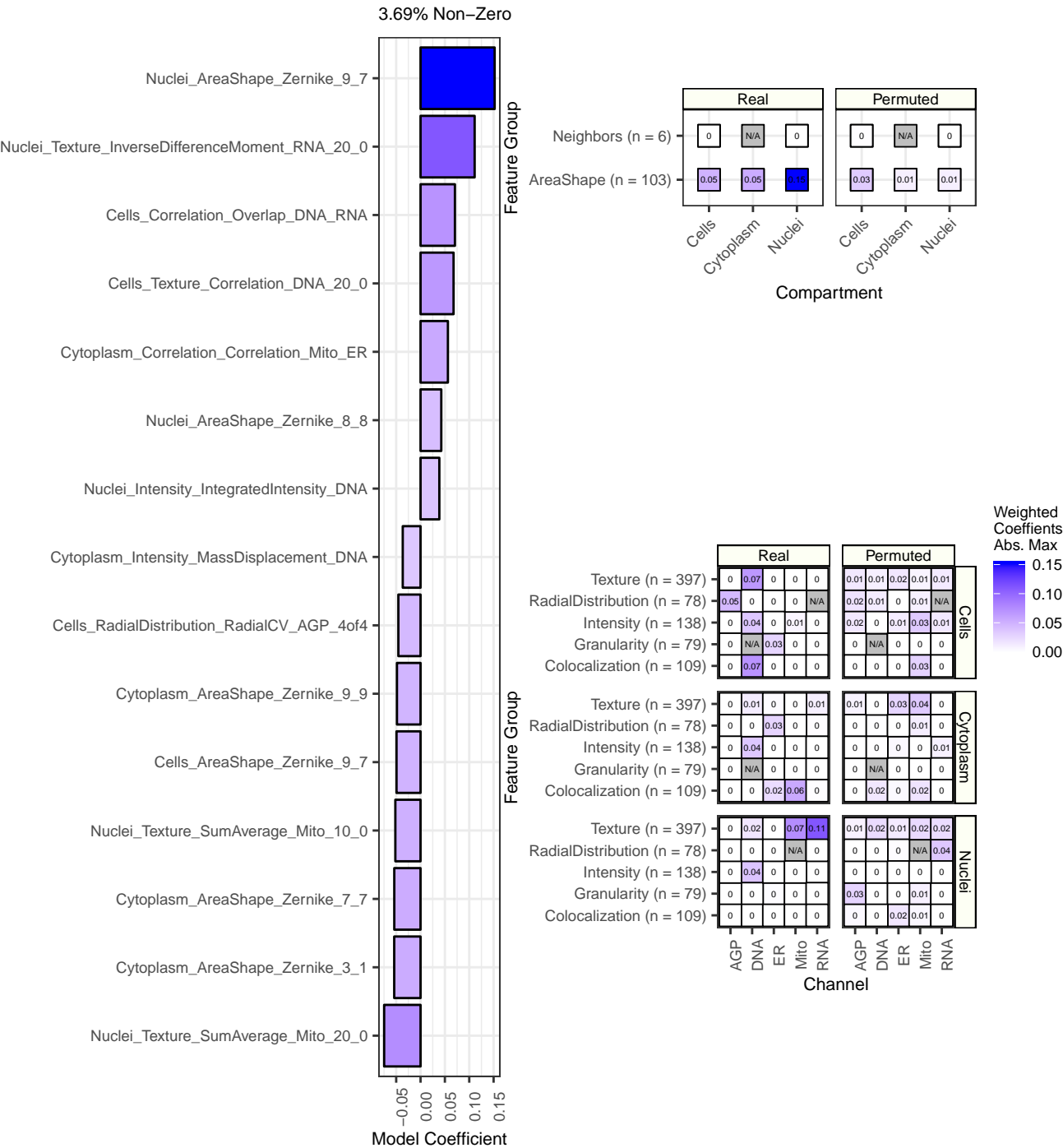
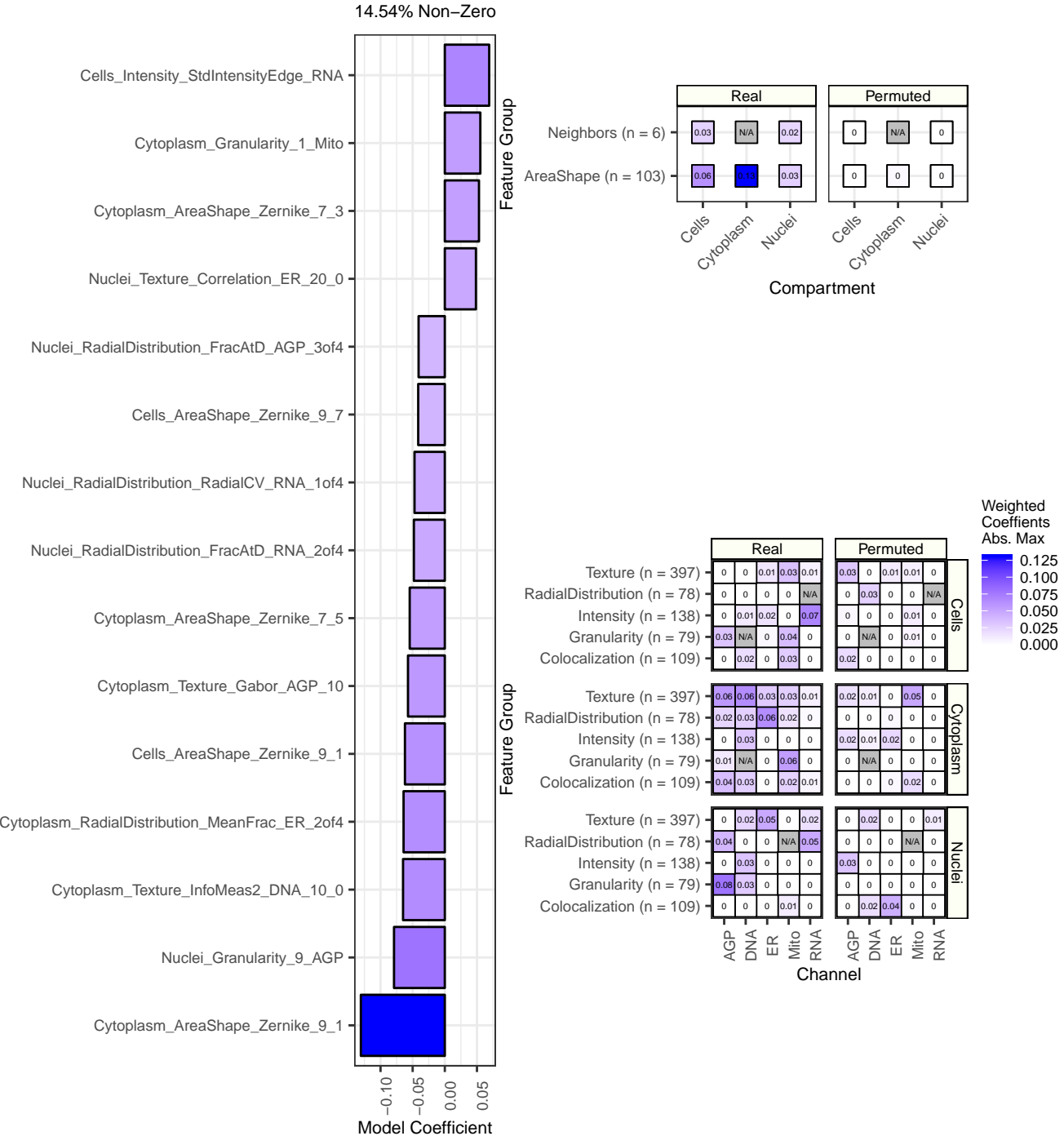


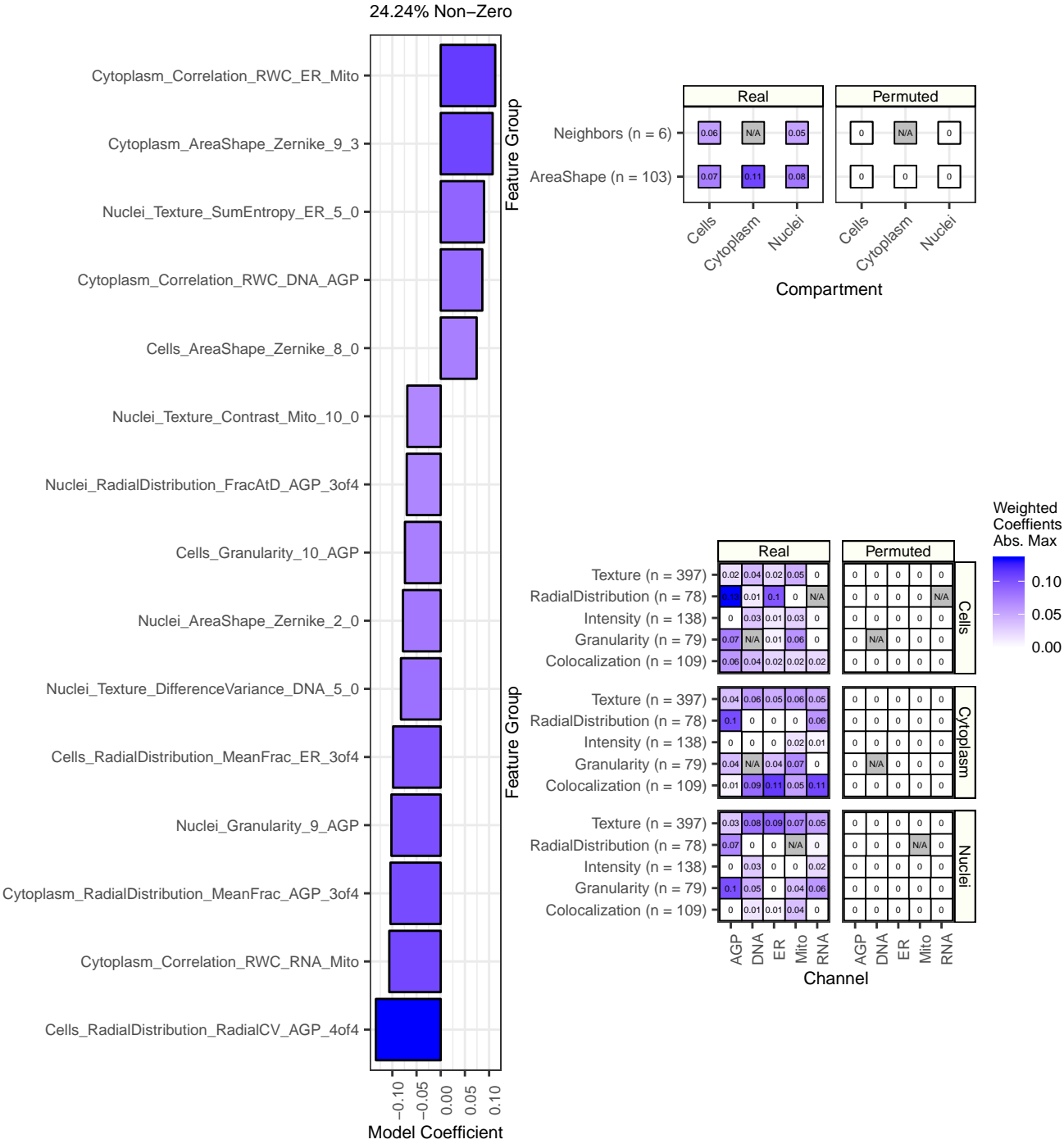
ALL – % High gH2AX Spots



ALL – Polynuclear

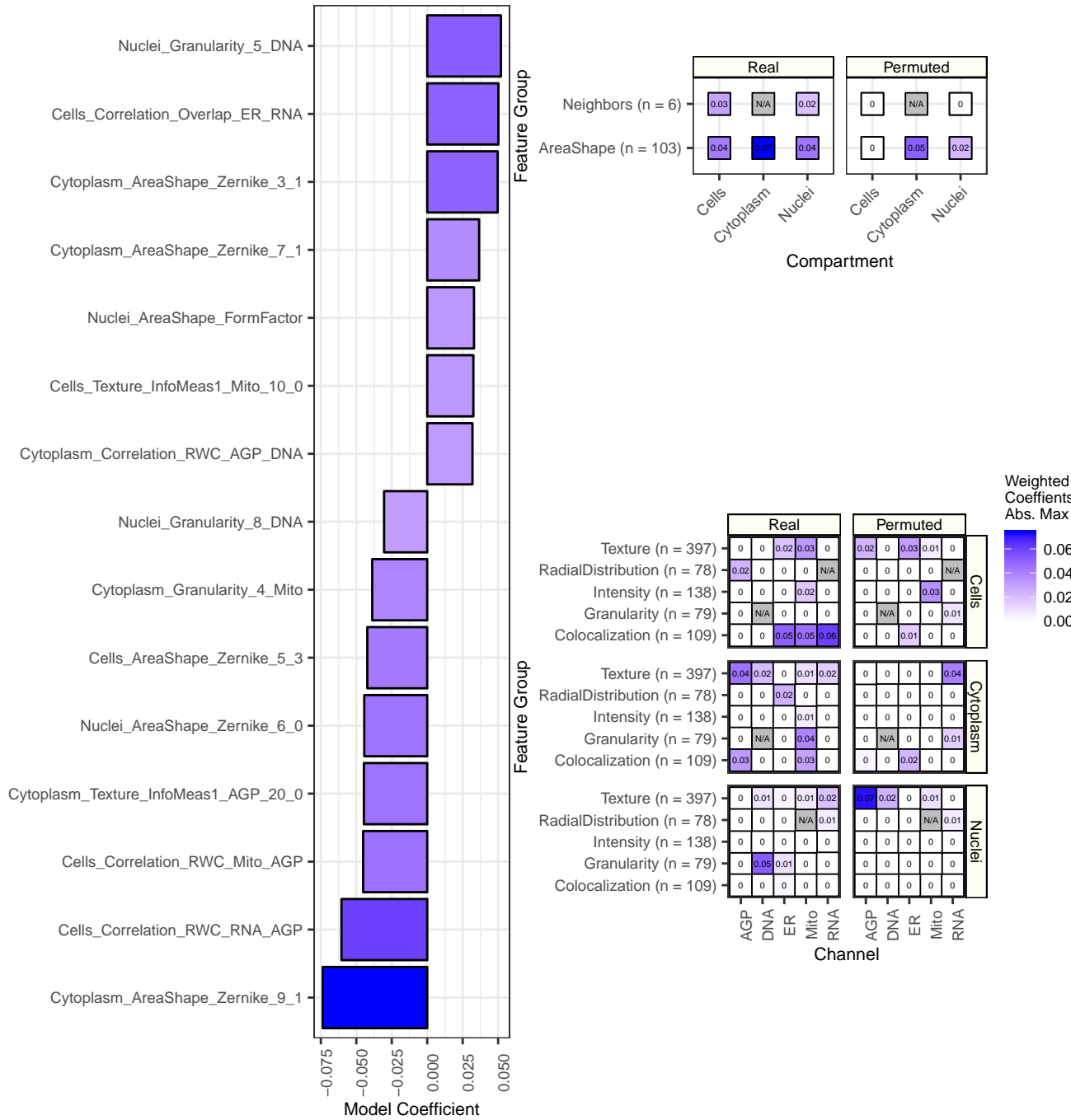


ALL – Polyploid



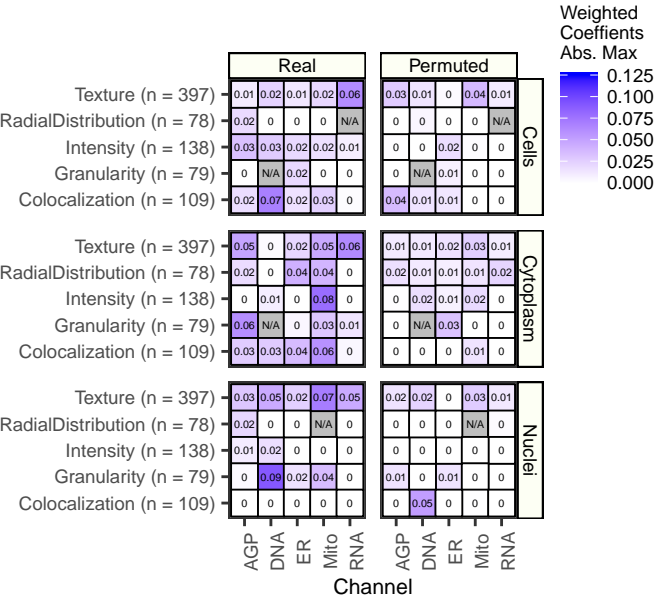
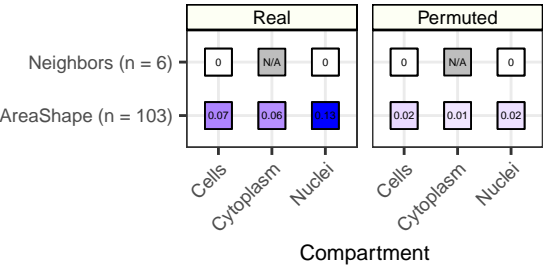
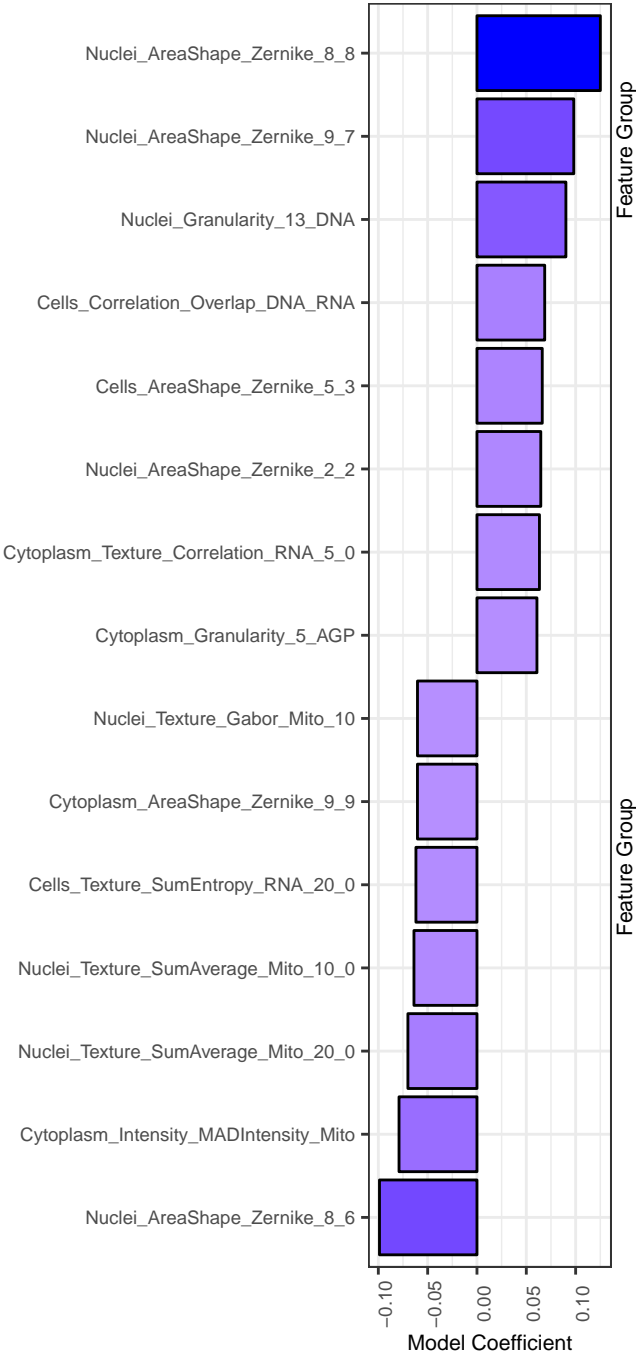
ALL – # cells

8.96% Non-Zero



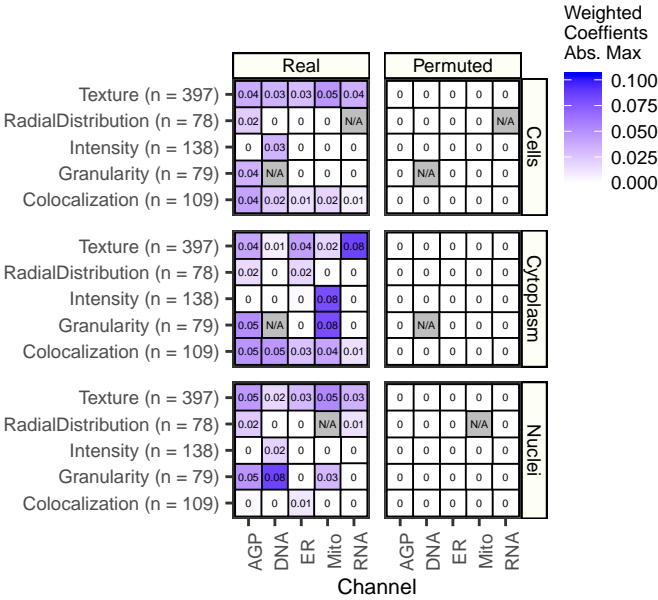
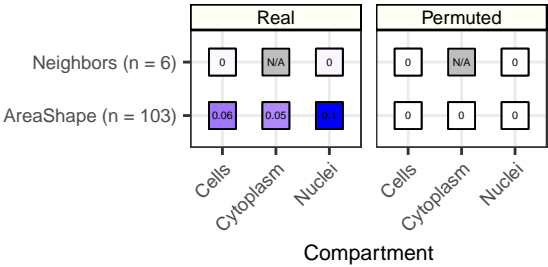
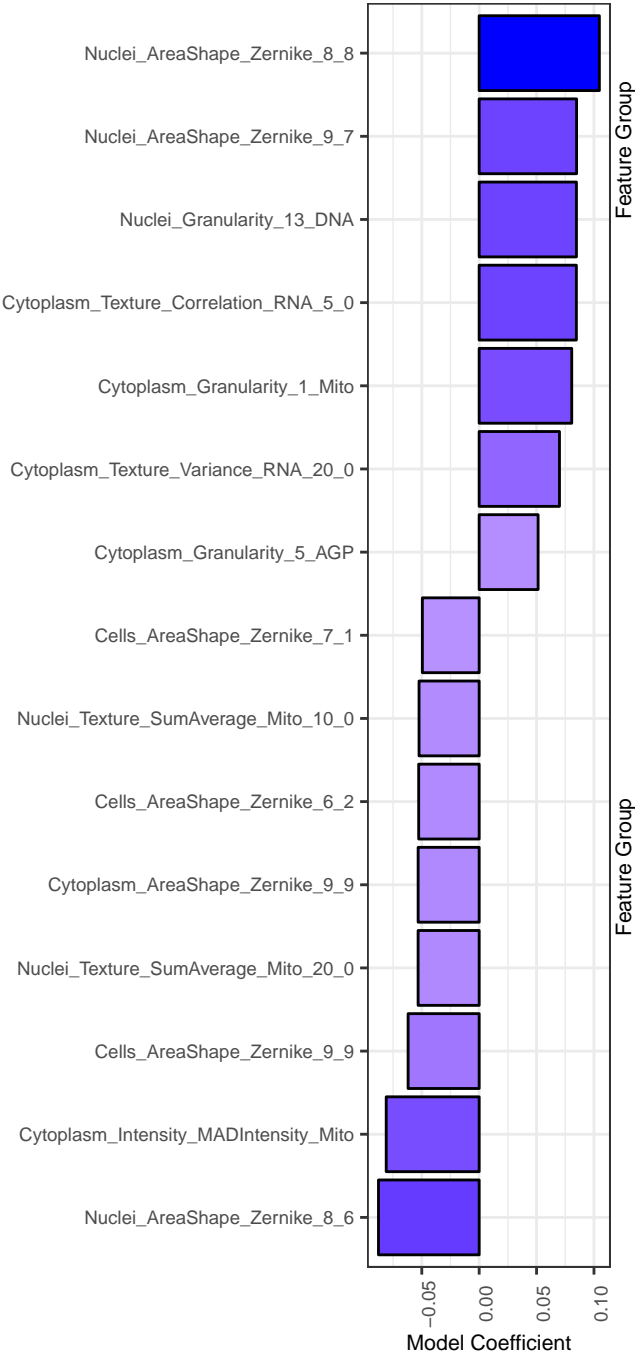
ALL – # of gH2AX Spots

