Fig. S1 Scheme of Super-SAGE data analysis. Numbers are compatible with Fig S2.

25%

37%

7%

31%

1
2
3
4
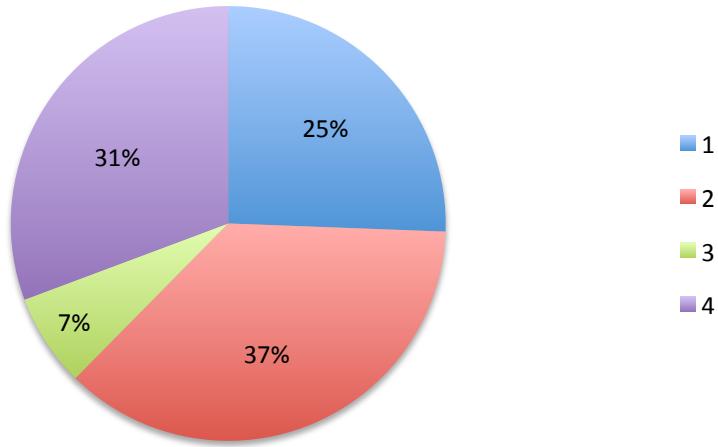
1: hit with predicted genes
2: hit with genome that contains predicted genes
3: hit with genome that does not contain predicted genes
4: no hit

Fig. S2 Matching results of Super-SAGE tags with predicted genes and reference genome sequence of *Lentinula edodes*. Numbers are compatible with Fig S1.
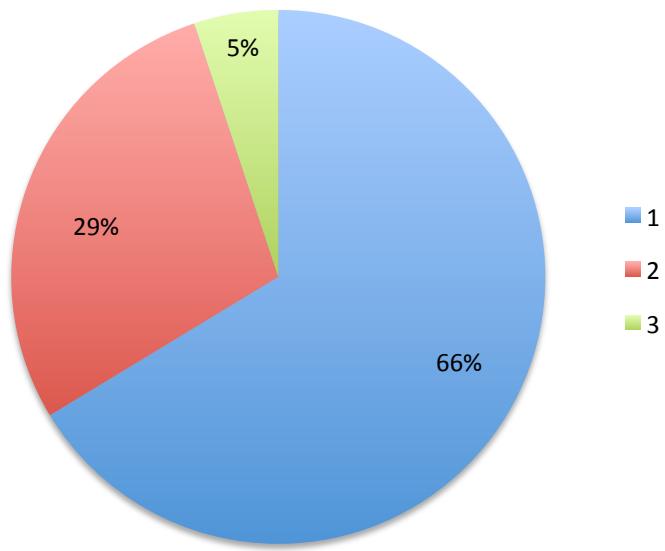
1 : expressed more than 2 fold change in postharvest fruiting body compare with fresh fruiting body, and estimated as DEG

2. expressed more than 2 fold change in postharvest fruiting body compare with fresh fruiting body, and not estimated as DEG

3. expressed less than 2 fold change in postharvest fruiting body compare with fresh fruiting body, and not estimated as DEG

