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# DESCRIPTION

## BACKGROUND TO THE INVENTION

[0001] The human intestine, thought to be initially sterile *in utero*, is exposed to a large variety of maternal and environmental microbes immediately after birth. The subsequent colonization and succession events in the gut remain dynamic during the first years of life, after which the microbiota becomes adult-like and relatively stable (1). The human gut microbiota contains more than 500 different phylotypes belonging essentially to two major bacterial divisions, the Bacteroidetes and the Firmicutes (2). The successful symbiotic relationships arising from bacterial colonization of the human gut have yielded a wide variety of metabolic, structural, protective and other beneficiary functions. The enhanced metabolic activities of the colonized gut ensure that dietary components, which are otherwise indigestible, are degraded with released byproducts providing an important nutrient source for the host. Similarly, the immunological importance of the gut microbiota is well-recognized and exemplified in germfree animals which have an impaired immune system that is functionally reconstituted following the introduction of commensal bacteria (3-5).

[0002] In sharp contrast to the production of secretory intestinal IgA which is influenced by microbial colonization *per se* (6, 7), T cell development and differentiation seems to require colonization of specific commensal micro-organisms. Clostridium species, in particular the spore-forming segmented filamentous bacteria (SFB), appear to be a major driver for the maturation of intestinal Th1, Th17 and Tregs (8, 9). Recent studies have, however, now shown that other gut bacteria including those of the altered Schaedler flora can induce *de novo* generation of Tregs while mono-colonization with *Bacteroides fragilis* can correct the Th1/Th2 imbalance in germfree mice by promoting the expansion of Tregs (5, 10).

[0003] The present invention seeks to elucidate other resident gut bacteria that can modulate metabolic activity in the gut and/or play a role in immunoregulatory processes.

## STATEMENT OF INVENTION

[0004] The present invention centres on the activity of the bacterial species *Roseburia hominis*, a member of the Firmicutes phylum. Studies by the applicant have demonstrated that this bacterial species plays an important part in immunoregulation and metabolic activity in the gut, as well as having an effect on appetite and satiety genes. The roles of bacterial genes participating in colonization and adaptation to the murine gut, as well as the host genes responding to colonization by this bacterium are described in more detail below.

[0005] Aspects of the invention, together with preferred embodiments, are set forth in the accompanying claims.

**[0006]** A first aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029; for use in medicine.

**[0007]** Another aspect of the invention relates to a pharmaceutical composition comprising a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029; and a pharmaceutically acceptable excipient, carrier or diluent.

**[0008]** Another aspect of the invention relates to a nutritional supplement comprising a bacterial having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029; and a nutritionally acceptable excipient, carrier or diluent.

**[0009]** Another aspect of the invention relates to a probiotic composition, feedstuff, food product, dietary supplement or food additive comprising (a) a bacterial strain having a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029.

**[0010]** Another aspect of the invention relates to a process for producing a pharmaceutical composition or a nutritional supplement comprising (a) a bacterial strain having a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, said process comprising admixing the bacterial strain with a pharmaceutically acceptable excipient, carrier or diluent or a nutritionally acceptable excipient, carrier or diluent.

#### **DETAILED DESCRIPTION OF THE INVENTION**

**[0011]** One aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number

NCIMB 14029 for use in one or more of:

- treating an immune disorder;
- treating an intestinal disorder;
- improving intestinal microbiota;
- regulating the innate immune system of a subject;
- regulating the adaptive immune system of a subject;
- promoting Tregs and immune tolerance;
- regulating appetite in a subject;
- promoting gut health in a subject; and/or
- maintaining immune homeostasis in a subject.

### ***Roseburia hominis***

**[0012]** *Roseburia hominis*, a recently described commensal gut anaerobe of the phylogenetic cluster XIVa within the Firmicutes phylum, belongs to a dominant group of bacteria in the human gut and is also a major butyrate producer (11). The present applicant has elucidated the complete genome sequence and annotation for this bacterium. Further studies investigated both bacterial and host transcriptome responses in germfree mice mono-colonized with *R. hominis*. The roles of bacterial genes participating in colonization and adaptation to the murine gut, as well as the host genes responding to colonization by this bacterium are described herein.

**[0013]** Experiments by the Applicant have shown that the activity of *Roseburia hominis* is highly specific. Studies have shown that important genomes of *Roseburia* species are very different, indicating diverse functionality. Indeed, experiments have shown that bacteria from Clostridium Cluster XIVa, including the bacterial species *Roseburia intestinalis*, *Roseburia hominis* and *Eubacterium rectale* (all of which are butyrate producers) surprisingly induce very different and distinct effects on gut cells.

**[0014]** In one preferred embodiment, the bacterial species is the strain deposited under the terms of the Budapest Treaty at National Collections of Industrial, Food and Marine Bacteria (NCIMB) at NCIMB Ltd, Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen, UK, AB21 9YA, on 21 October 2004 on behalf of the Rowett Research Institute of Nutrition and Health, University of Aberdeen, Greenburn Road, Aberdeen, AB21 9SB, Scotland, UK, under the accession number NCIMB 14029<sup>T</sup> *Roseburia hominis* A2-183<sup>T</sup> (DSM = 16839<sup>T</sup>).

**[0015]** The bacterial species is preferably *Roseburia hominis* as described in Duncan, S. H., Aminov, R. I., Scott, K. P., Louis, P., Stanton, T. B., & Flint, H. J. (2006) *Int. J. Syst. Evol. Microbiol.* 56: 2437-2441.

**[0016]** In one preferred embodiment, the bacterial species is in the form of a live bacterial population, a lyophilized bacterial population, a non-viable bacterial preparation, or the cellular components thereof. Preferably, where the bacterial species is in the form of a non-viable bacterial preparation, it is selected from heat-killed bacteria, irradiated bacteria and lysed bacteria.

**[0017]** In one preferred embodiment, the bacterial species is in the form of live bacteria or the cellular components thereof.

**[0018]** In one preferred embodiment, the bacterial species is in isolated form. As used herein, the term "isolated" means isolated from its native environment.

**[0019]** In one preferred embodiment, the bacterial species is in biologically pure form. As used herein the term "biologically pure" refers to a laboratory culture that is substantially free from other species of organism. Preferably, the bacterial species is in the form of a culture of a single species of organism.

**[0020]** The invention also encompasses the use of mutants of the bacterial species or strains described herein. As used herein, the term "mutant" includes derived bacterial strains having at least 96% homology, more preferably 98% homology to the polynucleotide sequence of a referenced strain, but otherwise comprising mutations in other sequences in the bacterial genome. Mutants are obtainable by genetic engineering techniques inferring alteration of the genetic material of the strains of the invention or inferring a recombination of the genetic material of the strains of the invention with other molecules. Typically, in order to obtain such mutant strains, a person skilled in the art can use standard mutagenesis techniques such as UV radiation or exposure to mutagenic chemical products.

**[0021]** As used herein, the term "mutations" includes natural or induced mutations comprising at least single base alterations including deletions, insertions, transversions, and other modifications known to those skilled in the art, including genetic modification introduced into a parent nucleotide or amino acid sequence whilst maintaining at least 95% homology with the parental sequence. As used herein, sequence "homology" can be determined using standard techniques known to those skilled in the art. For example, homology may be determined using the on-line homology algorithm "BLAST" program, publicly available at <http://www.ncbi.nlm.nih.gov/BLAST/>.

**[0022]** The invention also encompasses the use of homologues of the bacterial species or strains described herein. As used herein the term "homologue" refers to a bacterial strain having a nucleotide sequence having a degree of sequence identity or sequence homology with the nucleotide sequence of the parent bacterial strain (hereinafter referred to as a "homologous sequence(s)"). Here, the term "homologous" means an entity having a certain homology with the subject nucleotide sequence. Here, the term "homology" can be equated with "identity".

**[0023]** In the present context, a homologous sequence is taken to include a nucleotide sequence which may be at least 95%, 97%, 98% or 99% identical to the nucleotide sequence of the parent bacterial strain (the subject sequence).

**[0024]** Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These commercially available computer programs can calculate % homology between two or more sequences. % homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence is directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues.

**[0025]** Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus potentially resulting in a large reduction in % homology when a global alignment is performed.

**[0026]** Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the Vector NTI (Invitrogen Corp.). Examples of software that can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel et al 1999 Short Protocols in Molecular Biology, 4th Ed - Chapter 18), BLAST 2 (see FEMS Microbiol Lett 1999 174(2): 247-50; FEMS Microbiol Lett 1999 177(1): 187-8), FASTA (Altschul et al 1990 J. Mol. Biol. 403-410) and AlignX for example. At least BLAST, BLAST 2 and FASTA are available for offline and online searching (see Ausubel et al 1999, pages 7-58 to 7-60). Preferably, the degree of identity with regard to a nucleotide sequence is determined over at least 20 contiguous nucleotides, preferably over at least 30 contiguous nucleotides, preferably over at least 40 contiguous nucleotides, preferably over at least 50 contiguous nucleotides, preferably over at least 60 contiguous nucleotides, preferably over at least 100 contiguous nucleotides. Preferably, the degree of identity with regard to a nucleotide sequence may be determined over the whole sequence.

**[0027]** The traditional identification of bacteria on the basis of phenotypic characteristics is generally not as accurate as identification based on genotypic methods. Comparison of the bacterial 16S rRNA gene sequence has emerged as a preferred genetic technique and allows for new strains to be identified by comparison of sequences with known bacterial DNA sequences using BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). The 16S rRNA gene sequence is universal in bacteria, and so relationships can be measured across many different bacteria. In general, the comparison of the 16S rRNA sequence allows differentiation between organisms at the genus level across all major phyla of bacteria, in addition to classifying strains at multiple levels, including species and sub-species level. The 16S rRNA gene sequence has been determined for a large number of strains. GenBank, the largest databank of nucleotide sequences, has over 20 million deposited sequences, of which over 90,000 are of 16S rRNA genes. This means that many previously deposited sequences exist against which the

sequence of an unknown strain can be compared.

**[0028]** As used herein the term "16S rRNA identity" refers to the percentage identity with a known bacterial strain. In one preferred embodiment, the bacterial strain has a 16S rRNA identity of at least 99.5% with the strain deposited under the above accession number.

**[0029]** The invention also encompasses mutant strains, which can be obtained from the above-mentioned deposited strain, and strains exhibiting a DNA-DNA homology of at least 95 % and/or a 16S RNA identity of at least 99.5 % with the strain deposited under the above accession number.

**[0030]** In the context of the present invention, the term "DNA-DNA homology" refers to how closely related two or more separate strands of DNA are to each other, based on their nucleotide sequence. Typically, this is measured in terms of their % identity. In one preferred embodiment, the bacterial strain has a DNA-DNA homology of at least 95% with the strain deposited under the above accession number.

**[0031]** In one highly preferred embodiment, the bacterial strain has a DNA-DNA homology of at least 95% and a 16S rRNA identity of at least 99.5% with the strain deposited under the above accession number.

### **Therapeutic Applications**

**[0032]** Another aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 for use in medicine.

**[0033]** More particularly, the bacterial strain is for use in treating a disorder selected from an inflammatory disorder, an immune disorder and an intestinal disorder in a subject.

**[0034]** As used herein, the term "medicament" encompasses medicaments for both human and animal usage in human and veterinary medicine. In addition, the term "medicament" as used herein means any substance, which provides a therapeutic and/or beneficial effect. The term "medicament" as used herein is not necessarily limited to substances, which need Marketing Approval, but may include substances which, can be used in cosmetics, nutraceuticals, food (including feeds and beverages for example), probiotic cultures, nutritional supplements and natural remedies. In addition, the term "medicament" as used herein encompasses a product designed for incorporation in animal feed, for example livestock feed and/or pet food.

**[0035]** In one preferred embodiment of the invention, the disorder is selected from irritable

bowel syndrome (IBS), colitis, inflammatory bowel disorder (IBD), including Crohn's disease and ulcerative colitis, pouchitis, functional dyspepsia, functional constipation, functional diarrhoea (including antibiotic associated diarrhoea, traveller's diarrhoea and pediatric diarrhoea), functional abdominal pain, functional bloating, Epigastric Pain Syndrome, Postprandial Distress Syndrome, gastrointestinal reflux disease (GERD), autoimmune diseases such as diabetes, arthritis, multiple sclerosis and psoriasis allergies, atopic diseases e.g. atopic dermatitis, necrotising enterocolitis, other infections, and combinations thereof.

**[0036]** In one particularly preferred embodiment, the disorder is an inflammatory disorder. Preferably, the expression of pro-inflammatory genes is downregulated in the host subject. Further details of these studies are presented below.

**[0037]** More preferably, the inflammatory disorder is colitis, even more preferably, Crohn's disease, ulcerative colitis or pouchitis.

**[0038]** In one particularly preferred embodiment, the intestinal disorder is IBS. The precise pathophysiology of IBS remains to be elucidated. Recent studies have described mucosal inflammation and alterations in intestinal microbiota in IBS patients and a disease correlation with intestinal infections.

**[0039]** In one particularly preferred embodiment, the intestinal disorder is IBD. Preferably, the expression of barrier genes is enhanced in the host subject. Further details of these studies are presented below.

**[0040]** In one particularly preferred embodiment, the intestinal disorder is Crohn's disease.

**[0041]** In one particularly preferred embodiment, the disorder is an immune disorder. Preferably, the immune disorder is selected from ulcerative colitis, pouchitis, other autoimmune conditions including rheumatoid arthritis, psoriasis, multiple sclerosis, allergies, including coeliac disease, atopic dermatitis and rhinitis.

**[0042]** In one embodiment, the bacterial strain is for use in regulating the immune system of a subject. Immune regulation by bacterial species is known to be highly species-specific (8). In particular, the immune regulatory effect of Cluster XIVa and VI bacteria is very complicated, and independent of butyrate production (41).

**[0043]** In one preferred embodiment, the innate immune system of the subject is modulated.

**[0044]** In another preferred embodiment, the adaptive immune system of the subject is modulated towards immune regulation (and not immune activation, therefore reducing inflammation).

**[0045]** Another aspect of the invention relates to the bacterial strain for improving intestinal microbiota in a subject.

**[0046]** Intestinal microbiota refers to microorganisms that live in the digestive tract of the host animals. These microorganisms perform a wide variety of metabolic, structural, protective and other beneficiary functions. As used herein, "improving intestinal microbiota" refers to increasing the number and/or or type of microorganisms present in the intestine of a host, and/or increasing the activity of said microorganisms in terms of their metabolic, structural, protective and other beneficiary functions.

**[0047]** Preferably, the bacterial strain colonizes the colon and/or the ileum, more preferably the colon.

**[0048]** In one preferred embodiment, the bacterial strain regulates the expression of at least one mobilization or chemotaxis gene.

**[0049]** More preferably, the bacterial strain upregulates the expression of at least one mobilization or chemotaxis gene. More preferably still, the mobilization or chemotaxis gene is selected from *MobA* and *MobL*.

**[0050]** In another preferred embodiment, the bacterial strain regulates the expression of at least one gene selected from *FlaA1*, *FlaA2*, *Fla3* and *FlaB*.

**[0051]** Specific serum antibodies to FLA type proteins are present in inflammatory bowel disease. Thus, in one preferred embodiment, the bacterial strain is for use in treating inflammatory bowel disease.

**[0052]** In another preferred embodiment, the bacterial strain regulates the expression of one or more of the following: acetyl-CoA acetyltransferase, 3-hydroxyacyl-CoA dehydrogenase, butyryl-CoA dehydrogenase, electron transfer flavoprotein beta subunit, and electron transfer flavoprotein alpha subunit.

**[0053]** Another aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 for regulating the innate immune system of a subject.

**[0054]** As used herein, the term "innate immune system", also known as the non-specific immune system, comprises the cells and mechanisms that provide the host with immediate defence against infection by other organisms in a non-specific manner. This means that the cells of the innate system recognize and respond to pathogens in a generic way, but unlike the adaptive immune system, it does not confer long-lasting or protective immunity to the host.

**[0055]** As used herein, the term "regulating the innate immune system" means inducing the activity of the innate immune system, and/or increasing the level of activity relative to the

baseline level of activity such that it promotes immune homeostasis.

**[0056]** Loss or dysregulation of the innate immune function, either due to loss of epithelial barrier, innate immune peptides such as defensins, chemokines and cytokines or defective TLR signalling are associated with increased risk of inflammatory diseases, in several body organs including the gut. Such diseases include inflammatory bowel disease. Thus, in one highly preferred embodiment, the *Roseburia hominis* is for use in treating inflammatory bowel disease.

**[0057]** In one preferred embodiment, the bacterial strain regulates the expression of at least one gene selected from *Tlr5*, *Tlr1*, *Vnn1*, *Defb37*, *Pla2g*, *Muc16*, *Itln*, *Sprr1a*, *Cldn4*, *Pmp22*, *Crb3*, *Magi3*, *Marveld3*, *Mpp7*, *Defcr20*, *Pcgf2*, *Ltbp4*, *Igsf8* and *Tcfe2a*. Many of these genes are gut barrier genes and antimicrobials and hence work to reduce invasiveness of gut pathogens and also reduce the numbers of viable pathogens.

**[0058]** Another aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029 for regulating the adaptive immune system of a subject.

**[0059]** As used herein, the term "adaptive immune system", otherwise known as the "specific immune system" refers to highly specialized, systemic cells and processes that eliminate or prevent pathogenic growth. The adaptive immune response provides the vertebrate immune system with the ability to recognize and remember specific pathogens (to generate immunity), and to mount stronger attacks each time the pathogen is encountered.

**[0060]** As used herein, the term "regulating the adaptive immune system" means inducing the activity of the adaptive immune system, and/or promoting immune homeostatic mechanisms by increasing the level of activity relative to the baseline level of activity. Preferably, the adaptive immune system is modulated towards immune regulation (and not immune activation therefore reducing inflammation).

**[0061]** Defects and disorders associated with the adaptive immune system, particularly related to the function of T cells, are associated with many inflammatory and autoimmune diseases. T cell responses associated with Th1, Th2 and Th17 are associated with atopic, inflammatory and autoimmune diseases. Therapies which improve or increase T regulatory (Tregs) cell populations are important in controlling diseases driven by excessive Th1, Th2 and Th17 cell responses.

**[0062]** In one preferred embodiment, the bacterial strain activates at least one immune response gene in the colon or ileum.

**[0063]** In one preferred embodiment, the bacterial strain regulates the adaptive immune

system by modulating the expression of genes associated with T-cell regulation, more preferably in the colon. More preferably, the bacterial strain induces Tregulatory cells (Tregs). An increase in Treg numbers will combat the effects of other effector T cells, such as Th1, Th17 and Th2 which drive inflammation, autoimmunity and allergic/atopic conditions. Hence this property of the bacterial strain can be exploited to address many diseases where Teff/Treg cell balance is lost, e.g. Crohn's and ulcerative colitis

**[0064]** In one particularly preferred embodiment, the bacterial strain upregulates the expression of at least one gene selected from *Ly6g6c* and *Ly6g6e* in the ascending colon. Depletion of *Ly6g6c* and *Ly6g6e* increases infection risk, both gut and respiratory tract and is associated with diseases such as neutropenia. Thus, in one preferred embodiment, the bacterial strain is for use in treating neutropenia.

**[0065]** Another aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, for use in maintaining immune homeostasis in a subject. As used herein "maintaining immune homeostasis" refers to the self-regulation of the body's immune system to maintain oral tolerance or immune stability in response to changing conditions. Oral tolerance refers to the normal immune responses to food and commensal bacteria in a healthy gut. These are lost in coeliac disease and Inflammatory Bowel Diseases such as Crohn's disease and ulcerative colitis. Thus, in one particularly preferred embodiment, the bacterial strain is for use in treating coeliac disease and Inflammatory Bowel Diseases such as Crohn's disease and ulcerative colitis.

