

Table S1.1 List and annotation 24 single-copy genes of the *Armillaria cepistipes* with SNPs used in the study

Genes	SNPs	Mean identity, %	FUNYBASE annotation*	Sequences of nuclear DNA fragments with SNPs**
FG487	FG487_3	49.9	Gamma subunit of coatomer a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	TCAATGAATCCCCATAAGCCCAAGAAAGTGYCGAGCGTTGCTAACACGGATAGTCTACCTGCTCTATGTCGGCGAGACCTT TGGAACACAGGAGGCGACAACCCTGTTCTTTGGGACCACGAAGCTCTTCCAGCACAAAGATGTAAGCGGYG[A/G]CTTATTG TGCAGAAATTTGGGCTGATWGTAGTGACAGAGTGCAYTGAGGCAAGCCGTCTATCTYGCTATCAAGGAGCTCGCGACAACYG CCGAGGATGTWATCATGGTCACAAGCAGTATCATGAAGGACATG
FG524	FG524_2	70.9	Mitochondrial DNA-binding protein component of the mitochondrial nucleoid structure involved in mtDNA replication and segregation of mitochondrial genomes; member of the mitochondrial carrier protein family; Yhm2p	TCGGTACGCATATCATTCTACGATGCTCAGGTACGAATTGCTGATCGATY[C/T]TGTAACCTGGCAGCATGGGATTGCTCG TTTGACCGAAATTTTCATCCGGAGAGCCCGCGGTAAAGGGGAGAACGATTCTTTGAATGCTTTTCGAGAAAATTGCGGCCTCG ACTGTTGGTGGAAACCCTGGCTACT
FG529	FG529_4	52.3	Ubiquinol-cytochrome-c reductase a Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex; transfers electrons from ubiquinol to cytochrome c1 during respiration; Rip1p	CCCGGAGGGCAAGAACGTCATCATCAATGGCGTGGMAAGCCCGTATTCATCAGGCATCGRACRCAGGCAGAAATTGAGG AGGCCAGGAGGGAAGACTGGAAGAG[C/T]TTTAGGGACCCCGAGAGCGACGAGAGCCGTGCAAAAAGCCCGAATGGCTG GTATGTTGGGCGTTTGCACCCATCTGGGTT
	FG529_5			CCCGGAGGGCAAGAACGTCATCATCAATGGCGTGGMAAGCCCGTATTCATCAGGCATCGRACRCAGGCAGAAATTGAGG AGGCCAGGAGGGAAGACTGGAAGAGYTTTAGGGACCCCGAGAGCGACGAGAGCCGTGCAAAAAGCCCGAATGGCTGGT[C/T] ATGTTGGGCGTTTGCACCCATCTGGGTT
FG652	FG652_11	59.5	Delta-aminolevulinatase a homo-octameric enzyme catalyzes the conversion of delta-aminolevulinic acid to porphobilinogen the second step in the heme biosynthetic pathway; localizes to both the cytoplasm and nucleus; Hem2p	TTTATACGACCGTCCATCATGTCRCTGGGCGCTACRCAGTGGGCCCCRGCTTTTCGCGTAATTGACGGCAACCTCGGCRATA CGRTCCACAGAAGGARCRRTTGTGATAGTACCGTCGTCGTGGAGYAGRCCACAGTGACCRRTGGCTTGTGTACTCGCATAGA CAGAC[A/G]TCGCAGGCKATGTAGAGAGCGGGGAACAGTTCGCGAAGTTTCTTGATGGCAAGAATGACGGGTCCAGCGGGA TCRTCTGCTGGCGTTCCCTTCCGTCCTGCAGTRRCCATGAGAGCTGTTATATGYGCGAATAAAYAYACGCACCTTRATGC ATTCATCGGTACTCCGAAGAGAATCACRCTCTGTAGACCTTTCTTGACCAATGGACCCAGGAACCTCGTCCAATTTGTTCCACC CCCCATCGCTTCTGKCCCGRAGACTYTCAATAACCTCGCTCGCRTCCGGGTCTCCGTTATRAARATGGGATACATGAGC ATGGACTTCGT
