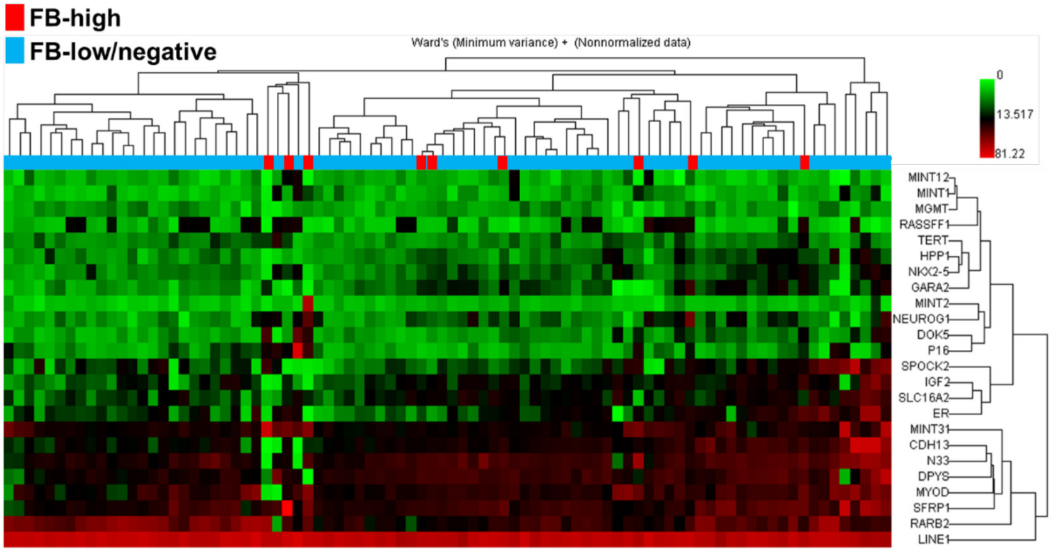
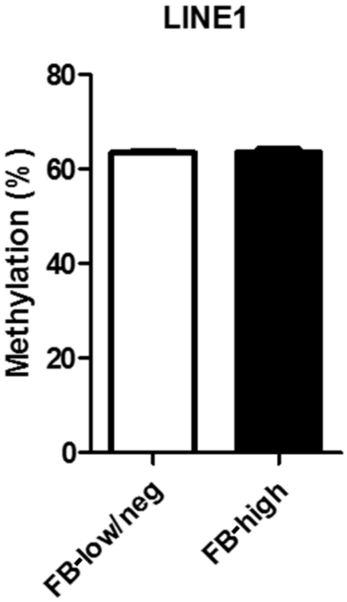
Potential link between Fusobacterium enrichment and DNA methylation accumulation in the inflammatory colonic mucosa in ulcerative colitis

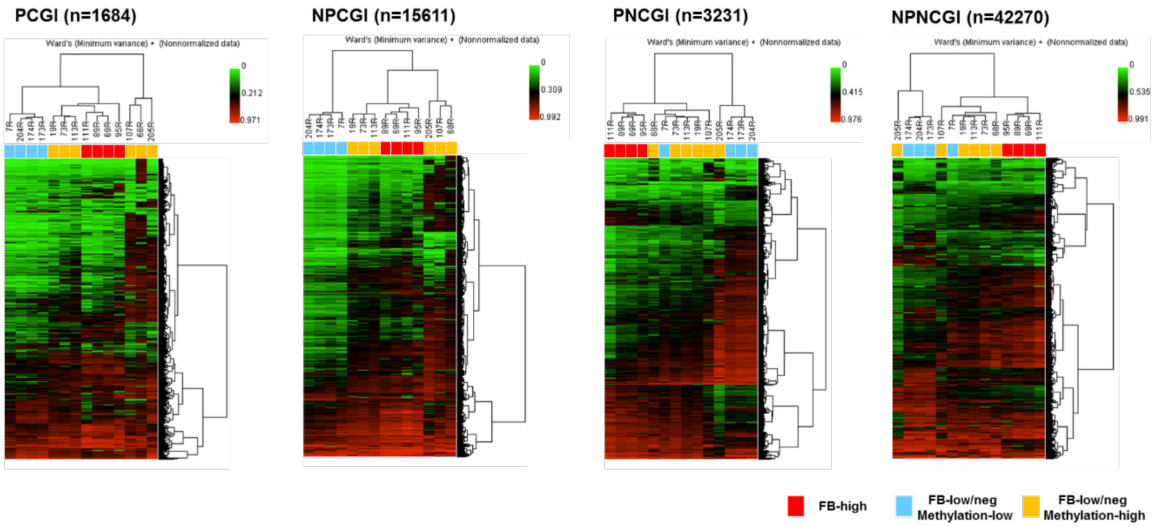
SUPPLEMENTARY MATERIALS



Supplementary Figure 1: Unsupervised hierarchical clustering analysis of 24 candidate panels using inflamed colonic mucosa from ten UC patients. Blue boxes, *Fusobacterium* low and negative (FB-low/neg) samples; Red boxes, *Fusobacterium* high (FB-high) samples;



Supplementary Figure 2: Methylation status of *LINE1* repetitive element among *Fusobacterium* low and negative (FB-low/neg) and *Fusobacterium* high (FB-high) samples. The statistical analysis was performed using Student’s t-test.



Supplementary Figure 3: Unsupervised hierarchical clustering analysis using 10% most variant probes among fourteen UC patients. PCGI, promoter CpG sites; NPCGI, outside promoter CpG sites; PNCGI, promoter non-CpG sites; NPNCGI, outside promoter non-CpG sites; Red boxes, *Fusobacterium* high (FB-high) samples; Blue boxes, *Fusobacterium* low and negative (FB-low/neg) with methylation-low samples; Yellow boxes, *Fusobacterium* low and negative (FB-low/neg) with methylation-high samples; Samples ID number were listed above the boxes.

Supplementary Table 1: List of candidate genes analyzed in this study and primer sequences used in pyrosequencing.

See Supplementary File1

Supplementary Table 2: Comparison of methylated genes in FB-high, FB-low/neg methylation-low and FB-ow/neg methylation-high groups.

See Supplementary File2

Supplementary Table 3: Summary of gene ontology analysis using methylated genes in specific groups

See Supplementary File3