

**Table S2.** Mulberry specific microsatellite markers utilized in screening of diverse set of genotypes along with their repeat motifs, primer sequences and annealing temperatures

Sl. No	GenBank acc. No.	Repeat motif	Primer name	Forward (F)	Reverse (R)	STS size	T <sub>a</sub> (°C)
1	GT629469.1	(GTT) <sub>5</sub>	MESTSSR 10	CATTGCACATTGCAGGTAGC	CGGCCATCCAAAATGTTGTTC	237	52.8
2	GT628644.1	(CAAAAG) <sub>2</sub> (AAAATA) <sub>2</sub>	MESTSSR 13	TCTATCTCAACCGGAAGTCC	CCAATTTGCTCGTCTTATGC	230	54.8
3	*	(TTGATT) <sub>2</sub>	MESTSSR 14	CGGCCACAGGTACTTTC	GGCAGCGATTTAGGATTGG	202	50.4
4	*	(TGA) <sub>5</sub>	MESTSSR 20	TCGCAAGTGCTCAACTGG	TTGGGAACGGATGGAGTAAG	200	49.1
5	*	(TAC) <sub>5</sub>	MESTSSR 23	AGGCCCAAACTCCATAGC	CCGCCAATTCTAGACCAATG	202	50.4
6	ES448362.1	(AGCTGG) <sub>2</sub>	MESTSSR 26	CGTGATTACCTTCGGATTGG	CCAACCCAGTAGACCCAGTG	219	57.9
7	ES448597.1	(CGG) <sub>5</sub>	MESTSSR 27	CCAACATTATCCGGAACACC	GGTAAAGCCATCCGTTGC	266	54.8
8	ES448403.1	(ATA) <sub>5</sub>	MESTSSR 28	GCCCAGTTTCCACAGAA	TTTGTGCGTGCCATAGTACC	217	47.9
9	ES448813.1	(GA) <sub>16</sub>	MESTSSR 31	CACCAATTAAGCGCAGTG	TACTTTGTGGTTGGCTCGTG	204	57.9
10	*	(AG) <sub>13</sub>	MESTSSR 35	CGTTTTCCGCTTCAGAGAG	GCCGATATCCTCCTTTCCTC	206	54.8
11	ES448476.1	(CTTTC) <sub>3</sub> (T) <sub>10</sub>	MESTSSR 37	CAAAAGCGGTTTGAATAGC	CCTCAACACAAAACCCACC	245	54.8
12	ES449069.1	(AAAAT) <sub>3</sub>	MESTSSR 40	TGAATCCTACAAGGGAGC	CATACAAGGATGCCACC	215	52.8
13	ES449022.1	(AAAAG) <sub>4</sub>	MESTSSR 41	GGAGTCGTACAGAAGGG	AAAGGCGTTCAAAGGG	121	56.7
14	ES448502.1	(AG) <sub>20</sub>	MESTSSR 42	TCTCCAACAGAATCACAACAG	GCAGGAGCCAAACTCCAGTA	254	54.8
15	ES448813.1	(AG) <sub>12</sub>	MESTSSR 46	GTTTGCGGAGGAAAATGAG	GGGATTTTCTGTCTGGGTG	200	56.7
16	ES448510.1	(CTC) <sub>5</sub>	MESTSSR 47	AATTGACTGCGGGAGAACAG	GAGTTCACCGAGGCTGAGAG	220	54.8
17	ES448516.1	(TC) <sub>8</sub>	MESTSSR 48	GTTGTTGTGGTGGTTGTTGC	CTTCACTTTCTCGCCCC	201	56.7
18	*	(GAAGA) <sub>2</sub>	MESTSSR 49	AGACTACGTCTGCCAGGG	GAGCGTCTCGAAGCAGTTG	184	56.7
