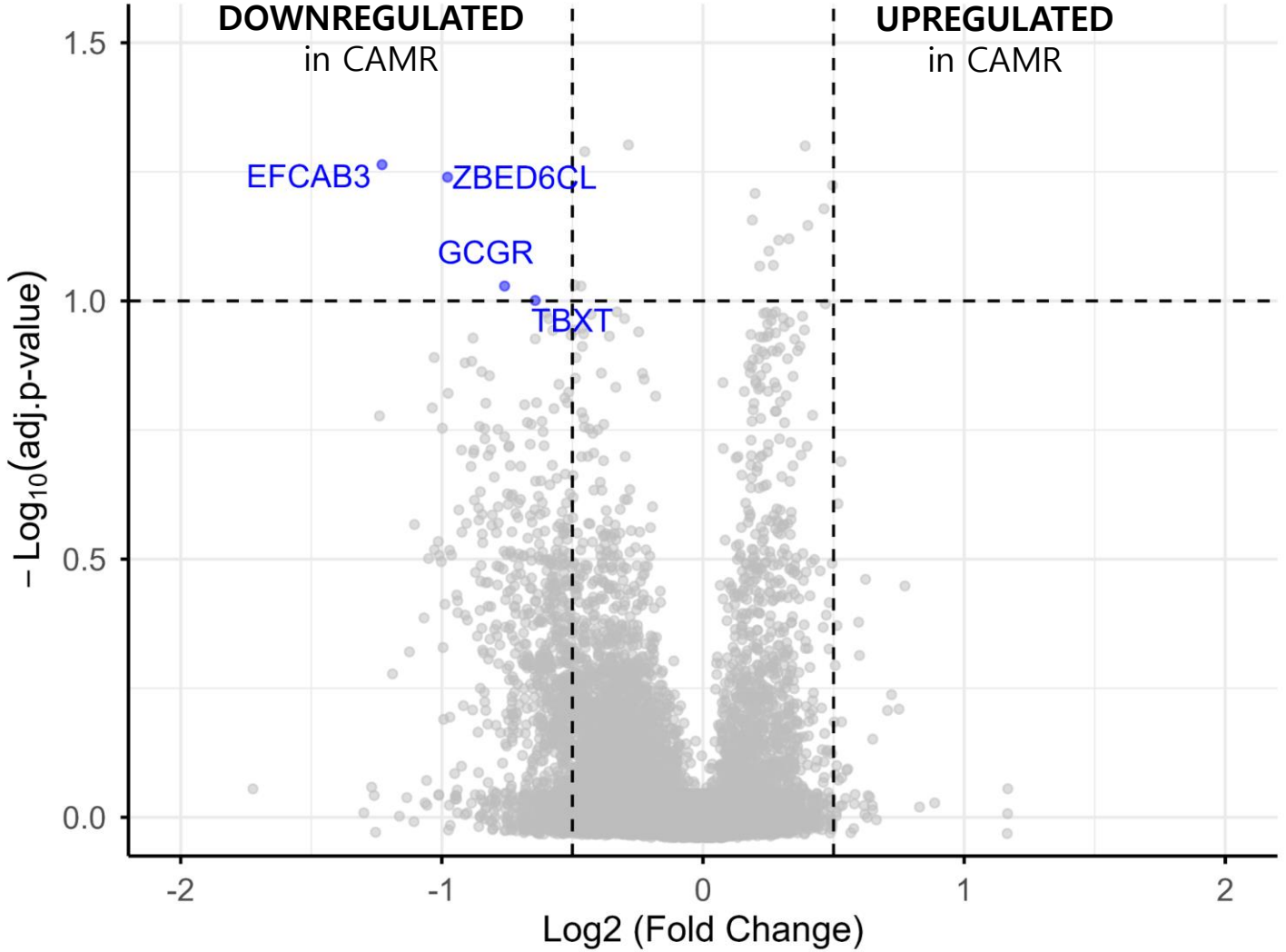
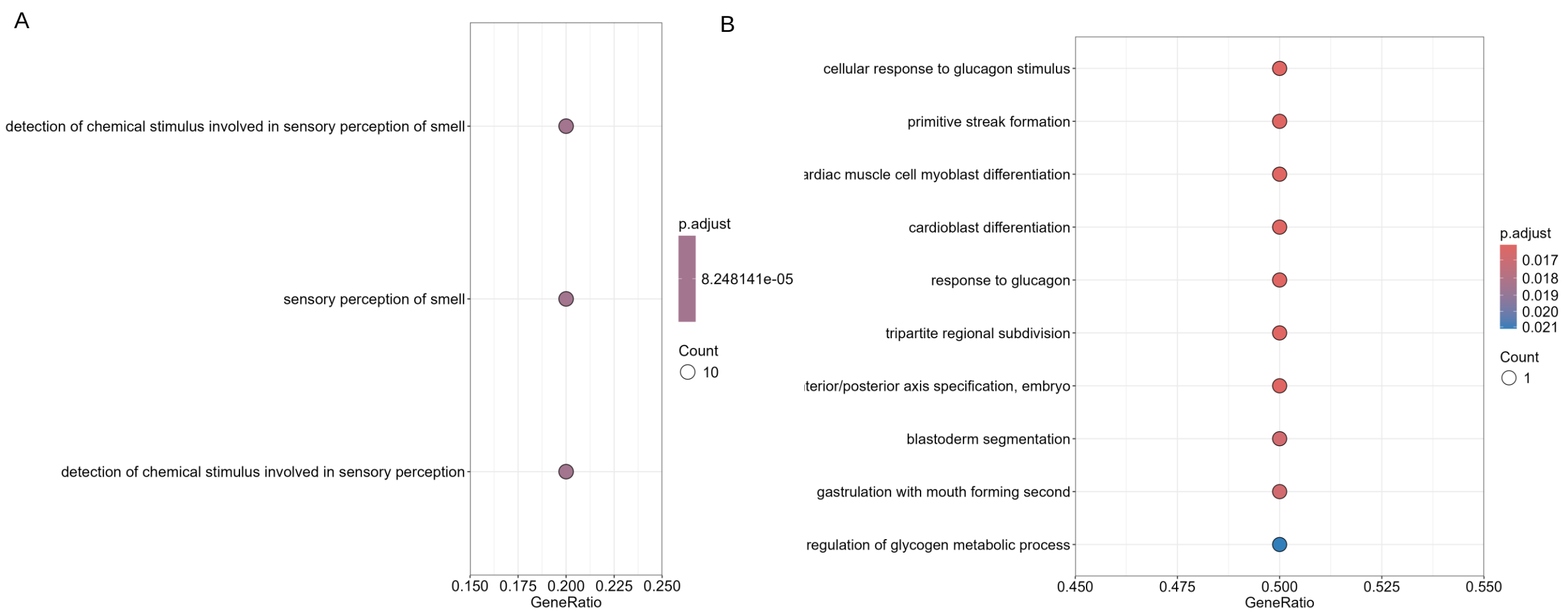
Supplementary Figures S1~8

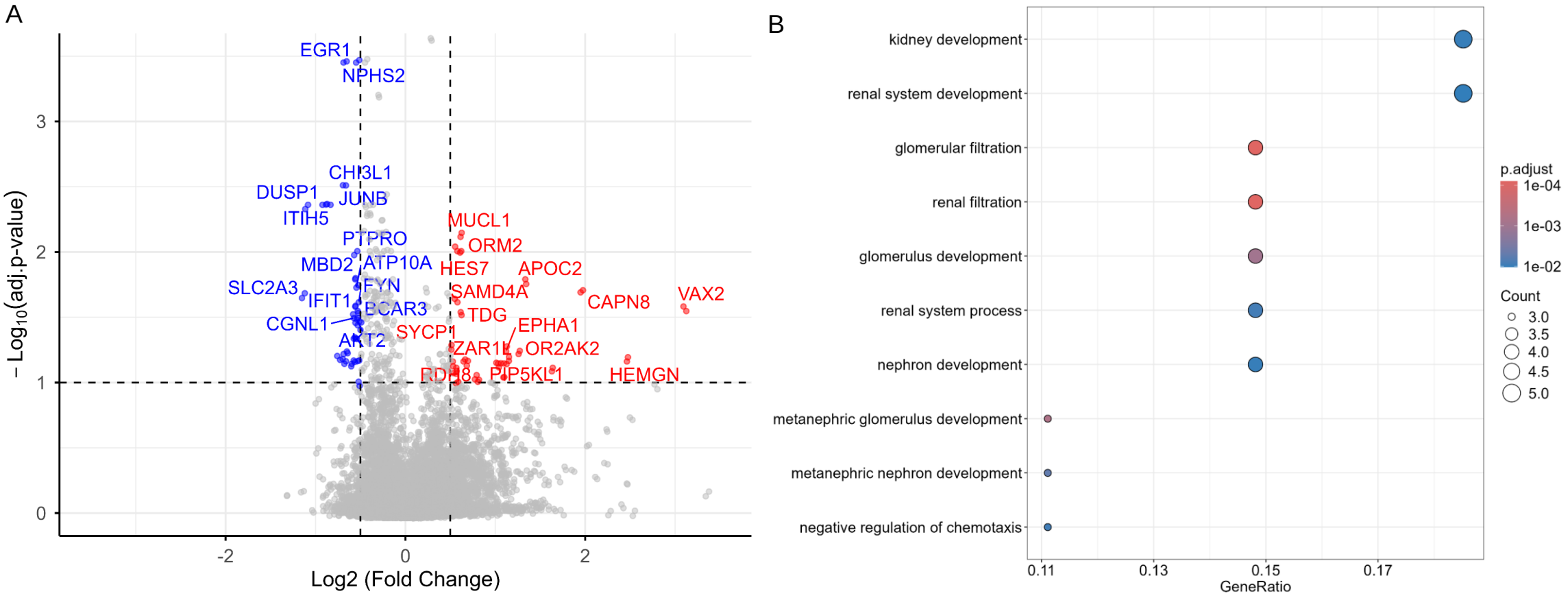
1. Supplementary Figure S1. Volcano plot: vascular ROIs (CAMR vs non-CAMR by model 1)
2. Supplementary Figure S2. GO enrichment dot plots (CAMR vs non-CAMR by model 1)
3. Supplementary Figure S3. Volcano plot and GO enrichment dot plot (allograft vs native-kidney by model 1)
4. Supplementary Figure S4. Volcano plots (CAMR vs non-CAMR by sensitivity analysis)
5. Supplementary Figure S5. Dot plots (ssGSEA scores for B-HOT pathways by 5 groups)
6. Supplementary Figure S6. Dot plots (ssGSEA score for complete B-HOT pathways)
7. Supplementary Figure S7. Dot plots (spatial deconvolution of inflammatory cells)
8. Supplementary Figure S8. Dot plots (spatial deconvolution of inflammatory cells)



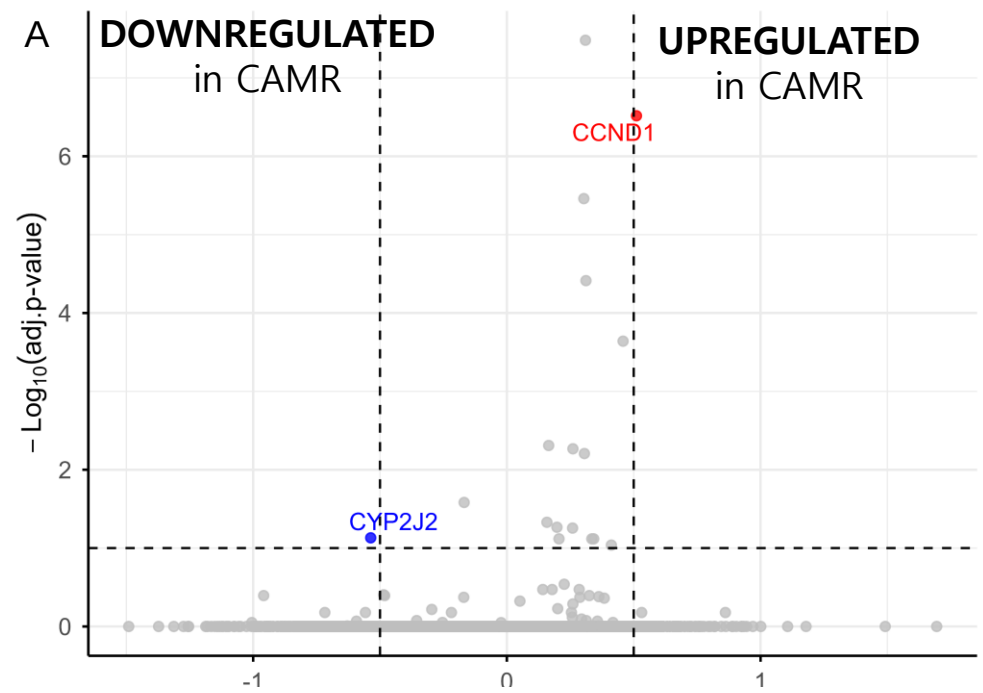
Supplementary Figure S1. Vascular CAMR ROIs (n=6; 3 DSA-positive, 3 DSA-negative) compared with non-CAMR ROIs (n=9; 3 DSA-positive NER, 3 DSA-negative NER, and 3 controls).
CAMR, chronic antibody-mediated rejection; ROI, regions of interest; DSA, donor-specific antibody; NER, no evidence of rejection.