17.18% Non-Zero

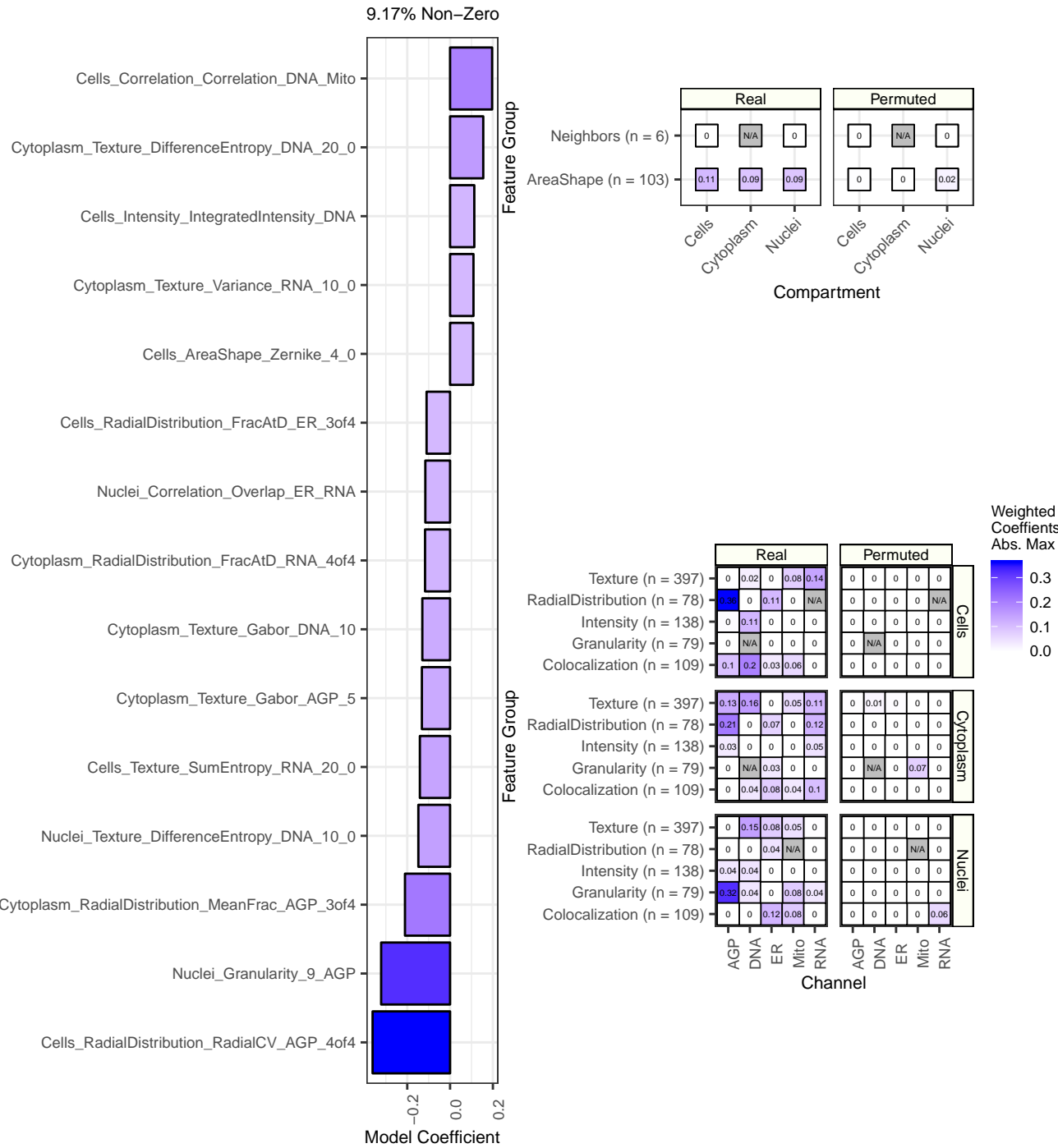


# ALL – # of gH2AX Spots per Area of Nucleus

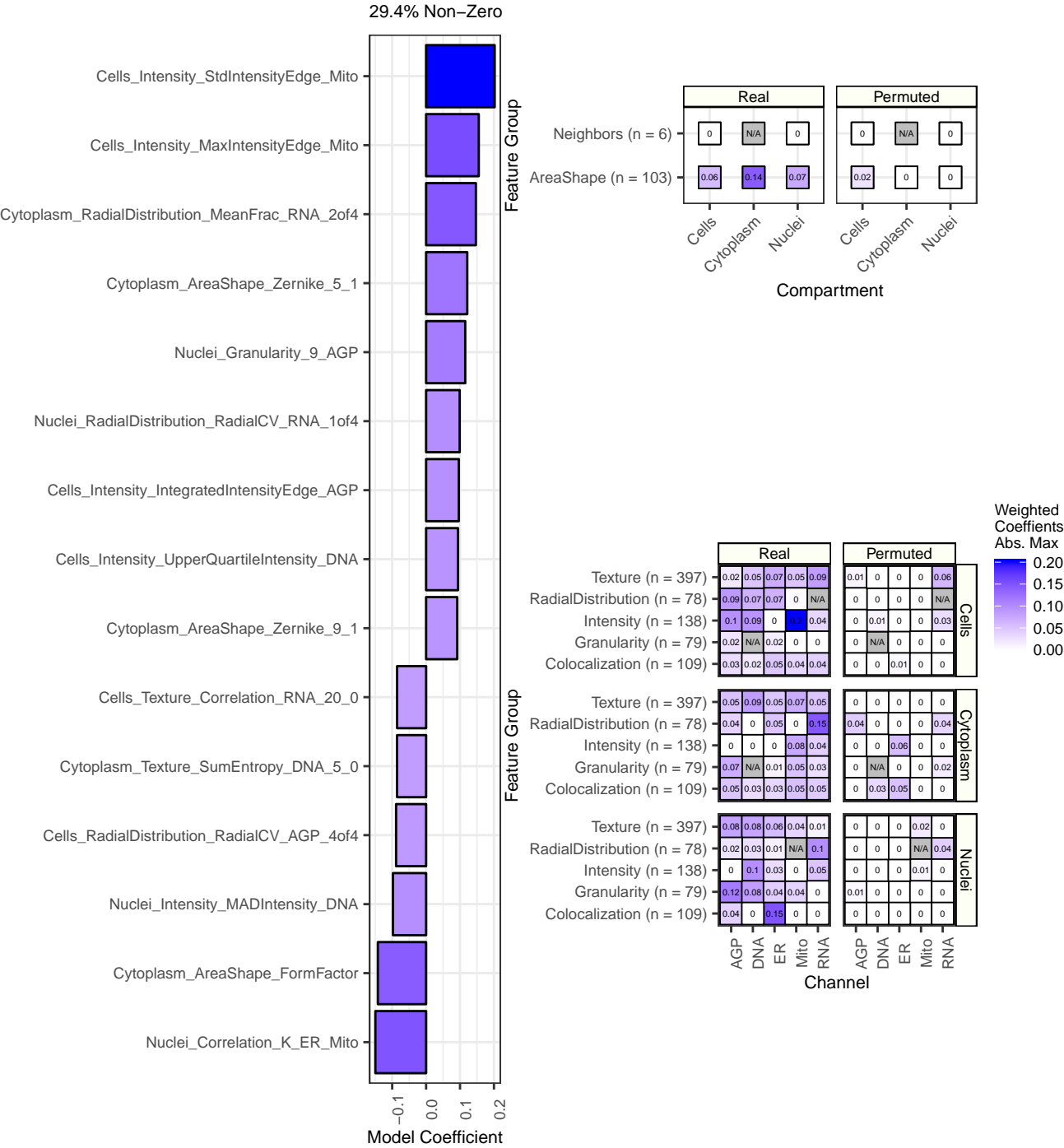
17.39% Non-Zero



ALL – Nucleus Area

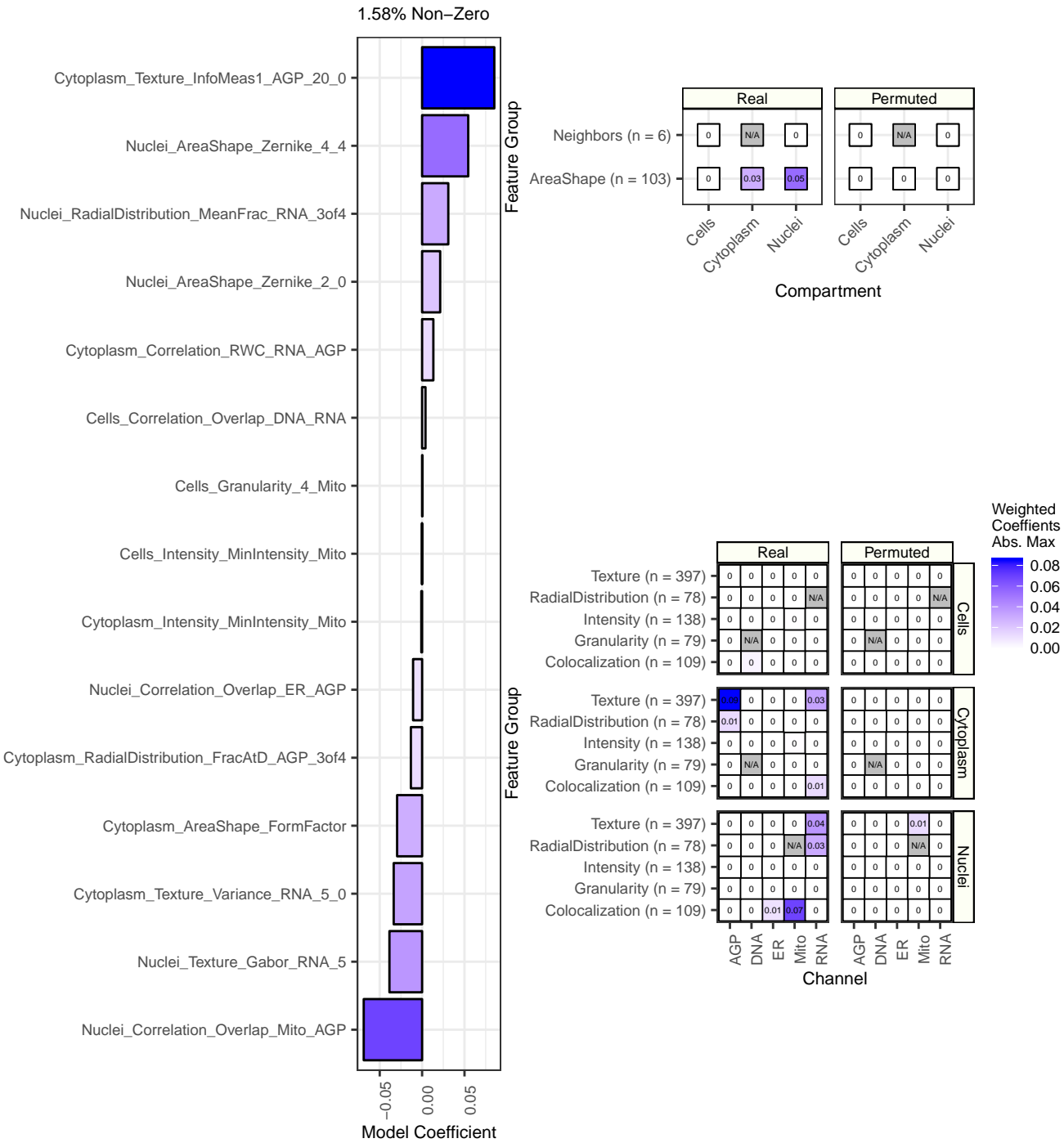


ALL – Nucleus Roundness

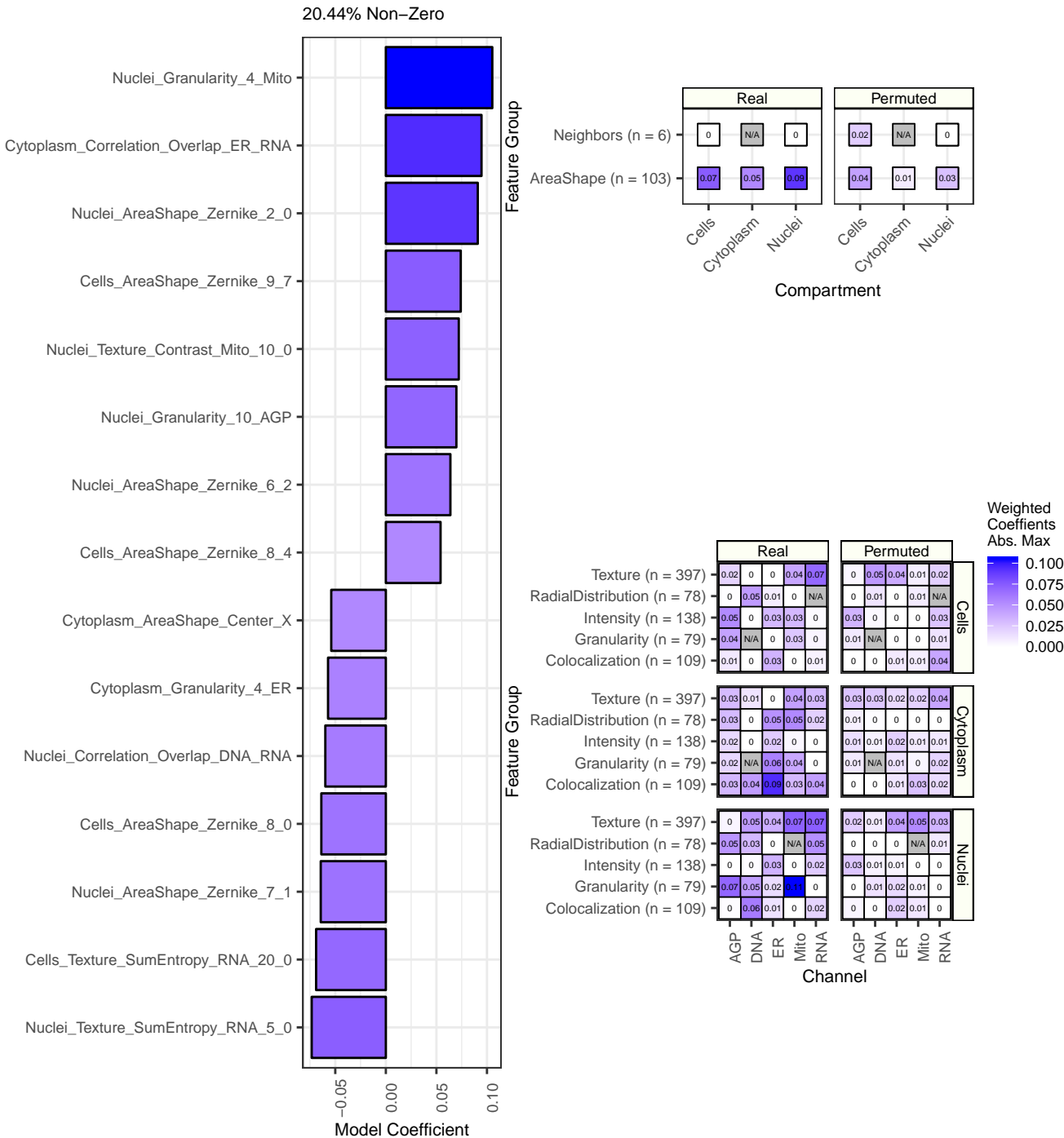




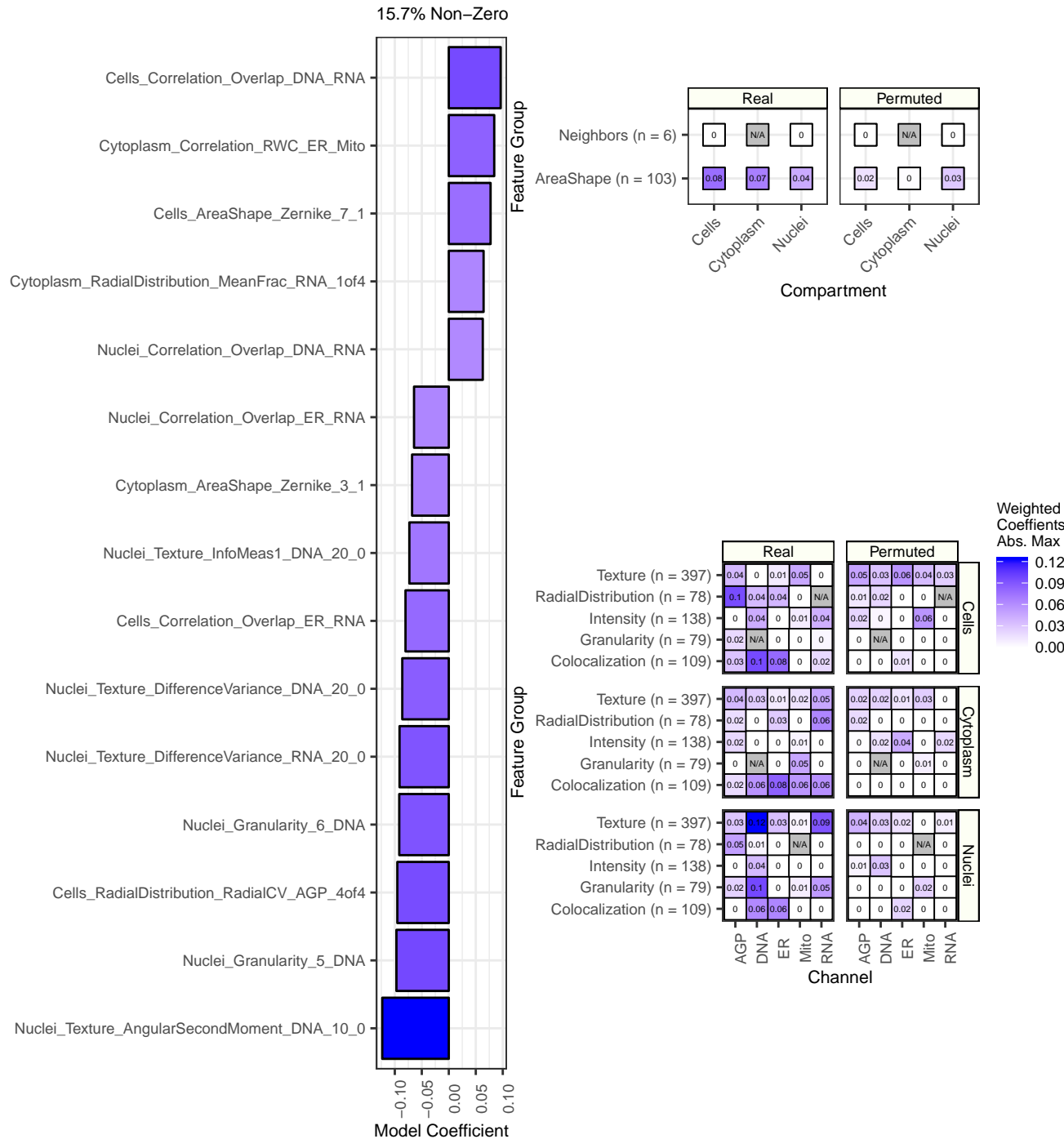
CC – % early M



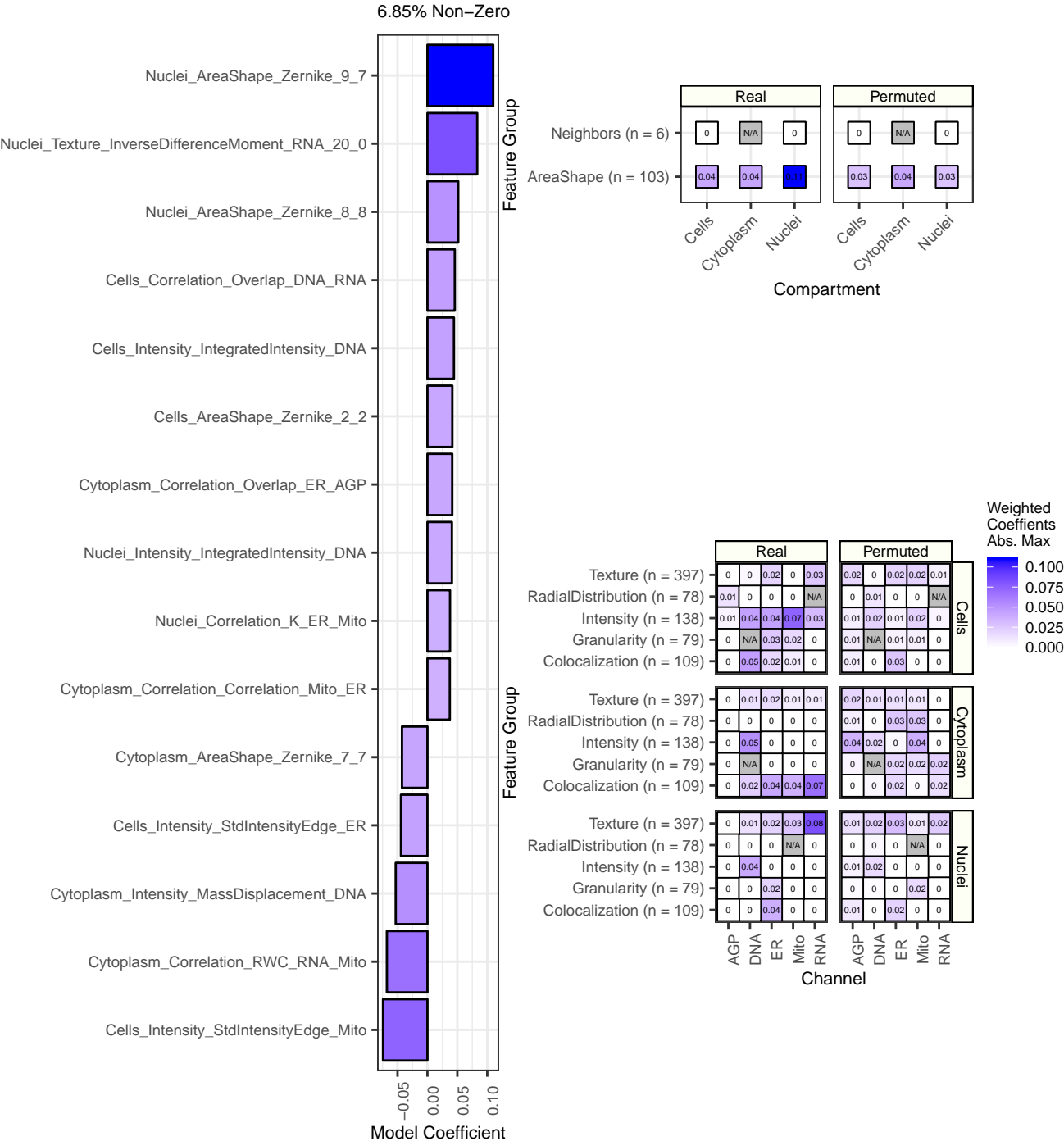
CC – % G1



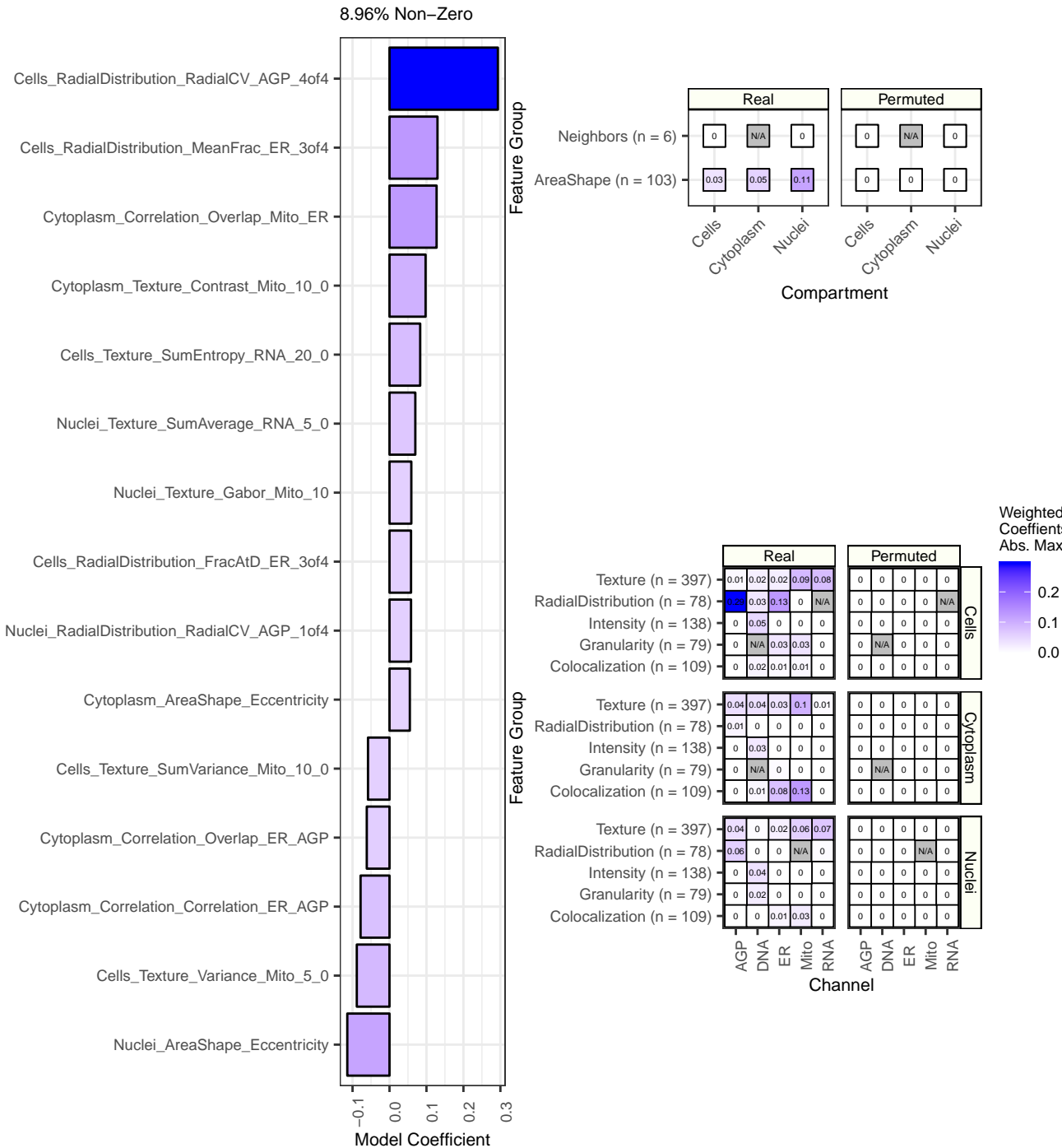
CC – % G2



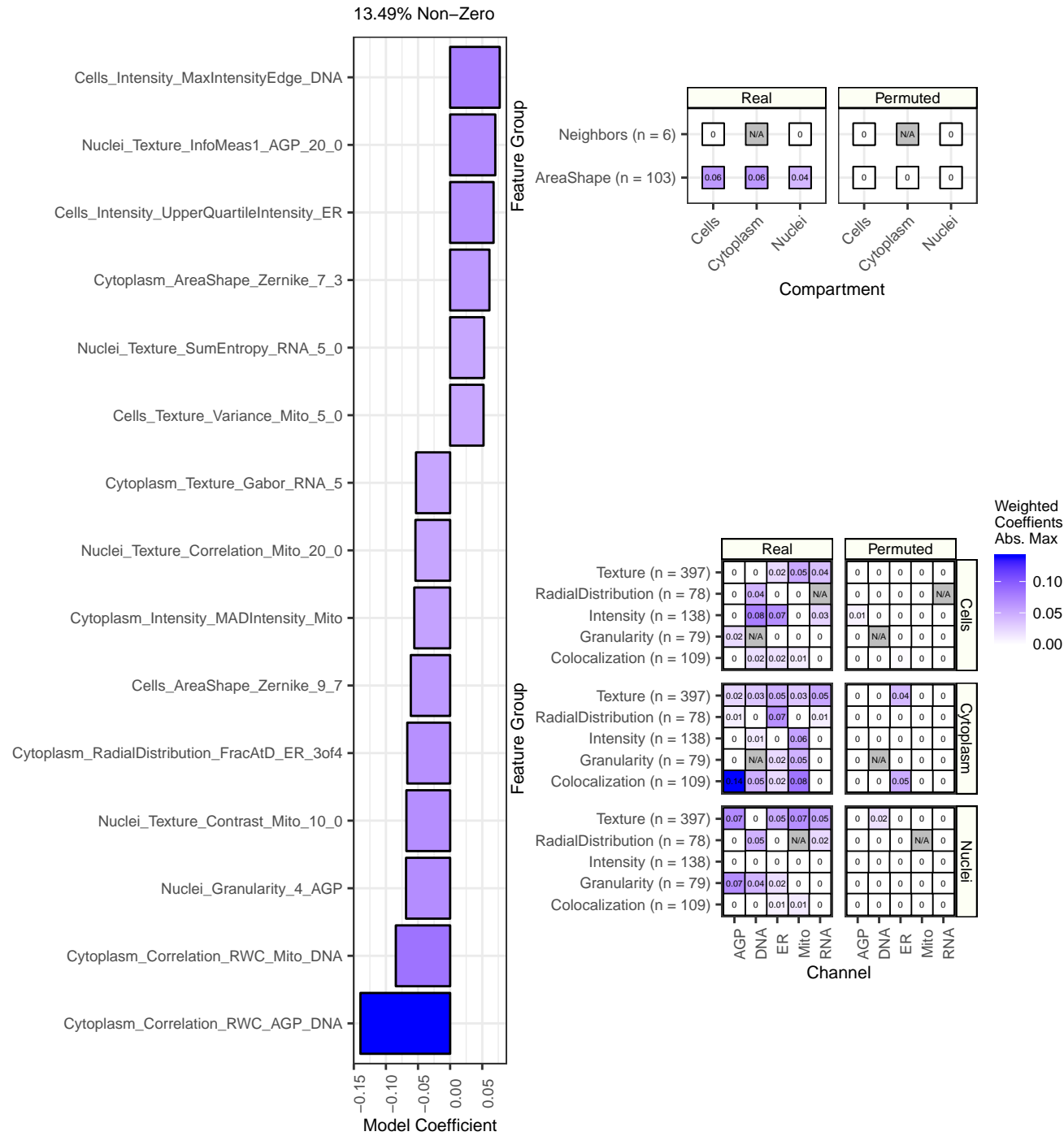
CC – % High gH2AX spots



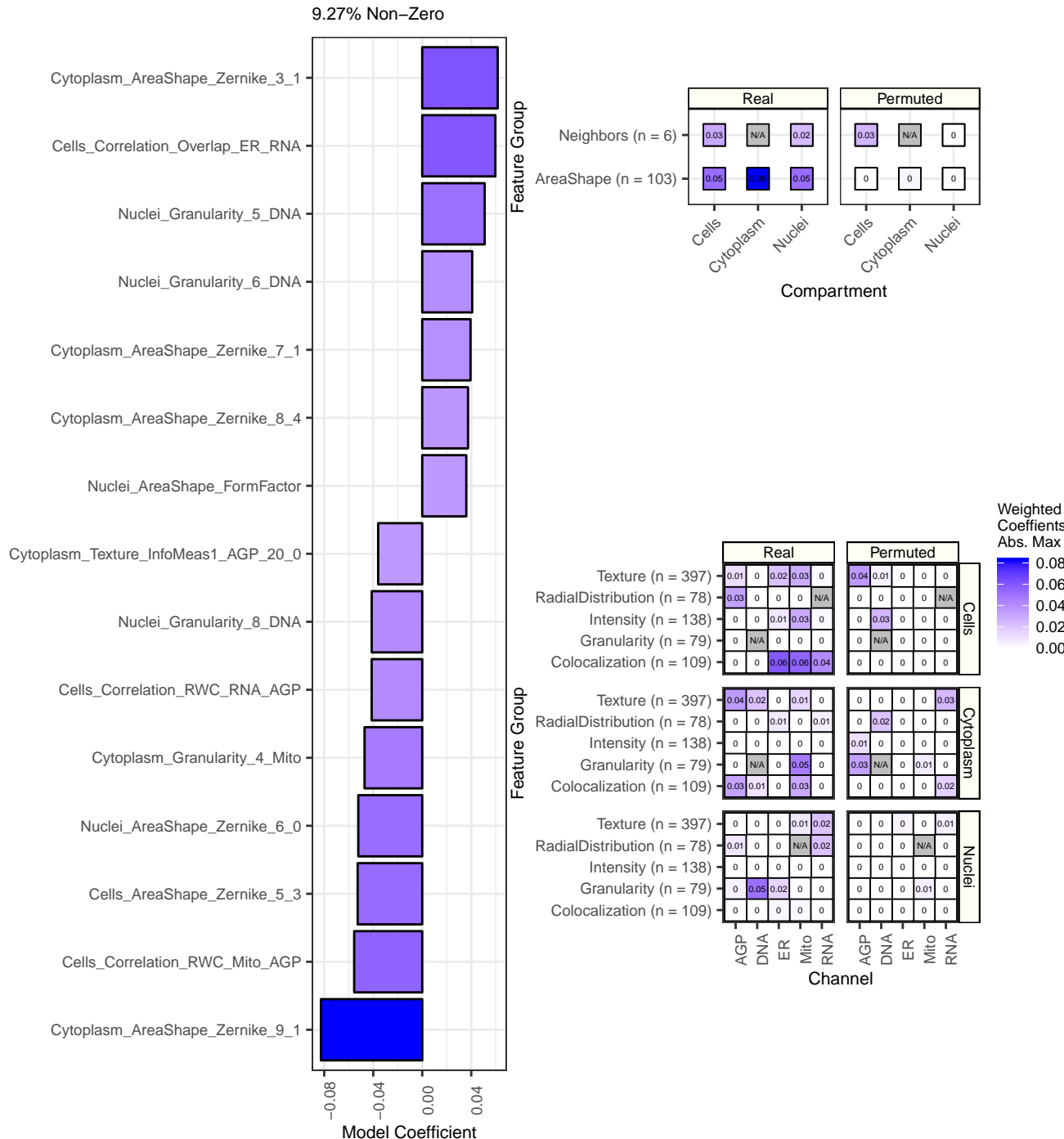
CC – % Late M



