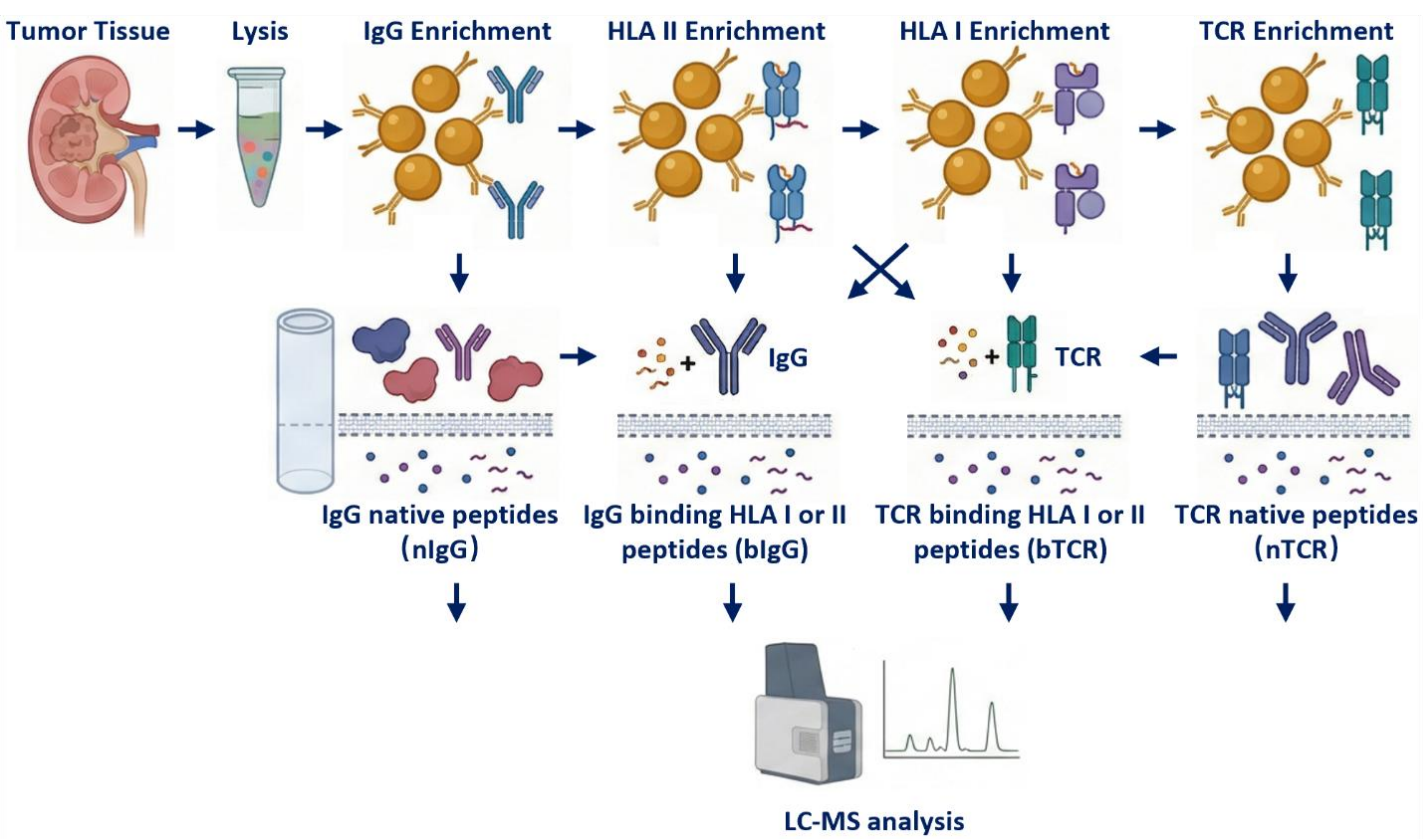
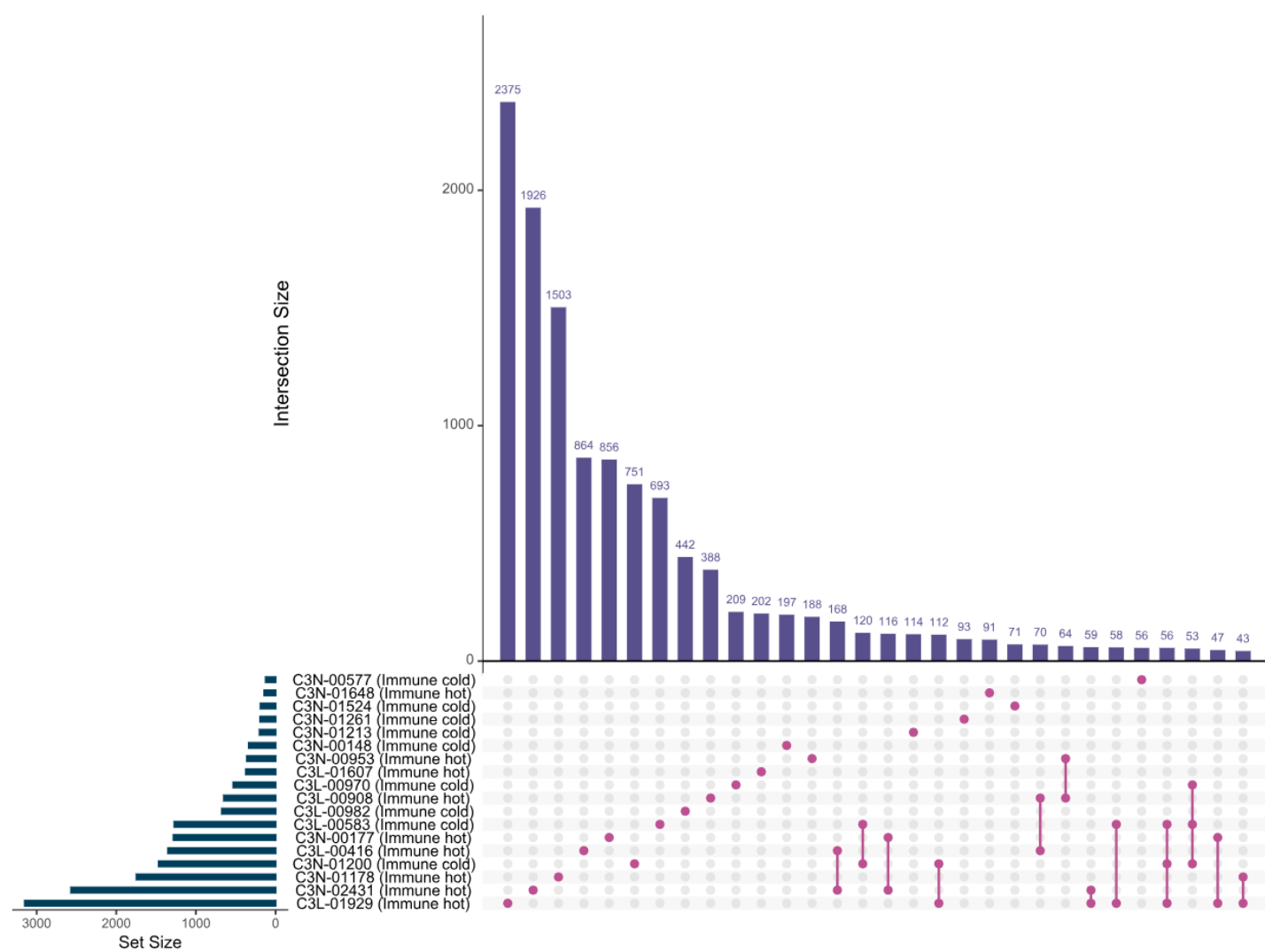


