



Relationship between Single Nucleotide Polymorphisms in the Peroxisome Proliferator-Activated Receptor Gamma Gene and Fatty Acid Composition in Korean Native Cattle

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- Supplementary Data -

Supplementary Table 1. The information of primer sequence about SNPs of PPAR γ gene in Hanwoo.

SNP	Gene ID	BTA		Sequences	TM	Product size
g.1159-71208 A>G	NC_007320	22	F ¹	GGCCTTTGCGAAGTGTAAGT	60	222
			R ²	CAGCCATCCATTTCAACACT		
			E ³	TCTCTTCTTGAGATGCTAC		
g.1492-70875 C>A	NC_007320	22	F	ATCAGGGCAGAATGTCCAAC	60	103
			R	TTTGTTGCACTGCATTCTGG		
			E	TTTTTCTACAAGCCATAAAA		
g.2267-70100 C>T	NC_007320	22	F	AAGATCTGGGTGCTGCTGTT	60	143
			R	ACATGCAGAAGTCCCCTTTG		
			E	TCCCCTTCATGAGACTTTTT		
g.2869-69498 A>G	NC_007320	22	F	CAGGCAGCTGTGTACTTGGA	60	275
			R	ACAAGCCCAGGACAATGAAC		
			E	CTGGCCGTATGCTTTCTGTG		
g.2896-69471 A>C	NC_007320	22	F	CAGGCAGCTGTGTACTTGGA	60	275
			R	ACAAGCCCAGGACAATGAAC		
			E	AAGCGTGTTCATCCATCCCCT		
g.4298-68069 A>G	NC_007320	22	F	TACTGGAGTGGGTTGCCATT	60	135
			R	GATAGTTGCTGGCAGGCTTC		
			E	GGGTCGTAAATGAAAAACA		
g.5248-67119 C>T	NC_007320	22	F	CCTCATGCCAGGATTTCTGT	60	183
			R	GCTCTCAAAGCCAGTGTTC		
			E	CTCATGCCAGGATTTCTGTA		
g.5831-66536 C>T	NC_007320	22	F	TGTTTCTTCTCTCCCCTCCA	60	222

			R	CAGGGTAAGAGGGGTGTTGA		
			E	TCTGTCCTTGTGCTCAACAC		
g.7504-64863 A>G	NC_007320	22	F	GGCCCCCTTACTTCTTTTCAG	60	262
			R	CTATGGGGTTCGCACAGAGTC		
			E	ACTATGTTGCTGCTGCTGCT		
g.7514-64853 T>A	NC_007320	22	F	GGCCCCCTTACTTCTTTTCAG	60	262
			R	CTATGGGGTTCGCACAGAGTC		
			E	TGCTGCTGCTACTGCTAAGT		
g.7523-64844 T>G	NC_007320	22	F	GGCCCCCTTACTTCTTTTCAG	60	262
			R	CTATGGGGTTCGCACAGAGTC		
			E	TACTGCTAAGTTGCTTCAGT		
g.7530-64837 A>T	NC_007320	22	F	GGCCCCCTTACTTCTTTTCAG	60	263
			R	TCTATGGGGTTCGCACAGAGT		
			E	AAGTTGCTTCAGTCGTGTCT		
g.7539-64828 C>T	NC_007320	22	F	GCTGCTGCTGCTACTGCTAA	60	206
			R	GCAATCCATGGGGTCACTAA		
			E	CAGTCGIGTCTGACTCTGTG		
g.7569-64798 C>T	NC_007320	22	F	GCTGCTGCTGCTACTGCTAA	60	206
			R	GCAATCCATGGGGTCACTAA		
			E	GACGGCAGCCCACCAGGCTC		
g.7573-64794 A>G	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	GCAGCCCACCAGGCTCCCCC		
g.7642-64725 A>C	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	TCTCCAATGCATGAAAGTGA		
g.7658-64709 T>G	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	GTGAGAAGTGAAAGTGAAGT		
g.7682-64685 T>C	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	CAGTCGIGTCTGACTCTTAG		
g.7694-64673 T>C	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	ACTCTTAGTGACCCCATGGA		
g.7700-64667 A>C	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	AGTGACCCCATGGATTGCAG		
g.7705-64662 T>G	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	CCCCATGGATTGCAGCCCAC		
g.7728-64639 T>G	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	GCTCCTCCGTCCATGGGATT		
g.7729-64638 A>T	NC_007320	22	F	GTTGCCATTCCTTCTCCAA	60	220

