



**Supplementary Figure 1. Criteria for identification of CMV-specific TCRβ clonotypes.** As an example, representative data from donor P01 for identification of CRV-specific T cells are shown. Diagrams on the left relate to the binary comparison of the CRV-stimulated sample and the TPR-stimulated sample (control peptide). Diagrams on the right relate to the comparison of the CRV-stimulated sample and the unstimulated PBMC sample. Only TCRs that fulfilled all criteria were categorized as CRV epitope-specific. In dot plots, a frequency of zero is plotted as a pseudofrequency of 0.5 reads. **(A)** Relative frequencies of TCRβ clonotypes. Red lines indicate the enrichment cut-off (diagonal line) and the specific sample read count cut-off (horizontal line). **(B)** The enrichment cut-off (red line) is defined as the local minimum of the weighted density distribution of the logarithm of clonotype enrichment. Clonotype enrichment is the ratio of clonotype frequencies in the CRV-stimulated sample and either control. **(C)** Read count cut-offs (red line) were defined as local minima of the distribution of the logarithms of clonotype counts, determined for clonotypes with a read count of 1 to 10 in the TPR-stimulated (left) or unstimulated (right) sample. The mean of these two cut-offs was used as the final specific sample read count cut-off. **(D)** Relative frequencies of TCRβ clonotypes as in A, but TCRβ clonotypes that fulfil all inclusion criteria for being CRV epitope-specific are shown in red. **(E)** Correlation of the log-transformed read frequencies of CRV-specific clonotypes in the unstimulated and CRV-stimulated sample, with Pearson correlation coefficient R.