**[0066]** Another aspect of the invention relates to a bacterial strain having (a) a 16S rRNA identity of at least 99.5% with the strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, or (b) a DNA-DNA homology of at least 95% identity to the bacterial strain belonging to the species *Roseburia hominis* deposited under accession number NCIMB 14029, for use in regulating appetite in a subject.

**[0067]** As used herein, "regulating appetite" refers to the ability to modulate (i.e. increase or decrease) the desire for a host to eat food. Preferably, the bacterial strain exerts a stimulatory effect on host appetite by downregulating the expression of genes associated with the suppression of appetite. Preferably, the bacterial strain downregulates the expression of at least one gene selected from *Agt*, *Cartpt*, *Cck*, *Cxcl12* and *Gcg*. More preferably, the bacterial strain downregulates, the expression of the satiety hormones *Cck* and *Gcg*.

**[0068]** The bacterial strain according to the invention may also be used in prophylactic applications. In prophylactic applications, bacterial species or compositions according to the invention are administered to a patient susceptible to, or otherwise at risk of, a particular disease in an amount that is sufficient to at least partially reduce the risk of developing a disease. Such an amount is defined to be "a prophylactic effective dose". The precise amounts

depend on a number of patient specific factors such as the patient's state of health and weight.

**[0069]** The present invention is further described by way of the following figures, wherein:

Figure 1 shows the abundance and localization of *R. hominis* in ascending colon. (A) *R. hominis*-colonized mouse ascending colon showing close association of bacteria with the host epithelium, using the A2-183 FISH probe. Original magnification x630. (B) PCR using *R. hominis*-specific primers showed a strong positive signal in faecal DNA post-colonization, while faeces of GF animals were negative for the presence of any bacteria. (C) Real-time PCR analysis showing colonization levels of *R. hominis*/mg faeces.

Figure 2 shows the sequence and annotation of *R. hominis* genome. (A) *R. hominis* circular genome map with the location of the PCR experiments indicated in the regions targeted by the primers. The tracks on the genome map, starting at the outer track 0, are: track 0 - (blue) Real-time PCR experiments indicated by numbered tick marks; track 1 - (pale blue) Forward CDS; track 2 - (pale blue) Reverse CDS; track 3 - (blue) rRNA; track 4 - (green) tRNA; track 5 - (red) STS marking regions targeted by Real-time PCR; graph 1 - GC content; graph 2 - GC bias. (B) Functional annotation of the *R. hominis* genome.

Figure 3 identifies transcripts differentially expressed in *R. hominis* after colonization and adaptation to the murine gut. (A) Bacterial RNA was isolated from mouse caecum contents, labeled with either dCTP-Cy3 or dCTP-Cy5 during cDNA synthesis and hybridized to microarray slides incorporating a dye swap. Data was considered significant when fold change > 2 and  $P < 0.05$ . 50 differentially expressed genes (*in vivo* vs. *in vitro*) were uncovered by microarray analysis. (B) Real-time PCR validation of genes involved in conjugation/mobilization transfer. (C) Real-time PCR validation of genes involved in Motility and Chemotaxis. (D) Western blot of ascending gut contents immuno-stained with affinity-purified Fla2 antibody at 14d (lane 1: ladder, lanes 2-6: gut contents from animals 1-5, lanes 7-8: empty, lanes 9-10: *R. hominis* biomass (positive control)). Picture of *R. hominis* showing flagella (black arrows) and (E) Real-time PCR validation of genes involved in butyrate metabolism. (F) Real-time PCR analysis of *R. hominis* transcripts during *in vitro* exposure to human intestinal epithelial cells. Real-time PCR results are means of triplicates, \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

Figure 4 identifies transcripts differentially expressed in the murine gut after mono-association with *R. hominis*. (A) Affymetrix microarray analysis of differentially expressed genes *R. hominis*-colonized mice relative to GF. Bar graphs represent number of genes higher and lower expressed after 14 and 28 days. (B) Heatmap generated from differentially expressed genes with functional significance - between GF and *R. hominis*-colonized mice at 14d and 28d. Columns represent individual arrays, and rows specific genes of interest. The Z-score depicts a measure of distance, in standard deviations, away from the mean. The relative value for each gene is depicted by colour intensity, with green indicating higher expression and red depicting lower expression. (C) Real-time PCR validation of genes shown to be significantly different between *R. hominis*-colonized and GF mice. Real-time PCR results are means of triplicates, \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

Figure 5 shows expression and localization of T cell markers in colon. Immunofluorescence and analysis of lamina propria cells labeled with anti-Ly6G (A), anti-CD3 (B) and anti-CD11b (C) in lamina propria of GF mice and *R. hominis*-treated mice. \* $P < 0.05$ .

Figure 6 shows the anti-inflammatory effects of *R. hominis* in an experimental model of colitis. IL-10KO mice were dosed three times a week for 14 weeks. (A) Untreated IL-10KO mice had strong elevation of all genes compared to wild-type mice, while differential gene expression was lower in *R. hominis*-treated animals. Real-time PCR results are means of triplicates, \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ . (B) Bodyweights of untreated IL-10KO and *R. hominis*-treated IL-10KO animals at the end of the study. (C) Ascending colon (haematoxylin/eosin stained) of IL-10KO and *R. hominis*-treated IL-10KO animals. Original magnification x100.

Figure 7 shows real-time PCR analysis of mRNA levels of IL-10, IL-17 and IFN- $\gamma$ . Real-time PCR was performed on ascending colon tissue for measurement of T cell markers. Real-time PCR results are means of triplicates, \* $P < 0.05$ , \*\* $P < 0.01$ .

Figure 8 shows the effects of mono-association of GF mice with *R. hominis* on body weight composition. Dry body weight and lipid carcass analysis was performed. (A) Dry carcass weights of *R. hominis*-associated mice were significantly heavier compared to GF animals. (B) Further carcass lipid analysis showed that total adiposity was also significantly higher in *R. hominis*-treated animals at 14d.

Figure 9 illustrates a comparison of gene expression data for three strains of bacteria from Cluster XIVa (Firmicutes), namely *Roseburia hominis*, *E. rectale* and *Roseburia intestinalis*.

Figure 10 shows that *Roseburia hominis* induces A20, a negative regulator of NF- $\kappa$ B signaling with potent anti-inflammatory activity, whereas other bacterial strains have no effect. The flagellin moiety of *Roseburia hominis* (FLA1 of *R. hominis*) also induces A20 unlike that of *Eubacterium rectale*, a related bacterium. In more detail, Figure 10 shows the fold-induction of A20 for *E. rectale*, *R. hominis*, FLA of *E. rectale*, FLA1 of *R. hominis*, EAV9, FLA of SV1400 relative to controls.

Figure 11 shows the Subsystem Category Distribution for *R. hominis* A2-183 as determined by RAST, showing functional subsystems and the number of genes in each subcategory.

Figure 12 shows the Subsystem Category Distribution for *R. inulinivorans* DSM 16841 A2-183 as determined by RAST, showing functional subsystems and the number of genes in each subcategory.

Figure 13 shows the Subsystem Category Distribution for *R. intestinalis* L1-82 as determined by RAST, showing functional subsystems and the number of genes in each subcategory.

Figure 14 shows the Subsystem Category Distribution for *R. intestinalis* M50/1 as determined by RAST, showing functional subsystems and the number of genes in each subcategory.

Figure 15 shows the Subsystem Category Distribution for *Eubacterium rectale* ATCC 33656 as determined by RAST, showing functional subsystems and the number of genes in each

subcategory.

### ***R. hominis* preferentially colonizes the colon**

**[0070]** Healthy adult C3H/HeN germfree (GF) mice were inoculated with three gavages of *R. hominis* on consecutive days. Successful colonization was achieved using an inoculation medium containing 3% ascorbic acid and 2% cysteine to protect the bacterium from oxygen exposure. Analysis of gut tissue by fluorescent *in situ* hybridization (FISH) revealed that *R. hominis* colonized both the ileum and colon, but was found in much higher numbers in the colon. Bacteria were also found closely associated with the colonic mucosa (Fig. 1A). Colonization was further validated and quantified by PCR using *R. hominis*-specific primers with numbers approximating  $1 \times 10^{10}$  bacteria/g faeces (Fig. 1B and 1C). Faeces of GF animals tested negative for the presence of any bacteria.

### **The *R. hominis* genome reveals unique genes promoting host interactions**

**[0071]** The complete genome sequence of *R. hominis* A2-183 was elucidated (Fig. 2A, which is represented by a single 3,592,125-bp chromosome (Fig. 2B). Automated and manual annotation of the genome using the RAST platform revealed the presence of four ribosomal operons, 66 RNAs and 3,273 predicted proteins. The largest group of genes belonged to the Subsystem Category Carbohydrates (271 genes), encoding proteins involved in carbohydrate metabolism, followed by Protein Metabolism (197) and Amino acids and Derivatives (175) (Fig. 2B). Other important functional categories included Motility and Chemotaxis (49) and Dormancy and Sporulation (12). Comparative genomic analysis established that the closest relative in terms of genomic structure and function among the complete bacterial genomes is *Eubacterium rectale* (12), which is not surprising given the close taxonomical relatedness of these organisms (11, 13). Comparative reconstruction of these two genomes with 1,095 genes revealed that they differed by approximately 25% of the genes. In particular, these differences encompassed genes encoding important functions for interaction with the host. For example, the Motility and Chemotaxis genes encoding type IV fimbrial assembly proteins PilB and PilC were present in *E. rectale* but absent in *R. hominis* whereas flagellar basal-body rod protein FlgC, flagellar hook-basal body complex protein FliE, flagellin protein FlaB and flagellar motor switch protein FliG were unique to *R. hominis*. The two bacterial genomes also differed by 42 carbohydrate genes, reflecting their divergent nutritional requirements.

### ***R. hominis* responds to the gut environment by up-regulating mobilization and chemotaxis genes**

**[0072]** To determine the genes differentially expressed by *R. hominis* in response to association with the host and diet, a microarray was constructed using 6,000 PCR fragments from the small-insert-size sequencing library. Subsequent Real-time PCR validation was performed on 42 differentially expressed genes which cluster at specific regions of the *R. hominis* genome as illustrated in Fig. 2B. To distinguish between the effects of gut environment and dietary components, bacterial RNA was isolated from four different experimental conditions: (i) *in vivo*, from the caecum of mono-associated mice; (ii) *in vitro*, from bacteria grown in culture media; (iii) *in vitro*, from bacteria grown in the presence of dietary components; and (iv) from bacteria incubated on the surface of confluent Caco-2 and HT-29 cells.

**[0073]** Fifty differentially expressed genes were identified (*in vivo* vs. *in vitro*) (Fig. 3A). The most surprising discovery was an extremely high up-regulation *in vivo* of genes involved in conjugation/mobilization transfer, the *mobA*- and *mobL*-like genes (Fig. 3B). The presence of such genes in the transcriptional studies was surprising as no identifiable genes were assigned to Phages, Prophages, Transposable Elements and Plasmids in the Subsystem Category feature. This difference in gene detection and allocation is likely due to the recognized limitations of the Subsystem Category annotation. The stimulatory effect of dietary compounds was much less pronounced, suggesting that the gut environment *per se* is a major inducer of genes involved in horizontal gene transfer.

**[0074]** Other gut environment-induced subsystems included Membrane Transport, in particular magnesium transport, and Motility and Chemotaxis including multiple methyl-accepting chemotaxis proteins and genes of the flagellar operon (Fig. 3C). *R. hominis* possesses multiple flagellin genes *flaA1*, *flaA2*, *flaA3*, and *flaB* and interestingly growth in the mouse gut environment promoted flagellin expression in this bacterium as seen by western-blotting of bacteria isolated from *in vivo* colonized mice using *R. hominis*-specific flagellin antibodies (Fig. 3D). This is consistent with previous reports indicating that only certain subsets of Firmicutes produce flagella *in vivo* (14).

Not surprisingly, the expression of catabolic metabolism genes in *R. hominis* in the gut environment was mostly affected by dietary compounds (Fig. 3E). The genes involved included acetyl-CoA acetyltransferase, 3-hydroxyacyl-CoA dehydrogenase, butyryl-CoA dehydrogenase and phosphoenolpyruvate carboxykinase [ATP]. Although the regulation of these genes was mostly diet-driven, at the later sampling point the host effect was also apparent. Unexpectedly, the host environment down-regulated some genes participating in the metabolism of host-derived substances such as glucuronate, which is common in carbohydrate chains of mucosal proteoglycans.

**[0075]** To further investigate the effects of host-adaptation on the *R. hominis* transcriptome, *in vitro* stimulation of human intestinal epithelial cells (Caco-2 and HT-29) was performed. This showed that the conjugation/mobilization transfer gene *mobA/mobL protein1*, which was induced by adaptation to the mouse gut, was also increased in both cell lines (Fig. 3F). Consistent with the *in vivo* data, the flagellin gene *MotA* was upregulated in Caco-2 cells. Genes involved in butyrate metabolism showed differences between the two cell lines, with

downregulation seen in Caco-2 cells and upregulation in HT-29 cells.

### ***R. hominis* affects T cell pathways mostly in the colon**

**[0076]** The colonization of GF mice with *R. hominis* correlated with increased gut gene expression which was highest in the colon. (Fig. 4A). Differential expression was most profound at 28d after colonization, with 159 genes up-regulated and 143 genes down-regulated. The number of differentially expressed genes in the ileum at 14d was similar to the ascending colon, with 79 genes up-regulated and 119 genes down-regulated. Differential expression in the ileum was very low at 28d, consistent with reduced colonization levels. The transcriptomic response differed at the two time-points, as shown by the clear separation of significant transcripts by heatmap analysis (Fig. 4B). Positive Real-time PCR validation of Affymetrix data is shown in Fig. 4C.

**[0077]** The majority of pathways affected at 14d in the ileum and the ascending colon grouped into the categories cell differentiation, cell cycle regulation and tissue remodeling. Importantly, immune response was the major pathway group induced at 28d in the ascending colon. The 36 significantly affected pathways in this category were mostly involved in T cell function and included the IL-10 signaling pathway, the ICOS pathway in T-helper cell and regulation of T cell function by CTLA-4. The genes involved in these pathways showed both up-regulation and down-regulation, so while these pathways were significantly affected by the presence of *R. hominis*, the precise net functional effects on T cell differentiation requires further investigation. However, enhanced IL-10, CD3 $\epsilon$  and IL-13 and changed expression of IFN- $\gamma$  was confirmed by Real-time PCR (Fig. 7), suggesting that *R. hominis* colonization may favor Treg and Th2 cell differentiation pathways. Gene Ontology analysis was applied to obtain additional information on the functional classification of differentially regulated genes. The GO-process for 'actin polymerization' (GO:0030041) (*Arpc3*, *Capg*, *Cdc42ep5* and *Rhoc*) was up-regulated at 28d in the colon in *R. hominis* colonized mice (Fig. 8). Actin polymerization at the immune synapse is required for T cell activation and effector function. Gene induction was further confirmed by Real-time PCR (Fig. 4C). Overall, this data indicates that *R. hominis* actively effects the adaptive immune response in the colon by positively influencing T cell regulation.

**[0078]** Related to these results was the induction of members of the Ly6 family in the ascending colon. In particular, the GPI-anchored gene product of *Ly6g6c* was up-regulated 25-fold, and the related gene *Ly6g6e* was up-regulated two-fold at 28d. Most hematopoietic cells express one or more members of the Ly6 family including neutrophils and plasmacytoid dendritic cells. Furthermore, a possible role of Ly6 in T cell activation, differentiation and maturation has been proposed (15).

**[0079]** Immunocytochemistry confirmed increased presence of Ly6G<sup>+</sup>, CD11b<sup>+</sup> and CD3<sup>+</sup> cells in *R. hominis*-colonized mice (Fig. 5). Consistent with the data showing T cell pathways mainly dominated by Treg responses, was a statistically significant increase in double-positive CD3<sup>+</sup>

FoxP3<sup>+</sup> T cells in the colon of *R. hominis*-inoculated mice. Clearly colonization of *R. hominis*, as a single bacterial species, induced a significant increase in a population of CD3<sup>+</sup> FoxP3<sup>+</sup> cells, particularly in the colon of these mice.

***R. hominis* modulates innate immune response genes in both the ileum and colon and attenuates colitis in IL10KO mice**

**[0080]** Genes involved in innate immunity and gut barrier function were significantly induced by the presence of *R. hominis* in the ascending colon. The GO-process 'innate immune response' (GO:0045087) was up-regulated and included the TLR-related genes *Tlr5*, *Tlr1* and *Vnn1*. The up-regulation of *Tlr5* was interesting, particularly given the corresponding induction of flagellar genes and the presence of flagellin protein in *R. hominis* during gut colonization, and may infer a role for this innate signaling pathway in mediating other innate and adaptive immune responses. The coupling between TLR5 signaling and CD4<sup>+</sup> T cell responses has recently been demonstrated for flagellate pathogens (16). Similarly, the role of TLR2 in facilitating the colonization of *Bacteroides fragilis*, Treg propagation and immune homeostasis has been shown (17).

**[0081]** Other innate immune genes affected in the colon by *R. hominis* included the antimicrobial peptides *Defb37*, *Pla2g3*, *Muc16* and *Itln* and the gut barrier function genes *Sprr1a*, *Cldn4*, *Pmp22*, *Crb3* and *Magi3*. Innate immune genes showing up-regulation in the ileum in response to *R. hominis* included *Defcr20*, *Pcgf2*, *Ltbp4*, *Igsf8* and *Tcfe2a*. Interestingly, *Pcgf2* negatively regulates the expression of different cytokines, chemokines, and chemokine receptors and may play an important role in controlling inflammatory responses in gut tissues in response to this commensal bacterium. Interestingly, we also showed negative regulation of the NF-κB pathway (GO:0043124) by *R. hominis*, which, like *B. thetaiotaomicron* (19), may contribute to immune homeostasis by down-regulating this inflammatory cascade.

**[0082]** The IL-10 knockout mouse model was used to test the therapeutic efficacy of *R. hominis*, due to the control of inflammatory pathways as well as the positive effects on Treg induction in mono-associated mice. Mice were dosed (~50 μl, 10<sup>10</sup>CFU) three times a week from weaning at 20d of age for a period of 14 weeks. Gene expression of a panel of pro-inflammatory biomarkers showed that untreated IL-10KO mice had strong elevation of all investigated genes compared to wild-type mice, with gene induction ranging from 4- to 49-fold (Fig. 6A). Pro-inflammatory gene induction was significantly lower in *R. hominis*-treated compared to untreated mice, indicating strong therapeutic benefits of oral administration of *R. hominis*. Bodyweights of *R. hominis*-treated animals were also heavier at the end of the study compared to untreated animals, and this effect was statistically significant in males (Fig. 6B). Finally, histological analysis showed the presence of severe inflammation in the ascending colon of untreated IL-10KO, while *R. hominis*-treated animals had a relatively healthy-looking colonic mucosa.

***R. hominis* colonization influences satiety genes and body composition**

**[0083]** Significant metabolic actions of *R. hominis* in mono-associated mice were also evident. The GO-processes 'negative regulation of response to food' (GO:0032096), 'negative regulation of appetite' (GO:0032099), and 'regulation of catecholamine secretion' (GO:0050433) were all down-regulated in the ascending colon after colonization with *R. hominis*. This data infers that *R. hominis* exerts a stimulatory effect on host appetite. The genes involved in these processes were *Agt*, *Cartpt*, *Cck* and *Cxcl12*, with fold-changes ranging from 2- to 12-fold. *Cck*, in particular, plays a major role in digestion and satiety as a hunger suppressant. *Gcg* also showed down-regulation at this gut site.

