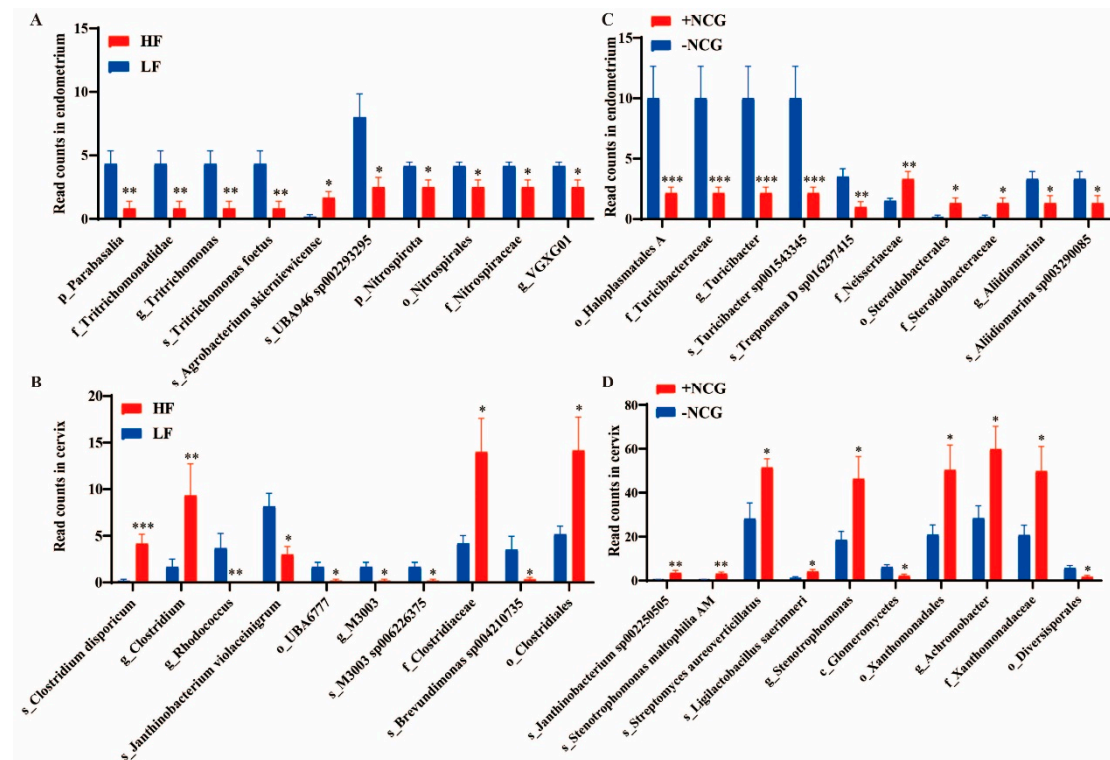


Figure S1. Dietary fiber and N-carbamylglutamate-induced modulations in uterine microbiota

