

Table S1. The modified formula of Gut microbiota medium (GMM)

<b>Component</b>	<b>Amount/L</b>	<b>Comments</b>
Tryptone Peptone	2 g	
Yeast Extract	1 g	
Raffinose	10 g	
L-cysteine	0.5 g	
Meat Extract	5 g	
KH <sub>2</sub> PO <sub>4</sub>	100 mL	1M stock solution pH 7.2
MgSO <sub>4</sub> -7H <sub>2</sub> O	0.002 g	
NaHCO <sub>3</sub>	0.4 g	
NaCl	0.08 g	
CaCl <sub>2</sub>	1 mL	0.8g/100mL stock
Vitamin K (menadione)	1 mL	1 mg/mL stock solution
FeSO <sub>4</sub>	1 mL	0.4 mg FeSO <sub>4</sub> /mL stock solution
Histidine Hematin Solution	1 mL	1.2 mg hematin/mL in 0.2M histidine
Tween 80	2 mL	25% stock solution
ATCC Vitamin Mix	10 mL	
ATCC Trace Mineral Mix	10 mL	
Resazurin	4 mL	0.25 mg/mL stock solution

**Table S2. Distribution of the homologous proteins of glycosidases related to raffinose utilization among human gut bacteria.**

No.	Human gut bacteria		Genes related to raffinose hydrolysis <sup>a, b, d</sup>			
	Species	Number of strains	$\alpha$ -galactosidase <sup>c</sup>	sucrose phosphorylase <sup>c</sup>	$\beta$ -fructosidase <sup>c</sup>	levansucrase <sup>c</sup>
1	<i>Actinobacillus suis</i>	1	1	0	0	0
2	<i>Actinomyces</i> sp.	1	0	1	0	0
3	<i>Alistipes indistinctus</i>	1	1	0	0	0
4	<i>Alistipes shahii</i>	1	1	0	0	0
5	<i>Anaerostipes caccae</i>	1	1	0	0	0
6	<i>Anaerostipes hadrus</i>	1	1	0	0	0
7	<i>Anaerostipes</i> sp.	1	1	0	0	0
8	<i>Bacillus smithii</i>	1	1	0	0	0
9	<i>Bacteroides caccae</i>	1	1	0	0	0
10	<i>Bacteroides cellulosilyticus</i>	1	1	0	0	0
11	<i>Bacteroides clarus</i>	1	1	0	0	0
12	<i>Bacteroides coprocola</i>	1	1	0	0	0
13	<i>Bacteroides coprophilus</i>	1	1	0	0	0
14	<i>Bacteroides dorei</i>	2	2	0	0	0
15	<i>Bacteroides finegoldii</i>	1	1	0	0	0
16	<i>Bacteroides fluxus</i>	1	1	0	0	0
17	<i>Bacteroides fragilis</i>	1	1	0	0	0
18	<i>Bacteroides intestinalis</i>	1	1	0	0	0
19	<i>Bacteroides oleiciplenus</i>	1	1	0	0	0
20	<i>Bacteroides ovatus</i>	4	4	0	0	0
21	<i>Bacteroides plebeius</i>	1	1	0	0	0
22	<i>Bacteroides salyersiae</i>	1	1	0	0	0
23	<i>Bacteroides</i> sp.	21	19	1	0	1
24	<i>Bacteroides stercoris</i>	1	1	0	0	0
25	<i>Bacteroides uniformis</i>	1	0	1	0	0
26	<i>Bacteroides vulgatus</i>	1	1	0	0	0
27	<i>Bacteroides xylanisolvens</i>	2	2	1	0	0
28	<i>Barnesiella intestinihominis</i>	1	1	0	0	0