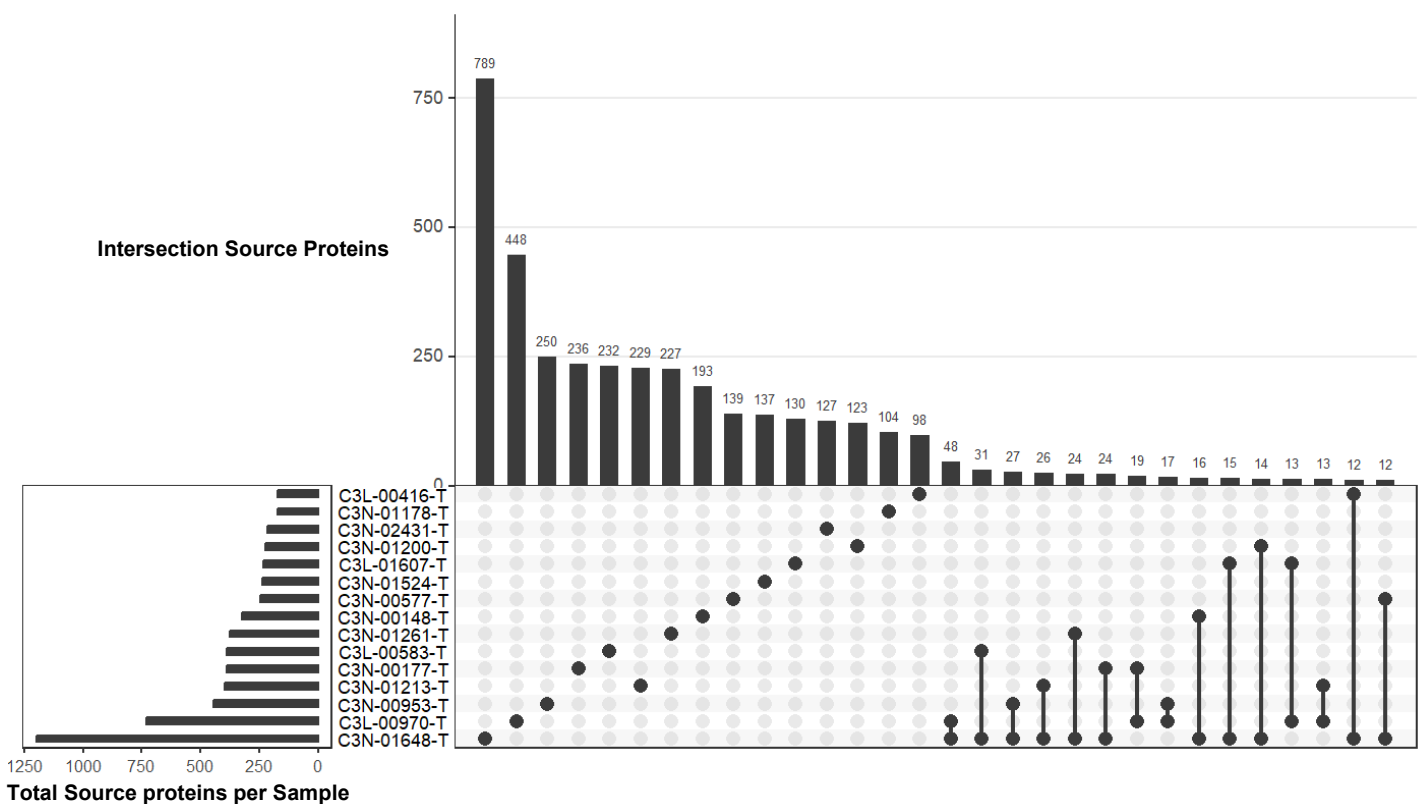
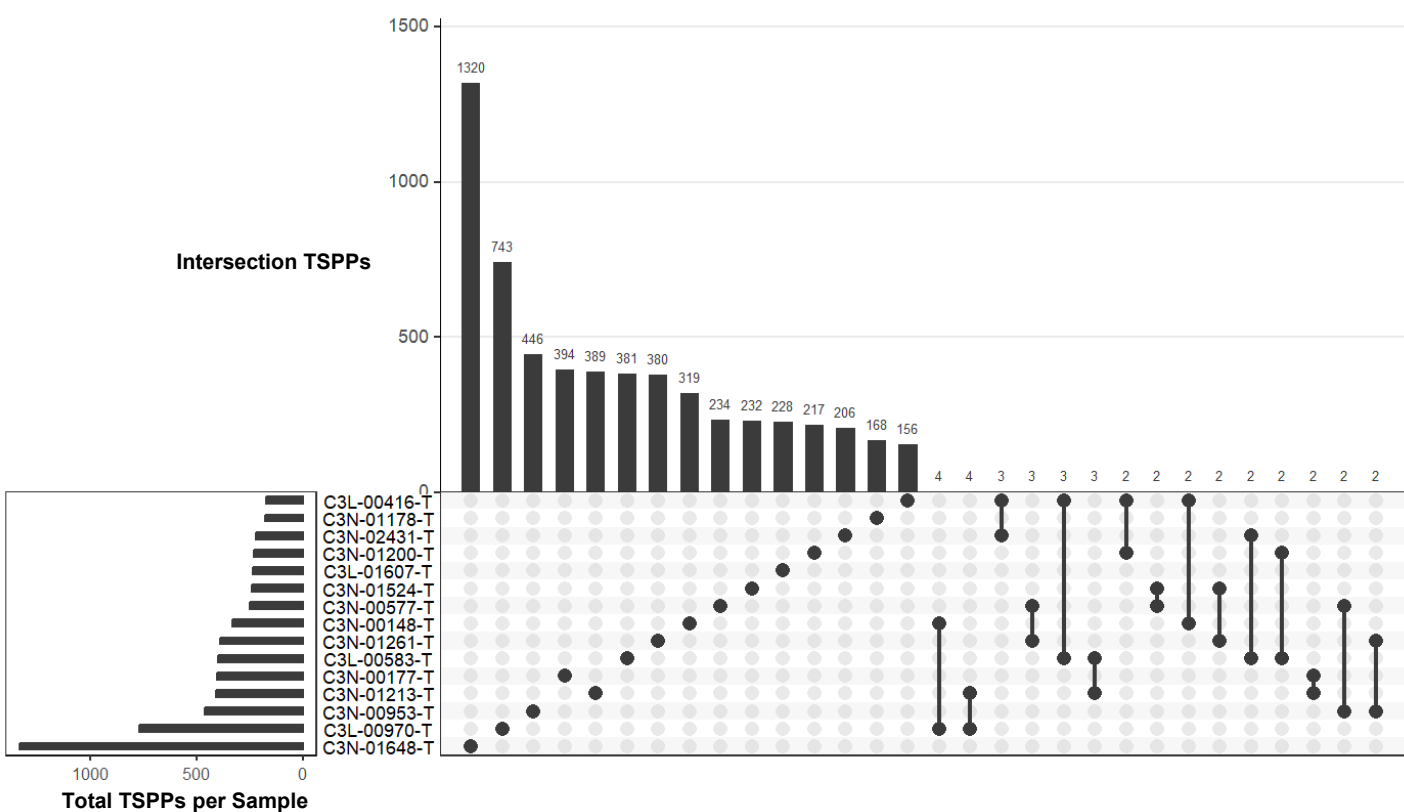
Supplementary Figures



Supplementary Figure 1. Schematic workflow of the functional immunopeptidomics for receptor-associated antigens platform.



