

Table S2 Primers sequences of of 151 EST-SSR markers for *P. chinensis*

Marker ID	Foward primer	Reverse primer	Repeat motif	Allele size(bp)	Amplified primer
PcSSR1	AGGCTTCAAAATCTTCCAATTC	GGATAAAATATGTGGGCTTGGTT	AAAAAT(4)	156	Yes
PcSSR2	GAAACACATCACAAATTTCTGGGT	TGTTGTAGGATTGCGTTATTGTG	AAAAT(4)	150	Yes
PcSSR3	TCCTGCATTTTCTTTCATTTC	GAAGAAGATACCCATCAACAAACA	AAAGA(4)	159	Yes
PcSSR4	AATGGAAAGAACAAAAGCAATGA	CCAACATCCTAATCTTCCAGAAA	AAAT(5)	143	Yes
PcSSR5	AAGTTGATGAGCTCACCCATAGA	AAGATATGGAGGTTGTGTCCAGA	AAC(6)	132	Yes
PcSSR6	AAACAAATCATCAAAACACACCC	GGCTATCAAAACTTAGCACATCA	AAG(12)	131	Yes
PcSSR7	CGAAAAGTCGTTTGATCCATAAG	TGTCATCTCCAGATTTTGTCTTC	AAG(6)	139	Yes
PcSSR8	CAGCGTTGAACTAACAAAATAA	CCTCTCTTCATACTCTTCTTCCG	AAG(7)	153	Yes
PcSSR9	AAGTAGGAGGGTCAAGAAAAGC	TTTAATCCTCCCAACCTTTCAT	AAGG(6)	131	No
PcSSR10	TTTCAAAGAGGATGAATGGTTTG	TTTGAATCTTGATGCCTCACAG	AAT(6)	149	Yes
PcSSR11	TTGCTTTAGTTTCAAGGACCAA	AAACTTACATCAGTCAGCAAGCC	AAT(7)	136	Yes
PcSSR12	AGAGCAATGCGCTCTAATAACAC	GTCGAGATGGGTGATTTCTATTG	AATC(5)	144	Yes
PcSSR13	TCAGTTCATAACATTCTGTCTCTTG	CCAAGACTGATAGCAGAATAAGGA	AC(8)	158	Yes
PcSSR14	GATTTGATCTCAGGAATCTCCTCT	AGCAAAGAGGACATGAAAACCTGA	ACA(6)	157	Yes
PcSSR15	CTTGGCCTAGACAATGATTCTGA	GTCTCTCTGCCTCCACCTCTAC	ACC(6)	137	Yes
PcSSR16	CACACTCTCCACTGACAAAAC	GGACCATGTGGTTAGGGATT	ACC(8)	135	Yes
PcSSR17	CAACCAAACTCGATCGTTTC	CACCTGAGGCTCACATGTCTT	ACTGCC(4)	141	Yes
PcSSR18	ACACAGACACAAACCCTTGAAAT	ATTAGTGAGGCCAAACAGAGACA	AG(11)	135	Yes
PcSSR19	AGCAAATAAGAGAAACAGGAGCC	TGACTTCTCTCTTTCCCTAACC	AG(12)	159	Yes
PcSSR20	TCTTCATGTCAATACAAAACGGA	CAGAGGCACCAGAATCTCTTTTA	AG(14)	143	Yes
PcSSR21	TTGGAGATATTGTGAGGTCTGC	CACTCATTCCAACAACAGAGACA	AG(8)	159	Yes
PcSSR22	GGAGGTAAAGTTGAAGCCAGAAC	TGCTACAAGAACAAGGTCCTCTC	AG(8)	158	Yes
PcSSR23	CATTACGTTCTGTCCCTGACTC	CATATTAAATCCGTACAACCCCA	AG(8)	153	Yes
PcSSR24	ATGCAGCAACTGGAGATGATAAG	CGTTTCATTGCCTTCAAACTAA	AG(9)	159	Yes
