

Supplementary Tables

Supplementary Table 1. Primers used for relative quantitative real-time PCR (qPCR) analysis.

Primer	Forward primer 5'-3'	Reverse primer 5'-3'
<i>β-actin</i>	ACAGTGCCCATCTATGAAGGCT	CTATCCAGGCAGTAGCTTTGAG
<i>akr1d1</i>	TCGCTCACTGAGGAAGAAATG	CATGGAATGGGTACTCTGGATG
<i>hrasls3</i>	CCGCGATCTGGTAACAATACT	CACCAGAGTCAATCGGAATCA
<i>elovl6</i>	GCAACACACACAACAGACATAC	CTCCTGCGGTGGAAACATAA
<i>scd</i>	GGTCCACTAGAGCACACTAAAG	AAAGGAGGAGAAGAAGCGAAG
<i>cers5</i>	CAAGGAGACTGCCACAGAAA	CACCGCAGGAACCAAGATAA
<i>ugt2a2</i>	CCAAGACTTTCCCTCCATCTAC	CCGACACTCTCGAATCTCTTTC
<i>ulk1</i>	CTCCTCCAATTCAGCGTAAGAC	CCAGTATGACTCCAGGGTAGAT

Supplementary Table 2. Effects of dietary fucoidan on proximate composition in muscle of black sea bream.

Parameter	CTRL	ASJ1	ASJ2
Moisture	75.74 ± 0.89	75.41 ± 1.68	75.74 ± 0.56
Protein	21.41 ± 0.95	21.34 ± 1.08	21.54 ± 1.26
Lipid	2.56 ± 0.15	2.50 ± 0.15	2.36 ± 0.18
Ash	0.85 ± 0.03	0.89 ± 0.07	0.91 ± 0.06

Data are presented as means ± SD, n = 3 cages (20 fish/cage).

Supplementary Table 3. Sequencing reads after filtering.

Sample	Clean Reads (Mb)	Clean Bases (Gb)	Q30 (%)	GC ratio (%)
CTRL	21.04	6.28	94.22	51.80
ASJ1	24.37	7.26	94.31	51.67

Supplementary Table 4. Annotation result of each functional database.

Values	Nr	eggNOG	Swissprot	Pfam	KOG	KEGG	GO	COG	Overall
Number, x10 ³ n	27.24	26.84	14.86	19.42	17.85	16.71	15.96	6.65	29.38
Percentage, %	92.72	91.37	50.58	66.11	60.74	56.89	54.33	22.65	100

Supplementary Table 5. Analysis of KEGG pathway on black seabream hepatic DEM between ASJ1 and CTRL group.

Type	ID	DEM	VIP	log2FC	Pvalue	KEGG pathway
Lipid metabolism	meta_20	Taurine	1.59	-0.52	0.01	Primary bile acid biosynthesis
	meta_3138	20-HETE	1.55	-0.46	0.01	Arachidonic acid metabolism
	meta_820	3-	1.49	-0.82	0.03	Sphingolipid metabolism
	meta_480	Choline	1.46	-0.26	0.03	Glycerophospholipid metabolism
	meta_50	Caprylic acid	1.51	-0.37	0.03	Fatty acid biosynthesis
	meta_2806	Dihydroceramide	1.54	-0.62	0.03	Sphingolipid metabolism
	meta_1058	Vitamin D3	1.43	-0.35	0.04	Steroid biosynthesis
	meta_1685	CDP-glycerol	1.44	-0.72	0.04	Glycerophospholipid metabolism
	meta_1218	PS(18:0/20:4(8Z,11Z	1.51	-0.89	0.04	Glycerophospholipid metabolism
	meta_202	LysoPC(20:2(11Z,14	1.39	-0.67	0.05	Glycerophospholipid metabolism
Amino acid metabolism	meta_3033	L-Threonine	1.58	-0.64	0.02	Glycine, serine and threonine
	meta_376	5'-	1.43	-0.48	0.04	Cysteine and methionine
	meta_275	1-Pyrroline-2-	1.55	-0.40	0.04	Arginine and proline metabolism
	meta_131	5-Hydroxy-L-	1.48	-0.43	0.05	Tryptophan metabolism
	meta_580	4-Oxo-1-(3-pyridyl)-	1.55	-0.45	0.01	Nicotinate and nicotinamide
Metabolism of cofactors and vitamins	meta_138	Vitamin A	1.50	-0.73	0.03	Retinol metabolism
	meta_1044	Gamma-Tocotrienol	1.44	-0.80	0.04	Ubiquinone and other terpenoid-
	meta_2838	Pipecolic acid	1.55	-0.48	0.01	Metabolic pathways
Global and overview maps	meta_5	L-Pipecolic acid	1.53	-0.76	0.02	Metabolic pathways
	meta_3009	L-3-Cyanoalanine	1.53	-0.45	0.05	Metabolic pathways
	meta_1319	Deoxyadenosine	1.52	-0.38	0.02	Purine metabolism
Nucleotide metabolism	meta_3114	Pseudouridine	1.54	-0.49	0.02	Pyrimidine metabolism
	meta_762	Digoxin	1.46	-0.77	0.04	Bile secretion
Digestive system	meta_2767	Pyridoxamine	1.42	-0.38	0.05	Vitamin digestion and absorption
Xenobiotics	meta_2686	6-Thioguanosine	1.51	-0.63	0.03	Drug metabolism - other
Signaling molecules and	meta_338	Anandamide	1.50	-0.76	0.03	Neuroactive ligand-receptor
Metabolism of	meta_143	Farnesol	1.53	-1.42	0.04	Terpenoid backbone biosynthesis
Membrane transport	meta_1230	L-Lysine	1.60	-0.65	0.01	ABC transporters
Cardiovascular disease	meta_74	Hyaluronic acid	1.57	-0.89	0.01	Fluid shear stress and
Carbohydrate	meta_3159	D-Sorbitol 6-	1.56	-0.87	0.03	Fructose and mannose