19	*	(CCTAAC) <sub>2</sub>	MESTSSR 50	GCCGGCATGTACGGATA	GTAAGGTTTCGCCCCAGG	235	54.8
20	ES448621.1	(GCG) <sub>5</sub>	MESTSSR 51	CCTAGGGTTTCCTTCGCTTC	AACGCTTAGGCTCCTTCCTC	223	54.8
21	ES448640.1	(TATTTT) <sub>3</sub>	MESTSSR 52	CTTCGTTACGCTCGCTATGC	CCCTTCTCTCAAGAATACTGG	261	56.7
22	*	(CCTAAC) <sub>2</sub>	MESTSSR 53	GGCCAACATGTACGGATAG	TCGCCAGGTACAACAAGAAG	203	56.7
23	ES449084.1	(TCATGA) <sub>2</sub>	MESTSSR 59	AAGAGCTCCGACGACCAC	GCGTCTCGACGTGAGAAATAAC	236	54.8
24	ES448647.1	(AAAAAC) <sub>3</sub>	MESTSSR 61	TCCCATAGCCTCAACGTTTC	ACGTCCGTATCATCGGATTC	239	54.8
25	ES448761.1	(TTTTTG) <sub>2</sub>	MESTSSR 66	ACGAAGGGGAAGGAAAAATTC	GCTCAAGGAGGTTGAAGCTG	258	53.8
26	*	(ATCGCC) <sub>3</sub>	MESTSSR 67	TGTGCTCGTAGCTTTGATGG	GCGAAGGAGAAGGAGGAGAG	215	54.8
27	*	(CT) <sub>12</sub>	MESTSSR 73	CCCCTGCGAACAATTTTCG	TTTGAGTTTCGGTTCTGAGC	237	52.8
28	*	(GAA) <sub>4</sub> (GAG) <sub>4</sub>	MESTSSR 74	GCGAAACGAAGAAGAGGATG	AGCTCCAGTGTTCTCTTG	238	52.8
29	ES448912.1	(CTCCGT) <sub>2</sub>	MESTSSR 76	TGATCCAGAACTCCCAAACC	GGTAATCCGAGTTCGAGACG	209	50.4
30	*	(AAAAAC) <sub>3</sub>	MESTSSR 77	TCCCATAGCCTCAACGTTTC	ACGTCCGTATCATCGGATTC	238	52.8
31	ES448921.1	(AAGTGG) <sub>2</sub>	MESTSSR 78	GCACTCTCAACAAATCCTC	CGTTTGGAACGGCTACTTC	242	52.8
32	ES448647.1	(AAAAAC) <sub>3</sub>	MESTSSR 79	TCCCATAGCCTCAACGTTTC	TCGACAACAACCGTCAAGTC	221	45.9
33	*	(ATACAT) <sub>9</sub>	MESTSSR 85	GTCATCTATGTCGGGTGGTC	CATGGAGCGTTTGTGTGTG	310	55.4
34	ES448967.1	(CCTAAC) <sub>2</sub>	MESTSSR 99	GGCCAACATGTACGGATAG	TCGCCAGGTACAACAAGAAG	203	50.4
35	ES448968.1	(CCATCA) <sub>3</sub> (TCT) <sub>7</sub>	MESTSSR 101	TATCGCCAGTCATCGTCATC	TCCGGAAGTCTGGCTTTAC	232	54.1
36	ES448289.1	(GAGTTG) <sub>3</sub>	MESTSSR 108	GGCTCTGAATGTCCGAGAAG	AGGGTGGTAGATTGGCAC	246	50.4
37	ES448647.1	(TTTGTT) <sub>3</sub>	MESTSSR 109	ACGTCCGTATCATCGGATTC	TCCATTCCTCATAGCCTCAAC	244	50.4

38	*	(AAAT) <sub>4</sub>	MESTSSR 111	CATCTATGTCGGGTGGTCG	CTATGCACAACAGGCTGC	299	45.9
