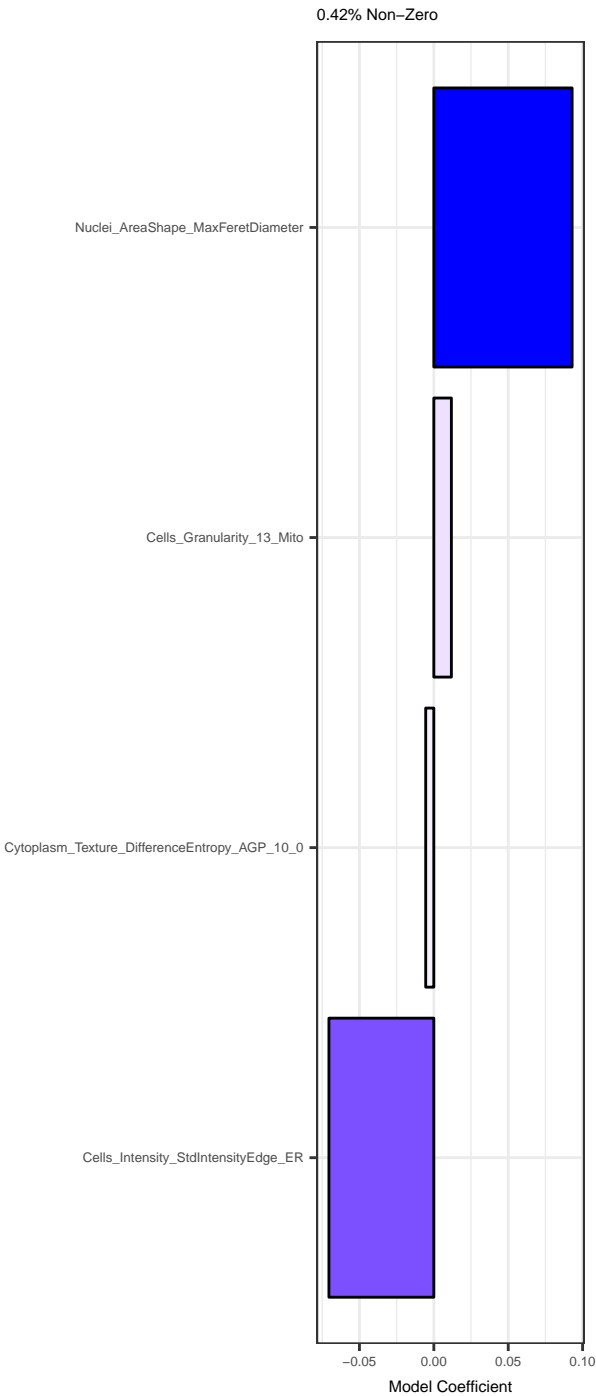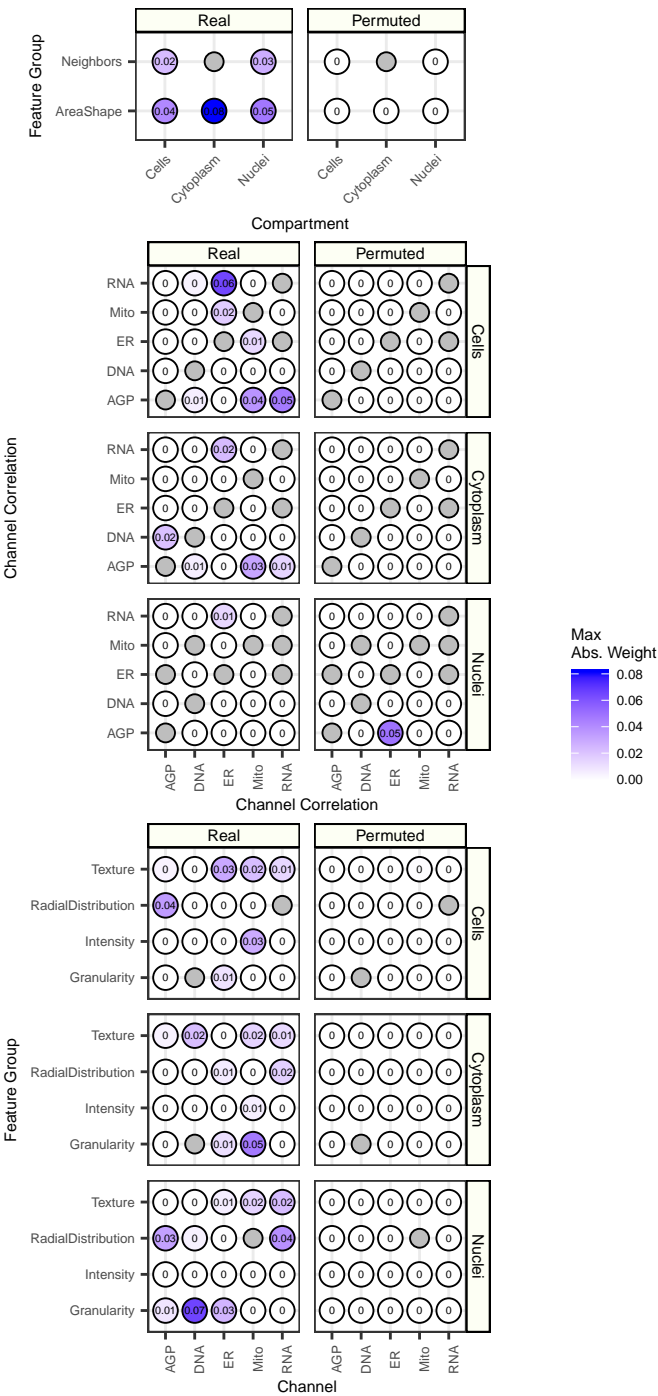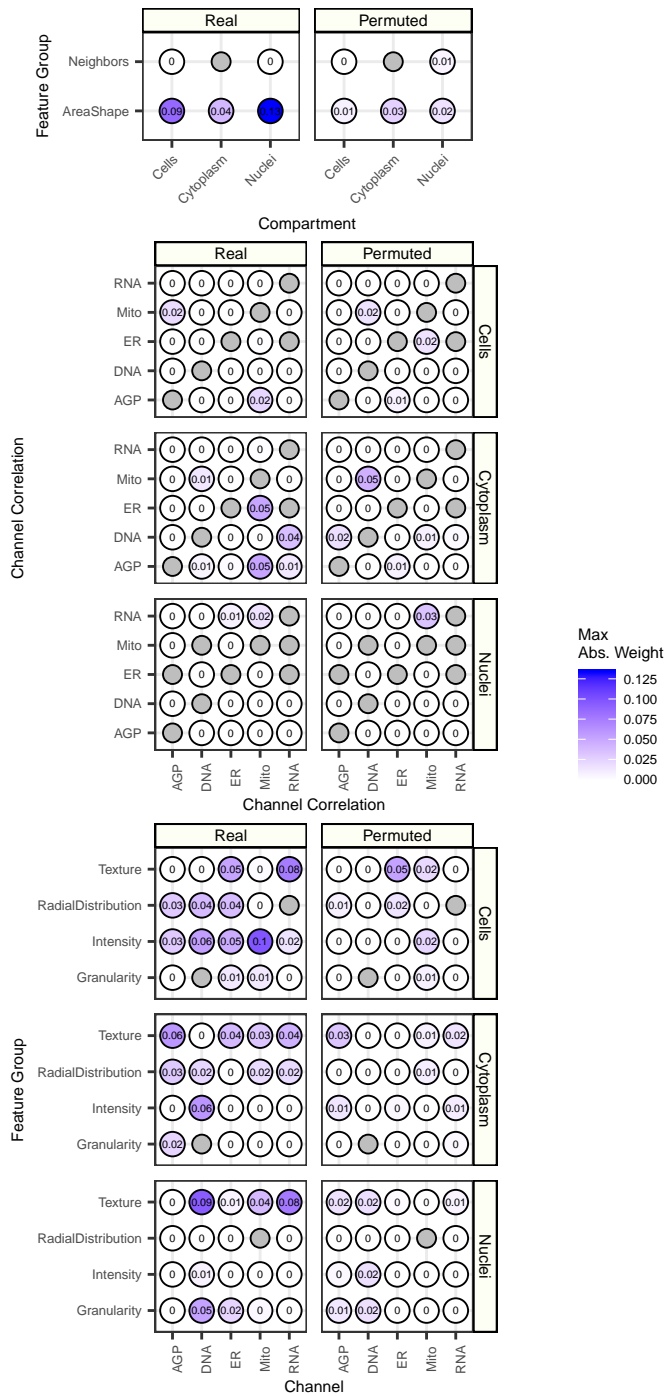# early M – # of gH2AX Spots

early M – # of gH2AX Spots per Area of Nucleus

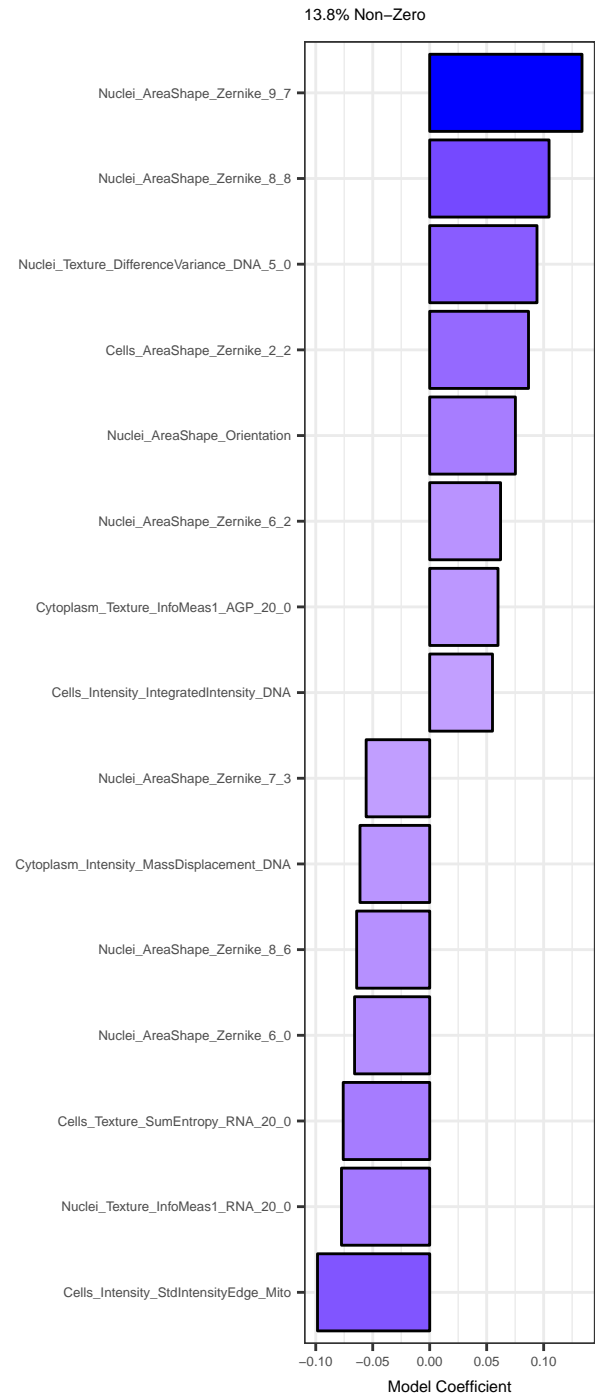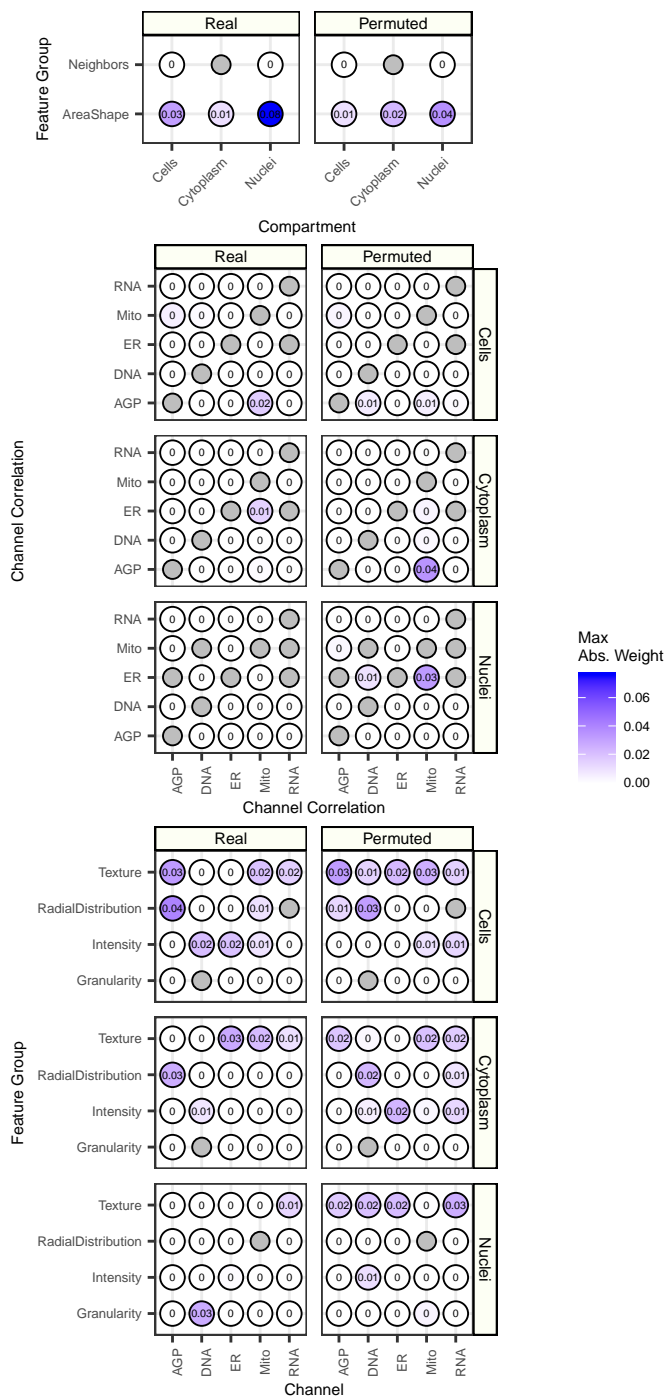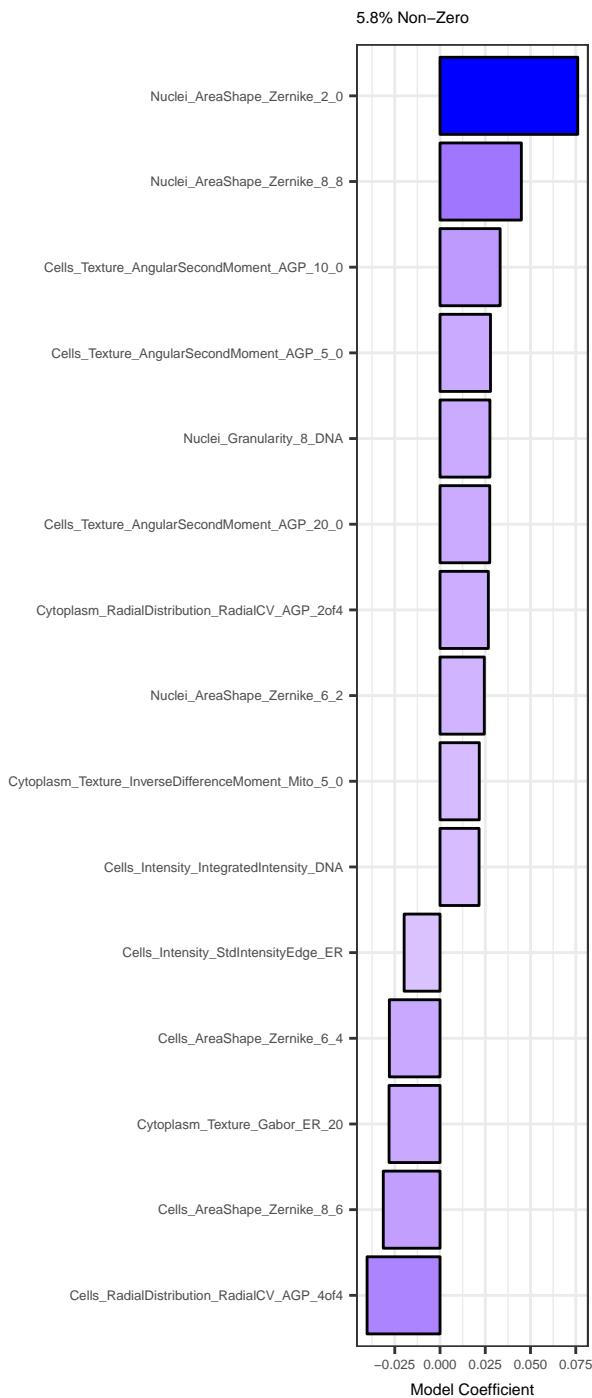# G1 – % High gH2AX Spots
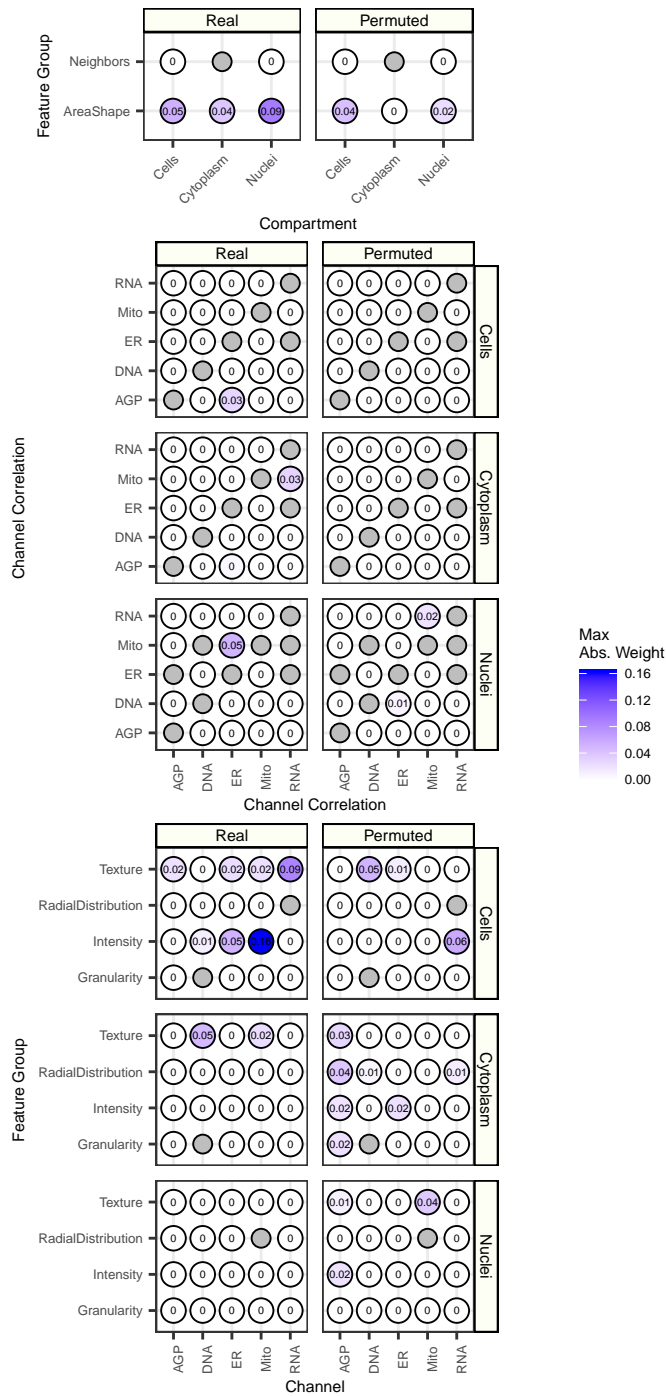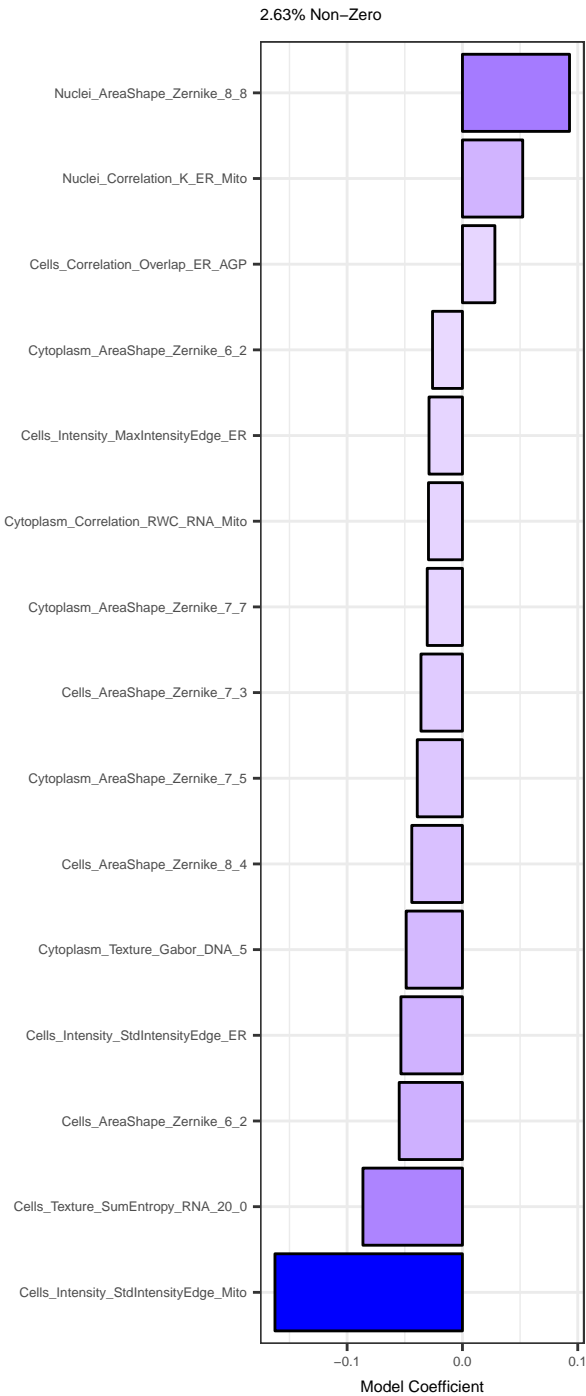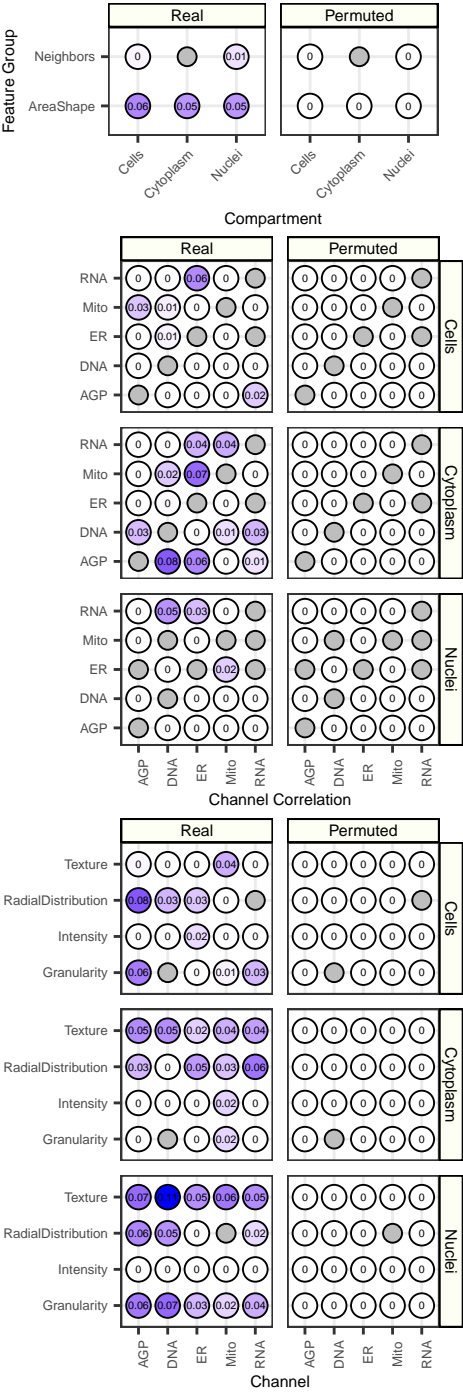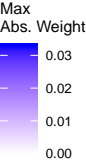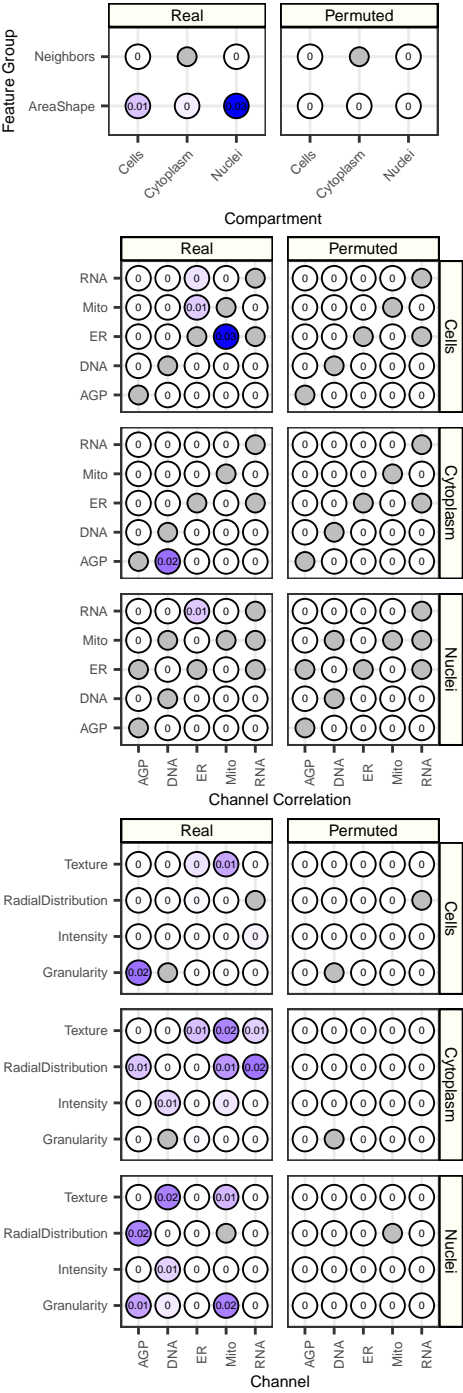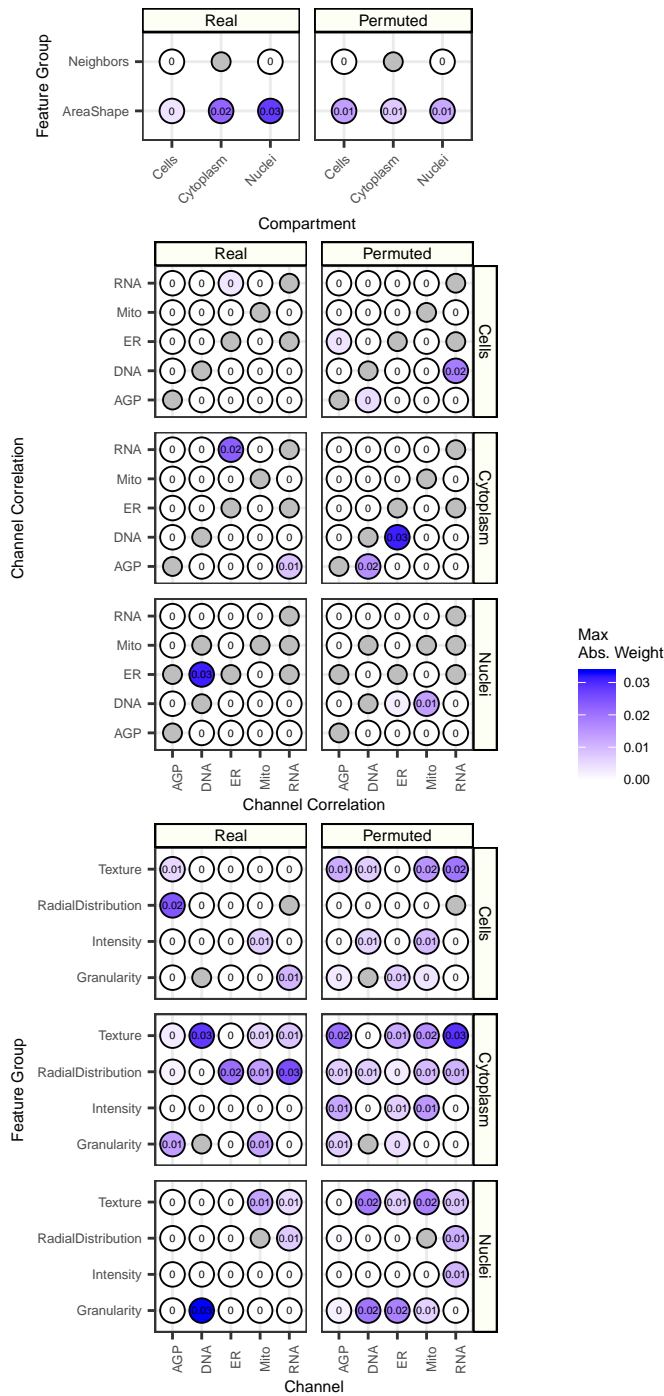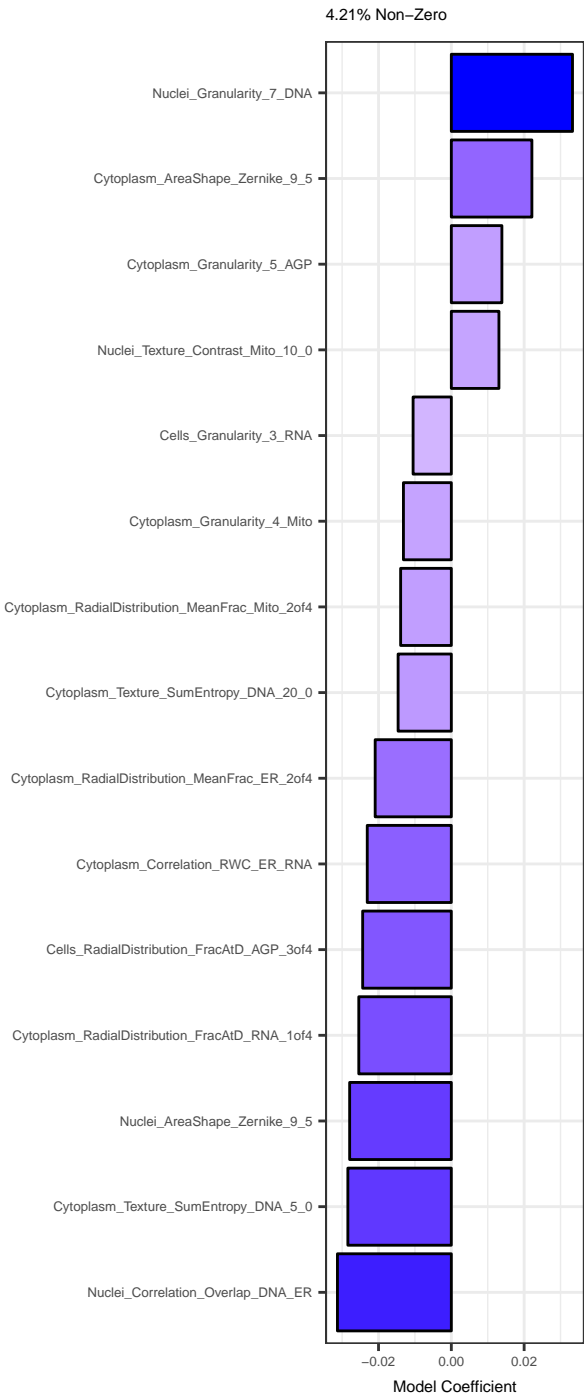

