

## Supplementary Material

### Integrated metagenomics identifies a crucial role for trimethylamine-producing *Lachnoclostridium* in promoting atherosclerosis

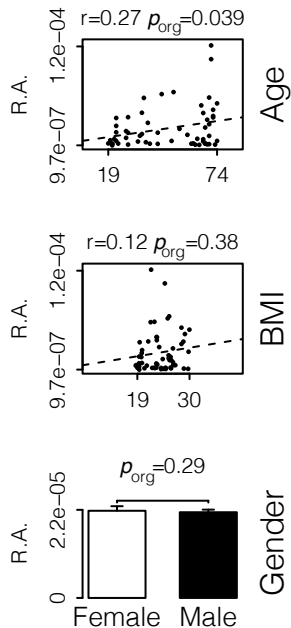
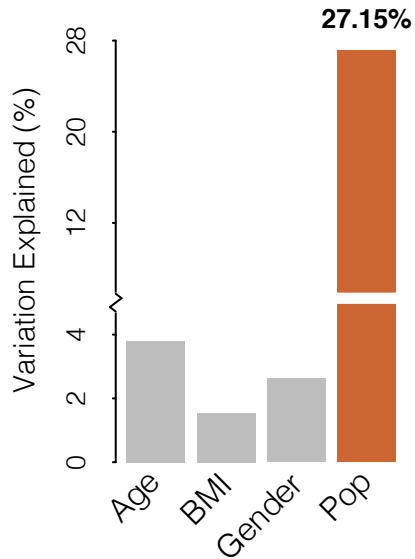
Yuan-Yuan Cai <sup>ab#</sup>, Feng-Qing Huang <sup>b#</sup>, Xingzhen Lao <sup>a</sup>, Yawen Lu <sup>b</sup>, Xuejiao Gao <sup>c</sup>, Raphael N. Alolga <sup>b</sup>, Kunpeng Yin <sup>b</sup>, Xingchen Zhou<sup>a</sup>, Yun Wang <sup>a</sup>, Baolin Liu <sup>b</sup>, Jing Shang <sup>b\*</sup>, Lian-Wen Qi <sup>b\*</sup>, Jing Li <sup>abd\*</sup>

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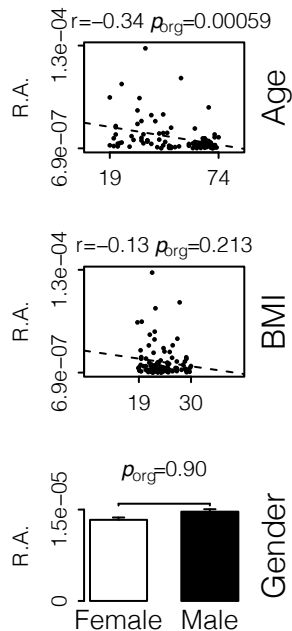
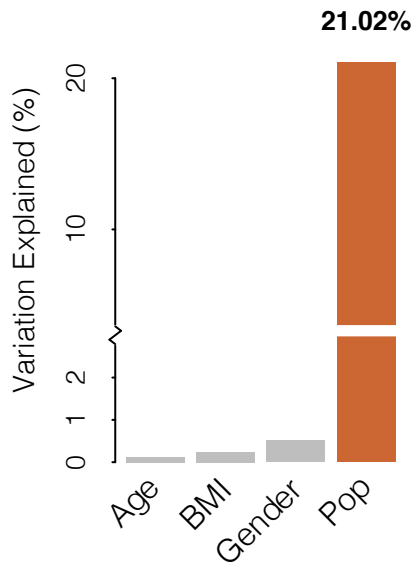
\*corresponding author: Jing Li, e-mail: lijing@cpu.edu.cn; Lian-Wen Qi, e-mail: Qilw@cpu.edu.cn; or Jing Shang, e-mail: shangjing21cn@163.com.

#These authors contributed equally to this work.

a.

***cntA***

b.

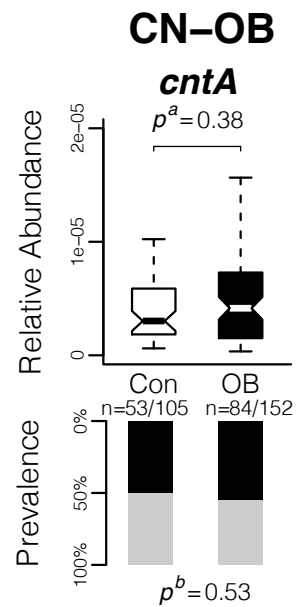
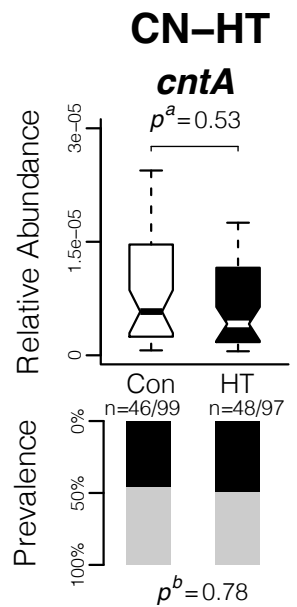
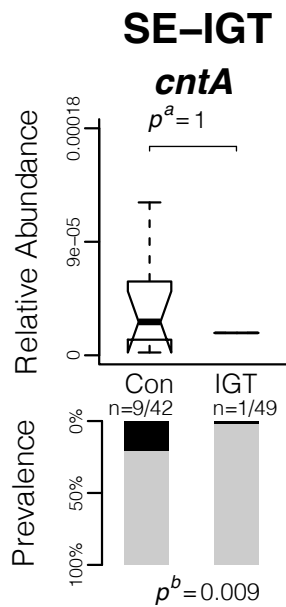
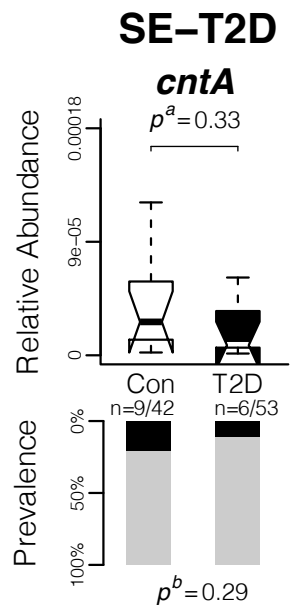
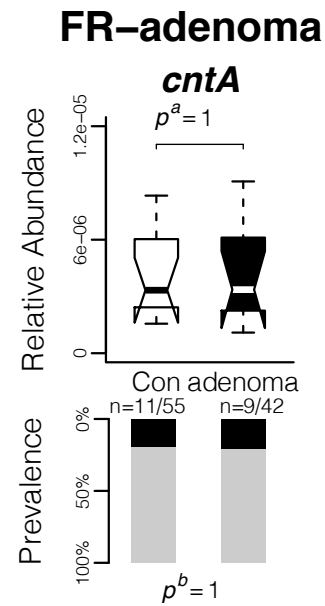
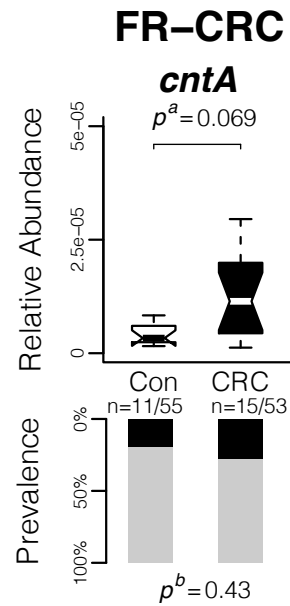
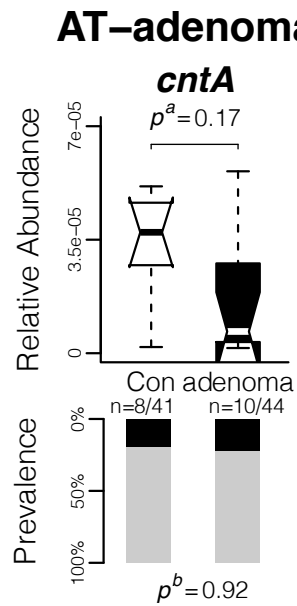
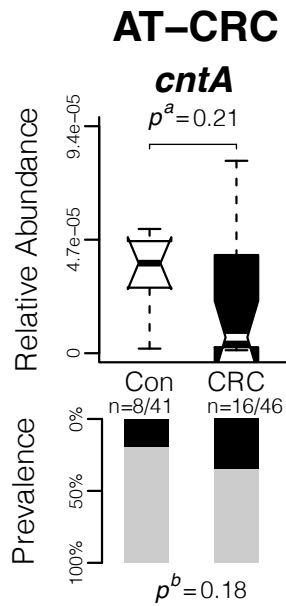
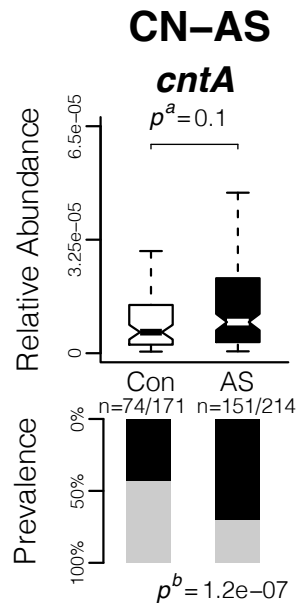
***cutC***

17 **Figure 1.** Multivariate analysis of covariance of *cntA* (**a**) and *cutC* (**b**) based on public  
18 metagenomes. Barplots show the sequence relative abundances against binary variables (i.e.  
19 gender), Error bars denote the means  $\pm$  s.e.m.  $p_{\text{org}}$  indicates the significance conducted by Mann-  
20 Whitney-Wilcoxon test; scatterplots indicate the pearson correlation between sequence relative  
21 abundances and continuous variables (i.e. age and BMI),  $p_{\text{org}}$  indicates the correlation significance.

