

Supplementary Material

Table S2 Number of neutral and potentially adaptive loci remaining after each quality-filtering step for auxiliary datasets (i.e. no-juveniles, PG-only, PG-joined and LUPS). MAF=Minor Allele Frequency; FDR=False Discovery Rate, HWE=Hardy Weinberg Equilibrium, LD=Linkage Disequilibrium.

	Primary	No Juvenile	PG-only	PG-joined	LUPS
Initial	38507	38507	38507	38507	38507
Duplicate Contigs	21102	21102	21102	21102	21102
Call Rate	6803	6985	7812	8317	6803
Heterozygosity	6751	6975	7812	8317	6751
Read Depth	6005	6179	6790	7030	6005
MAF	1479	1547	1752	1871	1479
FST Outliers	1395	1544	1752	1866	453
HWE	1390	1424	1663	1681	NA
LD	1373	1405	1632	1672	NA

Tables S3-S7 and Figure S1

Comparison of basic genetic analyses between the primary dataset and neutral subsets that were filtered after excluding PW08 (no Juveniles), after disregarding all samples except those from Papua New Guinea (PG-only), and after replacing the four PG sample groups with a single subset picked from across all four PG sample groups (PG-joined).

Table S3 Inbreeding coefficients F_{IS}

	Primary	No Juveniles	PG-only	PG-joined
FM08	0.001 ± 0.015	0.002 ± 0.015		0.0262 ± 0.011
GL09	-0.004 ± 0.012	-0.005 ± 0.011		0.022 ± 0.012
ID09	-0.058 ± 0.011	-0.057 ± 0.013		-0.022 ± 0.013
MH09	0.011 ± 0.014	0.011 ± 0.014		0.039 ± 0.013
PG07	0.067 ± 0.014	0.071 ± 0.013	0.085 ± 0.013	0.102 ± 0.011
PG09	0.062 ± 0.012	0.067 ± 0.012	0.084 ± 0.011	
PG11	0.095 ± 0.015	0.093 ± 0.013	0.120 ± 0.014	
PG12	0.058 ± 0.012	0.065 ± 0.013	0.084 ± 0.011	
PW08	0.013 ± 0.013			0.046 ± 0.011

Table S4 Heterozygosity

	Primary			No Juveniles			PG-only			PG-joined		
	H_{nb}	H_o	Diff	H_{nb}	H_o	Diff	H_{nb}	H_o	Diff	H_{nb}	H_o	Diff
FM08	0.249 ± 0.137	0.249 ± 0.156	<0.001	0.253 ± 0.138	0.253 ± 0.158	<0.001				0.250 ± 0.137	0.244 ± 0.152	0.006
GL09	0.249 ± 0.138	0.250 ± 0.155	0.001	0.255 ± 0.139	0.255 ± 0.156	<0.001				0.251 ± 0.138	0.246 ± 0.152	0.005
ID09	0.255 ± 0.136	0.270 ± 0.164	0.015	0.259 ± 0.138	0.273 ± 0.167	0.014				0.256 ± 0.135	0.261 ± 0.159	0.005
MH09	0.251 ± 0.138	0.249 ± 0.155	0.002	0.256 ± 0.139	0.252 ± 0.157	0.004				0.252 ± 0.140	0.243 ± 0.151	0.009
PG07	0.235 ± 0.135	0.220 ± 0.139	0.015	0.240 ± 0.136	0.223 ± 0.140	0.017	0.257 ± 0.138	0.235 ± 0.143	0.022	0.238 ± 0.132	0.214 ± 0.128	0.024
PG09	0.243 ± 0.134	0.228 ± 0.138	0.015	0.248 ± 0.134	0.232 ± 0.137	0.016	0.264 ± 0.135	0.242 ± 0.138	0.022			
PG11 1	0.233 ± 0.137	0.211 ± 0.132	0.022	0.238 ± 0.137	0.216 ± 0.134	0.022	0.255 ± 0.138	0.226 ± 0.135	0.029			
PG12	0.236 ± 0.137	0.223 ± 0.142	0.013	0.241 ± 0.138	0.226 ± 0.143	0.015	0.258 ± 0.139	0.237 ± 0.145	0.021			
PW08	0.245 ± 0.134	0.241 ± 0.150	0.004							0.246 ± 0.134	0.235 ± 0.144	0.011

