Legend to Supplementary Figure 1

Phylum-level classification of bacteria identified in individual biopsy samples belonging to the three study groups: Controls, Patients (active CD) and GFD-Patients. Each bar represents the percent relative contribution of phylum-level profiles grouped by disease status for each individual enrolled in the study. Twenty different phyla were identified and represented by different colors.

Legend to Supplementary Figure 2

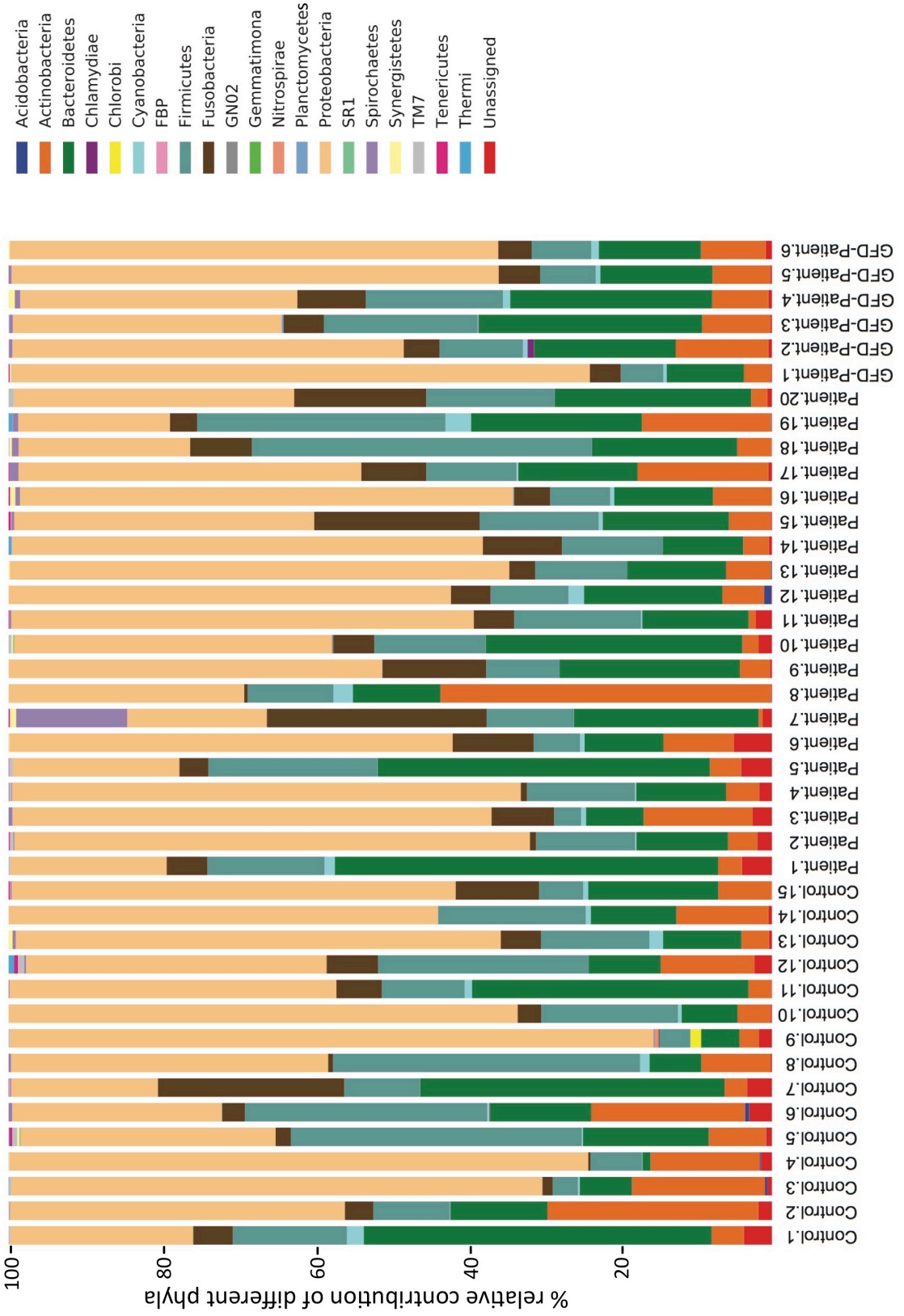
***Neisseria* isolated strains phylogenetic analysis.** Protein maximum likelihood tree derived from the concatenated alignments of 904 unambiguously orthologous single copy genes present in the genomes of all *Neisseria* isolates considered (93,642 amino acid sites). Bootstrap support values are shown when lower than 100%. Genbank Accession numbers are: *Neisseria elongata* ATCC 29315, NZ_ADBF00000000; *Neisseria weaveri* LMG 5135, NZ_AFWQ00000000; *Neisseria weaveri* ATCC 51223, NZ_AFWR01000000; *Neisseria wadsworthii* 9715, NZ_AGAZ00000000; *Neisseria shayeganii* 871, NZ_AGAY01000000; *Neisseria mucosa* ATCC 25996, NZ_ACDX00000000; *Neisseria sicca* ATCC 29256, NZ_ACKO00000000; *Neisseria macacae* ATCC 33926, NZ_AFQE00000000; *Neisseria cinerea* ATCC 14685, NZ_ACDY00000000; *Neisseria polysaccharea* ATCC 43768, NZ_ADBE00000000; *Neisseria lactamica* 020-06, NC_014752; *Neisseria lactamica* ATCC 23970, NZ_ACEQ00000000; *Neisseria meningitidis* MC58, NC_003112.2; *Neisseria meningitidis* 053442, NC_017501; *Neisseria meningitides MOI-240355,* NC_017517.1; *Neisseria gonorrhoeae* FA 1090, NC_002946; *Neisseria gonorrhoeae* NCCP11945, NC_011035; *Neisseria gonorrhoeae* MS11, NC_022240.1; *Neisseria flavescens* SK114, NZ_ACQV00000000; *Neisseria mucosa* C102, ACRG00000000; *Neisseria subflava* NJ9703, NZ_ACEO00000000; *Neisseria flavescens* NRL30031, NZ_ACEN00000000; *Neisseria bacilliformis* ATCC BAA-1200, NZ_AFAY00000000.1; Control-*Nf* (this study), LAEK00000000; CD-*Nf*3 (this study), LAEJ00000000; CD-*Nf*2 (this study), LAEI00000000; CD-*Nf*1 (this study), LAEH00000000).

