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MICROSATELLITE RECORDS

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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)
Hemifusus tuba (Gmelin)	HT001[a]	F: CTGGACATTGCTGAGGAA R: GCGGGTATGAATCGAGAT	$(CAAT)_8(TC)_{27}$	342–360	60	2	0.0667 (0.0655)
	HT002[a]	F: ATTGGACTTCTTCGGCATAGCG R: AATGAGACGACGGCAGACTTTG	$(GA)_{32}$	345–400	62	3	0.2333 (0.2164)
	HT005[a]	F: CCCAGCACAACAAACGACAGA R: TTCACCGTCACATCAACTTCCCT	$(GT)_{19}(TG)_{16}(TG)_{10}(TC)_7(TC)_9(TC)_9(TC)_{16}$	144–260	58	8	0.7500 (0.7883)
	HT007[a]	F: TTCCTGTATTTCTGCCTCT R: TGTCTTCTTACTGCCATTTC	$(AG)_{43}(TG)_4(TG)_4$	224–240	54	4	0.1852 (0.5304)
	HT009[a]	F: GGGTACATAAGGCTCGTTCA R: TTCTCGGACTTCGGTTTCTT	$(AG)_{62}(AG)_4$ $(AG)_7(GA)_4(GA)_8(GA)_{14}(AG)_7$	194–220	58	6	0.3571 (0.5552)
	HT012[a]	F: CAACTTCTGTAGCCTGTAATG R: GGGGAAAACCTAACCACT	$(CT)_5(TC)_{20}(TC)_{29}$	246–260	62	2	0.0667 (0.1831)
	HT015[a]	F: CGTGCATGTCGTGATAAGTCGG R: CTCAATCTCCAAGCAGAGTTGTCG	$(TC)_{12}(CT)_{17}(TC)_{28}$	288–308	56	7	0.4483 (0.6999)
	HT016[a]	F: CGTATTCGGCGGCAATCA R: GCCAGGGTTTTCCCAGTCA	$(GA)_6(AG)_8(AG)_{29}$	284–300	52	5	1.0000 (0.6101)
	HT018[a]	F: CTCCCTTGATTTCACCTTC R: TTGGTAATAGGGGCTTCC	$(GT)_{19}(TG)_{16}(TC)_7(TC)_9(TC)_9(TC)_{16}$	108–130	54	7	0.8214 (0.8169)
	HT023[a]	F: TGTACCACTTGAACTGGTCC R: GTAGGGGCTGTCAGAGATAA	$(TCC)_7(CT)_4$	172–180	56	2	0.0714 (0.0701)
	HT025[a]	F: GAGAGCGACGAACGGAAGGA R: CCGATTGACCAGAGACCCCA	$(AG)_{38}$	134–156	56	7	0.6207 (0.8149)
	HT027[a]	F: TGGTCACACTAGACTGACGACGCAT R: AGCCCAATACCCAAACCCCACTTAC	$(CT)_{32}(TG)_{19}$	198–244	52	12	0.6667 (0.8784)
	HT028[a]	F: TGGTCACACTAGACTGACGACGCAT R: TCGCAAAAAGTGAAGGGCGGTAG	$(GA)_{39}$	244–258	54	3	0.1429 (0.1377)
	HT029[a]	F: TTGACTGGGGTGTGGGGTT R: GAGAAAGTGAATGAGAGTGGGCG	$(TGTC)_4(TC)_5(CT)_{23}(CT)_{18}$	172–184	58	3	0.1333 (0.3774)
Osmoderma barnabita	Hermit_01[b]	F: ATTGCACGATTACTATG R: GTTCCTGGACGGGTTGT	$(AC)_{16}$	217–223	45	2	0.111 (0.145)
	Hermit_02[*,b]	F: GGCTGCTCCGAAGACA R: TTGCGACATAATAAAACAGG	$(AC)_{11}$	264–266	45	2	0.889 (0.501)
	Hermit_05[b]	F: GAACGCGAAGGTCCAATAAAT R: GTATCACTCTACATTAGGTTTGTGT	$(AC)_{14}$	291–315	45	4	0.111 (0.108)
	Hermit_06[b]	F: CACACCTCTAAAGTAATCGTT R: TGGCAATCGGGCAAGTT	$(AC)_{14}$	164–178	45	4	0.244 (0.288)
	Hermit_07[*,b]	F: GTTAACCGATCGGAAATGAAT R: CAATGAGATAGCGGTGATGAT	$(AC)_{12}$	385–387	45	2	0 (0.044)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
	Hermit_08[b]	F: AGTTCTTCGTTGAGGGATAAT R: GTGAAAAGCTGTAAACTGGATA	$(AC)_{12}$	248	45	1	–
	Hermit_09[b]	F: AATCATTTTCGGAGGTG R: GATTTAGATTCGCTTGTA	$(AC)_{10}(AG)_7$	353–357	45	3	0.067 (0.108)
	Hermit_10[b]	F: CATTGCCTTGCTACA R: AGACCTCGAACTTACAG	$(AG)_{18}$	249–261	45	5	0.289 (0.336)
	Hermit_11[b]	F: GAGTGAAGTAATACGCAAGTGAGAG R: TATTTAGGCAGCCAAGGAGGTG	$(AG)_{19}$	189–231	45	13	0.778 (0.868)
	Hermit_12*[,#,b]	F: GAATCACGGGTTAATTACCTACTAA R: GCGGCGCATTCATCAA	$(AG)_{18}$	310–322	45	5	0.244 (0.626)
	Hermit_13[b]	F: CAAGTTGGTCAGTAATAGGAGAA R: CGTCATGAGTTGGTGGTTT	$(AG)_4$ $GG(AG)_{11}$	219–235	45	3	0.044 (0.044)
	Hermit_14[b]	F: AGGAAATCGTGCATAGTCAATA R: TGGGCAGTCAGTAATAACC	$(AG)_{12}$	380–390	45	4	0.089 (0.087)
	Hermit_15[b]	F: CACGCCATGGATGTTGAAAA R: TACCGGAGCCGTTGGAGAT	$(AG)_{15}$	449–453	45	3	0.089 (0.087)
	Hermit_16[b]	F: GGAACGCGCAGATAGGACT R: AGGTGCCAGAGGTACATTTGAA	$(AT)_{11}$	370–372	45	2	0.044 (0.044)
Osmoderma eremita	Hermit_01[b]	F: ATTGCACGATTACTATG R: GTTCCTGGACGGGTTGT	$(AC)_{16}$	–	45		–
	Hermit_02*[,b]	F: GGCTGCTCCGAAGACA R: TTGCGACATAATAAAACAGG	$(AC)_{11}$	260	45	1	–
	Hermit_05[b]	F: GAACGCGAAGGTCCAATAAAT R: GTATCACTCTACATTAGGTTTGTGT	$(AC)_{14}$	–	45		–
	Hermit_06[b]	F: CACACCTCTAAAGTAATCGTT R: TGGCAATCGGGCAAGTT	$(AC)_{14}$	164	45	1	–
	Hermit_07*[,b]	F: GTTAACCGATCGGAAATGAAT R: CAATGAGATAGCGGTGATGAT	$(AC)_{12}$	–	45		–
	Hermit_08[b]	F: AGTTCTTCGTTGAGGGATAAT R: GTGAAAAGCTGTAAACTGGATA	$(AC)_{12}$	–	45		–
	Hermit_09[b]	F: AATCATTTTCGGAGGTG R: GATTTAGATTCGCTTGTA	$(AC)_{10}(AG)_7$	378	45	1	–
	Hermit_10[b]	F: CATTGCCTTGCTACA R: AGACCTCGAACTTACAG	$(AG)_{18}$	267–269	45	2	0.067 (0.065)
	Hermit_11[b]	F: GAGTGAAGTAATACGCAAGTGAGAG R: TATTTAGGCAGCCAAGGAGGTG	$(AG)_{19}$	189	45	1	–
	Hermit_12*[,#,b]	F: GAATCACGGGTTAATTACCTACTAA R: GCGGCGCATTCATCAA	$(AG)_{18}$	–	45		–

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Hermit_13[b]	F: CAAGTTGGTCAGTAATAGGAGAA R: CGTCATGAGTTGGTGGTTT	$(AG)_4$ $GG(AG)_{11}$	229–231	45	2	0.133 (0.164)
	Hermit_14[b]	F: AGGAAATCGTGCATAGTCAATA R: TGGGCAGTCAGTAATAACC	$(AG)_{12}$	–	45		–
	Hermit_15[b]	F: CACGCCATGGATGTTGAAAA R: TACCGGAGCCGTTGGAGAT	$(AG)_{15}$	–	45		–
	Hermit_16[b]	F: GGAACGCGCAGATAGGACT R: AGGTGCCAGAGGTACATTTGAA	$(AT)_{11}$	372	45	1	–
Opsaridium microlepis (N.Rukuru River)	Ops3[c]	F: ATGTTGCATGAAGCACCTG R: GGTTCGAAACGATATGAGGGTC	$(AAC)_{11}$	396–430	43	5	0.56 (0.72)
	Ops4[c]	F: TCAGCAATGCATCACCCTG R: GGTTTGGACAACAACCATGC	$(ATT)_{12}$	273–303	46	6	0.65 (0.63)
	Ops5[c]	F: AATGTGTGCAGCGCTCAAG R: CAAGTTAAGGCTGCTCTGGG	$(GAT)_{12}$	413–445	43	4	0.53 (0.56)
	Ops7[c]	F: TCATTTCTCTTGGGATTGTTTGG R: AGACACTGCTGAAGGACCG	$(ATT)_{11}$	385–400	45	4	0.42 (0.43)
	Ops9[c]	F: AGCATAGTGGACAGCTCAGT R: AGGGATCAAGAGTGTGCCTT	$(ATT)_{13}$	270–287	47	3	0.04 (0.04)
	Ops11[c]	F: GGGCTGAATGACGCTCTTAA R: AGCAGCTCGACCAAACTAGT	$(ATC)_{21}$	249–285	44	11	0.73 (0.76)
	Ops13[c]	F: ATTTCCACGCGCTGAACTC R: CGCTGAAACCGAGAGGTTG	$(CAAA)_5$	362	43	1	–
	Ops16[c]	F: GAAATGGAGTGTCATTTAGCATTAC R: CCGCTCCAATCTGGATTCAAC	$(AGAT)_{11}$	313–373	43	10	0.49 (0.83)
	Ops19[c]	F: CATTCACACCGTTCCTCTGC R: TGTGCCCTGATAAAAGCTGC	$(ATCT)_{11}$	241–277	44	9	0.80 (0.80)
	Ops20[c]	F: CACAGAATCAGGGATGCAGC R: GCATGGATTCCTGCCACAAA	$(ATCT)_{14}$	205	47	1	–
	Ops22[c]	F: TCCGGGCCACTGAAATAGAC R: AGGAATAACACAAATTATGGGACAG	$(GATT)_8$	384–410	46	4	0.54 (0.50)
Opsaridium microcephalum (Bua River)	Ops3[c]	F: ATGTTGCATGAAGCACCTG R: GGTTCGAAACGATATGAGGGTC	$(AAC)_{11}$	402–430	53	5	0.36 (0.53)
	Ops4[c]	F: TCAGCAATGCATCACCCTG R: GGTTTGGACAACAACCATGC	$(ATT)_{12}$	270–281	49	2	0.18 (0.17)
	Ops5[c]	F: AATGTGTGCAGCGCTCAAG R: CAAGTTAAGGCTGCTCTGGG	$(GAT)_{12}$	424	55	1	–
	Ops7[c]	F: TCATTTCTCTTGGGATTGTTTGG R: AGACACTGCTGAAGGACCG	$(ATT)_{11}$	377	46	1	–

