SUPPLEMENTARY DATA

Fig. S1. Origin of individuals from the French National Collection and scattered single founds from central and southern France.

Code-description:
SDXXX: French National Collection
Sampler: Eric Collin
Jean Thevenet
FrankreichXX: Individuals from forest canopy
Sampler: Jean Thevenet

Fig. S2. Change of the log probability between *K*-values 2–4.

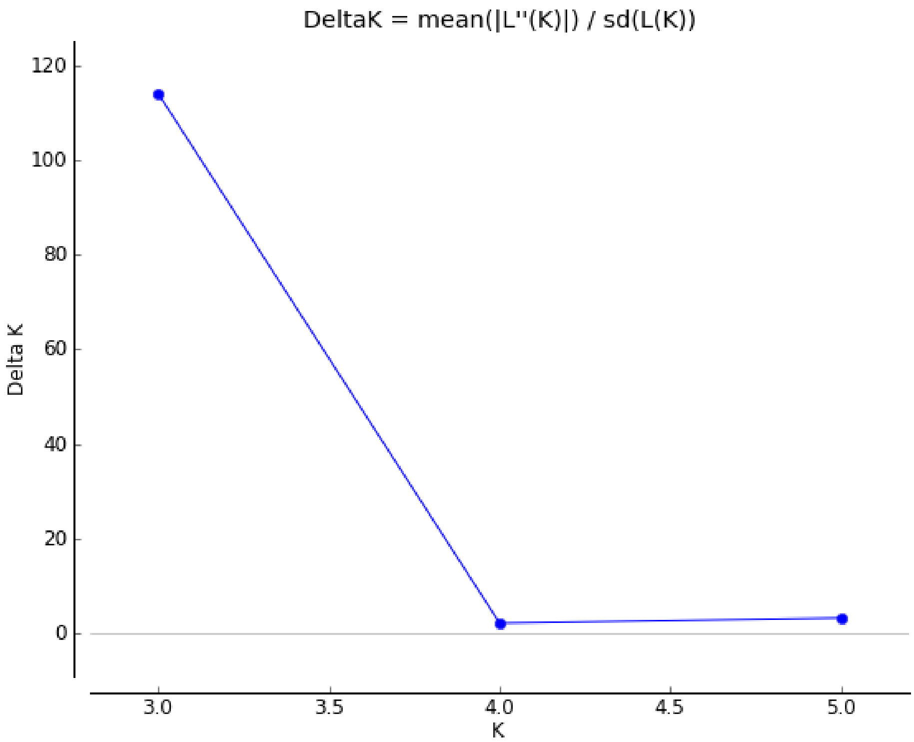

Fig. S3. Microspatial genetic structure for the population Merkenstein.

