

Supplemental Table 1: Real-Time PCR primers used in this study

Genes	Predicted	Sequences	Species
α V β 3	Integrin, alpha V	F: GTTGGACCGTCTGAAGC	<i>Danio rerio</i>
		R: CCGAAACTCACGGTCATC	
α V β 3-2	integrin beta-3-like	F: GGAGTCCCAGAAGAATTGAAC	<i>Oreochromis niloticus</i>
		R: AAGTACGGGTCTTCTCTTTG	
α V β 5	protein HEG-like	F: AGATTGTCCGTTCCGGTTAT	<i>Oreochromis niloticus</i>
		R: TGTCCTTCTTGGAGCTCT	
A2M	alpha-2-macroglobulin-like	F : ATGAGGACAACCTGTGTTGA	<i>Oreochromis niloticus</i>
		R : GAGGGACACATCCTTCG	
β -actin	β -actin	F : GAGAGGGAAATCGTGCG	<i>Epinephelus coioides</i>
		R : ACGGAACCTCTCATTGC	
BF	complement factor B-like	F : GTCAAGAGAAGAATATCTGGACATTTA	<i>Oreochromis niloticus</i>
		R : GACCACACAGACCCTTAAC	
Calnexin	calnexin-like	F: TGTGGAGAAGATTACAAACTGC	<i>Oreochromis niloticus</i>
		R: GTTCACCACCAGTGTGTAGA	
Cathepsin	Cathepsin L precursor	F: TGGAAGGTCCTACAACCTCTC	<i>Anoplopoma fimbria</i>
		R: GCGTCTGTACTCTTCGTTT	
Collectins	lactose-binding lectin I-2-like	F: GTCCGATGGGTCTAGAGT	<i>Oreochromis niloticus</i>
		R: GGGATACACAAACAGAAGCG	
C2r	C2r subcomponent-like	F : GAACCGTCCGTCCAAAC	<i>Danio rerio</i>
		R : GGTCTGATTATCCTGGCAGAA	

C1q	Complement C1q-like protein 2	F : ACTGATGCAGGATATATTGGAC	<i>Salmo salar</i>
		R : ACACACAGTGAAGTGGAG	
C1r	complement C1r subcomponent-like	F : GGTTTAATATCACTCTCAACTTTAGCGA	<i>Oreochromis niloticus</i>
		R : AGCTATCAGACCTGGACT	
C1s	haptoglobin-like	F : GGCAGAAACCTGTTTGTCA	<i>Oreochromis niloticus</i>
		R : GTAGTTCTGGAAGTGTGGATG	
C3	complement component C3	F : CCTCAACAAGTTTGCTTCC	<i>Epinephelus coioides</i>
		R : TTATAGTAGCCTGAGTTGATCCGTA	
C4	complement C4-like	F : CTGATTCTATCACCACATGGG	<i>Oreochromis niloticus</i>
		R : TAACAGGTGAAATGGATAGTTGC	
C4BP	Beta-2-glycoprotein 1 precursor	F : CCCTGACCCAGTGTCTAA	<i>Anoplopoma fimbria</i>
		R : CACAGGACACAGGTATGC	
C5	complement C5	F : CTGGAGAAGAAGCTGCG	<i>Oreochromis niloticus</i>
		R : AGCTGTGTTTGGACGA	
C6	complement component C6-like	F : ACAATGATGATGACTACACTATAGG	<i>Oreochromis niloticus</i>
		R : CAGTGTAGCACTGGAAGT	
C6-d	spondin-2-like	F : GGCCAGACGAATACTGAG	<i>Oreochromis niloticus</i>
		R : TGTCAGTTCCTGCGTCAT	
C7	complement component C7-like	F : CGTTTCTTGAGGAGGAAAGT	<i>Oreochromis niloticus</i>
		R : GAGGCCAGTTGTGCGTA	
C8	complement component C8 beta	F : CCTTGCCACAGTCCTAT	<i>Paralichthys olivaceus</i>
		R : CGTAGTCGTCCAAAGTGTAAATC	

