Global and temporal state of the human gut microbiome in health and disease

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# Abstract

The role of gut microbiota in humans is of great interest, and metagenomics provided the possibilities for extensively analysing bacterial diversity in health and disease. Here we explored the human gut microbiome samples across 19 countries, performing compositional, functional, and integrative analysis. We present the Human Gut Microbiome Atlas (HGMA), a tool available for public access. Through using the HGMA, the combination of interrogation of species across regions, diseases, and functional clusters allows for a more complete understanding of the importance a species has in human health and disease to aid in the generation of informed hypothesis.

# Introduction

Metagenomic studies of the human microbiome enable the characterization of the microbial and functional diversity in health and disease[1]. Advances in metagenome assembly and various clustering methods enabled the generation of metagenome species[2]–[6]. Most of these studies focused on unveiling new uncultured genomes, while only a few focused on investigating the functional potentials and dynamic changes of the gut microbiome[7]–[9]. Understanding the functional and temporal behaviour of the microbiome may have great implications for the identification of its global signature in health and disease[8], [10], [11]. Additionally, short-term perturbations may trigger gut microbiota dysbiosis and changes at compositional and functional levels. Specifically, the negative selective microbe-microbe and host-microbe interactions, in the context of metabolism or antimicrobial machinery, could be the main mechanism underlying microbial dysbiosis[12]. Large-scale integration of microbiome functional changes and their associations with clinical data may provide novel information on temporal changes in the microbiome and host physiology[13].

Herein, we integrated publicly available data from many studies across different countries from healthy and diseased individuals. The analysis is presented in an open-access Human Gut Microbiome Atlas (www.microbiomeatlas.org), allowing researchers to explore for the first time an integrative analysis on composition, functional, richness, diseases, and region signatures for the gut microbiota across 19 geographical regions and 23 diseases.

# Human Gut Microbiome Atlas; Pan-metagenomics study on compositional and functional changes of the human gut microbiome

We performed a large-scale integrative analysis of 6,014 publicly available shotgun metagenomics stool samples with addition to one Swedish cohort of 344 samples (under submission). There were at least 10 million high-quality sequencing reads from healthy and diseased cohorts from 19 different countries across five continents (Fig. 1a-b and Supplementary Table S1). We rarefied all metagenomic samples into 10 million reads per sample, which enables comparative analysis across different cohorts. We created the Human Gut Microbiome Atlas (HGMA) using quantitative analysis of shotgun metagenomics based on microbial genomes assembled using Metagenomic Species Pan-genomes (MSPs) (Fig. 1c). The MSP number was increased from 1,661 (previous release[5]) to 1,989 (average number of genes 1,894 ± 1,616) (Methods), and their taxonomy was updated. We generated gene counts and MSP abundances for all the samples using the 10.4 million gene catalogue[14]. We also characterized the functions and phenotype of the MSPs in 7 different categories (KO, PFAM, CAZyme, Mustard, JGI-GOLD phenotype, PATRIC virulence factor, and antiSMASH biosynthetic gene clusters) and identified co-conserved functional clusters across species (7,763 clusters) (Methods).All the data are freely available in the HGMA, without restrictions, in the public open access database (www.microbiomeatlas.org) that is part of the Human Protein Atlas program (www.proteinatlas.org). All MSPs and functions are highlighted together with the 6,014 samples across 19 countries with disease and healthy cohorts.

Using all samples obtained from individuals across 19 countries, we uncovered the geographical distribution of the gut microbiome. Enrichment of *Clostridium* and *Bacteriodes* were found to have higher mean relative abundance withing western countries whereas *Prevotella* were had higher mean relative abundance withing non-western countries (Fig. 1d). We applied the unsupervised clustering method, *monocle*, to MSP abundance profiles of all samples (Methods)[15], [16]. We observed that there were two distinct ordinations of non-westernized and European samples of subjects connected by a mixture of western/non-western samples belonging to China/Japan/US (Fig. 1e). Based on comparative analysis across different regions, we also identified 783 MSPs specifically enriched in certain countries (See Methods, and Supplementary Table S2). The following analysis was based on the western/non-western groups. Functional annotation-based analysis across geographical clusters revealed enrichment of CAZymes for degrading host mucins and storage carbohydrates in westernized populations, where antimicrobial resistance (AMR) and virulence factors were also more prevalent (Fig. 1f). Comparison of functions of region enriched MSPs in westernised countries revealed that genes encoding for vancomycin resistance, LPS biogenesis, and mucin degradation are overrepresented. An overrepresentation of genes encoding for complex polysaccharide binding proteins mostly belonging to *Prevotella* genus was found in the non-westernized cohorts.

