# Transcriptome analysis unravels spatiotemporal modulation of phytohormone-pathway expression underlying gibberellin-induced parthenocarpic fruit set in San Pedro-type fig (*Ficus carica* L.)

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**Table S1** Primer sequences of genes used for validation of RNA-Seq results by quantitative real-time PCR

| **Gene ID** | **Annotation in NR database** | **Forward primer (5’→3’)** | **Reverse primer (5’→3’)** |
|---|---|---|---|
| comp12280_c0 | gi:587835799/auxin-induced protein IAA4 [*Morus notabilis*] | CGGATCTGCCACACTTACTGCT | ACGCTGATCACGAGGACCAC |
| comp16786_c0 | gi:587939152/auxin-induced protein AUX22 [*Morus notabilis*] | AGCATCCAGTCTCCGTCT | ATTCGGATCTTGCAATGGCTT |
| comp29694_c0 | gi:587887925/hypothetical protein L484_011493 [*Morus notabilis*] | ACCTTTGTCCAGCCCCGGAAC | CCGACCGCGAAACCTACAAGTCCA |
| comp57463_c0 | gi:587886862/gibberellin 20 oxidase 3 [*Morus notabilis*] | CCCATTCGACAATGCCACAAAGGT | CCAGAACAACAAGTGGAACTCCGT |
| comp12680_c0 | gi:587893059/gibberellin 3-beta-dioxygenase 4 [*Morus notabilis*] | CGCCAATTTTCGCCCTATGTCC | CACCGTCAGCAGTCAACCCTC |
| comp16885_c0 | gi:587973425/gibberellin 2-beta-dioxygenase 1 [*Morus notabilis*] | ACATTCCTCGGCTGAATCGTC | GGGTCGAATACCTCCTCTTAACCAC |
| comp17110_c0 | gi:587942803/hypothetical protein L484_021647 [*Morus notabilis*] | GCAAAATCCCGAACCGCGACT | TTCCGACGATGATGCACGACT |
| comp19377_c0 | gi:587862256/hypothetical protein L484_024617 [*Morus notabilis*] | CCCTCCAGAGTCCCATACGGTT | ATCTACAAGCCTCGCAGACACGAT |
| comp23225_c0 | gi:587870483/putative protein phosphatase 2C 6 [*Morus notabilis*] | ACATCCCAAAGCCCATCACTTGC | AGGCCATGGATAATTCCCGTTCCAG |
| comp25377_c0 | gi:587848632/protein phosphatase 2C 16 [*Morus notabilis*] | CCCTTTTGTTCATGTAGGTGCTT | CCTTCTCCATCAACTCGCGTTC |

| | | | |
|---|---|---|---|
| comp18261_c1 | gi:375155309/ABA responsive element-binding protein [*Solanum torvum*] | GCACCGTTTCTTCGCTCCC | ACAAGGCTTATACAATGGAACTGGA |
| comp11492_c0 | gi:255556894/s-adenosylmethionine synthetase, putative [*Ricinus communis*] | ACACATCTCTTATTGCGGCCTC | TGTTAAGATCCTCAAGCCGAAGGT |
| comp9988_c0 | gi:587870860/1-aminocyclopropane-1-carboxylate oxidase 5 [*Morus notabilis*] | ACATCTTCCCAGTCAGCGTTGTCC | ACTTCAACAACTCCAAAGCCGTCA |

**Table S2** Summary of sequencing results for control and $GA_3$-treated female flowers and receptacles

| Sample | Total clean reads | Total base pairs | Total mapped reads | Error (%) | Q20 (%) | Q30 (%) | GC (%) |
|---|---|---|---|---|---|---|---|
| **Female flowers – control** | | | | | | | |
| **2 DAT** | 40,507,384 | 5,970,741,043 | 33,873,126 (83.62%) | 0.0094 | 98.68 | 96.27 | 47.19 |
| **4 DAT** | 33,382,198 | 4,921,053,317 | 27,890,594 (83.55%) | 0.0096 | 98.58 | 96.06 | 47.28 |
| **10 DAT** | 37,562,664 | 5,533,108,443 | 31,082,298 (82.75%) | 0.0095 | 98.66 | 96.27 | 46.81 |
| **Female flowers – $GA_3$ treatment** | | | | | | | |
| **2 DAT** | 31,825,922 | 4,691,836,332 | 26,549,828 (83.42%) | 0.0094 | 98.69 | 96.33 | 47.16 |
| **4 DAT** | 29,725,356 | 4,369,210,432 | 24,775,132 (83.35%) | 0.0097 | 98.52 | 95.91 | 47.09 |
| **10 DAT** | 35,042,510 | 5,161,255,990 | 29,241,540 (83.45%) | 0.0096 | 98.62 | 96.13 | 47.06 |
| **Receptacle – control** | | | | | | | |
| **2 DAT** | 32,072,882 | 4,725,438,484 | 26,724,548 (83.22%) | 0.0094 | 98.68 | 96.3 | 47.74 |
| **4 DAT** | 33,984,708 | 4,999,991,286 | 28,394,554 (83.55%) | 0.0096 | 98.61 | 96.11 | 47.7 |
| **10 DAT** | 39,066,466 | 5,751,772,897 | 32,078,648 (82.11%) | 0.0095 | 98.63 | 96.15 | 47.38 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Receptacle – $GA_3$ treatment** | | | | | | | |
| **2 DAT** | 36,232,880 | 5,330,791,349 | 30,257,864 (83.51%) | 0.0096 | 98.61 | 96.12 | 47.71 |
| **4 DAT** | 32,486,194 | 4,778,371,956 | 27,252,842 (83.89%) | 0.0096 | 98.59 | 96.06 | 47.84 |
| **10 DAT** | 31,798,676 | 4,681,066,843 | 26,272,570 (82.62%) | 0.0096 | 98.62 | 96.16 | 47.32 |

DAT, days after treatment.