			R	CATGTTGCTGCAAACCTGCAT		
			E	CTCCTCCGTCATGGGATTC		
g.7753-64614 G>A	NC_007320	22	F	GTTGCCATTTCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	GGCAAGAGTACTGGAGTGGG		
g.7762-64605 A>T	NC_007320	22	F	GTTGCCATTTCTTCTCCAA	60	220
			R	CATGTTGCTGCAAACCTGCAT		
			E	ACTGGAGTGGGGTGGCATTG		
g.8432-63935 G>T	NC_007320	22	F	CCAGCGTCAGAGTCTTTTCC	60	111
			R	AGGAGATAAGCCCTGGGTGT		
			E	TTCAAAAGCATCAATTCTTC		
g.8488-63879 A>G	NC_007320	22	F	CTTCAAAGAACACCCAGGA	60	364
			R	ATGGGGAAACAGTGGAAACA		
			E	CATACATGACCACTGGAAAA		
g.8527-63840 C>T	NC_007320	22	F	CATCACTTCATGGCAAATCG	60	269
			R	TTCGGAGCTCAGCTTTCTTC		
			E	AGACAGACCTTTGTGGCAA		
g.8612-63755 C>A	NC_007320	22	F	ACCACTGGAAAAACCACAGC	60	220
			R	TCCCATCACTTCATGGAACA		
			E	GTCTTTTAATATCATGGCTG		
g.8631-63736 T>G	NC_007320	22	F	ACCACTGGAAAAACCACAGC	60	385
			R	CAAGATTGCCGGGAGAAATA		
			E	GCAATCACCATCTGCAGTGA		
g.8632-63735 T>A	NC_007320	22	F	ACCACTGGAAAAACCACAGC	60	385
			R	CAAGATTGCCGGGAGAAATA		
			E	CAATCACCATCTGCAGTGAT		
g.8664-63703 T>C	NC_007320	22	F	GGAAGAAGCACAAGCTGGAA	60	198
			R	GAAGTGATGGGACCAGATGC		
			E	AAAAAATAAAGTCTCACACT		
g.8723-63644 C>G	NC_007320	22	F	TCCCCATCTATTTCCCATGA	60	221
			R	GGACTGGAAGAAGCACAAGC		
			E	GGACCAGATGCCATGATCTT		
g.8758-63609 C>A	NC_007320	22	F	CATGGCTGCAGTCACAATCT	60	231
			R	TGCAGATGACACCACCCTTA		
			E	GAGCTTTAAGCCAACCTTTT		
g.8766-63601 A>T	NC_007320	22	F	CATGGCTGCAGTCACAATCT	60	231
			R	TGCAGATGACACCACCCTTA		
			E	AGCCAACCTTTTTACTCTCC		
g.8768-63599 T>C	NC_007320	22	F	CATGGCTGCAGTCACAATCT	60	231
			R	TGCAGATGACACCACCCTTA		
			E	CCAACCTTTTTACTCTCCTC		
g.8792-63575 A>C	NC_007320	22	F	TGCAGATGACACCACCCTTA	60	225
			R	CTGCAATCACCATTTGCAGT		
			E	ACTTTCATCAAGAGGCTTTT		
g.8828-63539 A>C	NC_007320	22	F	TTCTGCCATAAGGGTGGTGT	60	223

