Supplement.1. Characteristics of 149 SSR loci and their primers

Marker name	**Forward primer（5'-3'）**	**Reverse primer（5'-3'）**	***Size (bp)***	***Tm*(°C)**	**Available primers**	**Polymorphic primers**
Cr0	TCTCTATTTATTCCTTGCTTCTCTCT	GTTGGGACTGGGAGGAATGG	221	59	+	++
Cr1	TCGCCGTATCTCGCTTCTTC	GACCACCAACCTCCTCATCG	276	60		
Cr2	GGAGGGCATCGATACAAGCA	TCCAATGGCATCGTCATCGT	208	60	+	++
Cr3	TGGATGCGCCTATTTTGATCG	CAAGCTGAAACATGTAGCGGT	252	59	+	++
Cr4	TTTCCTCCGATCTGGTTGCC	GACGCCAAACCGGAATTCAC	197	60	+	++
Cr5	CCATCCACCACAGTCACCTC	CGCCTTAGTAAGAGAGCGCA	244	60	+	++
Cr6	CCTCGGCAGCAAGAGGTAAT	AAATCCTGCAGCAGCTGACT	200	60	+	
Cr7	GAGGAGAGGGATTGGGGACT	ATTTCGTCGCTTTCCCTCCC	137	60	+	++
Cr9	TGGGCTTCTCATCTCTGCTG	CCTAGCAGCAGCAGCACTAA	265	60	+	++
Cr10	GGTTCTCATTTTCGCGCACA	AATAGCCTTTCGCCAGGGAC	265	60	+	
Cr11	CTCACACTGTGCACAACTGC	CCCCTCCCATTGCCACAATA	159	60	+	++
Cr12	GGAGAGCTTGTGCCATGACT	TGGACGGGAGAGAACACAGA	157	60	+	
Cr13	GAGGCTGAATCCCACACGAA	TTCTTTTCCGACAGGCGACA	161	60	+	
Cr14	CGAGGCAAGCTCACCTTCTA	TCGGTTGCTCTCTGATCAGC	231	60	+	
Cr19	ATCTCCCTTGGATCCGTGGA	CCTCTCCAGTTGCAGTCCAG	259	60	+	
Cr20	TCCAACCTCATAGACTCCTCTCT	GAGGCGGGGAAGAAGAAGAC	187	60	+	++
Cr21	AGGGAGTTGAGGCTGGTACT	GCTCCTCCTTCCCTCCCTAA	148	60	+	++
Cr22	TCTTTGTTGTGTCCCCGACC	AAGGAAGCGCATGTCCATGA	262	60	+	++
Cr23	AGCCACACGAAAGATCATACA	AGCCCTCAACCTGTCCATTG	190	59	+	++
Cr25	ATTGCAATTAGCCACAGCGC	AGGGCTCACAAGAGGAGCTA	275	60	+	++
Cr26	GTACACATCCACCGCCAGAA	GCCTTATCCTCCAGCTTGCT	268	60	+	++
Cr27	AGAGACAGAGAGGCCGACAT	ACTTCCGGGTCGCAAAGTAG	259	60		
Cr28	GGAGGAGGAAGCTTCTCCCT	TGAGCCGGATAAGCTTGCAA	258	60	+	++
Cr29	TGTACAGAAGGAGCTCTCTGC	ATTGCCCCCATATGTGCCAC	241	60	+	
Cr30	ACGCACCCGATATTCATCCC	CTCCCTCCGTCTGAAAACCC	249	60	+	
Cr31	CCCTGTCGCCTCCCTCTTT	TGGGGGTGAAATCACTACGC	260	61	+	++
Cr32	GCTCCCCACGAAAAACACAA	CGATCAAACCTTGAAAACCCGT	264	59	+	++
Cr33	GGTGTTCTCTGGAGGCCTTC	TGGTGCCATTGTGTGTAGCA	258	60	+	++
Cr38	GCGACCTTGCATCAATTGGG	GAACAAATGCCCGACTGCTG	220	60	+	
Cr39	TCAGAAGCGGCAGTCTCAAG	TCCACAGAGCTAGCAAAAGGT	219	60	+	
Cr40	TGACTTGTGGGCTTGTTGGA	AGTTTGGATCTTCCCCGCTT	255	60	+	++