	FG652_20			TTTATACGACCGTCCATCATGTCRCTGGGCGCTACRCAGTGGGCCCCRGCTTTTCGCGTAATTGACGGCAACCTCGGCRATA CGRTCCACAGAAGGARCRRTTGTGATAGTACCGTCGTCGTGGAGYAGRCCACAGTGACCRRTGGCTTGTGTACTCGCATAGA CAGACRTCGCAGGCKATGTAGAGAGCGGGGAACAGTTCGCGAAGTTTCTTGATGGCAAGAATGACGGGTCCAGCGGGATC RTCTGCTGGCGTTCCCTTCCGTCCTGCAGTRRCCATGAGAGCTGTTATATGYGCGAATAAAYAYACGCACCTTRATGCAT TTCATCGGTACTCCGAAGAGAATCAC[A/G]CTCTGTAGACCTTTCTTGACCAATGGACCCAGGAACCTCGTCCAATTTGTTCCACC CCCCATCGCTTCTGKCCCGRAGACTYTCAATAACCTCGCTCGCRTCCGGGTCTCCGTTATRAARATGGGATACATGAG CATGGACTTCGT
FG686	FG686_3	53.4	Imidazole glycerol phosphate synthase glutamine amidotransferase	ACCGTGCCTGRTACCACCARGCCTTTCCCTYTCCTCTATCACTTTGGARTCAGGGCGTCCCTCGAATTACCTCTCCCTTGT ATGGGCCGTCATA[C/T]GTCTCGGGGTCCACATACACCCGTCTAGGRTCAACAGACACGACGACCCGCTGTCTTCCATACGC ATAYGCAATCGTCTCGATCGCACTCGTCCCATCGCCCTCGTTCTTTTCCGACGCCAGCATCTTCTCCACAGCCAACACTGCT TCGCTGCCAATACTGACCTTGTGCGGCGCCRGCGCGGAAATAGGYGCCCGCGACTTCRAGYCGGGRTGCTTGGTGCCGTC WGGRTCGAYGGTGTCTTTATCCACCGCCGATAGTGAGAGGGACGAAGACGCGTTCTGCCGCGGTACGGACGACTGCGA TCATTGGCTGATCTCGGAGGGGGAGTGCCGGAAGGAKGTGATGTTGAGCA
FG691	FG691_2	73.6	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	>FG691_2 TCGTAGCGGTCCTTCTTCTCTCCAATTTCGACCTCGCTGCTGCCGCCGACTTTAATGACAGCAACACCACCGCTCAGCTTCG CGAGACGCTCCTGCAGACGTGTACGATCATAGTCGCTCGTACCCTTGTCAATCAAACCTCKAATCTGCTCGCACC CCTGGATCGCCGACCCTCGCCTTCGCCATTGAGAACGATCGTGTCTCTTGGTACTGTCAAGCTACCCGAGCTGCCGA GCATCTCCCGGGATGCATTCTCGAGCTTGTCAACGTCATTGCTGAACACGGTACCACC[A/T]GTAAGAACTGCCAAATC GCCAAGAATGTTCTTGGCGTTGTCTCCGAAGCCAGGAGCTTTGACCGCAACAACCTGCAATTGGCCGCGGAGCTTGTGAG AATAACAAGCAGCCAAAGCCTCGCCGTCAACATCTTCAGCGACAATGACCAATGGCCGTCTGTCCCAGCAGCAATCTCCAG AGACGGCAGGATATCAGCAAGCACACTGATCTTGCCTCGCTGAGTAAGATCAACGTTTCTCCATCTCGCATTCTGACCC TTGACRTCCGTGATGAAATACGGACTGATGAATCCCCGGTCAAGCGCATGCCYTC

Genes	SNPs	Mean identity, %	FUNYBASE annotation*	Sequences of nuclear DNA fragments with SNPs**