# Association study between metagenomic species and disease

To distinguish diseased and healthy microbiomes from multiple cohorts, we performed a pan-metagenomics association study (Pan-MGAS) of multiple disease cohorts (23 diseases across 43 cohorts from 14 countries). We determined the enriched and depleted species within disease cohorts compared to healthy samples from the same country, showing an effect size greater than 0.3 (Fig. 2g and Supplementary Table S3). In some cohorts a clear imbalance in the flora accompanies the disease. Some cohorts show a depletion of multiple species (i.e., NSCLC:FRA, RCC:FR, adenoma ITA (Fig. 2a). Conversely in some diseases, several species had enriched relative abundances, as we can see for most ColoRectal Cancer (CRC) cohorts. We also notice cohorts with minor changes in the microbiome composition, for example, adenoma cohorts.

Some species were either enriched or depleted across multiple cohorts, regardless of geographical differences. For example, *Anaerostipes hadrus,* *Coprococcus comes,* and *Blautia obeum* areamong the most depleted species withall these examples found depleted in at least six different cohorts (Fig. 2C, Supplementary Fig. S1)*.* The firsttwo have been described as butyrate producers and dominant species isolated from the healthy human colon[17]–[19], and the third has been associated with gut microbiota recovery after cholera infection and with normal maturation of the infant gut microbiota[20].

Between the species found enriched and in at least 6 different cohorts we find *Fusobacterium nucleatum, Clostridium bolteae, Clostridium clostridioforme, Clostriduium symbiosum, Peptostreptococcus stomatis, Flavonifractor plautii, Parvimonas micra*, among others (Fig. 2C, Supplementary Fig. S1). Several of them also have been isolated from oral samples (*Fusobacterium nucleatum*[21], *Peptostreptococcus stomatis*[22], *Parvimonas micra*[23]) and some of them have been identified in infections including bacteremia (*Clostridium bolteae*[24], *Clostridium clostridioforme*[25], *Parvimonas micra*[26]). Besides *Fusobacterium nucleatum* and *Clostridium symbiosum,* whichwere enriched in western countries and are linked with CRC[27]–[29], we also identify *Parvimonas micra* to be enriched in multiple cohorts of CRC and *Peptostreptococcus stomatis* enriched several times only in solid cancer studies (Supplementary Table S4, Supplementary Fig. S1).

Three different species belonging to the *Streptococcus* genus (*Streptococcus anginosus* *Streptococcus parasanguinis*, *Streptococcus vestibularis*) and three more species from the *Veillonella* genus (*Veillonella atypica*, *Veillonella dispar*, *Veillonella parvula*) were enriched in two different liver disease cohorts, all of which are common inhabitants of the oral cavity (Supplementary Table S4).

# Disease enriched-functional clusters showed distinct links to gut microbiome dysbiosis

We identified co-conserved functional clusters of the microbiome by applying an unsupervised clustering approach on MSPs (Fig. 3a-c, Supplementary Fig. 2 and Methods). This analysis provided a better representation of microbial functions than single annotations or known pathway definitions (e.g., KEGG). From the community detection algorithm, we identified 7,763 functional clusters, 6,297 singletons, and 591 representative clusters (Supplementary Table 5). For example, antimicrobial resistance and secondary biosy1nthetic genes were found to be singletons and not co-conserved with other functional genes. After excluding singletons and unreliable functional clusters detected in less than three species, we retained 591 representative clusters of microbial functions. One of the two largest clusters (CL-12 in Supplementary Table 5, named “*comm-cluster*” herewith) was over-represented among many commensal species, while the other (CL-10, named “*patho-cluster*”) was enriched in a few pathobionts, such as *Klebsiella* spp., *Enterobacter* spp., and *E. coli*. Interestingly, the *comm-cluster* was enriched with genes involved in the biosynthesis of amino acids indicative of functions. In contrast, the *patho-cluster* was enriched in functions associated with the uptake of several substrates. These included siderophore, ion, amino acid, and vitamin transport, thus competing with host and commensal bacteria. We also found other enriched-functional clusters, such as butyrate metabolism, propionate metabolism, vitamin B12, coenzyme metabolism, chemotaxis, ATPase, and mobile genetic elements (i.e., integrase and transposase) and the CRISPR-cas system (Fig. 4e); a number of these were correlated with phylum-level taxonomy (Extended Fig. 2c).

