Comparative Transcriptome Analysis Identified Candidate Genes Related to Mushroom Formation of Bailinggu and Genetic Markers for Genetic Analyses and Breeding

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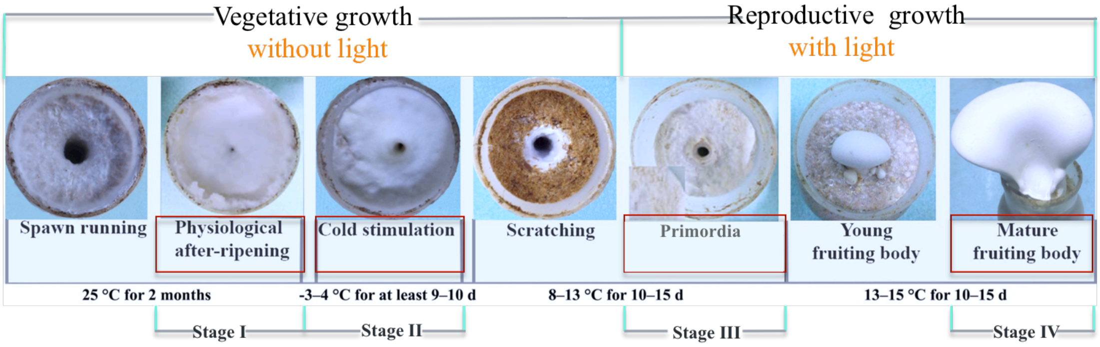
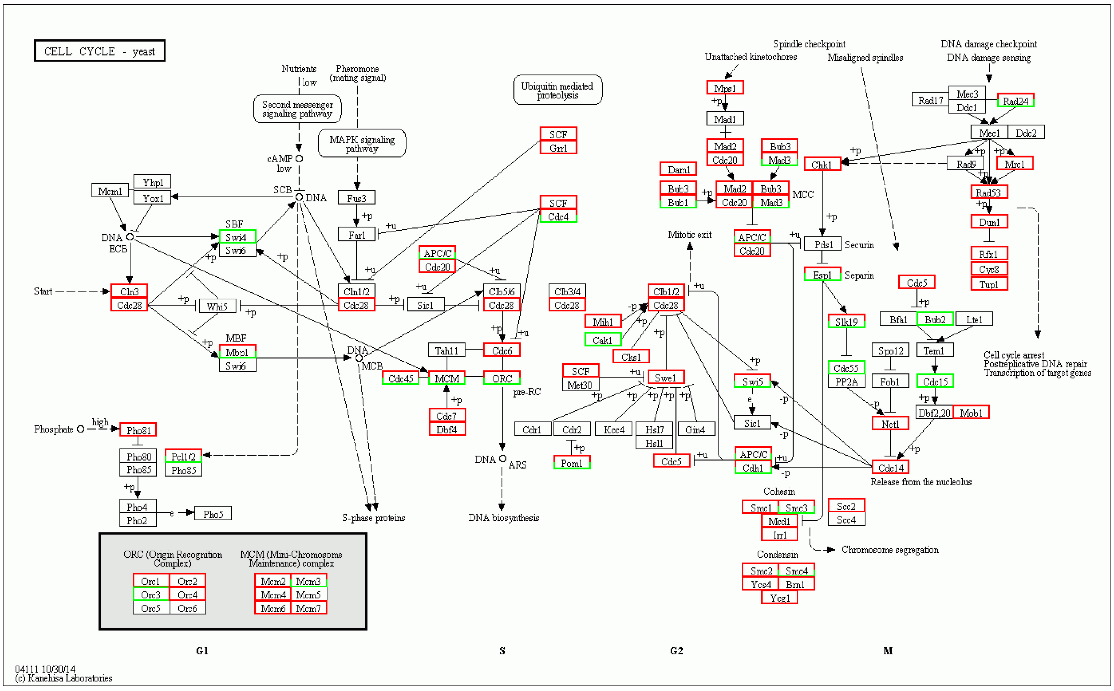
Supplementary Figure S1-6

