

Supplementary Materials: Optimizing Hybrid *de Novo* Transcriptome Assembly and Extending Genomic Resources for a Giant Freshwater Prawn (*Macrobrachium rosenbergii*): The Identification of Genes and Markers Associated with Reproduction

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Table S1. Table summary of Blast2Go results including Gene Ontology, KEGG, InterProScan domain search for all combined contigs in *M. rosenbergii*. Similarity of contigs generated with the CLC Genomic Workbench were searched and annotated using BlastX against the non-redundant database in NCBI with an *E*-value cutoff of 1×10^{-5} .

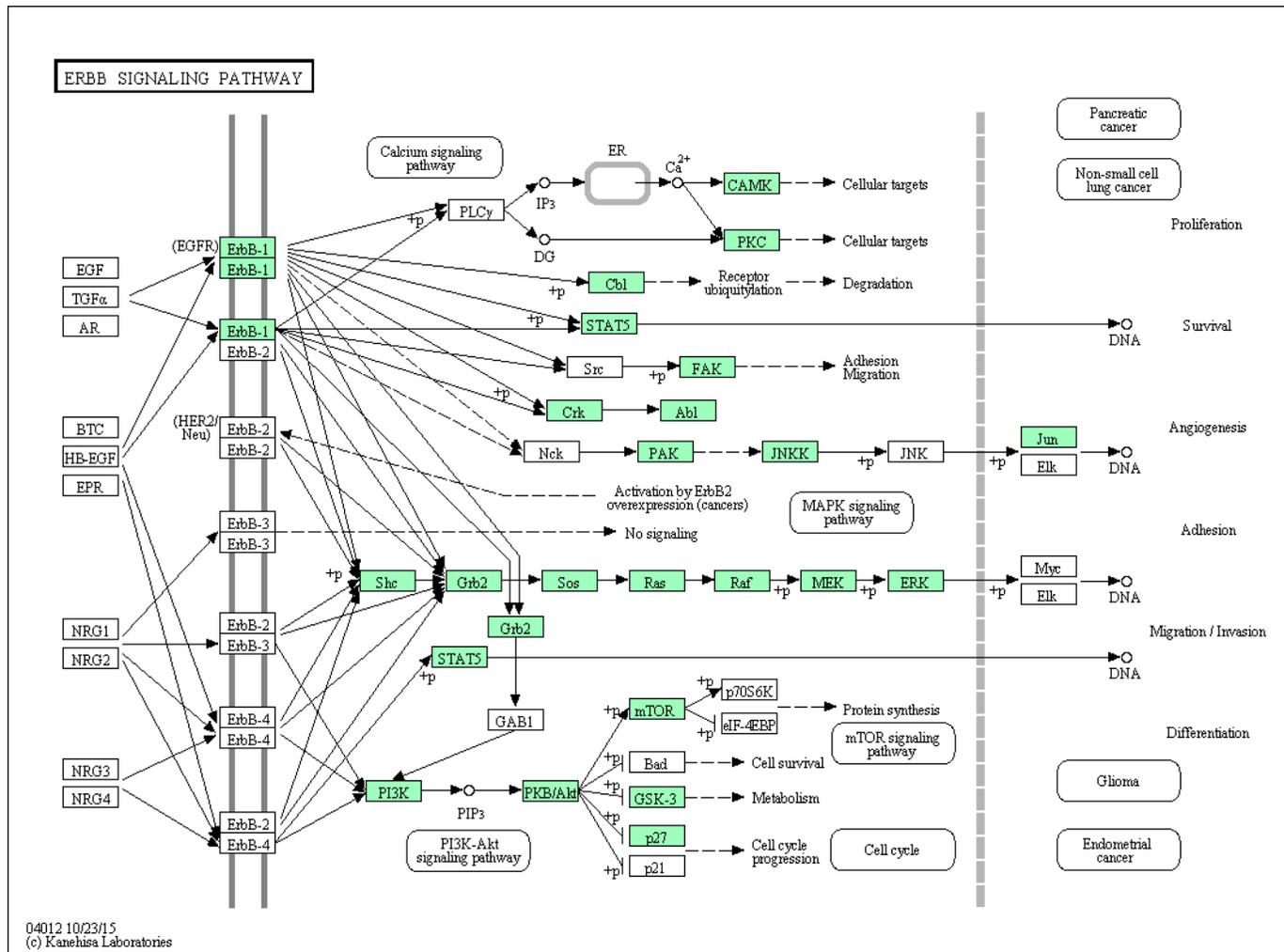
Table S2. Summary of KEGG IDs for all combined contigs in *M. rosenbergii*. Similarity of contigs generated with the CLC Genomic Workbench were searched and annotated using KAAS.

Table S3. Differentially expressed genes between ovary and testis tissues for all combined *M. rosenbergii* contig sequences. Contigs generated with the CLC Genomic Workbench were employed as a reference sequence.

Table S4. Gene lists potentially involved in reproductive-related development and sex differentiation for all combined *M. rosenbergii* contig sequences. Contigs generated with the CLC Genomic Workbench were employed to identify contigs.

