

Figure S1. Transcriptomic analysis pipeline. This figure describes the steps performed in the transcriptomic analysis.

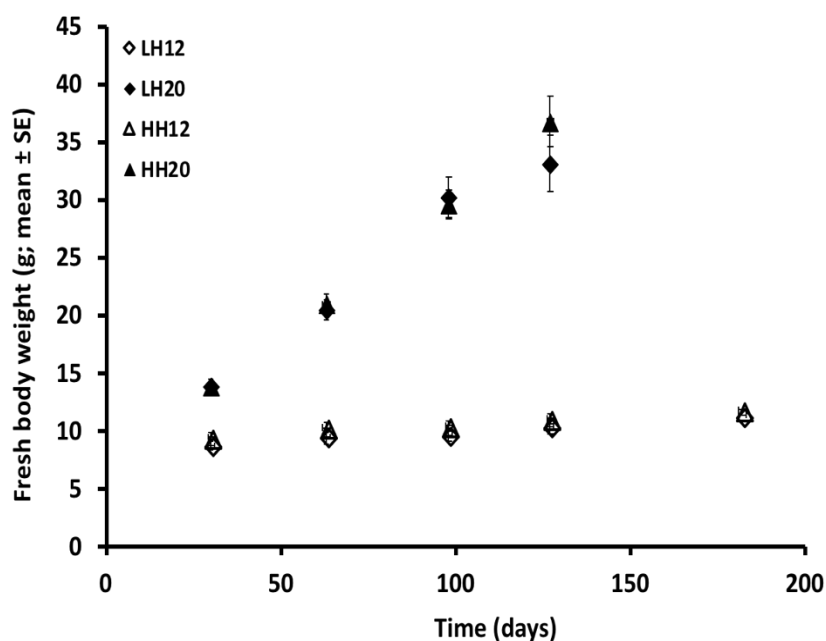


Figure S2. Growth curve of the four experimental groups of fish (HH12, LH12, HH20, LH20) tested and reared at 12°C or 20°C and fed the rich HUFA diet (HH) or the depleted HUFA diet (LH). The sample size was n = 34 (HH20), n = 20 (LH20), n = 37 (HH12) and n = 9 (LH12).

Table S1. Transcriptome assembly statistics. Assembly statistics based on the longest isoform per gene. The terminology corresponds to assembly with Trinity. BUSCO codes indicate the percentage of widely expressed genes that were recovered completely (C) (for single-copy (S) and duplicated (D) genes), that were only partially recovered (F for “Fragmented”), or that were missing (M). The total number of orthologous groups of genes (n) that was searched in BUSCO is also indicated.

Raw reads	661,022,788
Total assembled bases	123,209,874
Proportion of reads mapping back on the assembly (%)	92.1
Number of transcripts	328,877
Number of genes	189,77
Median contig length (bp)	349
Average contig length (bp)	649
Contig N50 (in bp, based on the longest isoform)	1474
BUSCO Eukaryota	C:95.7%[S:53.5%,D:42.2%],F:3.0%,M:1.3%,n:303
BUSCO Metazoa	C:95.0%[S:51.4%,D:43.6%],F:2.4%,M:2.6%,n:978
BUSCO Actinopterygii	C:74.4%[S:40.9%,D:33.5%],F:10.1%,M:15.5%,n:4584

Table S2. Summary table for GO terms summarised by REVIGO. Log₁₀ FDR refers to the GO enrichment test performed by Goseq. Other headers are defined in Supek et al (2011).

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Table S3. Results of the GO enrichment analysis performed by GSeq within the Trinity pipeline (see methods). The four parts of the tables correspond to the four treatment comparisons conducted (HH12 vs. HH20, LH12 vs. LH20, HH12 vs. LH20, LH12 vs. HH20). Go terms are defined by the fields category, term (P for iological Process, for ellular component, F for olecular Function) and ontology (GO term description). numDEIn at and numIn at provide the number of transcript detected within each GO term, and whether they were detected as being differentially-expressed or not, respectively. gene ids provides the list of transcripts detected as differentially expressed. Significance of the enrichment tests are provided in the over represented pvalue and under represented pvalue, with their associated False Discovery Rate value (over represented FDR).

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Table S4 List of the unique 33 differentially-expressed transcripts from the enriched GO Terms involved in calcium-mediated processes, specific to the HH12-LH20 comparison (compared to HH12-HH20: Fig. 7 and Table 2). These GO terms are linked to the combined effect of elevated temperature and lowered concentration of HUFA in the diet and are involved in the following five biological processes: regulation of voltage-gated calcium channel activity (GO:1901385, 11 differentially-expressed transcripts), positive regulation of calcium-transporting ATPase activity (GO:1901896, 7 differentially-expressed transcripts), calcium ion trans-membrane transport via high voltage-gated calcium channel (GO:0061577, 4 differentially-expressed transcripts), regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion (GO:0010881, 16 differentially-expressed transcripts), and regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (GO:0010880, 21 differentially-expressed transcripts). There are 59 differentially-expressed transcripts, 26 of which are involved in more than one GO term; we removed duplicates as to presenting the differentially-expression levels are Trinotate annotation results for the 33 transcripts involved in the set of five GO terms.

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