

Table S1 Sequence of primer pairs used in the real-time quantitative PCR reaction

Target gene	Primer sequences (5'-3')	Accession number	Annealing temperature (°C)
<i>prp7</i>	Forward: ACACCTTCCTGGCCTGTTTC Reverse: TAGCCATGATAGCAGCAGCC	ENSMALT00000031216.1	60
<i>cfi</i>	Reverse: GGATGATTCGTCCTCGCCAT Reverse: GCTGTCAAACAGGTGCTGTG	XM_020622172.1	60
<i>c5</i>	Forward: GCTCATCTCCCACTACGAGC Reverse: AGAGTCCAGAGGAAGGCGAT	XM_020595325.1	60
<i>maats1</i>	Forward: CACTCTGCCTCAGTGCTCAA Reverse: TCCACTCTCCTCAGCCTCTC	XM_020609566.1	60
<i>gmnc</i>	Forward: TGTTGTCAACGGCTCTCCTC Reverse: TTGGCAGTAGCTGTGGACAG	XM_020622727.1	60
<i>cpa1</i>	Forward: TGA CTGATGTGGCCATTCCC Reverse: GGGTGTAGGCGAAACCATCA	XM_020593509.1	60
<i>cdk14</i>	Forward: TCGGTCCCCAGCCATACTTA Reverse: GTGTTTGCTGCCACAGGATG	XM_020622249.1	60

<i>18s-1</i>	Forward: AGAAGAAGGAGAGGAGGAGAAGAC Reverse: CTGCATGAGTCAGAGCTAGAAATG	XM_020624505.1	60
<i>18s-2</i>	Forward: GTGGAGCGATTTGTCTGGTTA Reverse: CGGACATCTAAGGGCATCAC	ENSMALT00000018493.1	60
<i>bactin</i>	Forward: GCT GTG CTG TCC CTG TA Reverse: GAG TAG CCA CGA TCT	AAQ21403	60

Table S2 Quality evaluation of transcription sequencing data for *Monopterus albus* intestine tissue

Group	Samples	Raw reads	Clean reads	Clean bases	Q20 value (%)	Q30 value (%)
NI	NI1	38324422	37862874	5.66G	97.90	93.79
	NI2	39895726	39377246	5.89G	97.70	93.32
	NI3	38321892	37840114	5.66G	97.70	93.34
PI	PI1	47549926	46734122	6.99G	97.79	93.56
	PI2	43445040	42765292	6.40G	97.84	93.68
	PI3	41727682	41205128	6.16G	98.00	94.04

Table S3 The mapping result of transcription sequencing data for *Monopterus albus* intestine tissue

Group	Samples	Total reads	Total Mapping Ratio (%)	Uniquely Mapping Ratio (%)
NI	NI1	37862874	87.69	84.53
	NI2	39377246	87.15	84.16
	NI3	37840114	87.80	84.77
PI	PI1	46734122	87.36	84.28
	PI2	42765292	87.87	84.85
	PI3	41205128	88.10	85.00

Table S4 The Pearson correlation coefficient among six samples for intestine tissue

Correlation	NI-1	NI-2	NI-3	PI-1	PI-2	PI-3
NI-1	1	0.943	0.934	0.958	0.957	0.959
NI-2		1	0.91	0.876	0.887	0.850
NI-3			1	0.963	0.952	0.965
PI-1				1	0.994	0.988
PI-2					1	0.981
PI-3						1

