

Table S1: P values of correlations between microbial populations and cytokines in the jejunum.

	IL_2	IL_6	IL_10	IL_12	TNF α
<i>g_Paeniclostridium</i>	0.544	0.266	0.544	0.329	0.623
<i>g_Pseudomonas</i>	0.623	0.623	0.397	0.872	0.704
<i>g_unclassified_f_Peptostreptococcaceae</i>	0.156	0.111	0.787	0.329	0.623
<i>g_Candidatus_Saccharimonas</i>	0.872	0.872	0.623	0.397	0.208
<i>g_norank_c_WCHB1-41</i>	0.397	0.623	0.208	0.872	0.957
<i>g_norank_f_vadinBE97</i>	0.208	0.208	0.623	0.208	0.266
<i>g_Succinivibrio</i>	0.957	0.425	0.700	0.173	0.257
<i>g_Ruminococcaceae_UCG-014</i>	0.623	0.623	0.872	0.623	0.468
<i>g_norank_f_Rhodospirillaceae</i>	0.787	0.468	0.544	0.787	0.957
<i>g_Aeriscardovia</i>	0.544	0.468	0.787	0.329	0.208
<i>g_unclassified_f_Coriobacteriaceae</i>	0.397	0.623	0.208	0.872	0.957
<i>g_Succiniclasticum</i>	0.658	0.461	0.577	0.321	0.425
<i>g_Mogibacterium</i>	0.208	0.397	0.397	0.872	0.787
<i>g_Clostridium_sensu_stricto_1</i>	0.397	0.208	0.872	0.397	0.787
<i>g_norank_o_Gastranaerophilales</i>	0.623	0.623	0.872	0.623	0.468
<i>g_norank_f_Bifidobacteriaceae</i>	0.957	0.827	0.008 **	0.784	0.577
<i>g_Senegalimassilia</i>	0.329	0.266	0.957	0.156	0.266
<i>g_unclassified_f_Bifidobacteriaceae</i>	0.518	0.439	0.686	0.295	0.295
<i>g_Olsenella</i>	0.872	0.623	0.872	0.208	0.266
<i>g_Family_XIII_AD3011_group</i>	0.787	0.468	0.957	0.329	0.397
<i>g_Ruminococcus_2</i>	0.787	0.957	0.019 *	0.957	0.704
<i>g_Saccharofermentans</i>	0.872	0.872	0.072	0.623	0.329
<i>g_Ureaplasma</i>	0.468	0.329	0.957	0.704	0.872
<i>g_norank_f_Ruminococcaceae</i>	0.397	0.623	0.208	0.872	0.957
<i>g_[Eubacterium]_coprostanoligenes_group</i>	0.872	0.623	0.872	0.397	0.329
<i>g_Solobacterium</i>	0.518	0.439	0.686	0.295	0.295
<i>g_Erysipelotrichaceae_UCG-009</i>	0.787	0.468	0.544	0.787	0.957
<i>g_Turicibacter</i>	0.329	0.266	0.787	0.329	0.544
<i>g_unclassified_k_norank</i>	0.957	0.704	0.544	0.329	0.208
<i>g_Cellulosilyticum</i>	0.468	0.156	0.704	0.266	0.623

Correlations between microbial populations and cytokines detected in the jejunum of Altay sheep ($n = 12$). * Statistical significance is indicated by * $p < 0.05$, ** $p < 0.01$.

Table S2: R values of correlations between microbial populations and cytokines in the jejunum.

