Supplemental Figure legends

To promote understanding of the SINE insertion patterns, we have inserted explanations regarding the results of electrophoretic analyses in Supplemental Figure 1-4.

Supplemental Figure 1 Electrophoresis profiles of PCR products of SINE-inserted loci, and phylogenetic relationships of three major groups in Testuguria inferred from each electrophoretic pattern. Boxes A-D: The loci (indicated by lowercase letters to the left) are arranged to correspond to each clade of the phylogenetic tree. Arrowheads on the branches indicate positions at which a SINE insertion occurred in the loci of each box. The lane numbers indicate various species. Lane numbers and species correspond to the numbers assigned for each species in Figure 2. Lane numbers with a black background indicate the presence of a SINE unit, those with a gray background indicate the absence of a SINE unit, and those with a white background indicate that the presence or absence of a SINE unit is unknown. Arrowheads pointing to PCR bands indicate the presence (filled) or absence (open) of a SINE unit. The colored rectangles, containing abbreviations on the upper side in each box, indicate the classification of each group in the present study. The abbreviations are as follows: TES = Testudinidae (purple), GEO = Geoemydidae (yellow), EMY = Emydidae (orange), BG = *Batagur* group (red), SG = *Siebenrockiella* group (green), GG = *Geoemyda* group (blue).

Additional explanation for SINE loci in Supplemental Figure 1.

Box A;

For locus BHa25, two bands per specimen were observed in *Malayemys macrocephala* (lane 10) and *Heosemys grandis* (lane 20). We sequenced these additional products to confirm their identity. The upper band in lane 10 and the lower band in lane 20, whose lengths were equivalent to those of other Testuguria species, represented orthologous loci, whereas the lower band of lane 10 and the upper band of lane 20 were nonspecific. *Cu. mouhotii* (lane 18) yielded no PCR product at BHa25 locus. During the SINE insertion analysis, such occurrences were attributed to either a mutation in the primer binding site or a gross deletion within this locus. Therefore, data for such loci were categorized as “unknown”. At locus TTh26, the lower band of *Callagur borneoensis* (lane 7) and the single band of *Mal. macrocephala* (lane 10) were confirmed as nonspecific by sequencing analysis. Previous work using 16 species of Testudinoidea indicated that loci BCr01 and BCr06 would be useful for determining relationships among species of this superfamily (Sasaki et al, 2004; ref. in text). In this regard, we analyzed these loci using the 28 species of Testudinoidea.

To take into consideration the species for which no PCR product was obtained (lane 18 in BHa25; lane 8 in TKe30; lane 15 in TKe40; lanes 2 and 10 in TTh26; lane 11 in BOs240; lanes 1, 18 and 23 in BCr01) we performed a phylogenetic analysis using the maximum parsimony method with a data matrix showing the presence or absence of a SINE unit at 49 loci. The data clearly showed that those species are included in the Testuguria clade (100% bootstrap value (BP), stem A in Fig. 2). Thus, the results in Box A indicate that a SINE

insertion at each locus occurred in an ancestral species of Testuguria after the divergence of the two emydids.

Box B;

For locus TKe17, we sequenced the two PCR products observed in each of *Mal. macrocephala* (lane 10) and *Rhinoclemmys funerea* (lane 26). For *Mal. macrocephala*, the upper band represented the orthologous locus and the lower band was nonspecific. For *R. funerea*, the lower band represented the orthologous locus and the upper band was nonspecific. For specimens that yielded no PCR product at certain loci (i.e., “unknown”; lane 18 in TKe17; lanes 25 and 26 in TKe36), the MP analysis confirmed that those species form a clade that differs from the one suggested by the loci in Box B (88% BP, stem B in Figure 2).

Box C;

For locus BKs36, the specimens of lanes 5, 12, 27 and 28 did not yield a PCR product. MP analysis confirmed that the species of lanes 5 and 12 are in different clades (stem B containing the species of lane 5 with 97% BP, stem E containing the species of lane 12 with 88% BP; Fig. 2) from the one indicated by loci BKs36 and BKs52 (91% BP, stem C in Fig. 2), and that two emydids (lanes 27 and 28) are located outside of the Testuguria clade (100% BP, stem A in Fig. 2).

Box D;

K. homeana (lane 3) at locus BHa65 yielded multiple bands. Sequencing revealed that the lower band represented the respective orthologous locus (see the alignment in Supplemental Fig. 5-11). For specimens that yielded no PCR product at locus BHa65 of *K. erosa* (lane 2), the MP analysis confirmed that this species is included in a clade (97% BP, stem B in Fig. 2) that differs from the one suggested by loci BHa65 and BHa74 (88% BP, stem E in Fig. 2).

Supplemental Figure 2 Electrophoresis profiles of PCR products of SINE-inserted loci and phylogenetic relationships of the *Geoemyda* group inferred from each electrophoretic pattern. The abbreviations, color scheme and other details of each panel are defined in Supplemental Figure 1.

Additional explanation for SINE loci in Supplemental Figure 2.

Box A;

For locus BOs55, *B. baska* (lane 8) and *R. p. punctularia* (lane 25) both yielded two bands. Sequencing analyses revealed that the lower band of *B. baska* and the upper band of *R. p. punctularia* represented orthologous loci, whereas the upper band of *B. baska* and the lower band of *R. p. punctularia* were nonspecific (see the alignment in Supplemental Figure 5-16). Preliminary work (Sasaki et al., 2004) had shown that loci BCr61 and BMm105 contained a SINE unit that had inserted in a common ancestor of *Mau. reevesii* and *Mau. m. kami*. In the present study, loci BCr61 and BMm105 displayed a *Mauremys*-specific SINE insertion, as was indicated by the results of loci BOs55 and BOs74. At locus BMm105, *Mau. reevesii* (lane 14) yielded a longer product (722 bp) than that of the other *Mauremys* species (419 bp). This

longer product was due to an additional insertion unrelated to a SINE (Sasaki et al., 2004 and references therein; see the alignment in Supplemental Figure 5-19). *Emys orbicularis* (lane 28) yielded two bands for locus BCr61. Sequencing analysis showed that the upper band was nonspecific and that the lower band represented the orthologous locus.

For specimens that yielded no PCR product at certain loci (lane 18 in BCr61; lanes 5, 6 and 21 in BMm105), MP analysis confirmed that those species are in different clades (stem B containing the species of lane 5 with 97% BP, stem C containing the species of lane 6 with 91% BP, stem J containing the species of lane 18 with 63% BP, stem K containing the species of lane 21 with 99% BP; Fig. 2) from the one indicated by the loci in Box A (99% BP, stem F in Fig. 2).

Box B;

Details are described in the text.

Box C;

For locus BHg36, we sequenced multiple PCR products per specimen observed in each of *K. erosa* (lane 2) and *Mal. macrocephala* (lane 10). The middle band of *K. erosa* and the lower band of *Mal. macrocephala* represented the orthologous loci, whereas the upper and lower bands of *K. erosa* and the upper band of *Mal. macrocephala* were nonspecific (see the alignment in Supplemental Fig. 5-22). Similarly, at locus BHa59, we sequenced two bands per specimen observed in each of *K. homeana* (lane 3) and *B. baska* (lane 8). The lower bands of both species represented orthologous loci, whereas the upper bands were nonspecific (see the alignment in Supplemental Fig. 5-23).

For specimens that yielded no PCR product at certain loci (lane 1 in BHg36, lane 10 in BHa59, lane 11 in BM49), MP analysis confirmed that those species are in different clades (stem B containing the species of lane 1 with 97% BP, stem C containing the species of lane 10 with 91% BP; Fig. 2) from the one indicated by the loci in Box C (99% BP, stem K in Fig. 2) and that the species of lane 11 is outside of the *Geoemyda* group (88% BP, stem E in Fig. 2).

Supplemental Figure 3 Electrophoresis profiles of PCR products of SINE-inserted loci and phylogenetic relationships of the *Mauremys* lineage inferred from each electrophoretic pattern. The abbreviations, color scheme and other details of each panel are defined in Supplemental Figure 1.

Additional explanation for SINE loci in Supplemental Figure 3.

Box A;

At locus BOs68, the product observed in *B. baska* in Figure 5A-a (lane 8) was nonspecific. For specimens that yielded no PCR product at locus BOs68 (lanes 8 and 28), MP analysis confirmed that those species are in different clades (stem C containing the species of lane 8 with 91% BP; Fig. 2) from the one indicated by the loci in Box A (88% BP, stem G in Fig. 2) and that the species of lane 28 is outside of the Testuguria clade (100% BP, stem A in Fig. 2).

Box B;

For specimens that yielded no PCR product at locus BOs60 (lanes 3, 21, 27 and 28), MP analysis confirmed that those species are in different clades (stem B containing the species of lane 3 with 97% BP, stem K containing the species of lane 21 with 99% BP; Fig. 2) from the one indicated by the loci in Box B (86% BP, stem H in Fig. 2) and that two emydids (lanes 27 and 28) are outside of the Testuguria clade (100% BP, stem A in Fig. 2).

Box C;

For locus BMm103, we sequenced two bands per specimen observed in *Te. horsfieldii* (lane 1); the lower band represented an orthologous locus and the upper band was nonspecific. In preliminary work (Sasaki et al., 2004), loci BMm74 and BMm85 were characterized as having a SINE unit specifically inserted into the genome of *Mau. m. kami*. In the present study, *Mau. m. kami* and *Mau. annamensis* had insertions at these loci. In addition, at locus BMm74, a 46-bp deletion that was common to *Pa. smithii, Ca. borneoensis* and *Mal. macrocephala* was reported in preliminary work (Sasaki et al., 2004). The present study confirmed the deletion of this sequence at locus BMm74 in *B. baska* and *Or. borneensis*. This common sequence deletion supports a monophyletic relationship within the *Batagur* group. At locus BMm85, *Mau. sinensis* yielded a shorter product (227 bp) due to a 123-bp deletion upstream of the SINE 5' flanking region (see the alignment in Supplemental Fig. 5-33).

For specimens that yielded no PCR product at certain loci (lane 18 in BMm103, lanes 5 and 25 in BMm74), MP analysis confirmed that those species are in different clades (stem B containing the species of lane 5 with 97% BP, stem J containing the species of lane 18 with 63% BP; Fig. 2) from the one indicated by the loci in Box C (98% BP, stem I in Fig. 2) and that the species of lane 25 is outside of the clade of the *Mauremys* lineage (99% BP, stem F in Fig. 2).

Supplemental Figure 4 Electrophoresis profiles of PCR products of SINE-inserted loci and phylogenetic relationships of the *Heosemys* lineage inferred from each electrophoretic pattern. The abbreviations, color scheme and other details of each panel are defined in Supplemental Figure 1.

Additional explanation for SINE loci in Supplemental Figure 4.

Box A;

For specimens that yielded no PCR product at certain loci (lane 18 in BHg10; lanes 7, 8, 9, 13, 25 and 26 in BHg23), MP analysis confirmed that those species are in different clades (stem C containing the species of lanes 7, 8 and 9 with 91% BP, stem F containing the species of lane 13 with 99% BP, stem J containing the species of lane 18 with 63% BP; Fig. 2) from the one indicated by the loci in Box A (96% BP, stem L in Fig. 2) and that the species of lanes 25, 26, 27 and 28 are outside of the *Heosemys* clade (99% BP, stem K in Fig. 2).

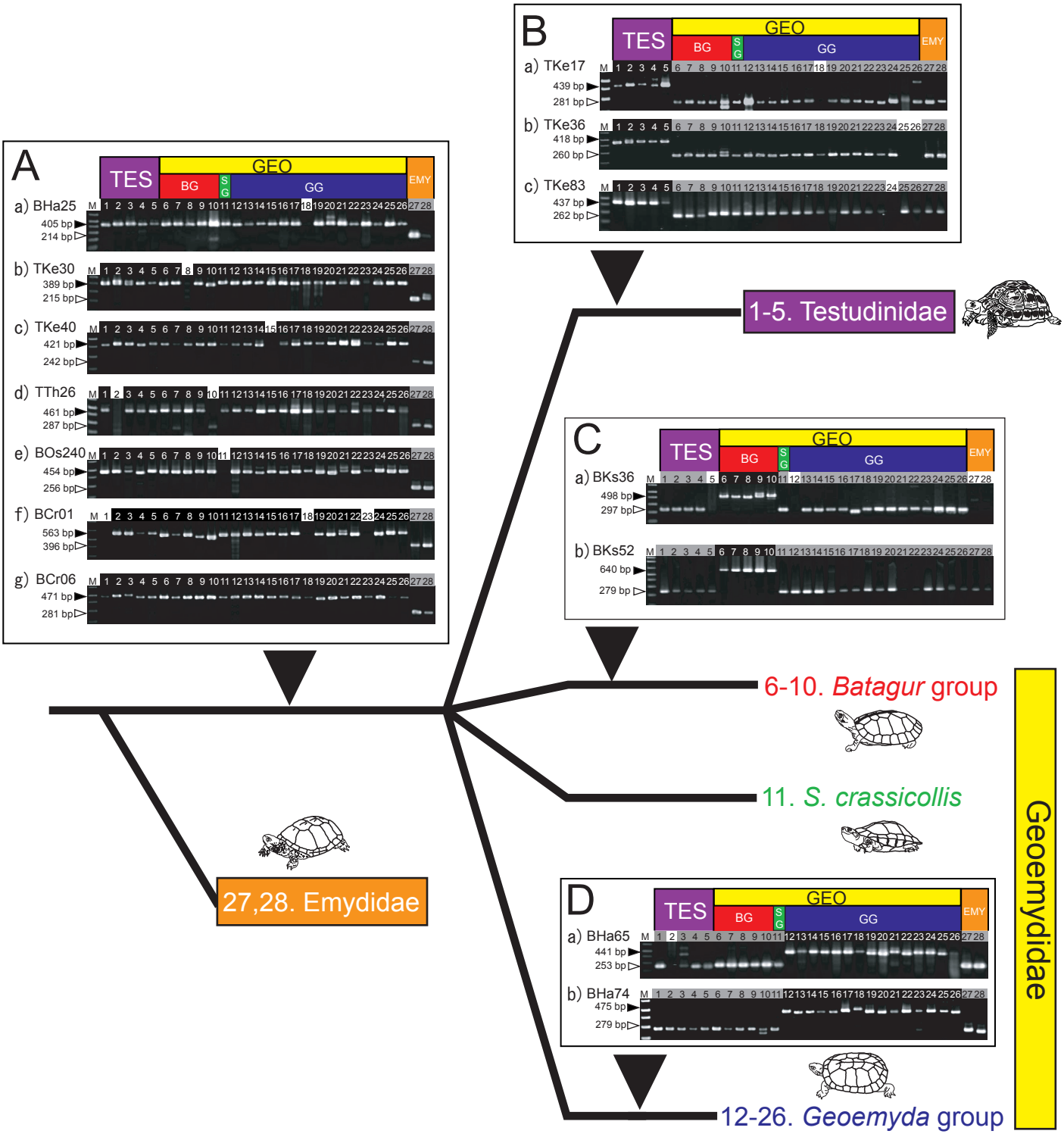
Box B;

For locus BHg12, we sequenced two PCR products per specimen observed in each of *Te.*

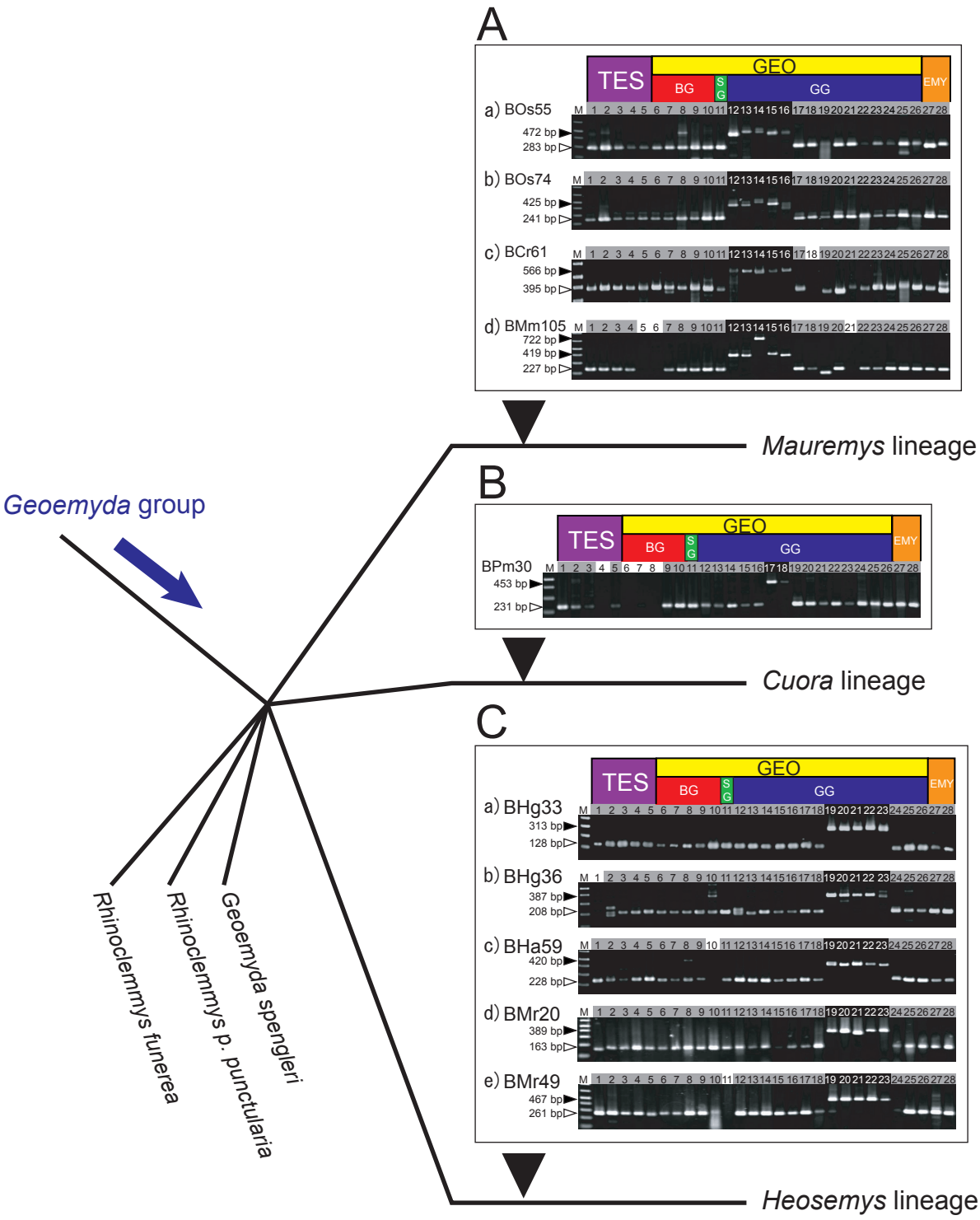
horsfieldii (lane 1) and *B. baska* (lane 8). The upper bands in each species were nonspecific and the lower bands represented the orthologous loci. For specimens that yielded no PCR product at locus BHg12 in the genome of *Tr. s. elegans* (lane 28), MP analysis confirmed that this species is outside of the Testuguria clade (100% BP, stem A in Fig. 2). Additionally, the monophyletic clade indicated by the loci in Box B is supported with 87% BP (stem M in Fig. 2).

Supplemental Figure 5 Sequence alignments of all 49 SINE loci from representative species. The sequence names are designated as a combination of a number and a locus name. The numbers correspond to each species used in this study. The correspondence between number and species is shown in Figure 2. Deletions or gap sequences are shown by dashes. GenBank accession numbers that were used in the sequence alignment are indicated below each alignment of loci.

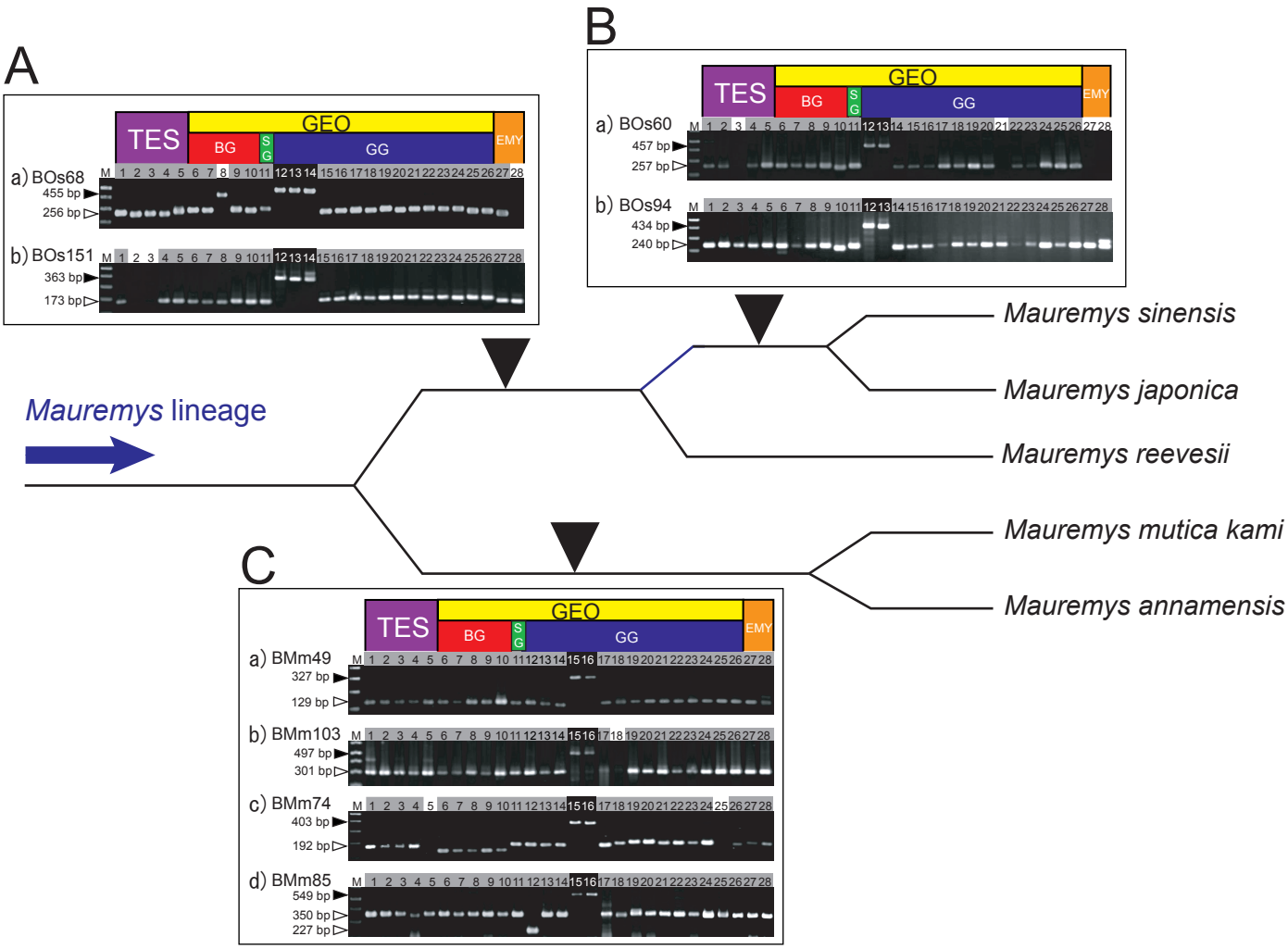
Supplemental Figure 6 Electrophoresis profiles of PCR products of SINE-inserted loci. The SINE insertions that occurred in these loci are species specific. The display method is identical to that indicated in Figure 3.



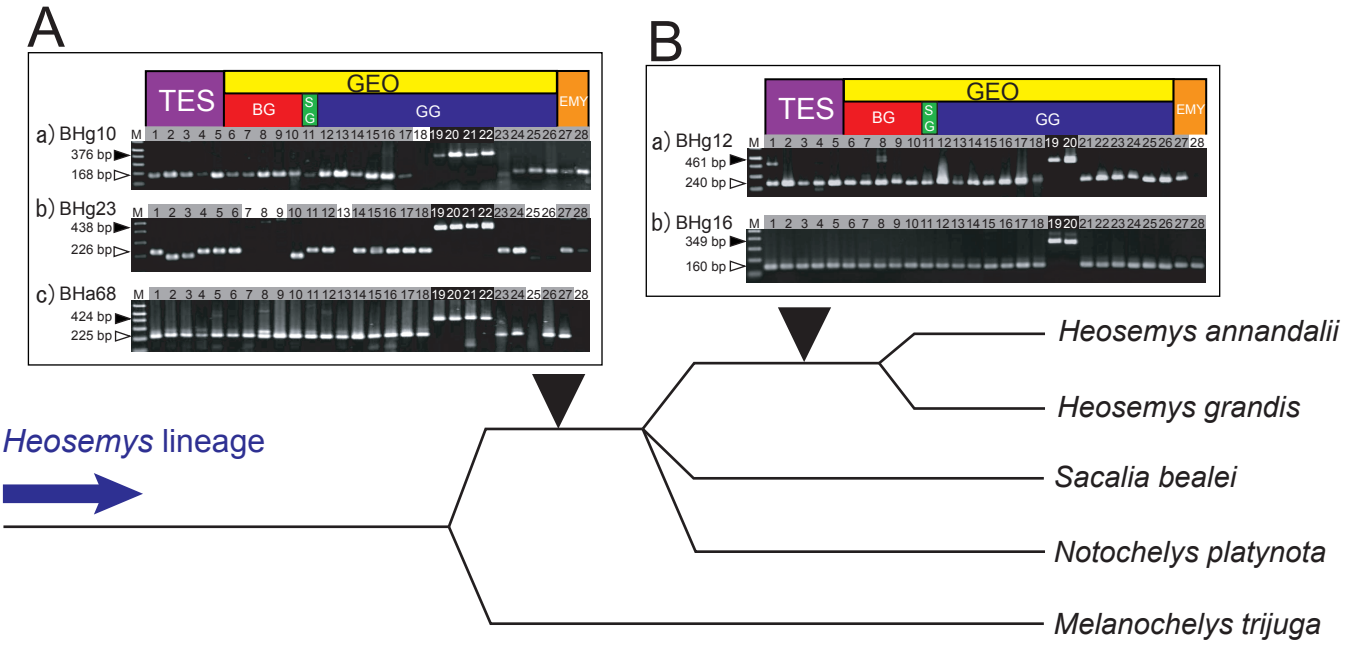
Sasaki et al._supplemental Fig.1



Sasaki et al._supplemental Fig.2



Sasaki et al._supplemental Fig.3



Sasaki et al._supplemental Fig.4

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01 BHa25 locus   1:-------------TTTTGGA-GAGAATGAGAAATGAATGACAGCCGTTAGTAGTGATAGG 46
06 BHa25 locus   1:GTTATTTGCAAACTTTTGGA-GAGAATGAGAAATGAGTGACAGCCGTTTGTAGTGAAAAG 59
10 BHa25 locus   1:GTTATTTGCAAACTTTTGGAAGAGAATGAGAAATGAGTGACAGCCGTTAGTAGTGATAGG 60
20 BHa25 locus   1:GTTATTTGCAAACTTTTGGAAGAGAATGAGAAATGAGTGACAGCCGTTAGTAGTGATAGG 60
27 BHa25 locus   1:GTTATTTGCAAA-TTTTGGA-GAGAATGAGAAATGAGTGACAGCCGATAGTAATGATAGG 58
                 .............******* ***************.*********.*.***.***.*.*

01 BHa25 locus  47:ATGATGCATAGTCCCTCACTCCTATGATAATCAGGGGTGGGGGAGGGAAAGCTCAGTGGT 106
06 BHa25 locus  60:ATGATGCATAGTCCCTCACTCCTATGATAAAC------GGGGGAGGGATAGCTCAGTGGT 113
10 BHa25 locus  61:ACGATGCATAGTCCCTCACTCCTATGATAATC------GAGGGAGGGATAGCTCAGTGGT 114
20 BHa25 locus  61:ATGATGCATAGTCCCTCACTCCTATGATAATC------AGGGGAGGGATAGCTCAGTGGT 114
27 BHa25 locus  59:ACGATGCATAGTCCCTCACTACTA---------------------------------- 82
                 *.******************.***........     ......................

01 BHa25 locus 107:TTGAGCATTGACCTGC-TAAATCCAGGGTTATGA-TTCAGTTTTTGAGGGGGCCATTTAG 164
06 BHa25 locus 114:TTGAGCATTGGCTTGCCTAAACCCAGGGTTATGAGTTCAATTCTTGAGGGGGCCATTTAG 173
10 BHa25 locus 115:TTGAGCATTGGCCTGC-TAAACCCAGGGTTATGAGTTGAATTCTTGAGGGGGCCATTTAG 173
20 BHa25 locus 115:TTGAGCATTGGCATGC-TAAACCCAGGGTTATGAGTTCAATTCTTGAGGGGGCCATTTAG 173
27 BHa25 locus  82:------------------------------------------------------------ 82
                 ............ ... ............................................

01 BHa25 locus 165:GGATCTGGGGCAAGAATCTTTCTGGAGATTGGTACTGCTTTGAGCATCAGGTTGGACTAG 224
06 BHa25 locus 174:GGATCTGGGGCAAAAATTTGTCTGCGGATTGGTACTGCTTTGAGCAGCAGGTTGGACTAG 233
10 BHa25 locus 174:GGATCTGGGGCAAAAATCTG----CGGACTGGTACTGCTTTGAGCAGCAGGTTGGACTAG 229
20 BHa25 locus 174:GAGTCTGGGGCAAAAATCTGTCTGGGGATTGGTACTGCTTTGAGCAGCAGGTTGGACTAG 233
27 BHa25 locus  82:------------------------------------------------------------ 82
                 ........................ ...................................

01 BHa25 locus 225:ATGACCTCCTGAGGTCCCTTCCAACCCTGATATGCTATGATTCTATGATACTAGGGGATA 284
06 BHa25 locus 234:ATGACCTCCTGAGGTCCCTTCCAACCCTGATACGCTATGATTCGATGATACTAGGGGATA 293
10 BHa25 locus 230:ATGACCTCCTGAAGTCCCTTCCAACCCTGATACGCTACGATTCTATGATACTAGGGGATA 289
20 BHa25 locus 234:ATGACCTCCTGAGGTCCCTTCCAACCCTGATATGCTATGATTCTATGATACTAGGGGATA 293
27 BHa25 locus  83:-----------------------------------------------------GGGGATA 89
                 ............................... ...................*******

01 BHa25 locus 285:TAATGGACAGAATTTTTTCTTATATATTCATATGCCTTTATTTGCACATTTTTG-GGGAT 343
06 BHa25 locus 294:TAATGGGCAGAATTTTTTCTTATATATTCATATGCCTT-ATTTGCAGATTTTTT-GCGAT 351
10 BHa25 locus 290:TAATAGGCAGAATTTTTTCTTATATATTCATATGCCTT-ATTTGCAGATTTTTT-GCGAT 347
20 BHa25 locus 294:TAATGGGCAGAATTTTTTCTTATATATTCATATGCCTT-ATTTGCACATTTTTT-GGGAT 351
27 BHa25 locus  90:TAATGGGCAGAATTTTTTCTTGTATATTCATATGCCTT-ATTTGCACATTTTTTTGGGAT 148
                 ****.*.**************.*************** *******.******. *.***

01 BHa25 locus 344:AGTGAACGATAAAGGTAGAATTTGATGTAATCTTCAACATTGTTTTGTCTAA-TCAAGGA 402
06 BHa25 locus 352:AGTGAACGAGAAAGGTAGAATCTGATGTAGTCTTGAACATTGTTTTGTCTA-G-CAAGGA 409
10 BHa25 locus 348:AGTGAACGATAAAGGTAGAATCTGATGTAGTCTTGAACATTGTTTTGTCTAAGTCAAGGA 407
20 BHa25 locus 352:AGTGAACGATAAAGGTAGAATCTGCTGTAGTCTTGAACATTGTTTTGTCTAAGTCAAGGA 411
27 BHa25 locus 149:AGTGAACGATAAAGGTAGAATCTGATGTGGTCTTTAACATTGTTTTGTCTAAGTCAAGGA 208
                 *********.***********.**.***..****.****************...******

01 BHa25 locus 403:A                                                        403
06 BHa25 locus 410:AGC                                                      412
10 BHa25 locus 408:AGC                                                      410
20 BHa25 locus 412:AGC                                                      414
27 BHa25 locus 209:AGC                                                      211
                 *
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Supplemental Figure 5-1. Sequence alignment of BHa25 locus. GenBank accession numbers are AB249019–AB249023.

```
01 TKe30 locus   1:-------------------------------------------TC-ACTTTGCATGCAT 15
06 TKe30 locus   1:TGCCTCCTTTAA-TGCAGTTAAATCCATTAGGATGTTAAGCAGATCCACTTTGCATCCAG 59
27 TKe30 locus   1:TGCCTCCTTTAAGTGCAGTTAAATCCATTAGGATGTTAAGCAGATCCACTTTGCATCCAG 60
                 ............ ...............................**.*********.**.

01 TKe30 locus  16:GAATGATGGAATTCTTCCACACCAGTCCATTTCCACAGCAACAGGGGGGGGAAATAGCTC 75
06 TKe30 locus  60:GAATGATGGAATTCTTCCACACCTGTCCATTTCAACAGCAACAAGGGGGGGAAATAGCTC 119
27 TKe30 locus  61:GAATGATGGAATTCTTCCACACCTGTCCATTTCAACAGCAACAG---------------- 104
                 **********************.*********.*********................

01 TKe30 locus  76:AGTGGTTTAAGCATTGGCCTGCTATTCACAGGGTTGTGAGTTCARTCCTTGAGGGGACCA 135
06 TKe30 locus 120:AGTGATTTAAGCATTGGCCTGCTATACCCAGGATTGTGAGCCCAATCCTTGAGGGGGCCA 179
27 TKe30 locus 104:------------------------------------------------------------ 104
                 .... ..................... . .... .......   .. ........... ...

01 TKe30 locus 136:TTTAGGGATCTGGGGCAAAA-TCTGTCTGGGGATTGGTCCTGCTTTGAGCAGGGGGTTGT 194
06 TKe30 locus 180:TTTAGGGATCTGGGGCAAAAATCTGTCTGGGGATTSGTCCTGGTTGGAG----------- 228
27 TKe30 locus 104:------------------------------------------------------------ 104
                 ..................... ............... ...... .. ...

01 TKe30 locus 195:ACTAGATAACCTCCTAAGGTCCCTTCCAAGCCTGACATTCTATGATTTCTATGATAAGAT 254
06 TKe30 locus 229:--TAGATGACCTCCTAAGATCCCTTCCAACCCTGACATTCTATGATTTCTATGATAAGAT 286
27 TKe30 locus 105:---------------------------------------------------GA-GAGAT 111
                  ..... .......... .......... .......................**..****

01 TKe30 locus 255:GCCAGCCCAATAACATTCACTATGGGAAATAACTTCTCTCTCTCTGCATGAGAGCTTTCT 314
06 TKe30 locus 287:GCCAGCCCAATAACATTCACTATGGGAAATAATTTCTCTCTCTCTACATGAGAGCTTCCT 346
27 TKe30 locus 112:GCCAGCCCAATAACATTCACTATGGGAACTAACCTCTCTCTCTCTGCATGAGAGCTTCCT 171
                   ****************************.***..***********.***********.**

01 TKe30 locus 315:TCTAATTTGGGTAACTTCAAACTCTGGC                            342
06 TKe30 locus 347:TGTAATTTGGGTAACTTCAAACTCTGGCATTTTTGTGAATT                 387
27 TKe30 locus 172:TCTAGTTTGGGTAACTTCAAACTCTGGCATTTTTGTGAATT                 212
                 *.**.**********************
```

Supplemental Figure 5-2. Sequence alignment of TKe30 locus. GenBank accession numbers are AB249024–AB249026.

```
01 TKe40 locus   1:ATCACAGGTTTCCCCTCTTATTTTCTTTACTCATAGGCTTTTCTATAGCTCTCACTATTG 60
06 TKe40 locus   1:ATCACAGGTTTCCCCTCTTATTTTCTTTAGTCATTGGCTTTTCTATAGCTCTCACTATTG 60
27 TKe40 locus   1:ATCACAGGTTTYCCCTCTTATTTTCTTTACTCATTGGCTTTTCTATAGCTCTCACTATTG 60
                 ***********.*****************.****.************************

01 TKe40 locus  61:TAGCAT-TAAGTGCCTACAAAACACTCCCTGTGAGGCAAAGAAGTGGCCAGGGGG-ATGG 118
06 TKe40 locus  61:TAGCATATAAGTGCCTAAAAAACACTCCCTGTGAGGCAGAGAAGTGGCCAGGGGGGAAGG 120
27 TKe40 locus  61:TAGCATATAAGTGCCTAAAAAACACCCTCTGTGAGGCAGAGAAGT--------------- 105
                 ******.**********.*******.*.**********.******.......... . ..

01 TKe40 locus 119:ATGGCTCAGTGGTTTGAGCACTGGCCAGCTAAACCCAGGGTTGTGAGCTCAATCCTTGAG 178
06 TKe40 locus 121:ATAGCTCAGTGGTTTGAGCACTGGCCTGCTAAACC-AGGGTTGTGAGTTCAATCCTTGAC 179
27 TKe40 locus 105:------------------------------------------------------------ 105
                 .. ........................ ........ ........... ...........

01 TKe40 locus 179:GGAACCATTTAGGGAC-------AAAAATCTGTCTGGGGATTGATCCTGCTTTGAGCAGG 231
06 TKe40 locus 180:AGGACCATTTAGGGACCTGGGGCAAAAATCTGTCTGGGGATTGATCCAGCTTTGAGCAGG 239
27 TKe40 locus 105:------------------------------------------------------------ 105
                . .............       ......................... ............

01 TKe40 locus 232:GAGTTGTACTAGACAACCTTTTGAGGTCCCTTCCAACCCTGATATTCTATAATTATTGTC 291
06 TKe40 locus 240:GAGTTGTACTAGATGACCTTCTGAGGTCCCTTCCAATTCTGATATTCTATGATTATCATC 299
27 TKe40 locus 106:--------------------------------------------------ATTATTATC 114
                .............  ..... ................  ............. *****..**

01 TKe40 locus 292:CTCTTTTTCTAGATGGGGACCTAGGACTTGCTGGTTAAGTTACTTAACTTCTCCACCACA 351
06 TKe40 locus 300:CTCTTTTTCTAGATGGGGACCTAGGACTTGCTGGTTAAGTTACTTAACTTCTCCATCACA 359
27 TKe40 locus 115:CTCTTTTTCTAGATGGGGACCTAGGACTTGCTGGTTAAGTTACTTAACTTCTCCATCACA 174
                 ******************************************************.****

01 TKe40 locus 352:TATATAAAGTGAGAGAAACAGGATATGAGCCCAGACCTCCCAAGATTCAATCCAAGTCTT 411
06 TKe40 locus 360:TATATAAAGTGAGAGAAACAGGATATGAACCCAGACCTCCCAAGATTCAATC-A      412
27 TKe40 locus 175:TATATAAAATGAGAGAAACAGGATATGAACCCAGACCTCCCAAGACTCAATCCAAGTCTT 234
                 ********.******************.***************.******.*......

01 TKe40 locus 412:TAGCCA                                                417
27 TKe40 locus 235:TAGCCA                                                240
                 ......
```

Supplemental Figure 5-3. Sequence alignment of TKe40 locus. GenBank accession numbers are AB249027–AB249029.

```
01 TTh26 locus   1:TTCATGATGTTTCACTCACCTATTTTATTGTTTCTC--------TCTTCTGCAAACCCAT 52
06 TTh26 locus   1:TTCATGATGTT-CACTCACCTATTTTATTATTTCTC--------TCTTCCACAAACCCAA 51
24 TTh26 locus   1:--------------------TATTTTATTGTTTCTCCCCATTTTATTGTTACAAACCCAT 40
27 TTh26 locus   1:----------------------------------------TTTTTTTTTCACAAACCCAT 20
28 TTh26 locus   0:------------------------------------------------------------ 0
                              ......... ......         . ..  ..........

01 TTh26 locus  53:TGTAATTTTTTTTT-------ATGTTAGTGATAGTGCTTGAGTCTGTGTCTGTGTTAAGG 105
06 TTh26 locus  52:TGTAATCTTTTTTTTTTTTTAATGTTAGTGATAGTGTTTGAGTCTGTACCTGTGTTAAGG 111
24 TTh26 locus  41:TGTAATCTTTTTTTTTT---AATGTTAGTGATAGTGCTTGAGTCTGYGTCTGTGTTAAGG 97
27 TTh26 locus  21:NGNANTTTTTTTTTTTT---AATGTTAGAGATATCGCTTGAGTCTGTGCCTGTGTTAAGG 77
28 TTh26 locus   1:-GTAATCTTTTTTTT-----AATGTTAGAGATATTGCTTGAGTCTGTGCCTGTGTTAAGG 54
                 .*.*.*.*******...   .*******.****..*.*********...***********

01 TTh26 locus 106:TATGGAGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTACTAAACCCCAGGTTGTGA 165
06 TTh26 locus 112:TACTGAAGGGAGGGATAGGTCAGTGGTTTGAGCATTGGTCTCCTAAACTCCAGGTTGAGA 171
24 TTh26 locus  98:TATGGAGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTACTAAACCCCACRTTGTGA 157
27 TTh26 locus  78:TACTGA------------------------------------------------------ 83
28 TTh26 locus  55:TACTGA------------------------------------------------------ 60
                 **..** ........... ................... .. ...... ...  ... ..

01 TTh26 locus 166:GTTTAATCCCTGAGGGGGCCATCTGGGGCAAAATCAGTACTTGGTCCTGCTAGTGAAGAC 225
06 TTh26 locus 172:GTTTATTCCCTTAGGAGGCCATCTGGGGCAAAATCAGTACTTGGTCCTGCTAGTGAAGGC 231
24 TTh26 locus 158:GTTTAATCCCTGAGGGGGCCATCTGGGGCAAAATCAGTACTTGGTCCTGCTAGTGAAGAC 217
27 TTh26 locus  83:------------------------------------------------------------ 83
28 TTh26 locus  60:------------------------------------------------------------ 60
                 ..... ..... ... ........................................... .

01 TTh26 locus 226:AGGGGGCTAGACTTGATGACCTTTTAGGGTCCCTTCCAGTTCTATGAGATAGGTATATTT 285
06 TTh26 locus 232:AGGGGGCTGGACTTGATGACCTTTTAGTGTCCCTTCCAGTTCTATGAGATATGTATATCT 291
24 TTh26 locus 218:AGGGGGCTGGACTTGATGACCTTTTAGGGTCCCTTCCAGTTCTATGAGATAAGTATATCT 277
27 TTh26 locus  83:------------------------------------------------------------ 83
28 TTh26 locus  60:------------------------------------------------------------ 60
                 ........ ................. ...................... ...... .

01 TTh26 locus 286:CCATATATTATAACCATCAGGTATTCCAGTGGACTGAGATAACACCAAGCAGTTTCATCC 345
06 TTh26 locus 292:TCATATATTATAACCATCAGGCATTCCAGTGGACTGAGAAAACACCAAGTAGTTTCATCC 351
24 TTh26 locus 278:CCATATATTATAACCATCAGGCATTCCAGTGGACTGAGATAACACCAAGTAGTTTCATCC 337
27 TTh26 locus  84:------------ACCATCAGGCATTCCAGTGGACTGAGATAACACCAAGTAGTTTCATCC 131
28 TTh26 locus  61:------------ACCATCAGGCATTCCAGTGGACTGAGATAACACCAAGTAGTTTCATCC 108
                  ...........*********.****************.*********.**********

01 TTh26 locus 346:TATAGTGTAAGAAGTTTTGAATAACACCCAAATCTTATCCATCCTAGTTGACCACTTTAT 405
06 TTh26 locus 352:TACAGTGTAAGAAGTTTTGAATATCACCCAAATCTTCACCATCCTAGTTGACCTCTTTAT 411
24 TTh26 locus 338:CATAGTATAAGAAGTTTTGAATAACACCCAAATTTTATCCATCCTAGTTGACCACTTTGT 397
27 TTh26 locus 132:TATAATGCAAGAAGTTTTTAATAACACCCNAATCATACCCATCCTAGTTGACCTCTTTGT 191
28 TTh26 locus 109:TATAATGCAAGAAGTTTTTAATACCACCCAAATCATACCCATCCTAGTTGACCTCTTCGT 168
                 .*.*.*..**********.****.*****.***..*. ***************.***..*

01 TTh26 locus 406:GGGTAATTCATCTGGCTGAAATAACTTTGTTTCCATGGAAGAACTTCATGGCATTA    461
06 TTh26 locus 412:GAGTAATTCATCTGGCCGAAATAACTTTGTTTCCATGGAAGA-CTT             456
24 TTh26 locus 398:GGGTAATTCATCTGGCTGAAATAACTTTGTTTCCAT                      433
27 TTh26 locus 192:GGGTAATTCATATGGCTGAAA                                   212
28 TTh26 locus 169:GGATAATTCATCTGGCTGAAATAACTTTGTTTCCAT                      204
                 *..********.****.****...............
```

