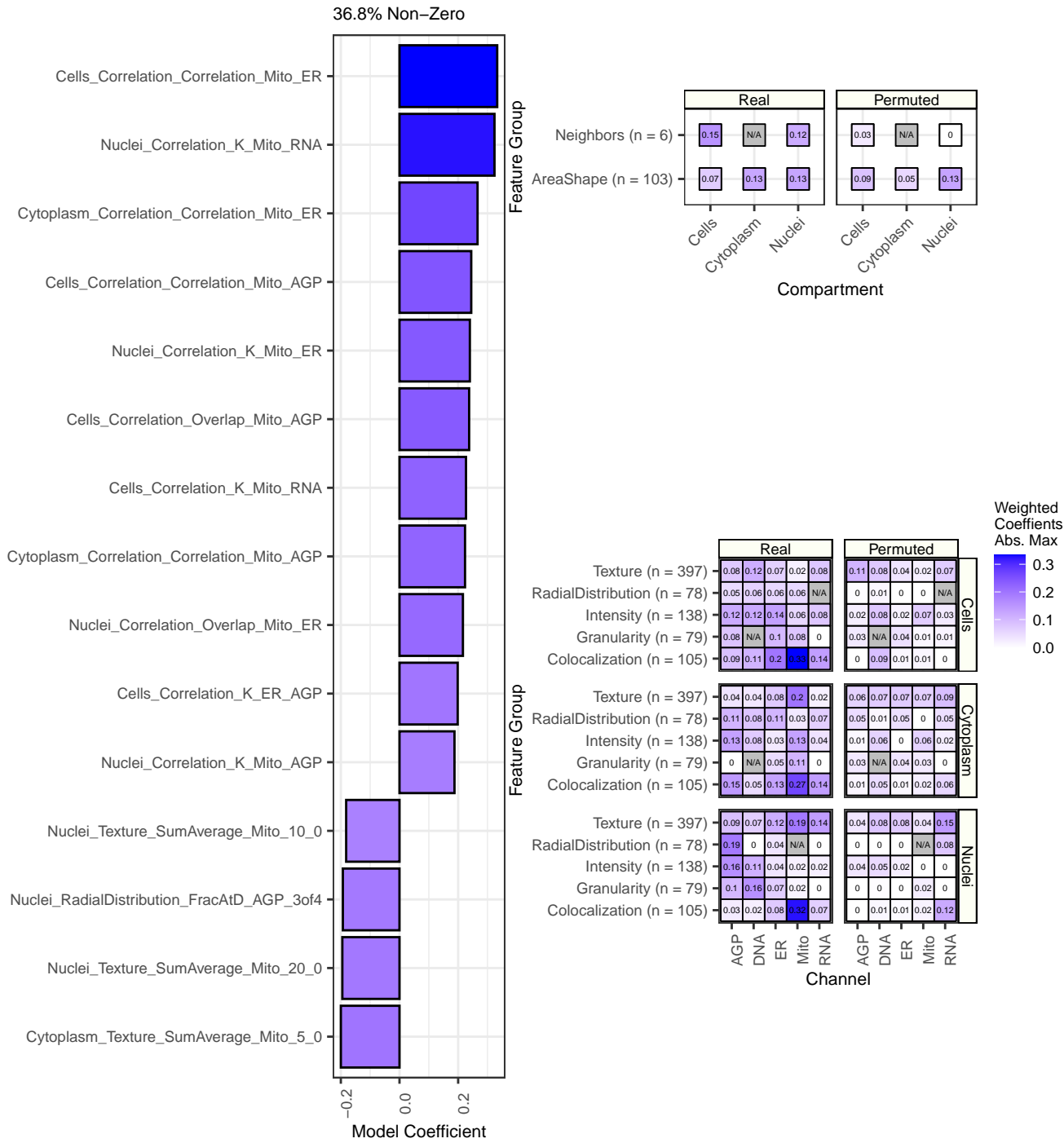
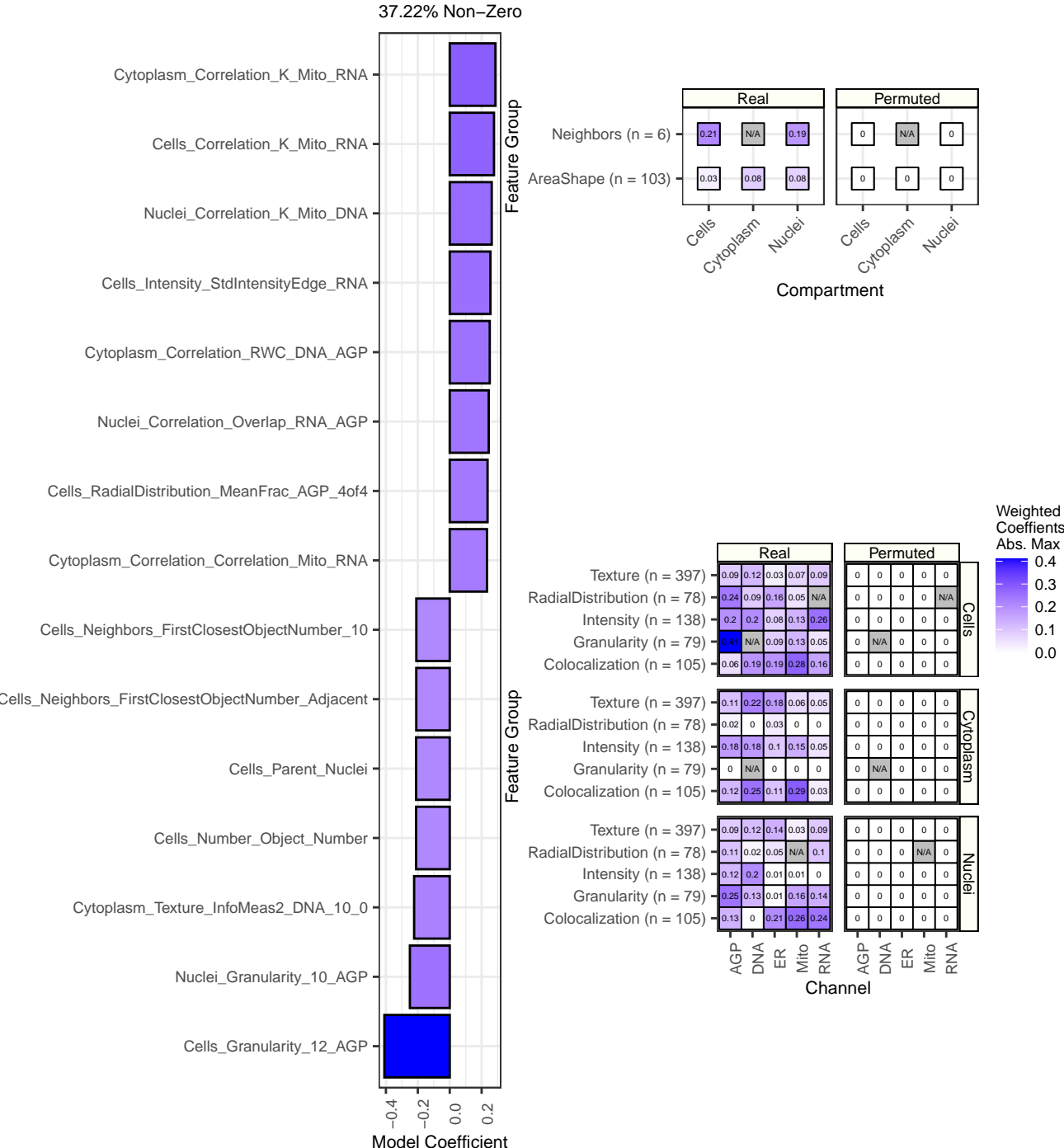


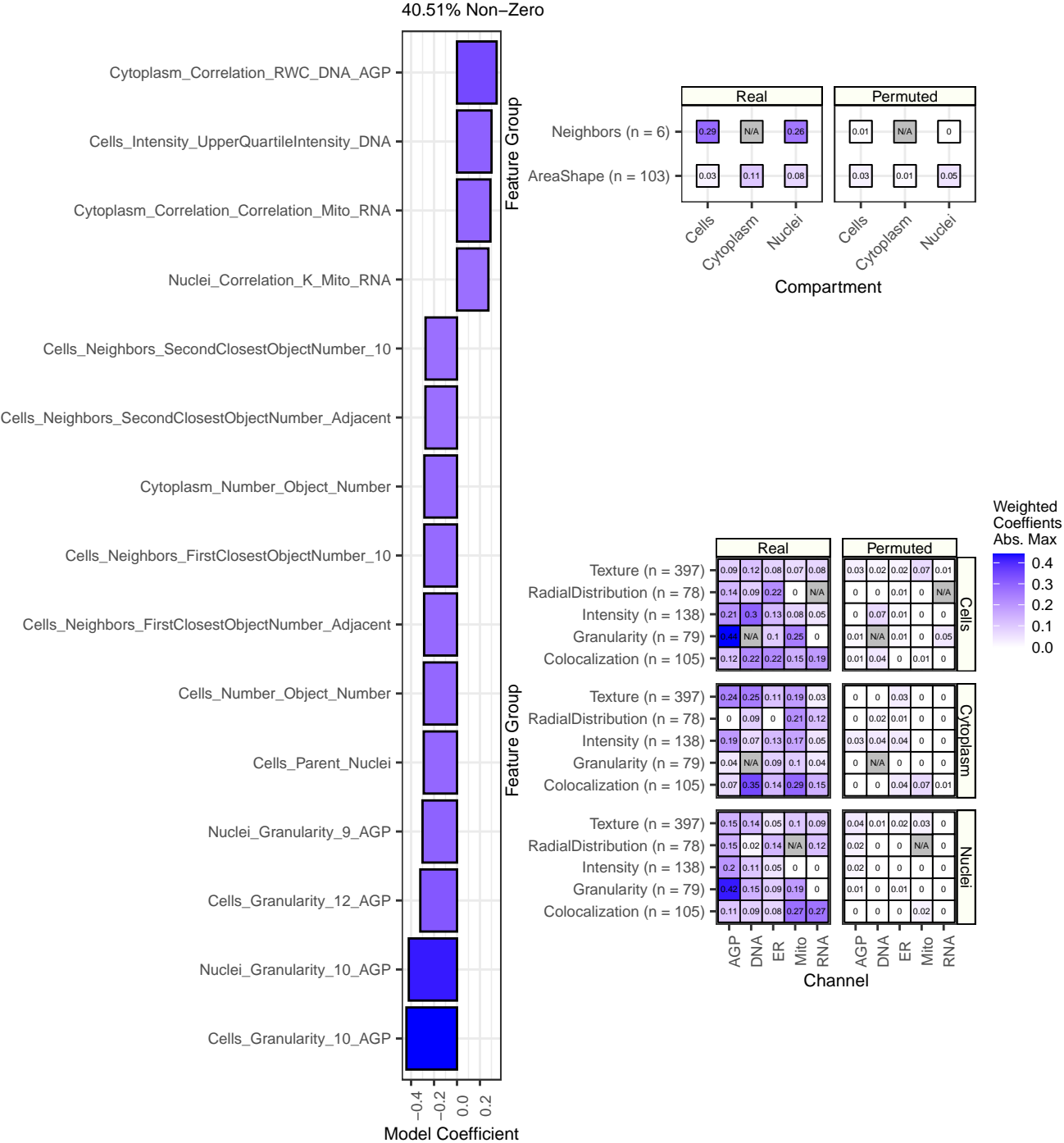
ALL – % High gH2AX Spots



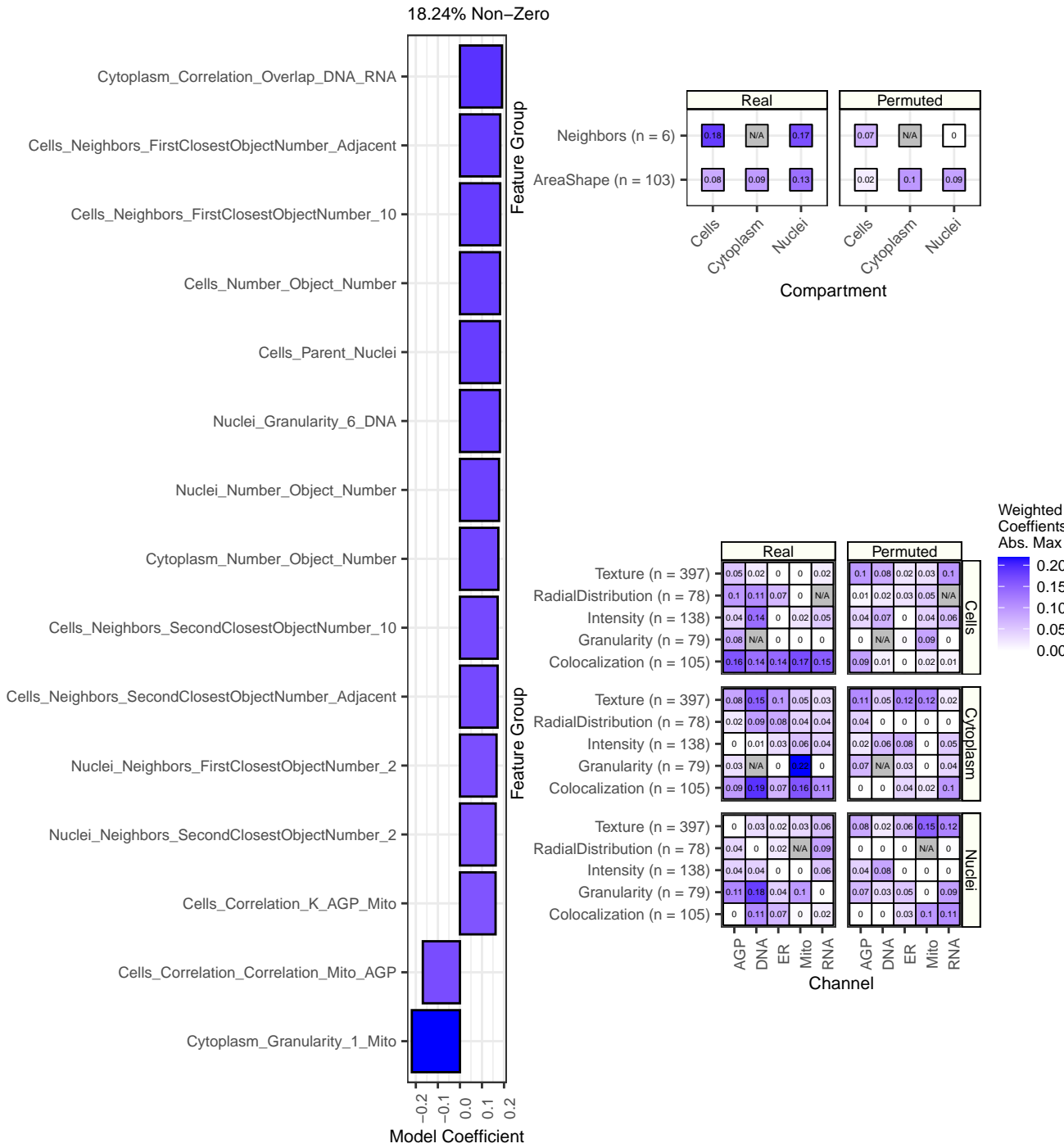
ALL – Polynuclear



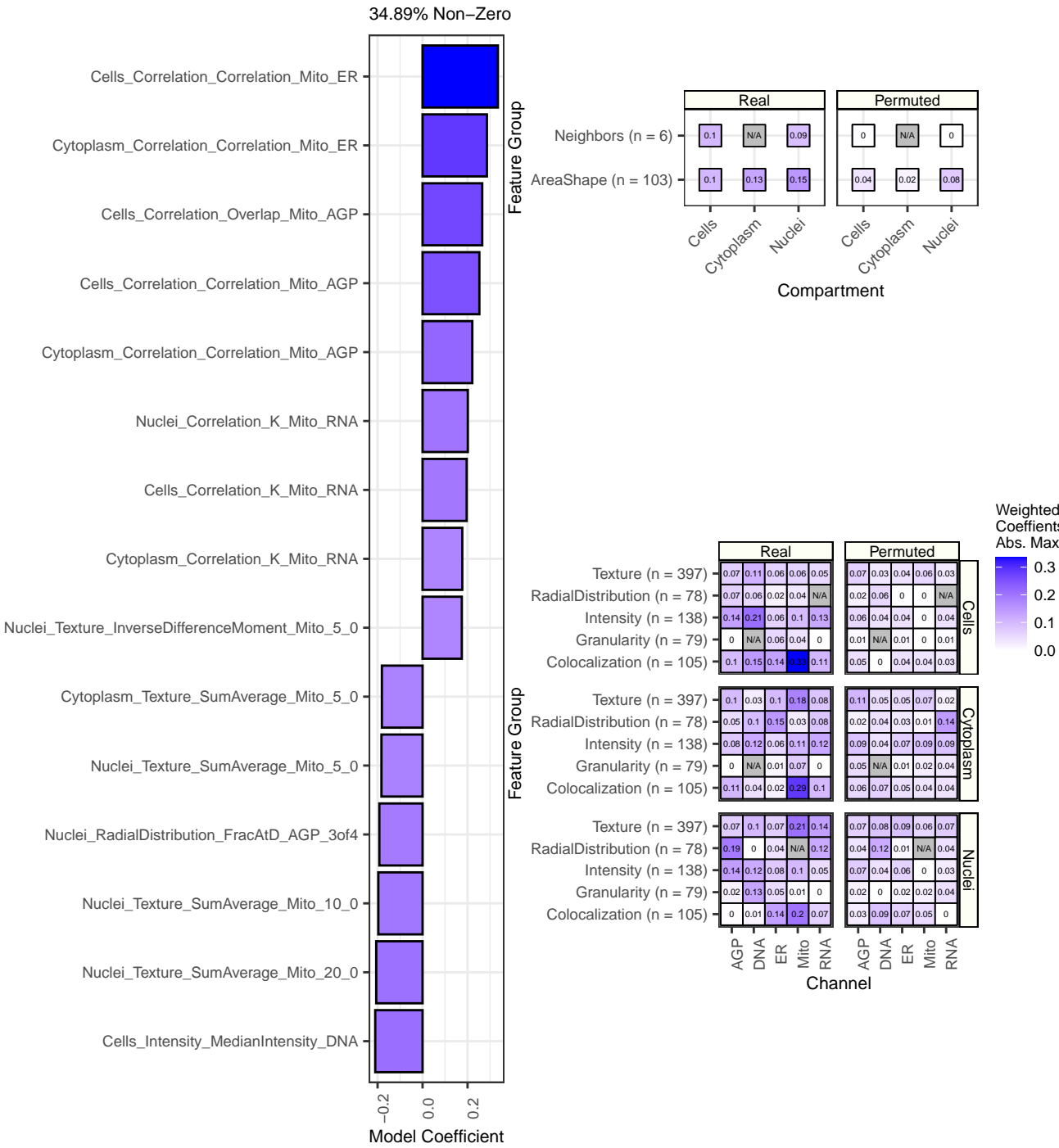
ALL – Polyploid



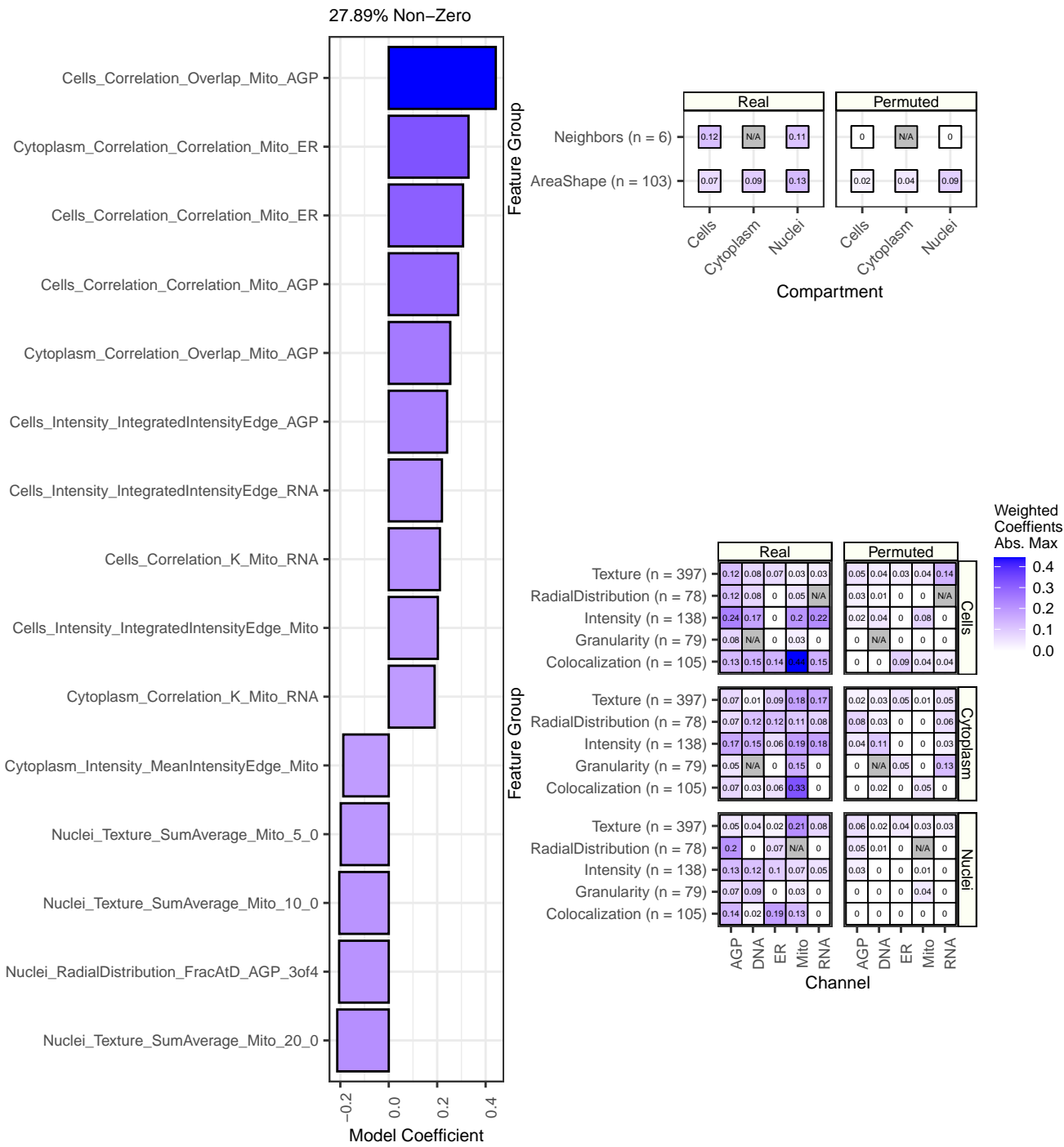
ALL – # cells



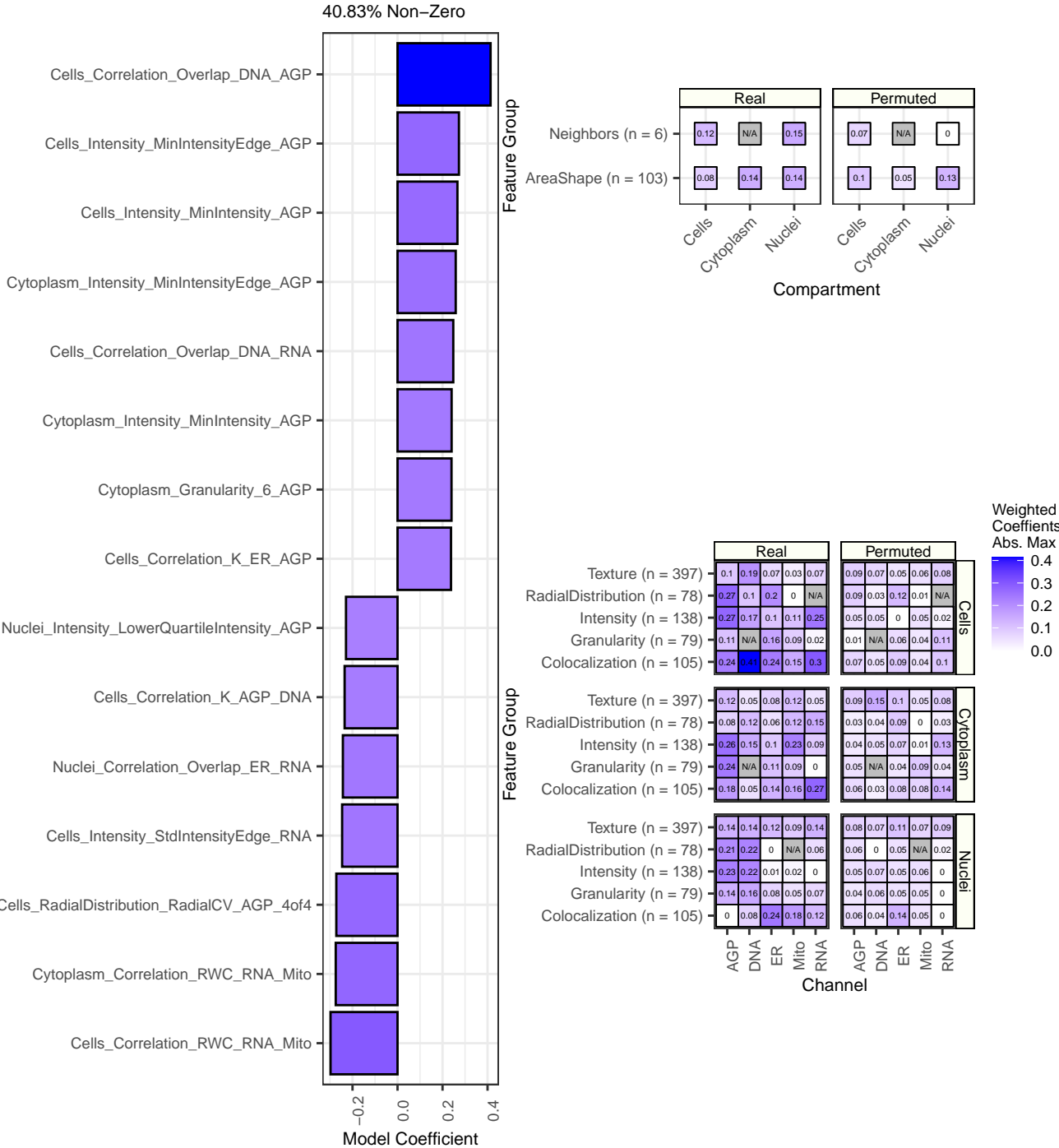
ALL – # of gH2AX Spots



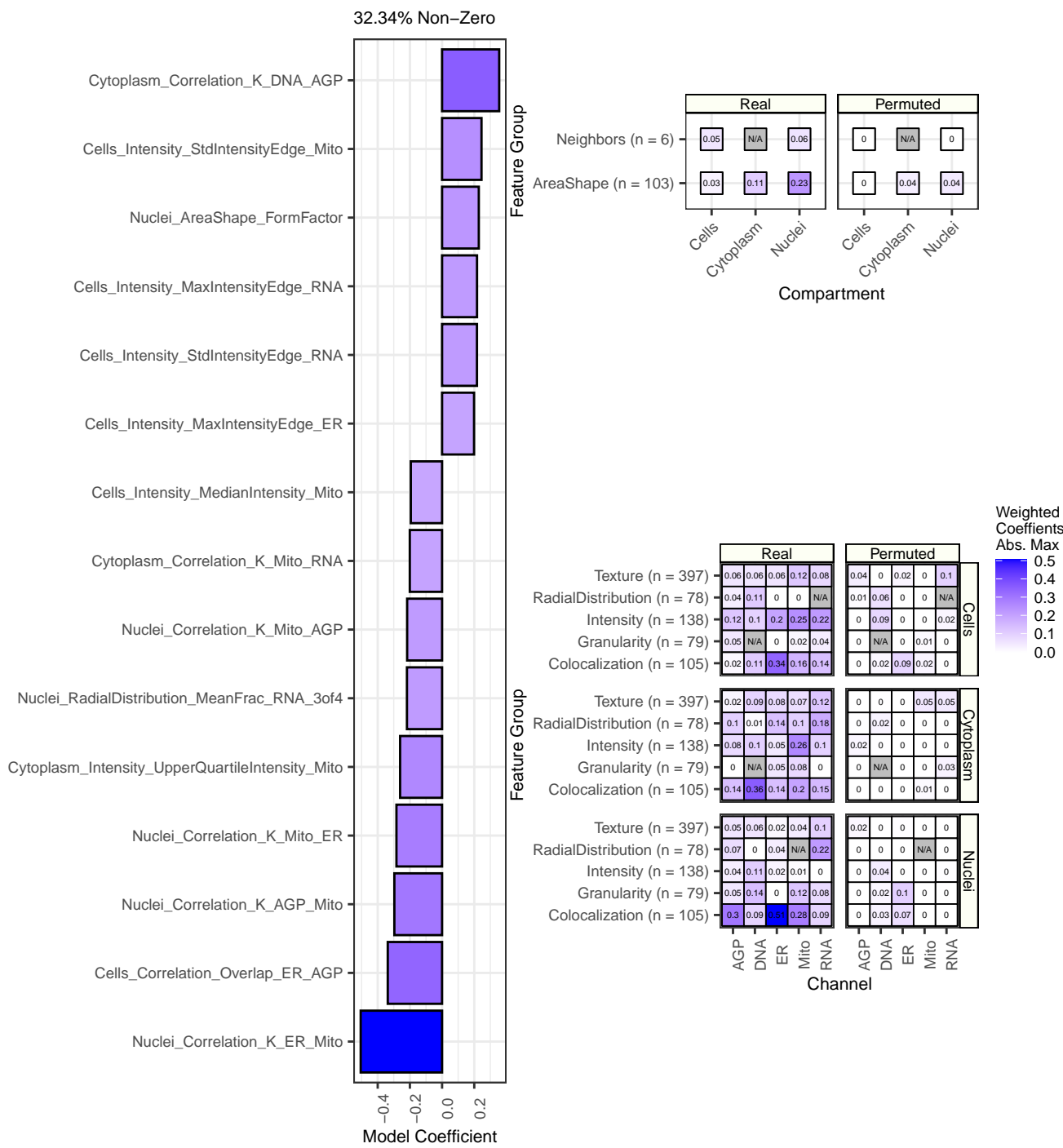
ALL – # of gH2AX Spots per Area of Nucleus



