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MICROSATELLITE RECORDS

Microsatellite records for volume 8, issue 2

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Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Xylocopa abbreviata	Xa1[a]	F:CCTCGCGGGAACCAAGCTCC	$(CT)_3CG(CT)_2A(T)_5(CT)_{13}(T)_2CT$	*Pop1* 193–229	*Pop1* 21	*Pop1* 7	*Pop1* 0.905 (0.774)
		R:GCGGTCGCGTCTCCAGGAAT		*Pop2* 221–229	*Pop2* 20	*Pop2* 5	*Pop2* 0.450 (0.731)
Xylocopa abbreviata	Xa2[a]	F:AGACACGCGTAAACAGTGTAAAT	$CT(TC)_{14}AC(TC)_2T_2(TC)_7$ $CATC(T)_2(TC)_3$	*Pop1* 252–282	*Pop1* 21	*Pop1* 10	*Pop1* 0.905 (0.839)
		R:GGGCAATGTATCGTCTTACATCT		*Pop2* 264–282	*Pop2* 20	*Pop2* 7	*Pop2* 0.600 (0.698)
Xylocopa abbreviata	Xa3[a]	F:TTACAGGGACGCGCGAACGG	$(GA)_3A_2(GA)A_2(GA)_{18}$	*Pop1* 200–238	*Pop1* 21	*Pop1* 14	*Pop1* 0.952 (0.892)
		R:GTCGGTGGCACGGTCGTGAT		*Pop2* 202–210	*Pop2* 20	*Pop2* 2	*Pop2* 0.100 (0.095)
Xylocopa abbreviata	Xa6[a]	F:ACCCTTTGGCTCGAAGCGAC	$(CT)_{16}CA(CT)_3C_2(CT)C_2G(CT)_3$	*Pop1* 227–245	*Pop1* 21	*Pop1* 9	*Pop1* 0.810 (0.837)
		R:CCCCGCGAATATACTTGATACCGA		*Pop2* 229–235	*Pop2* 20	*Pop2* 4	*Pop2* 0.550 (0.636)
Xylocopa abbreviata	Xa8[a]	F:CCGTCCTCCGAGCTTTCGCC	$(CT)_4T_2AC(CT)_2AT(CT)_{10}$	*Pop1* 254–268	*Pop1* 21	*Pop1* 7	*Pop1* 0.714 (0.696)
		R:CCCTCTCCCGTCCGGTGGTT		*Pop2* 260–266	*Pop2* 20	*Pop2* 4	*Pop2* 0.550 (0.615)
Xylocopa abbreviata	Xa9[a]	F:TGATGTGGCATCGCGCGGAC	$(CT)_{15}$	*Pop1* 222–248	*Pop1* 21	*Pop1* 9	*Pop1* 0.762 (0.718)
		R:ACGCGGACGTGAGAGAGTGT		*Pop2* 230–242	*Pop2* 20	*Pop2* 7	*Pop2* 0.750 (0.769)
Xylocopa abbreviata	Xa10[a]	F:CGTGCCCACGCAGCAGCTTT	$(CT)_{12}$	*Pop1* 231–267	*Pop1* 21	*Pop1* 7	*Pop1* 0.714 (0.787)
		R:CGCGACGCGAAGTGTCAGGA		*Pop2* 237–251	*Pop2* 20	*Pop2* 8	*Pop2* 0.650 (0.796)
Xylocopa abbreviata	Xa11[a]	F:TCGGCTGGCCAATCTCTTCG	$(AG)_{15}$	*Pop1* 197–231	*Pop1* 21	*Pop1* 9	*Pop1* 0.762 (0.773)
		R:ACGCGAGCCGTTCGTTTTCA		*Pop2* 199–225	*Pop2* 20	*Pop2* 12	*Pop2* 0.850 (0.881)
Xylocopa abbreviata	Xa12[a]	F:CACGATGATCGAGAAACGACT	$(GA)_4(GT)_3(GA)_{10}$	*Pop1* 251–273	*Pop1* 21	*Pop1* 11	*Pop1* 0.714 (0.834)
		R:CGGTCGAGCCTGCAACGTGT		*Pop2* 263–265	*Pop2* 20	*Pop2* 2	*Pop2* 0.050 (0.289)
Xylocopa abbreviata	Xa14[a]	F:TTACCGCACCGGAGGGCGAT	$(CT)_{21}$	*Pop1* 227–251	*Pop1* 21	*Pop1* 13	*Pop1* 0.857 (0.878)
		R:CACGACCCAGCCCACCAAGG		*Pop2* 227–237	*Pop2* 20	*Pop2* 6	*Pop2* 0.800 (0.810)
Xylocopa abbreviata	Xa19[a]	F:TGGCGAACGATCAGGTAAGCGA	$(TC)_{15}AT(TC)_2$	*Pop1* 183–203	*Pop1* 21	*Pop1* 9	*Pop1* 0.952 (0.836)
		R:ACGTTCAGCCAGCTTTCGGGA		*Pop2* 185–197	*Pop2* 20	*Pop2* 6	*Pop2* 0.700 (0.736)
Xylocopa macambirae	Xm1[a]	F:GGCCGCGTCTACGTGTGTGT	$(GA)_4A_2T(AG)_3G_3T(AG)_6$	*Pop1* 228–234	*Pop1* 21	*Pop1* 4	*Pop1* 0.571 (0.704)
		R:CGCCACGCCGCTTAATCCCT		*Pop2* 230–232	*Pop2* 20	*Pop2* 2	*Pop2* 0.200 (0.180)
Xylocopa macambirae	Xm2[a]	F:TCTCACTGCAATCGAGAAGAGCA	$(AG)_5A_2(AG)_{18}$	*Pop1* 245–267	*Pop1* 21	*Pop1* 9	*Pop1* 0.952 (0.842)
		R:ACGTTACTTAATCTGACCTCATCCT		*Pop2* 245–265	*Pop2* 20	*Pop2* 11	*Pop2* 0.700 (0.859)
Xylocopa macambirae	Xm3[a]	F:CGCTGCCATTCTGGCCTGCT	$(CT)_5C_2(CT)_4T_2(CT)_2T_2CT$	*Pop1* 243–245	*Pop1* 21	*Pop1* 2	*Pop1* 0.381 (0.308)
		R:ACACGAGAATGACTTGACGCGA		*Pop2* 243–245	*Pop2* 20	*Pop2* 2	*Pop2* 0.300 (0.455)
Xylocopa macambirae	Xm4[a]	F:ATCGGTCCAGCAGCGTGCAA	$(CT)_{15}$	*Pop1* 237–251	*Pop1* 21	*Pop1* 8	*Pop1* 0.714 (0.822)
		R:ACGCCACCGTATTCACGACCAC		*Pop2* 247–253	*Pop2* 20	*Pop2* 4	*Pop2* 0.300 (0.411)
Xylocopa macambirae	Xm5[a]	F:CGCACGCGAAAAGGGCCTAC	$(CTT)_{11}$	*Pop1* 258–273	*Pop1* 21	*Pop1* 5	*Pop1* 0.333 (0.438)
		R:CTGGCACAGGTTCGCGTCCA		*Pop2* 261–277	*Pop2* 20	*Pop2* 6	*Pop2* 0.650 (0.676)
Xylocopa macambirae	Xm6[a]	F:ACTTGCACTCGGCCGGCATC	$(GA)_{15}T(AG)_2$	*Pop1* 174–190	*Pop1* 21	*Pop1* 9	*Pop1* 0.810 (0.822)
		R:GCAGTCGGCCTTCACCACGA		*Pop2* 176–192	*Pop2* 20	*Pop2* 7	*Pop2* 0.750 (0.809)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Xylocopa macambirae	Xm7[a]	F:TCCACGATCGACCCCGCTCC R:CGCGGCTTATTTCCGTGCCG	$(TC)_{16}$	*Pop1* 190–222 *Pop2* 190–208	*Pop1* 21 *Pop2* 20	*Pop1* 14 *Pop2* 6	*Pop1* 0.810* (0.854) *Pop2* 0.600 (0.779)
Xylocopa macambirae	Xm9[a]	F:ACCGACGCACACGTCGGACA R:AGTTTTTACGTTCTTTCGAGCGAG	$(GA)_{17}A_2(GA)_5$	*Pop1* 224–254 *Pop2* 218–250	*Pop1* 21 *Pop2* 20	*Pop1* 12 *Pop2* 9	*Pop1* 0.714 (0.882) *Pop2* 0.300* (0.781)
Xylocopa macambirae	Xm11[a]	F:GTCACTCGACTCCCCGGCCA R:TACACACGCGTCACTCCGCC	$(CG)_4CACG(CT)_{11}CA(CT)_2$	*Pop1* 251–277 *Pop2* 251–279	*Pop1* 21 *Pop2* 20	*Pop1* 8 *Pop2* 8	*Pop1* 0.857 (0.764) *Pop2* 0.650 (0.784)
Xylocopa macambirae	Xm12[a]	F:ACTTCTCGAGCAGCTTGCGG R:AGATTCAGTCTACAACCGTTCG	$(GA)_{10}A_2(GA)_4$	*Pop1* 250–290 *Pop2* 254–280	*Pop1* 21 *Pop2* 20	*Pop1* 11 *Pop2* 7	*Pop1* 0.714 (0.854) *Pop2* 0.700 (0.806)
Xylocopa macambirae	Xm13[a]	F:GGCGTGTAACGTCGCGCAAA R:CCCACTCGTTTCTCAACGGA	$(AG)_{13}TG(AG)_3$	*Pop1* 203–221 *Pop2* 185–275	*Pop1* 21 *Pop2* 20	*Pop1* 8 *Pop2* 16	*Pop1* 0.857 (0.807) *Pop2* 0.700* (0.879)
Xylocopa macambirae	Xm14[a]	F:AGTTGGCCTCACCGAACCGA R:CCCTGCTGGGAAAATGGAAGACA	$(TC)_{13}AC(TC)_{13}$	*Pop1* 251–283 *Pop2* 255–279	*Pop1* 21 *Pop2* 20	*Pop1* 7 *Pop2* 5	*Pop1* 0.762 (0.723) *Pop2* 0.550 (0.510)
Xylocopa macambirae	Xm15[a]	F:CTCCTTTGATCTCCTCGATTAGC R:CGCTGCCATCGGTCGTCTCG	$(GAA)_{10}$	*Pop1* 238–258 *Pop2* 244–247	*Pop1* 21 *Pop2* 20	*Pop1* 7 *Pop2* 2	*Pop1* 0.571 (0.773) *Pop2* 0.550 (0.399)
Xylocopa macambirae	Xm17[a]	F:CGAGTGATCGATGAAACGGTTCGAG R:TCGCGGCTAGTGGACGTTCG	$(AG)_{10}C(GA)_5$ $A(AG)_3G(GA)_3GT(GA)_6$	*Pop1* 202–210 *Pop2* 196–224	*Pop1* 21 *Pop2* 20	*Pop1* 5 *Pop2* 3	*Pop1* 0.762 (0.721) *Pop2* 0.250 (0.429)
Xylocopa macambirae	Xm18[a]	F:TGGATGTTCTTGATCCTAACCAGTCA R:TCCAGTGAAAACCTGTCCCCGA	$(GA)_{13}GC_2(CA)_5$	*Pop1* 244–270 *Pop2* 252–268	*Pop1* 21 *Pop2* 20	*Pop1* 11 *Pop2* 6	*Pop1* 0.857 (0.837) *Pop2* 0.600 (0.650)
Xylocopa macambirae	Xm19[a]	F:TGCATACTCTTAACGCTACACGA R:ACCGCCTGTCCTTGGCGAAT	$(GAA)_{12}G_2A(GAA)_3$ $G_2AGA_4(GAA)_{14}$	*Pop1* 223–334 *Pop2* 239–267	*Pop1* 21 *Pop2* 20	*Pop1* 13 *Pop2* 7	*Pop1* 0.857 (0.880) *Pop2* 0.500 (0.578)
Xylocopa macambirae	Xm20[a]	F:CAGTGTAAGCTCTACGATAACACG R:CAAATCCCACGAAGAGATCGT	$(TC)_{16}$	*Pop1* 262–284 *Pop2* 264–278	*Pop1* 19 *Pop2* 18	*Pop1* 10 *Pop2* 5	*Pop1* 0.789 (0.850) *Pop2* 0.222* (0.613)
Gymnocypris potanini	GH01/ KT899335[b]	F:TTCGAAAGGCCAGTGCTATT R:TTGCATCCTCTTCCTTCTGG	$(AAAG)_{12}$	213–277	22	12	0.803 (0.873)
Gymnocypris potanini	GH05/ KT899336[b]	F:TGCATCTGCATTCAGACCAT R:TCTCTCTCTACCCATCCAGCA	$(GATG)_{13}$	172–224	22	11	0.636* (0.891)
Gymnocypris potanini	GH08/ KT899337[b]	F:TGCTCTAGATCAGTGGTTTTCAA R:TGTCTGCCTGTCTTTCTGTGAC	$(TCTA)_{10}$	228–292	22	12	0.894 (0.894)
Gymnocypris potanini	GH10/ KT899338[b]	F:TTCGAACACAGCCAAAACAG R:TGCACAAAACAGACATGCAA	$(GATT)_{12}$	187–231	22	10	0.795 (0.827)
Gymnocypris potanini	GH16/ KT899339[b]	F:ACACTGCATGAAAGGGCATT R:TCTTGGCAATGTGCGTGT	$(AAAC)_{10}$	203–249	22	4	0.568 (0.613)
Gymnocypris potanini	GH18/ KT899340[b]	F:TTTTGTTTCACTTAGATGTTGCAT R:CCAACCCTAACGATGGACAG	$(TCTG)_{11}$	227–299	22	14	0.848 (0.893)
Gymnocypris potanini	GH20/ KT899341[b]	F:TTACAGGCCCATATGCACAA R:CAACACGCTCATACGCTGAT	$(CACG)_{12}$	191–199	22	3	0.447 (0.419)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Gymnocypris potanini	GH24/KT899342[b]	F:TCTTCGATCCATCCATCCAT R:ACCAGTCCAGCACTGTGAGA	$(TCTT)_{11}$	171–235	22	13	0.674* (0.868)
Gymnocypris potanini	GH32/KT899343[b]	F:AATCTGCACATCCTGCGAGT R:ATGACGCTGGTTTCACTCAA	$(GAAT)_{12}$	238–266	22	28	0.758 (0.839)
Gymnocypris potanini	GH33/KT899344[b]	F:TCGGGGTCAGTAAGATTGTTT R:CATGCAAAACTCGCTGCTAT	$(GATA)_{10}$	187–239	22	9	0.758 (0.807)
Gymnocypris potanini	GH34/KT899345[b]	F:GTGCCAGAATGTTGCACTGT R:TCCTGACACAGGACAAAGGA	$(GTGC)_{11}$	185–221	22	6	0.788 (0.721)
Gymnocypris potanini	GH37/KT899346[b]	F:CACACAGCAGGAAAACAAACA R:GGAGAAATCGGTGACTCAGG	$(ATGG)_{11}$	206–262	22	8	0.811 (0.804)
Gymnocypris potanini	GH42/KT899347[b]	F:TCAATTGAACGCATTATTTCTGA R:AACACTTCAGCCATGCTTCA	$(GAAA)_{10}$	196–256	22	11	0.864 (0.883)
Gymnocypris potanini	GH43/KT899348[b]	F:TGCAAAGGGTTTCTGCTCTT R:CCCGCAATACAAAGTCAATG	$(AACA)_{11}$	160–228	22	10	0.856 (0.832)
Gymnocypris potanini	GH46/KT899349[b]	F:GAAATTTGGTTTGAGTGGATGTT R:CTGCCTTTCAGGAGTGTGCT	$(TCAT)_{11}$	201–237	22	27	0.530 (0.817)
Gymnocypris potanini	GH49/KT899350[b]	F:GATTAGATCGAGAAGGGACGA R:ATGCATGAACTGGCGTATGA	$(AGAC)_{10}$	194–254	22	11	0.886 (0.882)
Gymnocypris potanini	GH64/KT899352[b]	F:GGGTTCGTGACAGCTTCTGA R:TGGCAAAGCTGATTACTCCA	$(TGAA)_{11}$	124–184	22	8	0.803 (0.796)
Gymnocypris potanini	GH68/KT899353[b]	F:TTGATTTGACTGAATATTGCCATT R:AAGGCTGGAAAGTGCAAAAA	$(CTAA)_{15}$	205–249	22	9	0.788 (0.837)
Gymnocypris potanini	GH69/KT899354[b]	F:TGCCCTGAAAACACATACCA R:TTACTTGTCCACCGACACTGA	$(CTAT)_{13}$	196–296	22	14	0.826 (0.897)
Gymnocypris potanini	GH75/KU355887[b]	F:TGAAACAATAAAAGTTTCTGAAATTGA R:GCTTTCATTCCTATGTATTTGTTTG	$(AAAC)_{10}$	186–246	22	13	0.697 (0.884)
Gymnocypris potanini	GH76/KU355888[b]	F:CCATGACCCCCTTTAAGAGA R:GTATGGCACGGTACAGCAAG	$(ATTG)_{10}$	217–265	22	12	0.705 (0.857)
Gymnocypris potanini	GH77/KU355889[b]	F:AGGCCATGGACTGGATTCTT R:GGGTTTGAGGGATTGTTGAA	$(TTTC)_{11}$	220–272	22	11	0.886 (0.874)
Gymnocypris potanini	GH78/KU355890[b]	F:TTGAGTGATGCGATCTCCAG R:ATGTAAGCAGCCCCTCAAAA	$(TGTT)_{10}$	206–250	22	10	0.727 (0.884)
Gymnocypris potanini	GH79/KU355891[b]	F:CGGTACCTAATGGAACCTTATTG R:TCATCTACCAGCAATGCAGAG	$(AGAT)_{10}$	216–300	22	12	0.682 (0.898)
Gymnocypris potanini	GH80/KU355892[b]	F:GTCGTTTATTTTGCTCTAAGCTG R:CGCTGTGAAGCAGTGATGTT	$(AGAA)_{10}$	204–280	22	13	0.795 (0.882)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Gymnocypris potanini	GH81/KU355893[b]	F:CAAGAATAGGAAAGGAGTTGTGTG R:TCATTGCACATTTCACTTGGA	$(AAAG)_{11}$	206–270	22	13	0.614 (0.893)
Gymnocypris potanini	GH82/KU355894[b]	F:GAGGGACTGGGGTACAAACA R:GTCATTCGTTTCGTGCTCCT	$(GAAA)_{14}$	183–235	22	12	0.659 (0.858)
Gymnocypris potanini	GH83/KU355895[b]	F:CACTTTGAATTATTAGATGGTAGATGG R:TTTAAGGTAAGTGGTCGCAAA	$(AGAT)_{11}$	223–267	22	10	0.856 (0.853)
Gymnocypris potanini	GH84/KU355896[b]	F:TAAGTCCCCACCAAAATGGA R:CCCAGAATACCCTTACCTGCT	$(GCAC)_{12}$	196–208	22	4	0.598 (0.687)
Gymnocypris potanini	GH85/KU355897[b]	F:AGTGCAATGCCTTGCTGTAT R:AGATTCGGATTGGTTGGATG	$(ATCC)_{10}$	159–183	22	6	0.583 (0.632)
Gymnocypris potanini	GH86/KU355898[b]	F:CACATTCATTCAAGCAAGCA R:AACCAAGAGTTCTGTCCCAAA	$(TATC)_{14}$	204–252	22	11	0.917 (0.885)
Carcharhinus sorrah	CS 8[c]	F:CCCAACAACCTTTCCCTCCT R:TCTTTCACACTTGCTTCACACA	$(AC)_{13}$	132–186	40	13	0.900 (0.877)
