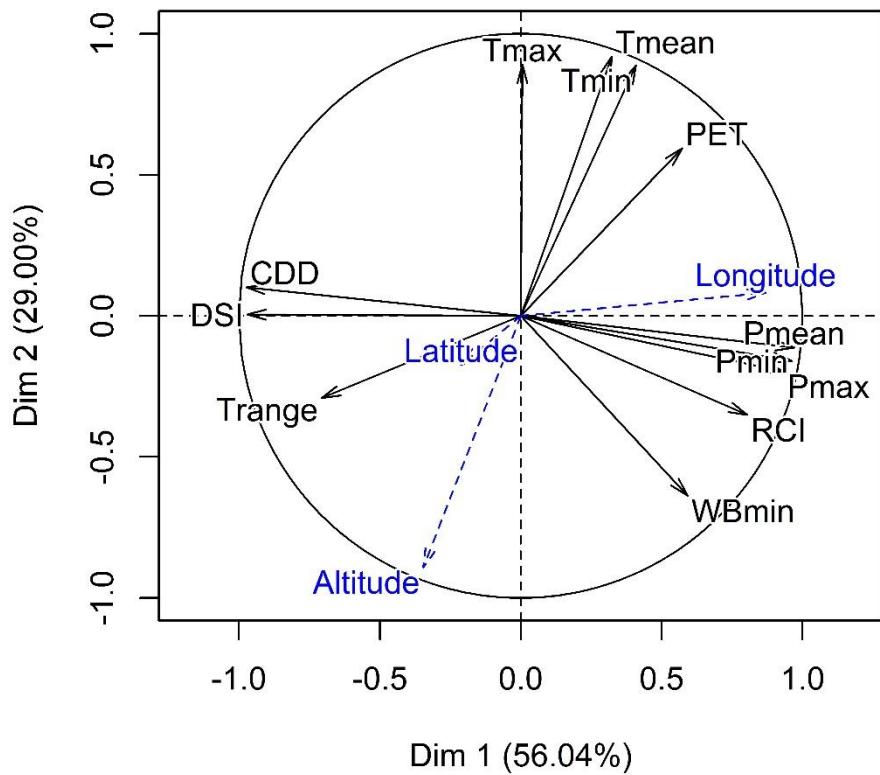
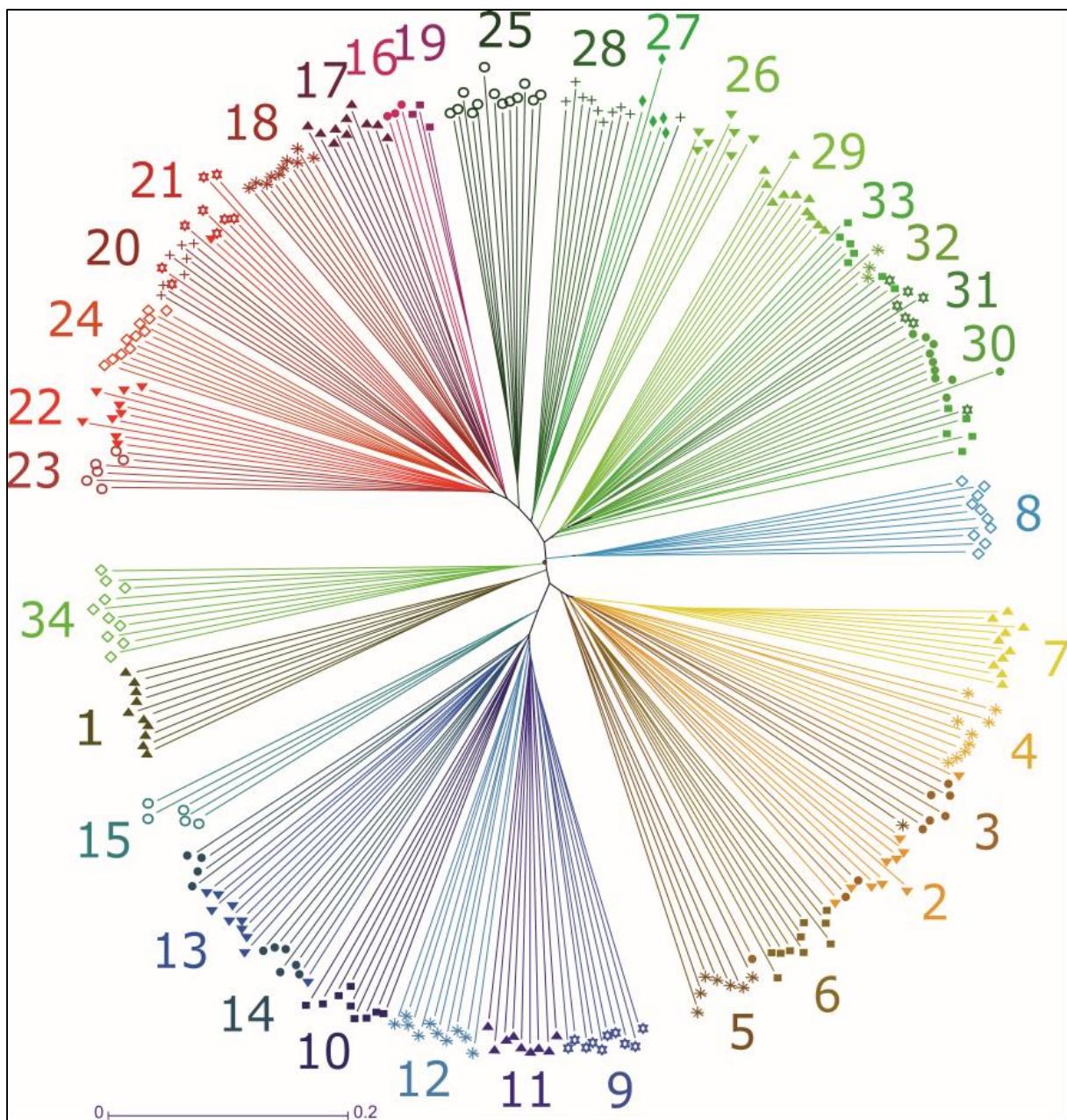


