

Table S1

List of analyzed edible fungal genomes their web sites.

Organism	Public web site
<i>Volvariella volvacea</i> V23	http://genome.jgi-psf.org/pages/dynamicOrganismDownload.jsf?organism=Volvo1
<i>Coprinus cinereus</i>	http://www.broadinstitute.org/annotation/genome/coprinus_cinereus/MultiDownloads.html
<i>Schizophyllum commune</i> H4-8 v2.0	http://genome.jgi-psf.org/Schco2/Schco2.download.html
<i>Agaricus bisporus</i> var <i>bisporus</i> (H97) v2.0	http://genome.jgi-psf.org/Agabi_varbisH97_2/Agabi_varbisH97_2.download.html
<i>Pleurotus ostreatus</i> PC15 v2.0	http://genome.jgi-psf.org/PleosPC15_2/PleosPC15_2.download.html

Table S2

Set of primers corresponding to the 100 microsatellite locus randomly selected from *V. volvacea* genome.

Microsatellite	Primer sequence	Position on <i>V. volvacea</i> genome
(TGCTGA)5	(F)ACGACGCGTATTTGTTTTCC (R)GCAGTTTGACCCCACTCATT	Scaffold1_431928-431957
(ACGAAG)6	(F)GAAAAGCGTGTGGTTGGATT (R)TACTCGTCCTCGTCCTCGTT	Scaffold1_612925-612960
(TCC)8	(F)ACTCCTCTGCAGCTTTCTCG (R)GGTTTACGAGCTCTTGGCTG	Scaffold1_1065146-1065169
(GTG)6	(F)AATGAAGCAACAGATTGGGG (R)GGGTGTGACAGAACTGCCTT	Scaffold1_1906218-1906235
(GTT)6	(F)GTCGAGGTTGATGTCGAGGT (R)GGCCTAATTGTCTCGAGTGC	Scaffold1_2488335-2488352
(CTG)7	(F)ATCCTTGTGCGGAAGTTGGTG (R)GGAAAAGGAACGGAAGAAGG	Scaffold1_2687794-2687814
(TGG)10	(F)TGATGGTGTAGCAGTGGCAT (R)CAGTCACAGTCTGGTGGTGC	Scaffold1_3470394-3470423
(TGCC)6	(F)GGTCAGAGGCTTGTACTCGG (R)TCTCTTTGCTCGAGCTCCTC	Scaffold1_3819500-3819523
(TCCGAG)5	(F)CTTACTCTGCTTCGCTGCCT (R)CGAAGACGAAGAGGATGAGG	Scaffold2_348331-348360
(T)15	(F)TTCAGAAATCGAATGGAGGG (R)TCCATCTCGTACGAAGACCC	Scaffold2_629590-629604
(A)38	(F)GTCGCTGATTGTCCCAGAAT (R)TATTGCGTAGTGTGCCAAA	Scaffold2_1281474-1281511
(CGTGTG)5	(F)AACACTCGACCTGACCCAAC (R)ATGCAAGGTCAAGGGACAAC	Scaffold2_1299385-1299414
(TTC)6	(F)GTTTGCCTGCTTACCATCT (R)CAATGGTACCCTGCTCGAAT	Scaffold2_1901177-1901194
(GTAGT)6	(F)GCCCCACCATGGTAGTGTAG (R)GGGAGAGGGAGGAAGAGAGA	Scaffold2_2144371-2144400
(AAAATA)5	(F)GATTTCCAAAGGTGGCTCAA (R)CTTTCTGCATGAGTTGTGGC	Scaffold2_2549073-2549102
(CCT)6	(F)CTATCCCCACCAGCATCACT (R)GTGCACCAGACCTGGTAAT	Scaffold3_131152-131169
(G)16	(F)CGTCACCTGCGTTCACCTCTA (R)AATTTCAAACACCCCAACCA	Scaffold3_631540-631555
(GAG)13	(F)AGTGCTGGACGACATGACTG (R)AGGTGGTAGAGGCATGGTTG	Scaffold3_1135265-1135303
(AAGGAC)9	(F)ACCAATGGGTCTAGGTGCTG (R)TGCCTCTCATCAAGATCACG	Scaffold3_1846823-1846876