FG698	FG698_1	60.2	Subunit of heteropentameric Replication factor C RF-C which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen PCNA processivity factor for DNA polymerases delta and epsilon; Rfc5p	CAGGTTGGACATGTATTTTTCCATTGTTTCGACGCAGGGCCGCTTGAGCATCGCGTGACAAAGAATCGGCCTCGTTGATAAAT ACCACTGATATTAAGC[A/G]CATGAAGACGTGGGACAACGGTGGCATGAAARTGGTCCTCACCTTTAAATCTTTGTTTAGCGT TTAGATCAACCTGCTGTGTCTGCGCAATTTCTTTGAGCAATTTCTGGATAACCACTCTGTTCATAGGACCCCGCTTCACTGCAT AAGAATTGTCCCATTATAACATATATCATTGCCAAAAACGACAACCATACTCGGCCTTATTTTCGATGTGGAAGTTGCTTTGA ACGAGGTTCACTTCGACTTTTCGTCTGGAAGGTGTTAGGAACACGCGTTGGTTCGATTTTTAGCTGTAAAAAGCTCTAAGTC ATCAATTGGATAACATGGCATGACACACACCTTCTCCACCCAGGTCCAAACAACCTGCCTCAAAGTACACGTTATACGCGTC TTCTTCCAGCTCCAGATGGGCCGTARAACAGCATGTGGGGAAAGTC
FG716	FG716_4	52.4	hypothetical protein; Yor356wp	GTGTTGCTGGGGAAGACGGAAGTCAGAATGACGGACGATACAGACCAGGGGAAGTCSTCCACACTCTTGGATGGCCCATT GAGCCACAGACATATGGCGGTGGTTGGGTGTATCACATGGATGGYGGACTAGTAAGTTTGGGACTGGTCATCGGGGCGGA TTGRAAAAATCCGTATAGAGAACCCTATCGGGATTTCCAGATGATGAAGCACCACCCTTACTTAAGGAAGCTTCT[G/T]ACGG CGTCCGATTCATCGTTCACACCAACCCGTGTTGCATACGGAGCTCGCGTGTGACGGAAGGAGGCCTGCAATCTATCCCC TTCTTCATTTCCCCGGCGGTGCACTCATTGTTGCTCCGC
FG730	FG730_11	43.7	Protein that forms a heterotrimeric complex with Erp1 Erp2p and Emp24 member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	AGAAATTGTTGATTCAAGCCCGCAGAAGAAYGTCTACCTCAGTAAGAGGAAYGTCAATGCAGAGACGAGGYTGGCTATAAC GACACACGCYAGGGAGARGTRGGAGTATGTTTCAAGAATCATCTTGACCCGGGTATGTTTCTACTTTGTTCTTTRCCGAG CATTGTCTYAYGYA[C/T]GGGTAGATGTACGGTCAGAGACGGCAAAAACGGCTCGCATAATCGACTTGGAYGTC
FG735	FG735_16	38.7	Subunit of the 26S proteasome substrate of the N-acetyltransferase Nat1p; Rpn2p	GGATACCARTACCAGAACTGACAAAACATGACCATGCCAACAATYGCCTTGGTATTCCGGCTTCTGCACGACTCAGYAAAC TGATAGTAACGTTCTACCACCAGCGTCRATGAGTCCCTGGCCAATAGCAGCACCAAATCGTGCGACAGGRTCCCTCGTGCT TGTCAGAAACCACTTTSGTRTACAGCGAACGRGTGGASGCAAGAGATGSCGACGACGCATCCGATTGTTCTACAAGGATCAT GCCYAGAGCGATAAACGCSCCTTGTGCAACGAAATCTACGCTATCYCGTGTTCATAGGTTCCAAAATCTCGACAGCGTCTAA TAATTGTAAGTCAACTCATGTTTCAGTGAGATCAAATRAGATACTGACTTGAAGCCCRGTTTCTGCACAAGCAATTCCCAACGC GAGAGTGGCACCACAACGCACGTGGGGGTTGTAGCTTT[C/A]CTCAATAGTTGCACGATTTCGAGGCACCTGGCCGGGGTT TTTGAATAAAAAGGAAAGCRAGGGATGTTACAGCTGCTCTTCCGAACATCGTCGGAGACATCTGACACGGCGATGTGAAGTARA CGGCGAACTGCATCATTGTTCCCGTTCAGCGTAGGCAAGGGCCAAAGTGTATACACCTCCGTAACGAAGAATGGGRTCC TACAAGACRGTAAGKAGSGGTTTAGGCAGAAGAAAACGGGGCTCACTTTTCCGCYAGGAGCAATTTTRATTGACTATCAGC TTCTTCTGACGACCATAATAAACAAGGCGACGCCGATTGCGAGACCACGAATAATCTTCTCRTGCTGAGTCTC
