

**Table A. Target proteins responsible for genome defense by fungi**

<b>Mechanism</b>	<b>Name</b>	<b>Description</b>	<b>Source organism</b>	<b>Length (aa)</b>	<b>GenBank accession</b>
Repeat-induced point mutation	Rid/Dim2 <sup>1</sup>	DNA methyltransferase	<i>Neurospora crassa</i>	1454	AAK49954.1
	Masc1 <sup>2</sup>	C5-DNA methyltransferase	<i>Ascobolus immersus</i>	537	AAC49849.1
	Masc2 <sup>3</sup>	C5-DNA methyltransferase	<i>Ascobolus immersus</i>	1356	AAC03766.1
Meiotic silencing by unpaired DNA	Sad-1 <sup>4</sup>	RNA dependent RNA polymerase	<i>Neurospora crassa</i>	1638	EAA35012.3
	Sms-3 <sup>4</sup>	dicer-like protein	<i>Neurospora crassa</i>	1584	EAA32662.1
	Sms-2 <sup>4</sup>	meiotic silencing suppressor	<i>Neurospora crassa</i>	989	EAA29350.1
Quelling	Qde-1 <sup>4</sup>	RNA-dependent RNA polymerase	<i>Neurospora crassa</i>	1402	EAA29811.1
	Dcl2 <sup>4</sup>	dicer-like protein	<i>Neurospora crassa</i>	1396	XP_963538.3
	Qde2 <sup>5</sup>	post-transcriptional gene silencing	<i>Neurospora crassa</i>	938	AAF43641.1

**Table B. Transcription factors involved in mushroom formation**

Protein name	GenBank Access	Length (aa)	Homologs in <i>Tricholoma matsutake</i>	Length (aa)	E-value	Identity (%)
Hom2	XP_003029756.1	723	Trima_14430	679	2.49e-57	33.4
Bri1	XP_003038897.1	776	Trima_08826	932	1.99e-159	39.2
Fst4	XP_003034563.1	826	Trima_15097	859	0.0	45.1
C2H2	XP_003026630.1	360	Trima_03635	486	7.59e-32	61.9
Fst3	XP_003031320.1	1120	Trima_16495	1056	0.0	64.8
Gat1	XP_003036589.1	449	Trima_00186	527	6.07e-66	39.1
Hom1	XP_003030056.1	316	Trima_12069	379	7.22e-31	75.6

**Table C. The summary of genome sequencing**

Platform	Insert size (bp)	Number of reads	Average read length (bp)	Total bases (bp)
HiSeq paired-end	500	99,204,510	100	10,019,655,510
HiSeq mate pair	5,000	310,061,732	100	31,316,234,932
MiSeq paired-end	250	24,712,074	250	6,165,993,276

**Table D. Transposable element Pfam domains**

Pfam ID	Pfam description
PF00075	RNase H
PF00078	Reverse transcriptase (RNA-dependent DNA polymerase)
PF00665	Integrase core domain
PF02925	Bacteriophage scaffolding protein D
PF02992	Transposase family tnp2
PF03184	DDE superfamily endonuclease
PF03221	Tc5 transposase DNA-binding domain
PF03732	Retrotransposon gag protein
PF04687	Microvirus H protein (pilot protein)
PF05699	hAT family C-terminal dimerisation region
PF05840	Bacteriophage replication gene A protein (GPA)
PF05970	PIF1-like helicase
PF07727	Reverse transcriptase (RNA-dependent DNA polymerase)
PF08283	Geminivirus rep protein central domain
PF08284	Retroviral aspartyl protease
PF10551	MULE transposase domain
PF13358	DDE superfamily endonuclease
PF13359	DDE superfamily endonuclease
PF13456	Reverse transcriptase-like
PF13837	Myb/SANT-like DNA-binding domain
PF13976	GAG-pre-integrase domain
PF14214	Helitron helicase-like domain at N-terminus
PF14223	gag-polypeptide of LTR copia-type
PF14529	Endonuclease-reverse transcriptase