(GTC)7	(F)AAGCTGTACGAGAAGGCGAC (R)AGCGACATAAGCCAACATCC	Scaffold3_2393769-2393789
(CCT)7	(F)CCGAGCTCGCATACTCTTCT (R)TAGAGGATTGTACGGGGCAG	Scaffold4_381002-381022
(CGAAA)6	(F)AAGCCCTACTCCAGCTCCTC (R)CAACTATTTTCCGCCACCAT	Scaffold4_570255-570284
(ACCG)5	(F)GATCAGGCCACACAAAAGT (R)ATCGAATAACTGGACCGACG	Scaffold4_1042332-1042351
(A)23	(F)AATTGGGACATTTGAGGCAC (R)CCTCGCTTCTCAAGGCAATA	Scaffold4_1688293-1688315
(CACGA)5	(F)GCTGATCACCGTTTTCGTTT (R)GTTGATGGGCACGGTAGACT	Scaffold4_2262668-2262692
(T)16	(F)TTGAAGCAAATGTTTGCAG (R)CTTGCATGATCCATCCTTT	Scaffold5_268766-268781
(GCC)6	(F)GATCCATTAATGATGCGGCT (R)CTTGCTTTGGCTCAAGGTTT	Scaffold5_982489-982506
(AT)10	(F)GATGAAGGTGTCGGTGGAAT (R)TTGCGTTTTCGAACTGTCTG	Scaffold5_1073542-1073561
(GAC)7	(F)TCTACGCAGGAACACACTGG (R)AAAATTGCTGCAAAGTGGCT	Scaffold5_1598143-1598163
(A)26	(F)TATACCATTGCTGGGGCATT (R)AGTGGGACTCTGCAAGGCTA	Scaffold6_315238-315263
(TGGT)6	(F)GGAAGGAAGGGGTGAGAGTC (R)ACGCTGGACCCCTAAAGAAT	Scaffold6_765056-765079
(CTTCGA)5	(F)GCGTGAATGCCGGTACTAAT (R)CCGGTAGTTGGACTCCAGAA	Scaffold6_1336082-1336111
(CAG)8	(F)TCACCATCAGTCCAGATGC (R)TCACGATTTACGCTCTCAC	Scaffold7_119885-119908
(GAC)8	(F)ATATCCTTCGCGATGACCTG (R)GTACTCCAGCACGGCATCTT	Scaffold7_320416-320439
(T)61	(F)CTTTCTGGGCTTTCGAGGTT (R)GGCAAAGAAACGAAATGGAA	Scaffold7_962608-962668
(GTG)9	(F)TGCGATAGCACTCAAAGGTG (R)GGCGTTCTATTCGTTCCAAA	Scaffold8_127150-127176
(TACGAA)5	(F)GAGCCGTCACATTTGACCT (R)CCATTCCTGCTTCTTCTTCG	Scaffold8_532402-532431
(GTC)7	(F)ATACGGGATACCGCTCTGTG (R)ACCTCCGTTTTGGTTCACTG	Scaffold8_1157968-1157988
(TTTCTT)5	(F)TGGCACTTGTCACTCCTCTG (R)AGACCTCTGAAGGTGGCTCA	Scaffold9_434842-434871
(GGATAT)5	(F)AGAGACCGATGGCAGAAAGA (R)TCCTTCCATACTCCCTGC	Scaffold9_814118-814147
(TCTTCG)5	(F)TTTCGGACAGGAGAGAGTCG	Scaffold10_162541-162570