0.42% Non−Zero

Nuclei_AreaShape_MaxFeretDiameter

Cells_Granularity_13_Mito

Cytoplasm_Texture_DifferenceEntropy_AGP_10_0

Cells_Intensity_StdIntensityEdge_ER

Model Coefficient

G1 − # cells

G1 – # of gH2AX Spots

G1 – # of gH2AX Spots per Area of Nucleus

Cell Count – G1+G2

9.91% Non−Zero

Cell Count – G2/G1

G2 – % High gH2AX Spots
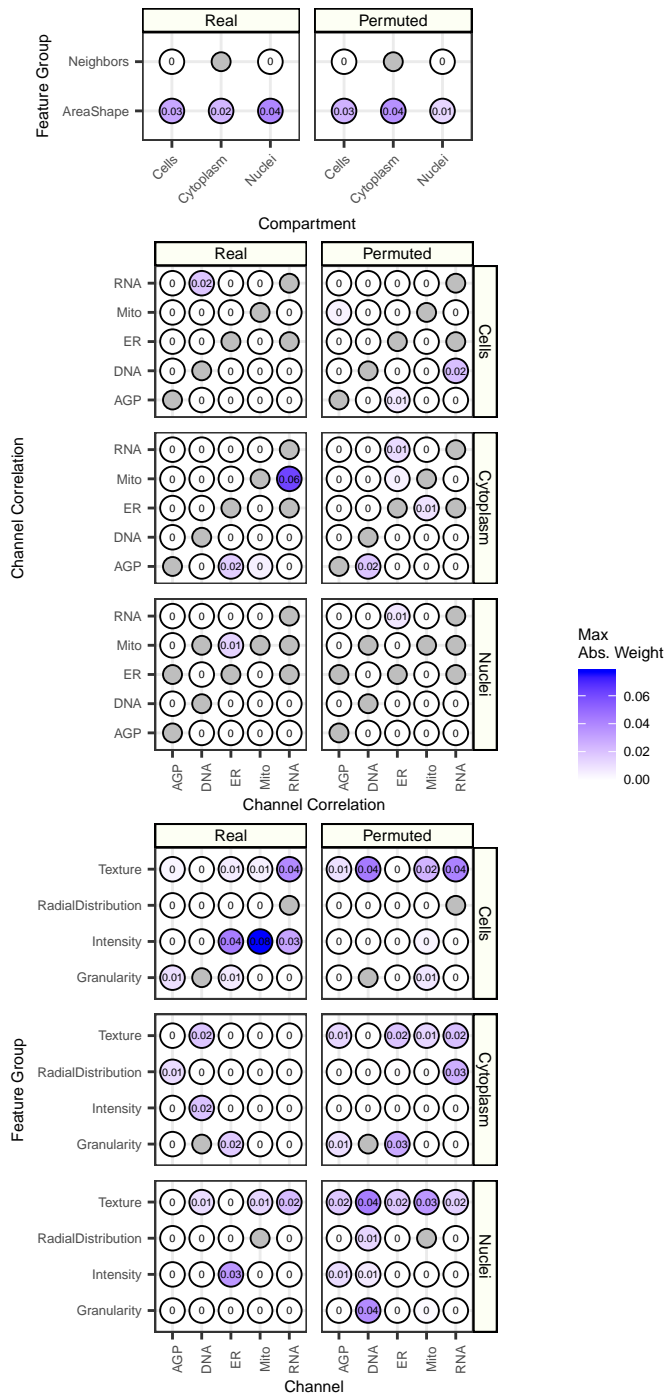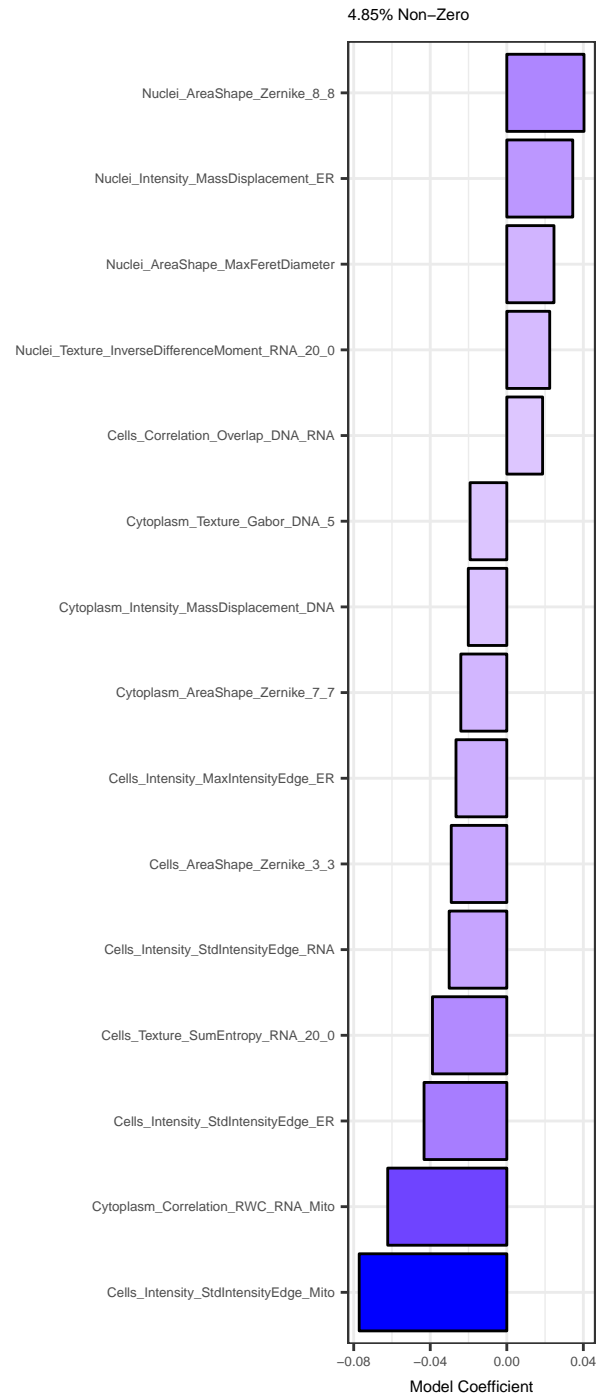
G2 − # cells
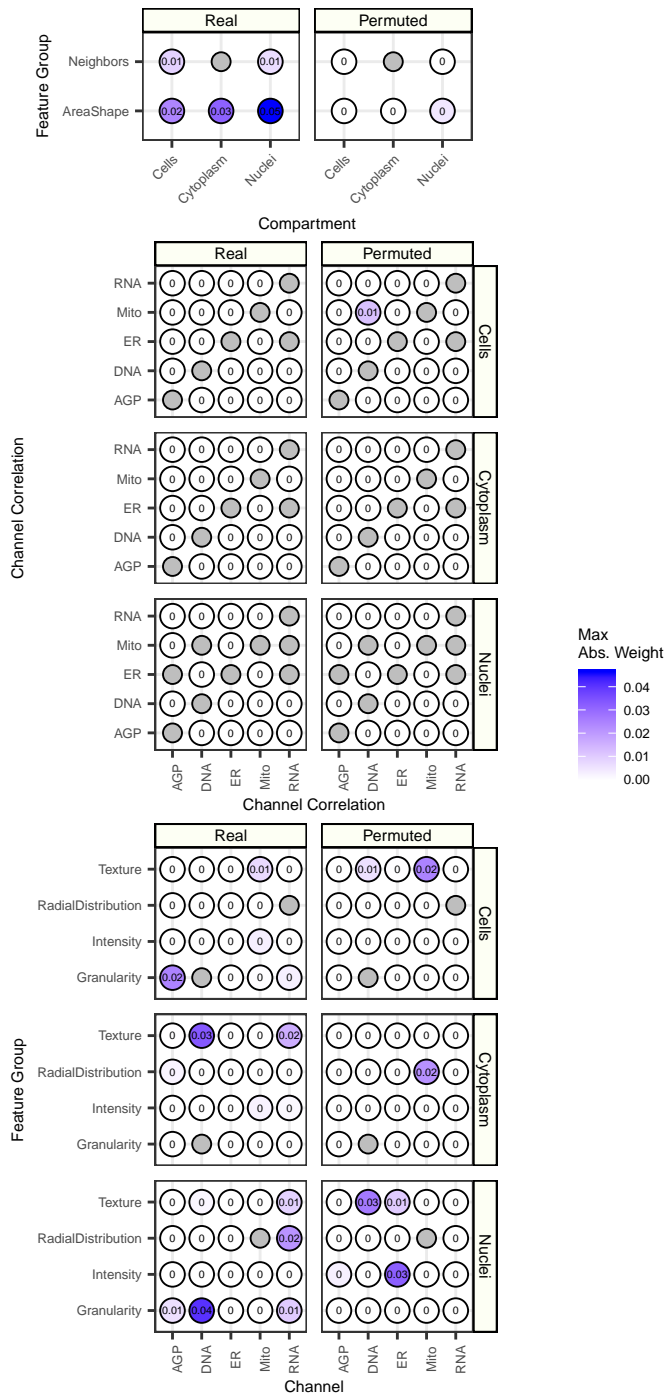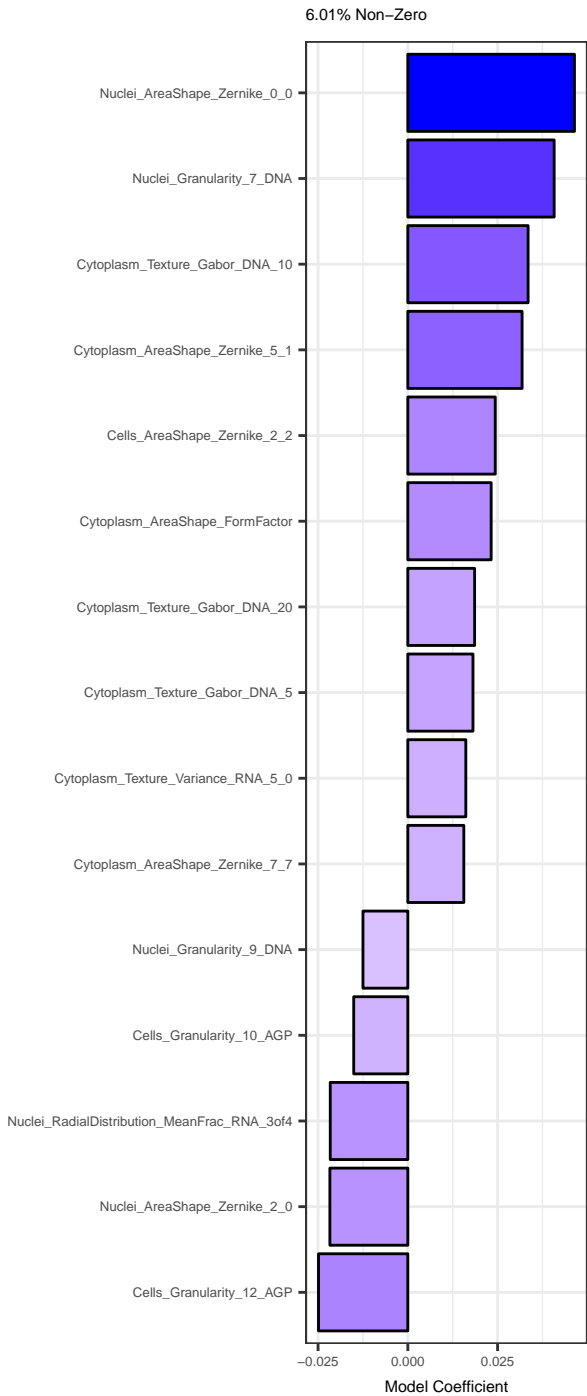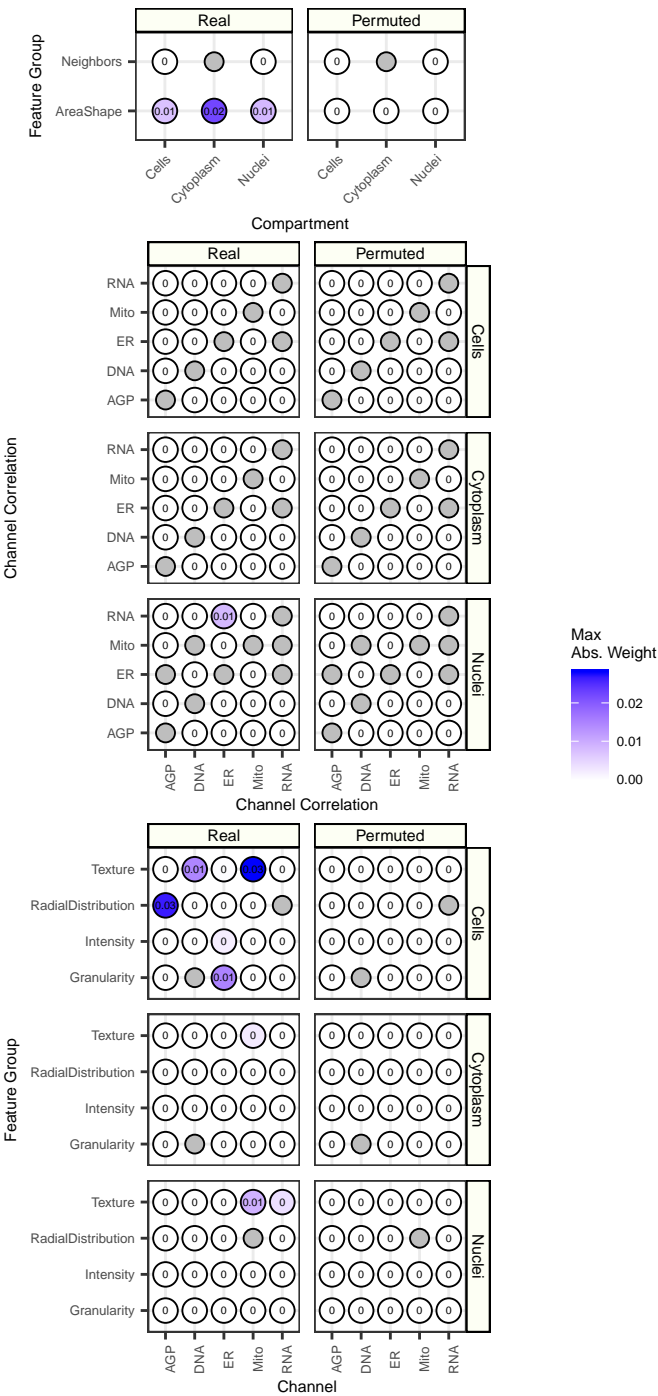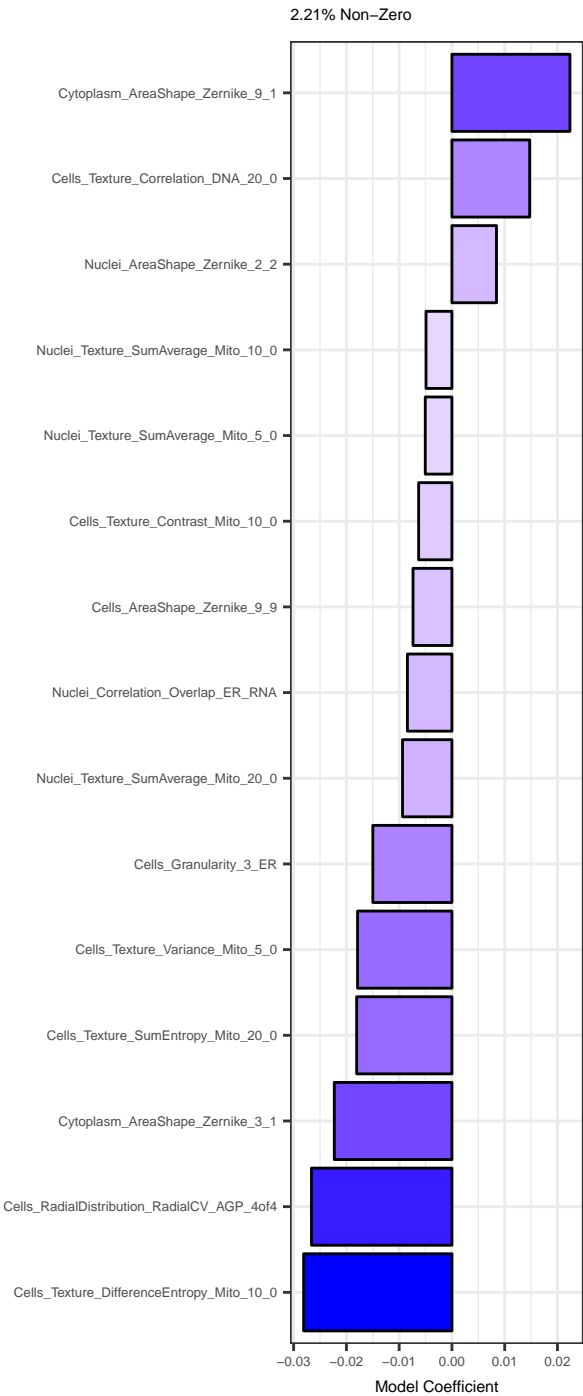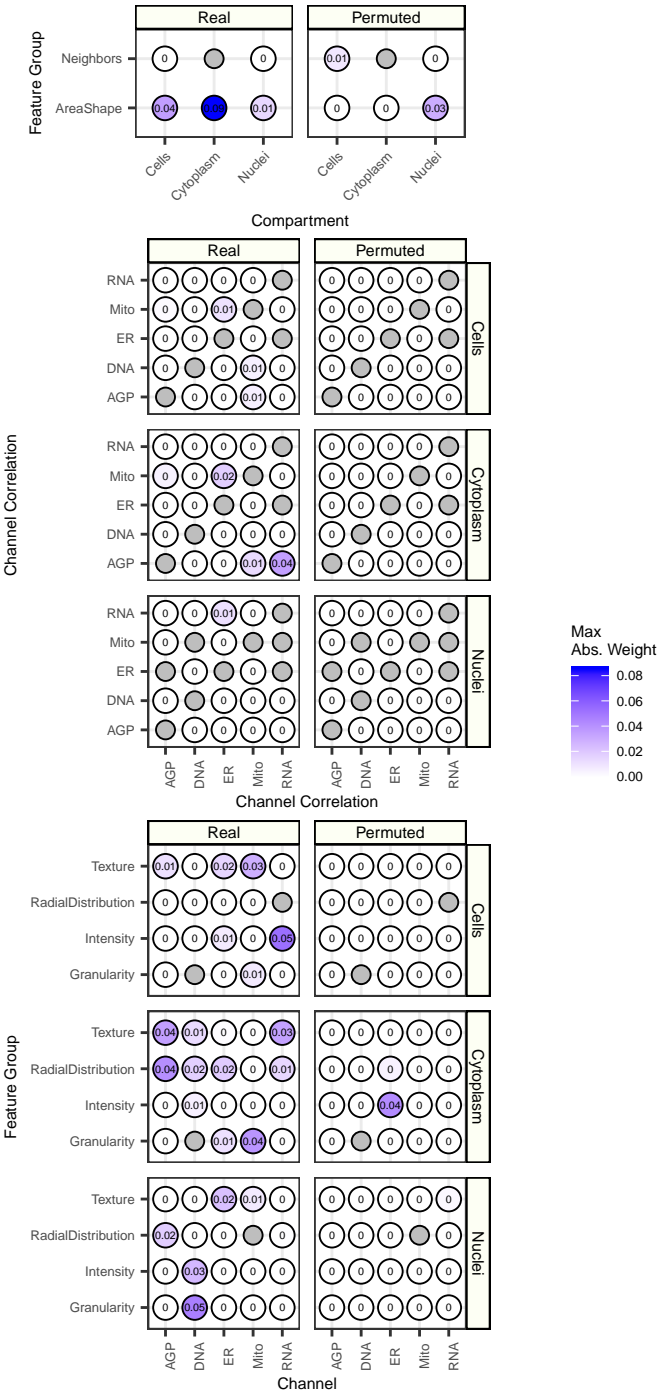
G2 – # of gH2AX Spots