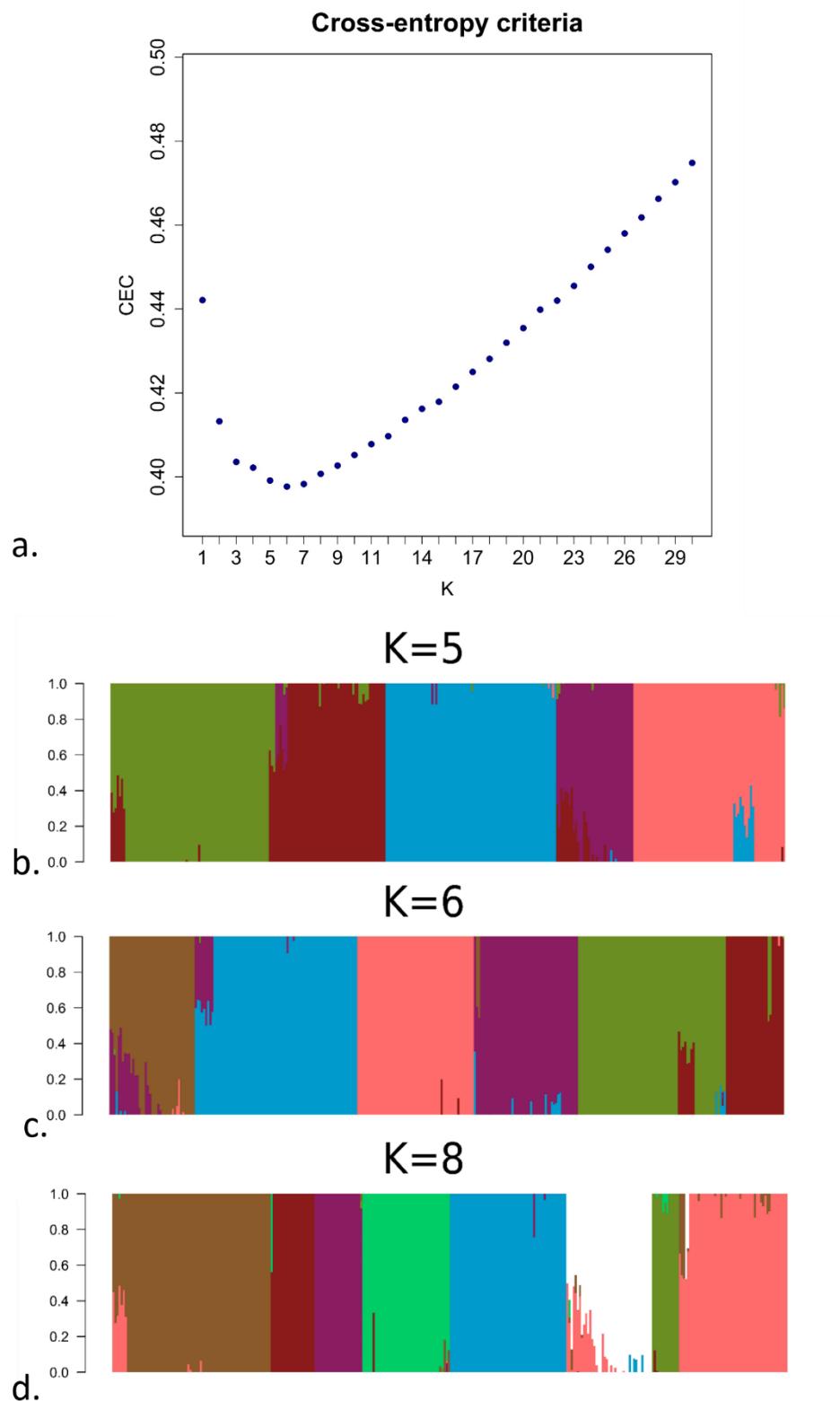
### Variables factor map (PCA)



