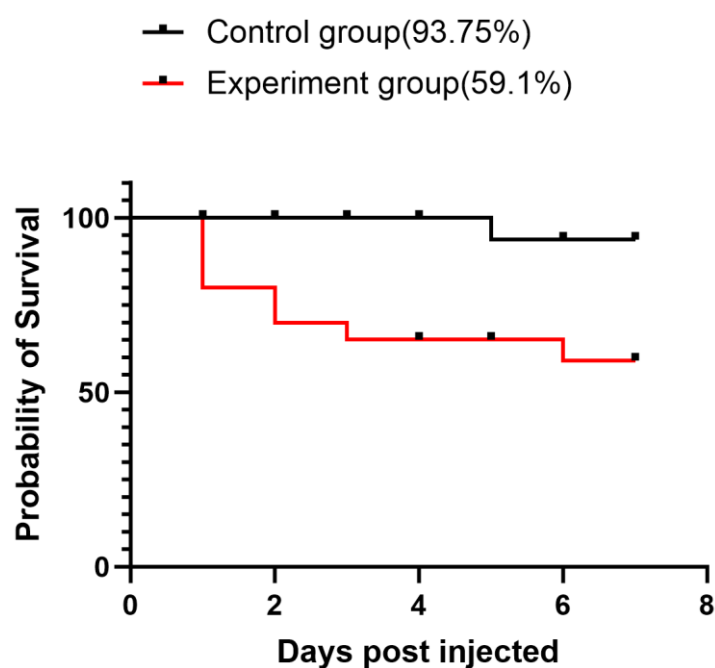


Table S1. The probability of survival within 7 days

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Table S2. Data of RNA-seq

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Sample	RawDatas	CleanData(%)	LowQuality(%)
K-48-1	47753060	47446946 (99.36%)	266958 (0.56%)
K-48-2	38889110	38684846 (99.47%)	181574 (0.47%)
K-48-3	38604484	38395500 (99.46%)	184456 (0.48%)
KE-48-1	39520362	39308420 (99.46%)	184330 (0.47%)
KE-48-2	48265518	47946866 (99.34%)	282456 (0.59%)
KE-48-3	41495260	41274004 (99.47%)	192802 (0.46%)
L-48-1	40172522	39956432 (99.46%)	183932 (0.46%)
L-48-2	45829704	45614952 (99.53%)	190136 (0.41%)
L-48-3	39742994	39552752 (99.52%)	171426 (0.43%)
LE-48-1	38716820	38520950 (99.49%)	15540 (0.04%)
LE-48-2	43943394	43724926 (99.50%)	22706 (0.05%)
LE-48-3	36814860	36637164 (99.52%)	17318 (0.05%)

