

Supplementary Data

Simple Sequence Repeat (SSR) markers for *Fraxinus*

Table A: PCR product size range and allele counts for successful primer multiplexes tested for SSR markers (screened for *in silico* polymorphism) developed from the European ash genome. Primers tested on 21 DNA extractions from the European ash diversity panel.

BATG -v.05 contig number_basepair coordinates	Repeat motif	PCR product size (BATG-v.04)	PCR product size range (RAP samples)	No. alleles (RAP Samples)	Forward primer sequence 5'-3'	Reverse primer sequence 5'-3'	Fluorescent tag	Multiplex
Contig679_76895_76745	(GA) ₈	151	145-149	2	GAGGACGGAGATGAAACTCG	CACTCTGTCTTGCTGCTGC	HEX	1
Contig6333_67506_67790	(GA) ₈	285	276-282	4	TCAAGGACAACGCATTTTCAG	AAATTGAATCTCTGGCGGAA	HEX	1
Contig1599_37272_37483	(AT) ₇	212	211-232	5	GAATACAATGGGACAAACAGCA	AGGGTTCGGATTGATGACTG	FAM	1
Contig2973_114859_115166	(CT) ₈	308	297-319	5	CTGGTCATTAAAGTTCGACTG	GCAAGAAGCACATGGTTCAA	FAM	1
Contig184_179564_179439	(AG) ₁₀	126	120-126	3	GCCATTGTTGGGTTTCACTC	CCGGGCTTAGTATCCAACCTG	HEX	2
Contig1992_131610_131822	(TA) ₇	213	208-216	4	CTCGGAGGTGGTTGATGAGT	AGAGCTCCCAACGCTCAATA	HEX	2
Contig383_57710_57981	(AT) ₈	272	266-274	4	CACCTTAGTGATTTCGCCCA	TTTGTGTTTCTCTGGCATCT	FAM	2
Contig2623_171328_171163	(GAA) ₇	166	159-179	5	GAAAGCTTTGCCAACTCCTG	CTGCCAGTTGAATTGATCAGAA	FAM	2
Contig4032_26441_26122	(CT) ₁₂	320	314-326	6	TCCCTACTAGCAATTGGCTCC	TGGTAATTTCCGCAACAGTG	HEX	2
Contig1308_65534_65760	(CA) ₇	227	224-228	3	GCTGCACATGGAATGCTAAA	CCCGGGTGTGGTGTAGATTA	FAM	3
Contig240_7943_7643	(GT) ₉	301	297-302	4	ATTGCCTCTTCCACATGCTT	GAATTCGCCCTAATGGTTCA	FAM	3
Contig2016_101810_102021	(CT) ₁₂	212	205-215 ¹	6	AACCACGTGAGGTCCAGAAC	GTGCTTGATTGATCGCCAG	HEX	3
Contig8028_30727_30850	(TC) ₉	124	122-134	6	GGCCGTGCAATTGACTAGAG	CAATGAAGGTGACTTGGTTCA	TAM	3
Contig65883_25650_25528 ²	(TC) ₉	140	129-145	8	CGTAGCTTGCAAGTTCAGCAC	ATTCTATCGCCGCCCATTA	FAM	3
Contig5748_109580_109480	(TA) ₈	101	98-112	4	ACATGCCTTCTCTTCGCC	TTCTAGGGCCTGCAAACAAC	TAM	4
Contig8097_39252_39512	(AG) ₈	261	241-262	4	TTATGTACATGCACGGCCAA	AACAGGAAGGTGCGTGAGAT	HEX	4
Contig918_100265_100431	(CT) ₁₃	167	157-173	7	TGTTAGTGGTATGGTGGAGGC	TTGCAGGCACAATTACATAAAG	HEX	4
Contig5418_11372_11513	(TG) ₉	142	135-148	12	TTATTGCCGATGTCTGTGGA	CGGGAAGTTTCACCTCAGAT	FAM	4
Contig8899_2905_3044	(GT) ₈	140	132-136	3	TGTACTCATGGGAACGGAGG	TTGAGAAGAGTTGAGCGAAGA	FAM	n/a ³
Contig5102_75169_75461	(GA) ₇	293	292-300	4	GATAAGGCATCGGAACTGC	AATAATGCACCCACGAAGGA	FAM	n/a ³

¹<95% blast match between target (BATG-0.5) and reference PCR product sequence (BATG-0.4). Allele peak at 155bp consistently recorded across all samples at microsatellite loci Fexmsat_599, the peak represents a third allele peak for individuals heterozygous for PCR products between 205- 215bp. ³Requires multiplex optimisation (failed to amplify in tested multiplex).

Table B: Primer sequences, locus information, and genome coordinates, successful primer multiplexes, for SSR sequences with the longest repeat motifs in European ash.

BATG -v.05 contig number_basepair coordinates	Repeat motif	Forward primer sequence 5'-3'	Reverse primer sequence 5'-3'	PCR product size (BATG-v.04)	Multiplex
Contig1_854544_854304	(TC) ₁₄	AATACAACCCAAGTGGTCGG	CCCTGGGTACATATCTCAGCTT	241	F
Contig1045_54054_53916	(AC) ₁₆	ATGTCAGATTTGTTGGATCACC	AGAGCAAAGTACGTCCGGG	139	n/a ³
Contig1063_27307_27504	(TC) ₁₄	TGGAATGCTGAGAATCGTAGTG	CGACGTTTCTCCTTCTCGAT	198	A
Contig11_153843_153680	(AG) ₁₆	GCAGTCTCGCATTCTGTTC	CCGAGCATGATAATCTGCAA	164	D
Contig147_7197_6904	(AG) ₁₅	TGTACAAGGGATGATTGCCA	TCACCTGGCATTAAAGTTGA	294	n/a ³
Contig1493_135476_135281 ²	(TC) ₁₅	AATTTAATTCTTCTGGCCTTATCT	TATCATCCATTAATTCGAGGTGG	190	n/a ³
Contig1650_119613_119498	(TG) ₁₄	AGCCAGCTCATGATTGAAGG	TGCTTGGAGTTTGTCTGTGG	116	C
Contig19606_643_486	(AT) ₁₆	TTGTTCAGCCTATTCTCGTTC	CACATTCAATAAGTTGCAGTATTGG	158	n/a ³
Contig2208_82901_82582	(TAT) ₁₄	GTAAATTGCTTTGGGCATGG	CAAGTTGCTGGTTAAATGAATG	320	A
Contig344_81629_81375	(AG) ₁₄	GGAGCAGTACCATATGCGCT	AGGAAGATCTAACGCTGCTTG	255	E
Contig364_284557_284416 ²	(TTA) ₁₇	GTAAGATGCAAATTAATGAATACTCG	CTTGGATAACCACAAGTTGGC	157	n/a ³
Contig3670_10994_10705	(CT) ₁₅	CACTTCAATGTCAGCATTCCA	CGAAAGTTCACCCAGTCAAAT	290	E
Contig413_266805_267049 ²	(AC) ₁₇	TGAACCTCAATACGTTCTTGTCAAA	AGGAAGGTCATCCAAGGCAT	243	C
Contig418_265110_264889	(TA) ₁₅	ATTGAATTATCTACCACATTTCAAAG	AGGGTTAAGTTGTAACGCC	160	F
Contig4412_3230_3361	(TC) ₁₉	TGACAATCTTGTCTTTGTTGG	CCTATTGTGAAACCCGCAAT	132	F
Contig4738_19258_19142	(AG) ₂₁	GCAAGGGAAGTAGCAACGAC	TGTGACTCAAATAGGGCTCAGA	260	A
Contig482_76777_77018	(ATA) ₁₄	CAGGTTATATTACTTCAGTTTATTGGG	GAATTCAGGTGAATGAAGTGGA	242	B
Contig50518_15111_15252 ¹	(CT) ₁₅	GGGAATCAGTTAGCATTGGG	GAAACTTTAACCTTGTCGCCA	142	A
Contig5308_65828_66003 ¹	(TC) ₂₂	CTCGAGGCAACCACTCTTC	AAACAAGCAGCTGAGGAGC	178	B
Contig608_143337_143131	(TC) ₁₄	CGGACTCTTCTAGTCTCCACG	TCCAATAAATAAACCGGCCT	207	E
Contig63036_11306_11509	(AG) ₁₈	TGCAATTCATTATACTCTACCCTACG	TGGGACTTCTATGAGGAGCAA	204	B
Contig636_38561_38744	(TC) ₁₇	GGTTTGGTATCGTGAGTGCA	TGATGGTATGTGTTGGGAGA	184	C
Contig6711_5568_5381	(AC) ₁₆	CATGCTTGTAATATCATAAATCTT	TTGTACGCTAGATGTTGCTTCA	188	n/a ³
Contig701_25705_25562	(GA) ₁₄	GGGTAGAGGGAGGCAGGT	CAGCCGATCTCGCACTTATT	144	B
Contig7018_133837_133642	(TC) ₁₅	TGCCATAAGAGTGGTAGGAG	TGAATCGGGTATTATAGAATGCAA	196	F
Contig7302_3643_3882	(TG) ₁₄	GAAGTGTAGGGACACATTAAGGTCA	ATTCTAGAAATCTTTAAAGGCAATGG	240	D
Contig77_117616_117440	(CT) ₁₄	GGGTTTGGAGTAGATGGTAGGG	TGGATGACAAATGACAACGG	177	n/a ³
Contig8881_19693_19904	(AT) ₁₆	CAGCAGAAGATTGGTTGTCTCA	TTAGGAGCCATGAATTTGGG	212	n/a ³

¹95% to <100% blast match between target (BATG-0.5) and reference PCR product sequences (BATG-0.4). ²<95% blast match between target (BATG-0.5) and reference PCR product sequence (BATG-0.4). ³Requires multiplex optimisation (failed to amplify in tested multiplex).

Table C: Primer sequences, locus information, and genome coordinates for 664 SSR sequences in European ash (*Fraxinus excelsior*).

BATG -0.4 scaffold number and base pair start position	BATG -0.5 scaffold number and base pair coordinates	Repeat motif	PCR product size	Forward primer sequence 5'-3'	Reverse primer sequence 5'-3'
scaffold1421_45465	Contig1_854544_854304	(TC) ₁₄	241	AATACAACCCAAGTGGTCGG	CCCTGGGTACATATCTCAGCTT
scaffold1115_76692	Contig100_156318_156573	(AG) ₉	256	CTTCAGAAACCGAAACTCG	CGACGTTTAAAGCCAAACGA
scaffold6062_24618	Contig1003_13283_13013	(AT) ₉	271	CACATGGGCCGTATATTCCT	CCATCAAACATGGCTTTCCT
scaffold3000_8058	Contig1003_81861_82044	(TC) ₇	184	CATCGATTAGGCTGATTGCC	CCGTGATCCTTTCGCTAAGA
scaffold2869_9155	Contig10098_3465_3653	(GA) ₁₂	189	ATTAGGTTTAACTTGGGACGAAA	TTTCCTGCCTTCAATAGCGT
scaffold2015_63419	Contig1022_142474_142191	(GAG) ₁₀	284	TCGTTGAAATCACCTACATATC	TTCCGGTATTTGAACATTTGA
scaffold18174_948	Contig10228_8104_8266	(GA) ₁₃	163	CGTTTCAACGTAGAACCATTAAA	CCTACAATGTCGCATGCTATT
scaffold4327_38483	Contig1027_98525_98386	(AG) ₇	140	TGGAATTGTGAGTCAGTACTCGT	CTACCTCCACGTGGCATA
scaffold1232_68606	Contig1040_82367_82072	(AT) ₁₀	296	CGGATCTGCACAAGTTACCA	GAAGGGAGCATCAGTGAAGG
scaffold4185_53016	Contig1043_189157_188930	(AC) ₇	228	TCCAATCTACAATCTTCGAGTCC	CAGCCCAGCATTGTTCATAA
scaffold9479_393	Contig1045_54054_53916	(AC) ₁₆	139	ATGTCAGATTGTTGGATCACC	AGAGCAAAGTACGTCCGGG
scaffold4403_2039	Contig1063_27307_27504	(TC) ₁₄	198	TGGAATGCTGAGAATCGTAGTG	CGACGTTTCTCCTCTCGAT
scaffold7502_17714	Contig1070_29343_29091	(TC) ₇	253	TTGGCAATGGAATCTCAGG	AAACGTGCAAATGACTGCAA
scaffold357_101598	Contig1086_11985_12130	(AT) ₈	146	CCGAACTTATATCGAATCAAACG	TCTCGACTAGTTTACTTCGCTTCT
scaffold1254_149835	Contig11_153843_153680	(AG) ₁₆	164	GCAGTCTCGATTCTGTTCA	CCGAGCATGATAATCTGCAA
scaffold144_178632	Contig1102_158789_158613	(AG) ₈	177	GAAGGAAATGGATGGTGCTT	ACAGAAATGATGTGGGAGCC
scaffold1101_30847	Contig1103_76718_76560	(TA) ₇	159	TCGATCCCATTACATCTCA	TAACGTTTGAGGTGGCCTTG
scaffold4549_16369	Contig1122_7564_7762	(TC) ₉	199	TTAGAGGCGACACATATGACAA	TGAGTTCCTATGAATAAGGCGA
scaffold2854_50169	Contig1125_13228_12987	(GA) ₁₂	242	CGAACACTGTATCACTCAGTTCC	AAGAACATTGAGGAAGTTGTGG
scaffold1387_239438	Contig1126_30667_30416	(TC) ₁₁	252	CGAGTTTGTTAGTCGTGGAGG	GAACAGTGCTACTACCGGACG
scaffold444_256046	Contig1130_126384_126685	(TC) ₇	302	TGCTGAATTGTTGCATGCTT	AAGGCATGTTCAATGGGAAA
scaffold595_61744	Contig1131_17765_17617	(CT) ₇	149	CATACCACTACCCGTCTACCTT	GAAGAAGTAGAAGCCACCGA
scaffold1381_94245	Contig1132_122689_122953	(GA) ₈	265	TGGCTTTGTGGAAGAACTCC	CTTGACCATGAAATACAACACG
scaffold4776_102341	Contig1136_11627_11736	(TC) ₁₂	110	CTAGTATGGGCAGGGCATGT	TTCACTGTATGACAGACAACAACCT
scaffold2686_44999	Contig1143_95954_95654	(TG) ₈	301	ATGCCACTGCTTTGCTCTT	CTGGTGAATTCTGGCAATCC
scaffold1460_82481	Contig1146_110970_111109	(AT) ₉	140	CAAGGTGCTAAGATAAACATGTCC	AAAGGACTGCTCAATCCCTAAA
scaffold2888_86856	Contig1146_43481_43343	(CT) ₁₂	139	GGGTAAGGAAGTCGAAGTCTA	TGCATGTTAATGTTGCCTGG
scaffold494_48060	Contig117_333724_333419	(TC) ₉	306	GAGCAGAGTCAAGCACATGG	GATGGAAAGCCAGGAGGAAT
scaffold1808_33971	Contig1170_18221_18339	(TA) ₈	119	GCTCTAAACCATGGAAGTGCA	TTCTTGTGTTGATAGATGTCCA

