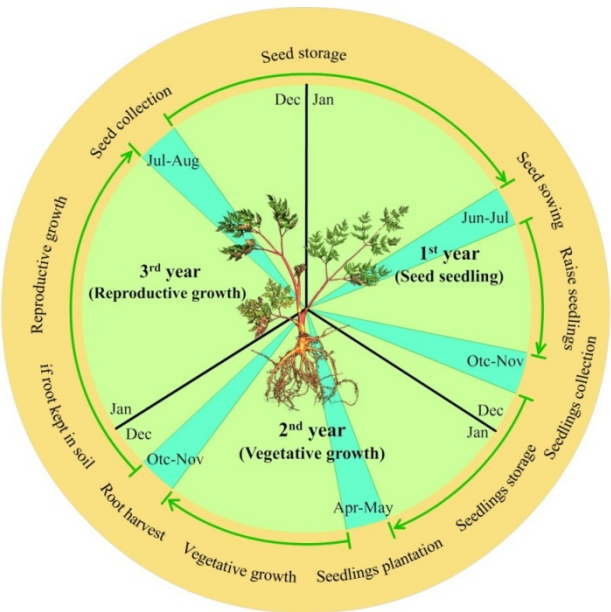
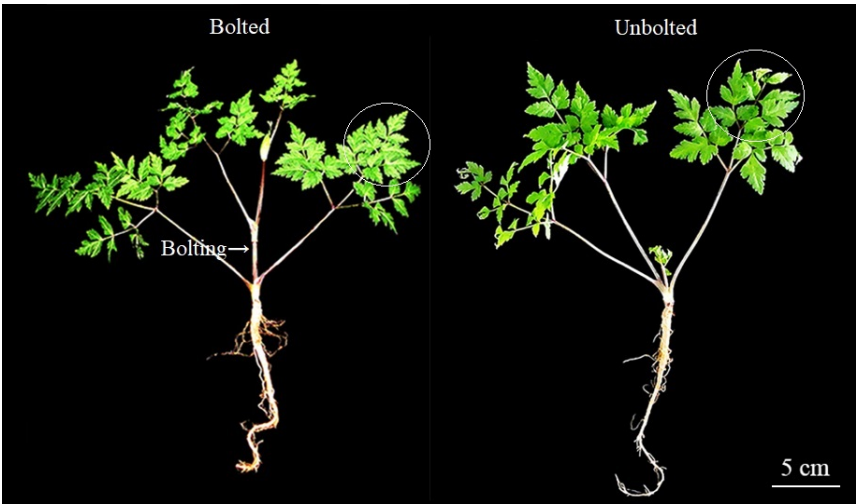


Supplementary Materials



**Figure S1:** Growth and development of *Angelica sinensis* in a commercial production process.



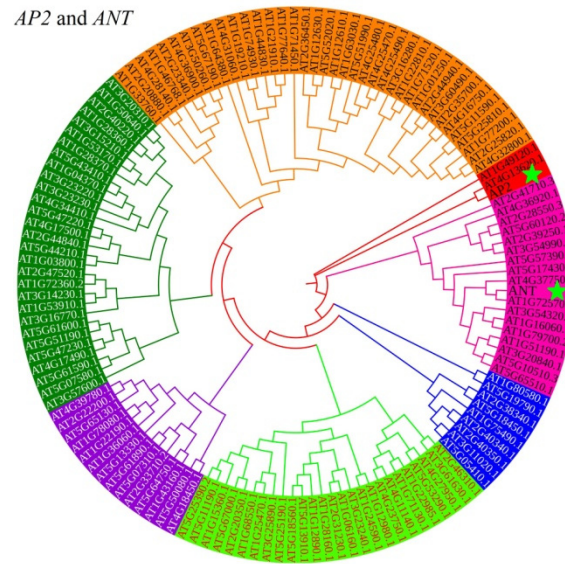
**Figure S2:** Two-year-old bolted and unbolted plants of *A. sinensis*. Bar represents 5 cm.

