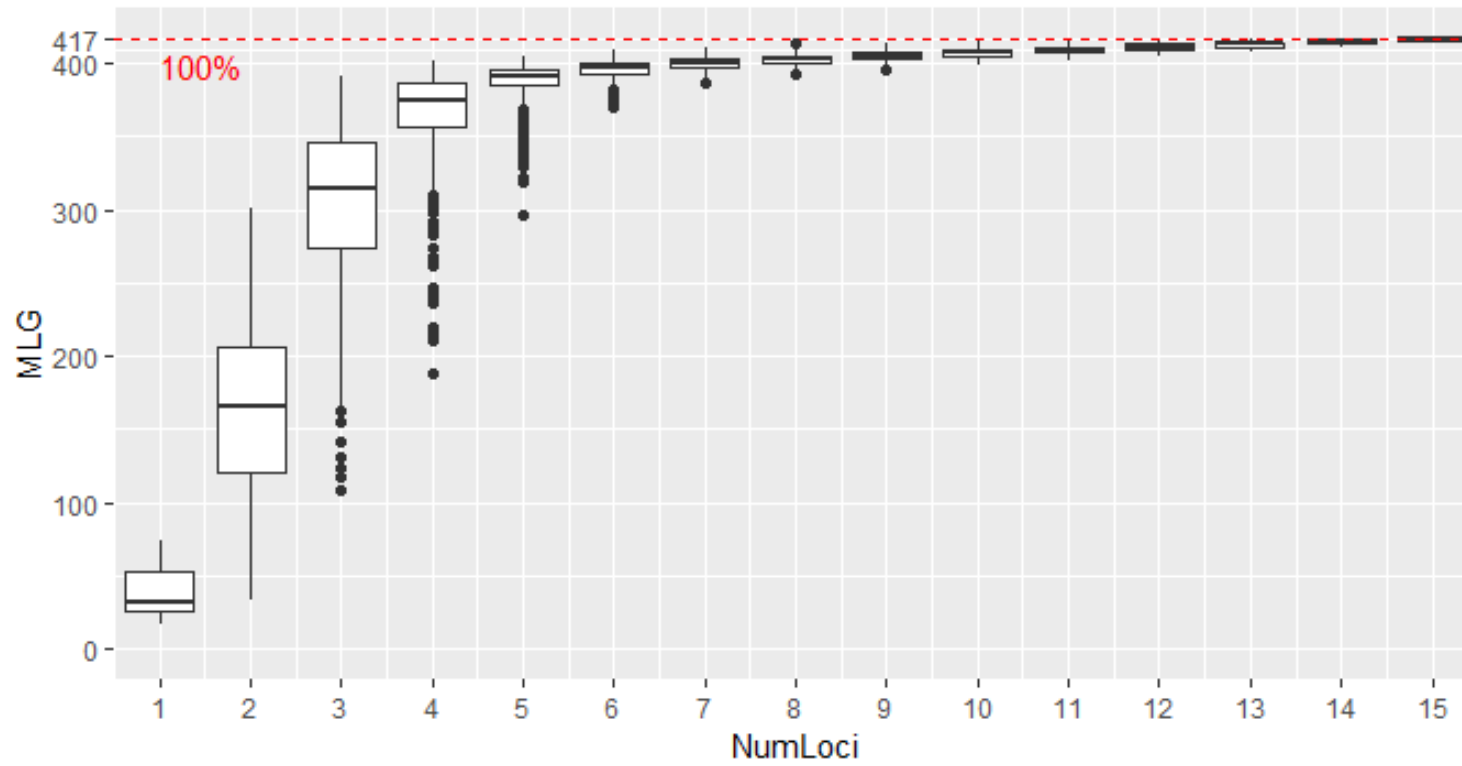
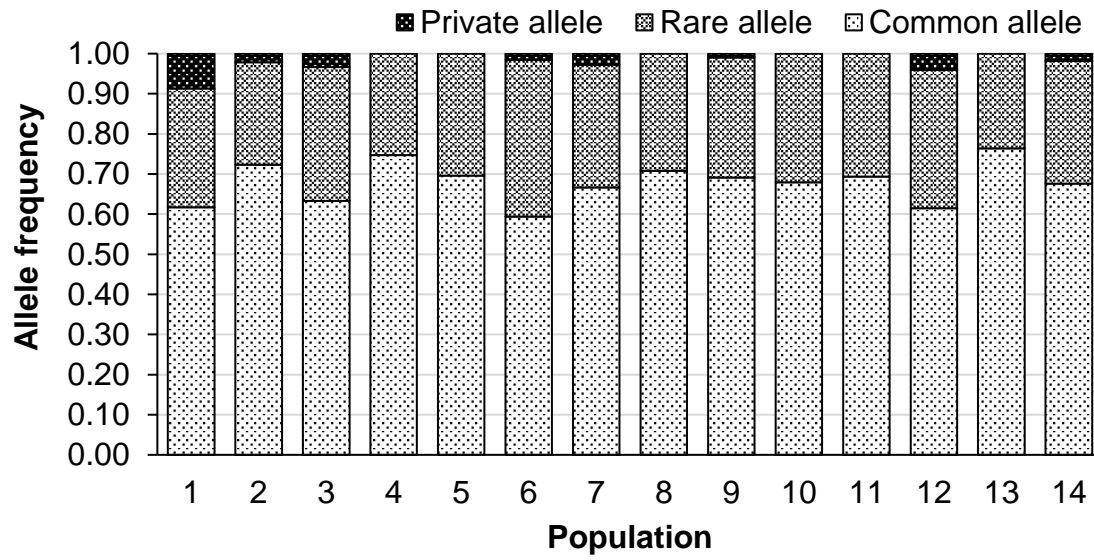


