

Supplementary Table 1. The Primer pairs of key flowering-related genes

Name	Forward primers	Reverse primers
<i>TUB</i>	TGACATTGAGCGCCCAACTTACA	ATCCACATTTCAGAGCACCATCGA
<i>CO</i>	GCACTTGAAGTTGGATTTGGT	GTTGGTCCGTTGATTGTCTG
<i>FT</i>	CGTATGCCACCACCTCAGA	CGTGATGGTGGACCCTGAT
<i>SOC1</i>	TCCTGCTCCCTCAACTCCA	GCAACTGGAGAAGAGCCTGA
<i>FLC</i>	CCTACCCTCGTCGCTCAAA	CCTTCCATCTGCTCATCCGT

Supplementary Table 2. Summary of RNA-Seq libraries for five biological replicates of the shoot buds at different growth stages of *Pleioblastus pygmaeus*

Sample	Raw Reads	Clean Reads	Clean Bases(G)	GC Content(%)	Q20(%)	Q30(%)
FE	58451642	54594345	8.19	51.84	95.91	90.16
FM	71934308	67682112	10.15	52.34	97.20	92.80
FL	61003625	56959102	8.54	50.40	95.93	90.12
NE	56978490	52944336	7.94	52.10	96.01	90.24
NM	63210037	59747064	8.96	51.64	95.95	90.11
NL	60205278	56415252	8.46	51.11	95.93	90.17

Note: Q20/30: The percentage of the bases with phred values greater than 20/30 accounted for the total bases, Qphred = $-10 \log_{10}(e)$.

Supplementary Table 3. Function annotation of the transcriptomes of the shoot buds at different growth stages of *Pleioblastus pygmaeus* in different databases

Database	Annotated number	Percentage (%)
Annotated in NR	201547	55.24
Annotated in NT	199699	54.73
Annotated in KO	76768	21.04
Annotated in SwissProt	144866	39.70
Annotated in PFAM	147740	40.49
Annotated in GO	154573	42.36
Annotated in KOG	54875	15.04
Annotated in all Databases	30935	8.47
Total unigene	364840	100.00

Supplementary Table 4. Differential expressed unigenes based on KEGG function annotation in transcriptome comparison of FE (dormant shoot bud of flowering plant) vs NE (dormant shoot bud of vegetative plant)

Pathway-term	Classification	Gene number
Plant hormone signal transduction	Environmental Information Processing	511
Spliceosome	Genetic Information Processing	539
Protein processing in endoplasmic reticulum	Genetic Information Processing	502
RNA transport	Genetic Information Processing	436
mRNA surveillance pathway	Genetic Information Processing	358
DNA replication	Genetic Information Processing	210
Nucleotide excision repair	Genetic Information Processing	204
Homologous recombination	Genetic Information Processing	187
Mismatch repair	Genetic Information Processing	155
SNARE interactions in vesicular transport	Genetic Information Processing	84
Starch and sucrose metabolism	Metabolism	424
Purine metabolism	Metabolism	385
Amino sugar and nucleotide sugar metabolism	Metabolism	325
Fatty acid degradation	Metabolism	166
Fatty acid biosynthesis	Metabolism	122
Nitrogen metabolism	Metabolism	77
Tropane, piperidine and pyridine alkaloid biosynthesis	Metabolism	55
Photosynthesis - antenna proteins	Metabolism	38
Synthesis and degradation of ketone bodies	Metabolism	30
Brassinosteroid biosynthesis	Metabolism	28

Supplementary Table 5. Differential expressed unigenes based on KEGG function annotation in transcriptome comparison of FM (Germinated shoot of flowering plant) vs. NM (Germinated shoot of vegetative plant)