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Ops9[c]	F: AGCATAGTGGACAGCTCAGT R: AGGGATCAAGAGTGTGCCTT	$(ATT)_{13}$	252–262	51	4	0.08 (0.08)
	Ops11[c]	F: GGGCTGAATGACGCTCTTAA R: AGCAGCTCGACCAAACTAGT	$(ATC)_{21}$	247–251	56	2	0.09 (0.09)
	Ops13[c]	F: ATTTCCACGCGCTGAACTC R: CGCTGAAACCGAGAGGTTG	$(CAAA)_5$	352–362	56	2	0.02 (0.02)
	Ops16[c]	F: GAAATGGAGTGTCATTTAGCATTAC R: CCGCTCCAATCTGGATTCAAC	$(AGAT)_{11}$	322–385	51	11	0.94 (0.84)
	Ops19[c]	F: CATTCACACCGTTCCTCTGC R: TGTGCCCTGATAAAAGCTGC	$(ATCT)_{11}$	249–326	56	6	0.09 (0.07)
	Ops20[c]	F: CACAGAATCAGGGATGCAGC R: GCATGGATTCCTGCCACAAA	$(ATCT)_{14}$	190–209	51	2	0.02 (0.02)
	Ops22[c]	F: TCCGGGCCACTGAAATAGAC R: AGGAATAACACAAATTATGGGACAG	$(GATT)_8$	409–421	45	2	0.02 (0.02)
Opsaridium tweddleorum (Ruhuhu River)	Ops3[c]	F: ATGTTGCATGAAGCACCTG R: GGTTCGAAACGATATGAGGGTC	$(AAC)_{11}$	403	18	1	–
	Ops4[c]	F: TCAGCAATGCATCACCCTG R: GGTTTGGACAACAACCATGC	$(ATT)_{12}$	279–282	18	2	0.33 (0.46)
	Ops5[c]	F: AATGTGTGCAGCGCTCAAG R: CAAGTTAAGGCTGCTCTGGG	$(GAT)_{12}$	–	–	–	–
	Ops7[c]	F: TCATTTCTCTTGGGATTGTTTGG R: AGACACTGCTGAAGGACCG	$(ATT)_{11}$	372–375	18	2	0.33 (0.36)
	Ops9[c]	F: AGCATAGTGGACAGCTCAGT R: AGGGATCAAGAGTGTGCCTT	$(ATT)_{13}$	267–273	18	2	0.06 (0.06)
	Ops11[c]	F: GGGCTGAATGACGCTCTTAA R: AGCAGCTCGACCAAACTAGT	$(ATC)_{21}$	249–253	18	2	0.17 (0.25)
	Ops13[c]	F: ATTTCCACGCGCTGAACTC R: CGCTGAAACCGAGAGGTTG	$(CAAA)_5$	183–354	18	2	0.06 (0.06)
	Ops16[c]	F: GAAATGGAGTGTCATTTAGCATTAC R: CCGCTCCAATCTGGATTCAAC	$(AGAT)_{11}$	353–373	17	5	0.18 (0.44)
	Ops19[c]	F: CATTCACACCGTTCCTCTGC R: TGTGCCCTGATAAAAGCTGC	$(ATCT)_{11}$	249–281	18	7	0.44 (0.72)
	Ops20[c]	F: CACAGAATCAGGGATGCAGC R: GCATGGATTCCTGCCACAAA	$(ATCT)_{14}$	181–209	18	3	0.33 (0.37)
	Ops22[c]	F: TCCGGGCCACTGAAATAGAC R: AGGAATAACACAAATTATGGGACAG	$(GATT)_8$	418–434	18	3	0.44 (0.45)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Chorthippus group *binotatus* (Orthoptera: Acrididae)	Cbin02[d]	F: CAGCAACCTGAAGCCTGTT R: GACATGTCGGATTGGACC	$(TGT)_{12}$	204–315	20	6	0.35 (0.68)
	Cbin05[d]	F: AGAATGAGCCACAAATTAAAACA R: CAAACTTCATATTGCAACCCC	$(CA)_{12}$	260–332	20	9	0.83 (0.88)
	Cbin07[d]	F: CAAGTGGACAAACTCGAGCA R: TCAGAGTGACGGCAATATACAA	$(GA)_{12}$	150–246	20	6	0.64 (0.75)
	Cbin08[d]	F: TCTGCACATTAATTTTGATAGGG R: CGATGTGTACATAGAGAAATCTAGTGA	$(TC)_{12}$	99–291	20	14	0.72 (0.91)
	Cbin12[d]	F: AGAGTAGCGTGGAGAGCTGC R: CACTGTATCATGCTGAAGGCA	$(CCA)_{13}$	60–153	20	4	0.38 (0.51)
	Cbin15[d]	F: TGAATGGGCTTTCAAAGAGAA R: ACAGCAGCCAATCTGGAGTT	$(CA)_{14}$	95–191	20	9	0.94 (0.77)
	Cbin16[d]	F: TTGCTTCGTAGCTTATCGGTG R: GCACCGGAGACTTGAAACAG	$(CA)_{15}$	240–382	20	11	0.21 (0.90)
	Cbin27[d]	F: GTTCGGTTGACCGATGTTC R: AACGTTCAGTTCGATTATCCG	$(CA)_{19}$	103–221	20	11	0.50 (0.89)
	Cbin31[d]	F: AACAAGTTTGGACGTTTCGC R: ATATCGAACCACGATTCGGC	$(AC)_{21}$	62–166	20	10	0.50 (0.71)
	Cbin33[d]	F: CACTTTGAATGATTAATCTCCTGATTT R: CGTCAAACGTAGTGAAGTTAGTAGG	$(GT)_{22}$	90–192	20	16	0.66 (0.91)
	Cbin36[d]	F: AGAGATTCCAGAGCTATGCTGG R: GCTGTAACACCACGACGGAC	$(AC)_{23}$	72–254	20	13	0.31 (0.92)
	Cbin48[d]	F: TTCAGAGATGAAGAGGCTTGC R: CGGCTTTCTAGCATTTGTGC	$(ACA)_{10}$	109–193	20	8	0.83 (0.87)
	Cbin50[d]	F: AGGCAGGAGCTTAGAAACGTC R: ATCATCTGGCGAGCAAAAGT	$(TCT)_{10}$	162–247	20	9	0.83 (0.87)
	Cbin56[d]	F: AACAGCCGCCGAGATAAAG R:CTGGACAATTCAACCGAAGG	$(CT)_{10}$	178–234	20	10	0.50 (0.80)
	Cbin57[d]	F: CGGAGAGCACAAACACAAAA R: GCAGTGGTGTGCAATAATCG	$(TC)_{10}$	64–138	20	6	0.44 (0.78)
	Cbin59[d]	F: TAAATTACCTCCCCTCAATCCA R: TCAATTCGAACTGGACAGTCA	$(ATC)_{10}$	132–237	20	11	0.88 (0.89)
	Cbin62[d]	F: CCTCTCGTTGTATACACTCCCA R: GGCCCTGGTCCAATAAGAAT	$(TG)_{10}$	244–358	20	8	0.35 (0.66)
	Cbin66[d]	F: AAGTCCCCTCTACATCCCCT R: CTCGAGCTTCCATCAGCTTC	$(GA)_9$	217–391	20	11	0.58 (0.86)
Cetorhinus maximus	Cmax01[e,1]	F: GAAATGAATCTCACAGGTATCAGG R: AACATTTCAAACCTAGCTCATCTTC	$(TG)_9$	161, 163	20	2	0.40 (0.51)
	Cmax02[e,1]	F: TGACTTTGGCAGTTGGTTTG R: CAGTGCAGGGTGTGCAAG	$(GA)_{10}$	189, 191	20	2	0.45 (0.36)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Cmax03[e,1]	F: CACATCAGGCCAGGTGAAC R: CTGCTTGGCACTAAGCTGTG	$(GA)_9$	121–127	20	3	0.65 (0.62)
	Cmax04[e,1]	F: AACCTTCCTTAAGAGCATTCTGC R: GCCAAGTTGCTGCTGTGTC	$(CA)_{12}$	91–105	20	5	0.80 (0.75)
	Cmax05[e,1]	F: TTTCCATGGCCAACCTAAAC R: TCTACCTTTCCTCAACCTCTAGTAGC	$(CT)_{11}$	145, 147	20	2	0.60 (0.49)
	Cmax06[e,1]	F: TGCTCGTAGTGTCTCATTCAAAC R: GTCATCCAGGGTTTCAGTCAC	$(TG)_{14}$	213–253	20	8	0.85 (0.81)
	Cmax07[e,1]	F: TGTGCTGGCCAATATTTATCC R: TTTCATGAGGGCTGGATACC	$(CA)_{21}$	203–227	20	10	0.90 (0.88)
	Cmax08[e,1]	F: CAGCACTTGGTCAGAGGTAGG R: TGGCGGGATATTGTGGTC	$(GA)_{14}$	194–212	20	7	0.65 (0.74)
	Cmax09[e,2]	F: CCAATAGCCTCAAGCCTGTC R: ATTGTTGTGGCCCGAGTTAG	$(TG)_{10}$	153–159	20	4	0.75 (0.65)
	Cmax10[e,2]	F: GGGAAATGATGGAAAATTGC R: GCTCTAACTGTTTCTGCCTTCC	$(CA)_9$	177–183	20	4	0.75 (0.68)
	Cmax11[e,2]	F: CACCAATTGGCTTCATCCTC R: GTCACCAACATTACCATGTCTCC	$(CA)_{13}$	99–111	20	7	0.95 (0.80)
	Cmax12[e,3]	F: TTATTATACTTTCGTCACACATACATGC R: ATGCATGTGACTGATTGTTGG	$(CA)_{12}$	358–376	20	6	0.70 (0.77)
	Cmax13[e,2]	F: AACCACTAGCCGAGCTGAAG R: TTGGTTCAAAGGTGGAGACC	$(CA)_{13}$	233–245	20	7	0.95 (0.80)
	Cmax14[e,2]	F: GCCTGACTGCCTTCTGTCTAA R: GGCTGAATTGCCTACTCCTG	$(CA)_{10}$	156–182	20	9	0.80 (0.69)
	Cmax15[e,1,4]	F: TCAAGCTCAGCCTTAACTCCG R: TCCATCTTGTCTTTGCTTTTGGG	$(TG)_9$	325–349	20	8	0.80 (0.81)
	Cmax16[e,2]	F: GAGCTGACTTTGGCAGTTGAG R: TAGGCATCCCTACAGCTTGG	$(GA)_{13}$	169–175	20	4	0.50 (0.65)
	Cmax17[e,2]	F: TCCACACAGCGTTAGTGACC R: AGGCCTGAGTGTCTCTCACC	$(CA)_{10}$	141–157	20	9	0.90 (0.84)
	Cmax18[e,2]	F: TGAGAGAGACAAACTTTAGCTCATAAATC R: GTCACCTGGATTAAATGCCATC	$(CA)_{17}$	135–155	20	10	0.90 (0.88)
	Cmax19[e,2]	F: GTCAGGCAGGTCTTGGAGAG R: ACTCCACCCAAGTTCCATTG	$(TG)_{11}$	179–189	20	4	0.70 (0.62)
Scapharca kagoshimensis (Mollusca: Bivalvia)	Sk01[f]	F: CTTTTCATTGGGCAGTCCTTA R: GGAACACACAAATACACATACG	$(CT)_{14}$	142–196	35	10	0.700 (0.786)
	Sk02[f]	F: ATTGTCAGCGTTTCGGTA R: ACCAACAACAAAAATACAGT	$(CA)_{26}$	360–430	35	8	0.667 (0.829)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Sk03[f]	F: GGGAATAAAGGGATAAACTC R: AGATAATTTGGTAATGGTCTT	$(CT)_{15}(CT)_{11}(CA)_4$	223–325	35	10	0.867 (0.856)
	Sk04[f]	F: ATAGTCACCATATTCCTACAA R: TATACTCTCTATTTTACGCTC	$(CA)_{23}$	220–256	35	9	0.727 (0.800)
	Sk05[f]	F: TTTAACCACGTGTAAACGAAA R: TTCAAATAGCTTAGATTCCGA	$(CT)_{13}$	425–505	35	7	0.656 (0.825)
	Sk06[f]	F: AACAACTTTGAACTATAACT R: AAACAGTTCTAACCAGTC	$(CT)_{19}$	385–418	35	5	0.600 (0.733)
	Sk07[f]	F: TATTAGTGGAGTTGGTTTCGTC R: ATTCACCGCTGGGTATTT	$(CA)_{19}$	282–370	35	11	0.886 (0.886)
	Sk08[f]	F: AGTCAGTAATTGTAGTCTTGT R: ACATAAATAGCTGGGACTC	$(CT)_{14}$	224–256	35	8	0.735 (0.862)
	Sk09[f]	F: GTAAGCAAATTGGACATC R: TTATGCAACACTTCCAGTA	$(CT)_9(CT)_8$	395–501	35	9	0.629 (0.867)
	Sk10[f]	F: GCAACCATTATTTGGAACAC R: GTCACGAATGTTATACTGGAG	$(CT)_{25}$	164–230	35	10	0.759 (0.872)
	Sk11[f]	F: CCTATTGACACACCTACACAT R: AAACGAGTAGCTCAATAATTCA	$(CT)_7(CA)_8$	280–330	35	7	0.655 (0.808)
	Sk12[f]	F: TTTGGACCACCTAGAATATGA R: TACAACTCTACTGCATCATCT	$(CA)_9(CA)_4\ (CA)_9$	406–444	35	11	0.655 (0.881)
	Sk13[f]	F: TGAACGGTATAATTCCTAGCTG R: AGAGATTGAAAGAGATTGCCT	$(CT)_{17}(CA)_6$	300–360	35	9	0.815 (0.850)
	Sk14[f]	F: TTATGTTTTGTTTAACCACG R: TCAAATAGCTTAGATTCCGA	$(CT)_{16}(CA)_{11}$	368–426	35	10	0.800 (0.862)
	Sk15[f]	F: TGGCAAGATAGGTATGTGCAA R: TAGGCAGACCAATCGTGAAGC	$(CT)_{19}$	220–296	35	26	0.829 (0.960)
	Sk16[f]	F: GTTCAAATAGCTTAGATTCCG R: GATGTGTATTGTTTAGTGTCA	$(CT)_{12}(CT)_9(CA)_4$	358–446	35	10	0.563 (0.868)
	Sk17[f]	F: AGAAACAGAAAAATAGTCCAAC R: CATACAAAAAATAGACAGTGCT	$(CT)_{11}(CT)_4(CT)_{13}$	270–345	35	14	0.700 (0.914)
	Sk18[f]	F: ACAATCAAATGCTTACATACTTC R: AGTCAATTTCATCTCTGTAGG	$(CT)_{22}$	132–210	35	21	0.704 (0.948)
	Sk19[f]	F: AGATGTAAAAGGCACAGACAAC R: TGGTAAGGTGGACCCTGT	$(CA)_{25}$	341–381	35	6	0.677 (0.821)
	Sk20[f]	F: AACGAGTAGCTCAATAATTCA R: AACCTATTGACACACCTACA	$(CA)_8(CT)_7$	245–320	35	11	0.759 (0.883)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
Bagrus docmak	Bd04^g	F: TGTGGACCAAGAGACAGGTG R: AATGAACAAGGCAGGTGATG	$(AGAT)^{18}$	200–208	16	3	0.563 (0.646)
	Bd18^g	F: ATGGGGAGGAAAAGTGGAG R: CCTGAGTGCATTGCTCATGG	$(AC)^{15}$	100–102	16	2	0.563 (0.451)
	Bd01^g	F: TTGCCAATCCTGATGACACTC R:TAAAGCTGGGCAACTGATCC	$(TTCT)^{15}$	203–219	15	4	0.333 (0.589)
	Bd02^g	F: TGTGCTCTGACCCCTACCTC R:GGGTATCGCATCCCAGATAG	$(AGAT)^{17}$	110–130	16	6	0.563 (0.541)
	Bd12^g	F: CCGACCATCTCAAATACAAGTC R: CTCTTCCCCAAGGCTATTCC	$(AAT)^{18}$	237–258	16	3	0.688 (0.508)
	Bd09^g	F: ACTGTTCCCATGAAGTTGGG R: TGGTCAACTTTAGATGTGCAGC	$(ATT)^{19}$	223–238	16	6	0.563 (0.734)
	Bd06^g	F: TTCTGAAGCCCAAAGTAGACG R: GCCCACACTATTGACACAGG	$(GATA)^{16}$	171–199	16	7	0.625 (0.609)
	Bd20^g	F: TCCTGGAGACCAAGACCAAG R: TGCAGGTTAAGAATGGAGGC	$(CA)^{11}$	156–168	16	4	0.688 (0.672)
	Bd05^g	F: GCTGGCAACATGCAGTAATC R: CAGCATTTCATTGCTATGTGC	$(ATAC)^{15}$	136–172	13	4	0.250 (0.719)
	BD07^g	F: GAGCACACGAAACATTGCAG R: TTGTAGATTCCCTTTGGGATG	$(GATA)^{15}$	125–157	4	5	0.538 (0.678)
	Bd16^g	F: GCAATCGCACTCTTGTTATCG R: TAGTAGCGCACCCAGGAAAC	$(ATT)^{13}$	83	13	1	–
	BD08^g	F: TTACCTCACACTCTGGGGTTG R: GGTAAAGGTTTACACTGTGGGG	$(ATCT)^{16}$	179–187	13	3	0.615 (0.544)
	BD03^g	F: CCTGCAGGAGTTTGTTTGTG R: CGTGCCATAGGCATTTATCC	$(TAGA)^{15}$	159–191	16	3	0.438 (0.568)
	BD14^g	F: CTTTAATGACACTGCGCTGC R: CTCAAAGCGCTTGAAGTGG	$(TAT)^{17}$	218–233	16	6	0.688 (0.781)
	Bd10^g	F: GTCCCACGGACTGAAAAGTG R:TCAACTTCTTAGCACAAAATCAGAC	$(TTA)^{15}$	266–287	16	7	0.375 (0.426)
Bagrus bajad	Bd04^g	F: TGTGGACCAAGAGACAGGTG R: AATGAACAAGGCAGGTGATG	$(AGAT)^{18}$	197–229	5	5	0.400 (0.760)
	Bd18^g	F: ATGGGGAGGAAAAGTGGAG R: CCTGAGTGCATTGCTCATGG	$(AC)^{15}$	125–133	5	4	0.600 (0.480)
	Bd01^g	F: TTGCCAATCCTGATGACACTC R:TAAAGCTGGGCAACTGATCC	$(TTCT)^{15}$	190–206	5	5	1.000 (0.740)
	Bd02^g	F: TGTGCTCTGACCCCTACCTC R:GGGTATCGCATCCCAGATAG	$(AGAT)^{17}$	110–126	5	4	0.600 (0.580)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Bd12[g]	F: CCGACCATCTCAAATACAAGTC R: CTCTTCCCCAAGGCTATTCC	$(AAT)^{18}$	236–239	5	2	0.400 (0.320)
	Bd09[g]	F: ACTGTTCCCATGAAGTTGGG R: TGGTCAACTTTAGATGTGCAGC	$(ATT)^{19}$	240–243	5	2	0.400 (0.480)
	Bd06[g]	F: TTCTGAAGCCCAAAGTAGACG R: GCCCACACTATTGACACAGG	$(GATA)^{16}$	203–215	5	4	0.800 (0.660)
	Bd20[g]	F: TCCTGGAGACCAAGACCAAG R: TGCAGGTTAAGAATGGAGGC	$(CA)^{11}$	148–150	5	2	0.200 (0.180)
	Bd05[g]	F: GCTGGCAACATGCAGTAATC R: CAGCATTTCATTGCTATGTGC	$(ATAC)^{15}$	125–133	5	2	0.200 (0.180)
	BD07[g]	F: GAGCACACGAAACATTGCAG R: TTGTAGATTCCCTTTGGGATG	$(GATA)^{15}$	134–158	5	4	0.750 (0.750)
	Bd16[g]	F: GCAATCGCACTCTTGTTATCG R: TAGTAGCGCACCCAGGAAAC	$(ATT)^{13}$	83–89	5	3	0.800 (0.540)
	BD08[g]	F: TTACCTCACACTCTGGGGTTG R: GGTAAAGGTTTACACTGTGGGG	$(ATCT)^{16}$	179–187	5	3	0.400 (0.460)
	BD03[g]	F: CCTGCAGGAGTTTGTTTGTG R: CGTGCCATAGGCATTTATCC	$(TAGA)^{15}$	179–203	5	6	1.000 (0.800)
	BD14[g]	F: CTTTAATGACACTGCGCTGC R: CTCAAAGCGCTTGAAGTGG	$(TAT)^{17}$	225–241	5	3	0.400 (0.340)
	Bd10[g]	F: GTCCCACGGACTGAAAAGTG R:TCAACTTCTTAGCACAAAATCAGAC	$(TTA)^{15}$	265–277	5	4	0.600 (0.480)
Acropora muricata (Linnaeus, 1758) (Scleractinia, Acroporidae)	Am01[h]	F: CGTCTCGCACTGGTTTACAA R: GAGGTGGAAAATGAGTAGCAAT	$(TC)_7$	313–319	46	3	0.50 (0.58)^{NS}
	Am02[h]	F: TGAAGTTACCAAAGTGCCTTAAA R: ACCATGTAAACTGGGCGAAT	$(CT)_7$	195–221	46	6	0.29 (0.61)[5]
	Am03[h,5]	F: GCGACCAGACAGGCTCTTA R: CGAAATGCGCTCCTTTACTA	$(GT)_7$	162–176	46	5	0.36 (0.44)^{NS}
	Am04[h]	F: GGGGAATTACTCCTCTAATTCAA R: TGGTTGTCAAGGGCAATTTT	$(AC)_7$	146–154	46	4	0.14 (0.14)^{NS}
	Am05[h]	F: GGTCAGCAGGTAGGCGGA R: CTTTTGAACCAGATTGATCGC	$(GT)_8$	137–155	46	3	0.21 (0.27)^{NS}
	Am06[h]	F: CAGCACGATAGTGGACAAAA R: GCAAAGTACGGATTCTGCAA	$(AG)_8$	114–120	46	3	0.36 (0.42)^{NS}
	Am07[h]	F: GGAATGAGGCACAAAGAAGG R: AGCAAAGTGAGGATGCCATT	$(AC)_7$	135–145	46	5	0.50 (0.49)^{NS}
	Am08[h]	F: TTGCAAACAGCAAGCCAG R: GGCTGCTTGATCACATCTAGTTT	$(CA)_7$	147–151	46	3	0.07 (0.07)^{NS}

