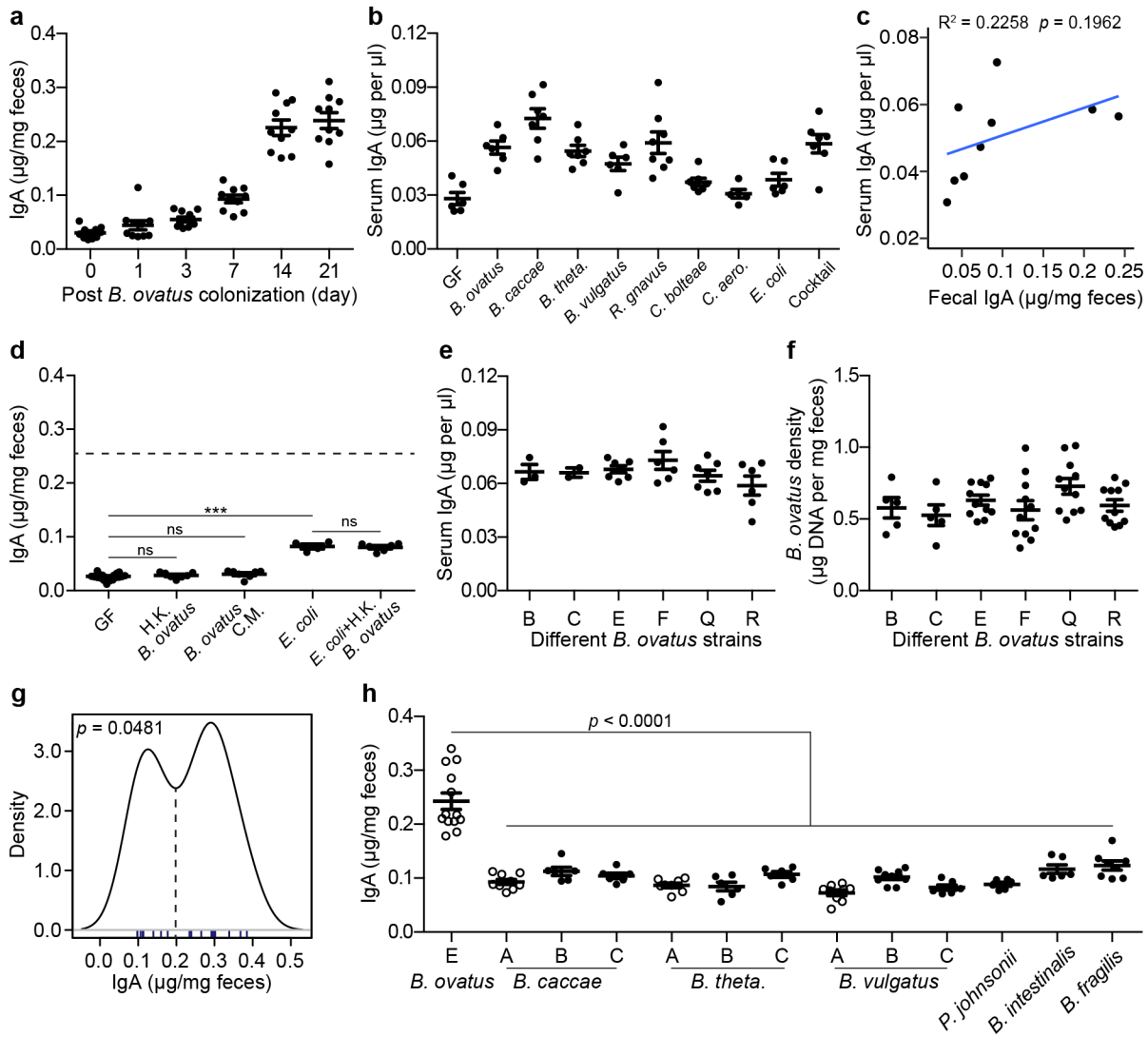


1 **Additional information**

2 **Supplementary figures**



3

4 **Supplementary Fig. 1. More information related to Fig. 1. (a)** Fecal IgA dynamics in

5 gnotobiotic mice after colonization with *B. ovatus* strain E. **(b)** Total serum IgA concentration in

6 gnotobiotic mice that were colonized with individual or a cocktail of eight bacterial species for

7 three weeks. **(c)** Correlation of IgA concentration in stool and serum in mice inoculated with

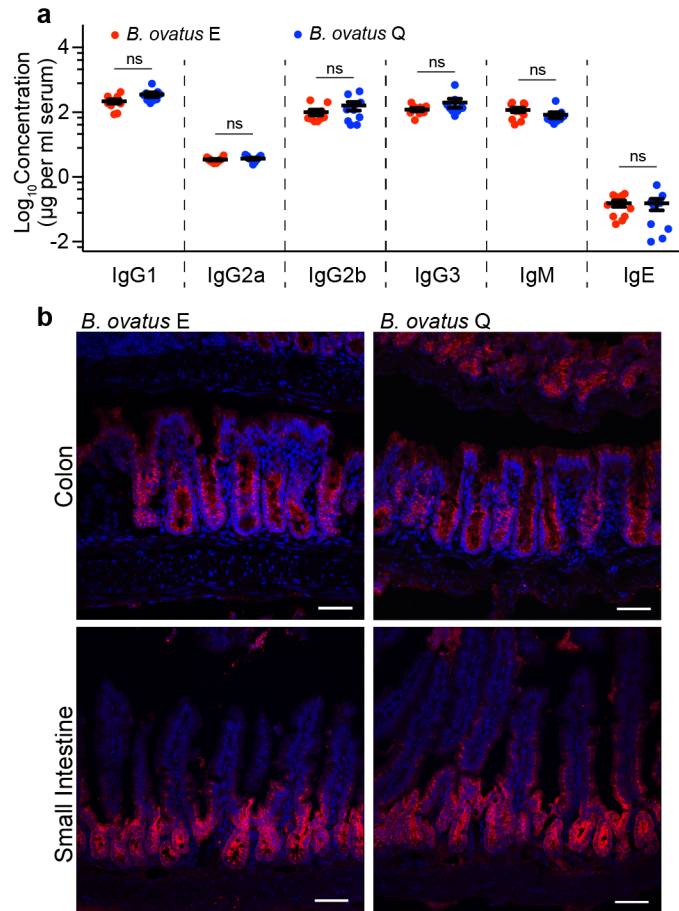
8 different bacterial species. The average concentrations of stool IgA in Fig. 1A and serum IgA in

9 [Supplementary Fig. 1b](#) were used for plotting. **(d)** Fecal IgA concentration in mice treated with

10 either heat-killed (H.K.) *B. ovatus* or *B. ovatus* metabolites. The right part of this plot

