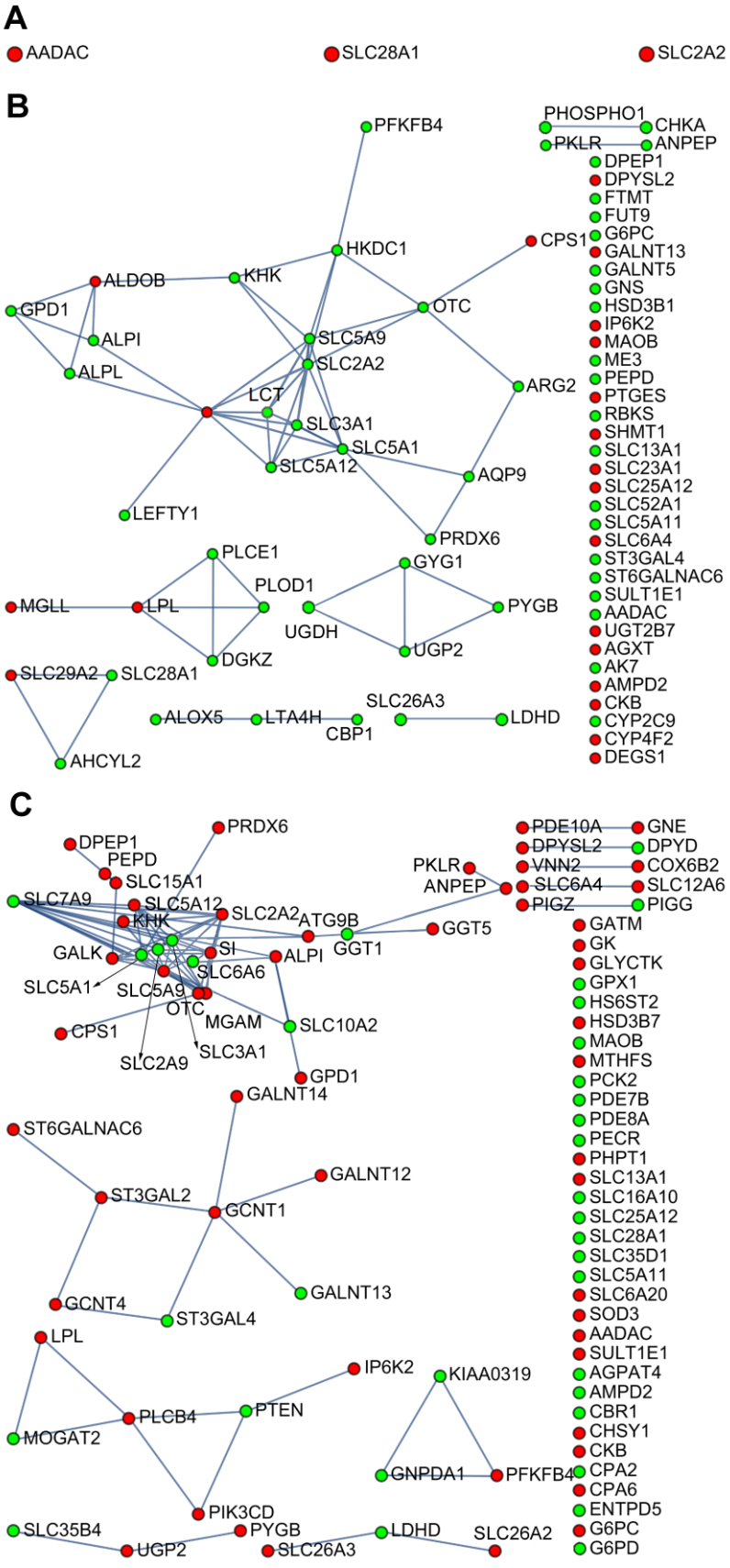
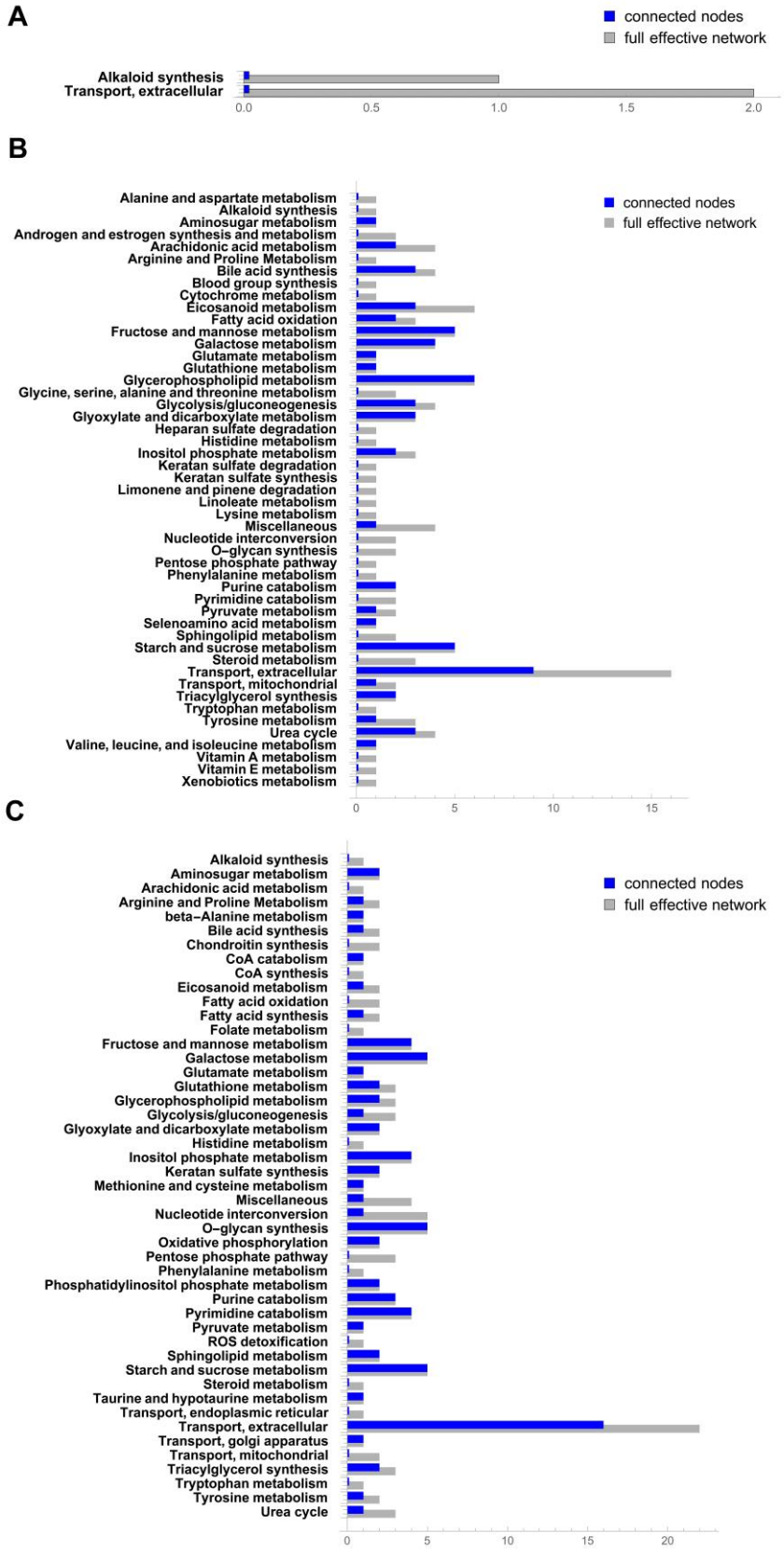
Supplementary Figure 1: Effective networks based on differentially expressed genes



