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(71) Applicant(s)
The Board of Trustees of the Leland Stanford Junior University;Novome Biotechnologies, Inc.

(72) Inventor(s)
Sonnenburg, Justin L.;Whitaker, Weston R.;Stanley, Elizabeth;Deloache, William C.

(74) Agent / Attorney
Spruson & Ferguson, GPO Box 3898, Sydney, NSW, 2001, AU

(56) Related Art
HEHEMANN JH ET AL: "Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota", NATURE, vol. 464, no. 7290, 8 April 2010, pages 908 - 912
HEHEMANN J.H. ET AL: "Bacteria of the human gut microbiome catabolize red seaweed glycans with carbohydrate-active enzyme updates from extrinsic microbes", PNAS, vol. 109, no. 48, 12 November 2012, pages 19786 - 19791
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(71) Applicants: THE BOARD OF TRUSTEES OF THE LE-

LAND STANFORD JUNIOR UNIVERSITY [US/US];
Office of the General Counsel, Building 170, 3rd
Floor, Main Quad, P.O. Box 20386, Stanford, California
94305-2038 (US). NOVOME BIOTECHNOLOGIES,
INC. [US/US]; 15 Westmont Drive, Daly City, California
94015 (US).

(72) Inventors: SONNENBURG, Justin L.; 1942 Stockbridge

Avenue, Redwood City, California 94061 (US). WHITAK-
ER, Weston R.; 15 Westmont Drive, Daly City, Califor-
nia 94015 (US). STANLEY, Elizabeth; 1168 Los Tran-
cos Road, Portola Valley, California 94028 (US). DE-
LOACHE, William C.; 5351 Belgrave Place #1C, Oak-
land, California 94618 (US).

(74) Agent: GURLEY, Kyle A.; 201 Redwood Shores Park-

way, Suite 200, Redwood City, California 94065 (US).

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(54) Title: COMPOSITIONS AND METHODS FOR MODULATING GROWTH OF A GENETICALLY MODIFIED GUT BACTERIAL CELL

(57) Abstract: Compositions and methods are provided for modulating growth of a genetically modified bacterial cell present in a human organ, for modulating growth of a genetically modified bacterial cell in an organ (e.g., gut), for displacing at least a portion of a population of bacterial cells in an organ, and for facilitating gut colonization by a genetically modified bacterial cell. Also provided are genetically modified bacterial cells, e.g., cells that include a heterologous carbohydrate-utilization gene or gene set that provides for the ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% of bacterial cells present in a human microbiome.

COMPOSITIONS AND METHODS FOR MODULATING GROWTH OF A GENETICALLY MODIFIED GUT BACTERIAL CELL

CROSS-REFERENCE

5 This application claims the benefit of U.S. Provisional Patent Application No. 62/435,048, filed December 15, 2016, which application is incorporated herein by reference in its entirety.

GOVERNMENT RIGHTS

10 This invention was made with Government support under contracts DK085025 and OD006515 awarded by the National Institutes of Health. The Government has certain rights in the invention.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING PROVIDED AS A TEXT FILE

15 A Sequence Listing is provided herewith as a text file, "STAN-1357WO_SeqList_ST25.txt" created on November 27, 2017 and having a size of 732 KB. The contents of the text file are incorporated by reference herein in their entirety.

INTRODUCTION

20 The gut microbiota is integral to many facets of human biology. Gut bacteria produce hundreds of metabolites that accumulate in human tissue, and the composition of the gut microbiota has been linked to pathogen susceptibility, immune disorders, heart disease, central nervous system diseases, diabetes and obesity. The rules governing gut ecology are
25 largely unknown, and colonization level of an introduced bacterial strain could theoretically be influenced by a wide range of factors including competition for a variety of macro- and micro-nutrients and the avoidance of inhibitory interactions from other bacteria, bacteriophage and the immune system.

 There is a need in the art for compositions and methods that facilitate the ability to
30 colonize the gut of a patient with a desired bacterial strain, e.g., a strain that is predicted to improve the patient's health. Prior to this disclosure, it has not been possible to colonize the gut of a patient with an introduced bacterial strain such that the population of the introduced strain can reliably be maintained at a predictable colonization level, despite variations in diet, host genetics, and composition of the bacteria already present.

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Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of the common general knowledge in the field.

Unless the context clearly requires otherwise, throughout the description and the claims, the words “comprise”, “comprising”, and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of “including, but not limited to”.

SUMMARY

According to an aspect, the present invention provides a method of colonizing the gut of a subject with a genetically modified, non-naturally occurring *Bacteroides* cell, the method comprising administering to the subject both:

a) the genetically modified *Bacteroides* cell, wherein the genetically modified *Bacteroides* cell comprises a carbohydrate-utilization gene set that provides the genetically modified *Bacteroides* cell with an ability to utilize as a carbon source a porphyrin and the carbohydrate-utilization gene set comprises one or more nucleic acids, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 80% or more sequence identity to SEQ ID NO: 14, a protein that has 80% or more sequence identity to SEQ ID NO: 15, a protein that has 80% or more sequence identity to SEQ ID NO: 16, a protein that has 80% or more sequence identity to SEQ ID NO: 17, a protein that has 80% or more sequence identity to SEQ ID NO: 18, a protein that has 80% or more sequence identity to SEQ ID NO: 19, a protein that has 80% or more sequence identity to SEQ ID NO: 20, a protein that has 80% or more sequence identity to SEQ ID NO: 21, a protein that has 80% or more sequence identity to SEQ ID NO: 22, a protein that has 80% or more sequence identity to SEQ ID NO: 23, a protein that has 80% or more sequence identity to SEQ ID NO: 24, a protein that has 80% or more sequence identity to SEQ ID NO: 25, a protein that has 80% or more sequence identity to SEQ ID NO: 26, a protein that has 80% or more sequence identity to SEQ ID NO: 27, a protein that has 80% or more sequence identity to SEQ ID NO: 28, a protein that has 80% or more sequence identity to SEQ ID NO: 29, a protein that has 80% or more sequence identity to SEQ ID NO: 30, a protein that has 80% or more sequence identity to SEQ ID NO: 31, a protein that has 80% or more sequence identity to SEQ ID NO: 32, a protein that has 80% or more sequence identity to SEQ ID NO: 33, and a protein that has 80% or more sequence identity to SEQ ID NO: 34; and

b) porphyrin;

wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^7 cells/mL in the feces of the subject.

According to an aspect, the present invention provides a method of colonizing the gut of a subject with a genetically modified, non-naturally occurring *Bacteroides* cell, the method

comprising orally administering to the subject both:

a) the genetically modified *Bacteroides* cell, wherein the genetically modified *Bacteroides* cell comprises a heterologous carbohydrate-utilization gene set that (i) provides the genetically modified *Bacteroides* cell with an ability to utilize as a carbon source a porphyran, (ii) is at least 40 kb, (iii) is encoded on a plasmid, encoded on a bacterial artificial chromosome, or artificially genomically integrated, and (iv) comprises one or more nucleic acids, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 80% or more sequence identity to SEQ ID NO: 14, a protein that has 80% or more sequence identity to SEQ ID NO: 15, a protein that has 80% or more sequence identity to SEQ ID NO: 16, a protein that has 80% or more sequence identity to SEQ ID NO: 17, a protein that has 80% or more sequence identity to SEQ ID NO: 18, a protein that has 80% or more sequence identity to SEQ ID NO: 19, a protein that has 80% or more sequence identity to SEQ ID NO: 20, a protein that has 80% or more sequence identity to SEQ ID NO: 21, a protein that has 80% or more sequence identity to SEQ ID NO: 22, a protein that has 80% or more sequence identity to SEQ ID NO: 23, a protein that has 80% or more sequence identity to SEQ ID NO: 24, a protein that has 80% or more sequence identity to SEQ ID NO: 25, a protein that has 80% or more sequence identity to SEQ ID NO: 26, a protein that has 80% or more sequence identity to SEQ ID NO: 27, a protein that has 80% or more sequence identity to SEQ ID NO: 28, a protein that has 80% or more sequence identity to SEQ ID NO: 29, a protein that has 80% or more sequence identity to SEQ ID NO: 30, a protein that has 80% or more sequence identity to SEQ ID NO: 31, a protein that has 80% or more sequence identity to SEQ ID NO: 32, a protein that has 80% or more sequence identity to SEQ ID NO: 33, and a protein that has 80% or more sequence identity to SEQ ID NO: 34; and

b) porphyran;

wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^7 cells/mL in the feces of the subject.

Compositions and methods are provided for modulating growth of a genetically modified bacterial cell present in a human organ, for modulating growth of a genetically modified bacterial cell in an organ, for displacing at least a portion of a population of bacterial cells in an organ, and for facilitating gut colonization by a genetically modified bacterial cell.

For example, in some cases a subject method includes introducing to a human organ (e.g., gut) a genetically modified bacterial cell capable of controlled entrenchment and/or controlled colonization. In some cases a method of the disclosure includes administering to a human a rare carbohydrate of interest that is utilized as a carbon source by a subject genetically modified bacterial cell present in a human organ (e.g., gut), where less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none;

e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ utilize the rare carbohydrate of interest as a carbon source. In some cases a method of the disclosure includes introducing a subject genetically modified bacterial cell to an organ (e.g., gut) *in vivo*, wherein the genetically modified bacterial cell utilizes as a carbon source a rare carbohydrate of interest, where less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ utilize the rare carbohydrate of interest as a carbon source. In some cases a method of the disclosure includes introducing to an organ (e.g., gut) a genetically modified bacterial cell capable of controlled entrenchment and/or controlled colonization, and displacing at least a portion of the population of bacterial cells in the organ with the genetically modified bacterial cell.

In some cases a method of the disclosure includes (a) introducing a genetically modified bacterial cell into a gut of an individual, where the genetically modified bacterial cell includes a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with the ability to use a carbohydrate of interest as a carbon source; and (b) administering the carbohydrate of interest to the individual, thereby providing the genetically modified bacterial cell with the carbon source.

Provided are genetically modified bacterial cells. In some embodiments such a cell utilizes as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%,

or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome (e.g., gut microbiome). In some cases, such a cell includes a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with an ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome (e.g., gut microbiome). In some cases, a genetically modified bacterial cell includes (i) a heterologous therapeutic transgene; and (ii) a carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with an ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome (e.g., gut microbiome). In some cases, a genetically modified bacterial cell includes a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with the ability to use a rare carbohydrate of interest as a carbon source.

Provided are methods of genetically modifying a bacterial cell. In some such cases, a subject method includes (i) providing a bacterial cell; and (ii) genetically modifying the bacterial cell to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome (e.g., gut microbiome). In some cases, a subject method includes (i) providing a bacterial cell that utilizes as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome (e.g., gut microbiome);

and (ii) genetically modifying the bacterial cell to express one or more therapeutic transgenes.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention is best understood from the following detailed description when read in conjunction with the accompanying drawings. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee. It is emphasized that, according to common practice, the various features of the drawings are not to-scale. On the contrary, the dimensions of the various features are arbitrarily expanded or reduced for clarity. Included in the drawings are the following figures.

Figure 1. Glycoside hydrolase representation in the healthy American microbiota. The incidence and mean abundance of glycoside hydrolase families in 87 Human Microbiome Project metagenomes are shown. The glycoside hydrolase family GH86 includes enzymes that can break down either porphyrin or agarose, and is underrepresented in these samples, with an incidence and mean abundance of 66% and 0.00015, respectively. GH32 is associated with utilization of inulin and is more highly represented with an incidence and mean abundance of 100% and 0.0049, respectively.

Figure 2 (panels A-E). The abundance of porphyrin-utilizing *Bacteroides* can be modulated by the addition of porphyrin. **(panel A)** A strain of *Bacteroides ovatus* capable of utilizing porphyrin (NB001) was isolated from the environment. **(panel B)** The porphyrin utilizing strain reaches a higher ($P = 0.02$) and more predictable ($P < 0.01$) abundance in eight different complex communities in culture when porphyrin is present. The average of two replicates for each community is shown. **(panel C)** Porphyrin increased abundance of porphyrin utilizer *in vivo*. Two groups of conventional mice, one fed a standard (std) diet and one fed a polysaccharide deficient (pd) diet, were colonized with porphyrin utilizing *Bacteroides*, strain NB006. Porphyrin was administered in the water, and abundance of both total anaerobic culturable bacteria and NB006 in the feces were monitored. Averages and standard deviation for replicates of four mice are shown. **(panel D)** Conventional mice being fed a standard diet (i.e. lacking porphyrin) were administered a *Bacteroides* strain that cannot utilize porphyrin, NB008. After seven days, these mice were challenged with NB006, a *Bacteroides* strain which can utilize porphyrin. NB006 was cleared from the mice after five days. Abundance of NB008 and NB006 in the feces was monitored by selective plating, averages and standard deviation for replicates of three mice are shown. **(panel E)** Porphyrin allowed for stable colonization of a porphyrin utilizer into a resistant microbiota. Conventional mice were administered NB008, and one week later given porphyrin in the water simultaneous to receiving NB006. Porphyrin was removed from the water and then

re-introduced, while abundances of both strains in the feces were monitored via selective plating. NB006 was able to displace NB008 with the addition of porphyrin, and inhibit it from re-invasion on day 48. Averages and standard deviation for replicates of three mice are shown.

Figure 3. Knockout of an eight-gene operon in the putative NB001 porphyrin PUL prevents growth on porphyrin. Genes corresponding to homologs of BACPLE_1692-1699 from *B. plebeius* were deleted from NB001. End-point cell density measurements were taken after growth in minimal media supplemented with either .2% glucose (blue) or .8% nori extract (orange).

Figure 4. Nucleotide alignment between the porphyrin mobile elements in *B. plebeius* (Hehemann et al., Nature 464, 908–912 (2010); Hehemann et al., Proc. Natl. Acad. Sci. U. S. A. 109, 19786–19791 (2012)) and NB001. Three truncations of the putative porphyrin polysaccharide utilization locus (PUL), shown in green, were cloned into a conjugation vector and transferred to a naive strain to assay growth on porphyrin.

Figure 5. Map of the medium-length porphyrin PUL conjugative plasmid pWD036. The medium-length porphyrin PUL genes were cloned from the NB001 genome and are homologs of BACPLE_1683-1706 from the *B. plebeius* genome (see e.g., Tables 5 and 6).

Figure 6. The medium-length porphyrin PUL is sufficient to confer growth on porphyrin in *B. vulgatus*. A *B. vulgatus* strain (NB004) containing either the small (pWD037) or medium-length (pWD036) porphyrin PUL were grown in minimal media supplemented with either .2% glucose (blue) or .8% nori extract (orange). End-point cell density measurements are shown. pWD037 contains homologs of BACPLE_1688-1699. pWD036 contains homologs of BACPLE_1683-1706 (see, e.g., Tables 5 and 6).

Figure 7 (panels A-D). Niche availability varied by microbiota and could be modulated by addition of a privileged nutrient. **(panel A)**, Schematic of experimental design. Groups of mice with three different gut communities, mouse (RF), or human (Hum-1, Hum-2), were colonized with NB001. NB001 was tracked in feces for seven days, and mice were switched to specialized polysaccharide chow containing either inulin (in.) or porphyrin (por.). **(panel B)**, Density of NB001 in feces in the three gut communities over the course of seven days (n=10) Kruskal-Wallis test, p<0.0001. **(panel C)**, Density of NB001 in feces prior to and upon addition of inulin in the diet (brackets/dotted lines, RF n=4, Hum-1 n=5) Kruskal-Wallis test, p=0.03. **(panel D)**, Density in NB001 in feces prior to and upon addition of nori extract in the diet (brackets/dotted lines, RF n=5, Hum-1 n=7, Hum-2 n=6). Kruskal-Wallis test, p=0.19. Error bars indicate s.e.m.

Figure 8 (panels A-F). Access to a privileged nutrient mediated population size and overcame isogenic self-exclusion. Density of NB001 (PUL+), NB001 lacking the ability to utilize porphyrin (PUL-), and total culturable anaerobes (Total) in feces of conventional mice.

Periods of administration of porphyrin extract in drinking water indicated by brackets/dotted lines (panels a-c: 1% w/v, panels d-f: 0.1% w/v). **(panel A)**, Mice colonized with PUL+ and fed a MAC-deficient diet or **(panel B)**, MAC-rich diet demonstrated toggling of strain abundance upon administration of porphyrin extract. **(panel C)**, Mice colonized with PUL- and fed a
 5 MAC-rich diet showed no change in strain abundance with administration of porphyrin extract. **(panels D-F)** Mice were colonized with PUL- for 6 days, and challenged with PUL+ on day 6. **(panel D)**, PUL+ is excluded by PUL- in the absence of porphyrin extract. **(panel E)**, PUL+ displaces PUL- with access to porphyrin for five days. **(panel F)**, PUL+ and PUL- stably co-exist after a three day pulse of porphyrin extract. Error bars indicate standard deviation,
 10 n=4 for all experiments.

Figure 9 (panels A-E). Control over population size was engineered, and was highly tunable. **(panel A)**, Schematic of porphyrin PUL from NB001 aligned to the previously published *B. plebeius* PUL. Shown below are the different minimal PULs (Long, Medium, and
 15 Short) designed and tested for ability to confer growth on porphyrin extract. The eight gene region deleted from NB001 PUL- is shown in gray ("Knockout"). **(panel B)**, Growth curves for natural and engineered strains on porphyrin extract as sole carbon source. **(panel C)**, *B. thetaiotaomicron* harboring the medium length PUL colonized in conventional mice demonstrates toggling upon administration of 1% w/v porphyrin extract in the drinking water
 20 (brackets/dotted lines, n=4). Error bars indicate standard deviation. **(panel D)**, NB001 PUL+ colonized in conventional mice demonstrates tunable response to porphyrin extract in the drinking water (brackets/dotted lines, n=4 per group). Error bars indicate standard deviation. **(panel E)**, NB001 expressing GFP colonized in conventional mice given 0.01% porphyrin extract (left) or 1% porphyrin extract (right). Host epithelium visualized by DAPI (nuclei, blue),
 25 epithelial border visualized by phalloidin (F-actin, white), background microbiota by DAPI segmented from host epithelium (bacteria, magenta), NB001 by endogenous GFP (bacteria, green). Scale bar represents 20 μ m.

Figure 10 (panels A-B). Three model background communities of gut microbes were distinct from each other. **(panel A)**, Principal Coordinates Analysis of weighted UniFrac
 30 distance for 16S rDNA amplicons from feces from the three background community groups from Figure 7 before diet switch, conventional (RF), or humanized (Hum-1 and Hum-2), n=10. **(panel B)**, Comparison of weighted UniFrac distances within each group (Intra) or across groups (AxB, AxC, BxC). One- way ANOVA, p<0.0001.

Figure 11 (panels A-C). NB001 can utilize both inulin and porphyrin extract as sole
 35 carbon sources for growth. NB001 demonstrates growth in minimal media with only one specified carbon source, either **(panel A)**, glucose (doubling time = 157 minutes), **(panel B)**,

inulin (doubling time = 127 minutes), or (**panel C**), porphyran extract (doubling time = 98 minutes).

Figure 12 (panels A-B). Porphyran extract did not significantly impact the gut microbiota in the absence of a known utilizer. Weighted UniFrac analysis was performed on fecal 16S data for conventional mice colonized with a porphyran utilization knockout (Figure 8c) before addition of porphyran extract (Pre, n=8) or after (Post, n=9). (**panel A**), Principal Coordinates Analysis (**panel B**), Unpaired two-tailed t-test, p=0.25

Figure 13 (panels A-B). Primary colonizer displacement was robust and contingent upon access to porphyran. (**panel A**), Conventional mice (n=7) colonized with NB001 (PUL- 1) containing an eight-gene deletion abrogating its ability to utilize porphyran (Figure 9b) demonstrate resistance to subsequent challenge with an isogenic knockout strain (PUL- 2) in the presence of 1% porphyran extract in the drinking water. Notably, conventionally raised mice were permissive to colonization by this strain and other species of *Bacteroides* tested (*B. thetaiotaomicron*, *B. fragilis*, *B. uniformis*, *B. vulgatus*, stable colonization range of 8×10^5 – 3×10^8 c.f.u. per ml feces), which differs from reports of tests on other conventionally raised mice, potentially reflecting inter-colony microbiota differences. (**panel B**), Mice from Figure 8e were challenged with the originally colonizing porphyran utilization knockout (PUL-) that was displaced by the utilizer (PUL+) and demonstrated colonization resistance to the previously displaced knockout strain.

Figure 14 (panels A-C). Data showing that access to porphyran allowed for crypt invasion and stable maintenance in the presence of an exclusionary primary colonizing strain.

DETAILED DESCRIPTION

As summarized above, compositions and methods are provided for modulating growth of a genetically modified bacterial cell present in a human organ, for modulating growth of a genetically modified bacterial cell in an organ (e.g., gut), for displacing at least a portion of a population of bacterial cells in an organ, and for facilitating gut colonization by a genetically modified bacterial cell. Also provided are genetically modified bacterial cells, e.g., cells that include a heterologous carbohydrate-utilization gene or gene set that provides for the ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% of bacterial cells present in a human microbiome.

Before the present methods and compositions are described, it is to be understood that this invention is not limited to a particular method or composition described, and as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose

of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limits of that range is also specifically disclosed. Each smaller range between any stated value or intervening value in a stated range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included or excluded in the range, and each range where either, neither or both limits are included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, some potential and preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited. It is understood that the present disclosure supercedes any disclosure of an incorporated publication to the extent there is a contradiction.

As will be apparent to those of skill in the art upon reading this disclosure, each of the individual embodiments described and illustrated herein has discrete components and features which may be readily separated from or combined with the features of any of the other several embodiments without departing from the scope or spirit of the present invention. Any recited method can be carried out in the order of events recited or in any other order which is logically possible.

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a cell" includes a plurality of such cells (e.g., a population of such cells) and reference to "the protein" includes reference to one or more proteins and equivalents thereof, e.g. polypeptides, known to those skilled in the art, and so forth.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

METHODS AND COMPOSITIONS

Provided are methods and compositions for modulating growth of a genetically modified bacterial cell present in an organ (e.g., human organ) of an individual. Modulation of growth can be achieved by administering an energy and/or carbon source (e.g., a nutrient, a carbohydrate, and the like) of interest to the individual, thereby providing the genetically modified bacterial cell with the energy and/or carbon source. The genetically modified bacterial cell can include a gene or gene set (e.g., a carbohydrate-utilization gene or gene set, e.g., in some cases a heterologous gene or gene set) that provides the genetically modified bacterial cell with the ability to use the energy and/or carbon source. As an example, in some cases a subject genetically modified bacterial cell includes a heterologous gene or gene set that provides the genetically modified bacterial cell with the ability to use a carbohydrate of interest as a carbon source.

In some cases a subject method includes a step of introducing the genetically modified bacterial into the organ (e.g., into a gut of an individual) prior to the modulating growth step. Thus, in some embodiments a genetically modified bacterial cell is introduced into an individual (e.g., into the individual's gut). The individual can be any mammalian species, e.g. rodent (e.g., mouse, rat), ungulate, cow, pig, sheep, camel, rabbit, horse, dog, cat, primate, non-human primate, human, etc. Thus, in some cases the individual is human. The individual may be a neonate, a juvenile, or an adult. In some cases, the introduction is by oral administration. Any convenient type of oral administration can be used. For example, oral administration can include delivery via eating (e.g., incorporated into food), drinking (e.g., incorporated into a solution such as drinking water), oral gavage (e.g., using a stomach tube), aerosol spray, tablets, capsules, pills, powders, and the like. In some embodiments, a genetically modified bacterial cell is introduced into an individual (e.g., into the individual's gut) by delivery into the individual's colon. Any convenient number of genetically modified cells can be introduced. For example, in some cases 10^3 or more cells (e.g., 10^4 or more, 10^5 or more, 10^6 or more, 10^7 or more, 10^8 or more cells, 10^9 or more, or 10^{10} or more) cells are introduced. In some cases 10^{11} or more cells are introduced. In some cases, between 10^7 and 10^{13} cells are introduced (e.g., between 10^8 - 10^{12} , 10^9 - 10^{12} , or 10^{10} - 10^{12} cells).

i. Growth control

Provided are methods for modulating growth of a genetically modified bacterial cell present in an organ (e.g., a gut) of an individual (e.g., a human). Growth can be controlled by providing (e.g., administering to the individual) a carbohydrate that can be utilized by the genetically modified bacterial cell as a carbon source. For example, growth can be controlled by adjusting the amount of carbohydrate provided and/or frequency with which the

carbohydrate is provided.

In some cases, a privileged niche is created by using a carbon source (e.g., carbohydrate) that is uncommon in the diet of the individual and is either rarely or not consumed by the gut bacteria in the population of interest (e.g., human population of interest).

5 The term 'privileged niche' is used herein to refer to a situation in which the genetically modified bacteria have 'privileged' access to a resource (e.g., a carbon source), which thereby provides them with a growth advantage (at least with respect to that resource). The use of a carbon source (e.g., a carbohydrate such as porphyran) to create a privileged niche for an introduced bacteria allows the bacteria to establish a population (e.g., colonize, entrench, etc.)

10 in the target organ (e.g., gut). Moreover, because the introduced bacteria has privileged access, the amount of the carbon source (e.g., carbohydrate) that is made available to the introduced bacteria can be manipulated (e.g., increased, decreased, or maintained) to control the growth of the population of introduced bacteria (e.g., in some cases without perturbing resident bacterial populations). In some embodiments, this results in a situation in which the

15 abundance of introduced bacteria at any given time is predictable, e.g., based on the amount of privileged resource (e.g., carbohydrate such as porphyran) that is being provided (e.g., introduced into the diet of the individual) (see, e.g., Figure 2, panel B). For example, in some cases the deviation in abundance of the introduced bacteria between different microbial communities by the 7th day after introduction (or 7th day after introduction, where the

20 introduced bacteria had access to the privileged resource) spans a range of 4-fold or less (e.g., 3-fold or less).

In some embodiments, e.g., to provide a privileged niche to the introduced genetically modified bacteria, the carbohydrate of interest is a rare carbohydrate of interest. By 'rare' carbohydrate of interest, it is meant a carbohydrate of interest that is utilized by less than 50%

25 (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in a target organ such as the gut (i.e., cells 'other' than

30 the introduced/genetically modified bacteria, e.g., cells of the resident population prior to introduction). Thus, in some cases (e.g., in any of the methods of the disclosure), a rare carbohydrate of interest is one that can be utilized by less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than

35 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ. In some cases (e.g., in any of the methods of the disclosure), the

rare carbohydrate of interest is one that can be utilized by less than 20% (e.g., less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none) of other bacterial cells present in the organ. In some cases (e.g., in any of the methods of the disclosure), the rare carbohydrate of interest is one that can be utilized by less than 5% (e.g., less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none) of other bacterial cells present in the organ. In some cases (e.g., in any of the methods of the disclosure), the rare carbohydrate of interest is one that can be utilized by less than 2% (e.g., less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none) of other bacterial cells present in the organ. In some cases (e.g., in any of the methods of the disclosure), the rare carbohydrate of interest is one that can be utilized by less than 0.5% (e.g., less than 0.2%, less than 0.1%, or none) of other bacterial cells present in the organ. In some cases (e.g., in any of the methods of the disclosure), the rare carbohydrate of interest is one that can be utilized by none of the other bacterial cells present in the organ.

A method of the disclosure can include a step of administering to an individual (e.g., a human) a carbohydrate of interest (e.g., a rare carbohydrate of interest) that is utilized as a carbon source by a subject genetically modified bacterial cell present in an organ of the individual (e.g., the gut), wherein less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ utilize the rare carbohydrate of interest as a carbon source. In some cases, such a method includes a step of introducing the genetically modified bacterial cell into the organ of the individual, e.g., prior to administering the carbohydrate of interest. In some embodiments, the organ (e.g., gut) of the individual includes at least 5 other bacterial species (other than the genetically modified bacteria), e.g., at least 8, at least 10, at least 15, at least 20, at least 50, at least 100, at least 200, at least 500, or at least 1,000 other bacterial species. In some cases, the organ (e.g., gut) of the individual includes at least 50 other bacterial species (other than the genetically modified bacteria). In some cases, the organ (e.g., gut) of the individual includes at least 100 other bacterial species (other than the genetically modified bacteria).

In some cases, two or more privileged niches (e.g., in some cases using dietary substrates from distinct geographic regions) can be used, e.g., to increase the effectiveness of this strategy even further. For example, this may allow robust colonization in the event that one of the two rare substrates is utilized by an individual's endogenous microbiota.

ii. Colonization and Entrenchment

In some cases, growth modulation is used to allow a bacterial cell (e.g., population of

bacterial cells) to colonize a target organ (e.g., gut). Thus, provided are methods that facilitate colonization of a bacterial cell (e.g., a population of bacterial cells) in an organ (e.g., gut) of an individual. By "colonize" it is meant that an introduced bacterial cell (e.g., population of bacterial cells) can establish a population of a desired abundance or level or can establish a large enough population in the target organ that the population is detectable, despite the presence of already established bacterial populations. In some cases, the introduced bacteria reaches a 'high level' of colonization (i.e., a 'high abundance'). In such cases, the introduced bacteria reaches an abundance of 10^5 CFU/ μ l or more (e.g., 10^6 CFU/ μ l or more, 10^7 CFU/ μ l or more) (e.g., by day 6 after introduction) (e.g., in the target organ). Thus, in some cases, introduced bacteria reaches an abundance of 10^7 CFU/ μ l or more. In some cases, the introduced bacteria reaches a 'low level' of colonization (i.e., a 'low abundance'), but the population is still detectable (e.g., by day 6 after introduction). For example, in some cases, the introduced bacteria reaches an abundance in a range of from 10^2 CFU/ μ l to 10^4 CFU/ μ l (e.g., 10^2 CFU/ μ l, 10^3 CFU/ μ l, 10^4 CFU/ μ l) (e.g., by day 6 after introduction) (e.g., in the target organ).

In some embodiments, the introduced/genetically modified bacteria reaches an abundance such that it attains a population level of 10% or more (e.g., 20% or more, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, or 90% or more) of total anaerobic CFUs (see e.g., Figure 2) (e.g., by day 6 after introduction) (e.g., in the target organ). In some embodiments, the introduced bacteria reaches an abundance such the population attains a population level in a range of from 10%-90% (e.g., from 10%-80%, 10%-70%, 10%-60%, 10%-50%, 20%-90%, 20%-80%, 20%-70%, 20%-60%, 20%-50%, 30%-90%, 30%-80%, 30%-70%, 30%-60%, or 30%-50%) of total anaerobic CFUs (e.g., by day 6 after introduction) (e.g., in the target organ).

In some embodiments, the introduced/genetically modified bacteria reaches an abundance such that it attains a population level of 1% or more (e.g., 2% or more, 5% or more, or 10% or more) of total bacterial cells in the organ (e.g., gut). In some embodiments, the introduced/genetically modified bacteria reaches an abundance such that it attains a population level in a range of from 1%-50% of total bacterial cells in the organ (e.g., from 1%-40%, 1%-30%, 1%-20%, 1%-15%, 2%-50%, 2%-40%, 2%-30%, 2%-20%, 2%-15%, 5%-50%, 5%-40%, 5%-30%, 5%-20%, or 5%-15% of total bacterial cells in the organ).

In some cases at least a portion of the population of bacterial cells in an organ (e.g., gut) is displaced as a result of modulating the growth (e.g., by administration of a carbohydrate of interest) of the genetically modified bacterial cell. For example, in some cases 5% or more (e.g., 10% or more, 15% or more, or 20% or more) of the population of bacterial cells in an organ (e.g., gut) is displaced as a result of modulating the growth (e.g., by administration of a carbohydrate of interest) of the genetically modified bacterial cell. In some cases, the

genetically modified bacterial cell and the bacterial cells in the population of bacterial cells are the same species. In some cases, the genetically modified bacterial cell and the bacterial cells in the population of bacterial cells are different species. In some cases, the genetically modified bacterial cell is generated by providing a bacterial cell from the population of bacterial cells and removing or inactivating one or more genes in the bacterial cell.

In some embodiments, colonization is stable for a long period of time. Thus, in some cases a genetically modified bacterial cell of the disclosure becomes entrenched in the gut. The term "entrench" (e.g., "entrenchment") is used herein to refer to a situation in which an introduced species becomes a stable/persistent member of the community into which it was introduced. For example, in some cases when entrenchment is not accomplished, an introduced bacterial species (e.g., introduced into the gut of an individual) might be cleared (reduced to undetectable levels) by approximately one week after introduction. If there is not a niche available to the introduced bacteria, it must compete with species that are already established (entrenched), and that share the same niche with the introduced bacteria (i.e., the introduced bacteria would have to compete for resources with already established species).

In some cases, entrenchment is accomplished when an introduced bacteria (e.g., a wild type species not normally present in the target organ, e.g., gut; a genetically modified bacterial cell; and the like) remains detectable or at a desired abundance or population level in the organ into which it was introduced (e.g., on day 6 after introduction). In other words, in some cases an introduced bacteria is entrenched if it remains detectable or at a desired abundance or population level for 6 or more days (e.g., 7 or more, 8 or more, 9 or more, or 10 or more) days after introduction. By detectable it is meant that the population of introduced bacteria includes a large enough number of individuals that their presence is detectable. In some cases, entrenchment is maintained by providing a sufficient amount of a carbohydrate (e.g., rare carbohydrate of interest) that can be utilized by the genetically modified bacterial cell at a sufficient frequency. In some cases, entrenchment can be maintained in the absence of a carbohydrate (e.g., rare carbohydrate of interest) that can be utilized by the genetically modified bacterial cell.

For any of the above metrics (e.g., abundance level, abundance range, population level, and the like), a time frame can be placed on the metric. For example, in some cases the metric is reached within 5 days of introduction of the bacteria. In some case, the metric is reached within 6 days of introduction of the bacteria. In some case, the metric is reached within 7 days of introduction of the bacteria. However, the time frame need not be relative to introduction of the bacteria. For example, in some cases the metric is relative to the introduction of the resource (e.g., carbohydrate of interest, rare carbohydrate of interest such as porphyrin). Thus, in some cases the metric is reached within 5 days of introduction of the resource (e.g., carbohydrate of interest, rare carbohydrate of interest such as porphyrin). In

some case, some cases the metric is reached within 6 days of introduction of the resource (e.g., carbohydrate of interest, rare carbohydrate of interest such as porphyran). In some case, the metric is reached within 7 days of introduction of the resource (e.g., carbohydrate of interest, rare carbohydrate of interest such as porphyran).

In some embodiments a method of the disclosure includes a step of detecting the presence of (e.g., measure the abundance of) the genetically modified bacterial cell after it has been introduced into an individual (e.g., 3 days, 4 days, 5 days, 6 days, and/or 7 days after introduction; and/or 3 days, 4 days, 5 days, 6 days, and/or 7 days after providing the carbohydrate of interest). In some such cases, the step of detecting includes measuring the colony forming units (e.g., CFU/ μ l) of the genetically modified bacterial cell present in the organ (e.g., gut) of the individual. In some such cases the detecting further includes measuring the colony forming units (e.g., CFU/ μ l) of other bacteria present in the organ.

In some cases, the term "controlled" is used in front of "colonization" and/or "entrenchment" (e.g., "controlled colonization" ; "controlled entrenchment"). The term "controlled" is used as such to refer to a situation in which the colonization and/or entrenchment of a bacteria is controllable by a user. For example, if the growth and/or survival of a given bacterial cell (e.g., a genetically modified bacterial cell) can be modulated by administering an energy and/or carbon source (e.g., carbohydrate of interest) to a host (e.g., a human) and/or a host organ, then the colonization and/or entrenchment of the bacterial is controllable. For example, in such a situation the population size and/or duration of colonization can depend on the amount and/or frequency with which the energy and/or carbon source (e.g., carbohydrate) is administered.

iii. Carbohydrate of interest

In some embodiments the carbohydrate of interest (e.g., rare carbohydrate of interest) is a polysaccharide. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is a sulfated carbohydrate. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is selected from the group consisting of porphyran, agarose, carrageenan, and any combination thereof. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is a carbohydrate cleaved by a glycoside hydrolase belonging to glycoside hydrolase family GH86. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is a marine carbohydrate. Examples of marine carbohydrates include but are not limited to: porphyran, agarose, agaropectin, carrageenan, and marine microbe exopolysaccharides. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is selected from porphyran and agarose. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is porphyran. In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is agarose.

In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is a carbohydrate that contains a glycosidic linkage selected from the group consisting of β -d-galactopyranose to α -l-galactopyranose-6-sulphate, β -d-galactopyranose to 3,6-anhydro- α -l-galactopyranose.

5 In some cases the carbohydrate of interest (e.g., rare carbohydrate of interest) is a sulfated polygalactan. In some such cases, one or more of the galactose residues of the sulfated polygalactan can be a 3,6-anhydro-galactose (e.g., in some cases joined by alternating α -1,3 and β -1,4-glycosidic linkage). In some cases, one or more of the galactopyranose residues of the sulfated polygalactan can be modified by one or more ester
10 sulfates. In some cases, one or more of the galactose residues of the sulfated polygalactan is a 3,6-anhydro-galactose (e.g., in some cases joined by alternating α -1,3 and β -1,4-glycosidic linkage); and one or more of the galactopyranose residues of the sulfated polygalactan is modified by one or more ester sulfates.

15 In some cases, the carbohydrate of interest is administered to an individual and in some such cases the carbohydrate of interest is isolated. The term "isolated" refers to the state in which a molecule (e.g., a carbohydrate) can be. In such a case, the carbohydrate will be free or substantially free of material with which it is naturally associated such as other carbohydrates with which it is found in the natural environment, or the environment in which it is prepared.

20 In some cases, less than 50% (e.g., less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1%, or none; e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ utilize
25 the carbohydrate of interest (e.g., rare carbohydrate of interest) as a carbon source. In some cases, the carbohydrate of interest (e.g., rare carbohydrate of interest) cannot be utilized or digested by mammalian (e.g., human) cells.

30 In some cases, the carbohydrate of interest is administered at a sufficient frequency and/or at a sufficient amount for controlled colonization and/or controlled entrenchment. For example, the carbohydrate of interest can be administered 1, 2, 3, 4, 5, 6, or more times per day, week, month, or year. The carbohydrate of interest can be administered over a period of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more days, weeks, months, or years. In some cases, the carbohydrate of interest can be administered by oral administration. Any convenient type of oral administration can be used. For example, oral administration can include delivery via
35 eating (e.g., incorporated into food), drinking (e.g., incorporated into a solution such as drinking water), oral gavage (e.g., using a stomach tube), aerosol spray, tablets, capsules, pills, powders, and the like.

iv. Genetically modified bacteria

In some cases a genetically modified bacterial cell includes a heterologous carbohydrate-utilization gene or gene set. "Heterologous," as used herein, means a nucleic acid and/or polypeptide that is not found in the native bacteria. For example, in a case where a bacterial cell includes a gene set (e.g., a nucleic acid encoding a set of proteins) that provides the cell with the ability to utilize a carbon source that the cell otherwise cannot use, and where that gene set is not naturally found in that bacteria, the gene set is 'heterologous' to the bacterial cell.

In some cases a subject method is a method of genetically modifying a bacterial cell to utilize as a carbon source a rare carbohydrate of interest. Any convenient method can be used to introduce a nucleic acid into a prokaryotic cell, e.g., by electroporation (e.g., using electro-competent cells), by conjugation, by chemical methods (e.g., using chemically competent cells), and the like.

In some embodiments, a genetically modified bacterial cell utilizes as a carbon source a rare carbohydrate of interest (as described elsewhere herein, e.g., wherein less than 50% of other bacterial cells present in the organ utilize the rare carbohydrate of interest as a carbon source). This is due to the fact that a subject genetically modified bacterial cell includes a carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with the ability to use a carbohydrate of interest as a carbon source. In some cases, the carbohydrate-utilization gene or gene set is native to the cell. In some case, the carbohydrate-utilization gene or gene set is heterologous to the cell (e.g., can be from a different species of bacteria). Thus, in some cases, the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of a heterologous carbohydrate-utilization gene or gene set. In some cases, the genetically modified bacterial cell is capable of utilizing the carbohydrate of interest as a carbon source in the absence of a heterologous carbohydrate-utilization gene or gene set, but the presence of the heterologous carbohydrate-utilization gene or gene set enhances that capability.

In some cases, a carbohydrate-utilization gene or gene set includes a porphyranase (e.g., one from GH family 86 (GH86)). In some cases, a carbohydrate-utilization gene or gene set includes an agarase (e.g., one from GH family 86 (GH86)).

In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1706 from the *B. plebeius* genome (or homologs thereof) (see, e.g., Table 6). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1687 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1700-1706 from the *B.*

plebeius genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1687 from the *B. plebeius* genome (or homologs thereof) and BACPLE_1700-1706 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1699 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1688-1706 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1687 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1700-1706 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding BACPLE_1683-1687 and BACPLE_1700-1706 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome (or homologs thereof).

As such, in some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1706 from the *B. plebeius* genome (see, e.g., Table 6). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1687 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1700-1706 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1687 from the *B. plebeius* genome (or homologs thereof) and BACPLE_1700-1706 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1699 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic

acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1688-1706 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1687 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1700-1706 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with BACPLE_1683-1687 and BACPLE_1700-1706 from the *B. plebeius* genome (or homologs thereof) as well as both porphyranases from within BACPLE_1688-1699 from the *B. plebeius* genome.

Table 6. SEQ ID NOs. and annotations for proteins encoded by *B. plebeius* genome (BACPLE_1669-1706).

B. Plebeius Homolog ID	SEQ ID NO	Annotation
BACPLE_01669	1	histidine kinase CDS
BACPLE_01670	2	beta-agarase CDS
BACPLE_01671	3	glycosyhydrolase CDS
BACPLE_01672	4	threonine synthase CDS
BACPLE_01673	5	hypothetical protein CDS
BACPLE_01674	6	altronate hydrolase CDS
BACPLE_01675	7	altronate oxidoreductase CDS
BACPLE_01676	8	sorbitol dehydrogenase CDS
BACPLE_01677	9	L-fucose:H ⁺ symporter permease CDS
BACPLE_01678	10	amidohydrolase CDS
BACPLE_01679	11	aldo/keto reductase CDS
BACPLE_01680	12	hypothetical protein CDS
BACPLE_01682	13	hypothetical protein CDS
BACPLE_01683	14	hypothetical protein CDS
BACPLE_01684	15	glycosyhydrolase CDS

B. Plebeius Homolog ID	SEQ ID NO	Annotation
BACPLE_01685	16	hypothetical protein CDS
BACPLE_01686	17	hypothetical protein CDS
BACPLE_01688	18	hypothetical protein CDS
BACPLE_01689	19	beta-porphyrinase B CDS
BACPLE_01692	20	hypothetical protein CDS
BACPLE_01693	21	beta-porphyrinase A CDS
BACPLE_01694	22	hypothetical protein CDS
BACPLE_01695	23	hypothetical protein CDS
BACPLE_01696	24	hypothetical protein CDS
BACPLE_01697	25	hypothetical protein CDS
BACPLE_01698	26	SusC/RagA family TonB-linked outer membrane protein CDS
BACPLE_01699	27	hybrid two component system
BACPLE_01700	28	alcohol dehydrogenase CDS
BACPLE_01701	29	acetylglucosamine-6-sulfatase CDS
BACPLE_01702	30	hypothetical protein CDS
BACPLE_01703	31	glycoside hydrolase CDS
BACPLE_01704	32	hypothetical protein CDS
BACPLE_01705	33	hypothetical protein CDS
BACPLE_01706	34	beta-galactosidase CDS

In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-34 (or homologs thereof) (see, e.g., Table 6). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-17 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 28-34 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-17 (or homologs thereof) and SEQ ID NOS.: 28-34 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-27 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 18-34 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-17 (or homologs thereof) as well as both porphyrinases from within SEQ ID NOS.: 18-27 (or homologs thereof). In some cases, a

subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 28-34 (or homologs thereof) as well as both porphyranases from within SEQ ID NOS.: 18-27 (or homologs thereof). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding SEQ ID NOS.: 14-17 and SEQ ID NOS.: 28-34 (or homologs thereof) as well as both porphyranases from within SEQ ID NOS.: 18-27 (or homologs thereof).

As such, in some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-34 (see, e.g., Table 6). In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-17. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 28-34. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-17 and SEQ ID NOS.: 28-34. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-27. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 18-34. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-17 as well as both porphyranases set forth as SEQ ID NOS.: 19 and 21. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 28-34 as well as both porphyranases set forth as SEQ ID NOS.: 19 and 21. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins that have 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID NOS.: 14-17 and SEQ ID NOS.: 28-34 as well as both porphyranases set forth as SEQ ID NOS.: 19 and 21.

In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding (i) at least one of SEQ ID NOs.: 19, 21, and 22 (or a homolog(s) thereof); (ii) at least one of SEQ ID NOs.: 26 and 33 (or a homolog(s) thereof); and (iii) at least one of SEQ ID NOs.: 25 and 32 (or a homolog(s) thereof). In some cases, a subject
5 carbohydrate-utilization gene or gene set encodes SEQ ID NOs.: 19, 21-22, 25, 26, and 32-33 (or a homologs thereof).

In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding (i) at least one protein that has 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with any one of
10 SEQ ID NOs.: 19, 21, and 22; (ii) at least one protein that has 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with any one of SEQ ID NOs.: 26 and 33; and (iii) at least one protein that has 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with any one of
15 SEQ ID NOs.: 25 and 32. In some cases, a subject carbohydrate-utilization gene or gene set includes one or more nucleic acids encoding proteins having 80% or more sequence identity (e.g., 85% or more, 90% or more, 95% or more, or 100% sequence identity) with SEQ ID
NOs.: 19, 21-22, 25, 26, and 32-33.