11 IgA concentration in *E. coli*-precolonized gnotobiotic mice, which were then treated with H.K.-*B.*
12 *ovatus*. Either metabolites of *B. ovatus* in culture medium or H.K.-*B. ovatus* was used to feed
13 mice, accordingly, for the duration of the experiments. Dot line indicates the average level of
14 stool IgA induced by live *B. ovatus* strain *E.* (e) Total serum IgA level in gnotobiotic mice
15 harboring different strains of *B. ovatus*. (f) *B. ovatus* density in the stool of gnotobiotic mice
16 colonized with different *B. ovatus* strains. (g) Binomial distribution of *B. ovatus* strains IgA
17 induction. (h) Fecal IgA concentration in mice colonized with different strains of *B. caccae*, *B.*
18 *theta.*, *B. vulgatus* and other Bacteroidales, such as *P. johnsonii*, *B. intestinalis* and *B. fragilis*.
19 Data with open circle were replotted from Fig. 1a to facilitate comparison. Data shown are mean
20 \pm standard error of the mean. Each dot represents a biological replicate. Detailed strain
21 information is listed in [Supplementary Tables 1, 2 and 7](#). *p*-values with statistical significance
22 (assessed by two-tailed Student's *t* test) are indicated: ****p* < 0.001; ns, not significant.

23



24

25 **Supplementary Fig. 2. *B. ovatus* strains *E* and *Q* induced comparable levels of serum**

26 **immunoglobulin isotypes and pIgR expression in both small intestine and the colon. (a)**

27 Total serum IgG1, IgG2a, IgG2b, IgG3, IgM and IgE in gnotobiotic mice colonized with either *B.*

28 *ovatus* strain *E* or *Q*. **(b)** Colonic and ileal sections from *B. ovatus* strain *E* or *Q* colonized mice

29 were stained with anti-pIgR (Red) and DAPI (4',6-diamidino-2-phenylindole) (Blue).

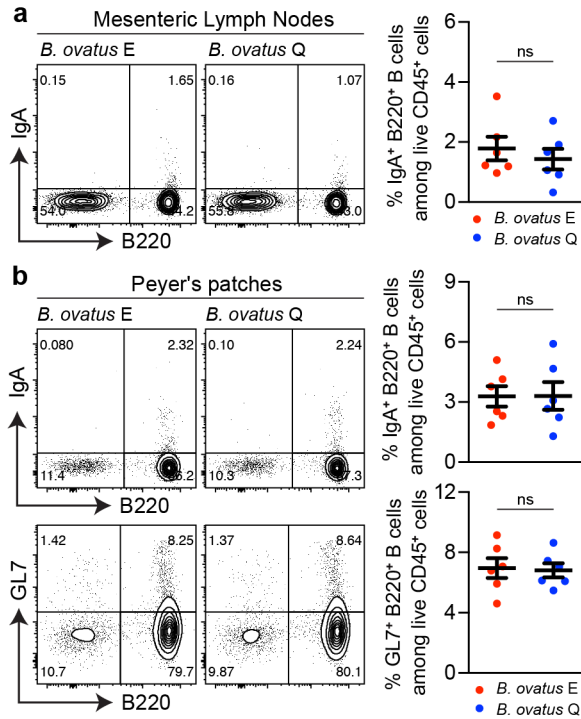
30 Representative images are shown (n = 4-6 mice per group). Scale Bars = 50 µm. Data shown

31 are mean ± standard error of the mean. Each dot represents a biological replicate. *p*-values with

32 statistical significance (assessed by unpaired two-tailed Student's *t* test) are indicated: **p* <

33 0.05; ns, not significant.

34



35

36 **Supplementary Fig. 3. Quantification of IgA⁺B220⁺ B cells in MLNs, PPs in *B. ovatus***

37 **strain *E* or *Q* harboring gnotobiotic mice. (a) Representative flow cytometry plot and**

38 **quantification of IgA⁺ B cells in mesenteric lymph nodes. (b) Representative flow cytometry plot**

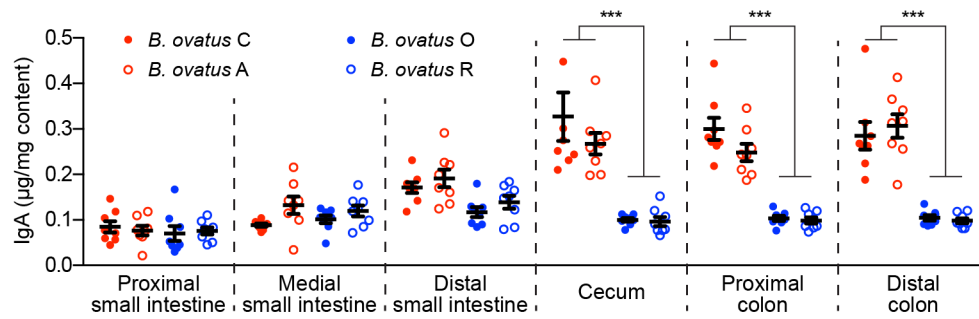
39 **and quantification of IgA⁺ B cell and germinal center B cells (GL7⁺B220⁺) in PPs. Number**

40 **adjacent to gate represents percentage. Data shown are mean ± standard error of the mean.**

41 **Each dot represents an individual mouse. *p*-values with statistical significance (assessed by**

42 **unpaired two-tailed Student's *t* test) are indicated: **p* < 0.05; ns, not significant.**