scaffold5949_17488	Contig1172_37344_37167	(AC) ₁₀	178	GAAGGTTTCGTGCGTGTA	CCAACCCAGGTGATGAATTT
scaffold1518_43981	Contig1185_76741_76966	(CT) ₁₀	226	CGTGGTCTCATCGCTCTACC	AGCTTCACATAATCGAGCCG
scaffold2256_150972	Contig12_143751_143536	(AT) ₇	216	TCACAGGTAGAGAAGAATATCAAAGA	CCTCTTGGAACCATTAAGAA
scaffold53_36587	Contig1202_64145_64292	(AC) ₇	148	ATGTGCTCACAGTCCACACC	ATTTACCTCCATCGCAACT
scaffold590_108430	Contig1203_120649_120846	(TC) ₇	198	GCACCTACCTACCAATGCAA	GAAGAGGTGAGGCGGTGTAG
scaffold351_221800	Contig1204_150931_151173	(AT) ₁₁	243	GGGTATTTACATGTCGAAGCCA	AGATTCTAATGTCGTTGTATGTTTGA
scaffold351_97500	Contig1204_27616_27894	(CA) ₈	279	CGATGGCGACAATCTTTG	CGTCTCAAGAACCTTCTGCAC
scaffold872_23662	Contig1211_20838_20960	(TA) ₁₃	123	AAAGGTACGAGGTTAACAACAAA	TCCAAGTGAATGTCACGCTCT
scaffold3697_166744	Contig1220_115635_115490	(AC) ₈	146	ATGAAGTCTTATTATTTGCCACAA	TGGGTACATGTAGCACGCTC
scaffold8870_37930	Contig1220_28923_29217	(AG) ₁₁	295	CATGCTAAACATGCGTCAAAT	CCAAGAATCTGACCCTGGAA
scaffold4548_313	Contig1230_94493_94325	(AAT) ₇	169	AATATAAAATACCAACAGGAGCTAGA	TCACTCCCATGTATTGATTTCCG
scaffold368_43648	Contig1231_140969_140680	(AAT) ₈	290	CTGGAGAAACACTATGGGTGC	TGCTCATTGTTACACGGAT
scaffold460_14155	Contig1235_187176_186976	(AT) ₇	201	AAGTTGAAATTTGGGCAAGG	TCATAGTTGGTATAGTGAATGGTCC
scaffold1124_1388	Contig1238_112578_112817	(TG) ₈	240	TTAGATTTAATGTACCCAGACTTCCC	AATTGCACAGGTGATAGGCAG
scaffold2423_25777	Contig1238_240859_241007	(AC) ₇	149	GCAATTTGAAACCGGAGAAG	CCACCAGAAGAATTCGGAAG
scaffold920_97857	Contig1241_91285_91546	(ACC) ₇	262	GAACGGAGTCTTGTATGACTATCAG	GATCATCCCCATCCAAAGCAT
scaffold4293_23417	Contig1245_61829_61699	(AT) ₈	131	CGATTGCAGATATCGCATGA	TGGCACTGATCCCATCATAA
scaffold768_38769	Contig125_378425_378127	(CT) ₁₀	299	GTCCCAACCAAAATTTCTGCT	AATGGGCCACCATAGAGAAC
scaffold14811_858	Contig1261_8364_8651 ¹	(AT) ₁₀	290	CTTGAGACCGGTATTCGAT	TCAGTATCCAACTTTAAATAACCTGAA
scaffold1265_178975	Contig1276_70187_70016 ²	(CAC) ₉	190	TGGTCAGAAATGCCATTCA	AAAGGTAGGTAGGGTACAAGCGAT
scaffold1246_32250	Contig1278_65064_64825	(AG) ₈	240	TTAATGAAAGAAATGCAAGCAGC	TGCTATTTAAACCTCCAAATAAGAAGT
scaffold1357_52846	Contig1281_146646_146512	(AT) ₁₂	135	TGGGCAAATAAATCGTTCCA	CACCAACTTATCTTTGACATTGTG
scaffold126_177556	Contig1293_79622_79464 ²	(GA) ₉	140	ATAACAAGAACGAAGGCCG	CTGCAGCAAATAGCATAAAGC
scaffold531_1418	Contig13_160964_160820	(AC) ₈	145	TCAGTTCCTCAAGTTTCGGA	TTCATAGTATAGATGCTTGATAGGTCC
scaffold64_125494	Contig13_81606_81765	(AAT) ₇	160	CATTTGAATGGACATTGGCA	GGCTCCTCTCAAGCTAACAAA
scaffold4442_61498	Contig1308_65534_65760	(CA) ₇	227	GCTGCACATGGAATGCTAAA	CCCGGGTGTGGTGTAGATTA
scaffold1080_62399	Contig131_159519_159228	(TA) ₈	292	TCATACGATCTTAGAGTCTCATGTGT	TGGCAATAATGAGATGTACTTACAGA
scaffold3060_66981	Contig1317_12597_12485	(AG) ₁₁	113	GCAAAGAAGTGCACCTGAGTT	GCCTGGTGTGCTGACAATAA
scaffold3060_14387	Contig1317_67197_67012	(AAT) ₈	186	AGCCACAGCATCTTCAGGTT	ACCTTGAAATCTTGATCATATCTATTT
scaffold6472_22955	Contig1321_37445_37554	(AT) ₉	110	TGAAATAATTAATTTACACTGTTTCG	CTGCGGCTGAATCAAATAA
scaffold3786_25487	Contig1324_193531_193672	(CT) ₈	142	AACCTGACTTTCCCTCCAATC	ATTAGAATTAGTCACTACAATCCTTT
scaffold2597_175241	Contig1334_31542_31406	(TAT) ₇	137	ACAATTTGGTGGGTGATGGT	CTTGTACTTTACTTTATGCTTTGTC
scaffold260_52026	Contig1338_199655_199794	(AT) ₁₀	140	CATCGCCTTTGAAGGAATCT	CTCTTAACAGCGTACCCTCCA
scaffold908_85208	Contig1341_196605_196744	(AT) ₉	140	GCACAATAAGAAAGTCAGTCTAGG	CATCTTGGTCTCTTCGTCTG

scaffold2653_44198	Contig1341_86956_87156	(GA) ₁₂	201	TCCAATTATCTTTACGAAGCAAA	ATCTTGAGATAAAATTTCCAGTATGTTT
scaffold5871_20297	Contig1351_72474_72377	(TA) ₈	98	TGCAAGGTTGGTTTGTGAGA	CCTCCAGTTGGTTGTACCT
scaffold1532_44022	Contig1358_178336_178048	(AC) ₉	289	TAAGCATGGAATCCCAGGAG	CGGGTATCAAGGTTTGCCT
scaffold1532_121743	Contig1358_91561_91385	(AG) ₉	177	TAATTCGAAATAACCGGCGT	GAAGGGCAGTAGCCTATATCTTCA
scaffold97_276133	Contig1360_336961_337226	(TG) ₇	266	ACGGACCAAATACCATCATCA	GTGGGTAATGAGATTATACAAGAATTT
scaffold1601_90158	Contig1360_55162_55032	(AT) ₈	131	AGACACAGCATGGCCAATTT	GGAATTGCTTTGAACCAACC
scaffold2127_99779	Contig1361_104542_104237	(AT) ₇	306	TTGAGCGCGAAGTGTATGTC	TTGGGTTATGAAGTGGACCC
scaffold2627_42817	Contig138_304328_304467	(GA) ₈	140	CCAGCCAAATCGATGCAAT	GCATCAAATCATAATTCTTCTGTC
scaffold32_453592	Contig1383_126586_126724	(AT) ₉	139	AACAAAGAACCGATTGAACAAA	GAAATCGTACTCGGACATCAA
scaffold529_13356	Contig1396_119143_118967	(TA) ₉	177	TTTGACCTCGTTAGCATGT	CATTGGATAGCTAGACCTCTGA
scaffold337_21303	Contig142_249780_249471	(AG) ₇	310	GCTGAAACTATGTAGTCAACACCA	TTCATATCCTCTTCGCTGG
scaffold5815_15420	Contig1430_93805_93600	(GA) ₇	206	CTATGGTGTGGAGGAACCCA	GCTCCACAACAATGAAGCTG
scaffold5815_10315	Contig1430_98691_98500	(AG) ₇	192	ACTAGGGTTTGCCTGCAATG	AAATTGCCGCCACTGAATC
scaffold6686_1199	Contig1432_11748_11991	(CTT) ₁₁	244	GGTGGTGTAGATTTATTTGATGC	GAGCAAATAAGGGCGAAATG
scaffold4929_27840	Contig1436_27544_27698	(AT) ₁₁	155	CAATTGGTTAAGCATGCCCT	GCCATGAAAGCCGATTTAGA
scaffold1696_112618	Contig1437_104570_104749	(TA) ₉	180	ATTCTCGGCTGGTTACTCA	AAGTTCGAATAGGAATGAAGATTGA
scaffold2410_102933	Contig1438_87062_86771	(TC) ₁₀	292	TTGTCCACCATATTCGTGCT	AACATGCGGTATTTGAAGGC
scaffold15_70602	Contig1448_57194_57433	(AT) ₇	240	ACTCTCAGTTGTTTCGCTAATTGA	TTTCAGTTAGTACAGCATGGG
scaffold10204_5112	Contig1449_31382_31170 ¹	(TA) ₈	213	CCGGTAGCGGTAAGGAAGAT	TTCGTCTCGAAAGAACTAACTCAA
scaffold1749_9668	Contig1450_10220_10379	(GA) ₈	160	AGAGCTTCGTTCTGTGAGAGG	TAACCCAAATCTCAGCCGTC
scaffold1648_111240	Contig1452_88308_88132	(AG) ₈	177	AACGCTATGGAAGGCTTTATTG	ATTTCCAAATCGACGCAAAC
scaffold13940_668	Contig1454_30426_30740	(AT) ₈	315	CGATGTCTGTACAACCTTGATCATT	AATGTCACTGCAGAAAGGATG
scaffold2453_37830	Contig1454_57323_57541	(CT) ₈	219	CCTACACAACCAATCTTTCGG	CTCGTGTTCCTTATTCTCCG
scaffold4450_34949	Contig1459_32738_32567	(AT) ₇	172	TCCGAAACTCGGTTTGTTC	AGAGAATGTGTTGAAGATGCTC
scaffold17997_48	Contig14611_980_854	(TG) ₇	127	TTCCCTATCTACCGAAGGCA	AAATCAAACCTAACATCAAGTCTAAAT
scaffold2384_1842	Contig1462_1711_1894	(TTA) ₁₀	184	TTCTTTACATCAGGCGGCTC	GGCTGGTTAAGGCCATGT
scaffold3773_87401	Contig147_5892_5693	(AG) ₇	200	GTTACGCAGCCACGGTAAG	AAATAATTCGTACGCCCGC
scaffold3773_86094	Contig147_7197_6904	(AG) ₁₅	294	TGTACAAGGGATGATTGCCA	TCACCTGGCATTAAAGGTTGA
scaffold3139_70777	Contig1470_49431_49288 ¹	(TCA) ₇	141	CAATGTGACGTGATTCCGTT	CGGTATCATCGTAAATATCCCAA
scaffold5935_27015	Contig14725_40565_40683	(CT) ₈	119	ACACGAGCAAATGACCATCA	CAACTATTCCAAACGCAGCC
scaffold1209_131057	Contig1482_143484_143335	(AGA) ₇	150	GGGTCTCCAGACCACTCGT	ATTATCCCATTGACCACCA
scaffold3920_38118	Contig1486_58916_58701	(AT) ₈	216	GATGCCAGAAATTGATTGGG	TGGATACCAATTCTCAGCTTCA
scaffold9729_1804	Contig1493_135476_135281 ²	(TC) ₁₅	190	AATTTAATTCTTCTTGGCCTTATCT	TATCATCCATTAAATCGAGGTGG
scaffold691_25437	Contig1520_45736_45497	(AG) ₉	240	CACCAACCTATTGTTTCTGGA	TTGACTGGTGTGCCAGGA

scaffold2230_33122	Contig1523_68813_69127	(AG) ₁₂	315	CTTTCGGTAGCCATCTGGG	CCCGTTAATACTAAGAGCCCCG
scaffold619_66508	Contig1531_58322_58525	(TA) ₇	204	CCTCTGCCAAGTTTGTATCCT	CAATGGCTATAAGAAATGGAAGTG
scaffold619_90039	Contig1531_79171_79298 ²	(AT) ₉	114	TTATCGATCACGAACAAAGTTTA	AGCTGTATTCTACTTTCATGGCA
scaffold15098_2744	Contig1533_611_870	(AG) ₉	260	TATTGCCGAGGAGGTTTCTC	TTCCACCTACTTCTGCTTATATTGG
scaffold7_62952	Contig154_293041_292819	(TG) ₈	223	CAATTTAGAGGCAGAAAGGG	CCGTTTGGGATTGAACAAAT
scaffold1901_55522	Contig1556_10696_10998	(AT) ₁₀	303	ACTACAGCCCACACGTCCTT	ACAGAATAAATGGGCGGAAA
scaffold10_102274	Contig1564_107074_107230	(TA) ₈	157	CCTCTCGAATAGCCTTGGA	TCCTCCTGCTGAAAGAACTGA
scaffold1940_57625	Contig1569_4630_4442	(AT) ₉	189	TGGTCACTACAGTCCAAGCAA	TTTGAAGGAGTCAGACGGC
scaffold913_283805	Contig157_185922_186204	(GA) ₁₀	283	CGCCGTGGAATATTAGCTTC	TTTGGTGAACAACCTGCGTGT
scaffold274_121017	Contig1572_38944_38755	(AT) ₇	190	CTTCCATGCACTATTTCTGTCG	ATCATTTGGTAATGACCGGG
scaffold26048_75	Contig1574_54891_54744	(AAT) ₉	148	GGTCATTGCGATATTTACTCCC	GCTCTTAAGGGTAATGTCTTTGC
scaffold1078_107861	Contig1599_37272_37483	(AT) ₇	212	GAATACAATGGGACAAACAGCA	AGGGTTCGGATTGATGACTG
scaffold174_113926	Contig1602_79835_79535	(TTA) ₁₂	301	TTTCCCTCTATCTCAGGTCTGT	GGGAAGAAGAGTTGGTTTGC
scaffold1020_98964	Contig1603_84306_84155	(CT) ₉	152	AAAGCACCAGGGTTCTCAA	CCAAGAAGCAAATGCGTAGA
scaffold2442_39213	Contig161_7245_7010	(CT) ₈	236	GCCTTCCAAATGACCCCTTCT	TCTTTAAAGGGTGTTCAATTTCA
scaffold2905_74343	Contig1626_80888_81037	(CAC) ₉	150	GGGTAAGCAAGGTGAAGCAA	CACAAGGTGGAAGTGGGATT
scaffold2663_53988	Contig1641_48779_48545 ²	(AT) ₁₀	221	TTCCCAAGTCTAACAATGGCA	CAAGAACTCAAAGCTAAAGAAACG
scaffold3460_8603	Contig16426_962_813	(TTA) ₈	150	CCAGATGGGACAGAACACCT	AAACATTGTTCAATTTCTGTCCAAA
scaffold6595_17376	Contig1650_119613_119498	(TG) ₁₄	116	AGCCAGCTCATGATTGAAGG	TGCTTGAGTTTGTCTGTGG
scaffold3161_51617	Contig1650_31977_31848	(CT) ₁₀	130	CATCGGTGTTGTCAAAGGAA	TTTCAAGTCACCGTGTCAG
scaffold3426_37716	Contig1661_111700_111982	(TG) ₇	283	AAGTGCCTGTTCTGAGCAATC	GCACTATTCTCTCCAAGTCGT
scaffold314_95003	Contig1667_94959_95107	(TG) ₉	149	GGTCACACTCAATGAGCCAGT	GCTCCGAAGATCATGGACA
scaffold1091_36116	Contig1675_92004_92139	(AC) ₉	136	TGTAAGTTCACACCAGAGGTGG	ATCCGCCATATTCCTCCAG
scaffold911_14661	Contig1687_50975_51264	(GA) ₉	290	TTTGCTAATGTATTAGAATGCAACAA	AGTGTTTCATCCGACAGACGAG
scaffold3822_32577	Contig1691_5081_5220	(AC) ₇	140	TCACTCCTAAGGTGACCATCTG	TATTAATTACGCAAGTTGCACTAACC
scaffold5164_92494	Contig17_213656_213846	(TG) ₁₁	191	CTCTGATTATGTATTCACTTGTGCC	AAGGCAAAGGCTTGAAGGG
scaffold3901_8336	Contig1702_13248_13487	(GA) ₁₀	240	AACATCCCTCATTCAAAGATCA	ATTTCAGAACGAAGAAGGAGAGG
scaffold3774_6772	Contig1721_86831_86710	(AT) ₇	122	CACAACCATTTCCAGCTTT	TGTAATAATGCCATTACCC
scaffold2952_68475	Contig1730_69134_69423	(TA) ₈	290	GCACTAGACGCCATATGACAGA	TGGACCTAAACCGCTAAACG
scaffold2411_51710	Contig1739_68647_68900	(GA) ₉	254	TCCGTGTAGTGCACTCTTGC	CTGGAACGACAAGATCTCCG
scaffold2656_16736	Contig1749_100482_100695 ¹	(CT) ₇	216	CCCAAATGACGAATTCCTCTAC	GCTCTAAATACCCTAGGCTTATCC
scaffold5525_92389	Contig1760_18575_18431	(AT) ₉	226	GCCAAACATGCTTAAACCAC	TTTGTCTTGCAATTTAGGTTTATTC
scaffold3609_11098	Contig1778_10988_11128	(CT) ₉	141	CCATAACAGCCACAAGGCAT	TGGCTCTTGAGCCTTCAGTT
scaffold4890_1805	Contig179_235231_235092	(TC) ₈	140	TGCAGATTCACTAAACCATACAA	GGTCGATAAAGGCCCTCC