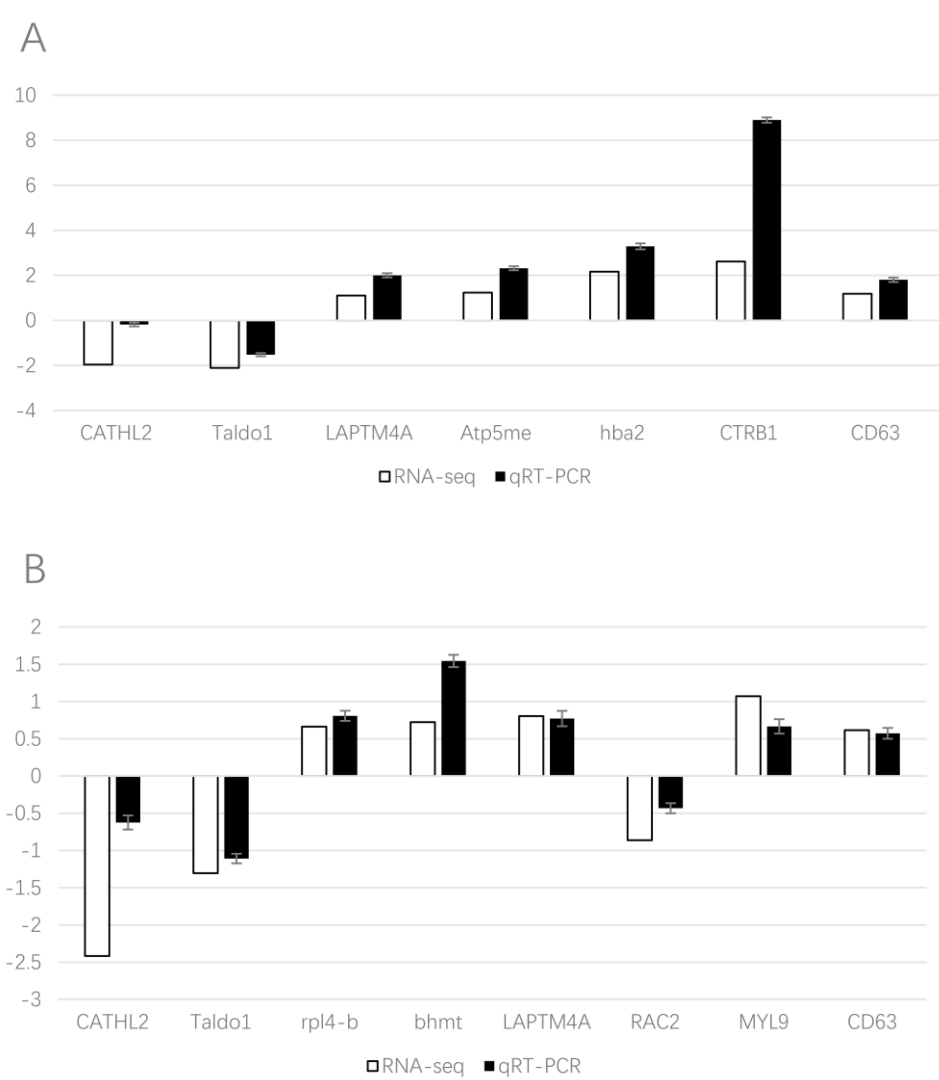


Fig. S1. Quantitative real-time RT-PCR for validation of RNA-seq. The expressions of these genes were detected by RNA-seq (white column) and qRT-PCR (black column). A and B represent the data of qRT-PCR in liver and kidney, respectively.

