# Table S2: Definition of lymphoid clusters for CITE-seq data, Related to STAR Methods, Figure 1 and Data S4

Related to **Figure 1B, C** and the **STAR Methods**: CITE-seq: multi-modal cluster annotation. The phenotypes of the identified sub-populations are shown in **Data S4: Multi-modal annotation of CITE-seq data**. Supporting GEX and ADT clustering analyses are shown in **Supplementary Figure 1E** and **Data S3: Analysis of Mass and Flow Cytometry, Repertoire and Proteomics, Related to STAR Methods**.

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## T and NK cell sub-population phenotypes

| Population | Subset | ADT phenotype | TCR phenotype | BCR phenotype | GEX phenotype | Cell count |
|---|---|---|---|---|---|---|
| **CD4** | | singlet, CD3+ CD4+ | singlet | <1% IgG, <20 HC umi | CD4+ | n = 270,003 |
| **CD8** | | singlet, CD3+ CD8+ | singlet | <1% IgG, <20 HC umi | CD8A+ | n = 106,245 |
| **DP** | | singlet, CD3+ CD4+ CD8+ | singlet | <1% IgG, <20 HC umi | | n = 7,102 |
| **DN** | | singlet, CD3+ CD4- CD8- | singlet | <1% IgG, <20 HC umi | | n = 4,644 |
| **MAIT** | **CD8+** | singlet, CD3+ CD8+ Vα7.2+ CD161+ | singlet, TRAV1-2, TRAJ33 , TRAJ12 , TRAJ20 | <1% IgG, <20 HC umi | Various | } n = 3,935 |
| | | singlet, CD3+ CD8+ Vα7.2+ CD161+ | singlet, TCR chains include Mait sequences | <1% IgG, <20 HC umi | MAIT | |
| | **DN** | singlet, CD3+ Vα7.2+ CD161+ | singlet, TRAV1-2, TRAJ33 , TRAJ12 , TRAJ20 | <1% IgG, <20 HC umi | Various- | } n = 639 |
| | | singlet, CD3+ Vα7.2+ CD161+ | singlet, TCR chains include Mait sequences | <1% IgG, <20 HC umi | MAIT | |
| **γδ T** | **Vδ2+ve** | singlet, CD3$^{+ve}$ Vδ2+ Vγ9+ | singlet | <1% IgG, <20 HC umi | TRDV2+ | n = 6,239 |
| | **Vδ2-ve Vγ9-ve** | singlet, CD3+ TCRγδ+ | singlet | <1% IgG, <20 HC umi | TRDV1+ (TRDV3+) | n = 2,238 |
| | **Vδ2-ve Vγ9+ve** | singlet, CD3+ Vδ2- Vγ9+ | singlet | <1% IgG, <20 HC umi | TRDV1+ (TRDV3+) | n = 1,227 |
| **iNKT** | **true** | singlet, Vα24Jα18+ | singlet, TRAV10, TRAJ18 | <1% IgG, <20 HC umi | | n = 293 |
| | **ADT** | singlet, Vα24Jα18+ | singlet, TRAV10, TRAJ18 + additional V/J chains | <1% IgG, <20 HC umi | | n = 93 |

| | | | | | |
|---|---|---|---|---|---|
| **NK** | singlet,<br>NCAM1+ | <50 TCRA & TCRB reads | <1% IgG, <20 HC umi | NCAM1+ | n = 69,997 |

Definition of T and NK cell identities. red: identifying features, green: additional criteria, blue: confirmatory observations.