PcSSR25	ATGCAGATTGTTTGGTGTTCCTT	ATATTATGGAGAAGCAGATGGCA	AG(9)	151	Yes
PcSSR26	GAAGAAGAGGAGGAAGAATTTGG	TACATTCTCACACGGGAACTTTT	AGA(6)	152	Yes
PcSSR27	GAAGGTCAAGGACAAGATCCAT	GATACGGATGTTAATCGCTGTC	AGA(6)	141	Yes
PcSSR28	TGGTAGAGAGGGTTGAGAGTGA	TCAAATGCTCCTTACCGTACCTA	AGA(8)	144	Yes
PcSSR29	CGTTCCTGTTCTAAGGACTTCAA	AAGAACTCACAGCAACCACAAC	AGAAAG(4)	151	Yes
PcSSR30	AATTTTGAAATTCGTTCTGTTG	GCAAAAATCCTAATTTTCGTTTTC	AGAAGG(4)	151	Yes
PcSSR31	ATGCGAAAAGTGTGTTAGCTTTTC	CCAATCTTTACTACCCACTCCCT	AGG(6)	158	Yes
PcSSR32	GGCAAAATTGGGTAGTGAAATTA	AGTTGTAAGTGAAGAAACCTCG	AGT(9)	148	Yes
PcSSR33	ATCACTATCGTCCAGCCAAGATA	TCAAGAGTAACCAAGGTAGGCAG	AT(10)	135	No
PcSSR34	CAGATGAAACAAAAATTCACACG	GCTCAGATGAAACAAAAATTCACA	AT(11)	145	No
PcSSR35	AACAACTGTCCCATCAATCAGT	GTTTCCTTGCTAACCAGCATTTA	AT(13)	137	Yes
PcSSR36	TTGCCTGTTAAATGTTGAAGGAC	ATGCAAGAAGAAGCACACCTAGT	AT(8)	145	Yes
PcSSR37	CCATCTAAAACCATTAAGGTCCC	TTACAGCTTCCATCTTTTTCAGC	AT(8)	84	No

PcSSR38	TTCCGAAATTAAGTTGCTTCTCA	AGATTGAACGAAGTGTGACTGGT	AT(8)	145	Yes
PcSSR39	TTATGATTGCATGACATTCTTGG	ATTCATGAGCAATCACCACCTTTT	AT(9)	143	Yes
PcSSR40	TAATAGGCCGAGAGGTTGATCTT	AAGAGTTGGGTGAAGTTTTAGGC	AT(9)	118	Yes
PcSSR41	TGGATGACTACAAAGTTTCAGCA	CATGTGTTCCAGGTGATGAGATA	ATAA(5)	131	Yes
PcSSR42	GCCCTAGCTGACTCTACCAAATC	TTTGATAGGGAGGCAAACAAATA	ATC(6)	135	Yes
PcSSR43	AAAGCAATGAAGCAGAGTTCATC	CTGAGAATGATTGGGGTTTTTC	ATC(8)	124	Yes
PcSSR44	TCTACTGAGGTTGGGAATCAGAC	TTGCAACAAATATTACTCCGCT	ATG(6)	130	Yes
PcSSR45	ACAACAACTTCAAATGTCGATGA	AAGAACAGAGGATATCCCATTGA	ATGGGA(4)	148	Yes
PcSSR46	ATTGAAAACCTCAAATTGTCCCAA	ATTGGACTTGATGGTTGCACTAC	ATT(6)	143	Yes
PcSSR47	GACTTTATTGAGCCCCTTCAAAT	GGGATCTATGTCATATTCATCTCTCA	ATTT(5)	139	Yes
PcSSR48	GCCATTTAACCCAAAGGAGTAAG	AGGCTAAGCGGAATTAGGTTTTA	CA(19)	152	Yes
PcSSR49	AAGAACATCTACAAGAGGGGGTC	CTAGTCTCTGTGGAGGGCCTAT	CA(8)	154	Yes
