# Supporting Informations

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**Manuscript Title**: Different types of dietary fibers trigger specific alterations in composition and predicted functions of colonic bacterial communities in BALB/c mice

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**Table S1** Macronutrient composition of experimental diets

| | **C** | **G** | **M** | **GM** |
|---|---|---|---|---|
| **Diet(g/kg)** | | | | |
| Casein | 233 | 200 | 233 | 212 |
| Corn starch | 316 | 280 | 316 | 280 |
| Sucrose | 60 | 60 | 60 | 83 |
| Palm kernel fat | 111 | 100 | 111 | 105 |
| bean oil | 10 | 10 | 10 | 10 |
| Linseed oil | 10 | 10 | 10 | 10 |
| Oat-derived β-glucan | 0 | 280 | 0 | 140 |
| MCC | 0 | 0 | 200 | 100 |
| bentonite clay | 200 | 0 | 0 | 0 |
| Mineral mixture[1] | 50 | 50 | 50 | 50 |
| Vitamin mixture[2] | 10 | 10 | 10 | 10 |
| Total amount of diet(g) | 1000 | 1000 | 1000 | 1000 |
| **Calculated macronutrient metabolizable energy(%)** | | | | |
| Protein | 25.51 | 20.00 | 21.41 | 19.98 |
| Carbohydrates | 46.22 | 55.49 | 54.88 | 56.02 |
| Fat | 28.27 | 24.50 | 23.72 | 23.99 |
| **Measured energy and protein** | | | | |
| Energy (Cal/g) | 4130.74 | 4307.28 | 4291.75 | 4204.88 |
| Protein (%) | 17.62 | 16.45 | 16.72 | 16.65 |
| Energy (Cal/g)/Protein (%) | 234.44 | 261.85 | 256.61 | 252.60 |

[1] Mineralswere added to the diets in the form of AIN-93G-MX mineral mix

[2] Vitaminswere added to the diets in the form of AIN-93-VX vitamin mix

C, control; G, glucan; M, MCC; GM, glucan and MCC.

As the β-glucan is extracted from oat, the remaining 29% is mainly composed by small amount of oat bran and protein. Thus only 70% of oat-β-glucan was considered as carbohydrate, and the left 30% was considered as protein which was calculated according to the proportion of protein in oat bran. In current study, not only total protein and carbohydrate, but also the balance of total energy between groups was considered. As the amount of the dietary fibers was too large (approximately 20%), total energy of diet of the four groups can only be calculated as closer as possible. Therefore, the total energy of feed in control diet was reduced by the supplement of bentoniteclay which is always used in swine feed for energy regulation as its inertcharacteristic.Alternatively, the measured energy (Cal/g) / protein (%) for each diet remained no significant change ($p > 0.05$).

**Table S2** OTU table summary

| Sample ID | Sequence counts | Observations (OTU number) |
|---|---|---|
| C1 | 109,010 | 943 |
| C2 | 91,608 | 887 |
| C3 | 88,607 | 950 |
| C4 | 78,438 | 791 |
| C5 | 54,282 | 972 |
| C6 | 76,028 | 988 |
| C7 | 77,422 | 966 |
| G1 | 86,313 | 591 |
| G2 | 83,659 | 699 |
| G3 | 92,349 | 467 |
| G4 | 90,202 | 562 |
| G5 | 69,899 | 511 |
| G6 | 56,753 | 443 |
| G7 | 78,127 | 570 |
| M1 | 101,396 | 871 |
| M2 | 79,105 | 789 |
| M3 | 74,422 | 692 |
| M4 | 73,145 | 797 |
| M5 | 86,767 | 1,287 |
| M6 | 94,271 | 982 |
| M7 | 102,035 | 926 |
| GM1 | 83,068 | 560 |
| GM2 | 79,849 | 726 |
| GM3 | 98,640 | 676 |
| GM4 | 86,321 | 681 |
| GM5 | 81,901 | 708 |
| GM6 | 69,042 | 573 |
| GM7 | 53,366 | 462 |

C, control; G, glucan; M, MCC; GM, glucan and MCC.