C8-d	complement component C8 alpha chain-like	F : ACTACCATACCTACCAGTTTG	<i>Oreochromis niloticus</i>
		R : TCAGTCCCACCTCCACATAAT	
C9	complement component C9	F : AGGGAAATGCTGAAAGAGAT	<i>Oreochromis niloticus</i>
		R : GTACTCTGAGACCTCACGA	
DAF	Decay accelerating factor	F : ATTGACATGGACAGAGGAAG	<i>Danio rerio</i>
		R : ATGGCTGTTTACCTGTGG	
DCSIGN	type II antifreeze protein I	F : GGTGTTTGGCTCTGGAA	<i>Epinephelus bruneus</i>
		R : TCTTGGCGCAGACAGAA	
DCSIGN2	nattectin	F : GCCTTCATTTATTGCGG	<i>Epinephelus bruneus</i>
		R : TCCTTTGAAGCATGGTGGTA	
Dynein	cytoplasmic dynein 1 heavy chain 1-like isoform 2	F : GACAGACCGCTGCTATC	<i>Oreochromis niloticus</i>
		R : ATGGCCTGGAAGTCGAA	
EEA1	early endosome antigen 1	F : GGAGGATGAATCTGAACGC	<i>Oreochromis niloticus</i>
		R : GCTTTGCTGCTGCAAAT	
F-actin	CDH1-D	F : AGTCAAGTTTGATCGTCTTCTC	<i>Gallus gallus</i>
		R : AGTAAGCGCGGGTCATA	
F-actin-d	beta-centractin-like	F : CTGGTGTGTGTTGGACT	<i>Oreochromis niloticus</i>
		R : TGTTGAAATTGTAGCCTTCCT	
Hepcidin	Hepcidin-like antimicrobial peptide precursor	F : GCTCAGTGTTCAGTTG	<i>Epinephelus coioides</i>
		R : CTCGATATTAATGGCATCATCC	
HF	complement regulatory plasma protein	F : ATGGAATCCAGATCCACTTT	<i>Paralabrax nebulifer</i>
		R : TCTGTGTTTCCGTATTCCT	

HSP70	heat shock 70 kDa protein 14-like	F : CCGAATTCAAACGCACC	<i>Oreochromis niloticus</i>
		R : TCTGGATATGTTGCATTCAAAGT	
IF	complement factor I-like	F : GGATGTGGTGAGGAGTTG	<i>Oreochromis niloticus</i>
		R : ACTCACACATTTGGTGGGTAA	
li	invariant chain-like protein	F : GAGCTTTGAGTCCTGGAT	<i>Epinephelus akaara</i>
		R : GGCTTGTAGGAACCGAT	
LAMP	lysosomal membrane glycoprotein 2 precursor	F : ATTCTTCCCTAAAGCATCAACAA	<i>Salmo salar</i>
		R : GCCTGTATGAGCACGTTT	
LAP2	Liver-expressed antimicrobial peptide 2-like	F : AGGTCAATTCCTGCCTGTA	<i>Oreochromis niloticus</i>
		R : GCAGATATTCTTCCTGCAGTA	
MASP1/2	Mannan-binding lectin serine protease 1	F : ACAAAGGACAAGAAGAGAAGG	<i>Oreochromis niloticus</i>
		R : GTTCTTTGTCATTTCCAGTTGAAATA	
MHC I	MHC class I alpha antigen	F : TTGAGATTGTAAAGCCACGC	<i>Oreochromis niloticus</i>
		R : CTTTGTGATTGTCCCCTTG	
MHC II	COP9 signalosome complex subunit 7a-like	F : ACCTCTTGCCTATGGAAC	<i>Oreochromis niloticus</i>
		R : TGCTGGAGGAGCAGTGA	
MPO-d	eosinophil peroxidase-like	F : ACCACCAATGACGCTAAT	<i>Oreochromis niloticus</i>
		R : GTAGAGTCTCTCCATCCC	
MR	macrophage mannose receptor 1-like	F : TCTCCAGCTCCTGATTG	<i>Oreochromis niloticus</i>
		R : CTCCATGCTGAGGATGGAAA	
MR-d	L-rhamnose-binding lectin CSL2-like	F : CGTAAACCTTGTTTCGTAACCTCTAA	<i>Oreochromis niloticus</i>
		R : TACACAAAGATAACCTGTCCTACATCA	

