Document S3. Chromosome mapping of *BmGr46*

Originally a tBLASTn search in KAIKObase using the amino acid sequence of *Gr46* suggested that it was split into two parts by the gap between Bm_scaf1_contig631 and contig630, i.e., exons 1 2 were located on the 5' edge of contig630, while exons 3 and 4 were on contig631 (Figure S5B in Supp. Document S2). However, as reported in Document S2, we found Bm_scaf444 harboring *BmGr41, 42* and *43* located in this gap, from which we predicted the gap between contig631 and Bm-scaf444 could contain exons 1 and 2 of *BmGr46.* We checked the original aa sequence of *Gr46* (Wanner and Robertson, 2008) by tBLASTn in KAIKObase and found [335-3bp] of Bm_scaf2386 (1739bp, unmapped) had 100% homology with 1-111 aa sequence of *Gr46*. Therefore, we designed a forward primer in this region on Bm_scaf2386 and a reverse primer in *Gr46* exon3, and performed PCR using BAC077B06 as template. Finally, we obtained a band of ~1.5kb which contained sequences corresponding to portions of exon1, intron1, exon2 and intron2, and part of exon3 of *BmGr46*. Combined with the KAIKObase BLAST results, we confirmed the full length sequence of *BmGr46*, especially the part of exon1 that should be located on Bm_scaf2386, which is located on the 5' side of Bm_scaf444. These results indicated the gene order on chr13 should be: *BmGr46, BmGr41, BmGr42, BmGr43, BmGr45,* and *BmGr48*.

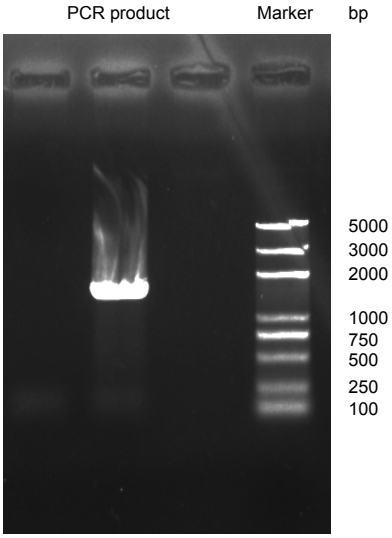

Figure S6A. PCR results for *BmGr46* using BAC077B06 as template. The experiment was conducted using specific primer set 2386F and exon3R (Table S2).

Figure S6B. Sequencing results of *BmGr46* showing the complete sequence of intron1 and intron2.