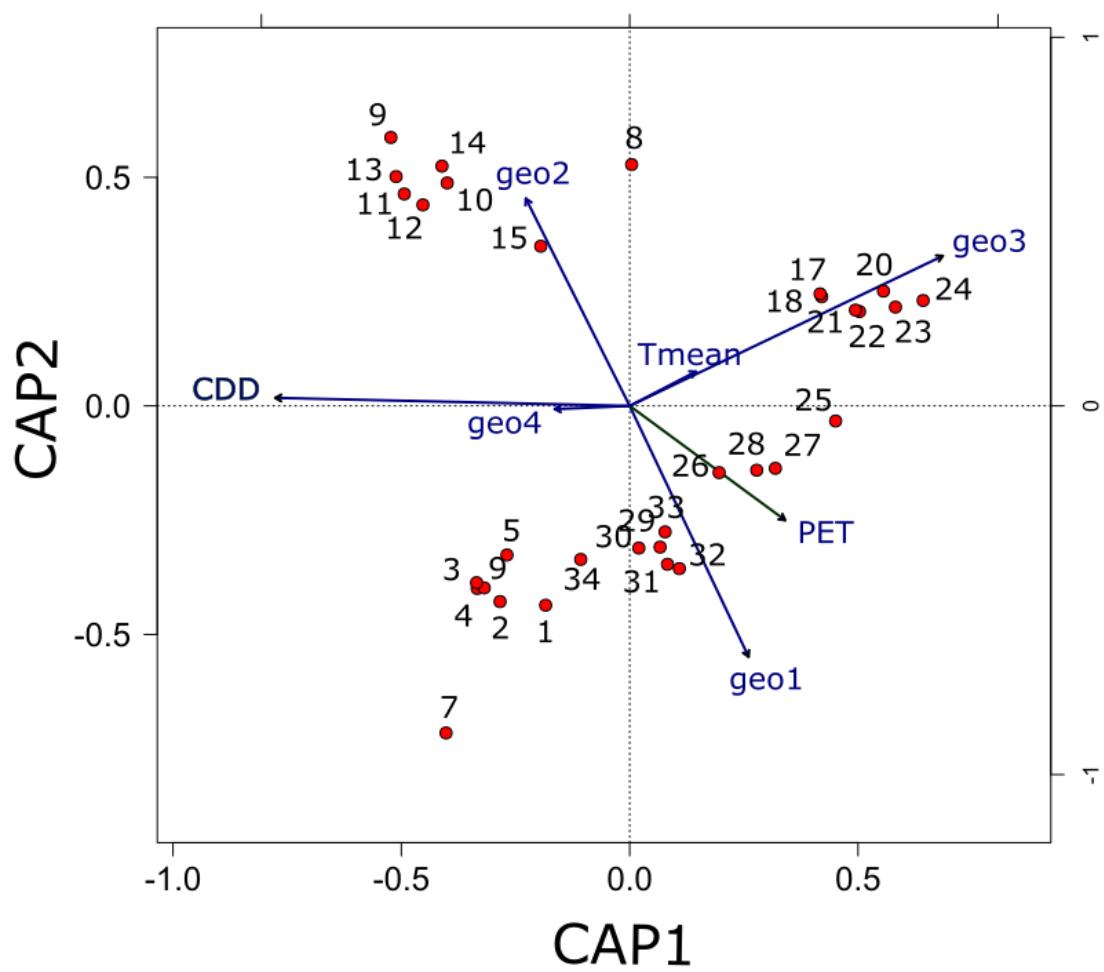
**Figure S1.** PCA results for the 12 climatic variables. Longitude, Latitude and Altitude were set as illustrative factors. Percentage of explained variance of each axis is given in parentheses.



