

Supplementary Materials

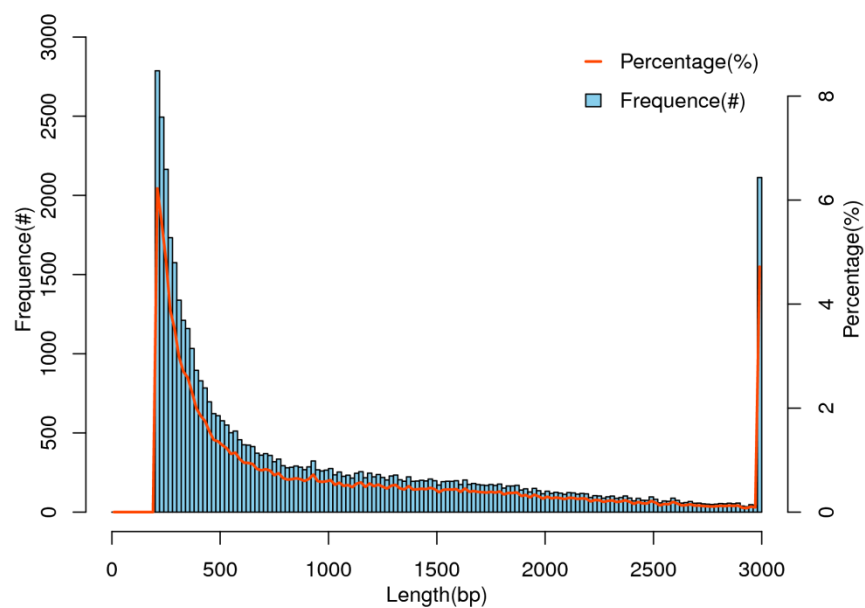


Figure S1: Length distribution of unigene.

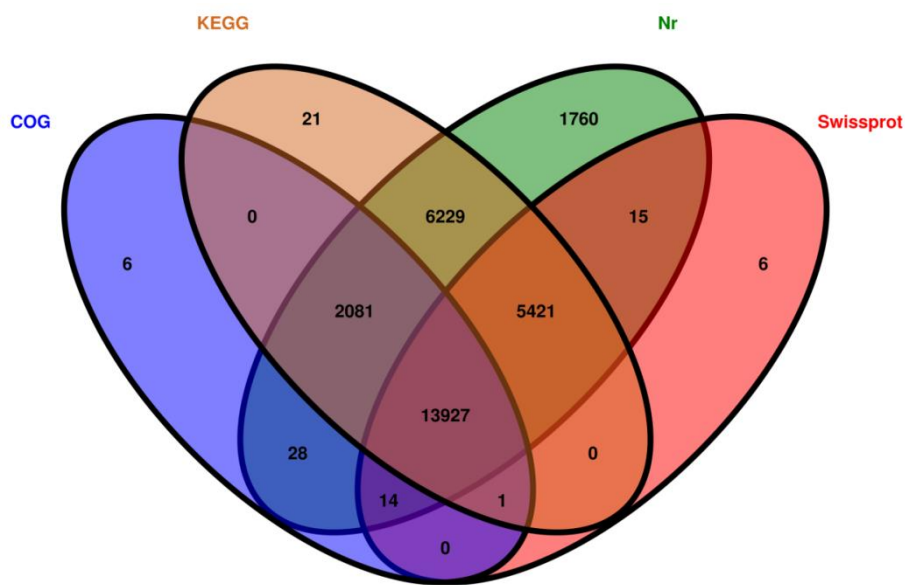


Figure S2: Basic annotation for all unigenes.

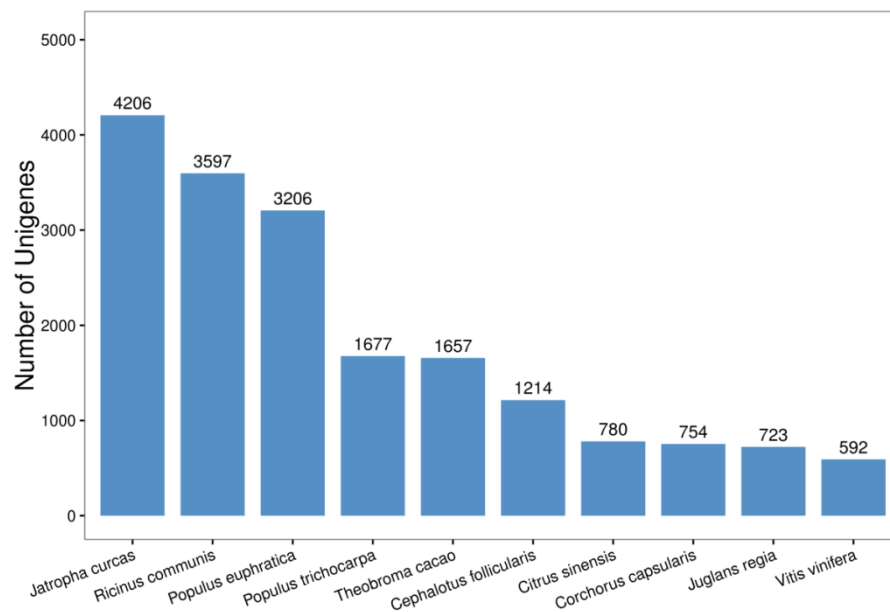


Figure S3: Top 10 plant species distribution of the total homologous sequences.