29	<i>Bifidobacterium adolescentis</i>	1	1	0	0	0
30	<i>Bifidobacterium angulatum</i>	1	1	1	0	0
31	<i>Bifidobacterium bifidum</i>	1	1	0	0	0
32	<i>Bifidobacterium breve</i>	2	2	2	1	0
33	<i>Bifidobacterium catenulatum</i>	1	1	1	0	0
34	<i>Bifidobacterium dentium</i>	1	1	1	1	0
35	<i>Bifidobacterium longum</i> subsp. <i>infantis</i>	3	3	3	0	0
36	<i>Bifidobacterium longum</i> subsp. <i>longum</i>	5	5	5	0	0
37	<i>Bifidobacterium pseudocatenulatum</i>	1	1	0	0	0
38	<i>Bifidobacterium</i> sp.	1	1	0	0	0
39	<i>Blautia hansenii</i>	1	1	1	0	0
40	<i>Brachyspira pilosicoli</i>	4	3	3	0	0
41	<i>Burkholderiales</i> bacterium	1	0	1	0	0
42	<i>Butyrivibrio fibrisolvens</i>	1	1	1	0	0
43	<i>Catenibacterium mitsuokai</i>	1	1	0	0	0
44	<i>Cedecea davisae</i>	1	0	1	0	0
45	<i>Citrobacter youngae</i>	1	1	1	0	0
46	<i>Clostridium asparagiforme</i>	2	1	0	0	0
47	<i>Clostridium bolteae</i>	2	1	0	0	0
48	<i>Clostridium citroniae</i>	2	1	0	0	0
49	<i>Clostridium clostridioforme</i>	2	2	1	0	0
50	<i>Clostridium hathewayi</i>	2	2	2	0	0
51	<i>Clostridium hylemonae</i>	2	1	1	0	0
52	<i>Clostridium nexile</i>	1	1	1	0	0
53	<i>Clostridium perfringens</i>	1	1	1	0	0
54	<i>Clostridium ramosum</i>	1	1	0	0	0
55	<i>Clostridium</i> sp.	7	3	1	0	0
56	<i>Coprobacillus</i> sp.	4	3	3	0	0
57	<i>Coprococcus comes</i>	1	1	1	0	0
58	<i>Coprococcus eutactus</i>	1	1	1	0	0
59	<i>Coprococcus</i> sp.	1	1	1	0	0
60	<i>Cronobacter sakazakii</i>	4	3	0	0	0

61	<i>Dysgonomonas gadei</i>	1	1	0	0	0
62	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1	1	0	0	0
63	<i>Enterococcus casseliflavus</i>	1	1	1	1	0
64	<i>Enterococcus faecium</i>	2	2	1	0	0
65	<i>Enterococcus saccharolyticus</i>	1	1	0	0	0
66	<i>Escherichia coli</i>	25	4	0	0	0
67	<i>Ethanoligenens harbinense</i>	1	1	0	0	0
68	<i>Eubacterium rectale</i>	2	2	1	0	0
69	<i>Eubacterium siraeum</i>	3	3	2	0	0
70	<i>Faecalibacterium prausnitzii</i>	5	2	2	0	0
71	<i>Fusobacterium mortiferum</i>	1	1	0	0	0
72	<i>Hafnia alvei</i>	1	1	1	0	0
73	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2	1	0	0	0
74	<i>Klebsiella</i> sp.	3	3	0	0	0
75	<i>Klebsiella variicola</i>	1	1	0	0	0
76	<i>Lachnospiraceae</i> bacterium	14	7	6	0	0
77	<i>Lactobacillus acidophilus</i>	1	1	0	0	0
78	<i>Lactobacillus antri</i>	1	1	1	0	0
79	<i>Lactobacillus brevis</i> subsp. <i>gravesensis</i>	1	1	0	0	0
80	<i>Lactobacillus buchneri</i>	1	1	0	0	0
81	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	1	0	0	0	1
82	<i>Lactobacillus fermentum</i>	2	2	0	0	0
83	<i>Lactobacillus hilgardii</i>	1	1	0	0	0
84	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i>	2	2	0	0	0
85	<i>Lactobacillus plantarum</i> subsp. <i>plantarum</i>	1	1	0	0	0
86	<i>Lactobacillus reuteri</i>	5	5	0	0	1
87	<i>Lactobacillus rhamnosus</i>	3	3	0	0	0
88	<i>Lactobacillus ruminis</i>	1	1	0	0	0
89	<i>Lactobacillus ultunensis</i>	1	1	0	0	0
90	<i>Leptotrichia buccalis</i>	1	1	1	0	0
91	<i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i>	1	0	0	0	1