**[0084]** To establish whether these gene changes had physiological relevance in relation to food intake and body composition, dry carcass weight and composition analyses were performed. Interestingly, the dry carcass weights of *R. hominis*-associated mice were significantly heavier compared to GF animals, and the differences were most discernable at 14d. Further carcass lipid analysis showed that total adiposity was also significantly higher in *R. hominis*-treated animals at 14d. These findings are consistent with recent data revealing the role of Firmicutes in energy harvest through dietary fermentation, but also support the notion that gut bacteria can in fact modulate the brain-gut axis and appetite-regulating hormones.

**Discussion**

**[0085]** The long-term co-evolution of host-microbe mutualism has likely driven the selection of functionally important bacterial species in the gut, the majority of which are not highly represented in other ecosystems. Currently, there is limited information regarding the contribution of individual members of the microbial community to intestinal functions, particularly in relation to development of the mucosal immune system.

**[0086]** Recent work using a reversible colonization model based on *E. coli* (HA 107) has demonstrated that live bacteria are required in numbers approaching  $10^8$  CFUs per gram of content for the immune-inducing effects on IgA (20). Recently, the specific functions of SFB and *Bacteroides fragilis* have been investigated in the mouse gut to define their individual contributions to T cell biology and both these bacteria have been shown to be potent inducers of Tregs and Th17 cells (5, 8, 9). The effects of individual members of the cluster XIVa Firmicutes have not been reported previously, although their presence in the ASF, which also affects T cell differentiation has been noted (10).

**[0087]** The applicant has demonstrated herein the first successful mono-association of the germ-free mouse gut with an anaerobic bacterium, *R. hominis*, which is a member of the Firmicutes phylum. The extreme oxygen sensitivity of bacteria like Roseburia requires strict anaerobic culture techniques, making it difficult to perform functional characterization. The

applicant established stable mono-colonization of *R. hominis* in germfree mice and produced the complete annotated genomic sequence to uncover its metabolic organization, physiology, and symbiotic properties. It was found that the transcriptional responses of *R. hominis* following colonization could be attributed to both the host gut environment and diet. The host-driven effects dominated the response of *R. hominis* following mono-association. These included gene transfer, membrane transport, chemotaxis and motility subsystems. The strong up-regulation of genes involved in mobilization transfer supports the view that the gut environment is highly conducive to horizontal gene exchange between members of the gut microbiota. Thus, this environment may accelerate the dissemination of genes important for bacterial survival, colonization and function within the gut ecosystem.

**[0088]** The role of motility and flagellar apparatus in host colonization is well-elaborated for pathogenic bacteria but much less is known about the role of flagellar proteins in commensal bacteria. *In vivo* experiments revealed a stimulatory effect of the host intestinal environment on the expression of flagellin genes. Flagellin signals are perceived by host TLR5 receptors (24) and many pathogenic flagellin structures induce strong pro-inflammatory responses (24). Signaling through TLR5 in response to by resident flagellated commensals may be important for homeostasis, since deletion of TLR5 results in spontaneous colitis in mice (25). The enhanced expression of *R. hominis* flagellin *in vivo* is therefore of potential interest. Other work has shown that *E. coli* flagellin mutants have a colonization advantage over wild-type flagellated strains, possibly due to absence of innate recognition by TLR5 signaling (26, 27). The applicant has shown that for certain Firmicutes, upregulation of flagellin is a natural response to gut colonization. *R. hominis* flagellin protein remains expressed *in vivo* and correlates with sustained colonization, absence of overt inflammation and expansion of T cells of regulatory phenotype. Hence, commensal flagellin structures through TLR5 may help direct immune tolerance responses. Additional data based on TLR5KO and flagellin mutants of *R. hominis* will further clarify the importance of commensal flagellins in relation to immune homeostasis but the observed protective effect of *R. hominis* in IL-10 KO mice supports this hypothesis, although other signaling moieties such as butyrate may also contribute to immune regulation.

**[0089]** A clear role was established for *R. hominis* in promoting gut barrier function and innate immunity in the mouse colon. Tight junctions, gap junctions and adherens junctions operate to limit bacterial translocation to the subepithelial layer (28). Both Crohn's disease and ulcerative colitis are characterized by loss of barrier function and tight junction integrity. Interestingly, dysbiosis of the gut microbiota in IBD is associated with a reduction in Firmicutes (1, 29). The observation that *R. hominis* actively enhances the expression of barrier genes suggests that their loss in IBD patients may be functionally significant. Activation of tight junction complexes is not just the prerogative of *R. hominis*; other commensals, such as *Bacteroides thetaiotaomicron* and *Lactobacillus acidophilus*, also enhance mucosal barrier function (18, 30), inferring probiotic opportunities with these bacteria in human IBD.

**[0090]** The effects of *R. hominis* on the gut immune system were intriguing. The strongest effects were noted in the ascending colon and genes such as *Ly6g6c* were strongly up-

regulated, as well as pathways involved in T cell regulation and differentiation and actin polymerization at the immune synapse, which are implicated in T cell activation and effector functions. Although the expression of Treg genes in response to *R. hominis* colonization was not very strong, the most affected T cell pathways included those related to IL-10, ICOS and CTLA-4, which are all involved in supporting Treg differentiation. Importantly, the applicant was able to demonstrate significant increases in CD3<sup>+</sup>FoxP3<sup>+</sup> cells in the colons of these mice. These findings complement the recent data on other Clostridium species that drive Treg differentiation. Clearly, *R. hominis* can promote mucosal T cell expansion and impacts on T cell differentiation.

**[0091]** It was interesting to note the strong immune effects in the colon compared to the ileum, especially at 28d after mono-colonization with *R. hominis*. The transcriptomic data at 14d suggests that some immune priming could be initiated in ileum at this time-point. The effects on the different T cell subsets in the ascending colon at 28d may thus reflect a trafficking and homing of cells from ileum to mesenteric lymph node to the colon.

**[0092]** An interesting additional biological effect of *R. hominis* colonization was the regulation of genes influencing responses to food and control of appetite. In particular, the satiety hormones *Cck* and *Gcg* were significantly reduced. The effects of *Cck* on food intake are mediated via a vagal afferent pathway. This is the major neural pathway by which information about ingested nutrients reaches the central nervous system to influence both gut function and feeding behavior. *Cck* acts on the vagal system to decrease expression of molecules that stimulate appetite and feeding, and to increase expression of molecules that inhibit feeding and decrease appetite (*Npy2r* and *Cartpt*, both down-regulated two-fold in the current study). No link between *Cck*, *Gcg* and commensal bacteria has been reported thus far, however, both fatty acids and proteins are potent inducers of *Cck* and *Gcg* (31). *R. hominis* produces short-chain fatty acids such as butyrate with aliphatic tails of less than six carbons; this metabolic activity has been reported to reduce the stimulatory effect on plasma *Cck* observed with longer chain fatty acids (32). Interestingly, carcass weight analysis revealed that both body weight and lipid content was indeed significantly increased with *R. hominis*, consistent with body weight increases observed in conventionalization of germfree mice (33). Whether this is a direct effect of a reduction in satiety hormones as seen in the current study remains to be seen, as the involvement of *Cck* and *Gcg* has not been reported previously. However, it is important to acknowledge that a link between microbiota colonization and energy harvest from the diet, in part through release of SCFAs, has been shown previously (34). Given that *R. hominis* is a major butyrate producer, this mechanism is likely also to contribute to the metabolic efficiency observed following *R. hominis* treatment.

**[0093]** In summary, mono-association of the murine gut with *R. hominis* induced strong bidirectional gene expression events consistent with changes in bacterial membrane transport, chemotaxis and motility of this gut-adapted bacterium and a concomitant activation of the innate and adaptive immune system of the host. This metabolically active bacterium also exerted important effects on appetite and satiety genes which correlated with enhanced body weight gain in colonized mice.

## Compositions

**[0094]** Another aspect of the invention relates to a composition comprising a bacterial strain as defined in the claims and a pharmaceutically acceptable excipient, carrier or diluent. Suitable excipients, diluents, carriers are described below.

**[0095]** The composition may be any composition, but is preferably a composition to be administered orally, enterally or rectally. For example, the composition may be an edible composition. "Edible" means a material that is approved for human or animal consumption.

**[0096]** Another aspect of the invention relates to a probiotic composition comprising a bacterial strain as defined in the claims.

**[0097]** As used herein, the term "probiotic" means microbial cell preparations or components of microbial cells with a beneficial effect on the health or well-being of the host. (Salminen S, Ouwehand A, Benno Y. et al "Probiotics: how should they be defined" Trends Food Sci. Technol. 1999:10 107-10).

**[0098]** Preferably, the probiotic composition is an orally administrable composition of metabolically active, i.e., live and/or lyophilized, or non-viable heat-killed, irradiated or lysed probiotic bacteria. The probiotic composition may contain other ingredients. The probiotic composition of the invention can be administered orally, i.e., in the form of a tablet, capsule or powder. Encapsulated products are favoured for *R. hominis* as it is an anaerobe. Other ingredients (such as vitamin C, for example), may be included as oxygen scavengers. Prebiotic substrates such as these improve the colonisation and survival *in vivo*. Alternatively, the probiotic composition of the invention may be administered orally as a food or nutritional product, such as milk or whey based fermented dairy product, or as a pharmaceutical product.

**[0099]** A suitable daily dose of the probiotic bacteria is from about  $1 \times 10^3$  to about  $1 \times 10^{11}$  colony forming units (CFU), more preferably from about  $1 \times 10^7$  to about  $1 \times 10^{10}$  CFU, more preferably, about  $1 \times 10^6$  to about  $1 \times 10^{10}$  CFU.

**[0100]** In one preferred embodiment, the composition contains the bacterial strain and/or cellular components thereof, as active ingredients, in an amount of from about  $1 \times 10^6$  to about  $1 \times 10^{11}$  CFU/g, respect to the weight of the composition, preferably from about  $1 \times 10^8$  to about  $1 \times 10^{10}$  CFU/g. The dose may be of 1 g, 3 g, 5 g, and 10 g.

**[0101]** Typically, a probiotic is optionally combined with at least one suitable prebiotic compound. A prebiotic is usually a non-digestible carbohydrate such as an oligo- or polysaccharide, or a sugar alcohol, which is not degraded or absorbed in the upper digestive

tract. Known prebiotics include commercial products such as inulin and transgalactooligosaccharides.

**[0102]** Preferably, the composition of the present invention includes a prebiotic in an amount of from about 1 to about 30% by weight, respect to the total weight composition, preferably from 5 to 20% by weight. Preferred carbohydrates are selected from: fructo-oligosaccharides (or FOS), short-chain fructo-oligosaccharides, inulin, isomalt-oligosaccharides, pectins, xylo-oligosaccharides (or XOS), chitosan-oligosaccharides (or COS), beta-glucans, arable gum modified and resistant starches, polydextrose, D-tagatose, acacia fibers, carob, oats, and citrus fibers. Particularly preferred prebiotics are the short-chain fructo-oligosaccharides (for simplicity shown hereinbelow as FOSs-c.c); said FOSs-c.c. are not digestible carbohydrates, generally obtained by the conversion of the beet sugar and including a saccharose molecule to which three glucose molecules are bonded.

### **Feedstuffs/products**

**[0103]** A further aspect of the invention relates to food products, dietary supplements, nutraceuticals, nutritional formulae, drinks and medicaments containing a bacterial strain as defined above, and use thereof.

**[0104]** In one preferred embodiment, the composition comprises additionally at least one other kind of other food grade bacterium, wherein the food grade bacterium is preferably selected from the group consisting of lactic acid bacteria, bifidobacteria, propionibacteria or mixtures thereof.

**[0105]** One aspect of the invention relates to a food product comprising the bacterial strain defined above. The term "food product" is intended to cover all consumable products that can be solid, jellied or liquid. Suitable food products may include, for example, functional food products, food compositions, pet food, livestock feed, health foods, feedstuffs and the like. In one preferred embodiment, the food product is a health food.

**[0106]** As used herein, the term "functional food product" means food that is capable of providing not only a nutritional effect, but is also capable of delivering a further beneficial effect to the consumer. Accordingly, functional foods are ordinary foods that have components or ingredients (such as those described herein) incorporated into them that impart to the food a specific functional - e.g. medical or physiological benefit - other than a purely nutritional effect.

**[0107]** Examples of specific food products that are applicable to the present invention include milk-based products, ready to eat desserts, powders for re-constitution with, e.g., milk or water, chocolate milk drinks, malt drinks, ready-to-eat dishes, instant dishes or drinks for humans or food compositions representing a complete or a partial diet intended for pets or livestock.

**[0108]** In one preferred embodiment the composition according to the present invention is a

food product intended for humans, pets or livestock. The composition may be intended for animals selected from the group consisting of dogs, cats, pigs, cattle, horses, goats, sheep or poultry. In a preferred embodiment, the composition is a food product intended for adult species, in particular human adults.

**[0109]** In the present invention, "milk-based product" means any liquid or semi-solid milk or whey based product having a varying fat content. The milk-based product can be, e.g., cow's milk, goat's milk, sheep's milk, skimmed milk, whole milk, milk recombined from powdered milk and whey without any processing, or a processed product, such as yoghurt, curdled milk, curd, sour milk, sour whole milk, butter milk and other sour milk products. Another important group includes milk beverages, such as whey beverages, fermented milks, condensed milks, infant or baby milks; flavoured milks, ice cream; milk-containing food such as sweets.

**[0110]** One aspect of the invention relates to a feedstuff or animal feed comprising the bacterial strain defined above.

**[0111]** The compositions of the present invention may be - or may be added to - food supplements, also referred to herein as dietary or nutritional supplements or food additives. Thus, another aspect of the invention relates to a dietary supplement or food additive comprising one or more bacterial strains according to the invention.

**[0112]** The bacterial strain and probiotic compositions according to the invention may also be used in animal nutrition (e.g. in pig nutrition), particularly in the early-weaned period and growing fattening period. The probiotics are expected to enhance immune function reduce and prevent infectious diseases, beneficially alter the microbiota composition, and improve growth and performance of animals, for example, through increased feed conversion efficiency.

#### **Diluents, excipients and carriers**

**[0113]** As mentioned above, the invention also relates to compositions, more preferably pharmaceutical compositions or nutritional supplements, comprising the bacterial strain defined above, and use thereof. The bacterial strain is generally administered in admixture with a pharmaceutically or nutritionally acceptable carrier, excipient or diluent, particularly for human therapy. The pharmaceutical compositions may be for human or animal usage in human and veterinary medicine.

**[0114]** Examples of such suitable excipients for the various different forms of pharmaceutical compositions described herein may be found in the "Handbook of Pharmaceutical Excipients, 2nd Edition, (1994), Edited by A Wade and PJ Weller.

**[0115]** Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co. (A. R. Gennaro edit. 1985).

**[0116]** Examples of suitable carriers include lactose, starch, glucose, methyl cellulose, magnesium stearate, mannitol, sorbitol and the like. Examples of suitable diluents include ethanol, glycerol and water.

**[0117]** The choice of pharmaceutical carrier, excipient or diluent can be selected with regard to the intended route of administration and standard pharmaceutical practice. The pharmaceutical compositions may comprise as, or in addition to, the carrier, excipient or diluent any suitable binder(s), lubricant(s), suspending agent(s), coating agent(s), solubilising agent(s).

**[0118]** Examples of suitable binders include starch, gelatin, natural sugars such as glucose, anhydrous lactose, free-flow lactose, beta-lactose, corn sweeteners, natural and synthetic gums, such as acacia, tragacanth or sodium alginate, carboxymethyl cellulose and polyethylene glycol.

**[0119]** Examples of suitable lubricants include sodium oleate, sodium stearate, magnesium stearate, sodium benzoate, sodium acetate, sodium chloride and the like.

**[0120]** Preservatives, stabilizers, dyes and even flavoring agents may be provided in the pharmaceutical composition. Examples of preservatives include sodium benzoate, sorbic acid and esters of p-hydroxybenzoic acid. Antioxidants and suspending agents may be also used.

**[0121]** Nutritionally acceptable carriers, diluents and excipients include those suitable for human or animal consumption and that are used as standard in the food industry. Typical nutritionally acceptable carriers, diluents and excipients will be familiar to the skilled person in the art.

### **Administration**

**[0122]** The compositions of the present invention may be adapted for oral, rectal, vaginal, parenteral, intramuscular, intraperitoneal, intraarterial, intrathecal, intrabronchial, subcutaneous, intradermal, intravenous, nasal, buccal or sublingual routes of administration. Preferably, the compositions of the present invention are adapted for oral, rectal, vaginal, parenteral, nasal, buccal or sublingual routes of administration.

**[0123]** For oral administration, particular use is made of compressed tablets, pills, tablets, gellules, drops, and capsules.

**[0124]** Other forms of administration comprise solutions or emulsions which may be injected intravenously, intraarterially, intrathecally, subcutaneously, intradermally, intraperitoneally or intramuscularly, and which are prepared from sterile or sterilisable solutions. The pharmaceutical compositions of the present invention may also be in form of suppositories,

pessaries, suspensions, emulsions, lotions, ointments, creams, gels, sprays, solutions or dusting powders.

**[0125]** An alternative means of transdermal administration is by use of a skin patch. For example, the active ingredient can be incorporated into a cream consisting of an aqueous emulsion of polyethylene glycols or liquid paraffin. The bacterial strain can also be incorporated into an ointment consisting of a white wax or white soft paraffin base together with such stabilisers and preservatives as may be required.

**[0126]** Compositions may be formulated in unit dosage form, i.e., in the form of discrete portions containing a unit dose, or a multiple or sub-unit of a unit dose.

### **Dosage**

**[0127]** A person of ordinary skill in the art can easily determine an appropriate dose of one of the instant compositions to administer to a subject without undue experimentation. Typically, a physician will determine the actual dosage which will be most suitable for an individual patient and it will depend on a variety of factors including the activity of the specific bacterial strain employed, the metabolic stability and length of action of that strain, the age, body weight, general health, sex, diet, mode and time of administration, rate of excretion, drug combination, the severity of the particular condition, and the individual undergoing therapy. The dosages disclosed herein are exemplary of the average case. There can of course be individual instances where higher or lower dosage ranges are merited.

**[0128]** The usual effective daily dose in humans is from about  $1 \times 10^3$  to about  $1 \times 10^{11}$ , more preferably, from about  $1 \times 10^7$  to about  $1 \times 10^{11}$ , even more preferably, from about  $1 \times 10^6$  to about  $1 \times 10^{10}$  CFU.

### **Combinations**

**[0129]** In a particularly preferred embodiment, the compositions of the invention are administered in combination with one or more other active agents. In such cases, the compositions of the invention may be administered consecutively, simultaneously or sequentially with the one or more other active agents.

**[0130]** The present invention is further described by way of the following non-limiting examples.

### **EXAMPLES**

## Materials and Methods

### Bacterial growth conditions

[0131] *R. hominis* A2-183<sup>T</sup> (=DSM 16839<sup>T</sup>=NCIMB 14029<sup>T</sup>) was grown anaerobically on synthetic YCFA or complex M2GSC media. Culture was inoculated from frozen stock into Hungate tubes and incubated overnight at 37°C. Bacteria were then grown on M2GSC agar plates for 48h in a MACS-MG-1000 anaerobic workstation (Don Whitley Scientific) under 80% N<sub>2</sub>, 10% CO<sub>2</sub>, and 10% H<sub>2</sub> at 37°C. The effect of mucin was investigated by adding 0.5% (w/v) mucin from porcine stomach type III (Sigma-Aldrich) to the YCFA medium.

[0132] For colonization of germfree mice, *R. hominis* was grown in YCFA media overnight at 37°C. The culture was spun down and the pellet was resuspended in one mL of YCFA media, supplemented with 2% cysteine (w/v, Sigma-Aldrich) and 3% ascorbic acid (w/v, Sigma-Aldrich).

