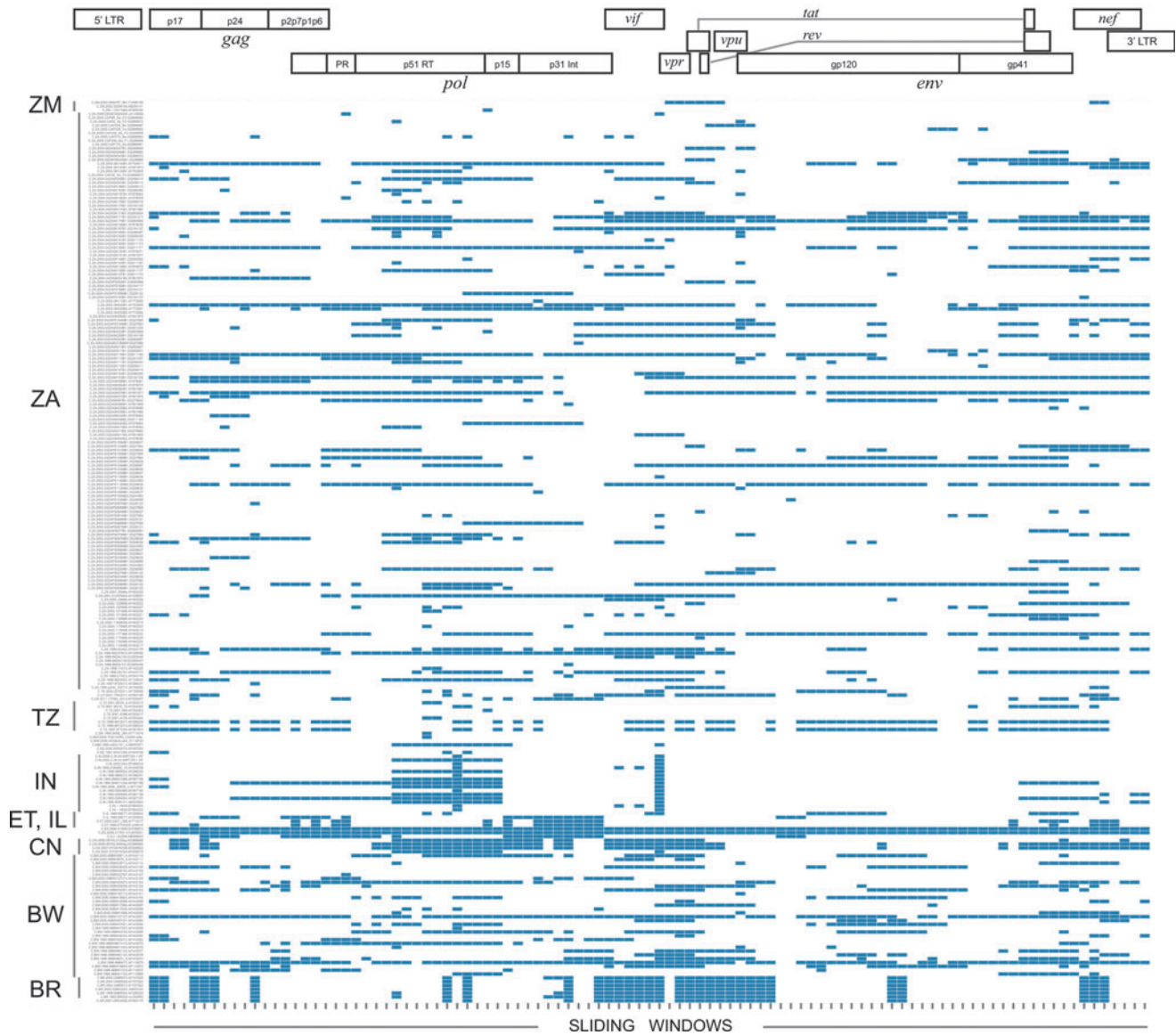SUPPLEMENTARY FIG. S2. Clustering of HIV-1C sequences across 99 sliding windows (window size 1,000 bp, step size 100 bp) in the bootstrapped $ML_{GTR+\Gamma}$ analysis at a bootstrap threshold of ≥ 0.80. The HIV-1 genome structure is shown at the *top* of the graph. The HIV-1 genome map was drawn according to the multiple sequence alignment of the near full-length genome sequences. Only HIV-1C sequences found in clusters at a bootstrap support of 0.70 in the near full-length genome analysis ($n = 236$) is shown. Clustering of the viral sequence within each sliding window is denoted by a *filled block*, while nonclustering is shown with a *blank block*. Viral sequences are listed on the *left* and grouped by country: BR, Brazil; BW, Botswana; CN, China; ET, Ethiopia; IL, Israel; IN, India; TZ, Tanzania; ZA, South Africa; and ZM, Zambia. Countries represented by small numbers of sequences are not delineated.