

## Supplementary data

**Table S1.** Distributions of bacterial community at different taxonomic levels.

Rank	Taxa	Normal (%)	PRE (%)	Post (%)
Phylum	<i>Proteobacteria</i>	0.0	6.2	2.6
	<i>Actinobacteria</i>	8.7	8.6	9.8
	<i>Bacteroidetes</i>	33.8	35.7	34.1
	<i>Firmicutes</i>	52.6	45.1	53.0
	<i>Verrucomicrobia</i>	0.0	3.2	0.0
	ETC (<1%)	1.0	1.2	0.5
Class	<i>Alphaproteobacteria</i>	1.2	2.6	0.0
	<i>Bacteroidia</i>	33.7	35.7	34.1
	<i>Bacilli</i>	1.2	1.1	1.6
	<i>Actinobacteria_c</i>	5.2	6.5	8.3
	<i>Coriobacteriia</i> <sup>*,c</sup>	3.5	2.0	1.5
	<i>Negativicutes</i> <sup>*,a</sup>	4.5	8.8	8.4
	<i>Betaproteobacteria</i> <sup>*,b</sup>	1.5	2.2	1.5
	<i>Erysipelotrichi</i> <sup>*,b</sup>	1.2	1.4	0.0
	<i>Clostridia</i> <sup>*,a</sup>	45.6	33.8	42.2
	<i>Verrucomicrobiae</i>	0.0	3.0	0.0
	ETC (<1%)	2.3	2.8	2.4
Order	<i>Bacteroidales</i>	33.7	35.7	34.1
	<i>Burkholderiales</i>	1.5	2.2	1.5
	<i>Clostridiales</i> <sup>*,a</sup>	45.6	33.8	42.2
	<i>Veillonellales</i>	1.3	5.0	5.4
	<i>Rhodospirillales</i>	1.2	2.6	0.0
	<i>Coriobacteriales</i> <sup>*,c</sup>	3.5	2.0	1.5
	<i>Acidaminococcales</i>	1.0	1.7	2.6
	<i>Erysipelotrichales</i> <sup>*,b</sup>	1.2	1.4	0.0
	<i>Selenomonadales</i>	2.2	2.1	0.0
	<i>Bifidobacteriales</i>	5.1	6.2	8.2
	<i>Lactobacillales</i>	1.2	1.1	1.6
	<i>Verrucomicrobiales</i>	0.0	3.0	0.0
	ETC (<1%)	2.6	3.2	3.0
Family	<i>Christensenellaceae</i>	1.9	1.1	0.0
	<i>Bifidobacteriaceae</i>	5.1	6.2	8.2
	<i>Rikenellaceae</i>	4.2	3.3	4.0
	<i>Rhodospirillaceae</i>	1.1	2.5	0.0
	<i>Bacteroidaceae</i>	17.8	20.9	18.4
	<i>Prevotellaceae</i>	8.6	8.4	8.3
	<i>Veillonellaceae</i>	1.3	5.0	5.4

	<i>Selenomonadaceae</i>	2.2	2.1	0.0
	<i>Acidaminococcaceae</i>	1.0	1.7	2.6
	<i>Sutterellaceae</i>	1.4	2.2	1.4
	<i>Porphyromonadaceae</i>	1.8	1.8	2.4
	<i>Coriobacteriaceae</i> <sup>*, c</sup>	3.5	2.0	1.5
	<i>Lachnospiraceae</i>	12.0	12.6	11.8
	<i>Erysipelotrichaceae</i> <sup>*, b</sup>	1.2	1.4	0.0
	<i>Ruminococcaceae</i> <sup>**, a</sup>	31.2	19.6	29.1
	<i>Akkermansiaceae</i>	0.0	3.0	0.0
	ETC (<1%)	5.5	6.1	7.0
Genus	<i>Ruminococcus_g2</i>	1.8	0.0	1.3
	<i>Subdoligranulum</i>	1.6	0.0	1.5
	<i>Oscillibacter</i>	4.3	3.8	4.1
	<i>Collinsella</i> <sup>*, c</sup>	2.6	1.2	0.0
	<i>Sutterella</i>	1.2	1.9	1.2
	<i>Prevotella</i>	7.7	7.5	7.8
	<i>Lachnospira</i>	1.6	1.5	1.5
	<i>Blautia</i>	1.3	1.6	1.3
	<i>PAC001207_g</i>	1.1	0.0	0.0
	<i>Clostridium_g24</i>	1.0	1.5	0.0
	<i>Sporobacter</i>	1.2	0.0	1.1
	<i>Bifidobacterium</i>	5.0	6.2	8.1
	<i>Eubacterium_g23</i>	2.4	1.3	1.7
	<i>Megamonas</i>	2.2	2.0	0.0
	<i>Roseburia</i>	3.0	1.8	2.4
	<i>Alistipes</i>	4.2	3.3	4.0
	<i>Bacteroides</i>	17.8	20.9	18.3
	<i>Parabacteroides</i>	1.8	1.8	2.4
	<i>Pseudoflavonifractor</i>	1.4	1.7	2.0
	<i>Ruminococcus</i>	1.0	0.0	0.0
	<i>LARJ_g</i>	1.1	2.5	0.0
	<i>Faecalibacterium</i> <sup>**, a</sup>	15.3	7.5	14.9
	<i>Veillonella</i> <sup>*, c</sup>	0.4	2.0	3.9
	ETC (<1%)	19.0	30.0	22.5

Relative abundances less than 1 % were expressed as ETC. Wilcoxon rank-sum test was used to analyze the significance between the groups (\*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ). Pre refers to the iron deficiency anemia (IDA) patient group, and Post refers to the group receiving iron supplementation and recovering from IDA. The superscripted a, b, and c denote the groups subjected to significance determination (a, Normal-Pre; b, Pre-Post; c, Normal-Post).