

Supplementary Materials

Table S1. Primers used in qRT-PCR.

Gene id			Primer	
evm.TU.Contig4.662	F*	5'	GCTTCACCGACCGCTACAACCTG	3'
	R*	5'	CAGCAGCAAGCAGGTTCGAGATAC	3'
evm.TU.Contig2.1111	F	5'	ACGAGAGCAGAGTGTCCAAGGAG	3'
	R	5'	GTTGACATCGGCCGAGAGGTTG	3'
evm.TU.Contig2.1123	F	5'	GGGAGAGACGGGAGCCTACATTC	3'
	R	5'	ACATCATCCTCACTCGGTCCAGAG	3'
evm.TU.Contig5.810	F	5'	GATCGCTCCAACCTCGCCTCAAC	3'
	R	5'	CGGCAGTTCGCTTCAAGACCTC	3'
evm.TU.Contig30.108	F	5'	CATCATCAGCGACTTCACCGTCTC	3'
	R	5'	GGATGTCACCGTTGGAAGCAGAG	3'
evm.TU.Contig17.77	F	5'	TGGTATGGATGGTTCGGTGGAGAG	3'
	R	5'	AGAGGCGGCGTAGGTGATGTAG	3'
evm.TU.Contig9.224	F	5'	CACTGCTTTGTTTGC GGGAATCAC	3'
	R	5'	CGATGTGGAACGAGTTGGTGTAGG	3'
evm.TU.Contig20.314	F	5'	GCCCTGGTTTCATCTGCCTACAC	3'
	R	5'	ACCGAGAAACAAACAGCGAGACAC	3'
evm.TU.Contig1.616	F	5'	CCAACGGCACTGACATCCACTG	3'
	R	5'	AGAGAAAGAAACACCAGGACAAGGC	3'
evm.TU.Contig16.341	F	5'	ATATACGCCTCCCTCCGAGTTAGTG	3'
	R	5'	AGCCGACAATATGATGCCTGTTACC	3'
evm.TU.Contig19.352	F	5'	TCACGAACTGGAGGGCTTAGAGG	3'
	R	5'	CCGTCATCTGCCACTTCTACATTCC	3'
evm.TU.Contig23.290	F	5'	CTTGCTGAGGTCAACGGCTATGG	3'
	R	5'	ACGAGGAACAGAGGGAAGTGAAG	3'
evm.TU.Contig18.225	F	5'	ACTCGGATGTTTGGGTTGGTTGG	3'
	R	5'	GTCATACGCAACGCCAGTAGAGG	3'
evm.TU.Contig13.313	F	5'	CGCTGCTCTTATCGCTGCTCTC	3'
	R	5'	ACTTCTTCATGCCACCATCGTAGC	3'
novel.1805	F	5'	TCTTGGCTTGGCTGGATCTTGAATG	3'
	R	5'	TGTGGTTGGATAAAACGACGGGAAG	3'
novel.2288	F	5'	CGGCTATGTTGTTGCGGAGGAC	3'
	R	5'	CAACCTTACCGGAACCGAGAAGTG	3'
novel.2293	F	5'	CCGTTCTTCTTGCCGTCCTCC	3'
	R	5'	TTCAAGGATGCGAAGCCGTCAG	3'

* Forward primer or Reversed primer

Table S2. Quality analysis of RNA-Seq sequencing data.