scaffold3286_61322	Contig179_61802_62043	(AG) ₈	242	GCGGATATCTCTTACTCCATTCC	TCCTCGATAGAAGGCACATCTT
scaffold32_266544	Contig1792_122379_122130	(AG) ₇	250	TTGAATCAAACGGCAGACTTT	TGATGGAACCTCACATTCCC
scaffold982_377105	Contig1795_237744_237898	(GA) ₁₀	155	TTCCTTTAACACCATCCAGC	TGGGTGGTATCGTAGAATGG
scaffold1165_197071	Contig18_3062_2865	(TA) ₇	198	ATTTGCCGAAATCCTCAACA	TTGAGCTCCTTAAGATTATCCTTGT
scaffold87_326421	Contig1808_82743_82881	(AT) ₁₀	139	TGCAACCTTGCAAAGATAAAC	CAACACTGTCTGCACCATCA
scaffold4515_15184	Contig1813_34262_33970	(GA) ₁₀	293	TCAGTGACAGAAAGGAATCCAA	CACGTTTCTGGTAGTCTCACTAAA
scaffold4515_7813	Contig1813_41525_41382	(TA) ₈	144	GCAATACAATGACCCACTGGA	CTGGCCTCAGTGAAGGACTC
scaffold1255_158018	Contig183_166184_166023	(CA) ₇	162	CATGGCACAGTAGTTCCGA	TGGAAGAGACAGTGGAATGC
scaffold1723_57473	Contig1830_90445_90206 ¹	(CT) ₇	240	AACCACTTATGTCGGCTGATG	ATGGAAGCCAAAGAAAGTTG
scaffold1745_188185	Contig184_179564_179439	(AG) ₁₀	126	GCCATTGTTGGGTTTCACTC	CCGGGCTTAGTATCCAACCTG
scaffold5840_57791	Contig184_264676_264969	(GA) ₈	294	GCTCTGTCCTCGTCAGGTTG	CAATGCATATTCTCAGACACCC
scaffold2319_123930	Contig1853_82397_82530	(TA) ₇	134	GGTGAAATGATGGACAAGGA	TGGTCTGAAATACATGGCCC
scaffold2191_126219	Contig1860_13016_12726	(TA) ₁₀	291	TTAACATGCTCAAACAGGCG	CGAGTCGATGAATAAGCTGTTCT
scaffold3555_57185	Contig1866_12174_11879	(CT) ₈	296	ACGGCAAACAATGCTATTCC	GGCTAAAGTTGAAATGTCATGATCTA
scaffold5599_61225	Contig1866_98945_99063	(CT) ₈	119	AGAATCGTCCAATTCCGGTT	CATGTAACACAATGCCTCCG
scaffold600_97825	Contig1878_104301_104597	(ATT) ₇	297	GGAACATTAAGGTTTGTGGTG	CAGAGTCTCGCAATCTGCAC
scaffold22_123387	Contig1883_119185_119047	(GA) ₇	139	GGGTCGTCGCACATAAACAT	TTCATAGTGAGCCGTTGACATC
scaffold305_80732	Contig1887_9178_9317	(TC) ₇	140	TAGGTTATGTAAGTCATCCAGCC	CACATCGACACGAACACCC
scaffold582_143556	Contig19_180808_181066	(GA) ₇	259	TCATTACAGCCATAGGTACAGG	TGCTAGCGAAATTTCTTGGG
scaffold582_191252	Contig19_225608_225747	(CT) ₁₀	140	AACATTTGAGGTCCTTTGTCA	GAGTATTGTACGCCCAAGTTCA
scaffold551_73366	Contig190_122939_122675	(TTA) ₇	265	TGGAACCCATGAAACTATGC	GCCGATGTTTAACAACATTCA
scaffold4956_43093	Contig1903_80370_80231	(AG) ₇	140	ATGGCACATGGAGGAACCTA	TTACGGCATCCTCAGTACCC
scaffold5624_2979	Contig1905_1542_1781	(TA) ₉	240	TCATTACCATATAAATCTCAGTTTCCA	GATCAAATGCCCAAATTAGCA
scaffold4431_75047	Contig191_35292_35108	(TC) ₉	185	TCCAGTTTCGAAAGGTGCTT	GCTCATAACCTAACACGCCC
scaffold728_232666	Contig1928_125340_125029	(AG) ₁₀	312	CCCACTCGTTCCTTACCA	TTGCAAATGAGTTGAACAGAGT
scaffold993_18458	Contig193_206542_206350	(AAT) ₇	193	TTCGATCCATCTAAGCCAAA	GGGCTCTAATGTTGAGAAA
scaffold772_100595	Contig1946_58207_58384	(CT) ₉	178	GTGTGACCTGCTTAGCTCC	TGTGGGACCTGCACTATGAA
scaffold3132_72707	Contig195_131553_131300	(TA) ₁₁	254	GGCAAAGAAAGGCAGTAGCA	GCCGCTGTTTGTATCTGGAA
scaffold2397_154606	Contig19606_643_486	(AT) ₁₆	158	TTGTTGAGCCTATTCTCGTTC	CACATTCAATAAGTTGCAGTATTGG
scaffold2353_110445	Contig1964_89743_89594	(TC) ₉	150	CCAAACATCCCTATGCTGGT	GGTCCTGCTGTACTGGTGGT
scaffold77697_140	Contig1965_23355_23144 ²	(AT) ₇	191	ACAATTCACAGGAACACCGC	TGAAAGGCTGGAGACTTCAGTT
scaffold512_72151	Contig197_121874_121676	(GGT) ₁₀	199	CCTCATTGGCCTTTCTGTTG	CCAAACAAGGACTTGGTTAGAGA
scaffold4742_32439	Contig19899_4210_4455	(TA) ₁₀	246	GGTGATGAGACCAAGTGCTG	ACACAGCAAAGCCTCCAAG
scaffold9278_2236	Contig1992_131610_131822	(TA) ₇	213	CTCGGAGGTGGTTGATGAGT	AGAGCTCCCAACGCTCAATA

scaffold39_145799	Contig2_213304_213560	(TG) ₇	257	TGCATTATGTGCACAAGATAACTAA	TTTGGCCAATTGAAACACTT
scaffold1694_380732	Contig2000_31035_31283	(GA) ₁₀	249	AACCAACGGCTGTTTCAAAT	TTAGGTTAGCAATCTGTCCTAGTTT
scaffold1302_91102	Contig2007_161300_161022	(AT) ₉	279	CAAATGCACCTAGGGAGGGA	CCACAATTGGGTATCATCTCC
scaffold599_63275	Contig2016_101810_102021	(CT) ₁₂	212	AACCACGTGAGGTCCAGAAC	GTGCTTGATTGATCGCCAG
scaffold5810_25983	Contig202_23413_23158	(GA) ₈	256	TGACCACCTCTTGCTATCCATTT	TCAGTAACATGTTGCCTCGG
scaffold2408_18434	Contig2022_29220_29346	(AG) ₇	127	TTTAAATAGCATAGTCAGATCGGG	CAAGTTCTGAAACAGCGGTC
scaffold235_195818	Contig203_101005_101201 ¹	(CA) ₈	196	TCTTGCGAATGCTCATTGG	CTTAGCAGGCTAGCAGCACA
scaffold893_103557	Contig203_327071_327262	(AGG) ₇	192	ACAGACGATTCTGCCTGGTC	TTGCTGAGCCTGTCCATACA
scaffold186_149560	Contig2035_28620_28893 ¹	(TA) ₉	276	GAACCGCTCAAATCGGTCTA	GTGCCCTCATTTAGCTCCAA
scaffold2542_66287	Contig2036_42079_41763 ¹	(TA) ₈	317	CCCACCTTTAGTTGAATAGATG	TGCTATTGCTCGACGAGATTT
scaffold1387_116635	Contig2043_30161_30000	(AG) ₉	162	TGAGATGGTATAGACTCCGAGAA	AAGGCTTACAATTTGATACCAAGG
scaffold2399_17361	Contig2062_64690_64450	(TG) ₇	241	TGCGATATGGCTAAAGATCAGA	GAGACATAAACTGCCCTCCAA
scaffold3926_19179	Contig2077_19774_20016	(AG) ₇	243	GATTGGCAACCCACACCTTA	TCACGTTGTTGGTTCATCA
scaffold1300_158203	Contig2090_7107_6923 ¹	(CT) ₁₂	185	GCTTATGGTCACGCTCCAAC	TCCAAATTAACAAAGGAGGA
scaffold873_60048	Contig2102_50609_50437 ²	(AT) ₈	191	TGCTAGAGTTCAAGAATAGCAATCA	GCAAGAGGTTCCCGAGAGTA
scaffold7382_48472	Contig2105_133030_132790	(TG) ₇	241	GGGATGGAGCCCTCATACTA	ACCTTCTGAGTTTGCTTGG
scaffold3386_3840	Contig21153_1865_2036	(TA) ₁₀	172	GCTTCTTGAACCTTGTGGC	CGCATGGTTACAGCCAACTA
scaffold1774_120260	Contig2119_45232_44995	(CT) ₈	238	ACGATCAGATCAGAATGCCC	CATTAGCGAGAACCAGAAAGG
scaffold2300_74915	Contig2126_60940_61131	(TC) ₁₂	192	CCTACGTCTCTATGAAACAAGCC	AACTTGTTATGCATTATCGTTGT
scaffold1495_86140	Contig213_8739_8588	(CT) ₇	152	GGCCAATCACATGTAAAGGAG	CGATCAATTTACCAACTAGCGA
scaffold498_53031	Contig217_248034_248271	(CT) ₇	238	ATTCTCGCCGATTGTTGAGA	AATTTGACTCAAGGGAGCA
scaffold530_494027	Contig2178_128906_128750	(CT) ₁₀	157	GTCAGAGAAGAGCTGCTGCC	GCGCTTATCCCATGTAAGC
scaffold448_62606	Contig21808_1608_1922	(AT) ₇	315	CACTGGACAGTCGCTTCATTT	AAACTAGGAAGAGACAGAATGGTG
scaffold153_133074	Contig21831_6045_5806	(AC) ₉	240	TGGAGCAGCTTCTGCTTTG	TGAAACCTGTAAGATGAGCTTGA
scaffold377_324566	Contig2190_132627_132474	(AC) ₁₃	154	GAAATCATCTCGTCCCTCAA	TTGTTCACTAGCATCTTCACCA
scaffold2654_64398	Contig2194_3445_3185	(AC) ₈	261	AGTCGGATTGGTGGATCAAG	TGGAACGCATTAGTTGTTTGT
scaffold1410_136600	Contig2198_32268_31958	(TAT) ₉	311	AGCACAAAGCTTTAAATGGGC	CTTGCAACATATCATAGTACAATCCA
scaffold1639_144757	Contig2200_140223_139940	(ATC) ₇	284	TCGACTGTTTGTGAAGCATTT	ATGGCAAGTGTGCAAGAGAA
scaffold3127_30775	Contig2208_82901_82582	(TAT) ₁₄	320	GTAAATTGCTTTGGGCATGG	CAAGTTGCTGGTTAAATGAATG
scaffold10170_9433	Contig2214_17394_17155	(GA) ₁₀	240	TCAACTAGCTAAAGTCAAGTTACAGG	CCAGCTCAGCATCTCTAACTG
scaffold5844_7859	Contig2215_27085_26967	(AC) ₁₁	119	GAGCACACTTGTGCATGGAG	GGTCATTCTGCAAGCAATTT
scaffold756_99932	Contig2219_77354_77673	(ATG) ₇	320	CGTCCCTTCACTCAGATCG	TGTCACGATGGACGTACTGAA
scaffold317_29874	Contig2234_109122_108978	(TA) ₇	145	AGCCAAGCCTTTCCATACG	GGCCTACACGTACAATTTG
scaffold2878_63103	Contig2241_78961_78671	(TAT) ₈	291	TTTCAGATCATCTTGGAACATC	GAGAGCTAGGTGATTATTGATAAAGGA