Supplemental Figure 5-4. Sequence alignment of TTh26 locus. GenBank accession numbers are AB249030–AB249034.

```
01 BOs240 locus   1:AGGTGACCCAGTGAGTCAGTGGAAAAGCCTGGAATAGAAGCCAGTTTTCTCAGCTCCCAA 60
06 BOs240 locus   1:AGGTGACCCAGTGAGTCAGTGGAAAAGTCTGGAATAGAAGCCAATTCTCCCAGCTCCCAA 60
27 BOs240 locus   1:AGGTGACCCAGTGAGTCAGTGGAAAAGTCCGGACTAGAAGCCAGTTCTCCCAGCTCCCAA 60
                  ***************************.*.***.*********.**.**.**********

01 BOs240 locus  61:CCCCACATTAAATCCTCAGGCTGCCCCATTCATGTTTAATGTTAACAGGAGGGAGGGATA 120
06 BOs240 locus  61:CCTCACATTAAATCCTCAGGCTGCCCCAGTCATGTTTAACGTTAACAGGAGGGAGGGATA 120
27 BOs240 locus  61:CCTCACATTAAATCC----------CCATTTATGTTTAATG------------------- 91
                  **.************..........***.*.********.*...................

01 BOs240 locus 121:TATCAGTGGTTTGAGCACTGGCCCATTAAATCCAGGGTTGTGAGTTCAATCCTTGAGGGG 180
06 BOs240 locus 121:GCTCAGTGGTTTGAGCATTGGCC----------AGGGTTGTGAGTTCAATCCTTGAGGGG 170
27 BOs240 locus  91:------------------------------------------------------------ 91
                  ............... .....          ...........................

01 BOs240 locus 181:GCCATTTAGGGAACTGGGGTAAAAATCTGTCTGGGGACTGGTCCCGCTCTGAGCAGCGGG 240
06 BOs240 locus 171:GCCATTTTGAGAACTGGGGTAAAAATCTGTCTGGGGACTGGTCCTGCTCTGAGCAGGGAG 230
27 BOs240 locus  91:------------------------------------------------------------ 91
                  ....... . ..................................... ........... . .

01 BOs240 locus 241:TTGGGCTAGATGACCTCCTGAGGTCCCTTCCAACCCTGATGTTCTATGATTCTATTAATG 300
06 BOs240 locus 231:CTGGGCAAGATGACCTCCTGAGGTCCCTTCCAACCCTGATGTTCTATGAGTCTGTGACCA 290
27 BOs240 locus  91:------------------------------------------------------------ 91
                    ..... ............................................ ... . .

01 BOs240 locus 301:CATCTCTAACTGTATCCTGTATTTTATACTGTGGGTAAACCAGCCAGGGCTTCAGCCTAC 360
06 BOs240 locus 291:CTWCTCTAACTGTATCCTGTATTTTATACTGTGGATAAACCAGACAGGGCTTCAGCCTAC 350
27 BOs240 locus  92:CATCTCTAACTGTATCCCGTATTTTATACTGTGGGTAAATCAGACAGGGCTTCAGCCCAC 151
                  *..**************.****************.****.***.*************.**

01 BOs240 locus 361:AATAGGCAGAATGTTTATTTTAGATGAATATTTGGGATACATGCTCATTTCCAAA--CAT 418
06 BOs240 locus 351:AATAGGCAGAAAGTTTATTTTAGATGAATATTTGGAATACATGCTCATTTCTAAAAACAT 410
27 BOs240 locus 152:AATAGGCAGAATGTTTATTTTAGATGAATATTTGGAATACATGCTCATTTCTAAA--CAG 209
                  ***********.**********************.***************.***  **.

01 BOs240 locus 419:CTCATATAATGCAGATTTCTTCCCAAAGTTTGTCTT                      454
06 BOs240 locus 411:CTCATATARTGCAKATTCCTTCCCAAAGTTTGTCTTCAAGGAGCCAC             457
27 BOs240 locus 210:CTCATATAATGCAGATTTCTTCCCAAAGTTTGTCTTCAAGGAGCCAC             256
                  ********.****.***.*****************
```

Supplemental Figure 5-5. Sequence alignment of BOs240 locus. GenBank accession numbers are AB249035–AB249037.

```
01 BCr01 locus   1:GTTCAATCCAGCCAAGTTTTGTA-GAGCCTTTTTTGACCTCATGAAGGAATGAATAAAAC 59
06 BCr01 locus   1:GTTCAATCCAGCCAAGTTTTGTACGAACCATTTTTGACCTCATGAAGGAATGAATAAAAC 60
10 BCr01 locus   1:------------CAAGTTT-GTACGAACCGTTTTTGACCTCATGAAGGAATGAATAAAAC 47
14 BCr01 locus   1:GTTCAATCCAGCCAAGTTTTGTACGAGCCATTTTTGACCTCGTGAAGGAATGAATAAAAC 60
20 BCr01 locus   1:----------------------------CCATTTT-GACCTCATGAAGGAATGAATAAAAC 32
22 BCr01 locus   1:------------------TTGTACGAGCCATTTT-GACCTCATGAAGGAATGAATAAAAC 41
27 BCr01 locus   1:GTTCAATCCAGCCAAGTTTTGTACAAGCCATTTTTGACCTCATGAAGGAATGAATAAAAC 60
                 ...........................**.****.******.******************

01 BCr01 locus  60:CACAACAGCTATTTTATTTGTTAGGGAGCACACTCCCCTATCTCTCTTTCTCTTATGGTT 119
06 BCr01 locus  61:CACAACAGCTATTTTATTTGTTAGGGAGCACACTCCCCTCTCTCTCTTTCTCTTATGGTA 120
10 BCr01 locus  48:CACAACAGCTATTTTATTTGTTAGGGAGCACACTCCCCTCTCTCT--TTCTCTTATGGTA 105
14 BCr01 locus  61:CACAACAGCTATTTTATTTGCTAGGGAGCACACTCCCCTCTCTCTCTTTCTCTTATGGTA 120
20 BCr01 locus  33:CACAACAGCCATTTTATTTGTTAGGGAGCACACTCCCCTCTCTCTCTGTCTCTTATGGTA 92
22 BCr01 locus  42:CACAACAGCTATTTTATTTGTTTGGGAGCACACTCCCTTCTCTCTCTTTCTCTTATGGTA 101
27 BCr01 locus  61:CACAACAGCTATTTTATTTGTTAGGGGGACACTTCTCCT-TCTCTCTTTCTCTCATGATA 119
                *********.**********.*.***.*.....**.*.*.*****...*****.***.*.

01 BCr01 locus 120:CTGTAAATATCAAAAACAATTTAAAATATCACAGTTGAACTCCTATAAAAGGTCCATTTA 179
06 BCr01 locus 121:CTGTAAATATCAAAAACAATTTAAAATACCAC-------------------------TTA 155
10 BCr01 locus 106:CTGTAAATATCAAAAACAAGTTAAAATACCAC-------------------------TTA 140
14 BCr01 locus 121:CTGTAAATATCAAAAACAATTTAAAATATCAC-------------------------TTA 155
20 BCr01 locus  93:CTGTAAATATCAAAAACAATTTAAAATACCAC-------------------------TTA 127
22 BCr01 locus 102:CTGTAAATATCAAAAACAATTTAAAATACCAC-------------------------TTA 136
27 BCr01 locus 120:CTGTAAATATCAAAAACAATTTAAAATACCACAGTTGAACTACTATAAATGGTCCACTTA 179
                *******************.********.***                        ***

01 BCr01 locus 180:AAATTCAATCCAATAAAAGCAAACAAGAGGGACCAATACAAAATAAGGGGAAAAGGAATG 239
06 BCr01 locus 156:AAATTCAAGCCAATAAAAGCAAACAAGAGGGACCAATACAAAATAAGGGGAAAAAGAATG 215
10 BCr01 locus 141:AAATTCAAGCCAATAAAAGCAAACAAGAAGGACCAATACAAAATAAGG--AAAAAGAATG 198
14 BCr01 locus 156:AAATTCAAGCTAATAAAAGCAAACAAGAGGGACCAATACAAAATAAGGGGAAAAAGAATG 215
20 BCr01 locus 128:AAATTCAAGCCAATAAAAGCAAACAAGAGGGACCAATACAAAATAAGGGGAAAAAGAATG 187
22 BCr01 locus 137:AAATTCAAGCCAATAAAAGCAAACAAGCGGGACCAATACAAAATAAGGGGAAAAAGAATG 196
27 BCr01 locus 180:AAATTCAAACGAATAAACGCAAACAAGAGGGCCCAATACAAAATAAGGGAAAAAGGAATG 239
                ********.*.******.*********..**.****************..****.*****

01 BCr01 locus 240:GGAGAGAAA---TGATACATGTGAGGTTAATCTTAACACATATTTGGAAATATTTGGGGG 296
06 BCr01 locus 216:AGAGAAAATAGATGATACATGTGAGGTTAATCTTTACACATATTTAGAACTATTTGGAGG 275
10 BCr01 locus 199:AGAGAAAAAAGATGATACATGTGAGGTTAATCTAAACACATATTTGGAAATATTTGGAGT 258
14 BCr01 locus 216:AGAGAAAAAAGATGATACATGTGAGGTTAATCTTAACACATATTTGGAAATATTTGGAGG 275
20 BCr01 locus 188:AGAGAAAAAAGAGGATACATGTGAGGATAATCTTAACACATATTTGAAAATATTTGGAGG 247
22 BCr01 locus 197:AGAGAAAAAAGATGATACATGTGAGGTTAATCTTAATACACATTTAGAAATATTTGGAGG 256
27 BCr01 locus 240:AGAGAGAAA-GATGATACATGTGAGGTTAATCTAAACACATATTTGGAAA---------- 288
                .****.**.....*************.******..*.***.****..**...........

01 BCr01 locus 297:GAGGGATAGCTCAGTGGTTTGAGCACTGGCCTACT-AAACACAGAGTTGTGAGTCCAATC 355
06 BCr01 locus 276:GAGGGATAGCTCAGTGGTTTGAGCAGTGGCCTACTTAAACCCAGGGTTGTGAGTTCAATC 335
10 BCr01 locus 259:GGGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAAACACAGGGTTGTGAGTTCAGTC 318
14 BCr01 locus 276:GAGGGATAGCTCAGTGGTTTGAGCATTGGC----TCAAAGCCAGGGTTGTGAGTTCAGTC 331
20 BCr01 locus 248:GAGGGATAGCTCAGTNGTTTGAGCATTGGCCTGCT-AAAGTGAGGGTTATTAGTTCAATC 306
22 BCr01 locus 257:GAGGGATAGCTCAGTGGTTTGAGCATTGGCCT-----------GGGTTATGAATTCAATC 305
27 BCr01 locus 288:------------------------------------------------------------ 288
                ............................... .. ...  ..................

01 BCr01 locus 356:CTTAAGAGGGCCACTTAGGAATCTGGGGCAAAAATCAGTACTTGGTCCTGCCAATGAAGG 415
06 BCr01 locus 336:CTTGAGAAGGCCACCCAGGGATCTGGGGCAAAAATTAGTACTTGGTCCTGCTAGTGAAGG 395
10 BCr01 locus 319:CTTGAGAGGACCACTTAGGGATCTGGGGCAAAAATTAGTACTTGGTCCTGCTAGTGAAGG 378
14 BCr01 locus 332:CTTGAGAGGGCCACTTAGGGATCTGGGGCAAAAATCAGAACTTGGTCCTGCTAGTGAAGG 391
20 BCr01 locus 307:CTTGAGAGGGCCACTTATGGATCTGGGGCAAAAATTAGTATGTGGTCCTGCTAGTGAAGG 366
22 BCr01 locus 306:ATCCAGAGAGCCACTTAGGGATCTGGGGCAAAAATTAGTACTTGGTCCTGCTAGTGAAGG 365
27 BCr01 locus 288:------------------------------------------------------------ 288
                ............................................................

01 BCr01 locus 416:CAGGGGCCTGGACTCAATGACCTTTCAAGGTCCCTTCTAGTTCTAGGACATAGGTATATC 475
06 BCr01 locus 396:CAGAGGATAGAACTCAATGATCTTTCAAGGTCCCTTCCGGTGATAGG-------TATATC 448
10 BCr01 locus 379:CAGAGGGTGGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGACAGGTATATC 438
14 BCr01 locus 392:CAGAGGGCTGGACTCAATGACCCTTCAGGGTCCCTTCCAGTTCTAGGAGATAGGTACATC 451
```

```
20 BCr01 locus 367:CAGAGGGCTGAACTCCATGACCTTTNAAGGGCC------ATCCTAGGAGATAGG------ 414
22 BCr01 locus 366:CAGAGGGCTGGAC--------CTTTCAAGGTCCCTCCCAGTTCTAGGAGATAGGTATATC 417
27 BCr01 locus 288:------------------------------------------------------------ 288
                ............................................................

01 BCr01 locus 476:TCCTATTATAATGAAAATAATTTTTTT-CAGATGCTTTTCAAAACAGAAACAAGATGACC 534
06 BCr01 locus 449:TCCTATTATAATGAAAAAGATGCTTTT-CA-----------AAACAGAAACAAGATAACC 496
10 BCr01 locus 439:TCCTATTATAATGAAAAAGATTCTT---------------------------------- 463
14 BCr01 locus 452:TCCTATTATAATGAAAAAGATTTTTTT-CAGATGCTTTTCAAAACAGAAACAAGATGACC 510
20 BCr01 locus 415:----AATGAAATGAAAAAGATTTTTTT-CAGATGCTTTTCAAAACAGAAACAAGATGACC 469
22 BCr01 locus 418:TTCTATTATAATGAAAAATATTTTTTTTCAGATGCTTTTCAAAACAGAAACAAGATGACC 477
27 BCr01 locus 289:----------------AAGAATTTTTT-CAGATGCTTTTCAAAACAGAAACGAGATGACC 331
                ................*..*...**.. ...............................

01 BCr01 locus 535:TGAGACAGAGTTCAGCAGCAAGAGTAGATTCCACATCTACCAGCACAAGTTCATGAGGGT 594
06 BCr01 locus 497:TGAGACAGAGTTCAGAAGCAAGAGTAGATTCCACATCTACCAGCACAAGTTCATGAGGGT 556
10 BCr01 locus 464:---------ACTCAGCAGCAAGAGTAGATTCCACATCT-CCA-CACAAGT-CATG     506
14 BCr01 locus 511:TGAGACAGAGTTCAGCAGCAAGAGTAGATTCCACATCTACCAGCACAAGTTCATGAGGGT 570
20 BCr01 locus 470:TGAGACAGAGTTCAGCAGCAAGAGTAGATTCCACATCT-CCACCA             513
22 BCr01 locus 478:TGAGACAGAGTTCAGCAGCAAGAGTAGATTCC-CATTTACCAGCACA            523
27 BCr01 locus 332:TGAGAGAG--TTCAGCAGCAAGAGTAGATTCCACATCTACCAGCACAAGTTCATGAGGGT 389
                ...........****.****************.***.*.***.**...............

01 BCr01 locus 595:GCTTTT                                                   600
06 BCr01 locus 557:GCTTTT                                                   562
14 BCr01 locus 571:GCTTTT                                                   576
27 BCr01 locus 390:GCTTTT                                                   395
                ......
```

Supplemental Figure 5-6. Sequence alignment of BCr01 locus. GenBank accession numbers are AB249038, AB125704-AB125708, and AB125525.

```
01 BCr06 locus   1:-------------GTTTCTAGATTTGGAATGTAGTCTAATATATCTATGTAGATAAATCC 47
14 BCr06 locus   1:GATTCTTCCCGGAGTTTCTAGATTTGGAATGCAGACTAACACATCTGTGTAGATAAATCC 60
27 BCr06 locus   1:GATTCTTCCCGGAGTTTCTAGATTTGGAATGCAGACTAACACATCTGTGTAGATAAATCC 60
28 BCr06 locus   1:GATTCTTCCCGGNGTT-CTAGATTTGGAATGCAGACTAATACATCTGTGTAGATAAATCC 59
                 ............ ***.**************.**.**** *.****.*************

01 BCr06 locus  48:CTGTAAAATGCAAAACATTTAA-ACAAGCATCACATGTTTACTGGATAGCACCTCTTTTT 106
14 BCr06 locus  61:CTGTAAAATGCAAAACAGTTAACACAAGCATCATATGTTTACTGGATAGCACCTCTTTTA 120
27 BCr06 locus  61:CTGTAAAATGCAAAACGTTTAA-ACAAGCATCATATTTTTACTGGATAGCACCTCTTTTT 119
28 BCr06 locus  60:CTGTAAAATGCAAAACGTTTAA-ACAAGCATCACATTTTTACTGGATAGCACCTATTTTT 118
                **************** .**** ********** ** *****************.****.

01 BCr06 locus 107:T-CATTTTAAAGGGGGAGGGATAGCTTAGTGGTTTGAGCATTGGCCTATTAAACCCAGAA 165
14 BCr06 locus 121:TTCATTTTAAAGGGGGAGGGATAGCTTAGTGGTTTGAGCATTGGCCTAGTAAACCCAGAA 180
27 BCr06 locus 120:T-TATTTTAAA------------------------------------------------ 129
28 BCr06 locus 119:T-CATTTTAAA------------------------------------------------ 128
                * .********

01 BCr06 locus 166:ATGTGAGCTCAATCTTTGAGGGGGCCACTTAGGGATCTAGGGCAAAAATCAGTACTTGGT 225
14 BCr06 locus 181:TTATGAGTTCAATCCTTGAGGGGACCACTTAGGGATCTAGGGCAAAAATCAGTACTTGGT 240
27 BCr06 locus 129:------------------------------------------------------------ 129
28 BCr06 locus 128:------------------------------------------------------------ 128


01 BCr06 locus 226:CCCACTAGTGAAAGCAGGGGGCTGGACTCAATGACCTTTCAGGGTCCCTTCCAGTTCTAT 285
14 BCr06 locus 241:CTCACTAGTGAAAGCAGGGGGCTGGACTCAATGACCTTTCAGGGTCCCTTCCAGTTCTAT 300
27 BCr06 locus 129:------------------------------------------------------------ 129
28 BCr06 locus 128:------------------------------------------------------------ 128


01 BCr06 locus 286:GAGATAGGTATATTTCCATATATTATATTATAAAAAGCTCTGTCAATTGTATAAACAAAT 345
14 BCr06 locus 301:GAGAGAGGTATATCTCCATATATTATATTATAAAAAGCTCTGTCAATTGTATAAACAAAT 360
27 BCr06 locus 130:----------------------------------AAGCTCTGTTAATTGTATAAACAAAT 155
28 BCr06 locus 129:----------------------------------AAGCTCTGTCANTTGTATAAACAAAT 154
                                             *********.*.**************

01 BCr06 locus 346:GCTATTTTCCAGTGTGAATGCACCATTGACAATTTGATACCAAACACTTAAGGG-TTTAA 404
14 BCr06 locus 361:GCTATTTTCCAGTGTAAATGCGCCATTGACAATTTGATACCAAACACTTAAGGG-TTTAA 419
27 BCr06 locus 156:GCTATTTTCCAGTGTGAATGCGCCATTGACAATTTGATACCAAACACTTAAGGG-TTTAA 214
28 BCr06 locus 155:GCTATTTTCCGGTGTGAATGTGCCATTGATAATCTGATACCAAACACTTAAGGGGTTTAA 214
                **********.****.****..*******.***.******************* *****

01 BCr06 locus 405:AA-CTAATTATGGCAATCTATCCCACAACTTTAACTTTTTTGTAACCCC          452
14 BCr06 locus 420:AAACTAATTATGACAATCTATCCCACAACTTGAACTTTTTTGTAACCCCTCAGTGAAAAC 479
27 BCr06 locus 215:AAACTAATTATGACAGTCTATCCCACAACTTGAACTTTTTTGTAACCCCTCAGTGAAAAC 274
28 BCr06 locus 215:AAACTAATTATGACAGTCTATCCCACAACTTGAACTTTTTTGTAACCC-TCA        265
                **.*********.** ***************.****************.

14 BCr06 locus 480:AC                                                   481
27 BCr06 locus 275:AC                                                   276
```

Supplemental Figure 5-7. Sequence alignment of BCr06 locus. GenBank accession numbers are AB249039, AB249040, AB125703, and AB125526.

```
01 TKe17 locus   1:TGTTTCATCCCAGTTCTCCTATGTAGGTCTTGTCTGCACTACAAAGCTGTACAGCATTAA 60
06 TKe17 locus   1:TGTTTCATCCCAGTTCTCCTACGTAGGTCTTGTCGGCACTACAAAGCTGTACAGCATTAA 60
14 TKe17 locus   1:TGTTTCATCCCAGTTCTCCTACGTAGGTCTTGTCGGCACTACAAAGCTGTACAGCATTAA 60
25 TKe17 locus   1:TGTTTCATCCCAGTTCTCCTACGTAGGTCTTGTCGGCACTACGAAGCTGCACAGCATTGA 60
27 TKe17 locus   1:TGTTTCATCCCAGTTCTCCTACGTAGGTCTTGTCTGCACTACAAAGCTGTACAGCATTAA 60
                 ********************.************.*******.******.********.*

01 TKe17 locus  61:CTCAATCTGATGCAGGGGGAGAGGGATAGCTCAGTGGTTTGAGCATTGGCCCATTAAACC 120
06 TKe17 locus  61:CTCAA------------------------------------------------------ 65
14 TKe17 locus  61:CTCAA------------------------------------------------------ 65
25 TKe17 locus  61:CTCAA------------------------------------------------------ 65
27 TKe17 locus  61:CTCAA------------------------------------------------------ 65
                 *****

01 TKe17 locus 121:CAGGGTTGTGAGTTCAGTCCTTGAGGGGGCCATCTGAGGAACTGGGGTAAAAATCTGGGG 180
06 TKe17 locus  65:------------------------------------------------------------ 65
14 TKe17 locus  65:------------------------------------------------------------ 65
25 TKe17 locus  65:------------------------------------------------------------ 65
27 TKe17 locus  65:------------------------------------------------------------ 65


01 TKe17 locus 181:ATTGGTCTTGCTTTGAGCAGAGGGTTGGACTAGATGACCTCCTGAGGATGCGTCCAACCC 240
06 TKe17 locus  65:------------------------------------------------------------ 65
14 TKe17 locus  65:------------------------------------------------------------ 65
25 TKe17 locus  65:------------------------------------------------------------ 65
27 TKe17 locus  65:------------------------------------------------------------ 65


01 TKe17 locus 241:TAGTATTCTATG-------------------------------------ATTATACCAA 262
06 TKe17 locus  66:------------CCCCCGGCAGGTGGATGCAGCTATGTACACACATACATATTATACCAA 113
14 TKe17 locus  66:------------CCCCCGGCAGGTGGATGCAGGTATGTACACACATACATATTATACCAA 113
25 TKe17 locus  66:------------CCCCCGGCAGGTGGATGCAGGTATGTTCACACATACATATTATACAAA 113
27 TKe17 locus  66:------------TCCCCGGAAGGTGGATGCAGGTATGTACACACATACATATTATACCAA 113
                           ......................................*******.**

01 TKe17 locus 263:TATAGCT--ATTCCCATATGGGAAGTAGAAAGGCTGTACTGCTATAAAACACTTTTACAC 320
06 TKe17 locus 114:TATAGCT--ATTCCCATGTGGGAAGTGGAA--------CAGCTATAAAACACTTTTATAC 163
14 TKe17 locus 114:TGTAGCT--ATTCCCATATGGGAAGTGGAA--------CAGCTATAAAACACTTTTATAC 163
25 TKe17 locus 114:TATATCTCTCTTCCCATATGGGAAGTGGAA--------CAGCTATAAAACACTTTTATAC 165
27 TKe17 locus 114:TATCGCT--CTTCCCATCTGGGAAGTGGAA--------CRGCTATAAAACACTTTTATAC 163
                  *.*..**  .*******.********.***       *.*****************.**

01 TKe17 locus 321:ACCCATACTAGTTGCATGCAGGATTGCACTGGGATAAT                   358
06 TKe17 locus 164:GCCCACACTAGTTGCATGCAGGCTTGCACTGGGATAAT                   201
14 TKe17 locus 164:ACCCATACTAGTTGCATTCAGGATTGCACTGGGATAAT                   201
25 TKe17 locus 166:ACCCATACTAGTTGCATGCAGGATTGCACTGGGATAAT                   203
27 TKe17 locus 164:ACCCGTTCTAGTTGCATGCAGGATTGCACTGGGATAAT                   201
                 .***...**********.****.***************
```

Supplemental Figure 5-8. Sequence alignment of TKe17 locus. GenBank accession numbers are AB249041–AB249045.

```
01 TKe36 locus   1:-----------------------------------CAGAAAGCAACAGGTCACAGAATTA 25
06 TKe36 locus   1:AATGTGTTGGAT-CCGTAATGCAGTTTGGAGGAGACAGAAGGCAACAGGTCACAGAATTA 59
14 TKe36 locus   1:AATGTGTTGGATGCCGTAATGCAGTTTGGAGGAGACAGAAGGCAACAGGTCACAGAATTA 60
27 TKe36 locus   1:AATGTGTTGGATGCCGTAATGCWGTTTGGAGGAGACAGAAGGCAACAGGTCACAGAATCA 60
                 ............ ......... ............*****.****************.*

01 TKe36 locus  26:TGTGGATGTCTTCCAGTAAAATGCATATGGGTTTGAGTTTGTAATATAAACCCCCCTGCT 85
06 TKe36 locus  60:TGTGGATGTCTTCCAGTAAAGTGCATATGGGTTTGAGTTTGTAATATAAATCCCCATGCT 119
14 TKe36 locus  61:TGTGGATGTCTTCCAGTAAAGTGCATATGGGTTTGAGTTTGTAATATAAATCCCTGTGCT 120
27 TKe36 locus  61:TGTGGATGTCTTCCAGTAAAGTGCATATGGGTTTGAGCTTGTAATATAAATCCCCATGCT 120
                ********************.***************.************.***. ****

01 TKe36 locus  86:TGGGGGGAGGGATAGCTCAGTGGTTTGAATATTGGCCTGCTAAACCCAGGGTTGTGAGCT 145
06 TKe36 locus 120:TG------------------------------------------------------- 121
14 TKe36 locus 121:TG------------------------------------------------------- 122
27 TKe36 locus 121:TG------------------------------------------------------- 122
                **

01 TKe36 locus 146:CAATCCTTGAGAGGGTCATCTACGGCAAAATCAGTACTTGGTCCTGCTAGTGAAGGCGGG 205
06 TKe36 locus 121:------------------------------------------------------------ 121
14 TKe36 locus 122:------------------------------------------------------------ 122
27 TKe36 locus 122:------------------------------------------------------------ 122


01 TKe36 locus 206:GGACTGGACTTAATGACCTTTCAAGGTCCCTTCCAGTGCTAGGAGATTGGTATATCTCCA 265
06 TKe36 locus 121:------------------------------------------------------------ 121
14 TKe36 locus 122:------------------------------------------------------------ 122
27 TKe36 locus 122:------------------------------------------------------------ 122


01 TKe36 locus 266:ATTTATTATTATTGAGTTTACTATTGTTTTGAGCTGACAGAACTGTGGCATCAACAGAAT 325
06 TKe36 locus 122:----------CTTGAGTTTACCATTGTTTGGAGCTGACAGAAGTGTGGCATCAACAGAAT 171
14 TKe36 locus 123:----------CTTGAGTTTACCATTGTTTGGAGCTGACAGAACTGTGGCATCAACAGAAT 172
27 TKe36 locus 123:----------CTTGAGTTTACCATTGTTTTGAGCTGACAGAACTGTGGCATCAACAGAAT 172
                        .**********.******* ************.*****************

01 TKe36 locus 326:CACTGCAGTGTTTAGCTCTACTAATATTTTAAATGTTCAGGTTACTATGAGGTGA     380
06 TKe36 locus 172:CACTGCAGTGTTTAGCTCTACTAATATTTTAAATGTTCAGGTTACTATGAGGTGAAAATC 231
14 TKe36 locus 173:CACTGCAGTGTTTAGCTCTACTAATATTTTAAATGTTCAGGTTACTATGAGGTGAAAATC 232
27 TKe36 locus 173:CACTGCAGTGTTTAGCTCTACTAATATTTTAAATGTTCAGGTTACTCTGAGGTGAAAATC 232
                ********************************************.********

06 TKe36 locus 232:AATACAAGCAGCATGGAATTCC-GGAGTTTA                        261
14 TKe36 locus 233:AATACAAGCAGCATGGAATTCCTGGAG                           259
27 TKe36 locus 233:AATGCAAGCAGCATGGAATTCCTGGAGTTT                         262
                ... ................... ....
```

Supplemental Figure 5-9. Sequence alignment of TKe36 locus. GenBank accession numbers are AB249046–AB249049.

```
01 TKe83 locus   1:AGGGGTTGCTACCTGTTTAAGACTGGGGTGAAAGACTTTTGCGTTGATTTGTGAACATGT 60
06 TKe83 locus   1:AGGGGTTG-TACCTGTTTAAGACTGGGGTGAAAGACTTTTGCATTGATTTGTAAACATAT 59
14 TKe83 locus   1:AGGGGTTGCTACCTGTTTAAGACTGGGGTGAAAGACTTTTGCATTGATTTGTAAACATAT 60
27 TKe83 locus   1:AGGGGT-GC-AC--GTTTAAGACTTRGGTGAAAGACTTTTGCGTTGATTTGTGAACATGT 56
                 ******.*..**..**********..*************** ********* ***** *

01 TKe83 locus  61:CAATAAAATCAGACCAGGAGGAGGAAGGCTGTTGTCATTAGGGGGAGGGATAGCTCAGTG 120
06 TKe83 locus  60:CAATAAAATCAGACCAGGAAGAGG---GCTGTTGTCATTAG------------------- 97
14 TKe83 locus  61:CAATAAAATCAGACCAGGAGGAGG---GCTGTTGTCATTAG------------------- 98
27 TKe83 locus  57:CAATAAAATCAGACCATGAGGAGG---GCTGTTGTCATTAG------------------- 94
                ***************.**.****   **************

01 TKe83 locus 121:GTTTGAGCATTGGCCACCTAAACCTAGGGTTGTGAGTTTAGTCCTTGAAGGGGCTATTTG 180
06 TKe83 locus  97:------------------------------------------------------------ 97
14 TKe83 locus  98:------------------------------------------------------------ 98
27 TKe83 locus  94:------------------------------------------------------------ 94


01 TKe83 locus 181:GGGCAAAAATCTGTCTGGGGATTTGTCCTGTTTTGAGCAGGGGGTTGGACTAGATGACCT 240
06 TKe83 locus  97:------------------------------------------------------------ 97
14 TKe83 locus  98:------------------------------------------------------------ 98
27 TKe83 locus  94:------------------------------------------------------------ 94


01 TKe83 locus 241:CCTGAGGTCCGTTCCAACCCTGATACTCTATGATTCTATGAAAGCTTGTGGGGAGTTTAT 300
06 TKe83 locus  98:--------------------------------ACTC-ATGAAAGCTTGTGTGCAGTTTAT 124
14 TKe83 locus  99:--------------------------------ACTC-ATGAAAGCTTGTGTGGAGTTTAT 125
27 TKe83 locus  95:--------------------------------ACTC-ATGAAAGCTTGTGTGGAGTTTAT 121
                                             *.** *************.*.*******

01 TKe83 locus 301:TTAAG-AAGCCCCTTCATAGAGGGAAATTGAGGTGAAGAGCTACTTACAGGGATGCC-TG 358
06 TKe83 locus 125:TTAAG-AAGCCCCTTGATAGGGGGAAATTGTGGTGAAGAGCTACTTACAGGGCTCCCCTG 183
14 TKe83 locus 126:TTAAGTAAGCCCCTTGATAGGGGGAAATTGAGGTGAAGAGCTACTTACAGGGCTCCCCTG 185
27 TKe83 locus 122:TTAAG-AAGCCCCTTGATAGGGGGAAATTGAGGTGAAGGGCTACTTACAGGGCTCCCCTG 180
                ***** *********.****.*********.*******.*************.*.**.**

01 TKe83 locus 359:AG--------------------AGCAGGCCACTCACTGACAGTCACTTGAATCACTGATG 398
06 TKe83 locus 184:AG--------------------AGCAGGCCACTCACTGACAGTCACTTGAATCACTGATG 223
14 TKe83 locus 186:AGGCCATACAGGGATGCCTGAGAGCAGGCCACTCACTGACAGTCACTTGAATCACTGATG 245
27 TKe83 locus 181:AGGCCATACAGGGATGCCTGAGAGCAG-CCACTCACTGACAGTCACTTGAATCACTGATG 239
                **                 *****.*******************************

01 TKe83 locus 399:ATTAATRTTTCCATCTTTAATTGCTGGTATTCCCACA                    435
06 TKe83 locus 224:GTTAATGTTTCCATCTTTAATTGCTGGTATTCCCACA                    260
14 TKe83 locus 246:ATTAATGTTTCCATCTTTAATTGCTGGTATTCCCAC                     281
27 TKe83 locus 240:ATTAATGTTTCCATCTTTAATTGCGGGTATTCCCAC                     275
                .*****.*****************.***********
```

Supplemental Figure 5-10. Sequence alignment of TKe83 locus. GenBank accession numbers are AB249050–AB249053.

```
01 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACCAGAA-TGTTCATGCTATCTGGCCTTATAGGA 59
03 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACCAGAA-TGTTCATGCTATCTAGTCTTACAGGA 59
06 BHa65 locus   1:------------------------------GAA-TGTTCATGCTATCTGGTCTTATAAAA 29
10 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACTAGAA-TGTTCATGCTATCTGGTCTTATAAAA 59
11 BHa65 locus   1:CATGGAGMGAGTT-GTTGTCAAGTAAACCAGAA-TGTTCATGCTATCTGGTCTTATAAAA 58
13 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACCAGAA-TGTTCATGCTATCTGGTTTTATAAAA 59
14 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACCAGAA-TGTTCATGCTATCTGGTTTTATAAAA 59
17 BHa65 locus   1:CATGGAGAGAGTTTGYTGTCAAGTAATCATAAAATGTTCATGCTATCTGGTCTTATAAAA 60
25 BHa65 locus   1:-----------------------------------TGTTCATGCTATCTGGTCTTATAAAA 26
27 BHa65 locus   1:CATGGAGAGAGTTTGTTGTCAAGTAAACCAGAA-TGTTCATGCTAGCTGGTCTCATAAGA 59
                 ................................. ***********.**.*..*.*.*..*

01 BHa65 locus  60:AATTTTGCGTACAAGTTTATTTTGTTT--TATGTAAAACTTAAACTTAACTTAAAAATGA 117
03 BHa65 locus  60:AATGTAGTGTGCAAGTTT-TTAAGTTT--TACATAAAACC-AAAC---ACTTAAAAATGA 112
06 BHa65 locus  30:A--TTAGTGTACAAGTTTGCTTTGTTT--CATGTAAAACTTTTAA--AACTTAAAAATGG 83
10 BHa65 locus  60:---TTAGTGTACAAGTTTGTTTTGTTT--TATGTAAAACTTTTAA--AACTTAAAAATGA 112
11 BHa65 locus  59:A--TTAGTGTACACGTTTGTTTT-------ATGTAAAACTTAA----AACTTAAAAATGA 105
13 BHa65 locus  60:A--TTAGTGTACACGATTGTTTTGTTT--TATGTAAAACTTAAACTTAACTTAAAAATGA 115
14 BHa65 locus  60:A--TTAGTGTACAAGATTGTTTTGTTT--TATGTAAAACTTAAACTTAACTTAAAAATGA 115
17 BHa65 locus  61:A--TTAGTGTACAAGATTGTTTTGTGT--TATGTAAAACTTAAACTTAACTTAAAAATGA 116
25 BHa65 locus  27:A--TTAGTGTACAAGTTTGTTTTGTTT--TATGTAAAACTTAAAC-----------ATGA 71
27 BHa65 locus  60:AA-TTAGTGTACAAGTTTGTTTTGTTTCTTATGTAAAACTTAAACTTAACTTAAAAATGA 118
                 .  .*.*.**.**.*.**..*......  .*..******.....  .........***.

01 BHa65 locus 118:CATTTTATCAATGACTCTTCT---CAAAGTATTAAA------------------------ 150
03 BHa65 locus 113:CATTTTATCAATAACTCTTCTTCTCAAAGTATTAAA------------------------ 148
06 BHa65 locus  84:TATTGTTTCAATTACTATTCTTTTCAAAGTATTAAA------------------------ 119
10 BHa65 locus 113:CATTGTTTCAATTACTATTCTTTTCAAAGTATTAAA------------------------ 148
11 BHa65 locus 106:CATTGTTTCAATGACTATACTTTTCAAAGTATTAAA------------------------ 141
13 BHa65 locus 116:CATTGTTTCAATGACTATTCTTCTCAAAGTATTAAAGAATATTTT-GGGGGGAGAGATAG 174
14 BHa65 locus 116:CATTGTTTCAATGACTATTCTTCTCAAAGTATTAAAGAATAGTTTGGGGGGGAGAGATAG 175
17 BHa65 locus 117:CATTGTTTCAATGACTATTCTTCTCAAAGTATTAAAGAATAGTTTT-GGGGGAGAGATAG 175
25 BHa65 locus  72:CATTGTTTCAATGACTGTTCTTCTYAAAGTATTAAAGACTAGCTT-GTGGGGAGAGATAG 130
27 BHa65 locus 119:CATTGTTTCAATGACTATTCTTCCCAAAGTATTAAA------------------------ 154
                 .***.*.*****.***.*.**....***********

01 BHa65 locus 150:------------------------------------------------------------ 150
03 BHa65 locus 148:------------------------------------------------------------ 148
06 BHa65 locus 119:------------------------------------------------------------ 119
10 BHa65 locus 148:------------------------------------------------------------ 148
11 BHa65 locus 141:------------------------------------------------------------ 141
13 BHa65 locus 175:CTCAGTGGTTTGAGCATTGGCCTGCTAAACCCCACATTCTGAGTTCAGTCCTTGAGGGGT 234
14 BHa65 locus 176:CTCAGTGGTTTGAGCATTGGTCTGCTAAACCCCACATTCTGAGTTCAGTCCTTGAGGAGG 235
17 BHa65 locus 176:CTCAGTGSTTCAAGCATTGGCCTACTAAACCCCAGGTTCTGAGTTCAATCCTTGAGGGGG 235
25 BHa65 locus 131:CTTAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGCAAGTTCAATCCTTGAAGGGG 190
27 BHa65 locus 154:------------------------------------------------------------ 154


01 BHa65 locus 150:------------------------------------------------------------ 150
03 BHa65 locus 148:------------------------------------------------------------ 148
06 BHa65 locus 119:------------------------------------------------------------ 119
10 BHa65 locus 148:------------------------------------------------------------ 148
11 BHa65 locus 141:------------------------------------------------------------ 141
13 BHa65 locus 235:ACCACTTAGGGATCTGGGGCAAAAATTGGTC-CTGCTAGTGAAGGCAGGGGGCTGGACTC 293
14 BHa65 locus 236:ACCACTTAGGGATCTGGGGCAAAAATTGGTC-CTGCTAGTGAAGGCAGGGGGCTAGACTC 294
17 BHa65 locus 236:ACCACTTAGGGATCTGGGGCAAAAATTGGTC-CTGCTAGTGAAGGCAGGGG-TTAGACTC 293
25 BHa65 locus 191:-CCACTTAGGGCTCTGGGGCAAAAATTGGACACTGCTAGTGAAGGCAGGGGGCTGGACTC 249
27 BHa65 locus 154:------------------------------------------------------------ 154


01 BHa65 locus 150:------------------------------------------------------------ 150
03 BHa65 locus 148:------------------------------------------------------------ 148
06 BHa65 locus 119:------------------------------------------------------------ 119
10 BHa65 locus 148:------------------------------------------------------------ 148
11 BHa65 locus 141:------------------------------------------------------------ 141
13 BHa65 locus 294:AATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCTATTATTATT-- 351
14 BHa65 locus 295:AATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATT-- 352
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17 BHa65 locus 294:AATGACCTTTCAAGGYCCCTTCCAGTTGTAGGAGATTGGTATGTCTCCTATTATTATTTA 353
25 BHa65 locus 250:AGTGACCTTTCAAGGTCCTTTCCAGTTCTAGGAGATAGGTATATCTCCAATTATTATTTA 309
27 BHa65 locus 154:------------------------------------------------------------ 154


01 BHa65 locus 151:-------TTCTGTATCATTACAGTACAGTATTATGGAAATTAATATACAATAGCTCTGTA 203
03 BHa65 locus 149:-------TTCTGTATCATTACAGTA-----TTATGGAAATTAATATACAATAGCTCTGTA 196
06 BHa65 locus 120:-------TTCTGTATCATTACAGTACAGTATTATGGAAATTAATATACAATAGCTCTGTA 172
10 BHa65 locus 149:-------TTCTGTATCATTACAGTACAGTATTATGGAAATTAATATACAATAGCTCTGTA 201
11 BHa65 locus 142:-------TTCTGTATCATTACAGTACAGTATTGTGGAAATTAATAAACAATAGCTCTGTA 194
13 BHa65 locus 352:--ATAAATTCTATATTATTACAGTACAGTATTATGGAAATGAATATACAATAGCTCTGTA 409
14 BHa65 locus 353:--ATAAATTCTATATCATTACAGTACAGTATTATGGAAATGAATATACAATAGCTCTGTA 410
17 BHa65 locus 354:TTATAAATTCTATATCATTACAGTACAGTATTATGGAAATGAATATACAATAGCTCTGTA 413
25 BHa65 locus 310:TTATAAATTCTGTATCATTACAGTA-----ATATGGAAATGAATATACAATAGCTCTGTA 364
27 BHa65 locus 155:-------TTCTGTATCATTACAGTACAGTATTATGGAAATTAATATACAATAGCTCTCTA 207
                      ****.***.*********......*.*******.****.***********.**

01 BHa65 locus 204:GCTGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            249
03 BHa65 locus 197:GCTGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            242
06 BHa65 locus 173:GATGTCTGAAACAACAATTGAAATGCATTGCTTTAGGGTTTCTGTT            218
10 BHa65 locus 202:GATGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            247
11 BHa65 locus 195:GATATCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            240
13 BHa65 locus 410:GATGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            455
14 BHa65 locus 411:GATGTCTGAAACAACAATGGAAATGCAT                            438
17 BHa65 locus 414:GATGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            459
25 BHa65 locus 365:GATGTCTGAAACAACAATGAAAATGTATTGCTTTAGGGTTTCTGTT            410
27 BHa65 locus 208:GATGTCTGAAACAACAATGGAAATGCATTGCTTTAGGGTTTCTGTT            253
                *.*.**************..******.**.................
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Supplemental Figure 5-11. Sequence alignment of BHa65 locus. GenBank accession numbers are AB249054–AB249063.

```
01 BHa74 locus   1:-------------ACATTTGTACTGATTTTTCTTATGACAGTTTTTTCTGTTTAGTTTTT 47
06 BHa74 locus   1:------------------------------------GACGATTTTTTCTGTTTA-TTTTT 23
10 BHa74 locus   1:AGGTTGGAAAGTTACATTTGTACTGATTTTTCTTATGACGATTTTTTCTGTTTAATTTTT 60
11 BHa74 locus   1:-GGTTGGAAAGTTACATTTGTACTGATTTTTCTTATGATGATTTTTTCTGTTTAATTTTT 59
14 BHa74 locus   1:--------------------------ATTT--CTT--GATGATTTTTTCTGTTTAATTTTT 31
18 BHa74 locus   1:AGGTTGGAAAGTTACATTTGTACTGATTTTTCTTATGACGATTTTTTCTGTTTAATTTTT 60
23 BHa74 locus   1:AGGTTGGAAAGTTACATTTGTACTGATTTTTCTTATGACGATTTTTTCTGTTTAATTTTT 60
24 BHa74 locus   1:AGGTTGGAAAGTTACATTTGTACTGATTTTTCTTATGACGATTTTTTCTGTTTAATTTTT 60
25 BHa74 locus   1:-----------------------------------TGACGATTTTTTCTGTTTAGTTTTT 25
27 BHa74 locus   1:-------------ACATTTGTACTGATTTTTCTTATGACAATTTTTTCTGTTTAGTTTTT 47
                            .......................**...*************.*****

01 BHa74 locus  48:AACCCCCAAACACCTGCTATTTTTGTTACA-TGTACTTAAAATGCAAAAATGAAAAGTAA 106
06 BHa74 locus  24:AAACCTCAAATACCTGCTATTTTTGTTAAA-TTTACACAAAATACAAAAATGAAAAGTAA 82
10 BHa74 locus  61:AAATCCCAAATACCTGCTATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 119
11 BHa74 locus  60:AAACCCCAAATACCTGCTATTTTTGGTAAA-TGTACATAAAATACAAAAATGAAAAGTAA 118
14 BHa74 locus  32:AA-CCCCAAATACCT---ATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 86
18 BHa74 locus  61:AAACCCCAAATACCTGCTATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 119
23 BHa74 locus  61:AAACCCCACATACCTGCTATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 119
24 BHa74 locus  61:AAACCCCACATACCTGCTATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 119
25 BHa74 locus  26:AA-CCCCAAATACCTGCTATTTTTGTTAAA-TTTACATAAAATACAAAAATGAAAAGTAA 83
27 BHa74 locus  48:AA-CACCAAATACCTGCTATTTTCATTAAAATGTACATAAAATACAAAAATGAAAAGTAA 106
                **....**.*.****...*****...**.* *.***..*****.***************

01 BHa74 locus 107:AGGTAT------------------------------------------------------ 112
06 BHa74 locus  83:AAGTAT------------------------------------------------------ 88
10 BHa74 locus 120:AAGTAT------------------------------------------------------ 125
11 BHa74 locus 119:AAGTAT------------------------------------------------------ 124
14 BHa74 locus  87:AAGTATTTATAAA--------------------------GAGGGGAGGGATAGCTCAGT 119
18 BHa74 locus 120:AAGTATTTATAAAGGGGGGAGGGGTAAGAGTATTTATAAAGGGGGGAGGGATAGTTCAGT 179
23 BHa74 locus 120:AAGTATTTATAAA--------------------------GGGGGGAGGGATAGCTCAGT 152
24 BHa74 locus 120:AAGTATTTATAAA--------------------------GGGGGGAGGGATAGCTCAGT 152
25 BHa74 locus  84:AAGTATTTATAAATGG-----------------------GGGGGGAGATATAGCTCAGT 119
27 BHa74 locus 107:AAGT-------------------------------------------------------- 110
                *.**..