**Table S3**The relative abundance of main bacterial taxa in the colon of mice in different treatments (%)

| Taxon | C | G | M | GM | SD-C | SD-G | SD-M | SD-GM | *p*-value |
|---|---|---|---|---|---|---|---|---|---|
| *[Prevotella]*§ | 0.141 | 0.730 | 0.251 | 0.390 | 0.34 | 0.62 | 0.29 | 0.62 | 0.16 |
| ***[Ruminococcus]**** | 1.170 | 0.457 | 0.787 | 0.458 | 0.68 | 0.33 | 0.40 | 0.33 | **0.02** |
| AF12 | 0.201 | 0.036 | 0.289 | 0.283 | 0.22 | 0.07 | 0.31 | 0.35 | 0.25 |
| *Anaeroplasma* | 0.249 | 0.247 | 0.119 | 0.615 | 0.28 | 0.58 | 0.19 | 1.56 | 0.72 |
| *Bacteroidales* | 1.456 | 6.062 | 3.214 | 1.461 | 0.82 | 9.76 | 2.88 | 1.24 | 0.31 |
| ***Bacteroides**** | 0.337 | 6.544 | 0.824 | 1.262 | 0.21 | 6.84 | 0.48 | 1.26 | **0.01** |
| *Christensenellaceae* | 0.067 | 0.098 | 0.210 | 0.068 | 0.06 | 0.19 | 0.30 | 0.16 | 0.50 |
| ***Clostridiales**** | 50.879 | 21.071 | 37.330 | 35.512 | 5.41 | 10.99 | 9.84 | 10.01 | **0.00** |
| ***Clostridiales*.Other.Other*** | 0.330 | 0.092 | 0.058 | 0.003 | 0.38 | 0.14 | 0.10 | 0.00 | **0.03** |
| *Clostridium*§ | 0.057 | 0.150 | 0.028 | 0.013 | 0.06 | 0.17 | 0.06 | 0.03 | 0.07 |
| ***Coprococcus**** | 0.856 | 0.301 | 0.859 | 0.355 | 0.49 | 0.21 | 0.40 | 0.31 | **0.01** |
| *Dechloromonas* | 0.031 | 0.111 | 0.029 | 0.032 | 0.03 | 0.14 | 0.05 | 0.06 | 0.20 |
| *Desulfovibrio*§ | 0.953 | 0.251 | 1.184 | 1.387 | 0.48 | 0.17 | 0.78 | 1.63 | 0.15 |
| ***Desulfovibrionaceae**** | 1.393 | 0.473 | 1.678 | 0.623 | 0.91 | 0.42 | 0.65 | 0.59 | **0.01** |
| *Dorea* | 0.124 | 0.180 | 0.054 | 0.095 | 0.15 | 0.17 | 0.05 | 0.07 | 0.30 |
| ***Enterobacteriaceae**** | 0.230 | 1.772 | 0.353 | 0.297 | 0.20 | 1.86 | 0.50 | 0.43 | **0.02** |
| ***Erysipelotrichaceae**** | 0.126 | 0.024 | 0.025 | 0.050 | 0.08 | 0.03 | 0.03 | 0.06 | **0.01** |
