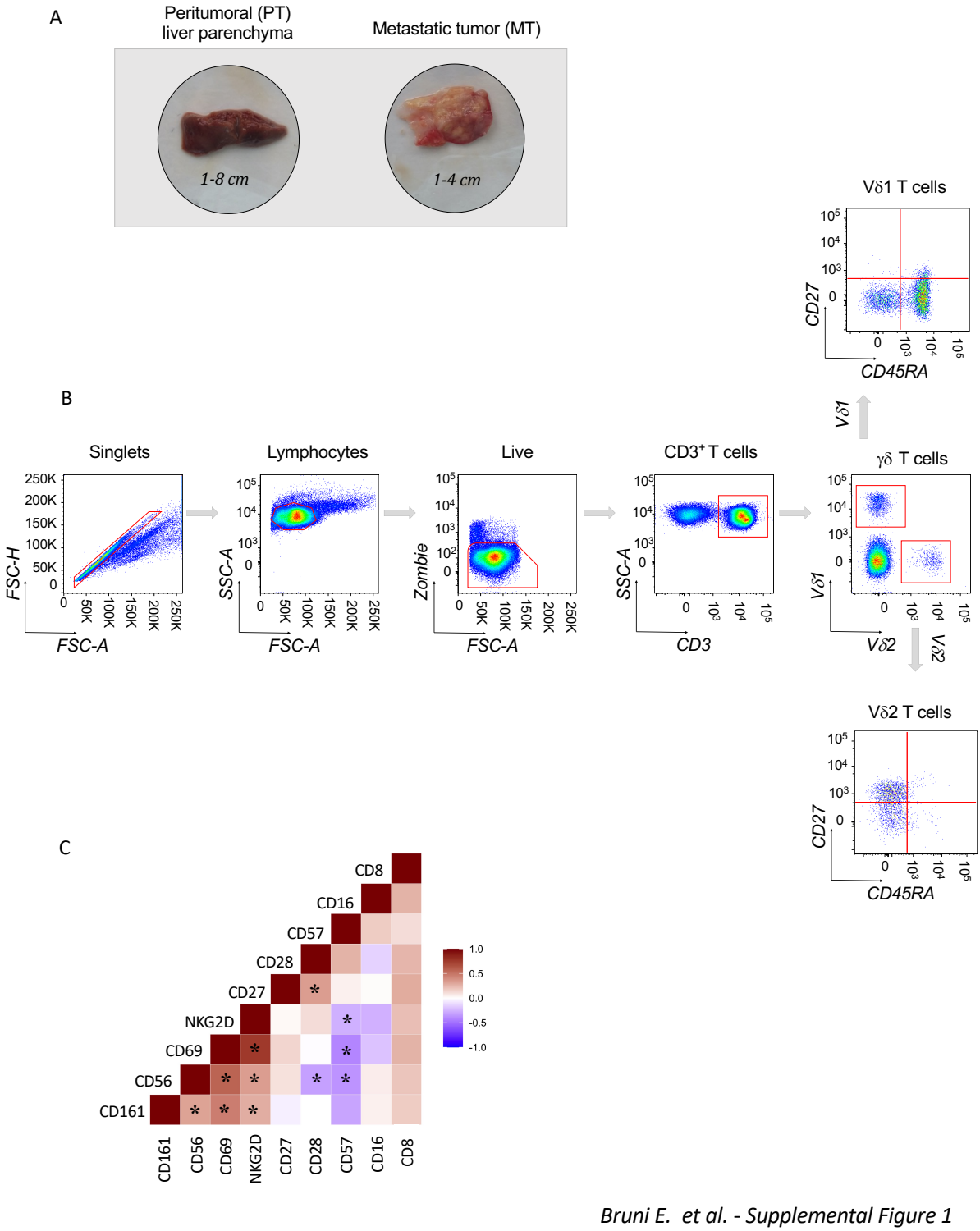
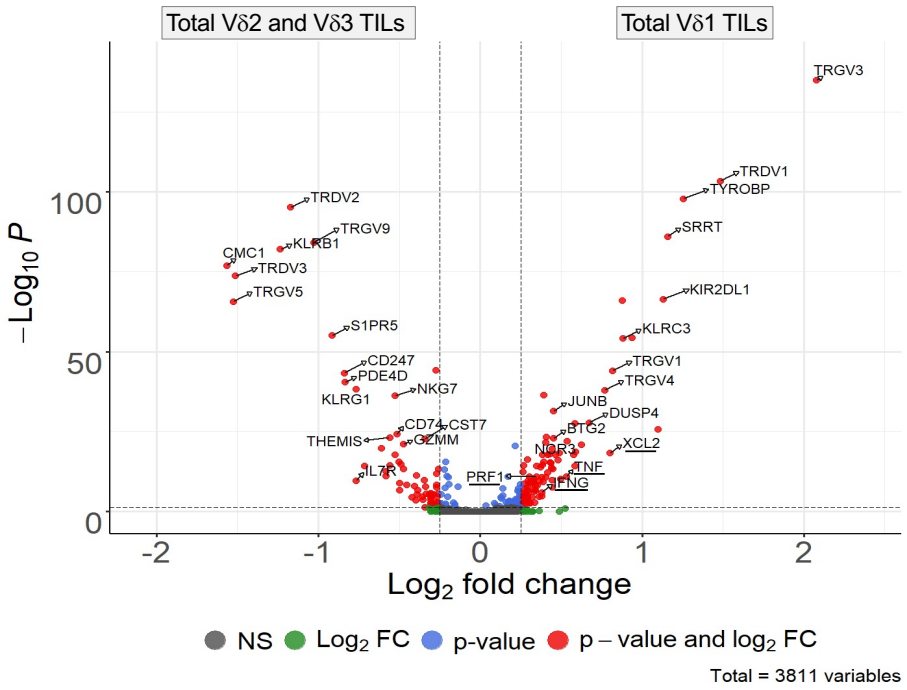



