

# Enterotypes of the human gut microbiome

Manimozhiyan Arumugam<sup>1\*</sup>, Jeroen Raes<sup>1,2\*</sup>, Eric Pelletier<sup>3,4,5</sup>, Denis Le Paslier<sup>3,4,5</sup>, Takuji Yamada<sup>1</sup>, Daniel R. Mende<sup>1</sup>, Gabriel R. Fernandes<sup>1,6</sup>, Julien Tap<sup>1,7</sup>, Thomas Bruls<sup>3,4,5</sup>, Jean-Michel Batto<sup>7</sup>, Marcelo Bertalan<sup>8</sup>, Natalia Borrueal<sup>9</sup>, Francesc Casellas<sup>9</sup>, Leyden Fernandez<sup>10</sup>, Laurent Gautier<sup>8</sup>, Torben Hansen<sup>11,12</sup>, Masahira Hattori<sup>13</sup>, Tetsuya Hayashi<sup>14</sup>, Michiel Kleerebezem<sup>15</sup>, Ken Kurokawa<sup>16</sup>, Marion Leclerc<sup>7</sup>, Florence Levenez<sup>7</sup>, Chaysavanh Manichanh<sup>9</sup>, H. Bjørn Nielsen<sup>8</sup>, Trine Nielsen<sup>11</sup>, Nicolas Pons<sup>7</sup>, Julie Poulain<sup>3</sup>, Junjie Qin<sup>17</sup>, Thomas Sicheritz-Ponten<sup>8,18</sup>, Sebastian Tims<sup>15</sup>, David Torrents<sup>10,19</sup>, Edgardo Ugarte<sup>3</sup>, Erwin G. Zoetendal<sup>15</sup>, Jun Wang<sup>17,20</sup>, Francisco Guarner<sup>9</sup>, Oluf Pedersen<sup>11,21,22,23</sup>, Willem M. de Vos<sup>15,24</sup>, Søren Brunak<sup>8</sup>, Joel Doré<sup>7</sup>, MetaHIT Consortium†, Jean Weissenbach<sup>3,4,5</sup>, S. Dusko Ehrlich<sup>7</sup> & Peer Bork<sup>1,25</sup>

**Our knowledge of species and functional composition of the human gut microbiome is rapidly increasing, but it is still based on very few cohorts and little is known about variation across the world. By combining 22 newly sequenced faecal metagenomes of individuals from four countries with previously published data sets, here we identify three robust clusters (referred to as enterotypes hereafter) that are not nation or continent specific. We also confirmed the enterotypes in two published, larger cohorts, indicating that intestinal microbiota variation is generally stratified, not continuous. This indicates further the existence of a limited number of well-balanced host–microbial symbiotic states that might respond differently to diet and drug intake. The enterotypes are mostly driven by species composition, but abundant molecular functions are not necessarily provided by abundant species, highlighting the importance of a functional analysis to understand microbial communities. Although individual host properties such as body mass index, age, or gender cannot explain the observed enterotypes, data-driven marker genes or functional modules can be identified for each of these host properties. For example, twelve genes significantly correlate with age and three functional modules with the body mass index, hinting at a diagnostic potential of microbial markers.**

Various studies of the human intestinal tract microbiome based on the 16S ribosomal-RNA-encoding gene reported species diversity within and between individuals<sup>1–3</sup>, and the first metagenomics studies characterized the functional repertoire of the microbiomes of several American<sup>4,5</sup> and Japanese<sup>6</sup> individuals. Although a general consensus about the phylum level composition in the human gut is emerging<sup>1,3,7</sup>, the variation in species composition<sup>1,2</sup> and gene pools<sup>5,8</sup> within the human population is less clear. Furthermore, it is unknown whether inter-individual variation manifests itself as a continuum of different community compositions or whether individual gut microbiota congregate around preferred, balanced and stable community compositions that can be classified. Studying such questions is complicated by the complexity of sampling, DNA preparation, processing, sequencing and analysis protocols<sup>9</sup> as well as by varying physiological, nutritional and environmental conditions. To analyse the feasibility of comparative metagenomics of the human gut across cohorts and protocols and to obtain first insights into commonalities and differences between gut microbiomes across different populations, we Sanger-sequenced 22 European metagenomes from Danish, French, Italian and Spanish individuals that were selected for diversity (Supplementary Notes section 1), and combined them with existing Sanger

(13 Japanese<sup>6</sup>, 2 American<sup>4</sup>) and pyrosequencing (2 American<sup>5</sup>) gut data sets—totalling 39 individuals.

## Global variation of human gut metagenomes

The vast majority of sequences in the newly sequenced 22 European samples belong to bacteria—only 0.14% of the reads could be classified as human contamination, all other eukaryotes together only comprised 0.5%, archaea 0.8% and viruses up to 5.8% (see Supplementary Notes section 2.1 for details).

To investigate the phylogenetic composition of the 39 samples from 6 nationalities, we mapped metagenomic reads, using DNA sequence homology, to 1,511 reference genomes (Supplementary Table 3) including 379 publicly available human microbiome genomes generated through the National Institutes of Health (NIH) Human Microbiome Project<sup>10</sup> and the European MetaHIT consortium<sup>11</sup> (Supplementary Methods section 4.1). To consistently estimate the functional composition of the samples, we annotated the predicted genes from the metagenomes using eggNOG<sup>12</sup> orthologous groups (Supplementary Methods section 6.2). We ensured that comparative analysis using these procedures was not biased by data-set origin, sample preparation, sequencing technology and quality filtering (see Supplementary Notes section 1).