			R	CGGTCAGCAAGCAACAATTA		
			E	TCTGCCATAAGGGTGGTGTC		
g.10645-61722 T>G	NC_007320	22	F	TCAGGGATTGAACCCTCATC	60	160
			R	GGCTCTGGGTGGTAACAGAA		
			E	TTGAACCCCTCATCTCCTGCA		
g.12138-60229 C>G	NC_007320	22	F	AAGGAACGCTCGGTAGGACT	60	277
			R	CACCCAGCCTGTCTTCAAAT		
			E	AGGATCCTGTCCTGGGTATC		
g.12729-59638 A>G	NC_007320	22	F	ACAGAGGATGAGACGGTTGG	60	299
			R	GCGGACACACCCAATAAGAT		
			E	GAAAGAAAAGACGAGAAACC		
g.12777-59590 A>G	NC_007320	22	F	ATGGGGTCACAAAGAGTTGG	60	255
			R	CAAGGCCTGGTGTCTCATCT		
			E	TTGAAATGGCAGTTTTAGGA		
g.13344-59023 A>T	NC_007320	22	F	TGGGGCTTCCTGAGAGTCTA	60	268
			R	CCGTTTCAGACCCTCACTGTT		
			E	ACCTACAGCACCTGATCTCT		
g.13346-59021 C>T	NC_007320	22	F	TGGGGCTTCCTGAGAGTCTA	60	268
			R	CCGTTTCAGACCCTCACTGTT		
			E	CTACAGCACCTGATCTCTTC		
g.13851-58516 T>G	NC_007320	22	F	GGGCACTGATGTTTCCTACC	60	209
			R	TCCCCAACATTTTAGTTTGA		
			E	TGTATGCATAGAAGGATGGA		
g.13862-58505 C>T	NC_007320	22	F	GGGCACTGATGTTTCCTACC	60	209
			R	TCCCCAACATTTTAGTTTGA		
			E	AAGGATGGATAGGAATGGGA		
g.13872-58495 G>A	NC_007320	22	F	ACGATTTGTGAAGGGCACTG	60	101
			R	TGTCCCATTTCCTATCCATCC		
			E	TAGGAATGGGACAAAGTAAGC		
g.14302-58065 G>A	NC_007320	22	F	CTTGCAGCATATGGGACCTT	60	131
			R	TGTCCTCAGCCCCTTAAAAA		
			E	GGTAATGAGTTTAAGGACAG		
g.14444-57923 T>A	NC_007320	22	F	CTTGCAGCATATGGGACCTT	60	304
			R	GGAGAGTGCTCTGTGCAGGT		
			E	AGTCCCAGGAACAGAATTTT		
g.16320-56047 C>T	NC_007320	22	F	CAGGACTCCTTCTCTGGGATT	60	208
			R	CTTTGGCAGGTCCTCAACAC		
			E	ATACTCTTGATGGGTCTTGA		
g.20851-51516 A>G	NC_007320	22	F	ACTTTCCTGGCTGCAGAAGA	60	162
			R	AGGGGACAGGAAGAGGAAGA		
			E	TTTCCTAAGTTTATTTGCC		
g.22327-50040 A>G	NC_007320	22	F	AGGAGCCTTGTTGGAAGTGA	60	217
			R	GAGGAGGGAGGAAGGTTTCAG		
			E	ACTGAAAAAATGAGATTGG		
g.25187-47180 C>T	NC_007320	22	F	GGATCTTAGCTCTCGGACCA	60	169