We next projected the functional clusters on enriched/depleted MSPs in HGMA disease cohorts (Fig. 3d: hypergeometric tests, p-value < 10-3). Among the functions of the clusters commonly associated with the enriched species in disease we found some of them were associated with antibiotic resistance, virulence regulation and several PTS systems. We found the *comm-cluster* Cl-12 (Fig. 3c-d) between functions commonly depleted, as mentioned above this cluster is related with commensal species. Interestingly we also observed the Methicillin resistance cluster commonly found depleted (Fig. 3d).

# Global view of the function, region, and composition of disease enriched/depleted gut microbiome species.

# A phylogenetic tree of the metagenomic species derived from IGC2 was calculated and taxonomic resolution of disease and region enriched species was investigated (Fig. 4, Methods). Employing this tree as a tool, it was possible to group species also by shared functional clusters that are enriched in disease in their phylogenetic context (Fig. 4).

An example of how this tool can be used to analyse a metagenomic species is demonstrated with *Streptococcus* (Fig. 4). Here, it’s enrichment in liver disease (ES=0.43) can be compared with its depletion in cancer (melanoma) (ES=0.30) across multiple species and cohorts. Another example can be found when looking at the species specificity of enrichment of *Fusobacterium nucleatum* in cancers. The species was not shown to be regionally enriched but shared functional clusters with this species also contribute to multiple cancers and in inflammatory diseases such as liver disease (Fig. 2c).

Diseases have different relationships with the microbiome

This could be enrichment or depletion of clades of species

Other enriched species as biomarker for disease

This is the first tool that allows for the comparison between metagenomic biomarkers between diseases and regions.

# Discussion

We have performed a comprehensive integrative analysis of global and temporal gut microbiomes, and we provide an open access HMGA portal (http://microbiomeatlas.org). This tool allows for the integration of several studies simultaneously that link species to disease, region, and function. It also presents a means of contextualising gene and species enrichments phylogenetically. We demonstrated that difference in origin (western/non-western) is reflected by the gut microbial composition with species/genes being over/under-represented in each origin. Finally, we also found that some species and functions are enriched or depleted across multiple diseases and studies.

Confirming previous observations[6], we have described the gut microbiome regional specificity, which needs to be considered before using the gut microbiome for the stratification of patients or for designing intervention studies. Beyond previous observations, our function-based analysis indicates that the western-enriched bacteria might dominate the gut microbial community with the production of antimicrobial peptides and homoserine lactone, which may inhibit their competitors.

The physiological changes caused by the disease might partly explain why some diseases have a pronounced compositional imbalance while others do not. Diseases affecting the bowel and CRC show a high species enrichment while some diseases affecting other body parts sometimes produce smaller imbalances. Some other factors might also be involved in the magnitude of the imbalance, for example, the changes in diet[30], [31] or the use of drugs for treating the disease [32]–[34]).

The loss of species actively contributing to maintain a healthy gut environment could increase the host’s vulnerability to further health complications. For example, we observed some of the more frequently depleted species have been described as butyrate producers. Butyrate has been associated with beneficial effects in the colon such as inhibition of inflammation, reinforcing the epithelial barrier and decreasing oxidative stress [35]. Conversely, some of the enriched species might worsen the health status, by leading to new infections, potentiating the disease symptoms and even weakening the immune response. Some reports suggest *Fusobacterium nucleatum* promotes CRC development and metastasis[36], [37]. A previous report found *Flavonifractor plautii*, a species we found enriched in 6 cohorts, suppresses the Th2 immune responses in mice[38] which makes us speculate it could exert a similar effect in the humans. The Pan-MGAS we present shows a clear bias toward CRC studies due to the increased availability of these studies. We expect new studies released in the future to include more countries and diseases that would help to update our analysis and balance this bias.