<sup>1</sup>European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany. <sup>2</sup>VIB—Vrije Universiteit Brussel, 1050 Brussels, Belgium. <sup>3</sup>Commissariat à l’Energie Atomique, Genoscope, 91000 Evry, France. <sup>4</sup>Centre National de la Recherche Scientifique, UMR8030, 91000 Evry, France. <sup>5</sup>Université d’Evry Val d’Essonne 91000 Evry, France. <sup>6</sup>Department of Biochemistry and Immunology, Universidade Federal de Minas Gerais, Av. Antônio Carlos 6627, 31270-901 Belo Horizonte, Minas Gerais, Brazil. <sup>7</sup>Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France. <sup>8</sup>Center for Biological Sequence Analysis, Technical University of Denmark, DK-2800 Lyngby, Denmark. <sup>9</sup>Digestive System Research Unit, University Hospital Vall d’Hebron, Ciberehd, 08035 Barcelona, Spain.

<sup>10</sup>Barcelona Supercomputing Center, Jordi Girona 31, 08034 Barcelona, Spain. <sup>11</sup>Marie Krogh Center for Metabolic Research, Section of Metabolic Genetics, Faculty of Health Sciences, University of Copenhagen, DK-2100 Copenhagen, Denmark. <sup>12</sup>Faculty of Health Sciences, University of Southern Denmark, DK-5000 Odense, Denmark. <sup>13</sup>Computational Biology Laboratory Bld, The University of Tokyo Kashiwa Campus, Kashiwa-no-ha 5-1-5, Kashiwa, Chiba, 277-8561, Japan. <sup>14</sup>Division of Bioenvironmental Science, Frontier Science Research Center, University of Miyazaki, 5200 Kiyotake, Miyazaki 889-1692, Japan. <sup>15</sup>Laboratory of Microbiology, Wageningen University, 6710BA Ede, The Netherlands. <sup>16</sup>Tokyo Institute of Technology, Graduate School of Bioscience and Biotechnology, Department of Biological Information, 4259 Nagatsuta-cho, Midori-ku, Yokohama-shi, Kanagawa Pref. 226-8501, Japan. <sup>17</sup>BGI-Shenzhen, Shenzhen 518083, China. <sup>18</sup>Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, DK-2800 Lyngby, Denmark. <sup>19</sup>Institució Catalana de Recerca i Estudis Avançats (ICREA), Pg. Lluís Companys 23, 08010 Barcelona, Spain. <sup>20</sup>Department of Biology, University of Copenhagen, DK-2200 Copenhagen, Denmark. <sup>21</sup>Institute of Biomedical Science, Faculty of Health Sciences, University of Copenhagen, DK-2200 Copenhagen, Denmark.

<sup>22</sup>Hagedorn Research Institute, DK-2820 Gentofte, Denmark. <sup>23</sup>Faculty of Health Sciences, University of Aarhus, DK-8000 Aarhus, Denmark. <sup>24</sup>University of Helsinki, FI-00014 Helsinki, Finland. <sup>25</sup>Max Delbrück Centre for Molecular Medicine, D-13092 Berlin, Germany.

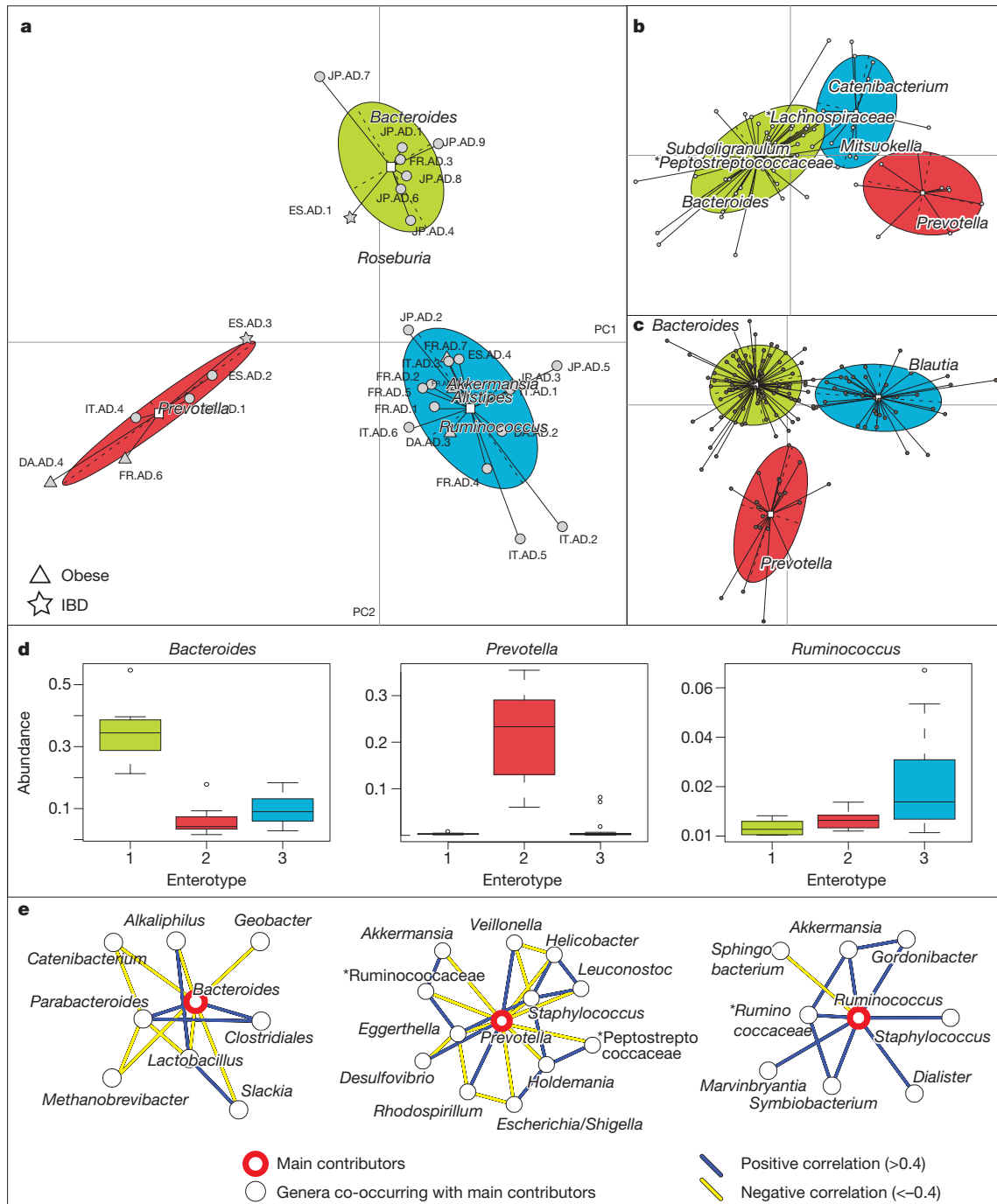
\*These authors contributed equally to this work.

