

**Supplementary File 1****Table S1** Sample sequencing data statistics

Sample	Raw reads	Clean reads	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
S0_T1	45790168	45407670	0.0233	98.68	95.86	52.49
S0_T2	47961938	47536530	0.0231	98.75	96.08	52.46
S0_T3	47953016	47546070	0.0233	98.71	95.96	52.69
S0_B1	47412630	46982928	0.0232	98.74	96.06	53.41
S0_B2	47152968	46728392	0.023	98.8	96.21	52.88
S0_B3	46082548	45688254	0.023	98.83	96.3	53.34
S1_T1	52051874	51640742	0.0232	98.73	96.03	54.55
S1_T2	51789682	51367640	0.023	98.82	96.29	54.37
S1_T3	49911624	49502850	0.0231	98.76	96.13	53.94
S1_B1	48014520	47622274	0.0228	98.88	96.52	55.48
S1_B2	56617666	56144040	0.023	98.78	96.25	55.12
S1_B3	52100624	51610414	0.0233	98.68	95.92	55.15
S2_T1	49891388	49475466	0.0229	98.84	96.35	54.01
S2_T2	49545084	49143304	0.0229	98.86	96.41	54.08
S2_T3	51848736	51438212	0.0228	98.91	96.52	54.66
S2_B1	52882350	52467454	0.0229	98.86	96.41	55.11
S2_B2	51963608	51534860	0.023	98.82	96.3	55.79
S2_B3	48934270	48524130	0.023	98.81	96.27	55.21
S3_T1	52737490	52324516	0.0231	98.76	96.12	54.55
S3_T2	56506580	56083198	0.0229	98.85	96.38	55.04
S3_T3	46930874	46454594	0.0229	98.86	96.4	54.37
S3_B1	52056954	51592478	0.023	98.8	96.29	55.83
S3_B2	53069056	52636282	0.023	98.79	96.24	56.26
S3_B3	51280482	50824242	0.0231	98.77	96.21	56.23

Note: (1)Sample:Name of Sample. (2)Raw reads: the total number of items in the original sequencing data (reads, representing a sequencing read, and one reads is one). (3)Clean reads: the total number of items in sequencing data after quality control. (4)Error rate(%): the average Error rate of sequencing bases corresponding to quality control data is generally less than 0.1%. (5)Q20(%), Q30(%): The quality of sequencing data after quality control is evaluated. Q20 and Q30 respectively refer to the percentage of bases with sequencing quality above 99% and 99.9% in the total base. Generally, Q20 is above 85% and Q30 is above 80%. (6)GC Content (%): The percentage of the sum of G and C bases corresponding to the quality control data in the total base.

**Table S2** Statistics of sample sequencing comparisons

Sample	Total reads	Total mapped	Multiple mapped	Uniquely mapped
S0_T1	45407670	43620948(96.07%)	2599937(5.73%)	41021011(90.34%)
S0_T2	47536530	45698283(96.13%)	2499514(5.26%)	43198769(90.87%)
S0_T3	47546070	45704650(96.13%)	2825575(5.94%)	42879075(90.18%)
S0_B1	46982928	44955531(95.68%)	2900819(6.17%)	42054712(89.51%)
S0_B2	46728392	44792089(95.86%)	2411767(5.16%)	42380322(90.7%)
S0_B3	45688254	43809830(95.89%)	2640729(5.78%)	41169101(90.11%)
S1_T1	51640742	49630914(96.11%)	2995237(5.8%)	46635677(90.31%)
S1_T2	51367640	49399605(96.17%)	3747791(7.3%)	45651814(88.87%)
S1_T3	49502850	47566464(96.09%)	3642912(7.36%)	43923552(88.73%)
S1_B1	47622274	45669788(95.9%)	2192025(4.6%)	43477763(91.3%)
S1_B2	56144040	53734630(95.71%)	2606886(4.64%)	51127744(91.07%)
S1_B3	51610414	49499407(95.91%)	2954516(5.72%)	46544891(90.19%)
S2_T1	49475466	47619992(96.25%)	4061209(8.21%)	43558783(88.04%)
S2_T2	49143304	47275738(96.2%)	4525766(9.21%)	42749972(86.99%)
S2_T3	51438212	49572253(96.37%)	2590947(5.04%)	46981306(91.34%)
S2_B1	52467454	50586905(96.42%)	2870212(5.47%)	47716693(90.95%)
S2_B2	51534860	49543705(96.14%)	2784079(5.4%)	46759626(90.73%)
S2_B3	48524130	46592980(96.02%)	2337374(4.82%)	44255606(91.2%)
S3_T1	52324516	50371552(96.27%)	3665287(7.0%)	46706265(89.26%)
S3_T2	56083198	53915589(96.14%)	4236462(7.55%)	49679127(88.58%)
S3_T3	46454594	44868554(96.59%)	5097932(10.97%)	39770622(85.61%)
S3_B1	51592478	49409203(95.77%)	3665671(7.11%)	45743532(88.66%)
S3_B2	52636282	50635595(96.2%)	3060208(5.81%)	47575387(90.39%)
S3_B3	50824242	48934792(96.28%)	2604650(5.12%)	46330142(91.16%)