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
	Am09[h]	F: GAAGGCTCTTGTGTTGCGAT	$(CA)_8$	113–129	46	4	0.43 (0.60)[NS]
		R: CGTTGATTTTGCTGACTTCAA					
	Am10[h]	F: CTCCCAACAGATGCTATTTAAGAGA	$(AG)_9$	145–151	46	3	0.14 (0.37)[5]
		R: CGACCAACCAATAACCACTT					
	Am11[h]	F: GCAATGCCATGGTTTCCA	$(TC)_9$	136–140	46	3	0.21 (0.20)[NS]
		R: TTGCAGCATCAAAGACCC					
Porites lutea Milne-Edwards & Haime, 1851 (Scleractinia, Poritidae)	Pl01[h]	F: TCATTCAATACCTTCTCAAGATTCA	$(AG)_{11}$	232–276	48	7	0.53 (0.74)[NS]
		R: TGGTATTTCATACATTATTTCCCTTG					
	Pl02[h]	F: GTCATCGTCATCACCATCCA	$(ACC)_6$	91–112	48	3	0.47 (0.54)[NS]
		R: GAGCCGAACAGATTTCAACC					
	Pl03[h]	F: TTGCCCCATTCCAATAACTG	$(AAC)_7$	185–200	48	6	0.37 (0.59)[NS]
		R: GGAAAGACGAAATTAAATAGCCC					
	Pl04[h]	F: TTTTATGGAGTGGCCATTTG	$(ACA)_7$	144–153	48	3	0.05 (0.40)[5]
		R: TTCAGTGTCAAAAGTGCAAGAAA					
	Pl05[h]	F: TGGTATATTATATTTCTGTTCCCTTTT	$(TC)_8$	131–143	48	2	0.16 (0.49)[NS]
		R: CTCGACATGAGCATTGCCT					
	Pl06[h]	F: ACGTGCAGGTTGAATGTATGC	$(GT)_{10}$	190–204	48	5	0.58 (0.71)[NS]
		R: GGTTTATAGATTCCATCACTAACCAA					
	Pl07[h]	F: CAACCAACCACTTCTGCTACA	$(TC)_6$	200–204	48	2	0.05 (0.15)[NS]
		R: TACTGCTTCTCAACATGCGG					
	Pl08[h]	F: GACCGCTGATCAAAGGCTTA	$(CT)_7$	182–226	48	3	0.05 (0.15)[NS]
		R: CGAAGAACCGAAACAGGAAG					
	Pl09[h]	F: TTGACTTTGTGGGCTTGAAA	$(AG)_7$	179–181	48	2	0.05 (0.05)[NS]
		R: CACGACTACCGGGTGAAGTT					
	Pl10[h]	F: CACCATAATCATGAGATTTACTATTGA	$(AC)_9$	123–143	48	4	0.53 (0.73)[NS]
		R: GAATCAACCAATGGCAGTCC					
	Pl11[h]	F: GCTGTTCAATGCACTTCTGG	$(AC)_9$	141–149	48	2	0.32 (0.51)[NS]
		R: GCTGTGAGCTTTAACCGACC					
Pelteobagrus vachelli	PV5[i]	F: GGACTGGAACACAACAGGCT	$(CA)_{10}$	214–222	32	5	0.688 (0.581)
	KP735111[i]	R: CCCAAACCGCACATTATTTC					
	PV11[i]	F: GCTTTTTATCATGCAGTGTGG	$(GA)_{10}$	258–278	32	8	0.938 (0.802)
	KP735112[i]	R: GAAAATTCAGCATTTCCAAGC					
	PV19[i]	F: CAGGCTAACCTTGGCTTGAC	$(GT)_9$	275–281	32	4	0.563 (0.537)
	KP735113[i]	R: CAGTCCCAGTCAGCTCTGC					
	PV20[i]	F: CCGTACACAGTTGCTCTCCA	$(AC)_9$	227–245	32	10	0.844 (0.782)
	KP735114[i]	R: CAAAACACTCCAGCAGTCCA					
	PV22[i]	F: CTGTCACACTCGCCTTCAAA	$(GT)_9$	251–255	32	3	0.188 (0.177)
	KP735115[i]	R: TTACTCGCAGTGCATTTTGG					