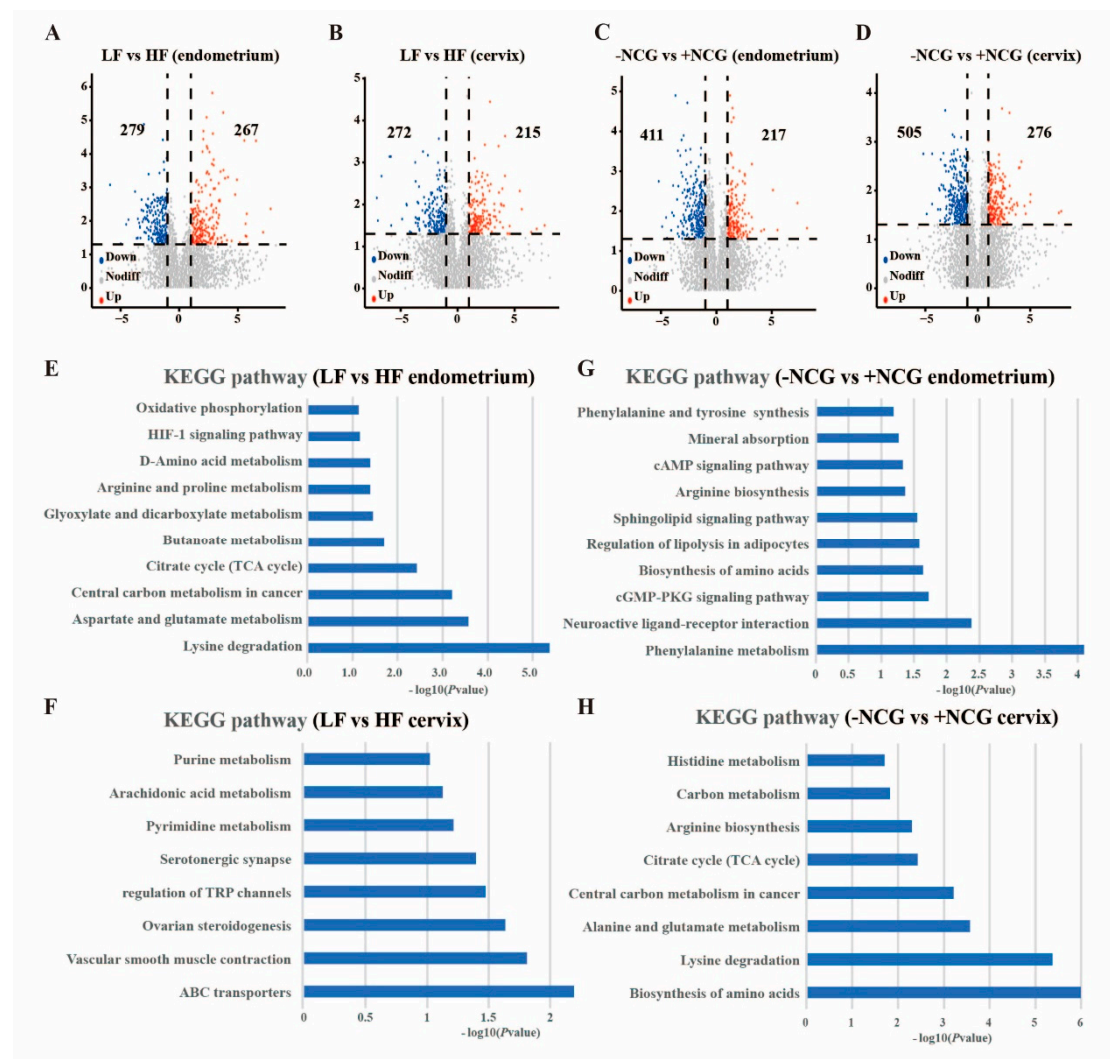


A-B: Read counts of differentially abundant microorganisms induced by dietary fiber in endometrium and cervix.

C-D: Read counts of differentially abundant microorganisms induced by N-carbamylglutamate in endometrium and cervix.

LF: low fiber; HF: high fiber; -NCG: without N-carbamylglutamate supplementation; +NCG: with N-carbamylglutamate supplementation.

Figure S2. Quantitative and functional analysis of differentially abundant metabolites induced by dietary fiber and N-carbamylglutamate



A-D: Volcano plots depicted differentially abundant metabolites between LF and HF groups, as well as between -NCG and +NCG group in endometrium and cervix.

E-F: KEGG pathway enrichment analysis of differentially abundant metabolites between LF and HF groups in endometrium (E) and cervix (F).

G-H: KEGG pathway enrichment analysis of differentially abundant metabolites between -NCG and +NCG groups in in endometrium (G) and cervix (H).

LF: low fiber; HF: high fiber; -NCG: without N-carbamylglutamate supplementation; +NCG: with N-carbamylglutamate supplementation.