

Supplementary Material

Table S1 Sample distribution across populations. FI = Flat Island, RI = Round Island, IAF = Ile aux Fouquets, IV = Ilot Vacoas, and IDLP = Ile de la Passe. For each population, the number of samples (n) are subdivided according to sampling year and we include the proportion of those samples successfully genotyped at 9 or 14 microsatellite loci or sequenced for mitochondrial cytochrome *b* gene

Island	Year	n	Microsatellites		mtDNA
			9 loci	14 loci	
FI	2009	25	-	25	5
RI	2009	37	-	37	6
IAF	2008	9	7	-	1
	2009	9	9	-	1
	2015	32	32	-	8
IV	2014	35	32	-	4
IDLP	2009	9	9	-	7
	2014	36	30	-	8
	2016	62	-	61	11

Table S2 Groups of microsatellite primers used for amplification and genotyping of samples

Multiplex	Loci	Forward primer sequence 5' to 3'	Reverse primer sequence 5' to 3'	Repeat motif	Characterised by
GongA	Gong2	CACTGTCTCAGAGCACCTGG	GATCCACAGGTACATACTAACTAGGAC	(GT) ₁₂ (GA) ₁₈	Dawson, D. and Freeman, K.
	Gong3	AGAAGAGCAAGCCAGCAAAG	GTTTGATCGCCCAAGTACAGCAT	(CT) ₂₅ (C) ₁₂	Dawson, D. and Freeman, K.
	Gong16	AAGGAGGCGATGCAGGTGAG	GTTTCTTTTCCCATCAAATGGTGGTGC	(GA) ₂₃	Dawson, D. and Freeman, K.
	Gong18	CCCAGTGGGAGCTTCAATGC	GTTTCTTTATGTGCTTGGCATAACGGGC	(GT) ₁₀ (GA) ₂₈	Dawson, D. and Freeman, K.
GongB	Gong15	TTCACACACTTTTAGTCCCTAATTTACA	CAAATTTCTAATTTAACCCTCTTCCA	(GA) ₂₄	Dawson, D. and Freeman, K.
	Gong22	TGATGCGGGTTCAAATGGAG	GTTTCAGCAGGGCTTTTCTTACATGTTC	(TTTC) ₂₅	Dawson, D. and Freeman, K.
GBC	GB01	GGTGTGACCAAACCCTAAGAACC	TGGCAAAAAGCAATGGAGC	(AAAG) ₁₇	Austin, J.
	GB03	CATCAATGTCAACAAGGAACTGGC	TGCTATCTACCAAAGTGGCTGCTG	(AAAG) ₁₇	Austin, J.
	GB04	GCCCAAGCACCAGAATAGTGC	CCCTCAAGCCTCAAACCACAG	(AAAG) ₁₇	Austin, J.
	GB06	ATTAGGGCTCTGTTACAAGCAG	CCACAGGTACATACTAACTAGGACC	(GT) ₁₂ (GA) ₁₈	Freeman, K.
GBD	GB08	TCACCTGTCCCTTTTCTGTGG	ATACTATCCCCATCATTGGC	(CA) ₁₀	Freeman, K.
	GB12	GGTGGTTACAGGCAGGTTTTAGG	TTCCCATCAAATGGTGGTGC	(GA) ₂₃	Freeman, K.
	GB14	CGGGTTCAAATGGAGAATAGTTC	GATCCAGCAGGGCTTTTCTTAC	(TTTC) ₂₅	Freeman, K.
	GB15	TGCTGCTGTTGCTGCCTTG	TTTGAGTACCTGCCTGTAAGCC	(CT) ₂₂	Freeman, K.

Table S3 Sample collection localities and ID codes for samples successfully genotyped at microsatellite loci and sequenced for mitochondrial cytochrome *b* gene. FI = Flat Island, RI = Round Island, IAF = Ile aux Fouquets, IV = Ilot Vacoas, and IDLP = Ile de la Passe

FI	RI	IAF	IV	IDLP 2009	IDLP 2014	IDLP 2016
E41	E08	GB246	GB174	GB07	GB227	S02
E49	E09	GB253	GB175	GB09	GB228	S03
E51	E10	GB255	GB176	GB11	GB229	S15
E55	E11	GB257	GB180	GB13	GB231	S16
E56	E12	GB258		GB17	GB232	S18
	E15	GB260		GB29	GB233	S30
		GB261		GB33	GB234	S43
		GB264			GB235	S49
		IF21				S51
		IF117				S61
						S62

