Document S1. Improvement of *BmGr65* structure and annotation

By tBLASTn searching in the KAIKObase, we found *BmGr65* was composed of four exons; however, exons 1 and 2 were on chr12 [4,086,094–4,085,241] and exons 3 and 4 were on chr23 [20,719,018–20,716,451]. Phylogenetic analysis indicated that a very recent gene duplication event produced *BmGr64* and *BmGr65*, suggesting that both genes were localized in the same site on the chromosome. KAIKObase showed that *BmGr64* and exons 1 and 2 of *BmGr65* were located on the same region of chr12, followed by about a 6kb gap. Hypothesizing that exons 3 and 4 could exist in this gap, we checked the sequences in KAIKObase and found two BAC clones covering this region, BAC072F19 [chr12: 4,004,155–4,209,359] and BAC089G09 [chr12: 4,014,245–4,185,183]. Accordingly, we made primer sets to cover exons 2 and 3 and exons 3 and 4, respectively, and used these BACs as templates to perform PCR. Then we cloned the amplified products into a T-vector for sequencing. Finally we found the complete structure of *BmGr65*, which should be located on chr12.

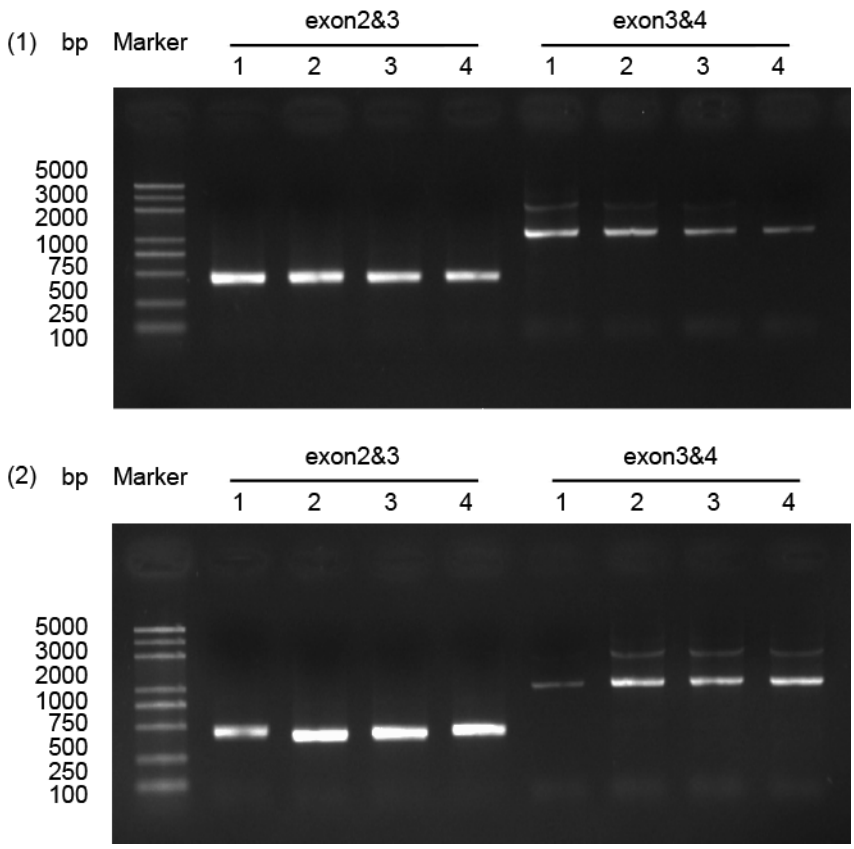

Figure S4A. PCR results for *BmGr65* gene structure. The experiment was conducted using primer sets Exon2-F/Exon3-R and Exon3-F/Exon4-R (Suppl. Table S2); we used 4 clones to check each sample primer set. (1) BAC072F17 PCR product confirmation. (2) BAC089G09 PCR product confirmation.

