

SUPPLEMENTARY INFORMATION:

**Moderate levels of dietary arachidonic acid reduced lipid
accumulation and tended to inhibit cell cycle progression in the liver
of Japanese seabass *Lateolabrax japonicus***

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Supplementary Table S1. Clean data and quality control.

Sample	Raw Reads	Clean Reads	Clean Bases	Error (%)	Q20 (%)	Q30 (%)	GC Content (%)
ARA-0.05_1	61,590,114	57,285,590	8.59 G	0.02	96.64	90.87	48.57
ARA-0.05_2	57,541,780	53,078,734	7.96 G	0.02	96.47	90.49	49.65
ARA-0.05_3	58,486,918	45,451,256	6.82 G	0.02	96.82	90.23	49.70
ARA-0.37_1	62,357,214	53,071,432	7.96 G	0.02	97.08	91.43	48.42
ARA-0.37_2	58,575,334	52,696,304	7.90 G	0.02	96.77	90.94	49.31
ARA-0.37_3	61,039,602	59,417,542	8.91 G	0.02	95.74	89.54	49.10

Q20 and Q30: the sequencing error rate 0.01 and 0.001 respectively.

Supplementary Table S2. Length distribution of transcripts and unigenes.

Transcript length interval	200-500 bp	500-1k bp	1k-2k bp	>2k bp	Total
Number of transcripts	145,811	42,334	33,836	39,966	261,947
Number of unigenes	133,117	29,326	15,570	13,844	191,857

Supplementary Table S3. Annotation of the unigenes.

Annotated in database	Number of unigenes	Percentage (%)
Annotated in NR	46,692	24.33
Annotated in NT	66,582	34.70
Annotated in KO	25,420	13.24
Annotated in SwissProt	38,541	20.08
Annotated in PFAM	37,741	19.67
Annotated in GO	37,959	19.78
Annotated in KOG	21,546	11.23
Annotated in all Databases	12,801	6.67
Annotated in at least one Database	81,636	42.55
Total Unigenes	191,857	100

Supplementary Table S4. Formulation and proximate composition of the experiment diets (% dry matter).

Ingredients	Dietary ARA level (% dry matter)					
	0.05	0.22	0.37	0.60	1.38	2.32
Fish meal	15.00	15.00	15.00	15.00	15.00	15.00
Soybean meal	20.00	20.00	20.00	20.00	20.00	20.00
Wheat meal	30.85	30.85	30.85	30.85	30.85	30.85
Casein	16.00	16.00	16.00	16.00	16.00	16.00
Gelatin	4.00	4.00	4.00	4.00	4.00	4.00
Mineral premix ^a	2.00	2.00	2.00	2.00	2.00	2.00
Vitamin premix ^b	2.00	2.00	2.00	2.00	2.00	2.00
Attractant ^c	0.30	0.30	0.30	0.30	0.30	0.30
Mold inhibitor ^d	0.10	0.10	0.10	0.10	0.10	0.10
Ethoxyquin	0.05	0.05	0.05	0.05	0.05	0.05
Soy lecithin	1.20	1.20	1.20	1.20	1.20	1.20
DHA enriched oil ^e	1.50	1.50	1.50	1.50	1.50	1.50
ARA enriched oil ^f	0.00	0.35	0.71	1.45	2.91	5.84
Tristearin ^g	7.00	6.65	6.29	5.55	4.09	1.16
<i>Proximate composition</i>						
Crude protein	43.64	43.53	44.40	44.36	43.39	44.13
Crude lipid	11.32	11.07	11.09	11.24	11.50	11.22
Ash	6.89	6.94	6.81	6.98	6.92	6.83

^aMineral premix (mg or g/kg diet): MgSO₄·7H₂O, 1200 mg; CuSO₄·5H₂O, 10 mg; ZnSO₄·H₂O, 50 mg; FeSO₄·H₂O, 80 mg; MnSO₄·H₂O, 45 mg; CoCl₂·6H₂O (1%), 50 mg; NaSeSO₃·5H₂O (1%), 20mg; Ca(IO₃)₂·6H₂O (1%), 60mg; CaH₂PO₄·H₂O, 10g; zoelite, 8.485 g.