[illegible][illegible][illegible][illegible]

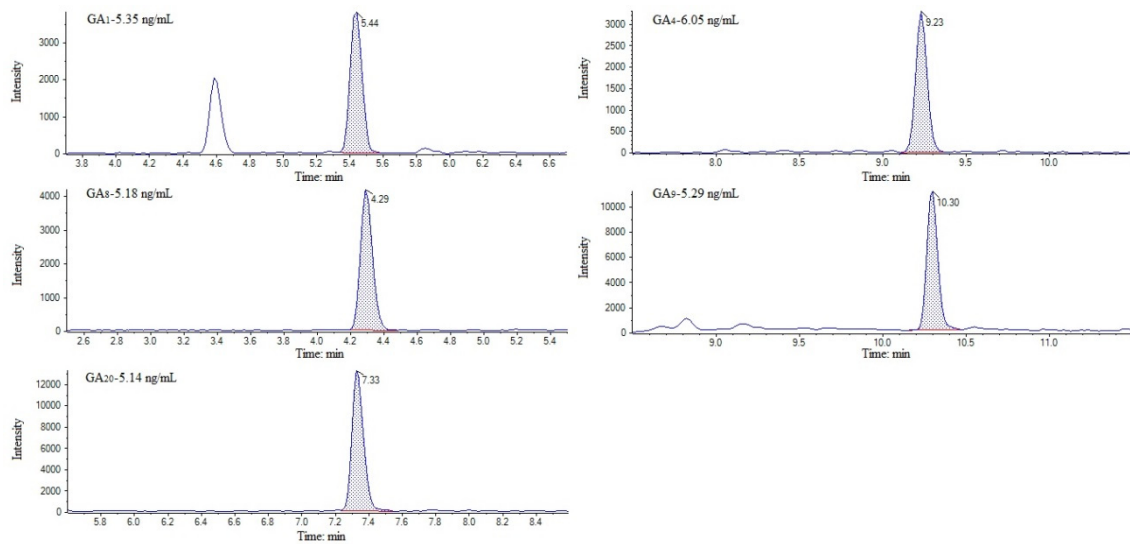
A circular phylogenetic tree representing the relationships between 100 *Arabidopsis thaliana* accessions. The tree is color-coded into segments corresponding to different populations: red (top), yellow, green, blue, purple, orange, and pink. Green stars are placed on the branches leading to specific accessions: AT1G53860, AT1G53861, AT1G53862, AT1G53863, AT1G53864, AT1G53865, AT1G53866, AT1G53867, AT1G53868, AT1G53869, AT1G53870, AT1G53871, AT1G53872, AT1G53873, AT1G53874, AT1G53875, AT1G53876, AT1G53877, AT1G53878, AT1G53879, AT1G53880, AT1G53881, AT1G53882, AT1G53883, AT1G53884, AT1G53885, AT1G53886, AT1G53887, AT1G53888, AT1G53889, AT1G53890, AT1G53891, AT1G53892, AT1G53893, AT1G53894, AT1G53895, AT1G53896, AT1G53897, AT1G53898, AT1G53899, AT1G53900, AT1G53901, AT1G53902, AT1G53903, AT1G53904, AT1G53905, AT1G53906, AT1G53907, AT1G53908, AT1G53909, AT1G53910, AT1G53911, AT1G53912, AT1G53913, AT1G53914, AT1G53915, AT1G53916, AT1G53917, AT1G53918, AT1G53919, AT1G53920, AT1G53921, AT1G53922, AT1G53923, AT1G53924, AT1G53925, AT1G53926, AT1G53927, AT1G53928, AT1G53929, AT1G53930, AT1G53931, AT1G53932, AT1G53933, AT1G53934, AT1G53935, AT1G53936, AT1G53937, AT1G53938, AT1G53939, AT1G53940, AT1G53941, AT1G53942, AT1G53943, AT1G53944, AT1G53945, AT1G53946, AT1G53947, AT1G53948, AT1G53949, AT1G53950, AT1G53951, AT1G53952, AT1G53953, AT1G53954, AT1G53955, AT1G53956, AT1G53957, AT1G53958, AT1G53959, AT1G53960, AT1G53961, AT1G53962, AT1G53963, AT1G53964, AT1G53965, AT1G53966, AT1G53967, AT1G53968, AT1G53969, AT1G53970, AT1G53971, AT1G53972, AT1G53973, AT1G53974, AT1G53975, AT1G53976, AT1G53977, AT1G53978, AT1G53979, AT1G53980, AT1G53981, AT1G53982, AT1G53983, AT1G53984, AT1G53985, AT1G53986, AT1G53987, AT1G53988, AT1G53989, AT1G53990, AT1G53991, AT1G53992, AT1G53993, AT1G53994, AT1G53995, AT1G53996, AT1G53997, AT1G53998, AT1G53999, AT1G54000. The