ALL – % High gH2AX Spots
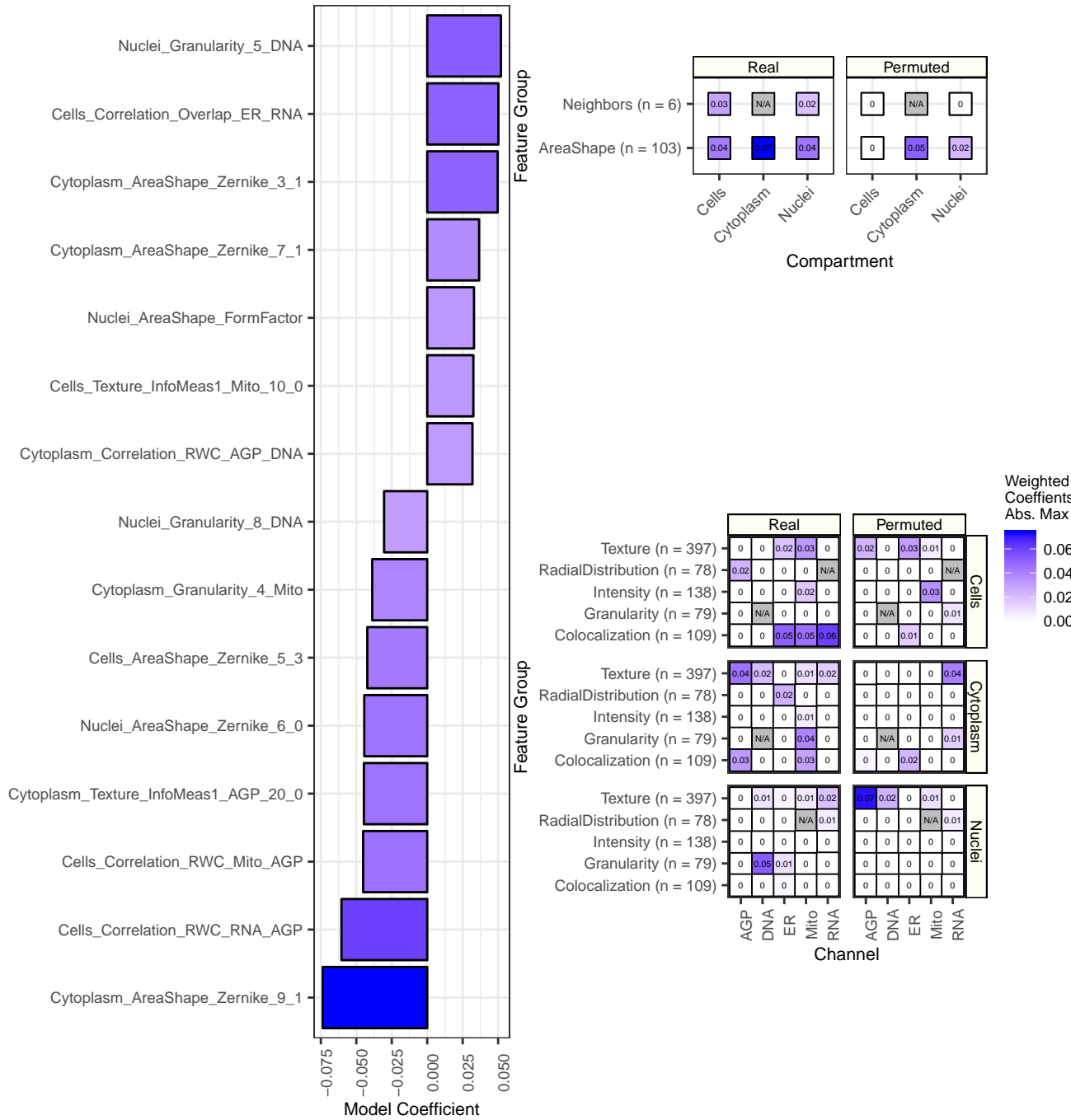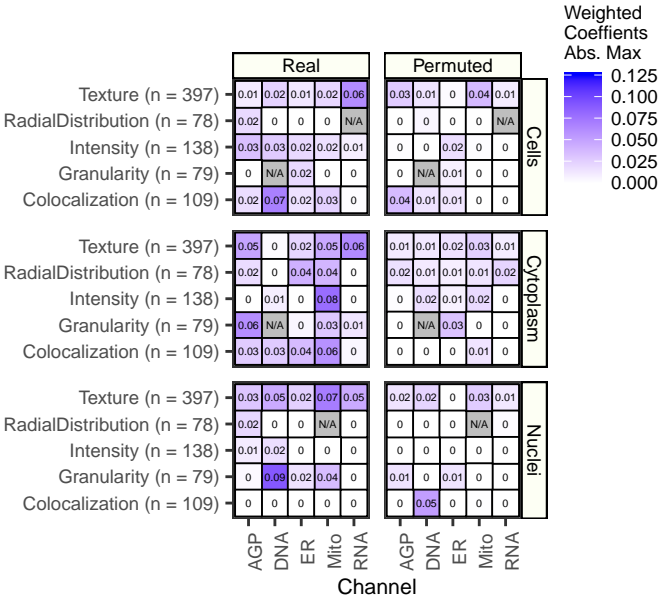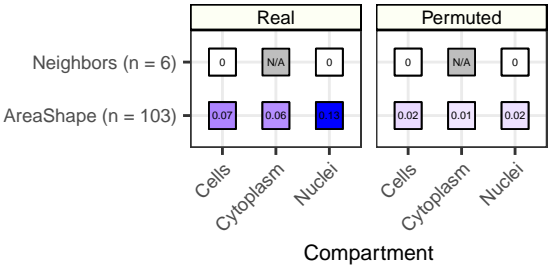

3.69% Non−Zero

ALL – Polynuclear

ALL – Polyploid
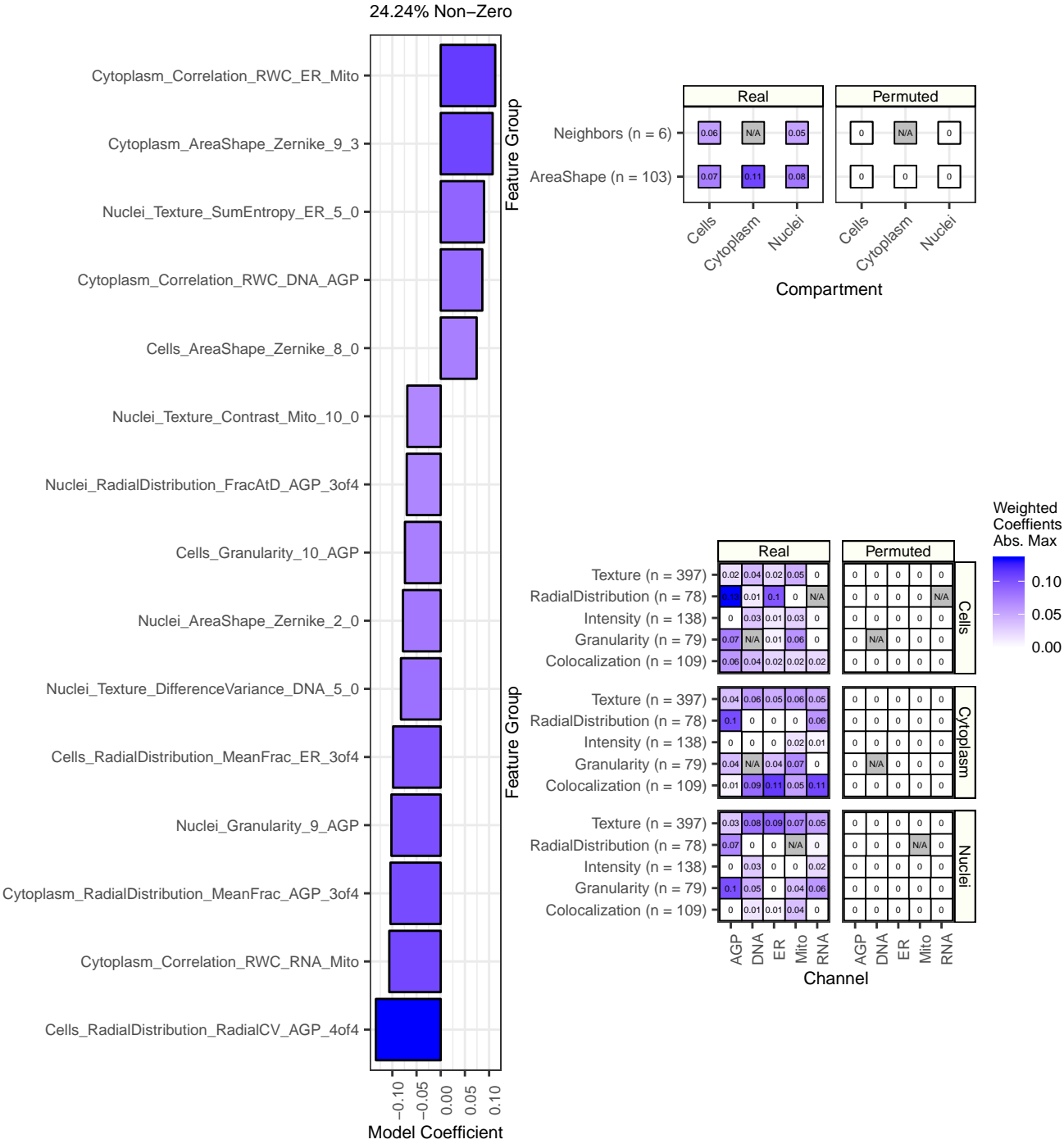
ALL – # cells

8.96% Non–Zero

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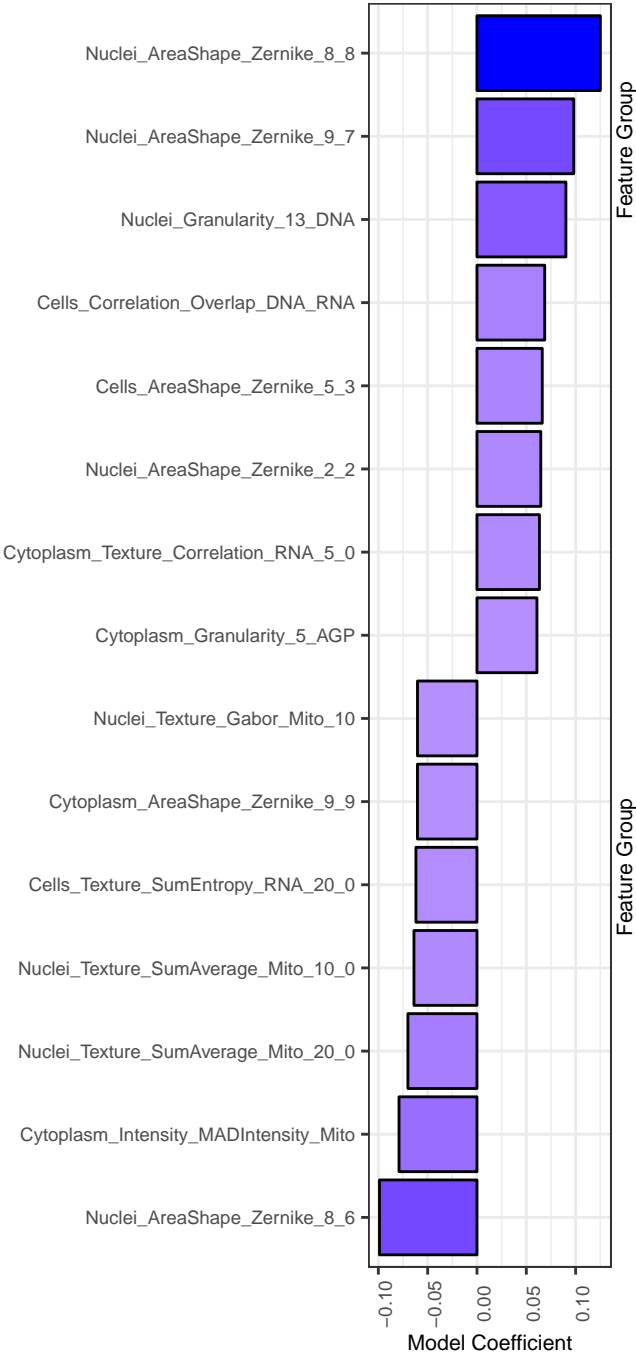
ALL − # of gH2AX Spots per Area of Nucleus
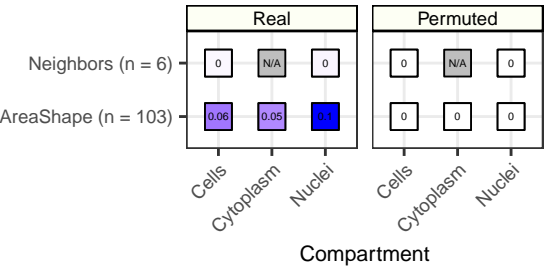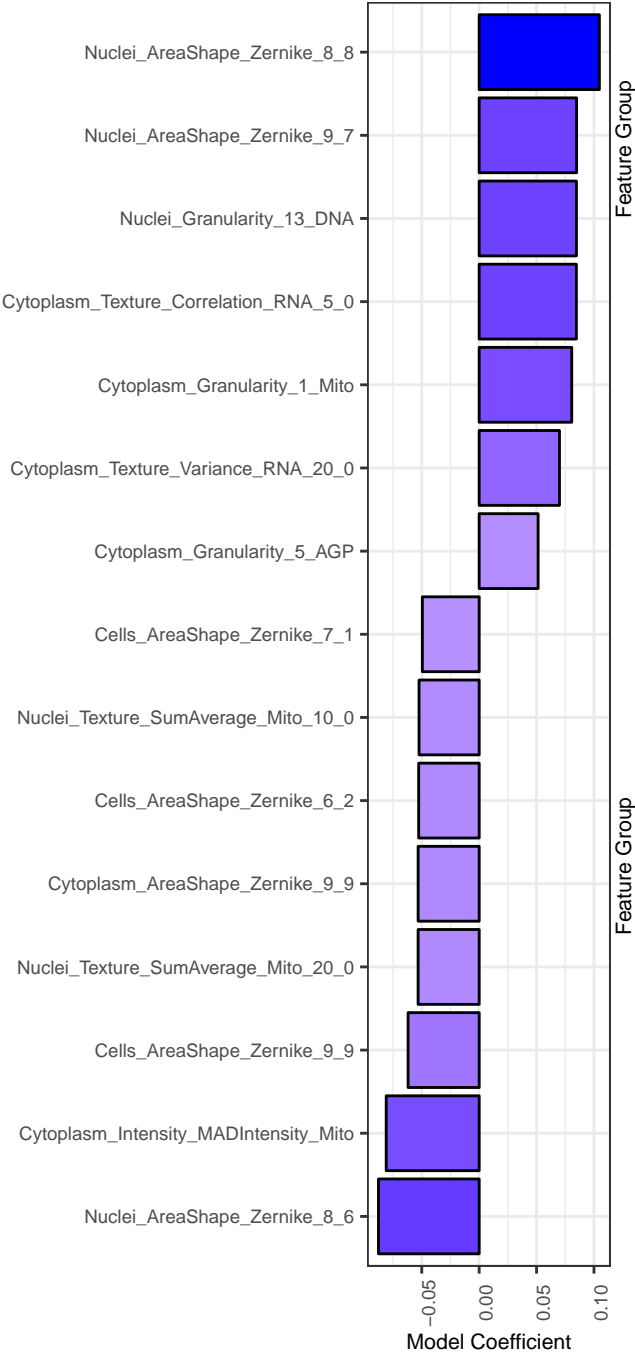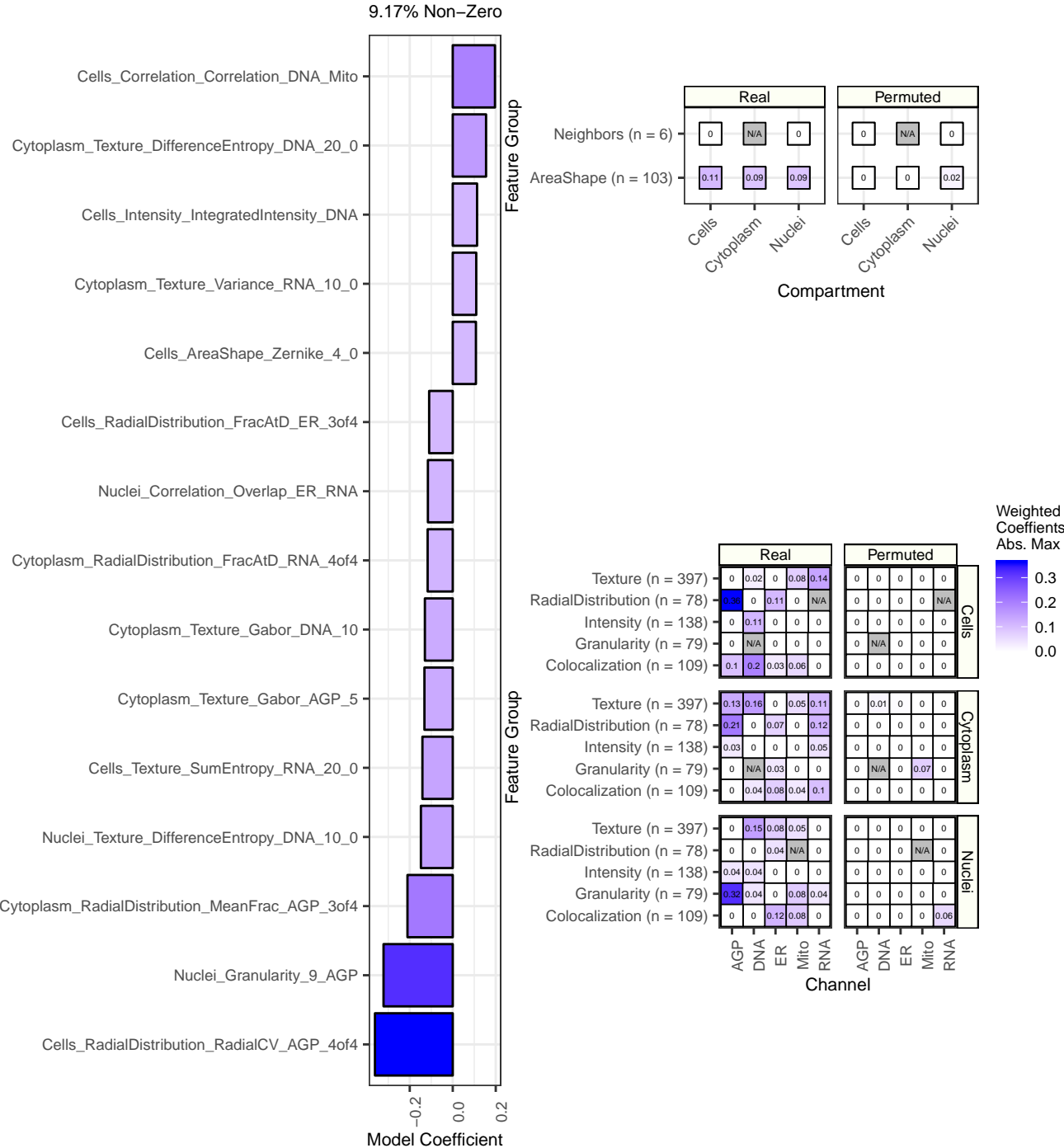
ALL – Nucleus Area

ALL – Nucleus Roundness
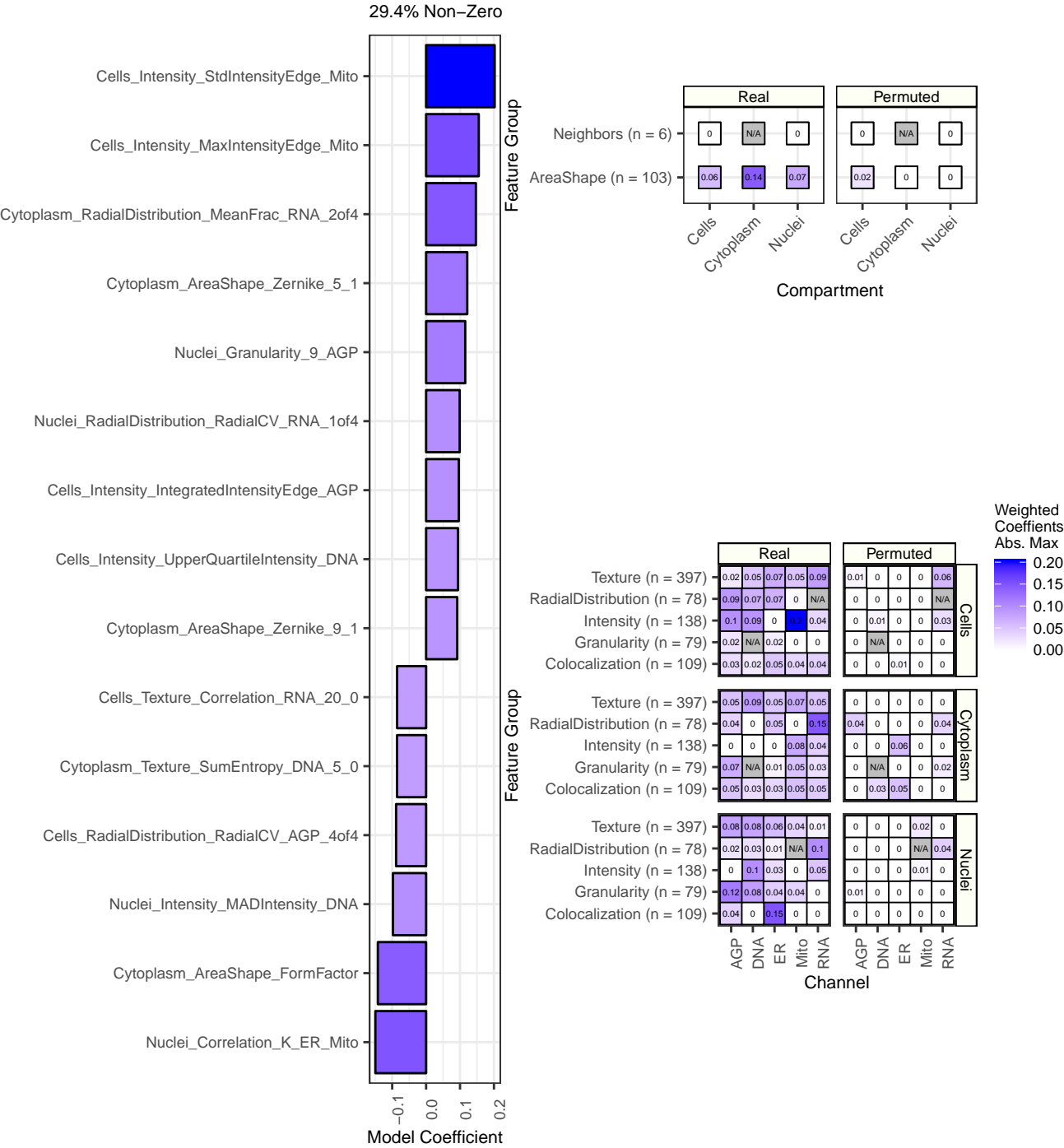
CC – % early M
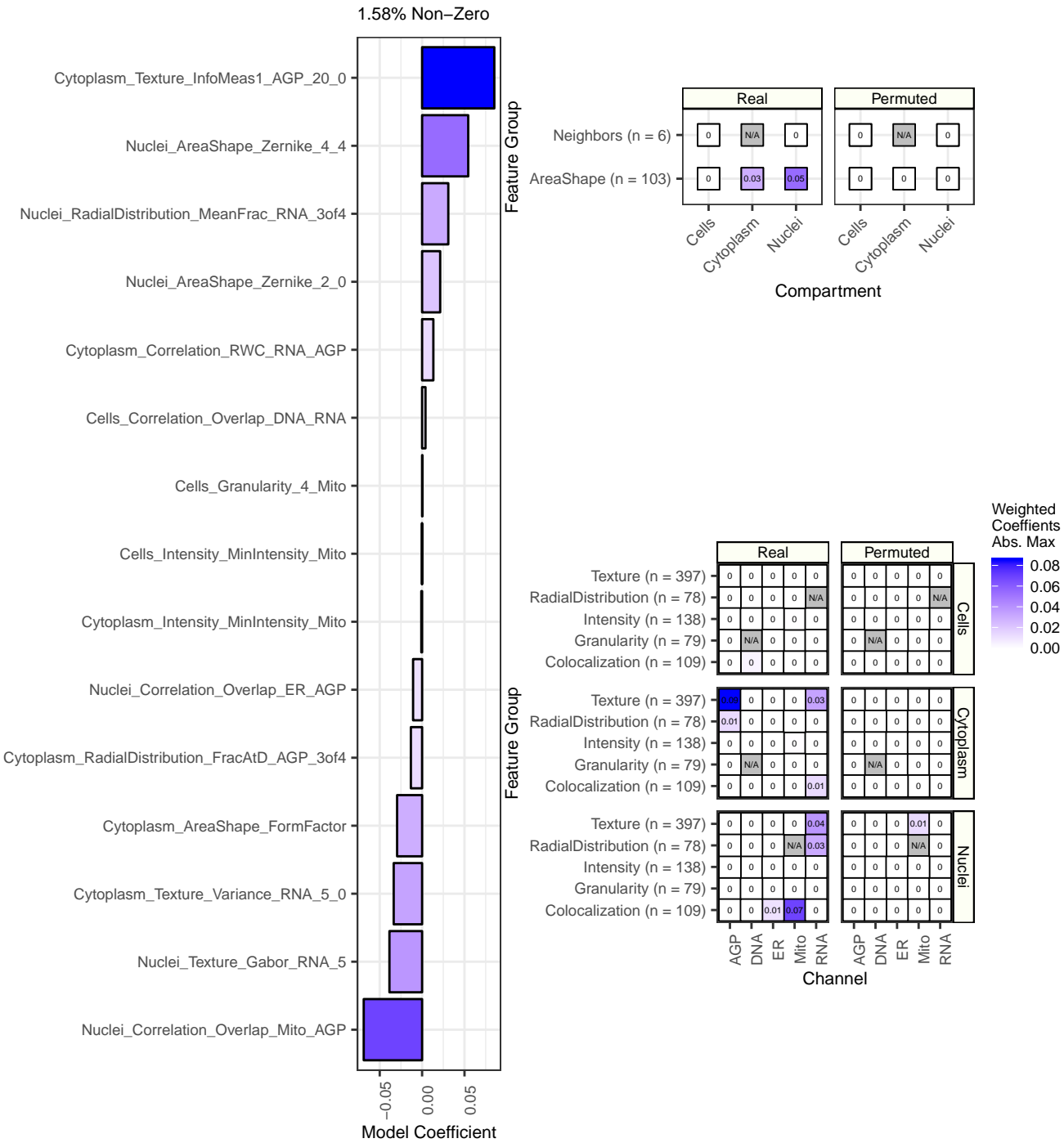
CC – % G1