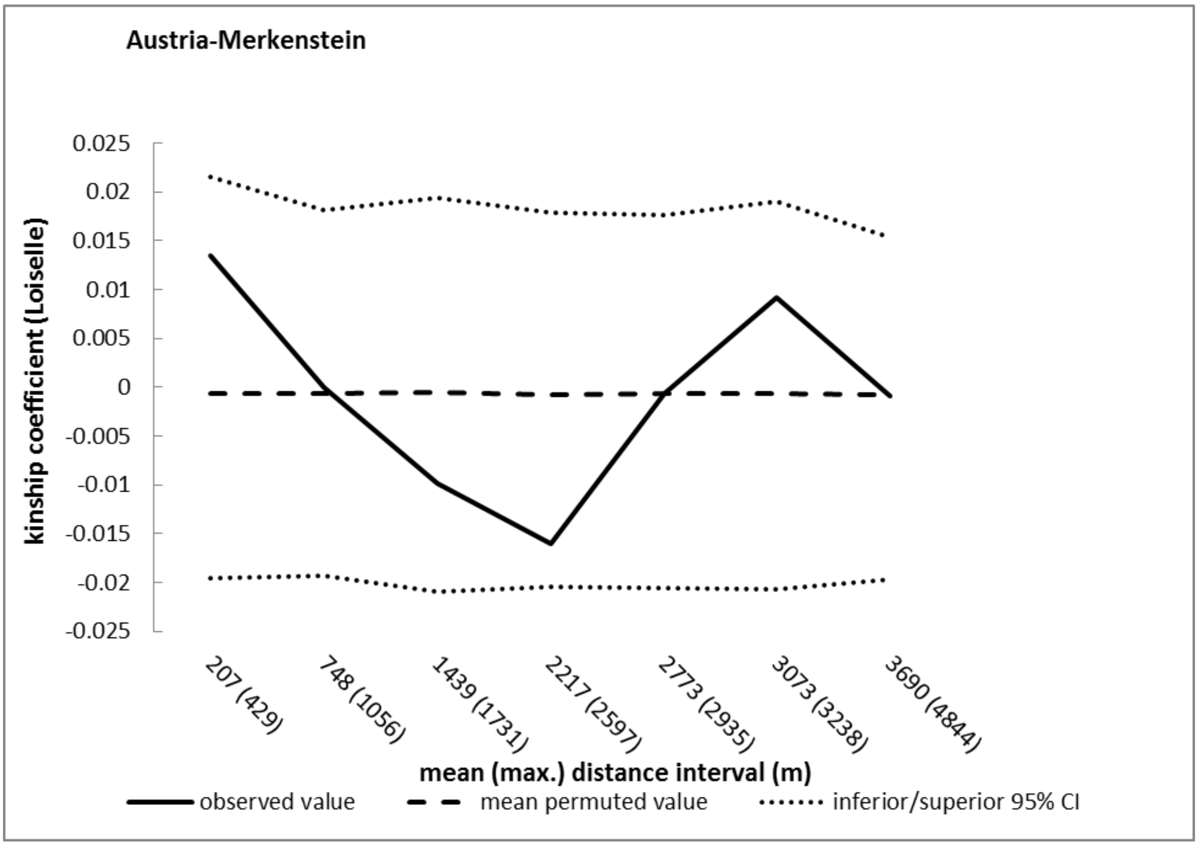

Fig. S4. Microspatial genetic structure for the population Wolkersdorf.

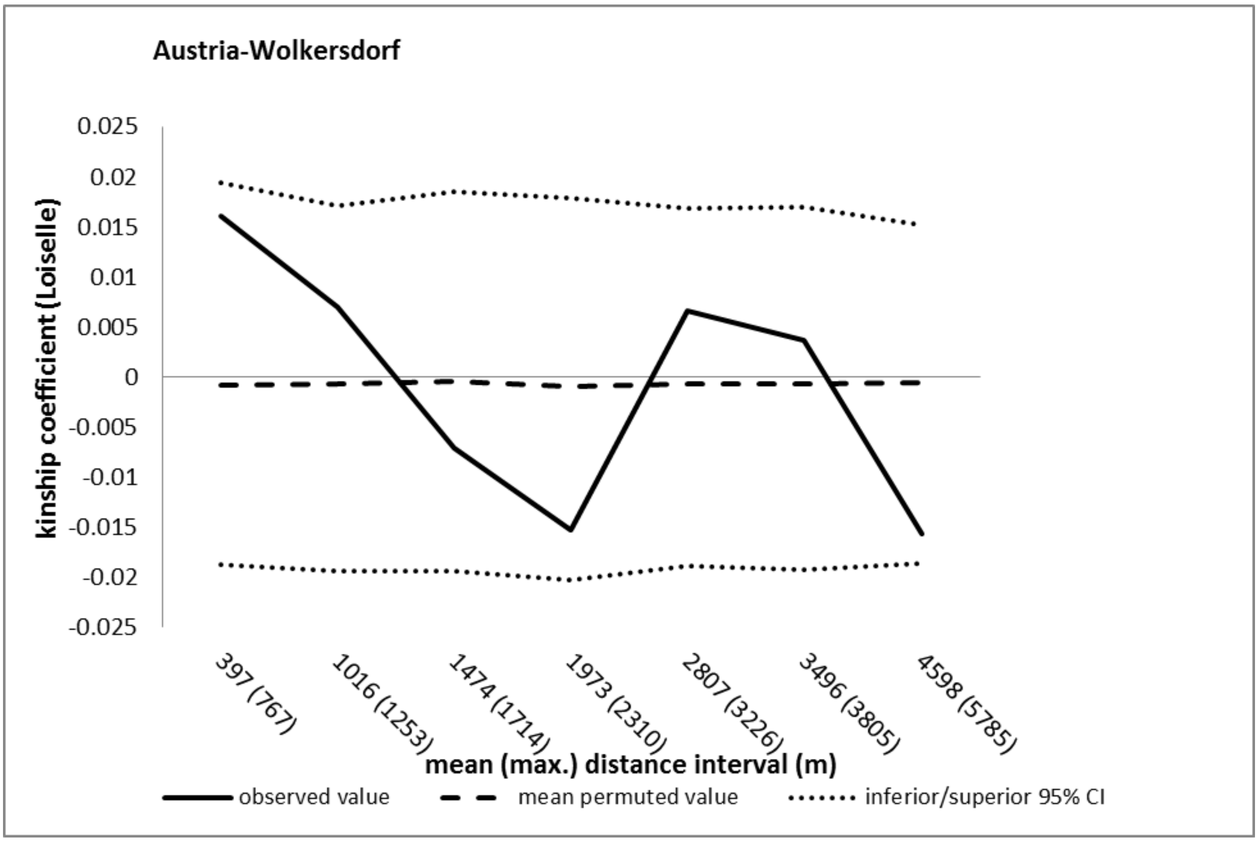

Table S1. Overview of all markers used.