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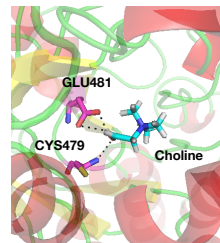
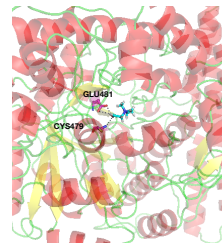
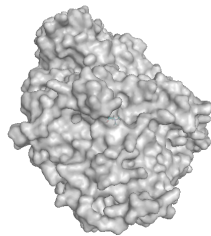
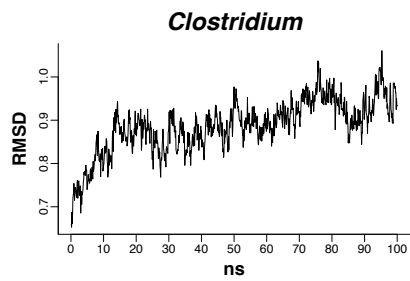
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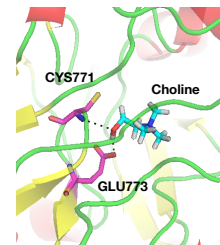
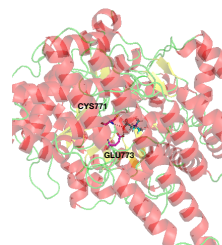
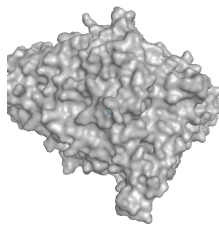
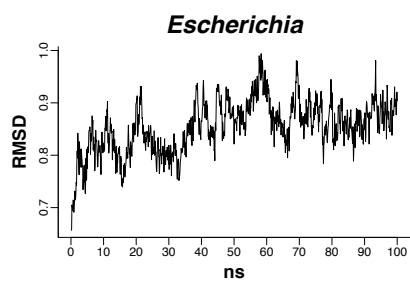
25 **Figure 2.** Relative abundance distribution of *cntA* in multiple case- control cohorts in the upper  
26 panel. Significant differences were conducted by Mann-Whitney-Wilcoxon test ( $p^a$ ). The bounds  
27 denote the interquartile range between the first and third quartiles and the center line denotes the  
28 median. The whiskers denote the lowest and highest value. Bar plots in the lower panel show the  
29 prevalence difference in multiple case-control cohorts. Significant differences were conducted by  
30 Chi-squared test ( $p^b$ ). CN-AS: atherosclerosis from China; AT-CRC: colorectal cancer from  
31 Austria; AT-adenoma: adenoma from Austria; FR-CRC: colorectal cancer from France; FR-  
32 adenoma: adenoma from France; SE-T2D: type 2 diabetes from Sweden; SE-IGT: impaired  
33 glucose tolerance from Sweden; CN-HT: hypertension from China; CN-OB: obesity from China.

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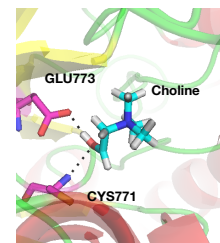
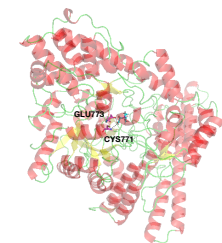
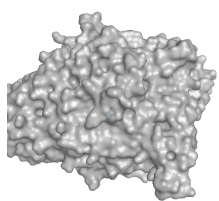
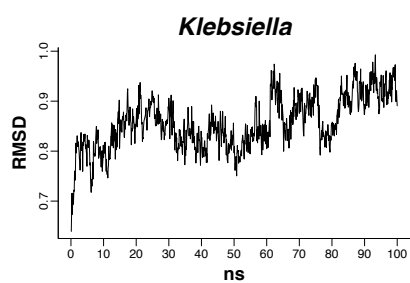
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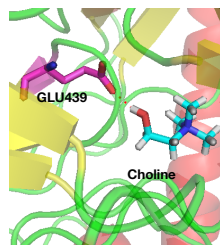
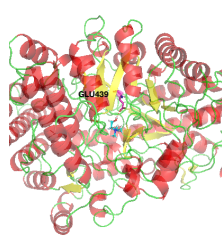
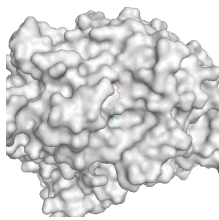
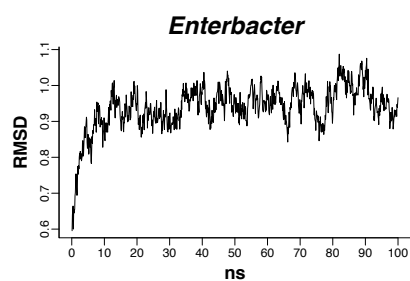
$E(\text{cutC}^{\text{Clostridium}}\text{-choline}) = -4.82 \text{ kcal/mol}$



$E(\text{cutC}^{\text{Escherichia}}\text{-choline}) = -4.87 \text{ kcal/mol}$



$E(\text{cutC}^{\text{Klebsiella}}\text{-choline}) = -4.88 \text{ kcal/mol}$



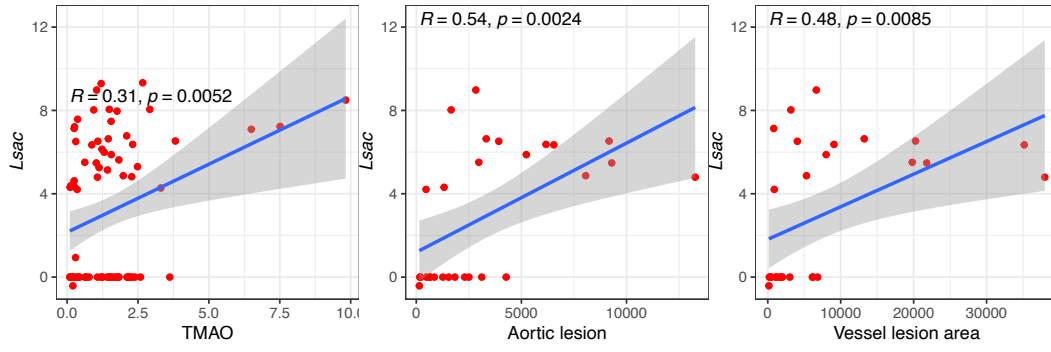
$E(\text{cutC}^{\text{Enterbacter}}\text{-choline}) = -4.34 \text{ kcal/mol}$

36 **Figure 3.** Molecular docking of the other 4 most abundant candidate TMA-producing genera and  
37 choline. The binding pockets are shown in the left panel of the figure, the active binding site on  
38 the macromolecular protein has been marked in bold, and the intermolecular hydrogen bond is  
39 shown by the black dotted line. Amber16 was used to calculate the dynamic changes within 100  
40 ns of the combined compound, and its RMSD is shown in the right column.

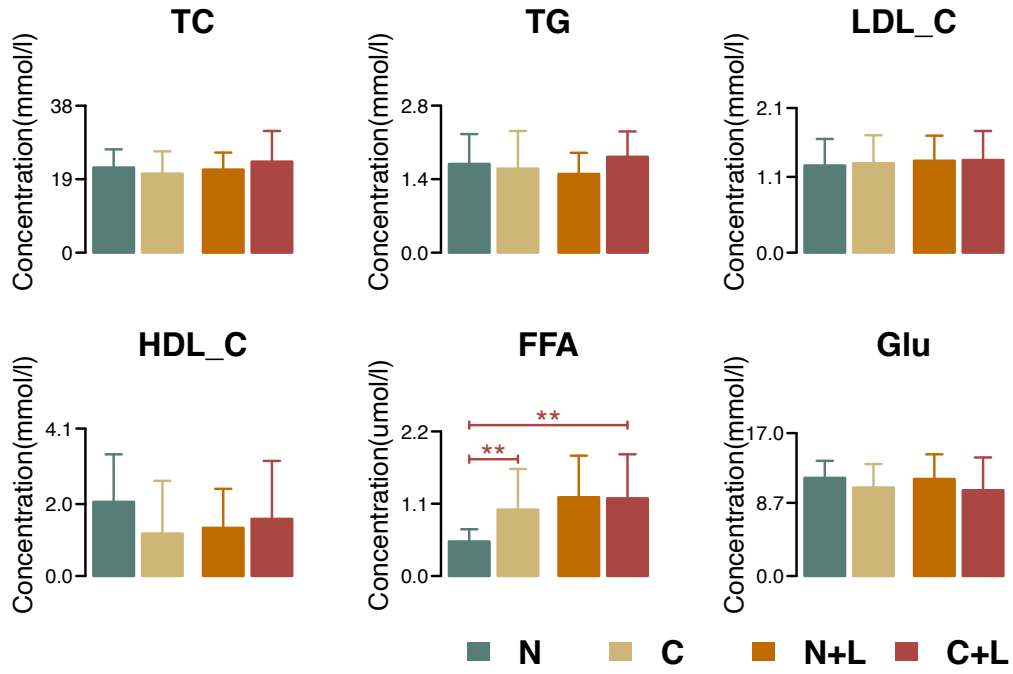
41

42

**a.**



**b.**



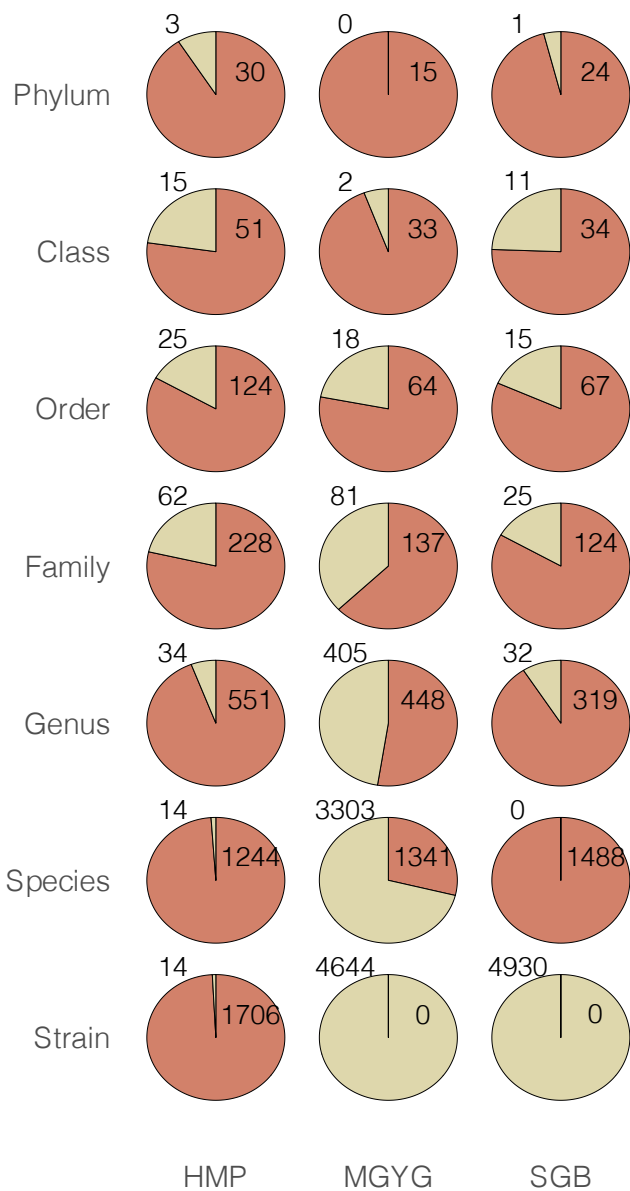


43 **Figure 4.** The effect of *L. saccharolyticum* on atherosclerosis in *ApoE<sup>-/-</sup>* mice. **(a)** Pearson  
44 correlation analysis between the level of *L. saccharolyticum* in feces and TMAO level in serum,  
45 aortic lesion and vessel lesion area. **(b)** Barplots show the concentration of glucose (Glu), non-  
46 esterified free fatty acids (FFA), triglycerides (TG), total cholesterol (TC), low-density lipoprotein  
47 (LDL\_C), and high-density lipoprotein (HDL\_C). Error bars denote the means  $\pm$  SEM. \*  $p < 0.05$ ,  
48 \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , the differences among groups were analyzed by single-factor ANOVA  
49 corrected with Tukey HSD test. N: normal group, mice fed with standard chow control diet and  
50 gavaged with the sterile medium; N+L: normal + *L.saccharolyticum* group, mice fed standard  
51 chow and gavaged live *L.saccharolyticum* at a dose of  $5 \times 10^8$  CFUs/100  $\mu$ l; C: choline group,  
52 mice fed with standard chow supplemented with 1.0% choline (Sigma-Aldrich, USA) and gavaged  
53 with the sterile medium; C+L: choline + *L.saccharolyticum* group, mice fed with standard chow  
54 supplemented with 1.0% choline and gavaged with live *L.saccharolyticum* at a dose of  $5 \times 10^8$   
55 CFUs/100  $\mu$ l.