Carcharhinus sorrah	CS 433[c]	F:AGTGAGCTGCGGAAGTCATT R:GGTCTCCCAGCAGAACTCTC	$(AC)_{13}$	205–221	40	3	0.575 (0.601)
Carcharhinus sorrah	CS 40[c]	F:TTTGAGGATCGTTGCTGCAG R:GCTCCTTCCTTCCCTTTCCT	$(AC)_{11}$	157–187	40	9	0.675* (0.820)
Carcharhinus sorrah	CS 295[c]	F:GGGCATCCTCCTTTCCATCT R:GACTTTTCCCTTCCCGCTTG	$(AC)_{10}$	207–237	40	5	0.550 (0.520)
Carcharhinus sorrah	CS 55[c]	F:GCCTCATATTCCCACCATGC R:CTTTCAGGGTTTGCTGGCTG	$(CA)_{10}$	138–168	40	6	0.350* (0.463)
Carcharhinus sorrah	CS 102[c]	F:TTGCTGCCAGTCCCCTAAG R:GACAGGTTCGATGGCCAATG	$(GA)_{12}$	185–221	40	12	0.800 (0.801)
Carcharhinus sorrah	CS 104[c]	F:GATTGCCATCCCAACATGCT R:AGCCTCAGGTGATGGTGATT	$(AG)_{11}$	145–167	40	7	0.650 (0.755)
Carcharhinus sorrah	CS 51[c]	F:CAATGAAGACACAGGACGCA R:TCAGAGGTGGGGAGGGATAA	$(AC)_{11}$	187–217	40	7	0.775 (0.731)
Carcharhinus sorrah	CS 288[c]	F:CGCAGGCAAAGGAAGAATGT R:CCTCTTTCCAGTCCTCAGCA	$(AC)_{12}$	133–169	40	10	0.825 (0.816)
Carcharhinus sorrah	CS 25[c]	F:GCACCGCACTTTTGTCTTTG R:CCCAGAGCCCCAGAACATTA	$(AC)_{11}$	184–204	40	7	0.625 (0.730)
Carcharhinus sorrah	CS 381[c]	F:GCATTCCTGAGAGTTGAAAGCT R:TCATATCACGCCCTCTCACC	$(AG)_{10}$	220–248	40	5	0.425 (0.493)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Carcharhinus sorrah	CS 179[c]	F:TGGGGTCTGTGCTGAAGAAT R:GTATGCGCTGGGATTGCTTT	$(AG)_{11}$	146–168	40	3	0.600 (0.585)
Carcharhinus sorrah	CS 109[c]	F:AGCAATCGTGGCAGCATTAC R:TCCTTCCACCCTTTTCTGCT	$(GA)_{12}$	141–171	40	8	0.575 (0.529)
Carcharhinus sorrah	CS 29[c]	F:TGGACACACATACATGCCCA R:GAAGCGATTCAGGAAGGCAG	$(AC)_{12}$	241–273	40	11	0.725 (0.815)
Carcharhinus sorrah	CS 94[c]	F:TTAGTGTGTCAGGCTCAGCT R:CCTCCCAACATAGACAGGCA	$(AG)_{10}$	150–182	40	7	0.750 (0.750)
Carcharhinus sorrah	CS 400[c]	F:CCATGGTCAGCAATGCCTTT R:GCCTGAATGTTGCAGCTCTT	$(AG)_{11}$	218–250	40	12	0.775 (0.758)
Carcharhinus limbatus	AG 5[c]	F:TGCAGCAAAACACAGAGTCC R:TGCTGGGGTTGAACTCTTGA	$(AG)_{13}$	170–192	50	5	0.260 (0.240)
Carcharhinus limbatus	AC 50[c]	F:AACCCACATACTCACCCACG R:TGCTAACCTTCTGACCAGCA	$(AC)_{13}$	205–273	50	9	0.560 (0.625)
Carcharhinus limbatus	AC 60[c]	F:ACAGACTCACACACGCAAAC R:TGGGGCAGAAAGGATGATCA	$(AC)_{10}$	215–270	50	10	0.440* (0.677)
Carcharhinus limbatus	AG 10[c]	F:CAAGCTCATCCAACAGGCAA R:ATCCCTCAGTACTGCGCTAG	$(AG)_{11}$	198–216	50	9	0.780 (0.783)
Carcharhinus limbatus	AC 35[c]	F:TTGCTACCACTGACCTTGCA R:GTGACTCACCTGCAATAAACCA	$(AC)_{11}$	132–156	50	8	0.760 (0.758)
Carcharhinus limbatus	AG 2[c]	F:GACAGAGACACAAAACGGGG R:GGACCTGATCTCCGGACTG	$(AG)_{12}$	176–194	50	9	0.580* (0.785)
Carcharhinus limbatus	AC 17[c]	F:TGGGTGTGACATGGTTCAGT R:GTTTGGCTCTTTCCCTGTGG	$(AC)_{13}$	138–168	50	10	0.440* (0.633)
Carcharhinus limbatus	AC 47[c]	F:AGAAGGATGAGGCTTTGGTTT R:ACATCTTCCACAGCTAGGCA	$(AC)_{13}$	182–220	50	5	0.680 (0.664)
Carcharhinus limbatus	AC 27[c]	F:CACACGCATGCAAACACAAA R:CTCTTCCCACAAATCCCAGC	$(AC)_{17}$	132–180	50	20	0.800 (0.884)
Carcharhinus limbatus	AG 11[c]	F:TGAGTGGGTGCAGAACAAAC R:TAGCTGCACTTTGACTGACAC	$(AG)_{13}$	117–139	50	4	0.700 (0.632)
Carcharhinus limbatus	AC 15[c]	F:GCCACTCAACCCATCTTGTC R:TGGAGGGAGGGTCAGAGATA	$(AC)_{12}$	210–232	50	7	0.720 (0.683)
Molgula manhattensis	M1–6[d]	F:CTCAGACAAAGCAGCCAAG R:TCGGACTATGTAGGAAGGC	CA	209–229	24	7	0.375 (0.482)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Molgula manhattensis	M3–60[d]	F:GTGTTCACAGGCAAGAGTAAAG R:GTTTGCCTTACCGCTTCATC	CTT	173–182	24	3	0.250 (0.297)
Molgula manhattensis	M3–68[d]	F:GGTCAGGCATCGCTTCTT R:GGGTTGTCCAAGTTCGTAGT	ATT	175–178	24	2	0.381 (0.316)
Molgula manhattensis	M4–16[d]	F:CTGCATATCGGTAGAATCCTC R:GATTCACCAATTCCAGACCA	TCT	168–171	24	2	0.429 (0.438)
Molgula manhattensis	M1–3[d]	F:GCCAGAGTATGCGTTCTGTGCG R:TCGGAGCGGTAGACCGTCCGGTTCA	GCC	178–184	24	3	0.217 (0.204)
Molgula manhattensis	M1–33[d]	F:CTTGCTGTCCTCAACCCATC R:GGACCACCTGCTGATCCT	GTT	211–229	24	5	0.958 (0.741)
Molgula manhattensis	M1–84[d]	F:GGGATACTCTGGACGGTAAT R:CGTAGTCGAGTGAATAATCCAA	TAT	215–224	24	3	0.250 (0.227)
Molgula manhattensis	M1–100[d]	F:GACTGTAATGAGTTCGATTGGGT R:ATTTACACGCAACCTTACAACC	TTA	217–226	24	4	0.950 (0.741)
Molgula manhattensis	M1–27[d]	F:CTGTAGCACCAAGCGAAGG R:CAGTGGCTCTCGACTACCT	TAT	86–113	24	2	0.125 (0.120)
Molgula manhattensis	M3–95[d]	F:AGCTTCGTGTTAATGTGACTGT R:GTGTGAGAGTTGTGACCGTTT	ATAC	223–227	24	2	0.500 (0.422)
Molgula manhattensis	M1–60[d]	F:CAACGGTTTAACCTGTAGTTACTTG R:GATGTAGGTTGTTGCAAACAGAA	CCA	185–289	24	3	0.333 (0.301)
Molgula manhattensis	M1–61[d]	F:GCTACTTAAAGTTTCATGCCTCC R:TGTACCCGGTTACCACATAG	AAT	184–235	24	4	0.286* (0.562)
Molgula manhattensis	M3–12[d]	F:TCCCAACAACTGCCAACT R:GCTCGCATCTGTTGTTCTTG	TGGAC	204–260	24	4	0.583 (0.580)
Molgula manhattensis	M3–13[d]	F:CCTCCTGCCGCGCTACCTTCT R:TCCTGGCCCCGACTCCATCTT	TTC	149–162	24	3	0.417 (0.637)
Molgula manhattensis	M3–35[d]	F:GAGATATCAGTGGGAAGG R:GAATACGATCAGCTCCAG	TAA	162–174	24	3	0.125* (0.492)
Molgula manhattensis	M1–101[d]	F:CACAAATTTTGTATTACAGTGGCGC R:GACATACTAATGCATGAATG	TAG	158–167	24	4	0.833 (0.608)
Molgula manhattensis	M1–109[d]	F:CAAATGGCTGAGGGTGGGTCTGACC R:AGCCTTCGCAGTTGATGGTG	TG	234–245	24	4	0.958 (0.734)
Molgula manhattensis	M2–16[d]	F:CTTTGTTTGACAACATACGAAATCA R:ACAAGCGGCAGTCATCATAC	CTG	152–155	24	2	0.286 (0.483)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Molgula manhattensis	M2–30[d]	F:AGTTTCAATATAGTTTGTGTGGTCA	TCTG	167–179	24	2	0.250 (0.296)
		R:TAGTACTCTTAGCAGACATT					
Molgula manhattensis	M3–7[d]	F:TCATTTTAAATGAGTTTTAGGAAAT	TGAC	197–201	24	2	0.176 (0.337)
		R:TTGATCCAGATATTGGGTGG					
Molgula manhattensis	M3–23[d]	F:CATATATAATAAAATGTATTTTGTG	AC	165–171	24	2	0.333 (0.438)
		R:ACTTAAACAACAGATGGAGC					
Molgula manhattensis	M3–65[d]	F:GTCTATTTTGCAATTTTCATTTATT	AGG	129–160	24	3	0.458 (0.430)
		R:TACGTTTGGTCCCGCACTTA					
Petroica traversi	PT1[e]	F:GGCCCATCTTTGAAGGTTCT	$(AAAG)_{23}$	322–360	30	3	0.567 (0.660)
Petroica macrocephala chathamensis		R:TCCAAAGTATCCCACCAGCA				0	0.000 (0.000)
Petroica traversi	PT10[e]	F:CCTGCTCAAACTGAAGTCCG	$(TTC)_{20}(TCC)_{11}$	325–338	30	2	0.300 (0.381)
Petroica macrocephala chathamensis		R:TGACATCCCCTTTGTGATGC				2	0.400 (0.325)
Petroica traversi	PT12[e]	F:CACAGGGGAGGACTTGAGAA	$(ATAC)_{11}(AT)_{15}$	192–198	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:AGTTCAGGTCTGCTTTGTACA				4	0.567 (0.610)
Petroica traversi	PT18[e]	F:TCCCACCCTGTTCTCCATTT	$(AGT)_{21}$	220–229	30	2	0.467 (0.364)
Petroica macrocephala chathamensis		R:TTAGGTGCCGTGACTTCTCA				3	0.600 (0.677)
Petroica traversi	PT19[e]	F:AGCAGGCATTTTCAGCACTC	$(AGTG)_{17}$	173–201	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:GCAACCCCACAAAACCTGAT				7	0.833 (0.812)
Petroica traversi	PT2[e]	F:GCTATTTGTGCAGGGAAGTG	$(AAAG)_{23}$	202–226	30	2	0.367 (0.305)
Petroica macrocephala chathamensis		R:TGTGCCAGATTTTCCACAGC				6	0.700 (0.754)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Petroica traversi	PT24[e]	F:GCCAGCAGGTAAGTTGTGCT	$(ATC)_{24}$	119–153	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:CCTCCCTTCTCCCTGTCTCT			29	3	0.200* (0.640)
Petroica traversi	PT25[e]	F:TAAAGGGAGCAAAGGAGGCA	$(ATGG)_{17}$	150–208	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:TGTCCAAAGTCCCTCTCCAG			29	10	0.586 (0.727)
Petroica traversi	PT26[e]	F:TGCCATGCTTATTCTGGGGA	$(ATGG)_{17}$	196–238	30	2	0.033 (0.033)
Petroica macrocephala chathamensis		R:CTATGGGAGTGTGCCTGTAG				4	0.467 (0.681)
Petroica traversi	PT27[e]	F:ACATACCACCTGCCACTTCA	$(ATT)_{28}$	214–240	30	3	0.300 (0.362)
Petroica macrocephala chathamensis		R:TGTCTGGGCTTTAATGTCTCAC			28	7	0.714 (0.690)
Petroica traversi	PT35[e]	F:CTGAAAGAGGGCACAGCTTC	$(AC)_{20}$	83–88	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:GAGATGCACTTCTTTGGCGA				3	0.467 (0.453)
Petroica traversi	PT37[e]	F:TCTTGGTGGGGATCTACACAC	$(AC)_{21}$	121–141	30	2	0.300 (0.305)
Petroica macrocephala chathamensis		R:ACTTCCCATGGCAGAACAGT				2	0.400 (0.506)
Petroica traversi	PT38[e]	F:CCTGCCCAGACCAACTCT	$(AC)_{21}$	101–105	30	2	0.233 (0.259)
Petroica macrocephala chathamensis		R:AAATGAATCCTCGCTGTCCA			8	0	0.000 (0.000)
Petroica traversi	PT39[e]	F:CCATGCAACTACGGGTGTTT	$(AC)_{21}$	99–109	30	2	0.367 (0.463)
Petroica macrocephala chathamensis		R:TGTCTGAGAACCCCAGAAGG				2	0.367 (0.345)
Petroica traversi	PT4[e]	F:TATCTCCACATGGTGCAGGC	$(AATG)_{14}$	281–300	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:TGCTATGGTTTTATGCCCTGG			29	6	0.897 (0.753)
Petroica traversi	PT40[e]	F:ACTTTGAAATACTCTCGAGGGC	$(AC)_{25}$	132–143	30	2	0.557 (0.508)
Petroica macrocephala chathamensis		R:TGGAATCCATTTTGTGCAAT				1	0.000 (0.000)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Petroica traversi	PT5[e]	F:GTCTCTGGTGAGTCCTGGGG	$(AGGG)_{10}(ATGG)_{10}$	246–254	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:GGGGTTTGGAACAATCATCC				3	0.433 (0.515)
Petroica traversi	PT6[e]	F:CAACCATGTGAACGGTCTGC	$(AGT)_{21}$	268–300	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:AAAGGAGTGGGATTTGGAAGC				5	0.467 (0.563)
Petroica traversi	PT7[e]	F:GCTCACCTTTTACAATCCTCTGC	$(ATCT)_{15}$	265–288	30	3	0.600 (0.594)
Petroica macrocephala chathamensis		R:CCTGCTGCTGTTTAGAAGCC				5	0.800 (0.755)
Petroica traversi	PT9[e]	F:CCTCTTGGAGAGGTTCTGCG	$(TGC)_{23}$	285–304	30	1	0.000 (0.000)
Petroica macrocephala chathamensis		R:GTGATGAGTCAGCTCCAGCG				4	0.300* (0.488)
Lateolabrax maculatus	LM05[f]	F:AGACAGATGGGAACGAGACG	$(AC)_{10}$	245–253	32	5	0.529 (0.579)
		R:CTGGTTCTCCTCCACTCTGC					
Lateolabrax maculatus	LM06[f]	F:CACAGCTTGCTAGAATGGCA	$(AC)_{17}$	183–223	32	14	0.667 (0.894)
		R:ACATTGTTACCGCCAGCTCT					
Lateolabrax maculatus	LM08[f]	F:TAAACCAGGAGGAGGTCTGC	$(CA)_{18}$	243–265	32	8	0.600 (0.823)
		R:CACACAAAACAACGTCCCTG					
Lateolabrax maculatus	LM09[f]	F:AGGCAGGGGAACTTACACAA	$(TG)_{10}$	217–227	32	5	0.556 (0.521)
		R:TTGAAGCTTTGCTGTTCCCT					
Lateolabrax maculatus	LM12[f]	F:CCGCTCAAAGGTTCCTACAA	$(GAA)_8$	142–160	32	5	0.938 (0.668)
		R:GGGATGTCCCCCTTTACATT					
Lateolabrax maculatus	LM13[f]	F:TGCAGTGAGTGGCTTCAGAC	$(GT)_{13}(GA)_6$	192–226	32	10	0.742 (0.746)
		R:CGAGCAGAAGGGAGAGTTCA					
Lateolabrax maculatus	LM14[f]	F:TCCTCTCTCTGCTTTGGCAT	$(TG)_{13}$	236–250	32	7	0.533 (0.768)
		R:TAAAAGCTTGTGAGCGCGTA					
Lateolabrax maculatus	LM15[f]	F:CGGAGAGTCCAGAGCAAGTC	$(TG)_{11}$	247–261	32	8	0.656 (0.793)
		R:ACGCCATACACTTCCACACA					
Lateolabrax maculatus	LM18[f]	F:AGAGCCAGGGTATGCATCAA	$(GT)_{10}$	182–244	32	8	0.517 (0.765)
		R:TAGATTAGGCATGCGCACAG					
Lateolabrax maculatus	LM19[f]	F:AGCGAGACCTCAGCCTGACT	$(GT)_{12}$	271–283	32	7	0.226* (0.726)
		R:GCTGTGCATGTCATTTGTCC					