Table S5 Enriched GO terms of DEGs among six samples in the intestine

Category	GO ID	Description	Gene Ratio	BgRatio	p value	padj
BP	GO:0038026	reelin-mediated signaling pathway	3/154	4/15370	3.92E-06	0.016808345
BP	GO:0021769	orbitofrontal cortex development	3/154	9/15370	7.93E-05	0.080503466
BP	GO:0001759	organ induction	4/154	24/15370	8.81E-05	0.080503466
BP	GO:0021541	ammon gyrus development	2/154	2/15370	9.97E-05	0.080503466
BP	GO:0045054	constitutive secretory pathway	2/154	2/15370	9.97E-05	0.080503466
BP	GO:0002673	regulation of acute inflammatory response	6/154	76/15370	0.000112566	0.080503466
BP	GO:0021837	motogenic signaling involved in postnatal olfactory bulb interneuron migration	2/154	3/15370	0.000297263	0.106296281
BP	GO:1903465	positive regulation of mitotic cell cycle DNA replication	2/154	3/15370	0.000297263	0.106296281
BP	GO:0021795	cerebral cortex cell migration	5/154	60/15370	0.000331521	0.108707157
BP	GO:0021800	cerebral cortex tangential migration	3/154	15/15370	0.000410843	0.108707157
BP	GO:0097089	methyl-branched fatty acid metabolic process	4/191	8/15370	1.56E-06	0.003154581
BP	GO:0003322	pancreatic A cell development	3/191	4/15370	7.49E-06	0.004688455
BP	GO:0006699	bile acid biosynthetic process	5/191	26/15370	1.50E-05	0.006893092
BP	GO:0001561	fatty acid alpha-oxidation	4/191	13/15370	1.51E-05	0.006893092
BP	GO:0015911	long-chain fatty acid import across plasma membrane	3/191	5/15370	1.85E-05	0.007146861
BP	GO:0019418	sulfide oxidation	3/191	6/15370	3.68E-05	0.011713786

BP	GO:0070221	sulfide oxidation, using sulfide:quinone oxidoreductase	3/191	6/15370	3.68E-05	0.011713786
BP	GO:0006642	triglyceride mobilization	4/191	16/15370	3.74E-05	0.011713786
BP	GO:0006790	sulfur compound metabolic process	15/191	359/15370	4.34E-05	0.012782325
BP	GO:0043903	regulation of biological process involved in symbiotic interaction	11/191	208/15370	5.90E-05	0.015127206
CC	GO:0005576	extracellular region	34/154	1815/15370	0.000210599	0.106296281
CC	GO:0044421	obsolete extracellular region part	26/154	1331/15370	0.000721282	0.117275522
CC	GO:0005579	membrane attack complex	2/154	6/15370	0.001457152	0.117275522
CC	GO:0060199	clathrin-sculpted glutamate transport vesicle	2/154	6/15370	0.001457152	0.117275522
CC	GO:0060200	clathrin-sculpted acetylcholine transport vesicle	2/154	6/15370	0.001457152	0.117275522
CC	GO:0060201	clathrin-sculpted acetylcholine transport vesicle membrane	2/154	6/15370	0.001457152	0.117275522
CC	GO:0060203	clathrin-sculpted glutamate transport vesicle membrane	2/154	6/15370	0.001457152	0.117275522
CC	GO:0070081	clathrin-sculpted monoamine transport vesicle	2/154	6/15370	0.001457152	0.117275522
CC	GO:0070083	clathrin-sculpted monoamine transport vesicle membrane	2/154	6/15370	0.001457152	0.117275522
CC	GO:0009986	cell surface	17/154	754/153	0.0014758	0.117275522

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CC	GO:0005576	extracellular region	46/191	1815/15370	1.51E-06	0.003154581
CC	GO:0005615	extracellular space	30/191	1050/15370	1.55E-05	0.006893092
CC	GO:0044421	obsolete extracellular region part	35/191	1331/15370	1.65E-05	0.006893092
CC	GO:0030141	secretory granule	23/191	782/15370	0.000109508	0.022855255
CC	GO:0071944	cell periphery	84/191	4849/15370	0.000191415	0.034242844
CC	GO:0005886	plasma membrane	81/191	4657/15370	0.000241332	0.037198051
CC	GO:0042583	chromaffin granule	3/191	11/15370	0.000289623	0.037198051
CC	GO:0099503	secretory vesicle	25/191	976/15370	0.000456511	0.049825829
CC	GO:0044224	juxtaparanode region of axon	3/191	13/15370	0.000492888	0.050385235
CC	GO:0030667	secretory granule membrane	11/191	272/15370	0.000605977	0.057270529
MF	GO:0038024	cargo receptor activity	5/154	58/15370	0.000282644	0.106296281
MF	GO:0030229	very-low-density lipoprotein particle receptor activity	2/154	3/15370	0.000297263	0.106296281
MF	GO:0038025	reelin receptor activity	2/154	3/15370	0.0002972	0.106296281

