

SUPPLEMENTAL MATERIAL

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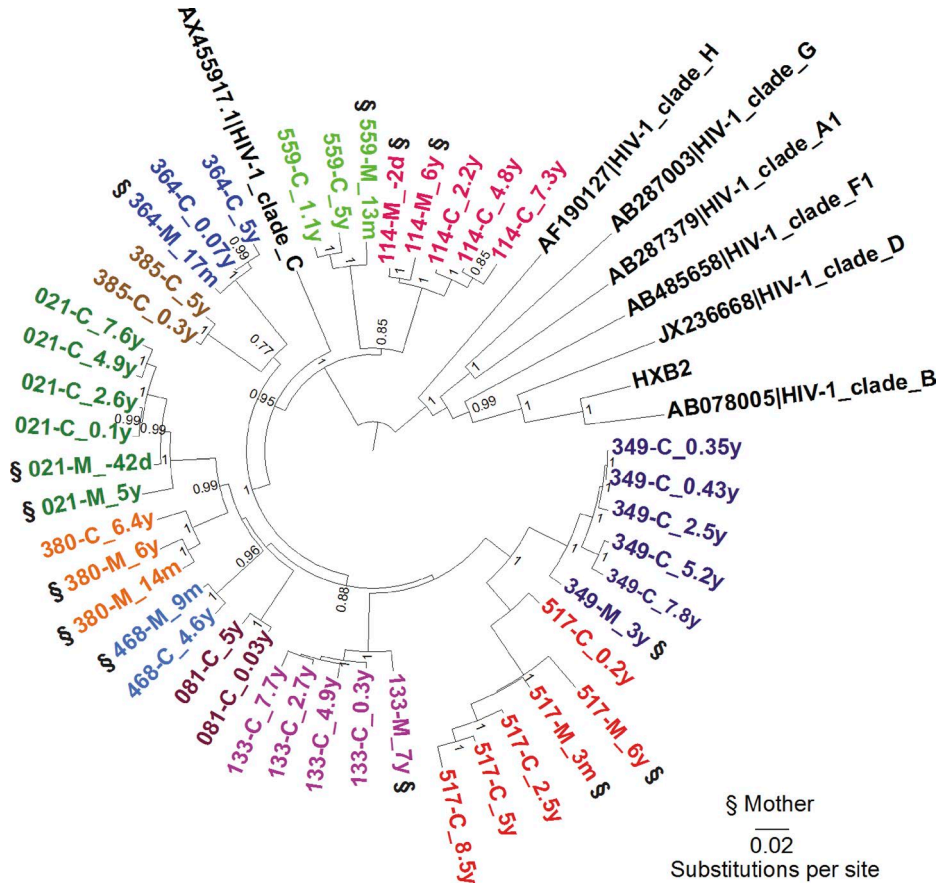


Figure S1. Maximum-likelihood phylogenetic tree from 43 full-genome sequences of the 11 PSP and their mothers. Partial genomes were not included. Mother-child pairs are distinguished by colors and maternal sequences are marked. HXB2 sequence and reference sequences for clades A, B, C, D, F, G, and H are included. Bootstrap values >0.75 based on 1,000 bootstrap replicates are shown. Scale bar shows number of substitutions per site.

Table S1 shows HLA-associated escape mutations that developed in the VNC child 517-C. Table S2 shows HLA-associated escape mutations that developed in the VNC child 021-C. Table S3 shows 11 HLA-B*42:01-positive and/or HLA-B*81:01-positive children from Southern Africa in whom autologous virus encoded a Gag-TL9 variant. Table S4 shows epitopes used in the analysis of pediatric deep-sequence data. Tables S1-S4 are provided as Excel files.