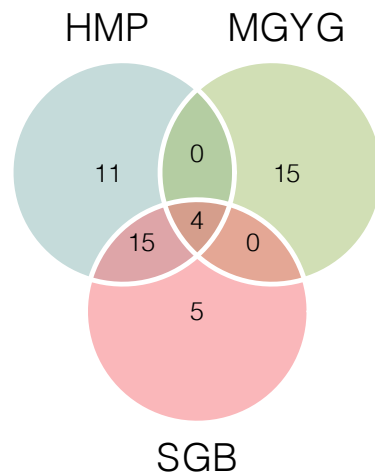
56

Defined Undefined

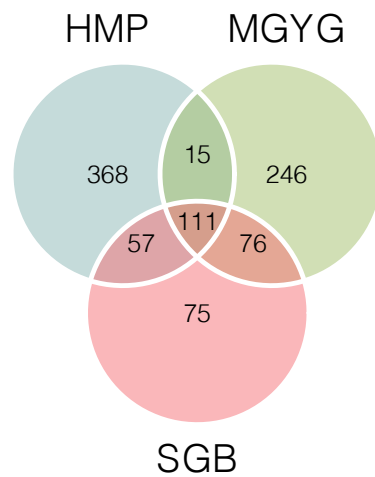
a.



b. Phylum:



c. Genus:



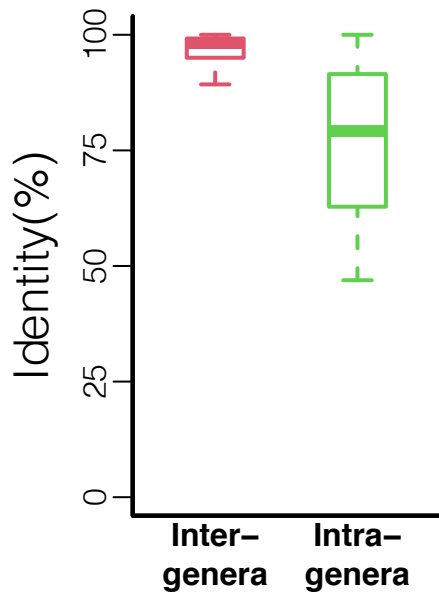
57 **Figure 5.** Taxonomic information of three reference genome resources. **(a)** Pie charts of the  
58 defined and undefined numbers of biological taxonomy. **(b)** Venn diagram analysis of phyla in the  
59 three resources. **(c)** Venn diagram analysis of the genera in the three resources.

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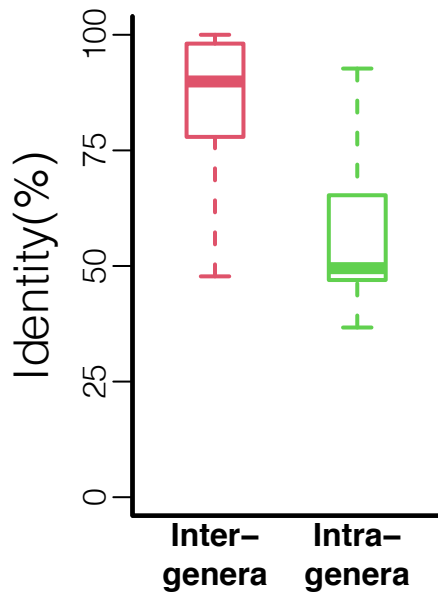
a.

***cutC***



b.

***cutD***



62 **Figure 6.** Inter- and intra-genera sequence identities of *cntA* (**a**) and *cutC* (**b**). The bounds denote  
63 the interquartile range between the first and third quartiles and the center line denotes the median.  
64 The whiskers denote the lowest and highest value.

65









HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli O157:H7 str. EC4024	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia albertii TW07627	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli D9	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia sp. 4_1_40B	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Yersinia	Yersinia pestis Pestoides A	yeaX
HMP	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Klebsiella	Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Achromobacter	Achromobacter piechaudii	yeaX
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Yersinia	Yersinia pestis biovar Mediaevalis str. K1973002	yeaX
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HMP	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii AB058	yeaX
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HMP	Firmicutes	Negativicutes	Selenomonadales	Sporosporaceae	Thermosinus	Thermosinus carboxydivorans Nor-1	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides ovatus ATCC 8483	cutD
HMP	Firmicutes	Clostridia	Clostridiales	NA	Pseudoflavonifractor	Pseudoflavonifractor capillosus ATCC 29799	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides stercoris ATCC 43183	cutD
HMP	Proteobacteria	Betaproteobacteria	Methylotenerales	Methyloteneraceae	Methylovorus	Methylovorus glucosotrophus SIP3-4	cutD
HMP	Proteobacteria	Aleromonadales	Shewanellales	Shewanellaceae	Shewanella	Shewanella benthica KT99	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium sporogenes ATCC 15579	cutD
HMP	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium	Rhizobium etli Kim 5	cutD
HMP	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium	Rhizobium etli CIAT 894	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcus	[Clostridium] hiranonis DSM 13275	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	Geobacter sp. M21	cutD
HMP	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Dickeya	Dickeya chrysanthemi Ech1591	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides coprophilus DSM 18228 = JCM 13818	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides sp. D2	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio magneticus RS-1	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium carboxidivorans P7	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium carboxidivorans P7	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminoclostridium	Ruminoclostridium thermocellum DSM 2360	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminoclostridium	[Clostridium] papyrosolvens DSM 2782	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminoclostridium	Ruminoclostridium thermocellum JW20	cutD
HMP	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	Vibrio	Vibrio alginolyticus 40B	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio aespoensis Aspo-2	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio sp. FW1012B	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides ovatus SD CMC 3f	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	Geobacter daltonii FRC-32	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteriaceae	Desulfatibacillum	Desulfatibacillum alkenivorans AK-01	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium carboxidivorans P7	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium carboxidivorans P7	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides sp. 1_1_14	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides sp. 3_1_23	cutD
HMP	Proteobacteria	Deltaproteobacteria	Syntrophobacteriales	Syntrophaceae	Syntrophus	Syntrophus aciditrophicus SB	cutD
HMP	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga	Thermotoga maritima MSB8	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	Geobacter sulfurireducens PCA	cutD
HMP	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	Geobacter sulfurireducens PCA	cutD
HMP	Spirochaetes	Spirochaetia	Brachyspirales	Brachyspiraceae	Brachyspira	Brachyspira pilosicoli 95/1000	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium ljungdahlii DSM 13528	cutD
HMP	Proteobacteria	Epsilonproteobacteria	Campylobacteriales	Campylobacteriaceae	Arcobacter	Arcobacter nitrofigilis DSM 7299	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Thermincola	Thermincola potens JR	cutD
HMP	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Prevotella ruminicola 23	cutD
HMP	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga	Thermotoga naphthophila RRU-10	cutD
HMP	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	Thermotoga	Thermotoga petrophila RRU-1	cutD
HMP	Firmicutes	Clostridia	Clostridiales	Symbiobacteriaceae	Symbiobacterium	Symbiobacterium thermophilum IAM 14863	cutD
HMP	Proteobacteria	Deltaproteobacteria	Myxococcales	Polysphondyliaceae	Sorangium	Sorangium cellulosum So ce36	cutD
UHGG	Actinobacteria	Coriobacteria	Coriobacteriales	Atopobiaceae	Atopobium	Atopobium minutum	cutD
UHGG	Actinobacteria	Coriobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella bonchedarhonensis	cutC
UHGG	Actinobacteria	Coriobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella tanakaei	cutC
UHGG	Actinobacteria	Coriobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella bouchedarhonensis	cutC
UHGG	Actinobacteria	Coriobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella tanakaei	cutC
UHGG	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio desulfuricans	cutC
UHGG	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio desulfuricans	cutC
UHGG	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio desulfuricans	cutC
UHGG	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio desulfuricans	cutC
UHGG	Desulfobacterota	Desulfovibrionia	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio desulfuricans	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus asini	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus dispar	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus raffinosus	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus avium	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus cacciae	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus asini	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus dispar	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus raffinosus	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus avium	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus cacciae	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus asini	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus dispar	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus raffinosus	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus avium	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus cacciae	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus asini	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus dispar	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus raffinosus	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus avium	cutC
UHGG	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus cacciae	cutC