01 BHa74 locus 112:------------------------------------------------------------ 112
06 BHa74 locus  88:------------------------------------------------------------ 88
10 BHa74 locus 125:------------------------------------------------------------ 125
11 BHa74 locus 124:------------------------------------------------------------ 124
14 BHa74 locus 120:GGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATTCTTGAGGGGGCCACTT 179
18 BHa74 locus 180:GGTTTGAGCACTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGG-CCACAT 238
23 BHa74 locus 153:GGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTCAAGGGGGCCACTT 212
24 BHa74 locus 153:GGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTCAAGGGGGCCACTT 212
25 BHa74 locus 120:GGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAACTNAATCCTTGAGGGGGCCACTT 179
27 BHa74 locus 110:------------------------------------------------------------ 110


01 BHa74 locus 112:------------------------------------------------------------ 112
06 BHa74 locus  88:------------------------------------------------------------ 88
10 BHa74 locus 125:------------------------------------------------------------ 125
11 BHa74 locus 124:------------------------------------------------------------ 124
14 BHa74 locus 180:AGGAATCTGGGGCAAAAA-TTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACC 238
18 BHa74 locus 239:AGGGATCTGGGGCAAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACC 298
23 BHa74 locus 213:AGGGATCTGGGGCAAAAA-TTGGTCCTGCTAGTGAGGGCAGGGGGATGGACTCAATGACC 271
24 BHa74 locus 213:AGGGATCTGGGGCAAAAA-TTGGTCCTGCTAGTGAAGGCAGGGGGATGGACTCAATGACC 271
25 BHa74 locus 180:AGGGATCTGGGGCAAAAA-TTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACC 238
27 BHa74 locus 110:------------------------------------------------------------ 110


01 BHa74 locus 112:------------------------------------------------------------ 112
06 BHa74 locus  88:------------------------------------------------------------ 88
10 BHa74 locus 125:------------------------------------------------------------ 125
11 BHa74 locus 124:------------------------------------------------------------ 124
14 BHa74 locus 239:TTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTTATTTATTA 298
18 BHa74 locus 299:TTTCAAGGTCCCTTCCAGTTCTAGGAGATAGGTATATCTCCAATTATTATTTATTTATTA 358
23 BHa74 locus 272:TTTCAAGGTCTCTTCCGGTTCTAGGAGATTGGTATACCTCCAATTATTATTTATTTATTT 331
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24 BHa74 locus 272:TTTCAAGGTCTCTTCCGGTTCTAGGAGATTGGTATACCTCCAATTATTATTTATTTATTT 331
25 BHa74 locus 239:TTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCT-----------------TTTA 281
27 BHa74 locus 110:------------------------------------------------------------ 110


01 BHa74 locus 113:---TT-ATATTTCTGCTAACATTTTTTTCTACATATTTAGAAAAATCAATGGTGGTCAAA 168
06 BHa74 locus  89:---TT-ATATTTCTGCTAACATTTTTTTCTACATATTTAGAAAAATTAATGGCGGCCAAA 144
10 BHa74 locus 126:---TT-ATATTTCTGCTAACATTTTTTTCTACATATTTAGAAAAACTAATGGCGGCCAAA 181
11 BHa74 locus 125:---TT-ATATTTCTGCTAACATTTTGT-CTACATATTTAGAAAAATTAATGGTGGCCAAA 179
14 BHa74 locus 299:TTATT-ATATTTCTGCTAACATTTTTT-CTACCTATTTAGAAAAATTAATGGTGGCCAAA 356
18 BHa74 locus 359:TTATT-ATGTTTCTGCTAACATTTTTT-CTACATATTTAGAAAAATTAATGGTGGCCAAA 416
23 BHa74 locus 332:TTATT-ATATTTCCGCTAACATTTTTT-CTACATATTTAGAAAAATTAATGGCGGCCAAA 389
24 BHa74 locus 332:TTATT-ATATTTCCGCTAACATTTTTT-CTACATATTTAGAAAAATTAATGGTGGCCAAA 389
25 BHa74 locus 282:TTATT-ATATTTCTGCTAACATTTTTT-CTACATATTTAGAAAAATTAATGGTGGCCAAA 339
27 BHa74 locus 111:--ATTGATATTTCTGCTAACATTTTT--CTACATATTTAGAAAAATTAATGGTGGCCAAA 166
                  .** **.****.***********.. ****.************..*****.**.****

01 BHa74 locus 169:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATAAATGGAATAAAATGATC 228
06 BHa74 locus 145:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 204
10 BHa74 locus 182:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 241
11 BHa74 locus 180:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAATGGAATAAAATGATC 239
14 BHa74 locus 357:ATAGCATAAACCAAGGAAGTAAATAAAAC--TTGTGCCAAATGAACGGAATAAAATGATC 414
18 BHa74 locus 417:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 476
23 BHa74 locus 390:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 449
24 BHa74 locus 390:ATAGCATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 449
25 BHa74 locus 340:ATAGCATAAACCAAGGAAGTAAATAAAAC                                368
27 BHa74 locus 167:ATAGTATAAACCAAGGAAGTAAATAAAACTGTTGTGCCAAATGAACGGAATAAAATGATC 226
                 ****.************************.............................

01 BHa74 locus 229:ATTTCTGTAATGTGTTTTTTACAG                                 252
06 BHa74 locus 205:ATTTCTGTAATGTGTTTTTTACAGGAAGAACATTTGAA                     242
10 BHa74 locus 242:ATTTCTGTAATGTGTTTTTTACAGGAAGAACATTTGAA                     279
11 BHa74 locus 240:ATTTCTGTAATGTGTTTTTTACAGGAAGAACATTTGA                      276
14 BHa74 locus 415:ATTTCTGTAATGTGTTTTTTACAG-AAGAACATTTGAA                     451
18 BHa74 locus 477:ATTTCTGTAATGTGTTTTTTACAGGAAGAAC                           507
23 BHa74 locus 450:ATTTCTGTAATGTGTTTTTTACAGGAAGAACATTTGAA                     487
24 BHa74 locus 450:ATTTCTGTAATGTGTTTTTTACAGGAAGAACATTTGA                      486
27 BHa74 locus 227:ATTTCTGTAATGTGTTTTTTAC                                   248
                 ........................
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Supplemental Figure 5-12. Sequence alignment of BHa74 locus. GenBank accession numbers are AB249064–AB249073.

```
06 BKs36 locus   1:TGCATGAATTTCTA-GCAAAGATTTTTCCTGTATAAAATGCTGCCAAGGAGACTTGACTG 59
10 BKs36 locus   1:TGCATGAATTTCTAAGCAAAGATTTTTCCTATATAAAATGCTACCAAGGAGACTTGACTG 60
11 BKs36 locus   1:TGCATGAATTTCTAAGCAAAGATTTTTCCTATATAAAATGCTGCCAAGGATACTTGACTG 60
17 BKs36 locus   1:TGCATGAATTTCTAAGCAAAGATTTTTCCTATATAAAATGCTGCCAAGGAGACTTGACTG 60
                 **************.***************.***********.*******.*********

06 BKs36 locus  60:CTTGATATTCAAATTCCAACAGATGTGCTATATTGGTTGC-TTACATAAGTCACATATT- 117
10 BKs36 locus  61:CTTGATATTCAAATTCCAACACTTGTGCTATATTGGTTAC-TTACATAAGTCACATATTA 119
11 BKs36 locus  61:CTTGATATTCAAATTCCAGCACTTGTGCTATATTGGTTACGTTACATAAGTCACATATTA 120
17 BKs36 locus  61:CTTGATATTCAAATTCCAACACTTGTGCTATATT----AC-------------------- 96
                ******************.**..***********.....* ..................

06 BKs36 locus 118:GGGGGAGAGGGATAGCTCAGTGGTTTGAGCATTGGCATGTTAAACCCAGGGTTGTG--AG 175
10 BKs36 locus 120:GGGGGGAAAGGATAGCTCAGTGGTTTGAGCATTGGTATACTAACCCCAGGGTGTTGTGAG 179
11 BKs36 locus 120:------------------------------------------------------------ 120
17 BKs36 locus  96:------------------------------------------------------------ 96


06 BKs36 locus 176:CTCAATCCTTGAGGAGGCCAMTTAGGGATCTGGGGCAAAAAYTGATCCTGC-TAGTGAAG 234
10 BKs36 locus 180:TTCAATCCTTGAGGGGACCACTTAGGGATCTGGGTCAAAAATTGGTCCTGCCTAGTGAAG 239
11 BKs36 locus 120:------------------------------------------------------------ 120
17 BKs36 locus  96:------------------------------------------------------------ 96


06 BKs36 locus 235:GCAGGGGGCTGGACTTGATGACCTTC------------TAGTTCTTGGAGAYTGGTATAT 282
10 BKs36 locus 240:GCAGGGGGCTGGACTTGATGACCTTCCAAGGTCCCTTCTAGCTCTAGGAGATTGGTATAT 299
11 BKs36 locus 120:------------------------------------------------------------ 120
17 BKs36 locus  96:------------------------------------------------------------ 96


06 BKs36 locus 283:CTCCATTTATTACCTTTAACTTATATCTCTTTCCTACATAAGATGACTTATTGTATGCAA 342
10 BKs36 locus 300:CTCCAATTATTACCTTTA-CTTATATCTCTTTCCTACATAAGATGACTTATTGTATGCAA 358
11 BKs36 locus 121:------------------------TATCTCTTTCCTACATAAGATGACTGATTGTATGCAA 157
17 BKs36 locus  97:------------------------ATCTCTTTCCTACATAAGATGACTTATTGTATGTAA 132
                                  .************************.********.**

06 BKs36 locus 343:CTAACACTGTGAATTTCACAAATTTTGAATATTTCAATCAAATGTGCAATTCACA-TTGA 401
10 BKs36 locus 359:CTAACACTGTGAATTTCACAAATTTAGAATATTTCAATCAAATGTGCAATTCACAATTGA 418
11 BKs36 locus 158:CTAACACTGTGAATTTCACAAATTTAGAATATTTCAA-CAAATGTGCAATTCACAATTGA 216
17 BKs36 locus 133:CTAACACTGTGAATTTCACAAATTTAGAATATTTCAATCAAATGTGCAATTCACAAT-GA 191
                 ************************.***********.*****************.*.**

06 BKs36 locus 402:CTTTTGGTG                                                410
10 BKs36 locus 419:CTTTTGGTG                                                427
11 BKs36 locus 217:CTTTTGGTG                                                225
17 BKs36 locus 192:CTTTTGGTG                                                200
                 *********
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Supplemental Figure 5-13. Sequence alignment of BKs36 locus. GenBank accession numbers are AB125715–AB125718.

```
01 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
02 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
06 BKs52 locus   1:GAAGAGGTAANNNGGAATTAGTATTTCAGAGTCTAGGCTCATTTATTTATGTTTGGGCCA 60
09 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
10 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
11 BKs52 locus   1:GAAGAGGTAGTGGGGAATTAGTATTTCAGAGTCTAGGCTCATTTATTTATGCTTGGGCCA 60
14 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
15 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
17 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
18 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
20 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
21 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
23 BKs52 locus   1:-------------------------------------------ATTTATGTTTGGGCCA 16
24 BKs52 locus   1:-------------------------------------------TATTTATGTTTGGGCCA 17
27 BKs52 locus   1:GAAGAGGTAGTGGGGAATTAGTATTTCAGAATCTAGGCTCATTTATTTATGCCTGGGCCA 60
                                                  .*******..*******

01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus  61:TTGCTATGGGGAAAAGCTATGCCAATAAGTCACAAACCATTTTCCCTTGGCTGTTAGAAG 120
09 BKs52 locus  18:TTGCTATGGGGAACAGCTATGCCAATAAGTCACAAACCATTTTCTCTTGGCTGTTAGAAG 77
10 BKs52 locus  18:TTGCTATGGGGAACAGCTATGCCAATAAGTCACAAACCATTTTCCCTTGGCTGTTAGAAG 77
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60


01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus 121:GCAGGATTGGGAGGAAAGGACCCTCTACCATGCATCAGAGAGTGATTCCTTAGTCTTATC 180
09 BKs52 locus  78:GCAGGATTGGGAGGAAAGGACCCTCTACCATCCATCAGAGAGTGAGCCCTTAGTCTTACC 137
10 BKs52 locus  78:GCAGGCTTGGGAGGAAAGGACCCTCTACCATCCATCAGAGAGTGAGCCCTTAGTCTTATC 137
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60


01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus 181:AACATTTGCTAATCCAAGCTCATTGTATGTAGAAGAGGGGG-GAGGGATAGCTCAGTGGT 239
09 BKs52 locus 138:AACTTTTGCTAATCCAAGCTCATGGTATGTGGAAGAGGGGGGGAAGGATAGCTTAGTGGT 197
10 BKs52 locus 138:AACTTTTGCTAATCCAAGCTCATTGTATATGGAAGAGGGGGAGAAGGATAGCTCAGTGGT 197
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60
```

```
01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus 240:TTGAGCATTGGCCTGCTAAACTCAGGGTTATGAGCTCTAATCCTTGAGGGGGCC--TTAG 297
09 BKs52 locus 198:TTGAGCATTGGCCCCCTAAACTCAGGGTTGTGAGCTCTAATCCTTGAGGGGGCCACTTAG 257
10 BKs52 locus 198:TTGAGGATTGGCCCCCTAAACTCAGGGTTGTGAGCTCTAATCCTTGGGGGGGCCACTTAG 257
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60


01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus 298:GGAGCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTT 357
09 BKs52 locus 258:GGAGCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACT----------- 306
10 BKs52 locus 258:GGAGCTGGGACAAAAATTGGTCCTGCTAGTGAAGGCAGAGGGCTGGACT----------- 306
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60


01 BKs52 locus  17:------------------------------------------------------------ 17
02 BKs52 locus  17:------------------------------------------------------------ 17
06 BKs52 locus 358:CAAGGTCCCTTCCAGCTCTAGGAGATTGGTATATCTCCAATAATTACCTT---------- 407
09 BKs52 locus 307:----GTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTACCTTTTTTATTACC 362
10 BKs52 locus 307:----GTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTACCTTTGT-ATTACC 361
11 BKs52 locus  60:------------------------------------------------------------ 60
14 BKs52 locus  17:------------------------------------------------------------ 17
15 BKs52 locus  17:------------------------------------------------------------ 17
17 BKs52 locus  17:------------------------------------------------------------ 17
18 BKs52 locus  17:------------------------------------------------------------ 17
20 BKs52 locus  17:------------------------------------------------------------ 17
21 BKs52 locus  17:------------------------------------------------------------ 17
23 BKs52 locus  16:------------------------------------------------------------ 16
24 BKs52 locus  17:------------------------------------------------------------ 17
27 BKs52 locus  60:------------------------------------------------------------ 60


01 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
02 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
06 BKs52 locus 408:--ATTACCTTGCTTCCAAGAGCACAAGAGTTGAAGGAATGATGTGCTCACAGATTGGTTT 465
09 BKs52 locus 363:TTATTACCTTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 422
10 BKs52 locus 362:TTATTACCTTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 421
11 BKs52 locus  61:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 112
14 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
15 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
17 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAACGATGTGCTCACAGATTGGTTT 69
18 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGTTCACAGATTGGTTT 69
20 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
21 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
23 BKs52 locus  17:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 68
24 BKs52 locus  18:--------TTGCTTCCAAGAGCACAAGAGTTGAGGGAATGATGTGCTCACAGATTGGTTT 69
27 BKs52 locus  61:--------TTGCTTCCAAGACCACAAGAGTTGAGGGAATGATGCGCTCACAGATTGGTTT 112
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                         ************.************.****.****.*.**************

01 BKs52 locus  70:AATTCAGGGGAATTAACACCACCAGAGTGTAACTACCACAAAAA-TTCTCTCTTGCTACC 128
02 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTACCACAAAAA-TTTTCTCTCGCTATC 128
06 BKs52 locus 466:AATTCAGGGGAATTAGCACCACCAAAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 524
09 BKs52 locus 423:AATTCAGGGGAATTAGCACCACCAAAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 481
10 BKs52 locus 422:AATTCAGGGGAATTAGCACCACCAAAGTGTAACTGCCACA-----TCTTCTCTAGCTACC 476
11 BKs52 locus 113:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 171
14 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 128
15 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTYTAGCTACC 128
17 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 128
18 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAAATCTTCTCTAGCTACC 129
20 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 128
21 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 128
23 BKs52 locus  69:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 127
24 BKs52 locus  70:AATTCAGGGGAATTAGCACCACCAGAGTGTAACTGCCACAAAAA-TCTTCTCTAGCTACC 128
27 BKs52 locus 113:AATTCAGGGGCATTAGCACCACCAGAGTGTAACAGCCACAAAAA-TCTTCTCTAGCTACC 171
                 **********.****.********.********..*****.... *..***.*.****.*

01 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTATTACTT 181
02 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------TAGCCTGTATTTAGTCTACTCCATCCTGTTACTC 181
06 BKs52 locus 525:TTTTAAAAAGCTGAC-TTCCCC-CCCCGGACTGTATTTAGTCTACTCCATCTTGTTATTT 582
09 BKs52 locus 482:TTTAAAAAAGCTGACCCCCCCTCCCCCAGCCTGTATTTAGTCTACTCCATCTTGTTATTT 541
10 BKs52 locus 477:TTTTAAAAAGCTGACCCCCCA--CCCCAGCCTGTATTTAGTCTACTCCATCTTGTTATTT 534
11 BKs52 locus 172:TTTTAAAAAGCTGACCCCC-----TGCAGCCTGTATTTAGTCTACTACATCCTGTTACTT 226
14 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
15 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
17 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
18 BKs52 locus 130:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTACATCCTGTTACTT 182
20 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
21 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
23 BKs52 locus 128:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 180
24 BKs52 locus 129:TTTTAAAAAGCTGACCTCC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 181
27 BKs52 locus 172:TTTTAAAAAGCTGACCTTC-------CAGCCTGTATTTAGTCTACTCCATCCTGTTACTT 224
                 ***.***********...*      ..*.****************.****.*.***.*.

01 BKs52 locus 182:CTGGTGGC                                                189
02 BKs52 locus 182:CTGGTGGC                                                189
06 BKs52 locus 583:CTGGTGGC                                                590
09 BKs52 locus 542:CTGGTGGC                                                549
10 BKs52 locus 535:CTGGTGGC                                                542
11 BKs52 locus 227:CTGGTGGC                                                234
14 BKs52 locus 182:CTGGTGGC                                                189
15 BKs52 locus 182:CTGGTGGC                                                189
17 BKs52 locus 182:CTGGTGGC                                                189
18 BKs52 locus 183:CTGGTGGC                                                190
20 BKs52 locus 182:CTGGTGGC                                                189
21 BKs52 locus 182:CTGGTGGC                                                189
23 BKs52 locus 181:CTGGTGGC                                                188
24 BKs52 locus 182:CTGGTGGC                                                189
27 BKs52 locus 225:CTGGTGGC                                                232
                 ********
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Supplemental Figure 5-14. Sequence alignment of BKs52 locus. GenBank accession numbers are AB249074–AB249085 and AB125719-AB125721.

```
01 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGGCTTTCATTTTAACAACATCCCTT 60
06 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCATTTTAACGACATCCCTT 60
10 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCATTTTAACAACATCCCTT 60
14 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCACTTTAACAACATCTCTT 60
15 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCATTTTAACAACATCTTTT 60
19 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCATTTTAACAACATCCCTT 60
27 BKs29 locus   1:CAGTTAAAGCATTTGAAAGGTAAAGTATTAAATAAGACTTTCATTTTAACAACATCCCTT 60
                 ************************************.******.******.*****..**

01 BKs29 locus  61:GTTCTTTCCCTTTAGTTGAAGAGTTTTAGAAAGGGGGTGGGGG-TGTTGTTTGACAGACT 119
06 BKs29 locus  61:GTTCTTTCCCTTTAGTTGAAGAGTTTTAGAAGGGGCGGGGG----ATTGTTTGACTGACT 116
10 BKs29 locus  61:GTTATTTCCCTTTAGTTGAAGAGTTTTAGAAGGGGTGGGGG-----TTGTTTGACAGACT 115
14 BKs29 locus  61:GTTCTTTCCCTTTAGTTGAAGAGTTTTAGAAGGGGGTGGGGG----TTGTTTGACAGACT 116
15 BKs29 locus  61:GTTCTTTCCCTTTAGTTGAAGAGTTTTAGAAGGGGGTGGGGG----TTGTTTGACAGACT 116
19 BKs29 locus  61:CTTCTTTCCCTTTAGTTGAAGAGTTTTA-AAAGGGCGGGGGGGGGGTTGTTTGAAAGACT 119
27 BKs29 locus  61:GTTCTTTCCCTTTAGTTGAAGAGTTTTAGAAAGGGGGGGTGGACC-TTGTTTGACAGACT 119
                .**.************************.**.***...*.*.    ********..****

01 BKs29 locus 120:TTTAG------------------------------------------------------ 124
06 BKs29 locus 117:CTTAG------------------------------------------------------ 121
10 BKs29 locus 116:CTTAG------------------------------------------------------ 120
14 BKs29 locus 117:TTTAGGGTAGGTTTACACTTACCTTCCGGGTCGACGCGGTGAGTTCGACTTCTTGGAGTT 176
15 BKs29 locus 117:CTTAG------------------------------------------------------ 121
19 BKs29 locus 120:TTTAG------------------------------------------------------ 124
27 BKs29 locus 120:CTTAA------------------------------------------------------ 124
                 .***.

01 BKs29 locus 124:------------------------------------------------------------ 124
06 BKs29 locus 121:------------------------------------------------------------ 121
10 BKs29 locus 120:------------------------------------------------------------ 120
14 BKs29 locus 177:CGAACTATCGCGTCTGATCTAGACGCGATAGTTCGAACTCCGGAAGCGCTGCGGTCAACT 236
15 BKs29 locus 121:------------------------------------------------------------ 121
19 BKs29 locus 124:------------------------------------------------------------ 124
27 BKs29 locus 124:------------------------------------------------------------ 124


01 BKs29 locus 124:------------------------------------------------------------ 124
06 BKs29 locus 121:------------------------------------------------------------ 121
10 BKs29 locus 120:------------------------------------------------------------ 120
14 BKs29 locus 237:CCGGTACTCCACCACTGCAAATGGTGGTGGCGGAGTCGACGGGGGAGCCGCGGAGTTTGA 296
15 BKs29 locus 121:------------------------------------------------------------ 121
19 BKs29 locus 124:------------------------------------------------------------ 124
27 BKs29 locus 124:------------------------------------------------------------ 124


01 BKs29 locus 124:------------------------------------------------------------ 124
06 BKs29 locus 121:------------------------------------------------------------ 121
10 BKs29 locus 120:------------------------------------------------------------ 120
14 BKs29 locus 297:CCCCGCCGCGTCTGGACGGGTGAGTAGGTCGAACTAGGGTACTTCGAATTCAGCTACGCT 356
15 BKs29 locus 121:------------------------------------------------------------ 121
19 BKs29 locus 124:------------------------------------------------------------ 124
27 BKs29 locus 124:------------------------------------------------------------ 124


01 BKs29 locus 124:------------------------------------------------------------ 124
06 BKs29 locus 121:------------------------------------------------------------ 121
10 BKs29 locus 120:------------------------------------------------------------ 120
14 BKs29 locus 357:ATTCACGTAGCTGAATTTGCGTACCCTAGTTCAACCCCCCCTTCTTAGTGTAGACCAGGC 416
15 BKs29 locus 121:------------------------------------------------------------ 121
19 BKs29 locus 124:------------------------------------------------------------ 124
27 BKs29 locus 124:------------------------------------------------------------ 124


01 BKs29 locus 125:-----ATTATG------------------------------------------------ 130
06 BKs29 locus 122:-----ATTATGATTATTAGGAGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTA 176
10 BKs29 locus 121:-----ATTATG------------------------------------------------ 126
14 BKs29 locus 417:CTTAGATTATG------------------------------------------------ 427
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15 BKs29 locus 122:-----ATTATG---------------------------------------------- 127
19 BKs29 locus 125:-----ATTATG---------------------------------------------- 130
27 BKs29 locus 125:-----ATTATA---------------------------------------------- 130
                    *****.

01 BKs29 locus 130:------------------------------------------------------------ 130
06 BKs29 locus 177:AAGCAAGGGTTGTGAGCTCAATCCTTGAGGAGGCCACTTAGGGATCTGGGGCAAAAAATT 236
10 BKs29 locus 126:------------------------------------------------------------ 126
14 BKs29 locus 427:------------------------------------------------------------ 427
15 BKs29 locus 127:------------------------------------------------------------ 127
19 BKs29 locus 130:------------------------------------------------------------ 130
27 BKs29 locus 130:------------------------------------------------------------ 130


01 BKs29 locus 130:------------------------------------------------------------ 130
06 BKs29 locus 237:GGTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCCAGTTC 296
10 BKs29 locus 126:------------------------------------------------------------ 126
14 BKs29 locus 427:------------------------------------------------------------ 427
15 BKs29 locus 127:------------------------------------------------------------ 127
19 BKs29 locus 130:------------------------------------------------------------ 130
27 BKs29 locus 130:------------------------------------------------------------ 130


01 BKs29 locus 131:-------------------------------TCAAGTTTGGTAAT---TGCCCTTTTGGG 156
06 BKs29 locus 297:TAGGAGGTTGGTATATCTTAAAAAAAAAATGTCAAGTTTGGTAATAACTGCCCTTTTGGG 356
10 BKs29 locus 127:-------------------------------TCAAGTTTGGTAATAACTGCCCTTTTGGA 155
14 BKs29 locus 428:-------------------------------TCAAGTTTGGTAATAACTGCCCTTTTGGG 456
15 BKs29 locus 128:-------------------------------TTAAGTTTGGTAATAACTGCTCTTTTGGG 156
19 BKs29 locus 131:-------------------------------TCAAGTTTGGTAATAACTGCCCTTTTGAG 159
27 BKs29 locus 131:-------------------------------TAAAGTTTGGTAATAACTGCCCTTTTGGG 159
                                         *.************...***.******..

01 BKs29 locus 157:TAAAAGGGAAGAAGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTGCTGCTATTGTTAAA 216
06 BKs29 locus 357:TAAAAGGGAAGACGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTTCTGCTATTGTTAAA 416
10 BKs29 locus 156:TAAAAGGTAAGAAGTTAGTTGAGATGGGCTGGAAGTGTTGTTGCTGCTGCTATTGTTAAA 215
14 BKs29 locus 457:TAAAAGGGAAGAAGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTGCTGCTATTGTTAAA 516
15 BKs29 locus 157:TAAAAGGAAAGAAGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTGCTGCTATTGTTAAA 216
19 BKs29 locus 160:TAAAAGGAAAGAAGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTGCTGCTATTGTTAAA 219
27 BKs29 locus 160:TAAAAGGGAAGAAGTTAGTTGAGATGGGCTGGAACTGCTGTTGCTGCTGCTATTGTTAAA 219
                *******.****.********************.**.*******.**************

01 BKs29 locus 217:GTTTGATACACTTTATCTCAGGTAATGTTGGGG                       249
06 BKs29 locus 417:GTTTGATACACTTTATCTCAGGTAATGTTGGGG                       449
10 BKs29 locus 216:GTTTGATACACCTTATCTCAGGTAATGTTGGGG                       248
14 BKs29 locus 517:GTTTGATACACTTTATCTCAGGTAATGTTGGGG                       549
15 BKs29 locus 217:GTTTGATACACTTTATCTCAGGTAATGTTGGGG                       249
19 BKs29 locus 220:GTTTGATACACTTTATCTCAGGTAATGTTGGGG                       252
27 BKs29 locus 220:GTTCGATACACTCTATCTCAGGTAATGTTGGGG                       252
                ***.*******..********************
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Supplemental Figure 5-15. Sequence alignment of BKs29 locus. GenBank accession numbers are AB249086–AB249092.

```
01 BOs55 locus   1:ATGGCTGCACATGTGGAGTACACAGCTACCACACAACAAAGATTAAATCTCTGTGCTAGT 60
08 BOs55 locus   1:ATGGCTGCACATGTGGAGTACGCAGCTACCCCAAAACAAAGATTAGGTCTCTGTGCTAGT 60
12 BOs55 locus   1:-------------------------------------AAGATTAGGTCTCTGTGCTAGT 22
13 BOs55 locus   1:ATGGCTGCACATGTGGAGTACACAGCTACCACACAACAAAGATTAGGTCTCTGTGCTAGT 60
15 BOs55 locus   1:ATGGCTGCACAT-TGGAGTACACAGCTACCACACAACAAAGATTAG-TCTCTGTGCTAGT 58
17 BOs55 locus   1:ATGGCTGCACATG-GGAGTAGACAGCTACCACACAACAAAGATTAGGTCTCTGTGCTAGT 59
19 BOs55 locus   1:ATGGCTGCTCATGTGGAGTACACAGCTACCACACAACAAAGATTAGGTCTCTGTGCTAGT 60
                 ......................................*******..*************

01 BOs55 locus  61:CTAGCATAAGCAACTGTGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTAATCTCACTGC 120
08 BOs55 locus  61:CTAGCATAAGCAACTGTGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCACTGC 119
12 BOs55 locus  23:CTAGCATAAGCAACTGTGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCACTGC 81
13 BOs55 locus  61:CTAGCATAAGCAACTGTGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCATTGC 119
15 BOs55 locus  59:CTAGCATAAGCAACTGTGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCACTGC 117
17 BOs55 locus  60:CTAGCATAAGCAACTGTGAAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCACTGC 118
19 BOs55 locus  61:CTAGCATAAGCAACTGAGGAAGGCCTCAGGATGTCTGTGCAGGGAGTTTA-TTTCACTGC 119
                ****************.*.****************************** *.***.***

01 BOs55 locus 121:TTCAGCCTCTAAGTGCTCCA---------------------------------------- 140
08 BOs55 locus 120:TTCAGCCTCTAAGTGCTCCA---------------------------------------- 139
12 BOs55 locus  82:TTCAGCCTCTAAGTGCTCCACGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGTCTGCT 141
13 BOs55 locus 120:TTCAGCCTCTAAGTGCTCCAGGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCT 179
15 BOs55 locus 118:TTCAGCCTCTAAGTGCTCCAGGGGGGAGGGATAGCTCAGTGGTTTGCACATTGGCCTGCT 177
17 BOs55 locus 119:TTCAGCCTCTAAGTACTCCA---------------------------------------- 138
19 BOs55 locus 120:TTCAGCCTCTAAGAGCTCCA---------------------------------------- 139
                 *************..*****

01 BOs55 locus 140:------------------------------------------------------------ 140
08 BOs55 locus 139:------------------------------------------------------------ 139
12 BOs55 locus 142:AAACTCAGGGTTGTGAATTCAATCCTTGAGGGGGCCACTTAGG-ATCTGGGGCAAAANNN 200
13 BOs55 locus 180:AAACCCAGGGTTGTGATTTCAATTCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATT 239
15 BOs55 locus 178:AAACGCAGCGTTGTGAATTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATT 237
17 BOs55 locus 138:------------------------------------------------------------ 138
19 BOs55 locus 139:------------------------------------------------------------ 139


01 BOs55 locus 140:------------------------------------------------------------ 140
08 BOs55 locus 139:------------------------------------------------------------ 139
12 BOs55 locus 201:NNNNNNNNNNNNNNNNNNNNNNNNNGGGACTCAATGACCTTTCAAAGTCCCTTCCAGCTC 260
13 BOs55 locus 240:GGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAAGTCCCTTCCAGTTC 299
15 BOs55 locus 238:GGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAAGTCCCTTCCAGTTC 297
17 BOs55 locus 138:------------------------------------------------------------ 138
19 BOs55 locus 139:------------------------------------------------------------ 139


01 BOs55 locus 141:------------------------------CCTAGGAAAGTCATGTGGGTTTTAGAGCAG 170
08 BOs55 locus 140:------------------------------CCTAGGTAAGTCACGTGGGTTTTAGAGCGG 169
12 BOs55 locus 261:TAGGAGATTGGTA------------TATCACCTAGGTAAGTCACATGGGTTTTAGAGCAG 308
13 BOs55 locus 300:TAGGAGATTGGTAGATTGATTGGTATATCACCTAGGTAAGTCACATGGGTTTTAGAGCAG 359
15 BOs55 locus 298:TAGGAGATTGGTAGATTGATTGGTATATCATCTAGGTAAGTCACATGGGTTTTAGAGCAG 357
17 BOs55 locus 139:------------------------------CCTAGGTAAGTCACATGGGTTTTAGAGYGG 168
19 BOs55 locus 140:------------------------------TCTAGGTAAGTCACGTGGGTTTAAGAGCGG 169
                                         .*****.******..*******.****..*

01 BOs55 locus 171:TAGCATTCATTTCACCTGTATTAATCCAATGTATATCATGCCCTTATATTGAAAATATTT 230
08 BOs55 locus 170:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATATTGAAAACATTT 228
12 BOs55 locus 309:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATAT-GAAAACATT- 365
13 BOs55 locus 360:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATATTGAAAACATTT 418
15 BOs55 locus 358:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATATTGAAAACATTT 416
17 BOs55 locus 169:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATATTGAAAACATTT 227
19 BOs55 locus 170:TAGCATTCATTTCACCTGTATTAATC-AATGTATATCATGCCCTTATATTGAAAACATTT 228
                 ************************* *********************.*****.***.

01 BOs55 locus 231:GGCACAGCTTAGCAGTGGATGTCTATGGATATATGGTGTGCATGGGGTTAAAT       283
08 BOs55 locus 229:GGCACAGCTTAGCAGTGGGTGTGTATGGATATACGGTGTGCATGGGGTTAAAT       281
12 BOs55 locus 366:GGCACAGC                                                 373
13 BOs55 locus 419:GGCACAGCTTAGCAGTGGGTGTGTATGGATATACGGTGTGCATGGGGTTAAATA      472
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15 BOs55 locus 417:GGCACAGCTTAGCAGTGGGTGTGTATGGATATACGGTGTGC-TGGGGTTAAAT       468
17 BOs55 locus 228:GGCACAGCTTAGCAGTGGGTGTATATGGATATACGGTGTGCATGGGGTTAAATA      281
19 BOs55 locus 229:GGCACAGTTTAGCAGTGGGTGTATATGGATATACGGTGTGCATGGGGTTAAATA      282
                *******............... ............................
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Supplemental Figure 5-16. Sequence alignment of BOs55 locus. GenBank accession numbers are AB249093–AB249099.

```
01 BOs74 locus   1:CTTGAAGGTCTGTTCGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGATGTGACAC 60
06 BOs74 locus   1:CTTGAAGGTCTGTTCGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGATGTGACAC 60
12 BOs74 locus   1:CTTGAAGGTCTGTTCGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGATGTGACAC 60
15 BOs74 locus   1:CTTGAAGGTCTGT-CGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGATGTGACAC 59
17 BOs74 locus   1:CTTGAAGGTCTGTTCGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGATGTGACAC 60
19 BOs74 locus   1:CTTGAAGGTCTGTTCGCATTCAGGGGAAGAATCCCACTCCTGTGGACAGAGCTGTGACAC 60
                 *************.************************************.********

01 BOs74 locus  61:CATGGTGGATCTCTCAACACCCCTTTGCTACAGGAGCTTATGCACTCTGGGAC------- 113
06 BOs74 locus  61:CATGGTGGGTCTCTCAACATCCCTTTGCTACAAGAGCTCATGCACTCTGGGAC------- 113
12 BOs74 locus  61:CATGGTGGATCTCTCAACACYCCTTTGCTACAGGAGCTCATGCACTCTGGGGCGAGGGAT 120
15 BOs74 locus  60:CATGGTGGATCTCTCAACACCCCTTTGCTACAGGAGCTCATGCACTCTGAGGGGAGGGAT 119
17 BOs74 locus  61:CATGGTGGGTCTCTCAACACCTCTTTGCTACAGGAGCTCATGCACTCTGGGAC------- 113
19 BOs74 locus  61:CATGGTGGATCTCTCAACATCCCTTTGCTACAGGAGCTCATGCACTCTGGGAC------- 113
                ********.**********...**********.*****.**********.*..

01 BOs74 locus 113:------------------------------------------------------------ 113
06 BOs74 locus 113:------------------------------------------------------------ 113
12 BOs74 locus 121:AGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAAKCCTTGAGGG 180
15 BOs74 locus 120:AGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGG 179
17 BOs74 locus 113:------------------------------------------------------------ 113
19 BOs74 locus 113:------------------------------------------------------------ 113


01 BOs74 locus 113:------------------------------------------------------------ 113
06 BOs74 locus 113:------------------------------------------------------------ 113
12 BOs74 locus 181:RGCCACTTAGGAATCTGGGGCAAAAATCTGTCTGGGGATTRGTCCTGCTTTGAGCAGAGG 240
15 BOs74 locus 180:GGCCACTTAGGGATCTGGGGCAAAAATCTGTCTGGGGATTGGTCCTGCTTTGAGCAGGGG 239
17 BOs74 locus 113:------------------------------------------------------------ 113
19 BOs74 locus 113:------------------------------------------------------------ 113


01 BOs74 locus 114:-------------------------------------------------------------AA 115
06 BOs74 locus 114:-------------------------------------------------------------AA 115
12 BOs74 locus 241:G----TTGGACTAGATGACCTCCTGAGGTCCCTTCCAATCCTGATAGTCTATGATTCTAA 296
15 BOs74 locus 240:GGGGGTTGGACTAGTTGACCTCCTGAAGTCCCTTCCAATCCTGATATTCTATGATTCTAA 299
17 BOs74 locus 114:-------------------------------------------------------------AA 115
19 BOs74 locus 114:-------------------------------------------------------------AA 115
                                                                **

01 BOs74 locus 116:CAACACTACTGGCCTTTTACATGCACATATAATGAGCACGGCCTGAAAGCTACATTCTTA 175
06 BOs74 locus 116:CAGTGCTACTGACCTTTTACATGCACAGATAATGAGCACGGCCTGAAAACTACATTCTTA 175
12 BOs74 locus 297:CAGTGCTACTGGCCTTTTACATGCACAGATAATGAGCACGGCCTGAAAACTACATTCTTA 356
15 BOs74 locus 300:CAGTGCTACTGGCCTTTTTCATGCACAGATAATGAGCACGGCCTGAAAACTACATTCTTA 359
17 BOs74 locus 116:CAGTGCTACTGGCCTTTCACATGCACAGATAATGAGCACGGCCTGAAAACTACATTCTTA 175
19 BOs74 locus 116:CAGTGCTCCTGGCCTTTTACATGCACAGATAATGAGCATGGCCTGAAAACTACATTCTTA 175
                 **...**.***.*****..********.**********.*********.***********

01 BOs74 locus 176:CAGAGTGAAAGCATTGGTGGGAAAAAGAGTCTAACACACTAAGTATATTTAGGAGCCCTT 235
06 BOs74 locus 176:CAAAGTGGAAGCATTAGTGGGAAAAAGAGTCTAACAC--TAAGTATATTTAGGAGCCCTT 233
12 BOs74 locus 357:TAGAGTGGAAGCATTGGTGGGAAAAAGAGTCTAACACACAAAGTATATTTAGGAGCCCTT 416
15 BOs74 locus 360:CAGAGTGGAAGCATTGGTGGGAAAAAGAGTCTAACACACTAAGTATATTTAGGAGCCCTT 419
17 BOs74 locus 176:CAGAGTGGAAGCATTGGTGGGAAAAAGAGTCTAACACACTAAGTATATTTAGGAGCCCTT 235
19 BOs74 locus 176:CAGAGTGGAAGCATTGGTGGGAAAAAGAGTCTAACACACTAAGTATATTTAGGAGCCCTT 235
                 .*.****.*******.********************...********************

01 BOs74 locus 236:CACTGC                                                   241
06 BOs74 locus 234:CACTGC                                                   239
12 BOs74 locus 417:CACTGC                                                   422
15 BOs74 locus 420:CACTGC                                                   425
17 BOs74 locus 236:CACTGC                                                   241
19 BOs74 locus 236:CACTGC                                                   241
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Supplemental Figure 5-17. Sequence alignment of BOs74 locus. GenBank accession numbers are AB24100–AB249105.

```
01 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACTATGCTCATGAGCCACATGCGGCTCTTTTACA 60
06 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGTGGCTCTTTTACC 60
11 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGCGGCTCTTTTACA 60
13 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGTGGCTCTTTTACA 60
14 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGTGGCTCTTTTACA 60
17 BCr61 locus   1:-----------------------------------ATGAGC-ACATGCGGCTCTTTTACA 24
19 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGCGGCTCTTTTACA 60
26 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGTGGCTCTTTTACA 60
28 BCr61 locus   1:GCTCCTAATATGTCAGGGATGGCCAAACCATGCTCATGAGCCACATGCAGCTCTTTTACA 60
                 ....................................******.*****..**********.

01 BCr61 locus  61:GTTCAAGTGCGGCATCAAAGA-GTCCCCAG-CCCCCCATTCTCTGCCTATCAGA-CTGGG 117
06 BCr61 locus  61:ATT-AAGTGCCGC-TCAAAGA-GTCCCCCCACCCCTCATTCTCTGCCTATCAGG-CTGGG 116
11 BCr61 locus  61:GTT-AAGTGCGGC-TCAAAGA-GTCCCCTG-CCCCTCATTCTCTGCCTATCAGG-GTGGG 115
13 BCr61 locus  61:GTT-AAGTGCGGC-TCAAAGA-GTCCCCCG-CCCCGCATTCTCTGCCTATCAGA-CTGGG 115
14 BCr61 locus  61:GTT-AAGTGCGGC-TCAAAGA-GTCCCCCG-CCCCCCATTCTCTGCCTATCAGA-CTGGG 115
17 BCr61 locus  25:GTT-AAGTGCGGC-TCAAAGAAGTCCCCCG-CCCCCCATTCTCTGCCTATCAGAACTGGG 81
19 BCr61 locus  61:GTT-AAGTGCGGC-TCAAAGA-GTCCCCCG-CTCCCCATTCTCTGCCTATTAGA-CTGGG 115
26 BCr61 locus  61:GTT-AAGTGCGGC-TCAAAGA-GTCCCCCG-CTCCCCATTCTCTGCCTATCAGA-CTGGG 115
28 BCr61 locus  61:GTT-AAATGCGGC-TCAAAGC-ATCCCC------CCCATTCTCTGCCTATCAGA-CTGAG 110
                 .** **.***.** ******. .*****.. ...*.**************.**. .**.*

01 BCr61 locus 118:G-GGGGGG-------TATTTTCCCTCAGGGCTTCTGACCTCAGGTCGGGTGGTAGGGCTA 169
06 BCr61 locus 117:GCAGGGGG-------TGTTTTGCCTCAGGGCTTCTGACCTCAGGTTGGGTGGTAGGGCTA 169
11 BCr61 locus 116:G------G-------TGTTTTGCCTCAGGGCTTCTGACCTCAGGTCAGGTGGTGGGGCTA 162
13 BCr61 locus 116:GGGGGTG--------TGTTTTGCCTCAGGGTTTCTGACCTCAGGTCAGGTGGTGGGGCTA 167
14 BCr61 locus 116:GGGGGGGG-------TGTTTTGCCTCAGGGCTTCTGACCTCAGGTCAGGTGGTGGGGCTA 168
17 BCr61 locus  82:GGGGGGGGGCGGCRGTGTTTTGCCTCAGGGCTTCTGACCTCAGGTCGGGTGGTGGGGCTA 141
19 BCr61 locus 116:G--GGCAG-------TGTTTTGCCTCAGGGCTTCTGACCTCAGGTCGGGTGGTGGGGCTA 166
26 BCr61 locus 116:GGTGTGTG-------TGTTTTGCCTCAGGGCTTCTGACCTCAGGTC-GGTGGTGGGGCTA 167
28 BCr61 locus 111:G------G-------GGTTGTGCCTCAGGGCTTCTGACCTGAGGTGGGGTGGTGGGGCTA 157
                 *  .....      ..**.*.********.*********.****..******.******

01 BCr61 locus 170:GGG-CTTCTTTCCAGCAGGGAGGGAGGTGTGCCTGCCAGAGCTCAGAGCTTCAGCCCTGC 228
06 BCr61 locus 170:GGG-CTTCTTTCCACCAGGAAGGGAGGTGTGCCTGCCAGGGCTCAGAGCTTCAGCTCTGC 228
11 BCr61 locus 163:GAG-CTTCTTTCCACCAGGAAGGGAGATGTGCCTGCCAGGGCTCAGAGCTTCAGCTCTGC 221
13 BCr61 locus 168:GGG-CTTCTTTCCAGCAGGGAGGGAGGGATAGCT--CAGTGGTTTGAGCATTGGCC-TGC 223
14 BCr61 locus 169:GGG-CTTCTTTCTAGCAGGGAGGGAGGGATAGCT--CAGTGGTTTGAGCATTGGCC-TGC 224
17 BCr61 locus 142:GGG-CTTCTTTCCAGCAGGGAGGGAGGTGTGCCTGCCAGGGCTCAGAGCTTCAGCCCTGC 200
19 BCr61 locus 167:GGG-CTTCTTTCCAGCAGGGAGGGAGGTGTGCCTGCCAGGGTTCAGAGCTTCAGCCCTGC 225
26 BCr61 locus 168:GGG-CTTCTTTCCAGCAGGGAGGGAGGTGTGCCTGCCAGGGCTCACAGCTTCAGCCCTGC 226
28 BCr61 locus 158:GGGGCTTCTGTCCAGCAGGGAGGGAGGTGTGCCTGCCAGGGCTCAGAGCTTCAGCCCTGC 217
                 *.* *****.**.*.****.******...*..**..***.*.*...***.*..**..***

01 BCr61 locus 229:T---------------------------------------------------------- 229
06 BCr61 locus 229:T---------------------------------------------------------- 229
11 BCr61 locus 222:T---------------------------------------------------------- 222
13 BCr61 locus 224:TAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCGCTTAGGGATCTGGGGCAAAAAT 283
14 BCr61 locus 225:TAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCGCTTAGGGATCTGGGGCAAAAAT 284
17 BCr61 locus 201:T---------------------------------------------------------- 201
19 BCr61 locus 226:T---------------------------------------------------------- 226
26 BCr61 locus 227:T---------------------------------------------------------- 227
28 BCr61 locus 218:T---------------------------------------------------------- 218
                 *

01 BCr61 locus 229:---------------------------------------------------------- 229
06 BCr61 locus 229:---------------------------------------------------------- 229
11 BCr61 locus 222:---------------------------------------------------------- 222
13 BCr61 locus 284:TGGTCCTGCTAGTGAAGGCAGGGGGC-TGGACTCAATGACCTTTCAAGGTCCCTTCCAGT 342
14 BCr61 locus 285:TGGTCCTGCTAGTGAAGGCAGGGGGCCTGGACTCGATGACCTTTCAAGGTCCCTTCCAGT 344
17 BCr61 locus 201:---------------------------------------------------------- 201
19 BCr61 locus 226:---------------------------------------------------------- 226
26 BCr61 locus 227:---------------------------------------------------------- 227
28 BCr61 locus 218:---------------------------------------------------------- 218


01 BCr61 locus 229:---------------------------------------------------------- 229
```

```
06 BCr61 locus 229:------------------------------------------------------------ 229
11 BCr61 locus 222:------------------------------------------------------------ 222
13 BCr61 locus 343:TCTAGGAGATTGGTATATCTCCAATTATTACCTACTACCTTTTATTACCTTCAGCCCTGC 402
14 BCr61 locus 345:TCTAGGAGATTGGTATATCTCCAATTATTACCTACTACCTTTTATTACCTTCAGCCCTGC 404
17 BCr61 locus 201:------------------------------------------------------------ 201
19 BCr61 locus 226:------------------------------------------------------------ 226
26 BCr61 locus 227:------------------------------------------------------------ 227
28 BCr61 locus 218:------------------------------------------------------------ 218


01 BCr61 locus 230:-CCTGCTGAAGTCCCTAGCCCCAGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 288
06 BCr61 locus 230:-CCTGCTGAAGTCCCTAGCCCTGGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 288
11 BCr61 locus 223:-CCTGCTGAAGTCCCTAGCCCCAGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 281
13 BCr61 locus 403:TCCTGCTGAAGTCCCTAGCTCCAGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 462
14 BCr61 locus 405:TCCTGCTGAAGTCCCTAGCTCCGGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 464
17 BCr61 locus 202:-TCTGCTGAAGTCCCTAACCCCGGCACGTGCACCTCCCCTCCTGCAGAGTTGAAGGCCCT 260
19 BCr61 locus 227:-CCTGCTGAAGTCCCTAGCTCCGGCAGGTGCACCTCGCC--------------------- 264
26 BCr61 locus 228:-CCTGCTGAAGTCWCTAGCCCCGGCAGGTGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 286
28 BCr61 locus 219:-TCTGCTGAAGTCCCTAGCCCTGGCAGGCGCACCTCCCCTCCTGCAGAGTTGAAGCCCCT 277
                  .***********.***.*.*..***.*.*******.**.....................