Fig. S3 Comparison between PCR-subtraction data and Super-SAGE data. Fold changes of in Super-SAGA data of genes that are estimated as true positive genes upregulated after harvest in PCR-subtraction data (Y. Sakamoto, K. Nakade, and T. Sato, Curr Genet 55:409-423, 2009, doi: 10.1007/s00294-009-0255-9) were summarized.
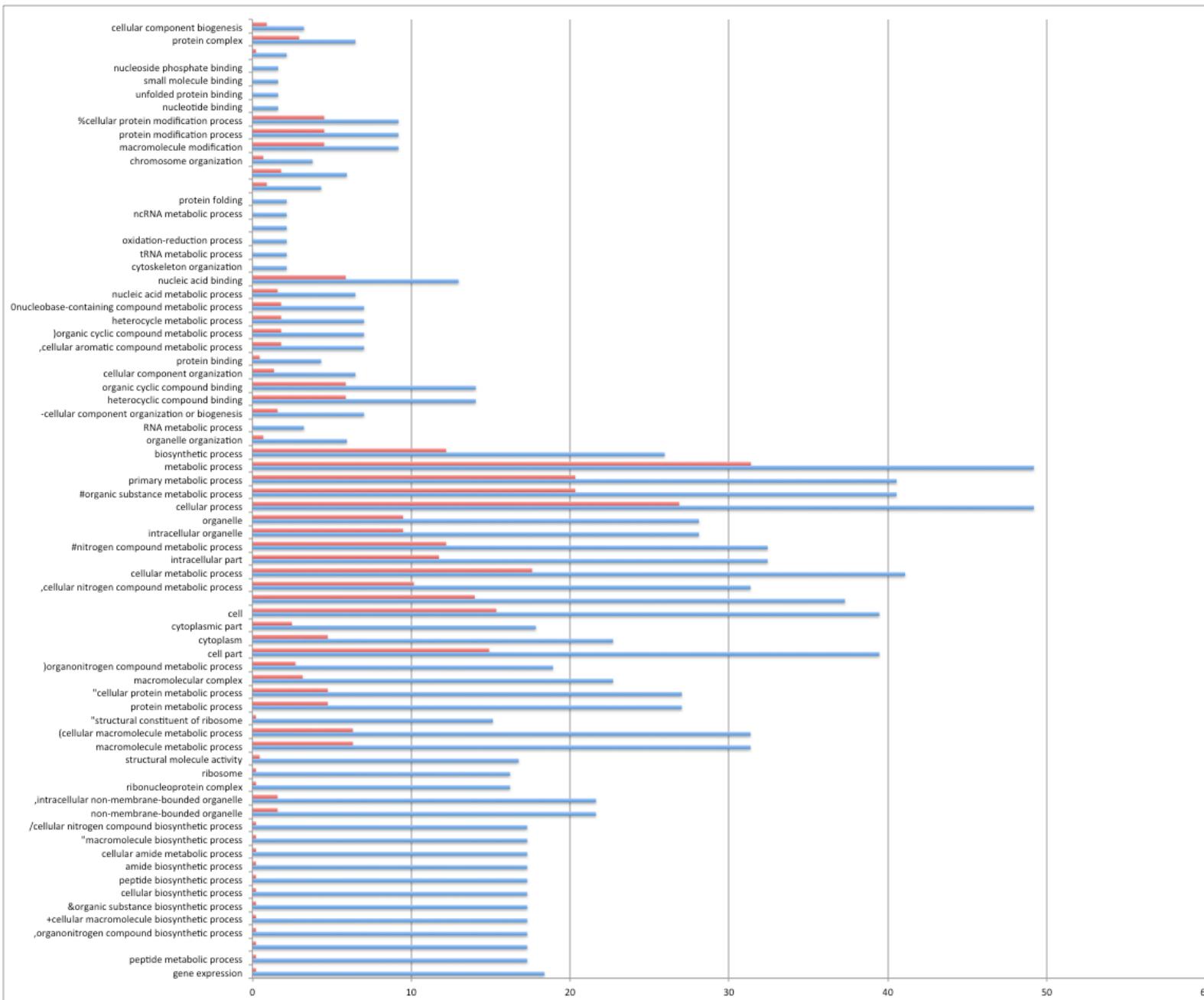
Fig. S4 Comparison of enriched gene ontology between fruiting body after harvest and fresh fruiting body (just after harvest) by using Blast2GO enrichment analysis (Fisher's Exact Test). Blue and red bars indicate enriched gene ontology in the fresh fruiting bodies and fruiting bodies after harvest, respectively. X-axis indicates number of genes enriched.
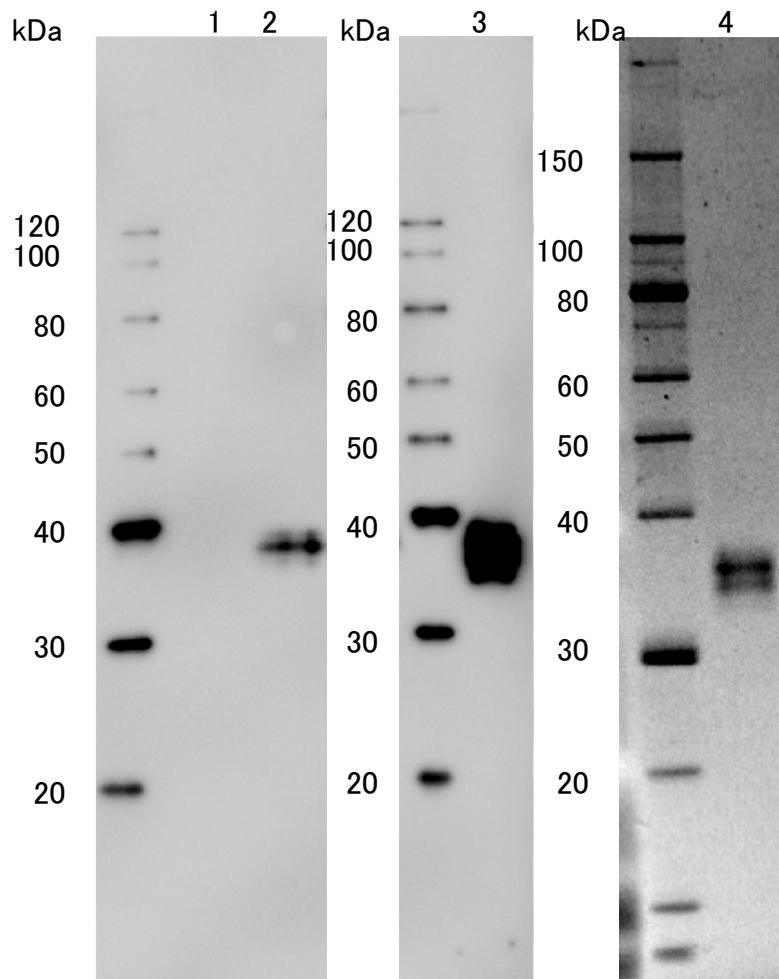
Fig. S5 Purification of GH16 enzyme, MLG1, using His-tag column, phenyl column, and MonoQ. (lane1) Western blot analysis of crude enzymes secreted from wild type *A. orizae* strain, RIB40 visualized by MLG1 antiserum, (lane2) western blot analysis of crude enzymes secreted from *A. oryzae* transformed *mlg1* expression vector visualized by MLG1 antiserum and (lane3) western blot analysis of purified rMLG1 visualized by MLG1 antiserum (lane 4) purified rMLG1 visualized by Oriole™ staining.

