

Table S2. The statistics of the fungal genomes used in this paper

S.No	Organism Name	Name	INSDC	Size (Mb)	GC%	Short Name	Short Name(JGI) Type	Family	Order	Genome_Source	
1	<i>Macrocybe gigangea</i>	—	—	41.23	49.82	<i>M. gigangea</i>	<i>Macgig</i>	SN	Tricholomataceae	Agaricales	—
2	<i>Armillaria ostoyae C18/9</i>	master WGS	FUEG000000000.1	60.11	0	<i>A. ostoyae</i>	<i>Armostl</i>	WR	Physalacriaceae	Agaricales	JGI
3	<i>Pleurotus eryngii</i>	master WGS	QCWS000000000.1	49.92	49.4	<i>P. eryngii</i>	<i>Pleeryl</i>	WD	Pleurotaceae	Agaricales	JGI
4	<i>Coprinopsis cinerea</i>	master WGS	AACS000000000.2	36.19	51.6	<i>C. cinerea</i>	<i>Copcil</i>	LD	Psathyrellaceae	Agaricales	JGI
5	<i>Clitocybe gibba</i>	—	—	—	—	<i>C. gibba</i>	<i>Cligibl</i>	SN	Tricholomataceae	Agaricales	JGI
6	<i>Lepista nuda</i>	master WGS	—	44.13	—	<i>L. nuda</i>	<i>Lepnudl</i>	WR	Tricholomataceae	Agaricales	JGI
7	<i>Tricholoma matsutake 945 v3.0</i>	master WGS	PKSN000000000.2	189	34.4	<i>T. matsutake</i>	<i>Trima3</i>	ECM	Tricholomataceae	Agaricales	NCBI
8	<i>Tricholoma saponaceum</i>	master WGS	QLOJ000000000.1	55.71	46.7	<i>T. saponaceum</i>	<i>Trisap</i>	ECM	Tricholomataceae	Agaricales	NCBI
9	<i>Tricholoma sp. MG77</i>	master WGS	QMFE000000000.1	118.32	45.5	<i>T. sp. MG77</i>	<i>TrispMG77</i>	ECM	Tricholomataceae	Agaricales	NCBI
10	<i>Tricholoma terreum</i>	master WGS	QFEU000000000.1	84.41	—	<i>T. terreum</i>	<i>Triter</i>	ECM	Tricholomataceae	Agaricales	NCBI
11	<i>Tricholoma flavovirens</i>	master WGS	QLOK000000000.1	119.32	44.3	<i>T. flavovirens</i>	<i>Trifla</i>	ECM	Tricholomataceae	Agaricales	NCBI
12	<i>Tricholoma bakamatsutake</i>	master WGS	QLOL000000000.1	140.67	43.2	<i>T. bakamatsutake</i>	<i>Tribak</i>	ECM	Tricholomataceae	Agaricales	NCBI
13	<i>Tricholoma sp. MG99</i>	master WGS	QOVE000000000.1	59.53	—	<i>T. sp. MG99</i>	—	—	Tricholomataceae	Agaricales	—

WR: wood-rotting, ECM:ectomycorrhizal, LD:litter decomposer, WD:wood-decay, SN:Saprotrrophic nutrition

*All statistics come from with NCBI and JGI