**Supplemental Table S3: Summary of reads and filtering process used for *de novo* transcriptome assembly.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Raw reads** | | **Reads after filtering process** | **Reads after normalization process** |
| **Sequence count** | 98,372,319 | 87,488,110 | | 17,664,763 |
| **Total nucleotides (bp)** |  | | 8,089,957,428 | 1,621,835,415 |
| **Average length (bp)** | 100 | | 92.46 | 91 |

bp: base pairs