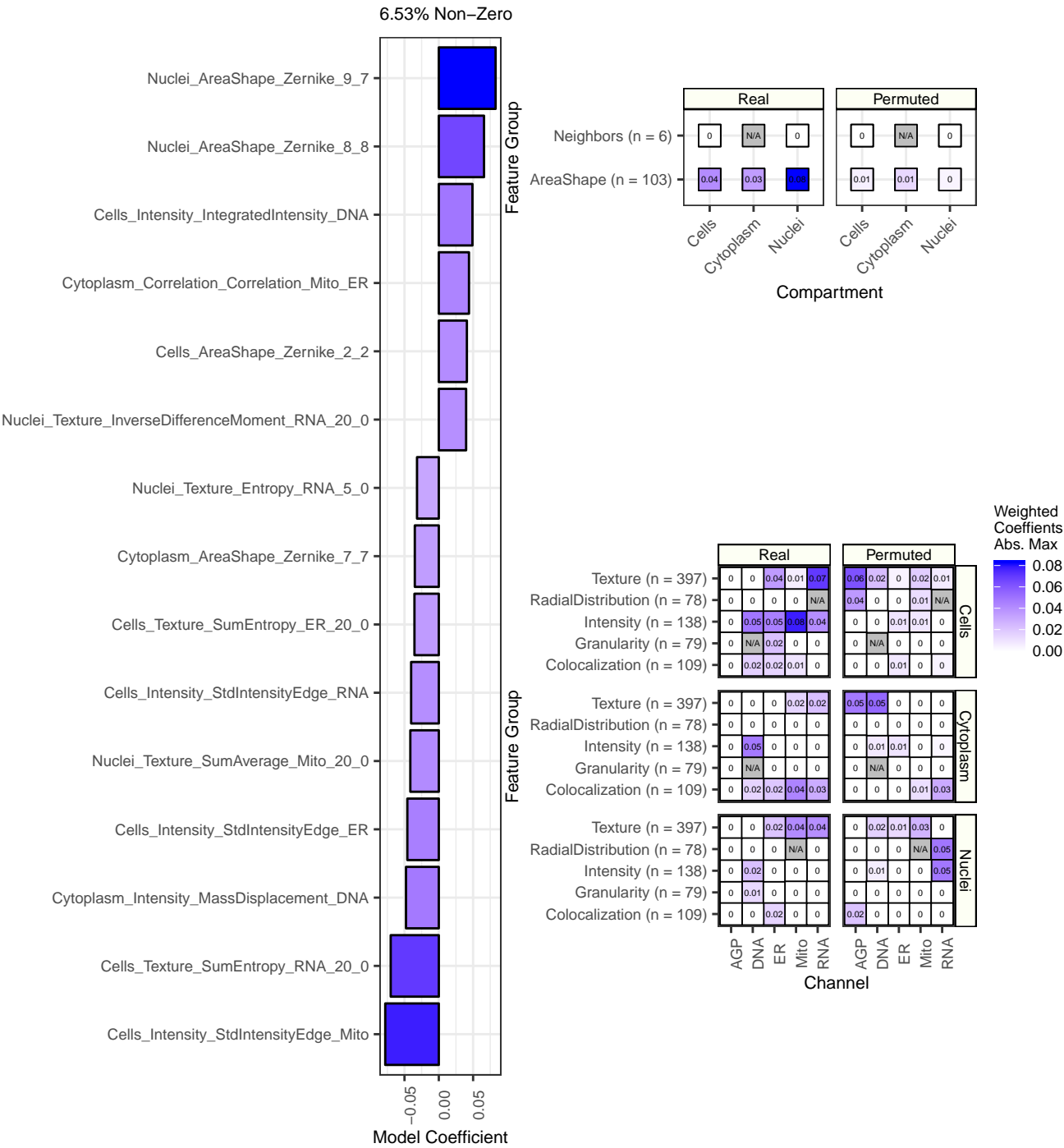
CC – % M



CC – # cells

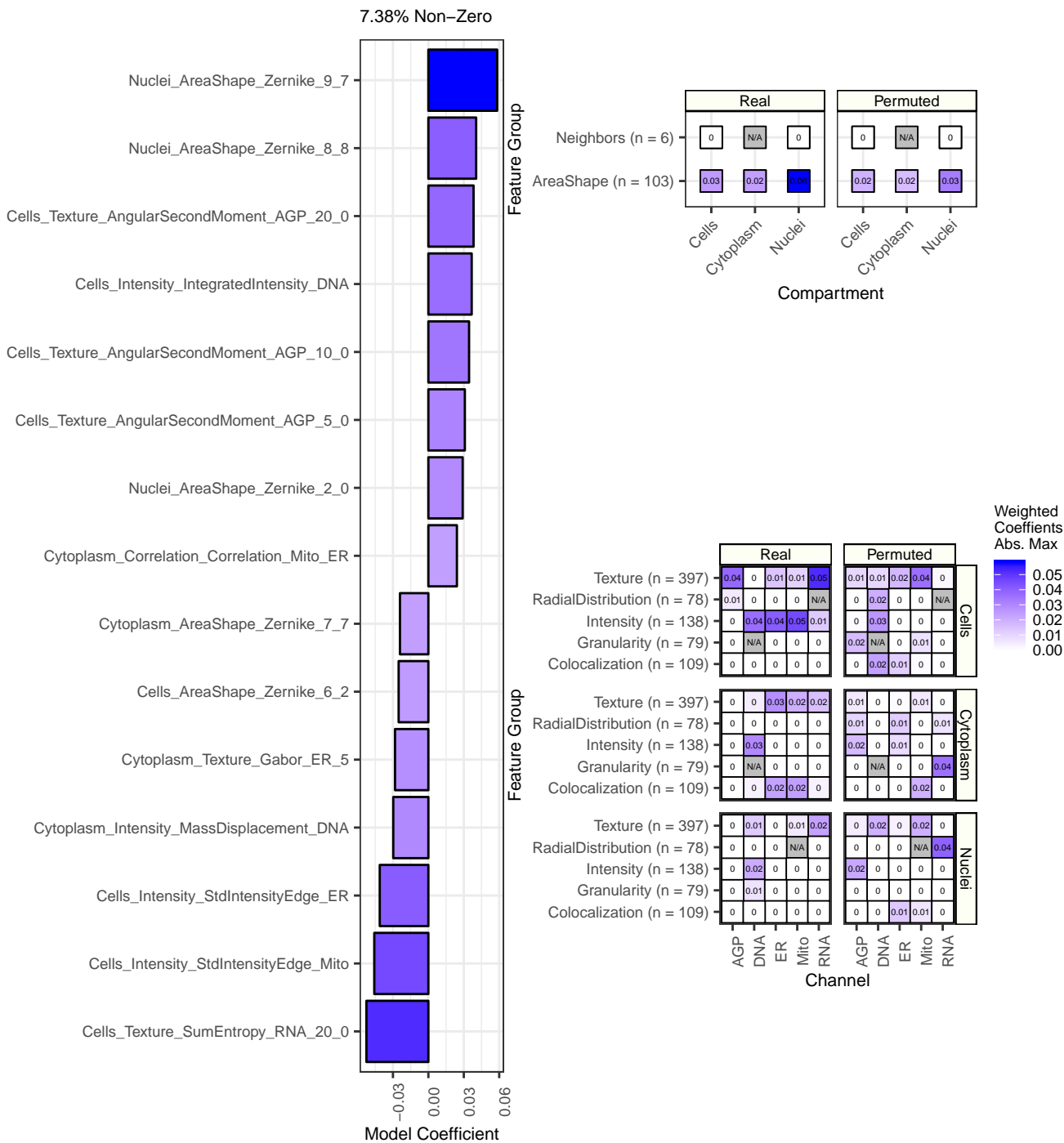


CC – # of gH2AX Spots

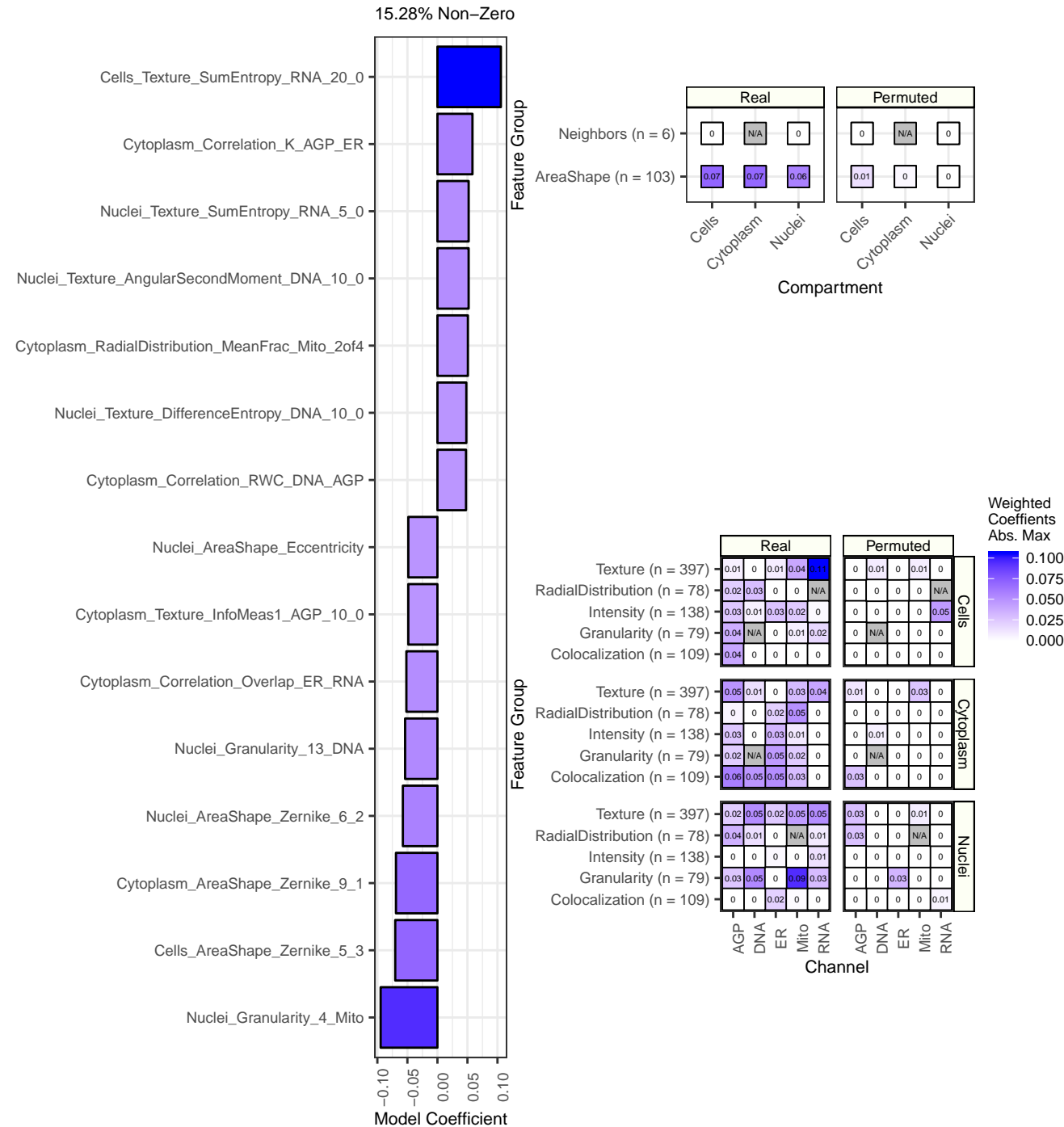




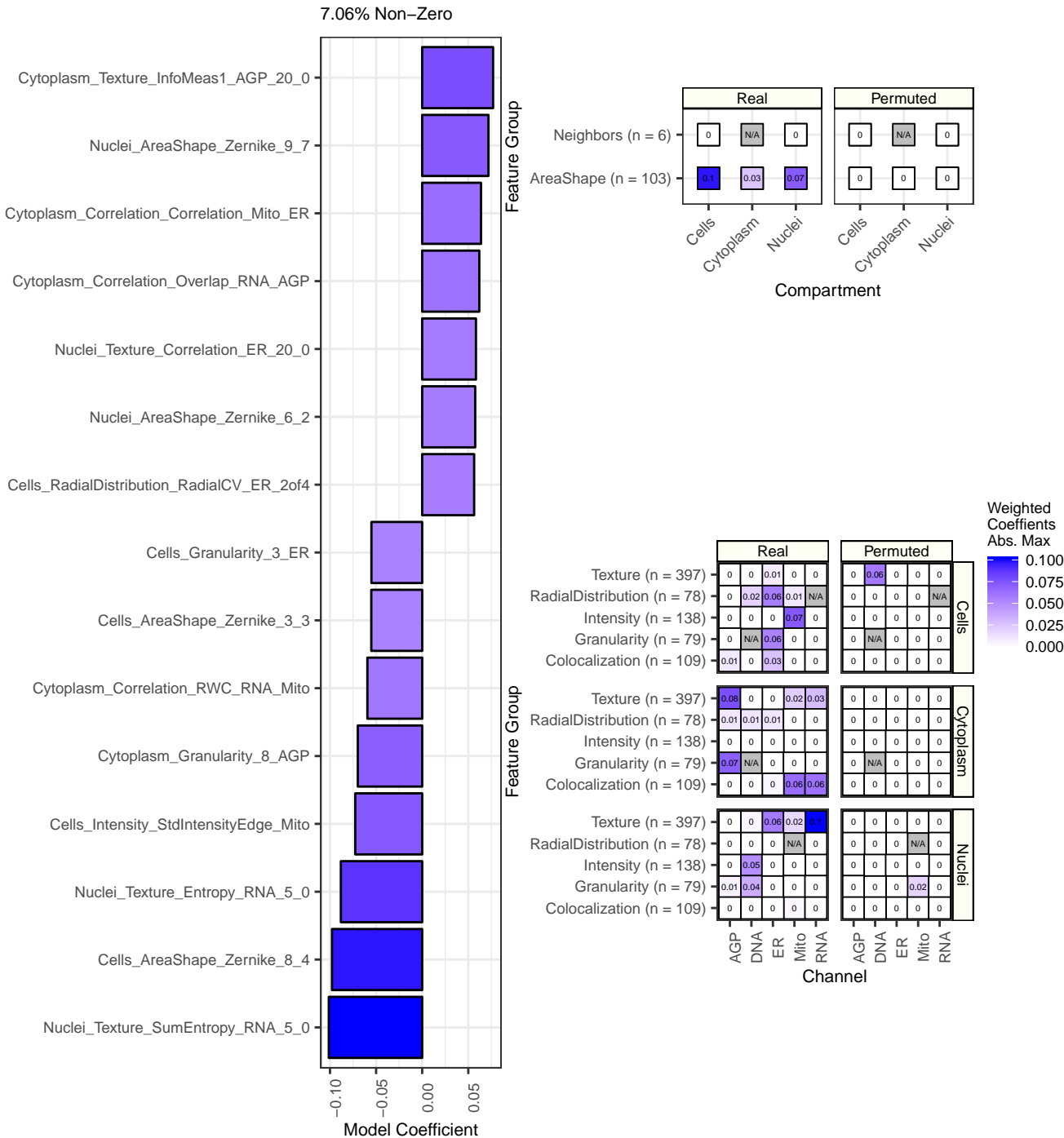
# CC – # of gH2AX Spots per Area of Nucleus



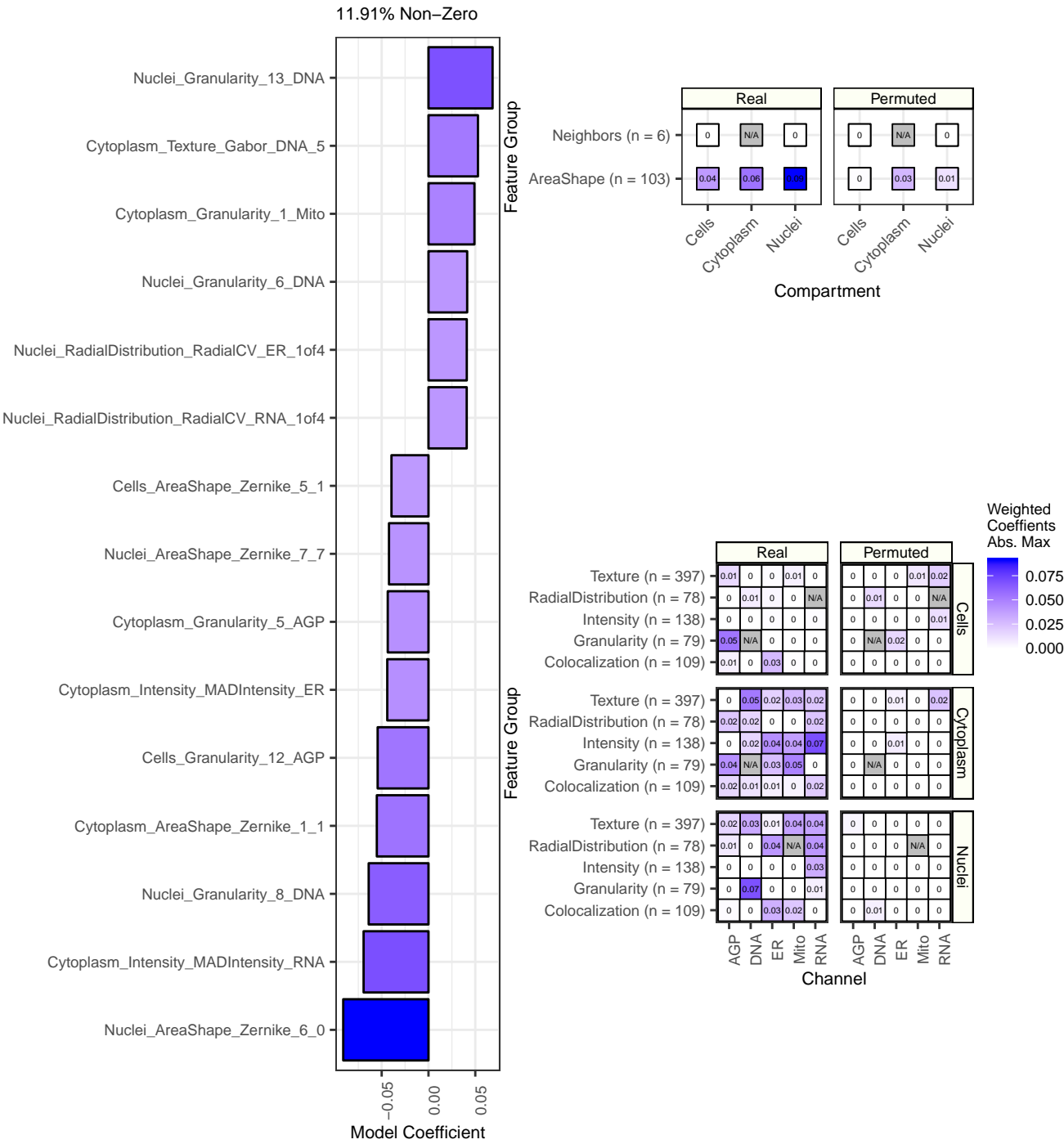
CC - % S



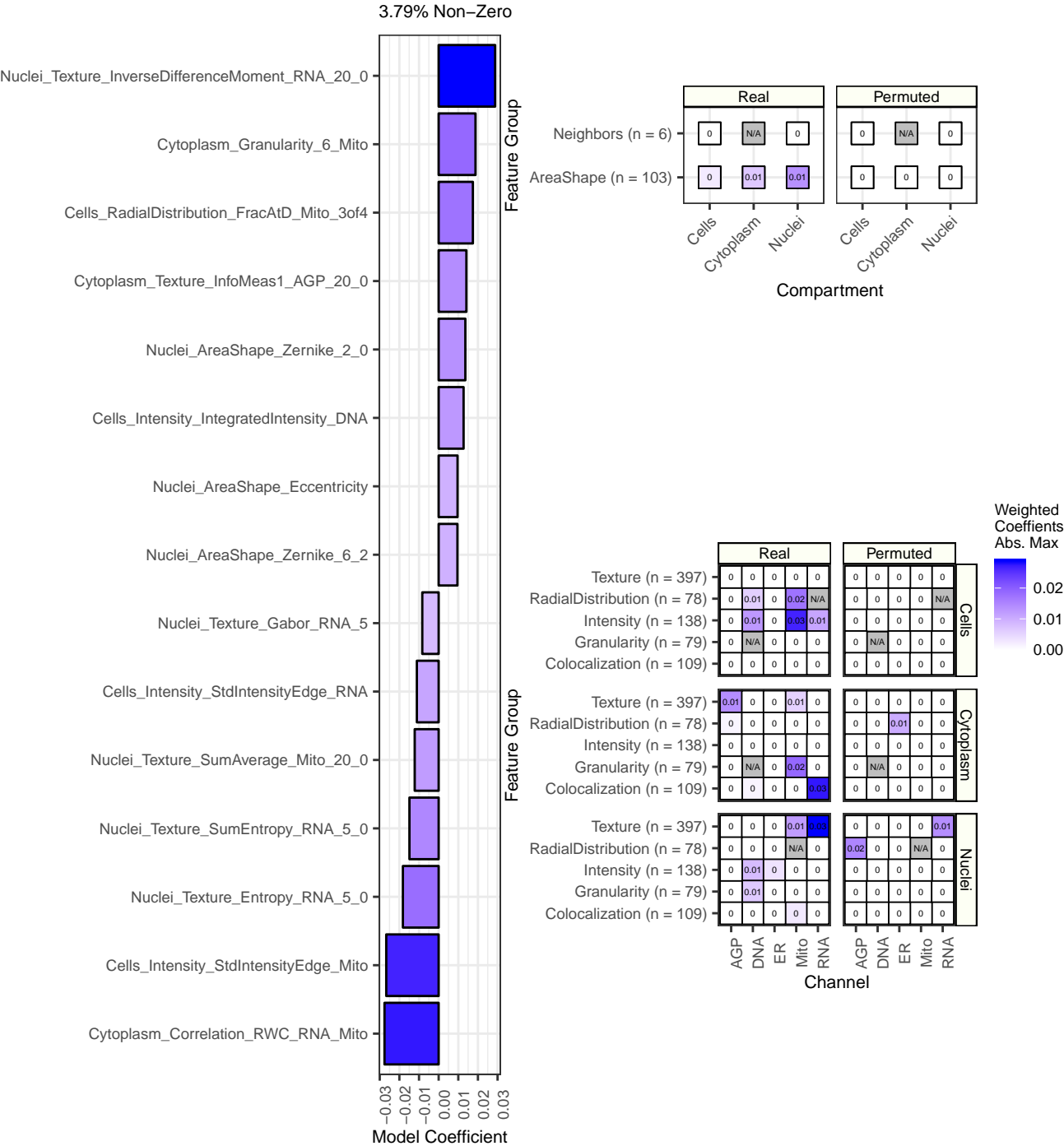
early M – % High gH2AX Spots



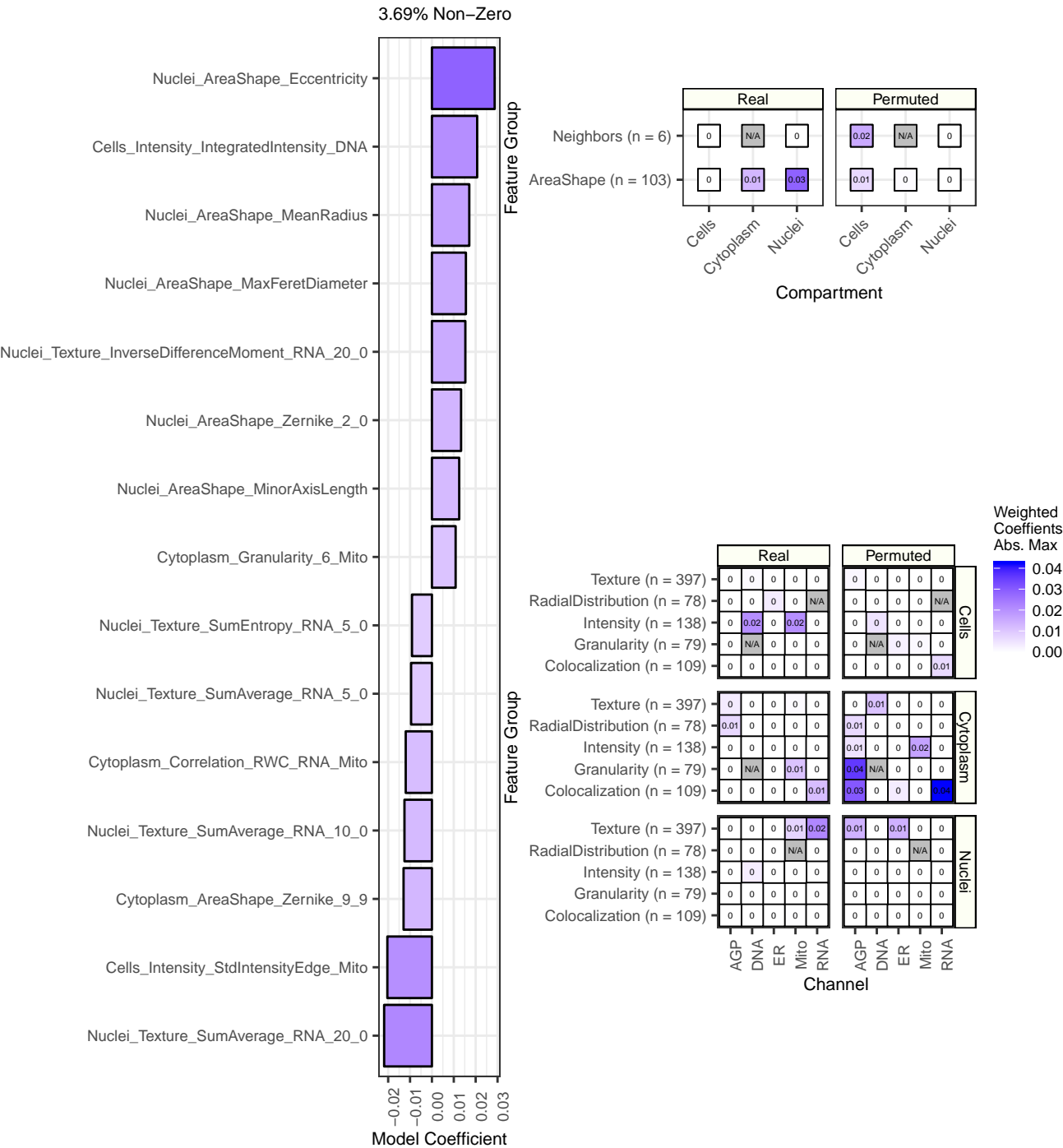
early M – # cells



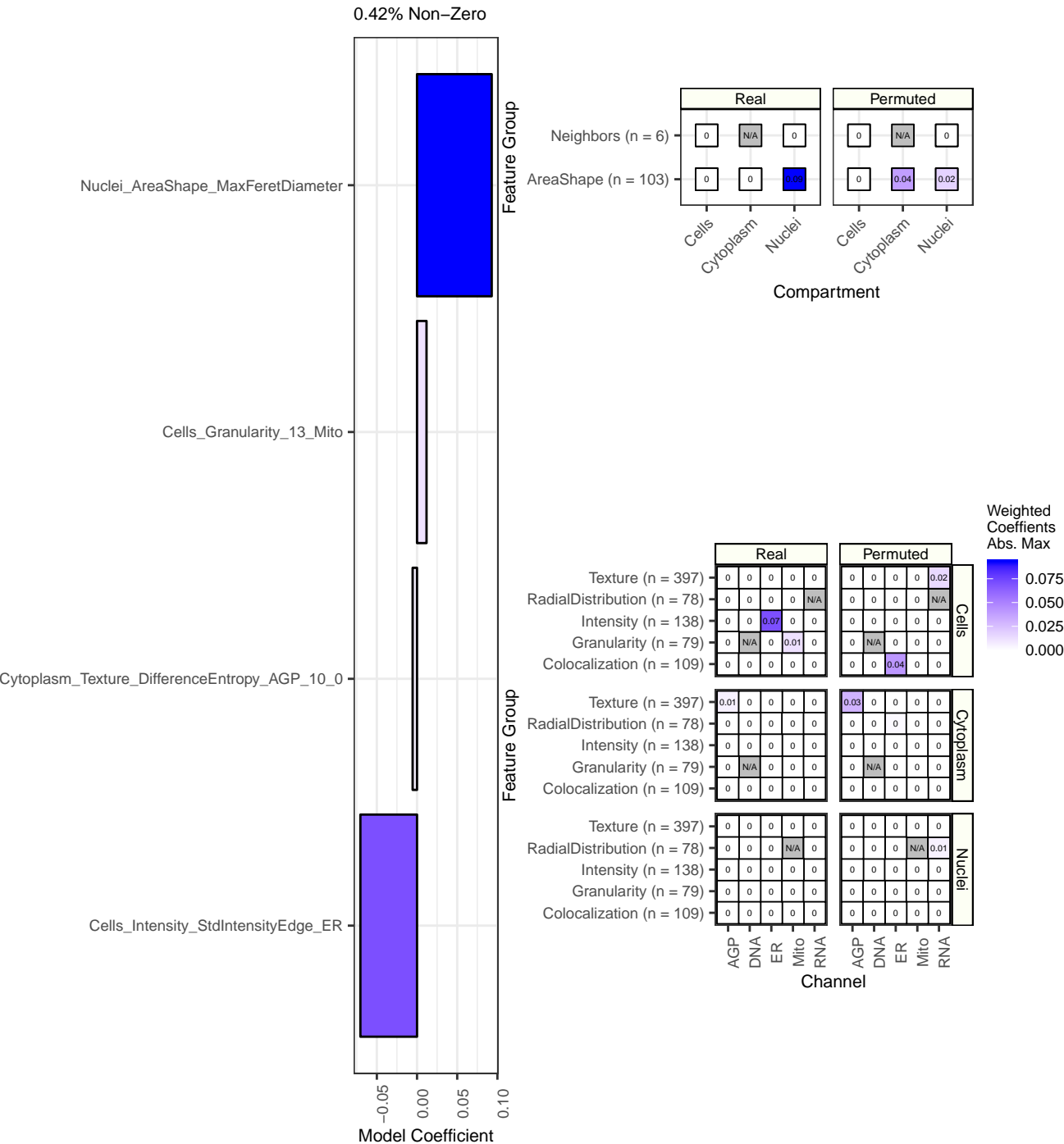
early M – # of gH2AX Spots



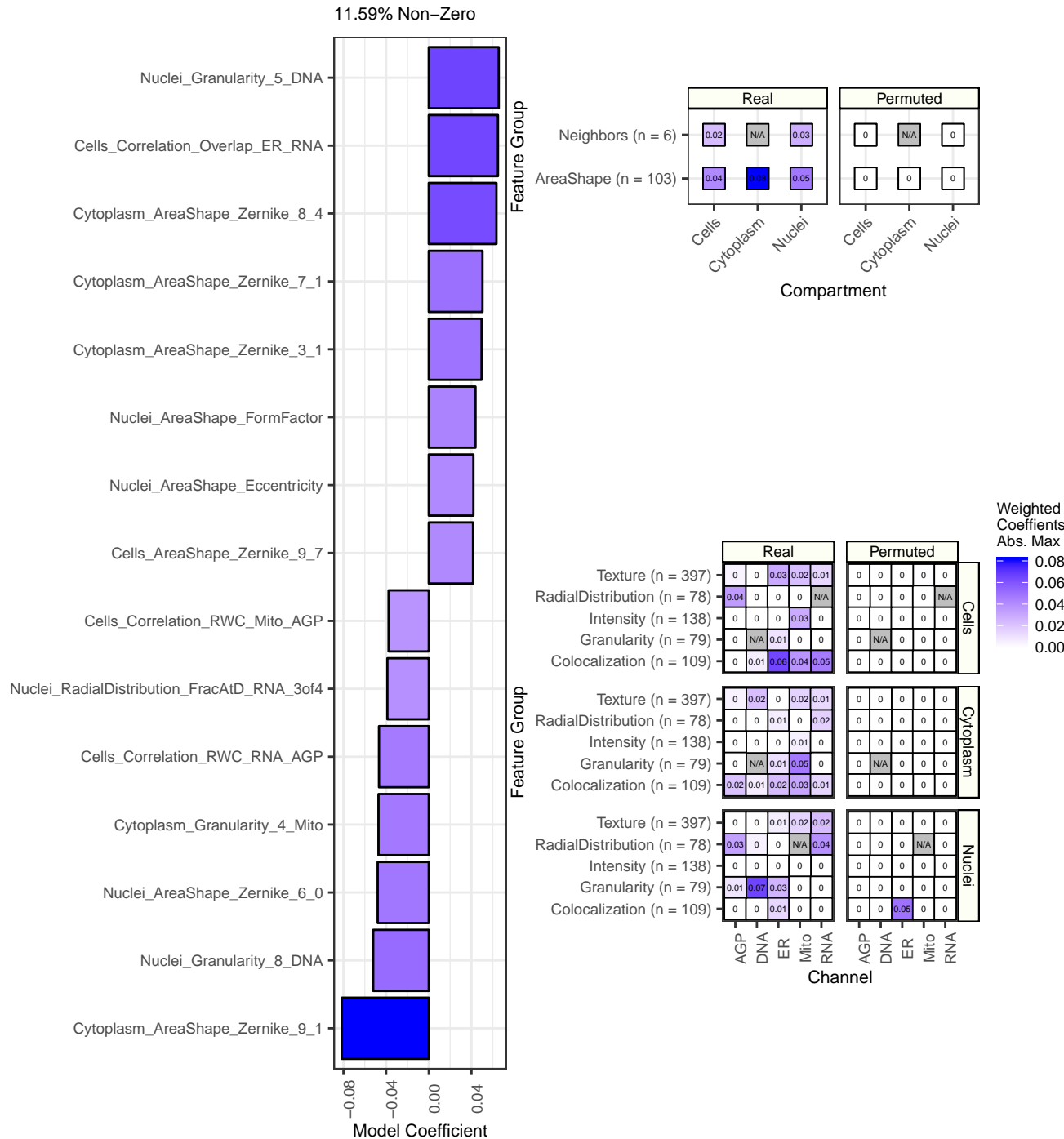
early M – # of gH2AX Spots per Area of Nucleus