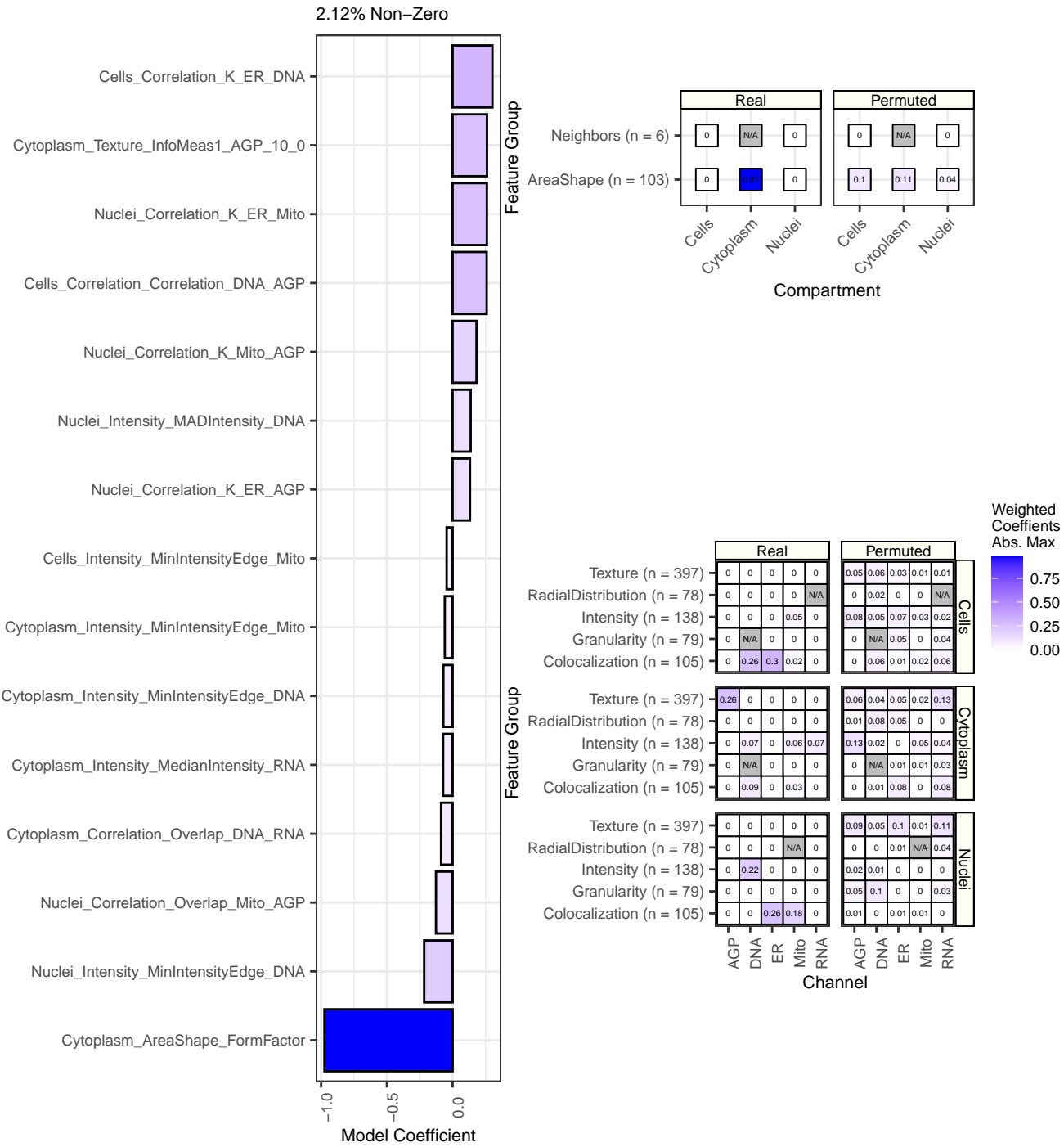
ALL – Nucleus Area



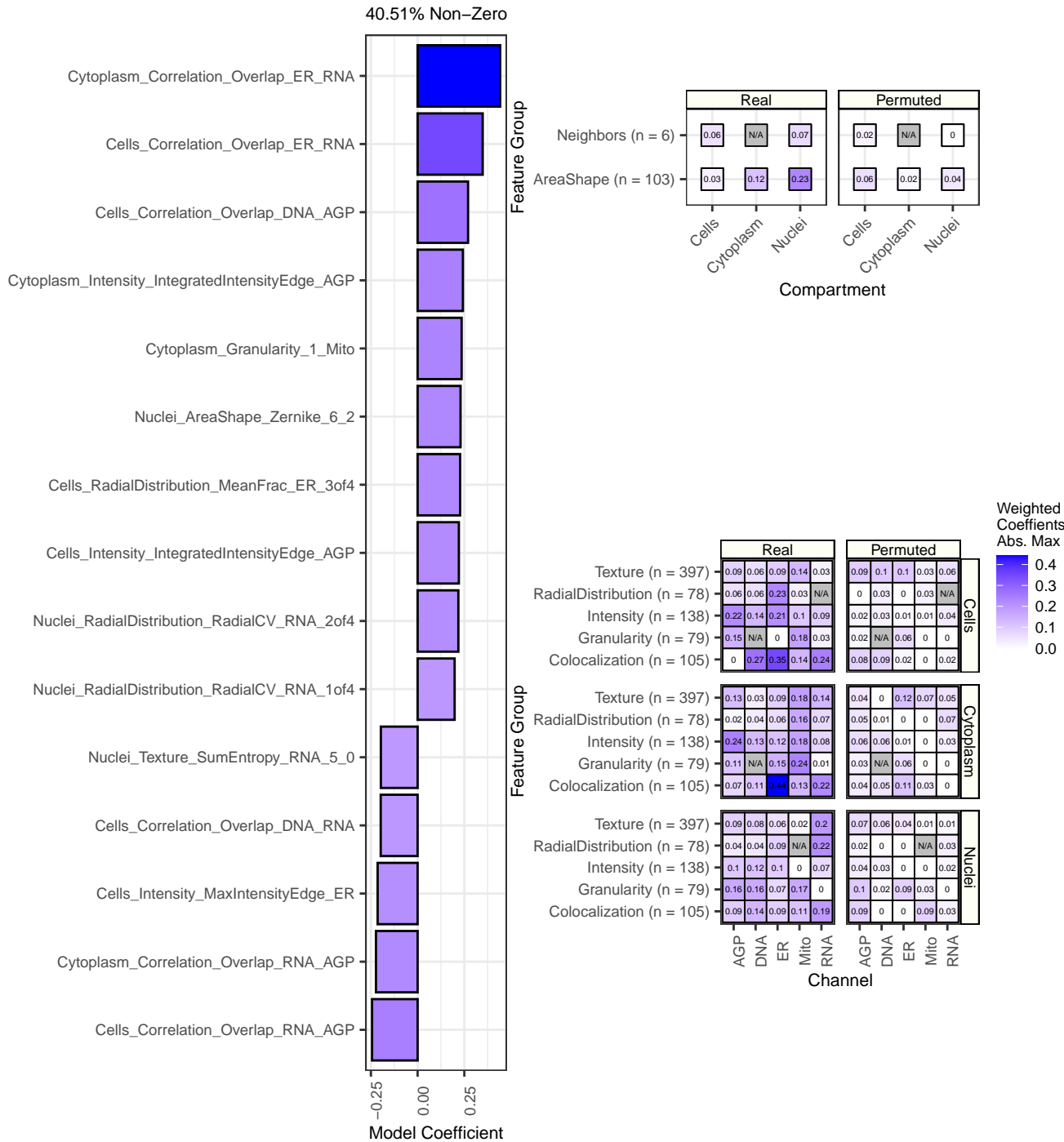
ALL – Nucleus Roundness



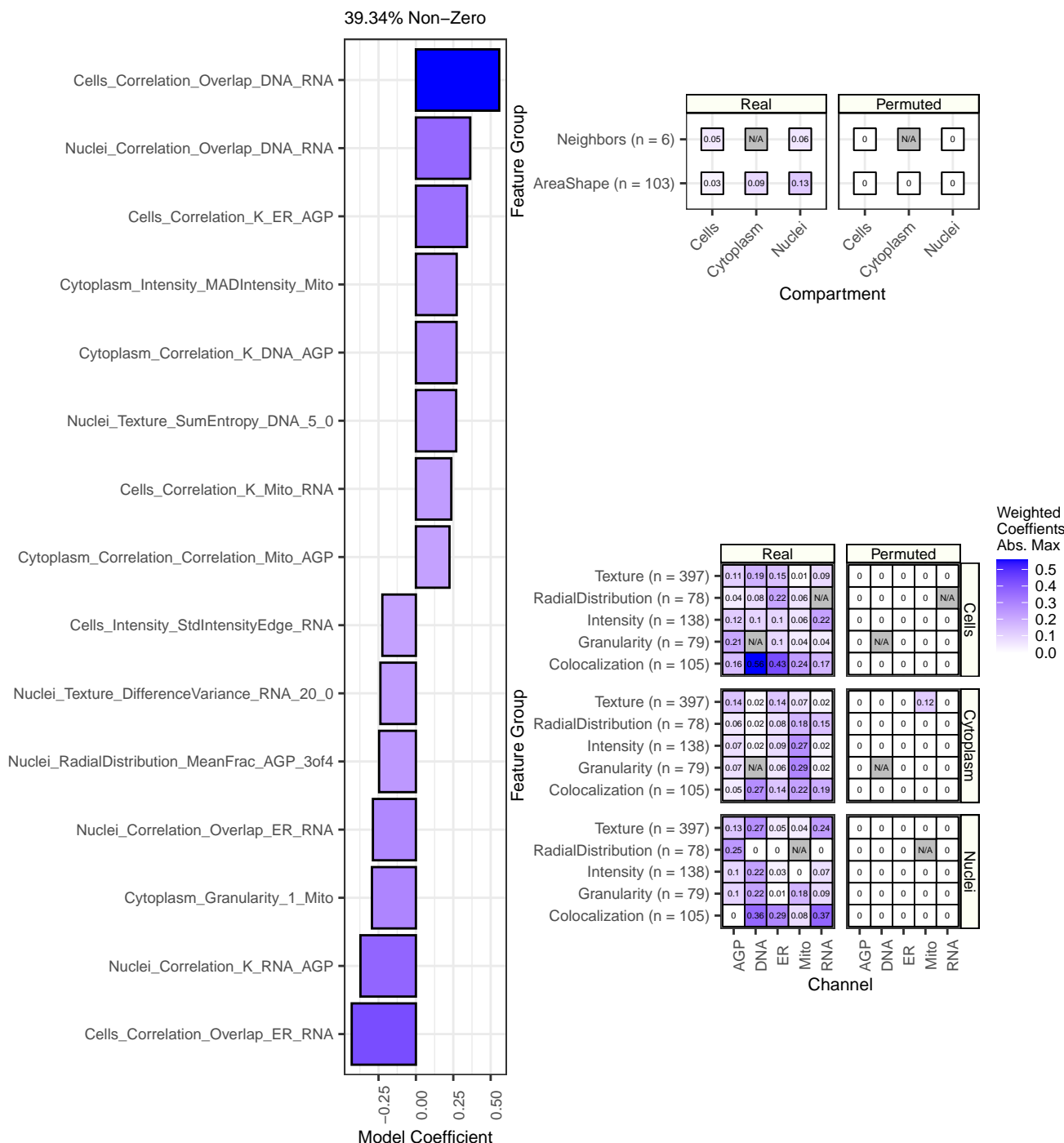
CC – % early M



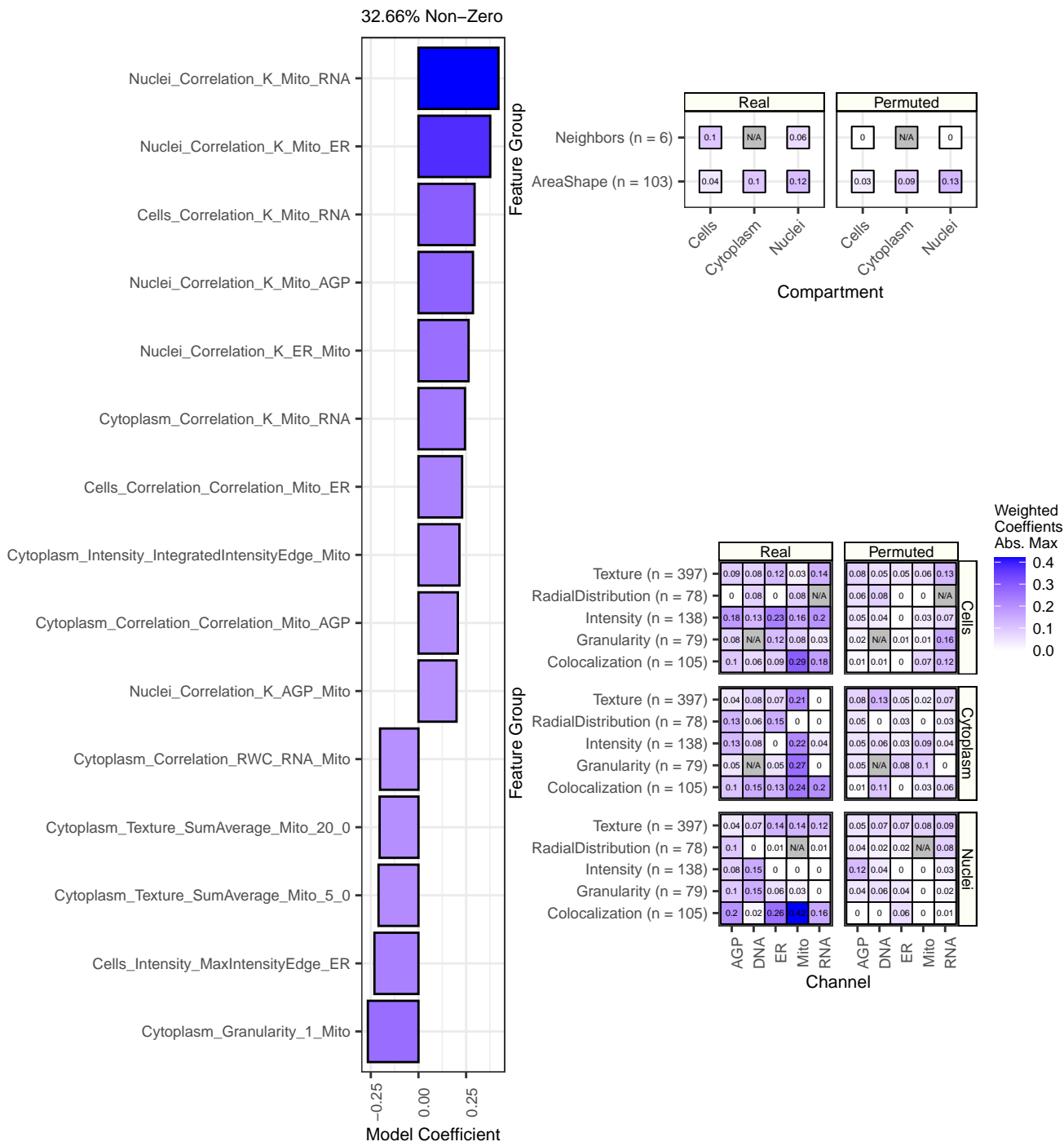
CC – % G1



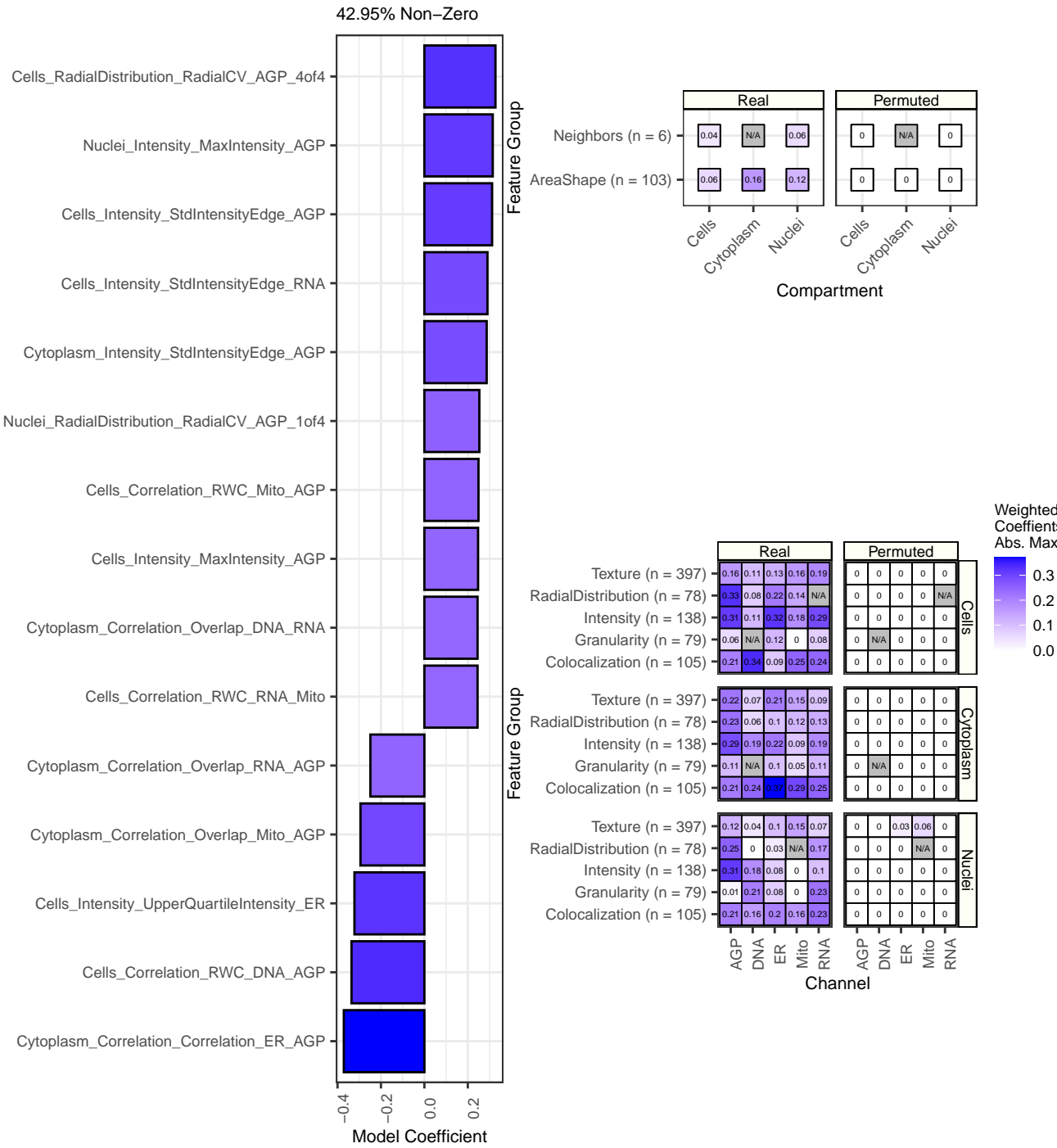
CC – % G2



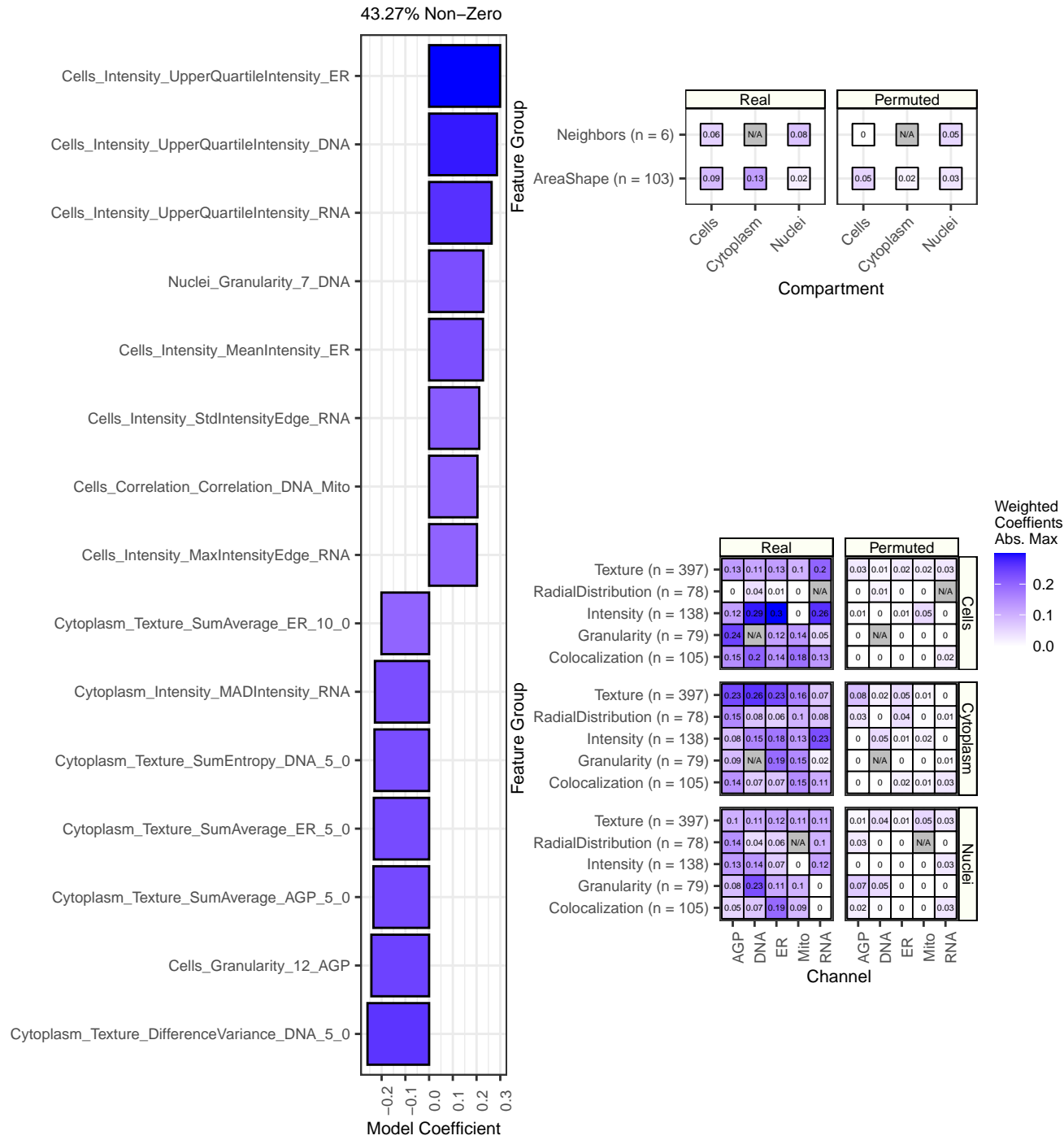
CC – % High gH2AX spots



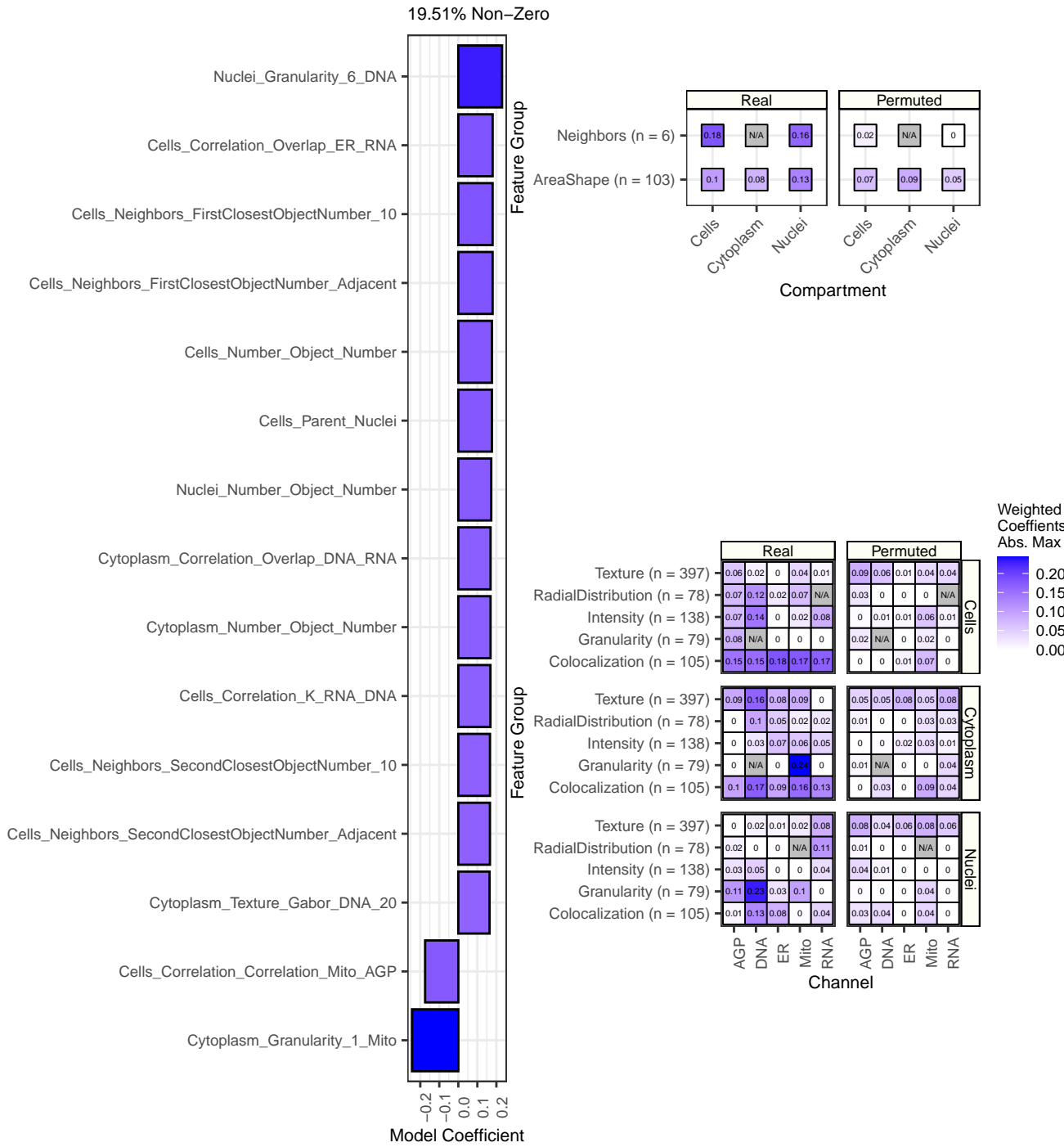
CC – % Late M



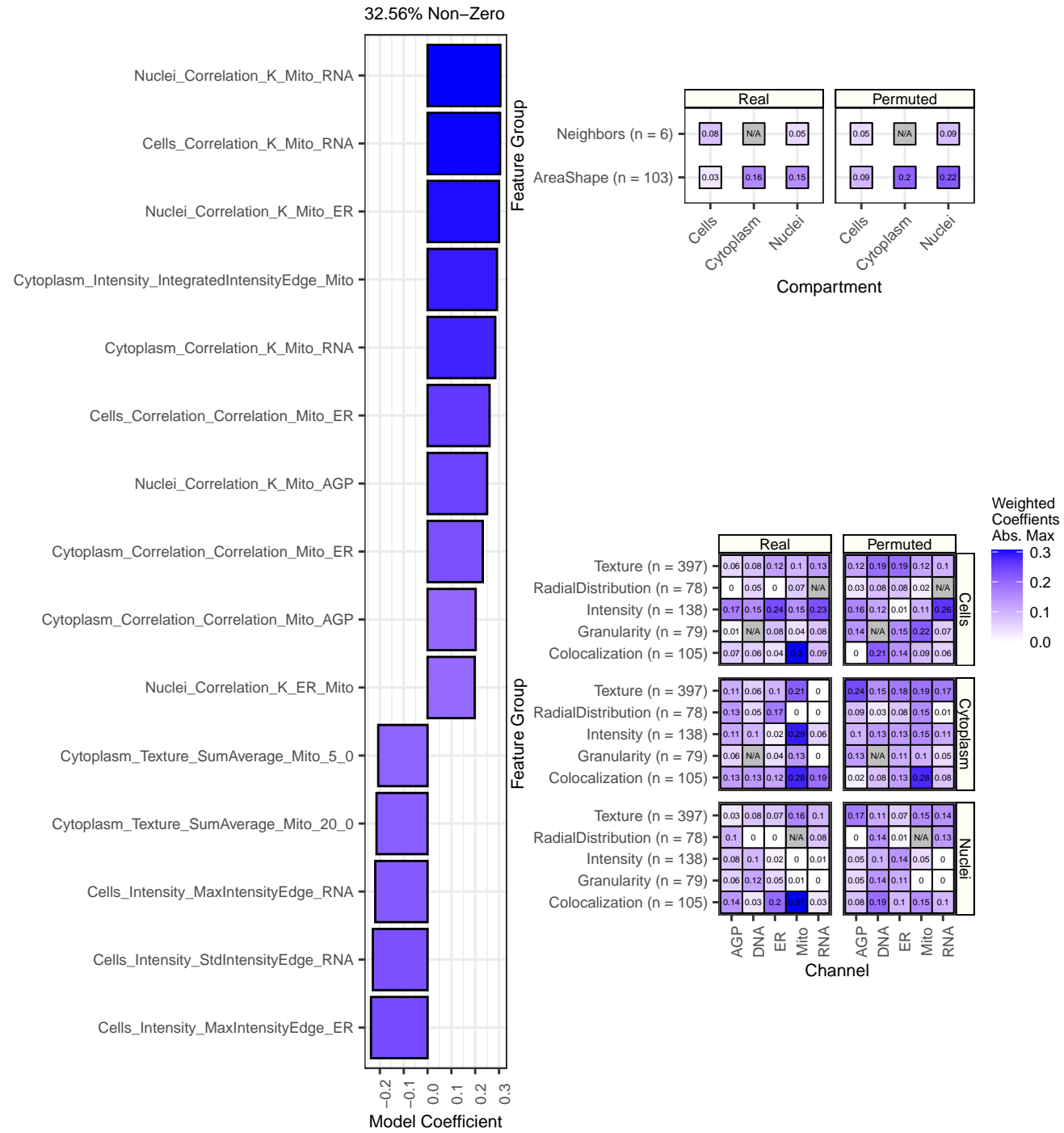
CC – % M



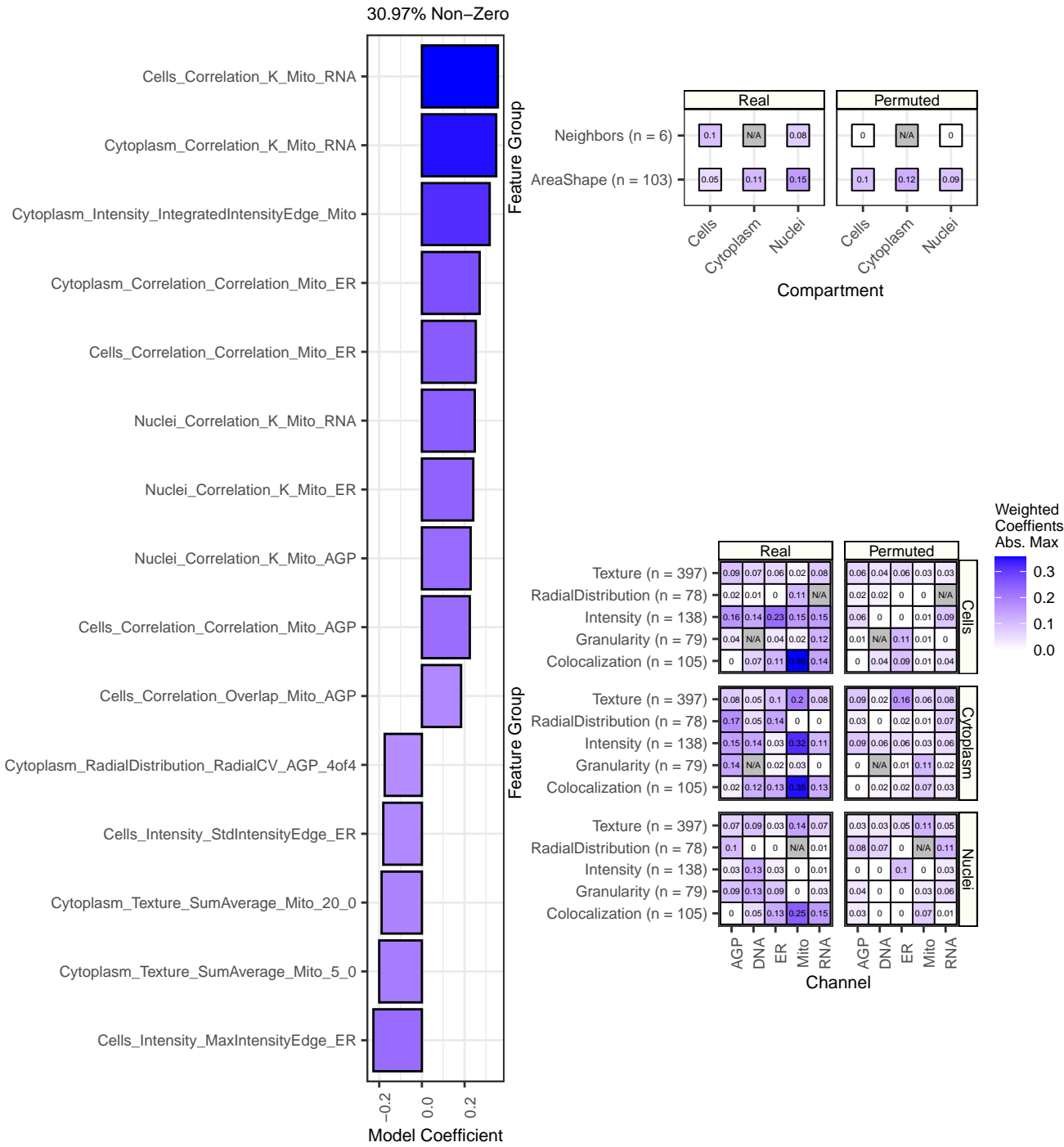
CC – # cells



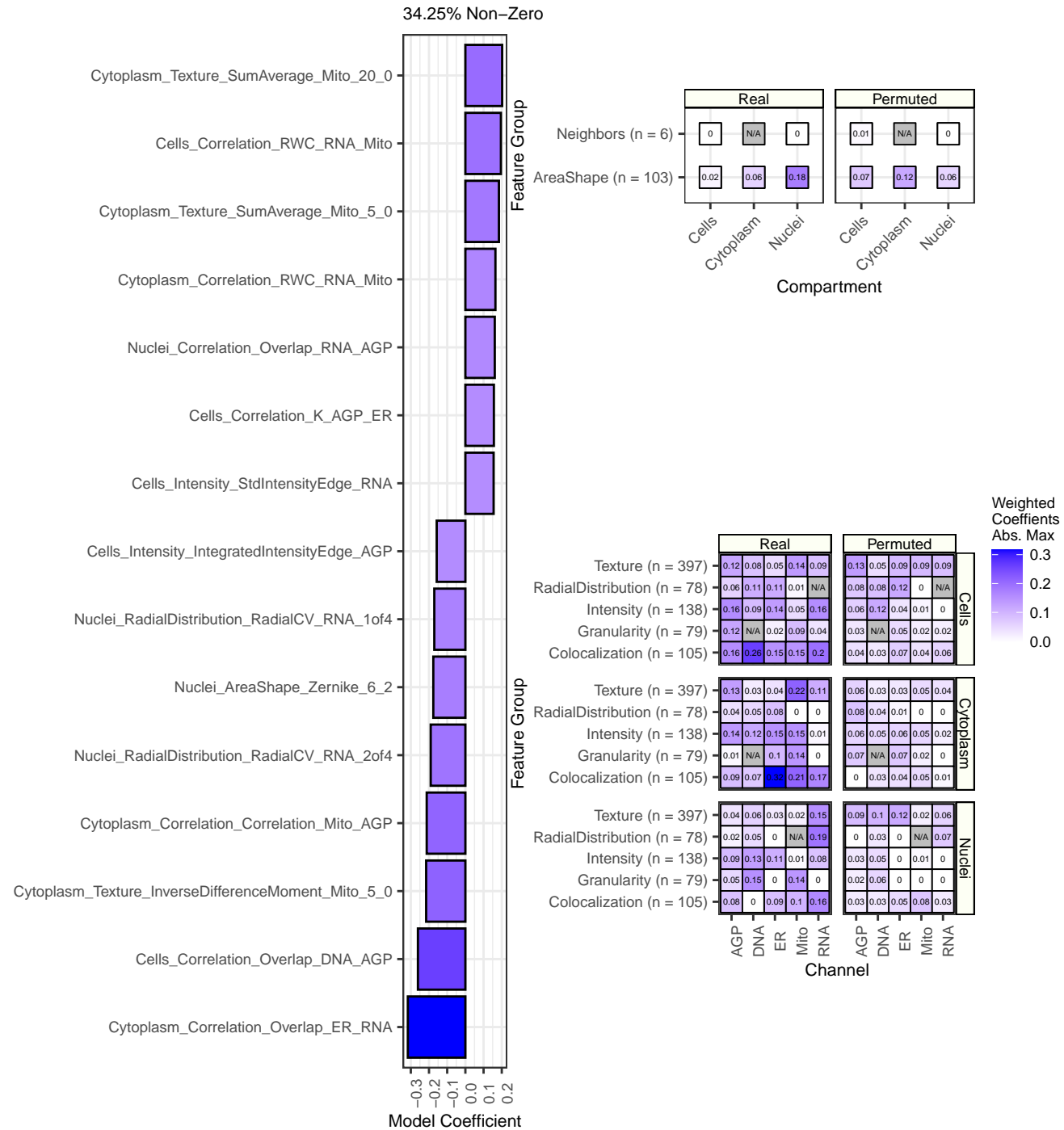
CC – # of gH2AX Spots



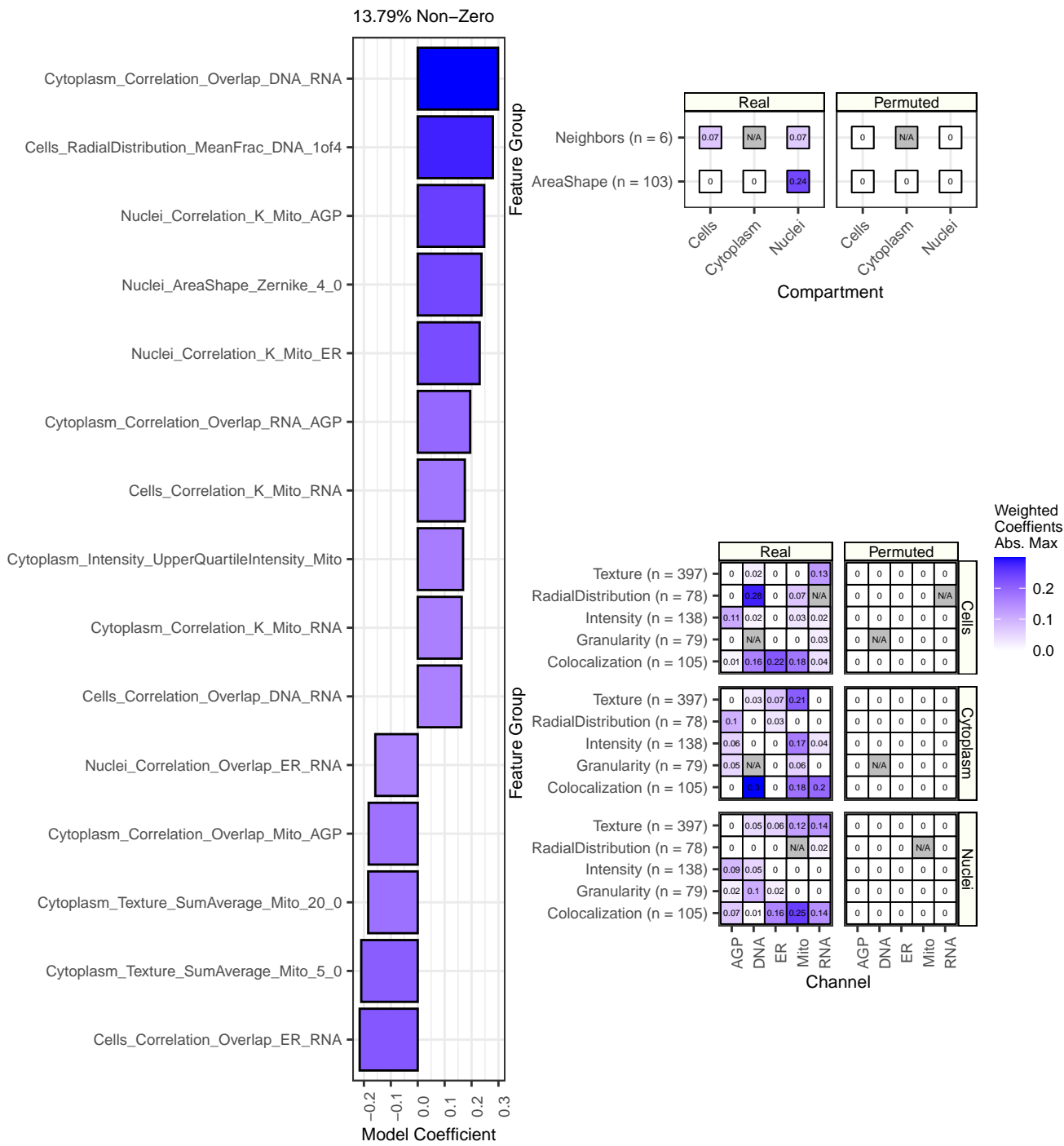
CC – # of gH2AX Spots per Area of Nucleus