**Figure S2.** Unweighted NJ tree based on Jaccard's distances estimated from 1860 filtered SilicoDArT markers among 296 *C. mauritiana* (individuals < 5% NA) samples originating from 34 source populations in Reunion Island. Source population codes are given in Table 1. Colors distinguish the main geographical regions of sampling.



**Figure S3.** Inference of spatial genetic structure using sNMF. **(a)** Values of cross-entropy criteria (CEC) estimated for each putative number of genetic clusters ( $K$ ). The best CEC value is displayed for each putative  $K$  value. **(b)** Group assignment at  $K=5$ . **(c)** Group assignment at  $K=6$ . **(d)** Group assignment at  $K=8$ .



**Figure S4.** Biplot of RDA analysis. Information on source populations is given in table 1. Eigenvalues for constrained axes: CAP1=34.37%; CAP2=10.09%. Tmean: average daily temperature; CDD: mean number of consecutive dry days; PET: average monthly potential evapotranspiration; geo1, geo2, geo3: uncorrelated descriptors of geographic distances

**Table S1.** Species sampled for DArTseq experiment

Species	Origin	Acc. Code*	Biogeographic group
<i>C. mauritiana</i>	Reunion Island	1 to 326	Mascarenes
<i>C. mauritiana</i>	Mauritius	RM-CF-00599	Mascarenes
<i>C. macrocarpa</i>	Mauritius	RM-CF-00615	Mascarenes
<i>C. bernardiniana</i>	Mauritius	RM-CF-00638	Mascarenes
<i>C. bernardiniana</i>	Mauritius	RM-CF-00655	Mascarenes
<i>C. bernardiniana</i>	Mauritius	MPL-B	Mascarenes
<i>C. myrtifolia</i>	Mauritius	MPL-M	Mascarenes
<i>C. myrtifolia</i>	Mauritius	RM-CF-00662	Mascarenes
<i>C. myrtifolia</i>	Mauritius	RM-CF-00658	Mascarenes
<i>C. bertrandii</i>	Madagascar	RM-CF-00515	Madagascar
<i>C. perrieri</i>	Madagascar	RM-CF-00513	Madagascar
<i>C. tsirananae</i>	Madagascar	RM-CF-00514	Madagascar
<i>C. dolichophylla</i>	Madagascar	MPL-D	Madagascar
<i>C. sessiliflora</i>	Kenya	RM-CF-00487	East Africa
<i>C. pseudozanguebariae</i>	Kenya	RM-CF-00471	East Africa
<i>C. eugeniooides</i>	Kenya	RM-CF-00422	East Africa
<i>C. canephora</i>	D.R. Congo	MPL-HD200-94	West and central Africa
<i>C. liberica</i>	Central African R.	RM-CF-00207	West and central Africa