G1 – % High gH2AX Spots

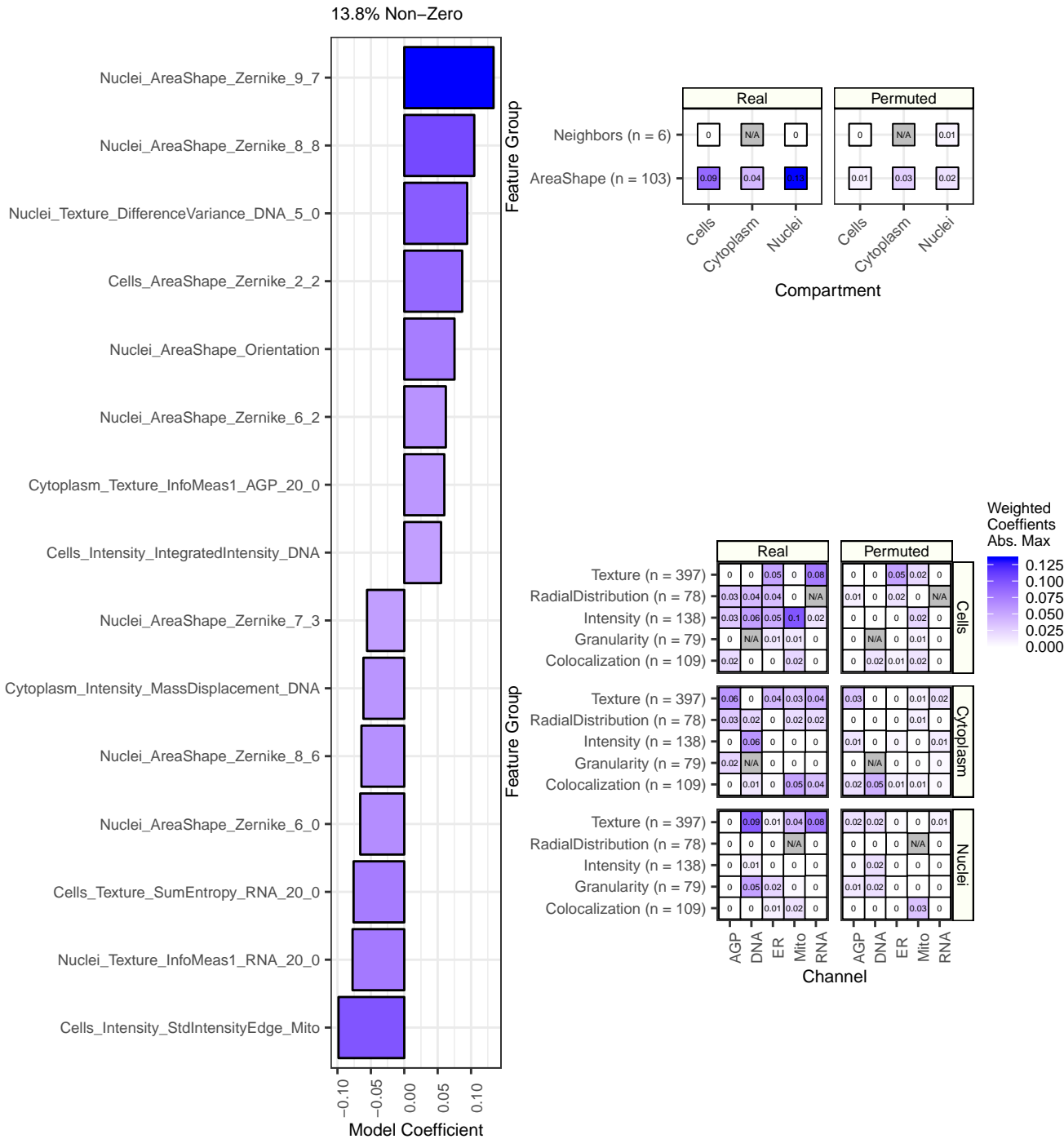


G1 – # cells

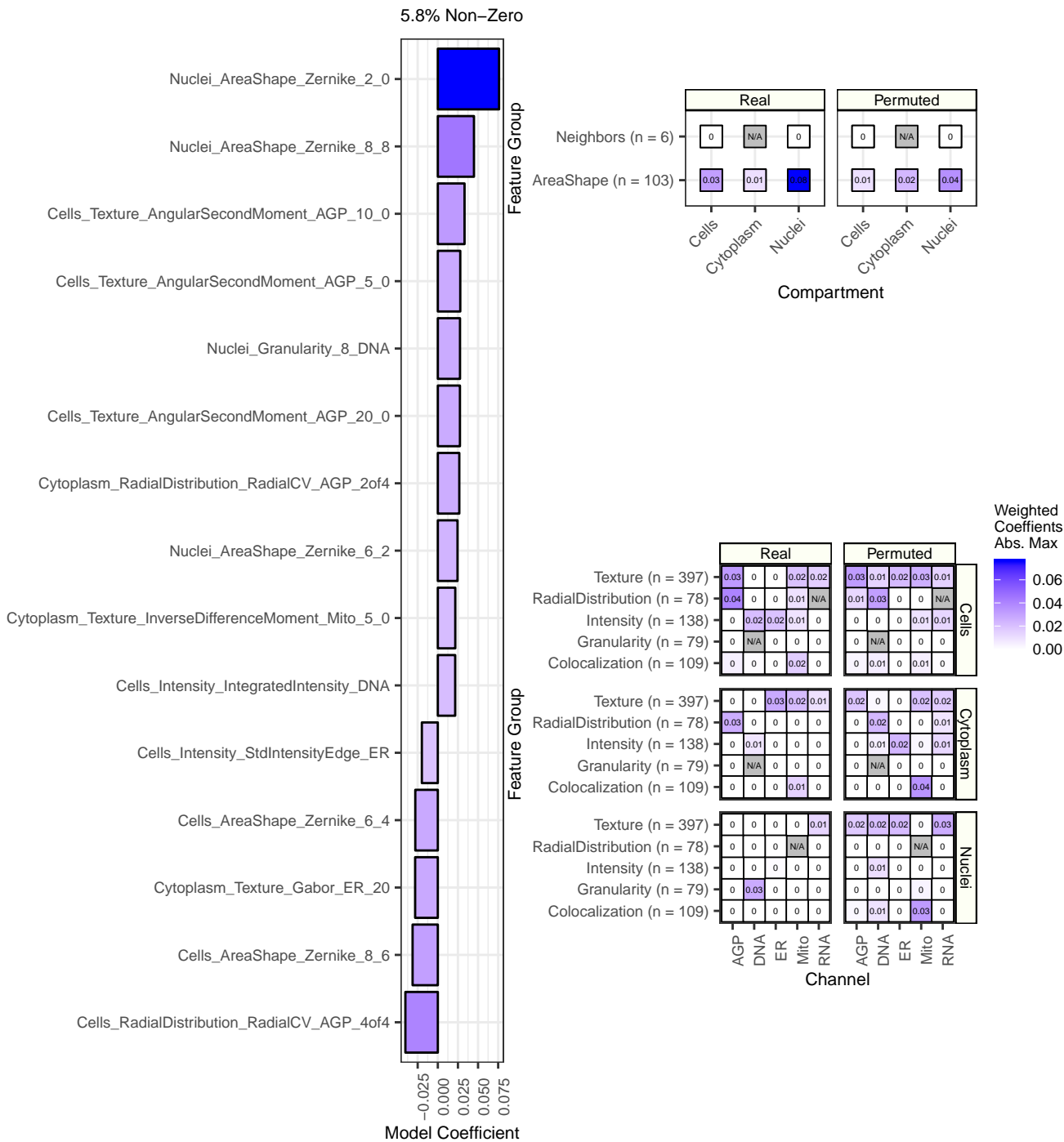




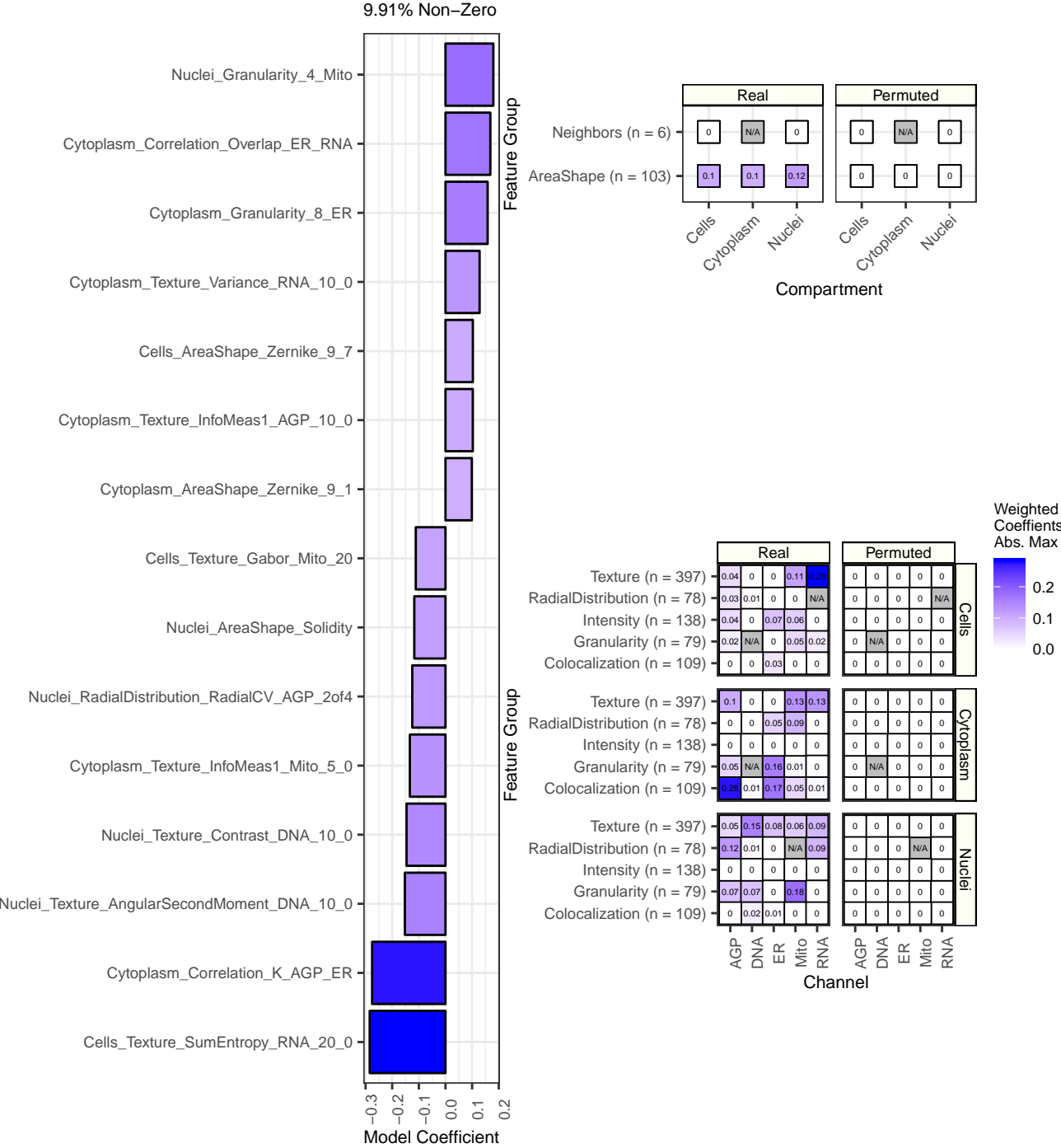
G1 – # of gH2AX Spots



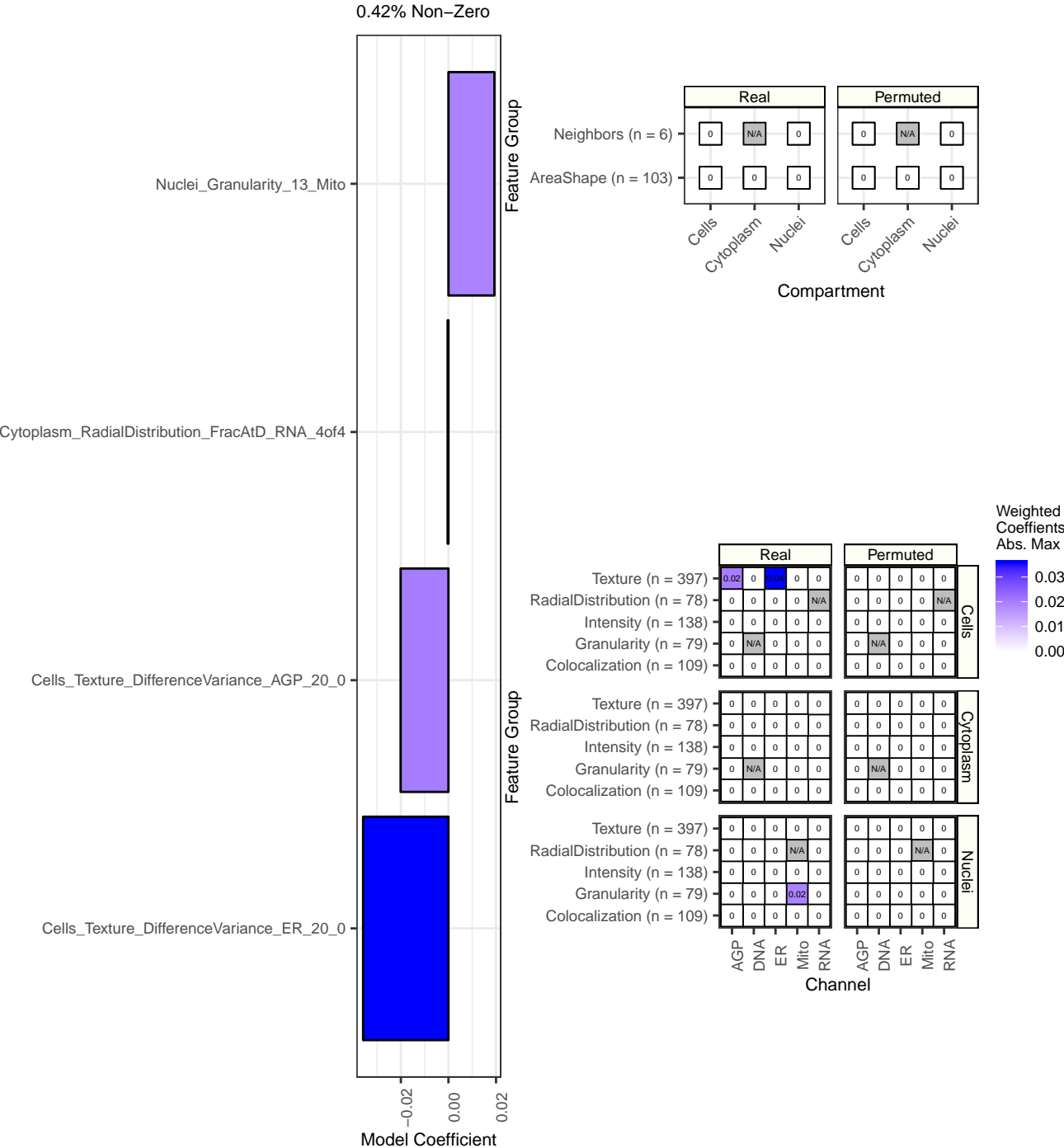
# G1 – # of gH2AX Spots per Area of Nucleus



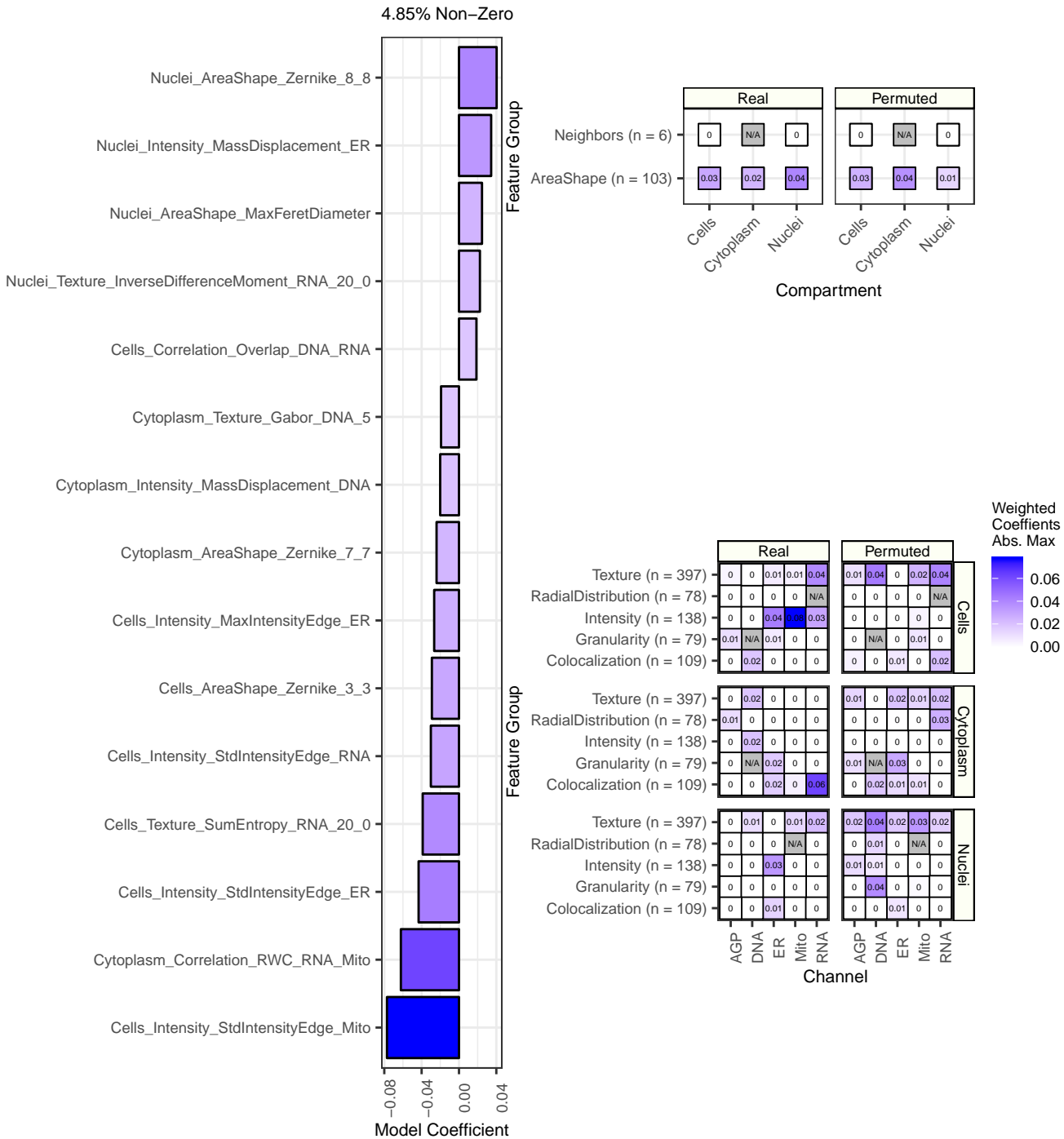
Cell Count – G1+G2



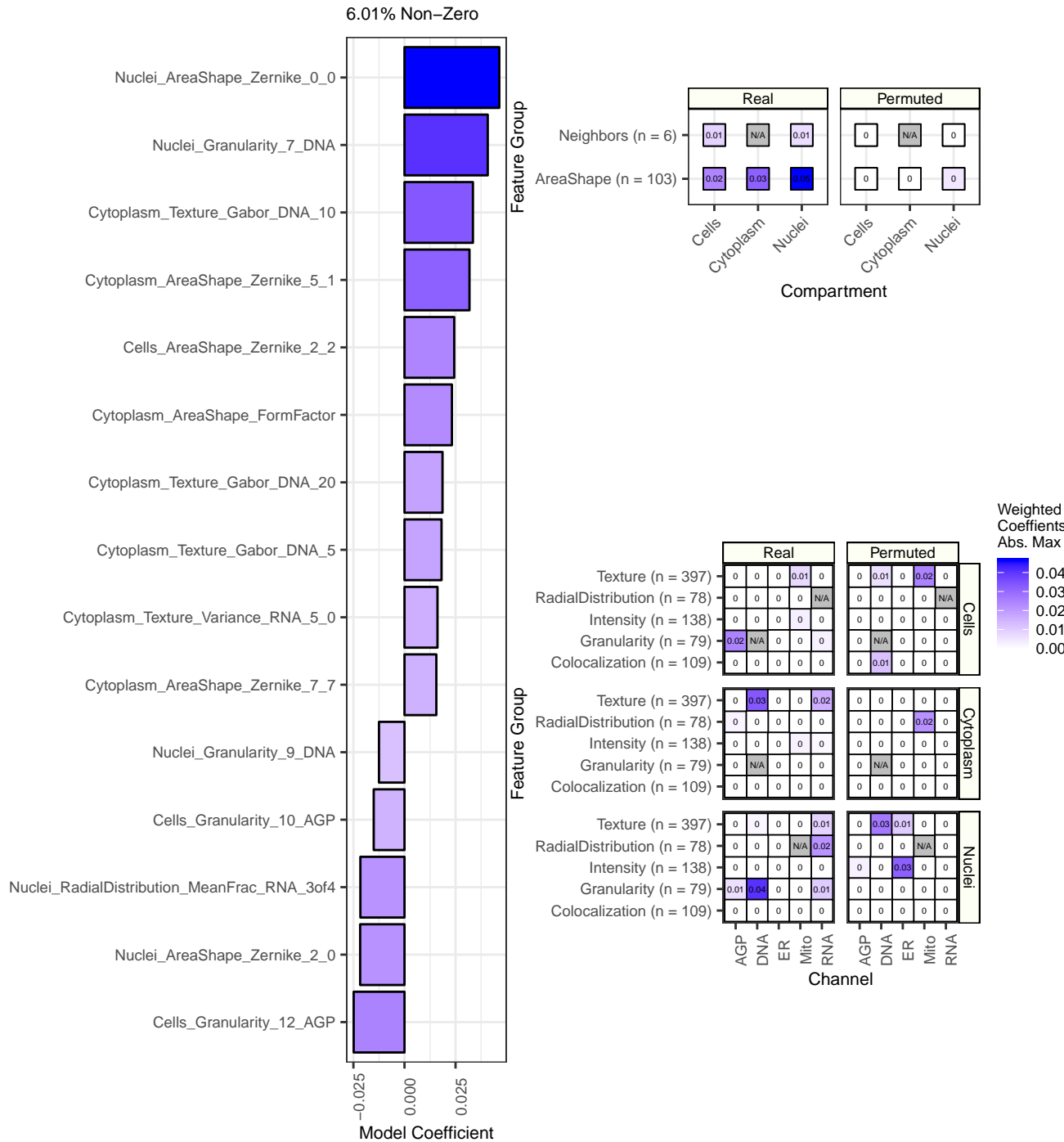
Cell Count – G2/G1



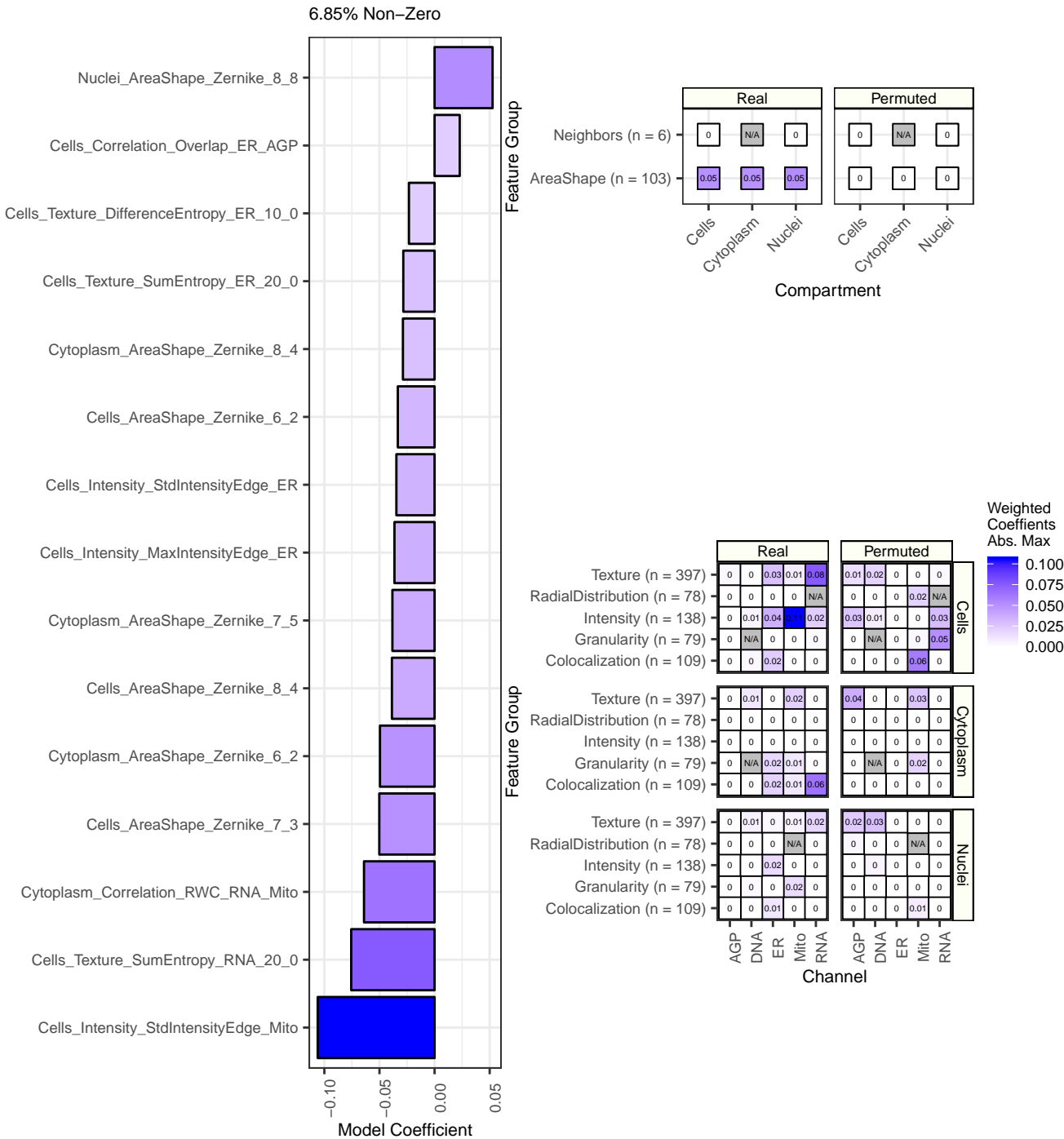
## G2 – % High gH2AX Spots



G2 – # cells

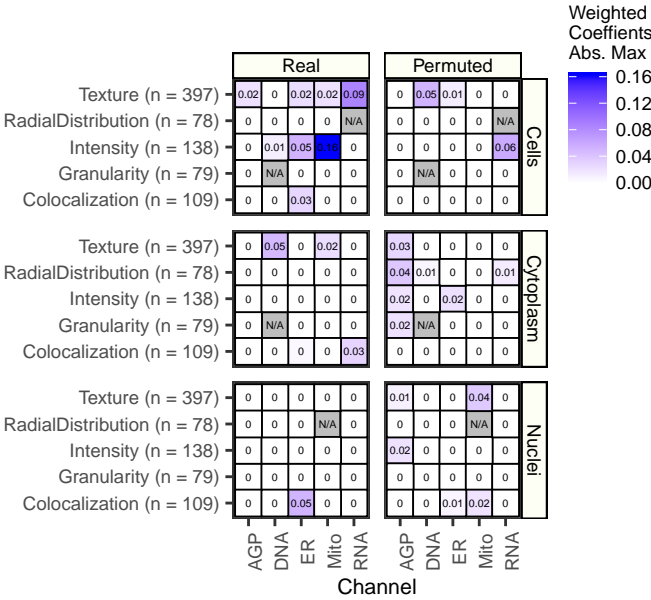
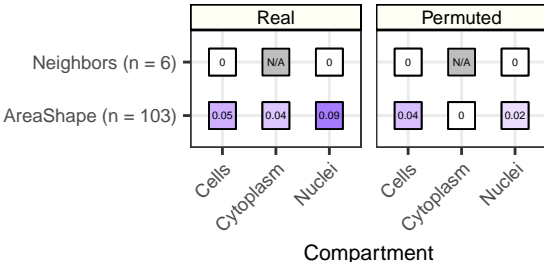
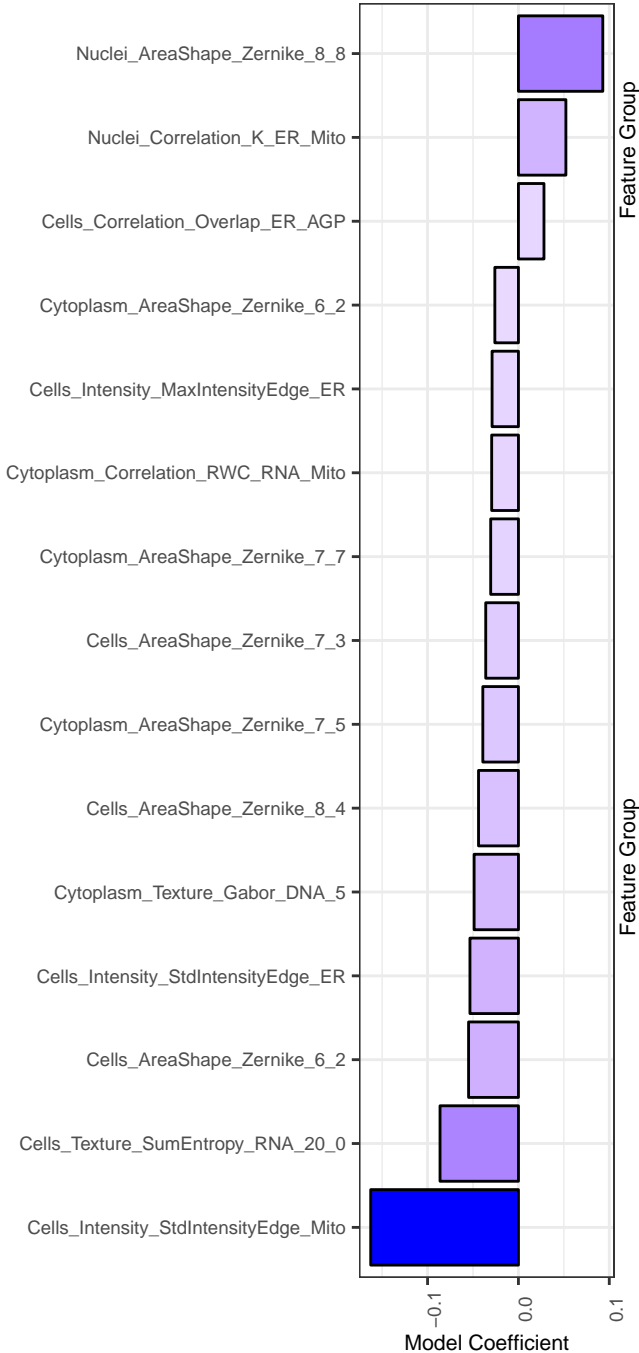


G2 – # of gH2AX Spots



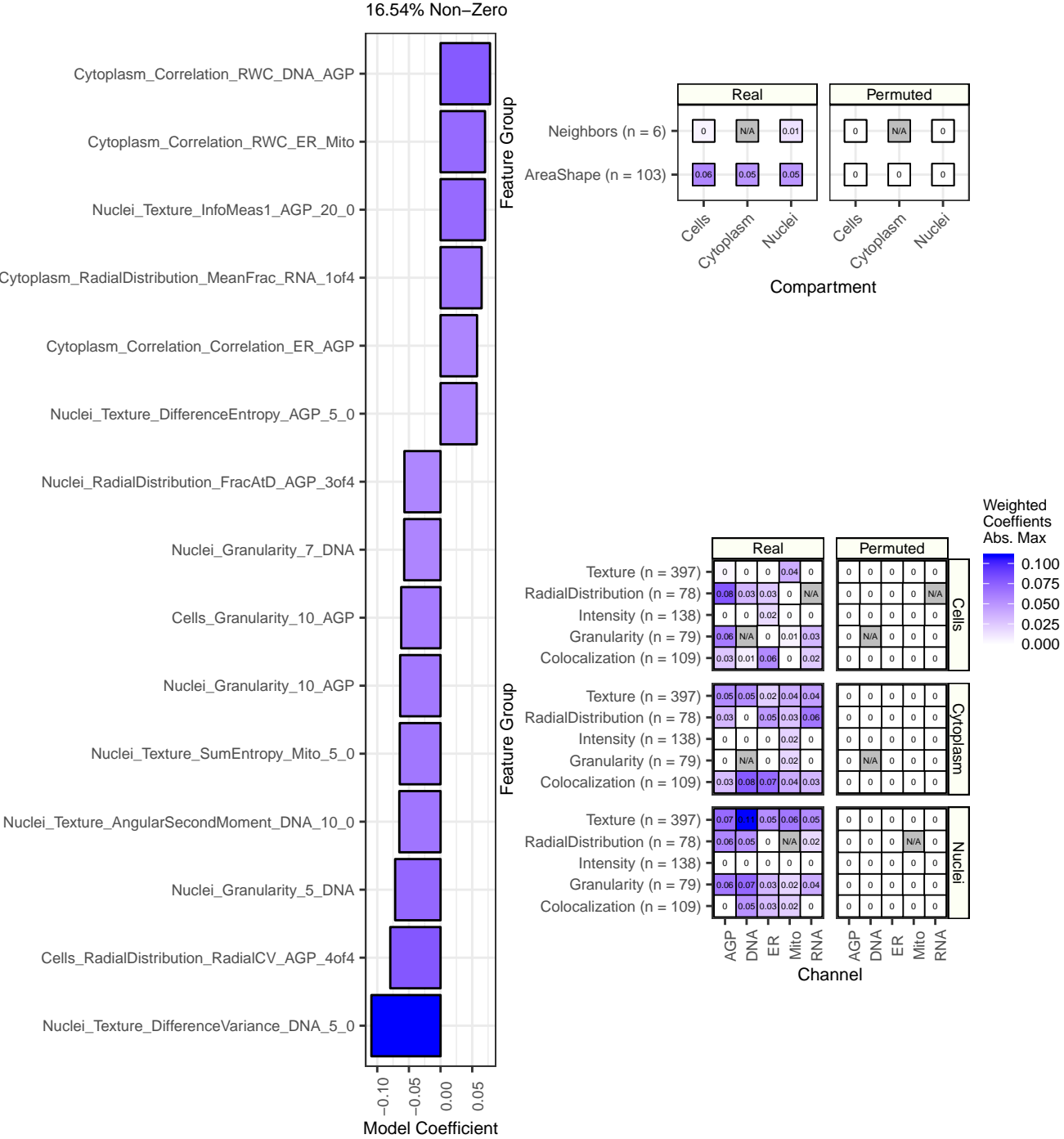
# G2 – # of gH2AX Spots per Area of Nucleus

2.63% Non-Zero



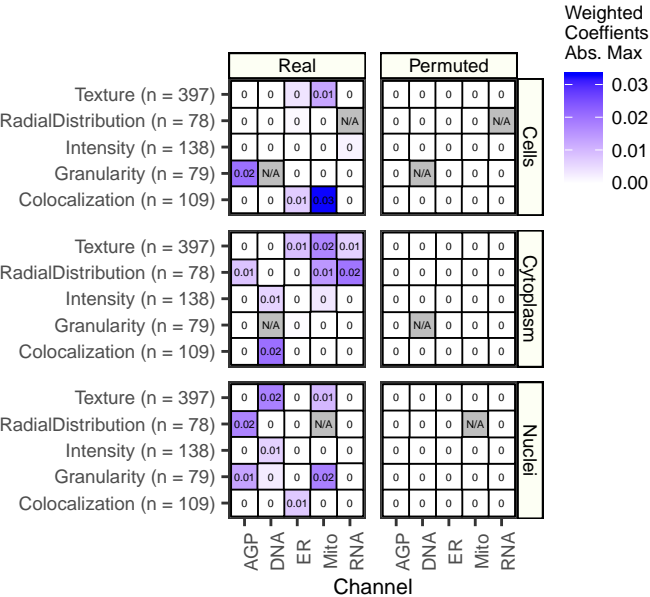
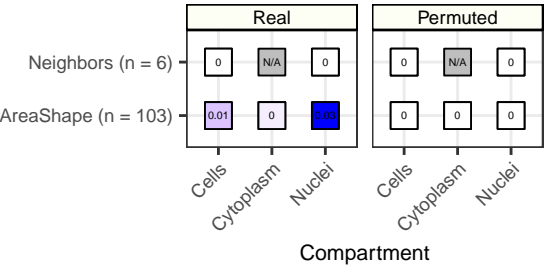
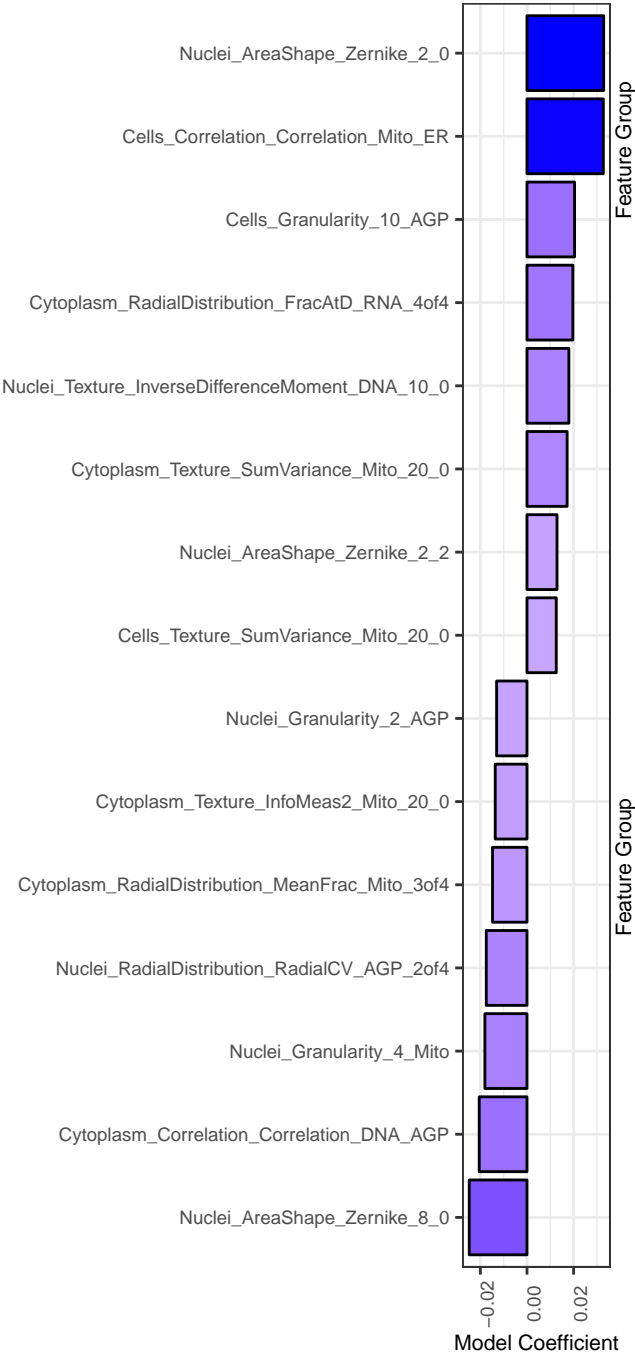