	(R)TGGAGAAGAGGCAGGGTATG	
(GCACAA)5	(F)CGACTGCTCAAGTACACCCA	Scaffold10_419127-419156
	(R)CTCCTCCTGTGCTTCGACTC	
(TGCTGG)5	(F)TATACGGCAGATTTGTTGCG	Scaffold11_139461-139490
	(R)AGCAGCAGCAGGGAATGTAT	
(CCGCAC)6	(F)CGTCTACATCCACAACACCG	Scaffold11_433434-433469
	(R)CTGTCGTCGTCTTCGTCTTG	
(GGT)5	(F)ATCGTCTACGGAGATCGGTG	Scaffold11_608487-608501
	(R)CTACCACCACCAAGTCCACA	
(GTGCTT)5	(F)CCTTGTTCGGTTTGCTTGT	Scaffold12_249930-249959
	(R)AAACTAGTCCCAAGGCGGAT	
(GAGTGC)5	(F)GAGCGATACTGCTGCTGTTG	Scaffold12_784704-784733
	(R)CCAACTCAAACAGCTCCCAT	
(CCGG)5	(F)CTTGCCTTGGTCAAATCCAC	Scaffold13_157743-157762
	(R)GCAGGCTAAAGGGTTCTTC	
(TTTTC)5	(F)TCTTGAGTGGCTATTGTCAGGA	Scaffold13_687861-687885
	(R)AATGACGCCACCGAGAATAC	
(GTG)7	(F)TTTATGACTGGCTGTGGCTG	Scaffold14_45258-45278
	(R)CGCAGGAGAGATGCATACAA	
(GT)8	(F)CAACCTCCTCTCCTCCCTC	Scaffold14_562610-562625
	(R)TCCTGCCCACACAGTCATAA	
(CAC)14	(F)TTTGCATCTAATGACGCCAC	Scaffold15_112434-112475
	(R)TTGTCTTTGAACATTCACATTGC	
(TTTTC)5	(F)CCTGGGCTCTGTCACTGTCT	Scaffold15_631004-631028
	(R)TAAGCAAGTCACGTGGTCCC	
(GTTCTG)5	(F)GGCTGATGACTTGGGTGACT	Scaffold16_224142-224171
	(R)AGATGATGATGAGGATCGGC	
(AAG)8	(F)AGGAGGAGGAAGAGGCAAAG	Scaffold16_721355-721378
	(R)ACAACGAGCGTCATAAGCCT	
(TTTCTT)5	(F)AAATACAGGCCTGGCAAGTG	Scaffold17_318630-318659
	(R)CACATGGTCCTTGGTGCTTA	
(T)20	(F)CCACCACCTCACACTATCCC	Scaffold17_615280-615299
	(R)GGGTGAGCAATCGGAAGATA	
(A)22	(F)GTCTCCCGATGTGTTCTGGT	Scaffold18_145216-145237
	(R)CACGCGTCTGCAGGTATAGA	
(ATT)8	(F)ACCGCCCCTTTCTTAATGTT	Scaffold18_541805-541828
	(R)ATCTGCAACAACGAACCACA	
(T)33	(F)TCTTAGGGTGCAGTCCGGATG	Scaffold19_440824-440856
	(R)AGCACATGGGAACCAGAAAG	
(ACC)9	(F)CGTCTTCACCTTACCCCAA	Scaffold19_646423-646449
	(R)GCTGTGATGGCAGACACACT	
(A)38	(F)CCAAGCAAGGAACAAGGAGA	Scaffold20_2127-2164
	(R)GGCATTCTGCCAAAGAGTC	