**Table S3** Significant GO terms (corrected *P*-value ≤ 0.05) identified between control and $GA_3$-treated female flowers and receptacles

| **No.** | **GO terms** | **ID** | **Number of genes** | | | |
|---|---|---|---|---|---|---|
| | **2 DAT** | | **Female flowers** | | **Receptacle** | |
| | **Molecular function** | | **up** | **down** | **up** | **down** |
| 1 | electron carrier activity | GO:0009055 | 3 | 2 | 4 | 0 |
| 2 | protein binding transcription factor activity | GO:0000988 | 0 | 1 | 2 | 0 |
| 3 | binding | GO:0005488 | 139 | 94 | 156 | 135 |
| 4 | transporter activity | GO:0005215 | 15 | 5 | 15 | 16 |
| 5 | catalytic activity | GO:0003824 | 145 | 83 | 186 | 136 |
| 6 | enzyme regulator activity | GO:0030234 | 3 | 7 | 4 | 4 |
| 7 | molecular transducer activity | GO:0060089 | 4 | 1 | 5 | 3 |
| 8 | receptor activity | GO:0004872 | 2 | 0 | 4 | 0 |
| 9 | nucleic acid binding transcription factor activity | GO:0001071 | 23 | 3 | 15 | 12 |
| 10 | antioxidant activity | GO:0016209 | 1 | 2 | 2 | 4 |
| 11 | structural molecule activity | GO:0005198 | 0 | 0 | 1 | 4 |
| | **Cellular component** | | | | | |
| 1 | symplast | GO:0055044 | 3 | 4 | 3 | 8 |
| 2 | organelle | GO:0043226 | 33 | 45 | 40 | 65 |
| 3 | cell part | GO:0044464 | 56 | 62 | 68 | 91 |
| 4 | membrane part | GO:0044425 | 35 | 23 | 37 | 36 |
| 5 | extracellular region | GO:0005576 | 3 | 4 | 9 | 8 |
| 6 | cell junction | GO:0030054 | 3 | 4 | 3 | 8 |
| 7 | membrane | GO:0016020 | 47 | 36 | 55 | 62 |
| 8 | macromolecular complex | GO:0032991 | 30 | 27 | 34 | 36 |
| 9 | cell | GO:0005623 | 56 | 62 | 68 | 91 |
| 10 | organelle part | GO:0044422 | 8 | 29 | 14 | 29 |
| | **Biological process** | | | | | |
| 1 | multiorganism process | GO:0051704 | 4 | 4 | 8 | 7 |
| 2 | developmental process | GO:0032502 | 7 | 4 | 7 | 6 |
| 3 | positive regulation of biological process | GO:0048518 | 4 | 1 | 1 | 1 |
| 4 | multicellular organismal process | GO:0032501 | 7 | 4 | 10 | 5 |
| 5 | cellular process | GO:0009987 | 141 | 83 | 158 | 135 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 6 | single-organism process | GO:0044699 | 130 | 59 | 151 | 112 |
| 7 | growth | GO:0040007 | 1 | 2 | 1 | 2 |
| 8 | signaling | GO:0023052 | 11 | 3 | 11 | 7 |
| 9 | negative regulation of biological process | GO:0048519 | 2 | 2 | 2 | 1 |
| 10 | metabolic process | GO:0008152 | 182 | 117 | 215 | 192 |
| 11 | biological regulation | GO:0065007 | 52 | 23 | 52 | 37 |
| 12 | reproductive process | GO:0022414 | 2 | 2 | 4 | 3 |
| 13 | regulation of biological process | GO:0050789 | 51 | 23 | 50 | 35 |
| 14 | cellular component organization or biogenesis | GO:0071840 | 4 | 10 | 17 | 13 |
| 15 | establishment of localization | GO:0051234 | 28 | 11 | 27 | 31 |
| 16 | rhythmic process | GO:0048511 | 1 | 0 | 1 | 0 |
| 17 | response to stimulus | GO:0050896 | 33 | 44 | 28 | 55 |
| 18 | localization | GO:0051179 | 28 | 11 | 28 | 32 |
| 19 | biological adhesion | GO:0022610 | 0 | 0 | 0 | 1 |
| | **4 DAT** | | **Female flowers** | | **Receptacle** | |
| | **Molecular function** | | **up** | **down** | **up** | **down** |
| 1 | electron carrier activity | GO:0009055 | 2 | 0 | 2 | 1 |
| 2 | protein binding transcription factor activity | GO:0000988 | 0 | 0 | 2 | 1 |
| 3 | binding | GO:0005488 | 37 | 73 | 159 | 121 |
| 4 | transporter activity | GO:0005215 | 2 | 4 | 20 | 10 |
| 5 | catalytic activity | GO:0003824 | 34 | 54 | 192 | 114 |
| 6 | enzyme regulator activity | GO:0030234 | 1 | 1 | 3 | 3 |
| 7 | molecular transducer activity | GO:0060089 | 0 | 2 | 3 | 2 |
| 8 | structural molecule activity | GO:0005198 | 1 | 3 | 12 | 0 |
| 9 | receptor activity | GO:0004872 | 0 | 0 | 2 | 0 |
| 10 | nucleic acid binding transcription factor activity | GO:0001071 | 2 | 7 | 10 | 16 |
| 11 | antioxidant activity | GO:0016209 | 0 | 2 | 1 | 0 |
| | **Cellular component** | | | | | |
| 1 | symplast | GO:0055044 | 0 | 3 | 11 | 2 |
| 2 | organelle | GO:0043226 | 8 | 24 | 69 | 38 |
| 3 | cell part | GO:0044464 | 16 | 31 | 119 | 58 |
| 4 | membrane part | GO:0044425 | 4 | 7 | 49 | 22 |
| 5 | extracellular region | GO:0005576 | 8 | 1 | 15 | 2 |
| 6 | cell junction | GO:0030054 | 0 | 3 | 11 | 2 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 7 | membrane | GO:0016020 | 10 | 11 | 76 | 32 |
| 8 | macromolecular complex | GO:0032991 | 3 | 17 | 56 | 28 |
| 9 | cell | GO:0005623 | 16 | 31 | 119 | 58 |
| 10 | organelle part | GO:0044422 | 4 | 9 | 35 | 17 |
|  | **Biological process** |  |  |  |  |  |
| 1 | multiorganism process | GO:0051704 | 0 | 7 | 5 | 6 |
| 2 | developmental process | GO:0032502 | 2 | 4 | 6 | 4 |
| 3 | positive regulation of biological process | GO:0048518 | 1 | 2 | 3 | 2 |
| 4 | multicellular organismal process | GO:0032501 | 2 | 6 | 10 | 4 |
| 5 | cellular process | GO:0009987 | 30 | 64 | 190 | 100 |
| 6 | single-organism process | GO:0044699 | 33 | 45 | 150 | 89 |
| 7 | growth | GO:0040007 | 0 | 1 | 2 | 0 |
| 8 | signaling | GO:0023052 | 0 | 4 | 15 | 0 |
| 9 | negative regulation of biological process | GO:0048519 | 1 | 3 | 3 | 1 |
| 10 | metabolic process | GO:0008152 | 39 | 84 | 227 | 150 |
| 11 | biological regulation | GO:0065007 | 8 | 17 | 52 | 31 |
| 12 | reproductive process | GO:0022414 | 1 | 6 | 4 | 5 |
| 13 | regulation of biological process | GO:0050789 | 8 | 17 | 49 | 30 |
| 14 | cellular component organization or biogenesis | GO:0071840 | 6 | 4 | 28 | 1 |
| 15 | establishment of localization | GO:0051234 | 4 | 6 | 37 | 15 |
| 16 | rhythmic process | GO:0048511 | 0 | 1 | 0 | 0 |
| 17 | response to stimulus | GO:0050896 | 4 | 35 | 37 | 48 |
| 18 | localization | GO:0051179 | 4 | 6 | 39 | 15 |
| 19 | reproduction | GO:0000003 | 0 | 0 | 1 | 1 |
|  | **10 DAT** |  | **Female flowers** |  | **Receptacle** |  |
|  | **Molecular function** |  | **up** | **down** | **up** | **down** |
| 1 | electron carrier activity | GO:0009055 | 4 | 1 | 6 | 3 |
| 2 | protein binding transcription factor activity | GO:0000988 | 1 | 0 | 1 | 1 |
| 3 | binding | GO:0005488 | 191 | 278 | 198 | 250 |
| 4 | transporter activity | GO:0005215 | 15 | 56 | 17 | 52 |
| 5 | catalytic activity | GO:0003824 | 253 | 399 | 279 | 320 |
| 6 | guanyl-nucleotide exchange factor activity | GO:0005085 | 1 | 0 | 1 | 0 |
| 7 | enzyme regulator activity | GO:0030234 | 2 | 12 | 12 | 8 |
| 8 | molecular transducer activity | GO:0060089 | 2 | 6 | 2 | 5 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 9 | structural molecule activity | GO:0005198 | 14 | 0 | 9 | 2 |
| 10 | receptor activity | GO:0004872 | 1 | 1 | 1 | 1 |
| 11 | nucleic acid binding transcription factor activity | GO:0001071 | 15 | 20 | 1 | 1 |
| 12 | antioxidant activity | GO:0016209 | 7 | 7 | 9 | 2 |
|  | **Cellular component** |  |  |  |  |  |
| 1 | symplast | GO:0055044 | 7 | 4 | 11 | 6 |
| 2 | extracellular matrix | GO:0031012 | 1 | 0 | 0 | 0 |
| 3 | extracellular region part | GO:0044421 | 3 | 1 | 0 | 0 |
| 4 | extracellular region | GO:0005576 | 0 | 0 | 24 | 11 |
| 5 | organelle | GO:0043226 | 74 | 68 | 64 | 69 |
| 6 | cell part | GO:0044464 | 108 | 109 | 106 | 109 |
| 7 | membrane part | GO:0044425 | 33 | 88 | 48 | 74 |
| 8 | extracellular region | GO:0005576 | 24 | 12 | 24 | 11 |
| 9 | cell junction | GO:0030054 | 7 | 4 | 11 | 6 |
| 10 | nucleoid | GO:0009295 | 0 | 1 | 0 | 0 |
| 11 | membrane | GO:0016020 | 65 | 132 | 89 | 115 |
| 12 | macromolecular complex | GO:0032991 | 49 | 48 | 38 | 49 |
| 13 | cell | GO:0005623 | 108 | 109 | 106 | 109 |
| 14 | organelle part | GO:0044422 | 39 | 32 | 27 | 32 |
|  | **Biological process** |  |  |  |  |  |
| 1 | reproduction | GO:0000003 | 1 | 0 | 2 | 2 |
| 2 | multiorganism process | GO:0051704 | 4 | 8 | 9 | 8 |
| 3 | developmental process | GO:0032502 | 12 | 13 | 11 | 7 |
| 4 | positive regulation of biological process | GO:0048518 | 4 | 4 | 1 | 5 |
| 5 | multicellular organismal process | GO:0032501 | 12 | 10 | 12 | 8 |
| 6 | cellular process | GO:0009987 | 188 | 290 | 203 | 263 |
| 7 | single-organism process | GO:0044699 | 195 | 314 | 206 | 261 |
| 8 | growth | GO:0040007 | 1 | 1 | 3 | 0 |
| 9 | signaling | GO:0023052 | 9 | 15 | 9 | 16 |
| 10 | negative regulation of biological process | GO:0048519 | 5 | 3 | 2 | 1 |
| 11 | metabolic process | GO:0008152 | 280 | 432 | 300 | 363 |
| 12 | biological regulation | GO:0065007 | 40 | 79 | 50 | 75 |
| 13 | reproductive process | GO:0022414 | 3 | 2 | 5 | 5 |
| 14 | regulation of biological process | GO:0050789 | 36 | 72 | 47 | 71 |
| 15 | establishment of localization | GO:0051234 | 27 | 77 | 29 | 69 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 16 | rhythmic process | GO:0048511 | 0 | 2 | 0 | 0 |
| 17 | cellular component organization or biogenesis | GO:0071840 | 36 | 6 | 32 | 8 |
| 18 | response to stimulus | GO:0050896 | 51 | 68 | 51 | 65 |
| 19 | biological adhesion | GO:0022610 | 1 | 1 | 1 | 0 |
| 20 | localization | GO:0051179 | 29 | 78 | 30 | 69 |