Sample	Raw reads	Clean reads	Clean bases	Error rate(%)	Q20 (%)	Q30 (%)	GC (%)	Total map
BF_R4d_1	49316358	48151054	7.22G	0.02	98.16	94.6	56.3	47254765(98.14%)
BF_R4d_2	48971862	47305862	7.1G	0.02	98.11	94.63	55.9	46257232(97.78%)
BF_R4d_3	49669084	48647556	7.3G	0.02	98.12	94.52	55.89	47745077(98.14%)
BF_R7d_1	47309784	46204562	6.93G	0.02	98.2	94.68	56.49	45361811(98.18%)
BF_R7d_2	48575250	47496712	7.12G	0.02	98.15	94.59	56.54	46717545(98.36%)
BF_R7d_3	48963314	47962720	7.19G	0.03	97.8	93.73	56.64	47058908(98.12%)
R4d_1	48905388	47588660	7.14G	0.02	98.09	94.49	55.57	46621126(97.97%)
R4d_2	47784000	46263794	6.94G	0.02	98.08	94.42	55.18	45376497(98.08%)
R4d_3	47735346	46341570	6.95G	0.02	98.19	94.73	55.51	45502131(98.19%)
R7d_1	50522322	49517844	7.43G	0.02	98.12	94.49	56.07	48434677(97.81%)
R7d_2	55207722	54225066	8.13G	0.02	98.25	94.78	56.52	53480130(98.63%)
R7d_3	47240898	46161110	6.92G	0.02	98.21	94.71	56.51	45376885(98.3%)

Table S3. Gene annotation and expression analysis of potential response genes in strain CBLJ-3.

	Log2 (Fold change)		Padj		
Gene id	BF_R4d vs R4d	BF_R7d vs R7d	BF_R4d vs R4d	BF_R7d vs R7d	Gene description
Genes encoding glucose transporter					
evm.TU.Con tig22.20	−1.227306797	-	0.006217354	-	Hexose transporter 13 / Multicopy suppressor of snf4 deficiency protein 1 / Sugar (and other) transporter
evm.TU.Con tig18.121	−1.091109424	-	0.009672643	-	High-affinity glucose transporter RGT2 / Sugar (and other) transporter
evm.TU.Con tig13.217	−1.115730235	-	0.010275477	-	High-affinity glucose transporter SNF3 / Sugar (and other) transporter
evm.TU.Con tig7.598	−1.54689462	-	0.011735671	-	High-affinity glucose transporter HXT2 / Sugar (and other) transporter
evm.TU.Con tig5.632	−1.449666379	-	0.048741531	-	Probable glucose transporter rco-3 / Sugar (and other) transporter
evm.TU.Con tig2.918	-	- 1.725870496	-	3.13519E−06	Hexose transporter 1 / Sugar (and other) transporter
Related genes to damage fungal cell wall					
evm.TU.Con tig11.337	1.945310073	-	3.71275E−13	-	Probable endo-β-1,4-glucanase D / Glycosyl hydrolase family 61
evm.TU.Con tig16.235	1.813632607	-	1.46054E−09	-	Endo-1,4-β-glucanase IV / Glycosyl hydrolase family 61
evm.TU.Con tig28.214	4.830898872	-	3.67092E−09	-	Probable xyloglucan-specific endo-β-1,4-glucanase A / Glycosyl hydrolase family 12
evm.TU.Con tig19.313	2.234198949	-	3.24014E−06	-	Probable xyloglucan-specific endo-β-1,4-glucanase A / Glycosyl hydrolase family 12
evm.TU.Con tig28.103	3.277833959	-	1.42353E−05	-	Probable xyloglucan-specific endo-β-1,4-glucanase A / Glycosyl hydrolase family 12
evm.TU.Con tig18.203	2.025644872	-	0.000281974	-	Glucan endo-1,6-β-glucosidase B / Glycosyl hydrolase family 5
evm.TU.Con tig18.225	5.385803234	-	0.000219848	-	Endo-β-1,4-glucanase B / Glycosyl hydrolase family 5
evm.TU.Con tig1.720	1.490552348	-	4.73746E−05	-	Probable endo-1,3(4)-β-glucanase / Glycosyl hydrolases family 16
evm.TU.Con tig20.16	-	2.925360733	-	5.55525E−05	Chitinase-1 / Glycosyl hydrolases family 18
evm.TU.Con tig30.145	-	1.127720541	-	0.039018451	Chitinase-1 / Glycosyl hydrolases family 18