G2 – # of gH2AX Spots per Area of Nucleus

Cell Count − G2 + M

Inf %

5.06% Non−Zero

Model Coefficient axis features (top to bottom):
- Nuclei_AreaShape_Zernike_2_0
- Cells_Correlation_Correlation_Mito_ER
- Cells_Granularity_10_AGP
- Cytoplasm_RadialDistribution_FracAtD_RNA_4of4
- Nuclei_Texture_InverseDifferenceMoment_DNA_10_0
- Cytoplasm_Texture_SumVariance_Mito_20_0
- Nuclei_AreaShape_Zernike_2_2
- Cells_Texture_SumVariance_Mito_20_0
- Nuclei_Granularity_2_AGP
- Cytoplasm_Texture_InfoMeas2_Mito_20_0
- Cytoplasm_RadialDistribution_MeanFrac_Mito_3of4
- Nuclei_RadialDistribution_RadialCV_AGP_2of4
- Nuclei_Granularity_4_Mito
- Cytoplasm_Correlation_Correlation_DNA_AGP
- Nuclei_AreaShape_Zernike_8_0

Late M – % High gH2AX Spots

0% Non−Zero

Model Coefficient

Late M – # cells

7.59% Non−Zero

Late M – # of gH2AX Spots

Late M – # of gH2AX Spots per Area of Nucleus

M – % High gH2AX Spots

0% Non−Zero
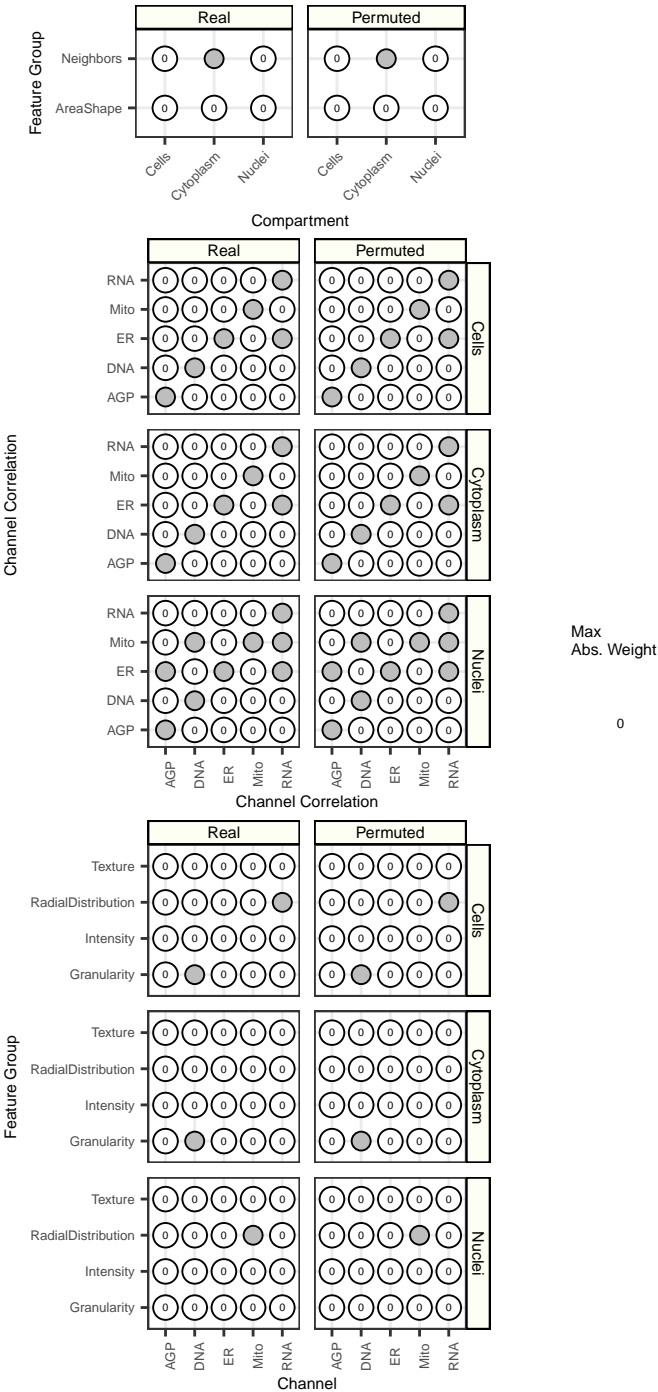
Model Coefficient
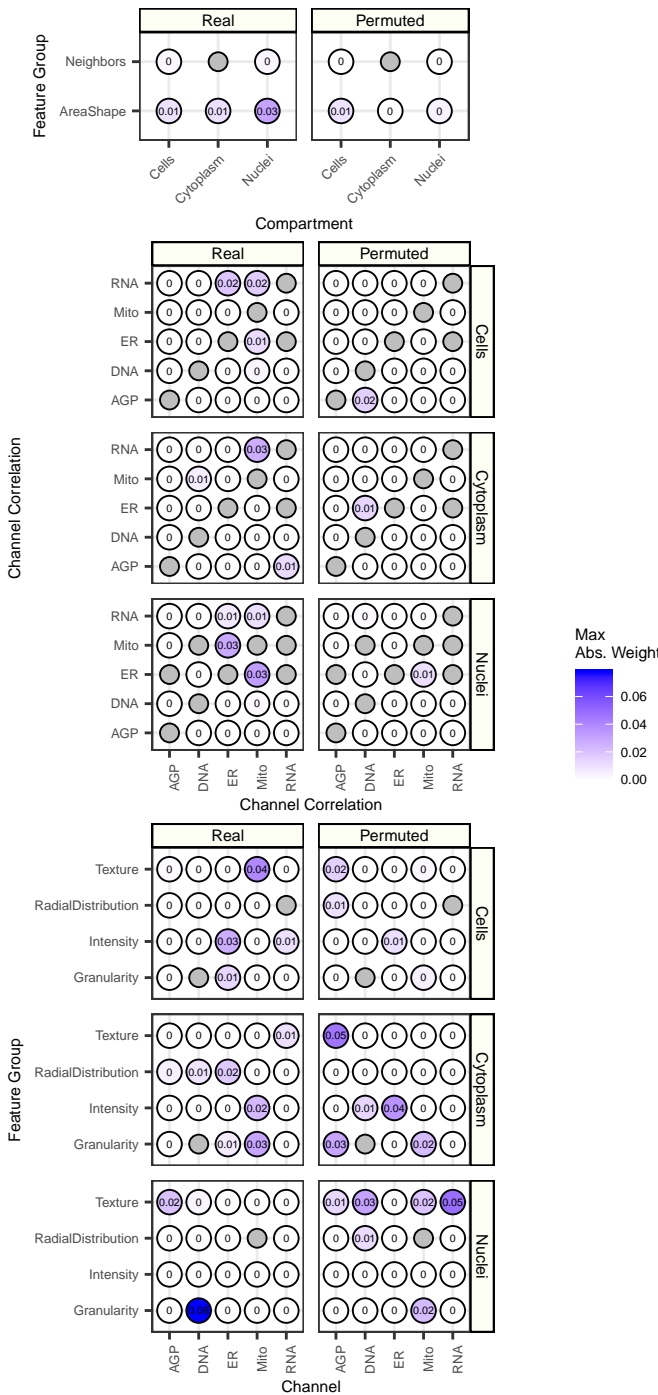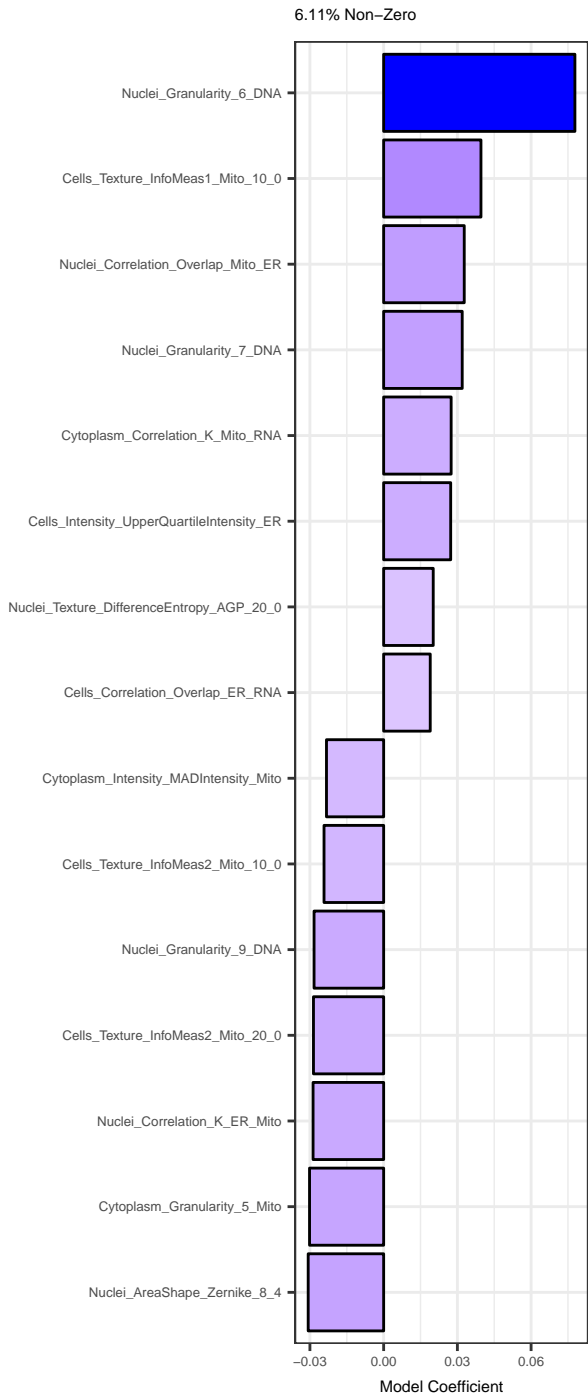
M – # cells

M − # of gH2AX Spots
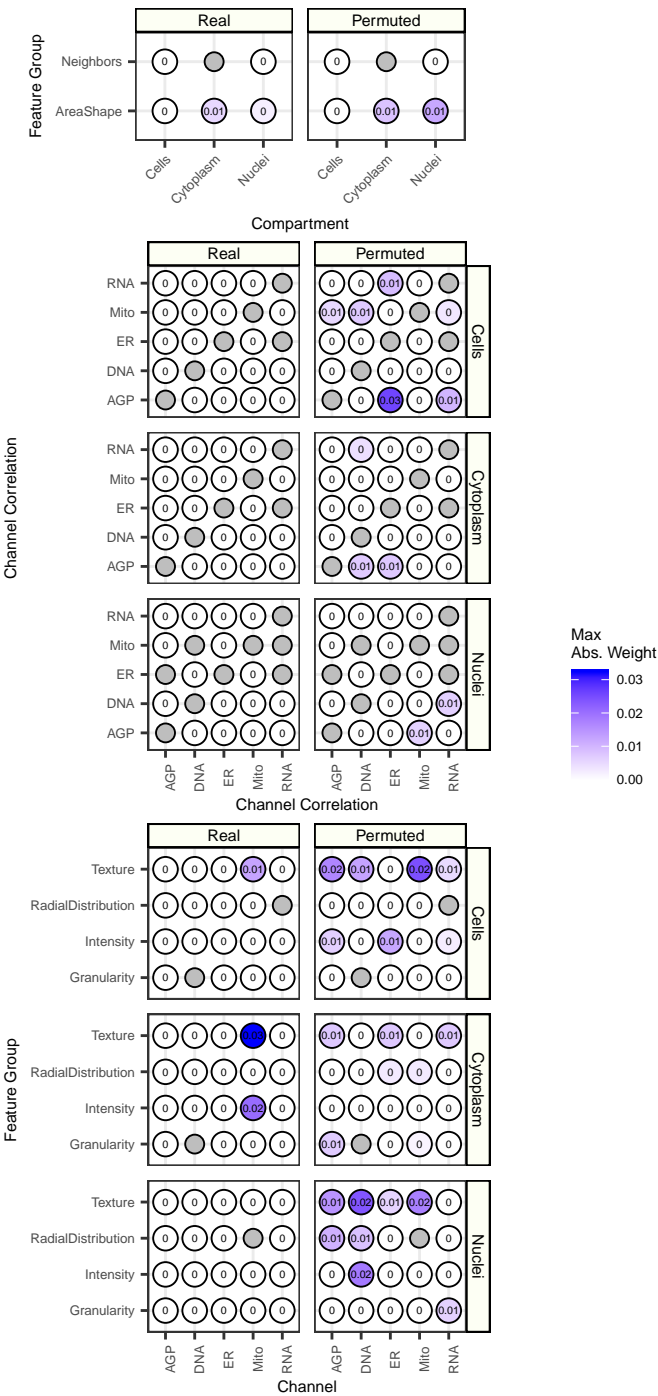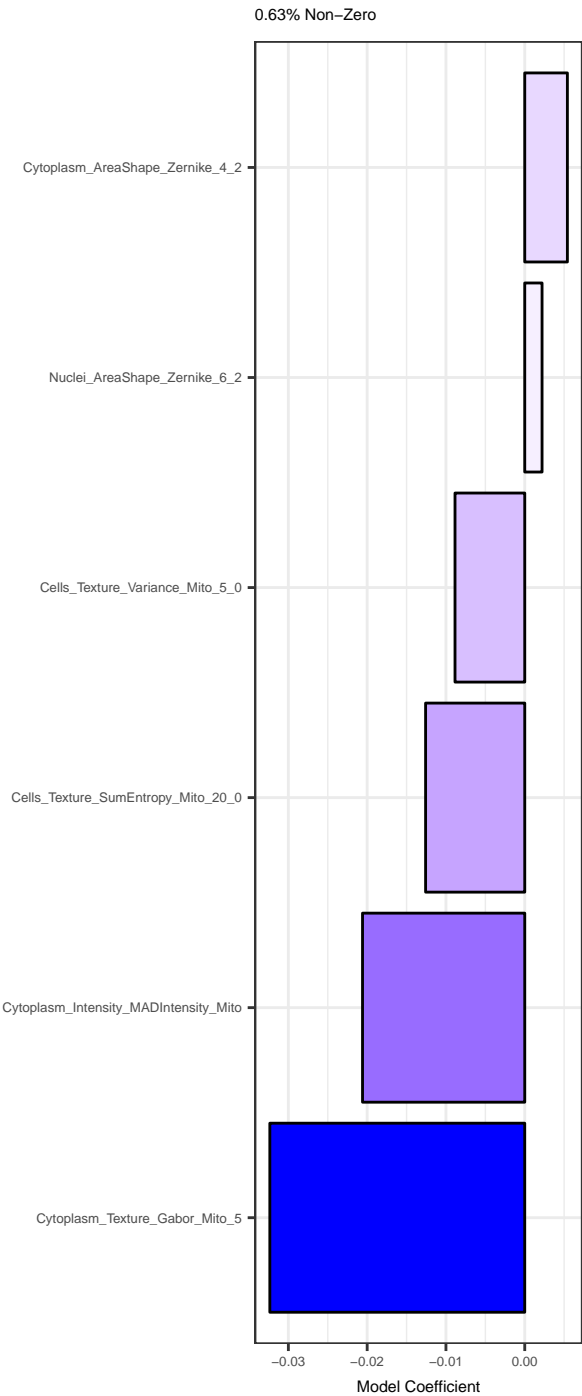
M – # of gH2AX Spots per Area of Nucleus
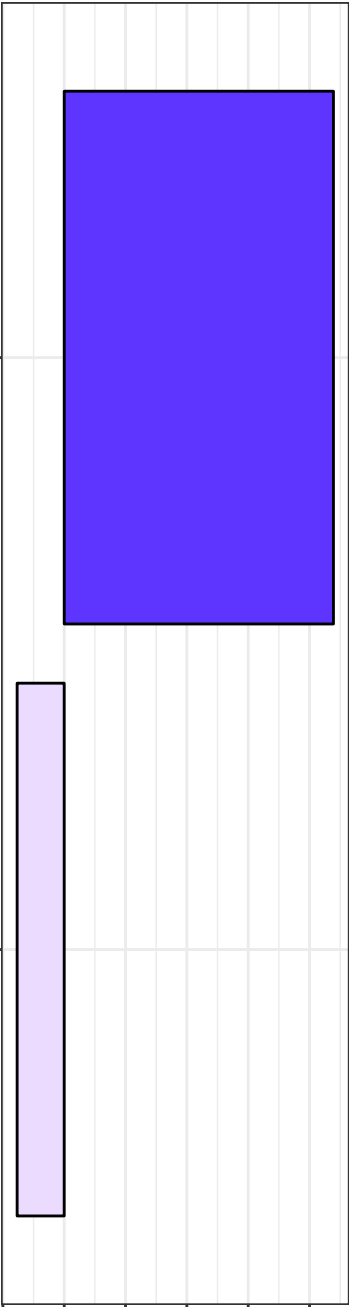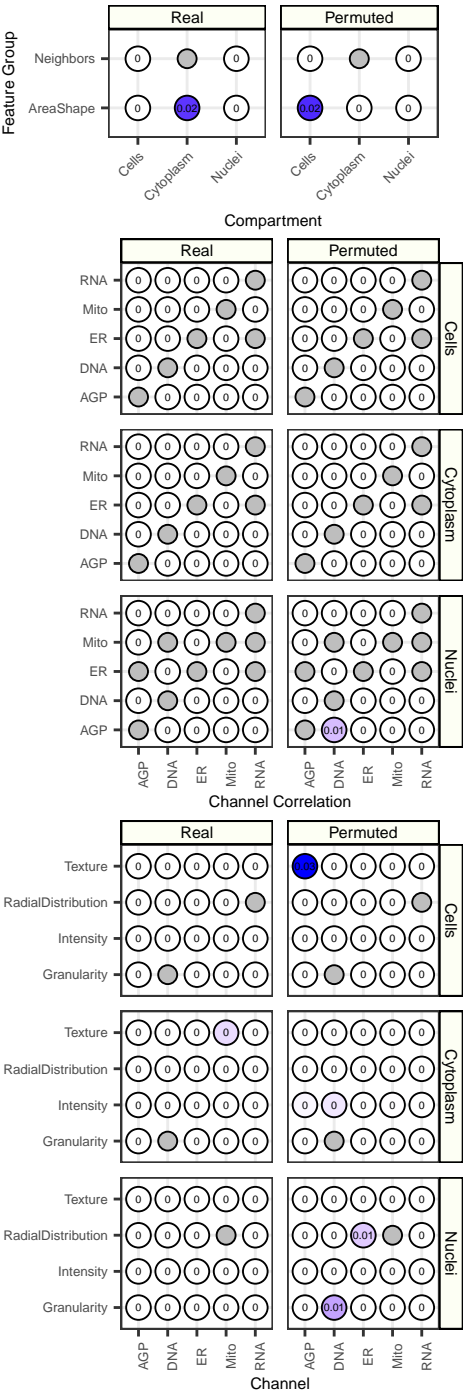
Polynuclear – % High gH2AX Spots