	IL_2	IL_6	IL_10	IL_12	TNF_a
<i>g_Paeniclostridium</i>	-0.314	-0.543	-0.314	-0.486	-0.257
<i>g_Pseudomonas</i>	0.257	0.257	-0.429	0.086	-0.200
<i>g_unclassified_f_Peptostreptococcaceae</i>	-0.657	-0.714	-0.143	-0.486	-0.257
<i>g_Candidatus_Saccharimonas</i>	0.086	0.086	0.257	0.429	0.600
<i>g_norank_c_WCHB1-41</i>	-0.429	-0.257	0.600	-0.086	-0.029
<i>g_norank_f_vadinBE97</i>	-0.600	-0.600	0.257	-0.600	-0.543
<i>g_Succinivibrio</i>	-0.029	-0.406	-0.203	-0.638	-0.551
<i>g_Ruminococcaceae_UCG-014</i>	-0.257	-0.257	-0.086	-0.257	-0.371
<i>g_norank_f_Rhodospirillaceae</i>	-0.143	-0.371	-0.314	-0.143	0.029
<i>g_Aeriscardovia</i>	-0.314	-0.371	-0.143	-0.486	-0.600
<i>g_unclassified_f_Coriobacteriaceae</i>	-0.429	-0.257	0.600	-0.086	-0.029
<i>g_Succiniclasticum</i>	-0.232	-0.377	0.290	-0.493	-0.406
<i>g_Mogibacterium</i>	0.600	0.429	0.429	0.086	0.143
<i>g_Clostridium_sensu_stricto_1</i>	-0.429	-0.600	-0.086	-0.429	-0.143
<i>g_norank_o_Gastranaerophiles</i>	-0.257	-0.257	-0.086	-0.257	-0.371
<i>g_norank_f_Bifidobacteriaceae</i>	-0.029	0.116	0.928	0.145	0.290
<i>g_Senegalimassilia</i>	0.486	0.543	-0.029	0.657	0.543
<i>g_unclassified_f_Bifidobacteriaceae</i>	-0.334	-0.395	0.213	-0.516	-0.516
<i>g_Olsenella</i>	0.086	-0.257	-0.086	-0.600	-0.543
<i>g_Family_XIII_AD3011_group</i>	-0.143	-0.371	0.029	-0.486	-0.429
<i>g_Ruminococcus_2</i>	-0.143	-0.029	0.886	0.029	0.200
<i>g_Saccharofermentans</i>	0.086	0.086	0.771	0.257	0.486
<i>g_Ureaplasma</i>	0.371	0.486	0.029	0.200	-0.086
<i>g_norank_f_Ruminococcaceae</i>	-0.429	-0.257	0.600	-0.086	-0.029
<i>g_[Eubacterium]_coprostanoligenes_group</i>	-0.086	-0.257	-0.086	-0.429	-0.486
<i>g_Solobacterium</i>	-0.334	-0.395	0.213	-0.516	-0.516
<i>g_Erysipelotrichaceae_UCG-009</i>	-0.143	-0.371	-0.314	-0.143	0.029
<i>g_Turicibacter</i>	-0.486	-0.543	-0.143	-0.486	-0.314
<i>g_unclassified_k_norank</i>	0.029	-0.200	-0.314	-0.486	-0.600
<i>g_Cellulosilyticum</i>	-0.371	-0.657	-0.200	-0.543	-0.257

Pearson's correlation analysis of microbial populations and cytokines in the colon ($n = 12$).

Table S3: P values of correlations between microbial populations and cytokines in the colon.

	IL_2	IL_6	IL_10	IL_12	TNF_α
<i>g_Ruminococcaceae_UCG-010</i>	0.266	0.397	0.072	0.468	0.397
<i>g_Prevotella_1</i>	0.111	0.468	0.208	0.329	0.787
<i>g_Fibrobacter</i>	0.544	0.468	0.329	0.623	0.042 *
<i>g_Christensenellaceae_R-7_group</i>	0.468	0.872	0.704	0.111	0.872
<i>g_Ruminococcaceae_UCG-005</i>	0.872	0.704	0.872	0.042 *	0.957
<i>g_Rikenellaceae_RC9_gut_group</i>	0.787	0.704	0.111	0.623	0.957
<i>g_norank_f_Bacteroidales_BS11_gut_group</i>	0.872	0.329	0.623	0.111	0.468
<i>g_unclassified_f_Lachnospiraceae</i>	0.704	0.872	0.329	0.208	0.397
<i>g_Treponema_2</i>	0.957	0.872	0.208	0.468	0.072
<i>g_Phocaecola</i>	0.872	0.872	0.872	0.957	0.208
<i>g_Bacteroides</i>	0.623	0.957	0.544	0.156	0.704
<i>g_Alistipes</i>	0.787	0.872	0.872	0.329	0.072
<i>g_Akkermansia</i>	0.872	0.329	0.623	0.111	0.468
<i>g_norank_f_Bacteroidales_UCG-001</i>	0.544	0.468	0.329	0.623	0.042 *
<i>g_norank_f_Clostridiales_vadinBB60_group</i>	0.019 *	0.397	0.156	0.872	0.872
<i>g_[Eubacterium]_coprostanoligenes_group</i>	0.397	0.329	0.544	0.468	0.111
<i>g_Phascolarctobacterium</i>	0.872	0.544	0.957	0.266	0.019 *
<i>g_Ruminococcaceae_NK4A214_group</i>	0.787	0.872	0.623	0.019 *	0.872
<i>g_Prevotellaceae_UCG-001</i>	0.329	0.329	0.072	0.266	0.957
<i>g_Elusimicrobium</i>	0.787	0.872	0.623	0.019 *	0.872
<i>g_unclassified_f_Ruminococcaceae</i>	0.266	0.872	0.397	0.329	0.872
<i>g_unclassified_p_Bacteroidetes</i>	0.872	0.329	0.266	0.397	0.544
<i>g_norank_f_Marinilabiaceae</i>	0.305	0.034 *	0.268	0.468	0.468
<i>g_Barnesiella</i>	0.704	0.704	0.397	0.468	0.111
<i>g_Ruminococcaceae_UCG-002</i>	0.156	0.872	0.872	0.957	0.623
<i>g_norank_o_Gastranaerophilales</i>	0.208	0.266	0.042 *	0.872	0.544
<i>g_Prevotellaceae_UCG-004</i>	0.389	0.913	0.036 *	0.354	0.913
<i>g_Prevotellaceae_UCG-003</i>	0.872	0.208	0.623	0.787	0.005 **
<i>g_Ruminococcaceae_UCG-014</i>	0.111	0.042 *	0.468	0.544	0.111
<i>g_Ruminococcaceae_UCG-013</i>	0.072	0.005 **	0.397	0.957	0.208

