S3 Table. Sequence-based diversity measures expressed as the median/IQR and calculated from NGS of 5 segments representing 5 selected HIV-1 env GP120 loop and 1 segment for a part of the GP41 ectodomain (NHR).

| HIV-1 env segment | Sequence-based diversity measure | Recent HIV-1 infected population | Chronic HIV-1 infected population |
|-------------------|---------------------------------|----------------------------------|----------------------------------|
|                   | Median | IQR       | Number of sample analyzed (n)  | Median | IQR       | Number of sample analyzed (n)  |
| GP120-V1          | Percent diversity | 0.01 [0.00-0.05] | 63 | 0.02 [0.00-0.09] | 35 |
|                   | Percent complexity | 0.00 [0.00-0.18] | 63 | 0.01 [0.00-0.25] | 35 |
|                   | Shannon Entropy | 0.05 [0.00-0.31] | 63 | 0.11 [0.00-0.54] | 35 |
|                   | Number of Haplotypes | 4 [1-7] | 63 | 6 [1-12] | 35 |
| GP120-V2          | Percent diversity | 0.01 [0.00-0.06] | 102 | 0.01 [0.01-0.09] | 77 |
|                   | Percent complexity | 0.00 [0.00-0.01] | 102 | 0.00 [0.00-0.02] | 77 |
|                   | Shannon Entropy | 0.02 [0.00-0.26] | 102 | 0.12 [0.00-0.32] | 77 |
|                   | Number of Haplotypes | 4 [1-13] | 102 | 8 [2-26] | 77 |
| GP120-V3          | Percent diversity | 0.01 [0.00-0.16] | 134 | 0.02 [0.00-0.17] | 115 |
|                   | Percent complexity | 0.00 [0.00-0.00] | 134 | 0.00 [0.00-0.00] | 115 |
|                   | Shannon Entropy | 0.02 [0.00-0.24] | 134 | 0.12 [0.00-0.32] | 115 |
|                   | Number of Haplotypes | 3 [1-16] | 134 | 7 [2-22] | 115 |
| GP120-V4          | Percent diversity | 0.01 [0.00-0.13] | 134 | 0.02 [0.00-0.14] | 115 |
|                   | Percent complexity | 0.00 [0.00-0.00] | 134 | 0.00 [0.00-0.00] | 115 |
|                   | Shannon Entropy | 0.01 [0.00-0.23] | 134 | 0.10 [0.00-0.27] | 115 |
|                   | Number of Haplotypes | 3 [1-17] | 134 | 6 [2-23] | 115 |
| GP120-V5          | Percent diversity | 0.02 [0.00-0.14] | 134 | 0.03 [0.00-0.17] | 115 |
|                   | Percent complexity | 0.00 [0.00-0.00] | 134 | 0.00 [0.00-0.00] | 115 |
|                   | Shannon Entropy | 0.01 [0.00-0.14] | 134 | 0.06 [0.00-0.25] | 115 |
|                   | Number of Haplotypes | 3 [1-13] | 134 | 4 [1-21] | 115 |
| GP41-NHR          | Percent diversity | 0.01 [0.00-0.05] | 131 | 0.01 [0.01-0.05] | 107 |
|                   | Percent complexity | 0.00 [0.00-0.08] | 131 | 0.00 [0.00-0.13] | 107 |
|                   | Shannon Entropy | 0.05 [0.00-0.30] | 131 | 0.13 [0.00-0.42] | 107 |
|                   | Number of Haplotypes | 5 [1-20] | 131 | 7 [2-35] | 107 |

*Median differences between recent and chronic infected individuals 4 sequence-based diversity measures of 6 env segments. IQR: interquartile range.*