tree is rooted at the bottom center, with branches radiating outwards. The color segments are: red (top), yellow (top-right), green (right), blue (bottom-right), purple (bottom), orange (bottom-left), and pink (left). Green stars are placed on the branches leading to specific accessions: AT1G53860, AT1G53861, AT1G53862, AT1G53863, AT1G53864, AT1G53865, AT1G53866, AT1G53867, AT1G53868, AT1G53869, AT1G53870, AT1G53871, AT1G53872, AT1G53873, AT1G53874, AT1G53875, AT1G53876, AT1G53877, AT1G53878, AT1G53879, AT1G53880, AT1G53881, AT1G53882, AT1G53883, AT1G53884, AT1G53885, AT1G53886, AT1G53887, AT1G53888, AT1G53889, AT1G53890, AT1G53891, AT1G53892, AT1G53893, AT1G53894, AT1G53895, AT1G53896, AT1G53897, AT1G53898, AT1G53899, AT1G53900, AT1G53901, AT1G53902, AT1G53903, AT1G53904, AT1G53905, AT1G53906, AT1G53907, AT1G53908, AT1G53909, AT1G53910, AT1G53911, AT1G53912, AT1G53913, AT1G53914, AT1G53915, AT1G53916, AT1G53917, AT1G53918, AT1G53919, AT1G53920, AT1G53921, AT1G53922, AT1G53923, AT1G53924, AT1G53925, AT1G53926, AT1G53927, AT1G53928, AT1G53929, AT1G53930, AT1G53931, AT1G53932, AT1G53933, AT1G53934, AT1G53935, AT1G53936, AT1G53937, AT1G53938, AT1G53939, AT1G53940, AT1G53941, AT1G53942, AT1G53943, AT1G53944, AT1G53945, AT1G53946, AT1G53947, AT1G53948, AT1G53949, AT1G53950, AT1G53951, AT1G53952, AT1G53953, AT1G53954, AT1G53955, AT1G53956, AT1G53957, AT1G53958, AT1G53959, AT1G53960, AT1G53961, AT1G53962, AT1G53963, AT1G53964, AT1G53965, AT1G53966, AT1G53967, AT1G53968, AT1G53969, AT1G53970, AT1G53971, AT1G53972, AT1G53973, AT1G53974, AT1G53975, AT1G53976, AT1G53977, AT1G53978, AT1G53979, AT1G53980, AT1G53981, AT1G53982, AT1G53983, AT1G53984, AT1G53985, AT1G53986, AT1G53987, AT1G53988, AT1G53989, AT1G53990, AT1G53991, AT1G53992, AT1G53993, AT1G53994, AT1G53995, AT1G53996, AT1G53997, AT1G53998, AT1G53999, AT1G54000.