Correlations between microbial populations and cytokines detected in the colon of Altay sheep ($n = 12$). * Statistical significance is indicated by * $p < 0.05$, ** $p < 0.01$.

Table S4: R values of correlations between microbial populations and cytokines in the colon.

	IL_2	IL_6	IL_10	IL_12	TNF_α
<i>g_Ruminococcaceae_UCG-010</i>	-0.543	0.429	0.771	-0.371	-0.429
<i>g_Prevotella_1</i>	0.714	-0.371	-0.600	0.486	0.143
<i>g_Fibrobacter</i>	-0.314	0.371	-0.486	-0.257	-0.829
<i>g_Christensenellaceae_R-7_group</i>	-0.371	0.086	0.200	-0.714	-0.086
<i>g_Ruminococcaceae_UCG-005</i>	-0.086	-0.200	0.086	-0.829	-0.029
<i>g_Rikenellaceae_RC9_gut_group</i>	-0.143	0.200	0.714	0.257	0.029
<i>g_norank_f_Bacteroidales_BS11_gut_group</i>	0.086	-0.486	0.257	-0.714	0.371
<i>g_unclassified_f_Lachnospiraceae</i>	0.200	0.086	-0.486	-0.600	-0.429
<i>g_Treponema_2</i>	0.029	-0.086	0.600	0.371	0.771
<i>g_Phocaecola</i>	0.086	-0.086	-0.086	0.029	-0.600
<i>g_Bacteroides</i>	0.257	-0.029	-0.314	0.657	-0.200
<i>g_Alistipes</i>	0.143	0.086	0.086	-0.486	-0.771
<i>g_Akkermansia</i>	-0.086	0.486	-0.257	0.714	-0.371
<i>g_norank_f_Bacteroidales_UCG-001</i>	0.314	-0.371	0.486	0.257	0.829
<i>g_norank_f_Clostridiales_vadinBB60_group</i>	-0.886	0.429	0.657	0.086	-0.086
<i>g_[Eubacterium]_coprostanoligenes_group</i>	-0.429	0.486	-0.314	-0.371	-0.714
<i>g_Phascolarctobacterium</i>	0.086	0.314	0.029	-0.543	-0.886
<i>g_Ruminococcaceae_NK4A214_group</i>	0.143	-0.086	0.257	-0.886	0.086
<i>g_Prevotellaceae_UCG-001</i>	-0.486	0.486	0.771	-0.543	-0.029
<i>g_Elusimicrobium</i>	-0.143	0.086	-0.257	0.886	-0.086
<i>g_unclassified_f_Ruminococcaceae</i>	-0.543	-0.086	0.429	-0.486	0.086
<i>g_unclassified_p_Bacteroidetes</i>	-0.086	0.486	0.543	0.429	0.314
<i>g_norank_f_Marinilabiaceae</i>	-0.507	0.845	0.541	-0.372	-0.372
<i>g_Barnesiella</i>	0.200	-0.200	-0.429	-0.371	-0.714
<i>g_Ruminococcaceae_UCG-002</i>	-0.657	-0.086	-0.086	0.029	-0.257
<i>g_norank_o_Gastranaerophilales</i>	-0.600	0.543	0.829	-0.086	-0.314
<i>g_Prevotellaceae_UCG-004</i>	-0.435	0.058	0.841	-0.464	0.058
<i>g_Prevotellaceae_UCG-003</i>	0.086	-0.600	0.257	0.143	0.943
<i>g_Ruminococcaceae_UCG-014</i>	-0.714	0.829	0.371	-0.314	-0.714
<i>g_Ruminococcaceae_UCG-013</i>	-0.771	0.943	0.429	-0.029	-0.600

Pearson's correlation analysis of microbial populations and cytokines in the colon ($n = 12$).