(TCG)7	(F)CTGTCCACCACCTCAATCG	Scaffold20_605184-605204
	(R)ACGTCTCATTCTTCACGGG	
(T)26	(F)AAGGAAACATGCCACAAAA	Scaffold21_20097-20122
	(R)TGCCTATGTATTCTTGCGACC	
(TCG)6	(F)CAGGAACAGCCATCTTCTC	Scaffold21_169819-169836
	(R)GTATGTGCATCTCGCTTGGGA	
(GAC)6	(F)ACGGAGCAGGTCGAGAGATA	Scaffold22_303125-303142
	(R)ATCAAACCAAAGAACAGCGG	
(TGC)7	(F)AGTTGTTGTCGTTGCTGACG	Scaffold22_601066-601086
	(R)AAACCAGAACCTGCAACACC	
(GCA)6	(F)ATGTGGCTAACTCCTGGGTG	Scaffold23_499139-499156
	(R)TGACGAGTAGCTGGTGATGC	
(T)21	(F)ATGTTGTCGTGTCGTGTCGT	Scaffold23_556485-556505
	(R)TTGATACTGCCTACCCCAGC	
(ACG)8	(F)GTGGGGATAGAACTGGGGTT	Scaffold24_291636-291659
	(R)GGCTTCAATCCCTAGATGGC	
(A)19	(F)TGCTCTTACGGTCTCGGTCT	Scaffold24_413622-413640
	(R)GGTTTGCGATTATGGTGGTC	
(T)22	(F)GCAGGAAGTCCTCCAAAGTG	Scaffold25_80676-80697
	(R)GGGTTCCGGTATTCTTGAT	
(GTCTT)5	(F)CACGTTTTTCGTGTTTCGTG	Scaffold25_335713-335737
	(R)AAACAGTCGAGACGGAGACG	
(TCA)8	(F)GCACTGCTTTCCTCATCTCC	Scaffold26_284037-284060
	(R)GCCTATGATATGGAGCGAGC	
(GTG)12	(F)AGTGCGACGAGCCCTAGTTA	Scaffold27_391371-391406
	(R)AGATTCTCCCTGACCCCATC	
(ACCAAA)5	(F)TCAGCGTCCATCACTCAAG	Scaffold28_255725-255754
	(R)GCTCTGCAGGAGCAATAAC	
(A)21	(F)AGGCGAGGAAAAATCACCTT	Scaffold29_291594-291614
	(R)GAACAGTCTGCTGGGGTGT	
(AAAATA)7	(F)GATTTCCAAAGGTGGCTCAA	Scaffold30_2671-2712
	(R)ATGCACTGCTCAAGATGCAC	
(ATCTAC)5	(F)ATGTACAGGATTGCCGCTC	Scaffold31_85372-85401
	(R)CCCGCTGAAATTAACGAAAA	
(TGACC)7	(F)CTTTCAGGAAGAGCCCAGC	Scaffold32_217019-217053
	(R)TGAAGGGCTTGAAGGAGAAA	
(CCTTT)5	(F)GTGGCTGAGTGATTCCCAT	Scaffold33_62403-62427
	(R)TTCAACAGTGCCCAGTTACG	
(GTG)7	(F)ATAACCGGAAGCAGAAGCAG	Scaffold34_109975-109995
	(R)TTCTATCACAACAAGCCCC	
(CCGAGT)5	(F)ATATCTGGCTTCGACGGTTG	Scaffold35_63354-63383
	(R)GATGTCCAAGTCCGAGTGGT	
(TTTCTC)5	(F)GCTGGCTGCATAAACGGTAT	Scaffold36_143288-143317

	(R)AGGGAAATCGAAAGCGGTAT	
(A)35	(F)TCCAAGCGTCTATCAATCCC	Scaffold37_171896-171930
	(R)CTTTTCGGCGACTTTTCTG	
(AAT)8	(F)TCAAGAGACAAAAAGTGAGCAAA	Scaffold38_108483-108506
	(R)TGTTGACTGCCACATTGAT	
(GGATTG)5	(F)GCGTCTTGGAGAAGCAAAAC	Scaffold39_179253-179282
	(R)AATCGTGCACAAAGGAAACC	
(G)16	(F)TTATGACCCCTTCCAGATCG	Scaffold40_34075-34090
	(R)GGTTGGAAGCAGACGAAGAG	
(CGT)6	(F)AAAAGCGCCCATTTGAACTT	Scaffold41_115044-115061
	(R)CGTCAACTACCTCCCAACA	
(CAC)6	(F)GTCATCTGACCGCCTGGTAT	Scaffold42_44443-44460
	(R)TTGGGTTTAAGCATTCTCGG	
(AT)8	(F)TGCTAGCCATGGCCTACTCT	Scaffold43_117069-117084
	(R)AGTCAAGTTTAGGGCTGCCA	
(TGA)7	(F)TTCTTTTGGATTATGGCGGC	Scaffold44_96228-96248
	(R)AACTCCACAACCACTACGCC	
(ACC)6	(F)GTTGGCACCCTACATCACG	Scaffold45_109122-109139
	(R)GGTGGGCTATCAGCATCATT	
(T)12	(F)CCAAGGAACTTCACACCAAA	Scaffold46_3720-3731
	(R)GTGACAGGGCAACAATTCAG	
(CCCATA)5	(F)GTGTTTCGTACTGGGCTTGGT	Scaffold47_20934-20963
	(R)TCAGAATGGTATGCGGATCA	
(T)10	(F)TTGGTGCATCTCCATCAAAA	Scaffold48_59215-59224
	(R)CAAACGTCAAATGAACGTGG	
(TC)8	(F)GGTTCTCTCTCCCTGCCTCT	Scaffold49_3987-4002
	(R)TCAAGCTGACAAGGAACACG	
(A)12	(F)ATTTTTAAACGGAGGGGTGG	Scaffold51_25191-25202
	(R)TAGCCCATGTGGACAAGACA	
(A)20	(F)TTTTAGGCTGCTCATGGCTT	Scaffold56_3669-3688
	(R)AGCTTGAGGTTGATGGGATG	
(TCG)5	(F)GTGATTGCTACGGGCTTGAT	Scaffold59_4798-4812
	(R)TCGATGGTGAAATGCGAATA	