Legend to Supplementary Figure 3

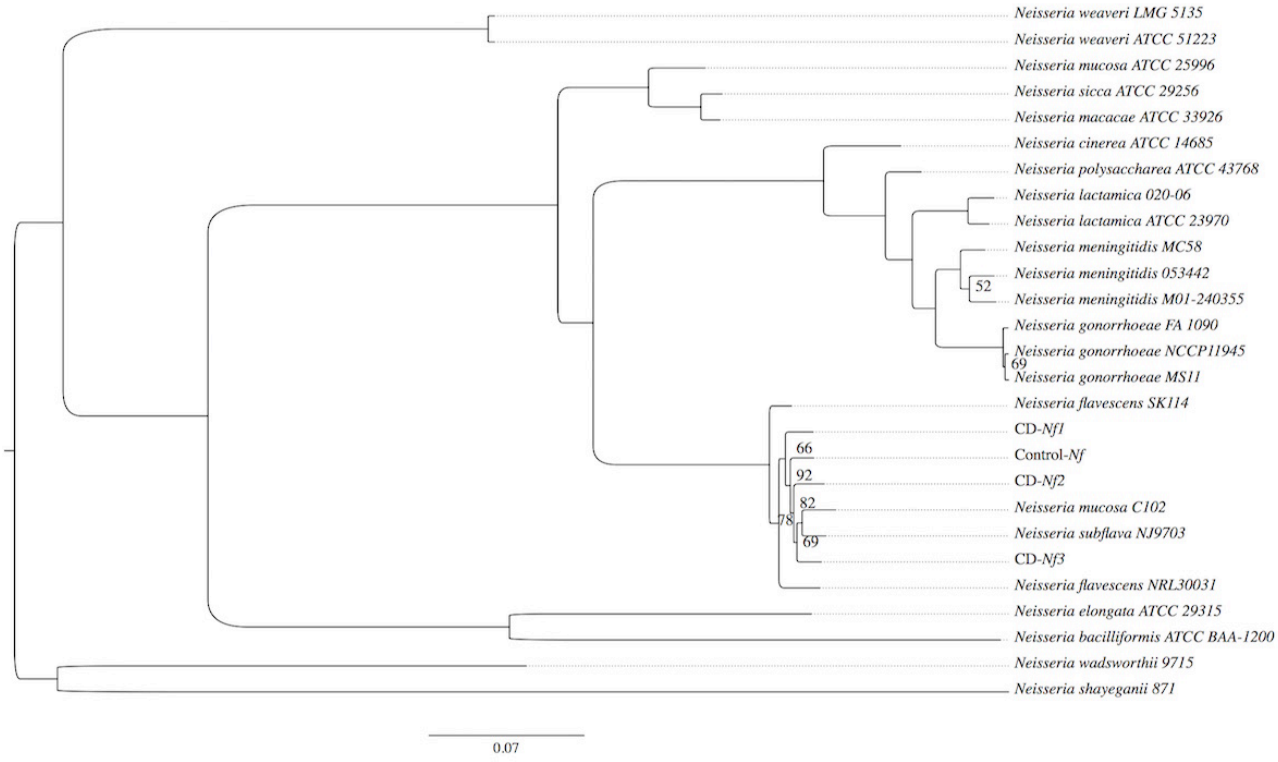
Immunofluorescence analysis showed that in *ex-vivo* mucosal explants from control subjects the CD-*Nf* challenge induced the epithelial expression of HLA-DR. After CD-*Nf* challenge HLA-DR (green) expression was noticeably enhanced in villus enterocytes, in the basal

