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Supplementary material

2 ***In vitro* fermentation reveals interplay relationship between oat β -glucan and**
3 **human gut *Bacteroides* and their potential role in regulating gut cytokines**

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24 **Table S1. Details for specific medium plates for *Bacteroides* isolation**

Reagents	Amount (/L)
Brucella agar	43.1 g
Sheep blood	50 mL
L-Cysteine hydrochloride	0.1 g
Hemin	10 mg
Vitamin K1	2 mg
Kanamycin	0.1 g
Vancomycin	0.75 mg

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27 **Table S2. Detailed information for primer sequence**

Gene	Sense sequence (5'→3')	Antisense sequence (5'→3')
TNF- α	GGTGCCTATGTCTCAGCCTCTT	GCCATAGAAGTACTGATGAGAGGGAG
IL-6	TACCACTTCACAAGTCGGAGGC	CTGCAAGTGCATCATCGTTGTTC
GAPDH	ACATCATCCCTGCATCCACT	GTCCTCAGTGTAGCCCAAG

Note: TNF- α , tumor necrosis factor- α ; IL-6, interleukin-6; GAPDH, glyceraldehyde-3-phosphate dehydrogenase

33 **Table S4. Gene annotation overview of two *Bacteroides* strains using different**

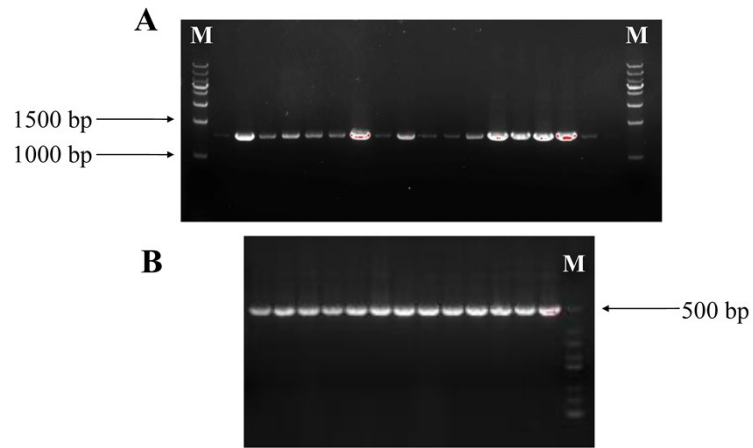
34 **databases**

No.	Strain	NR	Swiss-Prot	Pfam	COG	GO	KEGG
1	<i>Bacteroides xylanisolvens</i> Bac02	5483	2892	4151	3769	3330	1751
2	<i>Bacteroides koreensis</i> Bac08	5525	2966	4163	3763	3388	1748