In some embodiments, the carbohydrate-utilization gene set includes at least 3 genes (e.g., at least 4, at least 5, at least 6, at least 8 genes, at least 10 genes, at least 12 genes, at
20 least 15 genes, or at least 20 genes). In some cases, the carbohydrate-utilization gene set includes from 3-30 genes (e.g., from 5-30, 3-25, 3-20, 3-15, 3-10, 3-8, 5-25, 5-20, 5-15, 5-10, 5-8, 8-30, 8-25, 8-20, 8-15, 10-30, 10-25, 10-20, 10-15, 12-30, 12-25, 12-20, 15-30, 15-25, 20-30, or 20-25 genes). In some cases, the carbohydrate-utilization gene set includes from
3-10 genes.

A nucleic acid that includes the carbohydrate-utilization gene or gene set (e.g., a
25 heterologous carbohydrate-utilization gene or gene set) may or may not be integrated (covalently linked) into the genome of the cell. For example, in some cases, the nucleic acid that includes the carbohydrate-utilization gene or gene set is integrated into the genome of the cell (as a chromosomal integrant). In some cases, the nucleic acid that includes the
30 carbohydrate-utilization gene or gene set is maintained on an episomal element (extra chromosomal element) such as a plasmid.

In some cases the expression of genes from the carbohydrate-utilization gene or gene set is controlled by a high expression promoter. In some cases the expression of genes from the carbohydrate-utilization gene or gene set is controlled by an inducible promoter,
35 constitutive promoter, native promoter (e.g., native to the bacterial cell), heterologous promoter, or a promoter associated with the carbohydrate-utilization gene or gene set. Thus, for example, methods of the disclosure can be controlled by the type of promoter that is

present. As an illustrative example, in some cases, entrenchment (e.g., of a subject genetically modified bacterial cell into an organ of an individual, e.g., into the individual's gut) is controlled by a high expression promoter. Likewise, in some cases entrenchment (e.g., of a subject genetically modified bacterial cell into an organ of an individual, e.g., into the individual's gut) is controlled by an inducible promoter, constitutive promoter, native promoter (e.g., native to the bacterial cell), heterologous promoter, or a promoter associated with the carbohydrate-utilization gene or gene set.

Therapy etc.

The strategy disclosed here for facilitating robust colonization can facilitate a range of therapeutic applications, e.g., where it can be important to establish a high and/or predictable number of natural or engineered therapeutic microbes. For example, it may be important to colonize an organ (e.g., gut) at a high enough level to ensure that therapeutic activities may overcome competing activities of other microbes. As an example, this may be important when attempting to, for instance, change the short chain fatty acid profile or reduce the accumulation of harmful chemicals that are produced in the gut. Achieving predictable colonization can also be important for therapeutics that must be carefully dosed, such as bacteria with pro- or anti-inflammatory activities which could be used as an adjuvant for cancer immunotherapy or in the treatment of Inflammatory Bowel Diseases. The methods of the disclosure could also be used to, for example, ensure robust colonization to displace a harmful species by establishing a non-harmful version that can effectively compete for limiting resources with the harmful strain. As such, and as noted elsewhere, in some cases a subject method can result in displacement of bacteria present in the gut of an individual.

A subject genetically modified bacterial cell can be introduced into a variety of individuals with a variety of ailments. Diseases that can be treated with a subject genetically modified bacterial cell include but are not limited to diseases that are impacted by the gut microbiota, which include obesity, diabetes, heart disease, central nervous system diseases, rheumatoid arthritis, metabolic disorders, and cancer. For example, in some cases, the individual has gut inflammation, and in some such cases the individual has an inflammatory disease (e.g., Crohn's disease, ulcerative colitis, and the like), and in some cases gut inflammation can indirectly impact the disease, such as colorectal cancer or obesity.

In some cases, a subject bacterial cell is a therapeutic cell (has a positive impact on a clinical parameter of the individual). A therapeutic cell is not necessarily a genetically modified cell. For example, a cell that has not been genetically modified may serve a therapeutic purpose to an individual. In some cases, a therapeutic cell is genetically modified. For example, in some cases a therapeutic cell includes a transgene that encodes a therapeutic peptide (e.g., a peptide that when expressed by - and in some cases secreted by - a cell can

have a positive impact on the health of an individual). For example, a therapeutic cell and/or therapeutic peptide can have antimicrobial (antibiotic) activity (e.g., against one or more gut microbes), can function to change gut environmental parameters (e.g., pH control), can affect inflammation, can provide an enzymatic activity, and the like.

5 In some cases, a genetically modified bacterial cell includes a transgene that is an enzyme (e.g., a metabolic enzyme). For example, there are many small molecules produced in the gut (e.g., produced by microbes) that accumulate in the blood and cause or exacerbate diseases. Expressing an enzyme or a pathway (as a transgene) in a *Bacteroides* cell (or population of cells) to break down these products can be used in methods of treatment. For
10 example, a *Bacteroides* cell expressing such a transgene can be introduced into the gut of an individual (e.g., in order to break down small molecules, which in some cases may be produced by microbes, to reduce or even eliminate the amount absorbed by the gut of the individual, reducing the accumulation of the molecules in the blood of the individual).

In some cases, a genetically modified bacterial cell is tagged (e.g., to aid in tracking).
15 For example, in some cases, a genetically modified bacterial cell of the disclosure includes a detectable label (e.g., a nucleic acid that results in the presence of a detectable signal). As such, in some cases, a subject genetically modified cell (or population of cells) that is introduced into an individual (e.g., the gut), includes a transgene whose expression detectably labels the cell. The phrase "detectable label" as used herein refers to any expression product
20 (RNA, protein) that is detectable. The expression product (the label) can itself be detectable (directly detectable label) (e.g., a fluorescent protein), or the label can be indirectly detectable, e.g., in the case of an enzymatic label, the enzyme (e.g., luciferase or recombinase) may catalyze a chemical alteration of a substrate compound, composition or nucleic acid sequence and the product of the reaction is detectable (e.g. by fluorescence, chemiluminescence,
25 sequencing or presence and/or size of a PCR product). Thus in some cases, any of the methods of the disclosure can include a step of detecting (e.g., measuring) a detectable signal produced by a subject genetically modified bacterial cell. As an illustrative example, in some cases a genetically modified bacterial cell includes a transgene that encodes a fluorescent protein (e.g., green fluorescent protein (GFP) or any of a number of derivatives of GFP such
30 as YFP, CFP, RFP, etc.) or an enzyme that produces a fluorescent signal (e.g., luciferase), and a subject method includes a step of measuring the signal to detect the presence of (e.g., measure the abundance of) the genetically modified bacterial cell after it has been introduced into an individual (e.g., 3 days, 4 days, 5 days, 6 days, and/or 7 days after introduction; and/or 3 days, 4 days, 5 days, 6 days, and/or 7 days after providing the carbohydrate of interest).

35 In some cases, a genetically modified bacterial cell includes a transgene that is a "marker" or "marker gene" or "marker protein." A marker is an expression product (e.g., mRNA, protein, non-coding RNA) that marks a host cell such that the host cell is detectable

(e.g., detectably labeled). In some cases, the host cell is detectable by virtue of survival (e.g., the marker can be a “selectable marker”). In some cases, the host cell is detectable by observation (e.g., by direct visualization, by performing an assay, by performing a measurement step, and the like) and the marker can be referred to as a “reporter” or “reporter gene” or “reporter protein.”

As noted above, some markers are “selectable markers.” Selectable markers (a “selectable marker gene” can encode a “selectable marker protein”) provide for selection, i.e., for selective retention of cells (e.g., prokaryotic cells) that comprise the selectable marker gene, during culturing and propagation of the cells. An example of a selectable marker is a transgene that encodes a drug selectable marker protein that provides drug resistance for prokaryotic cells (e.g., Bacteroides cells). Such a selectable marker encodes a drug selectable marker protein that provides resistance for prokaryotic cells to one or more drugs (e.g., kanamycin, neomycin, ampicillin, carbenicillin, chloramphenicol, gentamicin, tetracycline, rifampin, trimethoprim, hygromycin B, spectinomycin, and the like). In some cases, a subject genetically modified bacteria can include an erythromycin resistance cassette. Proteins that provide drug resistance to cells (e.g., prokaryotic cells) in which they are expressed are known in the art. For example, wild type genes/proteins are known that provide resistance (e.g., for prokaryotic cells) to the above drugs. For example, aminoglycoside 3'-phosphotransferase (APH), is a wild type protein that provides for resistance to the drugs Kanamycin, Neomycin and Geneticin (G418); while beta-lactamase is a wild type protein that provides for resistance to the drugs ampicillin and carbenecillin. Chloramphenicol acetyltransferase (cat) confers resistance to chloramphenicol. Genes conferring resistance to aminoglycosides include aac, aad, aph and strA/B. Genes conferring resistance to β -lactams include ampC, cmv, tem and vim. Genes conferring resistance to sulfonamides include sull and sullI. Genes conferring resistance to tetracycline include tet(A), tet(B), tet(C), tet(D) and regulator, and tetR. Selectable markers can also be those useful in balanced lethal systems, e.g., in which an essential gene is maintained on a plasmid with a corresponding chromosomal deletion or suppressible mutation on the host cell genome, e.g. a tRNA selectable marker that suppresses a host chromosomal gene mutation; those useful in repressor titration systems, in which an operator sequences, e.g. the lac operator or tet operator, placed on a plasmid, derepresses a chromosomal gene; antidote/poison selection schemes, in which an antidote to a poison expressed from the host chromosome (e.g. the ccdB gene) is maintained on the plasmid; and those useful in RNA-based selection schemes, e.g. antisense regulators, or antisense regulators that inhibit the translation of a gene transcribed from the host chromosome that would otherwise promote cell death.

Bacteroides cells

In any of the embodiments of the disclosure, the bacterial cell of interest (e.g., the genetically modified cell, the cell being modified or introduced, or whose growth is being modulated, as part of a subject composition or method) can be a *Bacteroides* cell. In some cases, the bacterial cell of interest is not a *Bacteroides* cell. For example, the bacterial cell of interest can be any desired species, e.g., when the target organ is a gut the bacterial cell can be any species that can colonize a gut. In some cases the bacterial cell of interest is a *Clostridium* species (i.e., is a cell of the genus *Clostridium*).

The term "Bacteroides cell" is used herein to refer to a cell of the genus *Bacteroides*. As such, in some cases, a subject cell is a *Bacteroides* cell. Examples of species within the genus *Bacteroides* include but are not limited to: *B. fragilis* (Bf), *B. distasonis* (Bd), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), *B. eggerthii* (Be), *B. merdae* (Bm), *B. stercoris* (Bs), *B. uniformis* (Bu), and *B. caccae* (Bc). In some cases, a *Bacteroides* cell is a species selected from: *B. acidifaciens*, *B. amylophilus*, *B. asaccharolyticus*, *B. barnesiae*, *B. bivia*, *B. buccae*, *B. buccalis*, *B. caccae*, *B. capillosus*, *B. capillus*, *B. cellulolyticus*, *B. cellulosolvens*, *B. chinchilla*, *B. clarus*, *B. coagulans*, *B. coprocola*, *B. coprophilus*, *B. coprosuis*, *B. corporis*, *B. denticola*, *B. disiens*, *B. distasonis*, *B. dorei*, *B. eggerthii*, *B. endodontalis*, *B. faecichinchillae*, *B. faecis*, *B. finegoldii*, *B. fluxus*, *B. forsythus*, *B. fragilis*, *B. furcosus*, *B. galacturonicus*, *B. gallinarum*, *B. gingivalis*, *B. goldsteinii*, *B. gracilis*, *B. graminisolvans*, *B. helcogenes*, *B. heparinolyticus*, *B. hypermegas*, *B. intermedius*, *B. intestinalis*, *B. johnsonii*, *B. levvi*, *B. loescheii*, *B. macacae*, *B. massiliensis*, *B. melaninogenicus*, *B. merdae*, *B. microfus*, *B. multiacidus*, *B. nodosus*, *B. nordii*, *B. ochraceus*, *B. oleiciplenus*, *B. oralis*, *B. oris*, *B. oulorum*, *B. ovatus*, *B. paurosaccharolyticus*, *B. pectinophilus*, *B. pentosaceus*, *B. plebeius*, *B. pneumosintes*, *B. polypragmatus*, *B. praeacutus*, *B. propionificiens*, *B. putredinis*, *B. pyogenes*, *B. reticulotermitis*, *B. rodentium*, *B. ruminicola*, *B. salanitronis*, *B. salivorus*, *B. salyersiae*, *B. sartorii*, *B. splanchnicus*, *B. stercorisoris*, *B. stercoris*, *B. succinogenes*, *B. suis*, *B. tectus*, *B. termitidis*, *B. thetaiotaomicron*, *B. uniformis*, *B. ureolyticus*, *B. veroralis*, *B. vulgatus*, *B. xylanisolvans*, *B. xylanolyticus*, and *B. zooglyphiformans*. In some cases, a subject *Bacteroides* cell is a species selected from: *B. fragilis* (Bf), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), and *B. uniformis* (Bu).

In some cases, the *Bacteroides* cell is a species selected from: *B. fragilis* (Bf), *B. distasonis* (Bd), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), *B. eggerthii* (Be), *B. merdae* (Bm), *B. stercoris* (Bs), *B. uniformis* (Bu), and *B. caccae* (Bc). In some cases, the *Bacteroides* cell is a species selected from: *B. fragilis* (Bf), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), and *B. uniformis* (Bu). In some cases, the *Bacteroides* cell is a

species selected from: *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), and *B. uniformis* (Bu). In some cases, the Bacteroides cell is *B. thetaiotaomicron* (Bt).

KITS

5 Also provided are kits, e.g., for practicing any of the above methods. The contents of the subject kits may vary greatly. A kit can include, for example: (i) a subject genetically modified bacterial cell, and (ii) a rare carbohydrate of interest that can be utilized by the genetically modified bacterial cell. In some case, the genetically modified bacterial cell is a therapeutic cell.

10 In addition to the above components, the subject kits can further include instructions for practicing the subject methods. These instructions may be present in the subject kits in a variety of forms, one or more of which may be present in the kit. One form in which these instructions may be present is as printed information on a suitable medium or substrate, e.g., a piece or pieces of paper on which the information is printed, in the packaging of the kit, in a package insert, etc. Yet another means would be a computer readable medium, e.g., diskette, 15 CD, flash drive, etc., on which the information has been recorded. Yet another means that may be present is a website address which may be used via the internet to access the information at a removed site. Any convenient means may be present in the kits.

20 *Examples of Non-Limiting Aspects of the Disclosure*

 Aspects, including embodiments, of the present subject matter described above may be beneficial alone or in combination, with one or more other aspects or embodiments. Without limiting the foregoing description, certain non-limiting aspects of the disclosure numbered 1-98 are provided below. As will be apparent to those of skill in the art upon reading 25 this disclosure, each of the individually numbered aspects may be used or combined with any of the preceding or following individually numbered aspects. This is intended to provide support for all such combinations of aspects and is not limited to combinations of aspects explicitly provided below:

1. A method, comprising: introducing to a human organ a genetically modified bacterial cell capable of controlled entrenchment and/or controlled colonization.

2. A method for modulating growth of a genetically modified bacterial cell present in a human organ, comprising: administering to a human a rare carbohydrate of interest that is utilized as a carbon source by the genetically modified bacterial cell, wherein less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the human organ utilize the rare

carbohydrate of interest as a carbon source.

3. A method for modulating growth of a genetically modified bacterial cell in an organ, comprising: introducing the genetically modified bacterial cell to the organ *in vivo*, wherein the genetically modified bacterial cell utilizes as a carbon source a rare carbohydrate of interest, wherein less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ utilize the rare carbohydrate of interest as a carbon source.

4. A method for displacing at least a portion of a population of bacterial cells in an organ, comprising: introducing to the organ a genetically modified bacterial cell capable of controlled entrenchment and/or controlled colonization, and displacing at least a portion of the population of bacterial cells with the genetically modified bacterial cell.

5. The method of 4, wherein the genetically modified bacterial cell and the bacterial cells in the population of bacterial cells are the same species.

6. The method of 4 or 5, further comprising providing a bacterial cell from the population of bacterial cells and removing or inactivating one or more genes in the bacterial cell, thereby generating the genetically modified bacterial cell.

7. The method of 3 or 4, wherein the organ is a human organ.

8. The method of any one of the preceding, wherein the organ is a gut.

9. The method of 1 or 4, wherein the controlled entrenchment and/or controlled colonization is controlled by a high expression promoter.

10. The method of 1 or 4, wherein the controlled entrenchment and/or controlled colonization is controlled by an inducible promoter.

11. The method of 1 or 4, wherein the controlled entrenchment and/or controlled colonization is controlled by delivering a rare carbohydrate of interest to the organ.

12. The method of 11, wherein the rare carbohydrate of interest is a carbohydrate that can be utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other bacterial cells present in the organ, thereby generating a privileged niche.

13. The method of any one of 2-3 and 11-12, wherein the rare carbohydrate of interest is an isolated carbohydrate.

14. The method of any one of 2-3 and 11-13, wherein the rare carbohydrate of interest is a polysaccharide.

15. The method of any one of 2-3 and 11-14, wherein the rare carbohydrate of interest is a sulfated carbohydrate.

16. The method of any one of 2-3 and 11-14, wherein the rare carbohydrate of interest is

selected from the group consisting of porphyran, agarose, carrageenan, and any combination thereof.

17. The method of any one of 2-3 and 11-16, wherein the rare carbohydrate of interest is a carbohydrate cleaved by a glycoside hydrolase belonging to glycoside hydrolase family GH86.

18. The method of any one of 2-3 and 11-17, wherein the rare carbohydrate of interest is a sulfated polygalactan.

19. The method of any one of the preceding, wherein the genetically modified bacterial cell is a genetically modified gut resident bacterial cell.

20. The method of any one of the preceding, wherein the genetically modified bacterial cell is in the genus *Bacteroides*.

21. The method of any one of the preceding, wherein the genetically modified bacterial cell is selected from *B. acidifaciens*, *B. amylophilus*, *B. asaccharolyticus*, *B. barnesiae*, *B. bivius*, *B. buccae*, *B. buccalis*, *B. caccae*, *B. capillosus*, *B. capillus*, *B. cellulosilyticus*, *B. cellulosolvens*, *B. chinchilla*, *B. clarus*, *B. coagulans*, *B. coprocola*, *B. coprophilus*, *B. coprosuis*, *B. corporis*, *B. denticola*, *B. disiens*, *B. distasonis*, *B. dorei*, *B. eggerthii*, *B. endodontalis*, *B. faecichinchillae*, *B. faecis*, *B. finegoldii*, *B. fluxus*, *B. forsythus*, *B. fragilis*, *B. furcosus*, *B. galacturonicus*, *B. gallinarum*, *B. gingivalis*, *B. goldsteinii*, *B. gracilis*, *B. graminisolvens*, *B. helcogenes*, *B. heparinolyticus*, *B. hypermegas*, *B. intermedius*, *B. intestinalis*, *B. johnsonii*, *B. levvi*, *B. loescheii*, *B. macacae*, *B. massiliensis*, *B. melaninogenicus*, *B. merdae*, *B. microfus*, *B. multiacidus*, *B. nodosus*, *B. nordii*, *B. ochraceus*, *B. oleiciplenus*, *B. oralis*, *B. oris*, *B. oulorum*, *B. ovatus*, *B. paurosaccharolyticus*, *B. pectinophilus*, *B. pentosaceus*, *B. plebeius*, *B. pneumosintes*, *B. polypragmatus*, *B. praeacutus*, *B. propionificiens*, *B. putredinis*, *B. pyogenes*, *B. reticulotermitis*, *B. rodentium*, *B. ruminicola*, *B. salanitronis*, *B. salivosus*, *B. salyersiae*, *B. sartorii*, *B. splanchnicus*, *B. stercorisoris*, *B. stercoris*, *B. succinogenes*, *B. suis*, *B. tectus*, *B. termitidis*, *B. thetaiotaomicron*, *B. uniformis*, *B. ureolyticus*, *B. veroralis*, *B. vulgatus*, *B. xylanisolvens*, *B. xylanolyticus*, *B. zoogloformans*, and any combination thereof.

22. The method of any one of the preceding, wherein the genetically modified bacterial cell comprises a carbohydrate-utilization gene or gene set.

23. The method of 22, wherein the carbohydrate-utilization gene or gene set comprises one or more genes selected from the group consisting of porphyranase, glycoside hydrolase, sulfatase, galactosidase, and any combination thereof.

24. The method of 22, wherein the carbohydrate-utilization gene or gene set comprises one or more nucleic acids encoding proteins that have 80% or more sequence identity with BACPLE_1683-1706 from the *B. plebeius* genome.

25. The method of any one of 22-24, wherein the carbohydrate-utilization gene set comprises at least six genes.

26. The method of any one of 22-25, wherein the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of the carbohydrate-utilization gene or gene set.
27. The method of any one of 22-26, wherein the carbohydrate-utilization gene or gene set is heterologous.
28. The method of 27, wherein the carbohydrate-utilization gene or gene set is encoded on a plasmid, encoded on a bacterial artificial chromosome, or genomically integrated.
29. The method of any one of the preceding, wherein the genetically modified bacterial cell is capable of treating a metabolic disease or disorder.
30. The method of any one of the preceding, wherein the genetically modified bacterial cell comprises one or more therapeutic transgenes.
31. The method of 30, wherein the one or more therapeutic transgenes comprise one or more enzymes.
32. The method of any one of 2-3 and 11-18, further comprising administering the rare carbohydrate of interest for a sufficient amount of time and at a sufficient frequency to establish a population of the genetically modified bacterial cell.
33. The method of 32, further comprising maintaining the population of the genetically modified bacterial cell in the organ for at least 5 days.
34. The method of any one of 2-3 and 11-18, further comprising administering the rare carbohydrate of interest for at least 3 days.
35. The method of any one of the preceding, wherein the genetically modified bacterial cell is introduced orally.
36. The method of any one of the preceding, wherein the organ comprises at least 5 other bacterial species.
37. The method of any one of the preceding, further comprising colonizing the organ with the genetically modified bacterial cell at a level of at least 1% of total bacterial cells in the organ.
38. A genetically modified bacterial cell that utilizes as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiota.
39. A genetically modified bacterial cell, comprising:
 - a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with an ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than

0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiota.

40. A genetically modified bacterial cell, comprising:

(i) a heterologous therapeutic transgene; and

(ii) a carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with an ability to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiota.

41. The genetically modified bacterial cell of any one of 38-40, wherein the rare carbohydrate of interest is an isolated carbohydrate.

42. The genetically modified bacterial cell of any one of 38-41, wherein the rare carbohydrate of interest is a polysaccharide.

43. The genetically modified bacterial cell of any one of 38-42, wherein the rare carbohydrate of interest is a sulfated carbohydrate.

44. The genetically modified bacterial cell of any one of 38-42, wherein the rare carbohydrate of interest is selected from the group consisting of porphyran, agarose, carrageenan, and any combination thereof.

45. The genetically modified bacterial cell of any one of 38-44, wherein the rare carbohydrate of interest is a carbohydrate cleaved by a glycoside hydrolase belonging to glycoside hydrolase family GH86.

46. The genetically modified bacterial cell of any one of 38-45, wherein the rare carbohydrate of interest is a sulfated polygalactan.

47. The genetically modified bacterial cell of any one of 38-46, wherein the genetically modified bacterial cell is a genetically modified gut resident bacterial cell.

48. The genetically modified bacterial cell of any one of 38-47, wherein the genetically modified bacterial cell is in the genus *Bacteroides*.

49. The genetically modified bacterial cell of any one of 38-48, wherein the genetically modified bacterial cell is selected from *B. acidifaciens*, *B. amylophilus*, *B. asaccharolyticus*, *B. barnesiae*, *B. biviis*, *B. buccae*, *B. buccalis*, *B. caccae*, *B. capillosus*, *B. capillus*, *B. cellulosilyticus*, *B. cellulosolvens*, *B. chinchilla*, *B. clarus*, *B. coagulans*, *B. coprocola*, *B. coprophilus*, *B. coprosuis*, *B. corporis*, *B. denticola*, *B. disiens*, *B. distasonis*, *B. dorei*, *B. eggerthii*, *B. endodontalis*, *B. faecichinchillae*, *B. faecis*, *B. finegoldii*, *B. fluxus*, *B. forsythus*, *B. fragilis*, *B. furcosus*, *B. galacturonicus*, *B. gallinarum*, *B. gingivalis*, *B. goldsteinii*, *B. gracilis*, *B. graminisolvens*, *B. helcogenes*, *B. heparinolyticus*, *B. hypermegas*, *B. intermedius*, *B. intestinalis*, *B. johnsonii*, *B. levvi*, *B. loescheii*, *B. macacae*, *B. massiliensis*, *B. melaninogenicus*, *B. merdae*, *B. microfusis*, *B. multiacidus*, *B. nodosus*, *B. nordii*, *B.*

ochraceus, *B. oleiciplenus*, *B. oralis*, *B. oris*, *B. oulorum*, *B. ovatus*, *B. paurosaccharolyticus*, *B. pectinophilus*, *B. pentosaceus*, *B. plebeius*, *B. pneumosintes*, *B. polypragmatus*, *B. praeacutus*, *B. propionificiens*, *B. putredinis*, *B. pyogenes*, *B. reticulotermis*, *B. rodentium*, *B. ruminicola*, *B. salanitronis*, *B. salivorus*, *B. salyersiae*, *B. sartorii*, *B. splanchnicus*, *B. stercorisoris*, *B. stercoris*, *B. succinogenes*, *B. suis*, *B. tectus*, *B. termitidis*, *B. thetaiotaomicron*, *B. uniformis*, *B. ureolyticus*, *B. veroralis*, *B. vulgatus*, *B. xylanisolvans*, *B. xylanolyticus*, *B. zoogloformans*, and any combination thereof.

50. The genetically modified bacterial cell of 38, wherein the genetically modified bacterial cell comprises a carbohydrate-utilization gene or gene set.

51. The genetically modified bacterial cell of 39, 40, or 50, wherein the carbohydrate-utilization gene or gene set comprises one or more genes selected from the group consisting of porphyranase, glycoside hydrolase, sulfatase, galactosidase, and any combination thereof.

52. The genetically modified bacterial cell of any one of 39-40 and 50-51, wherein the carbohydrate-utilization gene or gene set comprises one or more nucleic acids encoding proteins that have 80% or more sequence identity with BACPLE_1683-1706 from the *B. plebeius* genome.

53. The genetically modified bacterial cell of any one of 39-40 and 50-52, wherein the carbohydrate-utilization gene set comprises at least six genes.

54. The genetically modified bacterial cell of any one of 39-40 and 50-53, wherein the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of the carbohydrate-utilization gene or gene set.

55. The genetically modified bacterial cell of 40 or 50, wherein the carbohydrate-utilization gene or gene set is heterologous.

56. The genetically modified bacterial cell of 39 or 55, wherein the carbohydrate-utilization gene or gene set is encoded on a plasmid, encoded on a bacterial artificial chromosome, or genomically integrated.

57. The genetically modified bacterial cell of any one of 38-56, wherein the genetically modified bacterial cell is capable of treating a metabolic disease or disorder.

58. The genetically modified bacterial cell of any one of 38-57, wherein the genetically modified bacterial cell comprises one or more therapeutic transgenes.

59. The genetically modified bacterial cell of 58, wherein the one or more therapeutic transgenes comprise one or more enzymes.

60. A method comprising:
 providing a bacterial cell; and
 genetically modifying the bacterial cell to utilize as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than

30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome.

61. A method comprising:

providing a bacterial cell that utilizes as a carbon source a rare carbohydrate of interest that is utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of bacterial cells present in a human microbiome; and

genetically modifying the bacterial cell to express one or more therapeutic transgenes.

62. The method of 60 or 61, wherein the rare carbohydrate of interest is an isolated carbohydrate.

63. The method of any one of 60-62, wherein the rare carbohydrate of interest is a polysaccharide.

64. The method of any one of 60-63, wherein the rare carbohydrate of interest is a sulfated carbohydrate.

65. The method of any one of 60-63, wherein the rare carbohydrate of interest is selected from the group consisting of porphyran, agarose, carrageenan, and any combination thereof.

66. The method of any one of 60-65, wherein the rare carbohydrate of interest is a carbohydrate cleaved by a glycoside hydrolase belonging to glycoside hydrolase family GH86.

67. The method of any one of 60-66, wherein the rare carbohydrate of interest is a sulfated polygalactan.

68. The method of any one of 60-67, wherein the genetically modified bacterial cell is a genetically modified gut resident bacterial cell.

69. The method of any one of 60-68, wherein the genetically modified bacterial cell is in the genus *Bacteroides*.

70. The method of any one of 60-69, wherein the genetically modified bacterial cell is selected from *B. acidifaciens*, *B. amylophilus*, *B. asaccharolyticus*, *B. barnesiae*, *B. bivius*, *B. buccae*, *B. buccalis*, *B. caccae*, *B. capillosus*, *B. capillus*, *B. cellulosilyticus*, *B. cellulosolvens*, *B. chinchilla*, *B. clarus*, *B. coagulans*, *B. coprocola*, *B. coprophilus*, *B. coprosuis*, *B. corporis*, *B. denticola*, *B. disiens*, *B. distasonis*, *B. dorei*, *B. eggerthii*, *B. endodontalis*, *B. faecichinchillae*, *B. faecis*, *B. finegoldii*, *B. fluxus*, *B. forsythus*, *B. fragilis*, *B. furcosus*, *B. galacturonicus*, *B. gallinarum*, *B. gingivalis*, *B. goldsteinii*, *B. gracilis*, *B. graminisolvens*, *B. helcogenes*, *B. heparinolyticus*, *B. hypermegas*, *B. intermedius*, *B. intestinalis*, *B. johnsonii*, *B. levvi*, *B. loescheii*, *B. macacae*, *B. massiliensis*, *B. melaninogenicus*, *B. merdae*, *B. microfus*, *B. multiacidus*, *B. nodosus*, *B. nordii*, *B. ochraceus*, *B. oleiciplenus*, *B. oralis*, *B. oris*, *B. oulorum*, *B. ovatus*, *B. paurosaccharolyticus*, *B. pectinophilus*, *B. pentosaceus*, *B.*

plebeius, *B. pneumosintes*, *B. polypragmatus*, *B. praeacutus*, *B. propionificiens*, *B. putredinis*, *B. pyogenes*, *B. reticulotermis*, *B. rodentium*, *B. ruminicola*, *B. salanitronis*, *B. salivorus*, *B. salyersiae*, *B. sartorii*, *B. splanchnicus*, *B. stercorisoris*, *B. stercoris*, *B. succinogenes*, *B. suis*, *B. tectus*, *B. termitidis*, *B. thetaiotaomicron*, *B. uniformis*, *B. ureolyticus*, *B. veroralis*, *B. vulgatus*, *B. xylanisolvans*, *B. xylanolyticus*, *B. zooglyphus*, and any combination thereof.

71. The method of any one of 60-70, wherein the genetically modified bacterial cell comprises a carbohydrate-utilization gene or gene set.
72. The method of 71, wherein the carbohydrate-utilization gene or gene set comprises one or more genes selected from the group consisting of porphyranase, glycoside hydrolase, sulfatase, galactosidase, and any combination thereof.
73. The method of 71 or 72, wherein the carbohydrate-utilization gene or gene set comprises one or more nucleic acids encoding proteins that have 80% or more sequence identity with BACPLE_1683-1706 from the *B. plebeius* genome.
74. The method of any one of 71-73, wherein the carbohydrate-utilization gene set comprises at least six genes.
75. The method of any one of 71-74, wherein the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of the carbohydrate-utilization gene or gene set.
76. The method of any one of 71-75, wherein the carbohydrate-utilization gene or gene set is heterologous.
77. The method of any one of 71-76, wherein the carbohydrate-utilization gene or gene set is encoded on a plasmid, encoded on a bacterial artificial chromosome, or genomically integrated.
78. The method of any one of 60-77, wherein the genetically modified bacterial cell is capable of treating a metabolic disease or disorder.
79. The method of 61, wherein the one or more therapeutic transgenes comprise one or more enzymes.
80. A method of facilitating colonization by a genetically modified bacterial cell, the method comprising:
 - (a) introducing a genetically modified bacterial cell into a gut of an individual, wherein the genetically modified bacterial cell comprises a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with the ability to use a carbohydrate of interest as a carbon source; and
 - (b) administering the carbohydrate of interest to the individual, thereby providing the genetically modified bacterial cell with the carbon source.
81. The method of 80, wherein the genetically modified bacterial cell is a genetically

modified gut resident bacterial cell.

82. The method of 80 or 81, wherein the genetically modified bacterial cell is a *Bacteroides* cell.

83. The method of 82, wherein the *Bacteroides* cell is a *B. fragilis* (Bf), *B. distasonis* (Bd), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), *B. eggerrthii* (Be), *B. merdae* (Bm), *B. stercoris* (Bs), *B. uniformis* (Bu), or *B. caccae* (Bc) cell.

84. The method of any one of 80-83, wherein the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of the heterologous carbohydrate-utilization gene or gene set.

85. The method of any one of 80-84, wherein the carbohydrate of interest is utilized as a carbon source by less than 50% (e.g., less than 30%, less than 10%, less than 3%, less than 1%, less than 0.3%, less than 0.1%, less than 0.03%, less than 0.01%, less than 0.003%, less than 0.001%, less than 0.0001%, or none) of other gut bacterial cells present in the gut of the individual.

86. The method of any one of 80-85, wherein the carbohydrate of interest is porphyran.

87. The method of 86, wherein the heterologous carbohydrate-utilization gene or gene set comprises one or more nucleic acids encoding the proteins that have 80% or more sequence identity with BACPLE_1683-1706 from the *B. plebeius* genome.

88. The method of any one of 80-87, wherein the genetically modified bacterial cell is a therapeutic bacterial cell.

89. The method of any one of 80-88, wherein the genetically modified bacterial cell comprises a nucleic acid molecule comprising a heterologous nucleic acid sequence that encodes a therapeutic polypeptide.

90. A genetically modified bacterial cell, comprising:
a heterologous carbohydrate-utilization gene or gene set that provides the genetically modified bacterial cell with the ability to use a rare carbohydrate of interest as a carbon source.

91. The genetically modified bacterial cell of 90, wherein the genetically modified bacterial cell is a genetically modified gut resident bacterial cell.

92. The genetically modified bacterial cell of 90 or 91, wherein the genetically modified bacterial cell is a *Bacteroides* cell.

93. The genetically modified bacterial cell of 92, wherein the *Bacteroides* cell is a *B. fragilis* (Bf), *B. distasonis* (Bd), *B. thetaiotaomicron* (Bt), *B. vulgatus* (Bv), *B. ovatus* (Bo), *B. eggerrthii* (Be), *B. merdae* (Bm), *B. stercoris* (Bs), *B. uniformis* (Bu), or *B. caccae* (Bc) cell.

94. The genetically modified bacterial cell of any one of 90-93, wherein the carbohydrate of interest cannot be utilized as a carbon source by the genetically modified bacterial cell in the absence of the heterologous carbohydrate-utilization gene or gene set.

95. The genetically modified bacterial cell of any one of 90-94, wherein the carbohydrate of

interest is porphyran.

96. The genetically modified bacterial cell of 95, wherein the heterologous carbohydrate-utilization gene or gene set comprises one or more nucleic acids encoding the proteins that have 80% or more sequence identity with BACPLE_1683-1706 from the *B. plebeius* genome.

97. The genetically modified bacterial cell of any of 90-96, wherein the genetically modified bacterial cell is a therapeutic bacterial cell.

98. The genetically modified bacterial cell of any of 90-97, wherein the genetically modified bacterial cell comprises a nucleic acid molecule comprising a heterologous nucleic acid sequence that encodes a therapeutic polypeptide.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1

To facilitate robust colonization, a privileged niche was created by introducing a carbohydrate into the diet that can only be utilized by the target bacteria. Remarkably, a single substrate was sufficient for boosting the colonization level of an introduced strain to more than half of the total microbes in the gut of conventional mice, which are expected to harbor hundreds of distinct bacterial strains. In addition to boosting total colonization levels, the data presented herein show that this privileged niche results in more predictable levels of target bacteria in different microbial communities. Finally, the data presented herein demonstrate that the ability to utilize the carbohydrate can be transferred to a naïve species.

Results

Selection of polysaccharides suitable for establishing a privileged niche

It was hypothesized that establishing a privileged niche that is inaccessible to other gut

microbes would enable a predictably high level of colonization in the gut by an introduced bacteria capable of occupying the privileged niche. Most substrates that are known to be safely consumable by humans and to be capable of supporting growth of bacteria are readily consumed by the host or native bacterial species in the gut and thus do not produce a privileged niche. Due to the wide diversity in carbohydrate utilization capabilities amongst gut bacteria, carbohydrates were chosen as the substrate for creating a privileged niche. It was reasoned that carbohydrates that are uncommon in the diet and are either rarely or not consumed by the gut bacteria in the human population of interest would be suitable substrates for creating a privileged niche. The marine carbohydrates porphyran and agarose are both known to be safe to consume yet are rare in Western diets. The glycoside hydrolase family containing agarases and porphyranases, GH86, was found to be underrepresented in deeply-sequenced metagenomic stool samples from healthy adult Americans in the Human Microbiome Project (Figure 1). Thus, these carbohydrates are likely to not be consumed by common American gut bacteria. In contrast to GH86, which was completely absent in 44% of samples and has a mean abundance of 0.00015, GH32, which hydrolyzes commonly consumed substrates such as the fructan polysaccharide inulin, was present in all samples and had a mean abundance of 0.0049.

Isolation of strains capable of consuming privileged substrates

To isolate a strain of gut bacteria from the environment that was capable of growing on a carbohydrate of interest, a minimal media (see Salyers et al., Appl. Environ. Microbiol. 33, 319–322 (1977)) was designed for *Bacteroides*, the most abundant bacterial genus present in the Western gut, in which the carbohydrate of interest was the sole carbon source. Strains capable of utilizing porphyran, NB001, (Figure 2, panel A) or agarose, NB002 and NB003, were isolated from the environment and the genomes of these strains were sequenced (Table 1). The porphyran utilizing strain NB001 contained a putative polysaccharide utilization locus (PUL) (SEQ ID NO: 67) on a mobile element that shares 71% identity with a previously identified porphyran-utilizing strain (Hehemann et al., Nature 464, 908–912 (2010); Hehemann et al., Proc. Natl. Acad. Sci. U. S. A. 109, 19786–19791 (2012)). The two agarose utilizers were found to have a putative PUL (SEQ ID NO: 68 and 69) sharing over 99% identity between the two strains and include genes with high homology to agarases of marine bacteria.

Table 1. Description of bacterial strains.

Name	Description	Species	Source
NB001	Porphyran consuming <i>Bacteroides</i>	<i>Bacteroides ovatus</i>	environmental isolate

NB002	Agarose consuming Bacteroides	<i>Bacteroides dorei</i>	environmental isolate
NB003	Agarose consuming Bacteroides	<i>Bacteroides uniformis</i>	environmental isolate
NB004	Porphyran naïve Bacteroides	<i>Bacteroides vulgatus</i>	environmental isolate
NB006	NB001 with GFP/Erm marker	<i>Bacteroides ovatus</i>	NB001 + pWW124 (SEQ ID NO: 60)
NB007	Porphyran strain with tdk deletion	<i>Bacteroides ovatus</i>	NB001 + UV mut.
NB008	Knockout of porphyran utilization	<i>Bacteroides ovatus</i>	NB001 +/- pWD034 (SEQ ID NO: 61)
NB009	NB004 + Short Porphyran PUL	<i>Bacteroides vulgatus</i>	NB004 + pWD037 (SEQ ID NO: 62)
NB010	NB004 + Medium Porphyran PUL	<i>Bacteroides vulgatus</i>	NB004 + pWD036 (SEQ ID NO: 63)

Porphyran establishes a privileged niche resulting in robust colonization

An *in vitro* experiment was performed to test the hypothesis that addition of porphyran can increase the ability of an introduced porphyran utilizing bacteria to colonize a complex community at a high (and predictable) level. The strain NB006 was created by modifying NB001 to contain an erythromycin resistance cassette expressing GFP to facilitate monitoring abundance via plating. NB006 was added to the complex communities, which were then grown and serially passaged in rich media either in the presence or absence of porphyran (Figure 2, panel B). In the absence of porphyran, NB006 colonization levels reached widely variable abundances across the 8 complex communities, spanning a 760-fold range by the seventh day. In the presence of porphyran, not only did the abundance of NB006 increase for all eight communities, but the deviation in abundance between the different communities also decreased considerably, spanning only a 3-fold range by the seventh day.

Next tested was the ability of porphyran to increase the abundance of NB006 in mice harboring a conventional complex microbiota (Figure 2). One group of mice was given the standard (STD) rodent diet, while a second group was fed a polysaccharide deficient (PD) diet. After three days on each diet, both groups of mice received NB006. When both groups received 1% porphyran in the drinking water, abundance of NB006 increased by almost 3 logs in mice on the STD diet, and almost 4 logs in mice on the PD diet. Based on monitoring total anaerobic colony forming units, this represents an increase in NB006 from roughly 0.1% of

total anaerobic CFU in both groups, to approximately 25% of total in mice fed the STD diet and 48% in mice fed the PD diet.

Additionally tested was the ability of porphyran to allow NB006 to stably colonize a microbiota that resists colonization. Mice were administered NB008, an isogenic strain to NB006 that cannot utilize porphyran, and this rendered them resistant to colonization by NB006 as this strain was cleared from the mice within five days after introduction (Figure 2, panel D). When mice were administered porphyran for three days simultaneous to introduction of NB006, NB008 decreased in abundance by three logs while NB006 remained constant and highly abundant (roughly 67% of total anaerobic CFU). After removal of porphyran, NB008 increased back to pre-challenge levels while NB006 decreased to one log lower abundance than NB008. After re-introduction of porphyran for seven days, NB006 displaced NB008 in a stable fashion, maintaining colonization of the mice in the absence of porphyran for thirty days. Additionally, NB008 was now excluded from the mice when re-introduced (Figure 2, panel E).

Transferring the key porphyran utilization genes is sufficient for conferring porphyran utilization to a naïve species

To confirm that the mobile element of interest in NB001 (see SEQ ID NO: 67) was necessary for the ability to grow on porphyran as a sole carbon source, an 8-gene operon was deleted that contained key glycoside hydrolases predicted to act on porphyran and constituted 16% of the mobile element. This deletion was sufficient to eliminate the ability to grow on porphyran (Figure 3).

The porphyran mobile element from NB001 contains an approximately 30kb deletion relative to the homologous mobile element from *B. plebeius*, suggesting many of the genes in the region are likely not to be involved in porphyran utilization (Figure. 4). To identify a minimal gene set necessary for porphyran utilization, portions of the PUL were synthesized of varying sizes and were integrated into the genome of a *Bacteroides* strain not capable of growth on porphyran (NB004). Initially protocols used previously to transfer a five gene PUL into a *Bacteroides* were followed, but it was found that the much larger porphyran PUL (up to 34 genes and 60kb) was not compatible with previously described techniques. Instead, the different sized porphyran PULs (Figure 4) were assembled into a plasmid with components necessary for yeast assembly, *E. coli* conjugation and *Bacteroides* genomic integration (Figure 5), which was sufficient to integrate correctly assembled porphyran PULs into naive *Bacteroides*. The shortest PUL candidate, containing 10 genes including both of the predicted porphyranases in the PUL, was not sufficient to impart porphyran utilization. However, when expanded to 24 of the 34 total genes, integration of this medium-sized PUL was sufficient to confer growth on porphyran (Figure 6).

DISCUSSION

Using a privileged niche strategy, an unprecedentedly high colonization level of an introduced strain was obtained in a complex community. Combining two or more privileged niches, potentially using dietary substrates from distinct geographic regions, could further
5 broaden the effectiveness of this strategy to allow robust colonization in the event that one of the two rare substrates is utilized by an individual's endogenous microbiota. Marine carbohydrates (e.g. porphyran, agarose, agarpectin, carrageenan, and marine microbe exopolysaccharides) offer promising substrates to establish a synthetic niche, as they are not typically found in human diets and thus are less likely to be utilized by human gut microbes. As
10 demonstrated in this disclosure, marine bacteria possess utilization genes that can be transferred to gut adapted species. For example, we were able to demonstrate this with the porphyran PUL (SEQ ID NO: 67) and with putative agarose utilization PULs (SEQ ID NO: 68 and 69), which conferred growth on agarose when present natively or when transferred to a naïve strain. Marine carbohydrates are typically easy to extract and generally safe to
15 consume.

This strategy for facilitating robust colonization can facilitate a range of therapeutic applications where it is important to establish a high or a predictable number of natural or engineered therapeutic microbes. For example, it may be important to colonize the gut at a high enough level to ensure that therapeutic activities may overcome competing activities of
20 other microbes. As an example, this may be important when attempting to, for instance, change the short chain fatty acid profile or reduce the accumulation of harmful chemicals that are produced in the gut. Achieving predictable colonization can also be important for therapeutics that must be carefully dosed, such as bacteria with pro- or anti-inflammatory activities which could be used as an adjuvant for cancer immunotherapy or in the treatment of
25 Inflammatory Bowel Diseases. This method of ensuring robust colonization could also be used to displace a harmful species by establishing a non-harmful version that can effectively compete for limiting resources with the harmful strain.

Materials and Methods

30 Identifying rare glycoside hydrolase subfamilies

87 fecal metagenomes sequenced by the HMP were downloaded and reprocessed (quality filtered and dynamically trimmed). These metagenomic sequences were then translated to their respective coding sequences and Hidden Markov Models were applied to identify all CAZymes. The data were normalized to the total count of assigned CAZyme
35 coding sequences per sample.

Porphyran extraction

Culinary Nori was added to ten times the weight of water and autoclaved for approximately 3 hours. The autoclaved Nori was then strained to remove particulates and then diluted five fold into 100% ethanol and allowed to settle for six hours. This was then
 5 centrifuged for 15 minutes at 30,000 g to pellet the precipitate, which was then dried at 80°C.