cytoplasmatic compartment as well as on the brush border and basolateral membranes. This overexpression was also detected in the lamina propria, particularly near the surface epithelium. Data were analyzed using a Fluorescence microscopy. The HLA-DR scoring was graded according to ref. 18 (from absent to very strong: 0 – 3) and measured the increase of HLA-DR expression.

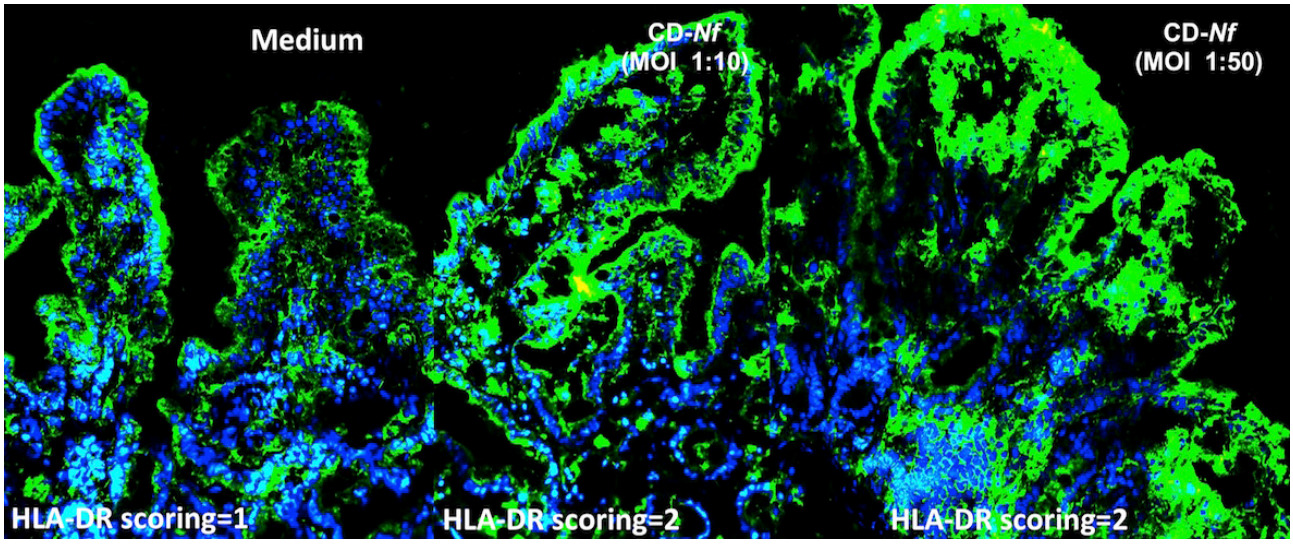
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