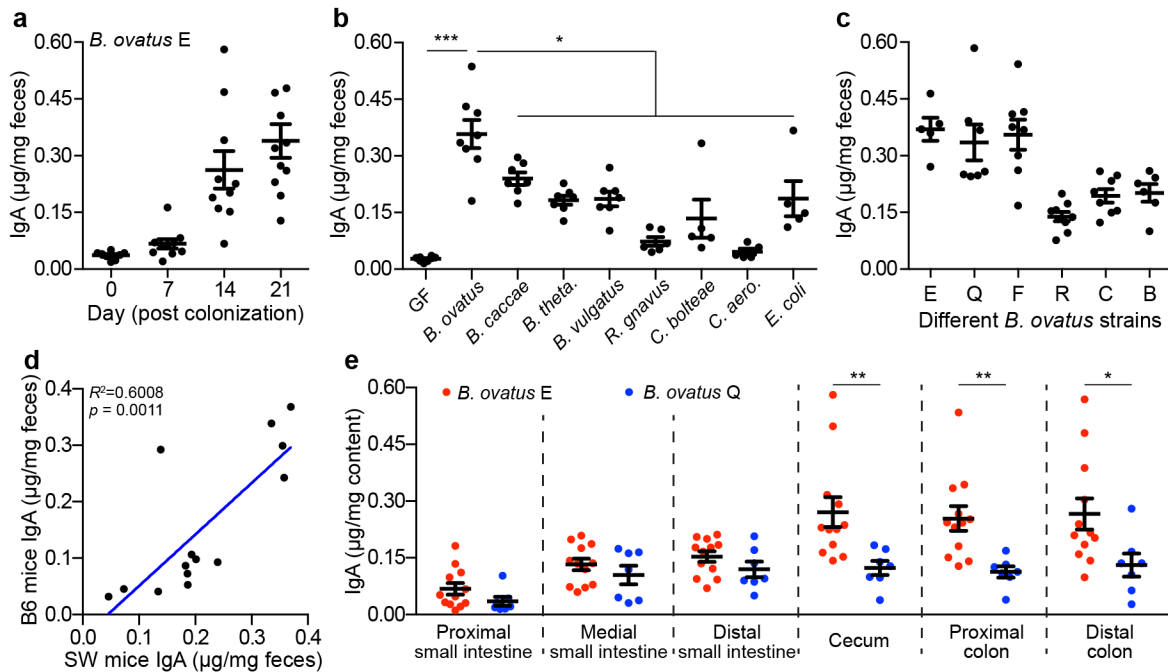
43



44

45 **Supplementary Fig. 4. IgA^{high} *B. ovatus* strains specifically induced more fecal IgA**
 46 **production in the large intestinal regions than IgA^{low} *B. ovatus* strains.** Free IgA
 47 concentration in different regions along the whole intestinal tract of mice that were colonized
 48 with individual *B. ovatus* strains (IgA^{high} *B. ovatus* strains A and C; IgA^{low} *B. ovatus* strains O and
 49 R) for three weeks. Data shown are mean ± standard error of the mean. Each dot represents a
 50 biological replicate. Detailed strain information is listed in [Supplementary Table 2](#). *p*-values with
 51 statistical significance (assessed by unpaired two-tailed Student's *t* test) are indicated: ****p* <
 52 0.001; ns, not significant.

53



54

55 **Supplementary Fig. 5. Host genetic background has little influence on human gut**

56 **bacteria induced fecal IgA production in mice. (a)** Dynamics of fecal IgA concentration in

57 gnotobiotic Swiss Webster mice colonized with *B. ovatus* strain E. **(b) and (c)** Fecal IgA

58 concentration in gnotobiotic Swiss Webster mice colonized with different bacterial species **(b)** or

59 various strains of *B. ovatus* **(c)**. **(d)** Correlation of fecal IgA produced by B6 mice and Swiss

60 Webster mice after the same bacteria colonization. The average fecal IgA level of Swiss

61 Webster mice in **(b)** and **(c)** were plotted against the average fecal IgA level in C57BL6/J mice

62 that were colonized with the same bacterial species or strain from Figure 1A and Figure 1F. **(e)**

63 Luminal IgA concentration along the whole intestine in Swiss Webster mice colonized with either

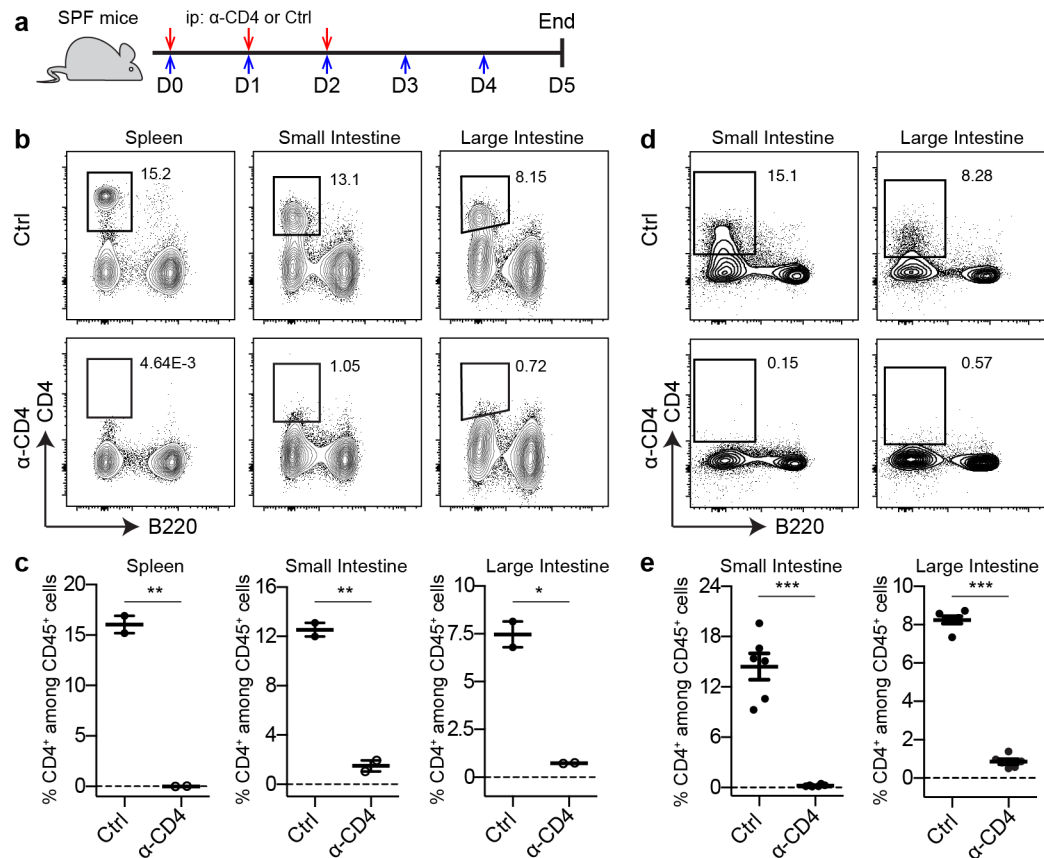
64 *B. ovatus* strains E or Q. Data shown are mean \pm standard error of the mean. Each dot

65 represents a biological replicate in **a**, **b**, **c** and **e**. Detailed strain information is listed in

66 [Supplementary Tables 1 and 2](#). p -values with statistical significance (assessed by two-tailed

