Supplementary Table 1. Enriched canonical pathways among the differentially abundant genes in ileum and caecum mucosa of pigs differing in feed efficiency.

Canonical Pathways	-log (p-value)	Z-score[1]	Molecules
Ileum			
4-hydroxyproline Degradation I	2.30	NA	*ALDH4A1, HOGA1*
CCR5 Signaling in Macrophages	1.94	-1.00	*CACNA1G, CD3G, CAMK4, CACNG4, MAPK8, CACNA1C, GNG13, PRKD1, PRKCB*
nNOS Signaling in Skeletal Muscle Cells	1.75	NA	*CACNA1G, CAMK4, CACNG4, SNTB1, CACNA1C*
UVB-Induced MAPK Signaling	1.65	-1.89	*PIK3R1, PIK3CG, MAPK8, EIF4E, PRKD1, PRKCB, ATM*
Chondroitin and Dermatan Biosynthesis	1.64	NA	*CHPF, CSGALNACT1*
Aldosterone Signaling in Epithelial Cells	1.53	-1.13	*CRYAB, PIK3R1, PIP4K2B, PLCL2, DNAJC15, DNAJB13, DNAJC5G, PIK3CG, DNAJC18, PRKD1, DNAJB5, PRKCB, ATM*
CREB Signaling in Neurons	1.51	-1.41	*CACNA1G, GRM2, CAMK4, CACNG4, PIK3R1, GNG13, CACNA1C, PLCL2, POLR2B, POLR2C, PIK3CG, GNAO1, PRKD1, PRKCB, ATM*
Crosstalk between Dendritic Cells and Natural Killer Cells	1.51	NA	*MICB, ACTA2, KLRD1, IL12B, FSCN1, IFNB1, CD83, TNFRSF1B*
Apelin Endothelial Signaling Pathway	1.43	-1.27	*CAMK4, PIK3R1, MEF2D, PIK3CG, GNAO1, MAPK8, HIF1A, PRKD1, ATM, PRKCB*
NRF2-mediated Oxidative Stress Response	1.37	0.00	*ABCC2, PIK3R1, MAPK8, DNAJC15, DNAJB13, DNAJC5G, ACTA2, RBX1, PIK3CG, DNAJC18, DNAJB5, PRKD1, PRKCB, ATM*
Ephrin A Signaling	1.37	NA	*EPHA10, EPHA8, PIK3R1, PIK3CG, EFNA1, ATM*
Androgen Signaling	1.34	0.82	*CACNA1G, CAMK4, POLR2C, CACNG4, GNAO1, CACNA1C, GNG13, POLR2B, PRKD1, PRKCB*
G Beta Gamma Signaling	1.34	1.67	*CACNA1G, CACNG4, PIK3CG, GNAO1, CAV1, CACNA1C, GNG13, PRKD1, PRKCB*
Nitric Oxide Signaling in the Cardiovascular System	1.32	-1.00	*BDKRB2, CAMK4, PIK3R1, PIK3CG, CAV1, CACNA1C, PRKD1, ATM, PRKCB*

