

Supplementary Figures

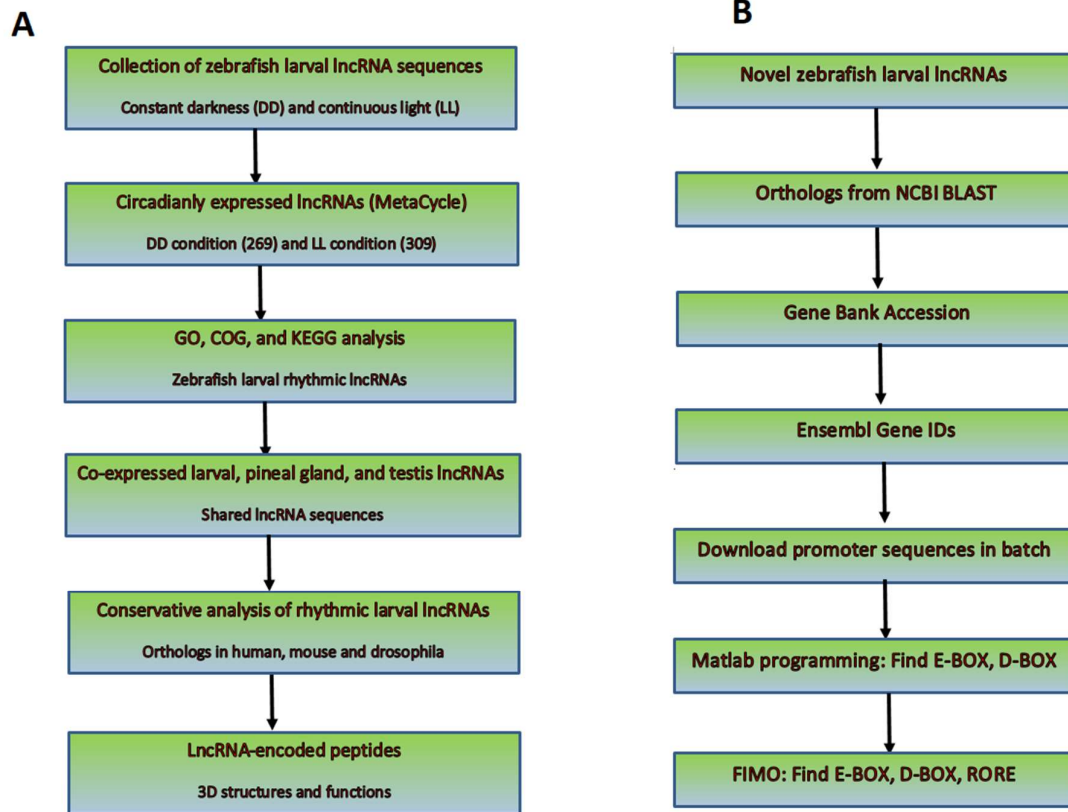


Figure S1. Research pipeline for investigating wild-type zebrafish larval lncRNAs under DD and LL conditions (A) and flow diagram for searching promoter motifs E-Box, D-Box and RORE for morning lncRNAs, evening lncRNAs and night lncRNAs, respectively (B).