The representative terms with a large number of differentially expressed genes are highlighted in yellow. DAT, days after treatment.

**Table S4** Significant KEGG pathways (corrected *P*-value ≤ 0.05) identified between $GA_3$-treated and control female flowers and receptacle

| **No.** | **Pathway** | **Number of genes** | **corrected *P*-value** | **Pathway ID** |
|---|---|---|---|---|
| **Female flowers (2 DAT)** | | | | |
| 1 | Protein processing in endoplasmic reticulum | 34 | 2.87E-13 | ko04141 |
| 2 | Photosynthesis – antenna proteins | 6 | 6.89E-04 | ko00196 |
| 3 | Photosynthesis | 9 | 0.00217 | ko00195 |
| 4 | Plant–pathogen interaction | 13 | 0.0224 | ko04626 |
| **Female flowers (4 DAT)** | | | | |
| 1 | Protein processing in endoplasmic reticulum | 25 | 1.02E-10 | ko04141 |
| **Female flowers (10 DAT)** | | | | |
| 1 | Alanine, aspartate and glutamate metabolism | 13 | 1.57E-06 | ko00250 |
| 2 | Phenylpropanoid biosynthesis | 23 | 4.46E-04 | ko00940 |
| 3 | Phenylalanine metabolism | 18 | 8.14E-04 | ko00360 |
| 4 | Flavonoid biosynthesis | 10 | 0.00556 | ko00941 |
| 5 | Cysteine and methionine metabolism | 15 | 0.00724 | ko00270 |
| 6 | Carbon fixation in photosynthetic organisms | 14 | 0.0117 | ko00710 |
| 7 | Tryptophan metabolism | 8 | 0.0143 | ko00380 |
| 8 | Arginine and proline metabolism | 13 | 0.0143 | ko00330 |
| 9 | Galactose metabolism | 11 | 0.0165 | ko00052 |
| 10 | Nitrogen metabolism | 8 | 0.0170 | ko00910 |
| 11 | Fatty acid metabolism | 9 | 0.0176 | ko00071 |
| 12 | Other glycan degradation | 5 | 0.0191 | ko00511 |
| 13 | Tyrosine metabolism | 8 | 0.0460 | ko00350 |
| **Receptacle (2 DAT)** | | | | |
| 1 | Protein processing in endoplasmic reticulum | 31 | 8.76E-08 | ko04141 |
| 2 | Photosynthesis – antenna proteins | 7 | 3.90E-04 | ko00196 |
| 3 | Nitrogen metabolism | 8 | 0.00257 | ko00910 |
| 4 | Phenylalanine metabolism | 12 | 0.00888 | ko00360 |
| 5 | Plant hormone signal transduction | 20 | 0.0150 | ko04075 |
| 6 | Cysteine and methionine metabolism | 11 | 0.0150 | ko00270 |
| 7 | Glycine, serine and threonine metabolism | 9 | 0.0154 | ko00260 |
| 8 | Carotenoid biosynthesis | 6 | 0.0154 | ko00906 |

