

**Supplementary Table 1. Summary of statistics of sequence reads**

| Parameter             | Pre-filtering | Post-filtering |
|-----------------------|---------------|----------------|
| Total no. of reads    | 11,138,100    | 8,668,014      |
| Total no. of bases    | 1,531,829,943 | 1,212,394,766  |
| Q <sub>20</sub> bases | 95.89%        | 99.27%         |
| Q <sub>30</sub> bases | 95.09%        | 98.98%         |
| GC content            | 39.79%        | 39.58%         |
| N bases ratio         | 0.0%          | 0.0%           |

**Supplementary Table 2. Statistics of *de novo* assembly**

| Parameter                          | Value    |
|------------------------------------|----------|
| Total no. of assembled transcripts | 133,246  |
| Total no. of assembled bases       | 91756717 |
| Median contig length (bp)          | 394      |
| Average contig length (bp)         | 688.63   |
| N50 contig length (bp)             | 1031     |
| Percent GC                         | 36.38    |