†Lists of authors and affiliations appear at the end of the paper.



species, which could shed light on their survival strategies in the human gut. In the samples analysed here, the most abundant molecular functions generally trace back to the most dominant species. However, we identified some abundant orthologous groups that are contributed to primarily by low-abundance genera (see Supplementary Fig. 2, Supplementary Table 6 and Supplementary Notes section 3). For example, low-abundance *Escherichia* contribute over 90% of two abundant proteins associated with bacterial pilus assembly, FimA (COG3539)

and PapC (COG3188), found in one individual (IT-AD-5). Pili enable the microbes to colonize the epithelium of specific host organs; they help microbes to stay longer in the human intestinal tract by binding to human mucus or mannose sugars present on intestinal surface structures<sup>18</sup>. They are also key components in the transfer of plasmids between bacteria through conjugation, often leading to exchange of protective functions such as antibiotic resistance<sup>18</sup>. Pili can thus provide multiple benefits to these low-abundance microbes in their efforts



**Figure 2 | Phylogenetic differences between enterotypes.** a–c, Between-class analysis, which visualizes results from PCA and clustering, of the genus compositions of 33 Sanger metagenomes estimated by mapping the metagenome reads to 1,511 reference genome sequences using an 85% similarity threshold (a), Danish subset containing 85 metagenomes from a published Illumina data set<sup>8</sup> (b) and 154 pyrosequencing-based 16S sequences<sup>5</sup> (c) reveal three robust clusters that we call enterotypes. IBD, inflammatory bowel disease. Two principal components are plotted using the ade4 package in

R with each sample represented by a filled circle. The centre of gravity for each cluster is marked by a rectangle and the coloured ellipse covers 67% of the samples belonging to the cluster. IBD, inflammatory bowel disease. d, Abundances of the main contributors of each enterotype from the Sanger metagenomes. See Fig. 1 for definition of box plot. e, Co-occurrence networks of the three enterotypes from the Sanger metagenomes. Unclassified genera under a higher rank are marked by asterisks in b and e.

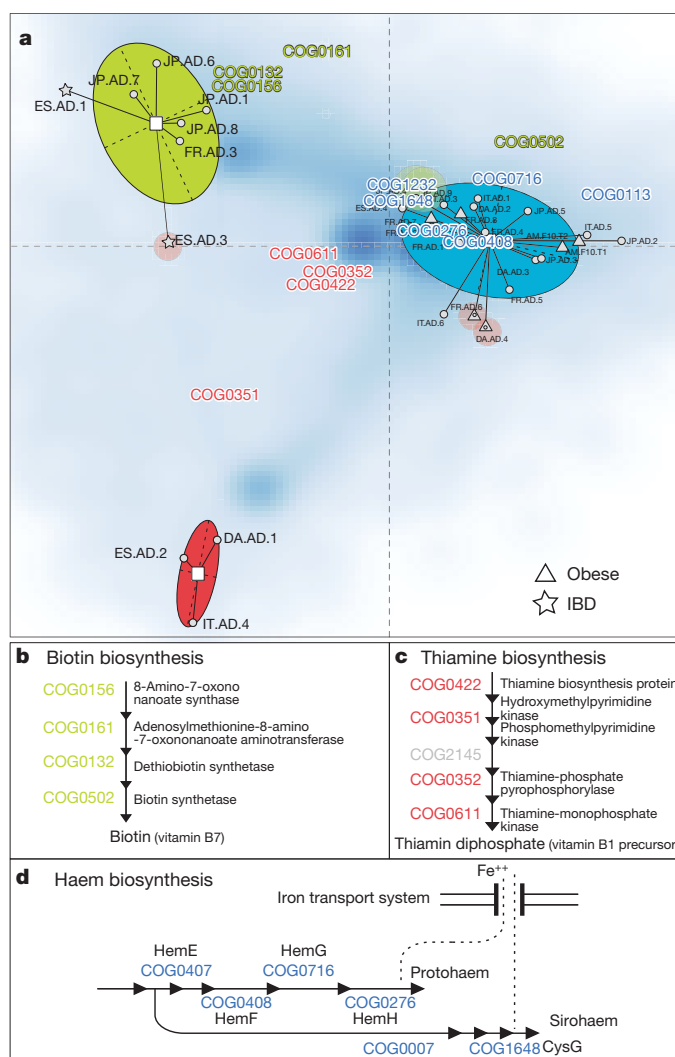
to survive and persist in the human gut. This example illustrates that abundant species or genera cannot reveal the entire functional complexity of the gut microbiota. More reference genomes will facilitate better taxonomic assignment from samples and thus the detection of more low-abundance species. However, there is not much room for as yet undetected, abundant genera. Even with our limited genus assignment rate of 52.8% of all reads, we estimate that we miss another 30.7% of the already classified genera owing to our strict assignment criteria (Supplementary Fig. 1); that is, only 16.5% of all reads are likely to belong to hitherto unknown genera.