Table S5. Putative SNPs for all combined *M. rosenbergii* contig sequences. Contigs generated with the CLC Genomic Workbench were employed as a reference sequence to identify polymorphisms.

Table S6. Putative microsatellite loci for all combined *M. rosenbergii* contig sequences. Contigs generated with the CLC Genomic Workbench were employed as a reference sequence to identify microsatellite motifs.



(A)

Figure S1. Cont.

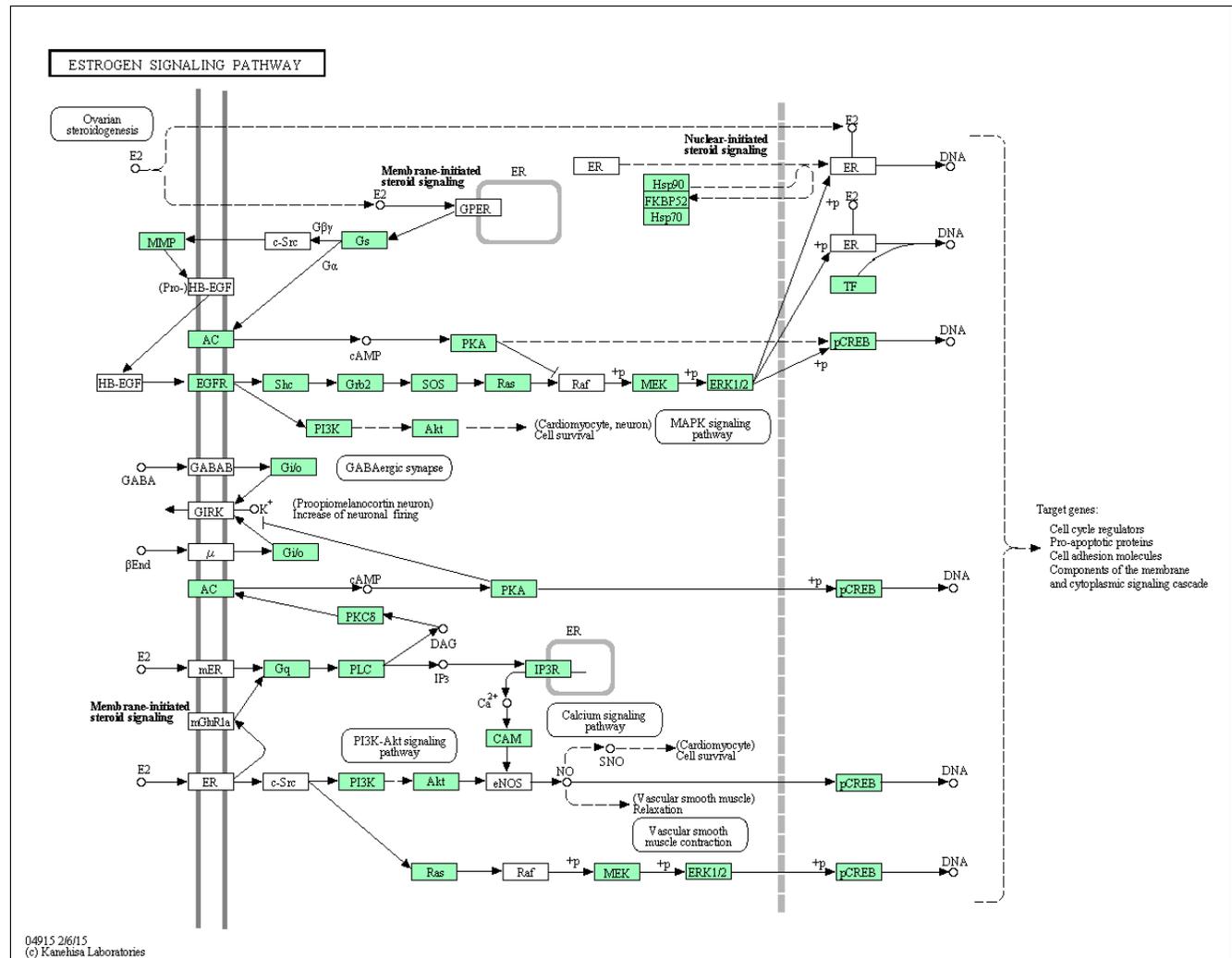
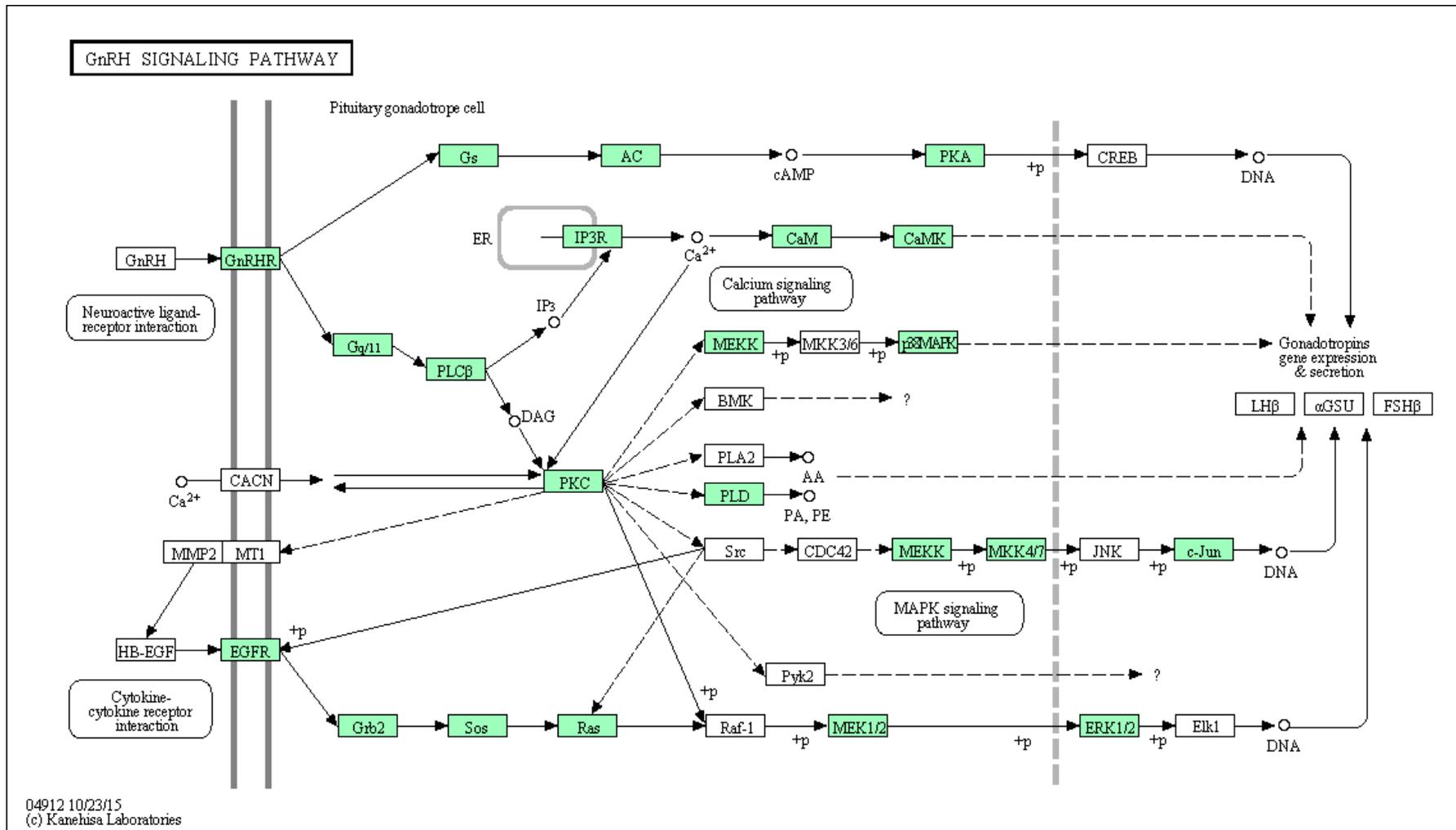
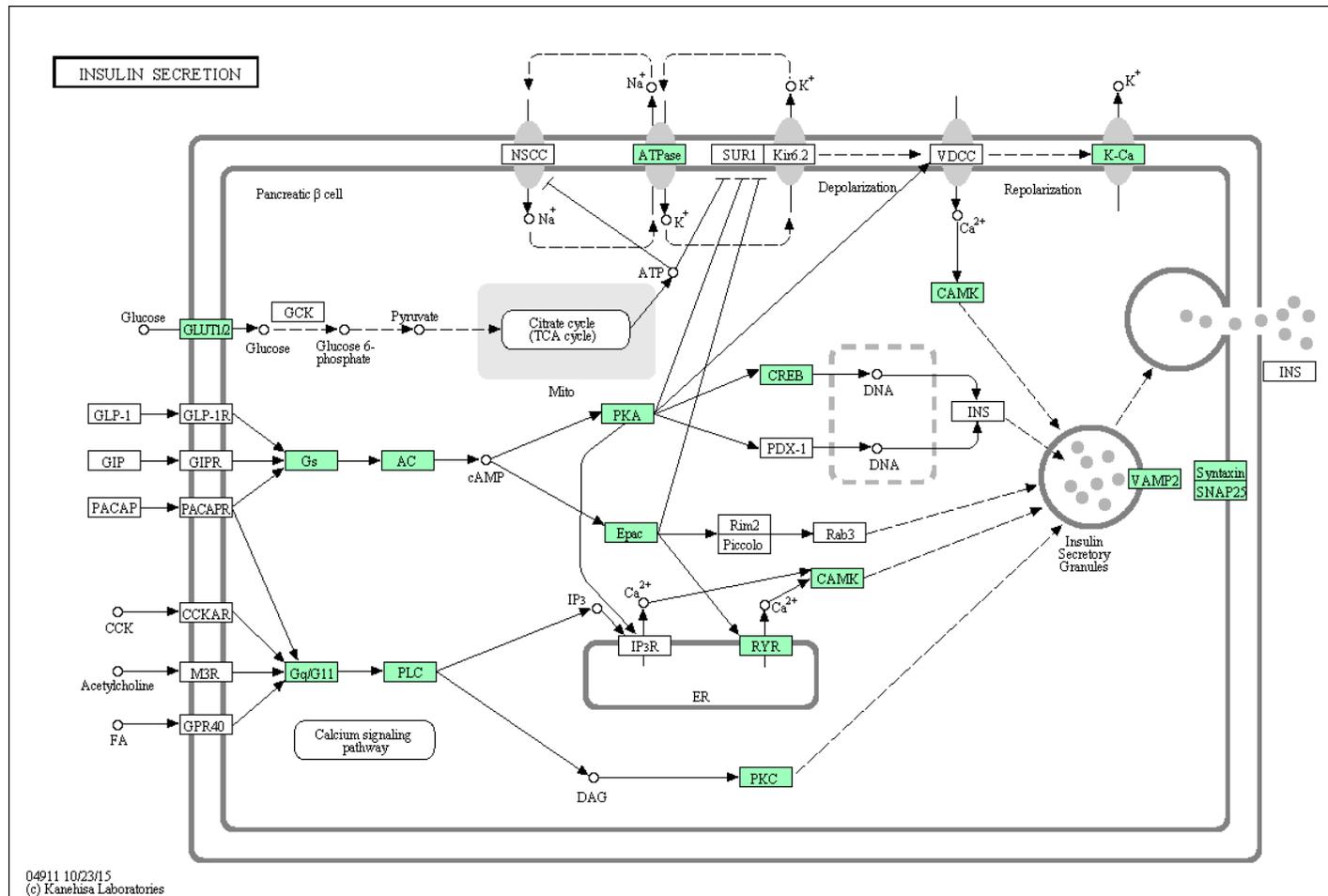