## B cell and plasmablast sub-population phenotypes

| Population | Subset | ADT phenotype | TCR phenotype | BCR phenotype | GEX phenotype | Cell count |
|---|---|---|---|---|---|---|
| **B** | | singlet, CD19+ | <50 TCRA & TCRB reads | singlet | CD19+ | n = 43,043 |
| | B.NAIVE.1 | IgD+ IgM+ CD27- | | IGHD, IGHM (<2 mutations) | IGHD+ IGHM+ TCL1A+ | n = 16,032 |
| | B.NAIVE.2 | IgD+ IgM+ CD27- | | | IGHD+ IGHM+ TCL1A+ | n = 2,547 |
| | B.NAIVE.3 | IgDint IgM+ CD27- | | IGHD, IGHM (<2 mutations) | IGHD+ IGHM+ TCL1A+ | n = 531 |
| | B.NAIVE.IgDlo | IgDlow IgMlow CD27- | | IGHD, IGHM (<2 mutations) | IGHD+ IGHM+ TCL1A+ | n = 71 |
| | B.NAIVE.IFN.resp | IgD+ IgM+ CD27- | | IGHD, IGHM (<2 mutations) | IGHD+ IGHM+ TCL1A+; IFN resp gene +ve (e.g. MX1+) | n = 1,176 |
| | B.NAIVE.CD1c | IgD+ IgM+ CD27- CD1c+ | | IGHD, IGHM (<2 mutations), or none | IGHD+ IGHM+ TCL1A+ | n = 922 |
| | B.int.1.IFN.resp | IgD+ IgM+ CD27int | | | IFN resp gene +ve (e.g. MX1+) | n = 199 |
| | B.int.1.early.act | IgD+ IgM+ CD27int | | IGHD, IGHM (≥2 mutations) | IGHD+ IGHM+ TCL1Aint | n = 388 |
| | B.int.1.early.act/sw.1 | IgDlow IgM+ CD27int | | IGHD, IGHM (≥2 mutations), or IGHA, IGHE, IGHG | IGHDlow IGHM+ TCL1Aint | n = 433 |
| | B.int.1.early.act/sw.2 | IgD- IgM-CD27int | | IGHD, IGHM (≥2 mutations), or IGHA, IGHE, IGHG | IGHD- IGHMlow TCL1A- | n = 168 |
| | B.int.2.unsw | IgD+ IgM+ CD27int | | IGHD, IGHM (<2 mutations) | IGHD+ IGHM+ TCL1Aint | n = 835 |
| | B.int.2.IFN.resp | IgDlow IgM+ CD27int | | | IGHDlow IGHM+ TCL1Aint; IFN resp gene +ve (e.g. MX1+) | n = 152 |
| | B.int.2.early.act.IFN.resp | IgD+ IgM+ CD27int | | IGHD, IGHM (≥2 mutations) | IGHD+ IGHM+ TCL1Aint; IFN resp gene +ve (e.g. MX1+) | n = 68 |
| | B.int.2.early.act/sw.1 | IgDlow IgM+ CD27int | | IGHD, IGHM (≥2 mutations), or IGHA, IGHE, IGHG | IGHDlow IGHM+ TCL1Aint | n = 3,978 |
| | B.int.2.early.act/sw.2 | IgD+ IgM+ CD27int | | IGHD, IGHM (≥2 mutations), or IGHA, IGHE, IGHG | IGHDlow IGHM+ TCL1Aint | n = 1,016 |
| | B.TRANSIT.CD10 | IgD+ IgM+ CD27- CD10+ | | | IGHD+ IGHM+ TCL1A+ | n = 1,116 |
| | B.mitohi.1 | | | | >4% mito | n = 1,632 |
| | B.mitohi.2 | | | | >4% mito | n = 470 |
| | B.cyc | | | | MKI67+ | n = 744 |
| | B.UNSW.MEM | IgD+ IgM+ CD27+ | | IGHD, IGHM | IGHD+ IGHM+ TCL1Aint | n = 2,597 |
| | B.SW.MEM.1 | IgD- IgM- CD27+ IgA+ or IgG+ | | IGHA, IGHE, IGHG | IGHD- IGHMlow TCL1A- | n = 5,855 |
| | B.SW.MEM.2 | IgD- IgM- CD27+ IgA+ or IgG+ | | | IGHD- IGHMlow TCL1A- | n = 1,970 |
| | B.SW.MEM.IFN.resp | IgD- IgM- CD27+ IgA+ or IgG+ | | IGHA, IGHE, IGHG or none | IGHD- IGHMlow TCL1A-; IFN resp gene +ve (e.g. MX1+) | n = 93 |
| **Plasma-blasts** | | singlet, CD19low CD20- CD38hi CD39hi | <50 TCRA & TCRB reads | singlet | XBP1+ SLAMF7+ PRDM1+ | n = 8,596 |
| | PB | | | >100 HC UMI | | n = 5,948 |
| | PB.IFN.resp | | | >100 HC UMI | IFN resp gene +ve (e.g. MX1hi) | n = 38 |
| | PB.mitohi | | | >100 HC UMI | >4% mito | n = 36 |
| | PB.cyc | | | >100 HC UMI | MKI67hi | n = 2,574 |

Definition of B and plasmablast subsets. red: identifying features, green: additional criteria, blue: confirmatory observations (thresholds checked but not applied).