### Animal experiments

[0133] Germ-free animal experiments were performed in the INRA gnotobiotic rodent breeding facility at Jouy-en-Josas (ANAXEM platform, Institut Micalis, INRA, Jouy-en-Josas, France). All animal experiments were approved by the local ethical committee. Eighteen germfree C3H/HeN male mice were allocated into control (N=8) and treatment (N=10) groups and caged individually in plastic isolators. The mice were fed ad libitum on a sterilized commercial diet (R03-40; UAR). At day 0, animals in the treatment group were given 100 µL of *R. hominis* culture by gavage, while control animals were given 100 µL YCFA media. At day 14 and 28, four control animals and five *R. hominis*-treated animals were sacrificed. C57/BL6 IL-10KO experiments were performed at the Rowett Institute of Nutrition and Health (Aberdeen, Scotland, UK). Wild-type mice (N=8), IL-10KO (N=12) and IL-10KO + *R. hominis* (N=11) were analysed 14 weeks from the outset of the experiment. Briefly *R. hominis* was administered 3 times per week at 10<sup>9</sup> cfu/day.

[0134] The ileum, ascending colon and descending colon were divided into four equal parts and transferred to RNAlater (Ambion), neutral buffered formalin (Sigma-Aldrich) or liquid nitrogen. The whole caecum and transverse colon were transferred to RNAlater. Histopathology was also evaluated in the IL-10KO mice.

### Tissue culture experiments

**[0135]** All cell culture reagents, unless specified otherwise, were supplied by Sigma-Aldrich. 2x10<sup>5</sup> Caco-2 or HT29 cells in 1.5 mL DMEM (high glucose, HEPES) medium supplemented with heat-inactivated fetal bovine serum (Gibco), penicillin, streptomycin, amphotericin B and L-glutamine were seeded into the upper compartments of a six-well transwell plate (Corning). The lower compartments contained 3.0 mL of the same medium. Cells were incubated at 37 °C in a 5% CO<sub>2</sub> atmosphere until 3 days post-confluence, washed with Hanks' solution to remove antibiotics and FCS and stepped down in DMEM supplemented with L-glutamine, sodium selenite and transferrin for 24h without antibiotics. Transwell inserts were then transferred to an anaerobic culture box within the anaerobic workstation at 37 °C. The upper compartment of each insert was filled with anaerobic DMEM cell medium, while the lower compartment was filled with oxygenated DMEM.

**[0136]** *R. hominis* A2-183 culture was harvested at exponential phase by centrifugation at 3,500xg for 5 min. The pellet was washed and resuspended in 0.8 mL anaerobic DMEM. One hundred microliters of bacterial suspension (10<sup>8</sup> CFU/mL) was added to experimental wells. The control wells received the same amount of medium without bacterial cells. Additional control included bacterial cells incubated without Caco-2 or HT29 cells.

**[0137]** Bacterial and eukaryotic cells were harvested after 2h and 4h incubation. Both non-adherent and adherent bacteria were aspirated and stored in RNAlater. The viability of *R. hominis* cells was tested by plating onto YCFA plates. Caco-2 cells or HT-29 cells were harvested from the wells and also stored in RNAlater.

### ***R. hominis* library construction**

**[0138]** *R. hominis* chromosomal DNA for small-size library construction and pyrosequencing was isolated using an UltraClean™ Microbial DNA Isolation Kit (Mo Bio Laboratories Inc) and high-molecular-weight DNA for fosmid libraries was isolated using a Wizard Genomic DNA Purification kit (Promega). DNA integrity was checked by gel electrophoresis.

**[0139]** DNA was mechanically sheared using a Nebulizer kit (Invitrogen) and fractionated by gel electrophoresis. DNA fragments of desired size were excised from the gel and purified using a Wizard® SV Gel and PCR Clean-Up System (Promega). End-repair was done with a DNA Terminator End Repair Kit (Lucigen). 1.5-3.5 kb fragments were cloned using the CloneSmart® LCamp kit (Lucigen) and a 4-8 kb library was constructed using the pJAZZ®-OC vector (Lucigen). Fosmid libraries were constructed using the CopyControl™ Fosmid Library Production Kit (Epicentre Biotechnologies). Colonies were picked using an automated colony picker (BioRobotics BioPick, Genomic Solutions) and archived into 384-well microtitre plates containing 70 µL 2xLB medium supplemented with 10% glycerol and corresponding antibiotic. Cells were grown overnight at 37 °C with shaking and stored at -80 °C.

### **Sequencing, assembly, and annotation**

**[0140]** Templates for sequencing of small-size libraries were generated by PCR using one  $\mu$ L of clone biomass and primers SL1 and SR2 surrounding the cloning site of pSMART-LCAmp. PCR products were purified using Multiscreen PCR Clean-up filter plates (Millipore). Recombinant DNA from the pJAZZ®-OC clones was isolated using the Wizard® SV 96 Plasmid DNA Purification System (Promega). Fosmid DNA was isolated using the FosmidMAX™ DNA Purification Kit (Epicentre). End-reads of DNA fragments from *R. hominis* WGS libraries with different insert sizes were obtained using CEQ8000 (Beckman Coulter) and ABI 3770 (Applied Biosystems) DNA sequencers. Genomic DNA from *R. hominis* was also sequenced using 454 GS20 (454 Life Sciences) and 454 FLX sequencers (Roche). The Sanger and 454 data were assembled with MIRA version 3 ([http://chevreux.org/projects\\_mira.html](http://chevreux.org/projects_mira.html); (35)). The RAST annotation pipeline (<http://rast.nmpdr.org>; (36)) was used for automatic and manual annotation of the genome and for comparative genomic analyses. The annotated genomic sequence of *R. hominis* A2-183 was submitted to GenBank under the accession number CP003040.

## **Microarray analyses**

### ***Bacterial microarray***

**[0141]** Bacterial RNA was isolated from mouse caecum contents using the RNeasy mini kit, and further processed with the MICROBEnrich™ kit (Ambion), the MICROBExpress™ bacterial mRNA enrichment kit (Ambion), and the MessageAmp™ II-bacteria RNA amplification kit (Applied Biosystems). RNA was labeled with either dCTP-Cy3 or dCTP-Cy5 during cDNA synthesis (CyScribe First strand cDNA labelling kit; Amersham). Labeled products were purified using the CyScribe GFX purification kit (Amersham). PCR products amplified from 6000 clones in the RA8 library were arrayed in duplicate on aminosilane-coated microscope slides (Corning) using a MicroGrid II TAS (BioRobotics). Amplified fragments of the housekeeping genes *rpoD* and *gyrA* were randomly distributed on the array as controls. Microarray hybridization was performed in the GeneTAC hybridization station (Genomic Solutions). Dye labeling was swapped for a second hybridization, and a separate RNA purification was also labeled and hybridized twice, to ensure reproducibility and to obtain statistically significant results. In total, four slides were hybridized for each comparison, for a total of 12 hybridizing spots per amplified clone. Fluorescence was measured in two channels using a GeneTAC LS IV (Genomic Solutions) with GeneTac Integrator version 3.0.1 software. Spot intensities were log-transformed and Loess normalization was applied to remove differences in probe labelling and hybridization efficiencies. One-sample t-tests were used on the log-ratio values to test for differential expression. Data was considered significant when fold change > 2 and  $P < 0.05$ .

### ***Mouse microarray analysis***

**[0142]** Ileum and ascending colon tissue was removed from RNAlater and lyzed in Trizol (Invitrogen). RNA was isolated using standard chloroform/isopropanol steps. Total RNA was further purified with the RNeasy kit (Qiagen), including an RNase-free DNase I (Qiagen) digestion step. RNA integrity was determined using the Agilent 2100 Bioanalyzer (Agilent Technologies). Total RNA was processed into biotin-labeled cRNA using the One-Cycle Target Labeling Kit (Affymetrix). Hybridization to the GeneChip Mouse Genome Array (Affymetrix) on a GeneChip Fluidics Station 450 (Affymetrix) was performed at the Institute of Medical Sciences Microarray Core Facility (University of Aberdeen, UK). Chips were scanned with an Affymetrix GeneChip Scanner 3000 (Affymetrix). Image quality analysis was performed using Gene Chip Operating Software (GCOS) (Affymetrix). Further data analysis was performed with the freely available software packages R (<http://www.r-project.org>) and Bioconductor (<http://www.bioconductor.org>). The moderated F-test provided by the Bioconductor package limma was used to test for differential expression. Data was considered significant when  $P < 0.05$  using the Benjamini and Hochberg false discovery method. Statistical analysis was performed separately for each of the two time-points. All differentially expressed genes ( $P < 0.05$ ) were imported into MetaCore analytical software (GeneGo, St Joseph, MI) to generate pathway maps. Integrated pathway enrichment analysis was performed using the knowledge-based canonical pathways and endogenous metabolic pathways. Ranking of relevant integrated pathways was based on p-values calculated using hypergeometric distribution. P-values represented the probability of a given number of genes from the input list to match a certain number of genes in the map by chance, considering the numbers of genes in the experiment versus the number of genes in the map within the full set of all genes on maps. Gene Ontology (GO) based functional interpretation of the data was performed using DAVID (<http://david.abcc.ncifcrf.gov>), an expanded version of the original web-accessible program (37). Significantly different transcripts ( $P < 0.05$ ) were allocated into the GO category 'Biological Process' to unearth patterns of gene expression significantly enriched for specific GO terms.

Microarray data were submitted to the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (accession number GSE25544; <http://www.ncbi.nlm.nih.gov/geo>).

### RT-PCR analysis

**[0143]** Bacterial PCR primers were designed using the on-line tool Primer3Plus (38) and purchased from Sigma-Aldrich. Real-time PCR analysis was performed using a 7500 Fast Real-Time PCR System (Applied Biosystems) with the Power SYBR Green PCR Master Mix (Applied Biosystems). PCR was performed as follows: one cycle at 95°C for 10 min, followed by 40 cycles at 95°C for 15 sec and 60°C for 1 min, ending with a dissociation step. All samples were run in triplicate. GyrA was used as a reference gene for normalization due to its low variation between samples.

**[0144]** For host gene expression, 2 µg of total eukaryotic RNA isolated from the ileum and ascending colon was reverse-transcribed into cDNA using the High Capacity cDNA Reverse

Transcription Kit (Applied Biosystems) with random primers. Real-time PCR analysis was performed using a 7500 Fast Real-Time PCR System (Applied Biosystems) with the QuantiFast SYBR Green PCR Kit (Qiagen) and QuantiTect Primer Assays (Qiagen). PCR cycling conditions were as follows: one cycle at 95 °C for 5 min, followed by 40 cycles at 95 °C for 10 s and at 60 °C for 30 s, ending with a dissociation step. All samples were run in triplicate. Hprt was selected as a reference gene for normalization because of its low variation between samples. All RT-PCR data were analyzed on a logarithmic scale with base 2 by Student's t test allowing unequal variances with a significance cut-off of  $P < 0.05$ . Differences were back-transformed to calculate fold changes.

### Western blot

**[0145]** Immuno-purified rabbit polyclonal antibodies against *Roseburia hominis* Fla2 was produced as described in Duck *et al* (39). In brief, New Zealand white female rabbits were immunized with synthetic peptide in complete Freund's adjuvant and boosted several times. For *R. hominis* fla2 peptide 261-275 (C-AQYNDDAKSVLEILK-COOH) and peptide 58-71 (C-GLNKASRNSQDGIS-CONH<sub>2</sub>) were used. Following immunization the antibodies were purified on an immunoaffinity column prepared by coupling the peptides to 1 mL of activated sepharose beads.

**[0146]** For the western blot, ascending colon gut contents were suspended in laemmli buffer containing 8M urea. *R. hominis* biomass (positive control) was diluted in the same buffer. Thirty  $\mu$ L of each sample was loaded into wells of a NuPAGE® Novex® 4-12% Bis-Tris gel (Invitrogen) and electrophoresed, followed by further processing using the WesternBreeze Chemiluminescent Immunodetection System (Invitrogen). Fla2 antibody was diluted 1:1000 in antibody diluent and incubated overnight at 4 °C, followed by 1h at room temperature with alkaline phosphatase conjugated anti-rabbit. Detection was accomplished using the Fuji LAS3000 image system.

### Dry body weight and lipid carcass analysis

**[0147]** Eviscerated mouse carcass was weighed, lyophilized to constant weight and then milled for analysis. Lipid content was determined by extraction (1:100 w/v) with chloroform/methanol (2:1 v/v) as described previously (40).

### FISH analysis

**[0148]** FISH analysis was performed on gut tissue sections using a general bacterial probe Eub338 and a newly designed *R. hominis* A2-183-specific probe.

**[0149]** Tissues fixed in neutral buffered formalin were embedded in Technovit 8100 (Heraeus Kulzer). Two-micron sections were cut using a rotary microtome (Leica/Reichert Autocut). Three sections were taken per slide at 100  $\mu\text{m}$ , 200  $\mu\text{m}$  and 300  $\mu\text{m}$  into the tissue, resulting in nine sections per animal.

**[0150]** Slides were dehydrated by consecutive incubation in 50% (v/v), 80% and 96% ethanol and dried at room temperature. 16S rRNA FISH probes used were a general bacterial probe Eub338 (GCTGCCTCCCGTAGGAGT; Cy3) and a newly designed *R. hominis* A2-183-specific probe (GTACATTACATACTCTGTCTCAGTG; FITC), which was extensively tested for specificity against a panel of intestinal bacterial isolates. Ten microliter probe (30 ng/ $\mu\text{L}$ ) in 100  $\mu\text{L}$  hybridization buffer was applied to the dehydrated sample and incubated at probe-specific temperature. The slides were washed in washing buffer at 50°C for 30 min, dipped in ice-cold water to remove residual washing buffer and dried under compressed air flow. Counterstaining was performed with 4',6-diamidino-2-phenylindole (DAPI; Vector Laboratories Inc) and slides were mounted with Vectashield Mounting Medium for fluorescence (Vector Laboratories Inc) to prevent fading. Bacteria were visualized using a Leica DM RBE fluorescence microscope (Leitz GMBH) and photographed with a Penguin 600CL camera (Pixera) and Viewfinder 3.0 software (Studio Lite). High-magnification images (x63) were retrieved using the Apochromatics system (Leica).

### **Immunofluorescence**

**[0151]** Immuno-localization of T cell markers was examined on sequential cryosections (8 $\mu\text{m}$ ). Sections were fixed either in pre-cooled methanol for 30 min at -20 °C (Ly6G FITC, CD3 FITC, CD11b FITC, all at 1:50 (BD Biosciences)), or, for the double-labeled FoxP3 (1:500, Abcam) with CD3 FITC (1:100, BD Biosciences) fixed in 1% paraformaldehyde (PFA) for 2 min at RT followed by 3 min in 0.01% Triton X in PBS. All sections were blocked with 10% BSA (Sigma) containing 10% relevant pre-immune sera in PBS (pH 7.4). Methanol-fixed tissues were incubated with primary antibodies for 1h at RT. PFA-fixed sections were incubated with antibodies over night at 4 °C. FoxP3 was visualized using Alexa goat anti rabbit 594 (1:1000, Molecular Probes). Sections were counter labeled with DAPI and mounted with Vectashield (Vector Laboratories). For quantification of positive cells, a minimum of five fields of view from each mouse section was examined, using imaging software and microscope settings described above.

### **Histology**

**[0152]** Tissue samples were fixed for three hours in Carnoy's fixative (60% (v/v) ethanol, 30% (v/v) chloroform and 10% (v/v) glacial acetic acid) at room temperature with constant agitation. The samples were transferred to 70 % ethanol and stored at room temperature until orientated for transverse sectioning and embedded in cold-curing resin using Technovit 8100 (Heraeus

Kulzer) according to the manufacturer's instructions. The embedded tissue was mounted onto Histoblocs using Technovit 3040 (Heraeus Kulzer). Four micron sections were cut using a rotary microtome (Leica Autocut) fitted with a glass knife (TAAB Laboratories Equipment Ltd.). Tissue sections were stained using standard haematoxylin/eosin methods and examined with a Zeiss Axioskop microscope equipped with x10 and x20 objectives. Images were taken using a QImaging camera and Image Pro Plus software.

### **Comparison of genomes of Roseburia-related species and strains**

**[0153]** The Applicant produced a complete genome sequence of *R. hominis* A2-183, which is represented by a single 3,592,125-bp chromosome. Automated and manual annotation of the genome using the RAST platform revealed the presence of four ribosomal operons, 66 RNAs and 3,273 predicted proteins. The Subsystem Category Distribution for *R. hominis* A2-183, *R. inulinivorans* DSM 16841, *R. intestinalis* L1-82, *R. intestinalis* M50/1 and *Eubacterium rectale* ATCC 33656 are shown in Figures 11-15 respectively.

**[0154]** This information illustrates the differences in number of genes (presented in brackets) in each functional subsystem. These genes are very important in mediating host response to each individual bacterium. Importantly these genes, both in number and function, are different between the various strains. The results are summarised below:

#### ***R. hominis* A2-183**

Cell Wall and Capsule (57)  
 Membrane Transport (24)  
 Motility and Chemotaxis (49)  
 Regulation and Cell signaling (16)  
 Dormancy and Sporulation (12)  
 Carbohydrates (271)

#### ***E. rectale* ATCC 33656**

Cell Wall and Capsule (41)  
 Membrane Transport (13)  
 Motility and Chemotaxis (16)  
 Regulation and Cell signaling (9)  
 Dormancy and Sporulation (6)  
 Carbohydrates (172)

#### ***R. intestinalis* L1-82**

Cell Wall and Capsule (35)  
 Membrane Transport (36)  
 Motility and Chemotaxis (15)  
 Regulation and Cell signaling (10)  
 Dormancy and Sporulation (17)

***R. intestinalis*** M50/1

Cell Wall and Capsule (28)

Membrane Transport (37)

Motility and Chemotaxis (17)

Regulation and Cell signaling (10)

Dormancy and Sporulation (17)

Carbohydrates (201)

***R. inulinovorans*** DSM 16841

Cell Wall and Capsule (69)

Membrane Transport (26)

Motility and Chemotaxis (14)

Regulation and Cell signaling (9)

Dormancy and Sporulation (17)

Carbohydrates (160)

**Percentage sequence identity of >3000 genes found in contig 1 highlights the differences between the bacterial genome of *R. hominis* and the bacterial of *E. rectale*, *R. intestinalis* and *R. inulinivorans***

**[0155]** Comparisons were made between the genomes of various Roseburia species and the related species *Eubacterium rectale*, the closest relative to *R. hominis*.

**[0156]** *R. hominis* reference genome 585394.12

*E. rectale* genome ATCC336556 515619.3

*R. intestinalis* L1-82166486.4

*R. intestinalis* M50/1166486.5

*R. inulinovorans* DSM16841 622312.3

**[0157]** The percentage identity of potential genes between the various Roseburia genomes ranges from 0% to around 90% sequence identity. Many genes are hypothetical and vary between the strains. Large numbers of genes are present in the *R. hominis* genomes that are absent from the genomes of the others Roseburia species

**[0158]** *Roseburia hominis* has 924 genes that are not found in the other genomes of other Roseburia species (0% identity) indicating that almost 25% of its genome is unique to *R. hominis*. Also the low homology between other genes (<10-70%) indicates that the functions of many others genes are also likely to differ.

**[0159]** The information provides compelling evidence that these bacteria are very different from a genome and functional perspective, and cannot be grouped other than by their

phylogenetic relatedness, which is generally based on the conserved gene 16S ribosomal gene which is a conserved piece of prokaryotic DNA found in all bacteria. 16S rRNA gene sequences are used for bacterial phylogeny and taxonomy studies (shared genetic marker).

