

Table 2 Validation and characterization of polymorphic SSR markers derived EST sequences

EST ID in Genbank	Code	Forward primer (5'-3')	Reverse Primer (5'-3')	Repeat	Expected Size of Allele (bp)	Allele Size Range (bp)	No. of Alleles	<i>He</i>	PIC
EG662973	RC02	CCTCCATTGGTTTCTCCATTTA	TGATTCGAGATCAGAGTTGACG	(GT) ₉	269	256-271	4	0.354	0.386
EG686206	RC03	TGATGCTAATGGCCTACTCAGA	TAATAGCACCACCATCAACTGC	(AT) ₈	264	260-268	3	0.226	0.212
EG682908	RC04	TGAAAGCCACACAATAGTCCTG	TGAGATTCACTTGTGGAGGTG	(CT) ₈	190	186-190	2	0.278	0.239
EE255832	RC05	CATCACCTCTATCCATCCGTTT	CCTTCATCAITGAACCTCCCTTC	(AC) ₈	200	200-227	4	0.709	0.658
EG663122	RC07	GGAAGAAGAGAAACAGCAAGGA	GTGGAGAGCCTCGACTAAGAAG	(GA) ₉	241	234-247	6	0.695	0.658
EG686478	RC09	GTCCAGGTTACCATCTTGATT	ACCACCGTAGAAAGTAGCATGG	(CT) ₉	280	280-288	3	0.226	0.212
EG678906	RC10	CAGAAGAGCTCATGTGTTGTGG	AGTCTTGTGATCCTCACACTGC	(CA) ₉	241	235-243	3	0.156	0.151
GE634375	RC11	TAGAAAGAAAGCGACCCCTTCTG	AAGAAGGAGGAGGAGGAGAAA	(TA) ₁₀	242	238-268	4	0.581	0.539
T14845	RC12	ACATTATAGCGAGTGTGCTTGC	TGGACTTCTCAAAGCTGCATTA	(AC) ₁₁	232	232-262	6	0.764	0.729
EG666688	RC14	TTCTGATGACATCCAGAAAC	AGATATCTGGGGAGACGAAGC	(TA) ₁₃	224	214-227	4	0.489	0.429
EE259292	RC16	CATGAACCCACAAATTTACAGA	GACAGACCCATCTCAAGATTCC	(AC) ₁₅	254	242-252	4	0.325	0.305
EG674726	RC17	CCTCCCAAATCATAGTCCATTG	GATCAAGGTGATTAGGGACCAA	(AT) ₁₆	255	249-261	4	0.503	0.456
EG670576	RC19	TCGTCTCCCTGCTTTTATTTA	GCACCAAATCTTTTAGGCAAG	(AT) ₁₈	192	278-296	6	0.521	0.490
EE259262	RC20	CGTTTAAGGATCCGCATATCTC	GCTCAACCACCTCAAGATTTTC	(AG) ₂₀	244	254-260	2	0.375	0.305
EE256592	RC22	ATGAAGTTCAGCGTAACCATT	ATCTGAAACCATGGGTCATCTC	(AT) ₂₂	254	272-294	4	0.573	0.483
EG662293	RC23	GCCGTCTATTCTCTCCTTCT	TTTCTACATCGGCAGTGAAAGA	(TC) ₂₂	208	249-255	3	0.288	0.264
EE255894	RC24	GAGAGCGTGGCTTCTCTACTTC	CAGTTTCACACCAAGCTGGTAA	(AT) ₂₃	233	259-273	3	0.594	0.523
GE633816	RC25	ACCCCTGCAAAACCCTAATAAT	TTGGGTGTAAAGAATCCGACTT	(CT) ₂₃	259	259-265	3	0.642	0.570
EG664176	RC26	CACCTTCTCTGATGCTCTCCT	AGGGGTGAAGGATTTGTTTAT	(AT) ₂₇	197	191-215	5	0.361	0.346
EG684662	RC27	AGATCTGGAGGCTGTTGTCAT	CTGCTTCAGGATCTCGAAAAGT	(AT) ₂₈	243	143-257	2	0.444	0.346
EE260610	RC28	CCCAAGTCCAGATCTCTCTAA	CAGAAGAAGCAGTAGCAGCAA	(AT) ₂₉	233	223-237	3	0.663	0.589

EE257519	RC29	ACGAGGCTCAGACTTGTGTCTA	GCTGCTAATTGGCTGAAATTG	(AT) ₃₂	264	250-266	4	0.538	0.482
