

Validation and Functional Analysis of Reference and Tissue-Specific Genes in Adipose Tissue of Freshwater Drum, *Aplodinotus grunniens* under Starvation and Hypothermia Stress

Miaomiao Xue¹, Haibo Wen^{1,2}, Pao Xu^{1,2}, Jianxiang Chen¹, Qingyong Wang¹, Yongkai Tang^{1,2}, Xueyan Ma^{1,2}, Guohua Lv^{1,2}, Changyou Song^{1,2,*}, Hongxia Li^{1,2,*}

Supplementary Materials:

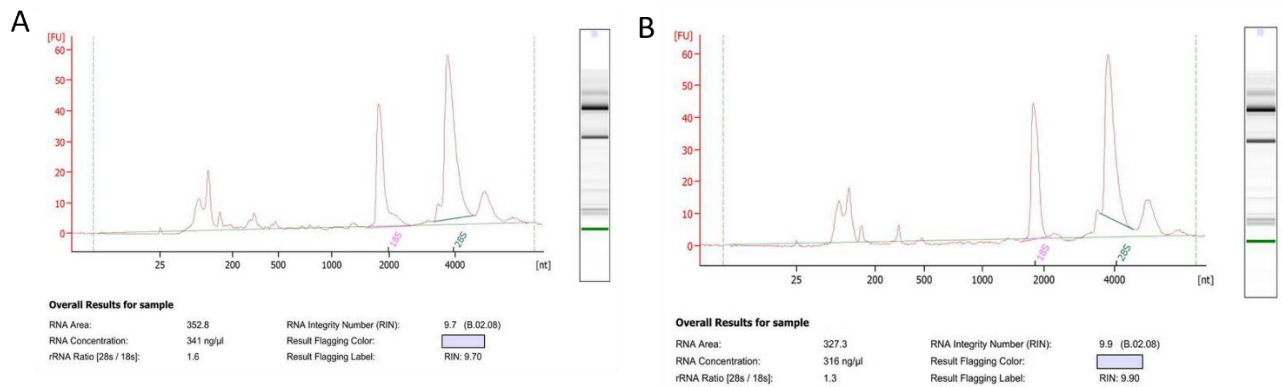


Figure S1. RNA integrity number by RNA 6000 Nano LabChip for the samples.

The concentration degree of each peak in the figure represents the integrity of RNA in the sample. The peak concentration represents a low degradation rate of RNA in the sample. The RIN value represents the integrity of the RNA sample, with higher values indicating better RNA integrity.

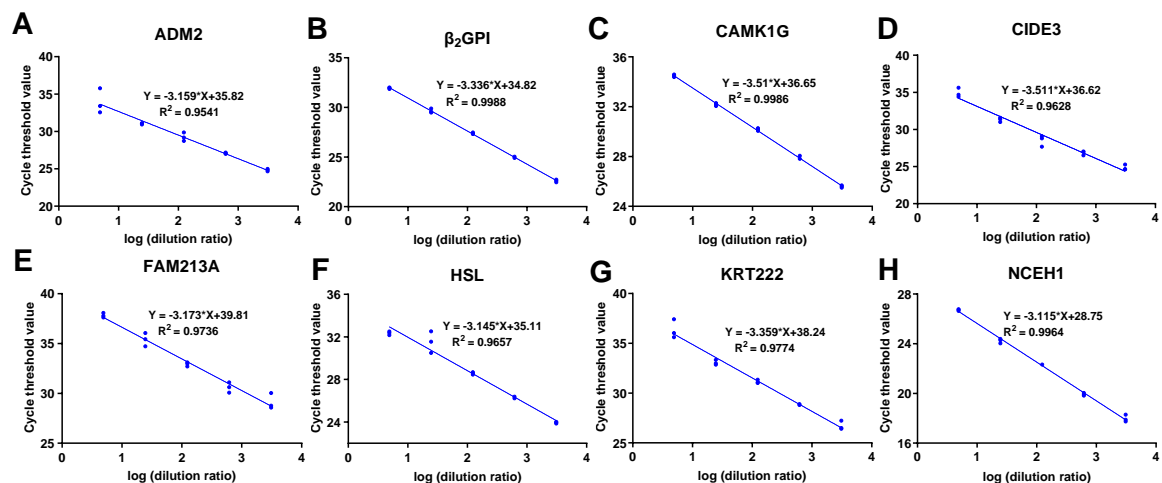


Figure S2. Standard curve of tissue-specific candidate genes in *A. grunniens*.

(A), adrenomedullin 2, ADM2; (B), beta-2-glycoprotein 1-like, β_2 GPI; (C), calcium/calmodulin-dependent protein kinase type 1G, CAMK1G; (D), cell death activator CIDE-3-like, CIDE3; (E), redox-regulatory protein FAM213A-like, FAM213A; (F), hormone-sensitive lipase, HSL; (G), keratin-like protein KRT222,

KRT222; (H), neutral cholesterol ester hydrolase 1, NCEH1.

Table S1. Bestkeeper Standard Deviation and coefficient of variation

| Reference gene | RPS4 | β -actin | RPI7 | 60SRP | EF1 α | ufm1 | B2M | EEF1B | SEC62 | 18S | GAPDH |
|-------------------|------|----------------|------|-------|--------------|------|------|-------|-------|-------|-------|
| SD | 0.91 | 0.93 | 1.04 | 1.14 | 1.37 | 1.79 | 1.81 | 1.85 | 2.15 | 3.46 | 3.80 |
| CV | 4.36 | 4.70 | 5.46 | 6.20 | 6.75 | 6.31 | 9.22 | 8.42 | 7.45 | 14.52 | 15.88 |