evm.TU.Con tig32.86	1.052093729	-	-	0.029231604	Glycosyl hydrolases family 18
evm.TU.Con tig19.330	-2.284435178	-	-	1.20E-12	Chitin synthase
evm.TU.Con tig1.1596	-2.073600898	-	-	0.010060275	Chitin synthase D / Chitin synthase
Sterol synthesis / transfer genes					
evm.TU.Con tig23.290	1.420367125	-	3.90E-06	-	Probable Delta(7)-sterol 5(6)-desaturase / C-5 sterol desaturase / Sterol-C5-desaturase
evm.TU.Con tig2.306	1.383905973	-	2.28E-05	-	Methylsterol monooxygenase / C-4 methylsterol oxidase
evm.TU.Con tig6.165	2.730195482	1.290754477	0.000187141	0.023512876	Sterol uptake control protein 2
evm.TU.Con tig6.163	2.64514561	1.579654627	0.000454146	0.0425209	Sterol uptake control protein 2
evm.TU.Con tig2.889	4.01990853	-2.140157526	2.73E-24	0.000129215	Sterol 24-C-methyltransferase erg-4 / Delta(24)-sterol C-methyltransferase
evm.TU.Con tig17.12	1.033408709	-	0.016699708	-	Sterol 24-C-methyltransferase erg-4 / Delta(24)-sterol C-methyltransferase
evm.TU.Con tig97.3	-1.797550935	-	7.58E-21	-	Sterol 3- β -glucosyltransferase UGT80B1 / UDP-glucose: sterol glucosyltransferase 80B1
evm.TU.Con tig19.352	-2.038076735	-	1.18E-08	-	Sterol 3- β -glucosyltransferase UGT80A2 / UDP-glucose: sterol glucosyltransferase 80A2
evm.TU.Con tig16.341	-1.501800564	-	4.65E-07	-	Sterol 3- β -glucosyltransferase UGT80A2 / UDP-glucose: sterol glucosyltransferase 80A2
evm.TU.Con tig29.33	-1.090541494	-	0.001046147	-	Sterol 3- β -glucosyltransferase UGT80A2 / UDP-glucose: sterol glucosyltransferase 80A2
evm.TU.Con tig13.242	-1.106797469	-	0.001354601	-	Sterol 3- β -glucosyltransferase UGT80A2 / UDP-glucose: sterol glucosyltransferase 80A2
Fungal metabolite synthesis genes					
evm.TU.Con tig2.1111	-6.044304189	-3.349124586	1.14E-42	0.008143923	Highly reducing polyketide synthase azaB / HR-PKS azaB
evm.TU.Con tig25.194	-1.762052148	-	3.77E-07	-	Reducing polyketide synthase PKS2 / T-toxin biosynthesis protein PKS2

evm.TU.Con tig4.114	−1.038261919	-	0.016361089	-	Fusarin C cluster PKS/NRPS FUS1 / Fusarin biosynthesis megasynthetase / Fusarin biosynthesis protein 1
evm.TU.Con tig2.1106	−4.873128	−3.191589465	1.03E−18	0.000369083	Nonribosomal peptide synthetase 8
evm.TU.Con tig2.1120	−4.881269357	−3.139340497	4.55E−43	0.007720758	Nonribosomal peptide synthetase dtxS1 / Destruxin synthase dtxS1 / Destruxin synthesis protein 1
evm.TU.Con tig2.1105	−2.668034775	-	0.000104188	-	Nonribosomal peptide synthetase 12
Drug resistance genes					
evm.TU.Con tig1.616	1.98265593	-	2.80E−13	-	Major facilitator superfamily
evm.TU.Con tig10.57	1.871783393	-	1.26E−08	-	Major facilitator super- family
evm.TU.Con tig20.314	1.517785056	-	3.72E−08	-	Major facilitator superfamily
evm.TU.Con tig17.77	2.679730677	-	0.029912132	-	Major facilitator superfamily
evm.TU.Con tig24.56	1.932600128	-	0.002120793	-	Pleiotropic ABC efflux transporter of multiple drugs CDR1/CDR ABC trans- porter
evm.TU.Con tig17.72	2.345504487	-	0.000415221	-	Multidrug resistance protein CDR1 / CDR ABC transporter
evm.TU.Con tig19.290	3.363687782	-	1.71E−09	-	ABC transporter CDR4 / CDR ABC transporter
evm.TU.Con tig5.810	5.280572337	-	0.021739634	-	Multidrug resistance protein CDR2 / CDR ABC transporter
DEGs of hub genes					
evm.TU.Con tig2.1115	−4.83003	-	7.59E−19	-	L-aspartate decarboxylase dtxS4 / Destruxin synthesis protein 4
evm.TU.Con tig23.121	−1.05853	-	0.000384	-	Glutamate/Leucine/Phe- nylalanine/Valine dehy- drogenase
evm.TU.Con tig13.145	-	−1.94912	-	3.57E−09	Heat shock protein 90 homolog / Hsp90 protein
evm.TU.Con tig3.801	-	−1.77591	-	5.79E−08	Heat shock 70 kDa protein / Hsp70 protein