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Lateolabrax maculatus	LM21[f]	F:CGCTCTGCTTTCATGTACCA R:GACAGGAGAGGAGCCAACAG	$(GT)_{14}$	145–163	32	10	0.750 (0.870)
Lateolabrax maculatus	LM23[f]	F:ACAGAGGAACCCATGCAAAC R:TTACCTCCGCTTGTGTCTCC	$(CAG)_7$	114–129	32	6	0.643 (0.716)
Lateolabrax maculatus	LM24[f]	F:TCGATAAACGGCAGATTGTG R:TGCCACAGACATGATACGGT	$(TG)_6$	184–188	32	3	0.467 (0.603)
Lateolabrax maculatus	LM30[f]	F:TAAGAGCACATGTGTCCCCC R:TACGAGGCATTGTGCAAGAG	$(AC)_{7t}(CA)_6$	240–256	32	9	0.625 (0.785)
Lateolabrax maculatus	LM36[f]	F:AAGGTAAGGCCCAGAACCAT R:GAAGGACCTGGTGTTTGGAA	$(AC)_7$	173–177	32	3	0.633 (0.595)
Lateolabrax maculatus	LM37[f]	F:AGTACAGTGGGGGAGGAAGG R:GTCAGAAGGTTGGCTCTTGC	$(GA)_{12}$	154–174	32	10	0.760 (0.895)
Lateolabrax maculatus	LM38[f]	F:AACGAGCTCCGACCTGTTTA R:CATCCCTTCACTTTTGGAGC	$(AATA)_4$	300–312	32	3	0.778 (0.586)
Lateolabrax maculatus	LM39[f]	F:ACATCAACAACTGTGGCAGG R:ATTTGTTGGCATCAAGTCCC	$(TG)_{13}$	294–332	32	11	0.708 (0.903)
Lateolabrax maculatus	LM40[f]	F:CGGTGGAAGTGGATCAGTAAG R:AGGAGGTGACATAACCACGG	$(GGT)_5$	297–320	32	7	0.807 (0.782)
Lateolabrax maculatus	LM42[f]	F:GCACCGCATTACATCATTCA R:GCACAATCGTATGCCAACAC	$(AC)_6$	233–255	32	7	0.667 (0.715)
Lateolabrax maculatus	LM44[f]	F:AGCACACATCACTTCCTTAGCA R:TCTCAGATGGCGTCTCACAG	$(TG)_{13}$	255–281	32	12	0.563 (0.894)
Lateolabrax maculatus	LM46[f]	F:ACAGTGCACGGAGTGATTGA R:GAACACGTGTGCGGTACATC	$(TG)_9$	249–261	32	7	0.567 (0.788)
Lateolabrax maculatus	LM47[f]	F:CTGCAGAGGGAAGACAGAGG R:CGCACTTCATCCTGTCAGTG	$(AC)_{10}$	191–207	32	9	0.563 (0.802)
Silurus lanzhouensis	SLsis43[g]	F:AGGCTCTGTCCCAAATGCT R:CACGGAGACGAATCTGACCT	$(AC)_{21}$	236–248	30	3	0.233 (0.660)
Silurus lanzhouensis	SLsis26[g]	F:CATGGGAATACGTGTCG R:CAGGTCTGATTAGTGGC	$(GA)_{16}$	201–210	30	6	0.200 (0.848)
Silurus lanzhouensis	SLsis14[g]	F:GGGATGGCGGAATGGGA R:CCCCGGATTCTGCACCA	$(AG)_{28}$	227–238	30	5	0.552 (0.752)
Silurus lanzhouensis	SLsis46[g]	F:TGCGAGACGAGTGAAGA R:CGCTGGAGCTATGATTT	$(AG)_{16}$	167–179	30	4	0.404 (0.708)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis2^{g}	F:GTGCTGCAAATGTTCTCAGTGAA R:CTGGAGATGGTGGGACAGTAGGT	$(AC)_{31}$	244–268	30	4	0.733 (0.756)
Silurus lanzhouensis	SLsis89^{g}	F:TGAGTCCTGAGTAAGTGGTGGAGGG R:CTGACACTCCATCTGTCTCGGGTGC	$(AC)_{26}$	124–141	30	3	0.243* (0.641)
Silurus lanzhouensis	SLsis30^{g}	F:AGCTGTATGAGAAGTTGGACACT R:TAATCCTATCCACTTCCTGCTTT	$(GA)_{22}$	259–291	30	5	0.702 (0.798)
Silurus lanzhouensis	SLsis272^{g}	F:AAATGCTAAGCCGCAGTGTTGTA R:ACAGGGAGGTAACTAGCCCAAAG	$(TG)_{25}$	220–230	30	5	0.625 (0.786)
Silurus lanzhouensis	SLsis260^{g}	F:GGAGTGAGTGACGCTGTGATGAT R:CTCCAAACATGATCCCTCACCTA	$(GT)_{23}$	140–150	30	5	0.667 (0.693)
Silurus lanzhouensis	SLsis6^{g}	F:CTGTGCCAAATGATATGTATGAG R:CCTTCAGTCTTTATCTCCTTCTC	$(AG)_{19}$	235–240	30	3	0.417 (0.414)
Silurus lanzhouensis	SLsis123^{g}	F:CACCTTCTTTCTGTCTGCCCTCT R:GGAGATGCAAATAAAGAACCCAC	$(CT)_{12}$	177–201	30	4	0.217 (0.312)
Silurus lanzhouensis	SLsis284^{g}	F:TCCAACCCCAACCTGAGGGAGAC R:CTCATCCAGGACGGCCTAACACG	$(CT)_{19}$	201–220	30	5	0.522 (0.568)
Silurus lanzhouensis	SLsis108^{g}	F:GCACATAATAATGATTCGTTTTC R:TATGTTTTCAGGACCGGAGTTAC	$(CT)_{27}$	156–167	30	4	0.609 (0.496)
Silurus lanzhouensis	SLsis118^{g}	F:ACATTCCTGGGTACATTCAGAGC R:AAGCAGTATGTGGAGTGTATGGG	$(GA)_{32}$	245–250	30	3	0.583 (0.504)
Silurus lanzhouensis	SLsis83^{g}	F:CCCCAACTGCTCGCTCTATTTAT R:TGGCATTTCTGCTTGACCCACAT	$(GT)_{26}$	244–277	30	5	0.582 (0.532)
Silurus lanzhouensis	SLsis18^{g}	F:GGAGGACCTGTGAAGTGTTTAGA R:CGCTCATGCTAATACACTGACTAT	$(TC)_{12}$	185–230	30	4	0.424 (0.213)
Silurus lanzhouensis	SLsis122^{g}	F:CCACCTCAGCAACAAGGAAGAAT R:ACAACCCAATCCCATACCCGATC	$(TC)_{17}$	322–340	30	5	0.623* (0.524)
Silurus lanzhouensis	SLsis137^{g}	F:TTCTCGATCTCCACCTCATCTGT R:AGACAGTCTGAGCGGTACGTGAG	$(TC)_{19}$	197–230	30	2	0.123 (0.131)
Silurus lanzhouensis	SLsis3^{g}	F:TAAGGGACAAGGCAATCATATGGCA R:CTATGGGATTTGTTTATTGTGGC	$(AC)_{36}$	215–230	30	5	0.679 (0.579)
Silurus lanzhouensis	SLsis98^{g}	F:AGGCCAAGGTACATCTCCAACCC R:CAGGTCCGTCTGCTCCACCATCA	$(TG)_{22}$	234–250	30	6	0.432 (0.411)
Silurus lanzhouensis	SLsis195^{g}	F:GTGCAGTGCGCCCACCAAAAAC R:TGTTGAAGGTGCGATACACTGAC	$(CA)_{21}$	261–282	30	4	0.429 (0.603)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis184^{g}	F:TGAGTCCTGAGTAAGGGTCTAA R:CACAAGTGCACCATTCCCAGAA	$(CA)_{10}$	190–202	30	3	0.543 (0.425)
Silurus lanzhouensis	SLsis186^{g}	F:AAGGCTCAATTCCCCTGAGATAC R:TAACGTCCCAAATGTAAGAAAAC	$(CA)_{18}$	139–150	30	3	0.497* (0.440)
Silurus lanzhouensis	SLsis187^{g}	F:GTGCTTTATTGTGGGCTGGTTAT R:CACCTGTGTAAGAACATACCTTC	$(CA)_{22}$	115–122	30	5	0.349 (0.645)
Silurus lanzhouensis	SLsis190^{g}	F:ATGGAGCTGAATGCTAAGAAGAG R:CTACTATTCAAATATAACACATT	$(AC)_{29}$	231–244	30	4	0.388 (0.382)
Silurus lanzhouensis	SLsis213^{g}	F:ATGCTCAGTGTTGTTACGACCTG R:AACCAGCCTGTTAGAATGGAAAT	$(AG)_{19}$	109–114	30	4	0.426 (0.352)
Silurus lanzhouensis	SLsis214^{g}	F:AGTCCTGAGTAACCAAAATCTG R:TGTCTTGCTTTCCTTCCTCTTCT	$(GT)_{9}$	201–223	30	6	0.662 (0.634)
Silurus lanzhouensis	SLsis216^{g}	F:ACTGCGGCTTAGCATTTTATT R:ACTAGTCTACCCCATTCTACACT	$(TG)_{10}$	133–136	30	2	0.383 (0.334)
Silurus lanzhouensis	SLsis225^{g}	F:CCTCGTTCATCTTGTATTGTT R:GAGATCCAGAACCCGATTTTA	$(CA)_{8}$	169–178	30	5	0.403 (0.626)
Silurus lanzhouensis	SLsis230^{g}	F:GTCTGTCAACACACAGCATAGC R:GCTGTTCAGCTCGTTCAGTCG	$(CA)_{16}$	175–198	30	3	0.381 (0.290)
Silurus lanzhouensis	SLsis233^{g}	F:TTCAGTCTCACTTCCCAAATA R:GAGTTATAGCTCATTCACCCT	$(CA)_{37}$	162–181	30	6	0.860 (0.754)
Silurus lanzhouensis	SLsis245^{g}	F:GTCCTGAGTAATAATCCATAAC R:TGATGAGAAACCGTCCCAAGC	$(TC)_{21}$	235–243	30	4	0.552 (0.509)
Silurus lanzhouensis	SLsis263^{g}	F:AAGCGTACTCGAATCTATCTC R:CACAGTATGGGGTGAAGGAGA	$(TG)_{13}$	221–224	30	3	0.282 (0.382)
Silurus lanzhouensis	SLsis267^{g}	F:AGTAACCATTACAACCAGCAC R:CTCAAAGACATCCAATCATCT	$(TG)_{19}$	130–138	30	3	0.431 (0.326)
Silurus lanzhouensis	SLsis272^{g}	F:CCAAGGTACATCTCCAACCCC R:GTCCGTCTGCTCCACCATCAT	$(TG)_{25}$	171–182	30	5	0.624 (0.573)
Silurus lanzhouensis	SLsis282^{g}	F:TCAGAGCGTTCAAGCGACAGA R:CTGGGAGTAAACTTGACTTCTTT	$(CT)_{17}$	121–127	30	3	0.423 (0.401)
Silurus lanzhouensis	SLsis301^{g}	F:ATTCATCACTCAGCGTCCCTC R:ACGGTCTGAAAACTAGCCCAT	$(GA)_{16}$	169–178	30	5	0.562 (0.533)
Silurus lanzhouensis	SLsis302^{g}	F:AGCTCTACACTGGAAGCTAAT R:TCCTGAGTAAGGGACTGAAAG	$(GA)_{26}$	244–248	30	3	0.412 (0.317)
Silurus lanzhouensis	SLsis9^{g}	F:ATCACCATTTTCTACACTCATC R:ACTCTATGGGACTATAATGGG	$(AG)_{34}$	156–167	30	4	0.833 (0.521)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis17[g]	F:AGAGATATCGATTTATTGGAGCT R:CAAGCAATGTGAGGGGAGGAA	$(CA)_{22}$	158–163	30	3	0.222 (0.210)
Silurus lanzhouensis	SLsis20[g]	F:TGATAGGATAATAAGCAGA R:CCGATTTCAAAGCAACT	$(CT)_{25}$	198–206	30	4	0.673 (0.562)
Silurus lanzhouensis	SLsis37[g]	F:AGGATGTAGCAAAGGCAGAG R:AGAGCCGGTTGAGTGGG	$(TC)_{24}$	121–129	30	4	0.524 (0.501)
Silurus lanzhouensis	SLsis165[g]	F:TAACCTGCACATATCATTGTATC R:GTGTAGGTGTGGACTACCAGC	$(CTG)_{8}$	205–220	30	3	0.288 (0.139)
Silurus lanzhouensis	SLsis180[g]	F:TCAACTATGGACTTGGATTACGC R:AGGAGGAGGTTTATGGATGTGGT	$(TCT)_{8}$	189–220	30	3	0.342 (0.334)
Silurus lanzhouensis	SLsis136[g]	F:GGAGCGAAAGGGAGTTGGCTAGT R:AGTGAAAGGACCACAGTGGAGGA	$(CAG)_{17}$	225–250	30	4	0.467 (0.327)
Silurus lanzhouensis	SLsis166[g]	F:TGGTTCTGTCTTCTGAATTCCAT R:TAAGGCCAGTGTAGGTGTGGACTAC	$(CTG)_{8}$	255–275	30	3	0.587 (0.412)
Silurus lanzhouensis	SLsis143[g]	F:GAGACGGAATAACACTGTGGGAGAC R:GAGGCAAAGCTGAGTATGGAAGG	$(GATA)_{12}$	308–330	30	5	0.305 (0.321)
Silurus lanzhouensis	SLsis150[g]	F:TAACTGGACCTCACATCATATTA R:CCATCCATCTATCTATCTGTCTG	$(ACAG)_{24}$	325–355	30	4	0.731 (0.632)
Silurus lanzhouensis	SLsis170[g]	F:CGGGACATGGTTCGGTTTAGGTG R:GGCCCATTGTCATTACTGTATTGGTCT	$(GATA)_{9}$	188–203	30	5	1.000* (0.730)