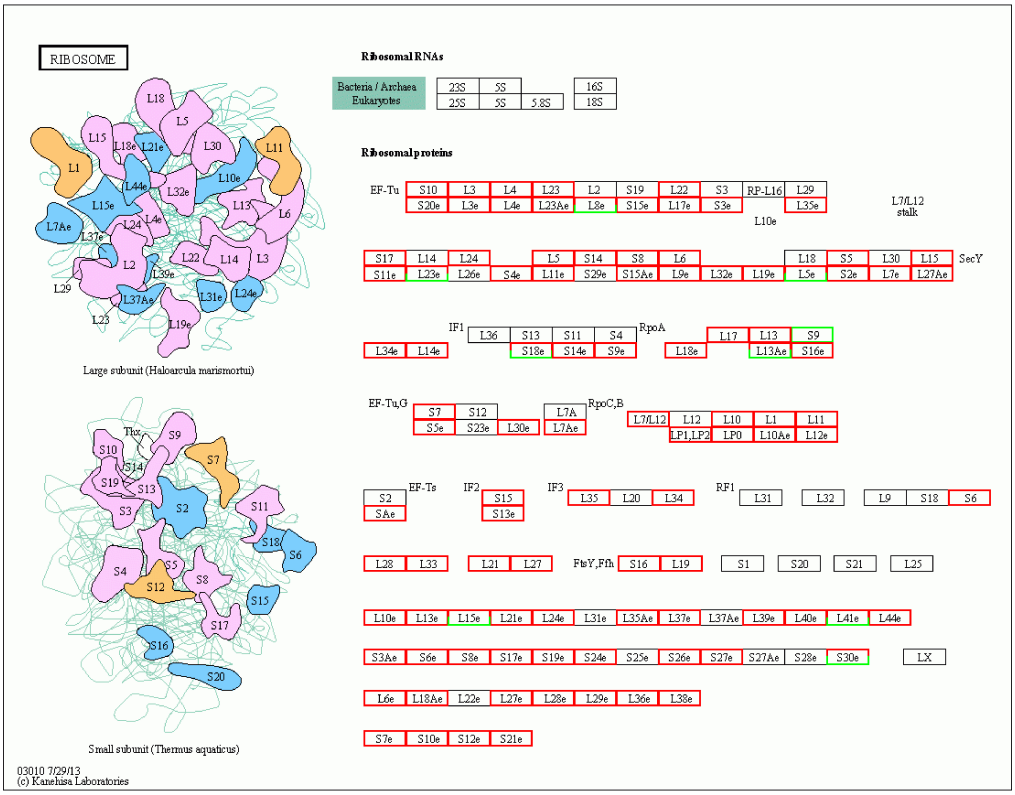
Supplementary Table S1-8



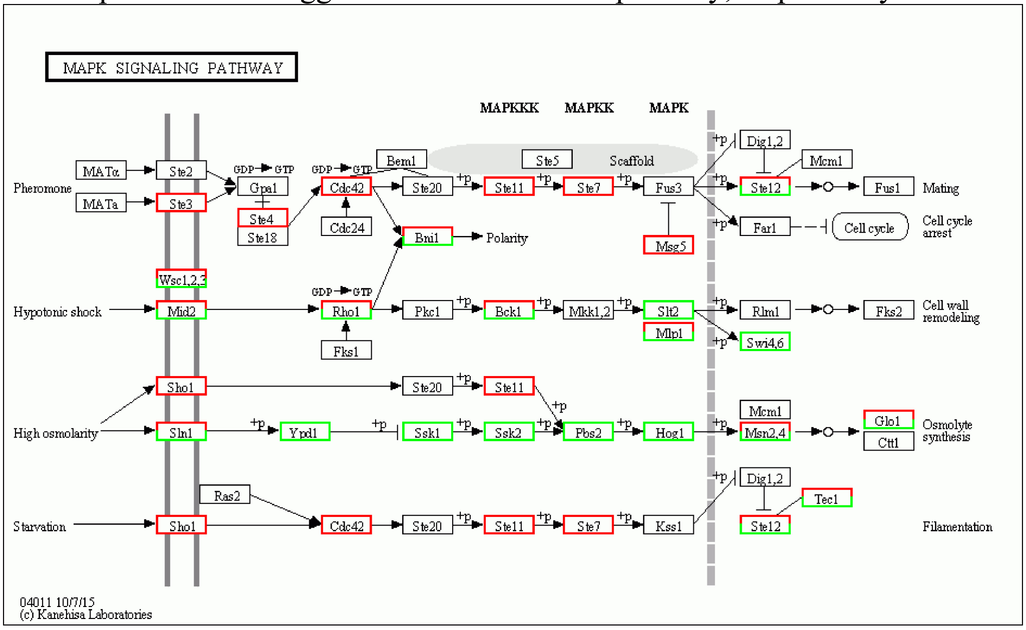
Supplementary Figure S1. Developmental stages of Bailinggu in year-round mushroom factory cultivation cycles. The vegetative (spawning, physiological ripening, cold stimulation) and fructification (primordia, fruiting body) phases are shown.



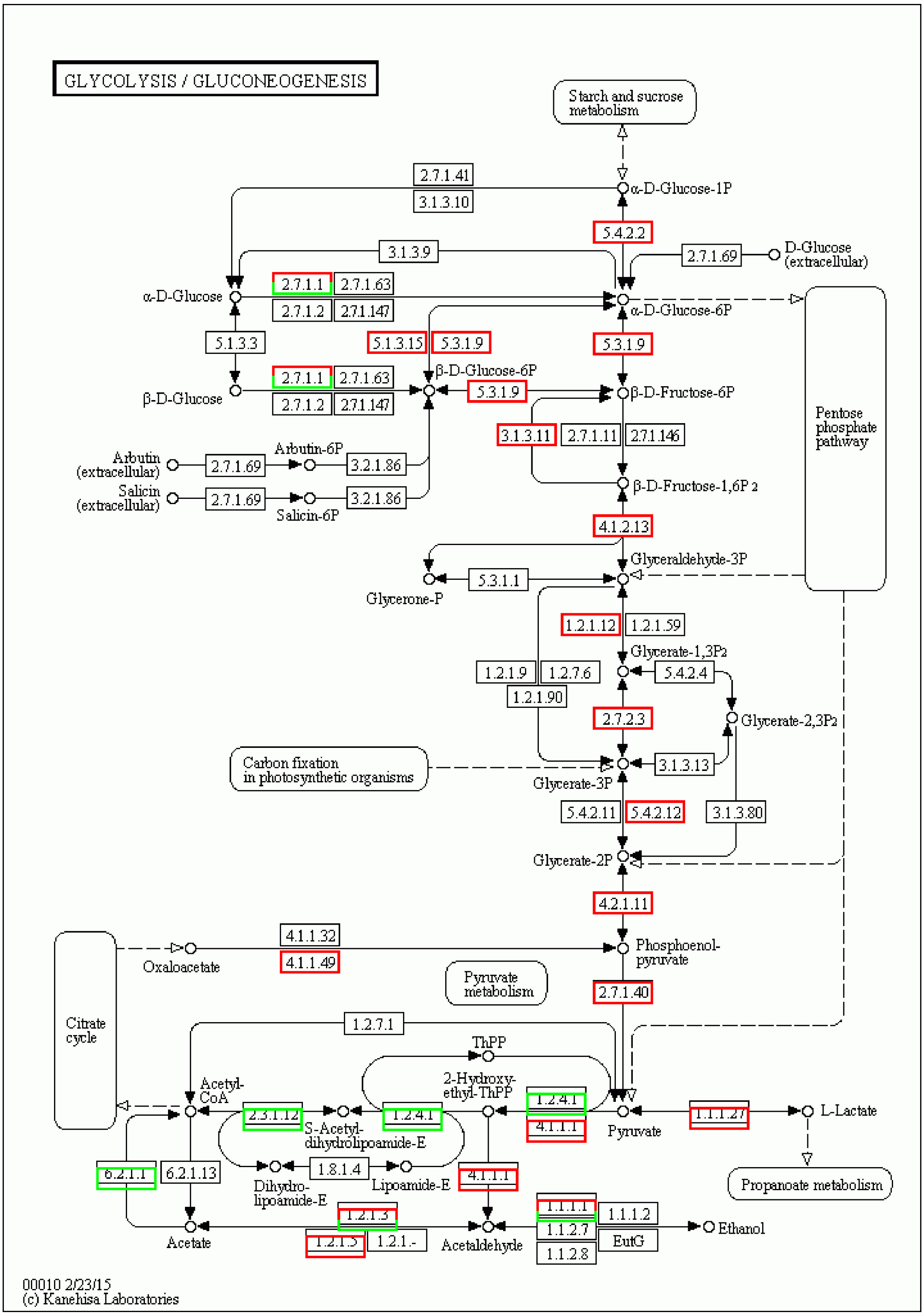
Supplementary Figure S2. The vegetative-to-reproductive transition stage related pathway-Cell cycle (http://www.kegg.jp/kegg/kegg1.html, derived from KEGG map04111) was identified by KEGG annotation [1-3]. The red and green boxes indicate that the up-regulation and down- regulation unigenes identified in the transcriptome of Bailinggu are annotated in the pathway, respectively.