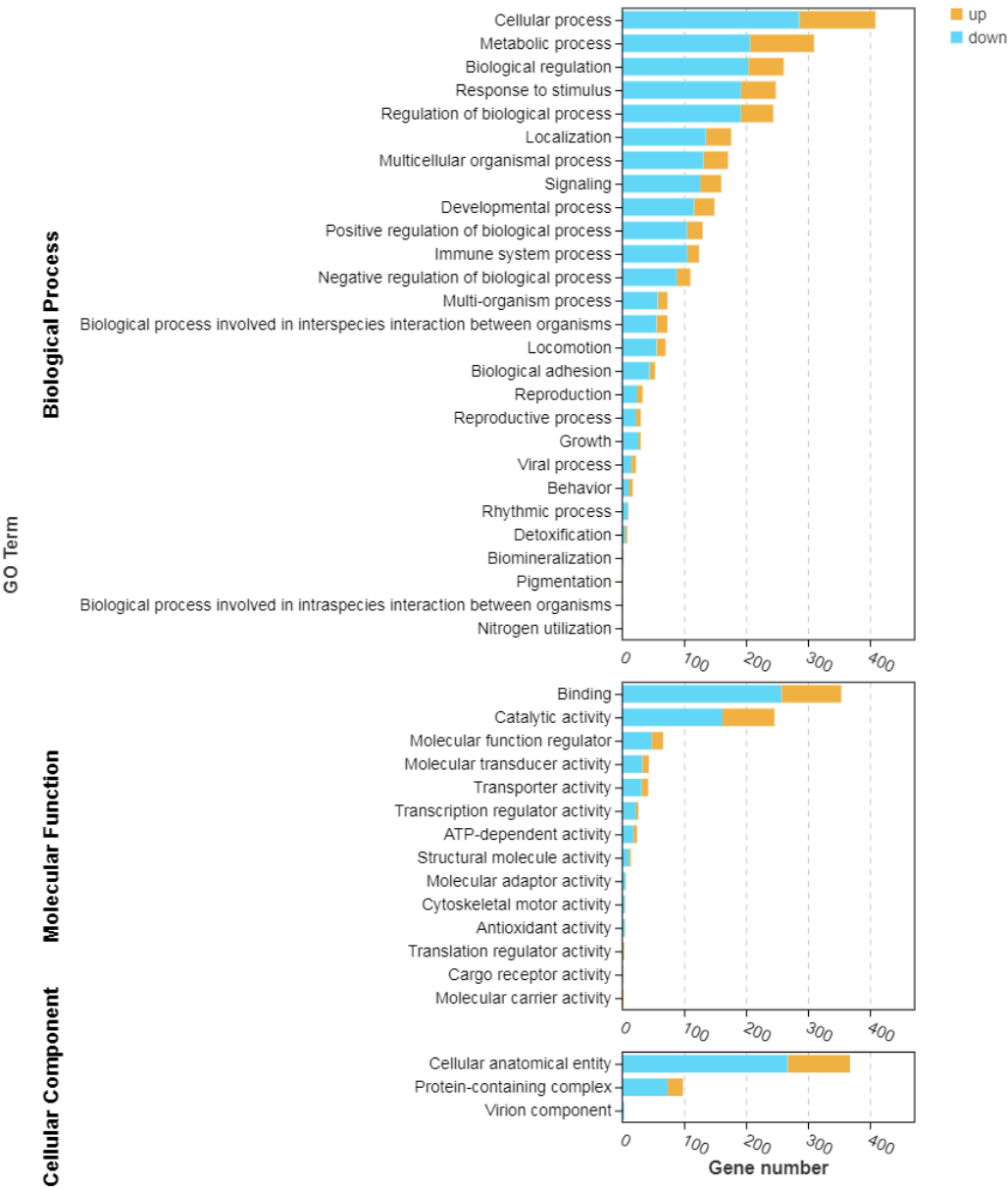


Fig. S2 Gene ontology (GO) enrichment analysis of DEGs in liver.

