OPEN ACCESS

Original research

A faecal microbiota signature with high specificity for pancreatic cancer

Ece Kartal ,[1,2] Thomas S B Schmidt ,[1] Esther Molina-Montes ,[3,4] Sandra Rodríguez-Perales ,[4,5] Jakob Wirbel ,[1,2] Oleksandr M Maistrenko ,[1] Wasiu A Akanni ,[1] Bilal Alashkar Alhamwe ,[6] Renato J Alves ,[1] Alfredo Carrato ,[4,7,8] Hans-Peter Erasmus,[9] Lidia Estudillo ,[3,4] Fabian Finkelmeier,[9,10] Anthony Fullam ,[1] Anna M Glazek,[1] Paulina Gómez-Rubio,[3,4] Rajna Hercog,[11] Ferris Jung ,[11] Stefanie Kandels ,[1] Stephan Kersting ,[12,13] Melanie Langheinrich ,[13] Mirari Márquez,[3,4] Xavier Molero,[14,15,16] Askarbek Orakov ,[1] Thea Van Rossum ,[1] Raul Torres-Ruiz ,[4,5] Anja Telzerow ,[11] Konrad Zych ,[1] MAGIC Study investigators, PanGenEU Study investigators, Vladimir Benes ,[11] Georg Zeller ,[1] Jonel Trebicka ,[9,17] Francisco X Real ,[4,18,19] Nuria Malats ,[3,4] Peer Bork [1,20,21,22]

ABSTRACT

Background Recent evidence suggests a role for the microbiome in pancreatic ductal adenocarcinoma (PDAC) aetiology and progression.

Objective To explore the faecal and salivary microbiota as potential diagnostic biomarkers.

Methods We applied shotgun metagenomic and 16S rRNA amplicon sequencing to samples from a Spanish case–control study (n=136), including 57 cases, 50 controls, and 29 patients with chronic pancreatitis in the discovery phase, and from a German case–control study (n=76), in the validation phase.

Results Faecal metagenomic classifiers performed much better than saliva-based classifiers and identified patients with PDAC with an accuracy of up to 0.84 area under the receiver operating characteristic curve (AUROC) based on a set of 27 microbial species, with consistent accuracy across early and late disease stages. Performance further improved to up to 0.94 AUROC when we combined our microbiome-based predictions with serum levels of carbohydrate antigen (CA) 19–9, the only current non-invasive, Food and Drug Administration approved, low specificity PDAC diagnostic biomarker. Furthermore, a microbiota-based classification model confined to PDAC-enriched species was highly disease-specific when validated against 25 publicly available metagenomic study populations for various health conditions (n=5792). Both microbiome-based models had a high prediction accuracy on a German validation population (n=76). Several faecal PDAC marker species were detectable in pancreatic tumour and non-tumour tissue using 16S rRNA sequencing and fluorescence in situ hybridisation.

Conclusion Taken together, our results indicate that non-invasive, robust and specific faecal microbiota-based screening for the early detection of PDAC is feasible.

Significance of this study

What is already known about this subject?

- Pancreatic ductal adenocarcinoma (PDAC) is on the rise worldwide, posing a high disease burden and mortality rate, yet accurate, non-invasive diagnostic options remain unavailable.
- Alterations in the oral, faecal and pancreatic microbiome composition have been associated with an increased risk of PDAC.

What are the new findings?

- Stool microbiota-based classifiers are described that predict PDAC with high accuracy and specificity, independent of disease stage, with potential as agents for non-invasive diagnostics.
- A faecal metagenomic classifier identified PDAC with an accuracy of 0.84 area under the receiver operating characteristic curve (AUROC) in a Spanish cohort, based on 27 species. The accuracy improved to up to 0.94 AUROC when combined with the less specific carbohydrate antigen (CA) 19–9 serum marker.
- The classifier was validated in an independent German PDAC cohort (0.83 AUROC), and PDAC disease specificity was confirmed against 25 publicly available metagenomic study populations with various health conditions (n=5792).
- The presence of marker taxa enriched in faecal samples (*Veillonella*, *Streptococcus*, *Akkermansia*) and also taxa with differential abundance in healthy and tumour pancreatic tissues (*Bacteroides*, *Lactobacillus*, *Bifidobacterium*) was validated by fluorescence *in situ* hybridisation.