### Detection of enterotypes, cross-national clusters

To get an overview of species variation we used phylogenetic profile similarities obtained by mapping metagenomic reads to the 1,511 reference genomes (Fig. 2a; see Supplementary Methods section 4.1). We excluded the two American Sanger-sequenced samples<sup>4</sup> from further analysis because of an unusual, very low fraction of Bacteroidetes and suspected technical artefacts<sup>19</sup>. Multidimensional cluster analysis and principal component analysis (PCA) revealed that the remaining 33 samples formed three distinct clusters that we designate as enterotypes (see Supplementary Notes section 4.1, Supplementary Fig. 3a and Supplementary Table 8). Each of these three enterotypes are identifiable by the variation in the levels of one of three genera: *Bacteroides* (enterotype 1), *Prevotella* (enterotype 2) and *Ruminococcus* (enterotype 3) (Fig. 2a, d), which was reproduced using independent array-based HITChip<sup>20</sup> data in a subset of 22 European samples (Supplementary Fig. 4 and Supplementary Notes section 4.5). The same analysis on two larger published gut microbiome data sets of different origins (16S pyrosequencing data from 154 American individuals<sup>5</sup> and Illumina-based metagenomics data from 85 Danish individuals<sup>8</sup>; Supplementary Methods section 5) shows that these data sets could also be represented best by three clusters (Supplementary Fig. 3b, c and Supplementary Tables 9, 10). Two of these are also driven by *Bacteroides* and *Prevotella*, whereas the third cluster is mostly driven by related groups of the order Clostridiales, *Blautia* and unclassified Lachnospiraceae in the 16S rDNA and Illumina data, respectively (Fig. 2b, c). This can be explained by a different reference data set in the instance of the 16S rDNA data, different mapping behaviour of short reads in the case of the Illumina data or current taxonomic uncertainties in the Lachnospiraceae and Ruminococcaceae clades (see Supplementary Notes section 4.2). The differences might also hint at community sub-populations within this enterotype, which might only be detectable with substantially more samples. Correlation analysis of the Sanger data revealed that abundances of each of the three discriminating genera strongly correlate (that is, they co-occur or avoid each other) with those of other genera (Fig. 2d; see Supplementary Methods section 11), indicating that the enterotypes are in fact driven by groups of species that together contribute to the preferred community compositions.

We demonstrate further the robustness of the enterotypes using two distinct statistical concepts. First, we used the silhouette coefficient<sup>21</sup> to validate that the three clusters are superior to clusterings obtained from various randomizations of the genus profile data, indicating a potential role for the interactions between co-occurring genera (see Supplementary Fig. 5 and Supplementary Notes section 4.3). Second, we used supervised learning and cross-validation to establish that these clusters have non-random characteristics that can be modelled and subsequently used to classify new samples (learning on clusters from randomized genus profiles led to considerably worse classification performance; see Supplementary Fig. 6 and Supplementary Notes section 4.4). These consistent results indicate that enterotypes will be identifiable in human gut metagenomes also from larger cohorts.

We then clustered the 33 samples using a purely functional metric: the abundance of the assigned orthologous groups (Fig. 3a). Remarkably, this clustering also showed a similar grouping of the samples with only minor differences (five samples placed in different clusters compared



**Figure 3 | Functional differences between enterotypes.** **a**, Between-class analysis (see Fig. 2) of orthologous group abundances showing only minor disagreements with enterotypes (unfilled circles indicate the differing samples). The blue cloud represents the local density estimated from the coordinates of orthologous groups; positions of selected orthologous groups are highlighted. **b**, Four enzymes in the biotin biosynthesis pathway (COG0132, COG0156, COG0161 and COG0502) are overrepresented in enterotype 1. **c**, Four enzymes in the thiamine biosynthesis pathway (COG0422, COG0351, COG0352 and COG0611) are overrepresented in enterotype 2. **d**, Six enzymes in the haem biosynthesis pathway (COG0007, COG0276, COG0407, COG0408, COG0716 and COG1648) are overrepresented in enterotype 3.

to Fig. 2a), indicating that function and species composition roughly coincide with some exceptions such as Spanish sample ES-AD-3, whose genus composition belongs to enterotype 2 whereas its functional composition is similar to members of enterotype 1. This individual has high levels of phage-related genes compared to the other samples (see Supplementary Fig. 7), hinting at partial temporal variability and dynamics of the microbiota, and perhaps indicating phage or virus bursts.