			R	GGGGAAGGGGTATAGGAGAA		
			E	TGGCAGTCCAGGGGTGAAGA		
g.25474-46893 C>T	NC_007320	22	F	CAACGTCAGGCTTCTCAACA	60	344
			R	CCGAGAGCTAAGATCCCACA		
			E	TTTCATTCTATTTATTACA		
g.25565-46802 C>T	NC_007320	22	F	AGGCGGTCACTGAGGTCATA	60	195
			R	TGCTGACTGCAAAGTGCTTC		
			E	GATTCCTGTGTTGAGAAGCC		
g.25582-46785 A>G	NC_007320	22	F	TGCTGACTGCAAAGTGCTTC	60	221
			R	TGTTGAGAAGCCTGACGTTG		
			E	GCCCCGACGTTGGTTGGCAGG		
g.26224-46143 T>A	NC_007320	22	F	TGTCACAGGCTGACTCTTGC	60	235
			R	GTCAGCAGCGTAGGGTTTGT		
			E	TTGTGTTTTCCAGGCACTTT		
g.26931-45436 C>T	NC_007320	22	F	AGTCCTGGGAGCATTACCC	60	230
			R	ACTCCCATGCCTTTGACATC		
			E	GAATTGGACTAAGCTCTCGT		
g.27009-45358 A>G	NC_007320	22	F	GCCAGGCTCCTCTGTCTATG	60	234
			R	CCAGGACTAATGGCTGTGGT		
			E	TTTATTCATCCACTTGCCA		
g.28071-44296 C>A	NC_007320	22	F	GTATGCCCAGCTTGAGGGTA	60	279
			R	TTGGCAGCCATTACTTGACA		
			E	TATGGAAATTTAATAGGCTT		
g.28234-44133 G>T	NC_007320	22	F	ACAACCTCTGGGCCTAACCT	60	275
			R	CTCAAGCTGGGCATACCATT		
			E	TTTCCTTCTCAGTTCCTTTT		
g.28877-43490 G>A	NC_007320	22	F	GAGGCACAGTAGCCTTGCTT	60	248
			R	GATAAAGCGTCAGGGTTCCA		
			E	AGGTACCTAGGTTTTTCATT		
g.28986-43381 C>T	NC_007320	22	F	GAGGCACAGTAGCCTTGCTT	60	248
			R	GATAAAGCGTCAGGGTTCCA		
			E	CTTGAAAACCTAAGAAAATC		
g.29025-43342 C>T	NC_007320	22	F	TTCAGGAGATCTGCGTTCTG	60	362
			R	GCTTGTGAAGGATGCAAGGT		
			E	GTGCCTCACTTCGTTTTTTC		
g.29043-43324 A>G	NC_007320	22	F	TTCAGGAGATCTGCGTTCTG	60	362
			R	GCTTGTGAAGGATGCAAGGT		
			E	TCCGAATTGGTCCTGTGCAG		
g.29170-43197 T>A	NC_007320	22	F	ATGGCTCACACTGATGCTGA	60	294
			R	CATGACAGTGATGGGCTGAC		
			E	TCTCCTGAATCTCCTAATGC		
g.29317-43050 C>A	NC_007320	22	F	ATGGCTCACACTGATGCTGA	60	294
			R	CATGACAGTGATGGGCTGAC		
			E	TGTCCTGAGATTTCCCCCA		
g.29439-42928 A>C	NC_007320	22	F	ATGGCTCACACTGATGCTGA	60	142

			R	TTTATGGCCACTTTGCAGGT		
			E	GGCAAAGAGATACAGCTGTT		
g.30339-42028 T>C	NC_007320	22	F	TGCTTTACCAGCCATAAAAA	60	294
			R	CTCCTGGCAAGAGATGCTTT		
			E	AGAAGTAGTTGAAGAAATCA		
g.31133-41234 G>A	NC_007320	22	F	CTTTGCAGCTCCACTGACTG	60	220
			R	AAGCTGAAGCTCCCTCCACT		
			E	TGAAGGACAGGGGAGCCTGC		
g.31670-40697 T>A	NC_007320	22	F	CAGGGACTGAACCCATGTCT	60	256
			R	CTCAACGTTTTGGGGTGAGT		
			E	GACCAAATGTTTGAGAACT		
g.31768-40599 C>G	NC_007320	22	F	CAGGGACTGAACCCATGTCT	60	256
			R	CTCAACGTTTTGGGGTGAGT		
			E	CCATCGTTAGACCAGTTAGA		
g.31777-40590 G>A	NC_007320	22	F	CAGGGACTGAACCCATGTCT	60	256
			R	CTCAACGTTTTGGGGTGAGT		
			E	GACCAGTTAGACCAGTGCCC		
g.32333-40034 G>A	NC_007320	22	F	TGGCAAGGGTCAAATAAACC	60	264
			R	CAGCCTTAGCTCACCAACAA		
			E	ACATATCTACATGCCAGGGG		
g.32487-39880 C>G	NC_007320	22	F	CCCACAGAGGCTGAATCAAT	60	387
			R	GACCCTTGCCAAAGTTCAGA		
			E	TACACTTTAGAACTTGCAAA		
g.32508-39859 A>T	NC_007320	22	F	CCCACAGAGGCTGAATCAAT	60	387
			R	GACCCTTGCCAAAGTTCAGA		
			E	CTGACATTGATTGCTTATAA		
g.32698-39669 A>G	NC_007320	22	F	TCCAACCTTCTCCTTATTGCT	60	150
			R	CATTGATTCAGCCTCTGTGG		
			E	GTTTTTAGTATATTCCCGTG		
g.33234-39133 G>A	NC_007320	22	F	GGCATGGTTGGAGATGAAGA	60	228
			R	CCAAGCTTGTACTGGGGTTT		
			E	CATGAACTTAGTCTTAAAAA		
g.33701-38666 T>G	NC_007320	22	F	TTTCCCCTGACTGATTCAC	60	183
			R	GATAGCCGAGCAGCATTTTC		
			E	ATCAGTCAGGGGAAAATGC		
g.34365-38002 A>T	NC_007320	22	F	TGCTGTGATTCTGCCCTCTA	60	105
			R	ACAGGCTTCTCCACCCCTAC		
			E	AATAAAAATTCTATGCAAGG		
g.34437-37930 G>A	NC_007320	22	F	TGCAGTGGCAAAAGTAAGGA	60	396
			R	GGCAGAATCACAGCAATGAA		
			E	ATGTGCAAAGAAGTTATTAA		
g.34821-37546 G>A	NC_007320	22	F	GGATTCCATTGGCTCTATGC	60	347
			R	TTTCCTTACTTTTGCCACTGC		
			E	AAACCATGATGCAGAAAACG		
g.35937-36430 G>A	NC_007320	22	F	ATTGCCTGTTCCCTCACTG	60	354