**Supplementary Figure 1.** Genotype accumulation curve for 417 *Ganoderma boninense* isolates collected from Sabah, Sarawak Peninsular Malaysia (Malaysia), and Sumatra (Indonesia). **MLG** indicates multilocus genotype; **NumLoci** indicates number of loci.



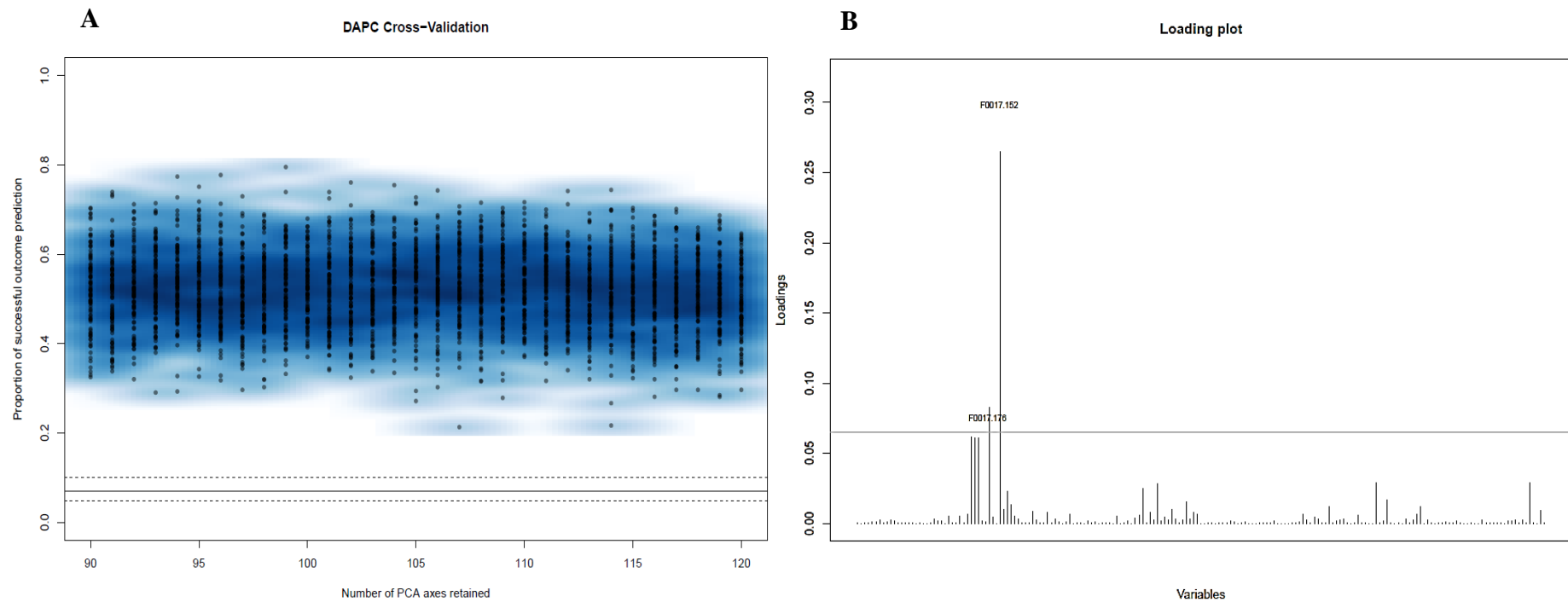
**Supplementary Figure 2.** The frequencies of private, rare and common alleles in the 14 populations of *Ganoderma boninense*.