Figure S1. Cont.



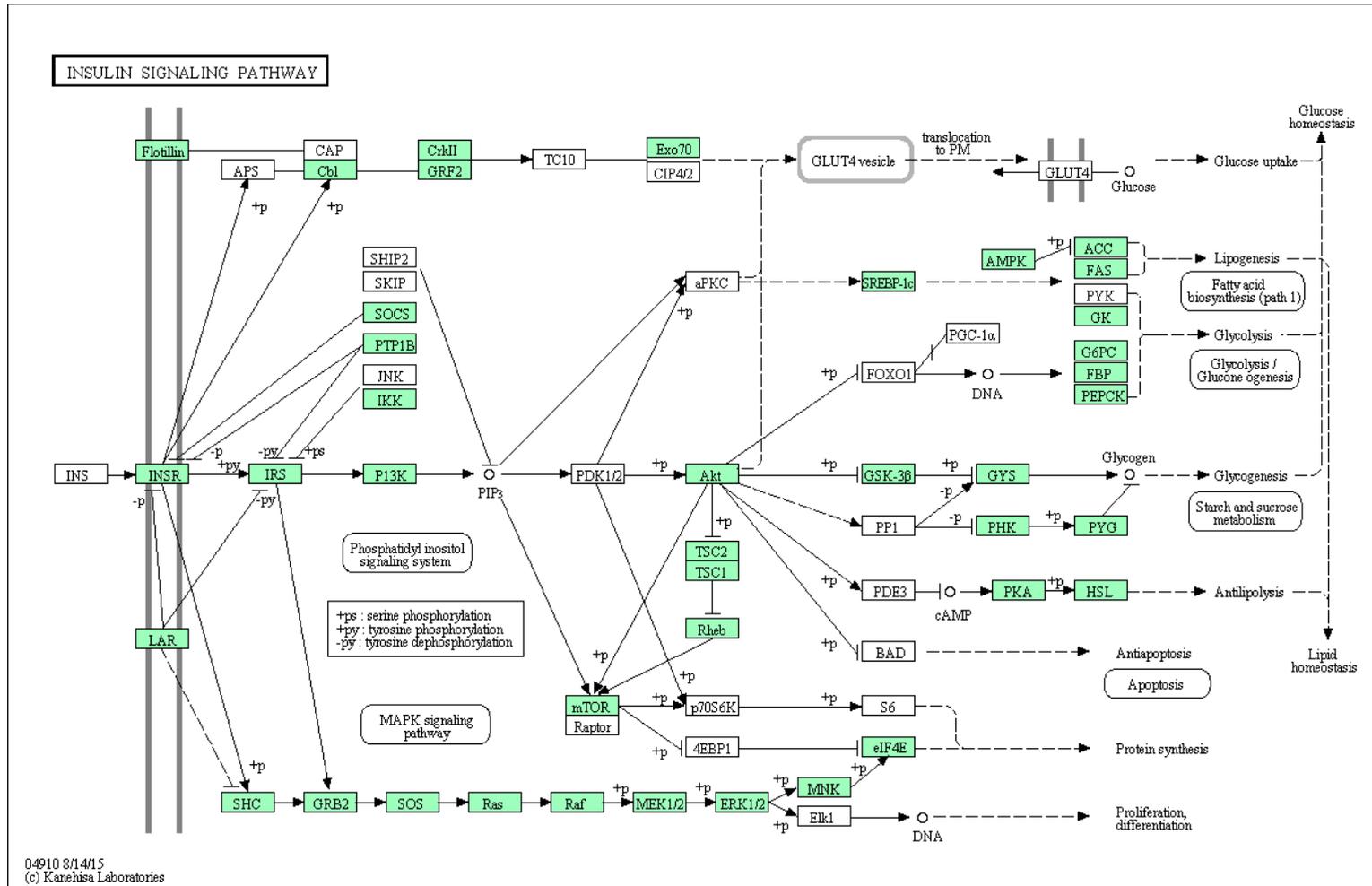
(C)

