

# Supplementary Materials: Comparative transcriptome analysis of *Penicillium citrinum* cultured with different carbon sources identifies genes involved in citrinin biosynthesis

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**Table S1.** Summary of RNA-Seq data. S-samples were grown with sucrose and the G-Samples were grown with glucose as sole carbon source.

Sample name	Total reads	Total nucleotide (nt)	Q <sub>≥</sub> 20	Adapter	Low quality
S1	41024262	6153639300	95.76%	10.27%	0.02%
S2	40904432	6135664800	95.24%	7.22%	0.02%
G1	40267398	6040109700	95.95%	8.66%	0.02%
G2	41064036	6159605400	95.68%	10.18%	0.02%

**Table S2.** Results of *de novo* assembly.

Unigene	N50	Average length	Total assembled bases
25491	3889	2048	52211935

**Table S3.** The primer sequences of 49 unigenes for qRT-PCR in this study.

Gene ID	Sequence of primer (5' to 3')
Unigene4605_All	For: ACTCATCTCTCGCACGCTGGATGT Rev: TCTCTTCTCAGCCGCCAACTTCAA
Unigene5443_All	For: CTTGGTGGCGATGCGAATGATGG Rev: CTTCTGAATAGCCTCTTCCTCCGTCTT
Unigene4470_All	For: AATGCTGGCGATGCTGGTATGGA Rev: GTGGCTGCTGGTGAAGTAGACGAT
Unigene1201_All	For: ATCTGATCGGTCGCATCCGTCTG Rev: ACCTATAAGCCTCCTCGTCCTTCGT
Unigene3306_All	For: GGAACCTGGAACCTTCATCACGCATT Rev: ACGGACGCAGGAAGCCCTTTATC
CL2002.Contig3_All	For: CGCTTCCGCTATGATCCGACCAT CAACAAGACCTATTTCAACGCCGAGAT
CL2002.Contig2_All	For: CGCTTCCGCTATGATCCGACCAT Rev: CAACAAGACCTATTTCAACGCCGAGAT
CL3211.Contig2_All	For: ACCTGACGATGTAATTATCCGACTCA Rev: GTCTCCTTATCATTCCAGCACATAGCA
Unigene3258_All	For: GAGATGGTGTCCGTGATTGCTGAG Rev: GTATTGTTCTGATGCCATAGTCACTCCTC
CL1938.Contig2_All	For: GTCAAATCCAGCCTGAGGAAAGTGT TGGTCGCCATTATGAGTCAACAACAAT
CL1093.Contig2_All	For: TCCAAGTATCAAGTGGTCTAGGCTCAT Rev: CTTGCGAATCTCGCTCTCCTTCAAG
CL2531.Contig1_All	For: AACAAATCGCTTACGCCTGCTTACA Rev: GAGCCTTGAGCACTATATCAACCACTT
Unigene950_All	For: GACTCGGTGGCTGGAGATGGAT Rev: GTGGTGAGACAGAAGAAGATTAGAGCAA
Unigene401_All	For: ATCTCCAACCTTGCCATTGCCATCA Rev: CTCTCCGTCCGAGCATCCAGAA
Unigene6956_All	For: CCTGATGACGAGTTCAAGCCTGAC Rev: GATCACCATTGCCGCTGTAGACAT
Unigene1095_All	For: AGACAGCCAGAAGAGTGAAGGAGAG CGACATCAGTTGACTTGGACCGTATT
CL1869.Contig6_All	For: TTCAACGGCAGTCCTATCATCATCATT Rev: GCCTCCATAATTAACACTGTCCTTCCA
Unigene3849_All	For: GGACGAACCACACCGCATTCTATT Rev: TTCCACGCCTCAAGAGCTTCCT
Unigene5620_All	For: CCGTGCGAATTACCATAGCCGATT Rev: CGAGACTCAATCCTACTCCAAGACCT
Unigene8542_All	For: GGAACCTCCGCACTCTGATGTATCG Rev: CTGCTGGACACTGTGGATCATTACG
CL2339.Contig4_All	For: AGACTGCTGAGGAGGCTCTTGAC Rev: GTAGAACTCGCTGGAGGCAACATC