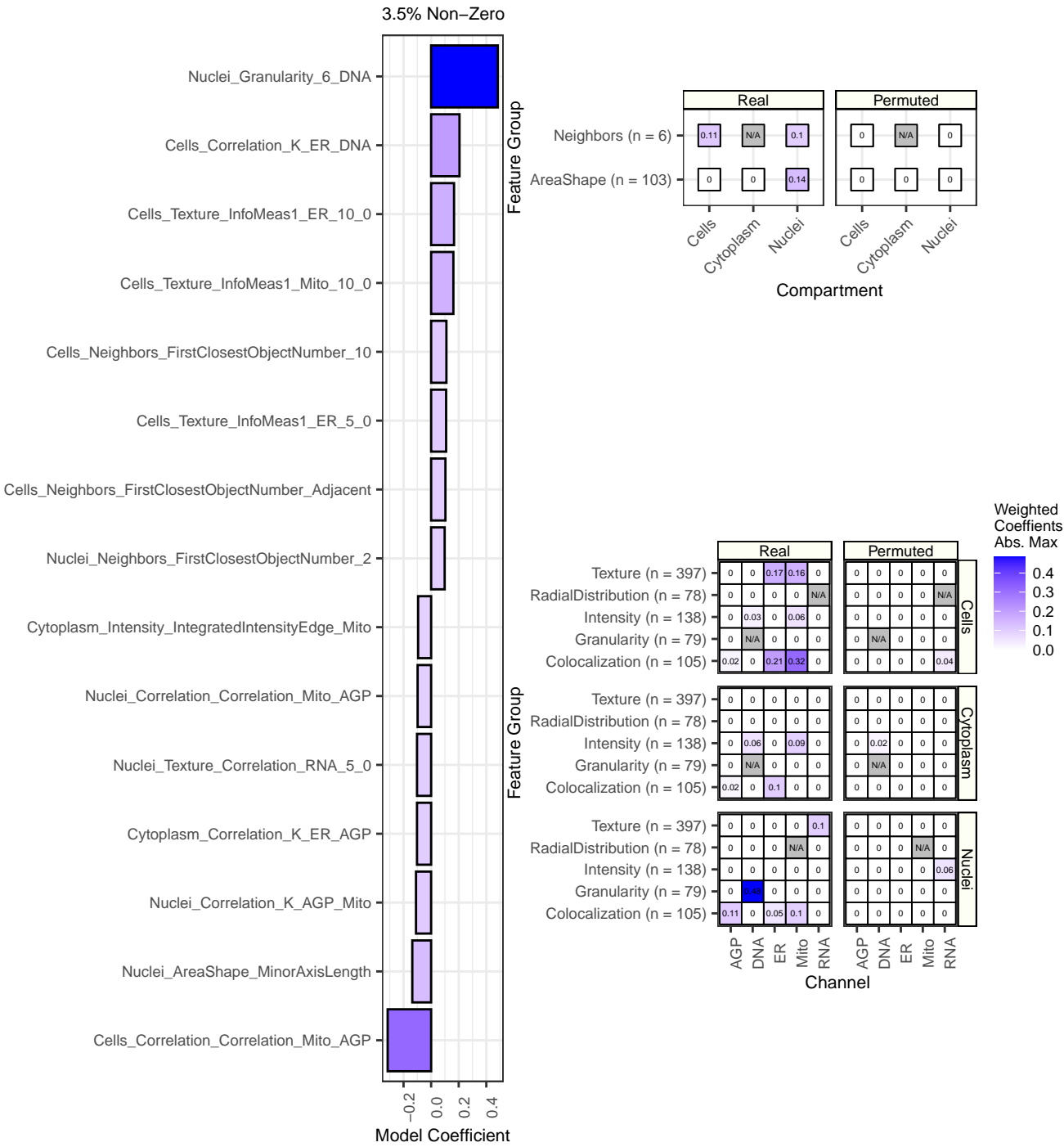
CC – % S



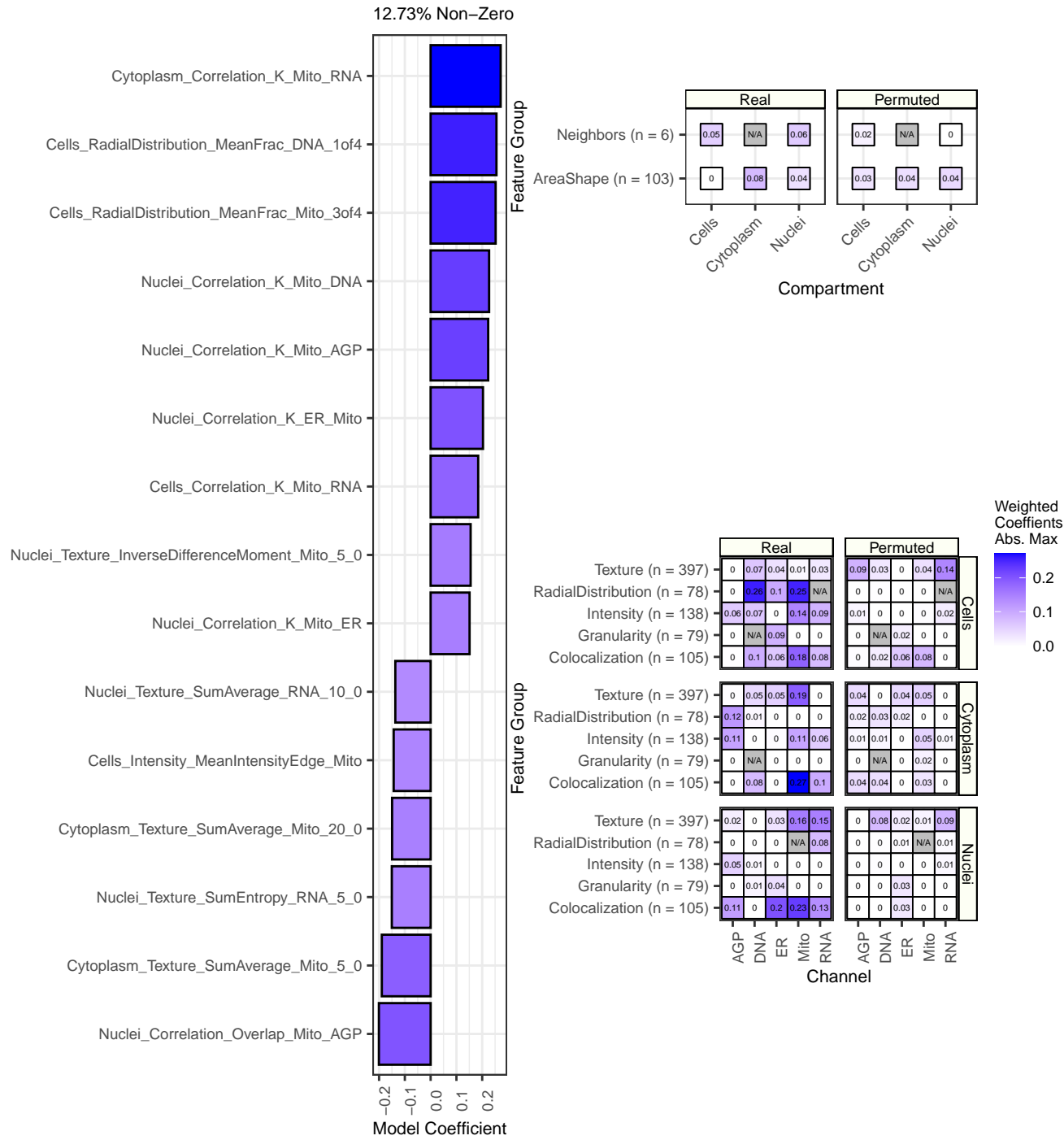
early M – % High gH2AX Spots



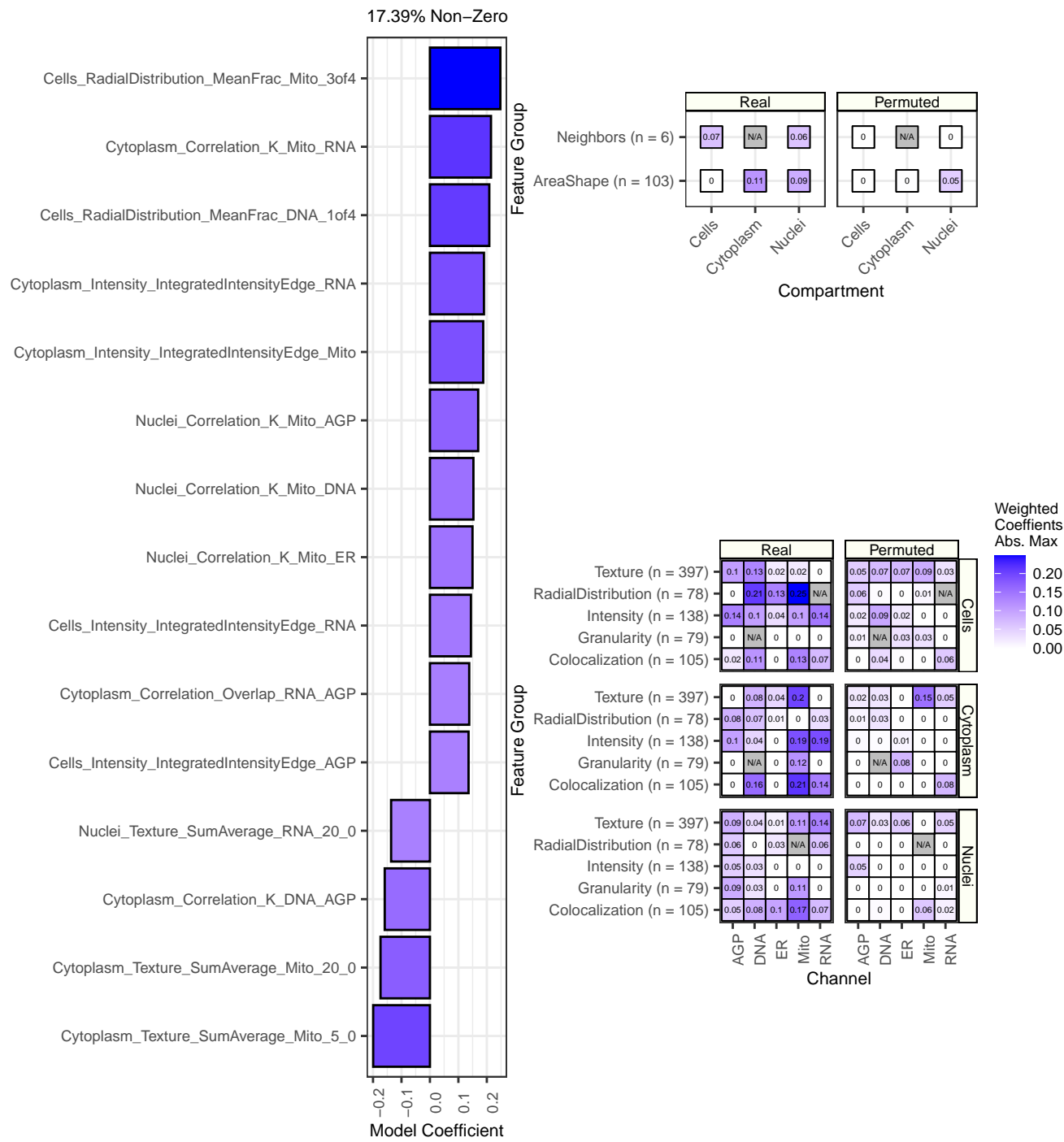
early M – # cells



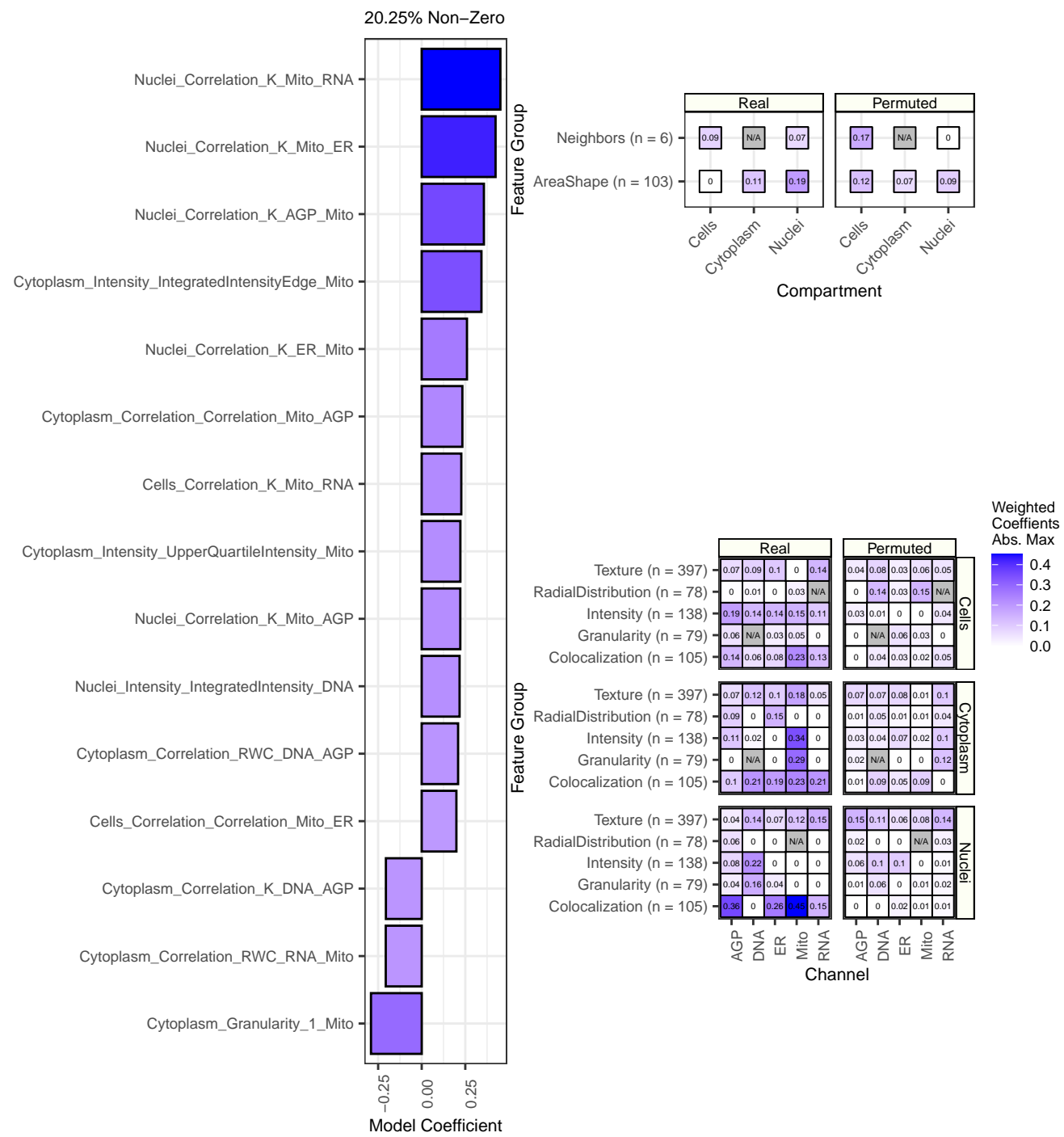
early M – # of gH2AX Spots



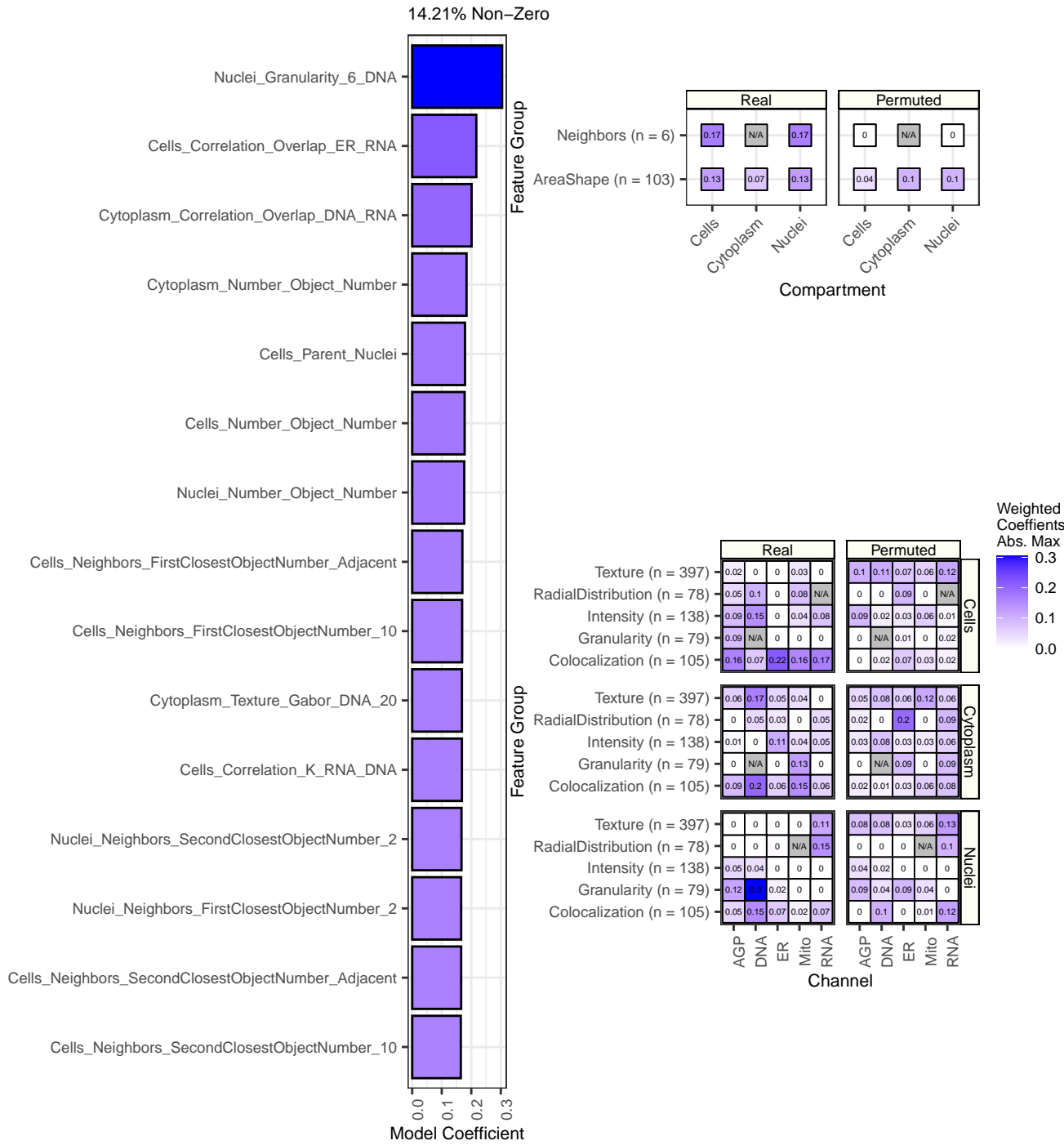
early M – # of gH2AX Spots per Area of Nucleus



