

1 **Supplementary Information**

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3 **Expression regulation of malate synthase involved in glyoxylate cycle during**
4 **protocorm development in *Phalaenopsis aphrodite* (Orchidaceae)**

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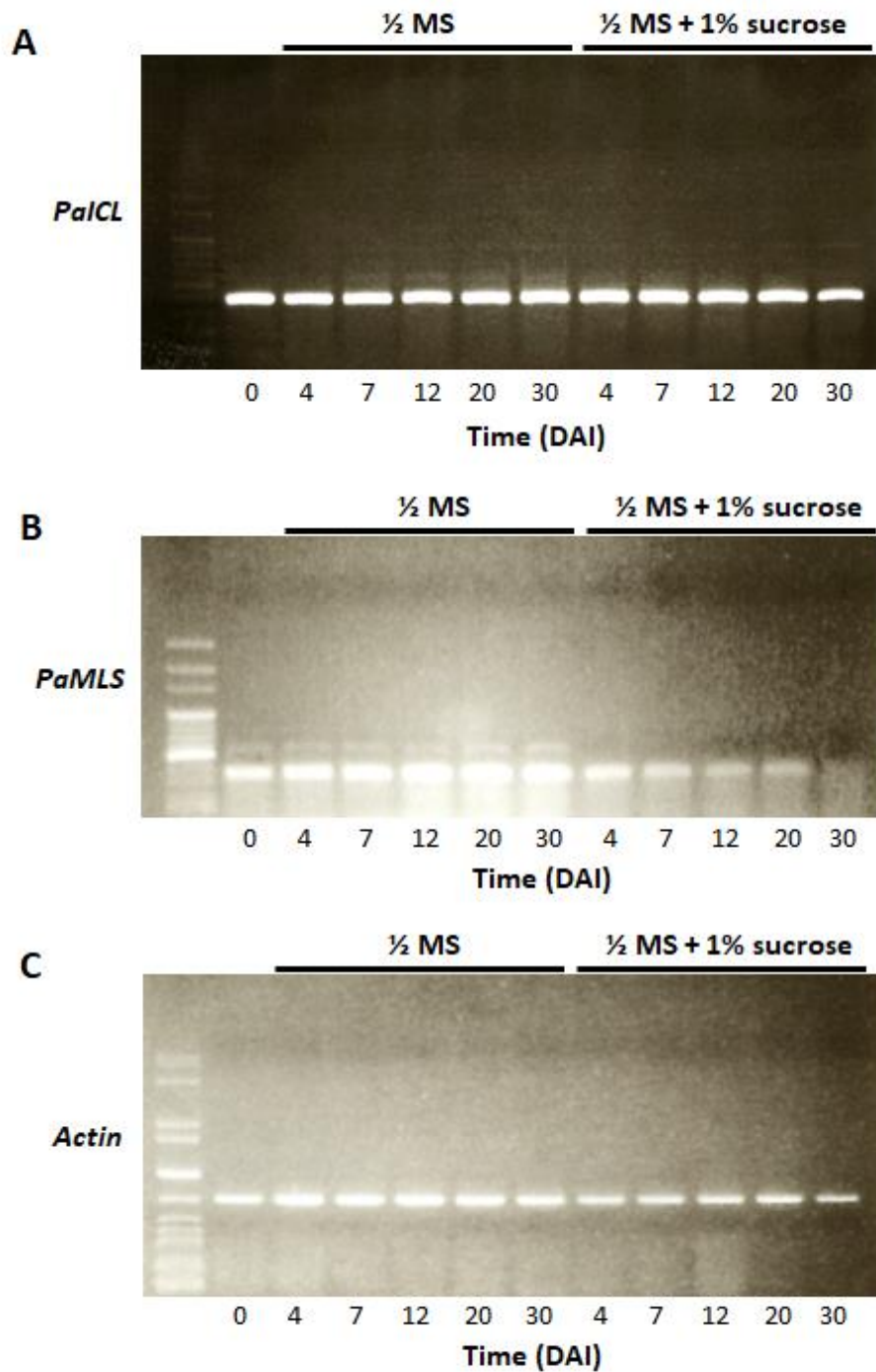


Figure S1. Expression profiles analysis of *PaICL* and *PaMLS* of different developmental protocorm stage in *P. aphrodite* by RT-PCR.