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Unigene548_All	For: CCGCCGTGCCGATTATCATCTC Rev: CCAGCCTCAACACAGAGCATCTTC
Unigene6764_All	For: ATTCTTCGGCTTCATTGAGTCCTTCC Rev: CCAGCAGATAAGAGAGCGTAGAGAGTA
Unigene2457_All	For: GACCGCTGATCTGATTGATTCACCTT Rev: TCGTTAGGCTGATGTGTACCATTGC
CL2164.Contig11_All	For: CGACACCGACCGCAAGTTCTAC Rev: ACCATCACCGCCCAGAGTAGTC
Unigene11940_All	For: GGCTGAGTTATATGGCGAAGATGGTATT Rev: TTAGGCAAGGCATCTGGTAGAGGAA
Unigene5219_All	For: CTCGTTGGTAGTGTCAAGGATGTTAAGT Rev: GCTGCTTCAGTTCGCTGCTGTA
CL1796.Contig2_All	For: TCAACACGCTATCATTCTCGCTAAG Rev: GCCTTCCCATTGCCATTGTCATTTC
CL1031.Contig3_All	For: TCGGTTGGACTCTACAGCAAGGAT Rev: CGGTGGTGAAGTATCTGAACGGATG
Unigene8156_All	For: GAACAGGAACTCCCGTCGGTGA Rev: CTGAAGGGTGCTTGCCAGTCTTT
CL1031.Contig5_All	For: GATGCGGCTTTTCACCTCACTACTT Rev: TTGTCTGACCAGCTCCATTGATGC
CL348.Contig2_All	For: GGAACCTACAACAGCACTCACCAGAAC Rev: CCAATCCACCAACACCAATGATACCAA
Unigene125_All	For: AAGCACACCATCTACAAGCAGTTCAA Rev: TTCACGAGCATAGCCAAGGAGGA
CL1559.Contig1_All	TCGGCACACCTGCGTACTTCAATA CGGTAGCAATGACATCAACATCCACAG
Unigene13097_All	CAGGAGACTCGTGCCAATCAGACA AGATGGGTGGTACACTTGCGTCAG
Unigene2872_All	GGCACTAGGCGGACCACTTGAT GCCAATCTTCATCTTCCAATCCAGCTC
Unigene4460_All	CACCGTTGCTTCTAAACTCACCGAAA TTCCATTGACCAGTGTAGAGCCTCC
Unigene5036_All	CCGTGAGCACTTGTTCCATGATGAC GCAGAAACCTGGGTAGGAGGAATAGAC
Unigene5396_All	TCTTGTTGGCTGCTGGATCTTCTGT GAGGAGGTCAGTTGCGTAGTCAGTT
CL1213.Contig1_All	CGGCTTCTGAAGTCGTTGGGATTG GCTCTGAGGTGAGTATCATCATCGGAAT
CL1213.Contig2_All	CCCAACGATGAGCGAGAGCAAGA CCCATATCCCTGTACCAGTCCCTAAATC
CL1213.Contig6_All	TCAGCATACAATGGCTCGATAAGCAATG TCTCGCTCATCGTTGGGCAAGAA
Unigene2855_All	GAGCCAGCGGTCATCACCAAGA GCAAGTAGCCCAACCCTCGTGTA

CL2103.Contig1_All	GCGAAGTCGAGGAGAATGTAGAGTATGT GCAATAATGTCTTCACCGCTGTCACTAT
CL2103.Contig5_All	TTCTGGACGAGTTGATGGTACTGTTGT CCTGAGAGATTGAATTTGGCGAGTGTG
CL2103.Contig6_All	ACCTAGCTTCTGGACGAGTGAATACG TGAGAGATTGAATTTGGCGAGTGTGAC
CL1659.Contig3_All	CTGAGCAAGACAGCAAGACTGAAGATG CTATGCGACGAAGGTTCTCCAGAAGA
Unigene7245_All	ACGTGCAACTCAAGGACTCTCAGC ATTTGGCCGTGAAGGACGACCA
CL1659.Contig1_All	GGCGTTGATAAGCGGTCGTATGC CATCCTTAGCGGTAGGCGAGTCAG
CL2661.Contig1_All	For: TCCGTGAGATCCGTCGCTACCA Rev: ACTCCTGAAGAGCACCGATGGC
Gene ID	Sequence of primer (5' to 3')
Unigene4605_All	For: ACTCATCTCTCGCACGCTGGATGT Rev: TCTCTTCTCAGCCGCCAACTTCAA
Unigene5443_All	For: CTTGGTGGCGATGCGAATGATGG Rev: CTTCTGAATAGCCTCTTCCTCCGTCTT
Unigene4470_All	For: AATGCTGGCGATGCTGGTATGGA Rev: GTGGCTGCTGGTGAAGTAGACGAT
Unigene1201_All	For: ATCTGATCGGTCGCATCCGTCTG Rev: ACCTATAAGCCTCCTCGTCCTTCGT
Unigene3306_All	For: GGAACCTGGAACCTTCATCACGCATT Rev: ACGGACGCAGGAAGCCCTTTATC
CL2002.Contig3_All	For: CGCTTCCGCTATGATCCGACCAT CAACAAGACCTATTTCAACGCCGAGAT
CL2002.Contig2_All	For: CGCTTCCGCTATGATCCGACCAT Rev: CAACAAGACCTATTTCAACGCCGAGAT
CL3211.Contig2_All	For: ACCTGACGATGTACTTATCCGACTCA Rev: GTCTCCTTATCATTCAGCACATAGCA
Unigene3258_All	For: GAGATGGTGTCCGTGATTGCTGAG Rev: GTATTGTTCTGATGCCATAGTCACTCCTC
CL1938.Contig2_All	For: GTCAAATCCAGCCTGAGGAAAGTGT TGGTCGCCATTATGAGTCAACAACAAT
CL1093.Contig2_All	For: TCCAAGTATCAAGTGGTCTAGGCTCAT Rev: CTTGGAATCTCGCTCTCCTTCAAG
CL2531.Contig1_All	For: AACAAATCGCTTACGCCTGCTTACA Rev: GAGCCTTGAGCACTATATCAACCACTT
Unigene950_All	For: GACTCGGTGGCTGGAGATGGAT Rev: GTGGTGAGACAGAAGAAGATTAGAGCAA
Unigene401_All	For: ATCTCCAACCTTGCCATTGCCATCA Rev: CTCTCCGTCCGAGCATCCAGAA
Unigene6956_All	For: CCTGATGACGAGTTCAAGCCTGAC Rev: GATCACCATTGCCGCTGTAGACAT

