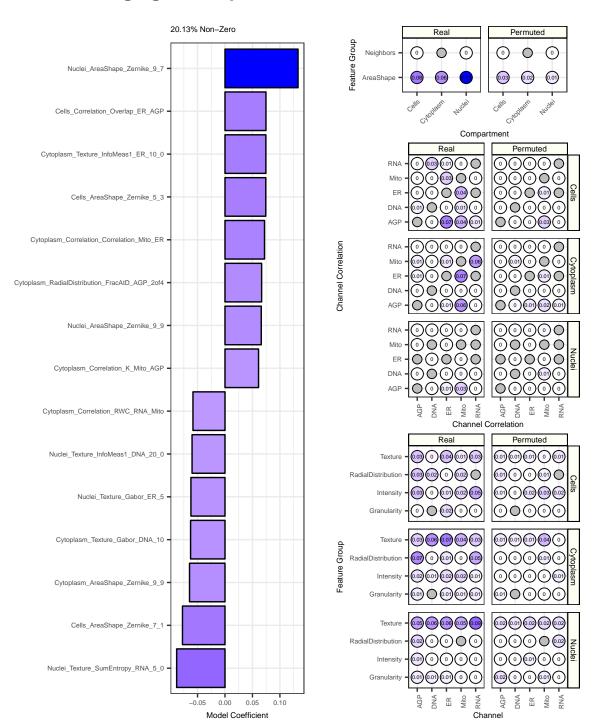
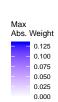
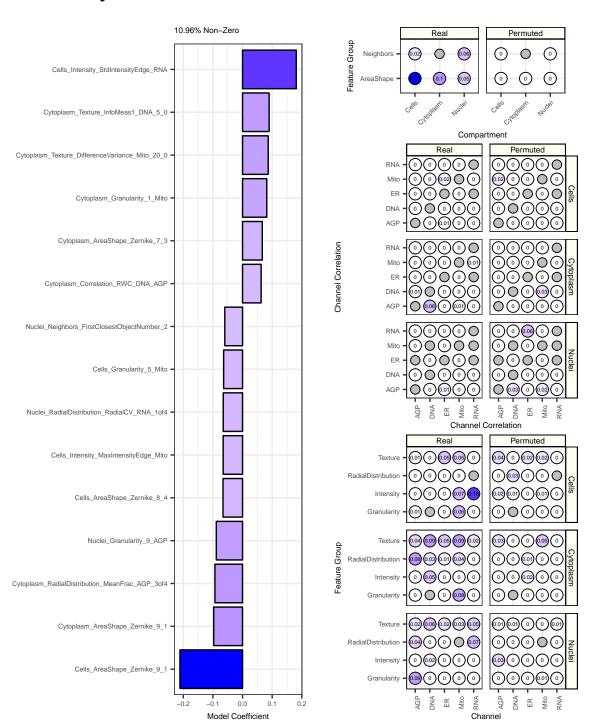
ALL - % High gH2AX Spots