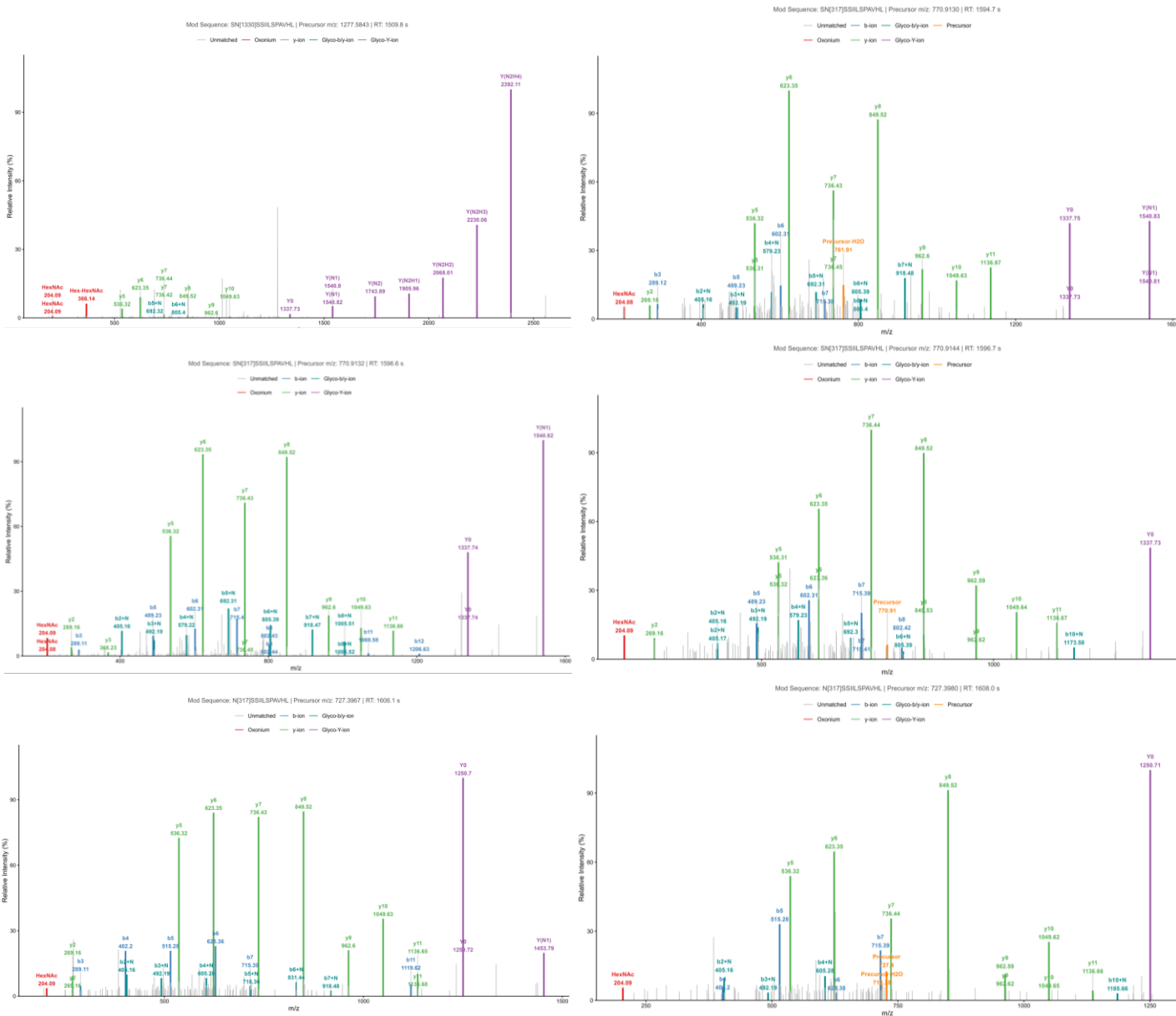
Supplementary Figure 2. UpSet intersection matrix delineating the cohort-wide cross-patient sharing profiles and exclusive partitioning of HLA-II restricted TSPs within the 18-patient tissue sample cohort.