The robustness and predictability of the enterotypes in different cohorts and at multiple phylogenetic and functional levels indicates that they are the result of well-balanced, defined microbial community compositions of which only a limited number exist across individuals. These enterotypes are not as sharply delimited as, for example, human blood groups; they are, in contrast, densely populated areas in a multi-dimensional space of community composition. They are nevertheless likely to characterize individuals, in line with previous reports that gut

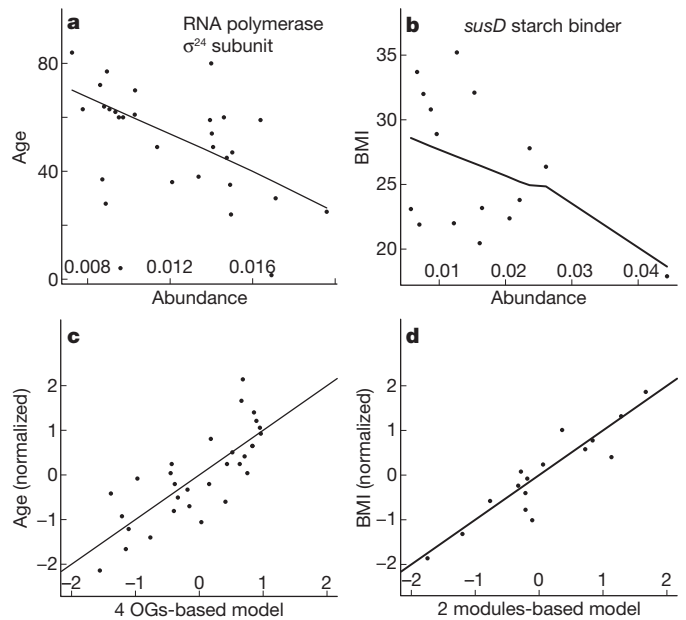
microbiota are quite stable in individuals and can even be restored after perturbation<sup>22–25</sup>.

### Variation between enterotypes

To determine the phylogenetic and functional basis of the enterotypes, we investigated in detail their differences in composition at the phylum, genus, gene and pathway level as well as correlations in abundance of co-occurring genera (Figs 2, 3; also see Supplementary Methods sections 10, 11 and 12). Enterotype 1, containing eight samples, is enriched in *Bacteroides* ( $P < 0.01$ ; Supplementary Fig. 8), which co-occurs, for example, with *Parabacteroides* (see Supplementary Table 11 for enriched genera and Fig. 2e for correlation networks of co-occurring genera in each enterotype). The drivers of this enterotype seem to derive energy primarily from carbohydrates and proteins through fermentation, as these closely related genera have a very broad saccharolytic potential<sup>26</sup> and because genes encoding enzymes involved in the degradation of these substrates (galactosidases, hexosaminidases, proteases) along with glycolysis and pentose phosphate pathways are enriched in this enterotype (see Supplementary Tables 12, 13). Enterotype 2 contains six samples and is enriched in *Prevotella* ( $P < 0.01$ ; Supplementary Fig. 9) and the co-occurring *Desulfovibrio*, which can act in synergy to degrade mucin glycoproteins present in the mucosal layer of the gut: *Prevotella* is a known mucin-degrader and *Desulfovibrio* may enhance the rate-limiting mucin desulphation step by removing the sulphate<sup>27</sup>. Enterotype 3 is the most frequent and is enriched in *Ruminococcus* ( $P < 0.01$ ; Supplementary Fig. 10) as well as co-occurring *Akkermansia*, both known to comprise species able to degrade mucins<sup>28</sup>. It is also enriched in membrane transporters, mostly of sugars, indicating the efficient binding of mucin and its subsequent hydrolysis as well as uptake of the resulting simple sugars by these genera. The enriched genera indicate that enterotypes use different routes to generate energy from fermentable substrates available in the colon, reminiscent of a potential specialization in ecological niches or guilds. In addition to the conversion of complex carbohydrates into absorbable substrates, the gut microbiota is also beneficial to the human host by producing vitamins. Although all the vitamin metabolism pathways are represented in all samples, enterotypes 1 and 2 were enriched in biosynthesis of different vitamins: biotin (Fig. 3b), riboflavin, pantothenate and ascorbate in the former, and thiamine (Fig. 3c) and folate in the latter. These phylogenetic and functional differences among enterotypes thus reflect different combinations of microbial trophic chains with a probable impact on synergistic interrelations with the human hosts.

### Functional biomarkers for host properties

Enterotypes do not seem to differ in functional richness (Supplementary Fig. 11), and virtually none of several measured host properties, namely nationality, gender, age or body mass index (BMI), significantly correlates with the enterotypes (with the exception of enterotype 1, which is enriched in Japanese individuals). However, some strong correlations do occur between host properties and particular functions, at the genes or module level (a module is a part of a pathway that is functionally tightly interconnected; see Supplementary Methods sections 6, 13 and Supplementary Notes section 6). The only significant correlation between a host property and a taxonomic group is a negative one between age and the abundance of an unknown Clostridiales genus ( $P < 0.02$ ) containing three obligate anaerobes (Supplementary Fig. 12a; see Supplementary Notes section 6.2). It should be noted that age is not constant across the nationalities (in our data set, Italians are relatively old and Japanese young), but that individuals did not stratify by nationality, indicating that this is not a confounding factor. Our data did not reveal any correlation between BMI and the Firmicutes/Bacteroidetes ratio and we thus cannot contribute to the ongoing debate on the relationship between this ratio and obesity<sup>29,30</sup>.