FG747	FG747_1 FG747_2	56.6	Glutamine-dependent NAD+ synthetase essential for the formation of NAD+ from nicotinic acid adenine dinucleotide; Qns1p	ATGCGATGGCGATCGACTGTATTA[C/T]GACGGATGCGCTATGATTGCTGTCAACGGCAGGATTGTAGCCCAGGGATCCCAG TTCTCTTTGAATGATGTCGAAGTYATAACTGCAACAATTGATATCGAGGATGTCCGCAGCCACCGTGCAATCAGCAGTCGAA GCATGCAGGCGGCCTCCGCGGAAAGATATCACCGTATCGAAGTTCCTTCTCGTTGTGACGCGGAAAATTTGAGGAGGTGA GGGACGAAGATATGGTGGGRTTTTTATCATCCCGCCCTTACGAAGTGAAGTACCACCGACCMGAAGAGGAGATCGCGTRA GTACTGTTTCGTTCAAACCATYCTAAAGCTCAGGTTTTCAAAGTTTGGGACCTGCR ATGCGATGGCGATCGACTGTATTAYGACGGATGCGCTATGATTGCTGTCAACGGCAGGATTGTAGCCCAGGGATCCCAGTT CTCTTTGAATGATGTCGAAGT[C/T]ATAACTGCAACAATTGATATCGAGGATGTCCGCAGCCACCGTGCAATCAGCAGTCGAA GCATGCAGGCGGCCTCCGCGGAAAGATATCACCGTATCGAAGTTCCTTCTCGTTGTGACGCGGAAAATTTGAGGAGGTGA GGGACGAAGATATGGTGGGRTTTTTATCATCCCGCCCTTACGAAGTGAAGTACCACCGACCMGAAGAGGAGATCGCGTRA GTACTGTTTCGTTCAAACCATYCTAAAGCTCAGGTTTTCAAAGTTTGGGACCTGCR
FG756	FG756_2	50.5	Ferrochelatase a mitochondrial inner membrane protein catalyzes the insertion of ferrous iron into protoporphyrin IX the eighth and final step in the heme biosynthetic pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	GGCTTGCTGGCGCATGAAGTTACTGCTCCRAGYATGAGAACRACGGCAAAGGAAAGAGCCRAAGAAGGGGTACAGACCTC AGAACACGAGCATCCGAAGTCAGACCAGCGATAGCGATACCAACATGGTCATCTATTCCGGAACATCTTCTGTTGGTATGAAG CCAGTTCRCCKGCGGAACGCTACAAGGGG[C/T]CAGTCAATAACCCAKTTGYRRATATTCRTTGKWAACAAGAACCTTGAGG GCCAGTAAGACTGAGTGKGTCTTTGAACGCAAGCCGACRGCCGACAGGCCTTGCTTACGGCTTCAAGGGCATATTCGACC TGGTGAAGRCGACCTTGRGGCGAGAAAACAGTGTTTRCCGAGTCGTATGT
FG762	FG762_7		20S proteasome alpha-type subunit; Pre5p	GGCTTGCTGGCGCATGAAGTTACTGCTCCRAGYATGAGAACRACGGCAAAGGAAAGAGCCRAAGAAGGGGTACAGACCTC AGAACACGAGCATCCGAAGTCAGACCAGCGATAGCGATACCAACATGGTCATCTATTCCGGAACATCTTCTGTTGGTATGAAG CCAGTTCRCCKGCGGAACGCTACAAGGGGYCAGTCAATAACCCAKTTGYRRATATTCRTTGKWAACAAGAACCTTGAGGGC CAGTAAGACTGAGTGKGTCTTTGAACGCAAGCCGACRGCCGACAGGCCTTGCTTACGGCTTCAAGGGCATATTCGACCTG GTGAAGRCGACCTTGRGGCGAGAAAACAGTGTTTRCCGAGTCGTATGT

Genes	SNPs	Mean identity, %	FUNYBASE annotation*	Sequences of nuclear DNA fragments with SNPs**