Silurus lanzhouensis	SLsis10[g]	F:CTTTTCTGTTTCATTTCTTCCTC R:ATGACCAGGCAAACATTAGATAG	$ATCT_{26}$	425–438	30	4	0.631 (0.582)
Silurus lanzhouensis	SLsis171[g]	F:TGCAGTTATGTCACATTACTCAC R:AGATGACAGTGGATCTAAGACAG	$(ATCT)_{15}$	192–202	30	3	0.254 (0.631)
Silurus lanzhouensis	SLsis85[g]	F:TAACAGGGCTGGCTTCAGGTAAC R:GAACTTATGGGCTGGATCATGGC	$(AC)_{17}(CA)_{8}$	226–243	30	6	0.662 (0.569)
Silurus lanzhouensis	SLsis52[g]	F:CCTCCCTGTGAGGACAACAAGAG R:CTTCACGCTGCCACGAATTAGCT	$(AC)_{15}(AC)_{18}$	217–228	30	4	0.479 (0.573)
Silurus lanzhouensis	SLsis168[g]	F:GCCAGCAACCCAATTCTCTGGAT R:ACCTGAGCCCTGCGAAAGGAAGT	$(GA)_{24}(GA)_{12}N(GA)_{16}$	325–335	30	7	0.437 (0.508)
Silurus lanzhouensis	SLsis226[g]	F:ACGTGTGAGGGAGAGAGAGC R:TTGTCATCCAGGACTCCACTT	$(CA)_{8}N(CA)_{20}$	234–238	30	3	0.383 (0.334)
Silurus lanzhouensis	SLsis215[g]	F:CTGTTCAGTCCTGGCCTCTACTT R:TGAGACACATCTCTAAACCAAC	$(CA)_{26}N(CA)_{7}$	187–104	30	5	0.748 (0.603)
Silurus lanzhouensis	SLsis189[g]	F:GCCACAGAACTGGTTTGGCTC R:TGTTTCCCCAGCCTGTCTTTACT	$(AC)_{28}N(CA)_{10}$	150–172	30	4	0.683 (0.509)
Silurus lanzhouensis	SLsis242[g]	F:GCACTATGGTACTGCTGATAA R:CTTTCTTTCCTTCAGTTTGTC	$(TC)_{11}N(CT)_{11}$	312–319	30	3	0.353 (0.440)
Silurus lanzhouensis	SLsis300[g]	F:ATGTCCATCAAGCCCTCCAAC R:TCATCGGCTGGTCTTCATCTC	$(GA)_{13}N(GA)_{9}$	193–203	30	4	0.479 (0.582)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis280^g	F:GGCTTTGTAATGCACAACAGG R:CAGACAGCAGAGTGGAAGGAA	$(TC)_{12}N(CT)_{11}$	191–202	30	4	0.578 (0.504)
Silurus lanzhouensis	SLsis310^g	F:AAACAACAACGATGCCTGATC R:GACTGAGTGAGCCCCACATAC	$(GT)_8N(TG)_6$	113–121	30	3	0.424 (0.451)
Silurus lanzhouensis	SLsis324^g	F:CATCTATCAATAAACCGAACA R:GAATGAAGTAGACAGGCAGAC	$(TC)_7N(CT)_{14}$	215–236	30	3	0.341 (0.422)
Silurus lanzhouensis	SLsis201^g	F:GAGTAAGGGGCGAAAAGAAAGTA R:GAGTCCTGAGTAAAATGAGTC	$(AG)_{22}N(ACAG)_5$	265–279	30	3	0.482 (0.382)
Silurus lanzhouensis	SLsis204^g	F:AAATGAAACCAAACCCCAACTCT R:ACAACCAATCACATTTAGCTTTAC	$(AG)_{32}N(TG)_{29}$	263–285	30	7	0.665 (0.503)
Silurus lanzhouensis	SLsis210^g	F:GAGTCCTGAGTAATGCACGTATG R:GTTTTCATGCAGGACTTCTCTC	$(GA)_7(CA)_{10}$ $N(CA)_6$	249–264	30	5	0.785 (0.660)
Silurus lanzhouensis	SLsis260^g	F:AATTCTTCTCGAAGCCTACAG R:CAAACATGATCCCTCACCTAA	$(TG)_8N(GT)_{23}$	157–164	30	4	0.617 (0.666)
Silurus lanzhouensis	SLsis264^g	F:ACATTCACTTCCCGTTCATTA R:CACGGCAGTCCTACAGTTGAG	$(TG)_{14}N(TC)_6$	212–230	30	5	0.447 (0.503)
Silurus lanzhouensis	SLsis19^g	F:TGACTGACGCTCGCTCTT R:CACCTCCAAATGACAAATC	$(CT)_{14}N(AC)_{18}$	239–254	30	2	0.316 (0.370)
Silurus lanzhouensis	SLsis1^g	F:TGAAACAGAAACTCGTG R:GTGAGACGTAGCCTCTT	$(AC)_{29}N(GA)_{24}$	237–255	30	2	0.133 (0.508)
Silurus lanzhouensis	SLsis76^g	F:ACTGTCTCTTTTTCTCTTCATTTAT R:GTCCTGAGTAAGGAGGGGTAGAG	$(AC)_{11}N(TC)_{23}$	193–208	30	3	0.417 (0.687)
Silurus lanzhouensis	SLsis47^g	F:CCTGTCATTCCTGATAACACCTA R:GTCCTGAGTAACCTACACTCAGTCA	$(AG)_{31}N(GT)_{32}$	187–215	30	3	0.281 (0.287)
Silurus lanzhouensis	SLsis8^g	F:GAACGAGGATGGACGAG R:CGATGTTGATTCTGGAT	$(AG)_{28}N(AC)_{14}$	232–238	30	2	0.097 (0.186)
Silurus lanzhouensis	SLsis249^g	F:ATCAGCACAGCAACACCTCACTT R:TTTCTATACTCTGTATGCGGCTC	$(TATC)_{15}(TCT)_{13}(TCTG)_{16}$	475–493	30	6	0.544 (0.500)
Silurus lanzhouensis	SLsis112^g	F:GAGACGGAATAACACTGTGGGAGAC R:GAGGCAAAGCTGAGTATGGAAGG	$(CA)_{40}(CA)_{33}$	264–288	30	4	0.569 (0.534)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis36^{g}	F:ATTAGCCAGTTTACATAC R:ATTGATTCTTGGAGGAG	$(TC_{)20}N(CT)_{14}$	221–236	30	2	0.310 (0.290)
Silurus lanzhouensis	SLsis31^{g}	F:CATGGGAATACGTGTCG R:CAGGTCTGATTAGTGGC	$(GA)_{22}N(AG)_{32}(CA)_{37}$	437–452	30	4	0.569 (0.498)
Silurus lanzhouensis	SLsis120^{g}	F:GGCTGGCACACAACAGGCAG R:AGTTTGCTTTATGAACAGAGGCT	$(AGAT)_{6}(TAG)_{15}N(AG)_{24}$	245–275	30	9	0.765 (0.747)
Silurus lanzhouensis	SLsis27^{g}	F:TAACTGATATGAAATGAAATATGAC R:CCACTCTCTCTATTTCTTTCTCTCT	$(GA)_{18}(AGAT)_{8}N(AG)_{24}$	316–349	30	5	0.640 (0.582)
Silurus lanzhouensis	SLsis159^{g}	F:AGCTCGGTACCCGGGGATCCTCT R:GCTCGTTTCGATGTGCTCTTTCT	$(CAG)_{6}N(CAG)_{6}$	196–230	30	4	0.683 (0.603)
Silurus lanzhouensis	SLsis181^{g}	F:CGAACTCAAGAGCTACATGG R:TTTGACATTCTCAGCAAGAATT	$(AAAT)_{5}N(CA)_{10}$	182–197	30	4	0.678 (0.599)
Silurus lanzhouensis	SLsis192^{g}	F:AAGTGTAGGCATAGTGGGAGGAT R:ATTGTGAGCGGATAACAATTTCA	$(AG)_{6}N(AG)_{11}N(AGAA)_{18}$	269–280	30	6	0.617 (0.666)
Silurus lanzhouensis	SLsis207^{g}	F:ACAACAGGCAGATAGATAGATAG R:CTGAGTAACCCAGGAAAAATCT	$(AGAT)_{20}N(AG)_{26}$	221–233	30	4	0.506* (0.399)
Silurus lanzhouensis	SLsis228^{g}	F:GTCCAAATAAAAGTCTGGAGG R:CCAATCTGCTGTCGTTTCTCA	$(GA)_{5}N(AAAG)_{18}$	316–332	30	8	0.660 (0.747)
Silurus lanzhouensis	SLsis285^{g}	F:AGTTTGCTTTATGAACAGAGG R:TCACTGCATTGTCTGCGTGAT	$(CT)_{40}N(AC)_{11}N\ (TC)_{18}N(CG)_{12}$	558–576	30	7	0.732 (0.694)
Silurus lanzhouensis	SLsis305^{g}	F:AAGGAAGGAATGAAGCAGACA R:TATGACCATGATTACGCCAAG	$(CAGA)_{12}N(GA)_{19}$	345–355	30	5	0.623 (0.600)
Silurus lanzhouensis	SLsis314^{g}	F:GATTTAGGTCCCAGTGTCGTG R:CTTCCGCTCCGTTACATCTGC	$(GT)_{13}N(GA)_{24}$	261–272	30	4	0.100 (0.529)
Silurus lanzhouensis	SLsis325^{g}	F:AAAATCTTCATGGAGTTTGCTT R:TGTGGAATTGTGAGCGGATAA	$(TC)_{8}N(CT)_{17}$ $N(TCTA)_{18}$	303–315	30	5	0.640 (0.435)
Silurus lanzhouensis	SLsis234^{g}	F:CACAGACACACACCAAACTCATCAC R:GCATACTCCATTGCACTGTCT	$(CACT)_{5}N(CT)_{6}(CTCA)_{8}$	146–155	30	5	0.401 (0.635)
Silurus lanzhouensis	SLsis235^{g}	F:CCTCACCTCTTCACTTACACCCAC R:GCTGATGACCGACCCCTAAAA	$(CAT)_{5}(GA)_{12}(AG)_{30}N(GA)_{8}N(GA)_{19}N(AG)_{11}$	409–421	30	9	0.890 (0.760)
Silurus lanzhouensis	SLsis244^{g}	F:CCTTTACATAACCTCTGCTAC R:GTCCTGACTAACCCGAGTGTC	$(TC)_{15}N(CT)_{14}(TCTA)_{13}N(GT)_{7}$	396–401	30	6	0.649 (0.645)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Silurus lanzhouensis	SLsis248^{g}	F:GGTCGAGATAACCGGGTTTGA R:AACGCTGGGGCAAGTACAATC	$(TCTG)_8N(TCTA)_5N(CTAT)_7$	251–266	30	5	0.518 (0.482)
Palaemon serratus	Pser–01^{h}	F:CTTCACGCTCGGTTCTGTCT R:TGGATTGCAGCGAACACTTA	$(AAG)_5$	105–108	20	2	0.050 (0.049)
Palaemon serratus	Pser-02^{h}	F:TTTGGTATAATCGTTATCATTC R:AAGGTGCATTAATTGTGGCG	$(AC)_7$	118–132	19	4	0.474 (0.539)
Palaemon serratus	Pser-03^{h}	F:AGGAATACCAGGAGGCGAAG R:TTTCGTCATCTATTCATTAAGCCC	$(AGG)_{15}$	206–215	20	4	0.600 (0.581)
Palaemon serratus	Pser-04^{h}	F:GACACCAGGAGTTGATGGGA R:AGGCTACTCCTTTCCGATGC	$(AG)_{32}$	212–258	13	12	0.308* (0.896)
Palaemon serratus	Pser-05^{h}	F:GGATGGATGTTTGTAAGCCG R:CCTTCAATCAATGGCATCGT	$(AG)_{27}$	93–135	20	8	0.500* (0.798)
Palaemon serratus	Pser-06^{h}	F:AGCGGATTTGTCAGCGAGT R:CTGCATCATTAGGGCATTCA	$(GA)_7$	109–113	20	3	0.700 (0.646)
Palaemon serratus	Pser-07^{h}	F:GAACCTCGCGCTGAGAATAA R:ACTAAGGTGTTTGGAGGCGG	$(AG)_8$	362–364	20	2	0.050 (0.049)
Palaemon serratus	Pser-08^{h}	F:TCTTGAATTTGGGCCACCTA R:AGAACCGCCATTGTTCTTCA	$(ACT)_{19}$	231–273	20	14	0.750 (0.901)
Palaemon serratus	Pser-09^{h}	F:TGTCGAAACAGGGTCACCAC R:GAACATCGAAATGTCCTGGC	$(AG)_6$	90–128	20	5	0.450* (0.716)
Palaemon serratus	Pser-10^{h}	F:GGAGCCCTTGGGAATATAGC R:GGAACGAGATAGGAATCGGG	$(ACT)_6$	140–146	19	3	0.789 (0.576)
Palaemon serratus	Pser-11^{h}	F:TCATTATCATTGGCATGATCCTT R:CCTTTATGTCATTAATTTGACCTTTG	$(AAG)_8$	111–117	19	3	0.368 (0.497)
Palaemon serratus	Pser-12^{h}	F:GCAGCATTGCTTAGCACGTT R:GAGAGAGAAGTGAACAGGAGCAA	$(ACG)_6$	104–113	20	4	0.600 (0.621)
Palaemon serratus	Pser-13^{h}	F:TCAAGGCCAGTCGTATGAAA R:CTCCTGGTCTCATTTGTCGC	$(AAT)_{22}$	391–448	20	17	0.950 (0.916)
Palaemon serratus	Pser-14^{h}	F:AGGCACTTCGATTGCTCTTT R:GTTGTGGAATGCACAGGTGA	$(AG)_{12}$	347–377	20	6	0.600 (0.661)
Palaemon serratus	Pser-15^{h}	F:TCGTTGTTCGTTGAAATAGGAA R:ACCGCTCAACTTTCCGGTTA	$(AAT)_7$	85–136	20	4	0.700 (0.516)
Palaemon serratus	Pser-16^{h}	F:GGGAAGATTTGGGATAAGGG R:GTGTCTGCCACCACGTAGC	$(ACG)_5$	100–103	20	2	0.400 (0.375)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Palaemon serratus	Pser-17^h	F:CAAGAACAACAACAACATTGACG R:CCCACCAAATTAAGCCAACA	$(AAC)_5$	489–507	20	2	0.800 (0.480)