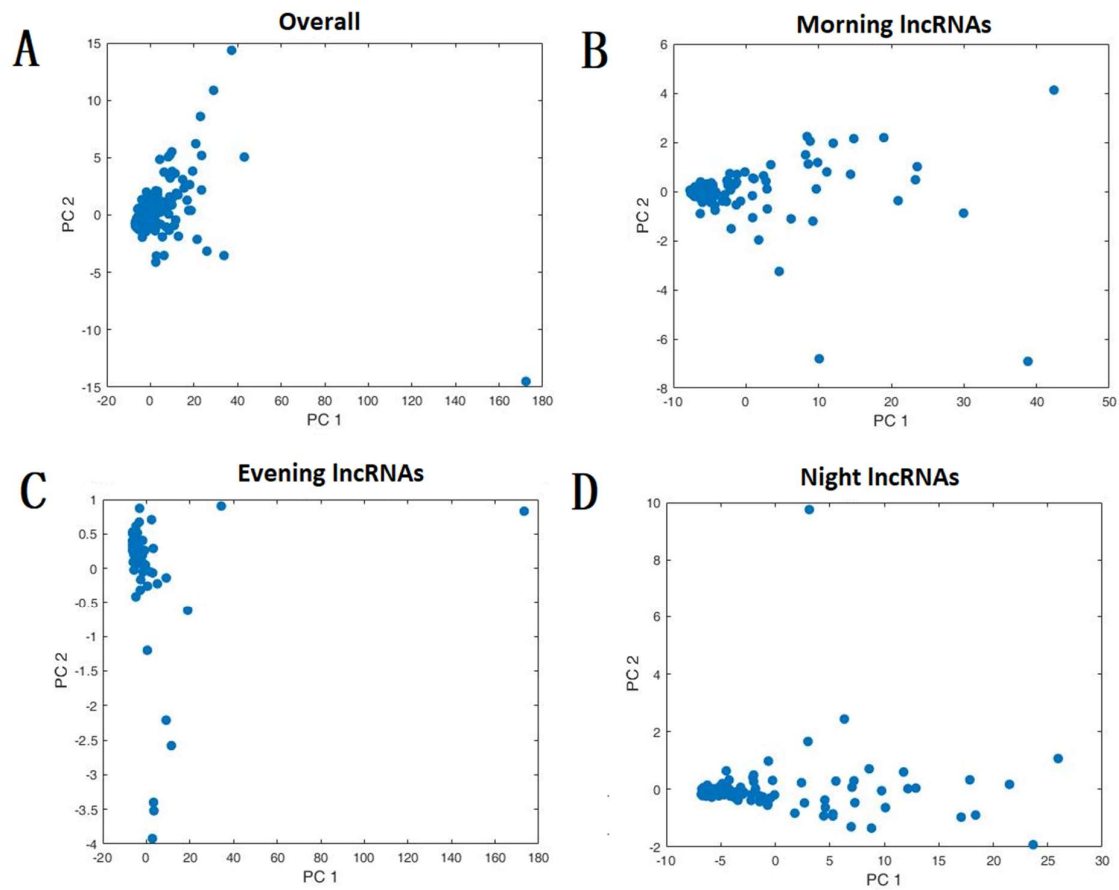


Figure S2. Principal Component Analysis (PCA) of circadianly expressed zebrafish larval lncRNAs under DD condition. All circadianly expressed larval lncRNAs (A), morning (CT0 and CT4) lncRNAs (B), evening (CT8 and CT12) lncRNAs (C), and night (CT16 and CT20) lncRNAs (D).