*Bruni E. et al. - Supplemental Figure 1*

**Supplemental Figure 1.**

**Peritumoral tissue (PT) and metastatic tumor (MT) areas CLM specimens and flow cytometry gating strategy.**

(A) Representative macroscopic examples (out of 93) of CLM liver specimen classified as peritumoral tissue (PT; left panel) or metastatic tumor (MT; right panel) parenchyma. **(B)** Representative (out of 93) flow cytometry pseudocolor plot graphs showing the gating strategy used to detect Vδ1 and Vδ2 T cell subsets among viable $CD3^+$ T lymphocytes and identification of differential phenotypes ($T_{EMRA}$, $T_{NAIVE}$, $T_{CM}$ and $T_{EM}$) based on CD27 and CD45RA markers expression among Vδ1 and Vδ2 T cells from PB of a CLM patient (out of 93). **(C)** Heatmap of flow cytometry data showing Spearman's rank between the mean of different cell markers expression (%) in PT Vδ1 TILs from CLM patients (*n=61*).




*Bruni E. et al. - Supplemental Figure 2*

**Supplemental Figure 2.**

**Analysis of differentially expressed genes between Vδ1 and Vδ2-3 TIL subsets from CLM.**

Volcano plot showing differentially expressed genes (DEGs) between total Vδ1 (cluster 0 and 3) versus total Vδ2 (cluster 2 and 5) and Vδ3 (cluster 1 and 6) TILs. Red circles represent genes with adj. *P value <0.05* and $Log_2$-FoldChange differential expression > 0.25, blue circles genes with adj. P value < 0.05 and $Log_2$-FoldChange < 0.25; green circles genes with *adj. P value* > 0.05 and $Log_2$-FoldChange > 0.25 and grey ones represent genes with adj. P value > 0.05 and $Log_2$-FoldChange < 0.25.



