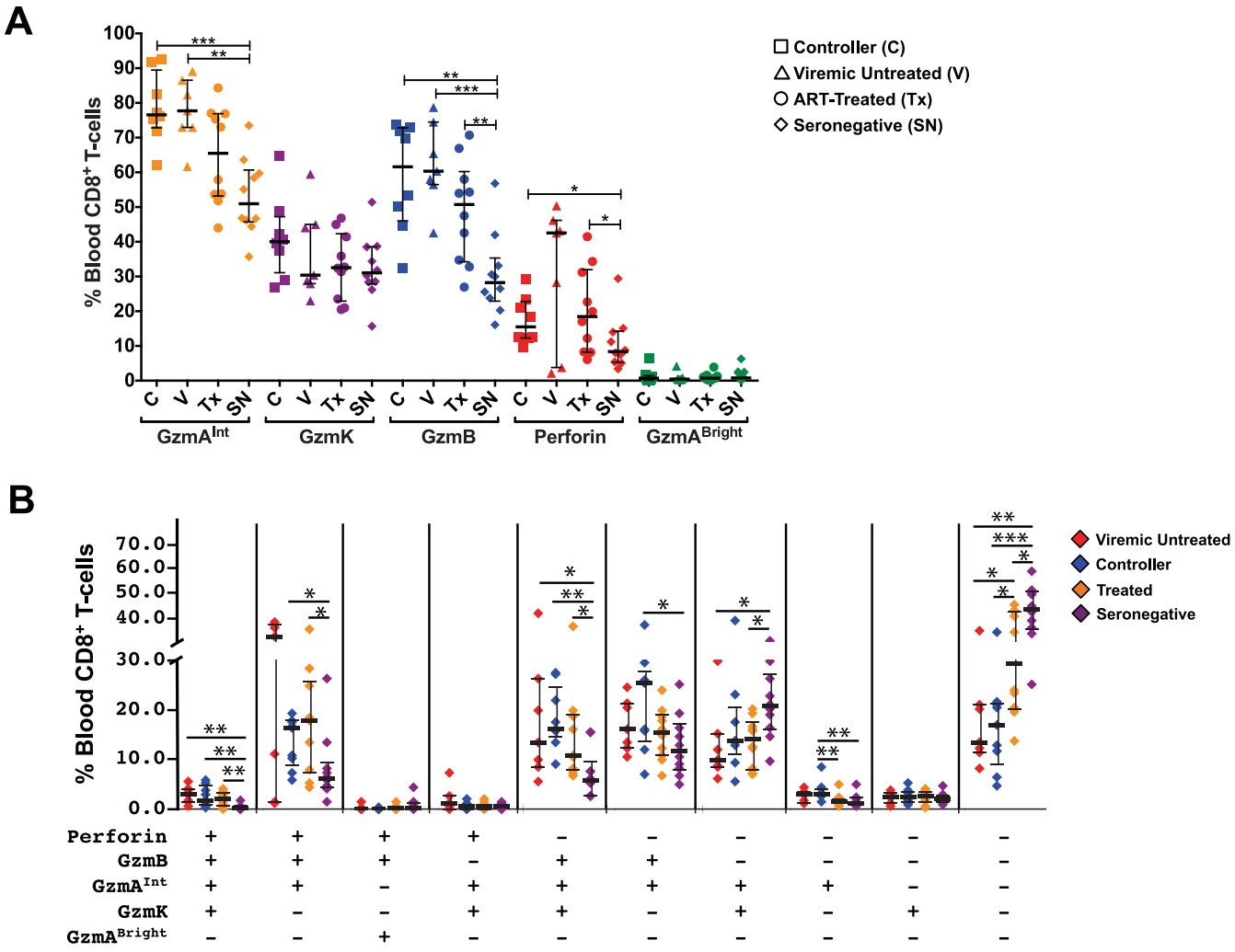
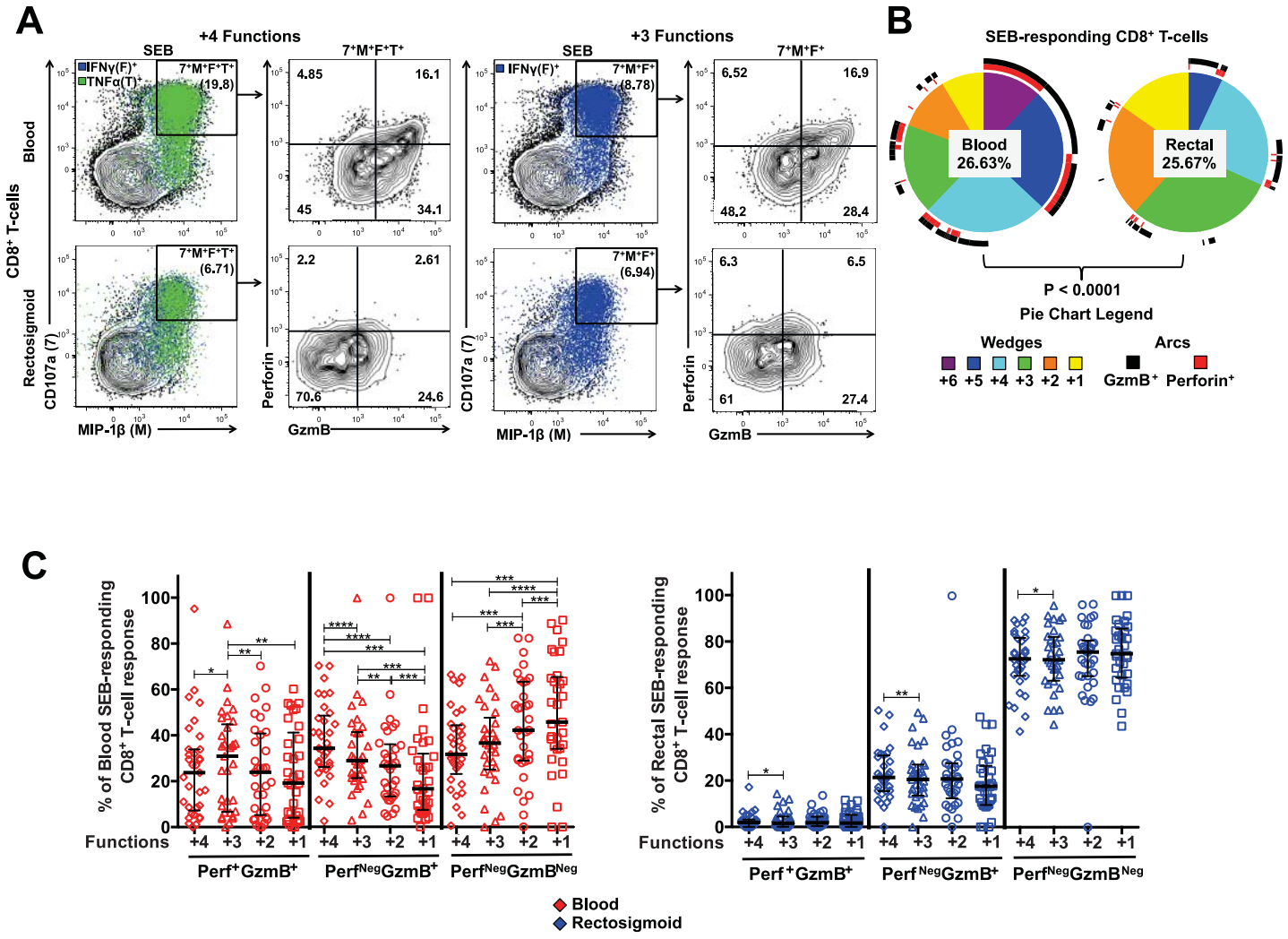
SUPPLEMENTAL FIGURE 1



