**Supplementary Table**

Supplementary Table 1 Relative abundance of gut microbiota at phylum level (%)

|  |  |  |  |
| --- | --- | --- | --- |
| Group  Community | Normal | Model | VOZB-HD |
| Firmicutes | 48.17 | 65.33 | 61.07 |
| Bacteroidetes | 46.30 | 28.32 | 33.44 |
| Proteobacteria | 4.14 | 3.65 | 3.16 |
| Deferribacteres | 0.26 | 1.93 | 1.54 |
| Actinobacteria | 0.58 | 0.40 | 0.33 |
| Tenericutes | 0.25 | 0.10 | 0.11 |
| others | 0.30 | 0.27 | 0.35 |

Supplementary Table 2 Relative abundance of gut microbiota at family level (%)

|  |  |  |  |
| --- | --- | --- | --- |
| Group  Community | Normal | Model | VOZB-HD |
| Lachnospiraceae | 20.27 | 42.11 | 37.43 |
| Bacteroidales\_S24-7\_group | 30.68 | 10.18 | 14.69 |
| Lactobacillaceae | 18.26 | 2.17 | 11.66 |
| Bacteroidaceae | 3.22 | 9.60 | 11.45 |
| Ruminococcaceae | 4.91 | 7.85 | 8.45 |
| Porphyromonadaceae | 3.39 | 5.71 | 1.59 |
| Erysipelotrichaceae | 1.92 | 6.96 | 1.58 |
| Prevotellaceae | 4.63 | 1.13 | 2.52 |
| Helicobacteraceae | 2.75 | 1.86 | 2.23 |
| Rikenellaceae | 3.30 | 1.07 | 2.31 |
| Streptococcaceae | 0.42 | 4.01 | 0.01 |
| Deferribacteraceae | 0.26 | 1.93 | 1.54 |
| Clostridiales\_vadinBB60\_group | 0.81 | 1.61 | 0.72 |
| Desulfovibrionaceae | 0.68 | 1.13 | 0.78 |
| Clostridiaceae\_1 | 0.73 | 0.12 | 0.68 |
| Bifidobacteriaceae | 0.33 | 0.35 | 0.23 |
| Enterobacteriaceae | 0.49 | 0.14 | 0.04 |
| Peptostreptococcaceae | 0.46 | 0.12 | 0.04 |
| Alcaligenaceae | 0.18 | 0.20 | 0.05 |
| Rhodospirillaceae | 0.03 | 0.28 | 0.06 |
| Unclassified Bacteria | 1.00 | 0.46 | 0.72 |
| others | 1.28 | 1.01 | 1.22 |