

**File S1.** Information of 8278 predicted protein-coding genes in *Sanghuangporus sanghuang*.

**Figure S1.** Pathway of terpenoid backbone biosynthesis in *Sanghuangporus sanghuang*. The blue and green boxes indicate the presence of single- and double-copy of homologous genes encoding the enzymes, respectively.

**Figure S2.** Pathway of sesquiterpenoid and triterpenoid biosynthesis in *Sanghuangporus sanghuang*. The blue boxes indicate the presence of single-copy of homologous genes encoding the enzymes.

**Figure S3.** Pathway of polysaccharide biosynthesis (starch and sucrose metabolism) in *Sanghuangporus sanghuang*. The blue, green, yellow and orange boxes indicate the presence of single-, double-, triple- and four- to nine-copy of homologous genes, respectively.

**Figure S4.** Genomic blocks of *Sanghuangporus baumii*, *S. sanghuang* and *S. vaninii*. Shared blocks of collinearity are linked by pink lines, blocks of translocation by blue lines, blocks of inversion by orange lines, and blocks of translocation and inversion by green lines.

**Table S1.** Putative genes involved in the pathway of terpenoid backbone biosynthesis in *Sanghuangporus sanghuang*.

Gene name and definition	Enzyme code	KO term	Gene ID
FDPS; farnesyl diphosphate synthase	2.5.1.1, 2.5.1.10	K00787	A1964
mvaD; diphosphomevalonate decarboxylase	4.1.1.33	K01597	A6841
FNTA; protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	2.5.1.58, 2.5.1.59	K05955	A6934
STE24; STE24 endopeptidase	3.4.24.84	K06013	A1904
HMGCR; hydroxymethylglutaryl-CoA reductase (NADPH)	1.1.1.34	K00021	A1041
atoB; acetyl-CoA C-acetyltransferase	2.3.1.9	K00626	A2749
GGPS1; geranylgeranyl diphosphate synthase, type III	2.5.1.1, 2.5.1.10, 2.5.1.29	K00804	A3347
mvaK2; phosphomevalonate kinase	2.7.4.2	K00938	A3410
E2.3.3.10; hydroxymethylglutaryl-CoA synthase	2.3.3.10	K01641	A2231
idi; isopentenyl-diphosphate Delta-isomerase	5.3.3.2	K01823	A5810
hexPS; hexaprenyl-diphosphate synthase	2.5.1.82, 2.5.1.83	K05355	A7458
FCLY; prenylcysteine oxidase/farnesylcysteine lyase	1.8.3.5, 1.8.3.6	K05906	A6316
FNTB; protein farnesyltransferase subunit beta	2.5.1.58	K05954	A1834
SRT1; ditrans, polycis-polyprenyl diphosphate synthase	2.5.1.87	K11778	A4415

**Table S2.** Putative genes involved in the biosynthesis of polysaccharides (starch and sucrose metabolism) in *Sanghuangporus sanghuang*.

Gene name and definition	Enzyme code	KO term	Identity (%)	E-value	Gene ID
SGA1; glucoamylase	3.2.1.3	K01178	84.1	4.10E-290	A2599
HK; hexokinase	2.7.1.1	K00844	74	7.30E-211	A2696
GBE1, glgB; 1,4-alpha-glucan branching enzyme	2.4.1.18	K00700	86.8	0	A2720
E3.2.1.4; endoglucanase	3.2.1.4	K01179	64.3	1.20E-170	A2968
PYG, glgP; glycogen phosphorylase	2.4.1.1	K00688	90.2	0	A3794
TSL1, TPS3; trehalose 6-phosphate synthase complex regulatory subunit	--	K22337	77.6	0	A3936
AMY, amyA, malS; alpha-amylase	3.2.1.1	K01176	73.5	7.70E-216	A4004
CBH1; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K01225	75.1	1.40E-208	A4217
CBH1; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K01225	74.7	3.00E-209	A4220
GYS; glycogen synthase	2.4.1.11	K00693	92.5	0	A4243
beta-glucosidase	3.2.1.21	K01188	80.4	0	A4328
CBH2, cbhA; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K19668	80.1	3.90E-164	A4452
AMY, amyA, malS; alpha-amylase	3.2.1.1	K01176	76.6	1.10E-241	A4496
1,3-beta-glucan synthase	2.4.1.34	K00706	89.9	0	A4637
bglX; beta-glucosidase	3.2.1.21	K05349	86.1	0	A4980
AMY, amyA, malS; alpha-amylase	3.2.1.1	K01176	54.6	9.60E-117	A5429
TREH, treA, treF; alpha,alpha-trehalase	3.2.1.28	K01194	88.7	0	A5537
otsA; trehalose 6-phosphate synthase	2.4.1.15, 2.4.1.347	K00697	88.4	8.90E-282	A5558