Caecum

Hepatic Fibrosis / Hepatic Stellate Cell Activation	3.29	NA	*MYH10, CD40LG, MYH6, COL4A6, MYL2, CXCR3, COL4A2, IFNAR2, MYL1, MYL9, COL1A1, CCL2, IL1RL2, TIMP1, IL10RA, CD14, TNFRSF1B, CCR7, TIMP2*
Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	3.19	-0.58	*MYO5A, PLD4, NCF1, ACTR3, ARPC1B, VAV3, PLCG1, NCK1, ACTC1, PRKD1, FCGR3A/FCGR3B, PTEN*
Th1 Pathway	3.06	0.28	*mir-146, MAP2K6, SOCS3, CD40LG, NOTCH3, CXCR3, PSEN2, HLA-DQB1, STAT4, PIK3C3, HLA-DMB, IL10RA, NOTCH1, ATM, PSEN1*
Glucose and Glucose-1-phosphate Degradation	3.03	0.00	*PGM3, PGM2L1, RGN, HK3*
Complement System	3.02	-2.65	*C1R, C4A/C4B, MASP2, C1QC, C1QA, C1QB, C2*
Actin Cytoskeleton Signaling	2.96	-0.24	*ABI2, MYH10, MYH6, ARHGEF12, ARPC1B, MYL2, MYLK2, FGD1, GSN, MYL1, MYL9, ACTR3, FGF18, PIK3C3, VAV3, CD14, ARHGAP35, FGF11, ACTC1, ACTN1, ATM*
Th1 and Th2 Activation Pathway	2.88	NA	*MAP2K6, mir-146, SOCS3, CD40LG, NOTCH3, CXCR3, PSEN2, HLA-DQB1, IL25, STAT4, PIK3C3, HLA-DMB, IL10RA, IL2RA, STAT5B, NOTCH1, ATM, PSEN1*
Urea Cycle	2.83	NA	*OTC, ARG2, CPS1*
Integrin Signaling	2.77	0.69	*ARPC1B, MYL2, MYLK2, MAPK8, PIKFYVE, PLCG1, NCK1, GSN, PTEN, MYL9, ITGAE, ACTR3, RHOB, PIK3C3, ITGAV, RHOU, CAPN2, ACTC1, ACTN1, ATM*
Axonal Guidance Signaling	2.49	-	*DPYSL2, PAPPA2, ARPC1B, MYL2, CXCL12, ADAMTS10, NCK1, NTN1, ACTR3, GLI3, SUFU, PIK3C3, ADAM19, DCC, SMO, ADAM32, PRKD1, ATM, ADAMTS4, KCNJ12, NGEF, ARHGEF12, FES, NRP2, GNAQ, PLCG1, PLXND1, MYL1, MYL9, PLCB4, FZD4, NTRK3, EPHB3, GLI1, FZD7*
Superpathway of Citrulline Metabolism	2.48	-1.00	*OTC, GLS, ARG2, CPS1*
TR/RXR Activation	2.41	NA	*AKR1C1/AKR1C2, SCARB1, SREBF1, DIO1, PIK3C3, NRGN, NCOR2, RCAN2, NCOA3, ATM, EP300*
Regulation of Actin-based Motility by Rho	2.27	-0.33	*MYL9, ACTR3, MYL2, RHOB, ARPC1B, PIKFYVE, RHOU, GSN, ACTC1, MYL1*
Epithelial Adherens Junction Signaling	2.25	NA	*MYH10, MYH6, NOTCH3, MYL2, ARPC1B, HNF1A, MYL1, PTEN, MYL9, ACTR3, NOTCH1, ACTC1, ACTN1, CTNND1*