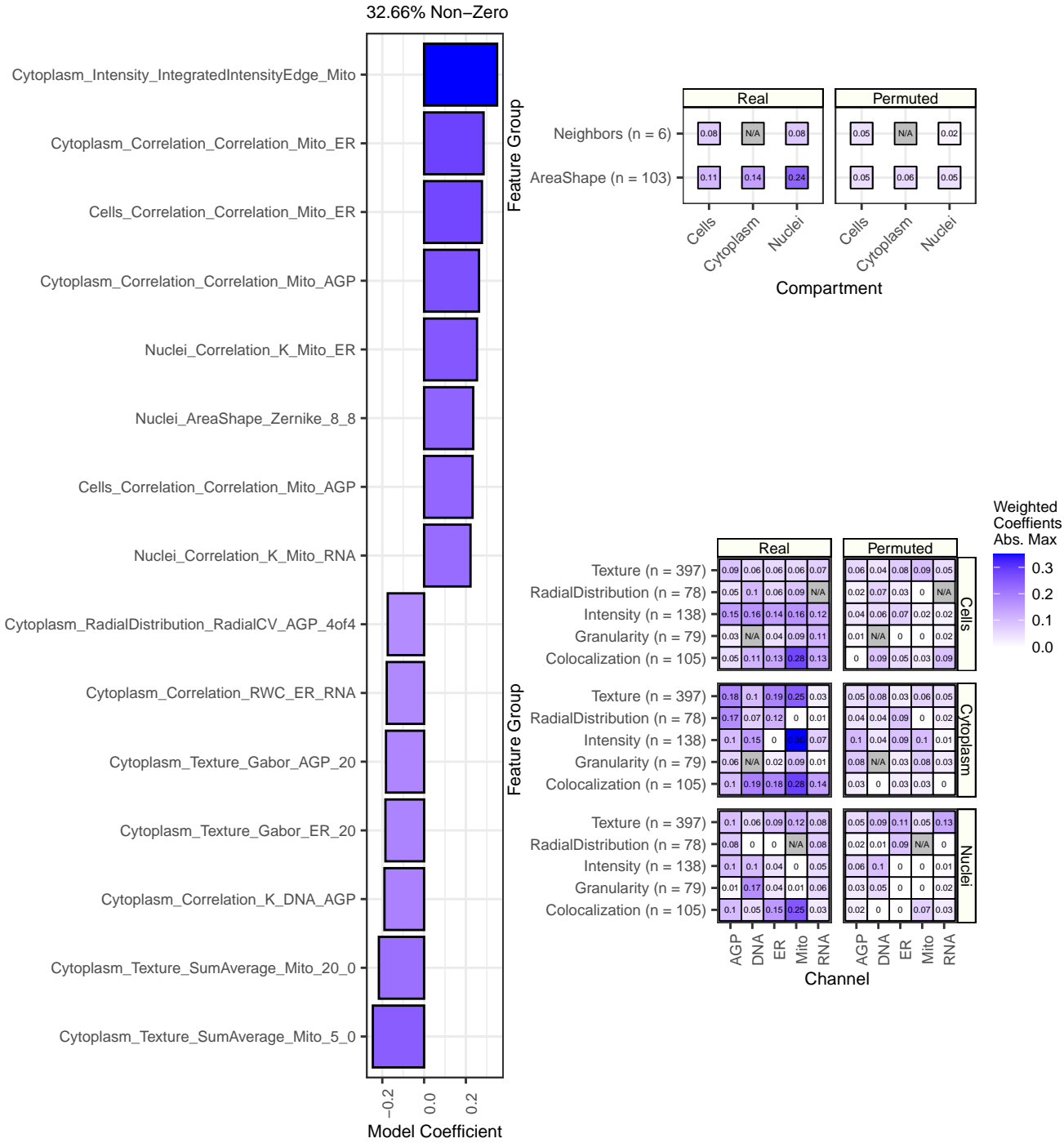
G1 – % High gH2AX Spots



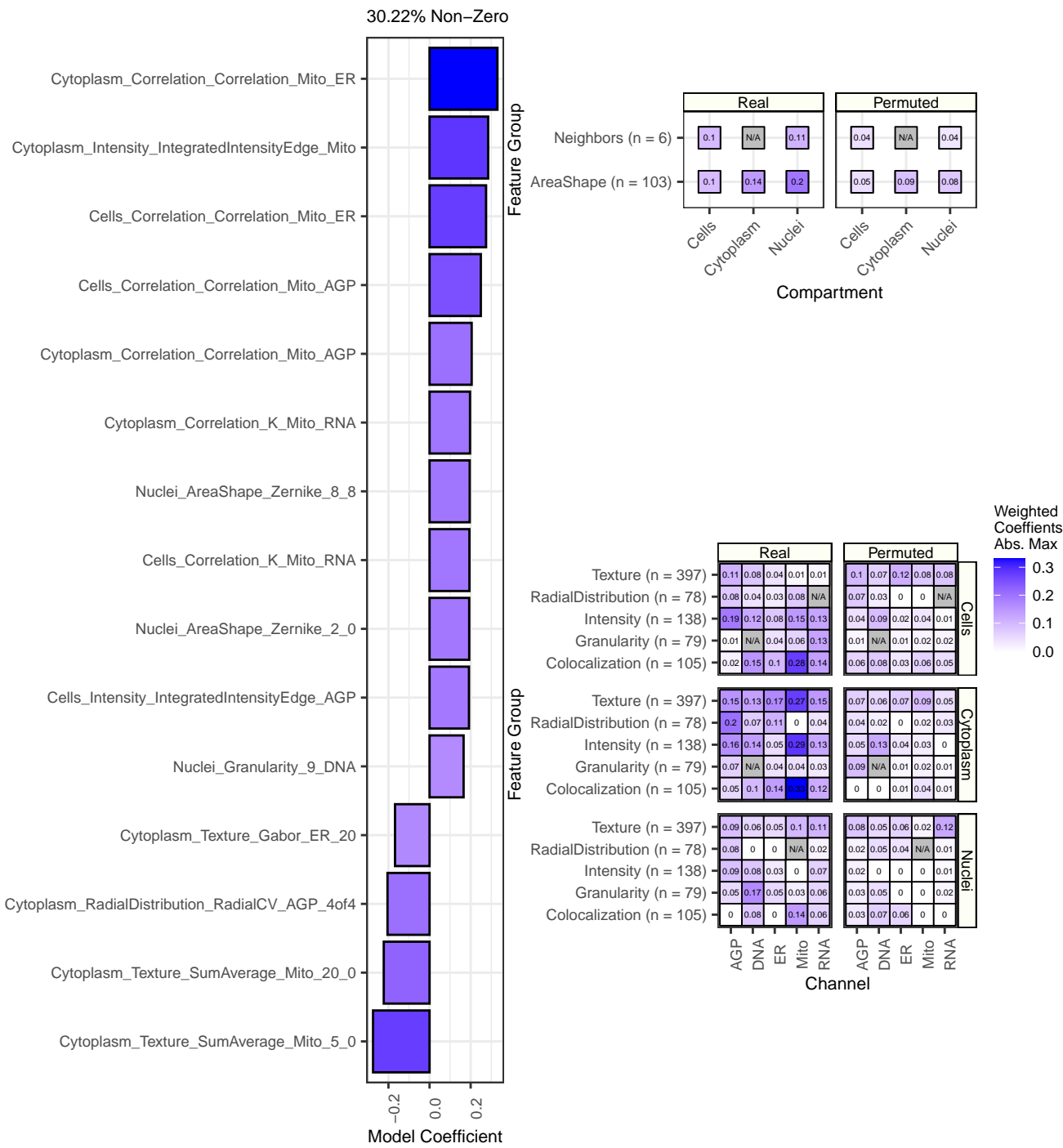
G1 – # cells



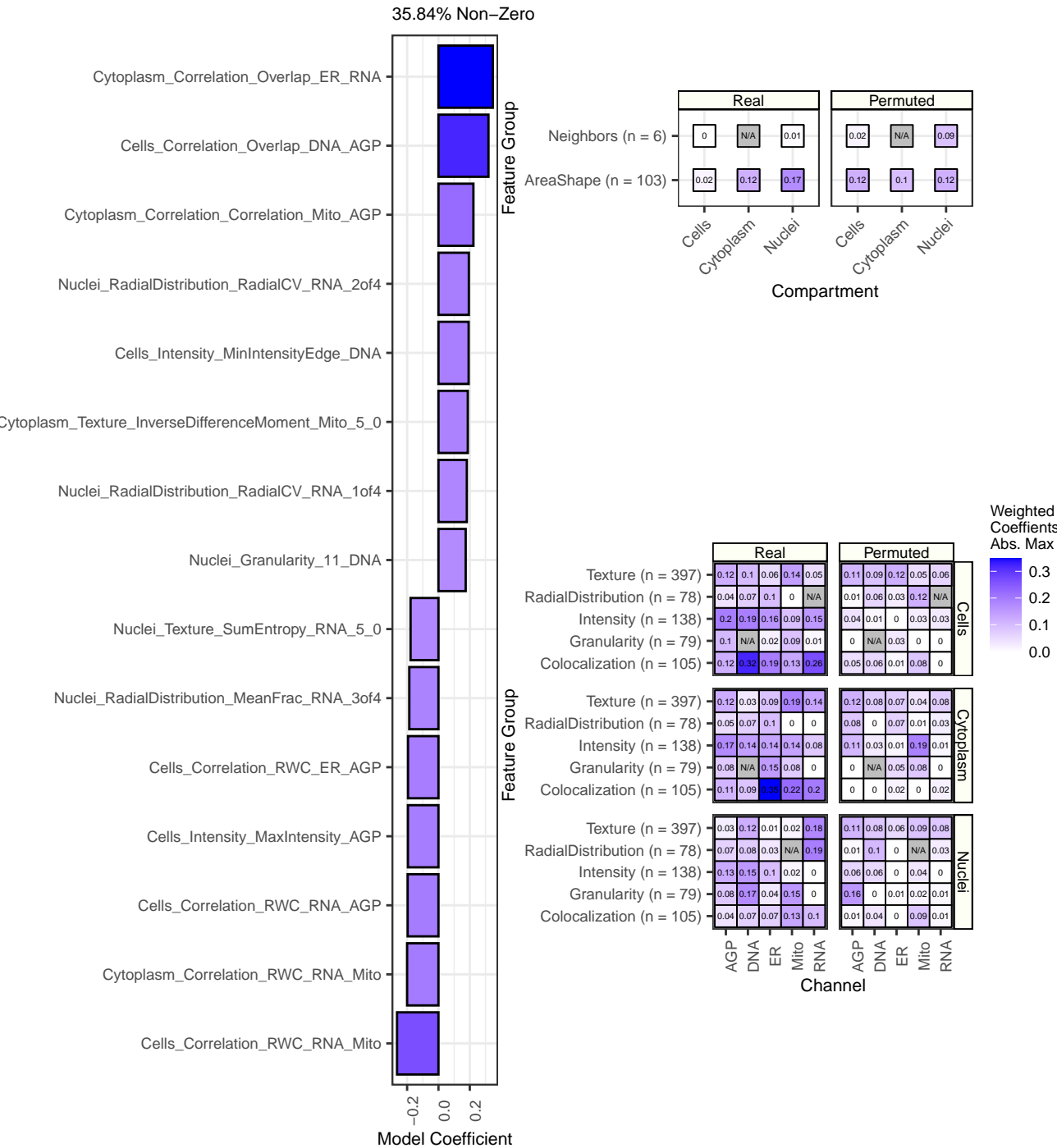
G1 – # of gH2AX Spots



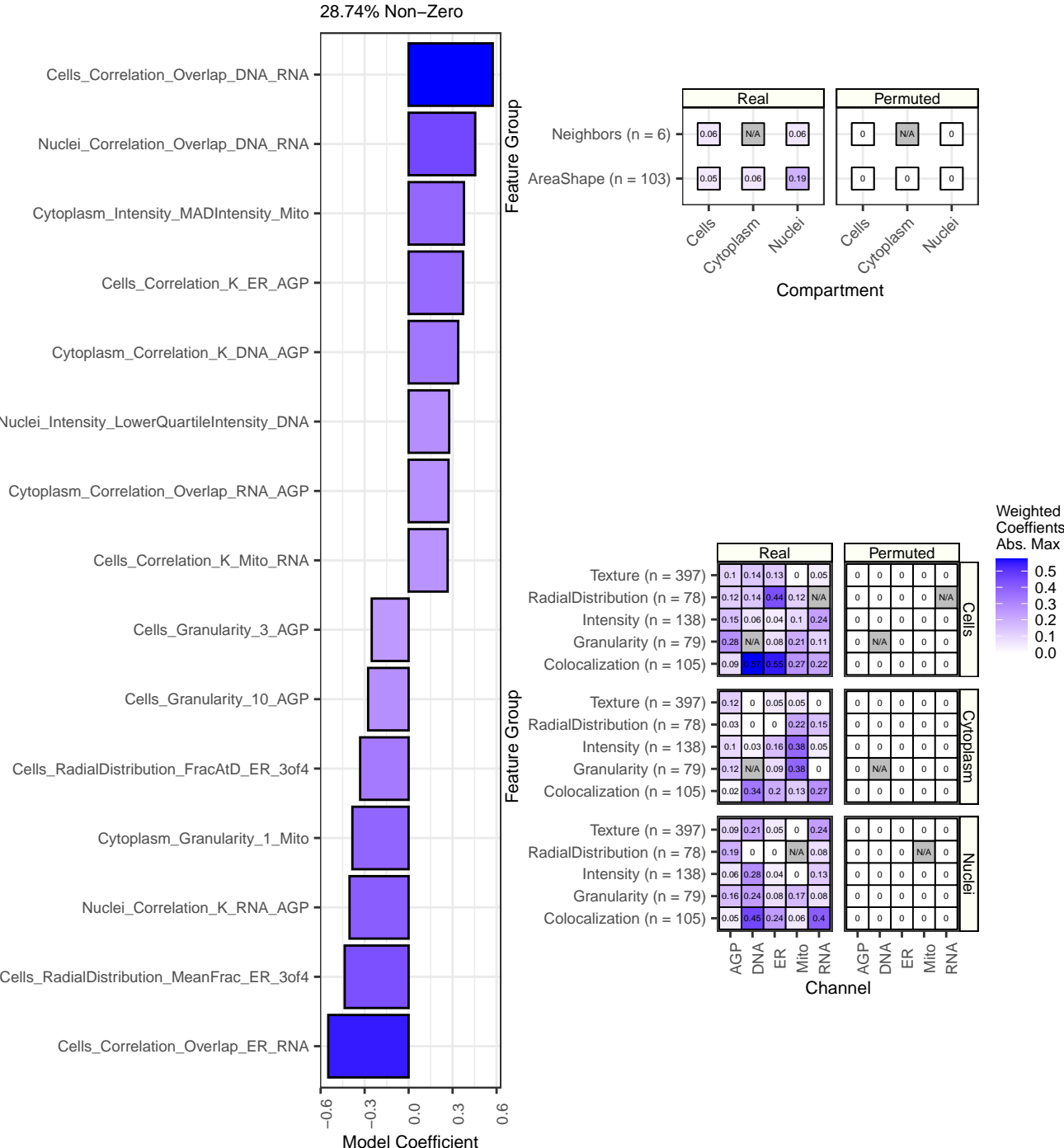
G1 – # of gH2AX Spots per Area of Nucleus



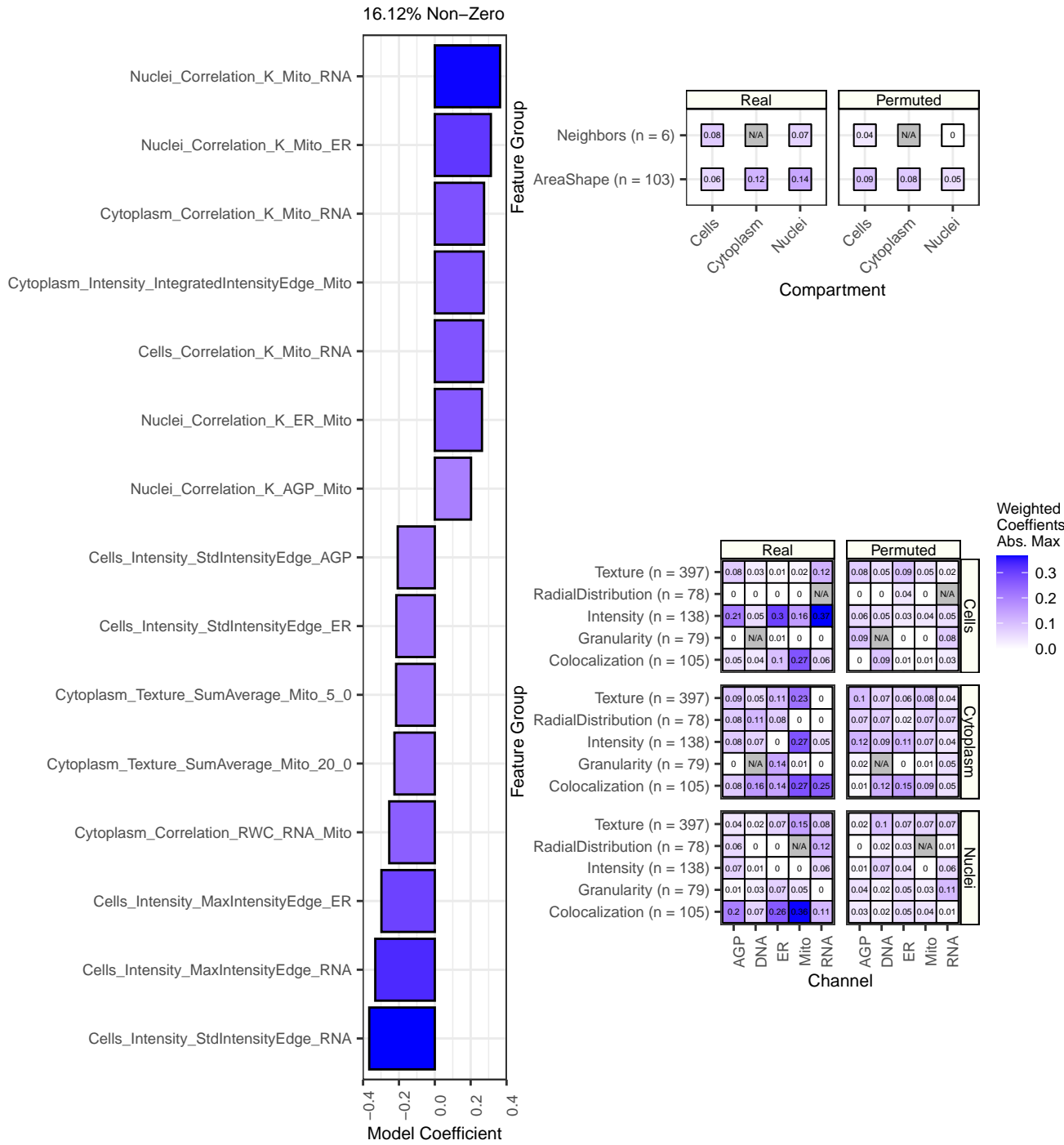
Cell Count – G1+G2



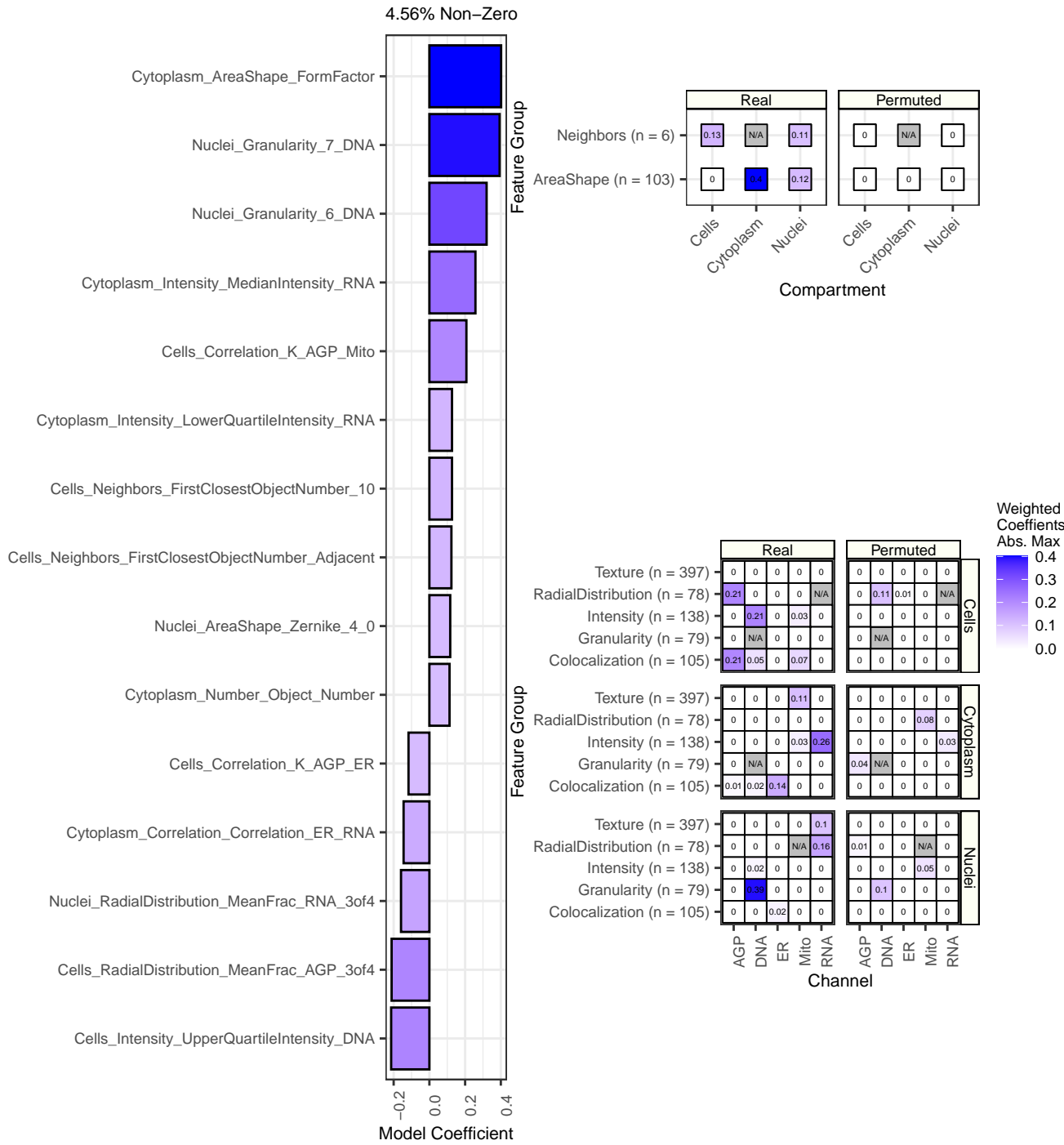
Cell Count – G2/G1



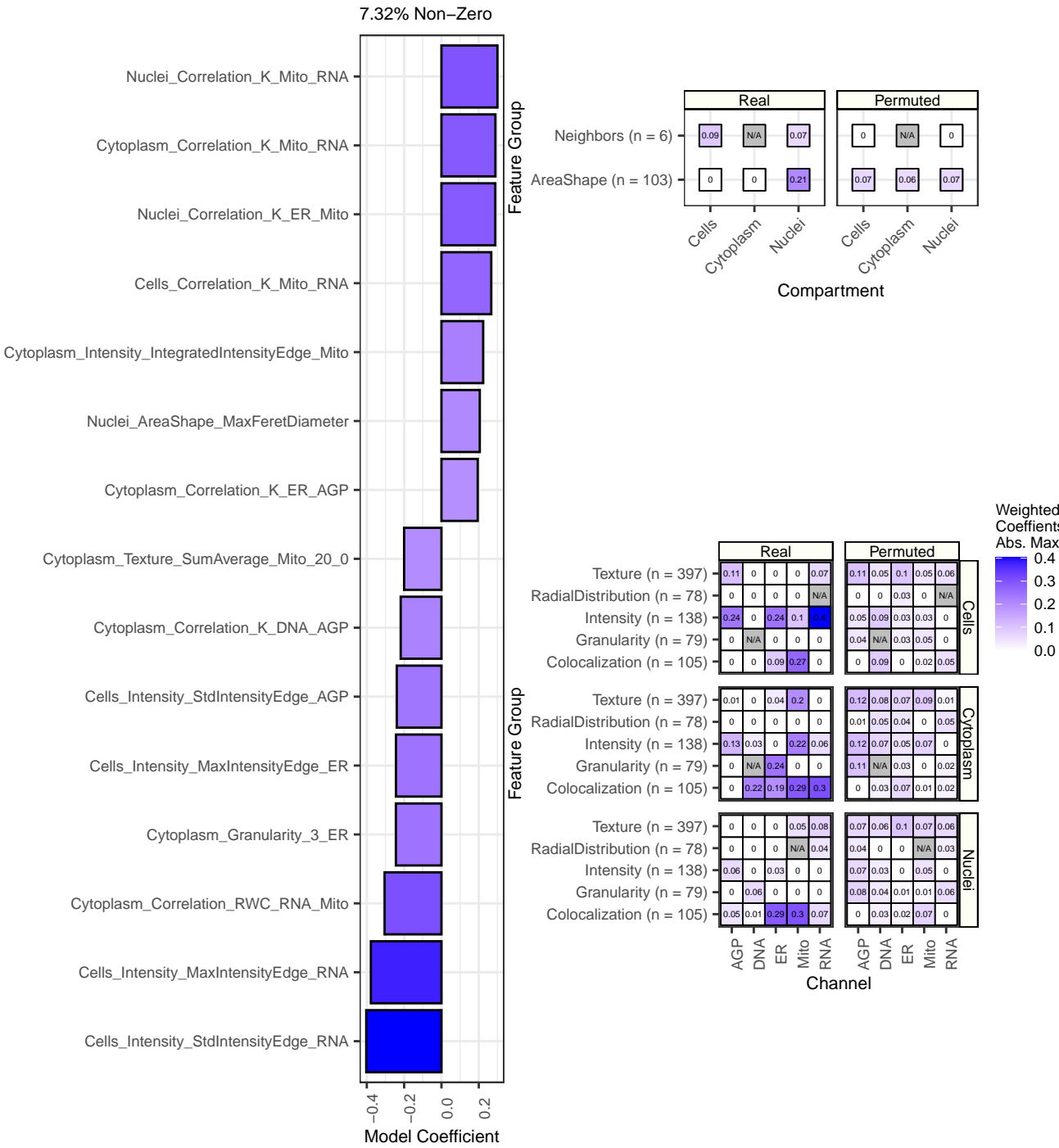
G2 – % High gH2AX Spots



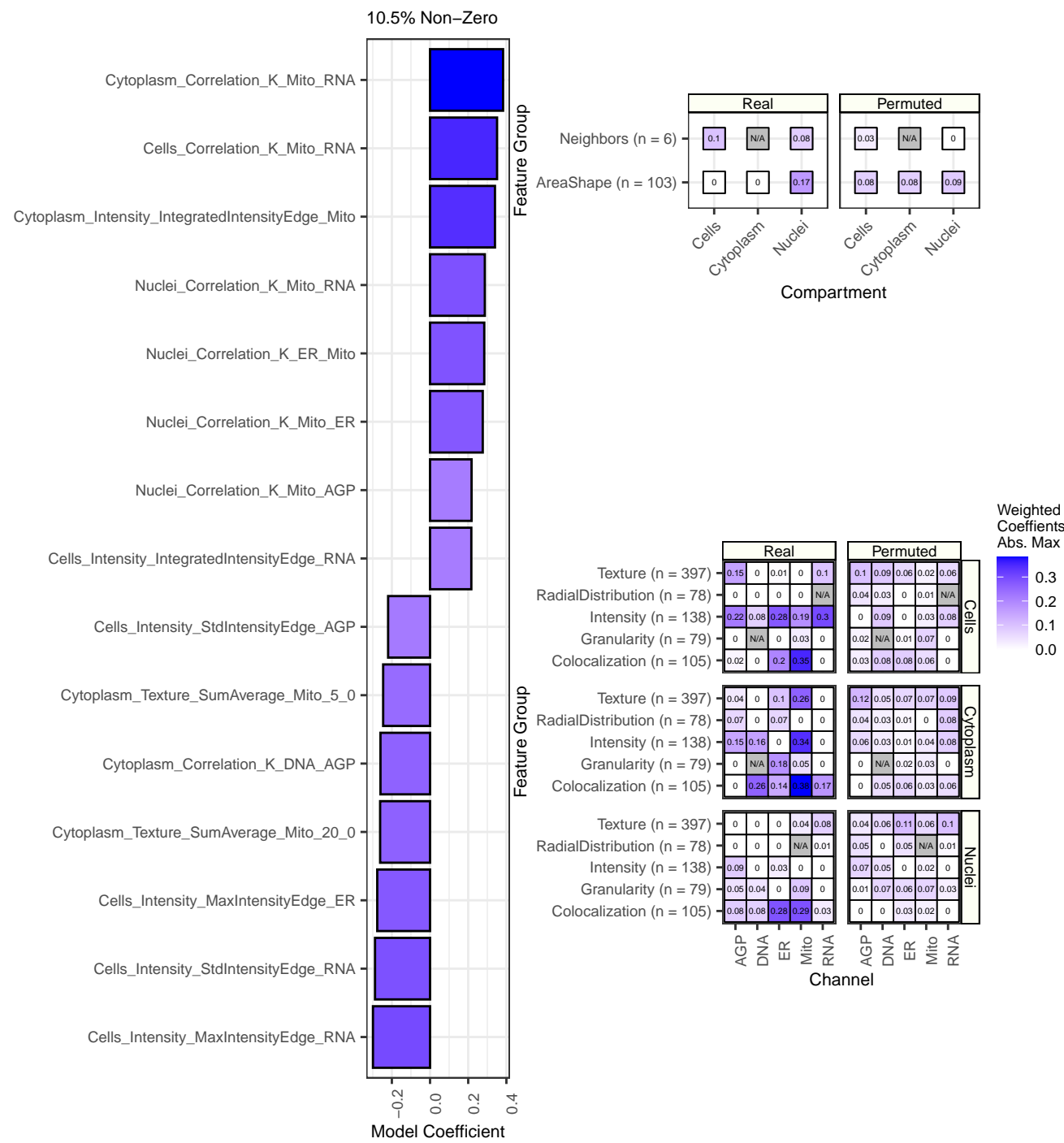
G2 – # cells



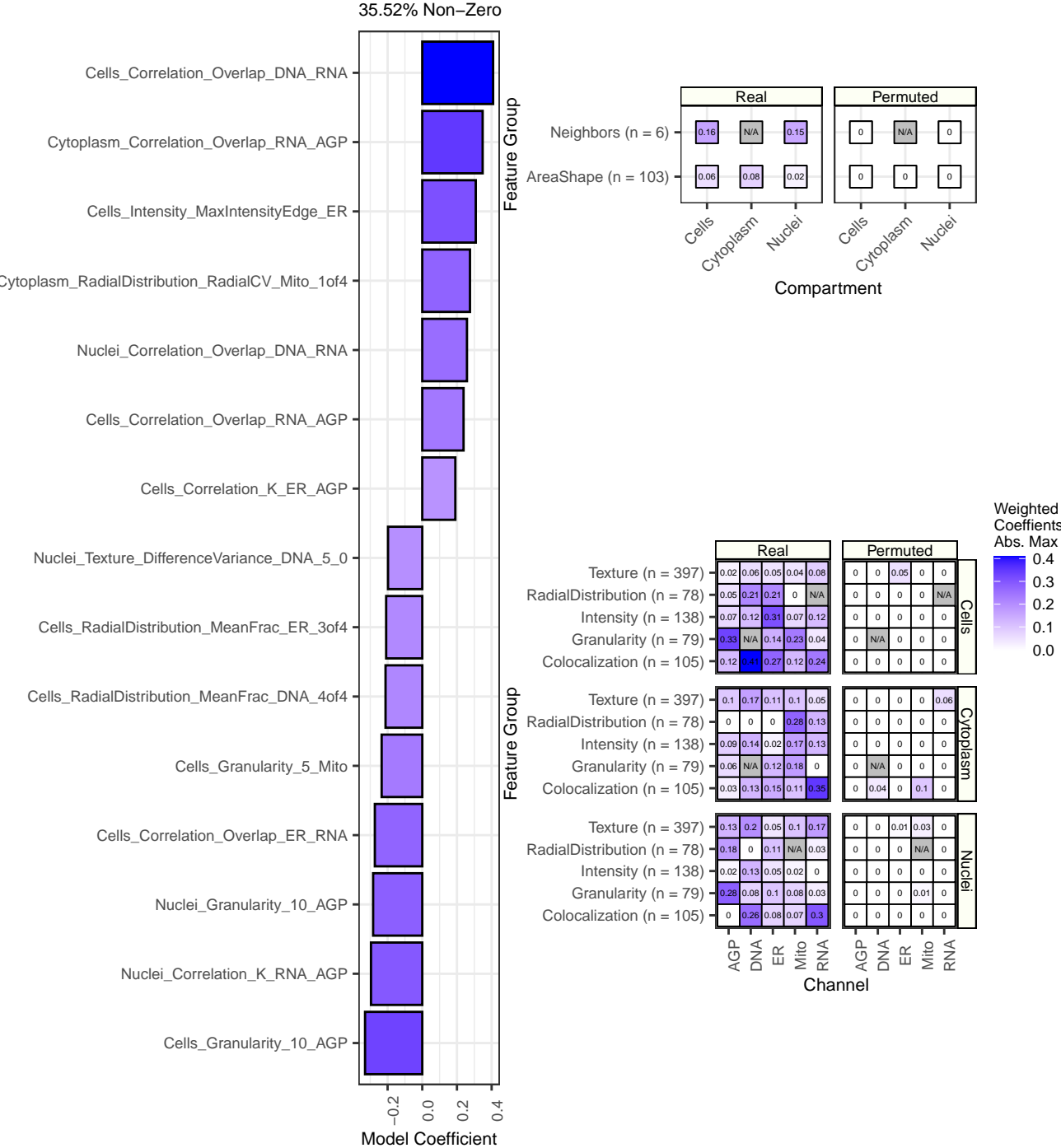
G2 – # of gH2AX Spots



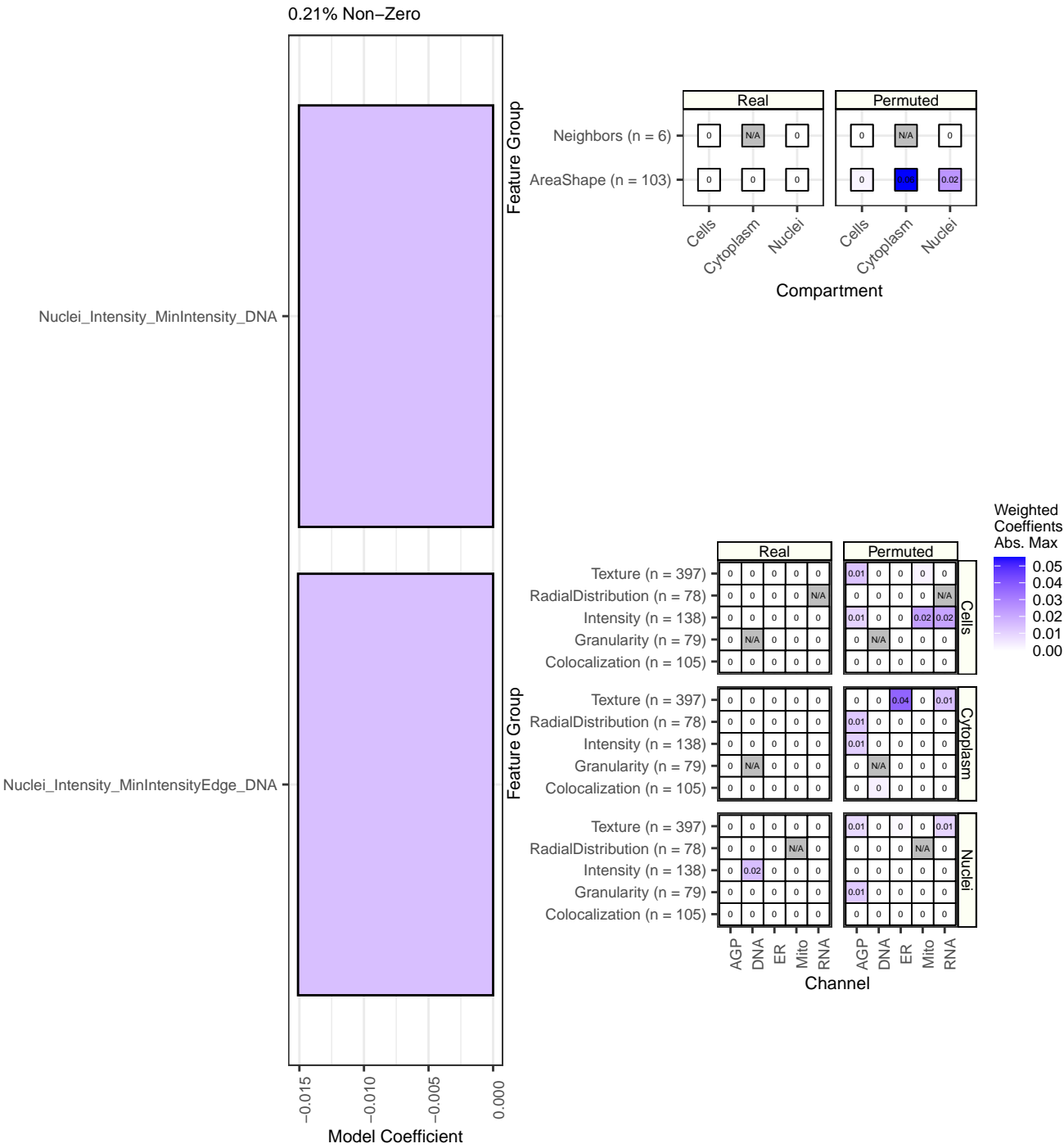
G2 – # of gH2AX Spots per Area of Nucleus



