

Supplementary Figure S1

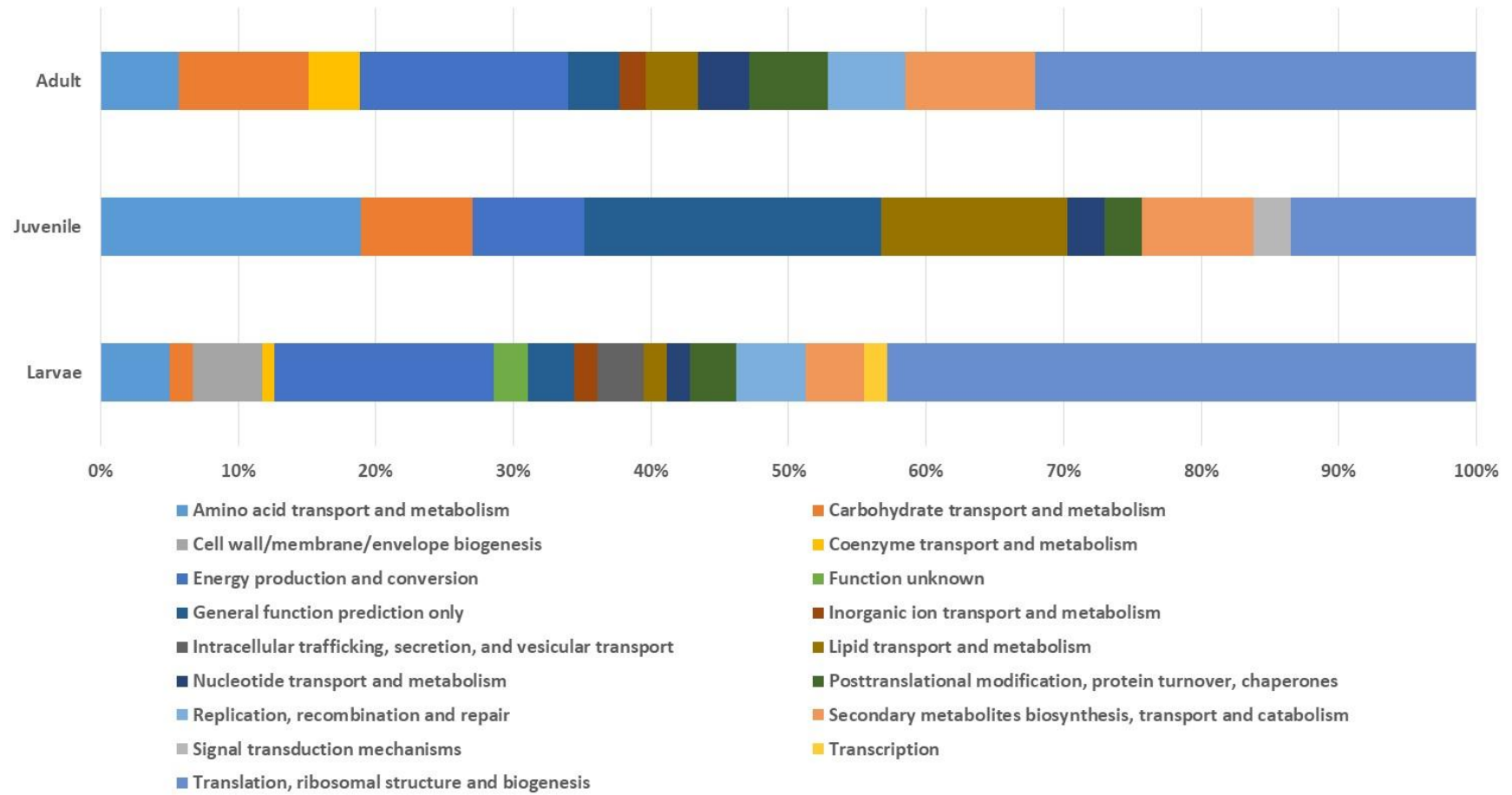


Figure S1. Functional classification based on level 2 of clustered orthologous groups in the microbiome of *L. vannamei* during different stages of development.