Supplementary Table 1. List of the primer' sequences used to amplify, by NGS, the bacterial 16S V4-V6 region. For each couple indicated on the same line, the sequences are reported from 5' to 3', on both forward and reverse primers. Each primer is a fusion primer resulting from the following sequences (from left to right): i) the 454-Roche adaptors sequences (adaptors A and B positioned on the left part of both forward and reverse primers respectively) required for emulsion amplification and sequencing reactions and reported in upper case characters; ii) the sample-specific 10 nucleotide tag sequences (MID 1-10) required to univocally tag each individual subject and reported in underlined characters; iii) the primer template-specific sequences are highlighted in bold characters on the right of the sequences themselves.

16S Primers for whole microbiota amplification					
F (5'-3')			**R (5'-3')**		
Adaptor A	MID (1-10)	Template Specific Primer	Adaptor B	MID (1-10)	Template Specific Primer
CGTATCGCCTCCCTCGCGCCATCAG-	ACGAGTGCGT	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	ACGAGTGCGT	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	ACGCTCGACA	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	ACGCTCGACA	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	AGACGCACTC	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	AGACGCACTC	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	AGCACTGTAG	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	AGCACTGTAG	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	ATCAGACACG	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	ATCAGACACG	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	ATATCGCGAG	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	ATATCGCGAG	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	CGTGTCTCTA	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	CGTGTCTCTA	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	CTCGCGTGTC	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	CTCGCGTGTC	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	TAGTATCAGC	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	TAGTATCAGC	-**TGACGACAGCCATGC**
CGTATCGCCTCCCTCGCGCCATCAG-	TCTCTATGCG	-**CAGCAGCCGCGGTAATAC**	CTATGCGCCTTGCCAGCCCGCTCAG-	TCTCTATGCG	-**TGACGACAGCCATGC**

F:forward; R:reverse.

Supplementary Table 2. Primers for *hmbR, hpuA/hpuB, tbpA/tbpB* gene amplification

Oligonucleotides	Sequences 5'-3'
hmbR Pr4-For	AGCTGTTTGCAGGGACCTTT
hmbR Pr5-Rev	GTTTACGTCATCGGCTTCGC
hmbR Pr6-F	GTTCCCGATGGATTATTCCACC
hmbR Pr6-Rbis	TGCTTTGATACAGGTTGGCATCC
hmbR Pr7-F	TGTCTGAAGAGCAGAAGC
hmbR Pr7-R	CTAAGCCTTTGCCATCG
hpuA 1 F	TTTGACTGCATGTGCAGG
hpuA 1 R	GACGGAGTGTAATAAGACG
hpuA 2 F	AGACCTGTTTGTCGG
hpuA 2 R	TACTGGCTGACAGG
hpuB 1 F	ATGAAGTCAAAGTCATTGGCGGCC
hpuB 1 R	TTGGAAGGTGTTGTTCCAGTAGGC
hpuB 3 F	ATGCTGGTCGAAAGC
hpuB 3 R	TGGTGAAGAGAAACGC
tbpA 1F	GTGATAACGAAGTAACCGG
tbpA 2R	ATATGCCTGAACTGCG
tbpA 3F	TCGCAATTGTCCCACAGC
tbpA 3R	AGACTCCCAAGTGGTATACC
tbpB 1F	TCACTTATTGCCCAAGCAGCC
tbpB 2R	TCGGTTTCGTTATGGGTAATCCG
tbpB 3F	TCTACCGCAATAACCGG

tbpB 4R	AAGCTGTTGGCGTTTCG
tbpAMC58_1F	ACAGTTGGATACCATACAGG
tbpAMC58_1R	TCAGGTTGTGGCGGATTTTG
tbpAMC58_2F	CAAAATCCGCCACAACCTGA
tbpAMC58_2R	GCCGCACATTTTCCCAAGTA
tbpbMC58_1F	ATACTACAGCCTTGAGGC
tbpbMC58_1R	AGTTGCACTGCTATTGCC

Supplementary Table 3. Metadata of 16S bacterial RNA samples in the whole study population (QIIME tool).