MS413	MS413_1	58	Component of the holoenzyme form of RNA polymerase transcription factor TFIIF has DNA-dependent ATPase/helicase activity and is required with Rad3p for unwinding promoter DNA; involved in DNA repair; homolog of human ERCC3; Ssl2p	GATGGAGTTTTTGACCTCTCGAGAATGGGGCTTCATGCTATTGGATGAAGTACATGTTGTACCCGCTGCAATGTTCCGTCGG GTTGTCGGAACGATCAAAGCGCACTCCAACTTGGT[C/T]TGACCGGTACGCTAATTCTTTCCCTTTCACTTTCTTTCGAAGGA ACCATGAAGCTCATGTTCTGACTTGTTCAGCTACCCTTGTCCGTGAAGATGACAAAATAGCGGACCTGAACTAYATGATCGG GCCCAAACGTACGAAGCGAATTGGATGTCAGTTGCTCACCATATGTCCATCACTGTAGTTAAATTGTTAATGACCGCTTTG CCTTTCTAGGGATCTTGCTGCCAAGGGACATATTGCAAATGTGCAGGTATTATCAACCTTACCTTAATTTTTGATATCAAGA TCGCTGAGTTCGGCGCATAGTGTGCGGAGGTATGGTGTCCAATGACACCCGAATTCTATCGTGAATACCTTCGGGAGCAAT CTAGAAAACGCATGCTTCTATAYTGCATGA
	MS413_2			GATGGAGTTTTTGACCTCTCGAGAATGGGGCTTCATGCTATTGGATGAAGTACATGTTGTACCCGCTGCAATGTTCCGTCGG GTTGTCGGAACGATCAAAGCGCACTCCAACTTGGTYTGACCGGTACGCTAATTCTTTCCCTTTCACTTTCTTTCGAAGGAAC CATGAAGCTCATGTTCTGACTTGTTCAGCTACCCTTGTCCGTGAAGATGACAAAATAGCGGACCTGAACTA[C/T]ATGATCGG GCCCAAACGTACGAAGCGAATTGGATGTCAGTTGCTCACCATATGTCCATCACTGTAGTTAAATTGTTAATGACCGCTTTG CCTTTCTAGGGATCTTGCTGCCAAGGGACATATTGCAAATGTGCAGGTATTATCAACCTTACCTTAATTTTTGATATCAAGA TCGCTGAGTTCGGCGCATAGTGTGCGGAGGTATGGTGTCCAATGACACCCGAATTCTATCGTGAATACCTTCGGGAGCAAT CTAGAAAACGCATGCTTCTATAYTGCATGA
MS428	MS428_4	55	Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles; component of the TRAPP transport protein particle complex; Bet3p	TTCGGTACACGGCTGATAGAAGATTTTCTGGCGAARAGYAGTTTGGGGCGGTGTTTTCAGATTTTCGGGAGGTTGGGGAGGTC GTTGCAAAGGTGCGTAGACTGCGCTGTGAATGYTGAGGGGGTTCGTCGCCGATCACTTCTCTCTCCTG[C/T]TAYTAGGTGCG GCTTCAAGTCGTTTCTCAACATTTTACCATCCGTCACACATGGCACTGCTGCCCCCCATCGTCACCGGGGGCGTCCGAATA GCGTGGGCTCYGTACCAGGATCATCGGGAGCGTATTTTACACTRGCTCTGGACGAGAACCCTCTGGCCGAGTTCGTTGARC TCCCAGAAGAAGTCTCGAAGGCGGTCTCTGGTTTTCAGCAACGTTTTATGA
	MS428_6			TTCGGTACACGGCTGATAGAAGATTTTCTGGCGAARAGYAGTTTGGGGCGGTGTTTTCAGATTTTCGGGAGGTTGGGGAGGTC GTTGCAAAGGTGCGTAGACTGCGCTGTGAATGYTGAGGGGGTTCGTCGCCGATCACTTCTCTCTCCTGYTAYTAGGTGCGC TTCAAGTCGTTTCTCAACATTTTACCATCCGTCACACATGGCACTGCTGCCCCCCATCGTCACCGGGGGCGTCCGAATAGC GTGGGCTC[C/T]GTACCAGGATCATCGGGAGCGTATTTTACACTRGCTCTGGACGAGAACCCTCTGGCCGAGTTCGTTGARC TCCCAGAAGAAGTCTCGAAGGCGGTCTCTGGTTTTCAGCAACGTTTTATGA
MS441	MS441_4	59.9	Bifunctional chorismate synthase and flavin reductase catalyzes the conversion of 5-enolpyruvylshikimate 3-phosphate EPSP to form chorismate which is a precursor to aromatic amino acids; Aro2p	ATGCTYTCCATYCCGGCYACTAAGGCTTTTCCAAATCGGGTCTGTTTTAAGGGGACAGAGGTACCTGGAAGCAAGCATAAC GATCCTTTTTGT[A/G]AAGCGTGATGACGGGCGACTCGGAACAAAGTCTAACTGGAGTGGCGGTGTGCAAGGAGGCATCACT AATGGGGAGGATATTTAYTTCCGGTTAGTTCTTGMTRCTTTSACTTCTTTTRGAYWCTGATGGTTCGGCTTCTAGGATCGGATT CAAGTCGCCAGCGACCATTTTCRCAGGCTCAAGAC