20.44% Non−Zero

CC − % G2

15.7% Non−Zero
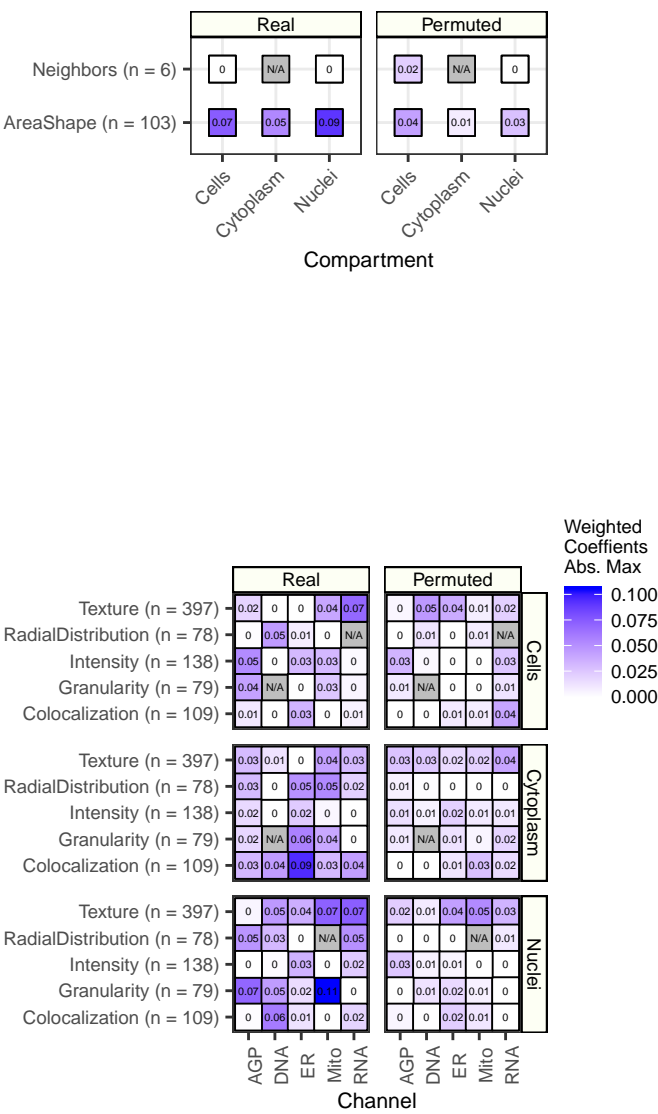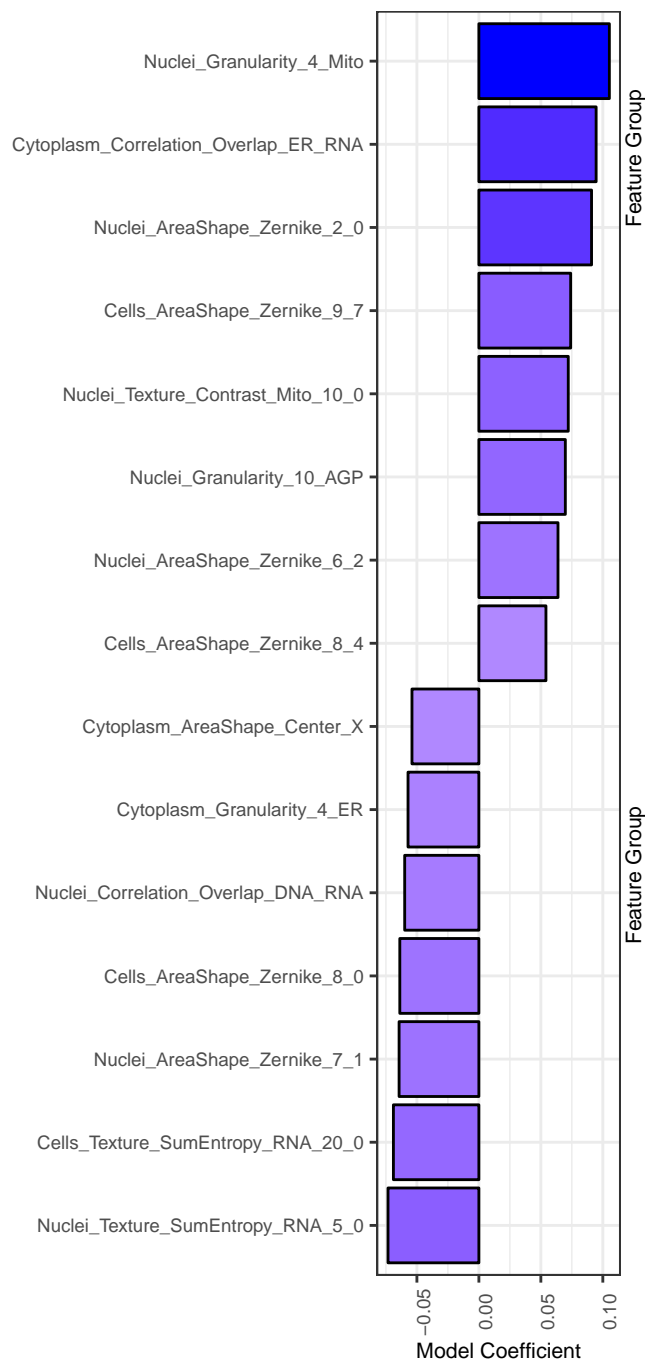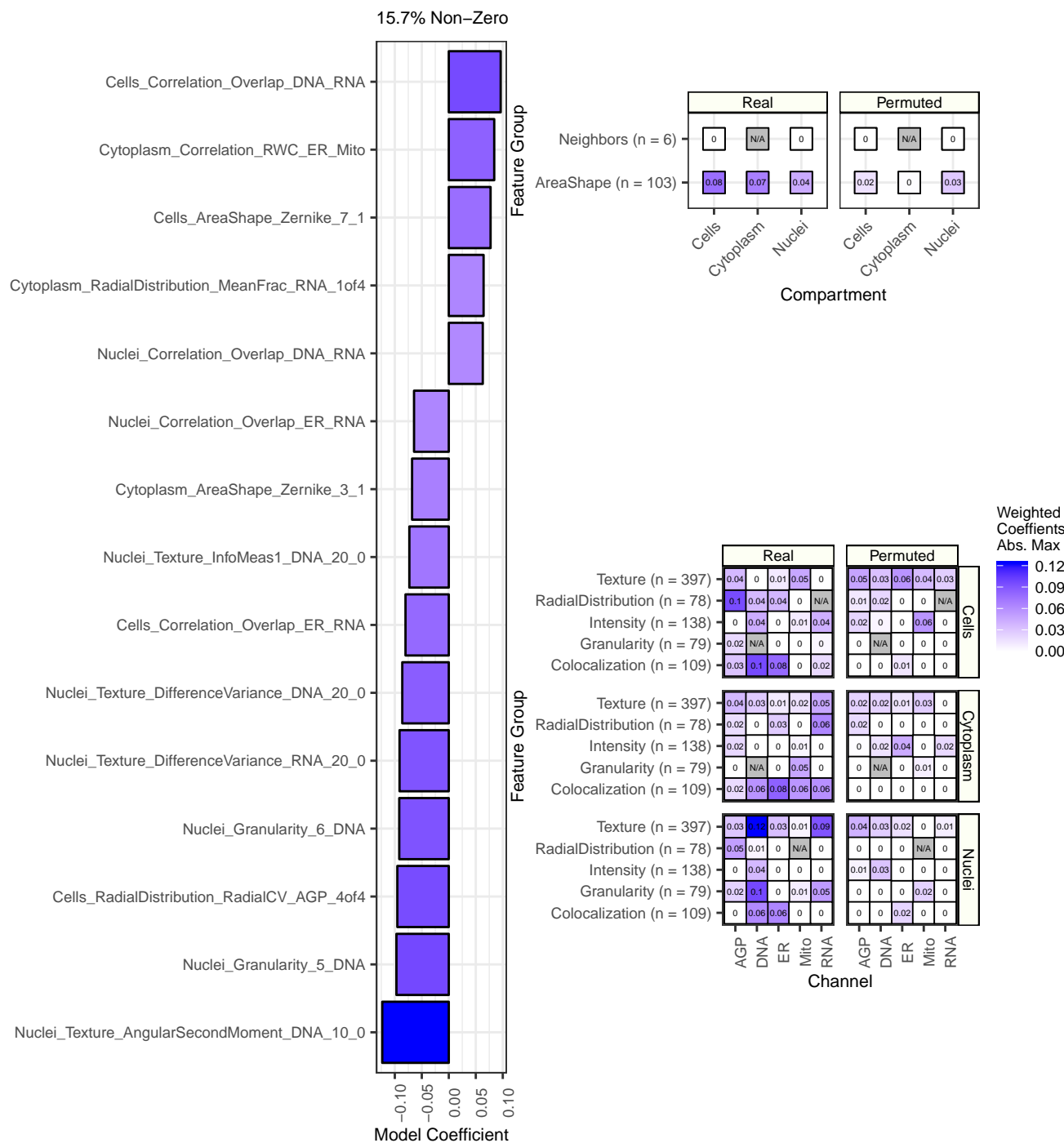
CC − % High gH2AX spots
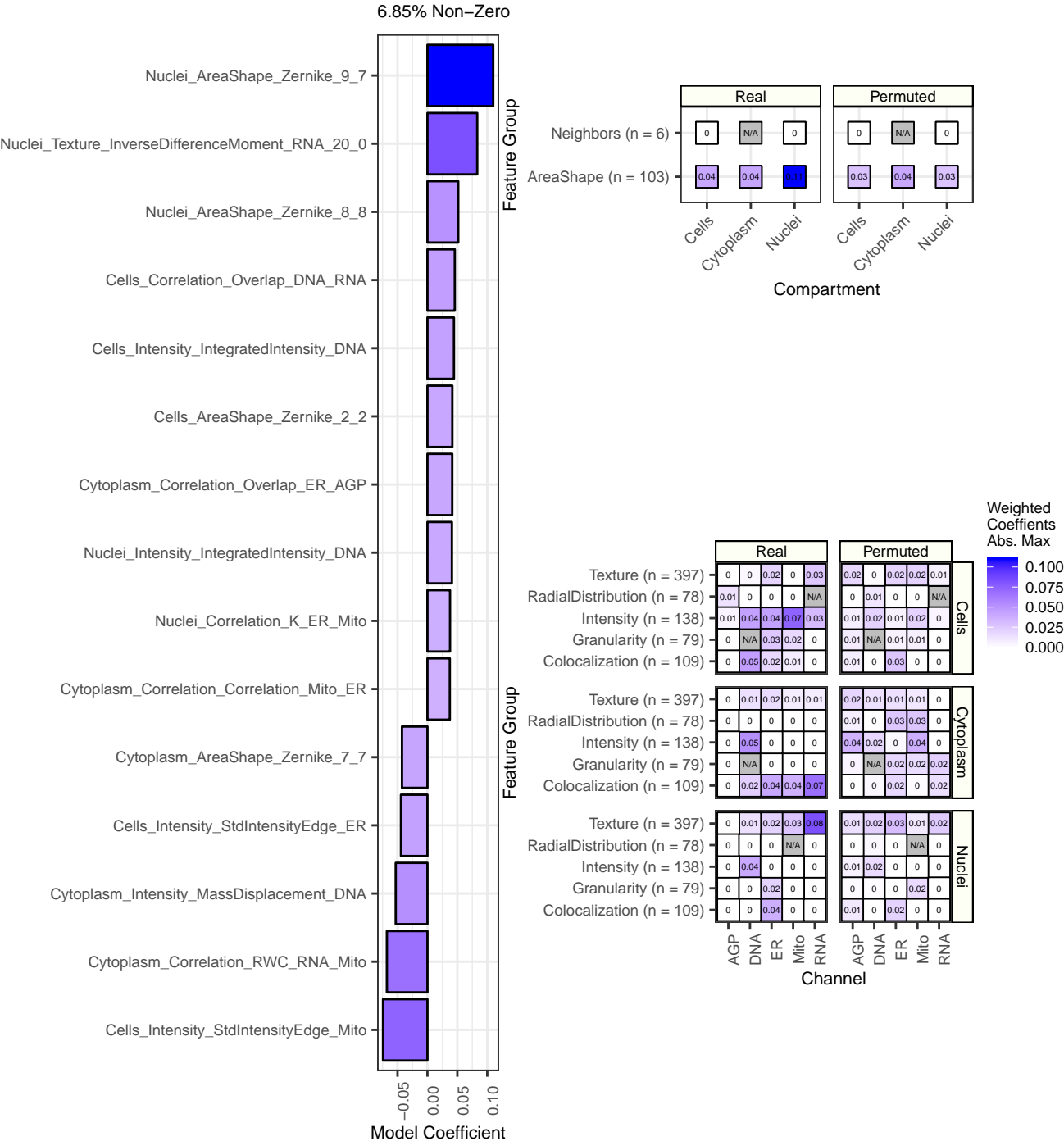
CC – % Late M

CC – % M

CC – # cells

9.27% Non-Zero

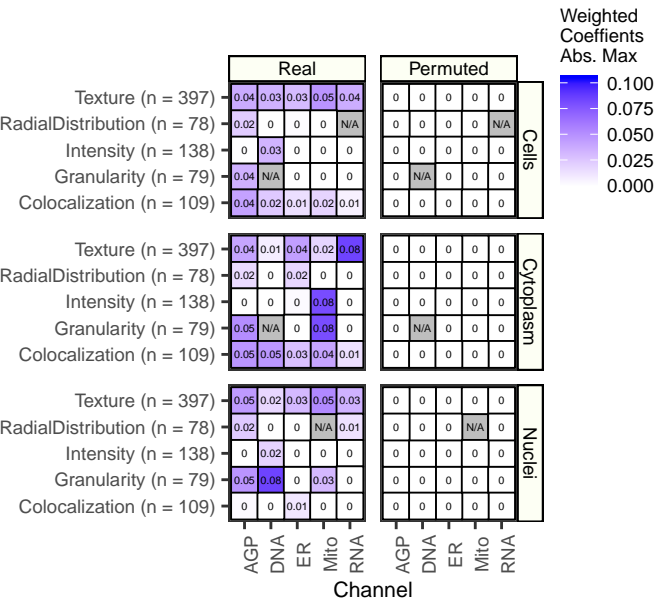# CC – # of gH2AX Spots

6.53% Non−Zero
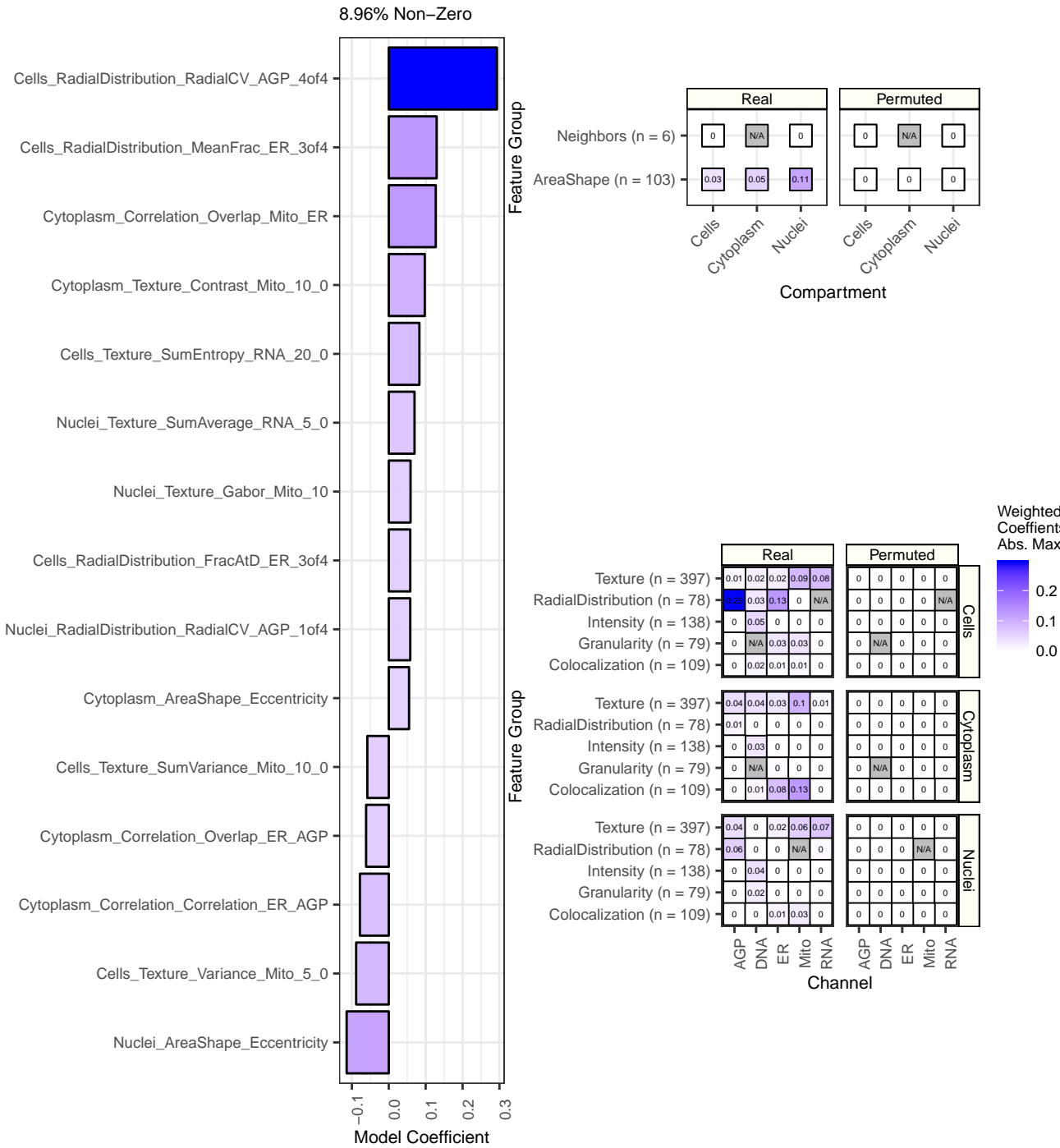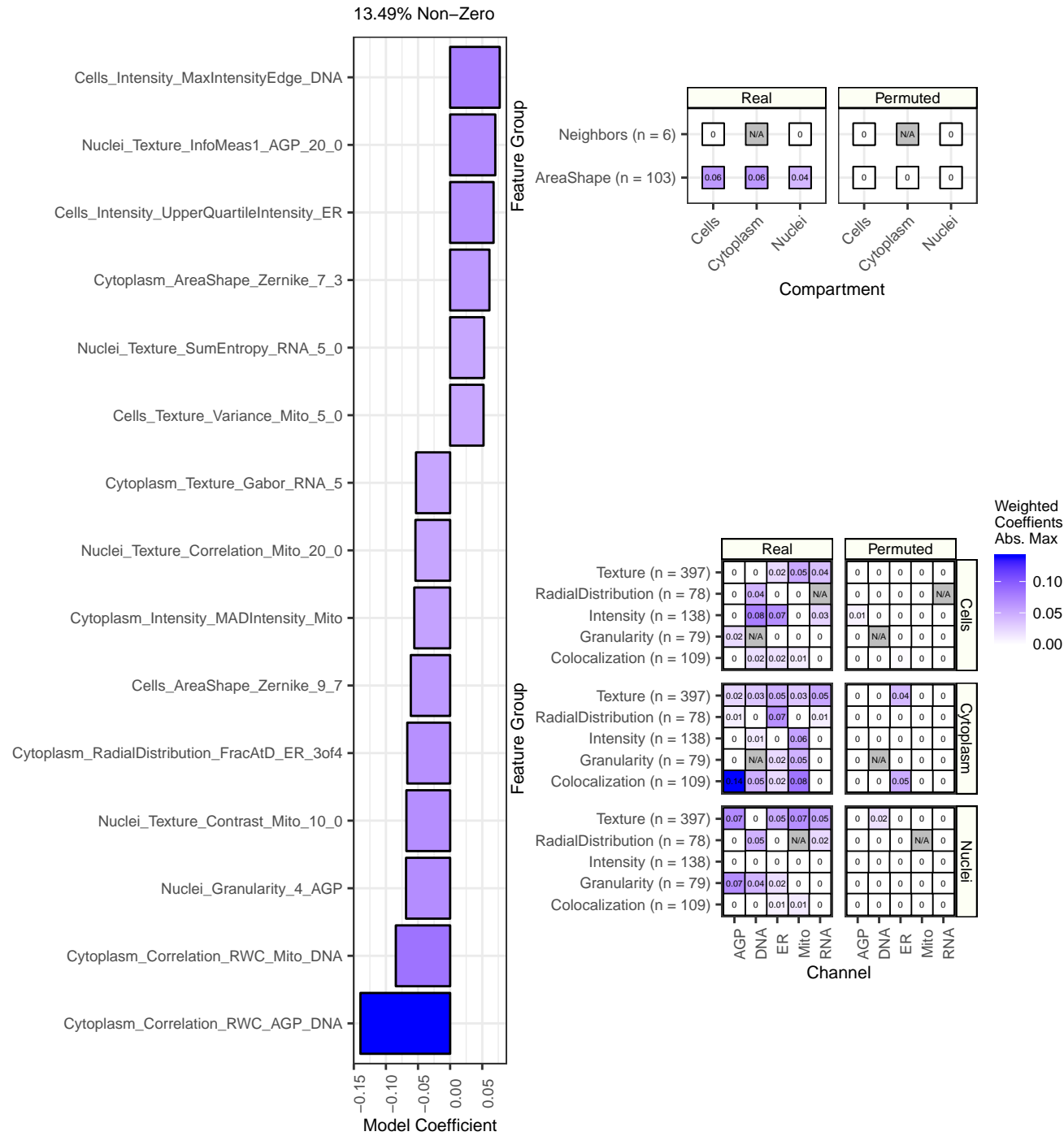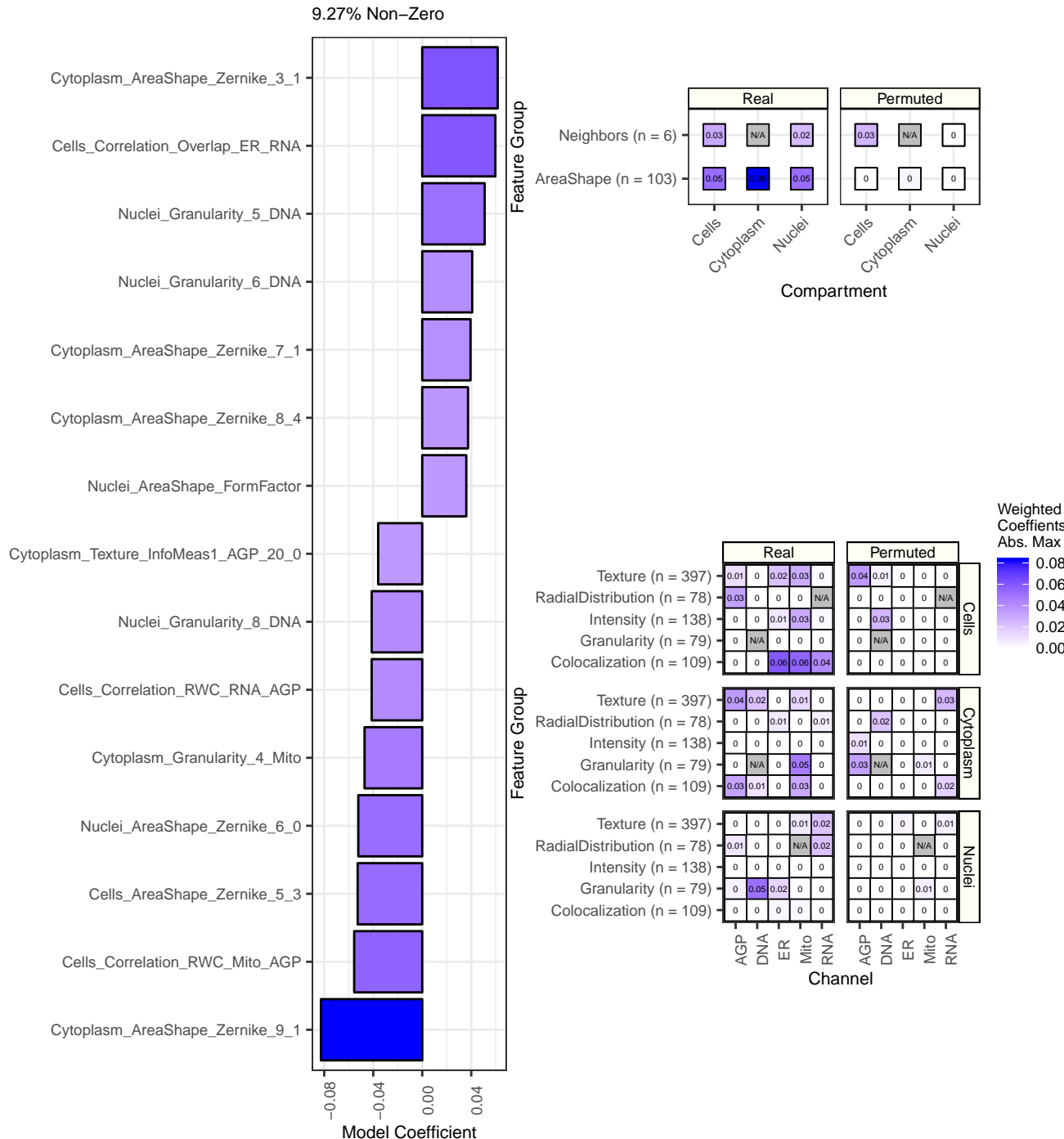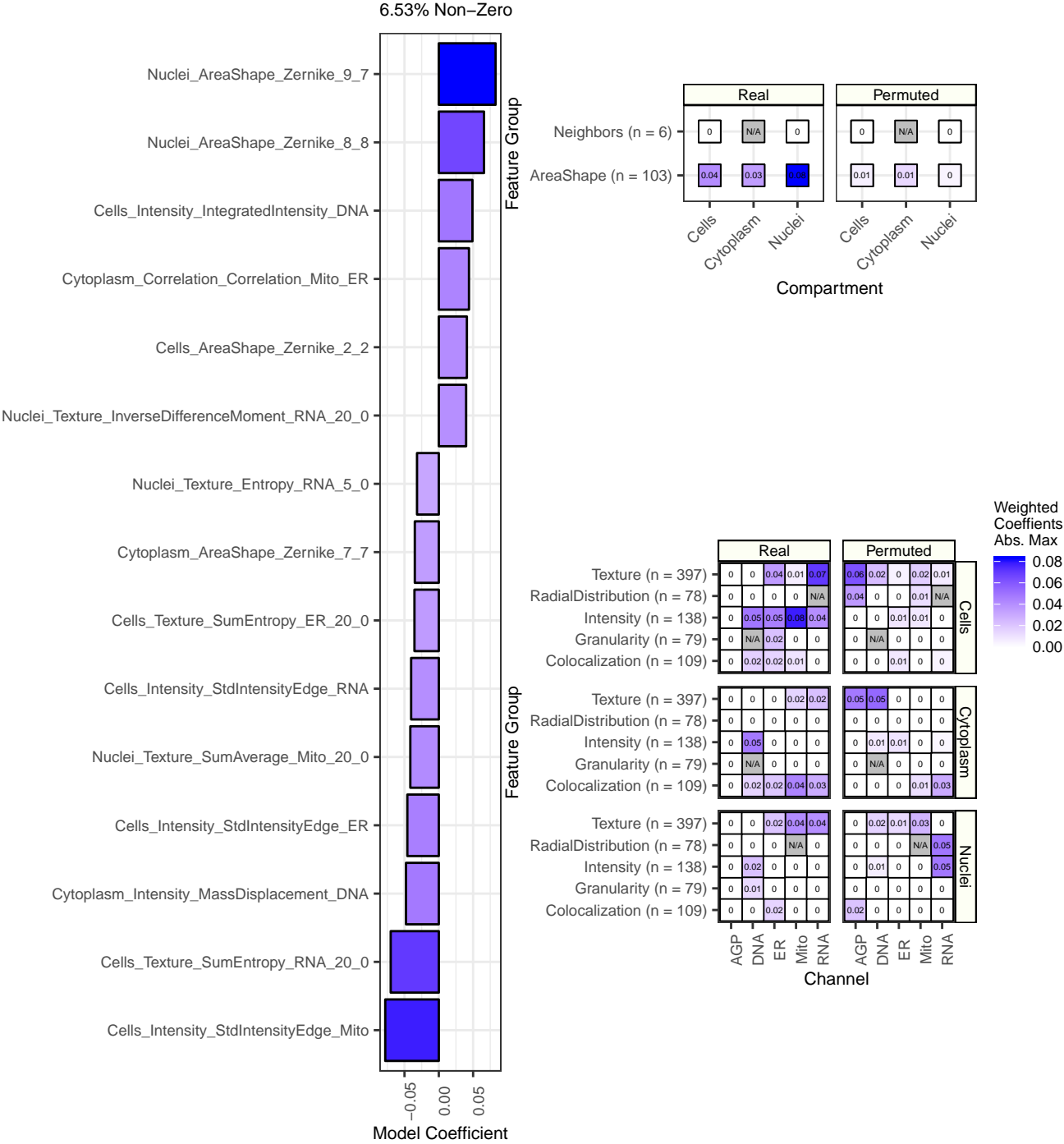
CC – # of gH2AX Spots per Area of Nucleus
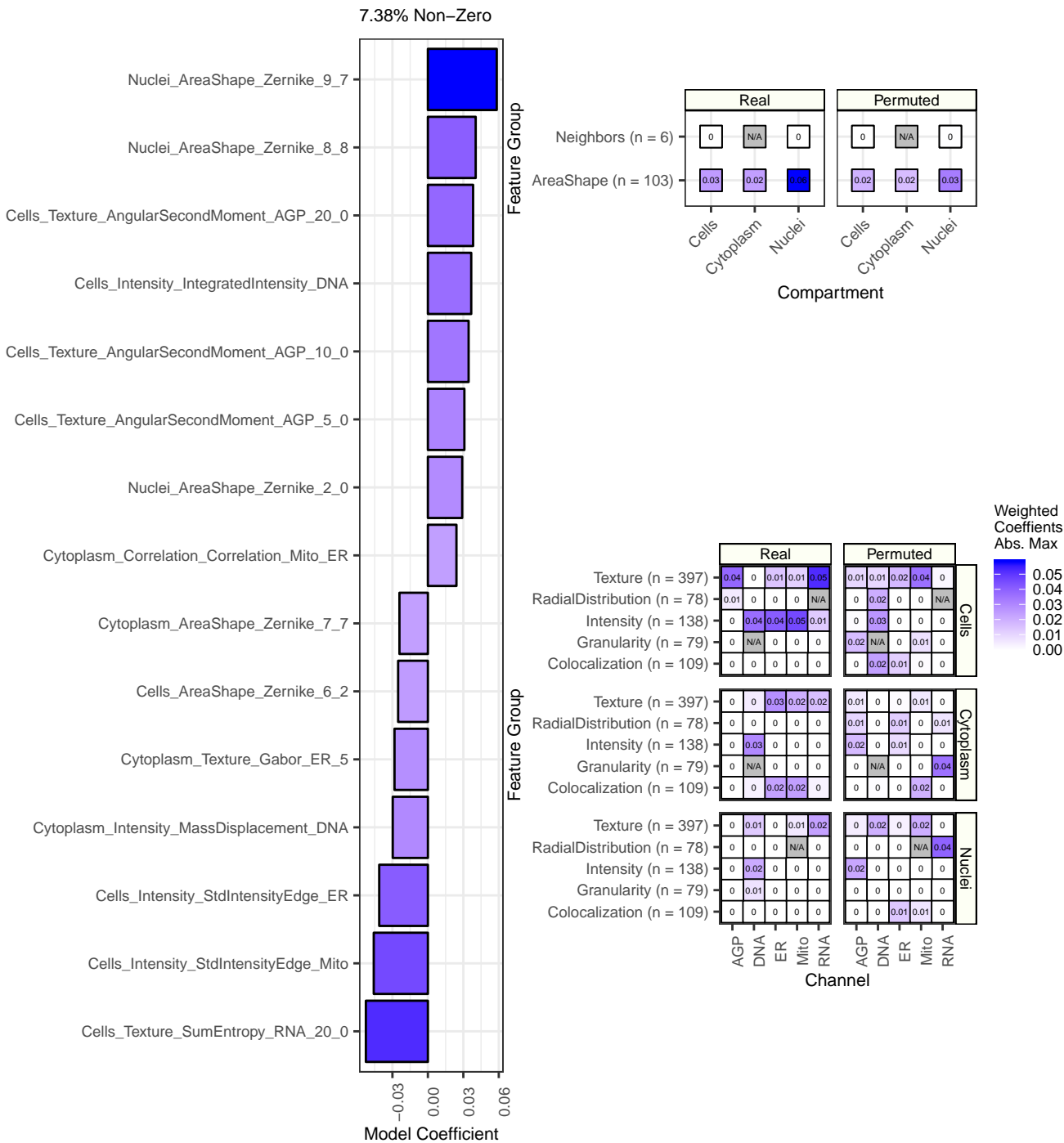
CC − % S
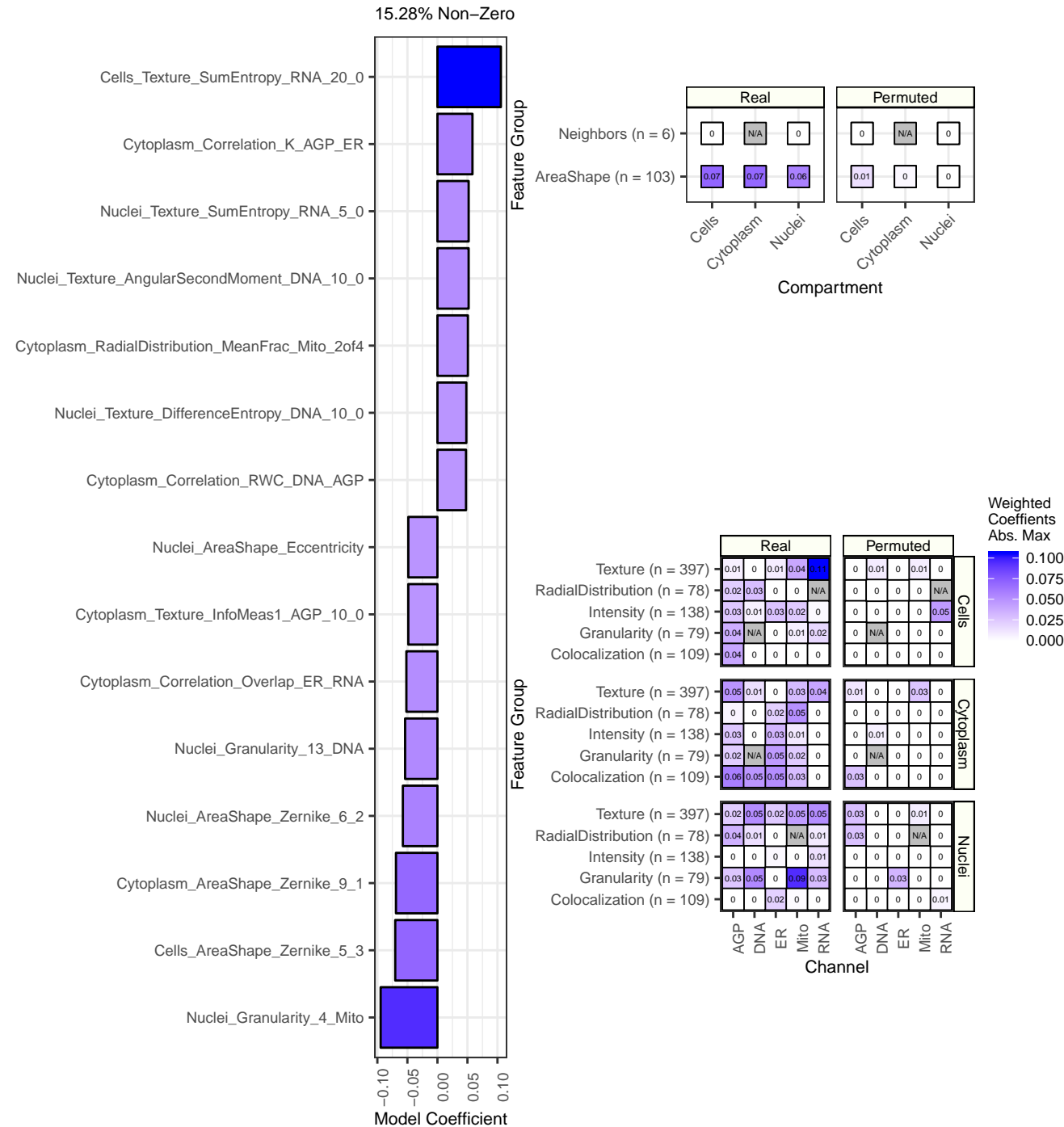
early M – % High gH2AX Spots

