

Figure S1 Result of specific sequence by BLAST N

The screenshot shows the BLAST N search results page. The header includes the BLAST logo and navigation links: Home, Recent Results, Saved Strategies, and Help. The search title is "NCBI/BLAST/blastn suite/ Formatting Results - MRCF83ZY015". Below the title are links for "Edit and Resubmit", "Save Search Strategies", "Formatting options", and "Download". A "YouTube" icon and links for "How to read this page" and "Blast report description" are also present. The main content area is titled "Nucleotide Sequence (120 letters)". It displays the following information:

Query ID	Id 37539	Database Name	nr
Description	None	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.2.28+ Citation
Query Length	120		

Below the table, a message states: "No significant similarity found. For reasons why, click here". A link for "Other reports: Search Summary" is provided. The footer contains copyright information, a disclaimer, and the NCBI logo.

Figure S2 Result of specific sequence by BLAST X

The screenshot shows the BLAST X search results page. The header includes the BLAST logo and navigation links: Home, Recent Results, Saved Strategies, and Help. The search title is "NCBI/BLAST/blastx/ Formatting Results - MRCKWTN101R". Below the title are links for "Edit and Resubmit", "Save Search Strategies", "Formatting options", and "Download". A "YouTube" icon and links for "How to read this page" and "Blast report description" are also present. The main content area is titled "Nucleotide Sequence (120 letters)". It displays the following information:

Query ID	Id 85685	Database Name	nr
Description	None	Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	nucleic acid	Program	BLASTX 2.2.28+ Citation
Query Length	120		

Below the table, a message states: "No significant similarity found. For reasons why, click here". A link for "Other reports: Search Summary" is provided. The footer contains copyright information, a disclaimer, and the NCBI logo.

Table S1 Information of the strains of *Hypsizygus marmoreus*

No.	Strain Code	Origin	Strain Type
1	ACCC50474	Dalian University of Technology, Dalian, Liaoning, China	storage stain
2	ACCC51149	Xin Yu Edible Fungi Institute, Wuhan, Hubei, China	storage stain
3	ACCC51533	Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing, China	storage stain
4	ACCC51661	Huan Yu Edible Fungi Institute, Jiayu, Hubei, China	storage stain
5	ACCC51729	Nanjing Agricultural University, Nanjing, Jiangsu, China	storage stain
6	ACCC51800	Shandong Agricultural University, Taian, Shandong, China	storage stain
7	GDGM26168	Shanghai Finc Bio-tech Inc., Shanghai, China	commercial cultivar
8	GDGM26169	Shandong Ronfun Group, Ltd., Dongying, Shandong, China	commercial cultivar
9	GDGM26171	Shanghai Tianchu Mushroom Co., Ltd., Shanghai, China	commercial cultivar
10	GDGM26713	Starway Bio-technology, Dongguan, Guangdong, China	commercial cultivar
11	FJNK-1	Fujian Academy of Agricultural Sciences, Fuzhou, China	commercial cultivar
12	FJNK-2	Fujian Academy of Agricultural Sciences, Fuzhou, China	commercial cultivar
13	GSGY-2	Gaoyou Institute of Edible Fungi, Gaoyou, Jiangsu, China	commercial cultivar
14	HN-1	Hunan Academy of Agricultural Science, Changsha, Hunan, China	commercial cultivar
No.	Strain Code	Origin	Strain Type
15	HN-2	Hunan Academy of Agricultural Science, Changsha, Hunan, China	commercial cultivar
16	HBYC	Yichang Kanghuiyuan Biology Technology Co., Ltd., Yichang, Hubei, China	commercial cultivar
17	SM-4	Sanming Mycological Institute, Sanming, Fujian, China	commercial cultivar
18	MYSYB	Mianyang Edible Fungi Research Institute of Sichuan, Mianyang, Sichuan, China	commercial cultivar
19	SCNK	Sichuan Academy of Agricultural Science, Chengdu, Sichuan, China	commercial cultivar

20 CBS-1

Changbaishan, Jilin, China

storage stain

Table S2 Fixed and arbitrary primers used in the TRAP analysis of *Hypsizygus marmoreus*