Isolation of porphyran and agarose utilizing strains

A bacteroides minimal media was prepared as described by Salyers *et al* (see Salyers et al., Appl. Environ. Microbiol. 33, 319–322 (1977)) with addition of 200 µg/ml Gentamycin
 10 and porphyran as 0.8% Nori extract added as the sole carbon source. Primary sewage effluent was collected, settled for approximately two hours and diluted ten-fold into the media, which was then incubated anaerobically for 24 hours at 37°C. The culture was then further diluted 200-fold into the fresh media and incubated another 24 hours anaerobically at 37°C. The saturated culture was then plated as serial dilutions onto Blood-Heart-Infusion media + 10%
 15 horse blood agar plates and incubated 24 hours anaerobically at 37°C. Colonies were then picked into fresh media, incubated 24 hours anaerobically at 37°C and prepared for analysis and cryogenic storage.

Assaying abundance of porphyran utilizer in complex cultures

An erythromycin resistance cassette was genomically integrated into NB001. The
 20 abundance of this strain, NB006, within each complex community could then be easily assessed via selective plating. The eight communities and NB006 were separately grown in rich media, and then NB006 was added to each community at a 1:20 dilution. The complex communities containing NB006 were subsequently grown and diluted 1:1000 daily in rich
 25 media either with or without a supplementation of 0.4% Nori extract, a culturing strategy that mimics the requirement for ongoing division necessary to sustain colonization of the gut. To determine the CFU/µL of NB006, 10 µL of each saturated culture was diluted into 200 µL of PBS, further successively diluted 1:10 in PBS seven times, 4 µL of each dilution was spotted onto a plate containing Brain Heart Infusion Blood agar with 200 µg/mL gentamycin and 10
 30 µg/mL erythromycin, and after 24 hours of anaerobic growth at 37°C colony counts were enumerated. Both significantly increased abundance and reduced variance of NB006 across the eight communities was observed over the course of a week.

Assaying abundance of porphyran utilizer in mice

35 To test ability of porphyran to toggle abundance of NB006 *in vivo*, one group of four male Restricted Flora Swiss-Webster mice (Taconic) were maintained on standard rodent

chow (STD diet), while an identical group was given a polysaccharide deficient diet (Bio-Serv, AIN-93G 68% glucose). Both groups were administered approximately 10^8 CFU of NB006. Abundance of NB006 in the feces was monitored by selective plating on Brain Heart Infusion Blood agar with 200 µg/mL gentamicin and 10 µg/mL erythromycin. Both groups received
 5 regular water for five days, 1% porphyran in the drinking water for five days, and then were switched back to regular water for the duration of the experiment.

To test ability of porphyran to allow for stable colonization of a porphyran utilizer into a resistant microbiota, two groups of three male Restricted Flora Swiss-Webster mice (Taconic) were administered NB008, an isogenic strain to NB006 that cannot use porphyran.

10 Abundance of NB008 was monitored by introducing a tetracycline-resistance cassette and selectively plating on Brain Heart Infusion Blood agar with 200 µg/mL gentamicin and 2µg/mL tetracycline. After one week, both groups of mice received NB006 and one group received 1% porphyran in the drinking water for three days, regular water for seven days, and then 1% porphyran in the drinking water for seven days, until being switched back to and maintained on
 15 regular water for the duration of the experiment. Abundance of NB006 was monitored by selectively plating as above with erythromycin selection. Finally, NB008 was re-introduced to mice at day 48 and monitored in the feces.

Genome sequencing and analysis

20 Genomic DNA was isolated from *Bacteroides* strains capable of growth on porphyran (NB001) (SEQ ID NO: 67) or agarose (NB002, NB003) (SEQ ID NO: 68 and 69, respectively) using a PureLink Genomic DNA Mini Kit (Invitrogen). Samples were prepared for multiplexed Illumina sequencing using a Nextera XT DNA Library Preparation Kit (Illumina) and run on an Illumina MiSeq using a 2 x 150bp paired-end kit. Approximately 10 million sequencing reads
 25 were obtained for each sample. De novo assembly of the reads was performed with the Geneious De Novo Assembler (Biomatters), yielding an average coverage of ~100 reads/bp. Gene annotation and alignment was also performed using Geneious.

Cloning and transferring the porphyran utilization genes.

30 Candidate porphyran PUL regions from the conserved mobile element of NB001 were transferred to *Bacteroides vulgatus* (NB004) via a three-step process, which is summarized here and expanded on in the sections below. First, the PUL genes of interest were amplified via PCR and assembled via yeast assembly into a custom shuttle vector capable of propagation in *S. cerevisiae* and *E. coli* as well as conjugation and genomic integration into
 35 *Bacteroides* species. Next, correctly assembled plasmids were transferred from yeast to the S17-1 conjugation strain of *E. coli* (see Simon et al., Nat. Biotechnol. 1, 784–791 (1983)) by electroporation. Finally, the plasmids were integrated into the genome of *B. vulgatus* via

conjugation and antibiotic selection, followed by sequence-verification using whole genome sequencing.

Design of porphyran PUL plasmids

A homolog (71% identity) of a porphyran mobile element was identified in the NB001 genome using the Mauve genome aligner (see e.g., Hehemann et al., Proc. Natl. Acad. Sci. U. S. A. 109, 19786–19791 (2012)). Based on gene annotations and the sequence alignment between these two regions (Figure 4), three candidate regions of varying sizes (20kb, 40kb, and 60kb) were selected that were predicted to potentially be sufficient to confer growth on porphyran to a naive *Bacteroides* strain. The shortest of these candidate PULs contained homologs of BACPLE_1688-1699 from the *B. plebeius* genome, the medium-sized PUL contained homologs of BACPLE_1683-1706, and the longest PUL contained homologs of BACPLE_1669-1706 (see, e.g., Table 6).

Previously-described techniques for PUL transfer (Sonnenburg et al., Cell 141, 1241–1252 (2010)) were insufficient to move PULs of this size between species. Therefore, a novel PUL transfer strategy was designed that utilized a custom shuttle vector containing a yeast selectable marker and origin of replication, a bacterial artificial chromosome origin and selectable marker for plasmid-based propagation of large DNAs in *E. coli*, a conjugative origin of transfer to enable conjugation from *E. coli* to *Bacteroides* species, as well as an integrase and selectable marker to enable integration into the *Bacteroides* genome. This vector was divided into three precursor fragments with flanking homology such that only upon proper assembly would the vector be capable of propagation in yeast (Tables 3 and 4). The first fragment (Vector_01) was an *Ascl* digestion of pWD011, which was custom built to contain all *Bacteroides*-specific machinery as well all yeast vector components aside from a portion of the KanMX selectable marker. The remainder of the KanMX marker was supplied via the PCR product Vector_02, which also served to bridge Vector_01 and Vector_03. Vector_03 was an *Ascl* digest of pWD012, which was derived from a blunt religation of the commercially-available pEZ-BAC vector (Lucigen). The PUL candidates were divided into multiple 6kb fragments to be used in a yeast assembly reaction (Tables 3 and 5), and PCR primers were designed such that neighboring fragments would share ~200bps of homology (Table 2).

Table 2: List of oligonucleotides used to build the porphyran PUL plasmid

ID	Sequence	SEQ ID NO:
AA34	GGGTACAGAAAATCTCGGTC	35

ID	Sequence	SEQ ID NO:
AA35	TTCATCATGTCGTACGAAGG	36
AA36	TACTTCCATTTGGGGTGAAG	37
AA37	TACAGTCCCTTTGGACAATG	38
AA38	CATACTTTAGCATCGTCGAAAAG	39
AA39	TTTCCATTTCCAGGATTCCC	40
AA40	GTAGCTCCGGTGACATTAC	41
AA41	TCTTTAGCTGAAGAAACGGC	42
AA42	AAGCTTGCGTATGTCGATAG	43
AA43	TTATCGCCATTCTTCAGCAG	44
AA44	TGGCATCCGACGAATATAAG	45
AA45	TTTGAATAGGCCAGTATGC	46
AA46	AGGTAAAGGCACTGTTTTCC	47
AA47	ATATAGCCGGAGATTCTCCG	48
AA48	CATCTACATCATGTCGGACG	49
AA49	CTGTCCGGTCATGATACATG	50
AA50	GATTCTCTTGGGGACAGAAC	51
AA51	AGTTTCCCATTTCACGTCTG	52
AE30	ATTTATCTATCCATTTCAGTTTGATTTCTCAGG ACTTTACATCGTCCTGAAAGTATTTGTTtttggg tgttgatatggcag	53
AE31	ATTTATCTATCCATTTCAGTTTGATTTCTCAGG ACTTTACATCGTCCTGAAAGTATTTGTTaatcc caatacagtctgttactg	54
AE45	GTGAGTTGATTGCTACGTAAATAACTTCGTA TAGCATACATTATACGAAGTTATGGACTAcgc aggccaatatccggaa	55
AE46	GTGAGTTGATTGCTACGTAAATAACTTCGTA TAGCATACATTATACGAAGTTATGGACTAggta aacctccccgatgg	56
AE47	GTGAGTTGATTGCTACGTAAATAACTTCGTA TAGCATACATTATACGAAGTTATGGACTAttag aacatattttccgattgccag	57
AE49	AAACAGCATTCCAGGTATTAGAAG	58

ID	Sequence	SEQ ID NO:
AE50	CACTGCCCGCTTTCCAGTCGGGAAACCTGT GCGGCCGCTTTCCTTCTTCTCTTCTGGc agtatagcgaccagcattc	59

Table 3: List of PCR products used to build the porphyran PUL plasmids.

ID	Length (bps)	Primer 1	Primer 2	Template	SEQ ID NO:
PCR_01	6,220	AA35	AA36	NB001 Genomic DNA	71
PCR_02	6,280	AA37	AA38	NB001 Genomic DNA	72
PCR_03	6,247	AA39	AA40	NB001 Genomic DNA	73
PCR_04	6,169	AA41	AA42	NB001 Genomic DNA	74
PCR_05	6,232	AA43	AA44	NB001 Genomic DNA	75
PCR_06	6,187	AA45	AA46	NB001 Genomic DNA	76
PCR_07	6,185	AA47	AA48	NB001 Genomic DNA	77
PCR_08	6,178	AA49	AA50	NB001 Genomic DNA	78
PCR_09	6,162	AE45	AA34	NB001 Genomic DNA	79
PCR_10	6,138	AA51	AE30	NB001 Genomic DNA	80
PCR_11	5,359	AE46	AA40	NB001 Genomic DNA	81
PCR_12	4,638	AE47	AA42	NB001 Genomic DNA	82
PCR_13	3,524	AA47	AE31	NB001 Genomic DNA	83
Vector_02	769	AE49	AE50	KanMX (SEQ ID NO: 70)	84

5

Table 4: List of digests used to build the porphyran PUL plasmids.

ID	Length (bps)	Plasmid	Restriction Enzyme
Vector_01	4,730	pWD011 (SEQ ID NO: 64)	Ascl
Vector_03	7,234	pWD012 (pEZ-BAC) (SEQ ID NO: 65)	Ascl

Table 5: List of porphyran PUL plasmids.

Plasmid Name	Description	Length (bps)	Parts used in yeast assembly
pWD035 (SEQ ID NO: 66)	Long Porphyrin PUL	72,558	PCR_01, PCR_02, PCR_03, PCR_04, PCR_05, PCR_06, PCR_07, PCR_08, PCR_09, PCR_10, Vector_01, Vector_02, Vector_03
pWD036 (SEQ ID NO: 63)	Medium Porphyrin PUL	53,695	PCR_04, PCR_05, PCR_06, PCR_07, PCR_08, PCR_10, PCR_11, Vector_01, Vector_02, Vector_03
pWD037 (SEQ ID NO: 62)	Short Porphyrin PUL	32,364	PCR_05, PCR_06, PCR_12, PCR_13, Vector_01, Vector_02, Vector_03

Yeast assembly of porphyrin PUL plasmids

All fragments were prepared for yeast assembly via PCR with NEB Q5 polymerase (Table 3) or restriction digest with *Ascl* from NEB (Table 4). Cleanup reactions were performed with a Zymo Clean and Concentrator kit, and the resulting DNA concentrations were measured using a Nanodrop 1000 (Thermo Scientific). Yeast assembly of plasmids pWD035-37 (Table 5) was carried as described (see, e.g., Chandran et al., *Methods Mol. Biol.* 1472, 187–192 (2017)), using 100 fmols of each part in a lithium acetate transformation of the *S. cerevisiae* strain BY4741. After rescuing the transformed cells for 1 hour at 30°C in YPD media, cells were plated on YPD plates supplemented with G418 (200µg/ml). After incubation for 48 hours at 30°C, colonies were grown up in YPD+G418 and screened for successful plasmid assembly using colony PCR. Approximately 90% of screened clones appeared to contain a correctly assembled plasmid.

Transfer of porphyrin PUL plasmids from yeast to E. coli

Yeast strains harboring properly assembled plasmids were back diluted 1:100 into YPD+G418 and grown at 30°C for 6 hours to an OD of 2. 500µl of each culture was transferred to a microcentrifuge tube, centrifuged, and resuspended in 100µl of PBS buffer. The cell mixture was then vortexed alongside ~50 0.5mm glass disruptor beads (USA Scientific) for 5 minutes to lyse the cells. 5µl of the lysate was used in an electroporation of 100µl of electrocompetent S17-1 *E. coli*. Transformations were rescued for 1 hour in LB media with shaking at 37°C and then plated onto agar plates with LB+ampicillin (100µg/ml). For large plasmids, fewer than 20 colonies were often obtained from a single electroporation. Colonies were grown up in LB+ampicillin and screened for successful plasmid transfer via colony PCR.

Conjugation of porphyran PUL plasmids into B. vulgatus

The PUL plasmids were then transferred from S17-1 *E. coli* into the genome of an environmental isolate of *B. vulgatus* (NB004). It was observed that larger plasmids resulted in fewer conjugants on erythromycin-selective plates, with the largest plasmid (pWD035) not yielding any successful plasmid integrants. Despite this size bias, both pWD036 and pWD037 were successfully integrated into NB004 as verified by whole genome sequencing of the resulting strains.

***In vitro* growth assays**

Strains were grown overnight anaerobically at 37°C in a tryptone-yeast extract-glucose (TYG) medium to saturation. Saturated cultures were diluted 1:50 into Salyer's Minimal Media supplemented with either .2% glucose or .8% porphyran extract. The diluted cultures were grown anaerobically at 37°C for 12 hours, and 100µL of each culture was transferred to a 96-well microtiter plate. The optical density at 600nm of each culture was measured using a Wallac Victor 2 1420 Multilabel Counter. OD600 readings were normalized by subtracting out the background detected when media lacking cells was measured.

Example 2

Synthetic niche generation enables strain integration in the gut microbiota

The dense microbial ecosystem in the gut is intimately connected to numerous facets of human biology, and manipulation of the gut microbiota has broad implications for human health. In the absence of profound perturbation, the abundance of bacterial strains that reside within an individual is largely stable over time. In contrast, the fate of exogenous commensal and probiotic strains applied to an established microbiota is variable, largely unpredictable, and greatly influenced by the background microbiota.

In this example, a synthetic metabolic niche was generated via administration of a privileged nutrient source, and reliable integration of an exogenous *Bacteroides* strain at predictable abundances into mice harboring diverse communities of gut microbes was demonstrated. Dietary marine polysaccharides not accessible to other members of the gut community, but utilized by the introduced strain facilitated predictable engraftment and boosted abundance by more than three orders of magnitude, independent of background microbiota. This targeted dietary support was sufficient to overcome priority exclusion by an isogenic strain, and facilitated strain replacement. Transfer of this privileged nutrient-utilization system into a naïve strain of *Bacteroides* is demonstrated, and finely tuned control of strain abundance in the gut by varying polysaccharide input is shown. The data presented here highlight the influence of nutrient availability in shaping microbiota membership, expand the ability to perform a broad spectrum of methods in the context of a complex microbiota, and

facilitate cell-based therapeutic strategies in the gut.

Results and Discussion

Changes to the microbial membership of the highly competitive and dynamic gut microbiota can impact numerous aspects of host biology. Despite the importance of gut microbe composition in human health, the rules governing invasion of commensal strains into an existing complex community are not well understood. Resident strains often appear to exclude similar invading strains although in some cases, the opposite is true: the niche occupied by existing strains can be exploited by a similar invading strain. The inability to predict or control the outcome of fecal microbiota transplants illustrates the need for basic insight into the factors that influence whether new strains of bacteria can integrate into a pre-existing, complex microbiota.

To characterize the extent to which incoming exogenous bacteria variably colonize hosts with distinct microbiotas, mice harboring a conventional mouse microbiota were used as were two groups of ex-germ free mice, each colonized with the gut microbiota from two different healthy human donors from the United States ("humanized") as model hosts. These three groups of mice were administered a strain of *Bacteroides ovatus* (NB001), a prominent gut commensal species, which was modified genetically, adding erythromycin resistance and GFP-expression cassettes for tracking purposes. NB001 was monitored by colony forming units (c.f.u.) in feces via selective plating, and colonies were verified by GFP-fluorescence (see Methods) over the course of seven days (Figure 7a). The different communities (Figure 10) varied in their ability to integrate NB001 (Figure 7b), and one human microbiota was resistant to colonization, with all mice in the group exhibiting decreased abundance of the challenge strain over the seven day period.

Inulin was then administered to the three aforementioned groups of mice seven days after inoculation with NB001, which grows at a similar rate *in vitro* in a minimal medium containing either glucose or inulin as the sole carbohydrates (MM-glucose doubling time = 157 min; MM-inulin doubling time = 127 min; Figure 11b). Over seven days of feeding an inulin-based diet (10% inulin w/v) to these three groups of mice, NB001 exhibited highly variable responses across the background microbiotas (range of mean c.f.u. per ml in feces $<4 \times 10^4$ to 2×10^{10} ; Figure 7c). This variability may be due to several factors that differentiate the three microbiotas including the varying degrees of competition from other community members for this MAC, common in the Western diet.

In contrast, microbiota utilization of the non-ubiquitous seaweed polysaccharide porphyran, found in the seaweed *Porphyra yezoensis* used to prepare culinary nori, is much less common in US microbiotas. The consumption of porphyran by some *Bacteroides* species can be facilitated by a horizontally-transferred PUL, which originated in marine bacteria. We

hypothesized that this exotic dietary MAC would create a privileged niche within the gut and promote integration of an exogenous strain competent in its use. NB001 was capable of growth on porphyran *in vitro* (doubling time = 98 min; Figure 11c), and so a custom nori diet (10% dried *Porphyra yezoensis* w/v) was administered to the three groups of mice seven days after inoculation with NB001. Indeed, in response to nori in the diet a robust increase in abundance of NB001 was observed, irrespective of background microbiota. Additionally, the variability in colonization levels across communities was eliminated (range of mean c.f.u. per ml in feces 3×10^{10} to 6×10^{10} ; Figure 7d), indicating specificity of an exotic nutrient source and cognate utilization system to promote bacterial growth *in vivo*. Access to nori substrates rescued NB001 from below the limits of detection in the most resistant microbiota and boosted its abundance to levels indistinguishable from those achieved in the other two microbiotas (Figure 7d). Together these data suggest a powerful approach to reproducibly control strain integration independent of the background microbiota, and implicate nutrient availability as a key modulator of strain integration into the gut community.

Given the context independence of strain integration via access to nori polysaccharides, it was next tested whether the population size could be toggled by addition and removal of the substrate *in vivo*. Conventional mice were colonized with NB001 and c.f.u. in feces was tracked. The mice were switched in five day intervals between regular water, water with 1% porphyran extract, and a regular water washout. To test the influence of competing polysaccharides in the diet, this experiment was performed on both standard, MAC-rich chow and a MAC-deficient chow that provides no exogenous polysaccharides to the microbiota. In both dietary contexts, with or without other competing dietary MACs, NB001 responded robustly to introduction of marine polysaccharides, showing a large and highly reproducible increase in abundance of four orders of magnitude in the absence of dietary MACs (Figure 8a) and three orders of magnitude in the presence of diverse dietary MACs (Figure 8b). This response was contingent upon access to porphyran, as deletion of eight genes required for its metabolism abolished the effect (Figure 8c, Figure 9a, 9b). Additionally, the extract alone did not significantly affect the composition of the background microbiota (Figure 12), further supporting the lack of porphyran use by members of the background community.

Bacteroides species engage in interesting colonization behavior in which an early colonizer will exclude a challenging isogenic strain, the phenomenon known as priority effects in the ecological literature. We hypothesized that this behavior, though previously demonstrated in gnotobiotic mice, would also occur in the context of a complex community, and that it could be overcome by providing a privileged nutrient to the challenging strain to create a distinct metabolic niche. Indeed, an early-colonizing NB001 strain excluded an NB001 challenge strain in conventional mice (Figure 8d). Supplementing porphyran in the

diet, accessible only to the challenging strain, allowed the challenging strain to overcome the priority effect, and resulted in displacement of the early colonizer by the challenging strain (Figure 8e). Replacement of the early-colonizing strain required that the challenging strain have access to porphyrin (Figure 13), and displacement was robust to subsequent challenge by the original colonizer (Figure 13). Interestingly, when porphyrin was supplemented for shorter periods of time, replacement of the original strain was incomplete: the early-colonizer recovered from below the levels of detection and co-existed with the secondary colonizer after cessation of porphyrin administration (Figure 8f).

The genome of NB001 was sequenced and the polysaccharide utilization locus (PUL) was identified (Figure 9a). Three different length PULs were constructed, ranging from 10 to 34 of the genes (20-60kb) from the full-length PUL (Figure 9a). Previous methods to transfer a five gene PUL were not sufficient for these much larger constructs, and so the constructs were assembled in yeast before transferring to conjugative *E. coli*, and the constructs were integrated into the chromosome of two target strains unable to utilize porphyrin for growth, *Bacteroides stercoris* and *Bacteroides thetaiotaomicron*. Transfer of the shortest PUL was insufficient to impart growth on porphyrin to either naïve species of *Bacteroides* tested (Figure 9b), but the medium PUL allowed for growth *in vitro* (Figure 9b). A significant drop-off in conjugation efficiency was observed with the long PUL, and only *B. stercoris* yielded transconjugants, suggesting inter-species differences in amenability to accepting large pieces of foreign DNA. When colonized into conventional mice, abundance of *B. thetaiotaomicron* harboring the medium length PUL could be toggled up and down through addition of porphyrin extract in the water (Figure 9c).

Finally, the tunability of strain abundance was assessed by varying the porphyrin supplemented in diet. Conventional mice were colonized with a GFP fluorescent NB001 strain and c.f.u. in the feces was tracked for five days. 1%, 0.1%, or 0.01% weight by volume porphyrin extract was then administered in the drinking water for five days, followed by a subsequent five-day washout with regular water. A ten-fold decrease in abundance of NB001 in the feces was observed with each ten-fold dilution of extract administered in the water (Figure 9d), indicating fine control over strain abundance through modulation of the porphyrin concentration. To visually assess the spatial distribution and abundance of NB001 *in vivo* in the presence of different amounts of porphyrin, frozen tissue sections were prepared and endogenous GFP of the NB001 strain was imaged via confocal microscopy. A substantial increase in GFP-positive cells was seen when comparing mice given 0.01% vs. 1% extract (Figure 9e).

Predicting amenability of a given community to the introduction of a new strain is a challenge given the diverse and divergent features of different individuals' pre-existing microbiotas, including whether or not it is already inhabited by a strain capable of excluding

the one being introduced. The results presented in this example demonstrate that privileged nutrient sources such as porphyran can modify resource partitioning in the gut microbiota, and systems such as those presented here can be deployed to enhance human health.

5 Methods

Bacterial Culture and Strain Isolation

All bacterial growth was performed at 37° C under anaerobic conditions. Growth for introduction into mice was performed in rich media (tryptone-yeast-glucose) with no antibiotics added. Growth curves and selective growth on nori extract were performed in Salyers Minimal Media (SMM 100mL in dH₂O: 0.1g (NH₄)₂SO₄, 0.1g Na₂CO₃, 0.05g L-cysteine, 10mL 1M KPO₄ pH7.2, 5mL Mineral Salts (1L in dH₂O: 18g NaCl, 0.53g CaCl₂*2H₂O, 0.4g MgCl₂*6H₂O, 0.2g MnCl₂*4H₂O, 0.2g CoCl₂*6H₂O), 1mL 0.4mg/mL FeSO₄, 0.1mL 1mg/mL Vitamin K₃, 0.1mL Histidine/Hematin*, 0.05mL 0.01mg/mL Vitamin B₁₂) with carbon source added to a final concentration of either 0.2% (Figure 9b, glucose), 0.5% (Figure 11), or 0.8% (Figure 9b, nori extract) weight by volume and filter sterilized. SMM was either made fresh the day of the experiment, or prepared without histidine/hematin or L-cysteine and stored at 4° C for up to four weeks, with the missing components added the day of the experiment.

C.f.u. were cultivated on brain-heart infusion blood agar (BHI-BA) with appropriate selective antibiotics (200 µg/mL gentamycin, and 25 µg/mL erythromycin or 2 µg/mL tetracycline), or on SMM agar plates (for GFP visualization, 2x SMM tempered to 50° C + equal volume 3% agar tempered to 50° C) with selective antibiotics.

NB001 (porphyran MAC utilizing *B. ovatus*) and NB004 (naïve *B. stercoris*) were isolated from primary waste effluent at the San Jose Wastewater Treatment Facility via selection in liquid culture (SMM) with 200ug/mL gentamycin (as *Bacteroides* are naturally gentamycin resistant*), and for NB001, growth on 0.8% nori extract. Briefly, settled primary effluent was diluted ten-fold into SMM and grown as above for 24 h, subcultured at 1:200 into fresh media and grown for 24 h, and plated in serial dilutions onto BHI-BA. Single colonies were picked into SMM for growth confirmation, cryogenic storage, and downstream analysis. A GFP-expressing, erythromycin-resistant variant of NB001 was generated as described previously.

Genome Sequencing and Analysis

Genomic DNA was isolated from NB001 and NB004 using a PureLink Genomic DNA Mini Kit (Invitrogen). Samples were prepared for multiplexed Illumina sequencing using a Nextera XT DNA Library Preparation Kit (Illumina) and run on an Illumina MiSeq using a 2x150bp paired-end kit. Approximately 10 million sequencing reads were obtained for each sample. De novo assembly of the reads was performed with the Geneious De Novo

Assembler (Biomatters), yielding an average coverage of ~100 reads/bp. Gene annotation and alignment was also performed using Geneious.

Porphyran PUL Transfer and Knockout

- 5 Generation of the porphyran utilization deficient mutant was performed using *tdk* counterselection as described previously. A thymidine kinase (*tdk*) deficient mutant (NB007) of NB001 was generated by exposing NB001 to ultraviolet light for 60 seconds and plating on BHI-BA supplemented with 200ug/mL of 5-fluoro-2'-deoxyuridine (FUdR). Eight genes predicted to be essential for growth on porphyran (homologous to BACPLE_1692-1699) were
- 10 knocked out using pWD034 (Table 7), a plasmid with 1.5kb of homology upstream and downstream of the target region assembled via Golden Gate Assembly into an erythromycin-resistant, *tdk*-containing vector.

Table 7: List of plasmids used in Example 2

Plasmid Name	Description	Length (bps)	Parts used in yeast assembly	Relevant Figure
pVW3452	High GFP, erythromycin resistance	6,031	N/A	Figure 7, Figure 9e
pNBU2-ermGb	Erythromycin resistance	4,909	N/A	Fig. 2, Figure 12
pNBU2-tetQb	Tetracycline resistance	6,662	N/A	Figure 8, Figure 12
pWD034	Porphyran PUL Deletion (main operon)	7,148	N/A	Figure 8c
pWD035	Long Porphyran PUL	72,558	PCR_01, PCR_02, PCR_03, PCR_04, PCR_05, PCR_06, PCR_07, PCR_08, PCR_09, PCR_10, Vector_01, Vector_02, Vector_03	Figure 9a, b
pWD036	Medium Porphyran PUL	53,695	PCR_04, PCR_05, PCR_06, PCR_07, PCR_08, PCR_10, PCR_11, Vector_01, Vector_02, Vector_03	Figure 9a, b, c
pWD037	Short Porphyran PUL	32,364	PCR_05, PCR_06, PCR_12, PCR_13, Vector_01, Vector_02, Vector_03	Figure 9a, b

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Generation of the porphyran PUL knock-in strains required expansion of previous

knock-in methods due to the large size of the PULs (20-60kb). Based on gene annotations and sequence alignment to a previously published mobile element conferring porphyran polysaccharide utilization capabilities, we designed three minimal PULs of varying sizes (20kb, 40kb, and 60kb, Figure 9a). To propagate such large pieces of DNA and integrate them into the *Bacteroides* genome we used a three-step process: performing yeast assembly into a custom shuttle vector, propagating it in *S. cerevisiae* and *E. coli*, and then performing conjugation and genomic integration into *Bacteroides* species. The minimal PULs were each divided into multiple 6kb fragments with 200bp homology between pieces and assembled in yeast with fragments containing the KanMX selectable marker and CEN6/ARS4 origin for selection and growth in yeast, the bacterial artificial chromosome origin and chloramphenicol selectable marker (from pEZ-BAC vector, Lucigen) for selection and growth in *E. coli*, and the conjugative origin and parts for integration and selection in *Bacteroides* (Tables 2, 3, 4 – see above). Yeast cells with successfully assembled constructs were lysed by mechanical disruption with 0.5mm glass disruptor beads (USA Scientific), and lysates mixed 1:20 with electrocompetent *E. coli* S17-1 cells and electroporated. Successfully transformed *E. coli* were then grown and conjugated with NB004 and *B. thetaiotaomicron* VPI-5482 (*Bt*) as previously described. NB004 successfully integrated all PULs, but *Bt* was initially unable to integrate any PUL constructs. To improve rates of genomic integration, we pre-integrated an NBU2 integrase-expressing plasmid with tetracycline resistance into *Bt*, and this improved efficiency such that *Bt* conjugants were obtained for both the short and medium length PUL constructs.

Nori Extract Preparation

Raw culinary nori derived from *Porphyra yezoensis* (<https://www.rawnori.com>) was added at 10% weight by volume to distilled water and subjected to hot water extraction by autoclaving for three hours. The mixture was then cooled and centrifuged at 11,000xg. Resulting supernatant was ethanol precipitated by combining with 200-proof ethanol to a final concentration of 80% ethanol, 20% supernatant and incubating at 4° C for 24-72 h. Precipitate was recovered by centrifugation at 26,000xg and dried for 24 h before manual grinding to generate a measurable powder.

Mice

Ex-germ free or restricted flora (RF) conventional Swiss-Webster mice (Taconic) were housed in gnotobiotic isolators and fed either an autoclaved standard diet (LabDiet 5K67) or a custom diet as indicated below (Bio-Serv) in strict accordance with a Protocol for Care and Use of Laboratory Animals approved by the Stanford University Administrative Panel of Laboratory Animal Care. Introduction of all *Bacteroides* strains into either ex-germ free or RF

mice was performed by oral gavage of 10^8 c.f.u. of the given strain in culture media.

Mice were humanized (Figure 7) with fecal samples from healthy human donors were stored at -80°C , thawed and resuspended in pre-reduced PBS in anaerobic conditions at a 1:1 dilution, and 0.2 mL gavaged orally into germ free mice. The mice were allowed to equilibrate the human microbiota for four weeks while consuming the standard lab diet. One week before introduction of NB001, mice were switched to MAC-deficient chow (AIN-93G, 68% glucose). Seven days after introduction of NB001, mice were switched to custom diets with inulin or nori as the only available MACs (AIN-93G, 10% unique polysaccharide, 58% glucose). RF mice (Figure 8, Figure 9) were administered nori extract in the water at the percent indicated, weight by volume.

16S rRNA Analysis

DNA was extracted from fecal samples using the PowerSoil 96-htp kit (MoBio), and amplified at the 16S v4 region (515F, 806R). Qiime 1.9 was used to analyze the resulting Illumina-generated sequencing reads as previously described*. Data were rarified to the sample with the lowest number of reads (16384), and open-reference OTU picking via UCLUST and taxonomy assignment through the Greengenes 13.8 database was performed.

Microscopy

Tissue was harvested and immediately fixed in 4% paraformaldehyde in PBS for 48 hours at 4°C . Cassettes were transferred to 20% sucrose for 24 h, and then samples were embedded in OCT Compound (Tissue-Tek) before sectioning at 30um on a Leica CM3050 S cryostat. Sections were stained for 30 minutes with 4',6-Diamidino-2-phenylindole dihydrochloride (DAPI; Sigma-Aldrich) and Alexa Fluor 594 Phalloidin (Life Technologies). Images were taken on a Zeiss LSM 700 confocal microscope.

Example 3

Figure 14 (panels A-C). Access to porphyrin allowed for crypt invasion and stable maintenance in the presence of an exclusionary primary colonizing strain. Germ-free mice were colonized with *B. thetaiotaomicron* strain VPI-5482 that was unable to utilize porphyrin. One week later, the mice were challenged with an isogenic strain harboring the medium-length porphyrin PUL, and continued drinking normal water (panel A) or were administered 1% porphyrin in the drinking water for four days (panel B, brackets). After four days, mice in panel B were switched to regular water, and two mice were sacrificed and images of the proximal colon were captured, demonstrating the challenge strain (panel C, green) colonizing the colonic crypts with the primary strain (panel C, red). Colony forming units were tracked in the feces for the duration of the experiment, demonstrating that without access

to 1% porphyran in the water (panel A) the challenge strain clears, but with short-term access the challenge strain maintains stable co-colonization with the primary colonizing strain. These data demonstrate that with access to porphyran, an incoming strain can enter the colonic crypts.

5

CLAIMS

That which is claimed is:

1. A method of colonizing the gut of a subject with a genetically modified, non-naturally occurring *Bacteroides* cell, the method comprising administering to the subject both:
 - a) the genetically modified *Bacteroides* cell, wherein the genetically modified *Bacteroides* cell comprises a carbohydrate-utilization gene set that provides the genetically modified *Bacteroides* cell with an ability to utilize as a carbon source a porphyrin and the carbohydrate-utilization gene set comprises one or more nucleic acids, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 80% or more sequence identity to SEQ ID NO: 14, a protein that has 80% or more sequence identity to SEQ ID NO: 15, a protein that has 80% or more sequence identity to SEQ ID NO: 16, a protein that has 80% or more sequence identity to SEQ ID NO: 17, a protein that has 80% or more sequence identity to SEQ ID NO: 18, a protein that has 80% or more sequence identity to SEQ ID NO: 19, a protein that has 80% or more sequence identity to SEQ ID NO: 20, a protein that has 80% or more sequence identity to SEQ ID NO: 21, a protein that has 80% or more sequence identity to SEQ ID NO: 22, a protein that has 80% or more sequence identity to SEQ ID NO: 23, a protein that has 80% or more sequence identity to SEQ ID NO: 24, a protein that has 80% or more sequence identity to SEQ ID NO: 25, a protein that has 80% or more sequence identity to SEQ ID NO: 26, a protein that has 80% or more sequence identity to SEQ ID NO: 27, a protein that has 80% or more sequence identity to SEQ ID NO: 28, a protein that has 80% or more sequence identity to SEQ ID NO: 29, a protein that has 80% or more sequence identity to SEQ ID NO: 30, a protein that has 80% or more sequence identity to SEQ ID NO: 31, a protein that has 80% or more sequence identity to SEQ ID NO: 32, a protein that has 80% or more sequence identity to SEQ ID NO: 33, and a protein that has 80% or more sequence identity to SEQ ID NO: 34; and
 - b) porphyrin;wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^7 cells/mL in the feces of the subject.
2. The method of claim 1, wherein the carbohydrate-utilization gene set is heterologous.
3. The method of claim 1, wherein the genetically modified *Bacteroides* cell further comprises one or more therapeutic transgenes.

4. The method of claim 1, wherein the *Bacteroides* cell is not a *B. plebeius* cell or a *B. ovatus* cell.
5. The method of claim 1, wherein the carbohydrate-utilization gene set is at least 40 kb.
6. The method of claim 1, wherein the carbohydrate-utilization gene set is encoded on a plasmid, encoded on a bacterial artificial chromosome, or artificially genomically integrated.
7. The method of claim 5, wherein the carbohydrate-utilization gene set is artificially genomically integrated.
8. The method of claim 1, wherein the genetically modified *Bacteroides* cell and porphyrin are administered orally.
9. The method of claim 1, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 90% or more sequence identity to SEQ ID NO: 14, a protein that has 90% or more sequence identity to SEQ ID NO: 15, a protein that has 90% or more sequence identity to SEQ ID NO: 16, a protein that has 90% or more sequence identity to SEQ ID NO: 17, a protein that has 90% or more sequence identity to SEQ ID NO: 18, a protein that has 90% or more sequence identity to SEQ ID NO: 19, a protein that has 90% or more sequence identity to SEQ ID NO: 20, a protein that has 90% or more sequence identity to SEQ ID NO: 21, a protein that has 90% or more sequence identity to SEQ ID NO: 22, a protein that has 90% or more sequence identity to SEQ ID NO: 23, a protein that has 90% or more sequence identity to SEQ ID NO: 24, a protein that has 90% or more sequence identity to SEQ ID NO: 25, a protein that has 90% or more sequence identity to SEQ ID NO: 26, a protein that has 90% or more sequence identity to SEQ ID NO: 27, a protein that has 90% or more sequence identity to SEQ ID NO: 28, a protein that has 90% or more sequence identity to SEQ ID NO: 29, a protein that has 90% or more sequence identity to SEQ ID NO: 30, a protein that has 90% or more sequence identity to SEQ ID NO: 31, a protein that has 90% or more sequence identity to SEQ ID NO: 32, a protein that has 90% or more sequence identity to SEQ ID NO: 33, and a protein that has 90% or more sequence identity to SEQ ID NO: 34.
10. The method of claim 1, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 95% or more sequence identity to SEQ ID NO: 14, a protein that has 95% or more sequence identity to SEQ ID NO: 15, a protein that has 95% or more sequence identity to SEQ ID NO: 16, a protein that has 95% or more sequence identity to SEQ ID NO: 17, a protein that has 95% or more sequence identity to SEQ ID NO: 18, a

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11. The method of claim 1, wherein said one or more nucleic acids encodes all of the proteins set forth in SEQ ID NOs: 14-34.

12. The method of claim 1, wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^7 cells/mL in the feces of the subject for at least 7 days.

13. The method of claim 1, wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^8 cells/mL in the feces of the subject.

14. The method of claim 13, wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^8 cells/mL in the feces of the subject for at least 3 days.

15. A method of colonizing the gut of a subject with a genetically modified, non-naturally occurring *Bacteroides* cell, the method comprising orally administering to the subject both:
a) the genetically modified *Bacteroides* cell, wherein the genetically modified *Bacteroides* cell comprises a heterologous carbohydrate-utilization gene set that (i) provides the genetically modified *Bacteroides* cell with an ability to utilize as a carbon source a porphyran, (ii) is at least 40 kb, (iii) is encoded on a plasmid, encoded on a bacterial artificial chromosome, or artificially genomically integrated, and (iv) comprises one or more nucleic acids, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 80% or more sequence identity to SEQ ID NO: 14, a protein that has 80% or more sequence identity to SEQ ID NO: 15, a protein that has 80% or more sequence identity to SEQ ID NO: 16, a protein that has 80% or more sequence identity to SEQ ID NO: 17, a protein that has 80% or more sequence identity to SEQ ID NO: 18, a protein that has 80% or

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b) porphyrin;

wherein the genetically modified *Bacteroides* cell reaches an abundance of at least 10^7 cells/mL in the feces of the subject.

16. The method of claim 15, wherein the genetically modified *Bacteroides* cell further comprises one or more therapeutic transgenes.

17. The method of claim 15, wherein the *Bacteroides* cell is not a *B. plebeius* cell or a *B. ovatus* cell.

18. The method of claim 15, wherein the carbohydrate-utilization gene set is artificially genomically integrated.

19. The method of claim 15, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 90% or more sequence identity to SEQ ID NO: 14, a protein that has 90% or more sequence identity to SEQ ID NO: 15, a protein that has 90% or more sequence identity to SEQ ID NO: 16, a protein that has 90% or more sequence identity to SEQ ID NO: 17, a protein that has 90% or more sequence identity to SEQ ID NO: 18, a protein that has 90% or more sequence identity to SEQ ID NO: 19, a protein that has 90% or more sequence identity to SEQ ID NO: 20, a protein that has 90% or more sequence identity to SEQ ID NO: 21, a protein that has 90% or more sequence identity to SEQ ID NO: 22, a protein that has 90% or more sequence identity to SEQ ID NO: 23, a protein that has 90% or more sequence identity to SEQ ID NO: 24, a protein that has 90% or more sequence identity to SEQ ID NO: 25, a protein that has 90% or more sequence identity to SEQ ID NO: 26, a protein that has 90% or more sequence identity to SEQ ID NO: 27, a protein that has 90% or

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20. The method of claim 15, wherein said one or more nucleic acids encodes all of the following proteins: a protein that has 95% or more sequence identity to SEQ ID NO: 14, a protein that has 95% or more sequence identity to SEQ ID NO: 15, a protein that has 95% or more sequence identity to SEQ ID NO: 16, a protein that has 95% or more sequence identity to SEQ ID NO: 17, a protein that has 95% or more sequence identity to SEQ ID NO: 18, a protein that has 95% or more sequence identity to SEQ ID NO: 19, a protein that has 95% or more sequence identity to SEQ ID NO: 20, a protein that has 95% or more sequence identity to SEQ ID NO: 21, a protein that has 95% or more sequence identity to SEQ ID NO: 22, a protein that has 95% or more sequence identity to SEQ ID NO: 23, a protein that has 95% or more sequence identity to SEQ ID NO: 24, a protein that has 95% or more sequence identity to SEQ ID NO: 25, a protein that has 95% or more sequence identity to SEQ ID NO: 26, a protein that has 95% or more sequence identity to SEQ ID NO: 27, a protein that has 95% or more sequence identity to SEQ ID NO: 28, a protein that has 95% or more sequence identity to SEQ ID NO: 29, a protein that has 95% or more sequence identity to SEQ ID NO: 30, a protein that has 95% or more sequence identity to SEQ ID NO: 31, a protein that has 95% or more sequence identity to SEQ ID NO: 32, a protein that has 95% or more sequence identity to SEQ ID NO: 33, and a protein that has 95% or more sequence identity to SEQ ID NO: 34.

21. The method of claim 15, wherein said one or more nucleic acids encodes all of the proteins set forth in SEQ ID NOs: 14-34.