Table S4 Msva input parameters. N_0 = current effective population size, N_1 = ancestral effective population size, t = time since demographic change in years, and π = mutation rate. Priors and hyperpriors for the three runs were the same for all analysed clusters. Values given are the mean followed by the variance as log10 values. For all hyperpriors, the variances around the mean and variance were 0 and 0.5 respectively, except π which were 0 and 2

Run	Priors				Hyperpriors			
	N_0	N_1	t	π	N_0	N_1	t	π
1	4 (2)	5 (2)	2 (2)	-4 (1)	4 (3)	5 (3)	2 (3)	-4 (0.5)
2	5 (2)	4 (2)	2 (2)	-4 (1)	5 (3)	4 (3)	2 (3)	-4 (0.5)
3	4 (2)	4 (2)	2 (2)	-4 (1)	4 (3)	4 (3)	2 (3)	-4 (0.5)

Table S5 Bojer's skink samples, collection localities and GenBank Accession numbers for selected samples from Austin *et al.* (2009) downloaded from GenBank. Samples representing extinct populations are denoted by an asterisk

Sample name	Collection locality	Accession Number
FJ790966.1	Flat Island	FJ790966
FJ790969.1	Flat Island	FJ790969
FJ790965.1	Gabriel Island	FJ790965
FJ790968.1	Gabriel Island	FJ790968
FJ790967.1	Gunner's Quoin	FJ790967
FJ790962.1	Gunner's Quoin	FJ790962
FJ790980.1*	Ile aux Fouquets	FJ790980
FJ790982.1*	Ile aux Fouquets	FJ790982
FJ790972.1	Ilot Vacoas	FJ790972
FJ790973.1	Ilot Vacaos	FJ790973
FJ790978.1	Pigeon House Rock	FJ790978
FJ790974.1	Round Island	FJ790974
FJ790977.1	Round Island	FJ790977
FJ790964.1	Serpent Island	FJ790964
FJ790970.1	Serpent Island	FJ790970

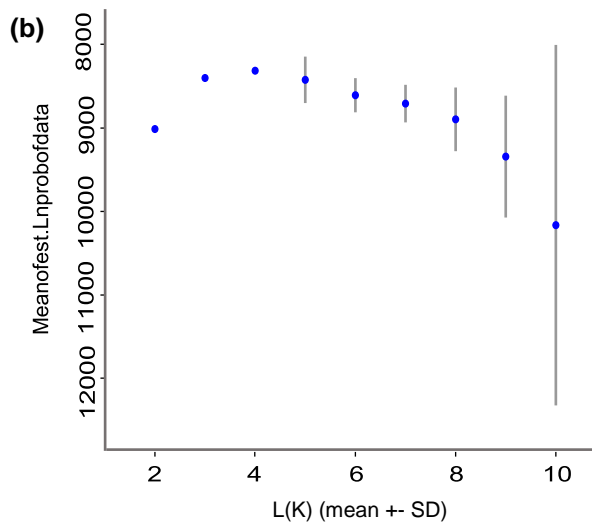
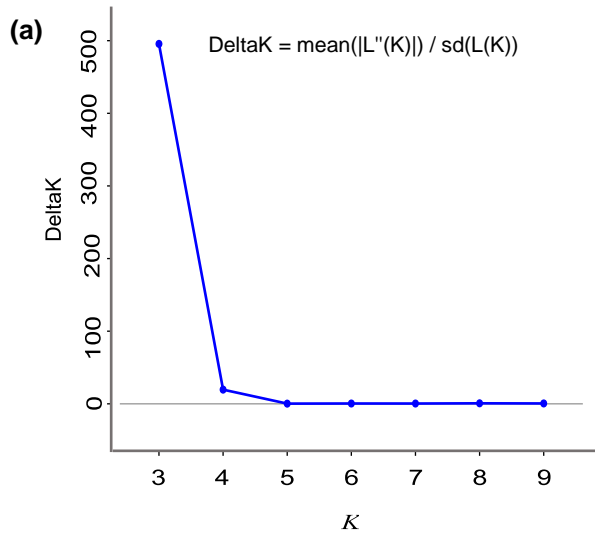