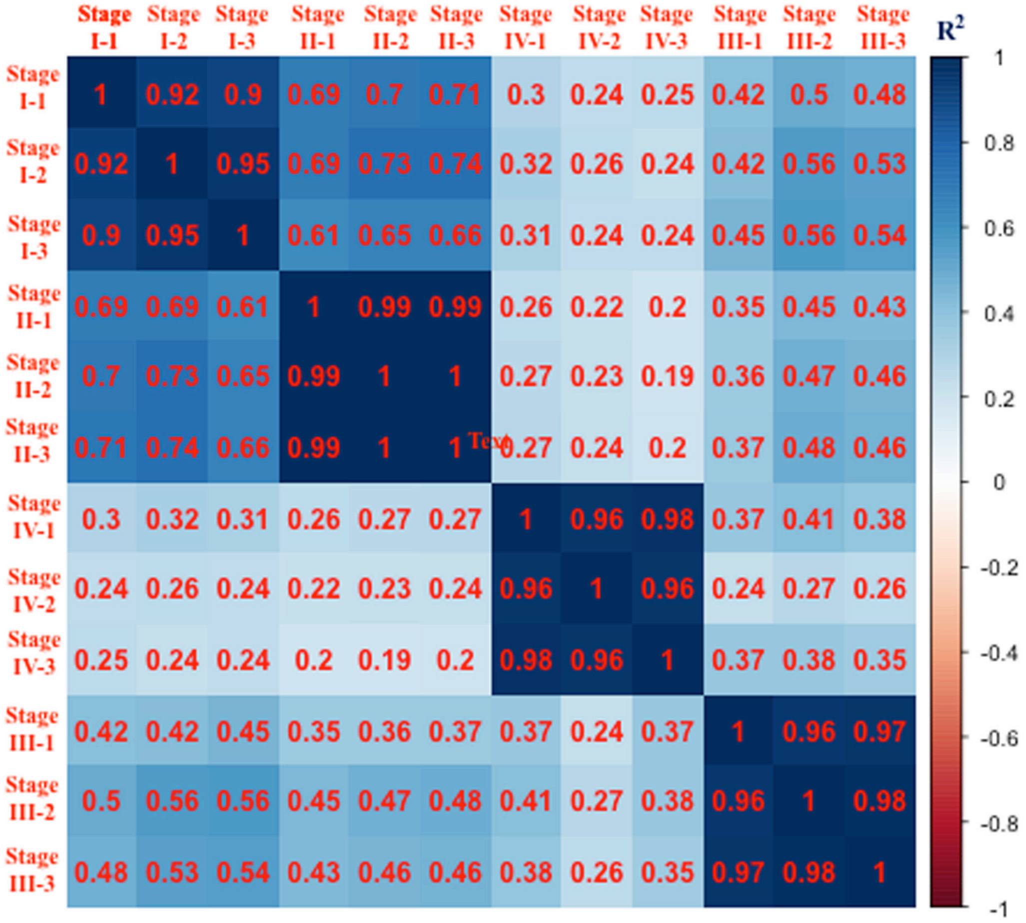
Supplementary Figure S3. The vegetative-to-reproductive transition stage related pathway-Ribosome (http://www.kegg.jp/kegg/kegg1.html, derived from KEGG map03010) was identified by KEGG annotation [1-3]. The red and green boxes indicate that the up-regulation and down-regulation unigenes identified in the transcriptome of Bailinggu are annotated in the pathway, respectively.



Supplementary Figure S4. The vegetative-to-reproductive transition stage related pathway-Mitogen-activated protein kinases (MAPK) signaling pathway (http://www.kegg.jp/kegg/kegg1.html, derived from KEGG map04011) was identified by KEGG annotation [1-3]. The red and green boxes indicate that the up-regulation and down-regulation unigenes identified in the transcriptome of Bailinggu are annotated in the pathway, respectively.



Supplementary Figure S5. The reproductive growth stage related pathway-Glycolysis (http://www.kegg.jp/kegg/kegg1.html, derived from KEGG map00010) was identified by KEGG annotation [1-3]. The red and green boxes indicate that the up-regulation and down- regulation unigenes identified in the transcriptome of Bailinggu are annotated in the pathways, respectively.



