

**Supplementary Table 1 Baseline demographic characteristics of the IBS-D patients and Controls.**

|                                          | IBS-D      | Controls     | <i>P</i> value |
|------------------------------------------|------------|--------------|----------------|
| Age, median and range, year              | 38 (17-75) | 37 (17-67)   | 0.170          |
| Sex, male/female                         | 39/21      | 38/22        | 0.849          |
| BMI, median and range, kg/m <sup>2</sup> | 22 (17-34) | 21.9 (18-29) | 0.846          |
| Anxiety, median and range                | 8 (0-16)   | 6 (2-12)     | <b>0.046</b>   |
| Depression, median and range             | 8 (2-19)   | 5 (0-11)     | <b>0.000</b>   |

*P* values < 0.05 are indicated in bold.

**Supplementary Table 2. Relative abundance of microbiota in IBS-D patients and healthy subjects. (only *P* values < 0.05 are shown).**

| Taxon name     | Healthy<br>(Mean±SD) (%) | IBS-D<br>(Mean±SD) (%) | <i>P</i> value | <i>FDR q</i><br>value |
|----------------|--------------------------|------------------------|----------------|-----------------------|
| <b>Phylum</b>  |                          |                        |                |                       |
| Bacteroidetes  | 31.46±18.40              | 41.14±18.84            | 0.036          | 0.304                 |
| Firmicutes     | 51.80±16.33              | 45.01±16.25            | 0.041          | 0.353                 |
| <b>Genus</b>   |                          |                        |                |                       |
| Prevotella     | 0.04438±0.1641           | 16.72±23.71            | 0.000          | <b>0.001</b>          |
| Staphylococcus | 0.006756±0.02016         | 0.00006122±0.0004586   | 0.000          | <b>0.011</b>          |
| Haemophilus    | 0.4533±0.5016            | 0.2341±0.6099          | 0.000          | <b>0.011</b>          |
| Sneathia       | 0.002265±0.004277        | 0.00006002±0.0004571   | 0.000          | <b>0.033</b>          |
| Halomonas      | 0.1029±0.3415            | 0.01176±0.07381        | 0.001          | 0.062                 |
| Pelomonas      | 0.0008717±0.00223        | 0                      | 0.001          | 0.065                 |
| Sphingomonas   | 0.09933±0.001717         | 0.1782±0.8680          | 0.003          | 0.092                 |
| Pedobacter     | 0.003678±0.008709        | 0.0002423±0.001156     | 0.005          | 0.142                 |
| Acinetobacter  | 0.004557±0.008629        | 0.08092±0.5365         | 0.007          | 0.166                 |

|                           |                   |                       |       |       |
|---------------------------|-------------------|-----------------------|-------|-------|
| Bradyrhizobium            | 0.003894±0.003894 | 0.02229±0.1249        | 0.008 | 0.169 |
| Microbacterium            | 0.001061±0.002820 | 0.00006056±0.00004612 | 0.010 | 0.171 |
| Ruminococcus2             | 0.1985±0.3273     | 0.5183±0.6833         | 0.011 | 0.730 |
| Megamonas                 | 1.775±6.821       | 4.897±8.942           | 0.012 | 0.730 |
| Clostridium XI            | 1.474±3.594       | 0.7125±2.547          | 0.012 | 0.172 |
| Veillonella               | 0.7115±0.9257     | 0.9711±3.354          | 0.013 | 0.172 |
| Ralstonia                 | 0.01497±0.02471   | 0.03544±0.1976        | 0.014 | 0.172 |
| Flavonifractor            | 0.1249±0.1456     | 0.05411±0.08119       | 0.014 | 0.172 |
| Solobacterium             | 0.01116±0.01252   | 0.003250±0.005630     | 0.015 | 0.177 |
| Clostridium sensu stricto | 2.791±7.818       | 1.072±3.634           | 0.016 | 0.177 |
| Coprococcus               | 0.5420±1.758      | 0.3318±0.4910         | 0.017 | 0.730 |
| Peptoniphilus             | 0.003841±0.0106   | 0.01956±0.1407        | 0.037 | 0.264 |
| Gemella                   | 0.01360±0.01218   | 0.01152±0.02822       | 0.039 | 0.264 |
| Dorea                     | 0.2095±0.3354     | 0.3845±0.5141         | 0.040 | 0.730 |
| Sarcina                   | 0                 | 0.07691±0.3774        | 0.042 | 0.730 |
| Olsenella                 | 0.004204±0.006913 | 0.001237±0.003436     | 0.046 | 0.264 |

*q* values <0.05 are indicated in bold.