Finally, the integration of metagenomics data from many studies spanning five continents provides valuable knowledge for researchers interested in the impact of the microbiome on individual health parameters. The open-access atlas will be updated routinely with the new publicly available gut metagenomics data, including the recently announced one million microbiome project aimed at providing comprehensive open-access metagenomics data from multiple research centres. In this manner, in-depth analysis of the impact of the gut microbiome on health and disease will be used to facilitate future studies to reveal the key role of the gut microbiome in human maintaining health.

# Data availability

The datasets used in this study, including Swedish wellness cohort, are available in http://www.microbiomeatlas.org, with relevant project accession codes of raw data provided in Supplementary Table S1. Other data access and research questions related to the Swedish wellness cohort can be made available by contacting the corresponding author, Mathias Uhlen (mathias.uhlen@scilifelab.se).

# Code availability

The functional cluster analysis can be applied on gene counts and species abundances. The other pipeline scripts for analysis are also shared publicly and can be found at https://github.com/theoportlock/ATLAS

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# Author contributions

S.S., S.D.E., and M.U. conceived the project. S.L., T.P, J.G. and S.S. led the design and analysis of the data. S.L., T.P, and J.G developed the temporal pipeline, analysis, and made the figures. L.E. and M.U. provided the wellness gut metagenomics samples. M.A., F.P., E.L., and S.D.E. generated the MSPs, performed quality check and taxonomy update. N.P. annotated the updated gut gene catalog. M.A., V.M. and F.P. performed the analysis on the Italian and American cohorts for validation. N.B., C.P., S.V., D. R. and A.H. analyzed part of the data and prepared the materials for the HGMA. K.F. and F.J. developed the HGMA website. V.L. and B.H. annotated the gut catalog with new CAZymes. J.P. and D.L. annotated the secondary metabolites of the gene catalog. M.A. and G.B. contributed to testing the pipeline, statistical and functional analysis. S.S., S.L., M.U. and S.D.E wrote and drafted the manuscript. L.A.E, D.L.S, A.M., G.P. J.N. provided critical feedback on the data and manuscript. All authors read, edited and reviewed the manuscript.

# Competing interests

The authors declare no competing financial interests.

# Additional information

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# Methods

## Metagenomics species pan-genome (MSP) creation

1601 metagenomic samples used to build the Integrated Gene Catalog of the human gut microbiome (IGC2) were downloaded from the European Nucleotide Archive [39]. Using the Meteor software suite[40], reads from each sample were mapped against the IG1C2 catalog and a raw gene abundance table was generated. This table was submitted to MSPminer[5] that reconstituted 1,989 clusters of co-abundant genes named Metagenomic-Species Pangenomes (MSPs). Quality control of each MSP was manually performed by visualizing heatmaps representative of the normalized gene abundance profiles. In addition, MSPs completeness and contamination were assessed by searching for 40 universal single copy marker genes[41] and by checking taxonomic homogeneity.

## MSP taxonomic annotation with phylogenetic tree.

MSPs taxonomic annotation was performed by aligning all core and accessory genes against *nt* and NCBI WGS (version of September 2018 restricted to the taxa Bacteria, Archaea, Fungi, Viruses and Blastocystis) using *blastn* (version 2.7.1, task = megablast, word\_size = 16)[42]. The 20 best hits for each gene were kept. A species-level assignment was given if more than 50% of the genes matched the RefSeq reference genome of a given species, with a mean identity ≥ 95% and mean gene length coverage ≥ 90%. The remaining MSPs were assigned to a higher taxonomic level (genus to superkingdom) if more than 50% of their genes had the same annotation.