| *Flexispira* | 1.166 | 0.528 | 0.505 | 1.015 | 1.51 | 0.43 | 1.03 | 1.75 | 0.70 |
| *Helicobacter* | 0.152 | 0.093 | 0.099 | 0.210 | 0.22 | 0.12 | 0.11 | 0.32 | 0.71 |
| *Helicobacteraceae*§ | 0.148 | 0.820 | 0.422 | 1.043 | 0.14 | 0.75 | 0.40 | 0.93 | 0.06 |
| *Helicobacteraceae.Other* | 0.233 | 0.103 | 0.000 | 0.000 | 0.62 | 0.27 | 0.00 | 0.00 | 0.53 |
| *Lachnospiraceae*§ | 14.221 | 7.723 | 10.685 | 10.079 | 3.82 | 5.78 | 4.24 | 3.50 | 0.08 |
| *Lactobacillus* | 0.116 | 0.196 | 0.199 | 0.128 | 0.15 | 0.14 | 0.21 | 0.10 | 0.65 |
| *Mucispirillum* | 1.229 | 0.232 | 0.751 | 1.320 | 0.88 | 0.21 | 1.20 | 1.47 | 0.22 |
| *Odoribacter*§ | 1.747 | 0.803 | 2.581 | 2.207 | 0.79 | 0.55 | 1.70 | 1.95 | 0.12 |
| *Oscillospira*§ | 3.828 | 2.842 | 4.398 | 5.737 | 1.62 | 0.95 | 1.31 | 3.07 | 0.06 |
| *Parabacteroides* | 0.076 | 0.000 | 0.074 | 0.199 | 0.14 | 0.00 | 0.13 | 0.52 | 0.62 |
| ***Prevotella**** | 0.099 | 1.380 | 0.251 | 0.294 | 0.08 | 1.52 | 0.20 | 0.38 | **0.02** |
| *Pseudomonadaceae* | 0.098 | 0.068 | 0.147 | 0.128 | 0.06 | 0.06 | 0.15 | 0.15 | 0.59 |
| *Pseudomonas* | 0.092 | 0.038 | 0.083 | 0.102 | 0.13 | 0.03 | 0.05 | 0.13 | 0.63 |
| ***Rikenella**** | 0.867 | 0.114 | 0.345 | 0.117 | 0.61 | 0.15 | 0.38 | 0.12 | **0.00** |
| ***Rikenellaceae**** | 3.823 | 1.587 | 6.471 | 3.559 | 1.91 | 0.74 | 3.39 | 3.11 | **0.01** |
| *Ruminococcaceae*§ | 5.500 | 3.638 | 7.065 | 5.122 | 1.20 | 2.68 | 3.97 | 3.36 | 0.23 |
| *Ruminococcaceae.*Other§ | 0.295 | 0.045 | 0.447 | 0.473 | 0.15 | 0.03 | 0.52 | 0.44 | 0.11 |
| *Ruminococcus*§ | 2.116 | 1.475 | 1.542 | 3.992 | 0.74 | 0.76 | 0.55 | 3.72 | 0.08 |
| **S24-7**** | 4.108 | 38.073 | 15.002 | 20.180 | 1.97 | 17.06 | 8.47 | 13.86 | **0.00** |
| ***Sutterella**** | 0.000 | 0.149 | 0.000 | 0.015 | 0.00 | 0.16 | 0.00 | 0.02 | **0.00** |