35 Note: NR, non-redundant protein database; COG, Clusters of Orthologous Groups of

36 proteins; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes

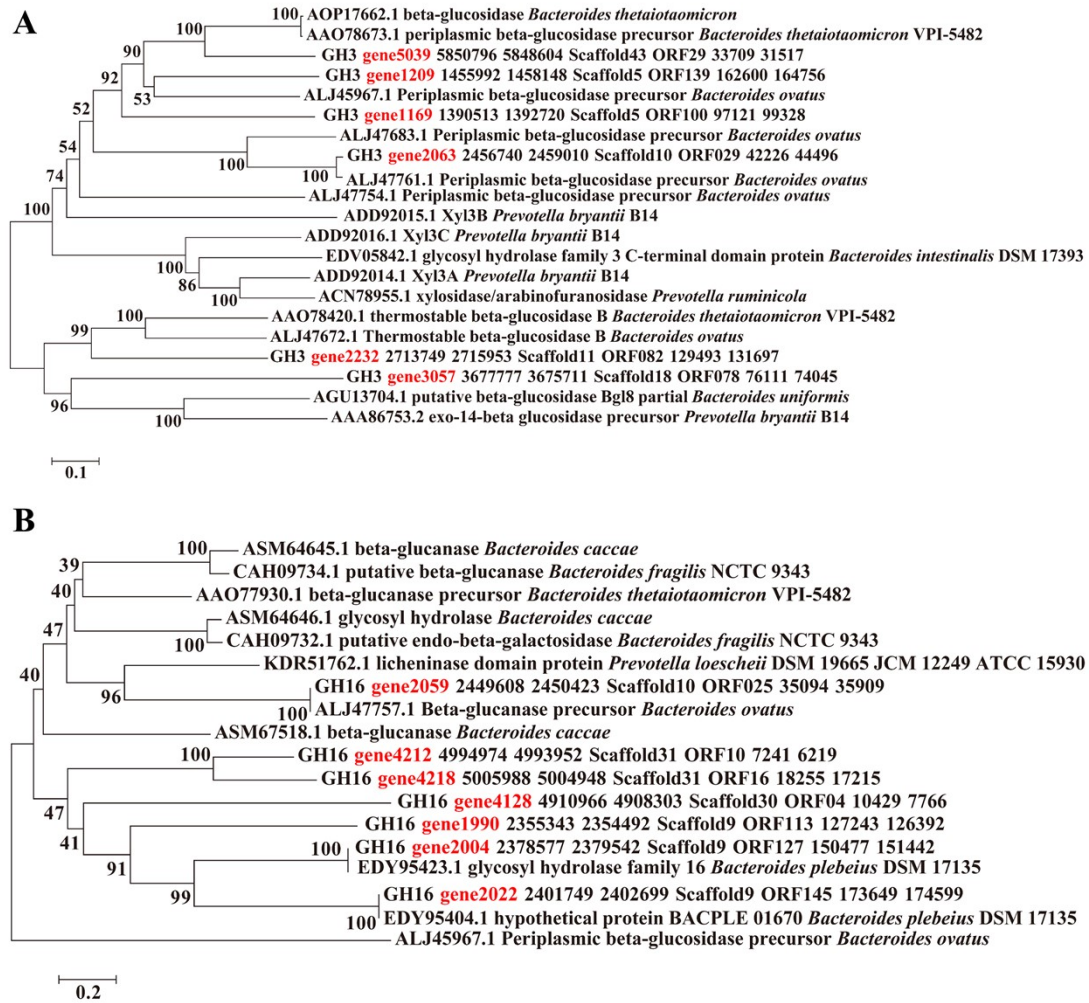
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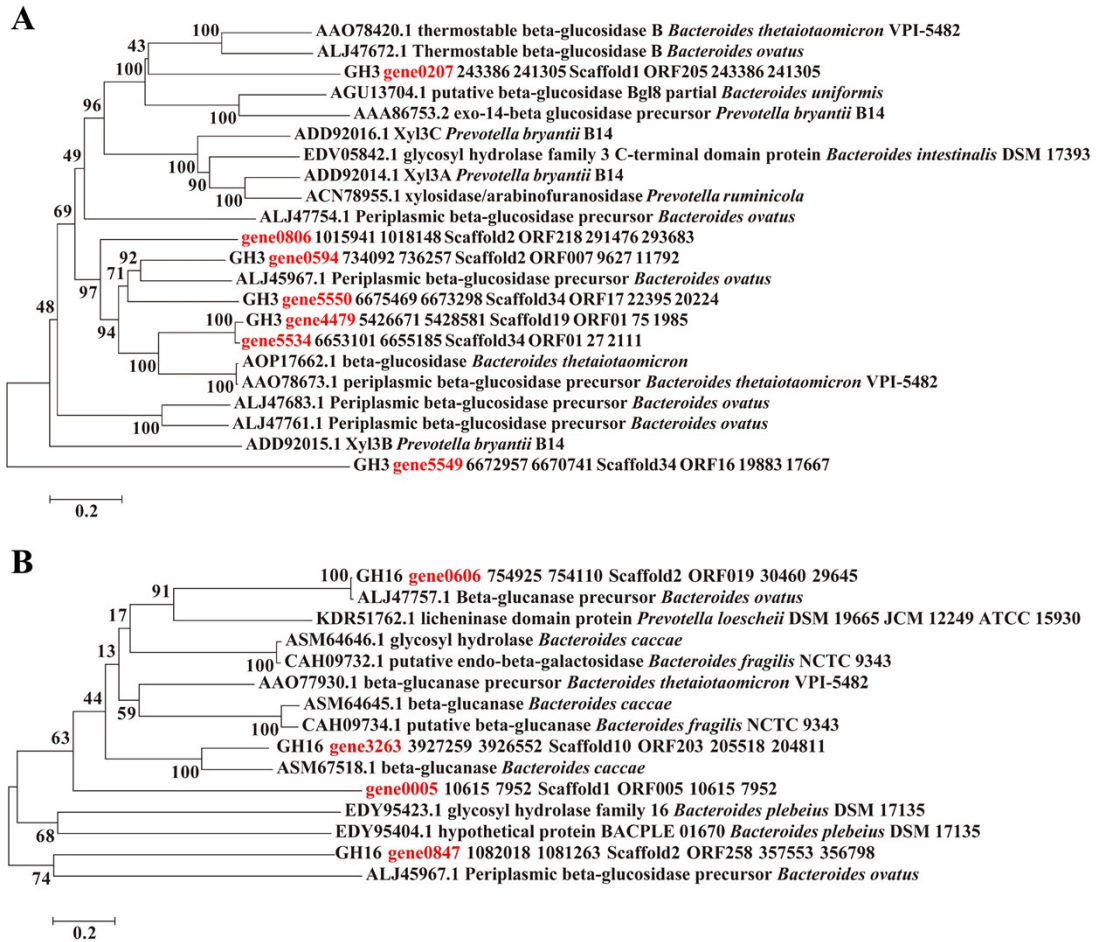
40 **Fig. S1.** Representative PCR detection of isolated gut microbes from healthy adult
 41 human. The DNA bands are shown on the gel and M indicates the marker (500 bp-
 42 15000 bp). The amplified fragments (A) using the universal primer for 16S rRNA and
 43 (B) using the specific primer for *Bacteroides* are respectively displayed.

