Table 1 | Statistics of *D. sissoo* genome assembly and assessment.

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| Assembly | *Dalbergia sissoo* |
| Genome-sequencing depth（X） | 10X genomics sequencing (Gb) | 214.42 |
| Hi-C (Gb) | 139.93 |
| Estimated genome size (Mb) | 756.56 |
| Estimated heterozygosity (%) | 0.68 |
| Assembly size (Mb) | 661.00 |
| GC content (%) | 33.59 |
| Scaffold N50 (Kb) | 7165.92 |
| BUSCO completeness of assembly (%) | 96.6 |
| Complete single-copy BUSCO (%) | 93.2 |
| Complete duplicated BUSCO (%) | 3.4 |
| Total length of pseudochromosome assembly (Mb) | 660.37 |
| Pseudochromosome number | 10 |
| Scaffold N50 of pseudochromosome assembly (Kb) | 56151.84 |
| BUSCO completeness of pseudochromosome assembly (%) | 96.2 |
| The rate of pseudochromosome anchored genome (%) | 99.9 |