

Figure S1. Bayesian phylogenetic tree constructed in Mr. Bayes based on mtDNA d-loop sequence. Numbers are posterior probabilities. Blue are *Mus musculus musculus* subspecies; orange are *M. m. castaneus*; red are *M. m. domesticus* with each region defined by a two or three letter code. Ge: Georgia, Ir: Iran, Sp: Spain, En: England, Fr: France, Ca: Cameroon, Ger: Germany, Sc: Scotland, Ire: Ireland, Gr: Greece, Au: Austria, Sw: Switzerland, Eg: Egypt, Tu: Turkey, Mo: Morocco, Un: United States, Po: Portugal, Is: Israel, Pe: Peru, It: Italy, Cr: Croatia, No: Norway, De: Denmark, Swe: Sweden.

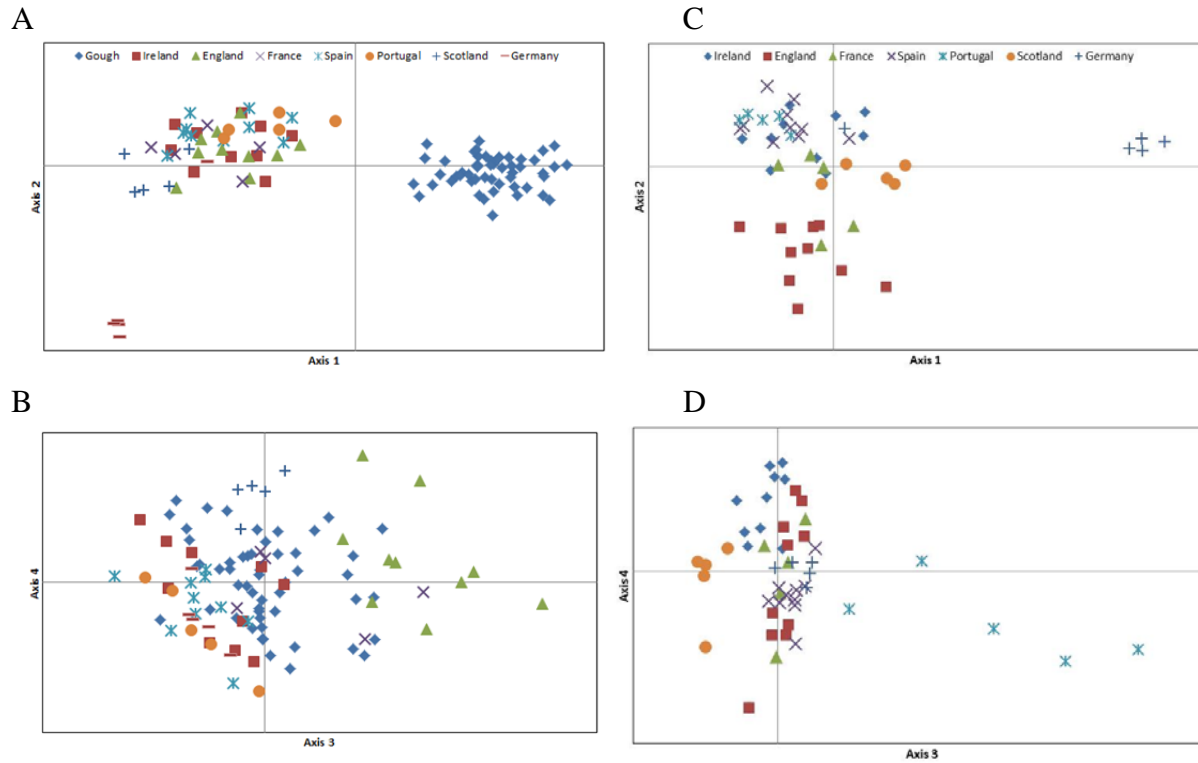


Figure S2. Principal coordinate analysis of 21 microsatellite loci. A.) Axis 1 and Axis 2 for all populations. B.) Axis 3 and Axis 4 for all populations. C.) Axis 1 and Axis 2 for just the European populations. D.) Axis 3 and Axis 4 for just the European populations.

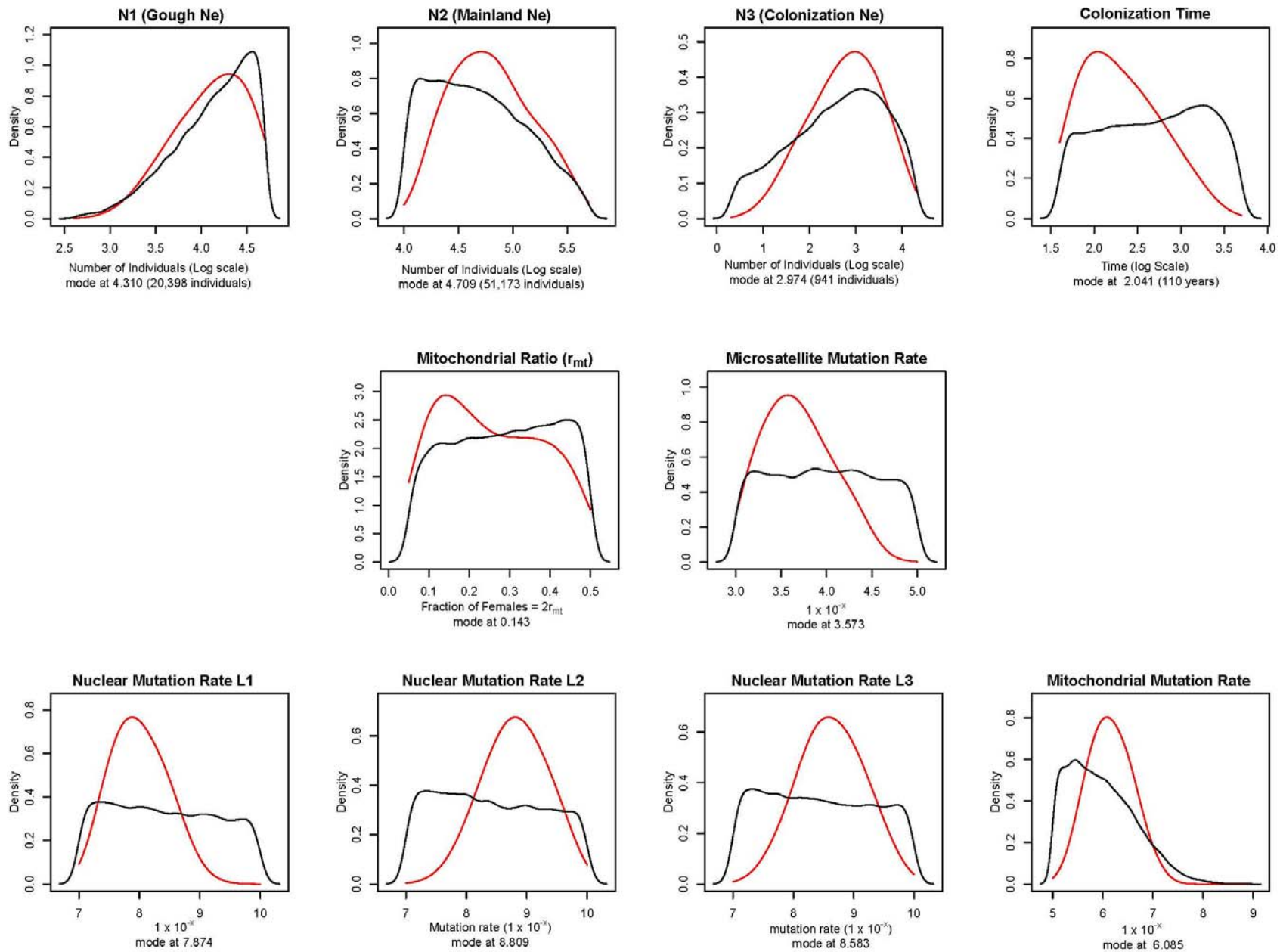


Figure S3. Posterior Density Distributions of the main model. Black lines indicate the prior distribution and the red lines indicate the posterior density distributions.

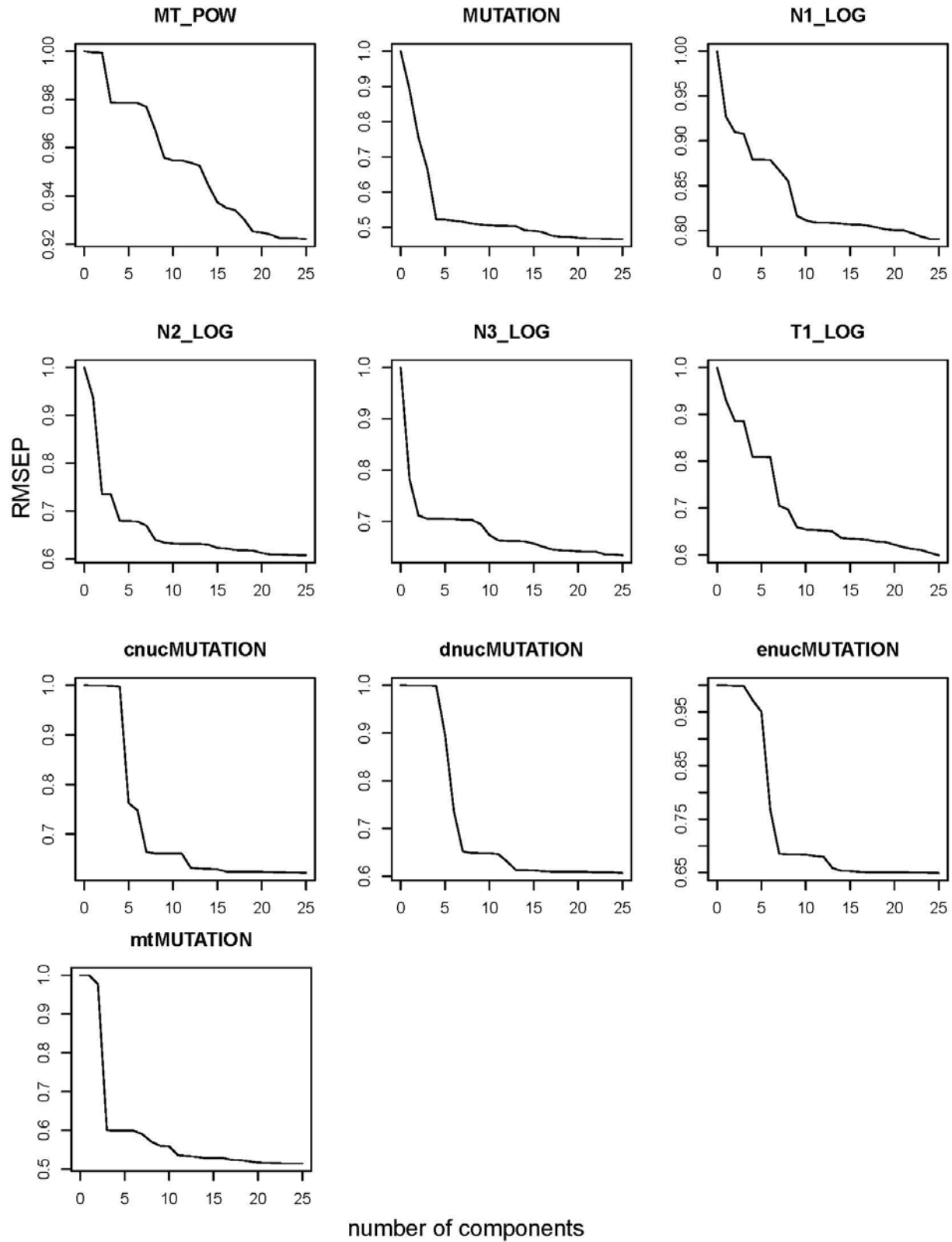


Figure 4. Root Mean Squared Error (RMSEP) plots of partial least squared components for each parameter inferred in the main demographic model.