^bVitamin premix (mg or g/kg diet): thiamin 25 mg; riboflavin, 45 mg; pyridoxine HCl, 20 mg; vitamin B₁₂ (1%), 10 mg; vitamin K₃, 10 mg; inositol, 800 mg; pantothenic acid, 60 mg; niacin, 200 mg; folic acid, 20 mg; biotin (2%), 60 mg; retinol acetate, 32 mg; cholecalciferol, 5 mg; alpha-tocopherol (50%), 240 mg; ascorbic acid, 5 g; choline chloride (50%), 5 g; wheat middling, 4.47 g.

^cAttractant: glycine and betaine.

^dMold inhibitor: contained 50% calcium propionic acid and 50% fumaric acid.

^eDHA enriched oil: DHA content, 43% of total fatty acid; in the form of triglyceride; Jiangsu Tiangkai Biotechnology Co., Ltd., Nanjing, China.

^fARA enriched oil: ARA content, 46% of total fatty acid; in the form of triglyceride; Jiangsu

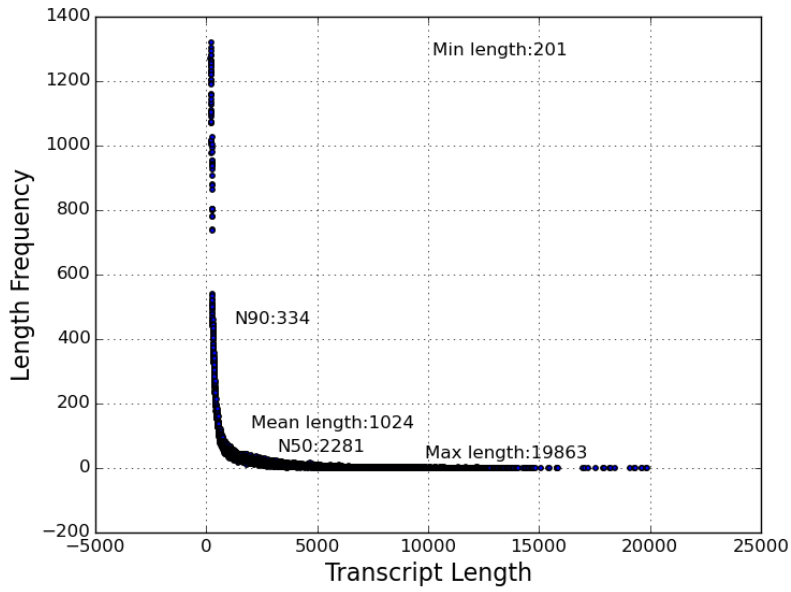
Tiankai Biotechnology Co., Ltd., Nanjing, China.

^gTristearin: HUDONG article of everyday use Co., Ltd., Jiaxing, China.

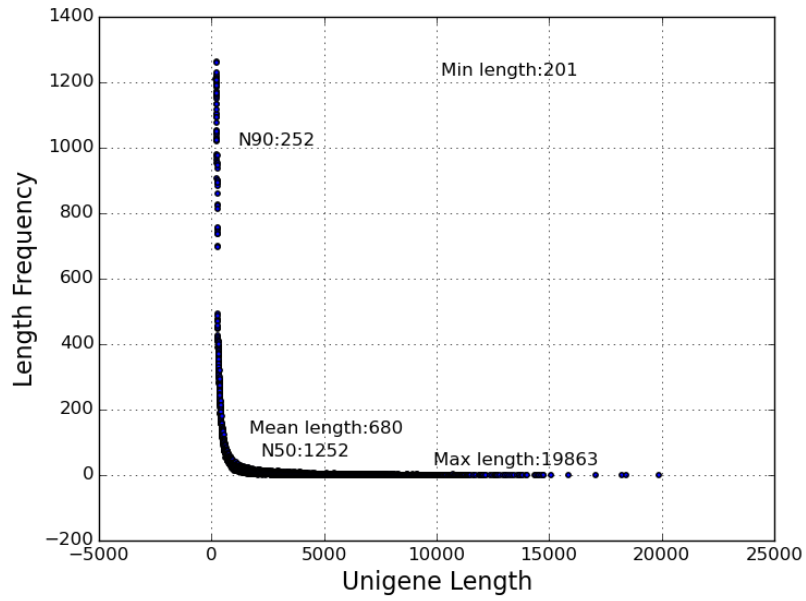
Supplementary Table S5. Fatty acid profiles of experimental diets (% total fatty acid).