**Figure 4 | Correlations with host properties.** **a**, Pairwise correlation of RNA polymerase facultative  $\sigma^{24}$  subunit (COG1595) with age ( $P = 0.03$ ,  $\rho = -0.59$ ). **b**, Pairwise correlation of *SusD*, a family of proteins that bind glycan molecules before they are transported into the cell, and BMI ( $P = 0.27$ ,  $\rho = -0.29$ , weak correlation). **c**, Multiple orthologous groups (OGs) (COG0085, COG0086, COG0438 and COG0739; see Supplementary Table 18) significantly correlating with age when combined into a linear model (see Supplementary Methods section 13 and ref. 40 for details;  $P = 2.75 \times 10^{-5}$ , adjusted  $R^2 = 0.57$ ). **d**, Two modules, ATPase complex and ectoine biosynthesis (M00051), significantly correlating with BMI when combined into a linear model ( $P = 6.786 \times 10^{-6}$ , adjusted  $R^2 = 0.82$ ).

In contrast to the minor phylogenetic signal, we found several significant functional correlations with each of the host properties studied (after correcting for multiple testing to avoid artefacts; see Supplementary Methods section 13), indicating that metagenomics-derived functional biomarkers might be more robust than phylogenetic ones. For example, the abundance of ten orthologous groups varies more between than within nationalities (Supplementary Table 14), although overall, the functional composition in total was remarkably similar among the nations (also with respect to the functional core; see Supplementary Fig. 13). For gender, we find five functional modules and one orthologous group that significantly correlate ( $P < 0.05$ ; for example, enriched aspartate biosynthesis modules in males; see Supplementary Table 16). In addition, twelve orthologous groups significantly correlate with age (Supplementary Table 17). For instance, starch degradation enzymes such as glycosidases and glucan phosphorylases increase with age (which could be a reaction to decreased efficiency of host breakdown of dietary carbohydrates with age<sup>31</sup>) and so does the *secA* preprotein translocase (Supplementary Fig. 14). Conversely, an orthologous group coding for the facultative  $\sigma^{24}$  subunit of RNA polymerase, which drives expression under various stress responses and is linked to intestinal survival<sup>32</sup>, decreases with age (Fig. 4a). One explanation for this could be the reduced need for stress response in the gut due to the age-associated decline in host immune response<sup>33</sup> (immunosenescence). Our analyses also identified three marker modules that correlate strongly with the hosts' BMI (Supplementary Table 19 and Supplementary Fig. 14), two of which are ATPase complexes, supporting the link found between the gut microbiota's capacity for energy harvest and obesity in the host<sup>34</sup>. Interestingly, functional markers found by a data-driven approach (derived from the metagenomes without previous knowledge) gave much stronger correlations than genes for which a link would be expected (for example, *susC/susD*, involved in starch utilization<sup>26</sup>;

Fig. 4b). Linear models combining the abundance of only a few functional modules correlate even better with host properties (Fig. 4c, d). It should be noted that given the possibility of many confounding variables owing to the heterogeneity and size of our cohort, these observations will need to be substantiated using larger, independent cohorts in the future. Furthermore, patterns in metagenomics data can (partly) reflect indirect factors<sup>9</sup> such as genome size<sup>35</sup> (the smaller the average genome size of a sample, the higher the relative fraction of single copy genes therein), which, however, does not matter for diagnostics.

Although individual host properties do not explain the enterotypes, the latter might be driven by a complex mixture of functional properties, by host immune modulation or by hitherto unexplored physiological conditions such as transit time or pH of luminal contents. Furthermore, the three major enterotypes could be triggered by the three distinct pathways for hydrogen disposal<sup>36</sup> (Supplementary Notes section 6.4). Indeed, despite their low abundance, *Methanobrevibacter* (a methanogen) and *Desulfovibrio* (a known sulphate-reducer) are enriched in enterotypes 3 and 1, respectively.

Taken together, we have demonstrated the existence of enterotypes in the human gut microbiome and have identified three of them that vary in species and functional composition using data that spans several nations and continents. As our current data do not reveal which environmental or even genetic factors are causing the clustering, and as faecal samples are not representative of the entire intestine, we anticipate that the enterotypes introduced here will be refined with deeper and broader analysis of individuals' microbiomes. Presumably, enterotypes are not limited to humans but also occur in animals. Their future investigation might well reveal novel facets of human and animal symbiotic biology and lead to the discovery of those microbial properties correlated with the health status of individuals. We anticipate that they might allow classification of human groups that respond differently to diet or drug intake. Enterotypes appear complex, are probably not driven by nutritional habits and cannot simply be explained by host properties such as age or BMI, although there are functional markers such as genes or modules that correlate remarkably well with individual features. The latter might be utilizable for diagnostic and perhaps even prognostic tools for numerous human disorders, for instance colorectal cancer and obesity-linked co-morbidities such as metabolic syndrome, diabetes and cardiovascular pathologies.

