

Supplementary Information

***De novo* assembly and annotation of the Zhe-Maidong (*Ophiopogon japonicus* (L.f.) Ker-Gawl) transcriptome in different growth stages**

HuijunLiu¹, Ying Wang^{2,3}, Tingzhang Wang^{2,3}, Xuhui Ying⁶, Rongrong Wu^{4,5,*}, Huan Chen^{1,2,3,*}

¹College of Pharmaceutical Science, Zhejiang University of Technology, Hangzhou 310014, China

²Zhejiang Institute of Microbiology, Hangzhou 310012, China

³Key laboratory of microbial technology and bioinformatics of Zhejiang Province, Hangzhou 310012, China

⁴Department of Cardiology, Second Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, 310009, China

⁵Cardiovascular Key Laboratory of Zhejiang Province, Hangzhou, 310009, China

⁶ChiaTaiQingchunbao Pharmaceutical Co., Ltd

*To whom correspondence should be addressed.

Huan Chen, E-mail address: chenhuan7809@gmail.com;

Rongrong Wu, E-mail address: realagatha@zju.edu.cn

Supplementary Figures

Figure S1 Three expression patterns were classified into biological process based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.

Figure S2 Three expression patterns were classified into cellular component based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.

Figure S3 Three expression patterns were classified into molecular function based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.

Figure S1

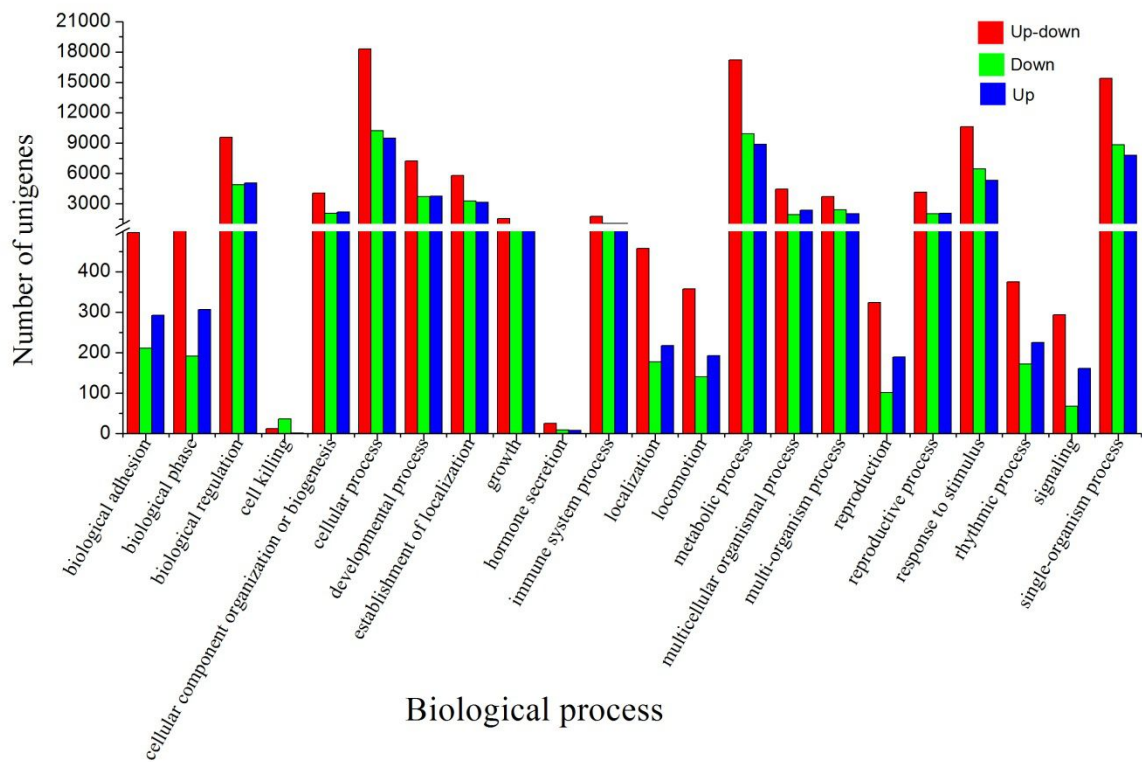


Figure S1 Three expression patterns were classified into biological process based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.

