

Table S3. Distribution of the Clean Reads of the sequencing.

Sample	Total Raw Reads(Mb)	Total Clean Reads(Mb)	Total Clean Bases(Gb)	Clean Reads Q20(%)	Clean Reads Q30(%)	Clean Reads Ratio(%)
White	52.66	52.65	7.9	97.19	92.89	99.99
Yellow	50.29	50.29	7.54	97.64	93.96	99.99

Table S4. Distribution of the lengths of the assembled unigenes.

Sample	Total Number	Total Length	Mean Length	N50	N70	N90	GC(%)
White	22823	57646679	2525	3805	2626	1353	45.33
Yellow	21023	47993042	2282	3506	2357	1218	45.45
All-Unigene	43750	1.06E+08	2424	3782	2529	1298	46.53

Table S5. Phylogenetic analysis of KOG species.

species	gene numbers	percentage
Agaricus bisporus var. bisporus H97	7274	20.32
Agaricus bisporus var. burnettii JB137-S8	6175	17.25
Galerina marginata CBS 339.88	4136	11.55
Laccaria amethystina LaAM-08-1	3885	10.85
Laccaria bicolor S238N-H82	2379	6.65
Hebeloma cylindrosporum h7	2019	5.64
Leucoagaricus sp. SymC.cos	1776	4.96
Hypholoma sublateritium FD-334 SS-4	1037	2.9
others	7085	19.88

Table S6. The primers used in this study.

Primer name	Sequence
FIMCH5-F	ATGGAACCCTCGATACACGA
FIMCH5-R	TCACACTATCTGGGTCCCTC
FIMCH5-GUS-F	ATGGAACCCTCGATACACGA
FIMCH5-GUS-R	CACTATCTGGGTCCCTC
FIMCH5-GUS attb1	AAAAAGCAGGCTTCATGGAACCCTCGATACACGATG
FIMCH5-GUS attb2	AGAAAGCTGGGTCCACTATCTGGGTCCCTCTTT
FIMCH5-XbaI	ggtctagaATGGAACCCTCGATACACGA
FIMCH5-BamHI	ggggatccTCACACTATCTGGGTCCCTC