	NGS-based duodenal microbiome profiles		
N QF reads	272,560		
N post-OTU picking reads	239,489		
N OTUs	9,674 (1% unclassified; 99% assigned)		
	Control	**CD patients**	**GFD patients**
Non-filtered-per- frequency taxonomic assignment	• 18 phyla • 35 classes • 57 orders • 98 families • 145 genera	• 14 phyla • 32 classes • 53 orders • 97 families • 139 genera	• 13 phyla • 25 classes • 40 orders • 68 families • 100 genera
Filtered-per-frequency >1% taxonomic assignment	• 5 phyla • 6 classes • 7 orders • 9 families • 10 genera	• 5 phyla • 6 classes • 7 orders • 9 families • 10 genera	• 5 phyla • 6 classes • 7 orders • 9 families • 10 genera

NGS: next generation sequencing; N: number; QF: quality filtered; OTU: operational taxonomic units.

Supplementary Table 4

Please, see the xls file in which Supplementary Table 4 is more readable.

Supplementary Table 5

Please, see the xls file in which Supplementary Table 5 is more readable.

Supplementary Table 6. Aerobic bacteria present in duodenal biopsies from active CD patients and controls as identified using culture methods and MALDI-TOF analysis.

Phylum	Species	Active CD patients		Control subjects	
		Lysate	Wash	Lysate	Wash
Firmicutes	*Bacillus cereus*	-	-	+	-
	Lactobacillus	-	-	+	-
	Micrococcus luteus	-	+	+	-
	Staphilococcus aureus	+	-	+	-
	Staphilococcus capitis	-	+	-	-
	Staphilococcus warneri	+	-	+	+
	Staphylococcus hominis	-	-	+	-
	Streptococcus parasanguinis	+	+	+	+
	Streptococcus salivarius	+	+	+	+
	Streptococcus viridans	+	+	+	+
Actinobacteria	*Actinomyces odontolyticus*	+	-	-	-
	Arthrobacter castelli	-	-	+	+
	Rothia dentocariosa	+	-	-	+
	Rothia mucilaginosa	+	+	+	+
	Kocuria rhizophila	-	+	-	-
	Microbacterium	+	-	+	+
Proteobacteria	*Burkholderia cepacia*	-	-	+	+
	Delftia acidovorans	-	+	-	-
	Enterobacter aerogenes	+	-	-	-
	Escherichia coli	-	+	-	-
	Kleibsiella oxytoca	+	-	-	-
	Neisseria flavescens	+	+	-	-
	Stenotrophmonas maltophilia	+	+	+	+

Supplementary Table 7. Whole genome sequencing using the NGS Roche-454 platform, and assembly features of the *Neisseria flavescens* (*Nf*) strains analyzed.

Strains	Number of reads	N50*	Number of contigs	Genome size (Mb)
CD-*Nf*1	184,277	181,117	68	2.22
CD-*Nf*2	117,511	89,374	119	2.28
CD-*Nf*3	159,621	181,822	59	2.30
CTR-*Nf*10	199,324	147,427	55	2,30

CD, Celiac Disease; CTR, Control; CD-*Nf*1/3 (*Nf* strains isolated from duodenal biopsies of CD patients); CTR-*Nf*10 (Nf strain isolated from pharyngeal swab of a control subject).
*Number of reads containing at least a half of the length of all contigs, thus indicating that in all cases they are sufficient for the complete sequencing assessment of the whole genome.

Supplementary Table 8. Presence of genes involved in the iron uptake (left panel) and iron acquisition ability (right panel) evaluated in the CD-*Nf* 1-3, 7, 8 (isolated from duodenal gut of active CD patients), in CTR-*Nf* 10 (isolated from oropharinx of a control subject) and in *N.meningitidis* (*Nm*) as pathogenic control (MC 58, serogroup B) strains. The presence/absence (+/-) of main genes involved in the iron uptake was tested by PCR and the iron uptake capacity yes/not (+/-) by an *in vitro* test using as iron sources: Hb, hemoglobin; Tf, transferrin; FeN, ferric nitrate (positive control) and H_2O, water (negative control).