scaffold3181_16944	Contig2242_75576_75314	(CT) ₁₁	263	TTTGGTCATGTTGTGATTCTATGA	CACAAGTCTGTTGAACATCTGGA
scaffold21_187515	Contig2263_76834_76621	(TC) ₁₂	214	GCCTAAATGGAAACCTCCAG	TGAGTACACAAATGGCTCCAA
scaffold1913_147237	Contig229_102582_102396	(AG) ₉	187	TAAAGGCCGTTTGAGAGTGC	GTCGTGCAGCTAATACGTCG
scaffold1395_149932	Contig2293_8666_8489	(AT) ₈	178	AAGCTCGTTAGATCATATGCCA	TCCCTACAGGACCAAATCCTT
scaffold672_156540	Contig2294_119511_119704	(AT) ₇	194	ATCGGAATCCCACAATTCT	TAATCTACTGCCAAAGTTTCACTG
scaffold1893_122360	Contig23107_8546_8372	(TC) ₁₃	175	TCAACCAAGTATGGTTAAATACCAA	TCATACCTTCTTGTATGCAG
scaffold7638_6553	Contig2319_11982_11864	(AT) ₉	119	TCCACTTCACAATCACAATCTTT	CGAGATCAGAGTATTGGTGCC
scaffold210_1610	Contig2333_114778_114487	(TA) ₈	292	TCCTAACCAGACATGTATACCAC	TGTTGAAAGGTGATGAGGTGA
scaffold646_64073	Contig235_122828_122527	(GA) ₁₃	302	GCTAGAACTGTGAACATAACAGACT	CTCAATCATGGGCTAAATCAG
scaffold359_43061	Contig2350_95396_95252	(TA) ₉	145	TGAACATACCTGTGGTAGCGA	CAAAGCAGTTGACATGACCG
scaffold1555_67253	Contig2357_38286_38389	(TC) ₇	104	TCCCAATTAATCTGCACCGT	TAGCGTGAGTTTCGTGTTCTG
scaffold661_108021	Contig2361_10592_10731	(TC) ₇	140	AAATAGCCTTGTCAAGACTCTACC	CCTTCTCCCTATAGATAAATCCAG
scaffold1237_20381	Contig2369_72797_72585	(CT) ₇	213	TGGTCTCAATCAAGCAATGG	TGGAATGGAAGGAAGGCTTA
scaffold3092_21321	Contig2371_54611_54413	(AG) ₁₂	199	CCGTGACAAACCACACGATA	CCCGGTTTGATTCTTGTGA
scaffold253_133484	Contig2376_12111_12301	(AT) ₉	191	GCATAGCTGGAACATTTGGA	TTGCACGTACGAGAATATTTGA
scaffold2476_52907	Contig2377_75657_75479	(CA) ₇	179	GCTAGCGGCATACATGTGAA	GCCACCTTAATCTTCGATCA
scaffold1167_128555	Contig2391_24342_24054	(CT) ₇	289	GAATATGGATGCACGAGGGT	CATTGGATGCCTTATCCGT
scaffold3867_23590	Contig2396_19779_19550	(TC) ₇	230	GCAACCAGCTGGATATAGGG	CCAAATCAAGGAGTCGACAA
scaffold1282_47454	Contig2396_51300_51598	(TG) ₁₁	299	CGAATTCCTTGTGATGAAATCT	GTAGGCCGAGCCGAGTTT
scaffold983_152568	Contig240_7943_7643	(GT) ₉	301	ATTGCCTCTTCCACATGCTT	GAATTGCGCCCTAATGGTTCA
scaffold1726_161386	Contig2405_111868_111711 ²	(GA) ₈	148	CGCATTGGTAAATATTGTCTGC	GTCTCGGGACCATGTTTGAT
scaffold4862_4143	Contig24144_4877_4585	(CAC) ₇	293	TCGTTCCACTAATACCGCAA	GGACCAATGTATTATTGCAAACC
scaffold1991_70118	Contig242_74263_74496	(AT) ₈	234	TTGTACCTAGATTGGTGCG	AACGAATCGAGCAGTTGAGC
scaffold8641_45256	Contig247_128564_128275	(TC) ₉	290	CGCAATCCTAAATCCTGAGC	GCATATAACCATTTCATGGAGG
scaffold1064_141132	Contig2477_170904_171091	(CT) ₉	188	TCTTCGATATTGCCTTGGTTG	CTACTCCGATTCCCAAAGGA
scaffold73_155413	Contig24839_29286_29413	(CAT) ₇	128	ACCAAGCTGCCTAACTGCAT	TCCAATAATTACTTTATGTGCAATTT
scaffold2364_20329	Contig2505_98759_98918	(AAT) ₈	160	TAACACCACAGTCCGACGAG	CCTGTGGAAGTGTGGATCA
scaffold2480_111153	Contig2506_100235_100527	(AG) ₈	293	TCGTAAATTCTGCGAAGAACAC	TGATCAAATGTTTGGGCCTT
scaffold4791_33852	Contig2507_152827_152637	(CCA) ₁₀	191	CATAAACACTCTTCATTTACCTCA	TTGTTTGCTCAAATTGCTCCT
scaffold257_119230	Contig251_147332_147647	(GT) ₇	316	TCTTTGTTGCTCCGTGAGTC	CATTGGAATCAATGTTGAAATTA
scaffold257_281726	Contig251_289061_289373	(TC) ₁₂	313	CGATGTTTCATGAGCCTGGTA	AGGAGCTTCGCCATATTGAA
scaffold520_238992	Contig2516_59232_59464	(TGG) ₇	233	GGGTTGATCACCATGCATT	GGCTTTCCTATGAACTTTCGG
scaffold1311_163296	Contig2541_221782_222085	(CA) ₁₃	304	TGTCCGCAACAAATACTGCT	CCTTTGGACAGCCTGATCTT
scaffold10129_4463	Contig2541_36104_35832	(ATA) ₁₀	273	CATAAACATTCTTGACGAAACCA	CAATCACCCAATTAGCCTGC

scaffold393_56099	Contig2546_53575_53814	(TG) ₇	240	AGAAATCTTCAACTGTCTTCGGA	TTATGAGCACATCAATGCCC
scaffold2947_8600	Contig2561_9418_9666	(AT) ₇	249	ACCCGATATGTTATTCGGCA	CAGCCTCCCATCTCTACCTG
scaffold6239_55796	Contig2564_131282_130980	(TGG) ₈	303	GCGACGGCATTCTTATGTT	ATTTGGATGATCAGGATCGC
scaffold1665_36850	Contig2568_37337_37579	(AT) ₁₁	243	ACACTGACCACTTGAGTGCC	GTTGAGGCTTCTTTAGTTACAAAT
scaffold1_410692	Contig2578_36418_36630	(ACC) ₇	213	GGGATCCCACTTCAATTCCT	GCATTCCTTCTCCTCATCCA
scaffold3529_9090	Contig258_148090_148230	(GAA) ₈	141	AAACCACAAACAGAACCGCT	CCACGCCTCATCATTCACTA
scaffold995_39209	Contig2584_137221_137416	(AT) ₁₀	196	CCAAAGGATCAATAAGAAGACTCC	CCGTGCCACGTTGAAATTA
scaffold403_106	Contig2606_88277_88559	(AG) ₇	283	GTGATTATCTTCCCTTGC GG	TTTATTTGCTGGCCCAATTT
scaffold1362_15106	Contig2607_14900_15181	(TA) ₉	282	GGTGGATCATAATCTATGGCTTC	TTGACTTTGGCACATGAGGT
scaffold1270_169264	Contig26148_9769_9478	(GT) ₉	292	CAAAATCCCTTCCAACCCCTT	AATCTTGATCGGACACTGCC
scaffold1935_26093	Contig2621_26525_26828	(AG) ₇	304	CCACGATCTTTCGAGCATTT	ATTGGTTGTTTGTGCTGGT
scaffold1876_16546	Contig2623_171328_171163	(GAA) ₇	166	GAAAGCTTTGCCAACTCCTG	CTGCCAGTTGAATTGATCAGAA
scaffold1854_76099	Contig2633_98476_98689	(AT) ₈	214	CGCAGTAGCAGTTTACCTCG	CGCTATAGACAATCAACGTGC
scaffold2857_36609	Contig2635_35043_35358	(TTC) ₇	316	TGCTTGGTGAGATCAATTC	ATCCCACCAAGCCTCCTTAT
scaffold3596_14363	Contig26633_2328_2538	(GGT) ₇	211	GCCTCAACTATGTTACCGGG	CACCTGCTAATCGGTGGAGT
scaffold1697_59350	Contig2667_66608_66796 ¹	(TC) ₉	190	GTCCGAACCTTCCATTTGC	CGAATGTCACTGACTCCACA
scaffold4786_83945	Contig2668_55311_55553	(TA) ₈	243	CCTTAAAGTTCTGTGCAGCATC	CAATGCAACATGGTGTTAATG
scaffold280_276461	Contig2679_141554_141833 ¹	(AG) ₁₁	290	AAACCTGTATGTGGTCGTCG	TTTGAGGAGAAATCGGAAGAT
scaffold2391_58136	Contig2694_42300_42460	(TCA) ₈	161	TGGAGAGCAAGTCACGAACA	TCTTTACCTCTTCTCCACAGC
scaffold338_90034	Contig27_25207_25404	(TC) ₇	198	GGTTAATAAATGCGACGGCA	ACCAACTTGCTACTAGTTATTGTCTCA
scaffold2272_10494	Contig27_286755_287018	(GT) ₁₀	264	TGAGAAGTCCGTTGTGACAAAT	GGAGGAATTAATACACTAGTTTGCG
scaffold2783_32749	Contig2737_66394_66276	(TG) ₈	119	CCACTGGTTCTCCATTACAT	GGAAAGGCTGTAGCATGAGC
scaffold2539_90392	Contig2743_3929_4221	(CA) ₇	293	TGTGGTCTTTGACTTGTGCAT	TTTCATCACTGTATTTCCATTCAAG
scaffold1431_61445	Contig2776_94267_94080	(AC) ₇	188	CGAGATGGGATAATCCACTTTG	ATTGCTGAATGGTGTGGTG
scaffold94_96448	Contig278_18842_19103	(GA) ₈	262	GCATATGGATTGTGCTTGCT	TCTTGTTGATTGCAATTGGTTT
scaffold6392_1388	Contig2780_17420_17228	(CAC) ₇	193	AAGTCCCATTCTCAATAAATTCTG	AAACTATCAACAAGCTAAAGGAAA
scaffold4227_6965	Contig2783_56422_56209	(CAC) ₇	214	AGCCGATCAATGAGCTTGAA	CGACTGCTCGATGTTGTCAT
scaffold686_115428	Contig2785_102733_102847	(AG) ₉	115	GGTAATTGGGCACGATCAAG	TATTAAGCTGACGGGCCAT
scaffold4058_19707	Contig2786_44725_44920	(GC) ₈	196	CCCTCAAGGGCATTTAAACA	AAAGTAACCGAGGTGGGACC
scaffold3807_76325	Contig2792_10481_10310	(AT) ₁₀	172	GCAGAGCTTCTCAACTGATGC	TAGAGATGTTCTCAACATGATATAAA
scaffold3292_4686	Contig2795_52506_52739	(GA) ₁₀	234	TGCAAGTGTAGAGAATGCTTTG	AAGAAGCATGCCAGCAATTT
scaffold3506_43911	Contig2803_28799_28964	(TA) ₇	166	TGGCAAACCTAACCCTCACTC	TGCTTGAATAATGGGTTTCTTTG
scaffold671_71684	Contig2833_57184_56994	(TC) ₉	191	GCAACTCAACTTGCAAAATCC	TGGATCAAGCATAAGACGCA
scaffold1119_94519	Contig2848_51040_51339	(TA) ₁₀	300	GTAATTTGTTGCAGCCGTGTT	GGAAGTCATATCAGGTAGAATCTCG

scaffold3714_28271	Contig286_124236_124043	(CT) ₉	194	ACCGAAACTCCGACTTGCTA	CAGAAAGCACCAAACGATCA
scaffold470_58362	Contig286_255340_255502	(TTA) ₈	163	CAAGCAATGTGCAATCATCA	TGCAAAACAGGTTATTCTACTGC
scaffold1554_190538	Contig2869_162477_162666	(CT) ₁₂	190	AAAGTTGATAATATTGCACCAAGA	TTCTTGATTTGTTGACTCTTTATCG
scaffold1094_133410	Contig2870_107932_108200	(TA) ₁₂	269	AAACAGACCAATAATAAAGGACCA	TTACGAGGCATTGACGTGTG
scaffold1094_27330	Contig2870_14588_14810	(AG) ₁₁	223	TTTGACCTTGCCTCAAATTACT	TAGTCGCCAAATTCAGGCTC
scaffold346_43795	Contig2870_199990_199751	(AAT) ₇	240	CCCTTCAAATTTGTGGATGTG	AATCAGCAATTCATAAGAGCTACCC
scaffold21_146188	Contig2891_64399_64562 ¹	(GA) ₁₃	165	GGGACACTTATAGAGTGAAATTTGG	TCTATTGGGCCATACGTCTCTT
scaffold301_80127	Contig2893_24569_24708	(CTTT) ₇	140	CATGTAATCTGAAGCACGCA	TCTCAATGTGGTCCAGAAACC
scaffold1060_232592	Contig2928_63062_62878	(TTA) ₇	185	GGTCGGTTCAAGTTGGATTT	GCATGGTGCTGTAGATCGTG
scaffold3647_6331	Contig2951_62401_62212	(AT) ₁₀	190	TTCATCTTCACATGTTGAACCG	GAGCATAAGTTGATACAAGGACTCAG
scaffold17_229684	Contig2972_46457_46262 ¹	(TG) ₈	196	GGTGGAATACAATTTAACAATAGAAA	TGTTTGCTTTTCAGTACCCGTTT
scaffold4547_7487	Contig2973_114859_115166	(CT) ₈	308	CTGGTCATTAAAGTCCGACTG	GCAAGAAGCACATGGTTCAA
scaffold15869_2040	Contig2996_1295_1039	(AC) ₈	257	CCTACCGATGATGGTTGATG	TTTGTCTCATACCTTGGTCAAGAA
scaffold7848_3021	Contig300_156451_156314	(AT) ₈	138	TCCGCAAGTGCTAAGTACCC	CCTGGGATTCATTTCTCCCT
scaffold38_85294	Contig3003_97176_96916	(GA) ₇	261	GTTCTCACATCCTTTCCCGA	TCCCTCGGTAACCACTTCAC
scaffold988_23227	Contig3020_75529_75335 ¹	(CA) ₁₀	193	GGGAAGATGAAGCACAACAA	AAATTCAAGGCCACACTGCT
scaffold183_34559	Contig3024_24640_24453	(GA) ₇	188	TGCTGGACTTGAGGAGATGTT	GCCATTGATTAATGCCTCGT
scaffold612_119902	Contig3035_148611_148911	(TC) ₈	301	CGCGACCTTGACTATCAACA	TGCCTAGTTTCACATCACTGC
scaffold2582_164694	Contig3049_4352_4072 ¹	(TA) ₉	271	CCCGTCTTCTGACAAGGTGA	CTGAGCCGGACAGAATTGTT
scaffold8870_1376	Contig3050_42167_42036	(TG) ₈	132	TGAAATGCAAGGCTGAGACA	CCTTCGGCGACTAATCCTTA
scaffold1834_14902	Contig3060_40874_41071	(AT) ₇	198	AATGGTGAAAGTTTAGCAAACAG	ACTATGCCTTGTGGCACCAT
scaffold2690_39877	Contig3086_43836_44047	(ATA) ₈	212	CAGTTGTTTGTTGCCGATGT	TGATATTTAAGGGAGCACACCA
scaffold429_152030	Contig310_169390_169646	(TC) ₈	257	TCTAAATCAAATAGGCCCTCAAA	ATATGCAGCCGCGTTAAGTT
scaffold1858_88773	Contig3101_30079_29789	(GT) ₁₃	291	TTCAATCATGCATAGCAGCC	ATGTGCACCAAATGTGGTCTT
scaffold828_99224	Contig3108_24618_24325	(TA) ₁₁	294	TCGTAGTAACAATTGGATGGG	CGCGTAACCTTCAGTGAGGA
scaffold5257_57281	Contig311_66705_66904	(CT) ₈	200	CATTTCTGAATCAGGCAGCA	AAGAACATAAATACGGCAATGAAT
scaffold195_184829	Contig3121_2865_2678	(AG) ₈	188	CGAGGGATGCTCTATCATTCA	AATCTCCAAATGCAGTCCCT
scaffold2093_72172	Contig3127_30315_30450	(TG) ₈	136	CGTGCCCTTCTAGACCTAGCC	AGGTACGACCCATATTGCCA
scaffold2093_51386	Contig3127_7991_8239	(AT) ₉	249	AATTCGACAGATTGGTGGC	CTGGTCTATGATTGCTTGGTT
scaffold2665_158219	Contig315_65194_65055	(TC) ₁₃	140	TCTGCGAGTCTTGTGCCTTA	CCTTGGCTCCTCCATTATGA
scaffold6900_16705	Contig315_89709_90000	(AT) ₁₀	292	CCACGTTATAACCCGTGCTG	TTACTTGTGGCGTACAATAATACAA
scaffold453_107274	Contig3161_55312_55001	(TA) ₇	312	GGGAACTGTAATCTTCTTGTTC	GCATCTAGCTTTACCCAAATGAC
scaffold2375_123174	Contig317_17295_17120	(GT) ₈	176	CGGCATCTTCTAATTCTCCTC	AGCGTAGAGTAAACACGAAGTTAAA
scaffold1744_58071	Contig3188_30708_30478	(TC) ₇	231	CGGCTTAGTGGTGGTTGTTT	TGATCAGGATGCGTCTCATT

