

# 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  $1 \times 10^{-5}$ .

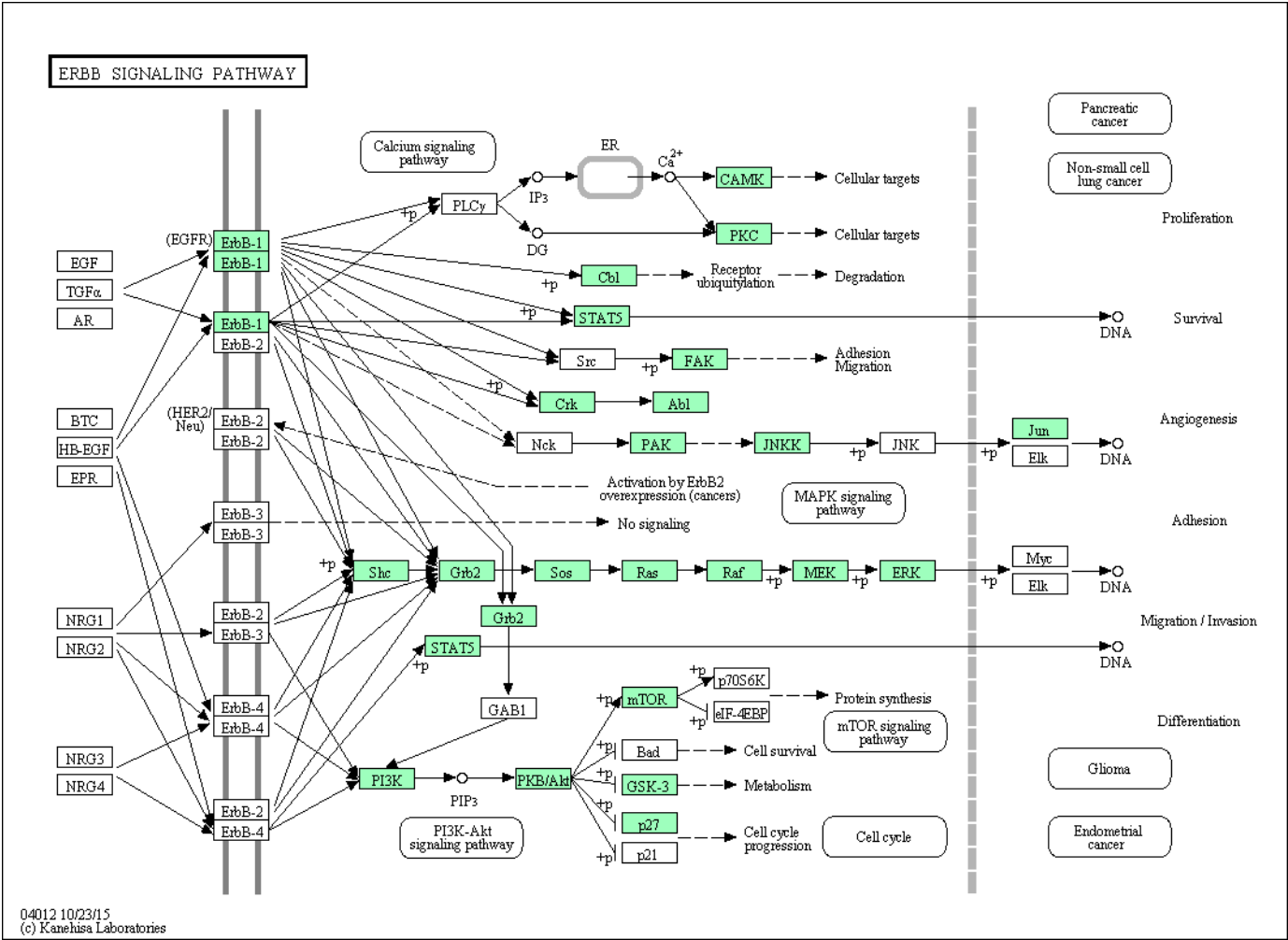
**Table S2.** Summary of KEGG IDs for all combined contigs in *M. rosenbergii*. Similarity of contigs generated with the CLC Genomic Workbench were searched and annotated using KAAS.

