Relationships of obtained cDNA, *B. floridiae* genomic scaffolds, and gene models of *bHLH-PAS* genes.

In panels showing cDNA and genomic scaffolds (A, B, D, E, G, H, J, K, M-Q, S, and T), the upper black band with coordinates represents part of the genomic scaffold, with scaffold number labeled. Some scaffolds are shown in minus direction. Gene models are shown in red segmented boxes above the genomic scaffolds. The lower black band represents obtained cDNA of each *bHLH-PAS* genes. Putative start and stop codons are labeled. Presumed exons are shown as cyan segmented boxes below the genomic scaffolds. Ambiguous gap regions, which were not sequenced and denoted as strings of “Ns” in the genome browser, are shown as black boxes in E, K, M, N, and T. cDNA regions that cannot be aligned may be due to these regions. Exons predicted in gene models but not present in cDNA are labeled with “x”. Predicted exons lacking evidence of its existence are labeled with “?”. In the comparisons of redundant models (panels C, F, I, L, and R), the upper schematic figures (drawn not to scale) show positional relationships of *bHLH-PAS* gene models (red boxes) and their neighboring gene models (black boxes), and the lower X-Y plots show the comparisons of sequences. In the schematic figures, ambiguous gap regions are shown as open boxes (labeled with “ambig.”) in scaffold 188, 792, and 83. The lower X-Y plots were made from comparing two scaffold regions showed above; compared regions are denoted by blue lines in C and I. The arrangement of gene models and the sequence similarity shown by comparison support that these two scaffolds or two scaffold regions are highly similar and may be one of the following: (1) two different haplotypes assembled separately, (2) mis-assembly of single region/allele, or (3) a product of local duplication occurred recently.

(A) The comparison of *BfNcoa* cDNA, the corresponding genomic scaffold, and gene model 212110. Five exons (2 upstream of and 3 downstream of the model) are not predicted in the model 212110, and the presumable start and stop codons of obtained cDNA are not predicted. (B) The comparison of *BfArnt* cDNA, the corresponding genomic scaffold, and gene model 124387. (C-E) The comparison of *BfHifa* cDNA and the two corresponding genomic regions. (C) The scaffold 35 contains two highly similar regions: both regions contain gene models of *BfHifa*, zinc finger protein (*Zfp808*, *Zfp112*, and *ZNF*, not sure of its assignment) and models of kelch-like proteins. The comparison of *BfHifa* cDNA, genomic scaffold regions, and gene model 208339 (D) or gene model 208408 (E) are shown. (F-H) The comparison of *BfbHLHPAS-orphan* cDNA and the two corresponding genomic regions. (F) Two regions neighboring the *BfbHLHPAS-orphan* gene models both contain gene models of *Ube3a* and *Trim23* genes. The comparison of *BfbHLHPAS-orphan* cDNA, genomic scaffolds, and gene model 117200 (G) or gene model 125569 (H) are shown. The blue box in H is predicted UTR, a presumed correct prediction. (I-K) The comparison of *BfClock* cDNA and the two corresponding genomic regions. (I) Two regions in the scaffold 2 show high similarity: the regions downstream of each *BfClock* model both have models representing *Hn1l* and *Intu* genes. The comparison of *BfClock* cDNA, genomic scaffolds, and gene model 63636 (J) or gene model 63642 (K) are shown. (L-N) The comparison of *BfBmal* cDNA and the two corresponding genomic regions. (L) Regions in two scaffolds show high similarity: both scaffold 279 and 792 have models representing *Lpar3*, *Eif3m* and *Slit1/3* genes just upstream of each *BfBmal* model. Some ambiguous regions in scaffolds 792 may contribute to the discrepancy between two scaffolds. The comparison of *BfBmal* cDNA, genomic scaffolds, and gene model 96140 (M) or gene model
110703 (N) are shown. In M, two redundant regions of scaffold 279 (labeled with “Re”) gave similar scores in comparison by BLAST (align two sequences), while the Spidey program suggests that the first region (coordinate: 592314-592206) be the exon. (O) The comparison of BfAhr cDNA, the corresponding genomic scaffold, and gene models 98840 and 235977. We suggest the two models, 98840 and 235977, should be joined together for a better model of BfAhr gene. (P) The comparison of BfNpas4 and the corresponding genomic scaffold and gene model 121518. The blue box is the predicted UTR. (Q) The comparison of BfSim and the corresponding genomic scaffold and gene model 265033. (R-T) The comparison of BfNpas1/3 cDNA and the two corresponding genomic regions. (R) Two scaffold regions in scaffold 84 and 83 containing BfNpas1/3 model show high similarity: both regions have gene models representing Akap6 and Pcdh15 genes. Many ambiguous regions in scaffolds 83 may contribute to the discrepancy between two scaffolds. The comparison of BfNpas1/3 cDNA, genomic scaffolds, and gene models on scaffold 84 (S) or gene model 220367 (T) are shown. In panel S, the model 163191 and the first exon of the model 220639 should be joined as a single exon, and four models showed should be joined to represent a single gene. The first exon including the presumable start codon of the BfNpas1/3 cDNA is not predicted.