early M – # cells

11.91% Non−Zero
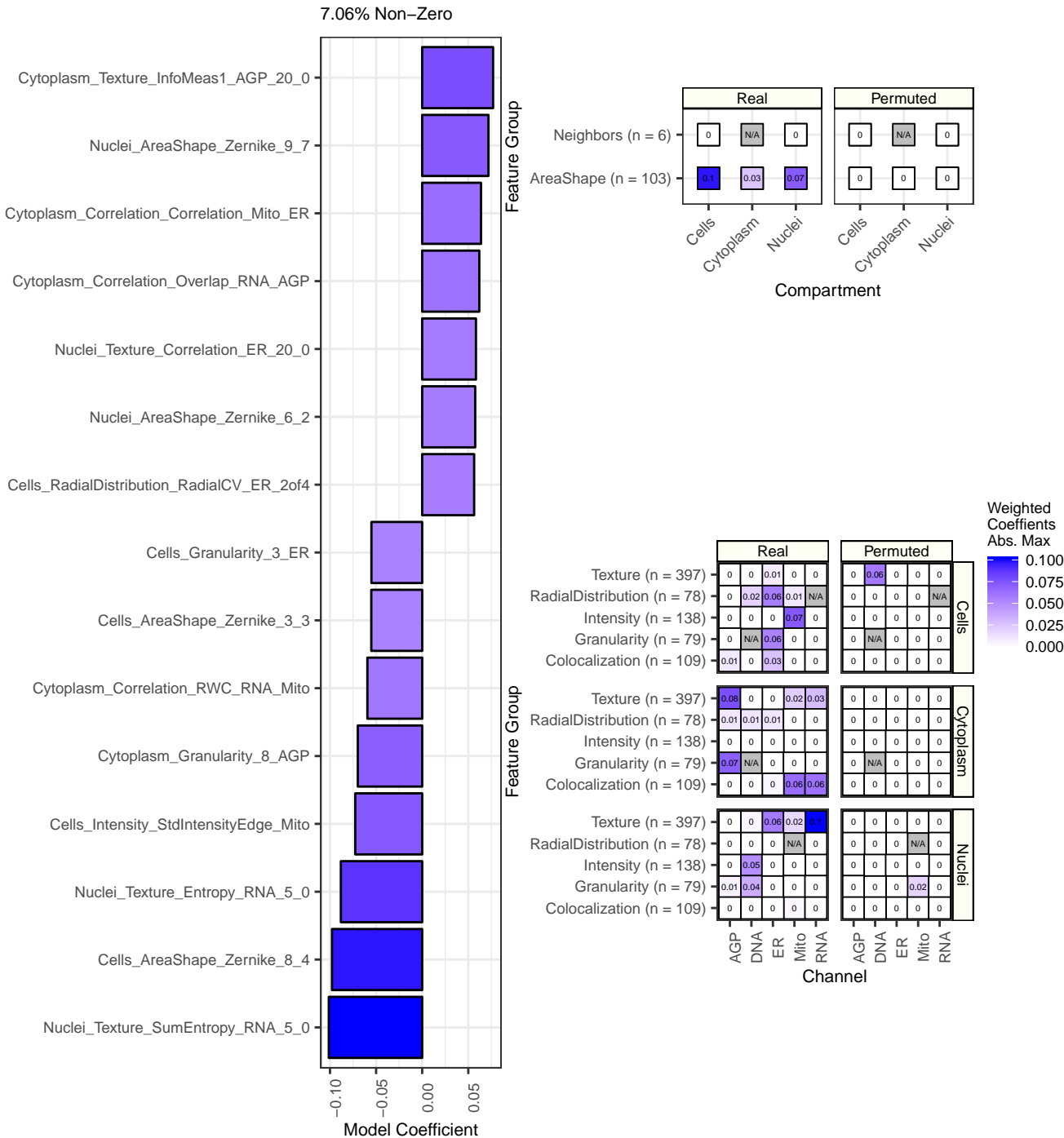
early M – # of gH2AX Spots

early M – # of gH2AX Spots per Area of Nucleus
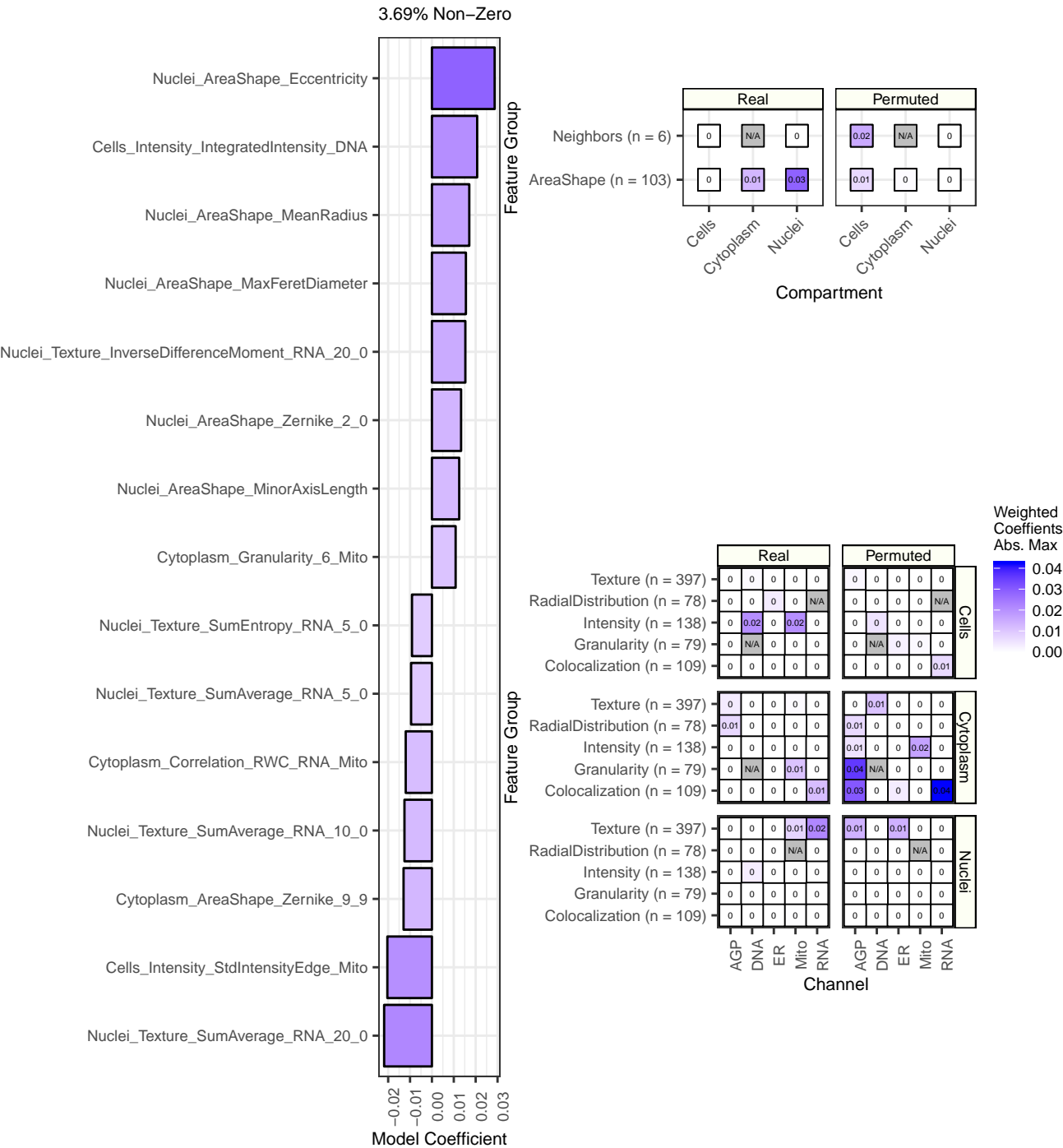
G1 – % High gH2AX Spots
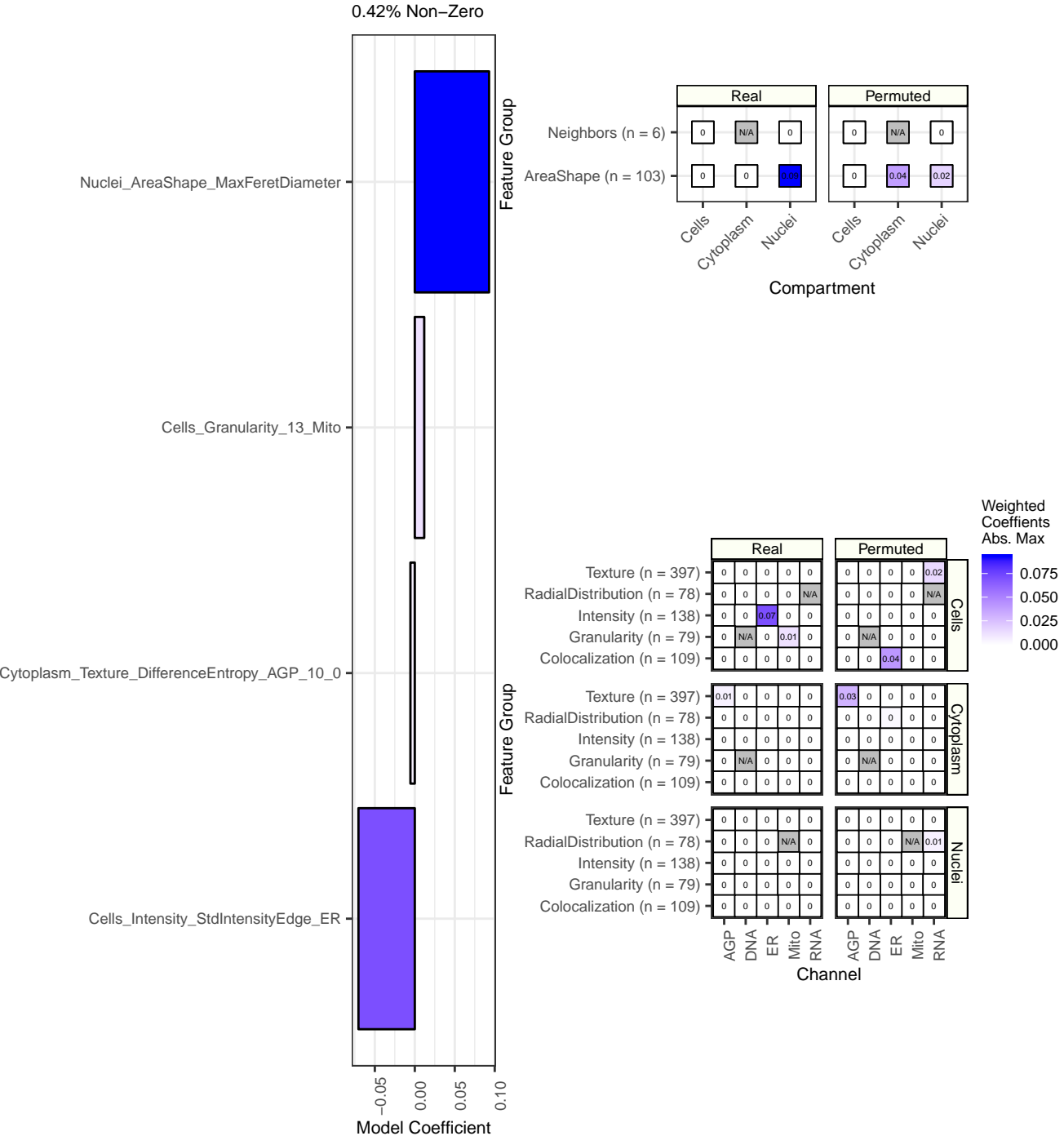
G1 − # cells

G1 – # of gH2AX Spots

G1 – # of gH2AX Spots per Area of Nucleus

Cell Count – G1+G2

Cell Count – G2/G1

G2 – % High gH2AX Spots

4.85% Non−Zero

G2 − # cells

G2 – # of gH2AX Spots
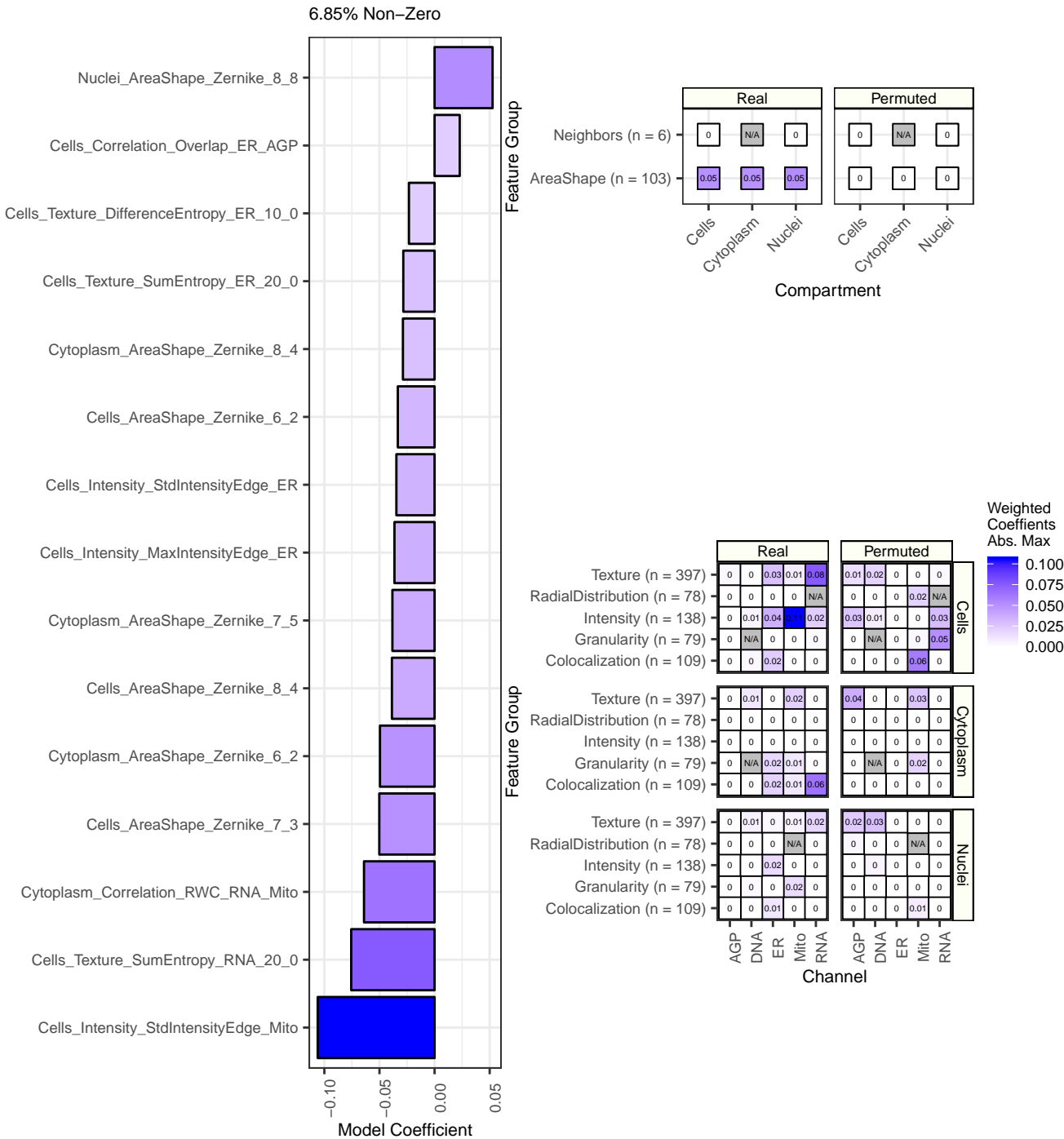
G2 – # of gH2AX Spots per Area of Nucleus

Cell Count − G2 + M

16.54% Non−Zero
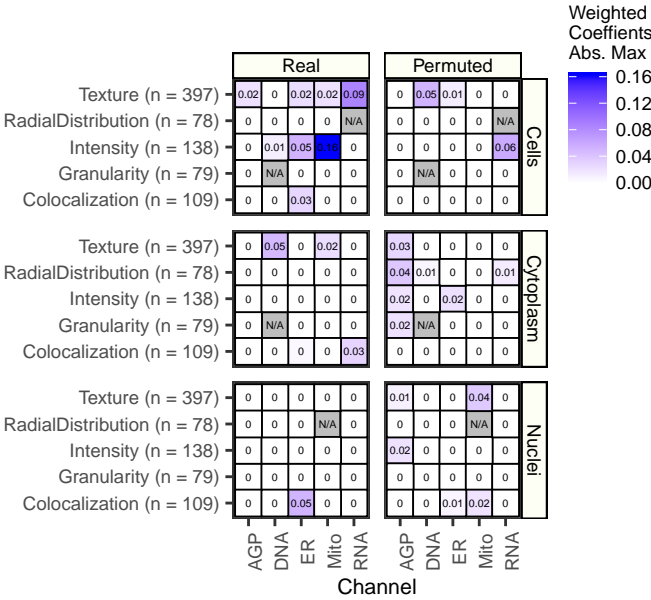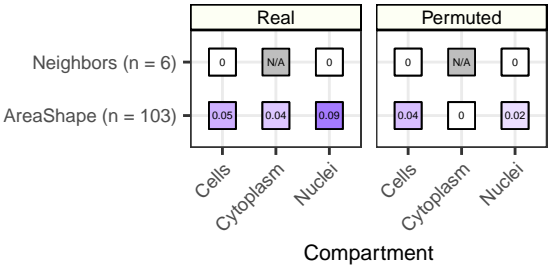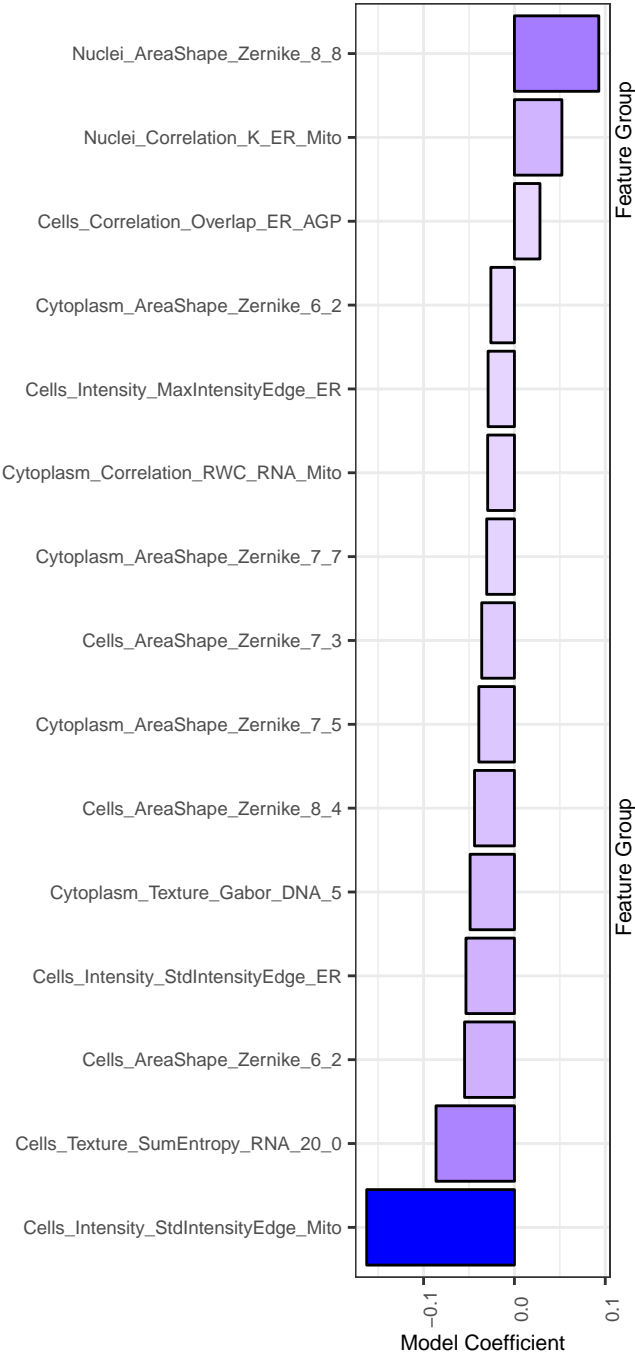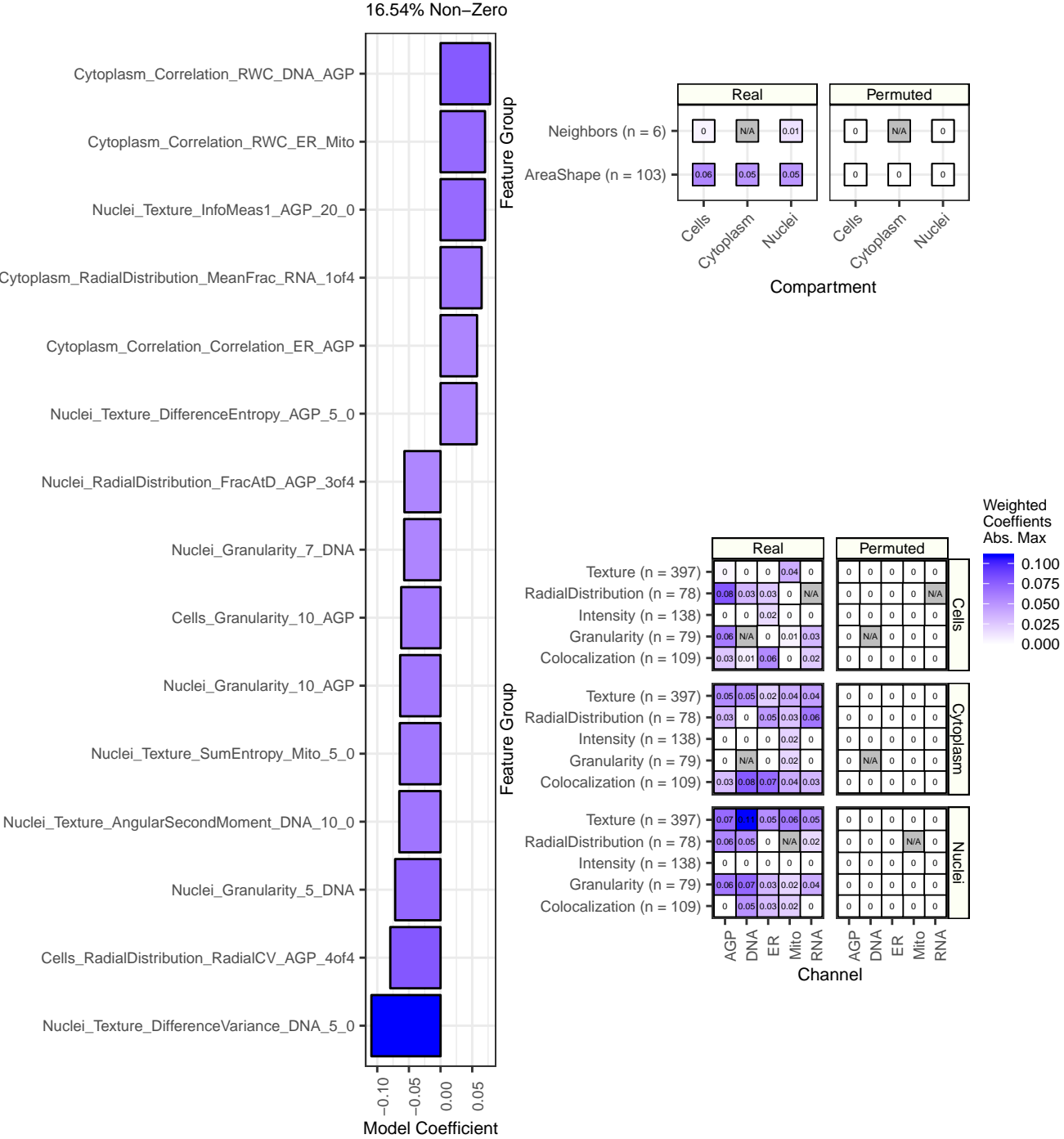
CC – Infection Efficiency

Late M – % High gH2AX Spots

0% Non−Zero

Feature Group

	Real			Permuted		
Neighbors (n = 6)	0	N/A	0	0	N/A	0
AreaShape (n = 103)	0	0	0	0	0	0
	Cells	Cytoplasm	Nuclei	Cells	Cytoplasm	Nuclei

Compartment

Weighted
Coeffients
Abs. Max

0

Feature Group

Real / Permuted — Cells

|	Real					Permuted				
Texture (n = 397)	0	0	0	0	0	0	0	0	0	0
RadialDistribution (n = 78)	0	0	0	0	N/A	0	0	0	0	N/A
Intensity (n = 138)	0	0	0	0	0	0	0	0	0	0
Granularity (n = 79)	0	N/A	0	0	0	0	N/A	0	0	0
Colocalization (n = 109)	0	0	0	0	0	0	0	0	0	0

Cytoplasm

	Real					Permuted				
Texture (n = 397)	0	0	0	0	0	0	0	0	0	0
RadialDistribution (n = 78)	0	0	0	0	0	0	0	0	0	0
Intensity (n = 138)	0	0	0	0	0	0	0	0	0	0
Granularity (n = 79)	0	N/A	0	0	0	0	N/A	0	0	0
Colocalization (n = 109)	0	0	0	0	0	0	0	0	0	0