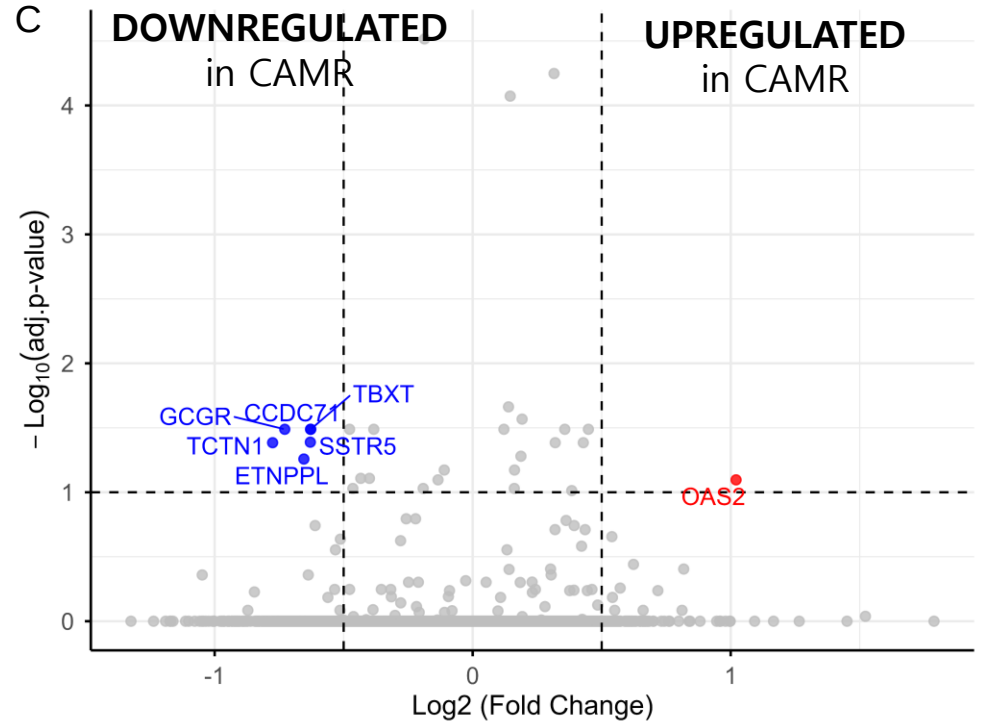


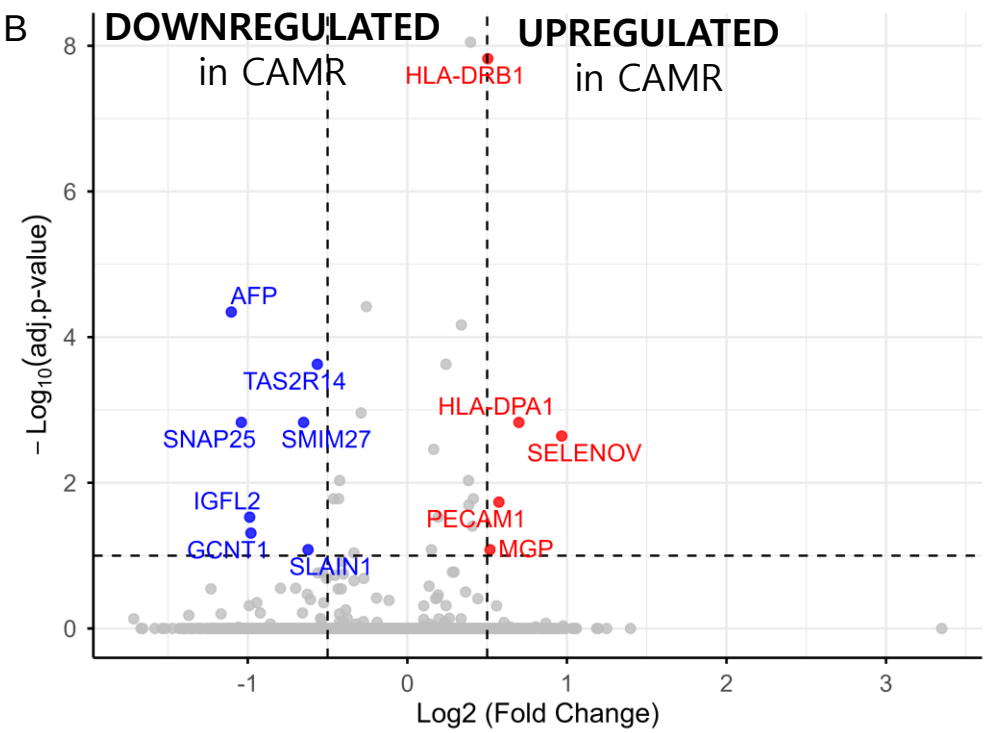
Supplementary Figure S2. Gene ontology biological process terms enriched among genes downregulated in CAMR glomerular (A) ROIs and vascular (B) ROIs.
CAMR, chronic antibody-mediated rejection; ROI, regions of interest.



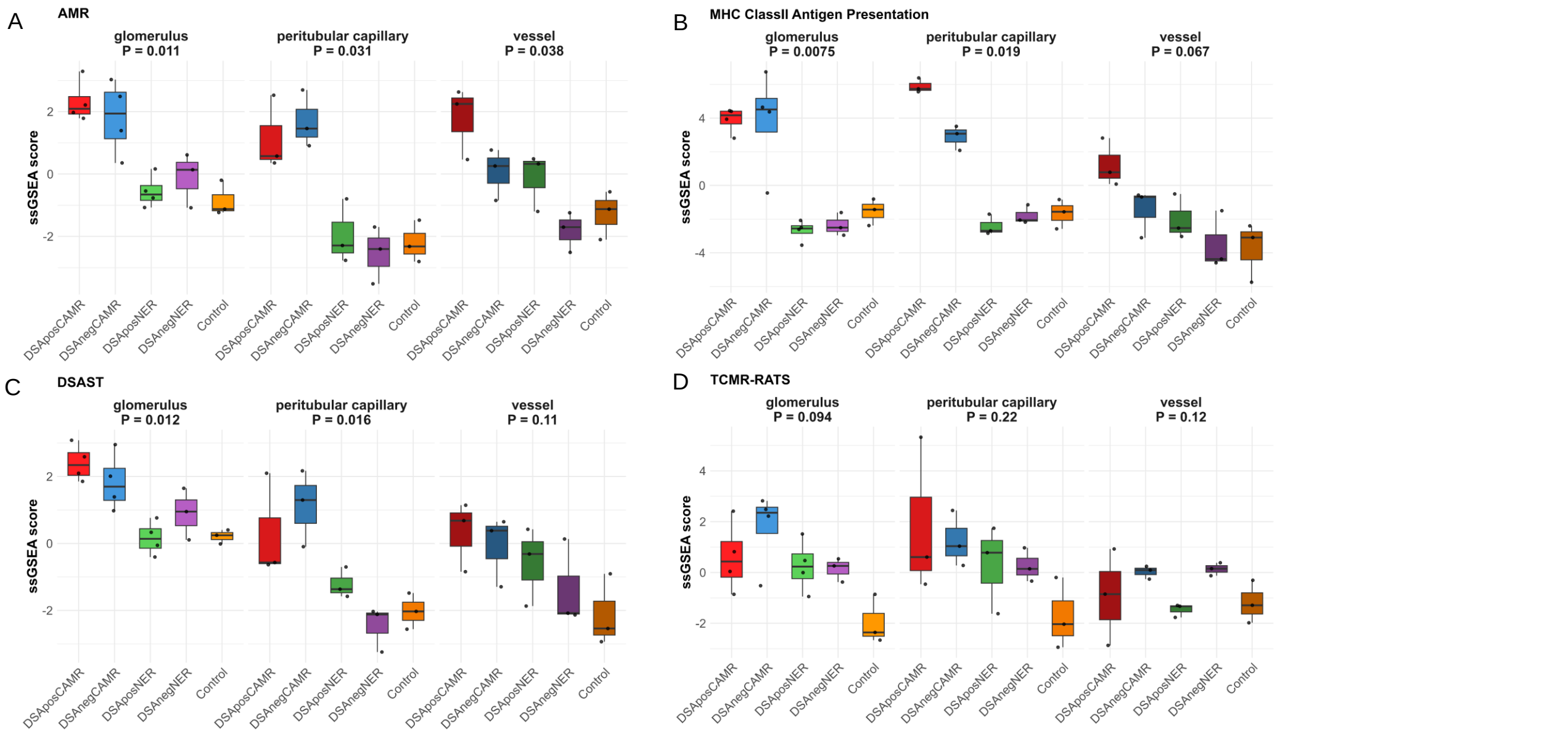
Supplementary Figure S3. Lower expression of kidney development and glomerular filtration-related genes was observed in the glomerular ROIs in allograft compared to native kidney.
(A) Volcano plot showing significantly upregulated (red) and downregulated (blue) genes in glomerular ROIs from allografts (n=15) compared with glomerular ROIs from native kidney (n=3). For visualization purposes, the x-axis was symmetrically centered at zero, and extreme log2 fold-change values were capped; no genes were excluded from the analysis. Only the top 15 genes were labeled by symbol.
(B) Gene ontology biological process terms enriched among genes downregulated in allograft glomerular ROIs.
ROI, regions of interest.