NFY	nuclear transcription factor Y subunit alpha-like	F: TGCCAACACCAACTACAAA	<i>Oreochromis niloticus</i>
		R: TCCTCCTCCAGCATCTCA	
Piscidin	Piscidin-like antimicrobial peptide precursor	F: CTCTTTCTTGTGTTGTGCGC	<i>Epinephelus coioides</i>
		R: GTCCAGCTCTTCCATGC	
PLG	plasminogen	F : CATGGACCTGTGCAAATA	<i>Perca flavescens</i>
		R : CATGTTTTGCCAGATTCAGTTAC	
SERPING1	minus strand C1 inhibitor	F : CCCTCATAATATGAATCTGAGCG	<i>Larimichthys crocea</i>
		R : AAATGTTGGATCTTATTGTTGGTC	
TAPBP	tapasin-like	F: AACAGCCGCTTAGGACA	<i>Oreochromis niloticus</i>
		R: TTTATATCCAGGCTGACGGAGA	
TfR	Transferrin receptor 1a	F: GATGTTATCACCGTGGAAGTC	<i>Danio rerio</i>
		R: CAACTGTTCGATGTGGCAA	
TUBB	Tubulin, beta 5	F: CTGCTCATCAGCAAGATCC	<i>Danio rerio</i>
		R: CCTCATTGTCAATACAGTAGGTTT	

Supplemental Table 2: Gene ontology analysis of *Epinephelus coioides* larvae

Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P-value
Cellular component			
myosin complex	45 out of 1129 genes, 4.0%	162 out of 28794 genes, 0.6%	1.46E-23
actin cytoskeleton	79 out of 1129 genes, 7.0%	656 out of 28794 genes, 2.3%	1.62E-16
contractile fiber	59 out of 1129 genes, 5.2%	501 out of 28794 genes, 1.7%	1.28E-11
extracellular region	106 out of 1129 genes, 9.4%	1483 out of 28794 genes, 5.2%	3.55E-07
myofibril	43 out of 1129 genes, 3.8%	433 out of 28794 genes, 1.5%	6.02E-06
sarcomere	36 out of 1129 genes, 3.2%	327 out of 28794 genes, 1.1%	6.05E-06
contractile fiber part	36 out of 1129 genes, 3.2%	332 out of 28794 genes, 1.2%	8.94E-06
cytoskeleton	173 out of 1129 genes, 15.3%	3012 out of 28794 genes, 10.5%	3.39E-05
extracellular region part	92 out of 1129 genes, 8.1%	1346 out of 28794 genes, 4.7%	3.53E-05
striated muscle thin filament	9 out of 1129 genes, 0.8%	25 out of 28794 genes, 0.1%	5.28E-05
cytoskeletal part	108 out of 1129 genes, 9.6%	1724 out of 28794 genes, 6.0%	0.00021
non-membrane-bounded organelle	237 out of 1129 genes, 21.0%	4673 out of 28794 genes, 16.2%	0.00230
Molecular function			
hydrolase activity	283 out of 1138 genes, 24.9%	5158 out of 28380 genes, 18.2%	2.08E-06
cytoskeletal protein binding	101 out of 1138 genes, 8.9%	1398 out of 28380 genes, 4.9%	2.80E-06
hydrolase activity, acting on acid anhydrides	132 out of 1138 genes, 11.6%	2114 out of 28380 genes, 7.4%	8.62E-05

pyrophosphatase activity	131 out of 1138 genes, 11.5%	2097 out of 28380 genes, 7.4%	9.39E-05
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	131 out of 1138 genes, 11.5%	2103 out of 28380 genes, 7.4%	0.00010
structural molecule activity	52 out of 1138 genes, 4.6%	613 out of 28380 genes, 2.2%	0.00013
nucleoside-triphosphatase activity	124 out of 1138 genes, 10.9%	1977 out of 28380 genes, 7.0%	0.00016
endopeptidase activity	44 out of 1138 genes, 3.9%	501 out of 28380 genes, 1.8%	0.00042
active transmembrane transporter activity	72 out of 1138 genes, 6.3%	1007 out of 28380 genes, 3.5%	0.00063
phosphorylase activity	5 out of 1138 genes, 0.4%	11 out of 28380 genes, 0.0%	0.01458
peptidase activity	66 out of 1138 genes, 5.8%	989 out of 28380 genes, 3.5%	0.01501
peptidase activity, acting on L-amino acid peptides	62 out of 1138 genes, 5.4%	912 out of 28380 genes, 3.2%	0.01503
transporter activity	155 out of 1138 genes, 13.6%	2861 out of 28380 genes, 10.1%	0.02337
oligopeptide transporter activity	4 out of 1138 genes, 0.4%	7 out of 28380 genes, 0.0%	0.03071
potassium-transporting ATPase activity	8 out of 1138 genes, 0.7%	38 out of 28380 genes, 0.1%	0.04100
potassium ion transmembrane transporter activity	8 out of 1138 genes, 0.7%	38 out of 28380 genes, 0.1%	0.04100
Biological process			
glucose metabolic process	42 out of 1105 genes, 3.8%	279 out of 27537 genes, 1.0%	2.39E-10
hexose metabolic process	48 out of 1105 genes, 4.3%	443 out of 27537 genes, 1.6%	7.72E-07
muscle system process	52 out of 1105 genes, 4.7%	520 out of 27537 genes, 1.9%	2.54E-06