39	ES449132.1	(AAAAA) <sub>2</sub>	MESTSSR 113	CAAGCCTCCCATTATGCAC	ATACGGATCTTCCAGGCTC	206	52.8
40	*	(A) <sub>19</sub> (AC) <sub>8</sub>	MESTSSR 115	GCTTATTTGGCTCGACGC	GATGGGATTTTGGGAAAG	294	53.8
41	*	(CGG) <sub>5</sub>	MESTSSR 117	ATTATCCGGAACACCAGACG	TTGCTAAGAACCTCGCTCG	247	53.8
42	*	(TTTGTT) <sub>3</sub>	MESTSSR 121	ACGTCCGTATCATCGGATTC	TCCATTCCCATAGCCTCAAC	244	52.8
43	ES448710.1	(CAACT) <sub>3</sub>	MESTSSR 122	CTGCTGATGAGGAGTGCAAG	TACAAATGACGCGGAAACC	246	52.8
44	*	(CT) <sub>12</sub>	MESTSSR 123	GGGGCTAAACTCCTTTTCC	TGTGTTTGCTGGACTTTGC	240	52.8
45	ES448693.1	(TTC) <sub>7</sub>	MESTSSR 126	CTGGTCTCCGTGACTTGGTC	AGCACAATCCATCCCAAGTG	200	52.8
46	ES448396.1	(CGG) <sub>5</sub>	MESTSSR 127	CCAACATTATCCGGAACACC	TACCTGGACGGAAGAAGTGG	285	52.8
47	*	(ATA) <sub>4</sub>	MESTSSR 131	CCTCATTGCGTTTCCTTGAG	CTGATTTGGGAGCCAAGAC	225	54.1
48	*	(TTTTCC) <sub>2</sub>	MESTSSR 132	GGGGTGGAAAGGAAATTTTG	GGTTAGCCCCTTGAAATGC	219	54.1
49	*	(TTTGTT) <sub>3</sub>	MESTSSR 134	ACGTCCGTATCATCGGATTC	GTACAAACCGAACGGGAAC	208	55.4
50	*	(ATCATG) <sub>2</sub>	MESTSSR 135	CCTCATTGCGTTTCCTTGAG	TGGGAGCCAAGACTCCTAAG	219	54.1
51	*	(AAAAAC) <sub>3</sub>	MESTSSR 136	TCCATTCCCATAGCCTCAAC	ACGTCCGTATCATCGGATTC	244	54.1
52	*	(AG) <sub>14</sub>	MUL3SSR 1	GGCCTCGATACAACTTGTGG	ACCATGATTACGCCAAGCTC	254	50.5
53	*	(TCTC) <sub>8</sub>	MUL3SSR 2	AGCTAGCAGATCCCTTCGTG	AGCCCAACATAAGGAACTCG	308	50
54	*	(ATATAC) <sub>2</sub> (TA) <sub>5</sub>	MUL3SSR 4	CAGTCAATGCTCTTGGCAG	TCTGGGGTTCAAACCTAAGC	313	54.8
55	*	(GT) <sub>14</sub>	MUL3SSR 6	GAGAGGTCGCCCTTAGA	AAACCAGCCTCACAGGAG	341	57.9
56	*	(CTG) <sub>5</sub> (TTTCCT) <sub>2</sub>	MUL3SSR 7	ACAAGTGACAAATGGCGTC	GCAGAATCCAGCTTTTTGG	255	56.7
57	*	(GT) <sub>7</sub> (GA) <sub>10</sub>	MUL3SSR 9	ATGACCAGCCATGAGCCTAC	ATCAAAAGGCAACCCAAGG	251	57.9
58	*	(CT) <sub>7</sub>	MUL3SSR 10	GAATCCAGCAATCCCCAC	CGGGATCCGATTGTTTAAGG	357	55.4
59	*	(AG) <sub>12</sub>	MUL3SSR 14	GGATAAAGGCGGTTTAGG	GAATCTCCACAGGGCAA	369	53.8