\* Accession numbers of either the IRD *Coffea* field genebank (RM-CF, [www.intertrop.antilles.inra.fr/Portail/](http://www.intertrop.antilles.inra.fr/Portail/)) or the greenhouse collection (MPL) are given.

**Table S2.** Pearson's correlation coefficients calculated between the 12 climatic variables, elevation, longitude and latitude. Pearson's correlation coefficients are below the diagonal and p-values calculated according to Holm's method are above.

	Tmin	Tmean	Tmax	Trange	Pmin	Pmean	Pmax	RCI	CDD	DSI	PET	WBmin	Elevation	Longitude	Latitude
Tmin		<0.001	<0.001	0.03	1	1	1	1	1	1	0.005	1	<0.001	1	1
Tmean	0.98		<0.001	0.85	1	1	1	1	1	1	0.01	1	<0.001	1	1
Tmax	0.82	0.91		1	1	1	1	1	1	1	0.86	1	<0.001	1	1
Trange	-0.59	-0.43	-0.02		0.06	0.002	0.14	1	0.001	<0.001	0.14	1	0.75	0.61	<0.001
Pmin	0.24	0.17	-0.1	-0.56		<0.001	<0.001	<0.001	<0.001	<0.001	0.24	<0.001	1	1	<0.001
Pmean	0.29	0.21	-0.12	-0.67	0.92		<0.001	<0.001	<0.001	<0.001	0.45	0.03	1	1	<0.001
Pmax	0.19	0.13	-0.14	-0.53	0.89	0.97		<0.001	<0.001	<0.001	1	0.01	1	1	<0.001
RCI	0.01	-0.02	-0.16	-0.25	0.85	0.79	0.88		<0.001	<0.001	1	<0.001	1	1	0.12
CDD	-0.29	-0.2	0.12	0.68	-0.97	-0.95	-0.89	-0.76		<0.001	0.08	0.01	1	1	<0.001
DSI	-0.41	-0.31	0.02	0.74	-0.92	-0.95	-0.89	-0.71	0.95		0.23	0.03	1	1	<0.001
PET	0.65	0.63	0.43	-0.53	0.5	0.47	0.41	0.28	-0.55	-0.5		1	0.02	1	0.03
WBmin	-0.24	-0.3	-0.41	-0.15	0.71	0.6	0.63	0.74	-0.62	-0.59	-0.24		1	1	1
Elevation	-0.98	-0.99	-0.89	0.44	-0.2	-0.22	-0.14	-0.01	0.22	0.34	-0.6	0.24		1	1
Longitude	-0.18	-0.13	0.1	0.45	-0.1	-0.32	-0.22	0.09	0.22	0.23	-0.31	0.28	0.14		0.02
Latitude	0.39	0.31	-0.04	-0.75	0.8	0.89	0.8	0.54	-0.88	-0.87	0.59	0.34	-0.33	-0.6	