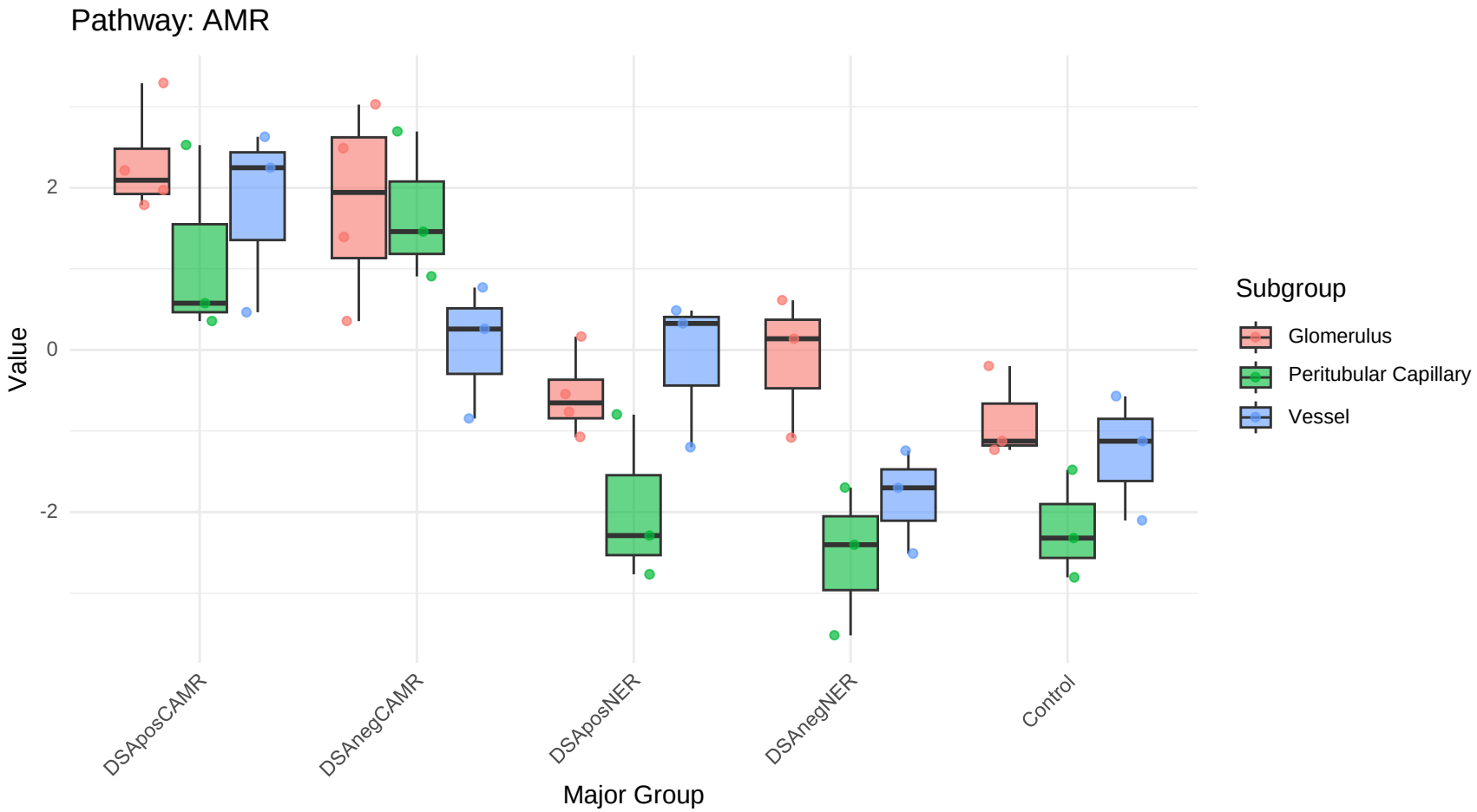
Supplementary Figure S4. Sensitivity analysis of differential gene expression in CAMR after excluding the early post-transplant NER case and reclassifying the low-MFI case as DSA-negative.
Volcano plots showing differentially expressed genes between CAMR and non-CAMR ROIs in glomerular **(A)**, peritubular capillary **(B)**, and vascular compartments **(C)**.
CAMR, chronic antibody-mediated rejection; ROI, regions of interest; DSA, donor-specific antibody; NER, no evidence of rejection.



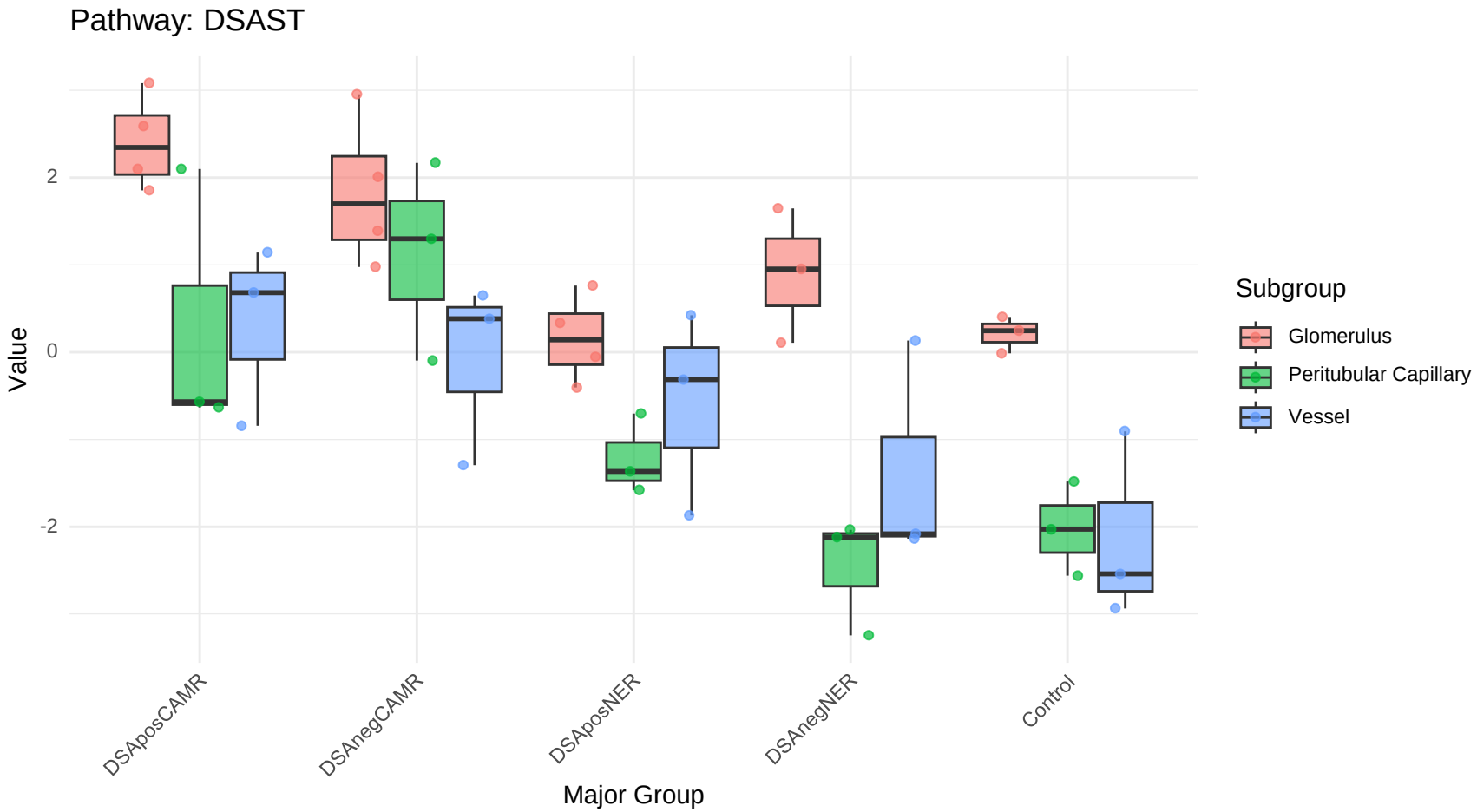
Supplementary Figure S5. Dot plot of single sample gene set enrichment analysis (ssGSEA) scores for each B-HOT pathway by renal compartment. Each dot represents the ssGSEA score of an individual ROI. The pathways associated with antibody-mediated rejection (AMR) (**A**), MHC class II antigen presentation (**B**), and donor-specific antibody-associated tissue signatures (DSAST) (**C**) show a consistent trend across compartments, with scores following the order: DSA-positive CAMR > DSA-negative CAMR > DSA-positive NER > DSA-negative NER. In contrast, T cell–mediated rejection-related acute tissue signatures (TCMR-RATS) scores (**D**) do not display prominent differences or consistent patterns among the groups in any renal compartment. *AMR, antibody-mediated rejection; DSAST, donor-specific antibody-associated tissue signatures; TCMR-RATS, T cell-mediated rejection-related acute tissue signatures; ROI, region of interest; DSA, donor-specific antibody; CAMR, chronic active antibody-mediated rejection; NER, no evidence of rejection.*

Supplementary Figure S6.