Table S1 De novo assemble and scaffolding of the *L. edodes* genome.

	clc genomics workbench (paired end)	SSPACE (mate pair)	PBJelly (long reads)
contig number	7,731	3,242	1,951
N50(bp)	36,146	69,696	103,018
total (bp)	35,042,971	34,981,635	38,944,209

Table S3 Number of CAZy enzymes involved in lignocellulose degradation in basidiomycetous fungi.

plant cell wall polysaccharide degrading

Cazy family	enzyme	Lened	Gymlu	Ompol	Monpe	Copci[1]	Schco[1]	Lacbi[1]	Phach[1]	Aurde[1]	Cryne[1]	Ustma[1]	repoted gene in *L. edodes*
GH1	β –glucosidase	3	3	3	7	2	3	0	2	1	0	0	
GH3	β –glucosidase	12	15	10	13	7	12	2	11	14	7	3	
GH6	endoglucanase	1	1	1	3	5	1	0	1	2	0	0	
GH7	endo–β–1,4–glucanase	4	7	3	5	6	2	0	9	8	0	0	
GH10	endo–1,4–β–xylanase	4	5	4	8	5	5	0	6	4	0	2	
GH28	polygalacturonase	13	19	8	4	3	3	7	4	14	1	1	
AA9	copper–dependent polysaccharide monooxygenases	12	13	12	17	33	22	13	15	20	1	0	

lignin degrading		Lened	Gymlu	Ompol	Monpe	Copci	Schco	Lacbi	Phach	Aurde	Cryne	Ustma	repoted gene in *L. edodes*
AA1	multicopper oxidase	14	19	9	27	17	6	13	5	8	5	4	*lcc1~14*
AA2	POD(Lip)	5(0)	5(0)	5(0)	1(0)	0	0	0	15(10)	5	0	0	*mnp1, mnp2*

Lened: *Lentinula edodes*, Gymlu: *Gymnopus luxurians*, Ompol: *Omphalotus olearius*, Monpe: *Moniliophthora perniciosa*, Copci:*Coprinopsis cinerea*, Schco:*Schizophyllum commune*, Lacbi:*Laccaria bicolor*, Phach: *Phanerochaete chrysosporium*, Aursu: *Auricularia subglabra*, Cryne:*Cryptococcus neoformans*, Ustma: *Ustilago maydis*

1) Data was based on each genome sequences in MycoCosm (http://genome.jgi.doe.gov/programs/fungi/index.jsf)

Table S5 Functional clustering of genes enriched in the fruiting bodies after harvest. The data were analyzed using DAVID.