### **Functionality in relation to host response and immunity is bacterial strain specific**

**[0160]** Figure 9 illustrates a comparison of gene expression data for three strains of bacteria from Cluster XIVa (Firmicutes), namely *Roseburia hominis*, *E. rectale* and *Roseburia intestinalis*. The data indicates the numbers of unique genes expressed by the phylogenetically related bacterial strains following exposure to human epithelial cells. Gene expression was determined by using Affymetrix human microarrays containing 56,000 genes. This difference reflects the differences in their respective genomes. [These experiments are similar to those described elsewhere in the specification using mouse microarrays but used specific human microarrays. The GeneChip® Human Genome U133 Plus 2.0 Array is the first and most comprehensive whole human genome expression array. The Affymetrix GeneChip® Human Genome U133 Plus 2.0 Array (HG-U133 Plus 2.0) microarray comprises 1,300,000 unique oligonucleotide features covering over 47,000 transcripts and variants, which, in turn, represent approximately 39,000 of the best characterized human genes. The cell lines used to evaluate the signalling responses induced by different commensal bacteria include the human colon cell line Caco-2 cells and HT-29 cells and bacteria including *R. hominis*, *E. rectale* and *R. intestinalis* where compared against *Salmonella enteritidis*, an enteric pathogen.

### **Functional differences in Cluster XIVa bacteria- comparison between *R. hominis* and *E. rectale***

**[0161]** Figure 10 shows that *Roseburia hominis* induces A20 a negative regulator of NF-κB signaling with potent anti-inflammatory activity whereas other bacterial strains have no effect. The flagellin moiety of *Roseburia hominis* also induces A20 unlike that of *Eubacterium rectale*, a related bacterium.

**[0162]** Cell culture reagents, unless specified otherwise, were supplied by Sigma-Aldrich. Caco-2 (ECACC Cat No. 860102002) and HT29 (ATCC) cell lines cultured in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% Foetal Bovine Serum (FBS) (Gibco,UK), 200 mM L-glutamine and 1% antibiotics/antimycotics were seeded in six-well transwell plate (Corning). Cells were incubated at 37 °C in a 5% CO<sub>2</sub> atmosphere until 3 days post-confluence, washed with Hanks' solution to remove antibiotics and FCS and stepped down in DMEM supplemented with L-glutamine, sodium selenite and transferrin for 24h without antibiotics. Transwell inserts were then transferred to an anaerobic culture box within the anaerobic workstation at 37 °C. The upper compartment of each insert was filled with anaerobic DMEM cell medium, while the lower compartment was filled with oxygenated DMEM.

**[0163]** *Roseburia hominis* A2-183 and *E.rectale* ATCC336556 in standard YCFA and M2 culture media and *Salmonella enteric* serovar *enteritidis* cultured in LB broth were harvested at exponential phase by centrifugation at 3,500xg for 5 min. The pellet was washed and resuspended in anaerobic DMEM. One hundred microliters of bacterial suspension ( $10^8$  CFU/mL) was added to experimental wells. The control wells received the same amount of medium without bacterial cells. Additional control included bacterial cells incubated without Caco-2 or HT29 cells.

**[0164]** Bacterial and eukaryotic cells were harvested after 2h and 4h incubation. Both non-adherent and adherent bacteria were aspirated and stored in RNeasy. Caco-2 cells or HT-29 cells were harvested from the wells and also stored in RNeasy.

### Luciferase Assay for determination of A20 luciferase gene expression

**[0165]** Fugene® 6 transfection reagent (Roche, UK) was used for the transfection of HT29 cells with the plasmids carrying the luciferase reporter gene under the control of the A20 promoter pLuc-A20 and pLuc-A20Δ NF-κB (mutated in 3 nucleotides in the A20 promoter region) and the GFP reporter gene under the control of the A20 promoter pCAGGS-GFP/A20 and pLuc-GL2\ NF-κB. After 48 h, the cells were stimulated with live bacteria *R. hominis*, *E. rectale* and *S. enteritidis* and recombinant flagellins; *S. enteritidis* and *R. hominis* (*Fla 1*) (100 ng/ml) for 9, 12 and 24 h. Recombinant flagellin were generated using full length sequences cloned into appropriate vectors and expressed in *E. coli* JM109, BL21 and Rosetta. Luciferase (Firefly - f-Luc and renilla - r-Luc) activities were determined using the Dual-Glo® luciferase assay system (Promega, UK) and an Envision 2102 Multilabel Reader. The relative luciferase reporter activity was obtained by normalization to renilla control.

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  - **SOKOL H. et al.***PNAS*, 2008, vol. 105, 4316731-16736 [\[0166\]](#)

**Patentkrav****1. Bakteriestamme med**

5 (a) en 16S rRNA-identitet på mindst 99,5% med stammen hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029, eller

(b) en DNA-DNA-homologi på mindst 95% med bakteriestammen hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029;

til anvendelse i medicin.

10

**2.** Farmaceutisk sammensætning omfattende en bakteriestamme med (a) en 16S-rRNA-identitet på mindst 99,5% med stammen hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029 eller (b) en DNA-DNA-homologi på mindst 95% med bakteriestammen hørende til slægten *Roseburia*  
15 *hominis* deponeret under accessionsnummer NCIMB 14029; og en farmaceutisk acceptabel excipiens, bærer eller fortyndingsmiddel.

**3.** Næringsmæssigt supplement omfattende bakteriestamme med (a) en 16S-rRNA-identitet på mindst 99,5% med stammen hørende til slægten *Roseburia*  
20 *hominis* deponeret under accessionsnummer NCIMB 14029 eller (b) en DNA-DNA-homologi på mindst 95% med bakteriestammen hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029; og en ernæringsmæssig acceptabel excipiens, bærer eller fortyndingsmiddel.

25 **4.** Probiotisk sammensætning, fodermiddel, næringsmiddelprodukt, kostsupplement eller næringsmiddeladditiv omfattende en bakteriestamme med (a) a 16S rRNA-identitet på mindst 99,5% med stammen hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029 eller (b) en DNA-DNA-homologi på mindst 95% med bakteriestammen hørende til slægten  
30 *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029.

- 5.** Bakteriestammen til anvendelse ifølge krav 1 eller farmaceutisk sammensætning, næringsmiddelsupplement, probiotisk sammensætning, fodermiddel, næringsmiddelprodukt, kostsupplement, eller næringsmiddeladditiv ifølge et hvilket som helst af kravene 2-4, hvor bakteriestammen er stammen 5 hørende til slægten *Roseburia hominis* deponeret under accessionsnummer NCIMB 14029.
- 6.** Bakteriestammen til anvendelse ifølge krav 1 eller farmaceutisk sammensætning, næringsmiddelsupplement, probiotisk sammensætning, 10 fodermiddel, næringsmiddelprodukt, kostsupplement, eller næringsmiddeladditiv ifølge et hvilket som helst af kravene 2-4, hvor bakteriestammen har et genom der består af et enkelt 3.592.125-bp kromosom med fire ribosomale operoner, 66 RNA'er og 3.273 forudsatte proteiner.
- 15 **7.** Bakteriestammen til anvendelse ifølge krav 1 eller farmaceutisk sammensætning, næringsmiddelsupplement, probiotisk sammensætning, fodermiddel, næringsmiddelprodukt, kostsupplement, eller næringsmiddeladditiv ifølge et hvilket som helst af kravene 2-4, hvor bakteriestammen er i form af en lyofiliseret bakteriel population.
- 20 **8.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i regulering af et individs immunsystem.
- 9.** Bakteriestammen til anvendelse ifølge krav 8, hvor reguleringen af 25 immunsystemet er regulering af det adaptive immunsystem hos et individ eller er regulering af det medfødte immunsystem hos et individ.
- 10.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i behandling af en forstyrrelse valgt fra en inflammatorisk forstyrrelse, 30 en immunforstyrrelse og en tarmlidelse, såsom en lidelse valgt fra: irritabel tarmsyndrom (IBS), colitis, irritabel tarmforstyrrelse (IBD), herunder Crohn's sygdom og ulcerativ colitis, pouchitis, funktionel dyspepsi, funktionel konstipation, funktionel diarré, herunder antibiotika-associeret diarré, rejse-diarré og pædiatrisk diarré, funktionel abdominalsmerter, funktionel blødning, epigastrisk 35 smertesyndrom, postprandial distress syndrom, gastrointestinal reflux sygdom

(GERD), autoimmun-sygdomme såsom diabetes, arthritis, multipel sclerose og psoriasis, allergier, atopiske sygdomme såsom atopisk dermatitis, nekrotiserende enterocolitis, andre infektioner, cøliakisygdom, og rhinitis og kombinationer deraf.

5 **11.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i forbedring af tarm-mikrobiota hos et individ, er til anvendelse i fremme af tarm-helbredstilstand hos et individ, er til anvendelse i fremme af T-regulatoriske celler og immuntolerans, eller er til anvendelse i opretholdelse af immunhomeostase hos et individ.

10

**12.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i øgning af et individs appetit.

**13.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i nedregulering af ekspresionen af gener associeret med suppressionen af appetit, eventuelt hvor genet er *Npy2r* eller *Cartpt*.

15

**14.** Bakteriestammen til anvendelse ifølge krav 1 eller krav 5, hvor stammen er til anvendelse i forøgelse af et individs legemsvægt.

20

**15.** Bakteriestammen til anvendelse ifølge et hvilket som helst af kravene 1 eller 5-14, hvor stammen:

25

(i) regulerer induktionen og/eller ekspresion på mindst ét mobiliserings- eller kemotaxi-gen, mere fortrinsvis opregulerer ekspresionen af et gen valgt fra *MobA* og *MobL*; eller

(ii) regulerer mindst ét gen valgt fra *FlaA1*, *Fla2*, *FlaA3*, og *FlaB*; eller

(iii) regulerer ekspresionen af mindst én af følgende: acetyl-CoA acetyltransferase, 3-hydroxyacyl-CoA dehydrogenase, butyryl-CoA dehydrogenase, elektron transfer flavoprotein beta underenhed, elektron transfer flavoprotein alfa underenhed; eller

30

(iv) nedregulerer ekspresionen på mindst ét gen valgt fra *Agt*, *Cartpt*, *Cck*, *Cxcl12* og *Gcg*; eller

(v) aktiverer mindst ét immunresponsgen i kolon eller ileum; eller

(vi) aktiverer det adaptive immunrespons ved regulering af induktionen og/eller ekspresion af gener associeret med T-cellerregulering; eller

5 (vii) opregulerer ekspresion på mindst ét gen valgt fra *Ly6g6c* og *Ly6g6e* i den opstigende kolon; eller

(viii) regulerer ekspresionen på mindst ét gen valgt fra *Tlr5*, *Tlr1*, *Vnn1*, *Dejb37*, *Pla2g*, *Muc16*, *Itln*, *Spr1a*, *Cldn4*, *Pmp22*, *Crb3*, *Magi3*, *Marveld3*, *Mpp7*, *Defcr20*, *Pcgf2*, *Ltbp4*, *Igsf8* og *Tcfe2a*.

10 **16.** Bakteriestammen til anvendelse ifølge et hvilket som helst af kravene 1 eller 5-15, hvor individet er et pattedyr, fortrinsvis et menneske.

**17.** Farmaceutisk sammensætning ifølge krav 2, hvor sammensætningen er tilpasset til oral administration.

15 **18.** Fremgangsmåde til fremstilling af en farmaceutisk sammensætning ifølge krav 2 eller næringsmæssigt supplement ifølge krav 3, hvilken fremgangsmåde omfatter blanding af bakteriestammen med en farmaceutisk acceptabel excipiens, bærer eller fortyndingsmiddel eller en ernæringsmæssig acceptabel excipiens, bærer eller fortyndingsmiddel.

20

# DRAWINGS

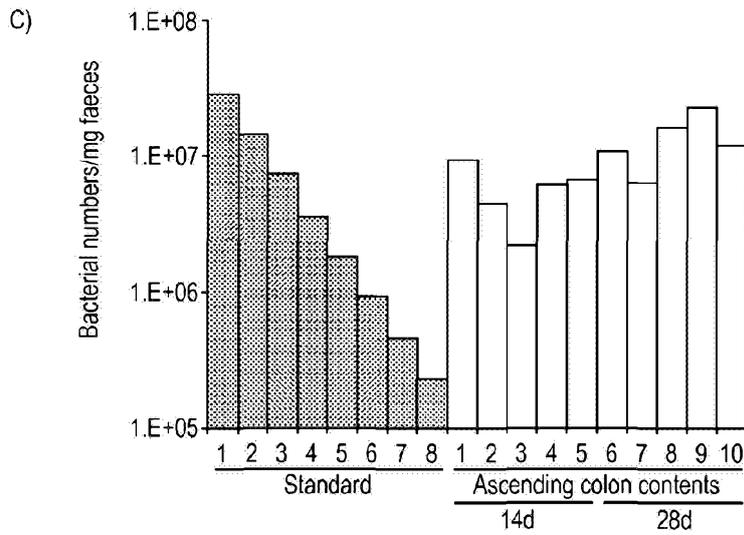
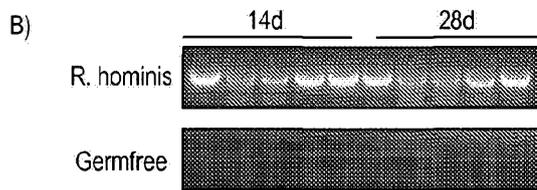
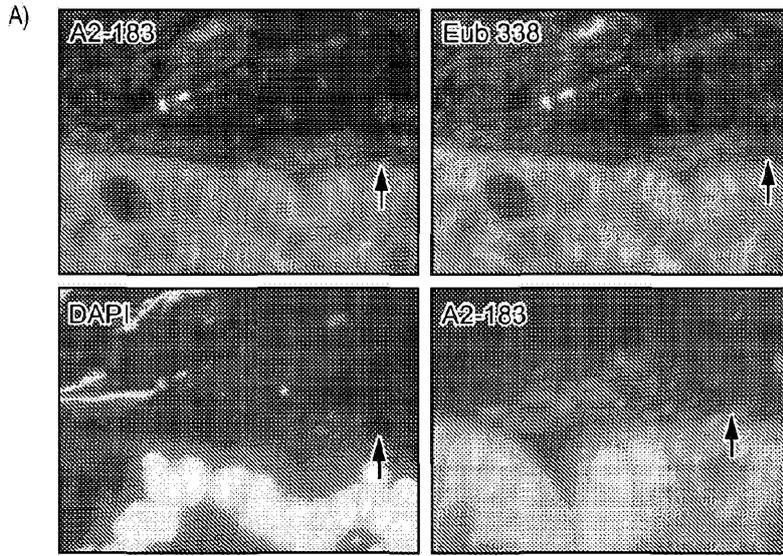