scaffold1744_35928	Contig3188_55885_55715	(GA) ₉	171	TCAATTTAAAGGGAAGCAACC	TTCGGAAATCTTTGATTCTCTTATG
scaffold1868_60442	Contig319_190045_189896	(AT) ₈	150	AATGACTTCCCAGCATCCAA	GATCAGTGCACATGAATCCAG
scaffold1209_32108	Contig3194_70445_70763	(AAG) ₇	319	GCGCTTTCTTCTCTGTATGAAC	GCCTCTTCAATCACACCACA
scaffold2820_33989	Contig328_5357_5219	(ACAT) ₇	139	GGAGGAGGTAACAGAGCCAG	CGCTATGCATCAACATCTCC
scaffold638_208507	Contig3283_12300_12065	(AG) ₈	236	GCACTGATTCTGTGAGTCCCT	CTCTATTGTCATCCCGCCAT
scaffold638_84814	Contig3283_128938_128696	(AC) ₇	243	CGAGTTCTGTTTACCTATTCTCTC	AGTTCCTCAGTCTCAGGGCA
scaffold5708_16752	Contig3287_34034_34231	(AG) ₁₀	198	CTGGATTAAAGGCTCCATCTG	TCACCTACTCGTTACCTCAATG
scaffold1599_35097	Contig3289_5759_6070	(AT) ₉	312	TGGATCCTATCAGCATGAATGT	GTTCCCGACTGATCACCCT
scaffold4222_16975	Contig329_12045_12202	(AC) ₈	158	TACACCAGGCATATGAGGGC	AAAGATGCAGGCGAAATAGG
scaffold72_70725	Contig3299_13703_13862	(TA) ₈	160	CCTGCTCTATTTGTGTTGTCTCTT	GCATACGTCATTAGAGCGTGAG
scaffold2034_210427	Contig3375_82131_82433	(TAA) ₁₀	303	CAGCCCATGGTTTCAACTACT	GTTTATGCTCTAGCAAGAACTTGT
scaffold9754_3399	Contig3375_89224_89506 ²	(CT) ₁₁	283	ACGAGAGTTGAACCAATCG	GGGTTCTCGTTACAGCCTTG
scaffold9367_6065	Contig33850_6505_6706	(TG) ₇	202	TTTGTGTTGTTTAAACATATTCCTT	GGGTCAATTCTGCAATAAGATG
scaffold1213_129712	Contig3390_47236_47357	(AT) ₈	122	CAATGCAGTTGAATATTTGTATCG	ATGATGACGCTTGGTGGATT
scaffold1392_65134	Contig3431_7576_7720	(AT) ₁₂	145	CGAAATTTAAGTTGGAAGCCA	CAGTCAAATGCAAGAATAAAGGC
scaffold584_129711	Contig3431_84537_84241	(GA) ₉	297	GGACAAACCGCTCTATTTGC	GGTGAATTCATTACTGGTGGG
scaffold31473_272	Contig34385_540_646	(TA) ₇	107	CAAATTTAATCTGTCGAACTATTCAT	GACTGACAAGGCATGTTCCA
scaffold3703_47644	Contig344_81629_81375	(AG) ₁₄	255	GGAGCAGTACCATATGCGCT	AGGAAGATCTAACGCTGCTTG
scaffold517_85339	Contig3449_88254_88055	(AG) ₈	200	ATACGAAAGGTGGCGACG	AAATGAGGGTGAAACGGG
scaffold1462_143845	Contig3460_102662_102812	(TC) ₇	151	GTGTCTCGGCAACCTCTTGT	CATGTTGCACCACCTCATCT
scaffold3497_20320	Contig3480_24353_24499	(AT) ₉	147	TACGCAATACCGCTGGAAGT	CATCCTGAAAGAATAATAAGGGTG
scaffold1803_111934	Contig3480_48656_48509	(GA) ₁₀	148	AAATCACAAGCCGCAATAGA	TGCCAGACTTTCAGTGATGG
scaffold2847_175691	Contig35_16776_16591	(GGTGG) ₇	186	GGTCACATGGGATTACATTCG	GAAACGAGTTGTCGTTGGTACA
scaffold63_12909	Contig3502_11925_12084	(TC) ₁₀	160	GGAATGTTGATAAAGCCACA	CACGATCACCAATCAAACCTGA
scaffold733_87978	Contig3512_70723_70533	(CA) ₁₁	191	CAATGCACGACTGCGATCT	TGGTTTGCTTGGTAGGAGTT
scaffold190_158771	Contig352_102804_102654	(GT) ₁₀	151	TGAAGGCTTTCTAAGCAGGAG	TGATAGAACTCATCCAACGGC
scaffold1916_43223	Contig352_277551_277870	(TC) ₁₃	320	TGGGCCGTAATTTGAGAAG	CCATAATCGTGATCAAACGG
scaffold8912_7343	Contig3528_23180_23014	(GA) ₉	167	CAACGAAGAAGCAACTGTGC	TTCTTCCAGTCCCACAAACC
scaffold902_59731	Contig353_105482_105333	(TC) ₁₀	150	TGCTCACTTCATACCATGCAA	AAGCAATTAGGCTCTTAAAGCAA
scaffold333_589732	Contig3542_31784_31495	(AT) ₁₁	290	CAAGTGCAGATGCTCGAATG	ATCCTATGAGATTTCCCTTCTGTTT
scaffold4881_3122	Contig3547_65361_65502	(AG) ₉	142	GCCGGAATACATGCTACTGT	TGGATCTTTCCCAATCATCA
scaffold251_206158	Contig355_106154_105963	(TA) ₁₃	192	CAAGTAACACGGTAAAGTTGATGA	CCATACCTTCATATAGAAGACGACA
scaffold725_23324	Contig356_159237_159402 ¹	(AT) ₈	166	TCGTGTGATTTGAGTGGACTG	ATGGTGTACACGGGATGCTT
scaffold1825_37401	Contig3561_19594_19847	(AG) ₈	254	GCCAGAAGTTCAATCTCTACCTATG	TCAACCTAAAGAATCTGGCTACTG

scaffold2193_24304	Contig3561_95076_95386	(CT) ₁₀	311	TGCTCTCCTTCTCCTGTTTC	AGATCCATCCGAAGTGGTGT
scaffold4070_6403	Contig357_65525_65368	(TA) ₈	158	GAACATGCCCAATTCATCC	TTTGACATGAATTGGGAGGAC
scaffold3265_115815	Contig3574_24363_24552	(TTA) ₁₀	190	GCCTCAGGAACTAACACTACTCA	TGCCTTCTCCTCCATACGAT
scaffold5114_18136	Contig36_254646_254407	(TC) ₉	240	GGTCATTCTATTACACATTCCTCA	CTAAGTTGTTAGGAGATGGCAGG
scaffold2192_49666	Contig36_304549_304405	(ATT) ₉	145	GACTGCTAACTAAAGAATCCATGC	TCTTGAGCTTCTGAACCTTTGA
scaffold1158_133769	Contig3617_90431_90552	(GA) ₉	122	TTATTCAGCATGGATATAGTTGATTT	GGGAGAAATTTCACTACACAGTTT
scaffold3288_36337	Contig362_103577_103822	(TC) ₁₀	246	TTCCACCCACGTTAAGTAATTC	GGCTATTCTTAGAAGTGTTAGCCA
scaffold1691_75271	Contig364_284557_284416 ²	(TTA) ₁₇	157	GTAAGATGCAAATTAATGAATACTCG	CTTGATAACCACAAGTTGGC
scaffold1172_1407	Contig365_44922_44732	(GA) ₁₂	191	AACTTGAGGTAAGAGAATGACTTGCG	CCAGATTTAAGAGCAATTTCTTCC
scaffold64_66527	Contig3651_44441_44287	(CT) ₁₀	155	CAATGGTCAGATCCCAGTCA	CCTAATCCTTCTAGCGAACCG
scaffold203_407918	Contig3666_7698_7836	(TC) ₈	139	GGCTTTCTTTGAATGATTTCTCTT	CAAGCATCGAGAAATGCATA
scaffold31039_1	Contig36679_1625_1505	(CT) ₉	121	CAATCTTGCTTTGTTTGGTATTTG	GGAAGACAACATTGGCCC
scaffold943_67867	Contig3670_10994_10705	(CT) ₁₅	290	CACTTCAATGTCAGCATTCCTCA	CGAAAGTTCACCCAGTCAAAT
scaffold119_129650	Contig3676_29006_29195	(CCA) ₈	190	ATTCTGGCTGCCTCATTCAT	CAACAGCACTTGCACTTCTGA
scaffold366_105796	Contig3685_92712_92482	(AT) ₁₀	231	GGGAACGATCAATACAAGATGC	AAATTAGTCCCTGGACGTTTATA
scaffold3281_28519	Contig369_77129_77278	(CT) ₈	150	GGTAAGTTGCAGCCGATGAT	CGGTTGGTTTGAGTAGCTGG
scaffold775_20244	Contig3708_84936_84641	(AAT) ₁₃	296	AAATCATATCTTAATGTGCACAGGTT	CCAGTGTAAGTGAATACCATTTGC
scaffold2803_70432	Contig3724_37789_37940	(GA) ₈	152	GAACAAATCCAGCCGTTACC	GATACACCGACGGAACGTG
scaffold6_107724	Contig3769_41073_40954	(GA) ₁₁	120	GAAGAATGGATCTGCACGGT	ATCCATGGTTCATCATGTGC
scaffold755_138063	Contig3794_61177_60941	(TA) ₁₀	237	TGGTCCCAAAATTTAGTTGGCT	CGACTACCGTAGGATTTCCA
scaffold1169_116348	Contig3800_28102_28298	(AG) ₁₂	197	CCAATGAATCTGTTACCTTCTTGA	CCAAGCTCTTTGACATCATCC
scaffold6088_2473	Contig3809_118941_119122	(CT) ₇	182	CTCAGCAATGAGAAGACCGA	TCTGGAGTAACTGGATCACCAA
scaffold2900_14208	Contig381_145793_145601	(TA) ₉	193	GGGTATTAATGGGACGAACC	GGGTTGAGTTCGATTGAGC
scaffold1856_79860	Contig383_57710_57981	(AT) ₈	272	CACTTTAGTGATTCGCCCCA	TTTGTGTTTCTCTTGGCATCT
scaffold68_190277	Contig3841_67393_67579	(GA) ₇	187	CCAACATTGAGTGATTGGAAG	ACTTGAACCCGGACCTTCTT
scaffold1000_53202	Contig3861_31038_30804	(CT) ₇	235	AGGGATTTGATGTGGATGGA	AACCCAAATAACAGCAAGCG
scaffold1000_43558	Contig3861_40909_40630	(GA) ₁₂	280	TGTGATTTGGAGTTTGGCTG	GTCGGACAGGCAAATCTTGT
scaffold1832_14465	Contig3899_16383_16576	(TC) ₁₀	194	CCTCCTTTCGTTAATTCTAGTCCA	TGTCAATGAGCAGGCAAAGA
scaffold85467_47	Contig3935_61941_61798	(CCACC) ₇	144	CATCGGTCACTTCACTTCCA	TTGTGAGATTTGGGTGGTTG
scaffold2615_12830	Contig3937_88043_88285	(GT) ₈	243	TTCTCAACAGCAACCAGGC	AATCATTTCCAGACATGCCC
scaffold2735_16402	Contig3945_32119_32309	(TG) ₈	191	GAATCCACTTGGAAATGTAAGG	CCCAAACATGCTCTAGCCTC
scaffold449_164362	Contig395_153187_153379	(TC) ₁₂	193	GGATGGAATTTGTTTCTTGGG	ATACCCACATCCACGTCACA
scaffold449_221192	Contig395_209430_209582	(TAG) ₇	153	GAACATGGTAGCTACGTGCG	AATCATCCCAAGTGCTTCA
scaffold2094_229914	Contig3960_10844_11117	(AG) ₁₃	274	TCCTGACATTGGATTTCTTC	CCATGCAGTGACCATCATA

scaffold3014_42518	Contig3964_18867_18695	(GA) ₁₀	173	TACAATGTCCTGTCTCGGCA	AATTGATCTTTCGGGCAATG
scaffold4179_34488	Contig3976_80529_80639	(GT) ₁₀	111	ATTTGTTGCACTCCTGGTCC	CAACTGACGCACTTATGGACA
scaffold3787_32905	Contig39775_15024_14819	(TG) ₁₀	206	CCAGGAGTACAACTTGTTGAAA	GGTTGGAGATGAATGGTTGA
scaffold4916_28306	Contig3981_77246_76991	(GA) ₉	256	TTTGGAATCTTGGATCAGCC	TCTTCCAAGTGAACCAACGAC
scaffold1235_88219	Contig3982_86165_86304	(TAT) ₇	140	ATTCAAAGGCTCGTGGAGTG	TTTACCACATTTAATCGCCC
scaffold2430_97925	Contig40_154348_154543 ¹	(GA) ₁₀	195	CAGAGATACCTTAACATTCTGCC	CTGCTTTGCTTTCGGATGAT
scaffold3530_10254	Contig4003_12699_12889	(TA) ₁₀	191	TCAAAGAAAGCGACCAAGAAA	ACCCACAGAACATTCCTAAG
scaffold5853_41518	Contig4006_41467_41656	(TA) ₁₁	190	TTGTCTCTCTCCAGAATCA	ACCACCTTATGAGGCCAATG
scaffold2049_31289	Contig403_1375_1222	(GA) ₁₀	154	TCTCTATCTAACAATGTAATCCCATCA	AAGCTCACAACCTGCCTCGTT
scaffold4296_51635	Contig4032_26441_26122	(CT) ₁₂	320	TCCCTACTAGCAATGGCTCC	TGGTAATTTCCGCAACAGTG
scaffold4222_3783	Contig40506_7131_6903	(AT) ₁₀	229	CATACGCTATATGCTCTCGATTG	TGTCCTATTGGCTGTTGATCC
scaffold6936_3513	Contig4054_64828_64519	(AT) ₈	310	GGTAAGGGCATCCTTCTGTTA	GCAAAGTCGACGGCTACC
scaffold1567_32963	Contig4102_14943_15258	(AC) ₇	316	GTCCTCCAACCTCCATTTGA	TTGTGAAGCACATAGAAATGAATG
scaffold3555_93726	Contig41184_11730_11439	(AG) ₇	292	GATTGAGCCTTGAAGTTGGG	GGTGGGACGGTCTTATATCC
scaffold3082_27586	Contig4128_31907_32093	(CTT) ₈	187	CATCCTCTGGATGAGCACAA	CAACAGACAGGCTGTGAAGC
scaffold3318_26919	Contig413_266805_267049 ²	(AC) ₁₇	243	TGAACTTCAATACGTTCTTGCAAA	AGGAAGGTCATCCAAGGCAT
scaffold1242_82782	Contig4133_123489_123597	(AG) ₈	109	GCCAACTCACCAGTACACCA	AAACAGCTGTCAACCATGC
scaffold3410_12194	Contig4133_33970_33824	(TC) ₈	147	GGTTTCTTGACCATATGCTTT	GCAAGTTGACATTCAAAGGG
scaffold2247_24860	Contig4137_25279_25419	(AG) ₇	141	TGTCAGCTACTCCTGCACAA	AGCATGGCCACTCCTATTCT
scaffold103_112265	Contig415_158351_158220	(TA) ₁₂	132	TTGATTCTTAAGGAAATCTGAATCC	TCTTCGTTTATCCGGCTTTG
scaffold103_100902	Contig415_169783_169544	(GA) ₈	240	CAAGACTTGAAGAGGATCTAATGC	TTCTTCCAATAAACTTTGGGC
scaffold635_106452	Contig418_265110_264889	(TA) ₁₅	160	ATTGAATTATCTACCACATTTCAAAG	AGGGTTAAGTTGTAACGCCC
scaffold1909_70690	Contig42_138327_138185	(TTC) ₈	143	TGAACTCCAGTGCTGTTGCT	CAAACCTGAGACATACAGCTCAACA
scaffold1989_92236	Contig42_64574_64393	AAG ₍₈₎	182	TGGTGGCTACTCAGCCAAG	CCCTAGTTGAAATGTGCCGT
scaffold692_60839	Contig4236_27256_27012	(CT) ₉	245	GAGTCCAACCACCGTTGAAT	GGTAACAAGCAAATGCAGAGC
scaffold39960_6	Contig42461_885_675	(TA) ₁₁	211	AGATGGAAATAATGGCTCCC	GCTATACCCTGTTTGAGCGG
scaffold632_221267	Contig4260_10603_10768	(ATA) ₈	166	CTGCGCCAATGGTATCAGAC	TCCAGTCACCAGTCTTGTC
scaffold758_59803	Contig4316_121671_121869	(GA) ₁₁	199	TCACAGTCTTTAGTTCACAGAGAAA	TTCATGGTTAACAAGTGGATATGT
scaffold119_80019	Contig4348_13495_13267	(TA) ₁₂	229	TCACGGATTGTTGAAGACG	GAATTTATTCTCTGCATCGTATTG
scaffold1067_79267	Contig43569_2511_2647	(AG) ₁₀	137	TCCTTAATTAATCAGAATAGCCCAA	TGCTAGGAAATTGAGGAGGAA
scaffold4146_44544	Contig4367_13023_13158	(TC) ₈	136	GCTGCAAGTTCATGTTGAG	GTAGTGCCCATGTTCCCT
scaffold123_197702	Contig4369_30507_30647	(TGG) ₈	141	TTGTCTTTGTTCTGTGTCGAAT	CCATCACACGTTACAGCTT
scaffold135_2678	Contig4371_4891_5081 ¹	(TA) ₈	190	TTCAGAATATTTGATTTCAATCGG	CGATATTTGACTTGTCGCTCA
scaffold3686_25786	Contig44_254170_254035	(TAT) ₈	136	TGTGATACTTTATCTTGATAAGACCGT	TTGTGTAGTTACGCCGTCCA

