

Supplementary Table S1 DEGs associated with cell growth in the intestines of *T. ovatus* in the antibiotic-treated and control groups

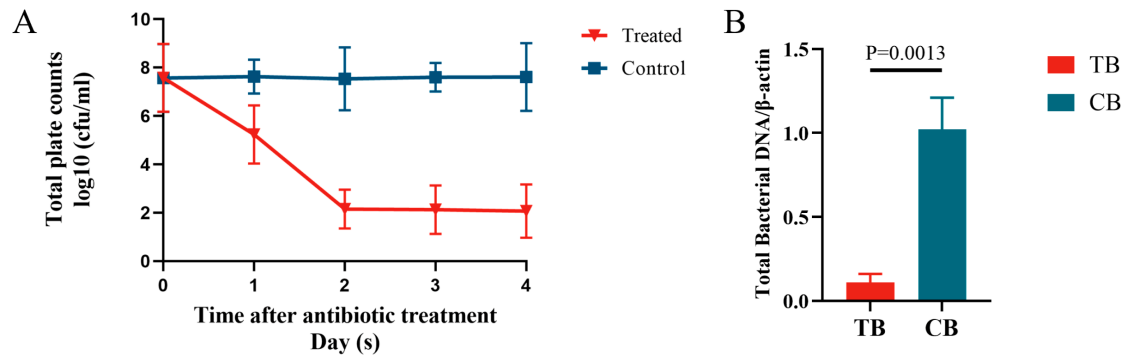
Gene name	Function annotation	TB vs CB
<i>socs1</i>	Suppressor of cytokine signaling 1 (SOCS1)	up
<i>cdkn1a</i>	Cyclin-dependent kinase inhibitor 1 (CDKN1A/P21)	up
<i>mapk1</i>	mitogen-activated protein kinase 1 (MAPK1)	down
<i>kras</i>	GTPase KRas (KRAS)	down
<i>sos1</i>	Son of sevenless homolog 1 (SOS1)	down
<i>shc1</i>	SHC-transforming protein 1 (SHC1)	down
<i>jak2</i>	Janus kinase 2 (JAK2)	down
<i>ghr</i>	Growth hormone receptor (GHR)	down
<i>stat3</i>	Signal transducer and activator of transcription 3 (STAT3)	down
<i>egfr</i>	Epidermal growth factor receptor (EGFR)	down

Supplementary Table S2 Quality assessment and comparison rate analysis of transcriptome data

Sample	Raw reads	Clean reads	Clean bases	Q20(%)	Q30(%)	GC content(%)	Total mapped(%)
TB_60d_1	42285646	41585244	6162702317	97.14	92.08	51.98	93.41%
TB_60d_2	46724810	46142572	6820776513	97.17	92.18	50.51	93.14%
TB_60d_3	39924258	39401806	5844522686	97.14	92.05	52.63	92.89%
CB_60d_1	44356266	43690662	6447839647	97.41	92.74	53.78	95.85%
CB_60d_2	44208538	43631108	6422153820	97.44	92.68	54.03	95.18%
CB_60d_3	45358888	44857758	6614827634	97.48	92.85	53.07	95.27%

Supplementary Table S3 Total ion number and identification statistics of metabolites

Ion mode	All peaks	Identified metabolites	Metabolites in Library	Metabolites in KEGG
pos	7192	569	440	197
neg	5272	250	214	92



Supplementary Fig. S1 Effect of antibiotic treatment on the intestinal bacterial quantity of *T. ovatus*. (A) Change of bacterial quantity of antibiotic treatment for 4 days. (B) qPCR analysis on the intestine ($n = 3$) was performed using universal primers for total intestinal bacterial genes. Three biological replicates were performed. Error bars indicate the mean values of SD. Significant differences were determined by the Student's *t* test, $p = 0.0013$.