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MF	GO:0008035	high-density lipoprotein particle binding	2/154	5/15370	0.0009778 68	0.117275522
MF	GO:0016494	C-X-C chemokine receptor activity	2/154	6/15370	0.0014571 52	0.117275522
MF	GO:0090722	receptor-receptor interaction	2/154	6/15370	0.0014571 52	0.117275522
MF	GO:0019958	C-X-C chemokine binding	2/154	7/15370	0.0020266 04	0.142559957
MF	GO:0005007	fibroblast growth factor-activated receptor activity	2/154	8/15370	0.0026843 91	0.171921223
MF	GO:0051021	GDP-dissociation inhibitor binding	2/154	8/15370	0.0026843 91	0.171921223
MF	GO:0001671	ATPase activator activity	3/154	35/1537 0	0.0051044 99	0.221838583
MF	GO:0070224	sulfide:quinone oxidoreductase activity	3/191	3/15370	1.89E-06	0.003154581
MF	GO:0016672	oxidoreductase activity, acting on a sulfur group of donors, quinone or similar compound as acceptor	3/191	4/15370	7.49E-06	0.004688455
MF	GO:0047747	cholate-CoA ligase activity	3/191	4/15370	7.49E-06	0.004688455
MF	GO:0050197	phytanate-CoA ligase activity	3/191	4/15370	7.49E-06	0.004688455
MF	GO:0070251	pristanate-CoA ligase activity	3/191	4/15370	7.49E-06	0.004688455
MF	GO:0061768	magnesium:sodium antiporter activity	2/191	2/15370	0.0001536 27	0.029596828
MF	GO:0031957	very long-chain fatty acid-CoA ligase activity	3/191	10/1537 0	0.0002125 78	0.035493437
MF	GO:0034930	1-hydroxypyrene sulfotransferase activity	3/191	10/1537	0.0002125	0.035493437

MF	GO:0015245	fatty acid transmembrane transporter activity	3/191	0 11/1537 0	78 0.0002896 23	0.037198051
MF	GO:0004062	aryl sulfotransferase activity	3/191	0 12/1537 0	38 0.0003826 38	0.045634082

Table S6 Downregulated and upregulated Enriched pathway terms of DEGs in the intestine between PI and NI

KEGGID	Description	Gene Ratio	BgRatio	P value	padj
ko04610	Complement and coagulation cascades	7/157	122/15607	0.00023 2181	0.055300548
ko00290	Valine, leucine and isoleucine biosynthesis	2/157	4/15607	0.00059 5382	0.055300548
ko00062	Fatty acid elongation	4/157	42/15607	0.00081 9267	0.055300548
ko01040	Biosynthesis of unsaturated fatty acids	4/157	42/15607	0.00081 9267	0.055300548
ko04090	CD molecules	13/157	539/15607	0.00314 5725	0.169869154
ko00537	Glycosylphosphatidylinositol (GPI)-anchored proteins	5/157	129/15607	0.00980 2239	0.303235997
ko00300	Lysine biosynthesis	1/157	1/15607	0.01005 9589	0.303235997
ko99994	Others	2/157	16/15607	0.01100 0373	0.303235997
ko04913	Ovarian steroidogenesis	4/157	87/15607	0.01150	0.303235997

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ko04061	Viral protein interaction with cytokine and cytokine receptor	4/157	91/15607	0.013394615	0.303235997
ko04972	Pancreatic secretion	16/225	188/15607	1.38E-08	4.00E-06
ko00920	Sulfur metabolism	4/225	15/15607	5.07E-05	0.007347758
ko05204	Chemical carcinogenesis - DNA adducts	6/225	60/15607	0.000219595	0.021227527
ko04974	Protein digestion and absorption	10/225	182/15607	0.000313562	0.022733276
ko04622	RIG-I-like receptor signaling pathway	7/225	95/15607	0.000444667	0.02579067
ko00120	Primary bile acid biosynthesis	4/225	32/15607	0.001101642	0.053246051
ko04146	Peroxisome	7/225	123/15607	0.002037072	0.084392987
ko01002	Peptidases and inhibitors	20/225	725/15607	0.004192938	0.115988483
ko04657	IL-17 signaling pathway	7/225	143/15607	0.004712017	0.115988483
ko01004	Lipid biosynthesis proteins	6/225	108/15607	0.00474258	0.115988483
