

Table S1. Mitochondrial DNA haplotype frequencies of the green turtles captured during 1997–1999 in the foraging ground around the Yaeyama Islands.

Haplotype	1997–1999
CmP1	6
CmP18	1
CmP20	30
CmP22	2
CmP32	14
CmP39	19
CmP49	5
CmP50	16
CmP53	2
CmP54	2
CmP57	5
CmP61	6
CmP67	1
CmP70	1
CmP77	3
CmP91	1
CmP121	2
CmP123	1
CmP126	2
CmP127	2
CmP128	2

Table S2. The contribution of each nesting population as estimated by MSA using mitochondrial DNA haplotypes. The numbers in brackets represent the 95% credible intervals.

	1997–1999	2016–2018
Population	Total	Total
Ogasawara	0.21 (0.10–0.36)	0.22 (0.07–0.43)
Central Ryukyus	0.19 (0.05–0.32)	0.21 (0.00–0.40)
Yaeyama	0.01 (0.00–0.05)	0.08 (0.00–0.21)
Taiwan	0.01 (0.00–0.05)	< 0.01 (0.00–0.01)
Eastern Borneo	0.04 (0.00–0.12)	< 0.01 (0.00–0.01)
Sipadan	0.01 (0.00–0.08)	< 0.01 (0.00–0.02)
Turtle Island Park	0.02 (0.00–0.08)	< 0.01 (0.00–0.01)
Sarawak	< 0.01 (0.00–0.01)	0.01 (0.00–0.06)
Penang & Perak	< 0.01 (0.00–0.02)	0.01 (0.00–0.07)
Vietnam	< 0.01 (0.00–0.02)	0.01 (0.00–0.07)
Perhentian	< 0.01 (0.00–0.02)	0.02 (0.00–0.13)
Redang	< 0.01 (0.00–0.02)	0.02 (0.00–0.11)
Terengganu	< 0.01 (0.00–0.02)	0.01 (0.00–0.08)
Penang	< 0.01 (0.00–0.02)	0.01 (0.00–0.06)
Mersing	< 0.01 (0.00–0.02)	< 0.01 (0.00–0.01)
Palau	< 0.01 (0.00–0.03)	0.04 (0.00–0.25)
Micronesia	0.39 (0.24–0.51)	0.23 (0.09–0.40)
CNMI/GUAM	< 0.01 (0.00–0.03)	0.05 (0.00–0.26)
Marshall Islands	0.06 (0.00–0.19)	0.01 (0.00–0.09)
Northern New Guinea	< 0.01 (0.00–0.03)	0.07 (0.00–0.30)
NW Hawaii	0.05 (0.02–0.09)	0.01 (0.00–0.03)

Table S3. The results of regional analysis using MSA. The numbers in brackets represent the 95% credible intervals.

	1997–1999 MSA	2016–2018 MSA
	Total	Total
Western Pacific	0.54 (0.45–0.63)	0.48 (0.37–0.59)
Ryukyus	0.20 (0.05–0.33)	0.29 (0.08–0.48)
Ogasawara	0.21 (0.10–0.36)	0.22 (0.07–0.44)
NW Hawaii	0.05 (0.02–0.09)	0.01 (0.00–0.03)

Table S4. Results of regional contributions calculated based on 103 individuals whose natal origins were estimated based on 1,676 single-nucleotide polymorphisms (SNPs) and one individual whose mitochondrial DNA was estimated to be from northwestern (NW) Hawaii.

	Total	< 55 cm SCL	55 > cm SCL
Western Pacific	0.41	0.50	0.29
Ryukyus	0.32	0.27	0.38
Ogasawara	0.26	0.23	0.31
NW Hawaii	0.01	0.00	0.02

