Contig ID (length) and ITS coordinates		No. repeats	Species involved
First contig found	**Other contig(s)**		
CM000577.1 (149 bp) 7964421–7964569	**CP064749.1** (149 bp) 11634–11782 **JAGDUS010000087.1** (149 bp) 2717–2865 **JAGDUV010000066.1** (149 bp) 7953–8101 **JAGDVB010000022.1** (149 bp) 13649–13797 **JAGDVF010000026.1** (149 bp) 2711–2859 **JAGDVJ010000033.1** (149 bp) 2819–2967 **CP088260.1** (149 bp) 7951857–7952005 **CP126887.1** (149 bp) 8019073–8019221	193	*Fusarium aethiopicum** *Fusarium asiaticum** *Fusarium boothii** *Fusarium cortaderiae** *Fusarium culmorum** *Fusarium graminearum*[§] *Fusarium louisianense** *Fusarium meridionale** *Fusarium mesoamericanum**
JAQJAR010000001.1 (174 bp) 11567–11740	**JAQJAG010000009.1** (174 bp) 100480–100653 **JAQJAG010000010.1** (174 bp) 103353–103526 **JAQJAG010000011.1** (174 bp) 115896–116069	52	*Penicillium lividum*[§] *Penicillium odoratum*[§]
CP021225.1 (220 bp) 2111426–2111644	**JAHFVN010000021.1** (220 bp) 82553–82771	39	*Antrodia cinnamomea*[§] *Taiwanofungus camphoratus*[§]
JAPZBT010000004.1 (177 bp) 15170–15345	**JAQJAW010000002.1** (177 bp) 3769092–3769267 **JAQJAW010000009.1**(177 bp) 18125–18300 **JAQJAW010000010.1** (177 bp) 16072–16247 **JAQJAW010000011.1** (177 bp) 13924–14099 **JAQJAW010000012.1** (177 bp) 10789–10964	36	*Penicillium concentricum*[§] *Penicillium robsamsonii*[§]
CM000580.1 (150 bp) 828406_828554	**DS022269.1** (150 bp) 13990–14138 **JAWLTA010000091.1** (150 bp) 2842–2990 **JAWLTM010000077.1** (150 bp) 2423–2571 **LJGR01000025.1** (150 bp) 5012–5160 **JACWFA010000008.1** (150 bp) 3200–3348 **JAWLSZ010000010.1** (150 bp) 2842–2990 **JAAQRH010000157.1** (150 bp) 3648–3796 + 11 additional contigs	33	*Aspergillus subversicolor** *Cladosporium antarcticum** *Fusarium guttiforme** *Fusarium pseudonygamai** *Fusarium sororula** *Fusarium temperatum** *Fusarium verticillioides*[§] + 11 additional species of *Fusarium*

Table S1. Partial list of fungal species sharing identical ITS sequences in FungITS_GB. For brevity purposes, data are shown for only five (rows) out of the 103 repeated sequences found among the 6211 sequences originally included in FungITS_GB. Species are ordered alphabetically. *Species not appearing in the final version of FugITS_GB (each of these species is represented by a single ITS sequence shared with another species). [§]Species sharing one ITS sequence with another species but still present in the final database because they are represented by another sequence. †For those sequences found in multiple positions of more than two contigs (genomes), only one representative per contig is shown in the columns on the left.

Contig ID (length) and ITS coordinates		No. repeats	Species involved
First contig found	Other contig(s)		
NW_026249951.1 (195 bp) 927298–927492	**NW_026249890.1** (195 bp) 3901–4095	2	*Alternaria arbusti* *Alternaria incomplexa**
NW_014574660.1 (166 bp) 4524–4689	**NW_026260342.1** (166 bp) 4216–4381	2	*Alternaria postmessia** *Metarhizium brunneum*
NC_036441.1 (183 bp) 2924696–2924878	**NC_054697.1** (183 bp) 2969554–2969736 2977350–2977532 2985146–2985328 2992942–2993124 3000738–3000920 3008534–3008716 3016330–3016512 3024126–3024308	9	*Aspergillus oryzae* *Aspergillus flavus**
NW_023336289.1 (187 bp) 1238883–1239069 1246938–1247124 1254989–1255175	**NC_054852.1** (187 bp) 735393–735579 743445–743631 751497–751683 759549–759735	7	*Aspergillus luchuensis** *Aspergillus tubingensis*
NW_025544790.1 (208 bp) 13158–13365 21648_21855 30138_30345 38621_38828 71250_71457	**NW_003101676.1** (208 bp) 2130074–2130281 2138547–2138754 2147026–2147233 2155508–2155715	9	*Blastomyces dermatitidis*[§] *Blastomyces gilchristii*[§]
NW_023501002.1 (148 bp) 887210–887357	**NW_024065882.1** (148 bp) 193587–193734 **NW_024066056.1** (148 bp) 642142–642289 **NW_024066232.1** (148 bp) 18020–18167 **NW_023501002.1** (148 bp) 887210–887357	18†	*Botrytis byssoidea* *Botrytis deweyae** *Botrytis fragariae* *Botrytis sinoallii**
NC_064679.1 (183 bp) 5451356–5451538	**NW_026518045.1** (183 bp) 6077–6259 **NW_026848238.1** (183 bp) 7945–8127 **NW_026849595.1** (183 bp) 32531–32713	9†	*Colletotrichum costaricense* *Colletotrichum fioriniae** *Colletotrichum lupine* *Colletotrichum tamarilloi**
NC_031677.1 (149 bp) 828406–828554	**NW_017387867.1** (149 bp) 13990–14138 **NW_025408615.1** (149 bp) 12764–12912 **NC_031677.1** (149 bp) 828406–828554 **NW_017387867.1** (149 bp) 13990–14138	14†	*Fusarium musae** *Fusarium verticilloides*
NW_026622757.1 (176 bp) 15170–15345	**NW_026643220.1** (176 bp) 3769092–3769267 **NW_026643227.1** (176 bp) 18125–18300 **NW_026643228.1** (176 bp) 16072–16247 **NW_026643229.1** (176 bp) 13924–14099 **NW_026643230.1** (176 bp) 52724–52899	36†	*Penicillium concentricum*[§] *Penicillium robsamsonii*[§]