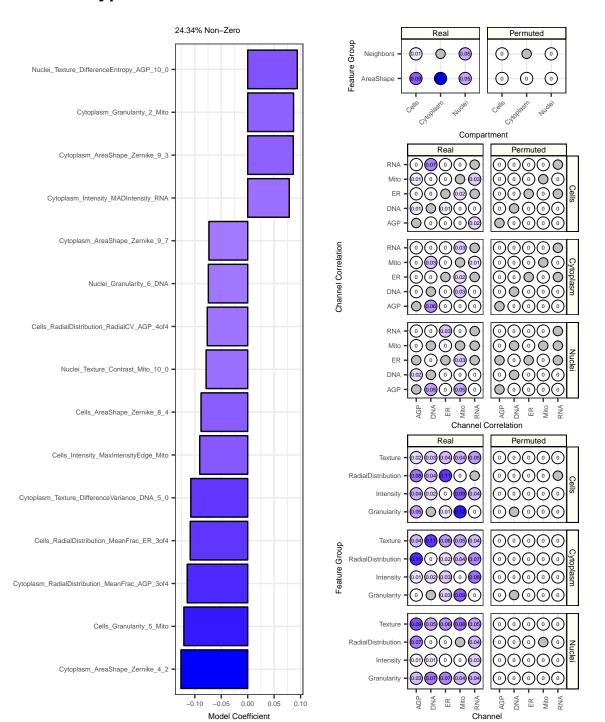


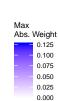
ALL - Polynuclear



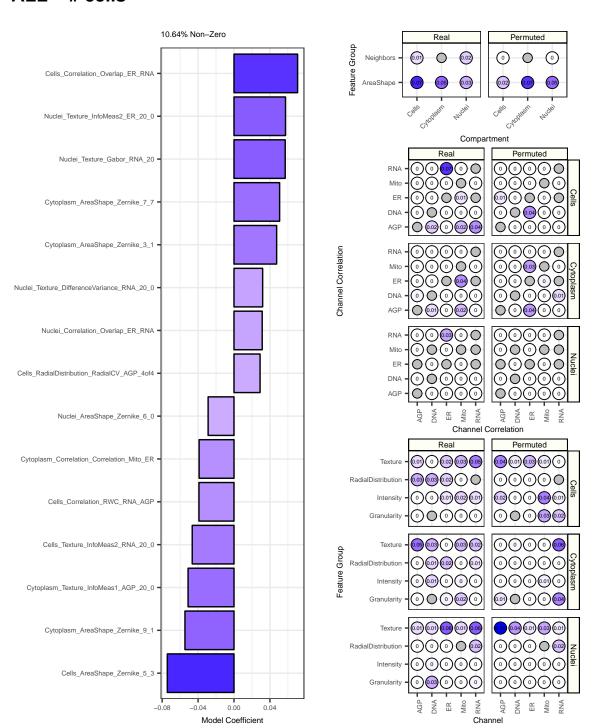


ALL - Polyploid



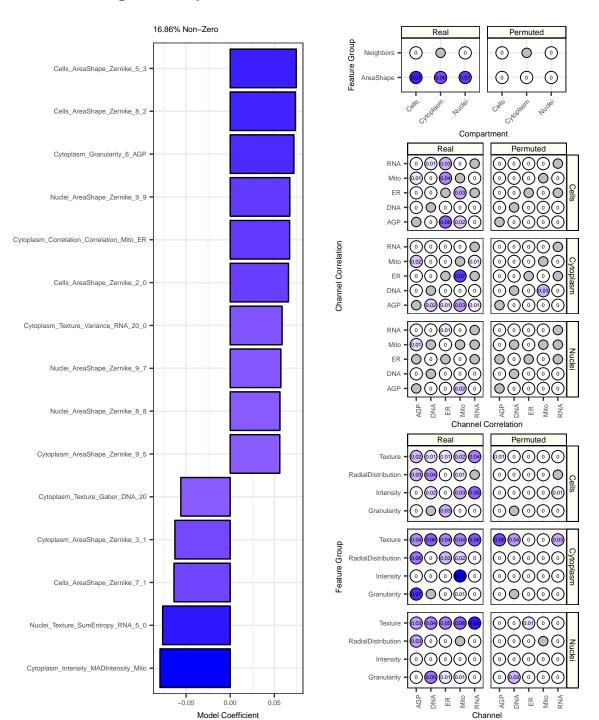


ALL - # cells



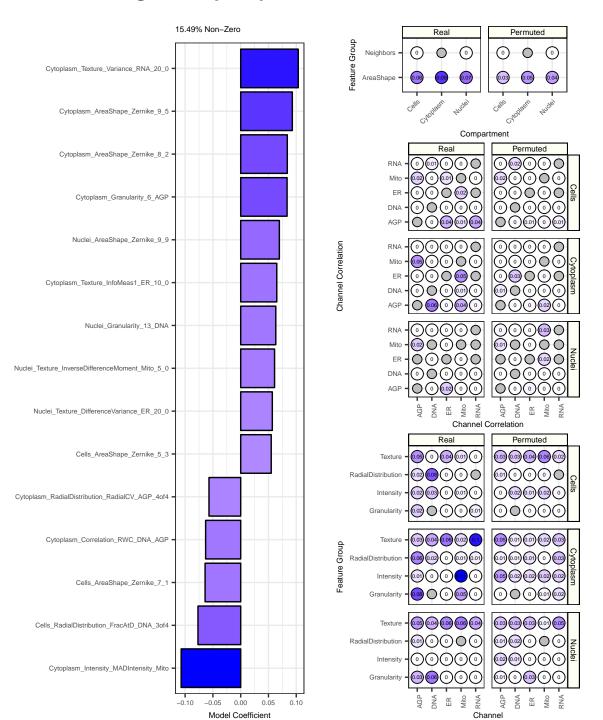


ALL - # of gH2AX Spots



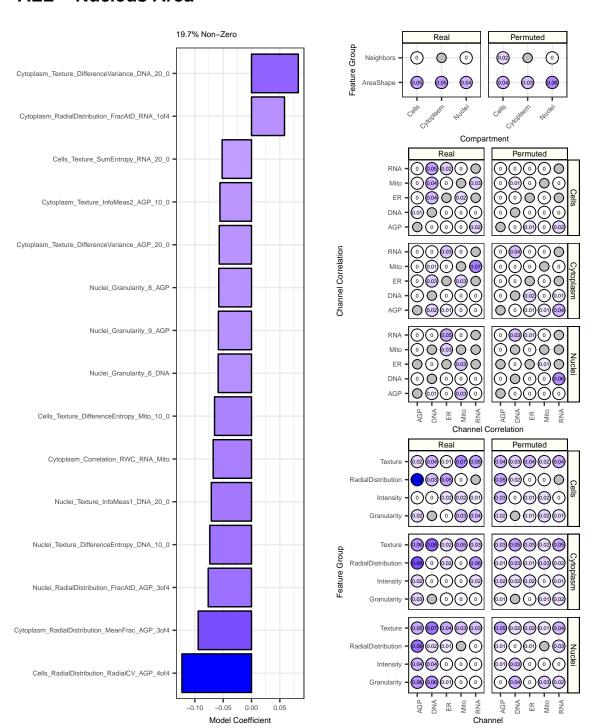


ALL - # of gH2AX Spots per Area of Nucleus



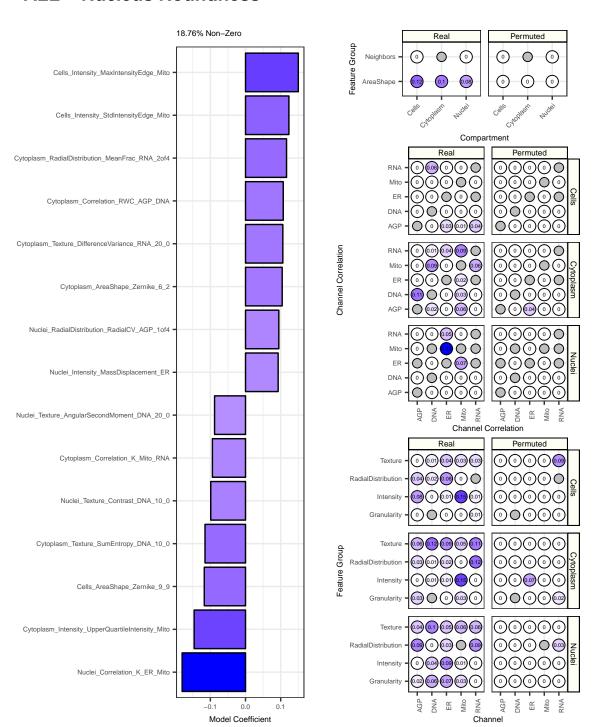


ALL - Nucleus Area



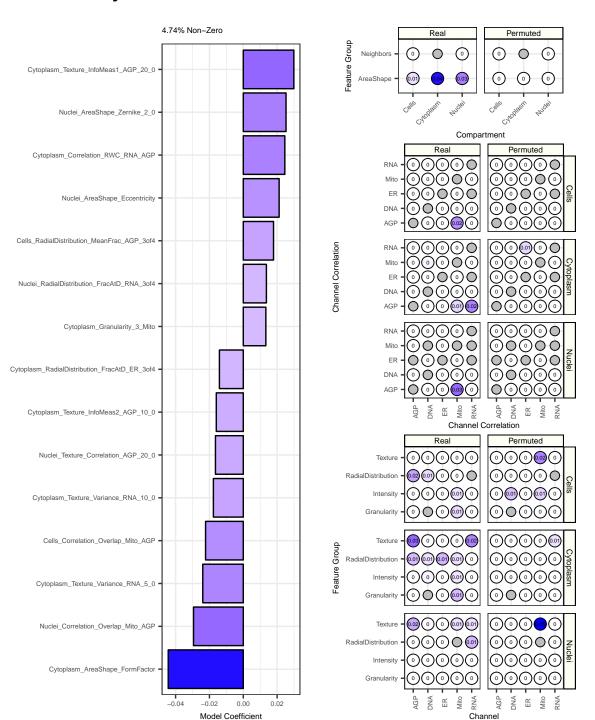


ALL - Nucleus Roundness



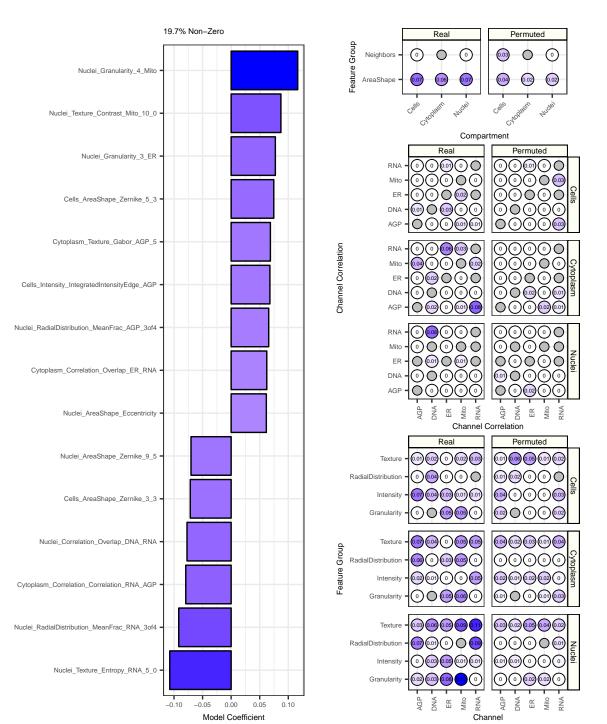


CC - % early M

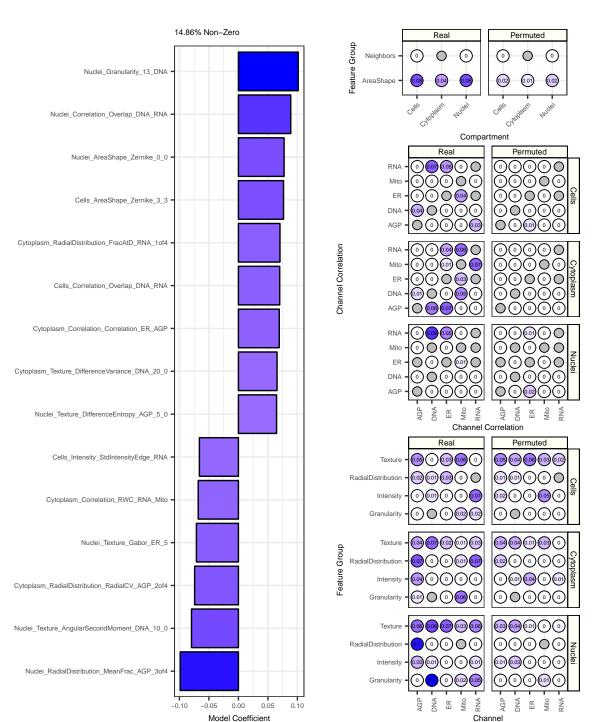


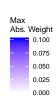


CC - % G1

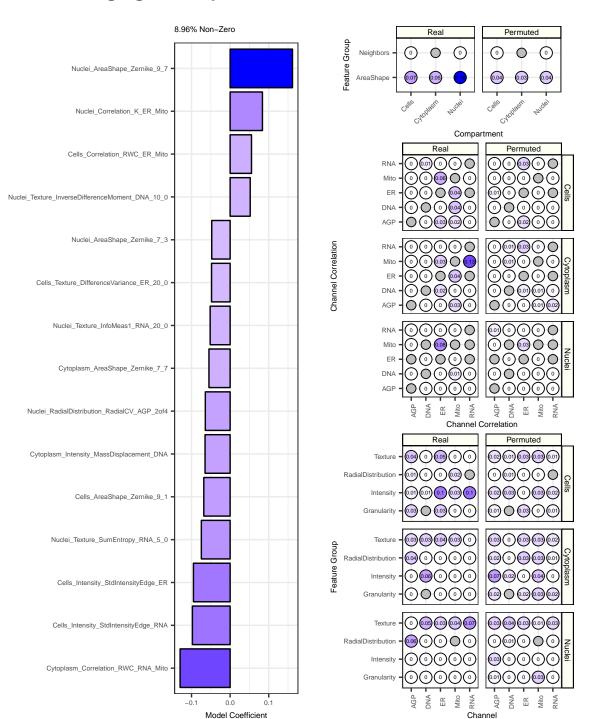






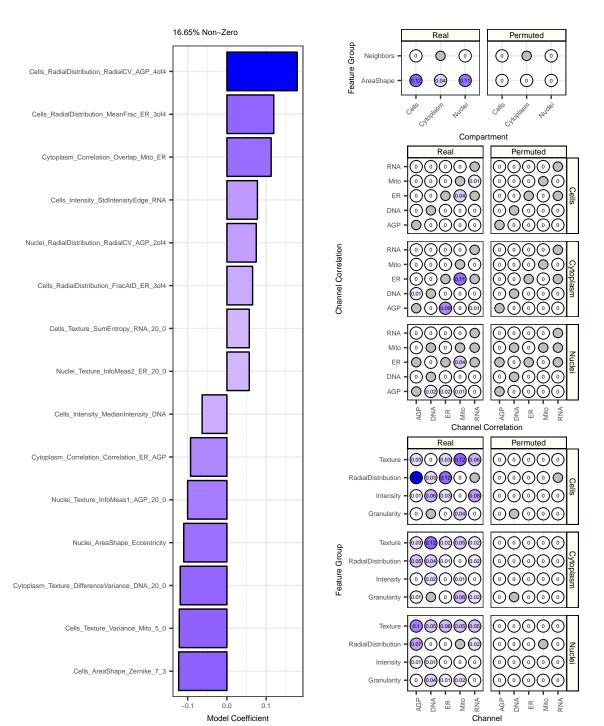


CC - % High gH2AX spots