**Table S3.** Orthodromic distances calculated between pairs of source populations

1	0
2	9,000 0
3	6,555 3,285 0
4	9,600 2,415 3,060 0
5	16,710 9,945 10,455 7,860 0
6	17,520 9,630 11,010 8,055 2,835 0
7	16,890 9,000 12,270 10,515 14,115 11,955 0
8	26,430 18,435 21,705 19,620 20,805 18,060 9,585 0
9	29,190 21,135 24,420 22,245 22,980 20,175 12,330 2,760 0
10	35,850 27,510 30,750 28,265 27,810 24,975 18,975 9,585 6,900 0
11	35,640 27,120 30,330 27,825 26,805 23,985 18,825 9,780 7,290 1,815 0
12	34,950 26,265 29,430 26,820 25,320 22,530 18,315 9,855 7,710 3,840 2,070 0
13	39,720 31,275 34,500 32,025 30,945 28,140 22,860 13,545 10,860 3,975 4,215 5,685 0
14	40,275 32,145 35,400 33,105 32,745 29,910 23,400 13,845 11,085 4,950 6,210 8,130 3,315 0
15	35,160 28,485 31,680 30,120 32,355 29,655 19,605 11,655 10,140 11,040 12,750 14,505 13,260 10,785 0
17	30,810 25,890 28,770 27,975 32,160 29,805 18,120 14,130 14,280 18,210 19,635 20,985 21,150 19,050 8,460 0
18	29,610 25,575 28,230 27,780 32,655 30,465 18,555 16,170 16,725 21,180 22,530 23,775 24,255 22,230 11,685 3,225 0
20	19,755 18,180 20,040 20,595 27,240 25,770 14,745 18,525 20,520 26,880 27,675 28,200 30,645 29,565 20,535 13,305 11,010 0
21	20,490 20,010 21,570 22,410 29,355 28,020 17,295 21,195 23,130 29,415 30,255 30,825 33,135 31,935 22,575 14,880 12,210 2,715 0
22	20,115 21,585 22,530 23,925 31,365 30,375 20,550 25,440 27,480 33,870 34,665 35,160 37,620 36,465 27,060 19,215 16,380 6,990 4,530 0
23	20,940 23,430 24,060 25,710 33,315 32,490 23,100 28,260 30,330 36,705 37,515 37,995 40,455 39,270 29,775 21,795 18,870 9,840 7,350 2,850 0
24	13,140 13,515 14,565 15,855 23,325 22,455 13,695 20,655 23,130 29,955 30,390 30,465 33,900 33,405 25,650 19,410 17,520 6,810 7,380 8,085 10,050 0
25	21,795 30,615 28,335 31,380 38,115 39,240 37,080 45,930 48,600 55,500 55,650 55,335 59,460 59,340 51,870 45,135 42,720 31,830 30,570 26,895 25,170 26,250 0
26	18,120 27,090 24,570 27,630 34,050 35,325 34,155 43,305 46,020 52,890 52,905 52,455 56,835 56,925 50,070 43,815 41,625 30,630 29,730 26,535 25,230 24,510 4,605 0
27	17,055 25,965 23,565 26,625 33,255 34,425 32,790 41,865 44,565 51,450 51,510 51,090 55,395 55,440 48,450 42,120 39,915 28,935 27,990 24,780 23,490 22,860 4,890 1,755 0
28	14,430 23,310 20,955 24,000 30,735 31,845 30,165 39,270 41,985 48,855 48,885 48,465 52,800 52,890 46,050 39,885 37,770 26,775 25,995 23,025 21,960 20,550 7,410 4,050 2,670 0
29	10,065 19,035 16,530 19,590 26,205 27,360 26,325 35,640 38,385 45,195 45,135 44,610 49,125 49,395 43,125 37,500 35,655 24,765 24,405 22,125 21,615 18,150 11,925 8,070 7,080 4,545 0
30	9,435 18,420 15,765 18,810 25,185 26,445 26,055 35,460 38,220 44,985 44,865 44,265 48,900 49,260 43,290 37,905 36,165 25,365 25,155 23,085 22,710 18,645 13,005 8,895 8,130 5,760 1,545 0
31	7,590 16,575 13,920 16,965 23,400 24,630 24,285 33,720 36,480 43,230 43,080 42,465 47,130 47,535 41,730 36,540 34,875 24,195 24,150 22,365 22,215 17,415 14,730 10,710 9,870 7,380 2,865 1,860 0
32	6,990 15,975 13,335 16,380 22,890 24,075 23,670 33,120 35,880 42,630 42,480 41,865 46,530 46,935 41,160 36,015 34,380 23,730 23,730 22,020 21,945 16,950 15,240 11,265 10,380 7,860 3,330 2,445 615 0
33	7,260 16,185 13,440 16,470 22,770 24,060 24,075 33,555 36,315 43,035 42,855 42,195 46,920 47,370 41,745 36,690 35,100 24,495 24,540 22,875 22,800 17,700 15,405 11,295 10,530 8,100 3,615 2,415 840 870 0
34	7,725 14,550 11,295 13,890 18,540 20,370 23,400 32,925 35,655 42,045 41,610 40,680 45,795 46,680 42,390 38,445 37,320 27,420 28,020 27,180 27,600 20,730 20,835 16,365 16,020 13,905 9,705 8,250 7,095 6,930 6,270 0
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34