Cell Count – G2 + M



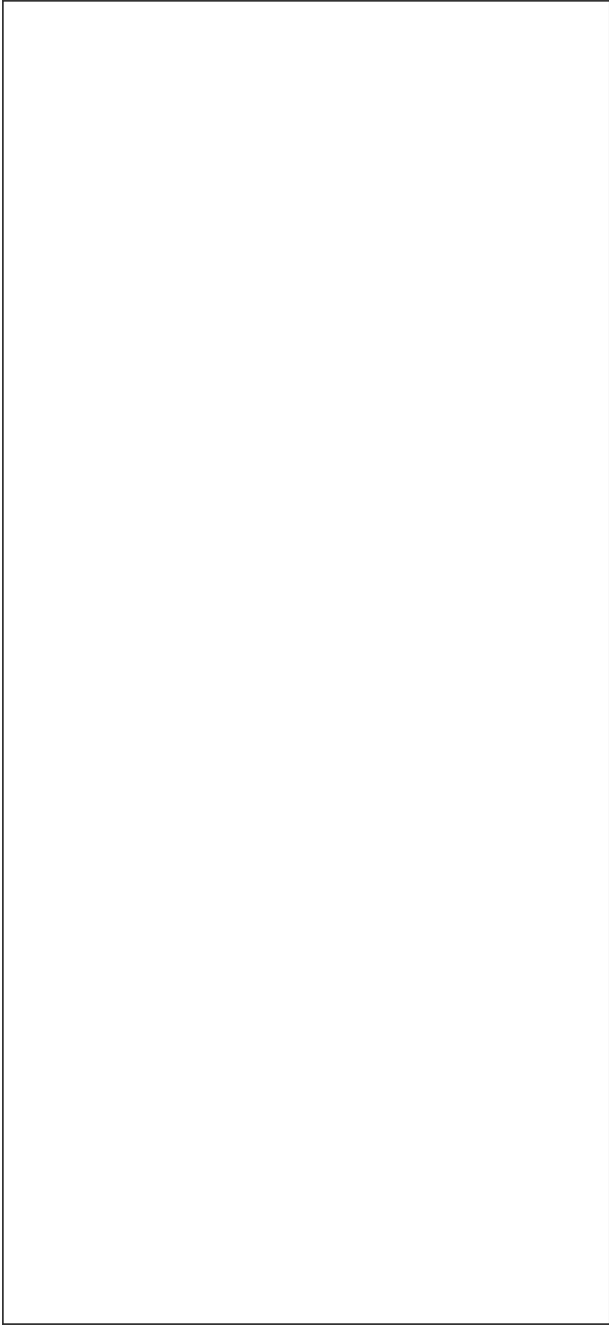
# CC – Infection Efficiency

5.06% Non-Zero

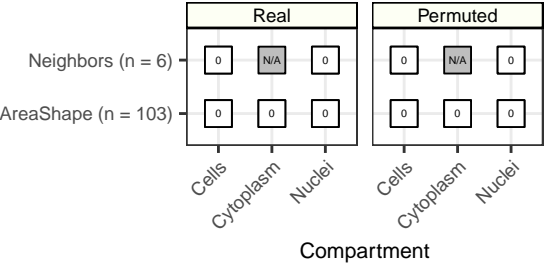


Late M – % High gH2AX Spots

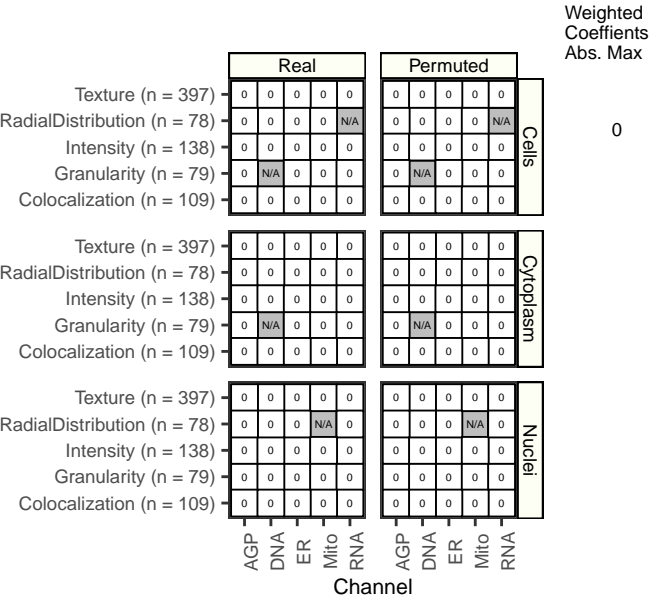
0% Non-Zero



Feature Group

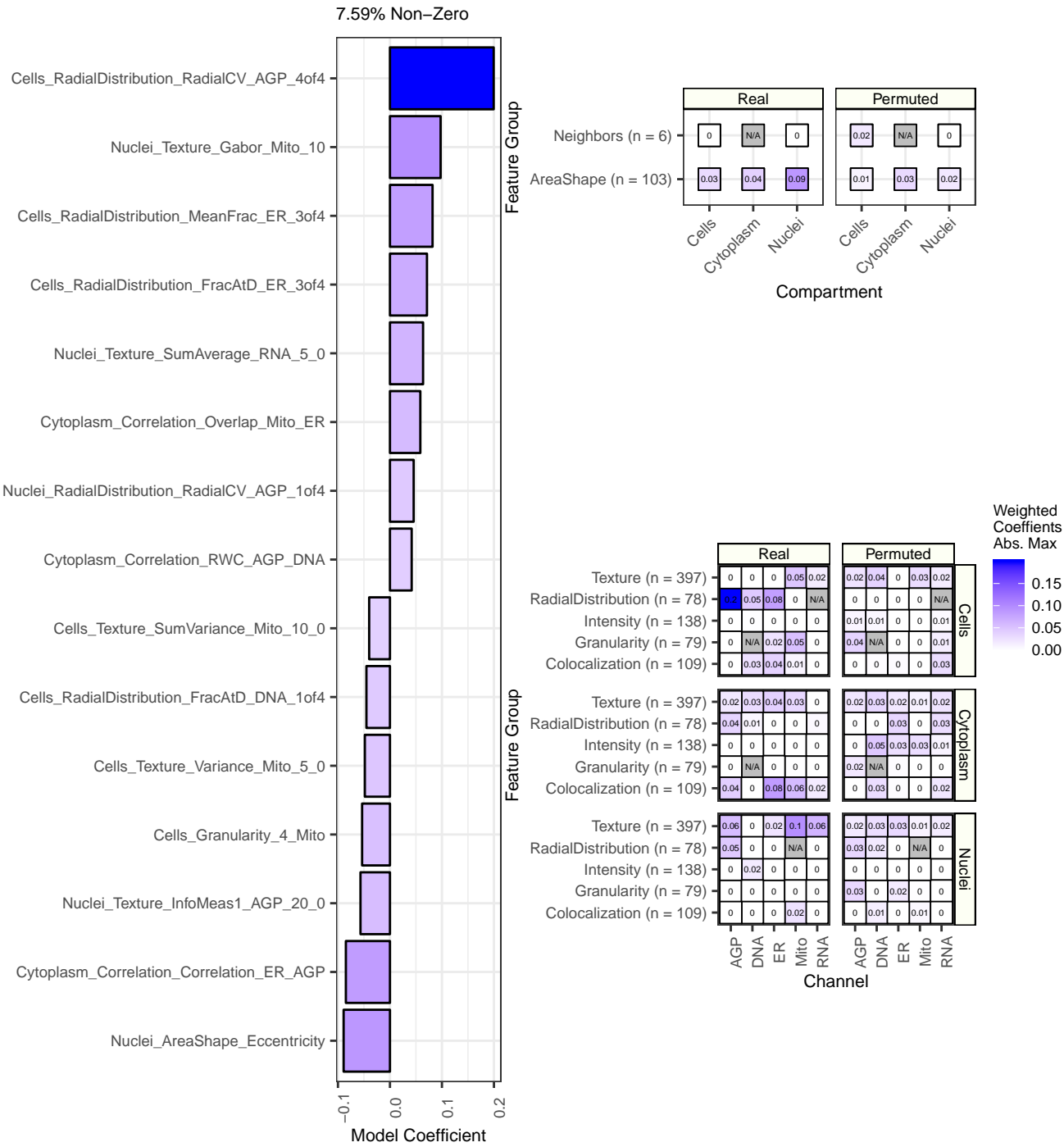


Feature Group

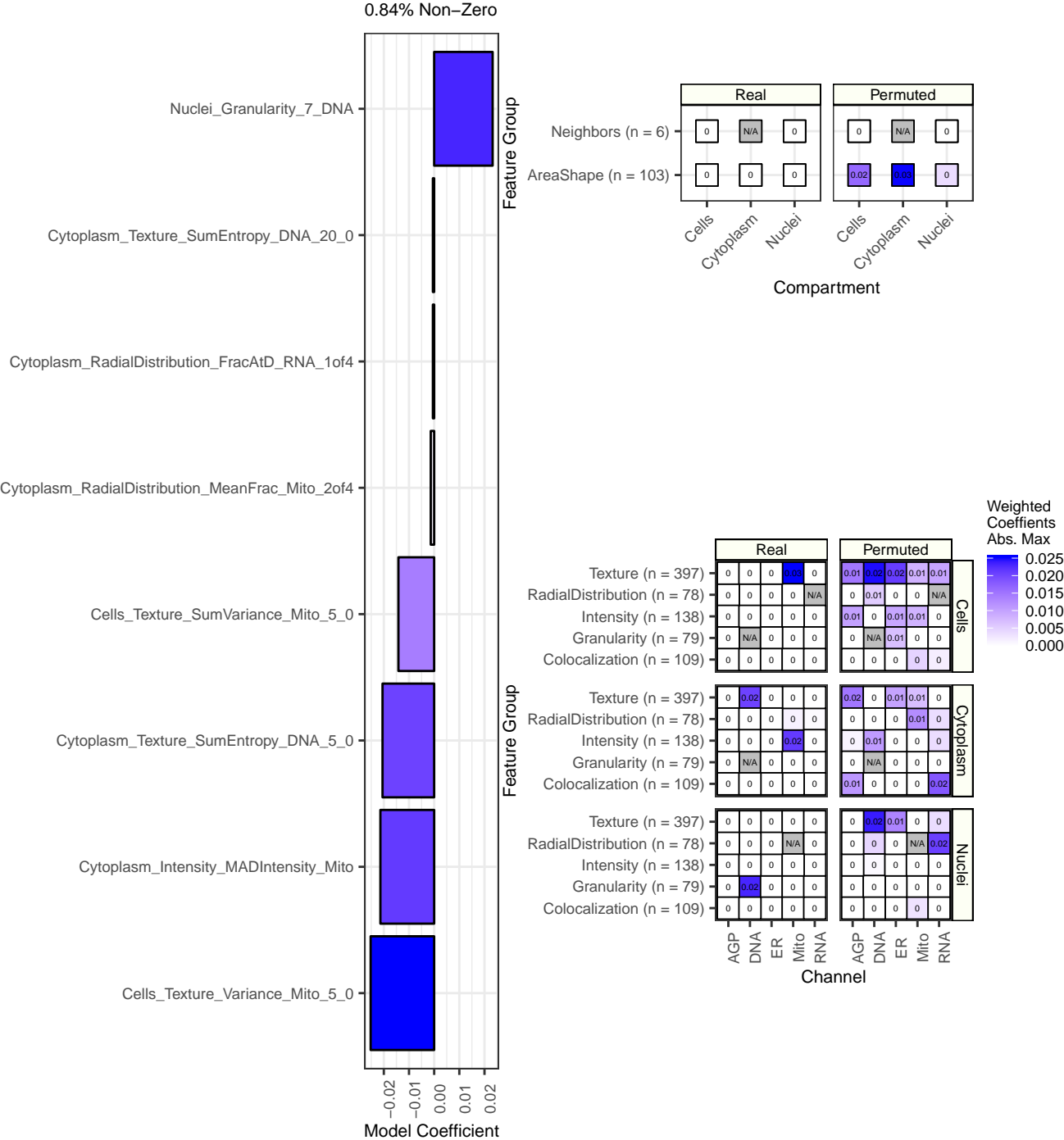


Model Coefficient

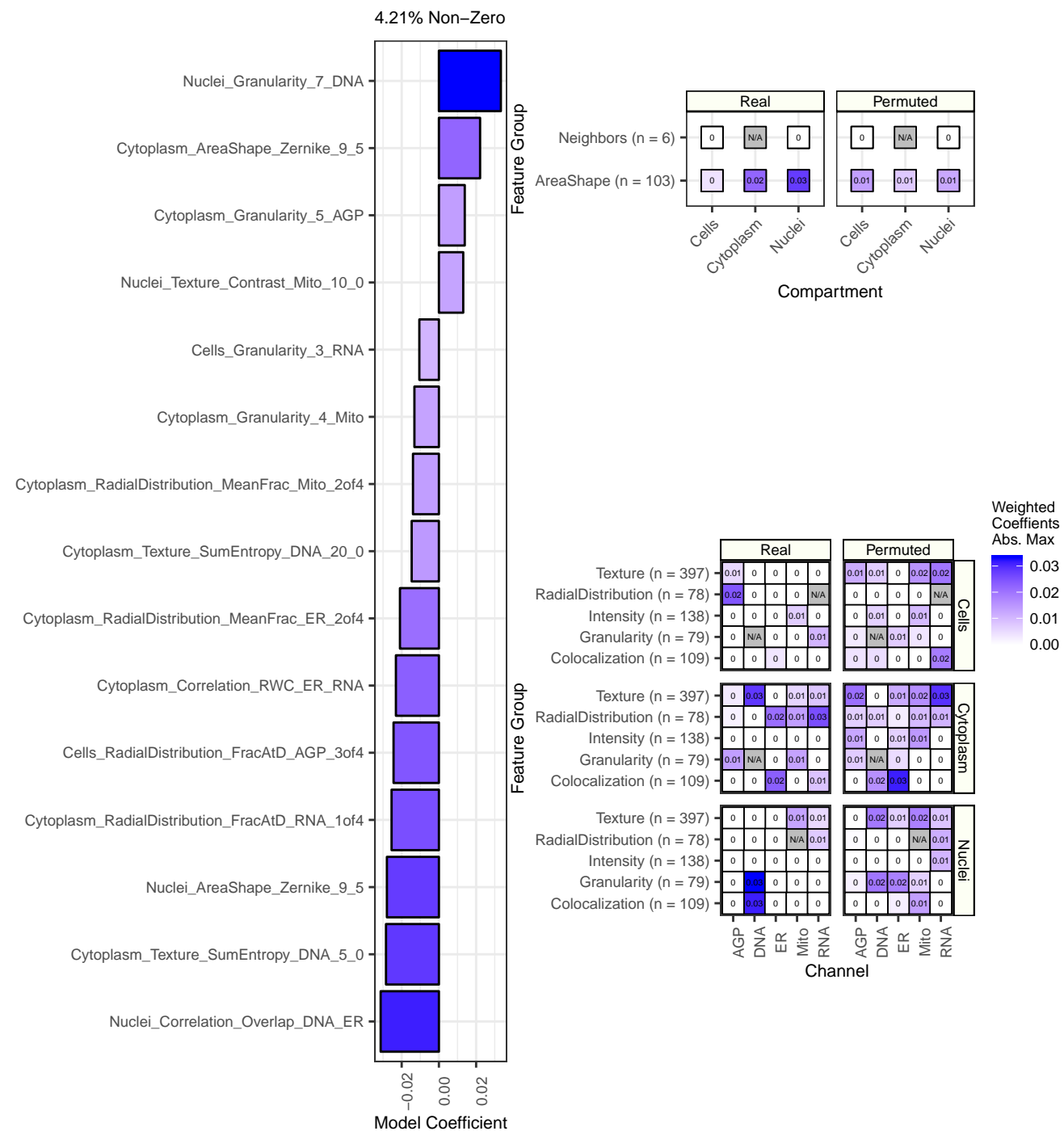
Late M – # cells



Late M – # of gH2AX Spots

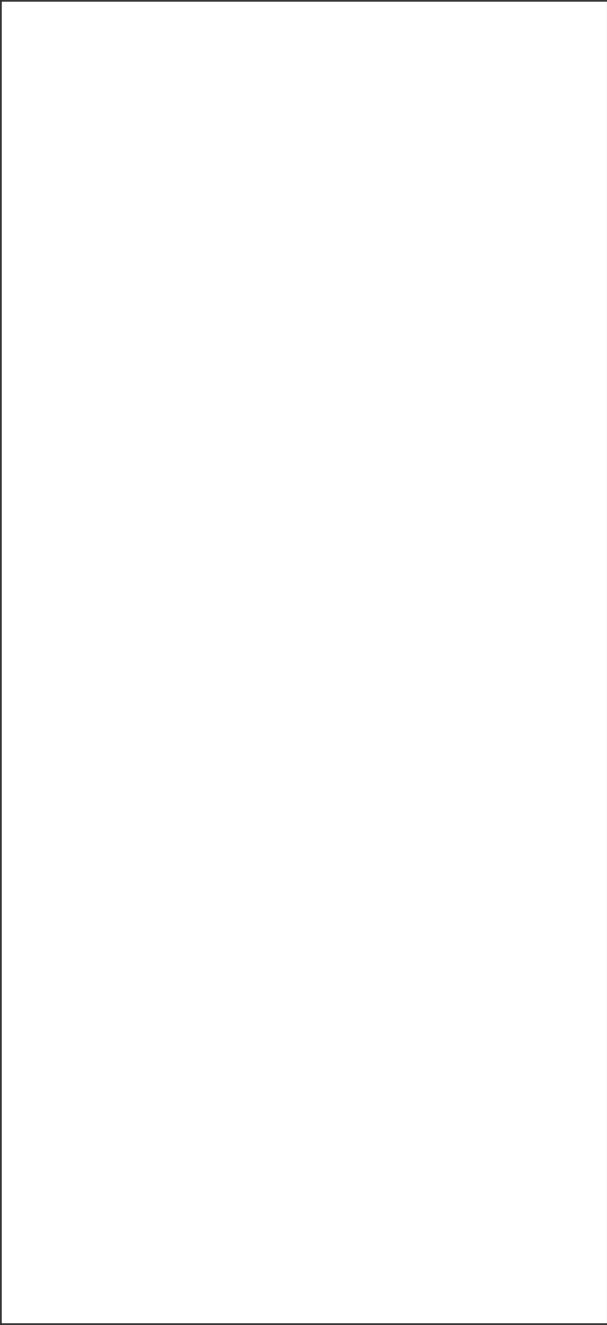


# Late M – # of gH2AX Spots per Area of Nucleus

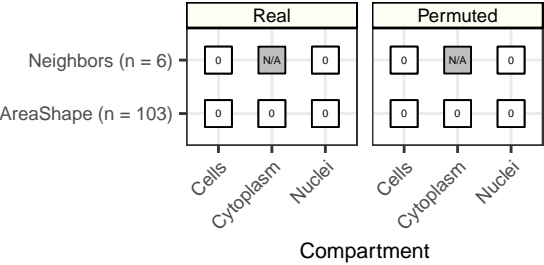


M – % High gH2AX Spots

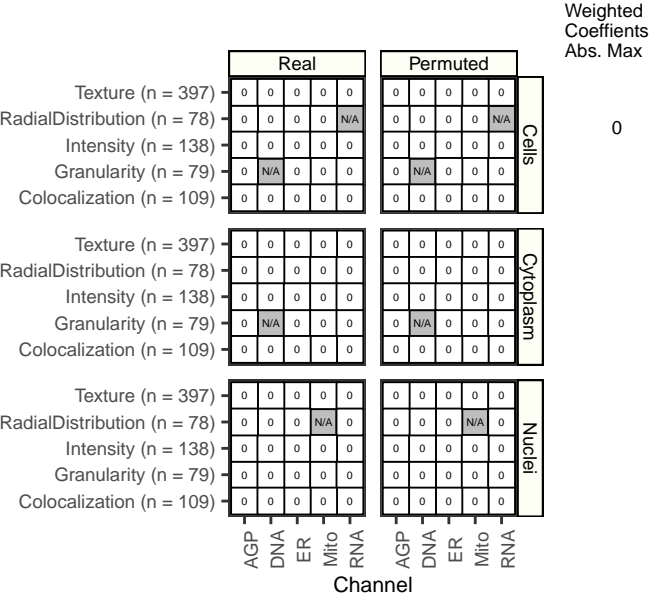
0% Non-Zero



Feature Group

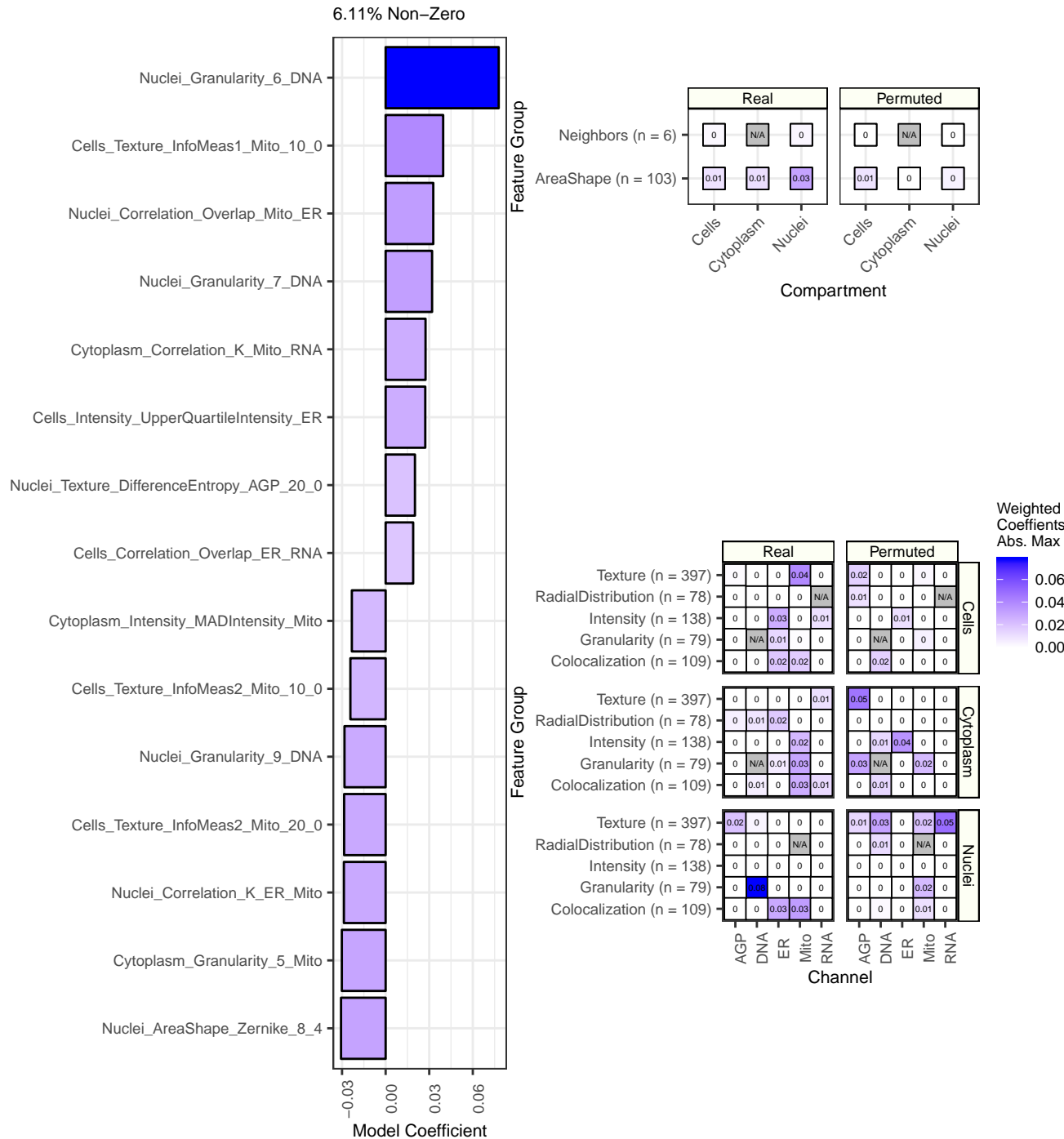


Feature Group



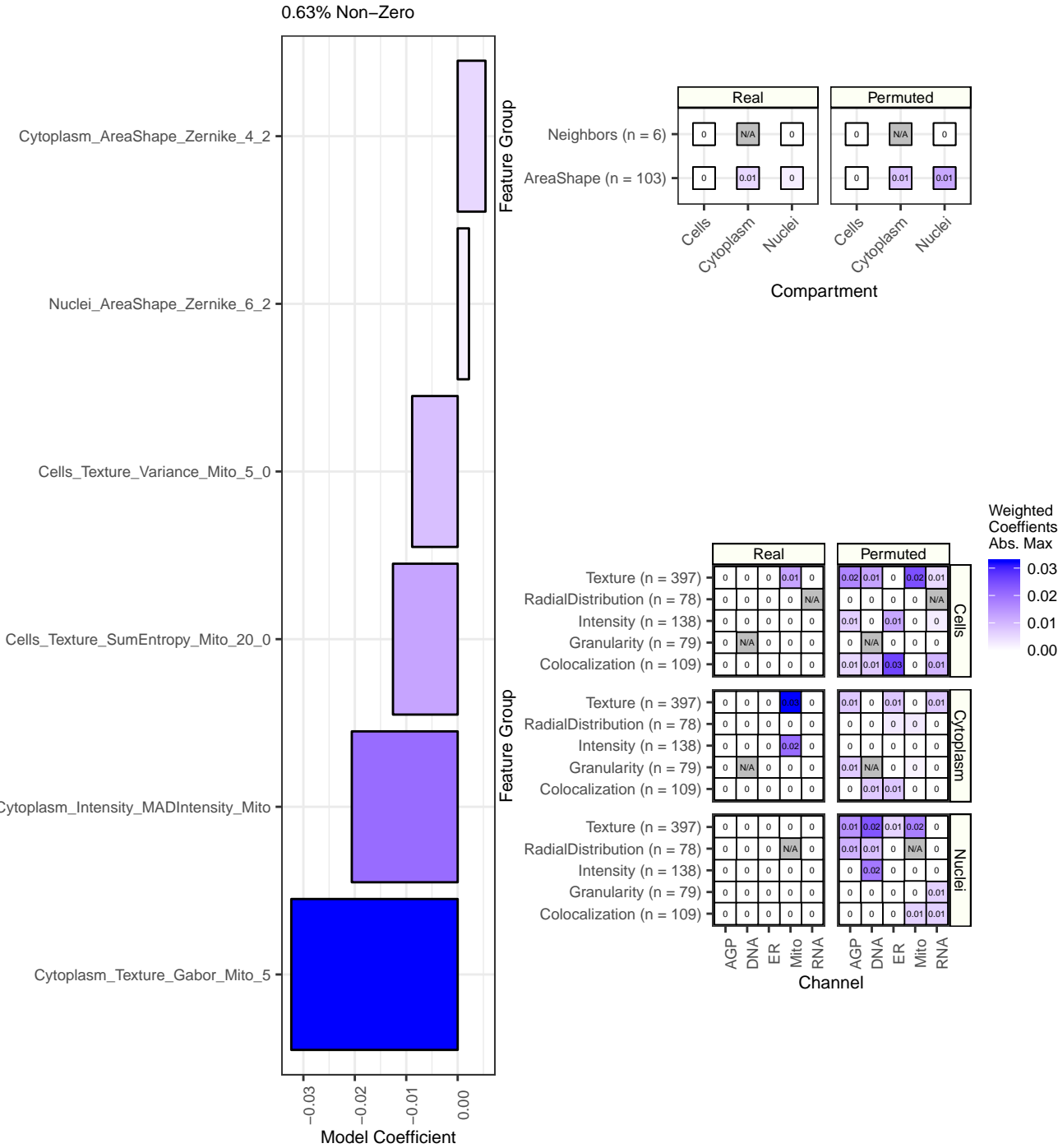
Model Coefficient

M – # cells

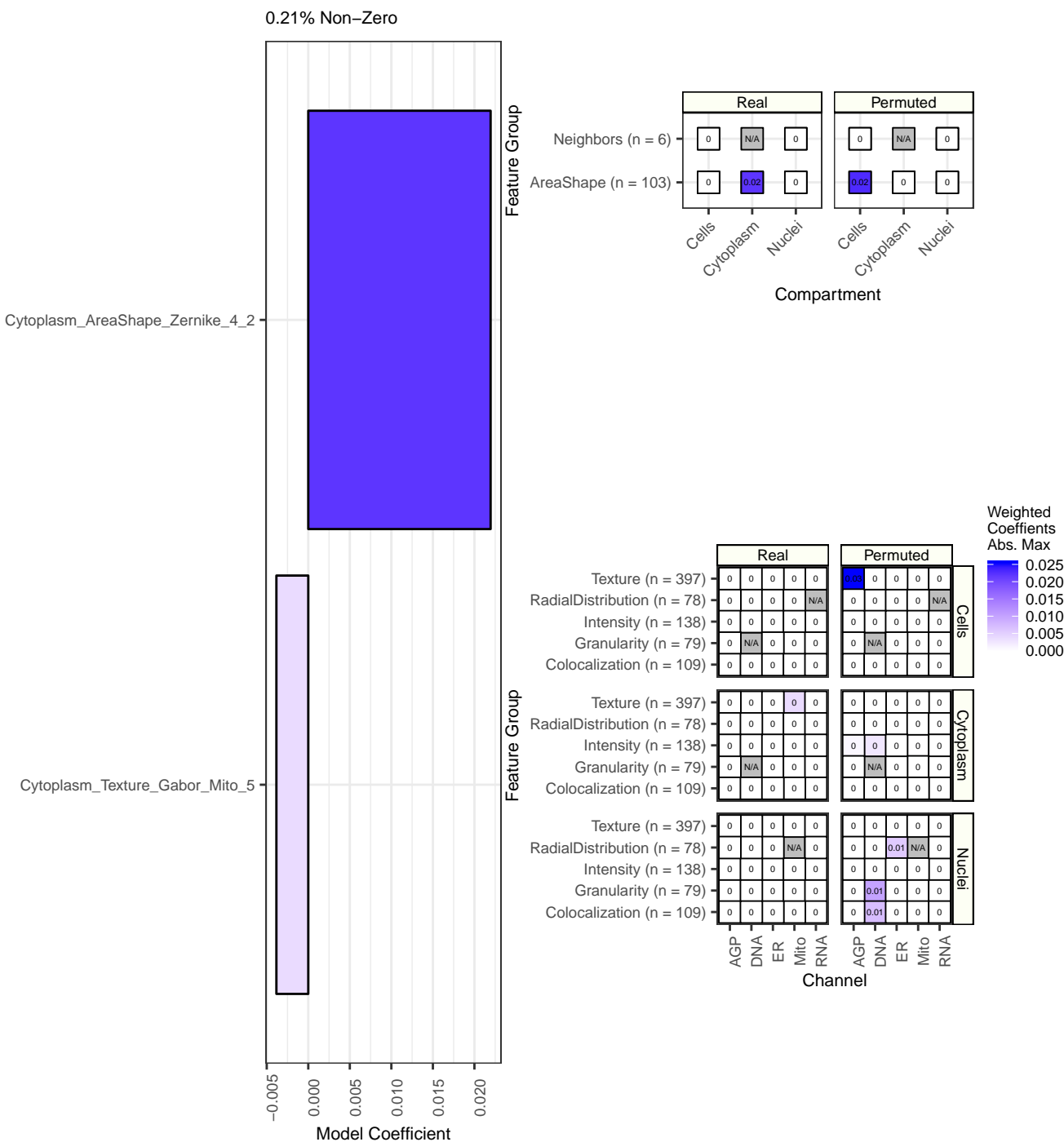




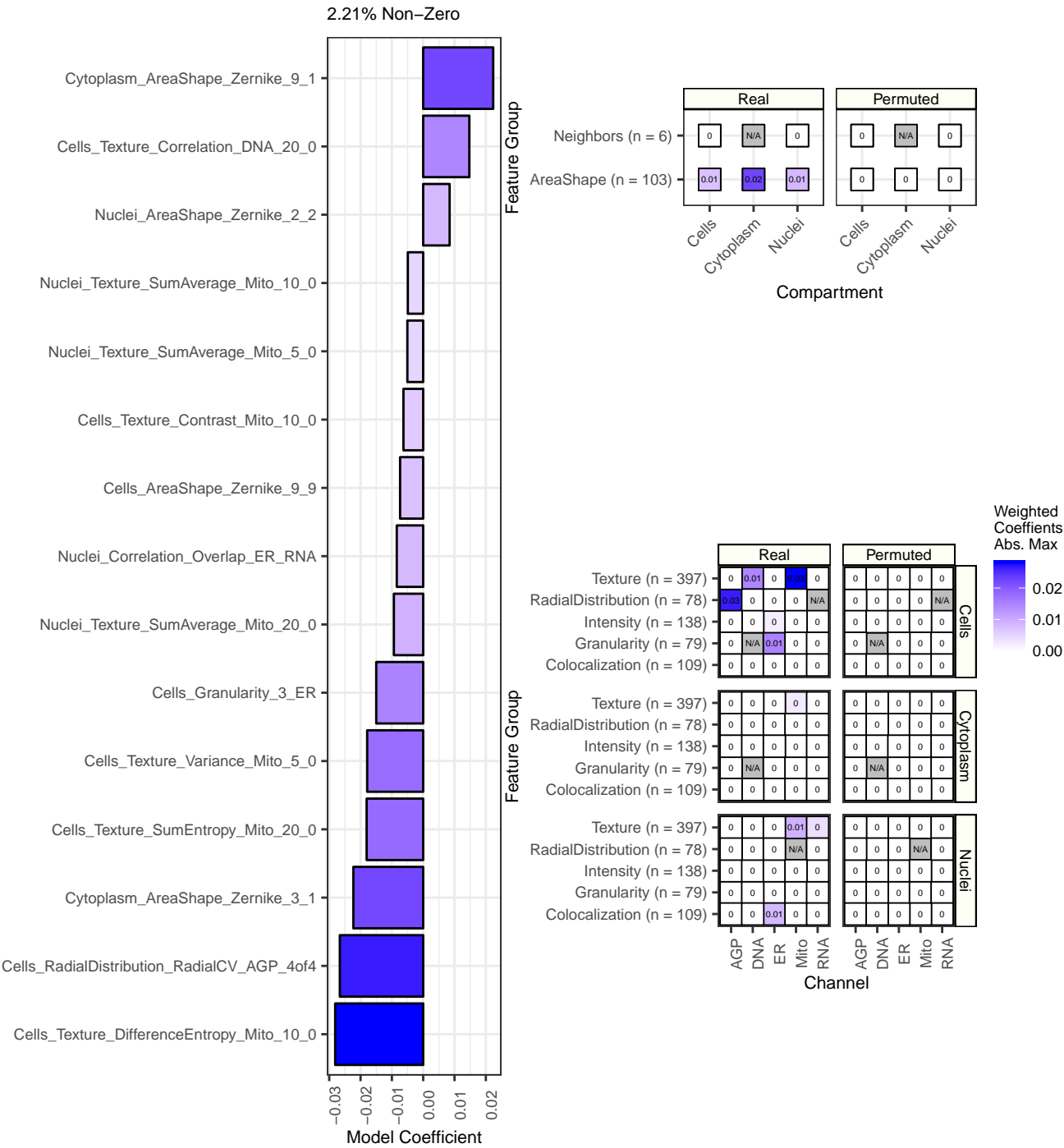
M – # of gH2AX Spots



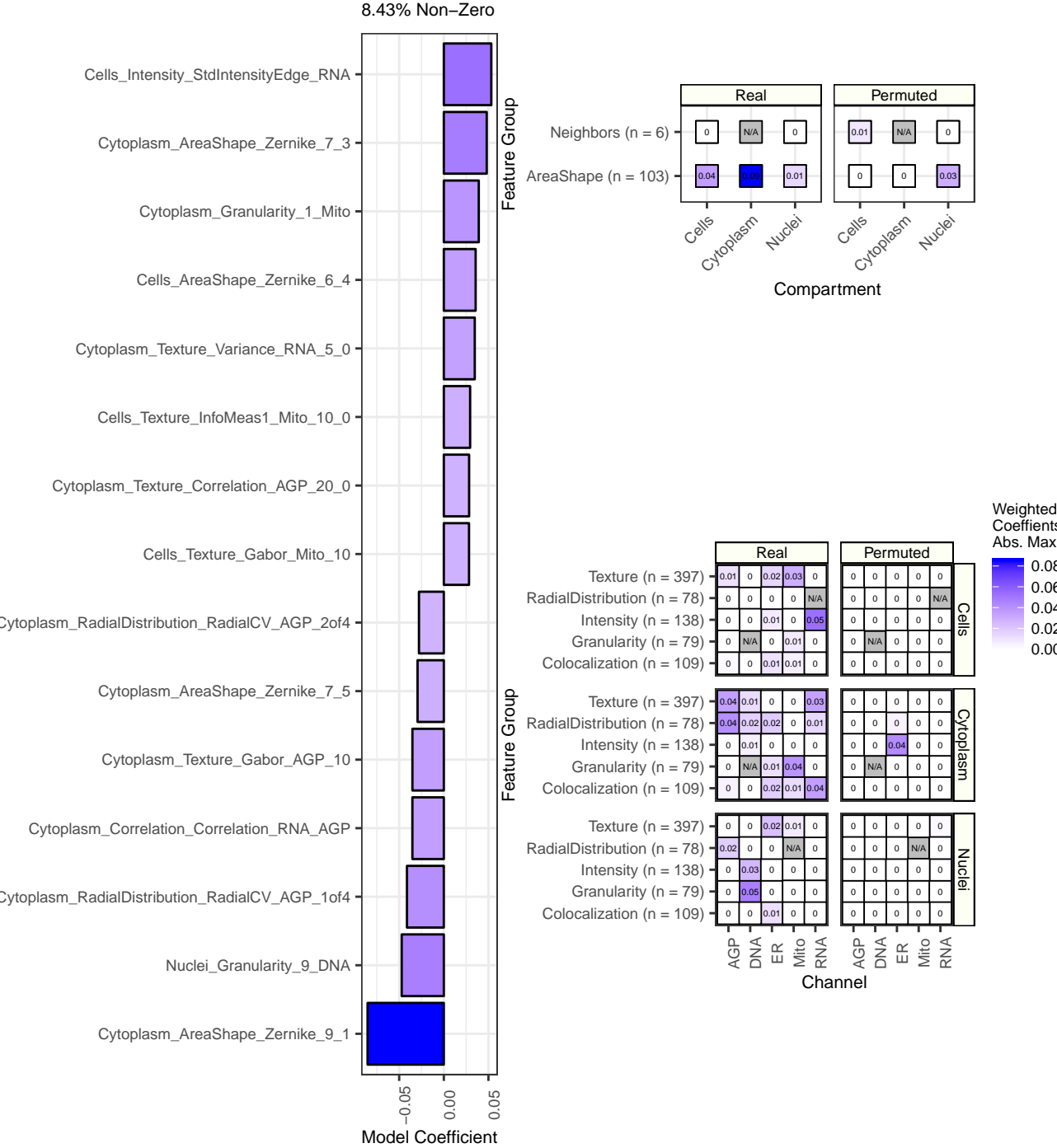
# M – # of gH2AX Spots per Area of Nucleus



