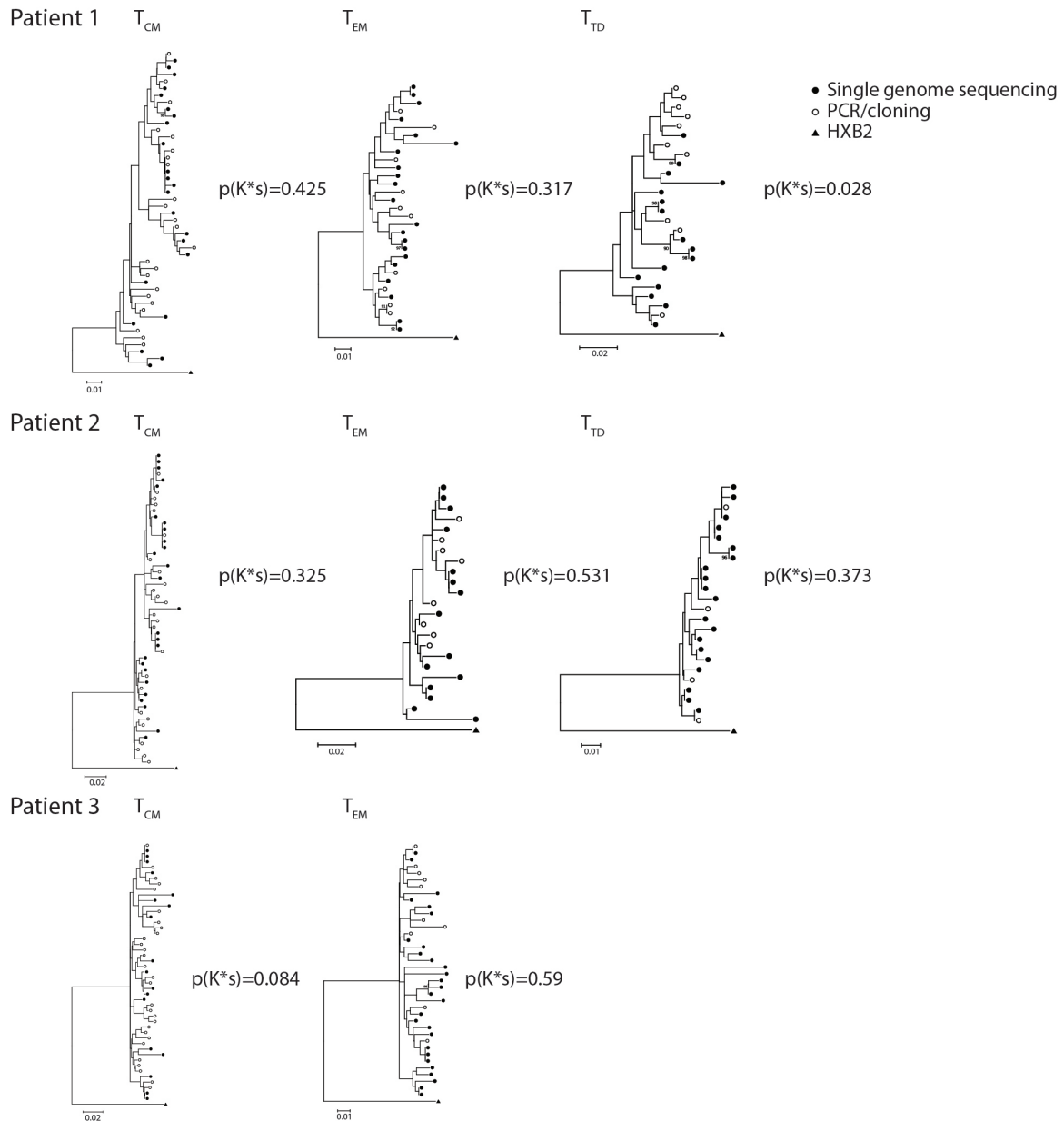


Supplementary Figure 9



Supplementary Figure 9: Comparison of HIV-1 sequences obtained by single-genome analysis vs PCR/cloning analysis. HIV-1 sequences were generated and analyzed by single-genome analysis as described in²⁵ from indicated CD4⁺ T cell populations. Phylogenetically-informative HIV-1 sequences generated by PCR/cloning were compared to sequences obtained by single-genome analysis from the same cell

populations, using neighborhood-joining phylogenetic trees. Solid symbols represent sequences derived by single genome sequencing and open squares represent sequences derived by PCR/cloning. Tests for panmixia ($p(K*s)$) were calculated as described before (<http://www.abi.snv.jussieu.fr/achaz/hudsonstest.html>)²⁴ and are indicated for each comparison; this algorithm assumes that if biases were introduced by the analysis type, the groups of sequences generated by single-genome analysis and PCR/cloning would be significantly different with a $p(K*s)$ value of <0.003 ²⁴.