40 universal phylogenetic markers genes were extracted from the MSPs with MOCAT[43]. MSPs with less than 5 markers were discarded. Then, the markers were separately aligned with MUSCLE[44]. The 40 alignments were merged and trimmed with trimAl[45]. Finally, the phylogenetic tree was computed with FastTreeMP[46] and visualized with iTOL[47]. Phylogenetic placement was further used to improve and correct taxonomic annotation. Pylogenetic data, species labels, and phylum colouring can be accessed from https://data.inrae.fr/dataset.xhtml?persistentId=doi:10.15454/FLANUP, with annotation for enriched species found at https://github.com/theoportlock/ATLAS.

## Functional annotation of the gut gene catalog and MSP

IGC2 catalog was annotated for the Antibiotic Resistant Determinants (ARD) described in Mustard database (v1.0) (http://www.mgps.eu/Mustard/)[48]. Protein sequences were aligned against 9,462 ARD sequences using *blastp* 2.7.1+ (option -evalue = 10-5). Best-hit alignments were filtered for identity ≥ 95% and bidirectional alignment coverage ≥ 90% (at query and subject level), giving a list of ARD candidates belonging to 30 families. Annotation of the carbohydrate-active enzymes (CAZymes) of the IGC2 catalog was performed by comparing the predicted protein sequences to those in the CAZy database and to Hidden Markov Models (HMMs) built from each CAZy family[49], following a procedure previously described for other metagenomics analysis[50]. Proteins of IGC2 catalog were also annotated to KEGG orthologous using Diamond (version 0.9.22.123)[51] against KEGG database (version 82). Best-hit alignments with e-value ≤ 10-5 and bit score ≥ 60 were considered. Proteins involved in virulence factors of PATRIC[52], [53] were matched against IGC2[14] by BLASTP (best identity > 50%, e-value < 10-10). Phenotype of MSP were manually checked and annotated based on JGI-GOLD phenotype (organism metadata)[54]. We identified biosynthetic genes of MSP with the use of standalone anti-SMASH program with minimal run option, focused on core detection modules (version 5)[55]. Loading antiSMASH into Amazon cloud computing (AWS) as docker image, we executed its mining process per MSP in a massive parallel setting.

## Quality control/normalization of gene counts and species abundance profiling

We filtered out human reads and then mapped metagenomic data (Supplementary Table S1) on IGC2 catalogue of human gut metagenome by METEOR[56] and based on the aligned reads, we estimated the abundance of each reference gene of the catalogue, normalizing multiple mapped reads by their numbers and summing up normalized counts for a given gene. Reducing the variability by sequencing depths, gene count values were downsized into 10 million reads per sample; and any samples less than 10 million mapped reads were excluded from our dataset. Normalized gene counts were used for the quantification of MSP abundance by R *momr* (*MetaOMineR*) package[57]. MSP abundances were estimated by the median abundance of the 25 marker genes representing the robust centroid of gene clusters of MSP. Sample metadata of all metagenomics data such as sequencing platform, geography, age, body-mass index, gender and the data source were provided under HGMA (http://microbiomeatlas.org).

## Tracing the diversifications of healthy metagenomic samples of different geography

After the quantification and per-million scaling of MSP abundance profiles, we employed trajectory analysis in R *monocle* ver.2 package to identify how samples were clustered[16]. In short, we selected the species profiles of all normal samples from different geographical origins and reduced the sample profiles into two dimensions by advanced nonlinear reconstruction algorithm, *DDRTree*. Based on the reduced two-dimensional components, we presented how samples were closely clustered as branches in scatter plots. Based on reduced profiles, we also calculated centroids and standard deviations of samples of given countries, except Finland population in toddlers (2 years).

## Identification of region-enriched species and genes from geographically distinct cohorts

Regional enrichment of species was calculated from calculating the Z-score for of each MSP. The Z-score is calculated as the difference between the country and the whole population. Displayed are the top 15 greatest mean Z-scores of western and non-western groups.

By selecting the top 100 overrepresented MSPs in western and non-western groups, two separate cumulative sums of their genes were filtered to have more than 90 genes. The genes in each of these lists were mapped against the CAZyme, PATRIC, and CARD databases. 18 of the max differences between the western and non-western gene count lists were calculated and plotted.