01 BCr61 locus 289:AGCCCCAGGAGGTAGGCCCCCCACCGC-----CACTCGCAAGGCTGAAGCCCTGAGCCCT 343
06 BCr61 locus 289:AGCTCCAGCAGATAGCACCCTCACCCCACCCCCACTCGCAAGGCTGAAGCCCTGAGCCCT 348
11 BCr61 locus 282:AGCCCCAGCAGATAG--CCCCCACCCC----CCACTCGCAAGGCTGAAGCCCTGAGCCCT 335
13 BCr61 locus 463:AGCCCCAGCAGATAG-CCCCCCACCCC-----CACTCGCAAGGCTGAAGCCCTGAGCCCC 516
14 BCr61 locus 465:AGCCCCAGCAGATAG-CCCCCCACCCC-----CACTCGCAAGGCTGAAGCCCTGAGCCCC 518
17 BCr61 locus 261:AGCCCCAGCAGATAG-CCCCCCACCCC-----CACT-G-AAGTTCTGAGCCCTG------ 306
19 BCr61 locus 265:----CCAGCAGATAG--CCCCCACCCCA-----ACTCGCAAGGCTGAAGCCCTGAGCCCT 313
26 BCr61 locus 287:AGCCCCAGCAGATAG-CCTCCCACCCC----CCACTCGCAAGGCTAAAGCTCTGA-CCCT 340
28 BCr61 locus 278:AGCCCCAGCAGGTAGCCCTCCCCCGCC---CCCACTCGCAAGGCTGAAGCCTTGA----- 329
                  ....****.**.*** .*.*.*.*..*    .***.*.***.....***..**......

01 BCr61 locus 344:GGCARATGCACCTGG-CTCTTAAACTTCTGAAAATTACTGTACGCA             388
06 BCr61 locus 349:GTCAGATGCACCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            395
11 BCr61 locus 336:AGCAGATGCATCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            382
13 BCr61 locus 517:GGCAGATGCACCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            563
14 BCr61 locus 519:AGCAGATGCACCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            565
17 BCr61 locus 307:-GCAGATGCACC                                     317
19 BCr61 locus 314:GGCAGATGCACCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            360
26 BCr61 locus 341:GGCAGATGCACCTGGGCTCTTGAACTTCTGAAAATTA-TGTACGCANC            387
28 BCr61 locus 330:--CAAATGCACCTGG-CTCTTGAACTTCTGAAAATTACTGTACGCAGC            374
                  ..**.*****.*... ............................
```

Supplemental Figure 5-18. Sequence alignment of BCr61 locus. GenBank accession numbers are AB24106–AB249111, AB125524, AB125726 and AB125727.

```
01 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCACATGTTATTGGTTCTAAGTGTGACCCACAGGGTGACCA 60
11 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCAAATGTTATTGGTTCTAAATGTGACCCACAGGGTGACCA 60
14 BMm105 locus   1:-AGTGCCAGTGCAGGTAAATCAAATGTTATTGGTTCTAAGTGTGACCCACAGGGTGATCA 59
15 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCAAATGTTATTGGTTCTAAGTGTGACCTATAGGGTGACCA 60
17 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCAAATGTTATTGGTTCTAAGTGTGACCCACAGGGTGACCA 60
19 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCAA------------------------------------ 23
28 BMm105 locus   1:TAGTGCCAGTGCAGGTAAATCAAATGTTATTGGTTCTAAGTGTGACCCACAGGGGGACCA 60
                  .********************.......................................

01 BMm105 locus  61:GATAGTAAATGTGAAAAATCAGGAAACTTTTCAGGGTTGGGGGAGTATAGTTGCCTTGT- 119
11 BMm105 locus  61:GATAGTAAATATGAAAAATCAGGAAACTTTTCAGGGTCGGAG-AGTATAGTTGCTTTGC- 118
14 BMm105 locus  60:GATAGTAAATGTGAAAAATCAGGAAACTTTTCAGGGTCGGGG-AGTATAGTTGCCTTGC- 117
15 BMm105 locus  61:GATAGTAAATGTGAAAAATCAGGAAACTTTTCAGGGTCGGGG-AGTATAGTTGCCTTGTG 119
17 BMm105 locus  61:GATAGTAAATGTGAAAAATCAGGAAACTTTTCAGGGTCGGGG-AGTATAGTTGCCTTGC- 118
19 BMm105 locus  24:----GTAAATGTGAAAAATCAGGAAACTTTTCAGGGTCGGGG-AGCATAGTTGCCTTGC- 77
28 BMm105 locus  61:GATAATAAGTGTGAAAAATCAGGACACTTTGCGGGGTGGGGG-AGTATAGTTGCCTTGC- 118
                  .....***.*.*************.*****.*.****.**.* **.********.***.

01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 118:--AGGGAGGGGTAGGTCAGTGGTTTGAGGATTGGCCTGCTAAACCCAGGGTTGTGAGTTC 175
15 BMm105 locus 120:GGGGGGAGGGATACGTCAGTGGTTTGAGCATTGGCCTGTTAAACCCAGGGTTGTGAGTTC 179
17 BMm105 locus 118:---------------------------------------------------------- 118
19 BMm105 locus  77:---------------------------------------------------------- 77
28 BMm105 locus 118:---------------------------------------------------------- 118


01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 176:AATCCTTGAGGAGGCCGCTTAGGGATCTGGGGCAAAAATTGGTCCTGATAGAATCATAGA 235
15 BMm105 locus 180:AATCCTTGAGGAGACCACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAG--------- 230
17 BMm105 locus 118:---------------------------------------------------------- 118
19 BMm105 locus  77:---------------------------------------------------------- 77
28 BMm105 locus 118:---------------------------------------------------------- 118


01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 236:ATTCAAGATCAGAAGGGACCATTATGATCATCTAGTCTGACCTCCTGCAAGATGCAGGCC 295
15 BMm105 locus 230:---------------------------------------------------------- 230
17 BMm105 locus 118:---------------------------------------------------------- 118
19 BMm105 locus  77:---------------------------------------------------------- 77
28 BMm105 locus 118:---------------------------------------------------------- 118


01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 296:ACATAAGCCGATCCACCCACTCCTTAGCAAGCGACCCCTGCCCCATGCTTCGGAGGAAGG 355
15 BMm105 locus 230:---------------------------------------------------------- 230
17 BMm105 locus 118:---------------------------------------------------------- 118
19 BMm105 locus  77:---------------------------------------------------------- 77
28 BMm105 locus 118:---------------------------------------------------------- 118


01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 356:CGAAAAACCTCCAGGGCCATTGCCAATCTTCCCTGGAGGAAAATTCCTTCCCGACCCCAA 415
15 BMm105 locus 230:---------------------------------------------------------- 230
17 BMm105 locus 118:---------------------------------------------------------- 118
19 BMm105 locus  77:---------------------------------------------------------- 77
28 BMm105 locus 118:---------------------------------------------------------- 118


01 BMm105 locus 119:---------------------------------------------------------- 119
11 BMm105 locus 118:---------------------------------------------------------- 118
14 BMm105 locus 416:ATATGGCGGTCAGCTGAACCCCGAGCATACGGGCAAGACTCTCCAGCCAAACCCTCTGGA 475
15 BMm105 locus 230:---------------------------------------------------------- 230
```

```
17 BMm105 locus 118:------------------------------------------------------------ 118
19 BMm105 locus  77:------------------------------------------------------------ 77
28 BMm105 locus 118:------------------------------------------------------------ 118


01 BMm105 locus 119:------------------------------------------------------------ 119
11 BMm105 locus 118:------------------------------------------------------------ 118
14 BMm105 locus 476:AAAGATTATATCATCCCATTGTACTATTTACCAGTGTGGCACTTAATTGACCTATTGACT 535
15 BMm105 locus 230:------------------------------------------------------------ 230
17 BMm105 locus 118:------------------------------------------------------------ 118
19 BMm105 locus  77:------------------------------------------------------------ 77
28 BMm105 locus 118:------------------------------------------------------------ 118


01 BMm105 locus 119:------------------------------------------------------------ 119
11 BMm105 locus 118:------------------------------------------------------------ 118
14 BMm105 locus 536:AAGCCCTATTGATAGCAAAGGCAGGGGGCTGGACTAGATGACCTTTCAAGGTCCTTTCCA 595
15 BMm105 locus 231:---------------TGAAGGCAGGGGGCTGGACTAGATGACCTTTCAAGGTCCTTTCCA 275
17 BMm105 locus 118:------------------------------------------------------------ 118
19 BMm105 locus  77:------------------------------------------------------------ 77
28 BMm105 locus 118:------------------------------------------------------------ 118


01 BMm105 locus 120:-----------------------------------ATATATAACAAAAAGCCCCCAATAT 144
11 BMm105 locus 119:-----------------------------------ATATATAACACAAAGCCCCCAGTAT 143
14 BMm105 locus 596:GTTT--GGAGATTGGTATATCTCCTGTTATTACC---------------------AATAT 632
15 BMm105 locus 276:GTTCTAGGAGATTGGTATATCTCCAATTATTACCTTTTTATTACCTATTATTACCAATAT 335
17 BMm105 locus 119:-----------------------------------ATATATAACACAAAGCCCCCAATAT 143
19 BMm105 locus  78:-----------------------------------ATATATAACACAAAGCCCCCAATAT 102
28 BMm105 locus 119:-----------------------------------GTATATAACACAAAACCCCCAATAT 143
                                                  ....................*.***

01 BMm105 locus 145:CAGGAAGTCTGGTCACCCTAGTGACTCACATGCTGTTAATTCATTACATGCAGCCAGATT 204
11 BMm105 locus 144:CAGGAAGTCTGGTCACCCTAGTGACTCAGG--CTGTTAATTCATTACATGCAGCCACATT 201
14 BMm105 locus 633:CAGGAAGTCTGGTCACCCTAGTGACTCACATGCTGTTAATTCATTACATGCAGCCAGATT 692
15 BMm105 locus 336:CAGGAAGTCTGGTCATCCTAGTGACTCACATGCTGTTAATTCATTACATGCAGCCAGATT 395
17 BMm105 locus 144:CAGGAAGTYTGGTCACCCTAGTGACTCACATGCTGTTAATTCATTACATGCAGCCAGATT 203
19 BMm105 locus 103:CAGGAAGTCTAGTCACCCTAGTGACTCACGTGCTGTTAATTCATTACATGCAGCCAGATT 162
28 BMm105 locus 144:CGGGAAGTCTGGTCACCCTCGTGACTCACATGGTGTTAATTCATTACATGCAGCCAAATT 203
                 *.******.*.****.***.********.....**********************.***

01 BMm105 locus 205:GCAATCTGAATGGTGCAAAGTTCT                                228
11 BMm105 locus 202:GCAATCTGAATGGTGCAAAGTTCT                                225
14 BMm105 locus 693:GTAATCTGAATGGTGCAAAGTTCT                                716
15 BMm105 locus 396:GCAATCTGAATGGTGCAAAGTTCT                                419
17 BMm105 locus 204:GCAATCTGAATGGTGCAAAGTTCT                                227
19 BMm105 locus 163:GCAATCTGAATGGTGCAAAGTTCT                                186
28 BMm105 locus 204:GCAATCTGAATGGTGCAAAGTTCT                                227
                 *.*********************
```

Supplemental Figure 5-19. Sequence alignment of BMm105 locus. GenBank accession numbers are AB24112–AB249116 and AB125728-AB125730.

```
01 BPm30 locus   1:GTTTATAACCATTTGAGGCATATGCTAAGTGAAAA---TCTTTCTTCCCCYGTGTATTGT 57
13 BPm30 locus   1:GTTTATAACCATTTGAGGCATATGCTAAGTGAAAA-TCTCTTTCTTCCCCCATGTATTGT 59
17 BPm30 locus   1:GTTGATAACCATNGGAGGCATATGGTAAGTGAAGAA--TCTTTCTTCCTCCATGTATTGT 58
18 BPm30 locus   1:GTTTATAACCATTTGAGGCATATGCTAAGTGAAAAA--TCTTTCTTCCTCCATGTATTGT 58
19 BPm30 locus   1:GTTTATAACCATTTGAGGCATATGCTAAGTGAAAA---TCTTTCTTCCCCCATGTATTGT 57
28 BPm30 locus   1:GTTTATAACCATTTGAGGCATATGCTAAGTGAAAA---TCTTTCTTCCCCCCTGTATTGT 57
                 ***.********..**********.********.*   **********.*..********

01 BPm30 locus  58:ACAGCCTGCCCAGATTT-CRCTCTTTACCATATATCAGAG-------------------- 96
13 BPm30 locus  60:ACAACCTGCCCGGATTT-CACTCTTTACCATATAACAGAG-------------------- 98
17 BPm30 locus  59:ACAACCTGCCCAGATTT-CACTCTTTACCATATMTCAGGGAGGGCTAGCTCAGTGGTGGG 117
18 BPm30 locus  59:ACAACCTGCCCGGATTT-CACTCTTTACCATATATCAGGGAGGACTAGCTCAGTGGCAGG 117
19 BPm30 locus  58:ACAACCTGCCCGGATTT-CACTCTTTACCATATATCAGAG-------------------- 96
28 BPm30 locus  58:ACAGCCTGCCTGGATTGGCACTCTTCACCATATATCAGAG-------------------- 97
                ***.******..****. *.*****.*******..***.*

01 BPm30 locus  96:------------------------------------------------------------ 96
13 BPm30 locus  98:------------------------------------------------------------ 98
17 BPm30 locus 118:GGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAATTCAATC 177
18 BPm30 locus 118:GGAGGGCTAGCTCAGTGGTTTGCGCATTAGCCTGCTAAACCCAGGGTTGTGAGTTCAATC 177
19 BPm30 locus  96:------------------------------------------------------------ 96
28 BPm30 locus  97:------------------------------------------------------------ 97


01 BPm30 locus  96:------------------------------------------------------------ 96
13 BPm30 locus  98:------------------------------------------------------------ 98
17 BPm30 locus 178:TTTGAGGGGGCCACTTAGGGATCTGTGGCAAAAAATTGGTCCTGCTAGTGAAGGCAGGGG 237
18 BPm30 locus 178:CTTGAGGAGGCCACTTAGGAATCTGGGGCAAAAAATTGGTCCTGCTAGTGAAGGCAGGGG 237
19 BPm30 locus  96:------------------------------------------------------------ 96
28 BPm30 locus  97:------------------------------------------------------------ 97


01 BPm30 locus  96:------------------------------------------------------------ 96
13 BPm30 locus  98:------------------------------------------------------------ 98
17 BPm30 locus 238:GCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTTTAGGAGATTGGTATATCTCCAAT 297
18 BPm30 locus 238:GCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATACCTCCAAT 297
19 BPm30 locus  96:------------------------------------------------------------ 96
28 BPm30 locus  97:------------------------------------------------------------ 97


01 BPm30 locus  97:------------------CACCTCACAGTCATTAATGATTTTTATCCTCTCAAAACWCCT 138
13 BPm30 locus  99:------------------CACTTCACGGTCATTAATGATTTTTATCCTCCCAAAACTCCT 140
17 BPm30 locus 298:TATTACCTTTTTTTATTACCTTTCACAGTCATTAATGATTTTTATCCTCACAAAACACCT 357
18 BPm30 locus 298:TATTACCTTTTTTTATTACCTTTCACAGTCATTAATGATTTTTATCCTCACAAAACTCCT 357
19 BPm30 locus  97:------------------CACTTCACAGTCATTAATGATTTTTATCCTCCCAAAACTCCT 138
28 BPm30 locus  98:------------------CACCTCACAGTCATTAATGATTTTTATCCTCCCAACACTCCT 139
                                *...****.********************** ***.**.***

01 BPm30 locus 139:GATTATATATTATTCCTCTTTTATAGATAGAAAACTGAGGCACAGGGTAAATTAAGTGAT 198
13 BPm30 locus 141:GATTATATATTATTCCTGTTTTATAGATAGAAAACTGAGGCACAGGGTAAATTAAGTGAT 200
17 BPm30 locus 358:GATTATATATTATTCCTGTTTTATAGACAGAAAACTGAGGCACAGGGTAAATTAANTGAT 417
18 BPm30 locus 358:GATTATATTTTATTCCTGTTTTATAGATAGAAAACTGAGGCACAGGGTAAATTAAGTGAT 417
19 BPm30 locus 139:GATTATATATTATTCCTGTTTTATAGATAGAAAACTGAGGCACAGAGTAAATTAAGTGAT 198
28 BPm30 locus 140:GATTATATATTATTCCTATTTTATAGATAGAAAACTGAGGTACAGGGTAAATTAAGTGAT 199
                 ********.********.*********.************.****.*********.****

01 BPm30 locus 199:TTGCCTGAGGTCACTCTAGAAGCCTCTGGTT                          229
13 BPm30 locus 201:TTGCCTGAGGTCACTCTAGAAGCCTCTGGTT                          231
17 BPm30 locus 418:TTCCCTGCGGTCACTCTANAANCCTCTGGTT                          448
18 BPm30 locus 418:TTGCCTGCGGTCACTCTAGAAGCCTCTGGTT                          448
19 BPm30 locus 199:TTGCCTGAGGTCACTCTAGAAGCCTCTGGTT                          229
28 BPm30 locus 200:TTGCCTGAGGTCACTCTAGAAGCCTCTGGTT                          230
                 **.****.**********.**.*********
```

Supplemental Figure 5-20. Sequence alignment of BPm30 locus. GenBank accession numbers are AB24117–AB249122.

```
01 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCCTCAAAGATCTGTTTTCCTCTCAG 60
06 BHg33 locus   1:GTTTGGATGCCATCTATCTCCANANNCACCTCCTCCTTCAAA-ATCTGTTTTCCTCTCAG 59
10 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAAATCTGTTTTCCTCTCAG 60
14 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAGAGATCTGTTTTCCTCTCAG 60
17 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAGATCTGTTTTCCTCTCAG 60
19 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAGAGCTGTTTTCCTCTCAG 60
20 BHg33 locus   1:GTTTGGATGCCAT-TATCTCCTCTCCCACCTCCTCCTTCAAAGAGCTGTTTTCCTCTCAG 59
23 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAGATCTGTTTTCCTCTCAG 60
24 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAGATCTGCTTTCCTCTCAG 60
25 BHg33 locus   1:GTTTGGATGCCATCTATCTCCTCTCCCACCTCCTCCTTCAAAGATCCGTTTTCCTCTCAG 60
                 *************.*******.....**********.***.*.*.*.*.***********

01 BHg33 locus  61:GCTTTGTGAAAGTATCATCAGGACATGGTGTTC--GCCATG------------------- 99
06 BHg33 locus  60:GCTCTGCGAAAGTATCATCAGGACATGGTGTTC--GCCATG------------------- 98
10 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATGGTGTTC--GCCATG------------------- 99
14 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATGGAGTTC--GCCATG------------------- 99
17 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATGGAGTTC--ACCATG------------------- 99
19 BHg33 locus  61:GCTCTGTGAAAGTACCATCAGGAGATAGGCTTT--GCCATGGAGGAGGGATAGCTCAGTG 118
20 BHg33 locus  60:GCTCTGTGAAAGTACCATCAGGAGATAGGCTTT--GCCATGGAGGAGGGATAGCTCAGTG 117
23 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATAGGGTTT--GCCATGGGGGAGGGCTAGCTCAGTG 118
24 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATGGGGTTC--GCCATG------------------- 99
25 BHg33 locus  61:GCTCTGTGAAAGTATCATCAGGACATAGTGTTCTCGCCATG------------------- 101
                 ***.**.*******.********.**.* .**.  .*****

01 BHg33 locus  99:------------------------------------------------------------ 99
06 BHg33 locus  98:------------------------------------------------------------ 98
10 BHg33 locus  99:------------------------------------------------------------ 99
14 BHg33 locus  99:------------------------------------------------------------ 99
17 BHg33 locus  99:------------------------------------------------------------ 99
19 BHg33 locus 119:GTTTGAGCATTGGCCTGCTAAGCCCAGGATTATGAGCTCACTCCTTGAGGGGGCCACTTA 178
20 BHg33 locus 118:GTTTGAGCATTGGCCTGCTAAGCCCAGGATTATGAGCTCACTCCTTGAGGGGGCCACTTA 177
23 BHg33 locus 119:GTTTGAGCATTGGCCTGCTAAACCCAGAGTTGTGAGTTCAATCCTTGAGGGGGCCGCTTA 178
24 BHg33 locus  99:------------------------------------------------------------ 99
25 BHg33 locus 101:------------------------------------------------------------ 101


01 BHg33 locus  99:------------------------------------------------------------ 99
06 BHg33 locus  98:------------------------------------------------------------ 98
10 BHg33 locus  99:------------------------------------------------------------ 99
14 BHg33 locus  99:------------------------------------------------------------ 99
17 BHg33 locus  99:------------------------------------------------------------ 99
19 BHg33 locus 179:CAGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGATGGACTTGATGACCTT 238
20 BHg33 locus 178:CAGATCTGGGGCAAAAATTGGTCCTGCTAGTGACGGCAGGGGGATGGACTTGATGACCTT 237
23 BHg33 locus 179:CAGATCTGGGGCAAACATTGGTCCTGCTAGTGAAGGCAGGGGGCTAGATCTGATGACCTT 238
24 BHg33 locus  99:------------------------------------------------------------ 99
25 BHg33 locus 101:------------------------------------------------------------ 101


01 BHg33 locus 100:----------------------------------------------TTTTCAGAGCTATT 113
06 BHg33 locus  99:---------------------------------------------TTTTCNNNGCTATT 112
10 BHg33 locus 100:----------------------------------------------TTTTCAGAGCTATT 113
14 BHg33 locus 100:----------------------------------------------TTTTCAGAGCTATT 113
17 BHg33 locus 100:----------------------------------------------TTTTCAGAGCTATT 113
19 BHg33 locus 239:TCAAGGTCCCTTCCAGTTCTAAGAGATTGGTGTATCTCCTATTATGTTTTCAGAGCTATT 298
20 BHg33 locus 238:TCAAGGTCCCTTCCAGTTCTAAGAGATTGGTGTATCTCCTATTATGTTTTCAGAGCTATT 297
23 BHg33 locus 239:TCAAGGTCCCTTCCAGTTCTAGGAGGTTGGTATATCTCTTATTATGTTTTCAGAGCTATT 298
24 BHg33 locus 100:----------------------------------------------TTTTCAGAGCTATT 113
25 BHg33 locus 102:----------------------------------------------TTTTCAGAGCTATT 115
                                                      *****...******

01 BHg33 locus 114:GTGCTTAATCCAC                                                126
06 BHg33 locus 113:GTGCTTAATCCAC                                                125
10 BHg33 locus 114:GTGCTTAATCCAC                                                126
14 BHg33 locus 114:GTGCTTAATCCAC                                                126
17 BHg33 locus 114:GTGCTTAAT                                                    122
19 BHg33 locus 299:GTGCTTAATCCAC                                                311
20 BHg33 locus 298:GTGCTTAATCCAC                                                310
```

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23 BHg33 locus 299:GTGCTTAATCCAC                                    311
24 BHg33 locus 114:GTGCTT                                          119
25 BHg33 locus 116:GTGCTTAATCCAC                                    128
                ******.......
```

Supplemental Figure 5-21. Sequence alignment of BHg33 locus. GenBank accession numbers are AB24123–AB249132.

```
02 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGCGTGGAATTTGGCCATGGAGTACACTTTTAAGTTTTG 60
06 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGCGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 60
10 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 60
11 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTACGTTTTG 60
12 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAATGCACTTTTAAGTTTTG 60
14 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTGTTAAGTTTTG 60
17 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 60
19 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCATTTTTAAGTTTTG 60
20 BHg36 locus   1:-------------AGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 47
23 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 60
24 BHg36 locus   1:--ACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 58
25 BHg36 locus   1:--ACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGCACTTTTAAGTTTTG 58
27 BHg36 locus   1:ATACAATGCCGTCAGACTGTCAGTGTGGAATTTGGCCATGGAGTGGACTTTTAAGTTCAG 60
                  .............**********.******************.*..*.*.***.***..*

02 BHg36 locus  61:AACTAAAACTATTCCCTCTTTGGTTTAAAAATTGTCCTATGGGGGG-------------- 106
06 BHg36 locus  61:AACTAAA-CAATTCCCCCTTTGGTTTAAAAATTGTCCTATGGCGGG-------------- 105
10 BHg36 locus  61:AACTAAAACTATTTCTCCTTTGGTTAAAAAATTGTCCTATGGGGGG-------------- 106
11 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCTTATGGGGGG-------------- 106
12 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCTGTGGGGGG-------------- 106
14 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCTGTGGGGGCAG------------ 108
17 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCTGTGGGGGGG------------- 107
19 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGATTTAAAAATTGTCCTG-GGGGGGAGGG-ATAGCTCAG 118
20 BHg36 locus  48:AACTAAAACTATTCCCCCTTTGATTTAAAAATTGTTCTG-GGGGGGAGGG-ATAGCTCAG 105
23 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCTG-GAGGGTAGGG-ATAGCTCAG 118
24 BHg36 locus  59:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCGG-GGGGGGGGG----------- 106
25 BHg36 locus  59:AACTAAA-CTATTCCCCCTTTGGTTTAAAACTTGTCCTATCGTYGGGGGGNATTTCT--- 114
27 BHg36 locus  61:AACTAAAACTATTCCCCCTTTGGTTTAAAAATTGTCCTATGGGGGG-------------- 106
                 *******.*.***.*..*****.**.****.****.........*.

02 BHg36 locus 106:------------------------------------------------------------ 106
06 BHg36 locus 105:------------------------------------------------------------ 105
10 BHg36 locus 106:------------------------------------------------------------ 106
11 BHg36 locus 106:------------------------------------------------------------ 106
12 BHg36 locus 106:------------------------------------------------------------ 106
14 BHg36 locus 108:------------------------------------------------------------ 108
17 BHg36 locus 107:------------------------------------------------------------ 107
19 BHg36 locus 119:TGGTTTGAGCATTAGCTTGCTAAACCCAGGGTTCTGAGTTCAATCCTGGAGGGGGCCACC 178
20 BHg36 locus 106:TGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACC 165
23 BHg36 locus 119:TGGTTGGAGCATTGGCCTGTTAAACCCAGCGTTGTGAG---------------------- 156
24 BHg36 locus 106:------------------------------------------------------------ 106
25 BHg36 locus 114:------------------------------------------------------------ 114
27 BHg36 locus 106:------------------------------------------------------------ 106


02 BHg36 locus 106:------------------------------------------------------------ 106
06 BHg36 locus 105:------------------------------------------------------------ 105
10 BHg36 locus 106:------------------------------------------------------------ 106
11 BHg36 locus 106:------------------------------------------------------------ 106
12 BHg36 locus 106:------------------------------------------------------------ 106
14 BHg36 locus 108:------------------------------------------------------------ 108
17 BHg36 locus 107:------------------------------------------------------------ 107
19 BHg36 locus 179:TAGGGATCTGAGGCAAAAATCAGTACTTGGTCCTGCTAGCAAAGGCAGGGGGCTGGACTA 238
20 BHg36 locus 166:TAGGGATCTGAGGCAAAAATCAGTACTTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTA 225
23 BHg36 locus 157:--GGAGTCTGGGGCAAAAATCAGTACTTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTA 214
24 BHg36 locus 106:------------------------------------------------------------ 106
25 BHg36 locus 114:------------------------------------------------------------ 114
27 BHg36 locus 106:------------------------------------------------------------ 106


02 BHg36 locus 107:-----------------------------------------------TAAAAATTAGAGA 119
06 BHg36 locus 106:-----------------------------------------------TAAAAATTAGAGA 118
10 BHg36 locus 107:-----------------------------------------------TAAAAATTAGAGA 119
11 BHg36 locus 107:-----------------------------------------------TAAAAATTAGAGA 119
12 BHg36 locus 107:-----------------------------------------------TAAAAATTAGAGA 119
14 BHg36 locus 109:-----------------------------------------------TAAAAATTAGAGA 121
17 BHg36 locus 108:-----------------------------------------------TAAAAATTAGAGA 120
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19 BHg36 locus 239:GATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATTATTATAAAAATTAGAGA 298
20 BHg36 locus 226:GATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATTATTATAAAAATTAGAGA 285
23 BHg36 locus 215:GATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATTATTATAAAAATTAGAGA 274
24 BHg36 locus 107:-----------------------------------------------TGAAA-TTAGAGA 118
25 BHg36 locus 115:-------------------------------------------------------------A 115
27 BHg36 locus 107:-----------------------------------------------TAAAAATTAGAGA 119
                                                        ............*

02 BHg36 locus 120:TATGATTAAACCCAGATTTTTGGGGATTTGTCAAGTCATTGATAGCAGCTACCAGTTTTC 179
06 BHg36 locus 119:TACGATTAAATCCAGCTTTTTGGG-ATTCGTCAAGTCATTGATAGCAGCTACCAGTTTTC 177
10 BHg36 locus 120:TATGATTAAATCCAGCTTTTTGGG-ATTCGTCAAGTCATTGATAGCAGTTACCAGCTTTC 178
11 BHg36 locus 120:GATGATTAAATCCAGCTTTTTGGG-ATTCGTCAAGTCATTGATAGCAGTTCCMAGTTTTC 178
12 BHg36 locus 120:TATGATTAAATCCAGCTTTTGGGG-ATTTGTCAAG----------------CCAGTTTTC 162
14 BHg36 locus 122:TATGATTAAATCCAGCTTTTTGGG-ATTTGTCAAGTCATTGATAGCAGCTACCAGTTTTC 180
17 BHg36 locus 121:TATGATTAAATCCAGCTTTTTGGG-ATTCGTCAAGTCATTGATAGCAGCTACCAGTTTTC 179
19 BHg36 locus 299:TATGATTAAATCCAGCTTTTTGGG-ATTCATCAAGTCATTGATAGCAGCTACCAGTTTTC 357
20 BHg36 locus 286:TATGATTAAATCCAGCTTTTTGGG-ATTCATCAAGTCATTGATAGCAGCTACCAGTTTTT 344
23 BHg36 locus 275:TATGATTAAATCCAGCTTTTTGGG-ATTCGTCAAGTCATTGATAGCAGCTACCAGTTTTC 333
24 BHg36 locus 119:TATGATTATATCCAGCTTTTTAGG-ATTTGTCAAGTTATTGATAGCAGCTACCAGTTTTC 177
25 BHg36 locus 116:TATGATTAAATCCAGCTTTTTGGG-ATTTGTCAAGTCATTGATAGCAGCTACCAGTTTTC 174
27 BHg36 locus 120:TATGATTAAATCCAGCTTTTGGGG-ATTTGTCAAGTCATTGATAGCGGCTACTAGTTTTC 178
                 .*.*****.*.****.****..** ***..*****................*.**.***.

02 BHg36 locus 180:AGGGAATGCACAATCCAAACCCAGATACT                           208
06 BHg36 locus 178:AGGGGATGCACAATCCAAACCCAGATACT                           206
10 BHg36 locus 179:AGGGGATGCACAATCCAAACCCAGATACT                           207
11 BHg36 locus 179:AGGGGATGCACAATCCAAACCCAGATACT                           207
12 BHg36 locus 163:AGGGGATGCACAATCCAAACCCAGATACT                           191
14 BHg36 locus 181:AGGGGATGCACAATCCAAACCCAGATACT                           209
17 BHg36 locus 180:AGGGGATGCACAATCCAAACCCAGATACT                           208
19 BHg36 locus 358:AGGGGATGCACAATCCAAACCCAGATACT                           386
20 BHg36 locus 345:AGGGGATGCACAATCCAAACCCAGATACT                           373
23 BHg36 locus 334:AGGGGATGCACAATCCAAACCCA                                356
24 BHg36 locus 178:AGGGGATGCACAATCCAAACCCAGATAC                            205
25 BHg36 locus 175:AGGGGATGGACAATCCAAACCCAGATACT                           203
27 BHg36 locus 179:AGGGGATGCACAATCCAAACCCAGATACT                           207
                ****.***.**************......
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Supplemental Figure 5-22. Sequence alignment of BHg36 locus. GenBank accession numbers are AB24133–AB249145.

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01 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATYTCTTTATCATCTACTTACAAATAAACCAGTTC 60
03 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTACCATCTACTTACAAATAAACCAGTTC 60
08 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTG---------TCATCTACTTACAAACAAACCAGTTC 51
09 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTACAAATAAACCAGTTC 60
10 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTGGAAANGAACCAGTTC 60
11 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTACAAATAAACCAGTTC 60
15 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTAGAAATAAACCAGTTC 60
17 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTAGAAATAAACCAGTTC 60
19 BHa59 locus   1:--------------------------TCTCTTTATCATCTACTTACA-ATAAACCAGTTC 33
23 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTACATATAAACCAGTTC 60
24 BHa59 locus   1:GGAAAAGAAACCTA-AAGCTGTTTGATCTCTTTATCATCTACTTAGAAATAAACCAGTTC 59
25 BHa59 locus   1:GGAAAAGAAACCTAGAAGCTGTTTGATCTCTTTATCATCTACTTAGAAATAAACCAGTTC 60
                 ..................................*********..*.*..*********

01 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAACAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
03 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAACAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
08 BHa59 locus  52:ATGAAACCTAAAACAGAGGAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 111
09 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAACAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
10 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
11 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
15 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
17 BHa59 locus  61:ATGAAACCTAAAACAGAGCAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTWTTA 120
19 BHa59 locus  34:ATGAAACTTAAACCAGAAGAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTG-A 92
23 BHa59 locus  61:ATGAAACCTAAACCAGAGGAAAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 120
24 BHa59 locus  60:ATGAAACCTAAAACAGAGCAGAAATAGCTGATGCTGCCACAACAAAGCATAAATGTTTTA 119
25 BHa59 locus  61:ATGAAACCTAAAACAGAGGAGAAGTAGCTGATGCTGCCACAGCGWAGCATAAATGTTTTA 120
                    *******.****.****..*.**..****************.*..***********...*

01 BHa59 locus 121:AG-TGCTTCAAAAA---------------------------------------------- 133
03 BHa59 locus 121:AG-TGCTTCAAAAA---------------------------------------------- 133
08 BHa59 locus 112:AGGTGCTTCAAAAA---------------------------------------------- 125
09 BHa59 locus 121:AG-TGCTTCAAAAA---------------------------------------------- 133
10 BHa59 locus 121:AGGTGCTTCAAAAA---------------------------------------------- 134
11 BHa59 locus 121:AGGTGCTTCAAAAA---------------------------------------------- 134
15 BHa59 locus 121:AGGTGCTTCAAAA----------------------------------------------- 133
17 BHa59 locus 121:AGGTGCTTCAAAAA---------------------------------------------- 134
19 BHa59 locus  93:AGGGGCTTCAAAAAAAGGGGAGGGAGGGATAGCTCANTGGTTTGAGCATTGGCCTACTA 152
23 BHa59 locus 121:AGGTGCTTCAAAAAAA--------GAGG------TCAGTGGTTTGAGCATTGGCCTGCTA 166
24 BHa59 locus 120:AGGTGCTTCAAAA----------------------------------------------- 132
25 BHa59 locus 121:AGGTACTTCAAAAA---------------------------------------------- 134
                    **...********.

01 BHa59 locus 133:------------------------------------------------------------ 133
03 BHa59 locus 133:------------------------------------------------------------ 133
08 BHa59 locus 125:------------------------------------------------------------ 125
09 BHa59 locus 133:------------------------------------------------------------ 133
10 BHa59 locus 134:------------------------------------------------------------ 134
11 BHa59 locus 134:------------------------------------------------------------ 134
15 BHa59 locus 133:------------------------------------------------------------ 133
17 BHa59 locus 134:------------------------------------------------------------ 134
19 BHa59 locus 153:AACTCAGGGTTGTGNNNNNNNNNNNNNNGGGGGGCCACTTAGGGATCTGGGGCAAAAATTG 212
23 BHa59 locus 167:AACTCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATTG 226
24 BHa59 locus 132:------------------------------------------------------------ 132
25 BHa59 locus 134:------------------------------------------------------------ 134


01 BHa59 locus 133:------------------------------------------------------------ 133
03 BHa59 locus 133:------------------------------------------------------------ 133
08 BHa59 locus 125:------------------------------------------------------------ 125
09 BHa59 locus 133:------------------------------------------------------------ 133
10 BHa59 locus 134:------------------------------------------------------------ 134
11 BHa59 locus 134:------------------------------------------------------------ 134
15 BHa59 locus 133:------------------------------------------------------------ 133
17 BHa59 locus 134:------------------------------------------------------------ 134
19 BHa59 locus 213:GTCCTGCTAGTGAAGGCAGGGG------GCTGGACTTGATGACCTTTCAAGGTCCCTTCC 266
23 BHa59 locus 227:GTCCTGCTAGTGAAGGCAGGGGAGGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCC 286
24 BHa59 locus 132:------------------------------------------------------------ 132
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25 BHa59 locus 134:------------------------------------------------------------ 134


01 BHa59 locus 134:---------------------------------------TAATGTCTATTTTGGTTTGGT 154
03 BHa59 locus 134:---------------------------------------TAATGTCTACTTTGGTTTGGT 154
08 BHa59 locus 126:---------------------------------------TAATGTCTATTTTGGTTTGGT 146
09 BHa59 locus 134:---------------------------------------TAATGTCTATTTTGGTTTGGT 154
10 BHa59 locus 135:---------------------------------------TAATGTCTATTTTGGTTTGGT 155
11 BHa59 locus 135:---------------------------------------TAATATCTATTTTGGTTTGGT 155
15 BHa59 locus 134:---------------------------------------TAATGTCTATTTTGGTTTGGT 154
17 BHa59 locus 135:---------------------------------------TAATGTCTATTTTGGTTTGGT 155
19 BHa59 locus 267:AGTTCTAGGAGATTGGTATATCTCCAATTATTATTACCTTAATGTCTATTTTGGTTTGGT 326
23 BHa59 locus 287:AGTTCTAGGAGATTGGTATATCTCCAGTTATTATTACCTTAATGTCTATTTTGGTTTGGT 346
24 BHa59 locus 133:---------------------------------------TAATGTCTATTTTGGTTTGGT 153
25 BHa59 locus 135:---------------------------------------TAATGTCTATTTTGGTTTGGT 155
                                                 ****.****.***********

01 BHa59 locus 155:TTCAGTTTACAAGCAACAAATTGGTTGATATAAAAATAAT-TCACATWTAGAATTATTAA 213
03 BHa59 locus 155:TTCAGTTTACAAGCAACAAATTGGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 213
08 BHa59 locus 147:TTCAGTTTACAAGCAACAAATTGGTAGACGTAAAAATAAT-TCACATTTAGAATTATTAA 205
09 BHa59 locus 155:TTCAGTTTACAAGCAACAAATTGGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 213
10 BHa59 locus 156:TTCCATTTACAAGCAACAAATTAGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 214
11 BHa59 locus 156:TTCAGTTTACAAGCAACAAATTGGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 214
15 BHa59 locus 155:TTCAGTTTACAAGCAACAAATTAGTAGATATAAAAATAATGTCACATTTAGAATTATTAA 214
17 BHa59 locus 156:TTCAGTTTACAARCAACAAATTAGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 214
19 BHa59 locus 327:TTCAGTTTACAAGCAACAAATTGGTAGATATAATAAATAA-TCACA             371
23 BHa59 locus 347:TTCAGTTTACAAGCAACAAATTGGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 405
24 BHa59 locus 154:TTCAGTTTACAAGCAACAAATTAGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 212
25 BHa59 locus 156:TTCAGTTTACAAGCAACAAATTGGTAGATATAAAAATAAT-TCACATTTAGAATTATTAA 214
                ***..*******.*********.**.**..***.**..*. *****...............

01 BHa59 locus 214:AAAAATCTGGTCCCC                                        228
03 BHa59 locus 214:AAAAATCTGGTCCCC                                        228
08 BHa59 locus 206:AAAAATCTGGTCCCC                                        220
09 BHa59 locus 214:AAAAATCTGGTCCCC                                        228
10 BHa59 locus 215:AAAAATCTGGTCCCC                                        229
11 BHa59 locus 215:AAAAATCTGGTCCCC                                        229
15 BHa59 locus 215:AAAAATCTGGTCCCC                                        229
17 BHa59 locus 215:AAAAATCTGGTCCCC                                        229
23 BHa59 locus 406:AAAAATCTGGTCCCC                                        420
24 BHa59 locus 213:AAAAATCTGGTCCCC                                        227
25 BHa59 locus 215:AAAAATCTGGTCCCC                                        229
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Supplemental Figure 5-23. Sequence alignment of BHa59 locus. GenBank accession numbers are AB24146–AB249157.

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01 BMr20 locus   1:GACTGGGGAAATCCTTAGAGACGGAGATCCAGATGCTTTCCAGTCCTTGCACAAGGACTA 60
06 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGGGAGATCCAGATGCTTTCCAATCCTTGCACAAGGACTA 60
14 BMr20 locus   1:GACTGGGGAAATCCT-AGAGAGGGAGATCCAGATGCTTT-CAGTCCTTGCACAAGGACTA 58
18 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGAGAGATCCAGATGCTTTCCAGTCCTTGCACAAGGACTA 60
19 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGGGAGATCCAGATGCTTTCCAGTCCTTGCACAAGGACTA 60
20 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGGGAGATCCAGATGCTTTCCAGGCCTTGCACAAGGACTA 60
23 BMr20 locus   1:---------------------------------------CCAGTCCTTGCACA-GGACTA 20
24 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGGGAGATCCAGATGCTTTTCAGTCCTTGCACAAGGACTA 60
25 BMr20 locus   1:GACTGGGGAAATCCT-AGAGAGGGAGATCCAGATGCTTTCCAGTCCTTGCACAAGGACTA 59
27 BMr20 locus   1:GACTGGGGAAATCCTTAGAGAGGGAGATCCAGATACTTTCCAGTCCTTGCACAAGGACCA 60
                 ........................................**..*********.****.*

01 BMr20 locus  61:GATCACAGCTTT------------------------------------------------ 72
06 BMr20 locus  61:GATCACAGTTTT------------------------------------------------ 72
14 BMr20 locus  59:GATCACAGCTTT------------------------------------------------ 70
18 BMr20 locus  61:GATCACAGCTTT------------------------------------------------ 72
19 BMr20 locus  61:GATTAGAGCTTTGATCCATCTCTTAGGGGGGAGGGATAGCTCAGTGGTTTGAGTATTGGC 120
20 BMr20 locus  61:GATTAGAGCTTTGATCTATCTCTTAGGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGC 120
23 BMr20 locus  21:GATAACAGCTTTGATTTATCTCTTAGGGRGGAGGGATARCTCAGTGGTTTGAGCATTGSC 80
24 BMr20 locus  61:GATCACAGCTTT------------------------------------------------ 72
25 BMr20 locus  60:GATCACAGCTTT------------------------------------------------ 71
27 BMr20 locus  61:GATCACAGCTTT------------------------------------------------ 72
                 ***.*.**.***

01 BMr20 locus  72:------------------------------------------------------------ 72
06 BMr20 locus  72:------------------------------------------------------------ 72
14 BMr20 locus  70:------------------------------------------------------------ 70
18 BMr20 locus  72:------------------------------------------------------------ 72
19 BMr20 locus 121:CTGCTAAACCCAGGGTTGTCAGTTCAATCCTTGAGGGTGCCACTTAGGGATGTGGGGCAA 180
20 BMr20 locus 121:CTGCTAAACCCAGGGTTGTCAGTTCAATCCTTGAGGGTGCCACTTAGGGATGTGGGGCAA 180
23 BMr20 locus  81:CTGCTAAACTCAGGGATGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGATGTGGGGCAA 140
24 BMr20 locus  72:------------------------------------------------------------ 72
25 BMr20 locus  71:------------------------------------------------------------ 71
27 BMr20 locus  72:------------------------------------------------------------ 72


01 BMr20 locus  72:------------------------------------------------------------ 72
06 BMr20 locus  72:------------------------------------------------------------ 72
14 BMr20 locus  70:------------------------------------------------------------ 70
18 BMr20 locus  72:------------------------------------------------------------ 72
19 BMr20 locus 181:AAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCC 240
20 BMr20 locus 181:AAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCC 240
23 BMr20 locus 141:AAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAACAACCTTTCAAGGTCCCTTCC 200
24 BMr20 locus  72:------------------------------------------------------------ 72
25 BMr20 locus  71:------------------------------------------------------------ 71
27 BMr20 locus  72:------------------------------------------------------------ 72


01 BMr20 locus  73:-----------------------------------------------GGATCTGGCTTCA 85
06 BMr20 locus  73:-----------------------------------------------GGATCTGGCTTCA 85
14 BMr20 locus  71:-----------------------------------------------GGATCTGGCTTCA 83
18 BMr20 locus  73:-----------------------------------------------GGATCTGGCTTCA 85
19 BMr20 locus 241:AATTCTAGGAGATTGGTATATCTTCAATTATTACCTTTATTACCTTTGGATCTGGCTTCA 300
20 BMr20 locus 241:AGTTCTAGGAGATTGGTATATCTCCAATTATTACCTTT---------GGATCTGGCTTCA 291
23 BMr20 locus 201:AGTTCTAGGAGATTGGTATATCTCCAATTATTACCTTTATTACCTTTGGATCTGGCTTCA 260
24 BMr20 locus  73:-----------------------------------------------GGATCTGGCTTCA 85
25 BMr20 locus  72:-----------------------------------------------AGATCTGGATTCA 84
27 BMr20 locus  73:-----------------------------------------------GGATCTGGCTTCA 85
                                                       .*******.****

01 BMr20 locus  86:GCATATTTGTTGTATATT-----------CAGTTGGCTTAGTATTATGTTTGCCTGTGAT 134
06 BMr20 locus  86:GCAAATCTGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 145
14 BMr20 locus  84:GCAAATCTGATTTATATTTATTGTATATGCAGTTGGCTTAGTATT--GTTTGCCTGTGAT 141
18 BMr20 locus  86:GCAAATCTGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 145
19 BMr20 locus 301:GCAAATATGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 360
20 BMr20 locus 292:GCAAATATGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 351
23 BMr20 locus 261:GCAAATCTGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATG           308
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24 BMr20 locus  86:GCAAATCTGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 145
25 BMr20 locus  85:GCAAATCTGATTTATATTTATTGTATGTTCAGTTGGCTTAGTATTATGTTTCCCTGTGAT 144
27 BMr20 locus  86:GCAAATCTGATTTATATTTATTGTATATTCAGTTGGCTTAGTATTATGTTTGCCTGTGAT 145
                ***.**.**.*.******...........***************..*............

01 BMr20 locus 135:GTTGAGGTACGGGCACAAAATTAGTGTAGA                          164
06 BMr20 locus 146:GTTGAGGTACGGGCACAAAATTAGTGTAG                           174
14 BMr20 locus 142:GTTGAGGTACGGGCACAAAATTAGTGTAG                           170
18 BMr20 locus 146:GTTGAGGTATGGGCACAAAATTAGTGTAGA                          175
19 BMr20 locus 361:GTTGAGGTACGGGCACAAAATTAGTGTAGA                          390
20 BMr20 locus 352:GTTGAGGTACGGGCACAAAATTAGTGTAGA                          381
24 BMr20 locus 146:GTTGAGGTACGGGCACAAAATTAGTGTAGA                          175
25 BMr20 locus 145:GTTGAGGTACGGGCACAAAATTAGTGTAG                           173
27 BMr20 locus 146:GTTGAGGTATGGGCACAAAATTAGTGTAGA                          175
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Supplemental Figure 5-24. Sequence alignment of BMr20 locus. GenBank accession numbers are AB24158–AB249167.

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01 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGGCTGTAAGTAATCTTTGATATGTTGAACC 60
09 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
14 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
17 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
19 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
20 BMr49 locus   1:------------------------------GCC-GTA-GTA-TCTTTGATATGTTGAACC 27
21 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
23 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAATAATYTTTGATATGTTGAACC 60
25 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAATCTTTGATATGTTGAACC 60
28 BMr49 locus   1:AACATTAGGCATCCCCAATAAGCCTGCAAGGCCCGTAAGTAGTCTTTGATATGTTGAACC 60
                 ...............................*.*.***..**.*.****************

01 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACAGGTATAAGTAAGATGATACTTGAGT 120
09 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACAGGTGTAAACAAGATGATACTTGAGT 120
14 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACTGATGTAAGCAAGATGATACTTGAGT 120
17 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACTGATGTAAGCAAGATGATACTTGAGT 120
19 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACAGGTGTAAGCAAGATGATACTTGAGT 120
20 BMr49 locus  28:AGGAGGTATTATTAACCTGACTGTAAANNCTGACAGGTGTAAGCAAGATGATACTTGAGT 87
21 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACAGGTGTAAGCAAGATGATACTTGAGT 120
23 BMr49 locus  61:AGGAGGTATTATTAACCTGACTATAAACCCTGACAGGTRTAAGCAAGATGATACTTGAGT 120
25 BMr49 locus  61:GGGAGGTACTATTAACCTGACTGTAAACCCTGACAAGTGTAAGCAAGATGATACTTAAGT 120
28 BMr49 locus  61:AGGAGGTATTATTAACCTGACTGTAAACCCTGACAGGTGTGAGCAAGATGATACTT---- 116
                 .*******.*************.****..*****...*.*.*..************....

01 BMr49 locus 121:GGTTCCATTCCTACCTT------------------------------------------ 137
09 BMr49 locus 121:GGTTCCATTCCTACCTT------------------------------------------ 137
14 BMr49 locus 121:GGTTCCATTCCTACCTT------------------------------------------ 137
17 BMr49 locus 121:GGTTCCATTCCTACCTT------------------------------------------ 137
19 BMr49 locus 121:GGTTCCATTCCTACCTTGGGGGGACAGATAGCTCAGTGGTTTAAGTACTGGCCTGCTAAA 180
20 BMr49 locus  88:GGTTCCATTCCTACCTTGGGGGGACAGATAGCTCAGTGGTTTAAGTACTGGCCTGCTAAA 147
21 BMr49 locus 121:GGTTCCATTCCTACCTTGGGGGGAGGGATAGCTCAGTGGTTTGAGCACTGGCCTGCTAAA 180
23 BMr49 locus 121:GGTTCCATTCCTACCTTGGGAGGAYAGATAG-----TGGTTTGAGCACTGGCCTGCTAAA 175
25 BMr49 locus 121:GGTTCCATTCCTACCTT------------------------------------------ 137
28 BMr49 locus 117:----CCATTCCTATCTT----------------------------------------- 129
                 ....*********.***

01 BMr49 locus 137:------------------------------------------------------------ 137
09 BMr49 locus 137:------------------------------------------------------------ 137
14 BMr49 locus 137:------------------------------------------------------------ 137
17 BMr49 locus 137:------------------------------------------------------------ 137
19 BMr49 locus 181:CCCAGGGTTGTGAGTTCAATCCTTGAGGGGACCACTTAGGGATYTGGAGCAAAAATTGGT 240
20 BMr49 locus 148:CCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGAGCAAAAATTGGT 207
21 BMr49 locus 181:CCTAGGGTTGTCAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGT 240
23 BMr49 locus 176:CCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACCTAGGGATYTGGGGCAAAAATTGGT 235
25 BMr49 locus 137:------------------------------------------------------------ 137
28 BMr49 locus 129:------------------------------------------------------------ 129


01 BMr49 locus 137:------------------------------------------------------------ 137
09 BMr49 locus 137:------------------------------------------------------------ 137
14 BMr49 locus 137:------------------------------------------------------------ 137
17 BMr49 locus 137:------------------------------------------------------------ 137
19 BMr49 locus 241:CCTGCTAGTGAAGGCAGGGG-CTGGACTCAATGACCTTTCAAGGTTCCTTCCAGCTYTAG 299
20 BMr49 locus 208:CCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGCTCTAG 267
21 BMr49 locus 241:CCTACTAGTGAAGGCAGGGGGCTGCACTTGATGACCTTTCAAGGTCCCTTCCAGCTCTAG 300
23 BMr49 locus 236:CCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGCTYTAG 295
25 BMr49 locus 137:------------------------------------------------------------ 137
28 BMr49 locus 129:------------------------------------------------------------ 129


01 BMr49 locus 138:----------------------------------------TCACAG-----TGTGTGGT 151
09 BMr49 locus 138:----------------------------------------TCACAGTGCACTGGGTGGT 156
14 BMr49 locus 138:----------------------------------------TCACAGTGCACTGGGTGGT 156
17 BMr49 locus 138:----------------------------------------TCACAGCGCACTGGGTGGT 156
19 BMr49 locus 300:GAGATTGGTATATCTCCAATTTTTT--TTTTTTTAAACCTTTCACAGTGCACTGAGTGGT 357
20 BMr49 locus 268:GAGATTGGTATATCTCCAATTTTTTTTTTTTTTTTAACCTTTCACAGTGCACTGGGTGGT 327
21 BMr49 locus 301:GAGATTGGTATATCTCCAAATTATTATTTTTTTTAAACCTTTCACAGTGCACTGGGTGGT 360
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23 BMr49 locus 296:GAGATTGGTATATCTCCAATTTTTT---TTTTTAATACCTTTCACAGTGCACTGGCTGGT 352
25 BMr49 locus 138:----------------------------------------TCACAGTGCACTGGGTGGT 156
28 BMr49 locus 130:----------------------------------------TCACAGTGCACTGGGTGGT 148
                                                 ******.....**..****

01 BMr49 locus 152:GTGTAACTGGTCATTGCCACAGAGGATCTTCTCACATAGGGTTCTGCAGAGTTTTAATC- 210
09 BMr49 locus 157:GTGTAACTGCTCATTGCCACAGAGAATCTTCTCACATAGGGTTCTGCAGGGTTTTAATC- 215
14 BMr49 locus 157:GTATAACTGCTCATTGCCACAGATAATCTTCTCACATAGGGTTCTGCGGGGTTTTAATC- 215
17 BMr49 locus 157:ATGTAACTGCTCATTGCCACAGAGAATCTTCTCACATAGGGTTCTGCGGGGTTTTAATC- 215
19 BMr49 locus 358:GTGTAACTGCTCATTGTCACAGAGAATCTTCTCACATAGA-TTAAAACCC-TGCAGAACC 415
20 BMr49 locus 328:GTGTAACTGCTNATTGTCACAGAGAATCTTCTCACATAGA-TTAAAACCCCTGCAGAACC 386
21 BMr49 locus 361:GTGTAACTGCTCATTGCCACAGAGAATCTTCTCACATAGGGTTCTGTGGGGTTTTAATC- 419
23 BMr49 locus 353:GTGTAACTGCTCATTGCCACAGAGAATCTTCTCACATAGGGTTCTGCAGGGTTTTAATC- 411
25 BMr49 locus 157:GTGCAACTGCTCATTGCCACAGAGAATCTTCTCGCATAGGGTTCTGCGGGGTTTTAATC- 215
28 BMr49 locus 149:GTGAAACTACTCATTGCCACAGAGAATCTTCTCACATAGGGTTCTGCAGGGTTTTAATC- 207
                .*..****..*.****.******..********.*****..**.... ...*....*.*

01 BMr49 locus 211:--TATCATCTGTCCTGTTCAACACTTGTGAGGTTGCTCGGAAGAGACAATTAG       261
09 BMr49 locus 216:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       266
14 BMr49 locus 216:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       266
17 BMr49 locus 216:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       266
19 BMr49 locus 416:C-TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       467
20 BMr49 locus 387:CCTATCATCTGTCCCTGTC                                    405
21 BMr49 locus 420:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       470
23 BMr49 locus 412:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAARARACAATTAG       462
25 BMr49 locus 216:--TATCATCTGTCCTGTTCAAAACTTGTGAGGTTGCTCGGAAGAGACAATTAG       266
28 BMr49 locus 208:--TATCATCTGTCCTGTTCAACACTTGTAAGGTTGCTCGGAAGAGACAATTAG       258
                  ************...**.................................
```