► Additional supplemental material is published online only. To view, please visit the journal online (http://dx.doi.org/10.1136/gutjnl-2021-324755).

For numbered affiliations see end of article.

Correspondence to
Dr Nuria Malats; nmalats@cnio.es
Dr Peer Bork, Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Baden, Germany; peer.bork@embl.org

EK, TSBS and EM-M contributed equally.

NM and PB are joint senior authors.

Received 5 April 2021
Accepted 5 December 2021

Check for updates

To cite: Kartal E, Schmidt TSB, Molina-Montes E, *et al*. *Gut* Epub ahead of print: [*please include* Day Month Year]. doi:10.1136/gutjnl-2021-324755

Significance of this study

How might it impact on clinical practice in the foreseeable future?

- Faecal microbiome-based detection of PDAC may provide a non-invasive, cost-effective and robust approach to early PDAC diagnosis.
- The presented PDAC-specific microbiome signatures, including links between microbial populations across tissues, provide novel microbiome-related hypotheses regarding disease aetiology, prevention and possible therapeutic intervention.

INTRODUCTION

Pancreatic ductal adenocarcinoma (PDAC) is the most common form of pancreatic cancer and a major cause of cancer-related deaths despite relatively low incidence rates.[1 2] The high lethality of PDAC is a consequence of both late diagnosis and limited therapeutic options[3]: symptoms are unspecific and often emerge only during late disease stages, at which point tumours can be either locally non-resectable or present as metastatic disease. At present, PDAC is diagnosed using imaging tests.[4] Sensitive and affordable tests for an early detection of PDAC could therefore improve outcome. PDAC markers have been explored in pancreatic tissue,[5] urine[6 7] and serum.[8 9] Yet to date, the sole Food and Drug Administration (FDA)-approved PDAC biomarker remains serum carbohydrate antigen (CA) 19-9. CA19-9 has limited disease specificity as levels can be elevated in several other concomitant conditions (eg, biliary obstruction) and is therefore mostly used as a marker for PDAC surveillance, rather than screening or diagnosis.[10–14]

PDAC has a complex aetiology, with established risk factors that include age, chronic pancreatitis, diabetes mellitus, obesity, asthma, blood group and lifestyle (eg, smoking and heavy alcohol consumption).[15 16] The role of these risk factors in PDAC aetiology may also be complemented—or sometimes indeed mediated—by alterations in the microbiome. For example, poor oral hygiene and periodontitis have been associated with an increased PDAC risk,[17] an observation that also extends to periodontitis- and caries-associated microbial species.[18 19] Shifts in these species are sometimes part of wider compositional changes in the oral microbiome[20 21] or have been explored as PDAC risk factors in their own right.[22] Similarly, microbial composition in the gut[23–25] and duodenum,[26 27] quantified via 16S rRNA amplicon sequencing, have previously been linked to PDAC risk.

The human pancreas harbours a microbiome that shares species with the mouth and the gut,[25 28–32] although its exact composition has remained elusive owing to the challenges associated with contamination control in low bacterial biomass samples.[33] In murine models, microbes originating from the intestine can contribute to carcinogenesis in the pancreatic duct,[25 30] suggesting a role for the microbiome in PDAC aetiology and progression that was recently extended to fungi.[34] Moreover, the pancreatic tumour microbiome may also be associated with disease progression and long-term survival in patients with PDAC.[31]

However, the translation of these advances into PDAC-specific microbiome signatures for clinical applications has so far remained largely unexplored. Here, we present the identification of robust, specific microbial PDAC signatures based on a metagenomic survey of a Spanish (ES) study population of 57 newly diagnosed and treatment-naïve patients with PDAC, 29 patients with chronic pancreatitis (CP), and 50 matched controls. We sampled saliva, faeces, pancreatic normal and tumour tissue and assessed microbial composition using whole-genome shotgun metagenomics, 16S rRNA amplicon sequencing, and fluorescence *in situ* hybridisation (FISH) assays. The best discrimination between patients with PDAC and non-PDAC subjects was achieved by statistical models based on a set of 27 faecal microbial species that could be quantified in a targeted manner in a diagnostic setting. The prediction accuracy of microbiome-based models was confirmed in an independent German (DE) PDAC validation population including 44 patients with PDAC and 32 controls and was further improved when combined with serum levels of CA19-9. We further validated the disease specificity of these models against existing data from 25 studies (n=5792) of nine diseases.[35–59] Several of the PDAC-enriched species were also detected in cancer tissue, with possible links to oral and intestinal populations, supporting their potential role in PDAC pathogenesis, as previously reported.[25 30 31 34]