## METHODS SUMMARY

**Sample collection.** Human faecal samples from European individuals were collected and frozen immediately, and DNA was purified as described previously<sup>37</sup>. Sequencing was carried out by Sanger-sequencing random shotgun DNA libraries of 3 kb using standard protocols established at Genoscope. For sequence processing, cloning vector, sequencing primers and low-quality bases were end-trimmed from raw Sanger reads, and possible human DNA sequences were removed. Reads were processed by the SMASH comparative metagenomics pipeline<sup>38</sup> for assembly and gene prediction.

Informed consent was obtained from the 22 European subjects. Sample collection and experiments were approved by the following ethics committees: MetaHIT (Danish), ethical committee of the Capital Region of Denmark; MetaHIT (Spanish), CEIC, Hospital Vall d'Hebron; MicroObes, Ethical Committee for Studies with Human Subjects of Cochin Hospital in Paris, France; MicroAge, Joint Ethical Committee of the University of Camerino.

**Phylogenetic annotation.** Phylogenetic annotation of samples was performed by (1) aligning reads (Sanger/Illumina) against a database of 1,511 reference genomes (listed in Supplementary Table 3); or (2) classifying 16S rDNA reads using RDP classifier<sup>39</sup>. Genus and phylum abundance was estimated after normalizing for genome size for the former, and for 16S gene copy number for the latter.

**Functional annotation.** Genes were functionally annotated using BLASTP against eggNOG (v2) and KEGG (v50) databases. Protein abundances were estimated after normalizing for protein length. Functional abundance profiles at eggNOG, KEGG orthologous group, functional module and pathway level were created.

**Clustering and classification.** Samples were clustered using Jensen-Shannon distance and partitioning around medoid (PAM) clustering. Optimal number of clusters was estimated using the Calinski-Harabasz (CH) index. We used the silhouette validation technique for assessing the robustness of clusters. Additionally, within a cross-validation scheme, we trained predictive decision tree models on clusters

obtained using the same clustering method and evaluated the classification of hold-out samples by accuracy, average precision and average precision gain.

**Statistics.** Correlations between metadata and feature abundances were computed as described previously<sup>40</sup>, based on multiple-testing corrected pairwise Spearman correlation analysis and stepwise regression for multi-feature model building. For categorical metadata and enterotype comparisons, samples were pooled into bins (male/female, obese/lean, one enterotype/rest, specific nationality/rest etc) and significant features were identified using Fisher's exact test with multiple testing correction of *P* values.

Received 12 March 2010; accepted 18 December 2010.

Published online 20 April 2011.

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**Supplementary Information** is linked to the online version of the paper at [www.nature.com/nature](http://www.nature.com/nature).

**Acknowledgements** The authors are grateful to C. Creevey, G. Falony and members of the Bork group at EMBL for discussions and assistance. We thank the EMBL IT core facility and Y. Yuan for managing the high-performance computing resources. The research leading to these results has received funding from the European Community's Seventh Framework Programme (FP7/2007-2013): MetaHIT, grant agreement HEALTH-F4-2007-201052, EMBL, the Lundbeck Foundation Centre for Applied Medical Genomics in Personalized Disease Prediction, Prevention and Care (LuCAMP), Novo Nordisk Foundation and the International Science and Technology Cooperation Project in China (0806). Obese/non-obese volunteers for the MicroObes study were recruited from the SU.VI.MAX cohort study coordinated by P. Galan and S. Herberg, and metagenome sequencing was funded by Agence Nationale de la Recherche (ANR); volunteers for MicroAge study were recruited from the CROWNALIFE cohort study coordinated by S. Silvi and A. Cresci, and metagenome sequencing was funded by GenoScope. Ciberehd is funded by the Instituto de Salud Carlos III (Spain). J.R. is supported by the Institute for the encouragement of Scientific Research and Innovation of Brussels (ISRB) and the Odysseus programme of the Fund for Scientific Research Flanders (FWO). We are thankful to the Human Microbiome Project for generating the reference genomes from human gut microbes and the International Human Microbiome Consortium for discussions and exchange of data.

**Author Contributions** All authors are members of the Metagenomics of the Human Intestinal Tract (MetaHIT) Consortium. Jun W., F.G., O.P., W.M.d.V., S.B., J.D., Jean W., S.D.E. and P.B. managed the project. N.B., F.C., T.H., C.M. and T. N. performed clinical

analyses. M.L. and F.L. performed DNA extraction. E.P., D.L.P., T.B., J.P. and E.U. performed DNA sequencing. M.A., J.R., S.D.E. and P.B. designed the analyses. M.A., J.R., T.Y., D.R.M., G.R.F., J.T., J.-M.B., M.B., L.F., L.G., M.K., H.B.N., N.P., J.Q., T.S.-P., S.T., D.T., E.G.Z., S.D.E. and P.B. performed the analyses. M.A., J.R., P.B. and S.D.E. wrote the manuscript. M.H., T.H., K.K. and the MetaHIT Consortium members contributed to the design and execution of the study.