GE632365	RC31	GCAGCTAGCCTTATTGAGGAAA	GAAAAATATCTCCACCACTTGC	(TA) ₁₁	174	174-176	2	0.486	0.368
EE254685	RC32	CAGTTTCACACCAAGCTGGTAA	GTTAAGGCAGGTAACGATACGG	(TA) ₂₃	259	259-265	2	0.375	0.305
GE632805	RC33	CTTGGCAGGTCACAAAGAACTA	GCCGTCCAGAATTGATAGGTAG	(TC) ₁₀	233	233-237	2	0.330	0.275
EE260187	RC35	AAGCGAATTCATACTCCTTCA	AAACCCACGTCTATCCTCAAAA	(AG) ₁₃	238	238-241	2	0.153	0.141
EE254189	RC40	GCATCATCACAGCCTCAAATTA	TATCTGAGCCTCCTCTTCCAG	(AG) ₁₅	163	163-184	3	0.642	0.570
EG698508	RC45	TATTACAATACCGCCCTATGC	ACCGCTGTTATTCCTGTCAAAT	(CAC) ₆	280	280-284	2	0.219	0.195
EG664367	RC51	AGGACTTATTCGACCCAGATGA	GATGAGTACTGAAGCGATGGTG	(GCC) ₆	207	260-266	2	0.278	0.239
EG697581	RC53	TGCAAGAACAAGATTGAGTCCA	GGCTCCAACAATAACAAAGGAG	(TGC) ₆	260	252-260	2	0.080	0.077
EG689318	RC57	TGTAGCAGAGAAATGCAAGGAA	ATTTAAGGTCAGCCCAAGAACA	(ATC) ₇	207	225-231	3	0.288	0.264
EG662586	RC61	GCACTGAGGGTTAATTCTGGAC	GTCGTAGACCACCTTAGCATCC	(GGC) ₇	232	205-211	2	0.492	0.371
EG701975	RC65	CGTAGCTGAAGCTGAACAAAGA	GCTTGACGGAGAGTAGAGCAAT	(AGA) ₈	261	271-286	3	0.508	0.415
GE633761	RC73	AGCCTGAATCCTCTGATGTAGC	GGTCTGGTTCAGGATCAGTAA	(CCA) ₉	178	178-184	2	0.486	0.368
EG698249	RC74	CTGAAGTTCCAGAGCTTCCTGT	TGAGAGGAAGGATTACGGAGAC	(CTG) ₉	200	200-208	2	0.469	0.359
EG696213	RC76	GGAGGGATATGGATTTTCAGATG	CGGAAGATGAGAGAACAGGTT	(ATA) ₉	225	223-230	3	0.431	0.392
EG695475	RC84	ACCTCTCCTTCCTCATCTCTC	GAATCTAACGGTGCTGATCCTC	(AAG) ₁₁	184	190-200	3	0.471	0.378
EG660729	RC85	GCCACTATGGTGTCTCTCGTA	CTTTTAATTTTAGGCGGTGGAG	(CAC) ₁₁	165	241-291	3	0.572	0.509
EG681190	RC86	GCAACTTCAGATGCAACAATC	TCATACATCTTGTGCAAGG	(CAG) ₁₁	245	275-284	2	0.153	0.141
EG687367	RC87	GCCACTCCGATTATTCTTTG	CGGTTCACACCCATCTCTTAT	(TAA) ₁₁	275	260-268	2	0.187	0.169
EG667050	RC88	CACCAATCTCATCACCAACT	GAATTGTGGGGTTTAGGGTTT	(TCT) ₁₁	246	252-264	3	0.344	0.307
EG679278	RC89	TCTGTAAACAACGGGAAAACC	CTACAAGAACAAAACGCCACCT	(TTC) ₁₁	261	252-261	2	0.249	0.218
EG666840	RC90	CACCTCCACAAGAACAAGAACA	CGGACGACGAACCTTTTAGATTC	(GAA) ₁₁	245	233-245	2	0.249	0.218
EG665468	RC91	AGTGGCATGGGCATATTATGTT	AACTCTCTAAGCCCCAAATTCC	(GAG) ₁₂	219	219-225	3	0.601	0.533
EG691818	RC94	ACGCCACAACACATATCAT	CAAGTGCATCTGAAACGACAAT	(GAA) ₁₅	248	231-248	3	0.601	0.516
EG699176	RC95	TAGACCCAGCAGTGCTCATAAA	CCACCTTTAGGTTGGATGTTGT	(CAA) ₁₉	235	211-241	3	0.594	0.511