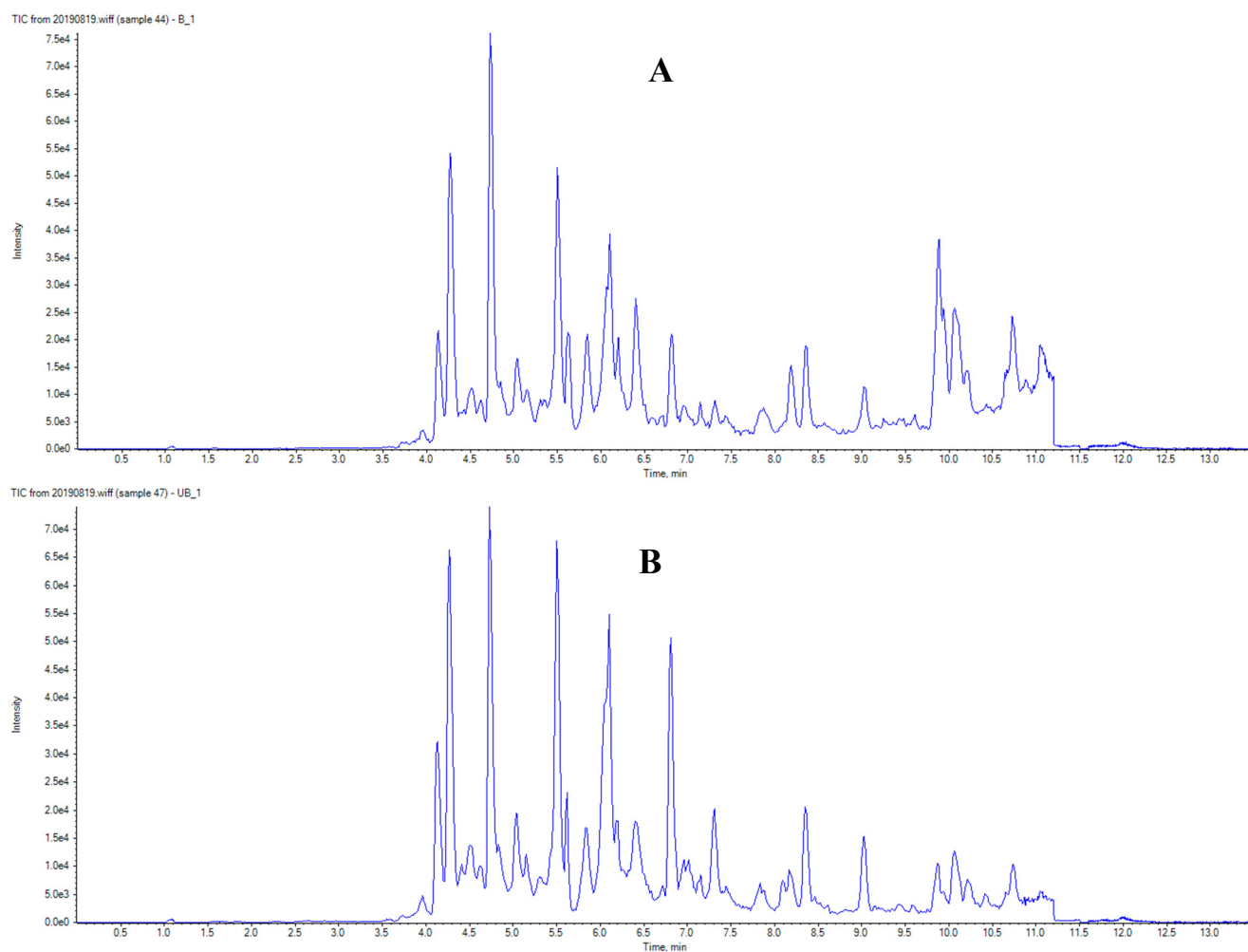
AP2 and ANT



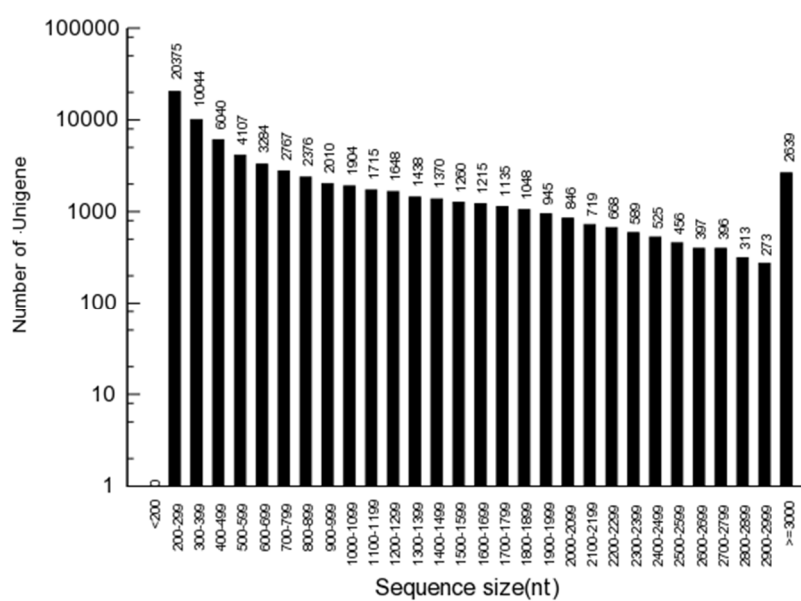
**Figure S3:** The cluster analysis of the 40 DEGs comparing with the families in *Arabidopsis thaliana*.



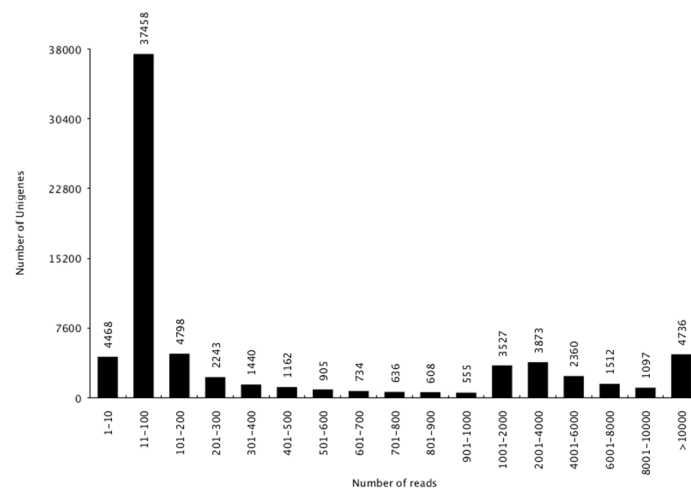
**Figure S4:** Representative chromatograms of reference standard of GA<sub>1</sub>, GA<sub>4</sub>, GA<sub>8</sub>, GA<sub>9</sub> and GA<sub>20</sub>.