METHODS

Subject recruitment and sample collection

A case–control design was applied. Subjects were prospectively recruited between 2016 and 2019 from the Hospital Ramón y Cajal in Madrid and Hospital Vall d'Hebron in Barcelona, Spain, using the same protocols for biological sample collection, processing and storage. Subjects with newly diagnosed PDAC (n=57), aged >18 years, were identified prior to any cancer treatment. Subjects in whom PDAC was suspected were recruited, and sampling was done before any treatment. Patients with chronic pancreatitis (CP, n=29) were recruited from the same hospitals. Controls matched for age, gender and hospital were selected from inpatients with a primary diagnosis for hospital admission not related to PDAC risk factors. Participants incapable of participating in the study owing to impairment of physical ability were excluded. Institutional review board ethical approval (CEI PI 26 2015-v7) and written informed consent were obtained from participating centres and study participants, respectively. Epidemiological and lifestyle data were collected by trained monitors during face-to-face interviews through a structured questionnaire. Clinical data, including stage of the diseases and follow-up data, were retrieved from hospital charts by the same monitors, likewise using structured questionnaires. Recorded jaundice status was additionally confirmed and extended by direct bilirubin measurements from blood samples in CNIO, Madrid. All data were entered, edited and managed using REDCap. Missing lifestyle and medication values in the metadata (missing overall in 3.1%) were imputed using a random forest-based algorithm for missing data imputation called missForest (n=100 trees).[60] The imputation accuracy was high according to the imputation error estimate (mean out-of-bag error=0.12). Serum CA19-9 levels were analysed by electrochemiluminescence immunoassay (ECLIA, Roche Diagnostics, Germany) following the manufacturer's instructions in the Institute of Laboratory Medicine and Pathobiochemistry, Marburg, Germany. Each sample was assayed in duplicate, with positive controls assayed in each plate (online supplemental table S1).

Stool and saliva (mouthwash) samples were preserved in RNALater and stored at 4°C immediately for 12 hours, then transferred to −20°C for another 24 hours, and then stored at −80°C until DNA extraction. Tumour and non-affected tissue samples were collected during surgery for a subset of individuals, immediately flash-frozen in liquid nitrogen after pathological

assessment, and preserved at −80°C. All the samples were shipped on dry ice.

An independent validation population was recruited at the Department of Surgery, University Hospital of Erlangen (32 PDAC and 32 control samples) and Section for Translational Hepatology, Department of Internal Medicine I, Goethe University Clinic, Frankfurt (12 PDAC samples) using the same protocols for biological sample collection, processing and storage. Matched controls were selected from inpatients with a primary diagnosis for hospital admission not related to PDAC risk factors. The study was approved by the local ethics committees (SGI-3–2019, 451_18 B), and written informed consent from study participants was obtained. Clinical data, including disease stage and follow-up data, were retrieved from the clinical records of the hospital charts of the respective patients (online supplemental table S2). Serum CA19-9 levels were analysed by a routine immunoassay (Roche Diagnostics, Germany) following the manufacturer's instructions. Stool samples were preserved in OMNIgene-Gut OM-200 vials (Steinbrenner Laborsysteme GmbH, Germany) and stored at −80°C immediately until DNA extraction.

Sample processing

Faecal and salivary samples were thawed on ice, aliquoted, and genomic DNA was extracted using the Qiagen Allprep PowerFecal DNA/RNA kit according to the manufacturer's instructions (Qiagen, Hilden, Germany). Genomic DNA from pancreatic tumorous and non-tumoral tissue samples was extracted using the Qiagen DNeasy blood and tissue kit in a protocol modified from Del Castillo *et al*[26]: cells were lysed mechanically (with 5 mm stainless steel beads at 25 Hz for 150 s), followed by lysozyme treatment (20 mg/mL) and protease and RNAse digestion (56°C for 2 h). All samples were randomly assigned to extraction batches. To account for potential bacterial contamination of extraction, polymerase chain reaction (PCR) and sequencing kits, we included negative controls (extraction blanks) with each tissue DNA extraction batch (online supplemental figure 1).