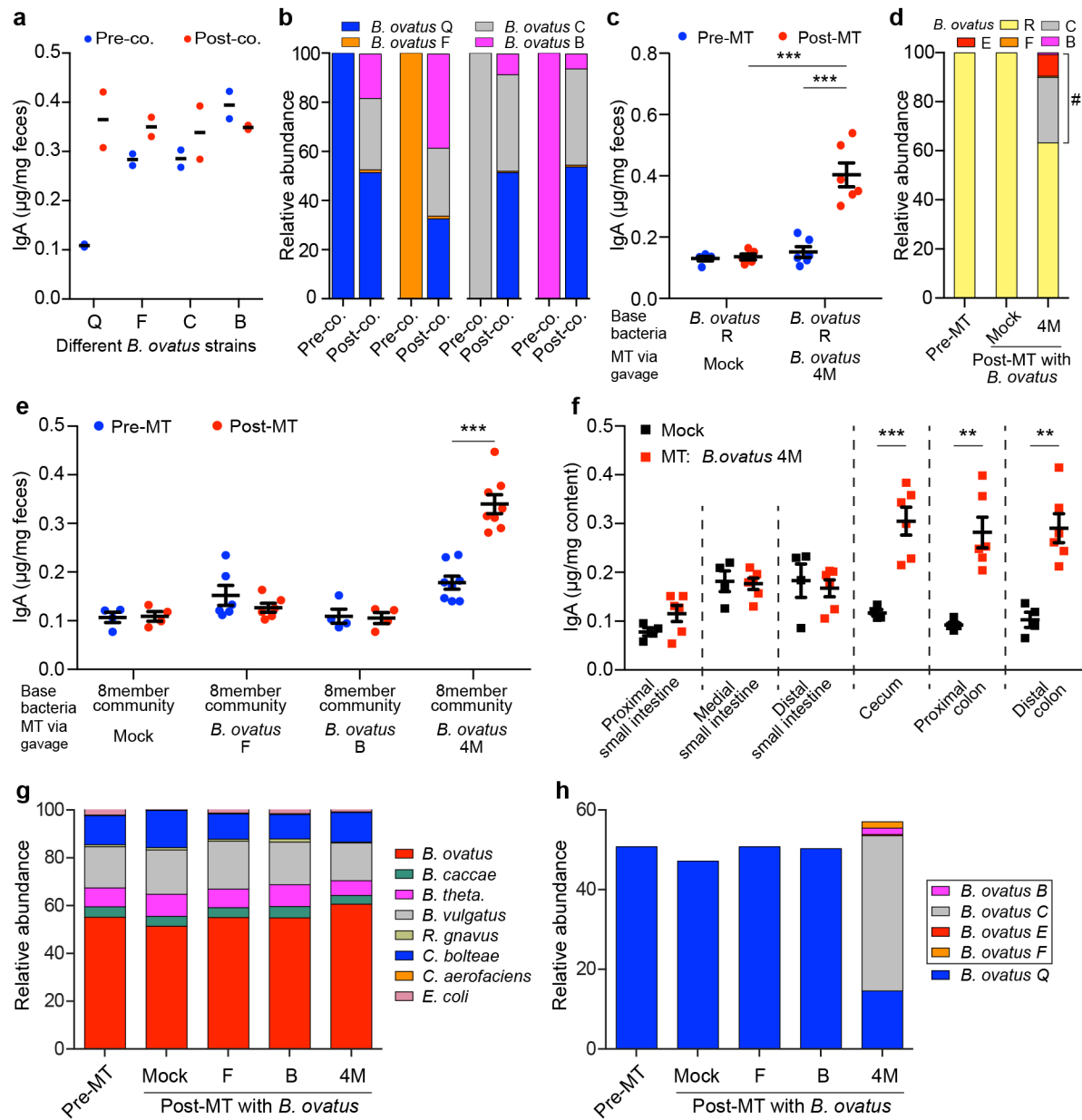
67 Student's t test) are indicated: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; ns, not significant.

68



69

70 **Supplementary Fig. 6. Anti-CD4 antibody promptly and robustly depleted CD4⁺ T cells in**
 71 **multiple organs of mice.** (a) Schematic representation of anti-CD4 antibody injection. Mice
 72 were injected Intraperitoneally with anti-CD4 antibody or isotype control for three consecutive
 73 days (0.5 mg/mouse/day). Two days after the last injection, tissues were collected and
 74 processed. Red arrows indicate antibody injection and blue arrows represent time. (b and c)
 75 Representative flow cytometry plot (b) and quantification (c) of CD4⁺ T cells in the spleen, LP of
 76 small and large intestines in SPF mice. (d and e) Representative flow cytometry plot (d) and
 77 quantification (e) of CD4⁺ T cells in spleen, LP of small and large intestines of gnotobiotic mice
 78 colonized with *B. ovatus* strain *E* with or without anti-CD4 antibody treatment. Number adjacent
 79 to gate represents percentage. Data shown are mean ± standard error of the mean. Each dot
 80 represents a biological replicate. *p*-values with statistical significance (assessed by unpaired
 81 two-tailed Student's *t* test) are indicated: **p* < 0.05, ***p* < 0.01, ****p* < 0.001; ns, not significant.



82

83 **Supplementary Fig. 7. Multiplex cocktail of microbial strains overcome phenotype**

84 **transfer resistance in gnotobiotic mice that were pre-colonized with simple bacterial**

85 **community. (a and b) Fecal IgA concentration (a) and relative abundance of each *B. ovatus***

86 **strain (c) in pre- and post-cohoused gnotobiotic mice. Before cohousing, four groups of mice**