small molecule metabolic process	215 out of 1105 genes, 19.5%	3657 out of 27537 genes, 13.3%	4.39E-06
protein activation cascade	11 out of 1105 genes, 1.0%	31 out of 27537 genes, 0.1%	2.49E-05
monosaccharide metabolic process	48 out of 1105 genes, 4.3%	493 out of 27537 genes, 1.8%	2.50E-05
muscle contraction	37 out of 1105 genes, 3.3%	328 out of 27537 genes, 1.2%	2.55E-05
complement activation	9 out of 1105 genes, 0.8%	20 out of 27537 genes, 0.1%	4.39E-05
alcohol metabolic process	69 out of 1105 genes, 6.2%	854 out of 27537 genes, 3.1%	4.72E-05
regulation of muscle contraction	17 out of 1105 genes, 1.5%	89 out of 27537 genes, 0.3%	0.00011
glucose catabolic process	21 out of 1105 genes, 1.9%	138 out of 27537 genes, 0.5%	0.00022
small molecule biosynthetic process	56 out of 1105 genes, 5.1%	665 out of 27537 genes, 2.4%	0.00025
regulation of muscle system process	19 out of 1105 genes, 1.7%	116 out of 27537 genes, 0.4%	0.00027
skeletal muscle contraction	13 out of 1105 genes, 1.2%	55 out of 27537 genes, 0.2%	0.00029
hexose catabolic process	21 out of 1105 genes, 1.9%	141 out of 27537 genes, 0.5%	0.00033
alcohol catabolic process	21 out of 1105 genes, 1.9%	141 out of 27537 genes, 0.5%	0.00033
monosaccharide catabolic process	21 out of 1105 genes, 1.9%	141 out of 27537 genes, 0.5%	0.00033
nucleobase, nucleoside and nucleotide biosynthetic process	45 out of 1105 genes, 4.1%	491 out of 27537 genes, 1.8%	0.0004
nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	45 out of 1105 genes, 4.1%	491 out of 27537 genes, 1.8%	0.0004
humoral immune response	10 out of 1105 genes, 0.9%	32 out of 27537 genes, 0.1%	0.00044
purine nucleoside triphosphate biosynthetic process	27 out of 1105 genes, 2.4%	223 out of 27537 genes, 0.8%	0.00052

purine ribonucleotide biosynthetic process	29 out of 1105 genes, 2.6%	251 out of 27537 genes, 0.9%	0.00053
striated muscle contraction	18 out of 1105 genes, 1.6%	111 out of 27537 genes, 0.4%	0.00066
cellular carbohydrate catabolic process	21 out of 1105 genes, 1.9%	151 out of 27537 genes, 0.5%	0.00106
nucleotide biosynthetic process	42 out of 1105 genes, 3.8%	465 out of 27537 genes, 1.7%	0.00146
purine ribonucleoside triphosphate biosynthetic process	26 out of 1105 genes, 2.4%	221 out of 27537 genes, 0.8%	0.00149
carbohydrate catabolic process	22 out of 1105 genes, 2.0%	168 out of 27537 genes, 0.6%	0.00166
nucleoside triphosphate biosynthetic process	27 out of 1105 genes, 2.4%	237 out of 27537 genes, 0.9%	0.00175
voluntary skeletal muscle contraction	11 out of 1105 genes, 1.0%	45 out of 27537 genes, 0.2%	0.00178
twitch skeletal muscle contraction	11 out of 1105 genes, 1.0%	45 out of 27537 genes, 0.2%	0.00178
ribonucleotide biosynthetic process	29 out of 1105 genes, 2.6%	271 out of 27537 genes, 1.0%	0.00259
purine nucleotide biosynthetic process	37 out of 1105 genes, 3.3%	398 out of 27537 genes, 1.4%	0.00325
musculoskeletal movement	14 out of 1105 genes, 1.3%	78 out of 27537 genes, 0.3%	0.00359
multicellular organismal movement	15 out of 1105 genes, 1.4%	89 out of 27537 genes, 0.3%	0.00361
cellular nitrogen compound biosynthetic process	52 out of 1105 genes, 4.7%	655 out of 27537 genes, 2.4%	0.00396
ribonucleoside triphosphate biosynthetic process	26 out of 1105 genes, 2.4%	233 out of 27537 genes, 0.8%	0.00404
fast-twitch skeletal muscle fiber	7 out of 1105 genes, 0.6%	18 out of 27537 genes, 0.1%	0.0053