Note: (1)Sample: Name of Sample. (2)Total reads: the number of filtered sequences (i.e. Clean reads). (3)Total mapped: number of Clean reads that can be mapped into the genome. (4)Multiple mapped: number of Clean reads with Multiple mapped locations in the reference sequence. (5)Unique mapped: Number of Clean reads with a Unique alignment position in the reference sequence.

**Table S3** Expression of DEGs in different stages of Moso bamboo shoots

Different stages	Total DEGs	Up DEGs	Down DEGs
S1_T	9633	5863	3770
S2_T	9749	5395	4354
S3_T	14388	7990	6398
S1_B	10470	6596	3874
S2_B	10771	6606	4165
S3_B	17852	9412	8440

Note: The differential gene expression numbers of S1\_T, S2\_T and S3\_T were all compared with S0\_T, and the differential gene expression numbers of S1\_B, S2\_B and S3\_B were all compared with S0\_B.

**Table S4** Heat map analysis of DEGs involved in starch and sucrose metabolism pathway at the top of Moso bamboo shoots

Gene_id	Gene Description	S0_T	S1_T	S2_T	S3_T
PH02Gene01052	RecName: Full=Soluble starch synthase 2-2, chloroplastic/amyloplastic; AltName: Full=Soluble starch synthase II-2; Flags: Precursor	1.7030	-0.2784	-0.6506	-0.7740
PH02Gene01266	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor	1.6772	-0.2139	-0.5440	-0.9193
PH02Gene06165	RecName: Full=1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic; AltName: Full=Starch branching enzyme I; Flags: Precursor	1.6682	-0.2360	-0.4557	-0.9766
PH02Gene07736	RecName: Full=Glucan endo-1,3-beta-glucosidase 4; AltName: Full=(1-3)-beta-glucan endohydrolase 4; Short=(1-3)-beta-glucanase 4; AltName: Full=Beta-1,3-endoglucan	1.7210	-0.4171	-0.5683	-0.7356
PH02Gene07829	RecName: Full=Probable sucrose-phosphate synthase 4; AltName: Full=Sucrose phosphate synthase 4F; Short=OsSPS4F; AltName: Full=UDP-glucose-fructose-phosphate gluco	1.6569	-0.1304	-0.5730	-0.9536
PH02Gene12545	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha	1.5759	-0.0072	-0.4060	-1.1626
PH02Gene13620	RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glu	1.6866	-0.4760	-0.2921	-0.9185
PH02Gene17166	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha	1.5785	0.0545	-0.5235	-1.1096
PH02Gene18798	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	1.6816	-0.5221	-0.2425	-0.9170
PH02Gene20456	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 4; AltName: Full=Cell wall beta-fructosidase 4; AltName: Full=Invertase 4; AltName: Full=OsCIN4; AltName:	1.6745	-0.1592	-0.6513	-0.8640
PH02Gene23984	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	1.7134	-0.5854	-0.3576	-0.7704
PH02Gene26491	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4	1.6790	-0.1838	-0.6267	-0.8685
PH02Gene39746	RecName: Full=Probable inactive beta-glucosidase 14; Short=Os4bglu14; Flags: Precursor	1.6034	-0.6435	0.0466	-1.0064
PH02Gene44838	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1,	1.6609	-0.3617	-0.2843	-1.0148

	chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-gl				
PH02Gene48441	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4	1.6844	-0.2068	-0.6198	-0.8579
PH02Gene03303	RecName: Full=Beta-glucosidase 12; Short=Os4bglu12; Flags: Precursor	1.7318	-0.5503	-0.5907	-0.5907
PH02Gene09014	RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor	1.7189	-0.4450	-0.7712	-0.5027
PH02Gene14465	RecName: Full=Nudix hydrolase 14, chloroplastic; Short=AtNUDT14; AltName: Full=ADP-sugar diphosphatase; Short=AtASPP; Flags: Precursor	1.7249	-0.4304	-0.6744	-0.6202
PH02Gene21236	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	1.7037	-0.7810	-0.2858	-0.6369
PH02Gene27242	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha	1.7311	-0.5667	-0.6278	-0.5366
PH02Gene48823	RecName: Full=Alpha,alpha-trehalose-phosphate synthase	1.7116	-0.8202	-0.4307	-0.4607
PH02Gene04423	RecName: Full=Sucrose synthase 1; Short=OsSUS1; AltName: Full=Sucrose synthase 2; Short=RSs2; AltName: Full=Sucrose-UDP glucosyltransferase 1	-1.7206	0.7370	0.4121	0.5715
PH02Gene04686	RecName: Full=Beta-glucosidase 31; Short=Os9bglu31; Flags: Precursor	-1.5823	0.5269	-0.0475	1.1029
PH02Gene05154	RecName: Full=Endoglucanase 23; AltName: Full=Endo-1,4-beta glucanase 23; AltName: Full=OsGLU12; Flags: Precursor	-1.6774	0.4422	0.2802	0.9551
PH02Gene09907	RecName: Full=Phosphoglucomutase, cytoplasmic 2; Short=PGM 2; AltName: Full=Glucose phosphomutase 2	-1.7001	0.5992	0.2817	0.8193
PH02Gene11050	RecName: Full=Beta-amylase 1, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 7; AltName: Full=Thioredoxin-regulated beta	-1.5489	0.4611	-0.0872	1.1750
PH02Gene13448	RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; AltName: Full=Phosphoglucose isomerase; Short=PGI; AltName: Full=Phosphohexose isomerase; Short=PH	-1.7234	0.6507	0.4118	0.6610
PH02Gene14729	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.6827	0.7143	0.1766	0.7918
PH02Gene15089	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.6714	0.5447	0.1925	0.9342

PH02Gene20325	RecName: Full=Probable trehalose-phosphate phosphatase 1; Short=OsTPP1; AltName: Full=Trehalose 6-phosphate phosphatase	-1.6522	0.2872	0.3246	1.0404
PH02Gene27125	RecName: Full=Fructokinase-1; AltName: Full=Fructokinase I; AltName: Full=OsFKI	-1.6510	0.4712	0.1678	1.0120
PH02Gene28586	RecName: Full=Glucan endo-1,3-beta-glucosidase 6; AltName: Full=(1-3)-beta-glucan endohydrolase 6; Short=(1-3)-beta-glucanase 6; AltName: Full=Beta-1,3-endoglucan	-1.7207	0.7469	0.4275	0.5463
PH02Gene30298	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphorylase; Short=UDPGP; Short=UGPase	-1.6661	0.5480	0.1725	0.9456
PH02Gene30801	RecName: Full=Alpha,alpha-trehalose-phosphate synthase	-1.7013	0.6926	0.2622	0.7465
PH02Gene32320	RecName: Full=Beta-amylase 3, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 8; AltName: Full=Chloroplast beta-amylase;	-1.6837	0.3910	0.3489	0.9437
PH02Gene35802	RecName: Full=Phosphoglucomutase, cytoplasmic 2; Short=PGM 2; AltName: Full=Glucose phosphomutase 2	-1.7269	0.5750	0.4675	0.6845
PH02Gene36763	RecName: Full=Lysosomal beta glucosidase; Flags: Precursor	-1.7173	0.4449	0.4890	0.7834
PH02Gene37603	RecName: Full=Fructokinase-2; AltName: Full=Fructokinase II; AltName: Full=OsFKII	-1.7278	0.5824	0.4735	0.6719
PH02Gene41019	RecName: Full=Hexokinase-3; AltName: Full=Hexokinase-8	-1.6151	0.4821	0.0579	1.0751
PH02Gene43583	RecName: Full=Fructokinase-2; AltName: Full=Fructokinase II; AltName: Full=OsFKII	-1.7149	0.5048	0.4152	0.7949
PH02Gene44962	RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor	-1.7094	0.4883	0.3940	0.8271
PH02Gene46034	RecName: Full=Sucrose synthase 1; Short=OsSUS1; AltName: Full=Sucrose synthase 2; Short=RSs2; AltName: Full=Sucrose-UDP glucosyltransferase 1	-1.7212	0.5877	0.4090	0.7245
PH02Gene47722	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP glucosyltransferase 7	-1.7280	0.4672	0.6064	0.6544
PH02Gene05641	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphorylase; Short=UDPGP; Short=UGPase	-1.6404	0.1072	0.5194	1.0138
PH02Gene09580	RecName: Full=Sucrose:sucrose 1-fructosyltransferase; AltName: Full=Sucrose 1(F)-fructosyltransferase; AltName: Full=Sucrose:sucrose 1(F)-beta-D-fructosyltransferase	-1.6889	0.2671	0.5300	0.8918
PH02Gene14100	RecName: Full=Lysosomal beta glucosidase; Flags: Precursor	-1.6140	0.1884	0.2985	1.1272