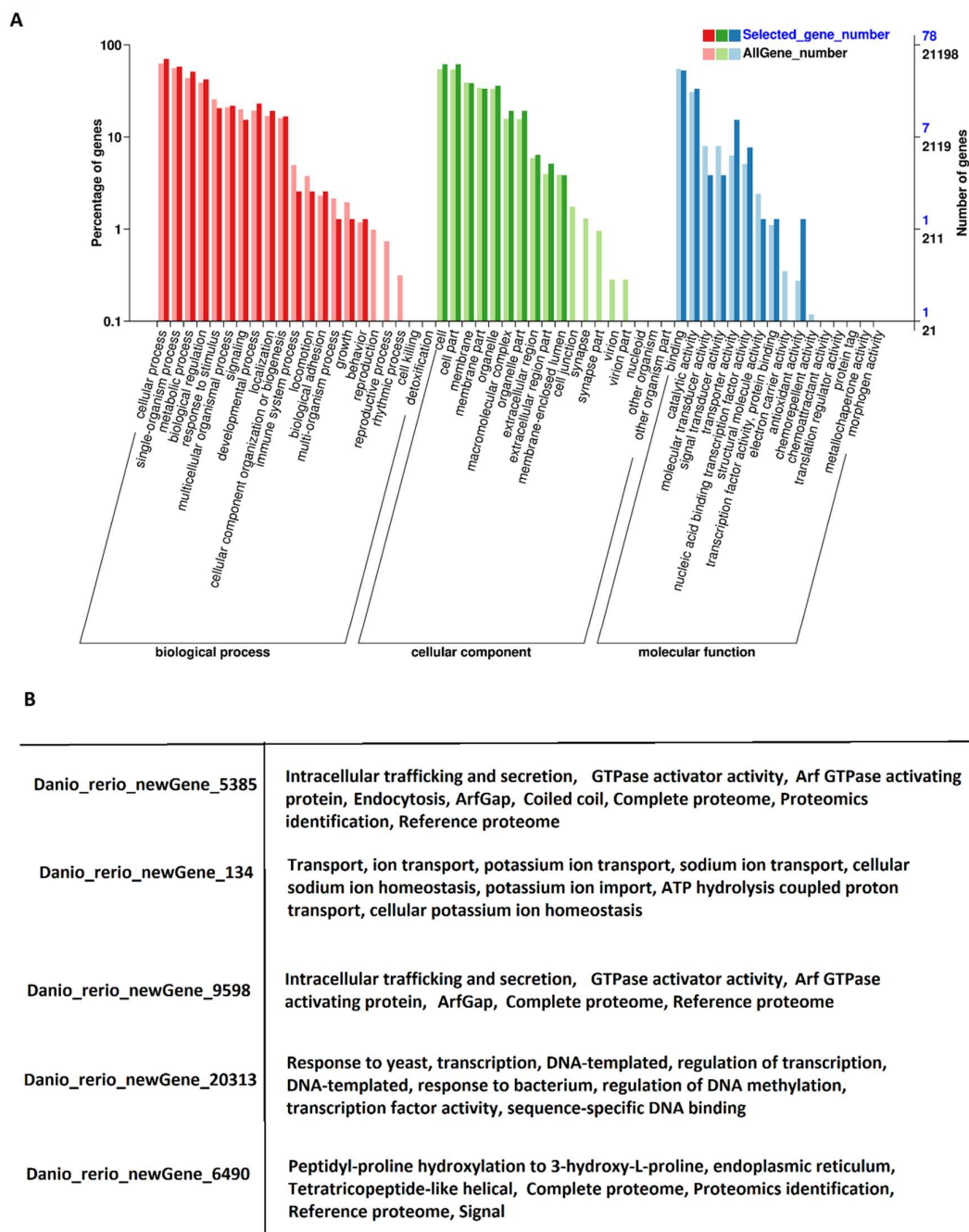


Figure S3. GO annotation and KEGG pathway analyses of zebrafish larval lncRNAs under DD condition: GO annotation revealed the percentage of genes involved in different biological processes (A), and KEGG pathways analysis of representative lncRNAs (B).