Cell Count – G2 + M

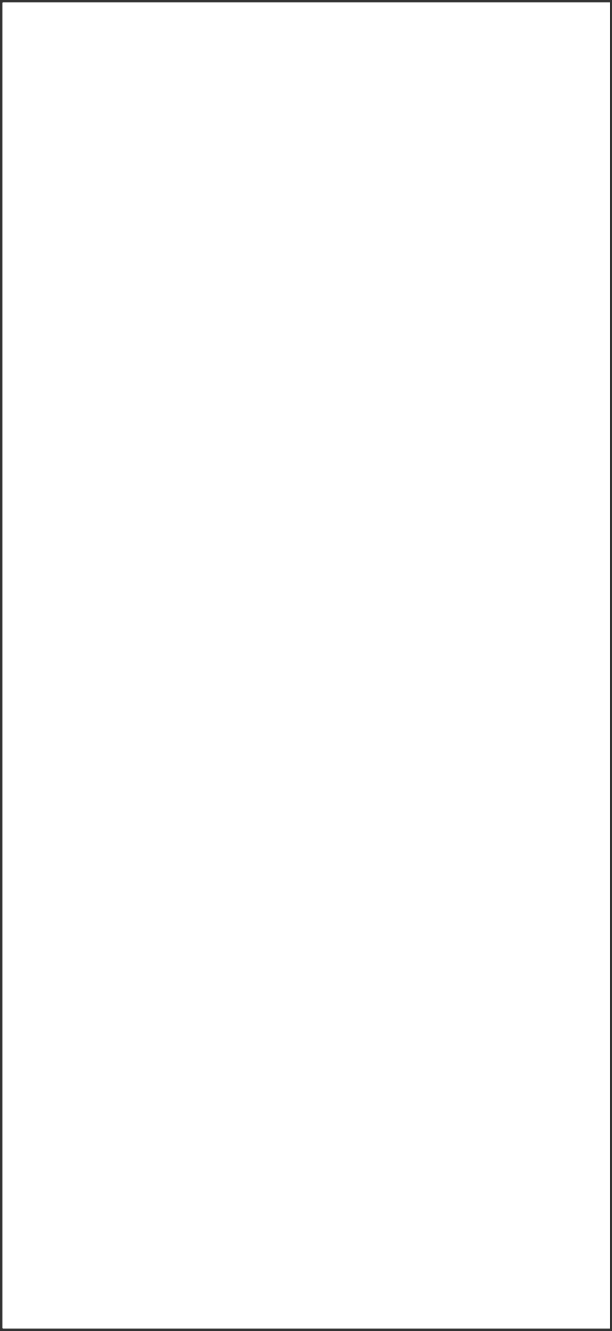


CC – Infection Efficiency



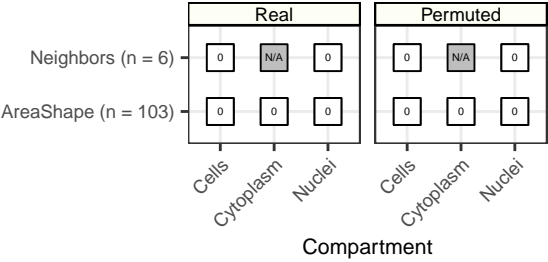
Late M – % High gH2AX Spots

0% Non-Zero

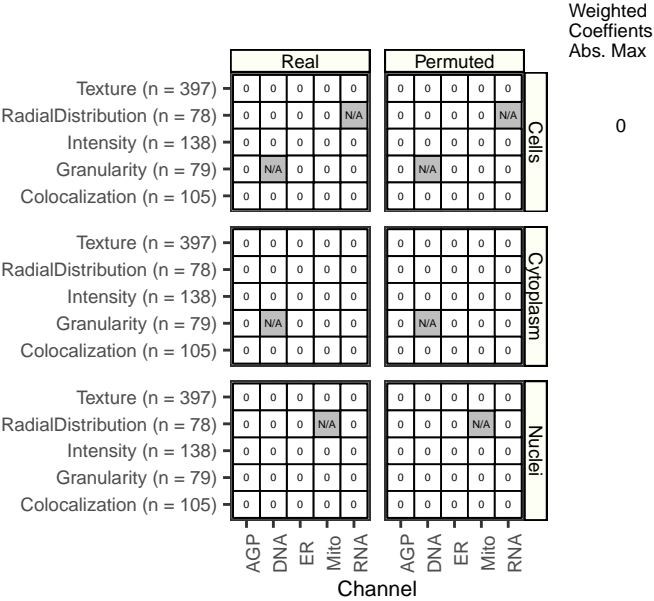


Model Coefficient

Feature Group

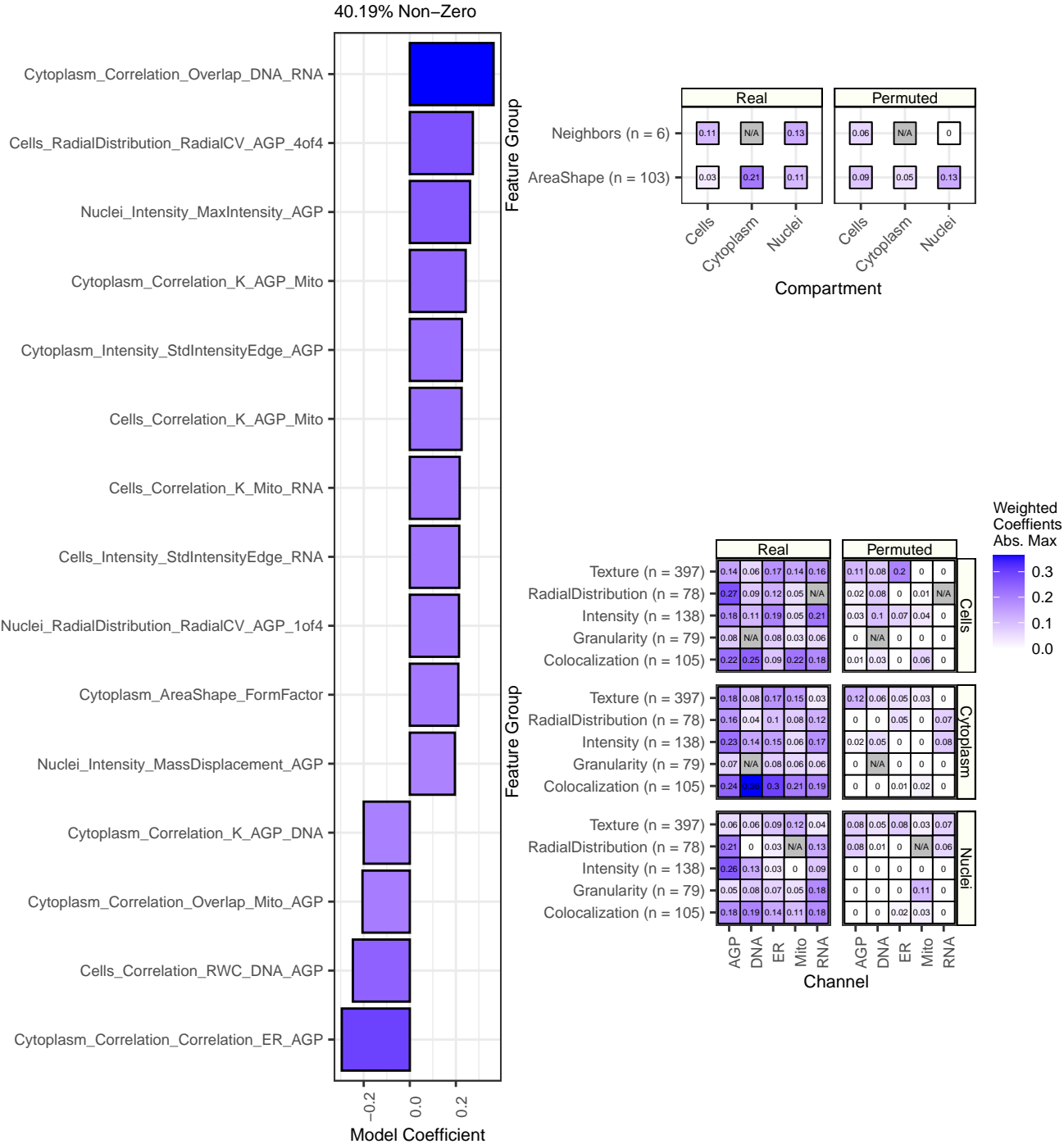


Feature Group



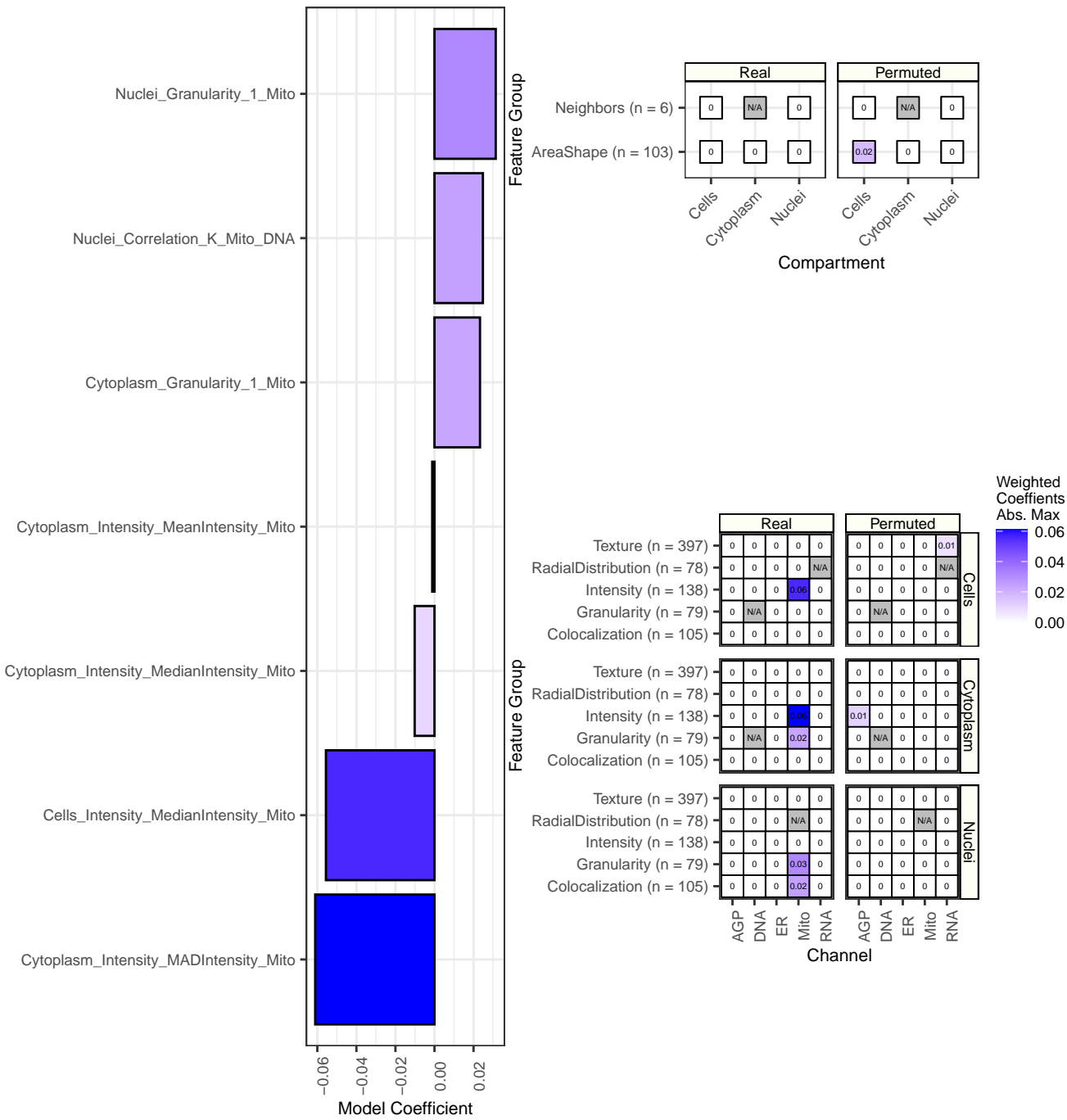
Weighted
Coefficients
Abs. Max

Late M – # cells



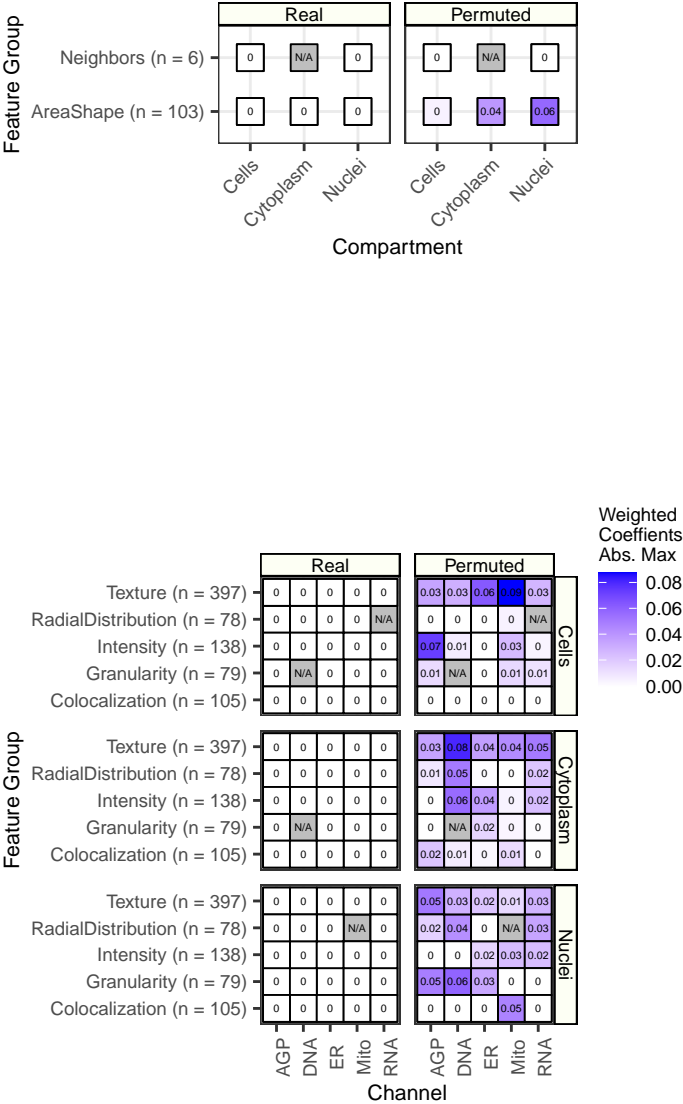
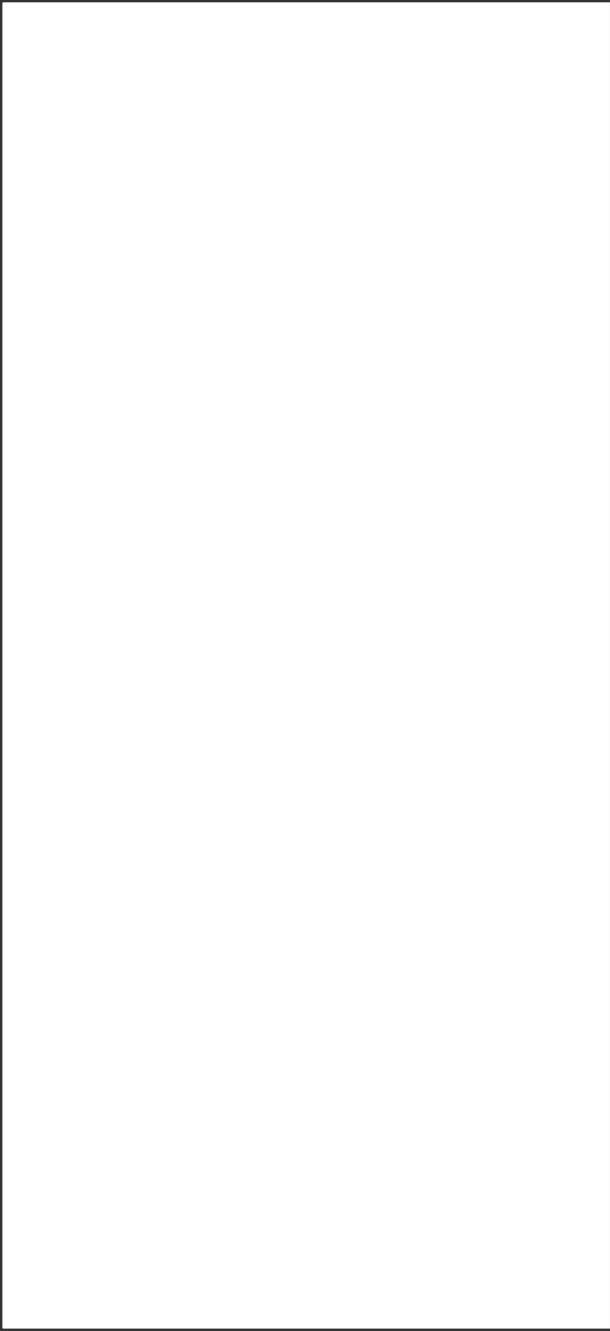
Late M – # of gH2AX Spots

0.74% Non-Zero



Late M – # of gH2AX Spots per Area of Nucleus

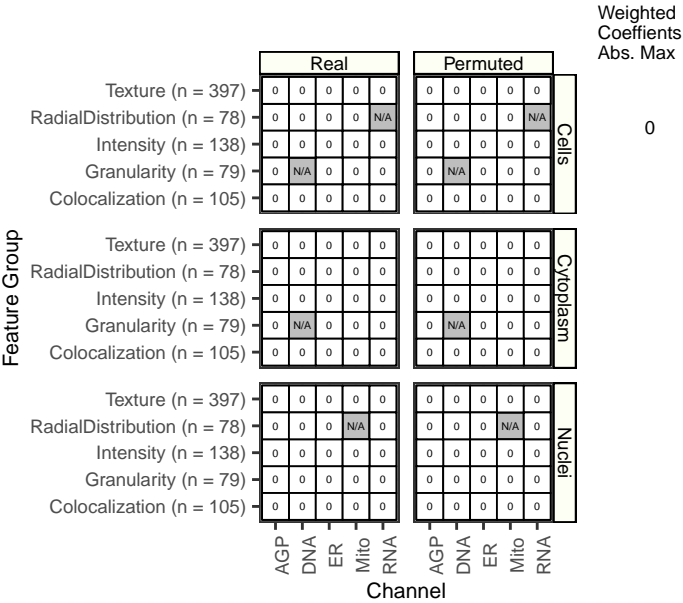
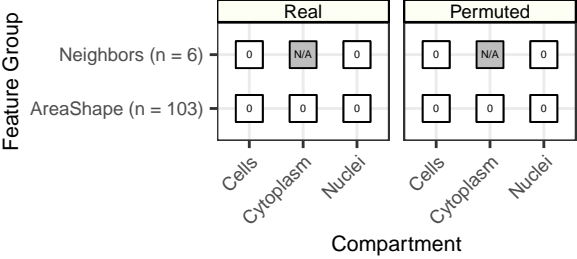
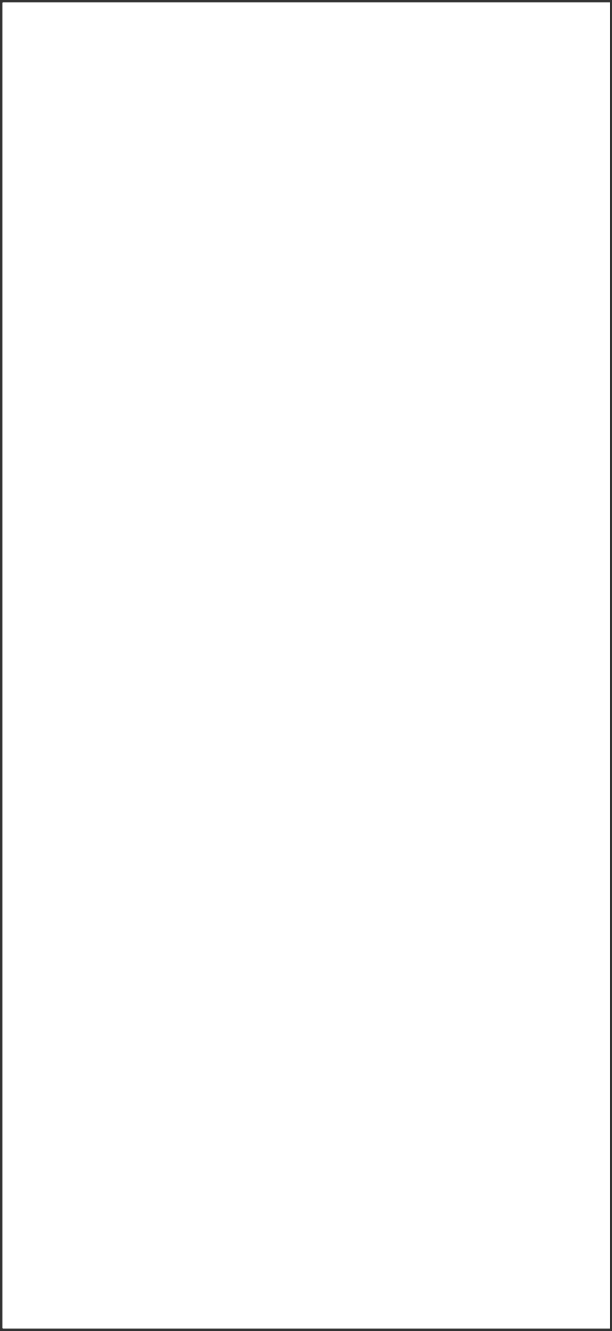
0% Non-Zero



Model Coefficient

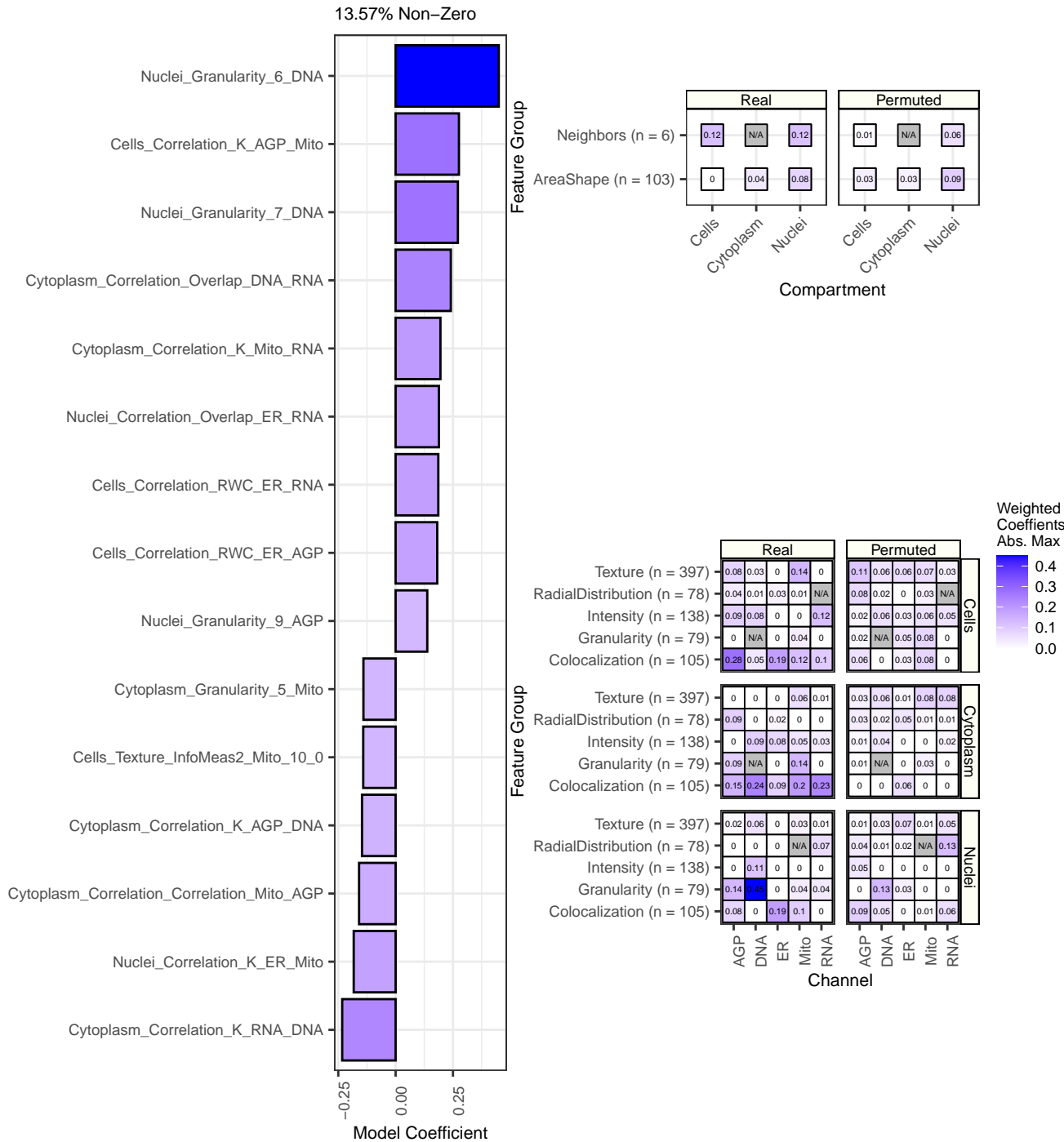
M – % High gH2AX Spots

0% Non-Zero



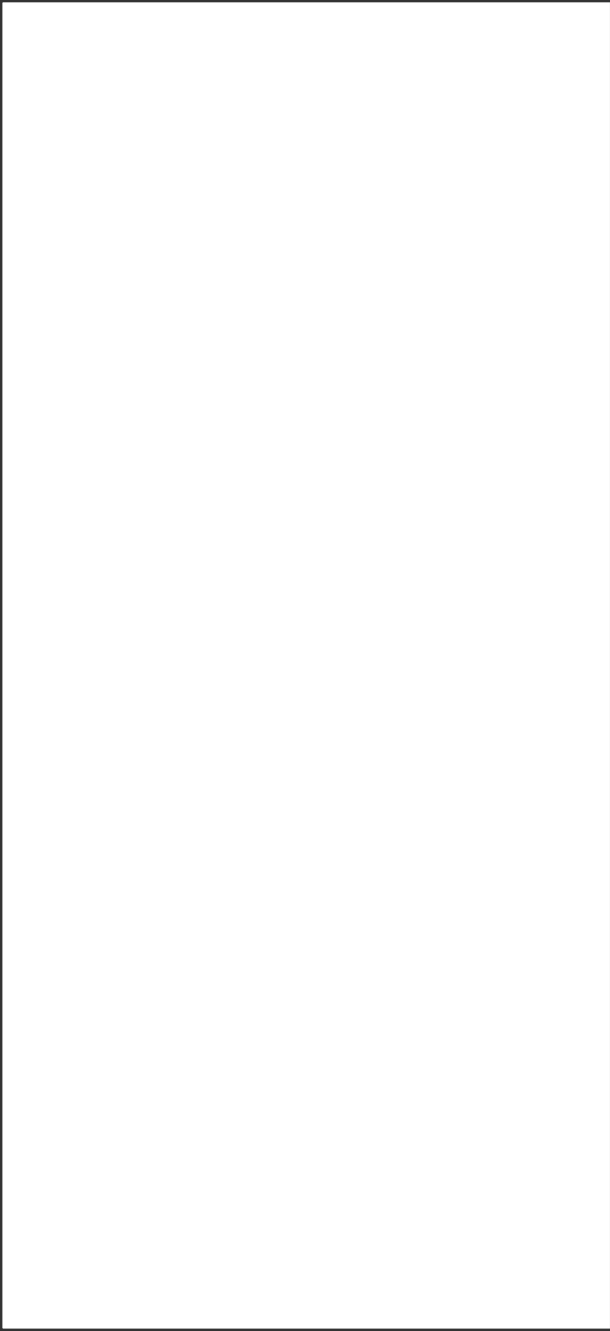
Model Coefficient

M – # cells

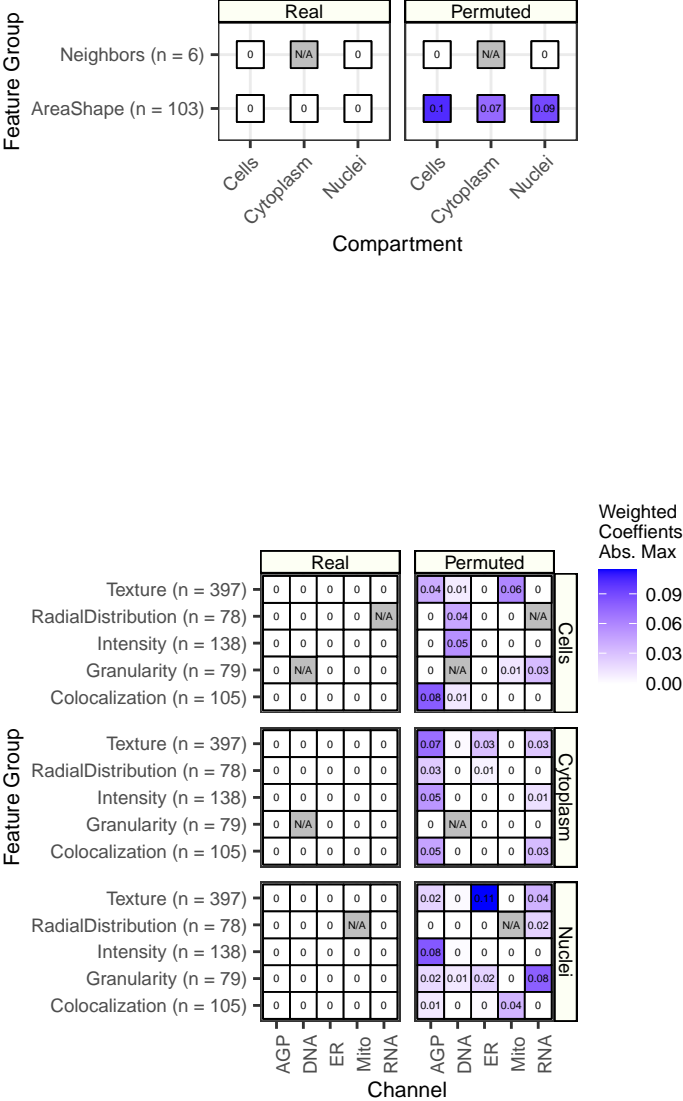


M – # of gH2AX Spots

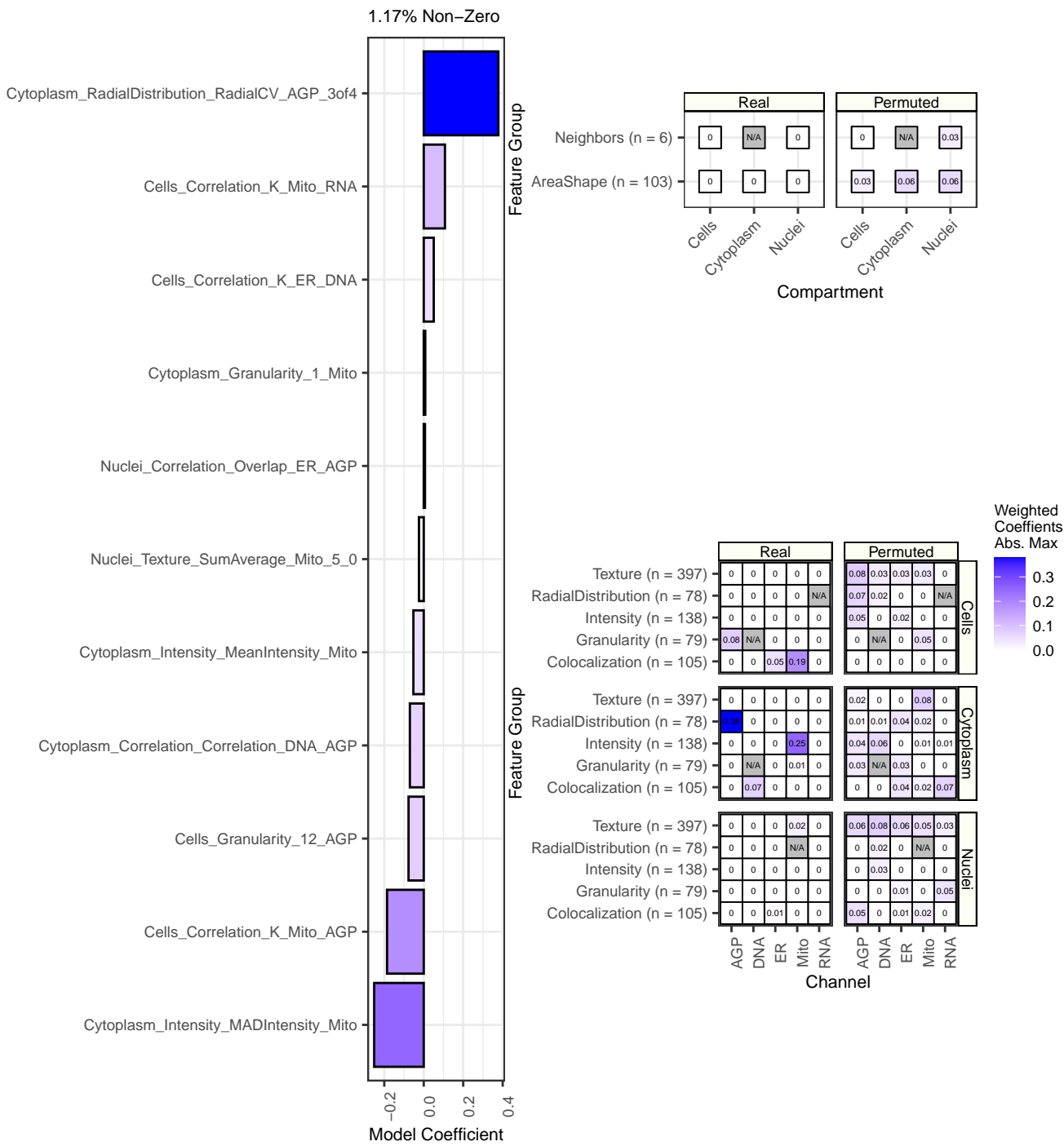
0% Non-Zero



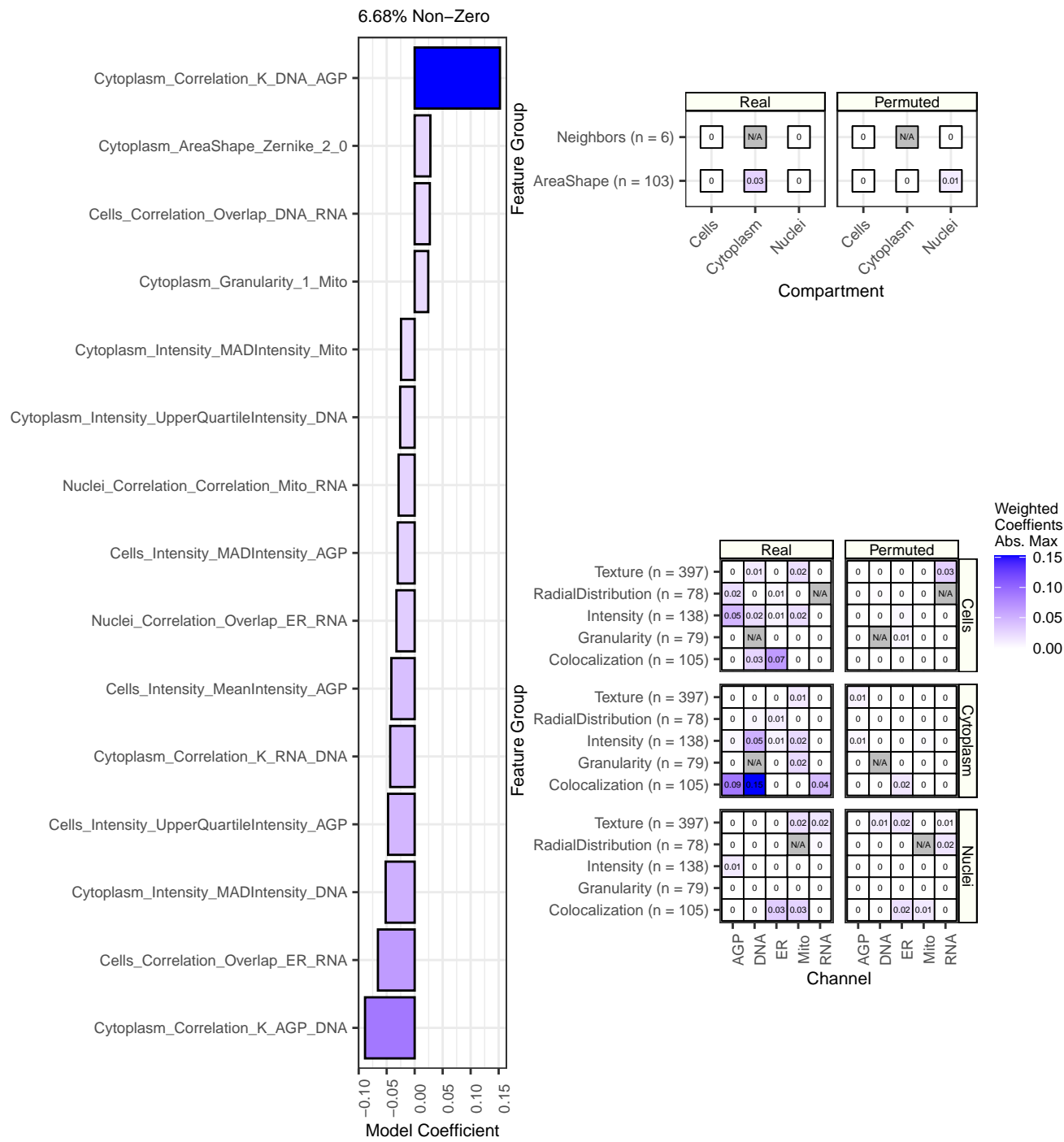
Model Coefficient



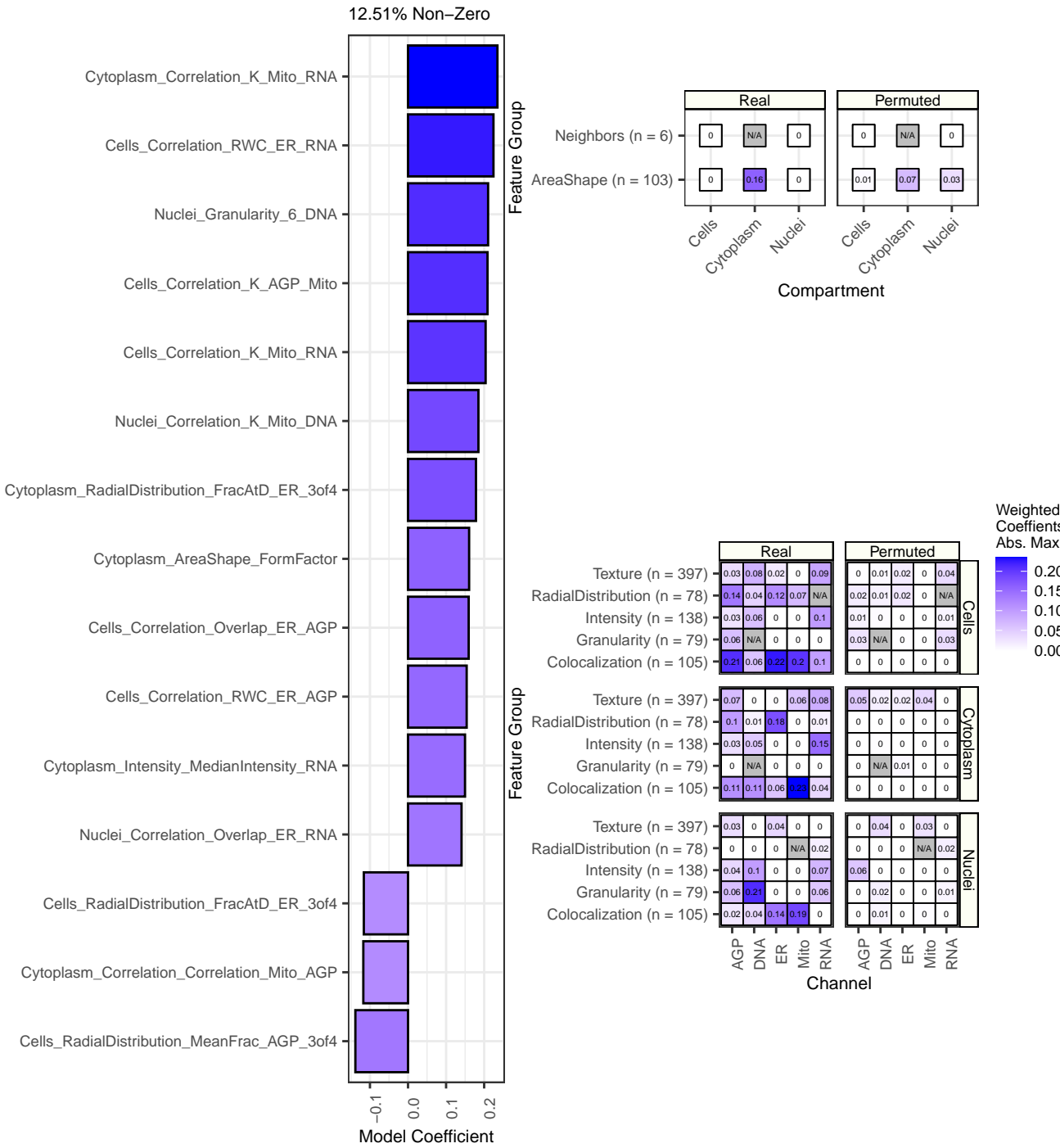
M – # of gH2AX Spots per Area of Nucleus



