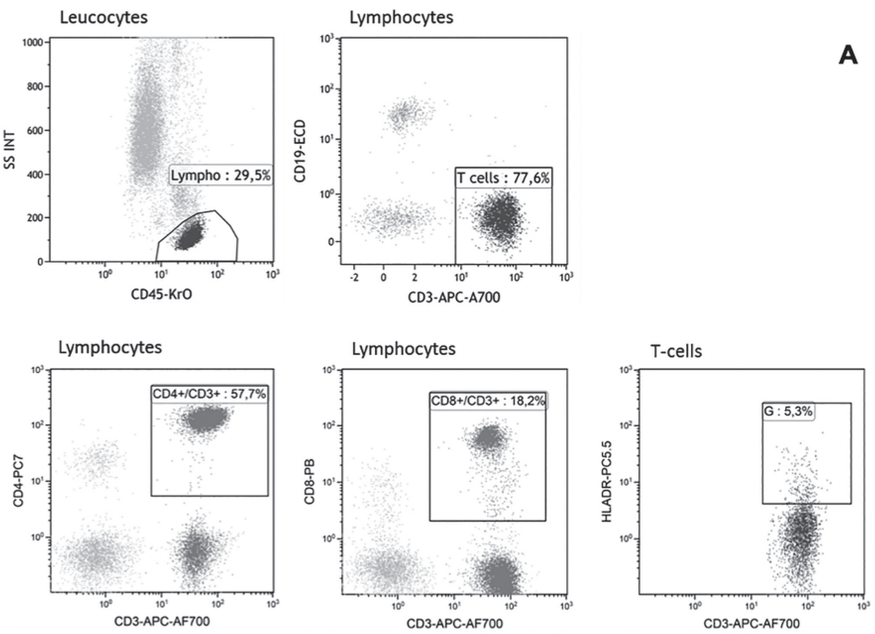
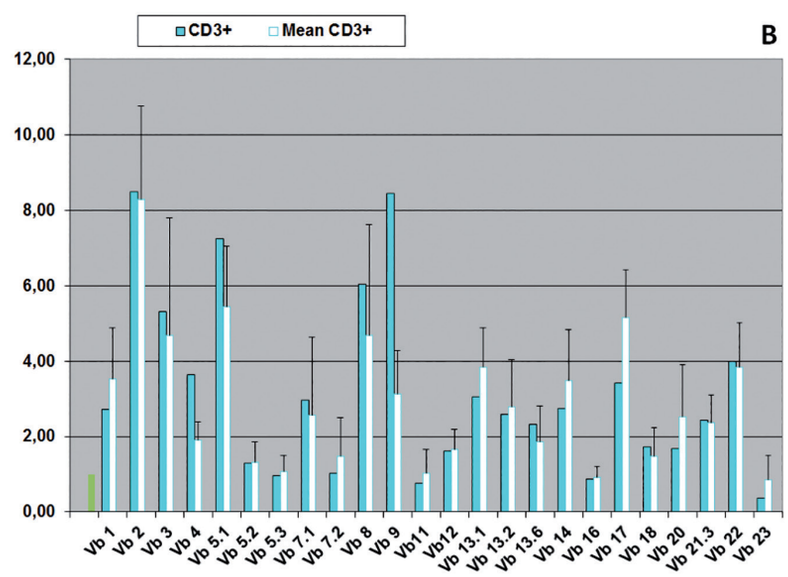
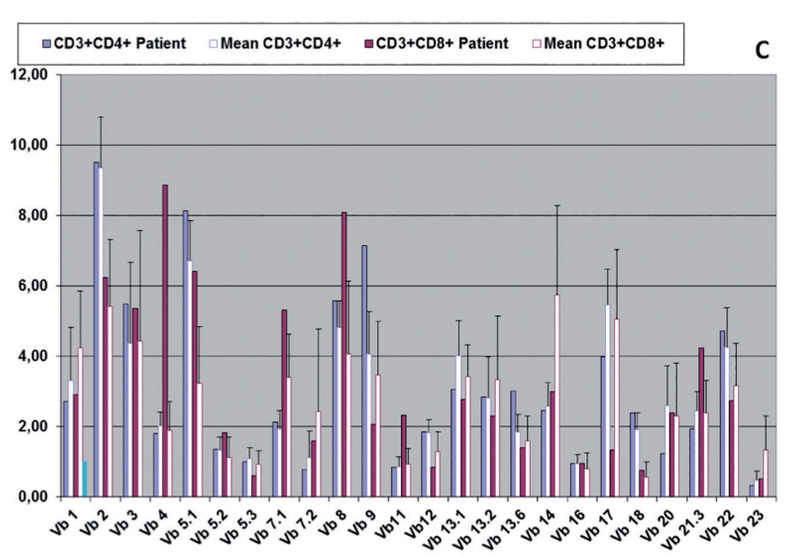
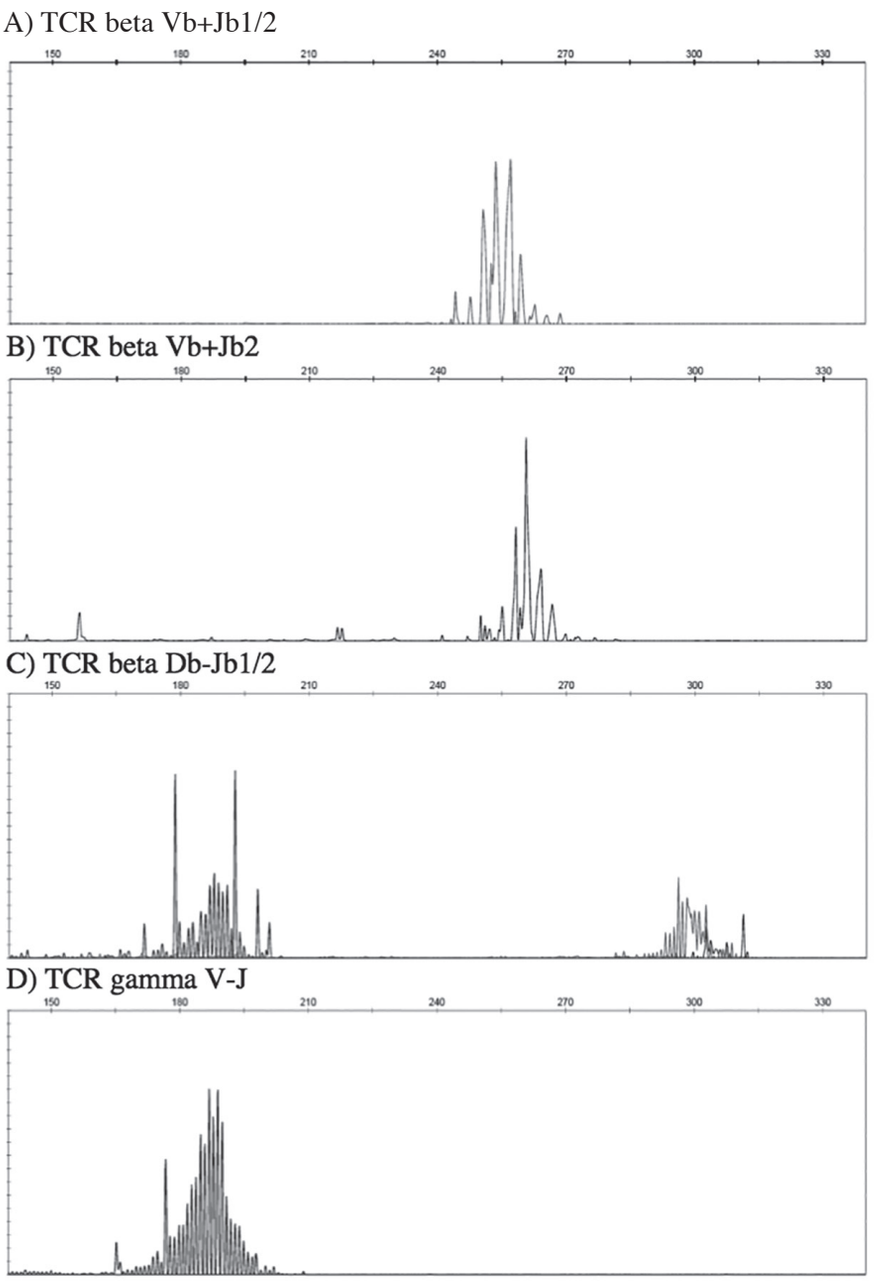
Supplementary Fig. 1.
A: Determination of lymphocyte subpopulations with immunophenotyping: Initially, a lymphocyte gate was established based on SS/CD45 of all leukocytes (**1**). Subsequently, T-cells were gated as CD19-/CD3+ (**2**), CD4+ T-cells as CD4+/CD3+ (**3**) and CD8+ T-cells as CD8+/CD3+ (**4**) of all lymphocytes. Activated T-cells are determined as CD3+/HLADR+ (**5**) of all T-cells.
B: Schematic overview showing the TCR-Vβ repertoire of all T-cells (CD3+) (upper diagram).
C: The CD4+/CD3+ and CD8+/CD3+ T-cell subpopulations (lower diagram) together with the mean normal values.









Supplementary Figure 2.
GeneScan analysis of PCR products of TCR beta (A-C) and TCR gamma (D) gene rearrangements using the multiplex BIOMED-2/Euroclonality primer system. (Oligo)clonal TCRB gene rearrangements in a polyclonal background could be identified in Db-Jb1/2, polyclonal TCR gene rearrangements can be identified in TCR beta Vb+Jb1/2, Vb+Jb2 and TCR gamma V-J. Pseudoclonality was excluded by determination of sufficient T-cell fraction by FACS, multiple PCR performances and blood draw at repeated times.