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	PV23[i]	F: GCTGAGAACTGAAACCCTGC	$(GA)_9$	241–251	32	6	0.688 (0.672)
	KP735116[i]	R: ACATGGACCTCCCATTGTGT					
	PV28[i]	F: TTTCAATGGCCTCCTGATTT	$(CT)_9$	273–283	32	6	0.563 (0.711)
	KP735117[i]	R: TTCTTCCCTTTTTCCCTCGT					
	PV30[i]	F: GCCAAGACGACATCACAGAA	$(TA)_9$	279–291	32	7	0.844 (0.712)
	KP735118[i]	R: TGTGCCAGGTTGTGTACGTT					
	PV34[i]	F: TCGGTCAGTTCAGATCACCA	$(TA)_8$	237–245	32	5	0.438 (0.643)
	KP735119[i]	R: CACACAACACAATCTGCCAA					
	PV35[i]	F: GATGAAAGAAACCCGGAACA	$(TC)_8$	220–222	32	2	0.031 (0.031)
	KP735120[i]	R: TGGAGAGAAAGAAGGCCAGA					
	PV36[i]	F: CAACGACTGGAGGTCAAACA	$(GT)_8$	285–315	32	12	0.625 (0.79)
	KP735121[i]	R: AGCTGACGGAACTGTTACTGC					
	PV37[i]	F: TGAAATAGCTTGCCGTTGTG	$(AC)_8$	251–257	32	4	0.5 (0.563)
	KP735122[i]	R: TGGATTGTTGTGAGGTTGGA					
	PV39[i]	F: GGGATTAGGGTGTAGGGAGC	$(AC)_8$	258–268	32	5	0.75 (0.655)
	KP735123[i]	R: CCCTAAGTTGAGCGCCTTTA					
	PV40[i]	F: TCACTACCGGGGACTGACTT	$(GT)_8$	258–260	32	2	0.125 (0.222)
	KP735124[i]	R: TAAAAATTCACCGGCCATTC					
	PV43[i]	F: AGCATTGGAGCCGATCATAC	$(TG)_8$	275–281	32	3	0.344 (0.304)
	KP735125[i]	R: AGGCACCCTCAGTAAGAGCA					
	PV44[i]	F: AGCAGCCTCTTCAACCGTTA	$(TG)_8$	257–261	32	3	0.188 (0.294)
	KP735126[i]	R: CAGGTAGAGTGGGAGTGATGG					
	PV45[i]	F: TCAAACTGGGCAAAAACTCC	$(AC)_8$	249–279	32	13	0.813 (0.864)
	KP735127[i]	R: AACGAAGGGGGTTTTCAGAT					
	PV49[i]	F: TTTTCTGAAGGAGACGTCGG	$(AC)_8$	272–278	32	4	0.563 (0.586)
	KP735128[i]	R: CCAGGCAGGATGGTTACCT					
	PV50[i]	F: CTTCCCAGAAGTCTGAACGG	$(AAG)_8$	268–289	32	7	0.938 (0.748)
	KP735129[i]	R: TCCAGGATCAGGACATCACA					
	PV65[i]	F: CCACTGGCAAAACATTGAAA	$(TCA)_7$	231–237	32	3	0.125 (0.121)
	KP735130[i]	R: TCAGACCCGCCTTAATATGC					
	PV71[i]	F: ATGATCAAACACAGTGGGCA	$(CAT)_7$	254–260	32	3	0.125 (0.354)
	KP735131[i]	R: AGAAGACGGGAGGAGGAGAG					
	PV84[i]	F: TGCTTCCTCTCCGCTATTGT	$(TCC)_6$	230–233	32	2	0.406 (0.484)
	KP735132[i]	R: GCAGCCACTATTATGAGCCC					
	PV86[i]	F: CTGGGAAACATCCTGGAAAA	$(TTG)_6$	228–243	32	6	0.938 (0.79)
	KP735133[i]	R: AACCATCCTGCAGGTGAGAC					
	PV88[i]	F: CACATGATCGTCACCTCGTC	$(ATG)_6$	218–220	32	2	0.781 (0.484)
	KP735134[i]	R: TGAGGATGATTCTGCACCTG					
	PV90[i]	F: TTCCCTAAATGACCTCGTGC	$(GTT)_6$	259–268	32	3	0.594 (0.549)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	KP735135[i]	R: ACTTTCCCCCTTTACATCCG					
	PV92[i]	F: CGTTCACCGTTTTTCAGAGA	(ATG)$_6$	222–240	32	7	0.938 (0.801)
	KP735136[i]	R: AGATGCAGCGGTGCTTTAGT					
	PV93[i]	F: TCACCTGCCGATTTCTATCC	(AAT)$_6$	249–255	32	3	0.656 (0.631)
	KP735137[i]	R: TGCAAATGAACAGAAGCAATG					
	PV97[i]	F: GAACTGTACGGCACACTGGA	(TTA)$_5$	250–253	32	2	0.125 (0.119)
	KP735138[i]	R: TTTGATCGTTGCTTTCTTTGTC					
	PV98[i]	F: GCTTTGTCGTGATTTGAGCA	(TCT)$_5$	268–289	32	7	0.844 (0.728)
	KP735139[i]	R: CTCATGTGGAATGAACGCAC					
	PV102[i]	F: GGGCATGCTGAGGAACTAAA	(ATT)$_5$	232–244	32	5	0.469 (0.785)
	KP735140[i]	R: GGTTTAAACACCTGTTCCATCA					
	PV103[i]	F: GGAGCTGCCTGTCTATCTCG	(GGT)$_5$	262–274	32	5	0.594 (0.667)
	KP735141[i]	R: TGGACTGAAAAACTACAGGAAAA					
	PV111[i]	F: AGAAGTGCTGCACACCAATG	(ATGT)$_5$	248–264	32	5	0.375 (0.354)
	KP735142[i]	R: TCCTGCCACTTGTCTAAGGAA					
	PV114[i]	F: AGCGTGCTGGAGTATTGCTT	(AAAT)$_5$	281–289	32	3	0.281 (0.466)
	KP735143[i]	R: CGGTTCAGAGGTTCACTCGT					
	PV117[i]	F: AGTCACAGACGCAGAAGCCT	(TAGC)$_5$	249–269	32	6	0.531 (0.605)
	KP735144[i]	R: TAGCCGGAGTTACCAAATGC					
	PV120[i]	F: AAACGCCAAAGAACCTGATG	(TCCA)$_5$	231–247	32	4	0.625 (0.58)
	KP735145[i]	R: CTGACAAGACTGCAGCAAGC					
	PV122[i]	F: GGCTGGTAAAATGGTGGTGT	(AT)8aaa(GT)$_7$	282–288	32	4	0.75 (0.614)
	KP735146[i]	R:GAACAGTGCATGCAGGCTAA					
	PV123[i]	F: GGCTAGCGGCTCAATTACTG	(CA)7cgttttccttttttatgatac agtacggccacagcagggtga(GT)$_6$	254–280	32	8	0.844 (0.769)
	KP735147[i]	R: CTCCTGGGACATACACACCC					
	PV128[i]	F: TAATGAGCGGAACAGGGAAG	(TG)7tacagggttgtgtgttggtgt gtgtacagggtggggtgtgctat gattgttgtgtgtgtactggatggtgtgagt(TG)$_6$	226–244	32	5	0.563 (0.61)
	KP735148[i]	R: ACACACAACTCACACCACCC					
	PV136[i]	F: CAGACAGGAGGTGTGTGTGG	(G)11cagatgtgggcaagaattcatcct ccctcagc(TG)8ttggactcgcct(TG)$_6$	273–293	32	6	0.719 (0.686)
	KP735149[i]	R: GCAGCTGTCAGTCATGTGGT					
	PV139[i]	F: CGCTGAACTACACACACGGT	(AC)7aaaaaaaa(AT)$_6$	288–294	32	4	0.531 (0.659)
	KP735150[i]	R: ATCAGAGCCCATGCTGAGTT					
	PV140[i]	F: TATGTGGTGGCCATGTCTGT	(TG)6cgcacgcgcaagtgtgcaaccccta tgtgaatgtccactgtgttgcagattttaagc(TG)$_7$	251–255	32	3	0.531 (0.493)
	KP735151[i]	R: TCAGACGGGAATTTGTCCTC					
	PV141[i]	F: TGCTAGCAATTAGCACTGGG	(AC)7agacaaacacacacacat(AC)$_6$	279–283	32	3	0.438 (0.405)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
	KP735152[i]	R: GGCATCAGGGTTTCTGGTTA					
	PV147[i]	F: GCGAGAGAGCCGTTATTTTG	(TG)7cattttcttttttctgtatggaaattgttac tgttttatgtgtgtgtaaatcctgtatttaaatc(CA)$_8$	232–240	32	5	0.5 (0.66)
	KP735153[i]	R: ATCTCTTTTGGCCTTTGCAC					
	PV148[i]	F: TGCACTTGAAGATCAGTTGTGTT	(GAT)5gtaatttaaatgtgtttctttaaaaattcttg agtcaagcctaaaactaaggtacaataaatac(TG) 7cgcgtccgtgtgtatgtgtgtattatagaatta(AT)$_8$	279–296	32	5	0.406 (0.357)
	KP735154[i]	R: TCGATAATTCATGATTGCCA					
	PV153[i]	F: GGGAGAGAAGAAGGGAATGG	(TC)7catcgctccaagtgcttcctcccca(TTG)$_5$	279–282	32	3	0.219 (0.35)
	KP735155[i]	R: CGAAAGACAAAATGGAGGGA					
	PV155[i]	F: AAACGTACCCACAGAGCCAC	(GT)9cctcaggttagaagtacttcaac(CA)$_6$	291–308	32	5	0.469 (0.628)
	KP735156[i]	R: TCCAAAAATGGTGTCGTTCA					
	PV156[i]	F: TCAATACACTCGCTGACCCA	(TG)6ttgtgtattagataataaagcaaaaataat aaggatccagaaaagtgtgggggtttaaata gaaataagg(ATA)$_5$	289–294	32	3	0.469 (0.458)
	KP735157[i]	R: AGCGTCCGAACAGAACAATC					
	PV165[i]	F: TCCTGGTACACTTTCGCACA	(TGT)5tttgtttgtttttagct(CAG)$_5$	274–280	32	3	0.625 (0.628)
	KP735158[i]	R: TGGATGGCGATCATACTGAA					
	PV169[i]	F: CACTTGCACTTCTCGTGTGA	(GAA)5aaaaa(AT)$_6$	290–293	32	4	0.656 (0.741)
	KP735159[i]	R: TAAACAGCCTCACCAAACCC					
	PV173[i]	F: TAGTGTTCCTGTGAAGCCCC	(AGC)5atcctcacagtgctgatgcgttcagtgtgcg actggtcctgagcggcagcagcattacgatcctaa cgtgataaactgagcaccgtctggtctggg(GT)$_9$	272–297	32	8	0.656 (0.821)
	KP735160[i]	R: AGGGAGAGCGTTTGTGCTAA					
	PV175[i]	F: TCTCCGGCGTTGTAGAAGTT	(GA)7atcacgtgagggttctgtcagctgcgcttcactcc tagctcaggggcagctgtgttacgtaaacaagt cggagatgaatgatttgtgttt(AC)$_8$	268–271	32	4	0.813 (0.648)
	KP735161[i]	R: TGGGAATCCTCGTGATTCAT					
	PV177[i]	F: TGTCTGCGTGTGTACCTGTG	(GT)8aagtttgtatgtccatgtgtcagtgtgt ttgtccagctattcctatgtc(TG)$_6$	275–285	32	4	0.625 (0.552)
	KP735162[i]	R: ACGGCTCTGCTTCAGTCTGT					
	PV184[i]	F: GTGAATTGGGTGAGTGGCTT	(GT)6(TG)$_6$	218–222	32	3	0.563 (0.5)
	KP735163[i]	R: GCCAAGTGGTGAAGGGATTA					
Sebasticus marmoratus	Sm31[j]	F: CAAACTGAGCAGGTTTGTGTAA R: AACTCTCTCCCCATAGAGGTCC	(ATA)$_{19}$	230–260	24	4	0.917 (0.727)
	Sm38[j]	F: GTCGTTGACAGAGCTTGACTTG R: TTTAAAAGCGGGCTCAATATGT	(CTT)$_{18}$	230–270	24	5	0.556 (0.748)
	Sm43[j]	F: CAGTTTGTAGTCAGCTGTCTGTG R: GGTGGTGGATTGGTGTTAATCT	(TAA)$_{11}$	150–180	24	5	0.250 (0.742)
	Sm49[j]	F: GCTGTTATCAGTGATCCTGGAG R: ACGAATGGCTTCAGTTCAATCT	(GAA)$_{10}$	120–160	24	6	0.556 (0.770)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Sm58[j,†]	F: ATCATCAACATATCGGAGCCTT R: GAGACTCGTGACATTGAGTTGC	$(TTA)_{14}$	130–170	24	6	0.611 (0.734)
	Sm92[j]	F: GGACTGATCTCCTTTAAGGTTCA R: TTCGATGTCTGCTCAGCATTAT	$(TTA)_{15}$	180–220	24	2	0.306 (0.497)
	Sm94[j,****]	F: GTGAAAGCTGTCAGAAGACACG R: ACGGTGTCAGTGCAGTTAAGAA	$(TGA)_{10}$	140–180	24	4	0.708 (0.724)
	Sm95[j]	F: GTGAGCTCTTCTGTTTTGGGAG R: ATATGTAAAGATGCTCAGCGCC	$(CTT)_{15}$	110–140	24	6	0.472 (0.745)
	Sm101[j]	F: GTGAGCTCTTCTGTTTTGGGAG R: ATATGTAAAGATGCTCAGCGCC	$(GGA)_{14}$	180–220	24	4	0.242 (0.667)
	Sm102[j]	F: AGACACTCCCACCTCCTACAGA R: CTATGGAACTGTGATGCTGGAA	$(AGAT)_{12}$	190–240	24	11	0.833 (0.896)
	Sm106[j]	F: GATTGCGTTAATGCGTTGAATA R: ACTGTGGACGGTCTGTACAATG	$(TAGA)_{16}$	220–350	24	9	0.889 (0.813)
	Sm117[j,****,†]	F: ACATGGTCCGTAGCAGAGTTTT R: TGCAAGTTGTCCTCTGTATGCT	$(AC)_{26}$	220–270	24	4	0.500 (0.713)
	Sm124[j]	F: AAGCGCATATTTTTCCACCTAA R: TGGGCCATCACAATAACAGTAG	$(TTA)_{18}$	120–160	24	9	0.861 (0.823)
	Sm131[j]	F: TCATTCAAGGTTTGTAGCTGGA R: AGGAGCAACGATGCATTTTATT	$(ATT)_{18}$	120–160	24	5	0.667 (0.766)
	Sm144[j]	F: AGTCAAAGGAATGGTCTGCAAT R: GCATGCAGAAAAGAGAACTTGA	$(ACA)_{18}$	230–260	24	6	0.722 (0.766)