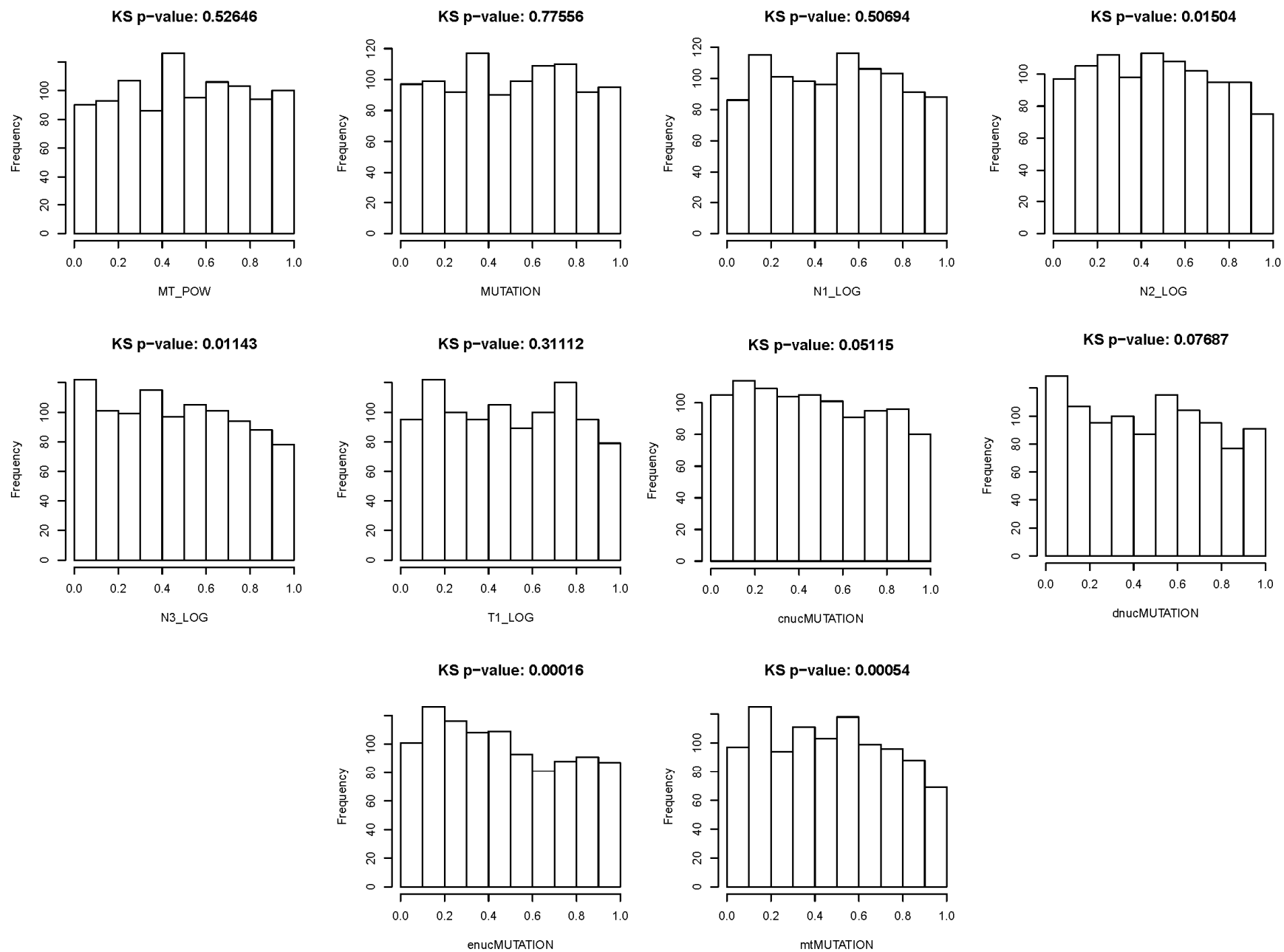


Figure S5. Distributions of the posterior quantiles for the parameters inferred in the main model of the ABC analysis. Values above the histograms are Kolmogorov-Smirnov test p-values.

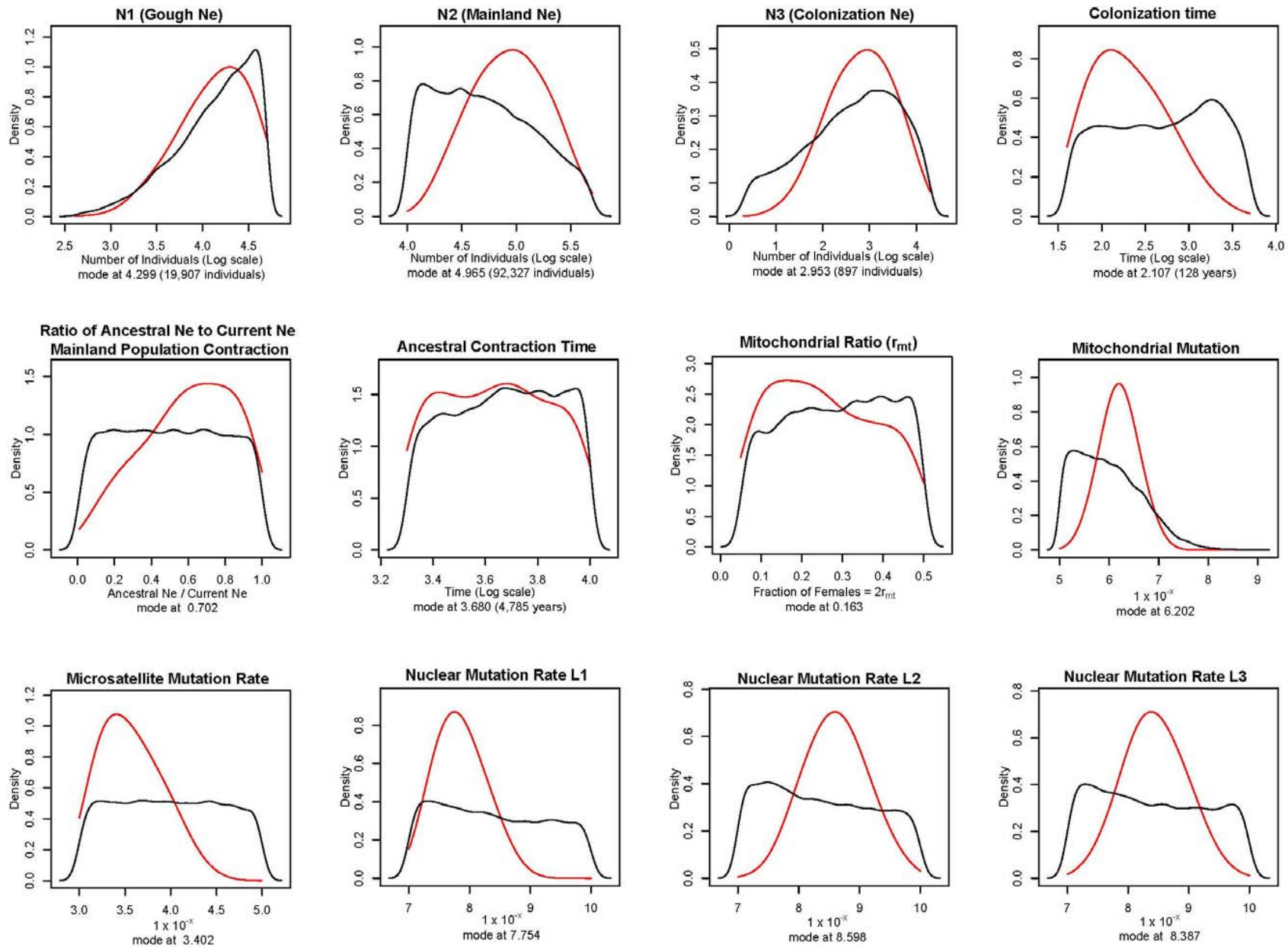


Figure S6. Posterior Density Distributions of Variation 1 model. Black lines indicate the prior distribution and the red lines indicate the posterior density distributions.

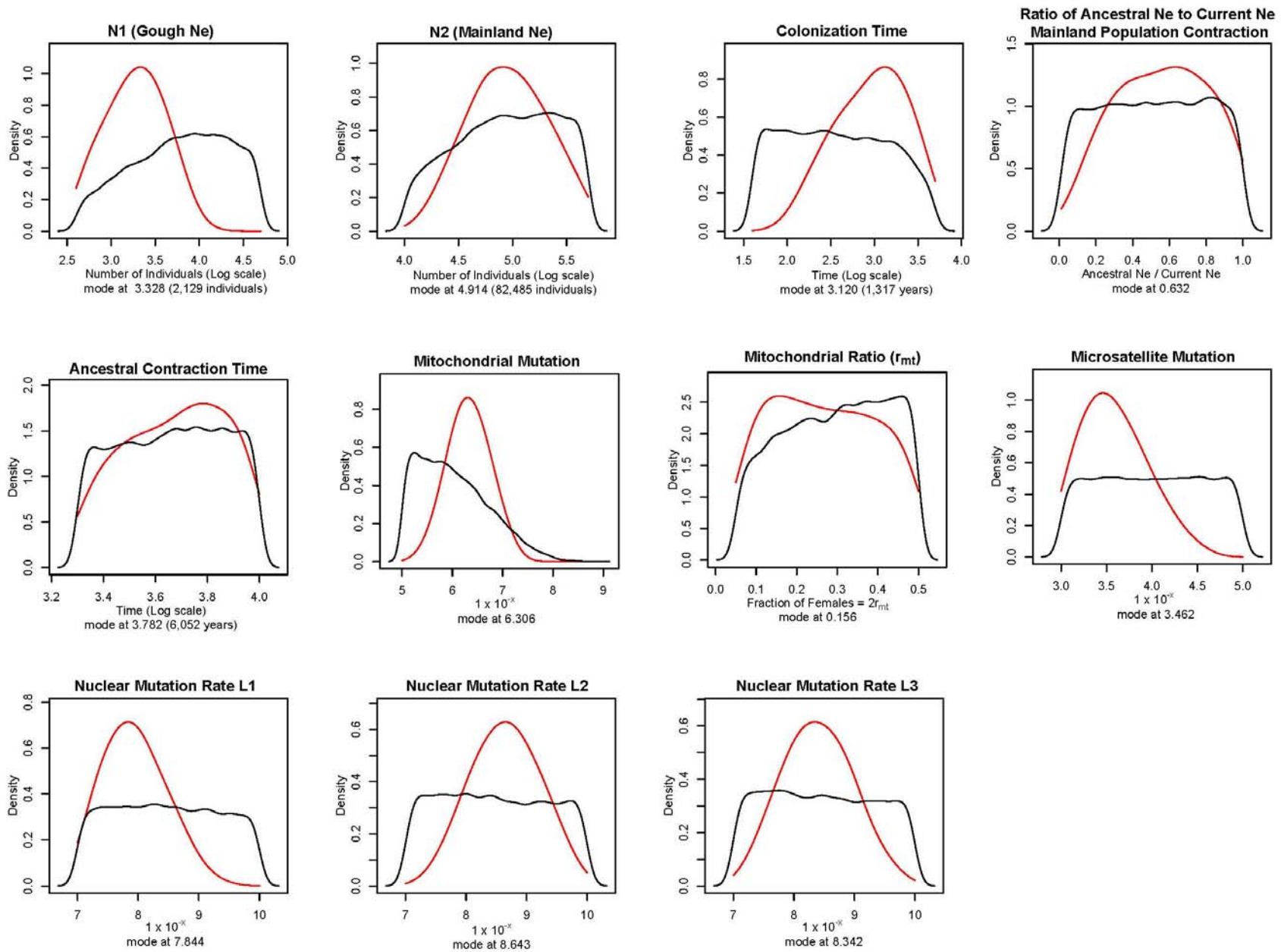


Figure S7. Posterior Density Distributions of Variation 2 model. Black lines indicate the prior distribution and the red lines indicate the posterior density distributions.