Nuclei

	Real					Permuted				
Texture (n = 397)	0	0	0	0	0	0	0	0	0	0
RadialDistribution (n = 78)	0	0	0	N/A	0	0	0	0	N/A	0
Intensity (n = 138)	0	0	0	0	0	0	0	0	0	0
Granularity (n = 79)	0	0	0	0	0	0	0	0	0	0
Colocalization (n = 109)	0	0	0	0	0	0	0	0	0	0

| AGP | DNA | ER | Mito | RNA | AGP | DNA | ER | Mito | RNA |

Channel

Model Coefficient

Late M – # cells

7.59% Non−Zero

Late M – # of gH2AX Spots

0.84% Non−Zero

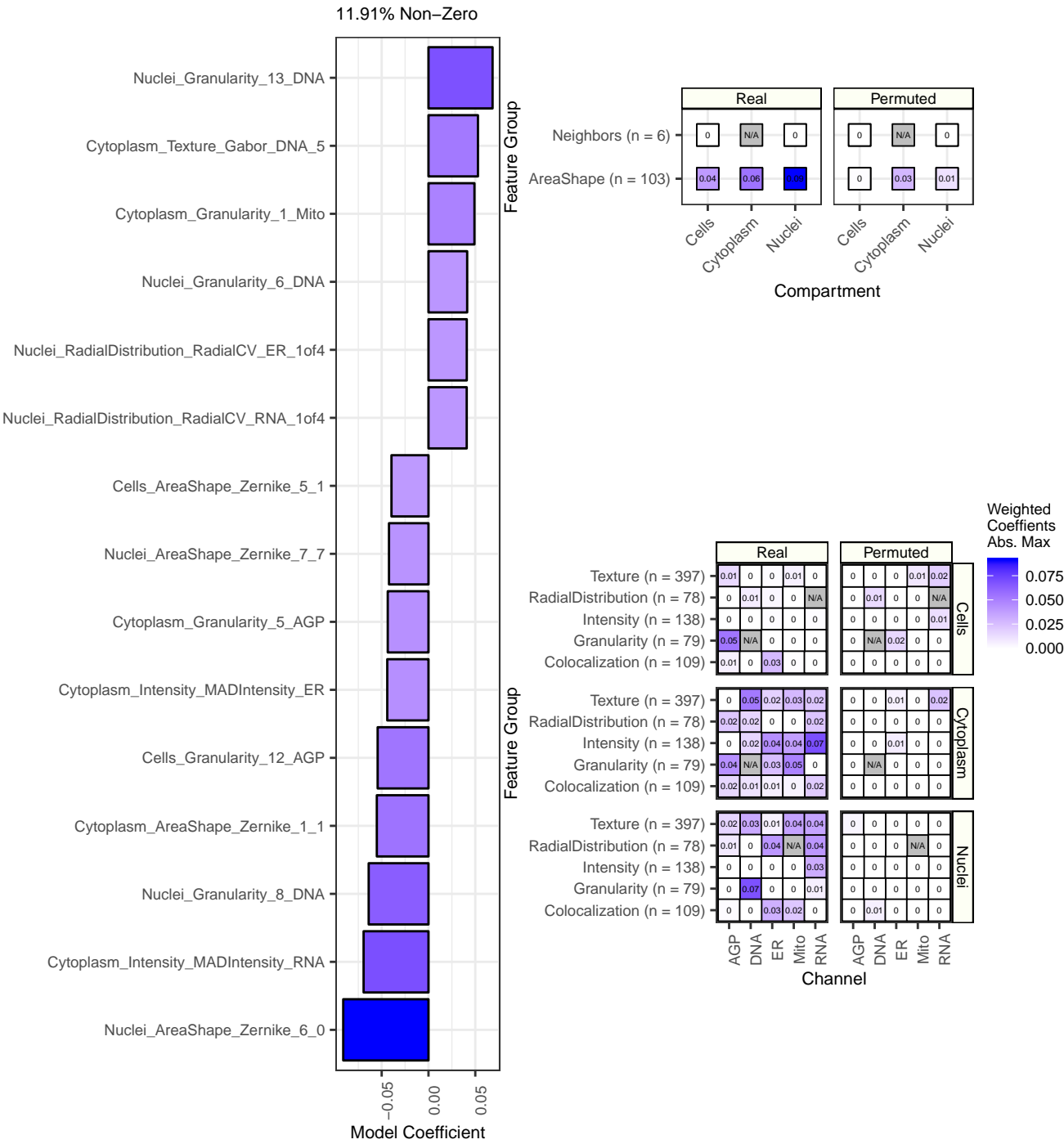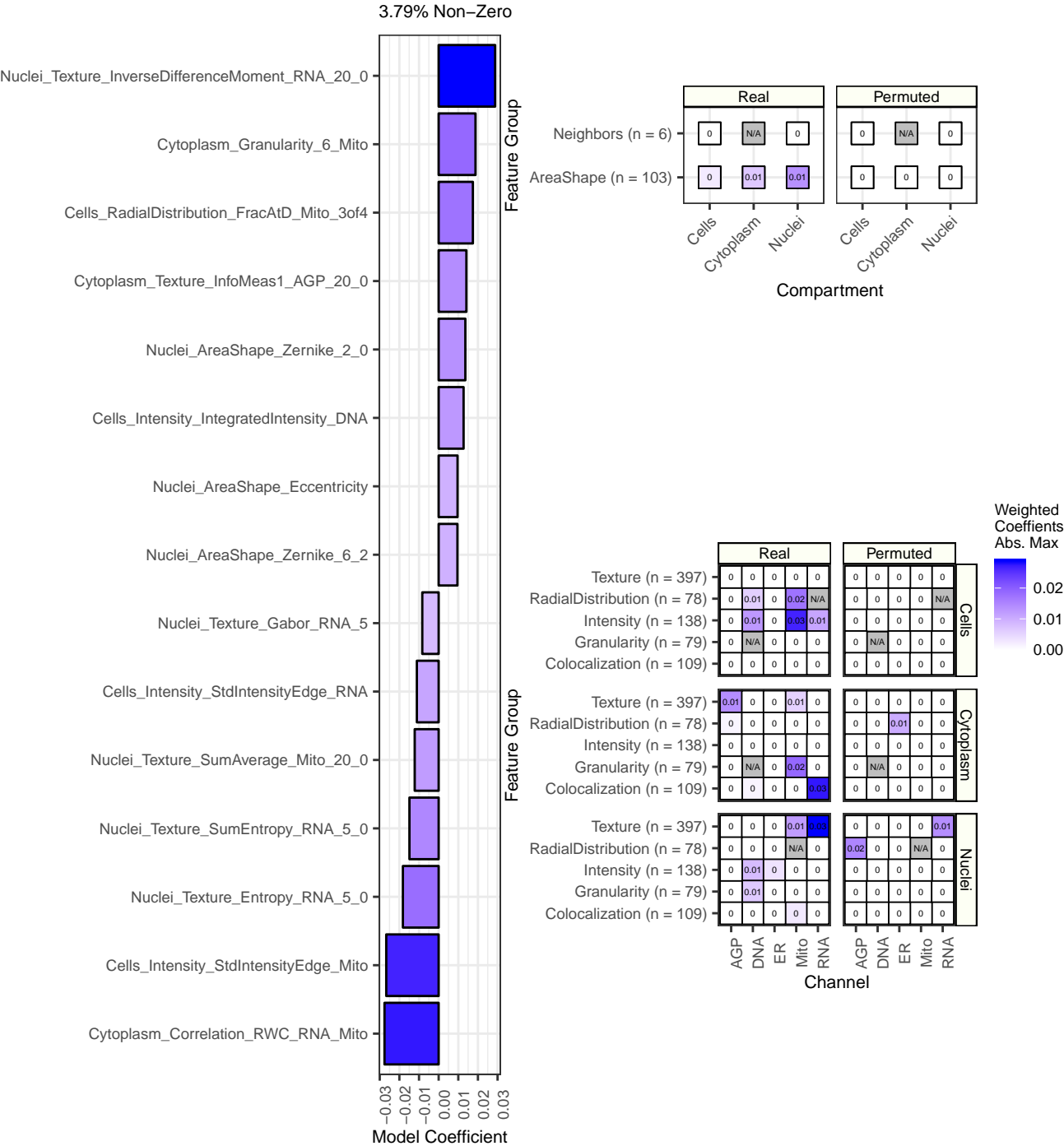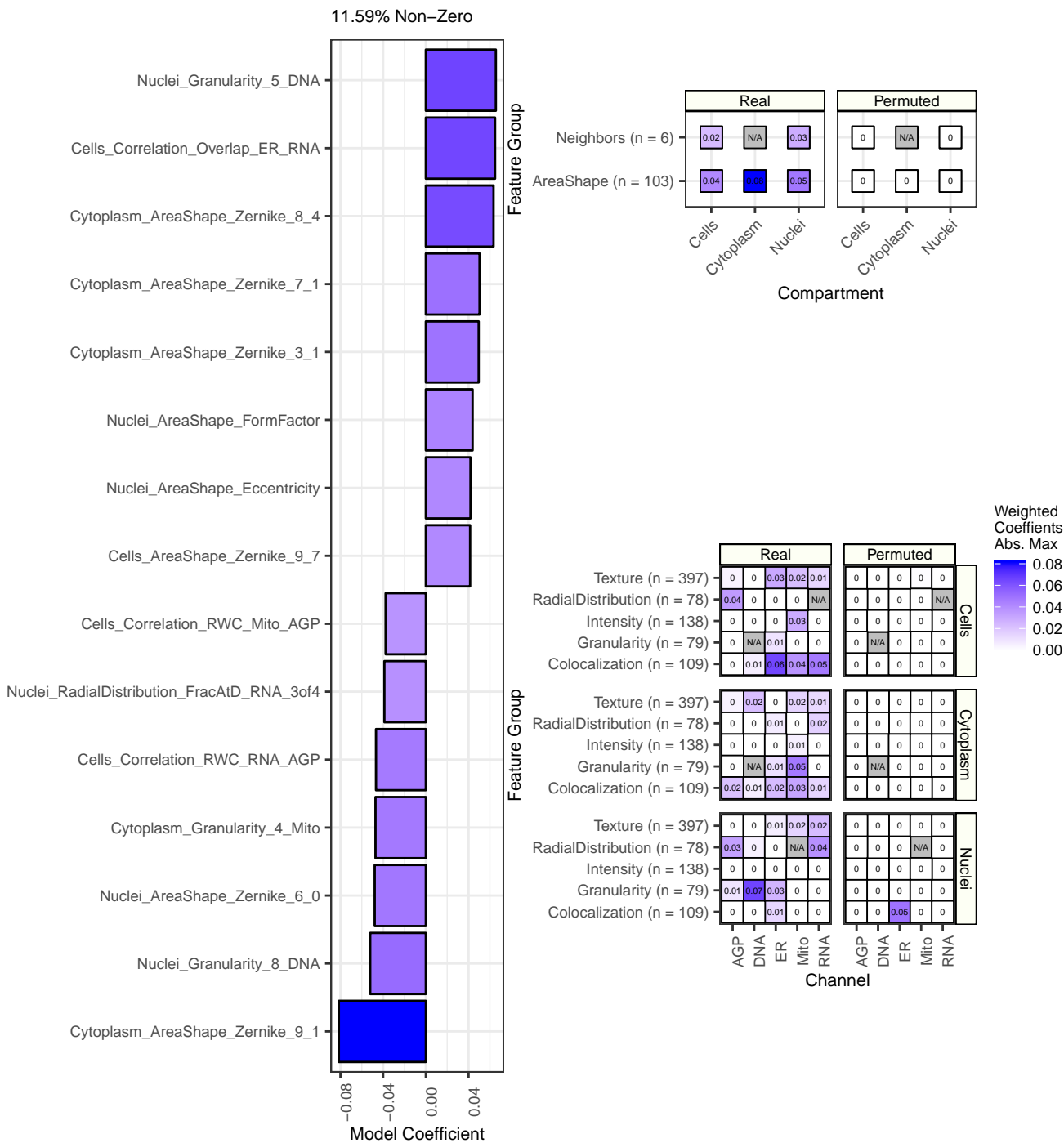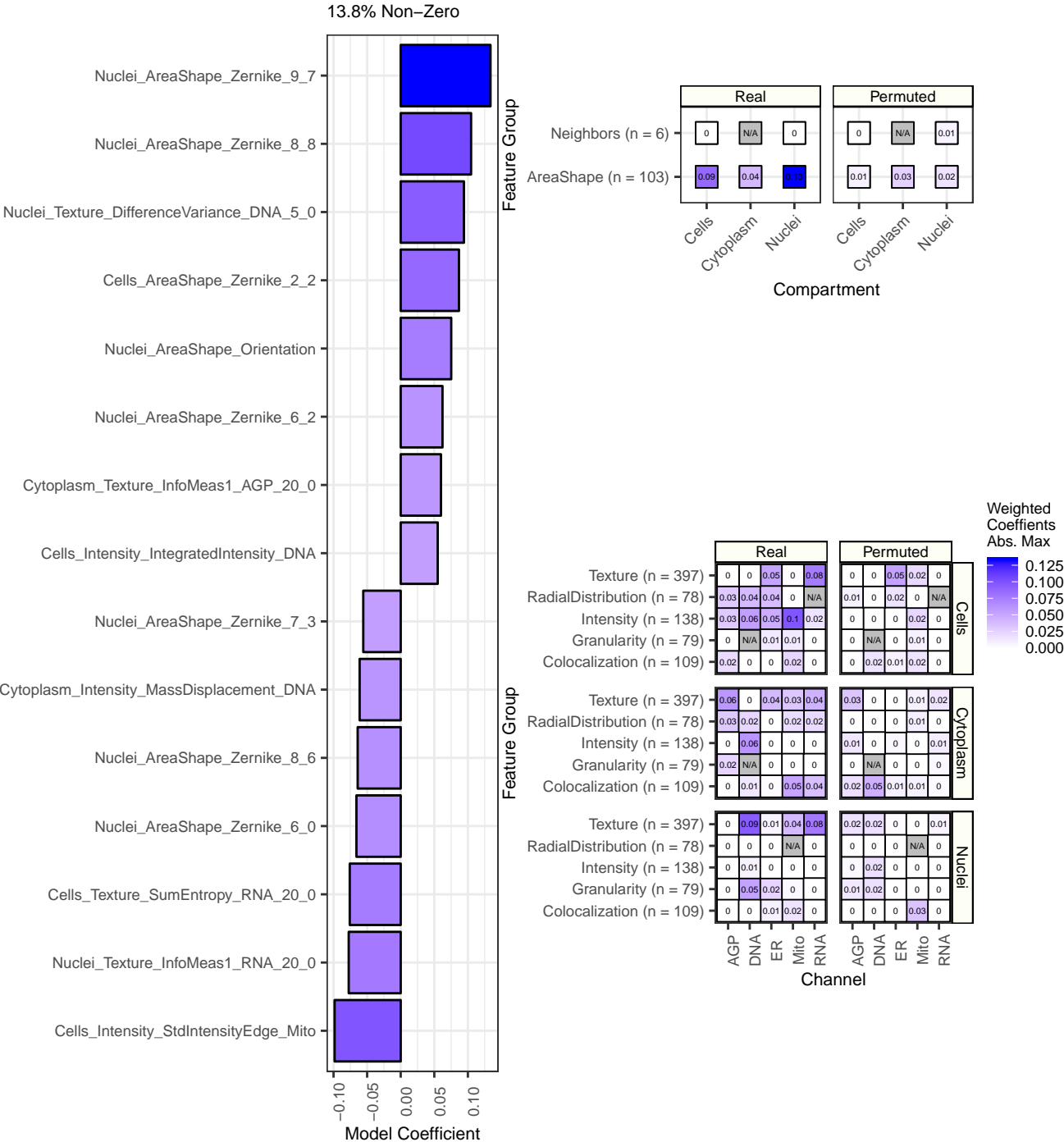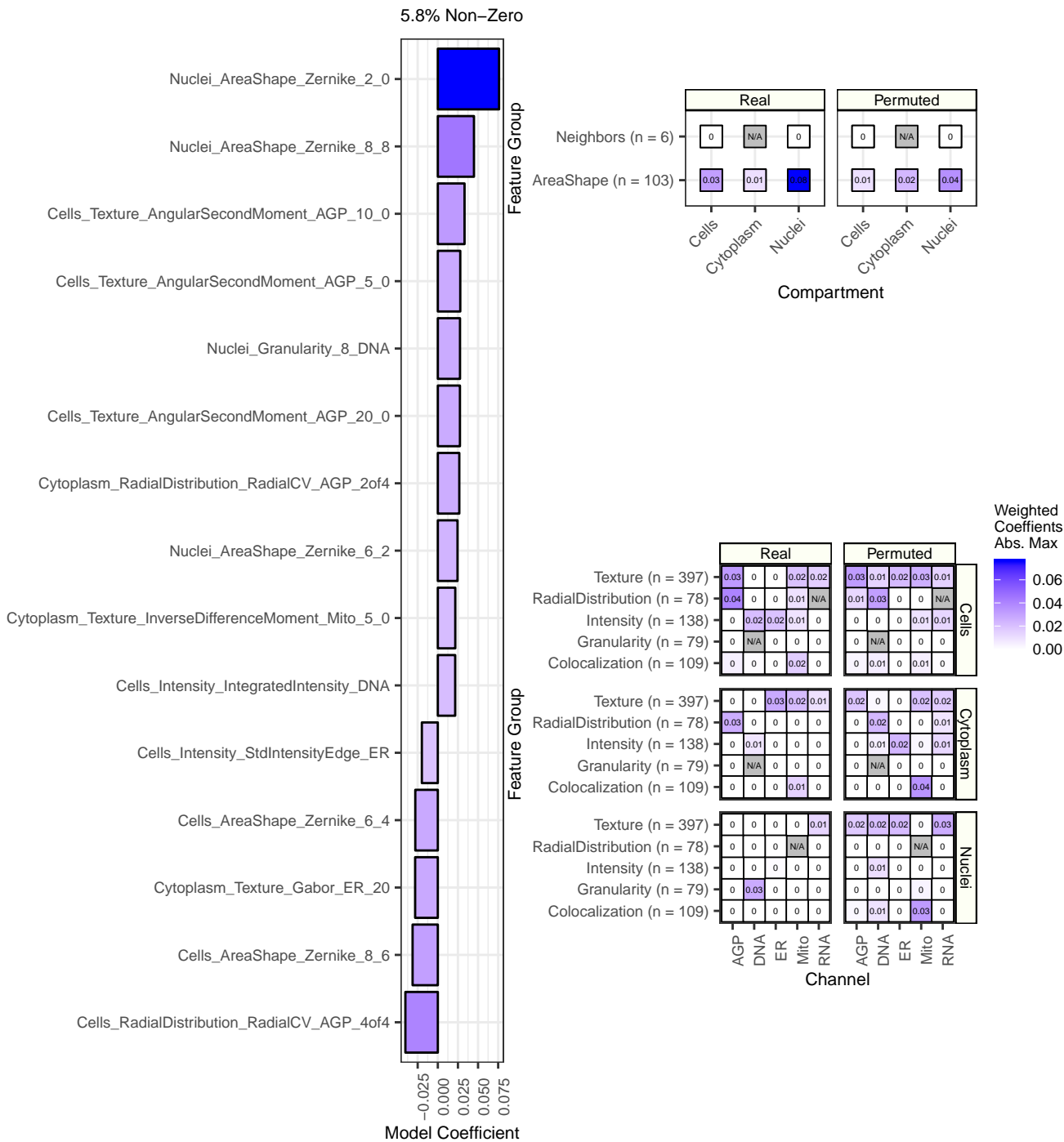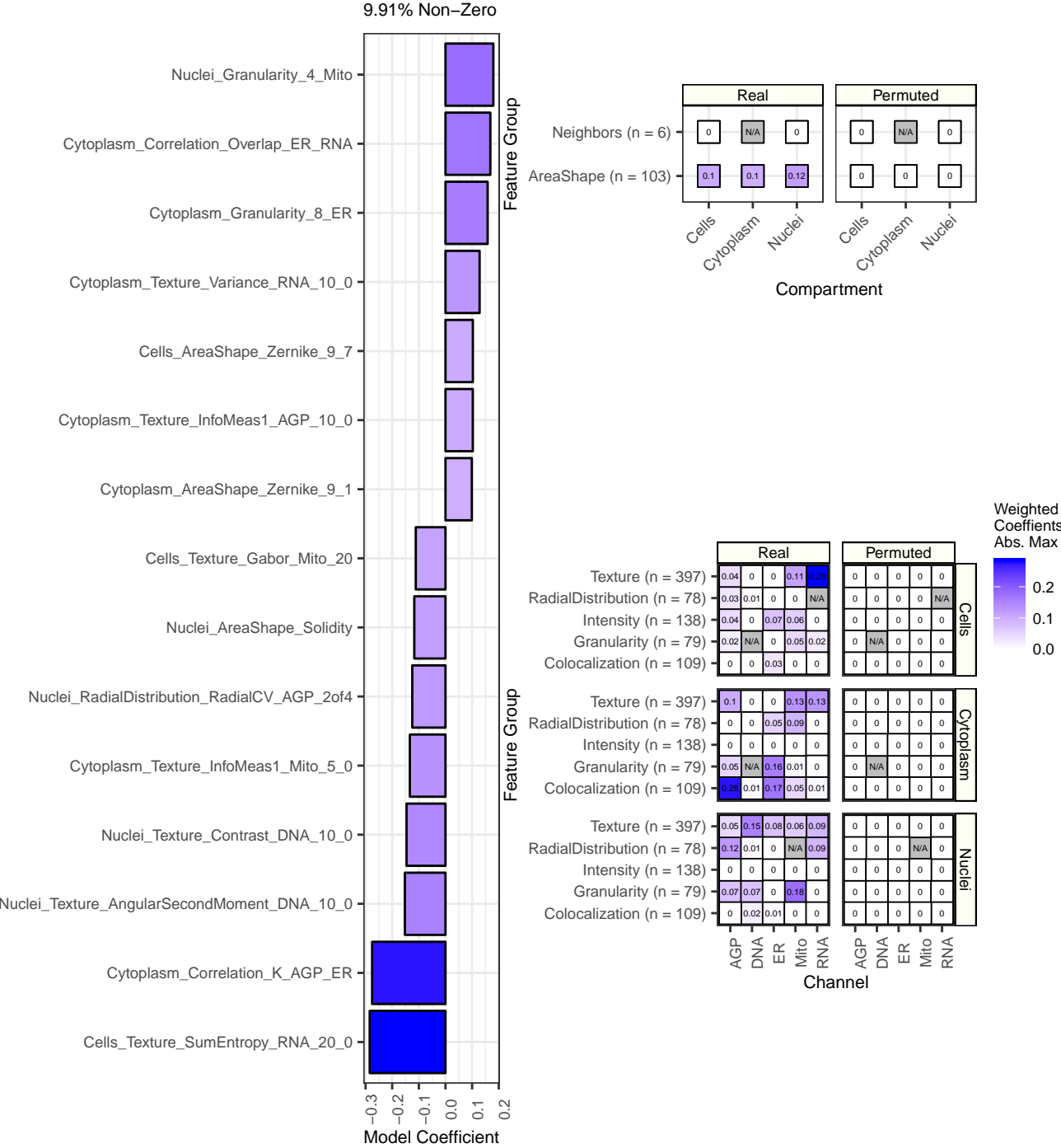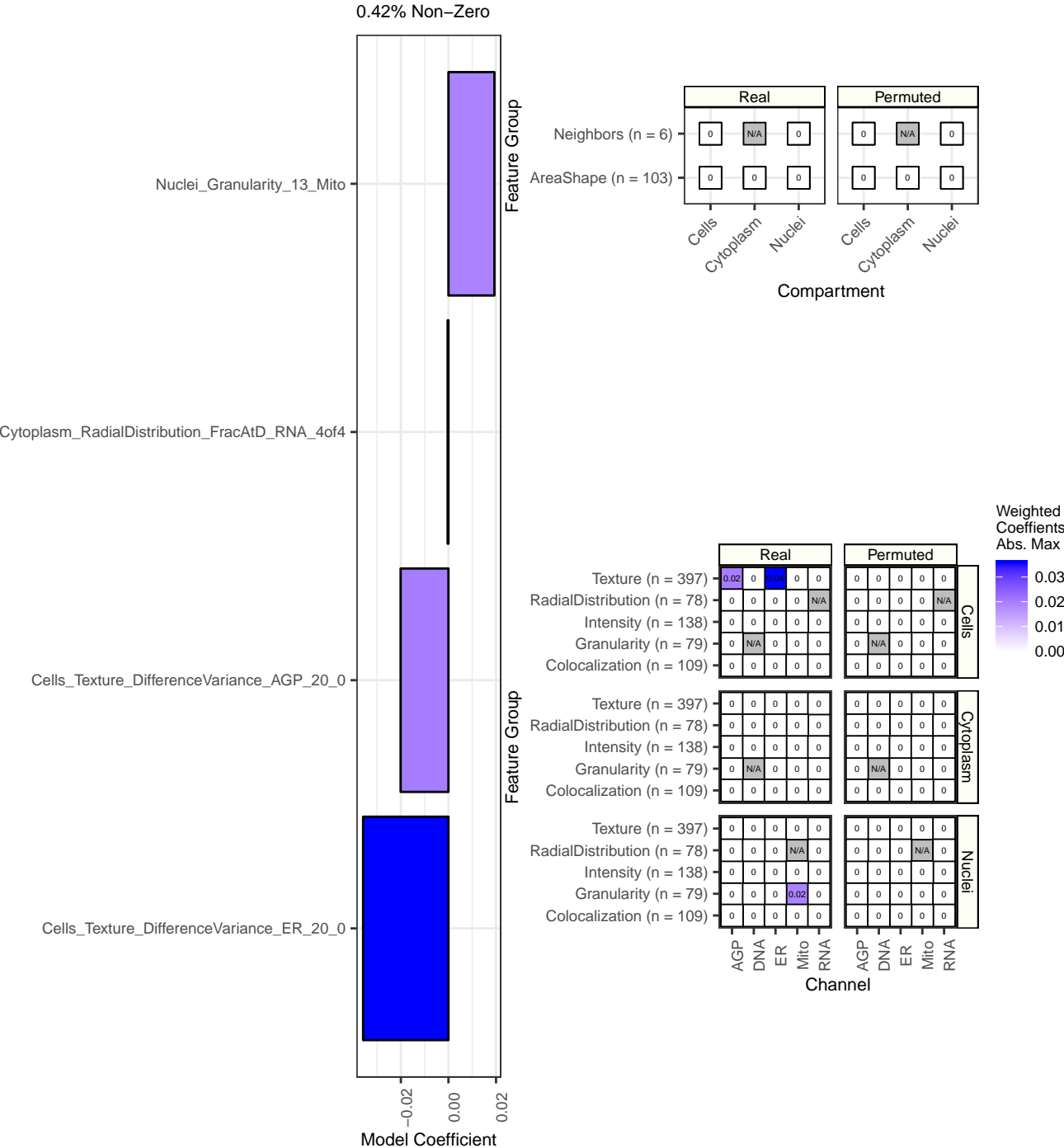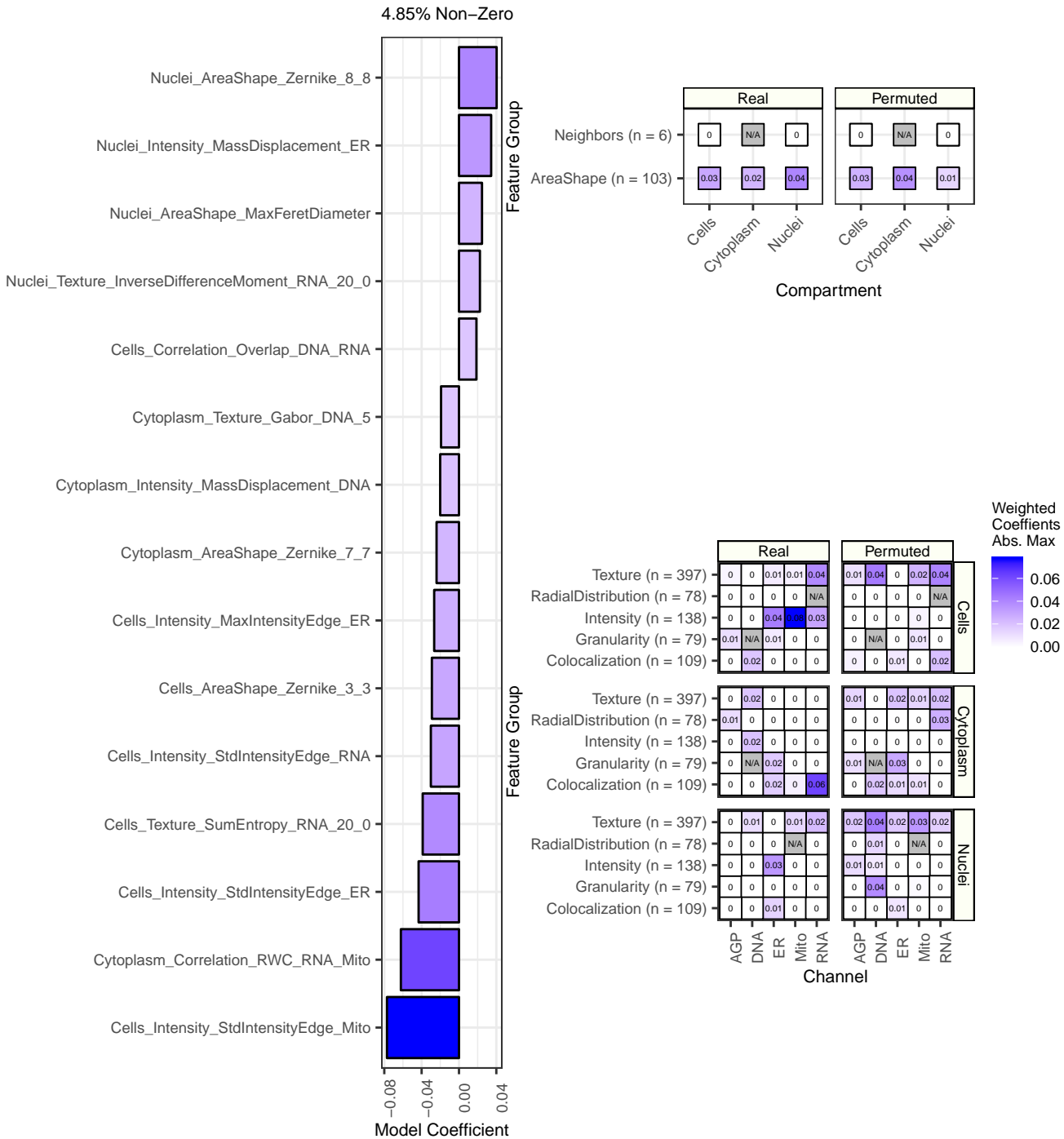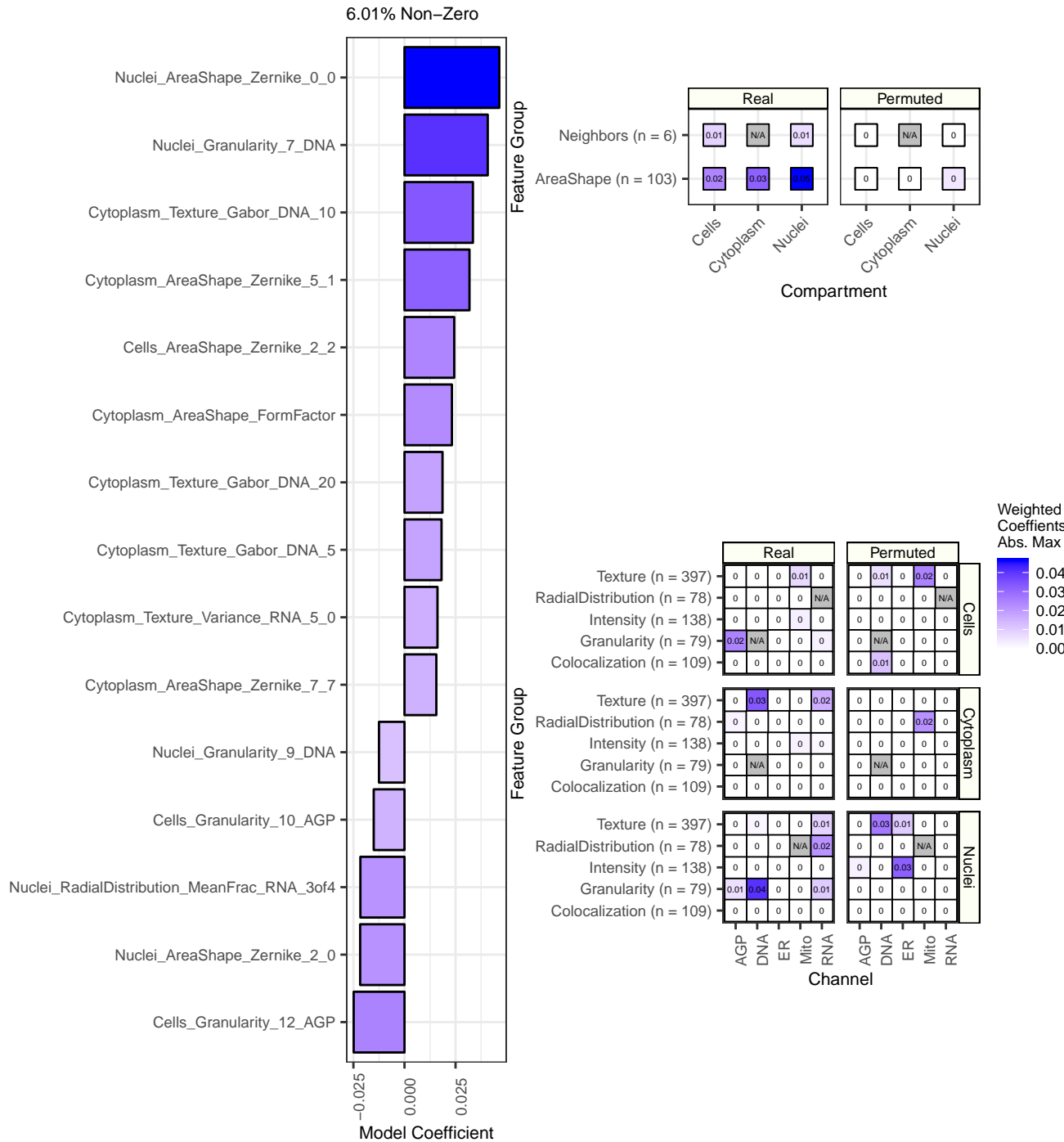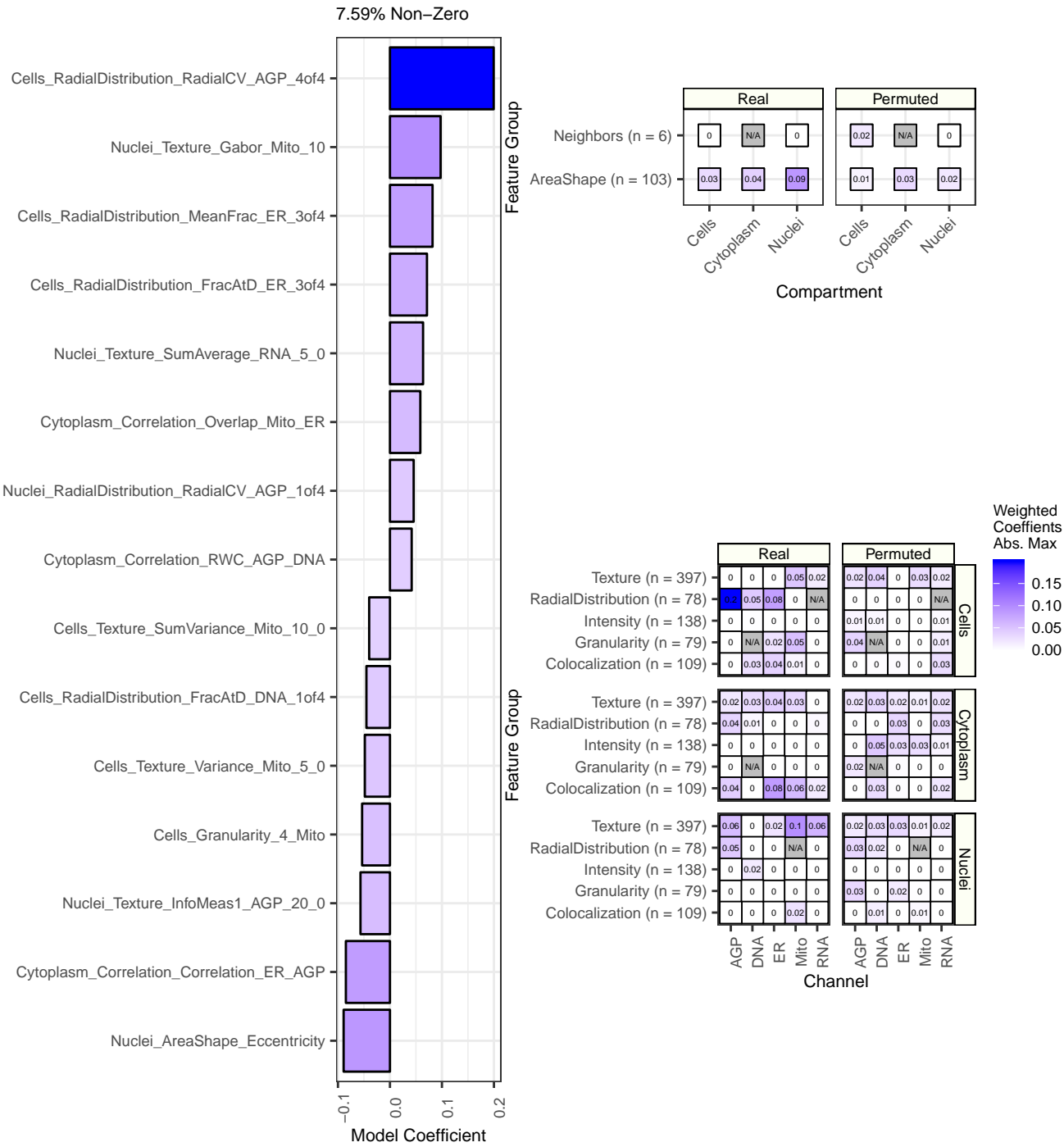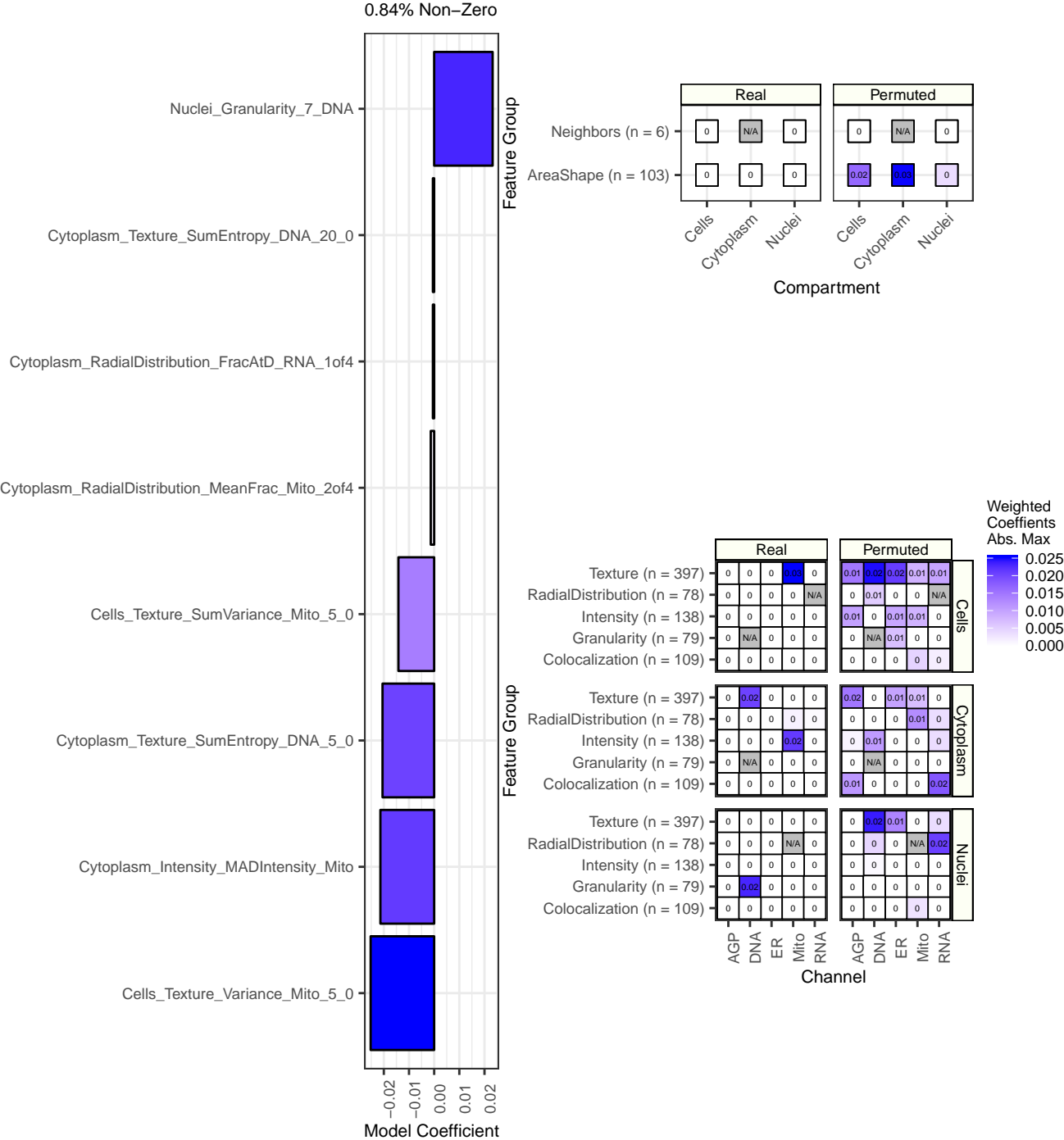# Late M – # of gH2AX Spots per Area of Nucleus
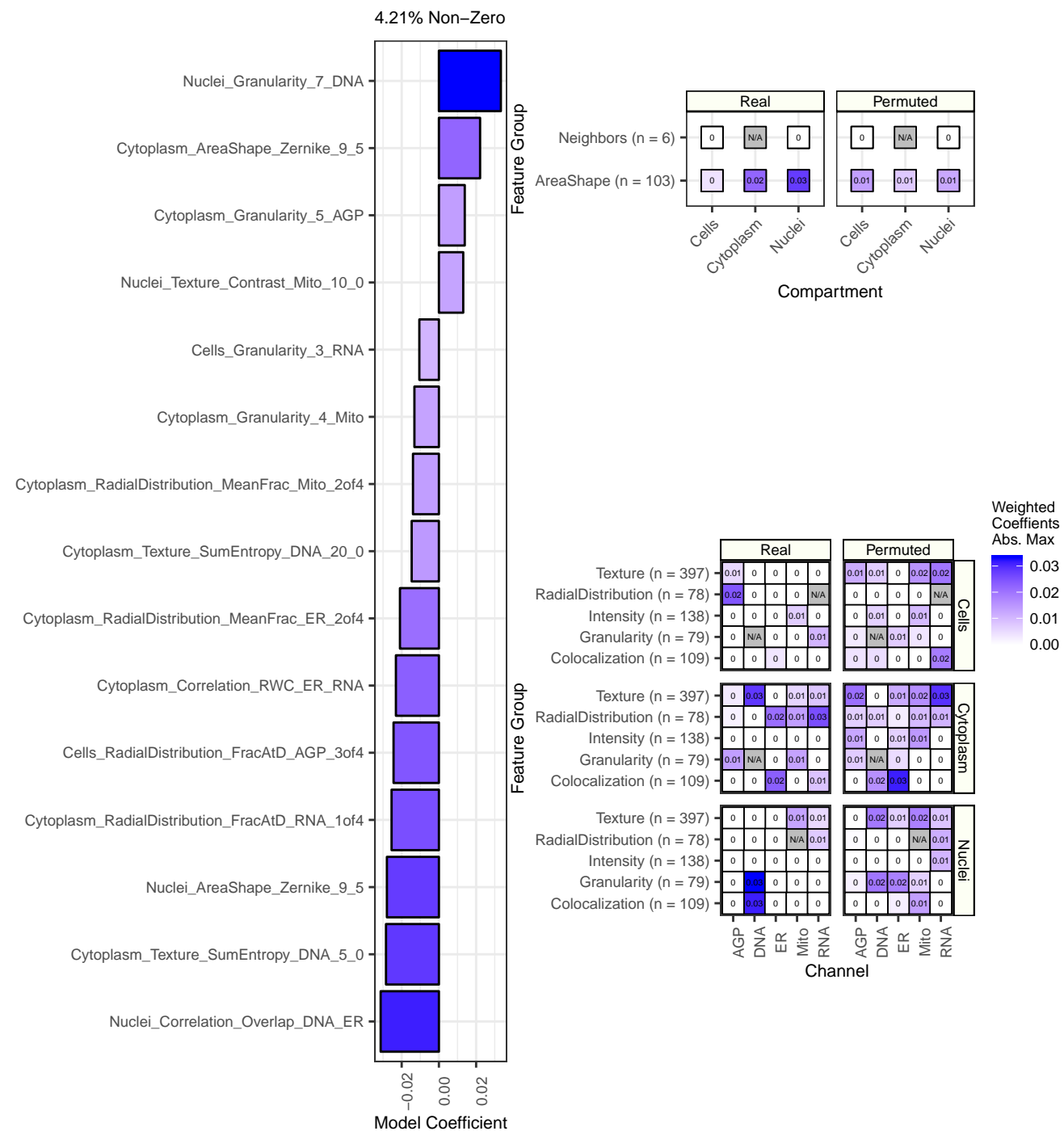
M – % High gH2AX Spots

