**Supplemental Table S3: Sequencing metrics for whole genome sequencing libraries.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Total sequenced read pairs** | **Adapter trimmed reads (%)\*** | **Median insert size (bp)** | **Duplicate rate (%)** | **Total mapped reads** | **Approximate whole genome read coverage (×)** |
| 1 | 92,068,418 | 1.41 | 302 | 2.93 | 181,727,776 | 9.1 |
| 2 | 55,667,435 | 1.43 | 312 | 2.17 | 110,933,201 | 5.6 |
| 3 | 97,997,942 | 1.39 | 282 | 2.90 | 194,123,836 | 9.8 |
| 4 | 88,648,438 | 1.37 | 268 | 2.76 | 178,365,771 | 9.0 |
| 5 | 108,487,732 | 1.39 | 275 | 3.07 | 213,764,765 | 10.8 |

\*As a proportion of the total reads processed.