	Stage I-1	Stage I-2	Stage I-3	Stage II-1	Stage II-2	Stage II-3	Stage IV-1	Stage IV-2	Stage IV-3	Stage III-1	Stage III-2	Stage III-3
Stage I-1	1	0.92	0.9	0.69	0.7	0.71	0.3	0.24	0.25	0.42	0.5	0.48
Stage I-2	0.92	1	0.95	0.69	0.73	0.74	0.32	0.26	0.24	0.42	0.56	0.53
Stage I-3	0.9	0.95	1	0.61	0.65	0.66	0.31	0.24	0.24	0.45	0.56	0.54
Stage II-1	0.69	0.69	0.61	1	0.99	0.99	0.26	0.22	0.2	0.35	0.45	0.43
Stage II-2	0.7	0.73	0.65	0.99	1	1	0.27	0.23	0.19	0.36	0.47	0.46
Stage II-3	0.71	0.74	0.66	0.99	1	1	0.27	0.24	0.2	0.37	0.48	0.46
Stage IV-1	0.3	0.32	0.31	0.26	0.27	0.27	1	0.96	0.98	0.37	0.41	0.38
Stage IV-2	0.24	0.26	0.24	0.22	0.23	0.24	0.96	1	0.96	0.24	0.27	0.26
Stage IV-3	0.25	0.24	0.24	0.2	0.19	0.2	0.98	0.96	1	0.37	0.38	0.35
Stage III-1	0.42	0.42	0.45	0.35	0.36	0.37	0.37	0.24	0.37	1	0.96	0.97
Stage III-2	0.5	0.56	0.56	0.45	0.47	0.48	0.41	0.27	0.38	0.96	1	0.98
Stage III-3	0.48	0.53	0.54	0.43	0.46	0.46	0.38	0.26	0.35	0.97	0.98	1

Supplementary Figure S6. Pearson correlation between samples using FPKM. The $\log_{10}$ (FPKM+1) of the samples are displayed along the x-axis and y-axis. R^2 represents the Pearson correlation coefficient squared.

Supplementary Table S1. Characteristics of the 100 novel EST-SSR markers used in this study.

Locus	Motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	T_a (℃)	Polymorphism/Monomorphism/No product		
					Bailinggu	Aweigu	Xingbaogu
BlgSSR1	(CTC)6	GCATTCGAACTCTCCACCTC	GACTTCGATTCGCAAGAACC	60	P	P	P
BlgSSR2	(TCG)5	TGATCGTGGTCATCTGGGTA	GTCCTATACCAGGCTGCTCG	60	P	P	P
BlgSSR3	(GAG)5	CGTCGGCATATCGACTATCA	CTGGCTATGACTCCCATCGT	60	P	P	P
BlgSSR4	(TA)7	ACTCGCACGACACTTCACTG	CAAGGATGTGGAATGCAATG	60	P	M	P
BlgSSR5	(CAG)5	GCATACTCTCAGCCGTCCTC	TTAGAGAGTGGCGGTCGAAT	60	P	P	P
BlgSSR6	(TA)7	ATCTCACGTTGAGCAGGTCC	ACCTATCACGAGCCGCATAC	60	P	P	P
BlgSSR7	(CGC)5	TTCAGTTCAGCGAACCCTCT	TTAGCCTTCTCGACGGTGTT	60	P	P	P
BlgSSR8	(AT)7	TCCTCTATCTCGCCCATCAC	GGGACAGCCTATTCGAGGAT	60	P	P	M
BlgSSR9	(TGA)5	TCTTGGTCGAAGAAAGCGAT	CTTTCCGAGATGTACGCTCC	60	P	M	M
BlgSSR10	(TTG)5	CCAGAGGGCGTATAGTGGTC	AACGACCAGGACACGATGAT	60	P	P	P
BlgSSR11	(CCA)5a(CAC)6ctcggtctcgatccctaccaaagctatctcgacgatcatcataatcatcgtaaccaccagggccgggaccaggg(CCT)6	TCCATAATTGTCATCTCCCCA	AAATAATTACGACGGTGGGC	60	P	P	P
BlgSSR12	(CGA)6	ACGGCGATACGAATGAAGTC	GGAAGACCATTGCTGATCGT	60	P	P	P
BlgSSR13	(AT)9	GCCGCAAGAAATATCCAAGA	TCAGTCAGGGGAAGTGAACC	60	P	M	P
BlgSSR14	(GTC)5gccgcc(GTCGGT)9	ATCTGTCTCGCGGTGATTCT	CTCGAGACCCTTCTTGACCA	60	P	P	P
BlgSSR15	(CCA)6	ACGTTGGAAACTCCGACATC	GTCGATGGTATCGGACGACT	60	P	P	P
BlgSSR16	(GCT)7gagcgggttgtccaaatagtccaccagaaggttgctgctgttgagaaggctgtccaaagagtccccccagtagtcccaga(CTG)5	ATGAACCGAATCCACCAAAA	GGTAGTTTGTTCGGTCAGCC	60	P	P	P
BlgSSR17	(TGC)6	AGTGTTTGTTCTCGGGGTTG	TTCTGTTCCGTCAGCATCAC	60	P	P	P
BlgSSR18	(GCAAC)5	GTCCTGTCCATCGATGTGTG	GTTGTCTCTCTTTCCGTCCG	60	P	P	P
BlgSSR19	(CAC)5	TGACCACCACCAATCGTAGA	CGTAACATCTGGGGAATGCT	60	M	P	P
BlgSSR20	(CCA)5	ATTGCACGATGACGCTACAG	AAAATGGCAAGATCTGCACC	60	P	P	P
BlgSSR21	(GTG)6	ATTATCCTCCCTGCCTTCGT	CGTCTGAATGTCCACCCTTT	60	P	P	P
BlgSSR22	(CGT)6	TTCGACATCTTCTTCCCCAC	ACCATCCATAGGTGCTCGTC	60	P	P	P
BlgSSR23	(GGT)6	GAAGGTGCGAATATAAGCGG	ACTACGAAGGCCGTCCCTAT	60	P	P	P
BlgSSR24	(GAG)14	ATCGGATTCGTTGTCGGTAG	CGGATTCCTCCTCTTCTTCC	60	P	P	P
BlgSSR25	(TG)6	TGCATCCTCCTCTGCTACCT	ATACAATCGCCTCCGATCAC	60	P	P	P
BlgSSR26	(ACA)5	AAGAGACCGCAAACGAAATG	CAAGGCGGGTGGTCTTAGTA	60	M	P	M