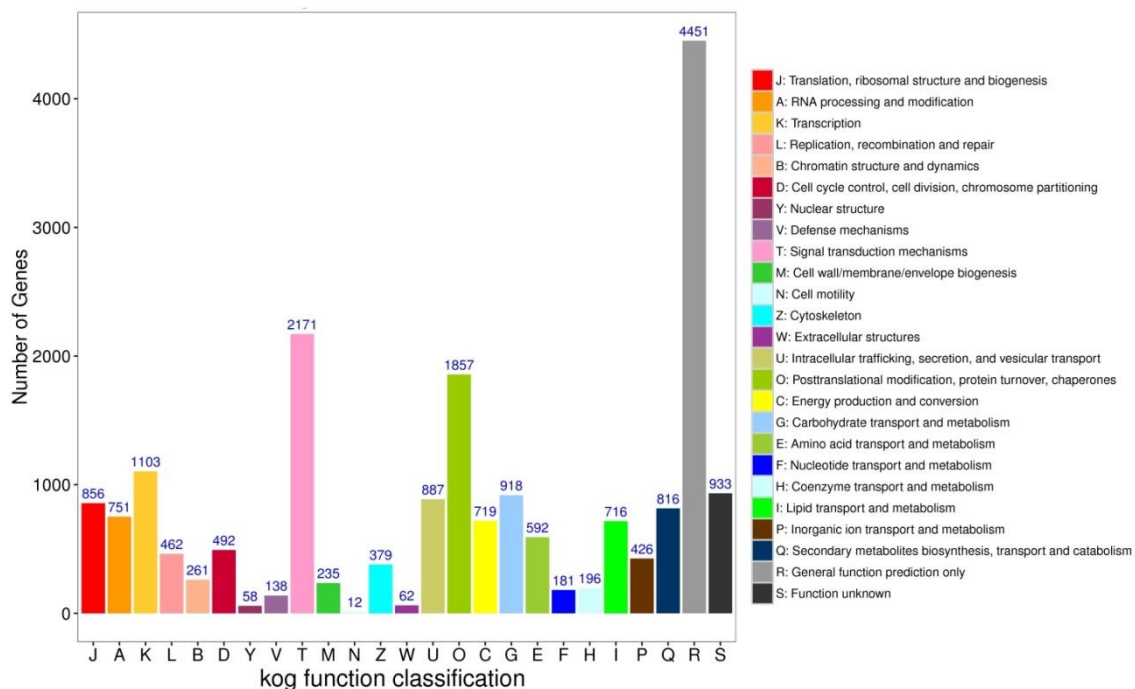


Figure S4: Distribution of unigenes in the transcriptome with KOG functional classification.

Sequences have a KOG classification among 25 categories. Note: [A] RNA processing and modification; [B] Chromatin structure and dynamics; [C] Energy production and conversion; [D] Cell cycle control, cell division, chromosome partitioning; [E] Amino acid transport and metabolism; [F] Nucleotide transport and metabolism; [G] Carbohydrate transport and metabolism; [H] Coenzyme transport and metabolism; [I] Lipid transport and metabolism; [J] Translation, ribosomal structure and biogenesis; [K] Transcription; [L] Replication, recombination and repair; [M] Cell wall/membrane/envelope biogenesis; [N] Cell motility; [O] Posttranslational modification, protein turnover, chaperones; [P] Inorganic ion transport and metabolism; [Q] Secondary metabolites biosynthesis, transport and catabolism; [R] General function

prediction only; [S] Function unknown; [T] Signal transduction mechanisms; [U] Intracellular trafficking, secretion, and vesicular transport; [V] Defense mechanisms; [W] Extracellular structures; [Y] Nuclear structure; [Z] Cytoskeleton.