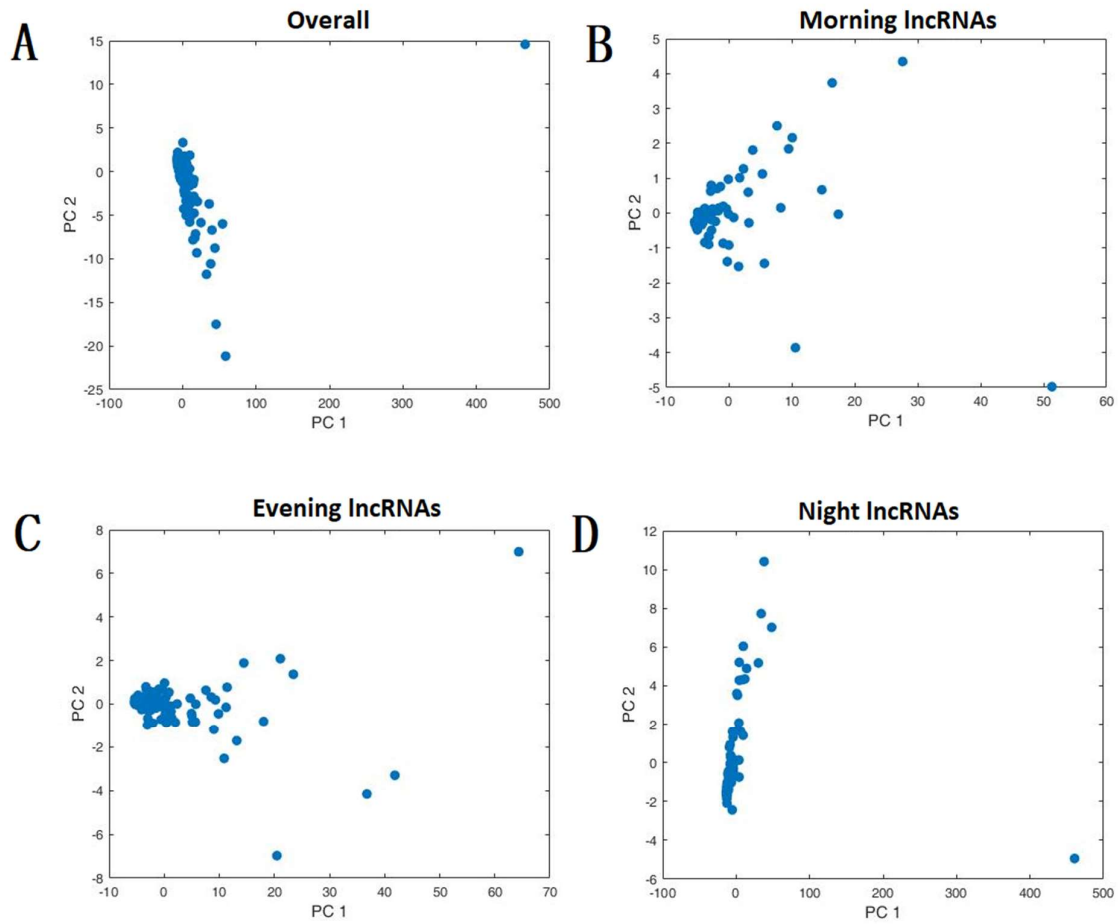


Figure S4. Principal Component Analysis (PCA) of circadianly expressed zebrafish larval lncRNAs under LL condition. All circadianly expressed larval lncRNAs (A), morning (CT0 and CT4) lncRNAs (B), evening (CT8 and CT12) lncRNAs (C), and night (CT16 and CT20) lncRNAs (D).