Cr41	ACATCATGTTTTCTATTTTTGAAAGCA	TCCAACTAAAATAGGTTTTGATTCAGA	265	57	+	
Cr43	TGGTACCCACAAACCCATCAG	CTTATACGCAGCCACGTCGA	232	60	+	++
Cr44	ATGGCGAAGATGTAGGTGGC	TCCCCTTCTCCCCATCTCTG	213	60	+	++
Cr45	TGGTTGGCAGACCTGTTGTT	GCAATGCCTACAAATTCTCTAATGC	120	60	+	++
Cr46	ATTAGCGGGCCCACATTTCA	ACCTCCATTAGCTACCACCTCT	261	60	+	++
Cr49	ACTCCCATTCAAGGTATTACATCTG	AAGCTGCTAGCCTGCTAGTG	225	59	+	
Cr50	TGCAACCTCAGATCAGTCGG	TGTTGCTTCTTTGAACACGTCT	278	59	+	
Cr51	GCCCATTTCGGATAGCAGTG	ACCTAGTTCCCTCGTCCTACA	280	59	+	
Cr54	GGGGAGATTTCGGGGATGTC	CCTCTCACGACTTCACAGGG	199	60	+	
Cr55	GAAAGTGGGCTCGGTTCGTA	CACAAAACGGAACTGAGCGT	191	60	+	
Cr56	CTCTTGACCCGTGGTGGAAA	CCCCACCAATCATTTCCCCA	189	60	+	
Cr57	GGCAGGAAAGGCAGGTAGAG	TTTCCTCTCTGTTGCAGCGA	221	60	+	
Cr58	TCTGTGATCTCTCTTGATCTGCA	CCAAGTACGAGGGAATTTGAGA	216	58	+	
Cr59	GCAAGCGATCGAAGTCGTTC	TCTTTCGCCTTCCCCAACAA	116	60	+	++
Cr60	TGCCCATATCAAAGGGGTTCC	ACATGCTCTAATGCAACCTGC	186	60	+	
Cr61	TCAAAATCGCGCACAAACGT	AGCATTCAACAGGGGTAGGC	209	60	+	++
Cr62	TTGAGCAGGCAGTGTGAACT	CCGACTAATGCCGGCTCATT	273	60	+	++
Cr63	GGCGGGACCTTATCTGACAC	GTATGAGGAAGAGGCGTCGG	175	60	+	++
Cr64	CCACAGATGAGACACATATCTGC	CAGCCTAACTTCTCTTCCGGT	245	59	+	
Cr65	TGGCCAGGAACATCGACAAT	ACATTTCACGTCACTAATTCACACA	253	60	+	
Cr66	CGACTCGACTACGACAAAATGG	GAGGAACCCTAGATGCTGCC	210	60	+	++
Cr67	GCAAGCAGAAGCAGAAGCAG	ACCTTGGGAAGTTGGAACCA	267	60	+	++
Cr69	GCCCGTGCTCATCCAGAATA	AGGCGGGGCATAACATACAC	255	60	+	
Cr70	CGGATTCACAGCCAAGAGGT	AGAACAACATGATTCTACATAGGGA	277	59	+	
Cr72	TGATCATGTCAGTTTGTACGTCA	TGGTGATGCAGTCATACGCC	236	59	+	++
Cr73	CTCCTGGCTCTTGTGAAGCA	TGAATTCATTCGCCCCTCCA	190	60	+	++
Cr74	AGCGGTTCAACAAGCAGACT	TCACAGACCTCCTGCACTTTC	272	60	+	
Cr75	TCGGATTGTTGTTTAGCTTGAGA	GCCTGGGTTCTGATTGGACA	196	59	+	++
Cr76	GCAAGGTGTAACAGCGCAAT	TCAGCAATAGGTGTCCTGTCA	260	59	+	++
Cr77	GGGGGCAAACCAACAAAACA	GCTGAGGTGGGAGAAGGAAC	198	60	+	
Cr78	ACCAGGAAATCTTTGTACCAGGA	GTGGTCTTTTTGTTGTTGGAACA	280	59	+	
Cr79	AGAGTGCTGGAGAGTGGAGT	ATTGGGTTGTATCCGCAGCA	203	60	+	++
Cr80	ATCGAAGACGGCCACTTCAG	AGCATGAAGAACTCGACCACA	236	60	+	++