			R	GGCCCAGGAAGGAAGTTAAA		
			E	GTCATAACTGCTAATGGAGC		
g.37405-34962 C>A	NC_007320	22	F	GGCAAATGCCCAACTACAAG	60	343
			R	TTCTCCGGAGGACAATCAG		
			E	CGAGGGCCGTGGCTGAAAAC		
g.37550-34817 T>G	NC_007320	22	F	GGCAAATGCCCAACTACAAG	60	230
			R	TGCTGTGGGGATGTCTCATA		
			E	ACGATGGGAGAAAAGACTGG		
g.37695-34672 A>T	NC_007320	22	F	AGCACAGGGAACCTTGCTCA	60	293
			R	CTGGGAAGTCTGGGTGGTAA		
			E	CTTTTTTTTATTTTATAGGC		
g.39018-33349 G>A	NC_007320	22	F	TGGTCACAAGAAGGCAAAAAG	60	342
			R	GGTGATGTGATCATGTTGCAG		
			E	TTTAAAAATTGTCACCTTTTC		
g.39148-33219 C>G	NC_007320	22	F	ACAAGGCTGCTCCTCTCTCT	60	175
			R	TCCCCTGTTGCTTGTTGTTT		
			E	GATGGTATAATTTTCTCTTT		
g.39790-32577 A>T	NC_007320	22	F	CTGCTGTCTATGGGGTCACA	60	267
			R	AGTCCCTGAGTCGGGAAGAT		
			E	CTGCTAAGTCACTTCAGTCG		
g.41072-31295 T>G	NC_007320	22	F	CACAGCCTCTGCCTTAGGAC	60	223
			R	TTTCTGTGGCTCTTCCCATC		
			E	TAAGGTAGTTCTCTTCTTTTC		
g.40613-31754 G>A	NC_007320	22	F	TCCTGATGGATTTCCCTGAC	60	295
			R	TGGCTGTTGCTGCAAATTAC		
			E	CACATTCTCAGAAAGCAAGG		
g.41072-31295 A>C	NC_007320	22	F	ACAGCCCCTCTTCCTTCATT	60	299
			R	GAAGATTCCCCTGGAGAAGG		
			E	CCCTGTGGACAGAGGAGCCT		
g.42346-30021 T>C	NC_007320	22	F	CTAAGGGGTGAATTCGCAGT	60	419
			R	CAGAGTCAGAAGATGAGGCTGT		
			E	TCCAAATGCGCATATTTTTT		
g.42499-29868 T>G	NC_007320	22	F	CCTTTCATCCGTCAGTGGAT	60	440
			R	GGTGATAAGACTGCCCTTG		
			E	ACTGACCATGAGACGAAGCC		
g.42523-29844 T>C	NC_007320	22	F	CCTTTCATCCGTCAGTGGAT	60	202
			R	CGAAGCCGTACTCATTGTCA		
			E	TCATTGTCAAAAAGCCTGATA		
g.42555-29812 C>T	NC_007320	22	F	AAGGGCAGGATGAATGAGTG	60	303
			R	CCATGAGACGAAGCCGTA		
			E	CACCCCTTAGATGTTAAAGG		
g.43637-28730 C>G	NC_007320	22	F	GCCCCACAGAGAACTTCTGA	60	210
			R	TGAACTCAGGCTTCCCTCAT		
			E	AGTCACTGGCCACATTTGTA		
g.43645-28722 G>A	NC_007320	22	F	GCCCCACAGAGAACTTCTGA	60	210