**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.

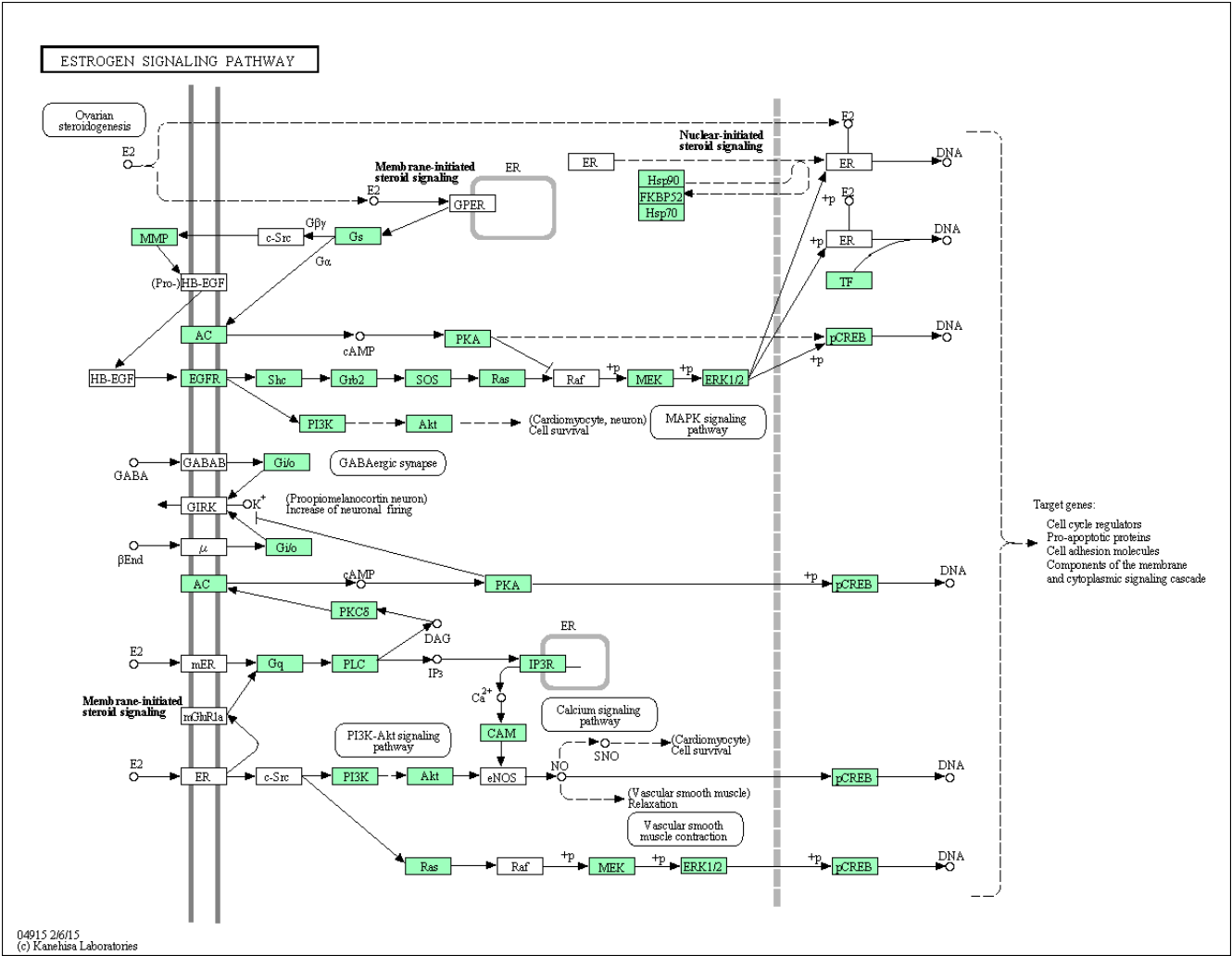
**Table S5.** Putative SNPs for all combined *M. rosenbergii* contig sequences. Contigs generated with the CLC Genomic Workbench were employed as a reference sequence to identify polymorphisms.