16S rRNA amplicon sequencing

Pancreatic tissue DNA was enriched for 16S rRNA in a preamplification PCR using primers 331F (5'-TCCTACGGGAGGCAGCAGT-3')[61] and 979R (5'-GGTTCTKCGCGTTGCWTC-3').[62] The cycling conditions consisted of an initial template denaturation at 98°C for 2 min, followed by 30 cycles of denaturation at 98°C for 10 s, annealing at 65°C for 20 s, extension at 72°C for 30 s and a final extension at 72°C for 10 min. This was followed by a size-selective cleanup using SPRIselect magnetic beads (0.8 left-sized; Beckman Coulter, Brea, California, USA). Faecal and salivary DNA were not preamplified.

Targeted amplification of the 16S rRNA V4 region (primer sequences F515 5'-GTGCCAGCMGCCGCGGTAA-3' and R806 5'-GGACTACHVGGGTWTCTAAT-3'),[63] was performed using the KAPA HiFi HotStart PCR mix (Roche, Basel, Switzerland) in a two-step barcoded PCR protocol (NEXTflex 16S V4 Amplicon-Seq Kit; Bioo Scientific, Austin, Texas, USA) with minor modifications from the manufacturer's instructions. PCR products were pooled, purified using size-selective SPRIselect magnetic beads (0.8 left-sized) and then sequenced at 2×250 bp on an Illumina MiSeq (Illumina, San Diego, California, USA) at the Genomics Core Facility, European Molecular Biology Laboratory, Heidelberg.

16S rRNA amplicon data processing

Raw reads were quality trimmed, denoised and filtered against chimeric PCR artefacts using DADA2.[64] The resulting exact amplicon sequence variants (ASVs) were taxonomically classified and mapped to a reference set of operational taxonomic units (OTUs) at 98% sequence similarity using MAPseq.[65] Reads that did not confidently map to the reference were aligned to bacterial and archaeal secondary structure-aware small subunit rRNA models using Infernal[66] and clustered into OTUs with 98% average linkage using HPC-CLUST,[67] as described previously.[68] As a result, we obtained taxa tables at two resolutions: 100% identical ASVs and 98% open-reference OTUs; unless otherwise indicated, analyses in the main text refer to OTUs.

Count tables were noise filtered by removing samples retaining less than 500 reads and taxa observed in fewer than five samples; this removed 2.5% of total reads from the dataset. For 18 salivary samples, technical replicates were merged after confirming that they strongly correlated with community composition. For pancreatic tissue and tumour samples, ASVs observed in negative control samples were removed, as were reads mapping to known reagent kit contaminants.[33] After these steps, we retained 308 16S rRNA amplicon samples from 143 subjects for further analyses (130 salivary, 118 faecal, 20 of unaffected pancreatic tissue, 23 of tumour tissue with 17 matching PDAC tissue samples).

Shotgun metagenomic sequencing

Metagenomic libraries for 212 faecal and 100 salivary samples were prepared using the NEB Ultra II and SPRI HD kits, depending on the concentration of starting material, with a targeted insert size of 350, and sequenced on an Illumina HiSeq 4000 platform (Illumina, San Diego, California, USA) in 2×150 bp paired-end setup to a target depth of 8 Gbp per sample at the Genomics Core Facility, European Molecular Biology Laboratory, Heidelberg. Sequencing statistics for each sample are provided in the associated git repository (https://github.com/psecekartal/PDAC.git). For three salivary and one faecal samples, technical replicates were merged after confirming that they strongly correlated in community composition.

Metagenome data processing

Metagenomic data were processed using established workflows in NGLess v0.7.1.[69] Raw reads were quality trimmed (≥45 bp at Phred score ≥25) and filtered against the human genome (version hg19, mapping at ≥90% identity across ≥45 bp). The resulting filtered reads were mapped (≥97% identity across ≥45 bp) against the representative genomes of 5306 species-level genome clusters obtained from the proGenomes database v2.[70]

Taxonomic profiles were obtained using the mOTU profiler v2.5[71] and filtered to retain only species observed at a relative abundance $\geq 10^{-5}$ in ≥2% of samples. Gene functional profiles were obtained from mappings against a global microbioal gene catalogue (GMGCv1, Coelho *et al*[72], http://gmgc.embl.de/), by summarising read counts from eggNOG v4.5[73] annotations to orthologous groups and KEGG modules. Features with a relative abundance of $\geq 10^{-5}$ in ≥15% of samples were retained for further analyses.