The difference on abundance of main bacterial taxa among the four groups was analyzed with One-Way ANOVA using SPSS 16.0. Only taxa that had a relative abundance of 0.01% in at least one of the treatments were shown and stated. The cutoff 0.01% was only for data in Table S3 but not for data shown in other tables or figures. The color depth of back ground of each cell based on red-yellow-green color gradation shows the abundance of each taxon. SD, standard deviation; C,

control; G, glucan; M, MCC; GM, glucan and MCC.
Differences were considered significant when $p < 0.05$. *$p< 0.05$; **$p < 0.01$; § Although the p-value showed no significant difference, at least two treatments showed significantly different.

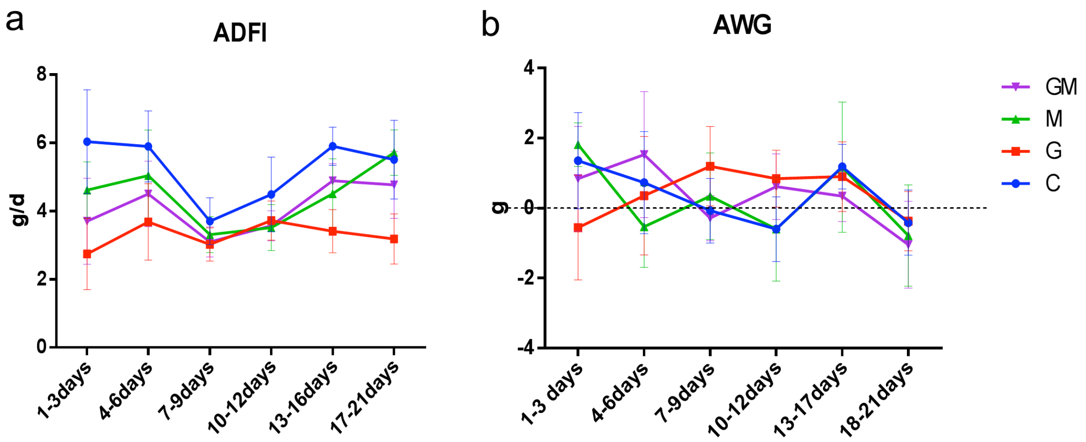

**Figure S1** Change of ADFI (a) and AWG (b) of mice in the four groups. C, control group; G, mice fed with oat-derived β-glucan; M mice fed with MCC; GM mice fed with the mixture of the two dietary fibers.

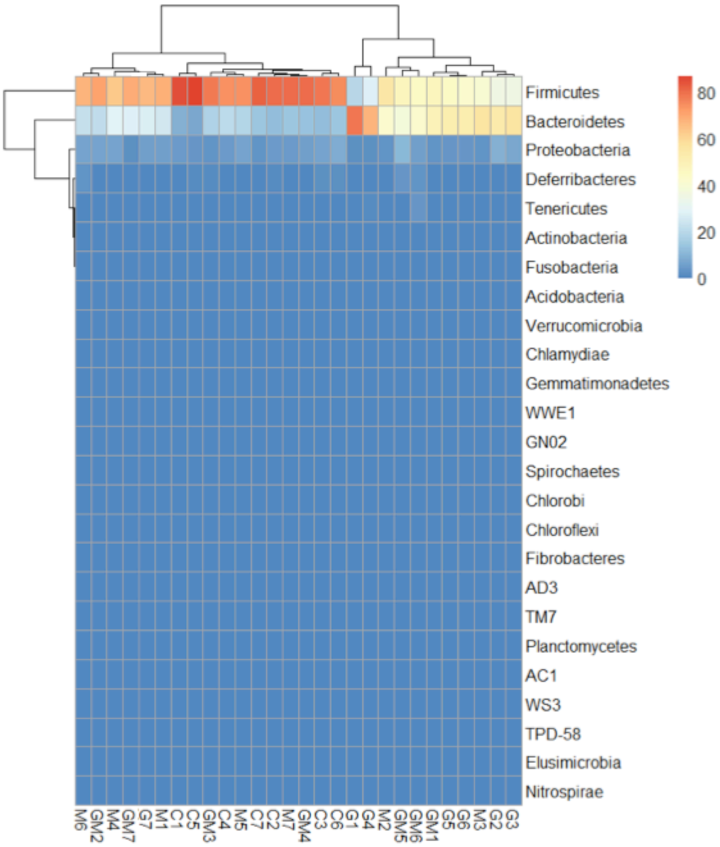

**Figure S2** Heatmap of bacterial phyla in the colonic samples. Phylaarearranged in rows and are clusteredon the vertical axis (y-axis).Samples arearranged vertically and are clustered on thehorizontal axis (x-axis).Clustering was done using Phylotrac’s heatmap optionwith Pearson correlations andcomplete lineage algorithms.Different colors indicate therelative abundance of the different phyla.C, control group; G, mice fed with oat-derived β-glucan; M mice fed with MCC; GM mice fed with the mixture of the two dietary fibers.

