Multiomics reveal the regulation of tryptophan metabolism by *Akkermansia muciniphila* in colitis

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Supplementary material

Figure S1. Method developed to measure the indicated Trp metabolites by ultra-performance liquid chromatography-Q Exactive hybrid quadrupole-orbitrap mass spectrometer (UPLC-Q Exactive MS), the indicated Trp metabolites (μg/ml) were spiked into serum, and the elution time for each was obtained.

Figure S2. Partial least squares discrimination analysis (PLS-DA) of metabolic profiling from colitis and control. (A) PLS-DA score plot between UC patients and healthy control. (B) PLS-DA score plot among control, DSS, DSS+ pasteurised *Akk* and DSS+Amuc_1100 group.

Figure S3. Integration of faecal microbiota and serum metabolomes identified a UC-associated network. The genus (top 50) identified as significantly differential between patients with UC and healthy controls and differential serum metabolites involved in Trp metabolism pathways were included. A positive correlation between the nodes is indicated by red connecting lines, and a negative correlation is indicated by green. Thicker lines indicate a larger correlation coefficient ($p < 0.05$). Higher taxonomy of genera (phylum) were Trp metabolites that are indicated by coloured dots.

Table S1. Differential metabolites between patients with UC and healthy controls.

Table S2. Differential metabolites between colitis mice induced by DSS and controls.

Table S3. Enriched pathways in colitis mice induced by DSS in comparison with controls.

Table S4. Enriched pathways in colitis mice upon pasteurised *Akk* treatment.

Table S5. Enriched pathways in colitis mice upon Amuc_1100 treatment.

Table S6. Enriched GO terms in colitis mice induced by DSS in comparison with controls.

Table S7. Enriched GO terms in colitis mice upon pasteurised *Akk* treatment.

Table S8. Enriched GO terms in colitis mice upon Amuc_1100 treatment.