0% Non−Zero

Feature Group / **Compartment**

Real / Permuted

	Cells	Cytoplasm	Nuclei		Cells	Cytoplasm	Nuclei
Neighbors (n = 6)	0	N/A	0		0	N/A	0
AreaShape (n = 103)	0	0	0		0	0	0

Weighted
Coeffients
Abs. Max

0

Feature Group / **Channel**
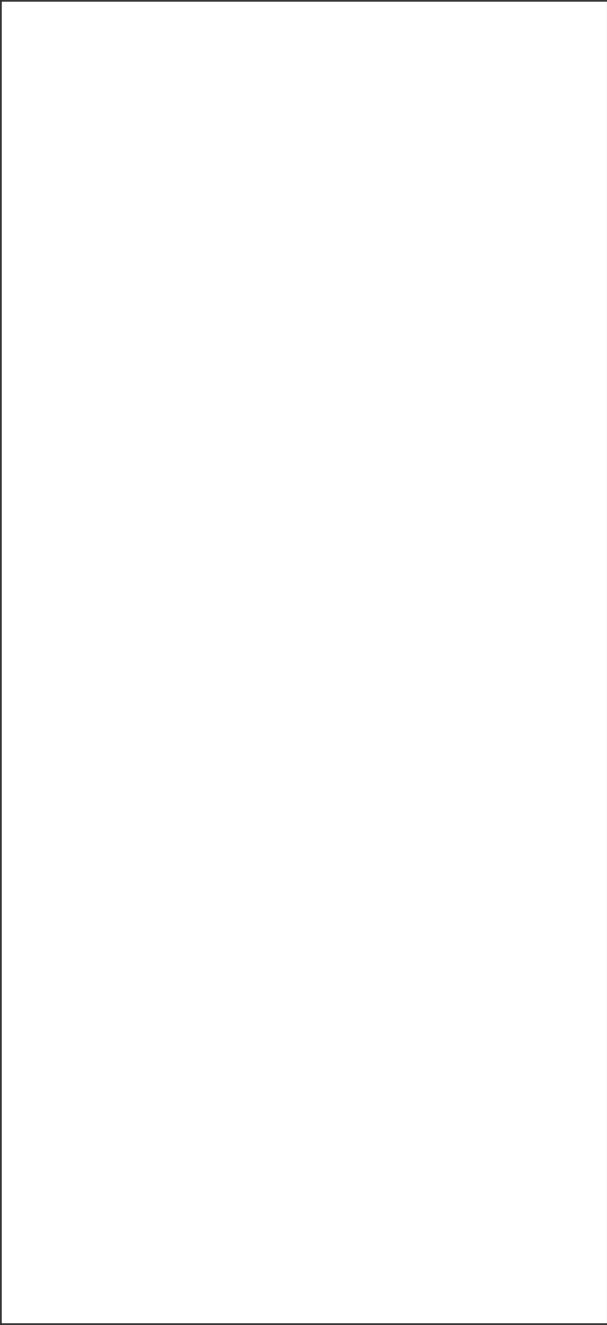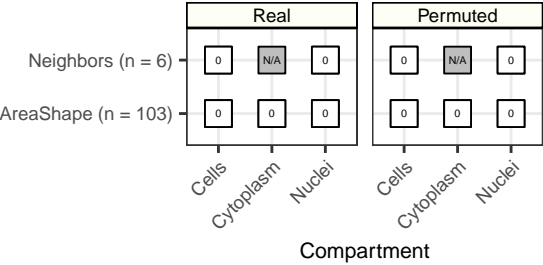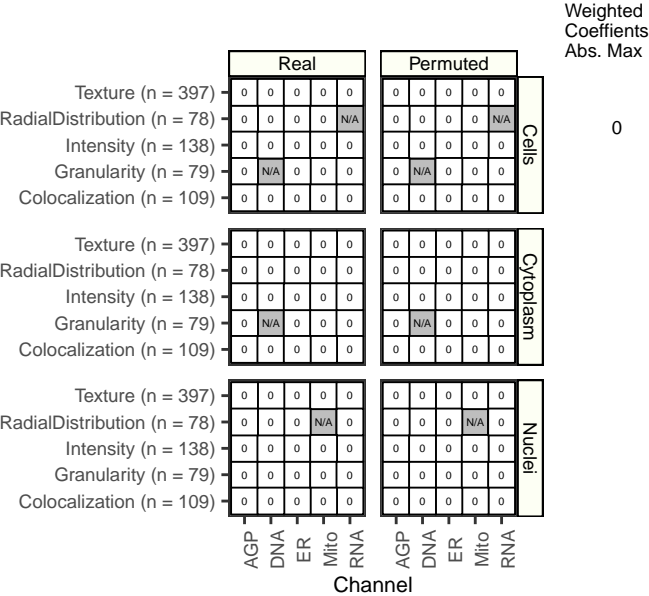
M – # cells

M – # of gH2AX Spots

0.63% Non−Zero

M – # of gH2AX Spots per Area of Nucleus

0.21% Non−Zero
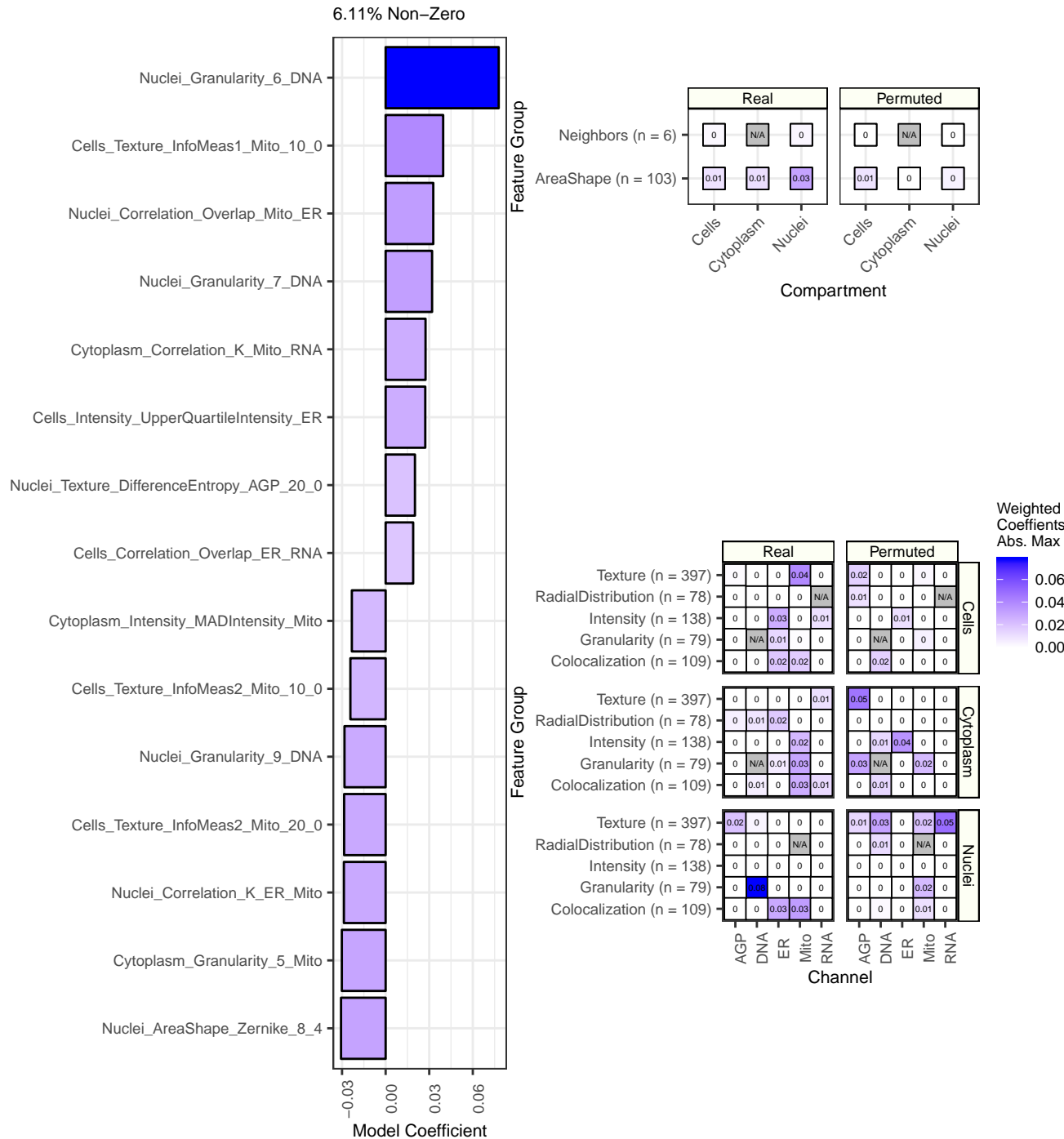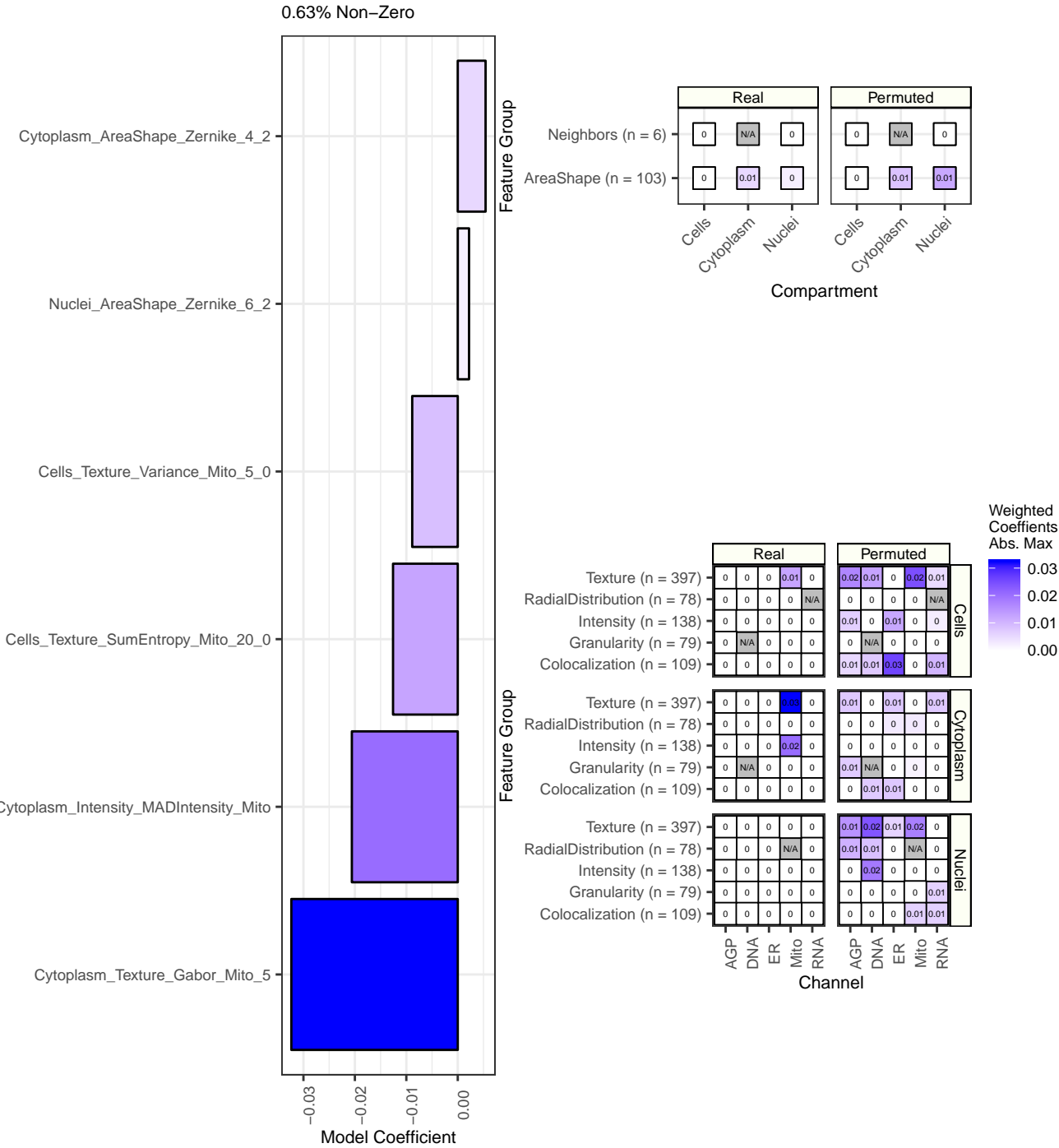
Polynuclear – % High gH2AX Spots
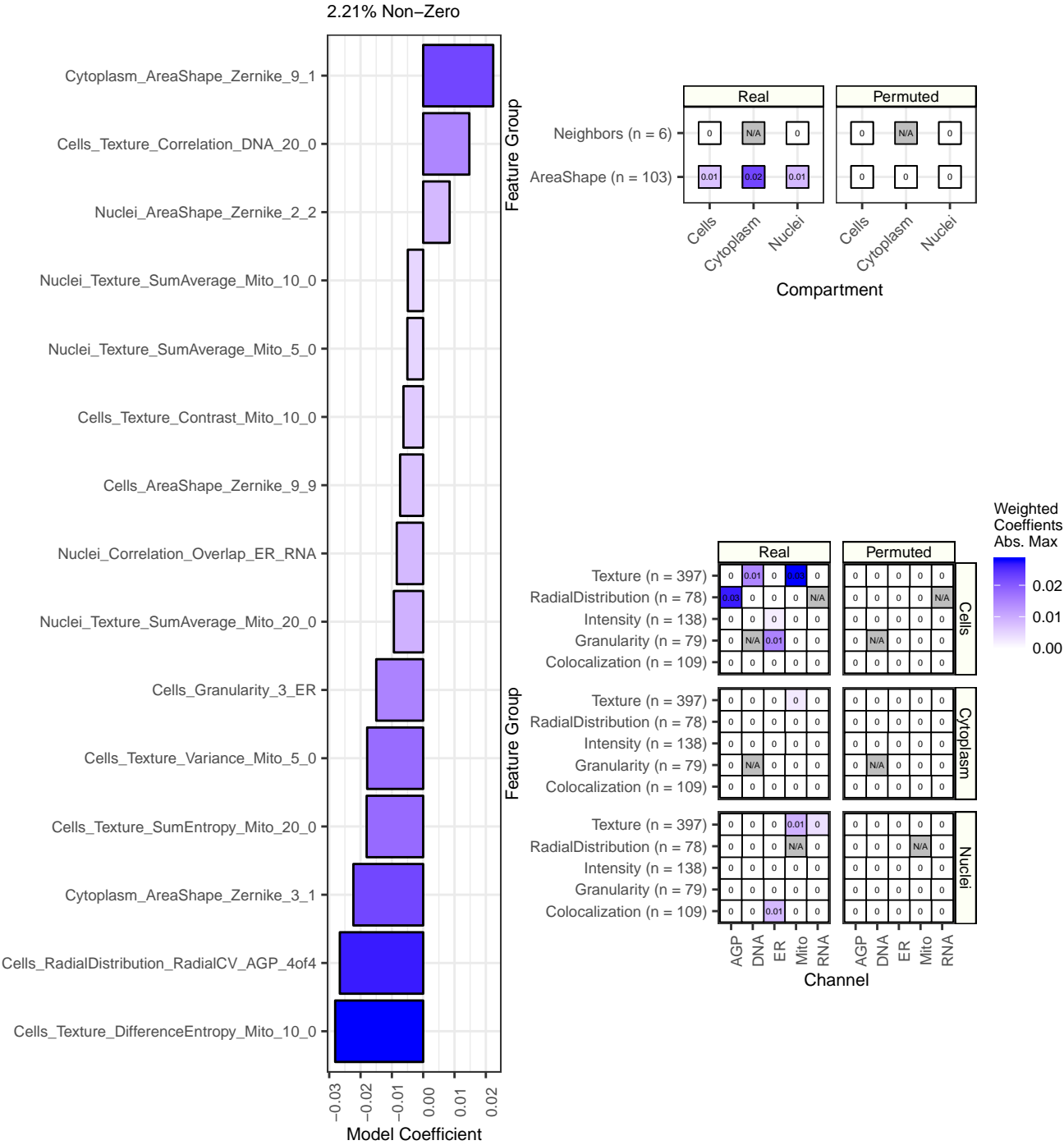
Polynuclear – # cells