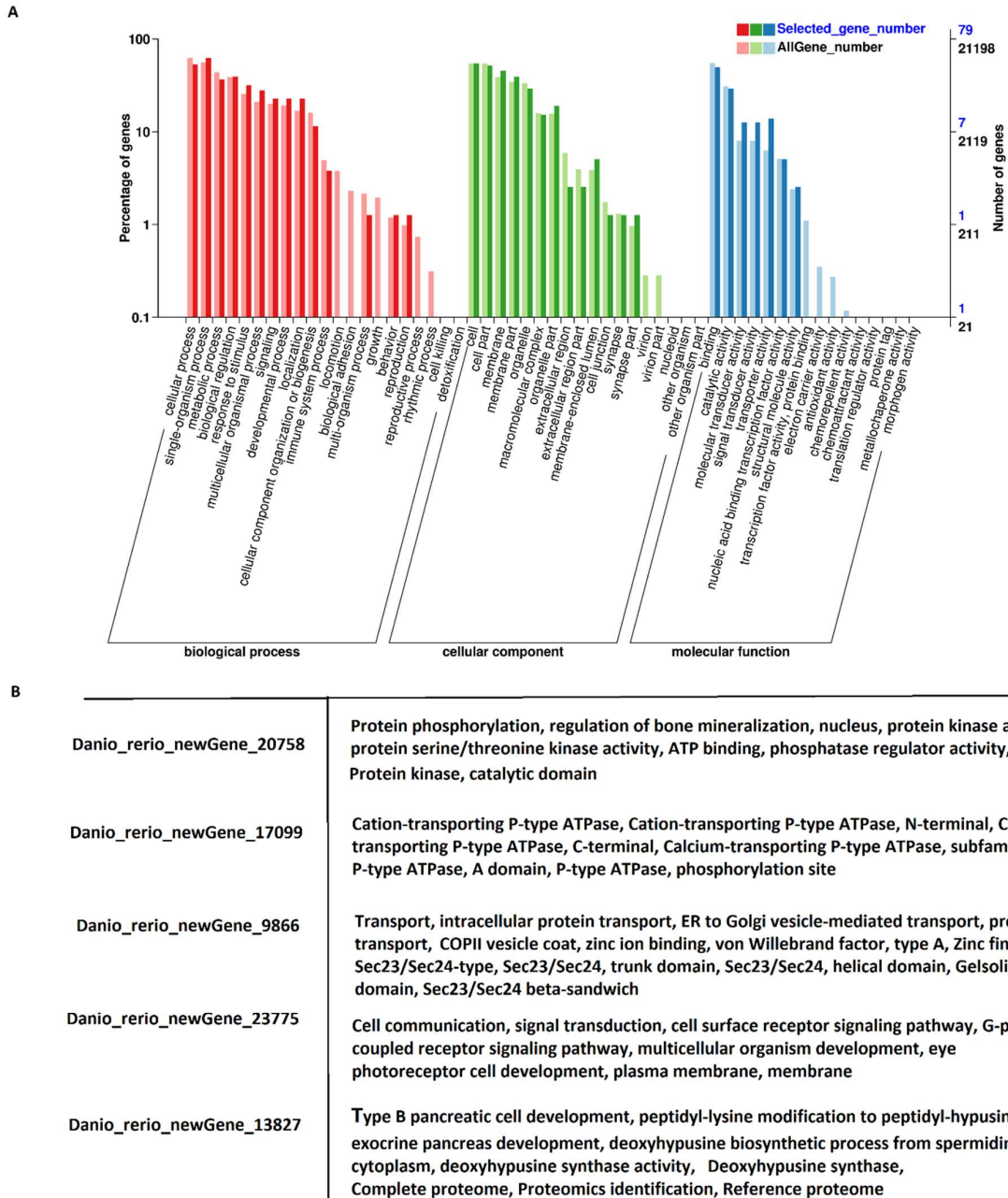


Figure S5. GO annotation and KEGG pathway analyses of zebrafish larval lncRNAs under LL condition: GO annotation revealed the percentage of genes involved in different biological processes (A), and KEGG pathways analysis of representative lncRNAs (B).

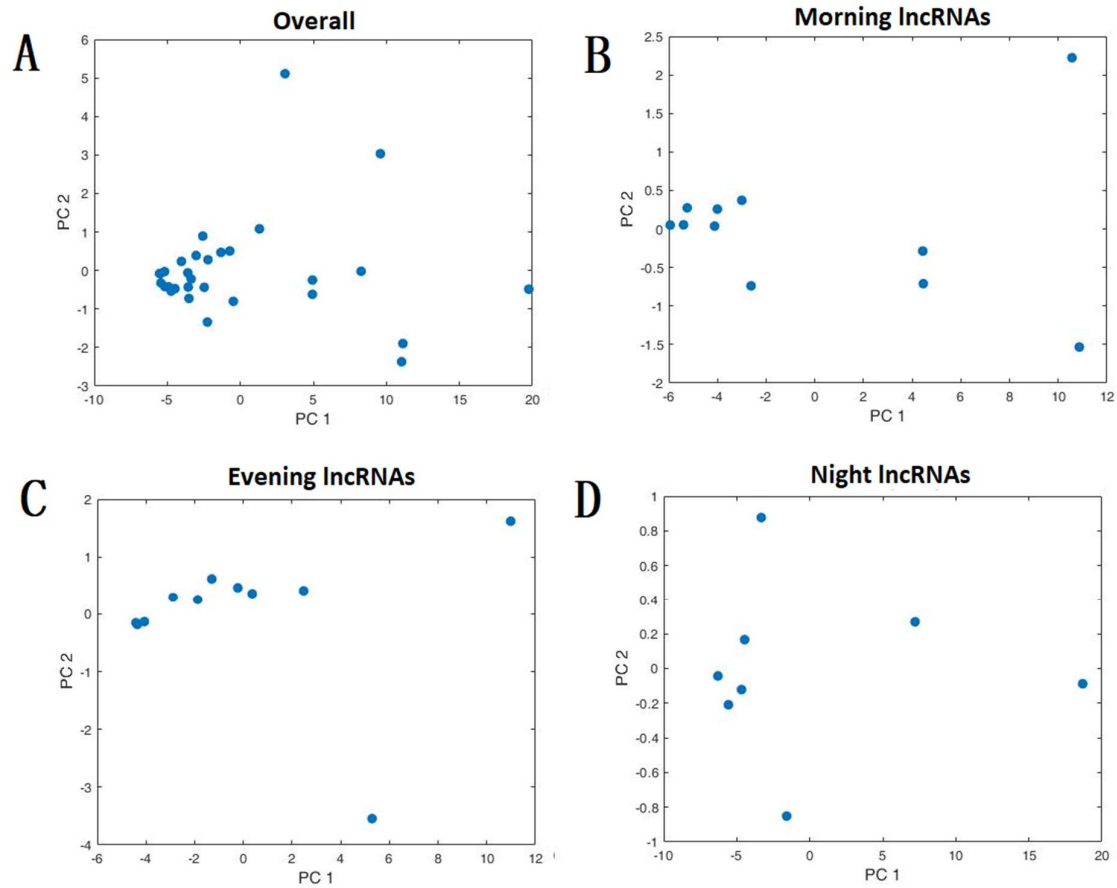


Figure S6. Principal Component Analysis (PCA) of 30 larval lncRNAs co-expressed under both DD and LL condition with expression profiles from DD condition. All circadianly expressed larval lncRNAs (A), morning (CT0 and CT4) lncRNAs (B), evening (CT8 and CT12) lncRNAs (C), and night (CT16 and CT20) lncRNAs (D).