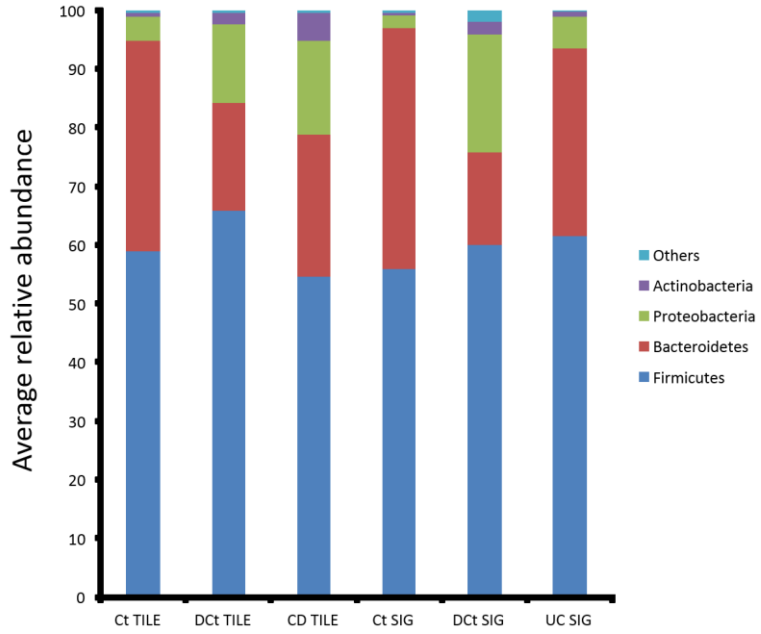
A) Effective network for the comparison of transcriptome profiles between the two tissue types, terminal ileum and sigmoid colon, for non-inflamed tissue and the control group. B) Effective network for the comparison of transcriptome profiles between inflamed and non-inflamed tissues for Crohn's disease in the terminal ileum. C) Effective network for the comparison of transcriptome profiles between inflamed and non-inflamed tissues for ulcerative colitis in the sigmoid colon. Nodes are those metabolic genes displaying a significant expression difference between the two conditions. Nodes depicted in green (red) represent upregulated (downregulated) genes. A link is drawn, when the corresponding reactions are connected in the reaction-centric projection of the (bipartite) metabolic network derived from Recon2.