<b>92</b>	<i>Marvinbryantia formatexigens</i>	1	1	1	0	0
<b>93</b>	<i>Megamonas funiformis</i>	1	1	1	0	0
<b>94</b>	<i>Megamonas hypermegale</i>	1	1	1	0	0
<b>95</b>	<i>Mitsuokella multacida</i>	1	1	1	0	0
<b>96</b>	<i>Odoribacter laneus</i>	1	1	0	0	0
<b>97</b>	<i>Paenibacillus</i> sp.	3	1	1	0	0
<b>98</b>	<i>Parabacteroides johnsonii</i>	1	1	0	0	0
<b>99</b>	<i>Parabacteroides merdae</i>	1	1	0	0	0
<b>100</b>	<i>Parabacteroides</i> sp.	3	3	0	0	0
<b>101</b>	<i>Paraprevotella clara</i>	1	1	0	0	0
<b>102</b>	<i>Paraprevotella xylaniphila</i>	1	1	0	0	0
<b>103</b>	<i>Prevotella copri</i>	1	1	0	0	0
<b>104</b>	<i>Prevotella stercorea</i>	1	1	0	0	0
<b>105</b>	<i>Roseburia intestinalis</i>	3	3	2	0	0
<b>106</b>	<i>Roseburia inulinivorans</i>	1	1	1	0	0
<b>107</b>	<i>Ruminococcaceae bacterium</i>	1	1	1	0	0
<b>108</b>	<i>Ruminococcus champanellensis</i>	1	1	0	0	0
<b>109</b>	<i>Ruminococcus gnavus</i>	1	1	0	0	0
<b>110</b>	<i>Ruminococcus obeum</i>	2	2	0	0	0
<b>111</b>	<i>Ruminococcus</i> sp.	2	2	0	0	0
<b>112</b>	<i>Ruminococcus torques</i>	1	1	0	0	0
<b>113</b>	<i>Selenomonas ruminantium</i> subsp. <i>lactilytica</i>	1	1	1	0	0
<b>114</b>	<i>Selenomonas sputigena</i>	1	1	1	0	0
<b>115</b>	<i>Streptococcus equinus</i>	1	0	0	0	1
<b>116</b>	<i>Streptococcus infantarius</i> subsp. <i>infantarius</i>	1	1	0	0	0
<b>117</b>	<i>Streptococcus sanguinis</i>	1	1	1	0	0
<b>118</b>	<i>Subdoligranulum</i> sp.	1	1	0	0	0
<b>119</b>	<i>Subdoligranulum variabile</i>	1	1	0	0	0
<b>120</b>	<i>Tannerella</i> sp.	1	1	0	0	0
<b>121</b>	<i>Treponema azotonutricium</i>	1	1	1	0	0

122	<i>Treponema denticola</i>	1	1	0	0	0
123	<i>Turicibacter sanguinis</i>	1	1	1	0	0
124	<i>Turicibacter</i> sp.	1	1	1	0	0
125	<i>Weissella paramesenteroides</i>	1	1	0	0	0

**Notes:** <sup>a</sup> The genes related to raffinose hydrolysis are classified into four groups and there are 17 genes, 4 genes, 2 genes, and 3 genes for  $\alpha$ -galactosidase, sucrose phosphorylase,  $\beta$ -fructosidase, and levansucrase, respectively. The genes for  $\alpha$ -galactosidase include La1438 melA, balac\_1601, RafA, aga-SM, agl1, agl2, agl3, aga1, aga2, agaN, agaT, aga-LR, aga36A, melA, aga-LM, aga-F75 and galA17. The genes for sucrose phosphorylase include La1437 GtfA2, ScrP, scrB and scrP. The genes for  $\beta$ -fructosidase include BfrA and bfrA. The genes for levansucrase include ftfA, m1ft and sucZE2. The information for the genes is indicated in Table 1.

