**Supplementary Data**

**Features and quality assessment of Phalaenopsis specialized microarray**

To examine genome-wide gene expression profiling of orchids, a customized microarray chip based on sequence information in the *Orchidstra* database [1] (http://orchidstra.abrc.sinica.edu.tw) was designed. The *Orchidstra* database contains 42,661 transcript contigs of *Phalaenopsis aphrodite* generated by *de novo* assembly procedure of reads generated from next generation sequencing (NGS) technologies such as Illumia Solexa and Roche 454 platforms. These transcript contigs were submitted to Agilent e-array (Agilent, CA) for microarray probe selection. Probe design of 39,431 transcript contigs was successful after software screening. Probes for the detection of common orchid viruses, Cymbidium mosaic virus (CymMV) and Odontoglossum ringspot virus (ORSV), were included to array design.

We have performed a series of quality test on the tailor made orchid array. Technical repeats showed reproducibility with correlation coefficients higher than 99.9% (after percentile shift normalization at 75%) between repeats (Supplementary Figure S1A). On average, 64-72% whole probe-sets on the array could be considered as detectable under Agilent scanner criteria or raw intensity more than 50. The detection rate was reasonable for basal expression since we have compared various orchid tissues including leaf, root, flower and germinating seeds under normal culture environment. The array performance between the diploid *Phalaenopsis aphrodite*, a Taiwan native species, and the tetraploid Sogo Yukidian 'V3', a popular commercial hybrid of *Phalaenopsis*, was satisfactory with correlation coefficients higher than 94% when same tissues were compared (Supplementary Figure S1B). The application of this array is therefore not limited to the rather scarce source of native *Phalaenopsis* orchid and can be extended to the more popular commercial hybrid.
Figure S1. Performance check of orchid specialized microarray with scatter plot. (A) Overall comparative profiling between tissue samples of *Phalaenopsis aphrodite*. (B) Overall comparative profiling between *Phalaenopsis aphrodite* and the commercial hybrid Sogo Yukidian ‘V3’.
Differentially expressed gene list

Table S1. Top 20 genes differentially expressed in specific tissue. Expression level was determined after normalization of microarray intensities and SPM value (Specificity Measure) was calculated accordingly. Maximum value of SPM is 1. Top 20 genes with the highest SPM value are listed.

| Probe Name | Description | SPM value |
|------------|-------------|-----------|
| **Flower** |             |           |
| PATC150065 (PaMYB-4) | Similar to ACB59077, Myb-like transcription factor EOBII [Petunia x hybrida] | 1 |
| PATC138068 | Similar to XP_002520171, ER glycerol-phosphate acyltransferase [Ricinus communis] | 1 |
| PATC144452 | Putative protein to AAG494418, MYB9 [Dendrobium sp. XMW-2002-9] | 0.999999 |
| PATC134411 | Weak similar to XP_002889772, DNA polymerase delta subunit 4 family [Arabidopsis lyrata subsp.lyrata] | 0.999999 |
| PATC156712 | Similar to CAD87008, MYB8 protein [Gerbera hybrid cv. 'Terr Regima'] | 0.999997 |
| PATC118359 | Weak similar to BAF98468, cytochrome P450 [Coptis japonica var. dissecta] | 0.999996 |
| PATC154654 | Homologue to ACC59773, flavonoid 3',5'hydroxylase-like protein [Vanda coerulae] | 0.999988 |
| PATC138772 (PaAGL6-2) | Homologue to ADI58464, AGL6 [Cymbidium goeringii] | 0.999987 |
| PATC136147 | Similar to CBH16443, unnamed protein product [Vitis vinifera] | 0.999987 |
| PATC112668 | Similar to EEC77471, hypothetical protein Osd16293 [Oryza sativa Indica Group] | 0.999987 |
| PATC140326 | Similar to XP_002512728, "ATP-binding cassette transporter, putative [Ricinus communis]" | 0.999986 |
| PATC145620 | Similar to XP_002516348, Sorting nexin-4, putative [Ricinus communis] | 0.999985 |
| PATC152417 | Similar to XP_002463916, hypothetical protein SORBIDRAFT_01g008880 [Sorghum bicolor] | 0.999985 |
| PATC009198 | Putative protein to CAA71513, putative cytochrome P450 [Glycine max] | 0.999984 |
| PATC209271 | Weak similar to XP_002518849, 3-oxoacyl-1-[acyl-carrier-protein] | 0.999984 |
| PATC124681 | Weak similar to BAD16430, putative AP2 domain-containing protein [Oryza sativa Japonica Group] | 0.999983 |
| PATC138420 | Similar to XP_002521076, Xyloglucan endotransglycosylase/hydrolase protein 2 precursor, putative [Ricinus communis] | 0.999981 |
| PATC143361 | Similar to EAY88298, hypothetical protein Osd_09755 [Oryza sativa Indica Group] | 0.999998 |
| PATC131581 | Similar to XP_002885644, hydrodase, alpha/beta fold family protein Arabidopsis lyrata subsp. lyrata | 0.999969 |
| ID            | Description                                                                                                                                       | Similarity |
|--------------|----------------------------------------------------------------------------------------------------------------------------------------------------|------------|
| PATC124610   | Putative protein to BAD44483, hypothetical protein [Arabidopsis thaliana]                                                                            | 0.997148   |
| PATC138503   | (PaMTN3) Similar to NP_001149087, MTN3, [Zea mays]                                                                                                 | 1          |
| PATC126569   | Similar to ADG34844, putative phenylacetaldehyde synthase [Vanda hybrid cultivar]                                                                    | 0.999911   |
| PATC034663   | Putative protein to BAF96951, flavone synthase II [Iris x hollandica]                                                                               | 0.999234   |
| PATC130766   | Putative protein to EAZ04731, hypothetical protein OsI_26893 [Oryza sativa Indica Group]                                                             | 0.998892   |
| PATC138606   | Similar to XP_002265207, 3-oxoacyl-[acyl-carrier-protein] synthase[Vitis vinifera]                                                                   | 0.998676   |
| PATC209271   | Weak similar to XP_002518849, 3-oxoacyl-[acyl-carrier-protein]                                                                                      | 0.998214   |
| PATC190376   | Weak similar to CAA58732, PAR-1c [Nicotiana tabacum]                                                                                               | 0.997444   |
| PATC201263   | Putative protein to ACP27626, beta-carotene hydroxylase [Oncidium Gower Ramsey]                                                                    | 0.996435   |
| PATC147953   | Similar to ABF93742, beta-carotene hydroxylase, putative, expressed [Oryza sativa(japonica cultivar-group)]                                        | 0.996286   |
| PATC177749   | Similar to NP_191000, WR11 (WRINKLED 1); DNA binding / transcription factor [Arabidopsis thaliana]                                                     | 0.995604   |
| PATC067105   | Similar to ABJ90468, beta-ketoacyl-ACP synthase I, [Jatropha curcas]                                                                               | 0.993919   |
| PATC187105   | Weak similar to ACG45585, cytochrome P450 CYP734A8 [Zea mays]                                                                                       | 0.993342   |
| PATC125229   | Similar to BAF02551, putative brassinosteroid hydroxylase [Solanum lycopersicum]                                                                   | 0.993267   |
| PATC132514   | Similar to XP_002301652, acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]                                                   | 0.993036   |
| PATC199654   | Weak Similar to NP_200018, MATE efflux protein-related [Arabidopsis thaliana]                                                                    | 0.992537   |
| PATC154379   | (PaAGL6-1) Homologue to AD67237, MADS box transcription factor 1 [Oncidium Gower Ramsey]                                                           | 0.992168   |
| PATC023454   | Similar to XP_002301652, acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]                                                   | 0.991833   |
| PATC030120   | Weak Similar to NP_194643, MATE efflux protein-related [Arabidopsis thaliana]                                                                    | 0.991163   |
| PATC166947   | Weak Similar to XP_002307962, acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]                                               | 0.9903     |
| PATC164233   | Similar to ACG32367, AP2/EREBP transcriptional factor WR11 [Zea mays]                                                                             | 0.990028   |