**Author Information** Raw Sanger read data from the European faecal metagenomes have been deposited in the NCBI Trace Archive with the following project identifiers: MH6 (33049), MH13 (33053), MH12 (33055), MH30 (33057), CD1 (33059), CD2 (33061), UC4 (33113), UC6 (33063), NO1 (33305), NO3 (33307), NO4 (33309), NO8 (33311), OB2 (33313), OB1 (38231), OB6 (38233), OB8 (45929), A (63073), B (63075), C (63077), D (63079), E (63081), G (63083). Contigs, genes and annotations are available to download from [http://www.bork.embl.de/Docu/Arumugam\\_et\\_al\\_2011/](http://www.bork.embl.de/Docu/Arumugam_et_al_2011/). The authors declare no competing financial interests. Correspondence and requests for materials should be addressed to P.B. ([bork@embl.de](mailto:bork@embl.de)) or S.D.E. ([dusko.ehrlich@jouy.inra.fr](mailto:dusko.ehrlich@jouy.inra.fr)).

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#### MetaHIT Consortium (additional members)

María Antolín<sup>1</sup>, François Artiguenave<sup>2</sup>, Hervé M. Blottiere<sup>3</sup>, Mathieu Almeida<sup>3</sup>, Christian Brechot<sup>1,2</sup>, Carlos Cara<sup>4</sup>, Christian Chervaux<sup>5</sup>, Antonella Cultrone<sup>3</sup>, Christine Delorme<sup>3</sup>, Gérard Denariáz<sup>5</sup>, Rozenn Dervyn<sup>3</sup>, Konrad U. Foerstner<sup>6,7</sup>, Carsten Friss<sup>8</sup>, Maarten van de Guchte<sup>3</sup>, Eric Guedon<sup>3</sup>, Florence Haimet<sup>3</sup>, Wolfgang Huber<sup>6</sup>, Johan van Hylckama-Vlieg<sup>5</sup>, Alexandre Jamet<sup>3</sup>, Catherine Juste<sup>3</sup>, Ghaliya Kaci<sup>3</sup>, Jan Knol<sup>5</sup>, Karsten Kristiansen<sup>1,3</sup>, Omar Lakhdari<sup>3</sup>, Severine Layec<sup>3</sup>, Karine Le Roux<sup>3</sup>, Emmanuelle Maguin<sup>3</sup>, Alexandre Mérieux<sup>1,2</sup>, Raquel Melo Minardi<sup>2</sup>, Christine M'rimi<sup>1,2</sup>, Jean Muller<sup>9</sup>, Raish Oozeer<sup>5</sup>, Julian Parkhill<sup>10</sup>, Pierre Renault<sup>3</sup>, Maria Rescigno<sup>11</sup>, Nicolas Sanchez<sup>3</sup>, Shinichi Sunagawa<sup>6</sup>, Antonio Torrejon<sup>1</sup>, Keith Turner<sup>10</sup>, Gaetana Vandemeulebroeck<sup>3</sup>, Encarna Varela<sup>1</sup>, Yohanhan Winogradsky<sup>3</sup> & Georg Zeller<sup>6</sup>

<sup>1</sup>Digestive System Research Unit, University Hospital Vall d'Hebron, Ciberehd, 08035 Barcelona, Spain. <sup>2</sup>Commissariat à l'Energie Atomique, Genoscope, 91000 Evry, France. <sup>3</sup>Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France. <sup>4</sup>UCB Pharma SA, 28046 Madrid, Spain. <sup>5</sup>Danone Research, 91120 Palaiseau, France. <sup>6</sup>European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany. <sup>7</sup>Heidelberger Strasse 24, 64285 Darmstadt, Germany. <sup>8</sup>Center for Biological Sequence Analysis, Technical University of Denmark, DK-2800 Kongens Lyngby, Denmark. <sup>9</sup>Institute of Genetics and Molecular and Cellular Biology, CNRS, INSERM, University of Strasbourg, 67404 Illkirch, France. <sup>10</sup>The Wellcome Trust Sanger Institute, Hinxton, Cambridge CB10 1SA, UK. <sup>11</sup>Istituto Europeo di Oncologia, 20100 Milan, Italy. <sup>12</sup>Institut Mérieux, 17 rue Burgelat, 69002 Lyon, France. <sup>13</sup>Department of Biology, University of Copenhagen, Ole Maaløes Vej 5, DK-2200 Copenhagen, Denmark.

## CORRIGENDUM

doi:10.1038/nature10187

## Enterotypes of the human gut microbiome

Manimozhiyan Arumugam, Jeroen Raes, Eric Pelletier, Denis Le Paslier, Takuji Yamada, Daniel R. Mende, Gabriel R. Fernandes, Julien Tap, Thomas Bruls, Jean-Michel Batto, Marcelo Bertalan, Natalia Borrueal, Francesc Casellas, Leyden Fernandez, Laurent Gautier, Torben Hansen, Masahira Hattori, Tetsuya Hayashi, Michiel Kleerebezem, Ken Kurokawa, Marion Leclerc, Florence Levenez, Chaysavanh Manichanh, H. Bjørn Nielsen, Trine Nielsen, Nicolas Pons, Julie Poulain, Junjie Qin, Thomas Sicheritz-Ponten, Sebastian Tims, David Torrents, Edgardo Ugarte, Erwin G. Zoetendal, JunWang, Francisco Guarner, Oluf Pedersen, Willem M. de Vos, Søren Brunak, Joel Doré, MetaHIT Consortium, Jean Weissenbach, S. Dusko Ehrlich & Peer Bork

*Nature* **473**, 174–180 (2011)

In this Letter, we inadvertently omitted Karsten Kristiansen, Department of Biology, University of Copenhagen, Ole Maaløes Vej 5, DK-2200 Copenhagen, Denmark, from the MetaHIT Consortium (additional members) list. This has been corrected in the HTML and PDF versions of the manuscript.