Unigene1095_All	For: AGACAGCCAGAAGAGTGAAGGAGAG CGACATCAGTTGACTTGGACCGTATT
CL1869.Contig6_All	For: TTCAACGGCAGTCCTATCATCATCATT Rev: GCCTCCATAATTAACACTGTCCTTCCA
Unigene3849_All	For: GGACGAACCACACCGCATTCTATT Rev: TTCCACGCCTCAAGAGCTTCCT
Unigene5620_All	For: CCGTGCGAATTACCATAGCCGATT Rev: CGAGACTCAATCCTACTCCAAGACCT
Unigene8542_All	For: GGAAC TTCCGCACTCTGATGTATCG Rev: CTGCTGGACACTGTGGATCATTACG
CL2339.Contig4_All	For: AGACTGCTGAGGAGGCTCTTGAC Rev: GTAGAACTCGCTGGAGGCAACATC
Unigene548_All	For: CCGCCGTGCCGATTATCATCTC Rev: CCAGCCTCAACACAGAGCATCTTC
Unigene6764_All	For: ATTCTTCGGCTTCATTGAGTCCTTCC Rev: CCAGCAGATAAGAGAGCGTAGAGAGTA
Unigene2457_All	For: GACCGCTGATCTGATTGATTCACCTT Rev: TCGTTAGGCTGATGTGTACCATTGC
CL2164.Contig11_All	For: CGACACCGACCGCAAGTTCTAC Rev: ACCATCACCGCCCAGAGTAGTC
Unigene11940_All	For: GGCTGAGTTATATGGCGAAGATGGTATT Rev: TTAGGCAAGGCATCTGGTAGAGGAA
Unigene5219_All	For: CTCGTTGGTAGTGTCAAGGATGTAAAGT Rev: GCTGCTTCAGTTCGCTGCTGTA
CL1796.Contig2_All	For: TCAACACGCTATCATTCTCGCTAAG Rev: GCCTTCCCATTGCCATTGTCATTTC
CL1031.Contig3_All	For: TCGGTTGGACTCTACAGCAAGGAT Rev: CGGTGGTGAAGTATCTGAACGGATG
Unigene8156_All	For: GAACAGGAACTCCCGTCGGTGA Rev: CTGAAGGGTGCTTGCCAGTCTTT
CL1031.Contig5_All	For: GATGCGGCTTTACCTCACTACTT Rev: TTGTCTGACCAGCTCCATTGATGC
CL348.Contig2_All	For: GGAAC TTACAACAGCACTCACCAGAAC Rev: CCAATCCACCAACACCAATGATACCAA
Unigene125_All	For: AAGCACACCATCTACAAGCAGTTCAA Rev: TTCACGAGCATAGCCAAGGAGGA
CL1559.Contig1_All	TCGGCACACCTGCGTACTTCAATA CGGTAGCAATGACATCAACATCCACAG
Unigene13097_All	CAGGAGACTCGTGCCAATCAGACA AGATGGGTGGTACACTTGCGTCAG
Unigene2872_All	GGCACTAGGCGGACCACTTGAT GCCAATCTTCATCTTCCAATCCAGCTC
Unigene4460_All	CACCGTTGCTTCTAAACTCACCGAAA TTCCATTGACCAGTGTAGAGCCTCC

Unigene5036_All	CCGTGAGCACTTGTTCATGATGAC GCAGAAACCTGGGTAGGAGGAATAGAC
Unigene5396_All	TCTTGTGGCTGCTGGATCTTCTGT GAGGAGGTCAGTTGCGTAGTCAGTT
CL1213.Contig1_All	CGGCTTCTGAAGTCGTTGGGATTG GCTCTGAGGTGAGTATCATCATCGGAAT
CL1213.Contig2_All	CCCAACGATGAGCGAGAGCAAGA CCCATATCCCTGTACCAGTCCCTAAATC
CL1213.Contig6_All	TCAGCATACAATGGCTCGATAAGCAATG TCTCGCTCATCGTTGGGCAAGAA
Unigene2855_All	GAGCCAGCGGTCATCACCAAGA GCAAGTAGCCCAACCCTCGTGTA
CL2103.Contig1_All	GCGAAGTCGAGGAGAATGTAGAGTATGT GCAATAATGTCTTCACCGCTGTCACTAT
CL2103.Contig5_All	TTCTGGACGAGTTGATGGTACTGTTGT CCTGAGAGATTGAATTTGGCGAGTGTG
CL2103.Contig6_All	ACCTAGCTTCTGGACGAGTGAATACG TGAGAGATTGAATTTGGCGAGTGTGAC
CL1659.Contig3_All	CTGAGCAAGACAGCAAGACTGAAGATG CTATGCGACGAAGGTTCTCCAGAAGA
Unigene7245_All	ACGTGCAACTCAAGGACTCTCAGC ATTGGCCGTGAAGGACGACCA
CL1659.Contig1_All	GGCGTTGATAAGCGGTCGTATGC CATCCTTAGCGGTAGGCGAGTCAG
CL2661.Contig1_All	For: TCCGTGAGATCCGTCGCTACCA Rev: ACTCCTGAAGAGCACCGATGGC