8.43% Non−Zero
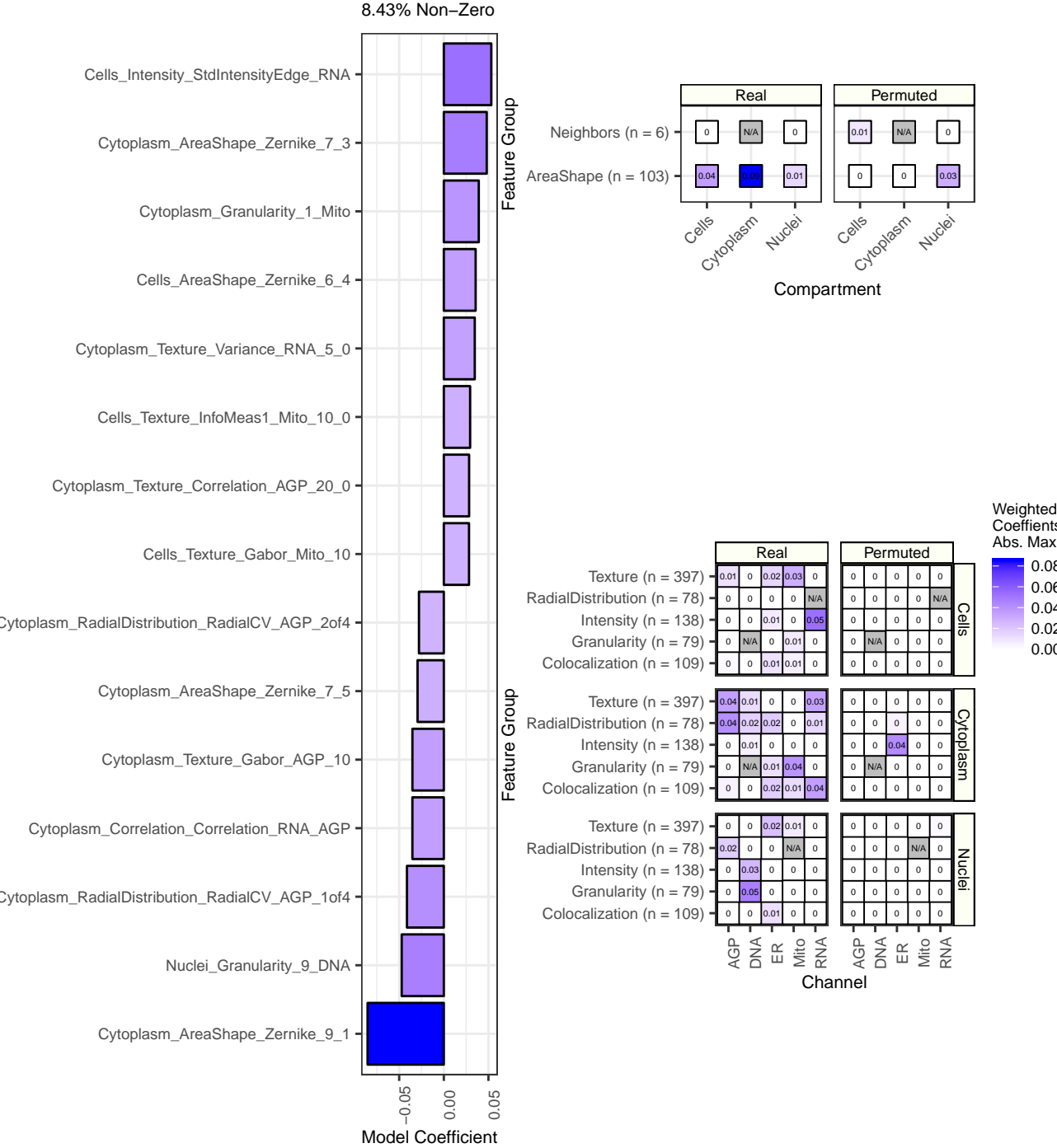
Polynuclear – # of gH2AX Spots
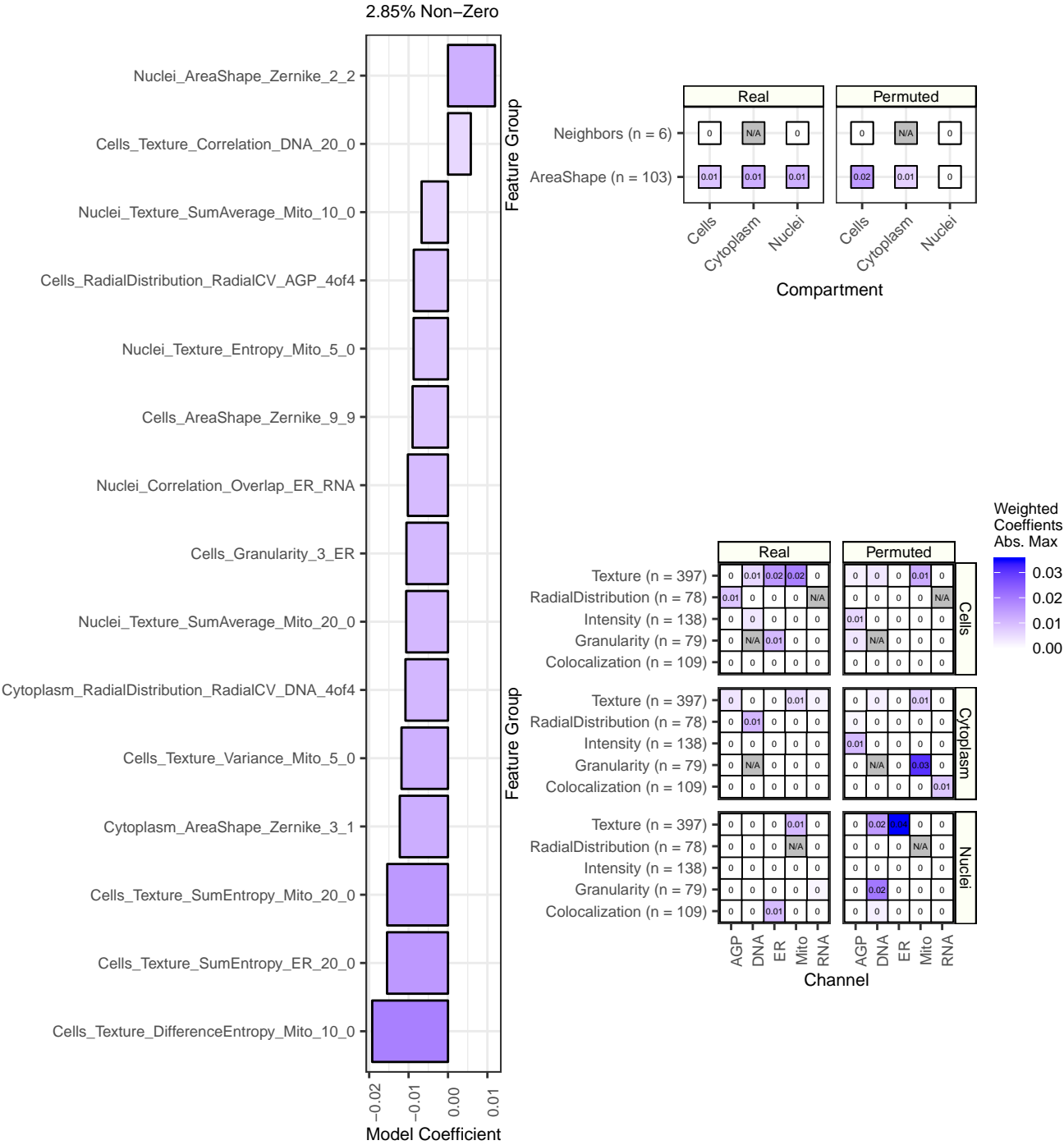
Polynuclear – # of gH2AX Spots per Area of Nucleus
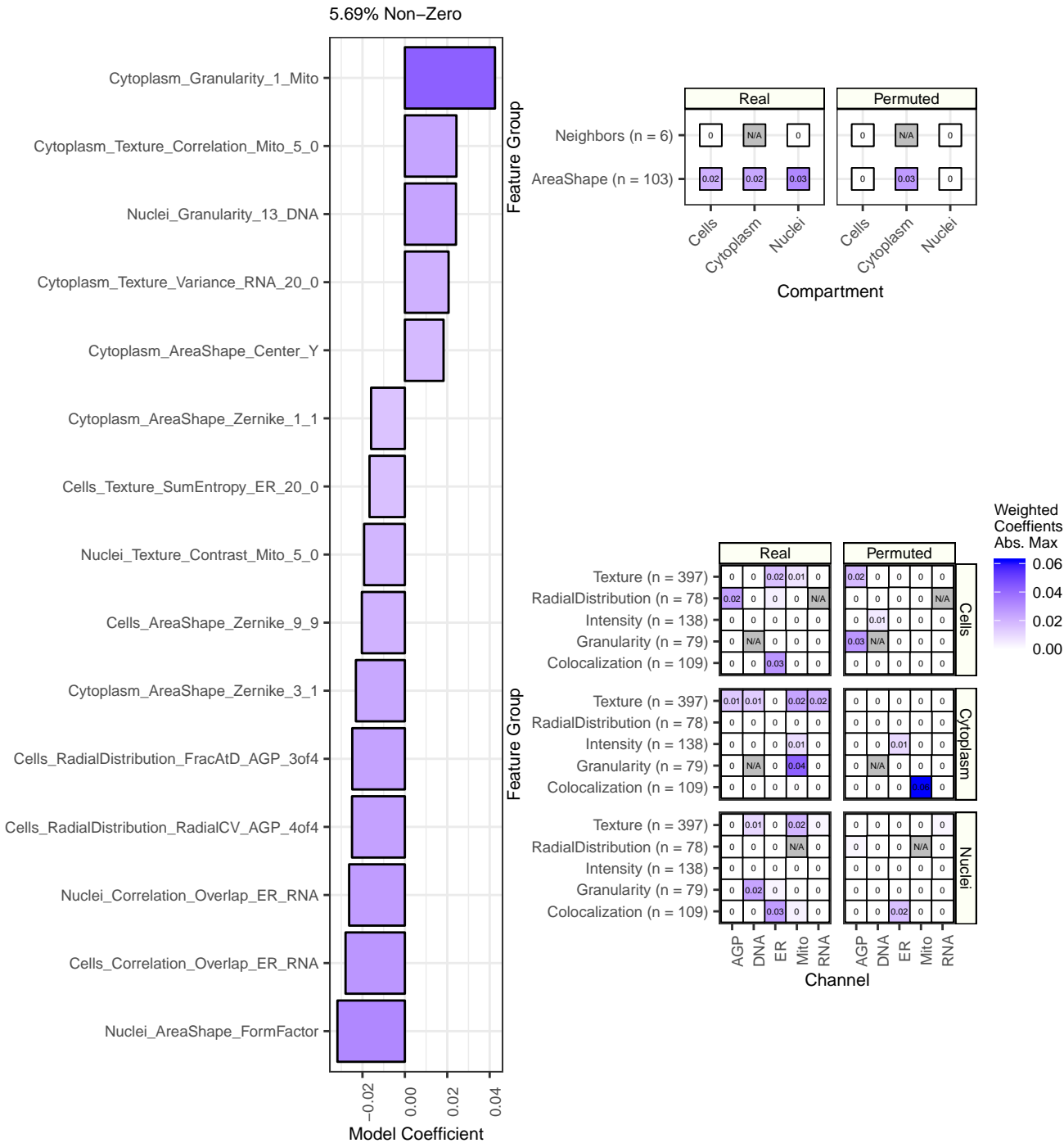
Polyploid – % High gH2AX Spots
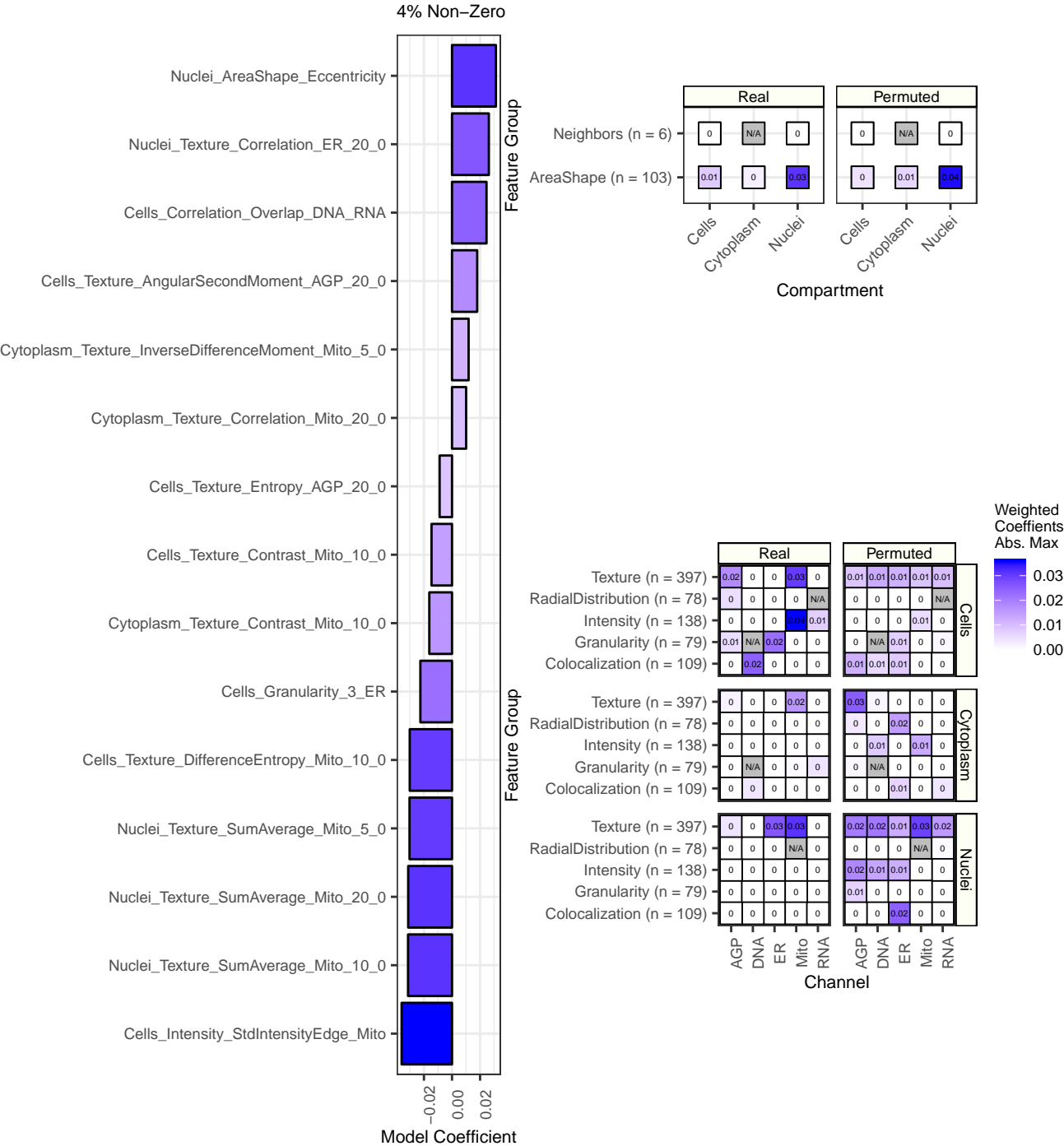
Polyploid – # cells
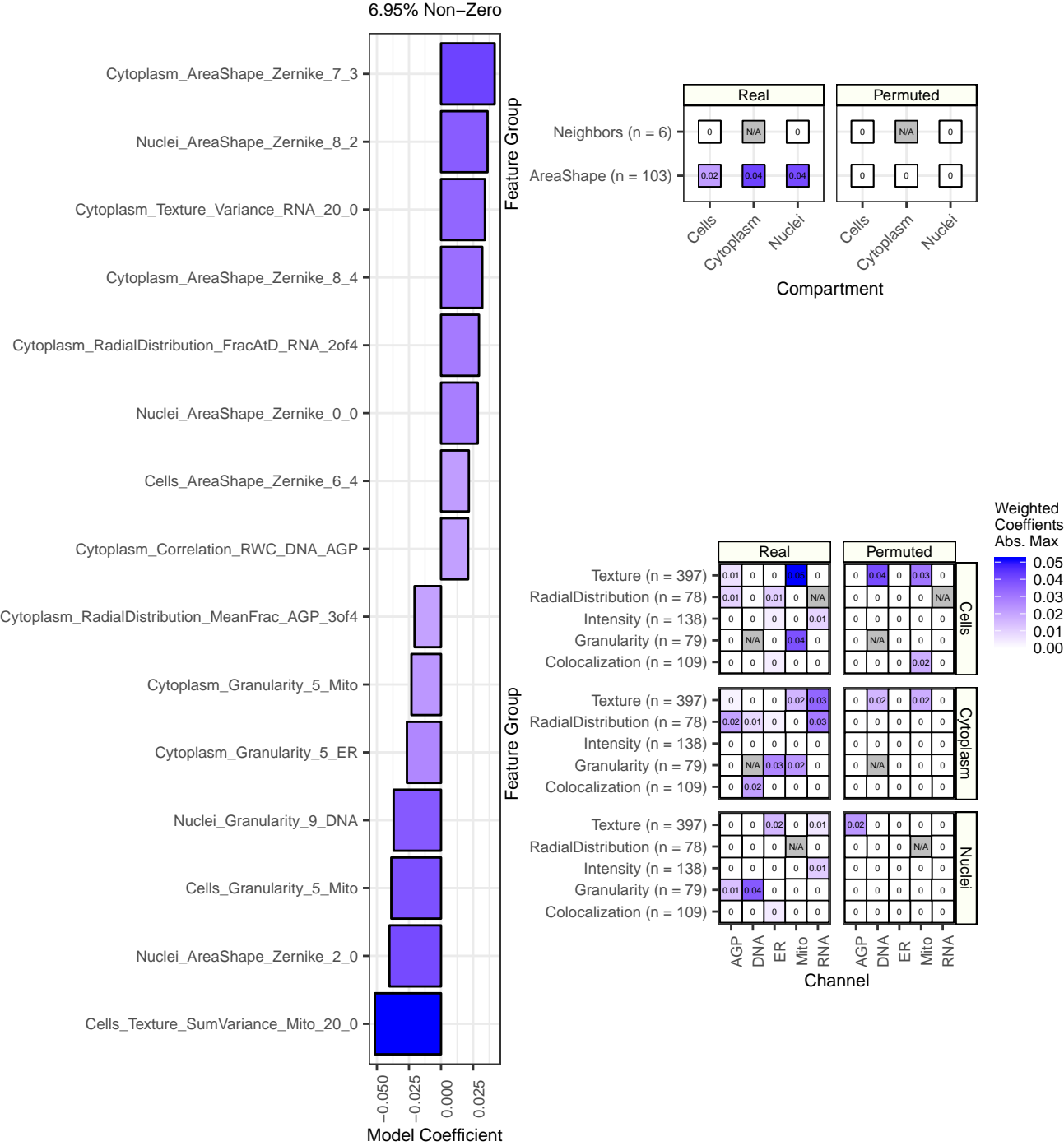
Polyploid – # of gH2AX Spots
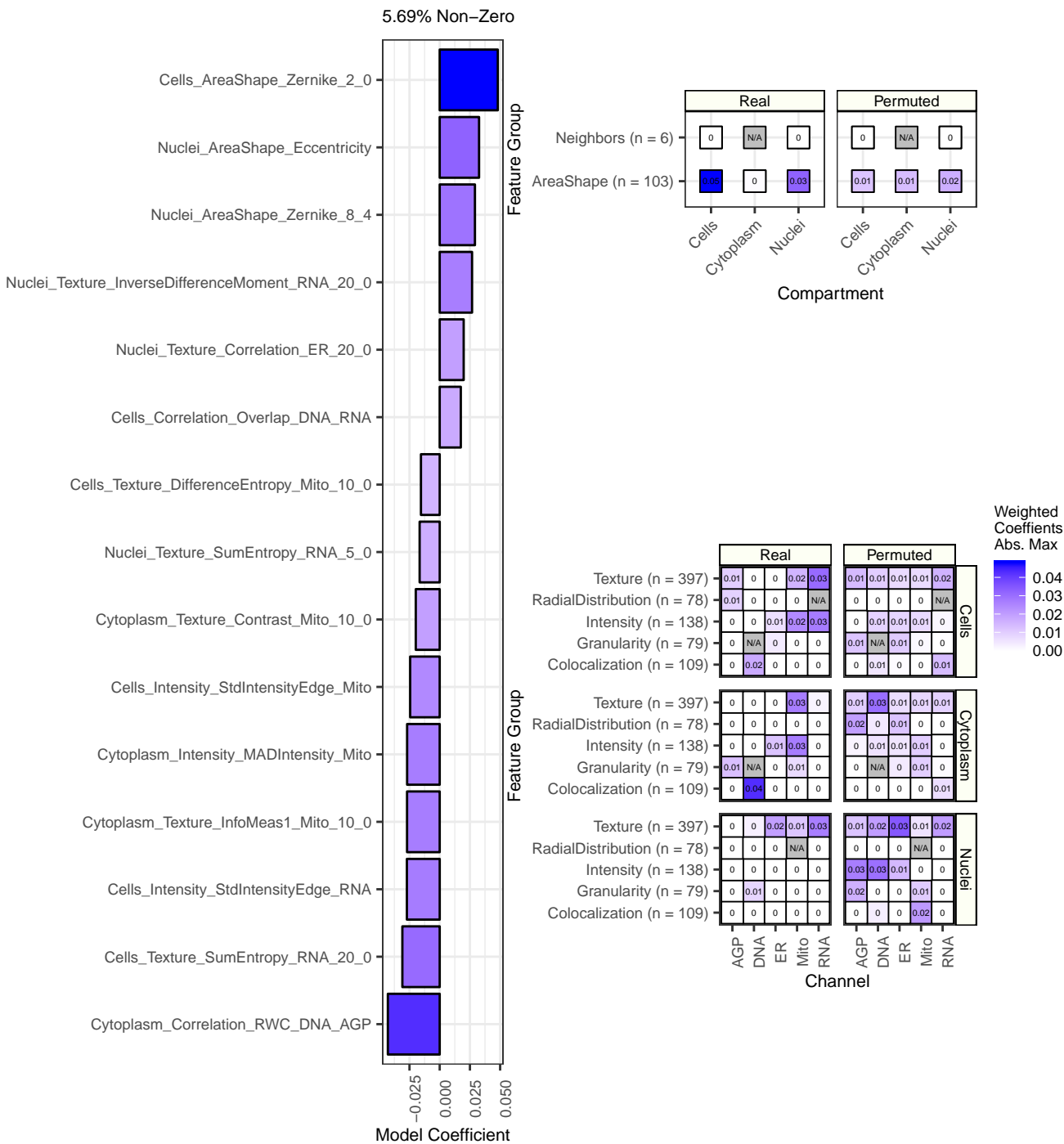
Polyploid – # of gH2AX Spots per Area of Nucleus
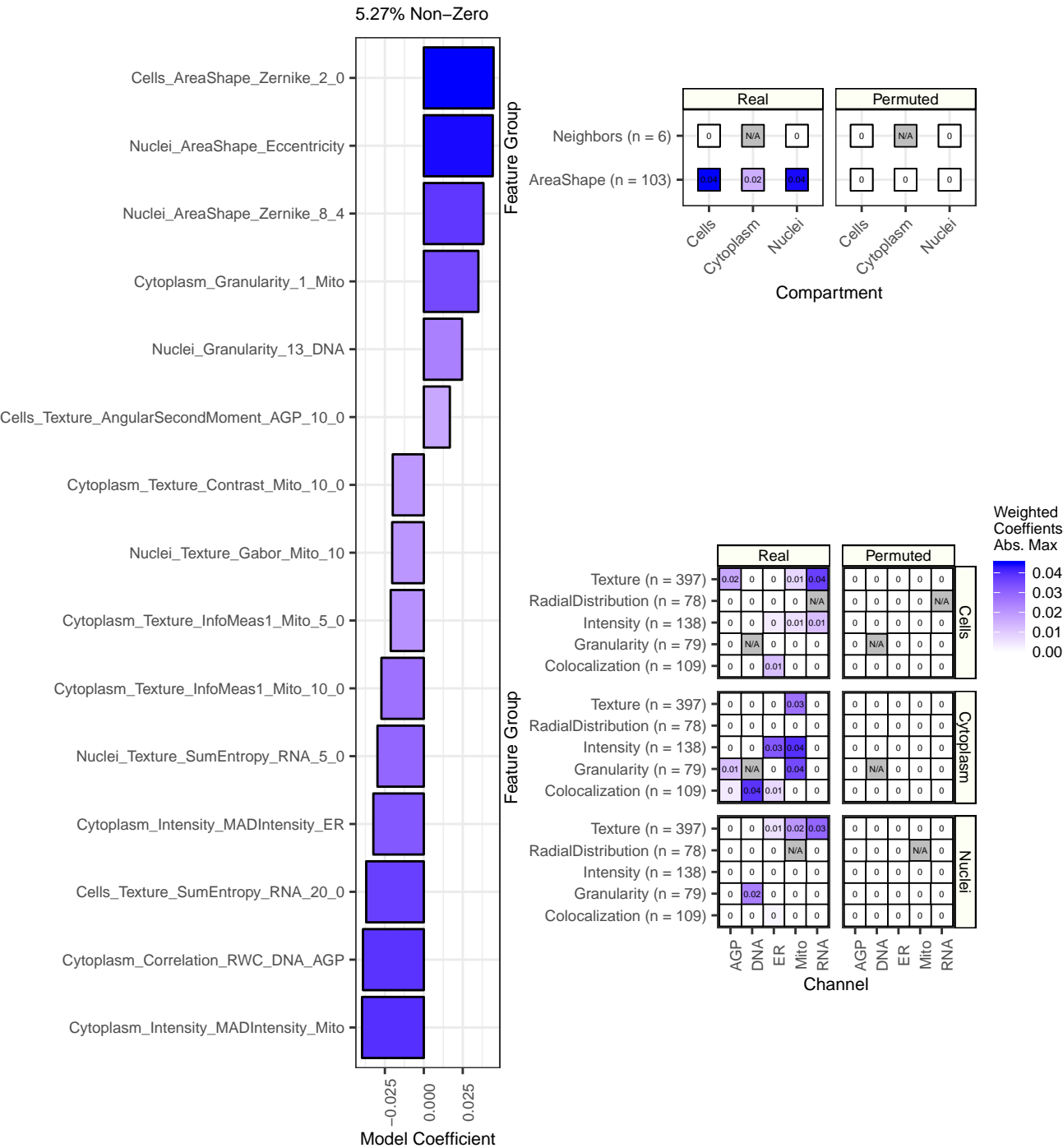
S – % High gH2AX Spots
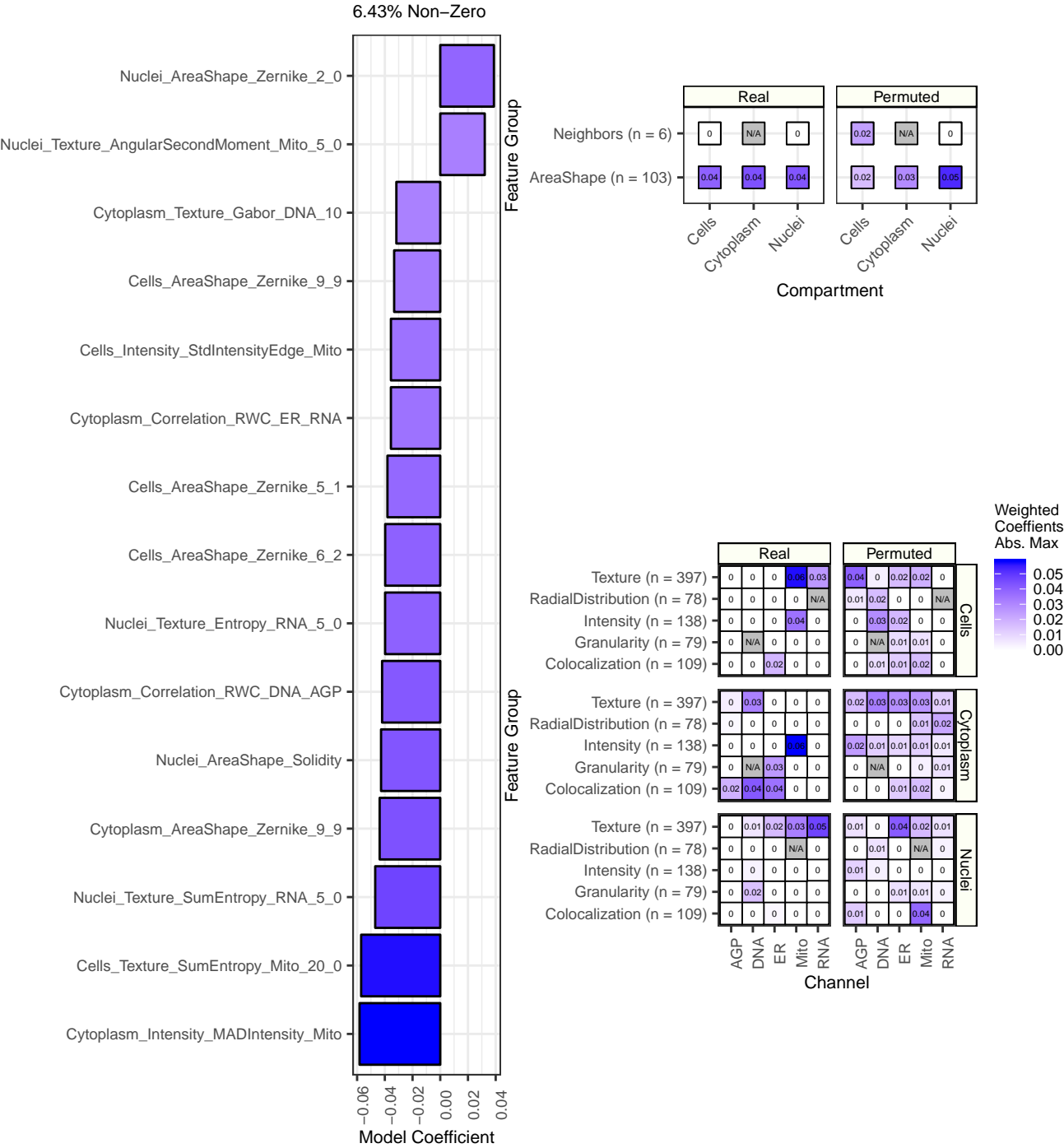
S – Intensity Nucleus EdU Mean

11.28% Non−Zero
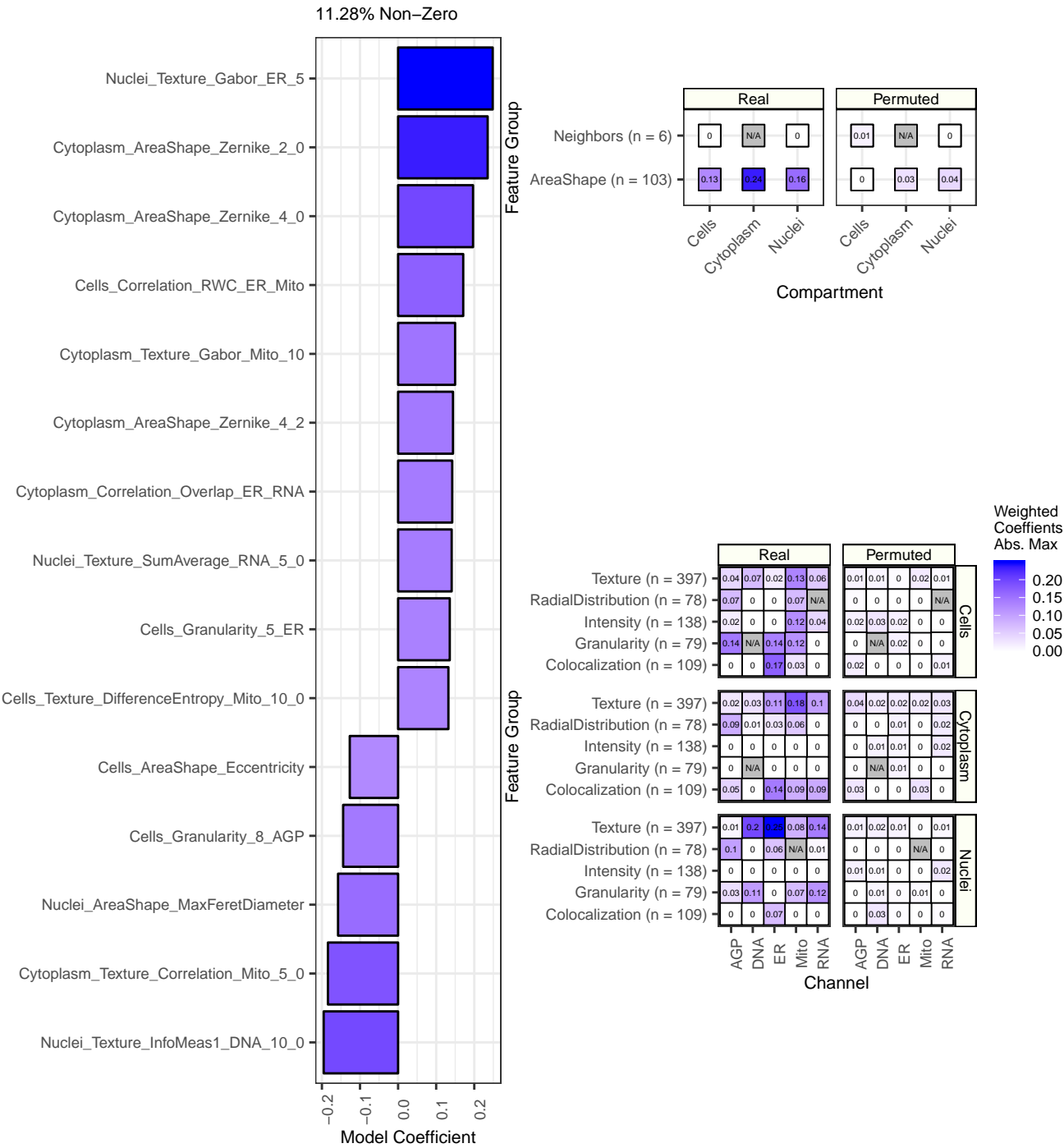
S – Intensity Nucleus EdU Sum