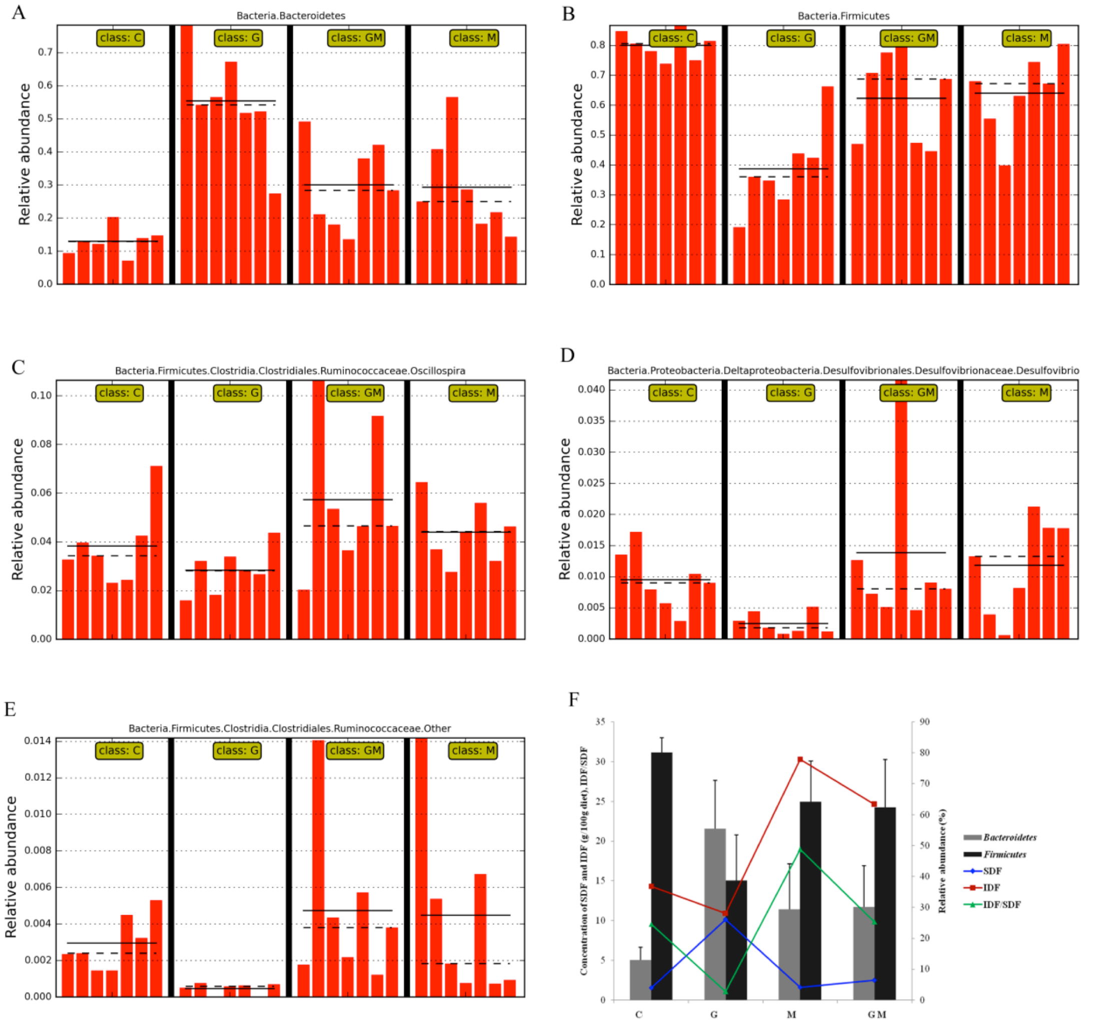

**Figure S3** Relative abundance of several bacterial phyla and genera in the colonic samples. (A) *Bacteroidetes*, (B) *Firmicutes*, (C) *Oscillospira* spp., (D) *Desulfovibrio* spp., (E) *Ruminoccaceae*, (F) the change of *Bacteroidetes* and *Firmicutes*, and their correlation with dietary SDF, IDF concentration and IDF/SDF ratio. C, control; G, glucan; M, MCC; GM, glucan and MCC.