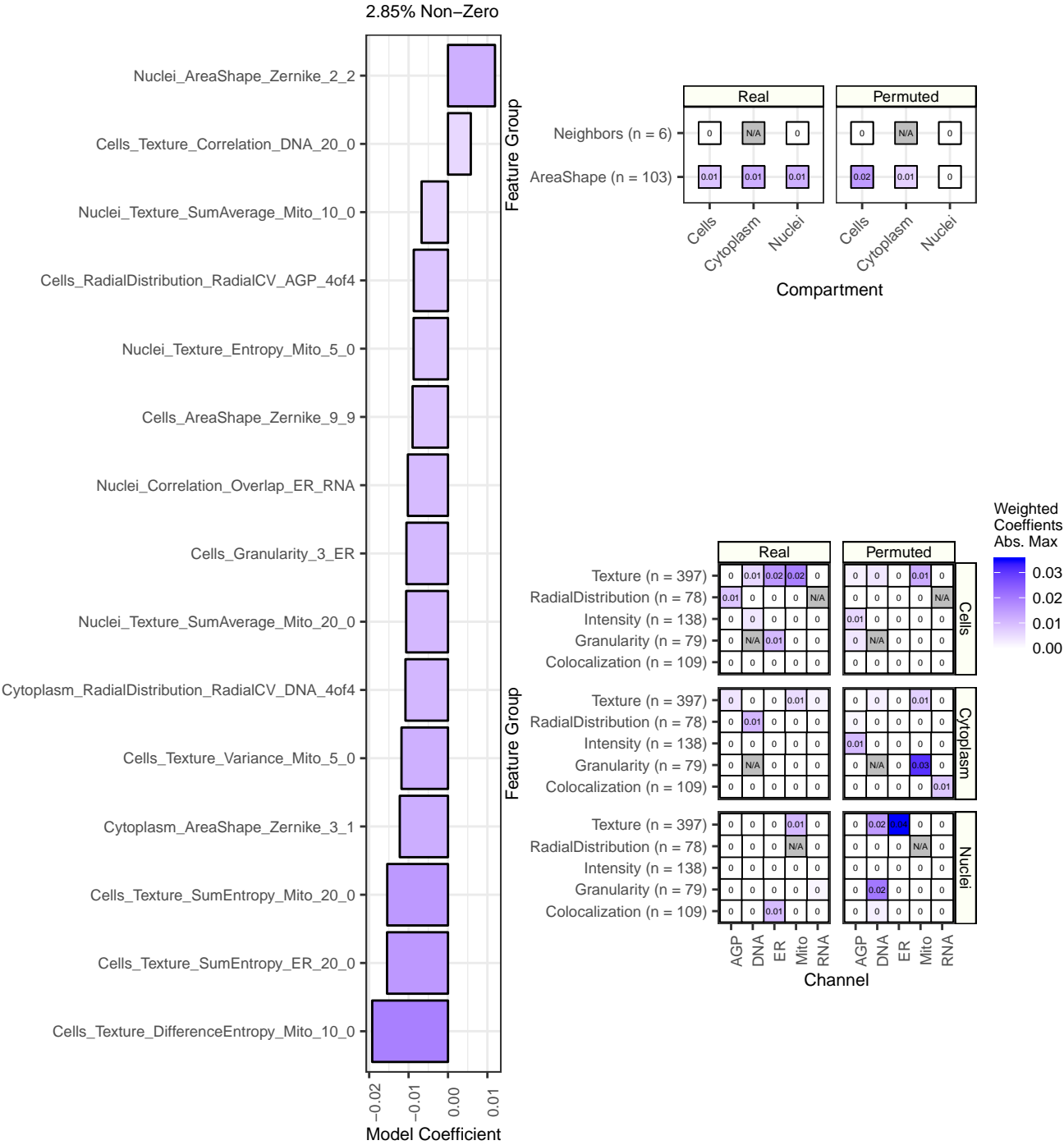
Polynuclear – % High gH2AX Spots



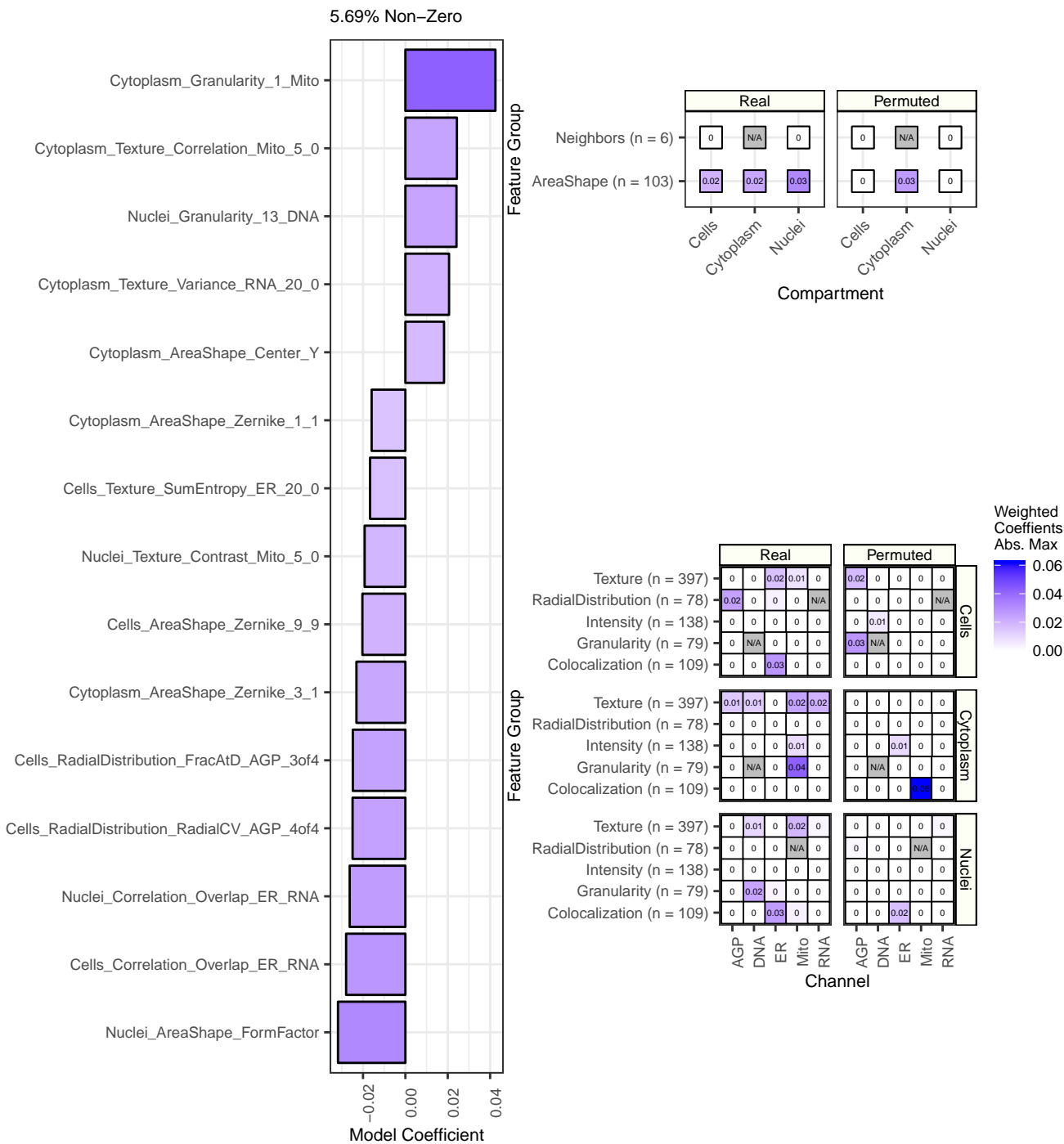
Polynuclear – # cells



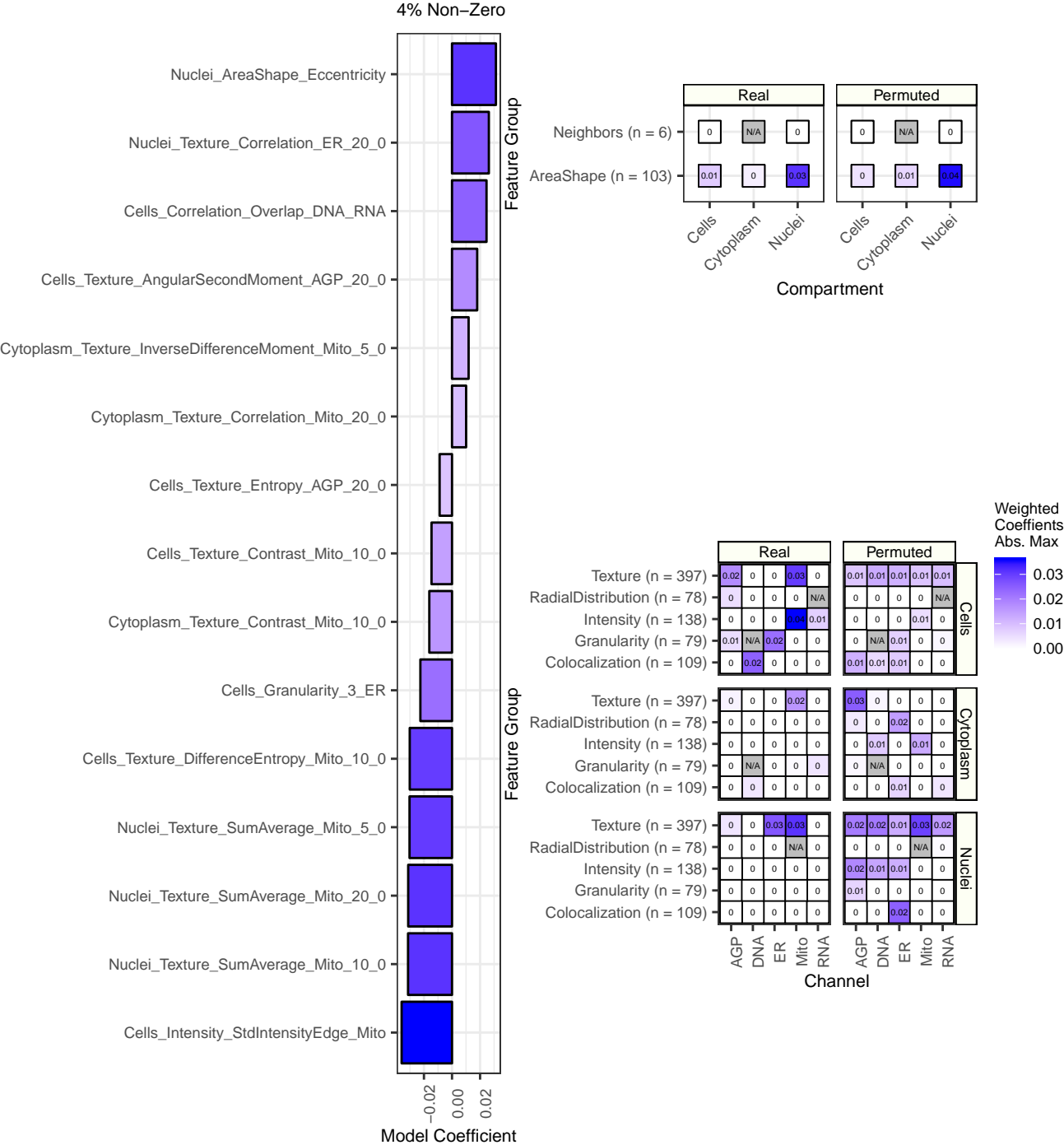
Polynuclear – # of gH2AX Spots



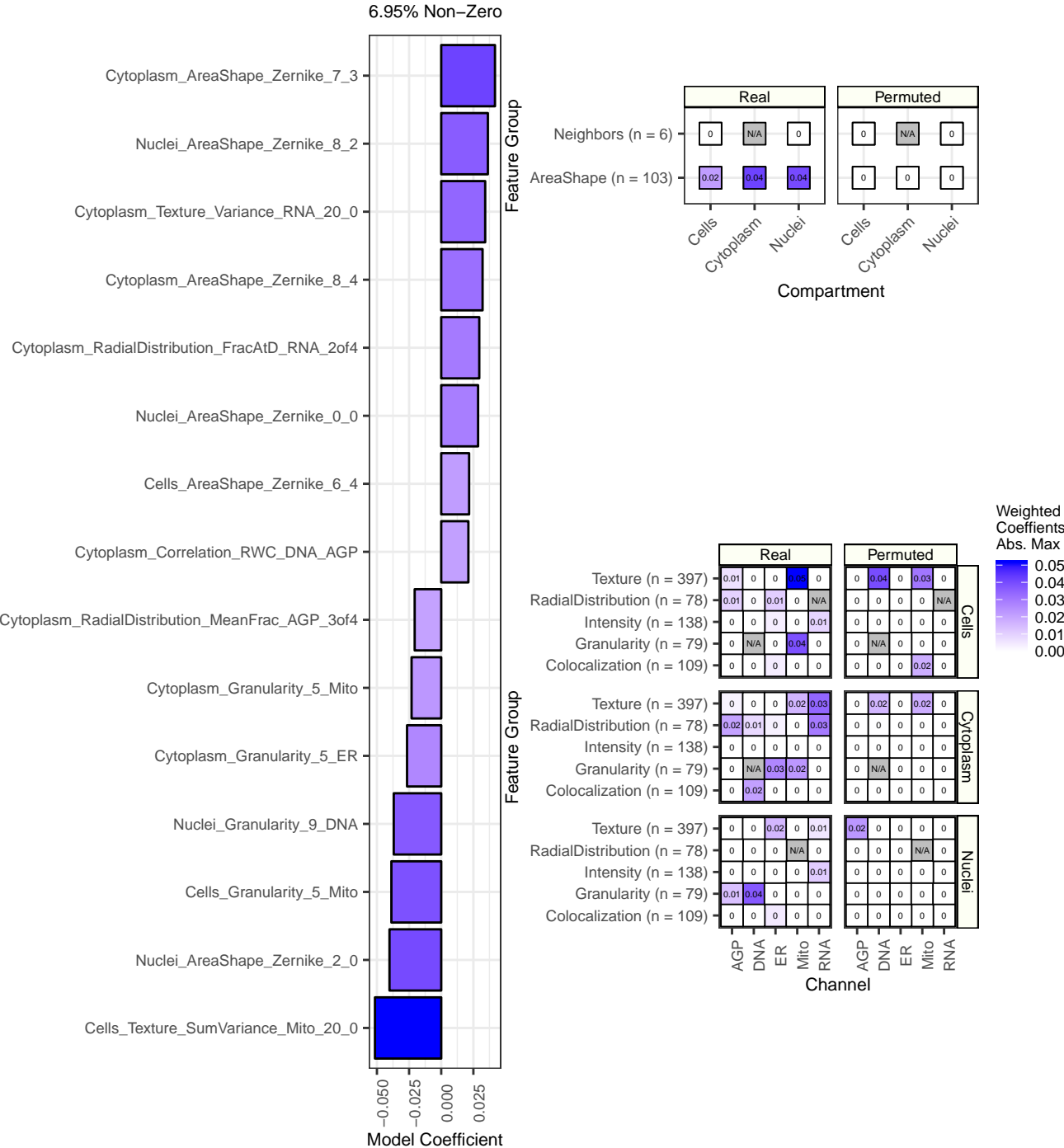
# Polynuclear – # of gH2AX Spots per Area of Nucleus



Polyploid – % High gH2AX Spots



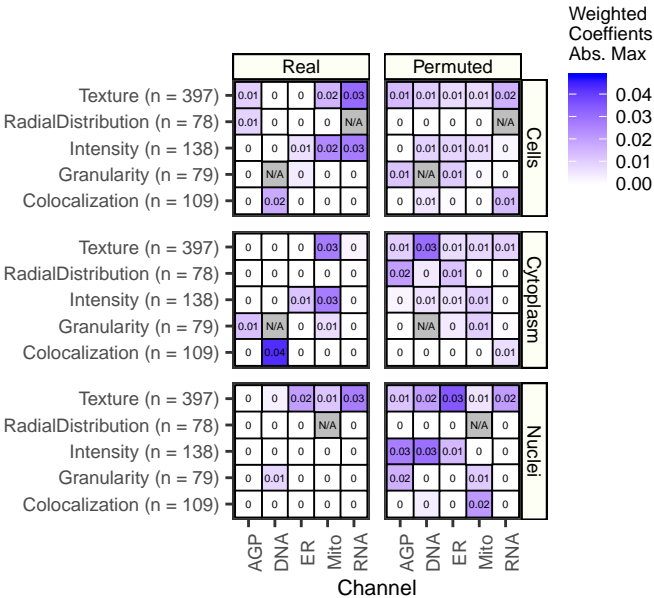
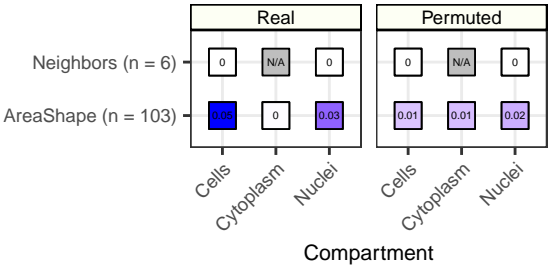
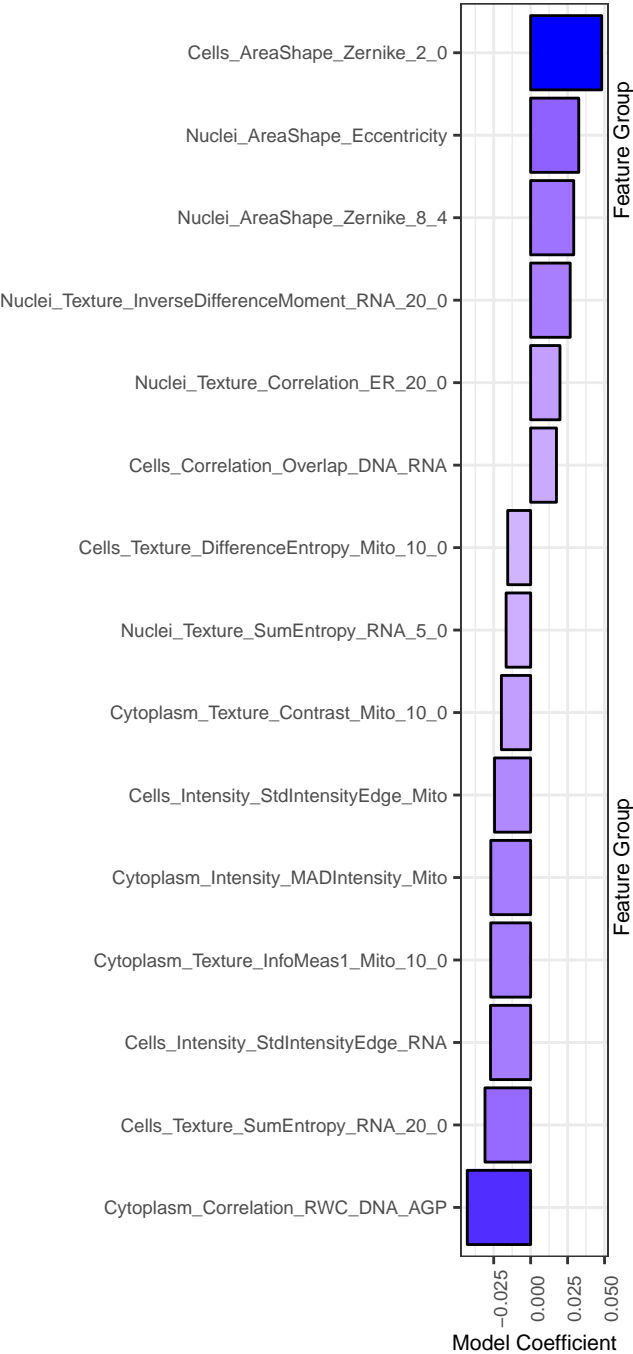
Polyploid – # cells



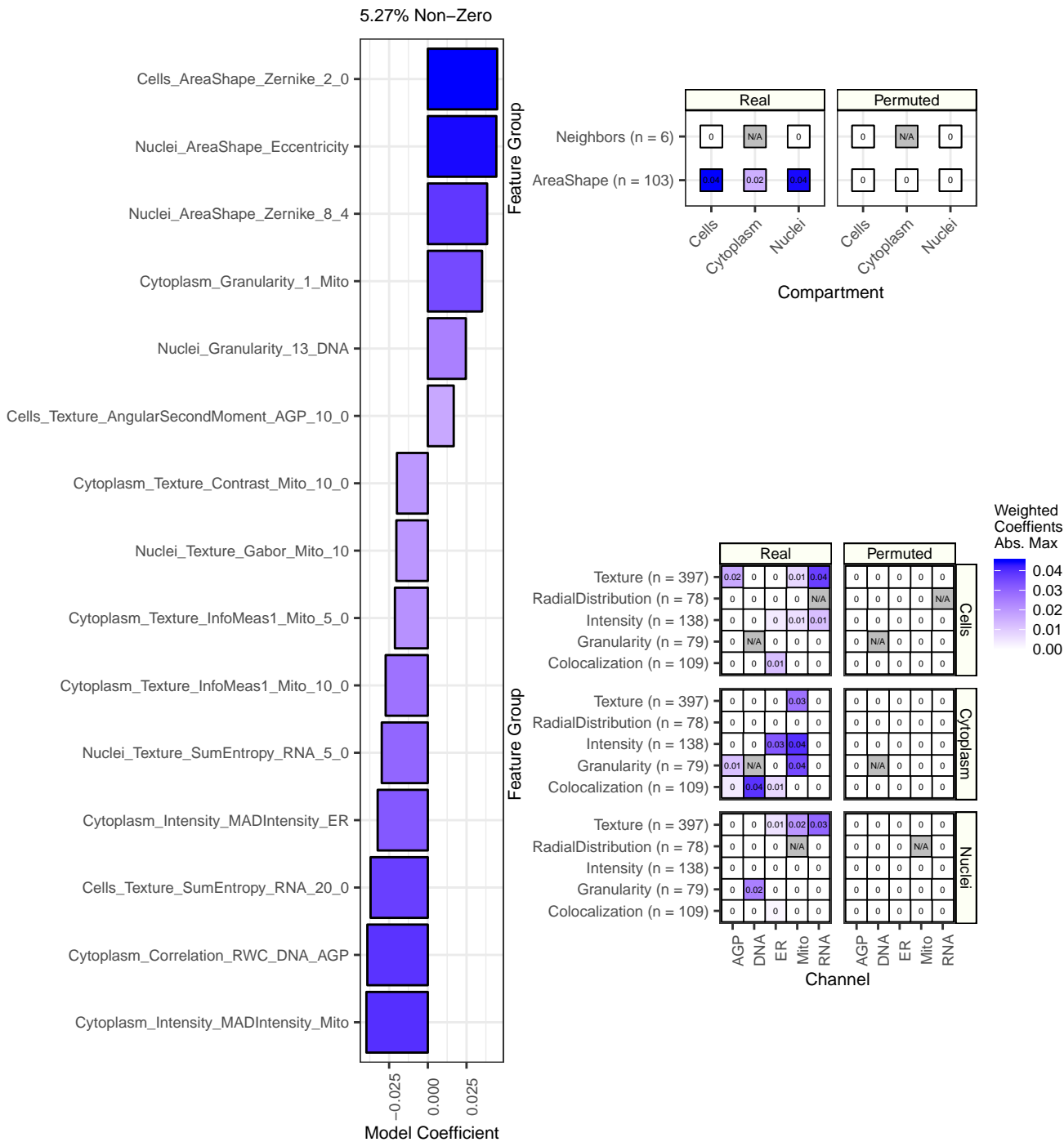


Polyloid – # of gH2AX Spots

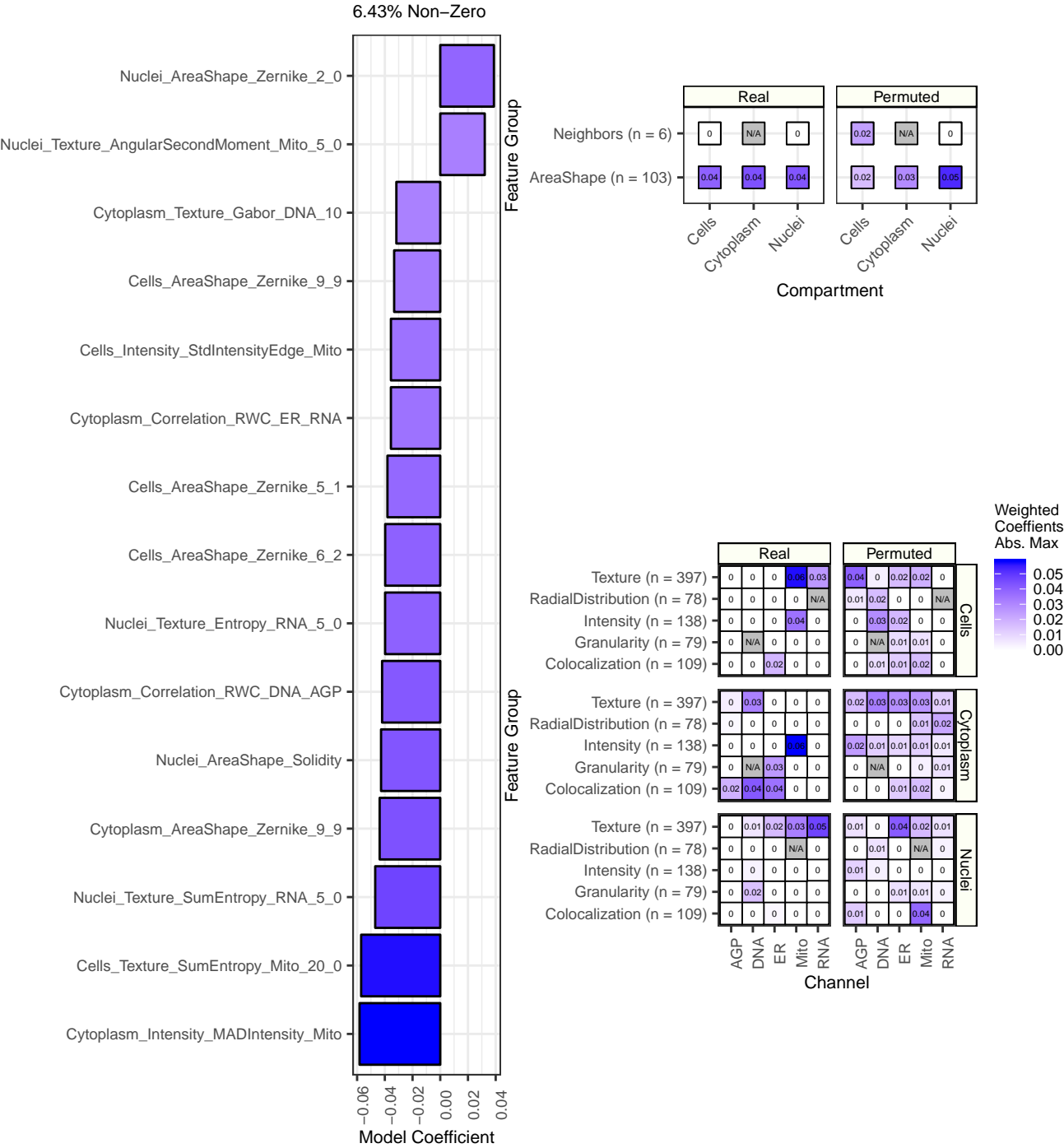
5.69% Non-Zero



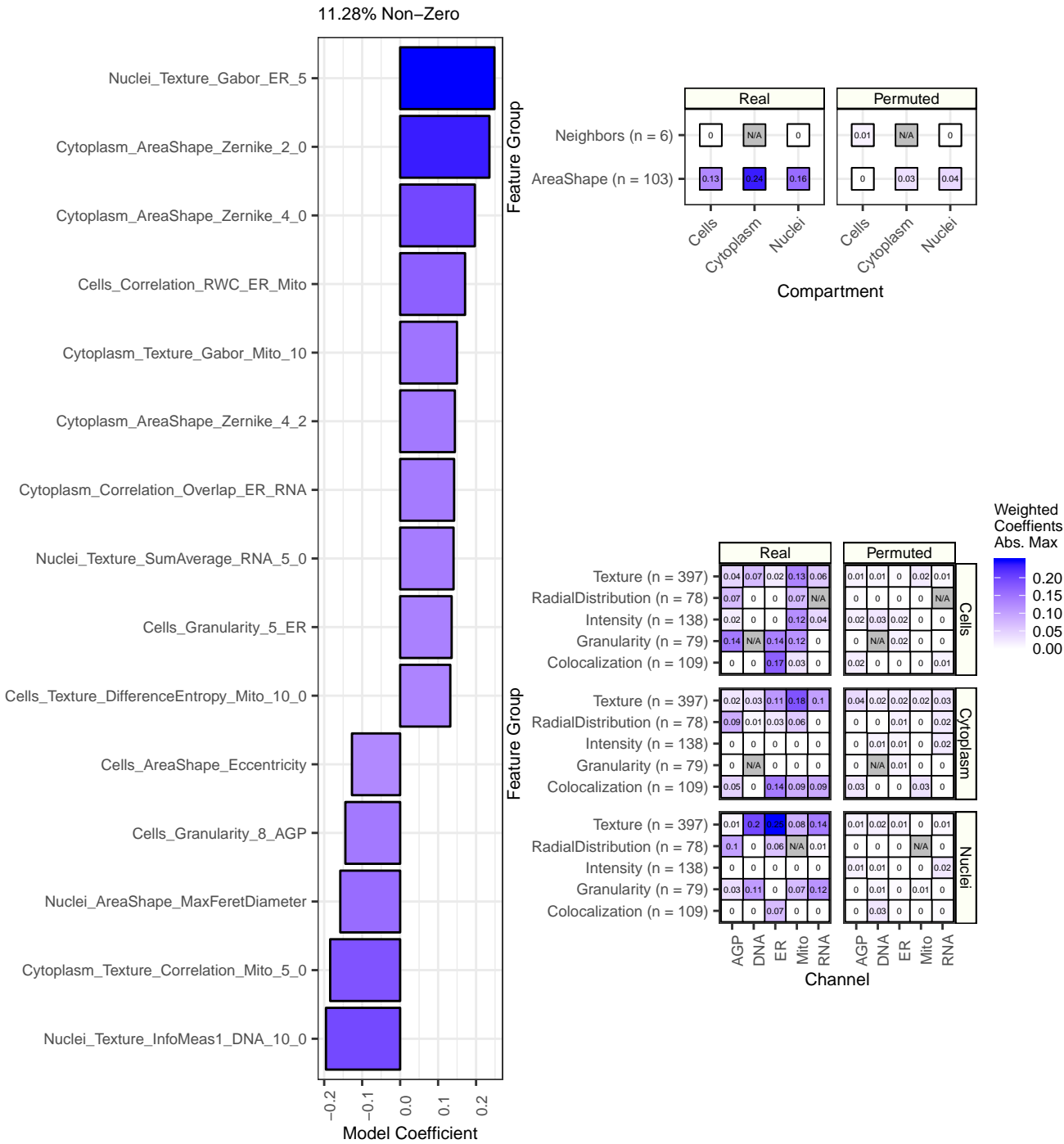
## Polyploid – # of gH2AX Spots per Area of Nucleus