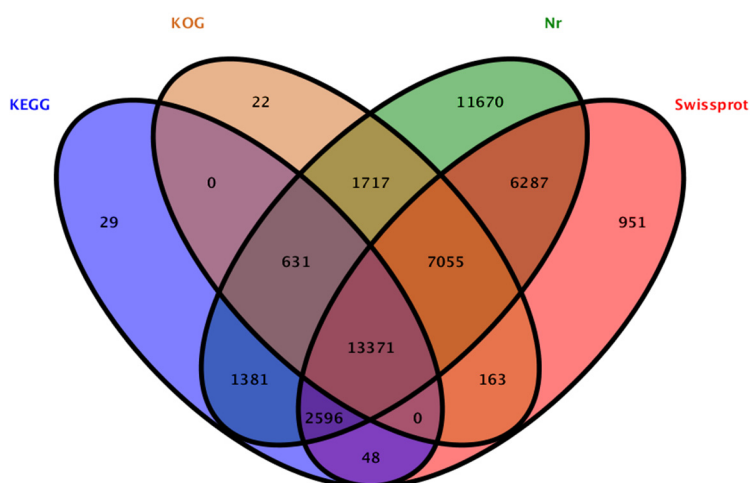
**Figure S5:** Representative chromatograms of bolted (A) and unbolted plants (B) of *A. sinensis*.



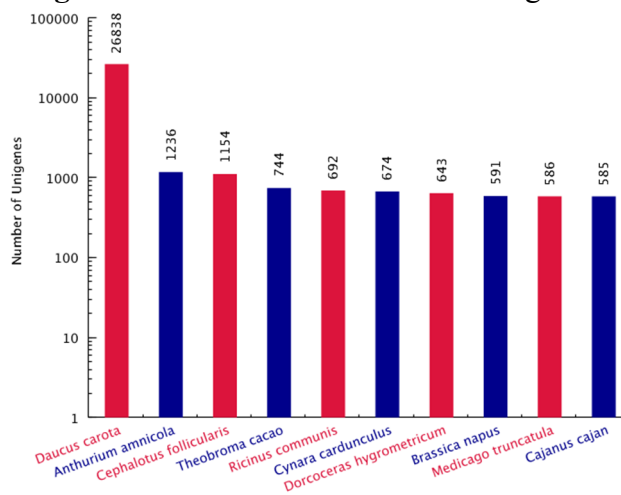
**Figure S6:** Length distribution of assembled unigenes.



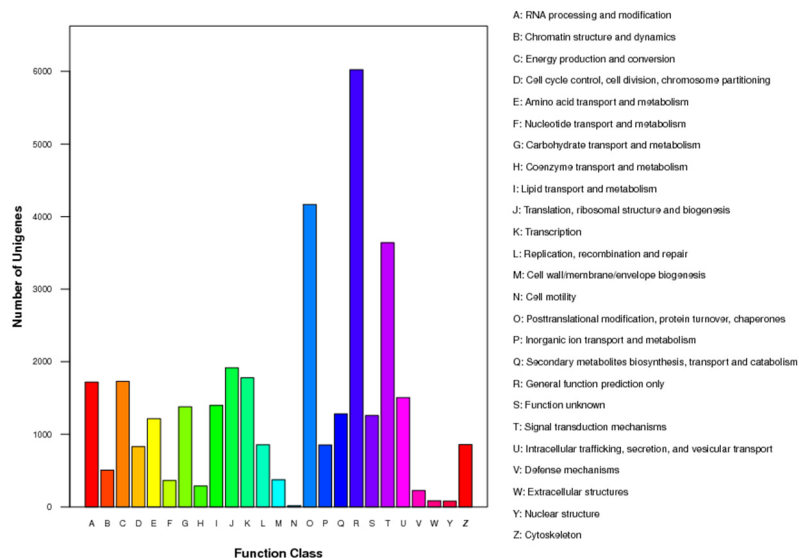
**Figure S7:** Read distribution of unigenes.