**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.



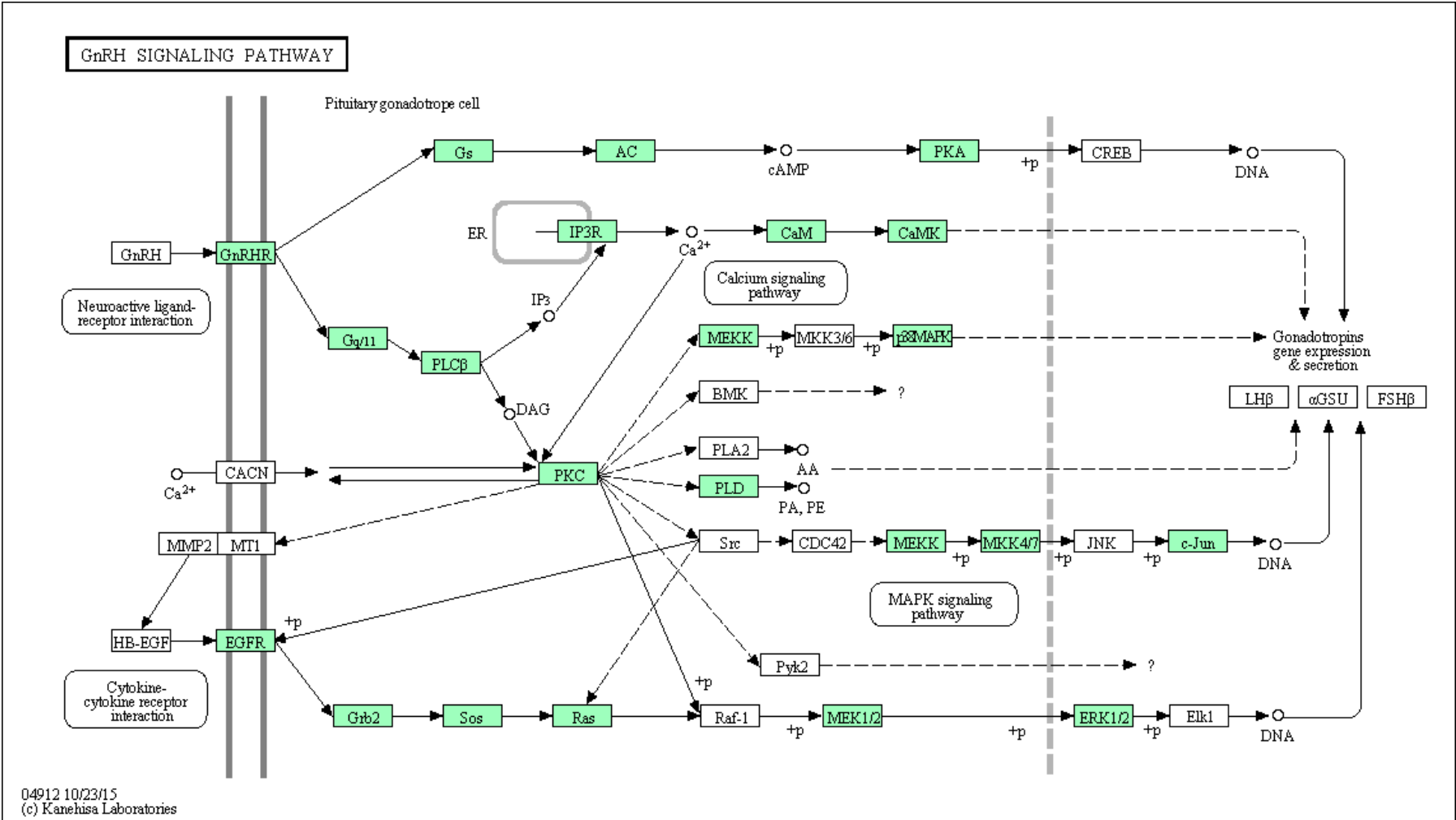
(A)

Figure S1. Cont.