	Sm148[j,****,†]	F: TTTAGCATGGTGGTTTGAAATG R: TCTTCCGGTCATGTACAACTCT	$(AAAC)_{12}$	110–190	24	7	0.723 (0.806)
	Sm149[j]	F: AGTCTGGATAGGAGGGGTTAGG R: ACTGTGATGCTGGAAACTTGAA	$(TATC)_{20}$	110–150	24	6	0.695 (0.798)
	Sm154[j]	F: ACTTGAATTTCCCTCTGGATCA R: CAGGGTCAGGATCTTTGAAAAC	$(TCTA)_{18}$	160–200	24	6	0.361 (0.758)
	Sm168[j]	F: GCAAGTGTGGAGCTAATCAGTG R: CACATCATCAAGATCGTGTCCT	$(GTT)_{12}$	180–240	24	6	0.556 (0.740)
	Sm198[j]	F: TCTCAGAAAGGTGCGTCACTTA R: GTGAGTGGGTGTGTGTGTTTTT	$(GAA)_{19}$	200–240	24	4	0.528 (0.654)
	Sm216[j]	F: ATGTTGTGTGACTCCCGTAATG R: TTGTTTTGTACAGTGACGTGGC	$(GTGA)_{16}$	220–280	24	4	0.667 (0.705)
	Sm289[j]	F: TGGTTGAATACATGACGAGAGG R: GGAACTGTGATGCTGAAACTTG	$(TAGA)_{14}$	220–260	24	6	0.667 (0.835)
	Sm290[j]	F: TGATCGACTGCAATATTTACGG R: TTGAATTCAGTGCATTTTAGGA	$(TAG)_9$	260–320	24	5	0.639 (0.760)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Sm309[j]	F: ACCAACTTCTCCCTCTTTCTCC R: ATGCAAAAGTAGACCTTGCACA	$(GT)_{20}$	340–380	24	3	0.556 (0.497)
Aquila chrysaetos japonica	AQJ03[k]	F: GGCTTGTAAATTTGTATGGCAGT R: TTTGGGCTAGAGAGGGATGA	$(CT)_{11}$	147–155	20	4	0.600 (0.569)
	AQJ08[k]	F: GGCCTTGCCTATTCTTCTCC R: TGTCTGGAGCTCTGCCTGAT	$(CTT)_{16}$	173–182	23	4	0.304 (0.387)
	AQJ10[k]	F: GAAAACATCCAGCACCATCA R: CATCGTGCTCGCTTAGATCA	$(ACT)_{17}$	193–220	25	7	0.440 (0.544)
	AQJ19[k]	F: TCATCTTCTTTCCCCACCAG R: TGATTTGAGCTGTCCCTTCC	$(AC)_{17}$	170–178	21	3	0.571 (0.632)
	AQJ22[k]	F: TGGTGAAACCATTCTCTTTTC R: TGGACTCCTTCTCAAAGAGG	$(CTTT)_{13}$	208–228	21	4	0.571 (0.573)
	AQJ27[k]	F: GAGACCTGAGGATTGGTGAC R: TGTGCCTGAATAGTGTGCTT	$(GT)_{14}$	174–184	23	4	0.522** (0.678)
	AQJ28[k]	F: CACTCTTGCTATAGGCTCACC R: CACGCACTGTAAAACAAAGG	$(AC)_{13}$	182–186	27	3	0.222 (0.313)
	AQJ30[k]	F: AAAGGTTTGGATAATCTGGATG R: GTCAATCAGGTTGTACGTTAGTATC	$(AAT)_{13}$	149–158	30	4	0.433* (0.518)
	AQJ34[k]	F: TGGCCACTGATTTCTATGTG R: CAAGTGTCCACTAGCACAGC	$(GT)_{13}$	157–165	22	4	0.364* (0.402)
	AQJ36[k]	F: TCCCAGTAAAATCACTGCAC R: ACTTTTAGACCAGCCTGACG	$(GT)_{12}$	185–195	22	6	0.727 (0.744)
	AQJ40[k]	F: GGATGCTAAAGTTAACACACACA R: TAAAGAAGCCATTTGGGAAA	$(AC)_{11}$	250–252	21	2	0.238* (0.500)
	AQJ41[k]	F: AGATAGGTTGGCAAAGATGC R: TTGCAAGCTAAAGCCTTTCT	$(AC)_{11}$	174–176	20	2	0.550 (0.439)
	AQJ49[k]	F: AGAAGCGATACGCATACACA R: AAACTAACAGCAGCAGCAAA	$(AC)_{11}$	215–221	22	4	0.182*** (0.449)
	AQJ52[k]	F: GACTGTGAGGACAGGGTCTC R: TGAAAGTTGATGGCAAAAGA	$(AC)_{12}$	168–174	21	4	0.714 (0.659)
	AQJ53[k]	F: TTGTTTTCATTGTGAAATACCTG R: TGACCTAGATTTTCTCCAGCTT	$(GT)_{12}$	140–152	26	3	0.692 (0.644)
	AQJ56[k]	F: AATATATTTATTGGCACATGCAC R: CAAAATTACCACTAGGAAAGCA	$(AT)_{11}$	154–158	26	3	0.538 (0.514)
	AQJ59[k]	F: GGCCAACCAGATATTAGACG R: GAAAGGTGGCAAAGAGGTAA	$(AAGG)_{11}$	184–200	22	3	0.591 (0.600)
	AQJ62[k]	F: CCTGTGAAAATGCATAGGTG R: TCCACAGAGTGCTAGCAAGA	$(AC)_{12}$	172–180	21	5	0.381* (0.594)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	AQJ63[k]	F: GCGATCAAATAAATCCCTCT R: GCGTTTTATCAAGCGTCTTT	$(GT)_{12}$	184–194	23	2	0.435 (0.476)
	AQJ66[k]	F: AGCAAAGTGCAGCATCAATA R: AGAGCTTGCTTTTCAGAACC	$(GT)_{12}$	154–158	22	3	0.545* (0.615)
***Araucaria rulei* chloroplast microsatellites**							
MP1							
Araucaria rulei	SSR2[l]	F: CGTCGGATGGAGTGGATTAT R: CCTGGCAAAAGATACAGAATAAAAAAA	$(T)_9$	253–255	28	3	(0.472)
	SSR11[l]	F: GGAATGGTTATTTGATCAAGGAGAT R: GAAAGGTGGTGAATTAAAAATAAAAAA	$(T)_{10}$	203–204	28	2	(0.337)
	SSR13[l]	F: GTGGTACGAGCGATCCATTT R: GGAGACAACCAGTAAACAAAAAAAAA	$(T)_9$	124–126	28	3	(0.446)
	SSR53[l]	F: CCATTGGGGATCTATTTTTCG R: GCGATCTTTAAGCGATCAGTG	$(A)_9$	253–255	28	2	(0.500)
MP2							
Araucaria rulei	SSR16[l]	F: TTCTACAAATCAATATCTGCCCTTA R: GGATTCAATCAATTTATTAATCTAAAAAAAA	$(T)_{13}$	337–338	28	2	(0.459)
	SSR23[l]	F: TGATTTTCTGGTGCACAATACC R: CAGTTTTTGAAATAGGAATATTTTTTTTTTTTTT	$(A)_{16}$	219–220	28	2	(0.459)
	SSR56[l]	F: CAAAGAGGATGCCAATTTGTT R: GTAGTTAGCGATTCTTTTCTCTATTTTTTTT	$(A)_{19}$	238–241	28	4	(0.651)
MP3							
Araucaria rulei	SSR4[l]	F: GGCTATCCCAATTTGACCAT R: GCAGCTGTAATTATTACAATAAAAAAA	$(T)_{11}$	147–148	28	2	(0.069)
	SSR27[l]	F: TCCATTTACAGATCATTATCGAAG R: CGATTCTCATAAAAAAAAAATATAGAAAAAA	$(T)_9(T)_9$	204–206	28	3	(0.401)
	SSR31[l]	F: AAGTTCAATTGGCCGAGATG R: CGGCAAGTCTGTTCCAGAGTA	$(TA)_{14}$	258–262	28	3	(0.349)
	SSR62[l]	F: TGGGTGCCATATTCACTTCA R: TATCGATCGGTCGCATAGG	$(TA)_9(T)_9(A)_{11}$	221–224	28	4	(0.625)
MP4							
Araucaria rulei	SSR9[l]	F: TAAAACACCTAAAACCCGACG R: CAGGTTATTCCATTCCCTAAA	$(T)_{12}$	170–172	28	3	(0.518)
	SSR21[l]	F: ACTTGCCTCTCCTAATGGTTGGT R: TTTCTTGGGACTTGTCGGAAATA	$(C)_9$	222–223	28	2	(0.069)
	SSR35[l]	F: TCAATTCCAACCGAGTAGGTG R: TCCGACAACTTCTATCCCATTC	$(T)_9(T)_{11}$	262–263	28	2	(0.245)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
***Araucaria rulei* nuclear microsatellites**							
MP1							
	572[l]	F: VIC-ACACACACGCATAAGAAACTAAAG R: AAGATCGAGCCCACTCCAAG	$(AC)_{11}$	151–182	29	6	0.483 (0.730)
	2821[l]	F: 6-FAM-GGAAGAGCTTGAACCACTCAAAG R: TGTGCAGGTGGAATGCAAAG	$(AC)_{22}$	132–185	29	9	0.862 (0.809)
	3612[l]	F: VIC-ATGGTGGTGATGTGCCAAAG R: ATGGATTTCATGCCCCAACC	$(AC)_{12}$	85–107	29	5	0.655 (0.738)
	3785[l]	F: PET-ATTTTTCAAGGGTGGGGGAC R: ATGTCCACCGCATTACAAGG	$(GT)_{11}$	214–241	29	2	0.172 (0.158)
	3956[l]	F: NED-ACTTCTCCACACTCTGATTCTAC R: TCTCTAGAAGAGGTGCAGGC	$(CA)_{11}$	99–143	29	6	0.690 (0.622)
MP2							
	8816[l]	F: PET-TTGTGGCTTATTGTGCCCTC R: CTATACACCAAGGCCTCCTC	$(AC)_{12}$	142–211	28	10	0.571 (0.819)
	9164[l]	F: PET-TCCCAAAGATACACCCCTTG R: TGCTTGTAGTTGAGAGTGAGTGAC	$(AC)_{17}$	70–130	28	9	0.857 (0.817)
	9465[l]	F: NED-AGGATGAAGGTTGGAGACCG R: CCTCTTCCTCTCGGCCTTAC	$(GA)_{12}$	219–245	29	6	0.517 (0.729)
	9996[l]	F: VIC-TGTGGGTAAGTGCATGAGGG R: AGGGTTGGACATCGTTGAGC	$(GT)_{14}$	79–124	28	9	0.464 (0.776)
	12152[l]	F: VIC-ACAGTGTCTTGCTCTCCTTTATG R: ACACTCACTATTCACTTAGCTACC	$(GA)_{12}$	186–267	29	10	0.552 (0.804)
	33936[l]	F: NED-AGCTTCTAATCCAATCCATATCATTCC R: TCTTGGAGTTGGGATGACCG	$(GT)_{12}$	73–139	29	8	0.862 (0.802)
	37789[l]	F: 6-FAM-GACCCATTGTTGTGTGTTTGTG R: GAGTCTTGTAAGAGAGCCAAGC	$(GT)_{11}$	130–159	29	4	0.759 (0.644)
Cyprinodon tularosa	Ctul_02[m]	F: TCTCTACAATTACACAATTACAGTTTCGG R: AGCCTTGCATTTCCTGTTCC	AATAG	252–280	50	7	0.88 (0.789)
	Ctul_03[m]	F: CCCTCTTACTCCGATTCCC R: CCTCTAAACACCAGAATTTCCC	AATAG	250–285	50	8	0.72 (0.783)
	Ctul_05[m]	F: GCAATTTGCCTGTACAAGAGAGG R: TGTTAAGTTATCCTGCATTAAACCG	AAAG	195–418	50	27	1 (0.943)
	Ctul_06[m]	F: AAGTAAAGTCACATCATACTGGTGC R: AACCCAGACAGATTAAGTGGG	ATCT	217–253	50	10	0.354 (0.861)
	Ctul_09[m]	F: CTCTGTGAATGGTTGGATACG R:TTTACAGAGATACATGCCCAGG	ATGG	231–263	50	7	0.7 (0.754)
	Ctul_12[m]	F: AAGCAGGAGCTAGATTGCCG R: GAAGTCAATTGAAAGTCAGCATAAGG	AGTC	307–359	50	13	0.88 (0.844)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
	Ctul_15[m]	F: TCTAAATGTCCAATGCTGGC R: TTCATTTCTTTGTGTTCAGTTCC	AATC	190–215	50	8	0.58 (0.606)
	Ctul_16[m]	F: CACCTACCAGGTCTTACAATGGG R: GTTGGAGTATTCACGCTCCG	ATGG	264–333	50	15	0.84 (0.825)
	Ctul_20[m]	F: CCCAGTTGAGATGTTAGGACG R: GGTGAAGCATTGTTTACCTTCC	ATCT	141–238	50	16	0.96 (0.903)
	Ctul_21[m]	F: ACACATGTAAACACCCTGTGC R: TTTGCCCACAGTTACAAATACC	AATC	263–295	50	8	0.5 (0.616)
	Ctul_23[m]	F: TACGCTTGCGACTCAACCC R: GCCTCTTGAATATTGAATCTGTGC	ATGG	129–225	50	12	0.88 (0.819)
	Ctul_29[m]	F: AAACTTCAACAATATGAGTCTCTGTGG R: CAACTTAACCATCAATTTCAACGC	AACT	159–204	50	10	0.86 (0.784)
	Ctul_33[m]	F: TGTGTTTGTCTGTCTGTGTAAAGG R: GCTGACAACCTCGGATAACG	ATGG	196–235	50	10	0.8 (0.796)
	Ctul_34[m]	F: AAATACTGCACGTTAGCAGGG R: GTGTGCAAACAGGGACACG	AATC	341–369	50	8	0.88 (0.81)
	Ctul_38[m]	F: CACCTACTGATCCTTGTCTAGAACCC R: CCATTTAACACATAGCGCAAAGC	AATC	204–253	50	5	0.74 (0.745)
	Ctul_39[m]	F: GCTGTTGTGATGCACTGAGG R: AATGCCATCACATCAAATGC	ATCT	257–394	50	25	0.98 (0.942)
	Ctul_40[m]	F: TGTGGTGTGTTTCTAATGTAATTATACC R: CCCACTTGGGATAAGAGTAAAGG	ATGG	123–143	50	6	0.64 (0.739)
	Ctul_41[m]	F: TTCAAGACATGAAACAACAGGG R: CAGATTCAACAGCATTCATCCC	TCTG	146–163	50	5	0.54 (0.553)
	Ctul_42[m]	F: TCTAGCGTCAAATCATAGTTACTGC R: AGTTTAATTGTTATAGATACTTGGCCC	AAAG	190–217	50	8	0.84 (0.795)
	Ctul_45[m]	F: GGGATTTGTGTGAAATAATGTGC R: GGGAAAGAGAGAGTGACGGG	ATCT	400–464	50	15	0.92 (0.905)
Pinus yunnanensis	PyTr01[n]	F: GAACATTCCCAAGACAAATACCA R: CATTTAAAACAAACACCTCCTGC	GGA	108	24	1	0.000 (0.000)
	PyTr02[n]	F: ATGACTTCTCCAAATGCTCAGTC R: ACCTTCATCGACAGTGTTGTTCT	ATG	100–145	24	6	0.750 (0.688)