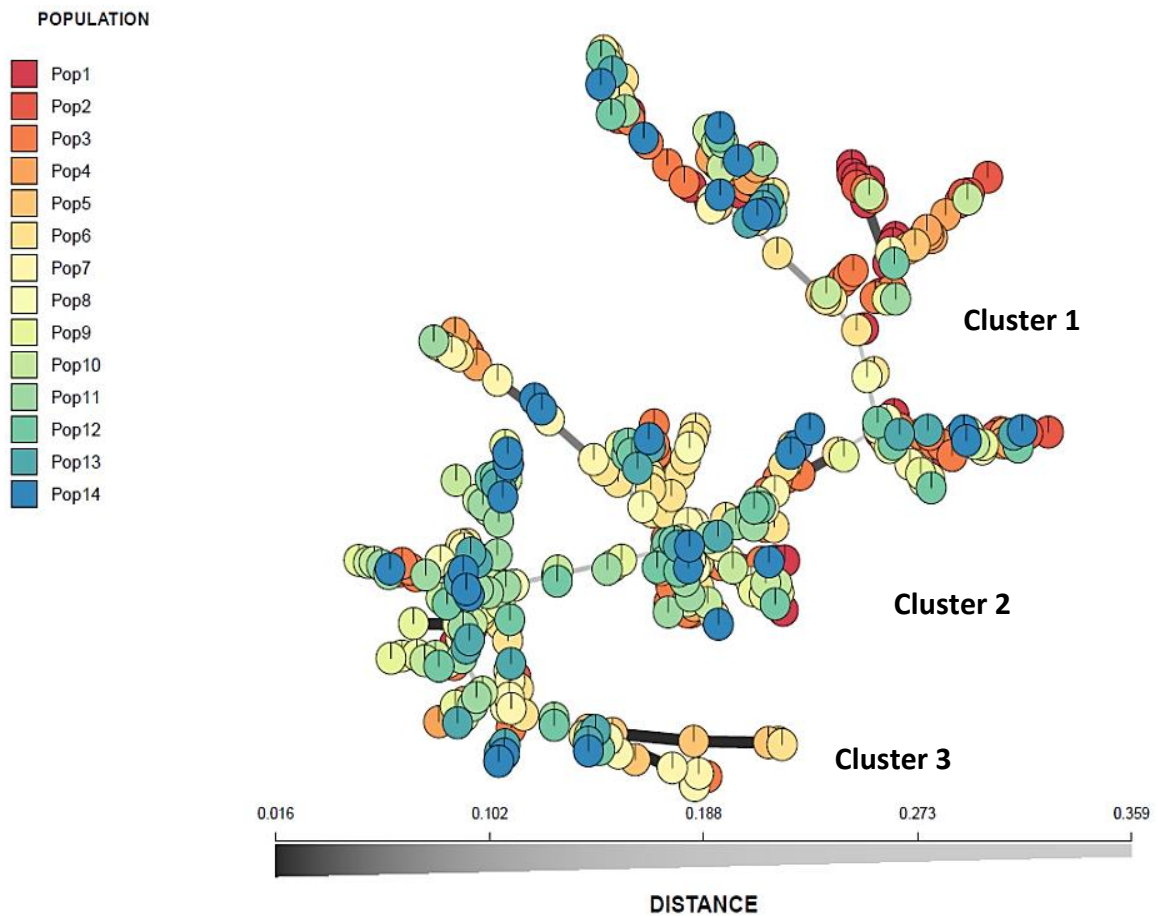
**Supplementary Figure 3.** Determination of first two principal components (PCs) for discriminant analysis of principal components (DAPC). **A.**

Initial DAPC cross-validation was performed from 10 to 200 PCs followed by narrow search from 90 to 120 PCs to determine the most appropriate PC for correct prediction with the lowest error. **B.** Alleles 152bp and 176bp from locus F0017 gave the largest contribution for

discriminating the pre-defined clusters in the current dataset (above threshold i.e. grey horizontal line).