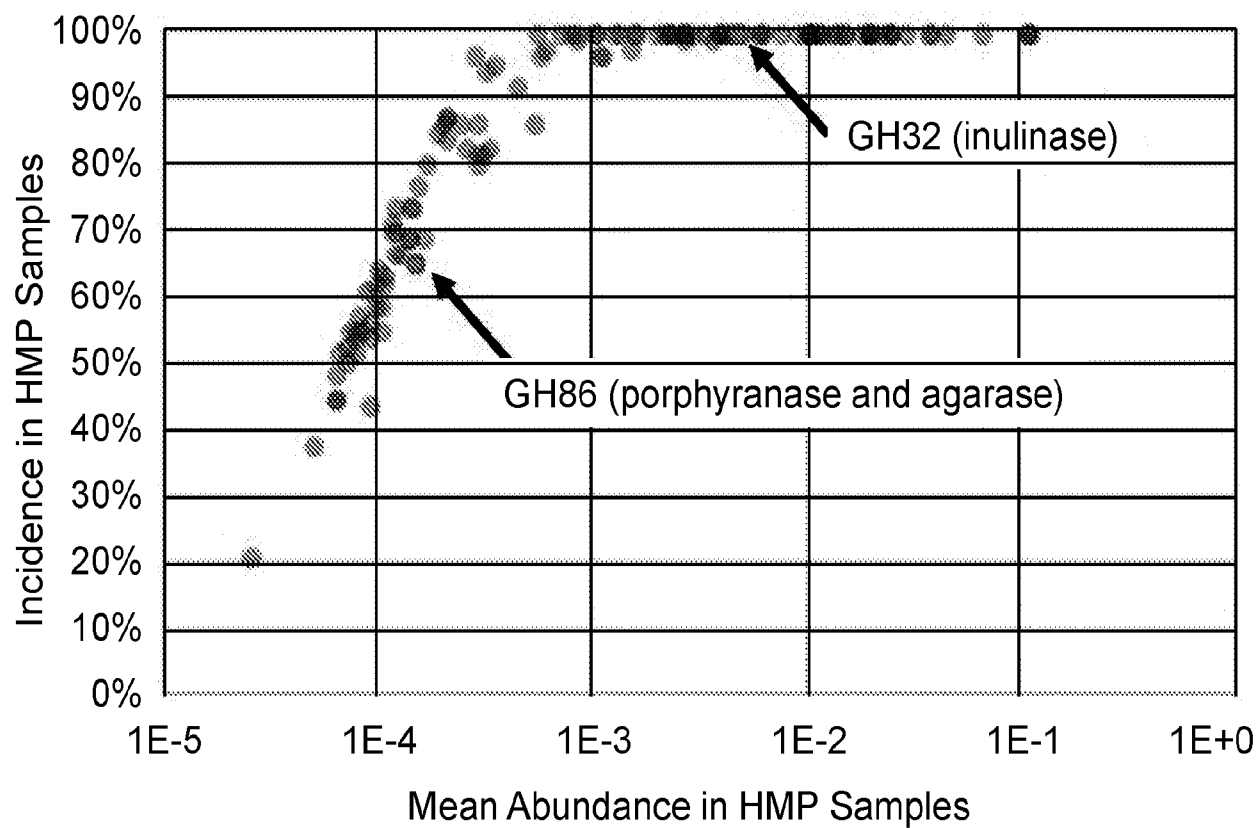
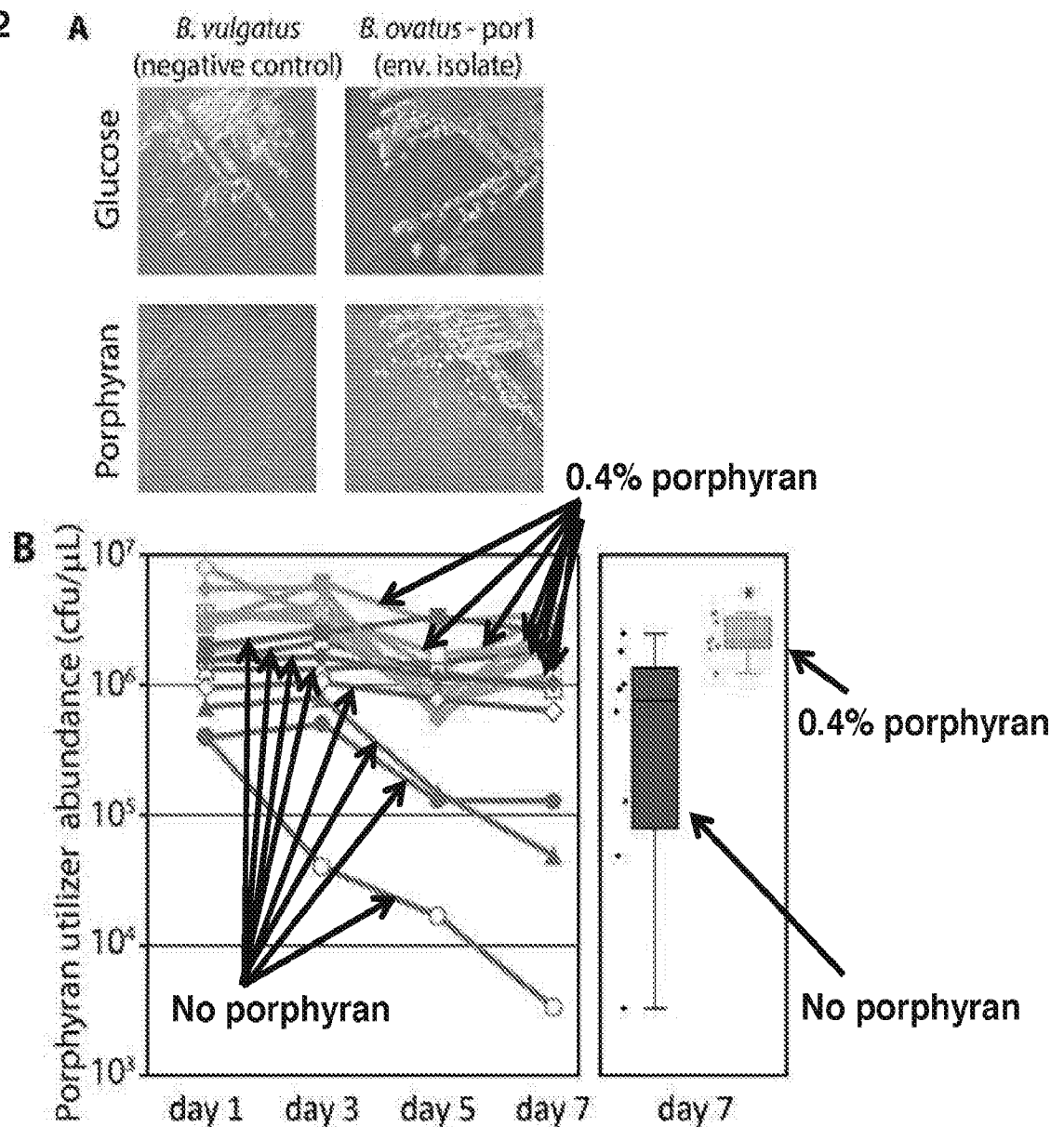
Figure 1

Figure 2

* Higher abundance ($P = 0.02$)

and

Lower deviation ($P < 0.01$)

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		2	Site 1 (Palo Alto, CA)	<i>Mus musculus</i>
		3	Site 2 (Palo Alto, CA)	<i>Mus musculus</i>
		4	Site 2 (Palo Alto, CA)	<i>Mus musculus</i>
		5	Site 3 (Daly City, CA)	<i>Mus musculus</i>
		6	Site 3 (Daly City, CA)	<i>Cavia porcellus</i>
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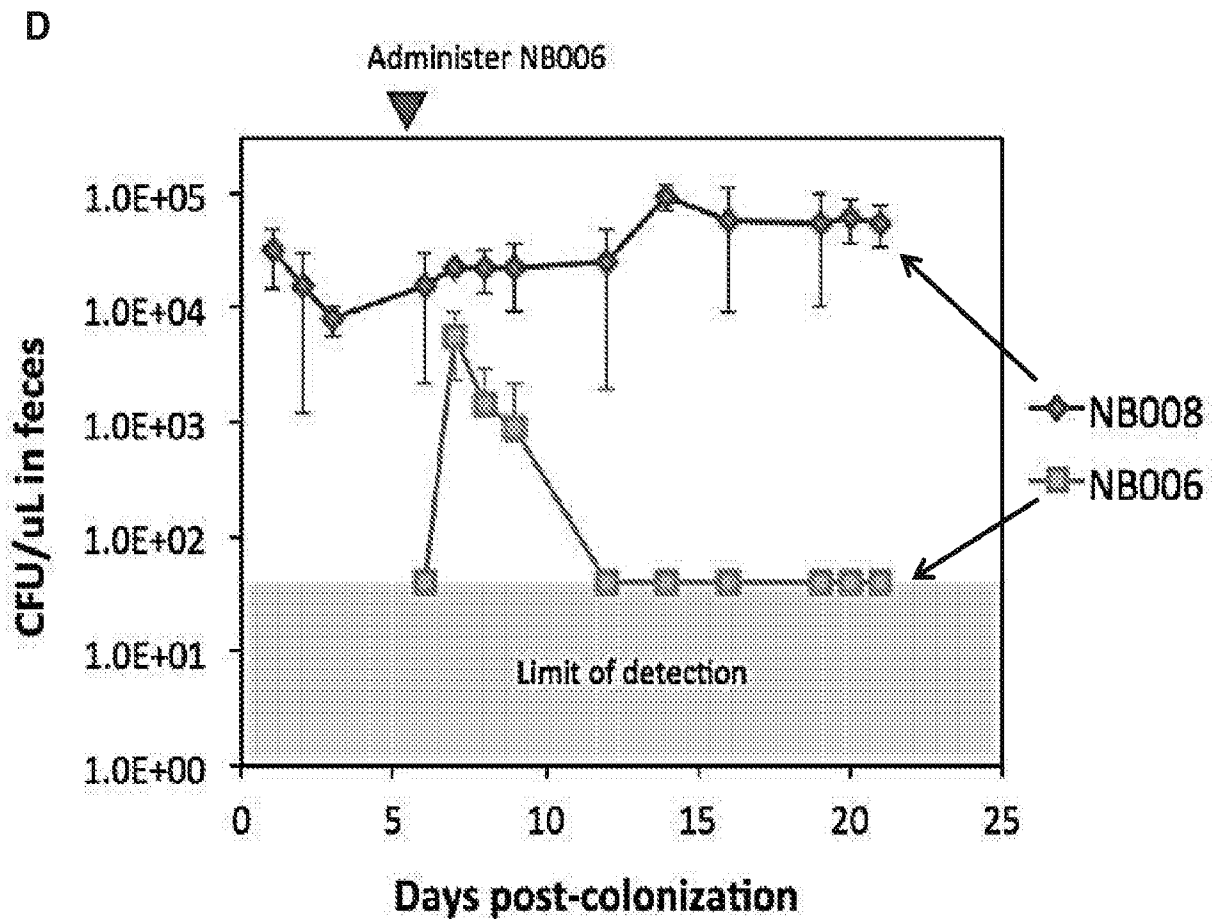
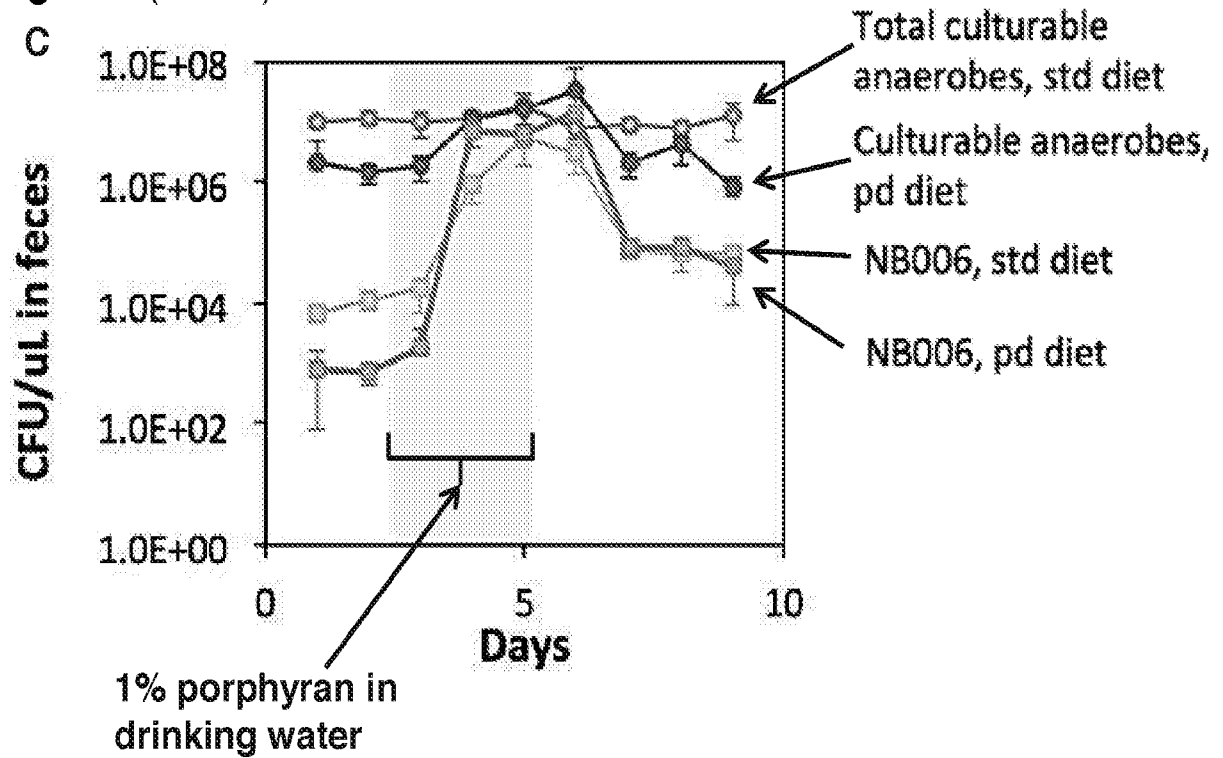
Figure 2 (Cont'd)

Figure 2 (Cont'd)

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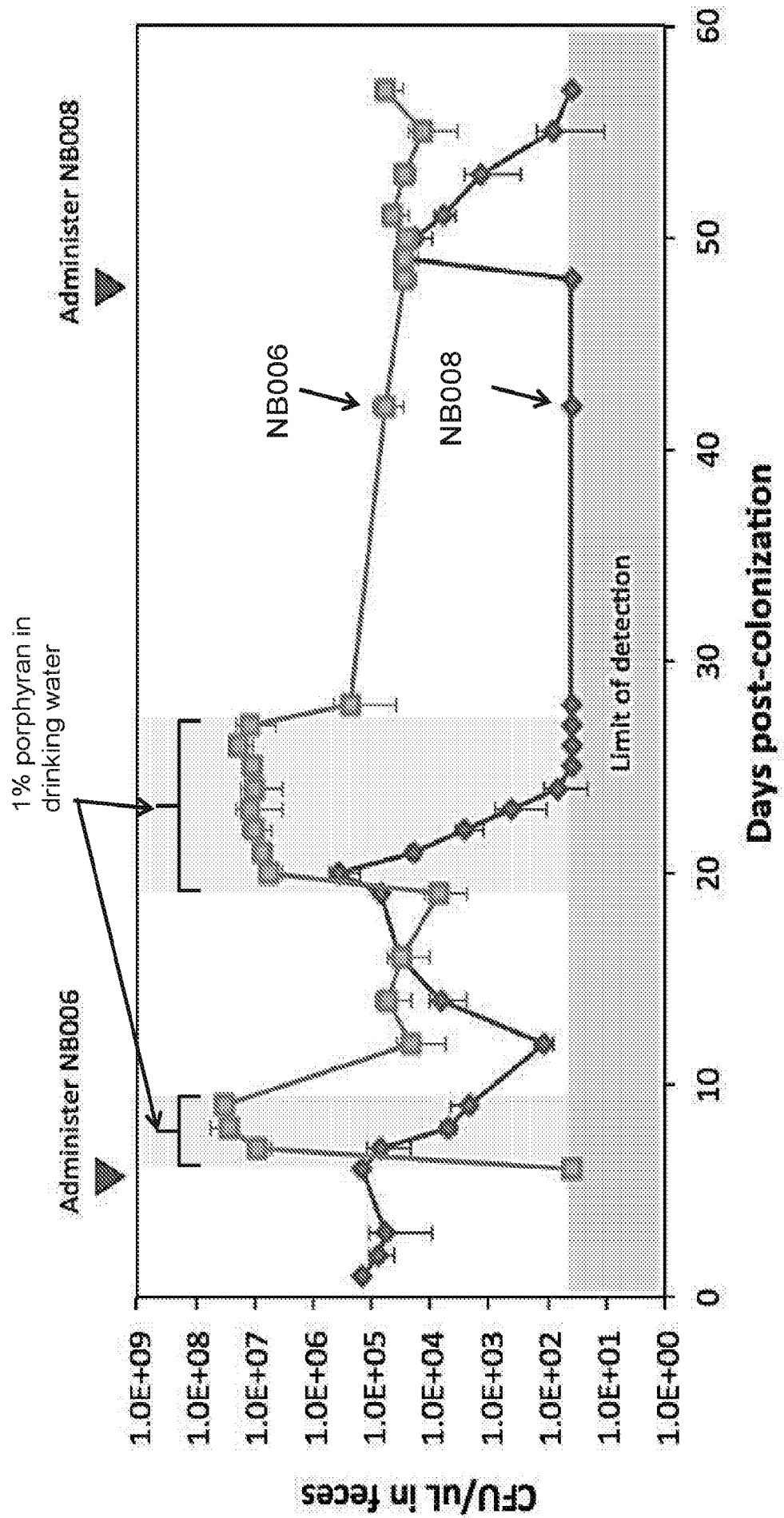


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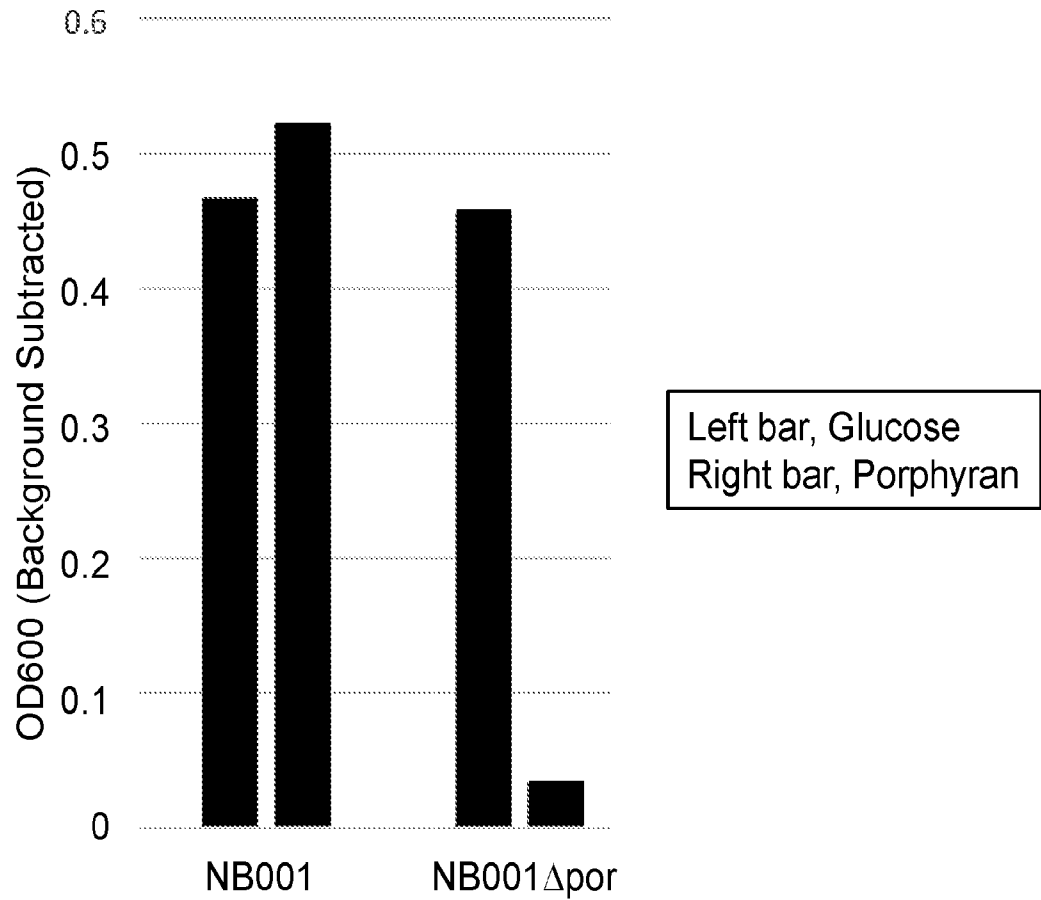
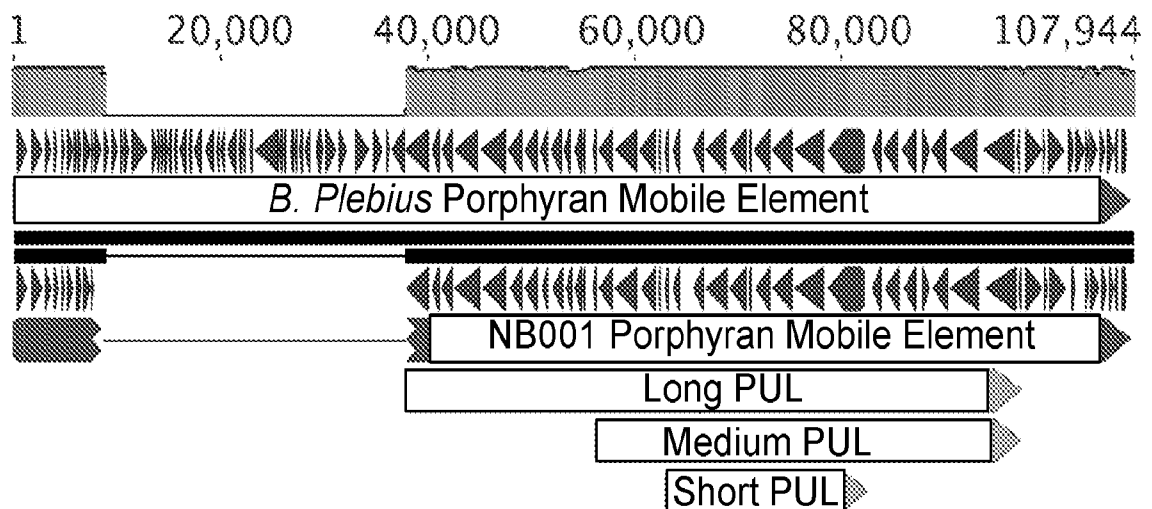


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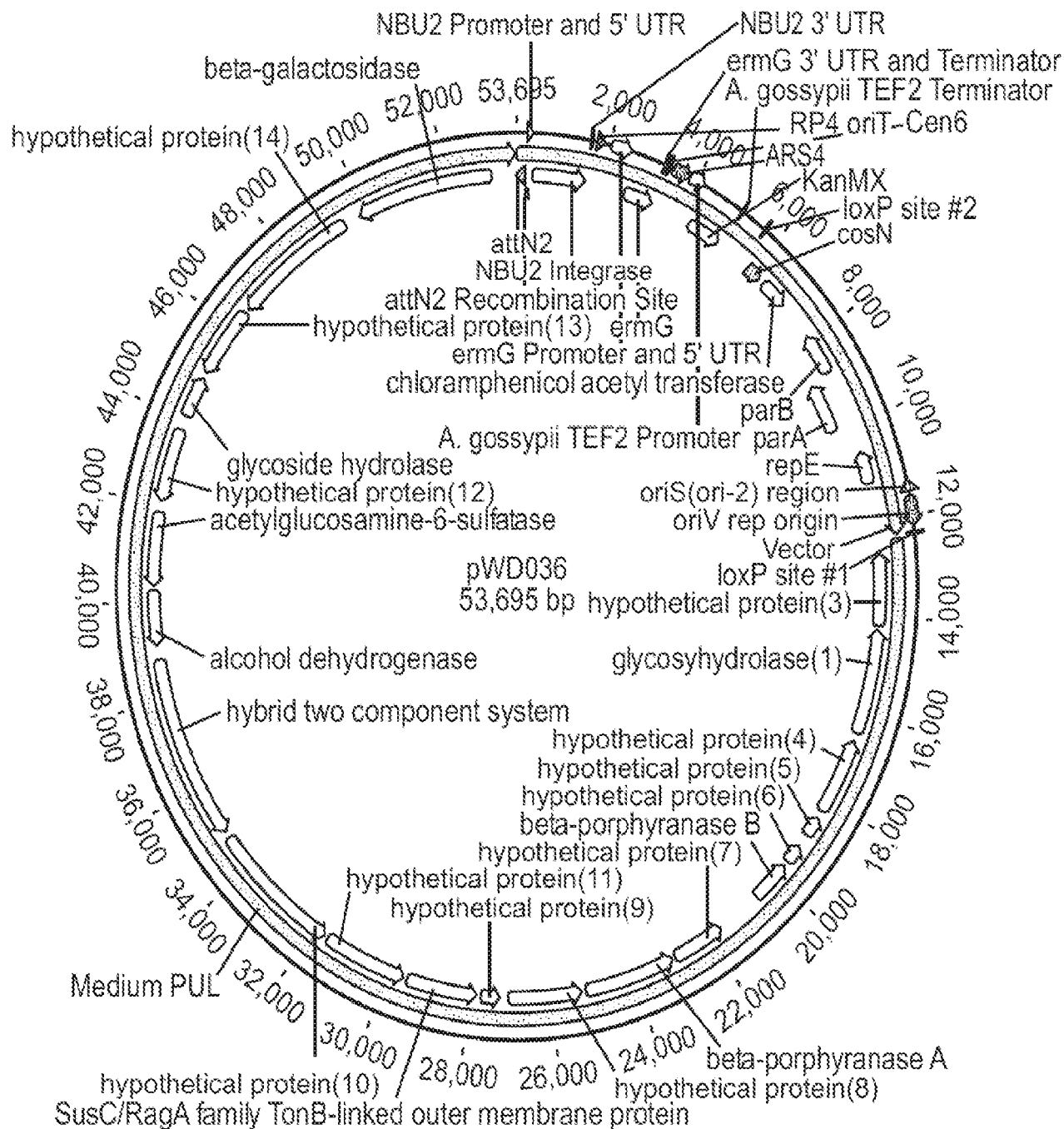


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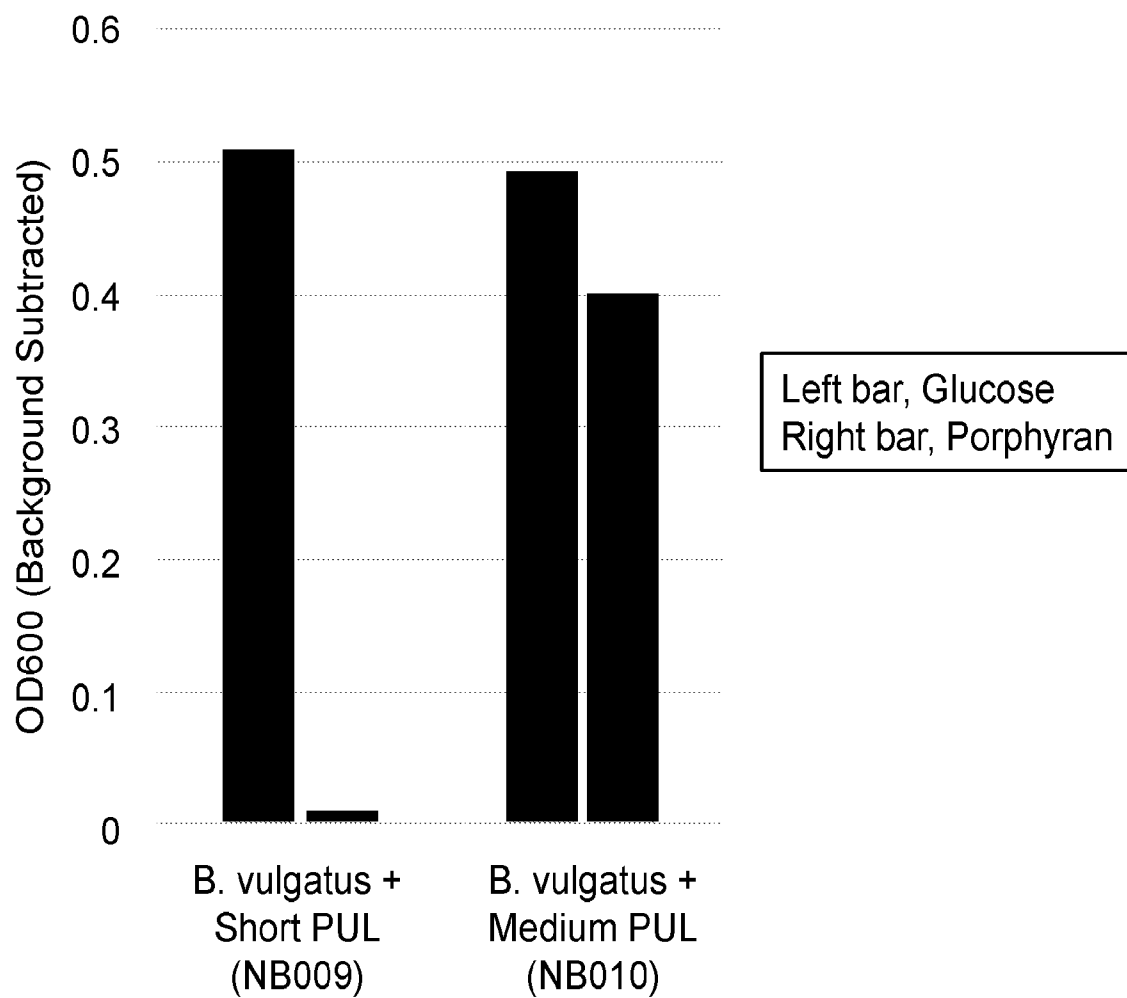
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Figure 7

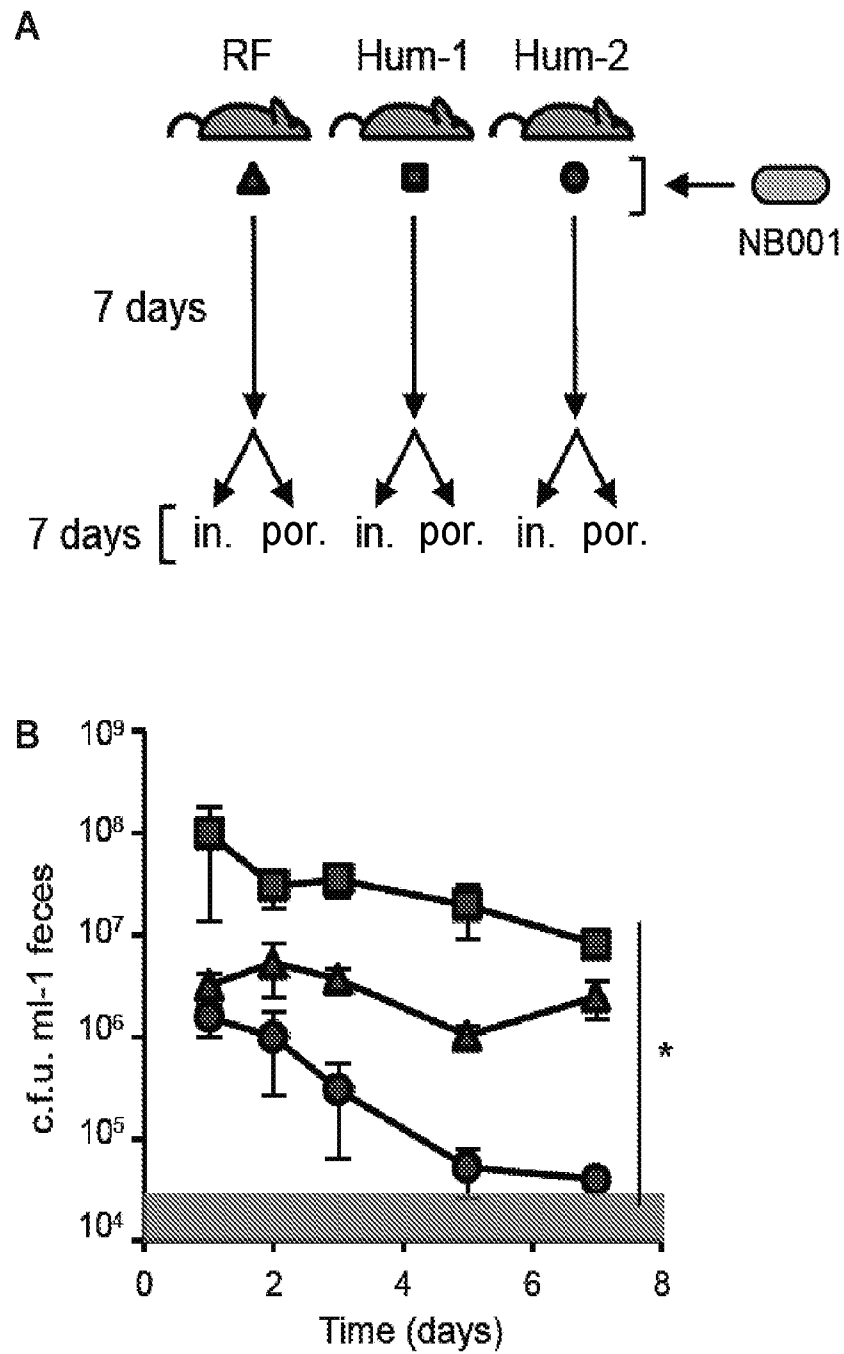


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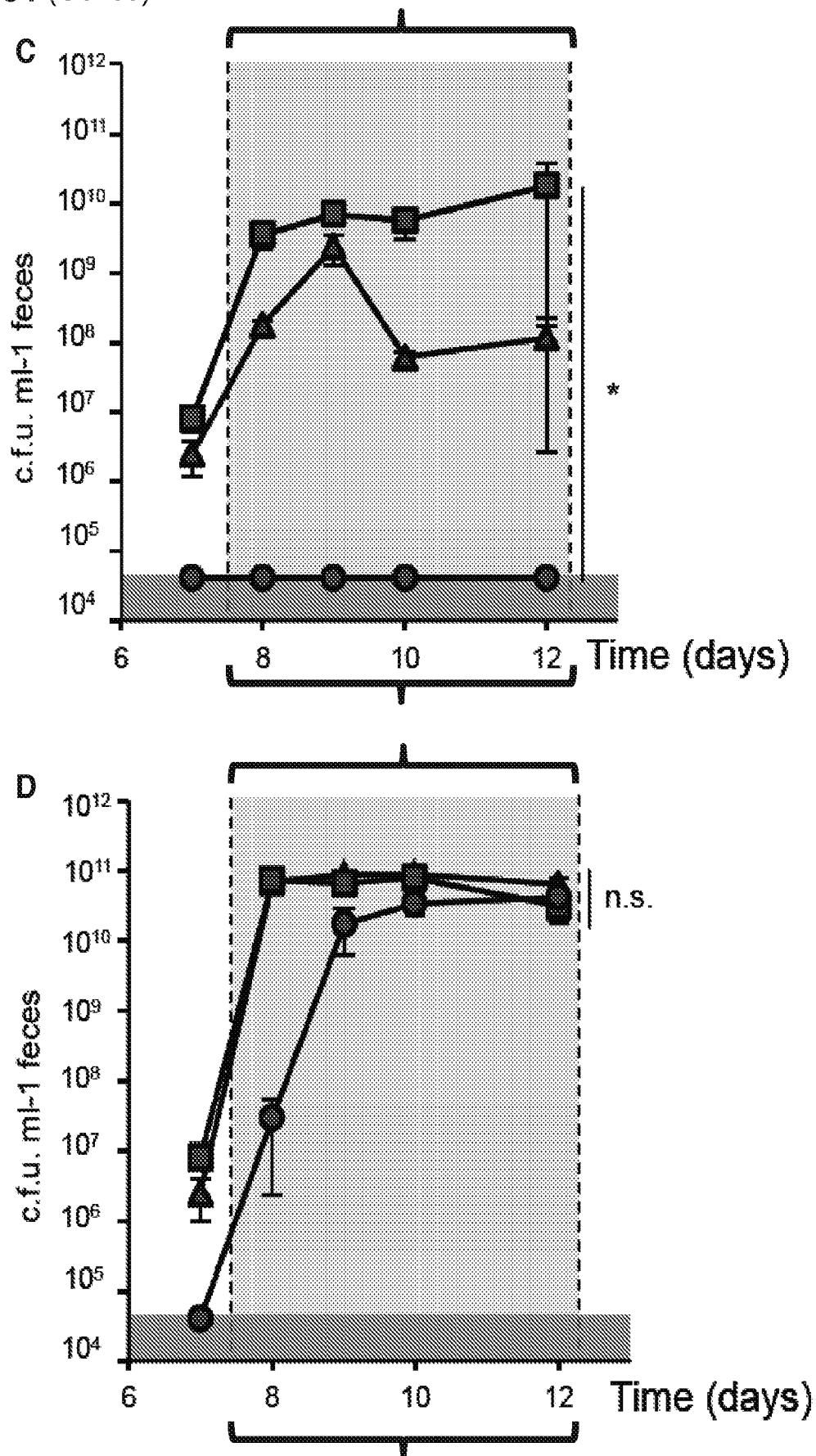
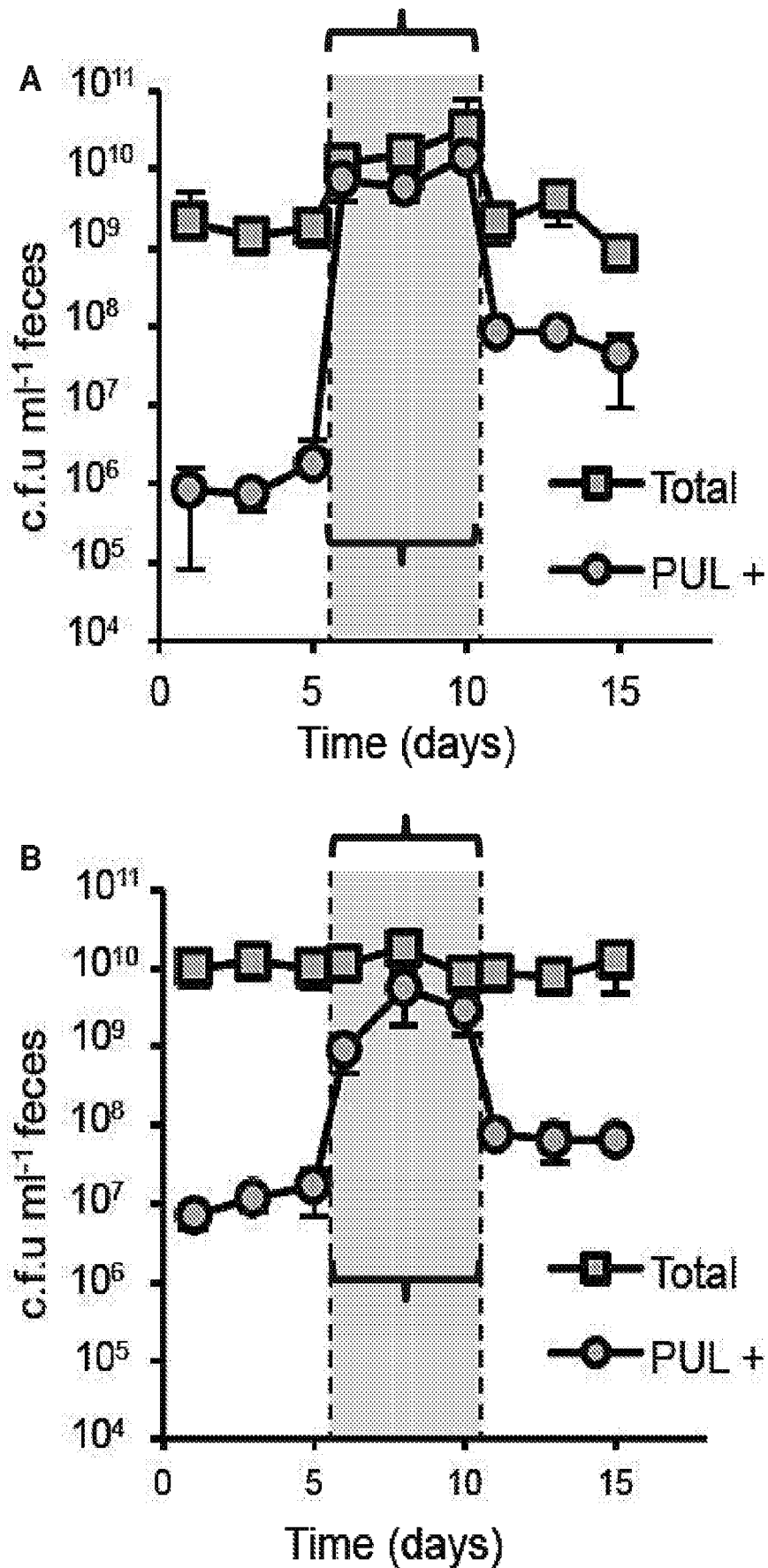


Figure 8



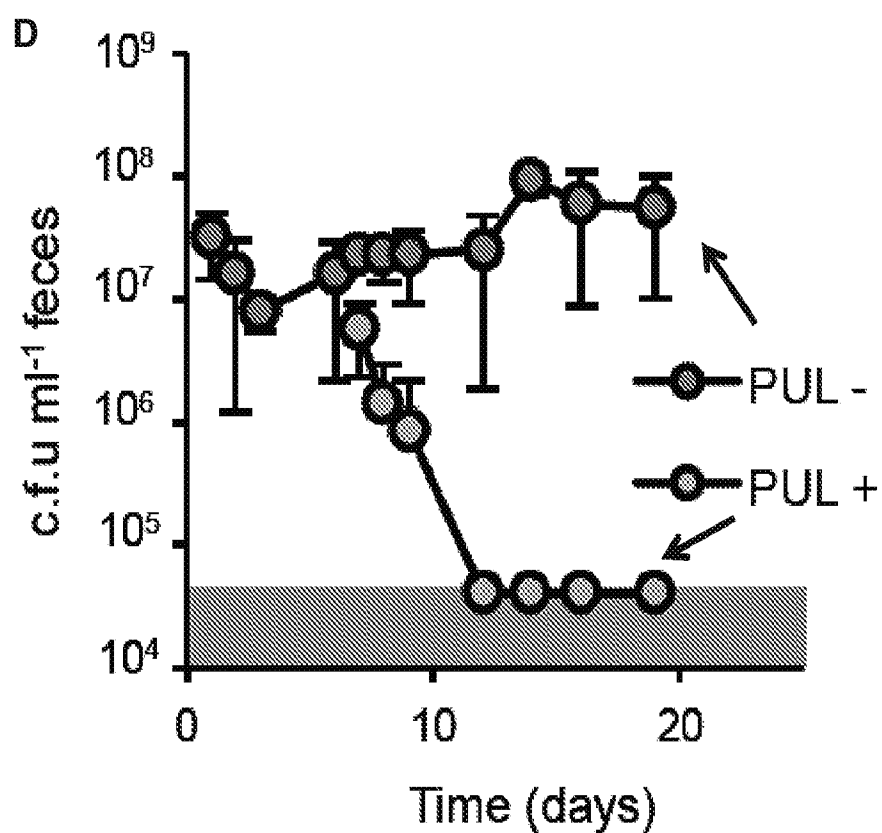
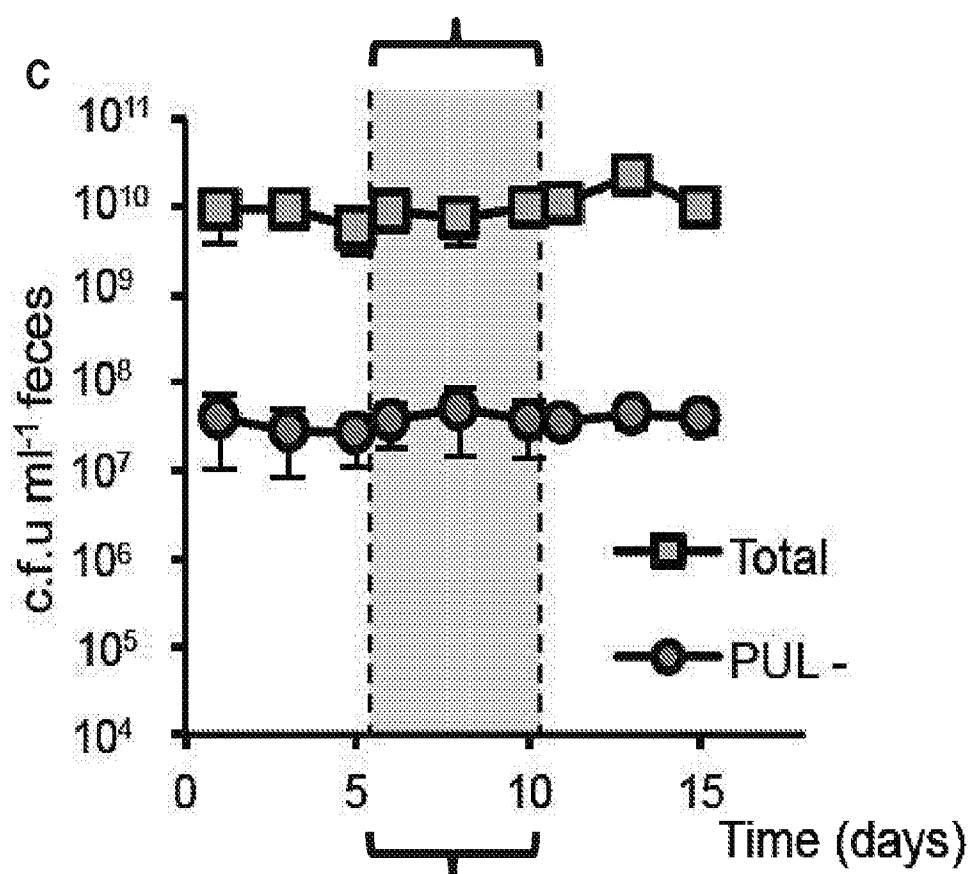
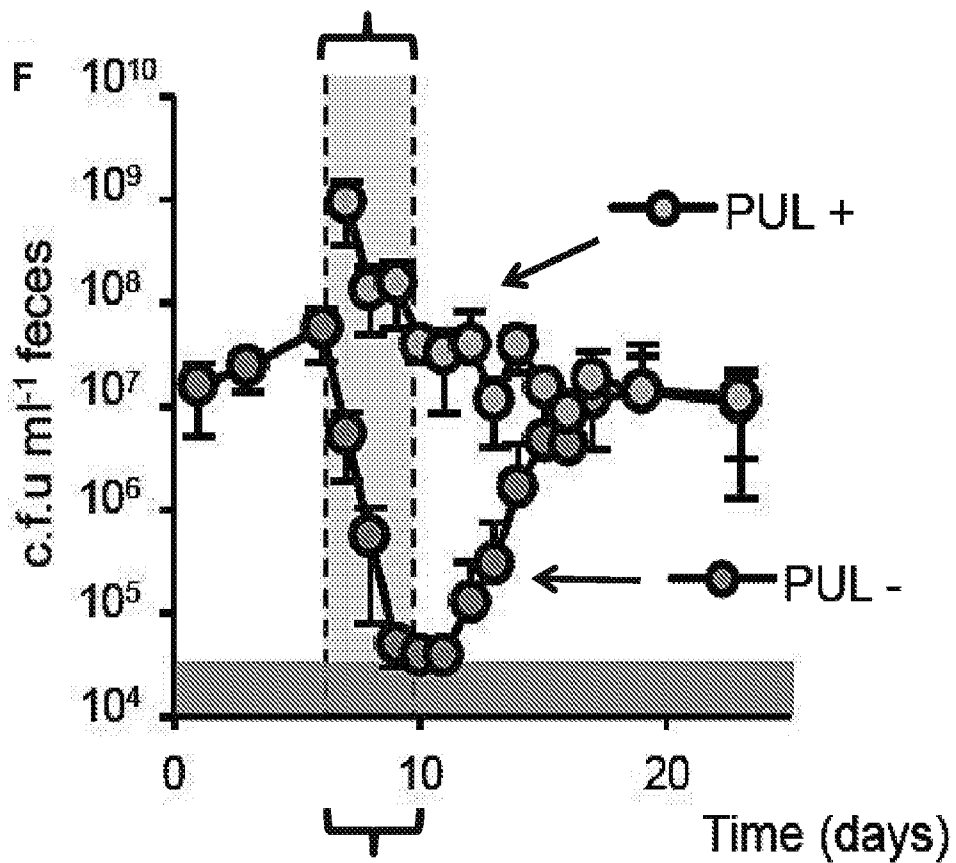
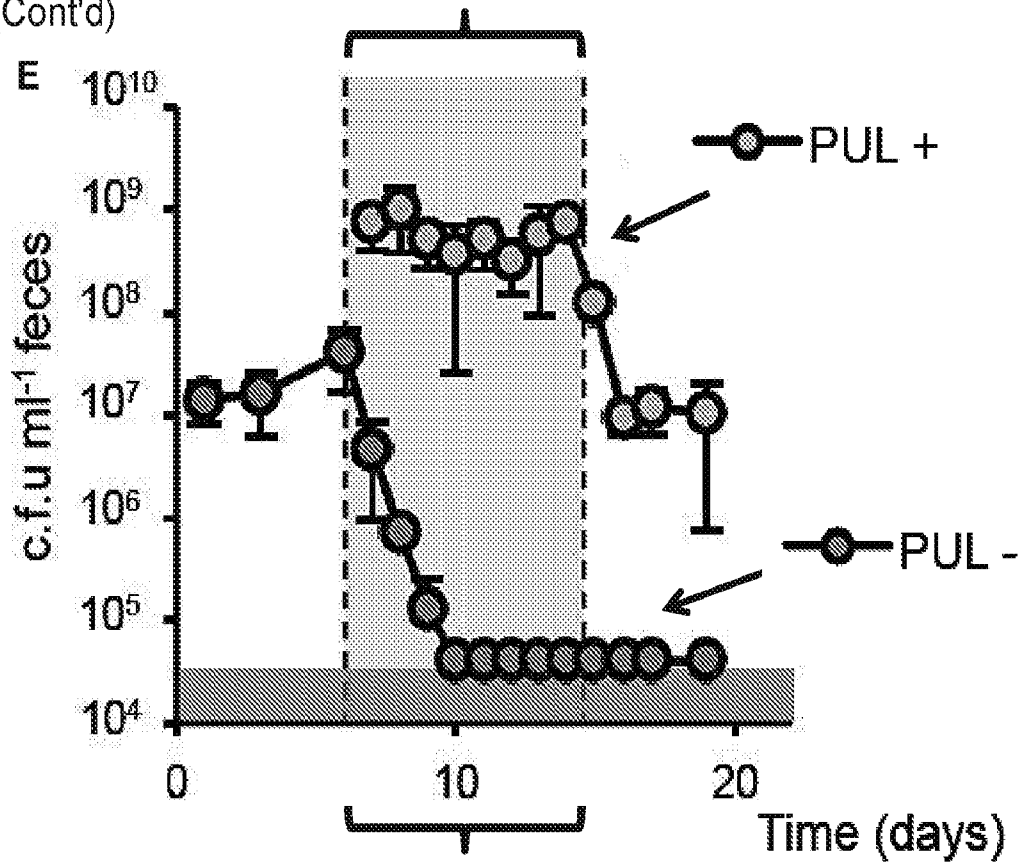