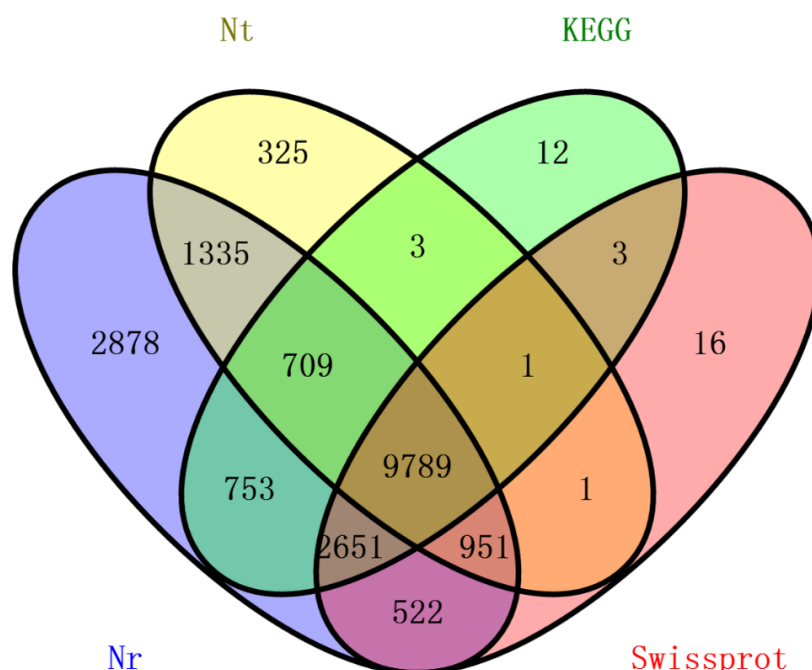
Gene ID	Sequence of primer (5' to 3')
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Unigene5443_All	For: CTTGGTGGCGATGCGAATGATGG Rev: CTTCTGAATAGCCTCTTCCTCCGTCTT
Unigene4470_All	For: AATGCTGGCGATGCTGGTATGGA Rev: GTGGCTGCTGGTGAAGTACGAT
Unigene1201_All	For: ATCTGATCGGTCGCATCCGTCTG Rev: ACCTATAAGCCTCCTCGTCCTTCGT
Unigene3306_All	For: GGAACCTGGAACCTTCATCACGCATT Rev: ACGGACGCAGGAAGCCCTTTATC
CL2002.Contig3_All	For: CGCTTCCGCTATGATCCGACCAT CAACAAGACCTATTTCAACGCCGAGAT
CL2002.Contig2_All	For: CGCTTCCGCTATGATCCGACCAT Rev: CAACAAGACCTATTTCAACGCCGAGAT
CL3211.Contig2_All	For: ACCTGACGATGTAATTATCCGACTCA Rev: GTCTCCTTATCATTCCAGCACATAGCA
Unigene3258_All	For: GAGATGGTGTCCGTGATTGCTGAG Rev: GTATTGTTCGTAGCCATAGTCACTCCTC

CL1938.Contig2_All	For: GTCAAATCCAGCCTGAGGAAAGTGT TGGTCGCCATTATGAGTCAACAACAAT
CL1093.Contig2_All	For: TCCAAGTATCAAGTGGTCTAGGCTCAT Rev: CTTGGAATCTCGCTCTCCTTCAAG
CL2531.Contig1_All	For: AACAAATCGCTTACGCCTGCTTACA Rev: GAGCCTTGAGCACTATATCAACCACTT
Unigene950_All	For: GACTCGGTGGCTGGAGATGGAT Rev: GTGGTGAGACAGAAGAAGATTAGAGCAA
Unigene401_All	For: ATCTCCAACCTTGCCATTGCCATCA Rev: CTCTCCGTCCGAGCATCCAGAA
Unigene6956_All	For: CCTGATGACGAGTTCAAGCCTGAC Rev: GATCACCATTGCCGCTGTAGACAT
Unigene1095_All	For: AGACAGCCAGAAGAGTGAAGGAGAG CGACATCAGTTGACTTGGACCGTATT
CL1869.Contig6_All	For: TTCAACGGCAGTCCTATCATCATCATT Rev: GCCTCCATAATTAACACTGTCCTTCCA
Unigene3849_All	For: GGACGAACCACACCGCATTCTATT Rev: TTCCACGCCTCAAGAGCTTCCT
Unigene5620_All	For: CCGTGCGAATTACCATAGCCGATT Rev: CGAGACTCAATCCTACTCCAAGACCT
Unigene8542_All	For: GGAACCTCCGCACTCTGATGTATCG Rev: CTGCTGGACACTGTGGATCATTACG
CL2339.Contig4_All	For: AGACTGCTGAGGAGGCTCTTGAC Rev: GTAGAACTCGCTGGAGGCAACATC
Unigene548_All	For: CCGCCGTGCCGATTATCATCTC Rev: CCAGCCTCAACACAGAGCATCTTC
Unigene6764_All	For: ATTCTTCGGCTTCATTGAGTCCTTCC Rev: CCAGCAGATAAGAGAGCGTAGAGAGTA
Unigene2457_All	For: GACCGCTGATCTGATTGATTACCTT Rev: TCGTTAGGCTGATGTGTACCATTGC
CL2164.Contig11_All	For: CGACACCGACCGCAAGTTCTAC Rev: ACCATCACCGCCCAGAGTAGTC
Unigene11940_All	For: GGCTGAGTTATATGGCGAAGATGGTATT Rev: TTAGGCAAGGCATCTGGTAGAGGAA
Unigene5219_All	For: CTCGTTGGTAGTGTCAAGGATGTTAAGT Rev: GCTGCTTCAGTTCGCTGCTGTA
CL1796.Contig2_All	For: TCAACACGCTATCATTCTCGCTAAG Rev: GCCTTCCCATTGCCATTGTCAATTTC
CL1031.Contig3_All	For: TCGGTTGGACTCTACAGCAAGGAT Rev: CGGTGGTGAAGTATCTGAACGGATG
Unigene8156_All	For: GAACAGGAACTCCCGTCGGTGA Rev: CTGAAGGGTGCTTGCCAGTCTTT
CL1031.Contig5_All	For: GATGCGGCTTTCACCTCACTACTT Rev: TTGTCTGACCAGCTCCATTGATGC
CL348.Contig2_All	For: GGAACCTTACAACAGCACTACCAGAAC Rev: CCAATCCACCAACACCAATGATACCAA