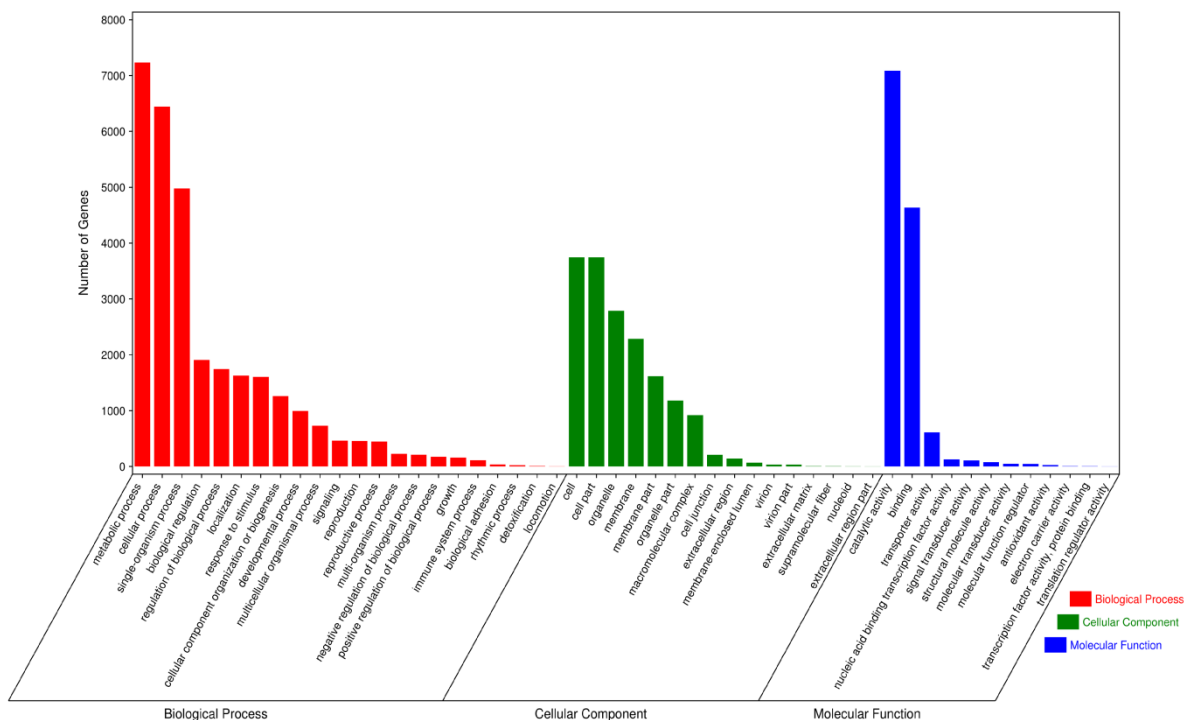


Figure S5: Functional classifications of GO terms of all assembled unigenes. Note: The results are summarized in three main categories: biological process, cellular component, and molecular function. The right y-axis indicates the number of genes in a category. The left y-axis indicates percentage of a specific category of genes.

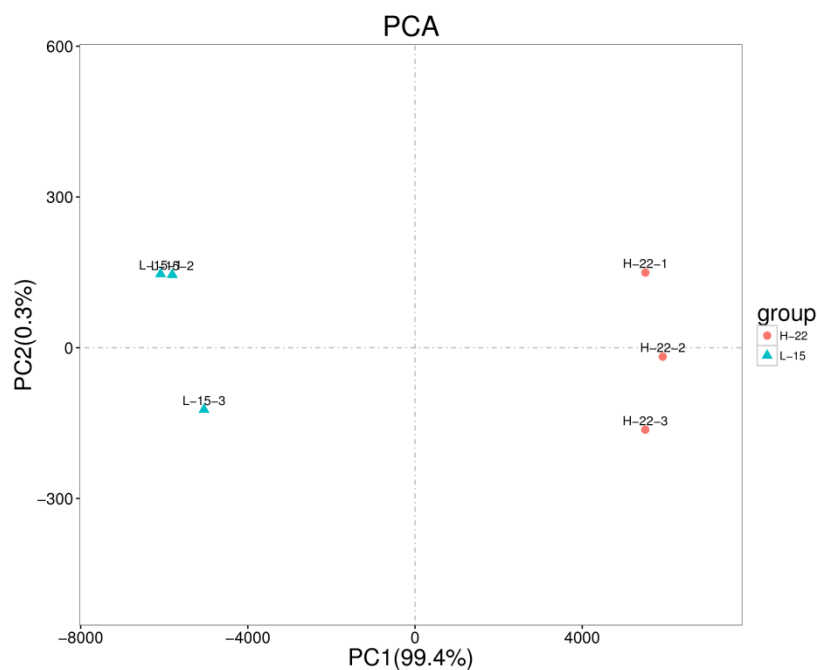


Figure S6: The PCA analysis between 15 and 22°C samples.

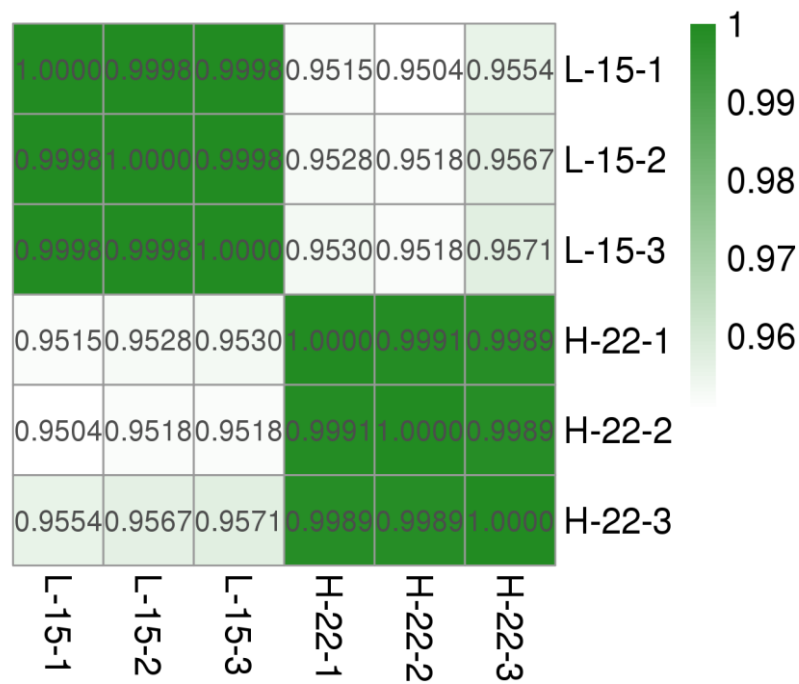


Figure S7: The correlation analysis of heat map between 15 and 22°C samples.

