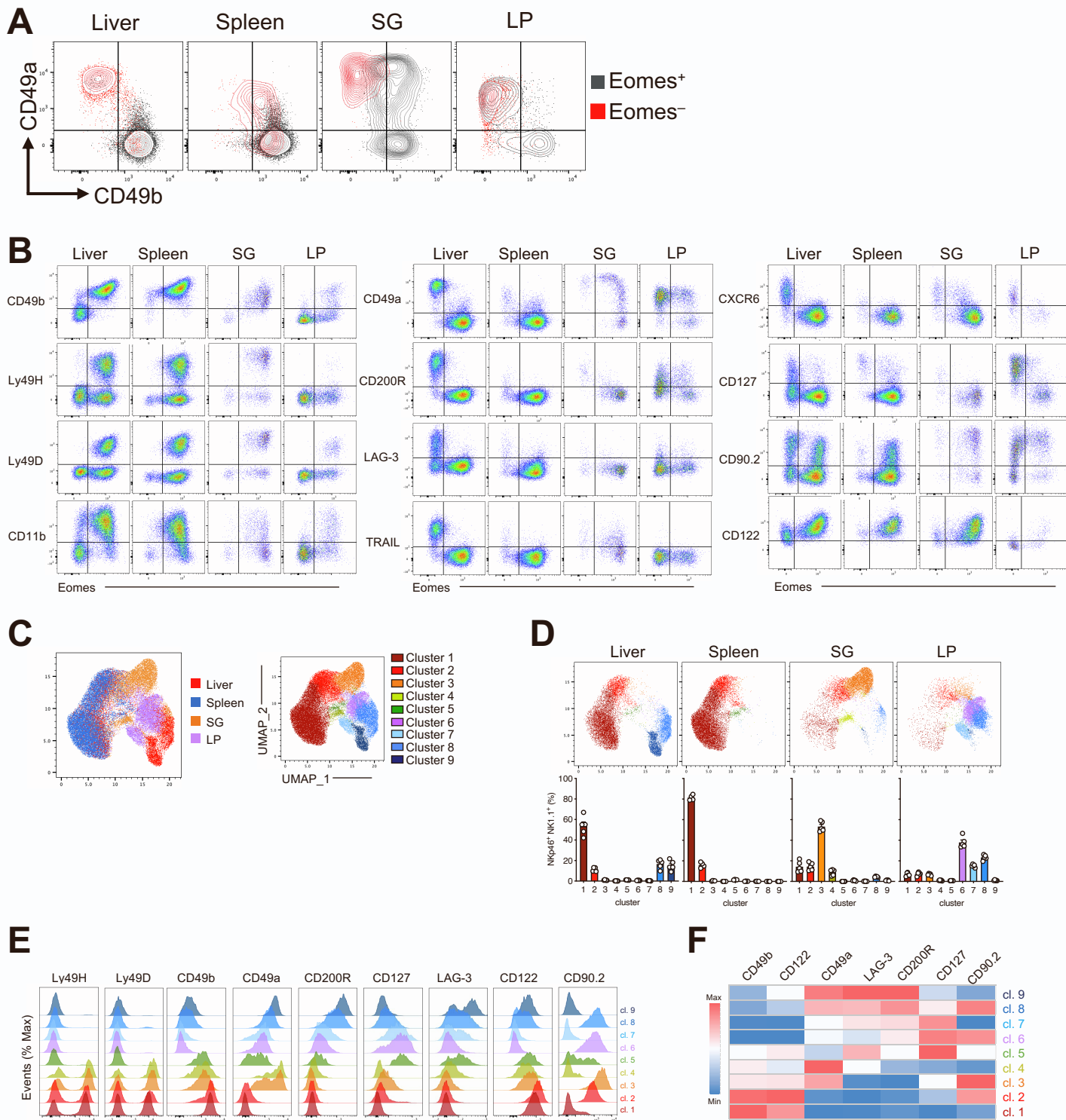


**Cell Reports Medicine, Volume 3**

**Supplemental information**

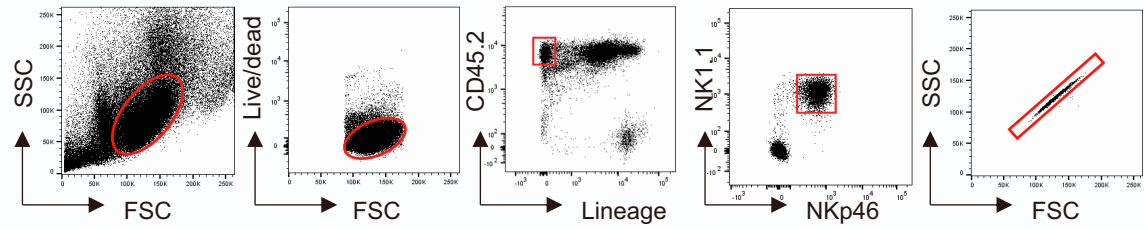
**Tissue-specific transcriptional profiles  
and heterogeneity of natural killer cells  
and group 1 innate lymphoid cells**

**Noella Lopes, Justine Galluso, Bertrand Escalière, Sabrina Carpentier, Yann M. Kerdiles, and Eric Vivier**

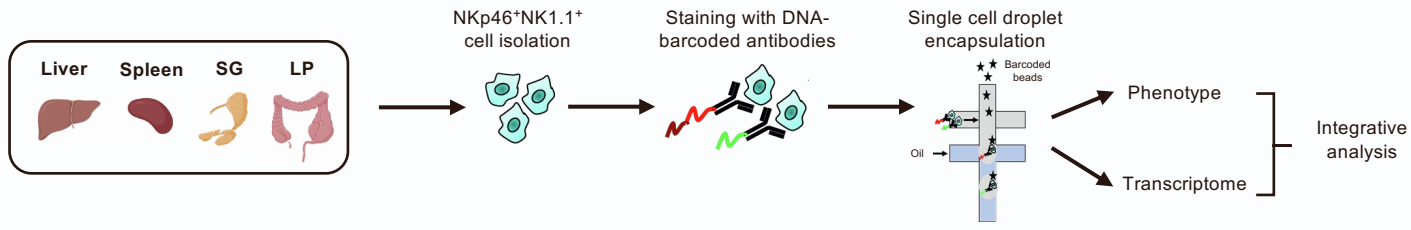


**Supplementary Figure 1. Phenotypic heterogeneity of tissue-restricted NKp46<sup>+</sup> NK1.1<sup>+</sup> cells, Related to Figure 1.** (A) Overlaid CD49a/CD49b expression profile of Eomes<sup>+</sup> and Eomes<sup>-</sup> NKp46<sup>+</sup>NK1.1<sup>+</sup> cells in liver, spleen, salivary glands (SG) and lamina propria (LP). (B) Detailed phenotypic analysis of total NKp46<sup>+</sup>NK1.1<sup>+</sup> cells. (C-D) UMAP dimensionality reduction, based on the expression of the markers in (E), overlaid with tissue of origin (C) and cell clusters identified using FlowSOM (D). (E, F) Phenotypic markers expression profiles (E) and heatmap representation of median expression values (F), for each FlowSOM cluster.