### Pollinia

| ID            | Description                                                                                                                                       | Similarity |
|--------------|----------------------------------------------------------------------------------------------------------------------------------------------------|------------|
| PATC024902   | Putative protein to XP_002308395, AP2 domain-containing transcription factor [Populus trichocarpa]                                                      | 1          |
| PATC138224   | Similar to XP_002325139, AP2 domain-containing transcription factor [Populus trichocarpa]                                                          | 1          |
| PATC056313   | Putative protein to XP_003027790, ubiquitin-conjugating enzyme E2 [Schizophyllum commune H4-8]                                                     | 1          |
| PATC142684   | Weak similar to XP_002278602, PREDICTED: hypothetical protein [Vitis vinifera]                                                                    | 1          |
| PATC154622   | Similar to ACG56678, tryptophan aminotransferase [Zea mays]                                                                                       | 1          |
| PATC138414 | Putative protein to ACG33223, pollen-specific protein C13 precursor [Zea mays] | 1 |
| PATC125413 | Similar to AAY86035, pyruvate kinase [Citrus sinensis] | 1 |
| PATC134337 | Similar to ACF06586, aluminum-induced protein [Elaeis guineensis] | 1 |
| PATC154983 | Putative protein to ACG33223, pollen-specific protein C13 precursor [Zea mays] | 1 |
| PATC155194 | Putative protein to XP_002325139, AP2 domain-containing transcription factor [Populus trichocarpa] | 1 |
| PATC055518 | Similar to NP_001063510, AP2 domain-containing transcription factor [Populus trichocarpa] | 1 |
| PATC059937 | Similar to AAW88315, expansin EXP A11, [Triticum aestivum] | 1 |
| PATC150528 | Weak similar to AAL99224, ubiquitin-conjugating enzyme E2 [Gossypium thurberi] | 1 |
| PATC194643 | Similar to ABM54492, expansin 2 [Cunninghamia lanceolata] | 1 |
| PATC138059 | Putative protein to XP_002308395, AP2 domain-containing transcription factor [Populus trichocarpa] | 1 |
| PATC138131 | Similar to CAQ58629, pyruvate kinase [Vitis vinifera] | 1 |
| PATC154132 | Putative protein to BAG80542, glycosyltransferase [Lycium barbarum] | 1 |
| PATC191966 | Putative protein to ABS32237, asymmetric leaves 2 [Carica papaya] | 1 |
| PATC133027 | Similar to BAI52955, calcium-binding EF-hand protein [Citrus lanatus subsp. vulgaris] | 1 |
| PATC118656 | Similar to BAC81184, putative glucose transport protein STP1 [Oryza sativa Japonica Group] | 1 |
| PATC036239 | Putative protein to XP_002519123, F-box and wd40 domain protein, putative [Ricinus communis] | 1 |
| PATC138345 | Putative protein to XP_002325139, AP2 domain-containing transcription factor [Populus trichocarpa] | 1 |
| PATC137385 | Similar to ABJ09596, pyruvate decarboxylase [Lycoris aurea] | 1 |

**Column**

| PATC154343 | Similar to XP_002529091, Polygalacturonase precursor, putative [Ricinus communis] | 0.999999 |
| PATC125905 | Homologue to CAA56277, bibenzyl synthase [Phalaenopsis sp. 'pSPORT1'] | 0.999712 |
| PATC130846 | Similar to 1Z3Q, Chain A, Resolution Of The Structure Of The Allergenic AndAntifungal Banana Fruit Thaumatin-Like Protein At 1.7a | 0.999641 |
| PATC197430 | Putative protein to XP_002265159, PREDICTED: hypothetical protein [Vitis vinifera] | 0.998959 |
| PATC138585 (PaAG-2) | Homologue to AAZ95250, AGAMOUS-like transcription factor [Dendrobium crumenatum] | 0.998456 |
| PATC038602 | Similar to XP_002514682, UDP-glucuronosyltransferase, putative [Ricinus communis] | 0.997282 |
| PATC190622 | Putative protein to XP_002513511, transferase, transferring glycosyl groups, putative [Ricinus communis] | 0.997046 |
| Accession   | Description                                                                                     | Similarity Score |
|------------|------------------------------------------------------------------------------------------------|------------------|
| PATC165907 | Similar to XP_002526116, UDP-glucuronosyltransferase, putative [Ricinus communis]               | 0.997042         |
| PATC147520 | Putative protein to BAD43783, putative bHLH transcription factor [Arabidopsis thaliana]          | 0.996157         |
| PATC036637 | Similar to XP_002526116, UDP-glucuronosyltransferase, putative [Ricinus communis]               | 0.996157         |
| PATC116847 | Putative protein to AAAJ32914, polygalacturonase [Persea americana]                             | 0.9954           |
| PATC119249 | Weak similar to AAL76415, MADS-box transcription factor [Phalaenopsis equestris]               | 0.995019         |
| PATC165547 | Similar to XP_002526116, UDP-glucuronosyltransferase, putative [Ricinus communis]               | 0.994654         |
| PATC002540 | Putative protein to BAC57273, putative polygalacturonase PG1 [Oryza sativa Japonica Group]     | 0.994233         |
| PATC009554 | Putative protein to XP_002526107, UDP-glucuronosyltransferase, putative [Ricinus communis]     | 0.993436         |
| PATC000227 | Putative protein to BAC10994, rhamnosyl transferase [Nierembergia sp. NB17]                    | 0.993142         |
| PATC061977 | Putative protein to AAY86364, AGAMOUS-like protein [Dendrobium thyrsiflorum]                   | 0.992483         |
| PATC052530 | Similar to XP_002520171, ER glycerol-phosphate acyltransferase [Ricinus communis]               | 0.992352         |
| PATC140136 | Similar to NP_001152613, MYB-CC type transfactor [Zea mays]                                    | 0.991949         |
| PATC198687 | Putative protein to NP_001064591, Osl0tg413400 [Oryza sativa Japonica Group]                  | 0.991353         |
| PATC155109 | (PaAG-3) Homologue to AAL76415, MADS-box transcription factor [Phalaenopsis equestris]        | 0.99129          |

**Pedicel**

| Accession   | Description                                                                                     | Similarity Score |
|------------|------------------------------------------------------------------------------------------------|------------------|
| PATC148981 | Weak similar to AAQ11882, knotted 1 [Hordeum vulgare]                                          | 0.999996         |
| PATC175072 | Putative protein to AC123247, COMPOUND INFLORESCENCE [Solanum lycopersicum]                   | 0.99991          |
| PATC022841 | Homologue to AD58462, flowering locus T [Cymbidium goeringii]                                 | 0.999904         |
| PATC173815 | Putative protein to ACL11801, WOX9-like protein [Phaeolus coccineus]                          | 0.999818         |
| PATC145039 | Similar to XP_002510423, cytochrome P450, putative, [Ricinus communis]                        | 0.999631         |
| PATC145786 | Similar to CAB88029, knotted1-like homeobox protein [Dendrobium greg Madame Thong-In]         | 0.999388         |
| PATC127065 | Similar to ABI74672, class I KNOX-like 1 protein [Elaeis guineensis]                           | 0.999125         |
| PATC150862 | Similar to ABU88887, S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase [Chimonanthus praecox] | 0.99827          |
| PATC155095 | Similar to CAD70566, carboxyl methyltransferase [Crocus sativus]                               | 0.997303         |
| PATC150515 | Putative protein to XP_002272432, PREDICTED: hypothetical protein [Vitis vinifera]             | 0.997057         |
| PATC166128 | Putative protein to BAH83538, DL related protein [Triticum aestivum]                          | 0.996476         |
| PATC144516 | Similar to BAJ49293, homedomain leucine zipper protein class 1 [Hordeum vulgare subsp. vulgare] | 0.994982         |
| PATC074709 | Putative protein to AAW83045, CRABS CLAW [Capparis flexuosa]                                 | 0.99446          |
| ID         | Description                                                                                                                                                                                                 | Identity Score |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|
| PATC147749 | Similar to BAF93480, class-I knotted1-like homeobox protein IBKN3 [Ipomoea batatas]                                                                                                                      | 0.992282       |
| PATC163884 | Weak similar to XP_002517072, conserved hypothetical protein [Ricinus communis]                                                                                                                             | 0.991868       |
| PATC069479 | Similar to ABF70015, zinc finger (Dof type) family protein [Musa acuminate]                                                                                                                                    | 0.989296       |
| PATC069726 | Putative protein to XP_002284464, PREDICTED: similar to bHLH transcription factor Upa20 [Vitisvinifera]                                                                                                | 0.988977       |
| PATC122106 | Putative protein to XP_002526340, LOB domain-containing protein, putative [Ricinus communis]                                                                                                                 | 0.987073       |
| PATC148697 | Similar to ACN21632, putative basic helix-loop-helix protein BHLH7 [Lotus japonicus]                                                                                                                         | 0.986846       |
| PATC202120 (PaAG-4) | Putative protein to AAZ95251, AGAMOUS-like transcription factor [Dendrobiurn crumenatum]                                                                                               | 0.985674       |
Quantitative PCR for validation of tissue specific expression pattern