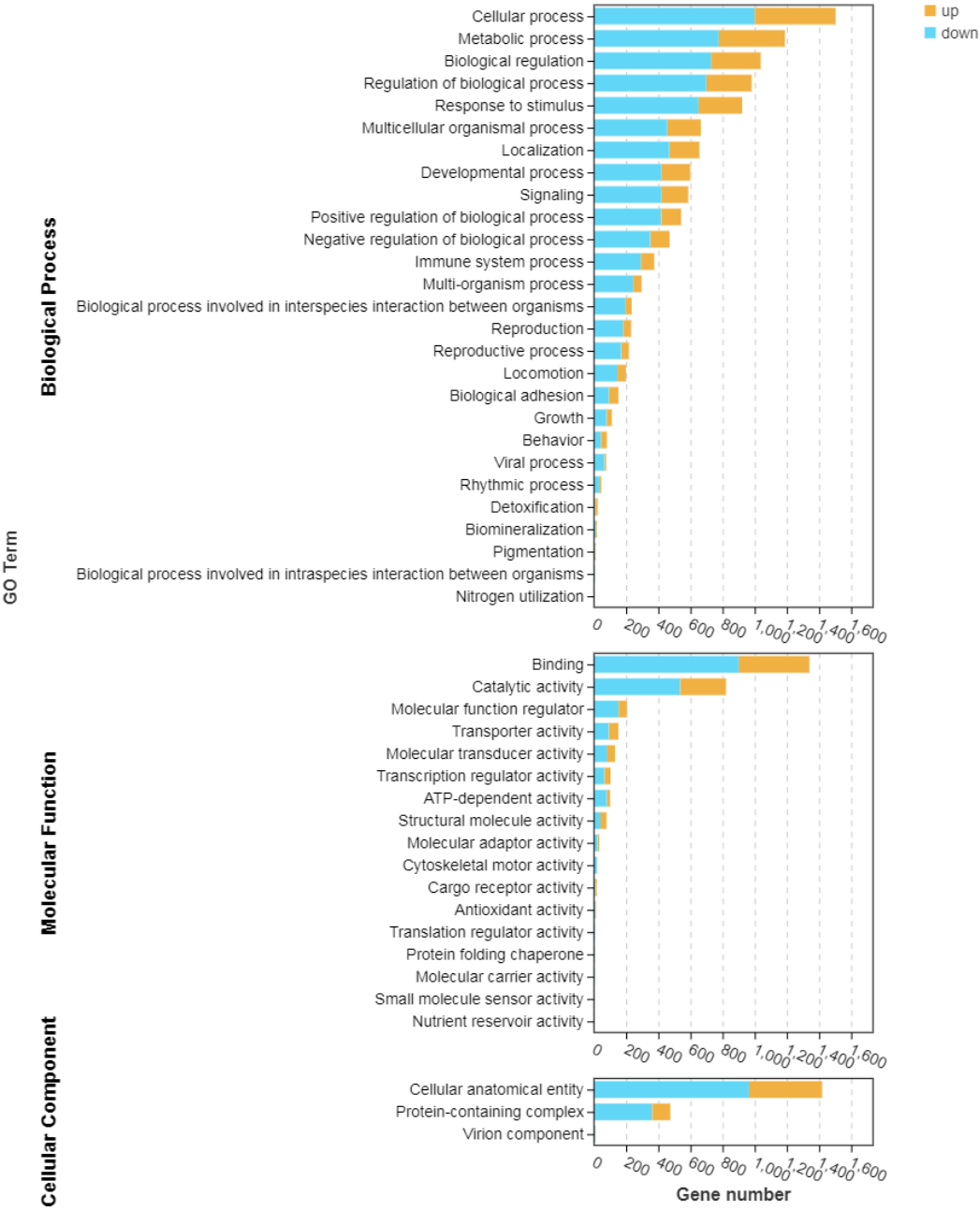


Fig. S3 Gene ontology (GO) enrichment analysis of DEGs in kidney.