Supplementary Figure 2: Contextualization of metabolic networks



For each of the genes in the effective network shown in supplementary Figure 1, the metabolic subsystem(s) associated to this gene in the Recon 2 model have been identified. Then the numbers of occurrence of each of these metabolic functional categories has been determined. This has been done for all nodes in the effective metabolic networks (gray bars), as well as for all nodes with a nonzero node degree (i.e. all connected nodes) (blue bars). (A) comparison of transcriptome profiles between the two tissue types, terminal ileum and sigmoid colon, for non-inflamed tissue and the control group. (B) comparison of transcriptome profiles between inflamed and non-inflamed tissues for Crohn's disease in the terminal ileum. (C) comparison of transcriptome profiles between inflamed and non-inflamed tissues for ulcerative colitis in the sigmoid colon.

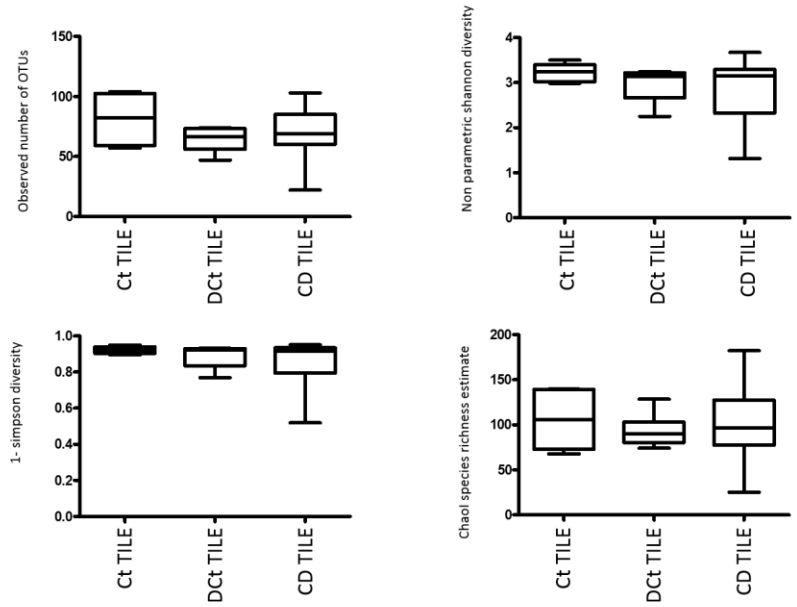
Supplementary Figure 3: Bacterial phyla abundance