7.9% Non−Zero
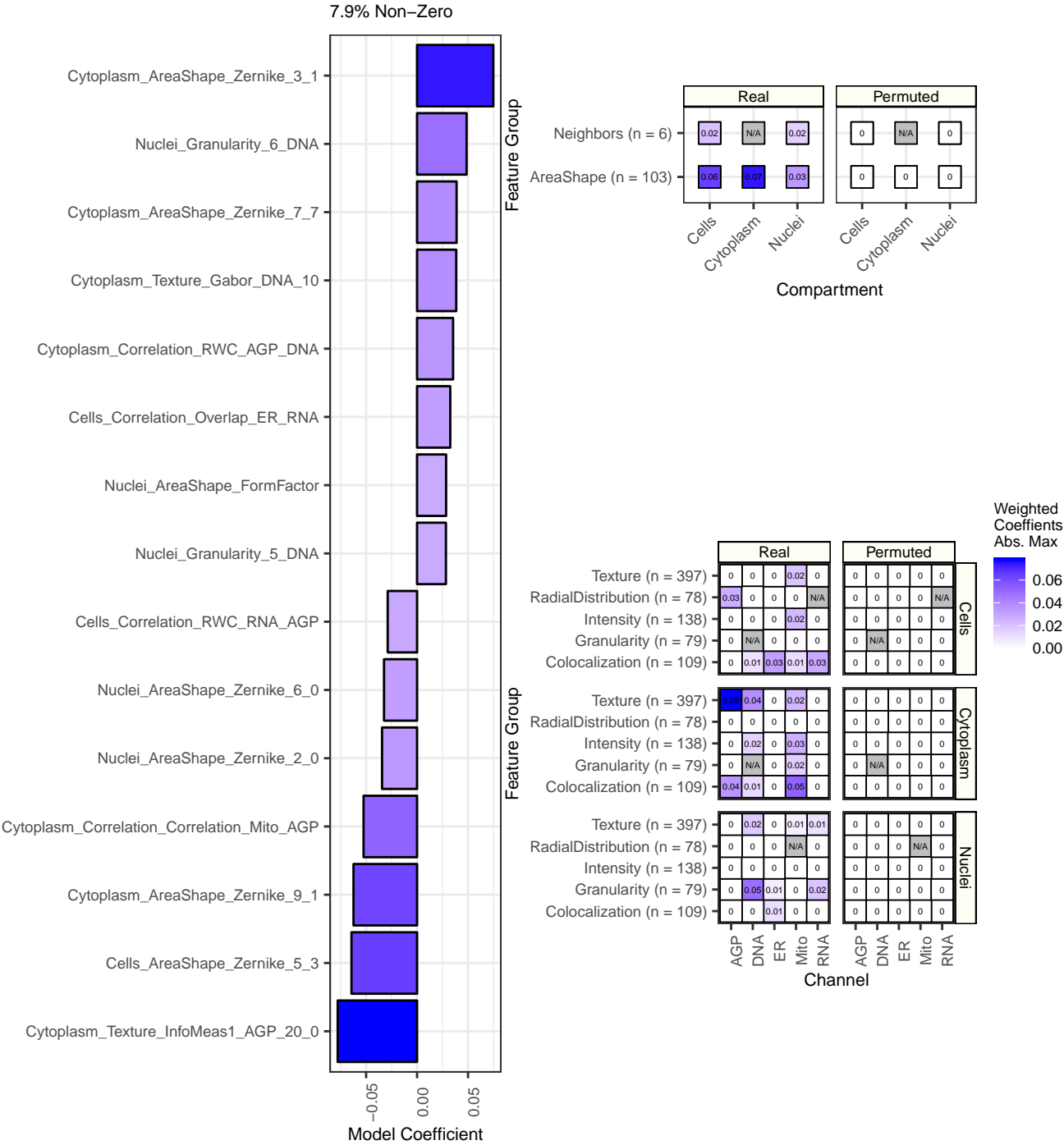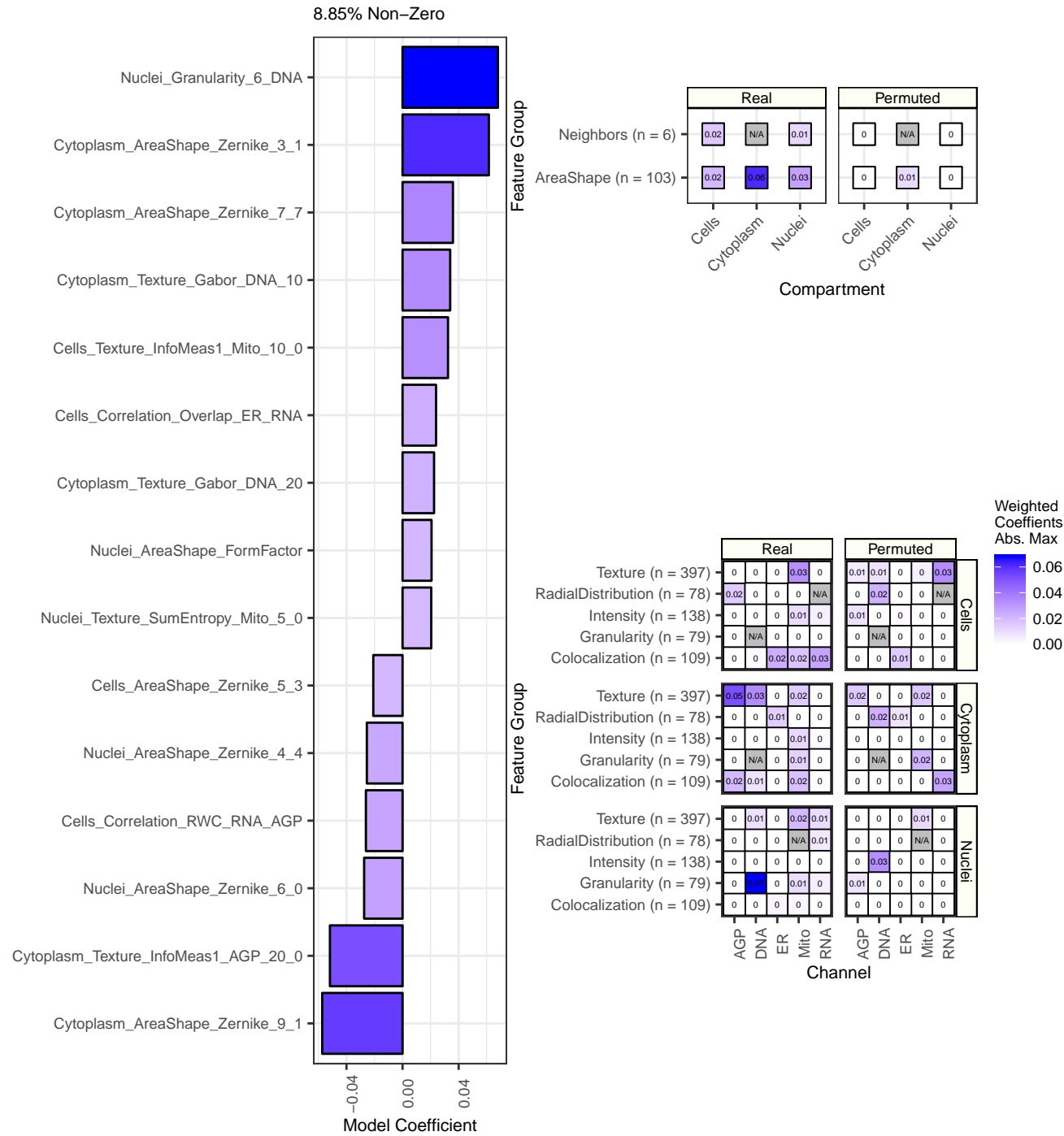
S – # cells

8.85% Non−Zero
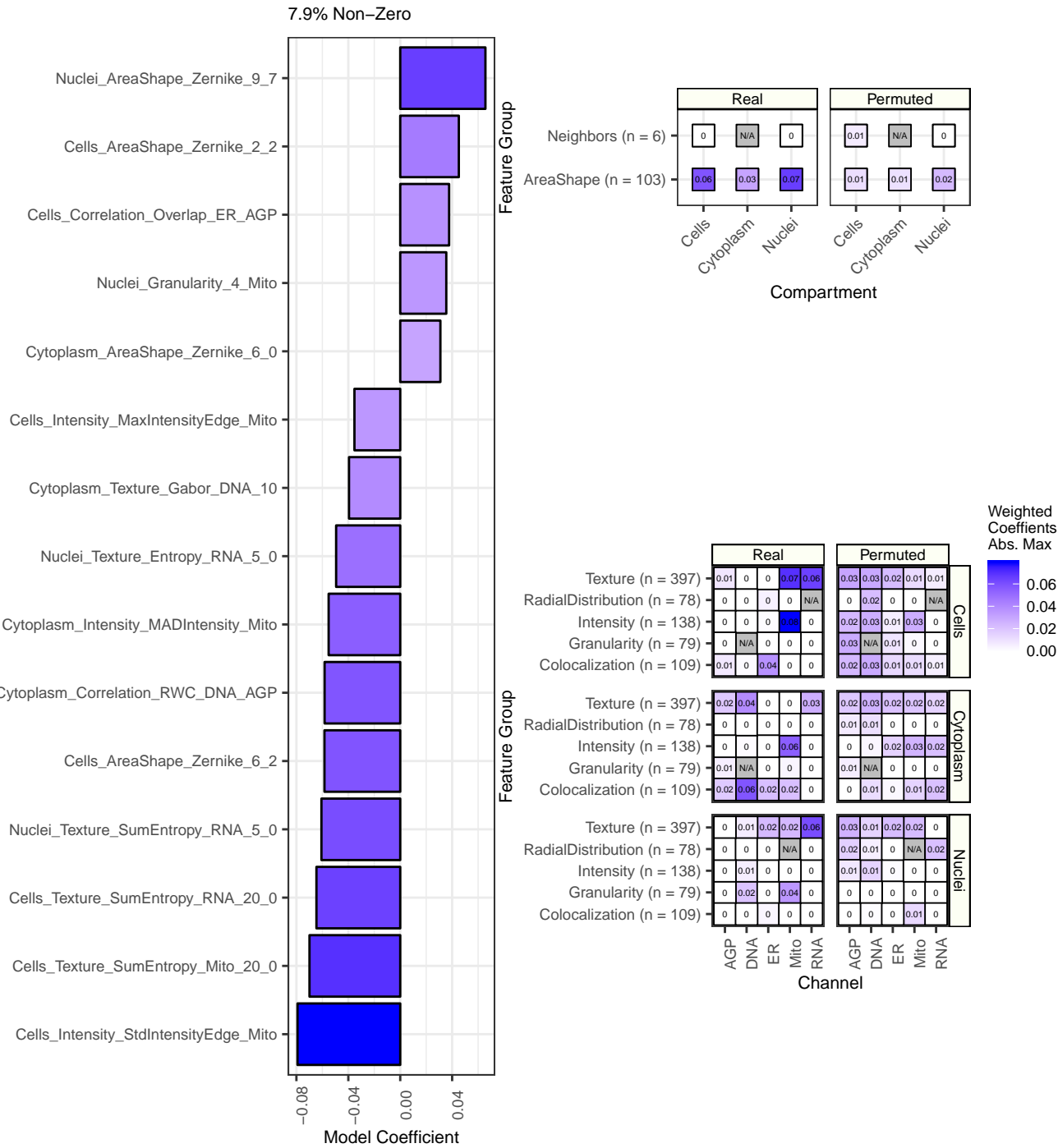
S – # of gH2AX Spots

S – # of gH2AX Spots per Area of Nucleus

VB – Infection Efficiency

5.06% Non−Zero

Live Cell Area

Live Cell Roundness

14.33% Non−Zero

Live Width / Length

15.17% Non−Zero

Feature Group (y-axis, top to bottom):
- Cells_RadialDistribution_RadialCV_AGP_4of4
- Cells_Texture_SumEntropy_ER_20_0
- Cytoplasm_AreaShape_Zernike_3_3
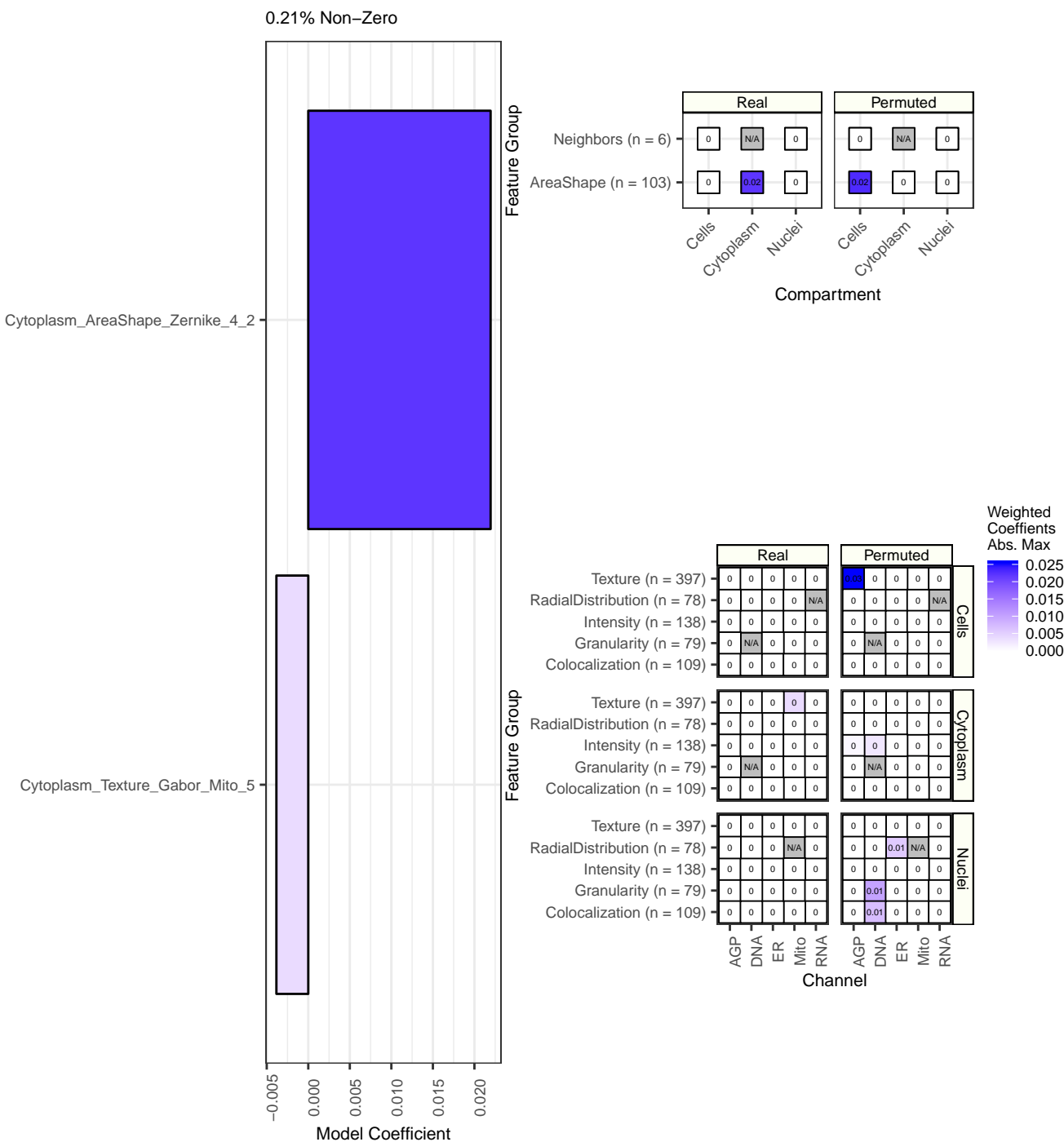- Nuclei_Granularity_7_DNA
- Cytoplasm_Correlation_RWC_RNA_Mito
- Cytoplasm_AreaShape_Zernike_3_1
- Cytoplasm_AreaShape_Zernike_7_1
- Cytoplasm_RadialDistribution_FracAtD_RNA_4of4
- Cells_Correlation_RWC_RNA_AGP
- Cells_AreaShape_Zernike_5_1
- Cytoplasm_Texture_Variance_RNA_10_0
- Nuclei_AreaShape_Zernike_6_2
- Cells_AreaShape_Zernike_7_1
- Cytoplasm_AreaShape_Zernike_6_4
- Cells_AreaShape_Zernike_5_3

Model Coefficient (x-axis): −0.05, 0.00, 0.05

Compartment heatmap

	Real Cells	Real Cytoplasm	Real Nuclei	Permuted Cells	Permuted Cytoplasm	Permuted Nuclei
Neighbors (n = 6)	0.02	N/A	0.02	0	N/A	0
AreaShape (n = 103)	0.08	0.07	0.05	0.03	0	0.02

Compartment

Channel heatmap

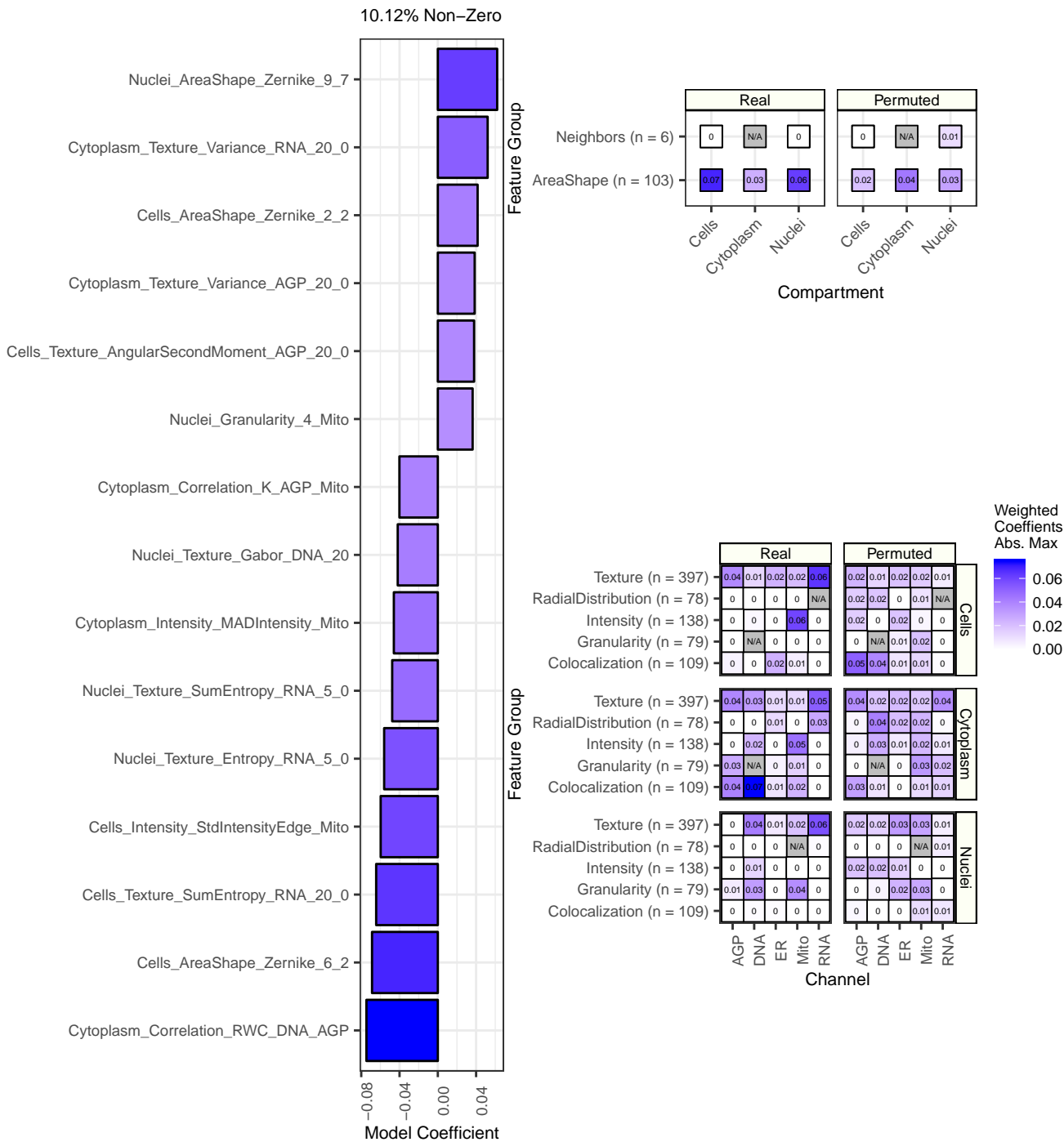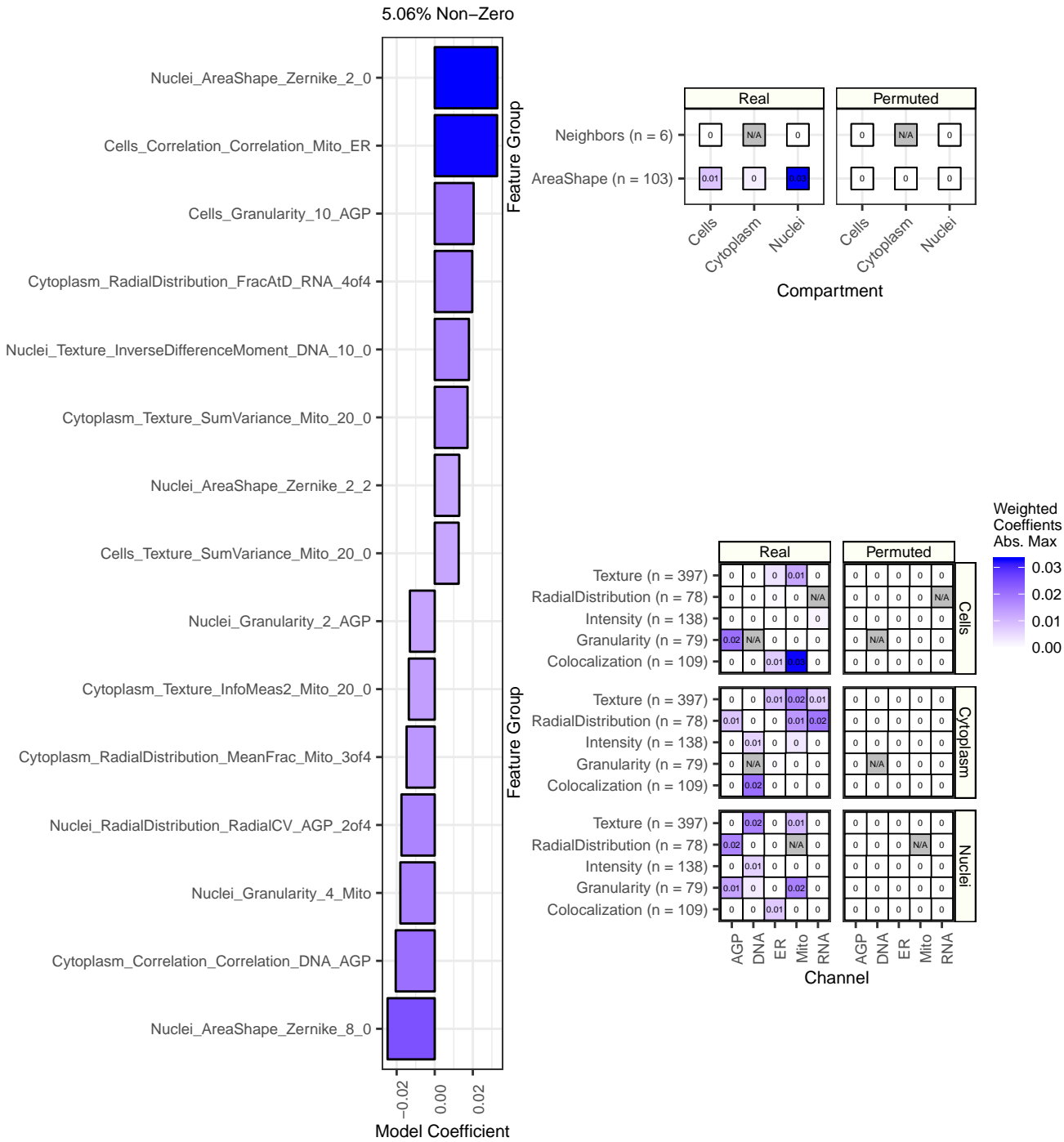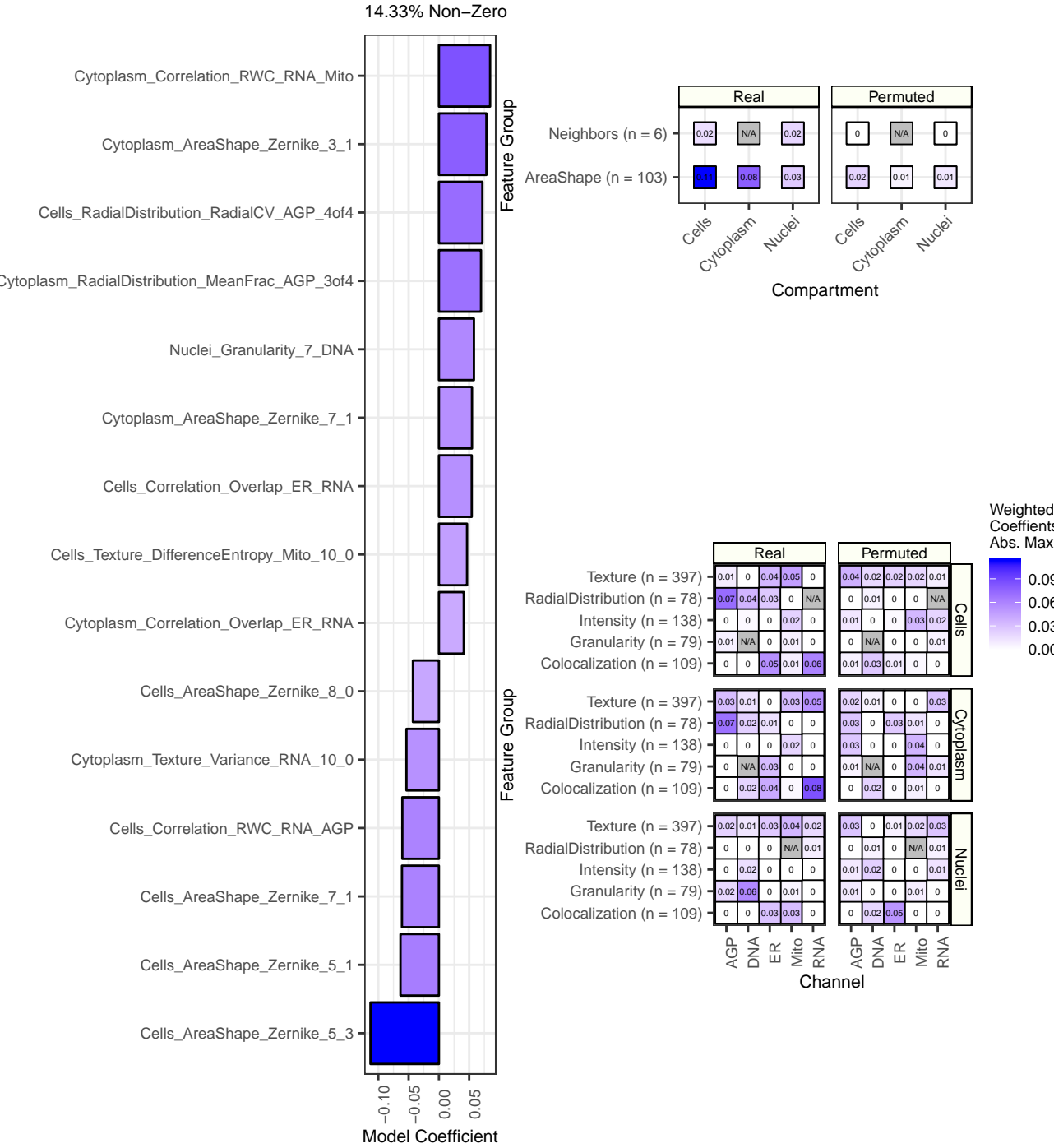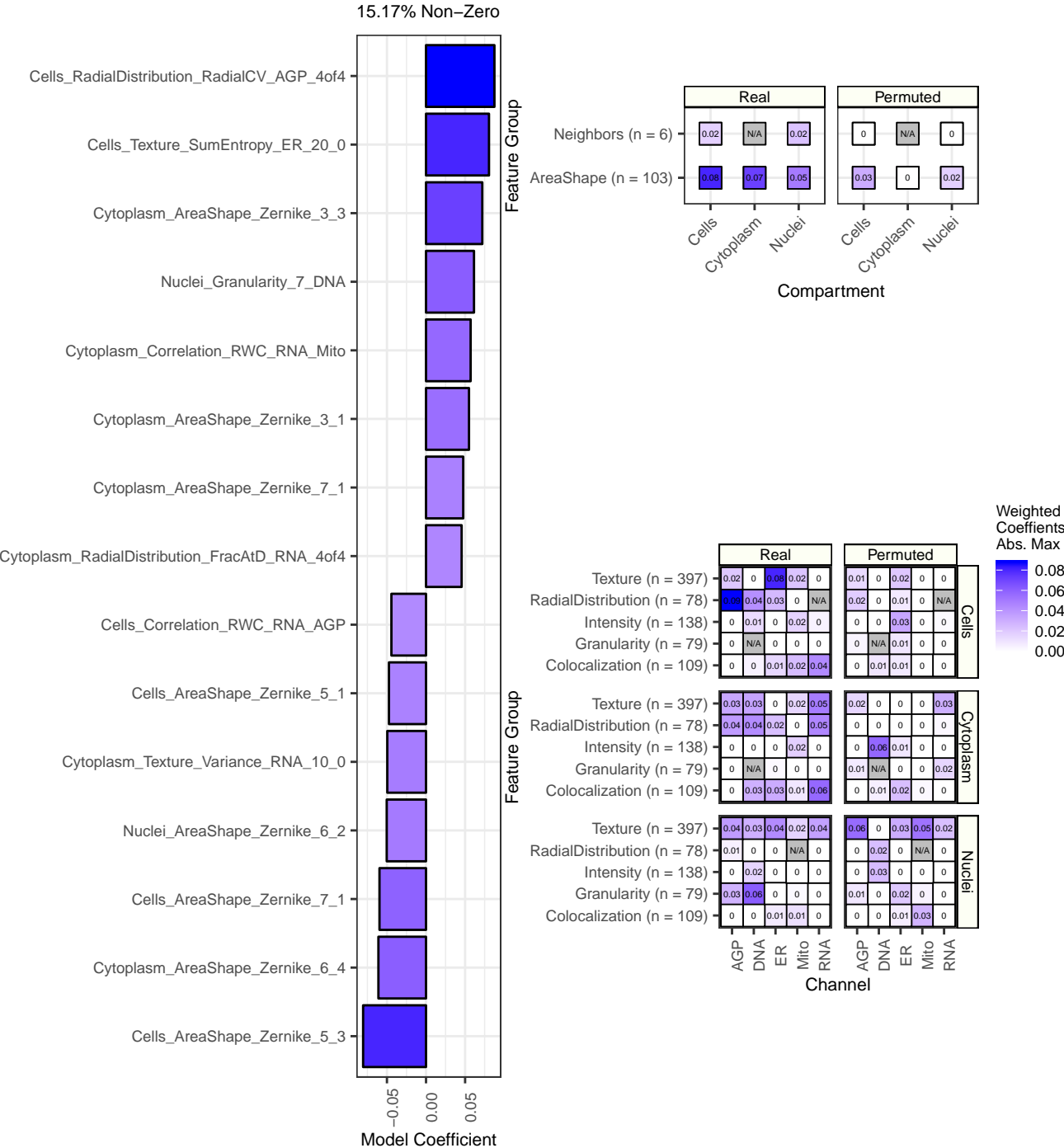Weighted Coeffients Abs. Max: 0.08, 0.06, 0.04, 0.02, 0.00