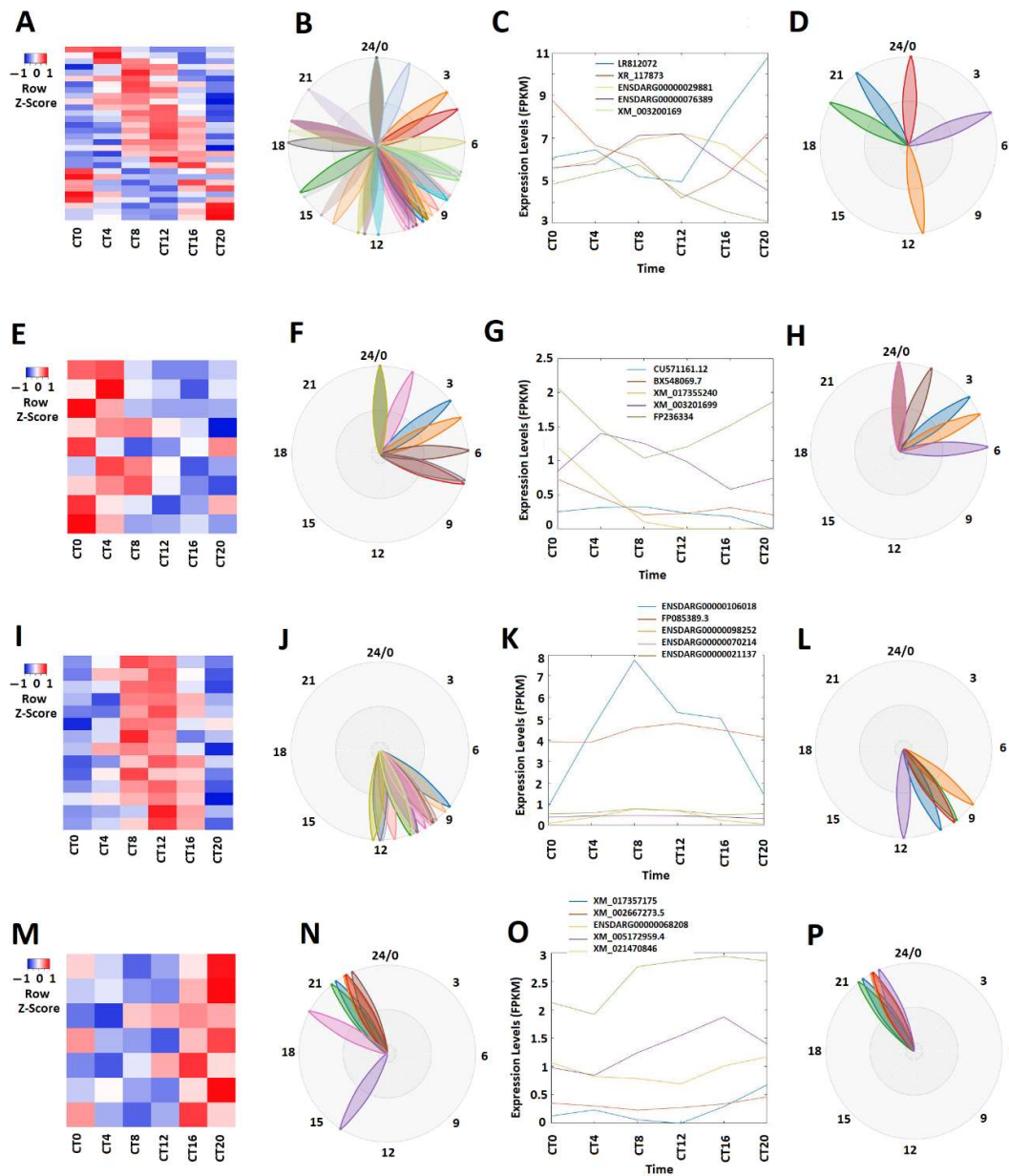


Figure S7. Expression profile analysis of morning (CT0 and CT4), evening (CT8 and CT12) and night (CT16, CT20) zebrafish larval lncRNAs co-expressed under both DD and LL conditions. Analysis of all 30 co-expressing larval lncRNAs with expression profiles from LL condition (**A–D**): Heat map (**A**) and BioDare2 plots (**B**) of all 30 co-expressing larval lncRNAs, expression profiles (**C**) and BioDare2 plots (**D**) of representative lncRNAs. (**E–H**) Analysis of 9 larval morning lncRNAs: Heat map (**E**) and BioDare2 plots (**F**) of 9 larval morning lncRNAs, expression profiles (**G**) and BioDare2 plots (**H**) of larval morning representative lncRNAs. (**I–L**) Analysis of 14 