Microbiome data statistical analyses

All data analyses were conducted in the R Statistical Computing framework v3.4 or higher.

Rarefied per-sample taxa diversity ('alpha diversity', averaged over 100 rarefaction iterations) was calculated as the effective number of taxa with Hill coefficients of q=0 (ie, taxa richness),

q=1 (exponential of Shannon entropy) and q=2 (inverse Simpson index), and evenness measures as ratios thereof. Unless otherwise stated, results in the main text refer to taxa richness. Differences in alpha diversity were tested using analysis of variance (ANOVA) followed by post hoc tests and Benjamini-Hochberg correction, as specified in the main text.

Between-sample differences in community composition ('beta diversity') were quantified as Bray-Curtis dissimilarity on raw or square-root transformed counts, abundance-weighted Jaccard index, and abundance-weighted and unweighted TINA index, as described previously.[74] Trends between these indices were generally consistent, unless otherwise stated. Results are reported for Bray-Curtis dissimilarities on non-transformed data. Associations of community composition to microbiome-external factors were quantified using the 'adonis2' implementation of PERMANOVA and distance-based redundancy analysis in the R package vegan v2.5.[75] To quantify potentially confounding univariate links between the abundance of individual taxa and subject-specific variables (see main text), we performed either ANOVA or non-parametric Kruskal-Wallis tests, depending on abundance distributions (online supplemental figure 2-3 and online supplemental table S4-S5). Bilirubin levels were measured from blood samples, and jaundice status was confirmed by clinical records. Owing to missing jaundice status for several individuals, values used for further analysis were imputed from existing data (figure 1, online supplemental table S1-S3).

Multivariable statistical modelling and model evaluation

In order to train multivariable statistical models for the prediction of pancreatic cancer, we first removed taxa with low overall abundance and prevalence (abundance cut-off point: 0.001). Then, features were normalised by log10 transformation (to avoid infinite values from the logarithm, a pseudo-count of 1e-05 was added to all values) followed by standardisation as centred log-ratio (log.clr). Data were randomly split into test and