**Supplementary Figure 4.** Minimum spanning network (MSN) constructed based on Bruvo's distance (Bruvo et al. 2004) for 417 *Ganoderma boninense* isolates (Pop 1–14) genotyped using 16 transcriptome-derived microsatellite loci. Each node represents an individual isolate and separated into three different subnetworks in Clusters 1 – 3.



**Supplementary Data 1.** The generation and age of oil palm planting at 14 sampling localities where *Ganoderma boninense* were sampled.

Region	Sampling locality	Pop	Generation of planting	Year of planting	Year of sampling
Sabah	Sigalong & Rimmer	1	First	1995, 1998 -1999	2018-2019
Sarawak	Sungai Balim, Lambir & Taniku	2	First, Second	Before 2004	2015
	Daro	3	First	2001	2015
	Balingian	4	First	2000 - 2003	2017
Peninsular Malaysia	Batu Lintang & Pelam	5	First	1991 - 1997	2016-2017
	Jeram	6	Second	1997	2015-2017
	Bekoh	7	First	1999, 2001	2019
	Random estates	8	Unidentified	Unidentified	2011-2018
Sumatra	Air Raya	9	First	1996	2017
	Bentaian	10	First	1996	2017
	Gunung Nayo	11	First	1995	2017
	Nilo	12	First	1999-2003	2015
	Tanjung Bringin	13	Third	2000	2015
	Padang Brahrang	14	First	1979	2015

**Supplementary Data 2.** The list of microsatellite loci and their molecular characteristics reported in Wong *et al.* (2021).

No.	Locus	Forward Primer Sequence (5' – 3')	Reverse Primer Sequence (5' – 3')	Repeat Motif	PCR annealing temperature, °C	Allele size, bp
1.	P5_13	CATGAGGGTAAGTTGAAATTG	TAGCGCTGTGATTGGTATTTA	(GAGAC) <sub>5</sub>	55	172 – 198
2.	P6_11	ACATATACACCTACCCGTCCT	ACCACGAGGGAGTTCGAC	(CAA) <sub>4</sub>	55	189 – 216
3.	F1_61	AACATTAATGGGAGCTGGA	CGTTGTTCTTCTTCTTCACAG	(CTG) <sub>3</sub>	55	213 – 243
4.	F44_93	CCAGCACTAGCACCAGTAGTA	GCGAGCACTACACGAACG	(CGT) <sub>6</sub>	55	170 – 236
5.	A0031	TGAATATTGAATGTTGTGCAG	ACGCCTGCTACTCTTACTACC	(AG) <sub>9</sub>	55	147 – 172
6.	A0050	GCACTGGTCGTAGAATACT	CTAGCGATACTCCAGTTTGTG	(ATA) <sub>6</sub>	55	168 – 186
7.	A0058	ACAAAGTGTACTCCCGAGTCT	GCCGTTTGGATATTCTTCTAT	(GGT) <sub>7</sub>	55	221 – 250
8.	F0017	CGGTCCTGTTTCTGTTTTT	GAGGGTTTACATAGGTGTGGT	(GT) <sub>6</sub>	55	152 – 178
9.	F0023	ATGTCGTCGAAGTACTCCTCT	GCGTATTTGAAGGATGTGTAT	(CA) <sub>6</sub>	55	139 – 175
10.	F0032	AGGAAGAATGATTGCAAGG	GGACACGGTAATTCAGATTTT	(GAA) <sub>6</sub>	55	135 – 164
11.	F0034	ACAAAGTGTACTCCCGAGTCT	GCCGTTTGGATATTCTTCTAT	(GGT) <sub>7</sub>	55	205 – 250
12.	F0035	CTATCACAGCAGGAACTCC	CACTCTACGAACGATGACAGT	(GTC) <sub>6</sub>	55	153 – 182
13.	F0046	TCAAGAGTTCTTCAAACAGGA	GATATGAGGAAGGGGACTACT	(GTC) <sub>7</sub>	55	194 – 227
14.	F0060	CCAGCACTAGCACCAGTAGTA	GCGAGCACTACACGAACG	(CGT) <sub>6</sub>	55	173 – 238
15.	F0064	ATTAGAGACGGAGAGAGATGG	TGTAGTTGTGTTGTTGTCGTC	(GA) <sub>6</sub>	55	143 – 173
16.	F0067	CAGATTTTATGATGGGTAACCT	GTGTCAGGGTAGAACTGCTG	(GCA) <sub>7</sub>	55	163 – 192