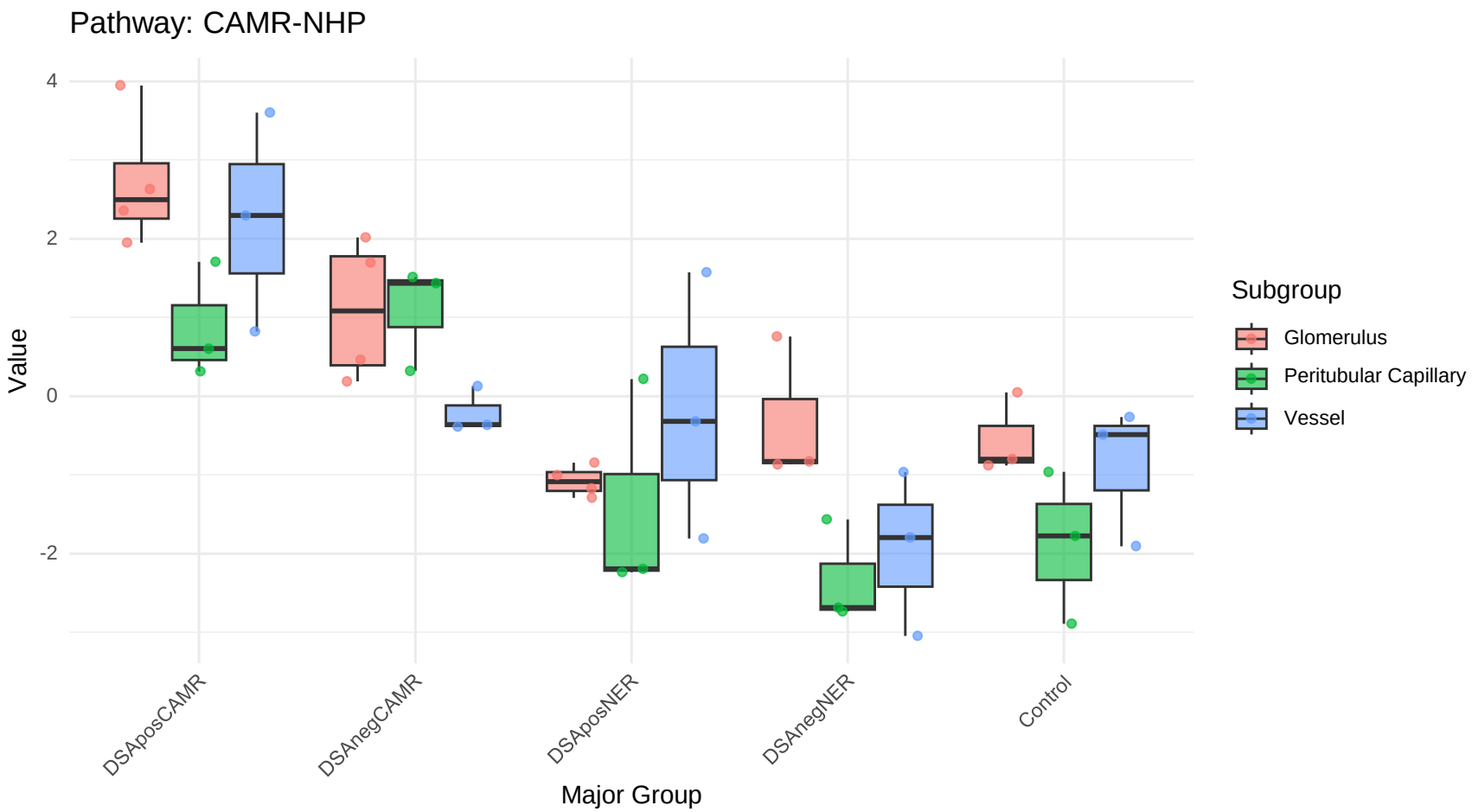
AMR


Pathway: AMR
Value
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

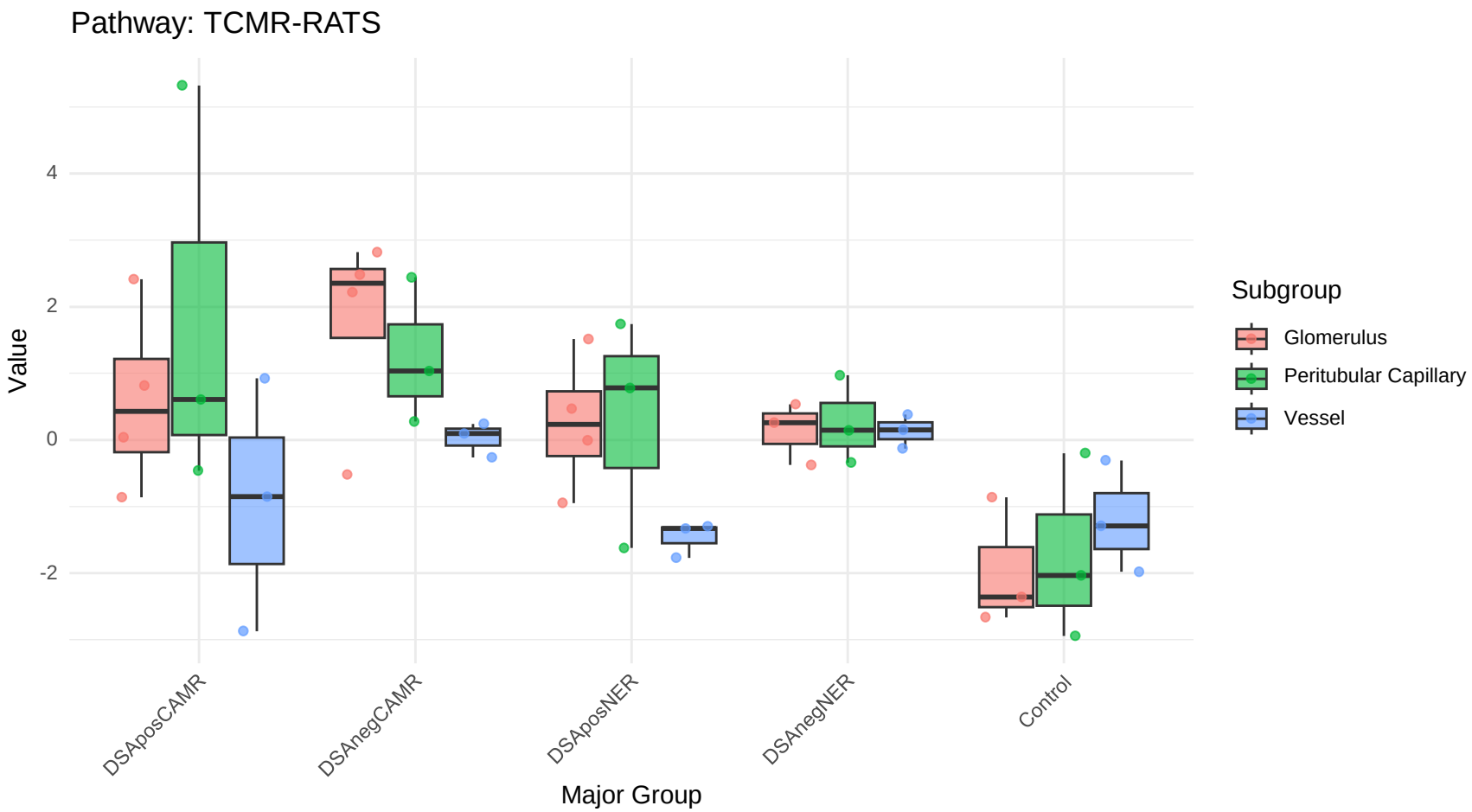
DSAST


Pathway: DSAST
Value
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

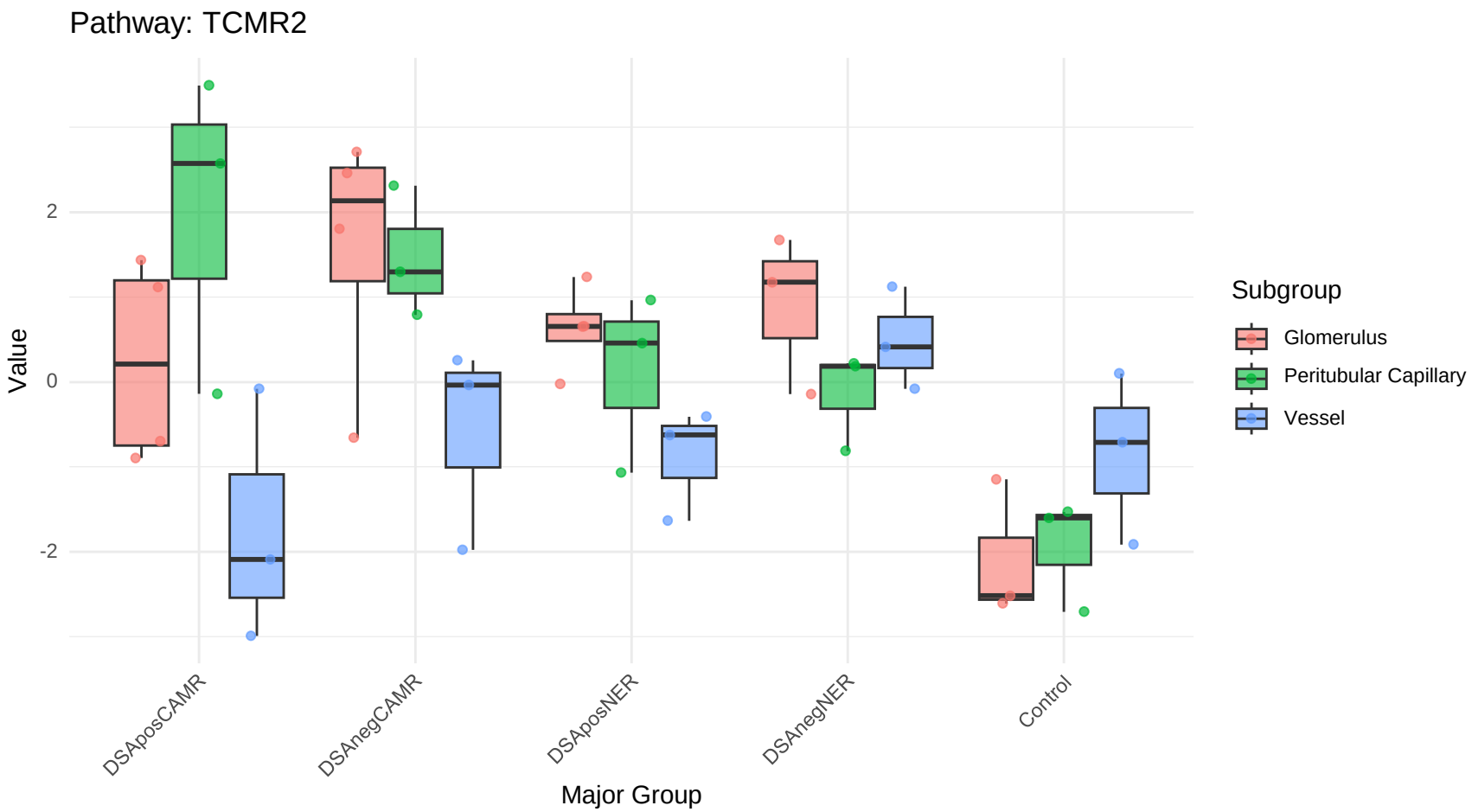
CAMR-NHP


Pathway: CAMR-NHP
Value
4
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

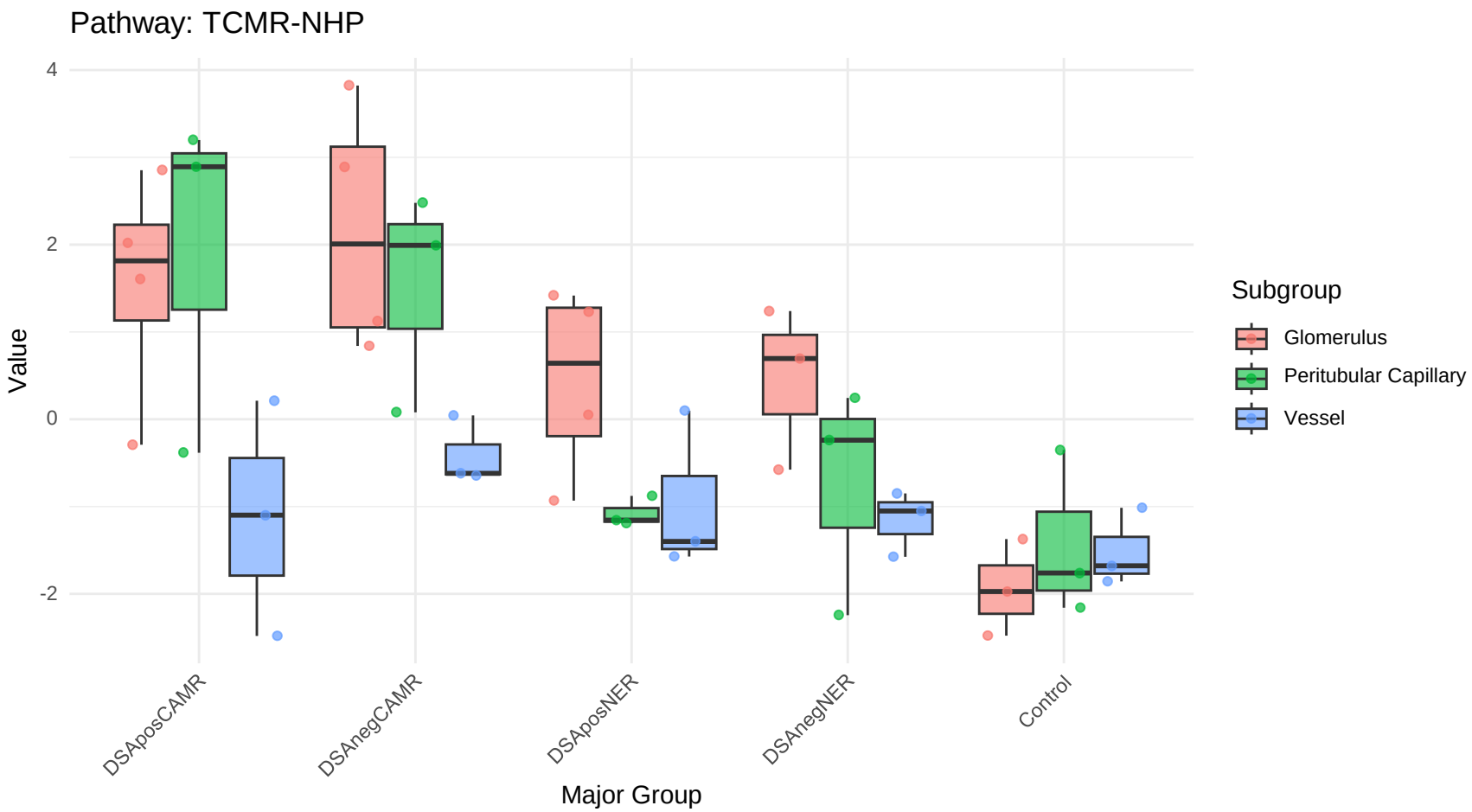
TCMR-RATS


Pathway: TCMR-RATS