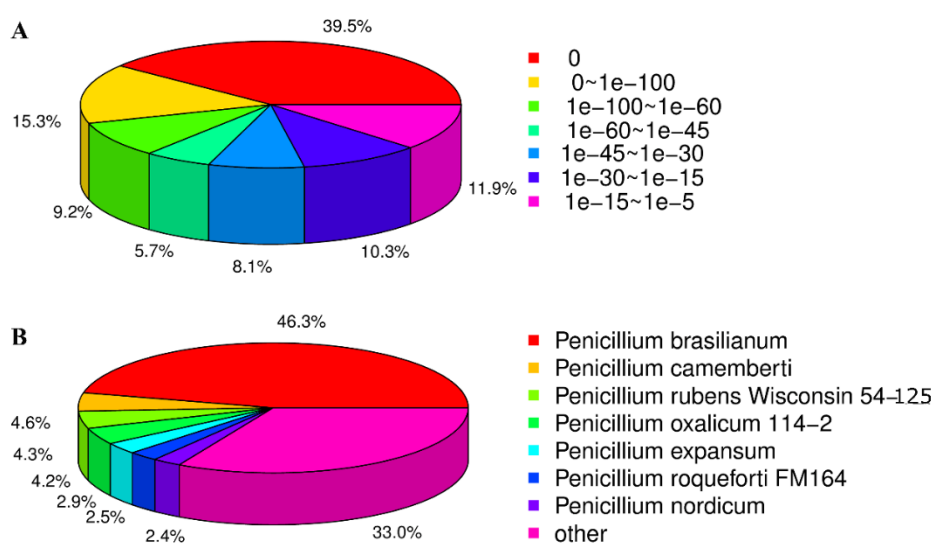
Unigene125_All	For: AAGCACACCATCTACAAGCAGTTCAA Rev: TTCACGAGCATAGCCAAGGAGGA
CL1559.Contig1_All	TCGGCACACCTGCGTACTTCAATA CGGTAGCAATGACATCAACATCCACAG
Unigene13097_All	CAGGAGACTCGTGCCAATCAGACA AGATGGGTGGTACACTTGCGTCAG
Unigene2872_All	GGCACTAGGCGGACCACTTGAT GCCAATCTTCATCTTCCAATCCAGCTC
Unigene4460_All	CACCGTTGCTTCTAAACTCACCGAAA TTCCATTGACCAGTG TAGAGCCTCC
Unigene5036_All	CCGTGAGCACTTGTTCCATGATGAC GCAGAAACCTGGGTAGGAGGAATAGAC
Unigene5396_All	TCTTGTTGGCTGCTGGATCTTCTGT GAGGAGGTCAGTTGCGTAGTCAGTT
CL1213.Contig1_All	CGGCTTCTGAAGTCGTTGGGATTG GCTCTGAGGTGAGTATCATCATCGGAAT
CL1213.Contig2_All	CCCAACGATGAGCGAGAGCAAGA CCCATATCCCTGTACCAGTCCCTAAATC
CL1213.Contig6_All	TCAGCATACAATGGCTCGATAAGCAATG TCTCGCTCATCGTTGGGCAAGAA
Unigene2855_All	GAGCCAGCGGTCATCACCAAGA GCAAGTAGCCCAACCCTCGTGTA
CL2103.Contig1_All	GCGAAGTCGAGGAGAATGTAGAGTATGT GCAATAATGTCTTCACCGCTGTCACTAT
CL2103.Contig5_All	TTCTGGACGAGTTGATGGTACTGTTGT CCTGAGAGATTGAATTTGGCGAGTGTG
CL2103.Contig6_All	ACCTAGCTTCTGGACGAGTGAATACG TGAGAGATTGAATTTGGCGAGTGTGAC
CL1659.Contig3_All	CTGAGCAAGACAGCAAGACTGAAGATG CTATGCGACGAAGGTTCTCCAGAAGA
Unigene7245_All	ACGTGCAACTCAAGGACTCTCAGC ATTGGCCGTGAAGGACGACCA
CL1659.Contig1_All	GGCGTTGATAAGCGGTCGTATGC CATCCTTAGCGGTAGGCGAGTCAG
CL2661.Contig1_All	For: TCCGTGAGATCCGTCGCTACCA Rev: ACTCCTGAAGAGCACCGATGGC