Supplemental Figure 5-25. Sequence alignment of BMr49 locus. GenBank accession numbers are AB24168–AB249177.

```
01 BOs68 locus    1:CCTGTGCCAAATTTATCTATGATAGAACAATAGAATTGTTCTGTATAACACATCAATATA 60
06 BOs68 locus    1:--------------ATCTATGATAGAACAATAAAATTGTTCTGTATAACACAACAATATA 46
12 BOs68 locus    1:-------------TATCTATGATAGAACAATAAAATTGTTCTGTATAACACAACAATATA 47
14 BOs68 locus    1:CCTGTGCCAAATTCATCTATGATAGAACAATAAAATTGTTCTGTATAACACAACAATATA 60
15 BOs68 locus    1:CCTGTGCCAAATTCATCTATGATAGAACAATAAAATTGTTYTGTATAACACAACAATATA 60
17 BOs68 locus    1:--------------------------------------TCTGTATAACACAACAATATA 21
19 BOs68 locus    0:------------------------------------------------------------ 0
                              ...............................................

01 BOs68 locus   61:ACAAT-GAA-ATTACACCAGGG-ATTATTTT-GGCCCATTACATGTAGCATG-------- 108
06 BOs68 locus   47:ACAAT-GAA-ATTACACTAGGG-ATTATTTT-GGCCCATTACATGTAGCATG-------- 94
12 BOs68 locus   48:ACAAT-GAA-ATTACACCAGGG-ATTATTTT-GGCCCATTACATGTAGCATGGGGGGAGG 103
14 BOs68 locus   61:ACAAT-GAA-ATTACACCAGGG-ATTATTTT-GGCCCATTACATGTAGTATGGGGGGAGG 116
15 BOs68 locus   61:ACAAT-GAA-ATTACACCAGGG-ATTATTTT-GGCCCATTACATGTAGCATG-------- 108
17 BOs68 locus   22:ACAATAGAACATTACACCAGGGGATTATTN-AGGCCCATTACATGTAGCATG-------- 72
19 BOs68 locus    1:-----------TTACACCAGGG-ATTATTTTAGGCCCATTAKATGTAGCATG-------- 40
                  ..... ... .******.**** ******.. *********.******.***

01 BOs68 locus  108:------------------------------------------------------------ 108
06 BOs68 locus   94:------------------------------------------------------------ 94
12 BOs68 locus  104:GATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAAGTCCTTG 163
14 BOs68 locus  117:GAAAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAA-TCCTTG 175
15 BOs68 locus  108:------------------------------------------------------------ 108
17 BOs68 locus   72:------------------------------------------------------------ 72
19 BOs68 locus   40:------------------------------------------------------------ 40


01 BOs68 locus  108:------------------------------------------------------------ 108
06 BOs68 locus   94:------------------------------------------------------------ 94
12 BOs68 locus  164:AGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGG 223
14 BOs68 locus  176:AGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGG 235
15 BOs68 locus  108:------------------------------------------------------------ 108
17 BOs68 locus   72:------------------------------------------------------------ 72
19 BOs68 locus   40:------------------------------------------------------------ 40


01 BOs68 locus  108:------------------------------------------------------------ 108
06 BOs68 locus   94:------------------------------------------------------------ 94
12 BOs68 locus  224:ACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTA 283
14 BOs68 locus  236:ACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTA 295
15 BOs68 locus  108:------------------------------------------------------------ 108
17 BOs68 locus   72:------------------------------------------------------------ 72
19 BOs68 locus   40:------------------------------------------------------------ 40


01 BOs68 locus  109:--------TGCTGTCAC-TCATGAGATTATAACAAC-TGTCTAGATACTTTTTTTTTAAA 158
06 BOs68 locus   95:--------TGCTGTCAC-TCATGGGATTATAGCAAC-TATCTAGATACTTTAAAAAAAAA 144
12 BOs68 locus  284:CCTTTATGTGCTGTCAC-TCATGGGATTATAGCAAC-TGTCTAGATACTTTAACAAAAAA 341
14 BOs68 locus  296:CCTTTATGTGCTGTCAC-TCATGGGATTATAGCAAC-TGTCTAGATACTTTAAAAAAAAC 353
15 BOs68 locus  109:--------TGCTGTCAC-TCATGGGATTATAGCAAC-TGTCTAGATACTTAAAAAAAAAA 158
17 BOs68 locus   73:--------TGCTGTCACATCATGG-ATTATAGCAACATGTCTAGATACTTNNAAAAAAAA 123
19 BOs68 locus   41:--------TGCTGTCAC-TCATGGGATTATAGCAAC-TGTCTAGATAGTTAAAAAAAAAA 90
                         ********* *****..******.**** *.********.**.......**.

01 BOs68 locus  159:AAAAAG------------CAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGGTTAAGGA 206
06 BOs68 locus  145:CAAACCACAAAAATAACCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGGTTAAGGA 204
12 BOs68 locus  342:AA-CACAAAAAA--CCCCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAAGTTAAGGA 398
14 BOs68 locus  354:ACACACAAAAA--CGCCCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGGTTAAGGA 411
15 BOs68 locus  159:-CACAAAAAAA----CCCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGATTAAGGA 213
17 BOs68 locus  124:AAACACAAA--CCCCCCCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGGTTAAGGA 181
19 BOs68 locus   91:ACACACAAAAAA--CCCCCAGCCATTCTGTATTGACCTTTAGGCTCCTAGAGGTTAAGGA 148
                  ...........   ...*********************************..*******

01 BOs68 locus  207:GATACTATCATGTGCAATATGCAGGGGT-GGGGGAGGGACAATGTTGAAGT        256
06 BOs68 locus  205:GATACTATCGTGTACAATATGCAGGAGAGGGGGGAGGGACA                 245
12 BOs68 locus  399:GATACTATCATATACAATATGCAGGGGT-GGGGGAGGG                   435
14 BOs68 locus  412:GATACTATCATGTACAATAAGCAGGGGT-GGGGGAGGGACAATGTTGAAGTA       462
```

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15 BOs68 locus  214:GATACTGTCATGTACAATATGCAGGGGT-GTGGGAGGG-CAATGTTGAAGTA        263
17 BOs68 locus  182:GATAC                                                  186
19 BOs68 locus  149:GATAC                                                  153
                 *****..................... ......... ..
```

Supplemental Figure 5-26. Sequence alignment of BOs68 locus. GenBank accession numbers are AB24178–AB249184.

```
01 BOs151 locus   1:TGGCGTTTCTAGAAGTTCTAAGGTACTATTAAAACAAAAATTACTTTTGTTCTACAT--- 57
12 BOs151 locus   1:-GGCGTTTCTAGGAGTTCTAAGGTACTATTAAAATAAAAATTACTTTTGTTCTAACTGTT 59
14 BOs151 locus   1:-GGCGTTTCTAGAAGTTNTAAGGTACTATTAAAATAAAAATTACTTATGTTCTAACTGTT 59
15 BOs151 locus   1:TGGCGTTTCTAGAAGTTCTAAGGTACTATTAAAATAAAAATTACTTTTGTTCTACAT--- 57
17 BOs151 locus   1:TGGCGTTTCTAGAAGTTCTAAGGTACTATTAAAATAAAAATTACTTTTGTTCTACAT--- 57
19 BOs151 locus   1:TGGCGTTTCTAGAAGTTCTAAGGTACTATTAAAATAAAAATTACTTTTGTTCTACAT--- 57
                  .***********.****.****************.***********.*******..*

01 BOs151 locus  57:------------------------------------------------------------ 57
12 BOs151 locus  60:GTTGTTTGGAGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTACTAAACCCACAGTT 119
14 BOs151 locus  60:GTTGTTTGGAGGGAAGGGCTAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACTCAGGGTT 119
15 BOs151 locus  57:------------------------------------------------------------ 57
17 BOs151 locus  57:------------------------------------------------------------ 57
19 BOs151 locus  57:------------------------------------------------------------ 57


01 BOs151 locus  57:------------------------------------------------------------ 57
12 BOs151 locus 120:GTGAGTTTAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGTCTTGCTAGT 179
14 BOs151 locus 120:ATGATTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAGT 179
15 BOs151 locus  57:------------------------------------------------------------ 57
17 BOs151 locus  57:------------------------------------------------------------ 57
19 BOs151 locus  57:------------------------------------------------------------ 57


01 BOs151 locus  57:------------------------------------------------------------ 57
12 BOs151 locus 180:GAAGGCAGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGT 239
14 BOs151 locus 180:GA---------------CTTGATGACCTTTCAAAGTCCCTTCCAGTTCTAGGAGATTGGT 224
15 BOs151 locus  57:------------------------------------------------------------ 57
17 BOs151 locus  57:------------------------------------------------------------ 57
19 BOs151 locus  57:------------------------------------------------------------ 57


01 BOs151 locus  58:------------------------TTTCCCCAGTGCATTTTTAGATATTAAAAAAATAGCA 94
12 BOs151 locus 240:ATATCTCCTATTATTTATTATATTTTCCCCAGTGCATTTTTAGATATTAAAAAA-TACCA 298
14 BOs151 locus 225:ATATCTCCAATTATT-ATTATATTTTCCCCAGTGCATTTTTAGATATTAAAAAA-TAGCA 282
15 BOs151 locus  58:------------------------TTTCCCCAGTGCATTTTTAGATATTAAAAAA-TAGCA 93
17 BOs151 locus  58:------------------------TTTCCCCAGTGCATTTTTAGATATTAAAAAA-TAACA 93
19 BOs151 locus  58:------------------------TTTCCCCAGTGCATTTTTAGATATTAAAAAA-TGGCA 93
                                   ****************************** *..**

01 BOs151 locus  95:AAACAAAAAAAACT-AGAATTTATATT-GAGGAAAGAGAGGGCAATAAGTAGATTATGTT 152
12 BOs151 locus 299:AAACAAAAAAAACC-AGAGTTTATATTTGAGGAAAGATAGGGCAATAAGTAGATTATGTT 357
14 BOs151 locus 283:AAACAAAAAAAACCC-AGAGTTTATATTTGAGGAAAGATAGGGCAATAAGTANATTATGTT 341
15 BOs151 locus  94:AAACAAAAAAACAACAGAGTTTATATTTGAGGAAAGAGAGGGCAATAAGTAGATTATGTT 153
17 BOs151 locus  94:AAACAAAAAAACAACAGAGTTTATATTTGAGGAAAGAGAGGGCAATAAGTAGATTATGTT 153
19 BOs151 locus  94:AAACAAAAAAACCCCAGAGTTTATATTTGAGGAAAGAGAGGGCAATAAGTAGATTATGTT 153
                  ***********..  ***.********.*********.*************.********

01 BOs151 locus 153:TATTTGGCACAATTTTGGGT                                    172
12 BOs151 locus 358:TATTTG                                                 363
14 BOs151 locus 342:TATTTGTCACAATTTTGGGT                                    361
15 BOs151 locus 154:TATTTGTCACAATTTTGGGT                                    173
17 BOs151 locus 154:TATTT                                                  158
19 BOs151 locus 154:TATTTGTCACAATTTTGGGT                                    173
                  *****. .............
```

Supplemental Figure 5-27. Sequence alignment of BOs151 locus. GenBank accession numbers are AB24185–AB249190.

```
06 BOs60 locus   1:CTCCATTATTACGG-ACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGC 59
12 BOs60 locus   1:CTCCATTATTACGG-ACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGC 59
13 BOs60 locus   1:CTCCATTATTACGGTACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGC 60
14 BOs60 locus   1:CTCCATTATTACGGTACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGC 60
17 BOs60 locus   1:CTCCATTATTACGGTACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGC 60
19 BOs60 locus   1:CTCCATTATTACGGTACCCATCTCACACAGTGATACAGACCAAAACAAAAACCTCTCTGT 60
                 **************.*********************************************.

06 BOs60 locus  60:GCTATGAAGTCTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCGAGTTT 119
12 BOs60 locus  60:TCTATGAAGTGTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCAAGTTT 119
13 BOs60 locus  61:TCTATGAAGTGTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCAAGTTT 120
14 BOs60 locus  61:TCTATGAAGTGTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCAAGTTT 120
17 BOs60 locus  61:TCTATGAAGTGTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCAAGTTT 120
19 BOs60 locus  61:GCTATGAAGTGTGCAGTGTAATAGACACTAGTACACACAACTAGCACCACAGTCAAGTTT 120
                 .*********.******************************************.*****

06 BOs60 locus 120:TCAAATGTTCTGCTACAAG---------------------------------------- 138
12 BOs60 locus 120:TCAAACATTCTGCTACAAGGAGGGGATGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTA 179
13 BOs60 locus 121:TCAAACATTCTGCTATAAGGGGGGGATGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTA 180
14 BOs60 locus 121:TCAAACGTTCTGCTACAAG---------------------------------------- 139
17 BOs60 locus 121:TCAAACGTTCTGCTACAAG---------------------------------------- 139
19 BOs60 locus 121:TCAAATGTTCTGCTACAAG---------------------------------------- 139
                 *****..********.***

06 BOs60 locus 138:------------------------------------------------------------ 138
12 BOs60 locus 180:AACCCAGGGCTGTGAGTTCAATCCTTGAGGGGACCACCTAGGAATCAGGGGCAAAAATTG 239
13 BOs60 locus 181:AACCCAGGGCTGTGAGTTCAATCCTTGAGAGGACCACCTAGGAATCAGGGGCAAAAATTG 240
14 BOs60 locus 139:------------------------------------------------------------ 139
17 BOs60 locus 139:------------------------------------------------------------ 139
19 BOs60 locus 139:------------------------------------------------------------ 139


06 BOs60 locus 138:------------------------------------------------------------ 138
12 BOs60 locus 240:GTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGATCTTTCAATGTCCCTTCCAGTTCT 299
13 BOs60 locus 241:GTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGATCTTTCAAGGTCCCTTCCAGTTCT 300
14 BOs60 locus 139:------------------------------------------------------------ 139
17 BOs60 locus 139:------------------------------------------------------------ 139
19 BOs60 locus 139:------------------------------------------------------------ 139


06 BOs60 locus 139:-----------------------------------AAAAAGAGG--GATCGCTCCTCCCA 161
12 BOs60 locus 300:AGGAGATTGGTATTTCTCCAATTATTACCTTTAAGAAAAAGAGGAGGATCACTCCTCCCA 359
13 BOs60 locus 301:AGGAGATTGGTATATCTCCAATTATTACCTTTAAGAAAAAGAGGAGGATCACTCCTCCCA 360
14 BOs60 locus 140:----------------------------------AAAAAAGAGGAGGATCACTCCTCCCA 165
17 BOs60 locus 140:----------------------------------AAAAAAGAGGAGGATCACTCCTCCCA 165
19 BOs60 locus 140:-----------------------------------TAAAAAAGGAGGATCACTCCTCCCA 164
                                                   .****.***..****.*********

06 BOs60 locus 162:TCGACTTGAATAGTTTCAAACTCTACCACTGTATTGCTATTCCAAGACATTAGCTATGCT 221
12 BOs60 locus 360:TCCACTTGAATAGTTTCAAACTCTACCACTGTATTGCTATTCCAAGACATTAGCTATGCT 419
13 BOs60 locus 361:TCCACTTGAATAGTTTCAAACTCTATCACTGTATTGCTATTCCAAGACATTAGCTATGCT 420
14 BOs60 locus 166:TCCACTTGAATAGTTTCAAACTCTACCACTGTATTGCTATTCCAAGACATTAGCTATGCT 225
17 BOs60 locus 166:TCCACTTGAATAGTT-CAAACTCTACCACTGTATTGCTATTCCAAGTCATTAGCTATGCT 224
19 BOs60 locus 165:TCCACTTGAATAGTTTCAAACTCTACCACTGTATTGCTATTCCA-GACGTTCGCTATGCT 223
                 **.************.*********.******************.*.*.**.********

06 BOs60 locus 222:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     257
12 BOs60 locus 420:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     455
13 BOs60 locus 421:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     456
14 BOs60 locus 226:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     261
17 BOs60 locus 225:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     260
19 BOs60 locus 224:GTGAAGTTTGTTATAGCAAGAGCTGAGTGTCACTGG                     259
                 ************************************
```

Supplemental Figure 5-28. Sequence alignment of BOs60 locus. GenBank accession numbers are AB24191–AB249196.

```
01 BOs94 locus   1:TCTCTTTCATTTTTCCATCCACACACAATGTCCATCCTGACTCATGCCATCCTCTT---A 57
06 BOs94 locus   1:-CTCTTTCATTTTTCCATCCACACACAATGTCCATCCTGACTCATGCCATCCTCTTCTTA 59
12 BOs94 locus   1:-CTCTTTCATTTT-CCATCCACACACAATGTCCATCCTGATTCATGCCATCCTCTTCTTA 58
13 BOs94 locus   1:TCTCTTTCATTTTTCCATCCACACACAATGTCCATCCTGACTCATGCCATCCTCTTCTTA 60
14 BOs94 locus   1:TCTCTTTCATTTTTCCATCCACACACAATGTCCATCCTGACTCATGCCATCCTCTTCTTA 60
17 BOs94 locus   1:TCTCTTTCATTTTTCCATCCACACACAATGTCCATCCTGACTCATGTCATCCTCTTCTTA 60
19 BOs94 locus   1:TCTCTTTCATTTTTCCATCCAGACACAATGTCCATCCTGACTCATGCCATCCTCTTCTTA 60
                 .************.*******.******************.*****.*********...*

01 BOs94 locus  58:TTCTCCATACCACAGCCCCTGCCATTCTGAACCCCTCCTCACGTTGTTC----------- 106
06 BOs94 locus  60:TTCTCCATACCTCAGCCCCTGCCATTCTGAACCCCTCCTCA---TGTTC----------- 105
12 BOs94 locus  59:TTCTCCATACCCCAGCCCCTGCCATTCTGAACCCCTCCTCACGTTGTTCATTCTTCTCTC 118
13 BOs94 locus  61:TTCTCCATACCCCAGCCCCTGCCATTCTGAACCCTTCCTCACGTTGTTCATTCTTCTCTC 120
14 BOs94 locus  61:TTCTCCATACCCCAGCCCCTGCCATTCT-------TCCTCACGTTGTTC----------- 102
17 BOs94 locus  61:TTCTCCATACCCCAGCCCCTGCCATTCTGAACCCCTCCTCACGTTGTTC----------- 109
19 BOs94 locus  61:TTCTCCATACCCCAACCCCTGCCATTCGGAACCCCTCCTCACATTGTTC----------- 109
                ***********.**.************........******...*****

01 BOs94 locus 106:------------------------------------------------------------ 106
06 BOs94 locus 105:------------------------------------------------------------ 105
12 BOs94 locus 119:TCCTCTGGTACATCTTGTAGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAA 178
13 BOs94 locus 121:TCCTCTGGTACATCTTGTAGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAA 180
14 BOs94 locus 102:------------------------------------------------------------ 102
17 BOs94 locus 109:------------------------------------------------------------ 109
19 BOs94 locus 109:------------------------------------------------------------ 109


01 BOs94 locus 106:------------------------------------------------------------ 106
06 BOs94 locus 105:------------------------------------------------------------ 105
12 BOs94 locus 179:ACCCAGGGTTGTGAGTTCAATCCTTGAGGAGGCCACTTAGGGATCTAGGGCAAAAATTAG 238
13 BOs94 locus 181:ACCCAGGGTTGTGAGCTCAATCCTTGAGGAGGCCACTTAGGGATCTGGGGCAAAAATTAG 240
14 BOs94 locus 102:------------------------------------------------------------ 102
17 BOs94 locus 109:------------------------------------------------------------ 109
19 BOs94 locus 109:------------------------------------------------------------ 109


01 BOs94 locus 106:------------------------------------------------------------ 106
06 BOs94 locus 105:------------------------------------------------------------ 105
12 BOs94 locus 239:TCCTGCTAGTGAAGGCAGGGGG-CTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCT 297
13 BOs94 locus 241:TCCTGCTAGTGAAGGCAGGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCT 300
14 BOs94 locus 102:------------------------------------------------------------ 102
17 BOs94 locus 109:------------------------------------------------------------ 109
19 BOs94 locus 109:------------------------------------------------------------ 109


01 BOs94 locus 107:-----ATTCTTCTCTCTCCTCTGGTACATCTTGTTGCTTTCCTACTCTGCATACAAACGC 161
06 BOs94 locus 106:-----ATTCTTCTCTTTCCTCTGGTACATCTTGTTGCTTTCCTACTCTGCATACAAACCC 160
12 BOs94 locus 298:AGGAGATTGGTATATCTCCTGTTATT-AT-TTGTTGCTTTCCTACTCTACATACAAACCC 355
13 BOs94 locus 301:AGGAGATTGGTATATCTCCT---ATT-AT-TTGTTGCTTTCCTACTCTACATACAAACCC 355
14 BOs94 locus 103:-----ATTCTTCTCTCTCCTCTGGTACATCTTGTTGCTTTCCTACTCTACATACAAACCC 157
17 BOs94 locus 110:-----ATTCTTCTCTCTCCTCTGGTACATCTTGTTGCTTTCCTACTCTGCATACAAACCC 164
19 BOs94 locus 110:-----ATTCTTCTCTCTCCTCTGGTACATCTTGTTGCTTTCCTACTCTGCATACAAACCC 164
                     ***..*.*.*.****....*..**.******************.*********.*

01 BOs94 locus 162:CAGACAAGTGAGGTGGAGCCCCTGAAGCCTGACTCTTTCCCCAAAGCAGGGCAGCTCTTA 221
06 BOs94 locus 161:CAGACAAGTGAGGTGTAGCCCCTGAAGCTTGACTCTTTCCCCAAAGCAGGGCAGCTCTTA 220
12 BOs94 locus 356:CAGACAAGTGAGGTGGAGCCC-TGAAGCCTGACTCTTTCCTCAAAGCAGGGCAGCTCCTA 414
13 BOs94 locus 356:CAGACAAGTGAGGTGGAGCCC-TGAAGCCTGACTCTTTCCTCAAAGCAGGGCAACTCCTA 414
14 BOs94 locus 158:CAGACAAGTGAGGTGGAGCCC-TGAAGCCTGACTCTTTCCCCAAAGCAGGGCAGCTCCTA 216
17 BOs94 locus 165:CAGACAAGTGAGGTKGAGCCCCTGAAGCCTGACTCTTTCCCCAAAGCAGGGCAGCTCCTA 224
19 BOs94 locus 165:CAGACAAGTGAGGTGGAACCCCTGAAGCCTGACTCTTTCCCCAAAGCAGGGCAGCTTCTA 224
                 **************..*.***.******.***********.************.**..**

01 BOs94 locus 222:CTAGGCTGCTGGATTTGTG                                      240
06 BOs94 locus 221:CTAGGCTGCTGGATTTGTG                                      239
12 BOs94 locus 415:CTAGGCTGCTGGATTTGTG                                      433
13 BOs94 locus 415:CTAGGCTGCTGGATTTGTG                                      433
```

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14 BOs94 locus 217:CTAGGCTGCTGGATTTGTG                                    235
17 BOs94 locus 225:CTAGGCTGCTGGATTTGTG                                    243
19 BOs94 locus 225:CTAGGCTGCTGGATTTGTG                                    243
               *******************
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Supplemental Figure 5-29. Sequence alignment of BOs94 locus. GenBank accession numbers are AB24197–AB249203.

```
01 BMm49 locus   1:TGATGACTGCATCCATAACAATATTTTCATGAGAGTAAAGCTTAGAGTAGTGTTCTAACC 60
06 BMm49 locus   1:TGATGACTGCATCCATAACAATATTTTCATGAGACTAAAGCTCAGAGTAGTGTTCTAACC 60
14 BMm49 locus   1:TGATGACTGCATCCATAACAATACTTTCATGAGAGTAAAGCTCAGAGTAGTGTTCTAACC 60
15 BMm49 locus   1:TGATGACTGCATCCATAACAATATTTTCATGAG--TAAAGCTCAGAGTAGTGTTCTAACC 58
16 BMm49 locus   1:TGATGACTGCATCCATAACAATATTTTCATGAG--TAAAGCTCAGAGTAGTGTTCTAACC 58
                 **********************.*********. *******.*****************

01 BMm49 locus  61:AGTGATCATTCTGCTTGGTCTCTTGATTGTTTCCCCTGTT-------------------- 100
06 BMm49 locus  61:AGTGATCATTCTGCTTGGTCT-TTGATTGTTTCCCCTGTT-------------------- 99
14 BMm49 locus  61:AGTGATCATTCTGCTTGGTCT-TTGATTGTTTCCCCTGTT-------------------- 99
15 BMm49 locus  59:AGTGATCATTCTGCTTGGTCT-TTGATTGTTTCCCCTGTTATCTCTCAGGGGGAGGGATA 117
16 BMm49 locus  59:AGTGATCATTCTGCTTGGTCT-TTGATTGTTTCCCCTGTTATCCCTCAGGGGGAGGGATA 117
                ******************** *****************

01 BMm49 locus 100:------------------------------------------------------------ 100
06 BMm49 locus  99:------------------------------------------------------------ 99
14 BMm49 locus  99:------------------------------------------------------------ 99
15 BMm49 locus 118:GCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTATGAGTTCAATCCTTGAGGAG 177
16 BMm49 locus 118:GCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTATGAGTTCAATCCTTGAGAAG 177


01 BMm49 locus 100:------------------------------------------------------------ 100
06 BMm49 locus  99:------------------------------------------------------------ 99
14 BMm49 locus  99:------------------------------------------------------------ 99
15 BMm49 locus 178:GCTACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCG 237
16 BMm49 locus 178:GCTACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCA 237


01 BMm49 locus 100:------------------------------------------------------------ 100
06 BMm49 locus  99:------------------------------------------------------------ 99
14 BMm49 locus  99:------------------------------------------------------------ 99
15 BMm49 locus 238:ATGACCTTTCAAGGTCCCTTCTAGTTCTAGGAGATTGGTATATCTCCAATAAAAAAAAAA 297
16 BMm49 locus 238:ATRACCTTTCAAGGTCCCTTCTAGTTCTAGGAGATTGGTATATCTCCAATAAAAAAAAAA 297


01 BMm49 locus 101:GTTGATTTCAATGGGGCTATCTTCTTTGAA                          130
06 BMm49 locus 100:ATTGATTTCAATGGGGCTATCTTCTTTGAA                          129
14 BMm49 locus 100:ATTGATTTCAATGGGGCTATCTTCTTTGAA                          129
15 BMm49 locus 298:ATTGATTTCTATGGGGCTATCTTCTTTGAA                          327
16 BMm49 locus 298:-TTGATTTCTATGGGGCTATCTTCTTTGAA                          326
                 .********.*******************
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Supplemental Figure 5-30. Sequence alignment of BMm49 locus. GenBank accession numbers are AB24204–AB249208.

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01 BMm103 locus   1:TAGTGAGTGCCAACAAGTCCCAGTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 60
06 BMm103 locus   1:TAGTGAGTGCCAACAAGTCCCACTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 60
14 BMm103 locus   1:TAGTGAGTGCCAACAAGTCCCACTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 60
15 BMm103 locus   1:TAGTGAGTGCCAACAAGTCCCACTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 60
16 BMm103 locus   1:-------------CAAGTACCACTGGATAGCCATCAGTCTTGGATGGTTTAGACACAGCA 47
17 BMm103 locus   1:-------TGCCAACAAGTCCCACTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 53
19 BMm103 locus   1:-AGTGAGTGCCAACAAGTCCCACTGGATAGCCATCTGTCTTGGATGGTTTAGACACAGCA 59
                  .............*****.***.************.************************

01 BMm103 locus  61:AACCCTGCCTCTTGTGGCAGTCAGAGGCTTAGATGGTGCTGTATCTTTATTT-------- 112
06 BMm103 locus  61:AACCNTGCCTCTTGCGGCAGTCAGAGGCTTAGATGTTGCTGTATCTTTATTT-------- 112
14 BMm103 locus  61:AACCCTGCCTCTTGTGGCAGTCAGAGGCTTAGATGGTGCTGTATCTTTATTT-------- 112
15 BMm103 locus  61:AACCCTGCCTCTTGTGGCAGTCAGAGGGTTAGATGGTGCTGTATCTTTATTTCAGAGGGG 120
16 BMm103 locus  48:AACCCTGCCTCTTGTGGCAGTCAGAGGGTTAGATGGTGCTGTATCTTTATTTCAAGGGGG 107
17 BMm103 locus  54:AACCCTGYCTCTTGTGGCAGTCAGAGGCTTAGATGGTGCTGTATCTTTATTT-------- 105
19 BMm103 locus  60:AACCCTGCCTCTTGTGGCAGTCARAGGCTTAGCTGGTGCTGTATYTTTATTT-------- 111
                  ****.**.******.********.***.****.**.********.*******

01 BMm103 locus 112:------------------------------------------------------------ 112
06 BMm103 locus 112:------------------------------------------------------------ 112
14 BMm103 locus 112:------------------------------------------------------------ 112
15 BMm103 locus 121:AAGAGATAGCTTAGTGGTTTGAGCATTGACCTGCTAAACCCAGGGTTGTGAGTTCAATCC 180
16 BMm103 locus 108:AAGAGATAGCTTAGTGGTTTGAGCATTAGCCTACTAAACCCAGGGTTGTGAGTTCAATCC 167
17 BMm103 locus 105:------------------------------------------------------------ 105
19 BMm103 locus 111:------------------------------------------------------------ 111


01 BMm103 locus 112:------------------------------------------------------------ 112
06 BMm103 locus 112:------------------------------------------------------------ 112
14 BMm103 locus 112:------------------------------------------------------------ 112
15 BMm103 locus 181:TTGAGGGGGCCACTTAGGGATCTAGGGCAAAAATTGGTCCTGC-TAGTGAAGGCAGGGGG 239
16 BMm103 locus 168:TTGAGGGGGCCACTTAGGAATCTGGGGCAAAAATCAGTCCTGCCTAGTGAAGGCAGGGGG 227
17 BMm103 locus 105:------------------------------------------------------------ 105
19 BMm103 locus 111:------------------------------------------------------------ 111


01 BMm103 locus 112:------------------------------------------------------------ 112
06 BMm103 locus 112:------------------------------------------------------------ 112
14 BMm103 locus 112:------------------------------------------------------------ 112
15 BMm103 locus 240:CTAGACTCAATAACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATAGCTCCAATT 299
16 BMm103 locus 228:CTGGACTCAATAACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATAGCTTCAATT 287
17 BMm103 locus 105:------------------------------------------------------------ 105
19 BMm103 locus 111:------------------------------------------------------------ 111


01 BMm103 locus 113:--------TACCGTTAAGTTGTTGTCTTGGGCTGGGGAGGCTGGCAGG-CTTGGAAACTG 163
06 BMm103 locus 113:--------NACCGTTAAGTTGTTGTCTTGGGCTGGGGAGGCTGGCAGGTCTTGGAAACTA 164
14 BMm103 locus 113:--------TACCGTTAAGTTGTTGTCTTGGGCTGGGGCGGCTGGCAGA-CTTGGAAACTA 163
15 BMm103 locus 300:ATTACCTTTACCATTAAGTTGTTGTCTTGGGCTGGGGCAGCTGGCAGG-CTTGGAAACTA 358
16 BMm103 locus 288:ATTACCTTTACCATTAAGTTGTTGTCTTGGGCTGGGGCAGATGGCAGG-CTTGGAAACTA 346
17 BMm103 locus 106:--------TACCGTTAAGTTGTTGTCTTGGGCTGAGGCGGCTGGCAGG-CTTGGAAACTA 156
19 BMm103 locus 112:--------TACCATTAAGTTGTTGTCTTGGGCTGAGGCGGCTGGCAGG-CTTGGAAACTA 162
                        .***.********************.**..*.******. **********.

01 BMm103 locus 164:TGAACAAGGAAAGTGCCTGCTG-TTGTTCAGGGAAA-CAGGATTTTTATGTACTTTCTTC 221
06 BMm103 locus 165:TGAGCAAGGAAAGTGCCTGCTGACTGTTCAGGGAAATCAGGATTT             209
14 BMm103 locus 164:TGAGCAAGGAAAGTGCCTGCTG-CTGTTCAGGGAAAT-AGGATTTTTATGTACTTTCTTC 221
15 BMm103 locus 359:TGAGCAAGGAAAGTGCCTGCTG-CTGTTCAGGGAAAT-AGGATTTTTATGTACTTTCTTC 416
16 BMm103 locus 347:TGAGCAAGGAAAGTGCCTGCTG-CTGTTCAGGGAAAT-AGGATTTTTATGTACTTTCTTC 404
17 BMm103 locus 157:TGAGCAAGGAAAGTGCCTGCTG-CTGTTCAGGGAAAT-AGGATTTTTATGTACTTTCTTC 214
19 BMm103 locus 163:TGAGCAAGGAAAGTGCCTGCTG-CTGTTCAGGGAAAT-AGGATTTTTATGTACTTTCTTC 220
                  ***.****************** .************. *******...............

01 BMm103 locus 222:ATAAACAAACAGGATTGCACCAAAGAACATACCTGACTCGTATCACCAATTTCTCCTCCT 281
14 BMm103 locus 222:ATAAATAAACAGGATTGCACCAAAGAACATACCTGACTTGGATCATCAATTTCTCCTCCT 281
15 BMm103 locus 417:ATAAATAAACATGATTGCACCTAAGAACATACCTGACTCGGATCATCAATTTCTCCTCCT 476
16 BMm103 locus 405:ATAAATAAACATGATTGCACCTAAAAACATACCTGACTCGGATCATCAATTTCTCCTCCT 464
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17 BMm103 locus 215:ATAAATAAACAGGATTGCCCCAAAGAACATACCTGACTCGGATCATCAATTTCTCCNCCT 274
19 BMm103 locus 221:ATAAATAAACAGGATTGCACCAAAGAACATACCTGACTCGGATCATCAATTTCTCCTCCT 280
                 ............................................................