MS452	MS454_7	39.3	Essential nucleolar protein of unknown function; contains WD repeats interacts with Mpp10p and Bfr2p and has homology to Spb1p; Enp2p	CCGAGTTGCGGAACGTAATAAGTRCCCATTTGAATGCCTTCGTTGGCAGTCATTAGAAGCCCACTCCCGGGAACGTGGTGA ACGTGAYTGAGGTCAGTGGCAGGTGTGATAGAAACGAAGTTGGTTGAGGGCTAGAAGTAAATCATTACCTTATGGTTCGAAGT GTGCACGGCGGGTACAACATAACCGTATTTTCGATCCCAAATTTTATCACCTTCTTGTGTCAGCACTGAGRATCATSCCGTCTCC AGCCATACGGCTACCACCCTCGATCCATAGGAGACTTTTACCAGGAAAGTCCGTAACCTTGGTCTTTCRTAGCAAACGGCCR CGCCGCTCGAATATCATA[A/G]CAGTGAATGGCCCGTTCGATGTTCCACCGCGTAAGTAAGCCCATCATCACGAGATGCC AACGCCGTCACTAACAACATCTGGCGTCGAAAGCCTGCTCGTTCGATTTTCGAGGACCCCTACGCAAGATCTCGATCGG GGATCCCAGAAATGAACCGAACCGTTGCCGTCTATCCCAAAGCCCCACAGTTGATGCGCTGGGTTGACATCAACAACGTTT ACTCCAGCGATTTCTTTCGTCAGCCTSCAGGACCAAGGGAGTCATAAATCGACCTTGTATGATTGAGGCGATATATCTCAT TACCGGAGGCGGAAAAYAGAGCGTCACACGAAGGGAAATGATAGGCAAGTGAACGTCCAAACCGCGGTATTCGTGTCCGG TAATGGAAACCGCCTTGTGTGTGA
MS481	MS481_16	36.1	Essential serine kinase involved in the processing of the 20S pre-rRNA into mature 18S rRNA; has similarity to Rio1p; Rio2p	TGCGCTGTGCTGACCATYTGAGGGAAATCRATRACGACAGGCTCCCCAGTGTCTCGCCGATCAGAATGTTGAACTCATTAA AGTCTCCATGAATYAACCCSGCGGAGCAAATCGCACRATRATGTCCATCAAGGTTGAATAAAGCTTYCCTGGWGATGCAA CCTCTGATATTTGTCGYCTTTAGAGCAGGTTAATRAGAAYATTGTAGCRTGCGTTAATTGAKAAACCTCACAAGGGATAWGC ATCAATGAATTCATCAGAATACAGTGTGCTGTTGATCGATAGGTTGGAACAGGAAAATCGTGTTCGTGAAGGACCTGA AACAT[C/T]RTTGGTTACAGAAGACGTTTTTACGATGAWTACTTACCTGCATGAAAGCCATTCTTTTTGAGCAGCTAAGCGAG ACATGTACATCCACG

* Putative single-copy orthologs of 21 fungal species used to compare identity: *Ashbya gossypii*, *Aspergillus fumigatus*, *Aspergillus nidulans*, *Candida glabrata*, *Candida lusitanae*, *Coccidioides immitis*, *Cryptococcus neoformans*, *Debaryomyces hansenii*, *Fusarium graminearum*, *Kluyveromyces lactis*, *Magnaporthe grisea*, *Neurospora crassa*, *Phanerochaete chrysosporium*, *Saccharomyces bayanus*, *Saccharomyces cerevisiae*, *Saccharomyces paradoxus*, *Schizosaccharomyces pombe*, *Sclerotinia sclerotiorum*, *Trichoderma reesei*, *Ustilago maydis*, *Yarrowia lipolytica* (Mathey et al. 2008).