**Table S4.** Pairwise  $F_{ST}$  of Weir and Cockerham calculated between 32 source populations of *C. mauritiana*. Population codes are given in Table 1.

	1	2	3	4	5	6	7	17	18	20	21	22	23	24	8	9	10	11	12	13	14	15	29	30	31	32	33	34	26	25	27	28	
	W	W	W	W	W	W	W	NE	NE	E	E	E	E	E	C	NW	SW	SW	SW	SW	SW	SE/	SE	SE	SE								
W	1	0.00																															
W	2	0.08	0.00																														
W	3	0.07	0.03	0.00																													
W	4	0.08	0.04	0.03	0.00																												
W	5	0.07	0.07	0.05	0.05	0.00																											
W	6	0.09	0.08	0.07	0.06	0.05	0.00																										
W	7	0.17	0.13	0.13	0.12	0.14	0.15	0.00																									
NE	17	0.21	0.24	0.24	0.25	0.22	0.24	0.30	0.00																								
NE	18	0.21	0.25	0.24	0.24	0.22	0.24	0.31	0.03	0.00																							
E	20	0.25	0.28	0.28	0.26	0.27	0.33	0.07	0.08	0.00																							
E	21	0.23	0.26	0.26	0.24	0.25	0.31	0.05	0.06	0.03	0.00																						
E	22	0.23	0.26	0.26	0.24	0.25	0.32	0.06	0.06	0.05	0.03	0.00																					
E	23	0.25	0.28	0.28	0.26	0.28	0.34	0.08	0.08	0.07	0.04	0.02	0.00																				
E	24	0.27	0.30	0.30	0.28	0.30	0.36	0.10	0.11	0.08	0.06	0.06	0.07	0.00																			
C	8	0.17	0.18	0.17	0.18	0.16	0.18	0.24	0.13	0.13	0.16	0.15	0.15	0.17	0.20	0.00																	
NW	9	0.20	0.19	0.17	0.18	0.18	0.19	0.26	0.29	0.29	0.32	0.31	0.31	0.33	0.35	0.15	0.00																
NW	10	0.17	0.16	0.15	0.15	0.17	0.24	0.25	0.25	0.29	0.27	0.27	0.29	0.31	0.14	0.09	0.00																
NW	11	0.17	0.16	0.14	0.15	0.14	0.17	0.23	0.27	0.27	0.31	0.29	0.29	0.31	0.34	0.14	0.05	0.05	0.00														
NW	12	0.17	0.16	0.14	0.15	0.14	0.17	0.23	0.26	0.26	0.30	0.28	0.28	0.30	0.32	0.15	0.08	0.07	0.04	0.00													
NW	13	0.18	0.17	0.16	0.16	0.15	0.18	0.24	0.28	0.28	0.32	0.30	0.30	0.32	0.34	0.16	0.09	0.07	0.04	0.06	0.00												
NW	14	0.18	0.16	0.15	0.16	0.15	0.17	0.24	0.25	0.26	0.29	0.27	0.27	0.29	0.32	0.14	0.10	0.06	0.05	0.07	0.04	0.00											
NW	15	0.14	0.15	0.13	0.14	0.13	0.15	0.23	0.19	0.19	0.23	0.21	0.21	0.23	0.26	0.12	0.14	0.10	0.11	0.11	0.10	0.09	0.00										