## Pan-metagenomics association studies (Pan-MGAS)

First, we selected of healthy and disease samples without interventions and redundant measurement (i.e., multiple visits) and performed comparative analyses of chosen samples (number of selected samples were shown in Supplementary Table S1). We estimated the effect sizes of Wilcoxon signed rank (one-sided) tests for MSP enrichment and depletion in diseases, compared to healthy controls of given country[58] and identified we identified significantly enriched or depleted species having medium effect sizes (effect size ≥ 0.3). Manhattan plots of pan-MGAS based on effect sizes were plotted with R *qqman* package[59].

## Unsupervised clustering of co-conserved functions of gut microbiota

We calculated Jaccard index among functional annotations to check how many species were sharing given a pair of functions together. We selected highly shared pairs of functions (Jaccard index >= 0.75) and merged into functional co-occurrence network using R *igraph* package[60]. Functional clusters within the network were identified by unsupervised community detection, short random work algorithm (*cluster\_walktrap* function)[61], [62] and identified singleton functions within the network as well. Among non-singleton functional clusters, we selected representative functional clusters if functions of given functional clusters were found more than three species, thereby excluding functional clusters sparsely annotated over MSPs. Associated MSPs to functional clusters were chosen if given MSP covered more than 75% functions of given functional cluster (Supplementary Table S5).

# Figure legends

**Fig. 1. Characterization of the global gut microbiome in health and disease.** Pan-metagenomics studies of health and disease. Corresponding datasets were publicly shared as a resource: human gut microbiome atlas (HGMA). **A,** geographical distribution of the datasets used in this study (the number of the samples is shown in parentheses). **B,** types of disease datasets of shotgun metagenomics used in this study. **C,** the workflow of the metagenomic species pan-genome (MSP) quantification together with functional characterization. In total, 6,014 shotgun metagenome samples, including 344 Swedish longitudinal samples, were aligned against the gene catalogue of the human gut microbiome and quantified at the level of MSP. **D,** heatmap showing the top 15 enriched MSPs between western and non-western cohorts coloured by mean species Z-score for each country against all samples. **E,** *monocle* ordination of the gut microbiome in healthy samples. Individual samples from non-westernized countries, European countries, and US/China/Japan were coloured green, orange, and blue, respectively. **F,** contrasted functions among region-enriched species are classified as non-westernized and westernized. Based on functional annotations of CAZyme, antimicrobial resistance (AMR), and virulence factors (PATRIC database), we checked the enrichment of functions of a geographical cluster. Functional genes from western/non-western enriched MSPs were cumulatively summed, filtered by top 18 maximal differences of gene count, and plotted (Methods).

**Fig. 2. Pan-metagenomics association studies (Pan-MGAS) of 43 cohorts from 23 different diseases and 14 countries (n=2,185).** **A,** We identified significantly enriched/depleted species of cohorts based on effect sizes (ESs) of Wilcoxon one-sided tests (ES ≥ 0.3). Acronyms are: ACVD, Acute Coronary Cardiovascular Disease; Ob, obesity; CRC, Colorectal Cancer; NSCLC, Non-Small Cell Lung Cancer; RCC Renal Cell Carcinoma; GDM, Gestational Diabetes Mellitus; T1D Type 1 diabetes; T2D, Type 2 diabetes; LC liver Cirrhosis; NAFLD Non-Alcoholic Fatty Acid Liver; UC, Ulcerative Colitis; CD, Crohn's disease; BD Becet’s; RA, Rheumatoid Arthritis; SPA, Ankylosing Spondylitis; ME/CFS Myalgic Encephalomyelitis/ Chronic Fatigue Syndrome; PD, Parkinson Disease. **B,** Jitter plots of frequency of the significantly enriched/depleted cohorts of all MSPs (effect size >0.3) were calculated: total frequency of enriched/depleted cohorts (number of enriched cohorts + number of depleted cohorts Y axis) and subtracted frequency between enriched cohorts and depleted cohorts (number of enriched cohorts - number of depleted cohorts X axis). Point colours changed from red (left) to blue (right) according to x-axis values. Common enriched/depleted species among cohorts were identified when total frequency ≥ 3 and absolute subtracted frequency ≥ 2. **c**, Species found depleted (*Anaerostipes hadrus*) and enriched (*Fusobacterium nucleatum subspecies animalis*) in most studies.