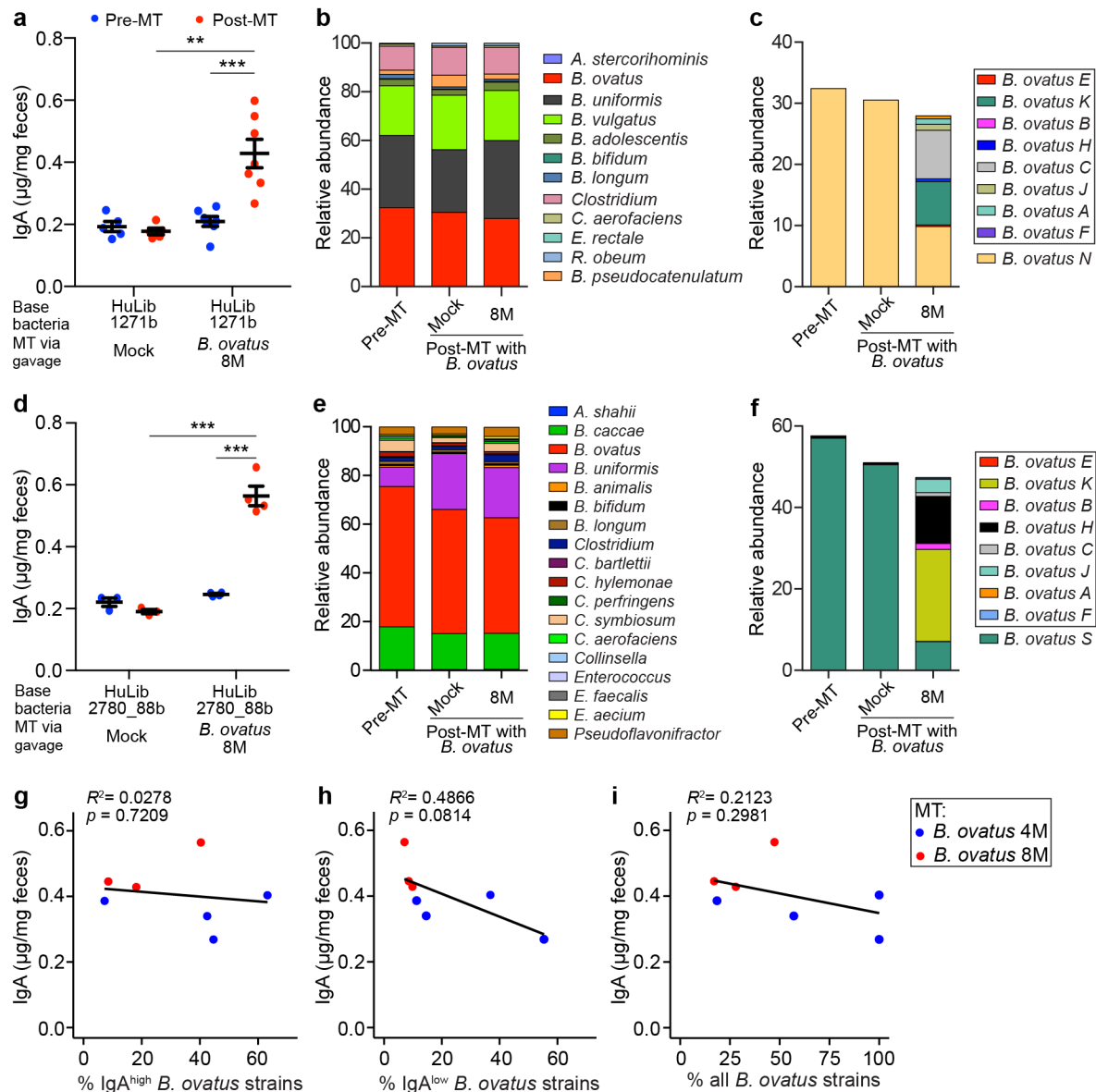
87 **were pre-colonized with four individual *B. ovatus* strains, respectively, for three weeks. Then, all**

88 **mice were cohoused together at a ratio of 1:1:1:1 for another three weeks. (c and d) Fecal IgA**

89 **concentration (c) and relative abundance of each *B. ovatus* strain (d) in mice pre- and post-MT.**

90 Mice were first colonized with *B. ovatus* strain *R* for three weeks. Then the microbial therapeutic
91 cocktail *B. ovatus* 4M was administered. (e) Fecal IgA concentration in mice pre- and post-MT,
92 which were pre-colonized with eight-member bacterial community for three weeks. The
93 microbial therapeutic consisted of either an individual IgA^{high} *B. ovatus* strain or *B. ovatus* 4M. (f)
94 Luminal IgA concentration along the intestinal tract of mice after gavage with Mock or *B. ovatus*
95 4M. (g) Relative abundance of each bacterial species in mice pre- and post-MT. (h) Relative
96 abundance of different *B. ovatus* strains in mice pre- and post-MT. Data shown are mean ±
97 standard error of the mean. Sequencing plots display the average abundance from five mice.
98 Each dot represents a biological replicate. Detailed bacteria information is listed in
99 [Supplementary Tables 2, 4 and 5](#). *p*-values with statistical significance (assessed by two-tailed
100 Student's *t* test) are indicated: ***p* < 0.01, ****p* < 0.001; ns, not significant.

101



102

103 **Supplementary Fig. 8. Robust modification of fecal IgA level with *B. ovatus* therapeutic**

104 **cocktails in gnotobiotic mice that were pre-colonized with microbiota arrayed culture**

105 **collections. (a-f) Fecal IgA concentration (a and d), relative abundance of each bacterial**

106 **species (b and e) and relative abundance of different *B. ovatus* strains (c and f) in gnotobiotic**

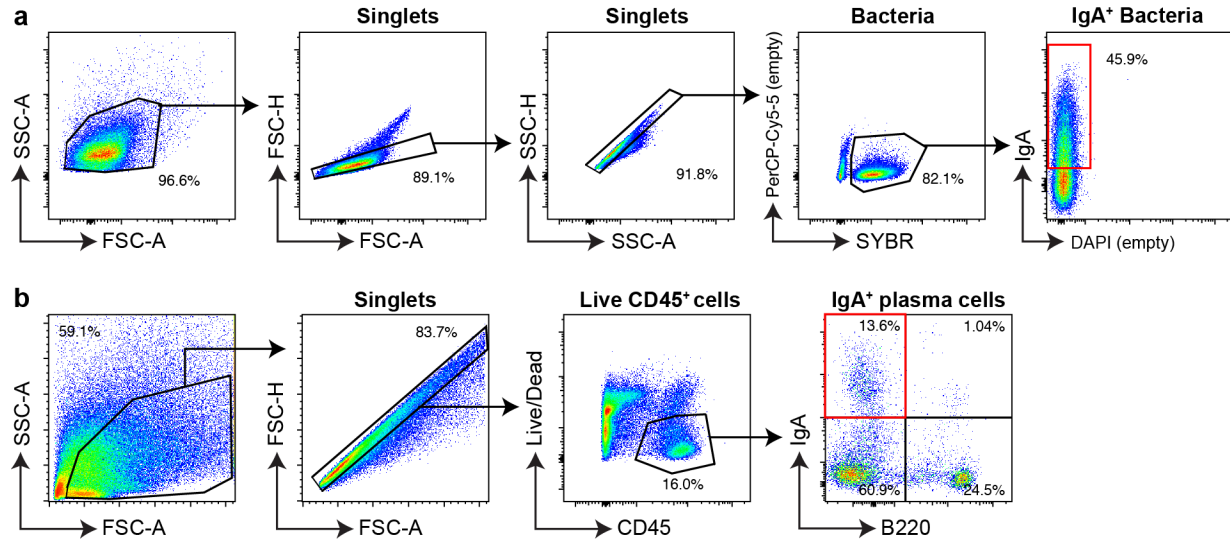
107 **mice pre- and post-MT. Mice were pre-colonized with microbiota arrayed culture collections (a:**

108 **HuLib1271b; d: HuLib2780_88b) for three weeks. Mice were then gavaged with *B. ovatus* 8M.**

109 **(g-i) Correlation between fecal IgA level and relative abundance of IgA^{high} (g), IgA^{low} (h) and**