Palaemon serratus	Pser-18^h	F:ACCTCCAAGATGGGCGAAC R:GTTCAACGCGGAGACCAACT	$(TCA)_4$	246–249	20	2	0.300 (0.320)
Palaemon serratus	Pser-19^h	F:CGGCACATGTAAAGTCCCAT R:TACCCTATCCCGACCAAAGA	$(AT)_{32}$	122–140	20	2	0.050 (0.049)
Palaemon serratus	Pser-20^h	F:CAATATACCGCCGTTACCAAA R:AACTAACCACCCATCCCACC	$(AG)_5$	58–112	19	4	0.158 (0.240)
Patinopecten yessoensis	comp98831_c0^i	F:GGAGGTAGCTGAAGCAGGTG R:TGAAGGGGATTTGTCCGTGG	$(AGG)_7$	176-182	30	3	0.233* (0.606)
Patinopecten yessoensis	comp78880_c0^i	F:GCGCTAGAAGAGGCCAAAGA R:TTGGACCGTCGCTTTGAAGA	$(TCC)_7$	191–194	30	2	0.233 (0.503)
Patinopecten yessoensis	comp97448_c0^i	F:GTGGGTTGGAGTGGACAGAG R:TCCTACCCTTCCACTCTCCC	$(AG)_{10}$	155-165	30	2	0.733 (0.488)
Patinopecten yessoensis	comp78253_c0^i	F:CCCCATCACCATCAACACCA R:GGCTGGTTGACTACGTCCTC	$(CCA)_8$	215–302	30	2	0.800* (0.488)
Patinopecten yessoensis	comp90979_c0^i	F:GTTCTATGCAAAAGGCCACGT R:CATCATTCACTGCGCCACAC	$(AT)_{10}$	251–291	30	3	0.967* (0.564)
Patinopecten yessoensis	comp86107_c0^i	F:TGGGCAAGACAAAAAGGGGT R:CCACGACATAAGGAACTGCCA	$(TGG)_7$	189–192	30	2	0.300 (0.381)
Patinopecten yessoensis	comp92083_c0^i	F:GACATTTTCGCGGTGTGGAC R:CACCTGGTTATTTTGTGCAGCA	$(CAC)_7$	263–269	30	3	0.700 (0.527)
Patinopecten yessoensis	comp96141_c0^i	F:TTCGGCAGGTTTGTGTTGTC R:TGCACTCTGGGATAAACCTCC	$(ATCA)_5$	100–104	30	2	0.267 (0.427)
Patinopecten yessoensis	comp98716_c1^i	F:TGCTCTCCGAGTGTTTTGTCT R:TAACGCGCCGAGTAACAAGT	$(TA)_{10}$	174–184	30	2	0.633 (0.494)
Patinopecten yessoensis	comp100333_c0^i	F:CTCGTGAGATTCGTCTCGCA R:CCACGGTCAGCTTCAGTCAT	$(AAC)_7$	193–199	30	3	0.533 (0.450)
Patinopecten yessoensis	comp88914_c1^i	F:TGCCTCACTTCCTTCTCCCA R:GGAACCTCGTCAATCATACTCCT	$(GACA)_5$	274–294	30	3	0.900* (0.552)
Patinopecten yessoensis	comp92015_c1^i	F:GGTACCGTGAACGAATGGGA R:TCGAAAGAGGGTGATGCAGA	$(TATC)_5$	225–233	30	3	0.500 (0.495)
Patinopecten yessoensis	comp89752_c1^i	F:TGCTAAACGTTGTATGGCACTC R:CATCAGAGTGTGCTGGGTGA	$(TAAA)_5$	225–229	30	2	0.133* (0.499)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Patinopecten yessoensis	comp95685_c0[i]	F:CATCTCCTGTACAGATGTGCC R:ACCCTCTAGATGGCGCTACA	$(AT)_{10}$	113–131	30	3	0.967* (0.564)
Patinopecten yessoensis	comp95797_c0[i]	F:ATCGACAACAACGACACCGA R:GGGGTCGGAGTGAATGTTGT	$(ACA)_7$	147–159	30	2	0.333 (0.499)
Patinopecten yessoensis	comp87586_c0[i]	F:GCCATGCAGACGTACAGAGA R:CGGAATGTTGCTGAAATGGACA	$(AT)_{10}$	200–240	30	5	0.700 (0.505)
Patinopecten yessoensis	comp99416_c0[i]	F:CGCACGGGGACAGTATAGAC R:AGGGCTGTACAGGTACGAAA	$(C)_{22}$	117–118	30	2	0.200 (0.283)
Patinopecten yessoensis	comp99275_c0[i]	F:ACAGCTCAATACTGGAAAAGTGT R:TTATCAACCCCGGCTGCTAC	$(TGTT)_5$	264–268	30	2	0.267 (0.506)
Patinopecten yessoensis	comp83689_c0[i]	F:AGCAGTGCAAGTAATGTCGGA R:GCGGTGGAGGAAGAGAAGAC	$(GGA)_7$	248–254	30	3	0.200* (0.472)
Patinopecten yessoensis	comp85798_c0[i]	F:GTGTTGAACACCCCTTCAATTT R:AATGTAGACCGTGTGTCCGT	$(AAC)_7$	236–308	30	3	0.833* (0.508)
Patinopecten yessoensis	comp62644_c0[i]	F:CGCTGTAGAATGAGACAAAACGA R:ATGCTCCTCTTGAGGGTTGG	$(AT)_{10}$	230–300	30	2	0.800* (0.499)
Patinopecten yessoensis	comp95299_c0[i]	F:CCCATGCAAGTAGTTCGATGT R:TCACTGTTCCATACACTTTCCA	$(TATGG)_9$	275–285	30	3	0.633 (0.450)
Patinopecten yessoensis	comp98805_c0[i]	F:TTGCCTGTTTTTCTTATCTATCCAAA R:AGATTTGTGGCAAGGGCAGT	$(AAC)_7$	259–268	30	4	0.500* (0.734)
Patinopecten yessoensis	comp92213_c0[i]	F:TGGATGTCCAGAATGTTTGCT R:TGGCTTTTCAAAACTTGACCCT	$(AT)_{10}$	240–280	30	2	0.833* (0.503)
Patinopecten yessoensis	comp165251_c0[i]	F:ATCCCTCAACCCCATACTCT R:CGGGGGTCAAATTTTGGGTT	$(AT)_{10}$	227–229	30	2	0.133 (0.364)
Patinopecten yessoensis	comp164313_c0[i]	F:CCAAGCAAAGTTACTGGCGT R:GACAGTTTGGTCCGCGTTTC	$(TTTA)_5$	176–180	30	2	0.067* (0.472)
Patinopecten yessoensis	comp93276_c0[i]	F:TGGCTCATAAGGGGAGACAT R:ACAGATTGAAACTCTTACAGCAAACT	$(GAAA)_5$	186–194	30	3	0.200 (0.242)
Patinopecten yessoensis	comp98499_c0[i]	F:TGCAGCCAGGGAATTCTTCA R:TCTGTCCTGACAATCAAGAACCA	$(GTCG)_6$	272–276	30	2	0.100* (0.508)
Patinopecten yessoensis	comp89675_c0[i]	F:GGAAGGTAGAGCAGATACAGGC R:CCCATGCCTCTCAGAGCATC	$(GGGA)_5$	244–248	30	2	0.300 (0.259)
Patinopecten yessoensis	comp91152_c0[i]	F:AGCACAGAGGAGAAGCTTGA R:CACGTTTCGATCTTTCCGCTC	$(ACTG)_5$	266–274	30	3	0.467 (0.420)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Patinopecten yessoensis	comp91359_c0[i]	F:TTGCGACCAGAGACGTATCG R:AGCACGATCACACGGCATAT	$(ACGA)_5$	187–195	30	2	0.367 (0.305)
Patinopecten yessoensis	comp100440_c1[i]	F:TCCCGGAGCTCATGGTCTTA R:CAGCACTGGTACTTCCTTGGT	$(TGTT)_5$	257–261	30	2	0.167 (0.210)
Patinopecten yessoensis	comp98790_c0[i]	F:TGTACACATGCACATCTACTACGA R:GGTCCATCAGCTTCACCCAA	$(ATA)_7$	262–313	30	2	0.667 (0.452)
Patinopecten yessoensis	comp96279_c0[i]	F:AAAGCATCTCATTCTTAGGTGAAG R:TCTTGCAATGCACACCATGT	$(AT)_{10}$	226–246	30	3	0.833* (0532)
Patinopecten yessoensis	comp91909_c0[i]	F:TGTGAACCGCTTTGAGACGA R:CAACGTTACACGATGGCCAC	$(ATT)_7$	246–258	30	3	0.867* (0.536)
Patinopecten yessoensis	comp60203_c1[i]	F:GCCTCCCCTGCTTTAAAAGG R:GCGGTTAGGAAGGGCAGATA	$(ATA)_7$	161–170	30	4	0.333* (0.646)
Patinopecten yessoensis	comp97858_c0[i]	F:CTGGCTGTTTTCACCGCAAA R:CACCTTATGTGGGCTAGCAA	$(TATG)_5$	286–290	30	2	0.233 (0.305)
Patinopecten yessoensis	comp88965_c0[i]	F:CCGGTTCTGAACTCGACCAA R:GGCCTCCAGGATTCTGTGTC	$(ACC)_7$	215–368	30	2	0.900* (0.503)
Patinopecten yessoensis	comp92499_c0[i]	F:ATGGGCTACCTCCCCTGATT R:TCGTTTGCATGCCAAAGTTGA	$(AATGT)_5$	202–207	30	2	0.133 (0.183)
Patinopecten yessoensis	comp98467_c0[i]	F:TGCTTTGGTGTGTTTGCTGG R:AGGCTGACTGGTGCTAACAA	$(TG)_{10}$	235–237	30	2	0.233 (0.381)
Patinopecten yessoensis	comp60442_c0[i]	F:TTGAGTATGGATGGCGGACG R:CACAACGTTTACTGCTATTGAGGA	$(GAT)_7$	246–249	30	2	0.200 (0.235)
Patinopecten yessoensis	comp94434_c0[i]	F:CCAACAACAGGCTCAACAGC R:ATCTGGTGCTGTGGTGATGG	$(ACA)_7$	189–192	30	2	0.100 (0.097)
Patinopecten yessoensis	comp87840_c0[i]	F:TCTCCCGGAAGTCGAATTCC R:TGCACAGAGAAACACAGAGACA	$(CTGT)_5$	246–254	30	3	0.100* (0.459)
Patinopecten yessoensis	comp100123_c2[i]	F:TGTTTGCAGACTGAAAACCAGG R:CGCTCCCTTCCTCTGAAACC	$(AT)_{10}$	273–275	30	2	0.267 (0.427)
Martes zibellina	Mz1[j]	F:GTAATGTCCACAATAGCCAAAC R:AAGCCAAGAATAGAAGAACCTC	$(AC)_{19}$	115–149	22	10	0.955 (0.838)
Martes zibellina	Mz2[j]	F:ACAGAGGACAGCCATCAC R:AGGGAGGGAAGAAGAGGT	$(GT)_{17}$	219–245	22	9	0.636* (0.797)
Martes zibellina	Mz3[j]	F:TCTCACGGAAAGAACACT R:TAAGCAGGCTAACACCAG	$(AC)_{26}$	183–193	22	6	0.546 (0.783)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Martes zibellina	Mz4^{j}	F:GATTTCTAACTTATCCCATTTC R:CAACCAACTCTTGACTTT	$(GT)_{15}$	271–281	22	5	0.546 (0.726)
Martes zibellina	Mz5^{j}	F:TCTCCCACTCACATTCCA R:AGAGGCTGAGAAACTGAT	$(GT)_{16}$	164–180	22	9	0.955 (0.850)
Martes zibellina	Mz7^{j}	F:TTTCCAGTCTTCCCATTT R:CCCATACACCACCTTACA	$(GT)_{15}$	236–248	22	6	0.818 (0.697)
Martes zibellina	Mz8^{j}	F:CCAAAGCATCACTAACCA R:ACTACACCACCAAACAGG	$(GT)_{21}$	184–212	22	11	0.727 (0.867)
Martes zibellina	Mz9^{j}	F:ACATTGTACCAGCTTCAC R:CCCAGGGATCTTATAGTT	$(AC)_{16}$	217–223	22	4	0.591 (0.578)
Martes zibellina	Mz10^{j}	F:TGGGTATTTATCACAAGG R:ATGGCAAGATTTCAGGTT	$(AC)_{17}$	216–226	22	5	0.955 (0.665)
Martes zibellina	Mz11^{j}	F:GGATTGGTCCCACTTTTG R:GGCTCCCCTATTCCCTTG	$(AC)_{19}$	123–147	22	10	0.727 (0.874)
Martes zibellina	Mz15^{j}	F:ATGATGTCAATAATGCTTCC R:ATGGATAATGACGGACGA	$(GT)_{17}$	222–228	22	4	0.636 (0.637)
Martes zibellina	Mz16^{j}	F:TAGTTCCACCCATCTCAG R:ATGCGTCCCTATGTTTAT	$(GT)_{20}$	200–218	22	8	0.955 (0.808)
Martes zibellina	Mz17^{j}	F:AGCGAAACTATGGAAAGA R:TTGACTACGGACCCTAAC	$(AC)_{19}$	186–210	22	9	0.773 (0.842)
Martes zibellina	Mz18^{j}	F:GCTTGCCTGGTGTTGATA R:GTCCCATTCTACCTGTTCTC	$(AC)_{15}$	203–215	22	6	0.773 (0.752)