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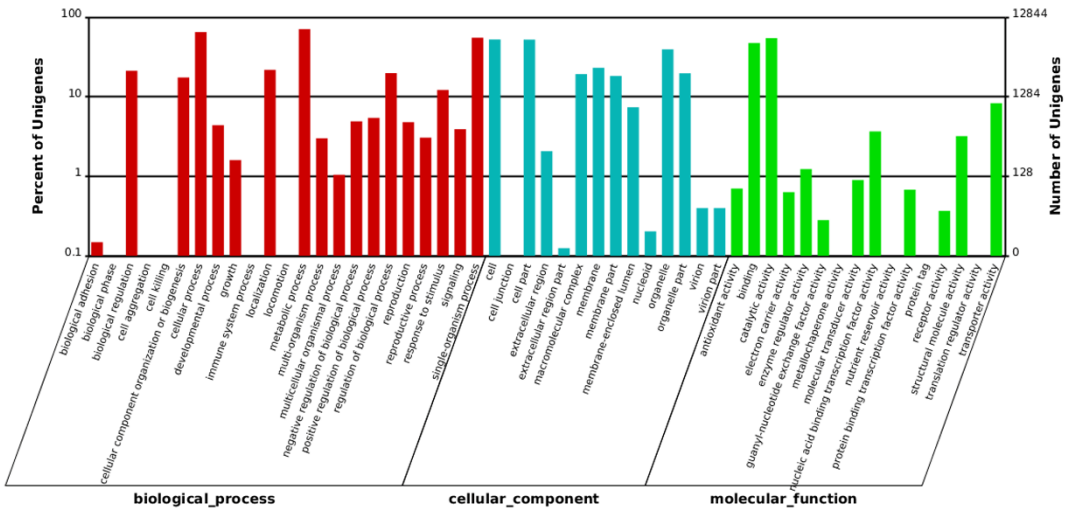




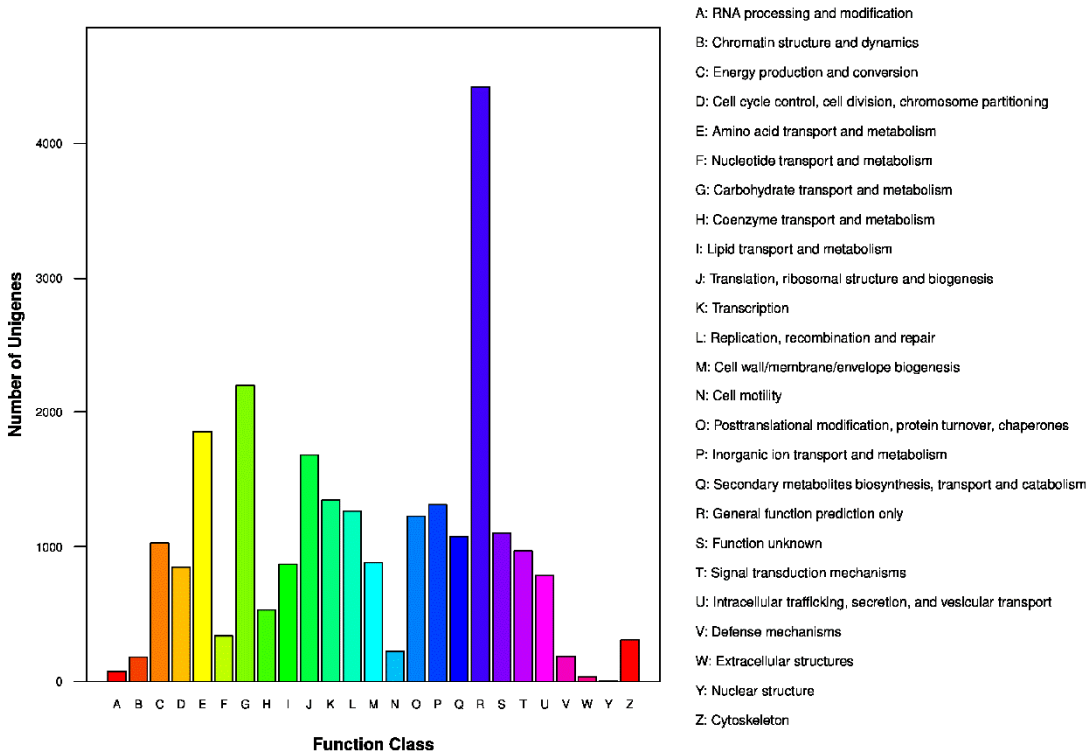
**Figure S1.** Number of the annotated genes against different databases.



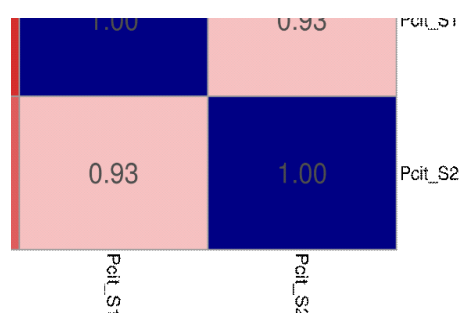
**Figure S2.** (A) E-value distribution of unigenes annotated in the nr database. (B) Species distribution of the first BLAST hits for each sequence with a cut-off E-value of 1.0E-5.