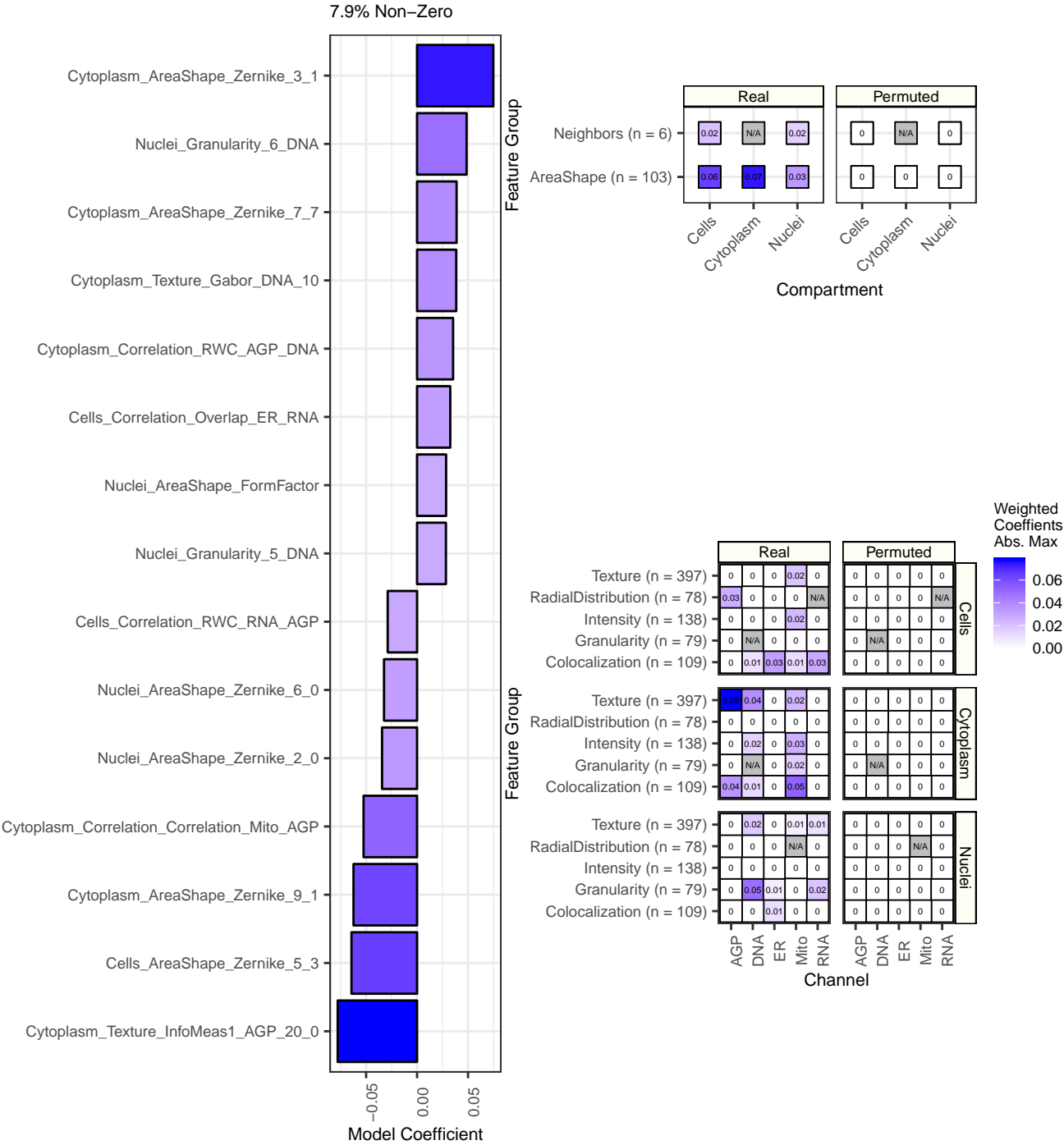
# S – % High gH2AX Spots



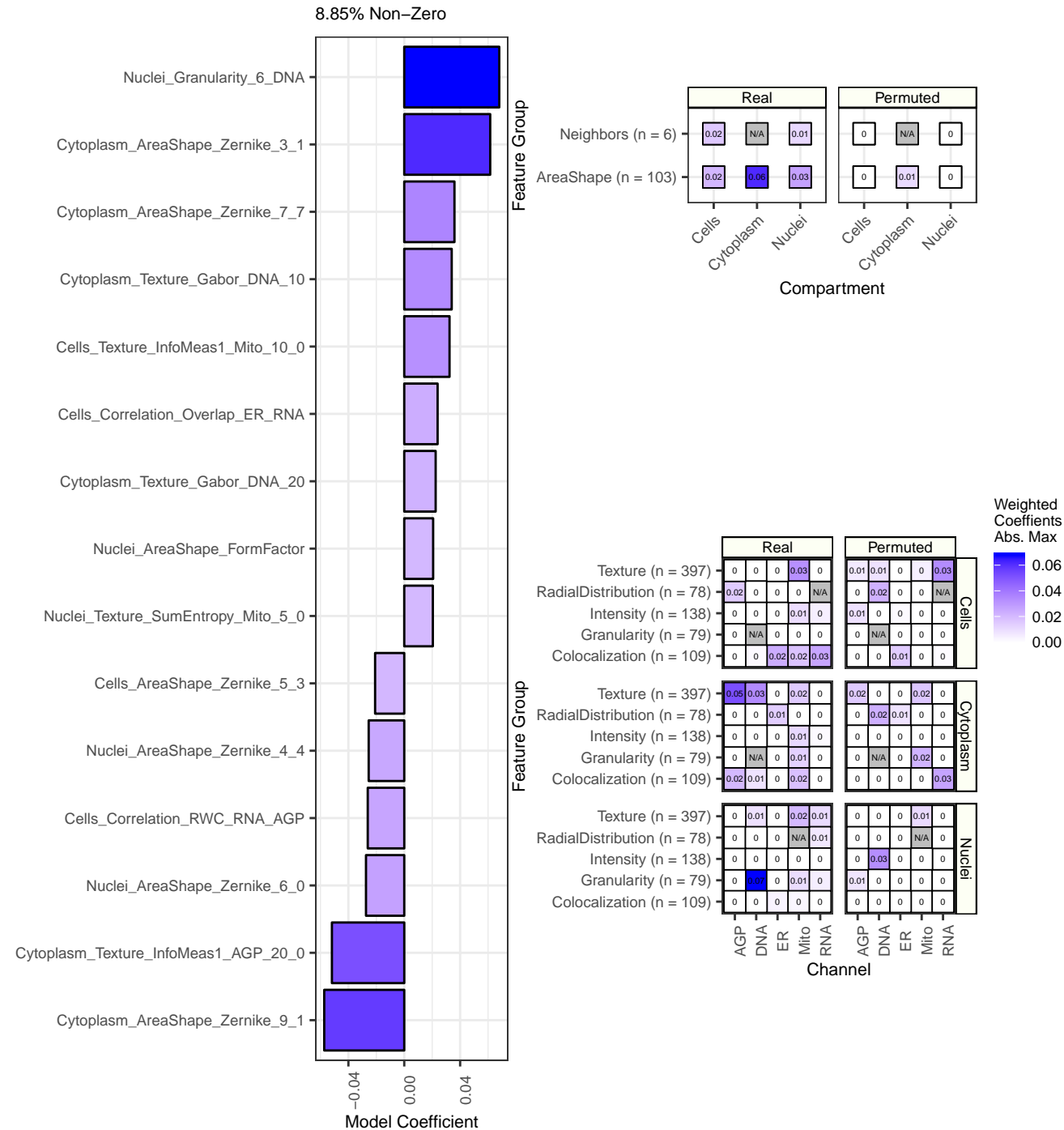
S – Intensity Nucleus EdU Mean



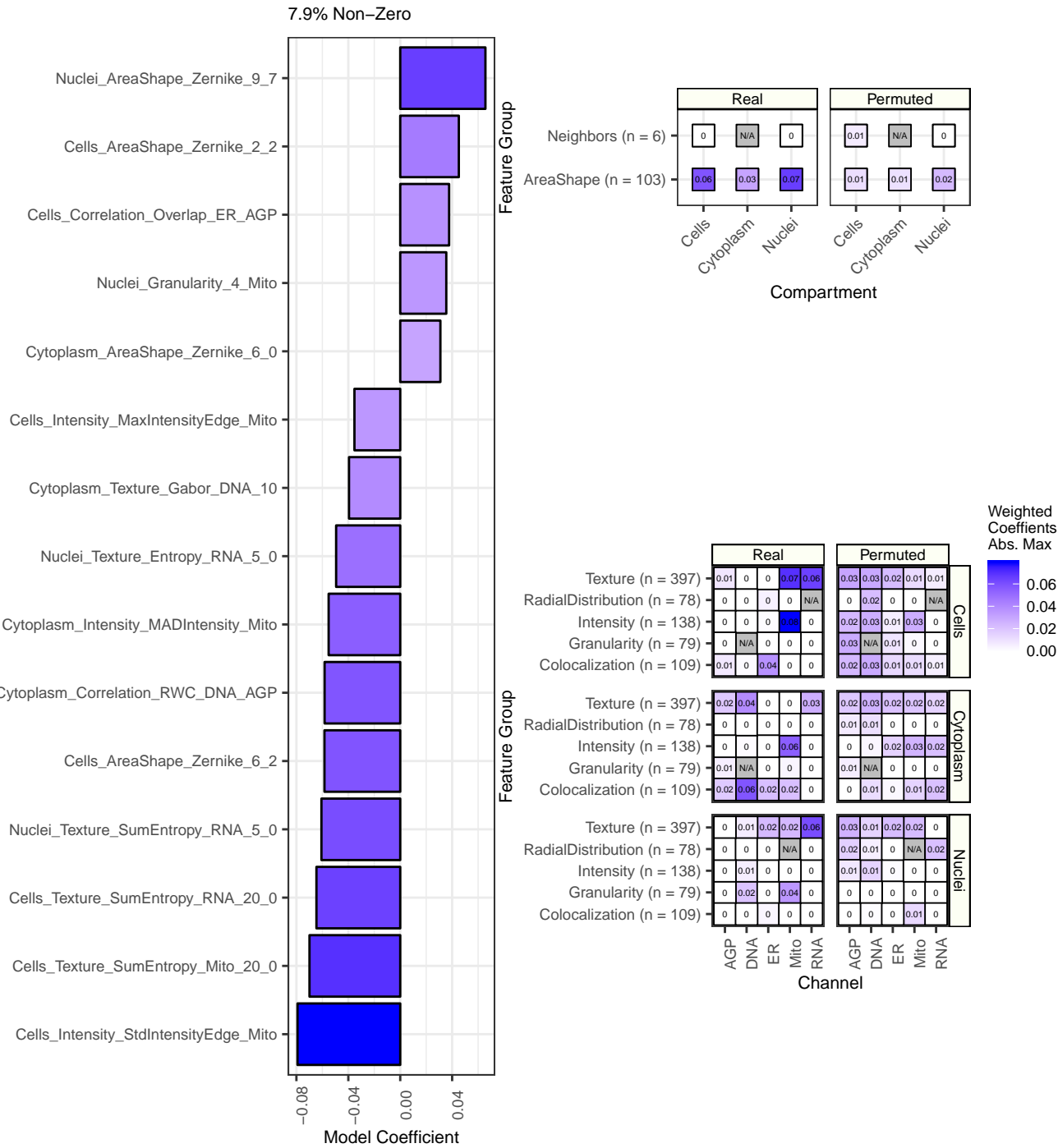
S – Intensity Nucleus EdU Sum



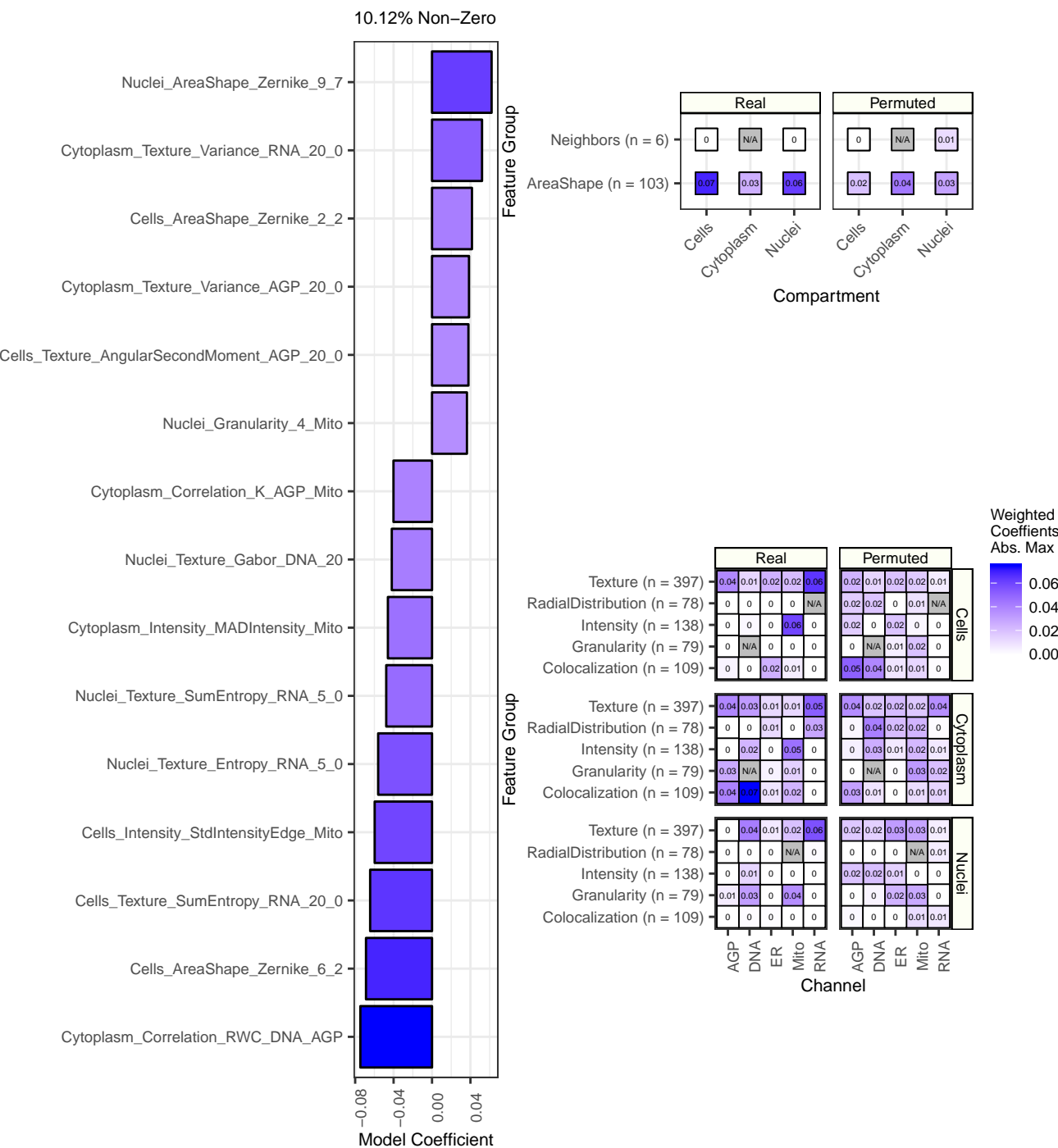
## S – # cells



S – # of gH2AX Spots

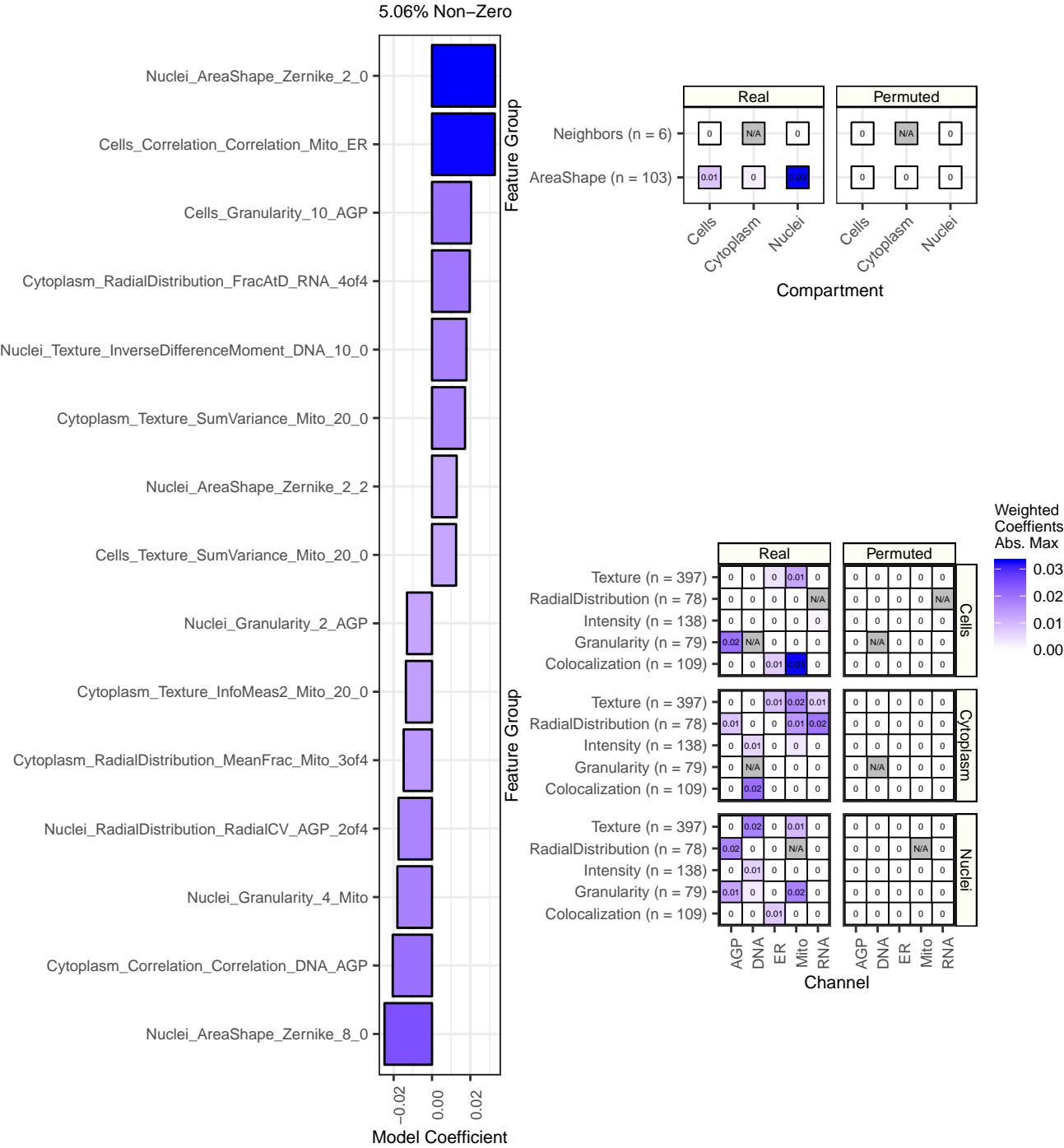


S – # of gH2AX Spots per Area of Nucleus

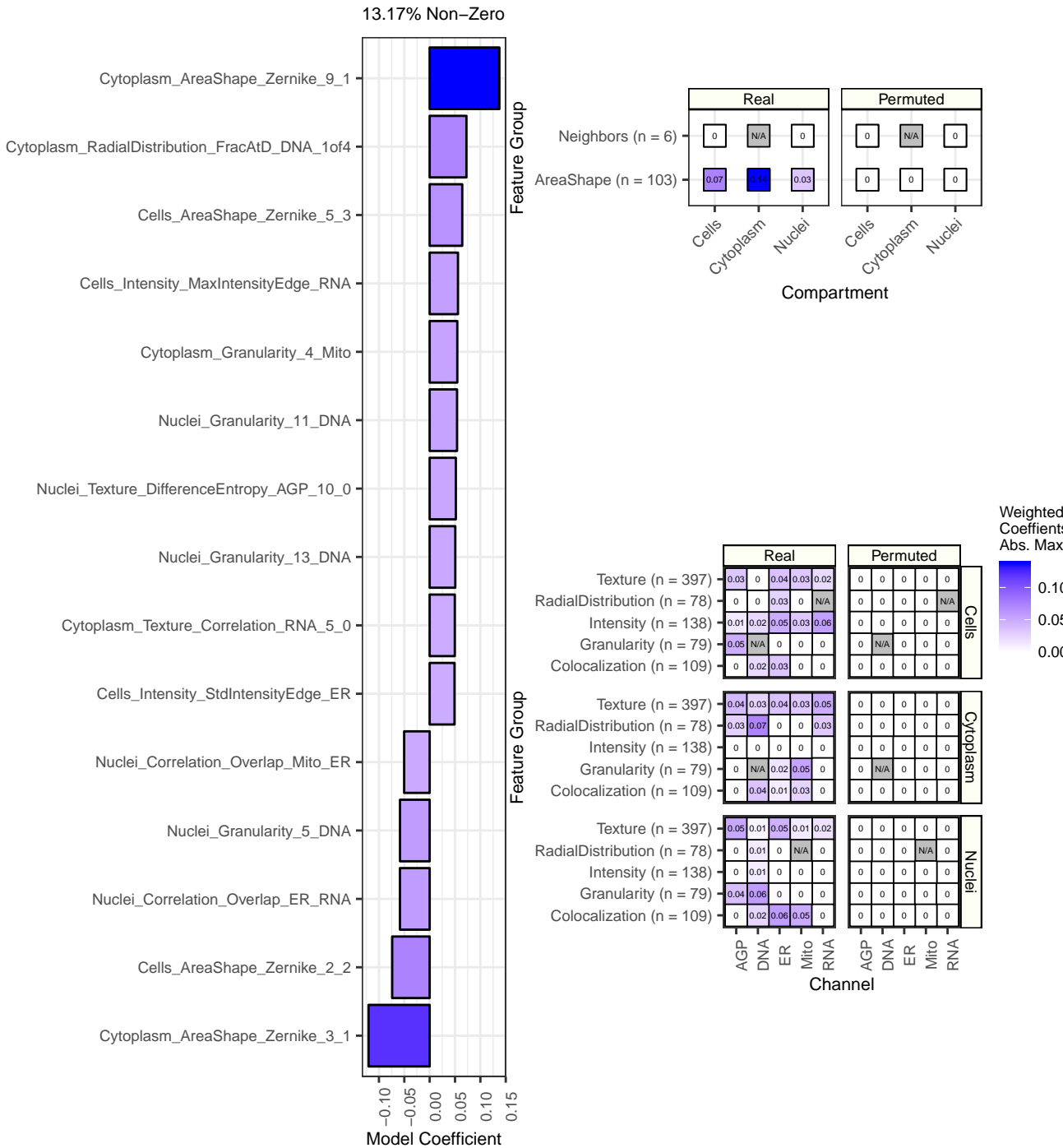




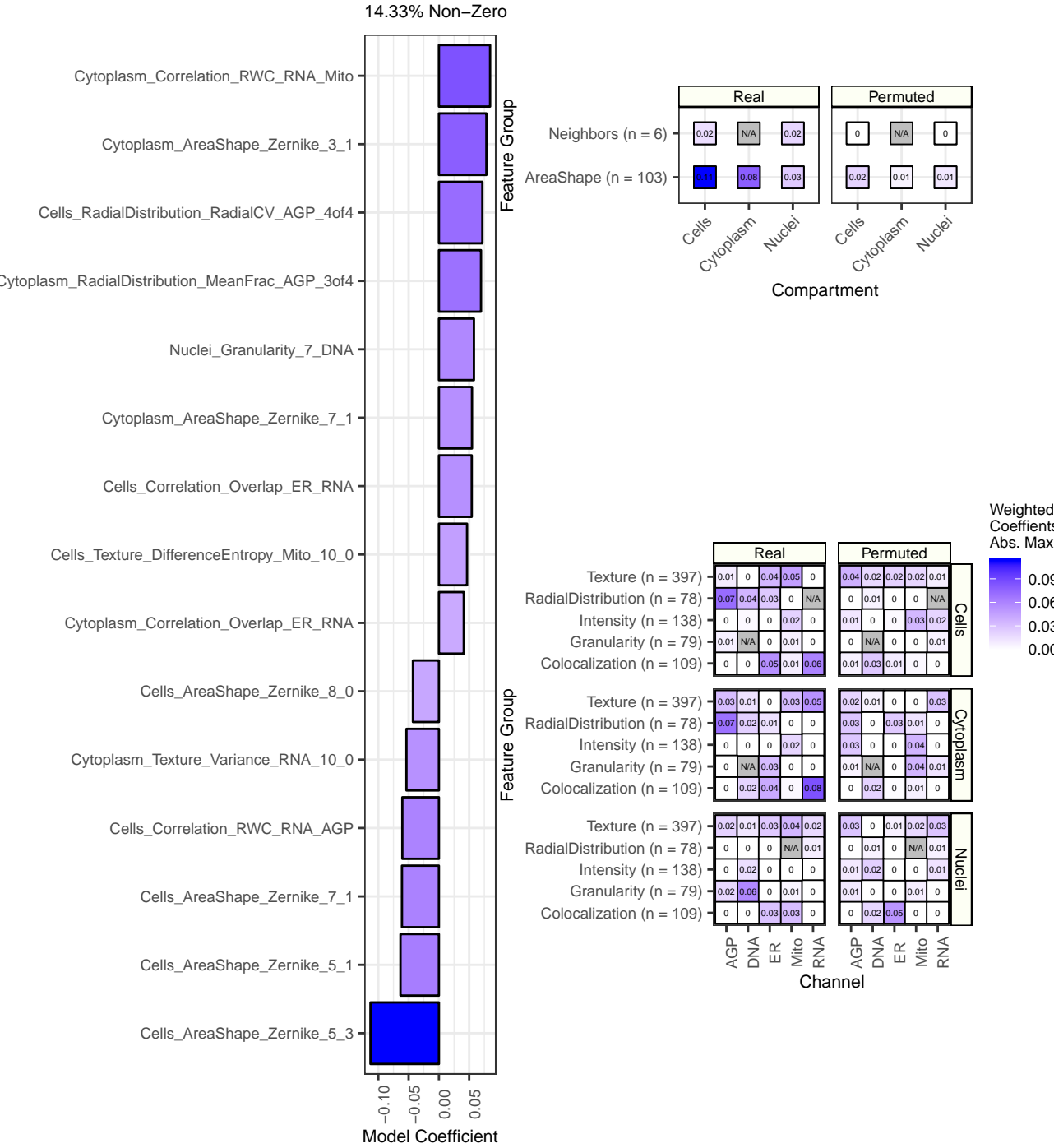
VB – Infection Efficiency



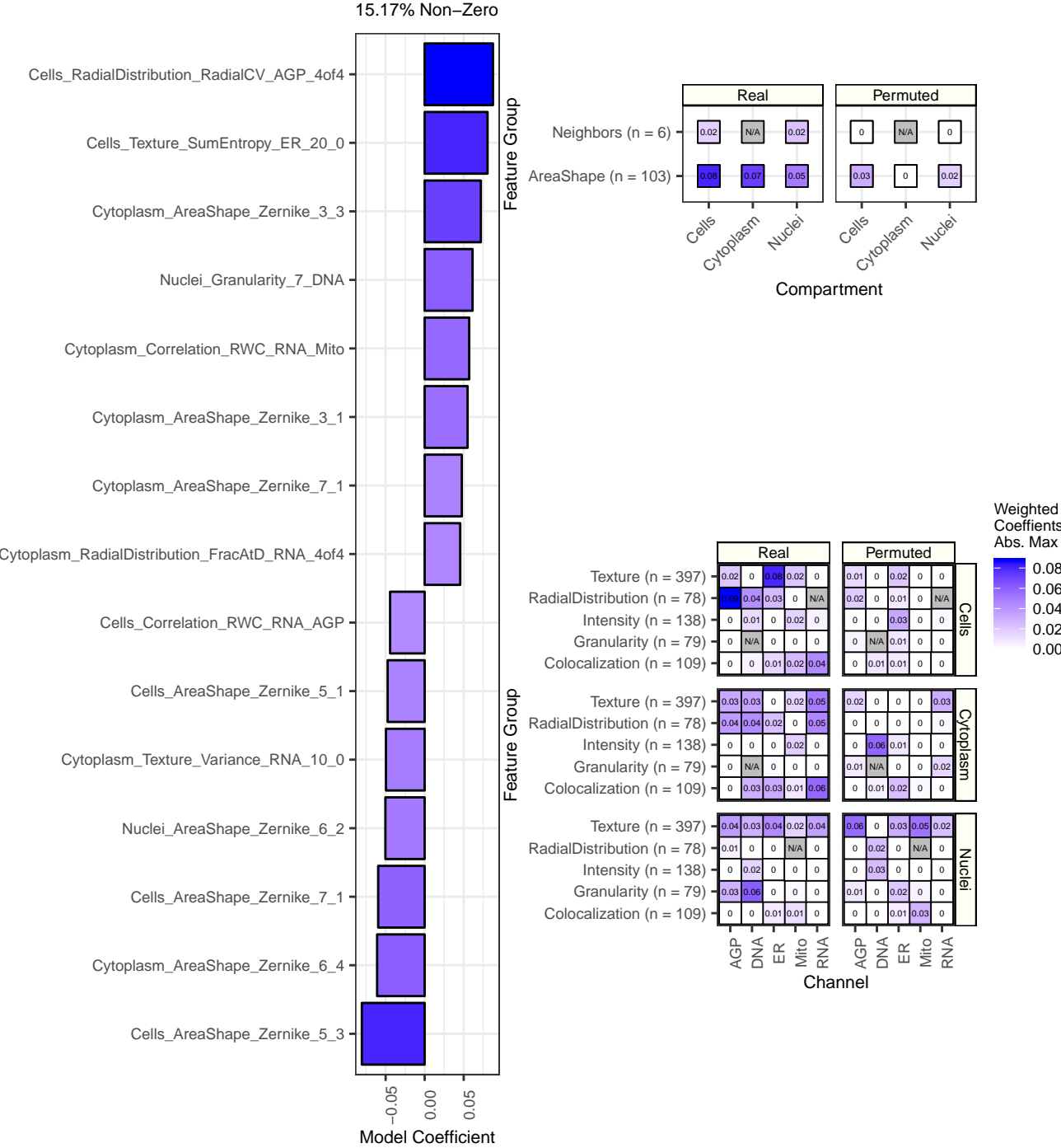
# Live Cell Area



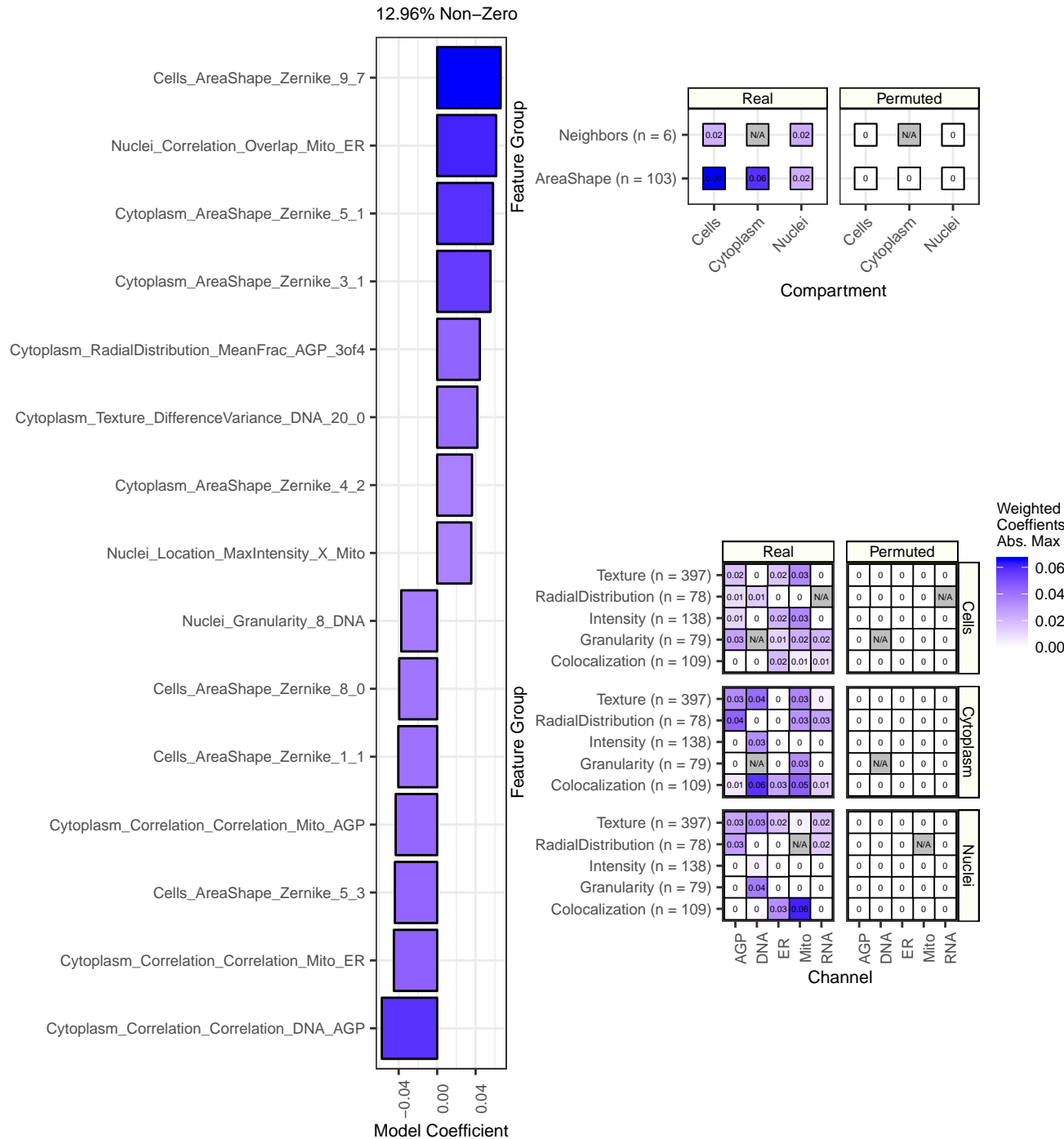
# Live Cell Roundness



# Live Width / Length

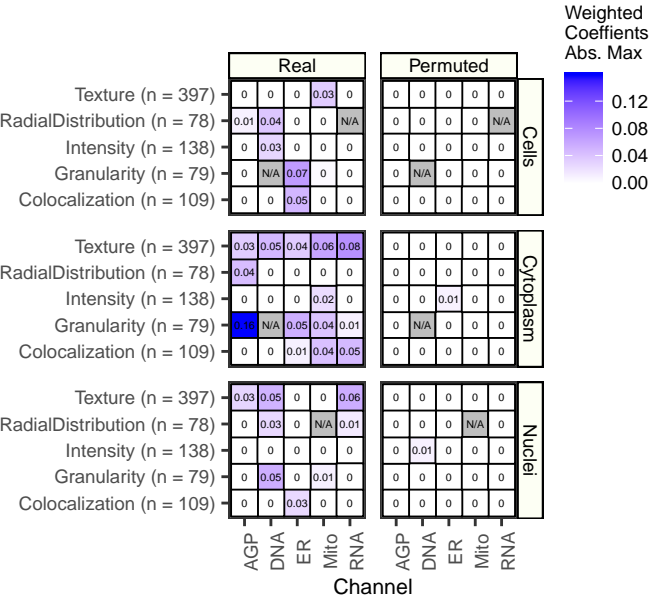