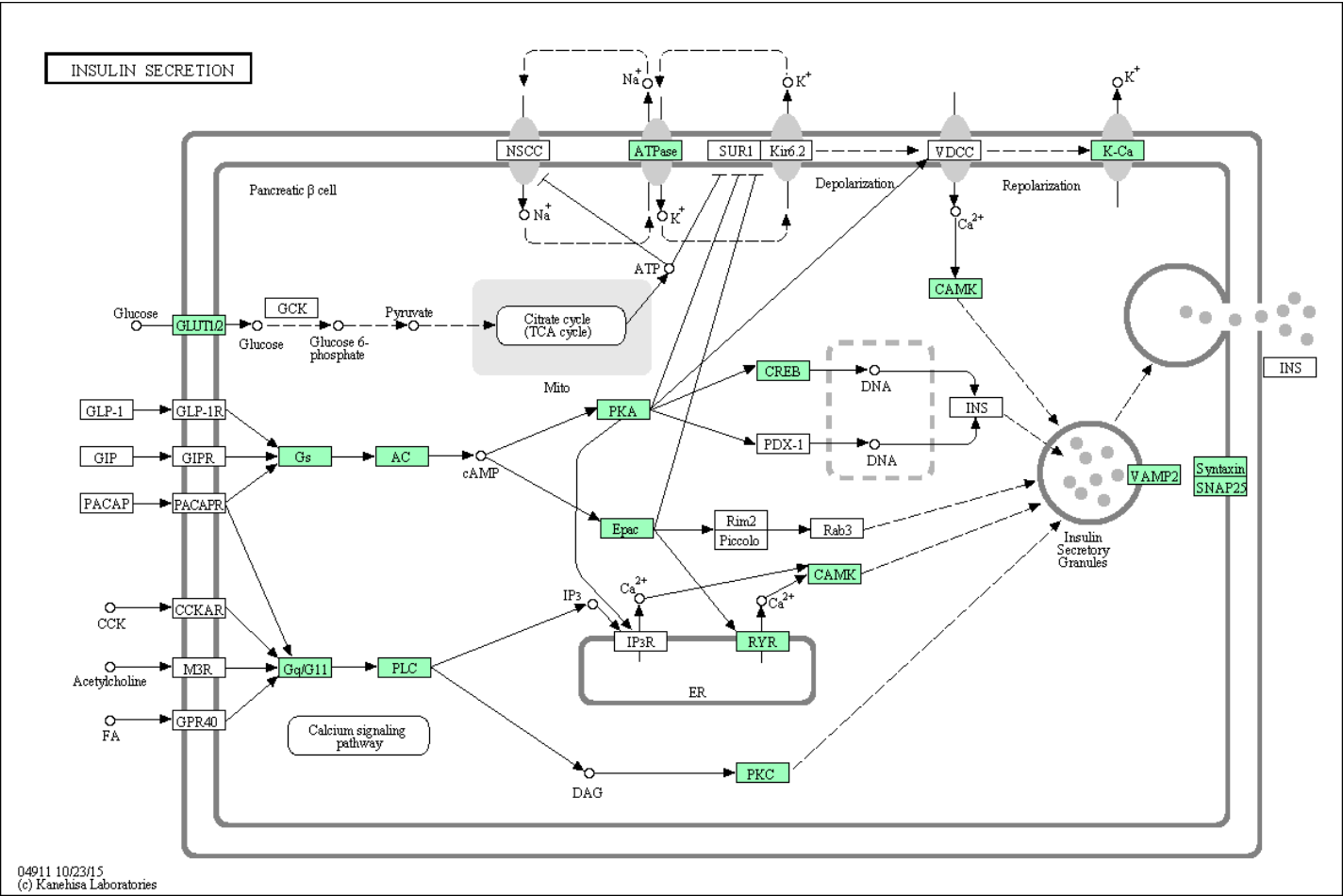
(B)

Figure S1. Cont.



(C)

Figure S1. Cont.



(D)