PH02Gene26917	RecName: Full=Probable trehalose-phosphate phosphatase 7; Short=OsTPP7; AltName: Full=Trehalose 6-phosphate phosphatase	-1.6302	0.0108	0.6848	0.9346
PH02Gene27917	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP glucosyltransferase 7	-1.5873	0.0725	0.3525	1.1623
PH02Gene33818	RecName: Full=Beta-amylase 1, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 7; AltName: Full=Thioredoxin-regulated beta	-1.4746	-0.1084	0.2619	1.3211
PH02Gene06193	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 2; AltName: Full=Cell wall beta-fructosidase 2; AltName: Full=Invertase 2; AltName: Full=OsCIN2; AltName	-1.5056	0.6623	-0.2635	1.1068
PH02Gene20078	RecName: Full=Sucrose:sucrose 1-fructosyltransferase; AltName: Full=Sucrose 1(F)-fructosyltransferase; AltName: Full=Sucrose:sucrose 1(F)-beta-D-fructosyltransferase	-1.4129	0.6516	-0.4222	1.1835
PH02Gene26446	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 1; AltName: Full=Cell wall beta-fructosidase 1; AltName: Full=Invertase 1; AltName: Full=OsCIN1; AltName	-1.6366	0.8507	0.0128	0.7731
PH02Gene47631	RecName: Full=Endoglucanase 23; AltName: Full=Endo-1,4-beta glucanase 23; AltName: Full=OsGLU12; Flags: Precursor	-1.6516	0.6660	0.0787	0.9069
PH02Gene08635	RecName: Full=Beta-glucosidase 31; Short=Os9bglu31; Flags: Precursor	1.4520	0.4059	-0.9532	-0.9046
PH02Gene10364	RecName: Full=Probable trehalase; AltName: Full=Alpha,alpha-trehalase; AltName: Full=Alpha,alpha-trehalose glucohydrolase	1.4685	0.3676	-0.8106	-1.0254
PH02Gene13763	RecName: Full=Alpha,alpha-trehalose-phosphate synthase	1.6269	0.0180	-0.8301	-0.8147
PH02Gene29656	RecName: Full=1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme IIB; Flags: Precursor	1.6028	0.0787	-0.7662	-0.9153
PH02Gene38601	RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside glucohydrolase A; AltName: Full=Cellobiase A; AltName: Full=Gentiobiase A; Flags: Precursor	1.5863	0.1130	-0.7326	-0.9666
PH02Gene12539	RecName: Full=Endoglucanase 10; AltName: Full=Endo-1,4-beta glucanase 10; AltName: Full=OsGLU2	-1.5594	1.2051	0.0141	0.3401
PH02Gene16852	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 2; AltName: Full=Cell wall beta-fructosidase 2; AltName: Full=Invertase 2; AltName: Full=OsCIN2; AltName	-1.6811	0.9078	0.2273	0.5460

PH02Gene23433	RecName: Full=Beta-glucosidase 4; Short=Os1bglu4	-1.7001	0.8317	0.2915	0.5769
PH02Gene24831	RecName: Full=Hexokinase-5; AltName: Full=Hexokinase I	-1.6639	0.9214	0.1402	0.6023
PH02Gene27250	RecName: Full=Endoglucanase 10; AltName: Full=Endo-1,4-beta glucanase 10; AltName: Full=OsGLU2	-1.6231	1.1034	0.1787	0.3410
PH02Gene30830	RecName: Full=Lysosomal beta glucosidase; Flags: Precursor	-1.6386	1.0310	0.1202	0.4875
PH02Gene32307	RecName: Full=Probable alpha-glucosidase Os06g0675700; AltName: Full=Maltase; Flags: Precursor	-1.6250	1.0945	0.1635	0.3670
PH02Gene19768	RecName: Full=Alpha-amylase type A isozyme; AltName: Full=1,4-alpha-D-glucan glucanohydrolase; AltName: Full=AMY1; AltName: Full=Low pI alpha-amylase; Flags: Precursor	-1.4410	1.2971	0.4115	-0.2676
PH02Gene26251	RecName: Full=Probable trehalase; AltName: Full=Alpha,alpha-trehalase; AltName: Full=Alpha,alpha-trehalose glucohydrolase	-1.3779	1.4479	0.0014	-0.0714
PH02Gene47638	RecName: Full=Beta-glucosidase 28; Short=Os8bglu28; Flags: Precursor	-1.5953	1.1301	0.4192	0.0460
PH02Gene20050	RecName: Full=Beta-glucosidase 34; Short=Os10bglu34; Flags: Precursor	-1.3525	-0.4644	0.5183	1.2986
PH02Gene41803	RecName: Full=Beta-glucosidase 16; Short=Os4bglu16; Flags: Precursor	-1.3692	-0.5329	0.8244	1.0778
PH02Gene22525	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.1097	-0.4318	-0.0641	1.6056
PH02Gene41109	RecName: Full=Probable trehalose-phosphate phosphatase 6; Short=OsTPP6; AltName: Full=Trehalose 6-phosphate phosphatase	-0.9198	-0.2185	-0.5396	1.6778
PH02Gene42897	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.2927	-0.2320	0.0164	1.5083
PH02Gene45438	RecName: Full=Hexokinase-7; AltName: Full=Hexokinase-6	-1.3082	0.1779	-0.3344	1.4647