**Supplementary Data 3.** The  $P$ -values of Chi Square ( $\chi^2$ ) statistic and permutation test ( $P \leq 0.001$ ) of each microsatellite loci in Hardy-Weinberg equilibrium over 14 populations of *Ganoderma boninense*.

<b>Locus</b>	<b><math>\chi^2</math></b>	<b>Degree of freedom</b>	<b><math>P</math>-value of <math>\chi^2</math> test</b>	<b><math>P</math>-value derived from 1000 permutations</b>
P5_13	681.86	28	0.000	0.000
P6_11	988.67	45	0.000	0.000
F1_61	456.65	55	0.000	0.000
F44_93	52.43	66	0.888	0.207
A0031	339.94	91	0.000	0.000
A0050	261.66	21	0.000	0.000
A0058	1391.78	45	0.000	0.000
F0017	888.64	66	0.000	0.000
F0023	1679.58	190	0.000	0.000
F0032	541.96	55	0.000	0.000
F0034	2013.01	91	0.000	0.000
F0035	89.56	55	0.002	0.000
F0046	165.67	55	0.000	0.000
F0060	54.65	45	0.154	0.177
F0064	537.71	136	0.000	0.000
F0067	321.20	55	0.000	0.000

**Supplementary Data 4.** The  $P$ -values of Chi Square ( $\chi^2$ ) statistic computed over 16 microsatellite loci under null expectation of Hardy-Weinberg equilibrium ( $P \leq 0.05$ ) across 14 populations of *Ganoderma boninense*.

<b>Loci</b>	<b>Pop 1</b>	<b>Pop 2</b>	<b>Pop 3</b>	<b>Pop 4</b>	<b>Pop 5</b>	<b>Pop 6</b>	<b>Pop 7</b>	<b>Pop 8</b>	<b>Pop 9</b>	<b>Pop 10</b>	<b>Pop 11</b>	<b>Pop 12</b>	<b>Pop 13</b>	<b>Pop 14</b>
<b>P5_13</b>	0.011	0.094	0.000	0.005	0.001	0.000	0.000	0.009	0.000	0.001	0.336	0.061	0.105	0.000
<b>P6_11</b>	0.000	0.346	0.000	0.000	0.000	0.000	0.000	0.002	0.006	0.429	0.400	0.000	0.019	0.000
<b>F1_61</b>	0.000	0.000	0.001	0.022	0.667	0.007	0.000	0.008	0.897	0.007	0.000	0.976	0.393	0.060
<b>F44_93</b>	0.983	0.990	0.929	0.840	0.025	0.373	0.154	0.011	0.881	0.766	0.151	0.891	0.332	0.691
<b>A0031</b>	0.994	0.007	0.000	0.000	0.595	0.000	0.001	0.164	0.106	0.000	0.996	0.564	0.298	0.420
<b>A0050</b>	0.594	0.040	0.632	0.161	0.002	0.000	0.000	0.040	0.030	0.029	0.095	0.025	0.806	0.002
<b>A0058</b>	0.000	0.021	0.000	0.000	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>F0017</b>	0.904	0.034	0.417	0.002	0.300	0.000	0.003	0.898	0.029	0.072	0.805	0.000	0.084	0.802
<b>F0023</b>	0.022	0.127	0.000	0.001	0.014	0.000	0.000	0.000	0.000	0.001	0.016	0.000	0.000	0.000
<b>F0032</b>	0.800	0.245	0.408	0.846	0.146	0.000	0.011	0.956	0.975	0.003	0.285	0.486	0.737	0.262
<b>F0034</b>	0.000	0.021	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.007	0.000	0.101	0.000	0.000
<b>F0035</b>	0.995	0.843	0.004	0.217	0.542	0.041	0.000	0.295	0.854	0.878	0.792	0.549	0.981	0.911
<b>F0046</b>	0.276	0.001	0.040	0.000	0.889	0.000	0.188	0.756	0.337	0.134	0.615	0.445	0.994	0.023
<b>F0060</b>	0.973	1.000	0.928	0.937	0.076	0.010	0.154	0.084	0.544	0.766	0.151	0.596	0.079	0.691
<b>F0064</b>	0.027	0.000	0.006	0.000	0.026	0.000	0.020	0.482	0.268	0.296	0.031	0.614	0.922	0.150
<b>F0067</b>	0.447	0.000	0.000	0.004	0.000	0.000	0.001	0.003	0.126	0.635	0.056	0.029	0.003	0.166