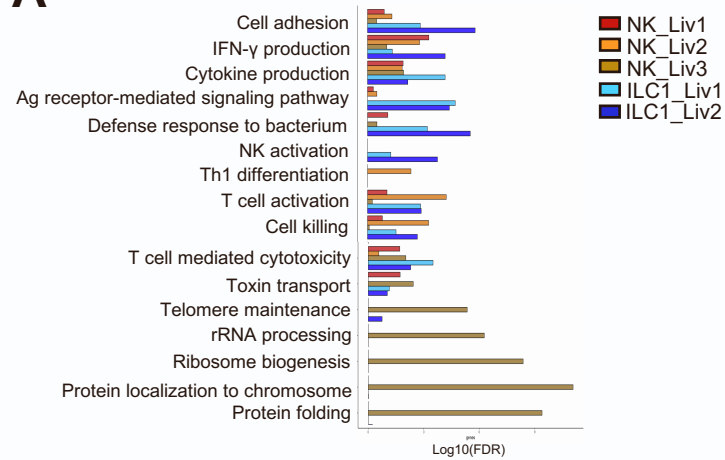
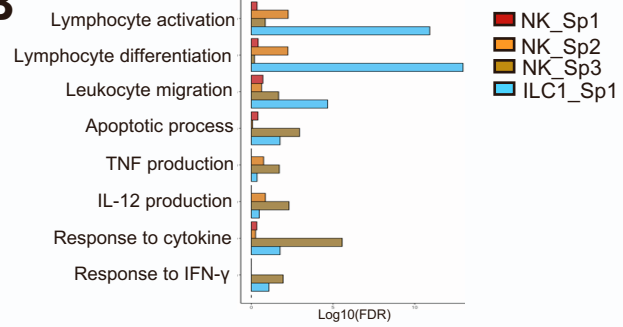
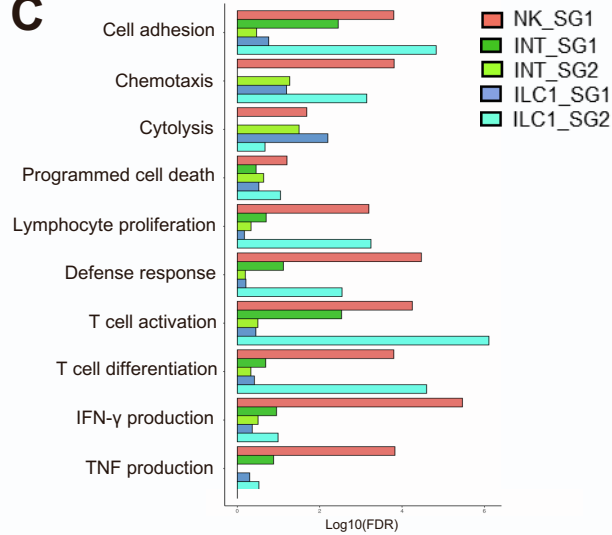
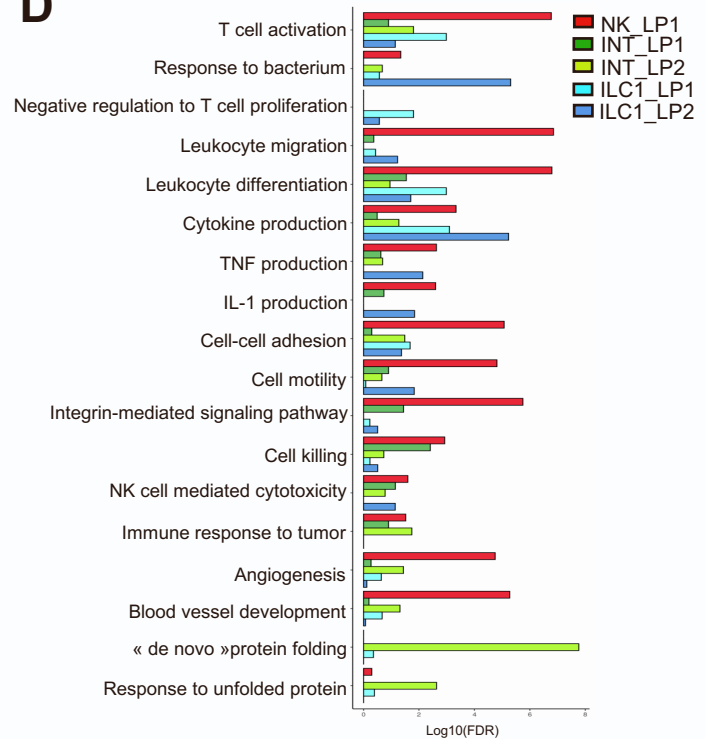
### A Sort gating strategy