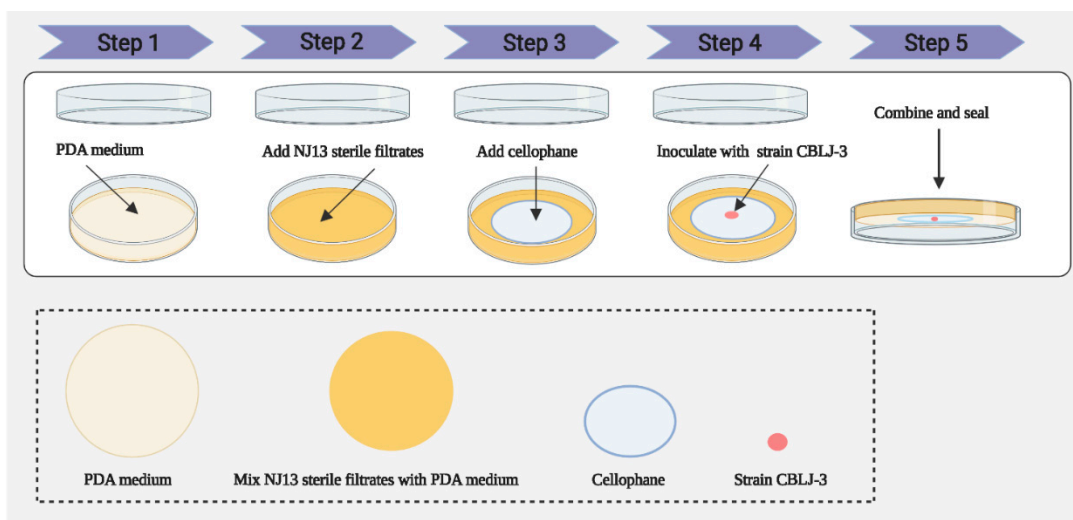


Figure S1. Procedure used for the interaction of CBLJ-3 with NJ13 sterile filtrates. Created with Biorender.com (<https://biorender.com>, accessed on 9 April 2020).