contraction			
system process	146 out of 1105 genes, 13.2%	2523 out of 27537 genes, 9.2%	0.00577
cellular carbohydrate metabolic process	58 out of 1105 genes, 5.2%	772 out of 27537 genes, 2.8%	0.00596
cardiac muscle tissue morphogenesis	14 out of 1105 genes, 1.3%	84 out of 27537 genes, 0.3%	0.00891
regulation of striated muscle contraction	9 out of 1105 genes, 0.8%	35 out of 27537 genes, 0.1%	0.01073
immune effector process	22 out of 1105 genes, 2.0%	204 out of 27537 genes, 0.7%	0.03947

Supplemental Table 3: KEGG pathway enrichment analysis of *Epinephelus coioides* larvae

List	Pathway	NGS with pathway annotation (1504)	All genes with pathway annotation (32664)	P value	Q value	Pathway ID
	Metabolism					
	Carbohydrate metabolism					
12	Glycolysis / Gluconeogenesis	25 (1.66%)	173 (0.53%)	4.10E-07	7.42E-06	ko00010
18	Starch and sucrose metabolism	21 (1.4%)	167 (0.51%)	2.98E-05	3.59E-04	ko00500
27	Fructose and mannose metabolism	16 (1.06%)	152 (0.47%)	0.001784423	1.43E-02	ko00051
35	Pentose phosphate pathway	10 (0.66%)	85 (0.26%)	0.005645537	3.45E-02	ko00030
37	Galactose metabolism	14 (0.93%)	146 (0.45%)	0.007629812	4.47E-02	ko00052
43	Amino sugar and nucleotide sugar metabolism	14 (0.93%)	171 (0.52%)	0.02701486	1.36E-01	ko00520
48	Pyruvate metabolism	9 (0.6%)	101 (0.31%)	0.04333364	1.93E-01	ko00620
	Amino acid metabolism					
26	Cysteine and methionine metabolism	14 (0.93%)	117 (0.36%)	0.000991208	8.27E-03	ko00270
33	Glycine, serine and threonine metabolism	10 (0.66%)	84 (0.26%)	0.005190363	3.41E-02	ko00260
	Metabolism of other amino acids					
38	Glutathione metabolism	11 (0.73%)	114 (0.35%)	0.01613945	9.22E-02	ko00480
	Metabolism of cofactors and vitamins					
47	Retinol metabolism	12 (0.8%)	149 (0.46%)	0.04291683	1.93E-01	ko00830

	Genetic Information Processing					
	Translation					
23	Aminoacyl-tRNA biosynthesis	16 (1.06%)	136 (0.42%)	0.000540022	5.09E-03	ko00970
	Cellular Processes					
	Cell communication					
9	Tight junction	112 (7.45%)	1224 (3.75%)	3.60E-12	8.68E-11	ko04530
	Transport and catabolism					
15	Phagosome	55 (3.66%)	651 (1.99%)	1.27E-05	1.84E-04	ko04145
	Cell motility					
16	Regulation of actin cytoskeleton	98 (6.52%)	1387 (4.25%)	1.81E-05	2.45E-04	ko04810
	Organismal Systems					
	Circulatory system					
1	Cardiac muscle contraction	108 (7.18%)	742 (2.27%)	1.81E-26	3.94E-24	ko04260
11	Vascular smooth muscle contraction	88 (5.85%)	988 (3.02%)	2.97E-09	5.86E-08	ko04270
	Digestive system					
2	Protein digestion and absorption	91 (6.05%)	575 (1.76%)	4.50E-25	4.88E-23	ko04974
10	Pancreatic secretion	70 (4.65%)	618 (1.89%)	4.61E-12	1.00E-10	ko04972
21	Vitamin digestion and absorption	17 (1.13%)	146 (0.45%)	0.000415018	4.29E-03	ko04977
24	Mineral absorption	24 (1.6%)	253 (0.77%)	0.000694997	6.28E-03	ko04978
28	Salivary secretion	39 (2.59%)	517 (1.58%)	0.001889861	1.46E-02	ko04970
29	Carbohydrate digestion and absorption	26 (1.73%)	316 (0.97%)	0.003268099	2.45E-02	ko04973