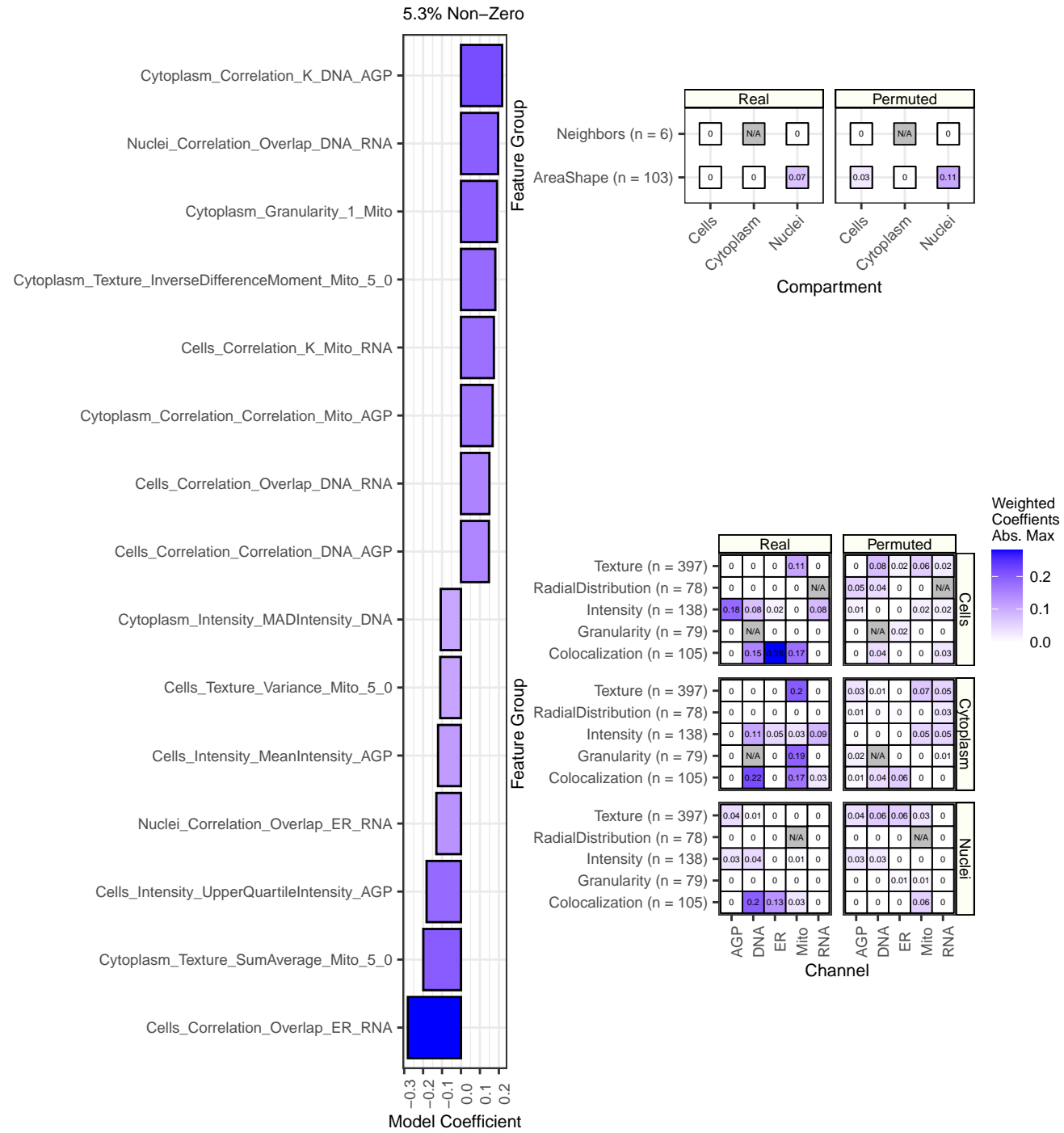
Polynuclear – % High gH2AX Spots



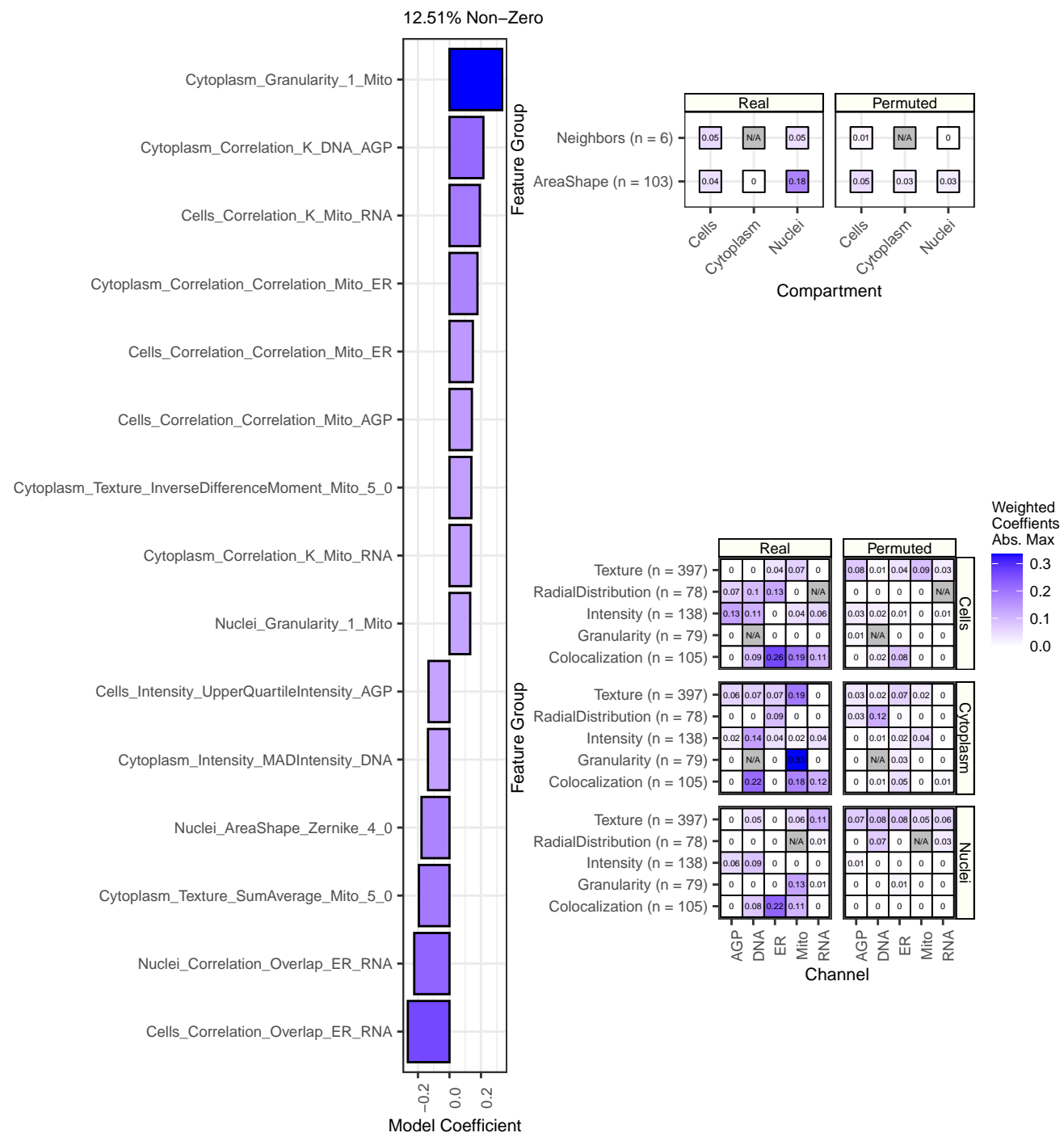
Polynuclear – # cells



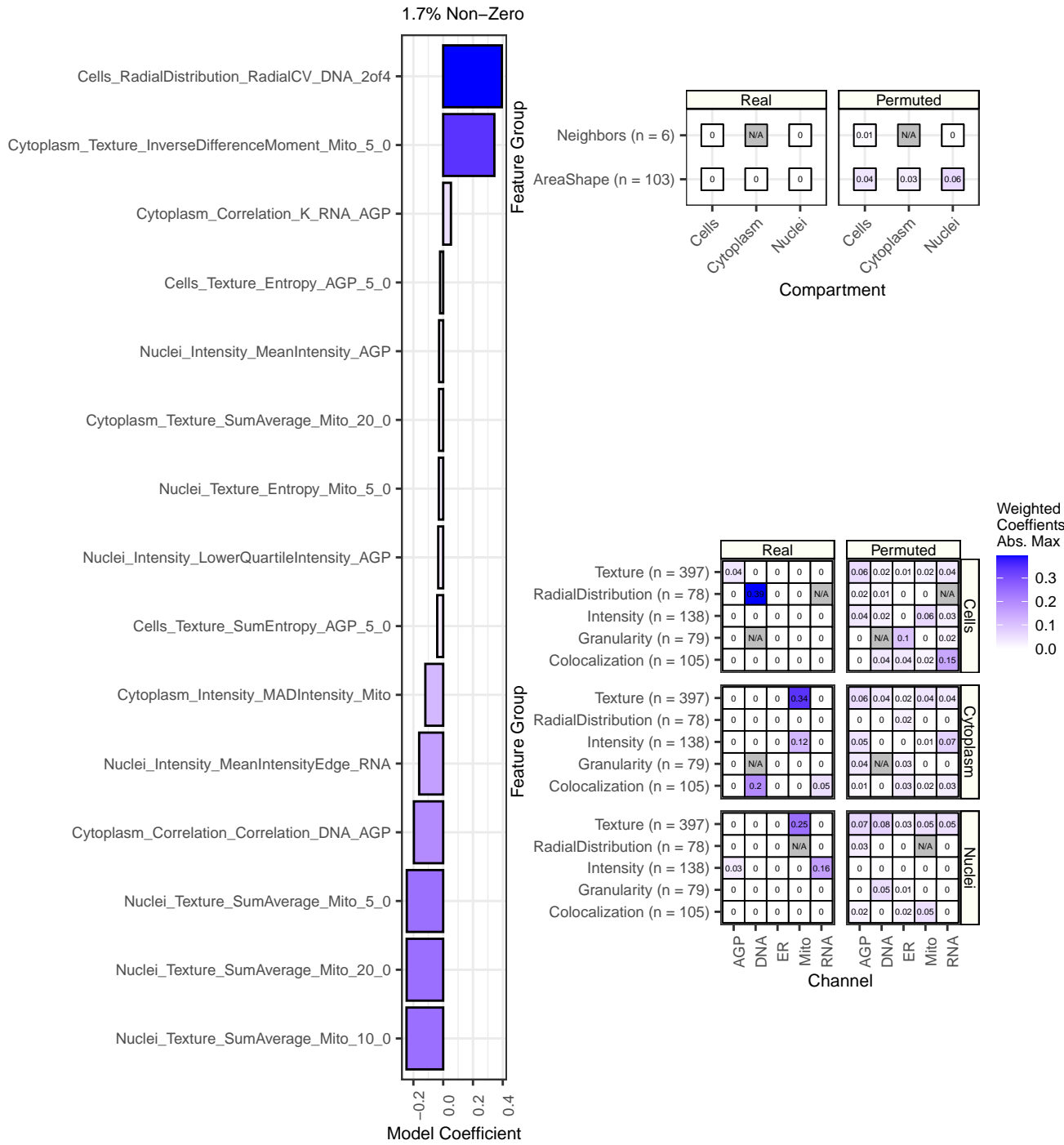
Polynuclear – # of gH2AX Spots



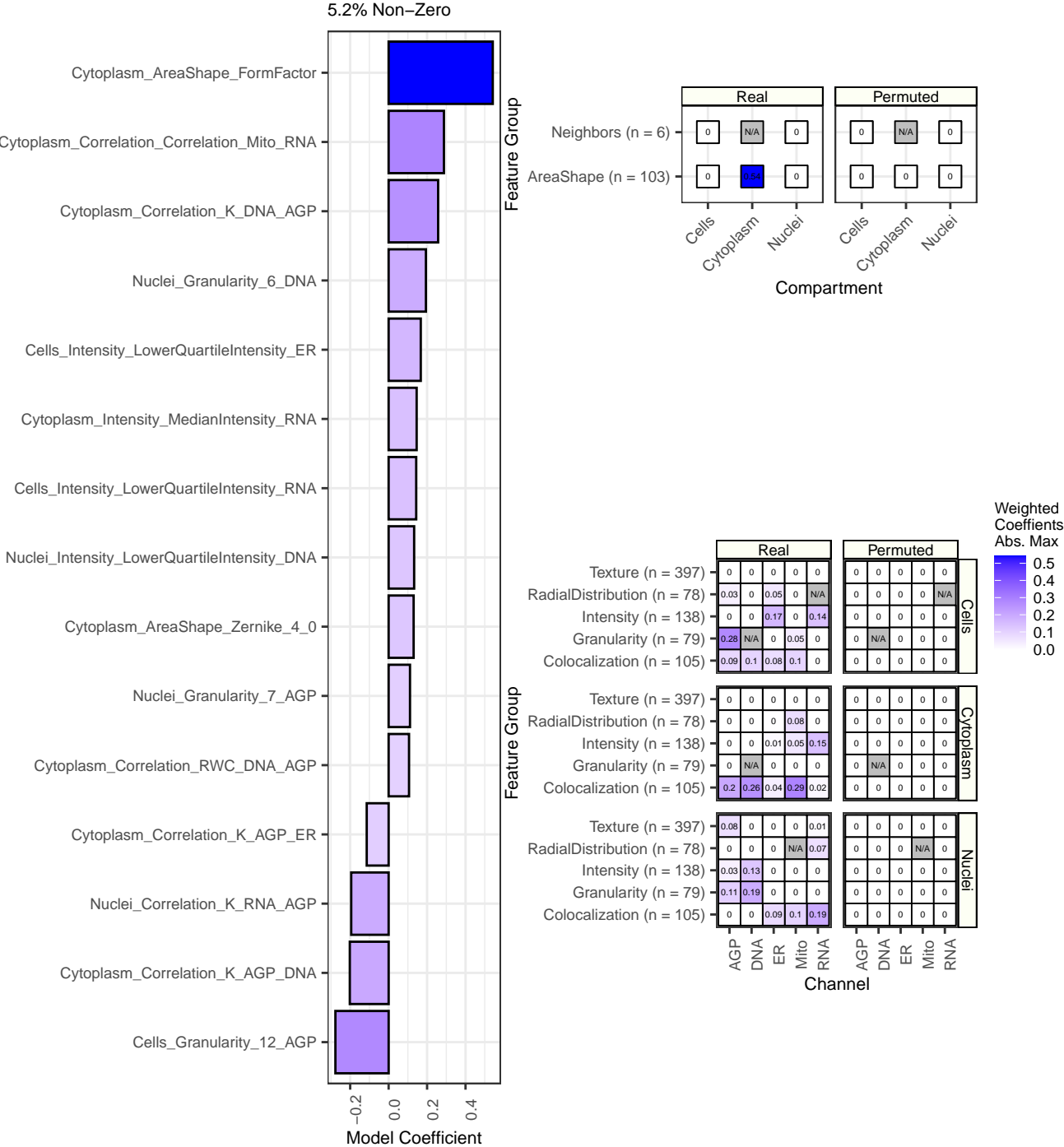
Polynuclear – # of gH2AX Spots per Area of Nucleus



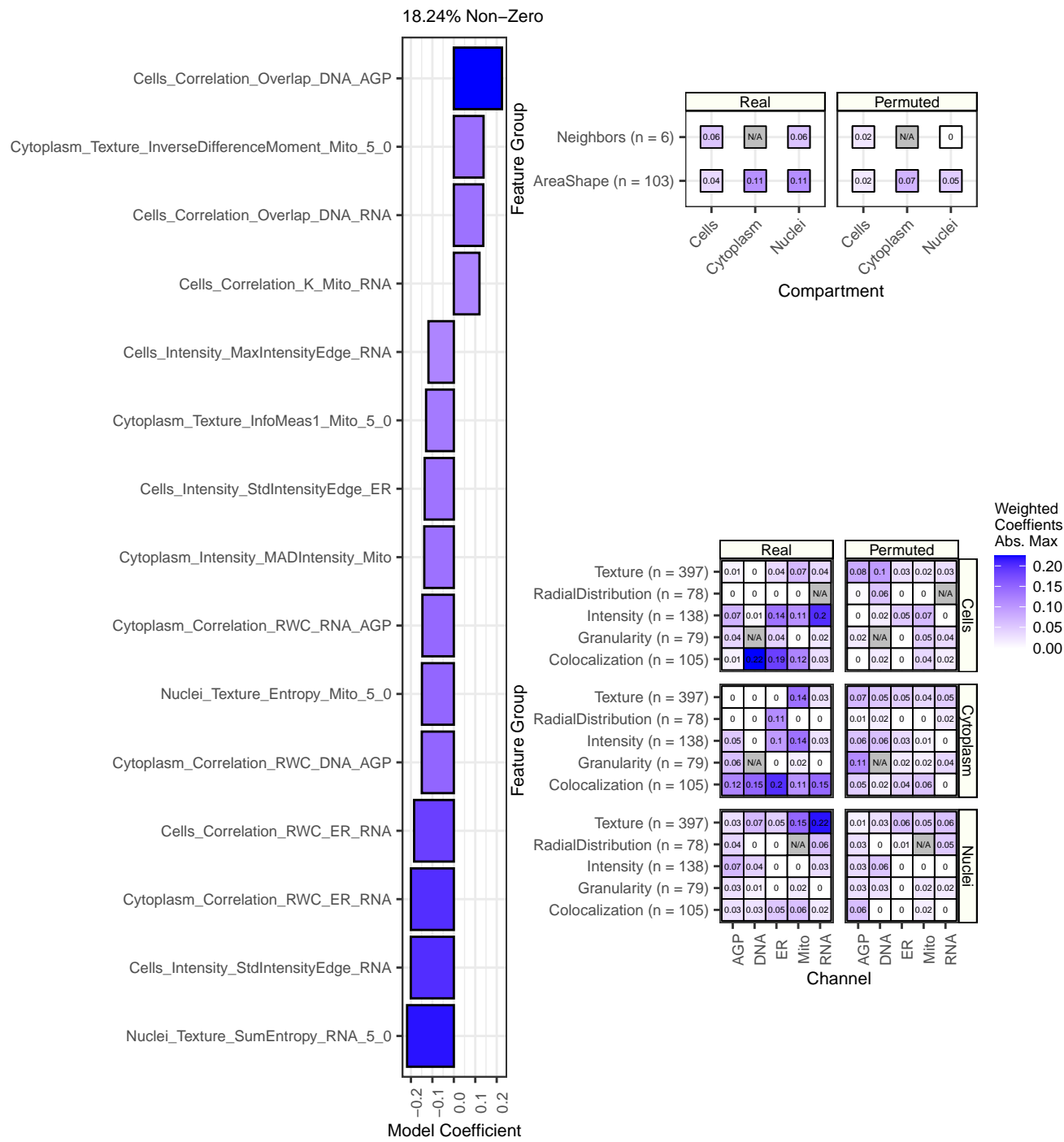
Polyploid – % High gH2AX Spots



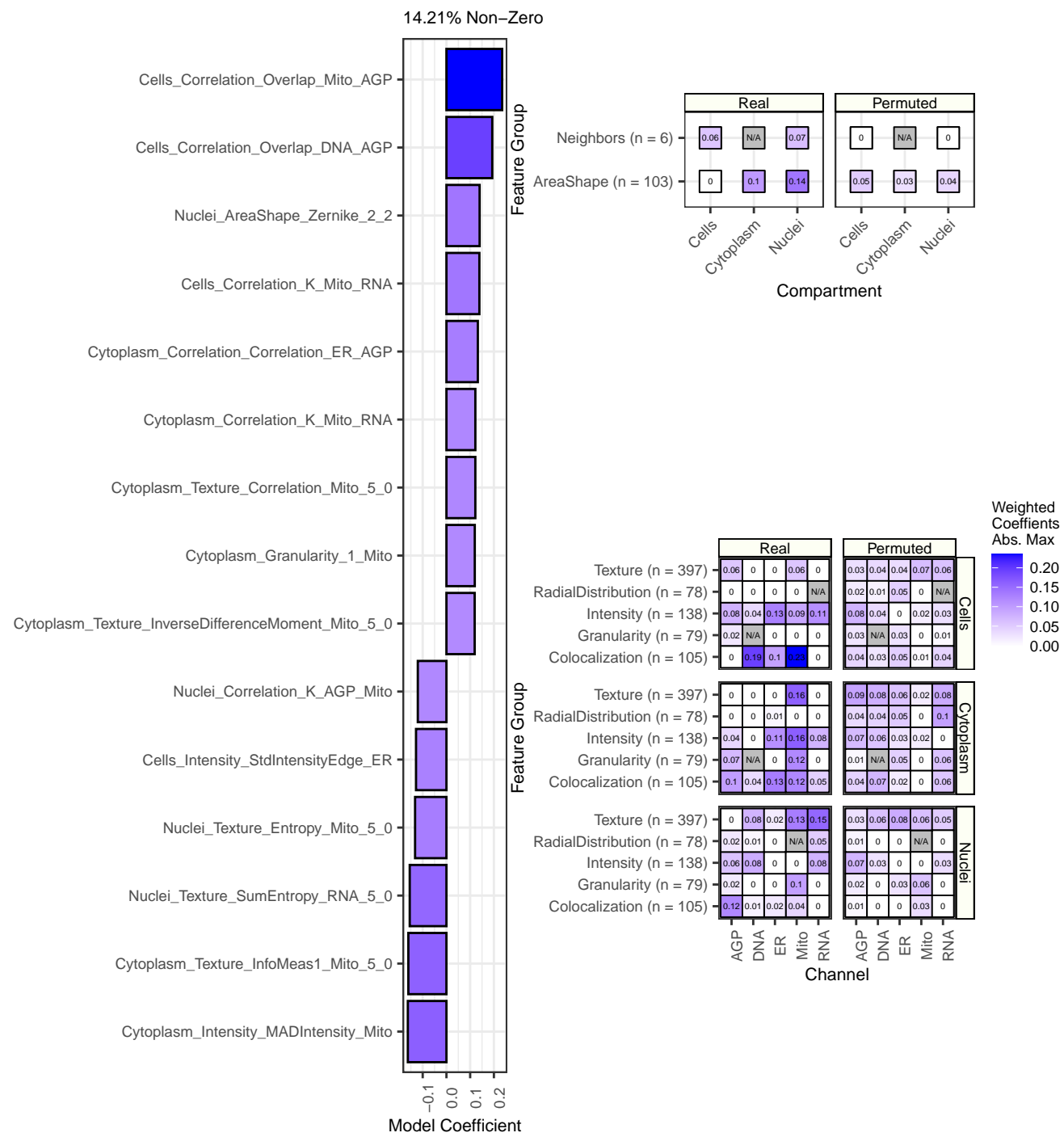
Polyploid – # cells



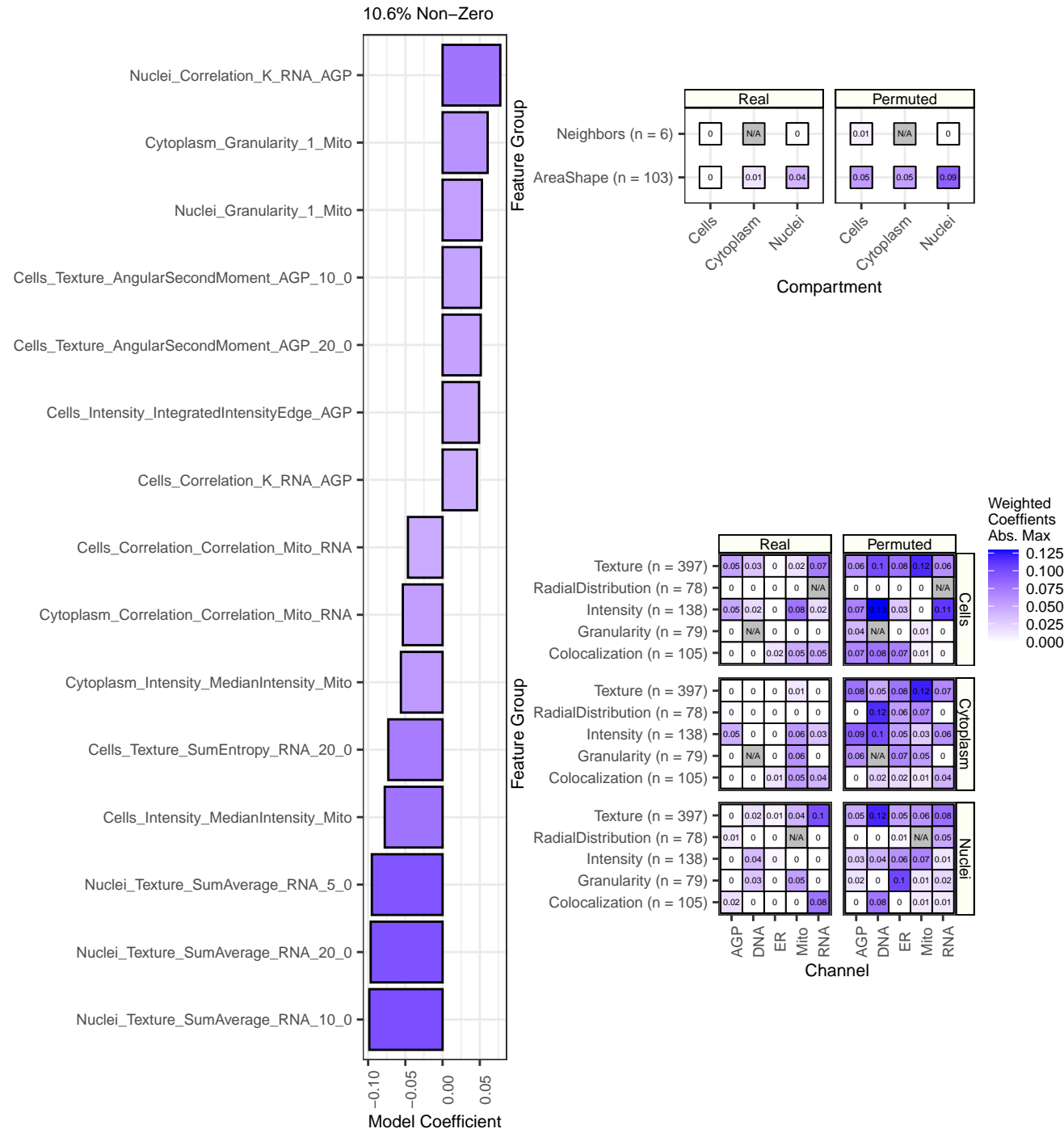
Polyloid – # of gH2AX Spots



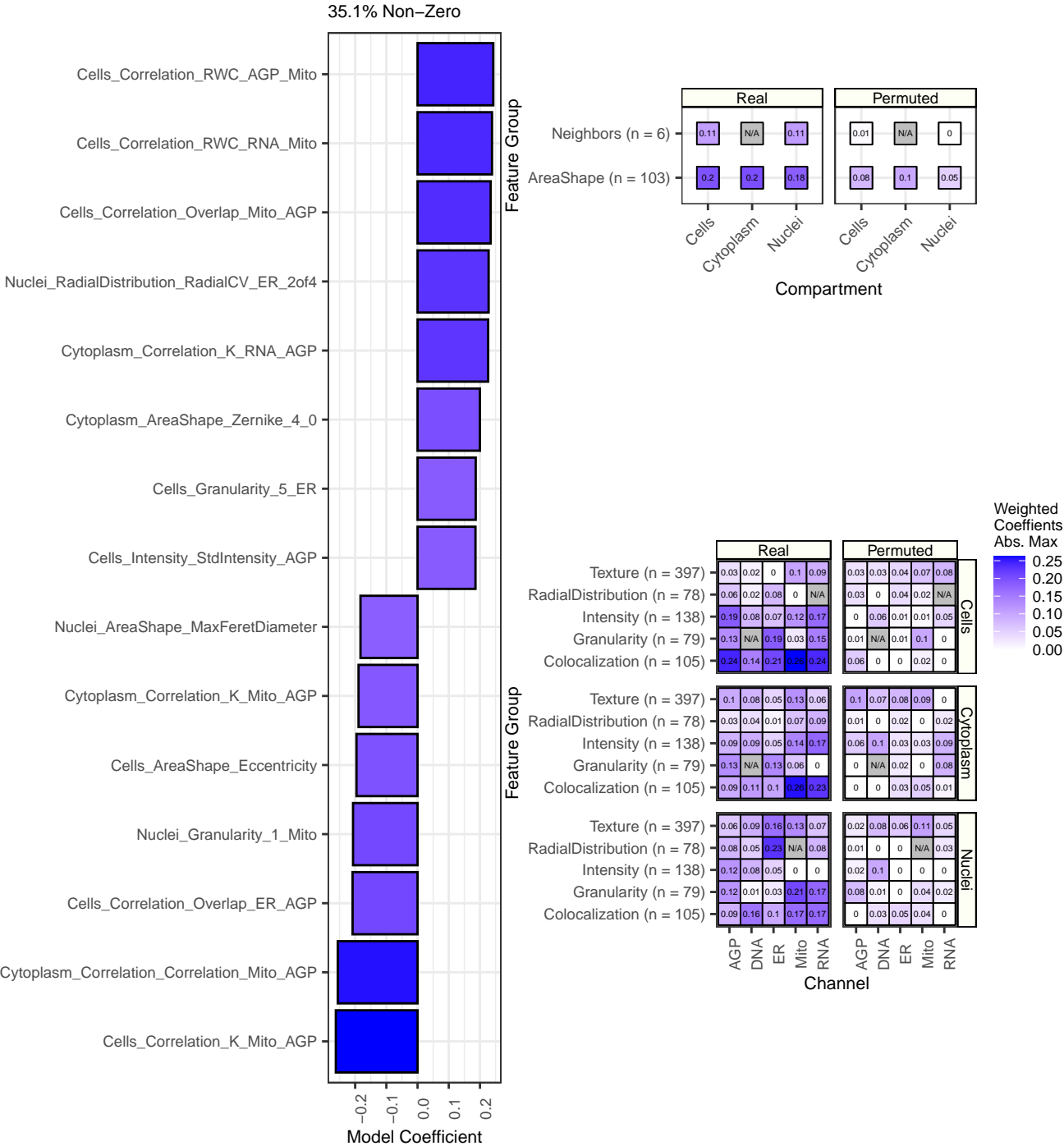
Polyploid – # of gH2AX Spots per Area of Nucleus