Value
4
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

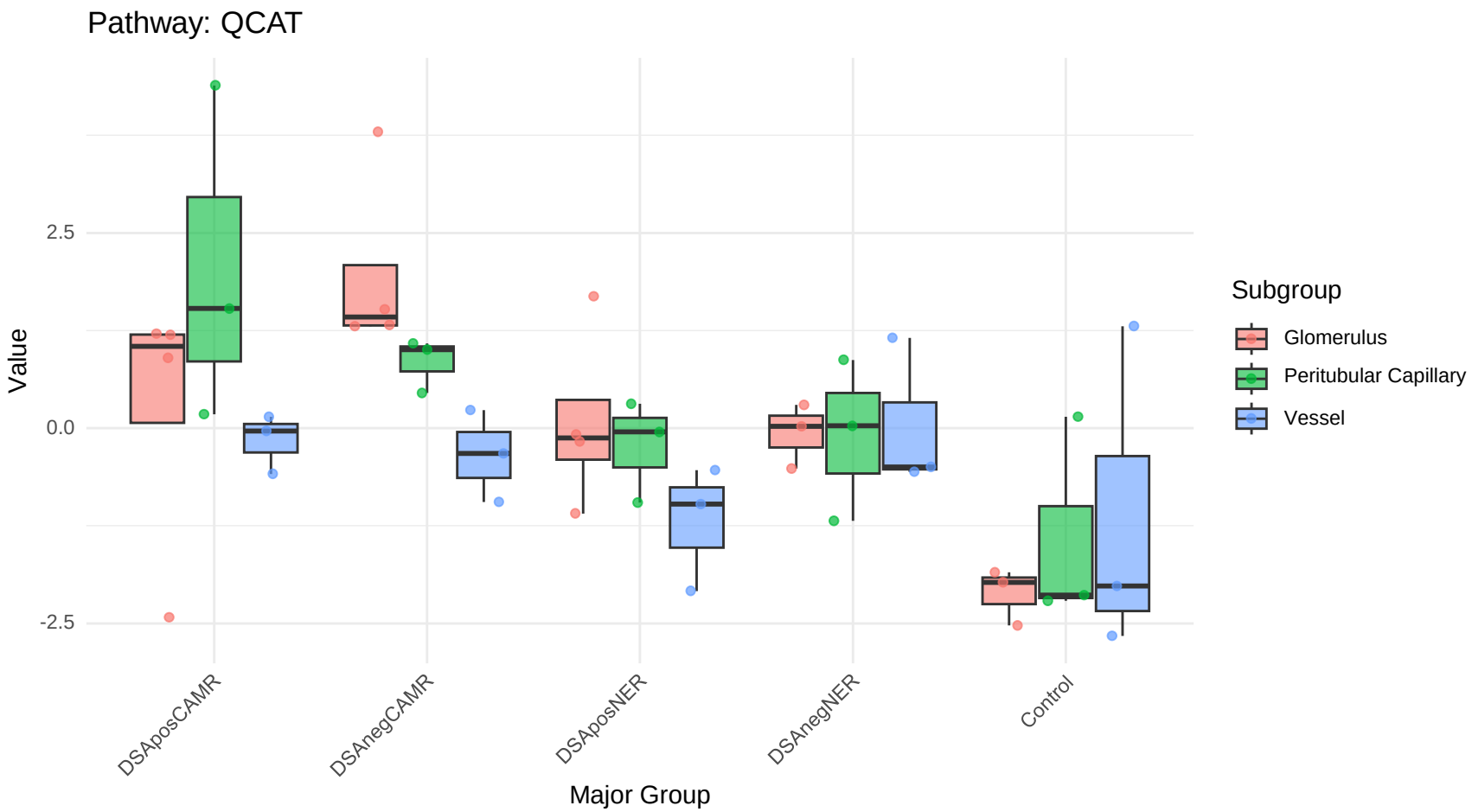
TCMR2


Pathway: TCMR2
Value
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

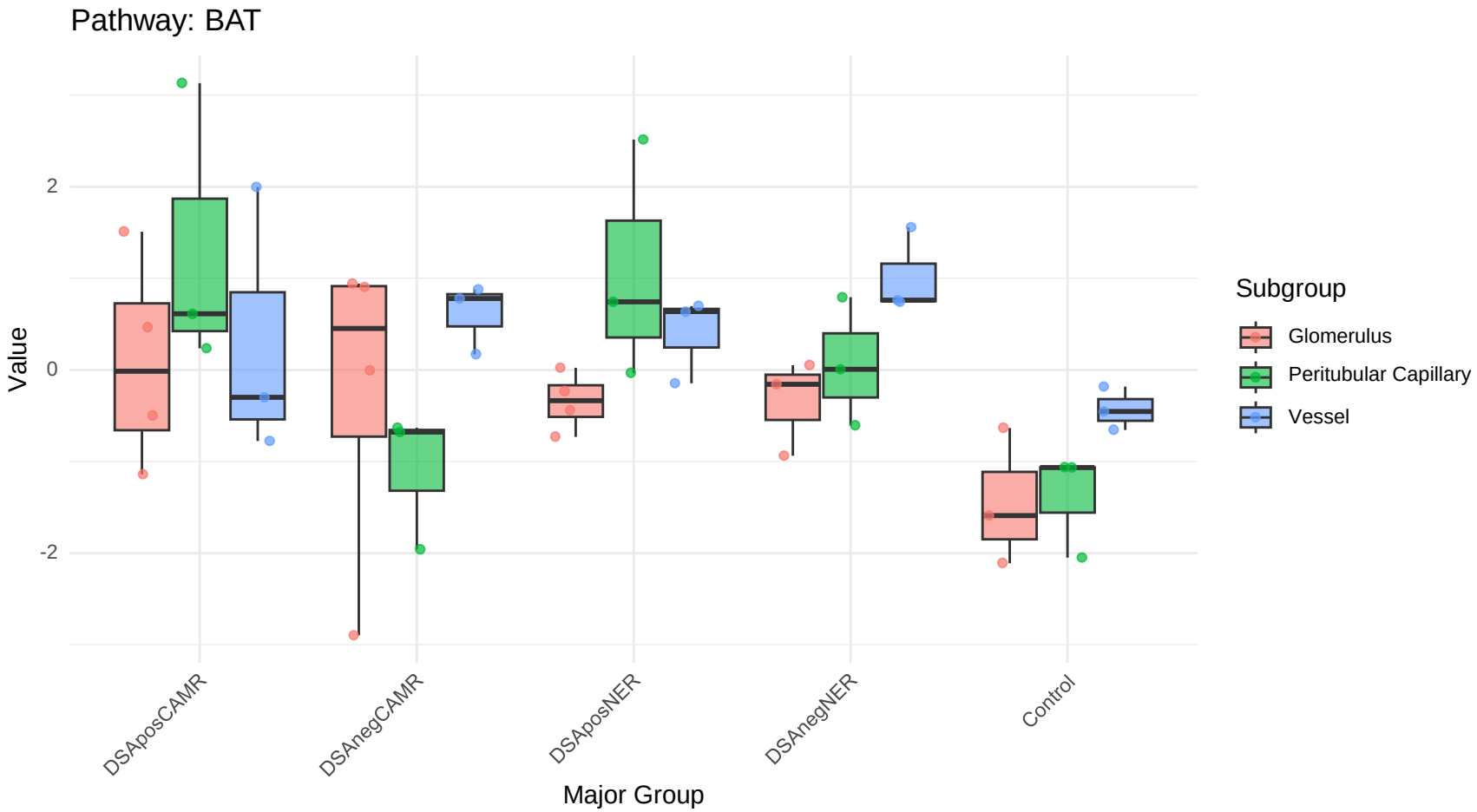
TCMR-NHP


Pathway: TCMR-NHP
Value
4
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

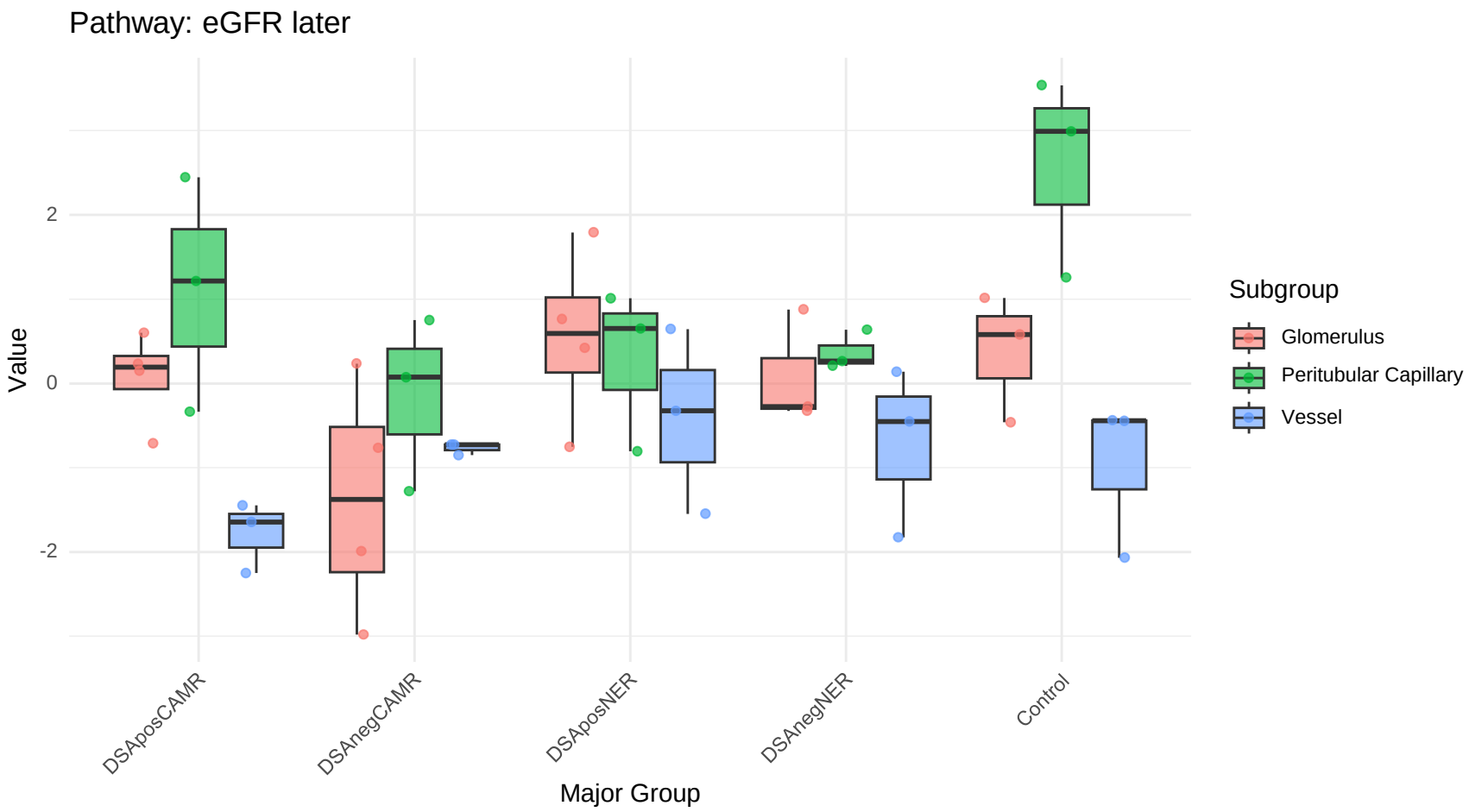
QCAT


Pathway: QCAT
Value
2.5
0.0
-2.5
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