|  |  |  |  |  |
|---|---|---|---|---|
| 9 | Photosynthesis | 8 | 0.0325 | ko00195 |
| **Receptacle (4 DAT)** |  |  |  |  |
| 1 | Protein processing in endoplasmic reticulum | 30 | 1.10E-06 | ko04141 |
| 2 | Circadian rhythm – plant | 8 | 0.00231 | ko04712 |
| 3 | Cysteine and methionine metabolism | 13 | 0.00281 | ko00270 |
| 4 | Endocytosis | 13 | 0.0326 | ko04144 |
| **Receptacle (10 DAT)** |  |  |  |  |
| 1 | Cysteine and methionine metabolism | 21 | 2.95E-07 | ko00270 |
| 2 | Carbon fixation in photosynthetic organisms | 15 | 9.82E-04 | ko00710 |
| 3 | Galactose metabolism | 12 | 0.00229 | ko00052 |
| 4 | Phenylalanine metabolism | 14 | 0.00863 | ko00360 |
| 5 | Pentose and glucuronate interconversions | 12 | 0.0120 | ko00040 |
| 6 | Starch and sucrose metabolism | 21 | 0.0120 | ko00500 |
| 7 | Plant hormone signal transduction | 24 | 0.0120 | ko04075 |
| 8 | Tyrosine metabolism | 8 | 0.0260 | ko00350 |
| 9 | Terpenoid backbone biosynthesis | 8 | 0.0260 | ko00900 |
| 10 | Arginine and proline metabolism | 11 | 0.0325 | ko00330 |
| 11 | Pentose phosphate pathway | 8 | 0.0427 | ko00030 |
| 12 | Carotenoid biosynthesis | 6 | 0.0460 | ko00906 |

DAT, days after treatment.

**Table S5** All gibberellin-, auxin- and cytokinin-synthesis, catabolism and response transcripts identified in this study which were differentially expressed (FDR < 0.01 and the absolute value of $\log_2$ ($\mathrm{FPKM}_{\mathrm{treatment}}/\mathrm{FPKM}_{\mathrm{control}}$) ≥ 1) in at least one pairwise comparison group

| **Gene name** | **Gene ID / Protein ID** | **Description in NR database** | **Similarity (%)** |
|---|---|---|---|
| **Gibberellin metabolism- and response-related genes** | | | |
| **GA20ox** | | | |
| comp57463_c0 | gi:587886862 / EXB75633.1 | Gibberellin 20 oxidase 3 [*Morus notabilis*] | 91% |
| **GA3ox** | | | |
| comp12680_c0 | gi:587893059 / EXB81619.1 | Gibberellin 3-beta-dioxygenase 4 [*Morus notabilis*] | 88% |
| comp13433_c0 | gi:587946228 / EXC32577.1 | Gibberellin 3-beta-dioxygenase 1 [*Morus notabilis*] | 89% |
| comp22862_c0 | gi:587893059 / EXB81619.1 | Gibberellin 3-beta-dioxygenase 4 [*Morus notabilis*] | 89% |
| **GA2ox** | | | |
| comp16885_c0 | gi:587973425 / EXC58248.1 | Gibberellin 2-beta-dioxygenase 1 [*Morus notabilis*] | 91% |
| comp26664_c0 | gi:587946750 / EXC33074.1 | Gibberellin 2-beta-dioxygenase 8 [*Morus notabilis*] | 93% |
| comp32778_c0 | gi:587942817 / EXC29353.1 | Gibberellin 2-beta-dioxygenase [*Morus notabilis*] | 93% |
| comp18866_c0 | gi:587906001 / EXB94107.1 | Gibberellin 2-beta-dioxygenase 8 [*Morus notabilis*] | 80% |
| comp53019_c0 | gi:587866532 / EXB55989.1 | Gibberellin 2-beta-dioxygenase 2 [*Morus notabilis*] | 85% |
| comp23223_c0 | gi:587917544 / EXC05108.1 | Gibberellin 2-beta-dioxygenase 8 [*Morus notabilis*] | 93% |
| **DELLA** | | | |
| comp26619_c0 | gi:645278651 / XP_008244327.1 | PREDICTED: scarecrow-like protein 21 [*Prunus mume*] | 80% |

| | | | |
|---|---|---|---|
| **Auxin metabolism- and response-related genes** | | | |
| **Aldehyde (IAld) dehydrogenase** | | | |
| comp9282_c0 | gi:595802986 / XP_007201943.1 | Hypothetical protein PRUPE_ppa004461mg [*Prunus persica*] | 95% |
| comp11862_c0 | gi:587899465 / EXB87864.1 | Aldehyde dehydrogenase family 2 member [*Morus notabilis*] | 82% |
| **IAA-amino acid hydrolase** | | | |
| comp20467_c0 | gi:587844298 / EXB34859.1 | IAA-amino acid hydrolase ILR1-like 4 [*Morus notabilis*] | 96% |
| comp25015_c0 | gi:587844301 / EXB34862.1 | IAA-amino acid hydrolase ILR1-like 5 [*Morus notabilis*] | 78% |
| comp12153_c0 | gi:587894121 / EXB82653.1 | IAA-amino acid hydrolase ILR1-like 2 [*Morus notabilis*] | 95% |
| **GH3** | | | |
| comp25108_c0 | gi:587861039 / EXB50903.1 | Hypothetical protein L484_021129 [*Morus notabilis*] | 96% |
| comp29694_c0 | gi:587887925 / EXB76648.1 | Hypothetical protein L484_011493 [*Morus notabilis*] | 96% |
| **AUX1** | | | |
| comp30772_c0 | gi:659131659 / XP_008465793.1 | PREDICTED: auxin transporter-like protein 3 [*Cucumis melo*] | 96% |
| **AUX/IAA** | | | |
| comp12280_c0 | gi:587835799 / EXB26568.1 | Auxin-induced protein IAA4 [*Morus notabilis*] | 62% |
| comp16786_c0 | gi:587939152 / EXC25824.1 | Auxin-induced protein AUX22 [*Morus notabilis*] | 82% |
| comp21990_c0 | gi:587939153 / EXC25825.1 | Auxin-responsive protein IAA17 [*Morus notabilis*] | 87% |
| comp20539_c0 | gi:388509620 / AFK42876.1 | Unknown [*Medicago truncatula*] | 77% |
| comp13087_c0 | gi:587905040 / EXB93236.1 | Auxin-responsive protein IAA3 [*Morus notabilis*] | 84% |
| comp12423_c0 | gi:587916406 / EXC04075.1 | Auxin-responsive protein IAA13 [*Morus notabilis*] | 86% |