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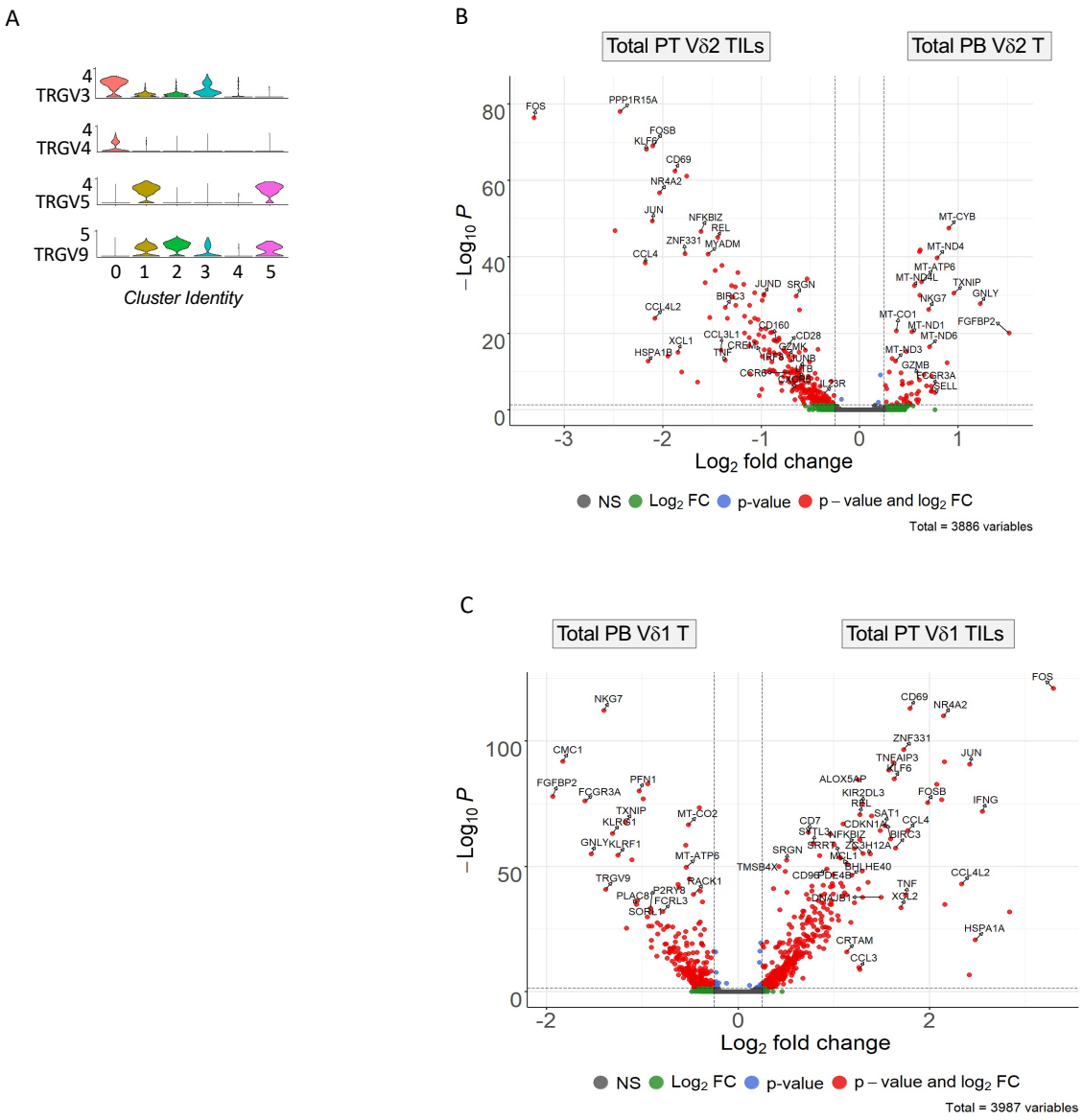


*Bruni E. et al. - Supplemental Figure 3*

**Supplemental Figure 3.**

**scRNA-seq integrated analysis comparing differentially expressed genes of circulating and tumor infiltrating γδT cells from CLM patients.**

**(A)** Violin plots showing the transcript levels of *TRGV* genes among the 6 γδT cell clusters identified by the integrated analyses of peripheral blood (PB) and peritumor (PT) samples from 3 CLM patients undergone surgical resections. **(B-C)** Volcano plots showing differently expressed genes (DEGs) between total PB and PT Vδ2 T cells **(B)**, and Vδ1 T cells **(C)**. Red circles represent genes with *adj. P value <0.05* and *$Log_2$-FoldChange differential expression > 0.25*, blue circles genes with *adj. P value < 0.05* and *$Log_2$-FoldChange < 0.25*; green circles genes with *adj. P value >0.05* and *$Log_2$-FoldChange > 0.25* and grey ones represent genes with *adj. P value >0.05* and *$Log_2$-FoldChange <0.25.*