			R	TGAACTCAGGCTTCCCTCAT		
			E	GCCACATTTGTAGGCCTTCA		
g.46012-26355 T>A	NC_007320	22	F	GGGGAAGCCGATAATTAAGC	60	201
			R	CCAGGCTCCTCTGTCCATAC		
			E	GTCTGACTCTTTATGACCCC		
g.46116-26251 A>G	NC_007320	22	F	GGGGAAGCCGATAATTAAGC	60	227
			R	TTTATGACCCCGTGGACTGT		
			E	GGATTTTCATGGCGGCGGGGG		
g.47009-25358 T>C	NC_007320	22	F	GGAAGGGAGAAGCTCTGGTT	60	248
			R	ACCCCACTGGAAGTGTGTC		
			E	GTTCTGTCTCATTGGTGAAG		
g.49232-23135 T>C	NC_007320	22	F	GGAGGAACTGGGGCTTCTAA	60	201
			R	TCCCTGTCCTTCACCATCTC		
			E	CCAGAGTTTGCTTAGACTCA		
g.52522-19845 C>T	NC_007320	22	F	TTCAACAACATTTCGCTGGAG	60	145
			R	GAGTCACCAGGCGAGCTTAC		
			E	TCGTTCTTGGCTTACTTGAA		
g.53828-18539 G>T	NC_007320	22	F	TATGATACCACGACCGGTGA	60	395
			R	CCTTATGCAGCTGCTCCTTC		
			E	AGAGGATTTTATCTAAAACA		
g.54191-18176 G>A	NC_007320	22	F	ACTGACACCCCTGGAAGATG	60	296
			R	CCAGAAGACAACCTGGAGGA		
			E	GGTGTGACCGTGAATGAGA		
g.55233-17134 G>T	NC_007320	22	F	CTGGTTCGGACTGCATTCTT	60	158
			R	CAGCGAGGTGTGACTTTGAA		
			E	CCCGTGTGGAGTCCCTCTGAC		
g.55383-16984 G>T	NC_007320	22	F	CCACACATCAGTTTCCATGC	60	289
			R	AACCAGAGAACACCCAGCAG		
			E	TGATCTAATTAACCAACTCC		
g.55672-16695 C>A	NC_007320	22	F	ACCTTTCAGGGCTTTGGTTT	60	209
			R	GAGCAAGGCCCACTCTGTAG		
			E	TCTTTTGTGGTCCAGTTAGT		
g.55896-16471 C>A	NC_007320	22	F	TCAAAACACGTCGGATAGCA	60	235
			R	AAACCAAAGCCCTGAAAGGT		
			E	ATGGAGTCAGGATGATGAAC		
g.55975-16392 T>G	NC_007320	22	F	TCAAAACACGTCGGATAGCA	60	235
			R	AAACCAAAGCCCTGAAAGGT		
			E	GCAAACAGATAACAGCACAG		
g.56135-16232 T>C	NC_007320	22	F	CACTGAGCTACTGGGGAAGC	60	326
			R	GCCCTTTGTCGTGTTATGCT		
			E	CCAGTTTATGTTAGGTCCAT		
g.56223-16144 T>C	NC_007320	22	F	CACTGAGCTACTGGGGAAGC	60	326
			R	GCCCTTTGTCGTGTTATGCT		
			E	TAAGGCCCATTTTATCTTTA		
g.57085-15282 T>C	NC_007320	22	F	CAGATGGGCGGATAGAGAAG	60	251
			R	TATCTTGGCAACCCCAAGTC		