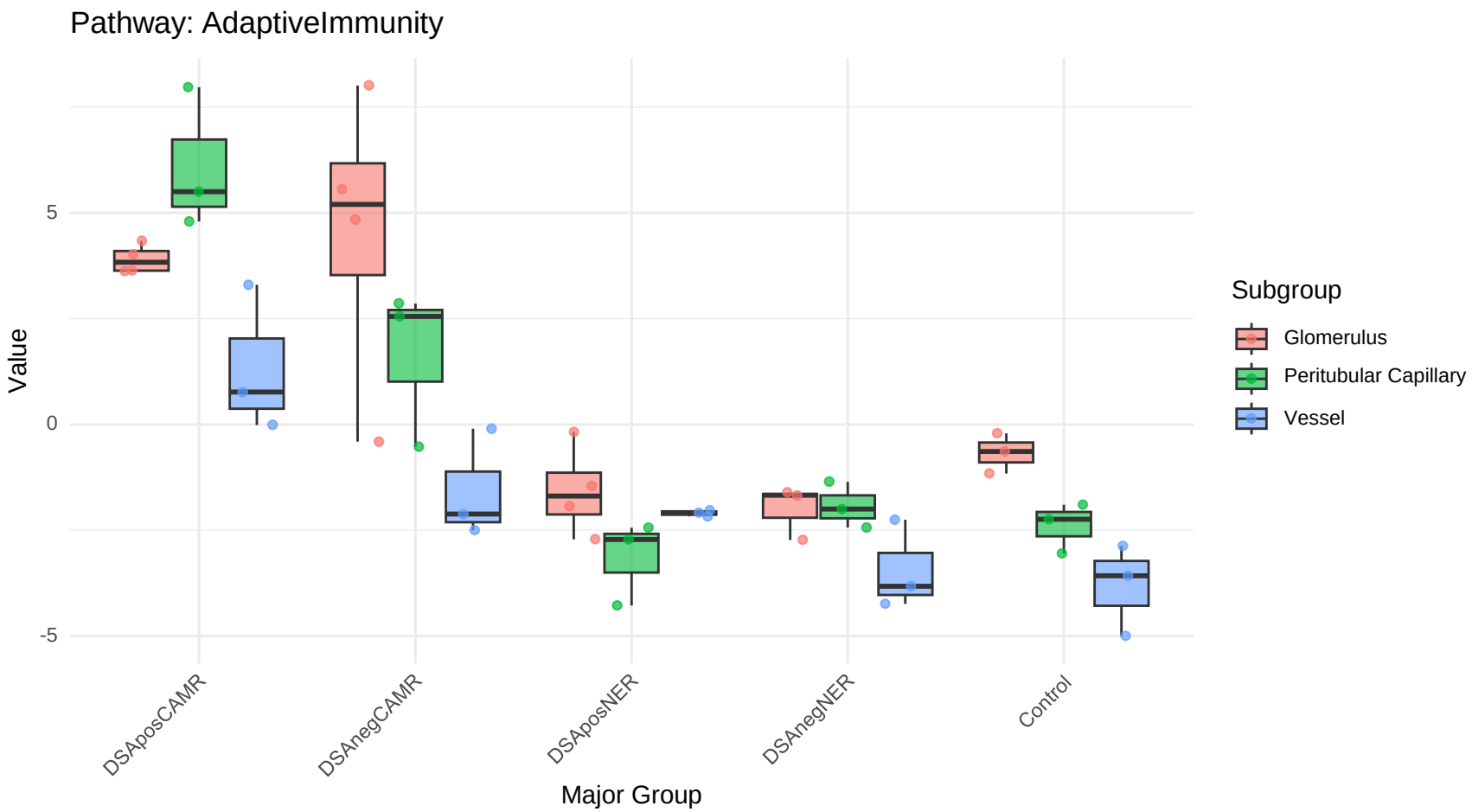
BAT


Pathway: BAT
Value
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

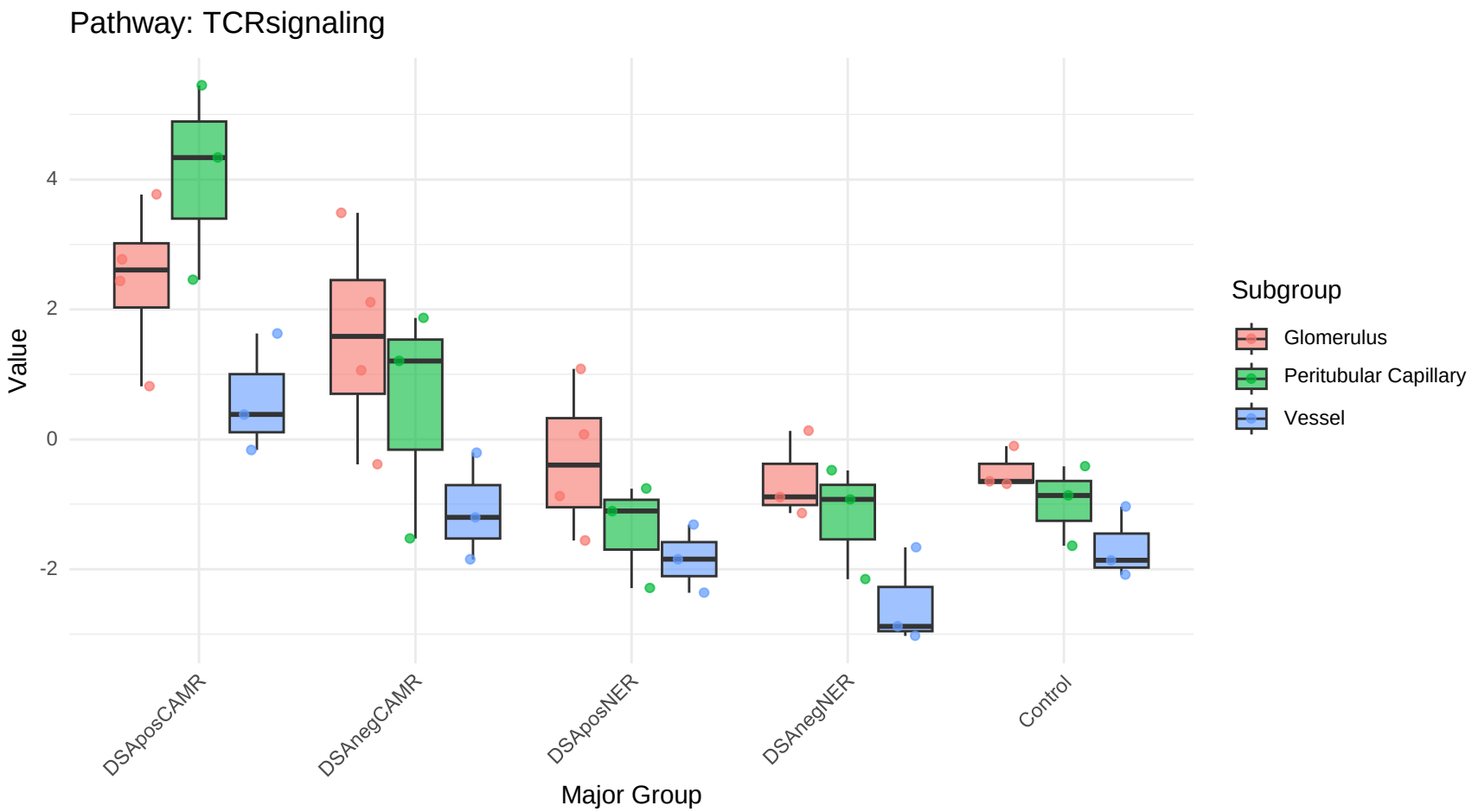
eGFR later


Pathway: eGFR later
Value
2
0
-2
DSAposCAMR
DSAnegCAMR
DSAposNER
DSAnegNER
Control
Major Group
Subgroup
Glomerulus
Peritubular Capillary
Vessel