	Iron uptake genes					***In vitro* iron uptake test**			
						Iron source			
***Nf* Strain**	***hpu*A**	***hpu*B**	***tbp*A**	***tbp*B**	***hmb*R**	**Hb**	**Tf**	**FeN**	**H_2O**
CD-*Nf*1	-	-	-	-	+	+	-	+	-
CD-*Nf*2	-	-	-	-	+	+	-	+	-
CD-*Nf*3	-	-	-	-	+	+	-	+	-
CD-N*f*7	-	-	-	-	+	+	-	+	-
CD-N*f*8	-	-	-	-	+	+	-	+	-
CTR-*Nf*10	+	+	+	+	-	+	+	+	-
Nm	-	-	+	+	+	+	+	+	-

Supplementary Materials and Methods

16S rRNA sequencing

An aliquot of the duodenal DNA was used for PCR amplification and sequencing of the bacterial 16S rRNA gene. To investigate the bacterial composition of duodenal samples in detail, a 548 bp amplicon, spanning from the V4 to V6 variable regions of the 16S rRNA gene, was amplified using the 519F and the 1067R primers.[1] Both primers were modified to obtain fusion primers so that each one contained, at the 5' end, a universal 454 adaptor (adaptor A for the forward primer and adaptor B for the reverse primer) and a specific 10-nucleotide tag/sample (Supplementary Table 1). PCR reactions were carried out with 25 µl of H_2O, 20 µl of 2.5X HotMaster PCR mix (Eppendorf, Hamburg, Germany), 1.5 µl of each primer 10 µM and 60 ng of DNA. The amplifications were performed on a DNA ENGINE Chassis (Bio-Rad Laboratories, Hercules, CA, USA) under the following conditions: 2 min at 94°C, 30 cycles of 94°C for 40 s, 50°C for 40 s, and 65°C for 40 s, and a final extension at 70°C for 7 min. After visualization by gel electrophoresis, each PCR product was individually purified with Ampure magnetic purification beads (Agencourt Biosciences, Beverly, MA, USA), assessed for quality on a Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA, USA) and quantified using the Quant-it PicoGreen dsDNA kit (Invitrogen, Carlsband, CA, USA). Equimolar amounts of each amplicon were pooled to obtain multiple amplicon libraries, each containing a total of 5 mixed subjects. Each library was pyrotag-sequenced on a 454 Genome Sequencer instrument (Roche, Penzberg, Germany), following the manufacturer's instructions and accordingly to Margulies et al.[2]

Bioinformatics evaluation of metagenomics data

16S rRNA barcoded amplicon sequences were analyzed using QIIME v. 1.9.1[3] Sequences were quality-filtered and demultiplexed using default QIIME parameters. The filtered reads were assigned to operational taxonomic units (OTUs) using an open-reference OTU picking approach on the basis of sequence similarity using UCLUST[4] against the Greengenes database (v. 13_8)[5] at 97% identity. A representative set of sequences was taken for each OTU and taxonomic classification was performed with uclust. The representative sequences were aligned using PyNAST[6] to the Greengenes Core reference alignment[7] and a phylogenetic tree was built using FastTree.[8] The phylogenetic tree was used for downstream phylogenetic community analyses. Community diversity analyses at a rarefaction depth of 792 sequences/sample were performed using QIIME related scripts. Principal coordinates analyses (PCoA) were generated from UniFrac weighted and unweighted distance matrices.[9] Alpha diversity, or the within-sample diversity, was computed using

two different metrics: the Faith's Phylogenetic Diversity (PD) richness estimator,[10] and the *observed species* metric, which reports the number of different bacterial OTUs at a rarefaction depth of 792 sequences/sample.

Microbiological analysis

Biopsy samples were collected in 2-ml tubes filled with 0.9 ml of phosphate saline buffer (PBS) and 0.1 ml of glycerol (Carlo Erba Reagents, Milan, Italy) and immediately frozen at -80°C. Each specimen was quickly washed three times in 0.5 ml of PBS and then lysed by vortexing in 0.5 ml of H_2O. Pharyngeal swabs were collected and stored in an appropriate transport medium. Viable cell counts were obtained by plating the samples on appropriate enriched, differential or selective culture media, namely, Becton Dickinson (BD) Trypticase Soy agar with 5% sheep blood, McConkey agar, BD Chocolate agar, BD Columbia CNA agar, BD Sabouraud agar, and BD Schaedler blood agar (Becton Dickinson, Franklin Lakes, NJ, USA). Bacterial species were identified by mass spectrometry using the Matrix Assisted Laser Desorption/Ionization (MALDI) mass spectrometer (Bruker Daltonics MALDI Biotyper, Fremont, CA, USA). All reagents were from Bruker Corporation (Fremont, CA, USA).