PcSSR50	AAACCTGAAGGTGTGTTGAAGAA	TGAAGAACAAAAAGACAAAGTTGA	CAAA(5)	143	Yes
PcSSR51	CACCACACATCCTGAATAACCAT	GTA TAGCACTGATCAAGGTGGC	CAC(6)	154	Yes
PcSSR52	TCACCTCCACCAACAACACTAC	CATTGATGATGACCACGTATCAG	CAC(8)	151	Yes
PcSSR53	GGCTCAAACCTCAGTCACACCTAC	ATTGTGACATAGCAGAGACAGCA	CAG(7)	158	Yes
PcSSR54	AAAACCACCTAACATTTACCAA	TATGTGAAGAAGATGACGAGCAA	CAT(6)	118	Yes
PcSSR55	TTCCCCTTCACTTTCTCACATAA	AGCGTCATTTGGAAGAATCAAT	CATTCT(4)	145	Yes
PcSSR56	TTATCCTCTGAATCACCAGAAC	CAGTCTGTAGAGGGTATGCTTCG	CCA(7)	138	Yes
PcSSR57	GAATGGTAAGAGTAGTGATGGCG	TATCCTGGTAAAACCGATGAACA	CCAGCT(4)	153	Yes
PcSSR58	GTAGTTGCAATTTCCCCTTCTTG	ATACAAAAGAAAGCAATGGCGTA	CCT(6)	155	Yes
PcSSR59	ACCCGTTTACCCTAATACAGCTC	ACTTGTGTCTCTCTTCAGAAACG	CCTTCT(4)	158	Yes
PcSSR60	TTCAAACCCAGATAGCGAACTTA	AAGGAAGTCTCCACCGTATTCTC	CGGTGG(4)	136	Yes
PcSSR61	TAGAAACAGTCCACCTCGAAAAA	CAGCAGGAGTTGGATTTGTAGTT	CT(11)	146	Yes
PcSSR62	ACATTCTCAGTTTCCCAACAGAA	CATAGAAAACACCGTCATCATCA	CT(13)	113	Yes
PcSSR63	CTCACACCAAACAGTCCCTAAAC	GATATTGCGGGAGAGTAGATGG	CT(8)	160	Yes
PcSSR64	TCACTACCTTGGTTCAGTCCATT	CGTTCAACGAGCTGAGTTACAG	CT(9)	138	Yes
PcSSR65	TCAAACCTCTTCTTCTTCCTTC	TCAGATTCTCTCTTGGGTTTGTT	CTC(7)	145	Yes
PcSSR66	AAAATCCAATGGAGAATACCCAG	CTGTTGAAGGAGATGGTGAAAAG	CTG(6)	113	Yes
PcSSR67	TGCTTCTAGGGCATGTTCTTTAG	AATTCAATATGGAGTTGGAGTGC	CTT(6)	149	Yes
PcSSR68	CTGCAGGTTATTGCATTAGGTTT	GAGTTATTTGAGCATGTGGTTCC	CTT(6)	155	Yes
PcSSR69	AGATCTTCTGTGTGAACCCCTG	TAAACGAGGCTTCTTCTTCTCC	CTT(7)	142	Yes
PcSSR70	GCTCTTTATCATCAATCTAGGGC	AACAGGCTTTATTGTTGGTGTTG	CTT(8)	128	Yes
PcSSR71	AGCTCCCCCTAATCTAGCTTTCT	GTTGTGTGTTTTTGTCCCTCTT	GA(10)	121	Yes
PcSSR72	GCTCTTTCAACTGTGCATTCTTT	TCCAGGTTCTCTCTTTTATCCC	GA(12)	151	Yes
PcSSR73	AGCTAGCAAATGAGACACCTGAC	TCTCTCACTTTTGCTCTTGCTCT	GA(8)	119	Yes
PcSSR74	ATGTGAAGGGGAGAAAGAAAAAG	ATTCAATTGTAGGCTTGGGAAAT	GA(8)	122	Yes
PcSSR75	AATAAGCAGAGCGGGAATAAAAG	TTTGCTCATGTACTTCTCTCTTTG	GA(9)	114	Yes