larval evening lncRNAs: Heat map (**I**) and BioDare2 plots (**J**) of 14 larval evening lncRNAs, expression profiles (**K**) and BioDare2 plots (**L**) of larval evening representative lncRNAs. (**M–P**) Analysis of 7 larval night lncRNAs: Heat map (**M**) and BioDare2 plots (**N**) of 7 larval night lncRNAs, expression profiles (**O**) and BioDare2 plots (**P**) of larval night representative lncRNAs.

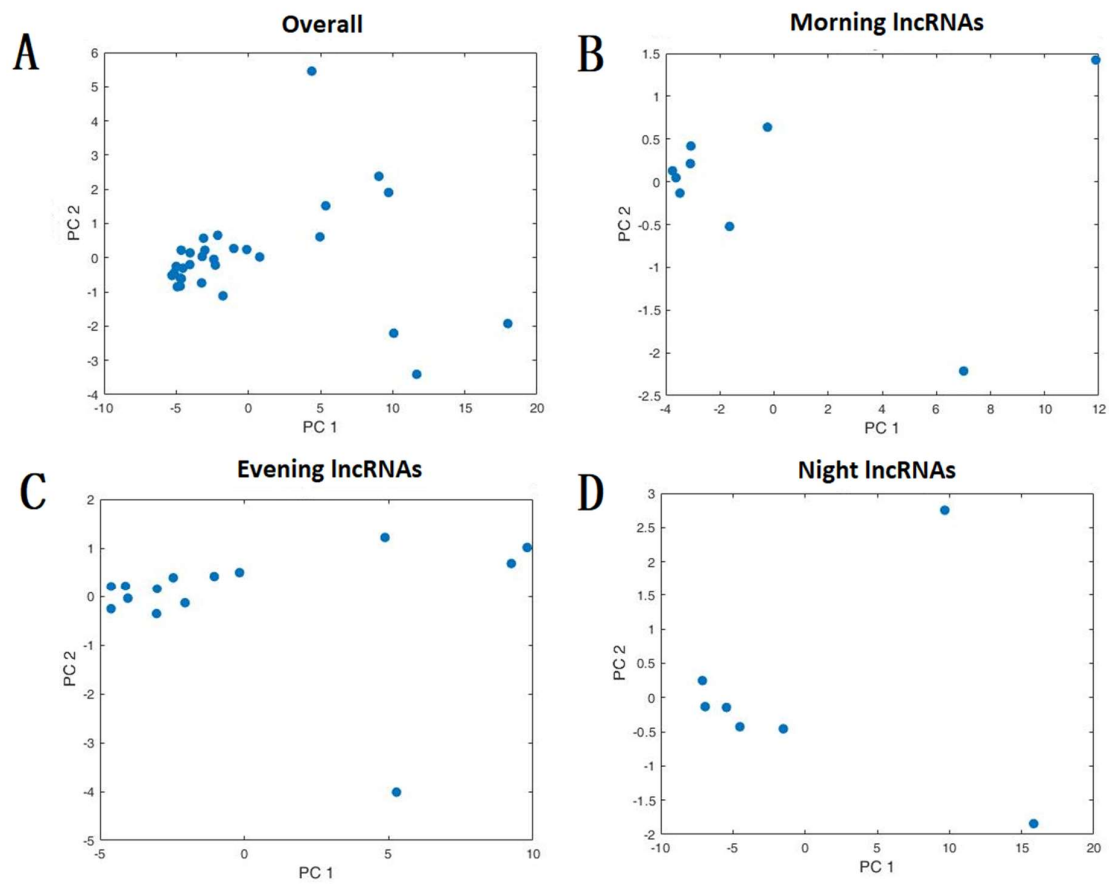


Figure S8. Principal Component Analysis (PCA) of 30 circadianly expressed zebrafish larval lncRNAs under both DD and LL condition with expression profiles from LL condition. All circadianly expressed larval lncRNAs (A), morning lncRNAs (B), evening lncRNAs (C), and night lncRNAs (D).