scaffold3022_17709	Contig440_84964_85234	(GA) ₇	271	TTAAGGGATCATCTTACTGTTCAAA	GATTTCCTCAGAAATTTGCAT
scaffold9824_3069	Contig4412_3230_3361	(TC) ₁₉	132	TGACAATCTTGCTTTGTTTGG	CCTATTGTGAAACCCGCAAT
scaffold1705_71653	Contig442_107088_107328	(AT) ₁₃	241	GCATTTATATCCGAATTGCC	GTGATGGTAGAGTGAAATTCCTCA
scaffold2645_114677	Contig4421_14382_14170	(CT) ₁₂	213	GGTGTGAATTCCACCTCTT	GGCCGGAATCAACAGAGTTA
scaffold3850_55030	Contig443_44585_44729	(TA) ₈	145	CGGATAAGCAATAACTAACAAGGAA	TTGATGATAATTAAGCTGACTCCA
scaffold736_220485	Contig4449_16814_16496	(AG) ₈	319	CCCGTCATCCATTTCAACTA	CGTGTCTCGTTGTTCTGTTT
scaffold1824_71415	Contig4462_61727_61547	(TA) ₁₂	181	ATTTACAGTTCGGCAGTCC	AACATTAAACATAGTAACACTGCAGACA
scaffold1917_4552	Contig448_36503_36722	(AG) ₇	220	TGAACTGCTCCTCGACTGAA	CAGTGGTACAACCTTGGCCT
scaffold6785_40196	Contig4493_30641_30357	(GGT) ₁₀	285	TCACCTTAGCATCGCAACACA	TACCACCAAGGAAGTGGAGG
scaffold6785_80093	Contig4493_8044_7905	(AG) ₁₁	140	AATGCATACTCCAGTTCCTTGT	ACCCTGAAGGTGACGAAGTG
scaffold747_89288	Contig450_163383_163692	(TC) ₁₂	310	CAATTCTATCAGGCATCAACACA	TCTTCCACATAATGGCCACA
scaffold1414_76197	Contig450_30829_30663	(AT) ₁₂	167	CCATATCGACTTGACAGAAGGA	TGAAACCAATGTGACCAACTT
scaffold2951_17131	Contig45104_17174_17457	(AC) ₉	284	TCATTTGCATAAGTTAGGACCG	CTTAGCGGGCTGGATATTG
scaffold16_416172	Contig452_192524_192821	(AG) ₇	298	TCAAGTATGACTAAAGGGAATTTGAT	CACTGGTTAGGTCGGTTAGGA
scaffold1460_4968	Contig4527_31021_30779	(TG) ₁₃	243	CATCTCACTGCCACAGCACT	TGATACACGGAGAAGAAGTGAA
scaffold909_172123	Contig4537_16254_16394	(AG) ₇	141	GGATATGGCATGCAGTGAGA	TTAAATTAATGGGCTTTCGGG
scaffold7794_40672	Contig4538_15545_15315	(TC) ₇	231	TGGCAACTGAACTCTAAGCC	CTCGTGTGCTCAGTTGACG
scaffold1244_29905	Contig4544_36812_36966	(TA) ₇	155	TCTCATGCCTCTCAATCTGTG	GCACAGGTGACATCAGTTGG
scaffold1547_44600	Contig458_27741_27569	(ATC) ₇	173	TTACCTTACATCAAGCAATCCA	CATGTTTGTACCACTTAAATCGTTG
scaffold1505_21935	Contig461_28849_29041	(ATT) ₇	193	AGATAGTGATGGGTGTTAAATTAGAGT	GCTAGAATCAATCTAAGATGGGCTA
scaffold2262_94714	Contig461_54895_55170	(ATT) ₁₀	276	GGTAGTGGCGGATTACTTCAA	TGGCCTGAGGATGTGGATA
scaffold951_191323	Contig4652_51938_51764	(TG) ₇	175	ACTGAAGCCTCTTGCCTTGA	GCATTACATAACATGTGGTTGGA
scaffold2797_62067	Contig4667_60869_61008	(ATT) ₇	140	AGGGTACCATCCACAGTTTCTC	TCATCTTCGAGGTATTGGCA
scaffold6142_13073	Contig468_119422_119259	(ATT) ₈	164	TGGATGCTTTGCTTTAGCCT	CCATGCTATTCGTGTAGTTGTGA
scaffold155_14519	Contig470_68703_68875	(CT) ₉	173	TGGACACAAGATTTCACTCG	CTGCTGAAACAATTGAGCATT
scaffold2114_88110	Contig4727_33247_33108	(GA) ₇	140	TCATGACCATTGTCTTTGCAC	TCCACTACCCAGAGTCAGGC
scaffold13360_3696	Contig473_1548_1844	(AC) ₈	297	GAGATAGGAAACCGCCACAA	GACGTTTAGCACCAACCAGC
scaffold4103_59368	Contig4738_19258_19142	(AG) ₂₁	260	GCAAGGGAAGTAGCAACGAC	TGTGACTCAAATAGGGCTCAGA
scaffold3568_11843	Contig4742_11832_12021	(ATT) ₉	190	AAATGCAATCAAGCACACTCT	AACTGGATCAGGTTGGTGGT
scaffold8521_11706	Contig47556_3131_3443	(CT) ₈	313	CGCATACATGCCATGCAAAT	CCAGTATGGGTATGCTAGGGAA
scaffold21742_1606	Contig48058_472_753	(AT) ₉	282	TGGCTATTGTGGCTGAATACAA	TGGAATTGAAATAACGAACCC
scaffold1932_113157	Contig4810_29495_29634	(TG) ₁₁	140	CTAAGTTGTTCCCTACCGTCG	GAGGGTTATCAATAGGAATGGAAA
scaffold20913_74	Contig482_106424_106243 ²	(AT) ₉	190	CTTCCATCCTGTCAATGCC	AGCCACAACACTGGTTTCCT
scaffold54868_1	Contig482_76777_77018	(ATA) ₁₄	242	CAGGTTATATTACTTCAGTTTATTGGG	GAATTCAGGTGAATGAAGTGGGA

scaffold4422_52526	Contig4838_29383_29253	(TG) ₁₀	131	CCATAGCCCATATTTCAATCAA	TGCTTGCAATGTTGTTGGC
scaffold2090_45808	Contig488_72614_72754	(GA) ₁₀	141	TGTGCGATTTCGATACAATTCA	TCCCTCTTACAAAGCCTCCT
scaffold1957_54008	Contig491_347278_346984	(CT) ₈	295	TGATCTGAATCCAAGTCTGAGGA	CACCTCATTAGCTGATATGTAACCA
scaffold8222_4002	Contig4941_19036_19226	(TC) ₁₁	191	GCAGAAACCTGAAGAGCCAG	CAGTCCATAACCAATTGCCC
scaffold1378_99507	Contig4976_850_1160	(TC) ₈	311	GCATCTGCAAAGTAGGCACA	TCGGGAACCAAGGTAAGTTT
scaffold10278_43824	Contig502_136114_135886	(ATT) ₈	229	GTGGAATTAGGATTCTCTGGAA	GCCTAGCAAACAGCTCCCTA
scaffold1522_46586	Contig5029_75633_75494	(CTT) ₇	140	ATGGAGTGCTTGCCAAGTG	GATATCAACCAAGAAGCAGCC
scaffold9_242007	Contig503_109727_109560	(TC) ₉	168	TGCCAATCTACCTTTTCATCA	CGTTCTCGGCGAAATAGAAC
scaffold3708_99193	Contig504_2737_3003	(AT) ₈	267	ATCTTCCGGGAGTGTTGAGA	ACGACCTTAAACGGATACGC
scaffold7586_9695	Contig5045_17888_17715	(AC) ₉	174	CATGACTGGTTATAATGTTGATGGA	TCTGTGTTTGTCTTTCTAGGAACTG
scaffold5278_14412	Contig50518_15111_15252 ¹	(CT) ₁₅	142	GGGAATCAGTTAGCATTGTTGGG	GAAACTTTAACCTTGTCGCA
scaffold476_52408	Contig507_25678_25535	(AAC) ₇	144	GCTAATAAAGCAGATCCCTTGC	ACGAAGATGGCAATATAAGGATG
scaffold924_60022	Contig5084_2478_2704	(CA) ₁₂	227	GCTGTGATCACCCATTCTTG	GGGTGATGAATACAACCTCTCA
scaffold6638_23107	Contig5086_11083_10798	(TA) ₇	292	TATTCCGGGATGTTTCCAGT	AATGCCAGCACTATAGAATTAGGT
scaffold1622_103581	Contig5102_75169_75461	(GA) ₇	293	GATAAGGCATCGGAACTGC	AATAATGCACCCACGAAGGA
scaffold55_161645	Contig513_253801_253612	(CTT) ₇	190	GGAATCAACTTCGTAGACTTATAAAGA	TTAACCAACTGTAACCTCTTCTGTTT
scaffold333_110552	Contig5149_55662_55851	(TA) ₉	190	TCACACCTCACTAACAACCACC	GTCTCAAAGCAAGAATTCCTCA
scaffold4184_7550	Contig51777_7710_7894	(TG) ₈	185	ACCTTGTCACCTGAACCAG	TCACAGAAGTATGCCTTTCCC
scaffold102_78683	Contig5194_81952_82170 ²	(TTA) ₉	239	ACAAGGAGATCAATGGCTGC	AAATTTGGGTGGCAACATAG
scaffold675_45902	Contig51943_6128_6300	(TC) ₉	173	TGAATTGATAATACAAATATCCAAAGG	TGGAAGATGAGTATGGTGGC
scaffold1706_23240	Contig5206_55037_54896	(AT) ₈	142	GGTAACGTATCTACAATTCCCGA	CATAAGAGGTAATAGCAATGATCTAGG
scaffold41062_544	Contig52187_3077_2917 ²	(AG) ₉	165	TCATTAATAACCACAGTCACGG	CTCGAGAGCGTGTGAATGAA
scaffold3639_35792	Contig5231_46268_46078	(GT) ₈	191	TTTGCAGTTCCAGAGATAGGC	GCATTTCTGTGATTAATTGGCA
scaffold1568_47698	Contig525_236033_235884	(TC) ₈	150	GGTTCTACGTACAATGTATCACACG	CAAATGAGGCACATCCCAGT
scaffold5856_51165	Contig5307_37536_37811	(AG) ₈	276	CGTGTTCTTTCTGCTTTCCGG	TTCCCACTTCATTATACTCATCCA
scaffold497_60320	Contig5308_65828_66003 ¹	(TC) ₂₂	178	CTCGAGGCAACCAACTCTTC	AAACAAGCAGCTGAGGAGC
scaffold5574_47088	Contig5324_54899_55109	(AAG) ₇	211	TTGATCCCACTACACAGG	TTCAATGGCTCAGTCTGTGG
scaffold2847_5678	Contig5329_29994_29742 ¹	(GA) ₉	252	ATCAATGGACAGGCAGAACC	GTTGCCAGGTAAGCATAGCA
scaffold1303_142574	Contig5333_30619_30430	(AT) ₈	190	AATTTGAGCATGAATTTAGTAACCA	TTTGTCCAGTGGCTTCGAT
scaffold3203_5060	Contig5344_5443_5718	(TTTA) ₉	276	GGATCTGTCTCTTTCCCGA	ATCCTTCTCTTGGGTGAGCA
scaffold1107_28884	Contig537_93599_93422	(AG) ₁₀	178	TCCCATCCATTTACAGCTTCTT	CCATCCCTTGCTTCTTCAAA
scaffold298_259104	Contig5385_139295_139433	(AC) ₁₀	139	TCAGCTTGCTGCTTGTAAG	CTTATTCGGATCCAGTTCGG
scaffold3906_47208	Contig5412_164597_164354	(ATT) ₇	244	AAATACAAGCCACGTTCTTCTC	TTCTAGGCCTGTCCTCAGGT
scaffold4050_45272	Contig5418_11372_11513	(TG) ₉	142	TTATTGCCGATGTCTGTGGA	CGGGAAGTTTCACCTCAGAT