Fig. S1 Plots to identify the optimal value of K . (a) the highest values of Delta K (ΔK) and (b) mean log likelihood (Mean $\text{LnP}(K)$) suggest $K = 3$ or $K = 4$, respectively, are most likely. Plots were produced using Structure Harvester

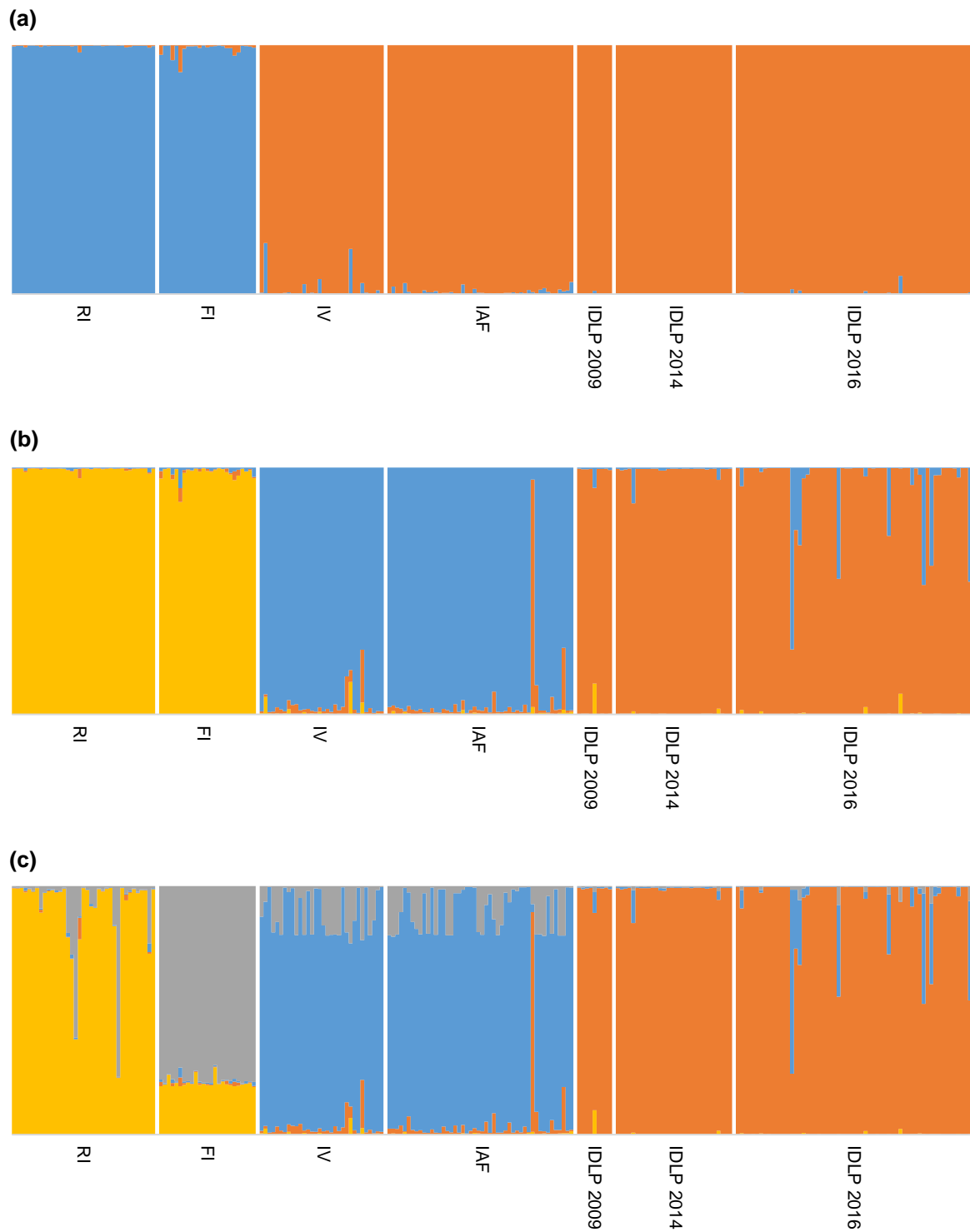


Fig. S2 Comparison of population clustering predicted by STRUCTURE at (a) $K = 2$, (b) $K = 3$, and (c) $K = 4$. Vertical bars represent individual genotypes, divided proportionately into coloured assignment probabilities to each cluster. White bars separate populations: FI = Flat Island, RI = Round Island, IAF = Ile aux Fouquets, IV = Ilot Vacoas, and IDLP = Ile de la Passe. Samples from IDLP are further split by year sampled