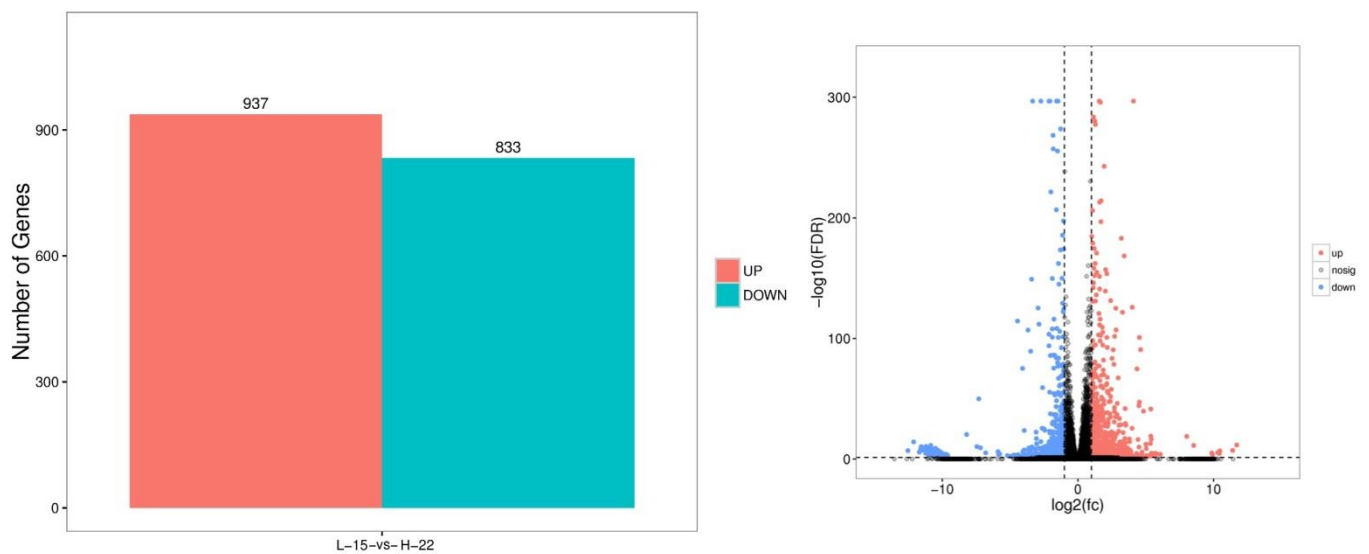


Figure S8: Number of differentially expressed genes and volcano plot when plants grown at 15 °C versus 22°C. Note: A total of 1,584 DEGs were obtained after excluding 186 repeated genes from the originally generated 1,770 genes.

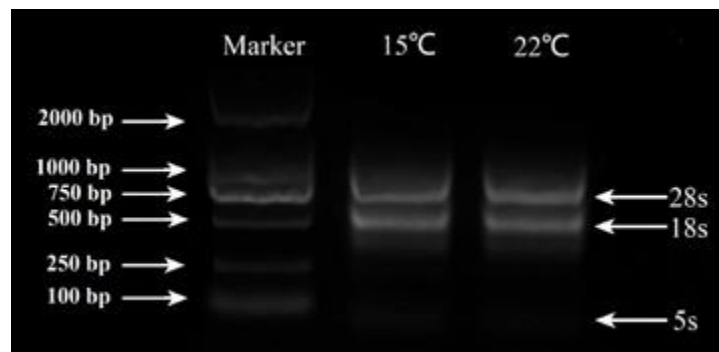


Figure S9: The quality of total RNA at 15 and 22°C was evaluated by 1.0% agarose gel electrophoresis.