Note:(1)description: name of gene code. (2)There are four growth and development stages of bamboo shoots: the expression level after standardization.

**Table S5** Heat map analysis of DEGs involved in starch and sucrose metabolism pathway at the base of Moso bamboo shoots

Gene_id	Gene Description	S0_B	S1_B	S2_B	S3_B
PH02Gene01052	RecName: Full=Soluble starch synthase 2-2, chloroplastic/amyloplastic; AltName: Full=Soluble starch synthase II-2; Flags: Precursor	1.6965	-0.2487	-0.6461	-0.8017
PH02Gene01266	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor	1.6725	-0.3381	-0.3525	-0.9820
PH02Gene05747	RecName: Full=Probable sucrose-phosphate synthase 1; AltName: Full=UDP-glucose-fructose-phosphate glucosyltransferase	1.7316	-0.5963	-0.5390	-0.5963
PH02Gene05928	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor	1.6990	-0.5285	-0.3120	-0.8584
PH02Gene06165	RecName: Full=1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic; AltName: Full=Starch branching enzyme I; Flags: Precursor	1.7136	-0.3379	-0.6493	-0.7265
PH02Gene13620	RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glu	1.7056	-0.6737	-0.2871	-0.7447
PH02Gene22653	RecName: Full=Beta-glucosidase 1; Short=Os1bglu1; Flags: Precursor	1.7032	-0.3619	-0.4857	-0.8556
PH02Gene25500	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-gl	1.7281	-0.4916	-0.5569	-0.6796
PH02Gene29656	RecName: Full=1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme IIB; Flags: Precursor	1.6540	-0.2667	-0.3540	-1.0333
PH02Gene37359	RecName: Full=Granule-bound starch synthase 1b, chloroplastic/amyloplastic; AltName: Full=Granule-bound starch synthase Ib; Flags: Precursor	1.6587	-0.2487	-0.3945	-1.0155
PH02Gene38601	RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside glucohydrolase A; AltName: Full=Cellobiase A; AltName: Full=Gentiobiase A; Flags: Precursor	1.6497	-0.1115	-0.5653	-0.9728
PH02Gene38723	RecName: Full=Alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic; AltName: Full=Starch phosphorylase L-2; Flags: Precursor	1.7085	-0.3942	-0.4814	-0.8329
PH02Gene44838	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1,	1.6503	-0.0865	-0.6299	-0.9339



	chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-gl				
PH02Gene02876	RecName: Full=Beta-amylase 3, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 8; AltName: Full=Chloroplast beta-amylase;	-1.2953	-0.3313	1.4802	0.1463
PH02Gene09572	RecName: Full=Sucrose synthase 5; Short=OsSUS5; AltName: Full=Sucrose-UDP glucosyltransferase 5	-1.3882	-0.2517	1.3966	0.2432
PH02Gene19719	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP glucosyltransferase 7	-1.5769	0.0608	1.1825	0.3337
PH02Gene04423	RecName: Full=Sucrose synthase 1; Short=OsSUS1; AltName: Full=Sucrose synthase 2; Short=RSs2; AltName: Full=Sucrose-UDP glucosyltransferase 1	-1.7233	0.7215	0.4373	0.5645
PH02Gene05641	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphorylase; Short=UDPGP; Short=UGPase	-1.7251	0.5176	0.4875	0.7201
PH02Gene09580	RecName: Full=Sucrose:sucrose 1-fructosyltransferase; AltName: Full=Sucrose 1(F)-fructosyltransferase; AltName: Full=Sucrose:sucrose 1(F)-beta-D-fructosyltransferase	-1.6580	0.0827	0.7454	0.8299
PH02Gene12539	RecName: Full=Endoglucanase 10; AltName: Full=Endo-1,4-beta glucanase 10; AltName: Full=OsGLU2	-1.7258	0.7114	0.4838	0.5305
PH02Gene14100	RecName: Full=Lysosomal beta glucosidase; Flags: Precursor	-1.7102	0.5218	0.3744	0.8141
PH02Gene14729	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.7115	0.3278	0.7467	0.6370
PH02Gene15089	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.6283	-0.0139	0.8257	0.8165
PH02Gene20325	RecName: Full=Probable trehalose-phosphate phosphatase 1; Short=OsTPP1; AltName: Full=Trehalose 6-phosphate phosphatase	-1.6977	0.2555	0.6425	0.7998
PH02Gene26446	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 1; AltName: Full=Cell wall beta-fructosidase 1; AltName: Full=Invertase 1; AltName: Full=OsCIN1; AltName	-1.7248	0.6106	0.4313	0.6828
PH02Gene27917	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP glucosyltransferase 7	-1.6827	0.3571	0.9478	0.3778
PH02Gene29429	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP	-1.6544	0.0680	0.8025	0.7839