	PyTr03[n]	F: GCGTACTGTTGTCTGTTTTCCAC R: AAGTGTTCGTGCAGAGAGAAGAC	GCC	115	24	1	0.000 (0.000)
	PyTr04[n]	F: GGAACCATAAACAATCCAAACAA R: TATCATCTCACTACGAAGGGGTG	GGT	115–163	24	12	0.167 (0.662)
	PyTr05[n]	F: CTCAGATTTATGCCCAAGCTTCT R: ACCACGATACCACATTAATGACC	AGAT	124	24	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)
	PyTr06^{n}	F: ATGCTGGTGACATTAAATCCAAG R: ATCACAATATCTTCTGCTGCGTC	AAG	138–147	24	4	0.458 (0.647)
	PyTr07^{n}	F: ATGTTAGAGCAACACAGGAGAGC R: GAGCTGTTGACACCCATACTAGC	TGA	147–201	24	7	0.542 (0.678)
	PyTr08^{n}	F: CCAATGAATGTACTGCTAGGACC R: TGTAAGGTATGTCGAGGAGCATT	ATG	135	24	1	0.000 (0.000)
	PyTr09^{n}	F: AGAGAATTAGCCAGATGATGTGC R: CAGATTCCATCATAATAGCAGCC	GAG	153–162	24	4	0.208 (0.261)
	PyTr10^{n}	F: AATTCTCATTCTCTCCTGCAGAC R: AAACTGAGAAACTTCTGGAAGGC	GAA	152–161	24	4	0.125 (0.259)
	PyTr11^{n}	F: TGTAAGTTTGTCCAAGAACCTGC R: CAGTGAAGGCTCGTATAAAGGAC	TTAT	146	24	1	0.000 (0.000)
	PyTr12^{n}	F: GAGCTTCTATTTCCTTTATCGGC R: CTTGAAAGTTGAGGAGTCTTTGC	TTC	162–174	24	5	0.208 (0.355)
	PyTr13^{n}	F: TCATACAGTGGATGTTGGAGAAC R: AGCTAATAGCAGTGAGCTTCTGG	CTG	164–194	24	5	0.833 (0.592)
	PyTr14^{n}	F: CATCACTTGGGTATCTCTTTGGA R: TATCCCTTTATTGCCCTATCACC	ATAG	155	24	1	0.000 (0.000)
	PyTr15^{n}	F: TGAAAGCGAAGTAGCTTTGGTAA R: ACAAGAACCATGATAAATCGCTG	TCC	173–176	24	2	0.875 (0.492)
	PyTr16^{n}	F: AGGAGGAGGACGATGATGTG R: ATTGCCTAGTTCGTTCAATGC	GGA	160	24	1	0.000 (0.000)
	PyTr17^{n}	F: ACAGCAACATTTAAGTCAGCGTT R: TGGAGAGGATTGCTGAGATACTT	CAG	143–152	24	4	0.167 (0.157)
	PyTr18^{n}	F: GAATAGGTAAGGGAGTGAAAGGG R: AAATTACCAGCAAAACCCAAGTT	GAG	134	24	1	0.000 (0.000)
	PyTr19^{n}	F: GGGGTTATCAAAGAACGAGACTT R: CCAGAGGGGTATCCATAGGTAAG	GGA	158–167	24	3	0.333 (0.312)
	PyTr20^{n}	F: CATCTTCATCTTCATCATCATCCT R: AAAATGTGGCCACTGGTACTAAA	TCA	143–176	24	5	0.375 (0.326)
	PyTr21^{n}	F: CAAGCAGGAGAGTCAATCATTTC R: GTTGGAAGAATGGTTGCAGATT	TCA	107	24	1	0.000 (0.000)
	PyTr22^{n}	F: GGGGTTATCAAAGAACGAGACTT R: AACCAATGTGTAGCGAGTATGGT	GGA	156–186	24	10	0.792 (0.800)
	PyTr23^{n}	F: CTAAGTGTGGAAAGTTTGTTGGC R: CTCTTACAGGCTGTGGAACCTCT	TA	165–185	24	6	0.792 (0.731)
	PyTr24^{n}	F: CAAAACCCAACGAATTAAGACAG R: CTGGATTCATTTGTGGCTAAGAC	AT	140–156	24	6	0.458 (0.761)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	PyTr25[n]	F: GAGAATTTATTCAGTGCCCGTAA R: AAACAAGCCAAACAAAAATGGTA	TA	150	24	1	0.000 (0.000)
	PyTr26[n]	F: AAGAACTTGACATTTTGAACCCA R: ATATATCCCCACGGTTCTTTACC	TA	124–132	24	5	0.750 (0.577)
	PyTr27[n]	F: GCATTGTGAGGGGTTTCTTAAAT R: CAAGTCTTTTTACCGTGTAAGGTG	AT	125–147	24	11	0.250 (0.805)
	PyTr28[n]	F: AGAAAAGTTTTGGTTGTGACACG R: GTTGTATGTTTATGTGCAGCGTT	CA	156–162	24	4	0.542 (0.459)
	PyTr29[n]	F: CCTACACCAGCTCCATTTTATCT R: ATCAGATATGGAGTTGTAAGCCT	TA	158	24	1	0.000 (0.000)
	PyTr30[n]	F: GGAGAATTCAAACACGAGAAAGA R: GAGAGAATGAAGAAGTTCACCCA	GA	153–167	24	7	0.500 (0.796)
	PyTr31[n]	F: AAAAGCTCATCATGCATTCTTTC R: AGAACAGTCTGGACATCATGGTT	AT	126–134	24	5	0.625 (0.571)
	PyTr32[n]	F: CGATAGTTTAGTTTGGCTGAGGA R: AGGCCCTTTAATGCACTAGACAC	AT	160–168	24	5	0.875 (0.698)
FN							
Pinus yunnanensis	PyTr02[n]	F: ATGACTTCTCCAAATGCTCAGTC R: ACCTTCATCGACAGTGTTGTTCT	ATG	103–145	24	3	0.667 (0.611)
	PyTr04[n]	F: GGAACCATAAACAATCCAAACAA R: TATCATCTCACTACGAAGGGGTG	GGT	115–163	24	6	0.500 (0.694)
	PyTr06[n]	F: ATGCTGGTGACATTAAATCCAAG R: ATCACAATATCTTCTGCTGCGTC	AAG	141–147	24	3	0.333 (0.500)
	PyTr07[n]	F: ATGTTAGAGCAACACAGGAGAGC R: GAGCTGTTGACACCCATACTAGC	TGA	147–201	24	4	0.667 (0.722)
	PyTr09[n]	F: AGAGAATTAGCCAGATGATGTGC R: CAGATTCCATCATAATAGCAGCC	GAG	156–162	24	3	0.333 (0.292)
	PyTr10[n]	F: AATTCTCATTCTCTCCTGCAGAC R: AAACTGAGAAACTTCTGGAAGGC	GAA	152–158	24	2	0.167 (0.153)
	PyTr12[n]	F: GAGCTTCTATTTCCTTTATCGGC R: CTTGAAAGTTGAGGAGTCTTTGC	TTC	165–171	24	3	0.333 (0.403)
	PyTr13[n]	F: TCATACAGTGGATGTTGGAGAAC R: AGCTAATAGCAGTGAGCTTCTGG	CTG	170–173	24	2	0.833 (0.486)
	PyTr15[n]	F: TGAAAGCGAAGTAGCTTTGGTAA R: ACAAGAACCATGATAAATCGCTG	TCC	173–176	24	2	1.000 (0.500)
	PyTr17[n]	F: ACAGCAACATTTAAGTCAGCGTT R: TGGAGAGGATTGCTGAGATACTT	CAG	149	24	1	0.000 (0.000)
	PyTr19[n]	F: GGGGTTATCAAAGAACGAGACTT R: CCAGAGGGGTATCCATAGGTAAG	GGA	164–167	24	2	0.500 (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)
	PyTr20[n]	F: CATCTTCATCTTCATCATCATCCT R: AAAATGTGGCCACTGGTACTAAA	TCA	143–176	24	3	0.333 (0.292)
	PyTr22[n]	F: GGGGTTATCAAAGAACGAGACTT R: AACCAATGTGTAGCGAGTATGGT	GGA	156–186	24	8	1.000 (0.847)
	PyTr23[n]	F: CTAAGTGTGGAAAGTTTGTTGGC R: CTCTTACAGGCTGTGGAACCTCT	TA	177–185	24	4	0.833 (0.694)
	PyTr24[n]	F: CAAAACCCAACGAATTAAGACAG R: CTGGATTCATTTGTGGCTAAGAC	AT	140–144	24	3	0.333 (0.486)
	PyTr26[n]	F: AAGAACTTGACATTTTGAACCCA R: ATATATCCCCACGGTTCTTTACC	TA	126–128	24	2	0.833 (0.486)
	PyTr27[n]	F: GCATTGTGAGGGGTTTCTTAAAT R: CAAGTCTTTTTACCGTGTAAGGTG	AT	131–145	24	6	0.167 (0.792)
	PyTr28[n]	F: AGAAAAGTTTTGGTTGTGACACG R: GTTGTATGTTTATGTGCAGCGTT	CA	158–160	24	2	0.500 (0.375)
	PyTr30[n]	F: GGAGAATTCAAACACGAGAAAGA R: GAGAGAATGAAGAAGTTCACCCA	GA	153–163	24	4	0.500 (0.583)
	PyTr31[n]	F: AAAAGCTCATCATGCATTCTTTC R: AGAACAGTCTGGACATCATGGTT	AT	126–128	24	2	0.833 (0.486)
	PyTr32[n]	F: CGATAGTTTAGTTTGGCTGAGGA R: AGGCCCTTTAATGCACTAGACAC	AT	160–166	24	4	1.000 (0.722)
	Mean					3.3	0.556 (0.500)
KM							
Pinus yunnanensis	PyTr02[n]	F: ATGACTTCTCCAAATGCTCAGTC R: ACCTTCATCGACAGTGTTGTTCT	ATG	103–145	24	3	0.500 (0.486)
	PyTr04[n]	F: GGAACCATAAACAATCCAAACAA R: TATCATCTCACTACGAAGGGGTG	GGT	118–163	24	3	0.000 (0.500)
	PyTr06[n]	F: ATGCTGGTGACATTAAATCCAAG R: ATCACAATATCTTCTGCTGCGTC	AAG	138–147	24	4	0.500 (0.708)
	PyTr07[n]	F: ATGTTAGAGCAACACAGGAGAGC R: GAGCTGTTGACACCCATACTAGC	TGA	147–171	24	4	0.667 (0.583)
	PyTr09[n]	F: AGAGAATTAGCCAGATGATGTGC R: CAGATTCCATCATAATAGCAGCC	GAG	156–162	24	3	0.167 (0.292)
	PyTr10[n]	F: AATTCTCATTCTCTCCTGCAGAC R: AAACTGAGAAACTTCTGGAAGGC	GAA	158–161	24	2	0.167 (0.153)
	PyTr12[n]	F: GAGCTTCTATTTCCTTTATCGGC R: CTTGAAAGTTGAGGAGTCTTTGC	TTC	162–174	24	4	0.333 (0.417)
	PyTr13[n]	F: TCATACAGTGGATGTTGGAGAAC R: AGCTAATAGCAGTGAGCTTCTGG	CTG	170–194	24	3	0.667 (0.486)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (*N*)	Number of alleles (N_A)	H_o (H_e)
	PyTr15^{n}	F: TGAAAGCGAAGTAGCTTTGGTAA R: ACAAGAACCATGATAAATCGCTG	TCC	173–176	24	2	1.000 (0.500)
	PyTr17^{n}	F: ACAGCAACATTTAAGTCAGCGTT R: TGGAGAGGATTGCTGAGATACTT	CAG	149–152	24	2	0.167 (0.153)
	PyTr19^{n}	F: GGGGTTATCAAAGAACGAGACTT R: CCAGAGGGGTATCCATAGGTAAG	GGA	158–167	24	3	0.500 (0.486)
	PyTr20^{n}	F: CATCTTCATCTTCATCATCATCCT R: AAAATGTGGCCACTGGTACTAAA	TCA	170–176	24	3	0.833 (0.569)
	PyTr22^{n}	F: GGGGTTATCAAAGAACGAGACTT R: AACCAATGTGTAGCGAGTATGGT	GGA	156–183	24	7	0.833 (0.806)
	PyTr23^{n}	F: CTAAGTGTGGAAAGTTTGTTGGC R: CTCTTACAGGCTGTGGAACCTCT	TA	165–185	24	6	0.667 (0.750)
	PyTr24^{n}	F: CAAAACCCAACGAATTAAGACAG R: CTGGATTCATTTGTGGCTAAGAC	AT	142–156	24	4	0.333 (0.597)
	PyTr26^{n}	F: AAGAACTTGACATTTTGAACCCA R: ATATATCCCCACGGTTCTTTACC	TA	126–130	24	3	1.000 (0.569)
	PyTr27^{n}	F: GCATTGTGAGGGGTTTCTTAAAT R: CAAGTCTTTTTACCGTGTAAGGTG	AT	125–147	24	8	0.333 (0.861)
	PyTr28^{n}	F: AGAAAAGTTTTGGTTGTGACACG R: GTTGTATGTTTATGTGCAGCGTT	CA	158–162	24	3	0.667 (0.486)
	PyTr30^{n}	F: GGAGAATTCAAACACGAGAAAGA R: GAGAGAATGAAGAAGTTCACCCA	GA	159–165	24	4	0.500 (0.722)
	PyTr31^{n}	F: AAAAGCTCATCATGCATTCTTTC R: AGAACAGTCTGGACATCATGGTT	AT	126–128	24	2	0.500 (0.375)
	PyTr32^{n}	F: CGATAGTTTAGTTTGGCTGAGGA R: AGGCCCTTTAATGCACTAGACAC	AT	160–166	24	4	0.833 (0.653)
	Mean				24	3.7	0.532 (0.531)
LG							
Pinus yunnanensis	PyTr02^{n}	F: ATGACTTCTCCAAATGCTCAGTC R: ACCTTCATCGACAGTGTTGTTCT	ATG	100–145	24	5	0.833 (0.736)
	PyTr04^{n}	F: GGAACCATAAACAATCCAAACAA R: TATCATCTCACTACGAAGGGGTG	GGT	136–160	24	4	0.167 (0.597)
	PyTr06^{n}	F: ATGCTGGTGACATTAAATCCAAG R: ATCACAATATCTTCTGCTGCGTC	AAG	141–147	24	3	0.333 (0.625)
	PyTr07^{n}	F: ATGTTAGAGCAACACAGGAGAGC R: GAGCTGTTGACACCCATACTAGC	TGA	147–201	24	5	0.667 (0.778)
	PyTr09^{n}	F: AGAGAATTAGCCAGATGATGTGC R: CAGATTCCATCATAATAGCAGCC	GAG	153–159	24	3	0.167 (0.292)
	PyTr10^{n}	F: AATTCTCATTCTCTCCTGCAGAC R: AAACTGAGAAACTTCTGGAAGGC	GAA	155–158	24	2	0.167 (0.486)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	PyTr12^{n}	F: GAGCTTCTATTTCCTTTATCGGC R: CTTGAAAGTTGAGGAGTCTTTGC	TTC	162–168	24	3	0.167 (0.486)
	PyTr13^{n}	F: TCATACAGTGGATGTTGGAGAAC R: AGCTAATAGCAGTGAGCTTCTGG	CTG	167–173	24	3	1.000 (0.569)