Table S1: Sequences of primer employed in qRT-PCR analysis

Gene name	Primer sequences (5' to 3')	Amplicon size (bp)
<i>ACT</i>	Forward: ATCTCCGTCTTGACCTTGC Reverse: ACGATTTCCTGCTGT	104
Hyp biosynthesis (19)		
Photosynthesis		
<i>CAB</i>	Forward: TACCCAGGAGGGAGCTTTGA Reverse: ATGGCCTGCACGAAGAATCC	131
<i>CAB1</i>	Forward: GAATCTCGCCGACCACTC Reverse: GGCAAACTAGCGAGGAAAAGT	100
<i>CAB1B</i>	Forward: GGGTCTCCATGAGGAAGGTC Reverse: TGGGAATTCGCCAGTCAAGT	134
<i>CAB3</i>	Forward: AAGCCCAACTCCAGTTTCCTC Reverse: TACTTGACACGCTCTGGGC	122
<i>CAB3C</i>	Forward: GGGTGCCCTTCAGGATGTAA Reverse: CAGTGTCCTCAACCGTAGTCA	188
<i>CAB96</i>	Forward: CTATTGGGAAACCCGAGCC Reverse: GGTCTCCGGCAATTCTACAG	108
Carbohydrate metabolism		
<i>BGLU11</i>	Forward: GGCCTGATAATGCACCCCAT Reverse: GCTTTGCTTCTGCTCTGTG	100
<i>CA</i>	Forward: ACCCCGAATGCGTGTTTATG Reverse: ATATTCAACAGCGGACCCGA	106
<i>CA1</i>	Forward: GCGAAACAAACGAGCCTAA Reverse: CAACAGCAGATCCAACCCCA	126
<i>LDHA</i>	Forward: TTATGGTGGTGTCGAACCCG Reverse: AGAACCAGAACCTGGAGCTA	120
<i>GAD</i>	Forward: GAATACCATCTGCGTTGCGG Reverse: GAGTGTCCTAGCCTGTGATT	116
<i>GAPC</i>	Forward: CTAGGGCTGTTGGGATGGTG Reverse: CCGGTTGAGGTCAGGAAACA	104
<i>PGAM</i>	Forward: TGTGGAAGGCGAGAAGAACC Reverse: CCAGCTCGGTCTGTCTGTTA	140
fatty acids metabolism		
<i>BEAT</i>	Forward: CCGCTAACCGGTCCATTAGG Reverse: CGTTGCACGAACATCCATCC	109
<i>BPS</i>	Forward: ATCGGGGCAAACCCTAACAC Reverse: ATCTCGTAGAAGTGGGCCGT	116
<i>PED1</i>	Forward: TGCCCTCAGAACAGTCAAC Reverse: CGCCAATGATGTCCAACGAC	138
<i>PLDZETA1</i>	Forward: TCGGAAGTCAGCAAGCCATT Reverse: TGCTTACCATCACGTAGCC	184
Cytochrome P450		
<i>CYP75B2</i>	Forward: TTCGTTCCGTTGCTAGAGCC Reverse: TCGCCTTGATCCTCCAAC	112
<i>CYP81E1</i>	Forward: TGATCAAGCTGGCCGAGAAG Reverse: AACTCGGGGTCTGTCTCCT	149
Plant growth (6)		
<i>CYP96A15</i>	Forward: AAGAGCTTGGGACACCTTCG Reverse: ATTGTTTCGGTCAGCCCTGT	148
<i>EMS1</i>	Forward: TCCTCAAGACCCTCTCCTCG Reverse: GCTATCCTCATTCGCCTGCT	184
<i>GEM</i>	Forward: ATCAGCAAGGAACGAAGGT Reverse: CGTTCCAGCTATGGGTCCAG	141
<i>MIZ1</i>	Forward: GGAATGGGGTTGGTTCGGAT Reverse: AACCCCGTACCCTGACTTCT	120
<i>SBT1.1</i>	Forward: CATGTACGCTGCAATGTCCG Reverse: CGTCTTCGATAGGGGAGTGC	164
<i>ZOG1</i>	Forward: CTAACGCCGAGTCCTACACC Reverse: CCTTCAAGCGAAGGGATGGT	121
Stress response (12)		
Heat shock protein and cold responsive protein		
<i>HSP70</i>	Forward: GACGACGCCTTCTTACGTGG Reverse: ATCGAAGACGGTGTTGACGG	100
<i>HSC-1</i>	Forward: GCTACCTCCAGCCGACAAAA Reverse: TCCATCGAACCACCATCAGC	186
<i>HSC-2</i>	Forward: CCAATGGCTTGATGGCAACC Reverse: AACTTCATCGTCCATCGGGG	145
<i>COR413IM1</i>	Forward: TGACCACCAGCGAGAAGAAG Reverse: TTGCAGTCCCCTTGGTAGC	168

<i>CRPK1</i>	Forward: TGTAGCTAGAGGGCTCGCAT Reverse: CTGGAATCAACTTGGCCAGC	140
<i>BAP1</i>	Forward: GAAGTCCACGAGAGCGGATT Reverse: CGGGTGTGTAGTCTCCCAAG	188
Transcription factor		
<i>ERF5</i>	Forward: GGTGACGGAGAGGAGACACT Reverse: ATCAACCGCCGTGTCATAGG	127
<i>ERF020</i>	Forward: ACGACTCTGGCTCGGTACTT Reverse: AAGGCAGCATCAGAGGGAAG	122
<i>MYB4</i>	Forward: CGTGAAACTTGGCGGCTACT Reverse: GATGGGTGTGCCAGTGATTC	143
<i>MYB14</i>	Forward: TCCTCAGCCACATGACACAG Reverse: GAGTCCGCGTTTTCGCTTAC	192
<i>NAC071</i>	Forward: AACGGGACATGGAGTGGTTC Reverse: GTAGCCTTCCAGTACCCAGC	100
<i>WRKY24</i>	Forward: CAATGAAGCGCCACGAAGAG Reverse: GTCCTCTGACCTCTCGACT	179

