

Supplementary Table 1. Gut microbiota at the phylum level in the indicated groups

|  | Young group          | Middle-age group     | Old group            | p value |
|--|----------------------|----------------------|----------------------|---------|
| "Other (median [IQR])"                       | 0.01 [0.00, 0.06]    | 0.01 [0.00, 0.10]    | 0.01 [0.00, 0.10]    | <0.001  |
| "p__Actinobacteria (median [IQR])"           | 5.80 [3.10, 9.40]    | 5.50 [2.91, 9.35]    | 3.77 [2.13, 6.60]    | <0.001  |
| "p__Bacteroidetes (median [IQR])"            | 39.23 [34.67, 43.61] | 38.81 [34.46, 43.21] | 37.78 [32.75, 42.94] | 0.003   |
| "p__Firmicutes (median [IQR])"               | 48.63 [43.41, 53.75] | 49.28 [44.04, 54.42] | 51.66 [46.02, 56.51] | <0.001  |
| "p__Fusobacteria (median [IQR])"             | 0.00 [0.00, 0.19]    | 0.00 [0.00, 0.11]    | 0.00 [0.00, 0.10]    | <0.001  |
| "p__Proteobacteria (median [IQR])"           | 4.03 [2.58, 6.01]    | 3.66 [2.33, 5.47]    | 3.43 [1.91, 5.91]    | <0.001  |
| Firmicute/Bacteroidetes ratio (median [IQR]) | 1.23 [1.01, 1.50]    | 1.26 [1.04, 1.55]    | 1.36 [1.12, 1.67]    | <0.001  |

Supplementary Table 2. Gut microbiota at the phylum level in the indicated groups

|                                    | Young group          |                      |                      |         | Middle-age group     |                      |                      |         | Old group            |                      |                      |         |
|------------------------------------|----------------------|----------------------|----------------------|---------|----------------------|----------------------|----------------------|---------|----------------------|----------------------|----------------------|---------|
|                                    | lean                 | normal               | obese                | p value | lean                 | normal               | obese                | p value | lean                 | normal               | obese                | p value |
| "Other (median [IQR])"             | 0.01 [0.00, 0.09]    | 0.01 [0.00, 0.06]    | 0.00 [0.00, 0.02]    | 0.001   | 0.01 [0.00, 0.14]    | 0.01 [0.00, 0.10]    | 0.01 [0.00, 0.04]    | <0.001  | 0.01 [0.00, 0.03]    | 0.02 [0.00, 0.12]    | 0.01 [0.00, 0.08]    | 0.127   |
| "p__Actinobacteria (median [IQR])" | 5.92 [3.00, 9.18]    | 5.85 [3.10, 9.52]    | 5.24 [3.13, 8.81]    | 0.52    | 5.50 [2.93, 9.43]    | 5.59 [2.97, 9.39]    | 5.06 [2.38, 8.74]    | 0.035   | 3.59 [1.80, 5.67]    | 3.77 [2.15, 6.93]    | 4.31 [2.17, 6.73]    | 0.681   |
| "p__Bacteroidetes (median [IQR])"  | 39.00 [34.24, 43.15] | 39.20 [34.67, 43.50] | 39.55 [35.13, 44.90] | 0.119   | 38.76 [34.12, 42.39] | 38.70 [34.29, 43.13] | 39.43 [35.52, 43.81] | 0.003   | 36.92 [31.73, 41.02] | 37.79 [32.74, 43.25] | 38.17 [33.09, 41.73] | 0.62    |
| "p__Firmicutes (median [IQR])"     | 48.65 [43.97, 54.16] | 48.78 [43.61, 53.79] | 47.53 [42.09, 52.71] | 0.018   | 49.33 [44.30, 55.05] | 49.38 [44.26, 54.44] | 48.98 [42.61, 53.74] | 0.026   | 52.79 [47.56, 55.78] | 51.38 [45.93, 56.87] | 51.02 [46.32, 55.08] | 0.863   |
| "p__Fusobacteria (median [IQR])"   | 0.00 [0.00, 0.12]    | 0.00 [0.00, 0.18]    | 0.00 [0.00, 0.59]    | 0.039   | 0.00 [0.00, 0.02]    | 0.00 [0.00, 0.09]    | 0.00 [0.00, 0.25]    | <0.001  | 0.01 [0.00, 0.14]    | 0.00 [0.00, 0.09]    | 0.00 [0.00, 0.10]    | 0.45    |
| "p__Proteobacteria (median [IQR])" | 4.27 [2.66, 6.34]    | 3.99 [2.58, 5.83]    | 3.99 [2.42, 6.42]    | 0.179   | 3.43 [2.33, 5.81]    | 3.66 [2.33, 5.45]    | 3.80 [2.35, 5.44]    | 0.833   | 3.54 [1.84, 5.41]    | 3.35 [1.92, 5.74]    | 3.68 [2.08, 6.73]    | 0.836   |
| "FB_ratio (median [IQR])"          | 1.26 [1.03, 1.52]    | 1.24 [1.02, 1.50]    | 1.20 [0.93, 1.47]    | 0.029   | 1.26 [1.07, 1.58]    | 1.27 [1.04, 1.56]    | 1.21 [1.01, 1.49]    | 0.003   | 1.41 [1.20, 1.64]    | 1.34 [1.12, 1.68]    | 1.40 [1.08, 1.62]    | 0.686   |