	glucosyltransferase 7				
PH02Gene43583	RecName: Full=Fructokinase-2; AltName: Full=Fructokinase II; AltName: Full=OsFKII	-1.6752	0.1876	0.5823	0.9053
PH02Gene44962	RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor	-1.7267	0.4615	0.6826	0.5826
	RecName: Full=Sucrose synthase 1; Short=OsSUS1; AltName: Full=Sucrose synthase 2;				
PH02Gene46034	Short=RSs2; AltName: Full=Sucrose-UDP glucosyltransferase 1	-1.6904	0.2550	0.5640	0.8715
PH02Gene04686	RecName: Full=Beta-glucosidase 31; Short=Os9bglu31; Flags: Precursor	-1.5126	-0.1998	0.5351	1.1772
	RecName: Full=Beta-fructofuranosidase 1; AltName: Full=Invertase 1; AltName:				
PH02Gene05690	Full=Sucrose 1; Flags: Precursor	-1.5279	-0.2227	0.6713	1.0794
PH02Gene22525	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.1977	-0.7713	0.8584	1.1107
	RecName: Full=Probable trehalose-phosphate phosphatase 7; Short=OsTPP7; AltName:				
PH02Gene26917	Full=Trehalose 6-phosphate phosphatase	-1.5229	-0.2629	0.7999	0.9859
PH02Gene30801	RecName: Full=Alpha,alpha-trehalose-phosphate synthase	-1.5951	-0.0212	0.5355	1.0809
	RecName: Full=Beta-amylase 1, chloroplastic; AltName: Full=1,4-alpha-D-glucan				
PH02Gene33818	maltohydrolase; AltName: Full=Beta-amylase 7; AltName: Full=Thioredoxin-regulated beta	-1.4523	-0.2924	0.4960	1.2487
PH02Gene41803	RecName: Full=Beta-glucosidase 16; Short=Os4bglu16; Flags: Precursor	-1.4784	-0.3501	0.8137	1.0147
PH02Gene42897	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase	-1.4696	-0.3450	0.7143	1.1004
	RecName: Full=Probable trehalose-phosphate phosphatase 7; Short=OsTPP7; AltName:				
PH02Gene46771	Full=Trehalose 6-phosphate phosphatase	-1.5282	-0.2592	0.8959	0.8915
	RecName: Full=Beta-fructofuranosidase, insoluble isoenzyme 2; AltName: Full=Cell wall				
PH02Gene06193	beta-fructosidase 2; AltName: Full=Invertase 2; AltName: Full=OsCIN2; AltName	-1.6795	0.9195	0.2297	0.5302
PH02Gene19810	RecName: Full=Beta-glucosidase 6; Short=Os3bglu6; Flags: Precursor	-1.4761	1.3079	-0.1354	0.3036
	RecName: Full=Endoglucanase 10; AltName: Full=Endo-1,4-beta glucanase 10; AltName:				
PH02Gene27250	Full=OsGLU2	-1.6451	0.9982	0.5335	0.1134
PH02Gene46133	RecName: Full=Hexokinase-6; AltName: Full=Hexokinase-2	-1.6491	0.8775	0.0597	0.7120
PH02Gene47637	RecName: Full=Beta-glucosidase 27; Short=Os8bglu27; Flags: Precursor	-1.6146	1.0084	-0.0071	0.6133
PH02Gene47638	RecName: Full=Beta-glucosidase 28; Short=Os8bglu28; Flags: Precursor	-1.5934	1.1711	0.2270	0.1952