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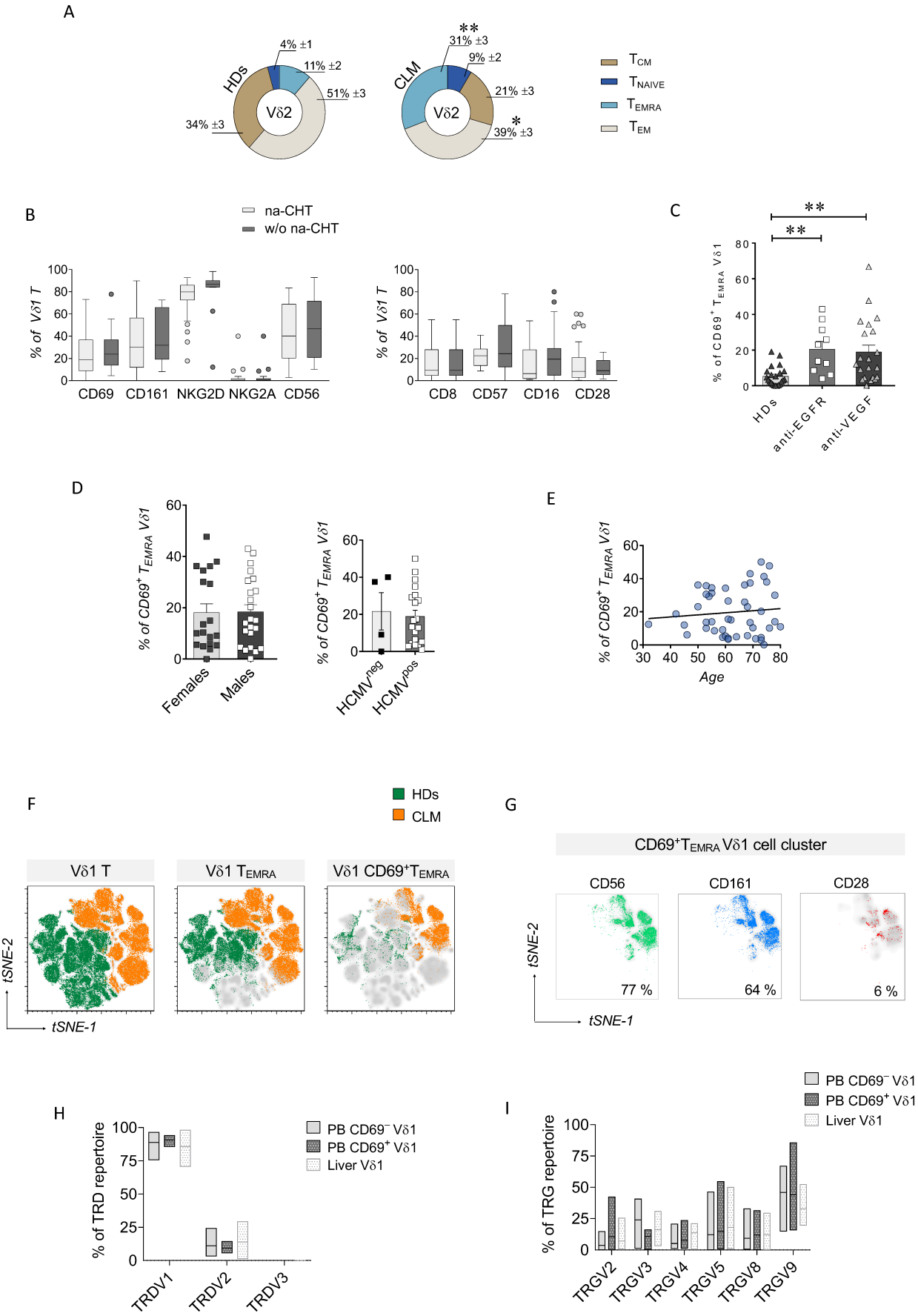


