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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table 1. Antibody repertoire analysis of an HIV-1-infected individual and two uninfected individuals. a** | | | | | | | | | |
| Exp.  index | Donor | PCR primers | PGM chip | Nread | Chain | Nchain | <Length> | Percno-gap | Percusable |
| **A. Validation of PGM for full-length antibody variable domain sequencing** | | | | | | | | | |
| 1 | IAVI donor | VH4 | 316 | 3,610,144 | H | 900,343 | 423.7 | 8.7% | 89.8% |
|  | 17 | VL3 |  |  | L | 2,675,687 | 429.8 | 10.1% | 90.8% |
| **B. Unbiased repertoire analysis based on 5’-RACE PCR** | | | | | | | | | |
| 2 | IAVI donor | 5’-RACE | 316 | 3,104,454 | H | 1,098,334 | 501.5 | 15.0% | 58.2% |
|  | 17 |  |  |  | L | 1,424,744 | 506.2 | 18.1% | 65.5% |
| 3 | Uninfected | 5’-RACE | 316 | 3,257,758 | H | 1,176,731 | 514.7 | 13.3% | 76.5% |
|  | donor #1 |  |  |  | L | 1,454,446 | 482.0 | 25.4% | 71.5% |
| 4 | Uninfected | 5’-RACE | 316 | 3,350,792 | H | 1,279,994 | 518.8 | 8.3% | 73.3% |
|  | donor #2 |  |  |  | L | 1,535,388 | 493.5 | 18.1% | 66.5% |
| **C. Comparison of repertoires obtained from 5’-RACE PCR and multiplex PCR** | | | | | | | | | |
| 5 | IAVI donor | GP-H1 | 316 | 4,732,217 | H | 4,732,217 | 429.1 | 30.0% | 79.7% |
| 6 | 17 | GP-H2 & | 318 | 6,802,786 | H | 2,508,220 | 495.0 | 7.7% | 43.2% |
|  |  | GP-L1 |  |  | L | 3,449,729 | 479.2 | 13.1% | 57.9% |
| **D. Validation of random barcoding in combined use with gene-specific primers** | | | | | | | | | |
| 7b | IAVI donor | VH4 | 316 | 3,109,512 | H | 1,133,165 | 448.2 | 18.1% | 84.2% |
|  | 17 | VL3 |  |  | L | 1,830,635 | 442.6 | 21.2% | 90.0% |
| **E. Assessment of new PGM technologies in the context of antibody sequencing** | | | | | | | | | |
| 8c | Uninfected | 5’-RACE | 316 | 3,902,464 | H | 2,079,766 | 565.6 | 28.4% | 86.5% |
|  | donor #2 |  |  |  | L | 1,416,722 | 554.8 | 33.7% | 91.8% |
| 9d | Uninfected | 5’-RACE | 316 | 3,888,807 | H | 1,924,743 | 435.8 | 38.8% | 65.0% |
|  | donor #2 |  |  |  | L | 1,360,189 | 453.0 | 42.5% | 71.1% |
| 10e | Uninfected | 5’-RACE | 316 | 4,205,538 | H | 1,261,313 | 560.5 | 33.3% | 85.3% |
|  | donor #2 |  |  |  | L | 2,255,705 | 559.1 | 33.2% | 81.1% |
| 11f | Uninfected | 5’-RACE | 316 | 4,183,209 | H | 1,107,022 | 461.6 | 41.5% | 73.1% |
|  | donor #2 |  |  |  | L | 1,889,100 | 455.7 | 40.7% | 72.8% |
| a Listed items include the index of sequencing experiment, donor name, PCR primers, PGM sequencing chip, total number of raw reads, antibody chain type, number of antibody chains, average read length, percentage of sequences without indel errors in the V gene, and total number of usable sequences after pipeline processing. Note that the 3’-trimming option was turned off in all PGM sequencing experiments except for #9 and #11 and the *Antibodyomics 1.0* pipeline was used for data processing and error correction.  b PGM sequencing using the standard setup and random barcoding technology.  c-d PGM sequencing using an improved emulsion-based template preparation method and Hi-Q enzyme (new OT2+Hi-Q) without 3-trimming (c) and with 3’-trimming (d).  e-f PGM sequencing using an emulsion-free template preparation method – isothermal amplification (IA) and Hi-Q enzyme (IA+Hi-Q) without 3’-trimming (e) and with 3’-trimming (f). | | | | | | | | | |