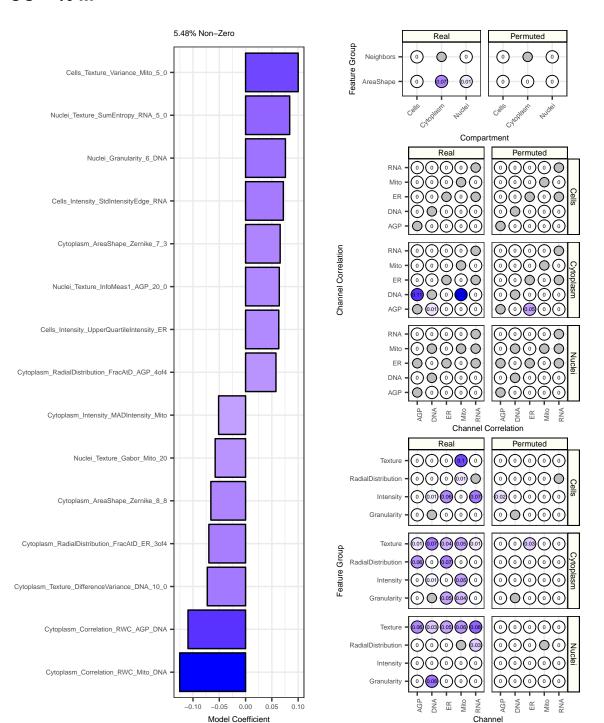


CC - % Late M



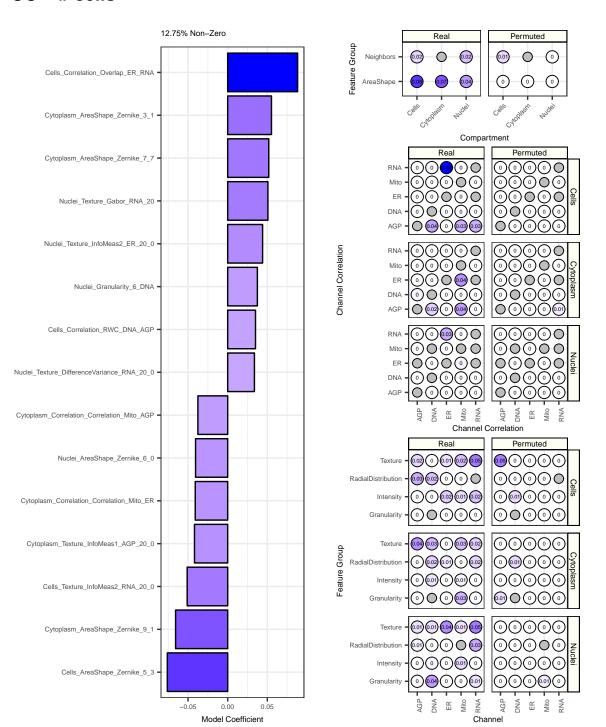


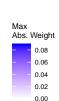
CC - % M



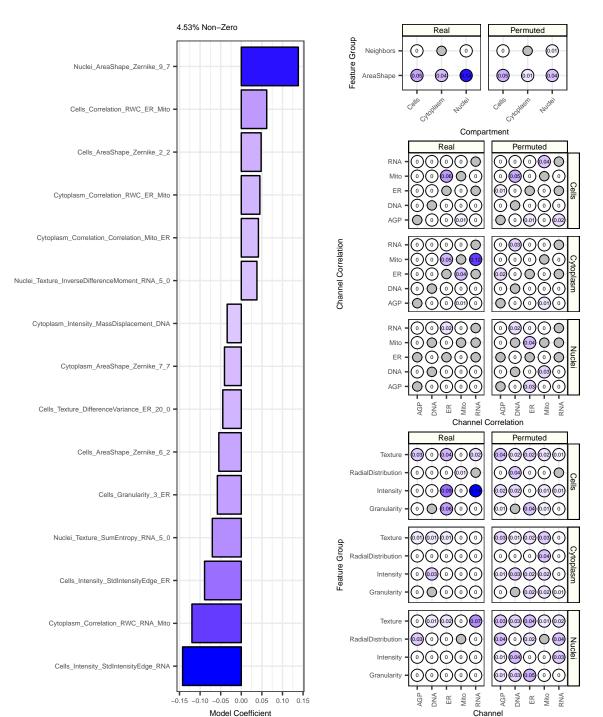


CC - # cells



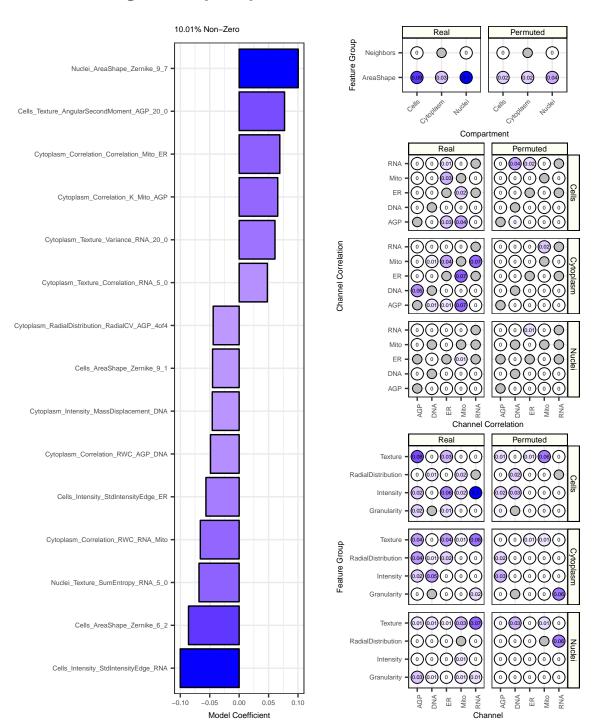


CC - # of gH2AX Spots

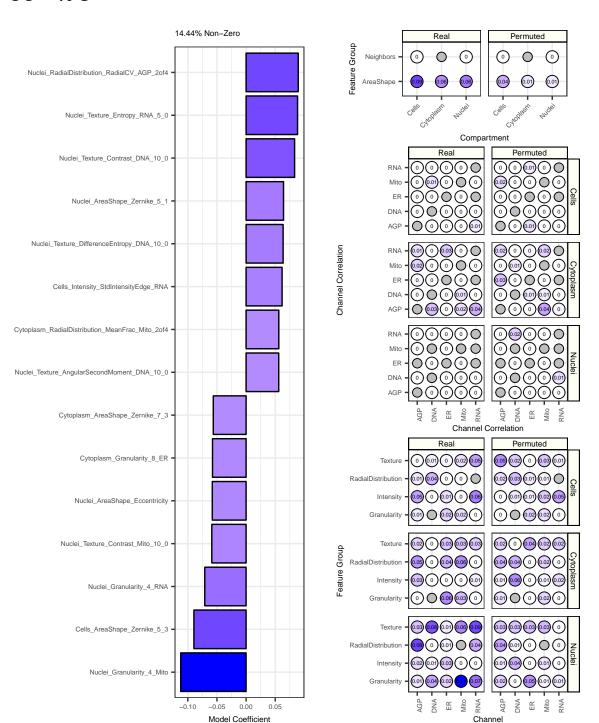




CC - # of gH2AX Spots per Area of Nucleus

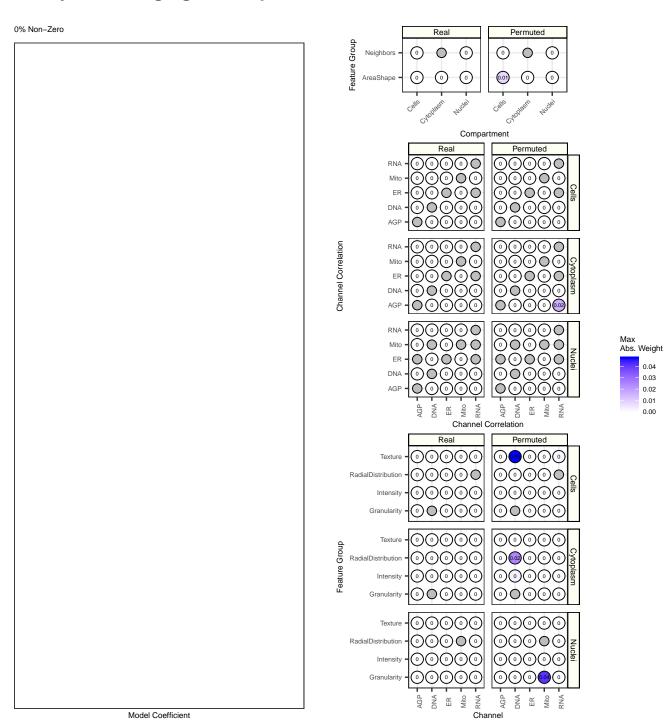




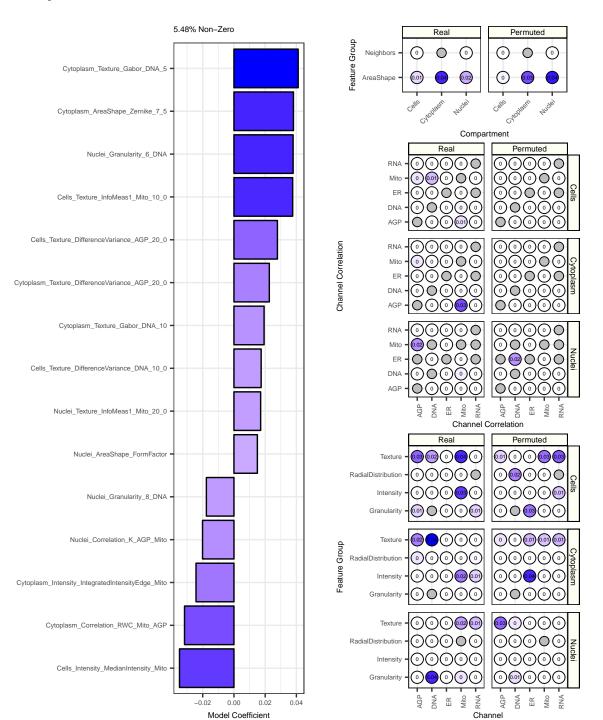


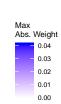


early M - % High gH2AX Spots

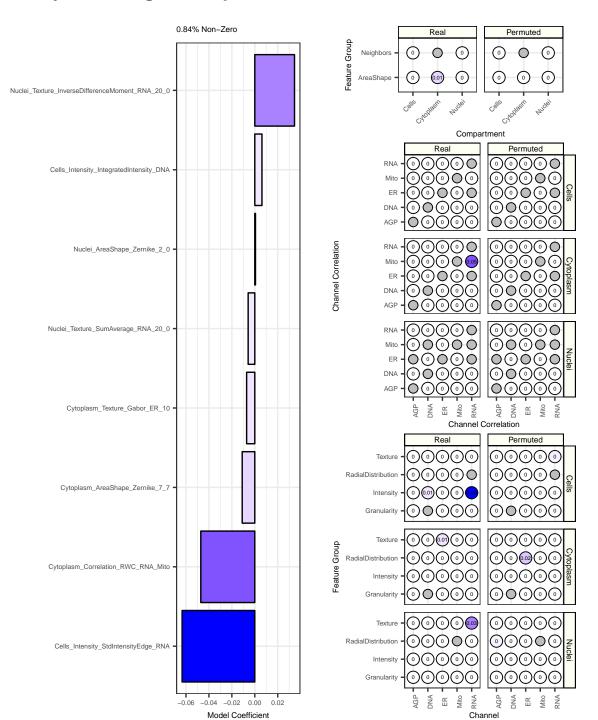


early M - # cells



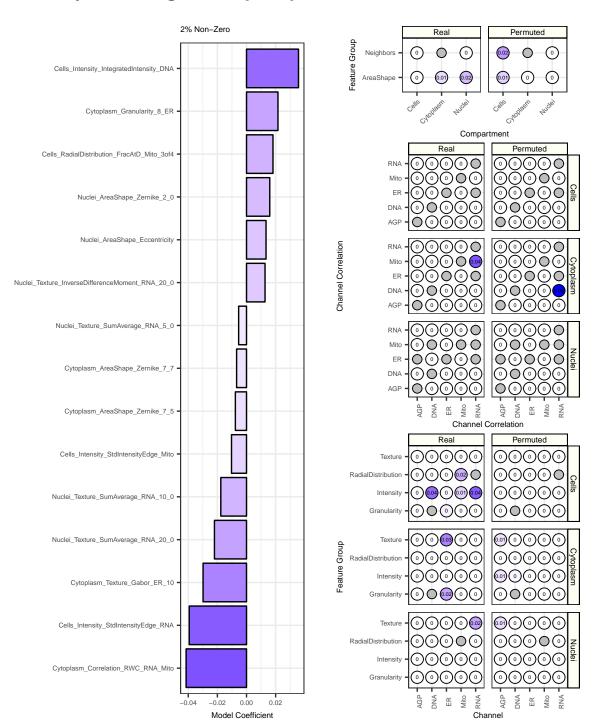


early M - # of gH2AX Spots



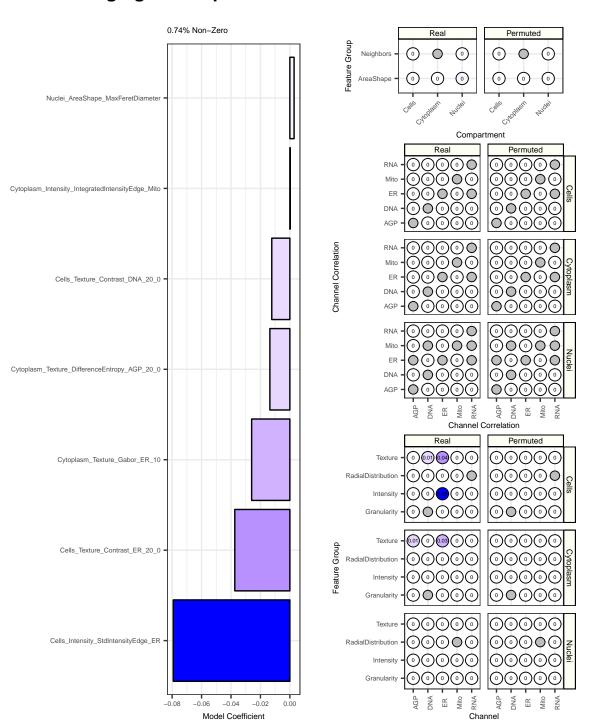


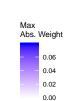
early M - # of gH2AX Spots per Area of Nucleus