Figure S2

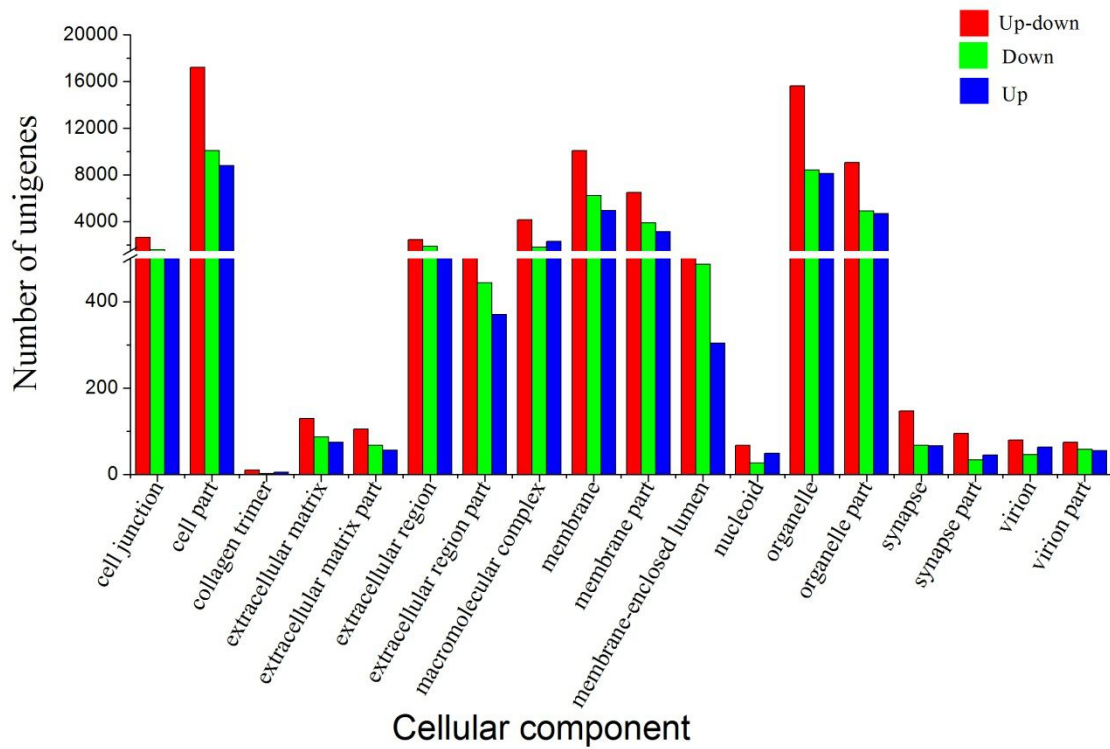


Figure S2 Three expression patterns were classified into cellular component based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.

Figure S3

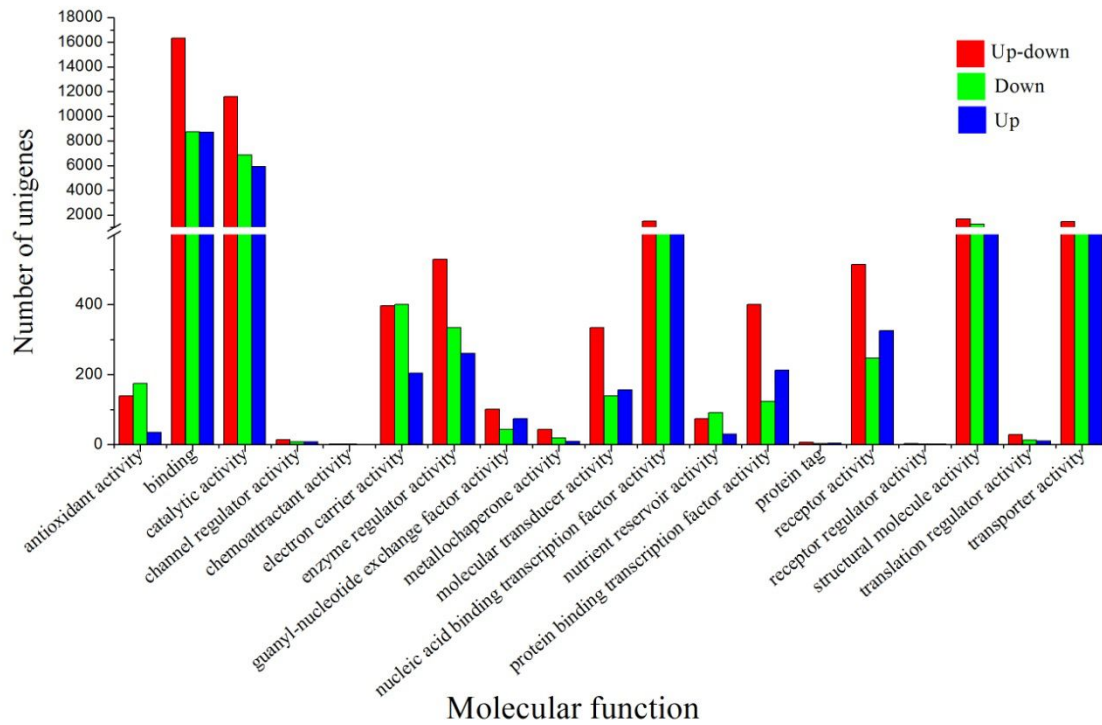


Figure S3 Three expression patterns were classified into molecular function based on gene ontology(GO). Abbreviations: Up-down(red bar), genes with expression first increased and then decreased pattern; Down(green bar), genes with decreased expression pattern; Up(blue bar), genes with increased expression pattern.