|  |  |  |  |
|---|---|---|---|
| comp7006_c0 | gi:470109762 / XP_004291159.1 | PREDICTED: auxin-responsive protein IAA26-like [*Fragaria vesca* subsp. *vesca*] | 68% |
| **ARF** |  |  |  |
| comp32528_c0 | gi:587869068 / EXB58397.1 | Auxin response factor 5 [*Morus notabilis*] | 95% |
| **SAUR** |  |  |  |
| comp33019_c0 | gi:587853002 / EXB43114.1 | Hypothetical protein L484_002582 [*Morus notabilis*] | 86% |
| comp36657_c0 | gi:587929004 / EXC16179.1 | Hypothetical protein L484_024347 [*Morus notabilis*] | 95% |
| comp16559_c0 | gi:587872564 / EXB61802.1 | Hypothetical protein L484_012234 [*Morus notabilis*] | 83% |
| comp31670_c0 | gi:587846607 / EXB37077.1 | Hypothetical protein L484_020868 [*Morus notabilis*] | 92% |
| comp19373_c0 | gi:587850151 / EXB40340.1 | Hypothetical protein L484_017482 [*Morus notabilis*] | 88% |
| **Cytokinin metabolism- and response-related genes** |  |  |  |
| **IPT** |  |  |  |
| comp9983_c0 | gi:587907848 / EXB95832.1 | Adenylate isopentenyltransferase 5 [*Morus notabilis*] | 85% |
| **CKX** |  |  |  |
| comp21589_c0 | gi:587938282 / EXC25031.1 | Cytokinin dehydrogenase 5 [*Morus notabilis*] | 91% |
| comp11524_c0 | gi:587923105 / EXC10466.1 | Cytokinin dehydrogenase 1 [*Morus notabilis*] | 95% |
| **CIS-ZOG** |  |  |  |
| comp18972_c0 | gi:587860262 / EXB50176.1 | Zeatin O-glucosyltransferase [Morus notabilis] | 88% |
| comp21293_c0 | gi:587860262 / EXB50176.1 | Zeatin O-glucosyltransferase [Morus notabilis] | 80% |

|  |  |  |  |
|---|---|---|---|
| comp20461_c0 | gi:604298708 / EYU18710.1 | Hypothetical protein MIMGU_mgv1a005799mg [*Erythranthe guttata*] | 86% |
| **CRE1** |  |  |  |
| comp16591_c0 | gi:587850113 / EXB40302.1 | Histidine kinase 3 [*Morus notabilis*] | 95% |
| **A-ARR** |  |  |  |
| comp4260_c0 | gi:587908595 / EXB96540.1 | Two-component response regulator [*Morus notabilis*] | 98% |
| comp16589_c0 | gi:587945862 / EXC32234.1 | Two-component response regulator [*Morus notabilis*] | 88% |

**Table S6** All abscisic acid- and ethylene-synthesis, catabolism and response transcripts identified in this study which were differentially expressed (FDR < 0.01 and the absolute value of $\log_2$ ($FPKM_{treatment}/FPKM_{control}$) ≥ 1) in at least one pairwise comparison group

| **Gene name** | **Gene ID / Protein ID** | **Description in NR database** | **Similarity (%)** |
|---|---|---|---|
| **ABA metabolism- and response-related genes** | | | |
| **NCED** | | | |
| comp22655_c0 | gi:587942803 / EXC29339.1 | Hypothetical protein L484_021647 [*Morus notabilis*] | 82% |
| comp17110_c0 | gi:587942803 / EXC29339.1 | Hypothetical protein L484_021647 [*Morus notabilis*] | 96% |
| comp26438_c0 | gi:587930726 / EXC17835.1 | Hypothetical protein L484_023189 [*Morus notabilis*] | 89% |
| comp19377_c0 | gi:587862256 / EXB52067.1 | Hypothetical protein L484_024617 [*Morus notabilis*] | 93% |
| **ABA2** | | | |
| comp12226_c0 | gi:587923076 / EXC10437.1 | Xanthoxin dehydrogenase [*Morus notabilis*] | 93% |
| **ABA 8'-hydroxylase** | | | |
| comp9528_c0 | gi:587945275 / EXC31689.1 | Abscisic acid 8'-hydroxylase 1 [*Morus notabilis*] | 94% |
| **PYR/PYL** | | | |
| comp25256_c0 | gi:587862606 / EXB52402.1 | Hypothetical protein L484_012047 [*Morus notabilis*] | 92% |
| **PP2C** | | | |
| comp23225_c0 | gi:587870483 / EXB59766.1 | Putative protein phosphatase 2C 6 [*Morus notabilis*] | 98% |
| comp25377_c0 | gi:587848632 / EXB38891.1 | Protein phosphatase 2C 16 [*Morus notabilis*] | 90% |
| comp14332_c0 | gi:587877015 / EXB66087.1 | Putative protein phosphatase 2C 8 [*Morus notabilis*] | 87% |

| | | | |
|---|---|---|---|
| comp16460_c0 | gi:587923379 / EXC10729.1 | Putative protein phosphatase 2C 24 [*Morus notabilis*] | 85% |
| comp25508_c0 | gi:645258105 / XP_008234728.1 | PREDICTED: probable protein phosphatase 2C 51 [*Prunus mume*] | 78% |
| comp19341_c0 | gi:587933921 / EXC20871.1 | Putative protein phosphatase 2C 75 [*Morus notabilis*] | 78% |
| **ABF** | | | |
| comp30505_c0 | gi:587946520 / EXC32855.1 | ABSCISIC ACID-INSENSITIVE 5-like protein 5 [*Morus notabilis*] | 91% |
| comp18261_c1 | gi:375155309 / AFA37978.1 | ABA responsive element-binding protein [*Solanum torvum*] | 98% |
| comp16514_c0 | gi:587946520 / EXC32855.1 | ABSCISIC ACID-INSENSITIVE 5-like protein 5 [*Morus notabilis*] | 87% |
| comp89455_c0 | gi:587848159 / EXB38447.1 | ABSCISIC ACID-INSENSITIVE 5-like protein 1 [*Morus notabilis*] | 86% |
| **Ethylene metabolism- and response-related genes** | | | |
| **SAM synthetase** | | | |
| comp11492_c0 | gi:255556894 / XP_002519480.1 | S-adenosylmethionine synthetase, putative [*Ricinus communis*] | 100% |
| comp28987_c0 | gi:460408090 / XP_004249481.1 | PREDICTED: S-adenosylmethionine synthase 2-like [*Solanum lycopersicum*] | 100% |
| comp28816_c0 | gi:449451048 / XP_004143274.1 | PREDICTED: S-adenosylmethionine synthase 2-like [*Cucumis sativus*] | 100% |
| comp30786_c0 | gi:255543014 / XP_002512570.1 | S-adenosylmethionine synthetase, putative [*Ricinus communis*] | 100% |
| comp7483_c0 | gi:470132951 / XP_004302338.1 | PREDICTED: S-adenosylmethionine synthase 1-like [*Fragaria vesca* subsp. *Vesca*] | 98% |
| **ACC synthase** | | | |
| comp27593_c0 | gi:587846852 / EXB37292.1 | 1-Aminocyclopropane-1-carboxylate synthase [*Morus notabilis*] | 94% |
| comp21829_c0 | gi:587861793 / EXB51626.1 | 1-Aminocyclopropane-1-carboxylate synthase 1 [*Morus notabilis*] | 95% |
| **ACC oxidase** | | | |