Fatty acid	ARA-0.05	ARA-0.22	ARA-0.37	ARA-0.60	ARA-1.38	ARA-2.32
C14:0	3.50	3.61	3.61	3.50	3.00	2.38
C16:0	26.62	27.12	26.62	25.91	22.38	17.35
C18:0	44.46	44.10	41.84	38.76	29.18	12.88
Σ SFA	74.58	74.83	72.07	68.17	54.56	32.61
C16:1n-7	0.79	0.81	0.84	0.88	0.87	0.92
C18:1n-9	3.87	3.42	3.69	3.85	5.16	6.72
Σ MUFA	4.66	4.23	4.53	4.73	6.03	7.64
C18:2n-6	7.32	8.05	8.21	8.72	9.71	12.19
C20:4n-6	0.26	1.24	3.04	5.97	11.44	22.86
Σ n-6 PUFA	7.32	9.29	11.25	14.69	21.15	35.05
C18:3n-3	0.70	0.76	0.81	0.80	0.85	0.92
C20:5n-3	1.37	1.44	1.49	1.49	1.65	1.57
C22:6n-3	6.26	6.39	6.59	6.63	6.60	6.66
Σ n-3 PUFA	8.33	8.59	8.89	8.92	9.10	9.15
Σ PUFA	15.65	17.88	20.14	23.61	30.25	44.20
Σ SFA/ Σ PUFA	4.77	4.19	3.58	2.89	1.80	0.74
Σ n-3/ Σ n-6	1.14	0.92	0.79	0.61	0.43	0.26

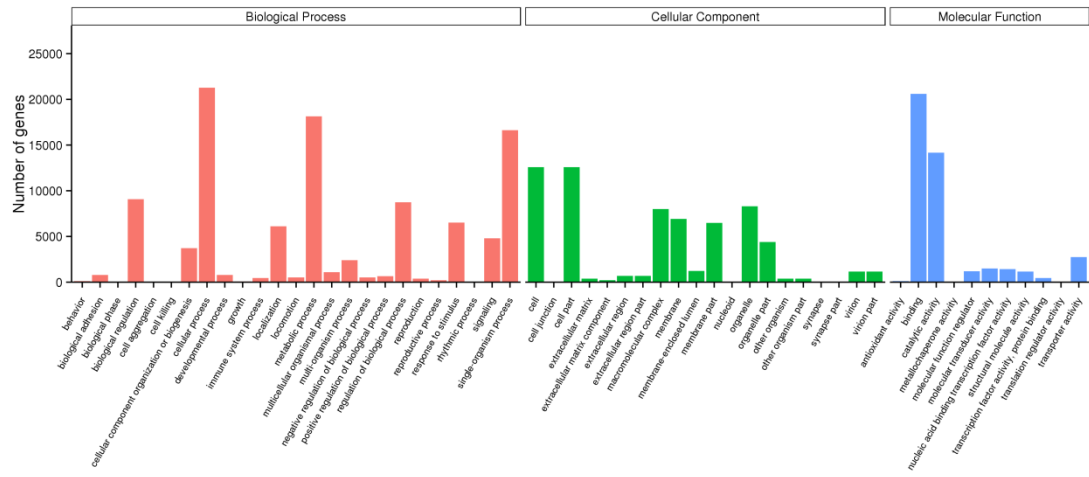
SFA, saturated fatty acid; MUFA, monounsaturated fatty acid; PUFA, polyunsaturated fatty acid.