			E	CACGTGTAAGTGACATCATA		
g.57182-15185 G>T	NC_007320	22	F	CAGATGGGCGGATAGAGAAG	60	251
			R	TATCTTGGCAACCCCAAGTC		
			E	TCCCTCTTTTTTGTGACTAA		
g.58062-14305 G>T	NC_007320	22	F	GTTTGTGTGTCATGCGGAGT	60	102
			R	TTCAGGGCTTTTTGAACCTG		
			E	TCCTACCACAGATATTAAGG		
g.58480-13887 A>C	NC_007320	22	F	AATCAAGTTCCTGGGTGCTG	60	313
			R	TTCCCCAGATTGTCTTCACA		
			E	TGGATCCTCACAATAATGAA		
g.59145-13222 C>G	NC_007320	22	F	TAGGGTTGAAGCCGAGTGAC	60	285
			R	GAGTGTTATGGGCAGGGAAC		
			E	TCACAGAAGAGCTTCGTCCC		
g.60868-11499 C>T	NC_007320	22	F	CCCCCTACATTGAAAGAGCA	60	209
			R	TGGCTCACAGTGAACCTGGTC		
			E	CCAGAGACATCCCGTAGATA		
g.60869-11498 C>A	NC_007320	22	F	CCCCCTACATTGAAAGAGCA	60	209
			R	TGGCTCACAGTGAACCTGGTC		
			E	CAGAGACATCCCGTAGATAC		
g.60917-11450 A>G	NC_007320	22	F	CCCCCTACATTGAAAGAGCA	60	209
			R	TGGCTCACAGTGAACCTGGTC		
			E	AGAATCAGAGCACAGAACCC		
g.61873-10494 G>T	NC_007320	22	F	TGTATAGCGAGCACCCCTCT	60	231
			R	CACCTGCCCTCTGGTCTTAG		
			E	CATTTTAACAGCAGAACTGT		
g.62494-9873 C>T	NC_007320	22	F	TGACACTGCTCCCTTCTCCT	60	211
			R	CCGAGGTCTCTGGTTTTTCAG		
			E	CAGGTGGCCGAGATGGCTTT		
g.62724-9643 C>T	NC_007320	22	F	TTCTCAACTGGCACCCAAAT	60	288
			R	ACGAATGATCCCAGCCTATG		
			E	CTCACACACTCTCACACACA		
g.63097-9270 A>G	NC_007320	22	F	CCACTTTGGGGAGCACTTTA	60	283
			R	TGGTAGAGTGAGGGGGTTTG		
			E	ACAGATCCTCTTCGAGTGAG		
g.63137-9230 A>T	NC_007320	22	F	CCACTTTGGGGAGCACTTTA	60	283
			R	TGGTAGAGTGAGGGGGTTTG		
			E	GCTCCAGAGGCCAGCACAGG		
g.67415-4952 C>T	NC_007320	22	F	AGGGAGTGCTGAAGACCAAA	60	289
			R	CACTAACCGGCTCTGTGACC		
			E	GTGTGAGCCTGTTAATGTGC		
g.68297-4070 A>C	NC_007320	22	F	CCCTGACACTTCCACACAGA	60	224
			R	TCCTGGCCTAGAGACTCACG		
			E	TTGCATAGCAACTGTGAGAA		
g.68712-3655 C>A	NC_007320	22	F	CTGAAAATCCCACCCGAGAC	60	402
			R	AGGACCTGGTGGGCTGTAGT		
			E	AAGAATTGTAGTTTTCAATC		

g.69435-2932 C>T	NC_007320	22	F	ACACAGGCAGGGTTTTGAAG	60	288
			R	AAGGCCACCACCTTCTTTTT		
			E	AAGAGTAAGCTTAAGTCAGT		
g.72367 G>T	NC_007320	22	F	GTGAAGCCCATTGAGGACAT	60	356
			R	CCTGTAGGAGTGGGTGGAGA		
			E	CTGCAAGCCTTGGAGCTGCA		

¹Forward sequence, ²Reverse sequence, ³Extension sequence