|  |  |  |  |
|---|---|---|---|
| comp23635_c1 | gi:166788505 / BAG06705.1 | 1-Aminocyclopropane-1-carboxylate oxidase [*Ficus carica*] | 100% |
| comp27433_c0 | gi:587864354 / EXB54016.1 | 1-Aminocyclopropane-1-carboxylate oxidase-3-like protein [*Morus notabilis*] | 90% |
| comp30808_c0 | gi:587929255 / EXC16422.1 | 1-Aminocyclopropane-1-carboxylate oxidase-1-like protein [*Morus notabilis*] | 86% |
| comp9988_c0 | gi:587870860 / EXB60136.1 | 1-Aminocyclopropane-1-carboxylate oxidase 5 [*Morus notabilis*] | 94% |
| comp11309_c0 | gi:587940644 / EXC27244.1 | 1-Aminocyclopropane-1-carboxylate oxidase 3 [*Morus notabilis*] | 97% |
| comp585_c0 | gi:645235671 / XP_008224379.1 | PREDICTED: 1-Aminocyclopropane-1-carboxylate oxidase homolog 1-like [*Prunus mume*] | 91% |
| **ETR** |  |  |  |
| comp16652_c0 | gi:587910281 / EXB98165.1 | Ethylene receptor 2 [*Morus notabilis*] | 92% |
| comp29504_c0 | gi:587907745 / EXB95735.1 | Ethylene response sensor 1 [*Morus notabilis*] | 96% |
| comp30741_c0 | gi:587905004 / EXB93200.1 | Protein EIN4 [*Morus notabilis*] | 94% |
| **EBF1/2** |  |  |  |
| comp9018_c0 | gi:587830385 / EXB21298.1 | Hypothetical protein L484_002248 [*Morus notabilis*] | 95% |
| **ERF** |  |  |  |
| comp16781_c0 | gi:587914274 / EXC02053.1 | Ethylene-responsive transcription factor 2 [*Morus notabilis*] | 82% |
| comp16998_c0 | gi:587864373 / EXB54035.1 | Ethylene-responsive transcription factor 1B [*Morus notabilis*] | 94% |
| comp17108_c0 | gi:587854580 / EXB44623.1 | Ethylene-responsive transcription factor 4 [*Morus notabilis*] | 82% |
| comp28870_c0 | gi:225455041 / XP_002282167.1 | PREDICTED: Ethylene-responsive transcription factor 5 [*Vitis vinifera*] | 60% |

|  |  |  |  |
|---|---|---|---|
| comp10854_c0 | gi:587944083 / EXC30582.1 | Ethylene-responsive transcription factor 12 [*Morus notabilis*] | 84% |
| comp22612_c0 | gi:587864369 / EXB54031.1 | Ethylene-responsive transcription factor [*Morus notabilis*] | 83% |
| comp25440_c0 | gi:587847245 / EXB37641.1 | Ethylene-responsive transcription factor 13 [*Morus notabilis*] | 79% |
| comp46255_c0 | gi:587945546 / EXC31946.1 | Ethylene-responsive transcription factor 15 [*Morus notabilis*] | 76% |
| comp7982_c0 | gi:587892625 / EXB81200.1 | Ethylene-responsive transcription factor [*Morus notabilis*] | 90% |
| comp24422_c0 | gi:587925050 / EXC12328.1 | Ethylene-responsive transcription factor [*Morus notabilis*] | 64% |
| comp18924_c0 | gi:587925050 / EXC12328.1 | Ethylene-responsive transcription factor [*Morus notabilis*] | 74% |
| comp33022_c0 | gi:587925344 / EXC12612.1 | AP2-like ethylene-responsive transcription factor ANT [*Morus* | 90% |
| comp7744_c0 | gi:587934118 / EXC21056.1 | Ethylene-responsive transcription factor 2 [*Morus notabilis*] | 81% |
| comp34364_c0 | gi:587935540 / EXC22410.1 | AP2-like ethylene-responsive transcription factor ANT [*Morus* | 85% |
| comp39079_c0 | gi:587892747 / EXB81318.1 | Ethylene-responsive transcription factor 3 [*Morus notabilis*] | 86% |