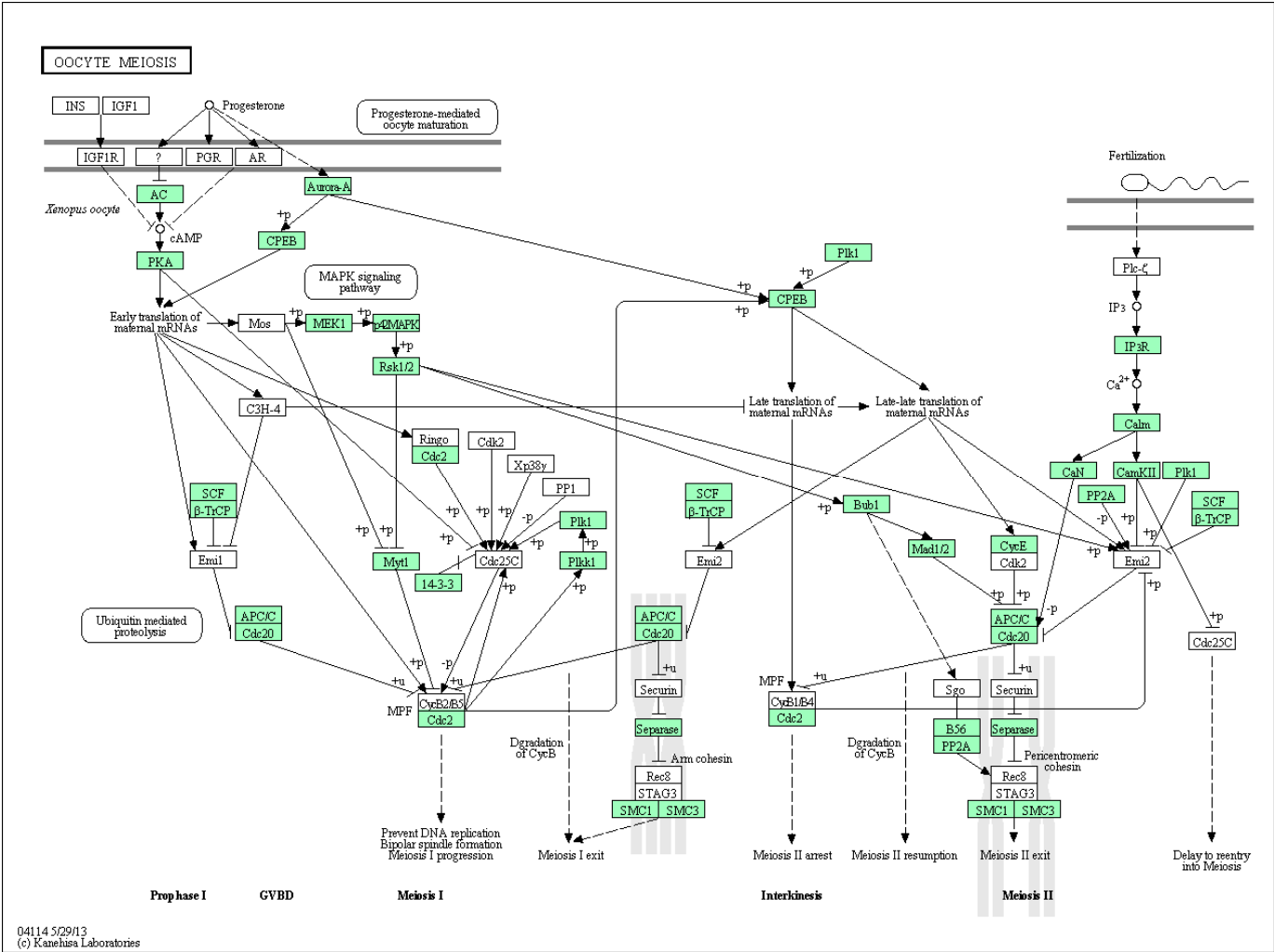
Figure S1. Cont.