Polynuclear – # cells
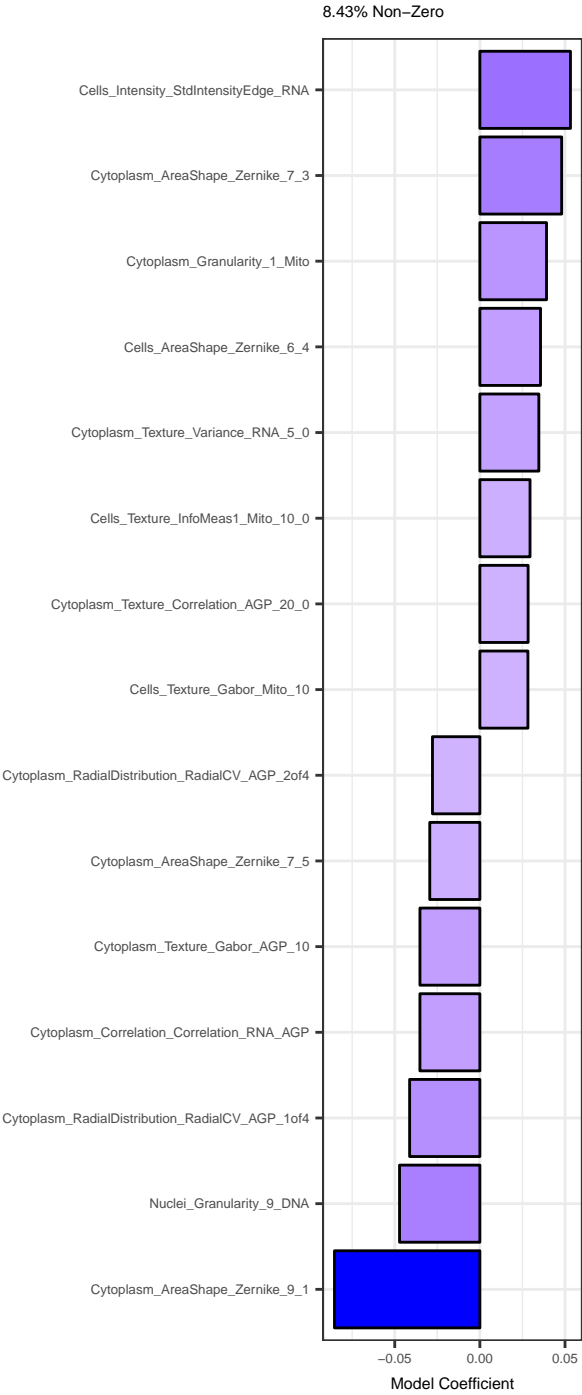
Polynuclear – # of gH2AX Spots
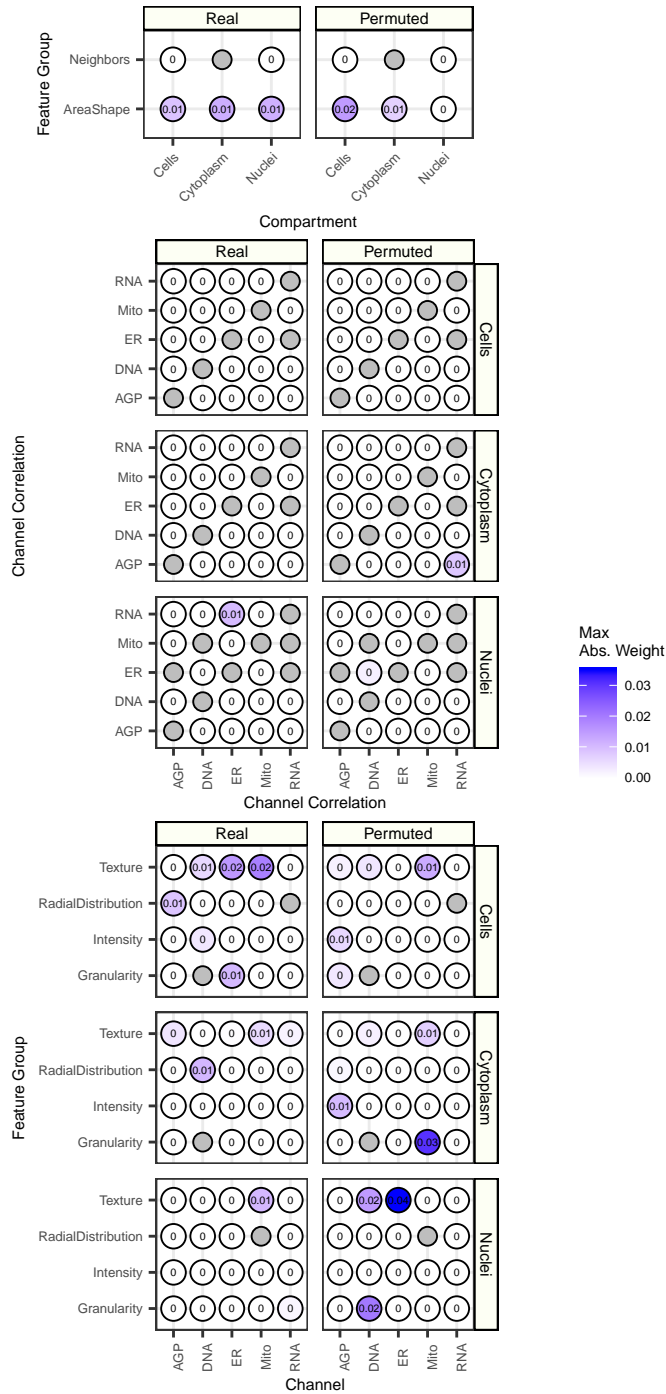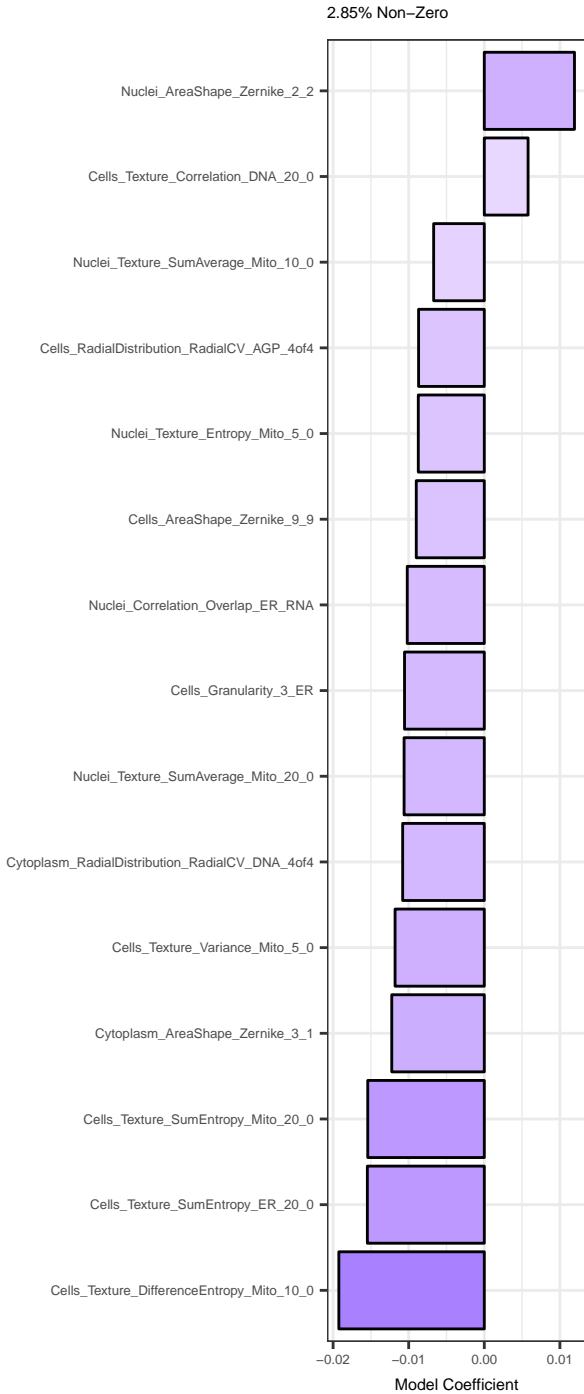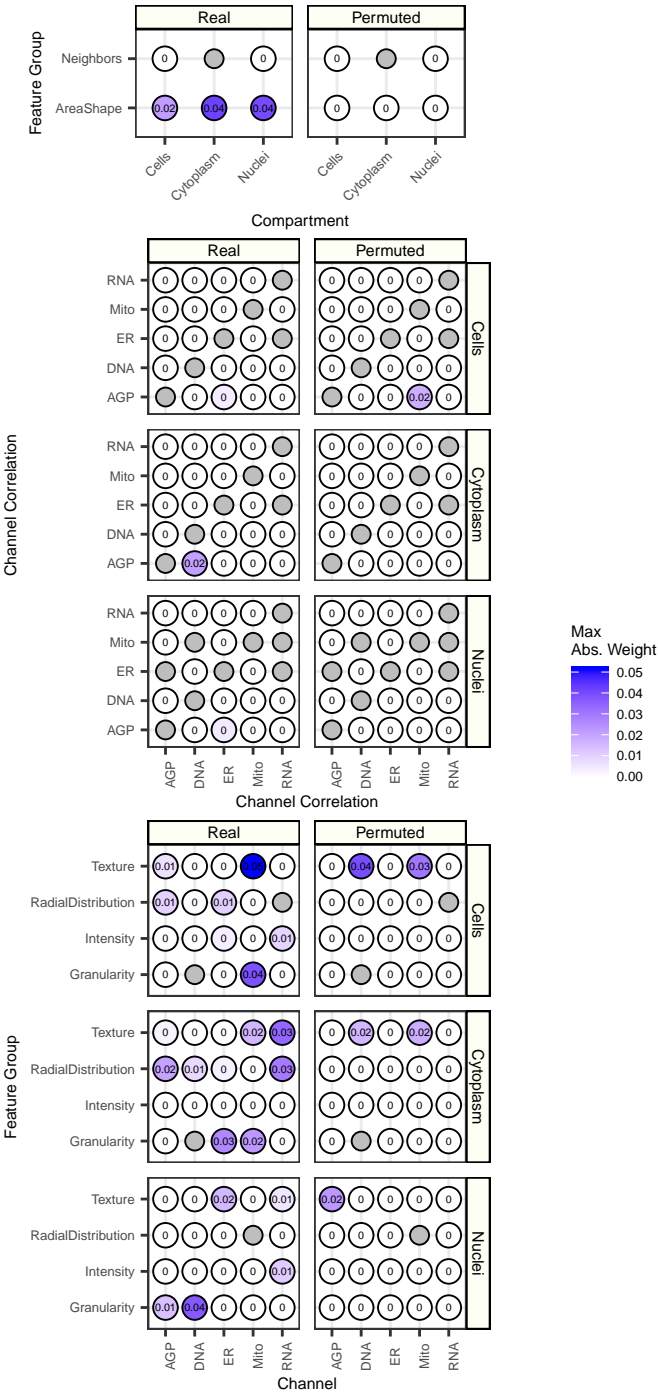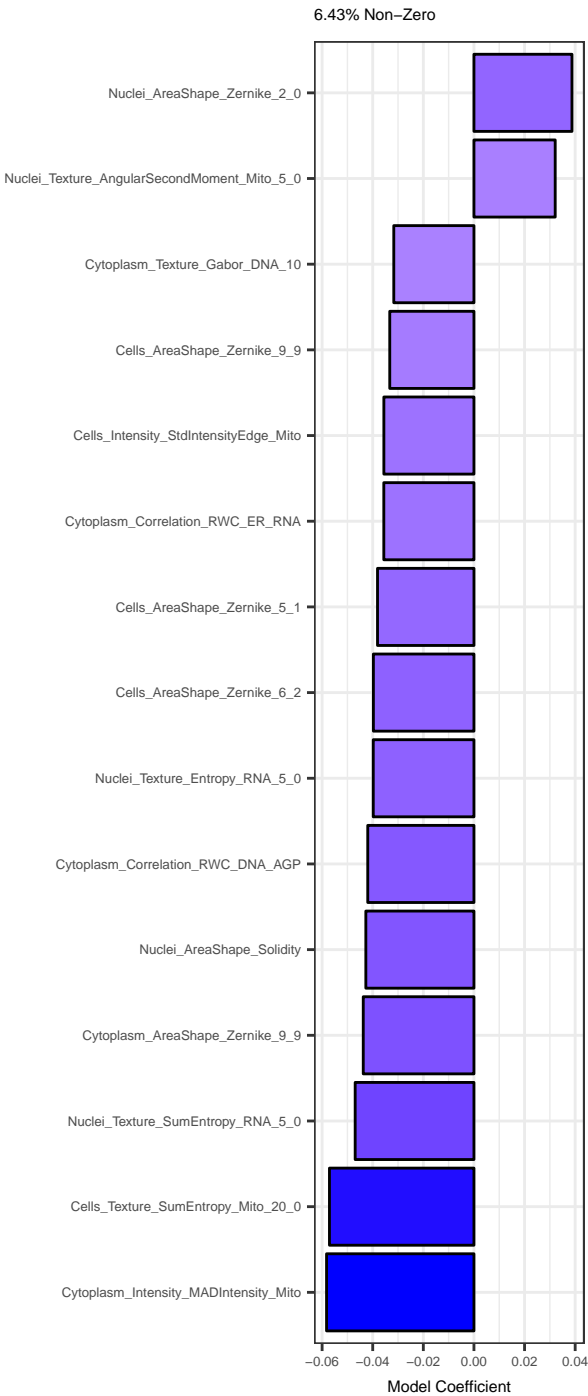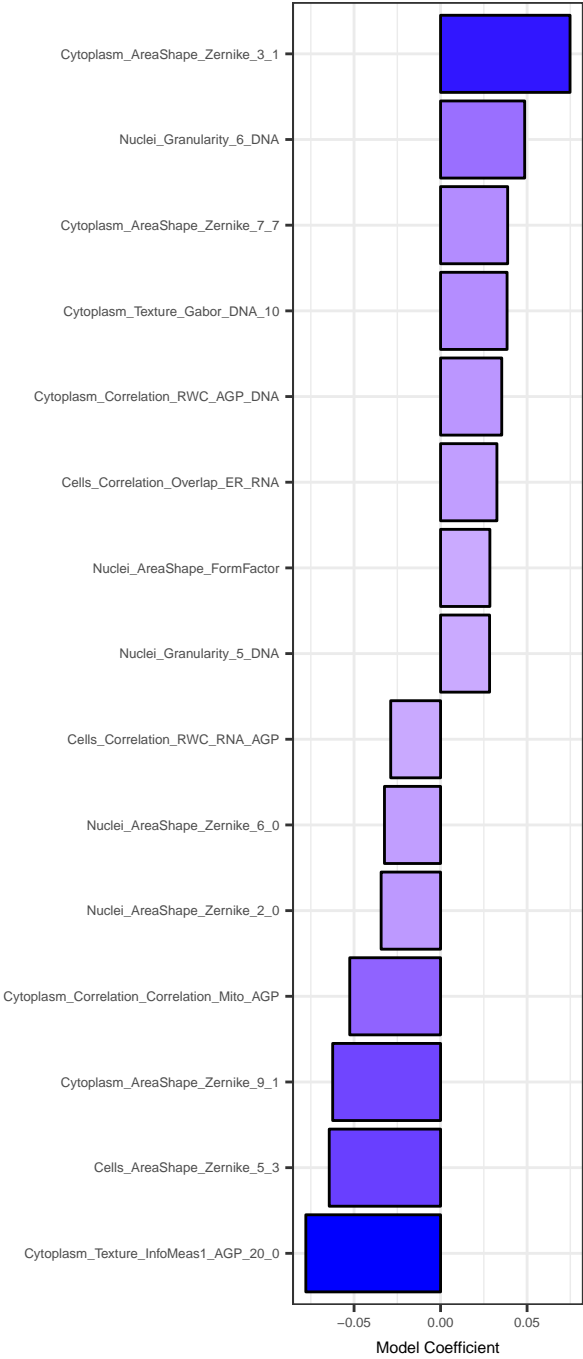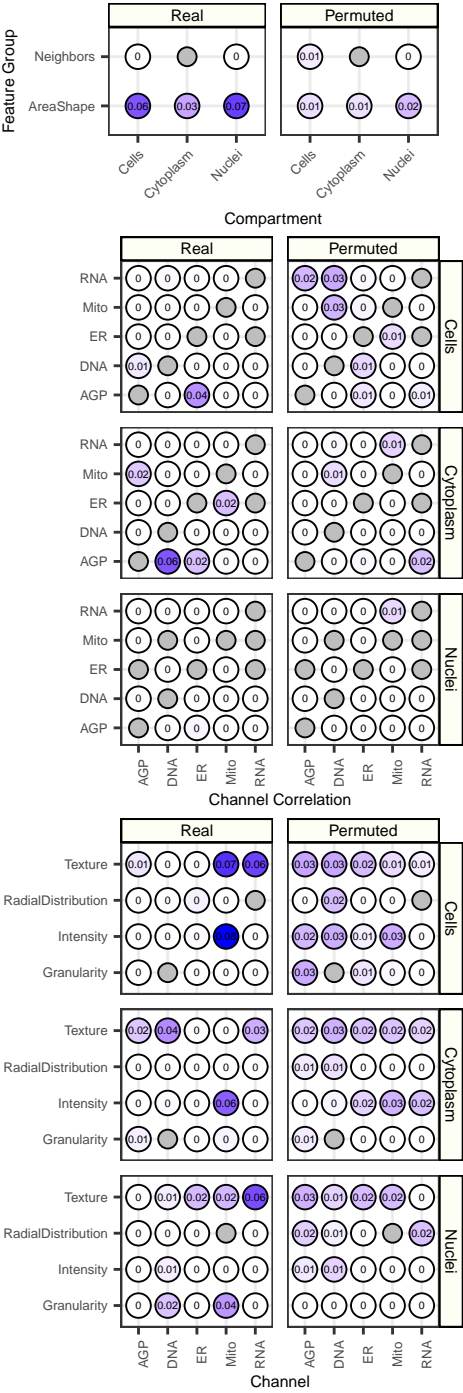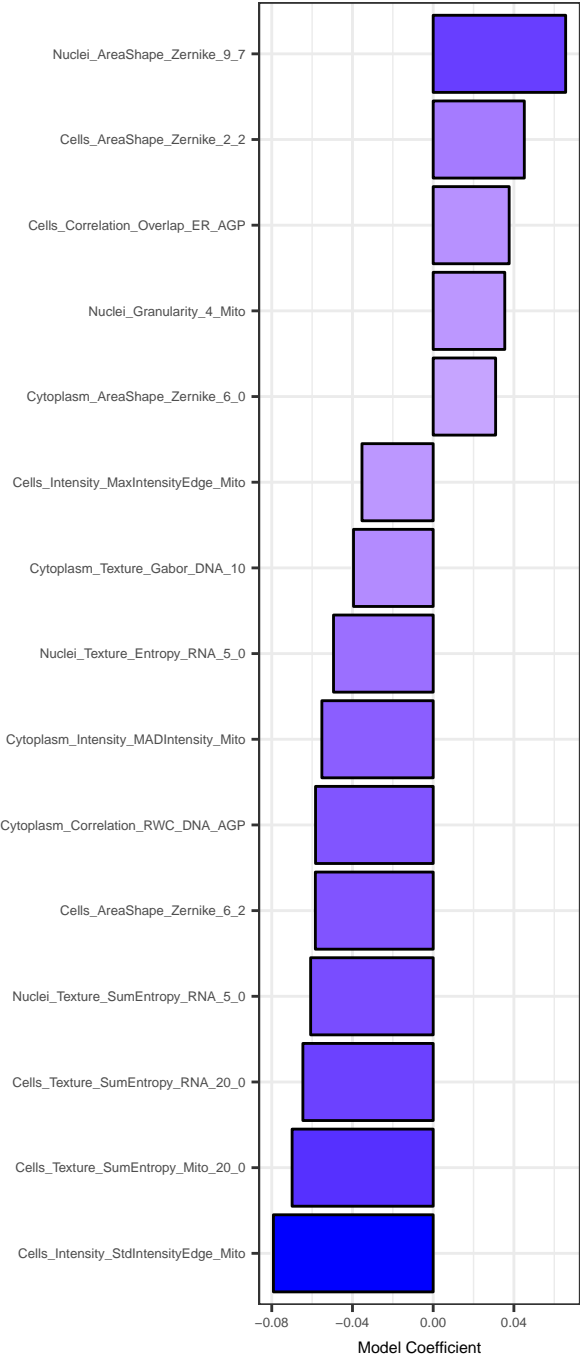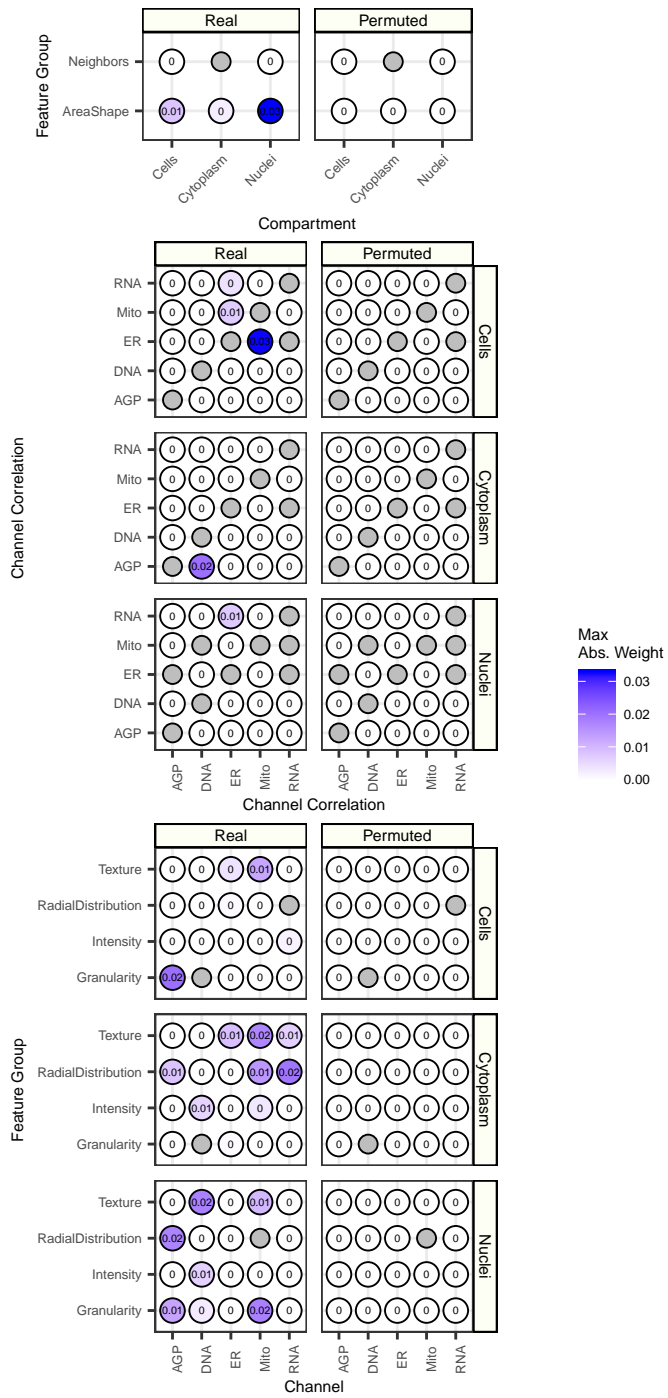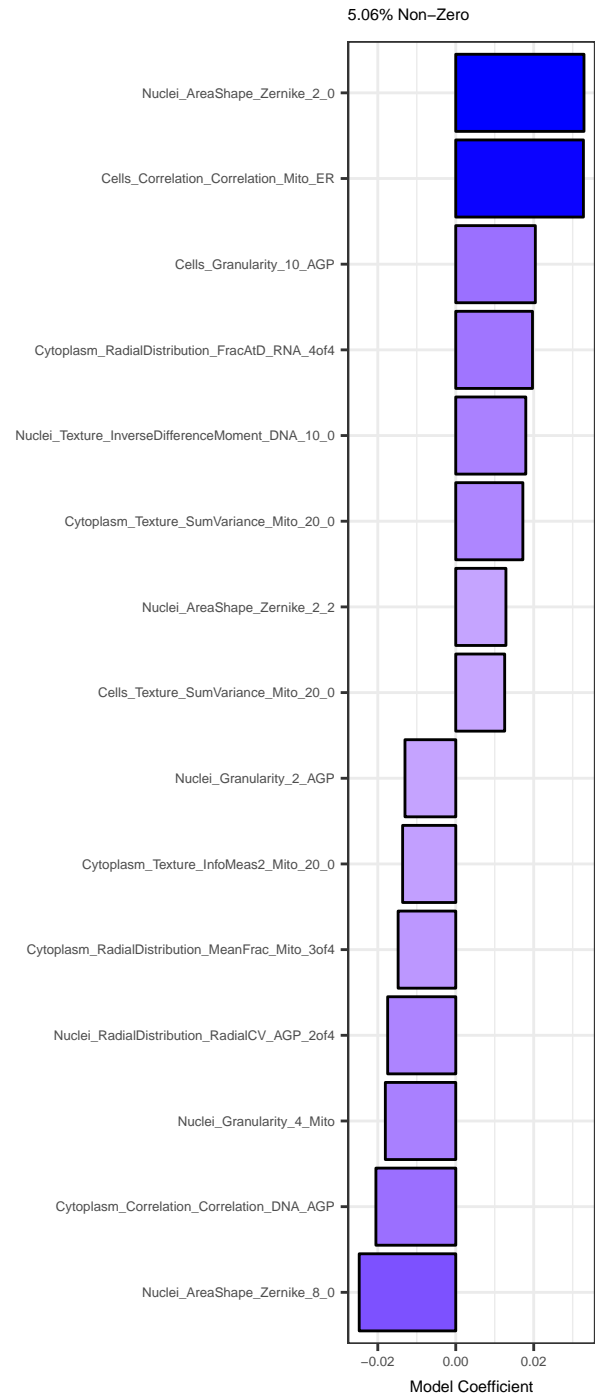
Polynuclear – # of gH2AX Spots per Area of Nucleus
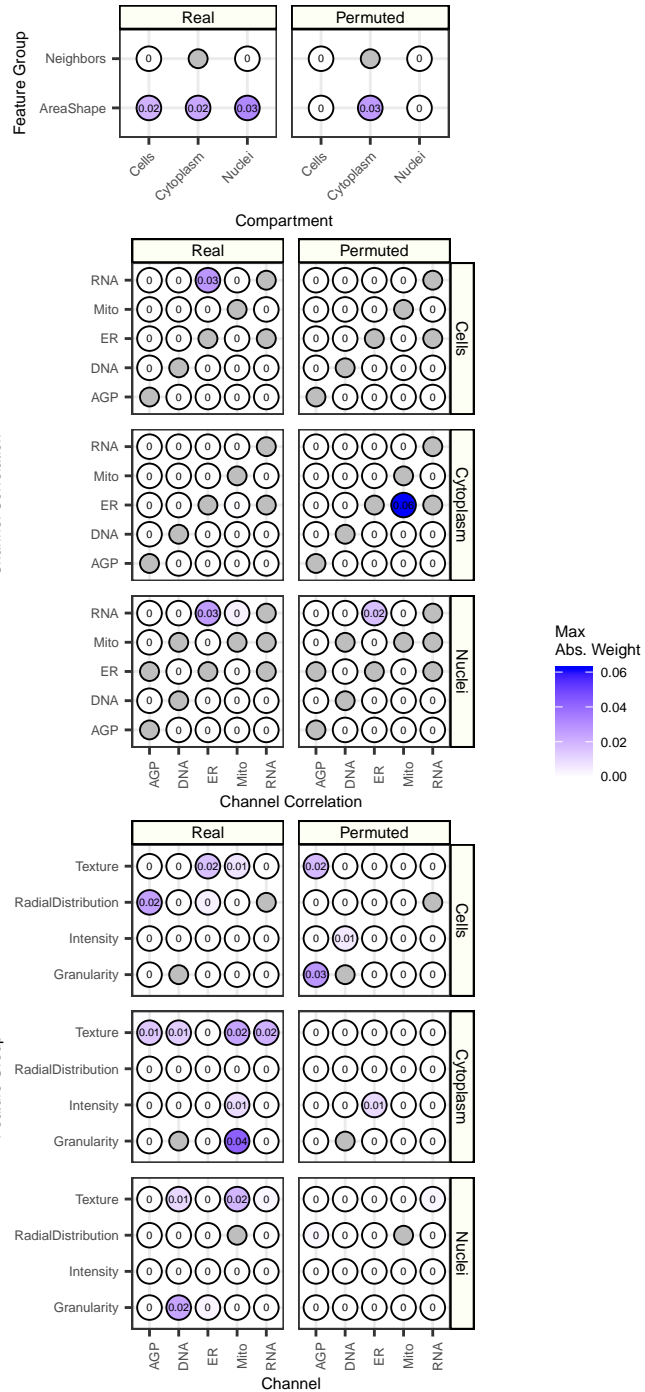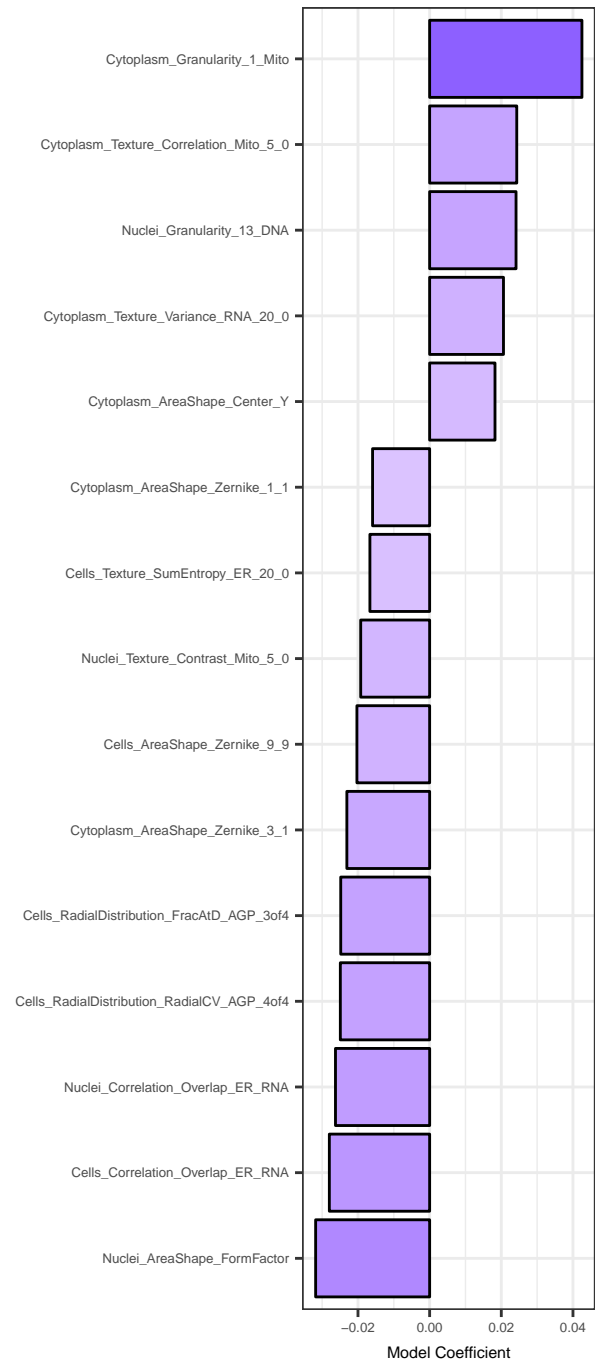
Polyploid − % High gH2AX Spots