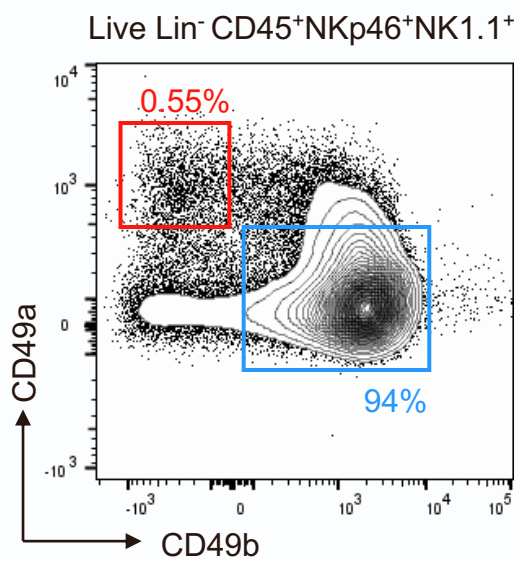
### B



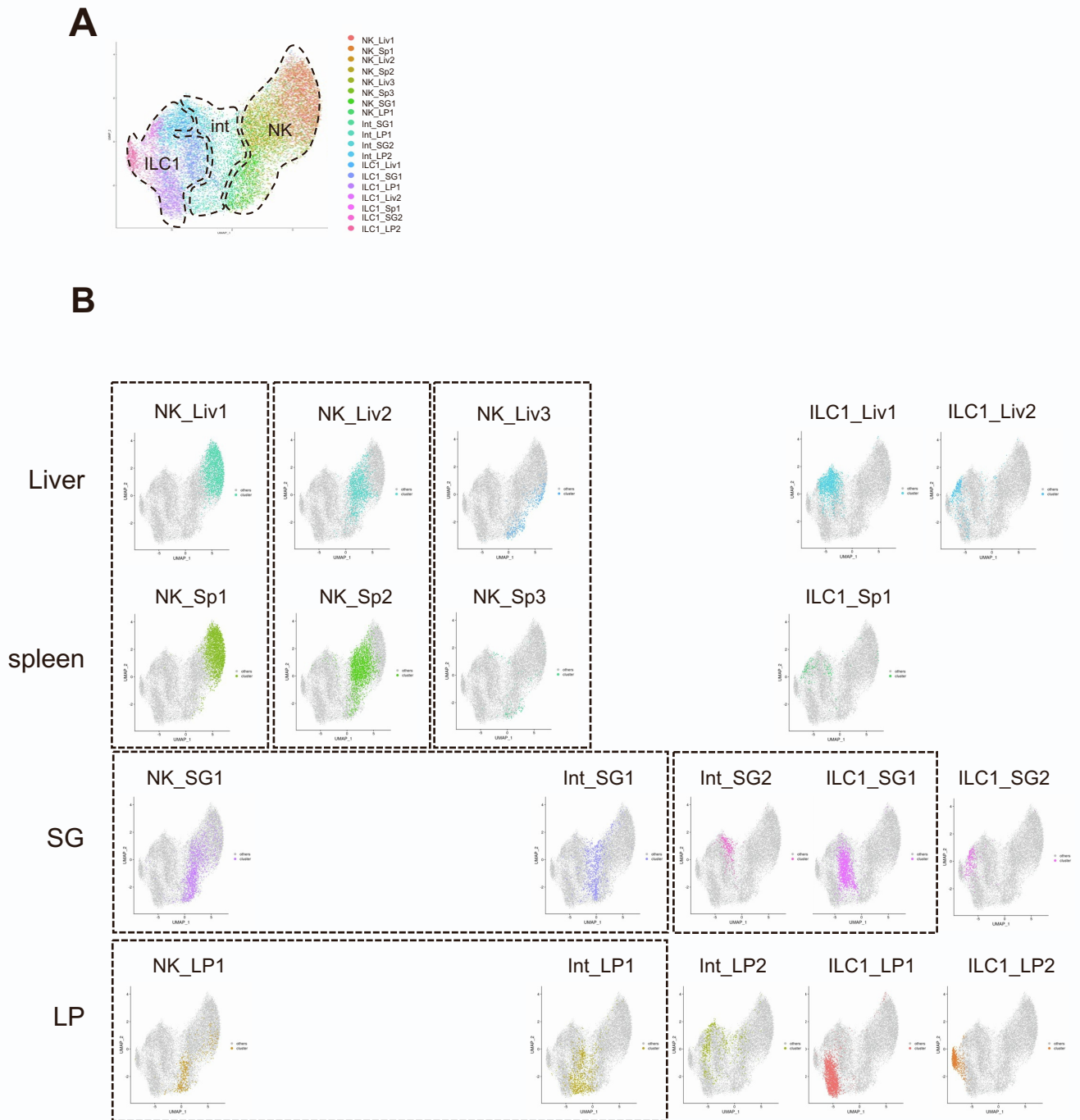
**Supplementary Figure 2. Experimental strategy, Related to Figure 1.** (A) Gating strategy used to analyse NK1.1<sup>+</sup>NKp46<sup>+</sup> cells. (B) Experimental setup: NKp46<sup>+</sup>NK1.1<sup>+</sup> cells from the indicated tissues were isolated, stained with oligonucleotide-labeled antibodies and subjected to classical droplet-based single cell sequencing.