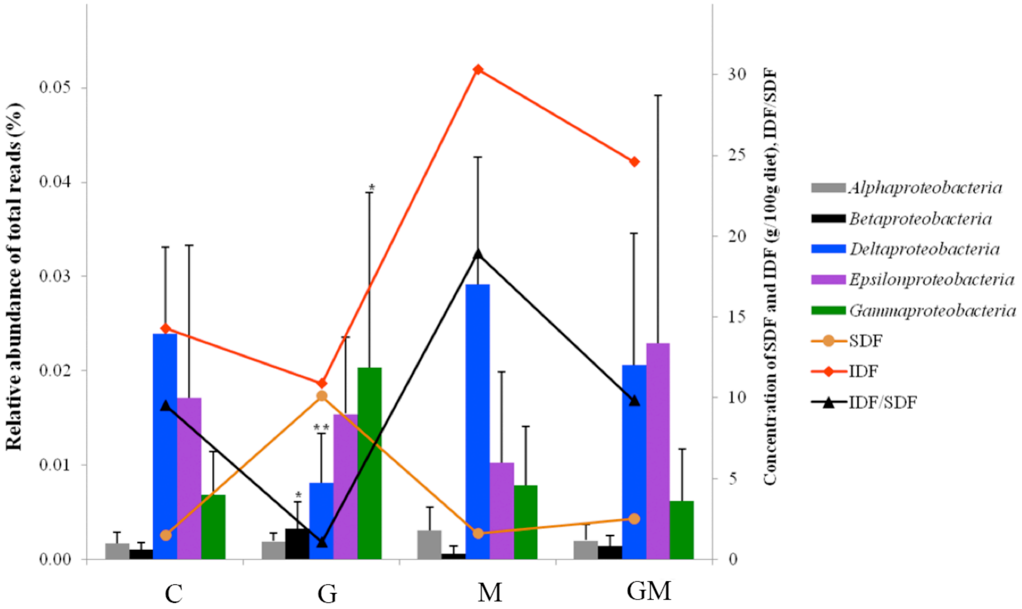

**Figure S4** Relative abundance of five classes of *Proteobacteria* in the four treatments. Broken lines show the change of dietary SDF and IDF concentration and IDF/SDF ratio in the four treatments. C, control; G, glucan; M, MCC; GM, glucan and MCC.