Table S2. List of fungal species sharing identical ITS sequences in FungITS_RS (continues in next page).

	NW_026643072.1 (174 bp)		
NW_026643117.1 (174 bp)	1650–1823	9	*Penicillium longicatenatum*
10013–10186	NW_026643072.1		*Penicillium pulvis**
	9501–9674		
NC_085887.1 (158 bp)	NC_085922.1 (158 bp)	2	*Podospora pseudoanserina*[§]
16980–17137	2188–2345		*Podospora pseudocomata*[§]

Table S2. List of fungal species sharing identical ITS sequences in FungITS_RS (continued). Species are ordered alphabetically. *Species not appearing in the final version of FungITS_RS (each of these species is represented by a single ITS sequence shared with another species). [§]Species sharing one ITS sequence with another species, but still present in the final database because they are represented by another sequence. †For those sequences found in multiple positions of more than two contigs (genomes), only one representative per contig is shown in the columns on the left.

Phylum	Database		
	FungITS_GB+	FungITS_RS_TL	"Clean UNITE"
Ascomycota	12560	11827	19241
Basidiobolomycota			9
Basidiomycota	5757	5336	14717
Blastocladiomycota	8	3	11
Calcarisporiellomycota			1
Chytridiomycota	70	67	142
Cryptomycota*	4	3	
Entomophthoromycota			9
Entorrhizomycota			7
Glomeromycota			471
Kickxellomycota			23
Microsporidia*	9	5	
Monoblepharomycota			4
Mortierellomycota			99
Mucoromycota	421	388	410
Neocallimastigomycota			43
Olpidiomycota	1	1	6
Rozellomycota			3
Sanchytriomycota*	1		
Zoopagomycota	33	25	28
Incertae sedis	2	2	

Table S3. Number of sequences per phylum included in the final databases. Phyla are ordered alphabetically. Those in bold marked with an asterisk are only represented in FungITS.
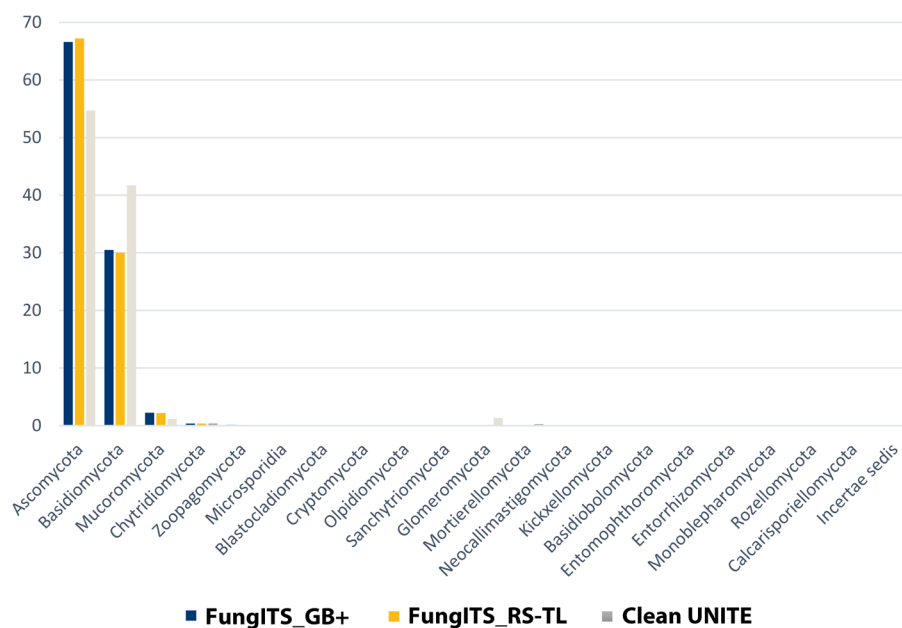
Figure S1. Distribution of the sequences of each database among different phyla. Note that, in all three databases, most sequences correspond to species belonging to the phylum Ascomycota, closely followed by Basidiomycota, and then Mucoromycota. The bars corresponding to sequences of species belonging to the three phyla unique to FungITS are not visible due to the scale of this plot.