PH02Gene06290	RecName: Full=Hexokinase-8; AltName: Full=Hexokinase-4	1.5426	-0.0753	-0.2150	-1.2523
PH02Gene09014	RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor	1.5938	-0.4220	-0.0405	-1.1314
PH02Gene12545	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha	1.5707	0.0796	-0.5382	-1.1122
PH02Gene14970	RecName: Full=1,4-alpha-glucan-branching enzyme 3, chloroplastic/amyloplastic; Short=AtSBE III; AltName: Full=Branching enzyme 1; Short=AtBE1; AltName: Full=Prote	1.5195	-0.0825	-0.1475	-1.2895
PH02Gene17166	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha	1.4768	0.1410	-0.3136	-1.3042
PH02Gene17228	RecName: Full=Starch synthase 1, chloroplastic/amyloplastic; AltName: Full=Starch synthase I-2; Short=SS I; Short=SS I-2; Flags: Precursor	1.4939	0.0442	-0.2290	-1.3091
PH02Gene26491	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4	1.4996	-0.2092	0.0162	-1.3066
PH02Gene29455	RecName: Full=1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme; Flags: Precursor	1.2281	0.2208	0.1102	-1.5591
PH02Gene31595	RecName: Full=1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme; Flags: Precursor	1.4987	0.0141	-0.2043	-1.3084
PH02Gene44935	RecName: Full=Phosphoglucomutase, chloroplastic; Short=PGM; AltName: Full=Glucose phosphomutase; Flags: Precursor	1.5559	0.0433	-0.4133	-1.1859
PH02Gene11050	RecName: Full=Beta-amylase 1, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 7; AltName: Full=Thioredoxin-regulated beta	-1.6649	0.4144	0.2546	0.9958
PH02Gene13448	RecName: Full=Glucose-6-phosphate isomerase, cytosolic; Short=GPI; AltName: Full=Phosphoglucose isomerase; Short=PGI; AltName: Full=Phosphohexose isomerase;	-1.6363	0.4109	0.1638	1.0616
PH02Gene20078	Short=PH RecName: Full=Sucrose:sucrose 1-fructosyltransferase; AltName: Full=Sucrose 1(F)-fructosyltransferase; AltName: Full=Sucrose:sucrose 1(F)-beta-D-fructosyltransferase	-1.6568	0.3025	0.3262	1.0281
PH02Gene24831	RecName: Full=Hexokinase-5; AltName: Full=Hexokinase I	-1.5935	0.6864	-0.0840	0.9912

PH02Gene27125	RecName: Full=Fructokinase-1; AltName: Full=Fructokinase I; AltName: Full=OsFKI	-1.6656	0.3489	0.3141	1.0027
	RecName: Full=Probable trehalose-phosphate phosphatase 6; Short=OsTPP6; AltName:	-1.6619	0.3374	0.3107	1.0138
PH02Gene31459	Full=Trehalose 6-phosphate phosphatase				
PH02Gene37603	RecName: Full=Fructokinase-2; AltName: Full=Fructokinase II; AltName: Full=OsFKII	-1.6749	0.4127	0.2936	0.9686
PH02Gene45438	RecName: Full=Hexokinase-7; AltName: Full=Hexokinase-6	-1.5557	0.2258	0.0972	1.2326
	RecName: Full=Probable trehalase; AltName: Full=Alpha,alpha-trehalase; AltName:	-1.0635	0.9789	1.0188	-0.9342
PH02Gene26251	Full=Alpha,alpha-trehalose glucohydrolase				
	RecName: Full=Alpha-amylase; AltName: Full=1,4-alpha-D-glucan glucohydrolase;	-1.3011	1.0523	0.8889	-0.6401
PH02Gene37127	AltName: Full=Alpha-amylase isozyme 1B; Flags: Precursor				
	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose	-1.4300	-0.1435	0.1967	1.3769
PH02Gene30298	pyrophosphorylase; Short=UDPGP; Short=UGPase				
	RecName: Full=Beta-amylase 3, chloroplastic; AltName: Full=1,4-alpha-D-glucan	-1.3938	-0.1313	0.1005	1.4247
PH02Gene32320	maltohydrolase; AltName: Full=Beta-amylase 8; AltName: Full=Chloroplast beta-amylase;				
	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP	-1.2869	-0.4207	0.2586	1.4491
PH02Gene47723	glucosyltransferase 7				
PH02Gene40204	_	-1.3790	0.3149	1.3785	-0.3144
	RecName: Full=Sucrose synthase 7; Short=OsSUS7; AltName: Full=Sucrose-UDP	-1.6349	0.6313	0.9628	0.0409
PH02Gene47722	glucosyltransferase 7				

Note:(1)description: name of gene code. (2)There are four growth and development stages of bamboo shoots: the expression level after standardization.