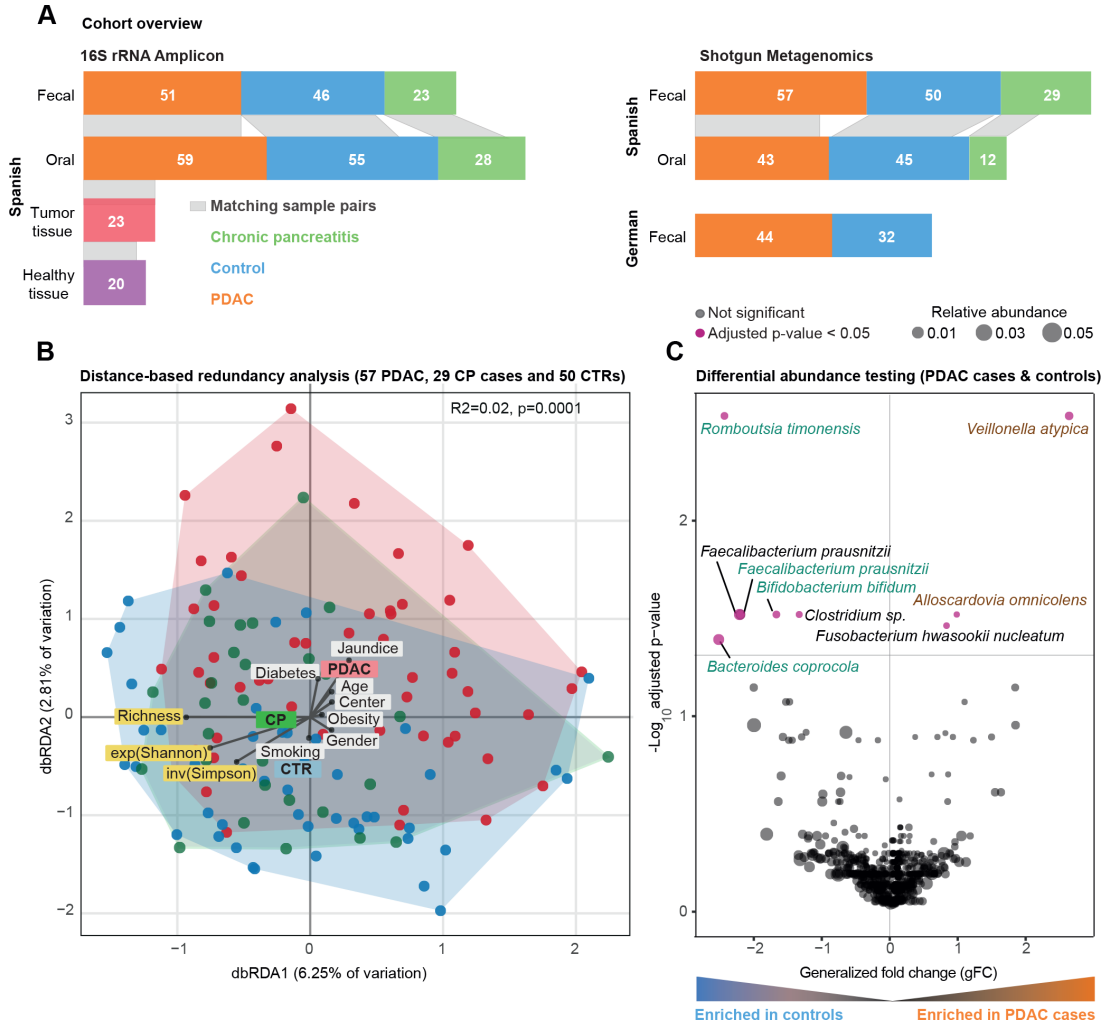

Figure 1 Community analysis of Spanish faecal microbiome data. (A) Study population overview. Grey bands between the bar plots indicate samples of matching body sites within individuals. (B) Bray-Curtis distance-based redundancy analysis (dbRDA) of pancreatic ductal adenocarcinoma (PDAC), chronic pancreatitis (CP) and control (CTR) faecal microbiome data in a Spanish (ES) cohort. PDAC samples are shown as red coloured circles, patients with CP as green and controls as blue. Richness, exponential Shannon (exp(Shannon)) and inverse Simpson (inv(Simpson)) diversity measures are also visualised with arrows similarly to tested metadata variables. The distance of the meta-variable from the centre represents the confounding effect size (see 'Methods'). (C) Wilcoxon test results of ES faecal microbiome data to test enriched taxa between PDAC and control cases (see 'Methods'). Y-axis is log10(FDR corrected p values), X-axis is generalised fold change, and dot size represents the relative abundance of a given species. Red dots represent significantly differentially abundant species in either group, while black dots show non-significant species after FDR correction. Green and brown-coloured species are selected in metagenomic model-1 as predictors of PDAC. FDR, false discovery rate.