Primers	Sequence(5'→3')	Origin
Fixed primers		
EF69R1	TTGTGAGCTTAGGCGTTA	<i>H. marmoreus</i> serine protease mRNA EF153269.2
GQ76L1	CGTTCCTGCATACTTCAA	<i>H. marmoreus</i> heat shock protein 70 GQ246176.1
GQ76R1	GCCTCTTCGATGAGATTC	<i>H. marmoreus</i> heat shock protein 70 GQ246176.1
EU94L1	CGGAAAGCGTTATAGGTT	<i>H. marmoreus</i> laccase mRNA EU375894.1
JN00R1	TCCTCGGTGTACTCAACA	<i>H. marmoreus</i> gene glyceraldehyde-3-phosphate dehydrogenase JN048800.1
JN00L1	GGGAGAAAGGGGTAGATT	
Arbitrary primers		
ME1	TGAGTCCAAACCGGATA	Li & Quiros (2001)
ME2	TGAGTCCAAACCGGAGC	
ME4	TGAGTCCAAACCGGACC	
ME6	TGAGTCCAAACCGGACA	
ME7	TGAGTCCAAACCGGACG	Budak et al.(2005)
ME8	TGAGTCCAAACCGGACT	
ME9	TGAGTCCAAACCGGAGG	
ME11	TGAGTCCAAACCGGAAC	
ME13	TGAGTCCAAACCGGAAG	
EM1	GACTGCGTACGAATTAAT	Li & Quiros (2001)
EM2	GACTGCGTACGAATTTGC	
EM4	GACTGCGTACGAATTTGA	

EM5	GACTGCGTACGAATTAAC	
EM6	GACTGCGTACGAATTGCA	
EM9	GACTGCGTACGAATTCAG	Budak et al.(2005)
EM10	GACTGCGTACGAATTCAT	
EM16	GACTGCGTACGAATTGTC	Ren et al (2012)
EM17	GACTGCGTACGAATTTAG	
EM24	GACTGCGTACGAATTATG	
EM26	GACTGCGTACGAATTCGG	

Table S3 Information of the sequences used to designed specific primers for *Hypsizigus marmoreus*.

Name	Sequence (3'-5')	Length	Size of prediction
KC906199SP	Forward: CGA CGA ACG AGA CTG AAT	18	321
	Reverse: ATA CTG CGA AGA TGT GAT GA	20	
KC906204SP	Forward: TCA GAA CAT CCA GCG TAA G	19	323
	Reverse: ACC TCT ACC ATC CAC CAT T	19	
KC906207SP	Forward: TCA GAA CAT CCA GCG TAA G	19	323
	Reverse: ACC TCT ACC ATC CAC CAT T	19	
KC906214SP	Forward: ATG CTG AGT TGT TGA ATG C	19	190
	Reverse: GCC ATC CGA TTG CTA CAT	18	
KC906215SP	Forward: TTG CTG GTA TTT GGC TGT A	19	191
	Reverse: CGA CTG GAG TAA TGT GAA TAG	21	
KC906223SP	Forward: GCT TGT ATC CGT CGT GTA T	19	244
	Reverse: GGT AGT GGT AAC CTG AGT C	19	

G	s						s	s	A
e	i						t	t	A
n	z						a	a	
b	e						r	r	n
a	o						t	a	u
n	f	Blast N	Blast X	Putative conserved domains (size, function name)	tBlast X	C	D	O	R
k	s					S	n	F	n
A	e						d	s	d
c	q						e		e
c	u						n		r
e	e						d		o
s	n						s		f

si	c						i	i	p
o	e						z	z	r
n							e	e	e
									d
									i
									c
									t
									e
									d
									p
									r
									o
									t
									e
									i
									n
K		26	No	Laccaria bicolor	Laccaria bicolor		6	8	
C		7	significant	S238N-H82	S238N-H82		-	-	
9	9	A	similarity	predicted	hypothetical		1	1	
0	0	20	found	protein partial	protein partial		7	7	
6	9	2		mRNA,	mRNA,		5/	5/	
1	9	7		Accession:	Accession:		2	2	
9		G		XP_001888969.	XP_001888934.1		2	2	
3		22		1			8	8	
		3					-	-	2
		T					5	5	2
							6	6	1
							9/	9/	
							6	6	
							8	8	
							8	8	
							-	-	
							8	8	
							4	4	
							2	0	