Table S2: Summary of sequencing data of *H. perforatum* transcriptome

	15°C	22°C
Unfiltered data		
Data of reads number (million)	39.44	45.60
Reads length	150	150
GC (%)	51.40	51.30
Data of reads number×read length (million)	5,916	6,840
Q20(%)	96.97	97.68
Q30(%)	92.26	93.50
Filtered data¹		
Data of reads number (million)	39.36	45.54
Data of reads number×read length (million)	5,879	6,802
GC (%)	51.38	51.29
Q20(%)	97.06	97.75
Q30(%)	92.38	93.59
Mapped data²		
Data of unique mapped reads (million)	28.60	33.37
Data of multiple mapped reads (million)	2.48	2.90
Mapping ratio (%)	78.96	79.64
Compiled data		
Total number of unigenes	44,776	
Total Length (bp) (million)	44.86	
N50 (bp)	1,694	
Max length (bp)	15,636	
Min length (bp)	201	
Average Length (bp)	1,001	
GC content (%)	46.00	

¹ Reads with a quality score < 30 and length < 60 bp were excluded;

² Mapping ratio = (Unique mapped reads + Multiple mapped reads) / Filtered reads

Table S3: Database searches for collected *H. perforatum* nucleotide sequences

BLASTx searching against specific platforms	Values	Percentage (%)
NR	29,475	65.83
SwissProt	19,384	43.29
KOG	16,057	35.86
KEGG	27,680	61.82
GO	12,038	26.88

Table S4: Photosynthesis genes differentially expressed at 15 versus 22°C

Gene name	Protein name	log ² Ratio (15°C _{RPKM} /22°C _{RPKM})
<i>CAB1</i>	Chlorophyll a-b binding of LHCII type 1 protein	1.18
<i>CAB1B</i>	Chlorophyll a-b binding protein 1B, chloroplastic	1.26
<i>CAB3</i>	Chlorophyll a-b binding protein 3, chloroplastic	1.13
<i>CAB3C</i>	Chlorophyll a-b binding protein 3C, chloroplastic	1.46
<i>CAB96</i>	Chlorophyll a-b binding protein AB96	1.16
<i>CAB</i>	Chlorophyll a-b binding protein, chloroplastic	1.42
<i>ELI_PEA</i>	Early light-induced protein, chloroplastic	1.97
<i>ELIP2</i>	Early light-induced protein 2, chloroplastic	-1.80
<i>OHP2</i>	Light-harvesting complex-like protein OHP2, chloroplastic	1.60
<i>RBCS-C</i>	Ribulose biphosphate carboxylase small chain C, chloroplastic	1.45
<i>RCA</i>	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic	-1.23
<i>RBCS-8B</i>	Ribulose biphosphate carboxylase small chain 8B, chloroplastic	-2.69

Table S5: Carbohydrate metabolism genes differentially expressed at 15 versus 22°C

Gene name	Protein name	log ² Ratio (15°C _{RPKM} /22°C _{RPKM})
<i>CA</i>	Carbonic anhydrase, chloroplastic	1.43
<i>CA1</i>	Carbonic anhydrase 1	1.23
<i>LDHA</i>	L-lactate dehydrogenase A	2.47
<i>PGAM</i>	Phosphoglycerate mutase-like protein	1.31
<i>AGLU2</i>	Alpha-glucosidase 2	1.16
<i>BGLU11</i>	Beta-glucosidase 11	1.38
<i>GINT1</i>	Glucosamine inositolphosphorylceramide transferase 1	-1.18
<i>GAD</i>	Glutamate decarboxylase	1.15
<i>GAPC</i>	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	1.84
<i>NonBGLU</i>	Non-cyanogenic beta-glucosidase	1.08
<i>TOGT1</i>	Scopoletin glucosyltransferase	1.14
<i>GAE6</i>	UDP-glucuronate 4-epimerase 6	-1.33
<i>USP1</i>	UDP-sugar pyrophosphorylase 1	-1.30

Table S6: Fatty acids metabolism genes differentially expressed at 15 versus 22°C

Gene name	Protein name	log ² Ratio (15°C _{RPKM} /22°C _{RPKM})
<i>FAD3</i>	Acyl-lipid omega-3 desaturase (cytochrome b5), endoplasmic reticulum	1.04
<i>YLR118C</i>	Acyl-protein thioesterase 1	1.59
<i>abhd17c</i>	Alpha/beta hydrolase domain-containing protein 17C	-1.29
<i>HOS3</i>	Elongation of fatty acids protein 3-like	1.81
<i>FAR3</i>	Fatty acyl-CoA reductase 3	-1.11
<i>MGD3</i>	Monogalactosyldiacylglycerol synthase 3, chloroplastic	1.22
<i>At1g06800</i>	Phospholipase A1-Igamma1, chloroplastic	2.41
<i>At4g16820</i>	Phospholipase A1-Ibeta2, chloroplastic	1.87
<i>PLDZETA1</i>	Phospholipase D zeta 1	1.69
<i>PLD1</i>	Phospholipase D alpha 1	1.27
<i>SQD2</i>	Sulfoquinovosyl transferase SQD2	1.11
<i>LIP2</i>	Triacylglycerol lipase 2	-1.11
<i>BEAT</i>	Acetyl-CoA-benzylalcohol acetyltransferase	1.45
<i>BPS</i>	2,4,6-trihydroxybenzophenone synthase	1.74
<i>PED1</i>	3-ketoacyl-CoA thiolase 2, peroxisomal	1.04