## Supplementary Figure legends

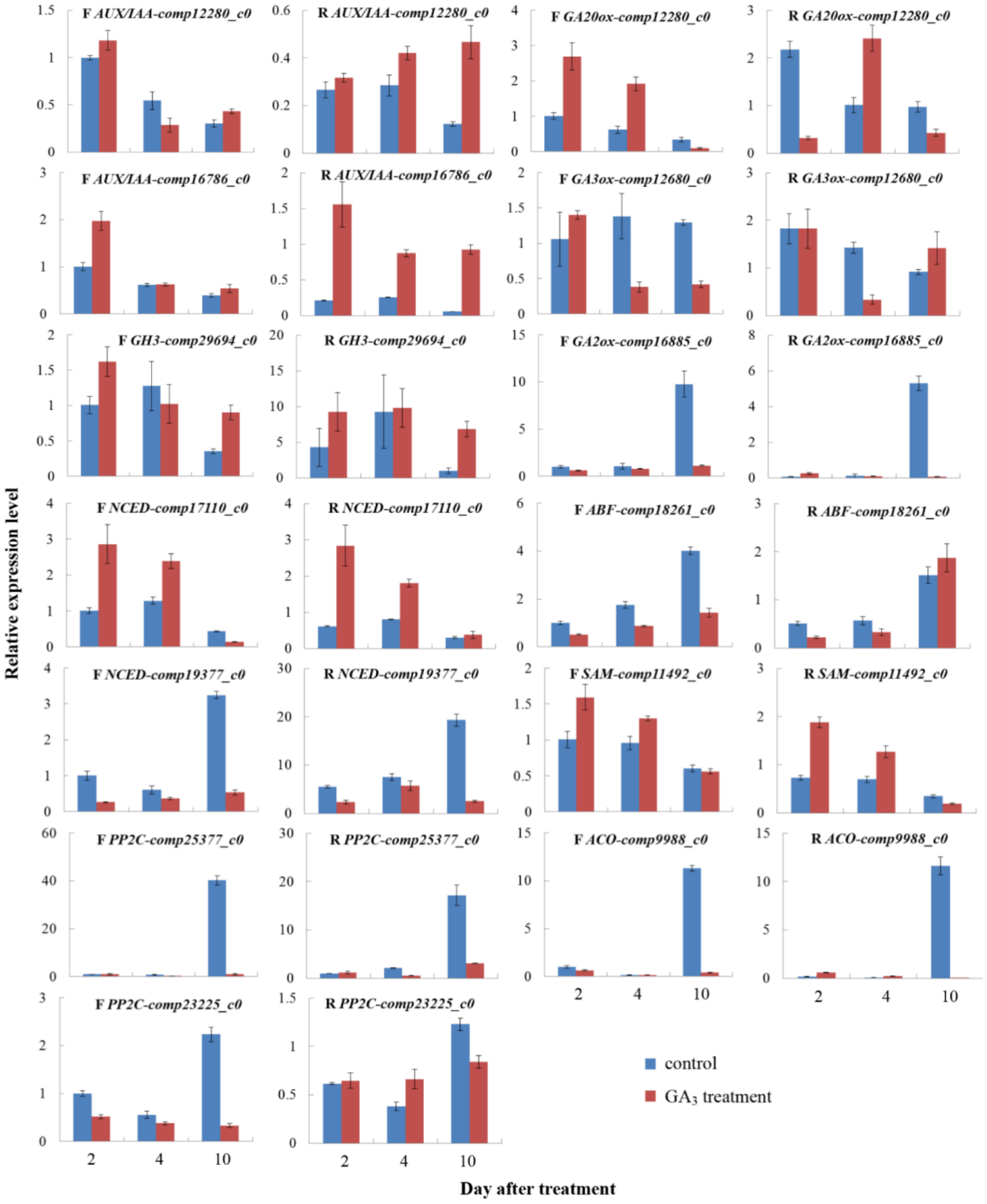
**Figure S1** Verification of RNA-Seq results by qRT-PCR. Bars represent standard deviation. F, female flowers; R, receptacle

**Figure S2** Correlation of fold changes in gene expression between RNA-Seq and qRT-PCR. Equation of linear regression and correlation coefficient ($R^2$) are shown. DAT, days after treatment

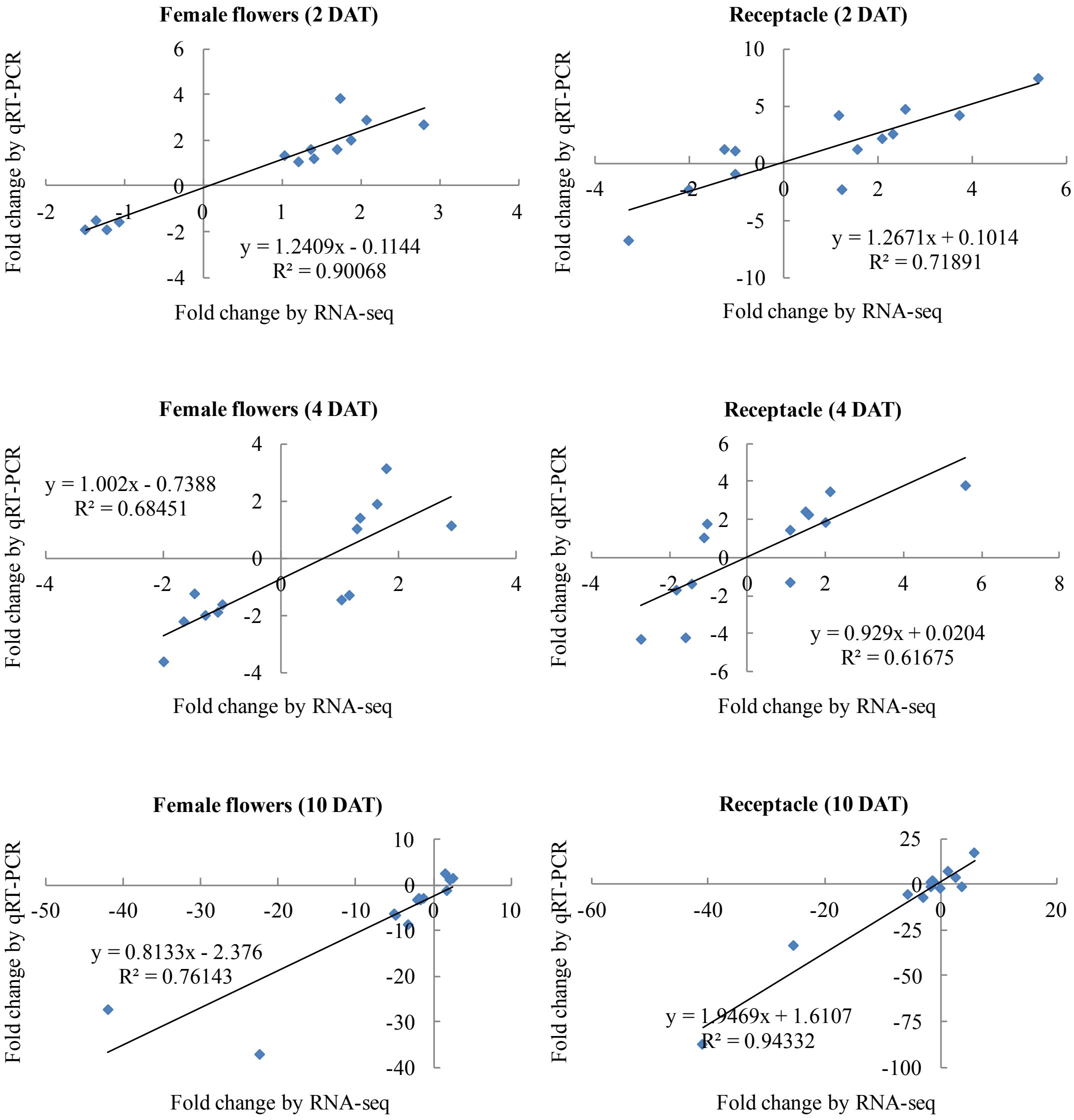
**Figure S3** Number of differentially expressed genes (FDR ≤ 0.001 and $\log_2(\mathrm{FPKM}_{\mathrm{treatment}}/\mathrm{FPKM}_{\mathrm{control}}) \geq 1$ or $\leq -1$) between control and $GA_3$-treated female flowers and receptacles. DAT, days after treatment