Supplementary Figure S2

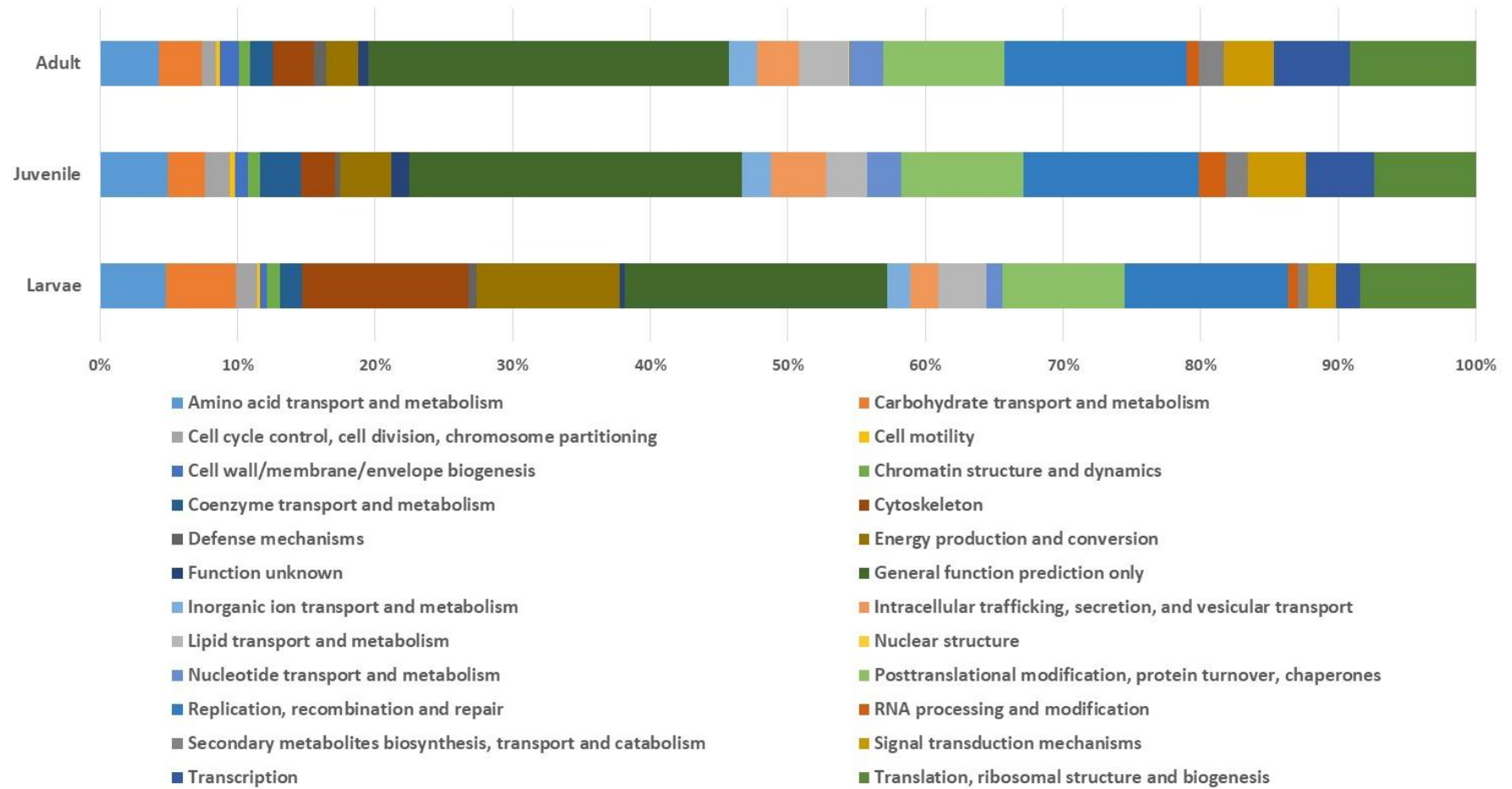


Figure S2. Functional classification based on level 2 clustered of orthologous groups in the eukaryotic transcripts during the development of *L. vannamei*.