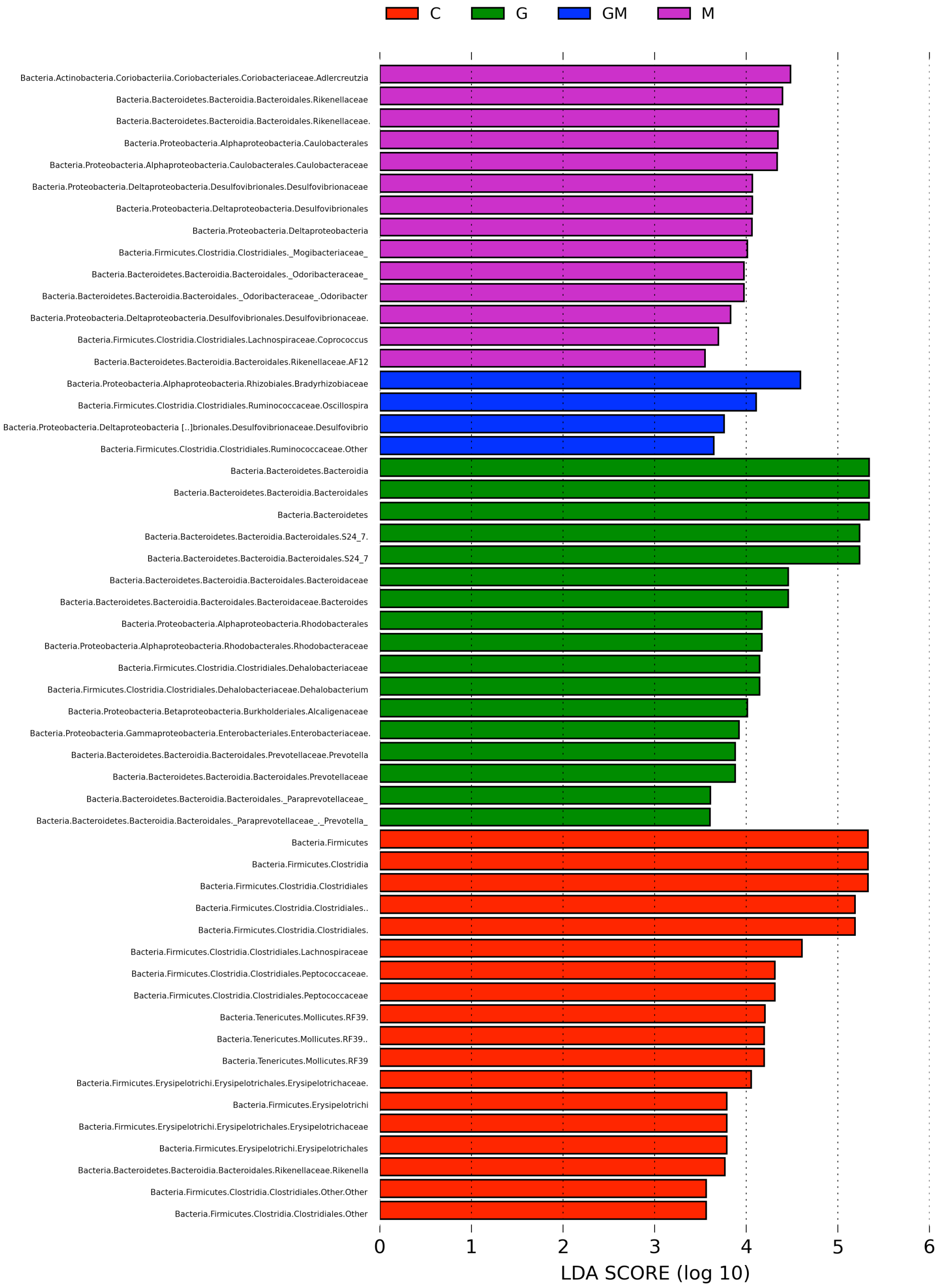

**Figure S5**. Bacterial taxa significantly different between the four treatments as identified by linear discriminant analysis coupled with effect size (LEfSe) using default parameters.