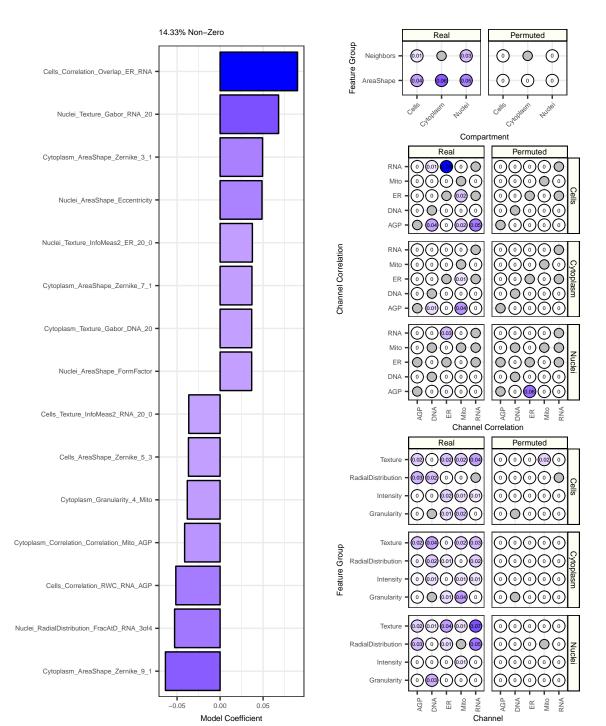


G1 - % High gH2AX Spots



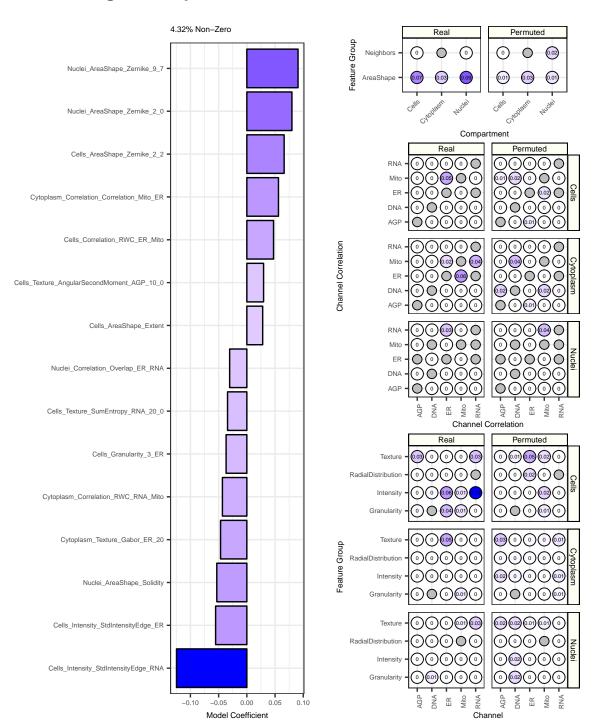


G1 - # cells



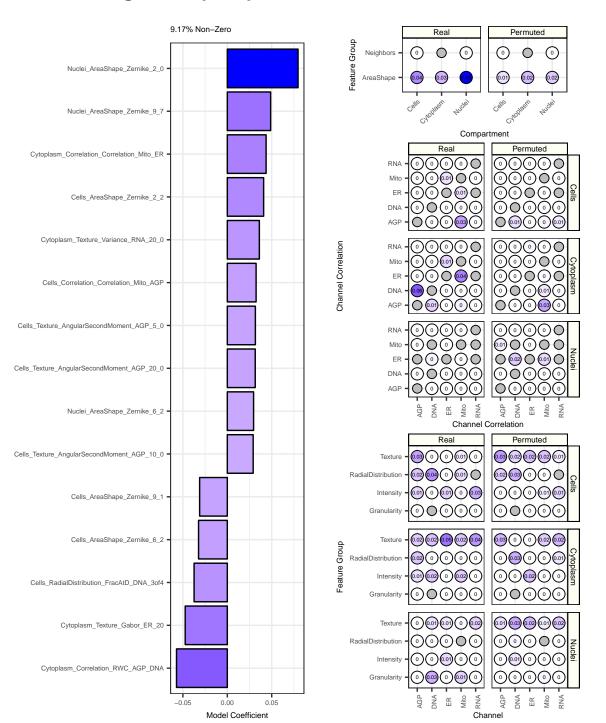


G1 - # of gH2AX Spots





G1 – # of gH2AX Spots per Area of Nucleus



Max Abs. Weight

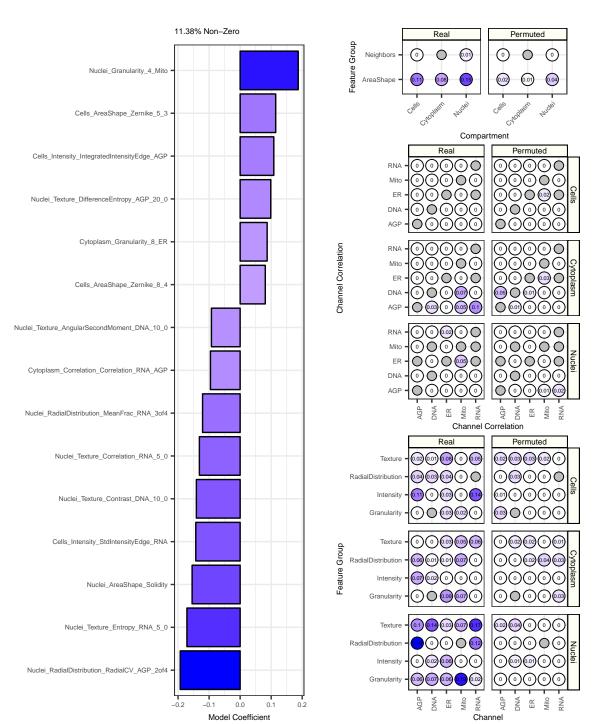
0.06

0.04

0.02

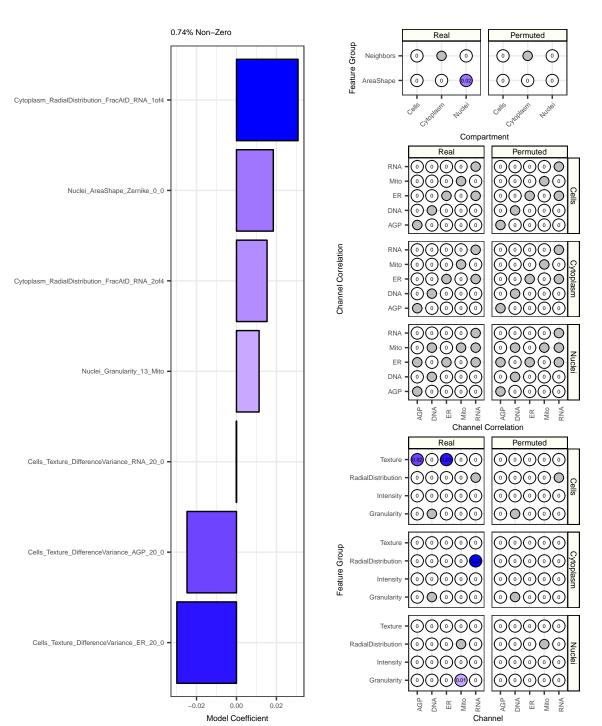
0.00

Cell Count - G1+G2



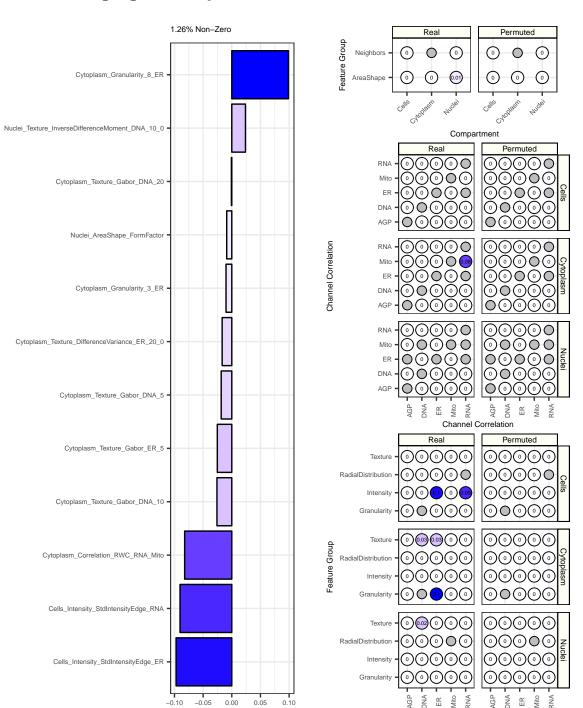


Cell Count - G2/G1

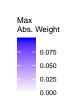




G2 - % High gH2AX Spots

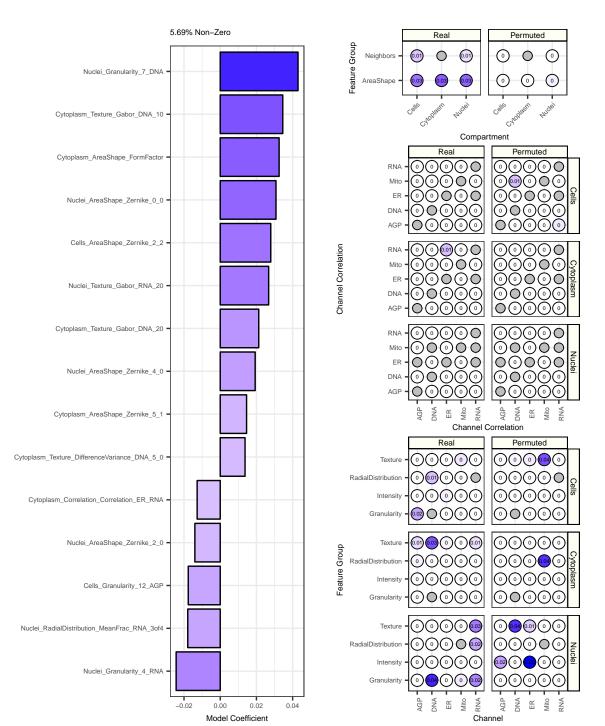


Model Coefficient



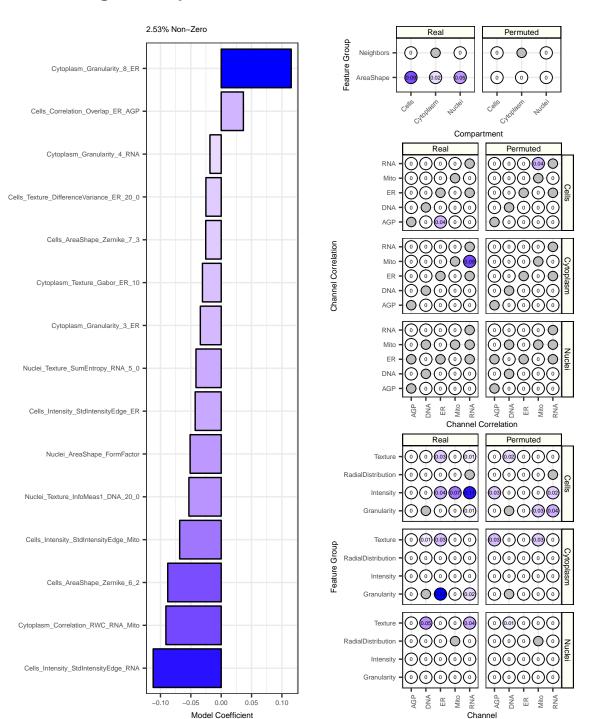
Channel

G2 - # cells



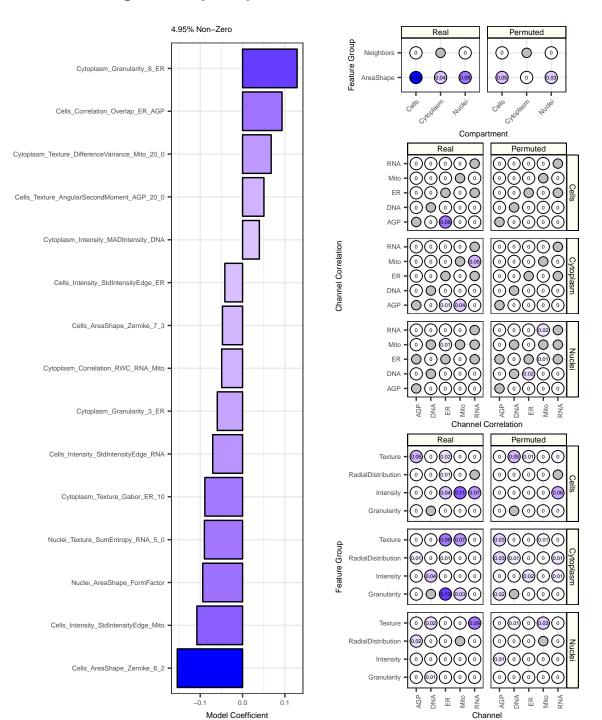


G2 - # of gH2AX Spots



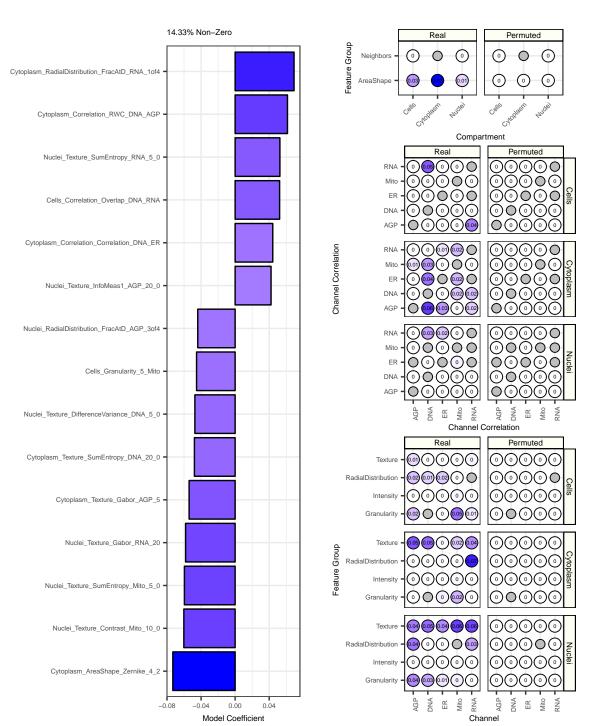


G2 – # of gH2AX Spots per Area of Nucleus



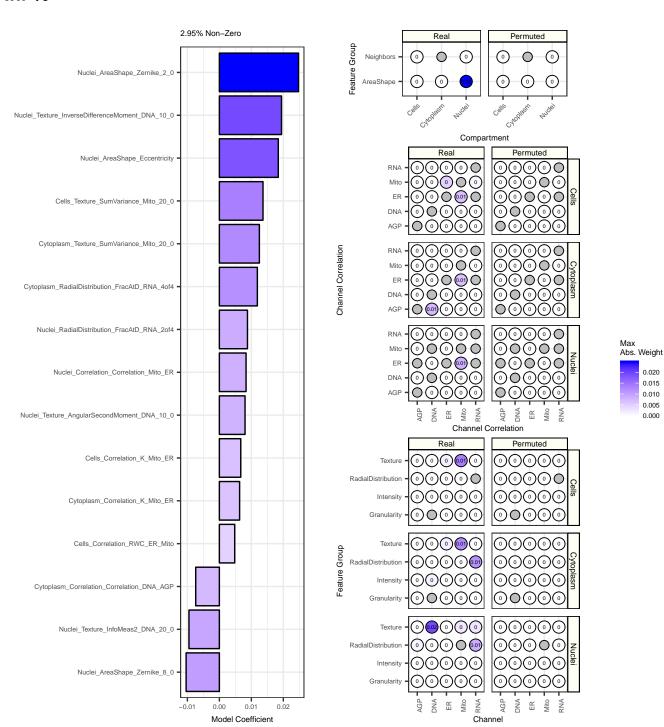