locus name	genome	repeat-motif	primer sequence (F)	primer sequence (R)	T_a	size range	references
MSS5	nuclear	$(CG)_n$	CCCCAACAACATTTTTCTCC	CCTCTCGCTCTTTGCCTCT	60°	119-143	Oddou-Muratorio *et al*. (2001b) Kamm *et al*. (2009)
MSS16	nuclear	$(CG)_n$	CTCCCCTTGTGTGATGCC	TTGCCCTCAAAGAATGCC	60°	145-156	Oddou-Muratorio *et al*. (2001b) Kamm *et al*. (2009)
BGT23b	nuclear	$(CG)_n$	CACATTCAAAGATTAAGAT	ACTCAGCCTTTTTTTCCCAC	50°	191-207	Yamamoto *et al*. (2002) Kamm *et al*. (2009)
MS14h03	nuclear	$(CG)_n$	CGCTCACCTCGTAGACGT	ATGCAATGGCTAAGCATA	50°	149-209	Liebhard *et al*. (2002) Kamm *et al*. (2009)
CH02C09	nuclear	$(CG)_n$	TTATGTACCAACTTTGCTAACCTC	AGAAGCAGCAGAGGAGGATG	50°	225-249	Liebhard *et al*. (2002) Kamm *et al*. (2009)
CH01h01	nuclear	$(CG)_n$	GAAAGACTTGCAGTGGGAGC	GGAGTGGGTTTGAGAAGGTT	60°	93-149	Gianfranceschi *et al*. (1998) Kamm *et al*. (2009)
CH01h10	nuclear	$(CG)_n$	TGCAAAGAAGGTAGATATATGCCA	AGGAGGGATTGTTTGTGCAC	60°	95-135	Gianfranceschi *et al*. (1998) Kamm *et al*. (2009)
CH02d08	nuclear	$(CG)_n$	TCCAAAATGGCGTACCTCTC	GCAGACACTCACTCACTATCTCTC	50°	237-265	Liebhard *et al*. (2002) Kamm *et al*. (2009)
rps16	chloroplast	$(CATTATATTATTGATTTTAGTT)_n$	GTATCCTCATAACTCAAGTTG	TCGGGATCGAACATCAATTGCAAC	58°	200-288	Chester *et al*. (2007) Oxelmann *et al*. (1997)

T_a: annealing temperature

Table S2. AMOVA results according to groups from PCoA based on Nei's standard genetic distance

Source of variation	F_{ST}			R_{ST}		
	sum of squares	variance components	percentage variation	sum of squares	variance components	percentage variation
among groups	122.16	0.20	8.10	301663.81	439.44	5.48
among populations within groups	71.88	0.15	6.00	228870.68	470.23	5.87
within populations	1261.64	2.14	85.90	4185151.63	7105.52	88.65
total	1455.69	2.49		4715686.10	8015.19	

Table S3. AMOVA results according to groups from UPGMA based on Cavalli-Sforza and Edwards chord distance

Source of variation	F_{ST}			R_{ST}		
	sum of squares	variance components	percentage variation	sum of squares	variance components	percentage variation
among groups	95.28	0.18	7.14	97168.22	-26.72	-0.34
among populations within groups	98.76	0.18	7.12	433366.28	833.70	10.54
within populations	1261.64	2.14	85.74	4185151.61	7105.52	89.80
total	1455.69	2.50		4715686.10	7912.51	

Table S4. AMOVA results based on genetic clustering calculated with *Structure*.

Source of variation	F_{ST}			R_{ST}		
	sum of squares	variance components	percentage variation	sum of squares	variance components	percentage variation
among groups	88.03	0.16	6.29	82623.91	-60.96	-0.77
among populations within groups	106.02	0.19	7.74	447910.58	858.96	10.87
within populations	1261.64	2.14	85.97	4185151.61	7105.52	89.90
total	1455.69	2.49		4715686.10	7903.51	