Figure S1. Cont.



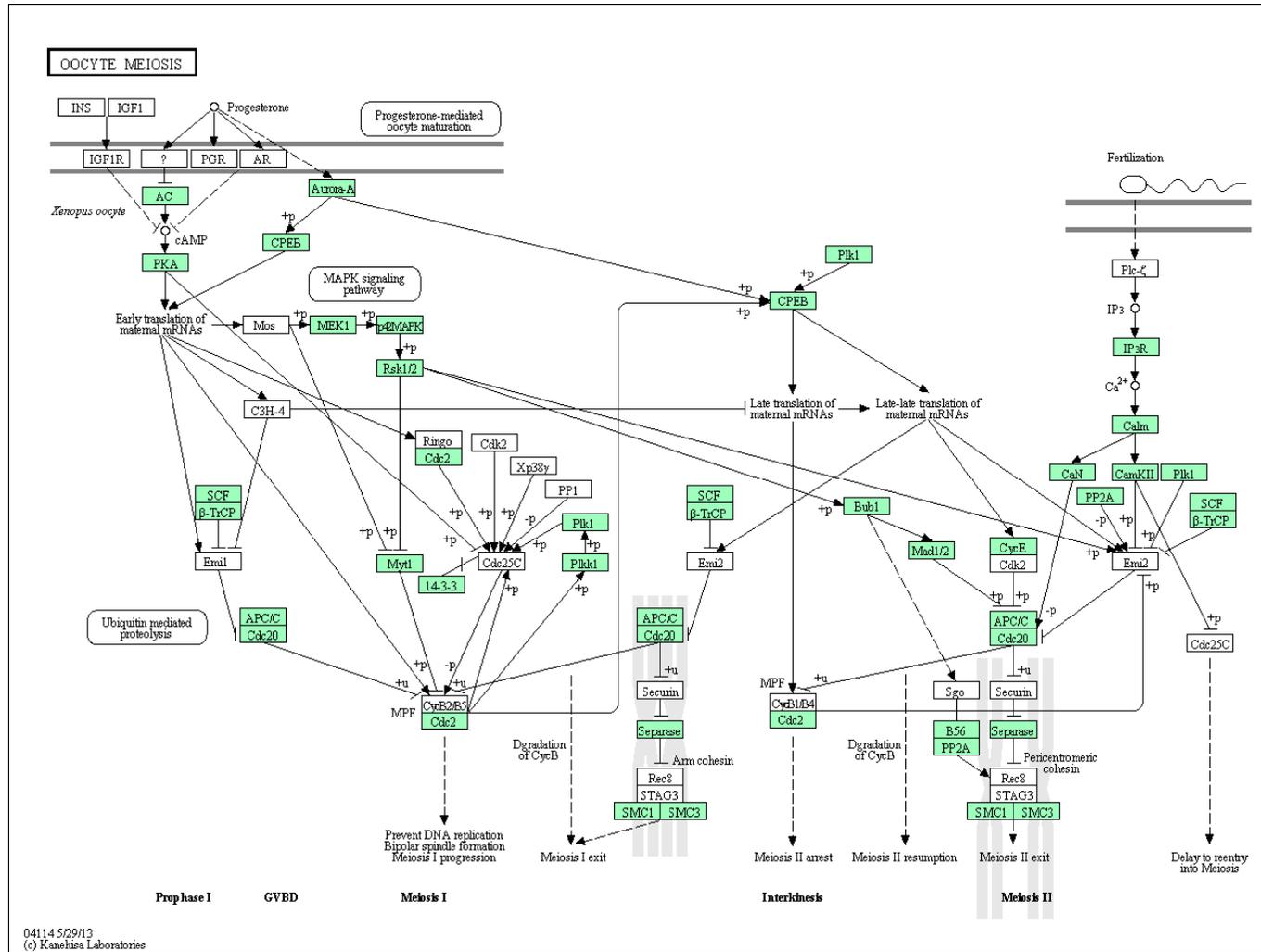
(D)

Figure S1. Cont.