EG693205	RC96	ATGGCAACTGTTGAGGTAATCC	CTACATGGCAGCACCAAGAAT	(AAAG) ₆	275	272-278	3	0.351	0.322
EG681785	RC100	CCAAGAAAACAACTCCGGTTAC	GAGGACATGGGTTGTGTGTTGAT	(CTCA) ₆	180	180-184	2	0.153	0.141
EG678636	RT103	CCAGAAATGCATCTGGATCG	TGGACTGGAGATGCTGATTATG	(TA) ₇	241	235-241	2	0.486	0.368
EG686206	RT104	TGATGCTAATGGCCTACTCAGA	TAATAGCACCACCATCAACTGC	(AT) ₈	262	262-266	2	0.353	0.291
EE254243	RT112	TATCTGAGCCTCCTCTTTCCAG	GGAACGACAAACACCACAATA	(TA) ₁₀	265	265-283	4	0.601	0.524
EG679802	RT113	TCAGTTGAACTCAAGGTCAGTCA	AAGCAGAGTGCTTCTTCAATCC	(AG) ₁₁	228	228-234	2	0.330	0.275
EG689244	RT116	TCCTTTCAGACCGAAGGAGATA	ATAACCATAACCCCATCCATCA	(AG) ₁₂	252	250-261	3	0.254	0.231
EG691558	RT117	CGTTTCCCTACGCTTCTACAT	TGATTACAGGTCCCATATTAGCC	(AT) ₁₂	232	222-238	3	0.559	0.470
EG663853	RT119	CAAACATAACACGCTTTCCA	ATTCTTCGTCGCTTCTTTTGC	(AG) ₁₃	189	195-203	2	0.486	0.368
EG697485	RT121	GCCACCATGTGAATTATCCTCT	TGTGAGAAGGAGAGGGTTTCAT	(TC) ₁₃	245	248-250	2	0.219	0.195
EG669444	RT122	CTGTCAAAACATTCTTCGCATC	AATGTTGTGGGATGAATAG	(CT) ₁₄	266	262-274	6	0.469	0.439
EE256105	RT124	GACAGACCCATCTCAAGATTCC	CATGAACCCACAAATTTACAGA	(AG) ₁₅	254	243-254	3	0.226	0.212
GE632416	RT126	CAGTATCACGCTGTGGTTGTTT	CTTTGCCGACTGGAATATCAAC	(TG) ₁₅	180	184-186	2	0.492	0.371
EG689641	RT128	TTGGGGACTATGATCAAACCTGA	TTTAAACTGCCATCAACGACAC	(TA) ₁₆	161	157-169	3	0.403	0.363
GE634251	RT129	TACTGCAACTCAATCCACTGCT	GATAGTGCCCTTTCGCTCTTTTC	(TC) ₁₆	247	241-253	4	0.580	0.523
EG692156	RT130	TGAACTCACAATCAGTCCCTTC	TCTGGTACAGGTGATGATTTTCG	(CT) ₁₇	229	227-233	3	0.403	0.363
EG685152	RT131	GATCATTTGCATGGCTGAAGTA	CCATAGCTTTGGACACACTCAC	(TA) ₁₇	180	168-180	3	0.344	0.307
EG694164	RT132	TCCTCACAGCTATTGGCAACAC	GGAAGCTAGGGATTAGGGATTG	(TC) ₁₇	189	183-189	2	0.330	0.275
GE634416	RT135	CTGCTTCTCTCTGCATTGTGTA	CCATTCCTTCTCTGGTTTCTTG	(GA) ₁₉	172	168-180	4	0.385	0.359
EG680179	RT138	CTTCCCAACAGCTCAATTTCTT	CACATGCATACATAAACACAGCA	(TC) ₂₁	269	265-269	2	0.413	0.328
EE254161	RT139	AGGTAACGATACGGTGTTGGAG	CAGTTTCACACCAAGCTGGTAA	(AT) ₂₃	225	213-231	5	0.733	0.687
EE259204	RT140	TCTAAGATGGTCTCGCCTCATT	GACCCATATAGGGCAAGGTTTA	(AT) ₂₄	179	163-183	6	0.780	0.748
EG700448	RT141	AATTGCCAGCCAAACATAAGAT	TAAATTGGGTTAATGGGTTTGG	(AG) ₂₅	176	176-190	3	0.351	0.322
EG693883	RT158	CCCCGACGATAACTACCATAAA	AGGTCATCGAATAACGACCAAG	(ACC) ₇	224	154-166	3	0.536	0.430
