**Table 1.** Statistics for genome assembly and annotation of *S. peregrina*.

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| Genome assembly | Parameter |
| Contig N50 size (bp) | 3,839,545 |
| Estimated genome size (bp) | 472,206,320 |
| Assembled genome size (bp) | 560,313,417 |
| Longest Contig Length | 20,896,554 |
| Total number of gene | 15,710 |
| Rate of chromosomes anchored | 97.76% |
| Average transcript length (bp) | 7,635.25 |
| Average CDS length (bp) | 1,404.03 |
| Average exons number per gene | 3.94 |
| Average exon length (bp) | 356.4 |
| Average intron length (bp) | 2,119.8 |
| *K*-mer depth | 61 |
| Heterozygosity | 3.0% |