Cr81	GAGCACCCTCTTTTTCTCAACA	CGAGACACAGAAATGATATTGAAATTT	262	58	+	++

Cr82	AGGCCGCAAAATCTTGGAGT	TGTGGTATCTTTTGTGGAGCA	280	59	+	
Cr83	CTGCCAAGTTAGGTGGGGAC	CACACACCAAACATCGTGCA	156	60	+	
Cr84	TGGGATCTTGATAATACGAAGCA	TGCTATGCTTAGTGTGTGATTCG	168	58	+	
Cr85	AGCTGTAACACAACACATGAAC	ATCGCCAGACAAGCTAGCAG	198	59	+	
Cr86	AACATATTAAACGAAATCCATGCTTC	ATCTGCCATTTGCTGGGACA	233	59	+	
Cr87	TTCCTGCCATTGAGCAAGGT	TGGTATCAGAGCGATCGAGT	156	59	+	
Cr88	CGCTTTGTTGTCACCTTTGGT	CCCACACGCACAAATAAGCC	212	60	+	
Cr90	ACCTGAGATGTCATTGGCAAGA	AGATGCTGAAAAACATGGGTATACC	278	60	+	
Cr92	GGGAGGGGTACTTCTACTGGT	ATCCAGAGCACTCCAACTGC	278	60	+	++
Cr93	TGAAGGCAACCAGTTCAGGC	TGGTCACAGATTACAAGTACCACT	262	60	+	
Cr94	TCCATATCTGTCCTACCTTCCTCA	ACACAGAAAGAAAGGAGGGGG	237	60	+	++
Cr95	ACGGAATTGGATCGGCAAAA	ATCACCTAAACCAAATTAATCACAATG	156	58	+	++
Cr96	AGCAGACAAAAGGGGAAGCA	TGACTGCAGTGTGTTACTCAACT	210	60	+	++
Cr97	TCCTCTGTGGTCAGTATCTGGT	GTGGCCGGGATTTGGAAGTA	247	60	+	
Cr98	TGTTGGTCACGGGGAAGAAG	TTGCGGCCTTTGTTCTCTCT	232	60	+	
Cr99	ACCCAAATTCAGCTGTGCAA	AGAAGAAACTGCGAAGGTTCCT	214	59	+	
Cr100	GCCCTCAGATGAGCCATCTC	GCCATGTGAGGTCACTTGCT	228	60	+	
Cr101	CCCTGCTAGCCTGGAGAAAC	GCACTCCTCATCTCGTACCC	275	60	+	
Cr102	AACCAGGCAGTGAATACCGG	TGACATTTTGAGCAGCGTGC	241	60	+	
Cr103	TAGGATGCATGGGGTGGTTG	ACATATCCCCTTGATCTTCCACA	150	59	+	
Cr104	ACTGAGCGGCTTATTGGAGG	TTCAAGCAAGCACAGGGTGA	224	60	+	
Cr105	ATCAGGCGTTAGTTGGTGCA	CACCGTGTGGATGGGACTAG	133	60	+	++
Cr107	TCTCAGTCTTCACCCCCAGA	TCTCAGCCCACCACCTATGA	165	60	+	++
Cr108	TGCTAGGCATAGTACAATAGACTCAC	GCCTCAACAAGTTAGTGGGC	118	60	+	
Cr110	GCTTCGATGGTGACCTGGAA	AGCTTCTGAGAGCTGCTCTT	271	59	+	
Cr111	CTGCCATGGATGACCTGCAT	CAGAAGTCTCAGGTTGCCCA	241	60	+	++
Cr112	ACCAAAGTAGCCCATCGGAC	TCCCTCCCCCGTATAGCTTC	168	60	+	
Cr116	ACCAGTGGCATATGCAAAAGC	AGTCACCCCAAATAGGACCA	221	59	+	
Cr117	CCAACAAATGCGACTGGACC	GCACAGAGCAAACAAGCACT	168	60	+	++
Cr118	CAGGAGCCGCACCATTAAGA	AGCTCTGCTCAGCCCAATTT	206	60	+	++
Cr119	AAGGTGGCAACTAGGGATGC	TGCCTCAATTACTCACTCCACC	147	60	+	++
Cr121	AGTACCCCTCCGCTCTTTCT	CACGTCCGAACTCTGTGACA	256	60	+	++