GE635881	RT165	ATTCTTTTCACACACGCTCTCT	GTATTTTAGGGGAATGGGGTTG	(GCA) ₇	249	240-249	3	0.468	0.411

EG684973	RT166	AGTTGCAGTTGAGGTTGTGATG	AAGGCCTCAGTTAACCAATGAA	(GGT) ₇	185	171-177	2	0.187	0.169
GE632520	RT167	GTCTGTGACAACAACCACGAAC	GAGATGGGAGAGATGAAGAGGA	(TTC) ₇	167	171-184	2	0.353	0.291
GE633169	RT168	TTCTTCCTCCTCCTCCACATAA	GAGGAGAAATGAAGCATTACGG	(AGA) ₈	213	214-219	2	0.187	0.169
GE633829	RT176	TACCCAATGACTGCAATCTTCA	GGGTTTGTGAGAAGGAGAAAA	(CTC) ₈	222	219-230	3	0.617	0.540
GE635438	RT182	GCCAATCTGTTACATACCTCA	GTCGAACTTTCATACCGGAAAA	(TCT) ₉	170	168-180	4	0.621	0.569
EG671871	RT184	CGCATCTTGCAATTTCTTTTGT	AGGATGGCCTGTGTCTAATAGC	(ATA) ₁₀	246	241-246	3	0.448	0.397
EG683300	RT186	AGATCAAATCGGGAAGAGAAT	CCATCATCAGTAGGTGGCATT	(GGA) ₁₀	175	172-178	2	0.492	0.371
EG662044	RT188	TCTTCTTCGCTCCAATAAAAC	TGTAGGGACAAAGCGATTTCATA	(TTC) ₁₀	157	157-160	2	0.278	0.239
EG666688	RT189	CCAGAAATGCATCTGGATCG	TGGACTGGAGATGCTGATTATG	(TTC) ₁₀	241	235-241	2	0.469	0.359
EE258383	RT193	CTACAAGAACAAAACGCCACCT	CGGACGACGAACTTTTAGATTTC	(GAA) ₁₁	227	233-239	2	0.249	0.218
EG662514	RT194	CCTCCTGCTCTTGAGAACCTTA	GGAGCAAAAGCATTGAAAGAAG	(TCT) ₁₁	249	249-252	2	0.08	0.077
EG673660	RT195	TATCTTTTGACCTGTGGAAGG	AAGGCTGCTTAAGACTCGGTTA	(TTC) ₁₁	222	219-225	3	0.469	0.391
EG667076	RT197	TTCCAAGAACAAAAGACCCTTC	CTGCGACACATTCAAGATTAGC	(CTTC) ₆	211	207-213	3	0.508	0.415
GE634515	RT206	TGAGTTGTGTGTCACCTTTGGT	CATCGGACGGTGCTAAAATAAT	(CT) ₆	193	193-228	2	0.375	0.305
EE259493	RT220	GTTGCTCCAAAGGACAATAACC	GATGGACTGTTGATTTCAGTGGA	(TG) ₆	180	182-184	2	0.413	0.328
EE255709	RT223	TAGAAAGAAAGCGACCCTTCTG	CACGATTGAAAGTTGAAACCAA	(TA) ₁₀	189	189-211	6	0.551	0.524
EG695020	RT224	CAAAGATTCCAAGTAGCAAGCA	CAGCAGCAACCATATTACCAAA	(TA) ₁₀	246	244-252	3	0.156	0.151
EE254893	RT226	CAAGACCAAAGAAACCGAAAAAC	AGCGACACAAGTCAAGTCCATA	(GA) ₁₀	243	239-243	2	0.219	0.195
EE254441	RT228	CCGCCAAAAATACCAAGATTAT	ATTACTGCAAGTGCTCCCTACC	(AT) ₁₁	236	232-236	2	0.153	0.141
EG657403	RT233	TTGGTACACAACCTACATGAGC	CTCCTCCAACATTCCTGGTAG	(GA) ₁₂	233	229-233	3	0.614	0.545
EG669717	RT234	AATCCAGAGAGGCAAAACATTC	CACCAATTGAAAGCCAGCTACTA	(TA) ₁₂	238	232-248	6	0.768	0.734
EE260480	RT236	TTGGTTGGA AAAACAGATTCTCT	AAACCCGCTTGAAATATGATTG	(CT) ₁₂	250	250-258	2	0.486	0.368
EG676447	RT239	CCAACAAATTCACCTCCCTCTCT	CCAAGATTGAAGCAAAAACACA	(TC) ₁₃	203	209-223	3	0.531	0.428