Table S3

Microsatellites in the gene models with some specialized function in *V. voluacea*.

Gene Product	Number of gene	Location
CYP547B1	1	Intron
CYP5080B3b	1	Intron
CYP627A1	1	Intron
Ectomycorrhiza-upregulated GH16 glucan endo-1,3-beta-glucosidase precursor	1	Intron
GH16 beta-1,3-glucan recognition protein	1	CDS, Intron×2
CAMK/CAMK1 protein kinase	1	CDS×4
CAMK/CAMKL/Kin1 protein kinase	1	CDS
CAMK/CAMKL/Kin4 protein kinase	1	CDS
CMGC/SRPK protein kinase	1	CDS
Hypothetical kinase	1	CDS
Mps one binder kinase activator-like 4	1	CDS
CAMKK/ELM protein kinase	1	CDS
HAL protein kinase	1	5'UTR
RAN protein kinase	1	Intron
Phosphatidylinositol phosphate kinase PIPK5	1	3'UTR
STE/STE11/cdc15 protein kinase	1	CDS
Candidate aryl-alcohol dehydrogenase	1	Intron
Dehydrogenase E1 and transketolase domain-containing protein 1	1	Intron, Intron
Dihydrolipoamide dehydrogenase	1	Intron
IMP dehydrogenase	1	CDS, Intron
Pyruvate dehydrogenase	1	CDS
Mitochondrial half-size ABC transporter	1	CDS
Multidrug resistance-associated ABC transporter	1	Intron
OPT oligopeptide transporter	1	Intron
Pleiotropic drug resistance ABC transporter	1	Intron
Sodium transport ATPase	1	Intron
Urea transporter	1	3'UTR
Vacuolar amino acid transporter 4	1	Intron×2
ZIP-like iron-zinc transporter	1	CDS
60S ribosomal protein L18-B	1	3'UTR
ABC domain-containing protein	1	CDS
Adaptor protein	1	CDS
Adenylate cyclase	1	CDS
ADP-ribosylation factor	1	CDS
Aminopeptidase	1	Intron
AMP dependent CoA ligase	1	Intron

Ankyrin repeat protein	1	CDS
Aspartic peptidase A1	1	3'UTR
ATP-dependent DNA helicase MER3	1	Intron
ATP citrate lyase isoform 2	1	3'UTR
Beta-tubulin 2 tubb2	1	Intron
Beta-xylosidase	1	CDS
C-4 methyl sterol oxidase	1	Intron
Calnexin	1	3'UTR
Carnitine/acyl carnitine carrier	1	Intron
CDC5	1	Intron
Clathrin-coated vesicle protein	1	Intron
Coiled-coil protein	1	CDS
COP8	1	CDS
Copper-fist transcription factor	1	5'UTR
Cytoplasmic protein	2	Intron×2
Deoxyuridine 5'-triphosphate nucleotidohydrolase Dut	1	CDS
Dienelactone hydrolase endo-1,3,1,4-beta-D-glucanase	1	Intron
DNA helicase	1	CDS
DNA repair and recombination protein pif1	1	Intron
Endoplasmic reticulum protein	1	3'UTR
Epsin domain-containing protein	1	CDS×2
Exo-beta-1,3-glucanase	1	Intron
Exosome component Rrp46	1	CDS
Expansin family protein	1	CDS×2
Expressed protein	2	CDS×2
Extracellular triacylglycerol lipase precursor	1	Intron
Fructose-bisphosphate aldolase	1	CDS, Intron
Glutamate-rich WD repeat containing	1	CDS
Glycoside hydrolase family 10 and carbohydrate-binding module family 1 protein	1	Intron
Glycoside hydrolase family 13 protein	1	CDS
Glycoside hydrolase family 15 protein	1	Intron
Glycoside hydrolase family 16 protein	1	Intron×2
Glycoside hydrolase family 18 protein	1	CDS, Intron
Glycoside hydrolase family 35 protein	1	Intron
Glycoside hydrolase family 38 protein	1	Intron
Glycoside hydrolase family 92 protein	1	Intron
Glycosyltransferase family 2 protein	2	CDS
Glyoxal oxidase	2	3'UTR
H3	1	Intron
Heparinase II/III family protein	1	Intron