**Supplementary Data 5.** STRUCTURE inferred membership coefficient for each population of *Ganoderma boninense* and the admixed genetic proportions from respective regions.

Region	Pop	Number of isolates	Inferred genetic clusters		
			1	2	3
Sabah	1	28	0.82	0.12	0.06
	2	19	0.80	0.04	0.16
Sarawak	3	52	0.73	0.16	0.11
	4	21	0.91	0.05	0.04
Peninsular Malaysia	5	15	0.00	0.35	0.65
	6	57	0.01	0.27	0.72
	7	37	0.07	0.43	0.50
	8	15	0.06	0.57	0.37
Sumatra	9	30	0.17	0.70	0.13
	10	29	0.21	0.75	0.04
	11	29	0.08	0.78	0.14
	12	31	0.11	0.67	0.22
	13	24	0.02	0.33	0.65
	14	30	0.01	0.34	0.65
<b>Admixed genetic proportion</b>					
Sabah	1	28	0.48	0.16	0.11
Sarawak	2-4	92	0.47	0.11	0.17
Peninsular Malaysia	5-8	124	0.01	0.28	0.46
Sumatra	9-14	173	0.03	0.45	0.27

**Supplementary Data 6.** Summary of global F-statistics and pairwise  $F_{ST}$  (Weir and Cockerham 1984) computed over 16 microsatellite loci across 14 populations of *Ganoderma boninense*. Number of random permutations = 10 000.  $F_{IT}$  indicates number of alleles within individuals relative to all population;  $F_{IS}$  indicates number of alleles within individuals relative to a population;  $F_{ST}$  indicates number of alleles within populations relative to all populations.

Locus	Global F-statistics			Pairwise $F_{ST}/(1-F_{ST})$
	$F_{IT}$	$F_{IS}$	$F_{ST}$	
P5_13	0.39	0.37	0.04	0.05
P6_11	0.46	0.43	0.05	0.06
F1_61	0.35	0.33	0.03	0.04
F44_93	0.10	0.09	0.02	0.02
A0031	0.13	0.12	0.02	0.02
A0050	0.36	0.33	0.04	0.05
A0058	0.65	0.63	0.06	0.08
F0017	0.23	0.17	0.07	0.08
F0023	0.26	0.20	0.07	0.08
F0032	0.19	0.15	0.05	0.08
F0034	0.66	0.63	0.08	0.10
F0035	0.13	0.08	0.06	0.06
F0046	0.20	0.14	0.07	0.08
F0060	0.10	0.09	0.02	0.02
F0064	0.24	0.21	0.04	0.05
F0067	0.20	0.17	0.03	0.03
<b>All Loci</b>	<b>0.30</b>	<b>0.27</b>	<b>0.05</b>	<b>0.06</b>

**Supplementary Data 7.** Pairwise  $F_{ST}/(1-F_{ST})$  values (Weir and Cockerham, 1984) among 14 populations of *Ganoderma boninense*. Shaded columns indicated low genetic differentiation ( $F_{ST}/(1-F_{ST}) < 0.05$ ) in Sabah (Pop 1), Sarawak (Pop 2 – 4), Peninsular Malaysia (Pop 5 – 8) and Sumatra (Pop 9 – 14). The classification of moderate and high genetic differentiation between the populations were  $0.05 \geq F_{ST}/(1-F_{ST}) \geq 0.15$  and  $F_{ST}/(1-F_{ST}) > 0.15$ , respectively.