Foraging turtles collected in 2016–2018 : n = 104

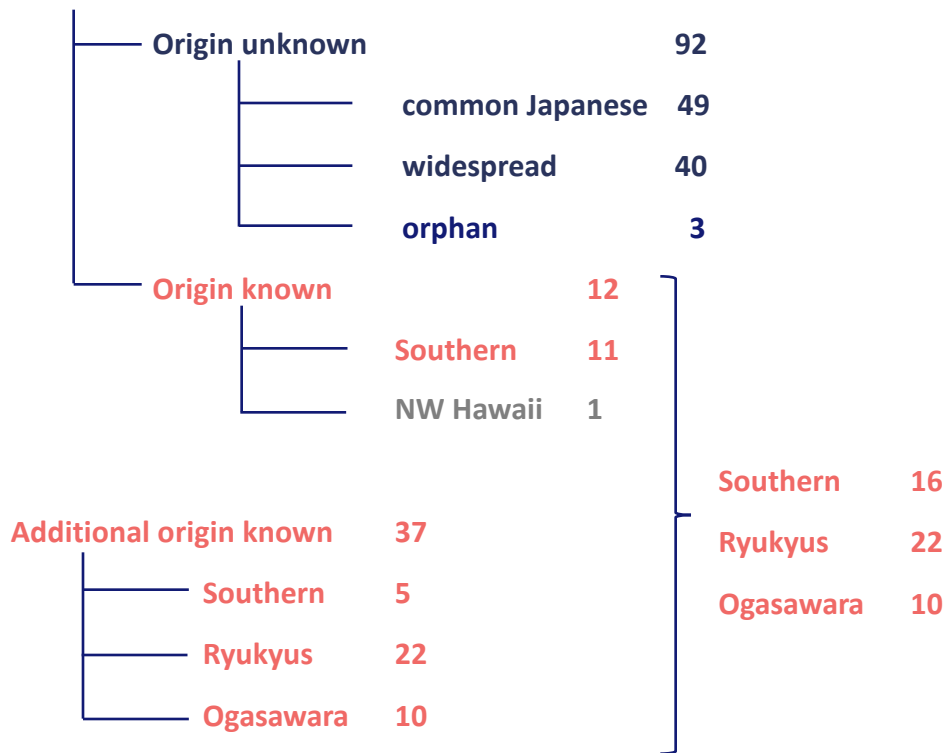


Figure S1. Breakdown of the number of samples sequenced via MIG-seq in this study and the category as which they were used. One sample for which the natal origin was probably NW Hawaii (with haplotype CmP2.1) was excluded from the analyses.

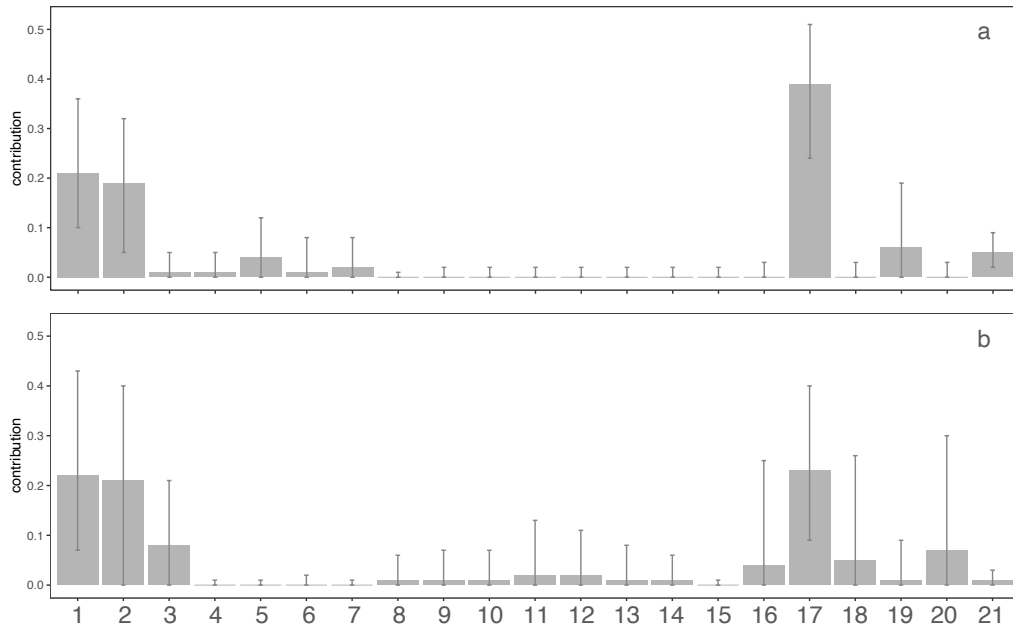


Figure S2. The mixed-stock analysis results estimated the contribution of the 21 distinct populations using the total samples collected in 1997 – 1999 (a) and 2016 – 2018 (b). Error bars represent 95 % credible intervals. Populations include: 1 Ogasawara, 2 Central Ryukyus, 3 Yaeyama, 4 Taiwan, 5 Eastern Borneo, 6 Sipadan, 7 Turtle Island Park, 8 Sarawak, 9 Penang and Perak, 10 Vietnam, 11 Perhentian, 12 Redang, 13 Terengganu, 14 Pehang, 15 Mersing, 16 Palau, 17 Micronesia, 18 CNMI/Guam, 19 Marshall Islands, 20 Northern New Guinea, and 21 Northwestern Hawaii.