PcSSR76	GCTCAGAACTTTAACCAACCAGA	ACTTTTCTTTTTCACTTGGGC	GAA(6)	142	Yes
PcSSR77	AGAAAGAATCAAATCTGGCACTG	CATCTTCTTCTTGATGTTCCG	GAA(6)	155	Yes
PcSSR78	TCAAAGTCGTAAAATGAAAGGGA	ATCTTCCAACCCCTTACACACT	GAA(7)	113	Yes

PcSSR79	AAGACATGATTTCATTGCTGGAGT	GATGAACTGAAAACAGCAACACC	GAA(8)	153	Yes
PcSSR80	TGATTGATGTTGTAAGCTATTTGG	TGGCCAGAAAACAAAAAGTAAGA	GAAA(5)	120	Yes
PcSSR81	TGGGAACGTTAAGGAGATACAAA	GGAGATAAGGAAAGGTAGAGCGA	GAAGAT(4)	146	Yes
PcSSR82	GACTTAGAGTTTGCGTTCAAGA	ACTCTCCTCTTCCACTTCCACTT	GAG(7)	150	Yes
PcSSR83	AAAAGAAAGGAGGGAGGGACTAA	CCCGCTCTCTGATTTTATTCTTC	GAT(7)	141	Yes
PcSSR84	GGGACGGAATCAGATAACTCTT	TGAGGTTCCACTACTCTTGAGAGA	GAT(8)	145	Yes
PcSSR85	AAAAAGAAATCAGCTCCGAAATC	ACCTTTGAATCTAATCACGACGA	GATCT(4)	105	Yes
PcSSR86	CTGAACTAACTGCACATCCACA	GTGAATGAATCATCAAACAGCAA	GCA(8)	100	Yes
PcSSR87	CATCCTGTAAATTTATGCTGCTTG	TGAATATAGCCATTTTCTTTTAGC	GCTAA(4)	160	Yes
PcSSR88	GGAAAGGAATATAAGGGAAAGGA	AGAAGGTGACTGGAATCTTCACC	GGAAAG(5)	152	Yes
PcSSR89	GTGGGATTGAACCTGACTTTGTA	GTCCTCCCAATTCTTCTACTGCT	GGAGGT(4)	150	Yes
PcSSR90	GAGGAGCTAAAAGAAGAAGGGTG	CTTCAAGTTAATAGAGCCCCTGC	GGGAAG(4)	156	Yes
PcSSR91	TTGATTGATTCACAGGAAAAGGT	GAGGAGAGTCATGTGGTATGTCC	GGT(6)	144	Yes
PcSSR92	ATTGTTTGAATAAGGTGGAGGTG	GTAAGGTGGAATCTTTAAAGCCG	GGTGA(4)	155	Yes
PcSSR93	TTCTTGAAGGAGCTCCAGAAGTT	CTCCACAACATCCTCCTCATC	GTG(6)	131	Yes
PcSSR94	TTCATCTGACAGAAAACCCAAAT	TTCATCCCAGTCTATACCCGATA	GTG(6)	158	Yes
PcSSR95	TCAAAATTCAGGTTCACTCCACT	CAAACACCTTCATCACACTACCA	GTT(7)	149	Yes
PcSSR96	TTTTCATGGATTGATGTGAACTG	ACCGTCAATCACAATCTTGTTTC	GTTTA(4)	156	Yes
PcSSR97	GATGCCATGAACTTCCACTCTTA	TGTTACATGCGAGAGAAACTGAA	T(31)	157	Yes
PcSSR98	TGTAACCTGTCTCAAGGGTGCTT	CATAGTGGTCTACTGGGTCACA	TA(10)	121	Yes
PcSSR99	TGCTGATTCTTTACTGTCCATGA	AACATTTCTGTGACAAATGGACT	TA(11)	148	Yes
PcSSR100	TCACAAAAGAAAAAGAAAAACGC	TCACAAAAGAAAAAGAAAAACGC	TA(12)	148	No