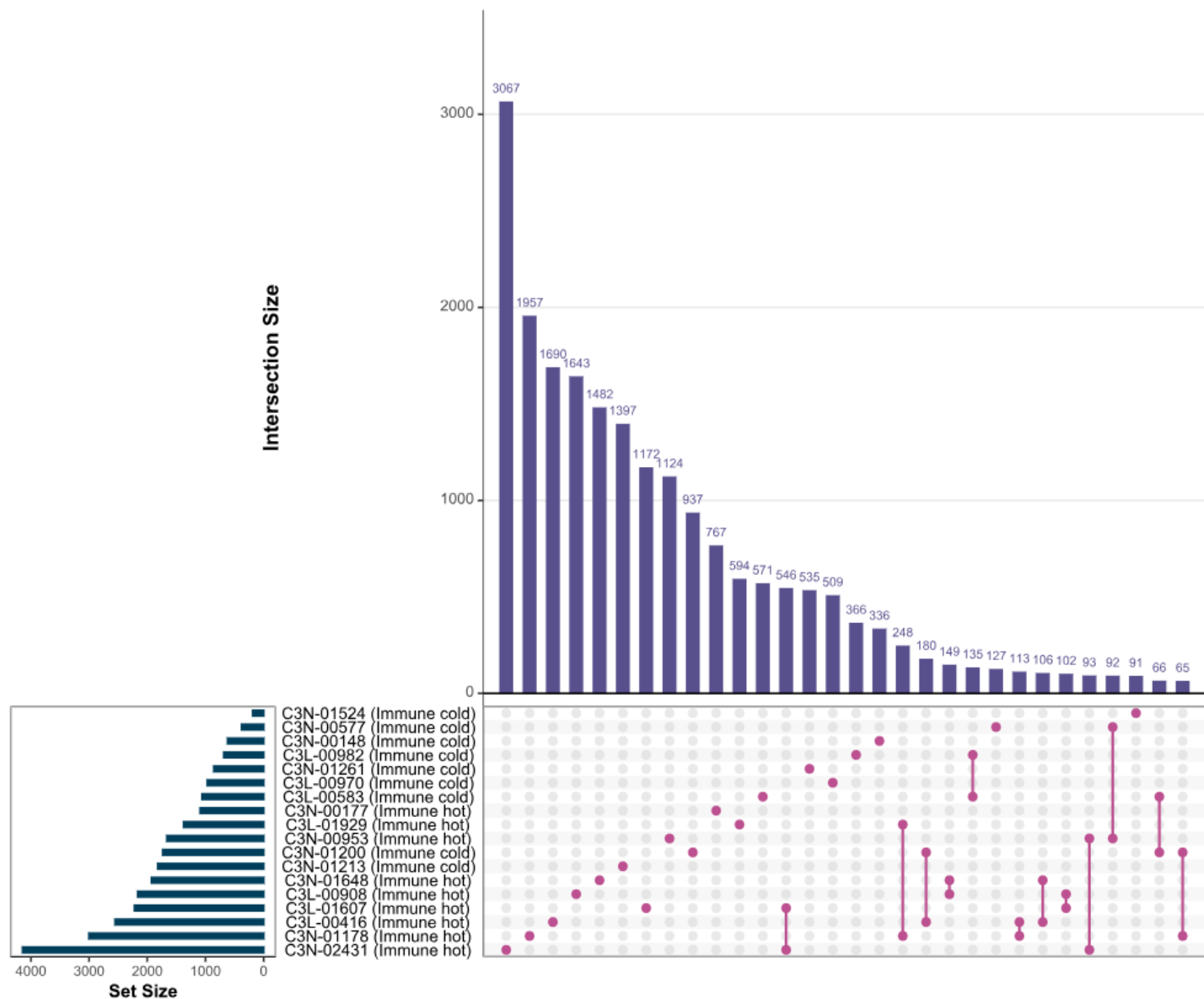
Supplementary Figure 3. UpSet plot analysis of tumor-specific phosphorylated peptides (TSPPs, top) and their corresponding source proteins (bottom) across renal cell carcinoma (RCC) tumor samples.