**Supplementary Table 3. Relative abundance of microbiota in the SIBO<sup>+</sup> and SIBO<sup>-</sup> subgroups. (only *P* values < 0.05 are shown).**

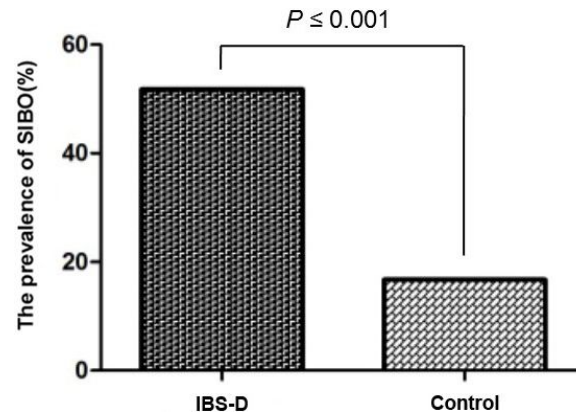
| Taxon name           | SIBO <sup>-</sup><br>(Mean±SD) (%) | SIBO <sup>+</sup><br>(Mean±SD) (%) | <i>P</i> value | <i>FDR q</i><br><i>value</i> |
|----------------------|------------------------------------|------------------------------------|----------------|------------------------------|
| <b>Phylum</b>        |                                    |                                    |                |                              |
| Bacteroidetes        | 34.74±15.73                        | 46.85±19.84                        | 0.005          | 0.074                        |
| Fusobacteria         | 4.241±7.578                        | 0.8687±3.407                       | 0.006          | 0.089                        |
| Proteobacteria       | 10.31±16.20                        | 4.708±6.739                        | 0.033          | 0.268                        |
| <b>Genus</b>         |                                    |                                    |                |                              |
| Prevotella           | 0.2592±0.6851                      | 32.29±24.25                        | 0.000          | <b>0.000</b>                 |
| Bacteroides          | 31.56±15.18                        | 12.12±12.47                        | 0.000          | <b>0.000</b>                 |
| Escherichia/Shigella | 8.500±16.49                        | 0.8999±1.359                       | 0.001          | 0.084                        |
| Fusobacterium        | 4.227±7.577                        | 0.8654±7.577                       | 0.003          | 0.262                        |
| Olsenella            | 0.001503±0.002419                  | 0.0004698±0.002016                 | 0.009          | 0.526                        |
| f-Prevotellaceae*    | 0.4823±0.0181                      | 0.3608±0.0184                      | 0.009          | 0.589                        |
| Megasphaera          | 0.1112±0.5409                      | 0.0611±0.1773                      | 0.010          | 0.589                        |
| Coprobacillus        | 0.002890±0.009229                  | 0                                  | 0.018          | 0.711                        |
| f-Fusobacteriaceae*  | 0.005773±0.01445                   | 0.0005827±0.003192                 | 0.018          | 0.711                        |
| Flavonifractor       | 0.07855±0.0883                     | 0.0311±0.0696                      | 0.021          | 0.721                        |
| Plesiomonas          | 0                                  | 0.0009377±0.002758                 | 0.025          | 0.589                        |
| Propionibacterium    | 0.0001247±0.000660                 | 0.002128±0.007845                  | 0.026          | 0.589                        |
| o-Bacteroidales**    | 0.0007512±0.002209                 | 0.2226±0.8374                      | 0.028          | 0.589                        |
| Sarcina              | 0.002619±0.01386                   | 0.1431±0.5277                      | 0.030          | 0.589                        |
| Parabacteroides      | 1.365±1.911                        | 0.5613±0.6994                      | 0.030          | 0.721                        |
| Leptotrichia         | 0.0006334±0.003351                 | 0.002749±0.010018                  | 0.034          | 0.589                        |
| Pseudomonas          | 0.01337±0.0448                     | 0.2784±1.366                       | 0.034          | 0.589                        |
| Streptococcus        | 0.8202±1.209                       | 4.767±9.697                        | 0.035          | 0.589                        |

|                 |                     |                    |       |       |
|-----------------|---------------------|--------------------|-------|-------|
| Ruminococcus2   | 0.3973±0.6224       | 0.6038±0.7117      | 0.035 | 0.589 |
| Proteus         | 0.002380±0.0101     | 0                  | 0.036 | 0.721 |
| Clostridium XIX | 0.00063242±0.002170 | 0                  | 0.036 | 0.721 |
| Enterococcus    | 0.0179343±0.04965   | 0.0009355±0.003298 | 0.039 | 0.721 |
| Sphingomonas    | 0.007639±0.01543    | 0.03384±1.203      | 0.041 | 0.589 |
| Pyramidobacter  | 0.001872±0.005661   | 0.0007064±0.003869 | 0.041 | 0.721 |
| Bradyrhizobium  | 0                   | 0.04159±0.1669     | 0.046 | 0.589 |
| Acidaminococcus | 0                   | 0.006752±0.03375   | 0.046 | 0.589 |
| Shuttleworthia  | 0                   | 0.0005883±0.001873 | 0.046 | 0.589 |
| Staphylococcus  | 0                   | 0.0005865±0.002087 | 0.046 | 0.589 |