01 BMm103 locus 282:AATGGAAACAACTCAGCAAG                                    301
14 BMm103 locus 282:AATGGAAACAACTCAGCAAG                                    301
15 BMm103 locus 477:AATGGAAACAACTCAGCAAG                                    496
16 BMm103 locus 465:AATGGAAACAACTCACCA-G                                    483
17 BMm103 locus 275:AATGGAAACAACNCAGCAA                                     293
19 BMm103 locus 281:AATGGAAACAACTCAGCAAG                                    300
                 ...................
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Supplemental Figure 5-31. Sequence alignment of BMm103 locus. GenBank accession numbers are AB24209–AB249215.

```
01 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT----------------- 43
02 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT----------------- 43
05 BMm74 locus   1:----------------------CCATTCAGGTCAGCTAATATAT----------------- 22
06 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAAAC 51
07 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAAAC 51
09 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAAAC 51
10 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAAAC 51
11 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
14 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
15 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
16 BMm74 locus   1:--------------------TCCATTCAGGTCCACTAATATAT---------GTTTAACC 31
17 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
18 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAATC 51
19 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATATATAATATATGTTTAACC 60
20 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATATATAATATATGTTTAACC 60
21 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
22 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
23 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAAGTCAGCTAATATAT---------GTTTAACC 51
24 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
26 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATAT---------GTTTAACC 51
27 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAGCTAATATCT---------GCTTAATC 51
28 BMm74 locus   1:ACAATAACAGGGATCAGACGTCCATTCAGGTCAACTAATATCT---------GCTTAATC 51
                 ....................*******.***..*******.*        ........

01 BMm74 locus  44:--GTGAATTATATTTGTAAATGTGGCTACCTGT----TAATCGCTAGAGAATTACAGAGT 97
02 BMm74 locus  44:--GTGATTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACTGGGT 97
05 BMm74 locus  23:--GTGATTTATATTTGTAAATGTAGCTACCCGT----TAATCGCTAGAGAATTACAGAGT 76
06 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
07 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
09 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCACTAGAGAATTACCGAGT 107
10 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGTTTGTTAATCGCTAGAGAATTACCGAGT 111
11 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
14 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTAGCGAGT 107
15 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACTTGT----TAATCGCTAGAGAATTACCGAGT 107
16 BMm74 locus  32:TTGTGGTTTATATTTGTAAATGTAGCTACTTGT----TAATCGCTAGAGAATTACCGAGT 87
17 BMm74 locus  52:TTGTGGTTTATATTTGTA------------------TAATCGCTAGAGAATTACCGAGT 92
18 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
19 BMm74 locus  61:TTGTGATTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 116
20 BMm74 locus  61:TTGTGATTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 116
21 BMm74 locus  52:TTGTGATTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
22 BMm74 locus  52:TTGTGATTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAGTTACCGAGT 107
23 BMm74 locus  52:GTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
24 BMm74 locus  52:TTGTGGTTTATATTTGTAAATGTAGCTACCTGT----TAATCGCTAGAGAATTACCGAGT 107
26 BMm74 locus  52:TTGTGATTT----TTAAAAATGTCGTTACCTGT----TAATCGCTAGAGAATTACTGAGT 103
27 BMm74 locus  52:TTGTGATTTATATTTGTAAATATAGCTAGCTGT----TAATCGCTAGAGAATTACTGAGT 107
28 BMm74 locus  52:TTGTGATTTATATTTGTAAATATAGGTAGCTGT----TAATCGTTAGAGAATTACTGAGT 107
                ..***..**....**..*...............   *****..******.***..*.**

01 BMm74 locus  98:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTTGGAGGTCGGG---GAGAGAGAG 154
02 BMm74 locus  98:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTTGGAGGTCGGG---GAGAGAGAG 154
05 BMm74 locus  77:CCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTTGGAGGTCGGG---GAGAGAGAG 133
06 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTAT---------------------------------- 132
07 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTAT---------------------------------- 132
09 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTAT---------------------------------- 132
10 BMm74 locus 112:GCATCAAGTGTTTGGGGTCCTGTAT---------------------------------- 136
11 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTAGGGGGTCGGG---GAGAGAGAT 164
14 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATATTGGGGGTCGGG---GAGAGAGAT 164
15 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGTGAATGTTGGGGGTCGGG---GAGAGAGAG 164
16 BMm74 locus  88:GCATCAAGTGTTTGGAGGCTTGTATTAGAGTGAATGTTGGGGGTCGGG---GAGAGAGAT 144
17 BMm74 locus  93:GCATCAAGTGTTTGGAGGCCTGTATTAGAGAGAATGTTGGGGGTCGAG---GAGAGAGAT 149
18 BMm74 locus 108:GCATCAAGTGTTTGGAGGCCTGTATTAGAGAGAATGTTGGGGGTCGAG---GAGAGAGAT 164
19 BMm74 locus 117:GCATCAAGTGTTTGGGAGCCTGTATTAGAGAGAATGTTGGGGGTCGGG---GAGAGAGAT 173
20 BMm74 locus 117:GCAGCAAGTATTTGGGAGCCTGTATTAGAGAGAATGTTGGGGGTCGGG---GAGAGAGAG 173
21 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTTGGGGGTCGGG---GAGAGAGAT 164
22 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGACTGTTGGGGGTCGGG---GAGAGAAAT 164
23 BMm74 locus 108:GCATCAAGTGTCTGGGGGCCTGTATTAGAGAGAATGTTGGGGGTCGGG---GAGAGAGAT 164
24 BMm74 locus 108:GCATCAAGTGTTTGGGGGCCTGTATTAGAGAGAATGTTGGGGGTCGAG---GAGAGAAAT 164
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26 BMm74 locus 104:GCATCAAGTGTTTGGAGGCCTGTATTAGAGAGAATGTTGGGGGT-------GAGGGA-AG 155
27 BMm74 locus 108:GCATCAAGTATTTGGGGGCCTGTATTAGAGAGAATCTGGGGGGGGGGGAGAGAGAGAGAG 167
28 BMm74 locus 108:GCATCAAGCGTTTGGGGGCCTGTATTAGAGAGAATGTTGTGGGTCGGG---GAGAGAGAT 164
                   .**.****..*.***...*.*****.......................  ........

01 BMm74 locus 155:AGAGTCTCAGTTATACTA---------------------------------------- 172
02 BMm74 locus 155:AGAGTCTCGGTTATACTA---------------------------------------- 172
05 BMm74 locus 134:TGAGTCTCGGTTATGCTA---------------------------------------- 151
06 BMm74 locus 133:--------------ACTA---------------------------------------- 136
07 BMm74 locus 133:--------------ACTA---------------------------------------- 136
09 BMm74 locus 133:--------------ACTA---------------------------------------- 136
10 BMm74 locus 137:--------------ACTA---------------------------------------- 140
11 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
14 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
15 BMm74 locus 165:AGACTCTCGGTTATACTAGGAGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAA 224
16 BMm74 locus 145:AGACTCTCGGTTATACTAGGAGGGAGGGATAGTTCAGTGGTTTGAGCATTGGCCTGCTAA 204
17 BMm74 locus 150:AGAGTCTCGGTTATACTA---------------------------------------- 167
18 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
19 BMm74 locus 174:ATAGTCTCGGTTATACTA---------------------------------------- 191
20 BMm74 locus 174:AGAGTCTCGGTTATACTA---------------------------------------- 191
21 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
22 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
23 BMm74 locus 165:AGAGTCTCGGTTATATTA---------------------------------------- 182
24 BMm74 locus 165:AGAGTCTCGGTTATACTA---------------------------------------- 182
26 BMm74 locus 156:AGTATCTCGCCTATACTA---------------------------------------- 173
27 BMm74 locus 168:AGAGTCTCGGTTATACTA---------------------------------------- 185
28 BMm74 locus 165:CGATTCTCGATTATACTA---------------------------------------- 182
                   ................**

01 BMm74 locus 172:------------------------------------------------------------ 172
02 BMm74 locus 172:------------------------------------------------------------ 172
05 BMm74 locus 151:------------------------------------------------------------ 151
06 BMm74 locus 136:------------------------------------------------------------ 136
07 BMm74 locus 136:------------------------------------------------------------ 136
09 BMm74 locus 136:------------------------------------------------------------ 136
10 BMm74 locus 140:------------------------------------------------------------ 140
11 BMm74 locus 182:------------------------------------------------------------ 182
14 BMm74 locus 182:------------------------------------------------------------ 182
15 BMm74 locus 225:ACCCAGCGTTGTGAATTCAATCCTTGAGAGGGCCACTTAGGGATCTGGGGCAAAAATTGG 284
16 BMm74 locus 205:ATCCGGCGTTGTGAATTCAAACCTTGAGAGGGCCACTTAGGGATCTGGGGCAAAAATTGG 264
17 BMm74 locus 167:------------------------------------------------------------ 167
18 BMm74 locus 182:------------------------------------------------------------ 182
19 BMm74 locus 191:------------------------------------------------------------ 191
20 BMm74 locus 191:------------------------------------------------------------ 191
21 BMm74 locus 182:------------------------------------------------------------ 182
22 BMm74 locus 182:------------------------------------------------------------ 182
23 BMm74 locus 182:------------------------------------------------------------ 182
24 BMm74 locus 182:------------------------------------------------------------ 182
26 BMm74 locus 173:------------------------------------------------------------ 173
27 BMm74 locus 185:------------------------------------------------------------ 185
28 BMm74 locus 182:------------------------------------------------------------ 182


01 BMm74 locus 172:------------------------------------------------------------ 172
02 BMm74 locus 172:------------------------------------------------------------ 172
05 BMm74 locus 151:------------------------------------------------------------ 151
06 BMm74 locus 136:------------------------------------------------------------ 136
07 BMm74 locus 136:------------------------------------------------------------ 136
09 BMm74 locus 136:------------------------------------------------------------ 136
10 BMm74 locus 140:------------------------------------------------------------ 140
11 BMm74 locus 182:------------------------------------------------------------ 182
14 BMm74 locus 182:------------------------------------------------------------ 182
15 BMm74 locus 285:TCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCCAGTTCTA 344
16 BMm74 locus 265:TCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCCAGTTCTA 324
17 BMm74 locus 167:------------------------------------------------------------ 167
18 BMm74 locus 182:------------------------------------------------------------ 182
19 BMm74 locus 191:------------------------------------------------------------ 191
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20 BMm74 locus 191:------------------------------------------------------------ 191
21 BMm74 locus 182:------------------------------------------------------------ 182
22 BMm74 locus 182:------------------------------------------------------------ 182
23 BMm74 locus 182:------------------------------------------------------------ 182
24 BMm74 locus 182:------------------------------------------------------------ 182
26 BMm74 locus 173:------------------------------------------------------------ 173
27 BMm74 locus 185:------------------------------------------------------------ 185
28 BMm74 locus 182:------------------------------------------------------------ 182


01 BMm74 locus 173:---------------------------------------GATGTTTTTCTTTTGAAGCT  192
02 BMm74 locus 173:---------------------------------------GATGTTTTTCTTTTGAAGCT  192
05 BMm74 locus 152:---------------------------------------GATGTTTTTCTTTTGAAGCT  171
06 BMm74 locus 137:---------------------------------------GATGTTTTTCTTTTGAAGCT  156
07 BMm74 locus 137:---------------------------------------GATGTTTTTCTTTTGAAGCT  156
09 BMm74 locus 137:---------------------------------------GATGTTTTTCTTTTGAAGCT  156
10 BMm74 locus 141:---------------------------------------GATGTTTTTCTTTTGAAGCT  160
11 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
14 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
15 BMm74 locus 345:GGCGATTGGTATATCTCCAATTATAAAAAAATAAAAAAAGATGTTTTTCTTTTGAAGCT  403
16 BMm74 locus 325:GGCGATTGGTATATCTCCAATTATAAAAAAA--------GATGTTTTTCTTTTGAAGCT  375
17 BMm74 locus 168:---------------------------------------GATGTTTTTCTTTTGAAGCT  187
18 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
19 BMm74 locus 192:---------------------------------------GATGTTTTTCTTTTGAAGCT  211
20 BMm74 locus 192:---------------------------------------GATGTTTTTCTTTTGAAGCT  211
21 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
22 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
23 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
24 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
26 BMm74 locus 174:---------------------------------------GATGTTTTTCTTTTGAAGCT  193
27 BMm74 locus 186:---------------------------------------GATGTTTTTCTTTTGAAGCT  205
28 BMm74 locus 183:---------------------------------------GATGTTTTTCTTTTGAAGCT  202
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Supplemental Figure 5-32. Sequence alignment of BMm74 locus. GenBank accession numbers are AB24216–AB249232, AB125733-AB125737.

```
01 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCCATGCATCTTTTTAGGGCATATATGGATAAAGCCAGGA 60
06 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
11 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
12 BMm85 locus   1:-------GATGGCCAGTGTTCCTATGCATC------------------------------ 23
14 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
15 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
16 BMm85 locus   1:-------------CAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 47
17 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATGCATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
19 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATACATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
20 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCTATACATCTTTTTAGTGTATATATGGATAAGGCCAGGA 60
28 BMm85 locus   1:GTTAGTAGATGGCCAGTGGTCCCATGCATCTTTTTAGGGCATATATGGATAAGGCCAGCA 60
                 .............*****.***.**.****.............................

01 BMm85 locus  61:GCAAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGAACT 118
06 BMm85 locus  61:GCCAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 118
11 BMm85 locus  61:GCCAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGCACC 118
12 BMm85 locus  23:------------------------------------------------------------ 23
14 BMm85 locus  61:GCCAGTTCATCTACACGCA--AACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 118
15 BMm85 locus  61:GCCAGTTCATCTACACGCACAGACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 120
16 BMm85 locus  48:GCCAGTTCATCTACACGCACAGACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 107
17 BMm85 locus  61:GCCAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 118
19 BMm85 locus  61:GCCAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 118
20 BMm85 locus  61:GCCAGTTCATCTACACGCA--GACTGTCCAGACTGATCAGAGTGCATATGTTTGGGTACT 118
28 BMm85 locus  61:GCCAGTTCATCTACATGCA--AGCCGTCCAAACTGATCAGAGTGCATATGTTTGGGTACT 118
                ...................  ......................................

01 BMm85 locus 119:CTGGACAACTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGT----------- 167
06 BMm85 locus 119:CTGGACAACTATGGGGATTACAGCGCATCTCACCAAGTCCTAAGGCAGT----------- 167
11 BMm85 locus 119:CTGGAGAACTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGT----------- 167
12 BMm85 locus  24:---------------------------------CAAGTCCTAAGGCAGT----------- 39
14 BMm85 locus 119:CTGGACAGCTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGT----------- 167
15 BMm85 locus 121:CTGGACAACTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGTCTTTAGGGGGG 180
16 BMm85 locus 108:CTGGACAACTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGTCTTTAGGGGGG 167
17 BMm85 locus 119:CTGGACAACTATGGGGATTACAGCCCATCTCACCAAGTCCTAAAGCAGT----------- 167
19 BMm85 locus 119:CTGGACAACTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGT----------- 167
20 BMm85 locus 119:CTGGACAGCTATGGGGATTACAGCACATCTCACCAAGTCCTAAGGCAGT----------- 167
28 BMm85 locus 119:CCAGACAACTATGGGGATTACAGCACATTTTACCAAGTACTAAGGCAGT----------- 167
                ..................................*****.****.*****

01 BMm85 locus 167:------------------------------------------------------------ 167
06 BMm85 locus 167:------------------------------------------------------------ 167
11 BMm85 locus 167:------------------------------------------------------------ 167
12 BMm85 locus  39:------------------------------------------------------------ 39
14 BMm85 locus 167:------------------------------------------------------------ 167
15 BMm85 locus 181:AGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCT 240
16 BMm85 locus 168:AGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCT 227
17 BMm85 locus 167:------------------------------------------------------------ 167
19 BMm85 locus 167:------------------------------------------------------------ 167
20 BMm85 locus 167:------------------------------------------------------------ 167
28 BMm85 locus 167:------------------------------------------------------------ 167


01 BMm85 locus 167:------------------------------------------------------------ 167
06 BMm85 locus 167:------------------------------------------------------------ 167
11 BMm85 locus 167:------------------------------------------------------------ 167
12 BMm85 locus  39:------------------------------------------------------------ 39
14 BMm85 locus 167:------------------------------------------------------------ 167
15 BMm85 locus 241:TGAGGGGGCTACTTAGGGATCTGGGGCAAAAAAAATTGGTCCTGCTAGTGAAGGCAGGGG 300
16 BMm85 locus 228:TGAGGGGGCTACTTAGGGATCTGGGGCAAAAAAAATTGGTCCTGCTAGTGAAGGCAGGGG 287
17 BMm85 locus 167:------------------------------------------------------------ 167
19 BMm85 locus 167:------------------------------------------------------------ 167
20 BMm85 locus 167:------------------------------------------------------------ 167
28 BMm85 locus 167:------------------------------------------------------------ 167


01 BMm85 locus 167:------------------------------------------------------------ 167
06 BMm85 locus 167:------------------------------------------------------------ 167
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11 BMm85 locus 167:------------------------------------------------------------ 167
12 BMm85 locus  39:------------------------------------------------------------ 39
14 BMm85 locus 167:------------------------------------------------------------ 167
15 BMm85 locus 301:GCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCTTT 360
16 BMm85 locus 288:GCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGCTCTAGGAGATTGGTATATCTCCTTT 347
17 BMm85 locus 167:------------------------------------------------------------ 167
19 BMm85 locus 167:------------------------------------------------------------ 167
20 BMm85 locus 167:------------------------------------------------------------ 167
28 BMm85 locus 167:------------------------------------------------------------ 167


01 BMm85 locus 168:------CTCCACAACATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAGGGATGCT 219
06 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTTTCACTATA--ATTAAAATATGCAGGGATGCT 219
11 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCACTGTA--ATTAAAATATGCAAGGATGCT 219
12 BMm85 locus  40:------CTCCACAGCATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAGGGATGCT 91
14 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAGGGATGCT 219
15 BMm85 locus 361:TATTACCTCCACAGCATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAAGGATGCT 418
16 BMm85 locus 348:TATTACCTCCACAGCATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAAGGATGCT 405
17 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCGCTGTA--ATTAAAATATGCAGGGATGCT 219
19 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCACTATATAATTAAAATATGCAGGGATGCT 221
20 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCATTATA--ATTAAAATATGCAGGGATGCT 219
28 BMm85 locus 168:------CTCCACAGCATGATTTTGCAGTGTCACTATA--ATTAAAATATGCAGGGATGCT 219
                      *******.**************.**..*.**  *************.*******

01 BMm85 locus 220:TCTTGGAGCTCTGTACACACCTT-ACATAGCATTATTATTTTAACAAGTCCCCAAGCTCT 278
06 BMm85 locus 220:TTTTGGAGCTCTGTACACACCTTTACGTAGCATTATTATTTTAACATGTCCTCTAGCTCT 279
11 BMm85 locus 220:TCTTGGAGCTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 279
12 BMm85 locus  92:TCTTGGAGCTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 151
14 BMm85 locus 220:TCTTGGAGCTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 279
15 BMm85 locus 419:TCTTGGAGTTCTGAACACACCTTTACAAAGCATTATTATTTTAACATGTCCTCTAGCTCT 478
16 BMm85 locus 406:TCTTGGAGTTCTGAACACACCTTTACATAGCATTATTATTTTAACATGTCCTCGAGCTCT 465
17 BMm85 locus 220:TCTTGGAGCTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 279
19 BMm85 locus 222:TCTTGGAGTTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 281
20 BMm85 locus 220:TCTTGGAGTTCTGTACACACCTTTACATAGCATTATTATTTTAACATGTCCTCTAGCTCT 279
28 BMm85 locus 220:TCTTGGAGCTCTGTACACACCTTTACATAGTATTATTATTTTAACATGTCCTCTAGCTCT 279
                *.******.****.*********.**..**.***************.****.*.******

01 BMm85 locus 279:GATGCTTAATTTGAAGGGGTAAAGTCTCGTTTCCGGTTATGGCATAGGGCGCTGAGGGTA 338
06 BMm85 locus 280:CATACTTAATTTGAAGGGGTAGTGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 339
11 BMm85 locus 280:GATACTCAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 339
12 BMm85 locus 152:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 211
14 BMm85 locus 280:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 339
15 BMm85 locus 479:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGG  536
16 BMm85 locus 466:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGG-A 524
17 BMm85 locus 280:GATACTTACTT-GAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGG-A 337
19 BMm85 locus 282:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 341
20 BMm85 locus 280:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 339
28 BMm85 locus 280:GATACTTAATTTGAAGGGGTAATGTCCTGTTTCCGGTTACTGCATAGGGCACTGAGGGTA 339
                .**.**.*.**.*********..***..***********..*********.*******..

01 BMm85 locus 339:CAAAGAGCAGT                                                349
06 BMm85 locus 340:CAAAGAGCAGT                                                350
11 BMm85 locus 340:CAAAGAGCAGT                                                350
12 BMm85 locus 212:CAAAGAGCAGT                                                222
14 BMm85 locus 340:CAAAGAGCAGT                                                350
17 BMm85 locus 338:CAAAGAGCAG                                                 347
19 BMm85 locus 342:CAAAGAGCAGT                                                352
20 BMm85 locus 340:CAAAGAGCAGT                                                350
28 BMm85 locus 340:CAAAGAGCAGT                                                350
                ...........
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Supplemental Figure 5-33. Sequence alignment of BMm85 locus. GenBank accession numbers are AB24233–AB249241, AB125738 and AB125739.

```
01 BHg10 locus   1:TCTTCCTGTGTGTTTGTACAACACCCAGCACAATGGANCCCAGATCTGTCTGGGGACTCT 60
06 BHg10 locus   1:TCTTCCTGTGTGTTTGTACAATACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 60
14 BHg10 locus   1:-CTTCCTGTGTGTTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 59
15 BHg10 locus   1:-CTTCCTGTGTGTTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 59
20 BHg10 locus   1:-CTTCCTGTGTGGTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 59
23 BHg10 locus   1:TCTTCCTGTGTGTTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 60
24 BHg10 locus   1:-CTTCCTGTTTGTTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 59
25 BHg10 locus   1:-CTTCCTGTGTGTTTGTACAACACCCAGCACAATGGAACCCAGATCTGTCTGGGGACTCT 59
27 BHg10 locus   1:TCTTCCTGTGTGTTTGTACAACACCCAGCACAGTGGAACCCAGATCTGTTTGGGGACTCT 60
                  ********.**.********.**********.****.***********.**********

01 BHg10 locus  61:GCATGCTACTGTAATAGAAATCAATGA--------------------------------- 87
06 BHg10 locus  61:GCATGCTACTATAATAGAAATCAGCGA--------------------------------- 87
14 BHg10 locus  60:GCATGCTACTATAATAGAAATCAATGA--------------------------------- 86
15 BHg10 locus  60:GCATGCTACTATAATAGAAATCAATGA--------------------------------- 86
20 BHg10 locus  60:GCATGCTACTATAATAGAAATCAATAATAATGACTGGAGGGGAGGGATAGCTCAGTGGTT 119
23 BHg10 locus  61:GCATGCTACTATAATAGAAATCAATGA--------------------------------- 87
24 BHg10 locus  60:GCATGCTACTATAATAGAAATCAATGA--------------------------------- 86
25 BHg10 locus  60:GCATGCTACTATAATAGAAATCAATGA--------------------------------- 86
27 BHg10 locus  61:GTGTGCTACTGTAATAGACATCAATGA--------------------------------- 87
                 *..*******.*******.****...*

01 BHg10 locus  87:------------------------------------------------------------ 87
06 BHg10 locus  87:------------------------------------------------------------ 87
14 BHg10 locus  86:------------------------------------------------------------ 86
15 BHg10 locus  86:------------------------------------------------------------ 86
20 BHg10 locus 120:TGAGGATTGGCCTGCTAAACCCAGGGTTGAGAGYTCAATCCTTGAGGGGGGCACTTAGGG 179
23 BHg10 locus  87:------------------------------------------------------------ 87
24 BHg10 locus  86:------------------------------------------------------------ 86
25 BHg10 locus  86:------------------------------------------------------------ 86
27 BHg10 locus  87:------------------------------------------------------------ 87


01 BHg10 locus  87:------------------------------------------------------------ 87
06 BHg10 locus  87:------------------------------------------------------------ 87
14 BHg10 locus  86:------------------------------------------------------------ 86
15 BHg10 locus  86:------------------------------------------------------------ 86
20 BHg10 locus 180:ATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTTCA 239
23 BHg10 locus  87:------------------------------------------------------------ 87
24 BHg10 locus  86:------------------------------------------------------------ 86
25 BHg10 locus  86:------------------------------------------------------------ 86
27 BHg10 locus  87:------------------------------------------------------------ 87


01 BHg10 locus  88:-------------------------------------------------------TAAT 91
06 BHg10 locus  88:-------------------------------------------------------TGAT 91
14 BHg10 locus  87:-------------------------------------------------------TAAT 90
15 BHg10 locus  87:-------------------------------------------------------TAAT 90
20 BHg10 locus 240:AGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTATTTATTATTTAAT 299
23 BHg10 locus  88:-------------------------------------------------------TAAT 91
24 BHg10 locus  87:-------------------------------------------------------TAAT 90
25 BHg10 locus  87:-------------------------------------------------------TAAT 90
27 BHg10 locus  88:-------------------------------------------------------TGAT 91
                                                                  *.**

01 BHg10 locus  92:GAACTACTAAACTGTCTTATCTCTATAAC-TATAGTACTTAATATGTTAATA-TATAATT 149
06 BHg10 locus  92:GAACTACTAAACTGTCTTATCTCTTTAAC-TATAGCTCTTAATATGTTAAT-GTGTAATT 149
14 BHg10 locus  91:GAACTACTAAACTGTCTTATCTCTATAAC-TATAGCACTTAATATGTTAATAGTATAATT 149
15 BHg10 locus  91:GAACTACTAAACTGTCTTATCTCTATAAC-TAT-------------------GTATAATT 130
20 BHg10 locus 300:GAACTACTAAACTGTCTTATCTCTATAAC-TATAGCACTTAATATGTTAAT-GTATAATT 357
23 BHg10 locus  92:GAACTGCTAAACTGTCTTATCTCTATAAC-TAT-------------------GTATAATT 131
24 BHg10 locus  91:GAACTACTAAACT--CTTATCTCTATAAC-TATAGCACTTAATATGTTAAT-GTATAATT 146
25 BHg10 locus  91:GAACTACTAAACTGTCTTATCTCTATAAC-TATAGCACGTAATATGTTAAT-GTATAATT 148
27 BHg10 locus  92:TAACTACTAAACTGTCTTATCTCTATAAGGTATAGCACTTAACATGTTCGT-GTATAATT 150
                 .****.*******..*********.***. ***................. .*.*****

01 BHg10 locus 150:CTGGAGTGCATATGTGCTG                                     168
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06 BHg10 locus 150:CTGGAGTGCATATGTGCTG                                    168
14 BHg10 locus 150:CTAGAGTGCATATGTGCTG                                    168
15 BHg10 locus 131:CTGGAGTGCATATGTGCTG                                    149
20 BHg10 locus 358:CTGGATGGCATATGTGCTG                                    376
23 BHg10 locus 132:CTGGAGTGCATATGTGCTG                                    150
24 BHg10 locus 147:CTGGAGTGCATATGTGCTG                                    165
25 BHg10 locus 149:CTGGAGTGCATATGTGCTG                                    167
27 BHg10 locus 151:CTGGAGTGCATATGTGCTG                                    169
                **.**..************
```

Supplemental Figure 5-34. Sequence alignment of BHg10 locus. GenBank accession numbers are AB24242–AB249250.

```
01 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
02 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTAGGAGTAGATAACTTGTGAAAGTTTATGGTT 60
06 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGTAGTAGATAAACTTTCACAAGTTAYGGTT 60
10 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTACGGTT 60
14 BHg23 locus   1:GAAGGGCTCCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
17 BHg23 locus   1:-AAGGGCTCCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAGGTTACGGTT 59
19 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
20 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
21 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
23 BHg23 locus   1:GAAGGGCACCATATTTTAGGGTTAGAGGTTGGAGTAGATAAACTTTCACAAGTTATGGTT 60
                  .******.********************.*.*********..*.*.*.*..***.****

01 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGATTAGGGTTGGAACAGG--------------- 105
02 BHg23 locus  61:TGGGCAGGTACAGTCCCCCCATCCTGGGATTAGGGTTGGAACAGG--------------- 105
06 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGATTAGGGTTGGAACAGG--------------- 105
10 BHg23 locus  61:TGAG------------------------------------------------------- 64
14 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGGTTAGGGTTGGAACAGG--------------- 105
17 BHg23 locus  60:TGGGCAGGTACAGTCCCCCAAGGCTAGGATTAGGGTTGGAACAGG--------------- 104
19 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGATTAGGGTTGGAATAGG------TTGGAATGT 114
20 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGATTAGGGTTGGAATAGGAATAGGTTGGAATGT 120
21 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCTGAGGATTAGGGTTGGAATAGGAATAGGTTGGCAGGT 120
23 BHg23 locus  61:TGGGCAGGTACAGTCCCCCAAGCCTAGGATTAGGGTTGGAACAGG--------------- 105
                  **.*.........................................

01 BHg23 locus 105:------------------------------------------------------------ 105
02 BHg23 locus 105:------------------------------------------------------------ 105
06 BHg23 locus 105:------------------------------------------------------------ 105
10 BHg23 locus  64:------------------------------------------------------------ 64
14 BHg23 locus 105:------------------------------------------------------------ 105
17 BHg23 locus 104:------------------------------------------------------------ 104
19 BHg23 locus 115:GGGGGGCAAGGGATAGCTCAGTGGTTTGAGCATTGACCTGCTAAATCCAGAGTTGTGAGT 174
20 BHg23 locus 121:GGGGGGCAAGGGATAGCTCAGTGGTTTGAGCATTGACCTGCTAAATCCAGGGTTGTAAGT 180
21 BHg23 locus 121:GGGAGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTATGAGT 180
23 BHg23 locus 105:------------------------------------------------------------ 105


01 BHg23 locus 105:------------------------------------------------------------ 105
02 BHg23 locus 105:------------------------------------------------------------ 105
06 BHg23 locus 105:------------------------------------------------------------ 105
10 BHg23 locus  64:------------------------------------------------------------ 64
14 BHg23 locus 105:------------------------------------------------------------ 105
17 BHg23 locus 104:------------------------------------------------------------ 104
19 BHg23 locus 175:TCAATCCTTGAGGGGGTTACTTAGGAATCTGGGGCAAAAACATTGGTCCTGCTAGTGAAG 234
20 BHg23 locus 181:TCAATCCTTGAGGGGGTTACTTAGGAATCTGGGGCAAAAACATTGGTCCTGCTAGTGAAG 240
21 BHg23 locus 181:TCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAAAATTGGTCCTGCTAGTGAAG 240
23 BHg23 locus 105:------------------------------------------------------------ 105


01 BHg23 locus 105:------------------------------------------------------------ 105
02 BHg23 locus 105:------------------------------------------------------------ 105
06 BHg23 locus 105:------------------------------------------------------------ 105
10 BHg23 locus  64:------------------------------------------------------------ 64
14 BHg23 locus 105:------------------------------------------------------------ 105
17 BHg23 locus 104:------------------------------------------------------------ 104
19 BHg23 locus 235:GCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATAT 294
20 BHg23 locus 241:GCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTTCAGTTCTAGGAGATTGGTATAT 300
21 BHg23 locus 241:GCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATAT 300
23 BHg23 locus 105:------------------------------------------------------------ 105


01 BHg23 locus 106:-----------------------------TAGGGCCTCCCACCCTAGGGTTAGCATTGGG 136
02 BHg23 locus 106:-----------------------------TAAGGCCTCCCACCCTAGGGTTAGCATTGGG 136
06 BHg23 locus 106:-----------------------------TAGGGCCTCCCACCCTAGGATTAGCATTGGG 136
10 BHg23 locus  65:-----------------------------TAGGGCCTCCCACCCTAGGGTTAGTATTGGG 95
14 BHg23 locus 106:-----------------------------TAGGGCCTCCCACCCTAGGGTTAGCATTGGG 136
17 BHg23 locus 105:-----------------------------TAGGGCCTCCCACCCTAGGGTTAGCATTAAG 135
19 BHg23 locus 295:CTCCAATTATTA---------CCTTTAGGTAGGGCCTCCCACCGAAGGGTTAGCATTGGG 345
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20 BHg23 locus 301:CTCCAATTATTA---------CCTTTAGGTAGGGCCTCCCACCGAAGGGTTAGCATTGGG 351
21 BHg23 locus 301:CTCCAATTATTATCTTTATTACCTTTAGGTAGGGCCTCCCACCCTAGGGTTAGCATTGGG 360
23 BHg23 locus 106:----------------------------TAGGGCCTCCCACCCTAGGGTTAGTATTGGG 136
                                            **.***********..***.****.***..*

01 BHg23 locus 137:GCAGAAAAGGTTTCTCAGGTTATGGCTGGGGTAGATAGTGCCCCTAGGGTTAGGGTTGGG 196
02 BHg23 locus 137:ACAGAAA-----------------------------GTGCTCCTAGGGTT------GGG 160
06 BHg23 locus 137:GCAGAAAAGGTTTCTCAGGTTATAGCTAGGGTAGATAGTGCTCCCAGGGTTAAGGTTGGG 196
10 BHg23 locus  96:GTAAAAAAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 155
14 BHg23 locus 137:GCAGAAAAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 196
17 BHg23 locus 136:GCAGAAAAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 195
19 BHg23 locus 346:GCAGAAAAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 405
20 BHg23 locus 352:GCAGAAAAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 411
21 BHg23 locus 361:GCAGAAGAGGTTTCTCAGGTTATGGCTAGGGTAGATAGTGCCCCCAGGGTTAGGGTTGGG 420
23 BHg23 locus 137:ACGGAAAAGGTTTCTCAGGTTATCGCTAGGGTAGATAGTGCTCCCAGGGTTAGGGTTGGG 196
                ....**.............................****.**.******......***

01 BHg23 locus 197:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           225
02 BHg23 locus 161:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           189
06 BHg23 locus 197:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           225
10 BHg23 locus 156:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           184
14 BHg23 locus 197:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           225
17 BHg23 locus 196:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           224
19 BHg23 locus 406:GCAGGTAGGGACCCAA-GTCTAGGCTTAG                           433
20 BHg23 locus 412:GCAGGTAGGGACCCAA-GTCTAGGCTTAG                           439
21 BHg23 locus 421:GCAGGTAGGGACCCAA-GTCTAGGCTTAG                           448
23 BHg23 locus 197:GCAGGTAGGGACCCAAAGTCTAGGCTTAG                           225
                ****************.************
```

Supplemental Figure 5-35. Sequence alignment of BHg23 locus. GenBank accession numbers are AB24251–AB249260.

```
06 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 60
11 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 60
14 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 60
17 BHa68 locus   1:----------------CTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATTTGGT 44
19 BHa68 locus   1:--------------GACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 46
20 BHa68 locus   1:--------------GACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 46
21 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATTTAGT 60
22 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 60
23 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 60
24 BHa68 locus   1:-CTTCCTTGGCATAGACTCATAGACTTTAAGGTAAGATGGGACCATCATGACCATCTAGT 59
27 BHa68 locus   1:TCTTCCTTGGCATAGACTCATAGACTTTAAGGTCAGATGGGACCATCATGACCATCTAGT 60
                 ...............*****************.********************.*.**

06 BHa68 locus  61:CTGGCCTCCTGCACATTGCAGGTCACAAAACCTCACCCACTCACTTGTGGCTTGTGGGAC 120
11 BHa68 locus  61:CTGGCCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGGCTTGTGGGAC 120
14 BHa68 locus  61:CTGACCTCTTRCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGGCTTGTGGGAC 120
17 BHa68 locus  45:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGGCTTGTGGGAC 104
19 BHa68 locus  47:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCGGCTTGTGG-------GAC 99
20 BHa68 locus  47:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCRGCTTGTGG-------GAC 99
21 BHa68 locus  61:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGGCTTGTGGGAC 120
22 BHa68 locus  61:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCGACTTGTGG-------GAC 113
23 BHa68 locus  61:CTGACCT---GCACATTGCAGGTCACAGAACCTCACTCACCCTCTTGTGGCTTGTGGGAC 117
24 BHa68 locus  60:CTGACCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGGCTTGTGGGAC 119
27 BHa68 locus  61:CTGATCTCCTGCACATTGCAGGTCACAGAACCTCACCCACCCACTTGTGG-------GAC 113
                 ***..**....****************.********.***...*******.......***

06 BHa68 locus 121:TGGAAGGATCTCAGAGAAGA-------------------------------------- 140
11 BHa68 locus 121:TGGAAGGATCTCAGAGAAGA-------------------------------------- 140
14 BHa68 locus 121:TGGAAGGATCTCAGAGAAGA-------------------------------------- 140
17 BHa68 locus 105:TGGAAGGATCTCAGAGAAGA-------------------------------------- 124
19 BHa68 locus 100:TGGAAAGATCTCAGAGAAGAGGAGTGATAGCTCAGTGGTTTGAGCATTRGCCTGCTAAAC 159
20 BHa68 locus 100:TGGAAAGATCTCAGAGAAGAGGAGTGATAGCTCAGTGGTTTGAGCATTGGCCTGCTAAAC 159
21 BHa68 locus 121:TGGAAGGCTCTCAGAGAAGAGGAAGGATAGCTCAGTGGTTTGAGCATTGACCTGCTAAAC 180
22 BHa68 locus 114:TGGCAGGATCTCAGCAAAGAGGAGGGATAGATCAGTGGTTTGAGCATTGGCCTGCTAAAC 173
23 BHa68 locus 118:TGGAAGGATCTCAGAGAAGA-------------------------------------- 137
24 BHa68 locus 120:TGGAAGGATCTCAGAGAAGA-------------------------------------- 139
27 BHa68 locus 114:TGGAAGGATCTCAGAGAAGA-------------------------------------- 133
                 ***.*.*.******..****

06 BHa68 locus 140:------------------------------------------------------------ 140
11 BHa68 locus 140:------------------------------------------------------------ 140
14 BHa68 locus 140:------------------------------------------------------------ 140
17 BHa68 locus 124:------------------------------------------------------------ 124
19 BHa68 locus 160:CCACANCTGTAAGTTCAATCCTCAAGGGGGCCCCTGAGGGATCTGGGGCAAAAATCAGTA 219
20 BHa68 locus 160:CCACAGCTGTAAGTTCAATCCTCAAGGGGGCCCCTGAGGGATCTGGGGCAAAAATCAGTA 219
21 BHa68 locus 181:CCAGGGTTATGAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGTCAAAAATCAGTA 240
22 BHa68 locus 174:CCAGGGCTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGAATCTGGGGCAAAAATCAGTA 233
23 BHa68 locus 137:------------------------------------------------------------ 137
24 BHa68 locus 139:------------------------------------------------------------ 139
27 BHa68 locus 133:------------------------------------------------------------ 133


06 BHa68 locus 140:------------------------------------------------------------ 140
11 BHa68 locus 140:------------------------------------------------------------ 140
14 BHa68 locus 140:------------------------------------------------------------ 140
17 BHa68 locus 124:------------------------------------------------------------ 124
19 BHa68 locus 220:CTTGGTCCTGCTAGTGAAAGCAGGGGGCTGGACTCAATG-----------TCCCTTCCAT 268
20 BHa68 locus 220:CTTGGTCCTGCTAGTGAAAGSAGGGGGCTGGACTCAATG-----------TCCCTTCCAT 268
21 BHa68 locus 241:CTTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTTCAAGGTCCCTTCCAG 300
22 BHa68 locus 234:CTTGGTCCTACTAGTGAAGGCAGGGAGCTAGACTCAATGACCTTTCAAGGTCCCTTCCAG 293
23 BHa68 locus 137:------------------------------------------------------------ 137
24 BHa68 locus 139:------------------------------------------------------------ 139
27 BHa68 locus 133:------------------------------------------------------------ 133


06 BHa68 locus 141:----------------------------------------TCATTTGGACATTCTTATGC 160
11 BHa68 locus 141:----------------------------------------TCATTTGGGCACTCTTGTGC 160
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14 BHa68 locus 141:----------------------------------------TCATTTGGACACTCTTATGC 160
17 BHa68 locus 125:----------------------------------------TCATTTGGACACTCTTATGC 144
19 BHa68 locus 269:TTCTAGGAGATTGGTATCTCTCCAGTTATTTAATTTAAGATCATTTGGACACTCTTATGC 328
20 BHa68 locus 269:TTCTAGGAGATTGGTATCTCTCCAGTTATTTAATTTAAGATCATTTGGACACTCTTATGC 328
21 BHa68 locus 301:TTCTAGGAGATTGGTATCTTTCCAATTATTTAATTTAAGATCATTTGGACACTCTTGTGC 360
22 BHa68 locus 294:TTCTAGGAGATTGGTATCTCTCCAATTATTTAATTTAAGATCATTTGGACACTCTTATGC 353
23 BHa68 locus 138:----------------------------------------TCATTTGGACACTCTTATGC 157
24 BHa68 locus 140:----------------------------------------TCATTTGGACACTCTTATGC 159
27 BHa68 locus 134:----------------------------------------TCATTTGGACACTCTTCTTC 153
                                                 ********.**.****.*.*

06 BHa68 locus 161:TTCAACATGCTTCCAAATTCCCTGAAGTCATC                          192
11 BHa68 locus 161:TTCAACATGCTTCCAAATTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 220
14 BHa68 locus 161:TTCAACATGCTTCCAAATTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 220
17 BHa68 locus 145:TTCAACATGCTTCCAAGTTCCCTGAAGTCWTCTACTATCTGTAAAATAGCCCACAACACA 204
19 BHa68 locus 329:TTCAACATGGTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCC-AC      381
20 BHa68 locus 329:TTCAACATGGTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATA           376
21 BHa68 locus 361:TTCAACATACTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 420
22 BHa68 locus 354:TTCAACATGCTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 413
23 BHa68 locus 158:TTCAACATGCTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 217
24 BHa68 locus 160:TTCAACATGCTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 219
27 BHa68 locus 154:TTCAACATGCTTCCAAGTTCCCTGAAGTCATCTACTATCTGTAAAATAGCCCACAACACA 213
                 ********..******.************.**

11 BHa68 locus 221:GAGT                                                    224
14 BHa68 locus 221:GAGT                                                    224
17 BHa68 locus 205:GAGT                                                    208
21 BHa68 locus 421:GAGT                                                    424
22 BHa68 locus 414:GAGT                                                    417
23 BHa68 locus 218:GAGT                                                    221
24 BHa68 locus 220:GAGT                                                    223
27 BHa68 locus 214:GAGT                                                    217
                 ....
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Supplemental Figure 5-36. Sequence alignment of BHa68 locus. GenBank accession numbers are AB24261–AB249271.