60	*	(A) <sub>15</sub> (AAAAAG) <sub>2</sub>	MUL3SSR 16	GTAGCAGATCACCCTTCG	TCATTGCCAGAACCCATG	392	52.8
61	*	(GT) <sub>14</sub>	MUL3SSR 17	GATGGCTTTGTCTTGACAC	CTCACAGGAGAACACCACC	356	52.8
62	*	(GAA) <sub>5</sub>	MUL3SSR 19	GGGCCTTTCTAAGACAGC	TAGCCGAAAAGGGACTCG	251	53.8
63	*	(CT) <sub>7</sub> (TC) <sub>6</sub>	MUL3SSR 20	AGCTAGCAGATCGTGGCA	CTCCGCCCAAAATATCACAC	255	54.8
64	*	(TC) <sub>16</sub>	MUL3SSR 21	TCGCAAATAGTGTGGAGTG	GGCAGTGAGAGCAAGGAG	237	45.9
65	*	(CTC) <sub>5</sub> (GAGACC) <sub>2</sub>	MUL3SSR 22	GCTAGCAGATCCCACCCCG	ACAGCTCCTCTTCCACAAGC	268	54.8
66	*	(TGCCAC) <sub>3</sub> (TCT) <sub>5</sub>	MUL3SSR 23	GCCCTCCACCATGAATTAGTC	GGAACCGTAACAACAAGACG	214	50.8
67	*	(AAG) <sub>6</sub>	MUL3SSR 24	GAGCCTTGTGACCACCA	CAAATCCAGTCCTTGGCTTC	283	57.9
68	*	(AAG) <sub>6</sub>	MUL3SSR 25	TCAAAGCAAATGAACCCAC	CCTATCCCTGACGAGGTC	260	53.8
69	*	(TC) <sub>7</sub> (TC) <sub>10</sub>	MUL3SSR 26	TATGAGAGCTTCGCACATGG	ATTGTCTCGGGAACAACAGC	201	53.8
70	*	(TA) <sub>7</sub> (TG) <sub>25</sub>	MUL3SSR 28	CTTCCACCTCTCAATGTTAGC	GCAGAATCATAGAGGACCAACC	215	50.8
71	*	(GTC) <sub>5</sub> (TCT) <sub>5</sub>	MUL3SSR 31	GATCCACTTCCACTCCCAG	GGACGCATGAGGTTTTAGG	382	47.9
72	*	(GAA) <sub>4</sub>	MUL3SSR 33	CCCGGATAAAAGACAACC	GCTCATCATCATCGGATTC	385	53.8
73	*	(GA) <sub>19</sub>	MUL3SSR 34	CAAACATTTTCTCTGACCCC	TCCAGTCCACGTCAGTTTC	221	57.9
74	*	(GAA) <sub>6</sub>	MUL3SSR 36	AGCAGAATCCCGGAGAAGAG	TAGCAGAATCCCCTGTTTGG	333	53.8
75	*	(TC) <sub>11</sub> (TC) <sub>8</sub>	MUL3SSR 38	TCAGCTTTAACCGAGCCAATAG	ACCATGATTACGCCAAGCTC	202	54.9
76	*	(CT) <sub>8</sub>	MUL3SSR 39	GCAGATCCCAATCACTCTGTC	AGTAATGGGCGTTCAACCTG	236	53.8

77	*	(CTT) <sub>10</sub> (TG) <sub>6</sub> (TA) <sub>8</sub>	MUL3SSR 41	CCCATGCCAAGAATTTCC	AACCTCGAGAAACCGGAG	295	52.8
78	*	(GAA) <sub>5</sub>	MUL3SSR 43	GAAAACCCGCATTCAATCTTG	GGCTTGTTCTGGATAAAACG	276	45.1
79	*	(CT) <sub>7</sub> (AC) <sub>12</sub>	MUL3SSR 44	CCCCTTTCCGTTTCAAATCC	TAGCAGAATCCCATCCCAAC	221	51.7
80	*	(ATC) <sub>6</sub>	MUL3SSR 49	CCAACATCAACACCGATCAC	ACCATGATTACGCCAAGCTC	242	53.8