Table S7: Cytochrome P450 genes differentially expressed at 15 versus 22°C

Gene name	Protein name	log ² Ratio (15°C _{RPKM} /22°C _{RPKM})
<i>CYP71A6</i>	Cytochrome P450 71A6	0.08
<i>CYP71A9</i>	Cytochrome P450 71A9	1.59
<i>CYP78A5</i>	Cytochrome P450 78A5	-2.31
<i>CYP82A1</i>	Cytochrome P450 82A1	2.17
<i>CYP82A3</i>	Cytochrome P450 82A3	-1.41
<i>CYP89A9</i>	Cytochrome P450 89A9	1.94
<i>CYP86B1</i>	Cytochrome P450 86B1	2.82
<i>CYP90B1</i>	Cytochrome P450 90B1	-1.11
<i>CYP94B1</i>	Cytochrome P450 94B1	1.79
<i>CYP96A15</i>	Alkane hydroxylase MAH1	1.37
<i>CYP714C2</i>	Cytochrome P450 714C2	1.22
<i>CYP81D1</i>	Cytochrome P450 81D1	1.86
<i>CYP81E8</i>	Cytochrome P450 81E8	0.53
<i>CYP716B1</i>	Cytochrome P450 716B1	1.22
<i>CYP736A12</i>	Cytochrome P450 CYP736A12	1.04
<i>CYP749A22</i>	Cytochrome P450 CYP749A22	-1.33
<i>CYP82D47</i>	Cytochrome P450 CYP82D47	1.80
<i>CYP75B2</i>	Flavonoid 3'-monooxygenase	1.19
<i>CYP93B1</i>	Licodione synthase	1.50
<i>CYP81E9</i>	Isoflavone 3'-hydroxylase	4.31

Table S8: Morpho-physiological traits genes differentially expressed at 15 versus 22 °C

Gene name	Protein name	log ² Ratio (15 °C _{RPKM} /22 °C _{RPKM})
<i>ZOG1</i>	Zeatin O-glucosyltransferase	-1.29
<i>DCR</i>	BAHD acyltransferase DCR	-1.33
<i>CYP96A15</i>	Alkane hydroxylase MAH1	1.37
<i>MIZ1</i>	Protein MIZU-KUSSEI 1	-0.09
<i>GEM</i>	GLABRA2 expression modulator	-1.02
<i>CET1</i>	CEN-like protein 1	1.54
<i>FPF1</i>	Flowering-promoting factor 1	-3.26
<i>FTIP1</i>	FT-interacting protein 1	1.47
<i>HD3B</i>	Protein HEADING DATE 3B	-1.25
<i>SWC6</i>	SWR1 complex subunit 6	-1.23
<i>SBT1.9</i>	Subtilisin-like protease SBT1.9	1.07
<i>SBT3.18</i>	Subtilisin-like protease SBT3.18	2.69
<i>SBT11.1</i>	Subtilisin-like protease SBT1.1	2.17
<i>EMS1</i>	Leucine-rich repeat receptor protein kinase EMS1	2.19
<i>MSP1</i>	Leucine-rich repeat receptor protein kinase MSP1	1.04

Table S9: Heat shock protein and cold responsive protein genes differentially expressed at 15 versus 22 °C

Gene name	Protein name	log ² Ratio (15 °C _{RPKM} /22 °C _{RPKM})
<i>HSP15.7</i>	15.7 kDa heat shock protein, peroxisomal	-2.39
<i>HSP17.3-B</i>	17.3 kDa class I heat shock protein	-1.60
<i>HSP17.4B</i>	17.4 kDa class III heat shock protein	-2.99
<i>HSP17.9-D</i>	17.9 kDa class II heat shock protein	-2.60
<i>HSP18.2</i>	18.2 kDa class I heat shock protein	-1.61
<i>HSP22.0</i>	22.0 kDa class IV heat shock protein	-1.83
<i>HSP70-8</i>	Heat shock 70 kDa protein 8	-1.15
<i>HSP70</i>	Heat shock cognate 70 kDa protein	-1.64
<i>HSC-I</i>	Heat shock cognate 70 kDa protein 1	-3.68
<i>HSC-2</i>	Heat shock cognate 70 kDa protein 2	-3.33
<i>HSF30</i>	Heat shock factor protein HSF30	-1.76
<i>HSP81-1</i>	Heat shock protein 81-1	-1.02
<i>HSP83A</i>	Heat shock protein 83	-2.73
<i>HSP21</i>	Small heat shock protein, chloroplastic	-2.69
<i>HSA32</i>	Protein HEAT-STRESS-ASSOCIATED 32	-1.57
<i>BAP1</i>	BON1-associated protein 1	1.43