```
01 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTGCATTAAATGAACTGGGTTCATGAACGTAAAGCTTTATC 60
06 BHg12 locus   1:CTTGTGGTTGGAGGTTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
08 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
14 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
17 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
19 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCCACATTAAATGAACTGGGTTCATGAACTTAAAGTTTTATC 60
20 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCCACATTAAATGAACTGGGTTCATGAACTTAAAGTTTTATC 60
21 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
23 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAATTTAAAGCTTTATC 60
24 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATGAACTGGGTTCATGAACTTAAAGCTTTATC 60
25 BHg12 locus   1:CTTGTGGTTGGAGTGTCATCTACATTAAATAAACTGGGTTCATGACCTTAAAACTTTATC 60
                 *************..*****..********.**************...****..******

01 BHg12 locus  61:AGAGCCTTCCCCA----CACCC-CACTTCTCCAAATCTGATGATAGGCAACTAAACTAGA 115
06 BHg12 locus  61:AGAGCCTTCCCCCCG--CACCCTCACTCTTCCAAATCTGGAGATAGGCAACTAAACTAGA 118
08 BHg12 locus  61:AGAGCCTTCCCCCC---CACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 117
14 BHg12 locus  61:AGAGCCTTCTCCCG---CACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 117
17 BHg12 locus  61:AGAGCCTTCCCCCG---CACCCTCACTTTTCCAAATCTGGAGATAGGCGACTAAACTAGA 117
19 BHg12 locus  61:AGAGCCTTCCCCCC---CACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 117
20 BHg12 locus  61:AGAGCCTTCCCCCC---CACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 117
21 BHg12 locus  61:AGAGCCTTCCCCCC---CACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 117
23 BHg12 locus  61:AGAGCCTTCCCCCCACCCACCCTCACTTTTCCAAATCTGGAGATAGGCAACTAAACTAGA 120
24 BHg12 locus  61:AGAGCCTTCCCCCG---CACCCTCACTTTTCCAGATATGGAGATAGGCAACTAAACTAGA 117
25 BHg12 locus  61:AGAGCCTTCCCCCC---TGCCCTCACTTTTCCAAATCTAGAGAGAGGCAACTAAACTAGA 117
                *********.**..   ..***.****..****.**.*...**.****.***********

01 BHg12 locus 116:ATTAATGCAGGGGGC---------AGGTAGACTCAAAC---------------------- 144
06 BHg12 locus 119:ATTGATGCGGGGGGG---------AGGTAGACTCAAAC---------------------- 147
08 BHg12 locus 118:ATTGATGCAGGGGGG---------AGGTAGACTCAAAC---------------------- 146
14 BHg12 locus 118:ATTGATGCGGGGGGGCGG------AGGTAGGCTCAAAC---------------------- 149
17 BHg12 locus 118:ATTGATGCGGGGGGGGAGGAG---AGGTAGGCTCAAAC---------------------- 152
19 BHg12 locus 118:ATTGATGCCGGGCGGGGG------AGGTAGGCTCAAACCCAGCTTTTTCGGGGGAGGGAT 171
20 BHg12 locus 118:ATTGATGCCGGGCGGGGG------AGGTAGGCTCAAACCCAGCTTTTTCGGGGGAGGGAT 171
21 BHg12 locus 118:ATTGATGCGGGGGGGGGGGGG---AGGTAGGCTCAAAC---------------------- 152
23 BHg12 locus 121:ATTGATGCGGGTGGGG--------AG-TAGACTCAAAC---------------------- 149
24 BHg12 locus 118:ATAGATGCGGGGGGGGGGGGGGGGAGGTAGGCTCAAAC---------------------- 155
25 BHg12 locus 118:ATTGATGCGGGGGGG---------AGATGGACTCAAAC---------------------- 146
                **..****.**..*.. .     **.*.*.*******

01 BHg12 locus 144:------------------------------------------------------------ 144
06 BHg12 locus 147:------------------------------------------------------------ 147
08 BHg12 locus 146:------------------------------------------------------------ 146
14 BHg12 locus 149:------------------------------------------------------------ 149
17 BHg12 locus 152:------------------------------------------------------------ 152
19 BHg12 locus 172:AGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGA 231
20 BHg12 locus 172:AGCTCAGTGGTTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGA 231
21 BHg12 locus 152:------------------------------------------------------------ 152
23 BHg12 locus 149:------------------------------------------------------------ 149
24 BHg12 locus 155:------------------------------------------------------------ 155
25 BHg12 locus 146:------------------------------------------------------------ 146


01 BHg12 locus 144:------------------------------------------------------------ 144
06 BHg12 locus 147:------------------------------------------------------------ 147
08 BHg12 locus 146:------------------------------------------------------------ 146
14 BHg12 locus 149:------------------------------------------------------------ 149
17 BHg12 locus 152:------------------------------------------------------------ 152
19 BHg12 locus 232:GGCCACTTAAGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTC 291
20 BHg12 locus 232:GGCCACTTAAGGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTC 291
21 BHg12 locus 152:------------------------------------------------------------ 152
23 BHg12 locus 149:------------------------------------------------------------ 149
24 BHg12 locus 155:------------------------------------------------------------ 155
25 BHg12 locus 146:------------------------------------------------------------ 146


01 BHg12 locus 144:------------------------------------------------------------ 144
06 BHg12 locus 147:------------------------------------------------------------ 147
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08 BHg12 locus 146:------------------------------------------------------------ 146
14 BHg12 locus 149:------------------------------------------------------------ 149
17 BHg12 locus 152:------------------------------------------------------------ 152
19 BHg12 locus 292:GATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTACCTT 351
20 BHg12 locus 292:GATGACCTTTCAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTACCTT 351
21 BHg12 locus 152:------------------------------------------------------------ 152
23 BHg12 locus 149:------------------------------------------------------------ 149
24 BHg12 locus 155:------------------------------------------------------------ 155
25 BHg12 locus 146:------------------------------------------------------------ 146


01 BHg12 locus 145:-----------------CCAGCTTGAAATAATTTGGCCCAAAAACCAAATTGTTAAAGCA 187
06 BHg12 locus 148:-----------------CCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 190
08 BHg12 locus 147:-----------------CCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 189
14 BHg12 locus 150:-----------------CCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 192
17 BHg12 locus 153:-----------------CCAGCTTGAAGTAATTTGGCCCCAAAACCAAATTGTTAAAGCA 195
19 BHg12 locus 352:TTTTATTACCTTTATTACCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 411
20 BHg12 locus 352:TTTTATTACCTTTATTACCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 411
21 BHg12 locus 153:-----------------CCAGCTTGAAATAATTTGGTCCCAAAACCAAATTGTTAAAGCA 195
23 BHg12 locus 150:-----------------CCAGCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 192
24 BHg12 locus 156:-----------------CCATCTTGAAATAATTTGGCCCCAAAACCAAATTGTTAAAGCA 198
25 BHg12 locus 147:-----------------CCAGCTTGAAATAATTTGTCCCCAAAACCAAATTGTTAAAGCA 189
                              ***.******.*******..**.********************

01 BHg12 locus 188:AATTGGCATCAGCCACGACCCCCCACATGATCTGACATTGCCATCTCTGT         237
06 BHg12 locus 191:AATTGGCATCAGCCACAACCCCCCACGCGATCTGACATTGCCATCTCTGT         240
08 BHg12 locus 190:AATTGGCATCAGCCACAACCCCCCACGCGATCTGACATTGCCATCTCTGT         239
14 BHg12 locus 193:AATTGGCATCAGCCTCAACCCCCCACATGATCTGACATTGCCATCTCTGT         242
17 BHg12 locus 196:AATTGGCATCAGCCAGAACTCCCCACATGATCTGACATTGCCATCTCTGT         245
19 BHg12 locus 412:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         461
20 BHg12 locus 412:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         461
21 BHg12 locus 196:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         245
23 BHg12 locus 193:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         242
24 BHg12 locus 199:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         248
25 BHg12 locus 190:AATTGGCATCAGCCACAACCCCCCACATGATCTGACATTGCCATCTCTGT         239
                ***************...**.******..*********************
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Supplemental Figure 5-37. Sequence alignment of BHg12 locus. GenBank accession numbers are AB24272–AB249282.

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01 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATACTTTTTGCTATATATAAAAATTG 60
07 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGGAAAATTATA-TTTTTGCTATATATAAAAATTG 59
14 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 60
17 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 60
19 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 60
20 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 60
21 BHg16 locus   1:-TGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 59
23 BHg16 locus   1:TTGCTTCCTGCAGATATATAAAAGGTGCAAAATTATATTTTTTGCTATATATAAAAATTG 60
24 BHg16 locus   1:-TGCTTCCTNCAGATATATAAAAGGTGCAAAATTTTATTTTTTGCTATATATAAAAATKG 59
25 BHg16 locus   1:TTGCTTGCAGCAGATATATAAAAGGTGCAAAATTRTA-TTTTTGCTATGTATAAAAATTG 59
                 .*****.*..****************.******.**.**********.*********.*

01 BHg16 locus  61:AAAGAGTAAATAAA---------------------------------------------- 74
07 BHg16 locus  60:AAAGATTAAATTAA---------------------------------------------- 73
14 BHg16 locus  61:AAAGAGTAAATAAA---------------------------------------------- 74
17 BHg16 locus  61:AAAGAGTAAATAAA---------------------------------------------- 74
19 BHg16 locus  61:AAATAGTAAATMAATATCTGGGGGAGGGATRGCTCAGTAGTGTGAGCACTGGCCTGCTAA 120
20 BHg16 locus  61:AAAKAGTAAATAAATATCTGGRGGAGGGATAGCTCAGTAGTGTGAGCACTGGCCTGCTAA 120
21 BHg16 locus  60:AAAGAGTAAATAAA---------------------------------------------- 73
23 BHg16 locus  61:AAAGAGTAAATAAA---------------------------------------------- 74
24 BHg16 locus  60:AAAGAGTAAATAAA---------------------------------------------- 73
25 BHg16 locus  60:AAAGAGTAAATAAA---------------------------------------------- 73
                ***.*.*****.**

01 BHg16 locus  74:------------------------------------------------------------ 74
07 BHg16 locus  73:------------------------------------------------------------ 73
14 BHg16 locus  74:------------------------------------------------------------ 74
17 BHg16 locus  74:------------------------------------------------------------ 74
19 BHg16 locus 121:AYACAGGGTTGTRAGTTCAATCCTTGAGGAGGCCACTTAGGGATCTGGGGCAAAAAAATT 180
20 BHg16 locus 121:ACACAGGGTTGTGAGTTCAATCCTTGAGGAGGCCACTTAGGGATCTGGGGCAAAAAAATT 180
21 BHg16 locus  73:------------------------------------------------------------ 73
23 BHg16 locus  74:------------------------------------------------------------ 74
24 BHg16 locus  73:------------------------------------------------------------ 73
25 BHg16 locus  73:------------------------------------------------------------ 73


01 BHg16 locus  74:------------------------------------------------------------ 74
07 BHg16 locus  73:------------------------------------------------------------ 73
14 BHg16 locus  74:------------------------------------------------------------ 74
17 BHg16 locus  74:------------------------------------------------------------ 74
19 BHg16 locus 181:GGTCCTGCTAGTGAAGTCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTC 240
20 BHg16 locus 181:GGTCCTGCTAGTGAAGTCAGGGGGCTGGACTCAATGACCTTKCAAGGTCCCTTCCAGTTC 240
21 BHg16 locus  73:------------------------------------------------------------ 73
23 BHg16 locus  74:------------------------------------------------------------ 74
24 BHg16 locus  73:------------------------------------------------------------ 73
25 BHg16 locus  73:------------------------------------------------------------ 73


01 BHg16 locus  75:-------------------------------------------AGTTTATTTGTAAAAAG 91
07 BHg16 locus  74:-------------------------------------------TGTTTATTTGTAAAAAG 90
14 BHg16 locus  75:-------------------------------------------TGTTTATTTGTAAAAAG 91
17 BHg16 locus  75:-------------------------------------------TGTTTATTTGTAAAAAG 91
19 BHg16 locus 241:TAGGAGATTGGTATATCTCCAATTATTACCTTTTTATTACCTATGTTTATTTGTAAGAAG 300
20 BHg16 locus 241:TAGGAGATTGGTATATCTCCAATTATTACC-----------TATGTTTATTTGTAAGAAG 289
21 BHg16 locus  74:---------------------------------------------TGTTTATTTGTAAAAAG 90
23 BHg16 locus  75:---------------------------------------------TGTTTATTTGTAAAAAG 91
24 BHg16 locus  74:---------------------------------------------TGTTTATTTGTAAAAAG 90
25 BHg16 locus  74:---------------------------------------------TGTTTATTTGTAAAAAG 90
                                                  .************.***

01 BHg16 locus  92:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          140
07 BHg16 locus  91:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          139
14 BHg16 locus  92:ACAGTAAATTACTTGTCATTTCCTTGAGCACATGGAATTTACAGGTAAT          140
17 BHg16 locus  92:ACAGTAAATTACTTGTCATTTCYTTCAGCACATGGAATTTACAGGTAAT          140
19 BHg16 locus 301:ACAGTAAATTACGTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          349
20 BHg16 locus 290:ACAGTAAATTACGTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          338
21 BHg16 locus  91:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          139
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23 BHg16 locus  92:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          140
24 BHg16 locus  91:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          139
25 BHg16 locus  91:ACAGTAAATTACTTGTCATTTCCTTCAGCACATGGAATTTACAGGTAAT          139
                ************.*********.**.**********************
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Supplemental Figure 5-38. Sequence alignment of BHg16 locus. GenBank accession numbers are AB24283–AB249292.

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01 BOs57 locus   1:CCAATGACAA TCT-CAAAAA CGTAATGCAT AATTATATCA GAGTTATTCC TATAAAGATA 59
06 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATGCAT AATTATATCA GAATTATTCC TATAAAGATA 60
10 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGGAACGCAT AATCATATCA GAATTATTCC TATAGAGATA 60
11 BOs57 locus   1:---------- ---------- ------GCAT AATTATATCA GAATTATTCC TATAAAGATA 34
12 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATGCAT AATTGTATCA GAATTATTCC TATAAAGATA 60
13 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATGCAT AATTATATCA GAATTATTCC TATAAAGATA 60
14 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATGCAT AATTATATCA GAATTATTCC TATAAAGATA 60
25 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATACAT AATTATATCA GAATTATTCC AATAAAGATA 60
27 BOs57 locus   1:CCAATGACAA TCTGCAAAAA TGTAATGCAT AATTATATCA GCATTATTCC TATAAAGAT- 59
                 .......... .......... .......*** ***..***** *..******* .***.****.

01 BOs57 locus  60:TAGATAT--- ---------- ---------- ---------- ---------- ---------- 66
06 BOs57 locus  61:TAGATATAAA GA-------- ---------- --TACAGATG TAGGGGGAGG GATAGCTCAG 100
10 BOs57 locus  61:TAGATAT--- ---------- ---------- ---------- --GGGGGAGG GATGTCTCAG 85
11 BOs57 locus  35:CAGATATAAA GA-------- ---------- --TACAGATG TAGAGGGAAG GATAGCTCAG 74
12 BOs57 locus  61:CAGATATAAA GAAAGATAAA GATAGAGATA GATATAGATA TAGGGGGAGG GATGGCTCAG 120
13 BOs57 locus  61:TAGATATA-- ---------- ---------- ----TAGATA TAGGGGGAGG GATGGCTCAG 94
14 BOs57 locus  61:TAGATATA-- ---------- ---------- ---------- --GGGGGAGG GATGGCTCAG 86
25 BOs57 locus  61:AAGATAAA-- ---------- ---------- ---------- --GGGGGAGG GATGGCTCAG 86
27 BOs57 locus  60:----CAT--- ---------- ---------- ---------- ---------- ---------- 62
                .....*..                                ........ ..........

01 BOs57 locus  66:---------- ---------- ---------- ---------- ---------- ---------- 66
06 BOs57 locus 101:TGGTCTGAGC ACTGGCCTGC TAAACCCAAG GTTGTGAGTT TAATCTTTGA GGGGGACACT 160
10 BOs57 locus  86:TGGTCTGAAC ATTGGCCTGC TAAACCCAGG GTTGTGAGTT CAATCTTTGA GGGGGCCACT 145
11 BOs57 locus  75:TGGTCTGAGC ATTGGCCTGC TAAACCCAAG GTTGTGAGTT CAATCTTTGA GGGGGACACT 134
12 BOs57 locus 121:TGGTTTGAGC ATTGGCCTGC TAAACCCAGG GTTGTGAGTT CAATCTTTGA GGGGGCCACT 180
13 BOs57 locus  95:TGGTTTGAGC ATTGGCCTGC TAAACCCAGG GTTGTGAGTT CAATCTTTGA GGGGGCCACT 154
14 BOs57 locus  87:TGGTTTGAGC ATTGGCCTGC TAAACCCAGG GTTGTGAGTT CAATCTTTGA GGGGGCCACT 146
25 BOs57 locus  87:TGGTTTGAGC ATTGGCCTGC TAAACCCAGG GTTGTGAGTT CAATCTTTGA GGGGGCCACT 146
27 BOs57 locus  62:---------- ---------- ---------- ---------- ---------- ---------- 62
                .... ..... .......... .......... .......... .......... ..........

01 BOs57 locus  66:---------- ---------- ---------- ---------- ---------- ---------- 66
06 BOs57 locus 161:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTACT GAAGACAGGG GGCTGGACTC 220
10 BOs57 locus 146:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTAGT GAAGGCAGGG GGCTGGACTC 205
11 BOs57 locus 135:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTACT GAAGACAGGG GGCTGGACTT 194
12 BOs57 locus 181:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTAGT GAAGGCAGGG GGCTGGACTC 240
13 BOs57 locus 155:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTAGT GAAGGCAGGG GGCTGGACTC 214
14 BOs57 locus 147:TAGGGATCTG GGACAAAAAT CAGTACTTGG CCCTGCTAGT GAAGGCAGGG GGCTGGACTC 206
25 BOs57 locus 147:TAGGGATCTG GGGCAAAAAT CAGTACTTGG CCCTGCTAGT GAAGGCAGGG GGCTGGACTC 206
27 BOs57 locus  62:---------- ---------- ---------- ---------- ---------- ---------- 62
                .......... .......... .......... .......... .......... ..........

01 BOs57 locus  66:---------- ---------- ---------- ---------- ---------- ---------- 66
06 BOs57 locus 221:GATGACCTTT TGAGGTCCCT TCCAGTTCTA GGAGATTGCT ATATCTCAAA TTATTA-TTA 279
10 BOs57 locus 206:GATGACCTTT CGAGGTCCCT TCTAGTTCTA GGAGATTGGT ATATCTCCAA TTATTAATTA 265
11 BOs57 locus 195:GATGACCTTT TGAGGTCCCT TCCAGTTCTA GGAGATTGCT ATATCTCAAA TTATTA-TTA 253
12 BOs57 locus 241:AATGACCTTT CGAGGTCCCT TCCAGTTCTA GGAGATAGGT ATATCTCCAA TTATTA-TTA 299
13 BOs57 locus 215:GATGACCTTT CGAGGTCCCT TCCAGTTCTA GGGGATAGGT ATATCTCCAA TTATTA-TTA 273
14 BOs57 locus 207:GATGACCTTT CAAGGTCCCT TCCAGTTCTA GGAGATAGGT ATATCTCCAA TTATTA-TTA 265
25 BOs57 locus 207:GATGACCTTT TGAGGTCCCT TCCAGTTCTA GGAGATAGGT ATATCTCCAA TTAT-A-TTA 264
27 BOs57 locus  62:---------- ---------- ---------- ---------- ---------- ---------- 62
                ..........  ......... .......... ...... ... .......... ...... ...

01 BOs57 locus  67:---------- ---------- -----TCCTA GAAGCTTCCA TCTTAAAAAG GAAGAACTTT 101
06 BOs57 locus 280:TTATTATTAT ---------- ---------- -AAGCTTCCA TCTTAAAAAG GAAGAACTTT 318
10 BOs57 locus 266:TTATTATTAT ---------- ---------- -AAGCTTCCA TCTTAAAAAG GAAGAACTTT 304
11 BOs57 locus 254:TTATTATTAT TAT------- ---------- -AAGCTTCCA TCTTAAAAAG GAAGAACTTT 295
12 BOs57 locus 300:T--------- ---------- ---------- -AAGCTTCCA TCTTAAAAAG GAAGAACTTT 329
13 BOs57 locus 274:TTATTAT--- ---------- ---------- -AAGCTTCCA TCTTAAAAAT GAAGAACTTT 309
14 BOs57 locus 266:TTATTAT--- ---------- ---------- -AAGCTTCCA TCTTAAAAAG GAAGAGCTTT 301
25 BOs57 locus 265:T-ATTATTAT TATTATTATT ATTAT----- -AAGCTTCCA TCTTAAAAAG GAAGAACTTT 317
27 BOs57 locus  63:---------- ---------- ---------- -TAGCTTCCA TCTTTAAAAG GAAGAACTTT 91
                .......                       .******** ****.****. *****.****

01 BOs57 locus 102:CCTTACATTA GTCATGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCATAT 161
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06 BOs57 locus 319:CCTTATATTG CTCATGTGCA TCTGAAGTAT GGAAAGTAAA CATTATCAAC TACTGCATAT 378
10 BOs57 locus 305:CCTTATATTA CTCACGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCAAAT 364
11 BOs57 locus 296:CCTTATATTG CTCATGTGCA TCTGAAGTAT GGAAAGTAAA CATTATCAAC TACTGCATAT 355
12 BOs57 locus 330:CCTTATATAT ---ATGCGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCATAT 386
13 BOs57 locus 310:CCTTATATTA GTCATGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCATAT 369
14 BOs57 locus 302:CCTTATATTA GTCATGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCATAT 361
25 BOs57 locus 318:CCTTATATTA GTCATGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCGAC TACTGCATAT 377
27 BOs57 locus  92:CCTTATATTA GTCATGTGCA TCTGCAGTAT GGAAAGTAAG CATTACCAAC TACTGCATAT 151
                 *****.**.. ...*.*.*** ****.***** *********. *****.*.** *******.**

01 BOs57 locus 162:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GATAGAAAGT 221
06 BOs57 locus 379:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 438
10 BOs57 locus 365:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 424
11 BOs57 locus 356:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 415
12 BOs57 locus 387:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAAAAAGT 446
13 BOs57 locus 370:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 429
14 BOs57 locus 362:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 421
25 BOs57 locus 378:TTAATGATCA TATTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 437
27 BOs57 locus 152:TTAATGATCA TACTATATCA TACAAGCACA CAACACTTTA TAGATATAAA GACAGAAAGT 211
                 ********** **.******* ********** ********** ********** **.*.*****

01 BOs57 locus 222:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTMTYGGA AATAATTTAA CTGTCAACC- 280
06 BOs57 locus 439:CCCTTAGTCA TAGAGCTTAA AATCTAAATG ATTTCTCTGA AATAATTTAA CTGTCAACGC 498
10 BOs57 locus 425:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTCAGAGA AATAATTTAA CTGTCAACCC 484
11 BOs57 locus 416:CCTTTATTCA TAGAGCTTAA AATTTAAATG ATTTCTCTGA AATAATTTAA CTGTCT-CCC 474
12 BOs57 locus 447:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTCTCTGA AATAATTTAA CTGTCAACCC 506
13 BOs57 locus 430:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTTTCTGA AATAATTTAA CTGTCAACCC 489
14 BOs57 locus 422:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTCTCTGA AATAATTTAA CTGTCAACC- 480
25 BOs57 locus 438:CCTTTAGTCA TAGAGCTTAA AATCTAAATT ATTTCTCTGA AATAATTTAA CTGTCAACCC 497
27 BOs57 locus 212:CCTTTAGTCA TAGAGCTTAA A-TCTAAATT ATTTCTCTGA AATTATTTAA CTGTCAACCC 270
                 **.***.*** ********** *.*.*****. ****....** ***.****** *****..*..

01 BOs57 locus 281:TTTCGTATTT G                                                 291
06 BOs57 locus 499:TTTCGTATT                                                    507
10 BOs57 locus 485:TTTCGTATTT G                                                 495
11 BOs57 locus 475:TTTCATATTT G                                                 485
12 BOs57 locus 507:TTTCGTATTT G                                                 517
13 BOs57 locus 490:TTTCGTATT                                                    498
14 BOs57 locus 481:TTTCGTATTT G                                                 491
25 BOs57 locus 498:TTTCGTATTT G                                                 508
27 BOs57 locus 271:TTTCGTATTT G                                                 281
                 ****.****. .
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Supplemental Figure 5-39. Sequence alignment of BOs57 locus. GenBank accession numbers are AB24293–AB249301.

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01 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
02 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGCTGTAAGTAGCAGGTTTCAAGTGA 60
06 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGTTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
09 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCGAGCTCCCATGGTCTTGTAAGTAGCAGGTTTCAAGTGA 60
10 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCTATGGTCTTGTAAGTAGTAGGTTACAAGTGA 60
11 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGATGTTGTAAGTAGCAGATTTCATGTGA 60
14 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGATTTCAAGTGA 60
15 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
17 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGNTGCCATGGTGTTGTAAGTAGCGGGTTTCAAGTGA 60
18 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
19 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGTCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
20 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGTCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
21 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
22 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAAGCTTCAAGTGA 60
23 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
24 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTAGCAGGTTTCAAGTGA 60
25 BKs11 locus    1:-GGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTGGTAAGTAGCAKGTTTCAWGTGA 59
26 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCACGGTGTNGTAAGTAGCAGGTTTCCAGTGA 60
27 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGATGCCATGGTGTTGTAAGTATCAGGTTTCA-GTGA 59
28 BKs11 locus    1:TGGAAAATGTGGTGCAGTAACCAAGCTGCCATGGTGTTGTAAGTATCAGGTTTCA-GTGA 59
                  .********************.**.*...*.*.*...*******......*.*..****

01 BKs11 locus   61:TTCACAATTTTTTTT--ATAGTTTTGTAATT----------------------------- 89
02 BKs11 locus   61:TTCACAATTTTTTTTT-ATAGTTTTGTAATT----------------------------- 90
06 BKs11 locus   61:TTCACAATTTTTTTT--ATAGCTTTGTAATT----------------------------- 89
09 BKs11 locus   61:TTCACAATTTTTTTTTTATAGTTTTGTAATTAAGTGTTATATTTTTGGTGGCAGCCAGTT 120
10 BKs11 locus   61:TTCACAATTTTTTTTT-ATAGTTTTGTAATT----------------------------- 90
11 BKs11 locus   61:TTCACAATTTTTTTT--ATAATTTTGTAATT----------------------------- 89
14 BKs11 locus   61:TTCACAATTTTTTTTT-ATAGTTTTGTAATT----------------------------- 90
15 BKs11 locus   61:TTCACAATTTTTTTT--ATAGTTTTGTAATT----------------------------- 89
17 BKs11 locus   61:GTCACAATTTTTTTTTTATAGTTTTGTAATT----------------------------- 91
18 BKs11 locus   61:GTCACAATTTTTTTTT-ATAGTTTTGTAATT----------------------------- 90
19 BKs11 locus   61:GTCACAATTTTTTTTTTATAGTTTTGTAATT----------------------------- 91
20 BKs11 locus   61:GTCACAATTTTTTTTTTATAGTTTTGTAATT----------------------------- 91
21 BKs11 locus   61:GTCACAATTTTTTTTTTATAGTTTTGTAATC----------------------------- 91
22 BKs11 locus   61:GTCACAATTTTTTTG--TTTGTTTTGTAATT----------------------------- 89
23 BKs11 locus   61:GTCACAATTTTTTTTTATAGTTTTGTAATG----------------------------- 91
24 BKs11 locus   61:TTCACAATTTTTTTT--ATAGTTTTGTAATT----------------------------- 89
25 BKs11 locus   60:TTCACAATTTTTTGTT-ATAGTTTTGTAATT----------------------------- 89
26 BKs11 locus   61:TTCACAATTTTTTGTT-ATAGTTTTGTAATT----------------------------- 90
27 BKs11 locus   60:TTCACAAAAAATGTA--ATAG--------------------------------------- 78
28 BKs11 locus   60:TTCACAAAAAAATTA--ATAG--------------------------------------- 78
                  .******......... .*............

01 BKs11 locus   89:------------------------------------------------------------ 89
02 BKs11 locus   90:------------------------------------------------------------ 90
06 BKs11 locus   89:------------------------------------------------------------ 89
09 BKs11 locus  121:TAGGAAGAAATCACT---------->1kb fragment----------CCATTTTATTTAC 1740
10 BKs11 locus   90:------------------------------------------------------------ 90
11 BKs11 locus   89:------------------------------------------------------------ 89
14 BKs11 locus   90:------------------------------------------------------------ 90
15 BKs11 locus   89:------------------------------------------------------------ 89
17 BKs11 locus   91:------------------------------------------------------------ 91
18 BKs11 locus   90:------------------------------------------------------------ 90
19 BKs11 locus   91:------------------------------------------------------------ 91
20 BKs11 locus   91:------------------------------------------------------------ 91
21 BKs11 locus   91:------------------------------------------------------------ 91
22 BKs11 locus   89:------------------------------------------------------------ 89
23 BKs11 locus   91:------------------------------------------------------------ 91
24 BKs11 locus   89:------------------------------------------------------------ 89
25 BKs11 locus   89:------------------------------------------------------------ 89
26 BKs11 locus   90:------------------------------------------------------------ 90
27 BKs11 locus   78:------------------------------------------------------------ 78
28 BKs11 locus   78:------------------------------------------------------------ 78


01 BKs11 locus   89:------------------------------------------------------------ 89
```

```
02 BKs11 locus   90:------------------------------------------------------------ 90
06 BKs11 locus   90:----------AAGAAATTAGGGTGGGAGGGATAACTCAGTGGTTTGAGCATTAGCCTACT 139
09 BKs11 locus 1741:ACACAACATTAAGAAATTAGGGTGGGAGGGCTAGCTCAGTGGTTTGCACATTAGCTTGCT 1800
10 BKs11 locus   91:----------AAGAAATTAGGGTGGGAGGAATTGCTCAGCGGTTTGAGCATTAGCTTGCT 140
11 BKs11 locus   90:----------AAGAAATTAGGGGCGCA-----------------------TTGGCCTGCT 116
14 BKs11 locus   90:------------------------------------------------------------ 90
15 BKs11 locus   89:------------------------------------------------------------ 89
17 BKs11 locus   91:------------------------------------------------------------ 91
18 BKs11 locus   90:------------------------------------------------------------ 90
19 BKs11 locus   91:------------------------------------------------------------ 91
20 BKs11 locus   91:------------------------------------------------------------ 91
21 BKs11 locus   91:------------------------------------------------------------ 91
22 BKs11 locus   89:------------------------------------------------------------ 89
23 BKs11 locus   91:------------------------------------------------------------ 91
24 BKs11 locus   89:------------------------------------------------------------ 89
25 BKs11 locus   89:------------------------------------------------------------ 89
26 BKs11 locus   90:------------------------------------------------------------ 90
27 BKs11 locus   78:------------------------------------------------------------ 78
28 BKs11 locus   78:------------------------------------------------------------ 78


01 BKs11 locus   89:------------------------------------------------------------ 89
02 BKs11 locus   90:------------------------------------------------------------ 90
06 BKs11 locus  140:ATAAACCCAGGGTTGTAAATTCAATCCTTGAGAGTACTACTTAAGGATCTGTCAAGGGAT 199
09 BKs11 locus 1801:A--AACCCAGGATTGTGAGTTCAATCCTTGAGAGGGCCACTTAGGGATCTGTCAAGGGAT 1858
10 BKs11 locus  141:A--AACCCAGGATTGTGAGTTCAATCCCTGAGATGGCCACTTAGGGATCTGTCAAGGGAT 198
11 BKs11 locus  117:A--AACCCAGTGTTGTAAATTCAATCCTTGAGGGGGCCACTTA------------GGGAT 162
14 BKs11 locus   90:------------------------------------------------------------ 90
15 BKs11 locus   89:------------------------------------------------------------ 89
17 BKs11 locus   91:------------------------------------------------------------ 91
18 BKs11 locus   90:------------------------------------------------------------ 90
19 BKs11 locus   91:------------------------------------------------------------ 91
20 BKs11 locus   91:------------------------------------------------------------ 91
21 BKs11 locus   91:------------------------------------------------------------ 91
22 BKs11 locus   89:------------------------------------------------------------ 89
23 BKs11 locus   91:------------------------------------------------------------ 91
24 BKs11 locus   89:------------------------------------------------------------ 89
25 BKs11 locus   89:------------------------------------------------------------ 89
26 BKs11 locus   90:------------------------------------------------------------ 90
27 BKs11 locus   78:------------------------------------------------------------ 78
28 BKs11 locus   78:------------------------------------------------------------ 78


01 BKs11 locus   89:------------------------------------------------------------ 89
02 BKs11 locus   90:------------------------------------------------------------ 90
06 BKs11 locus  200:CTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTTGAG 259
09 BKs11 locus 1859:CTGGGGCAAAAATTGGTCCTGCTAATGAAGGCAGGGGGCTGGACTCAATGACCTTTTGAG 1918
10 BKs11 locus  199:CTGGGGCAAAAATTGGTCCTGCTAATGAAGGCAGGGGGC-------------CTTTTGAG 245
11 BKs11 locus  163:CTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGATGGACTCAACAATCTTTTGAG 222
14 BKs11 locus   90:------------------------------------------------------------ 90
15 BKs11 locus   89:------------------------------------------------------------ 89
17 BKs11 locus   91:------------------------------------------------------------ 91
18 BKs11 locus   90:------------------------------------------------------------ 90
19 BKs11 locus   91:------------------------------------------------------------ 91
20 BKs11 locus   91:------------------------------------------------------------ 91
21 BKs11 locus   91:------------------------------------------------------------ 91
22 BKs11 locus   89:------------------------------------------------------------ 89
23 BKs11 locus   91:------------------------------------------------------------ 91
24 BKs11 locus   89:------------------------------------------------------------ 89
25 BKs11 locus   89:------------------------------------------------------------ 89
26 BKs11 locus   90:------------------------------------------------------------ 90
27 BKs11 locus   78:------------------------------------------------------------ 78
28 BKs11 locus   78:------------------------------------------------------------ 78


01 BKs11 locus   90:----------------------------------------------AAGAAAAGTATTTT 103
02 BKs11 locus   91:----------------------------------------------AAGCAAAGTATTTT 104
```

```
06 BKs11 locus  260:GTCCCTTTCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTATAAGAAAACTATTTT 319
09 BKs11 locus 1919:GTCCCTTCCTGTTCTAGGAGATTGGTATATCTCCAATTATTATTATAAGAAAACTATTTT 1978
10 BKs11 locus  246:GTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTATAAGCAAACTATTTT 305
11 BKs11 locus  223:GTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTATAAGAAAACTATTTT 282
14 BKs11 locus   91:----------------------------------------------AAGAAAACTATTTT 104
15 BKs11 locus   90:----------------------------------------------AAGAAAACTATTTT 103
17 BKs11 locus   92:----------------------------------------------AAGAAAACTATTTT 105
18 BKs11 locus   91:----------------------------------------------AAGAAAACTATTTT 104
19 BKs11 locus   92:----------------------------------------------AAGAAAACTATTTT 105
20 BKs11 locus   92:----------------------------------------------AAGAAAACTATTTT 105
21 BKs11 locus   92:----------------------------------------------AAGAAAACTATTTT 105
22 BKs11 locus   90:----------------------------------------------AAGAAAACTA---- 99
23 BKs11 locus   92:----------------------------------------------AAGAAAACTATTTT 105
24 BKs11 locus   90:----------------------------------------------AAGAAAATTATTTT 103
25 BKs11 locus   90:----------------------------------------------AAGAAAACTATTTT 103
26 BKs11 locus   91:----------------------------------------------AAGAAAACTATTTT 104
27 BKs11 locus   79:-------------------------------------------------------TTTT 82
28 BKs11 locus   79:-------------------------------------------------------TTTT 82
                                                        ..............

01 BKs11 locus  104:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAGAGACTTGAGGTGGATGAAAAAACATTA 163
02 BKs11 locus  105:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAGAGACTTGAGGTGGATGAAAAAACATTA 164
06 BKs11 locus  320:CTTCAAAAATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 379
09 BKs11 locus 1979:CTTCAAAAATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 2038
10 BKs11 locus  306:CTTCAAAAAGAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 365
11 BKs11 locus  283:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 342
14 BKs11 locus  105:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 164
15 BKs11 locus  104:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 163
17 BKs11 locus  106:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 165
18 BKs11 locus  105:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 164
19 BKs11 locus  106:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 165
20 BKs11 locus  106:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 165
21 BKs11 locus  106:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 165
22 BKs11 locus  100:-------TATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 152
23 BKs11 locus  106:CTTCAAATATAGCTGGTGCGTGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 165
24 BKs11 locus  104:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 163
25 BKs11 locus  104:CWTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 163
26 BKs11 locus  105:CTTCAAATATAGCTGGTGCATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 164
27 BKs11 locus   83:CTTCAAATATAGCTGGTGCATAAATTTACAAAAAGACTTGAGGTGGATGAAAAAACATTA 142
28 BKs11 locus   83:CTTCAAATATAGCTGGTG-ATGAGTTTTCAAAAAGACTTGAGGTGGATGAAAAAACATTA 141
                  ........*.********..*.*.***.****.***************************

01 BKs11 locus  164:G                                                    164
02 BKs11 locus  165:G                                                    165
06 BKs11 locus  380:G                                                    380
09 BKs11 locus 2039:G                                                    2039
10 BKs11 locus  366:G                                                    366
11 BKs11 locus  343:G                                                    343
14 BKs11 locus  165:G                                                    165
15 BKs11 locus  164:G                                                    164
17 BKs11 locus  166:G                                                    166
18 BKs11 locus  165:G                                                    165
19 BKs11 locus  166:G                                                    166
20 BKs11 locus  166:G                                                    166
21 BKs11 locus  166:G                                                    166
22 BKs11 locus  153:G                                                    153
23 BKs11 locus  166:G                                                    166
24 BKs11 locus  164:G                                                    164
25 BKs11 locus  164:G                                                    164
26 BKs11 locus  165:G                                                    165
27 BKs11 locus  143:G                                                    143
28 BKs11 locus  142:G                                                    142
                 *
```

Supplemental Figure 5-40. Sequence alignment of BKs11 locus. GenBank accession numbers are AB24302–AB249315 and AB125709-AB125714.

```
01 BKs85 locus   1:TCCCCAACTGCAGATTTAATGCTGATGCTAATTAGATGTACTCTGAAGACAAACCATCCT 60
06 BKs85 locus   1:TCCCCAACTGCAGATTTAATATTTATGCTAATTAGATGAACTCTGAAGACAAACCATCCT 60
11 BKs85 locus   1:-CCCCAACTGCAGATTTAATATTGATGCTAATTAGATGTACTCTGAAGACAAACCATCCT 59
14 BKs85 locus   1:-CCCCAACTGCAGATTTAATACTGATGCTAATTAGATGTACTCTGAAGACAAACCATCCT 59
15 BKs85 locus   1:TCCCCAACTGCAGATTTAATATTGATGCTAATTAGATGTACTCTGAAGACAAACCATCCT 60
                 .******************..*.**************.********************

01 BKs85 locus  61:TCTGAACAACA------------------------------------------------ 71
06 BKs85 locus  61:TCTGAACAACAGAAGGGAGGAGGGCTAGCTCAGCTGGGGGAGGGATAGCTCAATGGTTTG 120
11 BKs85 locus  60:TCTGAACAACAGAAAGGAGGAGGGATAGCTCAG--------------------TGGTTTG 99
14 BKs85 locus  60:TCTAAACCACA------------------------------------------------ 70
15 BKs85 locus  61:TCTAAACCACA------------------------------------------------ 71
                ***.***.***

01 BKs85 locus  71:------------------------------------------------------------ 71
06 BKs85 locus 121:AGCATTGGCCTGCTAAACCCATGGTTATGAGTTCAATCATTTAGGGGGC----------- 169
11 BKs85 locus 100:AGCATTGGCCTCCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGAT 159
14 BKs85 locus  70:------------------------------------------------------------ 70
15 BKs85 locus  71:------------------------------------------------------------ 71


01 BKs85 locus  71:------------------------------------------------------------ 71
06 BKs85 locus 170:-TGGGGCAAAAATTGGT--CCTGCTAGTGAAGGCAGCAGGCTGGACTTGATGACC--TTT 224
11 BKs85 locus 160:CTGGG-CAAAAGTTGGTGTCCTGCTAGTGAAGGCAGGGGGCTGGACGTGATGACCCTTTT 218
14 BKs85 locus  70:------------------------------------------------------------ 70
15 BKs85 locus  71:------------------------------------------------------------ 71


01 BKs85 locus  72:-----------------------------------------------------------C 72
06 BKs85 locus 225:CAAGGTTCCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTACTACCTTTTATTATTAC 284
11 BKs85 locus 219:CAAGGTCCCTTCCAGTTCTAGGAGATTGGTATATCTCCAA------CCTTTTATTATTAC 272
14 BKs85 locus  71:-----------------------------------------------------------C 71
15 BKs85 locus  72:-----------------------------------------------------------C 72
                                                                 *

01 BKs85 locus  73:TTACAGTTTATATCTCCATTAACTTGAGGTTGCAGTATTTATGGAGCCAATAGCCCTTTG 132
06 BKs85 locus 285:TTACAGTTTGTATCTCCATTAACTTGAGGTCACAGTATTTATGCAGCCAATAGCCCTTCA 344
11 BKs85 locus 273:TTACAGTTTGTATCTCCATTAACTTGAGGTCACAGTCTTTATGCAGCCAATAGCCCTTCA 332
14 BKs85 locus  72:TTACAGTTTGTATCTCCATTAACTTAAGGTCGTAGTATTTATGCAGCCAATAGCCCTTCG 131
15 BKs85 locus  73:TTACAGTTTGTATCTCCATTAACTTGAGGTCGCAGTATTTATGCAGCCAATAGCCCTTCG 132
                *********.***************.****...***.******.**************..

01 BKs85 locus 133:TACTAAATTTACTTCAGTAGGAGG-TCTGAGTTTGGGATCAGCAATCTC--GTTTCCCTC 189
06 BKs85 locus 345:TACTAAATTTACTTCAATAGGAGG-TCTGAGTTTGGGATCAGCAATCTCAAGTTTCCCTC 403
11 BKs85 locus 333:TACTAAATTTACTTCAATAGGGGGGTCTGAGTTTGGGATCAGCAATCTCAAGTTTCCCTC 392
14 BKs85 locus 132:TACTAAATTTACTTCAATAGGGGG-TCTGAGTTTGGCATCAGCAATCTCCAGTTACCCTC 190
15 BKs85 locus 133:TACTAAATTTACTTCAATAGGGGG-TCTGAGTTTGGCATCAGCAATCTCCAGTTACCCTC 191
                ****************.****.** ***********.************ .***.*****

01 BKs85 locus 190:ACTGCAGTTTGTTGAGGAGAAAGCAGATCTTCAGCCCTTTTTCTG              234
06 BKs85 locus 404:CCTGGGGTTTGTTGAGCAGAAAGCAGATCTTCAGCCCTTTTTCTG              448
11 BKs85 locus 393:ACTGGGGTTTGTTGAGCAGAAAGCAGATCTTCAGCCCTTTTTCTG              437
14 BKs85 locus 191:ACTGGGGTTTGTTGAGCAGAAAGCAGATCTTCAGCCCTTTTTCTG              235
15 BKs85 locus 192:ACTGGGGTTTGTTGAGCAGAAAGCAGATCTTCAGCCCTTTTTCTG              236
                .***..**********.***************************
```

Supplemental Figure 5-41. Sequence alignment of BKs85 locus. GenBank accession numbers are AB24316–AB249320.