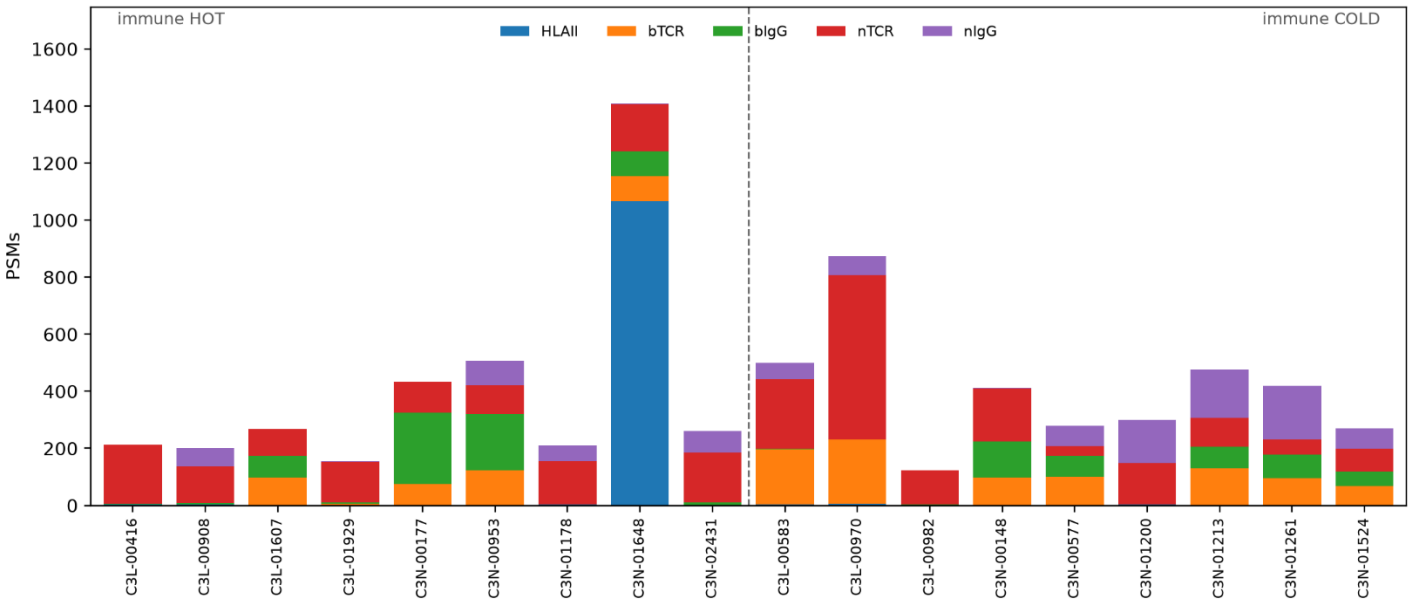
Supplementary Figure 4. Network visualization of shared tumor-specific phosphorylated peptides (TSPPs) and source proteins across renal cell carcinoma (RCC) tumor samples.



Supplementary Figure 5. Representative MS/MS spectra of identified N-glycopeptides. Tandem mass spectra (MS/MS) displaying structural identification and sequence coverage for N-glycosylated peptides containing the backbone sequences across retention times (RT) and m/z values. Peak annotations highlight diagnostic backbone and glycan fragment ions, including b-ion series (blue), y-ion series (green), characteristic low-mass glycan oxonium ions (red), intact peptide-glycan fragment Y-ions (purple), and precursor/neutral-loss ions (orange).



Supplementary Figure 6. UpSet intersection matrix delineating the cohort-wide cross-patient sharing profiles and exclusive partitioning of HLA-I restricted TSPs within the 18-patient tissue sample cohort.



Supplementary Figure 7. Distribution of HLA II-restricted phosphopeptide PSMs across RCC tumor samples. Stacked bar chart showing the total peptide-spectrum match (PSM) counts for HLA II phosphopeptides across individual patient tumor specimens. Total dataset yields comprise 7,310 PSMs, with direct baseline HLA-II capture accounting for 1,163 PSMs. Colors indicate the proportional contribution of each enrichment group: baseline HLA-II (blue), bound TCR (bTCR, orange), bound IgG (bIgG, green), native TCR (nTCR, red), and native IgG (nIgG, purple). Tumor samples are grouped by immune subtypes into immune HOT (left) and immune COLD (right), separated by the vertical dashed line.