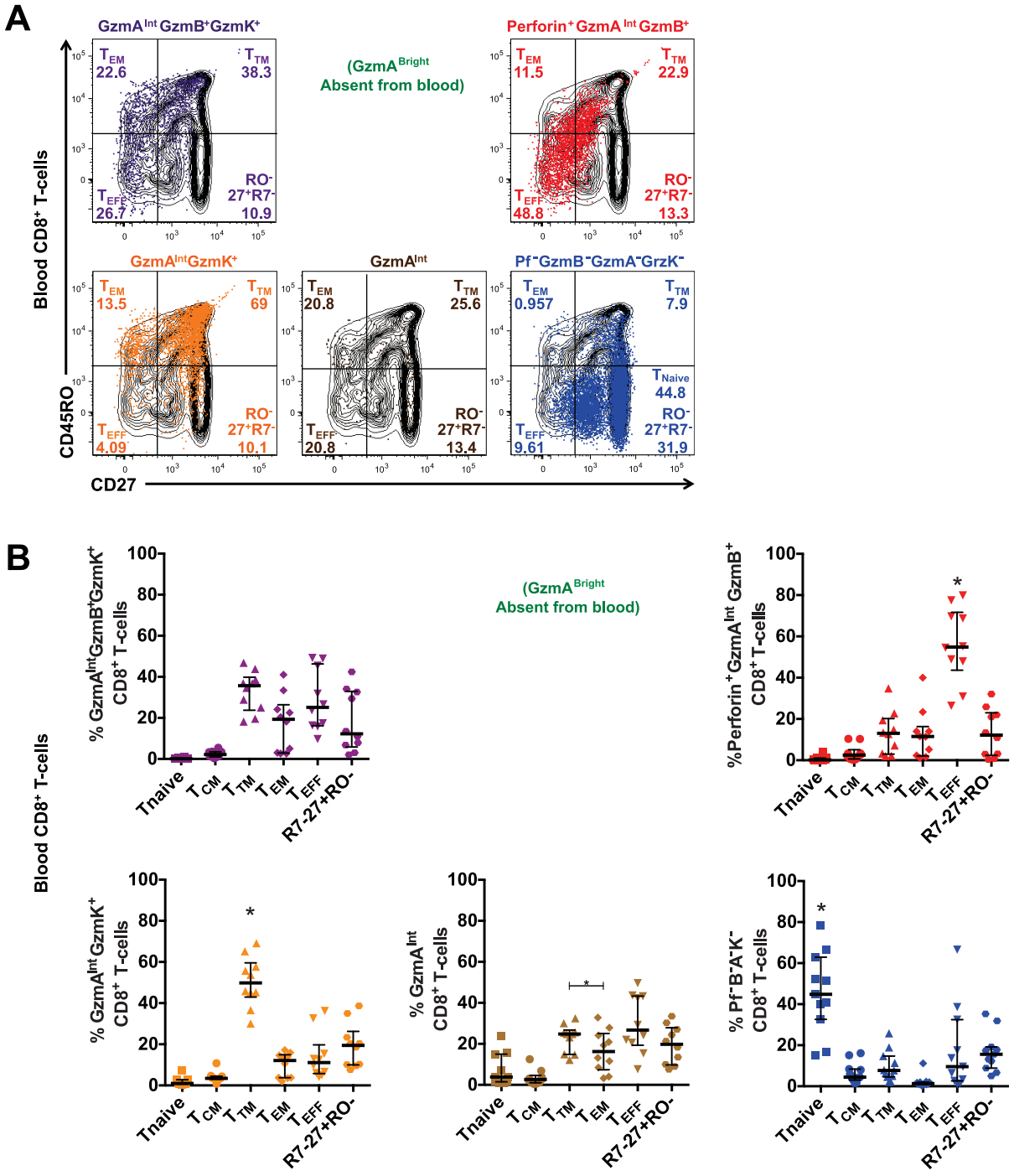
SUPPLEMENTAL FIGURE 1. Expression of cytotoxic effectors in unstimulated blood CD8$^+$ T-cells. (**A**) Differences in the intracellular expression of GzmA$^{Int/Bright}$, GzmK, GzmB, and perforin in unstimulated blood CD8$^+$ T-cells across HIV-1 disease status as follows: C (Controllers) n=8, V (viremic untreated) n=7, Tx (ART-suppressed) n=10, SN (seronegatives) n=10. (**B**) Differences in the abundance of blood CD8$^+$ T-cells co-expressing cytotoxic effectors across HIV-1 disease status as follows: Viremic Untreated (V) n=7, Controllers (C) n=8, ART-suppressed (Tx) n=10, and seronegatives (SN) n=10. Co-expression analysis was generated using SPICE software. Wide horizontal bars represent medians; narrow whiskers indicate interquartile ranges. Asterisks show level of significance as follows: * P <0.05, ** P <0.01, *** P <0.001.