**Fig. 3. Analysis of functional clusters.** For the functional characterization of human gut MSPs, we annotated respective genes with 19,540 features of microbial function/phenotype databases and identified 7,763 functional clusters better representing the microbiome. **A,** Identification of functional clusters based on co-conserved genes across species. Unlike the manually curated module database, we identified functional clusters based on high co-conservation across species using the unsupervised clustering method. **B,** among different sources of microbial functional annotations (e.g., KEGG module and pathway), we found that co-conservation of genes across different species was substantially low (Jaccard index < 0.5). **C**, Functional clusters identified by unsupervised community detection, the y-axis displays the number of genes within the functional cluster and the x axis displays the number of MSPs possessing more than 70% of the clusters’ genes. **D**, Functional clusters projected on enriched/depleted MSPs across disease cohorts. The Jitter plot display the frequency functional of functional clusters significantly associated with the enriched/depleted species (hypergeometric test p < 0.001) in disease cohorts. Y axis shows the total frequency of cohorts where a functional cluster was found significantly associated with enriched/depleted species. X axis shows the difference in the number of cohorts where a function was found enriched minus the frequency it was found depleted. Point colours changed from red (left) to blue (right) according to x-axis values. Common enriched/depleted species among cohorts were identified when total frequency ≥ 3 and absolute subtracted frequency ≥ 2.

**Fig. 4. Phylogenetic differences between species function, disease enrichment, and region enrichment.** Inner annotation of dendrogram is species phylum, second is enrichment of functional cluster, third is the total number of disease cohorts that the species is enriched/depleted in, and the outer annotation is the normalised, mean Z-score between western and non-western cohorts scaled between 0-1. Itol annotations and dendrogram are publicly available (Methods). Highlighted group are MSPs from the *Streptococcus* genus.

# Supplementary Figure Legends

**Supplementary Fig. 1.** Species found either depleted or enriched (effect size >0.3) in at least 6 different disease cohorts.

**Supplementary Fig. 2. Analysis of functional clusters. A,** Overview of the identification of functional clusters. **B,** community network detected from the co-occurrence network of functional annotations. All functional clusters were shown as nodes and significant co-occurrences of functional clusters across species were shown as edges in the network. “Comm-cluster” and “patho-cluster” were coloured blue and red, respectively. **C,**  number of functional clusters mapped with microbial function/phenotype databases and their singleton cluster fractions (singleton and non-singleton coloured green and red, respectively).

## Supplementary Tables Legends

**Supplementary Table S1.** Description of Human Gut Microbiome Atlas (HGMA) datasets used in this study. We showed the overall statistics of HGMA datasets, including total number of samples, number of samples without intervention and multiple visits, number of matched healthy controls, sequencing platform, geography, reference, and raw data link.

**Supplementary Table S2.** List of region enriched MSPs. Based on effect sizes (>0.3 in more than six countries of comparison), we identified total 782 regionally enriched MSPs among healthy samples of 17 countries.

**Supplementary Table S3.** Statistics of pan-metagenomics association study (pan-MGAS) results of 28 geographically distinct disease cohorts. We performed pan-MGAS analysis and identified enriched/depleted species in each cohort with effect sizes by each column.

**Supplementary Table S4.** Statistics of MSP common enriched/depleted in diseases. We examined the total and subtracted frequency of significantly enriched and depleted species in diseases.

**Supplementary Table S5.** Characteristics of 7,763 functional clusters. For more detailed understanding, per functional cluster we presented the size of cluster, number of enriched species, enriched MSP identifiers, enriched species names, enriched KEGG modules (hypergeometric tests p-value < 0.01), subsystems of enriched KEGG modules, and KEGG orthology terms, PFAM terms, virulence term, CAZyme terms, anti-microbial resistance (Mustard) terms, secondary metabolism (anti-SMASH) terms, phenotype (JGI-GOLD) terms, product names of virulence terms, and all functional terms of given cluster.