Table S1. European samples included in the study.

Sample	Locality	D-loop haplotype	Publication/Contributor
GERMANY			
MU205	Dortmund	MU205	S. Gabriel et al. unpublished
MU206	Dortmund	MU206	S. Gabriel et al. unpublished
MU212	Munster-Gievenback	MU212	S. Gabriel et al. unpublished
MU213	Munster-Gievenback	MU213	S. Gabriel et al. unpublished
MU209	Hamm (in Westfalen)	MU209	S. Gabriel et al. unpublished
ENGLAND			
SA	Steeple Ashton, nr. Trowbridge, Wiltshire	BritIsl.1	Searle et al. 09 PRS 276,201
52	Bristol	BritIsl.2	Searle et al. 09 PRS 276,201
MVZ162564	Culham College, Abingdon, Oxfordshire	MVZ162564	S. Gabriel et al. unpublished
MVZ162565	Culham College, Abingdon, Oxfordshire	MVZ162565	S. Gabriel et al. unpublished
EnLa1	Preston St Mary, nr. Lavenham, Suffolk	EnLa1	Jones et al. submitted
EnSB1	Sowerby Bridge, Yorkshire	EnSB1	Jones et al. submitted
EnTo1	Todmorden, Yorkshire	EnTo1	Jones et al. submitted
670M	Epworth, Lincolnshire	BritIsl.5	Searle et al. 09 PRS 276,201
Hesl	Heslington, near York	BritIsl.9	Searle et al. 09 PRS 276,201
York, Cara	York	BritIsl.1	Searle et al. 09 PRS 276,201
SCOTLAND			
2	West Canisbay, Caithness	BritIsl.17	Searle et al. 09 PRS 276,201
83	Mains of Olrig, Caithness	partial	Searle et al. 09 PRS 276,201
117	Dunnet, Caithness	partial	Searle et al. 09 PRS 276,201
119	John o'Groats, Caithness	BritIsl.31	Searle et al. 09 PRS 276,201
121	John o'Groats, Caithness	partial	Searle et al. 09 PRS 276,201
SPAIN			
98	Viladecans, near Barcelona	partial	Gunduz 1999 PhD thesis
115	Viladecans, near Barcelona	BARC 9	Johannesdottir et al. submitted
121	St Marti Sarroca, near Barcelona	partial	Gunduz 1999 PhD thesis
125	St Marti Sarroca, near Barcelona	BARC 2	Johannesdottir et al. submitted
132	Garraf, near Barcelona	BARC 12	Johannesdottir et al. submitted
SP1	Villamartin,Andalusia	SP1	Sofia Gabriel/ Jeremy Searle
SP30	Chiclana de la Fontera,Andalusia	SP30	Sofia Gabriel/ Jeremy Searle
SP66	Algeciras,Andalusia	SP66	Sofia Gabriel/ Jeremy Searle
SP82	Palos de la Frontera,Andalusia	SP82	Sofia Gabriel/ Jeremy Searle
SP106	Doñana,Andalusia	SP106	Sofia Gabriel/ Jeremy Searle
IRELAND			
ETL15	Tullamore,County Offaly	ETL15	Eleanor P Jones/JeremySearle
ECG5	Clonmel ,County Tipperary	ECG5	Jones et al 2011
EBFt3	Blarney ,County Cork	EBFt3	Jones et al 2011
EBD5	Blarney ,County Cork	EBD5	Jones et al 2011
EBE6	Blarney ,County Cork	EBE6	Eleanor P Jones/JeremySearle
ELR4	Letterkenny,County Donegal	ELR4	Eleanor P Jones/JeremySearle
ETM4	Tullamore,County Offaly	ETM4	Eleanor P Jones/JeremySearle
ERC10	Rathdrum ,County Wicklow	ERC10	Jones et al 2011

ECJ3	Clonmel ,County Tipperary	ECJ3	Jones et al 2011
EBD6	Blarney ,County Cork	EBD6	Eleanor P Jones/JeremySearle
FRANCE			
FrCs2	Calais,Pas-de-Calais	FrCs2	Jones et al 2011
FrFe2	Fecamp,Haute- Normandie	FrFe2	Jones et al 2011
FrCn1	Caen,Basse-Normandie	FrCn1	Eleanor P Jones/Jeremy Searle
FrAb9	Abbeville,Picardie	FrAb9	Jones et al 2011
FrSM1	Saint Malo,Bretagne	FrSM1	Eleanor P Jones/ Jeremy Searle
PORTUGAL			
PT38	Vila Franca de Xira	PT38	Sofia Gabriel / Daniel Förster / Jeremy Searle
PT46	Sines	PT46	Sofia Gabriel / Daniel Förster / Jeremy Searle
PT57	Figueira da Foz	PT57	Sofia Gabriel / Daniel Förster / Jeremy Searle
PT67	Porto	PT67	Sofia Gabriel / Daniel Förster / Jeremy Searle
PT80	Tavira	PT80	Sofia Gabriel / Daniel Förster / Jeremy Searle

Table S2. Genetic marker characteristics, primers, and reference sequence location.

Locus	Marker	Chr	Forward Primer	Reverse Primer	2011 Ref seq	Ref Seq Size	Dye	pool	Motif
Chr09_20	microsatellite	9	tgcaggaagactcccggacttg	agactccacttgggacaactgc	106198465	210	FAM	1	AC
Chr11_64	microsatellite	11	ttcagcagccatttggcaccag	agctacatagtgaggcactgtc	57516759	329	HEX	1	GT
Chr03_24	microsatellite	3	tcccatgctctaacaacctgg	acgtcttgataggcatctgtgc	122426201	389	FAM	1	AG
Chr02_01	microsatellite	2	agggtctctgacctgtagcag	tgagttcaagtccacactggtc	25427463	481	HEX	1	AG
Chr16_21	microsatellite	16	actcatgatcacacatgctctg	taagaggccaccagctacctg	30268016	209	FAM	2	AC
Chr19_08	microsatellite	19	tcagaggcagagtctcgctagg	agttgtggctccgccgggtgc	36737261	278	HEX	2	AC
Chr08_11	microsatellite	8	tggaacactcaagcaattcca	tagctccaaggacagttgacg	23410531	364	FAM	2	GT
Chr18_08	microsatellite	18	tctgcatgagttcaagaccagc	gctagagcaggacctccattgg	20509056	444	HEX	2	AC
Chr04_31	microsatellite	4	tgaataatgtggcactgacctg	agagataaggccagccattctg	14167775	134	FAM	3	AG
Chr12_05	microsatellite	12	gctctctcaaatcgatggctctc	ctttcatggtagcagaaggctc	70936323	172	HEX	3	AC
Chr17_09	microsatellite	17	aggctcattctagacagactcc	acaagggtcggtgtgtgtctg	35193776	239	FAM	3	AG
Chr13_22	microsatellite	13	tagctgatgccaagaccagtcc	agtctctccagacagcactacc	64159864	353	HEX	3	AC
Chr05_15	microsatellite	5	acgtgggtgctgtcgagtgtgc	ctccgagtgtagcagaaggctgac	113773172	140	FAM	4	GT
Chr03_21	microsatellite	3	atctgtgcaatgacgactcctg	ccgctactgatgacgaccagtg	131563768	192	HEX	4	GT
Chr07_38	microsatellite	7	atagagcaggacaccaatgtc	gggtgtgtccaccactgtccag	108932186	137	FAM	5	AC
Chr05_45	microsatellite	5	tctggcctgtgtcacctagtc	acaatgcttggtagctgtggtg	22613534	204	HEX	5	AC
Chr01_25	microsatellite	1	tcctgaacagaggactctgacc	gctagactgatactttccgacttagc	143737780	327	FAM	5	AC
Chr14_16	microsatellite	14	actgccattactgctgacatgg	gacatcggtgtgagccatctgc	122467400	477	HEX	5	GT
Chr10_45	microsatellite	10	gggacacatggtatgtctgcac	tacagtgttctccgactaagg	128924346	230	HEX	6	AG
Chr01_23	microsatellite	1	gctgcaagaagctcacggctac	agtgctcacgtcatccaggccag	134957479	278	FAM	6	TC
Chr02_02	microsatellite	2	gtaaggctgccccatcagag	agcctgacaacctggaaccac	94438926	218	HEX	7	GT
Ncap3	nuclear sequence	9	cgctgaacatcaggtatgaga	agggtgaatagcttcagggaaatagt	27034502	2216	PCR		
			tggaaagcaagtgtagattgtg	ggccacttcttgtgaaagtct	27034604	2015	PCR		
			aggaaggcaaattcagcactc	gcatgaagctcaaggtacaaaaga			SEQ		
			cactaacagactgactttctcaacc	aagtcctagattgtaagatcaacca			SEQ		
			gtggaagctcaagaacagtagaca	ttcccttcagctcatggt			SEQ		
			ggctacaggtacttccaattgac	ctggacaataatctcatgtcagaa			SEQ		
			cgtaaaccagtactaatactaccaa	agcccttctgcaaatatagga			PCR		
Rab21	nuclear sequence	10	tgtacacaacagagcaaacatga	aaaataagtcacctgtgaactttcc	115298895	1962	PCR		
			aattagttccacaacacctaacc	gtagttgtcctctacctgaggttc			SEQ		
			acattaaggaagcagctcagctat				SEQ		
			tcccacacagataacataacat	gctttacctcatcttgaatccac			SEQ		

			cttcctttaccaggtgaaatcttg				SEQ
			ggtatcactaactggccactttct	caggatgagttcctgtgtgac			SEQ
Mamdc2	nuclear sequence	19	gcatcaaactagttctctgtggg	tttctttcatgtagccagtgcttt	23443226	2278	PCR
			gttactaacagtgtgaggcctgg	tctacagatccaagtctcaacgg	23443329	2057	PCR
			ggcagtttaccagctatgtagag				SEQ
			agctggtgatgtctgggtc	tctctcctttactatgccaacctt			SEQ
			caaagtagctcttctcataaatgagt	tctgggaggaagaacaaactaaac			SEQ
				tttctacttatcgaagtaggtgac			SEQ
			cacacagagagagaaacacaatga	atgtgtgccagctgctgtact			SEQ
d-loop1a	mitochondria		ataaacattactctggtcttgtaaac	cctgaagtaagaaccagatg	15300	508	PCR
d-loop1b	mitochondria		ccaatgccccttctcgct	attaattataaggccaggaccaaacct	15722	676	PCR

Table S3. Summary Statistics and Partial Least Squared components calculated in the approximate Bayesian computation analysis.