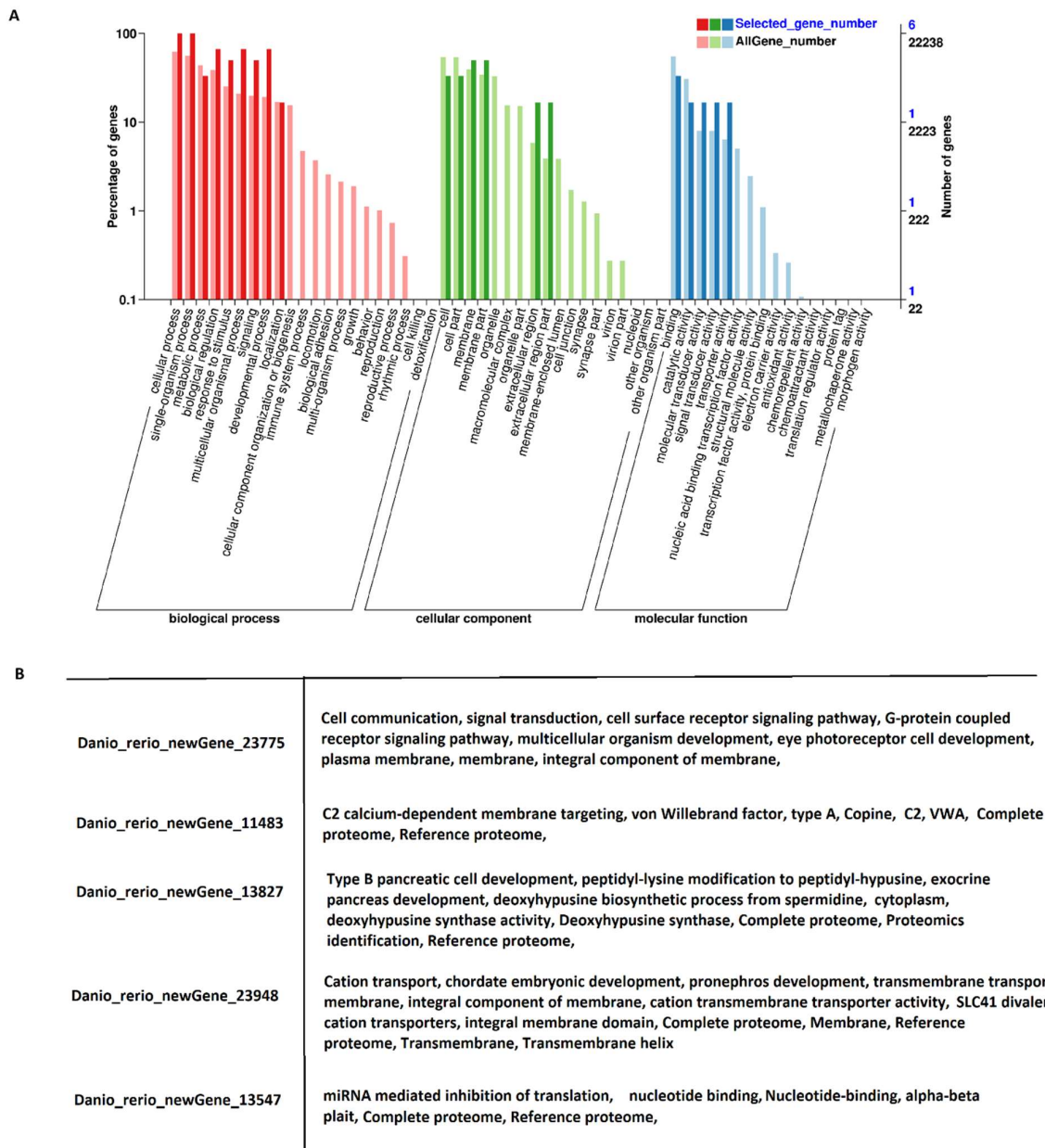


Figure S9. GO annotation and KEGG pathway analyses of zebrafish larval lncRNAs co-expressed under both DD and LL conditions: GO annotation revealed the percentage of genes involved in different biological processes (A), and KEGG pathways analysis of representative lncRNAs (B).