



Shaping Tomorrow's Nephrology: Insight-Driven Kidney Care

KSN SEOUL, KOREA
2026

The 46th Annual Meeting of the Korean Society of Nephrology



Jun 11 (Thu) – 14 (Sun), 2026

COEX, Seoul, Korea

Abstract Type : Oral presentation

Abstract Submission No.: A-0524

Abstract Topic : Transplantation

Spatial Transcriptomic Profiling of Vascular Compartments of Chronic Antibody-Mediated Rejection in Kidney Allografts Reveals Shared and Specific Signatures Among Compartments

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Objectives : Despite being a major cause of kidney allograft failure, compartment-specific molecular signatures underlying chronic active antibody-mediated rejection (CAMR) remain incompletely characterized.

Methods : We used GeoMx digital spatial profiling (18,677 genes) to analyze transcriptomic differences in glomeruli, peritubular capillaries, and vessels from four renal allografts with varying donor-specific antibody (DSA) and rejection statuses, and one control.

Results : Linear mixed model analysis identified differentially expressed genes enriched in antigen processing and presentation in CAMR versus non-CAMR, with major histocompatibility (MHC) class II predominating in glomeruli and MHC class I in peritubular capillaries. Three genes (C1QA, CTSS, IFI30) were commonly upregulated in both compartments. Banff Human Organ Transplant pathway scores for antibody-mediated rejection were significantly elevated across all compartments in CAMR. Comparison of DSA-positive versus DSA-negative CAMR revealed enrichment of antigen processing pathways across all three compartments. Cell type deconvolution demonstrated increased macrophages in glomeruli and myeloid dendritic cells in peritubular capillaries in CAMR.

Conclusions : Together, these findings demonstrate compartment-specific transcriptomic signatures in CAMR microvasculature and highlight mononuclear phagocytes as key drivers of antigen presentation in chronic rejection. These findings are exploratory given the limited sample size and require integration with other transcriptomic datasets.

Fig2.jpeg



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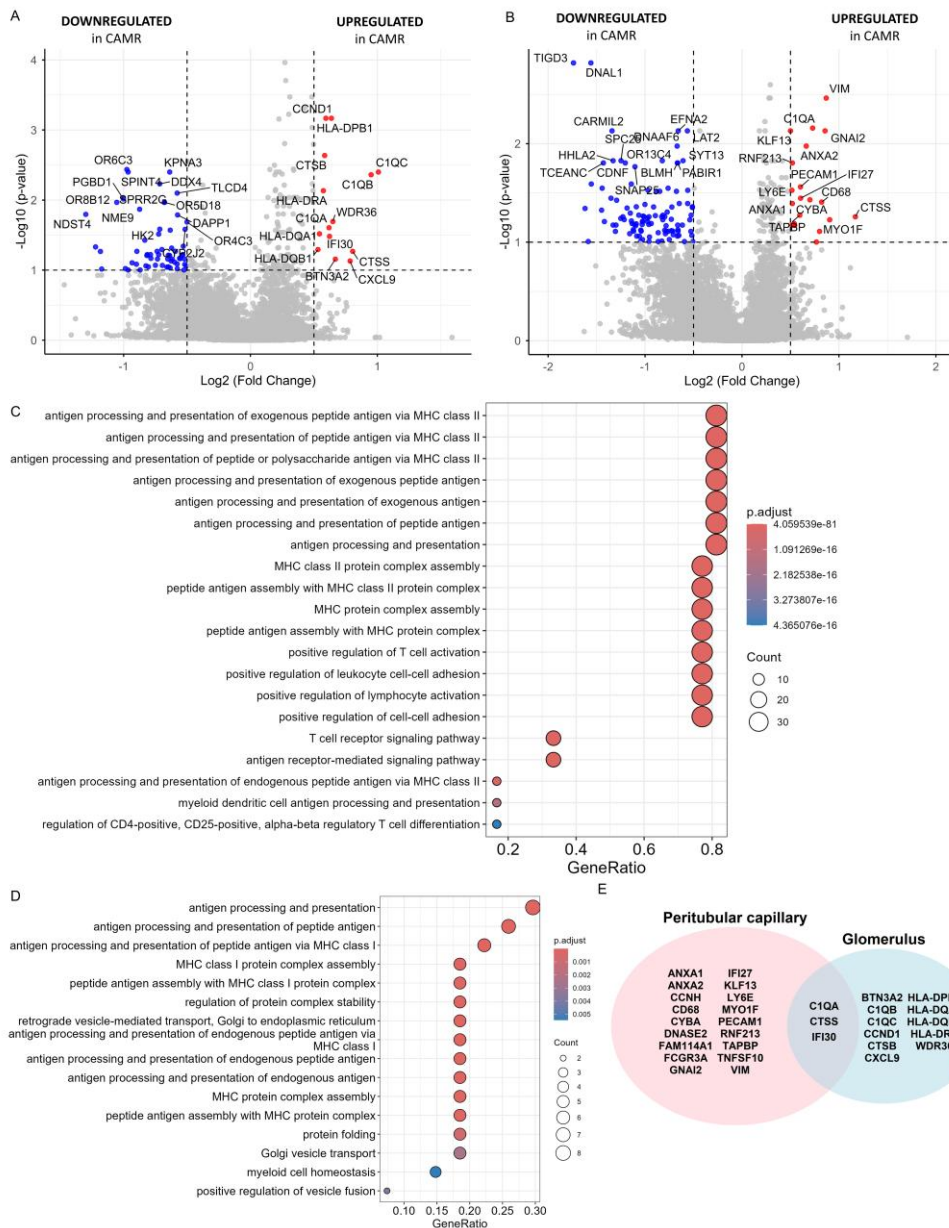


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