Table S5 N_e

	Primary				No Juveniles			
	LD		Het Excess		LD		Het Excess	
	Pt estimate	95% CI	Pt estimate	95% CI	Pt estimate	95% CI	Pt estimate	95% CI
FM08	363.8	309 - 442	Infinite	Infinite	357.9	306 - 431	Infinite	Infinite
GL09	513.3	411 - 680	Infinite	97 - Infinite	495.5	402 - 645	Infinite	172 - Infinite
ID09	248.9	219 - 287	13.9	11 - 19	277.4	242 - 325	14.2	11 - 19
MH09	564.3	438 - 790	Infinite	Infinite	592.4	458 - 838	Infinite	Infinite
PG07	907.7	650 - 1496	Infinite	Infinite	1036.7	720 - 1842	Infinite	Infinite
PG09	636.0	511 - 839	Infinite	Infinite	827.2	632 - 1192	Infinite	Infinite
PG11	1115.1	771 - 2003	Infinite	Infinite	1518.4	955 - 3680	Infinite	Infinite
PG12	363.9	313 - 435	Infinite	Infinite	392.7	335 - 474	Infinite	Infinite
PW08	574.4	463 - 754	Infinite	Infinite				

	PG-only				Joined-PG			
	LD		Het Excess		LD		Het Excess	
	Pt estimate	95% CI	Pt estimate	95% CI	Pt estimate	95% CI	Pt estimate	95% CI
FM08					421.0	360 - 506	Infinite	Infinite
GL09					670.1	530 - 909	Infinite	Infinite
ID09					262.9	235 - 298	61.6	27 - Infinite
MH09					584.1	469 - 772	Infinite	Infinite
PG07	1079.6	774 - 1777	Infinite	Infinite	1934.5	1242 - 4353	Infinite	Infinite
PG09	1078.2	802 - 1640	Infinite	Infinite				
PG11	1603.6	1044 - 3434	Infinite	Infinite				
PG12	449.4	385 - 540	Infinite	Infinite				
PW08					488.2	418 - 586	Infinite	Infinite

Table S6 AMOVA

	Primary	No Juveniles	PG-only	PG-joined
Within pop	0.995	0.994	0.998	0.992
Between pops	0.005 (p=0.001)	0.006 (p=0.001)	0.002 (p=0.001)	0.008 (p=0.001)

Table S7 Mantel

	Primary	No Juveniles	PG-only	PG-joined
r-value	0.6428 (p=0.0006)	0.7130 (p=0.0012)	0.47 (p=0.1323)	0.1344 (p=0.3008)

Table S8 F_{ST} Auxiliary neutral dataset (Significant values in bold).

	FM08	GL09	ID09	MH09	PG07	PG11	PG12	PW08
FM08								
GL09	0.00303							
ID09	0.00342	0.00430						
MH09	0.00476	0.00151	0.00671					
PG07	0.00415	0.00312	0.00601	0.00447				
PG09	0.00482	0.00400	0.00363	0.00385	0.00207			
PG11	0.00371	0.00343	0.00417	0.00471	0.00167	-0.00026		
PG12	0.00325	0.00422	0.00338	0.00637	0.00433	0.00303	0.00299	
PW08	0.00413	0.00305	0.00203	0.00564	0.00273	0.00281	0.00349	0.00083

Figure S1 DAPCs using neutral loci from the primary (47 principle components, 8 degrees of freedom) and auxiliary datasets after excluding PW08 (no Juveniles; 42 principle components, 7 degrees of freedom), after disregarding all samples except those from Papua New Guinea (PG-only; 25 principle components, 3 degrees of freedom), and after replacing the four PG sample groups with a single subset picked from across all four PG sample groups (PG-joined; 36 principle components, 5 degrees of freedom). Placement of individuals relative to each other reflects their genetic similarity and extent of genetic structure resulting in scatterplots that strongly overlapped all sample groups and thus, confirmed broadscale admixture irrespective of sample selection.