UHGG	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter pittii	MGY-GHUT-02346	yeaW
UHGG	Proteobacteria	Pseudomonadales	Moraxellaceae	Moraxellaceae	Acinetobacter baumannii	Acinetobacter baumannii	MGY-GHUT-02344	yeaX
UHGG	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter nosocomialis	Acinetobacter nosocomialis	MGY-GHUT-02345	yeaX
UHGG	Proteobacteria	Pseudomonadales	Moraxellaceae	Moraxellaceae	Acinetobacter pittii	Acinetobacter pittii	MGY-GHUT-02346	yeaX
UHGG	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas citronellolis	MGY-GHUT-04151	cntA
UHGG	Proteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas citronellolis	MGY-GHUT-04151	cntB
UHGG	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas citronellolis	MGY-GHUT-04151	cntB
UHGG	Proteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas citronellolis	MGY-GHUT-04151	yeaW
UHGG	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas citronellolis	MGY-GHUT-04151	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	ZeeviD_2015_PNP_DietIntervention_31_bin.3	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	LiJ_2014_VT.UC39-4_bin.41	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	CM_madagascar_A82_02_IFE_bin.3	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter werkmanii	VatanenT_2016_G80513_bin.7	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter freundii	KarlssonFH_2013_S389_bin.5	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter braakii	GeversD_2014_SKBSTL011_bin.2	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella quasipneumoniae	QinJ_2012_DLM028_bin.4	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	NielsenHB_2014_O2_UC38_2_bin.18	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	VatanenT_2016_G80555_bin.3	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella aerogenes	VogtmannE_2016_MMRS86168210ST-27-0-0_bin.16	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	Serratia liquefaciens	VatanenT_2016_G80472_bin.3	cntA
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter ursingii	BackhedF_2015_SID78_M_bin.21	cntA
SGB	Proteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Stenotrophomonas rhizophila	OhJ_2014_MET0293_bin.25	cntA
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. AU11447	OhJ_2014_MET0293_bin.22	cntA
SGB	Proteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. M1	XieH_2016_YSZC12003_37197R1_bin.69	cntA
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	ZeeviD_2015_PNP_DietIntervention_31_bin.3	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	LiJ_2014_VT.UC39-4_bin.41	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia albertii	BackhedF_2015_SID105_12M_bin.10	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	CM_madagascar_A82_02_IFE_bin.3	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter werkmanii	VatanenT_2016_G80513_bin.7	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter freundii	KarlssonFH_2013_S389_bin.5	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter braakii	GeversD_2014_SKBSTL011_bin.2	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella quasipneumoniae	QinJ_2012_DLM028_bin.4	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	NielsenHB_2014_O2_UC38_2_bin.18	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	VatanenT_2016_G80555_bin.3	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella aerogenes	VogtmannE_2016_MMRS86168210ST-27-0-0_bin.16	cntB
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	Serratia liquefaciens	VatanenT_2016_G80472_bin.3	cntB
SGB	Proteobacteria	Pseudomonadales	Moraxellaceae	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	WenC_2017_RA130_bin.22	cntB
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter ursingii	BackhedF_2015_SID78_M_bin.21	cntB
SGB	Proteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Stenotrophomonas rhizophila	OhJ_2014_MET0293_bin.25	cntB
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. AU11447	OhJ_2014_MET0293_bin.22	cntB
SGB	Proteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. AU11447	OhJ_2014_MET0293_bin.22	cntB
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. T	OhJ_2014_MET0241_bin.25	cntB
SGB	Proteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. M1	XieH_2016_YSZC12003_37197R1_bin.69	cntB
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. M1	XieH_2016_YSZC12003_37197R1_bin.69	cntB
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas sp. M1	YuJ_2015_SZAXP003412-1_bin.19	cntB
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Mogibacterium	Mogibacterium sp. CMS0	CM_periplantitiss SP_305SPI_T016_bin.15	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiales_Family XIII In	Mogibacterium	Mogibacterium sp. CMS0	ZeeviD_2015_PNP_Main_62_bin.36	cntC
SGB	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides vulgatus	VincentC_2016_MM058.1_bin.7	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus	Peptococcus niger	FengQ_2015_SID31477_bin.63	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Enterococcus	Enterococcus faecium	BackhedF_2015_SID184_4M_bin.17	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus casei	XieH_2016_YSZC12003_36116_bin.21	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Flavonifractor	Flavonifractor sp. An10	BackhedF_2015_SID335_M_bin.63	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus	Peptococcus niger	Bengtsson-PalmeJ_2015_TRAVELRES46_bin.63	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Blautia obeum	HMP_2012_SRS019125_bin.20	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Johnsonella	Johnsonella ignava	HeQ_2017_RSZAXP003069-101_bin.6	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium	Lachnoclostridium asparagiforme	HeQ_2017_RSZAXP003099-133_bin.12	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium	Lachnoclostridium	GeversD_2014_SKBSTL023_bin.2	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Hungatella	Hungatella hathewayi	NielsenHB_2014_V1_UC14_T_bin.35	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Hungatella	Hungatella hathewayi	HeQ_2017_RSZAXP003077-109_bin.16	cntC
SGB	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Megasphaera	Megasphaera sp. DJF_B143	ZellerG_2014_CCISI1362406ST-4-0_bin.75	cntC
SGB	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Megasphaera	Megasphaera sp. DJF_B143	HeQ_2017_SZAXP029575-90_bin.40	cntC
SGB	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Megasphaera	Megasphaera sp. DJF_B143	HeQ_2017_SZAXP029575-90_bin.40	cntC
SGB	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Megasphaera	Megasphaera micronuciformis	BackhedF_2015_SID565_4M_bin.4	cntC
SGB	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Cetobacterium	Cetobacterium somerae	YuJ_2015_SZAXP015255-46_bin.49	cntC
SGB	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Fusobacterium varium	QinN_2014_LD-78_bin.12	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium disporicum	FerrettiP_2018_CA_C10020IS2336FE_t1M15_bin.8	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium paraputrificum	FerrettiP_2018_CA_C10003IS2040FE_t3M15_bin.2	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium sporogenes	BackhedF_2015_SID515_4M_bin.18	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium sulfdigenes	HeQ_2017_RSZAXP003063-104_bin.17	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptoanaerobacter	Peptoanaerobacter	HMP_2012_SRS022725_bin.23	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptoanaerobacter	Peptoanaerobacter	HMP_2012_SRS015215_bin.44	cntC
SGB	Firmicutes	Tissierellales	Tissierellales	Peptoniphilaceae	Anaerococcus	Anaerococcus hydrogenalis	VincentC_2016_MM081_bin.7	cntC
SGB	Firmicutes	Tissierellales	Tissierellales	Peptoniphilaceae	Anaerococcus	Anaerococcus lactolyticus	VincentC_2016_MM004.2_bin.5	cntC
SGB	Firmicutes	Tissierellales	Tissierellales	Peptoniphilaceae	Anaerococcus	Anaerococcus tetradicus	HMP_2012_SRS011111_bin.13	cntC
SGB	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Veillonella	Veillonella seminalis	YuJ_2015_SZAXP003434-7_bin.67	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Vagococcus	Vagococcus teuberi	HeQ_2017_SZAXP029501-104_bin.19	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus raffinosus	BackhedF_2015_SID1_4M_bin.4	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus	FerrettiP_2018_CA_C10008IS2131FE_t5M16_bin.7	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus dispar	FengQ_2015_SID31870_bin.16	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	HeQ_2017_SZAXP029574-89_bin.4	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	HeQ_2017_SZAXP029545-129_bin.16	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia rettgeri	ZeeviD_2015_PNP_DietIntervention_31_bin.3	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella quasipneumoniae	LiJ_2014_VT.UC39-4_bin.41	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	QinJ_2012_DLM028_bin.4	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	NielsenHB_2014_O2_UC38_2_bin.18	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella aerogenes	VatanenT_2016_G80555_bin.3	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella aerogenes	VogtmannE_2016_MMRS86168210ST-27-0-0_bin.16	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella oxytoca	FengQ_2015_SID531155_bin.23	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella michiganensis	BackhedF_2015_SID608_B_bin.1	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella sp. Kd70_TUC_EEAO	FerrettiP_2018_CA_C10035IS2913FE_t4M16_bin.3	cntC
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Raoultella	Raoultella ornithinolytica	FerrettiP_2018_CA_C10029IS2503FE_t3M15_bin.8	cntC
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella uli	CM_periplantitiss SP_143SPI_T016_bin.9	cntC
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella umbonata	BritoIL_2016_W2.9.ST_bin.18	cntC
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella umbonata	QinJ_2012_T2D-103_bin.15	cntC
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella aerofaciens	ZellerG_2014_CCIS78100604ST-4-0_bin.15	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Lachnospiraceae	Lachnospiraceae	FengQ_2015_SID31455_bin.4	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Gemmiger	Gemmiger sp. An194	LiJ_2014_O2.UC48-1_bin.38	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio piger	ZellerG_2014_CCMDS0071957ST-21-0_bin.42	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio piger	LiJ_2014_MH0398_bin.77	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Bilophila	Bilophila sp. 4_1_30	LeChatelierE_2013_MH0239_bin.24	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Bilophila	Bilophila wadsworthia	FerrettiP_2018_CA_C10024IS2415FE_t3M15_bin.18	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Bilophila	Bilophila wadsworthia	LiJ_2017_H1M412837_bin.49	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Bilophila	Bilophila sp. 4_1_30	HeQ_2017_SZAXP029557-42_bin.30	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio piger	LeChatelierE_2013_MH0108_bin.24	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio desulfuricans	LouisS_2016_AS66_18_bin.13	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio desulfuricans	XieH_2016_YSZC12003_35387_bin.50	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio desulfuricans	QinN_2014_LD-22_bin.30	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio piger	RaymondF_2016_PIE0_bin.62	cntC
SGB	Proteobacteria	Desulfuovibrionales	Desulfuovibrionales	Desulfuovibrionaceae	Desulfuovibrio	Desulfuovibrio legallii	BackhedF_2015_SID624_M_bin.2	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus gallinarum	VatanenT_2016_G78762_bin.2	cntC
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Atopobium	Atopobium minutum	YuJ_2015_SZAXP003412-1_bin.19	cntC
SGB	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides xylanisolvens	HMP_2012_SRS042628_bin.29	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiales_Family XIII In	Mogibacterium	Mogibacterium sp. CMS0	CM_periplantitiss SP_305SPI_T016_bin.15	cntC
SGB	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides vulgatus	ZeeviD_2015_PNP_Main_62_bin.36	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus	Peptococcus niger	VincentC_2016_MM058.1_bin.7	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	Enterococcus faecium	FengQ_2015_SID31477_bin.63	cntC
SGB	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus casei	BackhedF_2015_SID184_4M_bin.17	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Flavonifractor	Flavonifractor sp. An10	XieH_2016_YSZC12003_36116_bin.21	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus	Peptococcus niger	BackhedF_2015_SID335_M_bin.63	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Blautia obeum	Bengtsson-PalmeJ_2015_TRAVELRES46_bin.63	cntC
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Johnsonella	Johnsonella ignava	CM_madagascar_A82_02_IFE_bin.3	cntC
SGB	Firmicutes	Clostridia	Clostrid					

SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_sp_Kd70_TUC_EEAO	FerrettiP_2018_CA_C10035IS2913FE_t4M16_bin.3	cutD
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Raouliella	Raouliella_ornitholytica	FerrettiP_2018_CA_C10029IS2503FE_t3M15_bin.8	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium_sp_ATCC_29733	XieH_2016_YSZC12003_36055_bin.93	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Ruminococcus_sp	XieH_2016_YSZC12003_37394_bin.53	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium	Eubacterium_siraeum	Obregon-TitoAJ_2015_SM20_bin.35	cutD
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella_uli	CM_periplantitis_SP_143SPI_T016_bin.9	cutD
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella_umbonata	BritoIL_2016_W2.9.ST_bin.18	cutD
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Atopobiaceae	Olsenella	Olsenella_umbonata	QinJ_2012_T2D-103_bin.15	cutD
SGB	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella_aerofaciens	ZellerG_2014_CCIS78100604ST-4-0_bin.15	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium	Clostridium_leptum	FengQ_2015_SID31455_bin.4	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Anaeromassilibacillus	Anaeromassilibacillus_sp_An250	LoombaK_2017_SID1050_bax_bin.11	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Anaeromassilibacillus	Anaeromassilibacillus_sp_An250	LiJ_2014_MH0370_bin.9	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Faecalibacterium_prausnitzii	LiJ_2014_V1.UC58-4_bin.44	cutD
SGB	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Gemmiger	Gemmiger_sp_An194	LiJ_2014_O2.UC48-1_bin.38	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_piger	ZellerG_2014_CCMD50071937ST-21-0_bin.42	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_piger	LiJ_2014_MH0398_bin.77	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila	Bilophila_sp_4_1_30	LeChateLierE_2013_MH0239_bin.24	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila	Bilophila_wadsworthia	FerrettiP_2018_CA_C10024IS2415FE_t3M15_bin.18	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila	Bilophila_wadsworthia	LiJ_2017_H1M412837_bin.49	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio	HeQ_2017_SZLXP029537-42_bin.30	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_piger	ChengpingW_2017_AS9raw_bin.35	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_piger	LeChateLierE_2013_MH0108_bin.24	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_desulfuricans	LouisS_2016_AS66_18_bin.13	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_desulfuricans	XieH_2016_YSZC12003_35387_bin.50	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_desulfuricans	QinN_2014_LD-22_bin.30	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_piger	RaymondF_2016_P1E0_bin.62	cutD
SGB	Proteobacteria	Dellaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	Desulfovibrio_legallii	BackhedF_2015_SID624_M_bin.2	cutD
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia_retgeri	ZeeviD_2015_PNP_DietIntervention_31_bin.3	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia_retgeri	LiJ_2014_V1.UC39-4_bin.41	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia_coli	CM_madagascar_A82_02_1FE_bin.3	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_werkmanii	VatanenT_2016_G80513_bin.7	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_freundii	KarlssonFH_2013_S389_bin.5	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_braakii	GeversD_2014_SKBSTL011_bin.2	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_quasipneumoniae	QinJ_2012_DLM028_bin.4	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_pneumoniae	NielsenHB_2014_O2_UC38_2_bin.18	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_pneumoniae	VatanenT_2016_G80588_bin.5	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_aerogenes	VatanenT_2016_G80555_bin.3	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_aerogenes	VogtmannE_2016_MMRS86168210ST-27-0-0_bin.16	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Yersiniaceae	Serratia	Serratia_liquefaciens	VatanenT_2016_G80472_bin.3	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ursingii	BackhedF_2015_SID78_M_bin.21	yeaW
SGB	Proteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Stenotrophomonas_rhizophila	OhJ_2014_MET0293_bin.25	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_sp_AU11447	OhJ_2014_MET0293_bin.22	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_sp_M1	XieH_2016_YSZC12003_37197R1_bin.69	yeaW
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia_retgeri	ZeeviD_2015_PNP_DietIntervention_31_bin.3	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Morganellaceae	Providencia	Providencia_retgeri	LiJ_2014_V1.UC39-4_bin.41	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia_albertii	BackhedF_2015_SID105_12M_bin.10	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia_coli	CM_madagascar_A82_02_1FE_bin.3	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_werkmanii	VatanenT_2016_G80513_bin.7	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_freundii	KarlssonFH_2013_S389_bin.5	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter	Citrobacter_braakii	GeversD_2014_SKBSTL011_bin.2	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_quasipneumoniae	QinJ_2012_DLM028_bin.4	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_pneumoniae	NielsenHB_2014_O2_UC38_2_bin.18	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_pneumoniae	VatanenT_2016_G80588_bin.5	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_aerogenes	VatanenT_2016_G80555_bin.3	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_aerogenes	VogtmannE_2016_MMRS86168210ST-27-0-0_bin.16	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	Serratia_liquefaciens	VatanenT_2016_G80472_bin.3	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_baumannii	WenC_2017_RA130_bin.22	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ursingii	BackhedF_2015_SID78_M_bin.21	yeaX
SGB	Proteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Stenotrophomonas_rhizophila	OhJ_2014_MET0293_bin.25	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_sp_AU11447	OhJ_2014_MET0293_bin.22	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_sp_M1	XieH_2016_YSZC12003_37197R1_bin.69	yeaX
SGB	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_oleovorans	OhJ_2014_MET0054_bin.5	yeaX



**Supplementary Table 2. Taxonomic information of TMA-lyase from Human Microbiome Project database, 4,644 gut prokaryotes (MGYG, Almeida et al. 2020 - PMID 32690973) and recapitulated 4,930 species-level genome bins (SGBs, Pasolli et al. 2019 - PMID 30661755).**

Phylum	Genus	Species	Database	cntA	cntB	cutC	cutD	yeaW	yeaX
Actinobacteria	<i>Atopobium</i>	<i>Atopobium minutum</i>	UHGG/SGB			+	+		
		<i>Collinsella bouchesdurhonensis</i>	UHGG			+	+		
		<i>Collinsella tanakaei</i>	UHGG			+	+		
		<i>Collinsella aerofaciens</i>	SGB			+	+		
		<i>Eggerthella lenta</i>	HMP					+	+
		<i>Olsenella uli</i>	HMP/SGB					+	+
		<i>Olsenella umbonata</i>	SGB			+	+		
		<i>Bacteroides coprophilus</i>	HMP					+	+
		<i>Bacteroides ovatus</i>	HMP					+	+
		<i>Bacteroides sp. 1_1_14</i>	HMP					+	+
Bacteroidetes		<i>Bacteroides sp. 1_1_6</i>	HMP					+	+
		<i>Bacteroides sp. 3_1_23</i>	HMP					+	+
		<i>Bacteroides sp. D2</i>	HMP					+	+
		<i>Bacteroides stercoris</i>	HMP					+	+
		<i>Bacteroides thetaiotaomicron</i>	HMP					+	+
		<i>Bacteroides vulgatus</i>	SGB			+	+		
		<i>Bacteroides xylanisolvens</i>	SGB					+	+
		<i>Prevotella ruminicola</i>	HMP					+	+
		<i>Desulfovibrio desulfuricans</i>	UHGG			+	+		
		<i>Dictyoglomus thermophilum</i>	HMP					+	+
Desulfobacterota_A		<i>Alkaliphilus metalliredigens</i>	HMP			+	+		
		<i>Alkaliphilus oremlandii</i>	HMP			+	+		
		<i>Anaerococcus hydrogenalis</i>	HMP/UHGG/SGB			+	+		
		<i>Anaerococcus obesiensis</i>	UHGG			+	+		
		<i>Anaerococcus tetradius</i>	HMP/SGB			+	+		
		<i>Anaerococcus vaginalis</i>	HMP/UHGG			+	+		
		<i>Anaerococcus lactolyticus</i>	SGB			+	+		
		<i>Anaerococcus sp. HMSC065G05</i>	SGB			+	+		
		<i>Anaeroglobus massiliensis</i>	UHGG			+	+		
		<i>Anaeromassilibacillus sp001305115</i>	UHGG					+	+
Dictyoglomi		<i>Anaeromassilibacillus sp002159845</i>	UHGG					+	+
		<i>Anaeromassilibacillus sp_An250</i>	SGB					+	+
		<i>Anaerosalibacter_A massiliensis</i>	UHGG			+	+		
		<i>Blautia obeum</i>	SGB			+	+		
		<i>Ruminococcus sp</i>	SGB					+	+
		<i>Caecibacter massiliensis</i>	UHGG			+	+		
		<i>Candidatus Desulforudis audaxviator</i>	HMP					+	+
		<i>Christensenella_A timonensis</i>	UHGG					+	+
		<i>Clostridium baratii</i>	UHGG			+	+		
		<i>Clostridium botulinum</i>	HMP/UHGG			+	+		
Firmicutes		<i>Clostridium carboxidivorans</i>	HMP			+	+		
		<i>Clostridium citroniae</i>	UHGG			+	+		
		<i>Clostridium clostridioforme</i>	UHGG			+	+		
		<i>Clostridium ihumii</i>	UHGG			+	+		
		<i>Clostridium ljungdahlii</i>	HMP			+	+		
		<i>Clostridium paraputrificum</i>	UHGG/SGB			+	+		
		<i>Clostridium senegalense</i>	UHGG			+	+		
		<i>Clostridium septicum</i>	UHGG			+	+		
		<i>Clostridium sporogenes</i>	HMP/SGB			+	+		
		<i>Clostridium tepidum</i>	UHGG			+	+		
Firmicutes		<i>Clostridium tetani</i>	HMP/UHGG			+	+		
		<i>Clostridium disporicum</i>	SGB			+	+		
		<i>Clostridium sp. ATCC_29733</i>	SGB					+	+
		<i>Clostridium sulfidigenes</i>	SGB			+	+		
		<i>Desulfitobacterium hafniense</i>	HMP/UHGG			+	+		
		<i>Desulfotomaculum reducens</i>	HMP			+	+		
		<i>Enterococcus asini</i>	UHGG			+	+		
		<i>Enterococcus avium</i>	UHGG			+	+		
		<i>Enterococcus caccae</i>	UHGG			+	+		
		<i>Enterococcus dispar</i>	UHGG/SGB			+	+		
Firmicutes		<i>Enterococcus raffinosus</i>	UHGG/SGB			+	+		
		<i>Enterococcus faecium</i>	SGB			+	+		
		<i>Enterococcus gallinarum</i>	SGB					+	+
		<i>Enterococcus sp. HMSC05C03</i>	SGB			+	+		
		<i>Faecalibacterium prausnitzii</i>	SGB					+	+
		<i>Flavonifractor sp. An10</i>	SGB			+	+		
		<i>Fournierella massiliensis</i>	UHGG			+	+		
		<i>Gemmiger sp. An194</i>	SGB			+	+		
		<i>Halothermothrix orenii</i>	HMP					+	+
		<i>Hungatella effluvii</i>	UHGG			+	+		
Firmicutes		<i>Hungatella hathewayi</i>	HMP/UHGG/SGB			+	+		
		<i>Johnsonella ignava</i>	SGB			+	+		
		<i>[Lachnoclostridium asparagiforme]</i>	HMP/UHGG/SGB			+	+		
		<i>Lachnoclostridium saccharolyticum</i>	HMP/SGB			+	+		
		<i>Clostridium lavalense</i>	UHGG/SGB			+	+		
		<i>Lachnoclostridium phytofermentans</i>	HMP			+	+		
		<i>Lactobacillus casei</i>	SGB			+	+		
		<i>Megasphaera elsdenii/SGB</i>	UHGG					+	+
		<i>Megasphaera micronuciformis</i>	SGB			+	+		
		<i>Megasphaera sp. DJF_B143</i>	SGB			+	+		
Firmicutes		<i>Megasphaera sp. NM10</i>	SGB					+	+
		<i>Mogibacterium sp. CM50</i>	SGB			+	+		
		<i>Paenibacillus_B thiaminolyticus</i>	UHGG			+	+		
		<i>Eubacterium_yurii</i>	SGB			+	+		
		<i>Peptoanaerobacter stomatis</i>	SGB					+	+