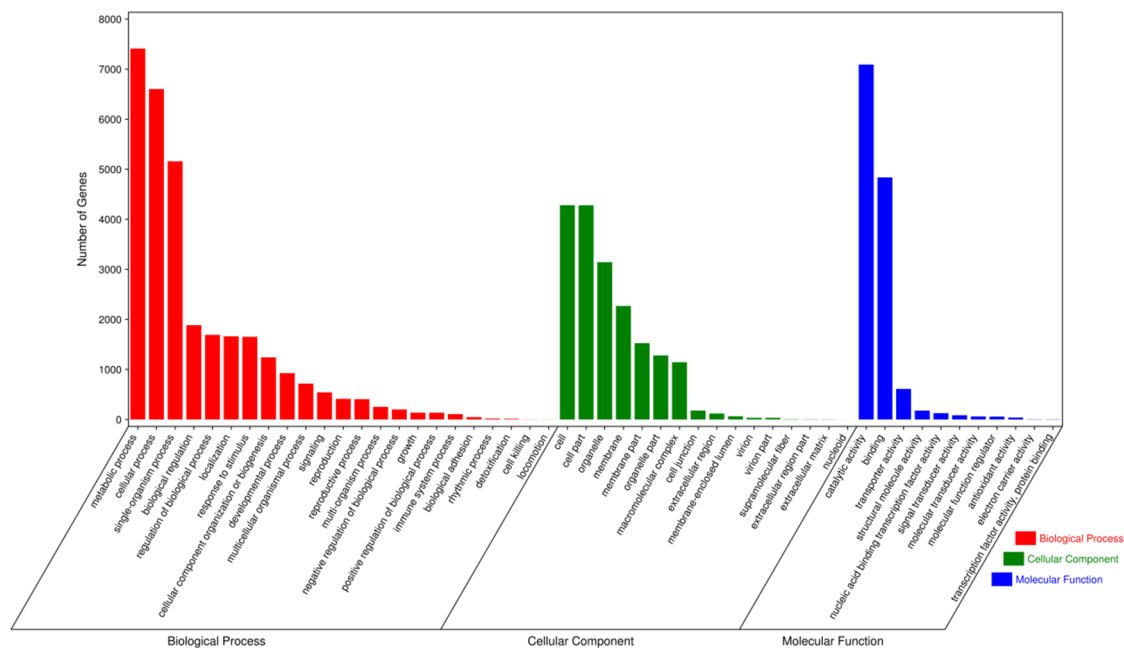
**Figure S8:** Basic annotation for all unigenes.



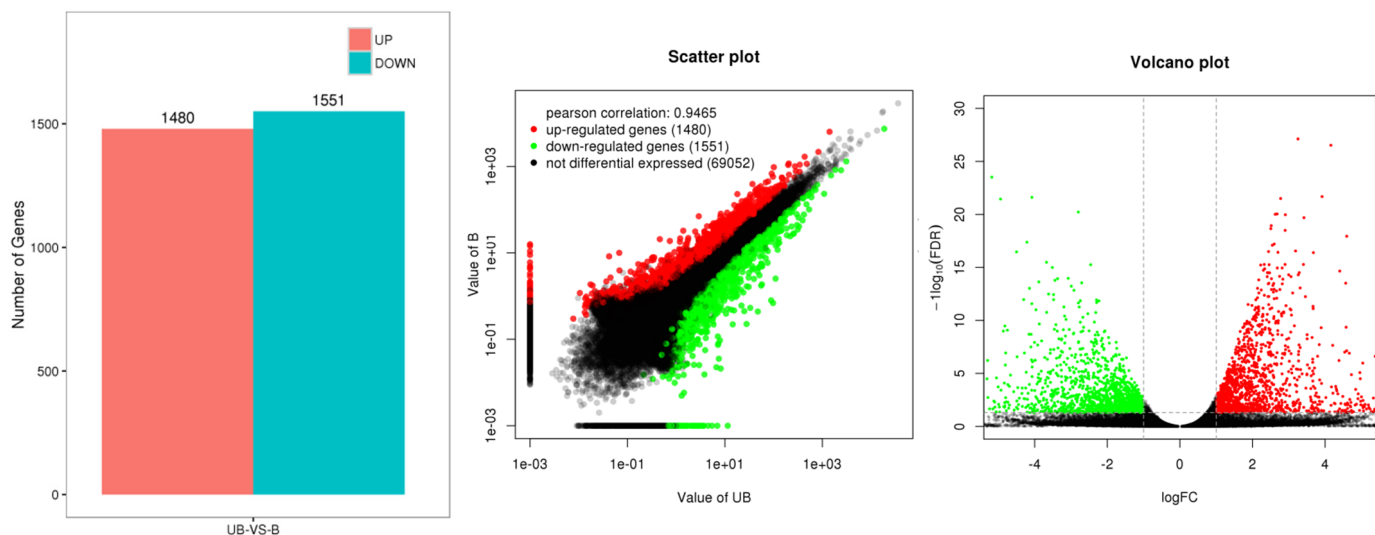
**Figure S9:** Top 10 plant species distribution of the total homologous sequences.