Polyploid – # cells

6.95% Non−Zero
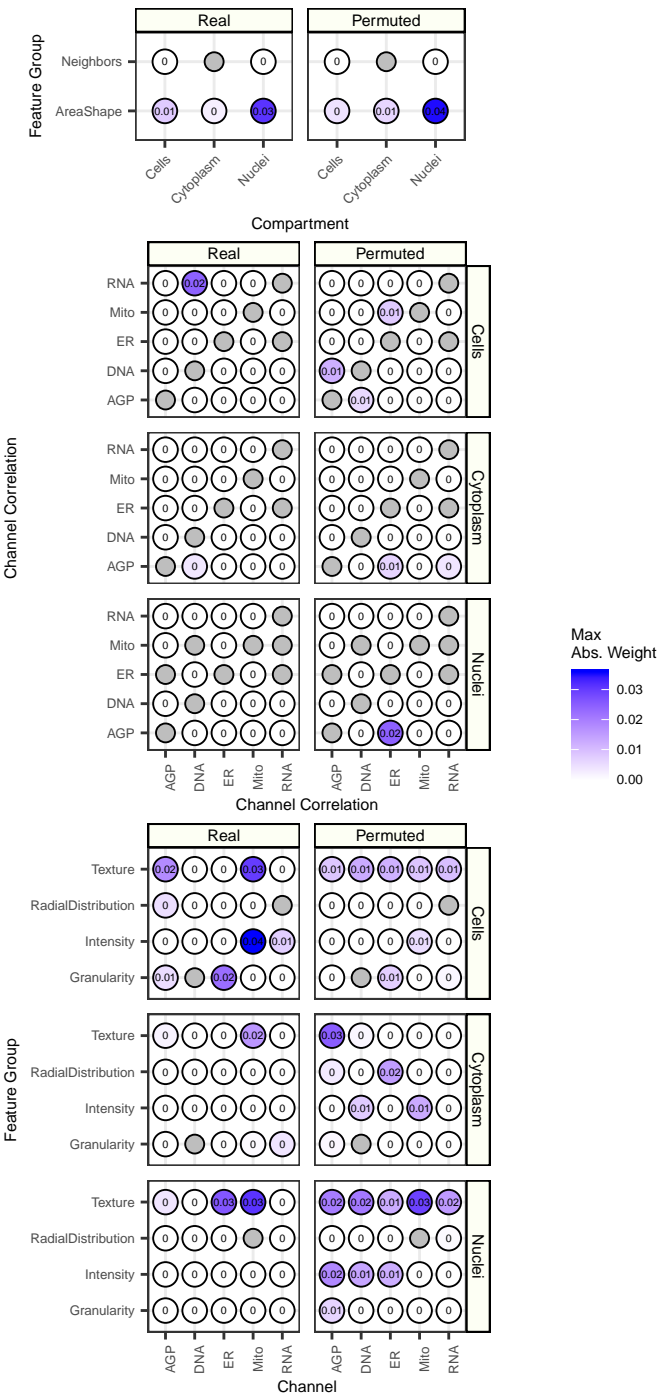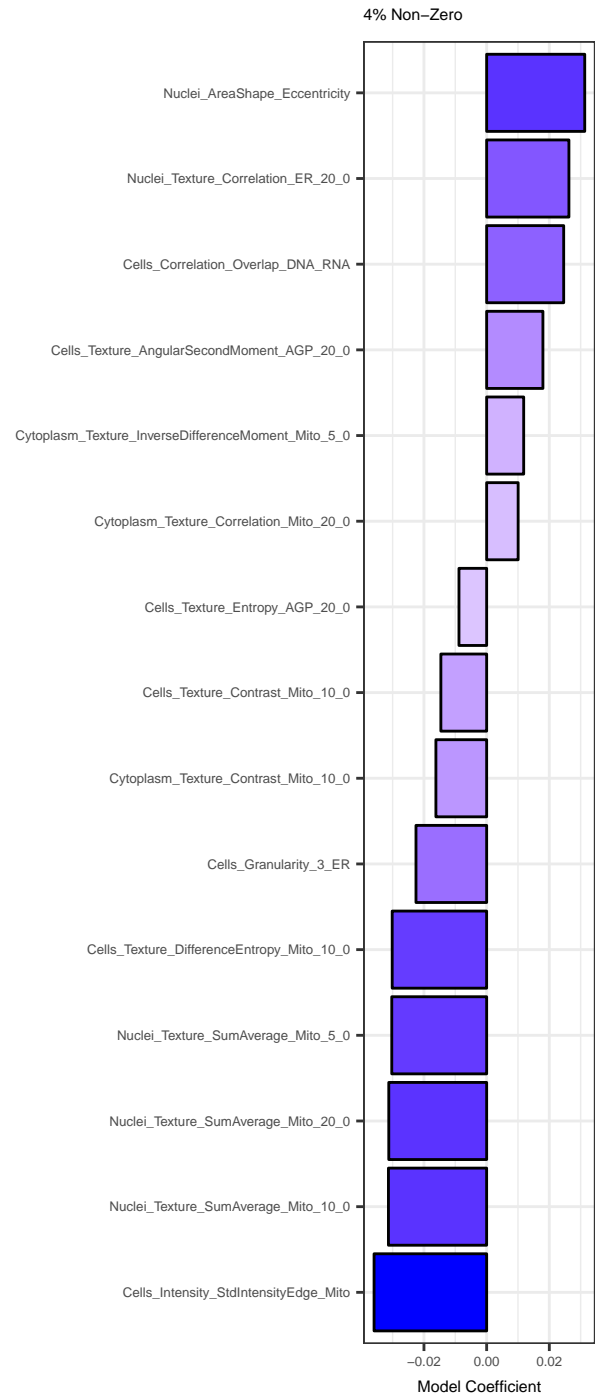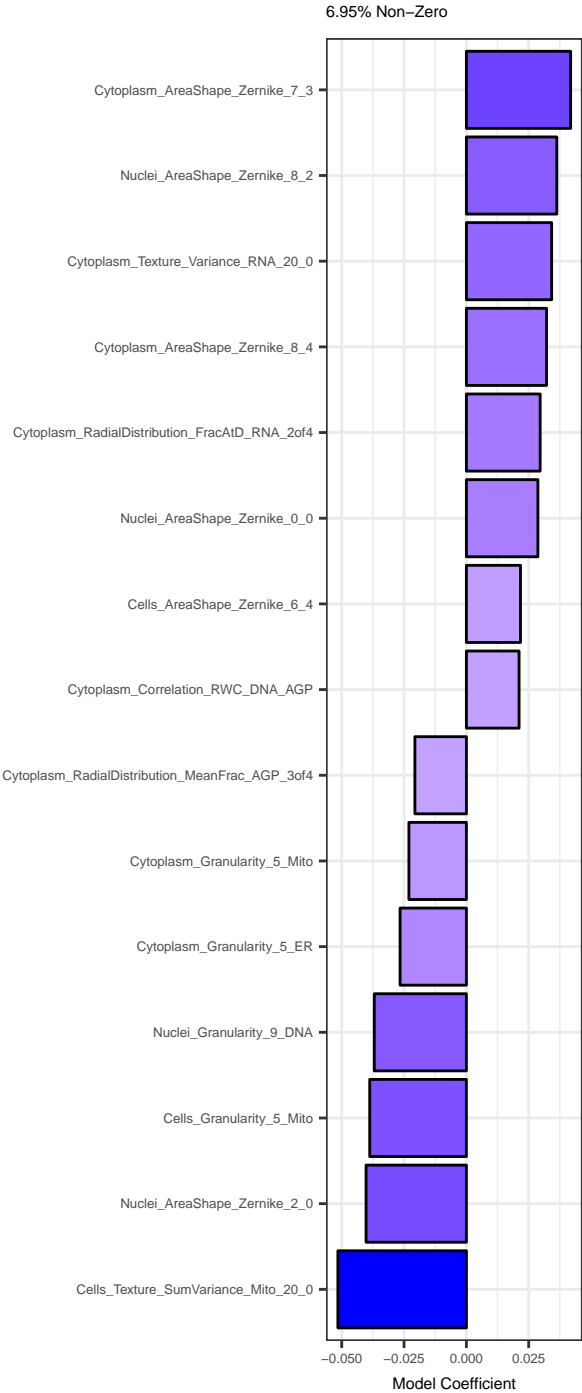
Polyploid – # of gH2AX Spots
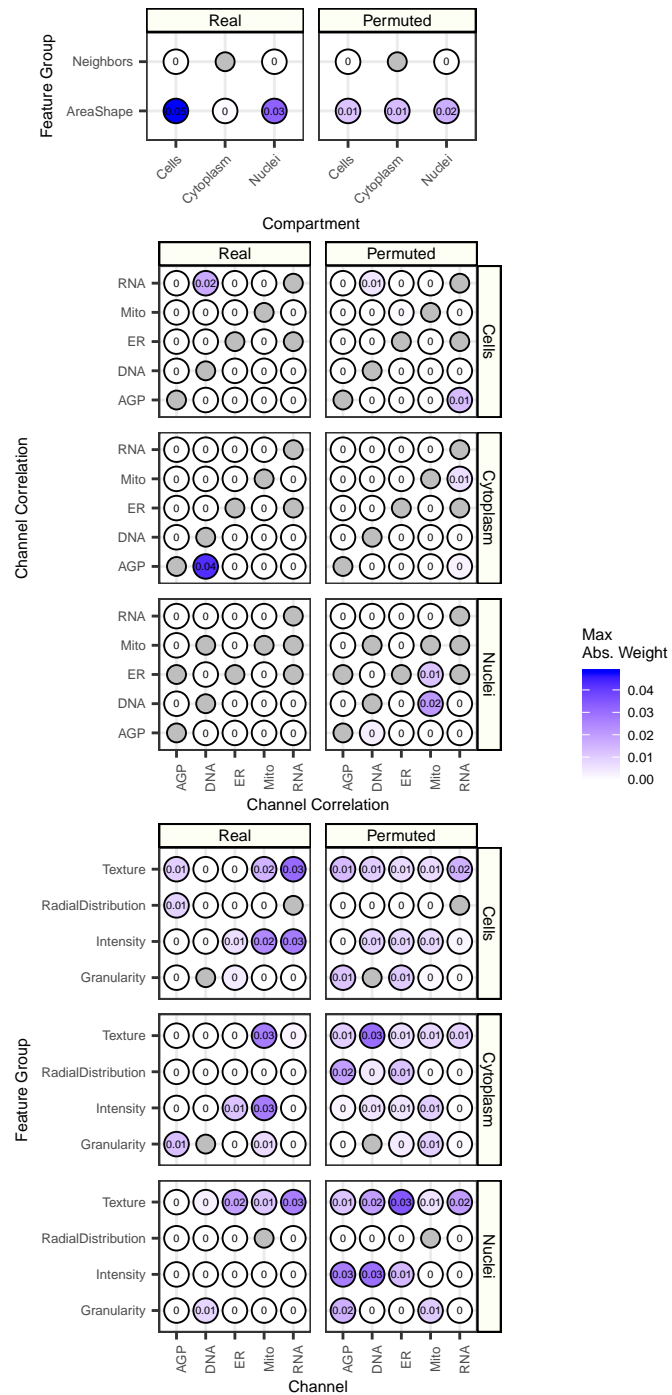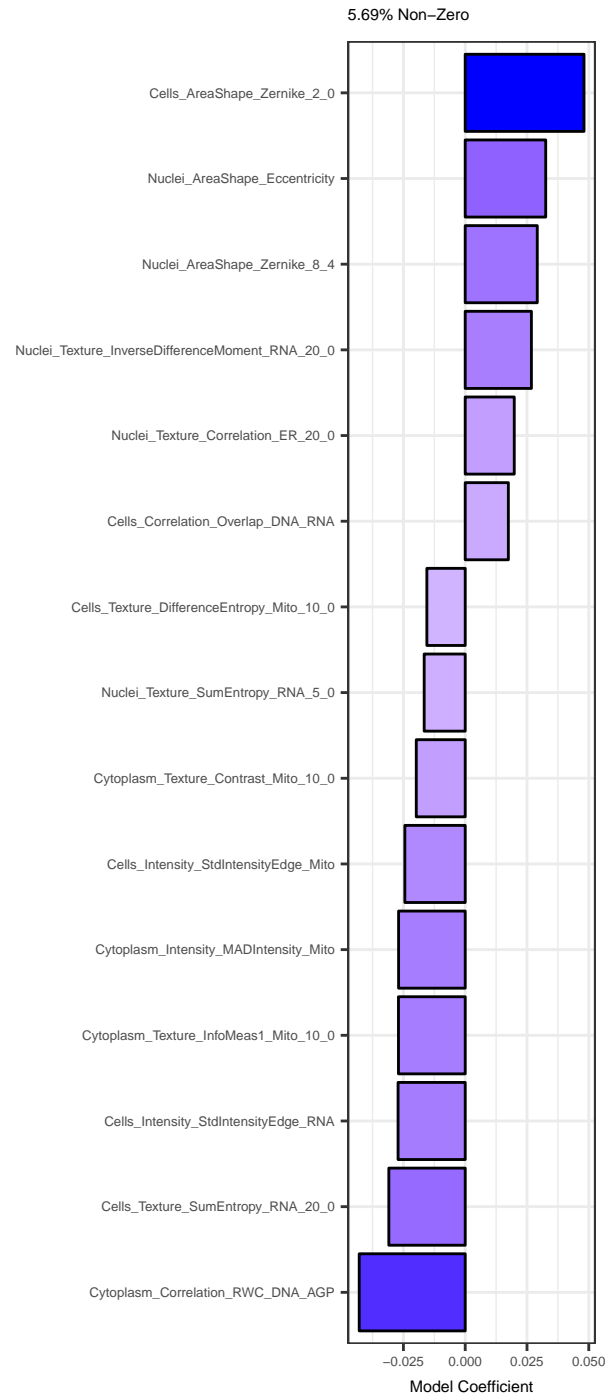
Polyploid – # of gH2AX Spots per Area of Nucleus
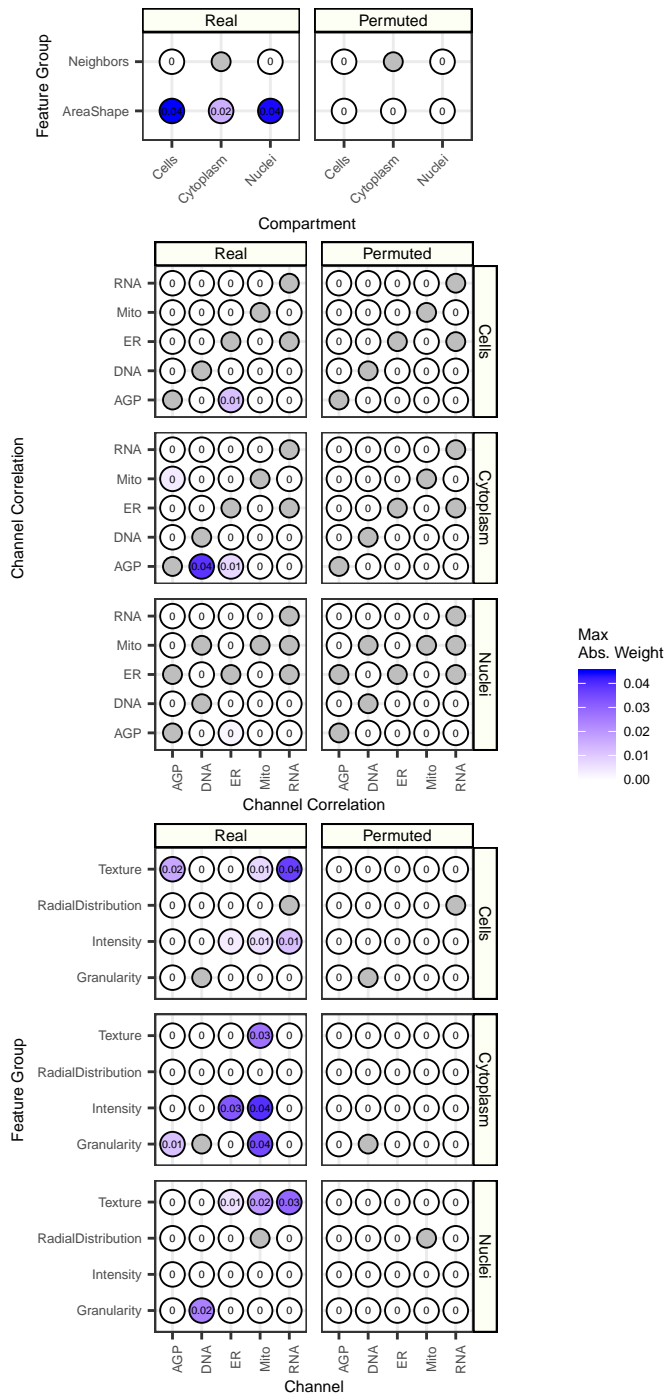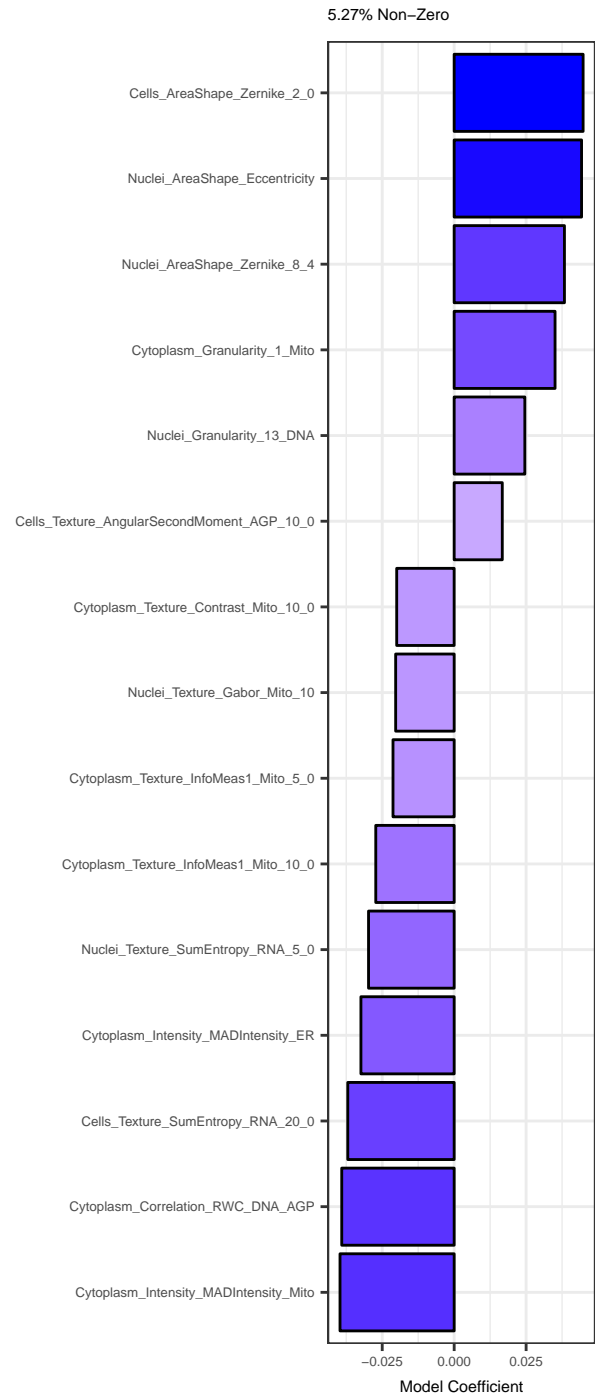
S – % High gH2AX Spots
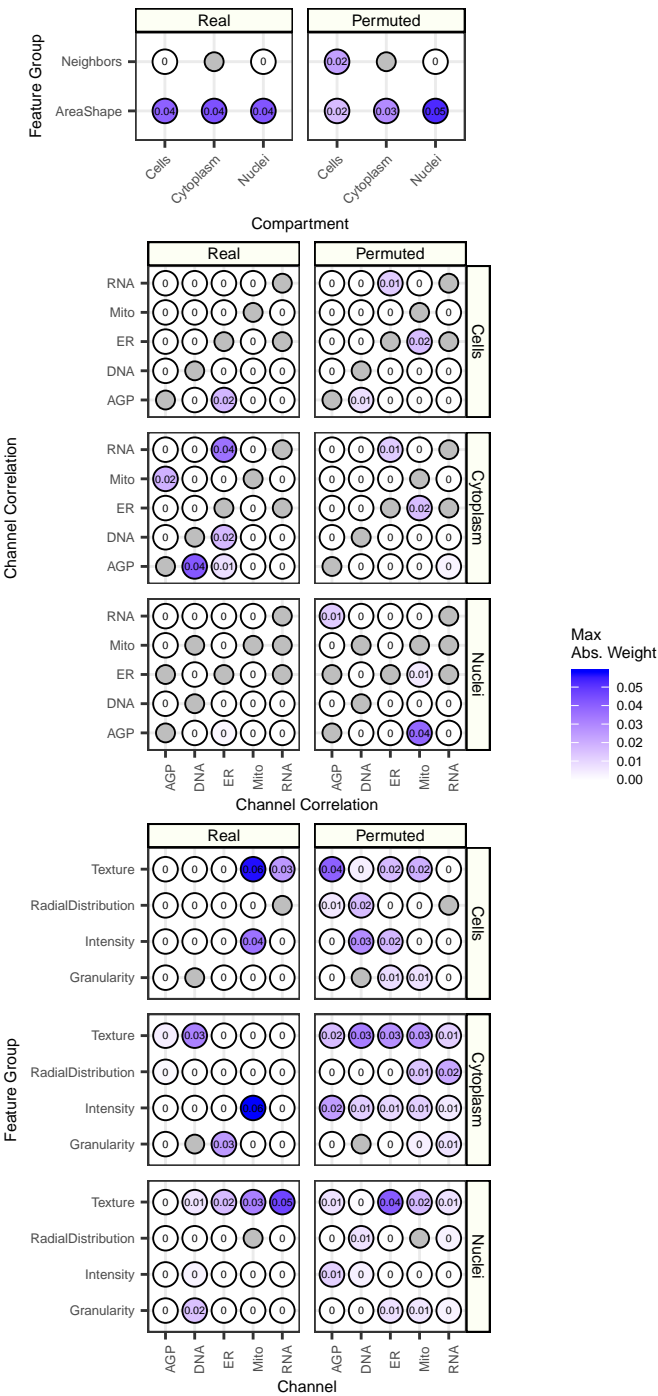
S – Intensity Nucleus EdU Mean
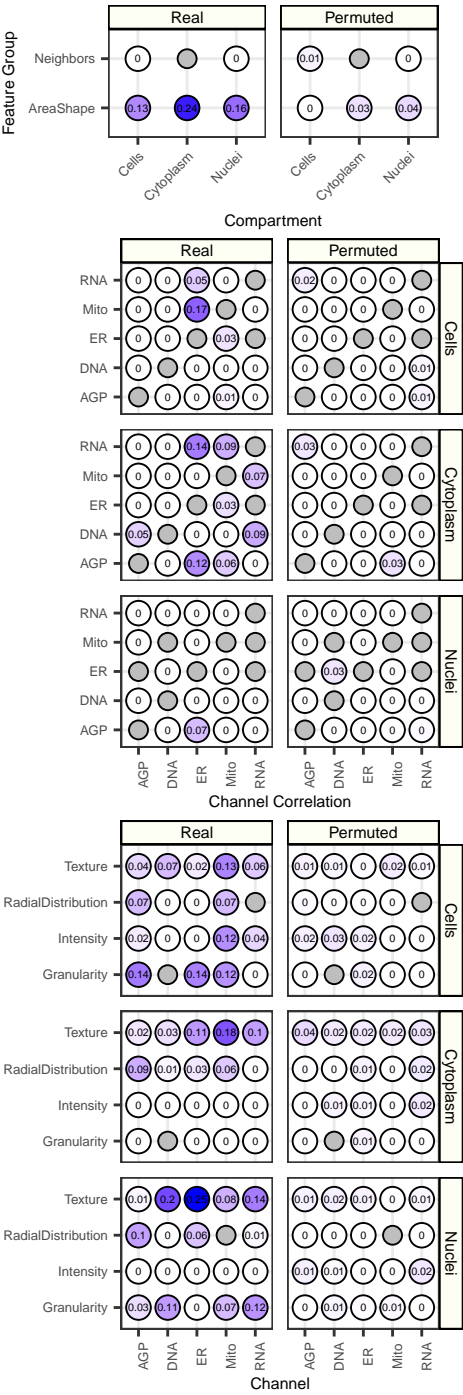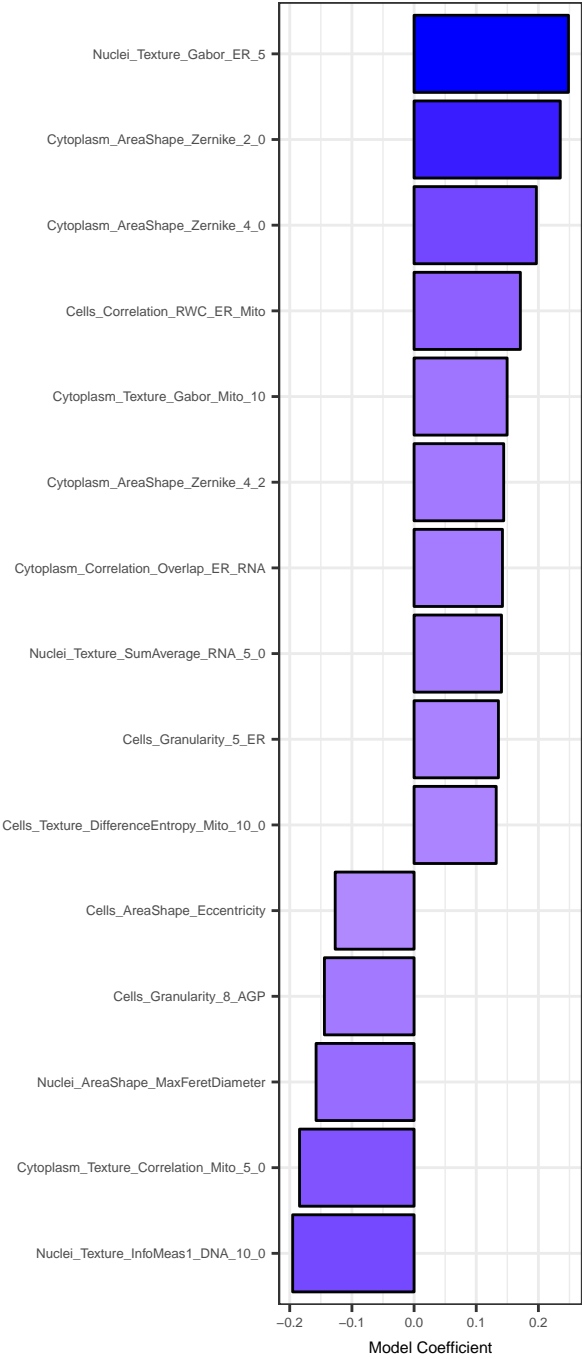
S – Intensity Nucleus EdU Sum