```
01 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTTTCTAGATTTACGTCATTCATTGAAGAGCTATAAA-- 58
02 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTTAAAAGCTATAAAAA 60
06 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTGAAGAGCTCTAA--- 57
11 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTGAAGAGCTCTAA--- 57
14 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTGAAGAGCTCTAA--- 57
20 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTGAAGAGCTCTAA--- 57
27 TTh23 locus   1:AAACAGCTCTTTCAAATTTTCCTCTCTAGATTTAAGTCATTCATTGAAGAGCTCTAA--- 57
                 **********************.**********.**********.**.****.***

01 TTh23 locus  59:GTCACCACAGAT-TTAAAAAAAA-GGTATATTAGTAAAAGAATGACTGATTTTTTGGAAA 116
02 TTh23 locus  61:GTCACCACAGAT-TTTAAAAAAA-GGTCTATTAGTAAAAGAATGACTGATTTCTTGGAAA 118
06 TTh23 locus  58:GTCACCACAGAT-TTTAAAAAAA-GGTATATTAGTAAAAGAATGACTGATTTTTTGGAAA 115
11 TTh23 locus  58:GTCATCACAGAT-TTTAAAAA--GGGTATATTAGTAAAAGAATGGCTGATTTTTTGGAAA 114
14 TTh23 locus  58:GTCACCACAGAT-TTTAAAAAA-GGGTATATTAGTAAAAGAATGACAGATTTTTTGGAAA 115
20 TTh23 locus  58:GTCACTACAGAT-TTTAAAGAA-GGGTATATTAGTAAAAGAATGACTGATTTTTTGGAAA 115
27 TTh23 locus  58:GTCACCACAGATGTTTAAAAAAAGGGTATATTAGTAAAGAAATGACTGATTTTTTTGAAA 117
                ****..****** **.***.*...***.**********..****.*.*****.**.****

01 TTh23 locus 117:TGGGGGCTGTTGGAATCTTGGGGAGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCT 176
02 TTh23 locus 119:TGGGGGCTATTGGAATCTTGGGGAGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCT 178
06 TTh23 locus 116:TGGGGGCTGTTGGAACCTTGGGGAGGAGGGATAGCTCAGTGGTTTGAGCACTGGCCTGCT 175
11 TTh23 locus 115:TGGGGGCTGTTGGAACCTT---------------------------------------- 133
14 TTh23 locus 116:TGGGTGCTGTTGGAACCTT---------------------------------------- 134
20 TTh23 locus 116:TGGGGGCTGTTGGAACCTT---------------------------------------- 134
27 TTh23 locus 118:TGGGGGCTGTTGGAACCTT---------------------------------------- 136
                ****.***.******.***

01 TTh23 locus 177:AAATCCAGGGCAGTGAGTTCAATCCTTGAGGGAGCCACTTAGGGATCTGGGGCAAAAATT 236
02 TTh23 locus 179:AAATCCAGGGCAGTGAGTTCAATCCTTGGTGGG-CCACTTAGGGATCTGGGACAAAAATT 237
06 TTh23 locus 176:AAACCCAGGGATGTGA-TTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATT 234
11 TTh23 locus 133:------------------------------------------------------------ 133
14 TTh23 locus 134:------------------------------------------------------------ 134
20 TTh23 locus 134:------------------------------------------------------------ 134
27 TTh23 locus 136:------------------------------------------------------------ 136

01 TTh23 locus 237:GGTCCTGCTAGTGAAGGCAGGG------------TGTCCTTTCAAGGTCCCTTCCAGTTC 284
02 TTh23 locus 238:GGTCCTGCTAGTGAAGGCACGGGGCTGGACTCGATGACCTTTCAAGGTCCCTTCCAGTTC 297
06 TTh23 locus 235:GGTCCTGCTAGTGAAGGTAGGGGGCTGGACTCAATGACCTGTCAAGGCCCCCTCCAGTTT 294
11 TTh23 locus 133:------------------------------------------------------------ 133
14 TTh23 locus 134:------------------------------------------------------------ 134
20 TTh23 locus 134:------------------------------------------------------------ 134
27 TTh23 locus 136:------------------------------------------------------------ 136

01 TTh23 locus 285:TAGGAGACTGGTATATCTGCAATTATTTCTTCTTTTCTTATTTCTATTT---ATCTTTTA 341
02 TTh23 locus 298:TAGGAGATAGGTATATCTCCAATTATTTCTTCTTTTCTTATTTCTGTTT---ATCTTTTA 354
06 TTh23 locus 295:TAGGAGATATACCTATCTCCAATTATTTCTTCTTTTCTTATTTCTATTTCTTATCTTTTA 354
11 TTh23 locus 134:-----------------------------------------------------ATCTTTTA 141
14 TTh23 locus 135:-----------------------------------------------------ATCTTTTA 142
20 TTh23 locus 135:-----------------------------------------------------ATCTTTTA 142
27 TTh23 locus 137:-----------------------------------------------------AT---TTA 141
                                                          **...***

01 TTh23 locus 342:TGTTTCTTGAGTTGGCAATTTAATTGCATTAACAAGGGTTATTTCTTCTTATATTTTTCT 401
02 TTh23 locus 355:TGTTTCTTGAGTTGGCAATTTAACTGCATTAACAAGGGTTATTTCCTATTATATTTTTCT 414
06 TTh23 locus 355:TGTTTCTTGAGCTGGCAATTTAACTGCATTAACAAGGGTTATTTCCCATTATATTTTTCT 414
11 TTh23 locus 142:TGTTTCTTGAGTTGGCAATTTAACTGCATTAACAAGGATTATTTCCCATTATATTTTTCT 201
14 TTh23 locus 143:CGTTTCTTGAGTTGGCAATTTAACTGCATTAACAAGGGTTATTTCCCATTATATTTTTCT 202
20 TTh23 locus 143:TGTTTCTTGAGTTGGCAATTTAACTGCAT-AACAAGGGTTATTTCCCATTATATTTTTCT 201
27 TTh23 locus 142:TGTTTCTTGATTTGGCAATTTAACTGCATAAACAAGGGTTATTTCCCATTATATTTTTCT 201
                 .*********..***********.*****.*******.*******...************

01 TTh23 locus 402:TTGTCTAAACGTAACATTAGCATTCAAAGGGTCCTAATT                  440
02 TTh23 locus 415:TTGTCTAAACTTAACATTAGCATTCAAATGGTCCTA                    450
06 TTh23 locus 415:TTGTCTAAACTTAATATTAGCATTCAAATGGTCCTAATTAA                455
11 TTh23 locus 202:TTGTCTAAACTTAACATTAGCATTCAAGTGGTCCTAATTAA                242
```

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14 TTh23 locus 203:TTGTCTAAACTTAACATTAGCATTCAAATGGTCCTAATTAA                 243
20 TTh23 locus 202:TTGTCTAAACTTAACATTAGCATTCAAATGGTCCTAATTAA                 242
27 TTh23 locus 202:TTGTCCAAACTTAACATTAGCATTCAAATGGTCCTAATTAA                 242
                *****.****.***.************..*******...
```

Supplemental Figure 5-42. Sequence alignment of TTh23 locus. GenBank accession numbers are AB24321–AB249326 and AB125509.

```
02 BKs31 locus   1:GTGCATTTTACACATGGGTAACTAATAAGCAGTAATCAAACAGGATATATAGATGTCAGC 60
06 BKs31 locus   1:GTGCATTTTACACATGGGTAATTA-TAAGCAGTAGTCAAACAGGATATATAGATGTCAGC 59
10 BKs31 locus   1:GTGCATTTTACACATGGGTAATTAATAAGCAGTAGTCAAACTGGATATATAGATGTCAGC 60
11 BKs31 locus   1:GTGCATTTTACACATGGGTAATTAATAAGCAGTAGTCAAACAGGATATATAGATATCAGC 60
14 BKs31 locus   1:GTGCATTTTACACATGGGTAATTAATAAGCAGTAGTCAAACAGGATATATANATGTCAGC 60
15 BKs31 locus   1:GTGCATTTTACACATGGGTAATTAATAAGCAGTAGTCAAACAGGATATATAGATGTCAGC 60
17 BKs31 locus   1:GTGCATTTTACACATGGGTAATTAATAAGCAGTAGTCAAACAGGATATATAGATGTCAGC 60
19 BKs31 locus   1:GTGCATTTTACACATGGGTAATGAATAAGCAGTAGTCAAACAGGATATATAGATGTCAGC 60
20 BKs31 locus   1:GTGCATTTTACACATGGGTAATGAATAAGCAGTAGTCAAACAGGATATATAGATGTCAGC 60
                 *********************..*.*********.******.*********.**.*****

02 BKs31 locus  61:AATACTGCTGTCCCCACAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
06 BKs31 locus  60:AATACTGCTGTCCCCATAGCTACATCTGCAGAATAGGTCTGGACTAATGTGTAATGTTTG 119
10 BKs31 locus  61:AATACTGCTGTCCCCACAGCTGTATCTGCAGAATAGGTCTGGACTAATGTGTAATGTTTT 120
11 BKs31 locus  61:AATACTGCTATCCCCACAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
14 BKs31 locus  61:AATACTGCTGTCCCCACAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
15 BKs31 locus  61:AATACTGCTGTCCCCACAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
17 BKs31 locus  61:AATACTGCTGTGCCCTCAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
19 BKs31 locus  61:AATACTGCTGTCCCCTCAGCTGCATCTGCAGAAGACGTCTGGACTAATGTGTAATGTTTT 120
20 BKs31 locus  61:AATACTGCTGTCCCCTCAGCTGCATCTGCAGAAGAGGTCTGGACTAATGTGTAATGTTTT 120
                *********.*.***..****..**********.*.**********************.

02 BKs31 locus 121:GGGAAAGTACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
06 BKs31 locus 120:GGGAAAGCACTTTGTTCAGTATAGGTACATCTTGAAGAGGAGGGAGGGATAGCTCAGTGG 179
10 BKs31 locus 121:GGGAAAGCACTTTGTTGAGTATAGGTACATCTTGAAGA---------------------- 158
11 BKs31 locus 121:GGGAAAGCACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
14 BKs31 locus 121:GGGAAAGCACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
15 BKs31 locus 121:GGGAAAGCACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
17 BKs31 locus 121:GGGAAAGTATTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
19 BKs31 locus 121:GGGAAAGTACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
20 BKs31 locus 121:GGGAAAGTACTTTGTTCAGTATAGGTACATCTTGAAGA---------------------- 158
                *******.*.******.********************

02 BKs31 locus 158:------------------------------------------------------------ 158
06 BKs31 locus 180:TTTGAGCGTTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGAGCCACTTAG 239
10 BKs31 locus 158:------------------------------------------------------------ 158
11 BKs31 locus 158:------------------------------------------------------------ 158
14 BKs31 locus 158:------------------------------------------------------------ 158
15 BKs31 locus 158:------------------------------------------------------------ 158
17 BKs31 locus 158:------------------------------------------------------------ 158
19 BKs31 locus 158:------------------------------------------------------------ 158
20 BKs31 locus 158:------------------------------------------------------------ 158


02 BKs31 locus 158:------------------------------------------------------------ 158
06 BKs31 locus 240:GAATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTTGATGACCTTT 299
10 BKs31 locus 158:------------------------------------------------------------ 158
11 BKs31 locus 158:------------------------------------------------------------ 158
14 BKs31 locus 158:------------------------------------------------------------ 158
15 BKs31 locus 158:------------------------------------------------------------ 158
17 BKs31 locus 158:------------------------------------------------------------ 158
19 BKs31 locus 158:------------------------------------------------------------ 158
20 BKs31 locus 158:------------------------------------------------------------ 158


02 BKs31 locus 159:-------------------------------------------------------GCAC 162
06 BKs31 locus 300:CAAGGTCCCCTCCAGTTCTAGGAGATAGGTATATCTCCCATTATTACCTTTTATTAGCAC 359
10 BKs31 locus 159:-------------------------------------------------------GCAC 162
11 BKs31 locus 159:-------------------------------------------------------GCAC 162
14 BKs31 locus 159:-------------------------------------------------------GCAC 162
15 BKs31 locus 159:-------------------------------------------------------GTAC 162
17 BKs31 locus 159:-------------------------------------------------------ACAC 162
19 BKs31 locus 159:-------------------------------------------------------ACAC 162
20 BKs31 locus 159:-------------------------------------------------------ACAC 162
                                                                     ..**

02 BKs31 locus 163:CAAGTTGCTTGTGCTGTAGTGGAGTGAGCTTTCACACCATCCAGGGGAGGAATATGCACT 222
```

```
06 BKs31 locus 360:CAAGTTGCTTGTGCTGTAGTGGAGTGGGCTCTCACACCATCCAGGGGAGGAATATGCAAT 419
10 BKs31 locus 163:CAAGTTGCTTGTGCTGTAGTGGAGTGGGCTCTCACACCATGCAGGGGAGGAATATGCACT 222
11 BKs31 locus 163:CAAGTTGCTTGTGCTGTAGTGGAGTGGTCTCTCACACCATCCAGGTGAGGAATATGCATT 222
14 BKs31 locus 163:CAAGTTGCTTGTGCTGTANTGGAGTGTGCTCTCACACCATCCAGGGGAGGAATATGCACT 222
15 BKs31 locus 163:CAAGTTGCTTGTGCTGTAGTGGAGTGGGCTCTCACACCATCCAGGGGAGGAATATGCACT 222
17 BKs31 locus 163:CAAGTTGCTTGTGCTGTAGTGGAGAGGGCTCTCACACCATCTAGGGGAGGAATATGCACT 222
19 BKs31 locus 163:CAAGTTGCTAGTGCTGTAGTGGAGTGGGCTCTCACACCATCCAGGGGAGGAATATGCACT 222
20 BKs31 locus 163:CAAGTTGCTAGTGCTGTAGTGGAGTGGGCTCTYACACCATCCAGGGGAGGAATATGCACT 222
                 *********.********.*****.*..**.*.*******..***.************.*

02 BKs31 locus 223:AGCTGATAAAGAATGATACAGTTAGAGG------------GTATCTGAGCAGAAAACGCT 270
06 BKs31 locus 420:AGCTGATAAAGAATGATCCAGTTGGAGA------------GTATCTGAGCAGAAAATGGT 467
10 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGGAGG------------GTATCTGAGCAGAAAACGGT 270
11 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGCAGGTCCACTTAAAGGGTATCTGAGCAGAAAACGGT 282
14 BKs31 locus 223:ANCTGATAAAGAATGATCCAGTTGGAGGTCCACTTAGAGGGTATCTGAGCAGAAAACGGT 282
15 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGGAGGTCCTCTTAGAGGGTATCTGAGCAGAAAACGGT 282
17 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGGAGGTCCACTTAGAGGGTATCTGAGCAGAAAGCGGT 282
19 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGGAGGTCCACTTAGAGGGTATCTGAGCAGAAAACGGT 282
20 BKs31 locus 223:AGCTGATAAAGAATGATCCAGTTGGAGGTCCACTTAGAGGGTATCTGAGCAGAAAACGGT 282
                 *.***************.*****..**.............***************..*.*

02 BKs31 locus 271:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          302
06 BKs31 locus 468:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          499
10 BKs31 locus 271:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          302
11 BKs31 locus 283:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
14 BKs31 locus 283:NGNCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
15 BKs31 locus 283:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
17 BKs31 locus 283:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
19 BKs31 locus 283:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
20 BKs31 locus 283:TGTCCTTTTGATTGTGCCACTAAAGGAACAAA                          314
                 .*.****************************
```

Supplemental Figure 5-43. Sequence alignment of BKs31 locus. GenBank accession numbers are AB24327–AB249331 and AB125722-AB125725.

```
01 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTGCATTGCTCTTACCATT 60
06 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTATCATT 60
12 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTACCATT 60
13 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTACCATT 60
14 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTACCATT 60
17 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTACCATT 60
19 BOs33 locus   1:TTTTCAGATTTATTTGGGGGCTGATGCCCTTTCTTTGCATCCTTCATTGCTCTTACCATT 60
                 ******************************************.***********.****

01 BOs33 locus  61:TGTGTATAATGGTCAAGCTTTCTTGAGCAGTTTGCTTGACCGGGTACTCATCTCTTGTGT 120
06 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTCGAGCAATTTGCTTGACTGGATACTCATCTCTTGTAT 120
12 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTCGAGCAGTTTGCTTGACTGGGTACTCATCTCTTGTGT 120
13 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTCGAGCAGTTTGCTTGACTGGGTACTCATCTCTTGTGT 120
14 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTCGAGCAGTTTGCTTGACTGGGTACTCATCTCTTGTGT 120
17 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTCGAGCAGTTTGCTTGACTGGGTACTCATCTCTTGTGT 120
19 BOs33 locus  61:CGTGTATAATGGTCAAGCTTTCTTGAGCAGTTTGCTTGACTGGGTACTCATCTCTTGTGT 120
                 .*********************.*****.**********.**.**************.*

01 BOs33 locus 121:TTTTACTAG-------------------------------------------------- 129
06 BOs33 locus 121:TTTTATTAG-------------------------------------------------- 129
12 BOs33 locus 121:TTTTACTAGATTGCTTGGGGGGAGGGGTAGCTCAGTGRTTTGAGTATTGGCCTGCTAAAC 180
13 BOs33 locus 121:TTTTACTAG-------------------------------------------------- 129
14 BOs33 locus 121:TTTTACTAG-------------------------------------------------- 129
17 BOs33 locus 121:TTTTACTAG-------------------------------------------------- 129
19 BOs33 locus 121:TTTTACTAG-------------------------------------------------- 129
                 *****.***

01 BOs33 locus 129:------------------------------------------------------------ 129
06 BOs33 locus 129:------------------------------------------------------------ 129
12 BOs33 locus 181:CCAGAGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGAATCTGGGGCAAAAATTGGTC 240
13 BOs33 locus 129:------------------------------------------------------------ 129
14 BOs33 locus 129:------------------------------------------------------------ 129
17 BOs33 locus 129:------------------------------------------------------------ 129
19 BOs33 locus 129:------------------------------------------------------------ 129


01 BOs33 locus 129:------------------------------------------------------------ 129
06 BOs33 locus 129:------------------------------------------------------------ 129
12 BOs33 locus 241:CTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTTCAAGGTCCCTTCCAGTTCTAGG 300
13 BOs33 locus 129:------------------------------------------------------------ 129
14 BOs33 locus 129:------------------------------------------------------------ 129
17 BOs33 locus 129:------------------------------------------------------------ 129
19 BOs33 locus 129:------------------------------------------------------------ 129


01 BOs33 locus 130:---------------------------TTTTTCCACCCTAGAGAATATCTT--AAGATTT 160
06 BOs33 locus 130:---------------------------CTTTTCCACCCCAGAGAATATCTTTTAAGATTT 162
12 BOs33 locus 301:AGATTGGTATATCTCTAATTATTATTACCTTTCCACCCTAGAGAATATCTTTTAAGATTT 360
13 BOs33 locus 130:---------------------------TTTTTCCACCCTAGAGAATATCTTTTAAGATTT 162
14 BOs33 locus 130:---------------------------TTTTTCCACCCTAGAGAATATCTTTTAAGATTT 162
17 BOs33 locus 130:---------------------------TTTTTCCACCCTAGAGAATACCTTTTAAGATTT 162
19 BOs33 locus 130:---------------------------TTTTTCCACCCTAGAGAATACCTTTTAAGATTT 162
                                        ..*********.********.***..*******

01 BOs33 locus 161:TTTTCAGGGAGTTCAGGTAARTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
06 BOs33 locus 163:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
12 BOs33 locus 361:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 418
13 BOs33 locus 163:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
14 BOs33 locus 163:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
17 BOs33 locus 163:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
19 BOs33 locus 163:TT--CAGGGAGTTCAGGTAAGTAGTAGTAGAGGATCCAGGCAACATCATGTCTCCAAATA 220
                 **  ****************.****************************************

01 BOs33 locus 221:TCAGTCTAGATGTCATTTGTCTTCTGTGCTTCACTCACACCTGATGA            267
06 BOs33 locus 221:T-AGGCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATG             265
12 BOs33 locus 419:TCAGTCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATGA            465
13 BOs33 locus 221:TTAGTCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATGA            267
```

```
14 BOs33 locus 221:TCAATCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATGA            267
17 BOs33 locus 221:TCAGTCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATGA            267
19 BOs33 locus 221:TCAGTCTAGATGTCACTTGTCTTCTGTGCTTCACTCACACCTGATGA            267
                *.*..**********.******************************.
```

Supplemental Figure 5-44. Sequence alignment of BOs33 locus. GenBank accession numbers are AB24332–AB249338.

```
01 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTTT-AGAAGTGCAGAAACTTCTGACTTATTGTATTG 59
06 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTTC-AGAAGTGCAGAAACTTCTGACTTATTGTATTG 59
12 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTGT-AGAAGTGCAGAAACTTCTGACTTATTGTATTG 59
13 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTGT-AGAAGTGCAGAAACTTCTGACTTATTGTATTG 59
17 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTTTTAGAAGTGCAGAAACTTCTGACTTATTGTATTG 60
19 BOs52 locus   1:AGGTGAGAGGATGGAGAAAATCTCTTT-AGAAGTGCAGAAACTTCTGACTTATTATATTG 59
                 *************************.. *************************.*****

01 BOs52 locus  60:GTTATCTCTGTAATAACAAGTGTTCTGTGTATTATAAGAATAATAAGTTTTCTGTCTGGG 119
06 BOs52 locus  60:GTTATCTCTGTAATAACAAGTGTTCTGTGTATTATAAGAATAA---GTTTTCTGTCTGGG 116
12 BOs52 locus  60:GTTATCTCTGTAATAACAAGTGTTCTGTGTATTATAAGAATAATAAGTTTTCTGTCTGGG 119
13 BOs52 locus  60:GTTATCTCTGTAATAACAAGTGTTCTGTAT--TATAAGAATAAGAAGTTTTCTGTCTGGG 117
17 BOs52 locus  61:GTTATCTCTGTAATAACAAGTGTTCTGTGTATTATAAGAATAATAAGTTTTCTGTCTGGG 120
19 BOs52 locus  60:GTTATCTCTGTAATAACAAGTGCTCTGTGTATTATAAGAATAATAAGTTTTCCGTCTGGG 119
                 *********************.*****.*..***********...******.*******

01 BOs52 locus 120:GGCATGTCCTCAGGTGGCATCTTC--CTTAGCA--------------------------- 150
06 BOs52 locus 117:GGAAGGTCCTCAGGTGGCATCTTCTTCTTAGCA--------------------------- 149
12 BOs52 locus 120:GGCAGGTCCTCAGGTGGCATCTTCTTCTTAGCAGGGGGAGGGATAGCTCAGTGGTTTGAG 179
13 BOs52 locus 118:GGCAGGTCCTCAGGTGGCATCTTCTTCTTAGCA--------------------------- 150
17 BOs52 locus 121:GGGAGGTCCTCAGGTGGCATCTTCTTCTTAGCA--------------------------- 153
19 BOs52 locus 120:GGCAGGTCCTCAGGTGGCATCTTCTTCTTAGCA--------------------------- 152
                 **.*.******************..*******

01 BOs52 locus 150:------------------------------------------------------------ 150
06 BOs52 locus 149:------------------------------------------------------------ 149
12 BOs52 locus 180:CATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGAGGCCACTTAGGGATCT 239
13 BOs52 locus 150:------------------------------------------------------------ 150
17 BOs52 locus 153:------------------------------------------------------------ 153
19 BOs52 locus 152:------------------------------------------------------------ 152


01 BOs52 locus 150:------------------------------------------------------------ 150
06 BOs52 locus 149:------------------------------------------------------------ 149
12 BOs52 locus 240:GGGGAAAAAATTGGTCCTGCTAGTGAAGGCAGGGGCTGGACTAGATGACCTTTCAAGGTC 299
13 BOs52 locus 150:------------------------------------------------------------ 150
17 BOs52 locus 153:------------------------------------------------------------ 153
19 BOs52 locus 152:------------------------------------------------------------ 152


01 BOs52 locus 151:--------------------------------------------------TATGTGCAA 159
06 BOs52 locus 150:--------------------------------------------------TATGTGCAA 158
12 BOs52 locus 300:CCTTCCAGTTCTAGGAGATTGGTATATCTCCAATTATTATTATTATTAGCATATGTGCAA 359
13 BOs52 locus 151:--------------------------------------------------TATGTGCAA 159
17 BOs52 locus 154:--------------------------------------------------TATGTGCAA 162
19 BOs52 locus 153:--------------------------------------------------TATGTGCAA 161
                                                         *********
01 BOs52 locus 160:-TGTGCCTCAGGTGCCACATGAACGTCATCACCGAATTTGGTCCACTGGTTGGATCATTA 218
06 BOs52 locus 159:-TGTGCCTCAG-TGCCATGTGAACGTCATCACCGAATTTGATCCRCTGGTTGGATCCTTA 216
12 BOs52 locus 360:-TGTGYCTCAGGTGCCACGTGAATGTCATCACCGAATTTGGTCCACTGGTTGGATCATTA 418
13 BOs52 locus 160:-TGTGCCTCAGGTGCCACGTGAATGTCATCACCGAATTTGGTCCACTGGTTGGATCATTA 218
17 BOs52 locus 163:ACGTGCTTCAGGTGCCACGTGAACATCATCACCGAATTTGGTCCACTGGTTGGATCATTA 222
19 BOs52 locus 162:-CGTGCCTCAGGTGCCACGTGAATGTCATCACCGAATTTGGTCCACTGGTTGGATCATTA 220
                  .***..****.*****..**** .***************.***.***********.***

01 BOs52 locus 219:CCTTCCATGGTCTGGGCCA-TGGGTACTGATGGGGAGTGCAACGTGAACACTGATCCATG 277
06 BOs52 locus 217:CCTTCCATGGC-TGGGCCACTAGGTACTGATGGGGAGCGCAACGTGAACACTGATCCATG 275
12 BOs52 locus 419:CCTTCCACAGCCTGGGCCGCTGGGTACTGATGGGGAGTGCAACGTGAACAC         469
13 BOs52 locus 219:CCTTCCACGGCCTGGGCCGCTGGGTACTGATGGGGAGTGCAACGTGAACACTGATCCATG 278
17 BOs52 locus 223:CCTTCCACGGCCTGGGCCGCTGGGTACTGATGGGTAGTGCAACGTGAACACTGATCCATG 282
19 BOs52 locus 221:CCTTCCACAGCCTGGGCCACTGGGTACTGATGGGGAGTGCAACGTGAACACTGATCCATG 280
                 *******..*..****** .*.************.**.*************........
```

Supplemental Figure 5-45. Sequence alignment of BOs52 locus. GenBank accession numbers are AB24339–AB249344.

```
01 BOs80 locus   1:TGAAAAGATAAAACNTGCAAGAGTTCAAGTCTAGAACATGTGTGT----TTTGGTGAGC- 55
06 BOs80 locus   1:-GAAAAGATAAAACCTGCAAGAGTTCAAGTCTAGAACATGTGTGT----TTTGGTGGG-- 53
12 BOs80 locus   1:-GAAAAGATAAAACACTGCAAGAGTTCAAGTCTAGAA--TGTGTGTGTGTTTTGGTGGGGT 57
13 BOs80 locus   1:-GAAAAGATAAAACCTGCAAGAGTTCAAGTCTAGAACGTGTGTGT----TTTGGTGGGGT 55
17 BOs80 locus   1:TGAAAAGATAAAACCTGCAAGAGTTCAAGTCTAGAACATGTGTGT----TTTGGTGGGGT 56
19 BOs80 locus   1:-GAAAAGATAAAACCTGCAAGAGTTCAAGTCTAGAACATGTGTGT----TTTGGTGGGGT 55
                  ***********...********************..*******   *******.*..

01 BOs80 locus  56:TTTTTTGTTTGT--TTTTGTTTTCTTT--------------------------------- 80
06 BOs80 locus  54:TTTTTTGTGTGTGTTTTTGCTTTCTGT--------------------------------- 80
12 BOs80 locus  58:TTTTTTGTTTGTGTTTTTGCTTTCTTTGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGG 117
13 BOs80 locus  56:TTTTTTGTTTGTGTTTTTGCTTTCTTT--------------------------------- 82
17 BOs80 locus  57:TTTTTTGTTTGTGTTTTTGCTTTCTTT--------------------------------- 83
19 BOs80 locus  56:TTTTTTGTTTGTGTTTTTGCTTTCTTT--------------------------------- 82
                 ********.***..*****.*****.*

01 BOs80 locus  80:------------------------------------------------------------ 80
06 BOs80 locus  80:------------------------------------------------------------ 80
12 BOs80 locus 118:CYTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGGG 177
13 BOs80 locus  82:------------------------------------------------------------ 82
17 BOs80 locus  83:------------------------------------------------------------ 83
19 BOs80 locus  82:------------------------------------------------------------ 82


01 BOs80 locus  80:------------------------------------------------------------ 80
06 BOs80 locus  80:------------------------------------------------------------ 80
12 BOs80 locus 178:AAAAATGGTCCTGCTAGTGAAGGCAGGGGCTGGACTAGATGACCTTTCAAGGTCCCTTCC 237
13 BOs80 locus  82:------------------------------------------------------------ 82
17 BOs80 locus  83:------------------------------------------------------------ 83
19 BOs80 locus  82:------------------------------------------------------------ 82


01 BOs80 locus  81:---------------------------------------------------AAAACTCCC 89
06 BOs80 locus  81:---------------------------------------------------AAAACCCCC 89
12 BOs80 locus 238:ACTTCTAGGAGATTGGTATATCTCCAATTATTATATTATTATTATTTCTTTAAAACCCCC 297
13 BOs80 locus  83:---------------------------------------------------AAAACCCCC 91
17 BOs80 locus  84:---------------------------------------------------AAAACCCCC 92
19 BOs80 locus  83:---------------------------------------------------AAAACCCCC 91
                                                          *****.***

01 BOs80 locus  90:-ATTTTATTCTTGTCTCTTCATCTTAGTAATGTGGAATTTCACAGCCATCCGTAGTAAGG 148
06 BOs80 locus  90:-ATTTTATTCTTGTCTTTTCACCTTAGTAATGTGGAATTTCACAGCCATCCATAGCAAGG 148
12 BOs80 locus 298:CATTTTATTCTTGTCTCTTCACCTTAGTAATGTGGAATTTCACAGCCATCCATAGCAAGG 357
13 BOs80 locus  92:-ATTTTATTCTTGTCTCTTCACCTTAGTAATGTGGAATTTCACAGCCATCCATAGCAAGG 150
17 BOs80 locus  93:-ATTTTATTCTTGTCTCTTCACCTTAGTAATGTGGAATTTCACAGCCATCCATAGCAAGG 151
19 BOs80 locus  92:-ATTTTATTCTTGTCTCTTCACCTTAGTAATGTGGAATTTCACAGCCCTCCATAGCAAGA 150
                  ***************.****.************************.***.***.***.

01 BOs80 locus 149:GTAGTACTTTCAAATGCAGTTCATTCTATCCTGTGGAACAAAGGATATTTCATTAGTTCC 208
06 BOs80 locus 149:GTAGTACTTTCAAATGCAGTTCATTCTATCCTGTGGAACAGAGGATATTTCAT-AGTTCC 207
12 BOs80 locus 358:GTAGTACTTTCAAATGCAGTTCATTCTATCCTGTGGAACAAAGGATTTTTCAT       410
13 BOs80 locus 151:GTAGTACTTTCAAATGCAGTTCATTCTATCCTGTGGAACAAAGGATATTTCATTAGTTCC 210
17 BOs80 locus 152:GTAGTACTTTCAAATGCAGTTCATTCTATCCTGTGGAACAAAGGATATTTCATTAGTTCC 211
19 BOs80 locus 151:GCAGTACTTTCAAATGCAGTTTATTCTATCCTGTGGAACAAAGGATATTTCATTAGTTCC 210
                 *.******************.*****************.*****.******.......

01 BOs80 locus 209:TGGCAA                                                   214
06 BOs80 locus 208:TGGCAAC                                                  214
13 BOs80 locus 211:TGGCAAC                                                  217
17 BOs80 locus 212:TGGCAAC                                                  218
19 BOs80 locus 211:TGGCAAC                                                  217
                 ......
```

Supplemental Figure 5-46. Sequence alignment of BOs80 locus. GenBank accession numbers are AB24345–AB249350.

```
01 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
02 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
06 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
12 BCr04 locus   1:AGCTTTTCCCCAGATCAC-AATGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
14 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
17 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
19 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAGAGGCATTGGCTTTCTTTCTTATTTTGCCTT 59
27 BCr04 locus   1:AGCTTTTCCCCAGATCACTACTGTGCTTAGAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 59
28 BCr04 locus   1:AGCTTTTCCCCAGATCAC-ACTGTGCTTAAAGGC-TTGGCTTTCTTTCTTATTTTGCCTT 58
                 ****************** *.********.**** *************************

01 BCr04 locus  59:TGTTTTGTGTTCTG-CCTTCCCT-CACATATG---------------------------- 88
02 BCr04 locus  59:TGTTCTGTGTTCTG-CTTTCCCT-CACATATG---------------------------- 88
06 BCr04 locus  59:TGTTCTGTGTTCTG-CCTTCCCT-CCCATATG---------------------------- 88
12 BCr04 locus  59:TGTTCTGTGTTCTG-CCTTCCCT-CACATATG---------------------------- 88
14 BCr04 locus  59:TGTTCTGTGTTCTG-CCTTCCCT-CACATATGCACATTATGGGGAGGGATAGCTCAGTGG 116
17 BCr04 locus  59:TGTTCTGTGTTCTGGCCTTCCCTTCACATATG---------------------------- 90
19 BCr04 locus  60:TGTTCTGTGTTCTG-CCTTCACT-CACATATG---------------------------- 89
27 BCr04 locus  60:TGTTCTGTGTTCTG-CCTTCCCT-CACATATG---------------------------- 89
28 BCr04 locus  59:TGTTCTGTGTTCTG-CCTTCCCT-CACATATG---------------------------- 88
                ****.********* *.***.** *.******

01 BCr04 locus  88:------------------------------------------------------------ 88
02 BCr04 locus  88:------------------------------------------------------------ 88
06 BCr04 locus  88:------------------------------------------------------------ 88
12 BCr04 locus  88:------------------------------------------------------------ 88
14 BCr04 locus 117:TTTGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATGCTTGAGGGGGCCACTTAG 176
17 BCr04 locus  90:------------------------------------------------------------ 90
19 BCr04 locus  89:------------------------------------------------------------ 89
27 BCr04 locus  89:------------------------------------------------------------ 89
28 BCr04 locus  88:------------------------------------------------------------ 88


01 BCr04 locus  88:------------------------------------------------------------ 88
02 BCr04 locus  88:------------------------------------------------------------ 88
06 BCr04 locus  88:------------------------------------------------------------ 88
12 BCr04 locus  88:------------------------------------------------------------ 88
14 BCr04 locus 177:GGATCTGGGGCAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTT 236
17 BCr04 locus  90:------------------------------------------------------------ 90
19 BCr04 locus  89:------------------------------------------------------------ 89
27 BCr04 locus  89:------------------------------------------------------------ 89
28 BCr04 locus  88:------------------------------------------------------------ 88


01 BCr04 locus  89:-----------------------------------------------CACATTTACCCAA 101
02 BCr04 locus  89:-----------------------------------------------CACATTTACCCAA 101
06 BCr04 locus  89:-----------------------------------------------CACATTTACCCAA 101
12 BCr04 locus  89:-----------------------------------------------CACATTTACCCAA 101
14 BCr04 locus 237:CAAGGTCCCTTCCAGTTCTAGGAGATTGGTGTATCTCCAATTATTACCACATTTACCCAA 296
17 BCr04 locus  91:-----------------------------------------------CACATTTACCCAA 103
19 BCr04 locus  90:-----------------------------------------------CACATTTACCCAA 102
27 BCr04 locus  90:-----------------------------------------------CACATTTACCCAA 102
28 BCr04 locus  89:-----------------------------------------------CGCATTTACCCAA 101
                                                   *.***********

01 BCr04 locus 102:AACAATACA-AGAAGAAC-----------ATGG-TACTAGTTTCCAGACAGACTCCACTA 148
02 BCr04 locus 102:AACAATACTTAGTTGAACTTTCTACCCACATGG-TGCTGGTTTCCAGACAGACTCCACTA 160
06 BCr04 locus 102:AACAATACTTAGTTGAACCCGCTACCCACATGG-TGCTAGTTTCCAGACAGACTCCACTA 160
12 BCr04 locus 102:AACAATACTTAGTTGAACCCTCTACCCACATGG-TGCTAGTTTCCAGACAGACTCCACTA 160
14 BCr04 locus 297:AACAATACTTAGTTGAACCCTCTACCCACATGG-TGCTAATTTCCAGACAGACTCCACTA 355
17 BCr04 locus 104:AACAATACTTAGTTGAACCCTCTACCCACATGG-TGCTAGTTTCCAGACAGACTCCACTA 162
19 BCr04 locus 103:AACAATACTTCGTTGAACCCTCTACCCACATGG-TGCTAGTTTCCAGACAGACTCCACTA 161
27 BCr04 locus 103:AACAATACTTAGTTGAACTCTCTACCCACATGGGTGCTAGTTTCCAGACAGACTCCACTA 162
28 BCr04 locus 102:AACAATACTTAGTTGAACCCTCTACGCACATGG-TGCTAGTTTCCAGACAGACTTCACTA 160
                ********...*..****...........**** *.**..**************.*****

01 BCr04 locus 149:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        179
```

```
02 BCr04 locus 161:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        191
06 BCr04 locus 161:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        191
12 BCr04 locus 161:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        191
14 BCr04 locus 356:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        386
17 BCr04 locus 163:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        193
19 BCr04 locus 162:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        192
27 BCr04 locus 163:GGTTGTATTTTAG-AGTAGGGGA                               184
28 BCr04 locus 161:GGCTGTATTTTAGGTGTGGACCATTAACTGT                        191
                **.**********..**.*...*........
```

Supplemental Figure 5-47. Sequence alignment of BCr04 locus. GenBank accession numbers are AB24351–AB249356, AB125519, AB125731 and AB125732.

```
06 BPm20 locus   1:TTTTTCAATTAAAG-GCCTGGCAGCAGCAAAGTTTGCAATGCTAGGGTTGTAACAAATTA 59
14 BPm20 locus   1:TTTTTCAATTAAAGTGCCTGGCAGCAGCAAAGTTTGCAATGCTAGGGTTGTAACAAATTA 60
17 BPm20 locus   1:TTTTTCAATTAAAGTGCCTGGCAGCAGCAAAGTTTGCAATGCTAGGGTTGTAACAAATTA 60
18 BPm20 locus   1:TTTTTCAATTAAAGTGCCTGGCAGCAGCAAAGTTTGCAATGCTAGGGTTGTAACAAATTA 60
19 BPm20 locus   1:TTTTTCAATTAAAGTGCCTGGCAGCAGCAAAGTTTGTAATGCTAGGGTTGTAACAAATTA 60
20 BPm20 locus   1:TTTTTCAATTAAAGTGCCTGGCAGCAGCAAAGTTTGCAATGCTAGGGTTGTAACAAATTA 60
                 **************.*********************.**********************

06 BPm20 locus  60:TTAGAGGGCCGTCTCTGTCTTAAATTCAAAT----------------------------- 90
14 BPm20 locus  61:TTAGAGGGCCATCTCTGTCTTAAATTCAAAT----------------------------- 91
17 BPm20 locus  61:TTAGAGGGCCATCTCTGTCTTAAATTCAAAT----------------------------- 91
18 BPm20 locus  61:TTAGAGGGCCATCTCTGTCTTAAATTCAAATTTAAGGGGGGGAGGGATAGCTCAGTGGTT 120
19 BPm20 locus  61:TTAGAGGGCCATCTCTGTCTTAAATTCAAAT----------------------------- 91
20 BPm20 locus  61:TTAGAGGGCCATCTCTGTCTTAAATTCAAAT----------------------------- 91
                **********.********************

06 BPm20 locus  90:------------------------------------------------------------ 90
14 BPm20 locus  91:------------------------------------------------------------ 91
17 BPm20 locus  91:------------------------------------------------------------ 91
18 BPm20 locus 121:TGAGCATTGGCCTGCTAAACCCAGGGTTGTGAGTTCAATCCTTGAGGGGGCCACTTAGGG 180
19 BPm20 locus  91:------------------------------------------------------------ 91
20 BPm20 locus  91:------------------------------------------------------------ 91


06 BPm20 locus  90:------------------------------------------------------------ 90
14 BPm20 locus  91:------------------------------------------------------------ 91
17 BPm20 locus  91:------------------------------------------------------------ 91
18 BPm20 locus 181:ATCTGGGGCAAAAAATTGGTCCTGCTAGTGAAGGCAGGGGGCTGGACTCAATGACCTTCT 240
19 BPm20 locus  91:------------------------------------------------------------ 91
20 BPm20 locus  91:------------------------------------------------------------ 91


06 BPm20 locus  91:----------------------------------------------------ACAAGT-G 97
14 BPm20 locus  92:----------------------------------------------------ACAAGTTG 99
17 BPm20 locus  92:----------------------------------------------------ACAAGT-G 98
18 BPm20 locus 241:GAGGTCCCTTCCACTTCTAGGAGATTGGTATATCTCCAATTATTACCTAAATACAAGT-G 299
19 BPm20 locus  92:----------------------------------------------------ACAAGT-G 98
20 BPm20 locus  92:----------------------------------------------------ACAAGT-G 98
                                                        ****** *

06 BPm20 locus  98:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAATCTACTTTGGCTTT 157
14 BPm20 locus 100:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAATCTACTTTGGCTTT 159
17 BPm20 locus  99:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAACCTACTTTGGCTTT 158
18 BPm20 locus 300:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAATCTACTTTGGCTTT 359
19 BPm20 locus  99:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAATCTACTTTGGCTTT 158
20 BPm20 locus  99:TGTTTTGCAGCAACACACAATAAAATTGTAGTTTCTTACTAAATAATCTACTTTGGCTTT 158
                ***********************************************.*************

06 BPm20 locus 158:GCTGACAACTTAAAATGTTGCT-GTCTTTCAGGCAAAG--TTTGAGTTAACTGCAACCTA 214
14 BPm20 locus 160:GCTGACAACTTAAATTGTTGCTTGTCTTTCAGGCAAAGTTTTTGAGTTAACTGCAACCTA 219
17 BPm20 locus 159:GCTGACAACTTAAATTGTTGCTTGTCTTTCAGGCAAAGTTTTTGAGTTAACTGCAACCTA 218
18 BPm20 locus 360:GCTGACAACTTAAATTGTTGCTTGTCTTTCAGGCAAAGTTTTTGAGTTAACTGCAACCTA 419
19 BPm20 locus 159:GCTGACAGCTTAAATTGTTGCTTGTCTTTCAGGCAAAGTTTTTGAGTTAACTGCAACCTA 218
20 BPm20 locus 159:GCTGACTACTTAAATTGTTGCTTGTCTTTCAGGCAAAGTTTTTGAGTTAACTGCAACCTA 218
                ******..******.*******.***************..********************

06 BPm20 locus 215:TNGCTTACAAGCC                                               227
14 BPm20 locus 220:TAGCTTACAAGCC                                               232
17 BPm20 locus 219:TAGCTTACAAGCC                                               231
18 BPm20 locus 420:TAGCTTACAAGCC                                               432
19 BPm20 locus 219:TAGCTTACAAGCC                                               231
20 BPm20 locus 219:TAGCTTACAAGCC                                               231
                *.***********
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Supplemental Figure 5-48. Sequence alignment of BPm20 locus. GenBank accession numbers are AB24357–AB249362.

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02 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATATTTCATTTATTATTGGAAATTGTATGATGATTTT 60
06 BMr15 locus   1:GCATGATTCGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATTGTATGATGATTTT 60
14 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATTGTATGATGATTTT 60
17 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATTGTATGATGATTTT 60
19 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTACAGTTAATTTATTACTGGAAATTGTATGATGATTTT 60
23 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATTGTATGATGATTTT 60
24 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATTGTATGATGATTTT 60
25 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCCATATTTAATGTATTATTAGAAATTGTATGATGATTTT 60
27 BMr15 locus   1:GCATGATTTGCTTAAGAAAATCTATAGTTAATTTATTATTGGAAATGGTGTGATGATTTT 60
                 ********.*************.*.*.**.**.*****.*.*****.**.**********

02 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAATAGACATTGGCAAAAGTGATATGAGTGAC-- 118
06 BMr15 locus  61:TGGAGAGAAAGTTCTACATATATTTTTAACAGACATTGGCAAAAGTGATATGAATGAC-- 118
14 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAACAGACATTGGCAAAAGTGAAATGAGTGAC-- 118
17 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAACAGACATTGGCAAAAGTGATATGAGTGAC-- 118
19 BMr15 locus  61:TGGAGAGAAAGTTCTATATGTATTTTTAACAGACATTGGCAAAAGTGATATGAGTGAC-- 118
23 BMr15 locus  61:TGGAGAGAAAGGTCTACATGTATTTTTAACAGACATTAGCAAAAGTGATATGAGTGACAT 120
24 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAACAGACATTGGCAAAAGTGATATGAGTGAC-- 118
25 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAACAGACATTGGCAAAAGTGATATGAATGAC-- 118
27 BMr15 locus  61:TGGAGAGAAAGTTCTACATGTATTTTTAACAGACATTGGCAAAAGTGATATGAGTG---- 116
                 ***********.****.**.*********.*******.**********.****.**..

02 BMr15 locus 118:------------------------------------------------------------ 118
06 BMr15 locus 118:------------------------------------------------------------ 118
14 BMr15 locus 118:------------------------------------------------------------ 118
17 BMr15 locus 118:------------------------------------------------------------ 118
19 BMr15 locus 118:------------------------------------------------------------ 118
23 BMr15 locus 121:ATATGAGTGGGGGGAGGGATAGCTCAGTGGTTTGAGCATTGGCCTGCTTAAACCCAGCAT 180
24 BMr15 locus 118:------------------------------------------------------------ 118
25 BMr15 locus 118:------------------------------------------------------------ 118
27 BMr15 locus 116:------------------------------------------------------------ 116


02 BMr15 locus 118:------------------------------------------------------------ 118
06 BMr15 locus 118:------------------------------------------------------------ 118
14 BMr15 locus 118:------------------------------------------------------------ 118
17 BMr15 locus 118:------------------------------------------------------------ 118
19 BMr15 locus 118:------------------------------------------------------------ 118
23 BMr15 locus 181:TGTGAGTTCAATCCTTGAGGGGGCCACTTAGGGATCTGGGGCAAAAATTGGTCCTGCTAG 240
24 BMr15 locus 118:------------------------------------------------------------ 118
25 BMr15 locus 118:------------------------------------------------------------ 118
27 BMr15 locus 116:------------------------------------------------------------ 116


02 BMr15 locus 118:------------------------------------------------------------ 118
06 BMr15 locus 118:------------------------------------------------------------ 118
14 BMr15 locus 118:------------------------------------------------------------ 118
17 BMr15 locus 118:------------------------------------------------------------ 118
19 BMr15 locus 118:------------------------------------------------------------ 118
23 BMr15 locus 241:TGAAGGCAGGGGGCTGGCCTCAATGACCTTTTAAGGTCCCTTCCAGTTCTAGGAGATTGG 300
24 BMr15 locus 118:------------------------------------------------------------ 118
25 BMr15 locus 118:------------------------------------------------------------ 118
27 BMr15 locus 116:------------------------------------------------------------ 116


02 BMr15 locus 119:-----------------------------------AGTTACATTGCTGGGGTAAGGGTAG 143
06 BMr15 locus 119:-----------------------------------AGTTACGTTGCTGGGGTAAAGGTAG 143
14 BMr15 locus 119:-----------------------------------AGTTACATTGCTGGGGTAAGAGTAG 143
17 BMr15 locus 119:-----------------------------------GGTTACATTGCTGGGGTAAGAGTAG 143
19 BMr15 locus 119:-----------------------------------AGTTACATTGCTGGGGTAAGAGTAG 143
23 BMr15 locus 301:TATATCTCCAATTATTACCTATTACCTTATCTGACAGTTACATTGCTGGGGTAAGAGTAG 360
24 BMr15 locus 119:-----------------------------------AGTTACATTGCTGGGATAAGAGTAG 143
25 BMr15 locus 119:-----------------------------------AGTTACATTGCTGGGGTAAGGGTAG 143
27 BMr15 locus 116:------------------------------------------------------------ 116
                                                   .......................

02 BMr15 locus 144:ATGCATCCTTATCTCATATGTGGCAGTACAGAGGAACCTGCAA-CAGAGTGTAATGG   199
```
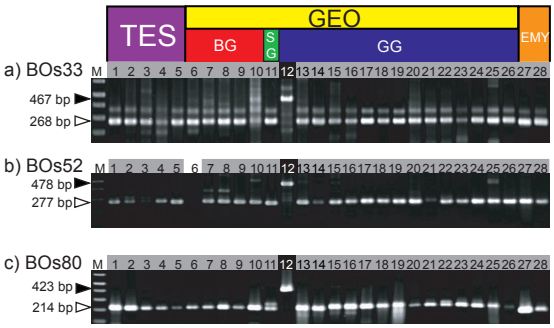
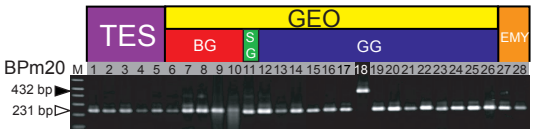

```
06 BMr15 locus 144:ATACATCCTTATCTCATATGTAGCACAACAGAGGAACCTGCAAACAGAGTGTAATGG   200
14 BMr15 locus 144:ATGCATCCTTATCTCATATGTGGCAGTACAGAGGAACCTGCAA-CAGAGTGTAATGG   199
17 BMr15 locus 144:ATGCATCCTTATCTCATATGTGGCATTACAGAGGAACCTGCAA-CAGAGTGTAATGG   199
19 BMr15 locus 144:ATGCATCCTTATCTCATTTGAGGCAGTGCAGAGGAACCTGCAAACAGAGTGTAATGG   200
23 BMr15 locus 361:ATGCATCCTTATCTCATATGTGGCAGTGCAGAGGAACCTGCAAACAGAGTGTAATGG   417
24 BMr15 locus 144:ATGCATCCTTATCTCATATGTGGCAGTACAGAGGAACCTGCAA-CAGAGTGTAATGG   199
25 BMr15 locus 144:ATGCATCCTTATCTCTCATGTGGCAGTACAGAGGAACCTGCAAACAGAGTGTAATGG   200
27 BMr15 locus 117:----------------------------CAGAGGGACCTGCAAACAGAGTGTAATGG   145
                ..........................******.********.*************
```

Supplemental Figure 5-49. Sequence alignment of BMr15 locus. GenBank accession numbers are AB24363–AB249371.

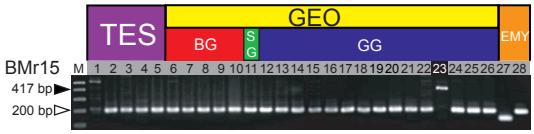
A *M. sinensis*-specific SINE insertion



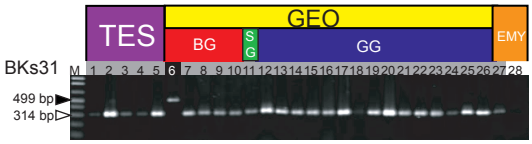
B *C. mouhotii*-specific SINE insertion



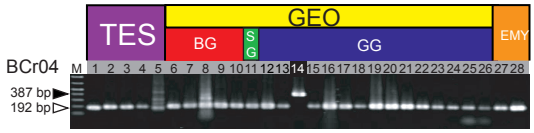
C *M. tirjuga*-specific SINE insertion



D *P. smithii*-specific SINE insertion



E *M. reevesii*-specific SINE insertion



Sasaki et al._supplement Fig.6