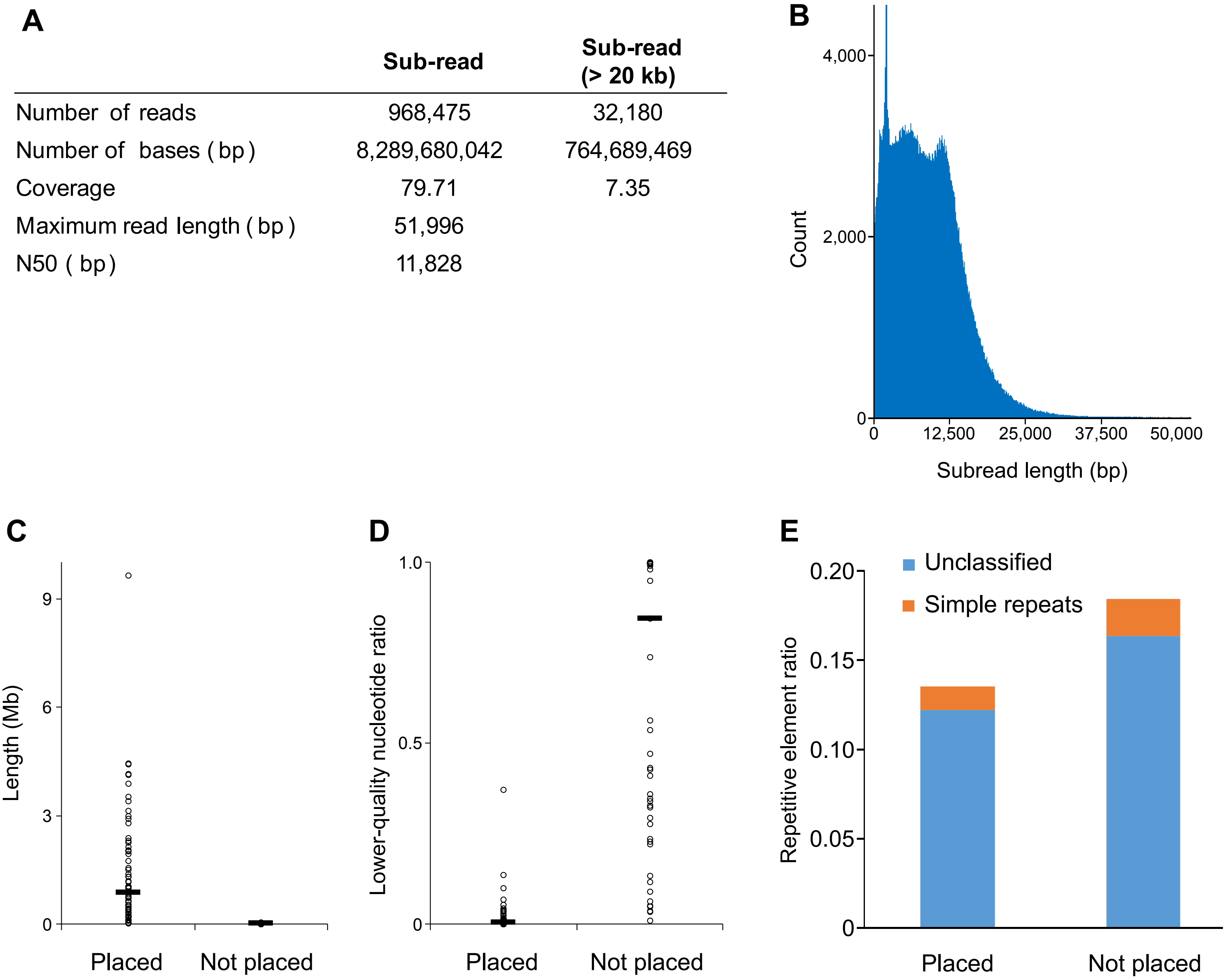

**A**

| | Sub-read | Sub-read (> 20 kb) |
|---|---|---|
| Number of reads | 968,475 | 32,180 |
| Number of bases (bp) | 8,289,680,042 | 764,689,469 |
| Coverage | 79.71 | 7.35 |
| Maximum read length (bp) | 51,996 | |
| N50 (bp) | 11,828 | |

**Supplemental Figure S1.** Stats of PacBio raw reads and not placed contigs. *(A)* PacBio raw sub-reads statistics. *(B)* PacBio raw reads length distribution. *(C)* length, *(D)* lower-quality nucleotides ratio, and *(E)* repetitive element types of placed and not placed contigs on the N2 genome. Black horizontal bars represent median values.