Supplementary Table 3. Gut microbiota at the genus level in the indicated groups

|   | Young group          | Middle-age group     | Old group            | p value |
|---|----------------------|----------------------|----------------------|---------|
| "f__Bacteroidaceae/g__Bacteroides (median [IQR])"         | 29.13 [21.16, 34.84] | 27.51 [18.39, 33.42] | 25.30 [15.55, 32.56] | <0.001  |
| "f__Bifidobacteriaceae/g__Bifidobacterium (median [IQR])" | 3.72 [1.26, 6.87]    | 3.27 [1.02, 6.78]    | 1.97 [0.60, 4.28]    | <0.001  |
| "f__Lachnospiraceae/g__ (median [IQR])"                   | 5.07 [3.74, 6.96]    | 5.04 [3.63, 6.92]    | 5.60 [4.07, 7.24]    | 0.01    |
| "f__Lachnospiraceae/g__Anaerostipes (median [IQR])"       | 1.51 [0.44, 3.17]    | 1.43 [0.44, 3.01]    | 1.00 [0.28, 2.50]    | <0.001  |
| "f__Lachnospiraceae/g__Blautia (median [IQR])"            | 5.65 [3.90, 7.83]    | 5.31 [3.69, 7.37]    | 4.41 [2.98, 6.32]    | <0.001  |
| "f__Lachnospiraceae/g__Dorea (median [IQR])"              | 1.23 [0.49, 2.10]    | 1.25 [0.55, 2.13]    | 0.96 [0.43, 1.55]    | <0.001  |
| "f__Lachnospiraceae/g__Fusicatenibacter (median [IQR])"   | 1.40 [0.27, 2.58]    | 1.37 [0.32, 2.56]    | 1.10 [0.36, 2.04]    | 0.047   |
| "f__Lachnospiraceae/g__Lachnoclostridium (median [IQR])"  | 1.38 [0.76, 2.38]    | 1.31 [0.70, 2.41]    | 1.00 [0.55, 2.11]    | <0.001  |
| "f__Ruminococcaceae/g__Faecalibacterium (median [IQR])"   | 7.39 [3.51, 10.39]   | 6.53 [3.07, 9.66]    | 6.82 [3.79, 9.50]    | <0.001  |
| "f__Tannerellaceae/g__Parabacteroides (median [IQR])"     | 2.53 [1.39, 4.15]    | 2.43 [1.28, 4.03]    | 2.17 [1.18, 3.59]    | 0.01    |
| "Other (median [IQR])"                                    | 35.39 [28.05, 47.25] | 38.92 [29.74, 52.04] | 45.40 [34.78, 59.45] | <0.001  |