BlgSSR27	(CGT)5	TCTTTGGTTCCAGTCCCAAC	GAGCAGAAGAAGGGCAGCTA	60	P	M	P
BlgSSR28	(GAG)7	GAGCCTTCGAAACGTAGCAC	CCCACATATCAACGTCATCG	60	P	M	M
BlgSSR29	(GGTA)5	CGGTACGCAGATAGAGGGAG	ATCGTCTACCCAATGCCAAG	60	P	M	P
BlgSSR30	(CT)7ccgtttccttctctctttctctttctctttctccg(TC)9	TTTCCCCGCTTTATTGTTTG	ATGGGGAATGGGGATAAGAG	60	P	N	N
BlgSSR31	(CTC)5	CAGCTCTGTCTTCTCCGTCC	GGTAAAGCAACTCGAGCGAC	60	P	N	N
BlgSSR32	(GTG)6	GTAAATGTGGCGGAGGAAAG	CCACATGGAATGCAGATGAG	60	M	P	M
BlgSSR33	(TGC)5	TCTCACGAGATGGTGGTGAC	CTACGGTGCAGTCGTGTTGT	60	M	M	M
BlgSSR34	(GCG)5	CATCCAAATCCAAATCCCAC	ATCTGAGCCTGGACATCGAC	60	P	M	P
BlgSSR35	(CGC)5	AACATGTTCTCCAAGGCCAC	ATGCGTGCTAACTGAACGTG	60	P	M	M
BlgSSR36	(TCG)6	TTCTTGGTGCTCGATATCCC	ACGGTGGCATTGAAGAAGAC	60	P	M	M
BlgSSR37	(CGA)7	ACAAAGGATACGGCCAACTG	TTGCTTCGCTTGAAGAGTGA	60	P	M	P
BlgSSR38	(CGT)6	TTCGCTTCTTCGTTTTTCGT	GCTAAATGGAGGGTGCGTTA	60	P	N	N
BlgSSR39	(GCA)7	AGAAGAATGGCGGTCAGCTA	TGGTATAGTATGGGTGGCGG	60	P	P	P
BlgSSR40	(CT)6	AAAGCTTAACTCACGCCCAG	TGGGACCATAGCTGGTTTTC	60	N	N	N
BlgSSR41	(GA)6	ATATGCGGAGGAGAGGGAGT	TGGCGTAGAGTTCTTCGGTT	60	P	P	P
BlgSSR42	(TC)7	CCACCCAAGTCATTCGTTCT	AGAATCTCCCGCGTTTACCT	60	P	M	M
BlgSSR43	(TC)8	AGTAGTGTGCGTGCGAAGTG	GTTGATGCGGCTGGAATACT	60	P	N	N
BlgSSR44	(AT)9	CTCAATCGACAAGCAATGGA	ATGTGATGCTGCGACTCAAG	60	P	M	N
BlgSSR45	(AGC)6	GCTCGAAGAAAAGGCAACTG	CGAAAAGCCTAGATGCTCCA	60	M	N	N
BlgSSR46	(TGTA)6	CCGTTCCTTCTTTTGCTCTG	AGGTATACAACCTGACGCGG	60	P	M	N
BlgSSR47	(GGC)7	CTTAACGTCGTCGTCCCATT	AACGTCGAGACATACCGGAC	60	P	P	M
BlgSSR48	(ACCG)7	ACCCCTTACGGACTAACGCT	CTGTTCTTGCTGTCCGTGAA	60	P	M	M
BlgSSR49	(AT)8	CCACCGATTCTTGGACTCAT	GAGTGTCCCGAAGTCTGAGC	60	P	M	M
BlgSSR50	(GGC)5	GGAGGTTGACGTGAACGAAT	GCGAAGATTCTACGAGTCCG	60	P	M	P
BlgSSR51	(CGA)6	CGGATCCGAACCTAGTCAAA	GCCGGTATATTCGTCCTTGA	60	M	M	M
BlgSSR52	(CCG)5	CATCCTCGGGTTGATGATTT	CAGCGGACCTTACTGAGGAG	60	N	N	N
BlgSSR53	(CG)8	CCCTCTGCAAATCGTCTAGG	GAAATACGGGTATGCCAACG	60	P	N	N
BlgSSR54	(AT)7	CTCATTGCGCACAACATTCT	CAATACCCTTTCTTGTCCGC	60	P	N	N
BlgSSR55	(GCG)7	AGGTGTGTTGGGAGGTGAAG	CGGCTCGTCATTTATCCATT	60	P	P	P
BlgSSR56	(CG)6	TCGCCGTCGTCTAATTCTTC	AGAAAGAATGGGGAGGAGGA	60	N	N	N
BlgSSR57	(AT)8	CGCTTGGAGCTACCTACTGC	AACGTAGATGACGGGAGGTG	60	P	N	N
BlgSSR58	(ACC)5	GCAGATATTGATGTCGCCCT	TGGAGTATAAGGTACGGCGG	60	P	P	N
BlgSSR59	(CTC)5	CCGAAAGTCCAAAGTCCAAA	ACCCATTGTCCGTTTTGTGT	60	P	N	N
BlgSSR60	(AAG)5	AAATGGGCTCTCGTGTCTTG	GCTTGGTGGACAGAGGAGAG	60	P	P	M
BlgSSR61	(GAC)5	GACGAGCTCATGAGTGGACA	CTCACTTCCGTAGTCGGCTC	60	M	M	M
BlgSSR62	(AT)6	TTGGTGGAGGAACTTTGAGG	GACGGATTCTTCGCACTCTC	60	P	P	M
BlgSSR63	(GAC)5	AGTTAGTAAA	GTGACCTTTGT	60	M	M	M