Method

All the RNA samples were treated with DNase treatment by TURBO DNA-free kit (Ambion, TX, USA) and quantified by RNA Bioanalyzer (Agilent, CA, USA). cDNA was synthesized from 1 µg of total RNA with M-MLV Reverse transcriptase kit (Invitrogen, CA, USA) and poly T primer. All primers used were designed by Primer Express version 3.0 (Applied Biosystems, CA, USA). A total of 20 µl real-time PCR reaction contained primers, cDNA and 10 µl 2X SYBR Green PCR master mix (Applied Biosystems, CA, USA). Real-time PCR was performed in the ABI Prism 7300 Sequence Detection System (Applied Biosystems, CA, USA) with programs recommended by the manufacturer (2 min at 50 °C, 10 min at 95 °C and 40 cycles of 95 °C for 15 sec and 60 °C for 1 min). Each sample was performed with real-time PCR for three independent biological replicates. The comparative CT method (cycle of threshold) was used to determine the relative level of gene expression, with the expression value of ubiquitin (PATC150470) or actin (PATC135993) used as internal controls. Relative expression level is determined by delta Ct of target gene normalized to the internal control. Genes for the validation are listed in Supplementary Table S2 and their primers were listed in Table S3.
(A) Whole flower specific
(B) Lip specific

1. PATC126569
2. PATC130766
3. PATC138503
4. PATC138606
5. PATC147953
6. PATC190376
7. PATC201263
(C) Pollinia specific

**PATC055518**

**PATC059937**

**PATC125413**

**PATC136224**

**PATC142684**

**PATC154622**

**PATC155194**

**PATC194643**
(D) Column specific

- **PATC125905**
  - Relative expression level (x 0.0001)
  - Tissue type:
    - Root
    - Leaf
    - Sepal
    - Petal
    - Lip
    - Pollinia
    - Column
    - Pedicel

- **PATC130864**
  - Relative expression level (x 0.0001)
  - Tissue type:
    - Root
    - Leaf
    - Sepal
    - Petal
    - Lip
    - Pollinia
    - Column
    - Pedicel

- **PATC138585**
  - Relative expression level (x 0.001)
  - Tissue type:
    - Root
    - Leaf
    - Sepal
    - Petal
    - Lip
    - Pollinia
    - Column
    - Pedicel

- **PATC154343**
  - Relative expression level (x 0.0001)
  - Tissue type:
    - Root
    - Leaf
    - Sepal
    - Petal
    - Lip
    - Pollinia
    - Column
    - Pedicel

- **PATC197430**
  - Relative expression level (x 0.0001)
  - Tissue type:
    - Root
    - Leaf
    - Sepal
    - Petal
    - Lip
    - Pollinia
    - Column
    - Pedicel
Figure S2. Quantitative PCR validation of genes differentially expressed in specific tissues. Relative expression level was normalized to a house-keeping gene, Ubiquitin (PATC150470),
with the determination of PCR cycle of threshold. Experiments with triple biological repeats were performed. Standard deviation was shown on figure. (A) Flower specific expression pattern. (B) Lip specific expression pattern. (C) Pollinia specific expression. (D) Column specific pattern. (E) Pedicel specific expression. Primers for the assay were listed in Supplementary Table S3.
Table S2. Genes from the microarray clustering assay that were validated by quantitative PCR. Ubiquitin gene (PATC150470) and actin (PATC135993) were used as internal controls for normalization. Gene-specific primers for validation were listed in Supplementary Table S3.

| Gene id       | Gene description                                                                                                                                                                                                 |
|---------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| **Flower specific (Figure S2A)** |                                                                                                                                                    |
| PATC131581    | Similar to XP_002885644, hydrolase, alpha/beta fold family protein Arabidopsis lyrata subsp. lyrata                                                                                                                  |
| PATC150065    | Similar to ACB59077, Myb-like transcription factor EOBII [Petunia x hybrida]                                                                                                                                   |
| PATC154654    | Homologue to ACC59773, flavonoid 3',5' hydroxylase-like protein [Vanda coerulea]                                                                                                                              |
| PATC144452    | Putative protein to AAO49418, MYB9 [Dendrobium sp. XMW-2002-9]                                                                                                                                                |
| PATC138772    | Homologue to ADIS8464, AGL6 [Cymbidium goeringii]                                                                                                                                                              |
| **Lip specific (Figure S2B)** |                                                                                                                                                    |
| PATC138503    | Similar to ref|NP_001149087.1|MTN3 [Zea mays] (Sugar efflux transporter for intercellular exchange)                                                                                                                                   |
| PATC126569    | Similar to ADG34844, putative phenylacetaldehyde synthase [Vanda hybrid cultivar] (PAAS – catalyzes the formation of PHA (floral scent)                                                                                           |
| PATC130766    | Putative protein to EAZ04731, hypothetical protein OsL_26893 [Oryza sativa Indica Group]                                                                                                                         |
| PATC138606    | Similar to XP_002265207, 3-oxoacyl-(acyl-carrier-protein) synthase [Vitis vinifera]                                                                                                                           |
| PATC190376    | Weak similar to emb|CAAS5732.1|PAR-1c [Nicotiana tabacum]                                                                                                                                                                        |
| PATC201263    | Putative protein to ACP27626, beta-carotene hydroxylase [Oncidium Gower Ramsey]                                                                                                                             |
| PATC147953    | Similar to >dbj|BAH10591.1|beta-ring hydroxylase [Lilium hybrid division I]                                                                                                                                                    |
| PATC177749    | Similar to NP_191000, WR11 (WRINKLED 1), DNA binding / transcription factor [Arabidopsis thaliana]                                                                                                             |
| **Pollinia specific (Figure S2C)** |                                                                                                                                                    |
| PATC199170    | Similar to ABM54492, expansin 2 [Cunninghamia lanceolata]                                                                                                                                                      |
| PATC138224    | Similar to XP_002325139, AP2 domain-containing transcription factor Populus trichocarpa                                                                                                                      |
| PATC142684    | Putative protein to >ref|NP_002522563.1|Heterogeneous nuclear ribonucleoprotein A1, putative [Ricinus communis]                                                                                                                                         |
| PATC154622    | Similar to >gb|ACG56678.1|tryptophan aminotransferase Zea mays                                                                                                                                                                        |
| PATC125413    | Similar to AAY86035, pyruvate kinase [Citrus sinensis]                                                                                                                                                           |
| PATC155194    | Putative protein to >ref|NP_002325139.1|AP2 domain-containing transcription factor Populus trichocarpa                                                                                                |
| PATC059937    | Weak similar to >gb|AAW88315.1|expansin EXPA11 [Triticum aestivum]                                                                                                                                                                        |
| PATC055518    | Similar to NP_001063510, Os09g0483500 [Oryza sativa Japonica Group]                                                                                                                                              |
Column specific (Figure S2D)

| Accession   | Description                                                                 |
|-------------|-----------------------------------------------------------------------------|
| PATC154343  | Similar to XP_002529091, Polygalacturonase precursor, putative [Ricinus communis] |
| PATC125905  | Homologueto CAA56277, bibenzyl synthase [Phalaenopsis sp. 'pSPORT1']         |
| PATC130846  | Similar to 1Z3Q, Chain A, Resolution Of The Structure Of The Allergenic And Antifungal Banana Fruit Thaumatin-Like Protein At 1.7a |
| PATC197430  | Putative protein to XP_002265159, PREDICTED: hypothetical protein [Vitis vinifera] |
| PATC138585  | Homologue to AAQ95250, AGAMOUS-like transcription factor [Dendrobium crumenatum] |