7.9% Non−Zero
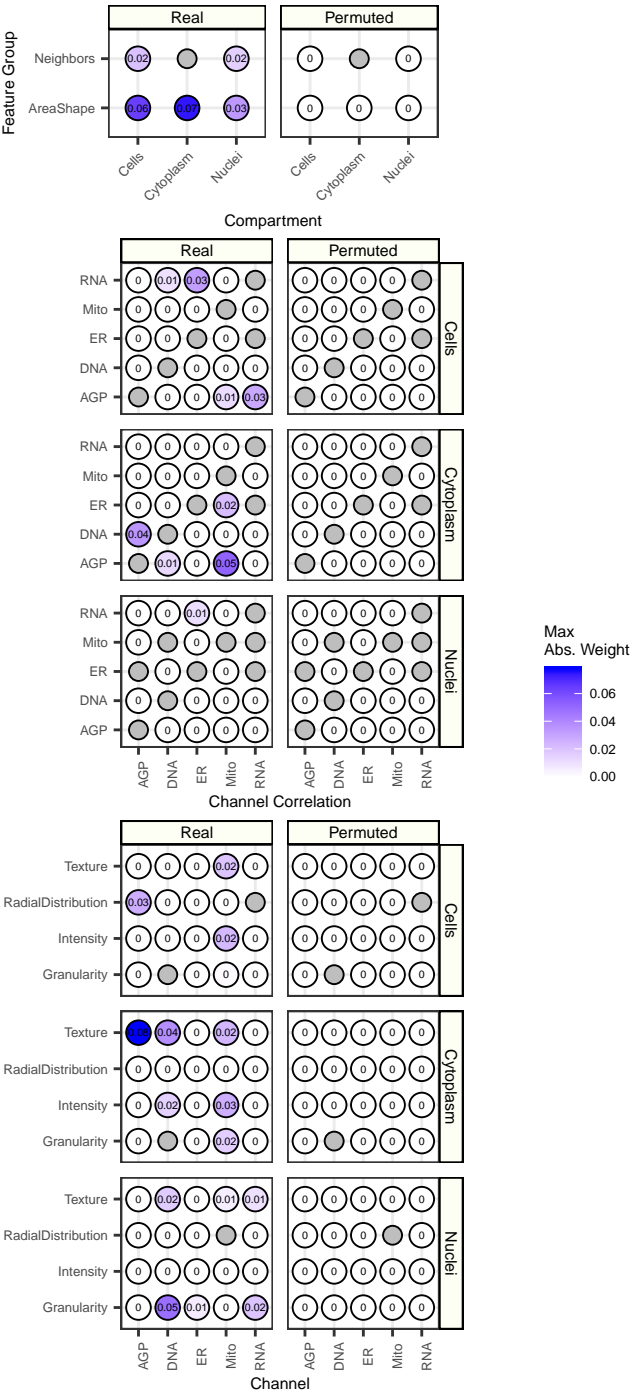
S – # cells
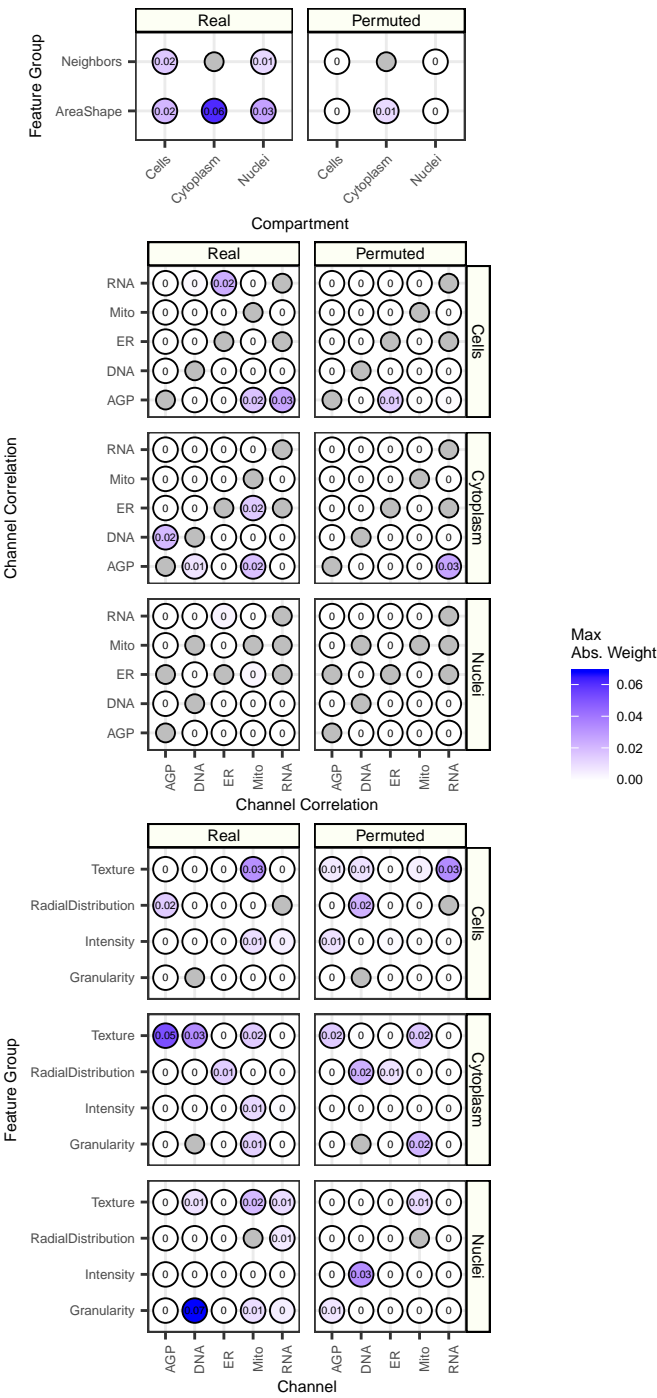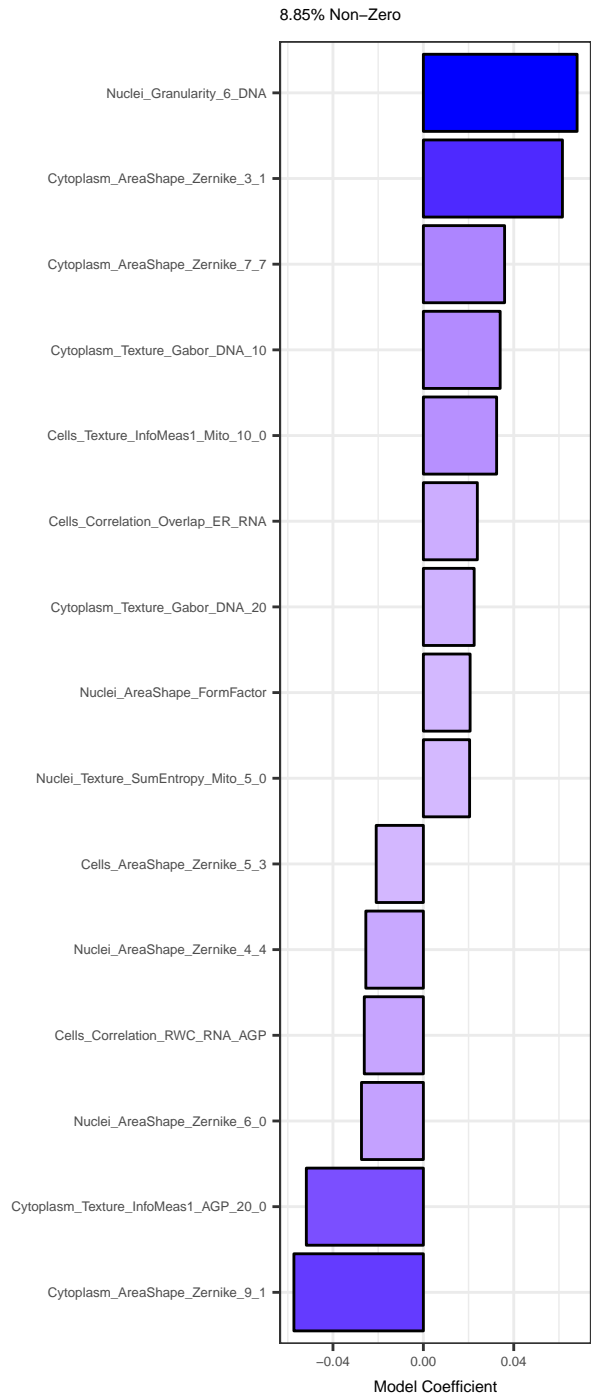
8.85% Non−Zero

S – # of gH2AX Spots
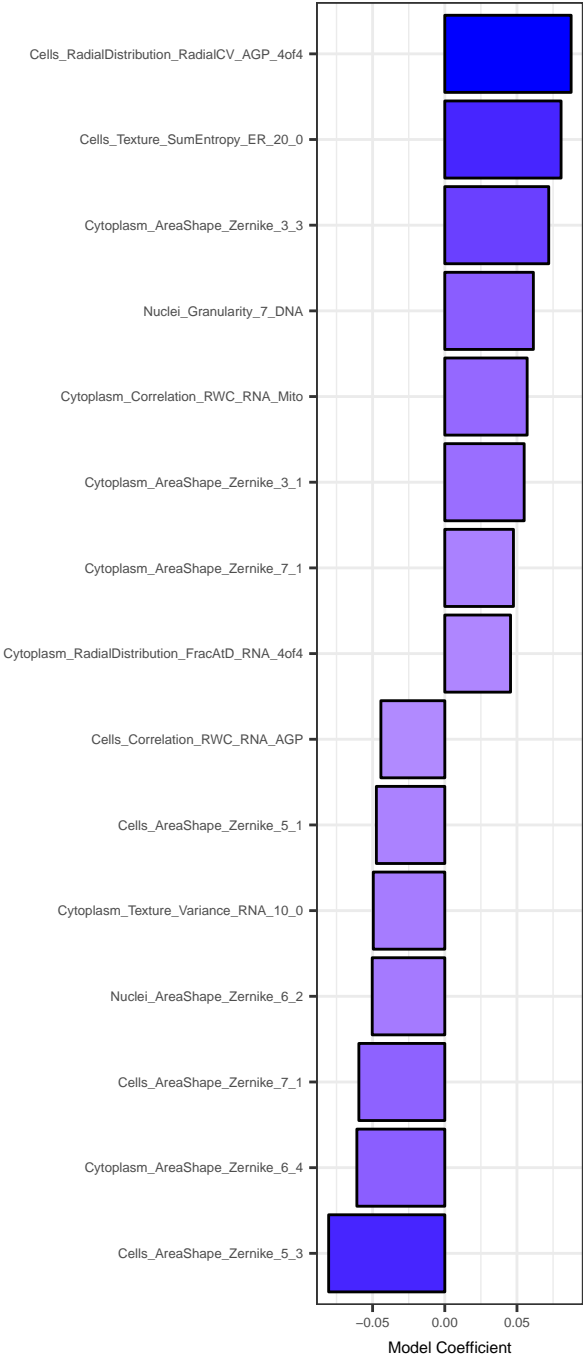
S – # of gH2AX Spots per Area of Nucleus

% Inf

5.06% Non−Zero
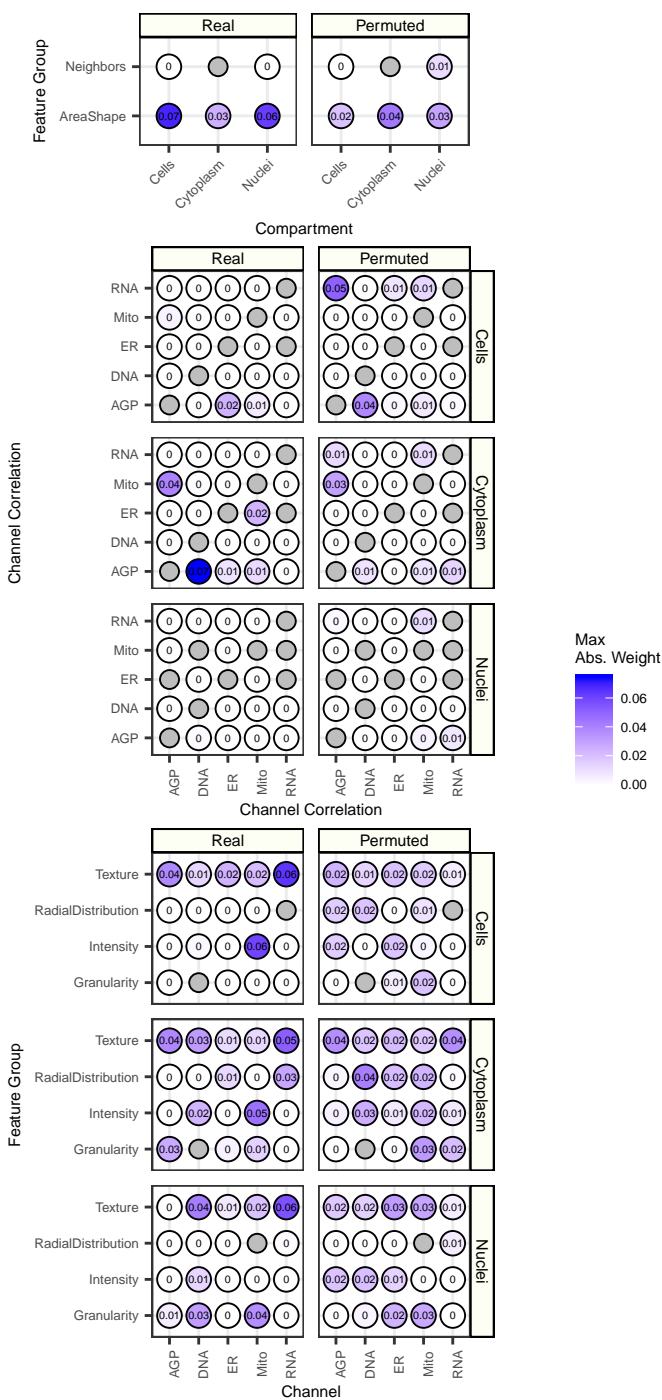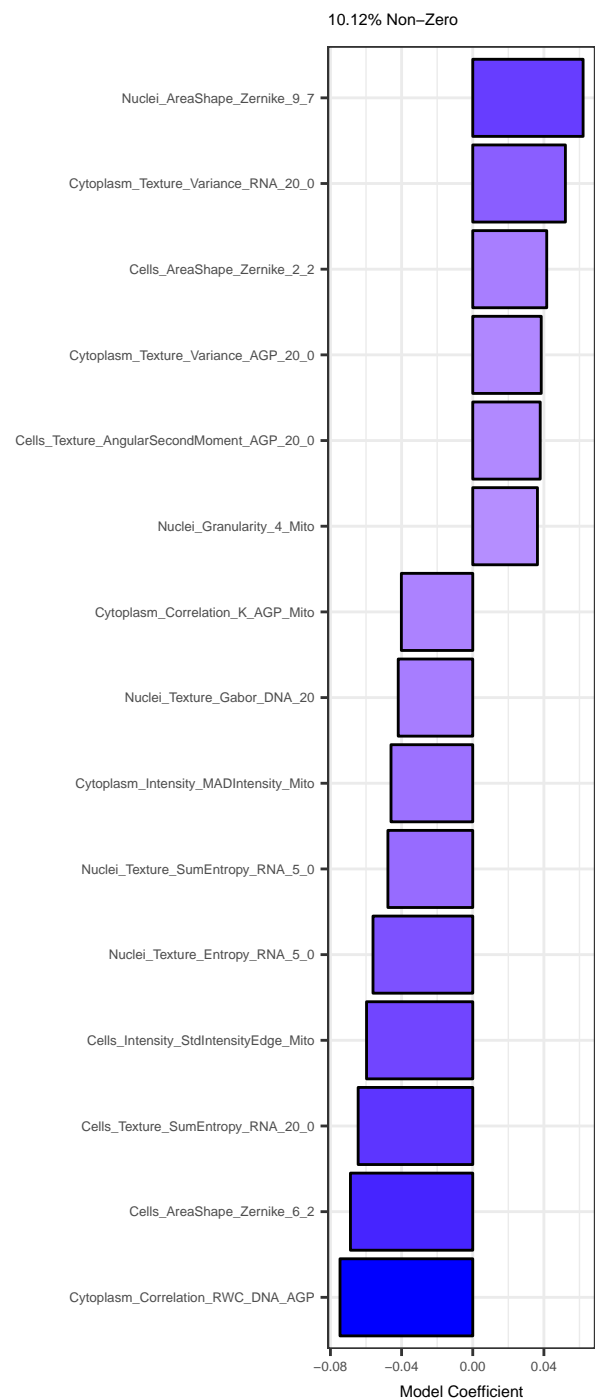
Live Cell Area
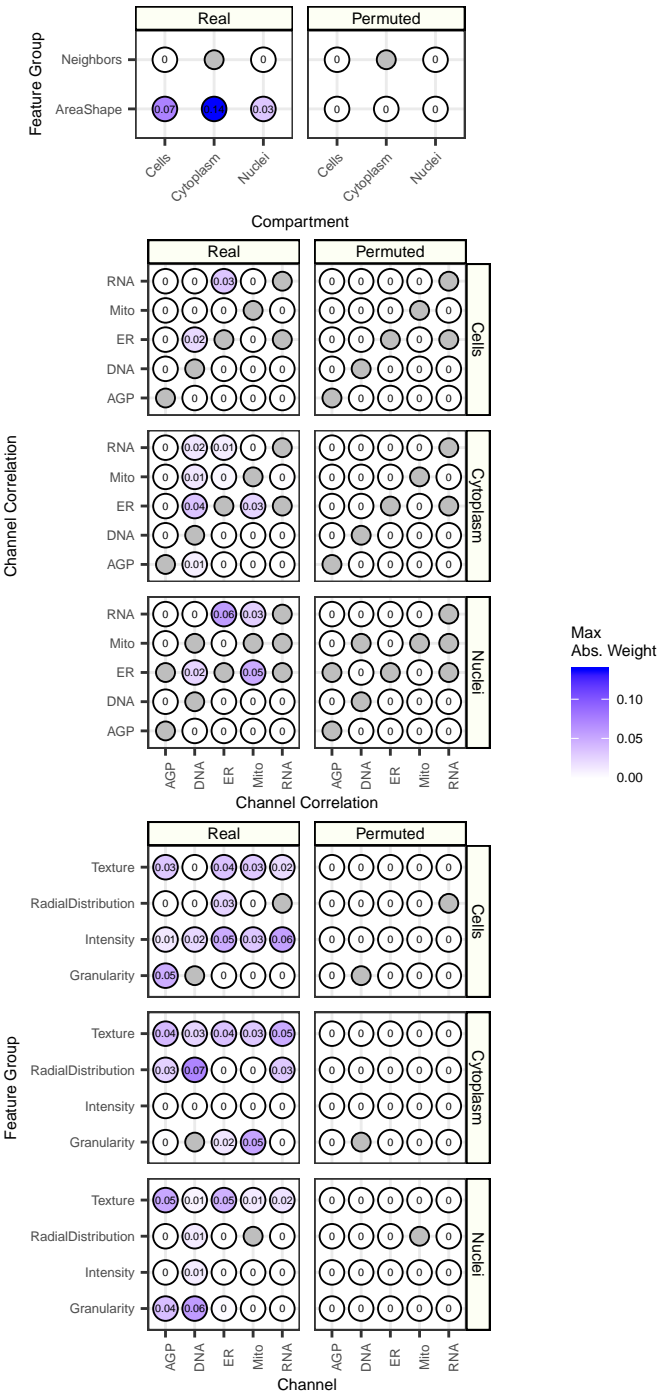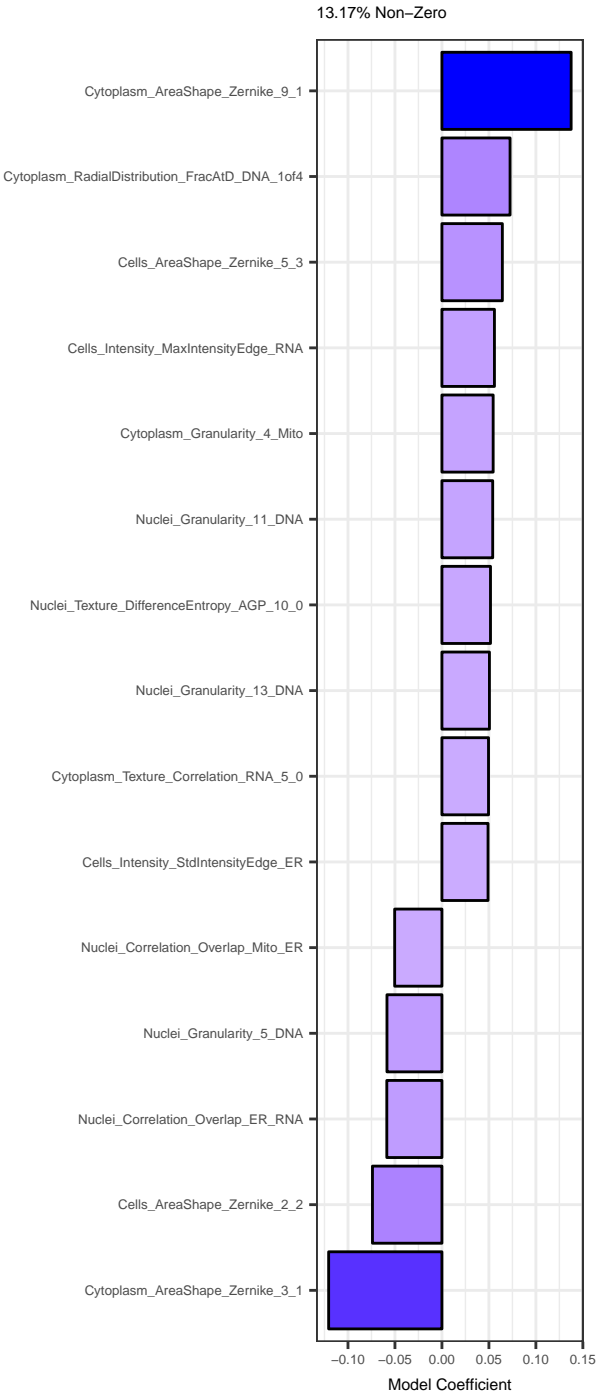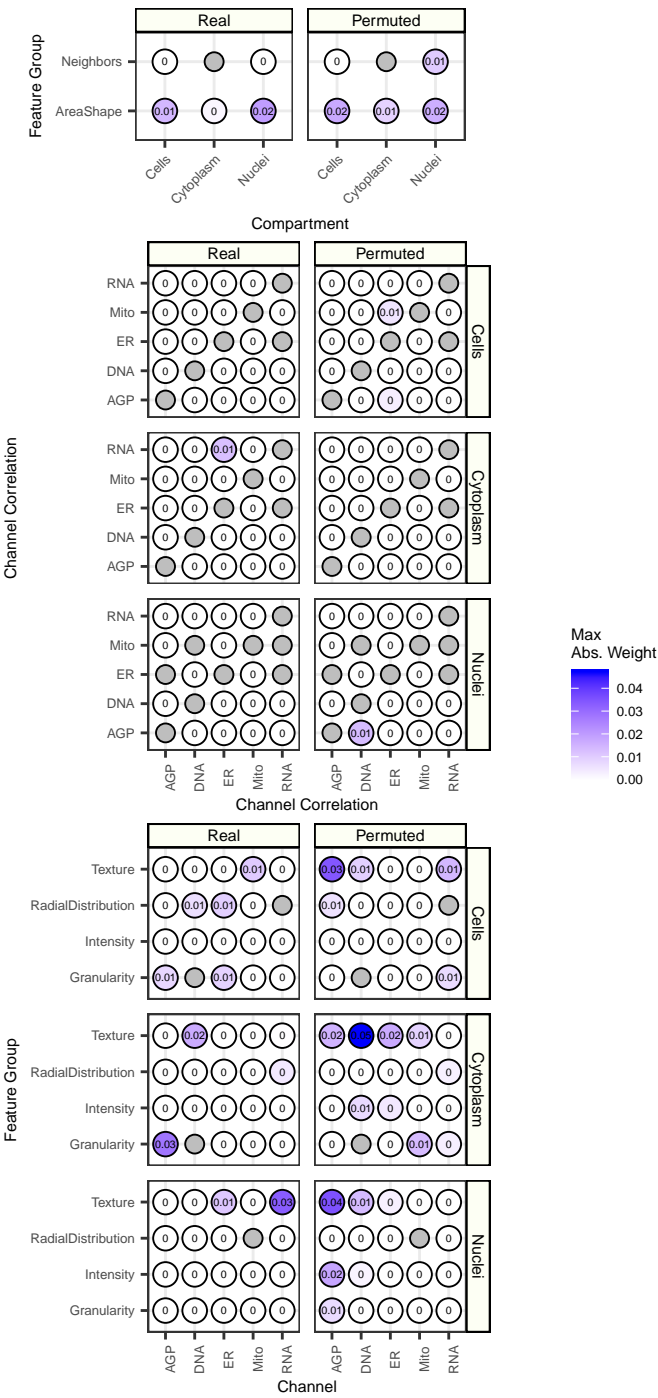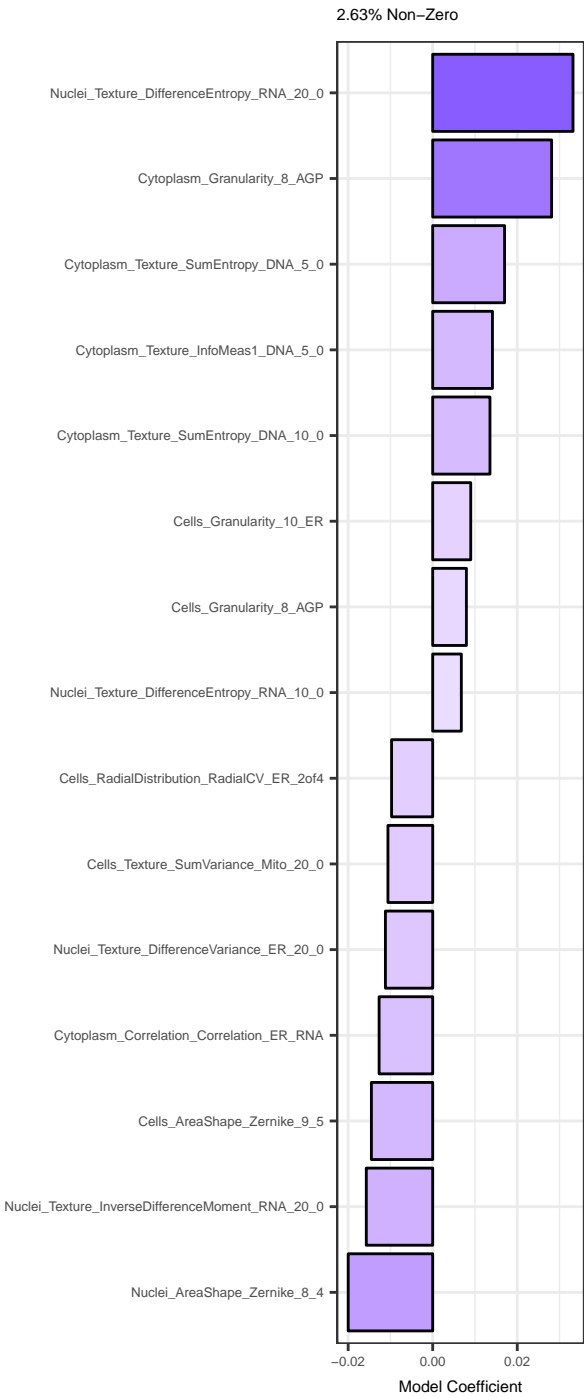
Live Cell Roundness