		CGCGCTCCGA	ACGCCGTCT				
BlgSSR64	(CG)6	AGTGGGAATACGAACGAACG	CACGACACCTTACCATGTGC	60	M	P	M
BlgSSR65	(GTC)5	CTAAATAACCGTTCGCCCAA	GTTCTGTGGAAGAAGCAGGC	60	M	M	M
BlgSSR66	(CT)6	TTCGCTCATCCTAAGGCACT	CGAGTGGGAAGAAGCGTAAG	60	M	P	P
BlgSSR67	(CTC)5	AAGGATCCCTGGACGTTTCT	ATCTCCGCTGTGGTCAATTC	60	M	M	M
BlgSSR68	(CAG)6	AATTCAAGGGAATTGGGGAC	GGTTGCTGTTGTGGTTGTTG	60	N	N	N
BlgSSR69	(CG)7	TCGAGTCTCCAAAGATGCCT	TGTGCCTCCTTAACCAGCTC	60	M	M	M
BlgSSR70	(TCC)5	TCGTGTCTCTACGTTCGTGC	AGACGAGAATGCGAACGACT	60	M	M	M
BlgSSR71	(CCA)5	ATTTCCATATCTTCCCCGCT	TCTTGAATCTGAGCACGCTG	60	P	M	M
BlgSSR72	(AG)7	CGGTGCCAGTGTTCCTTATT	TGATTCCTGCCCTTTCATTC	60	P	M	M
BlgSSR73	(CCGC)6	GCTAGTTTCTTGTCTGCCCG	ATTTAACGAGTGGGCCAGTG	60	P	M	M
BlgSSR74	(AATG)6	CATCTTAGCCGCTGGTTTTC	ATTCCGTAAGTTGGGCAGTG	60	P	P	M
BlgSSR75	(CGT)6	AGTGCCATATGACCCAAAGC	CCCTATCGCACAAAAAGCAT	60	M	N	P
BlgSSR76	(GAG)5	CGAGGAAGGCGAGACAATAC	GTCCTCGTCGTCCTCTTCAG	60	M	M	P
BlgSSR77	(TCA)6	ATGGTTACTTCGTGTTCCGC	CGTGCAGCAGACTTTCCATA	60	P	P	P
BlgSSR78	(CGA)5	GAAAGCTCGCCATCAGACTC	AGAAGAAGCCCGAAGAGAGC	60	M	P	P
BlgSSR79	(CAA)6	CCACCACCTCGTTTCACTTT	AACTTGATCCATGGGCTGAG	60	P	P	P
BlgSSR80	(TA)9	GCACCGACTATTTGCCGTAT	TTAGGAACATCCGGTGAAGC	60	M	M	P
BlgSSR81	(AC)7	ACTGCGTCGTGGTGTACAAG	GTCGCTAAGTATCGGTGGGA	60	P	N	N
BlgSSR82	(TCC)5	GTCCGCATCATCATCTTCCT	CATAAGCCCGGTAGATCGAA	60	P	M	M
BlgSSR83	(TA)7	GCTAAACCTCTCATCGCCAG	TGGGCTGCACAGACAATAAG	60	P	M	M
BlgSSR84	(GT)7	AAGGACACGCCAAAATGTTC	AAGTGGAACTGAAGCCATCG	60	P	N	N
BlgSSR85	(CGC)5	TTATTGAAGTTGCCTTGCCC	TTTCGGCTTCATATCCTTCG	60	M	P	P
BlgSSR86	(CT)6	CTCCAAGAAGATGTCGGAGC	GAGGACTTCCTCCTGCCTTC	60	P	N	N
BlgSSR87	(GGA)7	TGAAACTCGTCGTCTTGTGG	TTCACCAGGTCGTTCTCCTC	60	P	P	P
BlgSSR88	(GA)6	AGTCTCGAACCCAATCCCTT	CGTTGACCAAGACCCATTCT	60	P	P	P
BlgSSR89	(CG)6	GACCTCTGACCTCGTTCTGG	GAGGATGGAACAGTGGAGGA	60	P	M	M
BlgSSR90	(TC)6	CTTATCGTCCCCGTTCTCAA	GTCCGGATTACACGGTGAAG	60	P	P	M
BlgSSR91	(TGC)5	CTCCCGGTATACCTCGTTCA	ATGTCAATCGTCTAAGCCGC	60	P	M	P
BlgSSR92	(CT)7	GCATTTCACCAGTGTTGTGG	CGGTTCGTGTCTATGTGGTG	60	M	M	M
BlgSSR93	(TCA)5(TCG)7	AATACCGGTGTTCAAGCCAG	CCGCATCAAACCCACTATCT	60	M	P	M
BlgSSR94	(CAG)5	GTTGAGAAGGAGCGTTCCAG	GGGAGAATGGGATTGGACTT	60	P	M	M
BlgSSR95	(CG)6	GTCACCCCCTCCATCCTATT	GGTACGTCATGTTCTGCACG	60	P	M	M
BlgSSR96	(CCT)5	CTCGTCAATAACATCCGCCT	CCAAGAGGAGGACGAAGATG	60	P	M	M
BlgSSR97	(TA)7	CAATCTTGCTACTCTCCGCC	AATCAACGACTGTTGGAGGG	60	M	N	M
BlgSSR98	(GT)6(GC)6	GTACATCTGGGGAAGGGGAT	AGTGAGAAGTGGGGCTTCAA	60	P	P	P
BlgSSR99	(TCC)5	CGCATTGTCGGTCTCAGTAA	ATTAGGGCTGGTCGTTGTTG	60	M	P	P
BlgSSR100	(TCC)6	CCCCGTCCTCTAGTTCATCA	AATACGGGTCGTCAGATTCG	60	P	P	P

Supplementary Table S2. Detailed information for the three Pleurotus taxa populations.