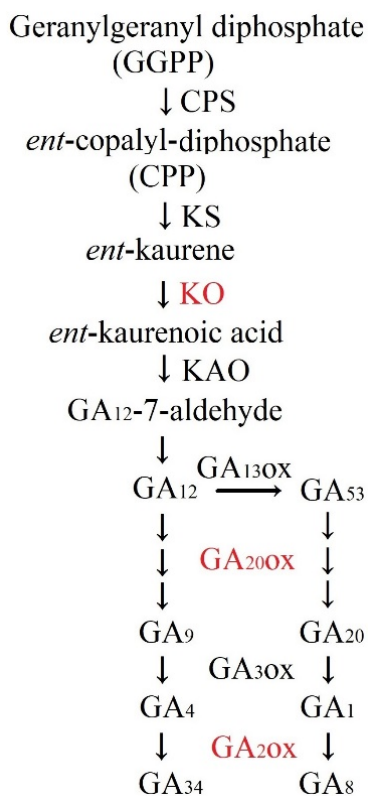
**Figure S10:** Distribution of unigenes in the transcriptome with KOG functional classification. Sequences have a KOG classification among 25 categories. Note: [A] RNA processing and modification; [B] Chromatin structure and dynamics; [C] Energy production and conversion; [D] Cell cycle control, cell 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 S11:** 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 S12:** Number of DEGs, correlation and volcano plot for unbolting versus bolting plants. Note: A total of 2,645 DEGs were obtained after excluding 386 repeated genes from the originally generated 3,031 genes.



**Figure S13:** The GA biosynthesis pathways and the differentially expressed genes are highlighted in red.

**Table S1:** Sequences of primer used in the qRT-PCR analysis

Gene name	Sequences (5' to 3')	Amplicon size (bp)
<i>ACT</i>	Forward: TGGTATTGTGCTGGATTCTGGT	109
	Reverse: TGAGATCACCACCAGCAAGG	
Floral development		
<i>SOC1</i>	Forward: CGAAACGGCGAAATGGACTG	200
	Reverse: CTGAATGTCTTGCCCAGCAG	
<i>MADS8</i>	Forward: GAGATGAGCGGAGGCCAAAG	101
	Reverse: AGCTTCCCCATGTTCTGTTCC	
<i>AGL8</i>	Forward: CGGAGCAACAAAACCAAGAGAG	102
	Reverse: CTCCGATGTTGCGTATGGCTT	
<i>AGL12</i>	Forward: ATGGATGAACTGCATGTGCTTG	191
	Reverse: ACCGGAACATCAATGTTACTAAACC	
<i>DEFA</i>	Forward: ACTCCGGAATGAGATCGGC	116
	Reverse: GCTCGCGTATGATGGCAAC	
<i>API</i>	Forward: TCGAAGTCCTGCAACGGAAC	200
	Reverse: CAGTTGGTTGTTCTGCCCC	
<i>AP2</i>	Forward: CTCTTCGACAGCCACCTTCA	163
	Reverse: AGGCTCCAACGACTCGAAC	
<i>ANT</i>	Forward: GCGAGGCGTAACAAAGACA	153
	Reverse: CTGCTGTGGGAACGATCTAGC	
Sucrose pathway		
<i>SUS1</i>	Forward: ATGAAGTCCACACAGGAAGCC	112
	Reverse: CGACGACAAGGTGATGAGTG	
<i>SUS3</i>	Forward: GGAGAGAAGACTAACGTGCCT	169
	Reverse: CGCGTAGCACTCTACTAGCC	
<i>SUS7</i>	Forward: TGACTTTATCGTCATCGGTTGG	166
	Reverse: AGAGCCGTGTTGAGTGTCT	
<i>INVA</i>	Forward: TAAGTTGTGCGGTTTGCGAG	174
	Reverse: ACTACACTCCTACCGCCAGT	
<i>INVB</i>	Forward: TTGCCGTCCTTTTCACCTCC	132
	Reverse: CTCATGCCCAAACGTTGACCT	
<i>INVE</i>	Forward: CAATTCGGGAAATCGAGTCCT	145
	Reverse: CTGCCGCACTAACACTTTCT	
<i>AMY1.1</i>	Forward: AAATCCAGACACCGGCACTC	128
	Reverse: ATCTCCAGCCAACGAATCCA	
<i>BAM1</i>	Forward: GGGAAGCTCAGGTACCACTT	127
	Reverse: GCACACATTTCTCTGCTCC	
<i>BAM3</i>	Forward: AGTCTCCGAGCAAGAAATTCG	127
	Reverse: TGCTATGTGGCCGAGATGAC	
<i>BAM9</i>	Forward: TTCCCGCAGAAAATCTGTTGA	118
	Reverse: TGCGGAAATTGCTTTTGCGT	
<i>INV Inh</i>	Forward: TCGAGCTTTATGATGATGCCCTC	180
	Reverse: TAGCATTGTTCTTGCGGTT	
GA pathway		
<i>KO</i>	Forward: ACTTGCTGTGAGTGGCCCG	104
	Reverse: AAGGAGGGAGATTCGAGGGTG	
<i>GA20OX1</i>	Forward: AACCGTTCTACCAAGCGAAT	175