Live Width / Length
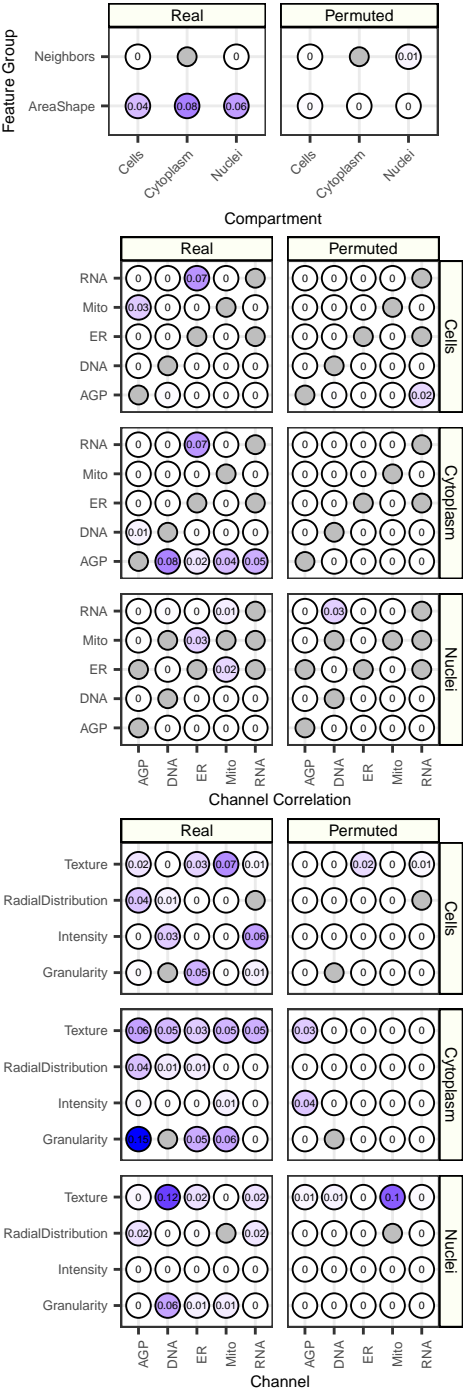
Live Cells

12.96% Non-Zero
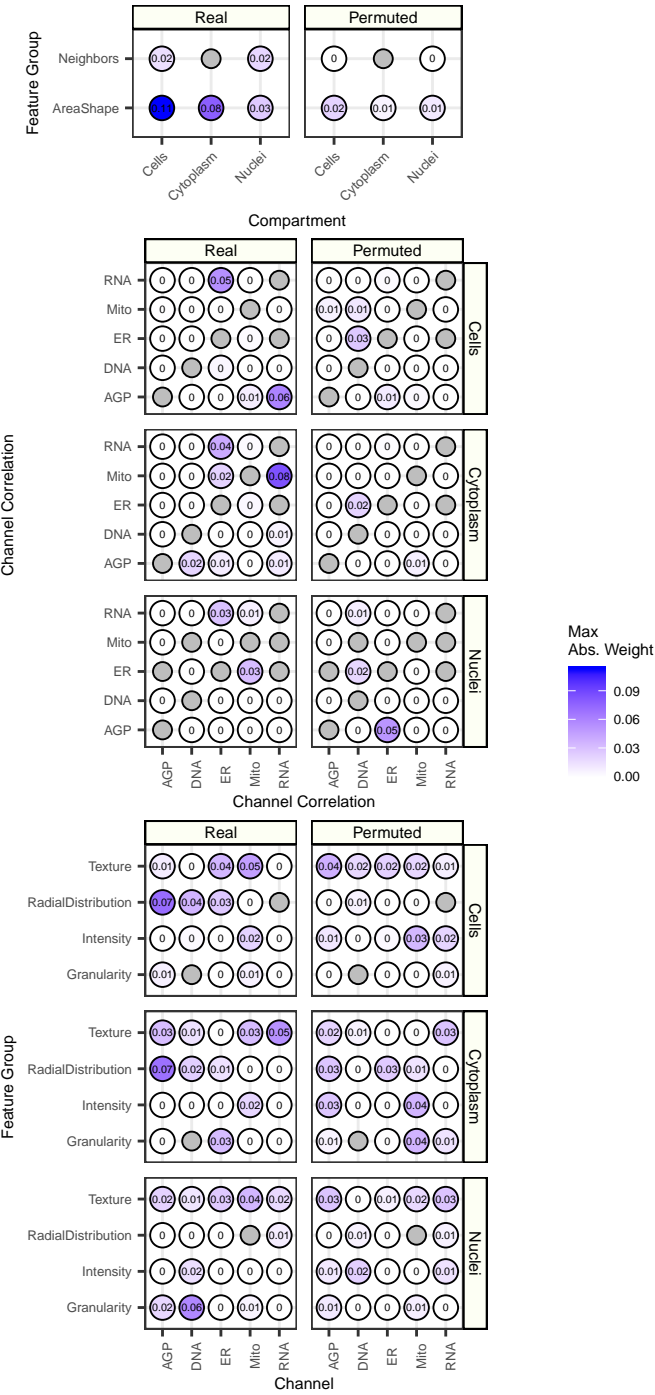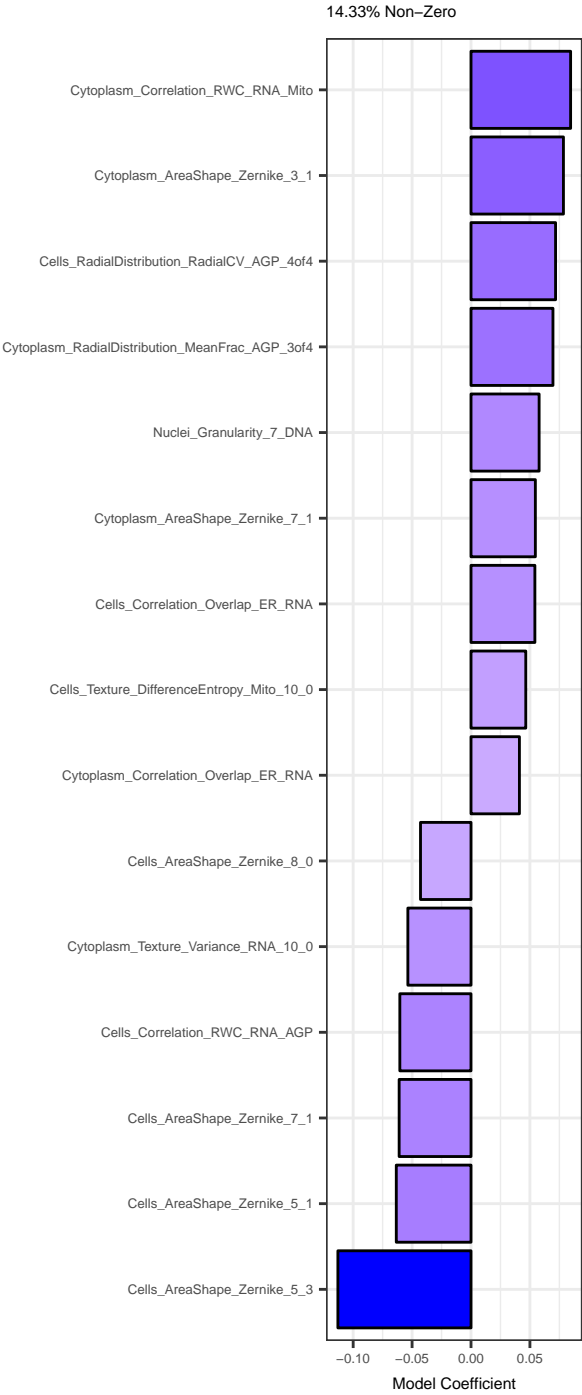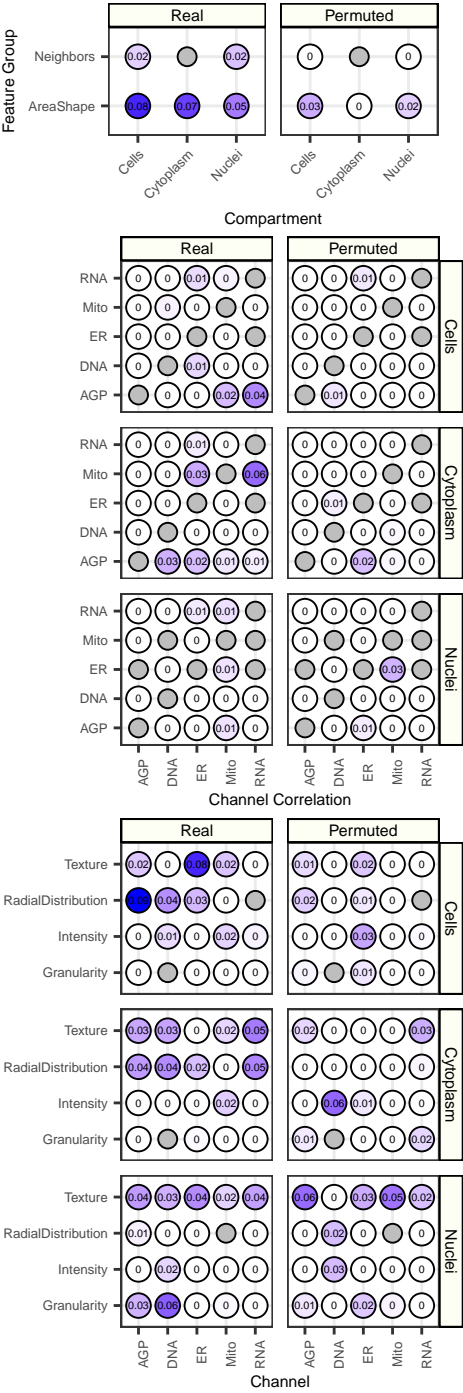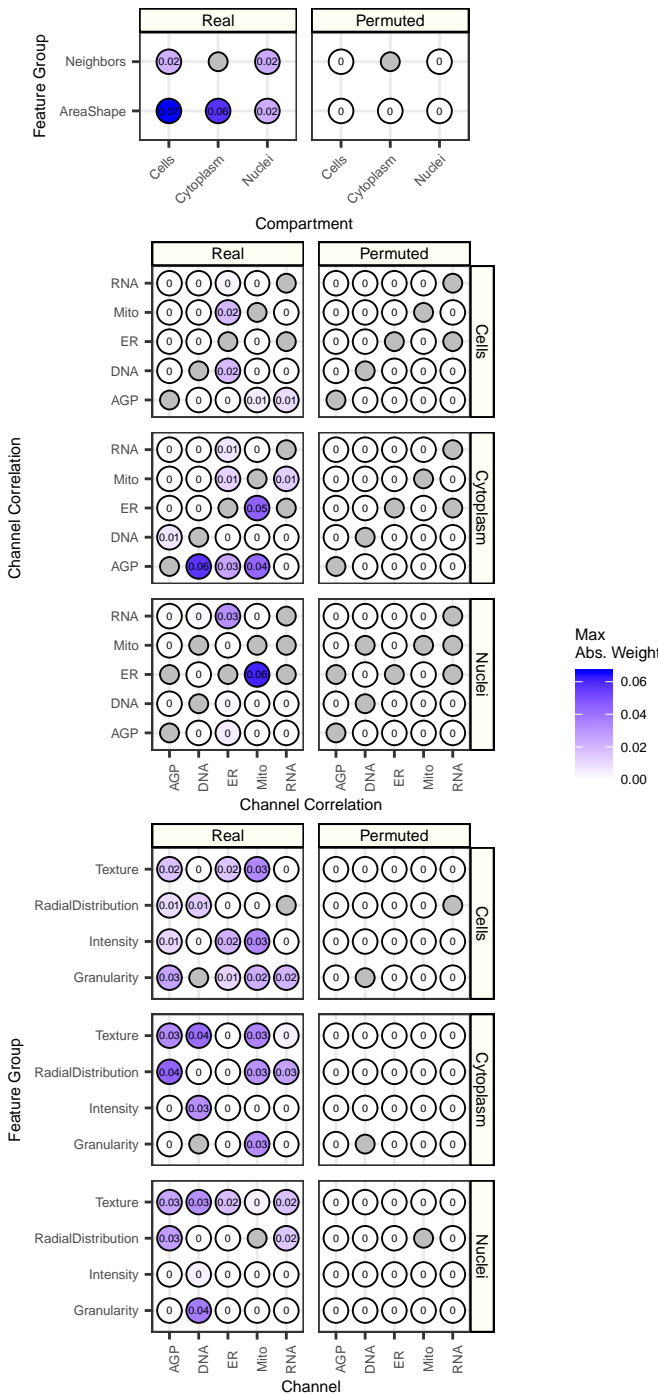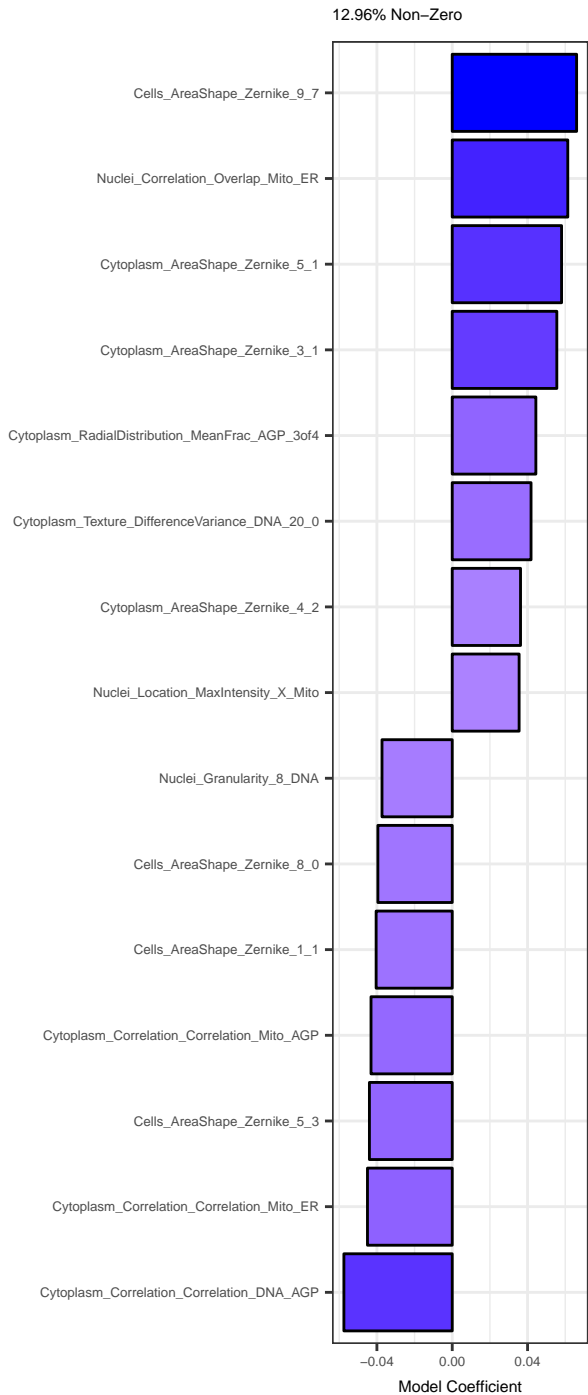
% All Apoptosis (CASP+)
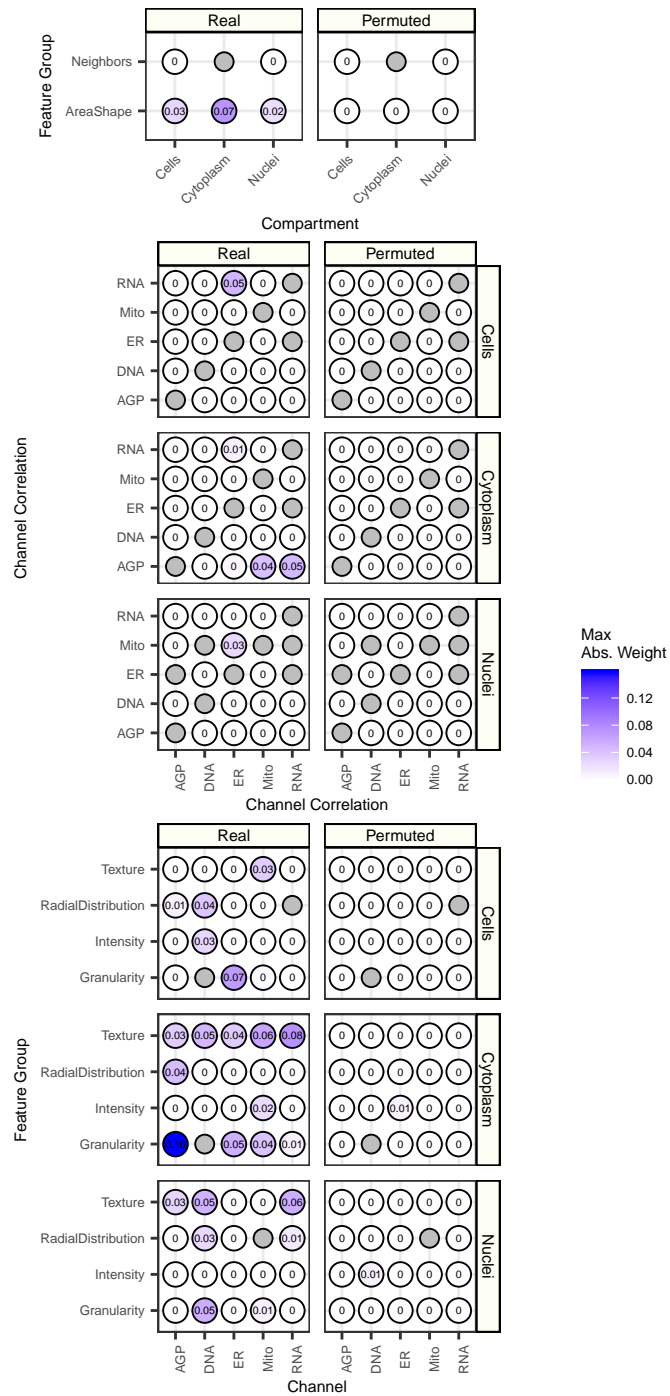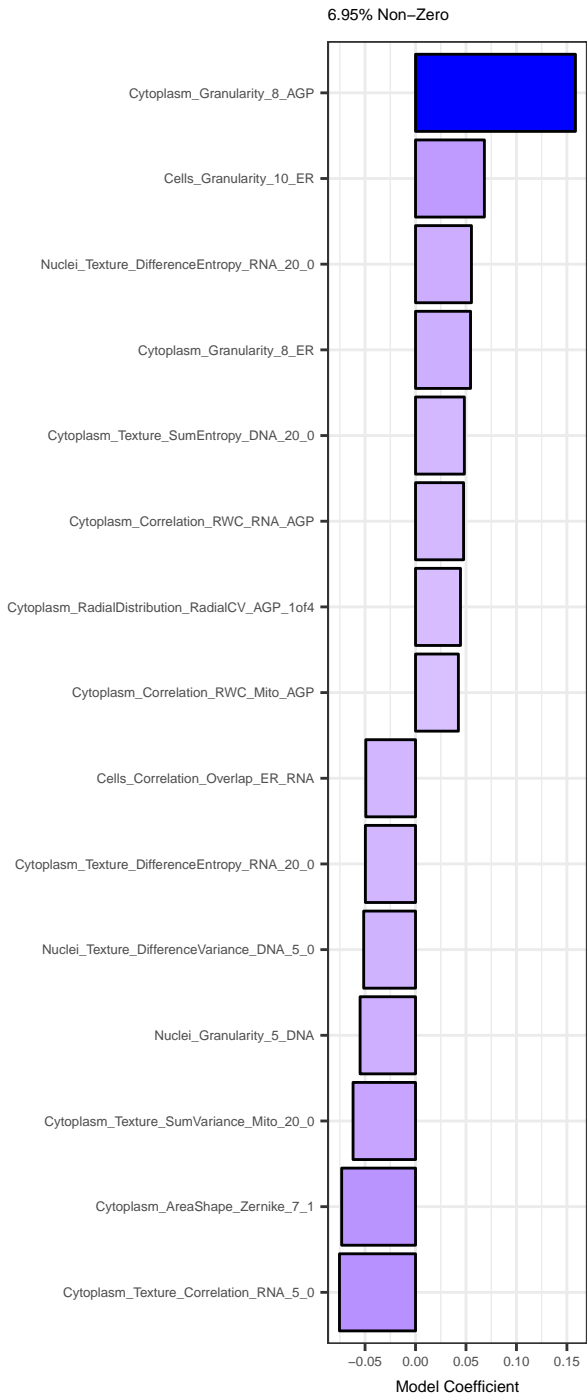
% Caspase / % Dead Only