**Figure S1. Cont.**



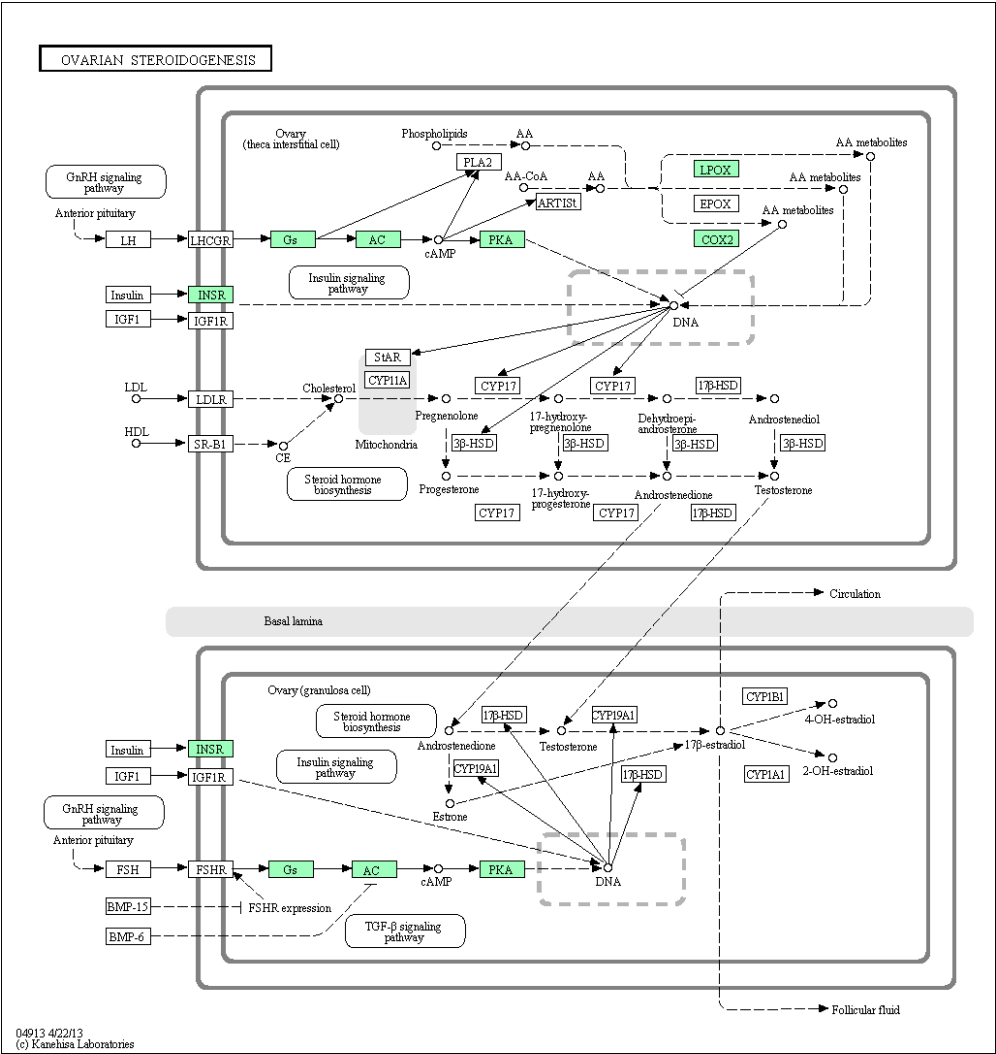
**Figure S1. Cont.**



(G)

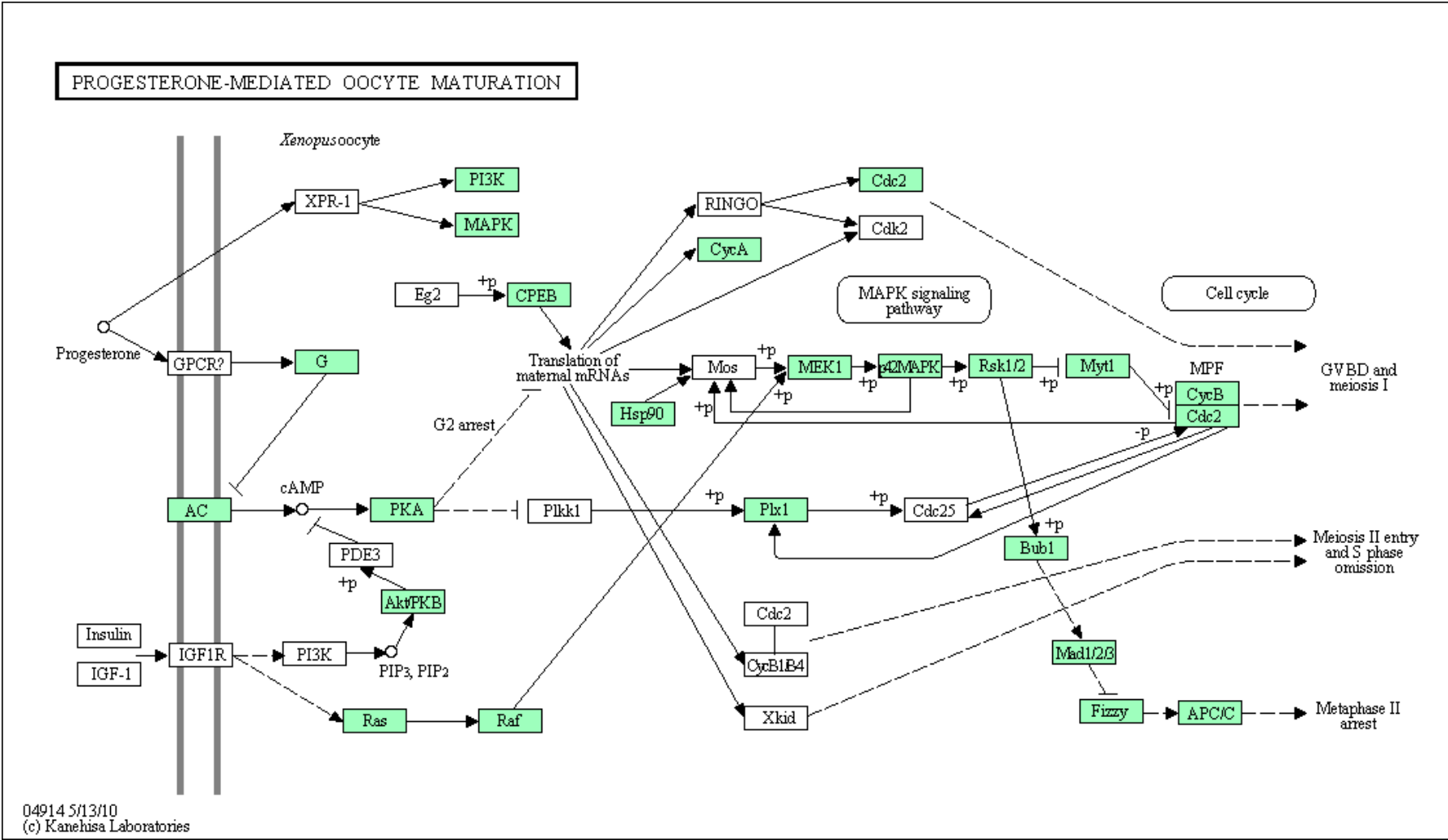
Figure S1. Cont.