K C 9 0 6 1 9 4	5 6 4	19 3 A 13 7 C 13 4 G 10 0 T	No significant similarity found	Trametes vericolor FP-10664 SS1, accession: EIW51173.1/ Agaricus bisporus var. bisporus H97 predictal protein AGABI2DRAF T, accession: EKV42031.1	Agaricus bisporus clone FWBA165-D07, complete sequenc, accession: AC253814.1	4 6 - 5 3 7	1	4 6 - 5 3 7	4 6 - 5 3 7	1 6 4
K C 9 0 6 1 9 5	8 0 0	18 6 A 14 8 C 24 9 G 21 7 T	No significant similarity found	Laccaria bicolor S238N-H82 predicted protein (Cover 22%)	Laccaria bicolor clone JGIAHZW-15X, complete sequence (Cover 21%)	6 1 - 3 0 0	1	6 1 - 3 0 0	6 1 - 3 0 0	8 0
K C 9 0 6 1 9 6	4 4 3	11 9 A 96 C 12 6 G 10 2 T	Lepista nebularis isolate AFTQL-1D 1495 18S ribosomal RNA gene partial sequence/Ric honiella asterospora 18 small subnit	Trametes versicolor FP-101664 SS1 checkpoint-link protein (CHK1), accession: EIW51416.1/ Medicago truncatula ATP synthase subunit beta, accession:	Richoniella asteropora 18S small subunit ribosomal RNA gene, partial sequence, accession JF76311.1/ unculturd Ascomycota clone BN4-51 18S ribosomal RNA gene,	0				

			ribosomal RNA gene, partial sequence	XP_003627732.1		partial sequence, accession GQ404768.1					
K C 9 0 6 1 9 7	7 0 8	18 0 A 17 9 9 C 15 4 G 19 5 T	Serpula lacrymans var. lacrmans S7.3 hypothetical protein (Cover 22%)	No significant similarity found		Zebrafish phospholipase mRNA (Cover 30%)	0				
K C 9 0 6 1 9 8	3 0 8	95 A 72 C 63 G 78 T	No significant similarity found	Laccaria bicolor S238N-H82 predicted protein partial mRNA, Accession: XP_001889811.1 (XP_001889801.1)		Laccaria bicolor S238N-H82 predicted protein partial mRNA, Accession: XP_001889811.1 (XP_001889801.1)	1 4 6 1 2 3 7	-	1 - 2 3 7	1 4 6 - 2 3 7	3 0
K C 9 0 6 1 9	9 0 9	12 9 A 11 2 C 11	No significant similarity found	No significant similarity found		No significant similarity found	0				

9		6 G 11 2 T								
K C 9 0 6 2 0 0	4 6 9	12 9 A 11 2 C 11 6 G 11 2 T	No significant similarity found	Moniliophihora perniciosa FA553 hypothetical protein MPER_13238, accession: XP_002387823. 1	RF+3: 42-200, EYA-cons_ domain	Pinus taeda clone PT_7Ba2882K18 , complete sequence, accession: AC241291.1	0			
K C 9 0 6 2 0 1	1 0 7 5 G 25 8 T	27 5 A 27 2 C 27 0 G 25 8 T	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete cds, Accession: GQ246176.1	Hypsizygos marmoreus heat shock protein 70, Accession: ACT33635.1	RF+2: 10-1035, NAD-GH (superfamili es); RF-3: 575-1060, NBD_sugar -kinase_HS P70_action superfamily ;1-1065, dnaK (Multi-dom ain)	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	6 2 - 1 0 7 5			3 0 3
K C 9 0 6 2	1 3 3 8 6 C	30 5 A 38 6 C	Laccaria bicolor S238N-H82 predicted protein (Query cover	No significant similarity found	RF-3: 500-600, Bactofilin	Laccaria bicolor S238N-H82 predicted protein partial mRNA (Query cover	1 4 0 - 9 7			1 9 4

0 2		31 6 G 33 1 T	39%)			36%)	0			
K C 9 0 6 2 0 3	5 1 0	12 4 A 12 6 C 12 6 G 13 4 T	No significant similarity found	Agaricus bisporus var. burnethii hypothetical protein AGABI2DEAF T_182914, accession: EKM82322.1		Laccaria bicolor S238N-H82 hypothetical protein partial mRNA, accession: XM_001994024. 1	0			
K C 9 0 6 2 0 4	9 2 7	26 7 A 21 2 C 24 5 G 20 3 T	No significant similarity found	No significant similarity found		No significant similarity found	0			
K C 9 0 6 2 0	8 9 3	24 3 A 19 7 C 21	No significant similarity found	Laccaria bicolor S238N-H82 glycoside hydrolase family 47 protein, accession:	RF-1: 740-550, Glyco_hydr o_47 Superfamily	No high similarity sequence over 25%	6 5 - 7 8 9	1		1 5 2

