Section S1: PCR reaction specifications and conditions:

Each 5 µL PCR reaction contained 1X MyTaq reaction buffer (Bioline, https://www.bioline.com/), 5 µg bovine serum albumin, 0.5 U MyTaq DNA polymerase (Bioline), 10 ng DNA and fluorescent-labelled primers according to the specifications shown in Table S1. The reaction conditions comprised of an initial denaturing step at 95°C for 3 minutes, followed by 35 cycles of 1 minute at 95°C, 1 minute at 60°C, 1 minute at 72°C, and a final extension at 72°C for 5 minutes.

Table S1. Details of multiplex PCR used to amplify thirteen microsatellite loci from whale shark genomic DNA using fluorescent-labelled primers from Vignaud et al. (2014) with respective mean allelic richness by locus.

	Locus	Repeats	Fluorescent label	Concentration in PCR reaction (µM)	Allelic richness by locus
Multiplex 1	A120	(CA)28	NED	0.35	11.1
	E105	(CT)12	FAM	0.2	5.3
	E115	(GA)13	NED	0.25	3.1
	Rty7	(CA)3TG(CA)3TA(CA)3(CT)4CC(CA)19	FAM	0.2	7.5
Multiplex 2	A9	(CG)3(CA)4AT(CA)4…(CA)12…(CA)4GA(CA)7CT(CA)3…(CA)4	VIC	0.25	4.8
	A101	(CT)6(CA)16	VIC	0.25	4.8
	D102	(GATA)12	PET	0.25	4.1
	Rty23	(CA)9…(CT)4(CA)15	VIC	0.25	-
Multiplex 3	A6	(CT)13(CA)6GA(CA)12GA(CT)4	NED	0.35	4.2
	Rty18	(AC)13	FAM	0.25	3.1
	Rty21	(AC)10	PET	0.5	2.1
	Rty3	(TG)14…(TG)5…(TG)4	NED	0.35	4.7
	Rty5	(CA)20	PET	0.35	6.5

Examples of matching genetic profiles obtained between whale sharks with matching spot patterns:

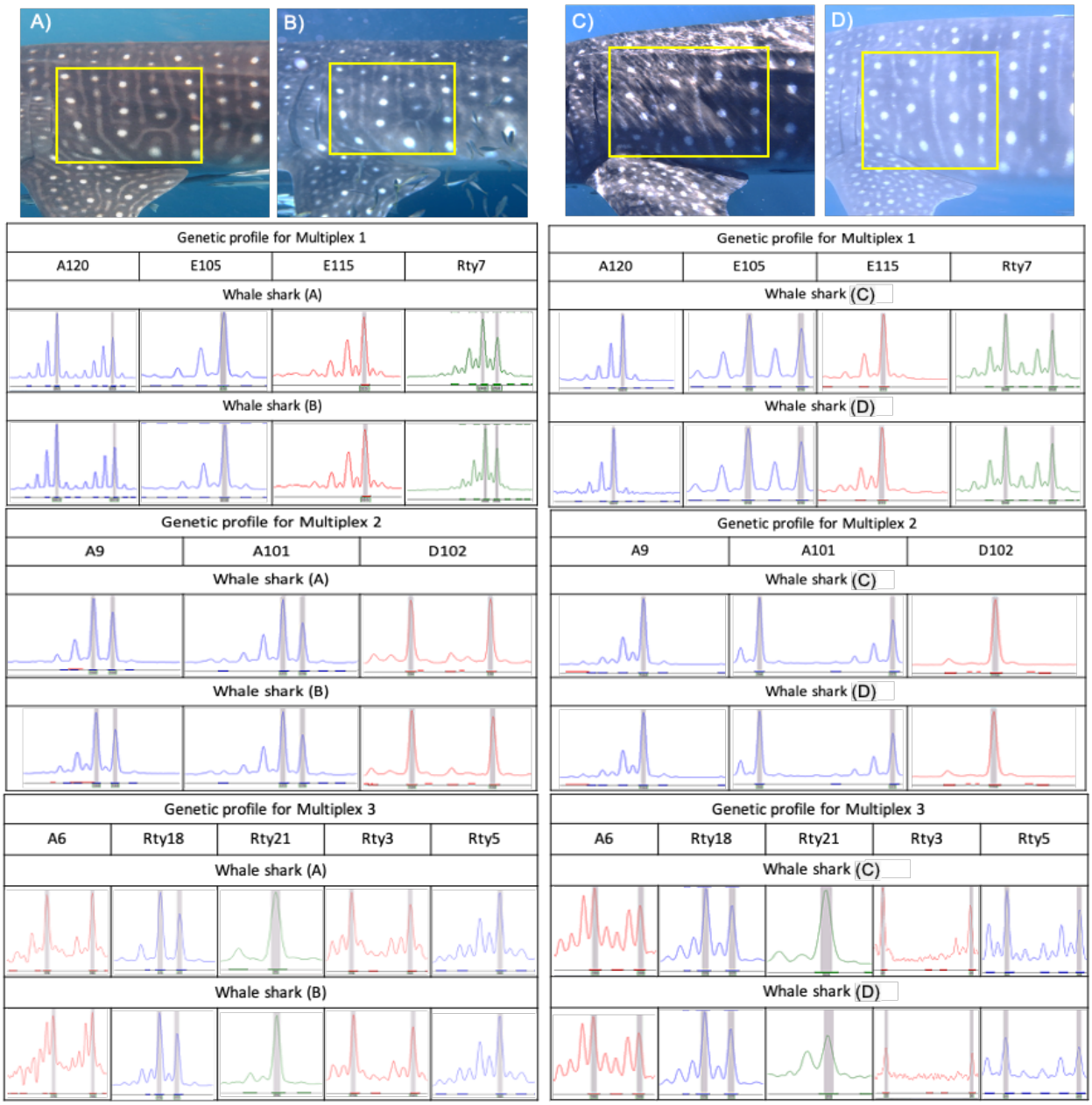

Fig. S1: Matches obtained between spot patterns of whale sharks photographed at Ningaloo Reef in example 1: 2016 (A) and 2017 (B) and example 2: 2017 (C) and 2018 (D) and their respective matching genetic profiles obtained from the tissue samples.

Section S2: Genetic analyses of the Ningaloo whale shark population (2016 – 2018):

The genetic data obtained from this study was further used to calculate indices of genetic diversity of the Ningaloo whale shark population between 2016 to 2018, as a decrease in genetic diversity could indicate decrease in population size. FSTAT software was used to calculate allelic richness, observed heterozygosity (H_o), expected heterozygosity (H_e) and inbreeding coefficient (F_{IS}). F_{IS} values were estimated, with a positive F_{IS} showing a deficit of heterozygotes relative to the levels expected under random mating, indicative of inbreeding in the population. Friedman's ANOVA was used to assess the significance of variation across all years. Friedman's ANOVA revealed no significant variation in H_e (χ^2 = 1.1, p-value = 0.58), F_{IS} (χ^2 = 2.6, p-value = 0.27) or allelic richness (χ^2 = 3, p-value = 0.23) across the three years. The results (Table S2) show no significant difference in genetic diversity between the years, with no occurrence of inbreeding, indicating a stable and large effective population size at Ningaloo Reef.

Table S2: Indices of genetic diversity and inbreeding coefficient of Ningaloo whale shark populations between 2016 – 2018. Standard errors are provided in parentheses.

Year	N	Observed heterozygosity (H_o)	Expected heterozygosity (H_e)	Inbreeding coefficient (F_{IS})	Allelic richness
2016	58	0.57 (0.05)	0.61 (0.04)	0.04 (0.03)	5.05 (0.7)
2017	71	0.62 (0.06)	0.63 (0.04)	0.007 (0.02)	5.17 (0.7)
2018	25	0.58 (0.06)	0.58 (0.05)	(-)0.009 (0.05)	4.98 (0.7)