SUPPLEMENTAL FIGURE 2



SUPPLEMENTAL FIGURE 2. Expression of perforin and GzmB in blood and rectosigmoid CD8$^+$ T-cells responding to *ex vivo* stimulation with SEB. (**A**) Intracellular expression of perforin (Perf) and GrzB in polyfunctional (CD107a$^+$MIP-1β$^+$IFNγ$^+$TNFα$^+$ and CD107a$^+$MIP-1β$^+$IFNγ$^+$) SEB-responding CD8$^+$ T-cells in blood and rectosigmoid mucosa. (**B**) Differences in intracellular expression of perforin and GzmB in SEB-responding CD8$^+$ T-cells visualized in a SPICE pie chart. Effector functions included CD107a, MIP-1β, IFNγ, and TNFα. Percentages indicate the median total SEB CD8$^+$ T-cell response. n=33. (**C**) Differences in perforin and/or GzmB expression between mono- and polyfunctional SEB-responding CD8$^+$ T-cells in blood and mucosa. n=33. Wide horizontal bars represent medians; narrow whiskers indicate interquartile ranges. In **B** and **C** asterisks show level of significance as follows: * P <0.05, ** P <0.01, *** P <0.001, **** P <0.0001.

SUPPLEMENTAL FIGURE 3



SUPPLEMENTAL FIGURE 3. Expression of memory markers by CD8$^+$ T-cell subsets in blood. (**A**) Representative flow cytometry plot showing expression of memory markers CD45RO and CD27 on blood CD8$^+$ T-cell subsets: GrzA^{Int}GrzB$^+$GrzK$^+$, GrzA^{Int}GrzK$^+$, GrzA^{Int}, GrzA^{Int}GrzB$^+$perforin$^+$, and cells lacking expression of cytotoxic effectors (Perforin$^-$GrzB$^-$GrzA$^-$GrzK$^-$). The proportions of naïve (T_{naive}), transitional memory (T_{TM}), effector-memory (T_{EM}), effector (T_{EFF}), and CD45RO$^-$CD27$^+$CCR7$^-$ cells within each subset are displayed within quadrants. (**B**) Differences in the frequencies of naïve (T_{naive}), central memory (T_{CM}), transitional memory (T_{TM}), effector memory (T_{EM}), effector (T_{EFF}), and CD45RO$^-$CD27$^+$CCR7$^-$ cells within each of the blood CD8+ T-cell subsets shown in (A). Large asterisk identifies memory phenotypes with a significantly greater median frequency compared to all other memory subsets. n=11. Wide horizontal bars represent medians; narrow whiskers indicate interquartile ranges; asterisks show level of significance as follows: * P <0.05.