Table S1. Summary of sequencing data generation and mapping on human reference genome hg19 (GRCh37)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample ID** | **Total raw reads** | **Raw data, Gb** | **Number of mapped reads** | **Rough coverage1** | **Average depth2** | **Number of unmapped reads** | **Het/Hom** | **Ti/Tv** |
| KAZ\_WG2 | 1,064,275,383 | 53.7 | 1,060,289,706 | 33X | 32,9 | 1,913,660 | 1,496 | 2,085 |
| KAZ\_WG4 | 987,687,090 | 49.4 | 976,807,984 | 31X | 30,4 | 2,924,412 | 1,353 | 2,074 |
| KAZ\_WG5 | 898,102,501 | 44.7 | 889,593,464 | 28X | 27,7 | 1,864,778 | 1,407 | 2,084 |
| KAZ\_WG6 | 864,441,400 | 41.7 | 855,564,629 | 27X | 26,6 | 2,243,220 | 1,483 | 2,084 |
| KAZ\_WG7 | 927,234,150 | 46.2 | 918,007,779 | 29X | 28,5 | 1,681,816 | 1,460 | 2,083 |

1 Coverage calculated on human reference genome GRCh37 (3,234,834,689 bp) for total raw reads.

2 Average depth calculated on human reference genome GRCh37 (3,234,834,689 bp) for mapped reads only.