|  |  |  |  |
| --- | --- | --- | --- |
| Sequencing run | Sample ID | Sequencing depth | |
| After quality control | After removing eukaryotes |
| First | BaZ2\_1 | 54,814 | 54,462 |
| BaZ2\_2 | 90,310 | 90,026 |
| BaZ2\_3 | 58,581 | 58,423 |
| MoZ2\_1 | 58,032 | 57,710 |
| MoZ2\_2 | 55,072 | 54,908 |
| MoZ2\_3 | 55,592 | 55,291 |
| StZ2\_1 | 48,153 | 48,127 |
| StZ2\_2 | 46,047 | 46,009 |
| **StZ2\_3** | 37,769 | **37,722** |
| TiZ2\_1 | 56,622 | 56,516 |
| TiZ2\_2 | 47,860 | 47,809 |
| TiZ2\_3 | 46,195 | 46,039 |
| Second | BaN5\_1 | 20,449 | 20,444 |
| BaN5\_2 | 28,298 | 28,284 |
| BaN5\_3 | 22,289 | 22,285 |
| BaM1\_1 | 70,419 | 70,386 |
| BaM1\_2 | 62,832 | 62,819 |
| BaM1\_3 | 121,240 | 121,062 |
| BaP1\_1 | 19,628 | 19,623 |
| BaP1\_2 | 19,168 | 19,168 |
| **BaP1\_3** | 18,182 | **18,180** |
| StN5\_1 | 26,864 | 26,863 |
| StN5\_2 | 29,756 | 29,755 |
| StN5\_3 | 26,750 | 26,747 |
| StM1\_1 | 56,653 | 56,651 |
| StM1\_2 | 54,629 | 54,624 |
| StM1\_3 | 54,842 | 54,823 |
| StP1\_1 | 18,824 | 18,824 |
| StP1\_2 | 19,035 | 19,030 |
| StP1\_3 | 21,187 | 21,187 |