Pedicel specific (Figure S2E)

| Accession   | Description                                                                 |
|-------------|-----------------------------------------------------------------------------|
| PATC148981  | Weak similar to AAQ11882, knotted 1 [Hordeum vulgare]                      |
| PATC022841  | Homologue to ADI58462, flowering locus T [Cymbidium goeringii]              |
| PATC173815  | Putative protein to >gb|ACL11801.1| WOX9-like protein Phaseolus coccineus |
| PATC145039  | Similar to XP_002510423, cytochrome P450, putative Ricinus communis         |
| PATC145786  | Similar to CAB88029, knotted1-like homeobox protein [Dendrobium grex Madame Thong-In] |
| PATC127065  | Similar to ABI74672, class I KNOX-like 1 protein [Elaeis guineensis]        |
| PATC150515  | Putative protein to XP_002272432, PREDICTED: hypothetical protein [Vitis vinifera] |

Transcription factors (Figure 5C, 5D)

| Accession   | Description                                                                 |
|-------------|-----------------------------------------------------------------------------|
| PATC135043  | (PaHLH-1) Similar to NP_001031255, basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] |
| PATC150065  | (PaMYB-4) Similar to ADGS8063, transcription factor [Lycoris longituba]      |
| PATC134262  | (PaZIP-2) Similar to NP_172097, "bZIP transcription factor, putative (bZIP69) [Arabidopsis thaliana]" |
| PATC133172  | Similar to ADJ67440, ethylene response factor 11 [Actinidia delicosa]       |
| PATC136849  | (PaZIP-3) Weak similar to AAK92213, bZIP transcription factor BZI-2 [Nicotiana tabacum] |
| PATC140443  | (PaHLH-3) Similar to ABR23669, Myc2 bHLH protein [Vitis vinifera]           |
| PATC152106  | (PaMYB-2) Similar to XP_002528315, r2r3-myb transcription factor, putative [Ricinus communis] |
| PATC138345  | (PaAP2-7) Putative protein to XP_002325139, AP2 domain-containing transcription factor [Populus trichocarpa] |
| PATC138298  | (PaNAC-3) Similar to ADGS57969, transcription factor [Lycoris longituba]     |

MADS box genes (Figure 5A, 5B)

| Accession   | Description                                                                 |
|-------------|-----------------------------------------------------------------------------|
| PATC154379  | (PaAGL6-1) Homologue to ADJ67237, MADS box transcription factor 1 [Oncidium Gower Ramsey] |
| PATC138772  | (PaAGL6-2) Homologue to ADIS8464, AGL6 [Cymbidium goeringii]                |
| PATC155109  | (PaAG-3) Homologue to AAL76415, MADS-box transcription factor [Phalaenopsis equestris] |
| Accession   | Description                                                                 |
|-------------|------------------------------------------------------------------------------|
| PATC138798  | Similar to NP_001148603, MADS-box protein AGL66 [Zea mays]                   |
| PATC138540  | Homologue to ADJ67238, MADS box transcription factor 6 [Oncidium Gower Ramsey] |
| PATC154853  | Homologue to AAR26629, MADS-box transcription factor [Asparagus officinalis]   |
| PATC138350  | Homologue to AAR26626, MADS box transcription factor [Phalaenopsis equestris] |
| PATC152852  | Homologue to AAV28175, MADS box PI-like protein 9 [Phalaenopsis hybrid cultivar] |

**Morphological genes (Figure 6)**

| Accession   | Description                                                                 |
|-------------|------------------------------------------------------------------------------|
| PATC154491  | Similar to ACV88635, SUPRESSOR OF OVEREXPRESSION OF CONSTANS1 [Magnolia virginiana] |
| PATC198032  | Weak similar to ADJ67237, MADS box transcription factor 1 [Oncidium Gower Ramsey] |
| PATC129930  | Similar to AAO64176, putative zinc finger protein [Arabidopsis thaliana]         |
| PATC138503  | Similar to NP_001149087, MTN3, [Zea mays]                                     |

**Internal control**

| Accession   | Description                                                                 |
|-------------|------------------------------------------------------------------------------|
| PATC150470  | Homologue to NP_001148325, ubiquitin-like protein SMT3 [Zea mays]             |
| PATC135993  | Similar to XP_002317939, actin related protein [Populus trichocarpa]            |
Table S3. List of primers used for quantitative PCR analysis.

| Gene id          | Forward primer (5’ to 3’)                      | Reversed primer (5’ to 3’)                  |
|------------------|------------------------------------------------|---------------------------------------------|
| **Flower specific (Figure S2A)** |                                                 |                                             |
| PATC131581       | TCAAGCATGGGCTGAAGAAATT                        | GCAAGGGAATGTGGTGGTT                        |
| PATC150065 (PaMYB-4) | GCACCTGCACGCTTAAATTG                           | GAAGAGTCTGGACGACGAAAA                      |
| PATC154654       | AATAAACCAATCATAAGCGATCAGAA                   | CCGACGGTTGGAAAACCTTTCA                    |
| PATC144452       | CATCTTCACGATAGGTGCCATCT                        | TTGCAAACCTAAAAGCAAAAGCTCAA               |
| PATC138772 (PaAGL6-2) | TTGTTCTCCAGAAAACGTGAAATCC                   | GCATCCATCCAAAGCATAAAAATATT               |
| **Lip specific (Figure S2B)** |                                                 |                                             |
| PATC138503 (PaMTN3) | TGGTGCGGCTCAAAATTATACTTT                | CAAGAGCGATTCAGAAAACCAT                    |
| PATC126569       | CGCAGTGGGTCGTAGGTTTC                        | CCAACAATATCGTCTGATGA                      |
| PATC130766       | CCCATCCGGTATCTCAA                                | CATCGCCGCTGATCGT                        |
| PATC138606       | GGCCTCGAGATTCGAAATTT                          | GCCCTGATCAGATTTTT                        |
| PATC190376       | CCGTGCGGTCTGTGAGAGAAG                       | CTTACGCCAGGATCTTCATTTGA                  |
| PATC201263       | GCTGAGCGAGGTTGTATTTG                         | GCCGTAATATGAAATCCAGAGCTTT               |
| PATC147953       | CCGTTTGGAGTCACGATGT                         | GGAGAGCAATGGCAGGATA                      |
| **Pollinia specific (Figure S2C)** |                                                 |                                             |
| PATC199170       | TAGCGCAAGGCTACGGCTTA                        | CAGCCCAATCGTGAACAGT                      |
| PATC138224       | TCTCATTTCCTCCGTTCAAAATCC                    | CATCAAAATTATCTACCTTTTCTAAAGGG            |
| PATC142064       | CCAACGCGTACCCCTCAA                             | TTTGTTCTGTGACATCGA                      |
| PATC154622       | GGCCTCGGCTAGTGAAGA                          | CTCGACACATTCACCATTCTTC                    |
| PATC125413       | CGATCTGTGCTGGTGTGTT                          | TGACCAGCACGTGATTTCT                      |
| PATC155194       | GTTCTGTGTTGTTACAAGCAGATG                   | TCTTGACGTCGCTCCTCCCA                    |
| PATC059937       | GCGAGGGAATGAGGTCA                           | CCACATCACAAGCAGATCATGTT                  |
| Accession | Sequence 1 | Sequence 2 |
|-----------|------------|------------|
| PATC055518 | GCGAAGGAGCTTACGAACATTC | CCGATTGCCGTAATGC |
| **Column specific (Figure S2D)** |
| PATC154343 | CGACAAAGGTGGCAGTGAAA | CGATTCACCTGCACGGATT |
| PATC125905 | AGCGGCTAAGGCTTACATTCA | GGTGGAAGTTTTTGATTTTG |
| PATC130846 | TGTCGGGACGTACACTTTATGCA | GCTGAGAAAAGCATTAAAGACATCCT |
| PATC197430 | CAATGCTTGTGGAAGTGATAG | TGAAGCTTATCCATCCATAATGG |
| PATC138585 (PaAG-2) | CTGATGGGAGGCACTTAGC | TCTCCAGTCTTTCTCAAGTGTGCT |
| **Pedicel specific (Figure S2E)** |
| PATC148981 | GAACGCTGCTGCTTTATATGG | AGGTCGAATCGATAATTCTCA |
| PATC022841 | TCCGGCAGTGAATAATGTTGCTA | ACAAGCGGTGTATGCCTAGACT |
| PATC173815 | CATGACATCAACACCTCTCTTT | CGGATCTGAAGCATAGGAGTT |
| PATC145039 | ACAGGAACCCAAAGCACAGCAA | TGGGCCAGCCACTCCATAAC |
| PATC145786 | TTTGATTTGTTGAGCTGCTCATA | CAGCGCAATTTTGCTGTGATTCT |
| PATC127065 | CAGTTTAAGTGCCTCGCTCTTTC | TCAAGCTCACCACCCACTTG |
| PATC150515 | TTCAAGACTGCGCCACAAACAT | TCTTTCCCACACTTATGTTG |
| **Transcription factors (Figure 5C, 5D)** |
| PATC138345 (PaAP2-7) | CCCTCGACAATGTCTGGATTAGA | GCCTCCCTAGGCAAAGTCA |
| PATC133172 (PaAP2-5) | CCGGGCTACCTACCTCTCTCTTCT | TGCCCTGCGGAATAGTAC |
| PATC135043 (PabHLH-1) | TGCGCTGCTGCTATGAG | GATAGCGCAATCGGAAGTCCTT |
| PATC140443 (PabHLH-3) | TTATCGTGAGGAGTTCAGATCA | GAATTGAGCCGGCCTT |
| PATC134262 (PabZIP-2) | TTAGTTGCCTGGAGGCTGACA | ACATCCCTGATAAAATTGCCCATTA |
| PATC136849 (PabZIP-3) | CATGTTTTTATAGTTCTGCTGTGAGT | CGGCTTTCGCAACCTATAA |
| PATC152106 (PaMYB-2) | GCGTGCGGCCTGACT | CAAATCAGCCTCCTACACTT |
| PATC150065 (PaMYB-4) | GCAACCTGCACCCCTGAAAATTG | GAAGAGTCTGGAAGCCGAAA |
| PATC138298 (PaNAC-3) | CTATCACTCTTTCCGCAGACCAA | ACTGCGATGTGGCTTCTAAC |
| **MADS box genes (Figure 5A, 5B)** |
| Accession | Gene | Primer 1 | Primer 2 |
|-----------|------|----------|----------|
| PATC154853 (PaAP3-4) | CCACCGATACCAAGAGTGTATATGA | GCTCGCTCCACAAATTTATGC |
| PATC152852 (PaPI-1) | AAAGAGCTTATTCGCCATTGGAGGA | TGTTTATCCCCGAAACGCTAGTGA |
| PATC138540 (PaSEP-1) | CCGATTTTATCGATTGCACCAA | CCAACCAGTGCGATGTAATT |
| PATC154379 (PaAGL6-1) | GAGGTACAATCAGTATGCTTCTG | TTGTAGGCTTGAGCAGATCGT |
| PATC138798 (PaMδS-1) | CAGATGCCTTGGCTCGTGA | TTGTAGGCTTGAGCAGATCGT |
| PATC155109 (PaAG-3) | CCACAAAAACTGCAGTCGCAA | GCATTCACCAGCAATTCC |
| PATC138772 (PaAGL6-2) | TTGTTCCTCCAGAAAACTGTAATTCC | GCATCCATCCAAGCATAAAATTATT |
| PATC138350 (PaAP3-3) | CCAGAAAACACACCCGGAACCTAA | CCATAAATGGGTGGTCCTCAA |
| PATC240636 (PaAP3-1) | GGGAAAACCTTACGCCTCTAATAC | CGTTCACCATTGGAAATCGAATT |