Summary Statistic	Marker	Observed	max	min	PLS1	PLS2	PLS3	PLS4	PLS5	PLS6	PLS7	Description
K_1	microsatellite	7.905	41.000	1.095	-0.181	-0.042	0.030	-0.100	0.002	-0.017	0.034	Average number of alleles across microsatellite loci in pop 1
K_2	microsatellite	13.667	41.286	1.667	-0.119	0.148	0.072	-0.058	0.004	-0.012	-0.012	Average number of alleles across microsatellite loci in pop 2
Ksd_1	microsatellite	3.097	6.715	0.000	-0.175	-0.044	0.026	-0.080	-0.002	-0.012	0.055	stdev of average number of alleles across microsatellite loci in pop 1
Ksd_2	microsatellite	3.322	7.309	0.463	-0.114	0.139	0.070	-0.056	0.003	-0.011	-0.008	stdev of average number of alleles across microsatellite loci in pop 2
mean_K	microsatellite	10.786	38.714	1.690	-0.159	0.100	0.066	-0.085	0.004	-0.016	0.005	Average of K as shown above for both populations
sd_K	microsatellite	4.074	28.217	0.000	0.008	0.188	0.059	0.022	0.002	0.002	-0.042	stdev of K as shown above for both populations
tot_K	microsatellite	14.857	57.048	1.905	-0.127	0.140	0.072	-0.069	0.004	-0.014	-0.013	Average of total number of alleles across loci for the two populations combined
H_1	microsatellite	0.704	0.970	0.002	-0.180	-0.060	0.020	-0.055	0.001	-0.009	0.075	Average expected Heterozygosity across microsatellite loci for pop 1
H_2	microsatellite	0.869	0.978	0.144	-0.119	0.146	0.072	-0.060	0.003	-0.012	-0.009	Average expected Heterozygosity across microsatellite loci for pop 2
Hsd_1	microsatellite	0.176	0.276	0.000	0.102	0.011	-0.018	0.109	-0.004	0.017	0.038	stdev of average expected Heterozygosity across microsatellite loci for pop 1
Hsd_2	microsatellite	0.047	0.257	0.005	0.115	-0.142	-0.069	0.059	-0.004	0.013	0.009	stdev of average expected Heterozygosity across microsatellite loci for pop 2
mean_H	microsatellite	0.786	0.971	0.117	-0.188	0.005	0.043	-0.068	0.000	-0.011	0.055	average of H as shown above for both populations
sd_H	microsatellite	0.117	0.671	0.000	0.131	0.140	0.020	0.037	-0.001	0.007	-0.079	stdev of H as shown above for both populations
tot_H	microsatellite	0.818	0.976	0.138	-0.179	0.048	0.056	-0.076	0.001	-0.013	0.034	Average expected heterozygosity across loci for the two populations combined
GW_1	microsatellite	0.645	1.048	0.078	0.134	-0.054	-0.028	-0.120	0.004	-0.017	-0.163	average Garza and williamson statistic across loci for pop 1
GW_2	microsatellite	0.816	1.000	0.360	0.115	-0.142	-0.073	0.058	-0.003	0.013	0.009	average Garza and williamson statistic across loci for pop 2
GWsd_1	microsatellite	0.206	0.685	0.000	-0.080	0.021	0.011	0.105	-0.008	0.013	0.167	stdev of average of Garza and williamson statistic for pop 1

GWsd_2	microsatellite	0.182	0.239	0.000	-0.070	0.081	0.055	-0.051	-0.007	-0.008	0.016	stdev of average of Garza and williamson statistic for pop 2
mean_GW	microsatellite	0.730	1.000	0.241	0.139	-0.110	-0.054	-0.056	0.002	-0.007	-0.106	average of GW as listed above for both populations
sd_GW	microsatellite	0.121	0.447	0.000	-0.013	0.148	0.040	0.090	-0.002	0.014	0.038	stdev of average GW as listed above for both populations
tot_GW	microsatellite	0.851	1.000	0.368	0.094	-0.157	-0.072	0.028	-0.001	0.008	0.005	average GW across loci for the two populations combined
NGW_1	microsatellite	0.467	1.000	0.012	-0.060	-0.182	-0.045	-0.043	0.000	-0.007	0.050	average new/adjusted Garza and williamson statistic across loci for pop 1
NGW_2	microsatellite	0.800	1.000	0.358	0.129	-0.110	-0.069	0.096	-0.005	0.022	0.018	average new/adjusted Garza and williamson statistic across loci for pop 2
NGWsd_1	microsatellite	0.203	0.313	0.000	0.012	-0.143	-0.035	0.013	-0.010	0.010	0.032	stdev of average of new/adjusted Garza and williamson statistic for pop 1
NGWsd_2	microsatellite	0.185	0.254	0.000	-0.041	0.023	0.030	-0.067	-0.001	-0.014	-0.002	stdev of average of new/adjusted Garza and williamson statistic for pop 2
mean_NGW	microsatellite	0.633	0.986	0.193	-0.012	-0.189	-0.061	-0.013	-0.002	-0.001	0.052	average of NGW as shown above for both populations
sd_NGW	microsatellite	0.235	0.587	0.000	0.115	0.145	0.021	0.073	-0.003	0.015	-0.045	stdev of average NGW as shown above for both populations
R_1	microsatellite	13.381	112.238	1.000	-0.191	0.015	0.040	-0.023	0.001	-0.007	0.095	average range in allele size across loci for pop 1
R_2	microsatellite	17.143	115.952	1.000	-0.120	0.148	0.073	-0.060	0.003	-0.013	-0.011	average range in allele size across loci for pop 2
Rsd_1	microsatellite	11.124	48.790	0.000	-0.172	0.042	0.043	0.013	0.000	-0.002	0.113	stdev of average range in allele size across loci for pop 1
Rsd_2	microsatellite	9.350	45.380	0.000	-0.118	0.143	0.074	-0.061	0.003	-0.014	-0.007	stdev of average range in allele size across loci for pop 2
mean_R	microsatellite	15.262	114.095	1.094	-0.154	0.116	0.068	-0.060	0.003	-0.013	0.021	average of R as shown above for both populations
sd_R	microsatellite	2.660	67.514	0.000	0.029	0.183	0.059	-0.016	0.004	-0.006	-0.076	stdev of average of R as shown above for both populations
tot_R	microsatellite	17.857	117.524	0.905	-0.123	0.145	0.074	-0.065	0.004	-0.014	-0.011	average of the total range in allele size across loci of the populations combined
FIS	microsatellite	0.291	0.570	0.028	0.126	0.109	0.018	-0.032	0.000	-0.001	-0.141	average Fis across loci of populations combined
FST	microsatellite	0.099	0.773	-0.011	0.142	0.120	0.024	-0.017	-0.003	0.000	-0.127	average Fst across loci of populations combined
FIT	microsatellite	0.360	0.867	0.027	0.141	0.121	0.023	-0.017	-0.002	0.001	-0.133	average Fit across loci of populations combined

RST_2_1	microsatellite	0.101	0.774	-0.008	0.142	0.120	0.024	-0.017	-0.003	0.000	-0.127	average Rst between loci between population 1 and 2
DMUSQ_2_1	microsatellite	3.946	1145.890	0.004	-0.017	0.169	0.065	-0.049	0.006	-0.013	-0.074	average Dmu across loci between population 1 and 3
XPi_1	microsatellite	656.963	9970.960	-	0.044	-0.054	-0.023	0.001	-0.013	0.003	0.038	sum of the variance in allele size across loci within pop1
				1.00E+10								
XPi_2	microsatellite	683.477	9985.970	-	0.044	-0.054	-0.022	0.002	-0.012	0.004	0.039	sum of the variance in allele size across loci within pop 2
				1.00E+10								
XPi_1_2	microsatellite	745.646	9873.910	-	0.044	-0.054	-0.023	0.001	-0.013	0.003	0.038	sum of the variance in allele size across loci between pop1 and 2
				1.00E+10								
K_1	mtDNA	3.000	48.000	2.000	-0.043	0.000	-0.209	-0.156	0.001	-0.024	-0.100	number of haplotypes for pop 1
K_2	mtDNA	22.000	39.000	2.000	-0.043	0.104	-0.203	0.051	-0.006	0.015	0.036	number of haplotypes for pop 2
Ksd_1	mtDNA	0.250	0.577	0.000	-0.051	-0.098	-0.065	-0.163	0.003	-0.024	-0.057	stdev of the number of alleles across bp. for pop 1
Ksd_2	mtDNA	0.315	0.577	0.000	0.035	-0.086	0.038	-0.177	0.006	-0.034	-0.129	stdev of the number of alleles across bp. for pop 2
mean_K	mtDNA	12.500	42.500	2.000	-0.047	0.072	-0.229	-0.028	-0.003	0.000	-0.013	average of the number of haplotypes across both populations
sd_K	mtDNA	13.435	26.163	0.000	-0.017	0.112	-0.090	0.162	-0.005	0.028	0.122	stdev of average number of haplotypes across both populations
tot_K	mtDNA	24.000	85.000	3.000	-0.040	0.078	-0.227	-0.025	-0.003	0.000	-0.017	total number of haplotypes in the whole sample set
H_1	mtDNA	0.112	0.997	0.038	-0.050	-0.018	-0.186	-0.168	0.000	-0.029	-0.110	gene diversity in pop 1
H_2	mtDNA	0.935	1.000	0.051	-0.041	0.097	-0.195	0.050	-0.004	0.016	0.045	gene diversity in pop 2
Hsd_1	mtDNA	0.015	0.294	0.000	-0.068	-0.095	-0.083	-0.154	0.002	-0.026	-0.038	stdev of expected heterozygosity across bp for pop 1
Hsd_2	mtDNA	0.164	0.296	0.000	-0.003	0.001	-0.022	-0.002	0.003	0.005	0.003	stdev of expected heterozygosity across bp for pop 2
mean_H	mtDNA	0.524	0.997	0.045	-0.052	0.019	-0.212	-0.113	0.000	-0.016	-0.067	average of gene diversity across populations
sd_H	mtDNA	0.582	0.680	0.000	0.036	0.062	0.113	0.204	-0.001	0.037	0.144	stdev of gene diversity across populations
tot_H	mtDNA	0.121	0.469	0.022	-0.008	-0.004	-0.033	-0.020	-0.005	0.000	-0.023	total expected heterozygosity of all populations
S_1	mtDNA	2.000	2537.000	1.000	-0.080	-0.024	-0.186	-0.120	-0.001	-0.014	-0.039	number of segregating sites in pop 1
S_2	mtDNA	29.000	7185.000	1.000	-0.044	0.108	-0.202	0.052	-0.009	0.014	0.016	number of segregating sites in pop 2