Supplementary Figure S3

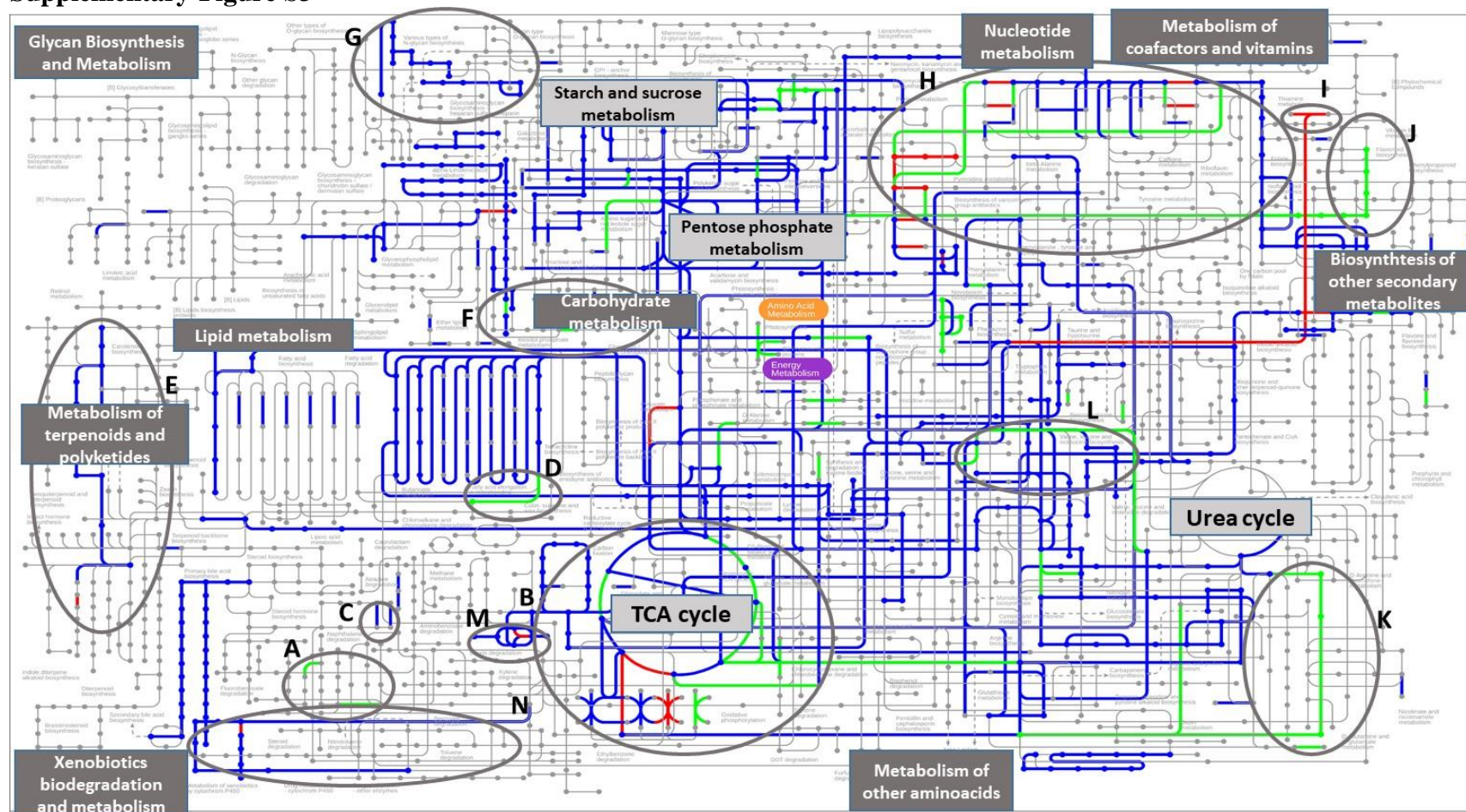


Figure S3. Global metabolic pathway analysis in larval stages of *L. vannamei*. Blue lines represent the host enzymatic modules, Red lines represents the microbiome enzymatic modules, Green lines represents shared enzymatic modules. (A) Xenobiotic degradation, (B) Energy metabolism (TCA, Oxidative phosphorylation), (C) Steroid biosynthesis, (D) Fatty Acid elongation, (E) Terpenoids and Polyketide metabolism, (F) Streptomycin biosynthesis, (G) Glycan biosynthesis (N-glycan, glycosaminoglycan), (H) Nucleotide metabolism, (I) Thiamine metabolism, (J) Vitamin B6 biosynthesis, (K) Aminoacid metabolism (Arg, Prol), (L) Glyoxylate and dicarboxylate metabolism (M) Carbon fixation, (N) Xenobiotic degradation (Toluene, Benzoate).