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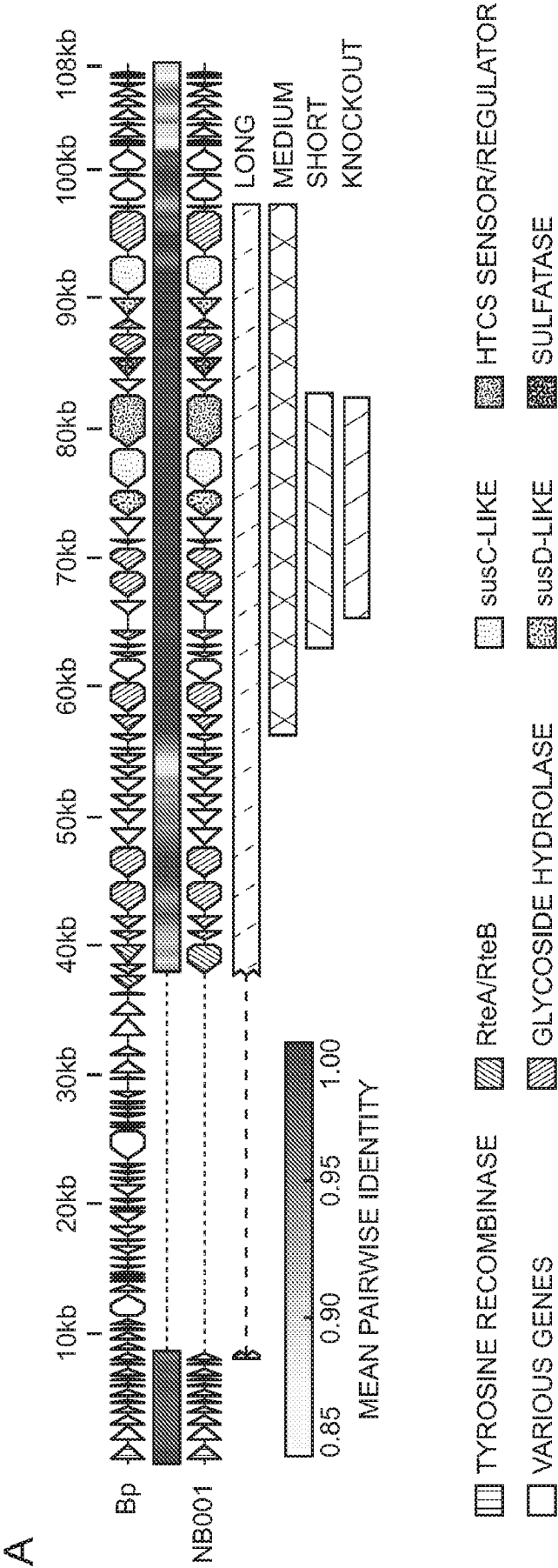


Figure 9

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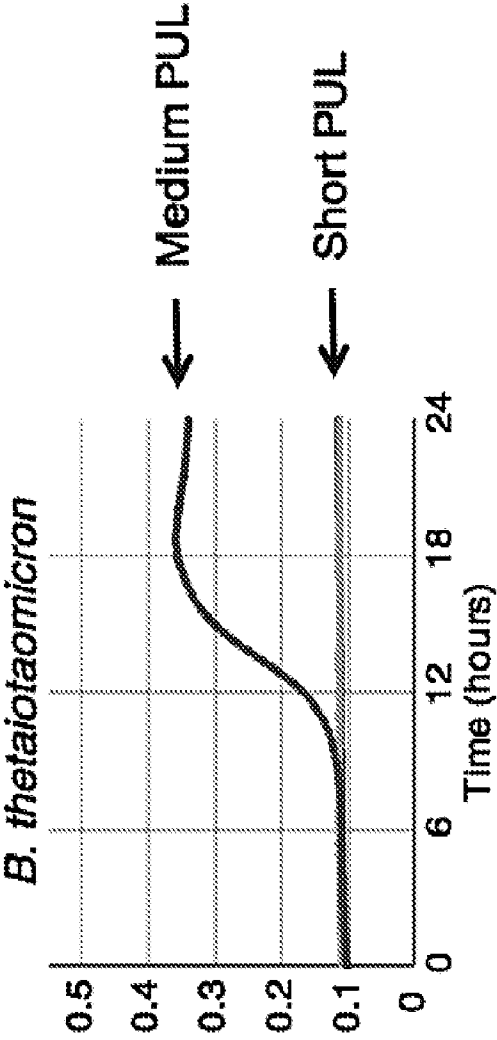
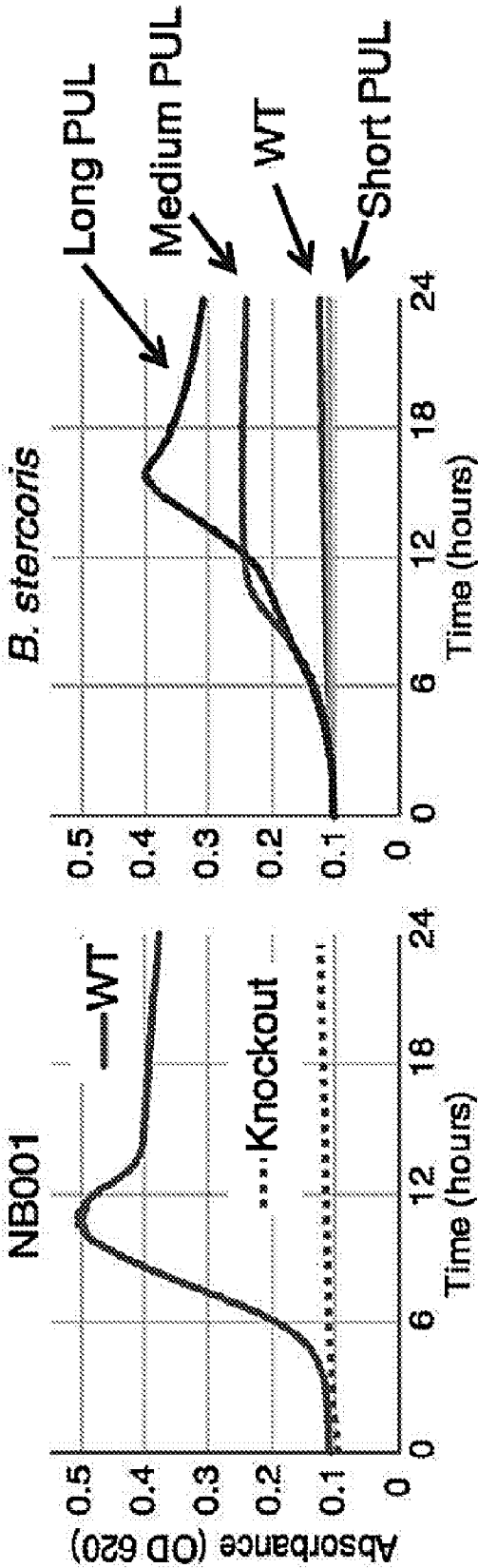


Figure 9 (Cont'd)

Figure 9 (Cont'd)

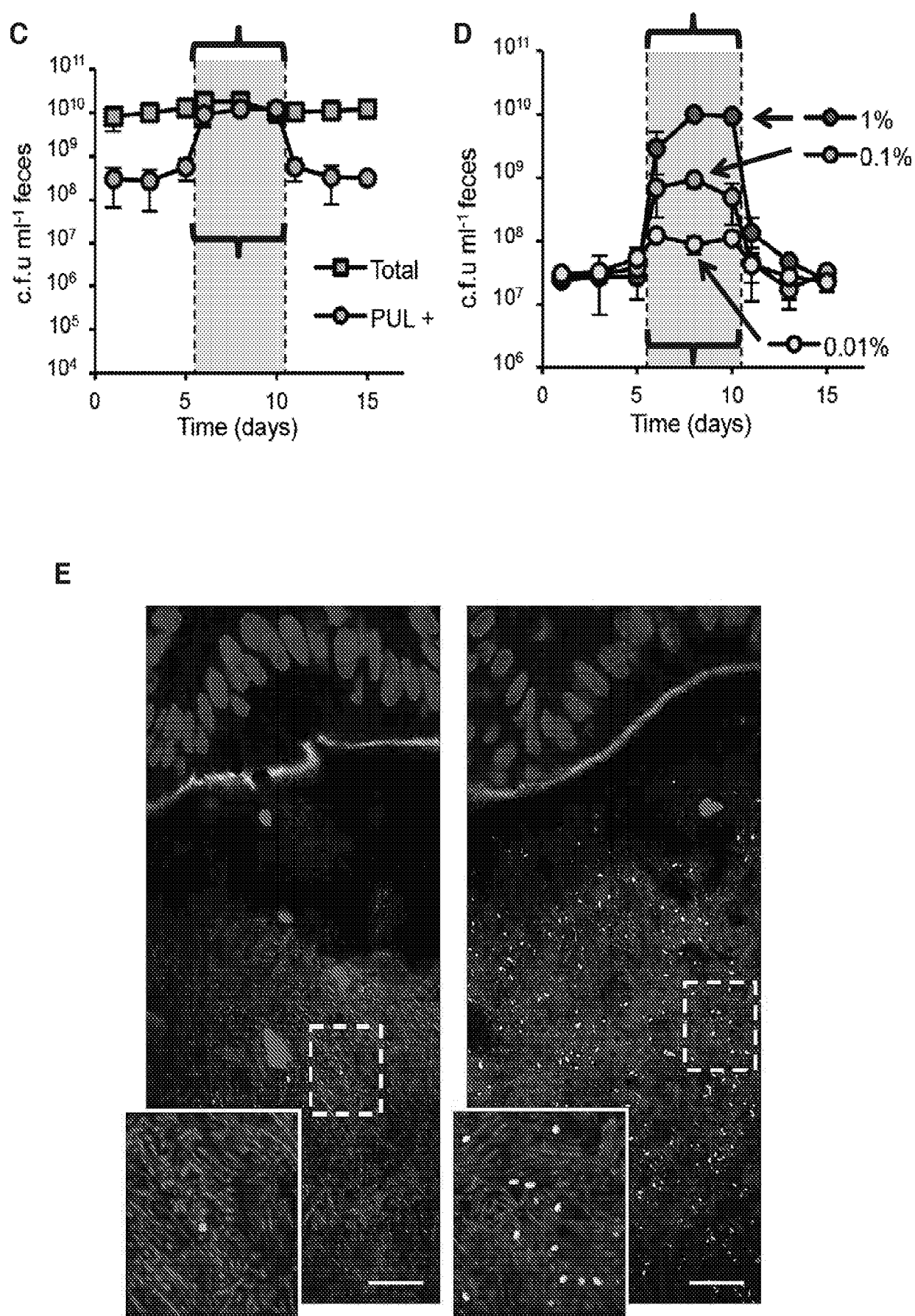
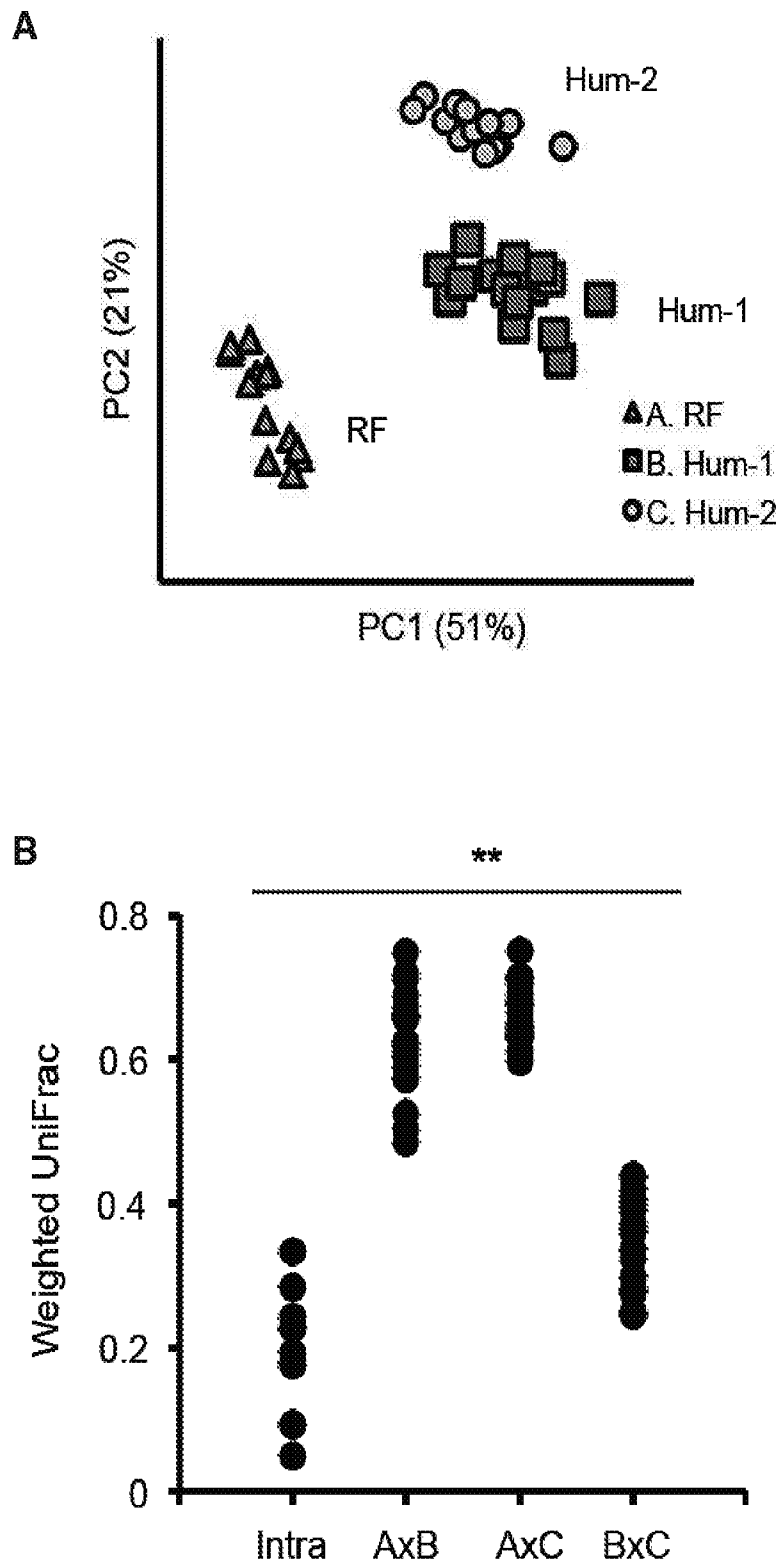


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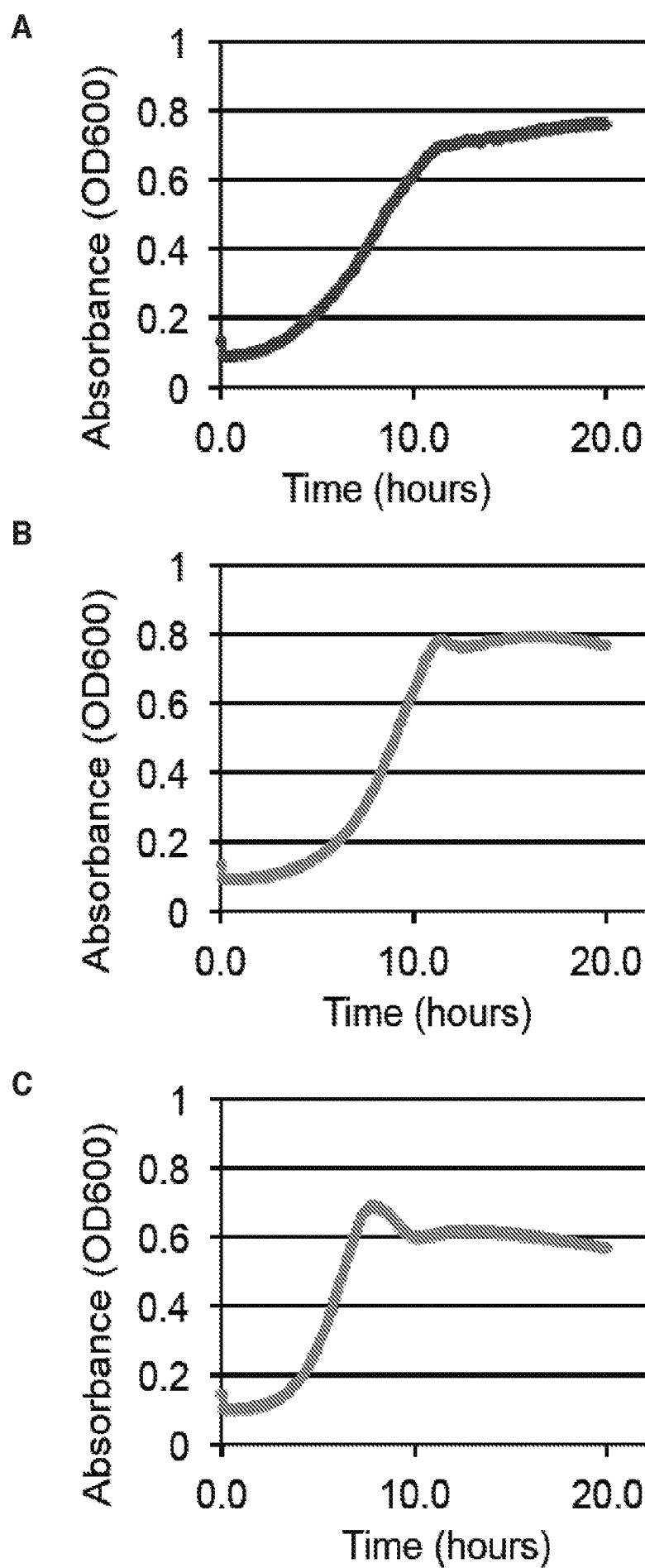


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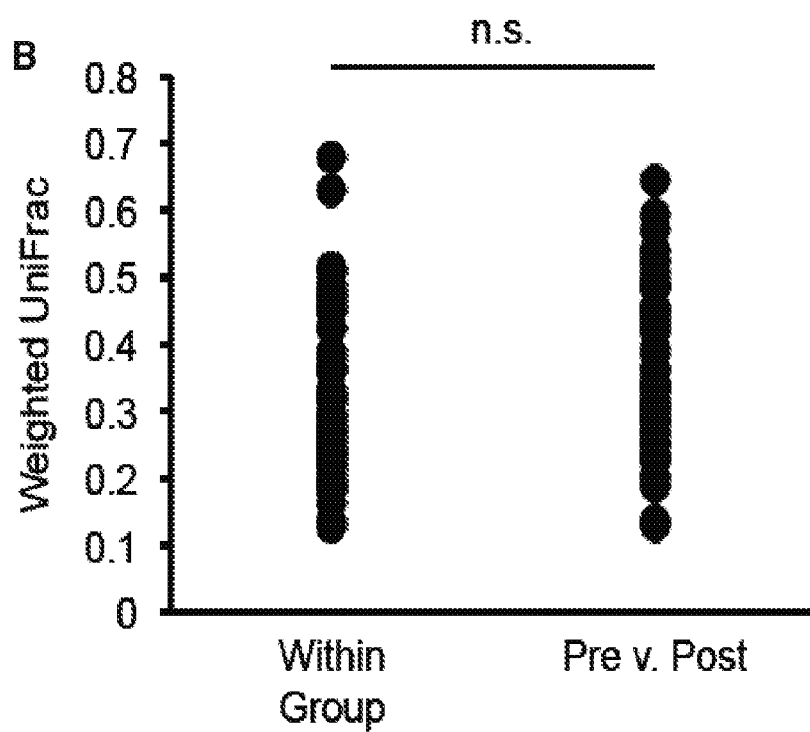
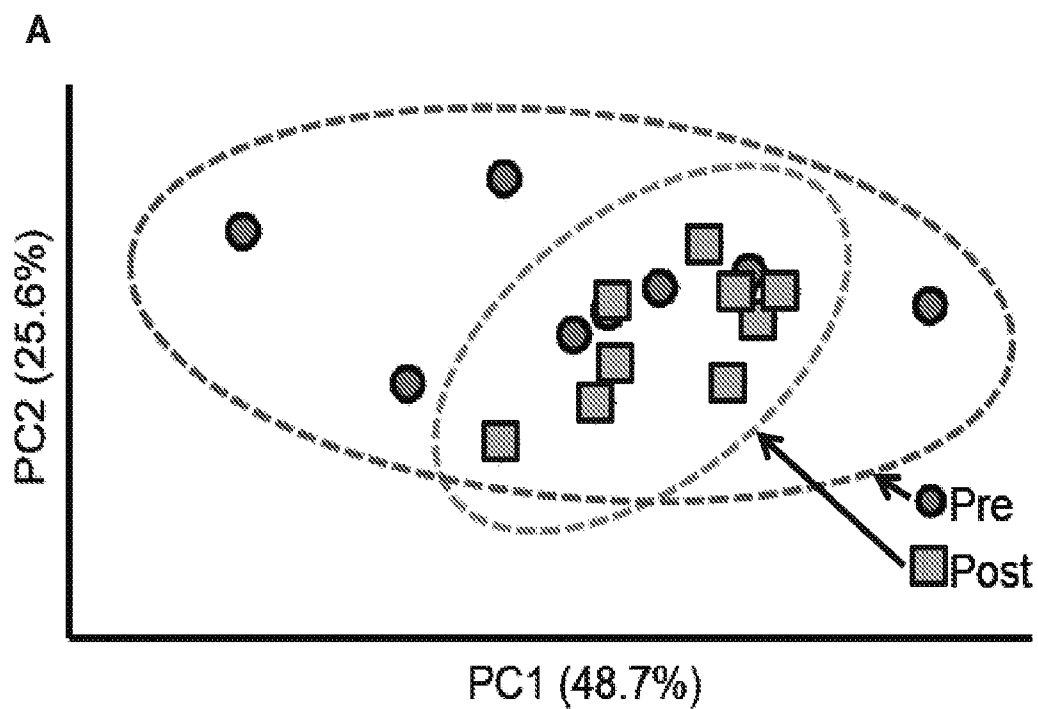


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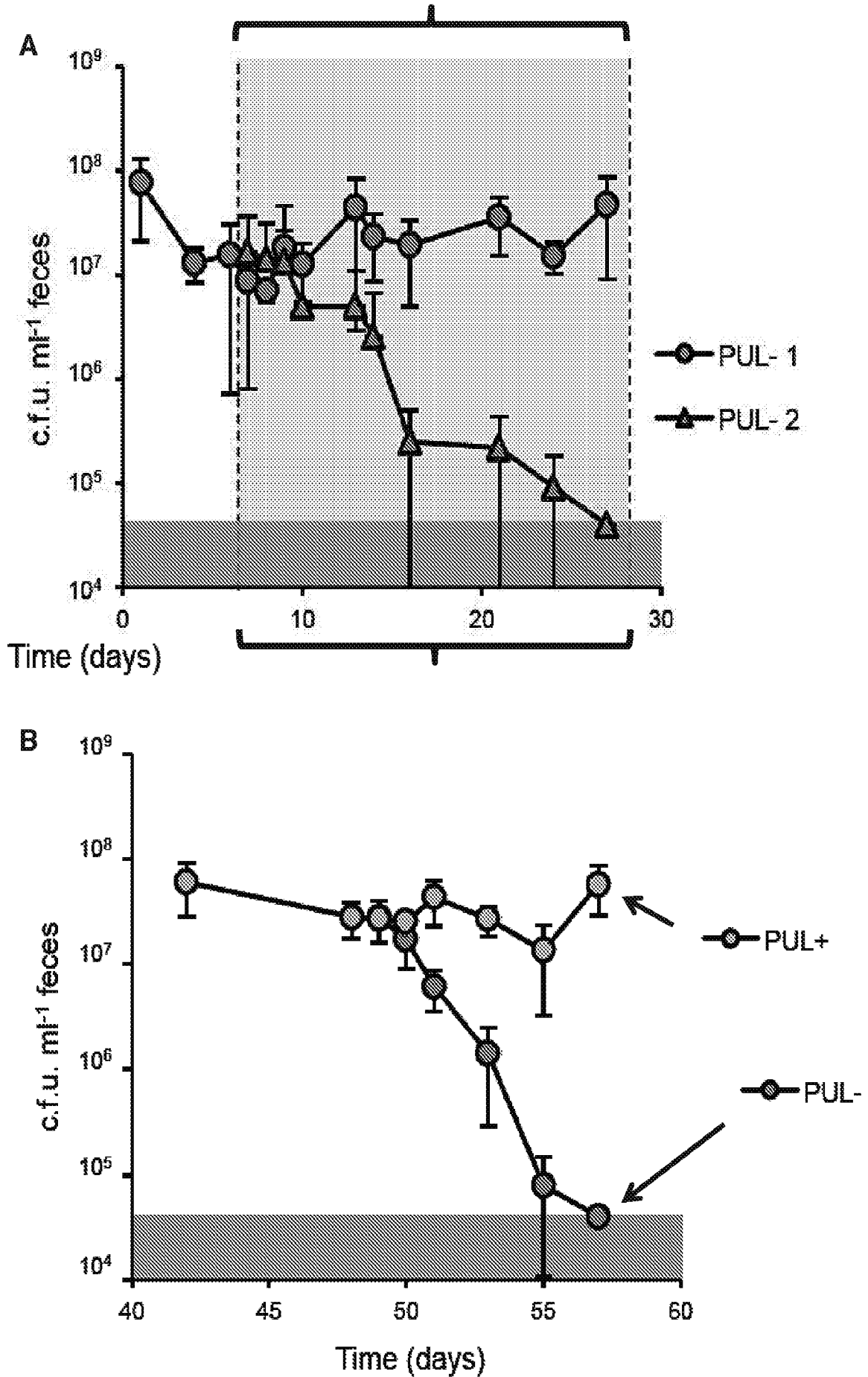


Figure 14

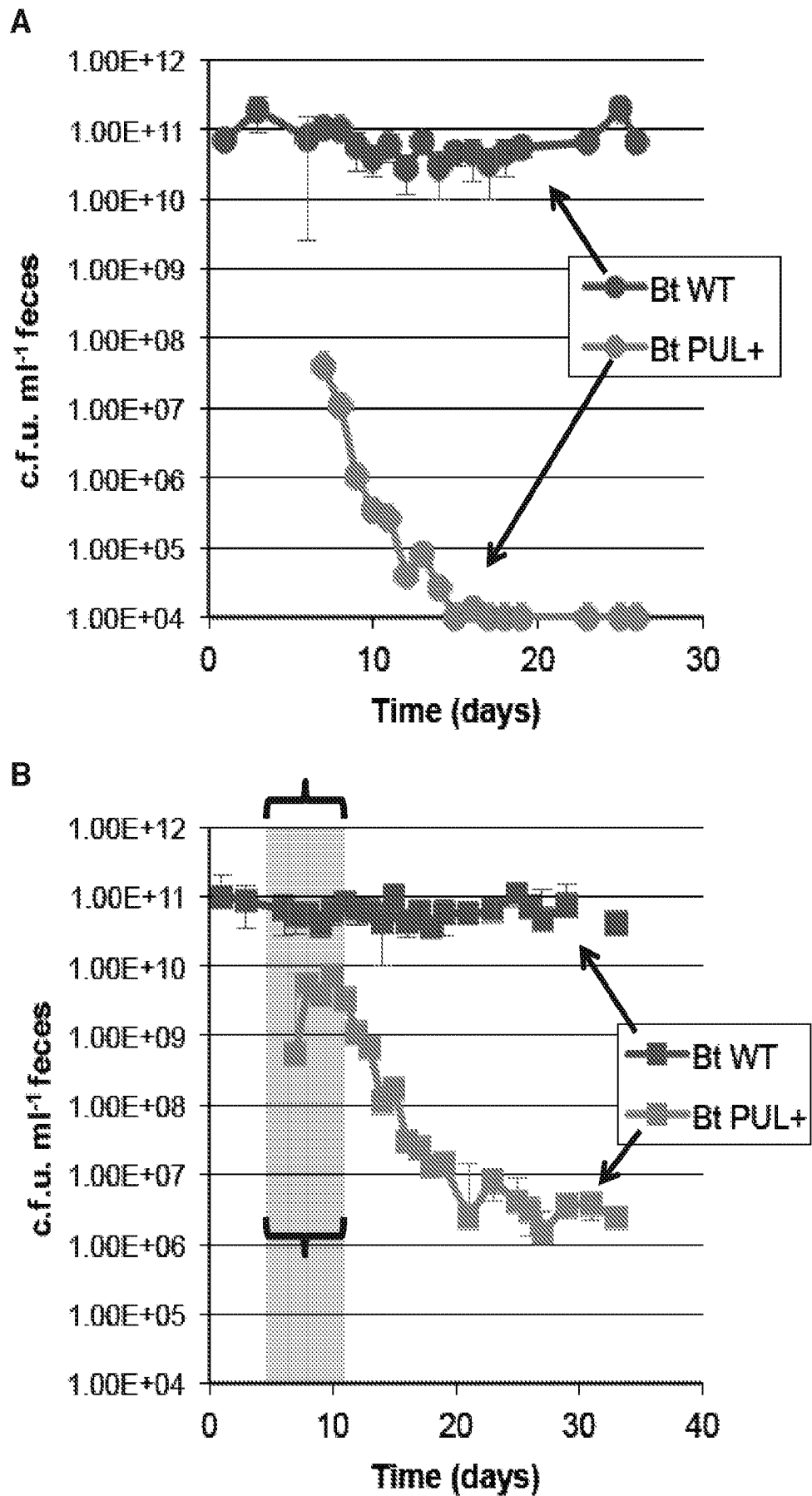
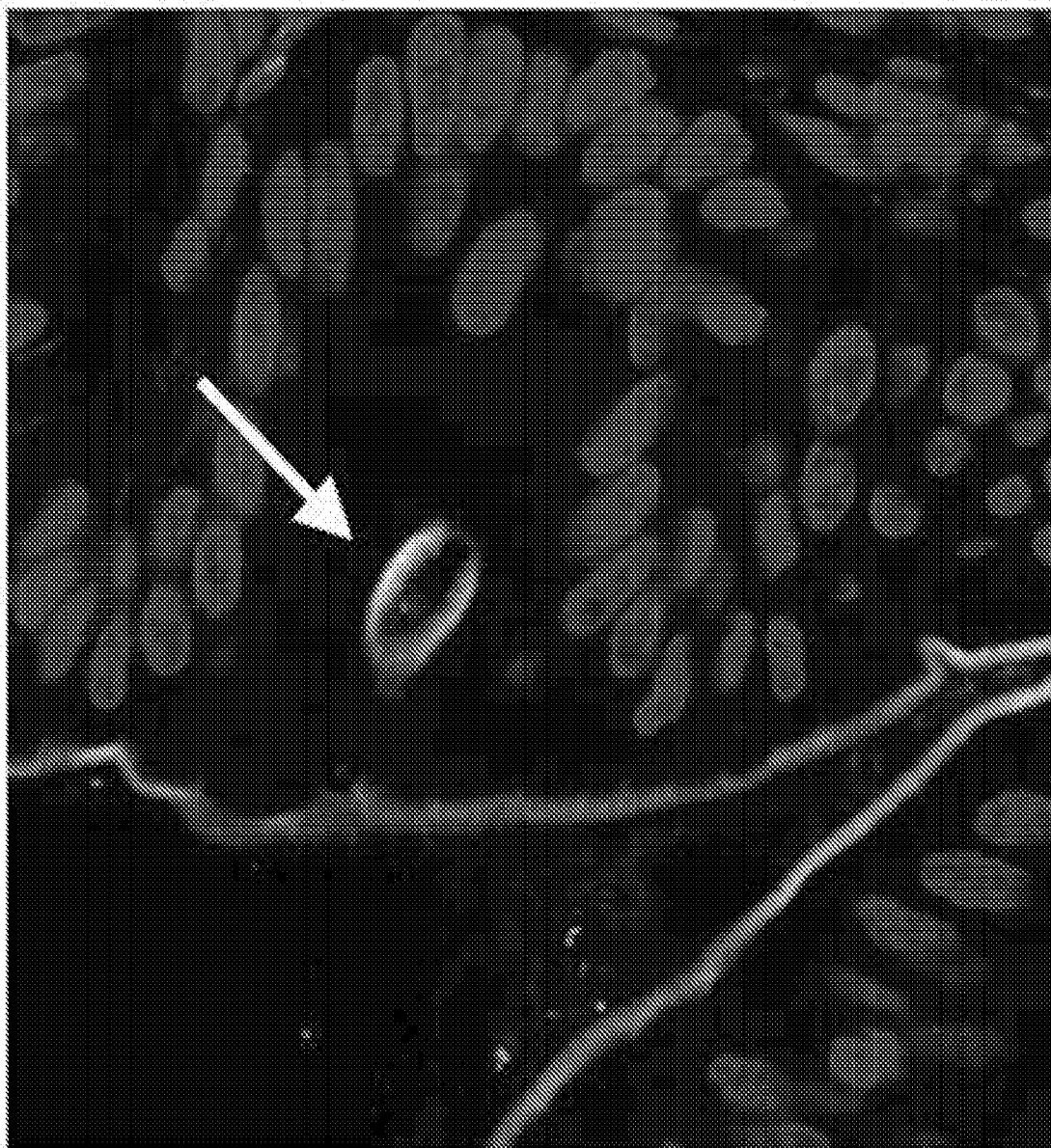


Figure 14 (Cont'd)

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deLoache, William C

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MODIFIED GUT BACTERIAL CELL

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Cys Ile Thr Ser Lys Thr Arg Val Lys Tyr Pro Val Tyr Val Glu Ala
130 135 140