<sup>b</sup> There are 286 strains within 177 species, which show negative results for BLASTP search. The species are listed as follows: *Achromobacter xylosoxidans*, *Acidaminococcus* sp., *Acinetobacter junii*, *Acinetobacter radioresistens*, *Actinobacillus pleuropneumoniae*, *Actinobacillus succinogenes*, *Aggregatibacter actinomycetemcomitans*, *Aggregatibacter aphrophilus*, *Akkermansia muciniphila*, *Alistipes putredinis*, *Anaerobaculum hydrogeniformans*, *Anaerococcus hydrogenalis*, *Anaerofustis stercorihominis*, *Anaerotruncus colihominis*, *Arcobacter butzleri*, *Atopobium parvulum*, *Bacillus* sp., *Bacteroides eggerthii*, *Bacteroides pectinophilus*, *Bifidobacterium gallicum*, *Bilophila* sp., *Bilophila wadsworthia*, *Blautia hydrogenotrophica*, *Brachyspira hyodysenteriae*, *Brachyspira intermedia*, *Brachyspira murdochii*, *Bradyrhizobium japonicum*, *Bradyrhizobium* sp., *Butyricoccus pullicaecorum*, *Butyrivibrio crossotus*, *Campylobacter coli*, *Campylobacter* sp., *Campylobacter upsaliensis*, *Capnocytophaga canimorsus*, *Capnocytophaga ochracea*, *Citrobacter freundii*, *Citrobacter* sp., *Clostridiales bacterium*, *Clostridiales butyrate-producing bacterium*, *Clostridiales pectinophilus*, *Clostridium bartlettii*, *Clostridium celatum*, *Clostridium cf. saccharolyticum*, *Clostridium difficile*, *Clostridium hiranonis*, *Clostridium leptum*, *Clostridium methylpentosum*, *Clostridium scindens*, *Clostridium spiroforme*, *Clostridium symbiosum*, *Collinsella aerofaciens*, *Collinsella intestinalis*, *Collinsella stercoris*, *Collinsella tanakaei*, *Coprococcus catus*, *Coralimargarita akajimensis*, *Corynebacterium ammoniagenes*, *Corynebacterium* sp., *Dehalobacter* sp., *Dermabacter* sp., *Desulfitobacterium hafniense*, *Desulfovibrio piger*, *Desulfovibrio* sp., *Dialister succinatiphilus*, *Dorea formicigenerans*, *Dorea longicatena*, *Dysgonomonas mossii*, *Edwardsiella tarda*, *Eggerthella* sp., *Enterobacter aerogenes*, *Enterobacter cancerogenus*, *Enterobacteriaceae bacterium*, *Enterococcus faecalis*, *Enterococcus* sp., *Erysipelatoclostridium ramosum*, *Erysipelotrichaceae bacterium*, *Escherichia fergusonii*, *Escherichia* sp., *Eubacterium bifforme*, *Eubacterium cylindroides*, *Eubacterium dolichum*, *Eubacterium hallii*, *Eubacterium* sp., *Eubacterium ventriosum*, *Finegoldia magna*, *Flavonifractor plautii*, *Fusobacterium gonidiaformans*, *Fusobacterium necrophorum*, *Fusobacterium necrophorum* subsp. *funduliforme*, *Fusobacterium nucleatum* subsp. *vincentii*, *Fusobacterium nucleatum* subsp. *animalis*, *Fusobacterium periodonticum*, *Fusobacterium* sp., *Fusobacterium ulcerans*, *Fusobacterium varium*, *Gordonibacter pamelaeeae*, *Haemophilus ducreyi*, *Haemophilus influenzae*, *Haemophilus parainfluenzae*, *Haemophilus parasuis*, *Haemophilus phage*, *Helicobacter bilis*, *Helicobacter canadensis*, *Helicobacter cinaedi*, *Helicobacter pullorum*, *Helicobacter pylori*, *Helicobacter winghamensis*, *Holdemania filiformis*, *Intestinibacter bartlettii*, *Janthinobacterium* sp., *Lactobacillus amylolyticus*, *Lactobacillus helveticus*, *Lactobacillus* sp., *Lactococcus garvieae*, *Lactococcus lactis* subsp. *lactis*, *Lactococcus phage*, *Lawsonia intracellularis*, *Listeria grayi*, *Listeria innocua*, *Megasphaera elsdenii*, *Methanobrevibacter smithii*, *Moraxella catarrhalis*, *Neisseria macacae*, *Olsenella uli*, *Oscillibacter valericigenes*, *Oxalobacter formigenes*, *Paenisporosarcina* sp., *Parasutterella excrementihominis*, *Parvimonas micra*, *Pasteurella multocida*, *Pasteurella phage*, *Pediococcus acidilactici*, *Peptoclostridium difficile*,