110 **total *B. ovatus* strains (i). The averages of fecal IgA level and bacteria relative abundance were**

111 used. All mice, being pre-colonized with either single bacterial strain or complex bacterial
112 community for three weeks, were gavaged either *B. ovatus* 4M or *B. ovatus* 8M. In **a** and **d**
113 plots, data shown are mean \pm standard error of the mean and each dot represents a biological
114 replicate. Sequencing plots display the average abundance from three to five mice. Detailed
115 strain information is listed in [Supplementary Tables 4 and 6](#). *p*-values with statistical significance
116 (assessed by two-tailed Student's *t* test) are indicated: **p* < 0.05, ***p* < 0.01, ****p* < 0.001; ns,
117 not significant.
118



119

120 **Supplementary Fig. 9. Representative flow cytometry gating strategies. (a)** IgA-coated

121 bacteria in stool were defined as SYBR⁺IgA⁺. **(b)** IgA-secreting B cells in the LP of small and

122 large intestines were defined as Live CD45⁺IgA⁺B220⁻.

123

124 **Supplementary tables**

125 **Supplementary Table 1. Information for each bacterial strain.**

Phylum	Species	Strain
Bacteroidetes	<i>Bacteroides ovatus</i>	ATCC®8483
Bacteroidetes	<i>Bacteroides caccae</i>	ATCC®43185
Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	ATCC®VPI5482
Bacteroidetes	<i>Bacteroides vulgatus</i>	ATCC®8482
Firmicutes	<i>Ruminococcus gnavus</i>	ATCC®29149
Firmicutes	<i>Clostridium bolteae</i>	ATCC®BAA-613
Actinobacteria	<i>Collinsella aerofaciens</i>	ATCC® 25986
Proteobacteria	<i>Escherichia coli</i>	ATCC®K-12 MG1655

126

127

128 **Supplementary Table 2. Details for different *B. ovatus* strains.**

Phylum	Species	Strain	Strain Abbreviation
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD2780_12_0875_150380_E1	<i>B. ovatus</i> A
Bacteroidetes	<i>Bacteroides ovatus</i>	1001095IJ_161003_A6	<i>B. ovatus</i> B
Bacteroidetes	<i>Bacteroides ovatus</i>	1001283B150210_160208_F9	<i>B. ovatus</i> C
Bacteroidetes	<i>Bacteroides ovatus</i>	1001217B_150727_E1	<i>B. ovatus</i> D
Bacteroidetes	<i>Bacteroides ovatus</i>	ATCC_8483	<i>B. ovatus</i> E
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD3178_07_1175_160815_A10	<i>B. ovatus</i> F
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD3448_08_0949_C3	<i>B. ovatus</i> G
Bacteroidetes	<i>Bacteroides ovatus</i>	1001099B_141217_E5	<i>B. ovatus</i> H
Bacteroidetes	<i>Bacteroides ovatus</i>	1001275B_160808_G11	<i>B. ovatus</i> I
Bacteroidetes	<i>Bacteroides ovatus</i>	1001713B_170207_170306_D4	<i>B. ovatus</i> J
Bacteroidetes	<i>Bacteroides ovatus</i>	J1101437_171009_F12	<i>B. ovatus</i> K
Bacteroidetes	<i>Bacteroides ovatus</i>	1001302B_F3	<i>B. ovatus</i> L
Bacteroidetes	<i>Bacteroides ovatus</i>	1001136B_E5	<i>B. ovatus</i> M
Bacteroidetes	<i>Bacteroides ovatus</i>	1001271B_150615_H2	<i>B. ovatus</i> N
Bacteroidetes	<i>Bacteroides ovatus</i>	1001262B_160229_F6	<i>B. ovatus</i> O
Bacteroidetes	<i>Bacteroides ovatus</i>	1001175B_160314_D1	<i>B. ovatus</i> P
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD2780_06_1687_150420_H2	<i>B. ovatus</i> Q
Bacteroidetes	<i>Bacteroides ovatus</i>	1001254J_160919_B1	<i>B. ovatus</i> R
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD2780_06_1688b_171218_A7	<i>B. ovatus</i> S

129

130

131 **Supplementary Table 3. % dissimilarity of genomic DNA sequences amongst various *B.***
 132 ***ovatus* strains.**

		Different <i>B. ovatus</i> strains																		
		D	B	L	K	A	R	O	J	N	P	Q	E	S	F	M	I	C	G	H
Different <i>B. ovatus</i> strains	D	0.00	0.83	0.85	0.73	0.72	0.72	0.73	0.73	0.74	0.74	0.74	0.74	0.74	0.70	0.73	0.73	0.73	0.74	0.74
	B	0.83	0.00	0.47	0.61	0.62	0.62	0.61	0.72	0.69	0.68	0.68	0.71	0.71	0.73	0.73	0.71	0.72	0.73	0.73
	L	0.85	0.47	0.00	0.67	0.67	0.63	0.64	0.68	0.69	0.70	0.70	0.71	0.70	0.73	0.71	0.72	0.73	0.73	0.72
	K	0.73	0.61	0.67	0.00	0.40	0.39	0.38	0.52	0.46	0.45	0.45	0.46	0.47	0.47	0.49	0.47	0.47	0.47	0.48
	A	0.72	0.62	0.67	0.40	0.00	0.33	0.33	0.52	0.48	0.47	0.48	0.50	0.49	0.48	0.52	0.49	0.49	0.49	0.49
	R	0.72	0.62	0.63	0.39	0.33	0.00	0.03	0.50	0.46	0.47	0.47	0.50	0.48	0.48	0.52	0.50	0.51	0.51	0.52
	O	0.73	0.61	0.64	0.38	0.33	0.03	0.00	0.51	0.46	0.46	0.46	0.49	0.49	0.47	0.51	0.49	0.50	0.51	0.51
	J	0.73	0.72	0.68	0.52	0.52	0.50	0.51	0.00	0.32	0.31	0.32	0.30	0.30	0.49	0.49	0.48	0.49	0.47	0.48
	N	0.74	0.69	0.69	0.46	0.48	0.46	0.46	0.32	0.00	0.09	0.09	0.27	0.29	0.46	0.42	0.40	0.43	0.43	0.44
	P	0.74	0.68	0.70	0.45	0.47	0.47	0.46	0.31	0.09	0.00	0.05	0.25	0.26	0.46	0.43	0.41	0.42	0.42	0.42
	Q	0.74	0.68	0.70	0.45	0.48	0.47	0.46	0.32	0.09	0.05	0.00	0.25	0.27	0.46	0.43	0.41	0.42	0.42	0.43
	E	0.74	0.71	0.71	0.46	0.50	0.50	0.49	0.30	0.27	0.25	0.25	0.00	0.12	0.44	0.43	0.42	0.42	0.42	0.43
	S	0.74	0.71	0.70	0.47	0.49	0.48	0.49	0.30	0.29	0.26	0.27	0.12	0.00	0.46	0.45	0.45	0.44	0.43	0.43
	F	0.70	0.73	0.73	0.47	0.48	0.48	0.47	0.49	0.46	0.46	0.46	0.44	0.46	0.00	0.40	0.41	0.41	0.40	0.41
	M	0.73	0.73	0.71	0.49	0.52	0.52	0.51	0.49	0.42	0.43	0.43	0.43	0.45	0.40	0.00	0.19	0.21	0.20	0.20
	I	0.73	0.71	0.72	0.47	0.49	0.50	0.49	0.48	0.40	0.41	0.41	0.42	0.45	0.41	0.19	0.00	0.11	0.11	0.11
	C	0.73	0.72	0.73	0.47	0.49	0.51	0.50	0.49	0.43	0.42	0.42	0.42	0.44	0.41	0.21	0.11	0.00	0.11	0.10
G	0.74	0.73	0.73	0.47	0.49	0.51	0.51	0.47	0.43	0.42	0.42	0.42	0.43	0.40	0.20	0.11	0.11	0.00	0.07	
H	0.74	0.73	0.72	0.48	0.49	0.52	0.51	0.48	0.44	0.42	0.43	0.43	0.43	0.41	0.20	0.11	0.10	0.07	0.00	