Tyr Ala Lys Leu Ser Asn Ser Thr Met Ala Ser Asp Val Trp Met Leu
145 150 155 160

Ser Pro Asp Asp Thr Gln Glu Ile Asp Ile Ile Glu Ala Tyr Gly Gly
165 170 175

Asp Arg Asp Gly Gly Gly Tyr Gly Ala Asp Arg Leu His Leu Ser His
180 185 190

His Ile Phe Ile Arg Gln Pro Phe Lys Asp Tyr Gln Pro Lys Asp Leu
195 200 205

Gly Ser Trp Tyr Lys Asp Asp Lys Gly Thr Leu Trp Arg Asp Asp Phe
210 215 220

His Arg Val Gly Val Phe Trp Lys Asp Pro Phe Thr Leu Glu Tyr Tyr
225 230 235 240

STAN-1357W0_SeqList_ST25.txt

Val Asp Gly Glu Leu Val Arg Thr Val Ser Gly Lys Asp Ile Ile Asp
245 250 255

Pro Asn Asn Tyr Thr Gly Gly Thr Gly Leu Val Lys Asp Met Asp Ile
260 265 270

Ile Ile Asn Met Glu Asp Gln Ser Trp Arg Ala Val Lys Gly Leu Ser
275 280 285

Pro Thr Asp Glu Glu Leu Lys Asn Val Glu Asp His Thr Phe Leu Val
290 295 300

Asp Trp Ile Arg Val Tyr Thr Pro Val Pro Glu Glu
305 310 315

<210> 3
<211> 402
<212> PRT
<213> Bacteroides Plebius

<400> 3

Met Arg Lys Ile Ile Leu Ala Ala Gly Met Met Ser Leu Leu Ala Ala
1 5 10 15

Cys Gly Asn Thr Gly Asn Thr Gln Thr Ile Ala Val Asp Asp Thr Gln
20 25 30

Asn Tyr Asp Glu Arg Lys Ala Asp Ser Leu Gly Ile Pro Lys Gly Asn
35 40 45

Lys Leu Ser Ala Ala Met Lys Arg Ala Met Lys Trp Glu Asn His Asp
50 55 60

Asn Lys Trp Phe Phe Glu Tyr Lys Met Glu Pro Leu Lys Gly Asp Leu
65 70 75 80

STAN-1357W0_SeqList_ST25.txt

Ala Tyr Glu Glu Gly Val Val Arg Arg Asp Pro Ser Ala Met Leu Lys
85 90 95

Ile Gly Asn Thr Tyr Tyr Val Trp Tyr Ser Lys Ser Tyr Gly Pro Thr
100 105 110

Gln Gly Phe Ala Gly Asp Ile Glu Lys Asp Lys Val Phe Pro Trp Asp
115 120 125

Arg Cys Asp Ile Trp Tyr Ala Thr Ser Lys Asp Gly Trp Thr Trp Lys
130 135 140

Glu Gln Gly Ile Ala Val Lys Arg Gly Glu Lys Gly Ala Tyr Asp Asp
145 150 155 160

Arg Ser Val Phe Thr Pro Glu Val Met Glu Trp Lys Gly Lys Tyr Tyr
165 170 175

Leu Cys Tyr Gln Ala Val Lys Ser Pro Tyr Thr Val Arg Val Lys Asn
180 185 190

Thr Ile Gly Met Ala Cys Ala Asp Ser Pro Glu Gly Pro Trp Ile Lys
195 200 205

Thr Asp Lys Pro Val Leu Glu Pro Ser Asn Thr Gly Glu Trp Glu Gly
210 215 220

Asp Glu Asp Asn Arg Phe Lys Val Val Ser Lys Gly Asp Phe Asp Ser
225 230 235 240

His Lys Val His Asp Pro Cys Ile Ile Pro Tyr Lys Gly Lys Phe Tyr
245 250 255

Met Tyr Tyr Lys Gly Glu Arg Met Gly Glu Glu Ile Thr Trp Gly Gly
260 265 270

STAN-1357W0_SeqList_ST25.txt

Arg Glu Ile Lys His Gly Val Ala Ile Ala Glu Asn Pro Met Gly Pro
275 280 285

Tyr Val Lys Ser Glu Tyr Asn Pro Ile Ser Asn Ser Gly His Glu Val
290 295 300

Cys Val Trp Pro Tyr Lys Gly Gly Ile Ala Ser Leu Ile Thr Thr Asp
305 310 315 320

Gly Pro Glu Lys Asn Thr Leu Gln Trp Ser Pro Asp Gly Ile Asn Phe
325 330 335

Glu Ile Met Ser Val Val Lys Gly Ala Pro His Ala Ile Gly Leu Asn
340 345 350

Arg Ser Ala Asp Ala Glu Lys Glu Pro Thr Glu Ile Leu Arg Trp Gly
355 360 365

Leu Thr His Ile Tyr Asn Ser Ser Asp Tyr Gln Ser Ile Met Arg Phe
370 375 380

Ser Thr Trp Thr Leu Gln Thr His Thr Ala Lys Gly Glu Ser Lys Glu
385 390 395 400

Arg Lys

<210> 4

<211> 851

<212> PRT

<213> Bacteroides Plebius

<400> 4

Met Thr Ser Lys Lys His Val Lys Pro Lys Ile Met Arg Asn Lys Asn
1 5 10 15

Leu Leu Ala Leu Ile Ile Leu Leu Ser Thr Leu Lys Val Ser Ala Ser

STAN-1357W0_SeqList_ST25.txt

20

25

30

Asp Ser Asn Val Asp Phe Asn Lys Asp Trp Lys Phe Val Leu Lys Asp
35 40 45

Ser Ala His Tyr Ser Tyr Thr Ser Tyr Val Pro Gly Asp Glu Trp Lys
50 55 60

Lys Val Asn Leu Pro His Asp Trp Ser Val Gly Leu Pro Tyr Asp Ser
65 70 75 80

Ile Ser Gly Glu Gly Cys Val Ala Phe Leu Gln Gly Gly Ile Gly Trp
85 90 95

Tyr Ser Lys Ser Phe Pro Thr Thr Ile Ser Ala Asn Gln Lys Cys Tyr
100 105 110

Ile Val Phe Asp Gly Val Tyr Asn Asn Ser Glu Tyr Trp Ile Asn Gly
115 120 125

Lys Lys Leu Gly Tyr His Leu Ser Gly Tyr Ala Pro Phe Tyr Phe Asp
130 135 140

Val Thr Asp Tyr Leu Asn Pro Asn Glu Asp Asn Arg Met Thr Val Arg
145 150 155 160

Val Asp His Ser His Tyr Ala Asp Ser Arg Trp Tyr Thr Gly Ser Gly
165 170 175

Ile Tyr Arg Asp Val Lys Met Ile Val Thr Asp Arg Leu His Ile Pro
180 185 190

Val Trp Gly Thr Phe Val Thr Thr Pro Val Val Thr Asp Lys Tyr Ala
195 200 205

Lys Val Asn Asn Gln Ile Thr Val Arg Asn Ser Tyr Ser Glu Pro Arg

STAN-1357W0_SeqList_ST25.txt

210

215

220

Thr Ala Val Val Glu Ile Val Tyr Lys Asp Asn Lys Gly Asn Ile Ala
225 230 235 240

Ala Phe Glu Val Phe Ser Ile Lys Leu Asn Ala Gly Glu Glu Lys Ile
245 250 255

Ile Asp Ile Val Ser Glu Ile Lys Gln Pro Asp Leu Trp Ser Val Glu
260 265 270

Ile Pro Val Leu Tyr Thr Ala Glu Thr Arg Ile Lys Asn Gly Asp Glu
275 280 285

Val Ile Ser Glu Asn Thr Val Arg Phe Gly Ile Arg Thr Phe His Phe
290 295 300

Asp Ala Asp Lys Gly Phe Phe Leu Asn Gly Lys Asn Met Lys Ile Lys
305 310 315 320

Gly Val Cys Leu His His Asp Ala Gly Ile Val Gly Thr Ala Met Ile
325 330 335

Arg Asp Val Trp Tyr Arg Arg Leu Lys Thr Leu Lys Glu Gly Gly Cys
340 345 350

Asn Ala Ile Arg Leu Ser His Asn Pro Gly Ala Asp Glu Phe Leu Ser
355 360 365

Leu Cys Asp Glu Ile Gly Leu Leu Val Gln Glu Glu Phe Phe Asp Glu
370 375 380

Trp Asp Tyr Pro Lys Asp Lys Arg Leu Asn Met Lys Glu Thr Val Glu
385 390 395 400

Asp Tyr Pro Thr His Gly Tyr Cys Glu His Phe Gln Glu Trp Ala Glu

STAN-1357W0_SeqList_ST25.txt

405

410

415

Arg Asp Leu Lys Asn Val Met Arg Arg Ser Arg Asn His Ala Cys Ile
420 425 430

Phe Gln Trp Ser Ile Gly Asn Glu Ile Glu Trp Thr Tyr Thr Gly Cys
435 440 445

Arg Glu Ala Thr Gly Phe Phe Gly Ala Asp Ser Asn Gly Asn Tyr Phe
450 455 460

Trp Asn Gln Pro Pro Tyr Ser Lys Glu Lys Ile Arg Glu Met Trp Lys
465 470 475 480

Ile Gln Pro Lys Gln Ala Tyr Asp Ile Gly Arg Thr Ala Gln Lys Leu
485 490 495

Ala Ala Trp Thr Arg Gln Met Asp Thr Thr Arg Val Val Thr Ala Asn
500 505 510

Cys Ile Leu Pro Ser Ile Ser Phe Glu Thr Gly Tyr Ile Asp Ala Leu
515 520 525

Asp Val Ala Gly Phe Ser Tyr Arg Arg Val Met Tyr Asp Tyr Ala Lys
530 535 540

Lys Asn Tyr Pro Asp Lys Pro Ile Met Gly Thr Glu Asn Leu Gly Gln
545 550 555 560

Trp His Glu Trp Lys Ala Val Ile Glu Arg Asp Phe Val Pro Gly Met
565 570 575

Phe Ile Trp Thr Gly Val Asp Tyr Leu Gly Glu Ser Gly Ser Arg Leu
580 585 590

Ser Arg Trp Pro Gln Lys Ser Ile Gly Cys Gly Leu Leu Asp Met Cys

STAN-1357W0_SeqList_ST25.txt

595

600

605

Gly Tyr Val Lys Pro Ser Tyr Asp Met Met Lys Ser Leu Trp Thr Asp
 610 615 620

Lys Pro Phe Ile Ala Ile Tyr Ser Gln Thr Pro Asp Lys Ser Ser Tyr
 625 630 635 640

Leu Gln Val Lys Asp Gly Phe Thr Asp Lys Lys Gly His Glu Trp Asp
 645 650 655

Arg Arg Leu Trp Val Trp Asp Asp Val Asn Ser His Trp Asn Tyr Gln
 660 665 670

Lys Gly Asp Ser Val Ile Val Glu Ile Tyr Ser Asn Cys Asp Glu Val
 675 680 685

Glu Leu Phe Val Asn Gly Lys Ser Met Gly Lys Lys Tyr Ile Asp Asp
 690 695 700

Phe Glu Asp His Ile Tyr Lys Trp Ala Val Gln Tyr Lys Pro Gly Thr
 705 710 715 720

Ile Thr Ala Lys Gly Lys Asn Lys Leu Gly Asn Thr Thr Thr Ala Ile
 725 730 735

Arg Thr Ser Gly Lys Glu His Ser Ile Leu Leu Ala Val Asp Lys Gln
 740 745 750

Ser Ile Ala Ala Asn Gly Lys Asp Val Leu His Val Thr Ala Gln Leu
 755 760 765

Thr Asp Lys Lys Gly Asn Pro Val Lys Thr Thr Glu Gln Met Leu Lys
 770 775 780

Phe Asn Ile Asp Gly Glu Tyr Arg Leu Leu Gly Ile Asp Asn Gly Asn

STAN-1357W0_SeqList_ST25.txt

Asp Met Asn Gly Lys Lys Val Phe Ile His Phe Glu Gly Val Tyr Asn
100 105 110

Asn Ser Lys Val Trp Ile Asn Gly His Met Leu Gly Phe Arg Pro Asn
115 120 125

Gly Tyr Val Gly Phe Glu Tyr Glu Leu Thr Gln Tyr Leu Lys Pro Lys
130 135 140

Gly Ser Met Asn Thr Ile Thr Val Cys Val Asp Arg Arg Ala Tyr Ala
145 150 155 160

Asp Ser Arg Trp Tyr Val Gly Ala Gly Ile Tyr Arg Asn Val Ser Leu
165 170 175

Ile Leu Arg Asn Glu Leu Tyr Ile Pro Ser Asp Gly Ile Phe Val Thr
180 185 190

Thr Pro Gln Val Gly Asn Arg Ser Met Val Asn Val Val Cys Glu Val
195 200 205

Lys Asn Ala Gly Thr Gly Val Lys Gly Val Thr Val Lys His Glu Val
210 215 220

Val Tyr Asp Gly Lys Thr Ile Ala Ser Val Ser Asp Asp Phe Val Ala
225 230 235 240

Leu Lys Gly Asp Phe Asn Glu Phe Thr Ala Ser Val Glu Leu Glu Asn
245 250 255

Cys His Leu Trp Ser Leu Glu Thr Pro Ser Met Tyr Glu Leu His Thr
260 265 270

Thr Leu Ile Ala Ser Asp Gly Tyr Val Met Asp Lys Lys Thr Thr Lys
275 280 285

STAN-1357W0_SeqList_ST25.txt

Phe Gly Ile Arg Asp Ile Lys Phe Asp Ala Asp Glu Gly Phe Leu Leu
290 295 300

Asn Gly Lys Ser Val Lys Ile Lys Gly Val Asn Ile His His Asp Leu
305 310 315 320

Gly Cys Met Gly Val Ala Ala Tyr Asp Asp Ala Leu Leu Arg Arg Leu
325 330 335

Leu Lys Leu Arg Ser Ile Gly Cys Asn Ala Ile Arg Thr Ala His Asn
340 345 350

Pro His Ser Glu Ser Leu Leu Glu Met Cys Asp Ser Leu Gly Leu Leu
355 360 365

Val Met Asn Glu Phe Ile Asp Glu Trp Lys Val Ala Lys Lys Lys Trp
370 375 380

Ile Thr Glu Arg Ala Lys Glu Asp Ala Pro Asp Ser Ile Ser Ile Gly
385 390 395 400

Tyr Thr Arg Tyr Phe Asp Thr His Ala Glu His Asp Leu Lys Ser Phe
405 410 415

Ile Arg Arg Asp Arg Asn His Pro Cys Val Ile Leu Trp Ser Ile Gly
420 425 430

Asn Glu Ile Glu Trp Thr Tyr Pro Tyr Tyr Trp Ala Ser Ser Lys Asp
435 440 445

Asn Lys Gly Phe Lys Gly Leu Ile His Thr Gly Asp Pro Glu Thr Asp
450 455 460

Asn Lys Ser Ile Leu Lys Glu Phe Asn Arg Leu Ser Gly Gly Lys Asp
465 470 475 480

STAN-1357W0_SeqList_ST25.txt

Asp Leu Ala Glu Thr Ala Ala Val Leu Ala Gly Trp Val Lys Asp Val
485 490 495

Asp Thr Thr Arg Pro Val Ser Ser Gly Val Val Val Pro Ser Val Ser
500 505 510

Arg Leu Ser Gly Tyr Thr Asp Val Leu Asp Val Val Gly Tyr Asn Tyr
515 520 525

Lys Asp Lys Tyr Tyr Glu Ile Asp His Lys Leu Tyr Pro Tyr Gln Pro
530 535 540

Ile Ile Gly Ser Glu Asn Val Gly Gln Leu Phe Glu Trp Thr Ala Val
545 550 555 560

Ala Asp Lys Lys Tyr Ile Ala Gly Ile Phe Val Trp Thr Gly Phe Asp
565 570 575

Tyr Leu Gly Glu Asn Gly Pro Trp Pro Ala Arg Gly Gly Asp Cys Ser
580 585 590

Phe Phe Asp Phe Val Gly Asn Lys Thr Ala Arg Gly His Phe Phe Glu
595 600 605

Cys Leu Trp Lys Asp Thr Pro Lys Thr His Ile Val Thr Ile Pro Glu
610 615 620

Lys Glu Ser Glu Phe Lys Met Asp Thr Asp Gly Ser Phe Thr Tyr Thr
625 630 635 640

Pro Arg Pro Gly Trp Ile Arg Arg Trp Glu Trp Tyr Asp Thr Arg Asp
645 650 655

Lys Trp Lys Tyr Arg Arg Asp Glu Asp Ile Leu Val Gln Val Tyr Thr
660 665 670

STAN-1357W0_SeqList_ST25.txt

Asn Ala Pro Glu Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Thr
675 680 685

Lys Lys Arg Ser Asp Phe Met Glu His Asn Ile Leu Met Trp Lys Val
690 695 700

Ala Tyr Lys Glu Gly Thr Leu Leu Ala Val Gly Lys Asp Gly Asp Arg
705 710 715 720

Ile Leu Ser Lys Asp Thr Leu Ser Thr Ser Gly Lys Pro Cys Arg Leu
725 730 735

Ala Leu Asn Cys Asp Arg Lys Thr Ala Thr Asp Asn Gly Tyr Asp Leu
740 745 750

Ile His Val Glu Val Ser Ile Glu Asp Lys Glu Gly Asn Thr Val Val
755 760 765

Asp Ile Pro Ser Asp Val Arg Ile Ile Leu Asp Asp Lys Leu Glu Leu
770 775 780

Ala Gly Leu Asp Asn Gly Ser Pro Ser Ile Glu Asp Leu Asn Ile Asn
785 790 795 800

Val Ile Asn Asn Ser Val Arg Thr Tyr Asn Gly Lys Cys Leu Phe Val
805 810 815

Leu Arg Thr Ile Arg Gly Lys Lys Gly Thr Ser Phe Val Lys Val Val
820 825 830

Gly Asp Gly Gly Ile Gln Gly Arg Cys Lys Ile Leu Ile Ser His Pro
835 840 845

Ile Ser His
850

STAN-1357W0_SeqList_ST25.txt

<210> 6
 <211> 495
 <212> PRT
 <213> Bacteroides Plebuis

<400> 6

Met Thr Glu Tyr Ile Gln Ile Asn Pro Ala Asp Asn Val Ala Val Ala
 1 5 10 15

Leu His Pro Leu Ser Lys Gly Thr Val Ile Glu Val Asn Gly Asn Ser
 20 25 30

Ile Glu Leu Met Glu Asp Ile Pro Ala Gly His Lys Ile Ala Leu Lys
 35 40 45

Asp Phe Ala Glu Gly Asp Met Val Ile Lys Tyr Gly Phe Pro Ile Ser
 50 55 60

His Ala Val Lys Glu Val Arg Lys Gly His Leu Leu Asn Glu Lys Thr
 65 70 75 80

Val Lys Thr Asn Leu Ser Gly Leu Ser Thr Tyr Thr Tyr Thr Pro Lys
 85 90 95

Phe Glu Lys Gln Thr Phe Thr Asn Glu Asn His Thr Phe Lys Gly Tyr
 100 105 110

Leu Arg Ala Asn Gly Glu Ala Gly Ile Arg Asn Glu Ile Trp Ile Ile
 115 120 125

Pro Thr Val Gly Cys Val Asn Gly Ile Val Asn Gln Leu Ala Glu Gln
 130 135 140

Leu Arg Lys Glu Thr Gly Cys Glu Gly Val Asp Ser Ile Ile Ser Phe
 145 150 155 160

STAN-1357W0_SeqList_ST25.txt

Pro His Asn Tyr Gly Cys Ser Gln Leu Gly Asp Asp His Glu Asn Thr
165 170 175

Arg Lys Ile Leu Arg Asp Met Val Leu His Pro Asn Ala Gly Ala Val
180 185 190

Leu Val Val Gly Leu Gly Cys Glu Asn Asn Gln Pro Asp Ala Phe Arg
195 200 205

Glu Phe Ile Gly Asp Tyr Asp Thr Gln Arg Ile Arg Phe Leu Val Ser
210 215 220

Gln Lys Val Asp Asp Glu Ile Glu Glu Gly Met Lys Leu Leu Arg Glu
225 230 235 240

Met Tyr Ala Ile Ala Arg Glu Asp Lys Arg Thr Asp Val Pro Leu Ser
245 250 255

Lys Leu Arg Ile Gly Leu Lys Cys Gly Gly Ser Asp Gly Leu Ser Gly
260 265 270

Ile Thr Ala Asn Pro Met Leu Gly Val Phe Ser Asp Tyr Leu Val Ala
275 280 285

Gln Gly Gly Thr Thr Val Leu Thr Glu Val Pro Glu Met Phe Gly Ala
290 295 300

Glu Thr Leu Leu Met Asn Arg Cys Arg Thr Lys Glu Ile Phe Asp Asp
305 310 315 320

Thr Val Ala Met Ile Asn Asp Phe Lys Asn Tyr Phe Ile Arg Asn Asp
325 330 335

Gln Pro Ile Tyr Glu Asn Pro Ser Pro Gly Asn Lys Ala Gly Gly Ile
340 345 350

STAN-1357W0_SeqList_ST25.txt

Ser Thr Leu Glu Glu Lys Ser Leu Gly Cys Thr Gln Lys Ser Gly Ser
355 360 365

Ser Met Val Glu Asp Val Leu Lys Tyr Gly Asp Arg Val Thr Thr His
370 375 380

Gly Leu Asn Leu Leu Ser Ala Pro Gly Asn Asp Leu Val Ala Ser Thr
385 390 395 400

Ala Leu Ala Ser Ala Gly Cys His Ile Val Leu Phe Thr Thr Gly Arg
405 410 415

Gly Thr Pro Phe Gly Thr Phe Val Pro Thr Val Lys Val Ser Thr Asn
420 425 430

Thr Pro Leu Tyr Glu Gln Lys His Thr Trp Ile Asp Phe Asn Ala Gly
435 440 445

Thr Leu Val Glu Gly Glu Ser Met Glu Ser Leu Ser Arg Arg Phe Ile
450 455 460

Asp Phe Val Val Glu Val Ala Ser Gly Lys Gln Ala Leu Asn Glu Lys
465 470 475 480

Lys Gly Tyr Arg Glu Ile Ala Ile Leu Lys Gln Gly Val Thr Leu
485 490 495

<210> 7

<211> 480

<212> PRT

<213> Bacteroides Plebuis

<400> 7

Met Lys Ala Leu Asn Ser Lys Thr Ala Val Lys Ala Val Arg Pro Glu
1 5 10 15

STAN-1357W0_SeqList_ST25.txt

Arg Ile Ile Gln Phe Gly Glu Gly Asn Phe Leu Arg Ala Phe Val Asp
20 25 30

Trp Ile Ile Ser Asn Met Asn Glu Lys Thr Asp Phe Asn Ser Ser Val
35 40 45

Val Val Val Gln Pro Ile Glu Lys Gly Met Val Asp Ala Leu Asn Ala
50 55 60

Gln Asp Cys Leu Tyr His Val Asn Leu Gln Gly Leu Asn Asn Gly Glu
65 70 75 80

Val Val Asn Ser Phe Arg Met Ile Asp Val Ile Ser Arg Ala Leu Asn
85 90 95

Pro Tyr Ser Gln Tyr Asn Asp Phe Met Ala Leu Ala Glu Gln Pro Asp
100 105 110

Met Arg Phe Val Ile Ser Asn Thr Thr Glu Ala Gly Ile Asn Phe Asp
115 120 125

Pro Ser Cys Lys Leu Glu Asp Ala Pro Ala Ser Ser Tyr Pro Gly Lys
130 135 140

Leu Thr Gln Leu Leu Tyr His Arg Phe Lys His Phe Asn Gly Asp Lys
145 150 155 160

Ser Lys Gly Leu Ile Ile Phe Pro Cys Glu Leu Ile Phe Leu Asn Gly
165 170 175

His Lys Leu Lys Glu Thr Ile Tyr Gln Tyr Ile Glu Leu Trp Asn Leu
180 185 190

Gly Glu Glu Phe Lys Ser Trp Phe Glu Thr Ala Cys Gly Val Tyr Ala
195 200 205

STAN-1357W0_SeqList_ST25.txt

Thr Leu Val Asp Arg Ile Val Pro Gly Phe Pro Arg Lys Asp Ile Asp
210 215 220

Asn Ile Lys Thr Lys Leu Tyr Phe Asp Asp Asn Leu Val Val Gln Gly
225 230 235 240

Glu Ala Phe His Leu Trp Val Ile Glu Ala Pro Glu Ser Val Ala Glu
245 250 255

Glu Phe Pro Ala Asn Lys Ala Gly Leu Asn Val Leu Phe Val Pro Ser
260 265 270

Glu Glu Pro Tyr His Glu Arg Lys Val Thr Leu Leu Asn Gly Pro His
275 280 285

Thr Val Leu Ser Pro Val Ala Phe Leu Ser Gly Val Asn Ile Val Arg
290 295 300

Asp Ala Cys Gln His Glu Val Ile Gly Lys Phe Ile Lys Arg Val Met
305 310 315 320

Phe Asp Glu Leu Met Glu Thr Leu Asn Leu Pro Lys Glu Glu Leu Lys
325 330 335

Lys Phe Ala Asp Asp Val Leu Glu Arg Phe Asn Asn Pro Phe Val Asp
340 345 350

His Gln Val Thr Ser Ile Met Leu Asn Ser Phe Pro Lys Tyr Ala Thr
355 360 365

Arg Asp Leu Pro Gly Val Lys Glu Tyr Leu Lys Arg Lys Gly Val Leu
370 375 380

Pro Glu Gly Leu Val Leu Gly Leu Ala Ala Ile Ile Val Tyr Tyr Lys
385 390 395 400

STAN-1357W0_SeqList_ST25.txt

Gly Gly Lys Arg Ala Asp Gly Val Glu Ile Val Pro Asn Asp Ala Gln
405 410 415

Glu Ile Met Ala Met Leu Thr Ser Leu Trp Asn Asp Gly Ser Val Glu
420 425 430

Asn Leu Val Lys Thr Val Leu Ala Asp Thr Ser Ile Trp Gly Glu Asp
435 440 445

Leu Asn Thr Ile Ser Gly Leu Ala Asp Arg Val Ile Tyr Tyr Ile Asn
450 455 460

Lys Ile Gln Ser Glu Gly Met Leu Gln Thr Val Lys Asp Leu Val Gly
465 470 475 480

<210> 8

<211> 338

<212> PRT

<213> Bacteroides Plebius

<400> 8

Met Lys Ala Val Gln Ile Thr Glu Ala Gly Lys Val Gln Val Ala Asp
1 5 10 15

Ile Val Lys Pro Thr Leu Gly Ala Gly Glu Ile Leu Leu Arg Ile Lys
20 25 30

Tyr Val Gly Phe Cys Gly Ser Asp Leu Asn Thr Tyr Leu Gly Arg Asn
35 40 45

Pro Met Val Lys Met Pro Val Ile Pro Gly His Glu Val Gly Ala Val
50 55 60

Ile Glu Glu Ile Gly Glu Gly Val Pro Val Gly Phe Glu Lys Gly Met
65 70 75 80

Asn Val Thr Val Asn Pro Tyr Thr Asn Cys Gly Lys Cys Ala Ser Cys

STAN-1357W0_SeqList_ST25.txt

85

90

95

Arg Asn Gly Arg Val Asn Ala Cys Glu His Asn Glu Thr Leu Gly Val
 100 105 110

Gln Arg Asn Gly Ser Met Gln Glu Phe Leu Val Leu Pro Trp Thr Lys
 115 120 125

Val Ile Pro Ala Ala Gly Leu Ser Asp Lys Glu Cys Ala Leu Ile Glu
 130 135 140

Pro Met Ser Val Gly Phe His Ala Val Ser Arg Ala Gln Val Thr Asp
 145 150 155 160

Ile Asp Thr Val Ala Val Ile Gly Cys Gly Met Ile Gly Leu Gly Ala
 165 170 175

Ile Val Arg Ala Ser Leu Arg Gly Ala Arg Val Ile Ala Leu Asp Ile
 180 185 190

Asp Asp Glu Lys Leu Glu Leu Ala Lys Arg Leu Gly Ala Ser Met Val
 195 200 205

Ile Asn Ser Lys Thr Glu Asn Val Val Glu Arg Val Arg Glu Leu Thr
 210 215 220

Asp Gly Tyr Met Ala Asp Val Val Ile Glu Ala Val Gly Ser Pro Ile
 225 230 235 240

Thr Tyr Val Thr Ala Ile Asp Ile Val Gly Phe Thr Gly Arg Val Ala
 245 250 255

Cys Ile Gly Tyr Ala Lys Ser Glu Val Ala Phe Gln Thr Lys Tyr Phe
 260 265 270

Val Gln Lys Glu Leu Asp Ile Arg Gly Ser Arg Asn Ala Met Pro Glu

STAN-1357W0_SeqList_ST25.txt

275

280

285

Asp Phe Arg Ala Val Ile His Tyr Leu Gln Asn Gly Asn Cys Pro Met
290 295 300

Asn Glu Leu Ile Ser Ala Val Val Lys Pro Glu Glu Ala Gly Glu Ala
305 310 315 320

Leu Gln Lys Trp Ser Glu Asn Pro Gly Lys Val Phe Arg Met Leu Val
325 330 335

Glu Phe

<210> 9

<211> 417

<212> PRT

<213> Bacteroides Plebius

<400> 9

Met Lys Asn Lys Tyr Phe Ile Pro Leu Leu Leu Ile Phe Ser Leu Phe
1 5 10 15

Phe Met Trp Ala Ile Ser Ser Asn Leu Leu Pro Thr Met Ile Arg Gln
20 25 30

Leu Met Lys Thr Cys Glu Leu Asn Ala Phe Glu Ala Ser Phe Thr Glu
35 40 45

Ala Ala Tyr Trp Leu Ala Tyr Phe Leu Phe Pro Ile Pro Ile Ala Met
50 55 60

Phe Met Lys Arg Phe Ser Tyr Lys Ser Gly Ile Ile Val Gly Leu Ile
65 70 75 80

Leu Ala Ala Ile Gly Gly Leu Leu Phe Phe Pro Ala Ala Glu Ile Lys
85 90 95

STAN-1357W0_SeqList_ST25.txt

Glu Tyr Trp Ala Tyr Leu Val Ile Phe Phe Ile Met Ala Thr Gly Met
100 105 110

Cys Phe Leu Glu Thr Ala Ala Asn Pro Tyr Val Thr Ala Leu Gly Thr
115 120 125

His Asp Thr Ala Ser Arg Arg Leu Asn Leu Ala Gln Ser Phe Asn Gly
130 135 140

Leu Gly Ala Phe Ile Ser Ala Met Phe Leu Ser Lys Leu Ile Leu Thr
145 150 155 160

Gly Gln Asn Tyr Thr Arg Glu Thr Leu Pro Ala Asp Phe Pro Gly Gly
165 170 175

Trp Asp Gly Phe Ile Gln Met Glu Thr Asp Ser Met Lys Met Pro Tyr
180 185 190

Leu Val Leu Ala Val Leu Leu Ile Ile Leu Ala Val Val Phe Ala Leu
195 200 205

Tyr Lys Leu Pro Asp Ile Asp Lys Glu Glu Ser His Gly Glu Lys Gly
210 215 220

Lys Leu Ile Asn Phe Ala Val Leu Lys Arg Lys His Leu Arg Trp Gly
225 230 235 240

Val Ile Ala Gln Phe Phe Tyr Asn Gly Gly Gln Thr Ala Ile Asn Ser
245 250 255

Leu Phe Leu Val Tyr Cys Cys Met Tyr Ala Gly Leu Ser Glu Asp Glu
260 265 270

Ala Thr Thr Phe Phe Gly Leu Tyr Met Leu Ala Phe Leu Gly Gly Arg
275 280 285

STAN-1357W0_SeqList_ST25.txt

Trp Ile Gly Thr Met Leu Met Ser Lys Phe Arg Pro Gln Asp Met Leu
290 295 300

Leu Thr Tyr Ala Ile Val Asn Ile Ile Leu Cys Gly Val Ile Ile Met
305 310 315 320

Phe Gly Gly Met Thr Gly Leu Tyr Ala Met Leu Ala Val Ser Phe Phe
325 330 335

Met Ser Ile Met Tyr Pro Thr Gln Phe Ser Leu Ala Leu Arg Asp Leu
340 345 350

Gly Glu Asp Thr Lys Ser Gly Ser Ala Phe Leu Val Met Ala Ile Ile
355 360 365

Gly Asn Ala Cys Ile Pro Gln Phe Thr Ala Phe Val Met Asn His Asn
370 375 380

Ala Asp Phe Tyr Gln Val Ala Tyr Val Ile Pro Leu Ile Cys Phe Phe
385 390 395 400

Phe Thr Ala Tyr Tyr Gly Trp Arg Gly Tyr Lys Ile Glu Lys Lys Gln
405 410 415

His

<210> 10

<211> 307

<212> PRT

<213> Bacteroides Plebius

<400> 10

Met Asp Tyr Thr Ile Ile Asp Ala His Ser His Leu Trp Leu Tyr Gln
1 5 10 15

STAN-1357W0_SeqList_ST25.txt

Asp	Thr	Glu	Val	Asp	Gly	Leu	Lys	Ile	Lys	Thr	Thr	Glu	Asn	Gly	Gln	20	25	30	
Ser	Leu	Phe	Met	Gly	Glu	Val	Arg	Gln	Met	Leu	Pro	Pro	Phe	Met	Ile	35	40	45	
Asp	Gly	Arg	Asn	Thr	Ala	Glu	Val	Phe	Leu	Ala	Asn	Met	Asn	Tyr	Ala	50	55	60	
Gln	Val	Gly	Gly	Ala	Val	Val	Thr	Gln	Glu	Tyr	Ile	Asp	Gly	Ile	Gln	65	70	75	80
Asn	Asp	Tyr	Leu	Leu	Glu	Val	Met	Thr	Asn	Tyr	Pro	Asp	Arg	Phe	Phe	85	90	95	
Val	Cys	Gly	Met	Cys	Glu	Phe	Arg	Lys	Gln	Gly	Tyr	Phe	Asn	Gln	Thr	100	105	110	
Val	Glu	Leu	Ile	Asp	Lys	Gly	Phe	Lys	Ala	Ile	Lys	Ile	Pro	Gly	His	115	120	125	
Arg	Leu	Gln	Leu	Lys	Asp	Gly	Arg	Val	Met	Leu	Asn	Ser	Asp	Glu	Met	130	135	140	
Met	Lys	Met	Phe	His	Leu	Met	Glu	Asp	Lys	Gly	Val	Ile	Leu	Ser	Ile	145	150	155	160
Asp	Met	Ile	Glu	Gly	Asp	Leu	Gln	Val	Gly	Glu	Met	Glu	Glu	Ile	Ile	165	170	175	
Ser	Glu	Cys	Pro	Gly	Leu	Lys	Ile	Ala	Ile	Gly	His	Phe	Gly	Met	Val	180	185	190	
Thr	Lys	Pro	Asp	Trp	Lys	Lys	Gln	Ile	Met	Leu	Ala	Arg	His	Lys	Asn	195	200	205	