Endoglucanase	3.2.1.4	K01179	81.5	7.70E-91	A5669
Endoglucanase	3.2.1.4	K01179	88.5	1.30E-185	A5687
bglX; beta-glucosidase	3.2.1.21	K05349	76.9	0	A5895
malZ; alpha-glucosidase	3.2.1.20	K01187	75.1	0	A6004
UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase	2.7.7.9	K00963	88.7	1.70E-257	A6356
TPS; trehalose 6-phosphate synthase/phosphatase	2.4.1.15, 3.1.3.12	K16055	83.6	0	A7139
beta-glucosidase	3.2.1.21	K01188	79	1.70E-250	A7142
CBH2, cbhA; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K19668	88.5	1.50E-192	A7429
glucan 1,3-beta-glucosidase	3.2.1.58	K01210	73.4	2.00E-173	A7446
glucan 1,3-beta-glucosidase	3.2.1.58	K01210	64.8	3.00E-165	A7447
glucan 1,3-beta-glucosidase	3.2.1.58	K01210	68.7	1.60E-171	A7449
GYG1, GYG2; glycogenin	2.4.1.186	K00750	64	0	A7574
AGL; glycogen debranching enzyme	2.4.1.25, 3.2.1.33	K01196	82.3	0	A8029
TREH, treA, treF; alpha,alpha-trehalase	3.2.1.28	K01194	78.1	8.30E-308	A0242
HK; hexokinase	2.7.1.1	K00844	90.5	4.70E-263	A0434
1,3-beta-glucan synthase	2.4.1.34	K00706	90.2	0	A0471
beta-glucosidase	3.2.1.21	K01188	89.1	4.10E-258	A0544
IMA, malL; oligo-1,6-glucosidase	3.2.1.10	K01182	62.3	1.20E-223	A1140
pgm; phosphoglucomutase	5.4.2.2	K01835	88.9	4.20E-294	A2275

CBH1; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K01225	83.3	2.40E-229	A2394
CBH1; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K01225	83.3	2.40E-229	A2395
CBH1; cellulose 1,4-beta-cellobiosidase	3.2.1.91	K01225	79.1	2.80E-222	A2404
GPI, pgi; glucose-6-phosphate isomerase	5.3.1.9	K01810	90.9	3.40E-299	A3598

**Table S3.** Putative genes involved in the biosynthesis of uridine diphosphate glucose in *Sanghuangporus sanghuang*.

Gene name and definition	Enzyme code	KO term	Identity (%)	E-value	Gene ID
1,3-beta-glucan synthase	2.4.1.34	K00706	90.2	0	A0471
1,3-beta-glucan synthase	2.4.1.34	K00706	89.9	0	A4637
ADP-ribosylation factor GTPase-activating protein 1	--	K12492	76.6	3.90E-197	A2453
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	45.6	1.20E-81	A7815
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	48.2	1.50E-86	A7766
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	62.8	2.80E-185	A7704
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	47.7	2.60E-78	A6709
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	50.8	1.00E-102	A6508
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	48.6	8.70E-87	A6470
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	48.2	3.30E-101	A4205
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	41.4	4.80E-66	A4142
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	59.9	3.60E-103	A3963
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	58.5	8.30E-192	A2927
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	52.5	2.70E-168	A2872
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	66.1	5.20E-89	A2858
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	49.2	6.00E-86	A2219
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	49.4	6.80E-157	A1496
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	41.1	2.80E-71	A1374
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	47.9	1.50E-50	A1344
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	64.9	3.30E-195	A1087
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	43.6	1.40E-81	A1034
endo-1,3(4)-beta-glucanase	3.2.1.6	K01180	54.2	5.00E-195	A0107
GTPase-activating protein BEM2	--	K19844	70.1	0	A5627
GTPase-activating protein SAC7	--	K19845	60	1.60E-171	A5513
GTPase-activating protein SST2	--	K19838	87	0	A2703
Hexokinase	2.7.1.1	K00844	70.7	7.60E-188	A3346
Hexokinase	2.7.1.1	K00844	90.5	4.70E-263	A2696
Hexokinase	2.7.1.1	K00844	74	7.30E-211	A0434
phosphoglucomutase	5.4.2.2	K01835	49.5	5.80E-133	A5826
phosphoglucomutase	5.4.2.2	K01835	88.9	4.20E-294	A2275

Ran GTPase-activating protein 1	--	K14319	85	1.00E-177	A7607
Rho GTPase-activating protein 1	--	K18470	71	1.50E-239	A2059
Rho-type GTPase-activating protein ½	--	K19839	76.8	5.90E-275	A6706
UTP--glucose-1-phosphate uridylyltransferase	2.7.7.9	K00963	88.7	1.70E-257	A6356

**Table S4.** Putative genes involved in the biosynthesis of flavonoid compounds in *Sanghuangporus sanghuang*.

Gene name and definition	Enzyme code	KO term	Identity (%)	E-value	Gene ID
isoflavonoid 7-O-beta-aposyl-beta-glucosidase	3.2.1.161	K20852	75.6	4.10E-231	A0544
isoflavonoid 7-O-beta-aposyl-beta-glucosidase	3.2.1.161	K20852	43.7	2.10E-112	A7142
isoflavonoid 7-O-beta-aposyl-beta-glucosidase	3.2.1.161	K20852	41.7	6.00E-111	A7157
chalcone 461beta-O-glucosyltransferase	2.4.1.286	K21372	46.6	2.60E-32	A4702
chalcone 486beta-O-glucosyltransferase	2.4.1.286	K21372	56.5	4.30E-238	A6287
Chalcone-flavanone isomerase	5.5.1.6	K01859	84	2.30E-276	A6232
Chalcone-flavanone isomerase	5.5.1.6	K01859	84	2.30E-276	A6233
Chalcone-flavanone isomerase	5.5.1.6	K01859	84	2.30E-276	A7868
flavonol L-rhamnosyltransferase	2.4.1.159	K22772	46.6	2.60E-32	A4702
flavonol L-rhamnosyltransferase	2.4.1.159	K22772	56.5	4.30E-238	A6287