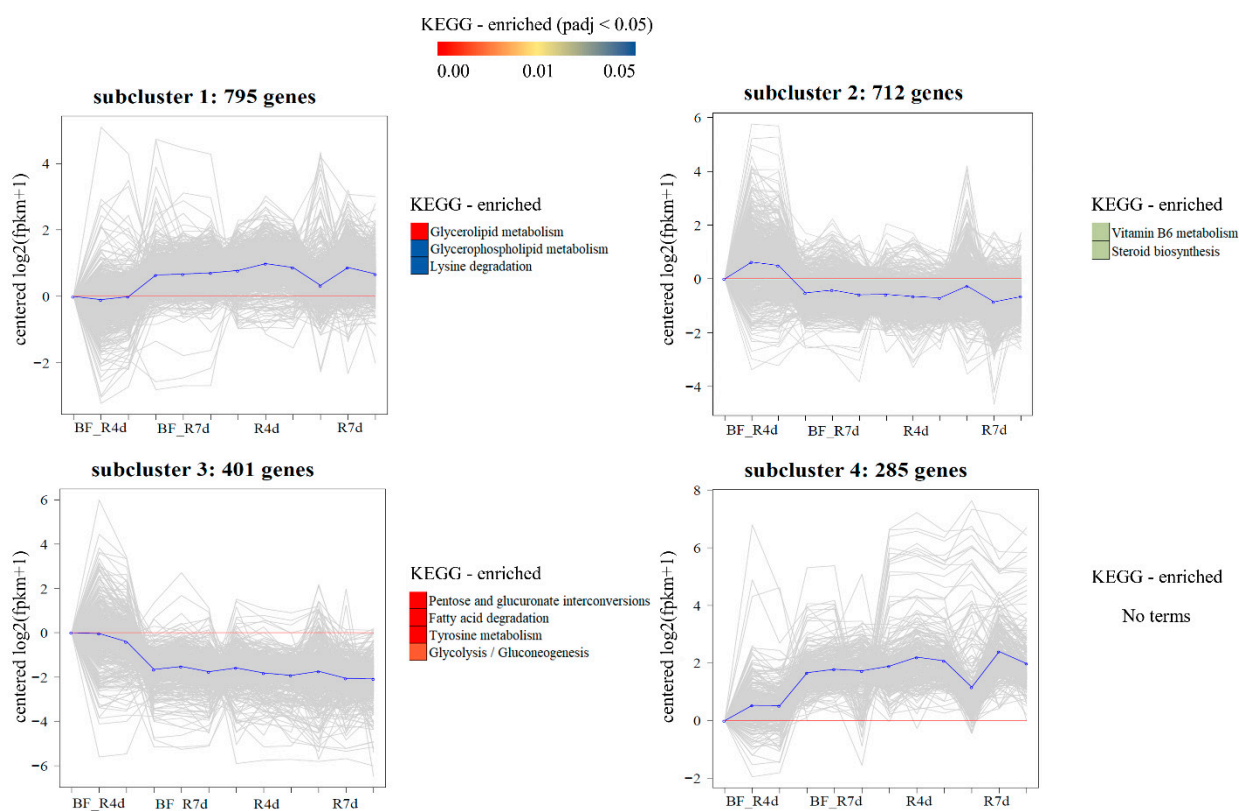


Figure S2. Analysis of KEGG category distribution of DEGs in the four co-expression subclusters constituting the transcriptome of CBLJ-3 under NJ13 sterile filtrates stress. The abscissa is the sample name, and the ordinate is the expression value corrected by the centralized logarithm. The gray line indicates the expression level of genes in the subclusters under different experimental conditions, and the blue line indicates the average expression value of all DEGs in the subcluster under different experimental conditions. By using clusterProfiler R package (Southern Medical University, Guangzhou, China) and $p \text{ adj} < 0.05$, the KEGG enrichment analysis was computed.