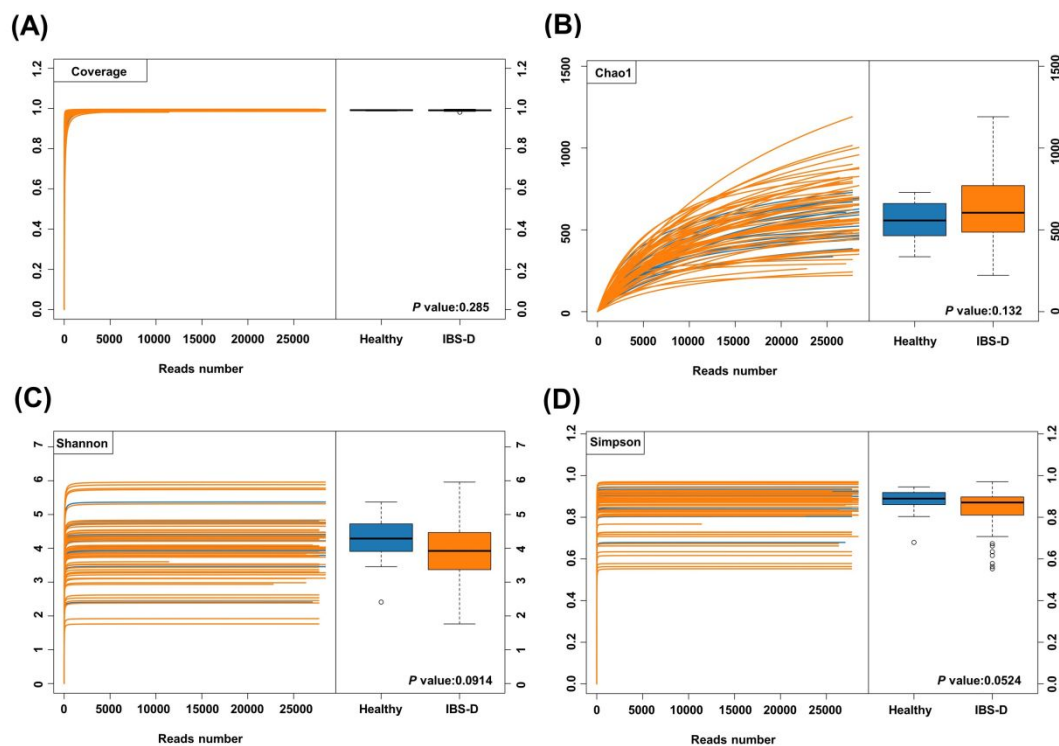
\*: A nameless genus in Prevotellaceae or Fusobacteriaceae respectively.

\*\*: A nameless genus in Bacteroidales.

*q* values < 0.05 are indicated in bold.



**Supplementary Figure 1. The prevalence of SIBO between the IBS-D and control groups.** The prevalence of SIBO in the IBS-D patients was significantly higher than that in the healthy controls ( $P \leq 0.001$ ).

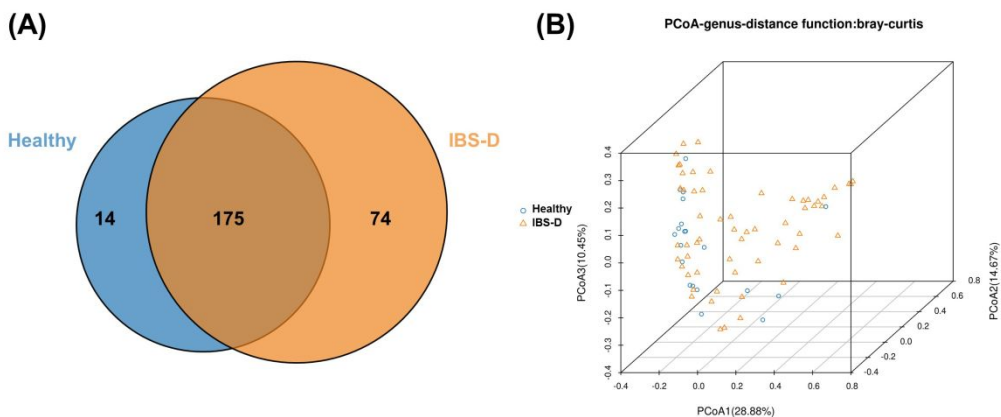


**Supplementary Figure 2. Richness and diversity of intestinal microbiota in IBS-D patients and healthy subjects.**

**(A)** Good's coverage index indicates the fine coverage of intestinal microbiota detected in IBS-D patients and healthy subjects.

(B) Chao1 diversity index revealing no altered richness between IBS-D patients and healthy subjects.

(C, D) Community diversity of IBS-D patients and healthy subjects. (C) Shannon diversity index and (D) Simpson diversity index suggests no significant difference in community diversity between IBS-D patients and healthy subjects.



**Supplementary Figure 3. IBS-D patients and healthy subjects exhibit different composition of the fecal microbiota.**

(A) Venn diagram of genera composing fecal microbiota in IBS-D patients and healthy subjects.

(B) IBS-D patients and healthy subjects exhibit different profile of fecal microbiota by Principal coordinates analysis (PCoA).