



Figure 5- figure supplement 2. Epigenetic and transcriptional program underlying the expression of perforin in Th1 cells. a) Methylation profiles of 450,000 CpG sites were measured in T cell subsets with Infinium arrays. 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 CM_{Th1} and naive CD4 (CD4_N) T cells (left panel), CD4_{CTX} and CM_{Th1} cells (right panel). Grey bars indicate the proportions of probes at the different gene locations. The differentiation of CM_{Th1} and CD4_{CTX} T cells was associated with the hypomethylation of large numbers of probes. **b)** The expression of candidate gene mRNA was measured by qPCR in purified T cell subsets from 3-4 donors. Data are median +/- interquartile range of log2 fold change as compared to naive CD4 (CD4_N) T cells. *:p<0.05. High levels of *ZEB2*, *HOPX*, and *ZNF683* (Hobit) were detected in all memory CD4 T cell subsets whereas increased levels of *ASCL2* were only detected in CD4_{CTX} T cells.