Supplementary information
Figure S1
Boxplot for cell-type frequency in four patient groups:
Control, mild, moderate and severe
**Figure S2:**
Correlation between NMF weight matrix and cell-type fraction
Figure S3: Microbe abundance correlation with clinical information.

A

B

Color Key
and Histogram

Value

0.5 0 0.5 1

Lactococcus
Bifidobacterium
Psychrobacter
Geobacter
Cellulosimicrobiurn
Collimonas
Acidovorax
Ensifer
Sulfurospirillum
Methylbium
Ralstonia
Malassezia
Megasphaera
Dialister
Cronobacter
Schwartzia
Synchococcus
Moraxella
Xanthomonas
Cupriavidus
Candida
Pasteurella
Brenneria
Haemophilus
Aeromonas
Proteus
Exiguobacterium
Figure S4: correlation between gene and microbe topic fraction in patients and clinical information.
Figure S5: microbe co-abundance network using the correlation with raw microbe abundance (A: in network view; B: heatmap view).
Figure S6
Top weighted microbe in the microbe topics.
Figure S7
Top weighted gene in gene topics
Figure S8: Heatmap of Gene topic fraction in patient (A) and Gene enrichment analysis of top weighted gene in topic 4 (B).
Figure S9
Function annotation finds the enriched gene pathway
Figure S9 continued: Metabolism network.