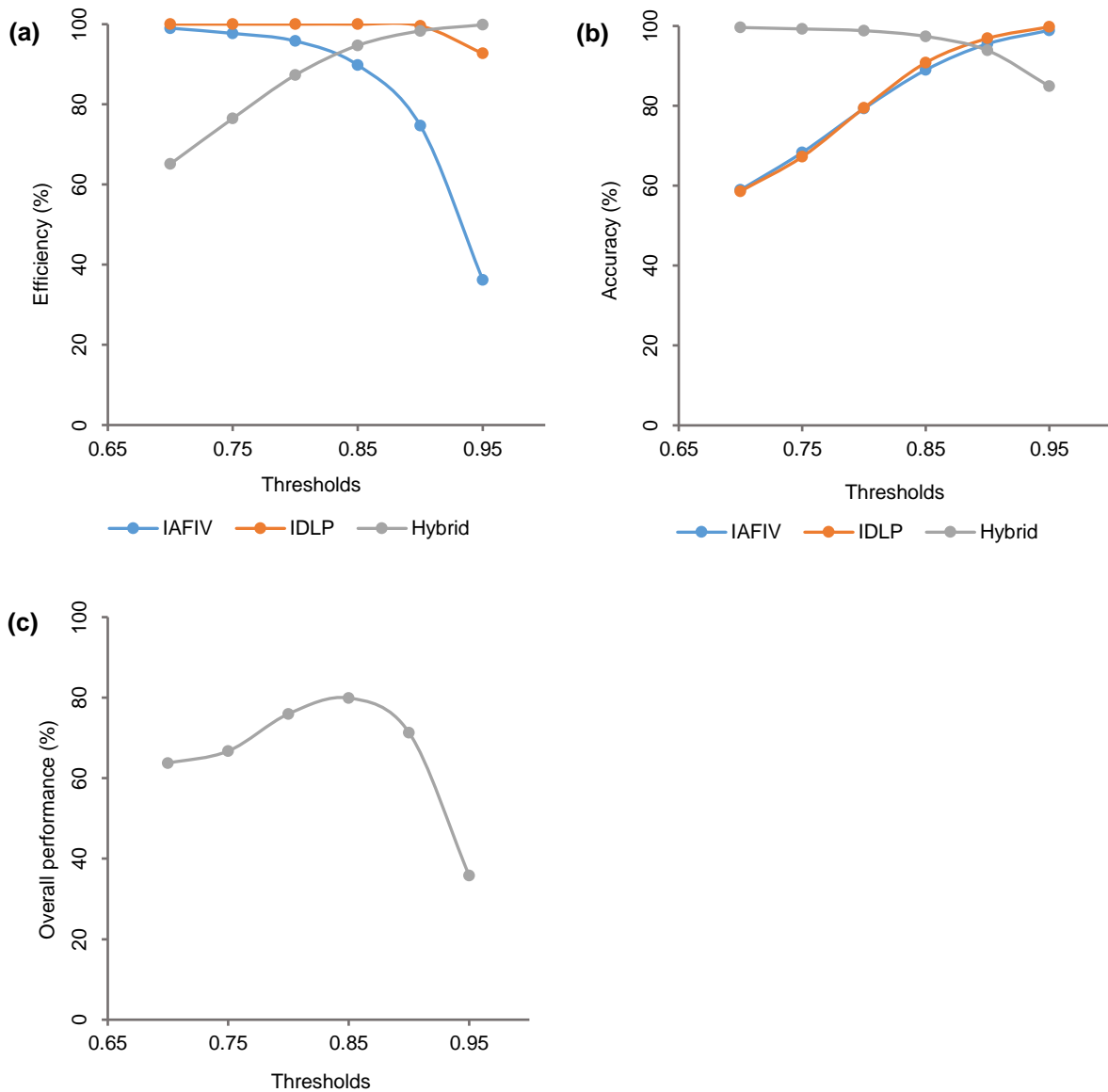


Fig. S3 Plots to show the performance of STRUCTURE for identifying 'pure' and hybrid individuals among south-eastern populations. Performance is assessed by (a) the efficiency, (b) the accuracy and (c) overall performance at different thresholds (T_q). IDLP = Ile de la Passe, and IAF/IV = Ile aux Fouquets/Ilot Vacoas

