

**Supplementary Table 1: Statistics of RNA-seq data and mapping rate**

<b>ID</b>	<b>Clean_reads</b>	<b>Clean_data(bp)</b>	<b>Mapping rate</b>	<b>Accession Number</b>
<b>W1</b>	<b>31,442,000</b>	<b>10,331,415,588</b>	<b>70.96%</b>	<b>SRR6476552</b>
<b>W2</b>	<b>31,710,704</b>	<b>11,107,735,274</b>	<b>64.32%</b>	<b>SRR1592738</b>
<b>W3</b>	<b>28,534,127</b>	<b>9,371,817,498</b>	<b>73.44%</b>	<b>SRR6476548</b>
<b>W4</b>	<b>24,894,384</b>	<b>8,170,702,308</b>	<b>73.91%</b>	<b>SRR6476599</b>
<b>L1</b>	<b>26,867,168</b>	<b>8,821,721,028</b>	<b>77.35%</b>	<b>SRR6476546</b>
<b>L2</b>	<b>29,706,661</b>	<b>9,758,753,718</b>	<b>84.84%</b>	<b>SRR6476594</b>
<b>L3</b>	<b>30,202,803</b>	<b>9,922,480,578</b>	<b>87.17%</b>	<b>SRR6476598</b>
<b>L4</b>	<b>24,789,438</b>	<b>8,136,070,128</b>	<b>84.86%</b>	<b>SRR6476551</b>
<b>I1</b>	<b>21,692,839</b>	<b>6,583,482,042</b>	<b>70.14%</b>	<b>SRR22571455*</b>
<b>I2</b>	<b>29,739,625</b>	<b>9,025,572,505</b>	<b>75.93%</b>	<b>SRR22571456*</b>
<b>I3</b>	<b>24,592,537</b>	<b>7,463,507,771</b>	<b>61.94%</b>	<b>SRR22571457*</b>
<b>I4</b>	<b>25,016,234</b>	<b>7,592,079,339</b>	<b>70.24%</b>	<b>SRR22571454*</b>

\*data were generated by this study.