Neisseria flavescens DNA isolation and whole genome sequencing

High-molecular-weight genomic DNA from *N. flavescens* isolated strains was prepared as previously reported.[11] DNA fragments were isolated by using acrylamide slab gels and recovered by electroelution as described previously.[12] The whole-genome shotgun sequencing of these isolated strains was carried out using the Genome Sequencer FLX System (454 Life Sciences and Roche, Basel, Switzerland), following the manufacturer's instructions as previously reported.[13] In particular, sequencing libraries were obtained from 500 ng of genomic DNA using a specific sequence tag/sample, so that all the obtained libraries were pooled in an equimolar ratio and sequenced together. Sequencing reads were subjected to quality trimming, error correction and assembly using the SPAdes software,[14] default parameters and genome annotation were performed with the RAST Genome Annotation Server.[15] Custom scripts were used to automate and parse the results of all-against-all tBlastx searches (incorporating 23 representative *Neisserial* genomes) were used to identify clusters of orthologous genes (COGs).

PCR amplification of iron uptake genes *in N. flavescens* isolates

The coding regions of the *hmbR* gene (2373 bp), *tbpA/tbpB* genes (2730 bp and 1779 bp, respectively) and *hpuA/hpuB* genes (996 bp and 2418 bp, respectively) were amplified from

genomic DNA of the isolated *N. flavescens* strains. Amplification reactions were as follows: 30 s of denaturation at 95°C, 45 s of annealing at 60°C or 50°C , and 1 min of extension at 72°C for a total of 30 cycles. Reactions were carried out in a My Cycler thermal cycler (Biorad) using primers indicated in Supplemental Table 2, and the amplicons were sequenced by Sanger methods. Primer synthesis and DNA sequencing were performed by Ceinge Biotecnologie Avanzate s.c.a r.l., Naples, Italy.

Bacterial lysates from *Nf* isolates

Crude extracts were prepared from *CD-Nf* isolates and *Nf*-control strain resuspended in brain heart infusion (BHI) broth until 1.0 OD_{600nm}. Bacterial cells were harvested by centrifugation at 3500 rpm for 20' at 4°C. Cells were mechanically broken by French press in PBS 1X. Total bacterial lysates were then purified by filtration with 0.22 μm syringe filters and protein concentration was assessed by Pierce BCA Protein Assay kit (Thermo Fisher Scientific, Waltham, MA, USA)

Iron uptake ability of CD-*Nf* and Control-*Nf* isolates

To test iron uptake ability*, N. flavescens* strains were grown overnight on Gonococcal (GC) agar supplemented with 1% (vol/vol) Polyvitox (Oxoid, Rodano, MI, Italy) at 37°C with 5% CO_2. Suspension of bacteria (Optical Density 600_{nm}= 0.2) were prepared and spread onto Mueller-Hinton agar (MHA) plates and MHA plates containing 40μM desferal. Disks were impregnated with 10μl of either human haemoglobin (Hb) (10mg ml^{-1}, Sigma-Aldrich, Milan, Italy) or transferrin (Tf) (50mg ml^{-1}, Sigma-Aldrich) and/or Iron (III) nitrate nonahydrate (FeN) (16,2mg ml^{-1}, Sigma-Aldrich) and plated onto a desferal-containing MHA plates along with a fourth disk without any added iron source. Plates were incubated overnight at 37°C in 5% CO_2.[16]

Immunofluorescence analysis

For analyses of antigen expression and tissue distribution by indirect immunofluorescence, 5 μm cryosections were separately incubated in the presence of the following antibodies: HLA-DR (1:5, Beckton Dickinson, San Jose, CA); COX-2 (1:10, Beckton Dickinson, San Jose, CA, USA). Antigen expression and distribution was visualized using a donkey anti-mouse IgGs conjugated to Alexa Fluor 488 for 60 min at room temperature. Isotype control antibodies (IgG1 or IgG2), isotype-matched non-immune IgGs, or isotype-matched antibodies against inappropriate blood group antigens were used as control of specificity. Data were analyzed under fluorescence examination using a fluorescence microscope. HLA-DR expression was graded from absent to very strong (0 – 3).[17] COX-2 –positive cells were counted per mm^2 of mucosa per 100 epithelial cells.