*Phascolarctobacterium succinatutens*, *Phenylobacterium zucineum*, *Porphyromonas asaccharolytica*, *Porphyromonas gingivalis*, *Prevotella oralis*, *Prevotella salivae*, *Propionibacterium* sp., *Proteus mirabilis*, *Proteus penneri*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudoflavonifractor capillosus*, *Pseudomonas putida*, *Pseudomonas* sp., *Ralstonia* sp., *Rothia dentocariosa*, *Rothia mucilaginosa*, *Ruminococcus bromii*, *Ruminococcus lactaris*, *Ruminococcus torques*, *Slackia piriformis*, *Sphingomonas phage*, *Sphingomonas* sp., *Sphingomonas wittichii*, *Sphingopyxis alaskensis*, *Staphylococcus* sp., *Streptococcus anginosus*, *Streptococcus* sp., *Streptomyces* sp., *Succinatimonas hippei*, *Sutterella parvirubra*, *Sutterella wadsworthensis*, *Synergistes* sp., *Treponema brennaborensense*, *Treponema pallidum* subsp. *pallidum*, *Treponema paraluis-cuniculi*, *Treponema pedis*, *Treponema primitia*, *Treponema succinifaciens*, *Tyzzereella nexilis*, *Veillonella* sp. and *Yokenella regensburgei*.

<sup>c</sup> The number of positive strains within the species.

<sup>d</sup> Aga36A and agaN are predicted to exist in 99 strains among the gut bacteria.

Table S3. Raffinose utilization by the selected gut bacteria

Strains	Raffinose utilization
<sup>a</sup> <i>Akkermansia muciniphila</i> FJLHD50M21	-
<sup>a</sup> <i>Akkermansia muciniphila</i> FGDLZ27M202	-
<sup>a</sup> <i>Clostridium butyricum</i> NXYCHL33	+
<sup>b</sup> <i>Bacteroides caccae</i> ELH-2.5MIC3	+
<sup>b</sup> <i>Bacteroides cellulosilyticus</i> ELH-2.5MIC4	+,w
<sup>b</sup> <i>Bacteroides dorei</i> HCK-B6	+
<sup>b</sup> <i>Bacteroides eggerthii</i> HCK-xy6	-
<sup>b</sup> <i>Bacteroides fragilis</i> HCK-B3	+
<sup>b</sup> <i>Bacteroides ovatus</i> HCM-XY1	+
<sup>b</sup> <i>Bacteroides salyersiae</i> ELI-BHI9	+
<sup>b</sup> <i>Bacteroides thetaiotaomicron</i> HCK-B2	+
<sup>b</sup> <i>Bacteroides uniformis</i> HCM-XY15	+
<sup>b</sup> <i>Bacteroides vulgatus</i> HCM-XY3	+
<sup>b</sup> <i>Bacteroides xylanisolvens</i> HCM-XY17	+
<sup>b</sup> <i>Odoribacter splanchnicus</i> ELH-2.5MIC5	-
<sup>b</sup> <i>Parabacteroides distasonis</i> HCM-4h5MIC2	+
<sup>b</sup> <i>Parabacteroides merdae</i> ELI-BHI4	+
<sup>b</sup> <i>Prevotella copri</i> ELH-xy3	+

+, positive utilization; w, weak utilization; -, negative utilization.

<sup>a</sup> The strains were isolated from healthy adult feces by Feng et al (data not published).

<sup>b</sup> The strains were isolated from seven healthy volunteers feces by Tan et al.

### References:

Tan H, Zhao J, Zhang H, et al. Isolation of low-abundant *Bacteroidales* in the human intestine and the analysis of their differential utilization based on plant-derived polysaccharides. *Frontiers in Microbiology*, 2018, 9:1319.