

Table S1. Primers for RNA-seq validation through RT-qPCR.

Gene name	Gene ID	Accession no	Forward primer	Reverse primer	Product size (bp)	Efficiency
<i>LY6E</i> ^a	ENSGALG00000041621	NM_204775.1	AGTCCATCTCCAAAGGCTGC	TCACTGTTGGAAGCCTGC	349	104.39%
<i>PLAC8</i>	ENSGALG00000011190	NM_001389397.1	GGTTTCTGTTCTGGGCTGAGT	CGTCGTCTCTACGGCATCAG	504	98.15%
<i>LOC771880</i>	ENSGALG00000052285	NM_205235.1	AGCCACGTCAACAAGGACAT	ACGATGGTGACGATCAGAGC	149	95.99%
<i>MLK</i> ^b	ENSGALG00000002766	XM_015279230.2	CACCGATAACCAGGAGCCAGT	AGCCAGCAAGTCCACGATCT	123	100.17%
<i>AVD</i> ^c	ENSGALG000000025945	NM_205320.1	GGCTCCAACATGACCATC	GGTGGACTCTGAAAACCTTC	193	100.29%
<i>IFI6</i>	ENSGALG00000013575	NM_001001296.5	GTCTGACCAGAACGTCCACA	TGCCTCACCAGACATGATCG	88	97.89%
<i>PLA2G4B</i>	ENSGALG000000008727	XM_015287124.2	GCTGGATGGCTTGTACTGGT	TCCAGCACAGTGTCTGCATATC	341	96.99%
<i>LBFABP</i>	ENSGALG000000004141	NM_204634.1	ACCCAGGCAGACTGTGACTAA	GCACACAAGCTTCCCATTG	115	104.17%
<i>GAPDH</i> *	ENSGALG00000014442	NM_204305.1	GGTGGCCATCAATGATCCCT	CCGTTCTCAGCCTTGACAGT	105	106.76%

^a The primers of *LY6E* were from Zhang et al. (2008) [1].

^b The primers of *MLKL* were from Zhang et al. (2020) [2].

^c The primers of *AVD* were from Dayabari et al. (2015) [3].

**GAPDH* is a housekeeping gene.

References

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2. Zhang, J.; Hao, X.; Xu, S. Selenium Prevents Lead-Induced Necroptosis by Restoring Antioxidant Functions and Blocking MAPK/NF-kappaB Pathway in Chicken Lymphocytes. *Biol. Trace. Elem. Res.* **2020**, *198*, 644–653. <https://doi.org/10.1007/s12011-020-02094-y>
3. Daryabari, H.; Akhlaghi, A.; Zamiri, M.J.; Pirsaraei, Z.A.; Mianji, G.R.; Deldar, H.; Eghbalian, A.N. Oral administration of supplementary biotin differentially influences the fertility rate and oviductal expression of avidin and avidin-related protein-2 in low- and high-fertility broiler line hens. *Poult. Sci.* **2015**, *94*, 289–295. <https://doi.org/10.3382/ps/peu073>

Table S2. Ensembl-derived GO terms associated with difference in FCR.

Category	GO ID	Term	p-value	Genes ¹
Enrichment of GO terms biological process (BP)	GO:0006749	glutathione metabolic process	0.0020	MMACHC , CHAC1
	GO:0006950	response to stress	0.0052	MLKL , RASGRF1 , PLAC8 , OASL , TRIM27.2 , CHAC1 , SPON2 , LAG3 , KNG1
	GO:0006952	defense response	0.0031	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0007162	negative regulation of cell adhesion	0.0033	MYOC , LAG3 , KNG1
	GO:0009605	response to external stimulus	0.0012	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , CDK5R1 , LAG3 , KNG1
	GO:0009607	response to biotic stimulus	0.0003	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0009615	response to virus	0.0035	MLKL , OASL , SPON2
	GO:0021700	developmental maturation	0.0057	MYOC , C1QL1 , CDK5R1
	GO:0035023	regulation of Rho protein signal transduction	0.0051	RASGRF1 , MYOC
	GO:0042551	neuron maturation	0.0017	MYOC , C1QL1
	GO:0043207	response to external biotic stimulus	0.0002	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0044419	interspecies interaction between organisms	0.0002	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0048640	negative regulation of developmental growth	0.0082	PLAC8 , CDK5R1
	GO:0051607	defense response to virus	0.0012	MLKL , OASL , SPON2
	GO:0051707	response to other organism	0.0002	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0071695	anatomical structure maturation	0.0032	MYOC , C1QL1 , CDK5R1
	GO:0098542	defense response to other organism	0.0002	MLKL , PLAC8 , OASL , TRIM27.2 , SPON2 , LAG3
	GO:0005102	signaling receptor binding	0.0086	RASGRF1 , MYOC , CHAC1 , C1QL1 , CDK5R1 , LAG3 , KNG1
Enrichment of GO terms molecular function (MF)	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	0.0049	PTPDC1
	GO:0033218	amide binding	0.0063	MMACHC , AVD , LAPTM4B
	GO:0035254	glutamate receptor binding	0.0007	RASGRF1 , CDK5R1