Supplementary Figure S4

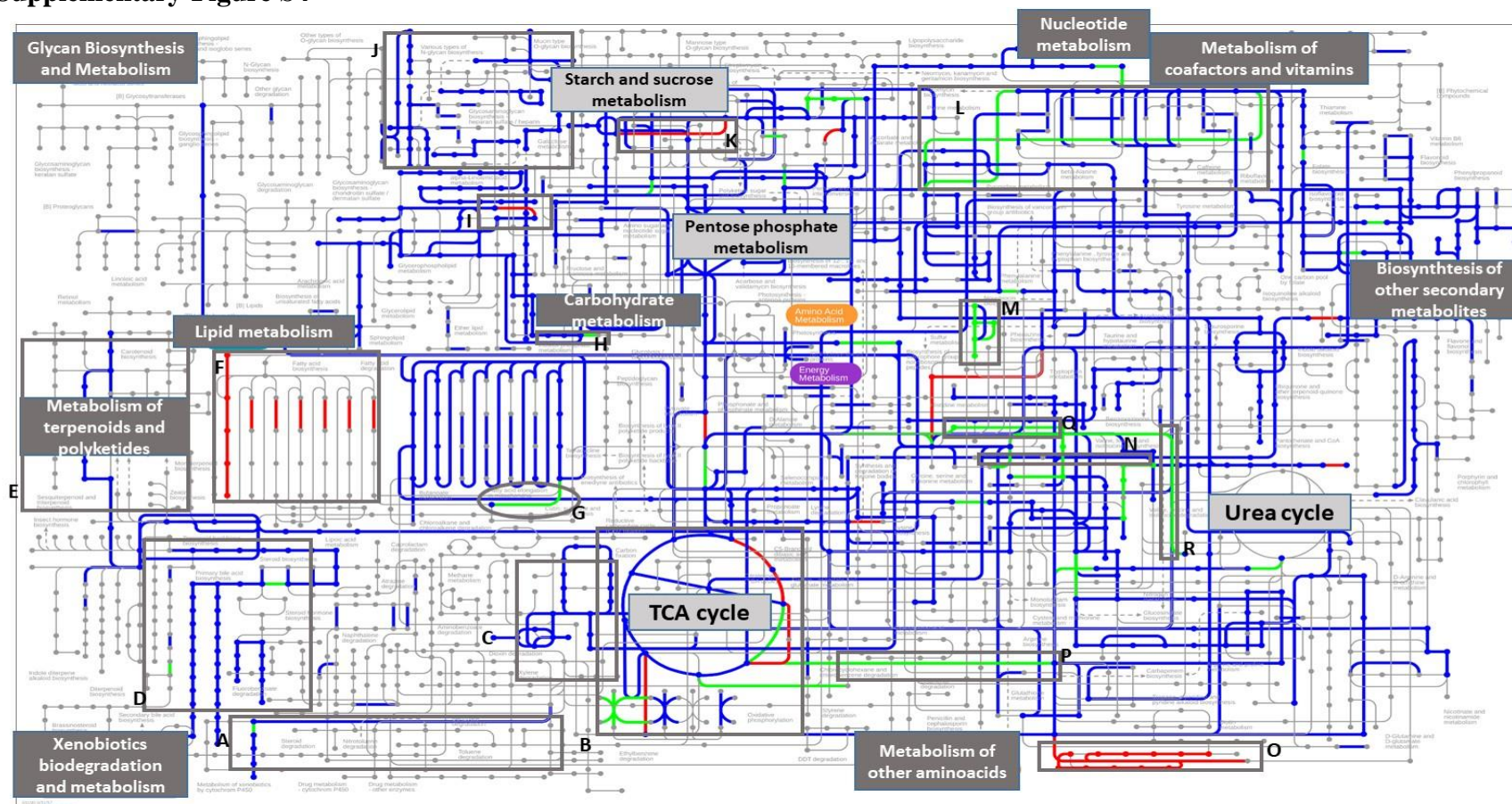


Figure S4. Global metabolic pathway analysis in juvenile stages of *L. vannamei*. Blue lines represents eukaryotic enzymatic modules, Red lines represents prokaryotic enzymatic modules, Green lines represents shared enzymatic modules. (A) Xenobiotic degradation (Toluene, Benzoate, Aminobenzoate), (B) Energy metabolism (TCA, Oxidative phosphorylation), (C) Carbon fixation in photosynthetic organisms, (D) Bile acids and steroid hormone biosynthesis, (E) Carotenoid biosynthesis, (F) Fatty acid biosynthesis, (G) Fatty acid elongation, (H) Streptomycin biosynthesis, (I) Glycerolipid metabolism, (J) Glycan biosynthesis (N-glycan, O-glycan, glycosaminoglycan), (K) Galactose metabolism, (L) Nucleotide metabolism, (M) Sulfur metabolism, (N) Porphyrin and Chlorophyll metabolism, (O) Biotin metabolism, (P) Nitrogen metabolism, (Q) Val, Leu and Ile biosynthesis, (R) Glyoxylate and dicarboxylate metabolism.

