

High throughput sequencing of small RNAs transcriptomes in two *Crassostrea* oysters identifies microRNAs involved in osmotic stress response

Xuelin Zhao¹, Hong Yu¹, Lingfeng Kong¹, Shikai Liu^{1,2}, Qi Li^{1*}

¹*Key Laboratory of Mariculture, Ministry of Education, Ocean University of China, Qingdao 266003, China*

²*The Fish Molecular Genetics and Biotechnology Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences and Program of Cell and Molecular Biosciences, Auburn University, Auburn, AL 36849, USA*

*Corresponding author: Q. Li, Fax: +86-532-82031765; E-mail address: qili66@ouc.edu.cn

Xuelin Zhao (xlzhao1989@163.com)

Hong Yu (hongyu@ouc.edu.cn)

Lingfeng Kong (klfaly@ouc.edu.cn)

Shikai Liu (szl0021@auburn.edu)

Qi Li (qili66@ouc.edu.cn)

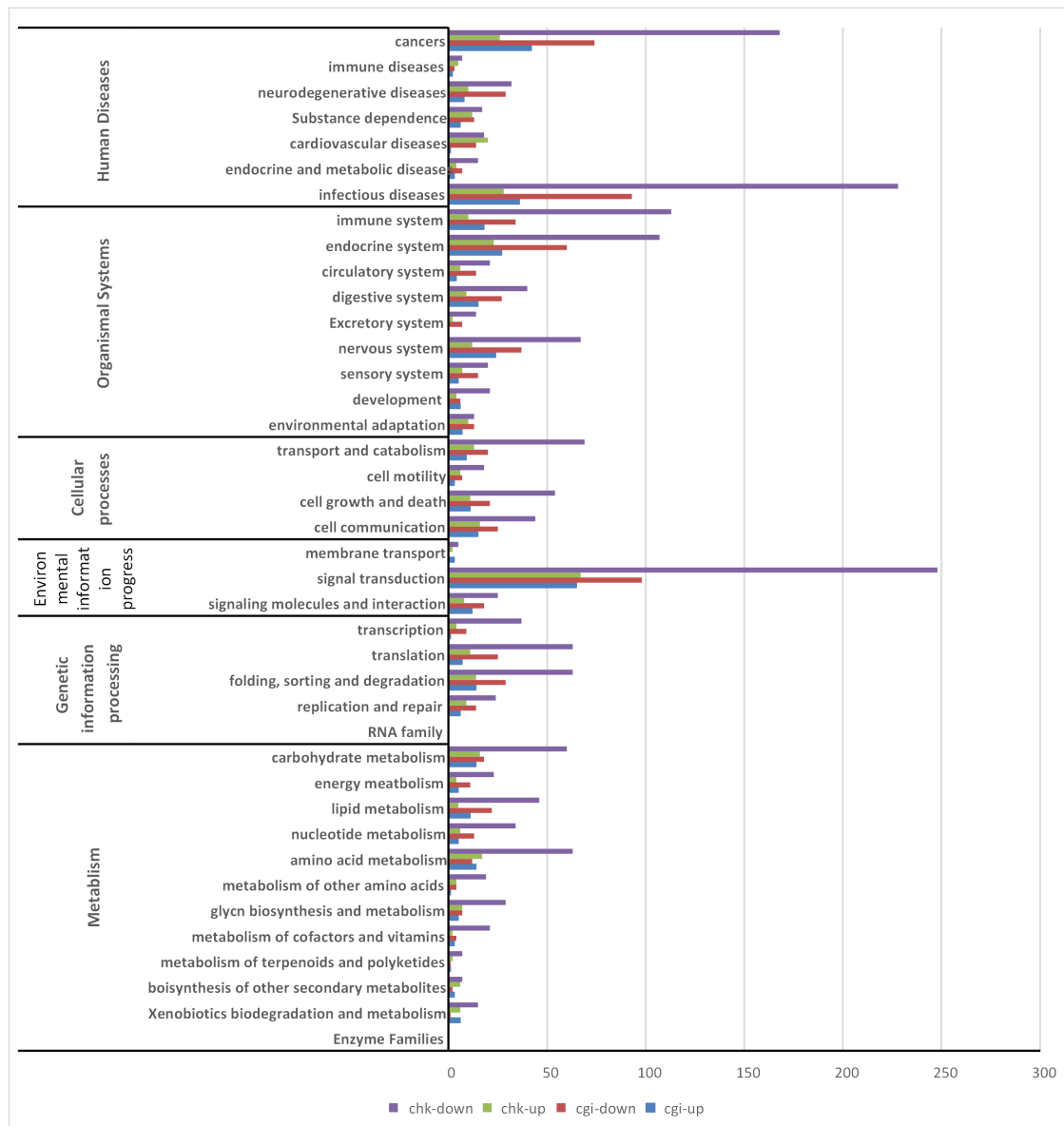


Figure S1. KEGG pathway distribution of target genes of differentially expressed miRNA of *C. gigas* and *C. hongkongensis*. Purple: target genes of down-regulated miRNAs in *C. hongkongensis*; Green: target genes of up-regulated miRNAs in *C. hongkongensis*; Red: target genes of down-regulated miRNAs in *C. gigas*; Blue: target genes of up-regulated miRNAs in *C. gigas*.