¹Genes in **bold** represent those higher expressed in low-FCR jejunum.

Table S3. KEGG pathways associated with difference in FCR.

Pathway ID	Term	Number of genes	q-value	Genes ¹
ko04977	Vitamin digestion and absorption	1	0.0128	<i>MMACHC</i>
ko04370	VEGF signaling pathway	1	0.0223	<i>PLA2G4B</i>
ko00350	Tyrosine metabolism	1	0.0133	<i>LOC100857280</i>
ko04668	TNF signaling pathway	1	0.0124	<i>MLKL, MMP10</i>
ko04660	T cell receptor signaling pathway	2	0.0133	<i>LOC107049158, LOC771880</i>
ko05323	Rheumatoid arthritis	1	0.0252	<i>MMP10</i>
ko00830	Retinol metabolism	1	0.0135	<i>LOC100857280</i>
ko04014	Ras signaling pathway	2	0.0262	<i>PLA2G4B, RASGRF1</i>
ko05340	Primary immunodeficiency	2	0.0086	<i>LOC107049158, LOC771880</i>
ko04913	Ovarian steroidogenesis	1	0.0156	<i>PLA2G4B</i>
ko04217	Necroptosis	2	0.0135	<i>MLKL, PLA2G4B</i>
ko00980	Metabolism of xenobiotics by cytochrome P450	1	0.0135	<i>LOC100857280</i>
ko04730	Long-term depression	1	0.0219	<i>PLA2G4B</i>
ko00591	Linoleic acid metabolism	1	0.0133	<i>PLA2G4B</i>
ko04657	IL-17 signaling pathway	1	0.0252	<i>MMP10</i>
ko04640	Hematopoietic cell lineage	2	0.0124	<i>LOC107049158, LOC771880</i>
ko04912	GnRH signaling pathway	1	0.0300	<i>PLA2G4B</i>
ko00010	Glycolysis / Gluconeogenesis	1	0.0160	<i>LOC100857280</i>
ko00480	Glutathione metabolism	1	0.0135	<i>CHAC1</i>
ko04664	Fc epsilon RI signaling pathway	1	0.0239	<i>PLA2G4B</i>
ko00071	Fatty acid degradation	1	0.0133	<i>LOC100857280</i>
ko00565	Ether lipid metabolism	1	0.0137	<i>PLA2G4B</i>
ko00982	Drug metabolism - cytochrome P450	1	0.0133	<i>LOC100857280</i>
ko04610	Complement and coagulation cascades	1	0.0262	<i>KNG1</i>
ko05030	Cocaine addiction	1	0.0137	<i>CDK5R1</i>
ko05204	Chemical carcinogenesis	1	0.0154	<i>LOC100857280</i>
ko04514	Cell adhesion molecules (CAMs)	3	0.0086	<i>LOC107049158, ENSGALG00000051068, LOC771880</i>
ko00590	Arachidonic acid metabolism	1	0.0156	<i>PLA2G4B</i>

ko04612	Antigen processing and presentation	2	0.0124	<i>LOC107049158, LOC771880</i>
ko00592	alpha-Linolenic acid metabolism	1	0.0128	<i>PLA2G4B</i>

¹Genes in ***bold*** represent those higher expressed in low-FCR jejunum.