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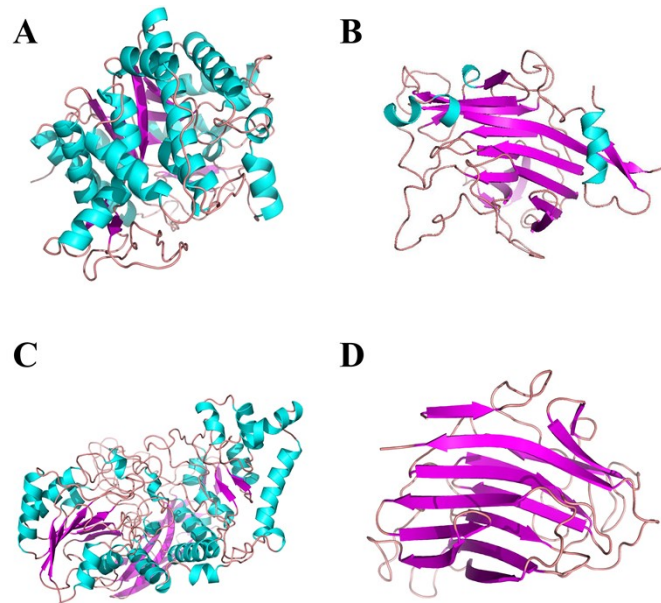
47 **Fig. S2.** Phylogenetic analysis of protein sequences of (A) GH3 and (B) GH16 from
 48 gut *Bacteroides* strains indicates the similarity and difference of *Bacteroides*
 49 *xylanisolvans* Bac02 strain sequences. The tree was inferred using the Neighbor-
 50 Joining method, and values of bootstrap were marked next to the branches.



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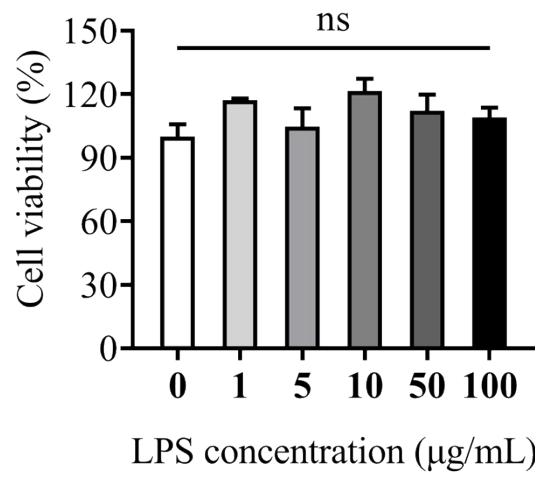
53 **Fig. S3.** Phylogenetic analysis of protein sequences of (A) GH3 and (B) GH16 from
 54 gut *Bacteroides* strains indicates the similarity and difference of *Bacteroides*
 55 *koreensis* Bac08 strain sequences. The tree was inferred using the Neighbor-Joining
 56 method, and values of bootstrap were marked next to the branches.

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60 **Fig. S4.** Tertiary structure homology modeling of GH3 and GH16 from *Bacteroides*
61 *xylanisolvans* Bac02 and *Bacteroides koreensis* Bac08 strains showing helical coils
62 and flat ribbon protein secondary structures in cartoon representation: (A) *BxGH3*₂₀₆₃,
63 (B) *BxGH16*₂₀₀₄, (C) *BkGH3*₄₄₇₉, and (D) *BkGH16*₃₂₆₃



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66 **Fig. S5.** The effect of LPS concentration on cell viability of Raw264.7 cells.

67 Differences were considered statistically not significant with a $P > 0.05$.

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