PcSSR101	GAATACGAGATTGGCATCACACT	CCTTGAGTCAAAAGGCTGTAAAGA	TA(8)	142	No
PcSSR102	AAACAGACCCCATTTTCTTTCTT	CTTGGTCATGTAGGGTTAGCAAG	TA(8)	152	Yes
PcSSR103	GTAAAAATCCATAACCATTTGCCA	AACATTTGTCTAGAAGCATTTTCC	TA(8)	157	Yes
PcSSR104	CACAAATAAACGAGCTTTACGGA	CACTCTGCCGTTGATAAAGTTTC	TA(9)	133	No
PcSSR105	CAGATCACATTACCCAGATCACA	TAGTGAATCAATGAACTGGGGC	TA(9)	142	No
PcSSR106	TTCCATTGATGTACCCATGAACT	TTTTTGACATCACAAGTACTCG	TAA(6)	160	Yes
PcSSR107	TGAAAAGAGGAATAAGAGTAATGCAA	TGAAGACAAGAAGAGGAGAGGTG	TAAA(5)	154	No
PcSSR108	CTCGGTTTCTTCTCTGGATTTTT	GGAGCTTCGTAAAAACAAGGATTT	TAG(7)	126	No
PcSSR109	GGCTTTATCCATTTGTCTCCATT	TTGCTTGTTTACGTGTTCAATTG	TAT(6)	111	Yes
PcSSR110	CTCTTACATCCATCATCCTCCTG	GAAATGGAGATGGCATTTGATTA	TATT(5)	145	Yes
PcSSR111	GACTTCGAATTAGAGCCAATCAA	GATTAGATGGCAACACAGAGAGA	TC(10)	94	Yes
PcSSR112	TCCAATCCCAGTCTTCTAGACCT	ACTGATGCCTAAAGGAGCACATA	TC(10)	157	Yes
PcSSR113	TTCCCCCTATAACATTTCAAACA	AACATCAAACGAAAGAGCAGAAA	TC(12)	120	Yes
PcSSR114	GTCCTTTTCTCATTTATGGGATT	CTCAGAAGCGATTCTACGTCTA	TC(17)	140	Yes
PcSSR115	ACCATGAGAACGAAAACCTAAT	CCATATTATCCAACCAGAAAATGA	TC(8)	145	Yes
PcSSR116	CAAAGAAGCCAACAAAGAAGGTA	AAACAAAAGAAAAACGGAAAAAGA	TC(8)	102	Yes
PcSSR117	TCAATTCAAATTGGTCTCTGCTT	TATGGAGGTATGGTATGGTGTCC	TC(9)	147	No

PcSSR118	TATTGGTTTCAAAATCACAAGGC	CGTCTTTCCTGTCAATGATTCT	TCA(7)	142	Yes
PcSSR119	TCTCAACAGAAACACCATGTCAG	AGAAGACTTTTGGGTTTGGTAGC	TCACAA(4)	150	Yes
PcSSR120	CAACATCAAGCTCATTCTCCTCT	GCTGTTCTTGATCTTCATTGCT	TCC(6)	158	Yes
PcSSR121	GACCATCATAAGAACCCTGAACA	CGGATTGGATTCTGAGAGTAATG	TCCCTA(4)	152	Yes
PcSSR122	TCCTCATCTGAAGCTCCTAACAC	CACAAAACCACACATCATAATCG	TCT(6)	156	Yes
PcSSR123	GCATTGCAAACCATTAAGAT	AGGTGAATGCTGAAGACAGAGAA	TCT(6)	123	Yes
PcSSR124	ATCAAATACCCTTTCAAGCCTTC	ACTGGATCAGGTGATGGAGTAGA	TCT(7)	113	Yes
PcSSR125	TTGCGCAAACATAAAGCTC	TCTGAGAGGTAGATTCTGCATGG	TCT(8)	122	Yes
PcSSR126	ACCCCAATTAATCAGATCAC	ATGGAATGTTTGATTTGCCTAA	TCTGAC(4)	159	Yes