Martes zibellina	Mz19^{j}	F:ATTTGACCTCTGACCCTT R:TTCCCACTGTTCCATCTT	$(GT)_{16}$	180–198	22	9	0.909 (0.747)
Martes zibellina	Mz20^{j}	F:GAGATTTCCTCATTCCCT R:GCTATCAATGTAGGAATAAAGA	$(AC)_{16}$	164–174	22	6	0.682 (0.736)
Martes zibellina	Mz21^{j}	F:GTGCCCAGACAATACGCT R:CCTTCCCAGCCACTCTAT	$(GT)_{20}$	131–147	22	8	0.727 (0.753)
Martes zibellina	Mz22^{j}	F:AGGTTAGGGTAGGAGGACA R:AACAGCGAAGGAGTGGAG	$(CA)_{20}$	162–178	22	8	0.864 (0.830)
Martes zibellina	Mz23^{j}	F:GACCCTCTATCCTCACCT R:CCCACTCTTGCCCTAAAT	$(TTTA)_9$	129–161	22	6	0.636 (0.732)
Martes zibellina	Mz24^{j}	F:TGACTTGAGCCCAAACCG R:TTACAGCCTCTACCTTCG	$(TTTA)_9$	244–260	22	4	0.455 (0.534)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Martes zibellina	Mz25[j]	F:TTCTCCTCGCTCTGTGCT R:CTGGGTGAAGTTCCTGTTT	$(AAAT)_9$	124–148	22	5	0.909 (0.715)
Martes zibellina	Mz26[j]	F:GAGGAAACGACCTGTGAA R:AGTAGGGAACCTGCTTAT	$(TTTA)_7$	129–141	22	3	0.636 (0.495)
Sinilabeo decorus tungting	SDT1[k]	F:TCCGGTCTTCTCTTTTTCCC R:AGGCGCAGGGTTTTTACTCT	$(AT)_{11}$	185–208	36	10	0.862 (0.672)
Sinilabeo decorus tungting	SDT6[k]	F:TTTGGTCTCTTCCTCTTGCC R:ACGCCTAGGTGTGAGCAGAT	$(GT)_{11}$	218–255	36	13	0.806* (0.794)
Sinilabeo decorus tungting	SDT7[k]	F:TGGGACAAAGTGAAGCAGTG R:GAAACACACAGAAACCCCAGA	$(AT)_{11}$	267–297	36	8	0.792 (0.668)
Sinilabeo decorus tungting	SDT9[k]	F:CCTCAAATAACAGAAACCTGCAT R:TTCCATTGATTGTGGGGAAT	$(AT)_{11}$	249–332	36	6	0.618 (0.764)
Sinilabeo decorus tungting	SDT12[k]	F:TTTTGATTTTGCTCTTCGCA R:TTCATCCTTTGCGTTGTCAG	$(AC)_{11}$	246–288	36	12	0.971 (0.772)
Sinilabeo decorus tungting	SDT13[k]	F:GCGTGCATATGGAGAGGAAT R:CCTGTTGGGAAGAGGTCAAA	$(AC)_{11}$	231–298	36	8	0.917 (0.813)
Sinilabeo decorus tungting	SDT16[k]	F:TGGGGTGGGCAGAGTATAAA R:ATGCACAGGAAATCCAGGAG	$(AG)_{11}$	103–158	36	6	0.833 (0.633)
Sinilabeo decorus tungting	SDT20[k]	F:TTTGGTCTCTTCCTCTTGCC R:ACGCCTAGGTGTGAGCAGAT	$(GT)_{11}$	255–281	36	14	0.967 (0.707)
Sinilabeo decorus tungting	SDT22[k]	F:AAACAAGCTTGGATTCCCCT R:GATCATGCTGTGCTGCTTGT	$(GT)_{11}$	276–306	36	16	0.926 (0.554)
Sinilabeo decorus tungting	SDT24[k]	F:GAGGACCCGAGAACGTACAA R:AAGCCAGCACCTGAAGTCAT	$(TA)_{11}$	204–233	36	8	0.867 (0.614)
Sinilabeo decorus tungting	SDT25[k]	F:GATCTCTCCGTCCGTTTCAC R:AAAGGGAGAGCAAGAGAGGG	$(TC)_{11}$	140–177	36	8	0.743 (0.706)
Sinilabeo decorus tungting	SDT31[k]	F:ATCCTGCAAAGGTTGTTTGG R:GAAACGTTGAGGGGATGAGA	$(CA)_{16}$	139–188	36	12	0.938 (0.778)
Sinilabeo decorus tungting	SDT36[k]	F:CGAAGAGATCGATGACACCA R: TGATTGTACCGAAAAGCGTTC	$(CA)_{10}$	240–274	36	16	0.953 (0.646)
Sinilabeo decorus tungting	SDT37[k]	F:CCAACCTGAAGATCGAGAGC R:TGACGTTGAACGGATAACCA	$(CA)_{11}$	177–211	36	7	0.888 (0.774)
Sinilabeo decorus tungting	SDT48[k]	F:TGATCTCAGGAAGCTGCAAA R:AAGAACCATTACGCCTATGGAA	$(CA)_{10}$	115–222	36	8	0.889 (0.618)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Sinilabeo decorus tungting	SDT49[k]	F:TCCCAAAACACAGGGAAGTC R:GGCGAGAGGCATAAAGAACA	$(CA)_{10}$	166–199	36	11	0.917 (0.619)
Sinilabeo decorus tungting	SDT50[k]	F:ATTGCACTGCTGACACCATC R:TCTGCCTTACTGCTACCAAATG	$(CT)_{10}$	265–292	36	16	0.978 (0.544)
Sinilabeo decorus tungting	SDT55[k]	F:CATGCCAAAACGTAGGGTCT R:TGTTCCGATTGATTTGTGGA	$(CT)_{10}$	123–128	36	9	0.733* (0.703)
Sinilabeo decorus tungting	SDT56[k]	F:CAGCCTTCAATCCTCAGTCC R:GTCTCGGCAAAAGAAGAACG	$(GA)_{10}$	149,174	36	4	0.688 (0.569)
Sinilabeo decorus tungting	SDT60[k]	F:ATTGGCTGTTTGAGCTGTCC R:TGGCCACTACAGTTTGTTCG	$(GA)_{10}$	273–320	36	8	0.856 (0.614)
Sinilabeo decorus tungting	SDT72[k]	F:CGGCTCCACATTCACTACTGT R:CCAAAGTCTGTGAAACGCAA	$(GA)_{10}$	273–315	36	3	0.323 (0.266)
Sinilabeo decorus tungting	SDT74[k]	F:AGAACAGCCACCTGTATGGG R:CGAAACCGCGTTATTTGTTT	$(GA)_{10}$	239–244	36	5	0.506 (0.441)
Sinilabeo decorus tungting	SDT78[k]	F:GCTTAGACAGCGCTTCCAGT R:CTCTGGTGTGGAAGGTTGGT	$(TG)_{22}$	219–252	36	8	0.885 (0.680)
Sinilabeo decorus tungting	SDT90[k]	F:ACCTCAGTCGATGGGATACG R: CAGGAACACCTGCTACCCAT	$(GT)_{17}$	267–288	36	6	0.662 (0.558)
Xantusia riversiana reticulata	Xari1[l]	F:ATATCAGGTGCGGATTTGGG R:AAAGGCTTCACTTGCCAGC	AAAG	195–239	32	11	0.813 (0.866)
Xantusia riversiana reticulata	Xari5[l]	F:CACACTCAAGCTCTCTTACATATGGG R:AAGGATGTCATTACTTCATGCCC	ATCT	164–204	32	10	0.844 (0.803)
Xantusia riversiana reticulata	Xari6[l]	F:GGAGCAGGCAACTATGTCACC R:ACTTTCTGTGGAAACTATCTTGAAGG	AAAG	172–212	30	9	0.467* (0.805)
Xantusia riversiana reticulata	Xari7[l]	F:AACGCCAAGGATTATGGAGG R:AGAATTTGGAAGGGCGGC	AACT	182–226	32	10	0.844 (0.851)
Xantusia riversiana reticulata	Xari9[l]	F:AATTGTCCTGTCCCAAAGGG R:AGCTTCCCATCTTCCACAGC	AAAG	264–312	32	11	0.781 (0.860)
Xantusia riversiana reticulata	Xari10[l]	F:TTTGTGTGTGTGAAATTGATTGG R:AGGGCTGTGGAGTTTCATGC	ATCT	172–220	32	13	0.844 (0.855)
Xantusia riversiana reticulata	Xari11[l]	F:TTACTAGACCTGTGTTTCTCGGG R:CACTTTAGCCAAAGGAAGAGTGC	AAAG	336–392	30	12	0.900 (0.871)
Xantusia riversiana reticulata	Xari13[l]	F:TTATGGAGAGCCCATTCACG R:CATCTTCAGGTGGTACAATATCTTCC	AAAG	223–283	30	14	0.967 (0.903)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Xantusia riversiana reticulata	Xari18[l]	F:AGAGCTGGCTCACAAGGAGG R:CTCCAATCAAAGCAAAGCCC	AAAG	168–208	28	9	0.893 (0.818)
Xantusia riversiana reticulata	Xari20[l]	F:GTGAAGGCTGCAGTTCGG R:CTGTGTGGGTCCAGAAGTGG	ATCT	190–218	30	7	0.667 (0.794)
Xantusia riversiana reticulata	Xari21[l]	F:GTTTAGTTCAGAACAAGCCAGGG R:CTGTTAACATTTCACCATTCCAGC	AAAG	180–240	32	13	0.938 (0.867)
Xantusia riversiana reticulata	Xari22[l]	F:TCTTTCCTTCACACCCACCC R:GAAGACAAGCGCCCTTCC	AAAG	246–322	32	16	0.844 (0.887)
Xantusia riversiana reticulata	Xari30[l]	F:TTGGTGGAACGTGCCTGG R:GCTCTTTCTCACCTGCCTGG	TTCC	176–228	32	10	0.719* (0.843)
Xantusia riversiana reticulata	Xari31[l]	F:CAGGAATGTACACTGATACAGAATATGG R:GCTTCTATCTTTACATCCTGTGATCC	ATCT	167–211	32	8	0.906 (0.805)
Xantusia riversiana reticulata	Xari33[l]	F:TCAGAACAAATAATTAACATGTGGC R:GGCTAGTACCATCTCCCTCCC	ATCT	148–176	31	8	0.742 (0.793)
Xantusia riversiana reticulata	Xari35[l]	F:CAAATTGTGAGTGTTATGCAAATAGC R:TCCAGAATAAGGATTCGCCC	AAAG	186–246	31	14	0.903 (0.883)
Xantusia riversiana reticulata	Xari38[l]	F:TGCATGTTATGTGAAGCAGCC R:TGCATGCATGGAAATCAAGC	AAAG	153–201	32	8	0.781 (0.811)
Xantusia riversiana reticulata	Xari41[l]	F:TCTGTATGTAGTGCTTTGACTATGCC R:TGGTTACCTATCCCAAAGGAGC	AAAG	131–155	32	7	0.563 (0.718)
Xantusia riversiana reticulata	Xari42[l]	F:TAAGCCTGTGGGAAGAGTGG R:TTATAAATTGAGGAAAGTCTCTAAACTAGG	ATCT	350–374	32	7	0.781 (0.783)
Xantusia riversiana reticulata	Xari44[l]	F:TGCCTCCACTTATGTTCTACAAGG R:TTGCACACTCTCCACATCCC	ATCT	158–198	31	9	0.677 (0.838)
Xantusia riversiana reticulata	Xari45[l]	F:TTGCAGTGTTTAAGGTGTCATAGG R:TTTCCCTTCTTGGCTTGTGG	AAAG	158–206	29	12	0.931 (0.880)
Xantusia riversiana reticulata	Xari46[l]	F:GACCCTCCTCTTTCTACAGTGC R:TTTCTGAACTACACGGAAATGC	AAAG	132–164	30	9	0.900 (0.857)
Xantusia riversiana reticulata	Xari47[l]	F:TTAAGCAGAAATGCACCCTCC R:TTTGCAGAAAGTAGCAAACTGC	AAAG	199–259	32	13	0.844 (0.875)
Xantusia riversiana reticulata	Xari48[l]	F:GCAATAATATCAAACCAACAAGCC R:TTTGGGCACTTGCTGACG	ATCT	215–247	32	9	0.844 (0.857)
Patinopecten yessoensis	Contig_141397[m]	F:CTCGGTTGCCAACGATGA R:ACGATCCCCTGTGACGTATT	$(AT)_{12}$	154–300	30	5	0.642* (0.632)
Patinopecten yessoensis	Contig_141159[m]	F:ACCTGATTTGGATGCCATTA R:GCTGTGGTGTGCTTGTCTGT	$(AC)_{12}$	114–150	30	3	0.608* (0.598)
Patinopecten yessoensis	Contig_1519946[m]	F:TCTTTCTTGACTTTTAAGGAACCG R:CGAACCATATCGTGATCCCT	$(AC)_{12}$	232–290	26	4	0.509* (0.499)
Patinopecten yessoensis	Contig_1217920[m]	F:CACCATGAAAACCTGACACG R:CGGAGTACCCAGAGAAAAACA	$(AC)_{11}$	140–190	30	4	0.593 (0.582)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Patinopecten yessoensis	Contig_1515729^{m}	F:CCTTTCTGGCACACAGTATGA R:CAACTTGGACCTCGATAAACG	$(AC)_{12}$	125–151	29	6	0.647* (0.636)