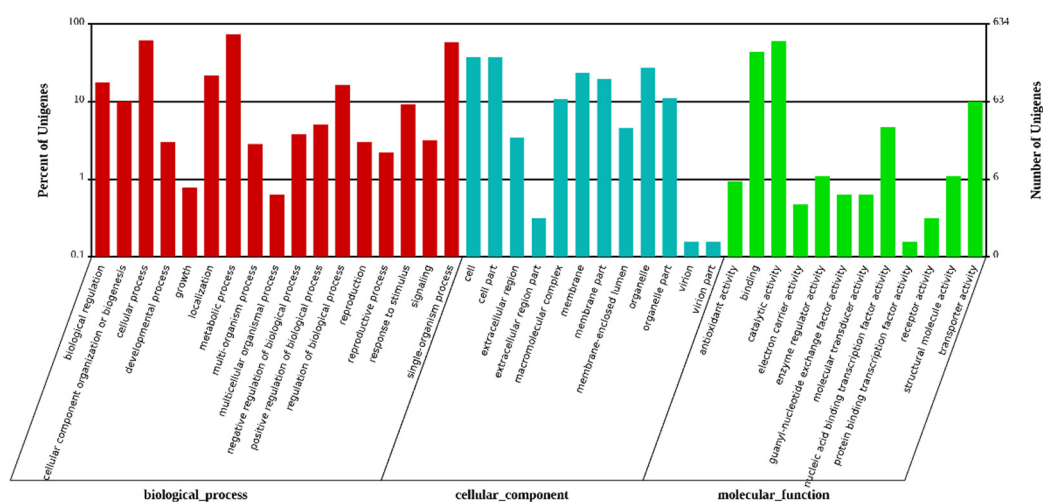
**Figure S3.** Gene Ontology (GO) classification of all unigenes. All unigenes were classified with respect to biological processes, molecular functions and cellular components.



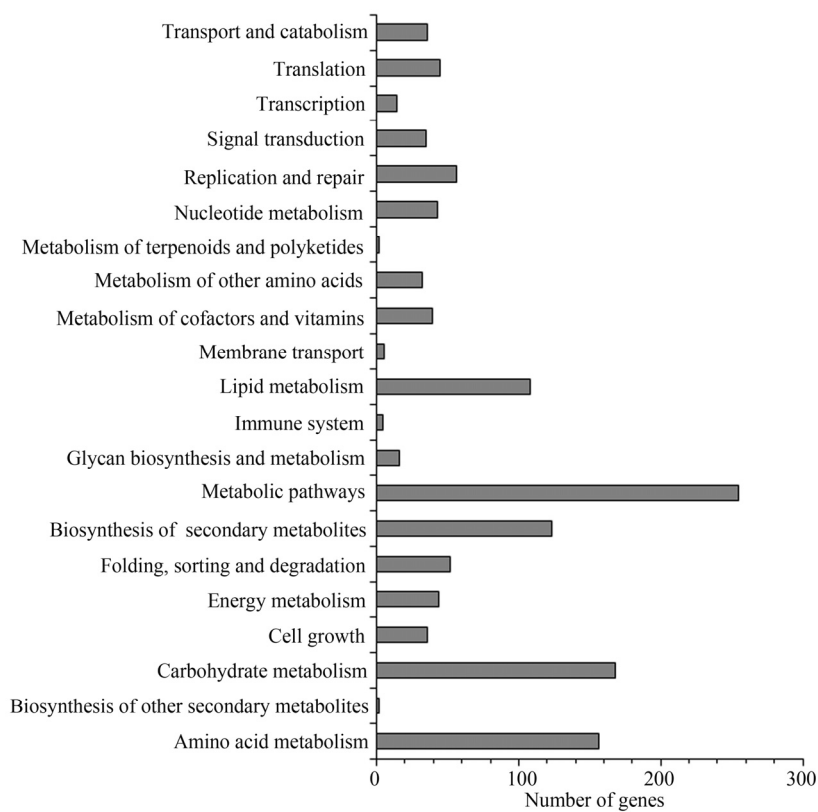
**Figure S4.** COG function classification of all unigenes.



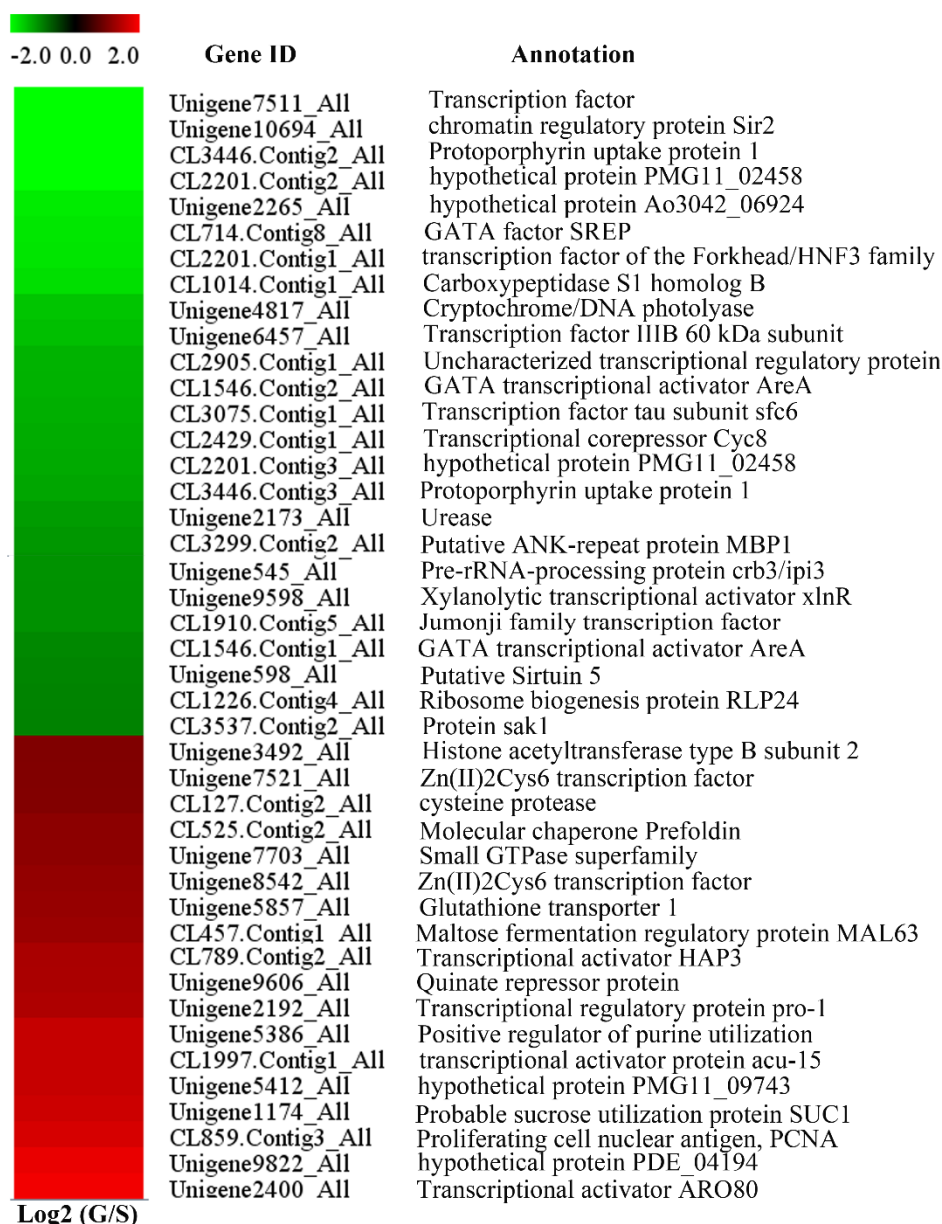
**Figure S5.** Spearman correlation analysis of the two replicates in each group. The vertical and horizontal axes represent the expression levels of all unigenes (log10 (FPKM)).



