**Library preparation and sequencing**

RNA was extracted from blood samples. Total RNA was extracted from blood samples using a PAXgene Blood RNA Kit according to the manufacturer’s instructions, with RNA quality then assessed using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). Total RNA was processed using a GlobinZero Kit (Epicentre, Illumina, Madison, WI, USA) and purified with a modified Qiagen RNeasy MinElute (Qiagen Inc., Valencia, CA, USA) cleanup procedure or ethanol precipitation. Blood samples with an RNA integrity number (RIN) higher than 6.5 were used for subsequent library construction and sequencing, with a specified amount of RNA from each sample used as input material. Lastly, the fecal and blood samples were subjected to transcriptomic and metagenomic sequencing at Novogene (Beijing, China), respectively, using the Illumina NovaSeq 6000 or Hiseq 4000 platforms, with a paired-end sequencing length of 150 bp (PE150).

**Transcriptome data analysis**

***Quality control and reads alignment.*** Adaptors and low-quality reads were removed using the fastp v0.23.4 with defalut parameter. Based on our previous treatment, samples in which more than 50% of reads were filtered out were considered contaminated and subsequently excluded from downstream analysis. The human reference genome was downloaded from Ensembl (Homo sapiens, GRCh38), and annotation information was downloaded from Ensembl release-110 ([www.ensembl.org](http://www.ensembl.org)). Following this, the genome index was constructed, and high-quality reads were mapped to the human reference genome using HISAT2 v2.2.1. The SAM files were converted to BAM files using SAMtools v1.19, with the BAM files sorted by chromosomal position. Finally, raw read count matrices for each gene and transcript were obtained using StringTie v2.2.1 based on the provided annotation information.