Patinopecten yessoensis	Contig_1431345^{m}	F:AAGTCCCCTAAACGAAAGGG R:TAGCACATTAAGGCACACGC	$(AC)_{12}$	16–669	29	4	0.424 (0.417)
Patinopecten yessoensis	Contig_1443641^{m}	F:CCCTGATGTGAAGTTGAATGTT R:CCGATTTGGTCATGTAAATAGC	$(AC)_{12}$	122–150	30	3	0.525* (0.516)
Patinopecten yessoensis	Contig_988858^{m}	F:TCACATTACCCACGTGCTTG R:AACTAGGTTGTGATAAAGCGGT	$(TG)_8$	149–156	30	4	0.188* (0.185)
Patinopecten yessoensis	Contig_490627^{m}	F:TGTAGCCCTCTCTTGATCGTT R:ACCTTCCCAGCCTTTCTCTC	$(TA)_9$	116–150	30	5	0.629* (0.618)
Patinopecten yessoensis	Contig_552733^{m}	F:AGGGCGCTATATCAAATAGTGTA R:TTGTGTGATTTCCAGATGGG	$(CA)_9$	131–134	30	2	0.259 (0.255)
Patinopecten yessoensis	Contig_421958^{m}	F:GGTAGGAAGAAACGGGAAGG R:TGTTGTGGTGATGTCACAATG	$(AT)_9$	171–201	30	4	0.637* (0.626)
Patinopecten yessoensis	Contig_627550^{m}	F:TGCACAGCTTGAATAGGTTACG R:CGTGTCAATCAATCAGGGTG	$(AC)_8$	192–200	29	3	0.597 (0.587)
Patinopecten yessoensis	Contig_1088861^{m}	F:TCAATAACAATCTACACCTGCCA R:TTCTTTTCCATCTGTTTTACCG	$(AT)_8$	110–150	30	4	0.572* (0.562)
Patinopecten yessoensis	Contig_1448634^{m}	F:TTTATTCAACTTCATTTCGATGAGA R:ACCACTCATTGTCCAGCCTC	$(AC)_{12}$	118–198	24	3	0.571 (0.559)
Patinopecten yessoensis	Contig_1391603^{m}	F:GCAAGCGTTTATAAAATCACGA R:AAAGAATTCCTCGGAGCGTA	$(AC)_{11}$	117–121	30	3	0.654 (0.643)
Patinopecten yessoensis	Contig_1092871^{m}	F:CGACGACGAGGATGATGATA R:TCTATCTTGAACGAGCGGTTT	$(AT)_9$	176–210	28	2	0.821 (0.494)
Patinopecten yessoensis	Contig_396763^{m}	F:TAGGCCACGACACGTCAGTA R:AATTGCAAACTTTCCATGCC	$(AT)_9$	150–190	29	3	0.532 (0.523)
Patinopecten yessoensis	Contig_760971^{m}	F:TTTGCAACCAATGAGAGATCC R:AAAATGCCCTTAAAACACTCCA	$(TA)_8$	200–230	23	4	0.653 (0.639)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Patinopecten yessoensis	Contig_897872[m]	F:GATTAGCAACAAATACTTACTTTACCG R:AACTGCACACTATCCAGACACAG	$(TG)_8$	111–175	25	4	0.510 (0.500)
Patinopecten yessoensis	Contig_915269[m]	F:GGCAGGGTCAGTGTGTATAGC R:ACAAGGCTGTGAGAAACGCT	$(TG)_8$	101–141	29	2	0.334 (0.328)
Patinopecten yessoensis	Contig_816331[m]	F:TGTAGAGGAGCGGAATTTCAA R:ATTTCGACCAAAATTGACCA	$(GT)_8$	202–282	29	2	0.313 (0.307)
Patinopecten yessoensis	Contig_585530[m]	F:AATCATTTGGTTCTGCGGTC R:CTTATACGCAGTTCAGGCGG	$(TA)_9$	116–150	27	2	0.409 (0.401)
Patinopecten yessoensis	Contig_245979[m]	F:CCTGTCGCATATTTCACAACA R:GACAAAACAATGCTATGTGAGTTTC	$(AC)_{12}$	225–275	30	2	0.440 (0.433)
Patinopecten yessoensis	Contig_1190024[m]	F:AACCCCTTCTTATGAAAATGTGA R:ACTCCATCGTGTGTATGGGA	$(TA)_9$	200–240	28	3	0.538 (0.528)
Patinopecten yessoensis	Contig_1697973[m]	F:TGCAGACTGTTGCTCCATTA R:TGAACCAGTGTAGCATCAGAGAA	$(AC)_{12}$	318–370	28	4	0.492 (0.483)
Patinopecten yessoensis	Contig_470364[m]	F:CACCAAACAAATGTTGTGTTCA R:CACATAATTATCATAGCTTTTGGTACA	$(AT)_9$	176–200	28	2	0.399 (0.392)
Patinopecten yessoensis	Contig_293601[m]	F:CTGTTGCGAACCGAGTTTGT R:CGAAATACTCATAATTTGTCCCG	$(AT)_9$	300–320	30	3	0.167 (0.156)
Patinopecten yessoensis	Contig_963940[m]	F:TATACGGTGCTTTTCCCGAC R:ACCTCGGGGCATTGTTACAG	$(TG)_8$	220–280	29	2	0.276 (0.452)
Patinopecten yessoensis	Contig_1475620[m]	F:CCCTTCTTTCACCTTTTCCC R:CGGGAATCTGAGGGTAACAA	$(AC)_{12}$	150–240	26	3	0.923* (0.553)
Patinopecten yessoensis	Contig_1696323[m]	F:CCAAGTTTCACCGTGTAGCA R:ATTAGAACGCACACCCACAT	$(AC)_{12}$	270–300	25	3	0.520 (0.441)
Patinopecten yessoensis	Contig_177175[m]	F:GGTACGCAAAAACACCCAAG R:TCTTGTACAAAAATTAGGGTTCATGT	$(AC)_{12}$	124–140	23	2	0.348 (0.287)
Patinopecten yessoensis	Contig_74709[m]	F:GCTTGCAGTGTGATCTTGGA R:CCCCTGAATGTTTTTCTGTG	$(AC)_8$	124–176	23	3	0.522 (0.420)
Patinopecten yessoensis	Contig_204398[m]	F:TCAAGGATACCCACAGTACAGC R:CAGACTTGCACTAGCATCCG	$(AC)_{12}$	280–310	28	3	0.643 (0.507)
Patinopecten yessoensis	Contig_1273600[m]	F:GTGCGGTTCTGTTCTTTCGT R:TCAGAGTTGTCGAGACAAGGA	$(ATC)_7$	116–182	25	2	0.560 (0.403)
Patinopecten yessoensis	Contig_878432[m]	F:CATCGTGCAATCAGTCGATA R:GCACAACAACGTGTTCCATC	$(TG)_8$	110–260	21	5	0.857 (0.776)
Patinopecten yessoensis	Contig_763705[m]	F:TGAGCACTAACAAGGCTGACTC R:ACTGTGCAACGCTTGATTTG	$(AT)_8$	100–120	29	3	0.613 (0.602)
Moerella iridescens	HGZ1–144[n]	F:TTTCATCGAAAAATAATGTAATGCC R:TTGGTAAGCCTTGACAGTATCTGTT	$(GT)_8$	95–234	42	7	0.667 (0.713)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Moerella iridescens	HGZ4–297^{n}	F:TGTGATTTCGAGACACACCGATGTA R:ACCTGTACGACGACAAGCCCTAGA	$(GT)_7$	317–351	36	5	0.278 (0.560)
Moerella iridescens	HGZ5–151^{n}	F:AGCATTTTCAGAGCTATGACAACTA R:ACTACACTGTCTGTTGAATAGCCAT	$(AC)_8$	130–177	48	6	0.542 (0.798)
Moerella iridescens	HGZ6–461^{n}	F:GTGTGGTCAGTTTTATCTGGTGG R:CCAGTTGATACATTGCTAAAGATAC	$(AC)_7$	413–487	42	5	0.666 (0.626)
Moerella iridescens	HGZ8–395^{n}	F:AACTGCGTATACCGAAGAAGTCAAC R:CCATAGAAATTATTGCATTGTCAGC	$(AC)_7$	408–423	32	2	0.125 (0.387)
Moerella iridescens	HGZ14–282^{n}	F:CTTGACAGATGGGTGATTTATTGGT R:GTTTAATGATAGCCTACCCCCTCTC	$(GT)_7$	260–338	48	6	0.583 (0.672)
Moerella iridescens	HGZ15–185^{n}	F:TCATCATGCCAACATACAAAAAGGG R:GCGGGGAACCAATTCATCAGTATTT	$(TG)_7$	160–238	46	6	0.652 (0.727)
Moerella iridescens	HGZ35–119^{n}	F:AGAAGAGGAAGGTGTAGAT R:AATAATTGAGGAAGTTGG	$(GAGG)_3$	100–172	38	7	0.737 (0.814)
Moerella iridescens	HGZ37–180^{n}	F:AAGGCTCAGAAAGGGAAC R:CCAGTGGTACTTCTGGTTG	$(ACAAAAAAAAG)_3$	100–404	26	7	0.462 (0.834)
Moerella iridescens	HGZ38–208^{n}	F:ATTTCCACTTCGCACATTG R:GGTGACTCGCACAAACAAAT	$(GAGGGA)_{13}$	120–192	40	10	0.050* (0.878)
Moerella iridescens	HGZ39–109^{n}	F:CGGGCAACATAGTGAGAC R:CGGGCAACATAGTGAGAC	$(AC)_{23}$	174–600	26	6	0.692 (0.828)
Moerella iridescens	HGZ40–202^{n}	F:ATTTCCACTTCGCACATTG R:GGTGACTCGCACAAACAAAT	$(GAGG)_{18}$	146–274	32	7	0.375 (0.768)
Moerella iridescens	HGZ41–144^{n}	F:TGTACAAGGGCGTCTAGAG R:CCGTTTAGGTGGACTGAC	$(AG)_{29}$	153–216	30	7	0.267* (0.846)
Moerella iridescens	HGZ43–100^{n}	F:AGTAAAATGCACCTAACCAT R:GGAGCGAGGAGTGAAGAG	$(TCCT)_8$	103–266	34	10	0.529 (0.849)
Moerella iridescens	HGZ45–227^{n}	F:ACATGCATAGGTCACTTG R:TGGCAAAATATCACTCAG	$(CAAGGT)_5$	137–232	36	9	0.389 (0.848)
Moerella iridescens	HGZ46–153^{n}	F:GGGACGATATTATAGCAAT R:GTGAACTTAGAACTGTGGAAC	$(TTCCAAAG)_3$	161–223	40	9	0.750 (0.845)
Moerella iridescens	HGZ47–182^{n}	F:TTTAAACTTTAGAGCACACAC R:TAGATACGCCTACCGATT	$(AG)_{18}$	124–185	32	9	0.625 (0.794)
Moerella iridescens	HGZ48–154^{n}	F:AGTAGTGTAACCACTTGCGTAT R:ATCACCGTGCTGTTTTCG	$(T)_{16}$	147–160	40	2	0.550 (0.409)
Moerella iridescens	HGZ49–122^{n}	F:CAGAAGTAGATCACTCATGCAC R:CACCAAGACTGGTATACAGAAG	$(TTGAAAA)_3$	100–158	30	6	0.133* (0.772)
Moerella iridescens	HGZ17–170^{n}	F:TTGTGAATAACTGCAGCCAATAAAC R:GGGAAAAATCGAGACTGGTAGGT	$(CA)_8$	154–208	28	10	0.786 (0.905)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Moerella iridescens	HGZ18–125[n]	F:AAAATCACAGTCAGTCTGCATTGTA R:ATACAAACAAACACAAGCAACCATC	$(TG)_8$	136–185	40	11	0.600 (0.910)
Moerella iridescens	HGZ19–169[n]	F:AATATAGCCAAATTGTAACCATTCC R:AAAAATACCAGTGAAAATGAAACAT	$(CA)_6$	167–169	28	10	0.786 (0.905)
Moerella iridescens	HGZ20–147[n]	F:GTAAGACGAGGGGTGCGGCAGTTG R:TGGGCAATGACGTATTCCTTCGATG	$(GT)_8$	130–164	40	9	0.900 (0.887)
Moerella iridescens	HGZ21–217[n]	F:ATGTTATTTACTTTAACGATTCCTT R:GTCGATTCATTCTTGATCTAGTTTT	$(TG)_8$	159–265	39	16	0.947 (0.947)
Moerella iridescens	HGZ22–127[n]	F:ATTCCATTTAGTGAAACTATGAGCA R:CTTTACTAAGAAGACGGTGTCATTT	$(TG)_9$	122–166	40	11	0.750 (0.874)
Moerella iridescens	HGZ23–198[n]	F:CACTATAGCACAGCTCACTGACATA R:ACAGAGAGGATTGCATTTGGTT	$(GT)_7$	164–194	40	11	0.400 (0.894)
Moerella iridescens	HGZ24–335[n]	F:AGTTCTCTGTAAGTCTAAATCCTAT R:TTGTTAGCTGTGTGTATAAAATG	$(TG)_7$	332–370	40	6	0.450 (0.681)
Moerella iridescens	HGZ55–276[n]	F:ACCTCTATCCACCTATGAC R:CTAGTAAACCCAGCAATT	$(TC)_8$	160–262	30	9	0.200 (0.846)
Moerella iridescens	HGZ56–492[n]	F:ACCTCTATCCACCTATGACG R:TGGTGCTGGTTGTTCTTG	$(CAG)_5$	153–457	38	16	0.684 (0.902)

