

**Supplementary material**

**Assessment of genetic structure among Australian east coast populations of snapper  
*Chrysophrys auratus* (Sparidae)**

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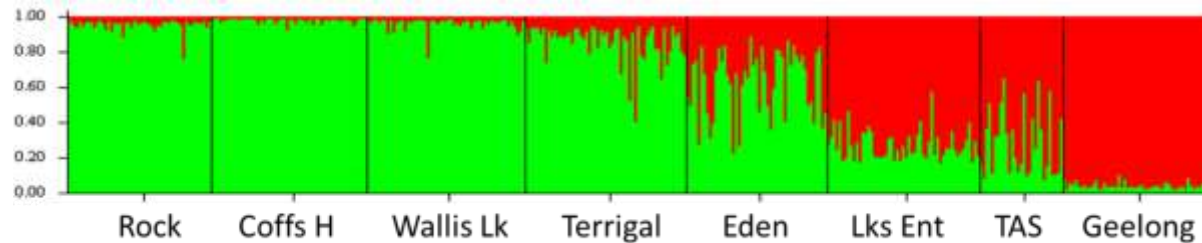
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**Table S1. Details of microsatellite loci targeted in study (modified from Le Port *et al.* 2017)**

The fluorescently labelled M13 primer (underlined section) was included at the same concentration as the reverse primer

Multiplex number	Locus	Primers (5'-3') with modified M13 tail underlined	FLU	Ta (°C)	Concentration (µM)	Allele repeat motif	Source
M1	Pma1	F <u>TAAAACGACGGCCAGTGCC</u> CATGCCAGTATTCCAATGTGC	NED	60	0.016	(GT)21	Takagi <i>et al.</i> (1997)
		R AGGACAAATTCCCAAGGTCATCC					
	Pma68-23	F <u>TTTCCCAGTCACGACGTTG</u> ATCCTGACACGCTGGAAACT	FAM	60	0.033	(CA)3AA(CA)18	Hatanaka <i>et al.</i> (2006)
		R TCTGGAAGTGGGAATAAAAAGG					
M2	Pma22-9	F <u>TTTCCCAGTCACGACGTTG</u> CAATGACTGGCACCGTATCA	FAM	62	0.02	(CA)22(TA)3	Hatanaka <i>et al.</i> (2006)
		R AAAGGGTTCATTTTGGATGG					
	CM003195	F <u>GCGGATAACAATTTACACAGG</u> AGTGTTATCACAGCTTTGCAG	VIC	62	0.016	(TG)13	Chen <i>et al.</i> (2005)
		R CTTGTGCTGTACCTATTCTGAG					
M3	Pma4-32	F <u>GCGGATAACAATTTACACAGG</u> CCTGCCACCTACTGTTTCCT	VIC	60	0.02	(CA)24	Hatanaka <i>et al.</i> (2006)
		R CGGTGATTACAGTCGGGTTT					
	Sal19	F <u>TAAAACGACGGCCAGTGC</u> ATTCTTCACAGGCCCAACACAAA	NED	60	0.02	(GT)25	Brown <i>et al.</i> (2005)
		R GAAAACACCGGCCAGTACGA					
S1	CM000278	F <u>TTTCCCAGTCACGACGTTGGT</u> GTGCGATCATCTTTGTGA	FAM	52	0.033	(TG)16	Chen <i>et al.</i> (2005)
S2	GA2A	F <u>GCGGATAACAATTTACACAGG</u> ACGGACAGAGAGGGAGTGG	VIC	59	0.02	(AG)16	Adcock <i>et al.</i> (2000)
		R CATCATCATCAGTCAGAGCTG					
S3	Sal10	F <u>CACAGGAAACAGCTATGACCT</u> CACGGGGGACCAAGACTG	PET	57	0.02	(GT)37	Brown <i>et al.</i> (2005)
		R CTCACACTGCCTAATTAGCACAGA					



**Fig. S1.** Predicted genetic stock structure of *C. auratus* based on population clustering of microsatellite data (reduced dataset removing Sunshine Coast and locus Pma68–23 due to possible deviations from HWE to leave 8 sampling locations and 8 loci) using a Bayesian model-based analysis. Vertical lines correspond to individual fish which are coloured by the posterior probability proportions of their genotype based on a  $K = 2$  cluster model.

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