prS_1	mtDNA	2.000	375.000	1.000	-0.035	0.013	-0.209	-0.147	0.000	-0.022	-0.105	number of private segregating sites in pop 1
prS_2	mtDNA	29.000	7185.000	1.000	-0.026	0.122	-0.187	0.065	-0.010	0.016	0.005	number of private segregating sites in pop 2
mean_S	mtDNA	15.500	3608.000	1.000	-0.053	0.094	-0.214	0.028	-0.008	0.010	0.012	average S across populations
sd_S	mtDNA	19.092	5058.640	0.000	-0.022	0.128	-0.170	0.084	-0.011	0.019	0.013	stdev of average S across populations
tot_S	mtDNA	31.000	7216.000	2.000	-0.044	0.102	-0.211	0.034	-0.009	0.010	0.007	total number of segregating sites in the sample set
D_1	mtDNA	-1.313	4.382	-2.979	-0.050	-0.062	0.024	-0.023	-0.001	-0.005	0.039	Tajima's D in pop 1
D_2	mtDNA	-0.133	3.343	-2.663	-0.001	0.002	-0.012	0.015	-0.002	0.007	0.008	Tajima's D in pop 2
mean_D	mtDNA	-0.723	3.435	-2.434	-0.043	-0.044	0.003	-0.005	-0.003	0.001	0.039	average Tajima's D for pop 1 and 2
sd_D	mtDNA	0.834	4.016	0.000	-0.017	0.014	-0.039	0.026	-0.010	0.008	0.024	stdev of average Tajima's D for pop 1 and 2
FS_1	mtDNA	-2.369	36.737	-27.703	-0.062	-0.055	0.046	0.049	-0.001	0.012	0.111	Fu's Fs for pop 1
FS_2	mtDNA	-6.667	30.639	-19.384	-0.004	0.004	-0.010	0.014	0.000	0.002	-0.007	Fu's Fs for pop 2
mean_FS	mtDNA	-4.518	21.819	-15.955	-0.060	-0.048	0.036	0.050	-0.001	0.011	0.098	average Fs of pop1 and pop2
sd_FS	mtDNA	3.039	28.115	0.001	-0.052	0.020	-0.127	-0.023	-0.002	0.007	-0.011	stdev of average Fs of pop1 and pop2
Pi_1	mtDNA	0.114	1117.060	0.038	-0.089	-0.038	-0.149	-0.087	-0.001	-0.010	0.003	mean number of pairwise differences in pop 1
Pi_2	mtDNA	6.594	1988.640	0.051	-0.043	0.107	-0.199	0.054	-0.010	0.014	0.016	mean number of pairwise differences in pop 2
mean_Pi	mtDNA	3.354	1096.780	0.045	-0.055	0.091	-0.210	0.033	-0.009	0.011	0.018	average pi of pop 1 and 2
sd_Pi	mtDNA	4.582	1404.880	0.000	-0.016	0.127	-0.166	0.080	-0.010	0.017	0.006	stdev of average pi of pop 1 and 2
FST_2_1	mtDNA	0.377	1.000	-7.211	0.077	0.062	0.006	-0.002	-0.003	0.000	-0.097	FST between pop 1 and 2
PI_2_1	mtDNA	6.318	3164.990	0.000	-0.030	0.103	-0.195	0.031	-0.010	0.009	-0.012	Average number of pairwise differences between populations (PiXY)
K_1	nucDNA L1	4.000	37.000	1.000	-0.098	-0.055	-0.001	0.035	-0.312	0.073	-0.181	number of haplotypes in pop 1
Ksd_1	nucDNA L1	0.277	0.577	0.000	-0.075	-0.029	0.003	0.071	-0.313	0.077	-0.152	stdev of the number of alleles across bp. in pop 1
H_1	nucDNA L1	0.619	0.989	0.000	-0.102	-0.053	-0.004	0.069	-0.308	0.078	-0.130	gene diversity in pop 1
Hsd_1	nucDNA L1	0.118	0.330	0.000	-0.096	-0.047	-0.004	0.075	-0.306	0.077	-0.121	stdev of expected heterozygosity across bp in pop 1
S_1	nucDNA L1	13.000	1274.000	0.000	-0.097	-0.034	-0.002	0.077	-0.295	0.080	-0.168	number of segregating sites in pop 1
D_1	nucDNA L1	3.144	4.184	-2.919	-0.046	-0.013	-0.009	0.095	-0.086	0.037	0.046	Tajima's D in pop 1
FS_1	nucDNA L1	10.888	36.737	-12.934	-0.061	0.001	-0.007	0.132	-0.168	0.062	-0.020	Fu's Fs for pop 1
Pi_1	nucDNA L1	6.015	435.212	0.000	-0.097	-0.030	-0.003	0.088	-0.285	0.080	-0.152	mean number of pairwise differences as calculated under Tajima's D in pop 1
HH	nucDNA L1	0.394	1.000	0.032	0.105	0.055	0.005	-0.069	0.308	-0.078	0.133	sum of squared frequency of haplotypes

													in pop 1
K_1	nucDNA L2	3.000	39.000	1.000	-0.099	-0.056	-0.010	0.026	0.206	0.244	-0.178		number of haplotypes in pop 1
Ksd_1	nucDNA L2	0.000	0.577	0.000	-0.077	-0.029	-0.004	0.066	0.202	0.243	-0.155		stdev of the number of alleles across bp. in pop 1
H_1	nucDNA L2	0.202	0.992	0.000	-0.107	-0.057	-0.011	0.059	0.199	0.245	-0.126		gene diversity in pop 1
Hsd_1	nucDNA L2	0.025	0.330	0.000	-0.099	-0.049	-0.008	0.070	0.193	0.237	-0.120		stdev of expected heterozygosity across bp in pop 1
S_1	nucDNA L2	22.000	1686.000	0.000	-0.100	-0.030	-0.008	0.068	0.183	0.234	-0.168		number of segregating sites in pop 1
D_1	nucDNA L2	-1.014	4.120	-2.975	-0.048	-0.013	-0.005	0.090	0.044	0.083	0.043		Tajima's D in pop 1
FS_1	nucDNA L2	8.136	36.737	-10.874	-0.066	0.002	-0.004	0.126	0.097	0.151	-0.019		Fu's Fs for pop 1
Pi_1	nucDNA L2	3.452	410.657	0.000	-0.100	-0.028	-0.008	0.081	0.183	0.238	-0.154		mean number of pairwise differences as calculated under Tajima's D in pop 1
HH	nucDNA L2	0.803	1.000	0.029	0.110	0.058	0.012	-0.058	-0.198	-0.244	0.130		sum of squared frequency of haplotypes in pop 1
K_1	nucDNA L3	3.000	37.000	1.000	-0.099	-0.053	-0.012	0.101	0.097	-0.271	-0.189		number of haplotypes in pop 1
Ksd_1	nucDNA L3	0.000	0.577	0.000	-0.076	-0.027	-0.008	0.130	0.098	-0.267	-0.177		stdev of the number of alleles across bp. in pop 1
H_1	nucDNA L3	0.425	0.991	0.000	-0.103	-0.050	-0.012	0.126	0.095	-0.268	-0.144		gene diversity in pop 1
Hsd_1	nucDNA L3	0.164	0.331	0.000	-0.094	-0.044	-0.012	0.131	0.095	-0.266	-0.156		stdev of expected heterozygosity across bp in pop 1
S_1	nucDNA L3	2.000	741.000	0.000	-0.098	-0.033	-0.010	0.131	0.089	-0.256	-0.191		number of segregating sites in pop 1
D_1	nucDNA L3	0.406	4.184	-2.849	-0.043	-0.008	-0.003	0.102	0.025	-0.083	0.017		Tajima's D in pop 1
FS_1	nucDNA L3	0.554	36.737	-9.855	-0.060	0.006	-0.004	0.146	0.041	-0.133	-0.044		Fu's Fs for pop 1
Pi_1	nucDNA L3	0.557	225.043	0.000	-0.097	-0.029	-0.009	0.142	0.085	-0.251	-0.177		mean number of pairwise differences as calculated under Tajima's D in pop 1
HH	nucDNA L3	0.584	1.000	0.030	0.105	0.052	0.012	-0.126	-0.095	0.268	0.148		sum of squared frequency of haplotypes in pop 1
K_1_vs_K_2	microsatellite	-0.238	0.134	-1.573	-0.089	-0.169	-0.034	-0.062	0.001	-0.010	0.047		Log10(K_1 / K_2)
H_1_vs_H_2	microsatellite	-0.091	0.122	-2.684	-0.148	-0.113	-0.006	-0.036	0.002	-0.008	0.085		Log10(H_1 / H_2)
R_1_vs_R_2	microsatellite	-0.108	0.172	-1.760	-0.125	-0.144	-0.029	0.003	0.000	-0.002	0.115		Log10(R_1 / R_2)
GW_1_vs_GW_2	microsatellite	-0.102	0.374	-0.786	0.072	-0.003	0.004	-0.171	0.001	-0.026	-0.168		Log10(GW_1 / GW_2)
NGW_1_vs_NGW_2	microsatellite	-0.234	0.137	-1.571	-0.087	-0.171	-0.034	-0.061	0.000	-0.010	0.046		Log10(K_1 / K_2)
K_1_vs_K_2	mtDNA	-0.865	0.929	-1.290	-0.009	-0.094	-0.047	-0.223	0.003	-0.040	-0.155		Log10(K_1 / K_2)
H_1_vs_H_2	mtDNA	-0.920	1.090	-1.415	-0.036	-0.050	-0.113	-0.176	0.000	-0.036	-0.125		Log10(H_1 / H_2)

S_1_vs_S_2	mtDNA	-1.161	1.230	-3.560	-0.030	-0.143	0.026	-0.191	0.005	-0.033	-0.082	Log10(S_1 / S_2)
prS_1_vs_p rS_2	mtDNA	-1.161	1.230	-3.560	-0.001	-0.134	0.038	-0.206	0.006	-0.037	-0.112	Log10(prS_1 / prS_2)
prS_1_vs_S _1	mtDNA	0.000	0.000	-2.068	0.109	0.088	0.048	0.041	0.000	0.007	-0.080	Log10(prS_1 / S_1)
prS_2_vs_S _2	mtDNA	0.000	0.000	-1.342	0.101	0.096	0.046	0.064	-0.001	0.011	-0.069	Log10(prS_2 / S_2)
prS_vs_S	mtDNA	0.000	0.000	-1.439	0.104	0.095	0.046	0.058	-0.002	0.010	-0.073	Log10((prS_1 + prS_2) / (S_1 + S_2))
mt_vs_nuc _K	MtDNA / nucDNA	-0.523	1.061	-1.462	0.058	0.058	-0.175	-0.170	0.008	-0.050	0.067	Log10(mt_K_1 / (nuc_L1_K_1 + nuc_L2_K_1 + nuc_L3_K_1))
mt_vs_nuc _H	MtDNA / nucDNA	-1.045	1.358	-1.838	0.079	0.053	-0.106	-0.194	0.006	-0.048	0.010	Log10(mt_H_1 / (nuc_L1_H_1 + nuc_L2_H_1 + nuc_L3_H_1))
mt_vs_nuc _S	MtDNA / nucDNA	-1.267	2.569	-2.666	0.059	0.030	-0.151	-0.205	0.015	-0.068	0.126	Log10(mt_S_1 / (nuc_L1_S_1 + nuc_L2_S_1 + nuc_L3_S_1))
mt_vs_nuc _Pi	MtDNA / nucDNA	-1.945	3.165	-3.452	0.056	0.023	-0.131	-0.222	0.013	-0.065	0.066	Log10(mt_Pi_1 / (nuc_L1_Pi_1 + nuc_L2_Pi_1 + nuc_L3_Pi_1))

Max and Min values are the maximum and minimum values across all simulations.

Table S4. Microsatellite population genetic measures per locus per population.