P. aphrodite seeds after resuspended in $\frac{1}{2}$ MS liquid medium for 48 hr which were defined as 0 DAI protocorms. 4 to 30 DAI protocorms incubated in the absence of sucrose or in the presence of 1% sucrose of $\frac{1}{2}$ MS medium. (A) *PaICL* (B) *PaMLS* (C) *Actin*. (DAI, days after incubation).

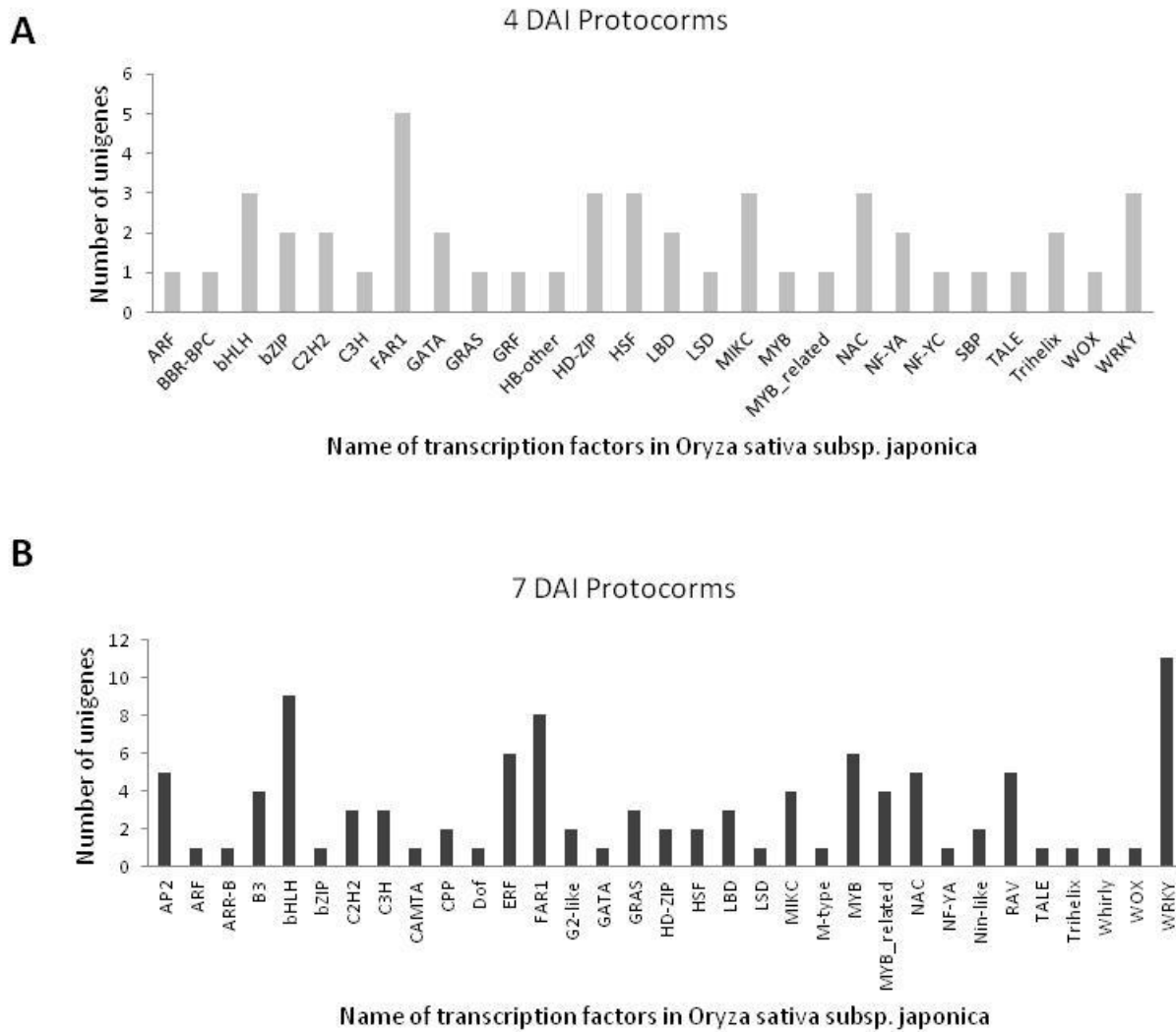


Figure S2. Number of unigenes related to transcription factors in each transcription factor family

Number of unigenes related to transcription factors 10-fold up-regulated in (A) 4-DAI protocorms and (B) 7-DAI protocorms.