	PyTr15^{n}	F: TGAAAGCGAAGTAGCTTTGGTAA R: ACAAGAACCATGATAAATCGCTG	TCC	173–176	24	2	0.833 (0.486)
	PyTr17^{n}	F: ACAGCAACATTTAAGTCAGCGTT R: TGGAGAGGATTGCTGAGATACTT	CAG	143–149	24	2	0.167 (0.153)
	PyTr19^{n}	F: GGGGTTATCAAAGAACGAGACTT R: CCAGAGGGGTATCCATAGGTAAG	GGA	164–167	24	2	0.333 (0.278)
	PyTr20^{n}	F: CATCTTCATCTTCATCATCATCCT R: AAAATGTGGCCACTGGTACTAAA	TCA	170	24	1	0.000 (0.000)
	PyTr22^{n}	F: GGGGTTATCAAAGAACGAGACTT R: AACCAATGTGTAGCGAGTATGGT	GGA	156–180	24	6	1.000 (0.806)
	PyTr23^{n}	F: CTAAGTGTGGAAAGTTTGTTGGC R: CTCTTACAGGCTGTGGAACCTCT	TA	177–183	24	4	0.667 (0.653)
	PyTr24^{n}	F: CAAAACCCAACGAATTAAGACAG R: CTGGATTCATTTGTGGCTAAGAC	AT	142–156	24	4	0.500 (0.708)
	PyTr26^{n}	F: AAGAACTTGACATTTTGAACCCA R: ATATATCCCCACGGTTCTTTACC	TA	126–132	24	3	0.500 (0.569)
	PyTr27^{n}	F: GCATTGTGAGGGGTTTCTTAAAT R: CAAGTCTTTTTACCGTGTAAGGTG	AT	129–141	24	3	0.167 (0.292)
	PyTr28^{n}	F: AGAAAAGTTTTGGTTGTGACACG R: GTTGTATGTTTATGTGCAGCGTT	CA	156–162	24	4	0.500 (0.514)
	PyTr30^{n}	F: GGAGAATTCAAACACGAGAAAGA R: GAGAGAATGAAGAAGTTCACCCA	GA	157–167	24	6	0.500 (0.806)
	PyTr31^{n}	F: AAAAGCTCATCATGCATTCTTTC R: AGAACAGTCTGGACATCATGGTT	AT	126–128	24	2	0.333 (0.278)
	PyTr32^{n}	F: CGATAGTTTAGTTTGGCTGAGGA R: AGGCCCTTTAATGCACTAGACAC	AT	160–164	24	3	0.833 (0.625)
	Mean				24	3.3	0.468 (0.511)
YJ							
Pinus yunnanensis	PyTr02^{n}	F: ATGACTTCTCCAAATGCTCAGTC R: ACCTTCATCGACAGTGTTGTTCT	ATG	103–145	24	4	1.000 (0.694)
	PyTr04^{n}	F: GGAACCATAAACAATCCAAACAA R: TATCATCTCACTACGAAGGGGTG	GGT	133–154	24	4	0.000 (0.667)
	PyTr06^{n}	F: ATGCTGGTGACATTAAATCCAAG R: ATCACAATATCTTCTGCTGCGTC	AAG	141–144	24	2	0.667 (0.500)
	PyTr07^{n}	F: ATGTTAGAGCAACACAGGAGAGC R: GAGCTGTTGACACCCATACTAGC	TGA	147–159	24	2	0.167 (0.153)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	PyTr09[n]	F: AGAGAATTAGCCAGATGATGTGC R: CAGATTCCATCATAATAGCAGCC	GAG	156–159	24	2	0.167 (0.153)
	PyTr10[n]	F: AATTCTCATTCTCTCCTGCAGAC R: AAACTGAGAAACTTCTGGAAGGC	GAA	158	24	1	0.000 (0.000)
	PyTr12[n]	F: GAGCTTCTATTTCCTTTATCGGC R: CTTGAAAGTTGAGGAGTCTTTGC	TTC	168	24	1	0.000 (0.000)
	PyTr13[n]	F: TCATACAGTGGATGTTGGAGAAC R: AGCTAATAGCAGTGAGCTTCTGG	CTG	164–173	24	4	0.833 (0.597)
	PyTr15[n]	F: TGAAAGCGAAGTAGCTTTGGTAA R: ACAAGAACCATGATAAATCGCTG	TCC	173–176	24	2	0.667 (0.444)
	PyTr17[n]	F: ACAGCAACATTTAAGTCAGCGTT R: TGGAGAGGATTGCTGAGATACTT	CAG	143–149	24	3	0.333 (0.292)
	PyTr19[n]	F: GGGGTTATCAAAGAACGAGACTT R: CCAGAGGGGTATCCATAGGTAAG	GGA	167	24	1	0.000 (0.000)
	PyTr20[n]	F: CATCTTCATCTTCATCATCATCCT R: AAAATGTGGCCACTGGTACTAAA	TCA	167–176	24	3	0.333 (0.292)
	PyTr22[n]	F: GGGGTTATCAAAGAACGAGACTT R: AACCAATGTGTAGCGAGTATGGT	GGA	159–168	24	3	0.333 (0.292)
	PyTr23[n]	F: CTAAGTGTGGAAAGTTTGTTGGC R: CTCTTACAGGCTGTGGAACCTCT	TA	179–185	24	4	1.000 (0.708)
	PyTr24[n]	F: CAAAACCCAACGAATTAAGACAG R: CTGGATTCATTTGTGGCTAAGAC	AT	144–156	24	4	0.667 (0.681)
	PyTr26[n]	F: AAGAACTTGACATTTTGAACCCA R: ATATATCCCCACGGTTCTTTACC	TA	124–128	24	3	0.667 (0.611)
	PyTr27[n]	F: GCATTGTGAGGGGTTTCTTAAAT R: CAAGTCTTTTTACCGTGTAAGGTG	AT	131–143	24	3	0.333 (0.500)
	PyTr28[n]	F: AGAAAAGTTTTGGTTGTGACACG R: GTTGTATGTTTATGTGCAGCGTT	CA	158–162	24	3	0.500 (0.403)
	PyTr30[n]	F: GGAGAATTCAAACACGAGAAAGA R: GAGAGAATGAAGAAGTTCACCCA	GA	157–165	24	5	0.500 (0.792)
	PyTr31[n]	F: AAAAGCTCATCATGCATTCTTTC R: AGAACAGTCTGGACATCATGGTT	AT	126–134	24	5	0.833 (0.750)
	PyTr32[n]	F: CGATAGTTTAGTTTGGCTGAGGA R: AGGCCCTTTAATGCACTAGACAC	AT	160–168	24	5	0.833 (0.667)
	Mean				24	3.0	0.468 (0.438)
Acrossocheilus wenchowensis	Awc 002[o]	F: TGTTATGTTCAGTGACTCCTC R: GTGTTCTACGGCTATGTCTC	$(CT)_{12}$	161–179	32	7	0.469 (0.731)
	Awc 004[o]	F: TCCTTCTCTTCCTCTACTACT R: CCTGGAGATACTGAACAACA	$(TC)_5$	180–200	32	3	0.094 (0.417)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	Awc 005^{o}	F: CTGTTGTAAGGTTGCTGTAG R: GACTGATAGACTGATAGACTGA	$(GT)_5…(TC)_6$	334–366	32	14	0.719 (0.908)
	Awc 009^{o}	F: CTTCCCTATTACTTCCCTACTA R: GAGAAAGAAGCAAGGACAAA	$(CTTC)_6$	302–330	32	2	0.219 (0.246)
	Awc 010^{o}	F: CTCCTTTCTCTCTTTCTCTCT R: TCAGACACAGTTCAGATACA	$(TC)5G(CT)_5$	292–368	32	10	0.813 (0.842)
	Awc 011^{o}	F: ACAAACCAAACCAATGAAGG R: TTACTGACGAGATGCTCATG	$(AAGA)_{10}$	342–344	32	2	0.000 (0.062)
	Awc 014^{*,o}	F: GCCTAGTATGTGTATGTATGTG R: TCAGAGGTCAGATGCAATAG	$(AG)_6$	361–441	32	15	0.423 (0.836)
	Awc 017^{o}	F: CATGACAGATAACAGGTGAT R: GATACAATAACGGACAGACA	$(GT)_{11}$	151–193	32	10	0.719 (0.663)
	Awc 019^{o}	F: CAACCAACAAACACAATACC R: TTACTGACGAGATGCTCATG	$(AAGA)_6$	114–144	32	14	0.875 (0.920)
	Awc 041^{*,o}	F: CACACTCCAAACATACTCAA R: AGAATCAGAATCCGTTTGAG	$(AACA)_5$	195–263	32	14	0.321 (0.843)
	Awc 042^{o}	F: AGCAGGTATCTAGTGTTACG R: GTGATGATGATTCAGCCTAAG	$(TC)_{21}$	309–337	32	5	0.469 (0.542)
	Awc 043a	F: TGTTGCTGACTTGTATGGAA R: TGCTGATGTGATCTGATGAG	$(GT)_{11}(AT)_2(TG)_5$	145–175	32	15	0.844 (0.902)
	Awc 043b^{*,o}	F: ATGCTCTCCATCATCACATT R: AGAGGACACAGAAACAGAAT	$(TC)_{23}$	173–209	32	17	0.469 (0.904)
	Awc 046^{o}	F: TCTCTTGTTCTTCTCTGTCT R: AGATACTGATGGAGGAAGTG	$(TC)_5$	111–139	32	13	0.906 (0.895)
	Awc 051^{*,o}	F: CAGAATGAATGAAGGAGACA R: CATGACAGATAACAGGTGAT	$(CA)_{17}$	172–200	32	7	0.469 (0.801)
	Awc 059^{o}	F: CCAAAGACACAACCACAAAG R: TTTACATTCTCTCAGCCTGT	$(AG)6AA(AG)_7$	92–128	32	17	0.839 (0.891)
	Awc 063^{o}	F: CTCTTCTGTCTTCACCTCTC R: AGTCAATGGATCTCTCTGTAG	$(TC)_7$	400–404	32	3	0.438 (0.469)
	Awc 069^{o}	F: TAATCCAGTAAGGCACCAGA R: CTCAACAGAGACAATACATCAG	$(AG)_9$	354–360	32	4	0.281 (0.307)
	Awc 070^{*,o}	F: TCTTTCTGCTGTGTTTCTTC R: ATCCCTCTTTGTGACTTTCT	$(AC)10T(CA)_{17}$	129–203	32	25	0.594 (0.954)
	Awc 071^{*,o}	F: GGTGCTTCATTACTCCTCTC R: GGTAAGACAGATGAGTGGAA	$(TC)_{14}$	281–311	32	12	0.719 (0.865)
	Awc 080^{o}	F: AGAACAAGAGACAGCAATCA R: GTCAGTAGTATCCACTCACAT	$(TG)_{21}$	309–351	32	18	0.719 (0.928)
	Awc 085^{o}	F: CAGATTGAATTTAGCGACAC R: ACACAATAATCCGACAGAGA	$(TC)_7$	274–278	32	3	0.214 (0.356)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pyrus betulaefolia Bunge	XL9^{P}	F: AAACTTGCATCCTCTAAATTGCTT R: GCTGGTATGAGCTAGGGTCG	AT	96–124	8	3	0.375 (0.633)
	XL10^{P}	F: CTGCTGGCATGAAATTCAAA R: TGCGCTCGTTAGACCATTT	AT	97–101	8	3	0.500 (0.648)
	XL21^{P}	F: CACCCAACCATAAAGCCTG R: CGCGTAATGACGTGACAGAT	AG	95–99	8	3	0.625 (0.625)
	XL22^{P}	F: CAGCTGCATGGGATAGAATG R: GTGACATTCAATGAGCCGAA	AG	98–102	8	3	0.500 (0.648)
	XL25^{P}	F: CAGTAGCTTGTGCGTGCTGT R: AATCGCTGCAGTGACACATC	AC	107–127	8	9	0.750 (0.844)
	XL31^{P}	F: CAACTTTCCAAATCCAAGGG R: GCGAGGGAGGAGATCAGAG	AG	90–108	8	3	0.625 (0.617)
	XL34^{P}	F: AGGGTAGCCAGAGTAGGCG R: TCTTACAAATGTTGTGCTTAGCC	AT	88–106	8	3	0.375 (0.586)
	XL65^{P}	F: TTGAAACTTGGATCTGGATGA R: TCGATGTCATACAACATGGATT	AC	106–110	8	3	0.125 (0.570)
	XL66^{P}	F: GGTCCAAAGAAGGAGAGGA R: CAGGGAGCAAGATAGATCCAA	AG	94–130	8	7	0.625 (0.805)
	XL68^{P}	F: AAAGTTCAAATGCTCCTCCG R: AGAGGACGATCACCAGCTTC	AG	109–127	8	8	0.750 (0.836)
	XL70^{P}	F: AATTTAGCAGTTTCGCTCATATTT R: GAAAGGCTTGAAACCGCC	AG	122–130	8	4	0.375 (0.711)
	XL71^{P}	F: CAGCTGAGATTATAGAACTGGTTACTT R: CCCACTATCTTCCTAGAAGCACC	AG	108–112	8	4	0.750 (0.664)
	XL105^{P}	F: CACCACTGAGCTTCCTCTCC R: AAGCACCAGAACAATGGAGG	AG	110–144	8	5	0.625 (0.766)
	XL106^{P}	F: TTCATTCTAACTCTGCCTTGAA R: GCTGTAGTTTCATACAGTTTCACTTG	AG	114–118	8	3	0.625 (0.664)
	XL114^{P}	F: CCAGGGCTATGAGTGTTCC R: TTCTCAACAGCCAAGCACTACT	AG	106–132	8	11	0.750 (0.875)
	XL118^{P}	F: CAAGCGCCCTAGATATTAGTTT R: ACTCCGATCCTTCTTCCCTT	AT	98–100	8	2	0.375 (0.492)
	XL122^{P}	F: GGAGTGCCAATAACTCTTCCC R: TAACTGTCTGTTTGAAGCAAACTT	AG	89–129	8	6	0.500 (0.797)
	XL124^{P}	F: CTTCTTAAGGTGATGCTCCAAA R: TGAAATAATCACTTGACATTTCCTTT	AT	121–125	8	3	0.625 (0.664)
	XL126^{P}	F: CTCCCGTAAGTATGGCTGGT R: TCGAATTATCGATGGTCGGT	AT	87–91	8	3	0.500 (0.625)
	XL130^{P}	F: CCGGACAAGGATATTTCCAG R: GCGGCTACTATCTCTGAGGC	AG	87–91	8	3	0.500 (0.633)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
	XL135[p]	F: ATTAGCCATTGACGGGATTC R: CAGTATCTCTTGGAGAAGAATTATTTG	AT	88–94	8	3	0.000 (0.594)
	XL138[p]	F: AAATCAATGACCCATGATGTGA R: AGAATCCTCTCTGGATCATTTCC	AG	88–120	8	5	0.625 (0.773)
	XL139[p]	F: TTAATCGTTGTTTATCTACTGTCGAG R: TGCATGCTTAAGATACCAACTAAA	AT	116–120	8	3	0.500 (0.586)
	XL141[p]	F: ATGTGGCTATCCGACAGTGC R: AACTTTGTAATTGAAACTGTTCATTCT	AT	89–93	8	3	0.500 (0.648)
	XL143[p]	F: AGAACTTACGCAATCTTGATGTT R: TTTCGCAATCACATATTGCAC	AC	114–118	8	3	0.750 (0.625)

