**Table S5. Genetic diversity of full-length HIV sequences**. Sequences with inversion mutations excluded from all calculations.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HLA-DR+ | | HLA-DR- | | Naïve | | CM | | TM | | EM | | Overall | |
| Hypermutated Sequences | Included | Excluded | Included | Excluded | Included | Excluded | Included | Excluded | Included | Excluded | Included | Excluded | Included | Excluded |
| Acutely Treated Participants (SCOPE ID) | | | | | | | | | | | | | | |
| 2302 | - | - | - | - | 0.2 | 0.1 | 2.7 | 0.2 | 1.9 | 0.0 | 1.3 | 0.2 | 1.8 | 0.2 |
| 2115 | 2.1 | 0.3 | 2.9 | 0.6 | - | - | 3.9 | 1.8 | 2.3 | 0.1 | 3.1 | 0.3 | 3.0 | 0.6 |
| 2275 | 0.1 | 0.1 | 0.2 | 0.2 | - | - | - | - | 4.5 | 2.9 | 0.1 | 0.1 | 1.0 | 0.5 |
| Average | 1.1 | 0.2 | 1.6 | 0.4 | 0.2 | 0.1 | 3.3 | 1.0 | 2.9 | 1.0 | 1.5 | 0.2 | 1.9 | 0.4 |
| Chronically Treated Participants (SCOPE ID) | | | | | | | | | | | | | | |
| 2452 | - | - | - | - | 2.7 | 0.8 | 2.4 | 0.8 | 0.2 | 0.2 | 0.6 | 0.4 | 1.6 | 0.6 |
| 2026 | 1.4 | 1.4 | 2.2 | 1.6 | 1.7 | 1.4 | - | - | 4.1 | 4.1 | 0.8 | 0.8 | 2.3 | 2.1 |
| 2046 | 1.3 | 1.3 | 4.3 | 4.1 | - | - | 3.1 | 2.3 | - | - | 1.1 | 1.1 | 2.8 | 2.3 |
| Average | 1.4 | 1.4 | 3.3 | 2.9 | 2.2 | 1.1 | 2.8 | 1.6 | 2.2 | 2.2 | 0.8 | 0.8 | 2.2 | 1.7 |