5		9 G 23 4 T		XP_001881296. 1							
K C 9 0 6 2 0 6	1 0 7 4 G 25 6 T	27 4 A 27 2 C 27 2 G 25 6 T	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete cds, Accession: GQ246176.1	Hypsizygos marmoreus heat shock protein 70, Accession: ACT33635.1	RF+3: 10-1065, NAD-GH (superfami les); RF-2: 560-1075, NBD_sugar -kinase_HS P70_actin superfamily ; RF-2: 1-1070, dnaK (Multi-dom ains)	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	6 3 - 1 7 0 4				3 0 2
K C 9 0 6 2 0 7	9 5 5	27 0 A 22 1 C 25 3 G 21 1 T	No significant similarity found	No significant similarity found		No significant similarity found	0				
K C 9 0 6	7 5 7	17 2 A 19 1	No significant similarity found	No high similarity sequence over 29%		No significant similarity found	0				

208	C170G224T									
KC906209	80719	1913214G199T	No significant similarity found	Lacaria bicolor S238N-H82 predicted protein, accession: XP_001880772.1	RF+3: 40-425, Anticodon_Ia_like superfamily (anticodon binding site & tRNA binding surface)	Lacaria bicolor S238N-H82 hyprothetical protein partial mRNA, accession: XM_001880737.1	1	4177		252
KC906210	758	1921014G210T	Clitocybe candicans isolate AFTOL-1D 541 18 ribosomal RNA gene, partial sequence, Accession: AY771609.1	Acinetobacter sp. P8-3-8 hypothetical protein, accession: ZP_0914283.1		Psilocybe montana isolate AFTOL-1D 820 18S ribosomal RNA gene, partial sequence, accession: DQ465342.1	0			
KC906216	669	202160C	No significant similarity found	Trametes versicolor FP-101664 SS1 hypothetical protein TRAVEDRAF		No high similarity sequence over 40%	0			

1		19		T_146600, accession: EIW60909.1						
1		3								
		G								
		11								
		4								
		T								
K		33								
C		7								
9	1	A	No	Laccaria bicolor		No high				
0	0	17	significant	S238N-H82		similarity				
6	6	9	similarity	predicted		sequence over	0			
2	1	C	found	protein, accession: XP_001883620. 1		40%				
1		20								
2		0								
		G								
		34								
		5								
		T								
K		22								
C		1								
9	7	A	No	Laccaria bicolor		Volariella				
0	7	18	significant	S238N-H82		volvacea	1			
6	7	0	similarity	glycoside		endoglucanase	8			
2	9	C	found	family 5		(egl) mRNA	4			8
1		20		protein, accession: XP_001879429. 1/ Volvarella		complete cds, accession: EU716328.1	-			2
3		1		volvacea			4			
		G		endoglucanase, accession: ACE06751.1			9			
		17					0			
		7								
		T								
K		20								
C	8	3	No	No significant		No significant				
9	6	A	significant	similarity found		similarity found	0			
0	8	19	similarity							
6		4	found							
2		C								

1 4		25 1 G 22 0 T									
K C 9 0 6 2 1 5	3 3 6	82 A 84 C 87 G 83 T	No significant similarity found	No significant similarity found		No high similarity sequence covered 50%	0				
K C 9 0 6 2 1 6	1 0 7 4	27 4 A 27 2 C 27 2 G 25 6 T	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete cds, Accession: GQ246176.1	Hypsizygos marmoreus heat shock protein 70, Accession: ACT33635.1	RF+3: 10-1045, NAD-GH (superfamilies); RF-2: 562-1065, NBD_sugar-kinase_HS P70_actin superfamily ; RF-2: dnaK (Multi-domains)	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	1	6 3 - 1 7 0 4			3 0 2
K C 9 0 6 2 1 7	3 0 2	79 A 71 C 89 G 63 T	No significant similarity found	Laccaria bicolor S238N-H82 predicted protein, accession: XP_001879074.1	RF-2: 183-273, mre11; RF-3: 53-123, mre11	Laccaria bicolor S238N-H82 predicted protein, accession: XP_001879039.1	0				

K C 9 0 6 2 1 8	1 0 7 4 1 9	27 5 A 27 2 C 27 1 G 25 6 T	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete cds, Accession: GQ246176.1	Hypsizygos marmoreus heat shock protein 70, Accession: ACT33635.1	RF+3: 10-1045, NAD-GH (Superfamil ies); RF-2: 555-1071, NBD_sugar -kinase_HS P70_actin superfamily ; RF-2: 1-1074, dnaK (Multi-dom ains)	Hypsizygos marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	6 3 - 1 7 0 4			3 0 2
K C 9 0 6 2 1 9	7 4 5 8 19 4 T	17 0 A 20 3 C 17 8 G 19 4 T	No significant similarity found	Coprinopsis cinere F-box/WD repeat-containin g protein 11, accession: XP_001832905. 2 / Stereum hirsutmu FP-91666 SS1 WD40 repeat-like protein, accession EIM89687.1	RF+1: 235-700, WD40 superfamily (structural tetrad); RF+1: 235-700, COG2319 (Multi-dom ains)	No significant similarity found	0			
K C 9 0 6 2 2 2	1 1 4 6 C 28	26 9 A 28 6 C 28	No significant similarity found	Sterpula lacrymans var. lacrymans S7.9 hypothetical protein SERLADRAFT _443947,	RF-2: 75-445, OTU-domai n-containin g protein (Superfamil ies)	No significant similarity found	4 8 - 9 8 0	1		2 7 0