Notch Signaling	2.25	-0.45	*DTX1, NOTCH3, PSEN2, LFNG, NOTCH1, PSEN1*
Citrulline Biosynthesis	2.25	NA	*OTC, GLS, ARG2*
Tight Junction Signaling	2.17	NA	*CPSF2, MYH10, MYH6, MYL2, PPP2R2A, CPSF1, MYL1, PTEN, MYL9, PPP2CB, CLDN8, STX4, TNFRSF1B, CSTF3, ACTC1*
DNA damage-induced 14-3-3σ Signaling	2.17	NA	*RAD17, CCNB2, RAD1, ATM*
RhoA Signaling	2.15	-0.91	*MYL9, NGEF, ARHGEF12, ACTR3, NRP2, MYL2, ARPC1B, MYLK2, PIKFYVE, ARHGAP35, ACTC1, MYL1*
Wnt/β-catenin Signaling	2.12	-0.83	*CSNK2A1, PPP2R2A, LRP6, GNAQ, HNF1A, EP300, APPL1, PPP2CB, FZD4, CDH5, TLE4, SMO, SFRP1, LRP1, FZD7*
GDP-glucose Biosynthesis	2.1	NA	*PGM3, PGM2L1, HK3*
Mechanisms of Viral Exit from Host Cells	2.09	NA	*CHMP6, CHMP4C, XPO1, SH3GL2, ACTC1, PRKD1*
ATM Signaling	2.02	0.33	*PPP2CB, FANCD2, PPP2R2A, GADD45G, RAD17, MAPK8, CCNB2, TP53BP1, PPM1D, ATM*
IL-10 Signaling	2.00	NA	*MAP2K6, SOCS3, IL1RL2, MAPK8, IL10RA, CD14, ARG2, ELK1*
Thymine Degradation	1.97	NA	*DPYSL2, UPB1*
Leukocyte Extravasation Signaling	1.93	0.50	*MAPK8, CXCL12, PLCG1, NCF1, CDH5, CLDN8, TIMP1, RAP1GAP, VAV3, PIK3C3, ARHGAP35, ACTC1, ACTN1, PRKD1, ATM, CTNND1, TIMP2*
Dendritic Cell Maturation	1.92	-1.29	*CD40LG, TYROBP, MAPK8, PLCG1, HLA-DQB1, STAT4, COL1A1, PLCB4, IL1RL2, PIK3C3, HLA-DMB, IGHG4, TNFRSF1B, CCR7, FCGR3A/FCGR3B, ATM*
ILK Signaling	1.90	-1.00	*MAP2K6, MYH10, MYH6, MYL2, PPP2R2A, MAPK8, MYL1, PTEN, MYL9, PPP2CB, RHOB, PIK3C3, RHOU, ACTC1, ACTN1, ATM*
Growth Hormone Signaling	1.90	-0.71	*SOCS3, PIK3C3, PLCG1, RPS6KA2, STAT5B, ELK1, SLC2A4, PRKD1, ATM*
Melatonin Signaling	1.89	0.38	*MAP2K6, PLCB4, RORA, GNAQ, PLCG1, SLC2A4, PRKD1, RORB*
Cleavage and Polyadenylation of Pre-mRNA	1.87	NA	*CPSF2, CPSF1, CSTF3*
Th2 Pathway	1.83	-1.51	*SOCS3, NOTCH3, PSEN2, HLA-DQB1, IL25, STAT4, PIK3C3, HLA-DMB, IL2RA, STAT5B, NOTCH1, ATM, PSEN1*

IL-6 Signaling	1.80	0.30	*MAP2K6, SOCS3, COL1A1, CSNK2A1, IL1RL2, CYP19A1, PIK3C3, MAPK8, CD14, TNFRSF1B, ELK1, ATM*
Tec Kinase Signaling	1.77	0.28	*FADD, STAT4, RHOB, PIK3C3, VAV3, RHOU, MAPK8, GNAQ, FCER1A, PLCG1, STAT5B, ACTC1, PRKD1, ATM*
Cholesterol Biosynthesis I	1.77	NA	*EBP, DHCR7, LSS*
RhoGDI Signaling	1.71	-0.28	*MYL9, ACTR3, ARHGEF12, CDH5, RHOB, ARPC1B, MYL2, RHOU, GNAQ, PIKFYVE, ARHGAP35, ACTC1, MYL1, EP300*
Death Receptor Signaling	1.70	-0.71	*TANK, FADD, ACIN1, PARP10, ZC3HAV1, MAPK8, PARP11, TNFRSF1B, ACTC1*
Apelin Cardiomyocyte Signaling Pathway	1.57	0	*MYL9, PLCB4, APLNR, MYL2, PIK3C3, MAPK8, PLCG1, MYL1, PRKD1, ATM*
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	1.55	0	*PLD4, PLCB4, PIKFYVE, PLCG1*
Superpathway of Cholesterol Biosynthesis	1.50	0	*EBP, DHCR7, LSS, GGPS1*

[1] negative and positive Z-scores indicating inhibition and activation in high RFI pigs, respectively. Absolute Z-scores above 2 were considered as significant. NA indicates pathways for which a prediction based on the Ingenuity Pathway Analysis knowledge base is not possible.