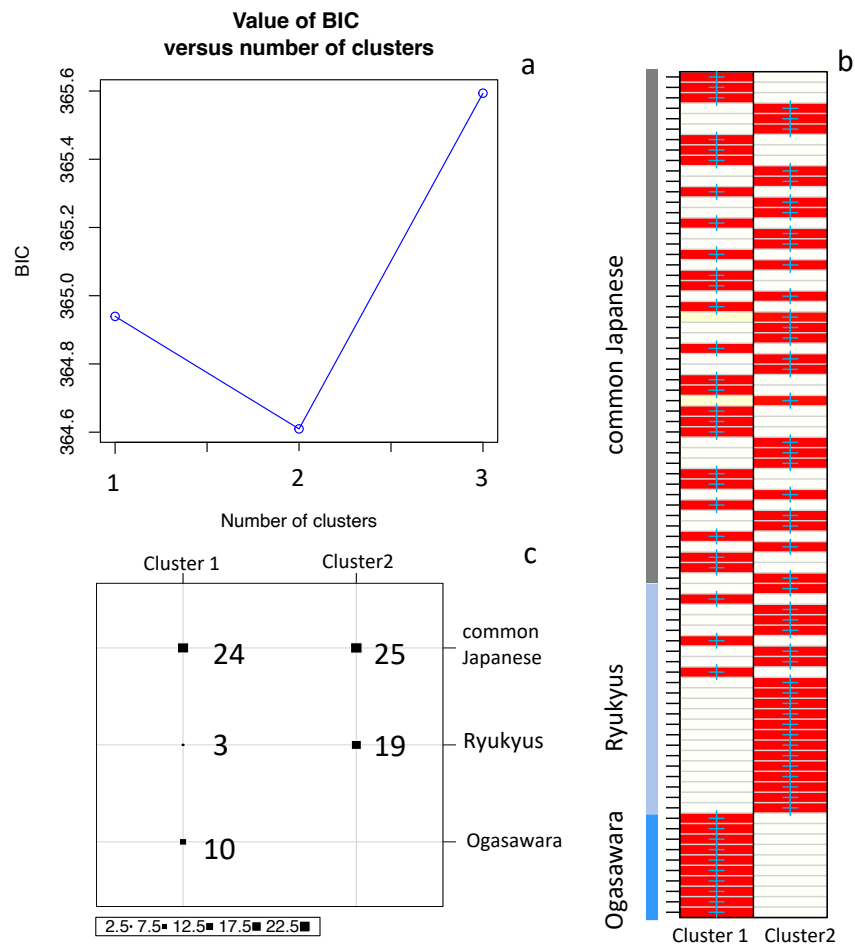


Figure S3. Values of the Bayesian Information Criterion (BIC) for k-means ($k = 1-3$) with 23 PCs and 49 individuals with common Japanese haplotypes and 32 individuals with a known origin (Ryukyus and Ogasawara) based on 1,676 single-nucleotide polymorphisms (SNPs) (a), the group assignment (b), and the table showing the number of individuals clustered with each cluster (c), respectively. Heatmap colors in the group assignment represent membership probabilities (red = 1, white = 0); blue crosses represent the prior cluster provided by the *find.clusters* function. Blue crosses on red rectangles show that the individuals successfully reassigned to the prior clusters based on the discriminant functions.