0		9 G 30 2 T		accession: EGO18612.1						
K C 9 0 6 2 2 1	4 2 5	11 3 A 10 7 C 11 3 G 97 T	No significant similarity found	Laccaria bicolor S238N-H82 predicted protein, accession: XP_001874648. 1 / Agaricus bisporus var. burnettii JB 137-S8 hypothetical protein AGABI2DRAF T_54902, accession EKM81845.1	RF-1: 320-423, snRNP component HSH155 (Multi-dom ains); RF-2: 5-272, snRNP component HSH155 (Multi-dom ains)	Agaricus bisporus clone FWBA189-L19, complete sequence, accession: AC253834.1	0			
K C 9 0 6 2 2 2	1 3 5 2	35 9 A 31 9 C 30 9 G 36 5 T	No significant similarity found	Agaricus bisporus var. bisporus H97 hypothetical protein AGABI2DRAF T_141320, accession: EKV50458.1	RF=1: 10-250, MutS_I (Superfamil ies)	No significant similarity found	1	4 9 - 1 3 1 5		3 4 3
K C 9 0 0	5 2 0	14 9 A 11	No significant similarity	No significant similarity found		No significant similarity found	1	6 3 - 1		4 4

6 2 2 3		5 C 12 6 G 13 0 T	found				9 9			
K C 9 0 6 2 2 4	1 0 7 4	27 4 A 27 4 C 27 1 G 25 5 T	Hypsizygyus marmoreus heat shock protein 70 (HSP70) mRNA complete cds (GQ246176.1)	Hypsizygyus marmoreus heat shock protein 70, Accession: ACT33635.1	RF+3: 10-1050, NAD-GH; RF-2: 565-1060, NBD_sugar -kinase_HS P70_actin superfamily ; 460-535, dnaK (Multi-dom ains)	Hypsizygyus marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	6 3 - 1 0 7 4	1		3 0 2
K C 9 0 6 2 2 5	1 0 7 4	25 5 A 27 2 C 27 4 G 27 3 T	Hypsizygyus marmoreus heat shock protein 70 (HSP70) mRNA complete cds, Accession: GQ246176.1	Hypsizygyus marmoreus heat shock protein 70, Accession: ACT33635.1	RF+2: 1-505, NBD_sugar -kinase_HS P70_actin superfamily ; 545-605, dnak (Mult-doma ins); RF-3: 25-1060, NAD-GH	Hypsizygyus marmoreus heat shock protein 70 (HSP70) mRNA complete CDS, Accession: GQ246176.1	1 - 1 0 1 2	1		3 0 2
K C 9 0	6 4 7	18 9 A 18	Laccaria bicolor S238N-H82 hypothetical	Laccaria bicolor S238N-H82 predicted protein,	RF-3: 305-625, thymidylate synthase_P	No high similarity sequence over	0			

6 2 2 6	0 C 14 7 G 13 1 T	protein partial mRNA, Accession: XM_0018894 59.1	accession: XP_001889494. 1	yrimidine_ HMase superfamily (Multi-domain)	50%					
K C 9 0 6 2 2 7	13 2 A 14 7 C 18 0 G 18 8 T	Laccaria bicolor S238N-H82 hypothetical protein partial mRNA, Accession: XM_0018894 59.1	Laccaria bicolor S238N-H82 predicted protein, accession: XP_001889494. 1	RF+2: 15-345, thymidylate synthase_P yrimidine_ HMase superfamily (Multi-domain)	No high similarity sequence over 53%	0				
K C 9 0 6 2 2 9	11 4 A 10 0 C 99 G 12 7 T	No significant similarity found	Agaricus bisporus var burnettii JB137-S8 hypothetical protein, accession: EKW80790.1 / Agaricus bisporus var. bisporus H97, accession: EKV47257.1	RF+2: 125-425, CypX superfamily	Coprinosis cinerea okayama 7#130 SeqLit hypothetical protein, mRNA, accession: XM_001830362. 2	1 5 5 - 4 2 9				7 8