FIG. 1

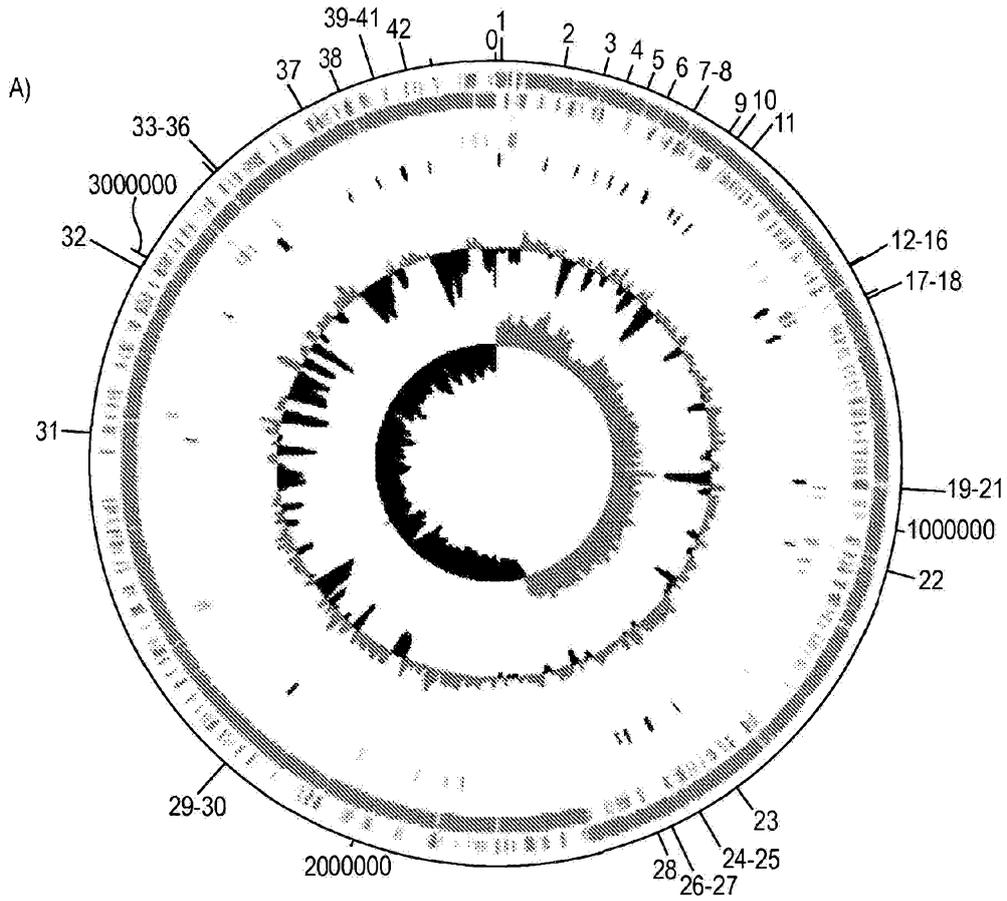


FIG. 2

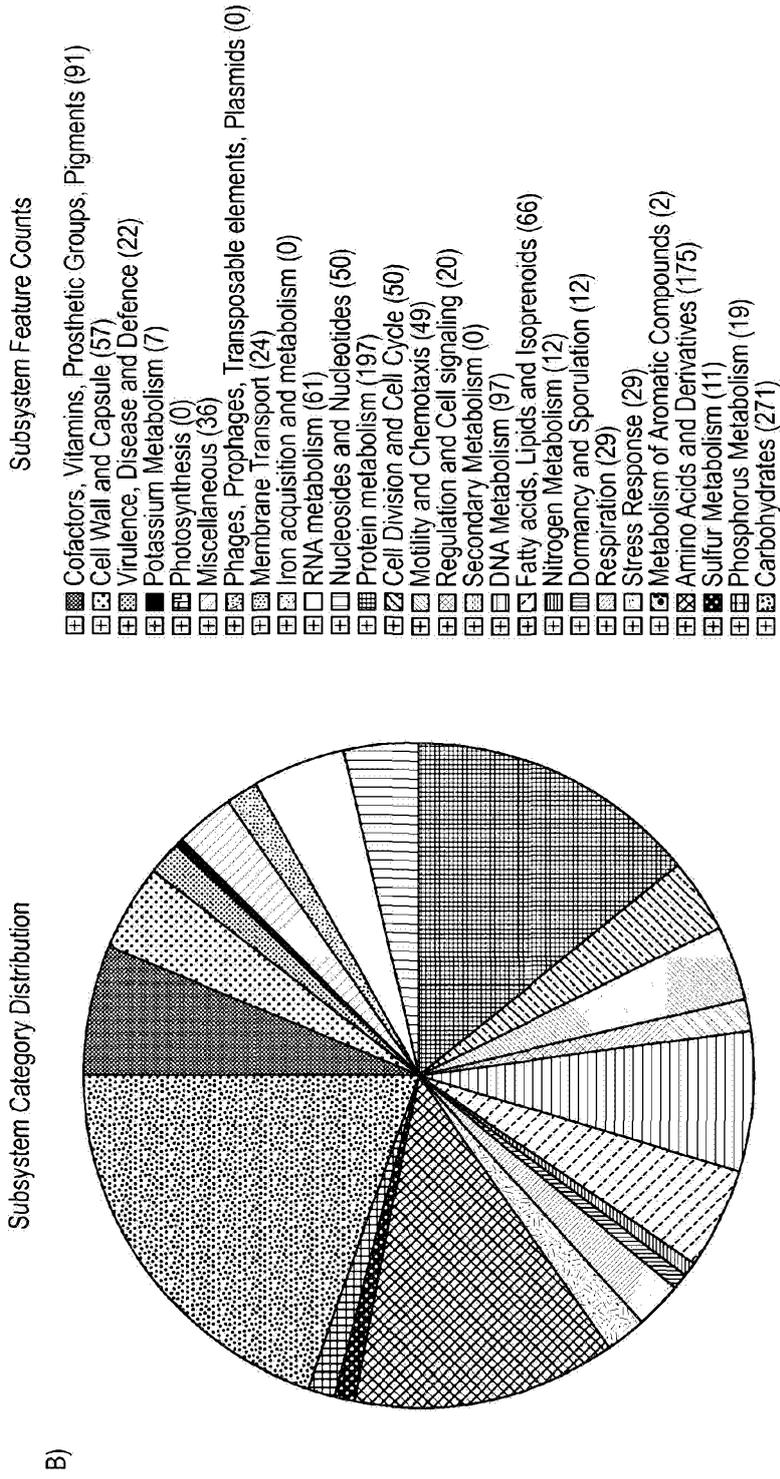


FIG. 2

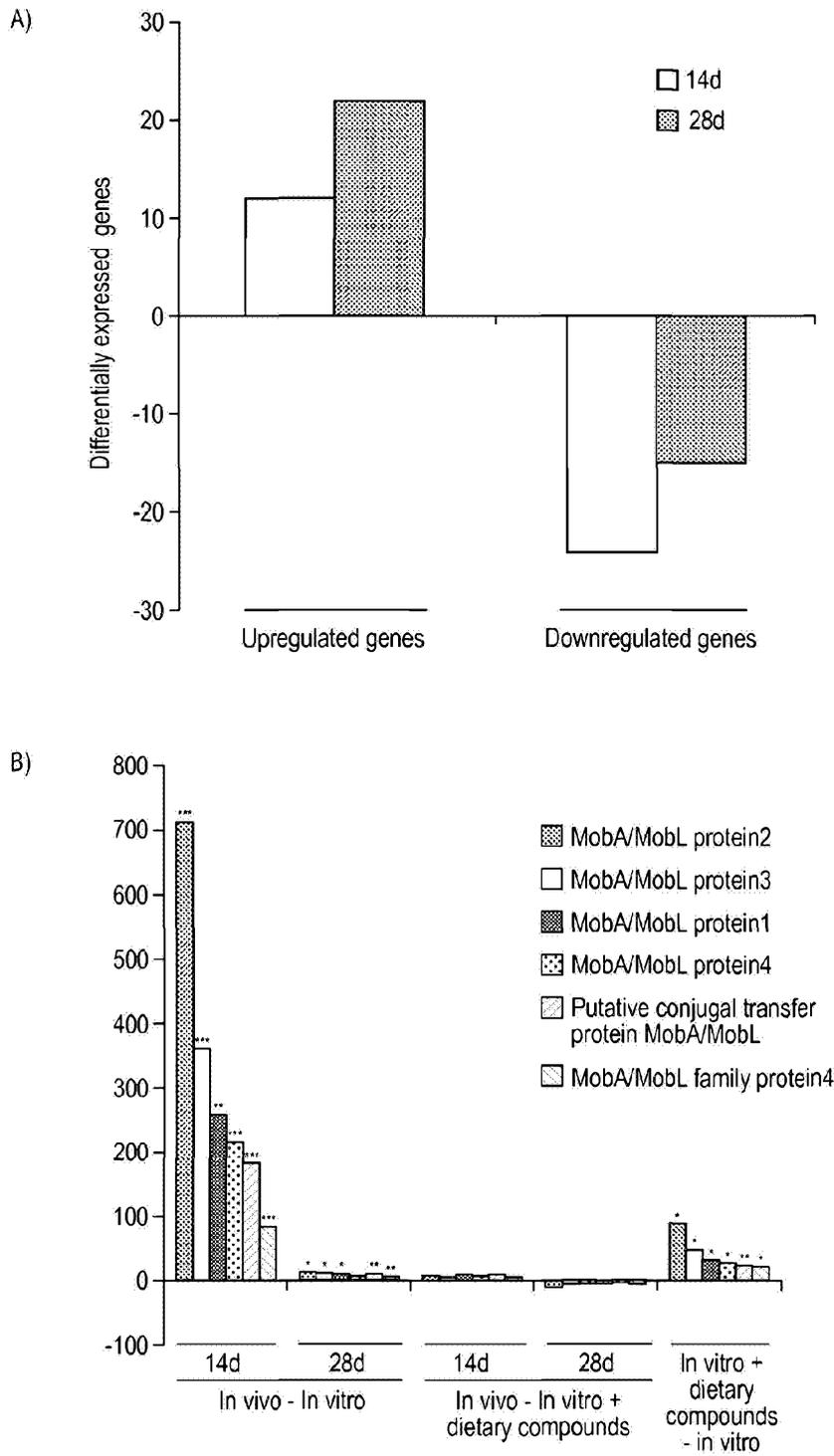


FIG. 3

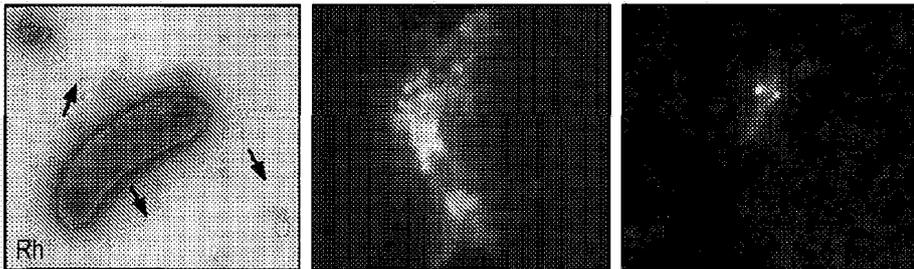
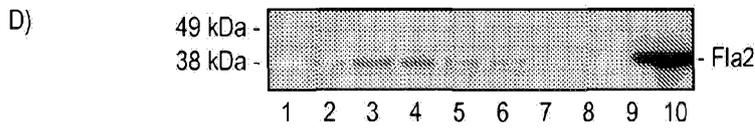
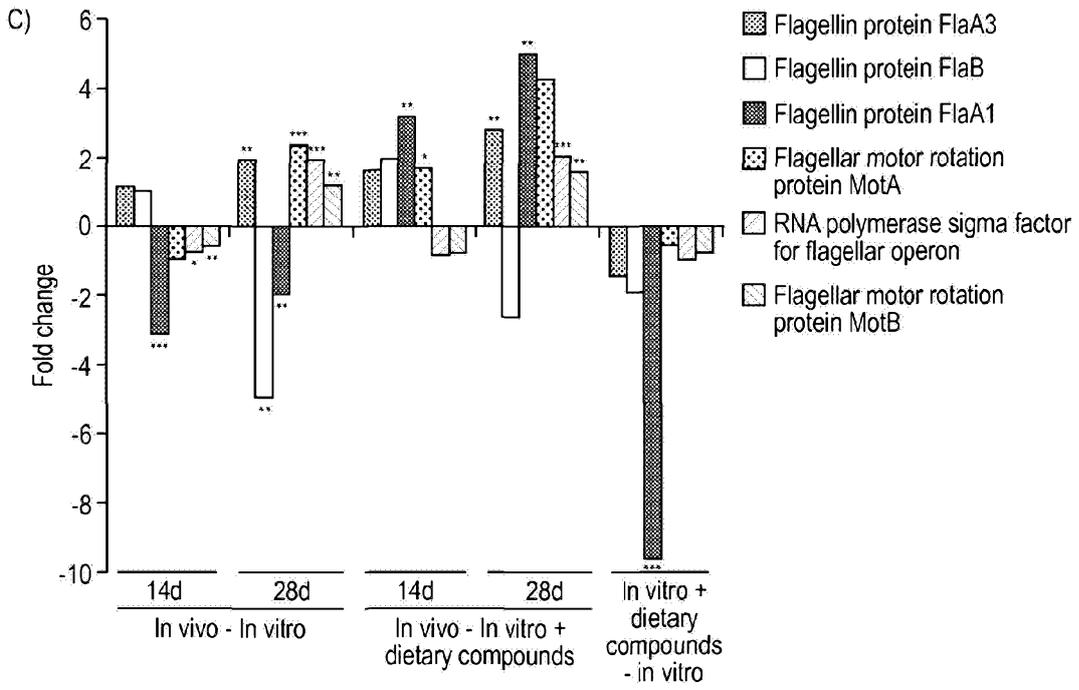


FIG. 3

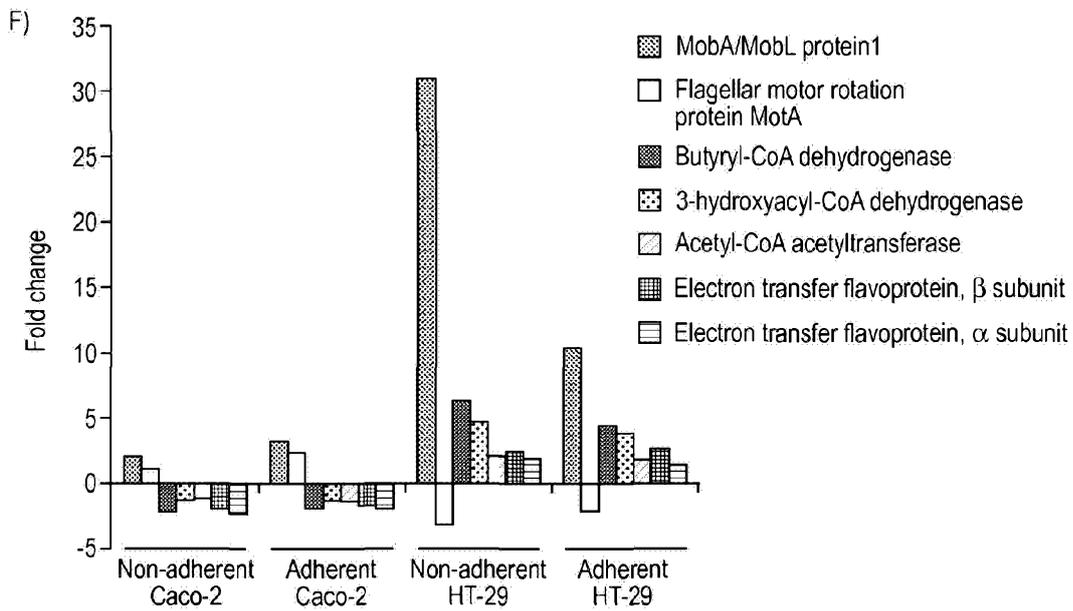
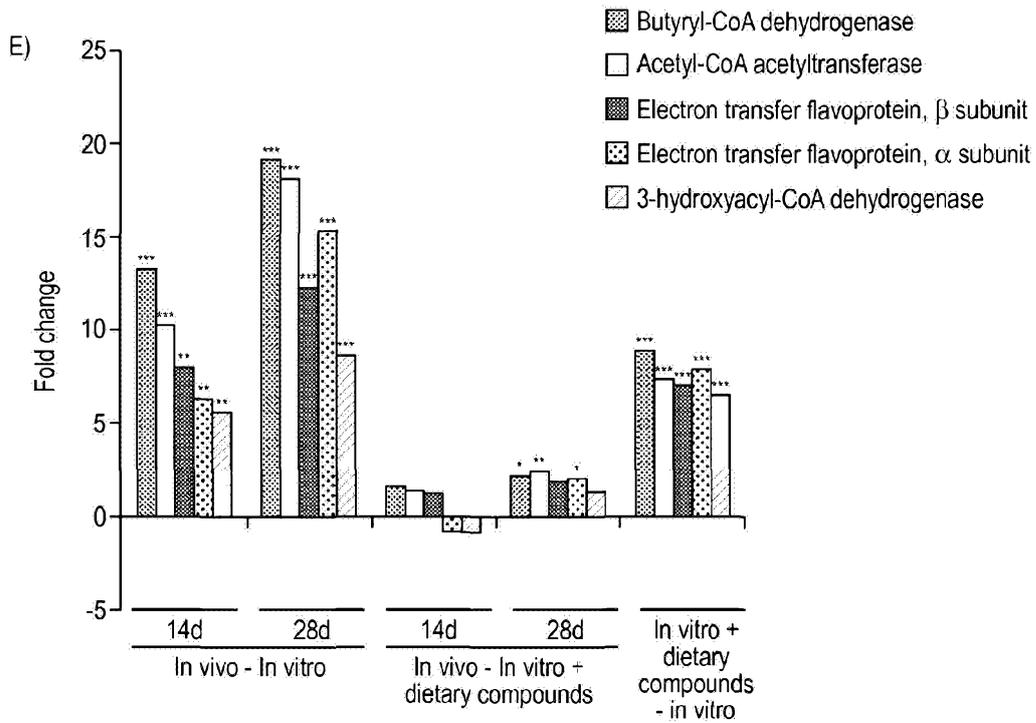