**Morphological genes (Figure 6)**

| Accession | Gene | Primer 1 | Primer 2 |
|-----------|------|----------|----------|
| PATC154491 (PaSOC1-3) | AGGAGATGTTCTCCAAATGTG | CGGGCCTCATCACATACAGTTC |
| PATC198032 | AGACAATCGGCGAGATATACGTCGTGC | CTGGATCCATGGCTGAGGCG |
| PATC129930 (PaZf) | TCTTAAAGGATCATGTCAAGGCATTT | CAAAAAATGCAACCCACAAG |
| PATC138503 (PaMTN3) | TGGTGCGGTCTCAAATTCTAAAAAT | CAAGAGCCGATTCAGAAACCAC |

**Internal Control**

| Accession | Gene | Primer 1 | Primer 2 |
|-----------|------|----------|----------|
| PATC135993 (Actin) | CTAGCGGAAACCGGCACAGA | CCAAGGGAGGCAAAAATGC |
| PATC150470 (Ubiquitin) | GATCGCCAGTCGGTTGATT | GAAGCCTACGGCCATCGA |
Phylogeny analysis of MADS box gene and AP2 transcription factors
Figure S3. Phylogenetic analysis of MADS box gene and AP2 gene family. (A) Phylogenetic analysis of MADS box gene family. 30 Arabidopsis (AT number) and 28 rice (LOC Os number) MADS box genes were collected for phylogeny analysis and used as the mainframe to support the classification. Sequences of all other orchid species were retrieved from GenBank or related references. Initials for gene symbol are indicated as Ce (Cymbidium ensifolium), Dc (Dendrobium crumenatum), DM (Dendrobium moniliforme), DO (Dendrobium grex Madame Thong-IN, hybrid), Dthyr (Dendrobium thyrsiflorum), Phal (Phalaenopsis hybrid cultivar), O (Oncidium Gower Ramsey, hybrid), Pe (Phalaenopsis equestris), PATC (Phalaenopsis aphrodite, from Orchidstra database). (B) Phylogenetic analysis of AP2 gene. 26 Arabidopsis and 33 rice AP2 genes were used for constructing the
structure of phylogenetic analysis. Zm is the initial for Zea mays. PHAP2 is petunia AP2 homologs and LIPLESS is snapdragon AP2 gene. 38 Phalaenopsis AP2 genes were included in the analysis. Numbers in the brackets indicate number of (PATC/overall) genes within each category. A complete gene list of the phylogenetic analysis is in Supplementary Table S4.
Table S4. MADS box genes and AP2 genes in phylogenetic analysis. Altogether, there are 120 MADS box transcription factors and 105 AP2 genes applied to Supplementary Figure S3 analysis. 28 MADS box genes and 38 AP2 genes of Phalaenopsis aphrodite (marked with *) were denoted with PATC initials used in the Orchidstra database. Additional MADS box genes, 16 others, were applied to Figure 2 (panel B and C) for detailed class A and class B functional groups.