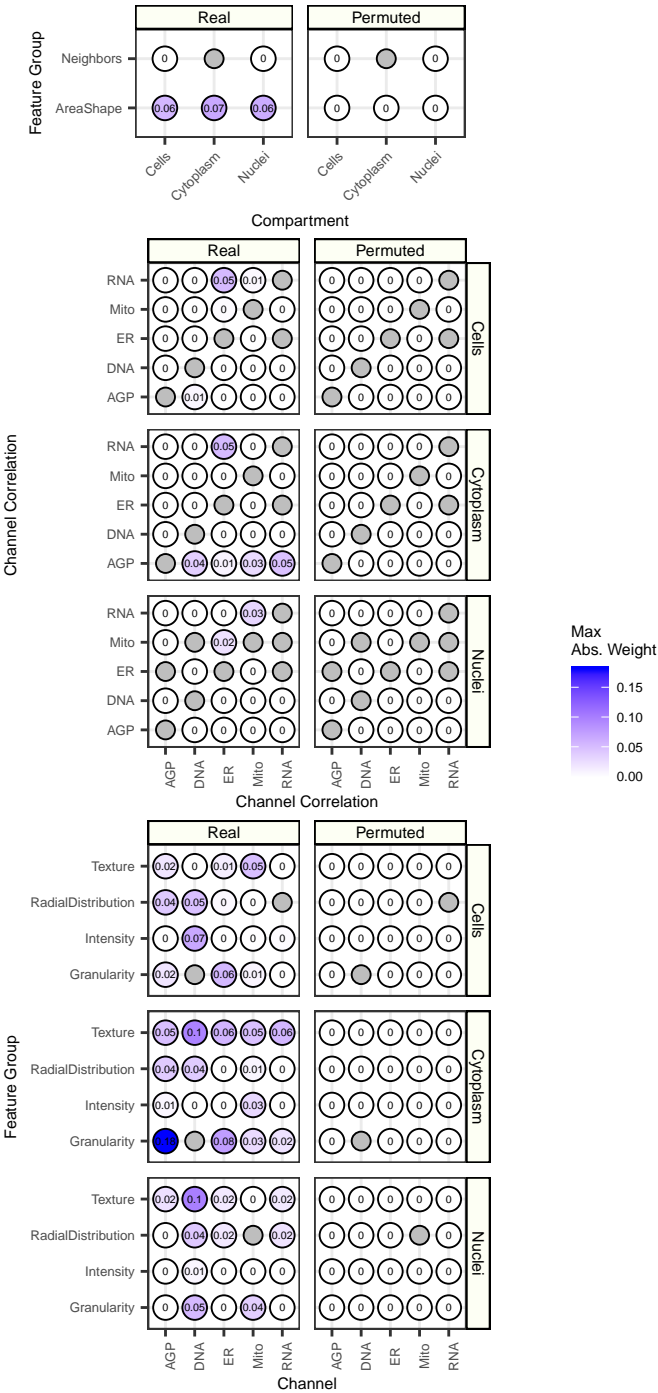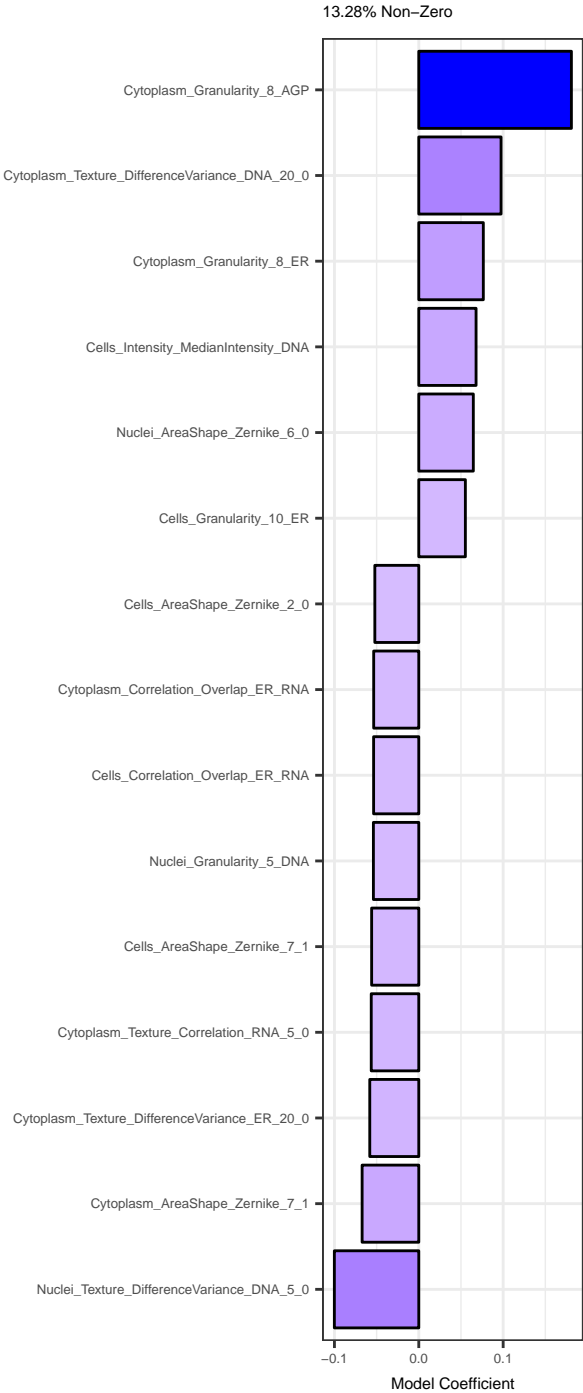# % All Dead (DRAQ7+)
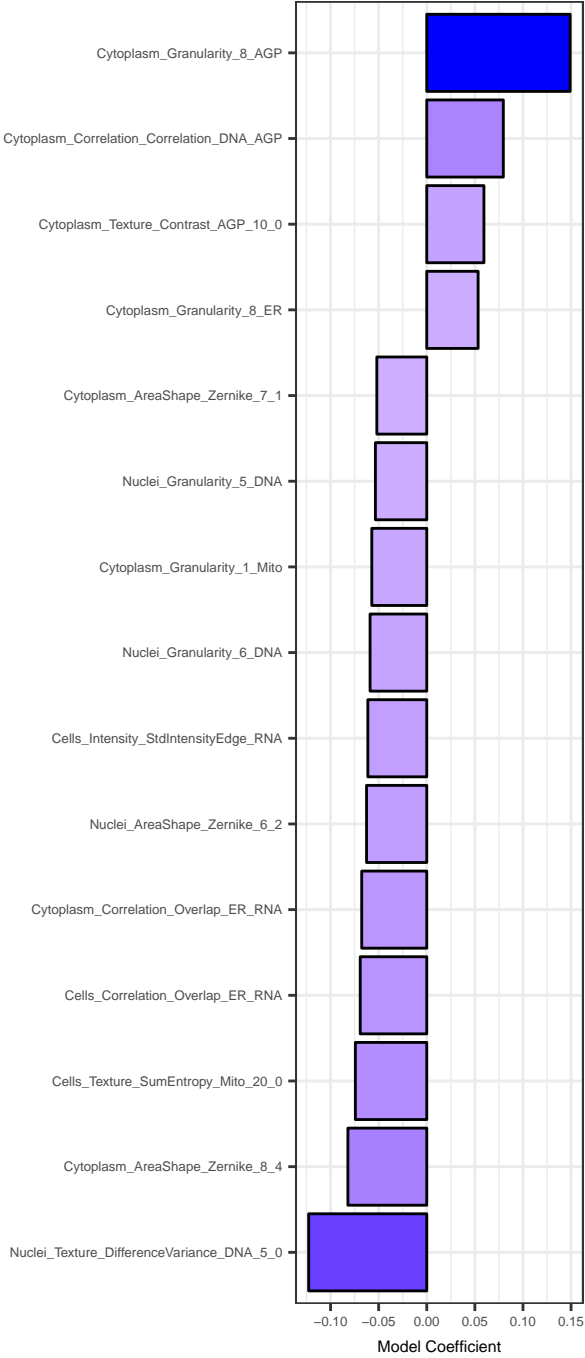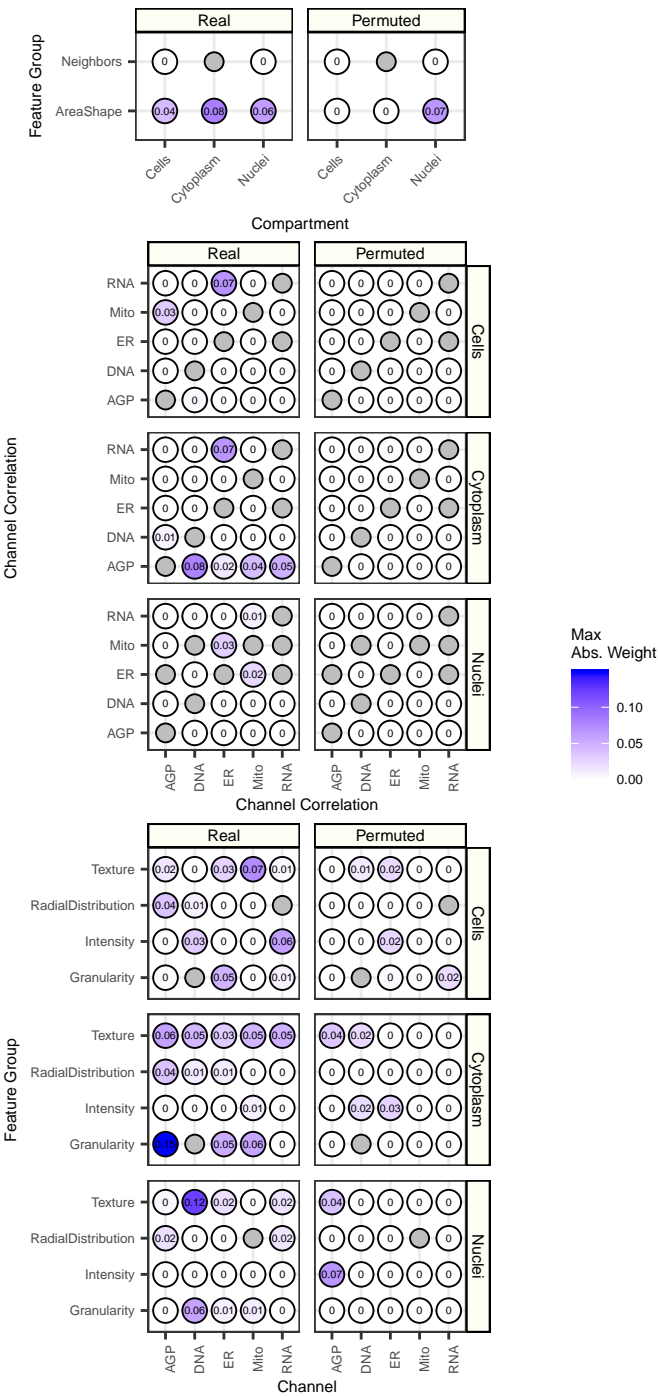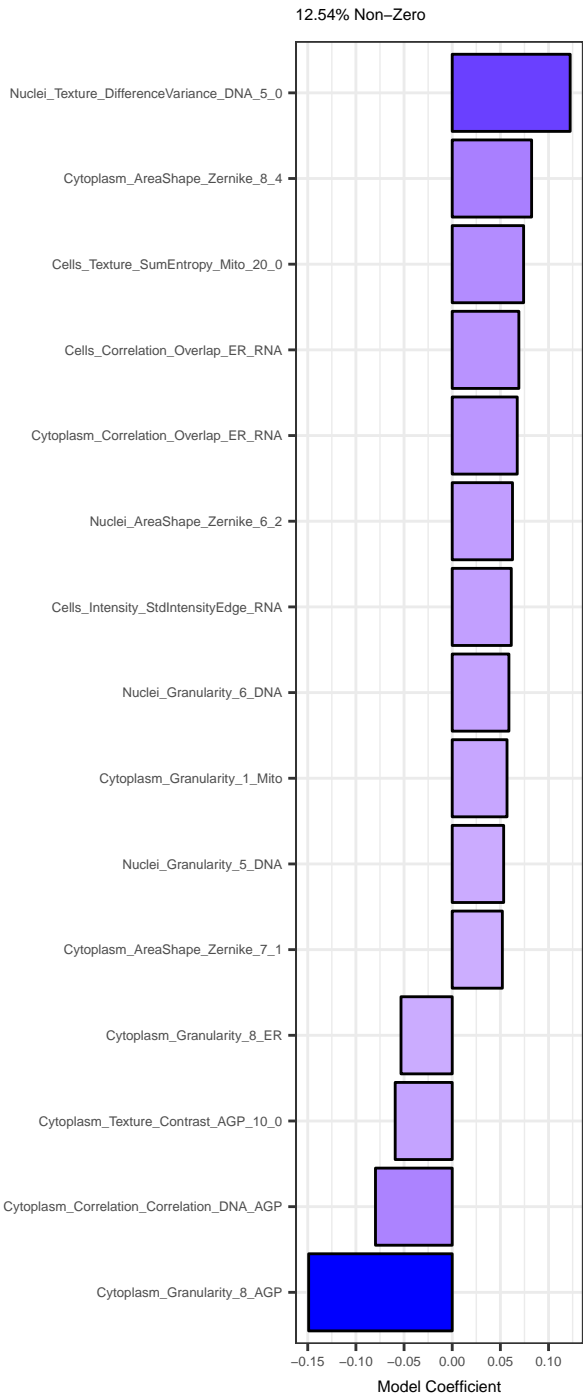
% Dead Only (CASP−; DRAQ7+)
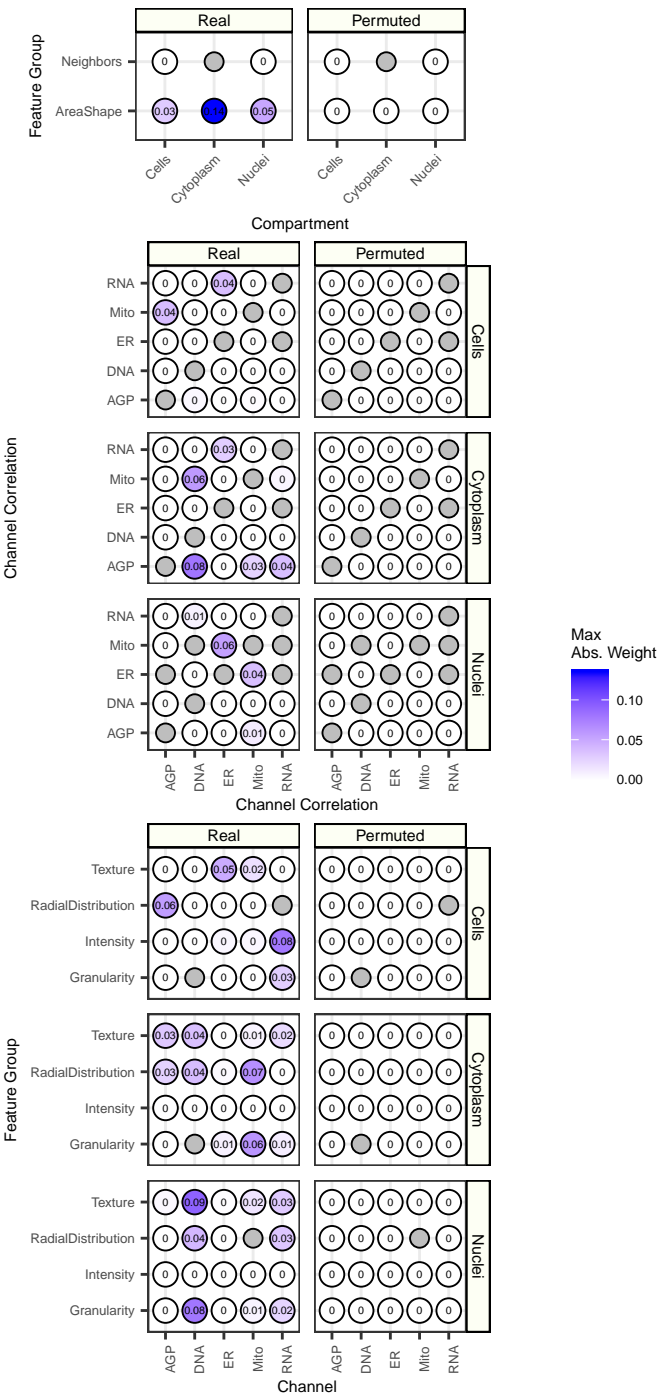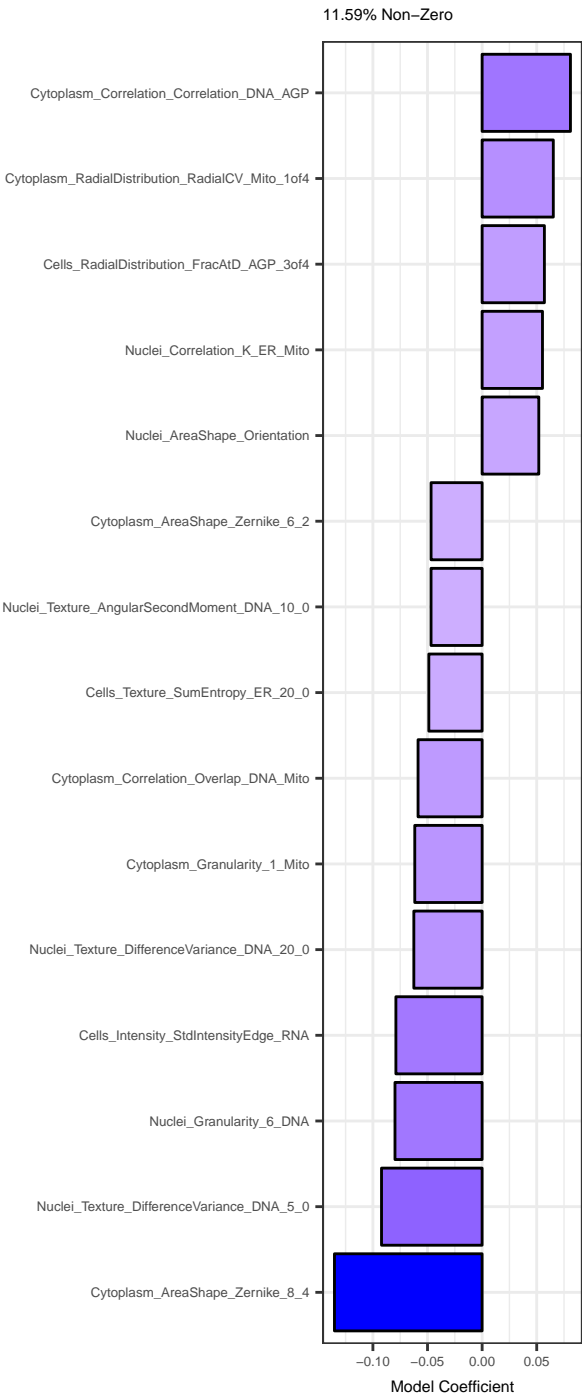
% Early Apoptosis (CASP+; DRAQ7−)
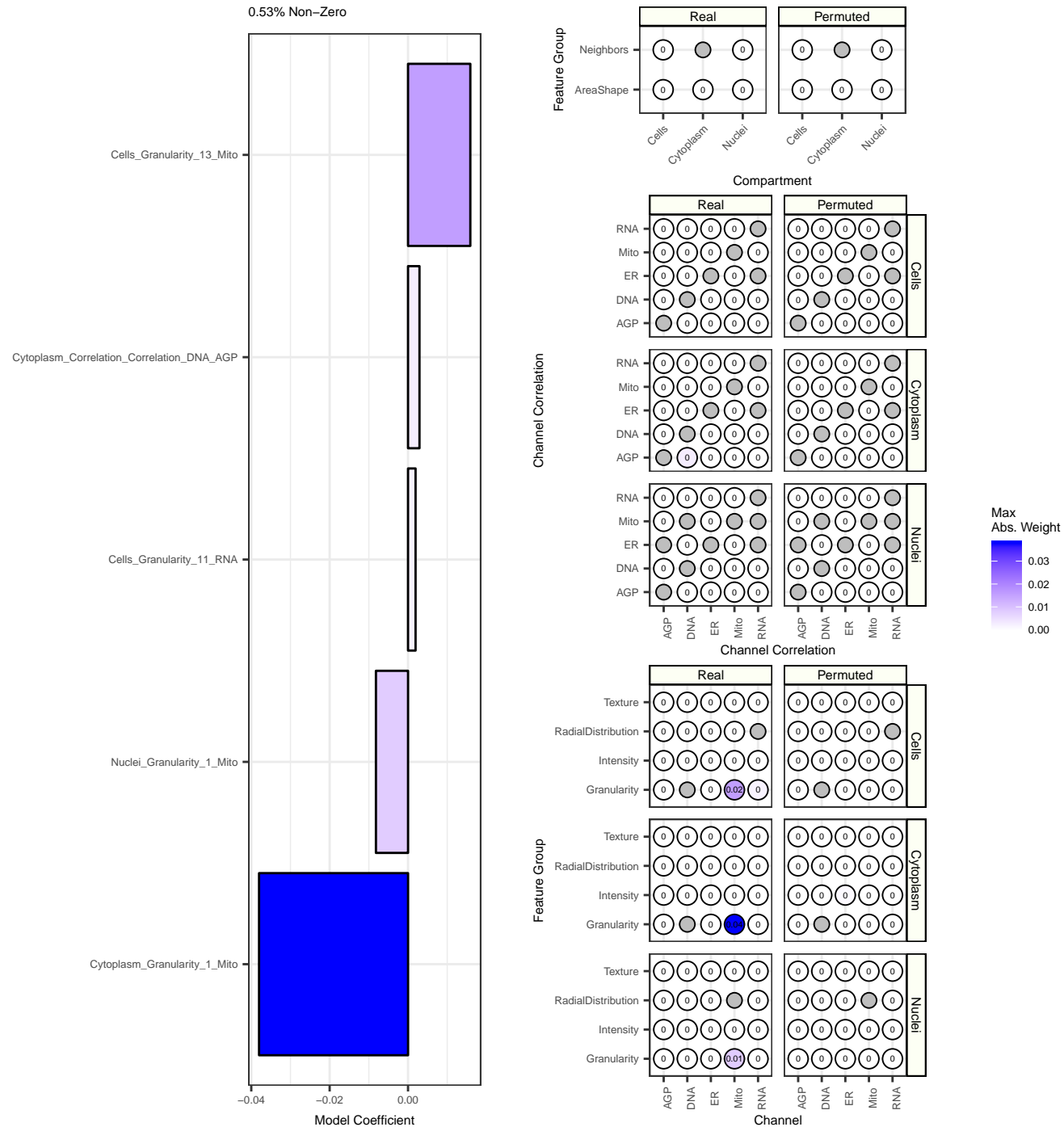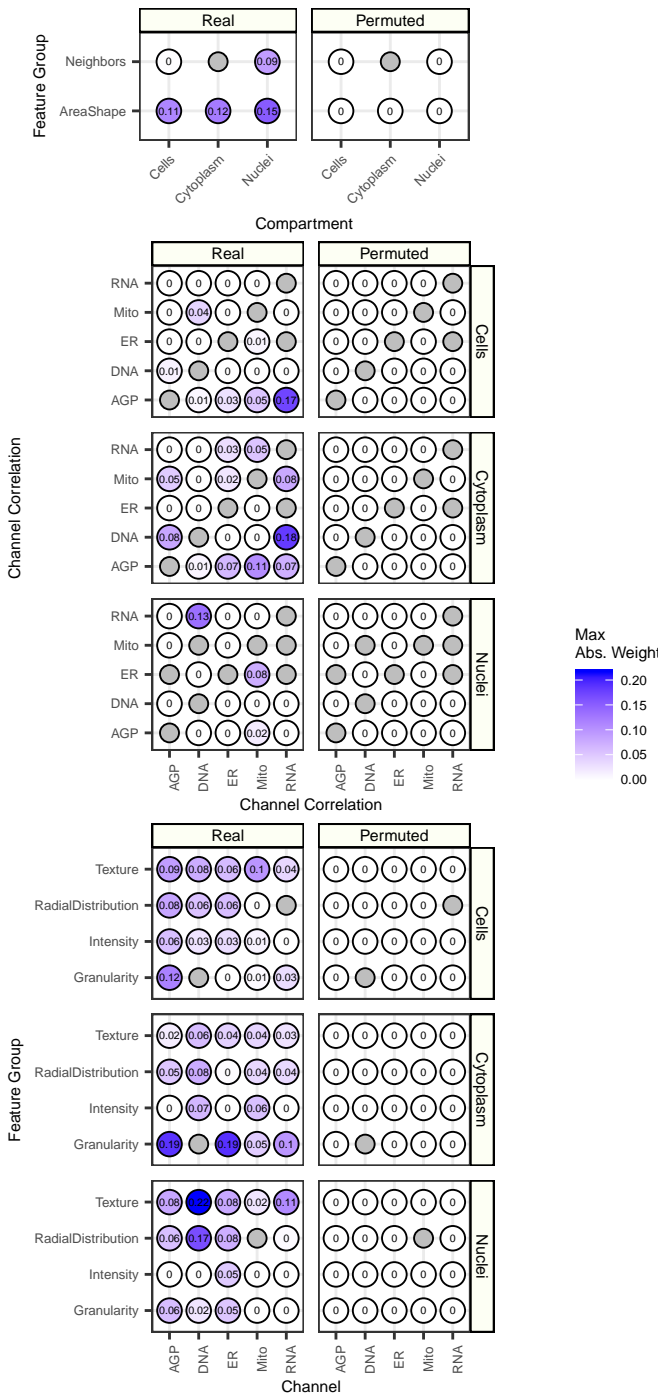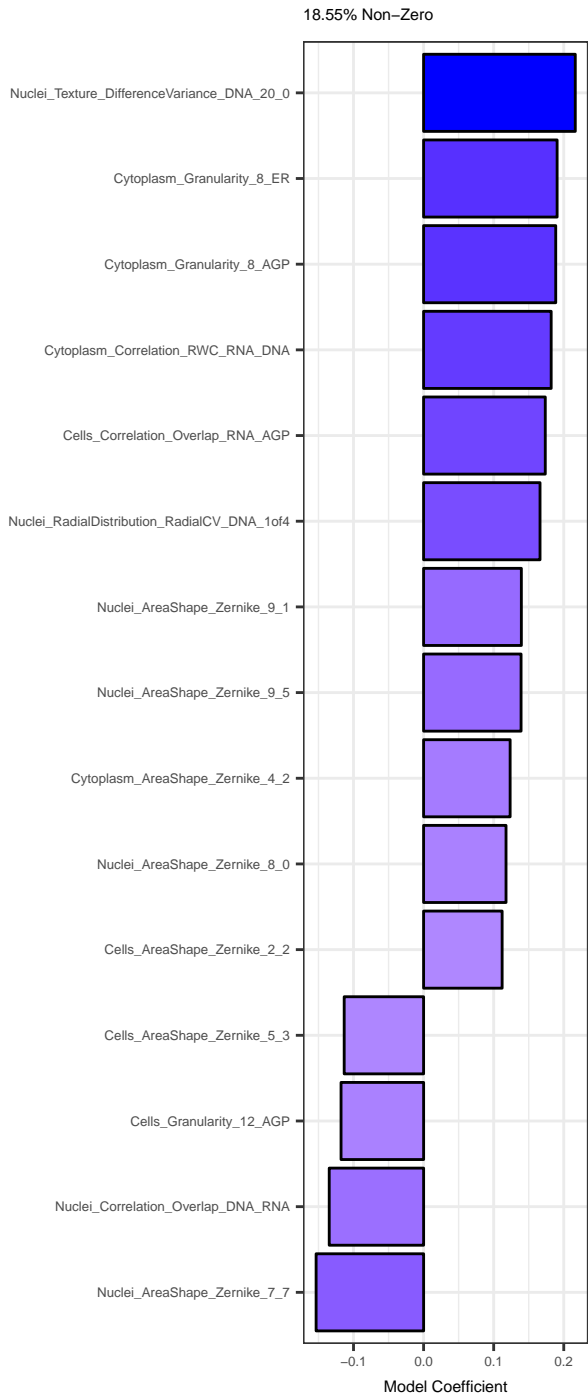
% Late Apoptosis (CASP+; DRAQ7+)

% Live (DRAQ7−; CASP−)

ROS−back

ROS

10.22% Non−Zero