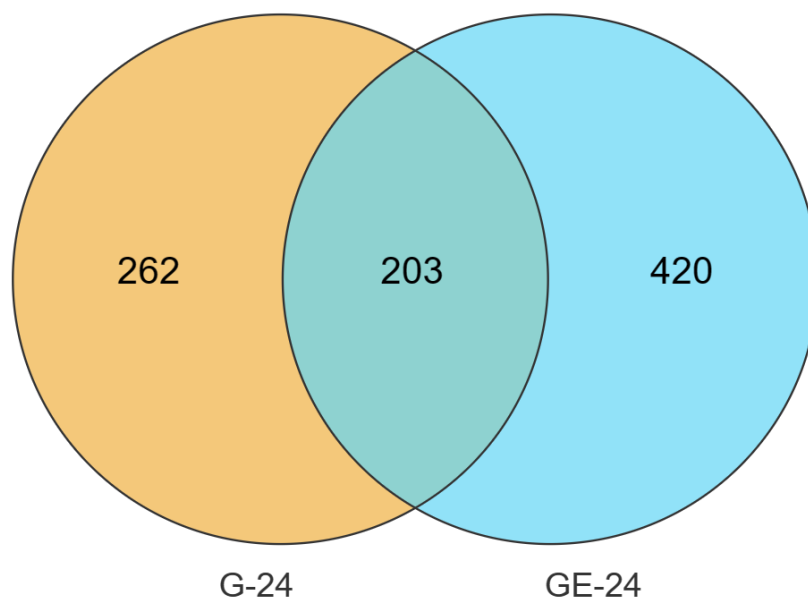
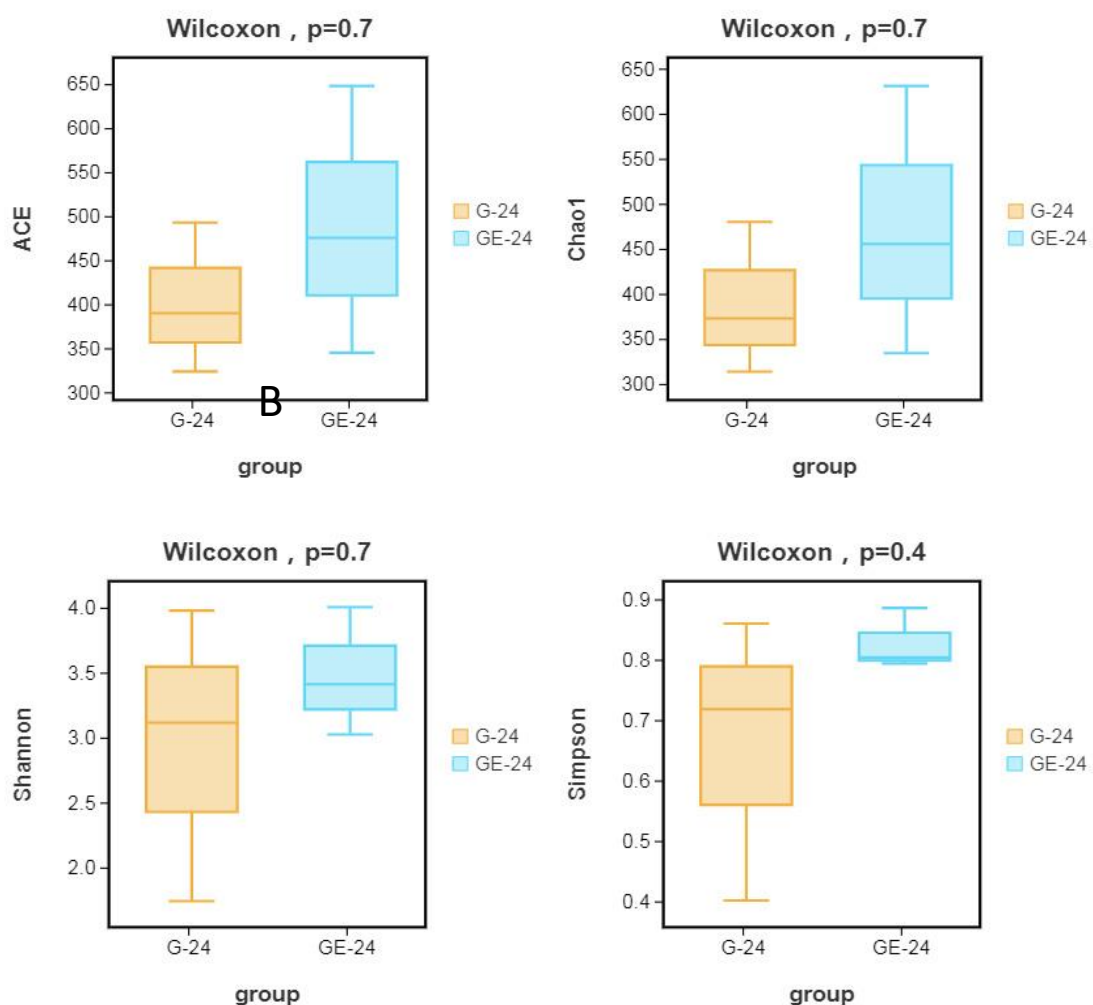


