Supplementary Table 1. Primers for the detection of bacterial groups

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Eubacteria (all bacteria)[1]

UniF340-Forward: 5’-ACTCCTACGGGAGGCAGCAGT-3’

UniR514-Reverse: 5’-ATTACCGCGGCTGCTGGC-3’

Ruminococcaceae (This study)

Forward: 5’-ATACCCTGGTAGTCCACGCT-3’

Reverse: 5’-GCGTCACTGGGATGTCAAGA-3’

***Eubacterium* rectale**[2]

UniF338-Forward: 5’-ACTCCTACGGGAGGCAGC-3’

C.cocR491-Reverse: 5’-GCTTCTTAGTCAGGTACCGTCAT-3’

Lachnospiraceae (This study)

Forward: 5’-TGGATCCGCGTCTGATTAGC-3’

Reverse: 5’- TGTCTCAGTCCCAATGTGGC-3’

***Lactobacillu*s group**[3]

LabF362-Forward: 5’-AGCAGTAGGGAATCTTCCA-3’

LabR677-Reverse: 5’-CACCGCTACACATGGAG-3’

Segmented filamentous bacteria-1[4]

SFB736F-Forward: 5’-GACGCTGAGGCATAGCAT-3’

SFB844R-Reverse: 5’-GACGGCACGGATTGTTATTCA-3’

Segmented filamentous bacteria-2[5]

SFB1F 5’-AGGAGGAGTCTGCGGCAC-3’

SFB2R 5’-CCTTCCTCTTCCCTGCT-3’

***Clostridium* coccoides**[6]

Forward-5’-AAATGACGGTACCTGACTAA-3’

Reverse-5’-CTTTGAGTTTCATTCTTGCGAA-3’

Clostridium leptum (This study)

Forward: 5’-CCTTCCGTGCCGSAGTTA-3’

Reverse: 5’-GAATTAAACCACATACTCCACTGCTT-3’

***Turicibacter* sp.** (This study)

Forward: 5’-ACGGGGACAACGATTGGAAA-3’

Reverse: 5’-AGTGATGCCAGGAGCATCTT-3’

***Bacteroides* sp.**[7]

BactF285-Forward: 5’-GGTTCTGAGAGGAGGTCCC-3’

UniR338-Reverse: 5’-GCTGCCTCCCGTAGGAGT-3’

***Anaerophaga* sp.** (This study)

Forward: 5’-TCTCCGTGGGTTTAAAGGAAG-3’

Reverse: 5’-CGTGTCTCAGTACCAGTGTG-3’

***Paludibacter* sp.** (This study)

Forward: 5’-AAGGAAGCGATTCCGGCTAC-3’

Reverse: 5’-CTCAGAACCCCTACGCATCG-3’

***Prevotella* sp.**[3]

Forward- 5’-GGTGTCGGCTTAAGTGCCAT-3’

Reverse- 5’-CGGACGTAAGGGCCGTGC-3’

***Helicobacter* pylori**[8]

Hp 547F-Forward: 5'-CTTAACCATAGAACTGCATTTGAAACTAC-3'

Hp 665R-Reverse: 5'-GGTCGCCTTCGCAATGAGTA-3'

Enterobacteriaceae[9]

Uni515F-Forward- 5'-GTGCCAGCAGCCGCGGTAA-3'

Ent826R-Reverse- 5'-GCCTCAAGGGCACAACCTCCAAG-3'

Akkermanisa muciniphila (This study)

Forward- 5'-CAGCACGTGAAGGTGGGGAC-3'

Reverse- 5'-CCTTGCGGTTGGCTTCAGAT-3'

The primer sets were either synthesized according to previous publications or designed based on DNA sequence information available in Ribosomal Database Project[10] and validated.