Cr122	GAACCTGCACCTGGTAAGCT	ACAATGCAACATGAACCCGC	224	60	+	
Cr123	CTGTTGATGAGGTCTGGCGT	CTGTTGCTGCTGTGGTTGAC	137	60	+	

Cr124	ATGACGAGGACAGTGATGGC	CCGTATCGGCTACACCTACC	260	60	+	++
Cr128	GGACACACGCACCCACATAT	ACCCATTGGTGCTAAGTCCAG	160	60	+	
Cr129	ACGCGTGGAGACTAGAGAGA	ACCATTTCCATCTCTTCTCTTTCT	221	59	+	
Cr130	TAGAGAGGTGTGGCAGCAGT	ATAAAACCCTGCCCAACCCC	208	60	+	++
Cr131	GCACCACTGTTGTTGGACAC	TGCGGTTTTTACCTCCCTCC	210	60	+	
Cr132	AGAGAGAACGCCCACTTTCG	TAAACCCAAACCCCAGCCTC	120	60	+	++
Cr133	GAGAGAGAAAGGTTGGGTGGA	ACCAGAGGCTCTTCTCCCTC	180	60	+	++
Cr134	GCGCGATTCTAAACTCCCCA	ACAGTAGAGAGGCGACCCTT	158	60	+	++
Cr135	GTCCCCAACCCAACTATTACCT	CTCAGTCCCAAGAACGACCA	240	59	+	
Cr136	TCTCTCCTCTTCCTCCACGG	TGCTGCTACTCCTTACTCCT	204	59		
Cr137	CCGTTCAAAGTTCACCGAGC	GAGCAAATTCGGGCATTCGG	243	60		
Cr138	GGAGCCAGAGACATGATCCG	GTTGTGACTCGGCTTCTCCA	280	60		
Cr139	AGGTTTCCTTTTTCTCTCCTCCT	CGCACAGAGCCATCACACTA	172	60		
Cr140	ACCTAGGGTTGCTTCTTGGC	TCCAGAGACTGCGCCATTTT	142	60	+	
Cr141	ACTCTTCATTTCCATCAACCCAGT	GGGGGTAAGAGAGGGATGGT	199	60		
Cr142	ACCTCAAACAACACAACGCT	TGACAACAGACCGACACGAA	225	59	+	++
Cr143	ACACAGCACAACAGAACACAC	CAAGGCGGTAAGGTCACTGT	223	60	+	
Cr144	TCACTCTGGCACACCTCCTT	CCCAATGCTGGTCTGGTCAT	220	60	+	++
Cr145	GAAAACCCTCTGCCCTCTCC	AGGATGAGAGTCGTGGTCGA	233	60		
Cr146	ACTGGATGTTCTGCCCACTG	TGTTCTAAGCAACCTGAGCA	245	59	+	++
Cr147	GCTCAGGCCAATATCTAATTTGAGG	GTTGCCAAGTACCGGAGTGA	156	60	+	++
Cr148	AGAACAACCGAACCAACCGA	AGAGAGAGGAGATGGGGCTG	236	60	+	++
Cr149	TCATTCCCCTTTTCGCCCTT	CGTTTCTTCGGCCACCAGAT	271	60	+	
Cr150	AAAACCTAACCTTCGCAGCG	AGGTAGCATGTGAAACGCCA	260	60	+	++
Cr151	AAAACAACGGGCCATGAAGC	TCACGAATCCCAGCCACTTC	276	60	+	++
Cr152	CCGCACTATCGCTCTTTCCT	GTTTTGTTGCCAACTTGCGC	231	60	+	
Cr153	AGATGGCAAGACACGCTCAA	GAACCGACCTAGGGTGAAGC	187	60	+	++
Cr154	GCTTGCCCCTACCTGAAGTT	TGTCGTTCTTCTGAGCCAGC	117	60		
Cr155	AAAACCCTAGCACGCCCTAC	CAACTGCAACCTGTCCGTTG	169	60		
Cr156	AAGCCCAGGCACTCAATCTC	GTTGGCGCAGATTGAGCAAT	210	60	+	
Cr157	AGCTAACTCGGAGGGAACAA	AAAACCCACAGCAAGACCCA	259	59	+	++