		<i>Proteus vulgaris</i>	UHGG/SGB			+	+		
		<i>Providencia alcalifaciens</i>	HMP/UHGG	+	+	+	+	+	+
	<i>Providencia</i>	<i>Providencia rettgeri</i>	HMP/UHGG/SGB	+	+	+	+	+	+
		<i>Providencia rustigianii</i>	HMP/UHGG			+	+		
		<i>Providencia stuartii</i>	HMP/UHGG	+	+			+	+
		<i>Pseudomonas citronellolis</i>	UHGG	+	+			+	+
		<i>Pseudomonas entomophila</i>	HMP	+	+			+	+
	<i>Pseudomonas</i>	<i>Pseudomonas putida</i>	HMP	+	+			+	+
		<i>Pseudomonas oleovorans</i>	SGB						+
		<i>Pseudomonas_sp_AU11447</i>	SGB	+	+			+	+
		<i>Pseudomonas_sp_M1</i>	SGB	+	+			+	+
		<i>Pseudomonas_sp_T</i>	SGB		+				
	<i>Raoultella</i>	<i>Raoultella ornithinolytica</i>	UHGG/SGB			+	+		
	<i>Rhizobium</i>	<i>Rhizobium etli</i>	HMP				+		
	<i>Ruegeria</i>	<i>Ruegeria pomeroyi</i>	HMP		+				
		<i>Serratia liquefaciens</i>	UHGG/SGB	+	+			+	+
	<i>Serratia</i>	<i>Serratia marcescens</i>	UHGG	+	+			+	+
		<i>Serratia ureilytica</i>	UHGG	+	+			+	+
		<i>Shewanella benthica</i>	HMP				+		
	<i>Shewanella</i>	<i>Shewanella oneidensis</i>	HMP				+		
		<i>Shigella boydii</i>	HMP	+	+			+	+
	<i>Shigella</i>	<i>Shigella flexneri</i>	HMP	+	+			+	+
		<i>Shigella sonnei</i>	HMP	+	+			+	+
	<i>Sorangium</i>	<i>Sorangium cellulosum</i>	HMP				+		
	<i>Stenotrophomonas</i>	<i>Stenotrophomonas rhizophila</i>	SGB	+	+			+	+
	<i>Syntrophobacter</i>	<i>Syntrophobacter fumaroxidans</i>	HMP				+		
	<i>Syntrophus</i>	<i>Syntrophus aciditrophicus</i>	HMP				+		
	<i>Thiobacillus</i>	<i>Thiobacillus denitrificans</i>	HMP				+		
	<i>unclassified Rhodobacteraceae</i>	<i>Rhodobacteraceae bacterium KLH11</i>	HMP		+				
	<i>Vibrio</i>	<i>Vibrio alginolyticus</i>	HMP				+		
	<i>Vitreoscilla</i>	<i>Vitreoscilla massiliensis</i>	UHGG	+	+			+	+
	<i>Xenorhabdus</i>	<i>Xenorhabdus nematophila</i>	HMP	+	+			+	+
		<i>Yersinia pestis</i>	HMP/UHGG	+	+			+	+
	<i>Yersinia</i>	<i>Yersinia pseudotuberculosis</i>	HMP	+	+			+	+
	<i>Yokenella</i>	<i>Yokenella regensburgei</i>	UHGG			+	+		
<i>Spirochaetes</i>	<i>Brachyspira</i>	<i>Brachyspira pilosicoli</i>	HMP				+		
	<i>Marinitoga</i>	<i>Marinitoga piezophila</i>	HMP				+		
		<i>Thermotoga maritima</i>	HMP				+		
<i>Thermotogae</i>	<i>Thermotoga</i>	<i>Thermotoga naphthophila</i>	HMP				+		
		<i>Thermotoga petrophila</i>	HMP				+		
		<i>Thermotoga sp. RQ2</i>	HMP				+		
	<i>Akkermansia</i>	<i>Akkermansia glycaniphila</i>	SGB				+		
<i>Verrucomicrobia</i>	<i>Verrucomicrobium</i>	<i>Verrucomicrobium sp. GAS474</i>	SGB				+		

Supplementary Table 3. Detailed information of public datasets used in this study.

Abbreviation	Country	Total number of individuals	The number of healthy individuals	Gender (F/M)	Age (mean±SD)	BMI (mean±SD)	Individuals with colorectal cancer (CRC)	Individuals with adenoma	Individuals with type 2 diabetes	Individuals with impaired glucose tolerance	Individuals with cardiovascular disease	Individuals with hypertension	Individuals with Obesity	Relative abundance of taxonomic classification						
														phylum	class	order	family	genus	species	
HZ	HADZA	26	26	9/18	32.00±14.93	-	-	-	-	-	-	-	-	0.787±0.06737	0.7059±0.08115	0.6969±0.08258	0.4731±0.09551	0.4142±0.09964	0.2638±0.0754	
CN	China	226	127	26/45	33.69±11.02	22.33±3.52	-	-	99	-	-	-	-	0.9155±0.03474	0.8795±0.05102	0.8762±0.05309	0.7269±0.08102	0.6614±0.09430	0.3540±0.08342	
JP	Japan	106	98	42/62	31.96±10.78	21.67±2.260	-	-	-	-	-	-	-	0.9329±0.02294	0.8920±0.03415	0.8875±0.03531	0.7042±0.05880	0.6172±0.06044	0.3804±0.06251	
KR	South Korea	35	35	-	-	-	-	-	-	-	-	-	-	0.8630±0.06961	0.8078±0.09593	0.8022±0.10110	0.6292±0.1330	0.5720±0.1363	0.3717±0.06883	
DK	Denmark	85	47	24/24	54.69±10.70	23.24±2.35	-	-	35	-	-	-	-	0.8579±0.05343	0.7964±0.07331	0.7875±0.07730	0.6065±0.08619	0.5614±0.09394	0.3300±0.05661	
SE	Sweden	145	35	36/0	70.36±0.73	24.32±2.93	-	-	53	49	-	-	-	0.8748±0.03471	0.8072±0.05319	0.7994±0.05695	0.6000±0.07385	0.5350±0.08098	0.3982±0.0653	
AT	Austria	156	41	19/22	66.37±7.21	25.63±3.21	46	44	-	-	-	-	-	0.8081±0.08061	0.8089±0.08903	0.8025±0.09075	0.6309±0.1050	0.5315±0.09511	0.4079±0.07749	
FR	France	156	51	30/25	60.62±11.88	23.97±2.41	53	42	-	-	-	-	-	0.8655±0.04605	0.8088±0.06319	0.8022±0.06595	0.6360±0.07894	0.5702±0.08355	0.3792±0.06439	
AU	Australia	25	25	-	-	-	-	-	-	-	-	-	-	0.8520±0.04775	0.8066±0.06033	0.7966±0.06714	0.6492±0.08069	0.6145±0.08653	0.3343±0.05526	
US	America	300	148	66/82	-	-	-	-	-	-	-	-	-	0.9178±0.04441	0.8876±0.064	0.8843±0.06679	0.7525±0.1006	0.7237±0.1196	0.3058±0.0755	
PE	Peru	36	12	12/19	20.43±15.55	20.55±4.15	-	-	-	-	-	-	-	0.7553±0.06890	0.6674±0.09728	0.6614±0.09986	0.4607±0.1286	0.4051±0.1214	0.2864±0.07902	
ACVD*	China	385	171	154/226	60.74±9.87	24.52±5.48	-	-	-	-	214	-	-	0.9144±0.03432	0.8706±0.05301	0.8667±0.05539	0.7131±0.08385	0.6304±0.09955	0.3709±0.07515	
HT	China	196	99	-	-	-	-	-	-	-	-	97	-	0.9101±0.04198	0.8754±0.06105	0.8704±0.06388	0.7265±0.09289	0.6770±0.1060	0.4171±0.1290	
OB	China	257	105	-	-	-	-	-	-	-	-	152	-	0.9198±0.03181	0.8838±0.04757	0.8810±0.04930	0.7298±0.07745	0.6784±0.09362	0.3827±0.08503	
Total		2134	1020				99	86	187	49	214	97	152							

**Supplementary Table 4. Homologous modeling and molecular docking between cutC sequences of trains from cutC abundant strains and coline.**

Genus	Source of strain	Protein sequence
	<i>Lachnoclostridium saccharolyticum</i> WMI	LKEREIRLDIREFSNKFVEATKNMTPEERASLMKMFETVSDEINKKESSSQAAACCEGGT EVPEGITPRLQKLKDNYLTHKPSITTYRARAITKIAKENPGMPKIMLRACFRYCCETAP LVIQDNELIVGAPCGAPRAGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMKEEL FPYWAGKSVDEYCEDQYREAGVWELSGESFVSDCSYHAINGGGDSNPGYDVILMKGMLD IQQEAKDHLKELDYENPDDIEKIYFYKSIIDTTEGVMIYAKRLSEYAAELAASETNPKRK EELLKISEVNAAYVPAHKPRTFWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMYPFYKDD IESGRMNDYQAFELAGCMLIKMSEMMWITSEGGSKFFAGYQPFVNMCVGGVTRSGHDATN DLTYLLMDAVRHVKIYQPSLACRIHNKSPKMYMKKIVDVVRSRGMGFPACHFDDAHIKMML AKGVSIEDARDYCLMGCVEPQKSGRLYQWTSTAYTQWPICIELVLNHGAPLWYGKQVCPD MGDLSNFKTYEEFEAAVKKEIKYITKWDVATVISQRVHRDLAPKPLMSIMYEGCMEKAK DVSAGGAMYNFGPGVVWSGLATYADSMIAIKKLVFEEKKYTLEQLNQALKADFGYDQIR TDCLNAPKYGNDDDYADLIAADLVDFTEHEHRKYKTLYSVLSHGTLSSISNNTPFQMTGA SANGRNAWLPLSDGISPTQGADFKGPTAIKSVSKMSNDSMNIGMVHNFKIMAGLLDTPE GEESLITLLRTACMFGNGEMQFNLYLDNDTLVEAQKHPELYRDLIVRVAGYSAFFVELCKD VQDEIISRTMLTHF
<i>Lachnoclostridium</i>	<i>[Lachnoclostridium asparagiforme]</i> DSM 15981	DEIDTIGSRPQDPFYISEEDKKIMREELFPFWKGSVDEYCEDQYREAGVWELSGESFVS DCSYHALNNGGGDSNPGYDVILMKGMLDIQQAAREHLEQLDYENPDDIEKIYFYKSIIDT TEGVMIYARRMSEYAAQLAAKEQNPRRREELLKISEVNARVPAHKPETFWEAIQAVWTIE SLLVVEENQTGMSIGRVDQYMYPFYKGDIASGRLNDRQAFELAGCMLIKMSEMMWITSEG GSKFFAGYQPFVNMCVGGVTRDGRDATNELTYLLMDAVRHVRIYQPSLACRIHNKSPKMY LKKIVDVVRSRGMGFPACHFDDAHIKMMLAKGVSIEDARDYCLMGCVEPQKSGRLYQWTST SYTQWPICIELALNHGVPLWYGKQVCPDMGDPDRFKTYEEFEAAVKDEIKFITKWTAVAT VISQRVHKELAPKPLMSIMYEGCMEKGRDVSAGGAMYNFGPGVIWSGLATYADSMIAIRK LVFDDRKYTLSQINEALKADFAFDQLRIDCLNAPKYGNDDDYADLIAADLVNFTEHEHR KYKTLYSTLSHGTLSSISNNTPFQMTGASANGRHAWLPLSDGISPTQGADFKGPTAIKS VSKMSNDSMNIGMVHNFKIMAGLLDTPEGEESLITLLRTACMFGNGEMQFNLYLDNNTLIE AQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTMLTHF
	<i>Lachnoclostridium phytofermentans</i> ISDg	LDIREFSNKFVEATKNMSPEERSLLMCMFETVSDEINKKETAPSTSNVCNEEGSNIPDGI TPRLHKLKENYLTHKPTITTYRARAITKIAKENPGMPKIMLRACFRYCCETAPLVIQDN ELIVGAPCGAPRAGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMKEELFPFWAG KSVDEYCEDQYREAGVWELSGESFVSDCSYHAINGGGDSNPGYDVILMKGMLDIQQA DHLKELDYENPDDIEKIYFYKSIIDTTEGVMIYAKRLSEYAAELAASETNPKRKEELKI SEVNAAYVPAHKPRTFWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMYPFYKDDIESGRM NDYQAFELAGCMLIKMSEMMWITSEGGSKFFAGYQPFVNMCVGGVTRSGRDATNDLTYLL MDAVRHVKIYQPSLACRIHNKSPKEYLKKIVDVVRSRGMGFPACHFDDAHIKMMLAKGVS IEDARDYCLMGCVEPQKSGRLYQWTSTAYTQWPICIELVLNNGVPLWYGKQVCPDMGALS NFKTYEEFEAAVKKEIKYITKWDVATVISQRVHRDLAPKPLMSIMYEGCMESAKDVSAGG AMYNFGPGVVWSGLATYSDSMIAIKKLVFDEKKYTLQNEALKADFAFDQIRTDCLNA PKYGNDDDYADLIAADLVDFTEHEHRKYKTLYSILCHGTLSSISNNTPFQMTGASANGRH AWLPLSDGISPTQGADFNPTAIKSSISKMANDSMNLGMVHNFKIMSGLLDTPEGEESLI TLLRTACMFGNGEMQFNLYLDNNTLIDAQKHPEKYRDLIVRVAGYSAFFIELCKDVQDEI SRTMLTHF
	<i>Clostridium sporogenes</i> ATCC 15579	MEATKNMSDEERAGLMKMFQSVSNEITKEEPATSKVACDNNGEIPDGMTERLVKLNENYM KHVPSITTHRARAITKIAKENPGIPKSVLRGKCFKHCCETAPLLIQDHELIVGAPNGKPR AGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMREELFPYWAGKSVDEYCEDQYR EAGVWELSGESFVSDCSYHAVNNGGGDSNPGYDVVLMKKGMLDIKREAEKLAELKYENPE DIDKIYFYKSLIDTAEGVMIYAKRMSDYAAELAQKETNPKRKAELQKISEINARVPAHKP STYWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMYPFYKADIEAGRMTDYEAFELSGCM LIKSEMMWITSEGGSKFFAGYQPFVNMCVGGVTRDGRDATNELTYLLMDAVRHVKIYQ PSLACRIHKGSPQKYLKIVDVIRAGMGFPACHFDDVHIKIMLAKGVSIEDARDYCLMGC VEPQKSGRLYQWTSTGYTQWPICIELVLNHGVPLWYGKQVCPDMGDLSQFKTYEQFEAAV KQIKFITKWTAVATVISQRVHKELAPKPLMSIMYEGCMENGGKVEAGGAMYNFGPGVVWS GLATYTDSMIAIKKLVFEDKKYTLQEMNEALKADFGYEQKQKDCLEAPKYGNDDDYADL IAADLINFTEQHRKYKTLYSVLSHGTLSSISNNTPFQMTGATANGRRAWMPLSDGISPS QGADFKGPTSIKSVSKMSCEDMNIGMVHNFKLISGLLDTPGEQGIITLLRSACALQLG EVQFNLYLDNNTLIEAQKHPDQYRDLIVRVAGYSAFFVELCKDVQDEIISRTMLTHF



