

**Table S7. Quality control of assembled genome.** Assembly quality validation was calculated by expressed sequence tags coverage against transcriptome assembled unigene sequences

| Dataset | Number | Total length<br>(bp) | Bases covered by<br>assembly (%) | Sequences covered<br>by assembly (%) | >90% sequence in one scaffold |          | >50% sequence in one scaffold |          |
|---------|--------|----------------------|----------------------------------|--------------------------------------|-------------------------------|----------|-------------------------------|----------|
|         |        |                      |                                  |                                      | Number                        | Percent  | Number                        | Percent  |
| >0bp    | 196627 | 64443253             | 92.22602248                      | 93.67228305                          | 165144                        | 83.98847 | 180712                        | 91.90599 |
| >200bp  | 105067 | 51703292             | 92.88031795                      | 95.21543396                          | 90652                         | 86.28018 | 97783                         | 93.06728 |
| >500bp  | 28988  | 28823107             | 93.58265575                      | 96.89871671                          | 25108                         | 86.61515 | 27256                         | 94.02511 |
| >1000bp | 9394   | 15425829             | 93.84311858                      | 97.93485203                          | 7957                          | 84.703   | 8883                          | 94.56036 |