Supplementary Table 2. Composition of ileal and caecal gene clusters deduced from correlation analysis between differentially expressed mucosal genes and digesta microbe abundance. The enrichment of genes in canonical pathways was analysed using Ingenuity Pathway Analysis.

Ileal Gene Cluster	Top canonical pathway (p-value)	Genes
1	ERK/MAPK Signaling (0.022), Cell Cycle Regulation by BTG Family Proteins (0.040)	*ADD2*, *C12H17orf78*, *CEP250*, *CNOT10*, *CRB2*, *CRKL*, *ENSSSCG00000028767*, *ENSSSCG00000033431*, *GPN3*, *GPR82*, *GRHL3*, *HBA2*, *KLRD1*, *LACTB2*, *LOC106509797*, *LOC110256510*, *MARCH8*, *MIR181B2*, *MYO5A*, *PPP2R2A*, *SULF2*, *TCTN3*, *TMEM229B*, *TRAK1*, *TRIM68*, *UBE2N*, *UPRT*, *ZNF662*, *ZSWIM7*
2	NER Pathway (0.003), BER pathway (0.009), DNA Double-Strand Break Repair by Non-Homologous End Joining (0.011)	*CCDC138*, *CHD2*, *CNTRL*, *COBL*, *EIF2S2*, *ERCC5*, *ISOC2*, *LIG3*, *LOC110257803*, *LSM8*, *MLLT6*, *NAT9*, *PARN*, *PHTF1*, *PTPRC*, *RLF*, *SESN3*, *ZNF473*
3	iCOS-iCOSL Signaling in T Helper Cells (<0.001), GP6 Signaling Pathway (<0.001), PI3K Signaling in B Lymphocytes (<0.001)	*ABRAXAS2*, *AFF3*, *AGMO*, *CAMK4*, *CD3G*, *CFP*, *CHML*, *COL24A1*, *DGKE*, *FUBP1*, *GAS8*, *GLMN*, *INPP4B*, *KLF8*, *LOC100515492*, *LOC100518286*, *LOC100620675*, *LOC110259525*, *MMADHC*, *PIK3R1*, *PLEKHA1*, *PPP1R9A*, *PRKCB*, *RABGAP1L*, *RASAL2*, *RORA*, *SIRT1*, *SLAMF6*, *SNORA19*, *SYTL5*, *TBCD*, *ZBTB38*, *ZKSCAN8*, *ZNF644*
4	Wnt/β-catenin Signaling (<0.001), Methylglyoxal Degradation VI (0.001), HIPPO signaling (0.003)	*BRINP3*, *CAMKV*, *CAVIN2*, *CD9*, *COL6A3*, *CORO6*, *GABRR1*, *GNAO1*, *HCAR2*, *LDHD*, *LOC100736871*, *LOC110260402*, *LURAP1L*, *LUZP4*, *MICB*, *MIR15A*, *MIR339-1*, *ONECUT2*, *OR2J2*, *PPP2R1A*, *PRR3*, *RPH3AL*, *SERPINA3*, *SFRP4*, *SP2*, *SUFU*, *YAP1*
5	PFKFB4 Signaling Pathway (0.044)	*ABCA2*, *AMPD1*, *ANKS3*, *CCDC103*, *CLEC3A*, *EDNRA*, *ENDOD1*, *FOXI1*, *GJD2*, *GSC*, *KLF4*, *LOXHD1*, *ODF3B*, *PABPC5*, *PRAG1*, *PRDM14*, *SKOR1*, *SMIM12*, *STK32A*, *STK32B*, *SYNE4*, *TACR2*, *TEX261*, *TMEM44*, *ZNF524*
6	Nitric Oxide Signaling in the Cardiovascular System (<0.001), Coagulation System (<0.001), Notch Signaling (<0.001)	*ASTN1*, *BATF3*, *BDKRB2*, *CAV1*, *CD300LF*, *DIP2C*, *ENSSSCG00000020314*, *ENSSSCG00000020581*, *ENSSSCG00000032809*, *EPS15L1*, *GATA2*, *HES7*, *HRG*, *IL12B*, *JAG2*, *LOC110257704*, *MAL*, *MTURN*, *NRM*, *OLFML2A*, *OR2W1*, *OTUB2*, *PRKD1*, *SHOX2*, *SLC6A1*, *THBD*, *TRIL*, *XCR1*
7	Glutamate Receptor Signaling (0.013), Neuropathic Pain Signaling In Dorsal Horn Neurons (0.026), Gαi Signaling (0.028)	*AAMP*, *C12orf45*, *GRM2*, *KCNH6*, *MIR432*, *SEL1L2*
8	Rapoport-Luebering Glycolytic Shunt (0.006), D-myo-inositol (1,3,4)-trisphosphate Biosynthesis (0.018), Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism (0.023)	*ACTRT2*, *C1QL2*, *CACNA1G*, *CLEC2B*, *CYP11B*, *ENSSSCG00000011967*, *ENSSSCG00000020634*, *FAM78A*, *FBLL1*, *GPR101*, *HOXD3*, *LOC102163402*, *LOXL1*, *MINPP1*, *MSRB3*, *MVB12B*, *NKX2-4*, *PDCD11*, *PDZD4*, *RAB9B*, *RHBDD2*, *RIMS4*, *SPACA9*, *TMEM114*, *TMEM201*, *TTC8*, *ZDHHC3*, *ZNF510*