Fig. S4 Numbers and sequence proportions of Shared OTUs between uninfected and infected groups



23

Fig. S5 Alpha diversity of microbial communities in the intestines of uninfected and infected black spotted frog

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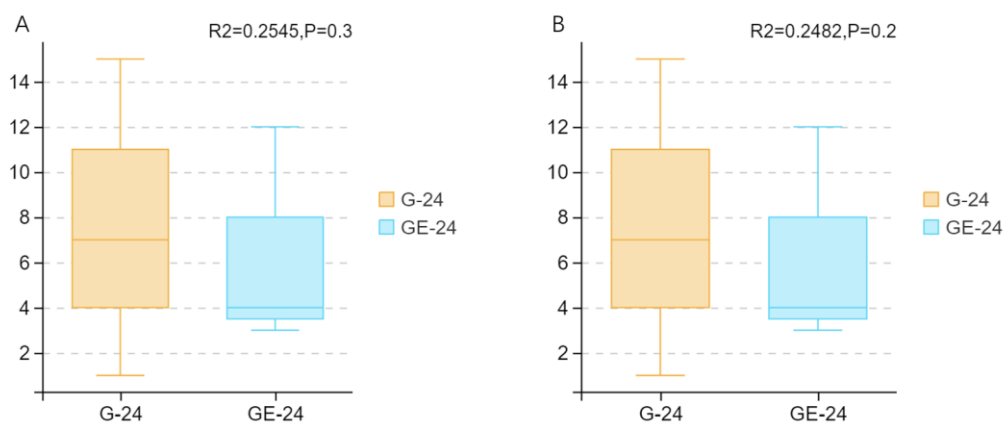


Fig. S6 Beta diversity of microbial communities in the intestines of uninfected and infected black spotted frog. (A) Bray-Curtis dissimilarity. (B) Jaccard dissimilarity.

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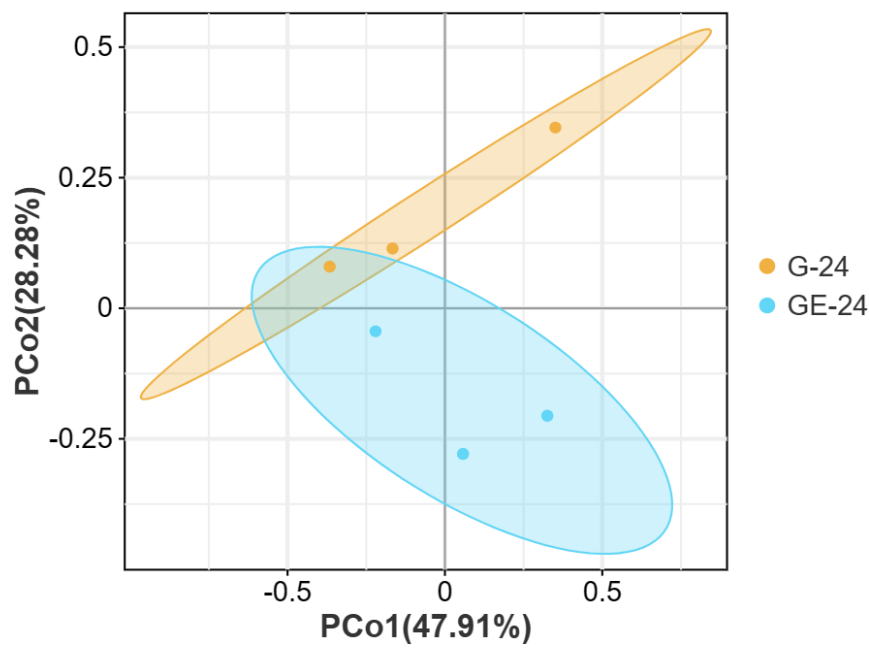


Fig. S7 Principal coordinates analysis (PCoA) of bacterial community structures