STAN-1357W0_SeqList_ST25.txt

Val Met Ile Glu Ser Gly Gly Ile Thr Trp Leu Phe Asn Asp Glu Phe
210 215 220

Tyr Pro Phe Asn Gly Ala Ile Arg Ala Ile Asn Glu Ala Ala Asp Leu
225 230 235 240

Val Gly Phe Glu Lys Leu Met Trp Gly Ser Asp Tyr Pro Arg Thr Ile
245 250 255

Thr Ala Ile Thr Tyr Lys Met Ser Tyr Asp Phe Val Ile Lys Ser Lys
260 265 270

Glu Leu Glu Glu Arg Ser Lys Lys Leu Phe Leu Gly Glu Asn Ala Lys
275 280 285

Ala Phe Tyr Gly Phe Lys Asn Leu Pro Glu Leu Pro Tyr Ile Lys Asn
290 295 300

Met Ser Glu
305

<210> 11
<211> 310
<212> PRT
<213> Bacteroides Plebuis

<400> 11

Met Glu Tyr Arg Glu Leu Gly Lys Thr Gly Leu Lys Val Pro Val Leu
1 5 10 15

Ser Tyr Gly Ala Ser Ser Leu Gly Gly Val Phe His Ser Ile Lys Glu
20 25 30

Ser Asp Ala Ile Gln Ser Val Phe Thr Ala Val Glu Arg Gly Leu Asn
35 40 45

STAN-1357W0_SeqList_ST25.txt

Phe Ile Asp Val Ser Pro Tyr Tyr Gly His Tyr Lys Ala Glu Thr Val
50 55 60

Leu Gly Lys Ala Leu Lys Glu Leu Pro Arg Glu Ser Phe Ile Leu Ser
65 70 75 80

Thr Lys Val Gly Arg Tyr Gly Lys Asp Gly Val Asn Thr Trp Asp Tyr
85 90 95

Ser Asp Lys Arg Ala Gln Glu Ser Val Tyr Glu Ser Met Glu Arg Leu
100 105 110

Asn Ile Asp Tyr Ile Asp Leu Ile Asn Val His Asp Val Glu Phe Ser
115 120 125

Asp Met Asn Gln Val Val Asn Glu Thr Leu Pro Ala Leu Val Glu Leu
130 135 140

Lys Lys Lys Gly Val Val Gly His Val Gly Ile Thr Asp Leu Gln Leu
145 150 155 160

Glu Asn Leu Lys Trp Ile Ile Asp His Ala Ala Pro Gly Thr Val Glu
165 170 175

Ala Val Leu Asn Phe Cys His Tyr Ser Leu Asn Asp Asp Lys Leu Val
180 185 190

Asp Phe Leu Asp Tyr Phe Asp Glu Asn Gly Val Gly Val Ile Asn Ala
195 200 205

Ser Pro Phe Gly Met Gly Leu Leu Thr His Arg Gly Val Pro Glu Trp
210 215 220

His Pro Ala Pro Lys Pro Leu Ile Glu Val Cys Ala Lys Ala Ala Lys
225 230 235 240

STAN-1357W0_SeqList_ST25.txt

Tyr Cys Ala Glu Gln Gly Tyr Pro Ile Glu Lys Leu Ala Val Gln Phe
245 250 255

Ser Val Ser Asn Pro Arg Ile Pro Thr Thr Leu Phe Ser Ser Ala Arg
260 265 270

Thr Glu Ser Val Leu Gln Asn Ile Lys Tyr Ile Glu Glu Pro Ile Asp
275 280 285

Trp Ser Leu Val Glu Lys Val Lys Glu Ile Ile Gly Asp Gln Gln Arg
290 295 300

Val Ser Trp Ala Asn Ser
305 310

<210> 12
<211> 127
<212> PRT
<213> Bacteroides Plebius

<400> 12

Met Lys Thr Glu Gly Tyr Lys Val Lys Ser Tyr Ser Leu Pro Val Lys
1 5 10 15

Arg Tyr Cys Gln Thr Leu Ser Leu Arg Glu Asn Pro Glu Leu Ile Glu
20 25 30

Ala Tyr Arg Lys Ala His Ser Lys Glu Glu Ala Trp Pro Glu Ile Arg
35 40 45

Ala Gly Ile Arg Glu Val Gly Ile Leu Glu Met Glu Ile Tyr Ile Leu
50 55 60

Gly Ser Lys Leu Phe Met Ile Val Glu Thr Pro Leu Asp Phe Asp Trp
65 70 75 80

Asp Thr Ala Met Ala Lys Leu Ala Thr Leu Pro Arg Gln Ala Glu Trp

STAN-1357W0_SeqList_ST25.txt

85

90

95

Glu Glu Tyr Val Ala Lys Phe Gln Gln Cys Ala Glu Gly Ala Thr Ser
100 105 110

Asp Glu Lys Trp Lys Met Met Glu Arg Met Phe Tyr Leu Tyr Glu
115 120 125

<210> 13

<211> 181

<212> PRT

<213> Bacteroides Plebuis

<400> 13

Met Ile His Ile Leu Ser Leu Asp Thr Cys Lys Tyr Lys Lys Arg Leu
1 5 10 15

Leu Ile Pro Val Phe Ile Phe Leu Ser Ala Asn Val Gln Ala Gln Leu
20 25 30

His Phe Ser Thr Thr Leu Gln Asn Met Ile Leu Trp Arg Gly Ile Glu
35 40 45

Val Ala Asp Gly Leu Ile Leu Ser Ser Asp Leu Ser Val Ser Asp Pro
50 55 60

Ser Gly Arg Phe Thr Ala Gly Phe Leu Gly Gly Ser Asn Thr Arg Gly
65 70 75 80

Ser Tyr Lys Glu Leu Ser Gln Tyr Ile Ala Tyr Thr His Gly Arg Phe
85 90 95

Gln Ile Lys Ala Ile Asp Thr Tyr Asn Phe Ser Pro Gly Ala Thr Tyr
100 105 110

Asn Asn Lys Glu Phe Phe Asn Tyr Lys Pro Asp Glu Thr Gly Arg Phe
115 120 125

STAN-1357W0_SeqList_ST25.txt

Val Asp Leu Met Val Asn Tyr Thr Gly Asp Arg Lys Phe Pro Leu Glu
130 135 140

Leu Ser Phe Ser Thr Leu Val Tyr Gly Arg Asp Arg Asp Leu Asp Asn
145 150 155 160

Ser Lys Asn Ile Tyr Ser Ser Phe Val Tyr Val Gly Tyr Thr Ile Tyr
165 170 175

Gln Asn Glu Lys Leu
180

<210> 14
<211> 523
<212> PRT
<213> Bacteroides Plebius

<400> 14

Met Lys Tyr Ser Thr Ile Ile Thr Lys Thr Ile Cys Leu Ser Val Pro
1 5 10 15

Phe Phe Ala Leu Ser Cys Glu Asp Pro Gln Glu Glu Phe Ser Tyr Ile
20 25 30

Pro Pro Glu Val Ile Tyr Ser Gln Pro Gly Asn Val Glu Asp Tyr Asn
35 40 45

Thr Pro Gly Asp Asn Ala Gly Asp Asn Asp Asp Asp Asp Val Glu Leu
50 55 60

Gln Leu Pro Val Pro Gly Pro Ala Glu Thr Tyr Pro Asn Ser Thr Lys
65 70 75 80

Gln Tyr Gln Pro Ile Ile Val Glu Tyr Ala Glu Lys Pro Asp Lys Ala
85 90 95

STAN-1357W0_SeqList_ST25.txt

Phe Ile Glu Ala Lys Thr Arg Ile Leu Pro Tyr Leu Val Gly Tyr Glu
100 105 110

Gln Gln Thr Lys Thr Gln Asp Glu Tyr Leu Gln Ser Val Asn Lys Tyr
115 120 125

Gly Ser Tyr Ala Lys Gly Gln Lys Ser Lys Ala Thr Gly Arg Phe Arg
130 135 140

Val Glu Lys Asn Ser Asn Gly Arg Ser Trp Ile Val Asp Pro Glu Gly
145 150 155 160

Tyr Pro Tyr Tyr Val Arg Gly Ile Ala Ser Phe Arg Met Asp Gly Asn
165 170 175

Ser Ser Ala Phe Gly Lys Leu Tyr Ser Ser Val Asp Asp Trp Val Ala
180 185 190

Lys Ser Gln Lys Gln Phe Ser Glu Ile Gly Phe His Ser Val Cys Ala
195 200 205

Phe Gly Lys Glu Glu Gly Asp Lys Ala Val Asn Asp Tyr Asn Lys Ser
210 215 220

Ala Ser Ser Pro Leu Thr Gln Ala Pro Ser Phe Ser Phe Leu Ala Glu
225 230 235 240

Phe Lys Asn Ser Lys Gly Ile Ser Tyr Pro Gly Gln Asn Val Asn Leu
245 250 255

Lys Ile Gly Leu Val Phe Tyr Asp Gly Trp Asp Glu Trp Cys Lys Glu
260 265 270

Tyr Leu Asn Ser Asp Ala Phe Gly Met Phe Arg Asn Asn Pro Asp Val
275 280 285

STAN-1357W0_SeqList_ST25.txt

Leu Gly Phe Phe Ser Asp Asn Glu Ile Asp Phe Ser Thr Trp Gly Asn
 290 295 300

Arg Leu Leu Asp Arg Phe Leu Lys Ile Ser Asn Lys Gln Asp Pro Ala
 305 310 315 320

Tyr Ile Ala Ala Ala Lys Phe Met Thr Asp Lys Asp Lys Ser Ala Asn
 325 330 335

Val Ser Asp Val Thr Asp Glu Leu Asn Asn Glu Phe Ala Gly Ile Cys
 340 345 350

Ala Glu Lys Tyr Tyr Ser Ala Ile Lys Asn Ala Val Lys Ala Ser Lys
 355 360 365

Asp Pro Glu Leu Leu Tyr Leu Gly Ser Arg Leu His Ser Leu Pro Lys
 370 375 380

Tyr Asn Ser Tyr Ile Ile Lys Ala Ala Gly Lys Tyr Cys Asp Val Ile
 385 390 395 400

Ser Ile Asn Tyr Tyr Ser Lys Trp Ser Pro Glu Lys Gly Tyr Met Asp
 405 410 415

Gly Trp Lys Asn Gln Ala Gly Gly Thr Pro Phe Met Val Thr Glu Phe
 420 425 430

Tyr Thr Lys Gly Glu Asp Thr Lys Leu Asp Asn Ser Ser Gly Ala Gly
 435 440 445

Phe Val Val Arg Asp Gln Gln Asn Arg Gly Phe Ala Tyr Gln His Phe
 450 455 460

Thr Leu Gly Leu Leu Glu Ala Lys Asn Cys Val Gly Trp Val Phe Phe
 465 470 475 480

STAN-1357W0_SeqList_ST25.txt

Lys Tyr Leu Asp Asp Glu Asp Cys Asn Lys Gly Met Leu Asp Tyr Asn
485 490 495

Tyr Lys Pro Tyr Thr Ser Leu Thr Lys Tyr Met Ser Asp Ile Asn Trp
500 505 510

Asn Val Tyr Asn Leu Ile Glu Tyr Phe Asp Lys
515 520

<210> 15

<211> 762

<212> PRT

<213> Bacteroides Plebuis

<400> 15

Met Leu Tyr Ile Leu Ile Ala Val Leu Pro Ser Phe Ser Phe Ala Lys
1 5 10 15

Lys Thr Asp Ala Gln Gln Val Arg Glu Met Ile Glu Gln Val Asn Asp
20 25 30

Ala Trp Gln Lys Asn His Ala Pro Glu Ala Arg Ser Phe Trp Asp Tyr
35 40 45

Ala Ala Tyr His Thr Gly Asn Met Glu Ala Tyr Phe Leu Thr Gly Lys
50 55 60

Glu Glu Tyr Arg Lys Tyr Ser Glu Ala Trp Ala Glu Tyr Asn Gln Trp
65 70 75 80

Met Gly Ala Lys Ser Asn Asn Lys Ser Glu Trp Lys Tyr Lys Tyr Gly
85 90 95

Val Lys Asp Asp Tyr Val Leu Phe Gly Asp Tyr Gln Val Cys Phe Gln
100 105 110

STAN-1357W0_SeqList_ST25.txt

Thr Tyr Ala Asp Leu Tyr Asn Ile Met Pro Glu Asn Tyr Lys Ile Lys
115 120 125

Arg Ala Arg Glu Val Met Glu Tyr Gln Met Ser Thr Pro Arg Lys Asp
130 135 140

Tyr Trp Trp Trp Ser Asp Gly Leu Tyr Met Val Met Pro Val Met Thr
145 150 155 160

Lys Met Tyr Lys Ile Thr His Asn His Arg Tyr Leu Lys Lys Leu Tyr
165 170 175

Glu Tyr Leu Cys Thr Ser Asp Ser Ile Met Tyr Asp Glu Glu Glu Gly
180 185 190

Leu Tyr Tyr Arg Asp Ala Lys Tyr Val Tyr Pro Lys His Lys Ser Leu
195 200 205

Asn Gly Lys Lys Asp Phe Trp Ala Arg Gly Asp Gly Trp Val Leu Ala
210 215 220

Ala Leu Ala Lys Val Leu Lys Asp Leu Pro Glu Gly Tyr Glu His Leu
225 230 235 240

Ser Phe Phe Glu Asp Lys Phe Val Arg Met Ala Lys Ala Val Ala Cys
245 250 255

Leu Gln Gln Pro Glu Gly Tyr Trp Thr Arg Ser Met Met Asp Pro Glu
260 265 270

His Ala Pro Gly Pro Glu Thr Ser Gly Thr Ala Phe Phe Thr Tyr Gly
275 280 285

Met Leu Trp Gly Ile Asn Asn Gly Tyr Leu Asp Lys Asp Glu Phe Met
290 295 300

STAN-1357W0_SeqList_ST25.txt

Pro Val Val Glu Lys Ala Trp Lys Tyr Leu Thr Lys Thr Ala Leu Gln
305 310 315 320

Lys Asp Trp Ser Val Gly Tyr Val Gln Pro Ile Gly Glu Lys Ala Ile
325 330 335

Pro Gly Gln Val Val Asp Ala Lys Ser Thr Ala Asn Phe Gly Val Gly
340 345 350

Ala Phe Leu Leu Ala Ala Cys Glu Tyr Val Arg Tyr Leu Glu Ala Asn
355 360 365

Asn Asn Glu Thr Arg Lys Tyr Trp Thr Asp Met Ala Tyr Arg Met Ala
370 375 380

Ala Pro Val Leu Ser Asn Met Ala Lys Gly Glu Leu Gln Lys Asn Met
385 390 395 400

Ile Leu Glu Val Ser Pro Asn Trp Asp Asn Arg Asn Lys Lys Val Ala
405 410 415

Tyr Met Glu Thr Phe Gly Arg Leu Met Ala Gly Ile Ala Pro Trp Leu
420 425 430

Ser Leu Pro Asp Asp Asp Thr Ala Glu Gly Gln Gln Arg Lys Gln Leu
435 440 445

Lys Glu Trp Ala Leu Lys Ser Tyr Ala Asn Ala Val Asp Pro Asn Ser
450 455 460

Pro Asp Tyr Leu Leu Trp Asn Gly His Gly Gln Ala Leu Val Asp Ala
465 470 475 480

Ala Tyr Ile Ala Glu Ser Phe Leu Arg Ala Phe Asp Gln Leu Trp Lys
485 490 495

STAN-1357W0_SeqList_ST25.txt

Pro Leu Asp Gln Thr Thr Lys Glu Arg Tyr Ile Lys Glu Phe Lys Gly
500 505 510

Leu Arg Arg Ile Asp Pro Pro Tyr Thr Asn Trp Leu Leu Phe Ser Ala
515 520 525

Thr Ile Glu Ser Phe Leu Ala Lys Ile Asp Ala Gly Gln Asp Thr Tyr
530 535 540

Arg Ile Asn Ser Thr Phe Arg Lys Val Glu Glu Trp Tyr Val Gly Asp
545 550 555 560

Gly Trp Tyr Ala Asp Gly Gln His Phe Ala Phe Asp Tyr Tyr Ser Ser
565 570 575

Tyr Val Phe His Pro Met Tyr Leu Glu Ser Ile His Ala Ile Met Glu
580 585 590

Ser Gly Val Arg Thr Arg Phe Asp Tyr Arg Lys Tyr Tyr Asp Arg Ala
595 600 605

Leu Met Arg Ala Gln Arg Phe Ala Met Ile Leu Glu Arg Phe Ile Ser
610 615 620

Pro Glu Gly Thr Phe Pro Val Phe Gly Arg Ser Ile Pro Tyr Arg Met
625 630 635 640

Ala Thr Ile Gln Pro Leu Ala Leu Ile Ala Trp Tyr Asn Glu Leu Pro
645 650 655

Ala Gly Val Ser Lys Ala Gln Val Arg Cys Ala Leu Thr Ala Cys Met
660 665 670

Lys Arg Met Phe Lys Ser Gly Asn Asn Phe Asn Glu Gly Gly Phe Leu
675 680 685

STAN-1357W0_SeqList_ST25.txt

Thr Ile Gly Phe Cys Gly His Gln Thr Gly Ile Ser Asn His Tyr Thr
690 695 700

Asn Asn Gly Ser Leu Tyr Met Thr Thr Leu Ala Phe Leu Pro Leu Gly
705 710 715 720

Leu Pro Ala Ser Asp Pro Phe Trp Thr Asp Ala Asp Gln Pro Trp Thr
725 730 735

Ser Val Lys Ala Trp Gly Glu Met Glu Phe Pro Ile Asp His Arg Trp
740 745 750

Gly Asp Thr Ile Arg Thr Trp Asp Leu Tyr
755 760

<210> 16
<211> 564
<212> PRT
<213> Bacteroides Plebius

<400> 16

Met Ser Ile Ala Met Leu Gln Ser Cys Thr Lys Asp Glu Leu Ser Asn
1 5 10 15

Val Asn Ala Val Ser Gly Pro Gln Asp Met Thr Phe Val Ala Gly Thr
20 25 30

Pro Ser Ser Arg Ser Ser Leu Gln Asn Gly Thr Thr Val Trp Trp Thr
35 40 45

Thr Gly Asp Ala Ile Asn Ile Phe Ser Gly Gln Glu Asn Asn Lys Phe
50 55 60

Thr Thr Ala Thr Gly Gly Ser Thr Val Thr Thr Phe Thr Gly Lys Ala
65 70 75 80

Thr Pro Asn Asn Ser Tyr Thr Ala Leu Tyr Pro Tyr Asn Ala Glu Ala

STAN-1357W0_SeqList_ST25.txt

85

90

95

Val Cys Leu Glu Gly Val Val Thr Thr Thr Leu Pro Ser Glu Gln Thr
 100 105 110

Ala Pro Ala Trp Gly Phe Asp Ala Asn Ala Asn Ile Ser Tyr Ala Thr
 115 120 125

Ala Thr Asp Asn Asn Lys Ser Leu Thr Phe Gln Asn Thr Cys Gly Leu
 130 135 140

Val Lys Phe Lys Asn Asn Leu Thr Asp Leu Thr Gly Ile Lys Leu Thr
 145 150 155 160

Ala Gly Gly Asp Val Lys Ile Ala Gly Asn Val Lys Ile Asp Ala Ser
 165 170 175

Ala Asn Leu Thr Val Glu Ser Gly Ser Asn Val Ile Thr Leu Thr Ala
 180 185 190

Lys Glu Gly Thr Phe Val Gly Pro Asn Glu Gln Asn Lys Asn Ala Lys
 195 200 205

Glu Tyr Ser Met Val Val Ala Pro Val Thr Phe Thr Asp Gly Phe Thr
 210 215 220

Leu Glu Leu Thr Arg Asn Ser Gly Thr Lys Thr Tyr Asn Phe Ser Gly
 225 230 235 240

Glu Asn Leu Ile Val Thr Lys Gly Gln Ile Val Thr Ile Val Leu Asn
 245 250 255

Asp Asp Gln Gly Gly Gly Glu Pro Pro Val Asp Leu Glu Lys Gln Thr
 260 265 270

Thr Val Ala Val Ser Ser Ala Lys Glu Ile Val Pro Asp Gln Thr Thr

STAN-1357W0_SeqList_ST25.txt

275

280

285

Gly Asn Asp Arg Ile Glu Leu Thr Leu Asp Lys Glu Val Ser Gly Thr
 290 295 300

Phe Thr Asp Ala Val Asn Lys Ala Phe Thr Ile Thr Val Ala Gly Lys
 305 310 315 320

Thr Ile Pro Val Ala Ser Gly Ser Val Asn Gly Thr Thr Met Thr Leu
 325 330 335

Ile Leu Gly Asp Lys Ile Tyr Ser Asn Asp Ala Asn Ile Ser Val Ser
 340 345 350

Tyr Asn Thr Asp Tyr Ala Val Ser Ala Leu Thr Ala Lys Asn Glu Asn
 355 360 365

Asn Glu Asp Ala Asn Ile Lys Ile Glu Ser Ala Asn Val Ala Leu Thr
 370 375 380

His Ala Asp Ala Phe Asp Phe Asn Phe Ala Asn Ile Asp Ala Val Lys
 385 390 395 400

Glu Tyr Leu Ala Glu Gly Val Ala Glu Lys Ile Asn Ala Ser Gly Glu
 405 410 415

Leu Glu Ile Val Pro Ala Asp Asn Gln Phe Pro Val Thr Lys Ser Met
 420 425 430

Ser Phe Arg Asp Gly Cys Thr Tyr Lys Phe Thr Tyr Thr Tyr Ala Ser
 435 440 445

Asn Asp Cys Ala Thr Thr Phe Arg Leu Gly Ala Ser Asp Lys Tyr Lys
 450 455 460

Phe Trp Ile Gly Arg Asn Thr Gly Ser Gly Thr Tyr Thr Asn Thr Phe

STAN-1357W0_SeqList_ST25.txt

465 470 475 480

Thr Ile Ser Ser Ser Thr Ser Ala Glu Thr Pro Ala Ser Arg Ala Asp
485 490 495

Gly Ser Leu Val Trp Pro Val Leu Glu Asn Val Ile Leu Thr Val Gln
500 505 510

Thr Asn Val Pro Gly Gly Thr Asp Ala Thr Gly Thr Ala Lys Ile Thr
515 520 525

Ser Phe Lys Ile Glu Glu Ile Thr Glu Arg Pro Ser Thr Gly Ala Asp
530 535 540

Ala Ser Phe Asp Ser Thr Thr Glu Gly Phe Asn Asn Gly Ala Glu Trp
545 550 555 560

Thr Pro Asn Lys

<210> 17

<211> 170

<212> PRT

<213> Bacteroides Plebuis

<400> 17

Met Val Asp Ile Lys Pro Arg Ile Leu Ser Val Tyr Asn Leu Phe Ile
1 5 10 15

Leu Leu Phe Ile Gln Phe Thr Ala Ile Ser Cys Asp Lys Asp Asp Asp
20 25 30

Gly Val Gly Gly Gly Asp Gly Thr Pro Ala Glu Glu Ile Lys Ile Glu
35 40 45

Tyr Val Val Phe Lys Asp Gly Gln Thr Asp Asn Lys Pro Val Ser Tyr
50 55 60

STAN-1357W0_SeqList_ST25.txt

Ile Glu Leu Pro Tyr Ser Gly Thr Val Glu Leu Gly Ile Asn Ile Thr
65 70 75 80

Lys Asp Asn Leu Pro Tyr Thr Gly Tyr Lys Ser Ile Val Trp Gly Thr
85 90 95

Ser Phe Pro Asp Val Leu Met Ile Thr Pro Ser Asp Asp Lys Met Arg
100 105 110

Cys Thr Val Val Ala Ile Asp Gly Gly Arg Asp Ser Asn Ile Gly Ala
115 120 125

Ser Val Asp Thr Gly Asn Gly Ile Lys Ser Ala Val Cys Arg Ile Ser
130 135 140

Ile Pro Pro Gly Ile Val Asp Gly Gly His Asp Asp Phe Glu Asp Asp
145 150 155 160

Gly Thr Glu Trp Lys Pro Asp Pro Lys Glu
165 170

<210> 18
<211> 156
<212> PRT
<213> Bacteroides Plebius

<400> 18

Met Met Ala Cys Gly Met Met Met Thr Ser Ala Tyr Ala Gln Glu Ile
1 5 10 15

Lys Asn Gly Asp Phe Glu Ser Gly Asp Leu Thr Ser Trp Asn Val Trp
20 25 30

Glu Lys Lys Asp Asn Lys Ile Val Asp Ala Lys Lys Ala His Ser Gly
35 40 45

STAN-1357W0_SeqList_ST25.txt

Asn Tyr Ala Val Glu Val Lys Val Gly Met Trp Gln Ala Val Asn Ile
50 55 60

Ser Tyr Glu Thr Gly Ala Glu Tyr Gln Ile Ser Ala Tyr Thr Lys Tyr
65 70 75 80

Ser Trp Gly Asp Lys Pro Asn Phe Arg Ile Glu Tyr Tyr Asn Pro Asp
85 90 95

Ser Lys Lys Leu Glu Glu Ile Ala Thr Ala Glu Val Lys Lys Asp Arg
100 105 110

Lys Asn Tyr Asn Leu Thr Thr Val Lys Phe Lys Leu Gln Glu Asn Gly
115 120 125

Phe Val Tyr Arg Phe Thr Ala Val Pro Gly Ser Gly Asn Gly Gly Cys
130 135 140

Phe Leu Leu Asp Asp Val Lys Ile Glu Lys Val Lys
145 150 155

<210> 19
<211> 321
<212> PRT
<213> Bacteroides Plebuis

<400> 19

Met Arg Lys Thr Val Leu Tyr Leu Ser Ala Ala Ser Leu Phe Leu Ser
1 5 10 15

Ser Tyr Thr Leu Lys Asn Asp Lys Glu Tyr Ser Leu Ala Glu Glu His
20 25 30

Ile Lys Asn Leu Pro Glu Ala Pro Glu Gly Tyr Lys Trp Val Val Asn
35 40 45

STAN-1357W0_SeqList_ST25.txt

Glu Asp Tyr Thr Asp Glu Phe Asn Gly Lys Arg Leu Asn Ala Ala Lys
50 55 60

Trp His Ala Lys Ser Pro Tyr Trp Thr Asn Gly Arg Pro Pro Ala Thr
65 70 75 80

Phe Lys Ala Glu Asn Val Ser Val Lys Lys Gly Cys Leu Arg Ile Ile
85 90 95

Asn Thr Val Leu Ser Pro Thr Glu Gly Leu Asp Gly Lys Pro Gly Asp
100 105 110

Lys Tyr Arg Leu Ala Gly Gly Ala Val Ala Ser Ala Lys Asn Gln Ala
115 120 125

His Tyr Gly Tyr Tyr Glu Thr Arg Met Lys Ala Ser Leu Thr Thr Met
130 135 140

Ser Ser Thr Phe Trp Leu Ser Asn Arg Pro Val Met Lys Glu Ile Met
145 150 155 160

Lys Gly Gly Lys Lys Ile Lys Thr Trp Ser Ser Gln Glu Leu Asp Ile
165 170 175

Ile Glu Thr Met Gly Ile Ile Arg Ser Val Asn Pro Asp Asn Pro Trp
180 185 190

Asn Lys Thr Trp Asn Met Gln Met Asn Ser Asn Thr His Tyr Trp Tyr
195 200 205

Gln Glu Gln Gly Gly Lys Arg Thr Asp Asn Thr Ala Lys Arg Ser Asp
210 215 220

Val Val Ser Tyr Met Thr Asp Pro Ser Ala Glu Asp Phe His Thr Tyr
225 230 235 240

STAN-1357W0_SeqList_ST25.txt

Gly Cys Trp Trp Val Asp Ala Asn Thr Val Lys Phe Tyr Tyr Asp Gly
245 250 255

Lys Tyr Met Tyr Thr Ile Lys Pro Thr Thr Lys Tyr Thr Asp Thr Pro
260 265 270

Phe Asp Arg Pro Met Phe Ile His Ile Val Thr Glu Thr Tyr Asp Trp
275 280 285

Glu Lys Gln Val Pro Thr Ala Glu Asp Leu Lys Asp Lys Asp Lys Ser
290 295 300

Thr Thr Tyr Tyr Asp Trp Val Arg Ala Tyr Lys Leu Val Pro Ile Glu
305 310 315 320

Glu

<210> 20

<211> 436

<212> PRT

<213> Bacteroides Plebius

<400> 20

Met Arg Asn Phe Ile Ser Phe Tyr Val Leu Ile Val Leu Cys Phe Thr
1 5 10 15

Ile Ile Ser Cys Lys Asp Glu Thr Glu Ile Ser Asp Phe Glu Val Ser
20 25 30

Glu Val Thr Phe Asp Thr Lys Leu Arg Asp Val Leu Thr Arg Lys Gly
35 40 45

Phe Asn Phe Ser Glu Asn Gly Glu Leu Ile Cys Asp Asn Gln Val Leu
50 55 60

Asn Thr Thr Ser Leu Asp Leu Ser Arg Cys Glu Leu Thr Ser Ile Ser

STAN-1357W0_SeqList_ST25.txt

65		70		75		80									
Gly	Leu	Arg	Ser	Phe	Pro	Ser	Leu	Ala	Asp	Val	Asn	Leu	Glu	Cys	Asn
				85					90					95	
Ser	Phe	Ser	Ile	Phe	Asp	Phe	Ala	Asp	Leu	Pro	Glu	Gly	Ile	Lys	Ser
			100					105					110		
Val	Ala	Leu	Arg	Gly	Asn	Asp	Gly	Ile	Thr	Ser	Tyr	Leu	Asn	Leu	Ile
			115				120						125		
Ser	Thr	Asp	Gly	Thr	Thr	Val	Leu	Cys	Lys	Ser	Leu	Thr	Asn	Leu	Lys
			130				135						140		
Leu	Pro	Tyr	Phe	Ala	Lys	Trp	Asn	Thr	Asp	Val	Ile	Pro	Ala	Phe	Tyr
145					150					155					160
Lys	Ala	Met	Thr	Asp	Lys	Cys	Leu	Val	Val	Met	Ser	Asp	Glu	Asp	Gly
				165					170					175	
Asn	Tyr	Thr	Glu	Tyr	Thr	Val	Asn	Arg	Arg	Val	Pro	Asp	Pro	Leu	Leu
			180					185					190		
Arg	Ser	Tyr	Leu	Tyr	Arg	Asn	Phe	Pro	Ser	Val	Phe	Val	Ser	Ser	Leu
			195				200					205			
Glu	Ile	Asp	Val	Thr	Lys	Arg	Ile	Thr	Glu	Gly	Asn	Asp	Leu	Ile	Phe
			210			215					220				
Leu	Ser	Gln	Thr	Ala	Asn	Leu	Glu	Gly	Val	Glu	Tyr	Ile	Leu	Ser	Asn
225					230					235					240
Pro	Gly	Phe	Arg	Gly	Lys	Val	Asp	Ile	Ser	Gly	Val	Lys	Ser	Lys	His
				245					250					255	
Tyr	Ser	Met	Ser	Tyr	Val	Lys	Pro	Ser	Ser	Gly	Val	Ser	Val	Phe	Ser

STAN-1357W0_SeqList_ST25.txt

260

265

270

Ile Ser Asn Ile Asp Thr Pro Leu Gly Met Asp Leu Ser Ser Ala Ser
275 280 285

Ser Leu Lys Val Leu Arg Val Glu Asn Asn Ser Ser Leu Gln Leu Val
290 295 300

Val Val Pro Ser Val Ile Leu Asn Asp Asp Val Ser Glu Thr Ser Ile
305 310 315 320

Phe Asp Ser Glu Ile His Ile Ser Gly Cys Ser Ser Leu Glu Ser Val
325 330 335

Ser Leu Gln Gly Ser Lys Gly Gly Asn Met Ile Gly Lys Leu His Phe
340 345 350

Ala Asp Leu Pro Ala Leu Asp Tyr Leu Asp Val Ser Ala Val Glu Ala
355 360 365

Val Asn Thr Val Val Leu Thr Asp Val Asn Pro Gly Ile Gly Ser Ile
370 375 380

Leu Leu Pro Ser Glu Leu Thr Ala Phe Leu Asp Gly Thr Gly Arg Phe
385 390 395 400

Ser Pro Thr Ser Gln Ile Ala Leu Cys Ile Asn His Pro Lys Val Ser
405 410 415

Ser Phe Met Glu Tyr Cys Lys Asn Val Ala Asp Ile Ile Asp Val Ser
420 425 430

Phe Phe Tyr Lys
435

<210> 21

STAN-1357W0_SeqList_ST25.txt

<211> 728

<212> PRT

<213> Bacteroides Plebuis

<400> 21

Met Ser Tyr Lys Tyr Ile Phe Leu Leu Ser Ala Phe Thr Leu Gly Val
1 5 10 15

Pro Pro Gly Ile Tyr Cys Gln Glu Arg Asn Glu Val Val Val Asp Tyr
20 25 30

Asn Thr Arg Arg Phe Leu Ser Gly Val Ser Glu Leu Asp Arg Ser Lys
35 40 45

Tyr Phe Asn Ile His Ser Thr Ser Asp Asp Asp Lys Asp Val Gly Lys
50 55 60

Phe Leu Ala Asp Tyr Gln Val Gly Leu Gly Arg Lys Phe Trp Gly Pro
65 70 75 80

Tyr Ser Tyr Ala Tyr Asn Lys Thr His Glu Val Gly Lys Tyr Pro Gln
85 90 95

Met Lys Pro Tyr Ser Gly Asn Ile Ser Val Lys Arg Tyr Ile Ala Thr
100 105 110

Glu His Pro Tyr Val Gln His Ile Gln Gly Gly Ile Asp Val Gln Ala
115 120 125

Ala Gly Ala Trp Ser Ala Glu Tyr Tyr Ser Asn Ser Glu Leu Val Pro
130 135 140

Glu Phe Phe Glu Pro Leu Asn Glu Pro Phe Val His Ala Asn Asp Ala
145 150 155 160

Gly Phe Thr Val Gln Gly Gln Ala Met Arg Glu Leu Met Val Asp Phe
165 170 175

STAN-1357W0_SeqList_ST25.txt

Tyr Ala Ser Ile Gly Lys His Ile His Asn Asn Pro Arg Leu Asn Gly
 180 185 190

Lys Met Lys Val Ile Gly Tyr Ala Ala Ala Tyr Pro Ala Trp Glu Asp
 195 200 205

Gly Asn Phe Asn Tyr Trp Asn Thr Arg Met Lys Met Phe Ile Asp Arg
 210 215 220

Ala Gly Ala Tyr Met Asp Gly Phe Ser Val His Leu Tyr Asp Gly Ile
 225 230 235 240

Asn Val Thr Gly Thr Asp Thr Lys Arg Ser Gly Ser Asn Ser Glu Ala
 245 250 255

Val Leu Asp Met Val Glu Ala Tyr Ser Tyr Ile Lys Phe Gly His Val
 260 265 270

Lys Pro Leu Ala Ile Ser Glu Phe Gly Gly Ile Asp Asn Ser Lys Pro
 275 280 285

Asp Asp Ser Tyr Asp Asp Ile Ser Ser Val Arg Ser Val Ser Ser Phe
 290 295 300

Asn His Phe Leu Phe Asn Leu Met Glu Arg Gln Asp Asn Leu Phe Ile
 305 310 315 320

Ser Ile Pro Phe Val Ser Asp Lys Ala Glu Trp His Ile Thr Ala Ala
 325 330 335

Asn Asn Tyr Thr Ser Tyr Ser Ala Ala Leu Phe Ile Pro Asp Asn Pro
 340 345 350

Gln Asn Leu Lys Asn Thr Thr Trp Arg Leu Asn Asp Lys Lys Tyr Phe
 355 360 365

STAN-1357W0_SeqList_ST25.txt

Phe Glu Leu Trp Lys Asn Val Lys Gly Glu Arg Val Asp Ile Thr Ser
370 375 380

Ser Asn Pro Asp Ile Gln Val Gln Ala Phe Lys Asp Gly Gly Arg Leu
385 390 395 400

Tyr Ile Ala Leu Asp Asn Leu Asp Asp Asn Pro Gln Thr Val Tyr Leu
405 410 415

Asn Asn Lys Asn Ser Trp Lys Asp Val Ser Asn Val Thr Lys Arg Ser
420 425 430

Leu Tyr Val Asn Tyr Asn Ala Gly Ile Glu Tyr Thr Glu Gln Asn Val
435 440 445

Pro Ser Met Pro Glu Ser Ile Ser Ile Val Pro Asn Gln Thr Ile Val
450 455 460

Leu Val Ala Asp Val Ser Ser Ser Ala Phe Thr Asn Ser Ile Ile Arg
465 470 475 480

Asn Lys Tyr Tyr Ser Ser Glu Tyr Leu Lys Pro Ile Ser Ala Gly Ser
485 490 495

Ser Leu Ser Phe Pro Phe Thr Gly Ile Glu Ser Gly Ser Gly Arg Ala
500 505 510

Ser Leu Arg Met Ser Ile Gly Arg Pro Val Ser Ala Ser Lys Lys Pro
515 520 525

Val Val Lys Ile Asn Gly Thr Ala Val Ser Val Pro Asp Asn Trp Lys
530 535 540

Gly Tyr Gly Gln Ser Asn Arg Asn Ile Phe Phe Gly Met Ile Glu Val
545 550 555 560

STAN-1357W0_SeqList_ST25.txt

Pro Phe Asp Ile Gln Leu Leu Lys Asn Gly Asp Asn Asn Val Asp Ile
565 570 575

Thr Phe Ser Asp Gly Gly Gly His Val Ser Ser Met Ile Leu Gln Val
580 585 590

Glu Lys Tyr Thr Val Ser Thr Leu Gln Asn Gly Thr Phe Ser Glu Gly
595 600 605

Leu Ser Ala Trp Gln Pro Leu Gly Asn Tyr Gly Thr Val Cys Val Gln
610 615 620

Thr Asp Asn Ala Gly Asn Asn Val Ala Cys Ile Ser Gly His Ala Gly
625 630 635 640

Leu Met Gln Arg Val Asp Met Glu Ser Gly Arg Thr Tyr Arg Phe Ser
645 650 655

Ala Asp Val Lys Thr Glu Gly Ala Cys Lys Leu Lys Val Met Leu Gln
660 665 670

Asp Met Ser Thr Gly Thr Val Tyr Thr Glu Glu Phe Ser Ser Pro Gly
675 680 685

Asn Tyr Lys Ala Val Ser Phe Asp Phe Asn Ser Thr Val Lys Lys Val
690 695 700

Val Cys Ala Ile Val Cys Glu Arg Gln Asn Asp Ala Ala Trp Ile Asp
705 710 715 720

Asn Ile Val Leu Leu Pro Gln Asn
725

<210> 22
<211> 595

STAN-1357W0_SeqList_ST25.txt

<212> PRT

<213> Bacteroides Plebuis

<400> 22

Met Ser Phe Ser Val Phe Pro Leu Ser Ser Ser Glu Asn Lys Thr Tyr
1 5 10 15

Asn Thr Thr Val Thr Val Asp Tyr Ala Thr Gln Arg Tyr Leu Asn Asp
20 25 30

Val Ser Ala Leu Asp Arg Gly Lys Tyr Phe Asn Ile His Thr Ser Lys
35 40 45

Asp Ser Asp Pro Asp Val Arg Lys Phe Leu Ala Asp Tyr Gly Val Gly
50 55 60

Ile Gly Arg Ser Phe Trp Gly Pro Phe Ser Tyr Ser Tyr Gly Lys Thr
65 70 75 80

Lys Lys Val Gly Glu Tyr Pro Phe Ser Glu Lys Pro Leu Asn Tyr Thr
85 90 95

Asp Leu Lys Glu Thr Lys Arg Tyr Val Ala Thr Glu His Ala Asn Ala
100 105 110

Arg Thr Ile Gln Trp Gly Ile Asp Pro Val Lys Ala Gly Ala Trp Ala
115 120 125

Ala Glu Tyr Tyr Ser Lys His Val Lys Gly Ala Val Pro Glu Phe Phe
130 135 140

Glu Pro Ile Asn Glu Pro Phe Val His Ala Arg Asp Lys Cys Phe Asn
145 150 155 160

Met His Gly Gln Glu Met Arg Met Leu Met Ala Asp Phe Tyr Ala Gln
165 170 175

STAN-1357W0_SeqList_ST25.txt

Thr Gly Lys His Ile His Ala Glu Pro Ser Leu Lys Lys Met Lys Ile
180 185 190

Ile Gly Tyr Ala Ala Ala Tyr Pro Ala Met Glu Leu Arg Asp Phe Asp
195 200 205

His Trp Asn Asn Thr Met Lys Met Phe Ile Asp Arg Ala Gly Glu Tyr
210 215 220

Met Asp Gly Leu Ser Val His Leu Tyr Asp Gly Ile Asn Ile Val Gly
225 230 235 240

Lys Ser Ser Arg Arg Ser Gly Ser Asn Ser Glu Ala Ile Leu Asp Leu
245 250 255

Met Glu Asn Tyr Ser Phe Ile Arg Leu Gly Lys Val Leu Pro Leu Ala
260 265 270

Val Thr Glu Tyr Gly Gly Ile Asp Asn Thr Ser Lys Gly Tyr Asn Pro
275 280 285

Ile Ala Ser Val Arg Thr Val Ala Ser Phe Asn His Ile Leu Phe Asn
290 295 300

Leu Leu Glu Arg Glu Asp Lys Met Leu Ile Ser Ile Pro Phe Val Ser
305 310 315 320

Asp Lys Ala Glu Trp His Ile Thr Lys Gln Tyr Asn Phe Glu Pro Tyr
325 330 335

Gly Ala Ala Leu Phe Val Ala Asn Asn Pro His Asp Leu Lys Asn Thr
340 345 350

Ala Trp Lys Leu Asn Asp Lys Lys Tyr Phe Phe Lys Leu Trp Lys Asp
355 360 365

STAN-1357W0_SeqList_ST25.txt

Val Lys Gly Glu Arg Val Asp Ile Val Ser Asp Asn Pro Asp Ile Gln
370 375 380

Val Ala Ala Phe Lys Asp Asp Asp Arg Leu Tyr Ile Ala Val Asp Asn
385 390 395 400

Leu Asp Asp Tyr Thr His Lys Val Asn Leu Lys Asn Val Leu Asn Trp
405 410 415

Lys Gly Val Asp Asn Val Ser Val Arg Ser Leu Lys Met Ile Phe Asp
420 425 430

Lys Gly Ile Val Tyr Asp Glu Lys Thr Leu Asn Ser Met Pro Gln Ser
435 440 445

Ile Asp Ile Ile Lys Asp Glu Thr Ile Ile Leu Cys Ala Asp Ile Ile
450 455 460

Arg Lys Lys Tyr Ser Asn Arg Ile Val Arg Thr Lys Tyr Tyr Ser Asn
465 470 475 480

Thr Tyr Leu Gln Pro Val Glu Ala Gly Lys Pro Ile Val Phe Asp Phe
485 490 495

Asp Gly Leu Lys Pro Gly Thr Gly Arg Ala Val Leu Arg Met Ser Ile
500 505 510

Gly Arg Lys His Glu Met Ser Lys Lys Pro Glu Ile Met Val Asn Gly
515 520 525

Lys Lys Val Asp Met Pro Asp Asn Trp Arg Gly Tyr Asp Gln Thr Gly
530 535 540

Arg Asp Asp Phe Phe Gly Met Ile Glu Ile Pro Phe Asp Tyr Arg Leu
545 550 555 560

STAN-1357W0_SeqList_ST25.txt

Ile Arg Lys Gly Lys Asn Ser Val Ser Val Thr Phe Pro Asp Asn Gly
565 570 575

Gly Arg Val Ala Thr Met Ile Leu Gln Thr Glu Arg Tyr Asp Lys Lys
580 585 590

Val Arg Lys
595

<210> 23
<211> 166
<212> PRT
<213> Bacteroides Plebuis

<400> 23

Met Phe Gly Ala Cys Asp Asn Asp Lys Trp Ala Glu Val Glu Leu Asp
1 5 10 15

Ser Thr Pro Val Tyr Glu Leu Thr Tyr Leu Lys Asn Val Glu Thr Gly
20 25 30

Lys Thr Gly Glu Val Ser Lys Phe Ser Val Tyr Arg Glu Leu Phe Asp
35 40 45

Leu Ile Ala Trp Lys Asn Asp Tyr Gln Thr Leu Arg Met Asn Lys Ile
50 55 60

Glu Phe Phe Ala Glu Ser Ser Glu Ala Pro Ser Glu Leu Pro Glu Trp
65 70 75 80

Leu Lys Ile Asn Ser Asp Thr Glu Lys His Leu Ser Phe Ser Phe Asn
85 90 95

Glu Val Tyr Thr Glu Lys Glu Glu Val Ile Asn Pro Glu Thr Gly Asp
100 105 110

STAN-1357W0_SeqList_ST25.txt

Lys Glu Glu Gln Glu Val Thr Lys Lys Arg Met Phe Met Phe Glu Gly
115 120 125

Lys Lys Glu Asn Asn Ser Ser Gly Gly Tyr Gly His Leu Thr Val Thr
130 135 140

Glu Asn Asp Gly Thr Glu Val Glu Tyr Glu Val Val Leu Asn Asp Val
145 150 155 160

Leu Lys Pro Ala Asp Phe
165

<210> 24
<211> 574
<212> PRT
<213> Bacteroides Plebuis

<400> 24

Met Lys Asn Arg Phe Leu Tyr Ile Ala Leu Ser Leu Ile Ser Val Leu
1 5 10 15

Thr Ser Cys Lys Asp Asp Glu Phe Glu Pro Leu Asn Asn Val Ala Glu
20 25 30

Cys Thr Trp His Val Ser Thr Asp Gln Glu Asn Val Ser Pro Ile Gln
35 40 45

Leu Asn Leu Asn Asn Tyr Ile Ser Ile Met Asp Leu Ser Gln Gly Met
50 55 60

Leu Ser His Gln Trp Val Val Ser Asp Asp Gly Thr Lys Phe Leu Asn
65 70 75 80

Gly Lys Met Glu Trp Gly Gln Thr Asp Tyr Thr Asn Leu Ile Asp Glu
85 90 95

Ser Ile Pro His Thr Asn Asp Leu Lys Thr Ile His Val Tyr Phe Thr

STAN-1357W0_SeqList_ST25.txt

100

105

110

Lys Pro Gly Asp His Thr Val Arg Leu Cys Asn Thr Phe Arg Arg Gln
 115 120 125

Val Val Tyr Pro Tyr Ser Val Tyr Asp Asp Asn Thr Gly Gly Tyr Ile
 130 135 140

Lys Lys Tyr Cys Tyr Ala Lys Gln Glu Gly Asp Val Tyr Val Met Asp
 145 150 155 160

Thr Thr Phe His Ile Arg Val Tyr Asp Pro Asn Leu Val Pro Ala Val
 165 170 175

Lys Val Tyr Ser Asp Pro Glu Cys Thr Gln Glu Ile Lys Thr Gly Ile
 180 185 190

Val Gly Gly Thr Glu Glu Ala Pro Glu Tyr Glu Lys Tyr Glu Leu Glu
 195 200 205

Tyr Gly Lys Ser Val Tyr Ile Lys Asp Asp Ser Tyr Gly Leu Pro Asn
 210 215 220

Lys Trp Thr Phe Lys Cys Ala Asp Thr Gly Val Asn Asp Glu Leu Thr
 225 230 235 240

Ser Phe Asp Thr Pro Tyr Gln Phe Thr Ala Lys Lys Phe Ser Asp Lys
 245 250 255

Pro Leu Leu Leu Ser Met Thr Ile Glu Arg Thr Ser Ala Ser Glu Gly
 260 265 270

Lys Gly Lys Tyr Thr Pro Lys Ala Ser Pro Lys Thr Leu Val Val Pro
 275 280 285

Leu Ala Ile Thr Val Val Pro Ser Asp Asp Pro Ile Thr Tyr Asn Ile

STAN-1357W0_SeqList_ST25.txt

290

295

300

Arg Gln Ile Asp Gln Thr His Ile Ala Ile Asp Leu Asp Asn Ser Glu
305 310 315 320

Phe Gly Tyr Lys Glu Ile Asn Pro Ser Ser Leu Lys Leu Thr Tyr Ser
325 330 335

Asn Ser Tyr Asn Arg Pro Ser Ala Val Arg Gly Ser Val Asn Ile Thr
340 345 350

Ala Ala Glu Val Asn Lys Gln Ser Arg Tyr Glu Leu Ile Leu Thr Leu
355 360 365

Val Glu Lys Ile Tyr Asn Thr Asp Glu Leu Thr Leu Thr Gly Thr Leu
370 375 380

Thr Glu Ala Leu Val Gly Tyr Gln Asn Leu Glu Ile Lys Ala Thr Ala
385 390 395 400

Pro Asn Val Ala Thr Thr Phe Gly Ala Phe Leu Asp Glu Asp Phe Glu
405 410 415

Asn Ser Asp Thr Tyr Ala Asp Trp Lys Val Ile Asp Ala Asp Thr Lys
420 425 430

Thr His Pro Val Val Pro Ser Gln Val Val Asp Asn Pro Leu Lys Asp
435 440 445

Gly Ile Asn Asn Ser Ala Lys Cys Met Phe Val Glu Ala Phe Asp Arg
450 455 460

Cys Arg Ala Leu Leu Ser Lys Thr Phe Thr Gly Gly Lys Gly Thr Tyr
465 470 475 480

Thr Phe Ser Tyr Lys Tyr Tyr Thr Pro Gly Tyr Lys Gln Gly Lys Gly

STAN-1357W0_SeqList_ST25.txt

485

490

495

Met Ser Pro Tyr Phe Val Pro Ala Gly Lys Glu Gly Ala Glu Asp Met
500 505 510

Thr Trp Gln Ser Asp Arg Pro Trp Cys Gly Ile Val Asn Gly Ser Asp
515 520 525

Ser Lys Trp Met Ser Ala Thr Thr Thr Val Thr Ser Lys Ala Glu Met
530 535 540

Asp Asn Ile Leu Leu Ser Met Arg Phe Asn Ala Phe Lys Asp Asn Ile
545 550 555 560

Tyr Phe Asp Asp Ile Phe Phe Gly Tyr Ile Glu Val Arg Pro
565 570

<210> 25
<211> 678
<212> PRT
<213> Bacteroides Plebuis

<400> 25

Met Asn Phe Arg Tyr Lys Thr Ile Val Phe Ser Leu Leu Met Ser Gly
1 5 10 15

Met Thr Leu Val Ser Cys Asp Asp Phe Leu Thr Gln Glu Asn Ile His
20 25 30

Gln Leu Thr Thr Gln Asn Phe Tyr Lys Thr Ile Gly Asp Cys Glu Lys
35 40 45

Gly Leu Ala Ala Val Tyr Asn Ala Leu Lys Asn Thr Asn Ile Tyr His
50 55 60

Pro Leu Asp Glu Asn Arg Arg Ser Asp Ile Ala Val Glu Gly Asn Lys
65 70 75 80

STAN-1357W0_SeqList_ST25.txt

Asp Arg Lys Gln Phe Asp Asn Glu Ala Tyr Lys Gln Thr Phe Asn Asp
85 90 95

Ser Tyr Gly Thr Val Arg Gly Lys Trp Ser Ala Leu Tyr Thr Gly Val
100 105 110

Phe Arg Ala Asn Gln Val Leu Ala Ser Ile Glu Lys Ile Arg Pro Asn
115 120 125

Val Thr Asp Glu Pro Gln Ile Thr Lys Leu Ala Gln Ile Glu Ala Gln
130 135 140

Ala Tyr Ser Leu Arg Gly Leu Phe Tyr Phe Tyr Leu Asn Asn Ser Phe
145 150 155 160

Asn Asn Gly Asn Val Pro Tyr Ile Asn Glu Ile Ala Glu Val Glu Glu
165 170 175

Asp Tyr Tyr Lys Lys Val Thr Pro Ser Asp Glu Ile Lys Lys Tyr Tyr
180 185 190

Arg Glu Asp Leu Gln Lys Ala Leu Asp Leu Gly Leu Asn Asp Lys Trp
195 200 205

Glu Lys Thr Asp Leu Gly Arg Ile Thr Ser Trp Ala Val Lys Ala Ile
210 215 220

Leu Gly Lys Ser Tyr Leu Tyr Asp Lys Glu Tyr Asn Lys Ala Ala Glu
225 230 235 240

Tyr Phe Lys Asp Ile Ile Asp Asn Gly Gly Phe Ala Leu Val Asp Asp
245 250 255

Ile Val Asp Asn Phe Thr Ala Ala Asn Glu Phe Asn Ser Glu Ser Ile
260 265 270

STAN-1357W0_SeqList_ST25.txt

Leu Glu Val Ser Tyr Ser Thr Gln Tyr Asn Thr Glu Phe Gly Thr Trp
275 280 285

Ser Glu Ser Thr Leu Tyr Asn Ile Trp Gly Met Asn Val Asn Gly Leu
290 295 300

Gly Asp Ala Trp Leu Asn Thr Val Pro Ala Phe Trp Leu Val Glu Ala
305 310 315 320

Phe Glu Thr Glu Pro Val Asp Arg Leu Asp Glu Arg Asn Trp Ile Lys
325 330 335

Met Gln Ser Asp Asn Tyr Gly Asp Pro Glu His Arg Asp Ile Ile Tyr
340 345 350

Asp Gln Leu Gly Thr Thr Phe Ser Ser Gln Val Asp Arg Gln Gly Val
355 360 365

Val Tyr Asn Arg Thr Tyr Val Tyr Thr Trp Asp Ala Thr Ala Gly Lys
370 375 380

Tyr Val Gly Val Arg Glu Arg Leu Val Ser Thr Val Gly Asp Asn Lys
385 390 395 400

Val Leu Tyr Asn Lys Ile Thr Gly Tyr Asp Asp Ile Val Pro Glu Phe
405 410 415

Lys Trp Glu Asp Gly Gln Ala Tyr Arg Leu Arg Ser Tyr Ser Met Arg
420 425 430

Ala Ser Ala Ser Leu Ala Ile Asn Gly Asp Glu Ser Leu Ile Tyr Tyr
435 440 445

Gln Ser Leu Pro Gln Gln Val Ser Lys Phe Asn Arg Gly Ser Ser Ala
450 455 460

STAN-1357W0_SeqList_ST25.txt

Tyr Phe Arg Lys Leu Ser Asn Trp Asp Thr Arg Lys Ser Glu Thr Glu
465 470 475 480

Phe Lys Pro Ala Met Ala Ser Gly Ile Asn Tyr Arg Leu Ile Arg Leu
485 490 495

Ala Asp Ile Tyr Leu Met Tyr Ala Glu Cys Leu Ile Lys Gly Gly Ala
500 505 510

Ser Asp Gly Asn Val Gln Ser Ala Ile Asn Ala Ile Asn Lys Val Arg
515 520 525

His Arg Ala Gly Val Val Leu Ile Gly Lys Ser Glu Gln Gly Glu Phe
530 535 540

Lys Arg Tyr Thr Tyr Asp Glu Lys Glu Tyr Ala Ala Ser Asp Val Met
545 550 555 560

Asn His Leu Met Tyr Val Glu Arg Pro Leu Glu Leu Cys Met Glu Gly
565 570 575

His Ala Ile Arg Val Ile Asp Leu Arg Arg Trp Asn Ile Thr Lys Glu
580 585 590

Arg Phe Asp Gln Leu Ala Ser Asp Glu Tyr Lys Tyr Cys Met Ile Gln
595 600 605

Thr Lys Tyr Leu Lys Pro Asn Pro Asp Asp Pro Asn Ala Leu Val Ser
610 615 620

Ala Phe Asn Phe Gly Lys Gln Tyr Arg Phe Tyr Glu Leu Pro Pro Glu
625 630 635 640

Lys Arg Gly Asn Ala Phe Val Asp Tyr Phe Gln Ala Ser Leu Asn Tyr
645 650 655

STAN-1357W0_SeqList_ST25.txt

Gly Pro Gln Val Ala Tyr Trp Pro Ile Pro Asn Ile Glu Ile Thr Ser
660 665 670

Asn Pro Asp Ile Asn Lys
675

<210> 26
<211> 1032
<212> PRT
<213> Bacteroides Plebius

<400> 26

Met Arg Asn Gln Lys Lys Trp Tyr His Gly Arg Tyr Met Leu Phe Val
1 5 10 15

Met Leu Ile Phe Tyr Thr Leu Ser Met Tyr Ser Gln Lys Ile Thr Val
20 25 30

Lys Gly Lys Val Ile Asp Ala Ala Asn Asn Leu Glu Val Ile Gly Ala
35 40 45

Ala Val Gln Val Glu Gly Thr Ser Leu Gly Thr Ile Thr Asp Met Asp
50 55 60

Gly Asn Phe Val Leu Gln Gly Val Pro Thr Lys Gly Asn Leu Val Phe
65 70 75 80

Ser Phe Val Gly Tyr Lys Thr Val Lys Ala Ala Ile Lys Asn Gly Gln
85 90 95

Ile Tyr Asn Ile Lys Leu Gln Glu Asp Thr Lys Val Leu Asp Glu Val
100 105 110

Val Val Val Gly Tyr Gly Ser Met Arg Lys Lys Glu Val Thr Gly Ala
115 120 125

STAN-1357W0_SeqList_ST25.txt

Val Ala Arg Val Asn Ser Asp Glu Ile Thr Lys Ile Ser Thr Ser Asp
130 135 140

Leu Gly Thr Ala Leu Gln Gly Met Val Ala Gly Val Asn Val Gln Ala
145 150 155 160

Ser Ser Gly Glu Pro Gly Ala Lys Ser Asn Ile Gln Ile Arg Gly Leu
165 170 175

Ser Ser Ile Ser Gly Asp Ser Ser Pro Leu Tyr Val Val Asp Gly Val
180 185 190

Pro Phe Glu Gly Asp Pro Gly Leu Ser Ser Ser Glu Ile Ala Ser Ile
195 200 205

Asp Ile Leu Lys Asp Ala Ala Ser Ala Ala Ile Tyr Gly Thr Arg Gly
210 215 220

Ala Ser Gly Val Ile Leu Ile Thr Thr Lys Lys Gly Lys Glu Gly Glu
225 230 235 240

Met Lys Ile Ala Val Asp Gly Tyr Tyr Gly Val Gln His Ile Thr Ser
245 250 255

Asn Ile His Leu Leu Asp Ala Asn Glu Ser Ile Phe Val Lys Val Met
260 265 270

Ser Asn Arg Met Met Glu Gly Asn Gln Asn Thr Asp Asp Leu Ala Trp
275 280 285

Ser Asn Leu Lys Thr Tyr Pro Val Asn Phe Phe Asn Asn Ser Ser Leu
290 295 300

Tyr Glu Tyr Val Val Asn Asn Asn Ala Pro Ile Gln Asn Tyr Ser Val
305 310 315 320

STAN-1357W0_SeqList_ST25.txt

Thr Ala Asn Gly Gly Lys Lys Asp Leu Thr Tyr Asn Leu Thr Ala Asn
325 330 335

Tyr Phe Asp Gln Lys Gly Val Leu Ile Asn Ser Asp Tyr Lys Arg Tyr
340 345 350

Asn Ile Arg Ser Asn Thr His Phe Gln Arg Gly Lys Trp Thr Ile Asn
355 360 365

Thr Asn Ile Ala Met Lys Ile Glu Asn Gln Leu Ser Pro Ala Trp Gly
370 375 380

Leu Leu Asn Glu Cys Tyr Asp Tyr Ser Pro Thr Arg Ser Gln Ile Tyr
385 390 395 400

Pro Gln Ala Ser Ile Val Asn Ala Ala Gly Asp Pro Ala Asp Leu Gln
405 410 415

Gly Val Ser Tyr Thr Leu Gly Arg Leu Lys Glu Glu Asn His Lys Asp
420 425 430

Thr Glu Ser Phe Asn Gly Asn Phe Tyr Leu Ala Tyr Asn Val Ile Pro
435 440 445

Gly Leu Asn Val Ser Thr Arg Leu Gly Phe Gly Tyr Asn Asn Gln Lys
450 455 460

Ala Val Ser Ile Arg Pro Glu Phe Glu Val Tyr Asn Gln Lys Gly Glu
465 470 475 480

Lys Val Thr Ser Ser Asn Tyr Arg Ser Gln Leu Lys Asp Thr His Ser
485 490 495

Lys Asn Thr Ser Leu Thr Trp Glu Thr Met Val Asn Tyr Asn Lys Lys
500 505 510

STAN-1357W0_SeqList_ST25.txt

Ile Lys Lys His Asp Ile Lys Phe Thr Gly Val Phe Ser Met Glu Lys
515 520 525

Tyr Thr Tyr Glu Met Phe Tyr Ala Ser Ile Met Asp Leu Val Thr Asn
530 535 540

Glu Ile Pro Asn Leu Asn Ala Gly Thr Ser Asp Met Thr Val Gly Thr
545 550 555 560

Gly Ser Gly Gln Trp Gly Gln Asp Arg Ile Ser Thr Met Val Gly Met
565 570 575

Leu Gly Arg Leu Gln Tyr Ser Tyr Ala Asp Lys Tyr Met Ala Ser Ala
580 585 590

Ser Ile Arg Arg Asp Gly Ser Ser Lys Phe Ser Glu Glu Asn Arg Trp
595 600 605

Gly Leu Phe Pro Ser Leu Ser Val Gly Trp Asn Ile Ser Glu Glu Ser
610 615 620

Phe Phe Asp Arg Phe Arg Trp Leu Val Asn Ser Leu Lys Leu Arg Phe
625 630 635 640

Ser Tyr Gly Thr Thr Gly Asn Gln Asn Phe Pro Asp Tyr Ser Tyr Ala
645 650 655

Pro Ala Ile Tyr Lys Asn Tyr Asp Tyr Thr Phe Gly Thr Gly Thr Ser
660 665 670

Glu Ile Leu Ala Asn Gly Phe Thr Gln Leu Gly Phe Ala Asn Pro Asn
675 680 685

Val Lys Trp Glu Thr Thr Gln Gln Leu Asn Ala Gly Ile Asp Met Ala
690 695 700

STAN-1357W0_SeqList_ST25.txt

Leu Tyr Asn Asn Lys Leu Ile Leu Gly Leu Asp Leu Tyr Lys Ser Asn
705 710 715 720

Lys Lys Asn Met Leu Phe Pro Met Val Val Pro Pro Ser Asn Gly Gly
725 730 735

Gly Gln Ser Ser Thr Val Thr Leu Asn Ala Gly Asp Met Glu Asn Arg
740 745 750

Gly Val Glu Phe Ser Leu Thr His Arg Asn Lys Ile Arg Gly Val Asn
755 760 765

Tyr Ser Leu Thr Gly Thr Phe Thr Lys Asn Val Asn Glu Ile Val Ser
770 775 780

Met Ala Gly Lys Asn Glu Leu Tyr Phe Phe Pro Asp Gly Lys Pro Val
785 790 795 800

Ser Ser Gly Ser Asp Tyr Val Thr Ala Ile Lys Lys Gly Tyr Glu Ala
805 810 815

Gly Ala Phe Phe Val Met Pro Thr Ala Gly Val Ile Asn Thr Glu Gln
820 825 830

Lys Leu Ala Glu Tyr Gln Lys Leu Gln Ser Ser Ala Arg Met Gly Asp
835 840 845

Leu Met Tyr Ile Asp Thr Asn Asn Asp Gly Val Leu Asn Asp Asp Asp
850 855 860

Arg Val Tyr Ala Gly Ser Gly Met Pro Asp Tyr Glu Leu Gly Leu Asn
865 870 875 880

Phe Ser Ala Asp Tyr Arg Gly Phe Asp Phe Ser Met Asn Trp Tyr Ala
885 890 895

STAN-1357W0_SeqList_ST25.txt

Ser Val Gly Asn Glu Ile Ile Asn Gly Thr Lys Ile Tyr Thr Tyr Gln
 900 905 910

Arg Arg Thr Asn Lys Glu Leu Ile Tyr Met Trp Thr Pro Thr Asn Tyr
 915 920 925

Thr Ser Thr Ile Pro Ser Tyr Arg Thr Glu Gly His Asn Asn Tyr Arg
 930 935 940

Ala His Thr Asp Met Trp Ile Glu Asp Gly Ser Phe Val Arg Leu Lys
 945 950 955 960

Asn Ile Met Leu Gly Tyr Ser Phe Pro Lys Ser Trp Val Ser Lys Leu
 965 970 975

Gly Leu Gly Lys Phe Arg Leu Tyr Val Ala Ala Asp Asn Leu Leu Thr
 980 985 990

Leu Thr Lys Tyr Asp Gly Tyr Asp Pro Glu Val Gly Ser Asn Gly Leu
 995 1000 1005

Ser Arg Arg Gly Leu Asp Tyr Gly Thr Tyr Pro Ile Ser Ile Gln
 1010 1015 1020

Met Arg Gly Gly Phe Gln Ile Asn Phe
 1025 1030

<210> 27
 <211> 1271
 <212> PRT
 <213> Bacteroides Plebius

<400> 27

Met Ala Thr Asn Asp Gly Leu Asn Arg Phe Asp Gly Tyr Glu Phe Lys
 1 5 10 15

STAN-1357W0_SeqList_ST25.txt

Val	Tyr	Gly	Tyr	Gln	Ser	Asn	Gly	Leu	Asn	Ser	Asn	Leu	Ile	Val	Cys
		20						25					30		
Ile	Asp	Glu	Asp	Ser	His	Gly	Asn	Leu	Trp	Ile	Gly	Thr	Ala	Asp	Arg
		35					40					45			
Gly	Val	Phe	Leu	Phe	Asn	Ser	Val	Lys	Asn	Glu	Phe	Val	Ser	Leu	Asn
	50					55					60				
Leu	Gly	His	Ser	Gly	Ile	Asp	Lys	Asn	Phe	Thr	Cys	Asp	Lys	Ile	Leu
65					70					75					80
Val	Asp	Ser	Lys	Asp	Arg	Val	Trp	Phe	His	Ser	Ser	Asp	Glu	Ser	Ile
				85					90					95	
Tyr	Leu	Val	Asn	Tyr	Asp	Phe	Gln	Asn	Gly	Lys	Ile	Asn	Thr	Val	Leu
			100					105					110		
Arg	Ser	Thr	Leu	Lys	Leu	Pro	Tyr	Ile	Ser	Asp	Ile	Ile	Glu	Ile	Asp
		115					120				125				
Asn	Thr	Ile	Met	Leu	Ser	Ser	Glu	Asp	Gly	Leu	Tyr	Glu	Cys	Asn	Val
	130					135					140				
Asp	Gly	Asp	Glu	Leu	Leu	Leu	Asn	Lys	Leu	Leu	Gly	Cys	Pro	Ile	Ala
145					150					155					160
Ser	Ala	Ile	Val	Ile	Ser	Ser	Ser	Gln	Ile	Leu	Tyr	Ser	Asn	Leu	Glu
				165					170					175	
Asn	His	Gln	Leu	Cys	Leu	Tyr	Asp	Lys	His	Thr	Cys	Lys	Val	Ser	Thr
			180					185					190		
Leu	Leu	Glu	Asn	Cys	Asp	Ile	Arg	Lys	Met	Val	Tyr	Lys	Asn	Lys	Arg
		195					200					205			