### MADS box gene family

| Gene Name          | Accession number | Source       | Reference                                      |
|--------------------|------------------|--------------|------------------------------------------------|
| Arabidopsis (30 genes) |                  |              |                                                |
| AT1G01530.1(AGL28) | NM_100035        | Arabidopsis thaliana | Plant Cell. 2003 Jul;15(7):1538-51.          |
| AT1G18750.1(AGL65) | NM_101733        | Arabidopsis thaliana | Plant Physiol. 2009 Apr;149(4):1713-23.     |
| AT1G24260.2(SEP3)  | NM_001198152     | Arabidopsis thaliana | Nature. 2000 May 11;405(6783):200-3.      |
| AT1G26310.1(CAL)   | NM_102395        | Arabidopsis thaliana | Science. 1995 Jan 27;267(5197):522-5.     |
| AT1G29962.1(AGL64) | NM_001084156     | Arabidopsis thaliana | Plant Cell. 2003 Jul;15(7):1538-51.      |
| AT1G65300.1(PHE2)  | NM_105204        | Arabidopsis thaliana | Genes Dev.2003 Jun 15;17(12):1540-53.    |
| AT1G69120.1(AP1)   | NM_105581        | Arabidopsis thaliana | Science. 1995 Jan 27;267(5197):522-5.     |
| AT1G69540.1(AGL94) | NM_105623        | Arabidopsis thaliana | Plant Physiol. 2009 Apr;149(4):1713-23    |
| AT1G77980.1(AGL66) | NM_106447        | Arabidopsis thaliana | Plant Physiol. 2009 Apr;149(4):1713-23    |
| AT2G03060.2(AGL30) | NM_001084404     | Arabidopsis thaliana | Plant Physiol. 2009 Apr;149(4):1713-23    |
| AT2G03710.1(SEP4)  | NM_201682        | Arabidopsis thaliana | Curr Biol. 2004 Nov 9;14(21):1935-40.    |
| AT2G14210.1(ANR1)  | NM_126990        | Arabidopsis thaliana | Plant J. 2008 Jun;54(5):820-8.            |
| AT2G22540.1(SVP)   | NM_001161056     | Arabidopsis thaliana | Plant J. 2000 Feb;21(4):351-60            |
| AT2G42830.2(SHP2)  | ABK59682         | Arabidopsis thaliana | Nature.2000 Apr 13;404(6779):766-70.     |
| AT2G45650.1(AGL6)  | NM_130127        | Arabidopsis thaliana | Plant Cell. 2012 Jun;24(6):2364-79.      |
| AT2G45660.1(SOC1)  | NM_130128        | Arabidopsis thaliana | Genes Dev. 2000 Sep 15;14(18):2366-76.   |
| Gene ID          | Accession | Species          | Journal Details |
|------------------|-----------|------------------|----------------|
| AT3G02310.1(SEP2)| AEE73791  | Arabidopsis thaliana | Curr Biol. 2004 Nov 9;14(21):1935-40. |
| AT3G04100.1(AGL57)| NM_111281 | Arabidopsis thaliana | Plant Cell. 2003 Jul;15(7):1538-51. |
| AT3G05860.1(AGL46)| NM_111460 | Arabidopsis thaliana | Plant Physiol. 2010 Sep;154(1):287-300. |
| AT3G54340.1(AP3)  | AEE79216  | Arabidopsis thaliana | Proc Natl Acad Sci U S A. 1996 May 14;93(10):4793-8. |
| AT3G58780.3(SHP1) | NP_001190130 | Arabidopsis thaliana | Nature.2000 Apr 13;404(6779):766-70. |
| AT4G002235.1(AGL51)| AT4G02235.1 | Arabidopsis thaliana | Plant Cell. 2003 Jul;15(7):1538-51 |
| AT4G09960.3(STK)  | AEE82818  | Arabidopsis thaliana | Plant Cell. 2005 Mar;17(3):722-9. Epub 2005 Feb 18 |
| AT4G18960.1(AG)  | AEE84112  | Arabidopsis thaliana | Plant Cell Physiol. 1997 Mar;38(3):248-58. |
| AT5G15800.2(SEP1) | NM_001125758 | Arabidopsis thaliana | Curr Biol. 2004 Nov 9;14(21):1935-40. |
| AT5G20240.1(PI)  | AED92817  | Arabidopsis thaliana | Plant Cell.1991 Nov;3(11):1221-1237. |
| AT5G38620.1(AGL73) | NM_123223 | Arabidopsis thaliana | J Mol Evol. 2003 May;56(5):573-86. |
| AT5G41200.1(AGL75) | BT030016  | Arabidopsis thaliana | Plant Physiol.2010 Sep;154(1):287-300 |
| AT5G48670.1(AGL80) | DQ056710  | Arabidopsis thaliana | Plant Physiol.2010 Sep;154(1):287-300 |
| AT5G60910(FUL)  | NM_125484 | Arabidopsis thaliana | Development. 1998 Apr;125(8):1509-17. |

**Rice (28 genes)**

| Gene ID          | Accession | Species          | Journal Details |
|------------------|-----------|------------------|----------------|
| LOC_Os01g10504.1_(OsMADS3) | Q40704  | Oryza sativa | Plant Mol. Biol. 29 (1), 1-10 (1995) |
| LOC_Os01g18440.1_(OsMADS89) | N/A     | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_Os01g66303.1_(OsMADS2)  | Q40702   | Oryza sativa | Plant Sci. 109, 45-56 (1995) |
| LOC_Os01g66290.1_(OsMADS21) | Q8RU31   | Oryza sativa | Plant J. 2007 Nov;52(4):690-9. Epub 2007 Sep 17 |
| LOC_Os02g36924.1_(OsMADS27) | Q6Ep49   | Oryza sativa | Plant Cell Physiol (2003) 44 (12): 1403-1411 |
| LOC_Os02g45770.1_(OsMADS6)  | Q6EU39   | Oryza sativa | Plant J. 2010 Nov;64(4):604-17 |
| LOC_Os02g49840.1_(OsMADS57) | Q6Z6W2   | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_Os02g52340.1_(OsMADS22) | Q9XJ66   | Oryza sativa | Mol Genet Genomics. 2005 Mar;273(1):1-9 |
| LOC_Os03g08754.1_(OsMADS47) | Q5K4R0   | Oryza sativa | J Exp Bot. 2008;59(8):2181-90 |
| LOC_Os03g11614.1_(OsMADS1)  | Q10PZ9   | Oryza sativa | Plant J. 2005 Sep;43(6):915-28 |
| LOC_Os03g54160.1_(OsMADS14) | Q10CQ1   | Oryza sativa | Plant Mol. Biol. 44 (4), 513-527 (2000) |
| LOC_ Os04g23910.1_(OsMADS25) | Q84NC5 | Oryza sativa | Plant Cell Physiol. 44(12): 1403–1411 (2003) |
| LOC_ Os04g49150.1_(OsMADS17) | Q7XUN2 | Oryza sativa | Cell Res. 2010 Mar;20(3):299-313. |
| LOC_ Os05g34940.1_(OsMADS4) | Q40703 | Oryza sativa | Plant Sci. 109, 45-56 (1995) |
| LOC_ Os06g06750.1_(OsMADS5) | Q0DEB8 | Oryza sativa | Mol Cells. 1997 Feb;7(1):45-51. |
| LOC_ Os06g11330.1_(OsMADS55) | Q69TG5 | Oryza sativa | Plant Sci. 2012 Apr;185-186:97-104 |
| LOC_ Os06g11970.1_(OsMADS63) | N/A | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_ Os06g49840.1_(OsMADS16) | Q944S9 | Oryza sativa | Plant Mol. Biol. 40 (1), 167-177 (1999) |
| LOC_ Os07g01820.1_(OsMADS15) | Q6Q912 | Oryza sativa | Plant Mol. Biol. 44 (4), 513-527 (2000) |
| LOC_ Os07g41370.1_(OsMADS18/28) | Q0D4T4 | Oryza sativa | Plant Physiol. 120 (4), 1193-1204 (1999) |
| LOC_ Os08g33488.1_(OsMADS23) | Q6VAM4 | Oryza sativa | Plant Cell Physiol (2003) 44 (12): 1403-1411. |
| LOC_ Os08g38590.1_(OsMADS62) | N/A | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_ Os08g41950.1_(OsMADS7/45) | Q0J466 | Oryza sativa | Mol Cells. 1997 Aug 31;7(4):559-66. |
| LOC_ Os09g32948.1_(OsMADS8/24) | Q9SAR1 | Oryza sativa | Plant J. 2010 Mar;61(5):767-81 |
| LOC_ Os10g39130.1_(OsMADS56) | P0C5B2 | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_ Os11g43740.1_(OsMADS68) | N/A | Oryza sativa | BMC Genomics. 2007 Jul 18;8:242. |
| LOC_ Os12g10540.1_(OsMADS13) | Q2QW53 | Oryza sativa | Dev. Genet. 25 (3), 237-244 (1999) |
| LOC_ Os12g31748.1_(OsMADS20) | Q2QQA3 | Oryza sativa | Plant Cell Physiol (2003) 44 (12): 1403-1411 |

**Cymbidium orchid (2 genes)**

CeMADS1 | GU123626 | Cymbidium ensifolium | Plant Cell Physiol. 2011 Mar;52(3):563-77. |

CeMADS2 | GU123627 | Cymbidium ensifolium | Plant Cell Physiol. 2011 Mar;52(3):563-77. |