Supplementary Table 4. Gut microbiota at the genus level in the indicated groups

|   | Young group          |                      |                      |         | Middle-age group     |                      |                      |         | Old group            |                      |                      |         |
|---|----------------------|----------------------|----------------------|---------|----------------------|----------------------|----------------------|---------|----------------------|----------------------|----------------------|---------|
|   | lean                 | normal               | obese                | p value | lean                 | normal               | obese                | p value | lean                 | normal               | obese                | p value |
| "f__Bacteroidaceae/g__Bacteroides (median [IQR])"         | 30.06 [22.99, 34.81] | 29.10 [21.26, 34.95] | 28.21 [18.18, 34.30] | 0.072   | 27.74 [19.64, 33.39] | 27.34 [18.32, 33.39] | 28.01 [18.35, 33.74] | 0.676   | 28.62 [19.25, 33.03] | 24.39 [14.86, 31.84] | 28.32 [18.22, 34.40] | 0.126   |
| "f__Bifidobacteriaceae/g__Bifidobacterium (median [IQR])" | 4.13 [1.26, 7.12]    | 3.73 [1.30, 6.91]    | 3.08 [1.05, 6.17]    | 0.189   | 3.56 [1.17, 7.10]    | 3.39 [1.06, 6.80]    | 2.79 [0.76, 6.37]    | 0.027   | 2.05 [0.54, 4.79]    | 1.89 [0.59, 4.29]    | 2.72 [1.03, 4.00]    | 0.684   |
| "f__Lachnospiraceae/g__ (median [IQR])"                   | 4.97 [3.73, 7.58]    | 5.15 [3.79, 6.97]    | 4.82 [3.48, 6.50]    | 0.033   | 5.22 [3.70, 7.40]    | 5.07 [3.65, 6.88]    | 4.87 [3.47, 6.76]    | 0.107   | 6.37 [5.02, 7.94]    | 5.51 [4.04, 7.24]    | 5.16 [3.89, 6.67]    | 0.064   |
| "f__Lachnospiraceae/g__Anaerostipes (median [IQR])"       | 1.46 [0.46, 3.27]    | 1.54 [0.46, 3.19]    | 1.27 [0.31, 2.79]    | 0.187   | 1.46 [0.43, 3.01]    | 1.45 [0.46, 2.96]    | 1.34 [0.35, 3.33]    | 0.939   | 1.25 [0.25, 2.98]    | 1.00 [0.29, 2.49]    | 0.86 [0.18, 2.64]    | 0.785   |
| "f__Lachnospiraceae/g__Blautia (median [IQR])"            | 5.78 [4.07, 7.75]    | 5.64 [3.92, 7.90]    | 5.54 [3.75, 7.56]    | 0.447   | 5.45 [3.87, 7.62]    | 5.33 [3.68, 7.35]    | 5.18 [3.67, 7.24]    | 0.257   | 4.18 [2.60, 6.03]    | 4.42 [2.96, 6.32]    | 4.56 [3.18, 6.42]    | 0.705   |
| "f__Lachnospiraceae/g__Dorea (median [IQR])"              | 1.01 [0.33, 1.75]    | 1.26 [0.51, 2.13]    | 1.47 [0.54, 2.30]    | <0.001  | 1.02 [0.42, 1.88]    | 1.24 [0.55, 2.09]    | 1.45 [0.70, 2.58]    | <0.001  | 0.79 [0.37, 1.25]    | 1.00 [0.43, 1.59]    | 0.98 [0.50, 1.65]    | 0.293   |
| "f__Lachnospiraceae/g__Fusicatenibacter (median [IQR])"   | 1.30 [0.03, 2.35]    | 1.43 [0.29, 2.60]    | 1.35 [0.40, 2.67]    | 0.2     | 1.26 [0.24, 2.73]    | 1.41 [0.32, 2.55]    | 1.29 [0.32, 2.48]    | 0.675   | 1.19 [0.47, 2.55]    | 1.12 [0.37, 2.03]    | 0.88 [0.22, 1.93]    | 0.492   |
| "f__Lachnospiraceae/g__Lachnoclostridium (median [IQR])"  | 1.30 [0.69, 2.25]    | 1.36 [0.75, 2.37]    | 1.53 [0.89, 2.68]    | 0.05    | 1.19 [0.69, 2.18]    | 1.27 [0.69, 2.30]    | 1.67 [0.80, 3.01]    | <0.001  | 1.32 [0.70, 2.38]    | 0.97 [0.51, 1.98]    | 1.08 [0.75, 2.51]    | 0.166   |
| "f__Ruminococcaceae/g__Faecalibacterium (median [IQR])"   | 6.99 [3.78, 10.50]   | 7.55 [3.60, 10.45]   | 5.85 [2.89, 9.90]    | 0.028   | 6.37 [2.98, 9.61]    | 6.61 [3.17, 9.83]    | 6.20 [2.69, 9.13]    | 0.08    | 7.28 [3.13, 9.25]    | 6.61 [3.78, 9.37]    | 8.64 [4.89, 10.62]   | 0.216   |
| "f__Tannerellaceae/g__Parabacteroides (median [IQR])"     | 2.68 [1.41, 4.34]    | 2.54 [1.41, 4.13]    | 2.44 [1.15, 4.15]    | 0.48    | 2.52 [1.23, 4.06]    | 2.46 [1.32, 4.06]    | 2.21 [1.15, 3.87]    | 0.202   | 1.50 [0.55, 2.94]    | 2.24 [1.28, 3.68]    | 2.15 [1.29, 3.57]    | 0.069   |
| "Other (median [IQR])"                                    | 35.27 [28.08, 44.97] | 35.03 [27.92, 47.00] | 37.23 [29.29, 52.21] | 0.009   | 38.38 [29.01, 49.85] | 39.15 [30.02, 52.06] | 38.11 [28.93, 52.84] | 0.629   | 36.71 [29.24, 52.33] | 45.82 [35.52, 60.64] | 41.39 [33.09, 54.60] | 0.094   |