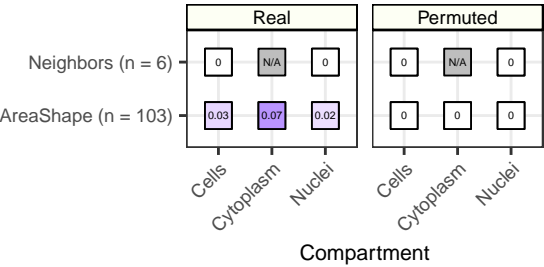
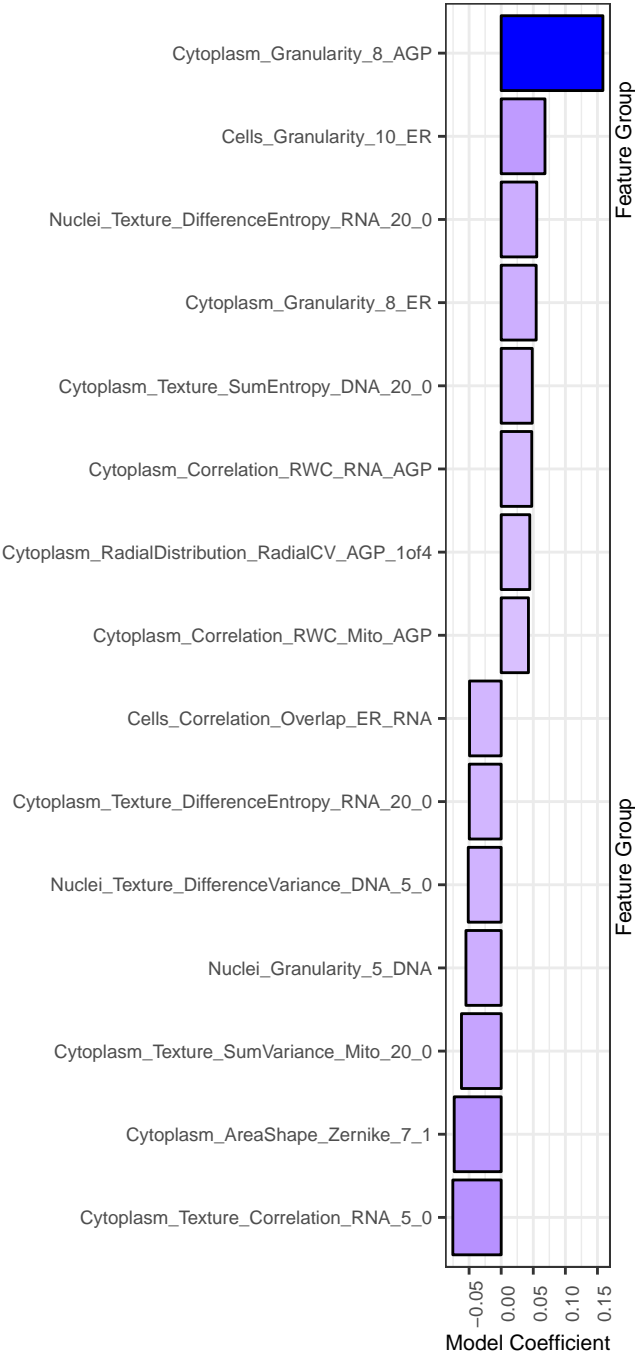


# Live Cells

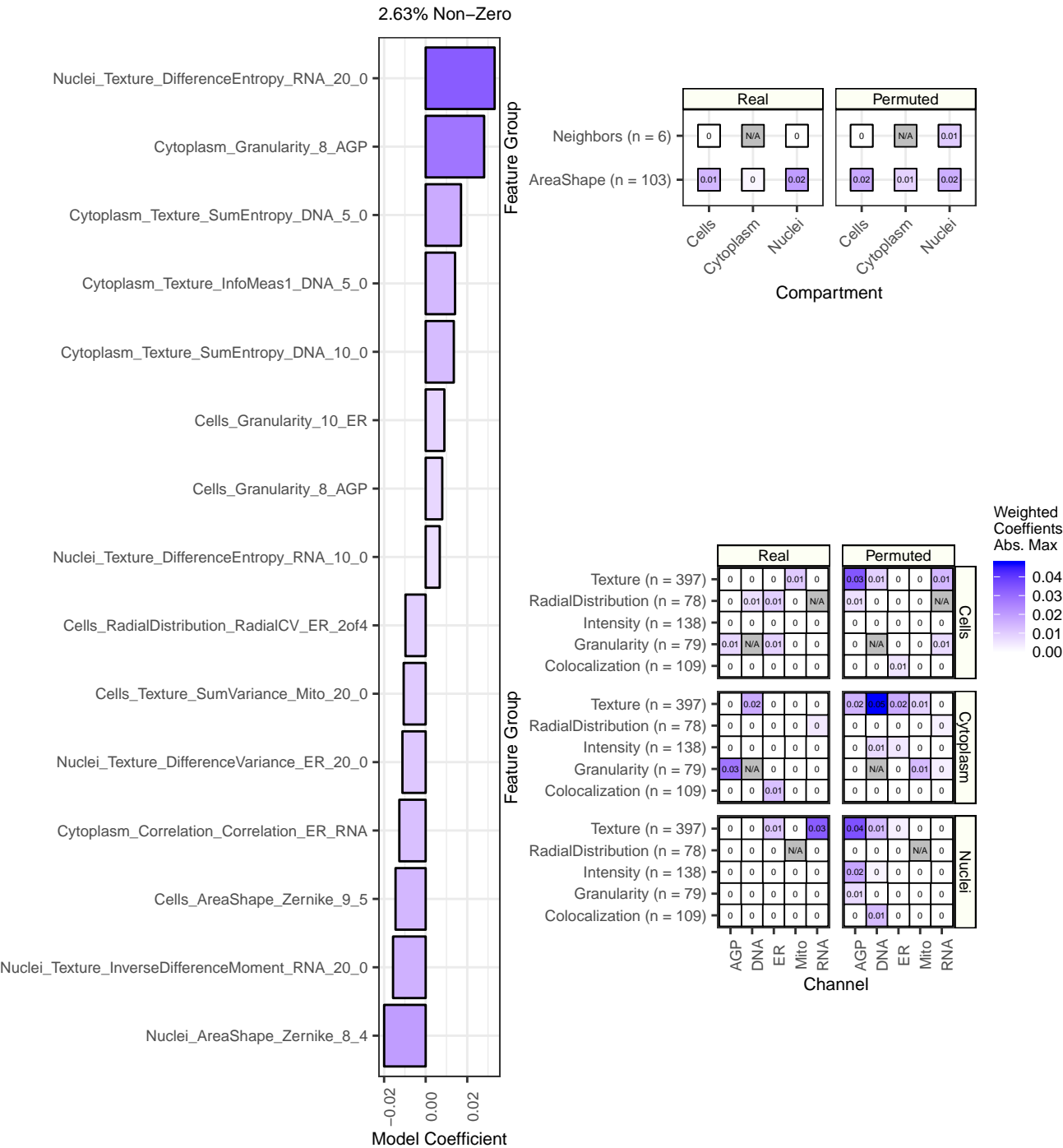


% All Apoptosis (CASP+)

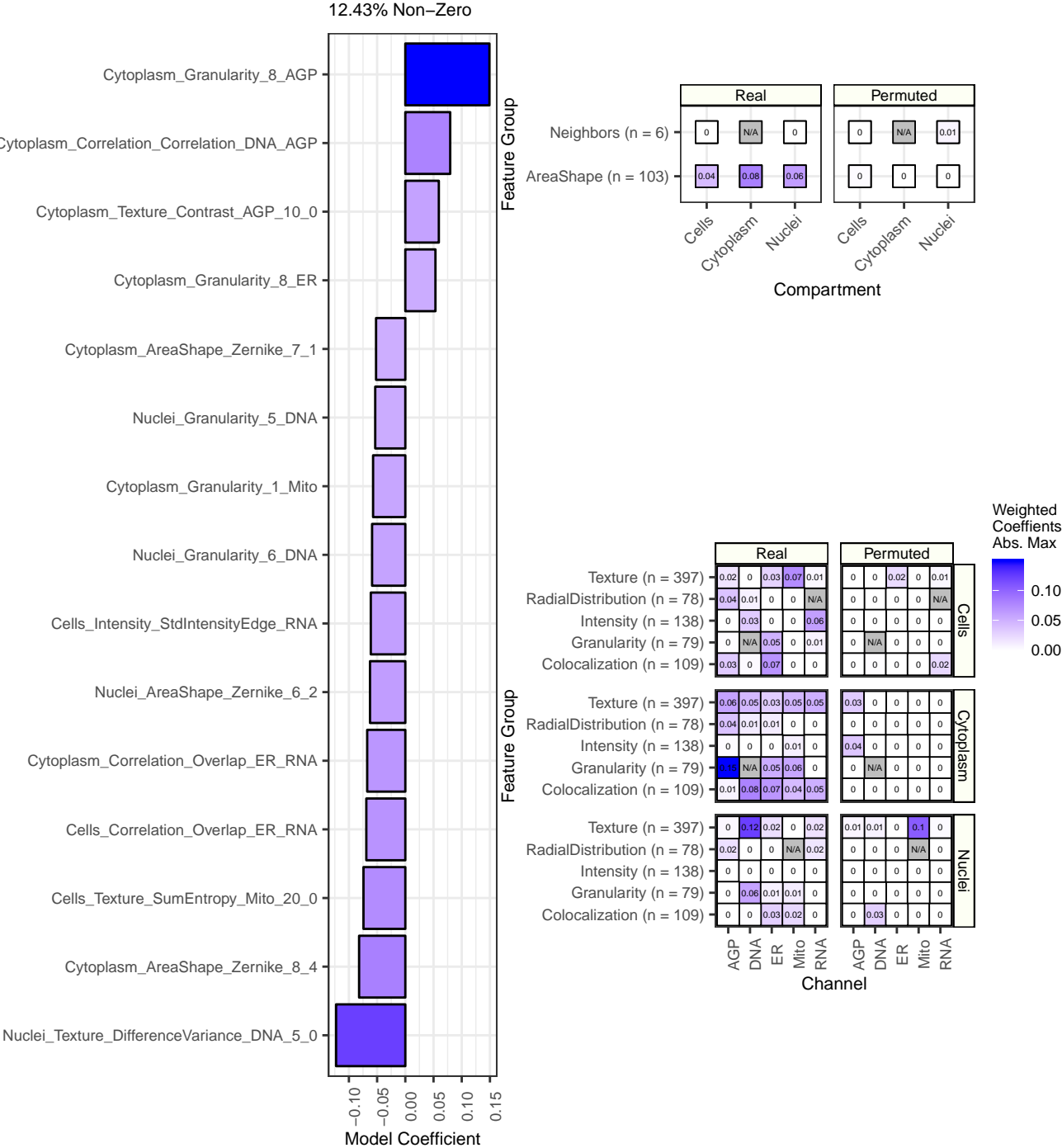
6.95% Non-Zero



% Caspase / % Dead Only

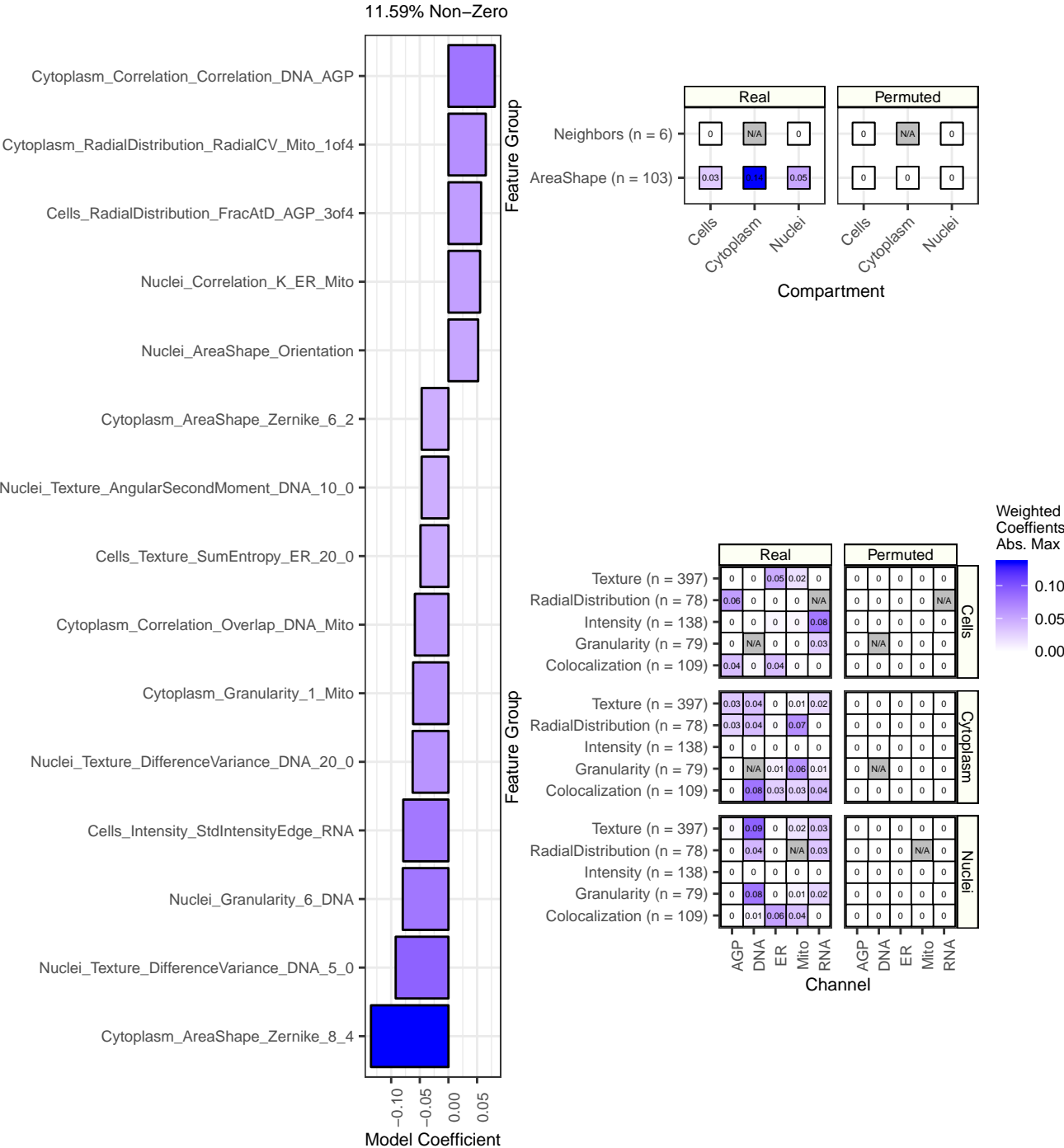


% All Dead (DRAQ7+)

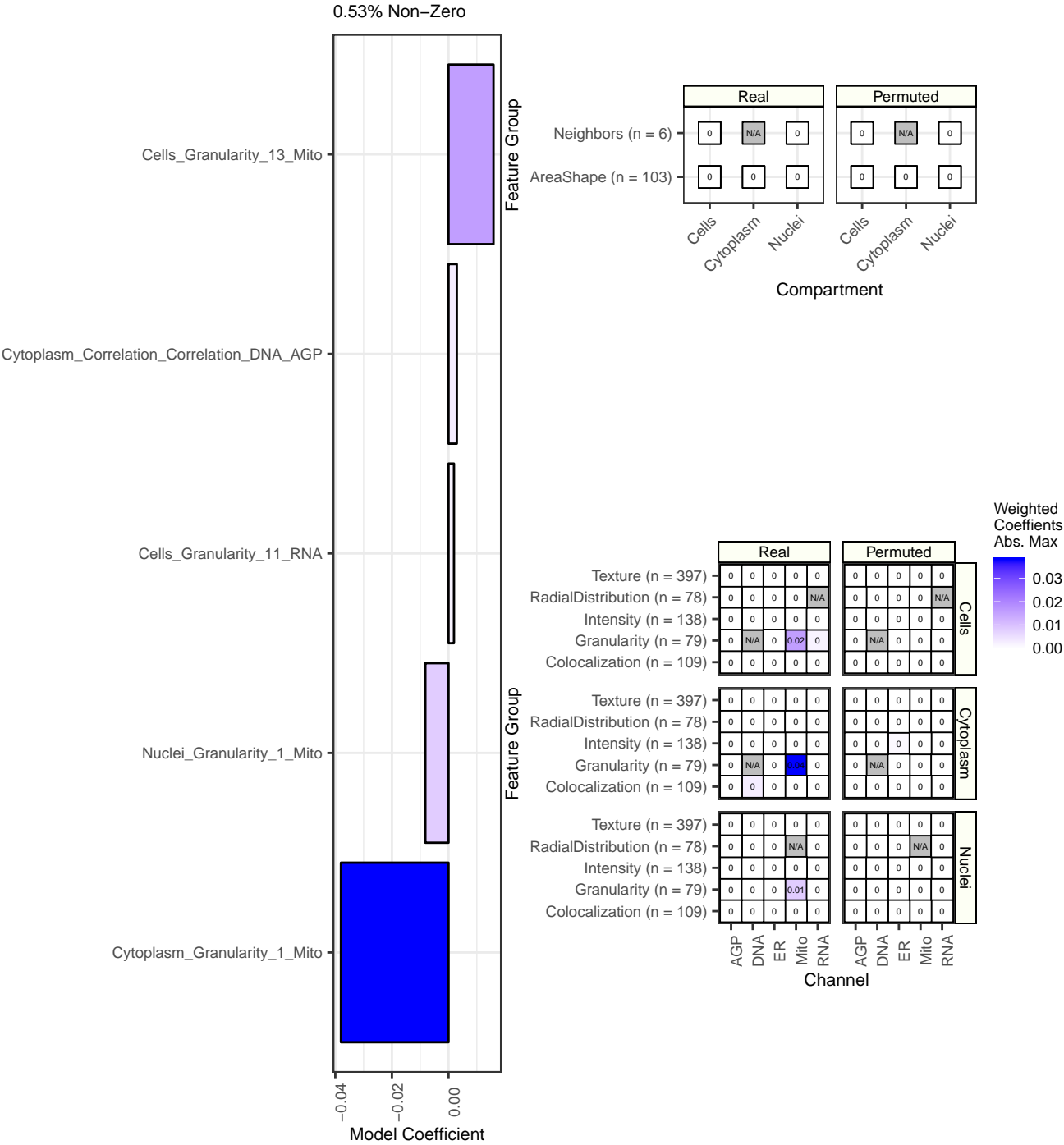




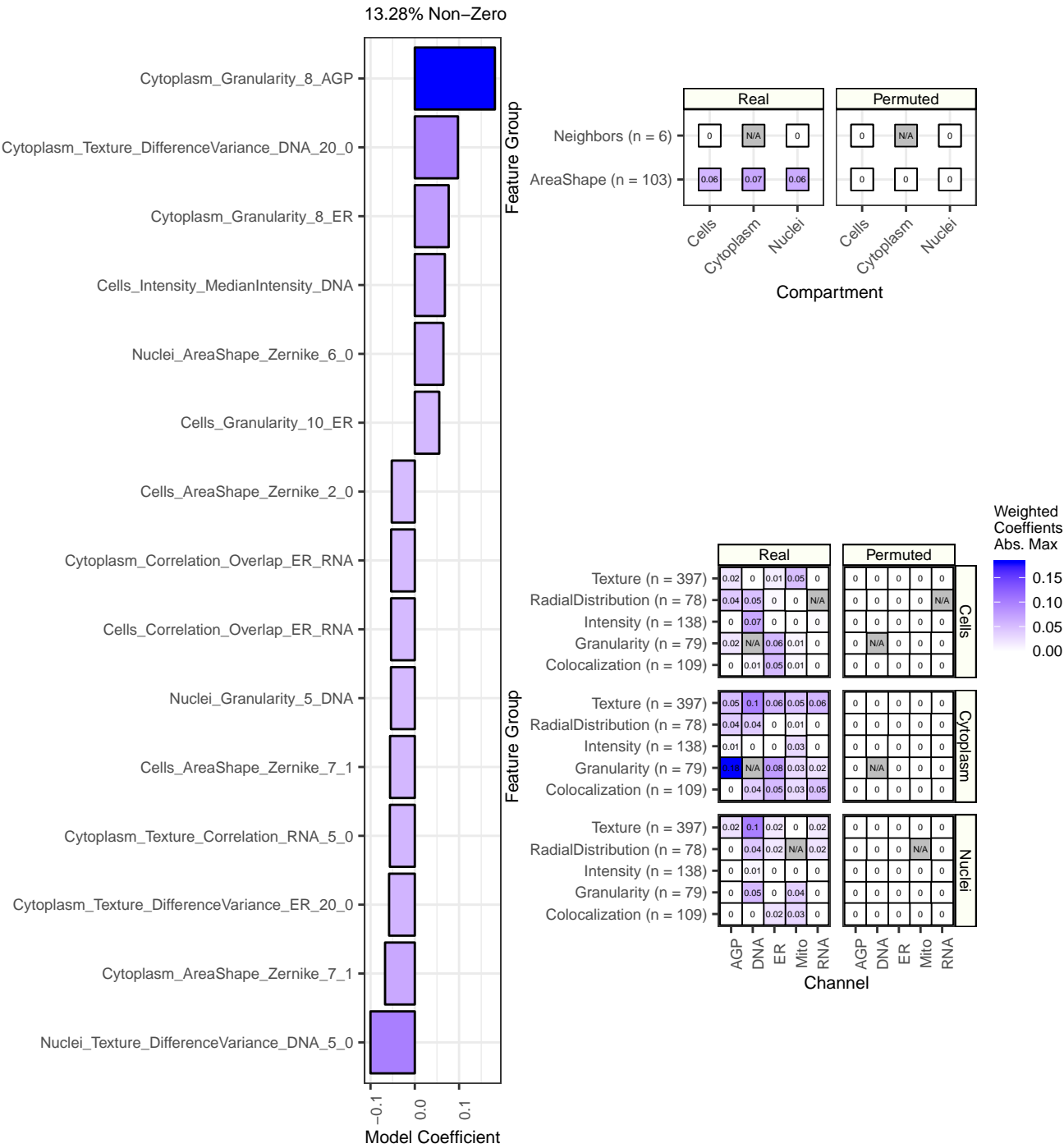
% Dead Only (CASP-; DRAQ7+)



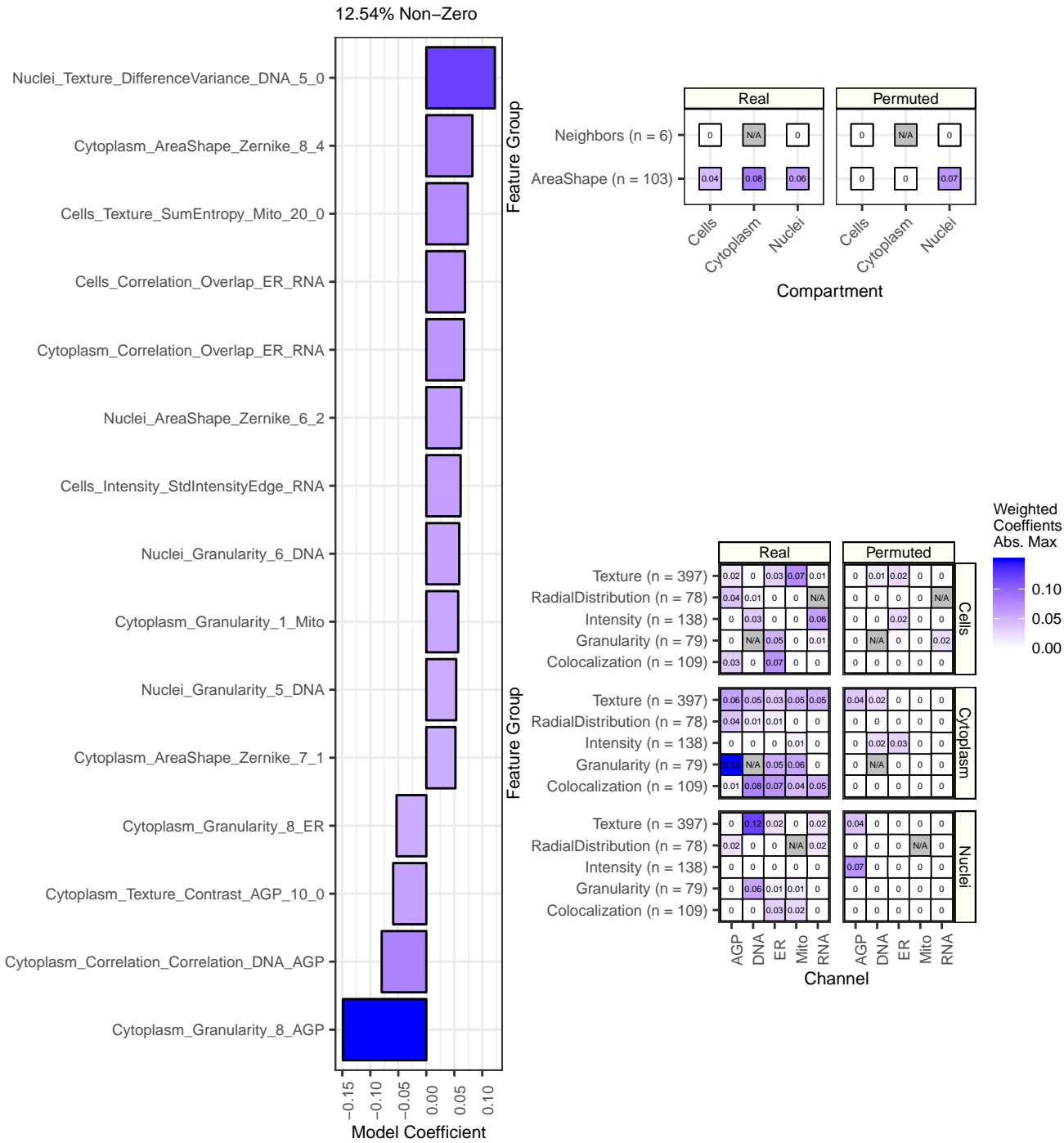
# % Early Apoptosis (CASP+; DRAQ7-)



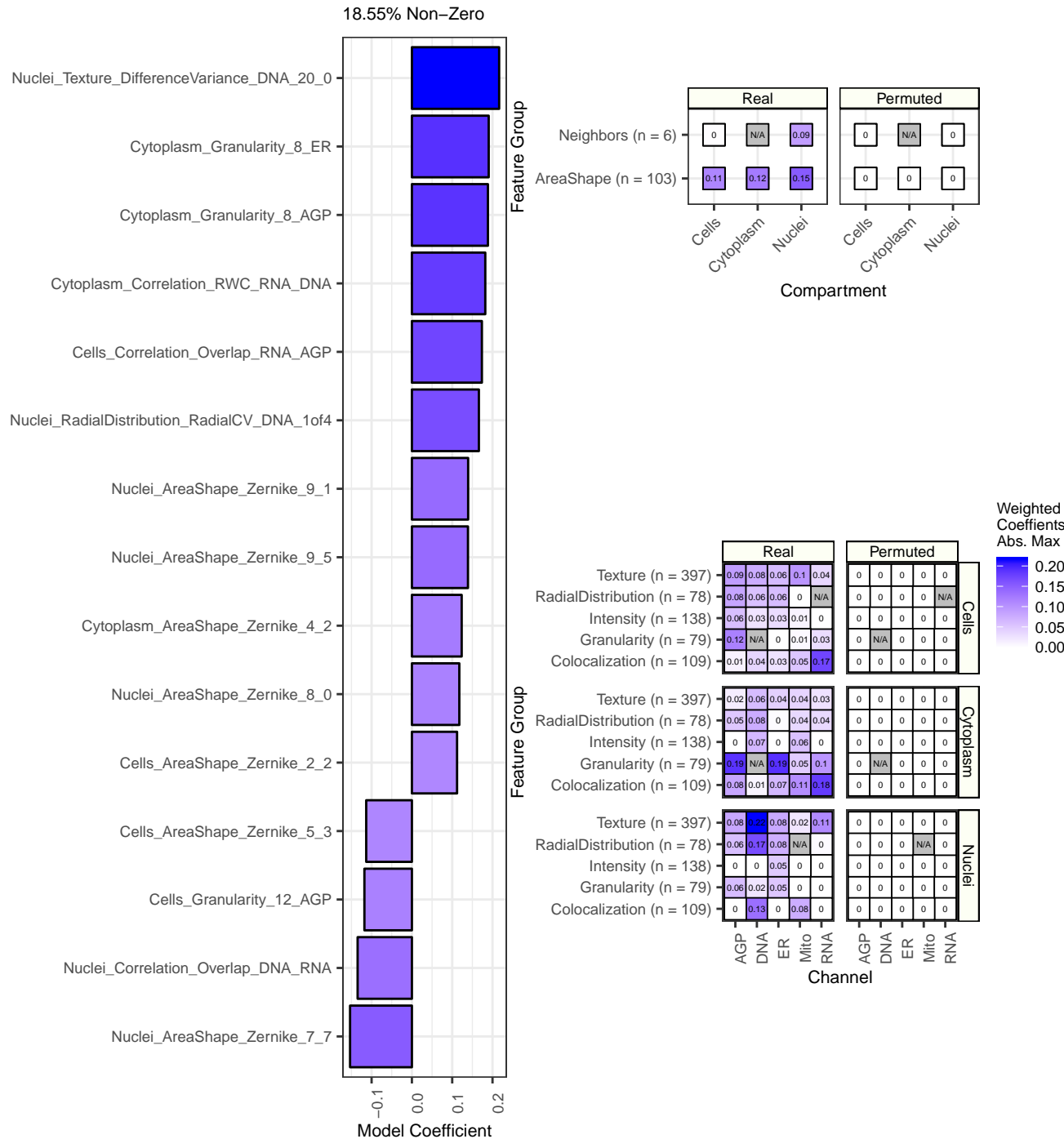
% Late Apoptosis (CASP+; DRAQ7+)



% Live (DRAQ7-; CASP-)



ROS-back



ROS