Pathway-term	Classification	Gene number
Phagosome	Cellular Processes	163
Plant hormone signal transduction	Environmental Information Processing	372
Protein processing in endoplasmic reticulum	Genetic Information Processing	412
Spliceosome	Genetic Information Processing	384
mRNA surveillance pathway	Genetic Information Processing	269
DNA replication	Genetic Information Processing	176
Nucleotide excision repair	Genetic Information Processing	158
Proteasome	Genetic Information Processing	124
Mismatch repair	Genetic Information Processing	122
Starch and sucrose metabolism	Metabolism	317
Phenylpropanoid biosynthesis	Metabolism	248
Amino sugar and nucleotide sugar metabolism	Metabolism	246
Fatty acid degradation	Metabolism	140
Fatty acid biosynthesis	Metabolism	103
alpha-Linolenic acid metabolism	Metabolism	90
Flavonoid biosynthesis	Metabolism	39
Sesquiterpenoid and triterpenoid biosynthesis	Metabolism	34
Photosynthesis - antenna proteins	Metabolism	34
Stilbenoid, diarylheptanoid and gingerol biosynthesis	Metabolism	30
Circadian rhythm - plant	Organismal Systems	86

Supplementary Table 6. Differential expressed unigenes based on KEGG function annotation in transcriptome comparison of FL (Flower bud of flowering plant) vs. NL (Leaf bud of vegetative plant)

Pathway-term	Classification	Gene number
Plant hormone signal transduction	Environmental Information Processing	341
Ribosome	Genetic Information Processing	618
Spliceosome	Genetic Information Processing	389
mRNA surveillance pathway	Genetic Information Processing	278
Proteasome	Genetic Information Processing	159
Oxidative phosphorylation	Metabolism	301
Pyruvate metabolism	Metabolism	242
Glyoxylate and dicarboxylate metabolism	Metabolism	206
Carbon fixation in photosynthetic organisms	Metabolism	201
Citrate cycle (TCA cycle)	Metabolism	179
Alanine, aspartate and glutamate metabolism	Metabolism	147
Fatty acid degradation	Metabolism	146
beta-Alanine metabolism	Metabolism	122
Fatty acid biosynthesis	Metabolism	109
Lysine degradation	Metabolism	102
Propanoate metabolism	Metabolism	98
Photosynthesis	Metabolism	97
Photosynthesis - antenna proteins	Metabolism	52
Limonene and pinene degradation	Metabolism	45
Circadian rhythm - plant	Organismal Systems	98

Supplementary Table 7. Differential expressed unigenes based on KEGG function annotation in transcriptome comparison of FE (Dormant shoot bud of flowering plant) vs. FM (Germinated shoot of flowering plant)

Pathway-term	Classification	Gene number
Plant hormone signal transduction	Environmental Information Processing	543
Spliceosome	Genetic Information Processing	565
mRNA surveillance pathway	Genetic Information Processing	404
Ribosome biogenesis in eukaryotes	Genetic Information Processing	278
Nucleotide excision repair	Genetic Information Processing	238
DNA replication	Genetic Information Processing	218
Base excision repair	Genetic Information Processing	141
Starch and sucrose metabolism	Metabolism	546
Phenylpropanoid biosynthesis	Metabolism	427
Amino sugar and nucleotide sugar metabolism	Metabolism	405
Glutathione metabolism	Metabolism	238
Cyanoamino acid metabolism	Metabolism	135
Photosynthesis	Metabolism	134
Fatty acid elongation	Metabolism	114
Photosynthesis - antenna proteins	Metabolism	66
Flavonoid biosynthesis	Metabolism	58
Sesquiterpenoid and triterpenoid biosynthesis	Metabolism	54
Stilbenoid, diarylheptanoid and gingerol biosynthesis	Metabolism	44
Flavone and flavonol biosynthesis	Metabolism	12
Circadian rhythm - plant	Organismal Systems	131

Supplementary Table 8. Differential expressed unigenes based on KEGG function annotation in transcriptome comparison of NE (Dormant shoot bud of vegetative plant) vs. NM (Germinated shoot of vegetative plant)