**Figure S6.** Cluster analysis of DEGs according to GO analysis. A total of 1085 DEGs were clustered using Blast2GO, and the analysis was performed with respect to biological processes, molecular functions and cellular components.



**Figure S7.** Cluster analysis of DEGs according to KEGG pathways. All those genes were classified according to the KEGG pathway database. Clusters of interest were selected for subsequent analysis.



**Figure S8.** Expression profiles of DEGs involved in transcription factors.

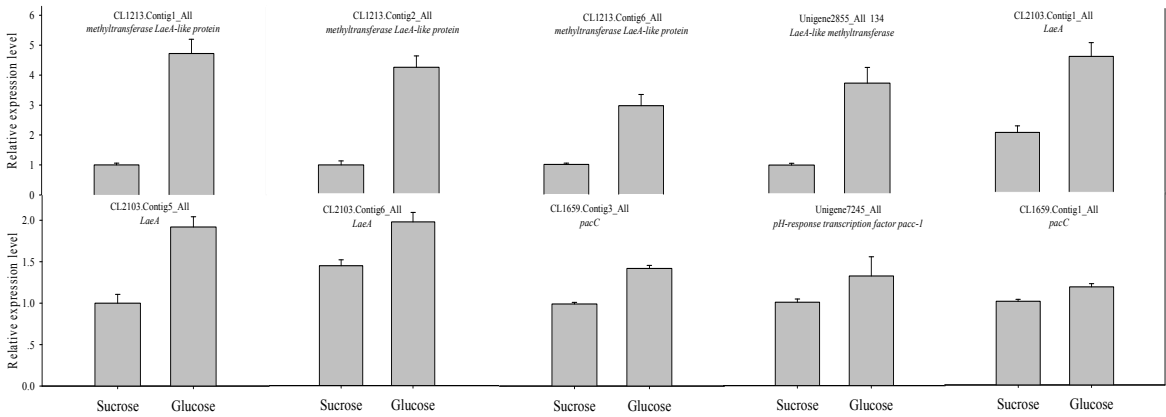


Figure S9. qRT-PCR analysis of expression levels of *LaeA* and *pacC* genes.

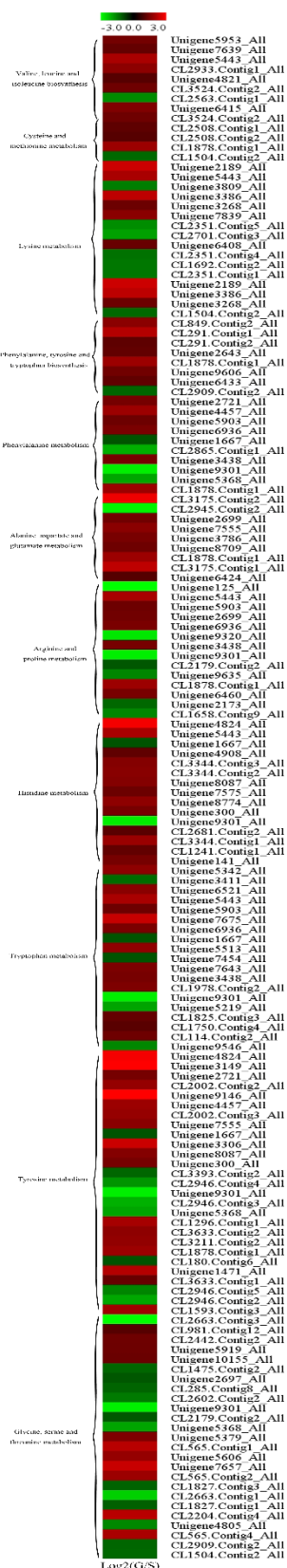


Figure S10. Expression profiles of DEGs involved in amino acids metabolism.