81	*	(TC) <sub>13</sub>	MUL3SSR 50	GCTAGCAGATCCACCAAACC	ACCATGATTACGCCAAGCTC	317	51.7
82	*	(TC) <sub>51</sub>	MUL3SSR 51	TGTGTATGAGCTTGGGGATG	GCACTTTTATCCAGGTGAAC	266	56.7
83	*	(TTTTTC) <sub>2</sub> (TTTCT) <sub>2</sub>	MUL3SSR 52	CCCATACACAAAGCCAAATG	CGTGAGAGAACCCGAGAAG	388	51.7
84	*	(AAAAC) <sub>4</sub>	MUL3SSR 53	TCAAATCAGGGAACGAATCC	CCATGATTACGCCAAGCTC	277	45.3
85	BV722881	(AC) <sub>11</sub>	MulSSR 2	TGCCTGAAGATATGTGGTTGGC	TGCTCGACTCTCTGAGGGAA	161	56.8
86	BV722890	(CCCCT) <sub>2</sub>	MulSSR 20	AAATTCCCCGGGCCTTGTGTG	GCGATTTTTTCTGGGCTCCCTTG	305	56.8
87	BV722891	(AC) <sub>11</sub>	MulSSR 26	GTGAAGAACCACCTGTTGCCTGA	TCGACTCTCTGAGGGAAGCAGA	174	56.8
88	BV722892	(TG) <sub>5</sub>	MulSSR 52	GATCGTGGAGAAGGCACG	CACCCATTCCAGCCCCTA	186	56.8
89	BV722893	(TTC) <sub>6</sub>	MulSSR 59	GGTTTCATTTTCCCTCTCGA	AAAGGCCGATGCGAACAGA	172	56.8
90	BV722895	(CT) <sub>19</sub>	MulSSR 82	AAGAGGGAAATCCCCTCG	AGAAGAACCCCGCCAAG	173	56.8
91	BV722896	(TC) <sub>9</sub>	MulSSR 85	CAATATTACCACCCTCAC	GAAATGGTTTGCATCCAG	290	56.8
92	BV722898	(CT) <sub>7</sub>	MulSSR 130	AATCTTCACCTCCACTCCGTG	GTAAAGTTTGGGCCCCGAGT	131	56.8
93	BV722899	(AC) <sub>11</sub>	MulSSR 147	GAAGAACCACCTGGTGCTG	ACTCTCTGAGGGAAGCAGAC	169	56.8
94	BV722883	(T) <sub>15</sub>	MulSSR 154	ACATCAGCGAACTAAACCG	ATTACTCCCGCCCTTCCC	281	56.8
95	BV722900	(CCTCT) <sub>2</sub>	MulSSR 162	GTTCTCTTCCCCGACGAATGG	AAGAGGCGGAGGGGGGAGAAGG	332	56.8
96	BV722901	(AAAG) <sub>3</sub>	MulSSR 165	TCCTTTTGCAATTTGCGGTGA	ATGGAAAGCGTCCCCATCCA	903	56.8
97	BV722902	(TC) <sub>9</sub>	MulSSR 183	GCCCTTAGACTTTGGCATAATAG	GCAACATTTTCTGTTAGCAGCCA	239	56.8
98	BV722886	(GCG) <sub>4</sub>	MulSSR 218	CCAGAAGAAGAGCGTGAGTTGC	ACCACTACCGCAATCACCGCA	140	56.8
99	GF101969	(ATTT) <sub>4</sub>	MulSSR 219	TGCAGTTCCGAATCACGAAATAG	CGGTGTACCTCAATATGGGTGTG	117	60
100	BV722903	(A) <sub>28</sub>	MulSSR 240	CATTTCAGAGAGTCCACAAAAGC	CAAAAAAGAACTTCTTCGGGGG	227	56.8