	Reverse: CCGGAGAGAAAGCCTCCTATG	
<i>GA2OX1</i>	Forward: ACCAACACATTGATTCCCCTC Reverse: GGACATAGGTGAAGAGAAAACTTG	171
<i>GAI</i>	Forward: GTATTGGCTGGTCCACGTT Reverse: AGCCAGCCACCTTACCAAAG	144
<i>GA2OX6</i>	Forward: GCCTTGACTTGCTAAGGGTG Reverse: AGCCTCAGACCAAGAGAGTT	152
<i>GA2OX8</i>	Forward: AGTTGGCAGAAATCTTAGCGG Reverse: CTCCGGTATTGGACATGGTGG	119
<i>GAIP</i>	Forward: TGTATCATCCCCCTCTGCT Reverse: GCATTCACTATCTCCTTTGCTTCC	132
<b>Photoperiodic induction</b>		
<i>CO3</i>	Forward: CTCAGCTTATGGGACCACC Reverse: CGAGCACGTTGGCGAC	101
<i>COL2</i>	Forward: TTCATCCCCAGCAAGAGCAG Reverse: GGATACAGAAACGCTGTGGC	131
<i>HD3A</i>	Forward: GAAAGTCCGAGGCCATCAGC Reverse: CGGCAAAGTCTCTAGTATTGAATTG	121
<i>FTIP1</i>	Forward: AACGCTGACAAAATCACAAGCA Reverse: GATTCCACTCGGGGTTCACT	193
<i>FD</i>	Forward: TACCACCCCCACCACTAAAC Reverse: AGAGCTGCTGCTAGGGTTG	160
<i>SVP</i>	Forward: GCCGGATTAAGTCGCGTGAT Reverse: TGGGATTAGCTTTCCACCTTTAGA	150
<i>COL3</i>	Forward: AAAGGTACAGAGCAAAGCGTG Reverse: CCTTGAGCTTCATCATTGCGT	127
<i>COL16</i>	Forward: GATGGGTCAGCAGAGACGAT Reverse: TCGCTGTTTGTCAATTCCGT	116
<i>AS1</i>	Forward: ATCCCGACCAACCTGCTTC Reverse: AAGTTGGGAGTGGAGCTGTT	138
<i>CDF2</i>	Forward: TCGATCCCCAACAACGAAGAG Reverse: ATGTTGTTGGACCACCCCTC	196
<i>MIP1A</i>	Forward: GCGATACAAGGGTTCATGCTG Reverse: GAGTCCGATGAGATAGCGGTG	104
<i>MIP1B</i>	Forward: TGATTGCCACGCTCTAACCC Reverse: GGCCTAATGAGTTGGTTGGTG	156
<i>HDR1</i>	Forward: GCAAGAGATCAGGACAGGGAG Reverse: TGGTTTTCCAGCATTGTGTTTTG	146
<i>EFM</i>	Forward: TGACTTGCACCGGAGATTTGT Reverse: TTTGAACTCGGGCCAACCA	200

**Table S2:** Calibration curves of GA<sub>1</sub>, GA<sub>4</sub>, GA<sub>8</sub>, GA<sub>9</sub> and GA<sub>20</sub>.

GAs	Calibration curves	Related coefficient
GA <sub>1</sub>	$y = 3549.48823 x + 133.18755$	( $r = 0.9923$ )
GA <sub>4</sub>	$y = 2527.09342 x + 574.86954$	( $r = 0.9905$ )
GA <sub>8</sub>	$y = 4004.18848 x + 320.37962$	( $r = 0.9934$ )
GA <sub>9</sub>	$y = 9565.89109 x + 339.64459$	( $r = 0.9949$ )
GA <sub>20</sub>	$y = 12108.82863 x + 1112.84346$	( $r = 0.9928$ )