PcSSR127	AATTCAATGATGTTGAAAGGAA	TGATATCACTAAATCAAACCCAAAA	TG(10)	106	Yes
PcSSR128	AAAGCTAAATCCTTCAATGCCTC	AATTTCAAATGGGCAAATTCTTT	TG(8)	158	Yes
PcSSR129	CCGTAATCCGAGAAGGTAAAAAT	CCCATCTACATGTTCAACACAGA	TG(9)	150	Yes
PcSSR130	GGATCTGCGTTCAAGAAACATAC	CATGGCAGACTGTACTCTTGATG	TGA(7)	151	Yes
PcSSR131	CAACACAATCTTCCCTTCATTTT	AGAGTGTTTGTGTTTGTGCTTCA	TGA(9)	160	Yes
PcSSR132	TTCTCTCTTCTGCTTCTTCTT	TCTCAGTTCTTGAAAAATGGCTC	TGC(6)	132	Yes
PcSSR133	AGCAGGGAGATGGTAGGAGTAGT	CTAACAACAGCGCCAATCTTATC	TGG(6)	160	Yes
PcSSR134	TTGATTCCATTTCTCCACTTTGT	AAAGGTCGAATTCTGATTGATT	TGG(7)	148	Yes
PcSSR135	CTTCTTGCATCTAGCACCAAGTT	TCAAAAAATAGAAACAGACGACAGG	TGGATC(4)	100	Yes
PcSSR136	TTGTTTTCTCCGAAGTGGTTAAA	AAACAACAAATAAAACAAAGAAGCG	TGT(7)	137	Yes
PcSSR137	GTTTTTCTTTCTTCTTGATGC	TAAGGGTTCGTTTCATTTGTGTTT	TTA(6)	157	Yes
PcSSR138	ATGGACATTCAAATCGCATAGAC	ATCGTTGCTCTACGATCTCTACG	TTC(11)	120	No
PcSSR139	TCCAGAGAAAAATGGGATGATTA	AACGCAAGTCAAAGTGCTAAAAG	TTC(6)	138	Yes
PcSSR140	AGTCTACCATTCGAATCCCGAGT	AATCCTCACACTGCAGCAGATAG	TTC(6)	141	Yes
PcSSR141	AACCAACTAAATGCACTCCAAAA	TATCGTCTTCCAGCTCAAACTC	TTC(6)	114	Yes
PcSSR142	AATTGACTCCACCAAGTTTGAA	AGGAGCAAAATTAAGGAGGAGAA	TTC(6)	158	Yes
PcSSR143	CCACCTGCCATCTGTAACTTTT	CTTCAACAAGAGGTTGAACGTAGG	TTC(8)	159	Yes
PcSSR144	ATCACACAAGAGGGAGTGAATGT	TCCAATGGCTTAATAGGAACAAA	TTCT(5)	136	Yes
PcSSR145	CAGTGGAAGTGTTCAGAGTTT	GAGAACTACAATGTTTTCGGAC	TTG(6)	160	Yes
PcSSR146	CTCTAGAGTTCGGAACAGCGTC	GATTCCATGAGGAAGAGTGTGAG	TTG(7)	160	Yes
PcSSR147	TGAAGACAAGAAGAGGAGAGGTG	TGAAAAGAGGAATAAGAGTAATGCAA	TTTA(5)	154	No
PcSSR148	TGACCTCGTTATGACAAAATTCA	TGAAGTAGTTTCTTATTCGCCCC	TTTA(6)	148	Yes
PcSSR149	AGGCTTAACCCACTTCTGTCTT	ACCTTGTTTGAGCAGGTTTACA	TTTC(5)	160	Yes
PcSSR150	AACACTCCAACCGCAGATATTTA	CCAGCAACTTTGCATAGAGATTA	TTTCTC(4)	158	Yes
PcSSR151	GGGTTTTCATGTTAATCATTTT	CCCTTCTCTCTTCAGAACCCTA	TTTTTC(4)	136	Yes