** SNPs selected for genotyping are marked with red color and square brackets

Study	Loci	Repeats	Primer sequences (5'-3')	Multiplex	#Scaffold *	Start position, bp	Length of the fragment, bp	Total length of scaffold, bp	Genomic fragments with the SSRs
This study	AC34	CTAC	F: NED- TTGACGCGTTGACGACTTACC R: CTTGTCGATAGCGGCTTCAC	7	23	463278	269	821663	TTGACGCGTTGACGACTTACCACCCTGGCCCGGGTTTAACAA TCAGTTTTCTGTGTGGACACTGCCGTGTAATACTACCTACCTAC CTACCTACCTACCTACCTACCTACCTACCTACCACGCCATCAGC GAGTATCTTAATTCTCCGTAGACTCGCACTTATGATAGCTCGGT GTATGTTAACGCTGCTTCCGCCGAGTCTAACTTACCATCCCGG CCGGTAACCGCGTGCTTTTGGCAGAGCTTGTGAAGCCGCTATC GACAAGT
	AC37	TGA	F: PET- AAGGACTAGGGAGGCTCTGG R: ATGATGACGCGCTGCGAATGG	6	25	922600	239	1000268	AAGGACTAGGGAGGCTCTGGAAGTTTAATTCAGGCGTGAAGT CACAGCCACAAATCGCAAAGGAAGGGCATGGGACAAGCTGAT GATGATGATGATGATGATGATGATCTGGATTGGTGACCCGCAA CACGTCTCGTGAGGGTATGGGACAAGCAAACCTTGGGTTGCGC CCACATCTTCAGGAACCGAAAAGAGGTCTCGAAGTGGTCCCTA CAGCCTACCATTGCGAGCGCGTCA
	AC38	TCT	F: FAM- ACAGCAGGATGTGATGGTGAC R: AGAAGCGTGCTGTAATTGAGG	7	28	844746	271	957909	ACAGCAGGATGTGATGGTGACGGGAAATAGTACGTTTCCGCGG TATCGTTTCTCGGTACCGTGTGGTTGTTTCTCCTCGTACTCTTCC TCTTCTCCTCCTCCTCGTCTGAGATCTTCTTCTTCTTCTTCT TCTTCTCCGGTTTTCGTATTCTTCTGTCCCGCAATTTGGGGTGG CCTGAACCTCCGATCTCCCGCTGAGCTTGAGCGTATCCAGAC AACATGCCCATCCGTCTGCCTTCTATCAAGGCCTCAAGTACAGC ACGCTTCT
Baumgartner et al. 2009	Am109	GTG	F: VIC- ATGAGACCCAGAAGTTGAAGA R: CACGTTGACAAATCCAATGC	4	7	148593	138	4682282	AATGAGACCCAGAAGTTGAAGATACCGCTGACCCCGCCGGCG GGGTTACCACAAATGTCCGGTGGCCTGAGTGGTGGTGGTGGT GTATTACTACTATCACCAGCCGGTTGCTGCGATGCGTCAACTT CGGGTAGAGCTCCAAGACCCGTTGGAAGCGAGCGCGTTGGA TTTGTCGACGT
Prospero et al. 2010	Arm02	CA	F: FAM- ATCGGAGAAGAAGCCAGACC R: AGGCAGGACATCGAGTTGAG	1	7	417266	185	4682282	GGAGAAGAAGCCAGACCGGTACAACCGCCACGTGCGTCCCTTA CCGGTACACACACACACACACACACACAGCCACCACTGCAAC TTCGAGAGGTATATCAGTTCAATTTCTTCTACGAATTCGATATC CCAACCCATATTCAGGATTCTCAACTCGATGTCCTGCCTCACC TGCAGCAATTGCGGA
	Arm05	GTC	F: FAM- GAGGAAGAGCTACGCACAGG R: CGGTTTCATCGGAGGTCTA	2	8	1111231	457	4279509	TGGACATCATGCTCGGGGTCCAGCCGACTACGAAGTCGATAT CTCCCTGATGGCACTGGCAGCAGGCCAGAGAGTCGACGTCCC AGTGCCAGAGGACAAGGCGGACACGAGTGAAAGCGAACCTGA GCCTGAACCGGAAGGAGAGTTGACTTCTTGTTCAGAGAAAA AAGGTGCCTCTTTATTTATTTATTTACTCCACATTTGCTGACAAC ACTGCAGAGGAAGAGCTACGCACAGGAATACTACGACATAAAT GACCCTTTTATTGACGACTCGGAGCTTGCAATTGATGAGCGCAA GTTTTTTGCTCAGACAAAACAGCGAGGATTCTATGTTTCTTCTGA CCAGGTTGCCTTGCTCAAGGATACTCCCAAAGAAAAGTTTCGTC GTCGTCGTCGTCGTCGTCGTCGTCATCGCCACTGACCGAATCG AGTCTAGACCTCCGATGAAACC