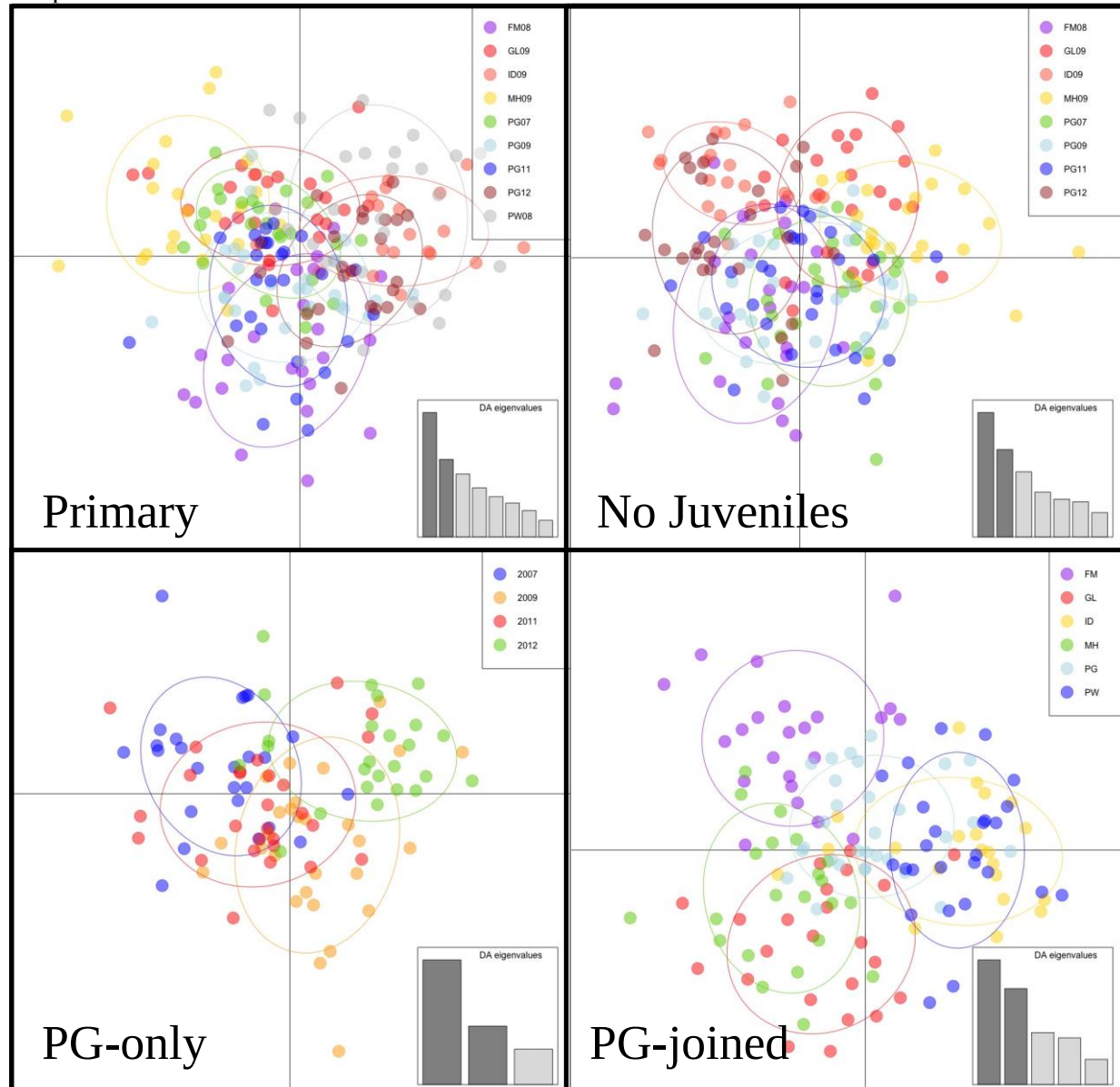


Figure S2 Population genetic structure network analysed using Netview R at mk-NN=6-30. Node sizes displayed are mapped to the relatedness of individual fish, where larger node diameters denote higher levels of relatedness.