**A****B****C****D**

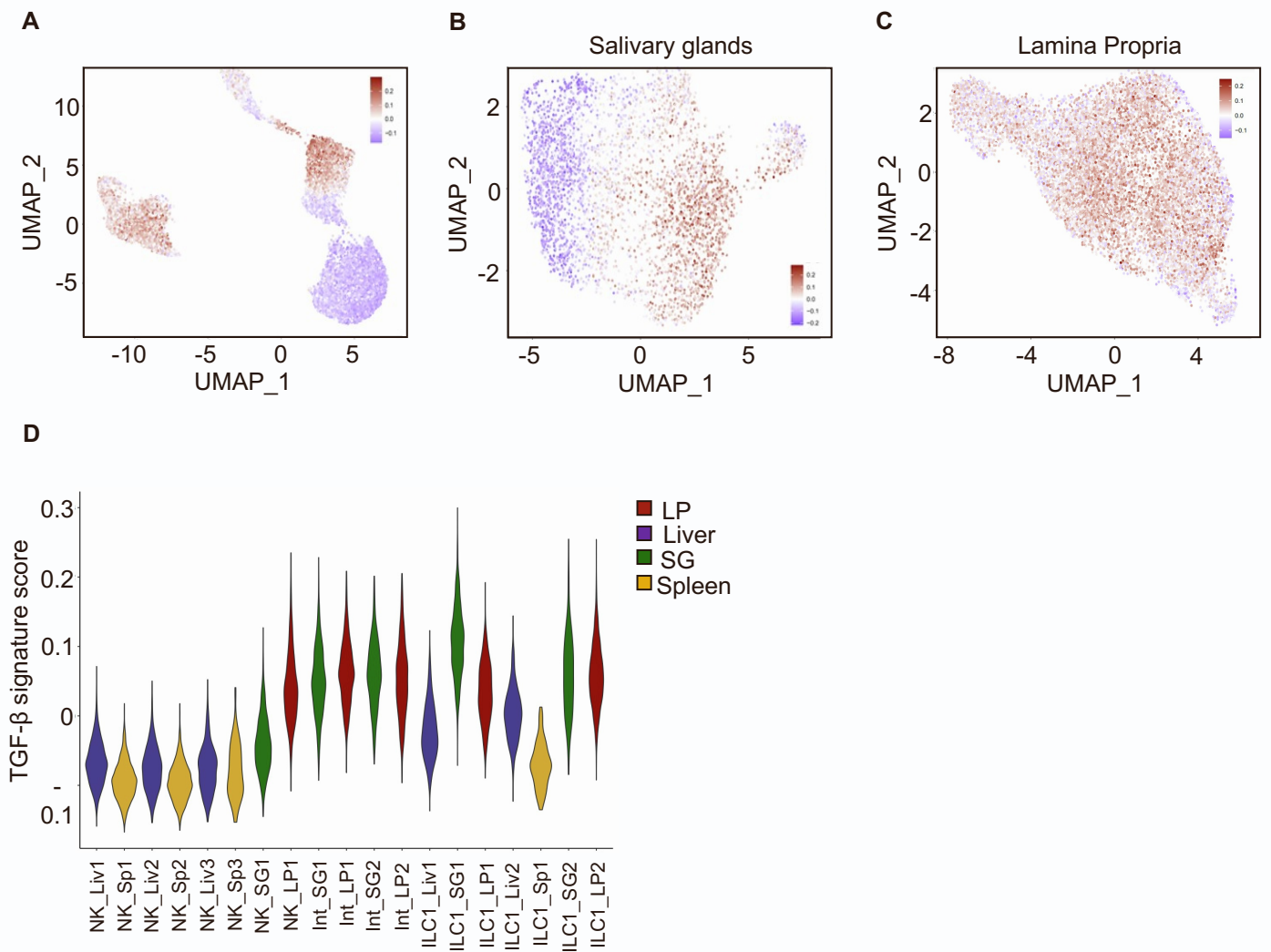
**Supplementary Figure 3. Gene ontology analysis of NK cell and ILC1 subset across organs, Related to Figure 3-5.** (A-D) Biological process gene ontology (GO) terms enriched among DEGs between different NKp46<sup>+</sup>NK1.1<sup>+</sup> subpopulations from liver (A), spleen (B), salivary glands (C) and lamina propria (D). The units for the x-axis are FDR-corrected log<sub>10</sub> p values for the hypergeometric test.