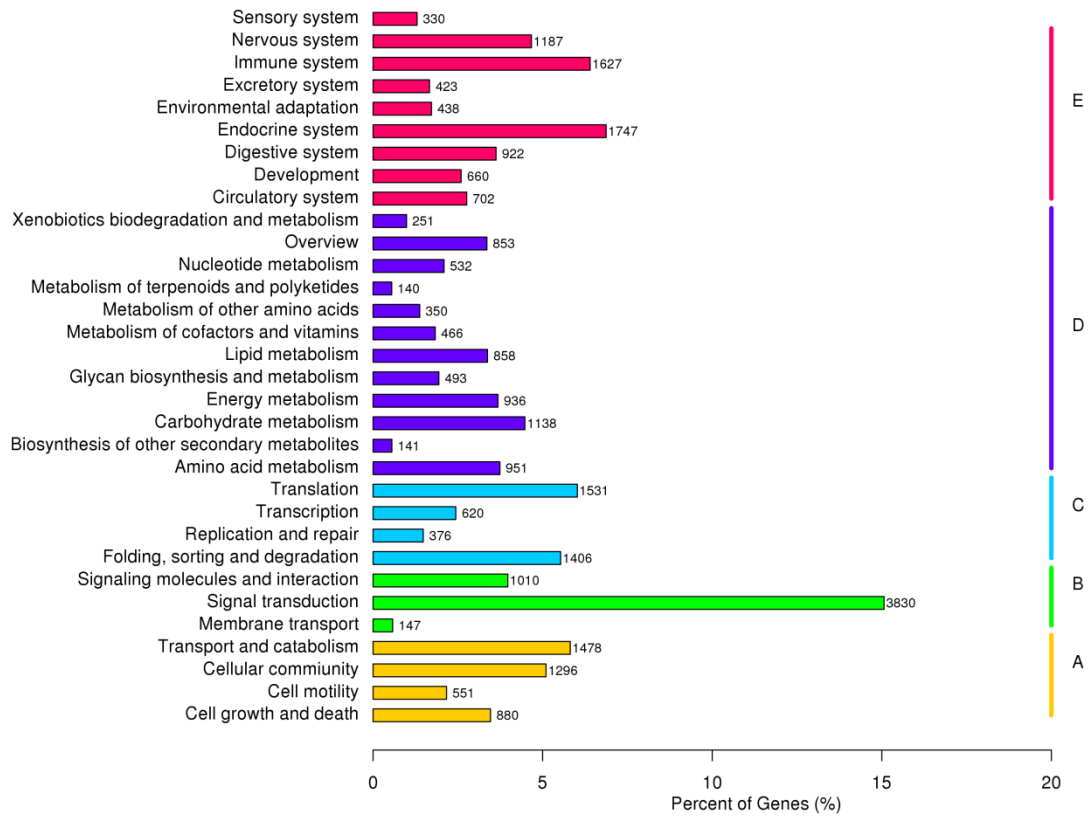
Supplementary Fig. S1. Length distribution of transcripts. N50 (N90): length of the transcript, longer than which the cumulative length of transcripts accounts for 50% (90%) of the total cumulative length.



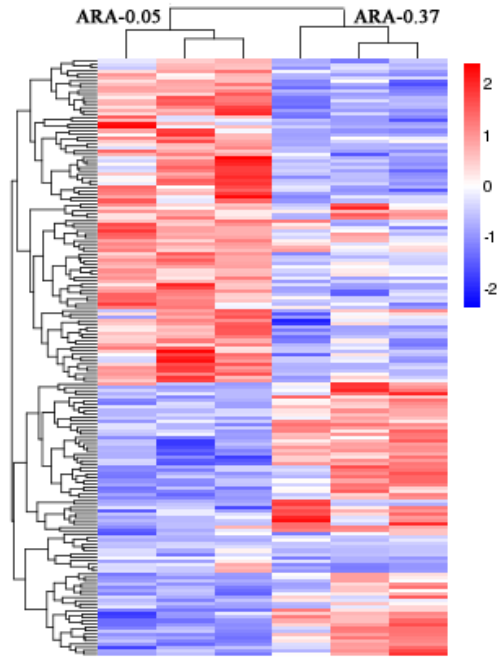
Supplementary Fig. S2. Length distribution of unigenes. N50 (N90): length of the unigene, longer than which the cumulative length of unigenes accounts for 50% (90%) of the total cumulative length.



Supplementary Fig. S3. Gene function classification (GO) of unigenes.



Supplementary Fig. S4. KEGG classification of unigenes. A: cellular processes; B: environmental information processing; C: genetic information processing; D: metabolism; E: organismal systems.



Supplementary Fig. S5. Cluster analysis of differentially expressed genes.