Cell Count - G2 + M

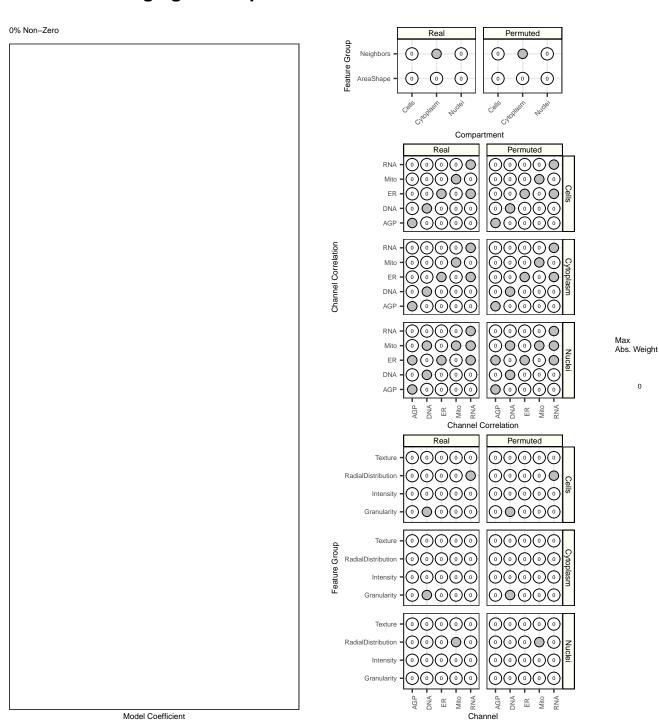




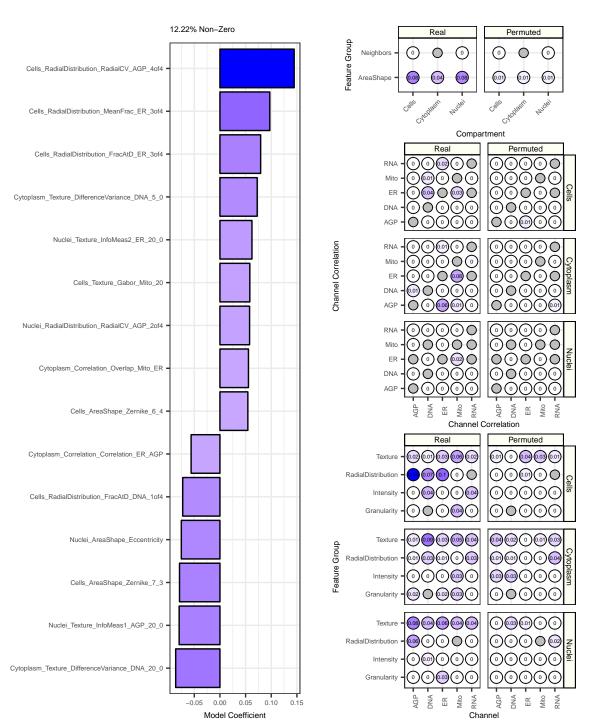
Inf %



Late M - % High gH2AX Spots

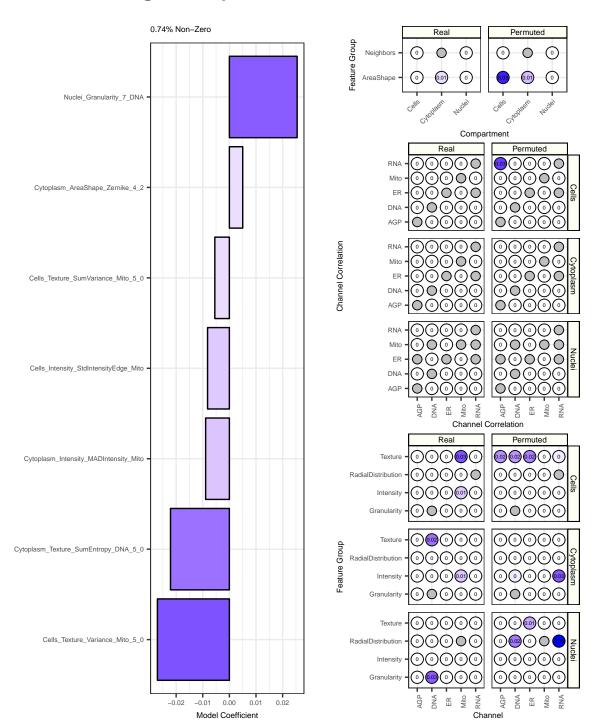


Late M - # cells





Late M - # of gH2AX Spots



Max Abs. Weight

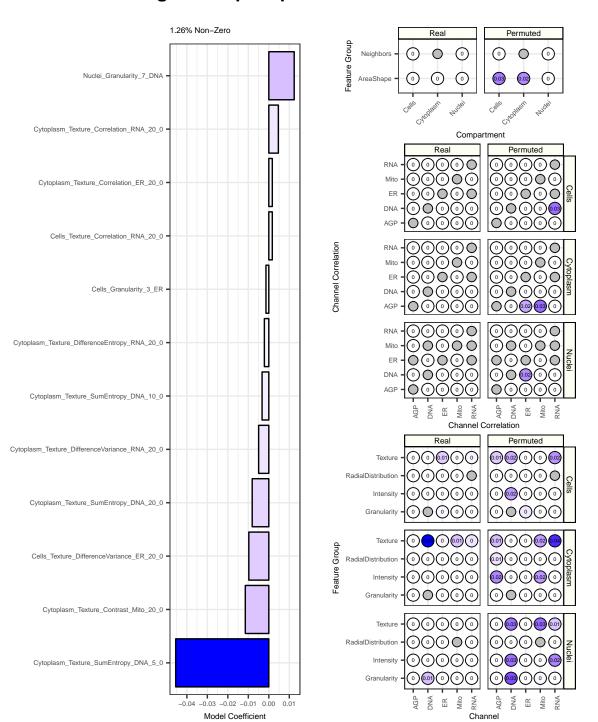
0.03

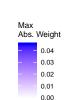
0.02

0.01

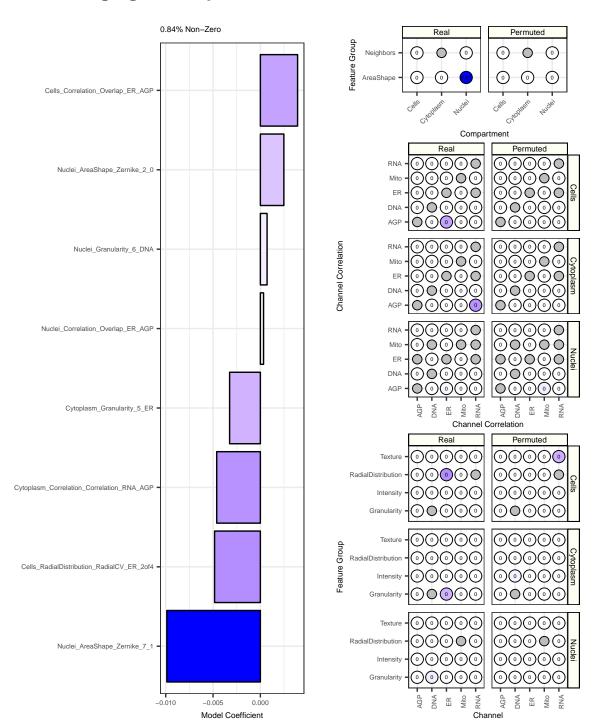
0.00

Late M - # of gH2AX Spots per Area of Nucleus





M - % High gH2AX Spots



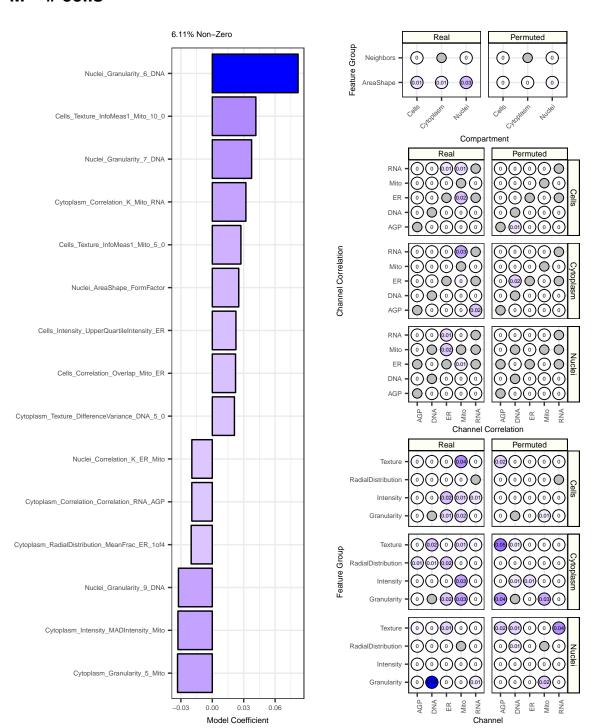
Max Abs. Weight

0.0050

0.0025

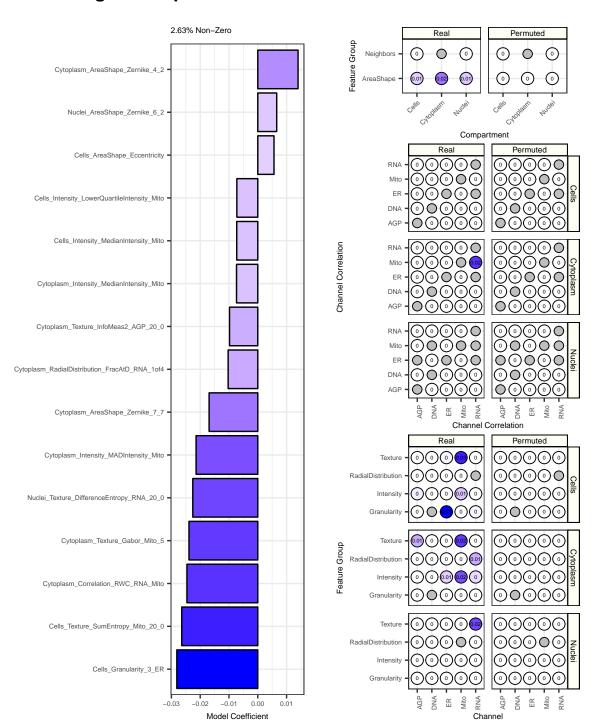
0.0000

M - # cells



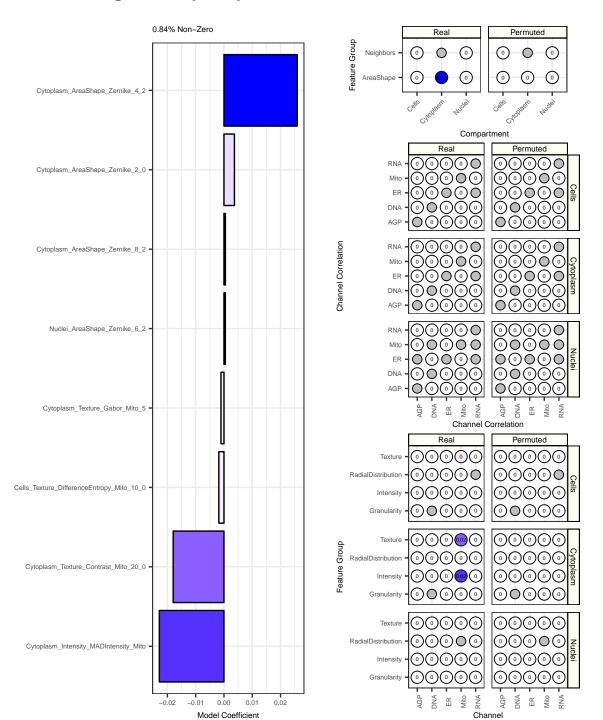


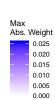
M - # of gH2AX Spots



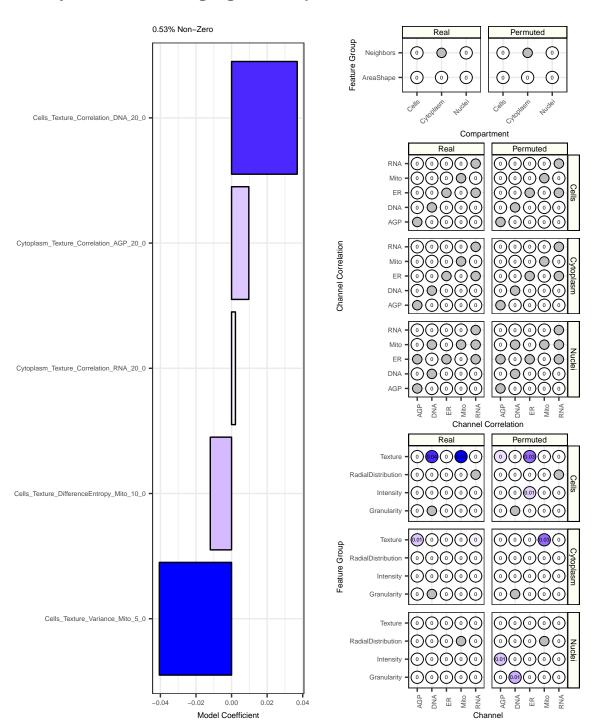


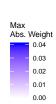
M - # of gH2AX Spots per Area of Nucleus