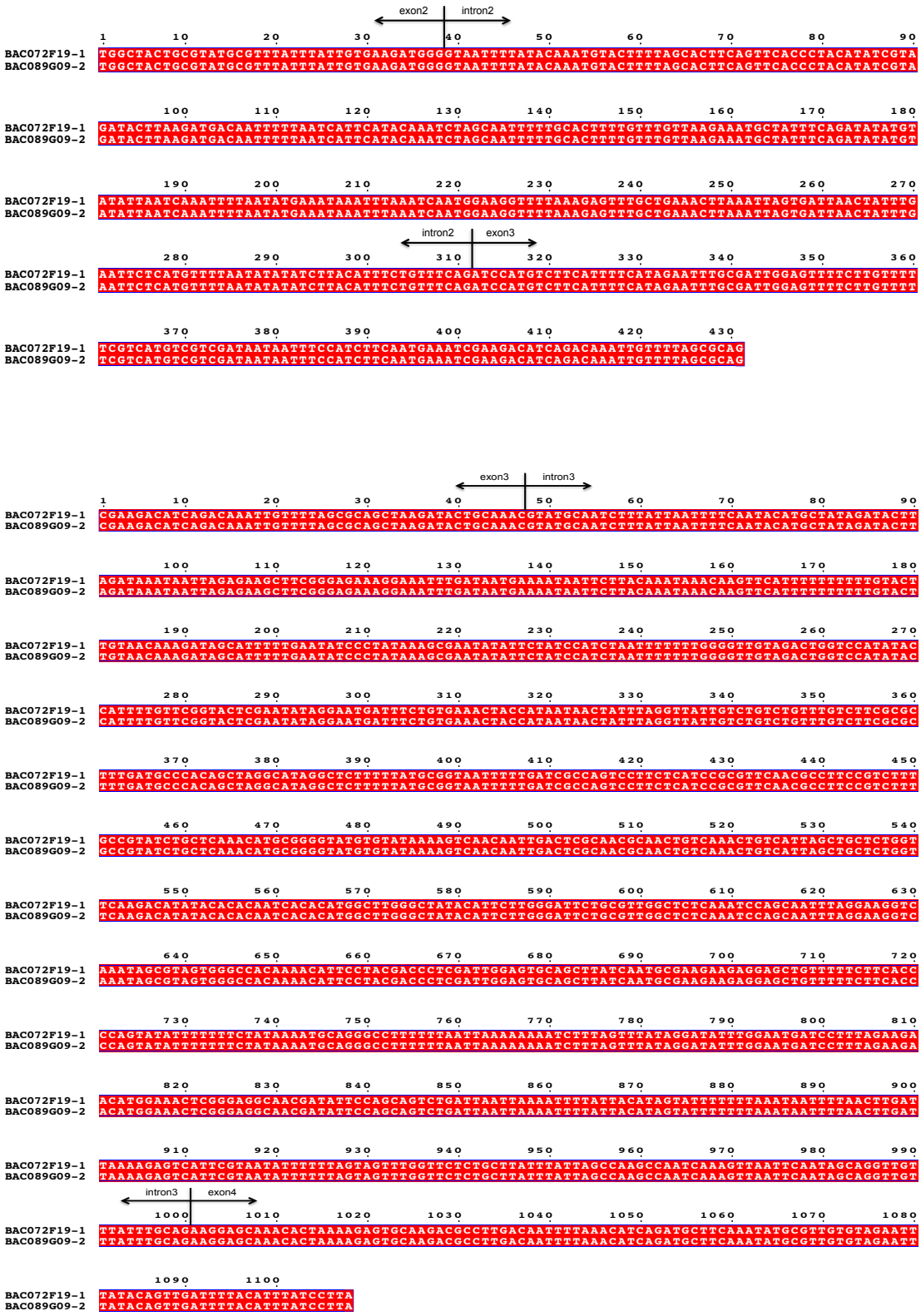

Figure S4B. Sequencing results for *BmGr65* intron2 and intron3. Templates and primer sets were the same as for Figure S1A.

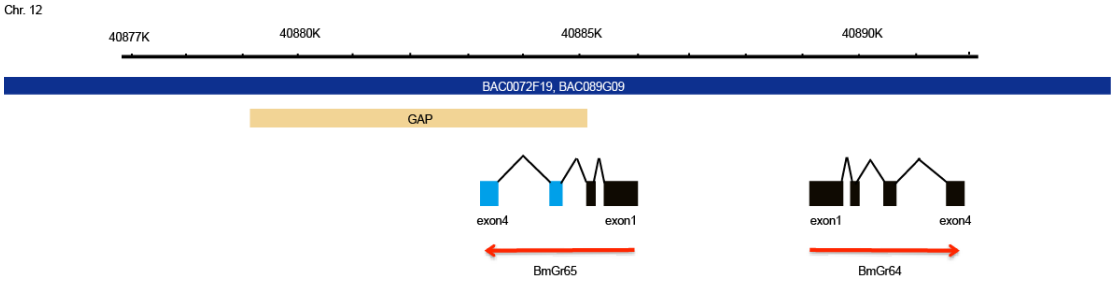

Figure S4C. Detailed gene distribution and structures of *BmGr64* and *BmGr65* on chr12. The blue boxes represent exons 3 and 4 of *BmGr65,* which are located in the gap and newly mapped to chr12. The red arrows indicate the direction of transcription.