**Supplementary Figure 4. Flow cytometry analysis of ILC1s (CD49a<sup>+</sup>CD49b<sup>-</sup>) and NK cells (CD49a<sup>-</sup>CD49b<sup>+</sup>) content in WT splenocytes, Related to Figure 3.**



**Supplementary Figure 5. Transcriptomic-based cell clusters projected onto harmony-integrated UMAP, Related to Figure 6.** (A) Transcriptome-based clusters identified for each organ were projected altogether (A) or individually (B) on the integrated UMAP obtained with Harmony.



**Supplementary Figure 6. NKp46<sup>+</sup>NK1.1<sup>+</sup> cells in SG and LP highly expressed genes associated with TGF- $\beta$  signature, Related to Figure 6.** (A) UMAP of NKp46<sup>+</sup>NK1.1<sup>+</sup> single cells from liver, spleen, SG and LP based on TGF- $\beta$  signature score. (B-C) UMAP plot of on TGF- $\beta$  signature among the identified clusters in SG (B) and LP (C). (D) Module score analysis for TGF- $\beta$  signature for each cluster identified in liver, spleen, SG and LP

Marker	Clone	Reference	Name
CD49a	Ha31/8	97858	TotalSeq™-A5154 Custom Oligo Conjugation
CD49b	HM $\alpha$ 2	96637	Total-Seq™-A0421 anti-mouse CD49b
CD90.2	30-H12	105345	TotalSeq™-A 0075 anti-mouse CD90.2
CD122	5H4	96465	TotalSeq™-A0227 anti-mouse CD122 (II-2Rb)
CD127 (II-7Ra)	A7R34	135045	TotalSeq™-A0198 anti-mouse CD127 (II-7Ra)
CD200R	OX-110	123913	TotalSeq™-A0807 anti-mouse CD200R (OX2R)
CD223 (LAG-3)	C9B7W	125229	TotalSeq™-A0378 anti-mouse CD223 (LAG-3)
NKG2A	16A11	97786	TotalSeq™-A0927 anti-mouse CD159a (NKG2A B6)

**Supplementary Table 1. List of antibodies used for CITE-seq analysis, Related to Figure 1**