Locus	Gough							Ireland						
	N	A	H _o	H _e	r	NGW	HWE	N	A	H _o	H _e	r	NGW	HWE
Chr02_01	104	13	0.808	0.833	17	0.591	0.614	20	15	0.900	0.968	20	0.682	0.313
Chr02_02	104	8	0.750	0.718	12	0.444	0.891	20	8	0.900	0.863	15	0.444	0.503
Chr12_05	104	5	0.558	0.674	5	0.227	0.303	20	6	0.600	0.800	5	0.273	0.194
Chr19_08	104	12	0.885	0.888	13	0.800	0.671	20	9	0.700	0.795	10	0.600	0.225
Chr18_08	104	13	0.500	0.770	57	0.203	0.000	20	8	0.600	0.900	11	0.125	0.012
Chr17_09	104	8	0.750	0.793	17	0.381	0.319	20	6	0.700	0.747	20	0.286	0.874
Chr08_11	104	8	0.750	0.748	10	0.571	0.353	20	7	0.900	0.842	7	0.500	0.966
Chr05_15	104	4	0.500	0.523	12	0.267	0.782	20	6	0.600	0.821	6	0.400	0.106
Chr14_16	104	6	0.808	0.813	13	0.353	0.374	20	9	0.800	0.858	11	0.529	0.543
Chr09_20	104	9	0.712	0.788	11	0.643	0.232	20	7	0.800	0.732	8	0.500	0.978
Chr03_21	104	7	0.692	0.779	9	0.700	0.030	20	7	0.700	0.800	9	0.700	0.393
Chr16_21	104	6	0.731	0.658	7	0.462	0.176	20	4	0.500	0.500	4	0.308	0.650
Chr13_22	104	8	0.712	0.774	8	0.800	0.041	20	7	0.900	0.826	6	0.700	0.986
Chr01_23	104	6	0.308	0.327	6	0.300	0.327	20	11	0.900	0.921	19	0.550	0.352
Chr03_24	104	11	0.788	0.757	18	0.440	0.139	20	12	0.900	0.937	18	0.480	0.654
Chr04_31	104	10	0.904	0.855	22	0.400	0.732	20	8	0.800	0.900	20	0.320	0.249
Chr07_38	104	2	0.192	0.176	1	0.118	1.000	20	8	0.600	0.837	10	0.471	0.148
Chr01_45	104	5	0.615	0.630	11	0.238	0.912	20	8	0.900	0.858	12	0.381	0.898
Chr05_45	104	10	0.788	0.799	12	0.714	0.083	20	7	0.700	0.811	10	0.500	0.573
Chr10_45	104	10	0.808	0.851	14	0.625	0.288	20	9	0.700	0.900	9	0.563	0.062
Chr11_64	104	4	0.558	0.625	6	0.308	0.458	20	5	0.400	0.663	6	0.385	0.154
Average		7.86	0.672	0.704	13.38	0.456	0.415		7.95	0.738	0.823	11.24	0.462	0.468
stdev		3.05	0.181	0.176	11.12	0.205	0.312		2.44	0.150	0.103	5.33	0.150	0.327

Locus	England							France						
	N	A	H _o	H _e	r	NGW	HWE	N	A	H _o	H _e	r	NGW	HWE
Chr02_01	20	6	0.700	0.768	7	0.273	0.760	10	7	1.000	0.933	13	0.318	1.000
Chr02_02	20	6	0.800	0.858	9	0.333	0.650	10	5	0.400	0.822	10	0.278	0.088
Chr12_05	20	7	0.700	0.821	15	0.318	0.551	10	5	0.600	0.867	14	0.227	0.284
Chr19_08	20	8	0.500	0.832	10	0.533	0.008	10	8	1.000	0.956	14	0.533	1.000
Chr18_08	20	12	0.700	0.942	54	0.188	0.006	10	6	0.400	0.844	29	0.094	0.011
Chr17_09	20	9	0.700	0.753	14	0.429	0.211	10	5	0.800	0.844	13	0.238	0.847
Chr08_11	20	8	0.700	0.884	9	0.571	0.119	10	5	0.800	0.844	4	0.357	0.353
Chr05_15	20	6	0.500	0.516	6	0.400	0.656	10	4	1.000	0.733	11	0.267	0.743
Chr14_16	20	8	0.700	0.837	10	0.471	0.350	10	9	0.800	0.978	14	0.529	0.116
Chr09_20	20	8	0.400	0.747	13	0.571	0.004	10	7	0.800	0.911	10	0.500	0.485
Chr03_21	20	3	0.300	0.668	5	0.300	0.017	10	6	0.800	0.889	7	0.600	0.148
Chr16_21	20	6	0.500	0.784	7	0.462	0.021	10	5	0.800	0.822	8	0.385	0.897
Chr13_22	20	6	0.300	0.726	5	0.600	0.005	10	3	0.200	0.733	2	0.300	0.048
Chr01_23	20	6	0.400	0.816	7	0.300	0.002	10	4	0.400	0.778	4	0.200	0.187
Chr03_24	20	9	0.600	0.900	17	0.360	0.003	10	7	0.600	0.911	12	0.280	0.049
Chr04_31	20	3	0.300	0.279	12	0.120	1.000	10	5	0.800	0.844	14	0.200	0.350
Chr07_38	20	9	0.400	0.795	13	0.529	0.012	10	6	0.600	0.889	9	0.353	0.155
Chr01_45	20	5	0.400	0.753	13	0.238	0.011	10	7	1.000	0.867	15	0.333	1.000
Chr05_45	20	4	0.300	0.700	3	0.286	0.030	10	5	0.600	0.756	10	0.357	0.232
Chr10_45	20	8	0.400	0.905	12	0.500	0.000	10	6	0.800	0.889	10	0.375	0.150
Chr11_64	20	5	0.600	0.758	9	0.385	0.287	10	5	0.400	0.756	4	0.385	0.046
Average		6.76	0.519	0.764	11.90	0.389	0.224		5.71	0.695	0.851	10.81	0.339	0.390
stdev		2.19	0.166	0.145	10.32	0.135	0.312		1.42	0.233	0.070	5.68	0.125	0.362

Locus	Spain							Portugal						
	N	A	H _o	H _e	r	NGW	HWE	N	A	H _o	H _e	r	NGW	HWE
Chr02_01	20	9	0.800	0.905	15	0.409	0.183	10	6	0.800	0.889	9	0.273	0.618
Chr02_02	20	7	0.600	0.863	11	0.389	0.022	10	6	0.800	0.778	9	0.333	0.876
Chr12_05	20	5	0.400	0.784	4	0.227	0.019	10	3	0.200	0.689	2	0.136	0.048
Chr19_08	20	9	0.800	0.921	11	0.600	0.411	10	7	0.800	0.911	11	0.467	0.498
Chr18_08	20	8	0.800	0.884	10	0.125	0.354	10	7	0.600	0.911	9	0.109	0.047
Chr17_09	20	8	0.500	0.868	12	0.381	0.013	10	7	0.800	0.911	14	0.333	0.500
Chr08_11	20	7	0.700	0.811	12	0.500	0.281	10	4	0.400	0.733	3	0.286	0.111
Chr05_15	20	9	0.600	0.832	13	0.600	0.045	10	7	0.800	0.867	13	0.467	0.616
Chr14_16	20	8	0.900	0.879	9	0.471	0.149	10	6	0.800	0.844	14	0.353	0.796
Chr09_20	20	8	0.700	0.889	8	0.571	0.322	10	5	0.800	0.822	9	0.357	0.337
Chr03_21	20	7	0.800	0.789	8	0.700	0.315	10	4	0.800	0.733	6	0.400	0.745
Chr16_21	20	8	0.800	0.868	7	0.615	0.813	10	5	0.600	0.822	4	0.385	0.334
Chr13_22	20	8	0.700	0.879	7	0.800	0.146	10	6	0.800	0.889	5	0.600	0.611
Chr01_23	20	8	0.700	0.853	8	0.400	0.257	10	5	1.000	0.844	6	0.250	0.851
Chr03_24	20	16	1.000	0.974	18	0.640	1.000	10	6	0.800	0.844	14	0.240	0.794
Chr04_31	20	8	0.800	0.884	16	0.320	0.752	10	5	0.200	0.867	10	0.200	0.003
Chr07_38	20	8	0.600	0.811	11	0.471	0.073	10	3	0.200	0.378	4	0.176	0.111
Chr01_45	20	7	0.700	0.879	8	0.333	0.448	10	7	0.600	0.911	17	0.333	0.054
Chr05_45	20	8	0.800	0.884	8	0.571	0.721	10	6	0.400	0.844	8	0.429	0.009
Chr10_45	20	8	0.700	0.889	9	0.500	0.312	10	6	1.000	0.889	6	0.375	0.617
Chr11_64	20	9	0.900	0.874	12	0.692	0.752	10	3	0.200	0.689	3	0.231	0.047
Average		8.24	0.729	0.868	10.33	0.491	0.352		5.43	0.638	0.813	8.38	0.321	0.411
stdev		2.00	0.138	0.044	3.34	0.166	0.295		1.36	0.265	0.122	4.28	0.119	0.320

Locus	Scotland							Germany						
	N	A	H _o	H _e	r	NGW	HWE	N	A	H _o	H _e	r	NGW	HWE
Chr02_01	10	4	0.800	0.778	4	0.182	0.071	10	5	0.600	0.756	18	0.227	0.496
Chr02_02	10	5	0.600	0.844	11	0.278	0.353	10	2	0.400	0.533	1	0.111	1.000
Chr12_05	10	4	0.600	0.711	4	0.182	1.000	10	3	0.400	0.622	16	0.136	0.241
Chr19_08	10	5	0.400	0.822	12	0.333	0.083	10	3	0.200	0.378	6	0.200	0.110
Chr18_08	10	3	0.600	0.511	4	0.047	1.000	10	4	1.000	0.778	12	0.063	0.239
Chr17_09	10	7	1.000	0.911	14	0.333	1.000	10	4	0.800	0.778	17	0.190	0.073
Chr08_11	10	5	0.800	0.667	8	0.357	1.000	10	2	0.000	0.356	1	0.143	0.112
Chr05_15	10	5	0.600	0.822	6	0.333	0.341	10	4	0.800	0.711	6	0.267	0.207
Chr14_16	10	3	0.400	0.711	6	0.176	0.187	10	3	0.200	0.689	5	0.176	0.047
Chr09_20	10	4	0.400	0.778	6	0.286	0.047	10	2	0.400	0.356	1	0.143	1.000
Chr03_21	10	2	0.200	0.200	4	0.200	1.000	10	2	0.200	0.467	1	0.200	0.334
Chr16_21	10	3	0.600	0.644	9	0.231	1.000	10	5	0.400	0.756	8	0.385	0.048
Chr13_22	10	3	0.400	0.600	2	0.300	0.623	10	2	0.200	0.200	1	0.200	1.000
Chr01_23	10	5	0.800	0.844	6	0.250	0.351	10	4	0.800	0.711	7	0.200	0.208
Chr03_24	10	4	0.600	0.778	4	0.160	0.693	10	3	0.200	0.511	12	0.120	0.113
Chr04_31	10	5	0.600	0.800	18	0.200	0.466	10	3	0.400	0.622	4	0.120	0.237
Chr07_38	10	5	0.600	0.844	7	0.294	0.349	10	3	1.000	0.644	5	0.176	0.175
Chr01_45	10	3	0.600	0.600	16	0.143	0.618	10	4	0.600	0.644	8	0.190	0.237
Chr05_45	10	5	0.600	0.756	7	0.357	0.490	10	3	0.200	0.378	3	0.214	0.110
Chr10_45	10	4	0.200	0.778	3	0.250	0.010	10	2	0.000	0.356	3	0.125	0.112
Chr11_64	10	2	0.200	0.200	3	0.154	1.000	10	2	0.000	0.356	4	0.154	0.112
Average		4.10	0.552	0.695	7.33	0.240	0.556		3.10	0.419	0.552	6.62	0.178	0.296
stdev		1.22	0.209	0.192	4.48	0.083	0.370		1.00	0.316	0.177	5.44	0.067	0.312

N, number of chromosomes sampled; A, number of alleles; H_o, observed heterozygosity; H_e, expected heterozygosity; r, range of allele sizes; NGW, new (adjusted) Garza-Williamson statistics, HWE, Hardy-Weinberg p-values computed by Fischer's exact test.