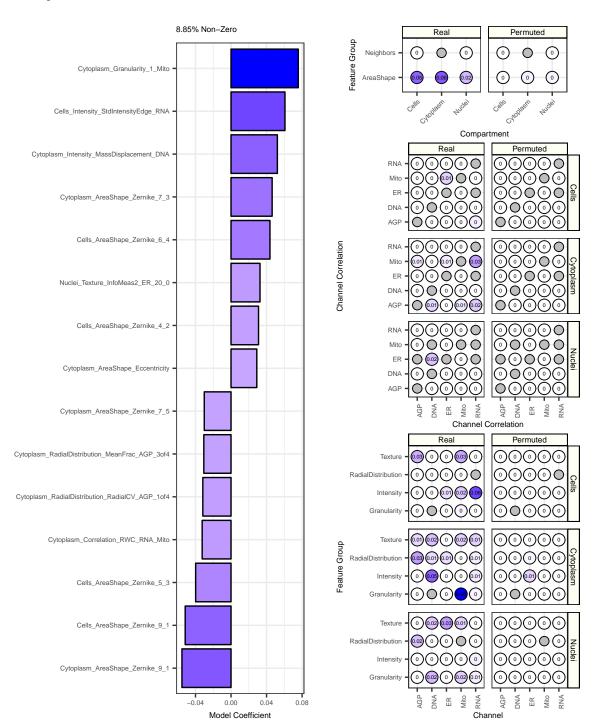


Polynuclear - % High gH2AX Spots



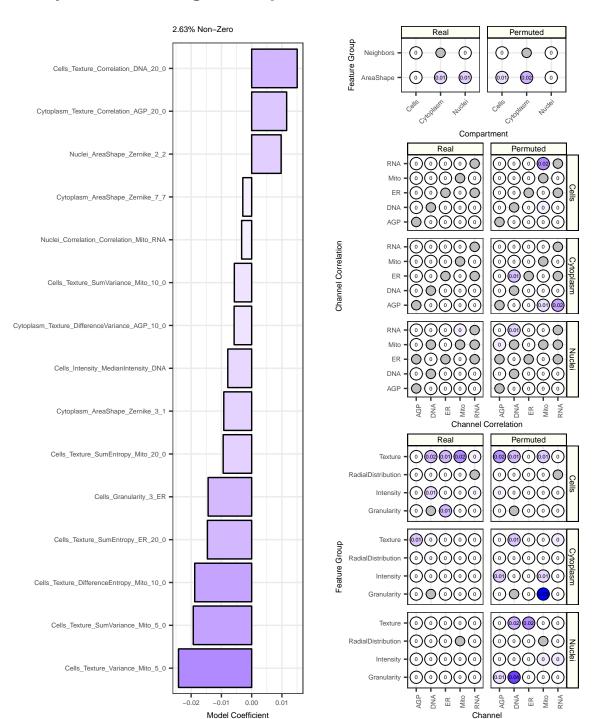


Polynuclear - # cells



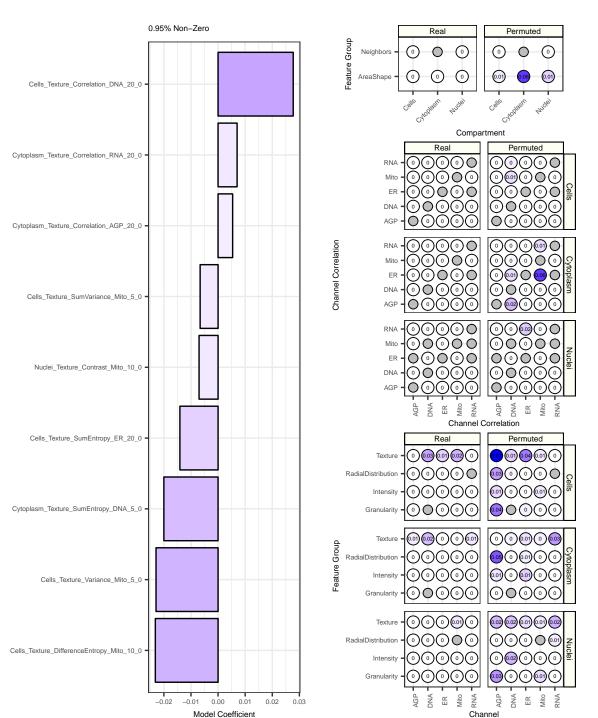


Polynuclear - # of gH2AX Spots



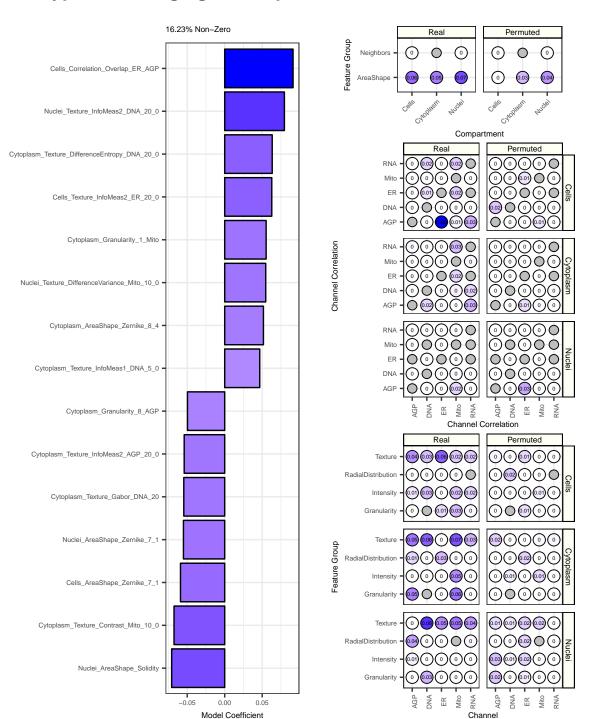


Polynuclear – # of gH2AX Spots per Area of Nucleus



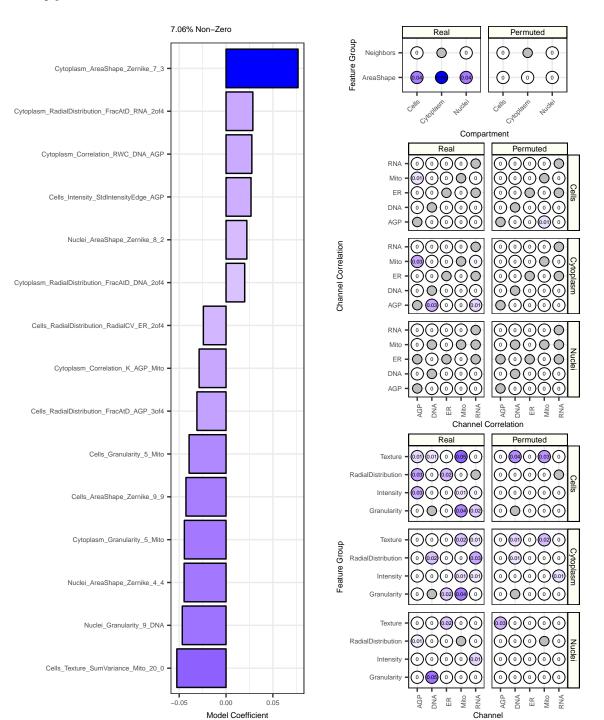


Polyploid - % High gH2AX Spots



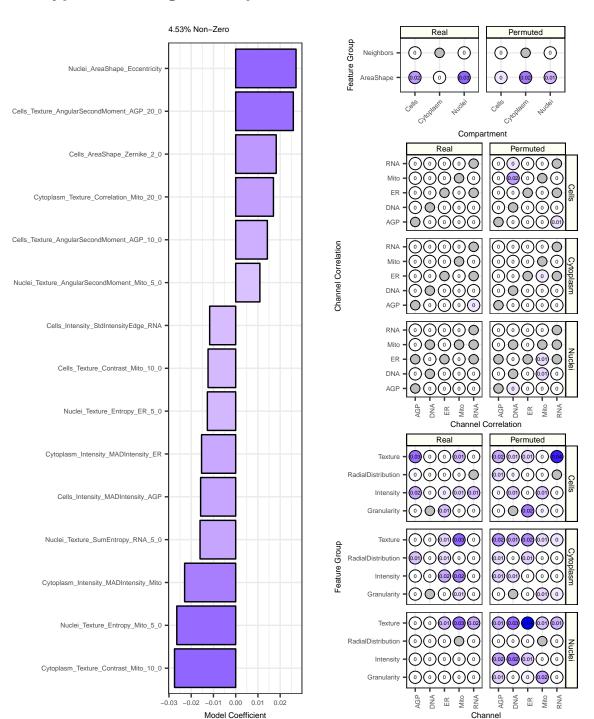


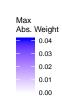
Polyploid - # cells



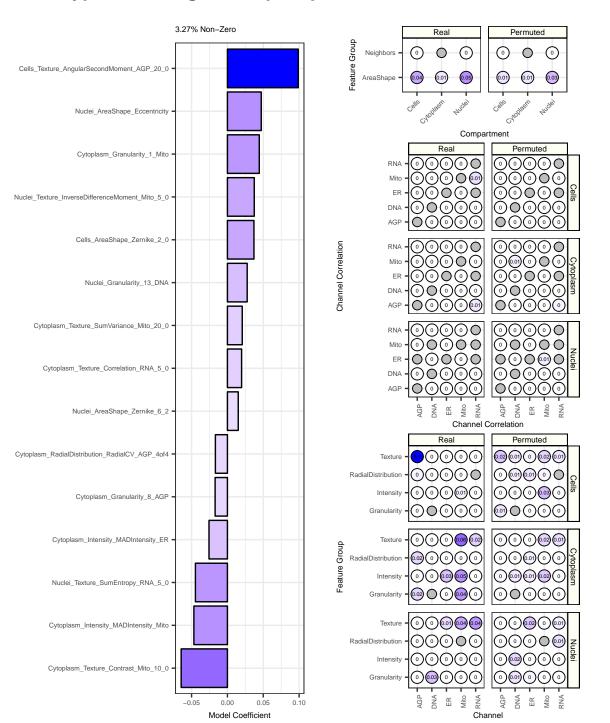


Polyploid - # of gH2AX Spots





Polyploid - # of gH2AX Spots per Area of Nucleus