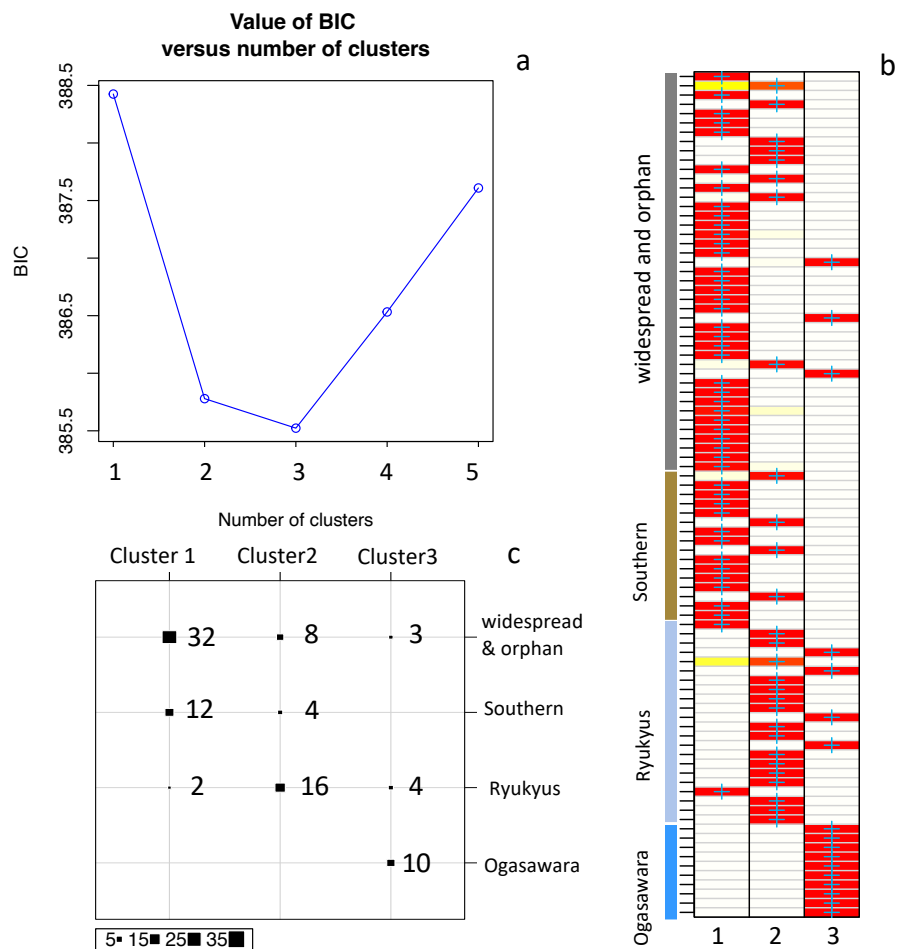


Figure S4. Values of the Bayesian Information Criterion (BIC) for k-means ($k = 1-5$) with 19 PCs and 40 individuals with widespread haplotypes and 3 individuals with orphan haplotypes and 48 individuals with a known origin (Southern, Ryukyus and Ogasawara) based on 1,676 single-nucleotide polymorphisms (SNPs) (a), the group assignment (b), and the table showing the number of individuals clustered with each cluster (c), respectively. Heatmap colors in the group assignment represent membership probabilities (red = 1, white = 0); blue crosses represent the prior cluster provided by the *find.clusters* function. Blue crosses on red rectangles show that the individuals successfully reassigned to the prior clusters based on the discriminant functions.

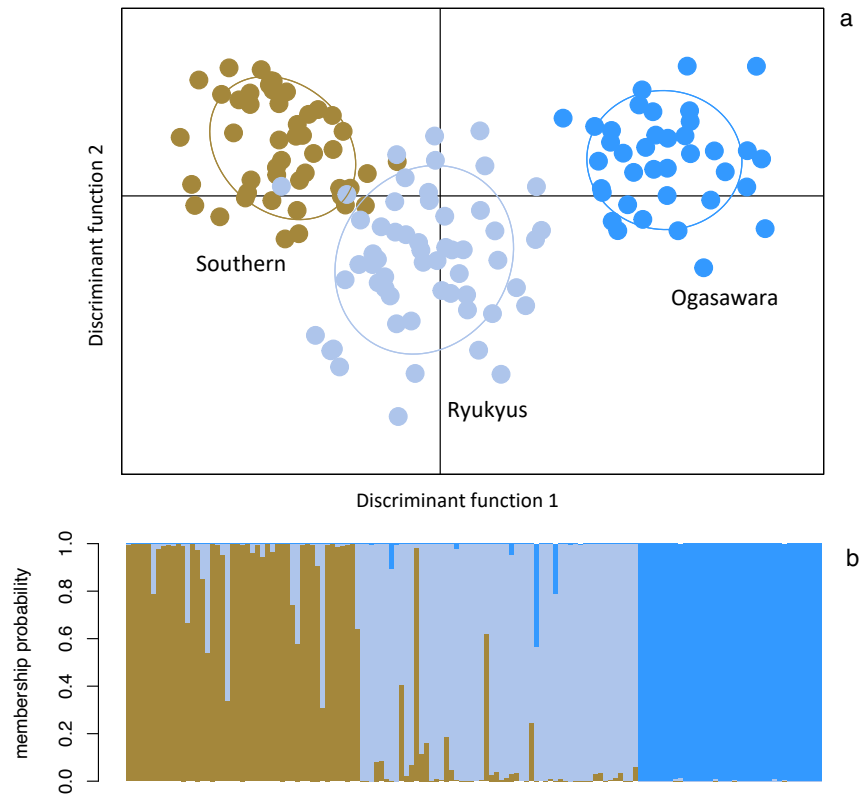


Figure S5. Scatterplot showing the structure patterns based on the results of group assignments of all 140 samples (a) and compo plot showing the admixed pattern of each individual (b). Both structures were generated from a discriminant analysis of principal components (DAPC) based on the three regional nesting groups and 1,676 single-nucleotide polymorphisms (SNPs).