<p><i>Clostridium botulinum E1</i> <i>str. BoNT E Beluga</i></p>	<p>MRGKKLDIREFSNKFVEATQNMSAEERECLMKIFEGVSKEITKEEPVLEHVVCTEGDKIP          DGITQRLLKLENYLKQVPSITTYRARAITKIAKENPGMPKILLRAKCFKYCCETAPLVI          QDNELIVGAPCGAPRAGAFSPDIAWRWMVDEIDTIGTRAQDPFYISEEDKKIMREELFPY          WAGKSVDEYCNQYREAGVWELSGESFVSDCSYHAINGGGDSNPGYDVILMKGMLDIQL          EAKEHLEKLDYENPEHIEKIYFYKAIIDTTEGVMYAKRLSKYAAELAEKETNPKRKSEL          QKISEINARVPAHKPSTFWIAIQAVWTIESLLVVEENQTGMSIGRVDQYMYEYYKNDIES          GRMNDFEAFELSGCMLIKMSEMMWITSEGGSKFFAGYQPFVNMVGGVDRQGRDATNELT          YLLMDAVRHVKIYQPSLACRIHNQSPQKYLKKIVDVIRAGMGFPACHFDDVHIKMMMLAKG          VSIEDARDYCLMGCVEPQKSGRLYQWTSTAYTQWPICIELVLNNGIPLWYEQVCPNMGD          INSFKNYEEFESAVKEQIKYITKWTSVATVISQRVHKELAPKPLMSIMYEGCMDNNGRVE          AGGAMYNFGPGVIWVSLATYTDMSMAAIKLVFEEKKYTLQELNEALKADFGVYKLRKDC          LEAPKYGNDDDYADYIAADLINFTELEHRKFKTLYSVLSHGTLSSISNNTPFQGLTGATAN          GRRAWMPLSDGISPSQGSYKGPATIIKSVSKMSCDSMNIGMVHNFKLISGLLDTKEGED          GIITLLRSACVGLGEVQFNLDNDTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQD          EIISRTMLTHF</p>	
<p><i>Clostridium botulinum</i> <i>A2 str. Kyoto</i></p>	<p>MEATKNMSDEERAGLMKMFQSVSNEITREEPATSKVACDNNGEIPDGMTERLVKLEKTYL          KHVPTITTHRARAITKIAKENPGTPKSVLRGKCFKHCCETAPLVIQDNELIVGAPNGQPR          AGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMREELFPYWAGKSVDEYCEDQYR          EAGVWELSGESFVSDCSYHAVNNGGDSNPGYDVVLMKKGMLDIKREAEKLAELKYENPE          DIDKIYFYKSLIDTAEGVMYAKRMSDYAAELAQKETNPKRKAELLKISEINARVPAHKP          STYWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMYPFYKADIEAGRMTDYEAFELSGCM          LIKSEMMWITSEGGSKFFAGYQPFVNMVGGVTREGRDATNELTYLLMDAVRHVKIYQPSL          ACRIHKSPPQKYLKKIVDVIRAGMGFPACHFDDVHIKIMMLAKGVSIEDARDYCLMGCV          EPQKSGRLYQWTSTGYTQWPICIELVLNNGVPLWYKQVCPMDGDLQFKTYEQFEAAVK          EQIKFITKWTSVATVISQRVHKELAPKPLMSMMYEGCMENGRGVEAGGAMYNFGPGVWVS          GLATYADSMAAIKLVFEDKKYTLQEMNEALKADFGVYEQRLKDCLEAPKYGNDDDYADL          IAADLINFTEQEHRKYKTLYSVLSHGTLSSISNNTPFQMTGATANGRRAWMPLSDGISPS          QGADFKGPTSIIKSVSKMSCEDMNIGMVHNFKLIAGLLDTPEGEQGIITLLRSACALQLG          EVQFNLDNKTLIEAQKHPDOYRDLIVRVAGYSAFFVELCKDVQDEIISRTMLTHF</p>	
<p><i>Clostridium</i></p>	<p><i>Clostridium botulinum Bf</i></p>	<p>MEATKNMSDEERAGLMKMFQSVSNEITKEETTAPKVACDNNGEIPDGMTERLVKLEKENYM          KHVPTITTHRARAITKIAKENPGTPKSVLRGKCFKHCCETAPLVIQDNELIVGAPNGQPR          AGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMREELFPYWAGKSVDEYCEDQYR          EAGVWELSGESFVSDCSYHAVNNGGDSNPGYDVVLMKKGMLDIKREAEKLAELKYENPE          DIDKIYFYKSLIDTAEGVMYAKRMSDYAAELAQKETNPKRKAELQKISEINARVPAHKP          STYWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMYPFYKADIEAGRMTDYEAFELSGCM          LIKSEMMWITSEGGSKFFAGYQPFVNMVGGVTREGRDATNELTYLLMDAVRHVKIYQPSL          ACRIHKGSPQKYLKKIVDVIRAGMGFPACHFDDVHIKMMMLAKGVSIEDARDYCLMGCV          EPQKSGRLYQWTSTGYTQWPICIELVLNHGVPLWYKQVCPMDGDLQFKTYEQFEAAVK          EQIKFITKWTSVATVISQRVHKELAPKPLMSMMYEGCMENGRGVEAGGAMYNFGPGVWVS          GLATYADSMAAIKLVFEDKKYTLQEMNEALKADFGVYEQRLKDCLEAPKYGNDDDYADY          IASDLINFTEQEHRKYKTLYSVLSHGTLSSISNNTPFQMTGATANGRRAWMPLSDGISPS          QGADFKGPTSIIKSVSKMTCEDMNIGMVHNFKLISGLLDTPEGEQGIITLLRSACALQLG          EVQFNLDNKTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTMLTHF</p>
<p><i>Clostridium</i> <i>carboxidivorans P7</i></p>	<p>MKYLKECEVINLDIREFSSKFMEATKNMTEERASLMKMFSSVSKEITKEEPAHICVTGD          NNGQIPDGITERLVKLEKTYLKHVPSITTHRARAITKIAKENPGIPKSVLRGKCFKHCC          TAPLVIQDNELIVGAPNGQPRAGAFSPDIAWRWMVDEIDTIGTRPQDPFYISEEDKKIMR          EELFPYWQKSVDEYCEDQYREAGVWELSGESFVSDCSYHAVNNGGDSNPGYDVILMKG          MLDIKREAEDKLAELNYENPEDIDKIYFYKSLIDTAEGVMYAKRMSDYAAELAASETNP          KRKAELQKISEVNARVPAHKPSTYWEAIQSVWTIESLLVVEENQTGMSIGRVDQYMYPFY          KADIEAGRMTDFEAFELSGCMLIKMSEMMWITSEGGSKFFAGYQPFVNMCLGGVTREGRD          ATNDLTYLLMDAVRHVKIYQPSLACRIHKASPPQKYLKKIVDVIRAGMGFPACHFDDVHIK          IMLAKGVSIEDARDYCLMGCVEPQKAGRLYQWTSTGYTQWPICIELVLNHGVPLWYKQV          CPNLGDLNFKTYEQFEAAVKEQIKYITKWTSVATVISQRVHKDLAPKPLMSMMYEGCME          KGRGVEAGGAMYNFGPGVWVWGLATYTDMSMAAIKLVFDDKKYTLQEMNEALKADFAGYE          QLRKDCLEAPKYGNDDDYADLIAADLINFTEQEHRKYKTLYSVLSHGTLSSISNNTPFQGL          TGATANGRRAWTPLSDGISPTQGADYKGPSTIIKSVSKMSCEDMNIGMVHNFKLIAGLLD          TPEGEQGIITLLRSACALQLGEMQFNLDNKTLDAQKHPEEYRDLIVRVAGYSAFFVEL          CKDVQDEIISRTVLTHF</p>	

