



**Figure 2-figure supplement 1. Whole genome methylation profiles of naive and cytotoxic CD4 and CD8 T cells.** Methylation profiles of 450,000 CpG sites were measured in T cell subsets with Infinium arrays in 5 CMV-seropositive healthy adults. The figure shows the proportions of hypomethylated (blue) and hypermethylated (red) probes identified in gene promoter, body, 3'UTR and intergenic regions following the comparison of  $CD4_{CTX}$  and naive  $CD4$  ( $CD4_N$ ) T cells (**a**),  $CD8_{CTX}$  and naive  $CD8$  ( $CD8_N$ ) T cells (**b**),  $CD8_N$  and  $CD4_N$  T cells (**c**) and  $CD4_{CTX}$  and  $CD8_{CTX}$  T cells (**d**). Grey bars indicate the proportions of probes at the different gene locations. The differentiation of naive in cytotoxic T cells was associated with the hypomethylation of large numbers of probes. Methylation values of 95,877 probes with a variance  $>0.01$  were submitted to unsupervised clustering analysis (**e**).