[a] X. Wu, M. Wu, X. Su, Y. Zhou, Y. Pan (ESM 1)

[b] A. Oleksa, K. Meyza, L. Cizek, L. Drag (ESM 2)

[c] H. Sungani, M.J. Genner (ESM 3)

[d] V. Noguerales, C. Cáliz-Campal, P.J. Cordero, J. Ortego (ESM 4)

[e] L. Lieber, D.A. Dawson, G.J. Horsburgh, L.R. Noble, C.S. Jones (ESM 5)

[f] C. Chen, Q. Li, H. Yu, L. Kong (ESM 6)

[g] R.K. Basiita, K.R. Zenger, D.B. Jones, D.R. Jerry (ESM 7)

[h] P. Gélin, C. Rougeux, V. Mehn, M.M.M. Guillaume, J.H. Bruggemann, H. Magalon (ESM 8)

[i] G. Zhang, J. Chen, S. Yin, P. Tao, R. Wang, X. Wang, Y. Ding, X. Wang (ESM 9)

[j] L. Liu, T. Yanagimoto, C.H. Li, N. Song, T.X. Gao (ESM 10)

[k] Y. Sato, H. Ito, M. Onuma, T. Maeda, R. Ogden, M. Inoue-Murayama (ESM 11)

[l] M. Ruhsam, A.S. Wulff, B. Fogliani, P.M. Hollingsworth (ESM 12)

[m] R.M. Martin, M.L. Robinson, W.D. Wilson (ESM 13)

[n] N. Cai, Y. Xu, Y. Xu, D. Wang, B. Tian, C. He, A. Duan (ESM 14)

[o] Y.Y. Jia, S.L. Liu, X.L. Li, Z.M. Gu, J.L. Zhao, W.P. Jiang, Q.P. Lian, J.L. Guo (ESM 15)

[p] J. Tian, B. Zeng, M. Liu, S. Luo, X. Li, J. Li (ESM 16)

[1] Microsatellite loci sequenced using Sanger from enriched individual BSUK05_17

[2] Microsatellite loci sequenced using MiSeq from enriched individual BSUK05_17

[3] Same microsatellite locus isolated from two separate Illumina paired-end libraries: the repeat enriched BSUK05_17 and unenriched BSUK05_35

[4] Cmax15 was homologous to *Isurus oxyrinchus* (shortfin mako shark), microsatellite CA1XD

[5] Corresponding to Acr1-60 (Tang et al. 2010), mentioned because the product size is different for designing new panels

N sample size; N_A number of alleles; H_O, observed heterozygosity; H_E, expected heterozygosity

* Significant deviation from Hardy -Weinberg equilibrium (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0021$)

[†] indicates locus may harbor null alleles (null allele frequency > 5%);

[#] high frequency of null alleles (19.5%), ×failed amplification