Table S5 Microsatellite allele frequencies per locus per country.

Locus	Allele	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
Chr02_01		n=52	n=10	n=10	n=5	n=10	n=5	n=5	n=5
	486	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
	488	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
	490	0.000	0.100	0.000	0.100	0.100	0.000	0.000	0.000
	492	0.212	0.100	0.000	0.000	0.000	0.000	0.000	0.200
	494	0.000	0.050	0.000	0.100	0.000	0.000	0.000	0.500
	496	0.000	0.050	0.000	0.000	0.000	0.100	0.000	0.000
	498	0.019	0.000	0.050	0.200	0.050	0.000	0.000	0.000
	500	0.000	0.050	0.050	0.000	0.000	0.000	0.200	0.100
	502	0.260	0.050	0.400	0.100	0.050	0.200	0.400	0.000
	504	0.183	0.150	0.200	0.200	0.100	0.000	0.100	0.000
	506	0.010	0.050	0.000	0.000	0.000	0.100	0.000	0.000
	508	0.154	0.050	0.000	0.200	0.100	0.300	0.300	0.000
	510	0.029	0.100	0.250	0.000	0.250	0.100	0.000	0.000
	512	0.010	0.050	0.050	0.000	0.150	0.000	0.000	0.000
	514	0.000	0.050	0.000	0.000	0.100	0.200	0.000	0.000
	516	0.010	0.000	0.000	0.100	0.000	0.000	0.000	0.000
	520	0.019	0.000	0.000	0.000	0.100	0.000	0.000	0.000
	522	0.058	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	524	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.100
	526	0.010	0.050	0.000	0.000	0.000	0.000	0.000	0.000
	528	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100
Chr02_02		Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
	215	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
	225	0.240	0.150	0.150	0.100	0.100	0.000	0.300	0.000
	227	0.019	0.200	0.000	0.000	0.000	0.000	0.000	0.000
	229	0.000	0.000	0.100	0.000	0.000	0.100	0.000	0.000
	231	0.010	0.000	0.000	0.000	0.050	0.100	0.000	0.000
	233	0.000	0.000	0.000	0.000	0.250	0.100	0.000	0.000
	237	0.000	0.050	0.200	0.200	0.250	0.500	0.000	0.000
	239	0.048	0.100	0.200	0.000	0.100	0.000	0.100	0.000
	241	0.000	0.050	0.250	0.400	0.150	0.000	0.200	0.000
	243	0.442	0.300	0.100	0.100	0.000	0.100	0.300	0.000

	245	0.173	0.100	0.000	0.200	0.000	0.000	0.000	0.600
	247	0.019	0.000	0.000	0.000	0.100	0.100	0.100	0.400
	249	0.048	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Chr12_05	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany	
	168	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
	174	0.000	0.000	0.000	0.200	0.000	0.000	0.000	0.000
	178	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200
	180	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
	186	0.144	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	188	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000
	190	0.202	0.050	0.200	0.000	0.000	0.000	0.500	0.000
	192	0.500	0.250	0.350	0.000	0.300	0.200	0.000	0.000
	194	0.144	0.050	0.200	0.000	0.250	0.500	0.100	0.000
	196	0.010	0.350	0.000	0.100	0.300	0.300	0.300	0.200
	198	0.000	0.200	0.050	0.200	0.050	0.000	0.100	0.000
	200	0.000	0.100	0.000	0.200	0.100	0.000	0.000	0.000
	202	0.000	0.000	0.000	0.300	0.000	0.000	0.000	0.000
	210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.600
Chr19_08	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany	
	291	0.106	0.000	0.100	0.200	0.000	0.000	0.200	0.000
	293	0.000	0.050	0.300	0.000	0.000	0.100	0.000	0.000
	295	0.087	0.050	0.000	0.100	0.000	0.000	0.000	0.000
	297	0.010	0.000	0.000	0.100	0.150	0.300	0.000	0.000
	299	0.029	0.100	0.050	0.100	0.150	0.000	0.000	0.000
	301	0.058	0.100	0.050	0.000	0.050	0.100	0.000	0.100
	303	0.202	0.050	0.300	0.100	0.150	0.100	0.000	0.000
	305	0.000	0.050	0.050	0.000	0.100	0.100	0.400	0.000
	307	0.144	0.000	0.000	0.000	0.150	0.200	0.000	0.000
	309	0.038	0.050	0.100	0.200	0.100	0.000	0.200	0.100
	311	0.125	0.450	0.050	0.100	0.000	0.000	0.000	0.000
	313	0.096	0.100	0.000	0.000	0.000	0.000	0.100	0.800
	315	0.096	0.000	0.000	0.000	0.100	0.100	0.100	0.000
	317	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	319	0.000	0.000	0.000	0.100	0.050	0.000	0.000	0.000
Chr18_08	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany	

445	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000
447	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000
451	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000
453	0.000	0.000	0.100	0.000	0.050	0.100	0.000	0.000
455	0.000	0.000	0.100	0.000	0.050	0.100	0.000	0.400
457	0.010	0.150	0.200	0.000	0.000	0.000	0.000	0.100
459	0.298	0.150	0.100	0.000	0.100	0.000	0.000	0.000
461	0.029	0.050	0.050	0.400	0.250	0.100	0.700	0.000
463	0.000	0.000	0.100	0.000	0.100	0.200	0.000	0.000
465	0.000	0.150	0.050	0.000	0.200	0.000	0.200	0.000
467	0.337	0.050	0.050	0.100	0.150	0.300	0.000	0.300
469	0.048	0.150	0.050	0.100	0.000	0.100	0.100	0.000
471	0.000	0.200	0.000	0.000	0.000	0.000	0.000	0.000
473	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.000
475	0.038	0.000	0.000	0.000	0.000	0.000	0.000	0.000
477	0.000	0.000	0.000	0.200	0.000	0.000	0.000	0.000
479	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.200
487	0.019	0.000	0.000	0.000	0.000	0.000	0.000	0.000
497	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
515	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
517	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000
519	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000
521	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
531	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
551	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
553	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
571	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Chr17_09	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
244	0.260	0.450	0.500	0.300	0.250	0.100	0.300	0.300
250	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
254	0.000	0.200	0.100	0.200	0.250	0.100	0.000	0.000
256	0.000	0.000	0.050	0.000	0.150	0.200	0.100	0.000
258	0.000	0.000	0.050	0.300	0.050	0.000	0.100	0.000
260	0.212	0.000	0.000	0.000	0.000	0.000	0.100	0.200
262	0.038	0.000	0.000	0.000	0.100	0.000	0.000	0.000

264	0.000	0.000	0.000	0.000	0.050	0.100	0.000	0.000
266	0.000	0.200	0.100	0.100	0.100	0.300	0.100	0.000
268	0.000	0.050	0.050	0.000	0.050	0.100	0.100	0.000
270	0.288	0.000	0.050	0.100	0.000	0.000	0.000	0.400
272	0.038	0.050	0.050	0.000	0.000	0.100	0.200	0.000
274	0.125	0.000	0.000	0.000	0.000	0.000	0.000	0.000
276	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
278	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.100
284	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000

Chr08_11	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
380	0.000	0.100	0.100	0.200	0.000	0.200	0.100	0.000
382	0.058	0.300	0.000	0.100	0.150	0.100	0.000	0.000
384	0.183	0.150	0.250	0.300	0.400	0.500	0.100	0.200
386	0.394	0.050	0.150	0.300	0.100	0.200	0.000	0.800
388	0.058	0.100	0.050	0.100	0.150	0.000	0.000	0.000
390	0.000	0.250	0.000	0.000	0.050	0.000	0.000	0.000
392	0.000	0.000	0.050	0.000	0.000	0.000	0.600	0.000
394	0.000	0.050	0.200	0.000	0.000	0.000	0.100	0.000
396	0.019	0.000	0.100	0.000	0.000	0.000	0.100	0.000
398	0.250	0.000	0.100	0.000	0.100	0.000	0.000	0.000
400	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
402	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.000
406	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000

Chr05_15	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
148	0.558	0.000	0.000	0.100	0.000	0.100	0.000	0.000
150	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
154	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
156	0.000	0.000	0.000	0.000	0.050	0.100	0.000	0.000
158	0.000	0.000	0.000	0.000	0.000	0.400	0.000	0.000
160	0.413	0.200	0.700	0.500	0.050	0.000	0.400	0.000
162	0.000	0.000	0.050	0.000	0.250	0.100	0.200	0.000
164	0.000	0.150	0.000	0.000	0.350	0.100	0.000	0.100
166	0.000	0.050	0.050	0.200	0.050	0.000	0.000	0.300
168	0.000	0.350	0.100	0.000	0.100	0.000	0.100	0.100
170	0.010	0.150	0.050	0.200	0.000	0.100	0.100	0.000

	172	0.019	0.100	0.050	0.000	0.000	0.000	0.200	0.000
	174	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000
	176	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.500
Chr14_16	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany	
	476	0.173	0.000	0.000	0.000	0.100	0.000	0.000	
	478	0.000	0.000	0.000	0.100	0.000	0.400	0.000	0.000
	480	0.000	0.000	0.050	0.000	0.000	0.100	0.000	0.000
	482	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
	484	0.000	0.050	0.150	0.000	0.000	0.000	0.400	0.000
	486	0.000	0.000	0.050	0.100	0.000	0.000	0.000	0.000
	488	0.000	0.000	0.000	0.100	0.100	0.000	0.000	0.000
	490	0.096	0.050	0.050	0.000	0.050	0.000	0.000	0.000
	492	0.000	0.050	0.100	0.100	0.000	0.100	0.000	0.000
	494	0.058	0.300	0.000	0.000	0.300	0.000	0.400	0.000
	496	0.000	0.200	0.050	0.200	0.100	0.000	0.200	0.000
	498	0.231	0.200	0.350	0.100	0.150	0.000	0.000	0.500
	500	0.250	0.050	0.200	0.100	0.100	0.100	0.000	0.000
	502	0.192	0.000	0.000	0.100	0.000	0.000	0.000	0.300
	504	0.000	0.050	0.000	0.000	0.100	0.200	0.000	0.000
	506	0.000	0.000	0.000	0.100	0.100	0.000	0.000	0.000
	508	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200
Chr09_20	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany	
	227	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000
	229	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.000
	231	0.279	0.000	0.500	0.300	0.100	0.400	0.000	0.000
	233	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
	235	0.048	0.050	0.000	0.100	0.200	0.200	0.300	0.000
	237	0.298	0.050	0.000	0.000	0.100	0.000	0.200	0.000
	239	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.000
	241	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
	243	0.010	0.150	0.050	0.100	0.100	0.000	0.000	0.000
	245	0.029	0.500	0.100	0.100	0.050	0.100	0.400	0.800
	247	0.038	0.050	0.100	0.200	0.000	0.100	0.100	0.200
	249	0.212	0.050	0.050	0.100	0.000	0.200	0.000	0.000
	251	0.038	0.150	0.000	0.100	0.000	0.000	0.000	0.000