	<p><i>Clostridium ljungdahlii</i> DSM 13528</p>	<p>LDIREFSNKFAEATKNMSAEEQAALMKIFQGVSQEITKEDNGAPAVSAEPCTNNGEVPNG MTERLKRIKENYLKQKPSITTYRAKAITKIAKENPGMPKILLRAKCFRYCCETAPLVIQD DELIVGAPCGAPRAGAFSPDIAWRWMQDEIDTIGTRPQDPFYVSEEDKKVMREELFPFWQ GKSVDEYCEDQYREAGVWELSGESFVSDCSYHATNGGGDSNPGYDVILMKKGMADIQQA KDHLAKLDYENPEDIEKIYFYKSVIDTTEGVMYAKRMSEYAAELAASETNPKRKAELQK ISEVNAHVPAHKPSNFWWEAIQSVWTIESLLVVEENQTGMSIGRVDQYMPFYKADIESGR MNNYEAFELAGCMLIKMSEMMWVTSEGASKFFAGYQPFVNMVGGVTRDGLDATNDLTYL LMDAVRHVKIYQPSLACRIHNKSPKKYLKIVDVVRAGMGFPACHFDDAHIKMMLAKGVS IEDARDY CIMGCVEPQKAGRLYQWTSTAYTQWPICIELVLNHGVPLWYGKQVCPDMGDLN RFKTYEEFDAAVKEEIKYITK WTDVATVISQRVHRDLAPKPLMSIMYEGCMEHGKDVSA GAMYNFGPGVWWTGLATYADSMAAIKVVFDKCTLEQLNQALKADDFVGYEELRNDCLK APKYGNDDDYADLIAADLINFTEMEHRKYKTLYSVLSHGTLSSISNNTPFQLTGASANGR KAWTPLSDGISPTQGADFKGPTAIKSVSKMSCDNMIGMVHNFKLMAGLLETPEGEEGI ITLLRTACLFNGQMNFNYLDNKTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEI ISRTMLTHF</p>
	<p><i>Clostridium tetani</i> E88</p>	<p>MEATKNMSDEERNGLMNMFQSSISKEIKKEEKVTSNVVFNNGEIPDGMTERLIKLENYM KQVPSITTHRARAITKIAKENPGVPSVLRGKCFKYCCETAPLVIQDNELIVGAPNGKPR AGAFSPDIAWRWMEDEIDTIANRPQDPFYISEEDKKIMREELFPYWKGSVDEYCEDQYR EAGVWELSGESFVSDCSYHAVNGGGDSNPGYDVILMKKGMLDIKREAEELASLSYERPE DIEKIYFYKSIIDTAEGVMYAKRMSDYAAELAASETDPKRKAELQKISKVNARVPAHKP STFWWEAIQAVWTIESLLVVEENQTGMSIGRVDQYMPFYKSDIESGRMTDFEAFELAGCM LIKMSEMMWITSEGGSKFFAGYQPFVNMVGGVTRDGLDATNELTYLLMDAVRHVKIYQPS SLACRIHKGSPQKYLKIVDVIRAGMGFPACHFDDVHIKMMMLAKGVSIEDARDYCLMGCV EPQKSGRLYQWTSTGYTQWPICIELVLNHGVPLWYGKQVCPDMGDLSDQFKTYEQFEGAVR EQIKYITKWTAVATTISQRVHRELAPKPLMSMMYEGCMEKGRGVEAGGAMYNFGPGVWVS GLATYTDSMAAIKLVFEEKKYTLEELSEALKADDFVGYERLRKDCLEAPKYGNDDDYADY IAADLVNFTEQHRKYKTLYSVLSHGTLSSISNNTPFQMTGATANGRRAWMPLSDGISPS QGSDFKGPSTSIKSVSKISCEDMIGMVHNFKLMGSLDTPEGEQGIIALLRSACALQLG EIQFNLYDNETLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTMLTHF</p>
<p><i>Klebsiella</i></p>	<p><i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i> ATCC 13884</p>	<p>MAHYNLTPRVKVLADRLLAQKSTLCTEHATTLNALDGDIAGVPAAVKPARRFYELMRQLP LTISADELIVGNQTRKPHGAIFHDENATRRPSVFQFLNLSNELDSPDYKLVVEKGVLAIK HQLEEKTRALGSAVSRSGMDEVNGCRAAIYACDALLALAQNLANSAEQAAAETNAYRKA ELLDSAAILHHVPAHPARNFKEACQAFYLFQALQLDNGSYAVNPQGADIALLPYFQDI NSGALNTQQAYEIVECLWFKLAELSEIRAACAIDGYPMLDAMLHGAAFDHAEVNELSAMF ISAQRNLSALNLPVRMFSGVQPVSHAPFAACADTPAMEGLTPRMQRLRNHYLTVRPSVSI YRALAFTEVVKANPGMPTILLRAKAFRHACETAPILIQDDELIVGHPCGKPRAGAFSPDI AWRWVRDELDTMSTRPQDPFEISEADKKTIREEIVPFWEGRSLDEICEAQYREAGVWAFS GETFVSDLSYHQINGGGDTCPGYDVLLFTKGMNGIKADAEAHLASLSMENPEDIDRIYYY KAAIETCEGVVNYARRIAAHARELAAKEQNAQRRRAELLTIAVYVNVNVPANPPKTLQEALQ SIWTVESLFEIEENQTGLSLGRVDQYSYPMFEADIREGRLTHDSALELLQAFIHKCAELM WMSELGAKYFAGYQPFINLTVGGQKRSBGDACCNDLTYLMDAVRFVKVYQPSLACRIHN QSPQKMEKIVDVVKAGMGFPACHFDDSHIKMMLRKGDFDFEDARDYCLMGCVEPQKSGRI YQWTSTGYTQWPPIAEFVLRNRMVLFDSYQGLDGTDLRDLRTFEDFDAAVKQQIAHIVR LSAIGTVISQRVHRDVAPKPLMSLLVEGCMESGKDVAAGGAMVNHGPGGLIFSGLATYVDS MAAIRKLVFEEKKYTLEQIRDALLANFEGYEALRRDCLNAPKYGNDDNYVDQYALDITEW TEKECRKYKMLYSTLSHGTLSSISNNTPIGELTNATPNGRLAWMPLSDGISPTQGADKQGP TAIIKSVSKMNVETMSIGMVHNFKFLKGLDTPEGRHGLITLLRTASILGNGQMQFSYVD NEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTVIEKF</p>
<p><i>Escherichia</i></p>	<p><i>Escherichia fergusonii</i> ATCC 35469</p>	<p>MANYNLTPRVKVLAEERLLAHPSTLCVEHAGILSGLDGDIAGIPAAVVKPARRFYELMRQLP LAVSPDELIVGNQTHRPHGAIFHDESTAHRPSVFQFLNLSNDLDAPDYKLVIEKGVLAIK QQLEEKTRSLGSAVSRSGMDEVNACRAAIYACDALMQLAQNLAESAELAAETNAYRKA ELSESAAILHHIPAHPARSFKEACQAFYLFQALQLDNGSYAVNPEGADKALLAYYQHDI ANGLLTEAQAYEIVECLWFKLAELSEVRAACAIDGYPMFDALLHGASLENVINPLSEMF LNAQRNLSALNLPVRLFHGAHKTVTTPFAACSETPVLEGLTPRIQRLRNHYLTVRPSVSI YRALAFTEVVKANPGMPAILLRAKAFRHACETAPILIQNDELIVGHPCGKPRAGAFSPDI AWRWVRDELDTMSTRPQDPFEISEEDKKTIREEIVPFWEGRSLDEICEAQYREAGVWSFS GETFVSDLSYHQVNGGGDTCPGYDVLLFTKGMNGIKADAEAHLAELSMENPEDIDRIYYY KAAIETCEGVINYAHRIAARARELAAVEQNAQRRRAELLTIAEVNQNVPANPPKTLQEALQ SIWTVESLFEIEENQTGLSLGRVDQYCYPMFEADIREGRLTHEGAELMQAFIHKCAELM WMSELGAKYFAGYQPFINLTVGGQKRSBGDACCNDLTYLMDAVRFVKVYQPSLACRIHN QSPQKMEKIVDVVKAGMGFPACHFDDSHIKMMLRKGDFDFEDARDYCLMGCVEPQKSGRI YQWTSTGYTQWPPIAEFVLRNRMVLFDSYQGLDGTDLKDLRTFEDFDAAVKQVAHIIR LSAIGTVISQRVHRDVAPKPLMSLLVEGCMESGKDVSAGGAMVNHGPGGLIFSGLATYVDS MAAIRKLVYEDKKYTLEQIRDALLANFEGYEGLRRDCLNAPKYGNDDNYVDQYALDITEW TEREKRKYKMLYSTLSHGTLSSISNNTPIGELTNATPNGRLAWMPLSDGISPTQGADKHGP TAIIKSVSKMNVETMNIGMVHNFKFLKGLDTPEGRNGLITLLRTASILGNGQMQFSYVD NEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTVIEKF</p>

<i>Enterobacter</i>	<i>Enterobacter cancerogenus</i> ATCC 35316	MKIDALSLRVRQLRDNYLQAKPFVSARRAISVTRVYKENPGMDNTLLRALAFRRACENAP LYVADNELIVSHPAGGARGGEISPEISWRWVADELDTLPQRAQDPYQIDDETKRLLREEV FPYWEGRSLDEMAQTQLQVLGLWEWCHDDGICDVTIKTQNGGGDSCPGYDNILLTKGIKG IREEAAARLAAVDPASPEGAEAFNFYTAMLHTCDGVLTYPARRYAARLSELAETEGDPLRQ DELRHLADICRRVPEHPPRHFDALQAIWFVHSLFTLEENQTGISLGRVDQYLWPLLERD LNDGVLTHAQAEELLCCWLIKMAETLWICSESTAMYFAGYQPFINLVVGGQKREGGDATN PLTLMIMDCSAQLKIYQPGLAVRIHNQSPQPFMRKVVDVVRSGMGFPACHFDDAHIRMML HKGFSYEDARDYCLMGCVEPQKAGKMYQWTSVGYTTFTAIEALRNGRSSAGKPCGPAT GEVSAFSCYDDVERAVRTQLSAIVRKAQAATLIVQKLHADYARKPLMSSLIDGCMATAKD VTQGGATLNAGPLIWTGLADCVNSLMAIRTLVFETQRFTLQQVVDALHNFGHDDILT ACLRAPKYGNDIRAVDEIARELVRFLEQHRQYRMLYAPFAFGTLSISNNTPFGLITGAL PSGRLAGKPLADGISPSQQTGYLGPTAIINSVSRINVEEMDIGMVHNIKLMYGMLETPEG QNSLIHLLRTASILGNAQLQFSYVDDDTLRQAQQNPGDYRNLNLMIRVAGYSAFFVELSKEV QDEIISRTTQRHF
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**Supplementary Table 5. List of primers for rt-qPCR.**

<b>Gene name</b>	<b>forward</b>	<b>reverse</b>
<i>I6S</i>	TGTGTAGCGGTGAAATGCG	CATCGTTTACGGCGTGGAC
<i>L.sac</i>	GCAGATGGGCCACTGGGTATA	TCCACAACAAGTCCCCGAAAA
<i>beta (Actb)</i>	GGGAAATCGTGCGTGAC	AGGCTGGAAAAGAGCCT
<i>IL-1<math>\beta</math></i>	GCAACTGTTCCCTGAACTCAACT	ATCTTTTGGGGTCCGTCAACT
<i>IL-6</i>	CCAAGAGGTGAGTGCTTCCC	CTGTTGTTTCAGACTCTCTCCCT
<i>TNF-<math>\alpha</math></i>	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG
<i>CD68</i>	TGTCTGATCTTGCTAGGACCG	GAGAGTAACGGCCTTTTTGTGA
<i>F4/80</i>	TGACTCACCTTGTGGTCCTAA	CTTCCCAGAATCCAGTCTTTCC
<i>Ccl 2(MCP-1)</i>	TTAAAAACCTGGATCGGAACCAA	GCATTAGCTTCAGATTTACGGGT
<i>Icam1</i>	GTGATGCTCAGGTATCCATCCA	CACAGTTCTCAAAGCACAGCG
<i>Vcam1</i>	AGTTGGGGATTTCGGTTGTTCT	CCCCTCATTCCCTTACCACCC