32	Fat digestion and absorption	15 (1%)	153 (0.47%)	0.004800051	3.26E-02	ko04975
45	Bile secretion	27 (1.8%)	403 (1.23%)	0.03405557	1.64E-01	ko04976
	Immune system					
5	Complement and coagulation cascades	60 (3.99%)	341 (1.04%)	3.13E-19	1.36E-17	ko04610
17	Antigen processing and presentation	20 (1.33%)	152 (0.47%)	2.36E-05	3.01E-04	ko04612
30	Hematopoietic cell lineage	21 (1.4%)	238 (0.73%)	0.003475879	2.51E-02	ko04640
	Excretory system					
19	Proximal tubule bicarbonate reclamation	17 (1.13%)	132 (0.4%)	0.00012283	1.40E-03	ko04964
46	Aldosterone-regulated sodium reabsorption	17 (1.13%)	228 (0.7%)	0.03537639	1.67E-01	ko04960
	Endocrine system					
31	Renin-angiotensin system	7 (0.47%)	45 (0.14%)	0.004232833	2.96E-02	ko04614
41	PPAR signaling pathway	22 (1.46%)	301 (0.92%)	0.02281113	1.21E-01	ko03320
	Sensory system					
49	Olfactory transduction	17 (1.13%)	234 (0.72%)	0.04347116	1.93E-01	ko04740
	Human Diseases					
	Cardiovascular diseases					
3	Viral myocarditis	86 (5.72%)	604 (1.85%)	1.19E-20	7.37E-19	ko05416
4	Hypertrophic cardiomyopathy (HCM)	124 (8.24%)	1091 (3.34%)	1.36E-20	7.37E-19	ko05410
7	Dilated cardiomyopathy	123 (8.18%)	1172 (3.59%)	1.19E-17	3.70E-16	ko05414
36	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	39 (2.59%)	552 (1.69%)	0.005718025	3.45E-02	ko05412

	Infectious diseases: Bacterial					
6	Staphylococcus aureus infection	44 (2.93%)	206 (0.63%)	1.00E-17	3.62E-16	ko05150
40	Pathogenic Escherichia coli infection	31 (2.06%)	457 (1.4%)	0.02117175	1.15E-01	ko05130
	Immune diseases					
8	Systemic lupus erythematosus	42 (2.79%)	248 (0.76%)	2.68E-13	7.28E-12	ko05322
14	Autoimmune thyroid disease	14 (0.93%)	72 (0.22%)	4.41E-06	6.84E-05	ko05320
20	Graft-versus-host disease	10 (0.66%)	57 (0.17%)	0.000248344	2.69E-03	ko05332
25	Allograft rejection	10 (0.66%)	66 (0.2%)	0.000834373	7.24E-03	ko05330
34	Asthma	6 (0.4%)	36 (0.11%)	0.005607425	3.45E-02	ko05310
	Neurodegenerative diseases					
13	Prion diseases	28 (1.86%)	225 (0.69%)	1.88E-06	3.14E-05	ko05020
	Endocrine and metabolic diseases					
22	Type I diabetes mellitus	12 (0.8%)	85 (0.26%)	0.000508753	5.02E-03	ko04940
44	Type II diabetes mellitus	21 (1.4%)	293 (0.9%)	0.03085919	1.52E-01	ko04930
	Infectious diseases: Parasitic					
39	Amoebiasis	39 (2.59%)	593 (1.82%)	0.01701984	9.47E-02	ko05146
42	Leishmaniasis	20 (1.33%)	269 (0.82%)	0.02469462	1.28E-01	ko05140

Supplemental Table 4: Summary of the variations in complement-related gene expression between controls and grouper challenged with *Vibrio alginolyticus*