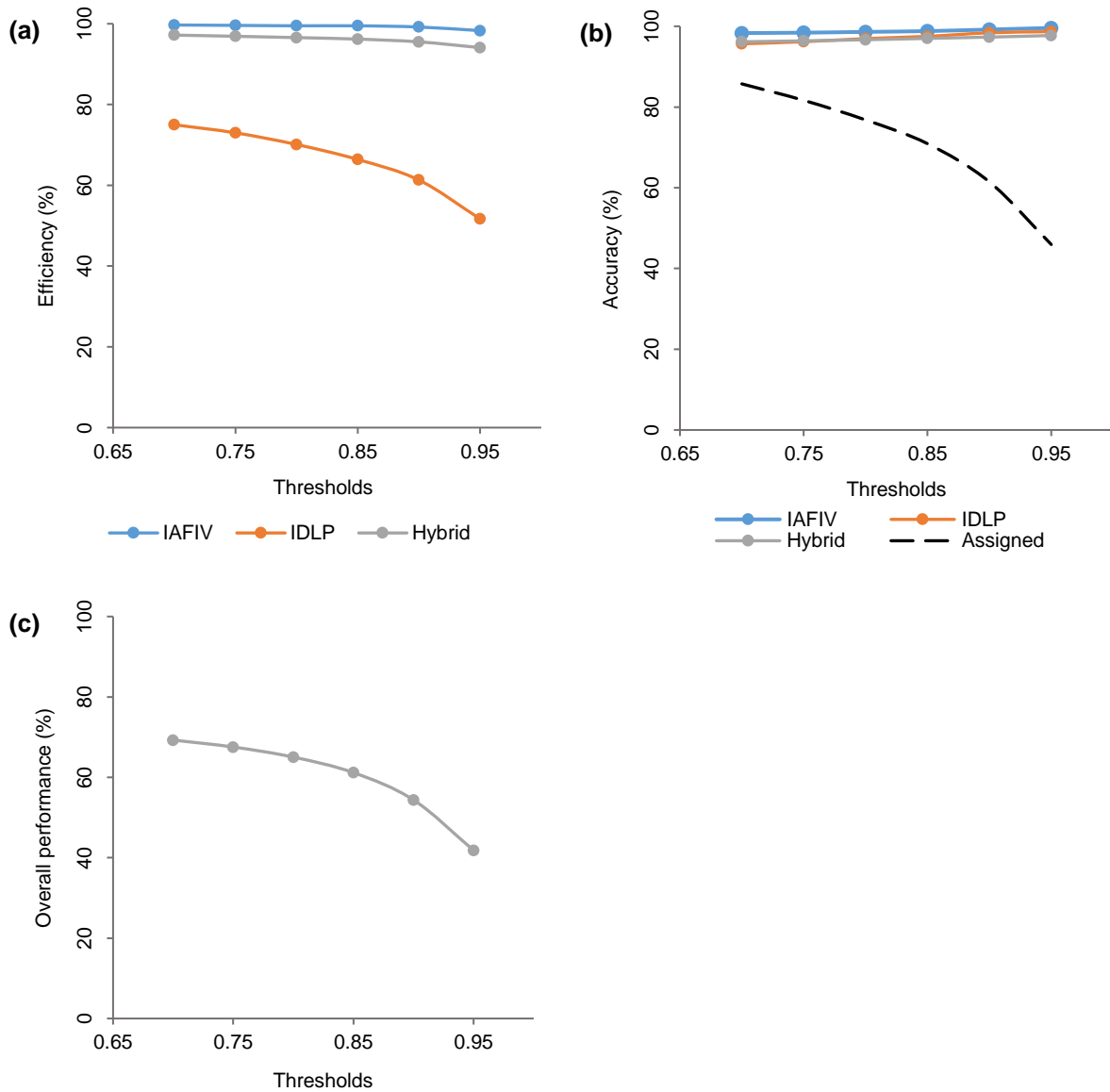


Fig. S4 Plots to show the performance of NewHybrids for identifying ‘pure’ and hybrid individuals among south-eastern populations. Performance is assessed by (a) the efficiency, (b) the accuracy and (c) overall performance at different thresholds (T_q). For accuracy (b), the proportion of individuals assigned to any hybrid category is given as ‘assigned’. IDLP = Ile de la Passe, and IAF/IV = Ile aux Fouquets/Ilot Vacoas