Supplementary Figure S5

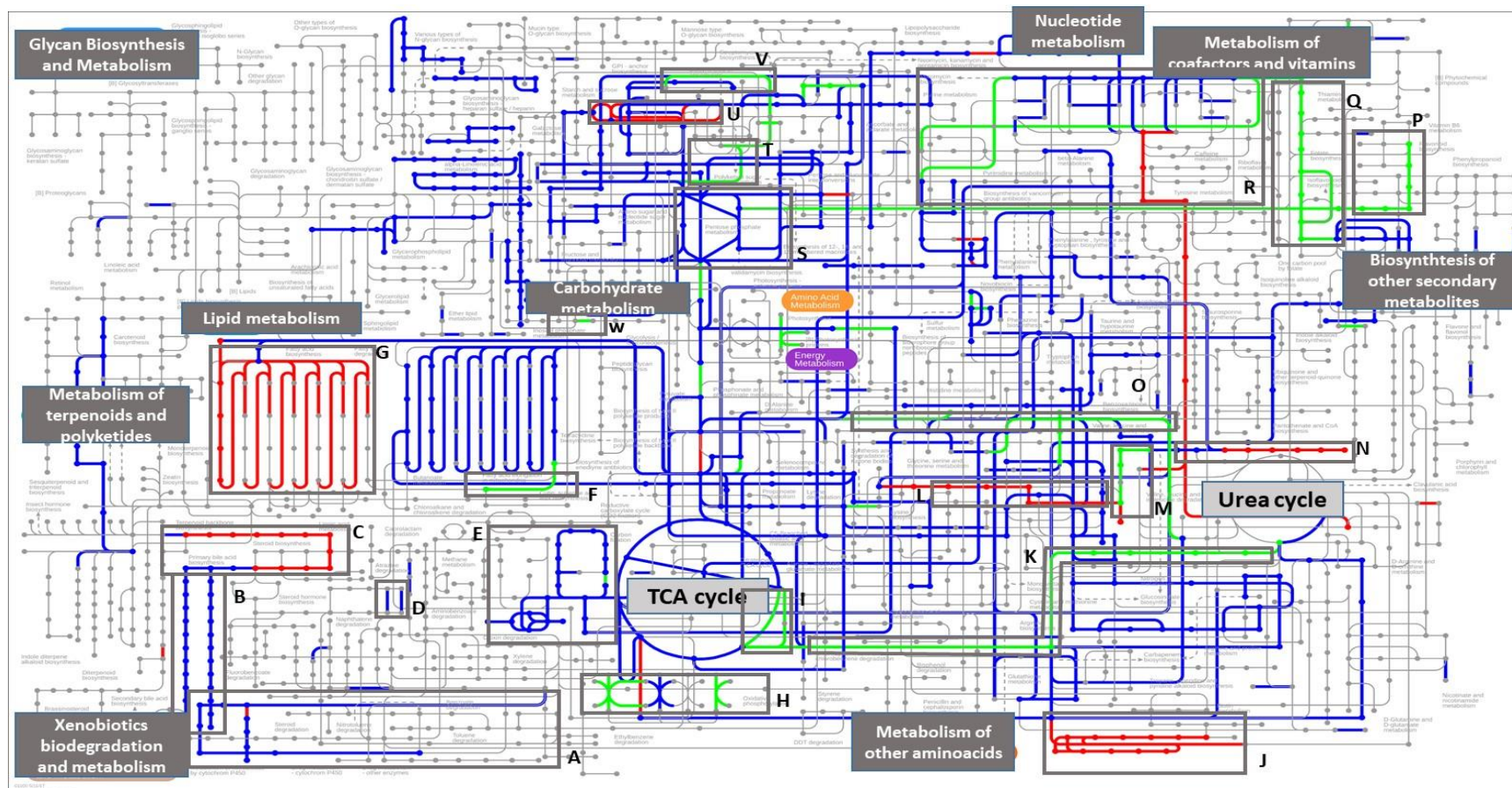


Figure S5. Global metabolic pathway analysis in adult stages of *L. vannamei*. Blue lines represents eukaryotic enzymatic modules, Red lines represents prokaryotic enzymatic modules, Green lines represents shared enzymatic modules. (A) Xenobiotic degradation, (B) Primary bile acid production, (C) Steroid biosynthesis, (D) Steroid hormone biosynthesis, (E) Photosynthetic carbon fixation, (F) Fatty acid elongation, (G) Fatty acid biosynthesis, (H) Oxidative phosphorylation, (I) Carbon fixation in prokaryotes, (J) Biotin, Arginine and Proline Metabolism, (K) Nitrogen metabolism, (L) Branched Aminoacid degradation, (M) Branched aminoacid biosynthesis, (N) Panthothenate biosynthesis, (O) Glyoxylate and dicarboxylate metabolism, (P) Vitamin B6 biosynthesis, (Q) Folate biosynthesis, (R) Nucleotide metabolism, (S) Ansamycin biosynthesis, (T) Galactose metabolism, (U) Aminosugar metabolism, (V) Starch and sucrose metabolism, (W) Streptomycin biosynthesis.

Supplementary Table S1.

Table S1. Metabolic pathway analysis of the microbiome of *L. vannamei* in different stages of development using the KEGG orthology classification.