Supplementary Table 2. Pyrosequencing of 16S rRNA genes in the stool of diabetic NOD mice

Number of NOD mice tested	5
Number of sequences analyzed	5784 ± 1223
Number of phyla examined	4.2 ± 0.8
Number of genera investigated	21.8 ± 1.3
Number of OTUs evaluated	1300
Phylum percentages:	
Firmicutes	72.9 ± 11.9
Bacteroidetes	26.7 ± 11.9
Tenericutes	0.12 ± 0.2
Actinobacteria	0.08 ± 0.09
Proteobacteria	0.04 ± 0.03
Ratio of *Firmicutes/Bacteroidetes*:	3.4 ± 1.9
Class percentages:	
Clostridia	70.4 ± 10.93
Bacteroidia	26.8 ± 11.94
Bacilli	1.8 ± 0.86
Erysipelotrichi	0.42 ± 0.33
Mollicutes	0.12 ± 0.25
Actinobacteria	0.08 ± 0.09
Alphaproteobacteria	0.02 ± 0.02
Gammaproteobacteria	0.01 ± 0.03
Order percentages:	
Clostridiales	70.74 ± 4.8
Bacteroidales	26.76 ± 5.3
Lactobacillales	1.8 ± 0.38
Erysipelotrichales	0.42 ± 0.14
Rhizobiales	0.22 ± 0.01
Anaeroplasmatales	0.12 ± 0.11
Micrococcales	0.08 ± 0.04
Enterobacteriales	0.01 ± 0.01
Rhodospirillales	0.003 ± 0.003
Family percentages:	
Lachnospiraceae	64.35 ± 11.77

Rikenellaceae	18.86 ± 14.42
Porphyromonadaceae	9.99 ± 3.74
Ruminococcaceae	3.56 ± 1.05
Lactobacillaceae	1.79 ± 0.87
Prevotellaceae	0.56 ± 0.45
Erysipelotrichaceae	0.40 ± 0.33
Anaeroplasmataceae	0.16 ± 0.25
Bacteroidaceae	0.15 ± 0.09
Micrococcaceae	0.09 ± 0.09
Clostridiaceae	0.04 ± 0.07
Methylobacteriaceae	0.03 ± 0.02
Enterobacteriaceae	0.02 ± 0.04
Rhodospirillaceae	0.003 ± 0.003
Species percentages:	
Firmicutes_*Clostridia_Clostridiales_Lachnospiraceae _Lachnospiraceae* sp.	66.58 ± 11.7
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus sp.	0.33 ± 0.11
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia sp.	0.31 ± 0.06
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_ Ruminococcaceae sp.	2.01 ± 0.31
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus sp.	0.22 ± 0.09
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Anaerotruncus sp.	0.46 ± 0.11
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium sp.	0.01 ± 0.01
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus johnsonii	0.86 ± 0.33
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus sp.	0.55 ± 0.20
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus reuteri	0.39 ± 0.1
Firmicutes_Clostridia_Clostridiales_Clostriaceae_Clostridium_Clostridium sp.	0.05 ± 0.03
Firmicutes_Clostridia_Clostridiales_Oscillospiraceae_Oscillibacter sp.	0.63 ± 0.05
Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turicibacter sp.	0.34 ± 0.15
Bacteroidetes_*Bacteroidia_Bacteroidales_Rikenellaceae_ Alistipes* sp.	16.2 ± 6.4
Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella sp.	0.33 ± 0.17
Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotellaceae sp.	0.14 ± 0.03
Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Paraprevotella sp.	0.04 ± 0.01
Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides sp.	0.13 ± 0.04
Bacteroidetes_Bacteroidia_Bacteroidales_Barnesiellaceae_Barnesiella sp.	8.86 ± 1.6
Bacteroidetes_Bacteroidia_Bacteroidales_Odoribacteraceae_Odoribacter sp.	1.19 ± 0.14
Tenericutes_*Mollicutes_Anaeroplasmatales_Anaeroplasmataceae_Anaeroplasma* sp.	0.12 ± 0.11
Actinobacteria_*Actinobacteria_Micrococcales_Micrococcaceae_Arthrobacter* sp.	0.08 ± 0.04
Proteobacteria_*Alphaproteobacteria_Rhizobiales_Methylobacteriaceae_Methylobacterium* sp.	0.02 ± 0.01
Proteobacteria_Gammaproteobacteria_ Enterobacterales_Enterobacteriaceae_ Escherichia/Shigella sp.	0.01 ± 0.01
unclassified sequences_metagenomes_organismal metagenomes_*wallaby gut metagenome*	0.01 ± 0.01

Phylum-Class-Order-Family-Genus-Species are listed according to the NCBI Taxonomy browser: https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi. The DNA was derived from the stools of 28-30-wk old diabetic female NOD mice and subject to pyrosequencing individually using the bTEFAP method[11]. The data were analyzed using a proprietary analysis pipeline by MR DNA Lab. Data shown are mean ± SD of 5 samples.

Supplementary References

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