Number	Strain name	Species	Strain types	Source
1	CCMJ964	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
2	CCMJ968	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
3	CCMJ969	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
4	CCMJ973	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
5	CCMJ979	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
6	CCMJ980	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
7	CCMJ981	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
8	CCMJ994	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
9	CCMJ997	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
10	CCMJ1002	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
11	CCMJ828	*P. tuolesis* (Bailinggu)	Cultivated strain	Jilin, China
12	CCMJ829	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
13	CCMJ1123	*P. tuolesis* (Bailinggu)	Cultivated strain	Shandong, China
14	CCMJ1157	*P. tuolesis* (Bailinggu)	Cultivated strain	Heilongjiang, China
15	CCMJ1160	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
16	CCMJ1161	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
17	CCMJ1162	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
18	CCMJ1165	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
19	CCMJ1166	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
20	CCMJ1170	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
21	CCMJ1172	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
22	CCMJ1173	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
23	CCMJ1668	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing, China
24	CCMJ1669	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing, China
25	CCMJ1676	*P. tuolesis* (Bailinggu)	Cultivated strain	Xinjiang, China
26	CCMJ812	*P. tuolesis* (Bailinggu)	Cultivated strain	Xinjiang, China
27	CCMJ1148	*P. tuolesis* (Bailinggu)	Cultivated strain	Sichuan, China
28	CCMJ1667	*P. tuolesis* (Bailinggu)	Cultivated strain	Liaoning, China
29	CCMJ1171	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
30	CCMJ1670	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing, China
31	CCMJ1077	*P. tuolesis* (Bailinggu)	Cultivated strain	Xinjiang, China
32	CCMJ814	*P. tuolesis* (Bailinggu)	Cultivated strain	Xinjiang, China
33	CCMJ983	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
34	CCMJ816	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing, China
35	CCMJ1176	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
36	CCMJ996	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
37	CCMJ987	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
38	CCMJ975	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
39	CCMJ976	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
40	CCMJ1097	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
41	CCMJ999	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
42	CCMJ1000	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
43	CCMJ1001	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
44	CCMJ1003	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
45	CCMJ1119	*P. tuolesis* (Bailinggu)	Cultivated strain	Shanghai, China

46	CCMJ1118	*P. tuolesis* (Bailinggu)	Cultivated strain	Shanghai, China
47	CCMJ819	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing, China
48	CCMJ1163	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
49	CCMJ1164	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
50	CCMJ1167	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
51	CCMJ1175	*P. tuolesis* (Bailinggu)	Wild stain	Xinjiang, China
52	CCMJ1044	*P. tuolesis* (Bailinggu)	Cultivated strain	Beijing,China
53	CCMJ1174	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
54	CCMJ991	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
55	CCMJ992	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
56	CCMJ993	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
57	CCMJ989	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
58	CCMJ990	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
59	CCMJ985	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
60	CCMJ986	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
61	CCMJ970	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
62	CCMJ971	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
63	CCMJ972	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
64	CCMJ1150	*P. eryngii* var. *ferulea* (Aweigu)	Cultivated strain	Sichuan, China
65	CCMJ825	*P. eryngii* var. *ferulea* (Aweigu)	Cultivated strain	Shandong, China
66	CCMJ984	*P. eryngii* var. *ferulea* (Aweigu)	Wild stain	Xinjiang, China
67	CCMJ1717	*P. eryngii* var. *ferulea* (Aweigu)	Cultivated strain	Shandong, China
68	CCMJ1732	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Jiangsu, China
69	CCMJ1066	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Sichuan, China
70	CCMJ656	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Fujian, China
71	CCMJ653	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Fujian, China
72	CCMJ657	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Fujian, China
73	CCMJ1072	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Beijing, China
74	CCMJ1130	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Fujian, China
75	CCMJ1683	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Jilin, China
76	CCMJ1102	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Shanghai, China
77	CCMJ1693	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Liaoning, China
78	CCMJ1699	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Shandong, China
79	CCMJ1707	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Shandong, China
80	CCMJ645	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Beijing, China
81	CCMJ1725	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Shandong, China
82	CCMJ1731	*P. eryngii* var.*eryngii* (Xingbaogu)	Cultivated strain	Liaoning, China

Supplementary Table S3. Characteristics of the 26 polymorphic EST-SSR markers in the three Pleurotus taxa populations.

Locus	Samples	Na	Ne	Ho	He	I	PIC
BlgSSR1	82	7	2.6204	0.268	0.622	1.2293	0.561
BlgSSR2	82	7	3.284	0.256	0.7	1.4534	0.659
BlgSSR3	82	7	2.1455	0.232	0.537	1.148	0.505
BlgSSR4	82	6	3.9705	0.317	0.753	1.5705	0.716
BlgSSR5	82	4	2.5245	0.244	0.608	1.1106	0.553
BlgSSR6	82	10	3.1815	0.244	0.69	1.5109	0.651
BlgSSR7	82	10	3.6915	0.195	0.734	1.7037	0.703
BlgSSR8	82	6	2.2541	0.085	0.56	1.0367	0.49
BlgSSR9	82	2	1.8299	0.305	0.456	0.6459	0.351
BlgSSR10	82	9	3.5057	0.39	0.719	1.5501	0.677
BlgSSR11	82	10	4.7319	0.549	0.794	1.7942	0.761
BlgSSR12	82	10	3.5605	0.512	0.724	1.6051	0.686
BlgSSR13	82	10	6.1016	0.378	0.841	1.9542	0.816
BlgSSR14	82	6	3.9002	0.488	0.748	1.4601	0.7
BlgSSR15	82	13	4.4179	0.402	0.778	1.7817	0.741
BlgSSR16	82	11	4.2289	0.683	0.768	1.7514	0.737
BlgSSR17	82	8	2.5728	0.354	0.615	1.2892	0.571
BlgSSR18	82	10	3.6623	0.573	0.731	1.5917	0.687
BlgSSR19	82	11	2.2417	0.122	0.557	1.2786	0.53
BlgSSR20	82	6	2.8425	0.195	0.652	1.3241	0.609
BlgSSR21	82	6	2.6928	0.207	0.633	1.1458	0.555
BlgSSR22	82	3	2.8282	0.183	0.65	1.0677	0.572
BlgSSR23	82	12	2.6816	0.354	0.631	1.5508	0.611
BlgSSR24	82	10	4.712	0.683	0.793	1.8009	0.761
BlgSSR25	82	12	6.1688	0.476	0.843	2.1353	0.825
BlgSSR26	82	4	1.642	0.098	0.393	0.6829	0.339
Mean		8.077	3.384	0.338	0.674	1.429	0.629