Cr158	ACCCCACCAAGGACTAGGTT	GCAGAGGCTTCATTAACCGC	277	60	+	
Cr159	CGGAAGTTCGCAAGCAAACA	GGATGTATGGTGGCGGTGAT	140	60		
Cr160	CCCACTTGAAACCCACTCCA	AAGAAGGGGAACGAGGAGGA	140	60	+	

Cr161	ACGATCCTCCTCCAGGGTAC	CAACAGAGAGCAGCCAGACA	271	60		
Cr162	GTCGACCTCCCAACTGAACC	GCGCTGCCATCCTTTTACCT	166	61	+	
Cr163	CCCAAATTTGCAAGTAGCTGCA	AGCAAAGAAAGCTGCAGCAC	266	60	+	++
Cr164	ACTATTGGGTAGCCAGGGGT	AGGAACACAGGGAAAAGACTT	250	59		
Cr165	GGTGGAGATCAGGTCGGTTC	CCATGCTGCAGCGAAAACAT	274	60		
Cr166	AAGGAGATGGCAAGGAAGGC	ACAAAAACCAACCTCTTTTAGCA	269	59	+	
Cr167	GTGCATCTAAACCCTCCTCGT	GCCATGAAAACTAAGTACATGTGAGT	150	60	+	
Cr168	ACCATCCGATGCGTCTTTGT	GAGCGGTACTCTCATCGGTG	280	60	+	
Cr169	CCCTGTCCATGGATGACACC	GTCCGACCATACACCATCTCC	203	60	+	++
Cr170	AAAGCAAGGCAAGAGGGAGG	TCTCTCCTTCTCCCTTCTGTT	148	59	+	
Cr171	GCTGCGTTGATCCTCTCCTT	AGCACATTGAACCCATCTAGCT	276	60		
Cr172	CTACCACCATCTCACCTCGC	ACTCAAATTTGGGCCTCCCT	205	60		
Cr173	CCTTGAAGAGAGAGAGGGGC	TGCTCAAGCCATGGTATGCA	271	60	+	
Cr174	AGAAACAATTGTGTGCGCGC	GGAACCCGACTTCTCACACC	186	61		
Cr175	GGAGACATGGGAATGGGCAA	GCACCTTCACCTCAACTCCA	245	60	+	
Cr176	ACTGAGGATGCTTGCTTGGG	ACCAAACCACCATGTGCAGA	132	60		
Cr177	TTATGGCCTTGCGCACCTAA	TCCAACCCAATCCAATCAGCA	256	60	+	
Cr178	ATAGAATGCACGCGGAACCA	GCATGAACAACAGCTACATCCA	241	60	+	++
Cr179	TTCAACCGTGTTGCCACCTA	GCAGTCCCAATCGCTAGTGT	262	60	+	
Cr180	GAGGAGGGAGGGGAGAAGAG	CCCTTCTTCCCCATCCAACC	194	60	+	
Cr181	ACCTGATAAGCGGAAGTGGC	ATTTCCACCACACCTGCCTT	280	60	+	
Cr182	ATAGGCGCTTGCTGTTCCTT	CCGGACTCTTTGCCTTCCTC	229	60	+	
Cr183	CTCAACTGAGCCGTTCATGT	GGGAATTAAAAATTGTCATTGGTGAGC	271	59		
Cr184	GCAGCACTCAACACAACTGG	GGGCCTACGATTCAGAGGTG	244	60	+	++
Cr185	CGGATTGGTCCAGTAGGTCG	CCAACTGGTTTCTGTTTTCCCT	277	59	+	++
Cr186	ATTGCAATTGCTCATGCCCC	CCAGAGCGCTACTGGCTTAG	255	60	+	
Cr187	GCAGACTTTGTTTGCGAACA	TGCTCCCAATGCACTGTTTT	163	58	+	++
Cr188	TCTTGGGTTTTGTTCCAGAGCT	GGATCCACTCCGTTCACAGG	264	60		
Cr189	TGAAGCGTGACGTACCAGTC	GGCACTTGCTGGTTCTGTTG	271	60	+	++
Cr190	ACAGCAACAACAACCAAGCC	TGGGACTAAAGGCTTGGTGG	145	60	+	++
Cr192	TGCAAAGATCATGTTGAGCAAT	TGCTTCCTCCTTTGACTTACCT	226	58	+	