

Single-cell analysis unveils distinct transcriptional alterations and cellular origins in IgD multiple myeloma

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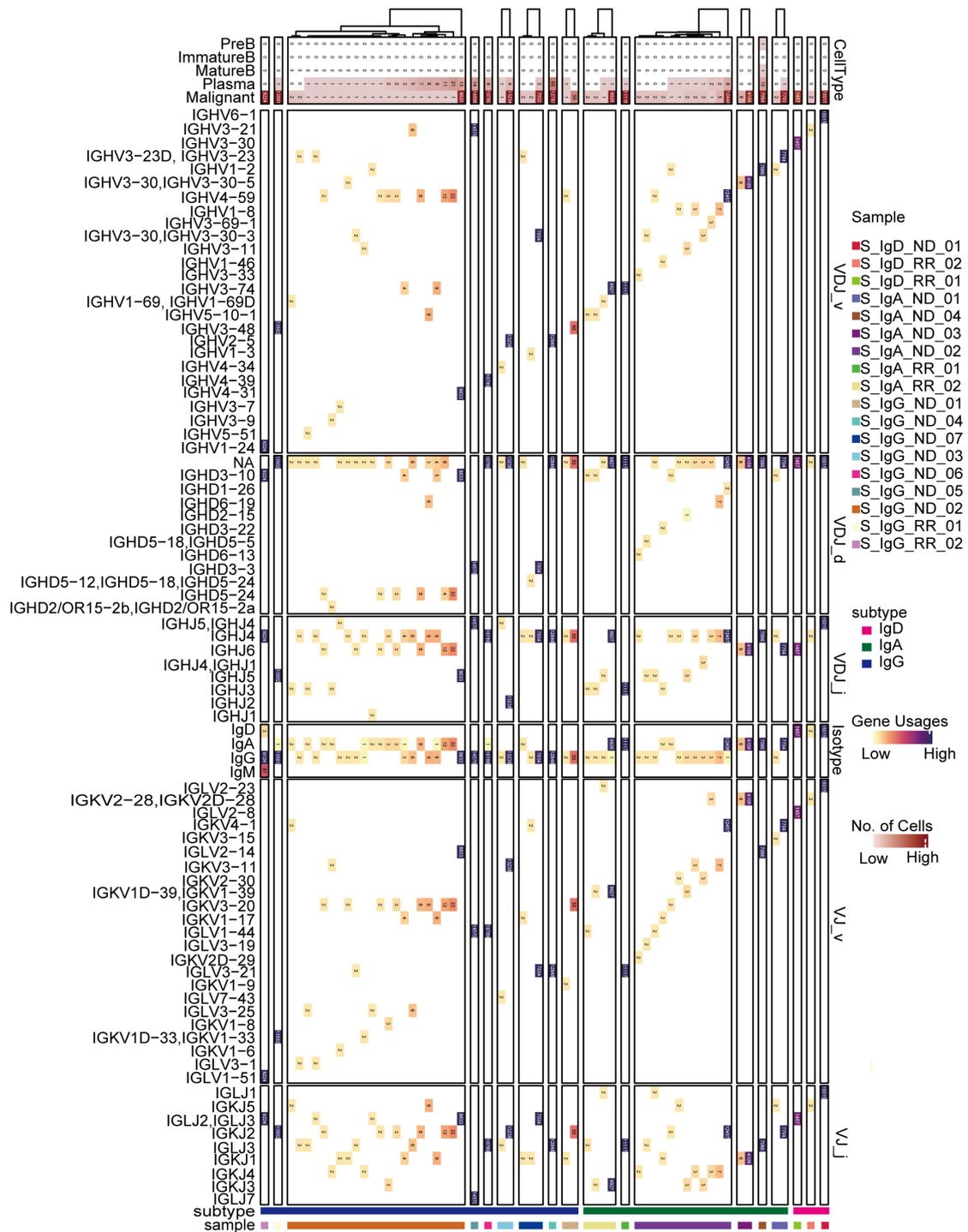
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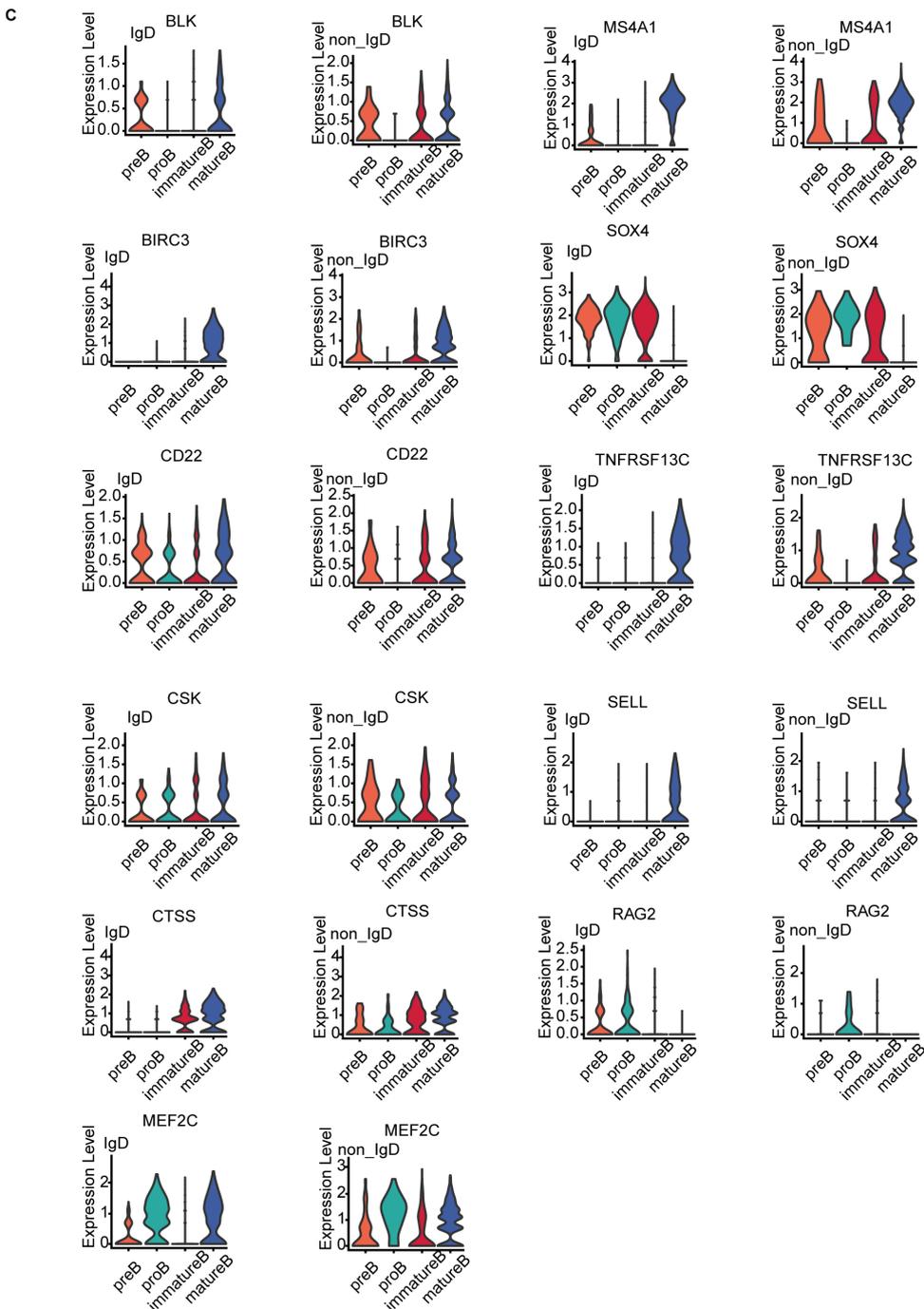
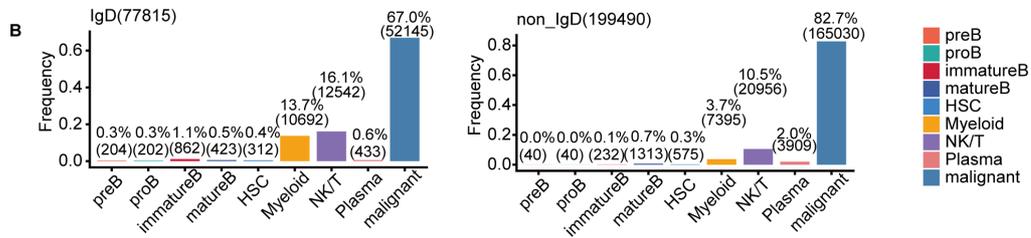
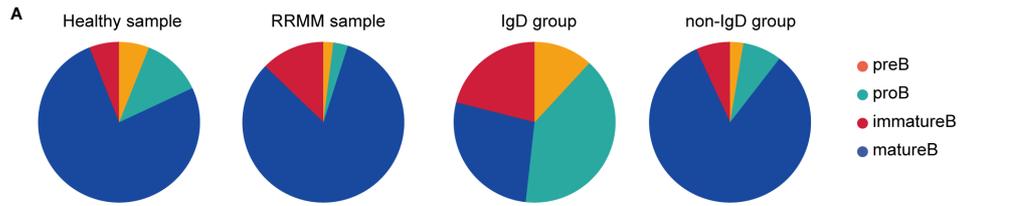
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Supplemental Figures