**Figure S4** Heat maps of hormone-related genes with low expression. FPKM of all samples was < 10

**Figure S1**


F AUX/IAA-comp12280_c0
R AUX/IAA-comp12280_c0
F GA20ox-comp12280_c0
R GA20ox-comp12280_c0
F AUX/IAA-comp16786_c0
R AUX/IAA-comp16786_c0
F GA3ox-comp12680_c0
R GA3ox-comp12680_c0
F GH3-comp29694_c0
R GH3-comp29694_c0
F GA2ox-comp16885_c0
R GA2ox-comp16885_c0
F NCED-comp17110_c0
R NCED-comp17110_c0
F ABF-comp18261_c0
R ABF-comp18261_c0
F NCED-comp19377_c0
R NCED-comp19377_c0
F SAM-comp11492_c0
R SAM-comp11492_c0
F PP2C-comp25377_c0
R PP2C-comp25377_c0
F ACO-comp9988_c0
R ACO-comp9988_c0
F PP2C-comp23225_c0
R PP2C-comp23225_c0
Relative expression level
2
4
10
Day after treatment
control
GA₃ treatment

# Figure S2



Female flowers (2 DAT)

Receptacle (2 DAT)

Female flowers (4 DAT)

Receptacle (4 DAT)

Female flowers (10 DAT)

Receptacle (10 DAT)

## Figure S3

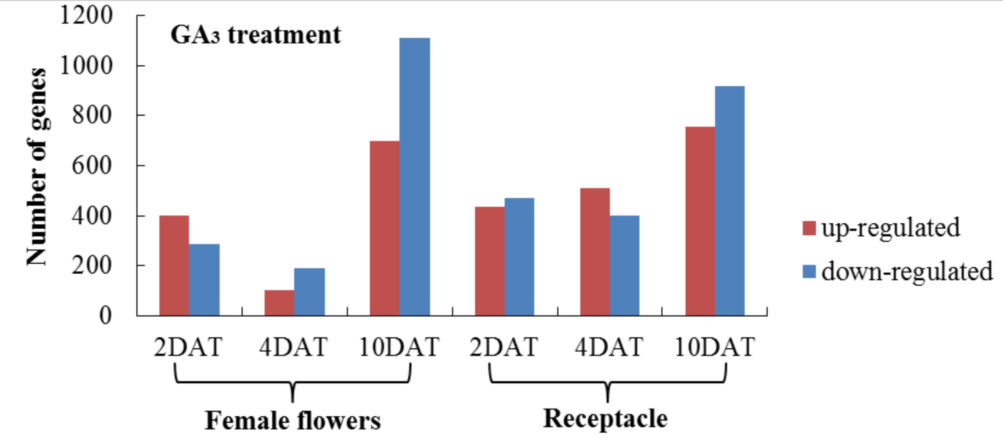
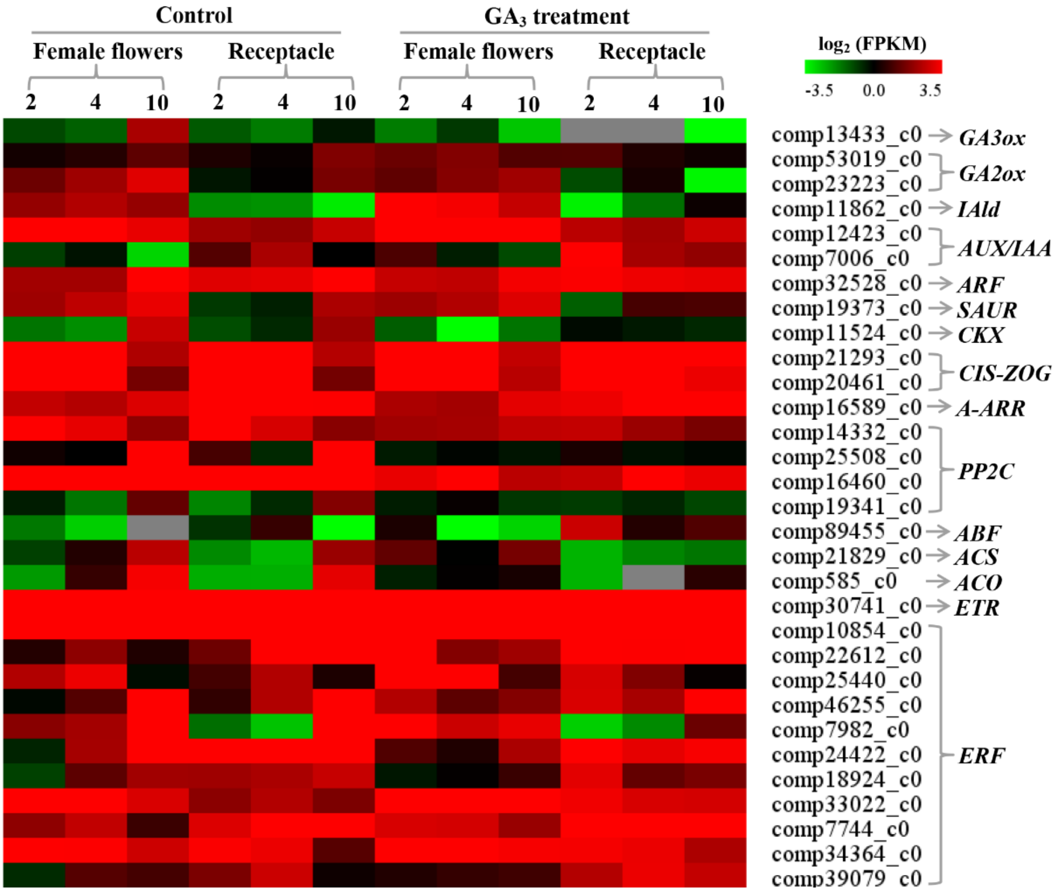

GA3 treatment
Number of genes
1200
1000
800
600
400
200
0
2DAT
4DAT
10DAT
2DAT
4DAT
10DAT
Female flowers
Receptacle
up-regulated
down-regulated

**Figure S4**


Control
GA₃ treatment
Female flowers
Receptacle
Female flowers
Receptacle
2
4
10
2
4
10
2
4
10
2
4
10
log₂ (FPKM)
-3.5
0.0
3.5
comp13433_c0 → GA3ox
comp53019_c0
comp23223_c0
GA2ox
comp11862_c0 → IAld
comp12423_c0
comp7006_c0
AUX/IAA
comp32528_c0 → ARF
comp19373_c0 → SAUR
comp11524_c0 → CKX
comp21293_c0
comp20461_c0
CIS-ZOG
comp16589_c0 → A-ARR
comp14332_c0
comp25508_c0
comp16460_c0
comp19341_c0
PP2C
comp89455_c0 → ABF
comp21829_c0 → ACS
comp585_c0 → ACO
comp30741_c0 → ETR
comp10854_c0
comp22612_c0
comp25440_c0
comp46255_c0
comp7982_c0
comp24422_c0
comp18924_c0
comp33022_c0
comp7744_c0
comp34364_c0
comp39079_c0
ERF