Annotation Cluster	Term	Enrichment Score
Annotation Cluster 1	Glucose/ribitol dehydrogenase	2.750051669
Annotation Cluster 2	General substrate transporter	2.269550536
Annotation Cluster 3	Cytochrome P450	1.427520501
Annotation Cluster 4	Amino acid/polyamine transporter	1.380667976
Annotation Cluster 5	cation antiporter activity	1.375886513
Annotation Cluster 6	ABC transporter-like	1.142828599
Annotation Cluster 7	cellular amino acid catabolic process	0.887506891
Annotation Cluster 8	peroxidase activity	0.84481625
Annotation Cluster 9	lipase activity	0.773952411
Annotation Cluster 10	transcription regulator activity	0.759688533
Annotation Cluster 11	GTPase regulator activity	0.672818778
Annotation Cluster 12	cellular amino acid biosynthetic proce	0.671932353
Annotation Cluster 13	pyridoxal phosphate binding	0.641612258
Annotation Cluster 14	DNA/RNA helicase	0.613633143
Annotation Cluster 15	ATPase activity	0.576822046
Annotation Cluster 16	Zinc finger, C2H2-like	0.534503138
Annotation Cluster 17	carbohydrate binding	0.513359865
Annotation Cluster 18	ATP binding	0.473831026
Annotation Cluster 19	Fungal specific transcription factor	0.464801781
Annotation Cluster 20	Tetratricopeptide TPR-1	0.363724625
Annotation Cluster 21	G-protein coupled receptor protein	0.317753313
Annotation Cluster 22	metal ion transport	0.263101544
Annotation Cluster 23	monosaccharide metabolic process	0.259391798
Annotation Cluster 24	Protein kinase	0.230133836
Annotation Cluster 25	cellular macromolecule localization	0.071841863
Annotation Cluster 26	nucleotide biosynthetic process	0.039185881
Annotation Cluster 27	peptidase activity	0.031918821
Annotation Cluster 28	WD40 repeat	0.008404691
Annotation Cluster 29	chromosome	0.000122783

Table S6 Functional clustering of genes enriched in the fresh fruiting body. The data were analyzed using DAVID.

Annotation Cluster	Term	Enrichment Score
Annotation Cluster 1	translation	10.96007435
Annotation Cluster 2	chromatin assembly	1.389517748
Annotation Cluster 3	monosaccharide catabolic process	1.082506148
Annotation Cluster 4	tRNA metabolic process	0.529486463
Annotation Cluster 5	pyridoxal phosphate binding	0.39308153
Annotation Cluster 6	WD40 repeat	0.387654065
Annotation Cluster 7	ATP binding	0.316090114
Annotation Cluster 8	Serine/threonine protein kinase	0.138631684
Annotation Cluster 9	peptidase activity	0.122788756
Annotation Cluster 10	oxidoreductase	0.06622579
Annotation Cluster 11	transcription regulator activity	0.015368224
Annotation Cluster 12	metal-binding	9.0021E-05

Table S7 Differentially expressed oxidative stress, signal transduction, and cell-death related genes judged as DEG.