101	BV722904	(CT) <sub>8</sub>	MulSSR 244	CCTACGACATATAACTGCACGTG	ATTGAAGTTTGGCATGTGGAG	180	56.8
102	BV722887	(CT) <sub>11</sub>	MulSSR 253	CCCAAATTTCCAATCAGGAAACC	GGAAGAGTAGGTCAGCGACA	217	56.8
103	BV722888	(CT) <sub>9</sub>	MulSSR 258	TGCATCTTTTCAGCCTATGGAA	ACATGGAAATGAAAATTGCTCG	155	56.8
104	BV722935	(CT) <sub>8</sub>	MulSSR 264	ACGACATATAACTGCACGTCTG	TTGAAGTTTGGCATGTGGAG	176	56.8
105	BV722939	(CT) <sub>8</sub>	MulSSR 270	TTTGGCGTGCGTTTGGGG	AACCACCCTCCTCACCAC	194	56.8
106	BV722940	(GTG) <sub>6</sub>	MulSSR 271	AGCGTGCGTCGAGTGTGG	CACCTCCACCACCTGCGA	205	56.8
107	BV722877	(TTG) <sub>4</sub>	MulSSR 306	TTTGTGTCTCGTGTGGC	TAATGCAGAATGGAGGGGCA	202	56.8
108	BV722874	(CT) <sub>8</sub>	MulSSR 313	ATAGATGAGCGGCAAAGCAG	TGTCTTTTTACTACACGCTCG	155	56.8
109	BV722906	(GGC) <sub>5</sub>	MulSSR 318	TGCTGTCTGTGGTTGCGGA	ACACAACTCCGCCTGCCA	259	56.8
110	BV722878	(TG) <sub>7</sub>	MulSSR 333	TCGATTCTGGGAAGATGAGC	AATCTTGATCTCCGAGCCCA	199	56.8
111	BV722889	(CT) <sub>8</sub>	MulSSR 338	TATAGATGAGCGGCAAAGCAG	GGTGATGTCTTTTTCTCACGCG	158	56.8
112	BV722875	(GC) <sub>7</sub>	MulSSR 356	GGAGGAGGCGACGTGTGA	TGCTCTCCCTCCGAGCT	158	56.8
113	BV722884	(CT) <sub>7</sub>	MulSSR 202A	TAATCTTCACCTCCACTCC	CCCGAGTAAAACAACCAATG	118	56.8
114	BV722885	(CT) <sub>7</sub>	MulSSR 202B	TCCAGAATGTGTATGGGCGCA	AGAGAAGCTCTGGACCGTGAGA	175	56.8
115	BV722936.1	(TGC) <sub>4</sub>	MulSSR 20S	GTATATTGTTGAGCGTGTGTGCAG	TAGCGCACAGCTCGCTGC	231	56.8

116	BV722937.1	(T) <sub>15</sub>	MulSSR 22S	CCGATCTTAGACTCTGCTCC	CCCTAAGCAAAACCGGCAAA	236	56.8
117	BV722938.1	(CT) <sub>6</sub>	MulSSR 25S	CTACTAGGGAATCCGCTC	GACACTAAGTAAAGTGGCGA	193	56.8
118	BV722931.1	(GT) <sub>6</sub>	MulSSR 27S	GCGTCTTGTGCCTCTTGG	ACGCACACACTCACGCCA	144	56.8
119	BV722939.1	(GGGGT) <sub>2</sub> (GTGGT) <sub>2</sub>	MulSSR 28S	TTTGGCGTGCCTTTGGGG	AACCAACCTCCTCACCAC	193	56.8
120	BV722905	(GTGG) <sub>3</sub>	MulSSR 312A	ACTAGGGCGGCGTGCAAA	CGCTTTAAACACAGCGCG	174	56.8
121	BV722876	(GCGGC) <sub>2</sub>	MulSSR 312B	AGGCTGACTGAGGAGCTG	TGCAGCAACCCAACTTCC	159	56.8