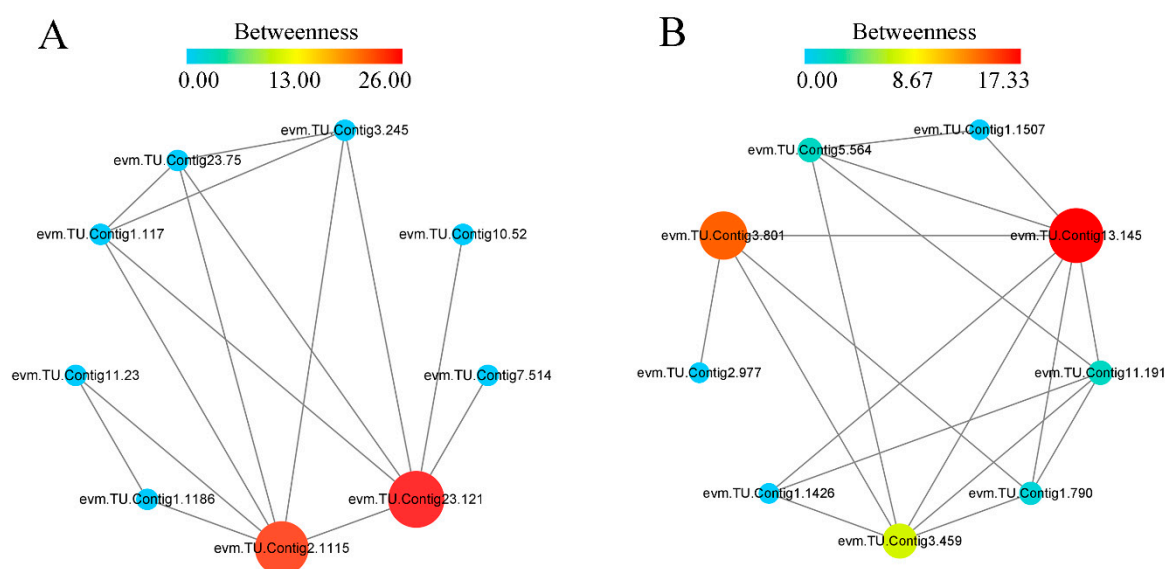


Figure S3. PPI analysis of DEGs at 4 dpi and 7 dpi by the "Betweenness Centrality" method. (A) BF_R4d vs R4d. (B) BF_R7d vs R7d.

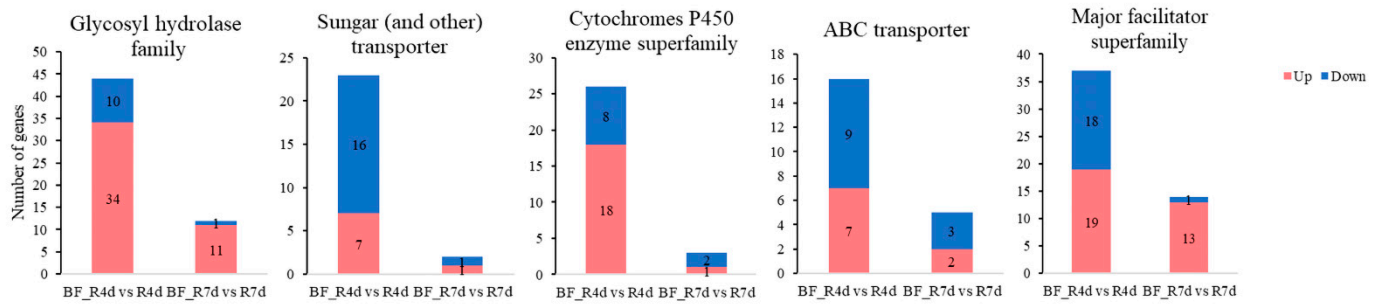


Figure S4. Based on transcriptomic annotation analysis, taxonomic analysis of DEGs. ($|\log_2(\text{fold change})| > 1$, $p_{\text{adj}} < 0.05$).