scaffold6500_51092	Contig5423_58760_59017 ²	(GA) ₇	251	TTGAAAGTTCTATACATCTTCATCCC	GTTGCTTCTGTAGACTATAATCGCT
scaffold3600_43471	Contig546_96233_96032	(TA) ₉	202	CAAGATTCTTCACTTACTTGGCCT	GACTCAGTCAGATTATCCAGCA
scaffold5868_67623	Contig5479_12015_12154	(AG) ₈	140	TTGATTGTTCCGAAACCCCTT	GTGATCAATCATATGAACCTAATGC
scaffold911_81623	Contig549_120196_120068	(GT) ₉	129	GTCACGGACAAACTTCACCA	TGTTATATTGATTCAGGGCG
scaffold5365_71709	Contig5495_29308_29100 ¹	(TG) ₁₀	205	AGCCGGCAACTTGTTAGAAA	AAGAACTCTACACCTTTAACTGGCA
scaffold2346_23061	Contig55_200702_200530	(AAT) ₇	173	ATCTTTACGAGCCACGAGC	AGCAAAGAAATTGTCGCAGC
scaffold2452_79828	Contig550_217073_216826	(TA) ₉	248	GGGCTGTCGAACTAGGTGTG	TATCGGATGTGACCGACAGA
scaffold1100_24047	Contig550_362764_362575	(CT) ₁₀	190	TGATGTGATGGAAGCTAATTTCA	ACCCACCAAATCTACCAATCC
scaffold1953_274511	Contig553_28510_28799	(AG) ₁₀	290	ATCAACCTACCTCAGTCTGC	CATCTGTATATGCCTTCTCACTTCC
scaffold54_41642	Contig554_280047_279858	(TA) ₉	190	TTCAAATTCATTAGCGTCGG	CAATAAGCTCATTGAAGCAA
scaffold1367_76252	Contig5552_25958_25694	(AT) ₉	265	AATTTGAGCCACGACTTTGC	AGGCAGTTGACCAAACACACA
scaffold8486_36252	Contig5572_36503_36642	(GA) ₈	140	CAATTCACGTAGAAGAGCCC	CATGTTTAGTATGGAAGTTTCTGC
scaffold4063_36887	Contig558_117347_117093	(GGT) ₇	255	AGAGGGCACAGGTTCTCAAG	GGACAACAAGCATGACAGGA
scaffold73_269398	Contig5602_52051_51924	(TA) ₁₀	128	TCTCATTTGTCTAAAGTTGAGC	TTTCTTGAATGGGCTATAATGAA
scaffold1993_189256	Contig5623_30715_30512	(GGC) ₈	204	ACTCTGCATTGGAGTCCCAC	CAGAAATGCTGGCACAAATG
scaffold140_72667	Contig563_298650_298468	(AG) ₉	183	CCATTAATAAGGCAACAAGATTT	CGCTCTATTTGGCGTATTCC
scaffold2477_30315	Contig566_8639_8928	(TA) ₈	290	TGATTCTGACTGCTAGTAGTATTCTTG	GAATTTGCCTAAAGCTTCAGAGTG
scaffold2160_65945	Contig5660_47455_47616	(GA) ₁₂	162	CTATCTGCGCTGTGCAGTGT	ACTCACGCTTCGGTGTCTCT
scaffold2942_40343	Contig5661_62823_62962	(TA) ₁₁	140	TACACCACCTCTGAACGCAT	CCCGGGTATTTATTCTAAGTTGA
scaffold2849_6870	Contig5666_39437_39675	(GA) ₈	239	GGTGTGGTTACCGCTCTTA	GGGAGGCTGCTATTTTCATGT
scaffold5835_12582	Contig5667_23980_24096	(TAT) ₈	117	TGCCTGAGAACCAGTTAGTGC	GGGTGGTTCTTGGAAGCATT
scaffold26484_1089	Contig5718_44044_44333	(TAT) ₈	290	TGTAATCACGAGATAAGTTGCTCC	AACCAAACCATAGATGGACACA
scaffold1561_152002	Contig572_138267_138124	(AT) ₉	144	AGGCATGATGACCCAAGAG	TCTTTATCGACAACCTCGGTG
scaffold10410_38911	Contig5728_8341_8210	(GA) ₁₂	132	CGCATACATCCTCTCTCTGC	CGTAAGGCGGATTATTGGAG
scaffold10809_2778	Contig5748_109580_109480	(TA) ₈	101	ACATGCCTTCTCTTCGCC	TTCTAGGGCCTGCAACAAC
scaffold3691_85702	Contig576_129000_129160	(TA) ₇	161	TCAGAATTCTACACAAGAAGCCA	TGGCGATTCAAGAAGAGTAGG
scaffold859_47658	Contig578_44559_44811	(AT) ₉	253	TTGGAGTTGCAAGCTTCTTT	TTTCTCCATAAGAACTCTAAGCTTAC
scaffold859_99780	Contig578_94385_94580	(TAA) ₈	196	CAACACTCTCAGAATTAACGCA	CCAGGACGCCGTCTTAGAAT
scaffold12_270834	Contig579_206145_206436	(GA) ₁₂	292	AAAGATAGATTAAATGATATGCTGGG	AAGAAATTACGCTCACGCCT
scaffold586_42667	Contig5790_52419_52738	(TC) ₈	320	CAGCGTGGTAGAAATGTATGGA	GAGCGCATAGTTCCTAACCAA
scaffold6940_18826	Contig5791_40931_41051	(AT) ₁₀	121	GCTAAATCGCACGACACTTG	CCATGCGCTTTACAAACCATA
scaffold362_44001	Contig58_153912_153725	(GA) ₈	188	AAGGACATAGGAGGTATAAGAACTGGT	GTGGCAGGTAGCCAGGTTT
scaffold428_41301	Contig5826_10018_10307	(TTA) ₇	290	GATGGATTTACATGGGAAGGG	TGTGGAATAACTCCTTTACCGA
scaffold428_68766	Contig5826_38505_38659	(AT) ₈	155	CATCCGGCTAATTTCCATCA	CTTTGGTCCACATACTCCGC

scaffold5107_19420	Contig583_19485_19662	(CT) ₁₁	178	CCATCCCAATTGACAAAATC	TCATTGCGCTTCGTACAGTG
scaffold6098_9312	Contig584_60987_60841	(GT) ₁₃	147	CCTTCTTCATGGCATTGCT	GATCGAGCTCATCGTCCTTC
scaffold73_245610	Contig5843_45879_46082	(AG) ₉	204	CGTTCAAACGAGTCACGCT	TCCCGTGTTCAGCTATTT
scaffold73_207803	Contig5843_9206_9498	(AG) ₁₀	293	ATAAACCCCTGCCATCTTCC	AGTCAGATGTCCAAATCCCG
scaffold138_290917	Contig5844_18371_18182	(AT) ₈	190	TTGTCATTCTCAGTAGCAATGAAG	GATGGCTCGATTAAACTTCAAA
scaffold300_232088	Contig5858_16664_16462	(AG) ₈	203	TTGTCCTAGCTCTGCCTGT	CAGAGATGGTGAAGTATTACCG
scaffold13027_4299	Contig5861_55720_55903	(TGG) ₈	184	ATGATGGATGGTGTCTTGTGA	ATTGGACCGTTACCAATGC
scaffold1024_56127	Contig5878_12528_12812	(TA) ₈	285	TCCAATAGTAGATGACAATATGACAA	ATTGGTTTACAGTCCCAGCC
scaffold1340_76597	Contig588_132246_132542	(CT) ₁₁	297	TTCATATGAACCAACCCATC	GTCAATTAATGCCACTGCC
scaffold4153_37452	Contig5885_21718_21930	(AG) ₈	213	TCAAACGGCCTATTCTGAGG	AAGCCTGAAAGAATGGCTGA
scaffold5960_32611	Contig591_30873_31028	(GA) ₈	156	GAGCTCGTATATTATAGAACAAAGGG	GATGTAAGCTTCTCATCCATGACT
scaffold524_101839	Contig5915_14680_14879	(CT) ₈	200	TTTCACAACATAACACCTTGATT	TTTCGAAGTGGGATTGATATT
scaffold524_118708	Contig5915_30703_30993	(CT) ₈	291	TCATCTCCGACTACGTACAA	TGGTAAACAGGAAACCTCAATGT
scaffold2765_16980	Contig5919_7884_7722	(AC) ₁₂	163	TAAGTTAAGGACCCAAAGGAAA	GGCTCTAAGCTCCCTTGACA
scaffold9705_5547	Contig5934_12052_11860	(AT) ₁₀	193	TCTTCAAGTTGTGGATTGATCTC	GCAACTTTGAATGTGAAAGCA
scaffold207_131753	Contig5941_55411_55568	(AT) ₉	158	AAAGGCAAGAGGTTTGCTATTTA	GGCGATTCTTGCAAGTTGA
scaffold1429_19864	Contig5974_72959_72813	(TC) ₇	147	CACCAATAGGAAATGTTGGGA	ACAGCTTAATTCCTGCTCGG
scaffold3849_26850	Contig5984_30262_30463 ¹	(CCT) ₁₀	202	CAATCTGGACTACTCTGGGTG	GGAAGAAGCAGTGCCAGAAA
scaffold92_104803	Contig6_464287_464426	(GA) ₇	140	ATTCCATTCACTAGGCCACC	AACTTGCTTGAAAGTCTAAGATAGC
scaffold3738_24976	Contig6004_42710_42950	(GA) ₉	241	GATCTTGTTAATGAGGTGGAACG	TAACAGCATTAACTACCAATCCA
scaffold6135_9211	Contig601_149523_149367	(AG) ₇	157	CCTGTCAACTTATATGTGCATCG	GATTGGCGCCAGACACTT
scaffold2552_84066	Contig6028_26567_26715	(AG) ₈	149	TGAAGCTAGCAGCATGTAGGA	CGTTTCATACGATGTACACAAACA
scaffold2755_83849	Contig6068_16692_16902	(TA) ₇	211	GGGAGTTAAGTGAATGAGCA	GTAGAGCTCGGTTCGGGAG
scaffold1837_118145	Contig608_143337_143131	(TC) ₁₄	207	CGGACTCTTCTAGTCTCCACG	TCCAACTAAATAAACCGGCCT
scaffold16_131981	Contig610_252819_252972	(GA) ₈	154	TGCCAATGCATCATTTGTTAAA	CCAAGAGTTGGTTTGAGGT
scaffold486_110716	Contig6115_70468_70215 ¹	(TA) ₇	254	GACACTGCAGCTCAATCAA	AATCTCCATCCCAAGCTCAC
scaffold1469_232395	Contig6165_114151_113912	(TAT) ₉	240	ATGGTTTCATACCACGCACC	TCTATCATGGGCATCAATCC
scaffold19035_956	Contig6191_2459_2328	(CCACC) ₇	132	CCATGTTGGAAGTAGTTGATTG	GACTGCAATACCTGAAATGTGAA
scaffold281_297286	Contig62_26633_26333	(TG) ₁₂	301	CAGTTGAAATGCAGCCATTG	ACACCACCCTACTGGTCAGC
scaffold265_113788	Contig622_30116_29911	(GC) ₈	206	AGATGAGCATCGCCATTGTT	CCAGATTCTAACCCTGTCCA
scaffold3095_55760	Contig6295_19460_19152	(AC) ₇	309	TGGATCATAGTGAACATGGGC	TCTATTAGAAGTATGACCAAGCGA
scaffold153_145921	Contig630_122460_122752	(GGT) ₇	293	TGAGCATGTTCAAGCAACATTA	CATGCCACCTCCACAACAT
scaffold6430_1677	Contig630_7049_6861	(GA) ₁₃	189	TCTGCTACCTTTAGTTCACTCAA	TGAATTTGCGCCTCAGTCT
scaffold4137_23970	Contig63036_11306_11509	(AG) ₁₈	204	TGCAATTCATTATACTCTACCCTACG	TGGGACTTCTATGAGGAGCAA

scaffold2029_167668	Contig631_271015_271170	(TC) ₇	156	GGAAGTCTCATCACAACCTCCC	GATCGGAAAGTGATGCGTTT
scaffold866_78585	Contig6333_67506_67790	(GA) ₈	285	TCAAGGACAACGCATTTCAG	AAATTGAATCTCTGGCGGAA
scaffold10121_7840	Contig6356_7907_8026	(GA) ₇	120	ACAATCTCACCAAGAAATGATTAGAA	TCCCTTTGTCTCCTTTGGAA
scaffold1091_115122	Contig636_38561_38744	(TC) ₁₇	184	GGTTTGGTATCGTGAGTGTCA	TGATGGTATGTGTTGGGAGA
scaffold588_220405	Contig641_101503_101229	(AG) ₇	275	GCACCACCTCAAACCATCTC	TGGCAGATTTTCATACACGGA
scaffold588_72381	Contig641_227069_226854	(TC) ₇	216	TCACGACGTTATTATTGATTATTGA	CGGCTGTATCTGATTGATTACTG
scaffold4734_16470	Contig6420_7359_7548	(TTA) ₇	190	TCGGAGATAGGAACATAATTAACAA	AAGCTGCTCAAGAAGATCCA
scaffold8684_2399	Contig644_198029_198227 ¹	(CT) ₈	290	TATCCACTCCATTCGGCTCATT	CTAATTAAGCACGTGACATGAGA
scaffold425_85064	Contig647_316352_316224	(TA) ₈	129	GACCATCGAGGGATCAATTT	CACCAAAATGTACAAGCAGCAA
scaffold425_48464	Contig647_352920_352797	(AT) ₇	124	GCAGCAATCCTTCTCCAGAC	TCCTGCTACAACTGAAAGCAA
scaffold669_109072	Contig65075_66546_66693	(TA) ₁₀	148	TGCTTCTATTCGGAGTGCTGT	TTCAACAAAGTCAAGATTCACGA
scaffold4824_16300	Contig65883_25650_25528 ²	(TC) ₉	140	CGTAGCTTGCACTTCAGCAC	ATTCTATCGCCGCCCATTA
scaffold5045_3287	Contig66_49060_48891	(ATA) ₉	170	CACGTGTTACCTAATCATCCA	GTGGCAGACAGAATTAGGGC
scaffold4199_167586	Contig6620_27775_27548	(AG) ₁₀	228	GCAATGAGTAGAATCTAGCAAGCA	TTGAAGGCAAAGAGGGAAGA
scaffold161_117870	Contig67_174139_174404	(AT) ₇	266	AGGACTGGTGTATGCCAAATC	AAACCCTATGTTTGTACAGTTTGAA
scaffold161_223535	Contig67_286317_286535 ¹	(TC) ₉	219	GCGTGAATTCAGTATCGACATC	AGTTCACTGAGTGAAGCCA
scaffold88574_1	Contig67045_3_142	(GA) ₇	140	TGGAATGGGAATGGATAAGC	AGGCAAGTCCAGCGCAAC
scaffold2534_64020	Contig6711_5568_5381	(AC) ₁₆	188	CATGCTTGTGAAATATCATAAATCTT	TTGTACGCTAGATGTTTGCTTCA
scaffold1030_78933	Contig674_247006_246816	(TC) ₉	191	TCAGCATGTGATTGATCTACCC	TAAACTGGGAAACGTGGCTA
scaffold3299_12970	Contig674_72681_72857	(CT) ₈	177	ACGTGGCACTTCATGATCC	GGAAATTTGAGGCTCACAGC
scaffold1864_42335	Contig6775_4915_5104	(AG) ₁₂	190	AAGTGCAACCAGAAGATCTTACCA	CAGCAATTCATTTAAGCTTTAGCTCC
scaffold6239_14113	Contig67771_13290_13539	(TA) ₉	250	CCCAACCATTATCTTCCACC	TCGGAGGAGTGATTGAGCTT
scaffold7485_1351	Contig679_76895_76745	(GA) ₈	151	GAGGACGGAGATGAAACTCG	CACTCTGTCTTGCTTGCTGC
scaffold7614_11834	Contig681_142664_142803	(AG) ₇	140	AGAGGAACCATATTTCCACCAC	TGATAACTTGGCATGATCTGG
scaffold1220_38443	Contig683_241864_242118	(GA) ₁₁	255	CCTAGATCTGCTGCAAACTATAACA	CCAGTTCTTCCAGACTTGCC
scaffold294_124857	Contig685_86937_87096	(GA) ₇	160	GAATAATGGGCTCGCAAGAA	GGTTATGCAATTGTTCTGCAAC
scaffold1016_39379	Contig689_259064_258795	(AG) ₁₀	270	AATCAAGAACGTGGGCTCC	CTACTTTACGGCACGGCTTC
scaffold5125_1059	Contig6920_6890_7193	(AG) ₇	304	AGTTTACATGCAACACATACGC	CAAACCTCTTCTCCTGCCACC
scaffold2572_112391	Contig6928_90421_90628	(AC) ₇	208	TCAACACCGTTAGTCAACAGG	TTTGCTTGACAAGATATGC
scaffold5718_26810	Contig6987_11586_11827	(AAT) ₇	242	CATGACTCGCCATGAGTTTC	GTGAGTTGTCCGTGGGAGTT
scaffold2904_41719	Contig7_233885_234165	(AT) ₁₁	281	TTTAAATAGTTTCCATGTGCTTCAA	TGTGGGCTCATTGATCCTT
scaffold1538_34585	Contig70_17422_17241	(AG) ₇	182	CATGTAATACGGGCAGCACA	CCACTGGGACATATCCTGCT
scaffold30_269845	Contig70_229547_229258	(AT) ₇	290	AAACCTTCTTTATCGCTGTAAGATA	ACTTACGCAAGGGCTCCAA
scaffold12369_998	Contig701_25705_25562	(GA) ₁₄	144	GGGTAGAGGGAGGCAGGT	CAGCCGATCTCGCACTTATT