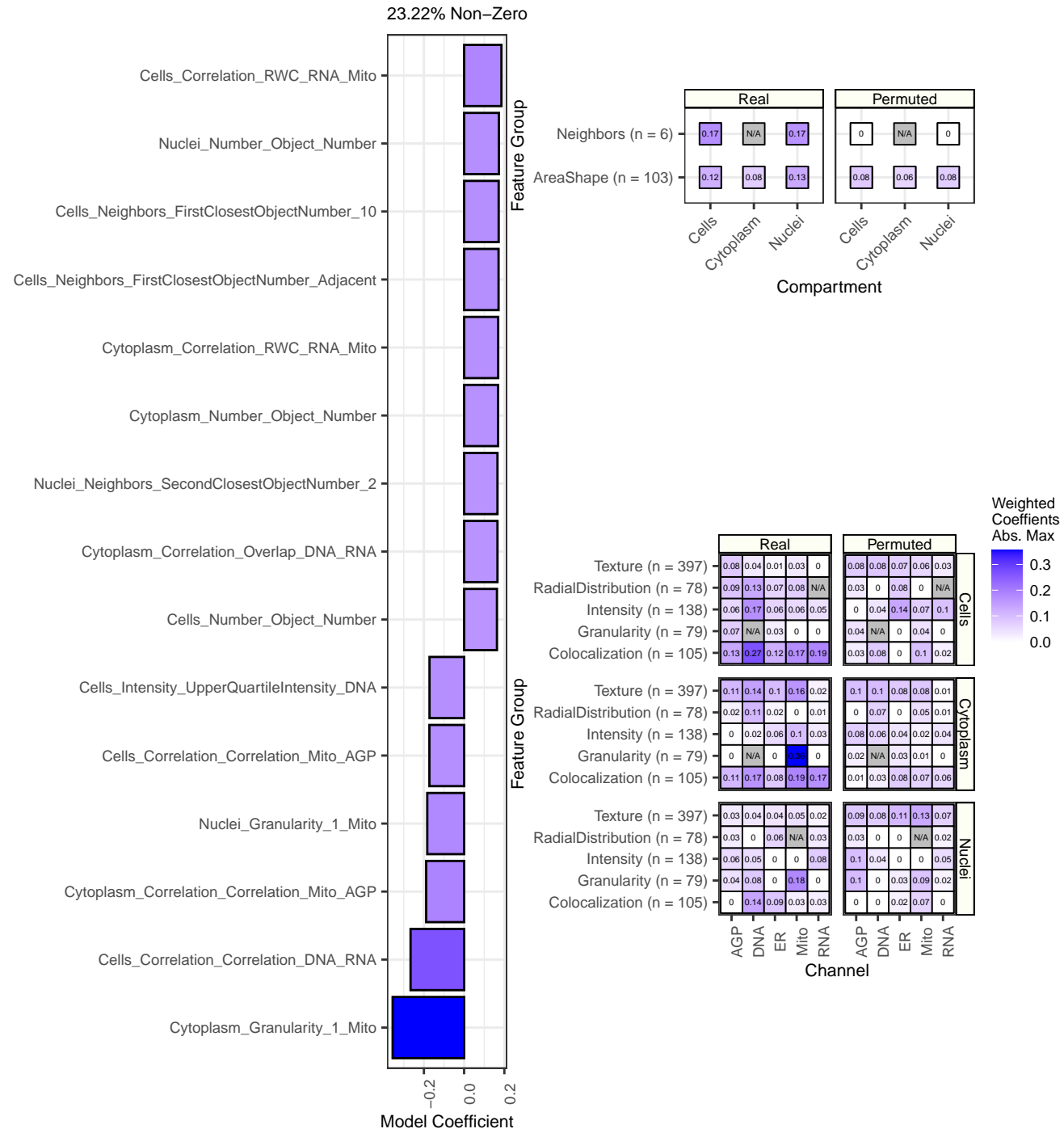
S – % High gH2AX Spots



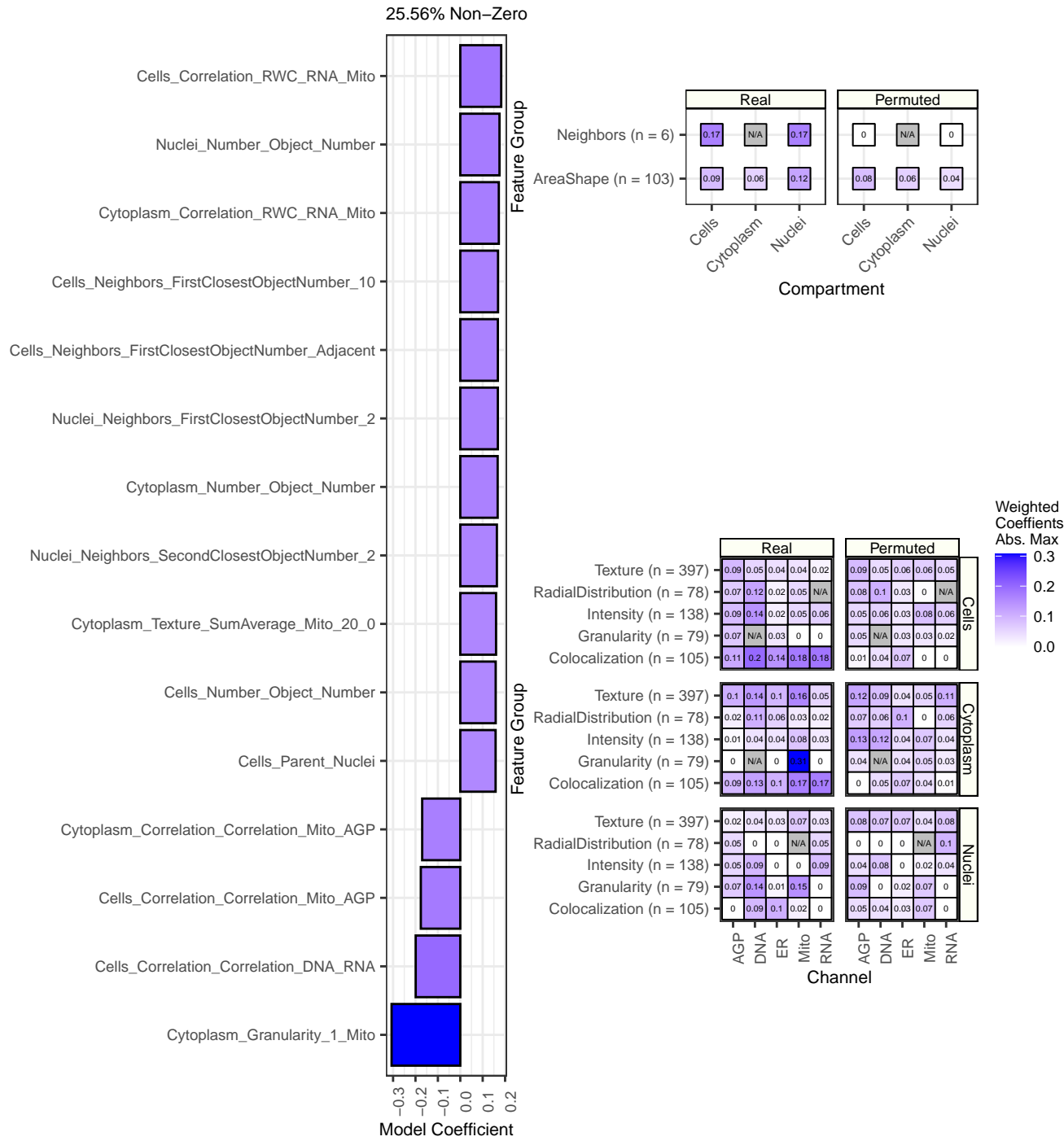
S – Intensity Nucleus EdU Mean



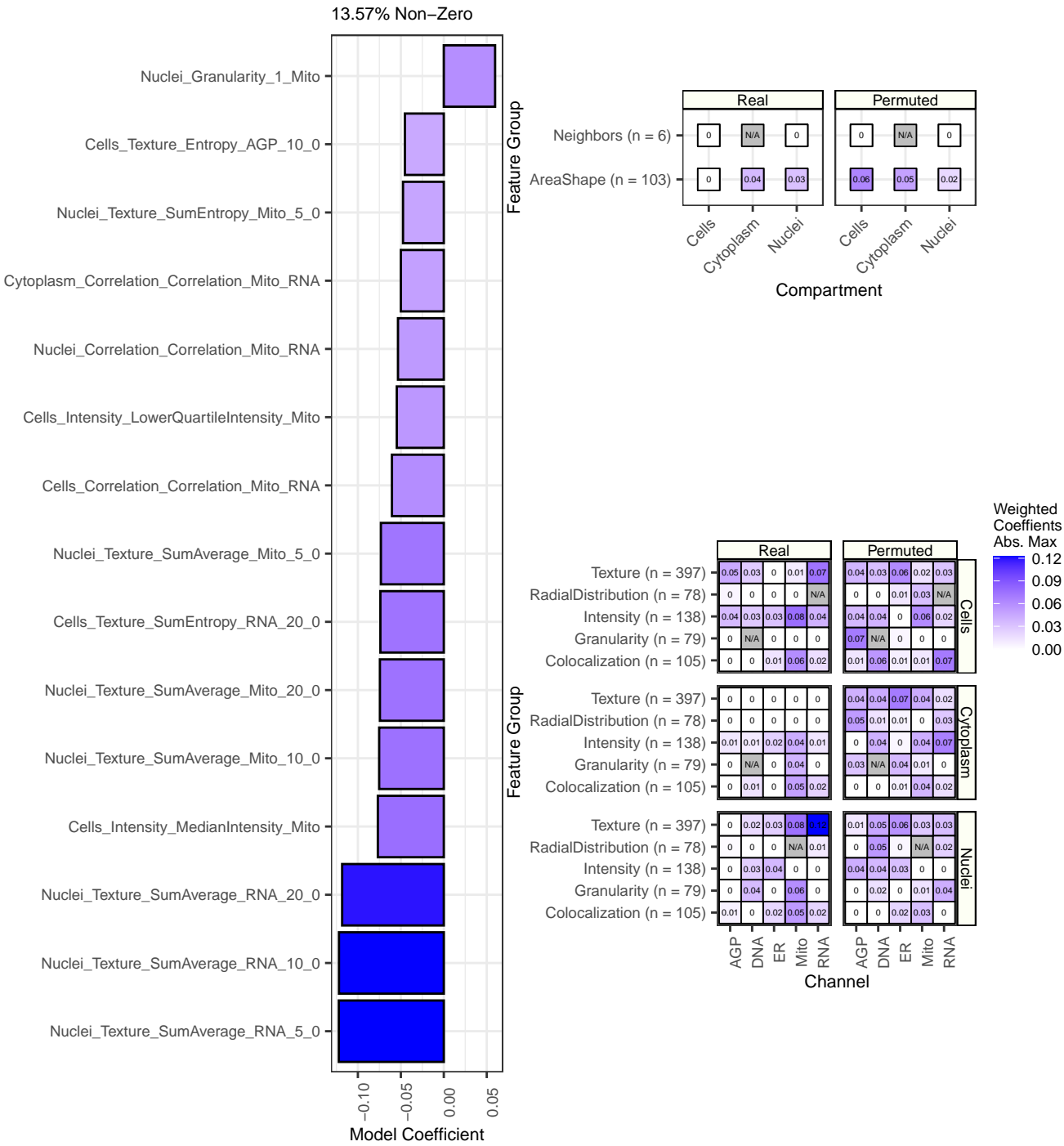
S – Intensity Nucleus EdU Sum



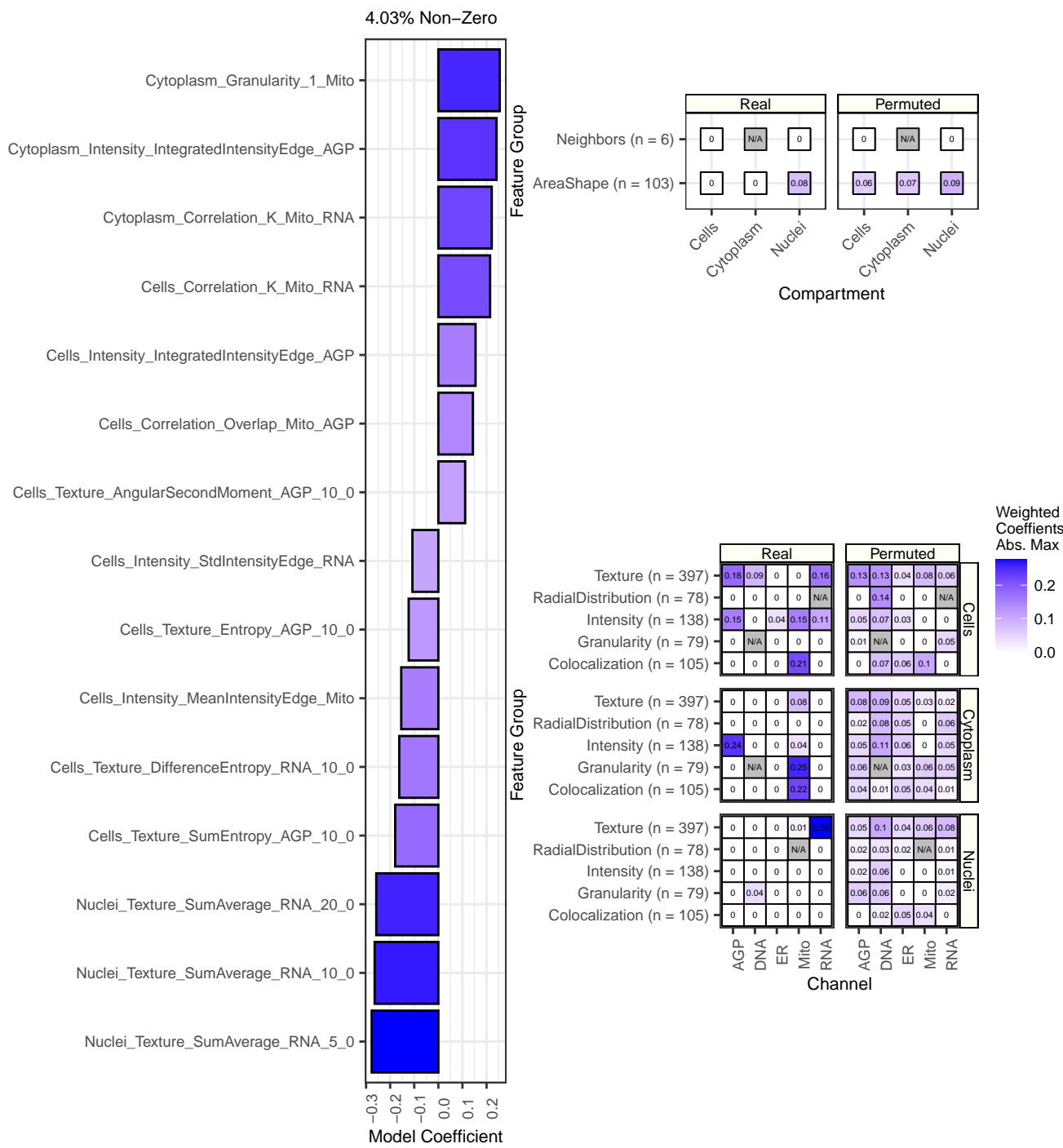
S – # cells



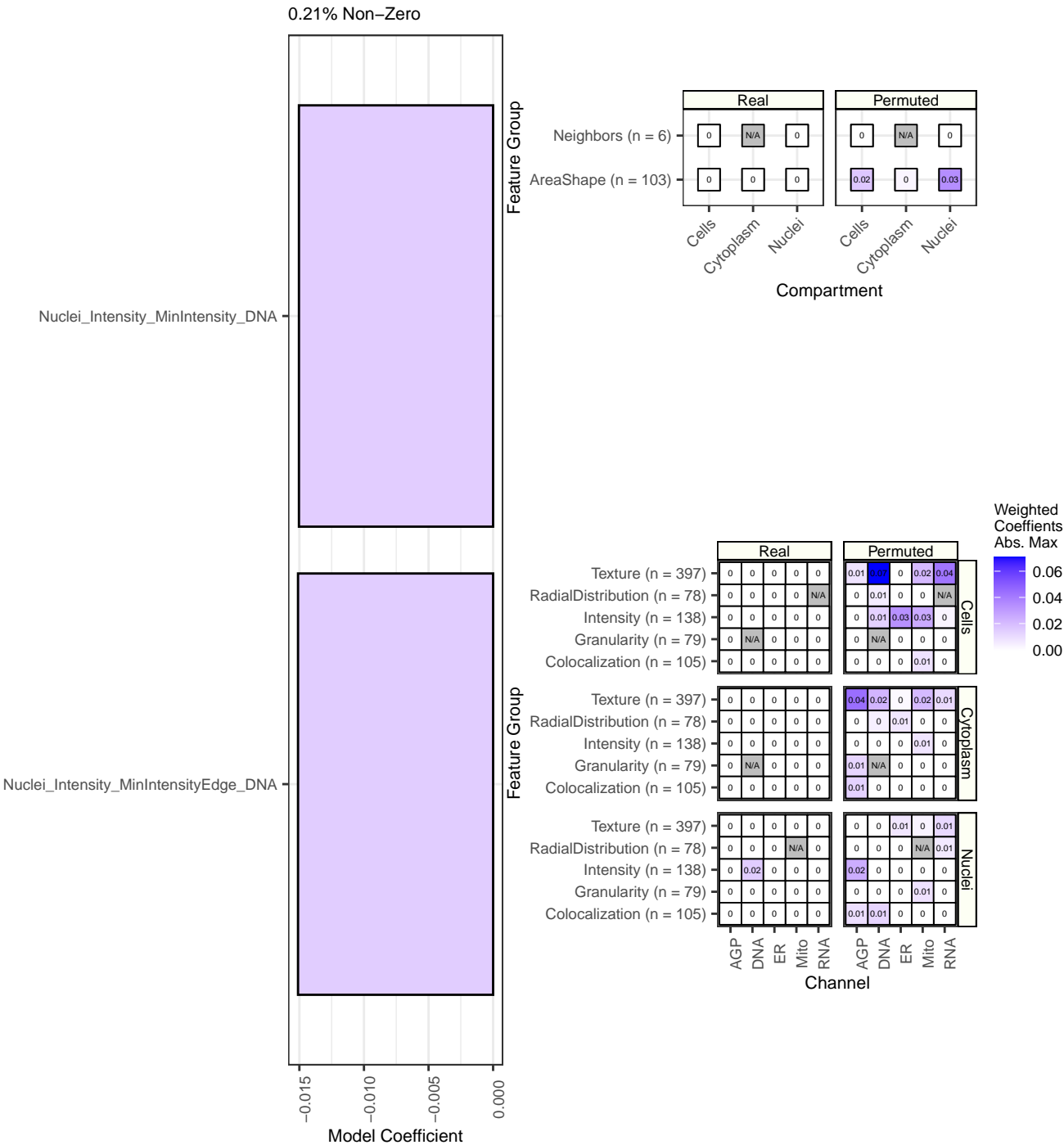
S – # of gH2AX Spots



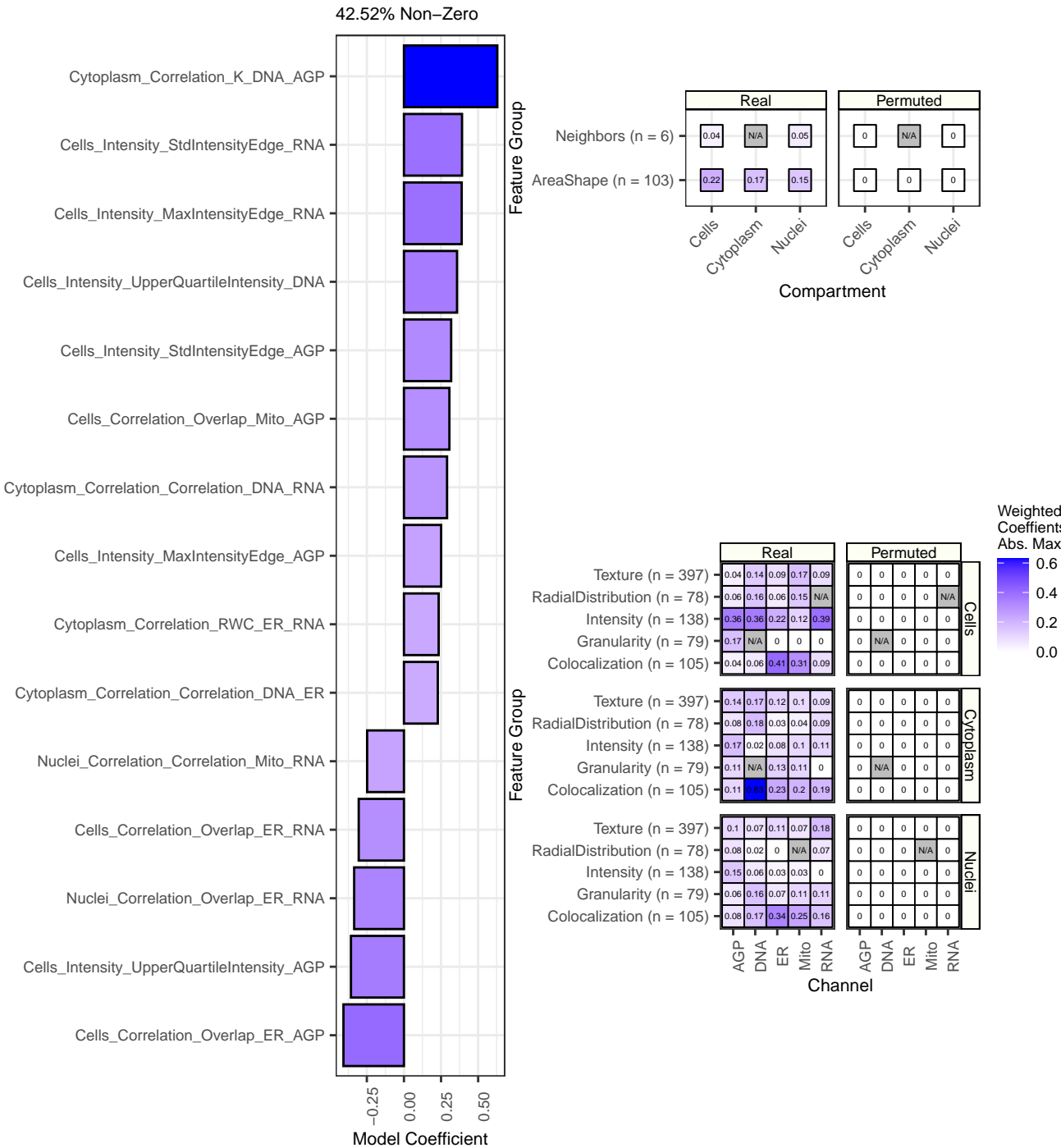
S – # of gH2AX Spots per Area of Nucleus



