

Figure S1: Comprehensive evolutionary alignment of SC3 RREs. The prevalence of each RRE sequence at a given visit was calculated as a percentage of the total number of sequences generated from that plasma sample without removing minority variants. RRE sequences were assigned a code in the form VXX-Y where XX refers to the visit number and Y refers to the prevalence rank order of that sequence. Nucleotide differences relative to the V08-1 presumptive founder sequence are highlighted. Sequences in red boxes have a prevalence of at least 5% and were included in the analysis presented in Figure 2 after excluding the minority variants.

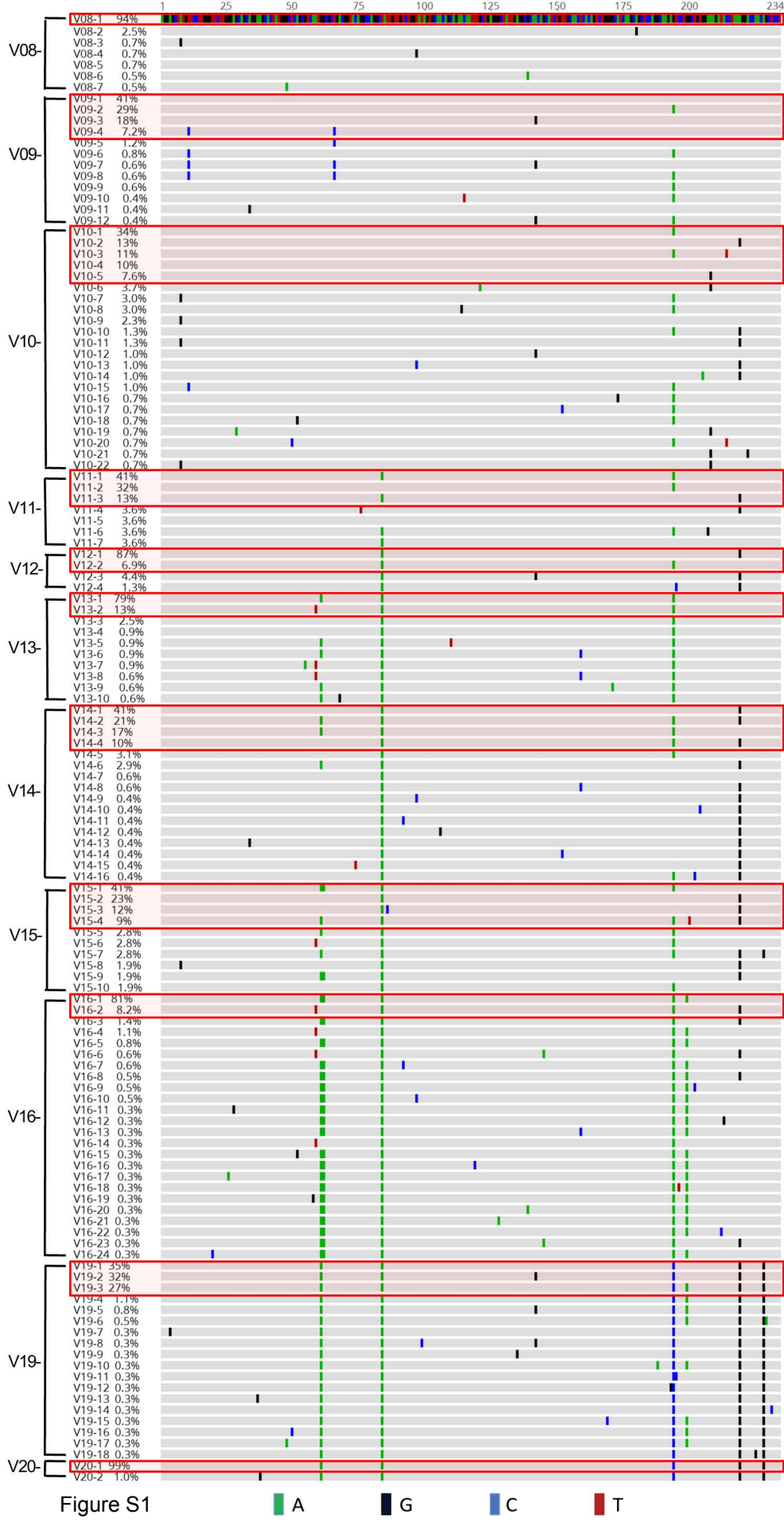


Figure S2: Evolutionary alignment of SC3 RREs at single-nucleotide resolution. The alignment includes only contigs that were present in at least 5% of the sequences at a given time point as explained in the Methods. Sequences obtained from different plasma samples corresponding to different time points are separated by horizontal red bars.



