

Table S1. Sea bass Group I NITR (“Intronless”) amino acid sites under positive selection identified using different methods.

AA position ^a	Protein domain ^b	Maximum Likelihood Method			
		PAML ^c	FEL ^d	REL ^e	MEC ^f
4	Signal P.		0.11	25.7	
6	Signal P.		0.13	24.6	
10	Signal P.		0.20		
17	Signal P.		0.11	36.6	
30	V		0.04	52.6	
66	V_CDR1		0.09	39.2	
72	V		0.07	59.4	
83	V_CDR2		0.06	20.9	[1, 3.1]
88	V_CDR2		0.17		
94	V		0.07	67.5	
120	V		0.16		
127	V		0.15		
133	V_CDR3		0.05	33.8	
136	V_CDR3	0.998			[3.1, 3.1]
140	V_CDR3	0.994			[1, 3.1]
143	V		0.06	81	
144	V		0.04	103.7	
148	V		0.17	20.6	
151	V		0.10	41.6	
209	V/C2		0.20		
218	V/C2		0.12	31.1	
234	V/C2		0.17		
246	V/C2		0.19		
264	TM		0.12	22.8	
266	TM		0.05	60.5	
272	TM		0.11	24.6	
275	TM		0.13	22.6	
286	TM		0.12	23.1	
291	TM	0.978	0.08		
292	TM		0.03	63	
295	TM	0.972			
300	TM		0.16	22.7	
302	TM		0.16	20.3	
323	Cyt1		0.20		
338	Cyt2	0.981	0.12		[1, 3.1]
340	Cyt2		0.13	28.6	
348	Cyt2	0.997	0.06		[3.1, 3.1]
350	Cyt2	1.00	0.02		[3.1, 3.1]
351	Cyt2		0.07	30.6	

^a Amino acid position refers to the sea bass Group I alignment reported in Fig. S1 (Supplementary File 2).

^b V: V-domain, V_CDR1: Complementarity determining region 1, V_CDR2: complementarity determining region 2, V_CDR3: Complementarity determining region 3, V/C2: I-domain, TM: Transmembrane domain, Cyt1 and Cyt2: cytoplasmatic domains.

^c Posterior probabilities of the BEB analysis.

^d P value.

^e Bayes factor.

^f Confidence interval.