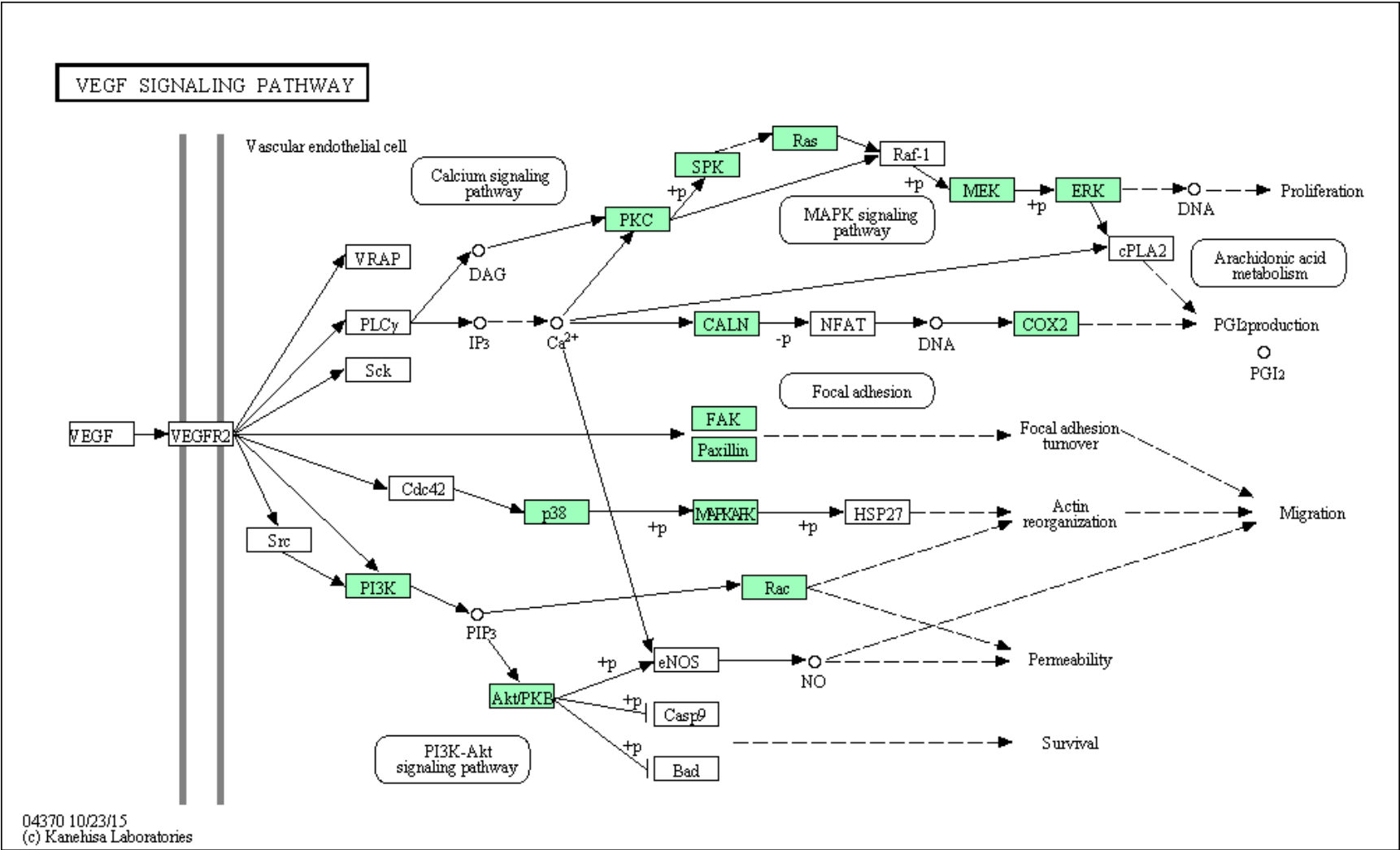
(H)