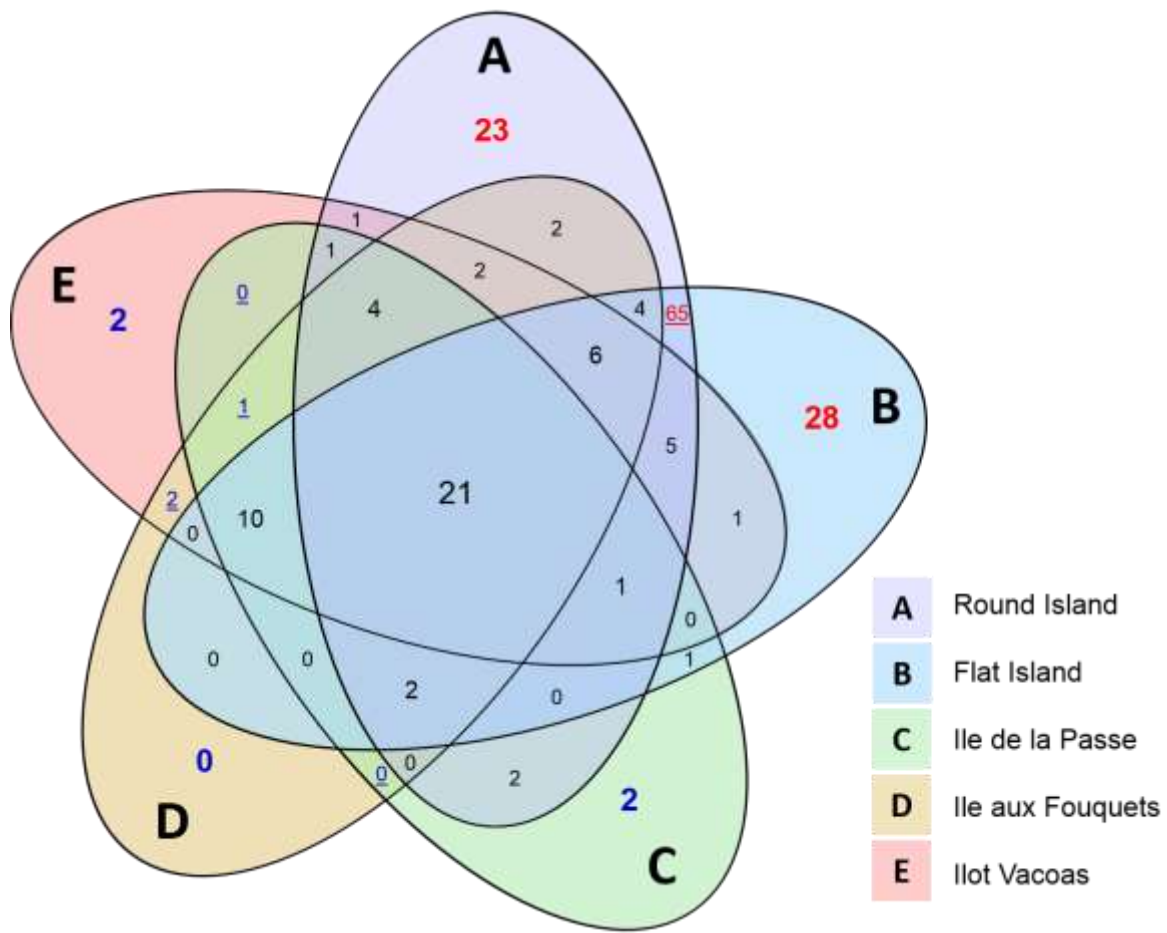


Fig. S5 Venn diagram showing the number of private and shared alleles within and between populations of Bojer’s skink. The number of alleles are based on the nine loci that were successfully genotyped in at least 65% of samples from each population. Overlapping segments represent shared alleles from the respective populations. Values in bold and highlighted red are the number of alleles private to each northern population, and values in bold and highlighted blue are the number of alleles private to each south-eastern population. Values underlined and highlighted red are the number of alleles shared but unique to northern populations, and values underlined and highlighted blue are the number of alleles shared but unique to south-eastern populations