Max Abs. Weight

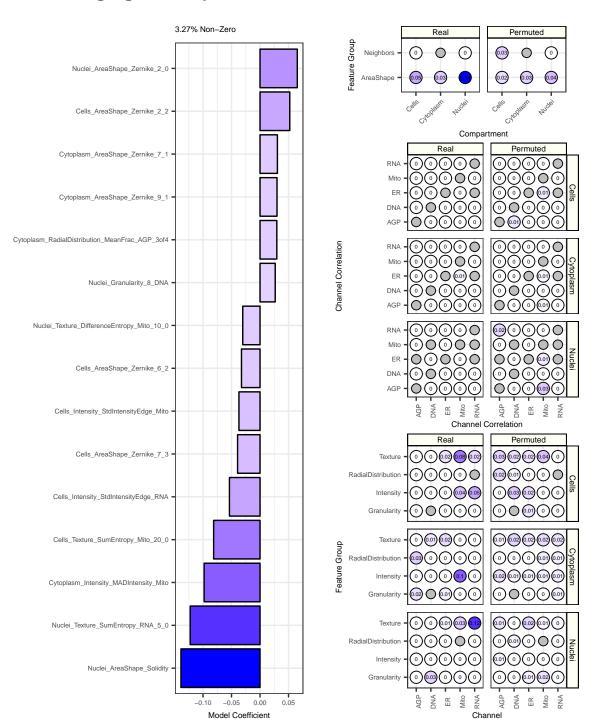
0.075

0.050

0.025

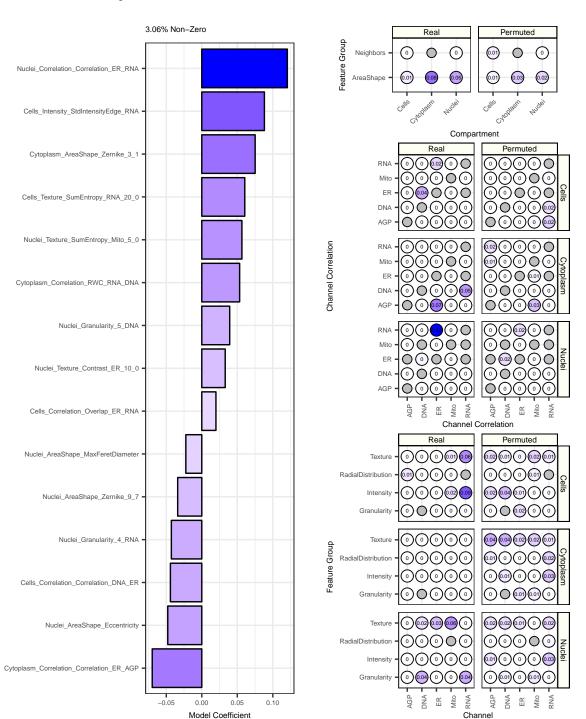
0.000

S - % High gH2AX Spots



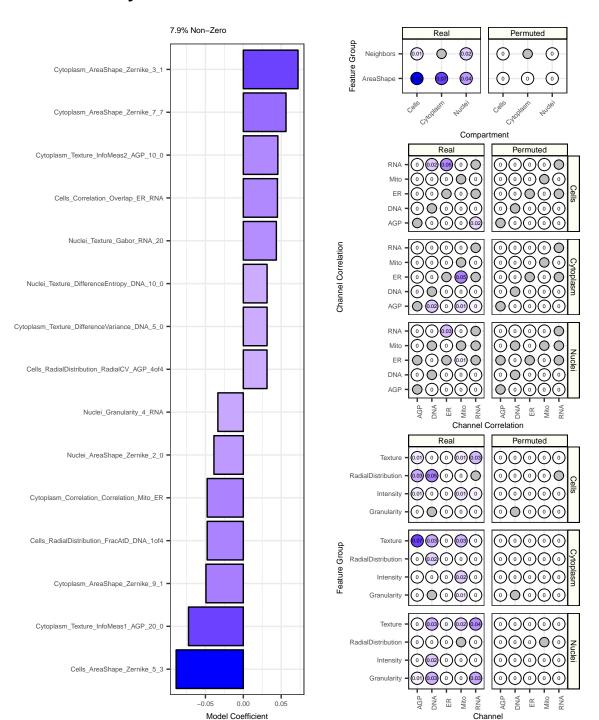


S – Intensity Nucleus EdU Mean



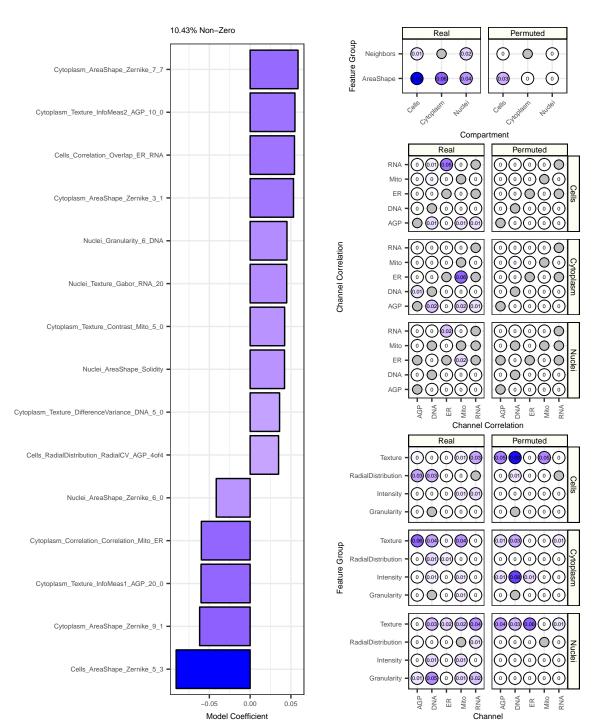


S - Intensity Nucleus EdU Sum



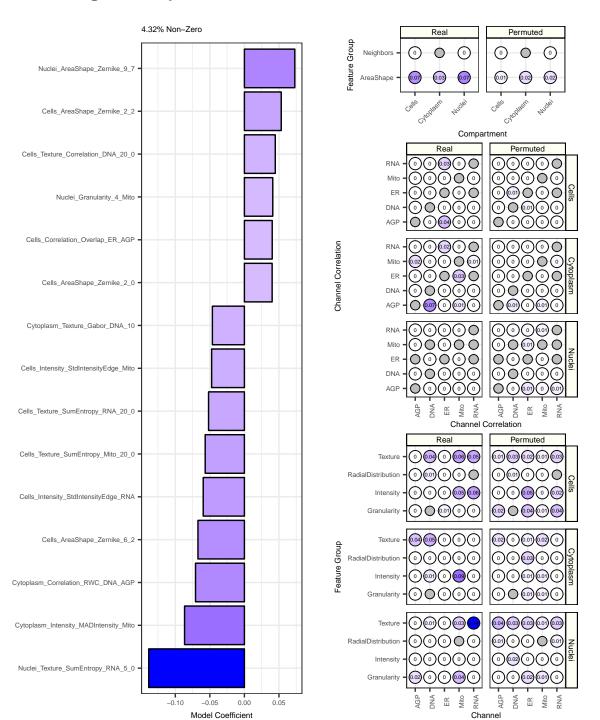


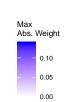
S - # cells



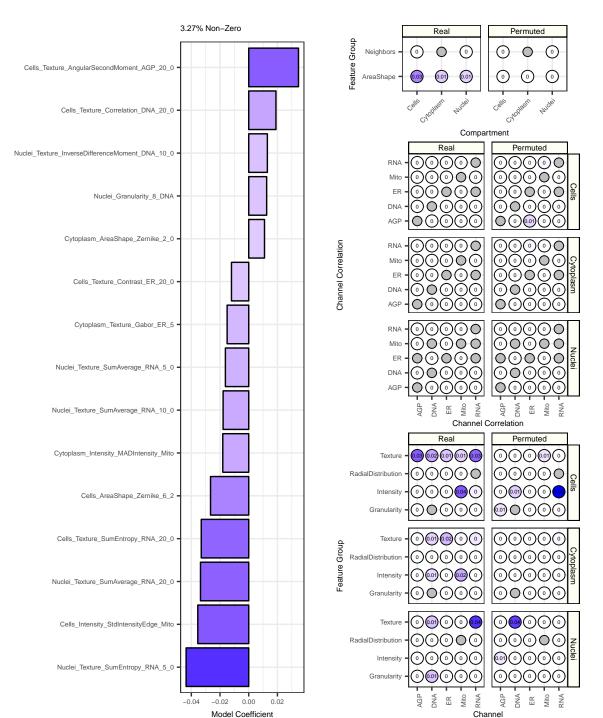


S - # of gH2AX Spots

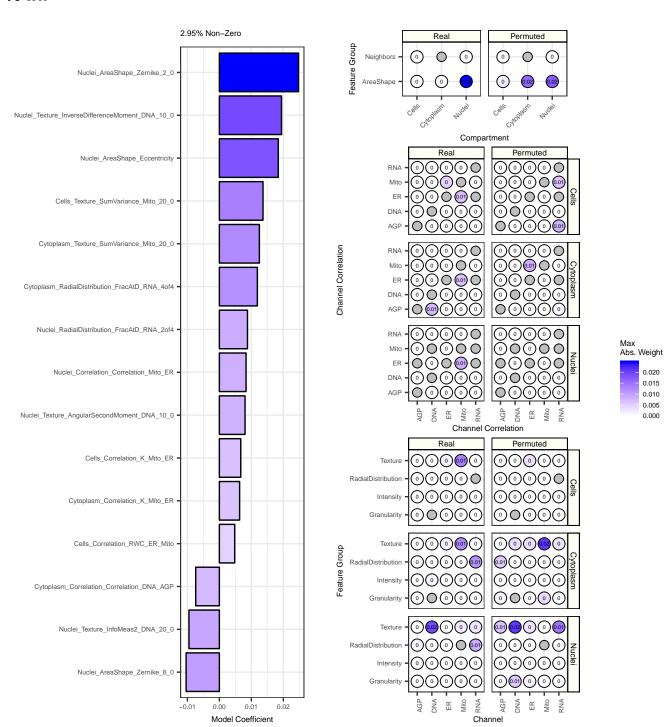




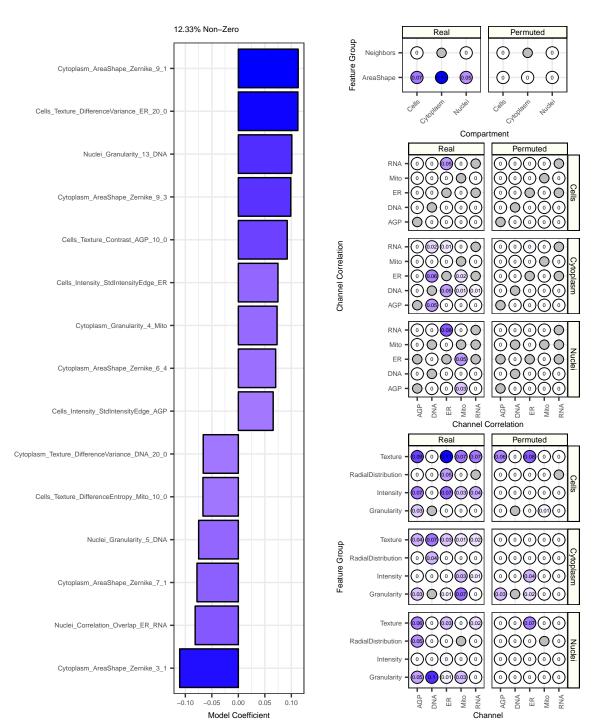
S - # of gH2AX Spots per Area of Nucleus