122	BV722907	(CGG) <sub>4</sub>	MulSSR 322A	ATGAGAGCGGCGAGAGAGA	CATCGTATGCCGCGTCTC	219	56.8
123	BV722934.1	(TC) <sub>10</sub>	MulSSR 57S	TCCTCACTTATTGATCCTGCCA	ACCTGTAACAACAGGACACG	220	56.8
124	BV722942.1	(GCT) <sub>4</sub>	MulSSR 60S	GTGGTGCAGGTGGACGTGTC	ACTACACCACTCACCGCCA	198	56.8
125	BV722943.1	(C) <sub>8</sub>	MulSSR 63S	CTTTCCTCTTACCCCCCA	ACCACATAACCAGAGAGTGGG	230	56.8
126	BV722944.1	(GT) <sub>5</sub>	MulSSR 65S	GCGGTGTATTGGCGGTAGTG	CACGCACACACACCCCTCA	206	56.8
127	BV722894	(CG) <sub>5</sub>	MulSSR 70A	AATCGAGGCGGAGCGCAA	AGCAATTCCAGGGCCTAACA	189	56.8
128	BV722894.1	(T) <sub>20</sub>	MulSSR 70A	AATCGAGGCGGAGCGCAA	AGCAATTCCAGGGCCTAACA	188	56.8
129	BV722897	(AC) <sub>11</sub>	MulSSR 96A	TGAAGAACCACTGGTGCCTGA	CGACTCTCTGAGGGAAGCAGA	171	56.8
130	BV722882	(CA) <sub>5</sub> (AC) <sub>11</sub>	MulSSR 96B	TGAAGAACCACTGGTGCCTGA	TCTACTACTGGGACATCCACG	286	56.8
131	AY714401	(CA) <sub>30</sub>	SS 01	CGGTCACGCCTTCTTCTCC	TGACCGAGAAATGAGGAAGGAG	115–190	55.7
132	AY714392	(CA) <sub>49</sub>	SS 02	GCTTCGATCAATCTAGCTTCCC	GCAAACCTACGCCACCCCG	325–420	55.4
133	AY714393	(TG) <sub>27</sub>	SS 04	CGAGGGAGGGATGAGGAGC	CACATTCATGCACCCTCCTATA	188–240	55.7
134	AY714400	(CA) <sub>5</sub> (CA) <sub>27</sub>	SS 05	TCCAGCAAAGATGTGACAAAAGTT	TTGCCTTCCCGATTATGCTG	342–478	52.4
135	AY714394	(TG) <sub>18</sub>	SS 06	ACTCAAAATGAAGGAAAAGGAATTATAC	TTTACTTAAATCCCAGCCACA	239–245	50.9
136	AY714395	(CA) <sub>56</sub>	SS 09	AGAACCCTTCCGCCCTATG	CCTTGGCGTAGGCAAAGTTG	358–364	54.1
137	AY714396	(CA) <sub>26</sub>	SS 17	TACAGGGCTCGGGCAAATG	TGATCCGAAGCTTGGGGTCT	249–243	54.1
138	AY714397	(CA) <sub>27</sub>	SS 18	TCTTCGCCCCTTGTTCGC	AGCAATTTTCTTCAACTCACCTTCT	181–210	53.1
139	AY714398	(TG) <sub>18</sub>	SS 19	TTCTGTGCTGTCTCCGTCAA	TGAGAACATACACTAATAGGTGAAAAC	352–367	54.3
140	AY714399	(CA) <sub>14</sub> (CA) <sub>12</sub>	SS 20	CCCTTTCATCGCCTCCTCC	CTCTGCCCATTAGTAGCGG	260–330	56.3

\*Personal communication with M. Sheshasayee, UAS, Bengaluru, India.