133

134

135 **Supplementary Table 4. Multiplex cocktails of *B. ovatus* strains used in MT.**

Cocktail name	Strain
<i>B. ovatus</i> 4M	<i>B. ovatus B</i>
	<i>B. ovatus C</i>
	<i>B. ovatus E</i>
	<i>B. ovatus F</i>
<i>B. ovatus</i> 8M	<i>B. ovatus B</i>
	<i>B. ovatus C</i>
	<i>B. ovatus E</i>
	<i>B. ovatus F</i>
	<i>B. ovatus A</i>
	<i>B. ovatus H</i>
	<i>B. ovatus J</i>
	<i>B. ovatus K</i>

136

137

138 **Supplementary Table 5. Bacterial strains in synthetic cocktail of diverse bacterial species**
 139 **(8member community).**

Phylum	Species	Strain	Strain Abbreviation
Bacteroidetes	<i>Bacteroides ovatus</i>	BSD2780_06_1687_150420_H2	<i>B. ovatus</i> Q
Bacteroidetes	<i>Bacteroides caccae</i>	ATCC®43185	<i>B. caccae</i>
Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	ATCC®VPI5482	<i>B. theta.</i>
Bacteroidetes	<i>Bacteroides vulgatus</i>	ATCC®8482	<i>B. vulgatus</i>
Firmicutes	<i>Ruminococcus gnavus</i>	ATCC®29149	<i>R. gnavus</i>
Firmicutes	<i>Clostridium bolteae</i>	ATCC®BAA-613	<i>C. bolteae</i>
Actinobacteria	<i>Collinsella aerofaciens</i>	ATCC® 25986	<i>C. aero.</i>
Proteobacteria	<i>Escherichia coli</i>	ATCC®K-12 MG1655	<i>E. coli</i>

140

141

142 **Supplementary Table 6. Bacterial composition in different microbiota arrayed culture**
 143 **collections.**