Table S1 List of primers used in this study

| Primer name | Sequence |
|---|--------------------------------------|
| For real-time quantitative PCR | |
| QPaMals-F | CGTGGAACAAGGTCGAGCTTTAGG |
| QPaMals-R | TGGGGAACAAGCTCCACAACCTTC |
| QPaICL-F | GCAAATCAGGTCCGGGACGATG |
| QPaICL-R | ATCCATCCACTCCTAAACATCGAATCC |
| QPaANT-F | AGTGGTGGAGTTGGAGGATTTG |
| QPaANT-R | GCATCGAGACTCCAAGCA |
| QPaHB5-F | GATGAGGGGGATGGAATGTATG |
| QPaHB5-R | CAGCTCCATATTTGTTATCACATTCC |
| QPaMADS2-F | AGGGAACTTACCGCGCTCTA |
| QPaMADS2-R | GAGATGGGGGATCTATTCAGAGAGA |
| QPaMYB4-F | ATCGAGTGATGATGAGGCTTATTTT |
| QPaMYB4-R | AACCCAAGTCATCCAAACTCC |
| QPaPIF3-F | GCGTGTTGTTTGGCGCAAGTGGCAT |
| QPaPIF3-R | AGGCGCCCAAATATCAGCACCGTTG |
| QPaRAV1-1-F | CAGTTATGGGGATTCATGATTTTTC |
| QPaRAV1-1-R | TTCTCCGCATCCAAATCCATC |
| QPaWRKY18-F | GAAGAACTCCGATAACTTTGAACAGA |
| QPaWRKY18-R | AATGCAAATGAGTTCAAGGTCTAGT |
| QPaWRKY71-F_2 | TCCCGCTTATCCGAAAACAT |
| QPaWRKY71-R | TCGAGCCGCAAGGTTCAA |
| For RACE | |
| 3'PaMLS_F1 | GTCCCTTCTTTTACCTCCCAA |
| 3'PaMLS_F2 | GCTCCGTTCTCACTCTGCTGG |
| 5'PaICL_R1 | GCCCCGAGAATGAACTGGTGGTC |
| 5'PaICL_R2 | CCTCTTGCTGCTTGCGGTCGTGGTAG |
| For PaMLS promoter-reporter plasmid construction | |
| PaMLSp_1000_5'_ <i>Bam</i> H I | GGATCCTTCAGATAGGTTACAGGTAAATTATATAGA |
| PaMLSp_3'_ <i>Nco</i> I | CCATGGCGTCACCACCGGAG |
| For PaHB5 plasmid construction | |
| PaHB5_5'_ <i>Xba</i> I | TCTAGAATGGAAGAAGAGAAGTCTCTGATCA |
| PaHB5_3'_ <i>Bam</i> H I | GGATCCTCATCCATCCCAAACCTCCC |

Table S2 Predicted ATHB5 binding sites on 2000 bp upstream sequence of *PaMLS*

| Putative binding site | Strand ^a | Putative binding sequence |
|-----------------------|---------------------|---------------------------|
| -1662 | + | ttcTTATTg |
| -1328 | + | ggcTTATTa |
| -1108 | + | aacTTATTt |
| -800 | + | caaTTATTt |
| -796 | + | tatTTATTt |
| -792 | + | tatTTATTt |
| -769 | - | aAATAAaaa |
| -756 | - | aAATAAgaa |
| -709 | + | tatTTATTa |
| -706 | + | ttaTTATTt |
| -702 | + | tatTTATTt |
| -611 | + | taaTTATTt |
| -598 | + | aagTTATTa |
| -590 | - | aAATAAtat |
| -559 | + | aaaTTATTt |
| -499 | + | aatTTATTt |
| -487 | - | tAATAAatt |
| -334 | - | aAATAAata |
| -330 | - | aAATAAtat |
| -296 | - | aAATAAtat |
| -278 | - | tAATAAaaa |
| -241 | - | aAATAAcga |

a: Forward or reverse directions of binding sequences