Pathway-term	Classification	Gene number
Phagosome	Cellular Processes	153
Plant hormone signal transduction	Environmental Information Processing	328
DNA replication	Genetic Information Processing	153
Proteasome	Genetic Information Processing	107
Starch and sucrose metabolism	Metabolism	371
Phenylpropanoid biosynthesis	Metabolism	289
Amino sugar and nucleotide sugar metabolism	Metabolism	252
Cysteine and methionine metabolism	Metabolism	190
Glutathione metabolism	Metabolism	150
Citrate cycle (TCA cycle)	Metabolism	148
Galactose metabolism	Metabolism	126
alpha-Linolenic acid metabolism	Metabolism	82
Steroid biosynthesis	Metabolism	79
Carotenoid biosynthesis	Metabolism	67
Flavonoid biosynthesis	Metabolism	44
Diterpenoid biosynthesis	Metabolism	32
Sesquiterpenoid and triterpenoid biosynthesis	Metabolism	32
Stilbenoid, diarylheptanoid and gingerol biosynthesis	Metabolism	31
Other types of O-glycan biosynthesis	Metabolism	15
Flavone and flavonol biosynthesis	Metabolism	11

Supplementary Table 9. The significantly enriched pathway-terms in transcriptome comparisons of
Pleuroblastus pygmaeus

Pathway-term	FE vs NE q-value	FM vs NM q-value	FL vs NL q-value	FE vs FM q-value	NE vs NM q-value
Circadian rhythm - plant	1.00	0.29	0.04	0.11	1.00
Plant hormone signal transduction	3.06E-09	1.34E-04	0.15	1.33E-04	1.08E-04
Protein processing in endoplasmic reticulum	0.86	0.19	1.00	1.00	1.00
Starch and sucrose metabolism	0.04	0.29	1.00	5.60E-05	1.27E-10

Supplementary Table 10. Flowering-related unigenes identified in different flowering pathways of *Pleioblastus pygmaeus*

Gene	Main participation way	Unigene number
<i>ADO1</i>	photoperiod pathway	3
<i>APL</i>	photoperiod pathway	83
<i>BBX19</i>	photoperiod pathway	4
<i>BHLH122</i>	photoperiod pathway	1
<i>CCA1</i>	photoperiod pathway	25
<i>CDF1</i>	photoperiod pathway	1
<i>CDF2</i>	photoperiod pathway	11
<i>CDF3</i>	photoperiod pathway	4
<i>CDF4</i>	photoperiod pathway	2
<i>CDF5</i>	photoperiod pathway	1
<i>CKB3</i>	photoperiod pathway	6
<i>CO</i>	photoperiod pathway	6
<i>COL5</i>	photoperiod pathway	13
<i>COL9</i>	photoperiod pathway	9
<i>COP1</i>	photoperiod pathway	17
<i>COP11</i>	photoperiod pathway	2
<i>CPK33</i>	photoperiod pathway	1
<i>CPK6</i>	photoperiod pathway	3
<i>CRY1</i>	photoperiod pathway	23
<i>CRY2</i>	photoperiod pathway	13
<i>ELF3</i>	photoperiod pathway	15
<i>ELF4</i>	photoperiod pathway	10
<i>ESD4</i>	photoperiod pathway	17
<i>FIO1</i>	photoperiod pathway	5
<i>FLR1</i>	photoperiod pathway	1
<i>FRS6</i>	photoperiod pathway	37
<i>FRS8</i>	photoperiod pathway	2
<i>FYPP3</i>	photoperiod pathway	2
<i>GI</i>	photoperiod pathway	22
<i>HAP2B</i>	photoperiod pathway	16
<i>HOS1</i>	photoperiod pathway	7
<i>LHY</i>	photoperiod pathway	19
<i>LWD1</i>	photoperiod pathway	9
<i>MED25</i>	photoperiod pathway	20
<i>MFT</i>	photoperiod pathway	11
<i>PCL1</i>	photoperiod pathway	26
<i>PFT1</i>	photoperiod pathway	1
<i>PHYA</i>	photoperiod pathway	19
<i>PHYB</i>	photoperiod pathway	35
<i>PHYC</i>	photoperiod pathway	9
<i>PHYE</i>	photoperiod pathway	1