ID	D0_mean	D4_Mean	Fold change (D4/D0)	p.value	Seq. Description	min. eValue
g4385.t1	0	495.33	∞	5.9E-08	phenylalanine tyrosine ammonia-lyase	0
g7820.t1	0	13.33	∞	5.1E-03	glutathione S-transferase C-terminal-like protein	3.87E-16
g6379.t1	0	16.67	∞	3.4E-05	glutathione transferase	9.97E-168
g884.t2	0	14.67	∞	2.0E-03	glutathione s-transferase	3.46E-100
g7820.t1	0	13.33	∞	5.1E-03	glutathione S-transferase C-terminal-like protein	3.87E-16
g6226.t1	1	29.67	29.67	6.4E-04	AChain Crystal Structure Of Glutathione Transferase	2.31E-24
g4124.t1	0.67	14.67	22	3.0E-03	glutathione s-transferase	4.91E-95
g7821.t1	65	1426.67	21.95	7.9E-05	glutathione S-transferase	1.72E-82
g8660.t1	17	179.33	10.55	2.4E-03	glutathione S-transferase C-terminal-like protein	5.95E-121
g10274.t1	25	1135	45.4	4.1E-08	thioredoxin	2.88E-48
g9281.t1	1.33	22	16.5	9.1E-04	l-ascorbate oxidase	0
g4567.t1	0	15.67	∞	6.9E-05	cytochrome p450	5.82E-174
g4711.t1	0	11.33	∞	4.4E-04	cytochrome P450 monooxygenase	0
g6252.t2	0	11	∞	1.3E-03	cytochrome p450	0
g691.t1	0	9.33	∞	3.2E-03	cytochrome p450	0
g1.t2	0	8.33	∞	2.1E-03	cytochrome p450	0
g7689.t4	0	7	∞	4.3E-03	cytochrome P450	5.45E-174
g2757.t1	1.33	487	365.25	9.3E-07	D-lactate dehydrogenase [cytochrome]	0
g2738.t1	3	333	111	8.0E-09	cytochrome p450	0
g11604.t1	7.67	508.33	66.3	2.5E-09	cytochrome c peroxidase	0
g2202.t1	3	66.67	22.22	5.3E-04	cytochrome P450 monooxygenase	0
g10671.t1	2	43.33	21.67	2.1E-04	cytochrome p450	0
g550.t1	3	52.33	17.44	7.3E-04	cytochrome p450	5.27E-141
g2157.t2	10.67	106.67	10	4.4E-04	QCR6 subunit6 of the ubiquinol cytochrome-c reductase complex	1.61E-126
g6572.t1	3	26.67	8.89	3.8E-03	cytochrome p450 monooxygenase pc-3	0
g7735.t1	9.33	81.33	8.71	6.3E-04	cytochrome c oxidase copper chaperone	2.04E-33
g3972.t2	12.67	80.67	6.37	4.5E-03	cytochrome P450	0
g11194.t1	0	110	∞	1.1E-10	CMGC MAPK protein kinase	0
g12.t1	0	13	∞	1.7E-04	protein kinase	1.5E-15
g640.t1	15.67	731	46.66	1.4E-11	TKL TKL-ccin protein kinase	0
g10411.t1	1.33	41.67	31.25	4.5E-03	CMGC MAPK protein kinase	0
g8811.t1	0.67	20.67	31	1.6E-03	kinase-like protein	0
g3286.t1	0.67	15.33	23	2.9E-03	bud32 protein kinase	9.11E-132
g10953.t1	1.33	21.33	16	9.8E-04	CMGC MAPK protein kinase	0
g3352.t1	3	42.67	14.22	5.2E-03	kinase-like protein	0
g4685.t1	24.33	288.67	11.86	1.3E-04	Pkinase-domain-containing protein	0
g5331.t1	70.67	837.67	11.85	5.8E-06	kinase-like protein	0
g3169.t1	12.33	131.33	10.65	5.1E-03	Pkinase-domain-containing protein	0
g11044.t3	17	168.67	9.92	7.6E-05	CMGC MAPK protein kinase	0
g509.t1	11	93.33	8.48	8.3E-04	serine threonine-protein kinase	0
g8053.t1	20	147.33	7.37	1.2E-03	other 1 protein kinase	6.84E-33
g1758.t1	161.67	992.33	6.14	1.7E-03	kinase-like protein	5.17E-108
g640.t1	15.67	731	46.66	1.4E-11	TKL TKL-ccin protein kinase	0
g615.t1	0	32.67	∞	7.4E-06	inositol hexakisphosphate kinase 1	4.03E-179
g11374.t1	0	8.67	∞	2.6E-03	Cullin-domain-containing protein	0
g9687.t2	17.67	244.33	13.83	4.1E-06	vacuolar assembling sorting protein VPS16	0
g10593.t1	5.67	60	10.59	5.3E-04	Programmed cell death protein 2-like	1.84E-131
g485.t1	13.33	944.67	70.85	2.7E-05	metacaspase	3.63E-165
g9815.t1	5.33	49	9.19	9.9E-04	subtilisin-like protease	0