EG695527	RT242	ACCCCTGCAAAACCTAATAAT	TTGGGTGTAAAGAATCCGACTT	(CT) ₁₃	243	243-259	3	0.469	0.391
EE254642	RT243	CAGAAGAAGCAGTAGCAGCAAA	CCCAAGTCCCAGATCTCTCTAA	(TA) ₁₄	203	196-228	4	0.503	0.456

EG669444	RT245	TCACTTTTACCTCCCTCTGCTC	ATGGGTTTAGGAATGTTGTGG	(CT) ₁₄	230	230-249	3	0.538	0.480
EE259040	RT246	TGCAGTTTCGTCTCCTTCACTA	AATGACAATGGCGACTGATAAA	(AG) ₁₄	193	193-196	2	0.375	0.305
EG680607	RT247	AACAAAATCCAAACCCCAATC	CAGCATATGATTGTTCCCTCCA	(AT) ₁₅	229	229-247	3	0.258	0.240
EG681668	RT248	CAATCACCACCAAAAACCAAAG	CAGCATATGATTGTTCCCTCCA	(AT) ₁₅	213	213-233	4	0.263	0.252
EG683395	RT249	GACTTCAACTTTCTACCTGACCTTG	CTACCACCTGATTCCCCATAA	(CT) ₁₅	226	226-245	3	0.288	0.264
EG661770	RT251	AAACAAACAACACCGAAATCCT	CGTAGCGACTCATTTACACCAA	(CT) ₁₅	187	181-195	4	0.605	0.526
EG667814	RT256	AGACAAACACATGCTGCCTTTA	ATGTGTGGTGGGGATGTTATCT	(AGAA) ₅	186	181-188	3	0.635	0.561
EG662055	RT258	GCAGTTAGGCATCAAAATCCTC	GAAGTGCAGCTGTTAGGGTTTC	(GAAA) ₅	201	194-202	3	0.655	0.581
EG692953	RT259	ACGACTCCGACTCCTCTTACAC	TTTCTTCTTTAATCGGCGTCTC	(AAAG) ₅	191	193-205	2	0.153	0.141
EG658641	RT260	GAAGTGCAGCTGTTAGGGTTTC	GCAGTTAGGCATCAAAATCCTC	(TTTC) ₅	201	201-209	2	0.457	0.353
EG664709	RT262	ACGACTCCGACTCCTCTTACAC	TTTCTTCTTTAATCGGCGTCTC	(AAAG) ₅	191	191-199	2	0.153	0.141
EV523864	RC272	ACGATCTGCTTGTCTCTGT	CAGGTCAAGATCTCCAACAT	(GCG) ₄	238	235-246	4	0.370	0.327
EV523770	RC287	CCTAAGGCAGCTAAGTCAAA	GCAACTGCTTATGCTTCTCT	(CTG) ₅	217	312-327	3	0.492	0.435
EV523693	RC294	GAATCCCAATGTCCAGTCTA	CCTGAAAGAGAACAAAGTGG	(TCT) ₅	155	152-161	3	0.469	0.391
EV523589	RC317	CGCCAAGCTTATAAGAGAAA	GAGTCTGAAGGGAGAGGAAT	(AAG) ₄	149	149-161	3	0.223	0.206
EV523460	RC325	ATCACCCACAATTACCCATA	CGAGAGAACGAAAAGAGAAA	(TC) ₅	132	130-136	2	0.080	0.077
EV523432	RC328	GCAGAAAGAACACGAATCTC	AGCAATAAAAACCAAGCAAG	(TC) ₁₂	107	105-123	5	0.654	0.596
EV523389	RC331	TTAGCTGCTTCGATTCTTC	CAACATTAGCAGGCTGTGTA	(GAG) ₄	208	208-216	2	0.413	0.328
EV521100	RC357	ATGGAGTTTGAGGATCAAGA	AACTCGCTGTCATTTTGA	(GAA) ₆	121	122-125	2	0.219	0.195
EV521100	RC358	AGTCAAAATGACAGCGAGTT	CGTGGTTCTTTAAGCACTCT	(CAG) ₆	119	121-130	2	0.278	0.239
EV520933	RC365	CCATCGCTTGCTAGTGTTT	CATTACCCAAAGAAGACTCG	(TAA) ₆	144	144-151	3	0.452	0.381
EV520791	RC374	GATCTCGTAATGAATGTTGG	CTCTCTTCTTGAGGCTCTTC	(GCT) ₅	143	266-272	3	0.312	0.274
						Average	2.97	0.414	0.361