**Dendrobium orchid (15 genes)**

DcOAG1 | DQ119840 | Dendrobium crumenatum | Plant J. 2006 Apr;46(1):54-68. |

DcOAG2 | AAZ95251 | Dendrobium crumenatum | Plant J. 2006 Apr;46(1):54-68. |

DcOAP3A | AAZ95248 | Dendrobium crumenatum | Plant J. 46 (1), 54-68 (2006) |

DcOAP3B | AAZ95249 | Dendrobium crumenatum | Plant J. 46 (1), 54-68 (2006) |

DcOSEP1 | DQ119842 | Dendrobium crumenatum | Plant J. 46 (1), 54-68 (2006) |
| Accession   | Name                      | Species                          | Journal/Reference                                  |
|-------------|---------------------------|----------------------------------|---------------------------------------------------|
| DMMADS4     | ADD60473                  | *Dendrobium moniliforme*         | Acta Hortic. 836, 259-264 (2009)                  |
| DOMADS1     | AF198174                  | *Dendrobium grex Madame Thong-In*| Unpublished                                       |
| DOMADS2     | AF198175                  | *Dendrobium grex Madame Thong-In*| Unpublished                                       |
| DOMADS3     | AF198176                  | *Dendrobium grex Madame Thong-In*| Unpublished                                       |
| Dthyr-PI    | AAY86363                  | *Dendrobium thyrsiflorum*        | Unpublished                                       |
| DthyrAG1    | DQ017702                  | *Dendrobium thyrsiflorum*        | Gene. 2006 Feb 1;366(2):266-74.                   |
| DthyrAG2    | AAY86365                  | *Dendrobium thyrsiflorum*        | Gene. 2006 Feb 1;366(2):266-74.                   |
| DthyrFL1    | AY927236                  | *Dendrobium thyrsiflorum*        | Plant Sci. 169 (3), 579-586 (2005)                |
| DthyrFL2    | AY927237                  | *Dendrobium thyrsiflorum*        | Plant Sci. 169 (3), 579-586 (2005)                |
| DthyrFL3    | AY927238                  | *Dendrobium thyrsiflorum*        | Plant Sci. 169 (3), 579-586 (2005)                |

**Oncidium orchid (9 genes)**

| Accession   | Name                      | Species                          | Journal/Reference                                  |
|-------------|---------------------------|----------------------------------|---------------------------------------------------|
| OMADS1      | HM140843                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 44 (8), 783-794 (2003)        |
| OMADS10     | HM140846                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 50 (8), 1425-1438 (2009)      |
| OMADS11     | HM140847                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 50 (8), 1425-1438 (2009)      |
| OMADS3      | AAO45824                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 43 (10), 1198-1209 (2002)     |
| OMADS5      | ADJ67234                  | Oncidium Gower Ramsey            | Plant Physiol. 152 (2), 837-853 (2010)            |
| OMADS6      | HM140844                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 2009 Aug;50(8):1425-38.       |
| OMADS7      | HM140845                  | Oncidium Gower Ramsey            | Plant Cell Physiol. 50 (8), 1425-1438 (2009)      |
| OMADS8      | ADJ67236                  | Oncidium Gower Ramsey            | Plant Physiol. 152 (2), 837-853 (2010)            |
| OMADS9      | ADJ67235                  | Oncidium Gower Ramsey            | Plant Physiol. 152 (2), 837-853 (2010)            |

**Phalaenopsis orchid (37 genes)**

| Accession   | Name                      | Species                          | Journal/Reference                                  |
|-------------|---------------------------|----------------------------------|---------------------------------------------------|
| PeMADS1     | AF234617                  | *Phalaenopsis equestris*         | Unpublished                                       |
| PeMADS2     | AAR26628                  | *Phalaenopsis equestris*         | Plant Cell Physiol. 45 (7), 831-844 (2004)        |
| PeMADS3     | AAR26629                  | *Phalaenopsis equestris*         | Plant Cell Physiol. 45 (7), 831-844 (2004)        |
| PeMADS4     | AAR26626                  | *Phalaenopsis equestris*         | Plant Cell Physiol. 45 (7), 831-844 (2004)        |
| PeMADS5     | AAR26630                  | *Phalaenopsis equestris*         | Plant Cell Physiol. 45 (7), 831-844 (2004)        |
| Gene       | Accession Number | Species                  | Publication Information                                      |
|------------|------------------|--------------------------|----------------------------------------------------------------|
| PeMADS6    | AAV83997         | *Phalaenopsis equestris* | Plant Cell Physiol. 46 (7), 1125-1139 (2005)                  |
| PeMADS7    | AFI61557         | *Phalaenopsis equestris* | Plant Cell Physiol. 53 (6), 1053-1067 (2012)                  |
| PhalAG1    | BAE80120         | *Phalaenopsis hybrid cultivar* | Dev. Genes Evol. 216 (6), 301-313 (2006)                      |
| PhalAG2    | BAE80121         | *Phalaenopsis hybrid cultivar* | Dev. Genes Evol. 216 (6), 301-313 (2006)                      |
| PaAG-1     | PATC052371*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAG-2     | PATC138585*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAG-3     | PATC155109*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAG-4     | PATC202120*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAGL6-1   | PATC154379*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAGL6-2   | PATC138772*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaANR-1    | PATC129763*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaANR-2    | PATC131704*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP1-1    | PATC145405*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP1-2    | PATC154931*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP3-1    | PATC240636*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP3-2    | PATC133864*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP3-3    | PATC138350*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaAP3-4    | PATC154853*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMdeltaP-1| PATC132082*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMdeltaS-1| PATC138798*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMgamma-1 | PATC171265*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMgamma-2 | PATC240637*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMgamma-3 | PATC240639*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaMgamma-4 | PATC240638*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaPI-1     | PATC152852*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| PaSEP-1    | PATC138540*      | *Phalaenopsis aphrodite*  | *Orchidstra* database                                         |
| Gene Name | Accession number | Species | Source | Reference |
|-----------|------------------|---------|--------|-----------|
| PaSEP-2   | PATC141808*      | Phalaenopsis aphrodite | Orchidstra database |
| PaSEP-3   | PATC152066*      | Phalaenopsis aphrodite | Orchidstra database |
| PaSOC1-1  | PATC136427*      | Phalaenopsis aphrodite | Orchidstra database |
| PaSOC1-2  | PATC150808*      | Phalaenopsis aphrodite | Orchidstra database |
| PaSOC1-3  | PATC154491*      | Phalaenopsis aphrodite | Orchidstra database |
| PaSVP-1   | PATC127095*      | Phalaenopsis aphrodite | Orchidstra database |
| Others (16 genes) | | | | |
| LMADS1    | AAM27456         | Lilium longiflorum | Plant Cell Physiol. 42 (10), 1156-1168 (2001) |
| TGEFA     | BAC75970         | Tulipa gesneriana | Plant Mol. Biol. 52 (4), 831-841 (2003) |
| BOBAP3    | AAB17139         | Brassica oleracea var. botrytis | Planta 201 (2), 179-188 (1997) |
| PMADS1    | Q07472           | Petunia x hybrida | Plant Physiol. 102 (3), 1051-1052 (1993) |
| ZMM16     | NP_001105136     | Zea mays | Science 326 (5956), 1112-1115 (2009) |
| ZMM29     | NP_001105137     | Zea mays | Plant Physiol. 134 (4), 1317-1326 (2004) |
| LRGLOA    | BAB91551         | Lilium regale | Mol. Biol. Evol. 19 (5), 587-596 (2002) |
| LRGLOB    | BAB91552         | Lilium regale | Mol. Biol. Evol. 19 (5), 587-596 (2002) |
| ORCPI     | BAC22579         | Orchis italica | Unpublished |
| VvAPI     | ACZ26528         | Vitis vinifera | Unpublished |
| LlAPI     | ADT78583         | Lilium longiflorum | Plant Cell Physiol. 49 (5), 704-717 (2008) |
| ZmAPl     | NP_001105333     | Zea mays | Plant J. 8 (6), 845-854 (1995) |
| MgAGL6    | AAY25579         | Magnolia grandiflora | Unpublished |
| AcAGL6    |AFX72880          | Aquilegia coerulea | Unpublished |
| GmAgl6    | XP_003528894     | Glycine max | Unpublished |
| TaAGL6    | ABF57913         | Triticum aestivum | Mol. Genet. Genomics 276 (4), 334-350 (2006) |

**AP2 gene family**

| Gene Name | Accession number | Species | Source | Reference |
|-----------|------------------|---------|--------|-----------|