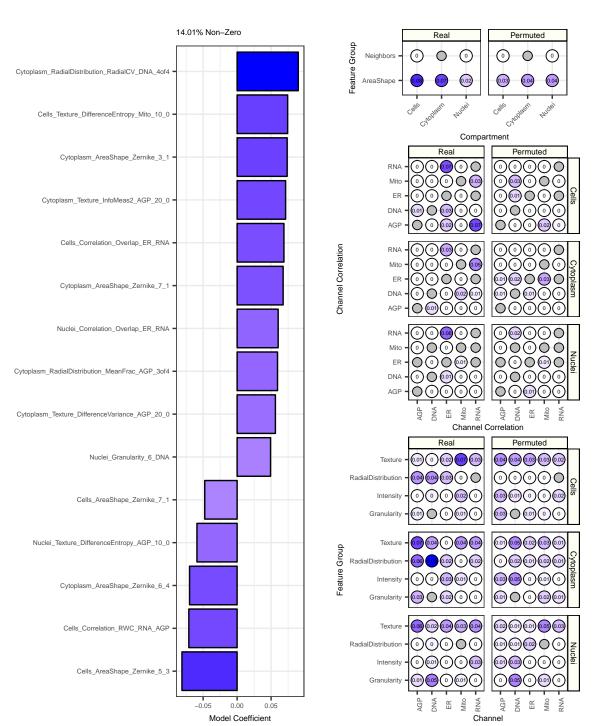


Live Cell Area



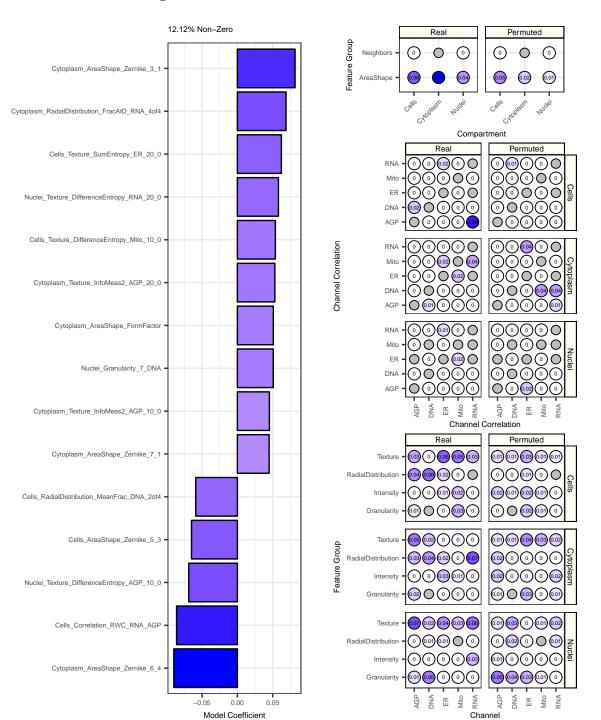


Live Cell Roundness



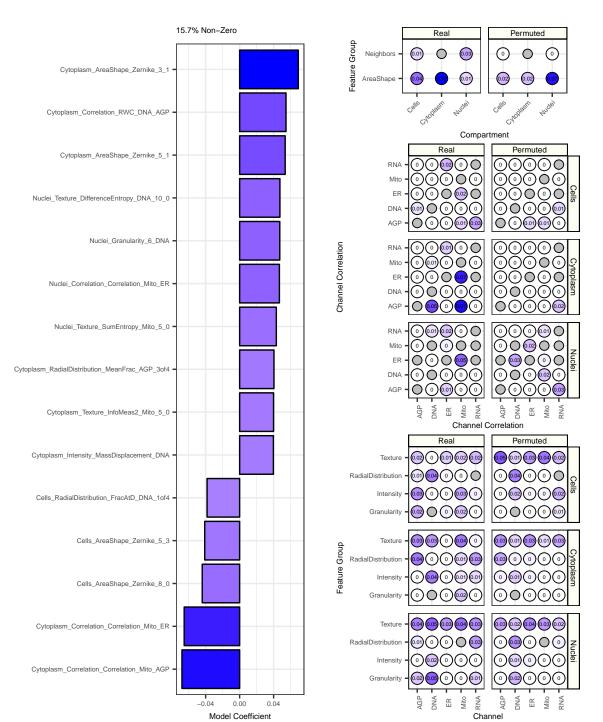


Live Width / Length



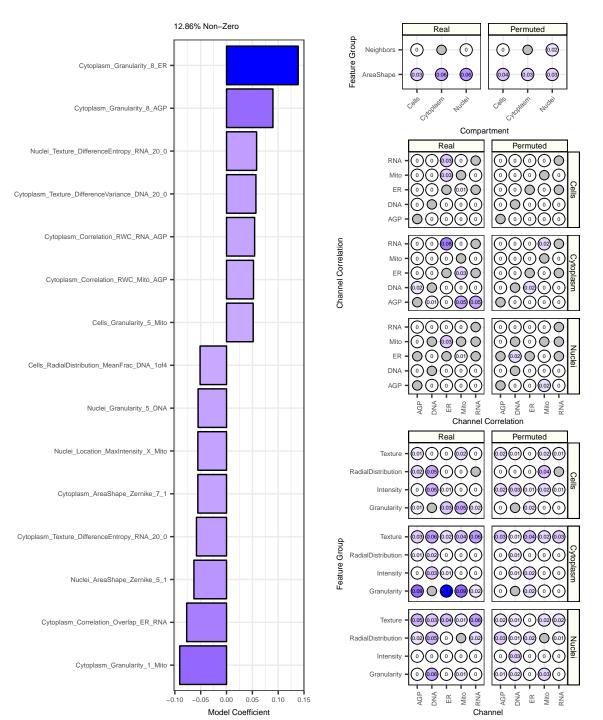


Live Cells



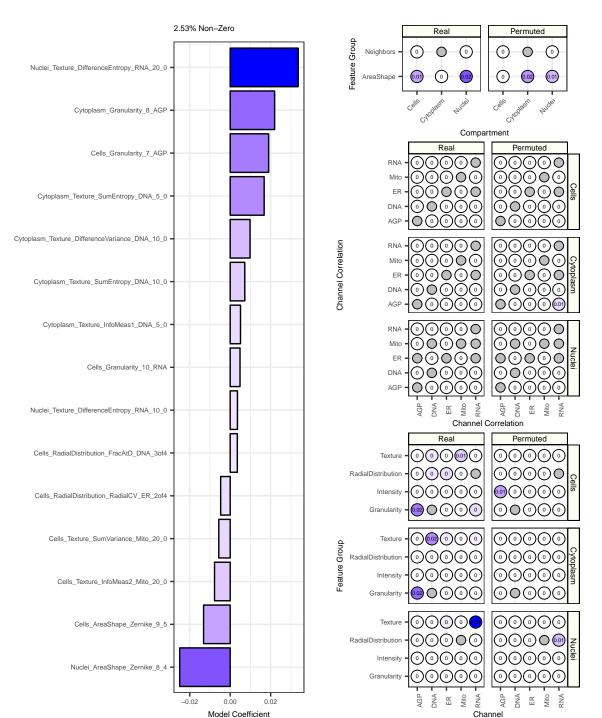


% All Apoptosis (CASP+)



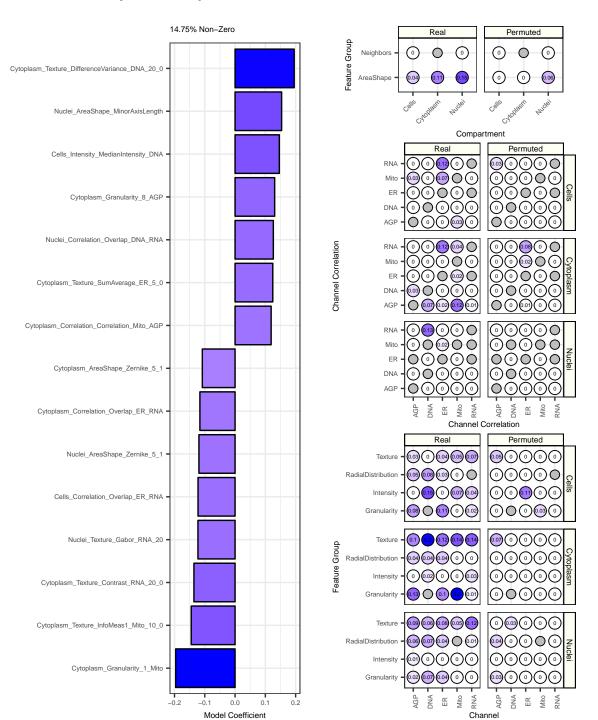


% Caspase / % Dead Only



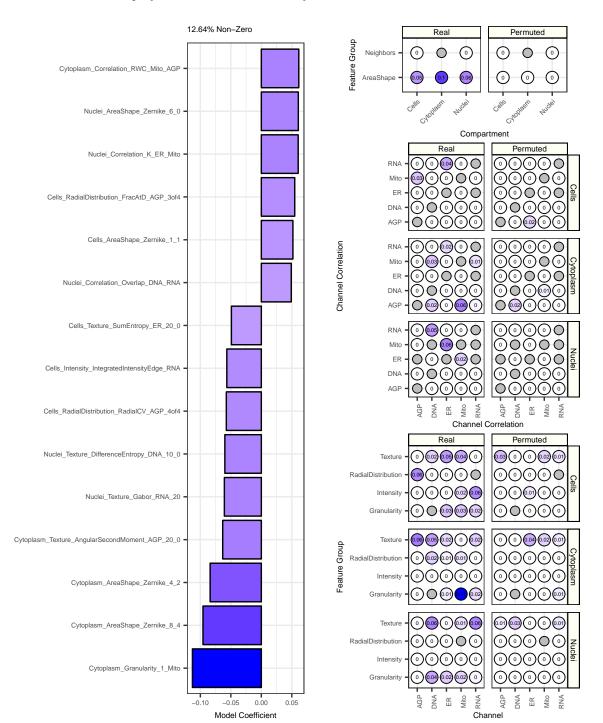


% All Dead (DRAQ7+)





% Dead Only (CASP-; DRAQ7+)



Max Abs. Weight

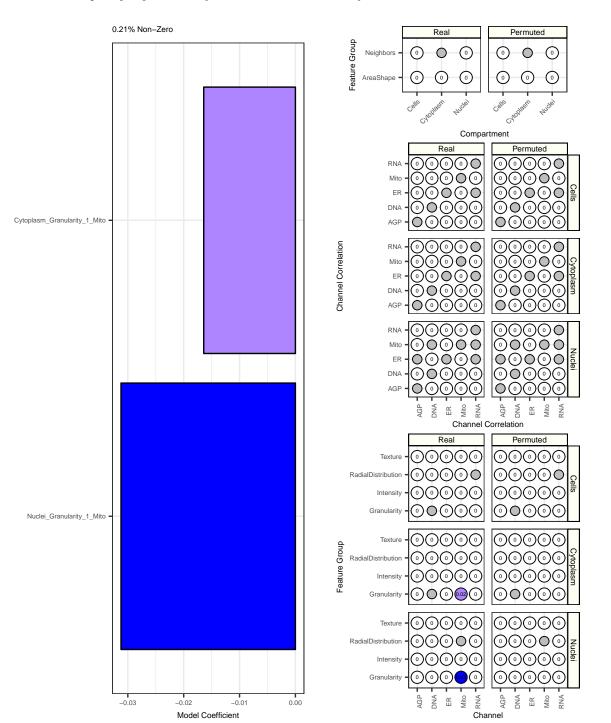
0.09

0.06

0.03

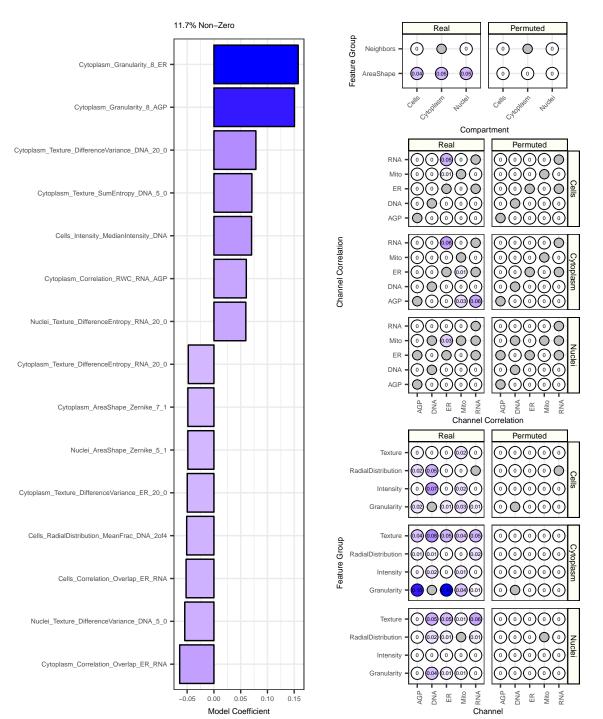
0.00

% Early Apoptosis (CASP+; DRAQ7-)



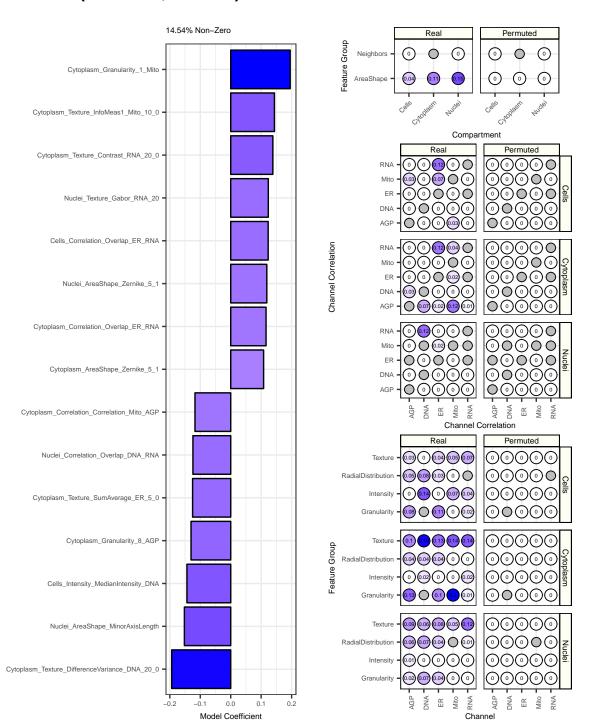


% Late Apoptosis (CASP+; DRAQ7+)



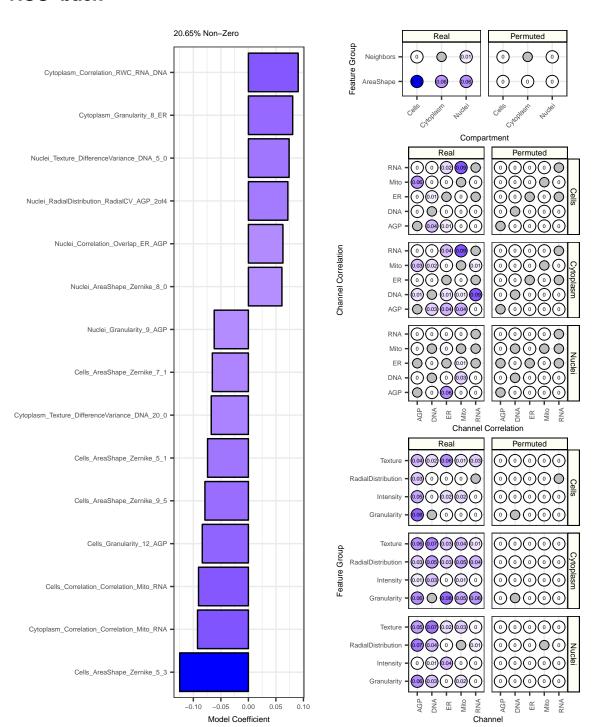


% Live (DRAQ7-; CASP-)





ROS-back





ROS

