Supplemental Figure 1: Distribution of naïve and memory cell subsets as a

function of time since seroconversion. The box (interquartile range) and whisker plots depict the relative frequencies of naïve, central-, transitional-, and effector-memory cells within CD4 or CD8 lineages.

Supplemental Figure 2: Overall distributions of the cell types examined in progression analyses. The box and whisker plots depict relative frequencies of central memory, naïve, and CD127⁺ T-cells. Interquartile ranges were used to group patients for the progression analyses; thus, data within the box represents individuals with

intermediate levels of a particular cell type (25th to 75th percentile), while data above and below the box represent patients in the highest and lowest groups, respectively.

Supplemental Figure 3: Cell sorting scheme. Cells from every sample were sorted into four subsets for quantification of the cell-associated viral load. Graphs illustrate the sequential gating to identify pure populations. The first gate eliminates doublets; the second restricts analysis to live, CD3⁺ T cells; small lymphocytes are selected; within those, CD4⁺ CD8⁻ T cells are selected. Within CD4⁺ T cells, naïve T cells were identified as CD28⁺CCR7⁺CD45RO⁻CD27⁺ (to exclude contaminating memory cells as well as possible). Effector memory cells were defined as CD28⁺CCR7⁺CD45RO⁺, and transitional memory cells as CD28⁺CCR7⁺CD45RO⁺.

Page 1 of 1

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Ganesan, et al. Suppl. Figure 2

Page 1 of 1

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Ganesan, et al. Supplemental Figure 3