Heterotrimeric G protein alpha subunit B	1	Intron×2
High-glucose-regulated protein 8	1	Intron
Histone acetyltransferase mst2	1	CDS
Histone deacetylase complex, catalytic component RPD3	1	Intron
HNWD1	1	Intron
Iron sulfur assembly protein 1	1	Intron
L-ascorbate oxidase	1	3'UTR
Laccase 1	1	3'UTR
Laccase 3	1	3'UTR
Laccase 6	1	Intron
Lipase	1	CDS×2
Lipase 2	1	CDS×2, Intron
Long-chain-fatty-acid-CoA ligase	1	3'UTR
Metalloprotease	2	Intron×2
Metalloprotease ATP23	1	3'UTR
MIP protein	1	CDS
Mitochondrial chaperone bcs1	1	Intron
Mitochondrial genome maintenance protein	1	CDS
Modular protein with glycoside hydrolase family 13 and glycosyltransferase family 5 domains	1	Intron
NADH-quinone oxidoreductase	1	Intron
Nonribosomal peptide synthetase 12	1	Intron
NUC153 and WD40 repeat-containing nucleolar rRNA processing-related protein	1	Intron
Nuclear condensin complex protein	1	Intron
Nuclear protein	1	3'UTR
Nucleolar protein	1	CDS
NWD2	1	Intron
Peptidase 1	1	Intron
Phosphatidylserine synthase 2	1	Intron
Plant senescence-associated protein	1	CDS, Intron
Pol-like protein Pol-2	1	CDS
Polyprotein	1	Intron
Polysaccharide synthase Cps1p	1	3'UTR
Potassium/sodium efflux P-type ATPase	1	CDS×3, Intron
Pre-mRNA-processing ATP-dependent RNA helicase PRP5	1	Intron
Protoporphyrinogen oxidase	1	Intron
RAB-protein geranylgeranyltransferase	1	3'UTR
Ras protein	1	Intron
Receptor expression-enhancing protein 4	1	CDS

Related actin-binding protein	1	CDS
Retrotransposable element Tf2 155 kDa protein type 1-like	1	Intron
Rho GTPase activating protein 22	1	CDS
ROT1 protein	1	3'UTR
RRM/R3H domain-containing protein	1	Intron
Sec7 guanine nucleotide exchange factor	1	3'UTR
Serine palmitoyltransferase 2	1	CDS
Serine protease inhibitor	1	Intron
SH3 domain-containing protein	1	3'UTR, Intron
Siderophore biosynthesis regulatory protein	1	Intron
Sim15	1	Intron
Sodium transport ATPase	1	Intron
Splicing factor SF1	1	Intron
STE-12 alpha	1	Intron
STE20	1	CDS
Structural maintenance of chromosome protein 3	1	Intron
Tetraspanin Tsp2	2	CDS
Trehalase	1	Intron
Ubiquitin-conjugating enzyme E2	1	CDS
Ubiquitin C-terminal hydrolase	1	CDS
Unnamed protein product	1	5'UTR
Vacuolar DHA amino acid exporter	1	Intron
Vacuolar membrane protein	1	CDS
Vacuole protein	1	Intron
XPG I-region protein	1	CDS
Xylanase	1	CDS
ZYRO0D15356p	1	CDS