Unigene	PREDICTED	1h	2h	3h	4h	5h	6h	7h	8h	12h	16h	24h	48h
A2M	Alpha-2-macroglobulin-like												
BF	Complement factor B-like			4.58	5.43	10.90	5.24	4.22	4.73	5.07			
C2r	C2r subcomponent-like		-2.22	-2.46									
C1q	Complement C1q-like protein 2								2.74				
C1r	Complement C1r subcomponent-like				2.39								
C1s	Haptoglobin-like				84.40	37.27	16.98	5.00	10.07				
C3	Complement component C3				3.21	4.40	3.74	2.23	3.21				
C4	Complement C4-like				2.13	4.01		2.45	3.60			4.11	

C4BP	Beta-2-glycoprotein 1 precursor					2.69			1.94	8.20		6.63	
C5	Complement C5								3.79	3.92	2.93	8.55	
C6	Complement component C6-like				10.90	16.08	19.77	22.38	14.82	23.19	9.81	16.39	
C6-d	Spondin-2-like	1.50				-2.95	-2.65	-6.95					
C7	Complement component C7-like				16.45	30.06	20.44	28.00	22.57	19.81	12.92		
C8	Complement component C8 beta					3.45			2.23	9.40	5.19	9.37	
C8-d	Complement component C8 alpha chain-like				2.48	3.48	2.55	3.86	4.05	6.83	2.74	9.04	
C9	Complement component C9				6.50	5.65	2.96	4.20	3.81	5.26	2.61	5.12	
DAF	Decay accelerating factor												

MASP1/2	Mannan-binding lectin serine protease 1		-1.81	-2.12	-1.84								
HF	Complement regulatory plasma protein					7.41	4.84	3.63	8.24				
IF	Complement factor I-like		11.83	11.23	16.61	16.71	7.55	5.13	4.47	7.20	2.36		
PLG	Ca ²⁺ -dependent complex C1R/C1S subunit	3.39						-3.12					
SERPING1	Minus strand C1 inhibitor												

Supplemental Table 5: Summary of the variations in phagocytosis-related gene expression between controls and grouper challenged with *Vibrio alginolyticus*

Unigene	PREDICTED	1h	2h	3h	4h	5h	6h	7h	8h	12h	16h	24h	48h
$\alpha V\beta 3$	Integrin, alpha V												
$\alpha V\beta 3-2$	Integrin beta-3-like												
$\alpha V\beta 5$	Protein HEG-like					2.57							
Calnexin	Calnexin-like							1.83					
Cathepsin	Cathepsin L precursor					3.95	2.93	89.3					
Collectins	Lactose-binding lectin I-2-like						20.48						
DCSIGN	Type II antifreeze protein I											4.85	1.65
DCSIGN2	Nattectin												
Dynein	Cytoplasmic dynein 1 heavy chain 1-like isoform 2												

EEA1	Early endosome antigen 1										2.07	3.48	
F-actin	CDH1-D									1.37			
F-actin-d	Beta-centractin-like												
HSP70	Heat shock 70 kDa protein 14-like					1.81							
li-d	Invariant chain-like protein			1.71									
LAMP	Lysosomal membrane glycoprotein 2 precursor							2.05	2.54				
MHCI	Beta-centractin-like			1146.74									
MHCII	COP9 signalosome complex subunit 7a-like												
MPO-d	Eosinophil peroxidase-like										-4.23		

MR	Macrophage mannose receptor 1-like					7.95	2.53	26.32	13.92				
MR-d	L-rhamnose-binding lectin CSL2-like												
NFY	Nuclear transcription factor Y subunit alpha-like												
TAPBP	Tapasin-like					2.23	1.70						
TfR	Transferrin receptor 1a				2.98								
TUBB	Tubulin, beta 5								-1.33		-1.51		

Supplemental Table 6: Summary of the variations in antimicrobial peptide gene expression between controls and grouper challenged with *Vibrio alginolyticus*

Unigene	PREDICTED	1h	2h	3h	4h	5h	6h	7h	8h	12h	16h	24h	48h
Hepcidin	Hepcidin-like antimicrobial peptide precursor				141.48	1924.44	467.00	6385.32	4798.65				
LAP2	Liver-expressed antimicrobial peptide 2-like												
Piscidin	Piscidin-like antimicrobial peptide precursor								-1.96				