SW	29	0.10	0.14	0.13	0.13	0.11	0.14	0.21	0.15	0.15	0.18	0.16	0.16	0.18	0.20	0.15	0.22	0.19	0.20	0.20	0.21	0.20	0.15	0.00									
SW	30	0.09	0.13	0.12	0.12	0.10	0.13	0.21	0.16	0.16	0.19	0.17	0.17	0.19	0.22	0.15	0.22	0.19	0.19	0.19	0.20	0.19	0.14	0.03	0.00								
SW	31	0.11	0.16	0.14	0.15	0.13	0.15	0.23	0.16	0.16	0.19	0.17	0.17	0.18	0.21	0.16	0.24	0.20	0.21	0.21	0.23	0.21	0.16	0.04	0.04	0.00							
SW	32	0.10	0.16	0.15	0.15	0.13	0.15	0.24	0.15	0.15	0.18	0.16	0.16	0.18	0.20	0.15	0.24	0.21	0.22	0.21	0.24	0.22	0.16	0.04	0.04	0.04	0.00						
SW	33	0.09	0.14	0.13	0.13	0.11	0.13	0.21	0.14	0.14	0.17	0.15	0.15	0.17	0.19	0.14	0.22	0.19	0.20	0.19	0.21	0.20	0.14	0.03	0.03	0.02	0.01	0.00					
SW	34	0.08	0.11	0.09	0.10	0.07	0.11	0.19	0.19	0.19	0.23	0.21	0.20	0.23	0.25	0.16	0.20	0.17	0.17	0.17	0.18	0.17	0.14	0.07	0.07	0.08	0.08	0.06	0.00				
SE/SW	26	0.14	0.18	0.17	0.17	0.15	0.17	0.25	0.13	0.12	0.15	0.13	0.12	0.14	0.17	0.15	0.25	0.21	0.22	0.22	0.23	0.21	0.16	0.08	0.08	0.09	0.09	0.07	0.11	0.00			
SE	25	0.21	0.25	0.24	0.25	0.23	0.24	0.31	0.10	0.11	0.12	0.09	0.08	0.08	0.12	0.18	0.31	0.27	0.29	0.28	0.30	0.27	0.21	0.15	0.15	0.15	0.15	0.13	0.19	0.09	0.00		
SE	27	0.17	0.21	0.21	0.21	0.19	0.21	0.28	0.12	0.13	0.14	0.11	0.11	0.12	0.15	0.17	0.28	0.24	0.26	0.25	0.27	0.24	0.19	0.09	0.11	0.11	0.09	0.14	0.06	0.09	0.00		
SE	28	0.15	0.19	0.18	0.19	0.17	0.18	0.26	0.10	0.10	0.12	0.10	0.09	0.10	0.13	0.14	0.26	0.22	0.24	0.23	0.25	0.23	0.17	0.07	0.09	0.08	0.08	0.07	0.12	0.05	0.07	0.04	0.00

**Table S5.** Results from *f3-statistic* tests among the seven clusters defined by sNMF analysis. Only negative Z-score are shown. According to Reich *et al.* (2009), results were considered as significant when Z-score < -2. Admixt population = population tested for admixture between parent 1 and 2.

Admixt population	Parent 1	Parent 2	f3-statistic	s.e.	Z-score
SW	W	NE	-0.00109	0.000615	-1.77402
SW	W	SE	-0.00132	0.0004	<b>-3.28951</b>
SW	NW	SE	-7.35E-05	0.000497	-0.14774
SW	W	E	-0.00196	0.000659	<b>-2.98648</b>
SE	W	E	-0.00127	0.000599	<b>-2.12336</b>
SE	E	SW	-0.00063	0.000414	-1.51478
C	NE	NW	-0.00165	0.000845	-1.94858
C	NW	E	-0.00164	0.000948	-1.73423