Chr01_23	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
281	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
291	0.000	0.050	0.300	0.000	0.000	0.000	0.000	0.000
293	0.000	0.000	0.000	0.000	0.000	0.100	0.200	0.100
295	0.000	0.000	0.000	0.200	0.200	0.300	0.100	0.000
297	0.029	0.000	0.100	0.300	0.000	0.000	0.000	0.000
299	0.067	0.000	0.300	0.400	0.200	0.000	0.300	0.100
301	0.817	0.200	0.150	0.000	0.050	0.200	0.300	0.000
303	0.019	0.000	0.100	0.100	0.300	0.300	0.000	0.300
305	0.048	0.100	0.050	0.000	0.050	0.100	0.100	0.000
307	0.000	0.050	0.000	0.000	0.050	0.000	0.000	0.500
309	0.019	0.100	0.000	0.000	0.050	0.000	0.000	0.000
311	0.000	0.050	0.000	0.000	0.100	0.000	0.000	0.000
313	0.000	0.200	0.000	0.000	0.000	0.000	0.000	0.000
315	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
317	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000
319	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000
Chr03_24	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
411	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
413	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
417	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
419	0.000	0.000	0.000	0.000	0.050	0.400	0.000	0.000
421	0.000	0.100	0.000	0.000	0.050	0.000	0.000	0.000
423	0.038	0.000	0.150	0.000	0.050	0.000	0.000	0.000
425	0.375	0.000	0.200	0.100	0.000	0.100	0.000	0.000
427	0.000	0.050	0.000	0.000	0.050	0.000	0.000	0.000
429	0.000	0.100	0.000	0.000	0.050	0.000	0.000	0.000
431	0.029	0.050	0.000	0.000	0.050	0.000	0.000	0.000
433	0.038	0.150	0.000	0.100	0.050	0.100	0.300	0.000
435	0.298	0.200	0.000	0.200	0.050	0.100	0.400	0.700
437	0.115	0.100	0.000	0.100	0.050	0.000	0.000	0.000
439	0.010	0.000	0.000	0.000	0.150	0.000	0.200	0.000
441	0.000	0.000	0.050	0.000	0.050	0.000	0.100	0.200
443	0.000	0.000	0.050	0.300	0.100	0.200	0.000	0.000
445	0.000	0.050	0.100	0.000	0.050	0.000	0.000	0.000

447	0.000	0.050	0.200	0.100	0.100	0.100	0.000	0.000
449	0.000	0.050	0.150	0.100	0.000	0.000	0.000	0.000
451	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000
453	0.048	0.000	0.000	0.000	0.000	0.000	0.000	0.000
455	0.019	0.050	0.000	0.000	0.000	0.000	0.000	0.000
457	0.019	0.050	0.000	0.000	0.000	0.000	0.000	0.000
459	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.100

Chr04_31	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
147	0.000	0.000	0.000	0.000	0.000	0.000	0.400	0.000
149	0.202	0.200	0.850	0.300	0.000	0.000	0.000	0.000
151	0.010	0.100	0.050	0.100	0.200	0.000	0.000	0.000
153	0.000	0.000	0.000	0.000	0.150	0.000	0.000	0.000
155	0.173	0.150	0.000	0.000	0.100	0.100	0.000	0.000
157	0.000	0.200	0.000	0.100	0.200	0.300	0.300	0.000
159	0.038	0.050	0.000	0.000	0.050	0.200	0.100	0.200
161	0.038	0.100	0.100	0.300	0.200	0.200	0.100	0.600
163	0.106	0.000	0.000	0.200	0.050	0.000	0.000	0.200
165	0.212	0.100	0.000	0.000	0.000	0.200	0.100	0.000
167	0.135	0.000	0.000	0.000	0.050	0.000	0.000	0.000
169	0.067	0.100	0.000	0.000	0.000	0.000	0.000	0.000
171	0.019	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Chr07_38	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
143	0.000	0.000	0.000	0.000	0.100	0.100	0.000	0.000
147	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000
149	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000
151	0.904	0.300	0.450	0.300	0.400	0.800	0.100	0.000
153	0.096	0.050	0.100	0.100	0.050	0.000	0.000	0.000
155	0.000	0.000	0.050	0.000	0.200	0.000	0.300	0.000
157	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.100
159	0.000	0.200	0.000	0.000	0.100	0.000	0.300	0.000
161	0.000	0.250	0.100	0.200	0.050	0.000	0.000	0.400
163	0.000	0.050	0.000	0.200	0.000	0.000	0.100	0.000
165	0.000	0.000	0.050	0.100	0.050	0.000	0.200	0.000
167	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.500
169	0.000	0.050	0.050	0.100	0.000	0.000	0.000	0.000

Chr10_45	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
243	0.010	0.000	0.150	0.200	0.000	0.000	0.000	0.200
245	0.000	0.000	0.150	0.300	0.000	0.000	0.000	0.000
249	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.800
251	0.000	0.000	0.100	0.000	0.100	0.000	0.000	0.000
253	0.000	0.000	0.000	0.000	0.100	0.100	0.200	0.000
255	0.163	0.050	0.000	0.000	0.050	0.200	0.400	0.000
257	0.087	0.100	0.050	0.100	0.200	0.200	0.100	0.000
259	0.221	0.250	0.200	0.200	0.200	0.300	0.300	0.000
261	0.221	0.050	0.150	0.100	0.100	0.100	0.000	0.000
263	0.077	0.150	0.000	0.100	0.000	0.000	0.000	0.000
265	0.029	0.100	0.100	0.000	0.000	0.100	0.000	0.000
267	0.067	0.150	0.100	0.000	0.050	0.000	0.000	0.000
269	0.115	0.050	0.000	0.000	0.000	0.000	0.000	0.000
271	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
273	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000
Chr11_64	Gough	Ireland	England	France	Spain	Portugal	Scotland	Germany
360	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000
362	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.000
364	0.000	0.050	0.000	0.000	0.050	0.000	0.000	0.000
366	0.154	0.000	0.100	0.000	0.000	0.000	0.000	0.000
368	0.000	0.150	0.350	0.100	0.050	0.000	0.900	0.800
370	0.000	0.050	0.150	0.200	0.200	0.200	0.000	0.000
372	0.327	0.550	0.350	0.500	0.300	0.500	0.000	0.000
374	0.000	0.000	0.000	0.100	0.100	0.000	0.000	0.000
376	0.500	0.200	0.000	0.100	0.050	0.300	0.000	0.200
378	0.019	0.000	0.000	0.000	0.100	0.000	0.000	0.000
384	0.000	0.000	0.050	0.000	0.050	0.000	0.000	0.000

Table S6. STRUCTURE group membership of European populations for K=5.

Population	Group Membership				
	1	2	3	4	5
Ireland	0.006	0.02	0.026	0.018	0.929
England	0.009	0.013	0.944	0.014	0.021
France	0.015	0.008	0.542	0.159	0.276
Spain	0.004	0.006	0.008	0.818	0.166
Portugal	0.004	0.006	0.009	0.97	0.011
Scotland	0.003	0.933	0.01	0.034	0.02
Germany	0.795	0.004	0.004	0.008	0.189

Table S7. STRUCTURE group membership of Gough Island with European populations set as known.

Population	Group Membership				
	1	2	3	4	5
Gough Island	0.191	0.078	0.374	0.059	0.298
Ireland	0.09	0.102	0.681	0.042	0.085
England	0.716	0.086	0.091	0.036	0.07
France	0.397	0.059	0.273	0.069	0.202
Spain	0.053	0.046	0.251	0.031	0.62
Portugal	0.062	0.045	0.073	0.028	0.793
Scotland	0.038	0.819	0.06	0.025	0.059
Germany	0.027	0.03	0.157	0.76	0.026

Table S8. Posterior distribution characteristics for model variations in the ABC analysis.

	Parameters	Priors				Posterior Distribution Characteristics							
		Distribution	Scale	min	max	mode	mean	median	q50_lower	q50_upper	q90_lower	q90_upper	
Variation1	N1 - Gough Ne	uniform	Log	2.6	4.7	19,907	12,048	13,495	6,671	24,179	2,346	41,266	
	N2 - Mainland Ne	uniform	Log	4	5.7	92,327	84,608	85,343	46,378	157,033	21,117	318,809	
	N3 - Colonization Ne	uniform	Log	0.3	4.3	898	641	680	195	2,266	35	8,674	
	T1 - Colonization Time	uniform	Log	1.6	3.7	128	221	198	98	441	51	1,349	
	T2 - Ancestral Contraction	uniform	Log			4,785	4,403	4,413	2,992	6,354	2,199	8,928	
	R - Contraction Severity	uniform	linear			0.702	0.588	0.612	0.408	0.786	0.154	0.940	
	Mitochondria Ratio	uniform	Log	0.05	0.5	0.163	0.259	0.249	0.156	0.360	0.077	0.462	
	Mitochondrial Mutation	uniform	linear	5	9	6.202	6.207	6.202	5.922	6.483	5.541	6.884	
	Microsatellite Mutation	uniform	linear	3	5	3.402	3.597	3.553	3.322	3.834	3.090	4.226	
	Nuclear Mutation L1	uniform	linear	7	10	7.754	7.863	7.829	7.528	8.161	7.196	8.628	
	Nuclear Mutation L2	uniform	linear	7	10	8.598	8.601	8.598	8.221	8.975	7.709	9.518	
Nuclear Mutation L3	uniform	linear	7	10	8.387	8.442	8.432	8.055	8.809	7.558	9.352		
Variation2	N1 - Gough Ne	uniform	Log	2.6	4.7	2,129	1,967	1,979	1,078	3,461	533	7,174	
	N2 - Mainland Ne	uniform	Log	4	5.7	82,048	87,341	87,038	47,301	163,332	21,536	344,897	
	T1 - Colonization Time	uniform	Log	1.6	3.7	1,317	859	937	420	1,851	155	3,654	
	T2 - Ancestral Contraction	uniform	Log			6,052	4,714	4,824	3,324	6,724	2,308	8,928	
	R - Contraction Severity	uniform	linear			0.632	0.549	0.557	0.353	0.746	0.139	0.930	
	Mitochondria Ratio	uniform	Log	0.05	0.5	0.156	0.268	0.263	0.163	0.369	0.082	0.464	
	Mitochondrial Mutation	uniform	linear	5	9	6.306	6.330	6.326	6.025	6.648	5.603	7.070	
	Microsatellite Mutation	uniform	linear	3	5	3.462	3.619	3.573	3.332	3.864	3.090	4.286	
	Nuclear Mutation L1	uniform	linear	7	10	7.844	7.974	7.935	7.573	8.327	7.181	8.900	
	Nuclear Mutation L2	uniform	linear	7	10	8.643	8.639	8.643	8.221	9.065	7.663	9.608	
	Nuclear Mutation L3	uniform	linear	7	10	8.342	8.396	8.387	7.965	8.824	7.422	9.397	