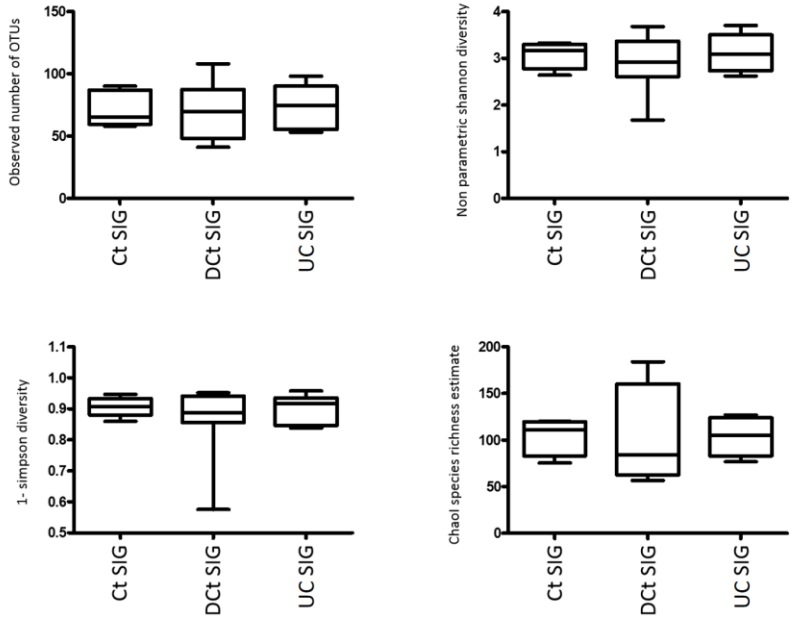
Relative abundance of major bacterial phyla stratified by disease and biopsy location. The individual groups are labelled UC (ulcerative colitis), CD (Crohn’s disease), Ct (healthy individuals), DCt (diseased controls), TILE (terminal ileum) and SIG (sigmoidal colon).

Supplementary Figure 4: Bacterial community richness and diversity

(A)

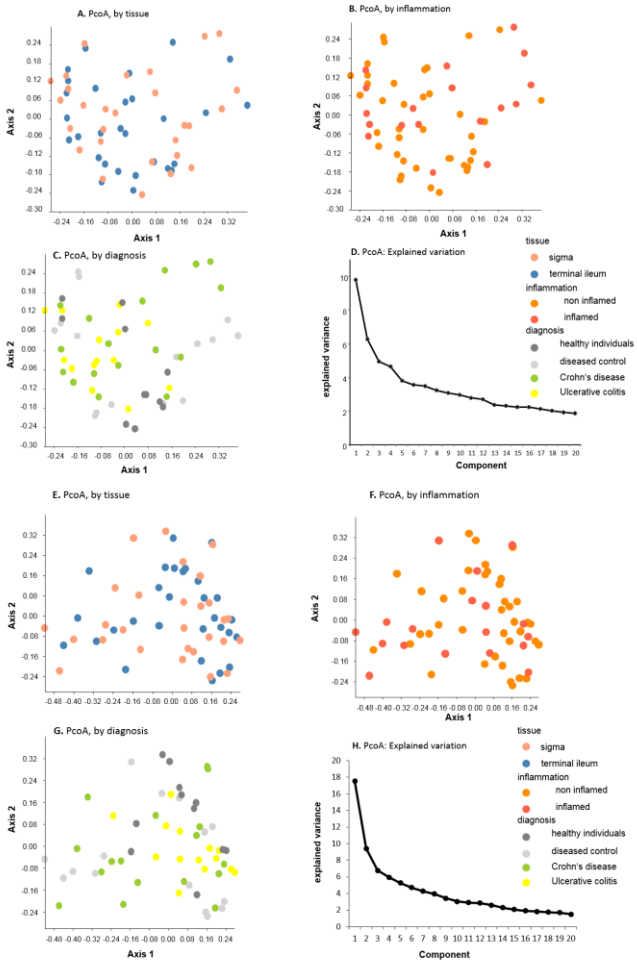


(B)



Bacterial community richness and diversity in biopsy samples collected from healthy individuals, disease control individuals, Crohn's disease patients (A) and ulcerative colitis patients (B). Box plot represents median line with 5 and 95% percentile whiskers. The individual groups are labelled UC (ulcerative colitis), CD (Crohn's disease), Ct (healthy individuals), DCt (diseased controls), TILE (terminal ileum) and SIG (sigmoidal colon).

Supplementary Figure 5: PcoA of samples, based on the microbiota variation.



Principal coordinate analysis depicting similarity in microbial composition and structure based on species level (97%) OTUs incidences (A-D: Jaccard) and their relative abundance (E-H: Bray Curtis). In both panels (A, E) shows PcoA pattern based on tissue, (B, F) shows inflammation based pattern, (C, G) shows PCoA pattern by diagnosis. (D, H) denotes top 20 principal coordinates explaining variance among microbial communities.