Study	Loci	Repeats	Primer sequences (5'-3')	Multiplex	#Scaffold *	Start position, bp	Length of the fragment, bp	Total length of scaffold, bp	Genomic fragments with the SSRs
Baumgartner et al. 2009	Am1 11	CAC	F: VIC- CGTCGTCCATTAGAGGCAAC R: GCCATTAGTTTGGCGTTGAG	4	8	1981033	194	4279509	GTCGTCCATTAGAGGCAATTAATTTCTTCACCACAACCACC ACCATCACACACACATTCTCACCAAACACGCAATGGCGAAATCA CTTCGATCCAAAACCAAACGGGATTTCCGTTTCAAGAAGCGAG AAGATGGAATTTATGCAGCAACAGAAGCTGCTCGCCTGCATAG GCTCAATGCCAAACTAATGGCCGTCATAT
Prospero et al. 2010	Arm1 6	TCG	F: HEX- ATTTGGAATCCTGACGTTGC R: GGCGCATTTGGTCAAAGTAA	2	8	3403536	189	4279509	GTCATTTGGAATCCTGACGTTGCAATAACTCGTCGTACCTGCAA AGGCACCAAGGCCGGTGTGTTGTAGCAGGCTGCCCGAAAACGCT AGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTTGATTGTTAG CGGCGTTACTTTGACCAAATGCGCCACCCTACCGAACGCGCT AGTACTTTTCAATGTCGG
	Arm1 1	CAG	F: FAM- CATCCCTTTTCGGACAGCAC R: TACCAGTCCATCTGGCATGA	2	10	3374956	217	5884921	CGGCATCCCTTTTCGGACAGCACGCGCAAGCCCAATTACACTTG CTTCAGCAGCAGCAGCAGCAGCAGCAGTTGCAGTCTCAGTCGCATC ATTTGCAGAATAACCGCCTCGAGCCGTTATATGAGAGCCGTCTC GATAACCGCAACTTCATGCCAGATGGACTGGTACCTGGCTTAC GGTCCGCCCTCCCCCGCGGAATCGTGAAAACGGTGGGATGT TTT
	Arm1 5	GAC GAC	F: FAM- CGAGCCGTCAACAGAGAATC R: TCCCCAACACAACCTTCTC	3	10	1186644	299	5884921	AGTTACACGCGTCTCCGAGCCGTCAACAGAGAATCAGACCAAG AAGAGGGAACGAAGCGATGACGACGACGGCGACGACGGCTCT GGCGAGCAAACGCCAGACTCTCCTGTCAAATTGACAGTGACCG AGGAGGAGCTAGACAGTCGGATTTCGAGAAAGGATGACAGAGCA GAGGAATTTTCGAGAAGGTTGTGTTTGGGGACTATGTCATAAGG ACATGGTGAGCACGCTCTGCCGCCTCTTATTGATTTACCTACTA TGCATCTAGGTATTTCTCGCCCTATGTGACGAGCGAAAAACC
	Arm0 9	GTT CTG	F: HEX- CGTCTCTGGTCCATGAAGGT R: GCCTCAGCAGCACCAGAT		12	1425084	448	4638314	TGTCGGTGTGCGCGGTGAGCATGTGGATGAGGGACGTGGTGC ATCTGGGATGTGCGCCGGTATGGTGAAGTCAGCGTAATCGACG ACGGCTGTCCCGCCCCATTCCCGCCGCTGACCGCATCTGTGA GTACATCGGCGCGCCATCTGTTTTGCGTCTGTCCCAGGCTCAT GTTTATTGGCTGCACCGTTTGGCCGTACGGCATGTTTATCATT CCATTGACTCTGGAGACAGGTATGTTTCCGTCTCTGGTCCATGA AGGTTTGTGTTTATCATGCNCGACGATGTGTGANAGTGGTGGT GGNGAGCAGTATGTGGTTGTTGTTGTTGTTGCTGTTGCTGTTGC TGCTGTTGCTGTTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTG CTGCTGGCGAGCAAGAGGCGGCACCCTCTGGTGTGCTGCTGAGG CGGCTGCTTGGGAGG

*Scaffold of draft genome assembly of the *A. cepistipes* (Sipos et al. unpublished)

Figure S1.1 Positions of SSRs and SNPs in the *Armillaria cepistipes* draft genome assembly (Sipos et al. unpublished) considered in the study:

