SUPPLEMENTARY FIGURES
Supplementary Figure 1: Analysis of the OTU number
The rarefaction curve plots the number of OTU (upper part) or Chao 1 index (lower part) as a function of the number of reads. Filled and open circles represent the samples from FD patients and HC volunteers, respectively.
Supplementary Figure 2: Intestinal type genera involved in the “32 Genera”
The “32 Genera” shown on Figure 2 are enlarged here. Those indicated by
triangles represent typical genera observed in the intestinal microbiota as
mentioned in the text. The genera in the parentheses represent those
recognized as top 10 major genera in the feces, which was report by Tsuda et
al.20

(Tsuda et al. Clinical and Translational Gastroenterology (2015) 6, e89)
Supplementary Figure 3: Gastric type genera involved in the “51 Genera”
The “51 Genera” shown on Figure 2 are enlarged here. Those indicated by
triangles represent typical genera observed in the gastric microbiota as
mentioned in the text. The genera in the parentheses represent those
recognized as top 10 major genera in the gastric fluid, which was reported by
Tsuda et al.\textsuperscript{20}
Supplementary Figure 4: Effect of LG21 treatment on the bacterial composition at the genus level
Samples from the FD patients before (red letters) and after the treatment (black letters) are represented on a double-hierarchical clustering heat map as mentioned in the legend to Figure 2. Note that, after LG21 treatment, 7 subjects out of the 8 subjects (FDs 33-2, 36-2, 39-2, 45-2, 46-2, 54-2, 56-2, and 62-2) were not densely inhabited any more with intestinal-type genera such as Bacteroides, Bifidobacterium, and Escherichia/Shigella.