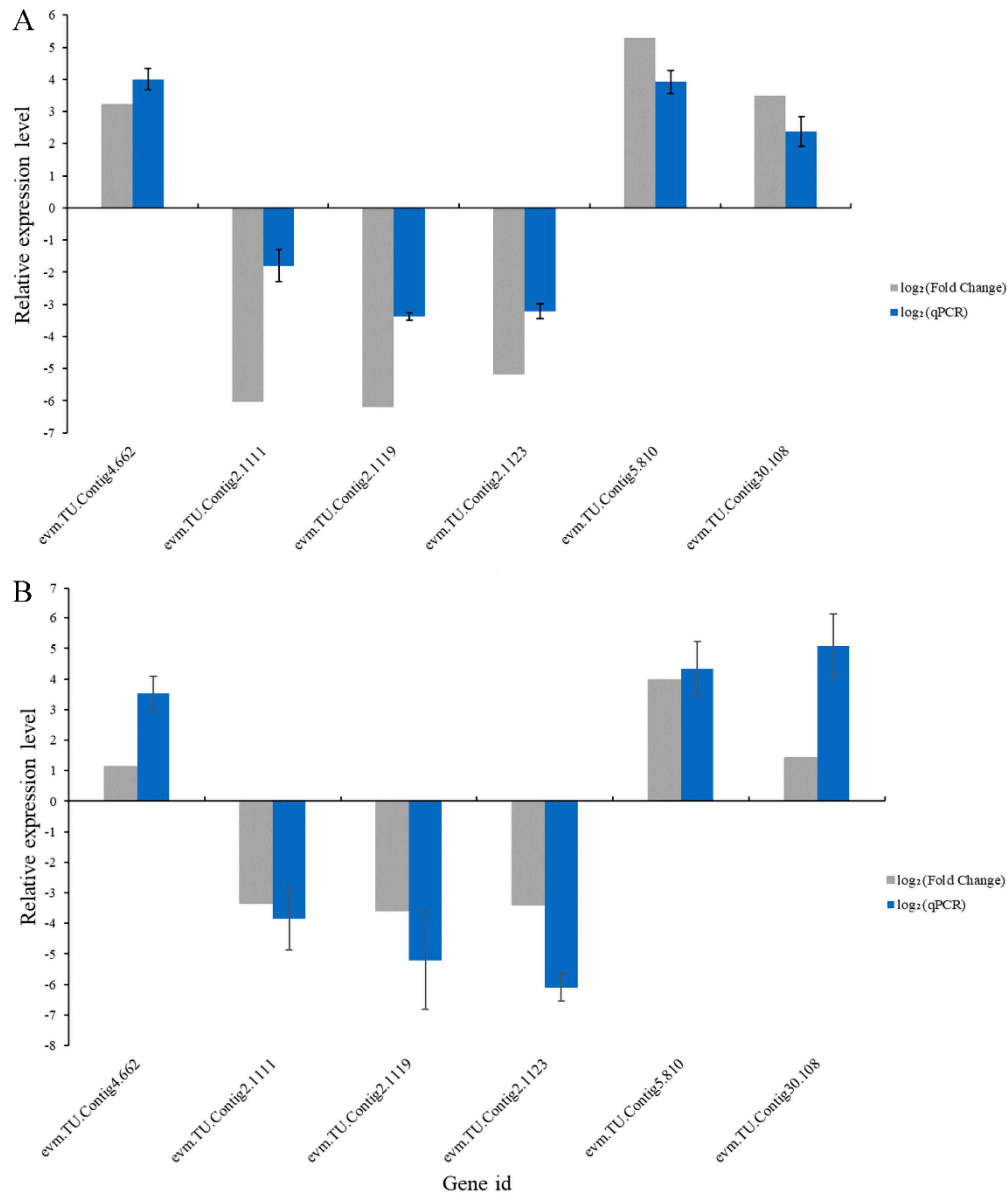


Figure S5. Relative expression level of 6 DEGs in (A) BF_R4d vs R4d and (B) BF_R7d vs R7d using reference gene β -actin for normalization by qRT-PCR included evm.TU.Contig4.662 (endo-1,4-beta-xylanase 1), evm.TU.Contig2.1111 (highly reducing polyketide synthase azaB), evm.TU.Contig2.1119 (acetohydroxy-acid synthase catalytic subunit AHAS), evm.TU.Contig2.1123 (putative sterigmatocystin biosynthesis peroxidase stcC), evm.TU.Contig5.810 (multidrug resistance protein CDR2), and evm.TU.Contig30.108 (pectate lyase). The X-axis indicates the name of the DEGs, and the Y-axis indicates the relative expression of the DEGs.