Pop1 Santo Inácio, Bahia, Brazil; Pop2 Pedra Venturosa, Pernambuco, Brazil

*Indicates significant deviations from Hardy–Weinberg expectations after Bonferroni corrections

[a] Françoso et al. Microsatellite loci for *Xylocopa* (*Monoxylocopa*) species: *Xylocopa abbreviata* and *Xylocopa macambirae* (Hymenoptera, Apidae, Xylocopini) (ESM1)

[b] Lei et al. Development of 31 tetranucleotide microsatellite loci in *Gymnocypris potanini* Herzenstein using next generation sequencing (ESM2)

[c] Almojil Development of new polymorphic microsatellite loci for the spot-tail shark *Carcharhinus sorrah* and the black-tip shark *Carcharhinus limbatus* (ESM3)

[d] Chen and Zhan Isolation and characterization of 22 polymorphic microsatellite markers for the invasive ascidian, *Molgula manhattensis*, using high-throughput sequencing (ESM4)

[e] Forsdick et al. Isolation and characterisation of microsatellite loci for the Chatham Island black robin *Petroica traversi* (ESM5)

[f] Liu et al. Isolation and characterization of 23 polymorphic microsatellites from Chinese spotted seabass *Lateolabrax maculatus* (ESM6)

[g] Wei et al. Isolation and characterization of 91 polymorphic microsatellite loci from *Silurus lanzhouensis* (ESM7)

[h] Perina et al. Isolation and characterization of 20 polymorphic microsatellite loci in *Palaemon serratus* and cross-amplification in *Palaemon* species by 454 pyrosequencing (ESM8)

[i] Zhang et al. Isolation and characterization of 44 microsatellite markers in Yesso scallop *Patinopecten yessoensis* by transcriptome mining (ESM9)

[j] Li et al. Development and characterization of 22 polymorphic microsatellite markers for the sable *Martes zibellina* (ESM10)

[k] Yuan et al. Characterization of 24 microsatellite markers for *Sinilabeo decorus tungting* (Cypriniformes, Cyprinidae) (ESM11)

[l] Rice et al. Development of 24 polymorphic microsatellite markers for the island night lizard (*Xantusia riversiana reticulata*) of San Clemente Island, California (ESM12)

[m] Sun et al. Development of genome-wide microsatellite genetic resources by using RAD tag sequencing in Yesso scallop *Patinopecten yessoensis* (ESM13)

[n] Wang et al. Isolation of 29 microsatellite markers for population genetics and conservation of the *Moerella iridescens* Benson, 1842 (ESM14)