Library Name	Phylum	Species	Strain	Strain Abbreviation	
HuLib1175B	Bacteroidetes	<i>Bacteroides eggerthii</i>	1001175st1_B5_1001175B_160314	<i>B. eggerthii</i>	
	Bacteroidetes	<i>Bacteroides fragilis</i>	1001175st1_C3_1001175B_160314	<i>B. fragilis</i>	
	Bacteroidetes	<i>Bacteroides intestinalis</i>	1001175st1_A4_1001175B_160314	<i>B. intestinalis</i>	
	Bacteroidetes	<i>Bacteroides ovatus</i>	1001175st1_E11_1001175B_160314	<i>B. ovatus</i>	
	Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	1001175st1_E5_1001175B_160314	<i>B. theta.</i>	
	Bacteroidetes	<i>Bacteroides uniformis</i>	1001175st1_F6_1001175B_160314	<i>B. uniformis</i>	
	Bacteroidetes	<i>Bacteroides vulgatus</i>	1001175st1_C6_1001175B_160314	<i>B. vulgatus</i>	
	Actinobacteria	<i>Bifidobacterium longum</i>	1001175st1_G10_1001175B_160314	<i>B. longum</i>	
	Firmicutes	<i>Clostridium 1001175sp1</i>	1001175st1_A10_1001175B_160314	<i>Clostridium</i>	
	Firmicutes	<i>Clostridium clostridioforme</i>	1001175st1_C5_1001175B_160314	<i>C. clostridioforme</i>	
	Firmicutes	<i>Clostridium perfringens</i>	1001175st1_F9_1001175B_160314	<i>C. perfringens</i>	
	Firmicutes	<i>Dorea longicatena</i>	1001175st1_H1_1001175B_160314	<i>D. longicatena</i>	
	Firmicutes	<i>Enterococcus avium</i>	1001175st1_D6_1001175B_160314	<i>E. avium</i>	
	Proteobacteria	<i>Escherichia coli</i>	1001175st1_F3_1001175B_160314	<i>E. coli</i> F3	
	Proteobacteria	<i>Escherichia coli</i>	1001175st2_F4_1001175B_160314	<i>E. coli</i> F4	
	Proteobacteria	<i>Escherichia coli</i>	1001175st3_A2_1001175B_160314	<i>E. coli</i> A2	
	Firmicutes	<i>Lachnospiraceae 1001136sp1</i>	1001175st1_C9_1001175B_160314	<i>Lachnospiraceae</i>	
	Firmicutes	<i>Lactobacillus 1001175sp1</i>	1001175st1_D8_1001175B_160314	<i>Lactobacillus</i>	
	Bacteroidetes	<i>Parabacteroides merdae</i>	1001175st1_A1_1001175B_160314	<i>P. merdae</i>	
	Firmicutes	<i>Roseburia 1001271sp1</i>	1001175st1_E3_1001175B_160314	<i>Roseburia</i>	
	Firmicutes	<i>Ruminococcus 1001175sp1</i>	1001175st1_E1_1001175B_160314	<i>Ruminococcus</i>	
	Firmicutes	<i>Streptococcus 1001175sp1</i>	1001175st1_H6_1001175B_160314	<i>Streptococcus</i> H6	
	Firmicutes	<i>Streptococcus 1001283sp2</i>	1001175st1_H3_1001175B_160314	<i>Streptococcus</i> H3	
	Firmicutes	<i>Streptococcus anginosus</i>	1001175st1_H11_1001175B_160314	<i>S. anginosus</i>	
	HuLib1271b	Firmicutes	<i>Anaerofustis stercorihominis</i>	1001271st1_D3_1001271B_150615	<i>A. stercorihominis</i>
		Bacteroidetes	<i>Bacteroides ovatus</i>	1001271st1_H2_1001271B_150615	<i>B. ovatus</i>
		Bacteroidetes	<i>Bacteroides uniformis</i>	1001271st1_A10_1001271B_150615	<i>B. uniformis</i>
		Bacteroidetes	<i>Bacteroides vulgatus</i>	1001271st1_G7_1001271B_150615	<i>B. vulgatus</i>
		Actinobacteria	<i>Bifidobacterium adolescentis</i>	1001271st1_A4_1001271B_150615	<i>B. adolescentis</i>
		Actinobacteria	<i>Bifidobacterium bifidum</i>	1001271st1_H11_1001271B_150615	<i>B. bifidum</i>
		Actinobacteria	<i>Bifidobacterium longum</i>	1001271st1_B4_1001271B_150615	<i>B. longum</i>
		Actinobacteria	<i>Bifidobacterium pseudocatenulatum</i>	1001271st1_F3_1001271B_150615	<i>B. pseudocatenulatum</i>
Firmicutes		<i>Clostridium 1001271sp1</i>	1001271st1_H5_1001271B_150615	<i>Clostridium</i>	
Actinobacteria		<i>Collinsella aerofaciens</i>	1001271st1_C3_1001271B_150615	<i>C. aerofaciens</i>	
Firmicutes		<i>Eubacterium rectale</i>	1001271st1_F12_1001271B_150615	<i>E. rectale</i>	
Firmicutes		<i>Ruminococcus obeum</i>	1001271st1_E5_1001271B_150615	<i>R. obeum</i>	
HuLib2780_88b	Bacteroidetes	<i>Alistipes shahii</i>	BSD2780061688st1_A10_BSD2780061688b_171218	<i>A. shahii</i>	
	Bacteroidetes	<i>Bacteroides caccae</i>	BSD2780061689st1_A4_BSD2780061688b_171218	<i>B. caccae</i>	
	Bacteroidetes	<i>Bacteroides ovatus</i>	BSD2780061688st1_C6_BSD2780061688b_171218	<i>B. ovatus</i>	
	Bacteroidetes	<i>Bacteroides uniformis</i>	BSD2780061689st1_G7_BSD2780061688b_171218	<i>B. uniformis</i>	
	Actinobacteria	<i>Bifidobacterium animalis</i>	BSD2780061688st1_E5_BSD2780061688b_171218	<i>B. animalis</i>	
	Actinobacteria	<i>Bifidobacterium bifidum</i>	BSD2780061688st1_G1_BSD2780061688b_171218	<i>B. bifidum</i>	
	Actinobacteria	<i>Bifidobacterium longum</i>	BSD2780061688st2_H1_BSD2780061688b_171218	<i>B. longum</i>	
	Firmicutes	<i>Clostridium BSD2780061688sp2</i>	BSD2780061688st1_H5_BSD2780061688b_171218	<i>Clostridium</i> E5	
	Firmicutes	<i>Clostridium BSD2780061688sp3</i>	BSD2780061688st1_E8_BSD2780061688b_171218	<i>Clostridium</i> E8	
	Firmicutes	<i>Clostridium bartlettii</i>	BSD2780061688st1_A9_BSD2780061688b_171218	<i>C. bartlettii</i>	
	Firmicutes	<i>Clostridium hylemonae</i>	BSD2780061688st1_A6_BSD2780061688b_171218	<i>C. hylemonae</i>	
	Firmicutes	<i>Clostridium perfringens</i>	BSD2780061688st3_G3_BSD2780061688b_171218	<i>C. perfringens</i>	
	Firmicutes	<i>Clostridium symbiosum</i>	BSD2780061688st1_G6_BSD2780061688b_171218	<i>C. symbiosum</i>	
	Actinobacteria	<i>Collinsella aerofaciens</i>	BSD2780061688st1_F5_BSD2780061688b_171218	<i>C. aerofaciens</i>	
	Actinobacteria	<i>Collinsella species</i>	BSD2780061688st1_H8_BSD2780061688b_171218	<i>C. species</i>	
	Firmicutes	<i>Enterococcus 1001136sp1</i>	BSD2780061688st2_D3_BSD2780061688b_171218	<i>Enterococcus</i>	
	Firmicutes	<i>Enterococcus faecalis</i>	BSD2780061688st3_G10_BSD2780061688b_171218	<i>E. faecalis</i>	
	Firmicutes	<i>Enterococcus faecium</i>	BSD2780061688st2_C8_BSD2780061688b_171218	<i>E. faecium</i>	
Firmicutes	<i>Pseudoflavonifractor BSD2780061688sp1</i>	BSD2780061688st1_E11_BSD2780061688b_171218	<i>Pseudoflavonifractor</i>		

144

145

146 **Supplementary Table 7. Detailed information about various bacterial strains.**

Phylum	Species	Strain	Strain Abbreviation
Bacteroidetes	<i>Bacteroides ovatus</i>	ATCC®8483	<i>B. ovatus E</i>
Bacteroidetes	<i>Bacteroides caccae</i>	ATCC®43185	<i>B. caccae A</i>
Bacteroidetes	<i>Bacteroides caccae</i>	1001285I_161205_F12	<i>B. caccae B</i>
Bacteroidetes	<i>Bacteroides caccae</i>	BSD3178_07_1176_160815_A7	<i>B. caccae C</i>
Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	ATCC®VPI5482	<i>B. theta. A</i>
Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	BSD2780_12_0875b_A6	<i>B. theta. B</i>
Bacteroidetes	<i>Bacteroides thetaiotaomicron</i>	BSD2780_06_1689_150309_F9	<i>B. theta. C</i>
Bacteroidetes	<i>Bacteroides vulgatus</i>	ATCC®8482	<i>B. vulgatus A</i>
Bacteroidetes	<i>Bacteroides vulgatus</i>	BSD2780_12_0874b_170522_A7	<i>B. vulgatus B</i>
Bacteroidetes	<i>Bacteroides vulgatus</i>	1001271B_150615_G7	<i>B. vulgatus C</i>
Bacteroidetes	<i>Parabacteroides johnsonii</i>	DSMZ_18315	<i>P. johnsonii</i>
Bacteroidetes	<i>Bacteroides intestinalis</i>	DSMZ_17393	<i>B. intestinalis</i>
Bacteroidetes	<i>Bacteroides fragilis</i>	J1001437_171009_C3	<i>B. fragilis</i>

147

148