**Table S3.** High throughput sequencing results. JM: *Juglans mandshurica*; QM: *Quercus mongolica*; CB: Conifer-broadleaf forest; LG: *Larix gmelinii*; PK: *Pinus koraiensis*. Note: N (%) is the ratio of fuzzy bases to the total number of bases; GC (%) is the GC content, that is, the ratio of G bases and C bases to the total number of bases; Q20 (%) and Q30 (%) The ratio of the bases whose measurement accuracy is 99% and 99.9% or more to the total number of bases, respectively. Statistical table of clean data set. JM: *Juglans mandshurica*; QM: *Quercus mongolica*; CB: Conifer-broadleaf forest; LG: *Larix gmelinii*; PK: *Pinus koraiensis*.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Samples | LIP | HQ Reads (%) | Clean reads | HQ Data (bp) | HQ Data (%) |
| QM | SPE | 98.75 | 8120943448 | 11928114547 | 96.06 |
| CB | SPE | 98.80 | 7643347816 | 11246232585 | 96.27 |
| PK | SPE | 99.03 | 8518216570 | 12556511820 | 96.67 |
| LG | SPE | 98.70 | 8452025858 | 12405448153 | 95.94 |
| JM | SPE | 99.03 | 7716146060 | 11370315732 | 96.64 |

Note: HQ Reads (%) refers to the percentage of high quality sequences in the original sequence number of the machine; HQ Data (bp) refers to the total number of bases of high-quality sequences; HQ Data (%) refers to the percentage of the total number of bases of high-quality sequences in the original sequence.