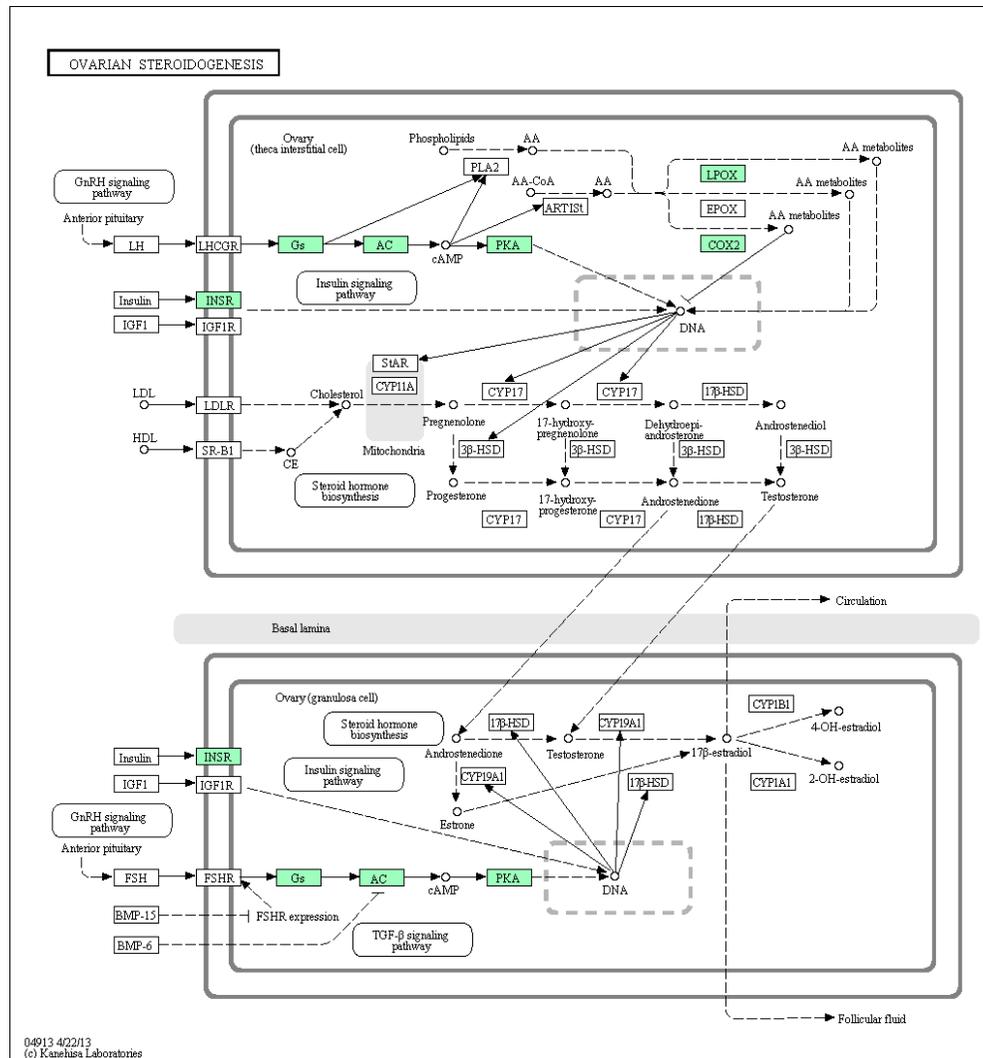
(F)

Figure S1. Cont.



(G)

Figure S1. Cont.



(H)

Figure S1. Cont.