<i>PIF1</i>	photoperiod pathway	50
<i>PIF3</i>	photoperiod pathway	8
<i>PIL1</i>	photoperiod pathway	4
<i>RUP1</i>	photoperiod pathway	1
<i>RVE2</i>	photoperiod pathway	8
<i>SRR1</i>	photoperiod pathway	2
<i>TCP21</i>	photoperiod pathway	6
<i>TFL1</i>	photoperiod pathway	1
<i>TGA4</i>	photoperiod pathway	22
<i>VOZ1</i>	photoperiod pathway	20
<i>ZTL</i>	photoperiod pathway	13
<i>CDC73</i>	vernalization pathway	12
<i>CUL3A</i>	vernalization pathway	10
<i>ICE1</i>	vernalization pathway	13
<i>POB1</i>	vernalization pathway	26
<i>VIL1</i>	vernalization pathway	8
<i>VIL3</i>	vernalization pathway	2
<i>VIN3</i>	vernalization pathway	14
<i>VIP1</i>	vernalization pathway	67
<i>VIP2</i>	vernalization pathway	34
<i>VIP3</i>	vernalization pathway	15
<i>VIP4</i>	vernalization pathway	11
<i>VRN1</i>	vernalization pathway	1
<i>VRN2</i>	vernalization pathway	1
<i>WDR5A</i>	vernalization pathway	6
<i>WRKY34</i>	vernalization pathway	2
<i>FES1</i>	vernalization pathway	16
<i>FLC</i>	vernalization pathway	49
<i>FRI</i>	vernalization pathway	5
<i>SUF4</i>	vernalization pathway	6
<i>FCA</i>	autonomous pathway	12
<i>FLK</i>	autonomous pathway	39
<i>FPA</i>	autonomous pathway	15
<i>FVE</i>	autonomous pathway	6
<i>FY</i>	autonomous pathway	11
<i>LD</i>	autonomous pathway	10
<i>RGA1</i>	gibberellins pathway	184
<i>RGA2</i>	gibberellins pathway	229
<i>RGA3</i>	gibberellins pathway	277
<i>RGA4</i>	gibberellins pathway	199
<i>RGA5</i>	gibberellins pathway	3
<i>ADC2</i>	gibberellins pathway	2
<i>GA20OX2</i>	gibberellins pathway	1
<i>GA2OX1</i>	gibberellins pathway	32

<i>GA2OX2</i>	gibberellins pathway	6
<i>GA2OX8</i>	gibberellins pathway	15
<i>GAI</i>	gibberellins pathway	8
<i>GASA4</i>	gibberellins pathway	1
<i>GASA5</i>	gibberellins pathway	7
<i>GID1B</i>	gibberellins pathway	3
<i>GID1C</i>	gibberellins pathway	3
<i>KAOI</i>	gibberellins pathway	15
<i>RGL1</i>	gibberellins pathway	3
<i>SLY1</i>	gibberellins pathway	9
<i>SNE</i>	gibberellins pathway	2
<i>SPY</i>	gibberellins pathway	24
<i>SPL1</i>	age pathway	13
<i>SPL2</i>	age pathway	6
<i>SPL3</i>	age pathway	6
<i>SPL4</i>	age pathway	9
<i>SPL5</i>	age pathway	4
<i>SPL6</i>	age pathway	10
<i>SPL7</i>	age pathway	7
<i>SPL8</i>	age pathway	6
<i>SPL9</i>	age pathway	16
<i>SPL10</i>	age pathway	6
<i>SPL11</i>	age pathway	10
<i>SPL12</i>	age pathway	13
<i>SPL13</i>	age pathway	2
<i>SPL14</i>	age pathway	8
<i>SPL15</i>	age pathway	9
<i>SPL16</i>	age pathway	8
<i>SPL17</i>	age pathway	9
<i>SPL18</i>	age pathway	14
<i>SPL19</i>	age pathway	7
<i>SPL21</i>	age pathway	3
<i>TPL</i>	age pathway	13
<i>AP51</i>	pentose phosphate pathway	29
<i>PGII</i>	pentose phosphate pathway	33
<i>PGM1</i>	pentose phosphate pathway	3
<i>SUS4</i>	pentose phosphate pathway	6
<i>AP1</i>	flowering signal integrator	3
<i>AP2</i>	flowering signal integrator	52
<i>FD</i>	flowering signal integrator	3
<i>FT</i>	flowering signal integrator	36
<i>LFY</i>	flowering signal integrator	1
<i>SOC1</i>	flowering signal integrator	21
<i>TSF</i>	flowering signal integrator	7