KO	Bacterial Metabolic Pathways	% Contigs		
		Larvae	Juvenile	Adult
Aminoacid metabolism	Ala, Asp and Glu metabolism	3.5	5.4	1.2
	Gly, Ser and Thr metabolism	1.2	13	3.7
	Cys and Met metabolism	1.7	5.4	NR
	Val, Leu and Ile degradation	1.7	9.1	1.2
	Arg and Pro metabolism	NR	3.6	2.5
	Trp metabolism	0.6	3.6	NR
Carbohydrate metabolism	Pyruvate metabolism	1.2	1.8	3.7
	Glycolysis / Gluconeogenesis	NR	3.6	1.2
	Pentose phosphate pathway	2.3	1.8	1.2
	Pentose and glucuronate interconversions	1.2	1.8	3.7
Lipid metabolism	Fatty acid biosynthesis	NR	1.8	2.5
	Steroid biosynthesis	NR	1.8	1.2
	Glycerolipid metabolism	NR	1.8	NR
	Fatty acid biosynthesis	8.7	0.5	5.5
Energy metabolism	Oxidative phosphorylation	1.7	NR	3.7
Nucleotide metabolism	Purine metabolism	2.3	1.8	2.5
Signal transduction	Two-component system	2.3	1.8	1.2
Transcription	RNA polymerase	42	13	30
Translation	Ribosome	2.3	1.8	1.2
Transport and Catabolism	Peroxisome	0.5	NR	5.0
Cancers	Pathways in cancer	NR	1.8	2.5

NR: Non represented pathways.

Supplementary Table S2.

Table S2. Metabolic pathway analysis of *L. vannamei* in different stages of development using the KEGG orthology classification.

KO	Eukaryotic Metabolic Pathways	% Contigs		
		Larvae	Juvenile	Adult
Aminoacid metabolism	Val, Leu and Ile degradation	2.5	1.5	1.1
	Gly, Ser and Thr metabolism	1.9	1.0	1.3
Carbohydrate metabolism	Citrate cycle (TCA cycle)	2.4	0.3	0.3
	Pentose and glucuronate interconversions	0.8	1.0	0.9
Cell communication	Tight junction	5.0	1.5	1.8
	Focal adhesión	4.6	2.9	4.0
Folding, sorting and degradation	Protein processing in endoplasmic reticulum	3.4	3.6	2.2
	Ubiquitin mediated proteolysis	1.5	4.6	3.7
Glycan biosynthesis and metabolism	Other types of O-glycan biosynthesis	0.2	0.4	0.1
	N-Glycan biosynthesis	NR	1.0	1.0
Lipid metabolism	Fatty acid metabolism	0.7	0.2	0.1
	Glycerolipid metabolism	0.1	1.0	1.0
Signal transduction	Calcium signaling pathway	2.1	0.7	0.6
	MAPK signaling pathway	1.3	2.7	1.7
Translation	Ribosome	6.0	1.5	3.0
	RNA transport	2.2	2.8	2.3
Infectious diseases	Vibrio cholerae infection	0.5	NR	0.1
	Malaria	0.1	0.5	0.3
Cancers	Chemical carcinogénesis	0.6	0.3	0.7
Cell growth and death	Cell cycle	1.8	3.6	2.4
Cell motility	Regulation of actin cytoskeleton	1.0	1.0	1.2
Digestive system	Protein digestion and absorption	0.1	0.2	0.5
Energy metabolism	Methane metabolism	0.7	0.2	0.1
Immune system	RIG-I-like receptor signaling pathway	NR	0.1	0.1
Membrane transport	ABC transporters	0.2	0.4	1.1

Nucleotide metabolism	Purine metabolism	0.5	0.9	1.4
Transcription	Spliceosome	3.0	5.7	5.7
Transport and catabolism	Lysosome	3.7	3.2	3.5
Biosynthesis of other secondary metabolites	Streptomycin biosynthesis	0.3	0.2	0.2

NR: Non represented pathways.