

Table S6 Differentially expressed genes related to the antigen processing and presentation pathways

Gene name	Gene ID	Description	Fold -change	<i>p</i> -value
<i>mhc1</i>	CL4289.Contig2_All	major histocompatibility complex, class I	-1.1758	3.22E-92
<i>mhc2</i>	Unigene8098_All	MHC class II antigen alpha chain, class II	1.0466	5.83E-09
<i>hsp27</i>	CL4186.Contig2_All	Heat shock 27kDa protein	3.9285	2.09E-30
<i>hsp70</i>	Unigene6318_All	Heat shock 70kDa protein	3.7239	2.05E-11
<i>b2m</i>	CL695.Contig1_All	Beta-2-microglobulin	1.2273	3.22E-24
<i>tap1</i>	Unigene30122_All	Transporter of antigen presentation	1.6031	3.90E-06
<i>ctsb</i>	Unigene4878_All	Cathepsin b	-1.006	9.39E-82
<i>ctse</i>	Unigene1543_All	Cathepsin E	3.6175	3.22E-24
<i>ctsf</i>	Unigene26177_All	Cathepsin F	1.9778	2.66E-76

The data are from the research of Qian et al. 2015 that the large yellow croakers at 21 days after fasting. Identification of all differentially expressed genes was based on $P < 0.05$. A P value < 0.05 indicated that the gene was significantly altered in fasting fish relative to that observed in normal feeding fish. The absolute value of “Fold-change” is the magnitude of up- or downregulation for each gene after fasting. “+” indicates upregulation and “-” indicates downregulation.

Qian, B.; Xue, L.; Huang, H. Liver transcriptome analysis of the Large yellow croaker (*Larimichthys crocea*) during fasting by using RNA-seq. *PLoS ONE* **2016**, *11*, doi:10.1371/journal.pone.0150240.