Supplementary Table S4. Characteristics of the 26 polymorphic EST-SSR markers in the Xingbaogu population.

Locus	Samples	Na	Ne	Ho	He	I	PIC
BlgSSR1	15	3.000	1.402	0.333	0.287	0.534	0.26
BlgSSR2	15	2.000	1.142	0.000	0.124	0.245	0.117
BlgSSR3	15	5.000	2.778	0.467	0.640	1.249	0.594
BlgSSR4	15	4.000	2.473	0.600	0.596	1.073	0.539
BlgSSR5	15	2.000	1.301	0.267	0.231	0.393	0.204
BlgSSR6	15	4.000	2.113	0.200	0.527	0.899	0.445
BlgSSR7	15	4.000	3.383	0.067	0.704	1.289	0.651
BlgSSR8	15	1.000	1.000	0.000	0.000	0.000	0
BlgSSR9	15	1.000	1.000	0.000	0.000	0.000	0
BlgSSR10	15	2.000	1.069	0.067	0.064	0.146	0.062
BlgSSR11	15	3.000	2.632	0.933	0.620	1.030	0.548
BlgSSR12	15	3.000	2.663	0.800	0.624	1.028	0.545
BlgSSR13	15	3.000	2.486	0.800	0.598	0.995	0.526
BlgSSR14	15	2.000	1.471	0.400	0.320	0.500	0.269
BlgSSR15	15	5.000	2.778	0.133	0.640	1.203	0.581
BlgSSR16	15	3.000	2.228	0.867	0.551	0.882	0.456
BlgSSR17	15	6.000	3.846	1.000	0.740	1.541	0.703
BlgSSR18	15	3.000	2.419	0.800	0.587	0.970	0.509
BlgSSR19	15	6.000	1.807	0.333	0.447	0.996	0.43
BlgSSR20	15	3.000	1.613	0.467	0.380	0.683	0.342
BlgSSR21	15	2.000	1.867	0.067	0.464	0.657	0.357
BlgSSR22	15	2.000	1.385	0.067	0.278	0.451	0.239
BlgSSR23	15	3.000	2.406	0.467	0.584	0.948	0.495
BlgSSR24	15	3.000	2.866	0.933	0.651	1.074	0.576
BlgSSR25	15	4.000	2.528	0.733	0.604	1.058	0.529
BlgSSR26	15	1.000	1.000	0.000	0.000	0.000	0
Mean		3.077	2.064	0.415	0.433	0.763	0.384

Supplementary Table S5. Characteristics of the 26 polymorphic EST-SSR markers in the Aweigu population.

Locus	Samples	Na	Ne	Ho	He	I	PIC
BlgSSR1	15	2.000	1.385	0.200	0.278	0.451	0.239
BlgSSR2	15	2.000	1.142	0.133	0.124	0.245	0.117
BlgSSR3	15	2.000	1.642	0.000	0.391	0.580	0.315
BlgSSR4	15	1.000	1.000	0.000	0.000	0.000	0
BlgSSR5	15	3.000	1.402	0.333	0.287	0.534	0.26
BlgSSR6	15	4.000	2.239	0.067	0.553	1.057	0.515
BlgSSR7	15	4.000	3.285	0.067	0.696	1.282	0.644
BlgSSR8	15	3.000	2.018	0.400	0.504	0.831	0.428
BlgSSR9	15	1.000	1.000	0.000	0.000	0.000	0
BlgSSR10	15	5.000	3.543	0.667	0.718	1.385	0.67
BlgSSR11	15	2.000	1.965	0.200	0.491	0.684	0.371
BlgSSR12	15	7.000	3.237	0.533	0.691	1.484	0.659
BlgSSR13	15	1.000	1.000	0.000	0.000	0.000	0
BlgSSR14	15	3.000	1.495	0.267	0.331	0.591	0.294
BlgSSR15	15	9.000	3.689	0.733	0.729	1.682	0.704
BlgSSR16	15	6.000	4.286	0.733	0.767	1.580	0.731
BlgSSR17	15	2.000	1.142	0.133	0.124	0.245	0.117
BlgSSR18	15	2.000	1.142	0.133	0.124	0.245	0.117
BlgSSR19	15	6.000	3.879	0.333	0.742	1.522	0.702
BlgSSR20	15	3.000	1.226	0.067	0.184	0.389	0.175
BlgSSR21	15	3.000	1.145	0.133	0.127	0.291	0.123
BlgSSR22	15	2.000	1.069	0.067	0.064	0.146	0.062
BlgSSR23	15	5.000	3.409	0.267	0.707	1.315	0.649
BlgSSR24	15	7.000	3.383	0.400	0.704	1.474	0.661
BlgSSR25	15	5.000	2.446	0.667	0.591	1.058	0.507
BlgSSR26	15	4.000	2.184	0.533	0.542	1.000	0.495
Mean		3.615	2.129	0.272	0.403	0.772	0.3675

Supplementary Table S6. The differentially expressed unigenes (DEGs) between four different developmental stages.

Supplementary Table S7. FPKM data of all samples.

Supplementary Table S8. All GeneExpression FPKM data.

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