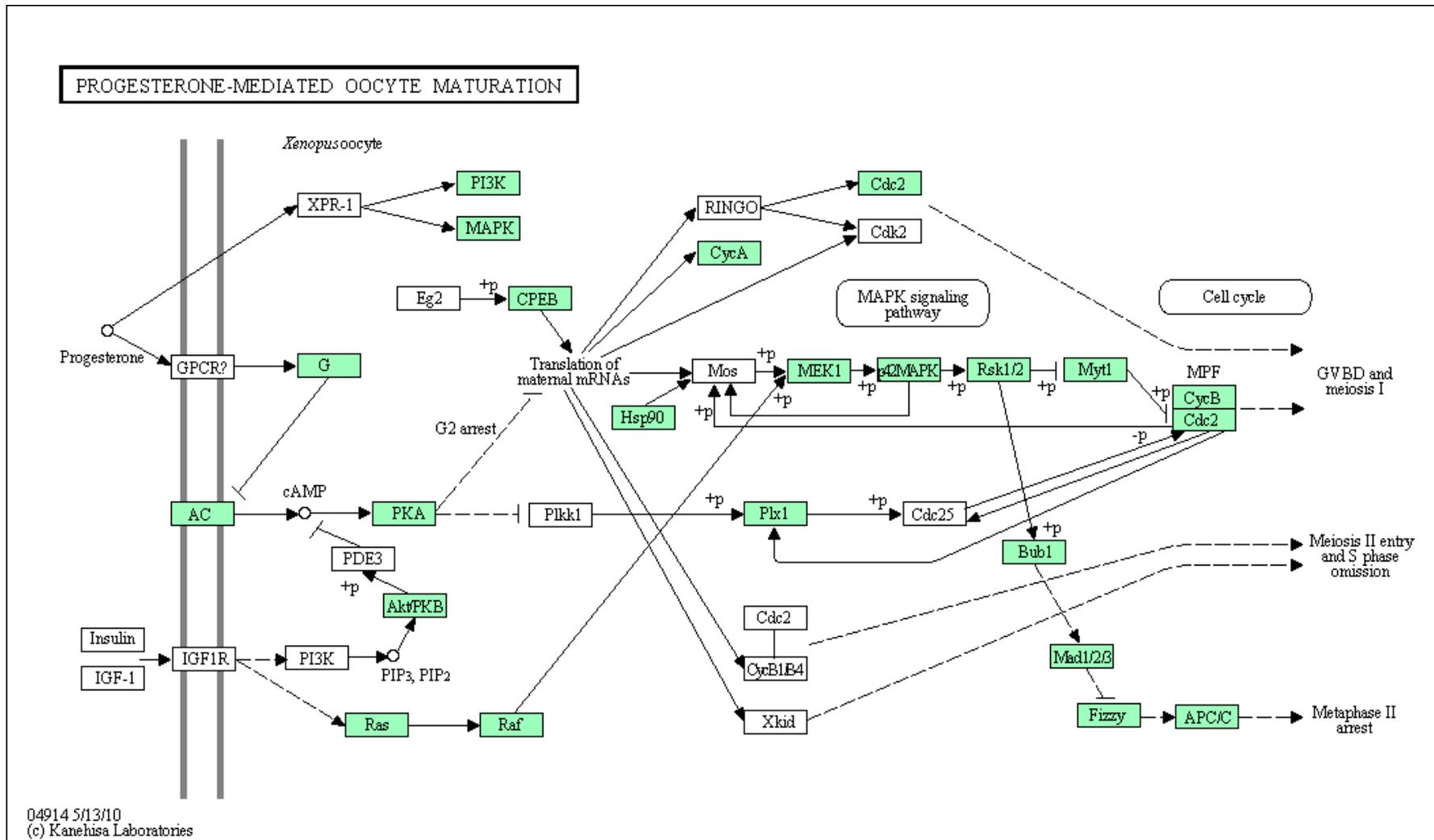
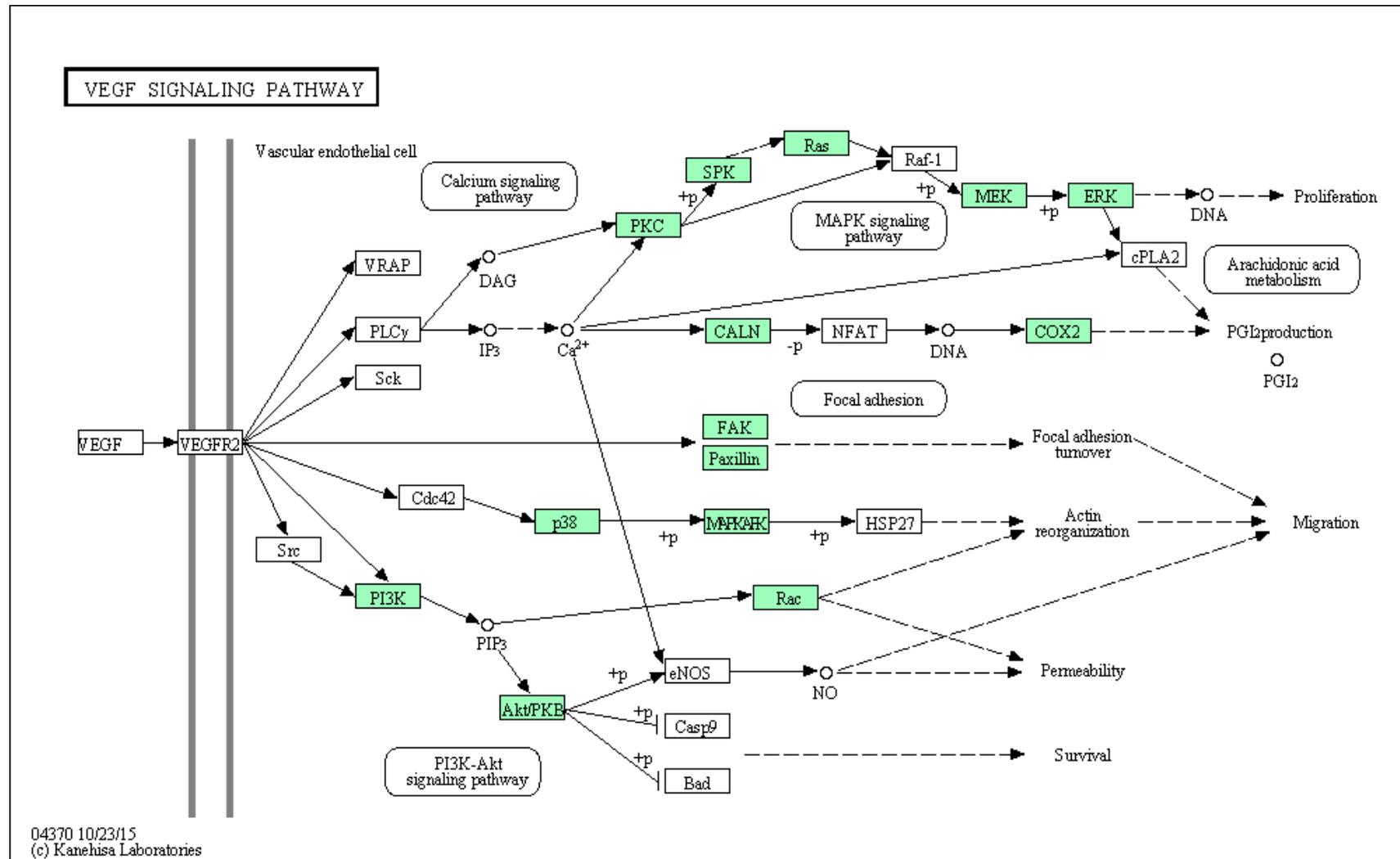
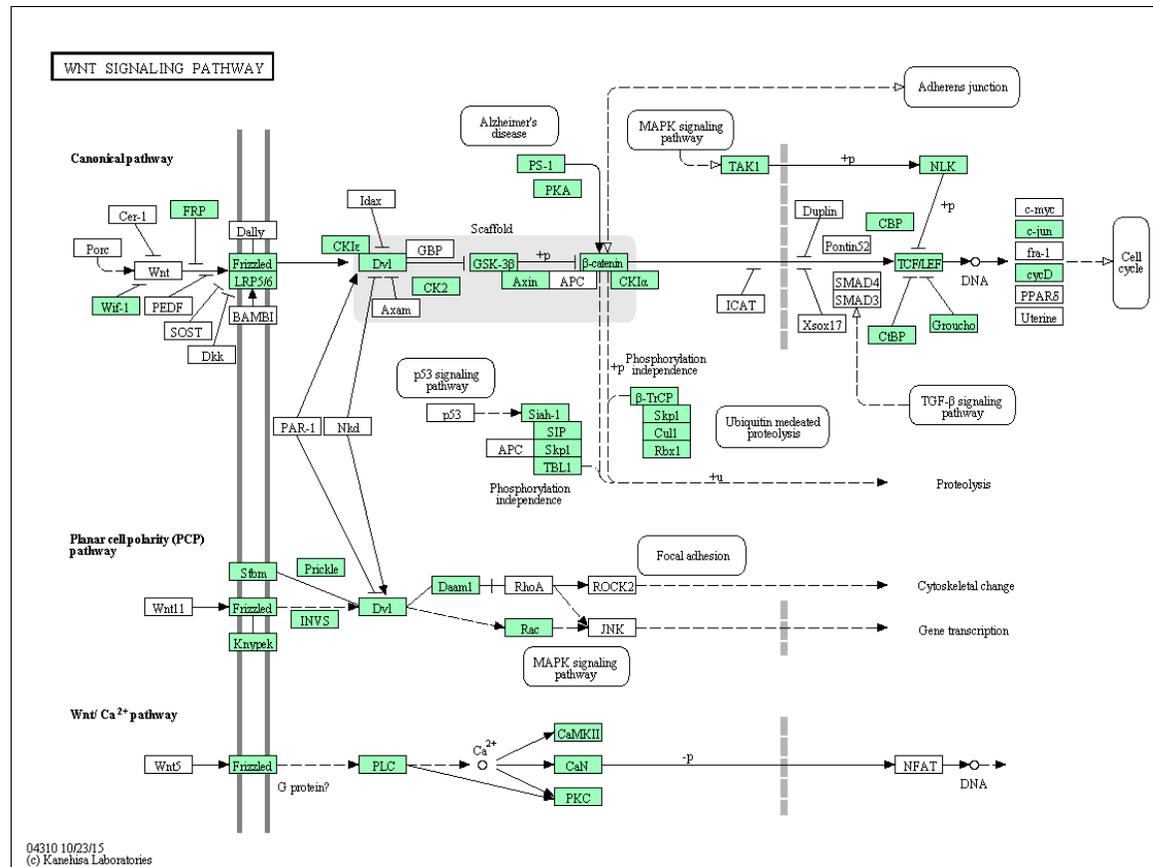


Figure S1. Cont.



(J)

Figure S1. Cont.



(K)

Figure S1. Summary of KEGG MAPs for all combined contigs in *M. rosenbergii*. Similarity of contigs generated with the CLC Genomic Workbench were searched and annotated using KAAS (KEGG Automatic Annotation Server). A few selected KEGG pathway maps potentially involved in sex differentiation and gonadal reproduction are presented. (A) ERBB signalling pathway; (B) estrogen signalling pathway; (C) GnRH signalling pathway; (D) insulin secretion; (E) insulin resistance; (F) insulin signalling pathway; (G) oocyte meiosis; (H) ovarian steroidogenesis; (I) progesterone-mediated oocyte maturation; (J) VEGF signalling pathway; (K) WNT signalling pathway.