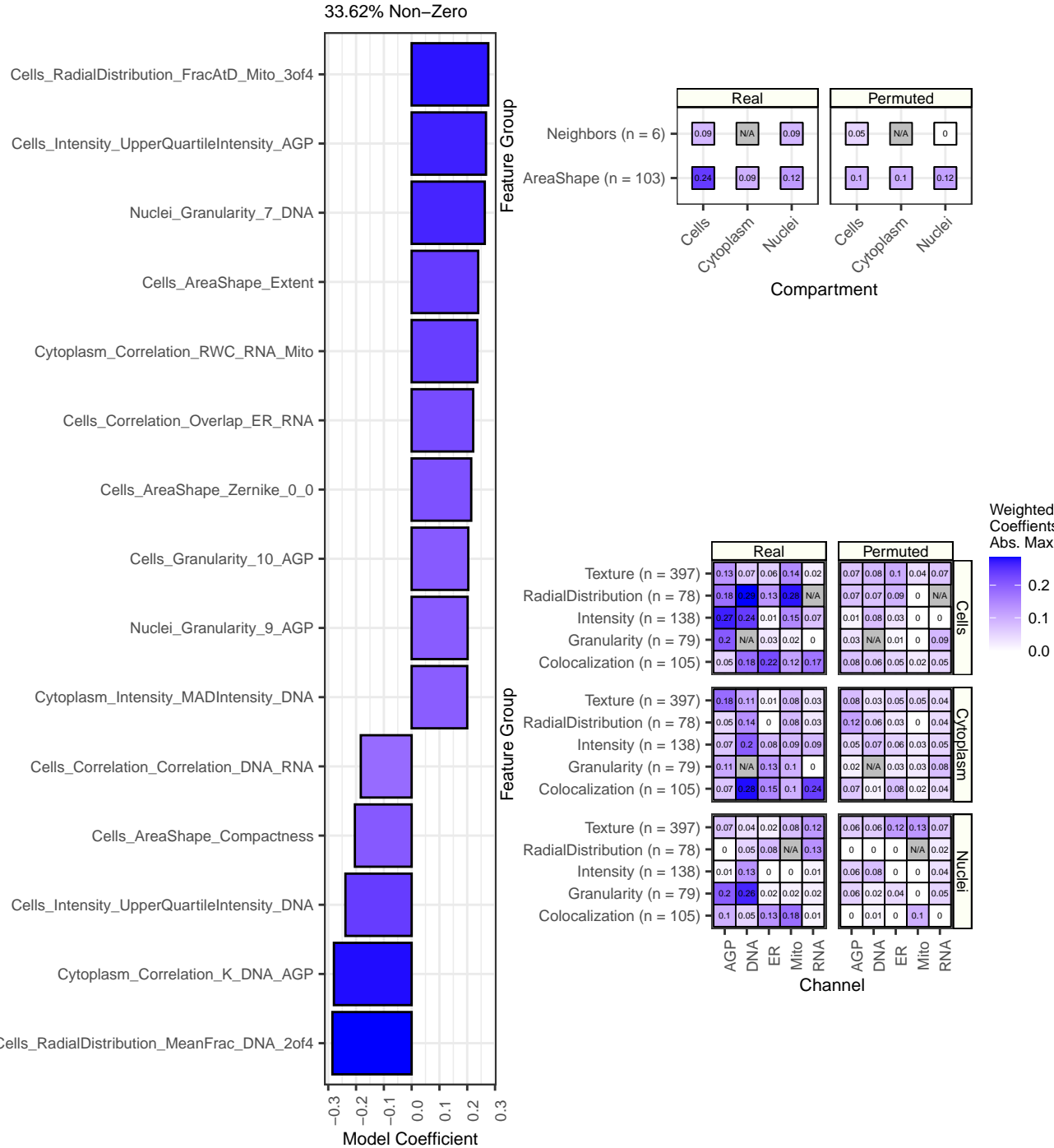
VB – Infection Efficiency



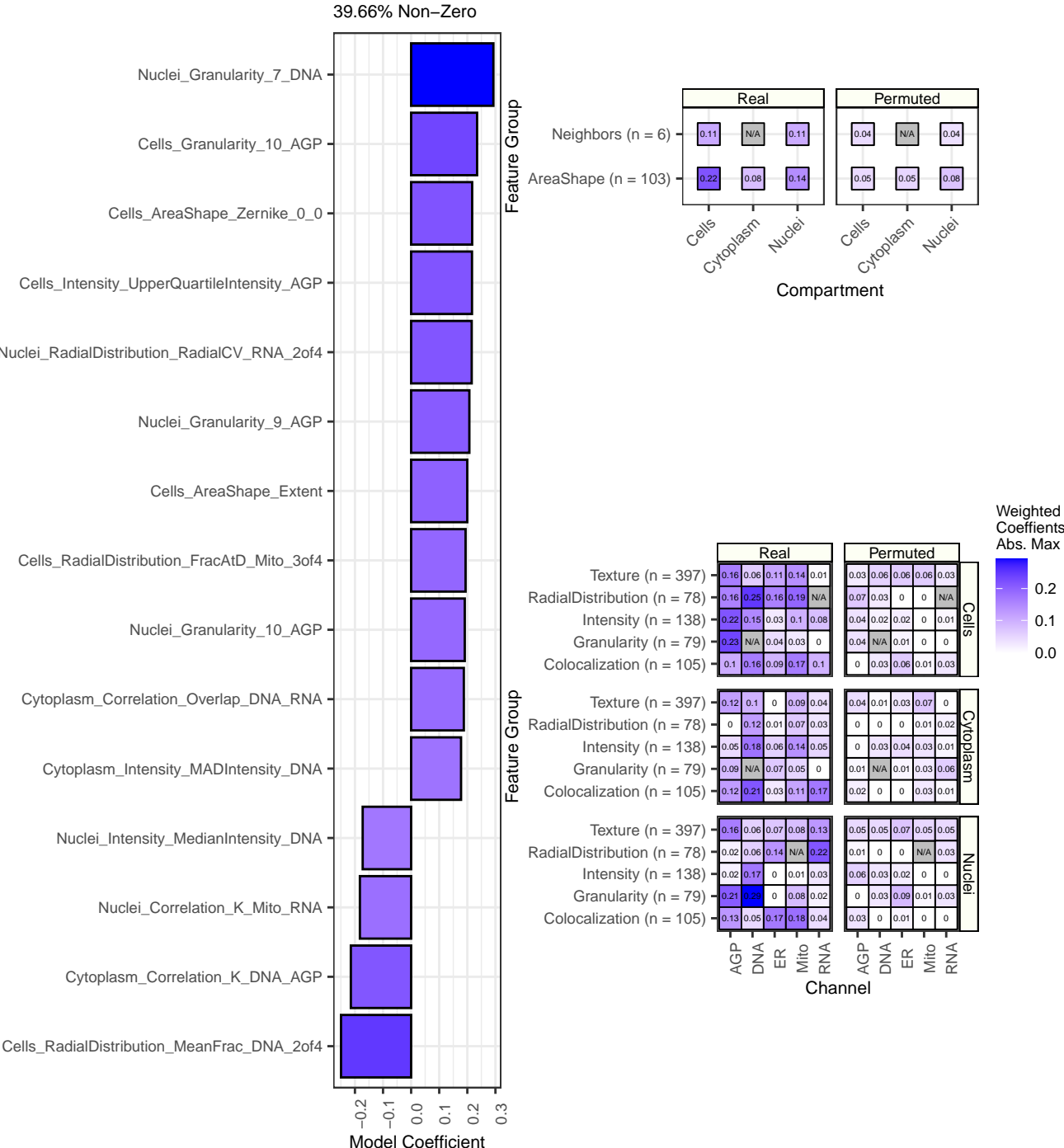
Live Cell Area



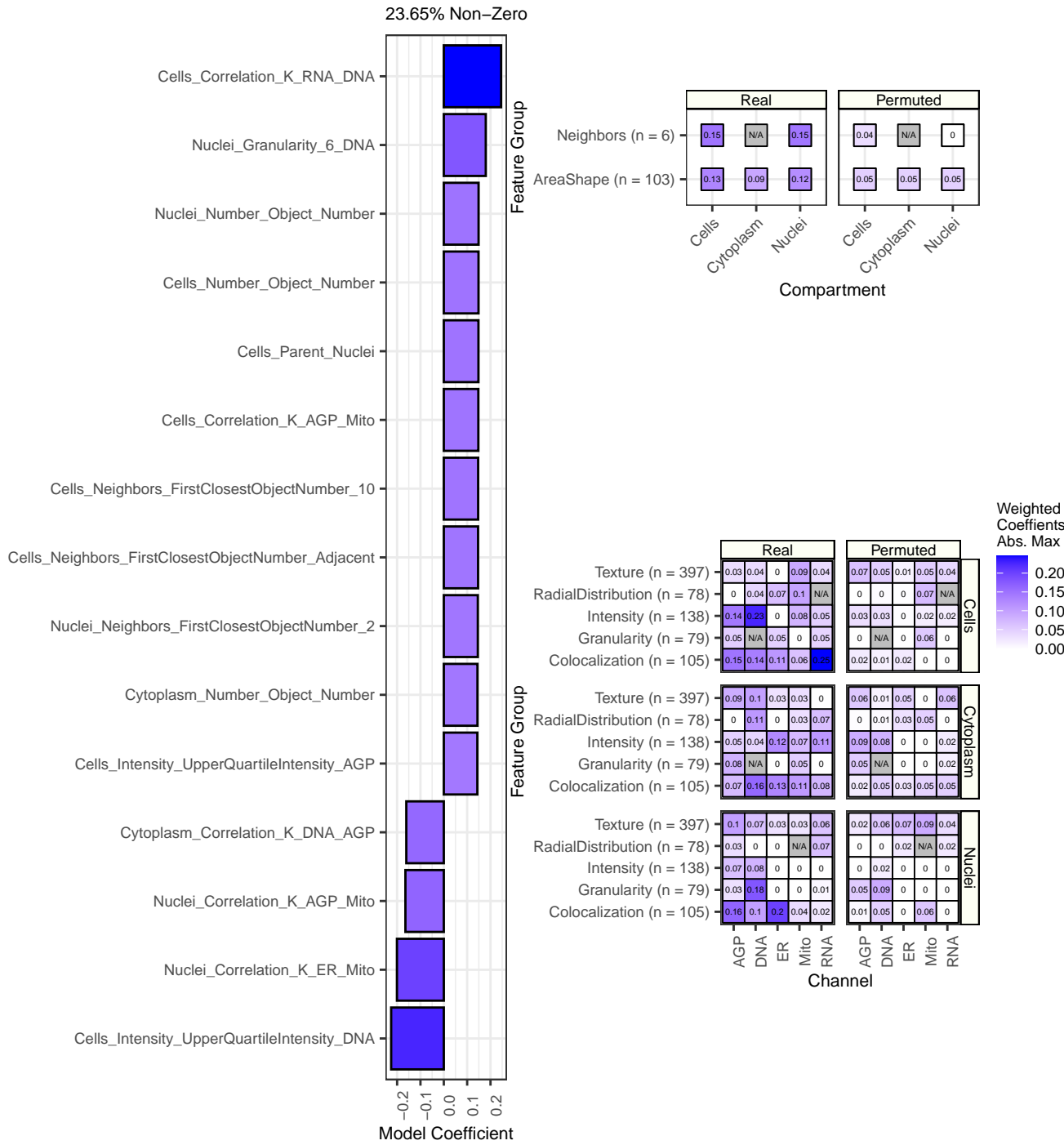
Live Cell Roundness



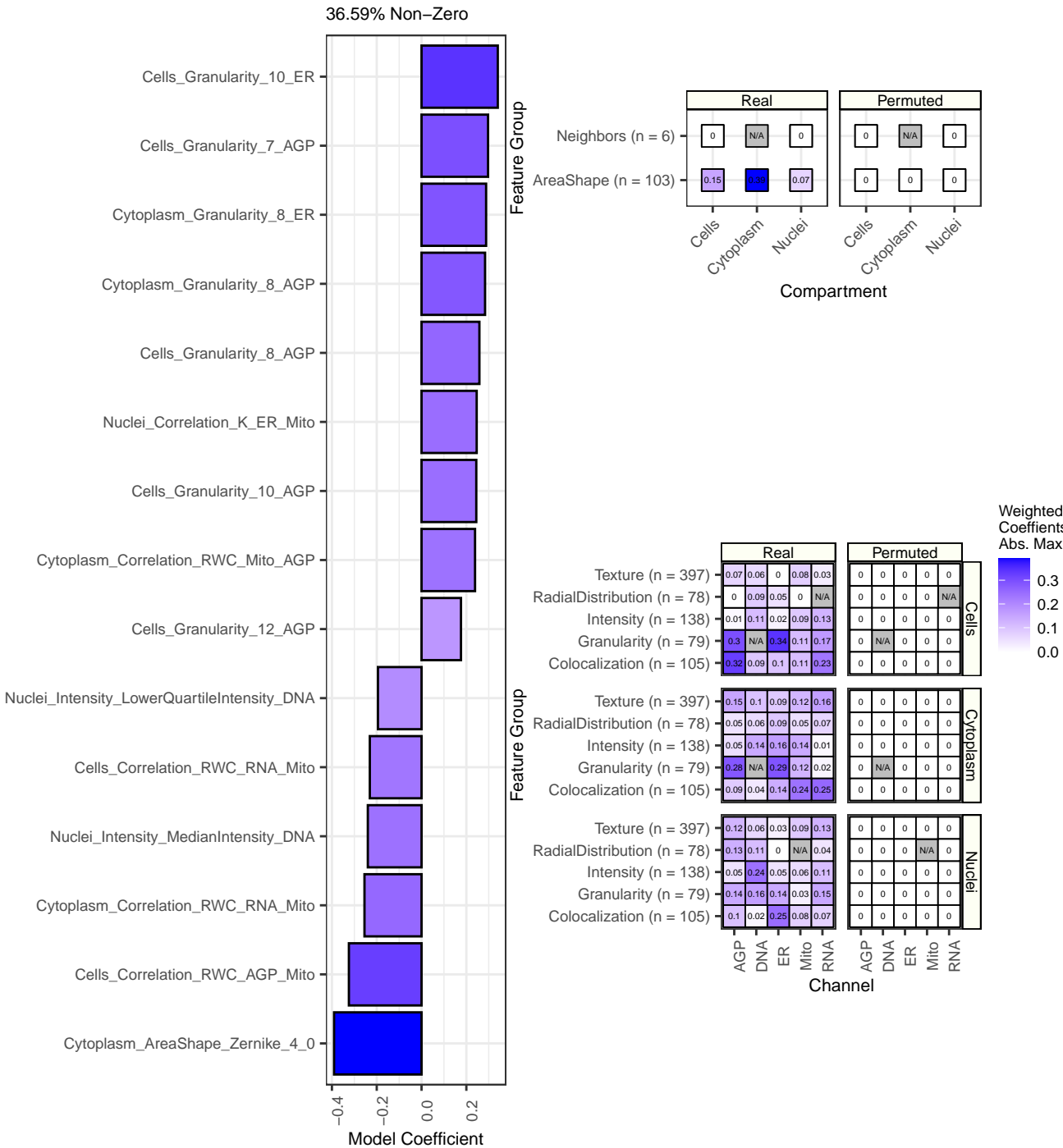
Live Width / Length



Live Cells

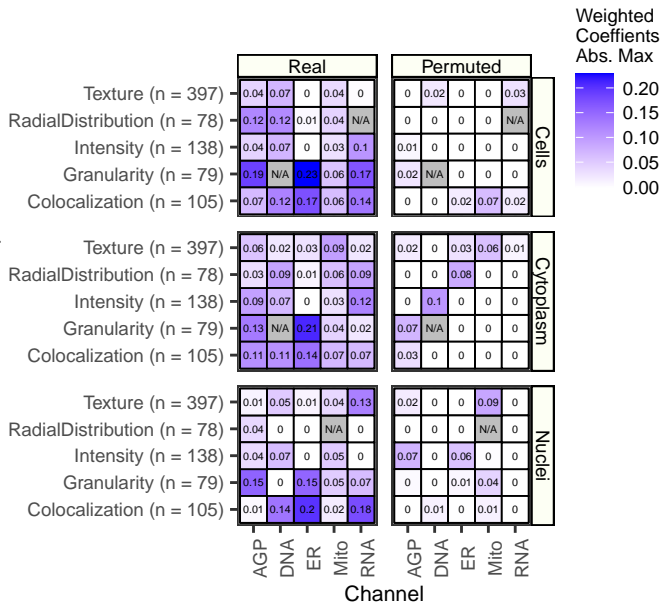
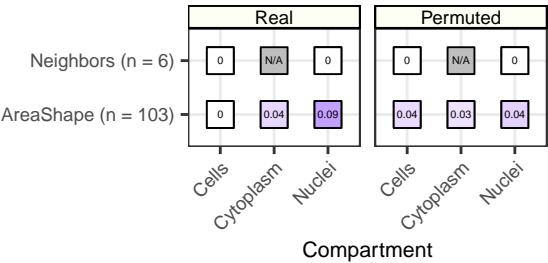
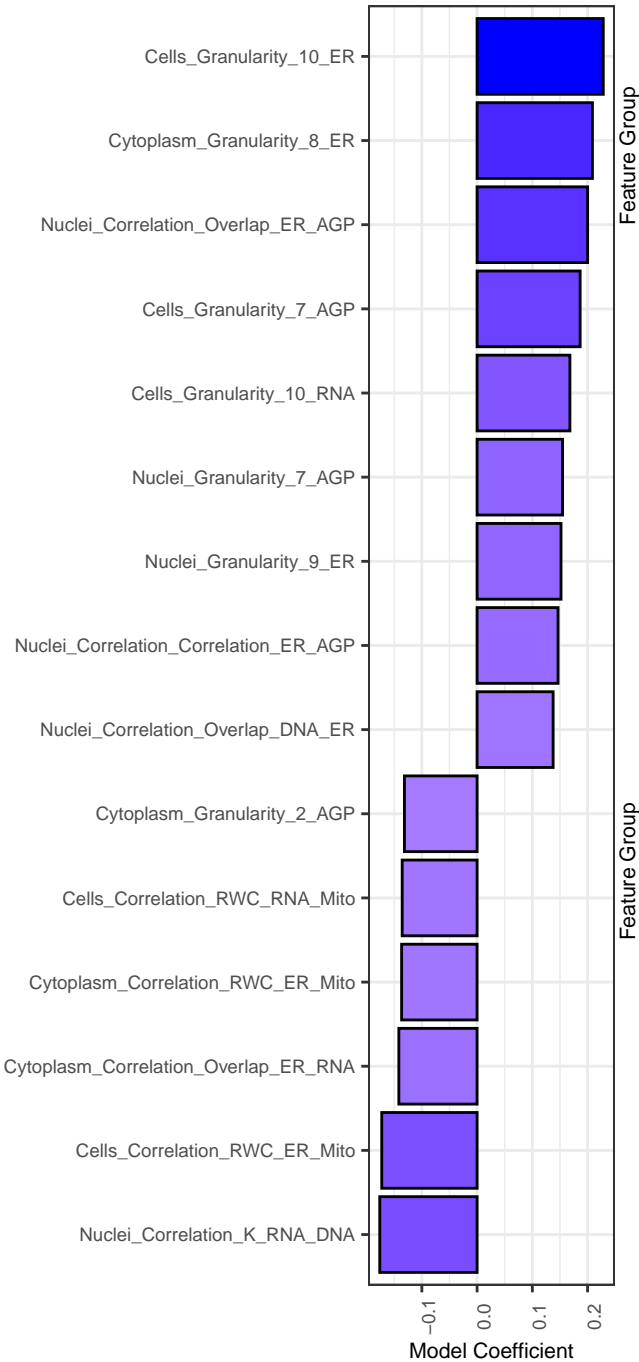


% All Apoptosis (CASP+)



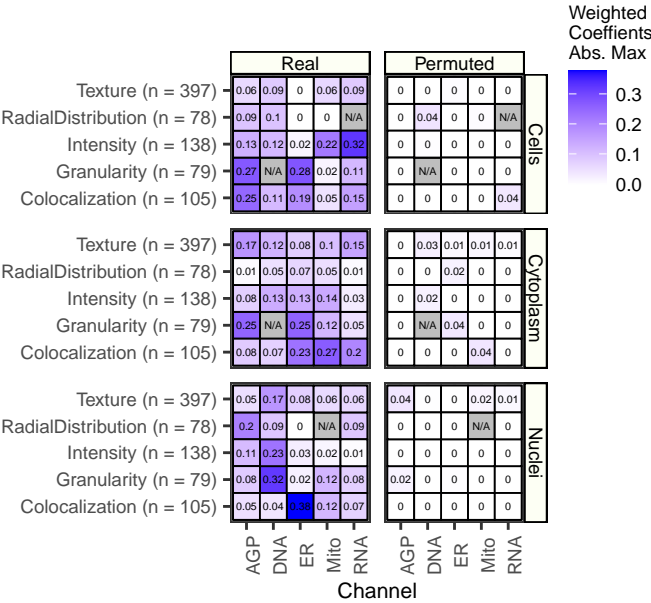
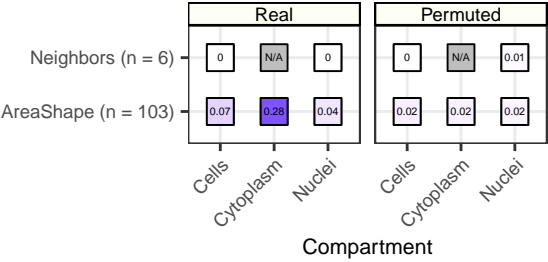
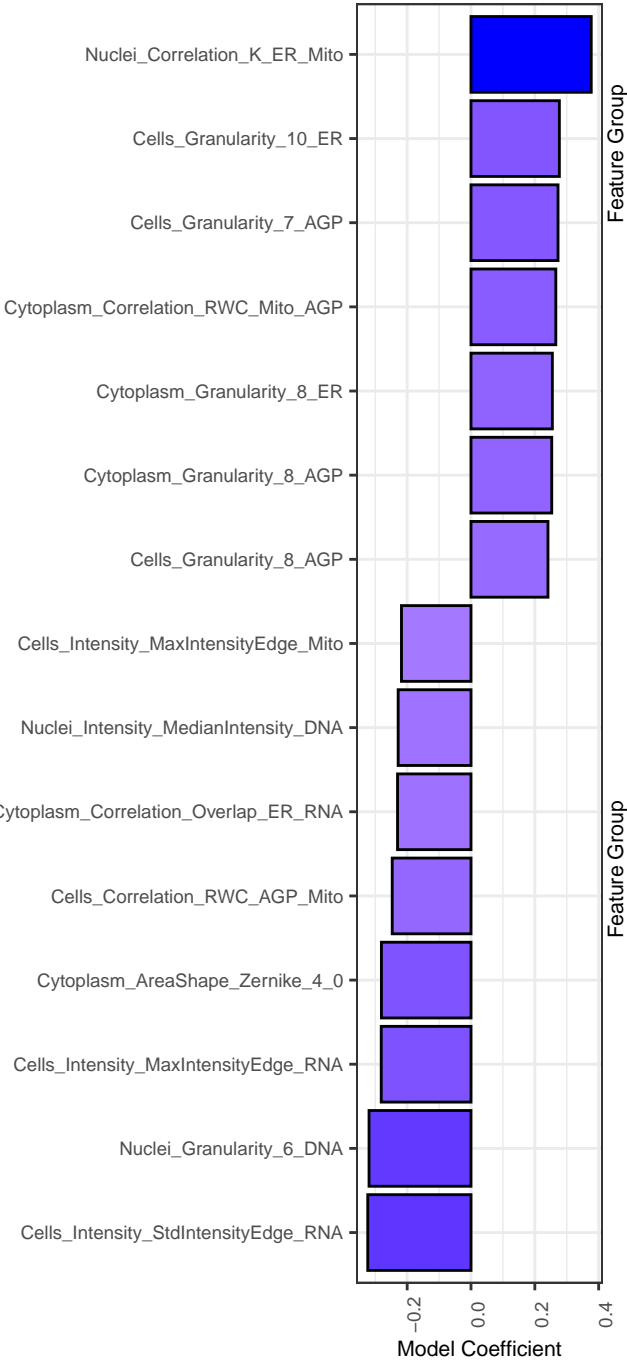
% Caspase / % Dead Only

27.25% Non-Zero

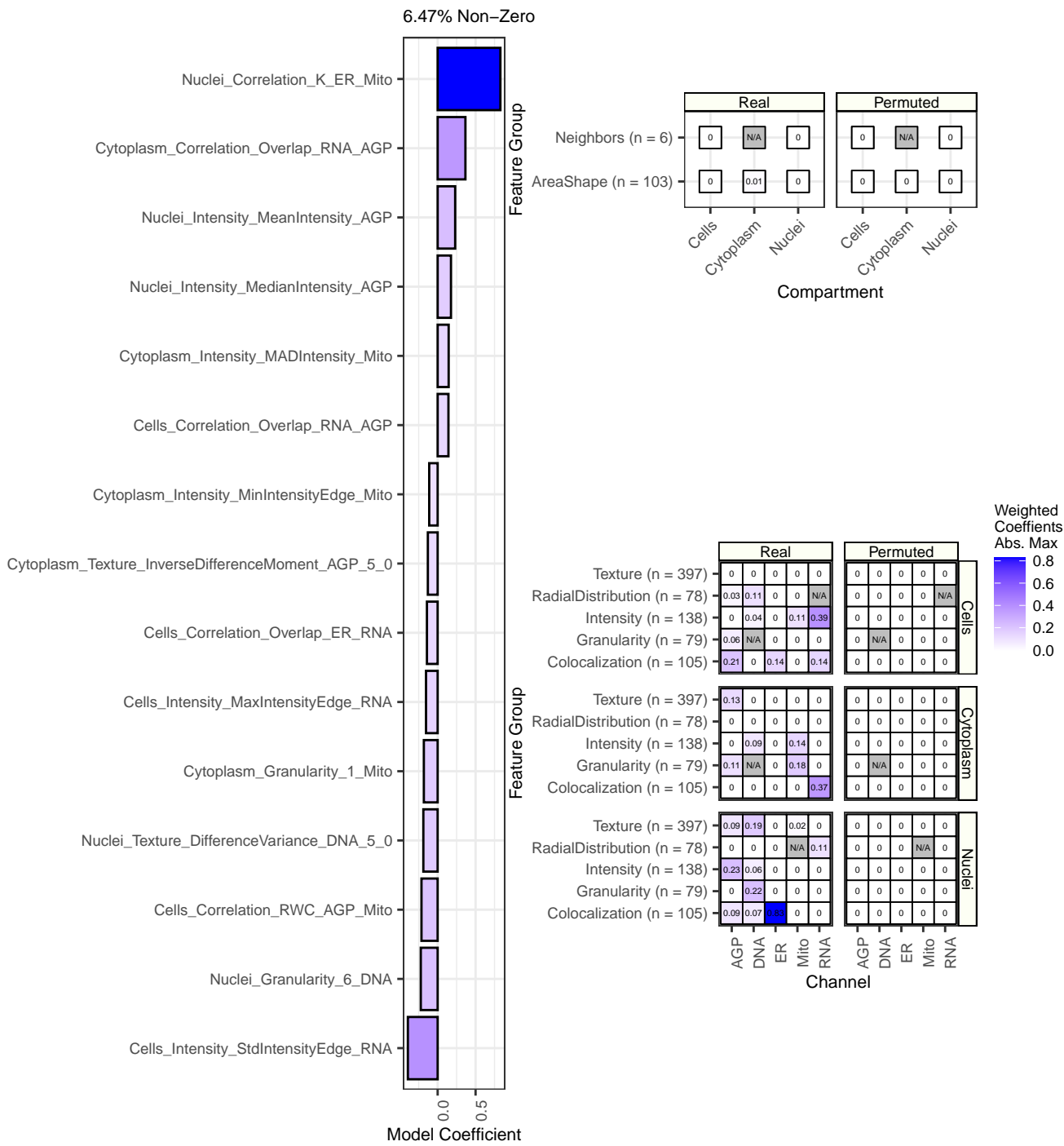


% All Dead (DRAQ7+)

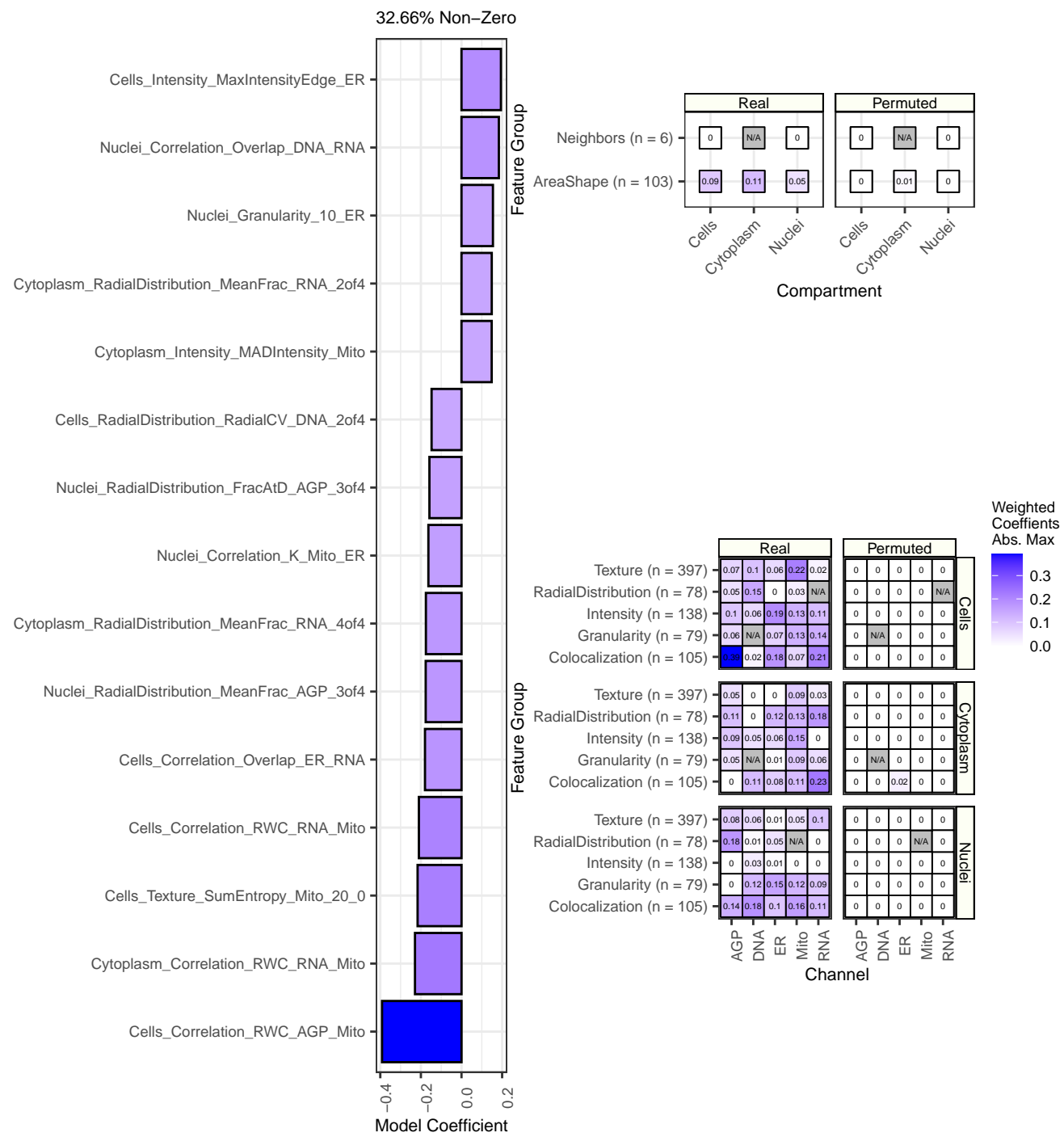
33.93% Non-Zero



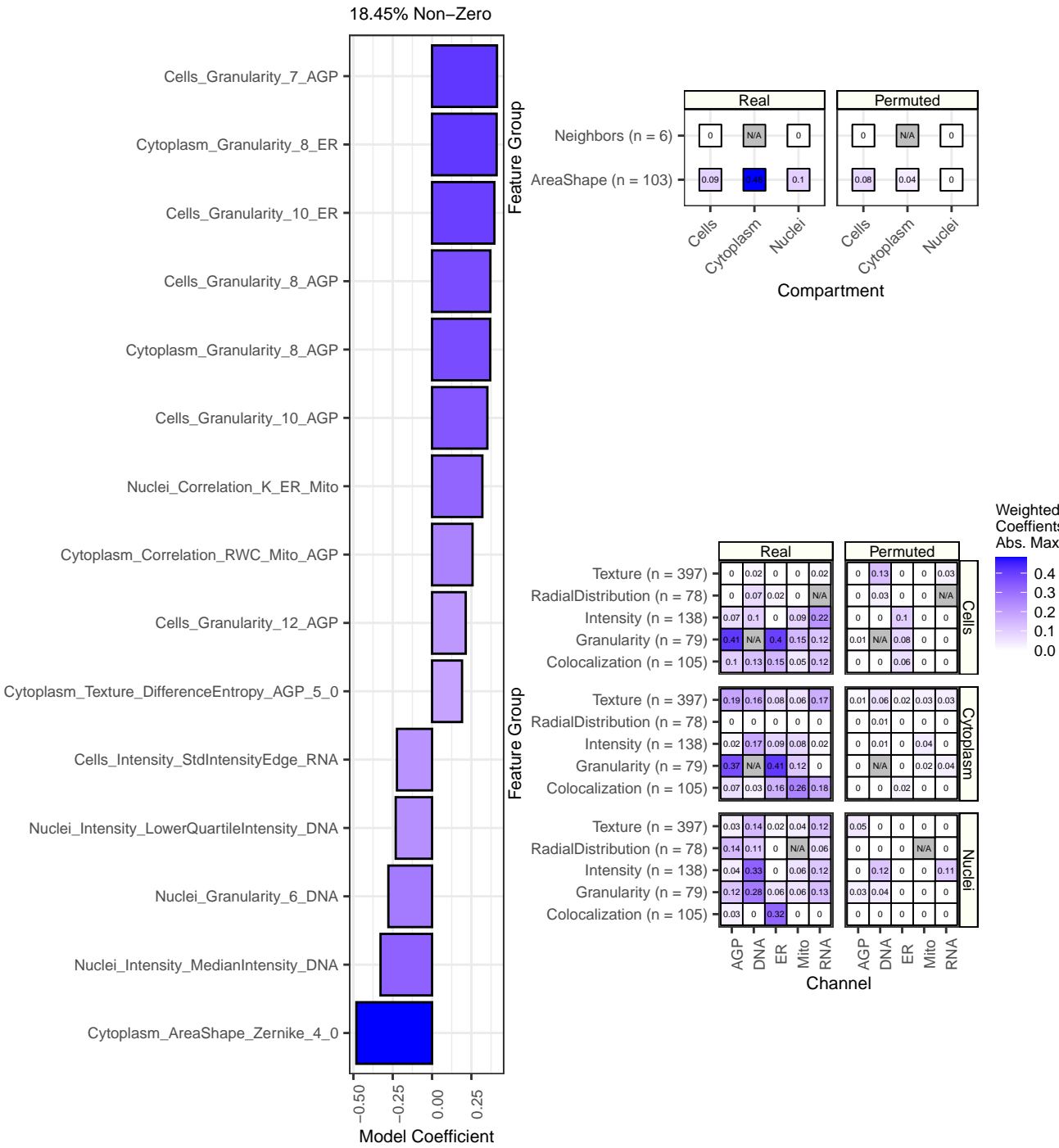
% Dead Only (CASP-; DRAQ7+)



% Early Apoptosis (CASP+; DRAQ7-)

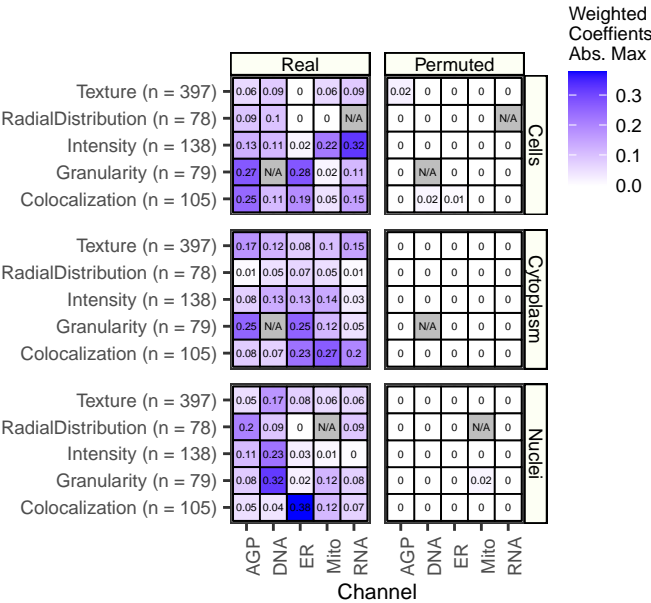
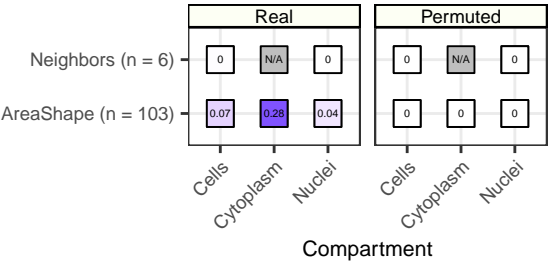
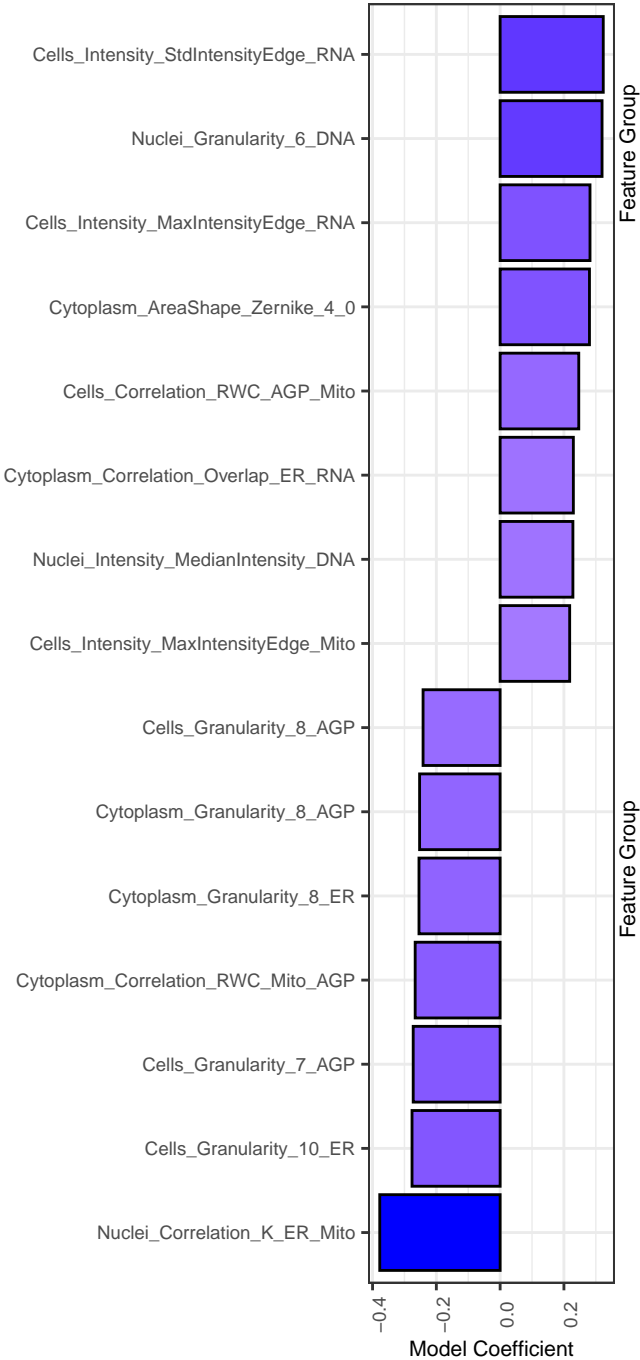


% Late Apoptosis (CASP+; DRAQ7+)

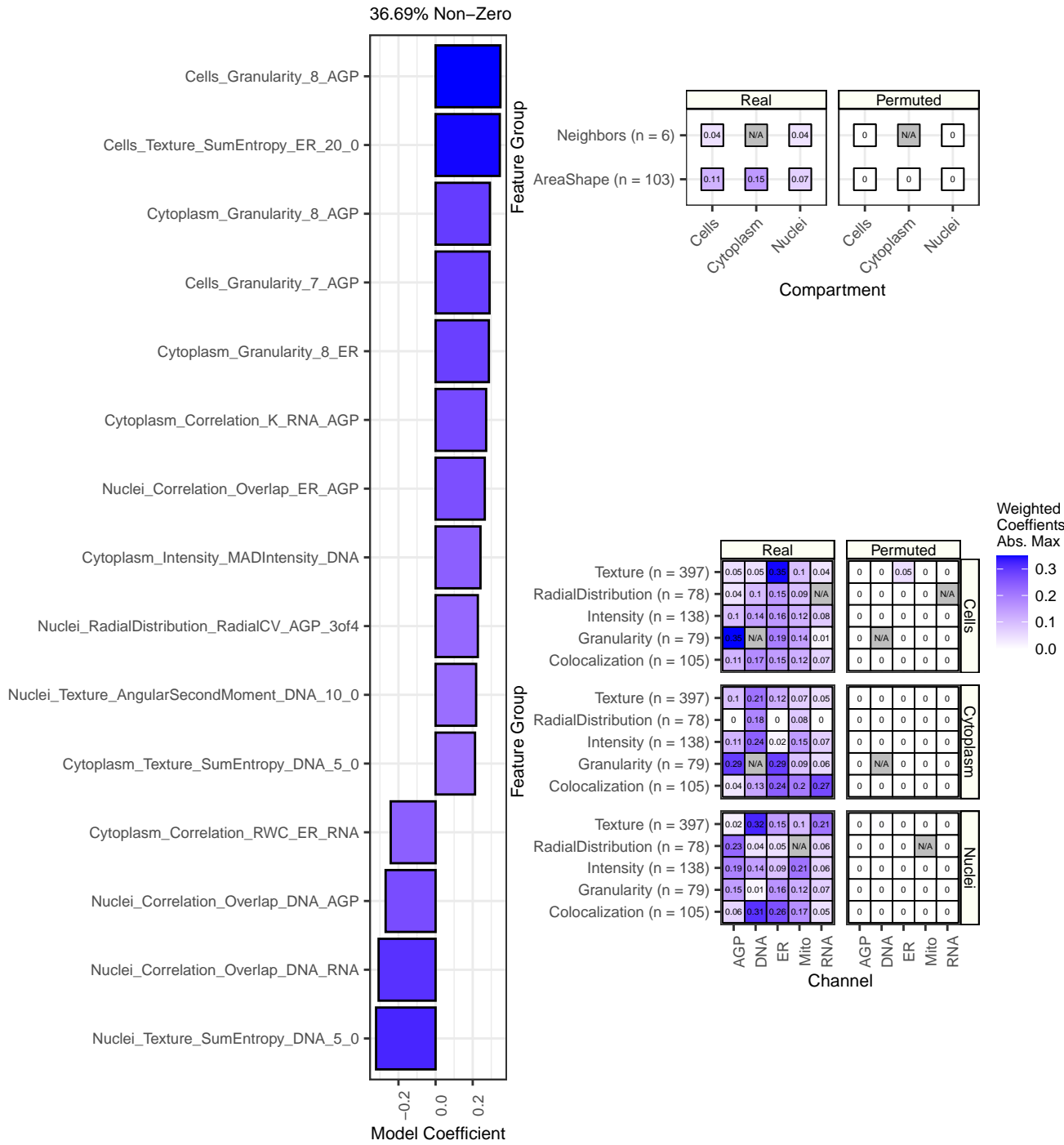


% Live (DRAQ7-; CASP-)

33.83% Non-Zero



ROS-back



ROS