scaffold1068_62316	Contig7018_133837_133642	(TC) ₁₅	196	TGCCATAAGAGGTGGTAGGAG	TGAATCGGGTATTATAGAATGCAA
scaffold8512_11324	Contig7032_11530_11707	(AT) ₉	178	TCGAAGACAAACACATTTACACA	CCATCTTGATAGAGAATTTGGG
scaffold3294_25371	Contig705_105582_105716	(GT) ₈	135	CCCTCGATCCATTTAACAGC	GGTTACCTTAGGAATGCTGGTCT
scaffold559_105806	Contig711_272569_272758	(AG) ₉	190	TCTTTATGCAAGAATTGTACCTACC	AAGAAATGCTAAAGGTTTGGGAG
scaffold383_46071	Contig7237_36932_37149	(TC) ₁₂	218	GTACAGCAACCGGCTTATCC	CTGCTTCCATTTCCACTTCC
scaffold77225_285	Contig72492_290_459	(AC) ₉	170	AATGCCAGAAACCTGCAGAC	TTCTGGAAGTTTGATTACGTT
scaffold3332_62168	Contig73001_869_1017 ²	(TC) ₇	180	CACATGTGACGCACCTTAATCA	ACGGCAACTTAGGGAATCA
scaffold154_365243	Contig7302_3643_3882	(TG) ₁₄	240	GAAGTGAGGGACACATTAAGGTCA	ATTCTAGAAATCTTTAAAGGCAATGG
scaffold4166_111298	Contig7325_6928_6789	(TA) ₁₃	140	TCTTAGCTAATTTCTTCTACCA	AAAGTAATGATCTCCTAAGCACCG
scaffold3241_19752	Contig7342_36524_36424	(AG) ₇	101	ACAATCCTGACACAGGCCAT	AGTGACAGATGTGGGAAGGG
scaffold1280_24456	Contig74_203690_203916	(TC) ₇	227	GCACAGATTAGCTTAGCTGGATT	TCGAATGCGATTTCTAACA
scaffold357_77157	Contig74148_30854_30662	(GA) ₇	193	GGCCCTCAAACAGAATGGT	CGTATGAAGAGTAGTGAGTACGG
scaffold93_138939	Contig750_42677_42972	(GA) ₇	296	AGGGCATAAGATCAAGCTGAA	CAAGATTTCAATCAGTGGACTTG
scaffold3304_78477	Contig754_78519_78709	(AT) ₉	191	TTCTACCCTTTGCTTTCGT	AACACATCAAGATAGACCCAGAA
scaffold1230_121054	Contig75683_3180_3456	(ATT) ₇	277	GCAACCCAAATGGAAGTTCT	AATCACAAACAGGCTCTGGG
scaffold6977_21867	Contig75691_16032_15754 ²	(AT) ₇	275	TAGCAGCCACTACAATGTTGA	CTTCGAGGCTCAGGTTTCAC
scaffold5842_18657	Contig757_21744_21902	(TA) ₁₁	159	CAAGTAGGGCAATGAAGATCG	TTGGTAGGTATAGCGCCCG
scaffold1365_132815	Contig760_17506_17347	(GA) ₈	160	ACCTGTTCTGACGTGGCATA	GTTCTAATTTGCCCGTTGA
scaffold1695_87074	Contig77_117616_117440	(CT) ₁₄	177	GGGTTTGGAGTAGATGGTAGGG	TGGATGACAAATGACAACGG
scaffold8625_4121	Contig77204_4155_4467	(AG) ₈	313	CTGTACATAGAACTCAGGAAACAAT	TTGGCTTTACAGATTGACATTCAT
scaffold1232_349428	Contig77337_9143_9338	(TC) ₁₀	196	ATGAAAGCAGTGGGTGTCG	GTGAAGGCAGGCTTGACTA
scaffold2598_14803	Contig7764_2022_1833	(TC) ₉	190	GCTGAAGGCCTTTCAAAGAA	AATCAATCATCAGTGAAACACGC
scaffold146_143814	Contig79_154365_154197	(TA) ₁₂	169	GGACAGATTATACTGTGCCTGAA	GGCTTGTAATCCGATCCTGA
scaffold4788_106044	Contig798_133854_134118	(AG) ₉	265	CGAAGGCTTAATCTTGAGCAG	CAAAGTCCAAACGTACGAACC
scaffold5063_38290	Contig7993_23181_23344	(TG) ₈	164	TGGTTGATGAACCTCAAGTTTCC	AGGCCATATAATTTGACGCG
scaffold4335_20587	Contig80_347291_347033	(AT) ₇	259	GTGAGCCATATGACCACGG	AACGTAGCCTATCACCTCGC
scaffold3905_30354	Contig8028_30727_30850	(TC) ₉	124	GGCCGTGCAATTGACTAGAG	CAATGAAGGTGACTTGGTTCA
scaffold3882_73250	Contig8029_8183_8372	(TTA) ₈	190	CCGATGGTAAATGATGGTCG	CCTGCTTTGGTCAACTCAAC
scaffold6329_9533	Contig80522_17239_17134	(AG) ₉	106	GGGAGATGAGGTGTAATAAATTAAGT	TCTTGAATTGGAAGAGGGCT
scaffold3460_40659	Contig807_49714_49533	(GA) ₁₁	182	TGGCTGTTACGGTGCTACAG	TGATTCCTGCTTTCCTCTT
scaffold4113_44992	Contig8097_39252_39512	(AG) ₈	261	TTATGTACATGCACGGCCAA	AACAGGAAGGTGCGTGAGAT
scaffold175_134242	Contig81_190923_191188	(AG) ₇	266	CGACACAATTGTCCAATCCA	ATTTCTGGATGATCGAAGG
scaffold250_11821	Contig82614_12862_12710	(TG) ₁₂	153	TGCGATCTTAGCAAAGTTCATT	CATCGGCCTGAAACACAAA
scaffold12793_4907	Contig8284_43183_43333	(AG) ₈	151	TTCAGGTTGCTTTGCACATT	ACATTGGCAAGCTGATCTTT

scaffold6307_28415	Contig8304_19176_19332	(GA) ₉	157	TCAGCCTCCATGCTCTTCTT	TGGGTATGTTGGAGGGAAA
scaffold1013_146112	Contig84_196846_196652	(TC) ₁₂	195	CACCTCCTTCATCCGTTTCGT	TGACTTCTTGCAAGCCGGT
scaffold1952_74256	Contig8472_980_848	(CA) ₇	133	AGTGGTTTGGTTCCGTTCAA	CGCACCCCTCAAAGTTTAGTTC
scaffold7946_10186	Contig8539_14245_14448 ¹	(GA) ₈	204	CTTTCCAGATCCACGTAGC	GGCAAGAATCGCTTGTCTTA
scaffold2216_78731	Contig854_85190_85394	(GCTCTT) ₈	205	TGAGGGATCTTCTAGCACTTACAA	TCGCTGATGGGAGTTATCTTCT
scaffold9528_6257	Contig8608_19702_19890	(GA) ₁₀	189	TTGAGGAAGAAAGAAGTGGGT	CATAGAAGCCCACTGCCACT
scaffold2938_68780	Contig864_98345_98208	(TG) ₈	138	GGGAAACCACTCTTTACCGA	TTTATGTATCCATGATCCATCTGA
scaffold1023_97033	Contig86573_855_654	(AG) ₁₀	202	GGCATATCTTATCTGAATTTGAGGA	CATGAGAATAGAAACACGGCA
scaffold5861_290	Contig86759_2247_2090	(TG) ₇	158	GCAAGTCTCTTCCACCCAT	GCTATGCATCGCATCATACTAAA
scaffold239_31603	Contig87_333704_333466	(AG) ₁₃	239	GTAGAGACGAATCGATGCCA	GGAGGTTCTCAGATGTTTGA
scaffold239_30365	Contig87_334888_334663	(AT) ₇	226	CCAAATTCTCCGTTTGGCTA	CGATCAACTCGCCAATTAAAG
scaffold5178_2408	Contig8715_2556_2820	(TTC) ₇	265	ACGCCAACAGTTTCAAAGGA	TGTGGTTGATGAACTGGAGC
scaffold196_372695	Contig879_112474_112599 ¹	(TC) ₈	126	ACGAATCTAGTCGTGCTCGG	GCGGTACACGAAATACACCC
scaffold406_6007	Contig8824_10635_10419	(AT) ₇	217	AGACCCAAGTTCAGCCTCAG	TCAAACCTTTCGATATGACTTCC
scaffold1843_16557	Contig8850_41173_40971	(AT) ₉	203	AGGTTGTGGGAGATAATACAAGTAA	TTGCACGATACATTCTCC
scaffold297_191750	Contig8881_19693_19904	(AT) ₁₆	212	CAGCAGAAGATTGGTTGTCTCA	TTAGGAGCCATGAATTTGGG
scaffold3065_62937	Contig8895_40303_40010	(CT) ₉	294	TTTGACATAACGTTGAATCCC	ACATGCAAATTGGAATCTGA
scaffold643_126335	Contig8896_2964_2750	(TA) ₁₀	215	TCAATTGTAAAGAGCCAACTTT	CAAGTTTCACCTCTATGTCTCAATG
scaffold8320_636	Contig8899_2905_3044	(GT) ₈	140	TGTACTCATGGGAACGGAGG	TTGAGAAGAGTTGAGCGAAGA
scaffold2661_58140	Contig89_298305_298110	(TA) ₇	196	TTTCAAGACGAGCAAGCAAG	AACAATTGCTGGAGAAGGG
scaffold1394_8929	Contig8902_137544_137396	(CT) ₁₂	149	ATCCTTCGCGTAATTGGAAA	ACGTCGACAGTCAGAAGCCT
scaffold1777_51808	Contig891_137531_137363	(CT) ₁₀	169	TTCTCGAGACTTAAACCCAAA	CGTCCTACAGACCCACCATT
scaffold4274_35660	Contig894_223251_223444	(CA) ₇	194	CCCTGTACTGGTTAATCCAATC	CAGAAGGAGGAATCACTTCTCAA
scaffold1054_137220	Contig8974_30719_30845	(AG) ₇	127	TGGAATGATCACATTTCTTCCA	TTTGAATTGACGTTATCTCCG
scaffold5449_29169	Contig8993_16694_16548	(GA) ₁₁	147	TTTGCCAGGCAGAGATAAACT	GCTGCAAGGTGTACGGTAGG
scaffold8353_8030	Contig904_166213_166039	(GT) ₈	175	TGAAGAACTGATGCAATAAGTATCAA	GTTGTTTCATGGTGCAGGTTG
scaffold892_95305	Contig906_159486_159658	(GA) ₈	173	GGCGACAATGTTGGAGAAT	TTGAGCACGTCTAATGCCTG
scaffold581_9089	Contig9078_6750_7011	(ATT) ₁₂	262	TTCAGTGATTGTGGATGGAA	TCACCATTACAGTCAAGATTTGC
scaffold3134_140889	Contig9088_15720_15912 ¹	(TA) ₈	193	CACCTGACGCCAACTATTCA	TCGTGTTCTGTAGCTTAGTTCG
scaffold1671_102209	Contig9096_75353_75515	(TA) ₁₁	163	TGACACCTGCAACATTGTAA	TGCTAGTGATGTCATTCTGAAA
scaffold4887_18725	Contig91_192767_192598	(TC) ₉	170	CGAGCACCGATTCAATTCT	GATTTGCGGGACGGTAACT
scaffold509_113463	Contig915_215617_215803	(AT) ₁₃	187	AGGAAGGATGGAGAAGGGAA	TTCCACGAAACATCAACCTT
scaffold579_196639	Contig915_58276_58492	(AG) ₇	217	CGTGCAATTATGATGACCCAG	CGTATTGAAATGAAAGCCGC
scaffold5457_16885	Contig9175_10014_10238	(CT) ₁₁	225	TGGCTAAATGGTGGTTAGGG	ACCAAACATGTAATGTTCCCA

scaffold3550_29189	Contig918_100265_100431	(CT) ₁₃	167	TGTTAGTGGTATGGTGGAGGC	TTGCAGGCACAATTACATAAAG
scaffold4665_23163	Contig919_11691_11591	(CT) ₉	101	CATTTCAAAGTCGGTCAGCC	CAAGCAGCATACAGCCAACA
scaffold120_153679	Contig921_141205_141027	(TA) ₁₀	179	TTGTGTGTAATGATAGCCAC	CAAGGACTCGATGCGAGATT
scaffold120_94435	Contig921_199374_199114	(ATT) ₁₁	261	GGACGAGCTCATGGGATAAG	CAACGATCGGAATCTTGACA
scaffold2715_35821	Contig922_240864_240562	(CAC) ₈	303	TGACGACGTTACCATTCAAA	TGGGCAATATTTAGGTTGA
scaffold5306_25480	Contig923_26153_26306	(CCA) ₈	154	CATTGTGTCCTTGTTTCCA	GGAGTGATTTCGTAGCATTGAA
scaffold61_181001	Contig927_81894_82163	(GT) ₁₀	270	TGCTTCCAGATTGATACCG	TCAGCCGATAAATTGAAGCC
scaffold5676_31376	Contig9459_67189_66983	(AT) ₇	207	GGGACTTCCATTTGCCTAGC	ACACAGCCAGATAACTCCCA
scaffold3806_2920	Contig9481_48006_47845	(AG) ₉	162	TGAGGTTCAAGGGTTCCAC	ACATGACAGAAGATTGGTGACG
scaffold2082_57964	Contig951_110976_110830	(TC) ₈	147	AGAGCTGTGATTGACCTGGG	GGGTGCTCTGGTGTATTCA
scaffold2082_56018	Contig951_112987_112685	(AT) ₇	303	GGAAGCGCGTGATAATAATTTG	CCTTCTTGACAGGCACTA
scaffold2082_16008	Contig951_148225_148079	(TC) ₈	147	TTCAAATGAAGTCGTAATTCTCAAC	CCACCCAGATTGACACCTCT
scaffold4409_57635	Contig9516_55685_55973	(GA) ₇	289	TGGGACTCAATCTGGAAGG	TATTCTCGTTGTGGTGCCAA
scaffold940_55713	Contig9543_25865_25711	(AG) ₉	155	GGTAAATTGGATAGTGAAATAGGAAA	TGGTAATGATATCCAATCTCCA
scaffold7313_11911	Contig961_131923_131665	(AT) ₇	259	TTGTACAATCAAGAACTGCGA	GGGACAGAAAGTGTTCGGA
scaffold459_29247	Contig9619_56592_56451	(TG) ₈	142	TTGATTTGGCAATGAGACCA	TTGCAATCACCATTGAACC
scaffold7233_50796	Contig9815_20731_20920	(AG) ₇	190	CACCGCACGTTAGAAGATGA	ACCCTAACCCATTCAAACCTCA
scaffold1751_114312	Contig9821_53600_53789	(TG) ₈	190	ACAATGTTTGTCTCTCTCA	TTTGCCTAAGCTGAAAGTTGG
scaffold1990_113063	Contig988_93529_93828	(AT) ₇	300	CCAAATTCGAGTTAGAGCCAA	GCACCTTACCTCTAACGGTTACATA
scaffold243_10766	Contig9897_18988_18776	(AG) ₈	213	CCACAGGCCATTTAAGCAGT	TAAATACTGAGGCCGATGCG
scaffold4257_5405	Contig9901_5526_5648	(AG) ₉	123	GTGAAGCCGAGATATGGAGG	CAATTAACAAATAAGCCTTCACCA
scaffold9126_2470	Contig9929_11010_10708	(TA) ₁₁	303	GGAAATCAGAGCTTGGAATAGA	GCCAATAGCTTGATTTGTCCA
scaffold8402_11491	Contig9956_1393_1135	(AAT) ₇	259	TTGGTAGGAATTTCTGTCTACCC	ATGTTTGGCAATTGTGGGAT

¹95% to <100% blast match between target (BATG-0.5) and reference PCR product sequences (BATG-0.4). ²<95% blast match between target (BATG-0.5) and reference PCR product sequence (BATG-0.4).