Supplemental Fig. 1. Single-cell BCR repertoire landscape of MM in sorted samples

In the top panel, cell numbers for each patient are plotted. The middle panel displays VDJ and VJ usage, isotypes, and cell numbers in a heatmap format, with MM subtypes labeled at the bottom, providing insights into the BCR profiles across different MM samples.



Supplemental Fig. 2. Comparison of cell proportions and genes in the B cell receptor (BCR) signaling pathway

(A) Comparison of B cell type fractions between healthy donors and patients with RRMM (adapted from <https://doi.org/10.1038/s41467-021-26951-z>), IgD MM, and non-IgD MM (from this study).

(B) Bar plot illustrating the proportions of various cell types (IgD MM vs. non-IgD MM)

(C) Violin plot depicting the expression levels of differentially expressed genes in immature B cells comparing IgD and non-IgD multiple myeloma (MM), with a focus on the BCR signaling pathway. Genes such as MEF2C, BLK, MS4A1, BIRC3, SOX4, CD22, TNFRSF13C, CSK, SELL, CTSS, and RAG2 are highlighted for comparison between IgD MM and non-IgD MM

Supplemental Fig. 3. Analysis of communication patterns between IgD and non-IgD MM from the LIANA and Tensor-cell2cell framework (all unsorted samples and ND unsorted samples).

(A) Left, sample loadings were statistically compared between IgD MM and non-IgD MM within the same cell-cell communication program for all unsorted samples. Right, the heatmap illustrates the cell type loadings for Factor 4 for all unsorted samples.

(B) Left, sample loadings were statistically compared between IgD MM and non-IgD MM within the same cell-cell communication program for ND unsorted samples. Right, the heatmap illustrates the cell type loadings for Factor 4 for ND unsorted samples.

(C) The heatmap displays the ligand-receptor interactions loadings across all programs for all unsorted samples.

(D) The heatmap displays the ligand-receptor interactions loadings across all programs for ND unsorted samples.