29
| Gene Name (Gene ID) | Accession Number | Species | Source |
|--------------------|------------------|---------|--------|
| AT1G06160.1(ORAI59) | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT1G13260.1(RAV1)  | Arabidopsis thaliana | Nucleic Acids Res. 1999 Jan 15;27(2):470-8 |
| AT1G15360.1(SHIN1) | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT1G16060.1(ADAP)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT1G25560.1(TEM1)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT1G51120.1        | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT1G53910.1(RAP2.12)| Arabidopsis thaliana | Proc Natl Acad Sci U S A. 1997 Jun 24;94(13):7076-81 |
| AT1G73730.1(EIL3)  | Arabidopsis thaliana | J Mol Biol. 2005 Apr 29;348(2):253-64 |
| AT2G28550.3        | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT2G41710.3        | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT3G14230.1        | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT3G16770.1(RAP2.3)| Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT3G20840.1(PLT1)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT3G54320.1(WRI1)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT4G17490.1(ATERF6)| Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT4G34410.1(RRTF1) | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT4G36920.1(AP2)   | Arabidopsis thaliana | Plant Cell. 1989 Jan;1(1):37-52 |
| AT4G37750.1(ANT)   | Arabidopsis thaliana | Sex Plant Reprod. 2010 Jun;23(2):115-21 |
| AT5G05410.1(DREB2A)| Arabidopsis thaliana | Plant Cell. 1998 Aug;10(8):1391-406 |
| AT5G11590.1(TINY2) | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT5G44210.1(ERF9)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT5G51190.1        | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT5G51990.1(CBF4)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT5G53290.1(CRF3)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
| AT5G57390.1(AIL5)  | Arabidopsis thaliana | http://www.arabidopsis.org/ |
AT5G64750.1 (ABR1)  
*Arabidopsis thaliana*  
http://www.arabidopsis.org/

**Rice (33 genes)**

| LOC_Os01g04800.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os01g07120.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os01g12440.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os01g46870.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os01g67410.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g10760.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g13710.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g40070.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g42585.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g43790.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g43820.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os02g45450.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os03g56050.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os03g64260.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os04g44670.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os04g46240.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os04g46250.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os04g55560.3 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os04g55970.2 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os05g03040.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os05g32270.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os05g47650.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os05g49700.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| LOC_Os06g03670.1 | *Oryza sativa* | http://rice.plantbiology.msu.edu/ |
| Accession  | Genotype          | Location          | Description                  |
|------------|-------------------|-------------------|-------------------------------|
| LOC_Os06g07030.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os06g09390.2 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os08g36920.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os08g45110.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os09g26420.2 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os09g31400.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os09g39850.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| LOC_Os12g39330.1 | *Oryza sativa* | [http://rice.plantbiology.msu.edu/](http://rice.plantbiology.msu.edu/) |  |
| OsAP2-1     | AB247626         | *Oryza sativa*    | [Sex Plant Reprod (2006)19:197-206](https://doi.org/10.1007/s00470-006-7004-9) |

**Phalaenopsis orchid (38 genes)**

| Accession  | Genotype          | Location          | Description                  |
|------------|-------------------|-------------------|-------------------------------|
| PaAP2-20(CBF.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-18(ANT.4) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-32(RAP2.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-33(CRF3.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-34(CRF3.2) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-11(AP2.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-38(RAV.2) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-37(RAV.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-29(ERF9.2) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-15(ANT.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-2(RAP2.2) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-35(CRF3.3) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-23     | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-22(TINY2.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-26(RRTF1.1) | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| PaAP2-10     | *Phalaenopsis aphrodite* | [Orchidstra database](http://www.orchidstra.com) |  |
| Gene          | Accession   | Species        | Database                 |
|--------------|-------------|----------------|--------------------------|
| PaAP2-21(CBF.2) | PATC128464* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-39(ORA59.1) | PATC129684* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-5(ERF6-2) | PATC133172* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-14(AP2-4) | PATC133311* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-9(EIL3.1) | PATC133419* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-27(ABR1.1) | PATC134172* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-11(ANT.5) | PATC135200* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-24(DREB.1) | PATC135602* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-13(AP2.3) | PATC135984* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-25(DREB.2) | PATC138022* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-8(RAV.3)  | PATC138224* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-7(EIL3.2) | PATC138345* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-3(RAV.4)  | PATC138625* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-31(ERF6.1) | PATC139218* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-16(ANT.2) | PATC140258* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-28(ERF9.1) | PATC140664* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-40(RAP2.4) | PATC141619* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-17(ANT.3) | PATC141638* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-30(ERF9.3) | PATC142390* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-4(RAP2.3)  | PATC143144* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-12(AP2.2)  | PATC147704* | Phalaenopsis aphrodite | Orchidstra database     |
| PaAP2-11(ERF6-3) | PATC152393* | Phalaenopsis aphrodite | Orchidstra database     |
| Others (8 genes) |             |                |                          |
| PHAP2A        | AAD39439    | Petunia x hybrida | Plant Cell. 2001 Feb;13(2):229-44. |
| PHAP2B        | AAD39440    | Petunia x hybrida | Plant Cell. 2001 Feb;13(2):229-45. |
| ZmIDS1        | NP_001104904 | Zea mays       | Development 135 (18), 3013-3019 (2008) |
| Protein   | Accession | Species                | Journal/Volume | Page/Year       |
|-----------|-----------|------------------------|----------------|-----------------|
| ZmSID1    | NP_001139539 | Zea mays              | Development 135 (18), | 3013-3019 (2009) |
| DcOAP2    | AAZ95247  | *Dendrobium crumenatum* | Plant J. 46 (1), | 54-68 (2006)    |
| LIPLESS1  | AAO52746  | *Antirrhinum majus*    | EMBO J. 22 (5), | 1058-1066 (2003) |
| LIPLESS2  | AAO52747  | *Antirrhinum majus*    | EMBO J. 22 (5), | 1058-1066 (2004) |
| NsAP2     | BAL04981  | Nymphaea hybrid cultivar | Plant Cell Rep. 30 (10), | 1909-1918 (2011) |
Subcellular localization of *Phalaenopsis aphrodite* MADS box genes

**Method**

*GFP* fusion constructs were prepared followed by particle bombardment and confocal microscopy with the same procedures on previous report [2]. Full length cDNA of target genes were PCR amplified and cloned into a smGFP vector (326-GFP) [3]. Nuclei marker construct of mCherry with NLS signal peptide fusion (E3170) was kindly provided by Dr. Gelvin (Purdue University, IN) [4]. The *GFP* construct and nucleus mCherry construct were co-bombarded into the petal of *Phalaenopsis* Sogo Yukidian ‘V3’ (a commercial hybrid) for further observation with confocal microscopy and image taken (Supplementary Figure S3). Free GFP construct was also bombarded to orchid petals and showed diffused cytoplasmic pattern (data not shown) as described before [2]. All transient expression experiments were repeated at least three times of bombardments and more than three images were taken from each bombardment.
Figure S4. Subcellular localization of MADS box genes according to particle bombardment. All GFP fusion patterns exhibit nuclei localization and co-localized with nuclear marker of NLS-mCherry except for PaAP3-4 (PATC154853) and PaSVP-1 (PATC127095), showing both nuclei and cytoplasmic punctured pattern. (Scale bars in the photo of nuclei pattern indicate 5µm; and bars in PaAP3-4 and PaSVP-1 indicate 20µm.)
Morphology of the peloric mutants

Figure S5. Peloric flowers of orchids. Peloric mutants can be found in several orchid cultivars including commercial hybrids. P. Little Mary and P. Nobby’s Amy are commercial hybrids of crossing between *Phalaenopsis* spp. Dtps stands for *Doritaenopsis* and is a commercial hybrid of crossing between *Doritis* and *Phalaenopsis* orchids. Box a and b are *Phalaenopsis* Little Mary; c and d are *Phalaenopsis* Nobby’s Amy; e and f are Dtps I-Hsing Helen; g and h are *Phalaenopsis equestris*. Box a, c, e and g are wild type flowers. Box b, d, f and h are peloric flowers. Box i and j are illustrations of the morphology of wild type and peloric flowers.
Reference

1. Su CL, Chao YT, Yen SH, Chen CY, Chen WC, et al. (2013) Orchidstra: an integrated orchid functional genomics database. Plant Cell Physiol 54: e11.

2. Su CL, Chao YT, Alex Chang YC, Chen WC, Chen CY, et al. (2011) De novo assembly of expressed transcripts and global analysis of the Phalaenopsis aphrodite transcriptome. Plant Cell Physiol 52: 1501-1514.

3. Davis SJ, Vierstra RD (1998) Soluble, highly fluorescent variants of green fluorescent protein (GFP) for use in higher plants. Plant Mol Biol 36: 521-528.

4. Lee LY, Fang MJ, Kuang LY, Gelvin SB (2008) Vectors for multi-color bimolecular fluorescence complementation to investigate protein-protein interactions in living plant cells. Plant Methods 4: 24.