*Bruni E. et al. - Supplemental Figure 4*

**Supplemental Figure 4.**

**Frequencies, phenotype and TCR repertoires of PB Vδ1 and Vδ2 T cells from CLM patients.**

**(A)** Pie charts showing the mean frequency distribution (%) of PB $T_{NAIVE}$, $T_{CM}$, $T_{EM}$ and $T_{EMRA}$ Vδ2 T cells in healthy donors (HDs) (*n=33*) and in CLM (*n=50*). **(B)** Statistical bar graph showing the mean (±SEM) frequency (%) of several surface markers differentially expressed on PB Vδ1 T cells in CLM patients either in the absence (*n=13) (grey)* or in the presence (*n=40*) (white) of na-CHT. **(C)** Mean (±SEM) frequency (%) of $CD69^+T_{EMRA}$ Vδ1 cell cluster in HDs and CLM patients underwent either anti-EGFR (*n=10*) or anti-VEGF (*n=20*) mAbs therapy. (**D**) Statistical bar graph showing the mean (±SEM) frequency (%) of PB $CD69^+T_{EMRA}$ Vδ1 cells in CLM patients according to sex (Female, *n=18;* Male, *n=26*) (left panel) and HCMV infection status ($HCMV^{neg}$, *n=4;* $HCMV^{pos}$, *n=20*) (right panel). (**E**) Pearson's rank correlation between frequency (%) of PB $CD69^+T_{EMRA}$ Vδ1 cells and age of CLM patients (*n=49*). **(F-G)** *t-distributed Stochastic Neighbor Embedding (t-SNE)* plots showing projection of total Vδ1 T cells or either the specific $T_{EMRA}$ or $CD69^+T_{EMRA}$ Vδ1 cells in HDs (*n=22*; green) and CLM (*n=22*; orange) **(F)**, and the overlapping of different cell surface markers in CLM $CD69^+T_{EMRA}$ Vδ1 cells (*n=22*) (**G**). **(H-I)** TCR-repertoire analysis of the liver and PB Vδ1 T cells. Quantification (%) of V chains for TCR-δ (TRD) **(H)** and TCR-γ (TRG) **(I)** repertoires of PB $CD69^+$ and $CD69^-$ Vδ1 and liver PT Vδ1 of CLM patients (*n=5*).

**Supplemental Table 1|**
**Monoclonal antibodies (mAbs) used for flow cytometry analysis.**

| Marker | Fluorochrome | Clone | Company | Catalogue Number |
|---|---|---|---|---|
| **CD3** | BUV661 | UCHT1 | BD | 565065 |
| **CD8** | BUV805 | SK1 | BD | 564912 |
| **CD16** | BUV496 | 348 | BD | 564653 |
| **CD16** | PR-CY7 | 3G8 | BD | 557744 |
| **CD45** | AF700 | HI30 | BD | 560566 |
| **CD45RA** | BUV737 | HI100 | BD | 564442 |
| **CD56** | BUV563 | NCAM16.2 | BD | 565704 |
| **CD56** | PE-CF594 | B159 | BD | 562289 |
| **CD107a** | PE | H4A3 | BD | 555801 |
| **CCR7** | AF700 | 150503 | BD | 561143 |
| **CXCR3** | APC | 1C6 | BD | 550967 |
| **NKG2D** | BV780 | 1D11 | BD | 743560 |
| **Vδ2** | BUV395 | B6 | BD | 743754 |
| **Vδ2** | FITC | IMMU 389 | Beckman Coulter | IM1464 |
| **CD3** | BV650 | OKT3 | BioLegend | 317324 |
| **CD28** | PE-CY7 | CD28.2 | BioLegend | 302926 |
| **CD69** | BV605 | FN50 | BioLegend | 310938 |
| **CD161** | BV421 | HP-3G10 | BioLegend | 339914 |
| **CD14** | BV570 | M5E2 | BioLegend | 301832 |
| **CD27** | APC eFluor780 | 0323 | eBioscience | 47027942 |
| **CD45** | APC-Vio770 | 5B1 | Miltenyi | 130096609 |
| **CD57** | PE-Vio615 | REA769 | Miltenyi | 130111815 |
| **Vδ1** | PE | REA173 | Miltenyi | 130120440 |
| **Vδ1** | PE-Vio770 | REA173 | Miltenyi | 130117697 |
| **CD19** | APC-Vio770 | REA675 | Miltenyi | 130113643 |