FIG. 3

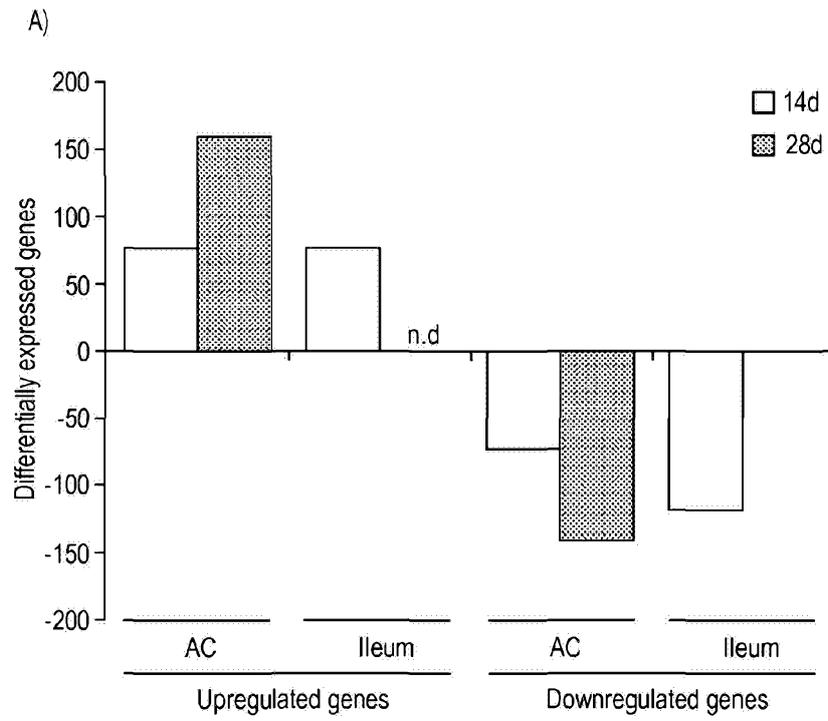


FIG. 4

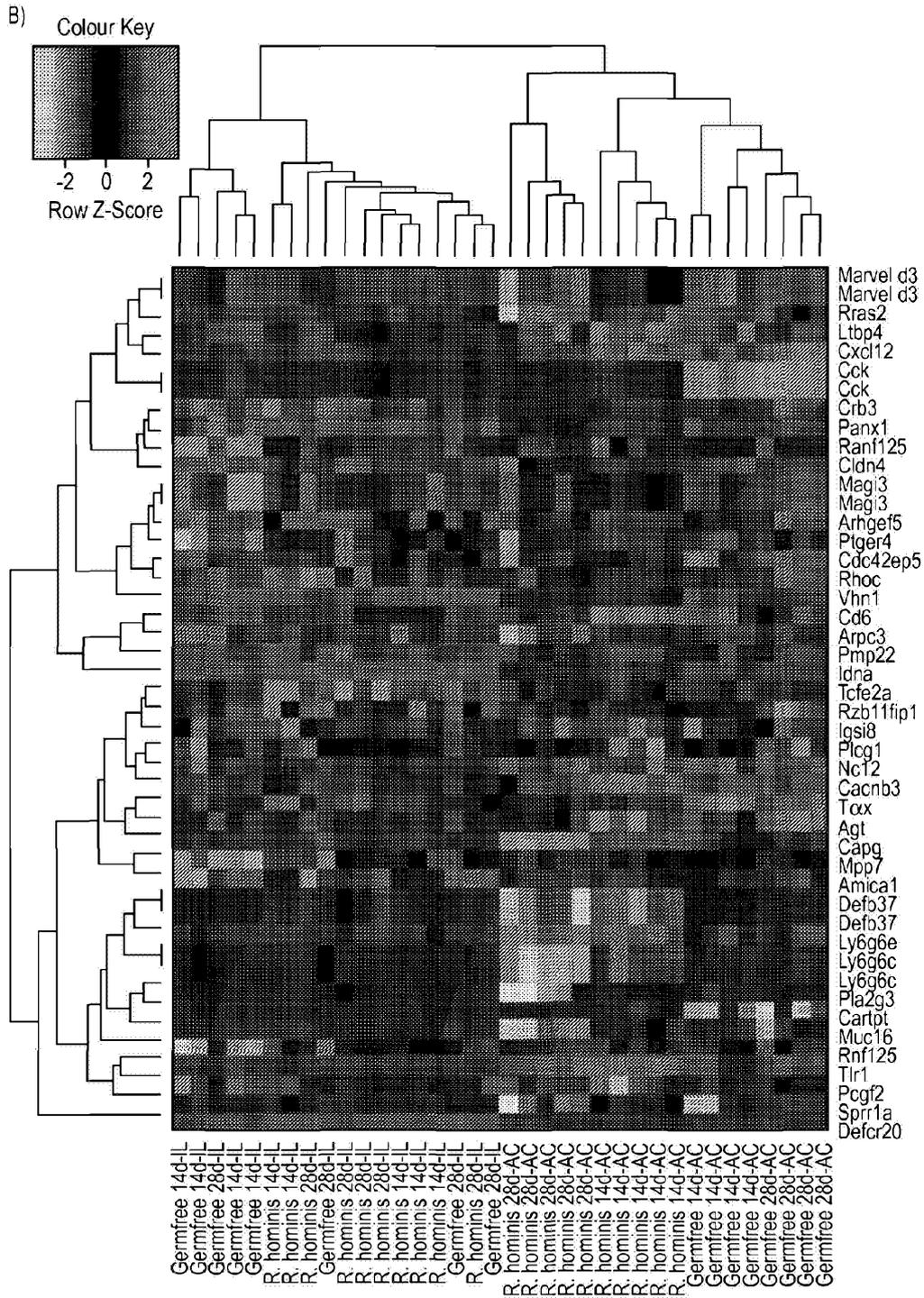


FIG. 4

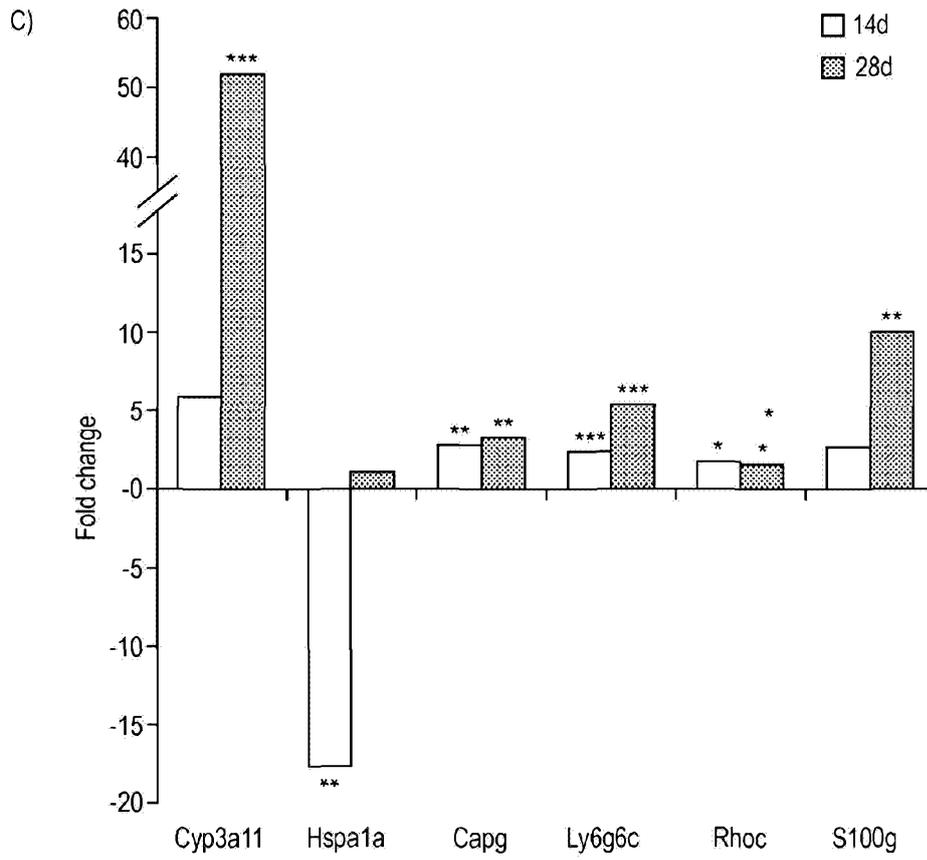


FIG. 4

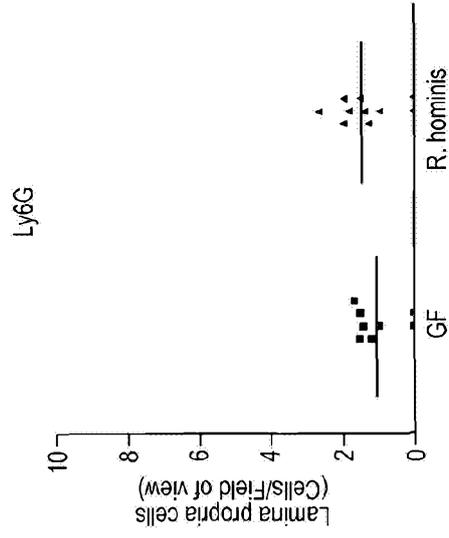
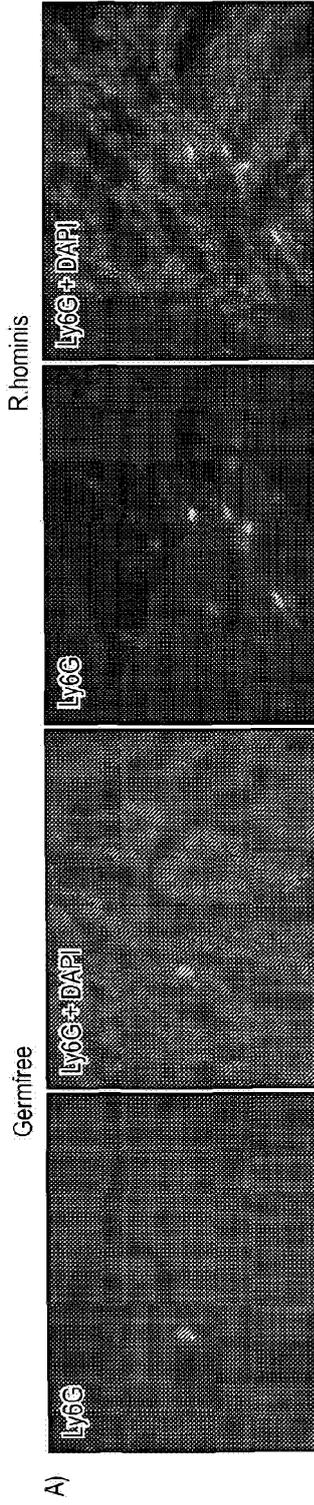


FIG. 5

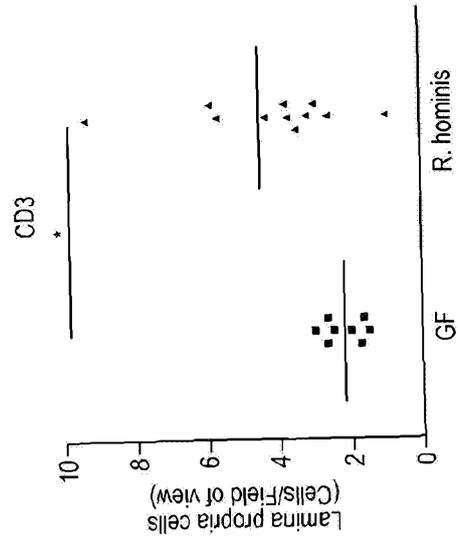
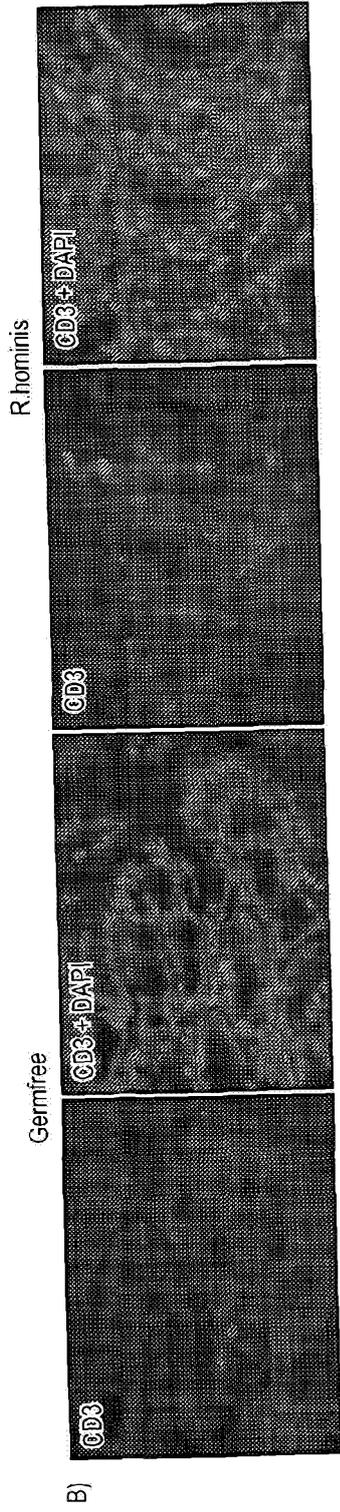


FIG. 5

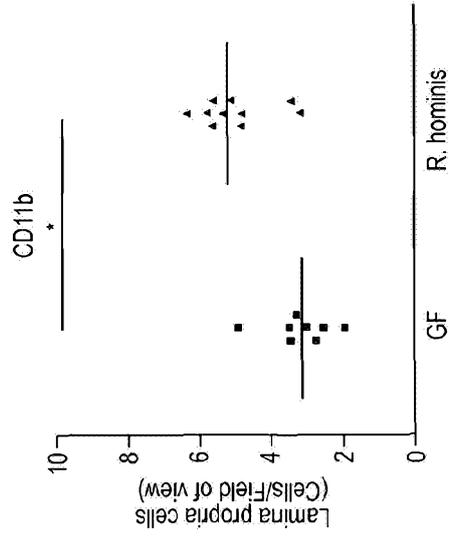
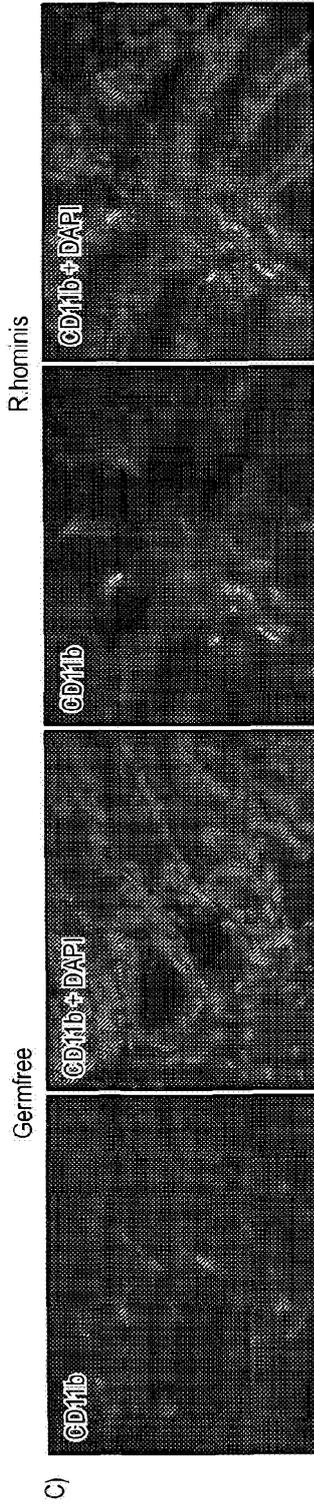


FIG. 5

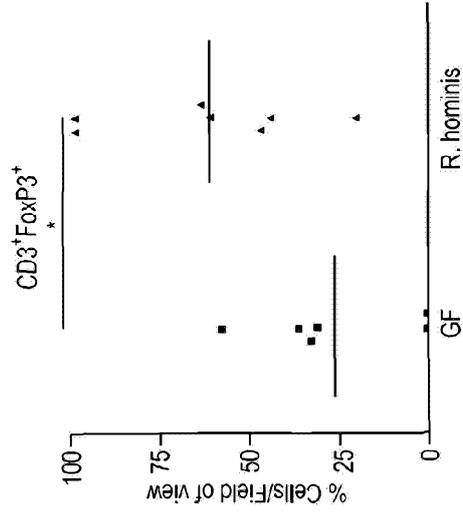
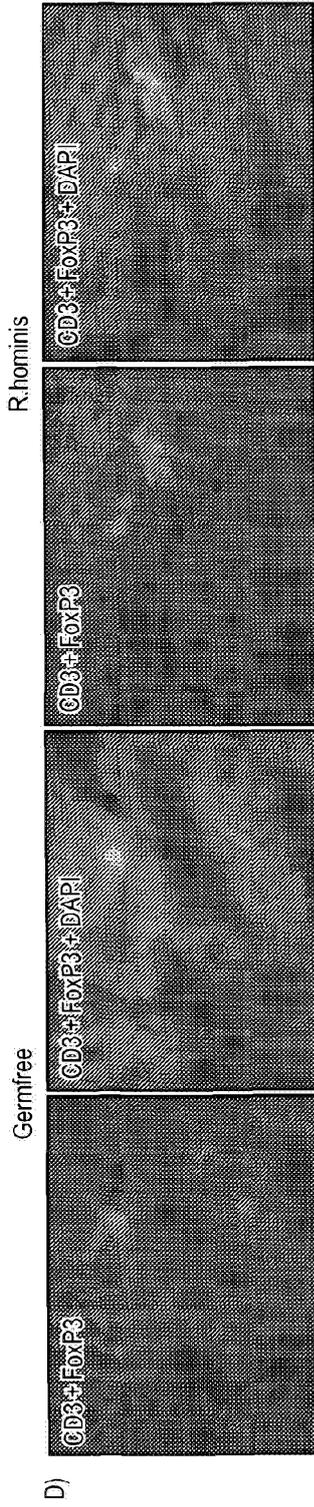


FIG. 5

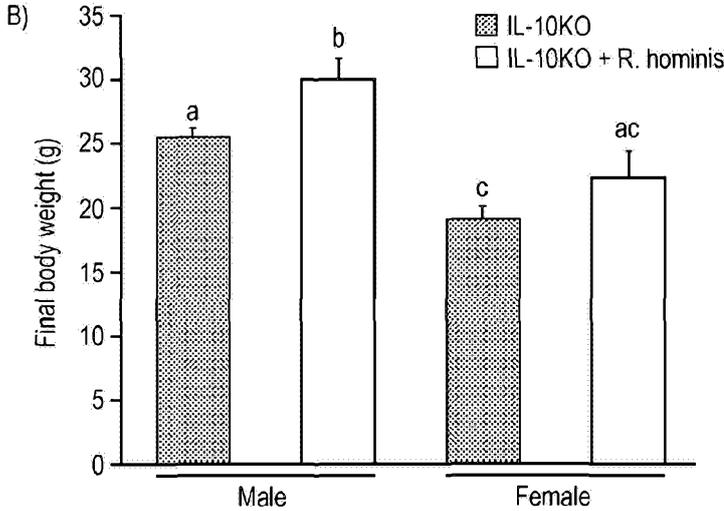
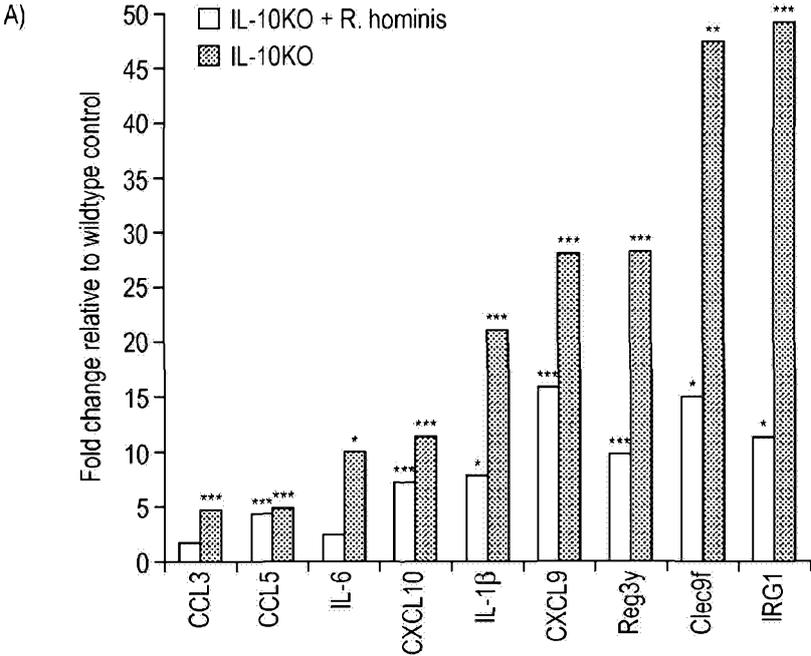