**Table S6** Co-expression network of DEGs at the top of Moso bamboo shoots

gene id	degree	description
PH02Gene26491	15.54354	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4
PH02Gene07829	15.03386	RecName: Full=Probable sucrose-phosphate synthase 4; AltName: Full=Sucrose phosphate synthase 4F; Short=OsSPS4F; AltName: Full=UDP-glucose-fructose-phosphate gluco
PH02Gene01052	14.97322	RecName: Full=Soluble starch synthase 2-2, chloroplastic/amyloplastic; AltName: Full=Soluble starch synthase II-2; Flags: Precursor
PH02Gene48441	14.91505	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4
PH02Gene13620	14.41779	RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glu
PH02Gene17166	14.16257	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha
PH02Gene12545	13.99325	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha
PH02Gene39746	13.91867	RecName: Full=Probable inactive beta-glucosidase 14; Short=Os4bglu14; Flags: Precursor
PH02Gene01266	13.79487	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor
PH02Gene38601	13.55319	RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside glucohydrolase A; AltName: Full=Cellobiase A; AltName: Full=Gentiobiase A; Flags: Precursor
PH02Gene13763	13.42544	RecName: Full=Alpha,alpha-trehalose-phosphate synthase

PH02Gene06165	13.40999	RecName: Full=1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic; AltName: Full=Starch branching enzyme I; Flags: Precursor
PH02Gene44838	13.19952	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-gl
PH02Gene18798	13.12174	RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase
PH02Gene14465	12.72853	RecName: Full=Nudix hydrolase 14, chloroplastic; Short=AtNUDT14; AltName: Full=ADP-sugar diphosphatase; Short=AtASPP; Flags: Precursor

Note:(1) degree: Node connectivity. The larger the degree, the more important it is(2) description:Name of gene code

**Table S7** Co-expression network of DEGs at the base of Moso bamboo shoots

gene id	degree	description
PH02Gene01266	14.90276	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor
PH02Gene37359	14.69078	RecName: Full=Granule-bound starch synthase 1b, chloroplastic/amyloplastic; AltName: Full=Granule-bound starch synthase 1b; Flags: Precursor
PH02Gene29656	14.03499	RecName: Full=1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme IIB; Flags: Precursor
PH02Gene01052	13.97282	RecName: Full=Soluble starch synthase 2-2, chloroplastic/amyloplastic; AltName: Full=Soluble starch synthase II-2; Flags: Precursor
PH02Gene31595	13.81575	RecName: Full=1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic; AltName: Full=Q-enzyme; AltName: Full=Starch-branching enzyme; Flags: Precursor
PH02Gene06290	13.75796	RecName: Full=Hexokinase-8; AltName: Full=Hexokinase-4
PH02Gene26491	13.37804	RecName: Full=Sucrose synthase 4; Short=OsSUS4; AltName: Full=Sucrose-UDP glucosyltransferase 4
PH02Gene14970	13.20047	RecName: Full=1,4-alpha-glucan-branching enzyme 3, chloroplastic/amyloplastic; Short=AtSBE III; AltName: Full=Branching enzyme 1; Short=AtBE1; AltName: Full=Prote

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PH02Gene06165	13.00712	RecName: Full=1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic; AltName: Full=Starch branching enzyme I; Flags: Precursor
PH02Gene17228	12.77285	RecName: Full=Starch synthase 1, chloroplastic/amyloplastic; AltName: Full=Starch synthase I-2; Short=SS I; Short=SS I-2; Flags: Precursor
PH02Gene38723	12.54154	RecName: Full=Alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic; AltName: Full=Starch phosphorylase L-2; Flags: Precursor
PH02Gene12545	12.43129	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose syntha
PH02Gene44838	12.40378	RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic/amyloplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-gl
PH02Gene05928	12.18266	RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor
PH02Gene38601	12.10717	RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside glucohydrolase A; AltName: Full=Cellobiase A; AltName: Full=Gentiobiase A; Flags: Precursor

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Note:(1) degree: Node connectivity. The larger the degree, the more important it is(2) description:Name of gene code

**Table S8** Sequences of qRT-PCR primers used in this study

Target gene	Primer	5'----3'
PH02Gene04423	PH02Gene04423-F	TGCGGTCTTCCGACATTC
	PH02Gene04423-R	GGGTCTTGCTGGCACTTA
PH02Gene46034	PH02Gene46034-F	AGGGTGGGCTTCAGCGTAT
	PH02Gene46034-R	AGGTAGCGGCGGGTTTCA
PH02Gene06165	PH02Gene06165-F	TGAAGCGAGCACAAACAGT
	PH02Gene06165-R	TCTTTCCAGCATAGGGTC
PH02Gene11050	PH02Gene11050-F	CGAAATGGGTATCGGAGGAGA
	PH02Gene11050-R	CGCATGAAGTCGGCGTAGCA
Internal control gene	ACT-F	TACGCTTCCTCACGCTATTCTTC
	ACT-R	TTCTCGCTCGGCAGTTGTTG