STAN-1357W0_SeqList_ST25.txt

Leu Phe Tyr Ala Thr Thr Ser Thr Val Asn Val Leu Thr Phe Asp Val
210 215 220

Leu His Ala Ile Glu Ser Lys Pro Gln Val Ile Ala Thr Tyr Ser Tyr
225 230 235 240

Ser Tyr Pro Gln Thr Val Val Leu Asp Lys Asn Asp Ile Leu Trp Ile
245 250 255

Gly Phe Phe Lys Ser Gly Phe Met Ser Ile Arg Glu Asn Asn Lys Pro
260 265 270

Ile Asp Leu Phe Arg Gly Ile Gly Asn Asp His Ile Ser Ser Val Tyr
275 280 285

Thr Phe Ala Lys Ser Asp Ile Tyr Leu Gly Thr Glu Gly Ser Gly Leu
290 295 300

Tyr His Phe Asn Ser Ile Thr Gly Asn Ala Arg Leu Ile Pro Phe Thr
305 310 315 320

Ala Asn Arg Ile Val Tyr Ser Thr Ala Tyr Ser Asn Tyr Thr Asp Cys
325 330 335

Met Tyr Val Ser Leu Met Tyr Asp Gly Ile Tyr Ser Phe Thr Ser Asp
340 345 350

Asn Asp Tyr Lys Lys Ile Ser Gly Leu Arg Asn Val Arg Ala Met Leu
355 360 365

Ala Asp Gly Lys Tyr Leu Trp Ile Gly Thr Tyr Asn Lys Gly Leu Phe
370 375 380

Arg Tyr Asp Leu Ser Thr Gly Val Met Lys Glu Ile Lys Thr Ser Asp
385 390 395 400

STAN-1357W0_SeqList_ST25.txt

Asn Lys Glu Leu Lys Ile Val Arg Asn Ile Ile Lys Asp His Lys Gly
405 410 415

Asn Ile Trp Val Ala Ser Ser Phe Gly Leu Lys Val Leu Glu Ser Ala
420 425 430

Asp Leu Tyr Ile Asp Asn Pro Val Leu Asn Ser Val Lys Gly Leu Asp
435 440 445

Glu Leu Asp Tyr Ile Val Pro Val Cys Glu Asp Leu Asn His Asn Ile
450 455 460

Trp Tyr Gly Thr Leu Gly Arg Gly Leu Arg Lys Ile Val Asp Leu Asp
465 470 475 480

Glu Asn His Asn Ala Cys Val Glu Asn Phe Ser Ser Ala Asp Gly Leu
485 490 495

Ser Ser Asn Thr Ile Lys Ser Ile Val Asn Gly Thr Asp Gly Thr Leu
500 505 510

Trp Ile Ser Thr Asn Lys Gly Ile Asn Ser Leu Asn Ile Asn Thr Gln
515 520 525

Arg Ile Arg Ser Tyr Asp Ile Phe Asp Gly Leu Gln Asp Tyr Glu Phe
530 535 540

Met Glu Leu Ser Ala Gly Val Met Thr Asp Gly Thr Met Ile Phe Gly
545 550 555 560

Gly Val Asn Gly Ile Asn Val Phe Arg Pro Asn Asp Phe Asp Val Ile
565 570 575

Asp Phe Asn Gly Ser Pro Thr Leu Val Asp Phe Lys Ile Phe Asn His
580 585 590

STAN-1357W0_SeqList_ST25.txt

Ser Val Glu Ala Asp Ser Thr Tyr Ser Ala Tyr Phe Asp Lys Ser Val
595 600 605

Ser Phe Thr Glu His Ile Glu Leu Pro Tyr Asn Leu Asn Thr Phe Ser
610 615 620

Phe Gln Phe Ser Ser Leu Asp Tyr Arg Ser Pro Tyr Lys Val Gly Tyr
625 630 635 640

Glu Tyr Met Leu Glu Gly Val Asp Asp Ser Trp Ile Ser Thr Ser Ala
645 650 655

Phe His Arg Glu Ala Phe Tyr Thr Lys Leu Pro Ser Gly Glu Tyr Met
660 665 670

Phe Arg Leu Arg Val Arg Asn Ser Asp Gly Val Tyr Ser Leu Asn Glu
675 680 685

Leu Ser Ile Pro Val Ile Ile Asn Pro Pro Phe Trp Arg Thr Trp Tyr
690 695 700

Ala Tyr Thr Leu Tyr Phe Ile Leu Leu Val Leu Ser Leu Tyr Arg Phe
705 710 715 720

Lys Val Tyr Tyr Thr Ser Arg Val Gln Arg Arg Asn Ala Leu Tyr Ile
725 730 735

Ala Asn Met Glu Lys Arg Lys Thr Glu Glu Leu Leu Glu Lys Glu Thr
740 745 750

Thr Phe Phe Thr Asn Ile Ser His Glu Leu Arg Thr Pro Leu Thr Leu
755 760 765

Ile His Ser Pro Leu Ser Met Ile Ile Glu Ser Gly Lys Tyr Ser Ser
770 775 780

STAN-1357W0_SeqList_ST25.txt

Asp Lys Tyr Leu Ala Gly Met Leu Gln Thr Met Glu His Asn Ser Lys
785 790 795 800

Phe Leu Leu Ser Leu Val Asn Gln Leu Met Asn Phe Ser Lys Ser Glu
805 810 815

Lys Gly Met Leu Ser Leu Asn Leu Lys Tyr Gly Asn Phe Ser Ser Phe
820 825 830

Ser Lys Glu Val Phe Gln Gln Phe Thr Tyr Trp Ala Lys Gln Lys Gly
835 840 845

Val Gly Leu Glu Tyr Ser Val Ser Arg Ser Asp Ile Ser Phe Leu Phe
850 855 860

Asp Pro His Leu Met Glu Gln Ile Ile Tyr Asn Leu Val Ser Asn Ala
865 870 875 880

Ile Lys His Thr Pro Ala Gly Gly Phe Val Ser Phe Thr Val Asn Glu
885 890 895

Gln Asp Asn Lys Ile Asn Ile Ser Val Ala Asp Ser Gly Asn Gly Ile
900 905 910

Ser Asp Asn Leu Lys Thr His Leu Phe Glu Arg Phe Tyr Ser Gln Asn
915 920 925

Lys Asn Ser Ala Glu Gly Gly Thr Gly Ile Gly Leu Phe Leu Thr Lys
930 935 940

Arg Leu Val Glu Ile His Asn Gly Asn Ile Thr Phe Val Ser Glu Glu
945 950 955 960

Gly Lys Gly Thr Val Phe His Val Val Ile Pro Met Ile Thr Glu Gly
965 970 975

STAN-1357W0_SeqList_ST25.txt

Asp Met Val Thr Glu Asn Ile Ser Ala Asn Ser Gly Glu Asp Glu Lys
980 985 990

Phe Ala Asp Val Leu Arg Ser Glu Ser Cys Glu His Glu Glu Met Ile
995 1000 1005

Asp Ile Glu Val Asp Gly Glu Ser Pro Ala Ile Leu Ile Val Asp
1010 1015 1020

Asp Asn Lys Asp Ile Cys Asn Met Leu Ser Leu Leu Leu Ser Asp
1025 1030 1035

Lys Tyr Lys Ile Met Ile Ala His Asp Gly Glu Met Ala Trp Asn
1040 1045 1050

Met Ile Pro Asp Leu Gln Pro Asp Leu Val Leu Ser Asp Ile Met
1055 1060 1065

Met Pro Gly Met Asn Gly Leu Glu Leu Cys Glu Arg Ile Lys Gln
1070 1075 1080

Asp Val Arg Thr Ser His Ile Pro Val Val Leu Leu Ser Ala Lys
1085 1090 1095

Thr Thr Leu Gln Asp Tyr Phe Ile Gly Tyr Lys Phe His Ala Asp
1100 1105 1110

Ala Tyr Cys Pro Lys Pro Phe Asp Asn Lys Ile Met Lys Glu Leu
1115 1120 1125

Leu Asn Ser Ile Ile Thr Asn Arg Lys Arg Ile Leu Gln His Lys
1130 1135 1140

Lys Val Pro Ala Ile Lys Ile Ser Glu Val Ser Thr Thr Ser Thr
1145 1150 1155

STAN-1357W0_SeqList_ST25.txt

Asp Asp Lys Phe Leu Glu Lys Leu Val Lys Ile Ile Glu Asp Asn
1160 1165 1170

Ile Thr Asp Ser Ser Phe Gln Ile Glu Asp Ile Cys Lys Gly Leu
1175 1180 1185

Gly Val Thr Ala Leu Val Leu Asn Lys Lys Leu Lys Ala Leu Met
1190 1195 1200

Gly Val Thr Ala Asn Ala Phe Val Arg Ser Ile Arg Met Lys Arg
1205 1210 1215

Ala Ala Glu Leu Leu Lys Thr Gly Arg Tyr Ser Val Ser Glu Val
1220 1225 1230

Thr Tyr Asp Val Gly Phe Asn Asp Leu Lys Tyr Phe Arg Glu Cys
1235 1240 1245

Phe Lys Lys Glu Phe Gly Val Leu Pro Gln Gln Tyr Lys Glu Gln
1250 1255 1260

Ser Ile Gln Thr Asp Leu Asp Ser
1265 1270

<210> 28

<211> 390

<212> PRT

<213> Bacteroides Plebius

<400> 28

Met Asp Asn Asn Phe Val Phe Gly Tyr Asn Ile Pro Thr Lys Ile Leu
1 5 10 15

Phe Gly Cys Gly Glu Leu Lys Arg Leu Ser Thr Glu Thr Leu Pro Gly
20 25 30

Lys Lys Ala Leu Ile Val Ile Ser Ser Gly Thr Ser Met Arg Lys Tyr

STAN-1357W0_SeqList_ST25.txt

35

40

45

Gly Tyr Leu Asp Lys Val Ile Gly Leu Leu Lys Glu Asn Asn Val Asp
 50 55 60

Ala Val Val Tyr Asp Lys Ile Leu Pro Asn Pro Ile Lys Asp His Val
 65 70 75 80

Met Glu Gly Thr Ala Ile Cys Arg Glu Glu Asn Cys Asp Met Ile Ile
 85 90 95

Gly Leu Gly Gly Gly Ser Ser Ile Asp Thr Ala Lys Ser Ile Ala Ile
 100 105 110

Met Ala Cys Asn Asp Gly Asp Tyr Trp Glu Tyr Val Glu Gly Gly Thr
 115 120 125

Gly Lys Gly Leu Pro Tyr Ser Lys Ala Leu Pro Ile Ile Ala Ile Pro
 130 135 140

Thr Thr Ala Gly Thr Gly Thr Glu Ala Asp Pro Trp Thr Val Ile Thr
 145 150 155 160

Asn Leu Glu Thr Asn Glu Lys Ile Gly Ile Gly Ser Thr Leu Thr Phe
 165 170 175

Pro Cys Leu Ser Ile Ile Asp Pro Glu Leu Met Val Ser Val Pro Pro
 180 185 190

His Leu Thr Ala Tyr Gln Gly Phe Asp Ala Phe Phe His Ala Ala Glu
 195 200 205

Gly Tyr Ile Ala Asn Cys Ala Thr Pro Ile Ser Asp Ile Phe Ala Leu
 210 215 220

Glu Ala Ile Arg Leu Leu Tyr Lys Tyr Leu Pro Val Ala Val Lys Asp

225 230 — 235 — 240

STAN-1357W0_SeqList_ST25.txt

<400> 29

Met Lys Thr Asn Leu Lys Asn Asn Ile Met Lys Gly Met Ala Val Met
1 5 10 15

Pro Phe Leu Ser Val Cys Val Gly Val Ala Ala Gln Gln Lys Gln Met
20 25 30

Asn Val Ile Tyr Ile Met Ser Asp Asp His Thr Ser Gln Ala Ile Gly
35 40 45

Ala Tyr Gly Ser Arg Leu Ala Val Leu Asn Pro Thr Pro Thr Ile Asp
50 55 60

Glu Leu Ala Arg Asp Gly Met Leu Phe Glu Asn Cys Phe Cys Thr Asn
65 70 75 80

Ser Ile Ser Thr Pro Ser Arg Ala Cys Ile Met Thr Gly Gln Tyr Ser
85 90 95

His Arg Asn Lys Val Leu Thr Leu Asp Glu Val Leu Gln Pro Asp Gln
100 105 110

Glu Tyr Leu Val Asp Glu Phe His Asn Met Gly Tyr Gln Thr Ala Met
115 120 125

Ile Gly Lys Trp His Leu Gly Cys Glu Pro Ser His Phe Asp Tyr Tyr
130 135 140

Ser Val Phe Asn Gly His Gly Gly Gln Gly Glu Tyr Phe Asp Pro Ile
145 150 155 160

Phe Leu Thr Ser Asp Val Thr Asp Lys Lys Trp Pro Asn Asn Gln Ile
165 170 175

Lys Lys Met Gly Tyr Ser Ser Asp Ile Val Thr Asn Leu Ala Ile Asp
180 185 190

STAN-1357W0_SeqList_ST25.txt

Trp Leu Lys Asn Arg Arg Asp Lys Ser Lys Pro Phe Phe Met Met His
195 200 205

His Tyr Lys Ala Pro His Asp Met Phe Glu Tyr Ala Pro Arg Tyr Glu
210 215 220

Tyr Tyr Leu Asp Asp Val Glu Val Pro Val Pro Leu Ser Leu Phe Asp
225 230 235 240

Thr Asp Lys Trp Gly Ser Glu Gly Thr Arg Gly Lys Asn Asp Ser Leu
245 250 255

Arg His Phe Ile Gly Thr Ser Val Ser Ser Arg His Glu Ile Arg Asn
260 265 270

Tyr Val Met Glu Tyr Lys Cys Asn Thr Gly Asp Glu Met Glu Asn Thr
275 280 285

Tyr Leu Ala Tyr Gln His Tyr Leu Lys Ser Tyr Leu Arg Cys Val Lys
290 295 300

Gly Val Asp Asp Asn Leu Lys Arg Leu Phe Asp Tyr Leu Lys Lys Glu
305 310 315 320

Gly Leu Trp Glu Asn Thr Ile Ile Val Tyr Thr Gly Asp Gln Gly Met
325 330 335

Met Leu Gly Glu His Asp Leu Gln Asp Lys Arg Trp Met Tyr Glu Glu
340 345 350

Ser Gln Arg Met Pro Phe Ile Val Arg Asp Pro Arg Cys Pro Tyr Lys
355 360 365

Gly Ala Lys Ser Asp Leu Met Ile Asn Asn Ile Asp Phe Ala Pro Thr
370 375 380

STAN-1357W0_SeqList_ST25.txt

Leu Ile Glu Met Val Gly Gly Lys Glu Pro Ser Tyr Met Asp Gly Lys
385 390 395 400

Ser Phe Ala Ser Val Phe Glu Gly Lys Lys Pro Glu Asn Trp Lys Asp
405 410 415

Ala Val Tyr Tyr Arg Tyr Trp Met His Met Ile His His Asp Val Pro
420 425 430

Ala His Ile Gly Ile Arg Thr Glu Asn Tyr Lys Leu Ile Leu Phe Tyr
435 440 445

Gly Arg His Tyr Asp Asp Lys Arg Tyr Gly Gln Lys Ser Met Ser Trp
450 455 460

Leu Lys Asn Ser His Lys Ile Val Pro Thr Pro Val Ser Phe Glu Leu
465 470 475 480

Tyr Asp Val Lys Asn Asp Pro Tyr Glu Met Val Asn Leu Ala Asp Asn
485 490 495

Pro Lys Tyr Ala Lys Val Leu Lys Asp Met Lys Lys Lys Leu Arg Glu
500 505 510

Leu Arg Lys Gln Val Gly Asp Thr Asp Glu Ala Tyr Pro Glu Leu Lys
515 520 525

Lys Val Ile Asp Glu Ala Leu Arg
530 535

<210> 30

<211> 519

<212> PRT

<213> Bacteroides Plebuis

<400> 30

STAN-1357W0_SeqList_ST25.txt

Met Lys Thr Val Leu Gly Val Ala Ala Leu Ser Leu Leu Ala Ser Cys
1 5 10 15

Asn Ser Thr Tyr Ala Pro Asn Val Asp Ser Thr Val Ser Leu Lys Gly
20 25 30

Thr Asp Val Phe Lys Ala Asp Ser Ala Ser Ile Ala Gln Asn Tyr Thr
35 40 45

Ile Pro Glu Trp Phe Lys Asp Ala Lys Phe Gly Ile Phe Ile His Trp
50 55 60

Gly Val Tyr Ser Val Pro Ala Tyr Gly Ser Glu Trp Tyr Ser Arg Trp
65 70 75 80

Met Tyr Lys Glu Gly His Pro Ile Asn Lys Tyr His Val Gln Thr Tyr
85 90 95

Gly Pro Leu Thr Lys Phe Gly Tyr Lys Asp Phe Ile Pro Met Phe Lys
100 105 110

Ala Glu Asn Phe Asn Ala Asp Glu Trp Leu Ala Val Val Lys Ser Ser
115 120 125

Gly Ala Gln Tyr Ile Val Pro Val Ala Glu His His Asp Gly Phe Ala
130 135 140

Met Tyr Ser Ser Thr Phe Asn Lys Trp Asn Ala Val Asp Met Gly Pro
145 150 155 160

Lys Arg Asp Ile Ile Gly Glu Leu Lys Glu Ala Thr Lys Lys Ala Gly
165 170 175

Leu Arg Phe Gly Leu Ser Ser His Arg Cys Glu Asn Ala Trp Phe Tyr
180 185 190

STAN-1357W0_SeqList_ST25.txt

Glu Tyr Gly Met Glu Thr Pro Ser Asp Val Gln Asp Thr Thr Ile Thr
195 200 205

Leu Tyr Gly Glu Arg Leu His Glu Pro Glu Gly Gln Gly Met Thr Pro
210 215 220

Tyr Cys Gly Lys Tyr Glu Gly Ser Asn Glu Arg Ser Arg Arg Gln Phe
225 230 235 240

Leu Met His Thr Tyr Glu Leu Ile Asp Lys Tyr Gln Pro Glu Leu Ile
245 250 255

Trp Phe Asp Trp Thr Val Gly Lys Tyr Pro Phe Gln Pro Thr Phe Tyr
260 265 270

Lys Phe Met Ala Tyr Tyr Tyr Asn Ser Ala Leu Asp Trp Asn Lys Glu
275 280 285

Val Val Val Asn Thr Lys Phe Gly Tyr Gly Asp Asn Ile Gln Val Phe
290 295 300

Asp Ile Glu Arg Gly Lys Ser Asp Arg Ile Arg Glu Tyr Pro Trp Gln
305 310 315 320

Thr Asp Thr Ser Val Gly Lys Lys Ser Trp Ser Tyr Cys Val Gly Glu
325 330 335

Glu Asn Lys Ser Pro Asp His Ile Ile Asp Asp Phe Val Asp Ile Val
340 345 350

Ser Lys Asn Gly Asn Leu Leu Leu Asn Ile Gly Pro Lys Ala Asp Gly
355 360 365

Thr Ile Thr Asp Glu Gln Lys Asn Val Leu Ala Glu Ile Gly Lys Trp
370 375 380

STAN-1357W0_SeqList_ST25.txt

Leu Lys Thr Asn Gly Glu Ala Ile Tyr Gly Ser Arg Pro Trp Val Ile
385 390 395 400

Ala Phe Glu Gly His Asn Ala Gly Thr Ala Gly Tyr Met Thr Asp Asn
405 410 415

Thr Lys Thr Glu Tyr Thr Ala Asp Asp Ile Arg Phe Thr Thr Arg Asp
420 425 430

Asn Asn Leu Tyr Ala Val Ser Leu Ala Trp Thr Asp Gly Ser Val Thr
435 440 445

Ile Lys Ser Phe Ala Pro Lys Tyr Cys Gln Asn Val Glu Ile Glu Ser
450 455 460

Val Glu Met Leu Gly Ser Ser Glu Lys Ile Asp Tyr Lys Met Thr Asp
465 470 475 480

Glu Gly Leu Val Val Asn Phe Pro Lys Asn Lys Pro Thr Glu Tyr Ala
485 490 495

His Val Phe Lys Ile Lys Leu Lys Gly Ala Val Val Ser Lys Pro Leu
500 505 510

Tyr Asp Lys Val Asp Asn Gly
515

<210> 31
<211> 299
<212> PRT
<213> Bacteroides Plebuis

<400> 31

Met Lys Asn Tyr Leu Ile Tyr Leu Leu Ala Ala Val Ser Cys Thr Thr
1 5 10 15

STAN-1357W0_SeqList_ST25.txt																
Val	Ala	Asp	Leu	Asn	Ala	Gln	Val	Ser	Thr	Lys	Thr	Gly	Asn	Glu	Thr	
			20				25						30			
Thr	Glu	Leu	Thr	Ile	Pro	Lys	Lys	Phe	Tyr	Lys	Asp	Ser	Ile	Asp	Phe	
			35				40						45			
Ser	Asn	Ala	Pro	Lys	Arg	Leu	Asn	Asn	Lys	Tyr	Pro	Leu	Ser	Asp	Gln	
			50				55						60			
Lys	Asn	Glu	Gly	Gly	Trp	Val	Leu	Asn	Lys	Lys	Ala	Ser	Asp	Glu	Phe	
65							70						75			
Lys	Gly	Lys	Lys	Leu	Asn	Glu	Glu	Arg	Trp	Phe	Pro	Asn	Asn	Pro	Lys	
						85						90				
Trp	Lys	Gly	Arg	Gln	Pro	Thr	Phe	Phe	Ala	Lys	Glu	Asn	Thr	Thr	Phe	
			100						105						110	
Glu	Asp	Gly	Cys	Cys	Val	Met	Arg	Thr	Tyr	Lys	Pro	Ala	Gly	Ser	Leu	
			115						120						125	
Pro	Glu	Gly	Tyr	Thr	His	Thr	Ala	Gly	Phe	Leu	Val	Ser	Lys	Glu	Leu	
			130						135						140	
Phe	Leu	Tyr	Gly	Tyr	Phe	Glu	Ala	Arg	Leu	Arg	Pro	Asn	Asp	Ser	Pro	
145							150						155			
Trp	Val	Phe	Gly	Phe	Trp	Met	Ser	Asn	Asn	Glu	Arg	Asn	Trp	Trp	Thr	
			165						170						175	
Glu	Ile	Asp	Ile	Cys	Glu	Asn	Cys	Pro	Gly	Asn	Pro	Ala	Asn	Arg	His	
			180						185						190	
Asp	Leu	Asn	Ser	Asn	Val	His	Val	Phe	Lys	Ala	Pro	Ala	Asp	Lys	Gly	
			195						200						205	

STAN-1357W0_SeqList_ST25.txt

Asp Ile Lys Lys His Ile Asn Phe Pro Ala Lys Tyr Tyr Ile Pro Phe
210 215 220

Glu Leu Gln Lys Asp Phe His Val Trp Gly Leu Asp Trp Ser Lys Glu
225 230 235 240

Tyr Ile Arg Leu Tyr Ile Asp Gly Val Leu Tyr Arg Glu Ile Glu Asn
245 250 255

Lys Tyr Trp His Gln Pro Leu Arg Ile Asn Leu Asn Asn Glu Ser Asn
260 265 270

Lys Trp Phe Gly Ala Leu Pro Asp Asp Asn Asn Met Asp Ser Glu Tyr
275 280 285

Leu Ile Asp Tyr Val Arg Val Trp Tyr Lys Lys
290 295

<210> 32
<211> 531
<212> PRT
<213> Bacteroides Plebius

<400> 32

Met Phe Ala Ala Ile Ala Ser Ser Ser Cys Ser Asp Ser Phe Leu Asp
1 5 10 15

Thr Ala Pro Ile Met Ser Glu Thr Glu Ser Ser Phe Tyr Arg Thr Asp
20 25 30

Glu Gln Met Phe Lys Ala Leu Thr Ala Cys Tyr Asp Pro Leu Ala His
35 40 45

Ile Gly Gly Ala Ser Gly Asn Ala Leu Ala Ser Ile Val Pro Met Gly
50 55 60

Glu Ile Arg Ser Asp Asn Ala Arg Thr Gly Gly Gly Ser Asp Gln Asp

STAN-1357W0_SeqList_ST25.txt

65		70		75		80
Gln	Pro	Tyr	Met	Gln	Ala	Ile
			85			
				Glu	Asp	Tyr
					90	
				Ser	Asn	Thr
						Ser
						Val
						Asn
						95
Ser	Ile	Ser	Asp	Asn	Leu	Trp
			100			
				Lys	Thr	Arg
					105	
				Tyr	Arg	Gly
						Ile
						Tyr
						Arg
						110
Cys	Asn	Leu	Val	Ile	Asn	Ser
			115			
				Glu	Tyr	Asp
					120	
				Ser	Pro	Glu
						Ala
						Lys
						Val
						125
Tyr	Lys	Ala	Glu	Ala	Lys	Phe
						Leu
						Arg
						Ala
						Trp
						Tyr
						His
						Phe
						Glu
						Leu
						130
						135
						140
Leu	Arg	Tyr	Tyr	Gly	Pro	Cys
						Phe
						Ile
						Ser
						Leu
						Glu
						Thr
						Leu
						Tyr
						Pro
						145
						150
						155
						160
Glu	Gly	Phe	Lys	Phe	Thr	Arg
						Asp
						Thr
						Arg
						Glu
						Asn
						Val
						Asn
						Lys
						Ala
						165
						170
						175
Ile	Glu	Lys	Asp	Leu	Leu	Glu
						Ala
						Ile
						Pro
						Ser
						Leu
						Lys
						Asp
						Asn
						Phe
						180
						185
						190
Pro	Asp	Thr	Met	Lys	Gly	Arg
						Ile
						Thr
						Lys
						Thr
						Ala
						Ala
						Gln
						Ala
						Leu
						195
						200
						205
Leu	Ala	Lys	Val	Tyr	Leu	Tyr
						Trp
						Ala
						Asp
						Trp
						Ser
						Asn
						Asp
						Asp
						Ala
						210
						215
						220
Lys	Ile	Phe	Asp	Lys	Ala	Lys
						Pro
						Leu
						Leu
						Glu
						Asp
						Val
						Ile
						Ser
						Ser
						225
						230
						235
						240
Gly	Asn	Tyr	Thr	Leu	Thr	Asp
						Asp
						Tyr
						Ser
						Lys
						Leu
						Phe
						Ala
						Ala
						His
						245
						250
						255
Gln	Glu	Asn	Asn	Glu	Glu	Ser
						Ile
						Phe
						Glu
						Ile
						Gln
						Thr
						Ser
						Thr
						Lys

STAN-1357W0_SeqList_ST25.txt

260

265

270

Ser Gly Asn Thr Asn Trp Gly Asn Ile Asp Ala Gly Glu Gly Ala Met
 275 280 285

Trp Val Thr Phe Cys Gly Pro Arg Gln Leu Lys Asn Ser Pro Asp Tyr
 290 295 300

Asp Asn Gly Tyr Gly Phe Cys Leu Pro Thr Lys Glu Leu Tyr Asp Tyr
 305 310 315 320

Phe Leu Pro Asp Asp His Val Arg Arg Asp Ala Ala Ile Phe Thr Tyr
 325 330 335

Asp Glu Leu Val Thr Lys Pro Asn Ala Asn Ile Gln Asp Glu Ser Lys
 340 345 350

Lys Val Val Trp Glu Thr Gly Ser Tyr Gly Pro Asp Phe Gln Gly Tyr
 355 360 365

Ala Gln Lys Lys Tyr Pro Pro Phe Lys Asn Tyr Asp Met Ile Gly Asn
 370 375 380

Pro Asn Leu Asn Lys Pro Gly Asn Val Arg Val Ile Arg Tyr Gly Glu
 385 390 395 400

Val Tyr Leu Met Leu Ala Glu Ala Tyr Leu Arg Gly Thr Asn Pro Asp
 405 410 415

Glu Ala Lys Ala Lys Tyr Tyr Ile Asn Glu Leu Arg Lys Lys His Val
 420 425 430

His Ala Asp Asp Gly Ser Tyr Ile Asp Val Asp Lys Leu Met Gln Met
 435 440 445

Tyr Pro Asp Arg Phe Lys Ser Val Ile Asp Val Leu Trp Tyr Glu Arg

STAN-1357W0_SeqList_ST25.txt

450

455

460

Arg Cys Glu Leu Ala Cys Glu Gly Asp Arg Trp Phe Asp Leu Val Arg
465 470 475 480

Ser Gly Arg Ala Glu Glu Val Met Met Pro Ile Leu Arg Arg Asp Tyr
485 490 495

Gly Ile Ser Ala Trp Ser Lys Lys Phe Asn Tyr Leu Pro Ile Gly Ser
500 505 510

Ile Glu Ile Ser Asn Ser Gly Asn Ser Leu Thr Glu Tyr Pro Asp Glu
515 520 525

Val Asn Glu
530

<210> 33
<211> 982
<212> PRT
<213> Bacteroides Plebius

<400> 33

Met Ile Gly Ala Ser Ile Leu Val Lys Gly Thr Thr Asn Gly Ile Ile
1 5 10 15

Ser Asp Leu Asp Gly Asn Tyr Ile Leu Glu Asn Val Pro Met Glu Ser
20 25 30

Thr Leu Ile Tyr Ser Phe Val Gly Tyr Asp Thr Gln Asn Ile Val Tyr
35 40 45

Lys Gly Gln Ser Lys Ile Asp Val Gln Leu Lys Thr Ser Ala Ile Ala
50 55 60

Leu Glu Glu Val Val Ala Ile Gly Tyr Glu Val Lys Lys Lys Ser Val
65 70 75 80

STAN-1357W0_SeqList_ST25.txt

Val Thr Gly Ala Ile Ser Ser Ile Asp Ser Asp Asp Leu Leu Gln Ser
85 90 95

Lys Pro Ala Asn Ala Val Asn Ala Leu Ser Gly Arg Val Ser Gly Val
100 105 110

Asn Val Val Thr Asn Ser Gly Gln Pro Gly Thr Ala Pro Lys Leu Val
115 120 125

Ile Arg Gly Val Gly Thr Asn Gly Asn Ser Asn Pro Leu Phe Val Ile
130 135 140

Asp Gly Leu Pro Met Asp Asp Met Asn Ser Val Asn Pro Asn Asp Ile
145 150 155 160

Glu Ser Met Glu Val Leu Lys Asp Ala Thr Ser Ala Ala Ile Tyr Gly
165 170 175

Ala Arg Ala Ala Asn Gly Val Val Leu Ile Thr Thr Lys Lys Gly Lys
180 185 190

Lys Gly Lys Thr Ser Leu Ala Tyr Asp Gly Tyr Tyr Gly Phe Ser Thr
195 200 205

Val Ala Lys Lys Pro Thr Met Leu Asn Asp Glu Gln Tyr Ile Met Leu
210 215 220

Met Lys Glu Phe Ala Asp Asn Asp Asp Met Pro Leu Ala Gly Gly Val
225 230 235 240

Pro Thr Ala Pro Thr Gly Tyr Asn Thr Asp Trp Phe Asn Glu Ile Leu
245 250 255

Asn Thr Ala Pro Val Thr Glu His Asn Ile Thr Ala Asn Phe Gly Ser
260 265 270

STAN-1357W0_SeqList_ST25.txt

Asp Lys Gly Ser Ser Leu Leu Ser Leu Asn Tyr Leu Asp Gln Asn Gly
275 280 285

Ile Ile Gly Glu Asp Ala Ser Phe Tyr Lys Arg Phe Ser Thr Arg Leu
290 295 300

Asn Ser Ser Tyr Ser Ile Asn Asp Phe Leu Ser Val Gly Ala Asn Val
305 310 315 320

Asn Tyr Ala Tyr Ile Glu Asn Ser Gly Val Ala Thr Gly Ile Asn Gly
325 330 335

Tyr Asn Pro Ile Ser Tyr Ala Tyr Asn Ile Asp Pro Thr Thr Pro Val
340 345 350

Tyr Asp Glu Asn Ser Asn Asp Thr Phe Gly Tyr Gly Val Ser Pro Val
355 360 365

Pro Tyr Ser Arg Met Trp Asn Pro Ile Ala Phe Met Asp Glu Ala Pro
370 375 380

Lys Asn Lys Asn Ile Thr Gln Gln Phe Phe Gly Asn Val Tyr Ala Glu
385 390 395 400

Ile Thr Phe Ile Lys Asp Leu Val Phe Arg Thr Asp Phe Gly Ile Asn
405 410 415

His Arg Asn Phe Arg Gly Arg Met Phe Ala Pro Lys Phe Phe His Ser
420 425 430

Ala Glu Cys Lys Glu Asp Asn Ser Arg Val Glu Gln Ser Thr Asn Ala
435 440 445

Asn Ser Ser Trp Gln Trp Glu Asn Thr Leu Arg Tyr Lys Lys Ser Phe
450 455 460

STAN-1357W0_SeqList_ST25.txt

Gly Glu His Ser Thr Ser Val Leu Leu Gly Thr Ser Ala Ser Arg Asp
465 470 475 480

Val Tyr Glu Phe Met Ala Gly Thr Arg Asn Lys Tyr Pro Asn Glu Ala
485 490 495

Met Thr Asn Glu Asn Tyr Trp Tyr Leu Asn Ala Gly Asp Val Met Thr
500 505 510

Ser Ala Asn Ser Gly Gly Ala Asn Pro Arg His Ser Met Phe Ser Tyr
515 520 525

Phe Ala Arg Leu Ser Tyr Asn Tyr Ala Glu Lys Tyr Met Ala Glu Val
530 535 540

Val Val Arg Arg Asp Gly Ser Ser Asn Phe Gly Pro Asn Asn Arg Tyr
545 550 555 560

Ala Thr Phe Pro Gly Val Ser Leu Gly Trp Asn Val Ser Asn Glu Lys
565 570 575

Phe Trp Lys Ile Lys Asn Phe Asp Val Phe Lys Leu Arg Phe Ser Trp
580 585 590

Gly Gln Asn Gly Asn Glu Arg Ile Ser Pro Phe Ser Tyr Thr Ser Ile
595 600 605

Ile Gly Asn Asn Tyr Asn Tyr Thr Phe Gly Asn Ala Ile Thr Val Gly
610 615 620

Ser Ala Pro Asn Asn Leu Val Asn Pro Asp Val Lys Trp Glu Thr Ser
625 630 635 640

Glu Gln Phe Asn Val Gly Ala Asp Met Thr Phe Tyr Asn Gly Met Ile
645 650 655

STAN-1357W0_SeqList_ST25.txt

Arg Ala Ser Phe Asp Trp Phe Lys Lys Ser Thr Lys Asp Leu Leu Phe
660 665 670

Gln Pro Thr Val Glu Ala Ile Arg Gly Asn Asn Ala Ala Phe Arg Asn
675 680 685

Leu Gly Asn Ile Thr Asn Gln Gly Val Glu Met Gln Met Thr Phe Asn
690 695 700

Lys Asn Trp Asn Glu Ile Asn Phe Ser Ile Ser Ala Asn Ala Ser Tyr
705 710 715 720

Leu Lys Asn Glu Val Val Lys Ile Gly Asn Val Asn Gly Tyr Thr Asp
725 730 735

Gly Gly Ser Trp Arg Thr Ser Val Asn Val Thr Arg Met Glu Glu Gly
740 745 750

His Ala Met Gly Tyr Phe Arg Leu Tyr Lys Asn Leu Gly Ile Phe Gln
755 760 765

Asn Glu Glu Gln Ile Gln Asn Tyr Lys Ser Lys Asp Gly Lys Val Ile
770 775 780

Gln Pro Asp Ala Val Pro Gly Asp Phe Ile Trp Gln Asp Thr Asn Asn
785 790 795 800

Asp Gly Gln Ile Thr Asp Glu Asp Arg Thr Asp Cys Gly Asn Pro Trp
805 810 815

Pro Lys Trp Thr Phe Gly Leu Asn Leu Gly Ala Asp Trp Arg Gly Ile
820 825 830

Asp Met Thr Ile Phe Leu Thr Gly Lys Ala Gly Tyr Lys Val Phe Ser
835 840 845

STAN-1357W0_SeqList_ST25.txt

Asp Ile Tyr Arg Gln Glu Ala Tyr Gly Arg Ser Asn Leu Pro Ser Phe
850 855 860

Tyr Leu Asp Arg Trp Arg Lys Glu Gly Asp Asp Asn Gly Val Pro Arg
865 870 875 880

Leu Ser Ser Lys Asp Pro Asn Gly Asn Phe Gly Lys Pro Ser Asp Phe
885 890 895

Tyr Leu Tyr Asp Gly Ser His Leu Lys Ile Ser Ser Leu Glu Val Gly
900 905 910

Tyr Ser Phe Pro Thr Lys Leu Ile Asn Lys Leu Met Leu Asn Lys Ala
915 920 925

Arg Ile Tyr Ala Ala Ile Asp Asn Leu Ala Thr Phe Thr Ser Tyr Pro
930 935 940

Phe Met Asp Pro Glu Val Gly Asn Met Ala Gly Gly Asn Ile Leu Ser
945 950 955 960

Thr Gly Ile Asp Tyr Gly Thr Tyr Pro Gln Ala Arg Thr Phe Arg Phe
965 970 975

Gly Leu Ser Leu Asn Phe
980

<210> 34
<211> 1086
<212> PRT
<213> Bacteroides Plebius

<400> 34

Met Gln Phe Leu Ser Ala Ser Asp Asn Gly Ala Asn Gln Trp Arg Asn
1 5 10 15

STAN-1357W0_SeqList_ST25.txt

Asn Gln Asn Val Trp Gln Asp Gln Thr Ile Asn Gly Ile Asn Arg Leu
20 25 30

Pro Ser Arg Ser Thr Thr Tyr Ser Phe Arg Arg Val Asp Trp Ala Leu
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Asp Gly Asp Arg Glu Lys Ser Glu Tyr Met Ser Leu Asn Gly Gln Trp
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Lys Phe Asn Phe Ser Glu Asp Met Ala Leu Ala Pro Ala Gly Phe Tyr
65 70 75 80

Lys Val Glu Tyr Asn Ser Ser Ser Trp Lys Thr Ile Pro Val Pro Ser
85 90 95

Cys Trp Glu Met Gln Gly Tyr Gly Tyr Pro Ile Tyr Thr Asn Thr Ile
100 105 110

Tyr Pro Phe Pro Ala Arg Pro Pro Tyr Ile Asp Arg Asn Asn Gln Thr
115 120 125

Gly Cys Tyr Ile Lys Glu Phe Val Val Pro Asp Lys Trp Lys Ser Asp
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Arg Ile Ile Leu His Phe Gly Gly Val Tyr Ser Gly Phe Asn Val Trp
145 150 155 160

Ile Asn Gly Gln Lys Val Gly Tyr Ser Glu Asp Ser Cys Leu Pro Thr
165 170 175

Glu Phe Asp Ile Thr Glu Tyr Val Lys Lys Gly Glu Asn Lys Leu Ala
180 185 190

Val Gln Val Tyr Lys Trp Thr Asp Gly Ser Tyr Met Glu Asp Ala Asp
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His Trp Arg Met Ala Gly Ile His Arg Glu Val Tyr Ile Met Ser Ile
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Arg Lys Asn Ile Ala Arg Leu Gln Ile Arg Pro Glu Ile Thr Asn Gln
245 250 255

Asn Met Asp Asp Leu Lys Gly Trp Asn Leu Ser Ala Gln Leu Tyr Asp
260 265 270

Ala Asp Gly Lys Pro Val Phe Gly Lys Asp Ile Thr Val Thr Ala Asp
275 280 285

Tyr Val Val Asn Glu Pro Tyr Pro Gln Arg Asp Asn Val Tyr Tyr Gly
290 295 300

Met Met Glu Gly Ile Val Ser Lys Pro Lys Leu Trp Asn Ser Glu His
305 310 315 320

Pro Tyr Leu Tyr Thr Leu Val Ile Lys Leu Thr Asp Lys Lys Gly Asn
325 330 335

Val Val Asp Ala Arg Ser Asn Lys Val Gly Phe Arg Asp Ile Lys Ile
340 345 350

Thr Gly Asn Gln Ile Leu Val Asn Asp Thr Pro Ile Lys Leu Ile Gly
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Val Asn Arg His Asp His Ser Glu Thr Gly Gly Lys Thr Val Thr Arg
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Asp Glu Met Leu Glu Asp Val Leu Leu Met Lys Arg Tyr Asn Phe Asn
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Phe Met Glu Arg Val Val Arg Met Ala Val Arg Asp Arg Asn His Pro
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Ser Val Phe Met Trp Ser Leu Gly Asn Glu Ser Gly Cys Gly Pro Asn
465 470 475 480

His Ala Ala Leu Ser Gly Trp Leu Lys Asp Tyr Asp Pro Thr Arg Pro
485 490 495

Val His Tyr Glu Gly Ala Gln Gly Gln Pro Glu Asn Pro Leu Tyr Lys
500 505 510

Pro Ile Gly Arg Lys Glu Ala Ser Ile Val Thr Ser Glu Ile Asp Phe
515 520 525

Asn Val Asn Glu Asp Val Lys Pro Ala Lys Lys Glu Leu Cys Val Tyr
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Ala Asn Pro Asp Asp Pro Leu Tyr Val Asp Val Ile Ser Arg Met Tyr
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Pro Met Val Asp Glu Leu Ile Ala Met Thr Lys Asn Pro Val Met Asn
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Arg Pro Ile Ile Met Cys Glu Tyr Ala His Ser Met Gly Asn Ser Thr
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625 630 635 640

Lys Gly Glu His Asn Asp Gln Asn Phe Cys Ile Asn Gly Val Ile Ser
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Ala Asp Arg Ser Ile Lys Pro Ala Thr Glu Glu Cys Lys Tyr Val Phe
660 665 670

Ala Pro Val Ser Phe Thr Thr Asp Asn Val Tyr Ser Gly Glu Ile Thr
675 680 685

Val Lys Asn Arg Asn Phe Phe Leu Ser Thr Asp Glu Tyr Arg Tyr Phe
690 695 700

Trp Gln Leu Lys Asp Glu Asp Ser Val Leu Gln Glu Gly Glu Ile Ile
705 710 715 720

Val Pro Thr Thr Pro Ala Gly Glu Ser Cys Lys Leu Lys Leu Pro Ile
725 730 735

Gln Asn Phe Lys Ala Asp Asp Gly Ala Glu Tyr Trp Leu Phe Leu Ser
740 745 750

Ala Arg Leu Lys Asn Asp Asn Leu Tyr Ala Lys Ala Gly Tyr Glu Val
755 760 765

Ala Trp Glu Gln Phe Lys Tyr Leu Ser Leu Pro Lys Ile Val Glu Cys
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820 825 830

Lys Pro Asn Phe Trp Arg Ala Ser Thr Asp Asn Asp Trp Arg Gly Trp
835 840 845

Lys Val Asp Arg Leu Phe Ala Phe Trp Lys Asp Ala Pro Leu Lys Leu
850 855 860

Lys Thr Val Ser Ile Asp Val Arg Lys Ser Glu Gly Asn Leu Glu Val
865 870 875 880

Lys Val Leu Lys Ala Ile Asp Glu Arg Leu Arg Leu Thr Leu Asn Tyr
885 890 895

Lys Val Lys Ala Asp Gly Thr Ile Gly Val His Tyr Ser Met Met Lys
900 905 910

Ser Pro Glu Ile Ser Glu Met Leu Arg Val Gly Leu Gln Cys Glu Cys
915 920 925

Thr Asn Arg Leu Ser Asp Val Thr Tyr Tyr Gly Arg Gly Pro Trp Glu
930 935 940

Asn Tyr Ser Asp Arg Lys Ala Ser Ala Met Val Ser Ile Tyr Asn Cys
945 950 955 960

Lys Val Ser Ala Leu Gly Phe Asp Tyr Val Met Pro Gln Glu Asn Gly
965 970 975

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 995 1000 1005

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 1010 1015 1020

Lys Asp Leu Tyr Ser Asn Thr Leu Asn Ile Asp Leu Val Gln Ala
 1025 1030 1035

Gly Val Gly Gly Thr Asp Ser Trp Ser Leu Lys Ala Arg Pro Ser
 1040 1045 1050

Ile Asp Lys Arg Leu Leu Lys Gly Ser Tyr Ser Tyr Gly Phe Thr
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