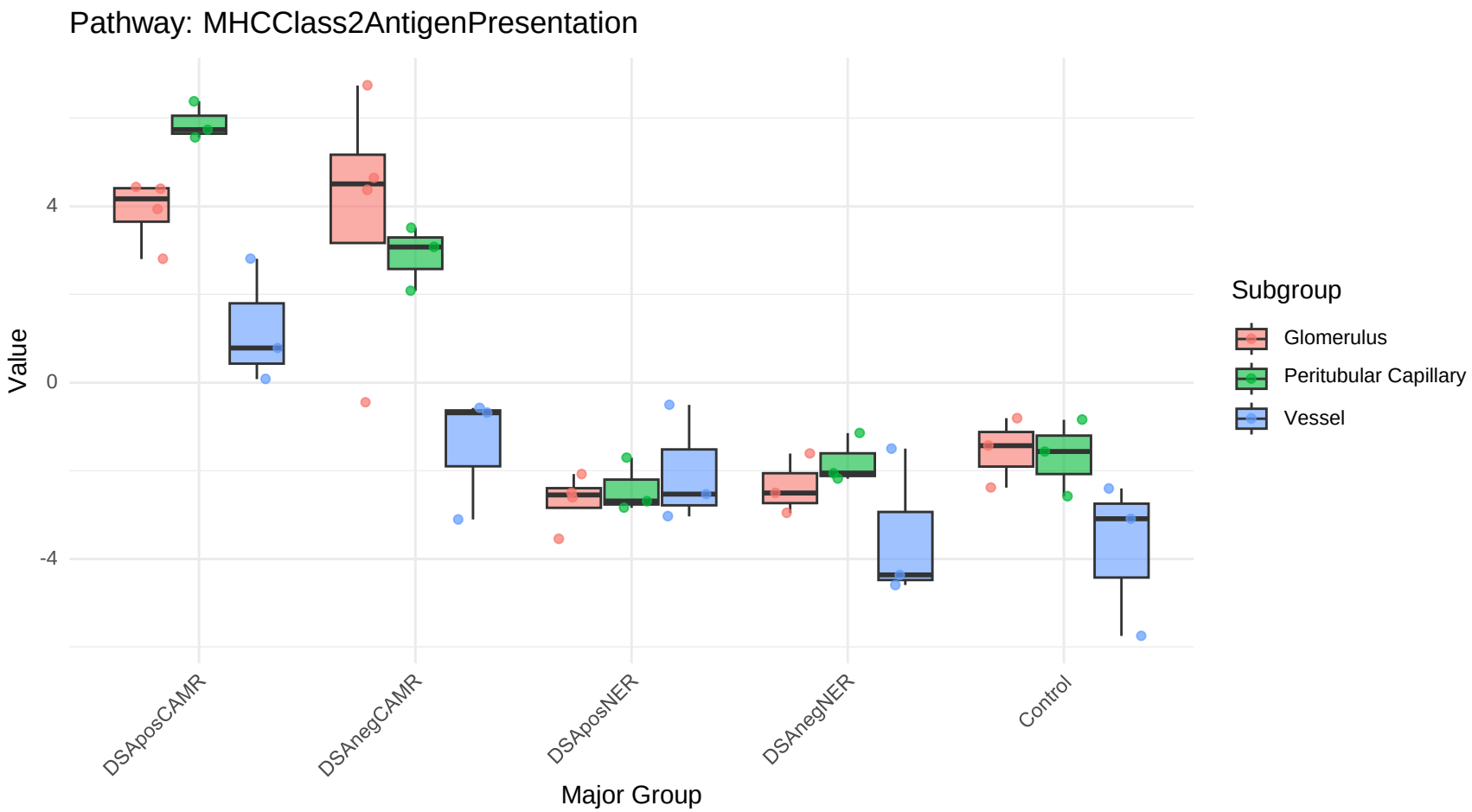
AdaptiveImmunity



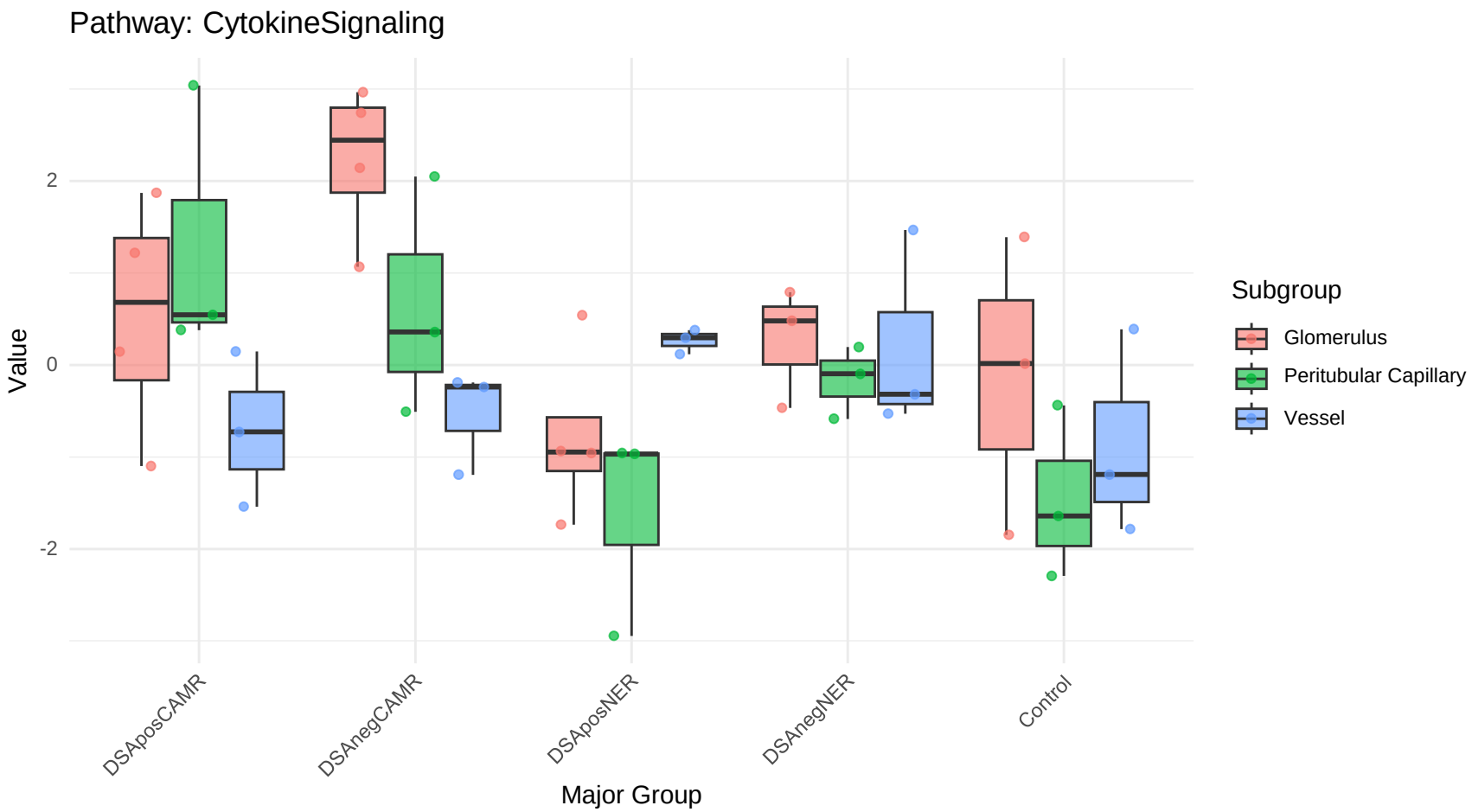
TCRsignaling



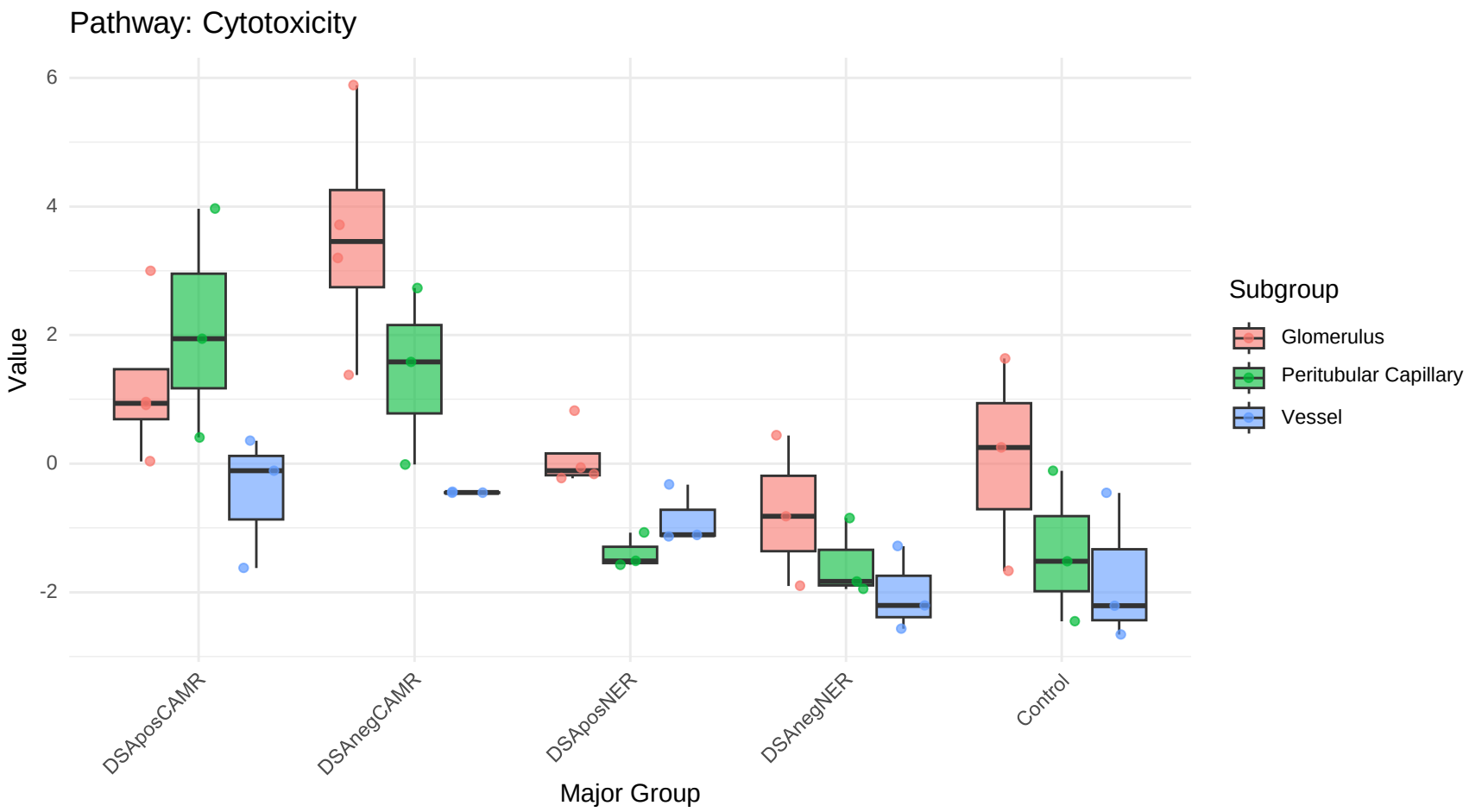
MHC-Class2 AntigenPresentation

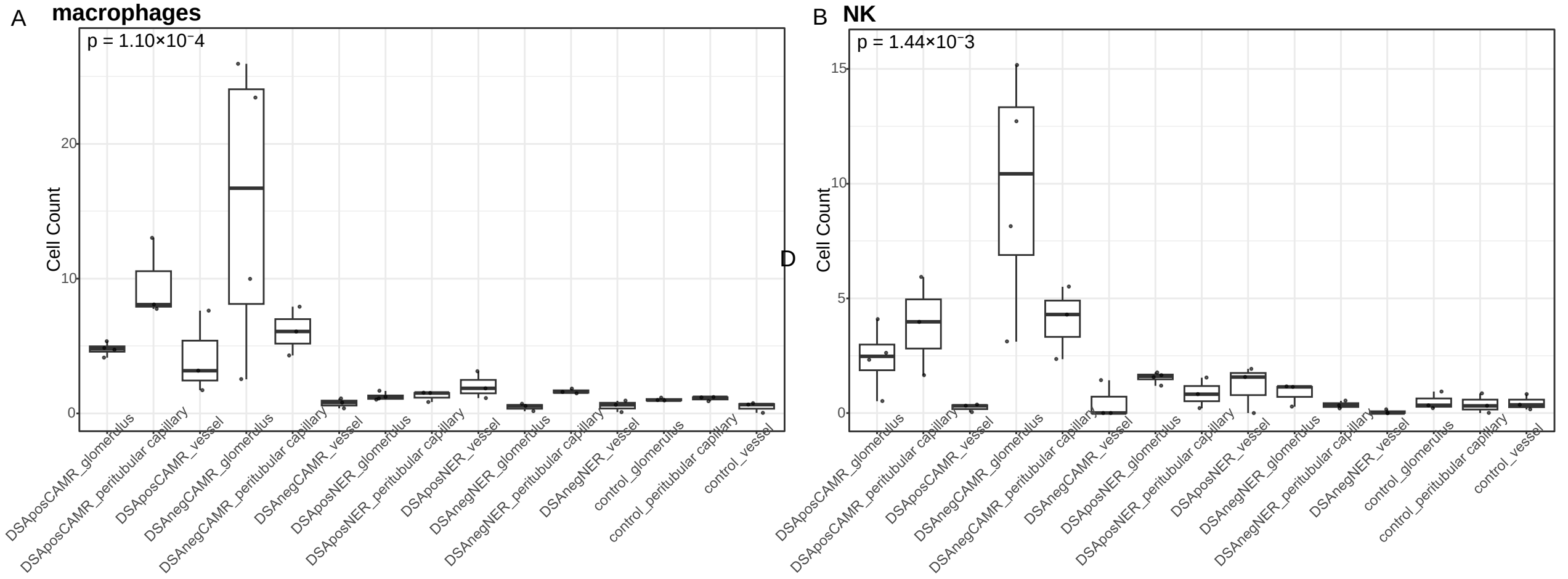


CytokineSignaling



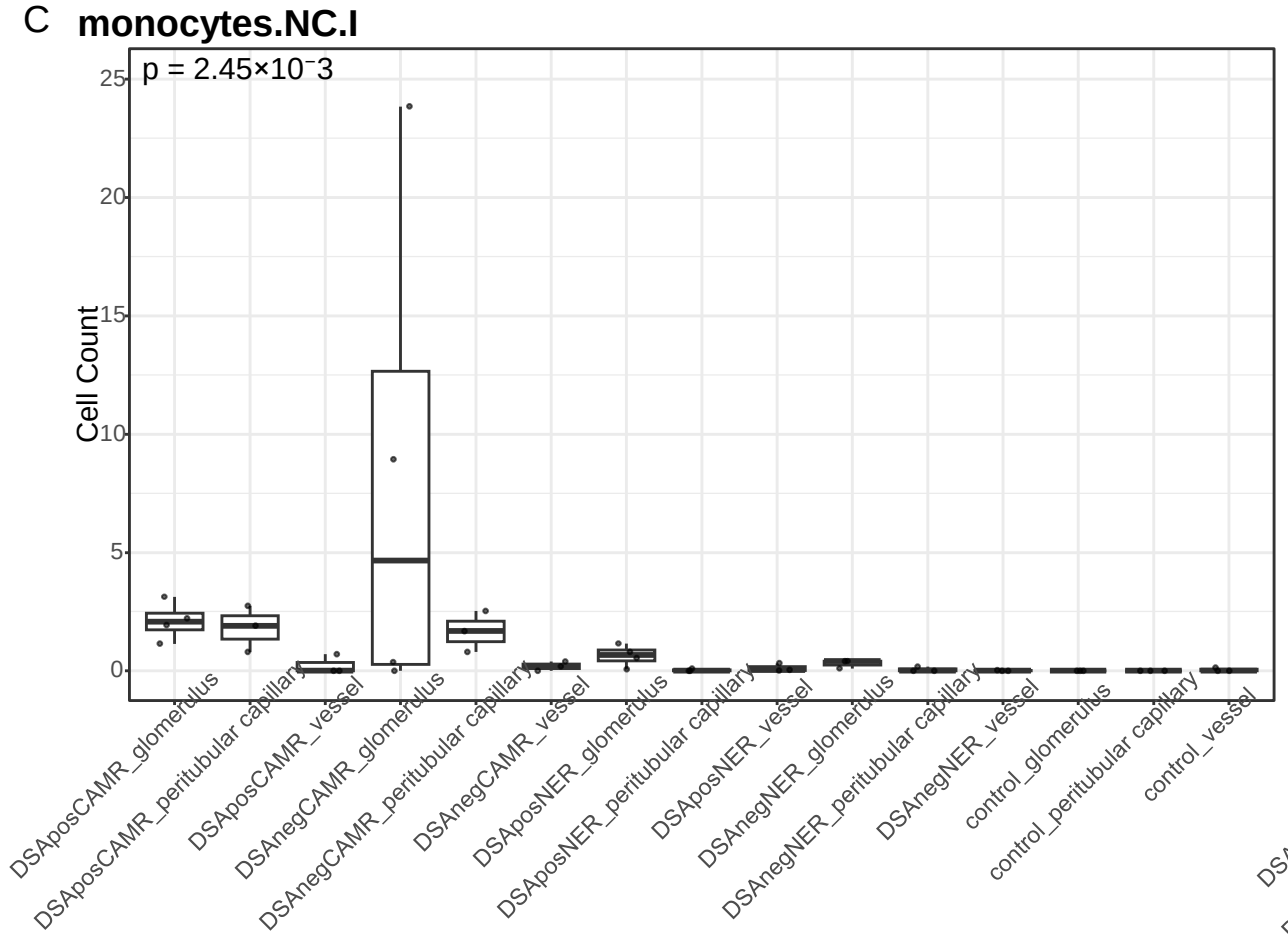
Cytotoxicity

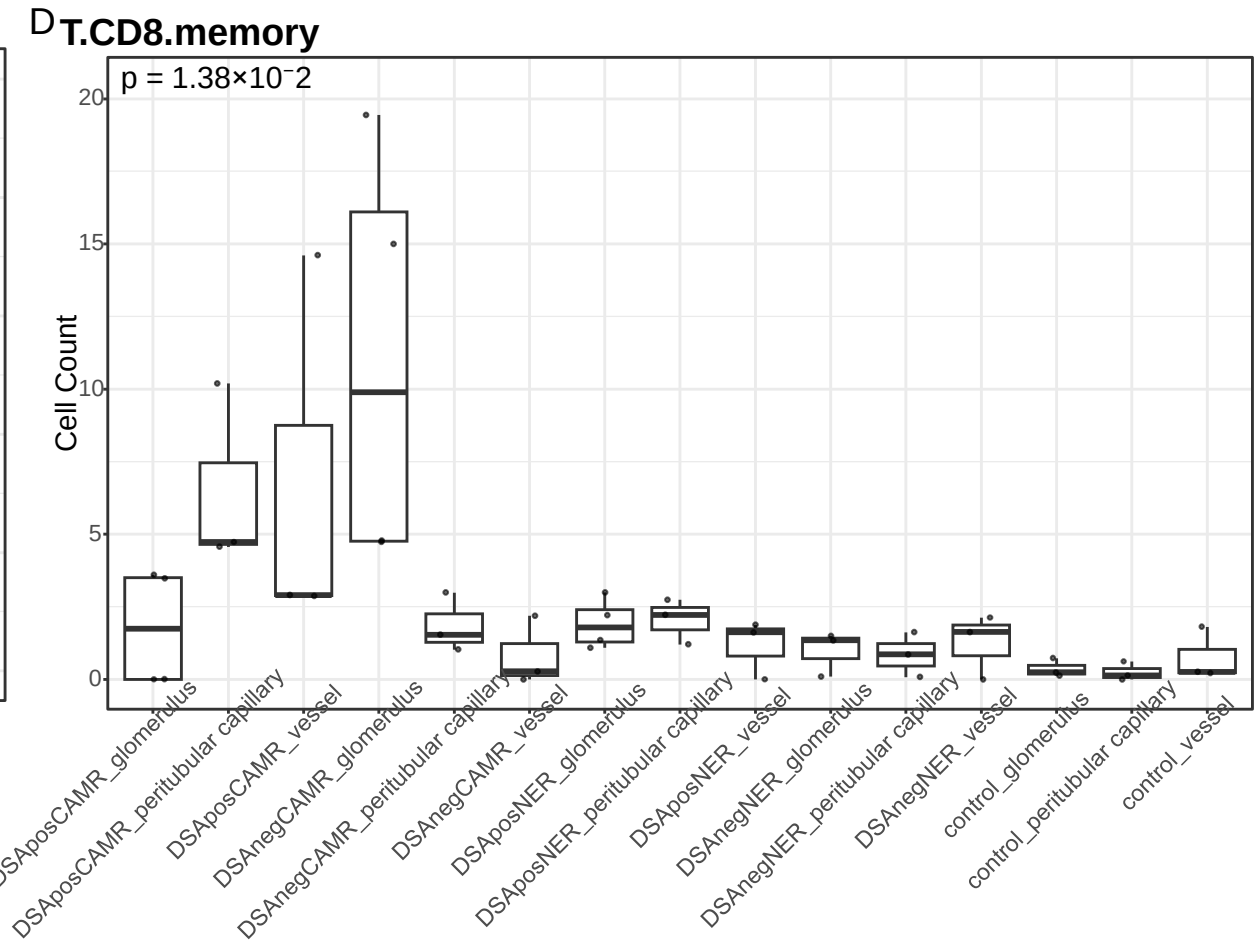




Supplementary Figure S7. Spatial deconvolution of inflammatory cells across ROIs. Comparative analysis of cell count revealed that glomerular ROIs from DSA-negative CAMR exhibited significantly higher number of macrophages **(A)** and NK cells **(B)**.

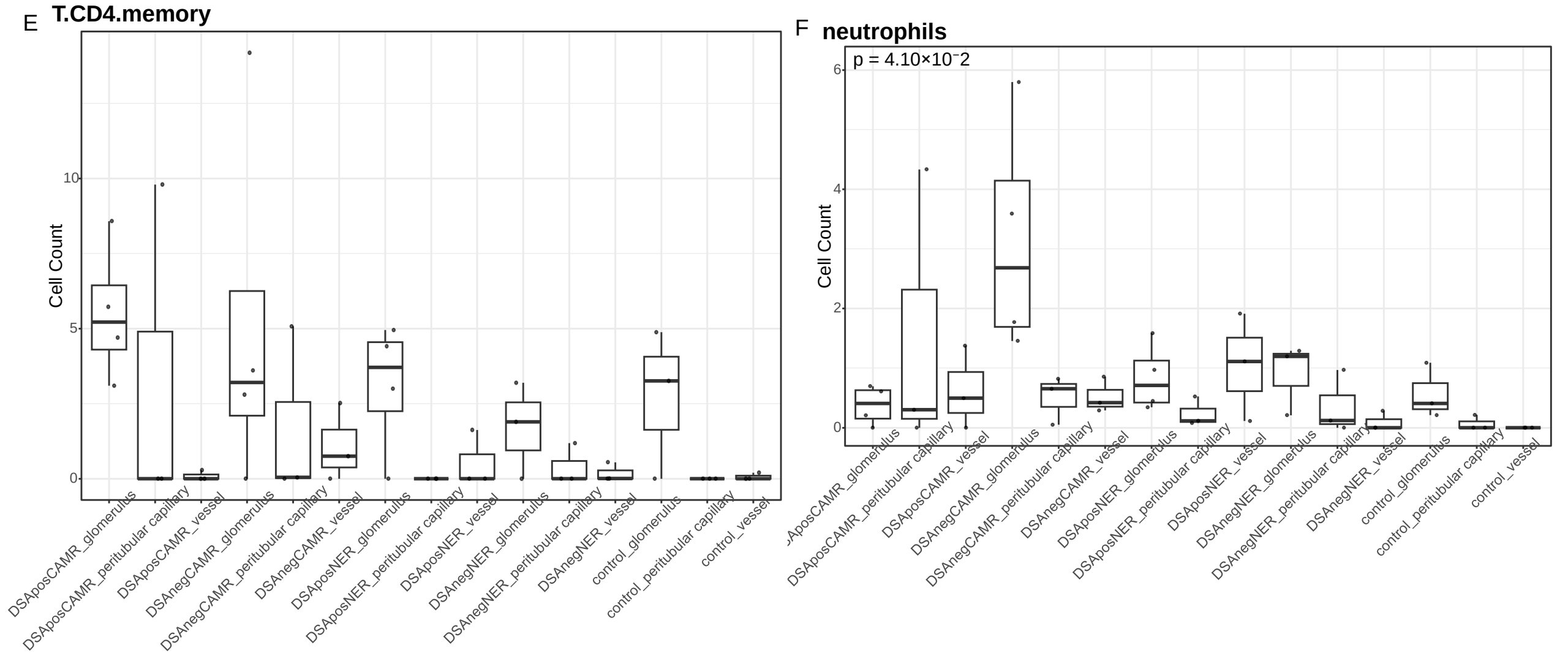
ROI, region of interest; DSA, donor-specific antibody; CAMR, chronic antibody-mediated rejection; NER, no evidence of rejection; monocytes.NC.I., non-classical/intermediate monocytes.



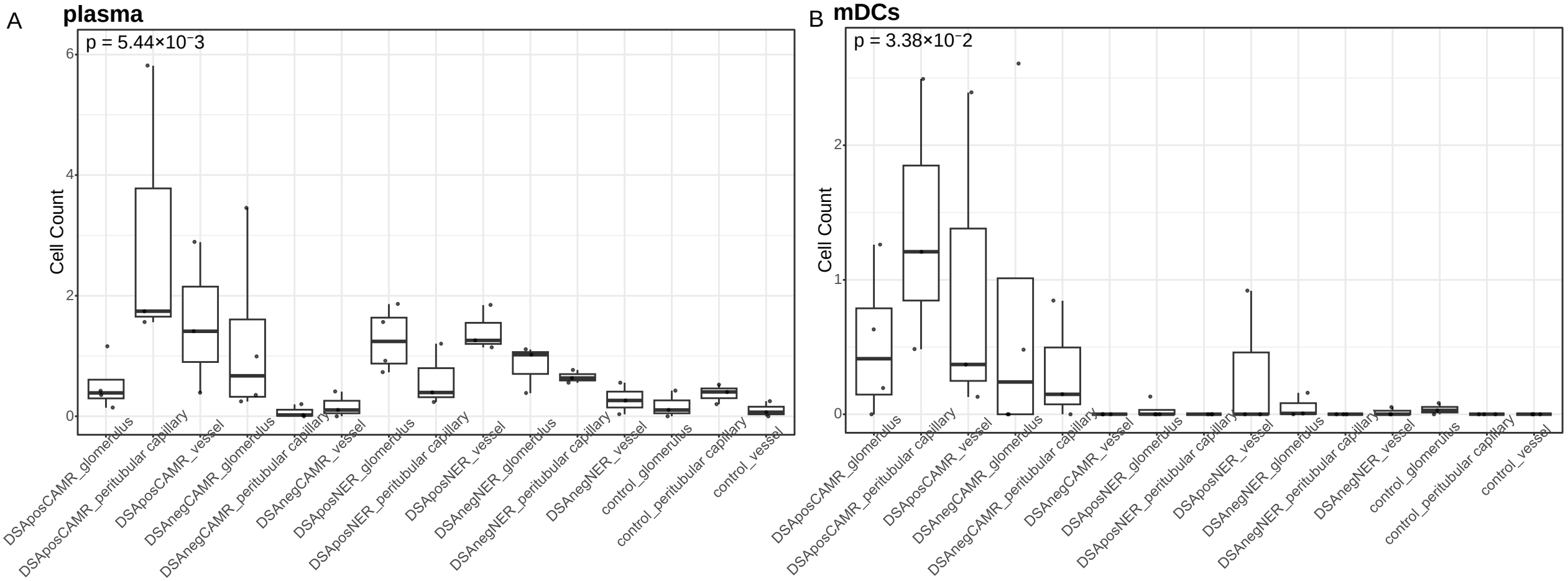


Supplementary Figure S7 (continued). Spatial deconvolution of inflammatory cells across ROIs. Comparative analysis of cell count revealed that glomerular ROIs from DSA-negative CAMR exhibited significantly higher number of non-classical/intermediate monocytes **(C)** and memory CD8 T cells **(D)**.

ROI, region of interest; DSA, donor-specific antibody; CAMR, chronic antibody-mediated rejection; NER, no evidence of rejection; monocytes.NC.I., non-classical/intermediate monocytes.



Supplementary Figure S7 (continued). Spatial deconvolution of inflammatory cells across ROIs. Comparative analysis of cell count revealed that glomerular ROIs from DSA-negative CAMR exhibited significantly higher number of memory CD4 T cells **(E)** and neutrophils **(F)**.
ROI, region of interest; DSA, donor-specific antibody; CAMR, chronic antibody-mediated rejection; NER, no evidence of rejection; monocytes.NC.I., non-classical/intermediate monocytes.



Supplementary Figure S8. Spatial deconvolution of inflammatory cells across ROIs. Number of plasma cells **(A)** and myeloid dendritic cells **(B)** within the peritubular capillary ROIs of DSA-positive CAMR was higher than in other ROIs, despite the relatively low cell count within the ROIs.
ROI, region of interest; DSA, donor-specific antibody; CAMR, chronic antibody-mediated rejection; NER, no evidence of rejection; mDC, myeloid dendritic cells.