**Table E. Genomes used for comparative analysis**

Species	Order	GenBank ID	Ecotype	Number of genes	Genome Size (Mbp)
<i>Agaricus bisporus</i> var. <i>bisporus</i> H97	Agaricales	GCF_000300575.1	Saprotroph	10,448	30.2
<i>Agaricus bisporus</i> var. <i>burnettii</i> JB137-S8	Agaricales	GCF_000300555.1	Saprotroph	11,278	32.6
<i>Amanita muscaria</i> Koide BX008	Agaricales	GCA_000827485.1	Ectomycorrhizal	18,093	40.7
<i>Auricularia subglabra</i> TFB-10046 SS5	Auriculariales	GCF_000265015.1	White-rot	23,555	74.9
<i>Botryobasidium botryosum</i> FD-172 SS1	Cantharellales	GCA_000697705.1	White-rot	16,502	46.7
<i>Coprinopsis cinerea</i> okayama7#130	Agaricales	GCF_000182895.1	Saprotroph	13,356	36.2
<i>Cylindrobasidium torrendii</i> FP15055 ss-10	Agaricales	GCA_000934385.1	White-rot	13,936	31.6
<i>Exidia glandulosa</i> HHB12029	Auriculariales	GCA_001632375.1	Saprotroph	26,690	78.2
<i>Fibularhizoctonia</i> sp. CBS 109695	Atheliales	GCA_001630335.1	Saprotroph	32,854	95.1
<i>Fistulina hepatica</i> ATCC 64428	Agaricales	GCA_000934395.1	Brown-rot	11,244	33.8
<i>Fomitiporia mediterranea</i> MF3/22	Hymenochaetales	GCF_000271605.1	White-rot	11,338	63.4
<i>Fomitopsis pinicola</i> FP-58527 SS1	Polyporales	GCA_000344655.2	Brown-rot	13,852	41.6
<i>Galerina marginata</i> CBS 339.88	Agaricales	GCA_000697645.1	White-rot	21,391	59.4
<i>Gloeophyllum trabeum</i> ATCC 11539	Gloeophyllales	GCF_000344685.1	Brown-rot	11,755	37.2
<i>Gymnopus luxurians</i> FD-317 M1	Agaricales	GCA_000827265.1	Saprotroph	22,046	66.3
<i>Hebeloma cylindrosporum</i> h7	Agaricales	GCA_000827355.1	Ectomycorrhizal	15,376	38.2
<i>Heterobasidion irregulare</i> TC 32-1	Russulales	GCF_000320585.1	Plant pathogen	13,275	33.6
<i>Hypholoma sublateritium</i> FD-334 SS-4	Agaricales	GCA_000827495.1	White-rot	17,771	48
<i>Jaapia argillacea</i> MUCL 33604	Jaapiales	GCA_000697665.1	White-rot	16,375	45
<i>Laccaria amethystina</i> LaAM-08-1	Agaricales	GCA_000827195.1	Ectomycorrhizal	21,033	52.2
<i>Laccaria bicolor</i> S238N-H82	Agaricales	GCF_000143565.1	Ectomycorrhizal	18,215	64.9
<i>Moniliophthora roreri</i> MCA 2997	Agaricales	GCF_000488995.1	Plant pathogen	17,910	52.2
<i>Neolentinus lepideus</i> HHB14362 ss-1	Gloeophyllales	GCA_001632425.1	Saprotroph	13,157	35.6
<i>Peniophora</i> sp. CONT	Russulales	GCA_001632445.1	White-rot	18,945	46
<i>Piloderma croceum</i> F 1598	Atheliales	GCA_000827315.1	Ectomycorrhizal	21,524	59.3
<i>Pleurotus ostreatus</i> PC15	Agaricales	GCA_000697685.1	White-rot	12,296	34.3
<i>Plicaturopsis crispa</i> FD-325 SS-3	Amylocorticiales	GCA_000827205.1	White-rot	13,617	34.5
<i>Punctularia strigosozonata</i> HHB-11173 SS5	Corticiales	GCF_000264995.1	White-rot	11,540	34.2
<i>Pycnoporus coccineus</i> BRFM310	Polyporales	GCA_002092935.1	White-rot	12,693	32.8
<i>Rhizoctonia solani</i> AG-1 IA	Cantharellales	GCA_000334115.1	Plant pathogen	10,489	36.9
<i>Schizophyllum commune</i> H4-8	Agaricales	GCF_000143185.1	White-rot	13,194	38.5
<i>Scleroderma citrinum</i> Foug A	Boletales	GCA_000827425.1	Ectomycorrhizal	20,995	56.1
<i>Serendipita indica</i> DSM 11827	Sebacinales	GCA_000313545.1	Endophyte	11,791	25
<i>Serendipita vermifera</i> MAFF 305830	Sebacinales	GCA_000827415.1	Orchid mycorrhizal	15,245	38.1

<i>Sistotremastrum niveocreum</i> HHB9708	Trechisporales	GCA_001630475.1	Saprotroph	13,076	35.4
<i>Sistotremastrum suecicum</i> HHB10207 ss-3	Trechisporales	GCA_001632355.1	Saprotroph	13,654	33.9
<i>Suillus luteus</i> UH-Slu-Lm8-n1	Boletales	GCA_000827255.1	Ectomycorrhizal	18,303	37

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**Table F. Total bases and read counts for the three developmental stages of *Tricholoma matsutake***

Development stage	Total bases	Read count	N (%)	GC (%)	Q20 (%)	Q30 (%)
Hyphae	10,954,625,640	108,461,640	0.004	49.58	94.12	86.92
Primordia	13,424,362,278	132,914,478	0.004	49.85	93.95	86.82
Fruiting Body	12,872,445,152	127,449,952	0.004	49.79	94.34	87.42

**Table G. Repeat families predicted by RepeatModeler**

Repeat family	Number of families	Average length (bp)
LTR	289	1832
DNA	130	2398
LINE	39	2228
RC	22	2103
Simple_repeat	14	756
buffer	2	2098
Unknown	1879	676



## Supplementary references

- 1 Kouzminova, E. & Selker, E. U. *dim-2* encodes a DNA methyltransferase responsible for all known cytosine methylation in *Neurospora*. *The EMBO journal* **20**, 4309-4323, doi:10.1093/emboj/20.15.4309 (2001).
- 2 Malagnac, F. *et al.* A gene essential for de novo methylation and development in *Ascobolus* reveals a novel type of eukaryotic DNA methyltransferase structure. *Cell* **91**, 281-290 (1997).
- 3 Chernov, A. V., Vollmayr, P., Walter, J. & Trautner, T. A. *Masc2*, a C5-DNA-methyltransferase from *Ascobolus immersus* with similarity to methyltransferases of higher organisms. *Biological chemistry* **378**, 1467-1473 (1997).
- 4 Galagan, J. E. *et al.* The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature* **422**, 859-868, doi:10.1038/nature01554 (2003).
- 5 Catalanotto, C., Azzalin, G., Macino, G. & Cogoni, C. Gene silencing in worms and fungi. *Nature* **404**, 245, doi:10.1038/35005169 (2000).