	Pop1	Pop2	Pop3	Pop4	Pop5	Pop6	Pop7	Pop8	Pop9	Pop10	Pop11	Pop12	Pop13	Pop14
Pop1		0.06	0.04	0.08	0.11	0.08	0.08	0.08	0.07	0.07	0.10	0.10	0.08	0.08
Pop2	0.06		0.03	0.02	0.09	0.06	0.05	0.06	0.05	0.06	0.08	0.08	0.06	0.06
Pop3	0.04	0.03		0.06	0.09	0.05	0.06	0.05	0.05	0.04	0.06	0.06	0.05	0.05
Pop4	0.08	0.02	0.06		0.11	0.09	0.10	0.08	0.09	0.09	0.12	0.12	0.11	0.10
Pop5	0.11	0.09	0.09	0.11		0.04	0.07	0.06	0.05	0.07	0.09	0.07	0.06	0.03
Pop6	0.08	0.06	0.05	0.09	0.04		0.03	0.03	0.04	0.04	0.04	0.03	0.01	0.01
Pop7	0.08	0.05	0.06	0.10	0.07	0.03		0.02	0.05	0.03	0.04	0.05	0.04	0.03
Pop8	0.08	0.06	0.05	0.08	0.06	0.03	0.02		0.04	0.03	0.05	0.06	0.04	0.04
Pop9	0.07	0.05	0.05	0.09	0.05	0.04	0.05	0.04		0.01	0.01	0.04	0.04	0.04
Pop10	0.07	0.06	0.04	0.09	0.07	0.04	0.03	0.03	0.01		0.01	0.03	0.04	0.03
Pop11	0.10	0.08	0.06	0.12	0.09	0.04	0.04	0.05	0.01	0.01		0.04	0.05	0.04
Pop12	0.10	0.08	0.06	0.12	0.07	0.03	0.05	0.06	0.04	0.03	0.04		0.04	0.03
Pop13	0.08	0.06	0.05	0.11	0.06	0.01	0.04	0.04	0.04	0.04	0.05	0.04		0.00
Pop14	0.08	0.06	0.05	0.10	0.03	0.01	0.03	0.04	0.04	0.03	0.04	0.03	0.00	

**Supplementary Data 8.** Distribution of private alleles over eight populations of *Ganoderma boninense*.

Region	Sampling location	Pop	Locus	Allele, bp	Frequency		
Sabah	Sigalong & Rimmer	1	A0031	172	0.018		
			F0035	164	0.018		
				182	0.018		
			F0060	178	0.036		
				196	0.018		
			F1_61	239	0.036		
				170	0.018		
			F44_93	176	0.036		
			178	0.036			
			194	0.018			
Sarawak	Sungai Balim, Lambir & Taniku	2	F0060	238	0.026		
			F44_93	236	0.026		
	Daro	3	A0050	182	0.019		
				186	0.010		
			F0032	135	0.010		
			F0046	227	0.010		
Peninsular Malaysia	Jeram	6	F0032	164	0.036		
				F1_61	216	0.009	
				F0023	139	0.081	
	Bekoh	7		F0064	143	0.014	
					146	0.041	
Sumatra	Air Raya	9	F44_93	212	0.017		
				152	0.481		
	Nilo	12	F0017	155	0.058		
				162	0.077		
				164	0.096		
				209	0.032		
	Padang Brahrang	14	F0023	143	0.017		
					F0046	224	0.017

Summary of private alleles by locus:

No.	Locus	Private allele, bp
1.	F1_61	239, 216
2.	F44_93	170, 176, 178, 194, 212, 236
3.	A0031	172
4.	A0050	182, 186
5.	F0017	152, 155, 162, 164
6.	F0023	139, 143
7.	F0032	135, 164
8.	F0034	209
9.	F0035	164, 182
10.	F0046	224, 227
11.	F0060	178, 196, 238
12.	F0064	143, 146