Cells

	AGP	DNA	ER	Mito	RNA		AGP	DNA	ER	Mito	RNA
Texture (n = 397)	0.02	0	0.05	0.02	0		0.01	0	0.02	0	0
RadialDistribution (n = 78)	0.08	0.04	0.03	0	N/A		0.02	0	0.01	0	N/A
Intensity (n = 138)	0	0.01	0	0.02	0		0	0	0.03	0	0
Granularity (n = 79)	0	N/A	0	0	0		0	N/A	0.01	0	0
Colocalization (n = 109)	0	0	0.01	0.02	0.04		0	0.01	0.01	0	0

Cytoplasm

	AGP	DNA	ER	Mito	RNA		AGP	DNA	ER	Mito	RNA
Texture (n = 397)	0.03	0.03	0	0.02	0.05		0.02	0	0	0	0.03
RadialDistribution (n = 78)	0.04	0.04	0.02	0	0.05		0	0	0	0	0
Intensity (n = 138)	0	0	0	0.02	0		0	0.06	0.01	0	0
Granularity (n = 79)	0	N/A	0	0	0		0.01	N/A	0	0	0.02
Colocalization (n = 109)	0	0.03	0.03	0.01	0.06		0	0.01	0.02	0	0

Nuclei

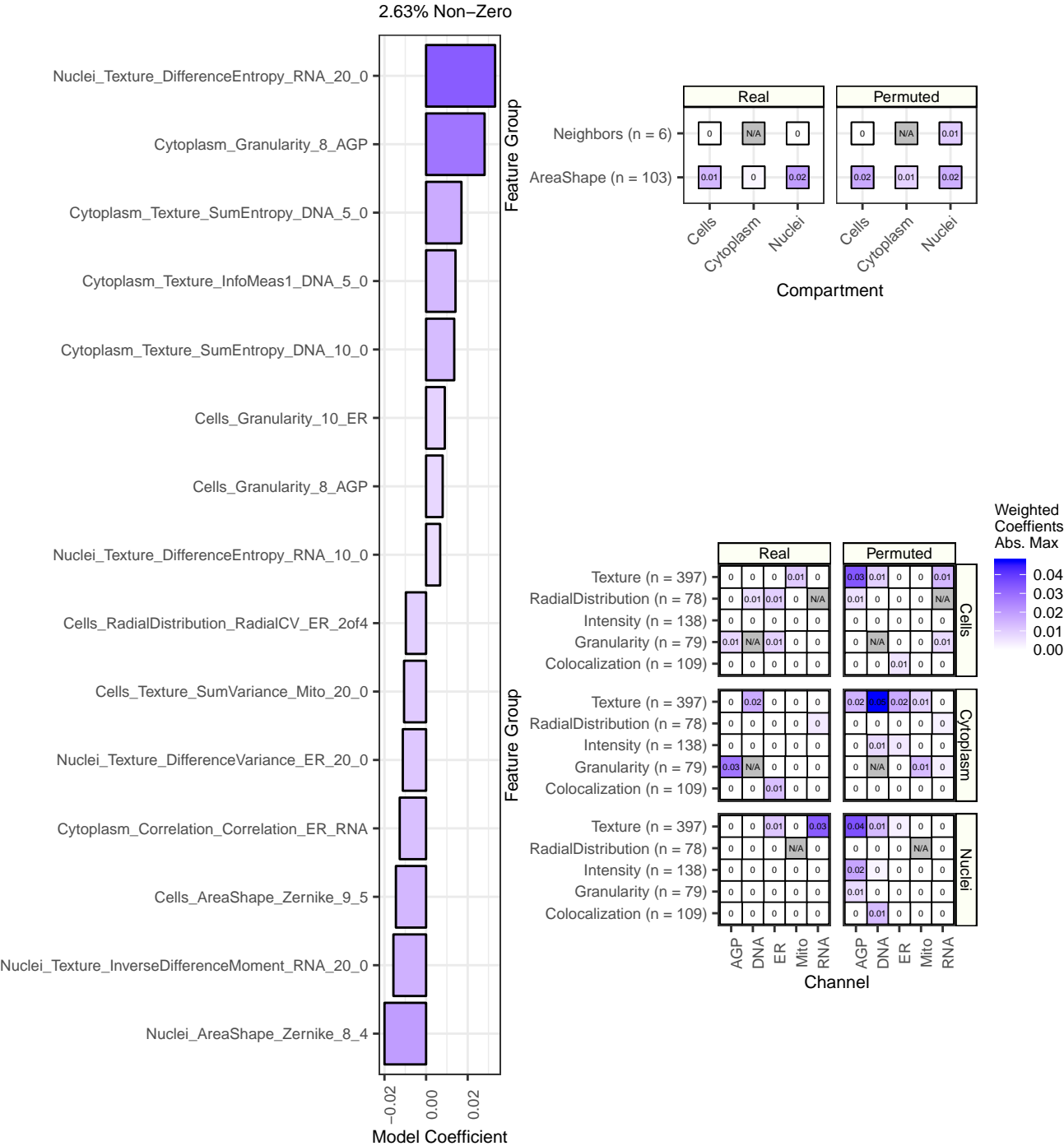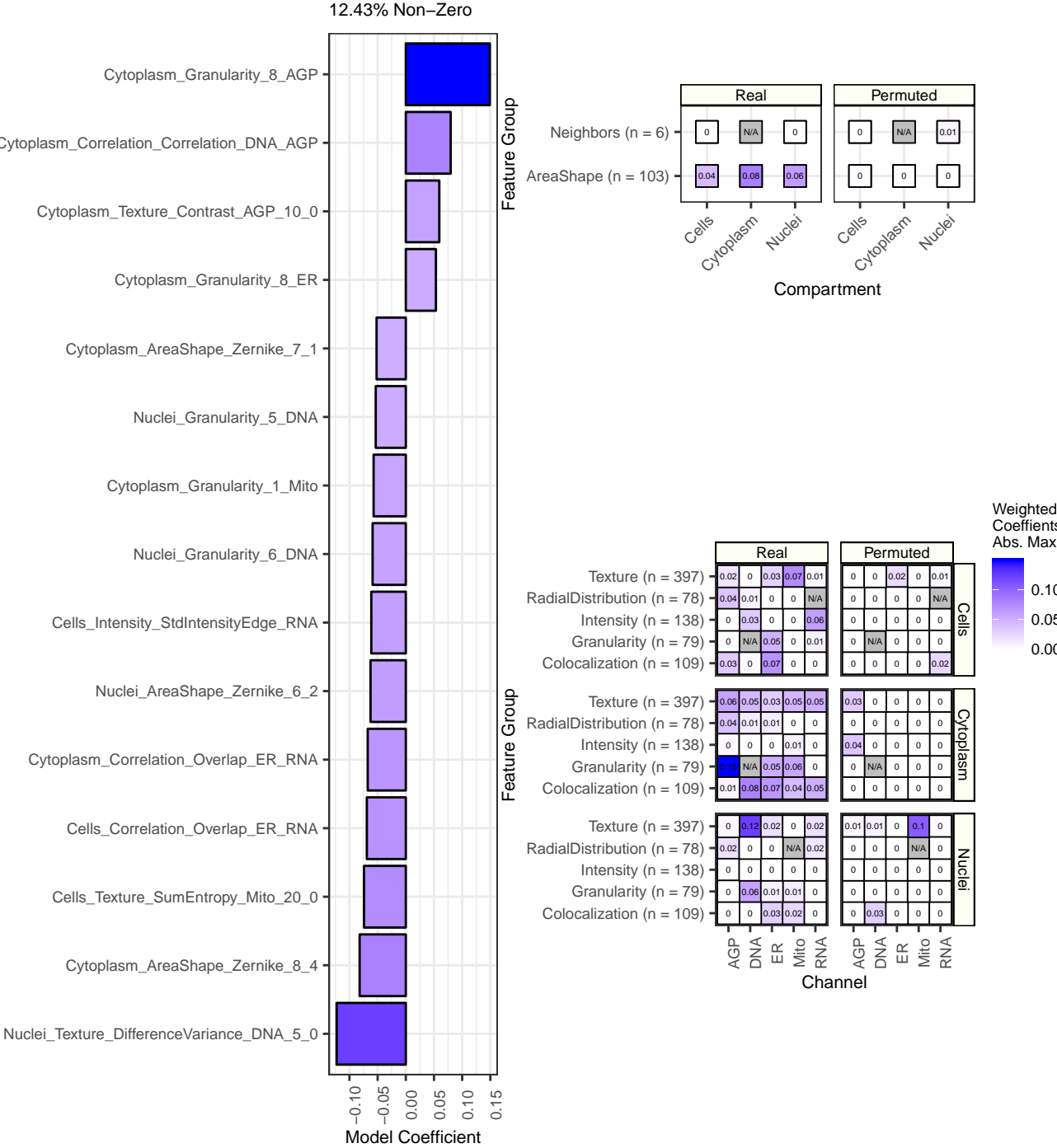|	AGP	DNA	ER	Mito	RNA		AGP	DNA	ER	Mito	RNA
Texture (n = 397)	0.04	0.03	0.04	0.02	0.04		0.06	0	0.03	0.05	0.02
RadialDistribution (n = 78)	0.01	0	0	N/A	0		0	0.02	0	N/A	0
Intensity (n = 138)	0	0.02	0	0	0		0	0.03	0	0	0
Granularity (n = 79)	0.03	0.06	0	0	0		0.01	0	0.02	0	0
Colocalization (n = 109)	0	0	0.01	0.01	0		0	0	0.01	0.03	0

Channel

Live Cells

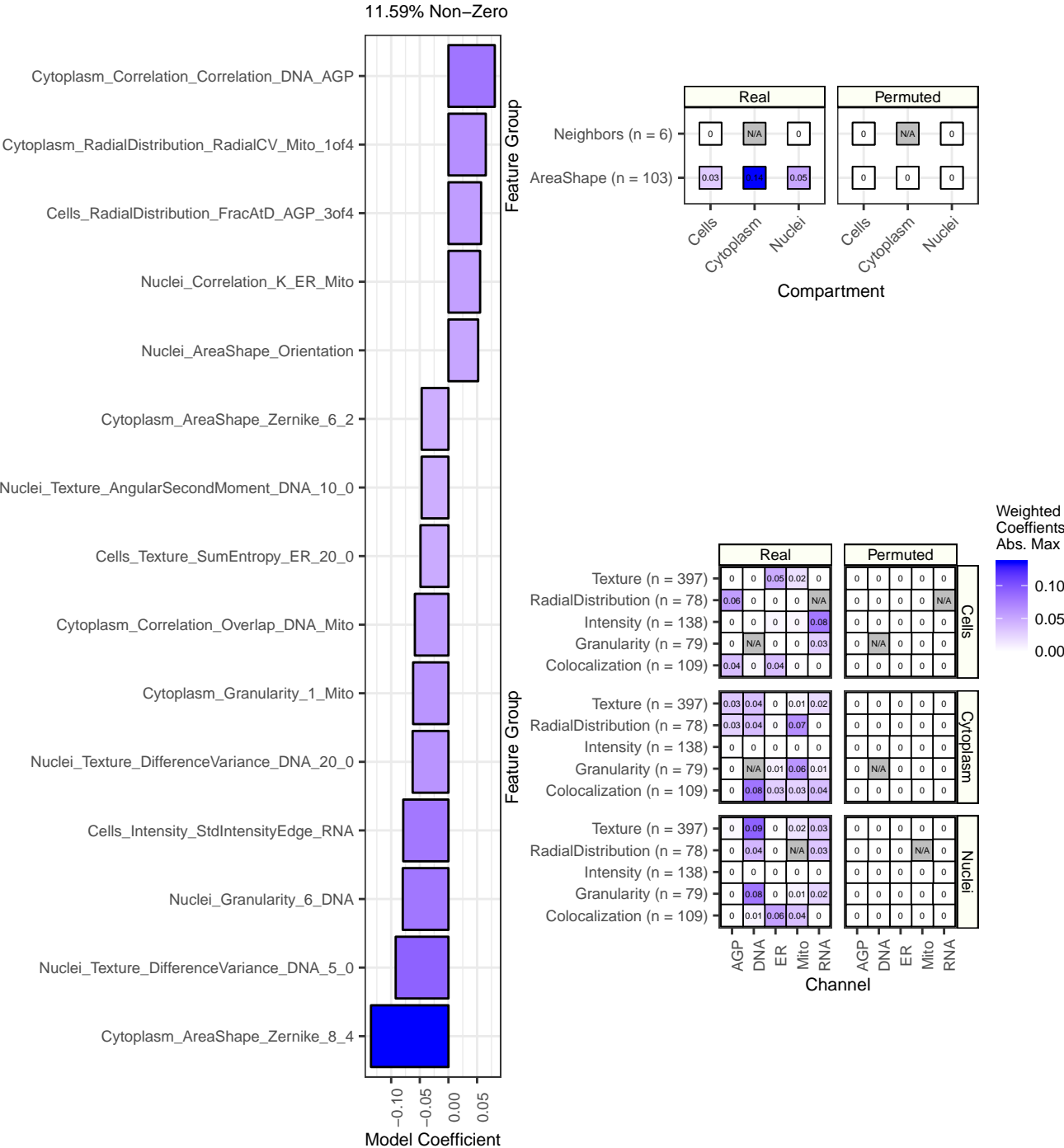12.96% Non−Zero
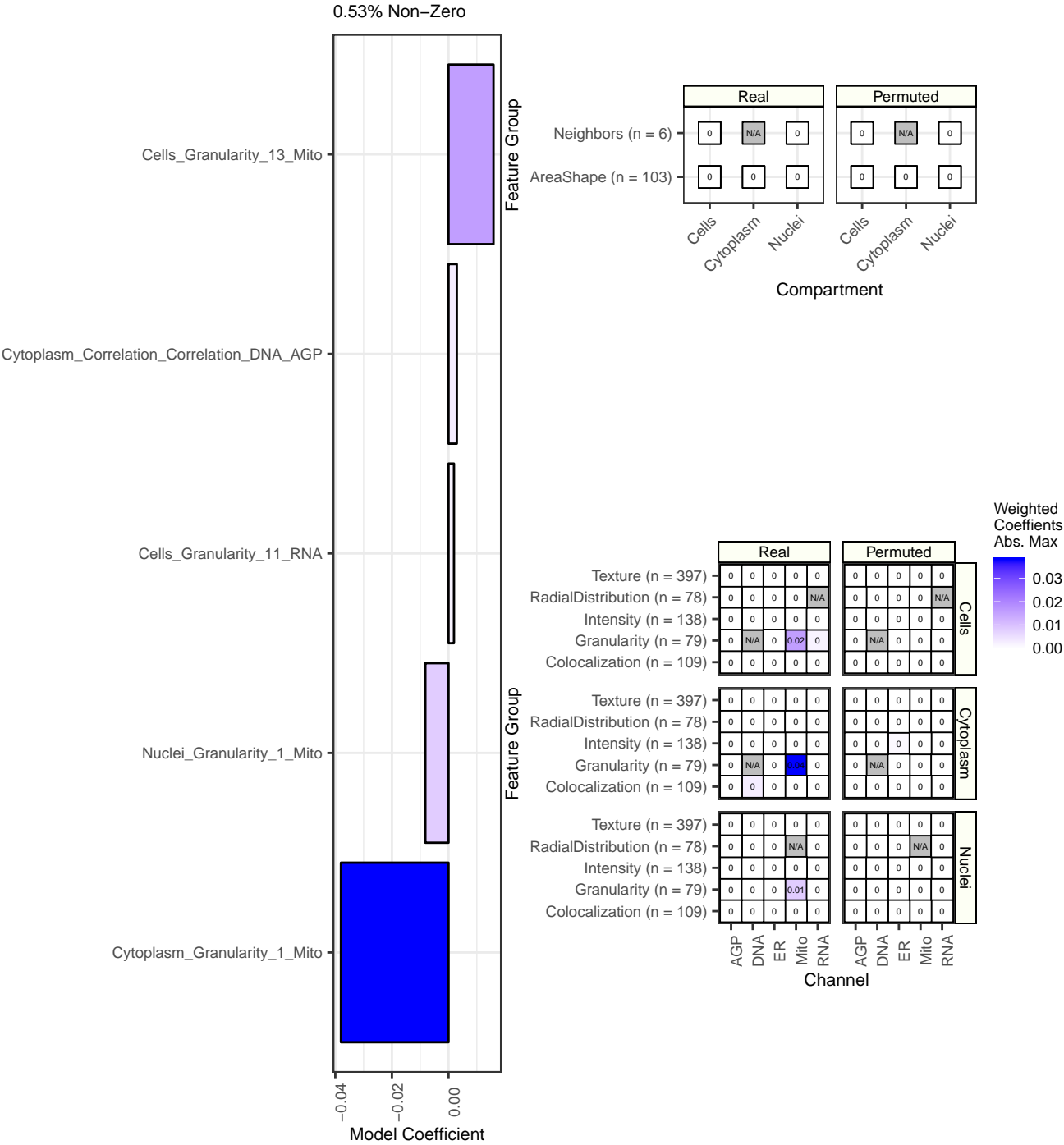
% All Apoptosis (CASP+)
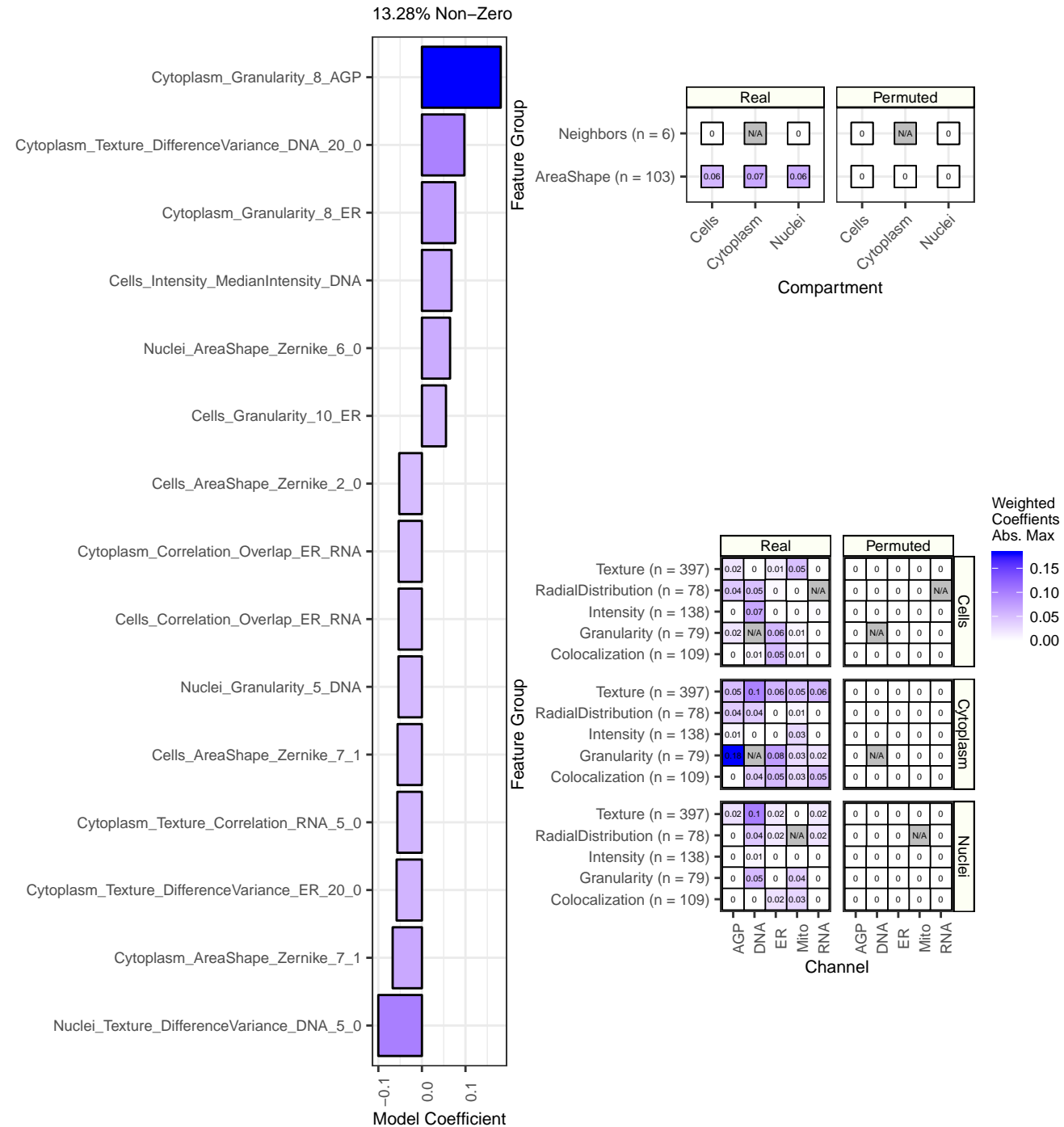
% Caspase / % Dead Only

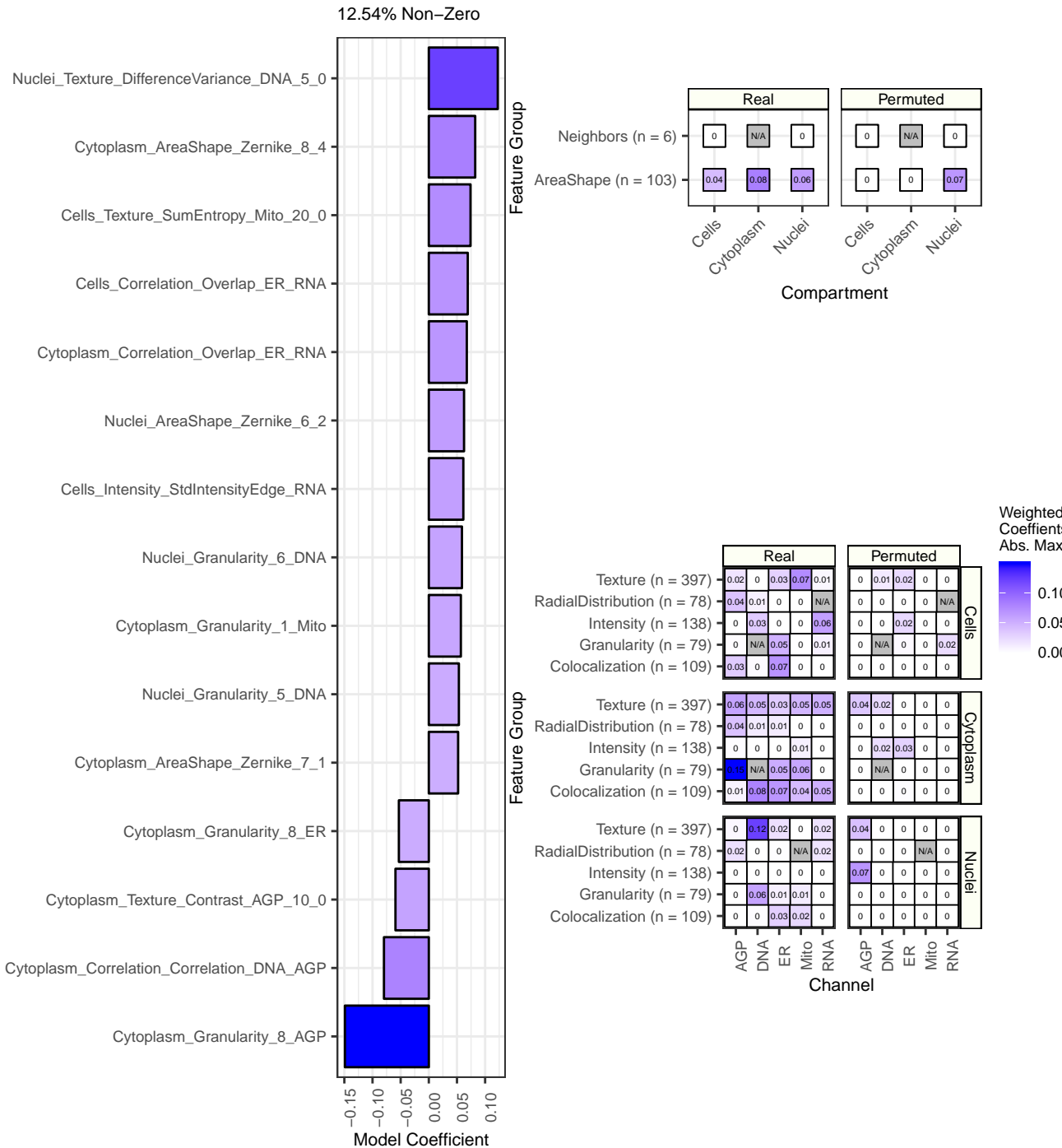# % All Dead (DRAQ7+)

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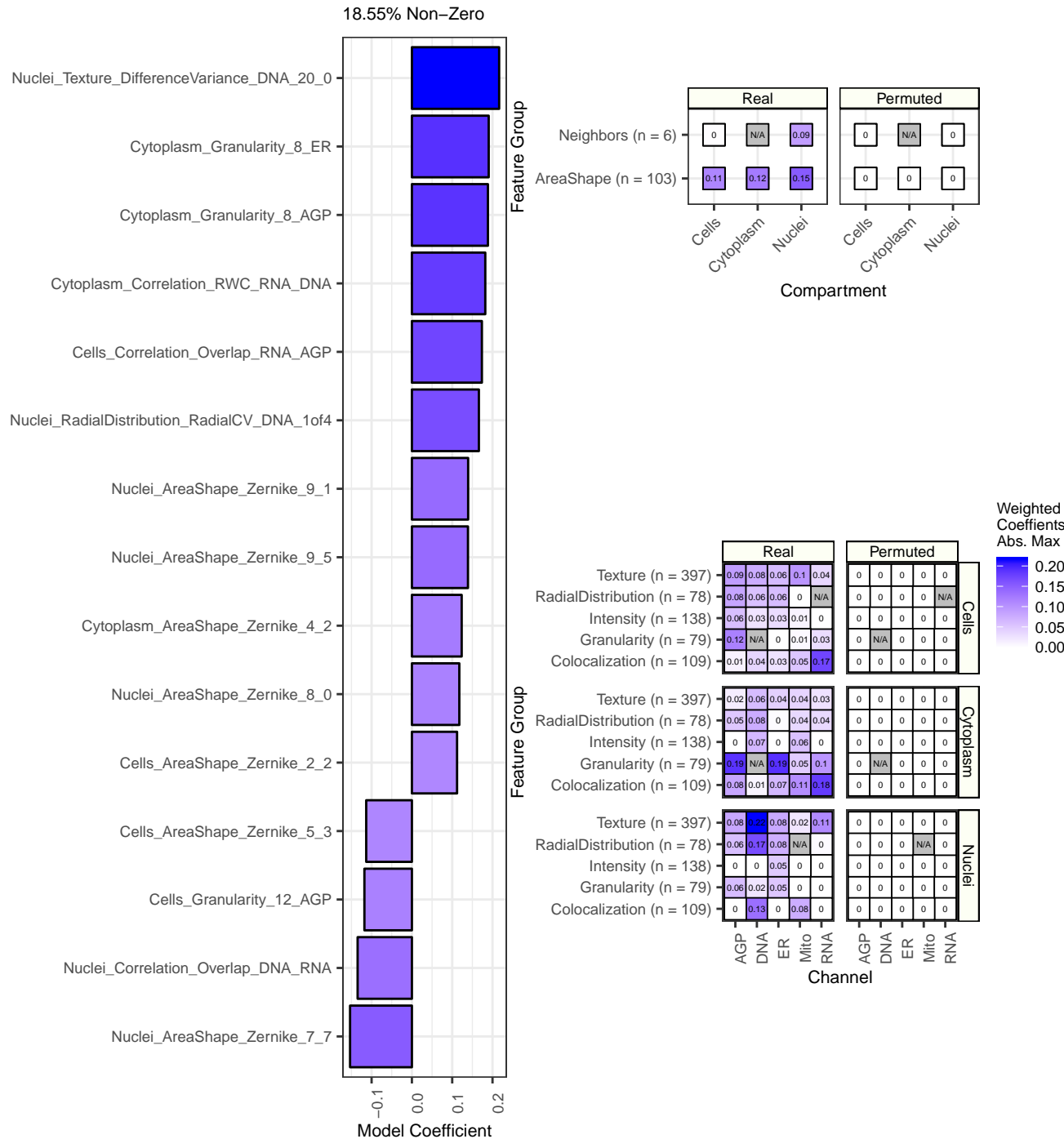
% Early Apoptosis (CASP+; DRAQ7−)

% Late Apoptosis (CASP+; DRAQ7+)

% Live (DRAQ7−; CASP−)

ROS−back

ROS