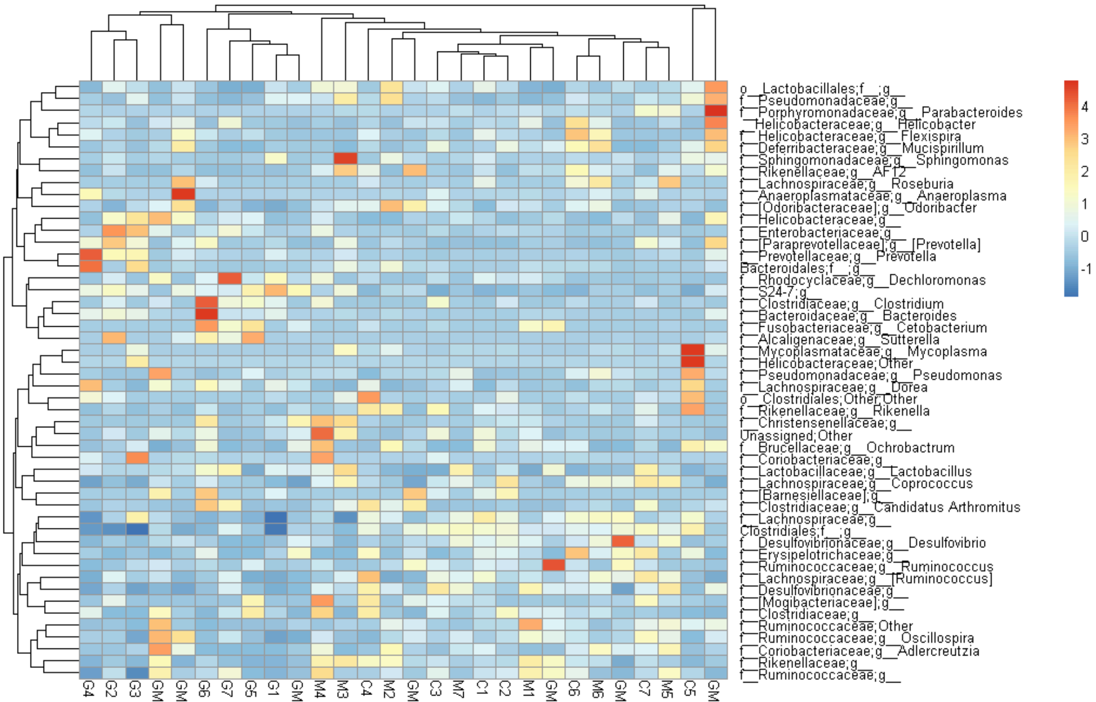

**Figure S6** Heatmap of top 50 bacterial genera in the colonic samples. OTUs arearranged in rows and are clusteredon the vertical axis (y-axis).Samples arearranged vertically and are on thehorizontal axis (x-axis).Clustering was done for eachusing Phylotrac's heatmap optionwith Pearson correlations andcomplete lineage algorithms.Different colors indicate therelative abundance of the taxons.C control group, G mice fed with oat-derived â-glucan, M mice fed with MCC, GM mice fed with the mixture of the two dietary fibers.

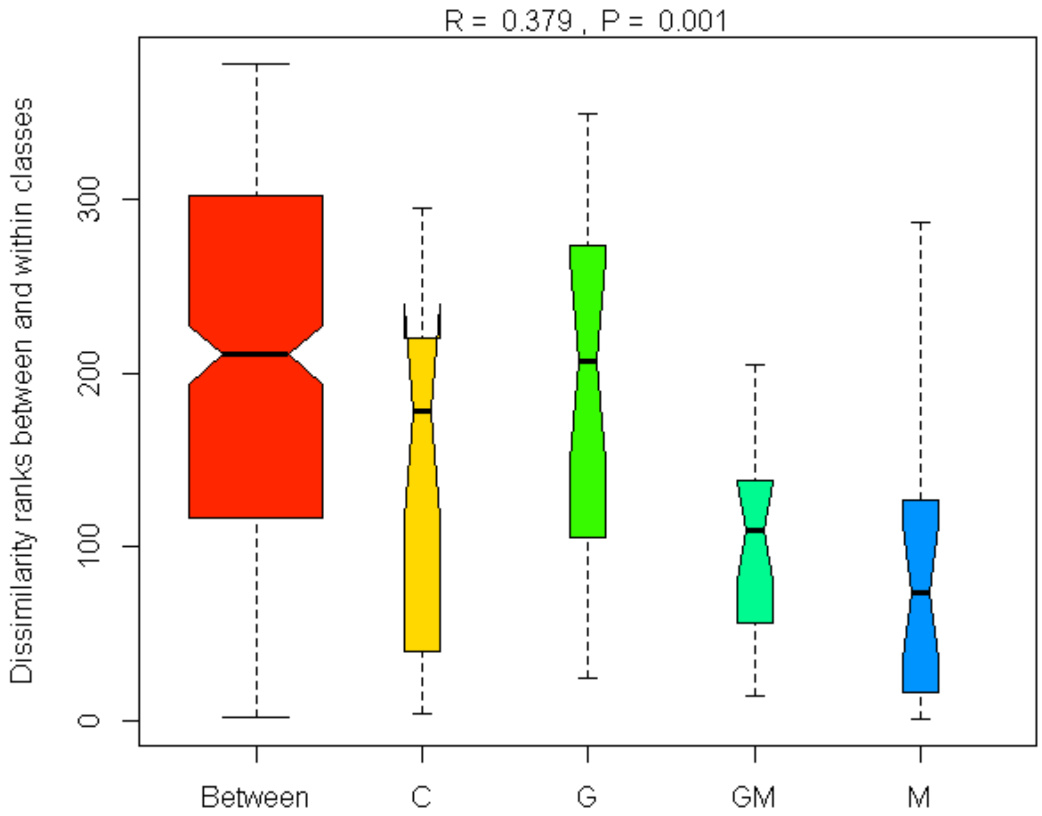

**Figure S7** Analysis of similarities (ANOSIM) of bacterial diversity of the four groups. ANOSIM statistic R is 0.379, *p* = 0.001. C control group, G mice fed with oat-derived â-glucan, M mice fed with MCC, GM mice fed with the mixture of the two dietary fibers.