Caecal gene cluster	Top canonical pathway (p-value)	Genes
1	Autophagy (<0.001), Sirtuin Signaling Pathway (0.001), Glutamine Degradation I (0.001)	*ARMT1*, *ATG4A*, *BLOC1S2*, *CDC5L*, *CHD9*, *CKAP2L*, *CPSF2*, *CSTF3*, *EIF2AK3*, *FAM102B*, *GLS*, *HMG20A*, *LDAH*, *March5*, *MFF*, *MIOS*, *N4BP2L2*, *NAA25*, *NCBP2*, *NCK1*, *NSD3*, *NUFIP2*, *PHF6*, *PIK3C3*, *PIKFYVE*, *PPP2R2A*, *PSMD7*, *PTEN*, *RRP15*, *SMG1*, *TCEA1*, *THUMPD1*, *TOP1*, *TP53BP1*, *UBE2W*, *UBR3*, *ZNF644*
2	DNA damage-induced 14-3-3σ Signaling (<0.001), Role of NFAT in Regulation of the Immune Response (0.003), Role of CHK Proteins in Cell Cycle Checkpoint Control (0.003)	*ACTR3*, *ASB3*, *ASNSD1*, *ATM*, *CFAP97*, *DYNC1LI2*, *FAM83B*, *FAM98A*, *FBXO28*, *FEM1B*, *FGD6*, *KMT2C*, *LOC100525309*, *LRP6*, *MMADHC*, *MPHOSPH8*, *MYO5A*, *NCAPG*, *NKTR*, *OPA1*, *PAFAH1B2*, *PREPL*, *RAB2A*, *RAB3GAP1*, *RAD17*, *RCAN1*, *STX18*, *TM9SF2*, *TMBIM4*, *TMEM263*, *TMEM59*, *UBR5*, *WFDC3*, *XPO1*
3	Rapoport-Luebering Glycolytic Shunt (0.002), D-myo-inositol (1,3,4)-trisphosphate Biosynthesis (0.007), Superpathway of D-myo-inositol (1,4,5)-trisphosphate Metabolism (0.009)	*ENSSSCG00000018772*, *ENSSSCG00000036968*, *GEMIN2*, *IRAK1BP1*, *JSRP1*, *MINPP1*, *PRC1*, *RETREG1*, *SLC35A5*, *STUM*, *ZUFSP*
4	GDP-glucose Biosynthesis (0.012), Glucose and Glucose-1-phosphate Degradation (0.013), Glycogen Degradation II (0.015)	*ANK2*, *C13H21orf59*, *CA2*, *CNTNAP2*, *CXXC4*, *CYP2D25*, *ENSSSCG00000000659*, *ENSSSCG00000001458*, *ENSSSCG00000007512*, *ENSSSCG00000020137*, *ENSSSCG00000035996*, *EP300*, *FAM219A*, *FHAD1*, *FZD7*, *GUCY1B1*, *HDHD5*, *KCNJ12*, *LCN9*, *LNX2*, *LOC100519221*, *LOC100626387*, *MEOX2*, *MFHAS1*, *MIR342*, *MOB3C*, *MROH2A*, *PGM2L1*, *PLXNA4*, *RNU6-77P*, *SLC19A2*, *SVOP*, *TTC8*, *UPK3A*, *WFIKKN2*, *ZNF461*
5	Granzyme B Signaling (0.015), Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F (0.022), Tumoricidal Function of Hepatic Natural Killer Cells (0.023)	*ANXA6*, *AP3S2*, *ARSA*, *AXL*, *C2*, *CDH5*, *COL4A6*, *DAP*, *DEFB103A*, *DSG3*, *ENSSSCG00000022506*, *ENSSSCG00000034481*, *EPHX3*, *FSIP2*, *GSN*, *GZMB*, *LOC110256886*, *MIR1296*, *MRPS23*, *NOTCH1*, *RNU6ATAC31P*, *SLC7A8*, *SNORA61*, *VENTX*, *WDR87*, *WIPI1*
6	Autoimmune Thyroid Disease Signaling (0.020), Primary Immunodeficiency Signaling (0.020), Retinoic acid Mediated Apoptosis Signaling (0.025)	*ADORA3*, *AGO3*, *CD40LG*, *FCER1A*, *INVS*, *LGI1*, *PARP11*, *RBCK1*, *YPEL5*
7	Histidine Degradation III (0.005), Histidine Degradation VI (0.010), CDP-diacylglycerol Biosynthesis I (0.017)	*ABCB5*, *C1QTNF2*, *GPAT2*, *GPR26*, *IGLV3-21*, *LOC100626988*, *MIR146B*, *NHS*, *NRGN*, *PIANP*, *RCC1L*, *RFPL4B*, *UBAC1*, *UBAP2*, *UROC1*, *ZNF282*
8	Gαs Signaling (0.005), Adrenomedullin signaling pathway (0.019), April Mediated Signaling (0.039)	*ATXN7L2*, *CCDC107*, *CTIF*, *CYLC1*, *ELK1*, *ENSSSCG00000035556*, *ETV3L*, *FRAS1*, *GNLY*, *GPR182*, *HRH2*, *LOC100739359*, *LOC110256774*, *LOC110259674*, *LOC110261361*, *MRPL38*, *MRPS2*, *NRM*, *PFKFB2*, *SLC12A7*, *SLC35G2*, *SPAG11*, *SSU72*, *STAB1*, *TBC1D2B*, *VPS72*, *XPNPEP2*, *ZDHHC7*