<i>COR413IM1</i>	Cold-regulated 413 inner membrane protein 1, chloroplastic	1.29
<i>CRPK1</i>	Cold-responsive protein kinase 1	1.22

Table S10: Transcription factors differentially expressed at 15 versus 22°C

Gene name	Protein name	log ² Ratio (15°C _{RPKM} /22°C _{RPKM})
Myb family transcription factor		
<i>PHL5</i>	Myb family transcription factor PHL5	-1.27
<i>MYB2</i>	Transcription factor MYB2	-3.01
<i>MYB3</i>	Transcription factor MYB3	-1.05
<i>MYB4</i>	Transcription factor MYB4	2.48
<i>MYB14</i>	Transcription factor MYB14	1.40
<i>MYB17</i>	Transcription factor MYB17	1.82
<i>MYB48</i>	Transcription factor MYB48	10.44
<i>MYB52</i>	Transcription factor MYB52	-1.02
<i>MYB62</i>	Transcription factor MYB62	-1.36
<i>MYB73</i>	Transcription factor MYB73	-1.08
<i>MYB78</i>	Transcription factor MYB78	1.53
<i>MYB108</i>	Transcription factor MYB108	1.15
MADS-box transcription factor		
<i>AGL80</i>	Agamous-like MADS-box protein AGL80	-1.32
<i>SVP</i>	MADS-box protein SVP	-1.26
<i>CMB1</i>	MADS-box protein CMB1	-2.85
<i>MADS50</i>	MADS-box transcription factor 50	-2.09
Transcription factor bHLHs		
<i>BHLH62</i>	Transcription factor bHLH62	-1.10
<i>BHLH92</i>	Transcription factor bHLH92	1.11
<i>BHLH96</i>	Transcription factor bHLH96	-1.30
<i>BHLH154</i>	Transcription factor bHLH154	-1.35
<i>BHLH162</i>	Transcription factor bHLH162	2.64
Transcription factor TCPs		
<i>TCP1</i>	Transcription factor TCP1	-1.60
<i>TCP12</i>	Transcription factor TCP12	-2.00
<i>TCP20</i>	Transcription factor TCP20	-1.00
WRKY transcription factor		
<i>WRKY7</i>	Probable WRKY transcription factor 7	1.56
<i>WRKY40</i>	Probable WRKY transcription factor 40	2.16
<i>WRKY41</i>	Probable WRKY transcription factor 41	2.18
<i>WRKY53</i>	Probable WRKY transcription factor 53	3.02
<i>WRKY72</i>	Probable WRKY transcription factor 72	1.53
<i>WRKY6</i>	WRKY transcription factor 6	1.11
<i>WRKY28</i>	WRKY transcription factor 28	1.75
<i>WRKY55</i>	WRKY transcription factor 55	2.83

<i>WRKY24</i>	WRKY transcription factor WRKY24	1.52
bZIP transcription factor		
<i>BZIP44</i>	bZIP transcription factor 44	-1.12
<i>BZIP61</i>	Basic leucine zipper 61	-1.04
<i>TGA10</i>	bZIP transcription factor TGA10	-1.37
Ethylene-responsive transcription factor		
<i>At1g50680</i>	AP2/ERF and B3 domain-containing transcription factor At1g50680	-0.52
<i>At1g51120</i>	AP2/ERF and B3 domain-containing transcription factor At1g51120	-1.32
<i>ERF2</i>	Ethylene-responsive transcription factor 2	4.72
<i>ERF2</i>	Ethylene-responsive transcription factor 2	1.93
<i>ERF5</i>	Ethylene-responsive transcription factor 5	1.89
<i>ABR1</i>	Ethylene-responsive transcription factor ABR1	1.32
<i>ERF003</i>	Ethylene-responsive transcription factor ERF003	-1.34
<i>ERF013</i>	Ethylene-responsive transcription factor ERF013	-1.22
<i>ERF017</i>	Ethylene-responsive transcription factor ERF017	3.03
<i>ERF020</i>	Ethylene-responsive transcription factor ERF020	4.50
<i>ERF071</i>	Ethylene-responsive transcription factor ERF071	3.06
<i>ERF095</i>	Ethylene-responsive transcription factor ERF095	4.00
<i>ERF109</i>	Ethylene-responsive transcription factor ERF109	2.48
NAC domain-containing protein		
<i>NAC014</i>	NAC domain-containing protein 14	1.10
<i>NAC043</i>	NAC domain-containing protein 43	-1.16
<i>NAC048</i>	NAC domain-containing protein 48	2.19
<i>NAC071</i>	NAC domain-containing protein 71	2.54
<i>NAC087</i>	NAC domain-containing protein 87	1.15
<i>NAC090</i>	NAC domain-containing protein 90	4.53
<i>NAC100</i>	NAC domain-containing protein 100	-0.76