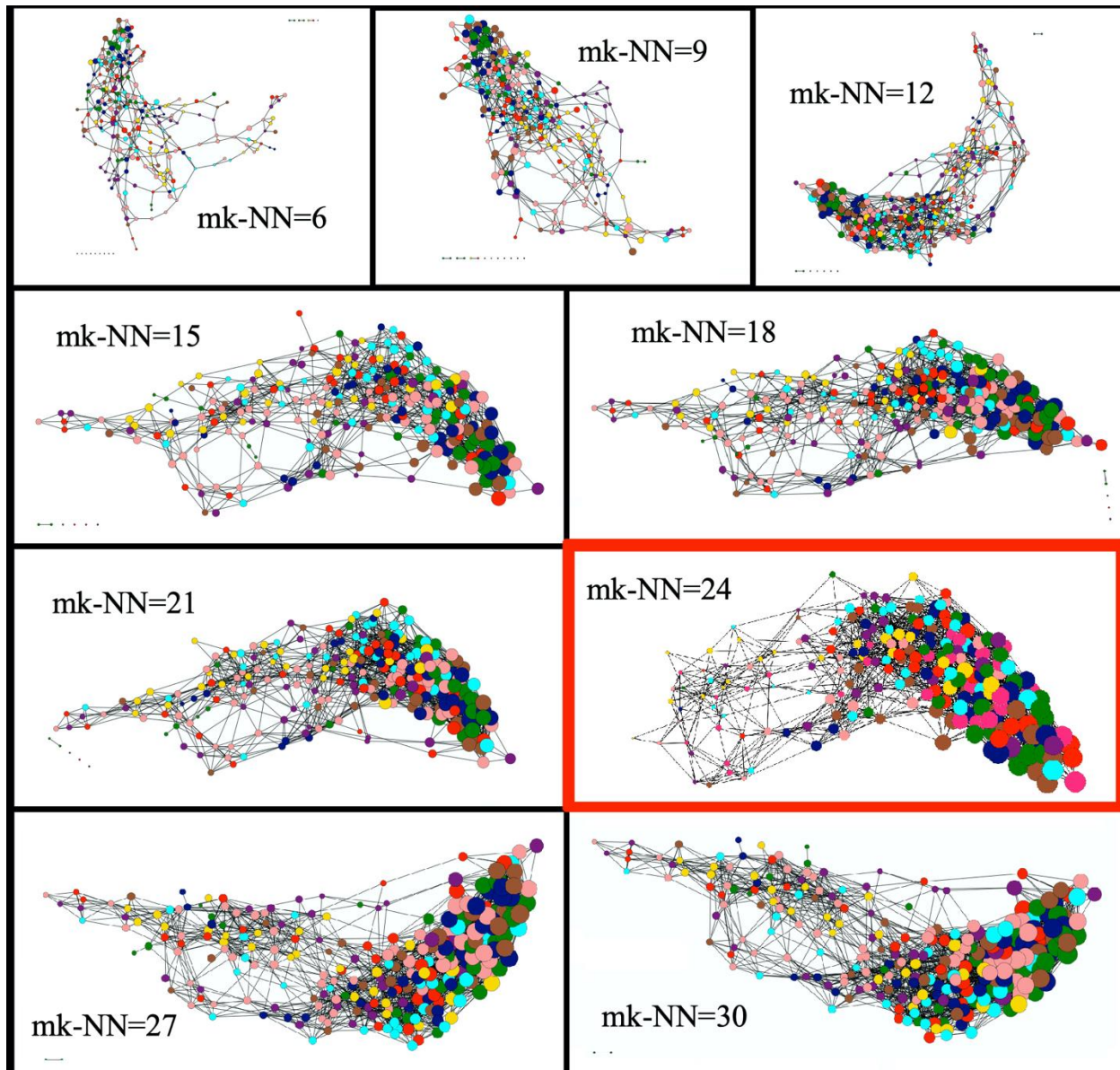


Figure S3 Population dendrogram based on 1-psa genetic distance matrix and NJ approach.