Figure S1. Cont.



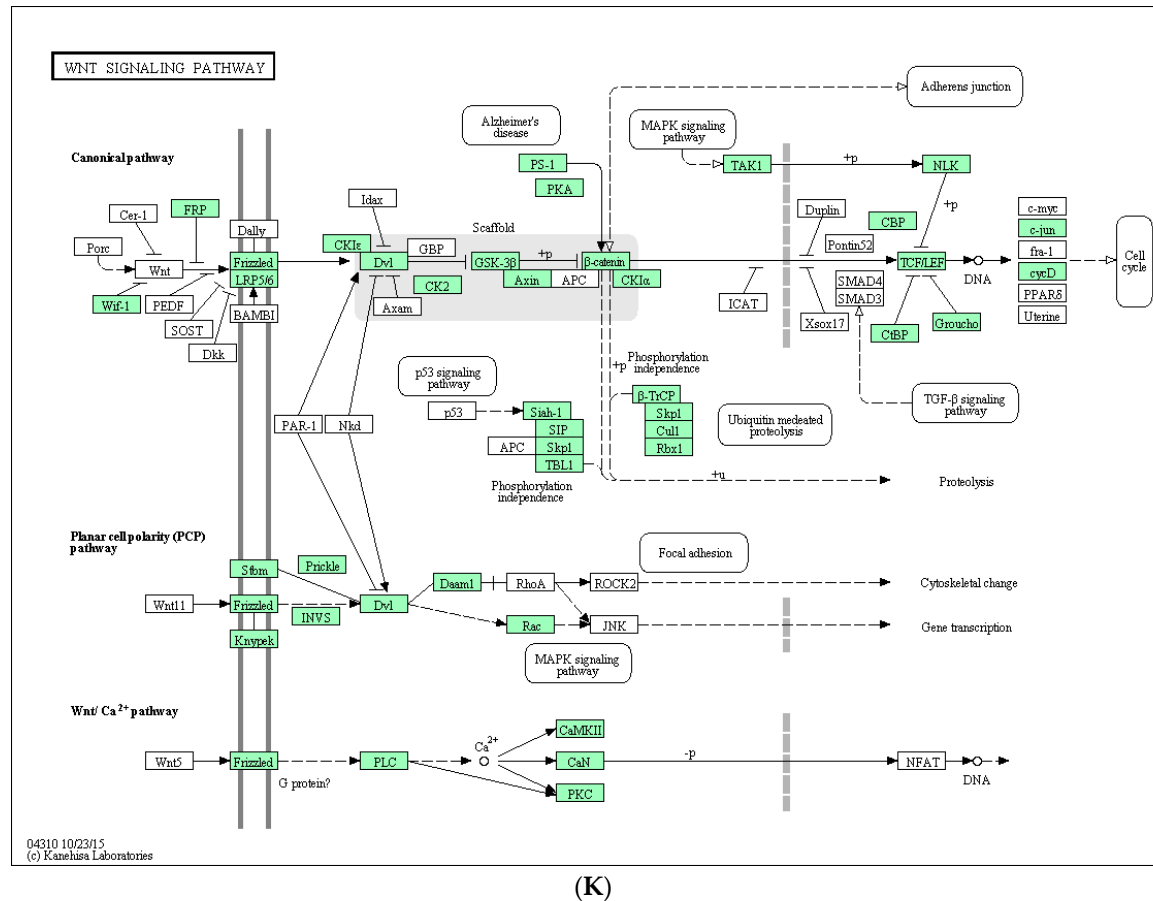
(I)

Figure S1. Cont.



(J)

Figure S1. Cont.



**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.