Internalization and intracellular localization of *N. flavescens* in epithelial cells

After infection at a multiplicity of infection of 1:50 for the times indicated, cells were washed with PBS and fixed with 3% paraformaldehyde. Incubation with primary antibody was carried out for 20 min at room temperature to stain extracellular bacteria. After washes in PBS, cells were incubated with secondary antibody (Cy5-conjugated) for 20 min. Then, the cells were permeabilized with 0.1% saponin for 15 min, incubated with primary antibodies to stain bacteria and lysosomes, and then incubated with secondary antibodies (secondary antibodies Alexafluor-546 and Alexafluor-488 conjugated, respectively). Gentamicin (100 mg/ml) was used to kill extracellular bacteria 30 min before completion of the internalization assay at 37°C. Rabbit polyclonal anti-*N. meningitidis* antibody was obtained from ViroStat (6121) and monoclonal CD107a (cod. 555798) anti-Lamp1 was from BD Pharmingen (Milan, Italy). Primary and secondary antibodies were used at a 1:500 dilution.

Supplementary References

1. Baker GC, Smith JJ, Cowan DA. Review and re-analysis of domain-specific 16S primers. J Microbiol Methods 2003; 55:541-555.

2. Margulies M, Egholm M, Altman WE, et al. Genome sequencing in microfabricated high-density picolitre reactors. Nature 2005;437:376-380.

3. Caporaso JG, Kuczynski J, Stombaugh J, et al. QIIME allows analysis of high-throughput community sequencing data. Nat Methods 2010;7:335-336.

4. Edgar RC. Search and clustering orders of magnitude faster than BLAST. Bioinformatics 2010;26:2460-2461.

5. McDonald D, Price MN, Goodrich J, et al. An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. ISME J 2012;6:610–618.

6. Caporaso JG, Bittinger K, Bushman FD, et al. PyNAST: a flexible tool for aligning sequences to a template alignment. Bioinformatics 2010;26:266-267.

7. DeSantis TZ, Hugenholtz P, Larsen N, et al. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. Appl Environ Microb 2006;72:5069-5072.

8. Price MN, Dehal PS, Arkin AP. FastTree 2-Approximately Maximum-Likelihood Trees for Large Alignments. PlosOne 2010;5:e9490.

9. Lozupone C, Knight R. UniFrac: a new phylogenetic method for comparing microbial communities. Appl Environ Microbiol 2005;71: 8228-8235.

10. Faith DP, Baker AM. Phylogenetic diversity (PD) and biodiversity conservation: some bioinformatics challenges. Evolutionary Bioinformatics 2007;2:121-128.

11. Bucci C, Lavitola A, Salvatore P, et al. Hypermutation in pathogenic bacteria: frequent phase variation in meningococci is a phenotypic trait of a specialized mutator biotype. Mol Cell 1999;3:435-445.

12. Sambrook J, Russell DW. Molecular Cloning, A Laboratory Manual, 3rd ed. New York: Cold Spring Harbor Laboratory, 2001.

13. D'Argenio V, Petrillo M, Cantiello P, et al. De novo sequencing and assembly of the whole genome of Novosphingobium sp. strain PP1Y. J Bacteriol 2011;193:4296.

14. Bankevich A, Nurk S, Antipov D, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 2012;19:455-477.

15. Aziz RK, Bartels D, Best AA, et al. The RAST Server: rapid annotations using subsystems technology. BMC Genomics 2008;9:75.

16. Lucidarme J, Findlow J, Chan H et al. The distribution and 'in vivo' phase variation status of haemoglobin receptors in invasive meningococcal serogroup B disease: genotypic and phenotypic analysis. PLoS One 2013;8:e76932.

17. Bucci C, Zingone F, Russo I, et al.Gliadin does not induce mucosal inflammation or basophil activatuion in patients with nonceliac gluten sensitivity. Clin Gastroenterol Hepatol 2013;11:1294-1299.