FIG. 6

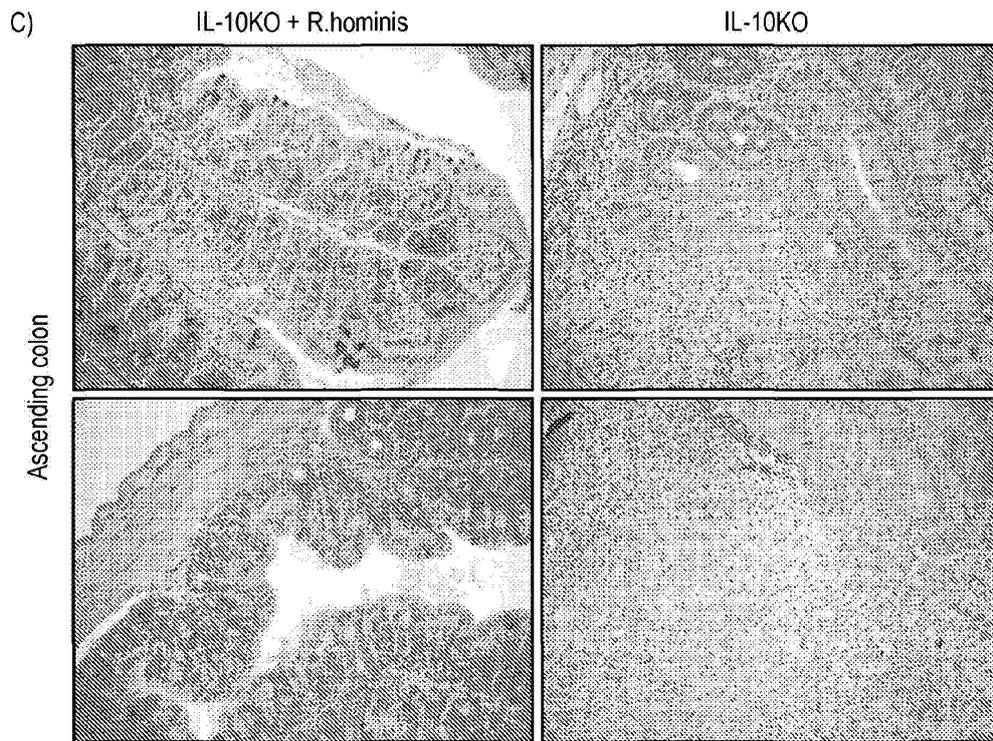


FIG. 6

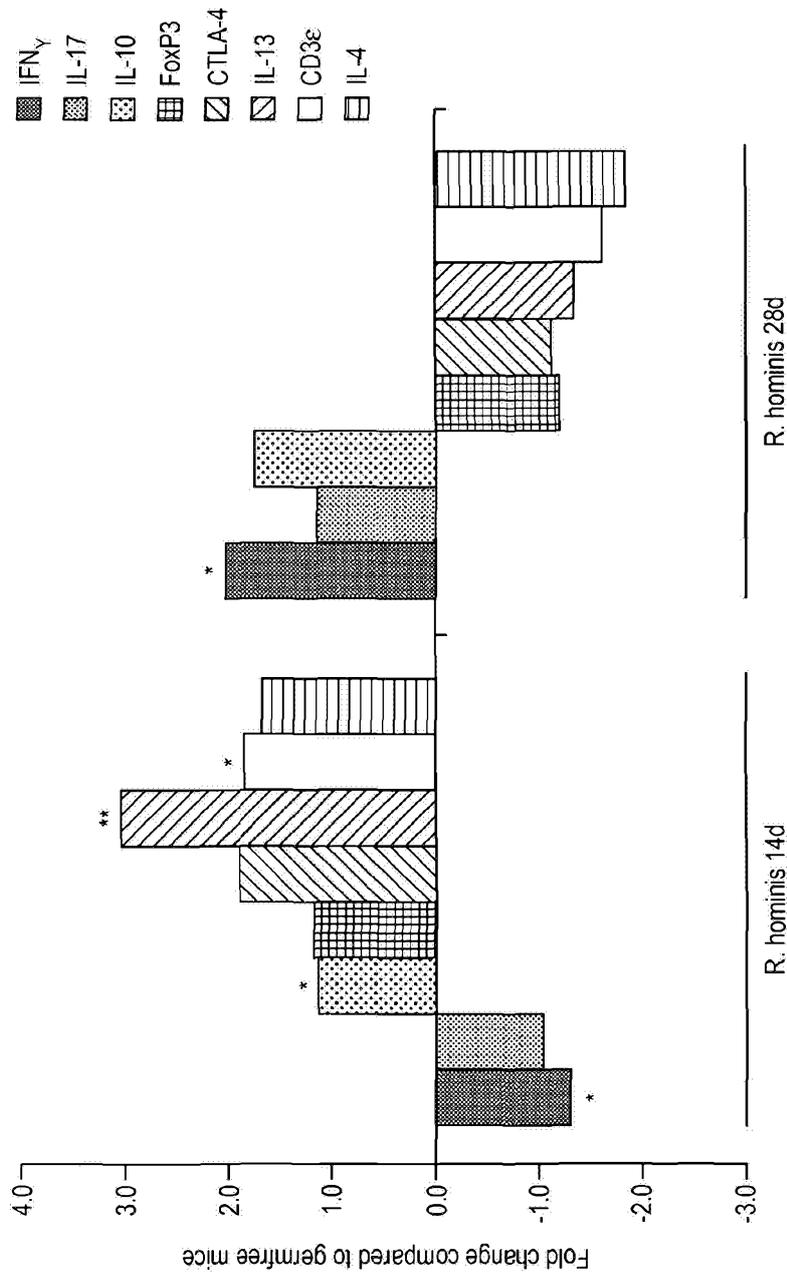


FIG. 7

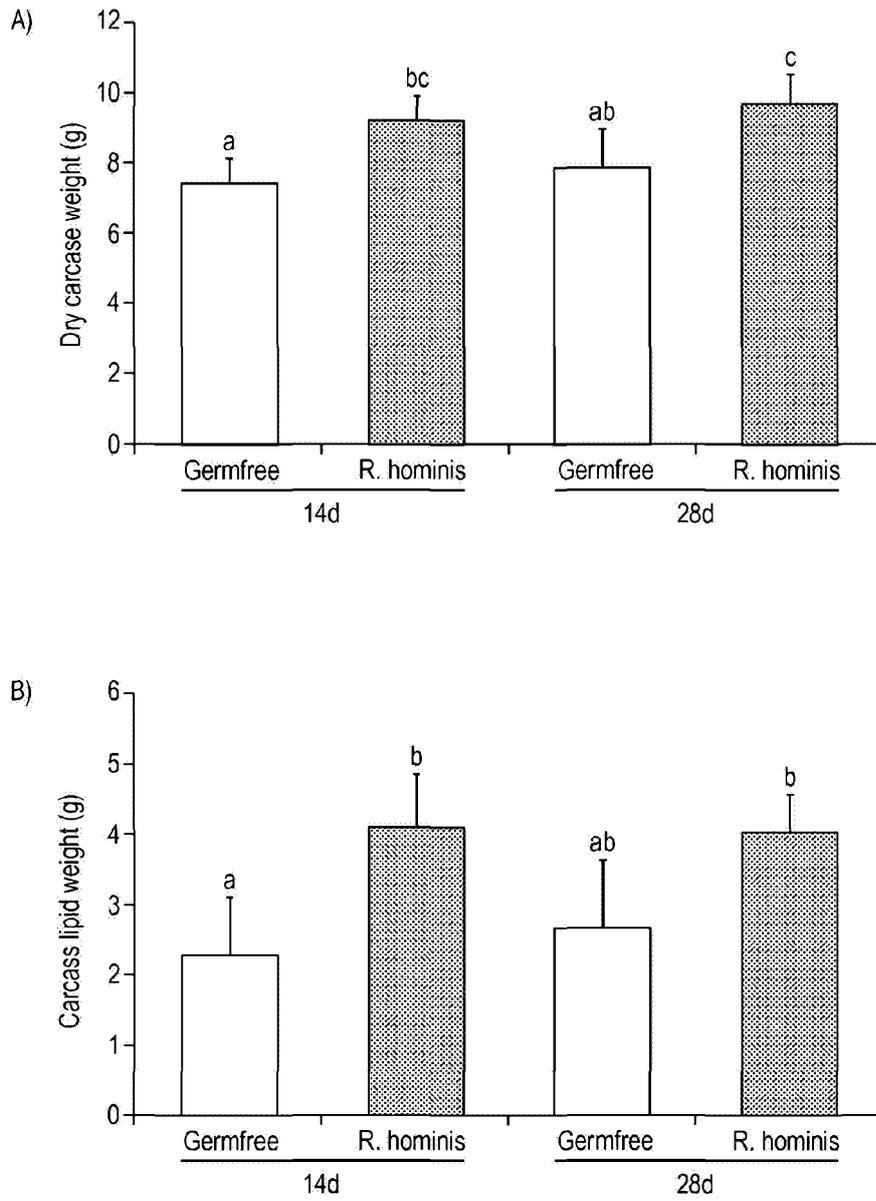


FIG. 8

#	Colour	Experiment name	Species
1		R. hominis-Control none	Mus musculus
2		E. rectale-Control none	Mus musculus
3		R. intestinalis-Control none	Mus musculus

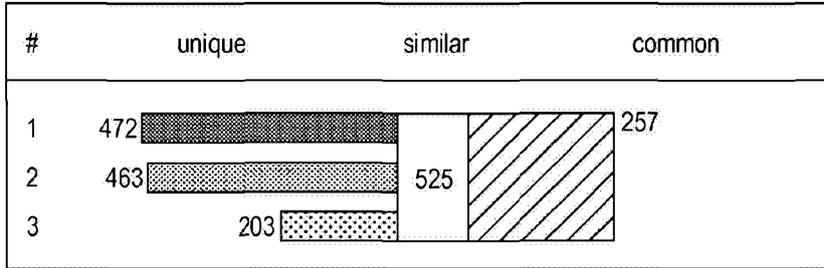


FIG. 9

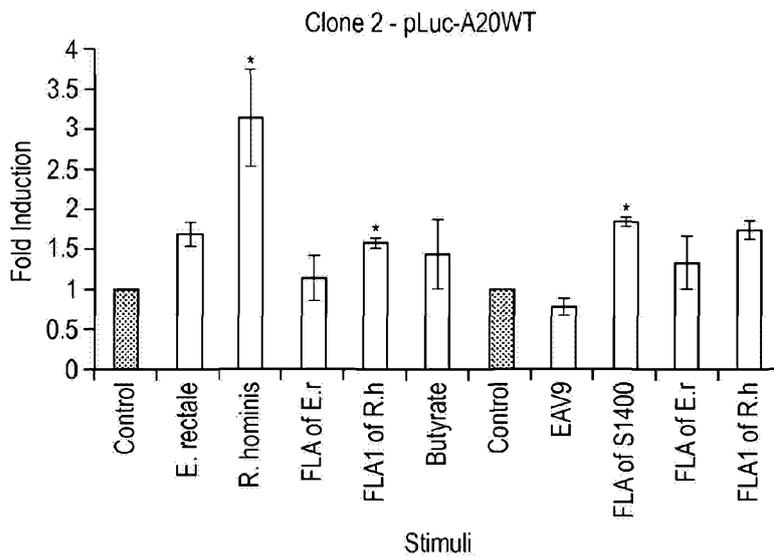


FIG. 10

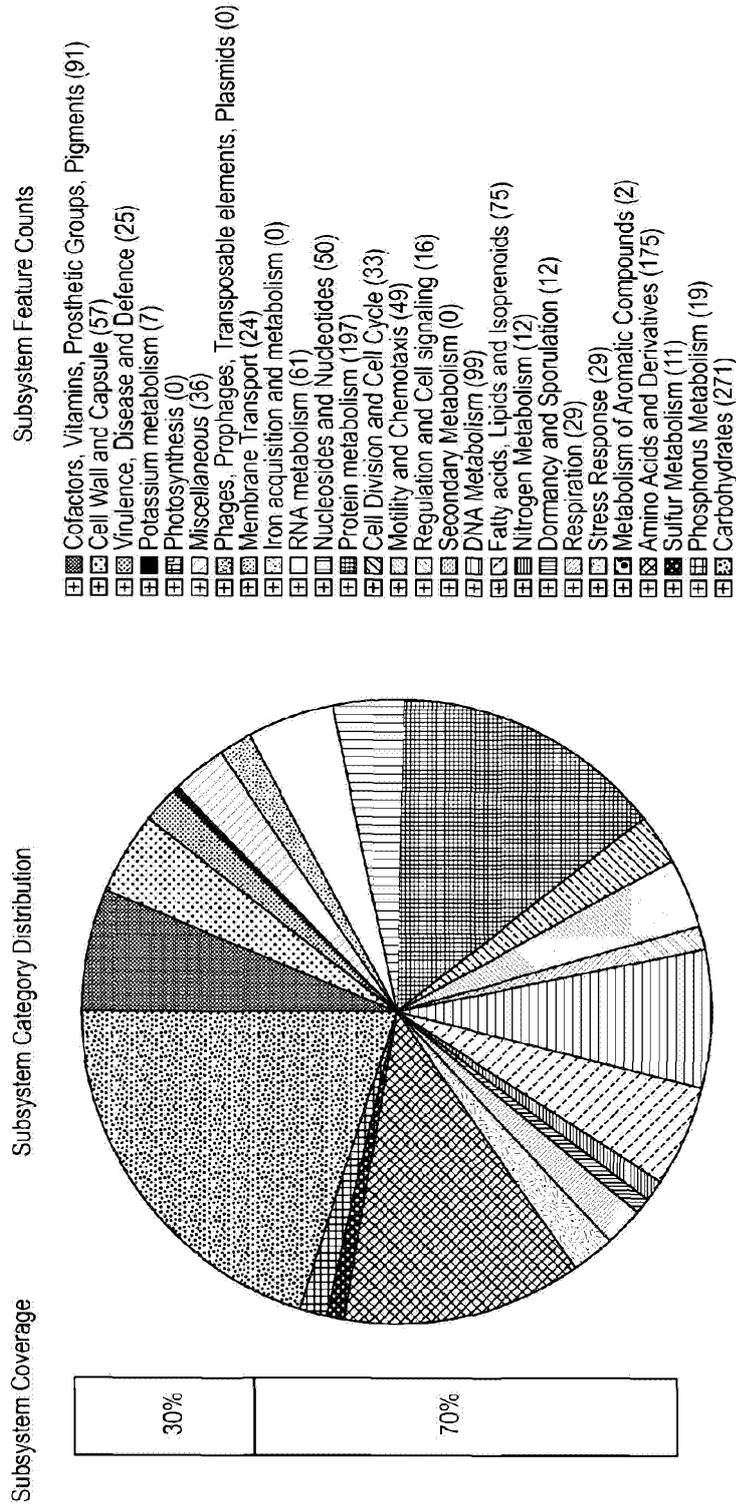


FIG. 11



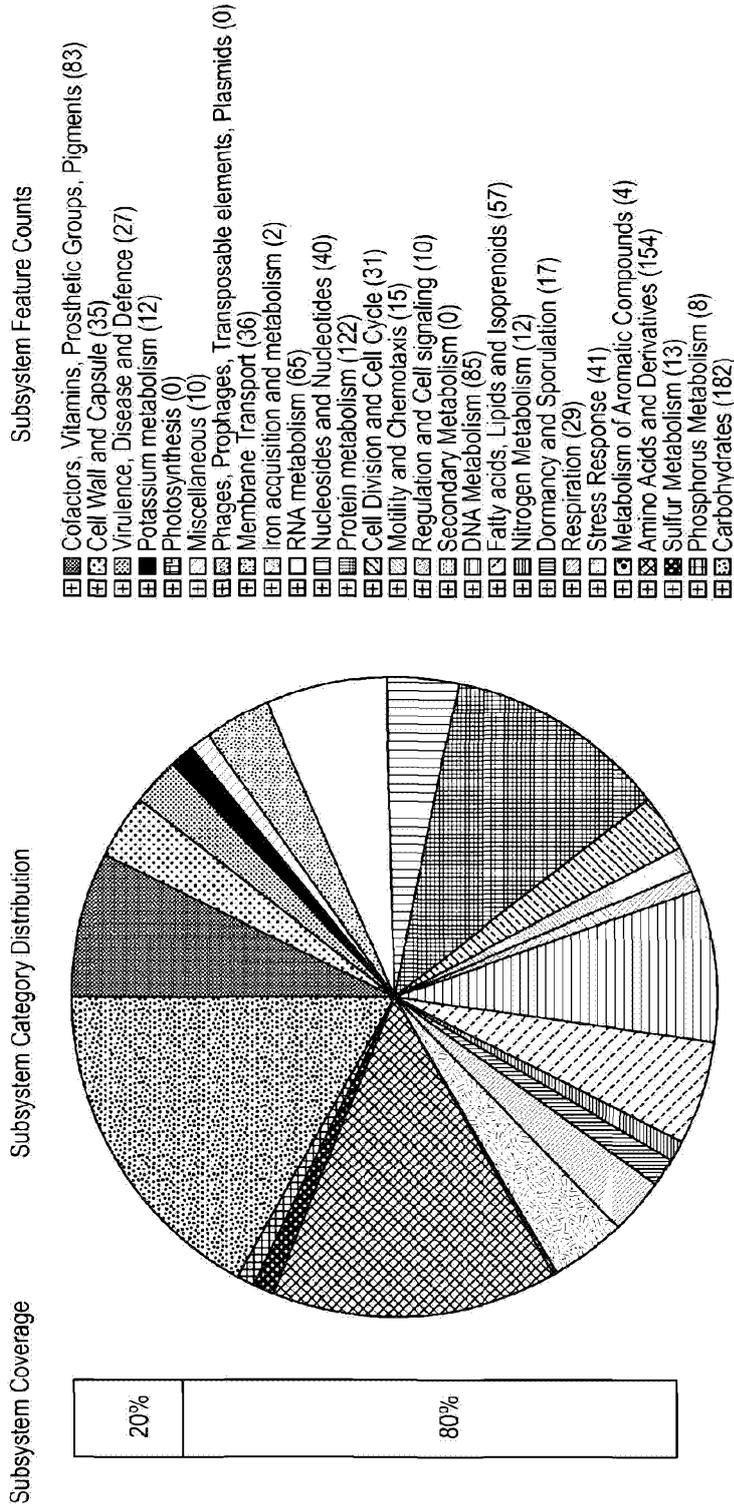


FIG. 13

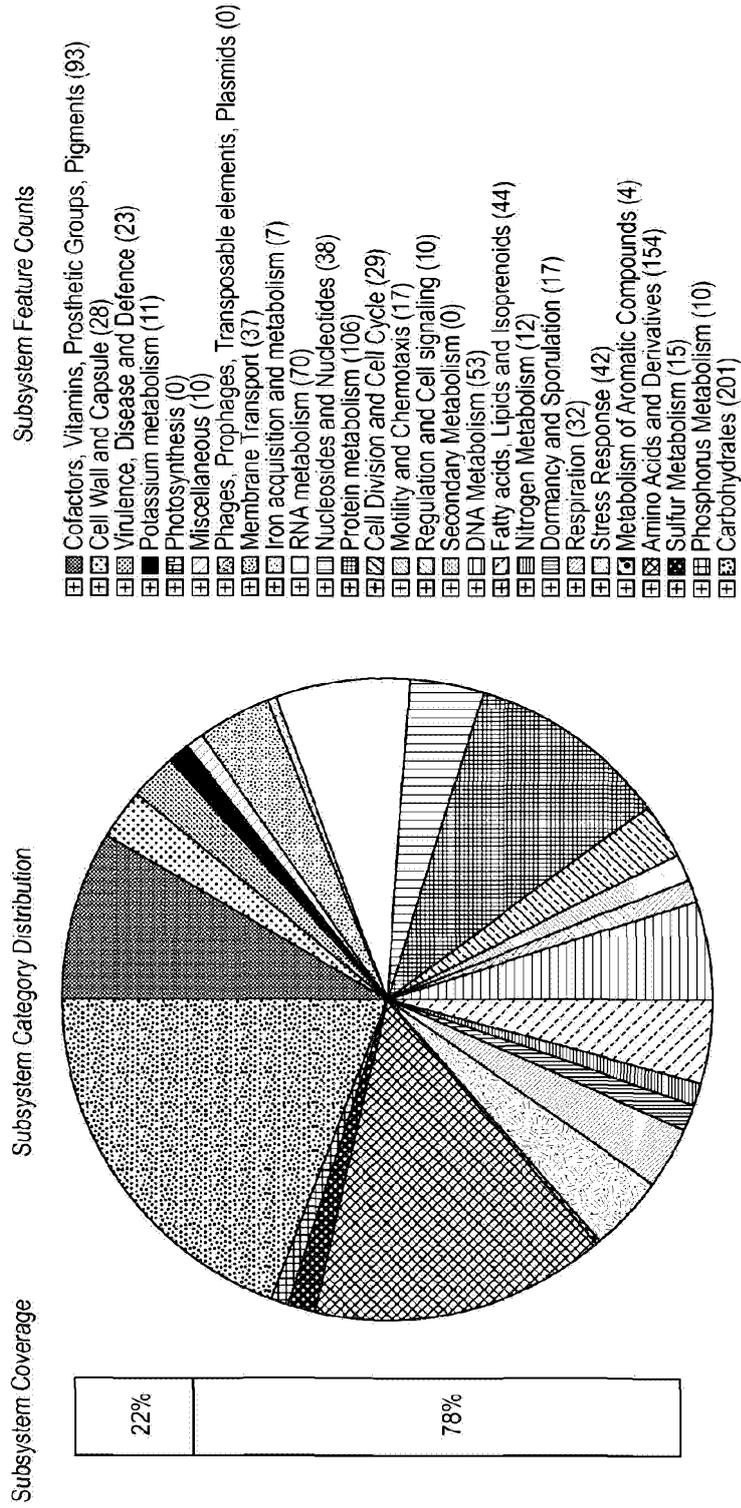


FIG. 14

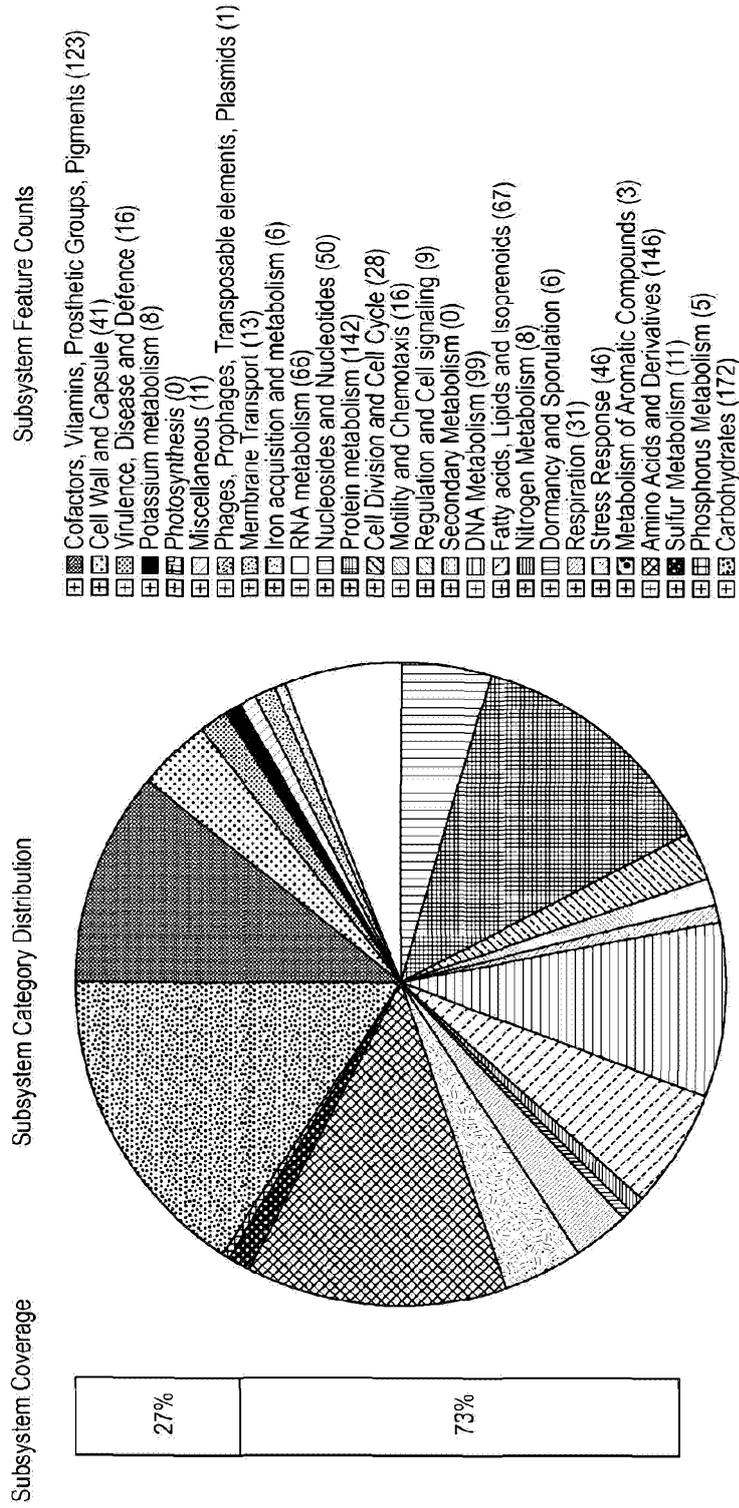


FIG. 15