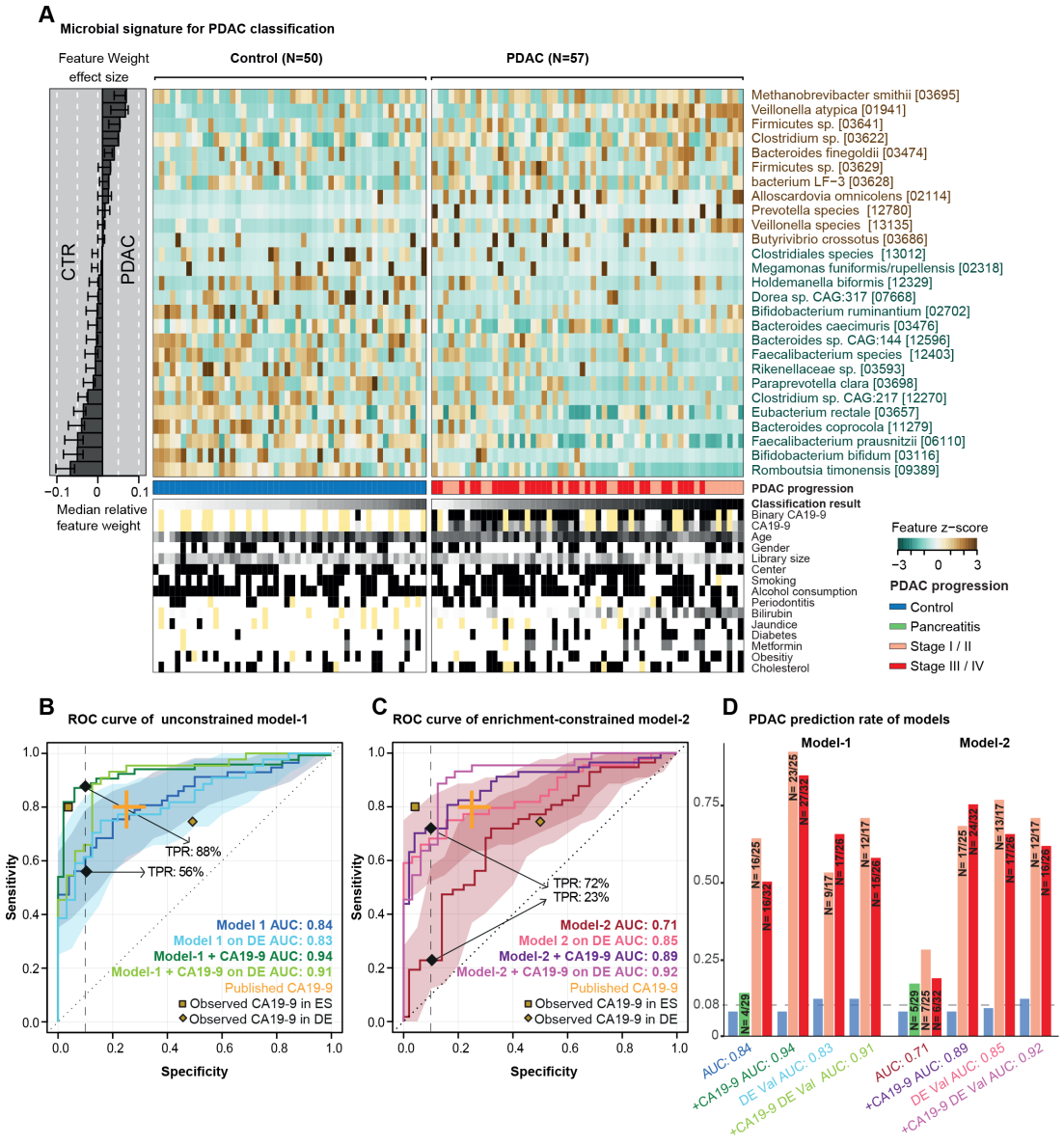

Figure 2 Predictive microbiome signatures of pancreatic ductal adenocarcinoma (PDAC). (A) Normalised abundance of 27 selected species in the faecal microbiome across samples shown as a heat map. The right panel represents the contribution of each selected feature to the overall model-1, and the robustness (the percentage of models in which the feature is included as predictor) of each feature is presented as percentage. Classification scores from cross-validation of each individual and condition for tested meta-variables are displayed at the bottom of the panel, yellow representing missing information. (B–D) Internal cross-validation results of unconstrained model-1 (without feature selection), enrichment-constrained model-2 (constrained to positive features) and combination of carbohydrate antigen (CA)19-9 (using a threshold of 37 µL/mL) with microbial features (see 'Methods') are shown as receiver operating characteristic (ROC) curve with 95% CI shaded in corresponding colour. True positive rates (TPRs) are given as a percentage at a 90% specificity cut-off. Validation of all models on an independent German (DE) PDAC test population (n=76) is represented as well. Published CA19-9 accuracy from a meta-study shown in orange. The yellow dots represent observed CA19-9 accuracies in our populations (data available for 33/50 controls (CTRs) and 44/57 patients with PDAC in the Spanish (ES) and for 8/32 CTRs and 44/44 patients with PDAC in the German (DE) population) (D) TPRs of all models at different PDAC progression stages and in addition, the false-positive rate for patients with chronic pancreatitis and controls at a 90% specificity cut-off are shown as bar plots. Stages I and II and stages III and IV are combined owing to the overall low sample size. The number of predicted cases compared with the total is also shown on the top of each bar. DE-Val, German validation population.

training sets in a 10 times repeated 10-fold cross-validation. For each test fold, the remaining folds were used as training data to train an L1-regularised (LASSO) logistic regression model[76] using the implementation within the LiblineaR R package v2.10.[77] The trained model was then used to predict the left-out test set and finally, all predictions were used to calculate the area under the receiver operating characteristics curve (AUROC) (figure 2).

In a second approach, features were filtered within the cross-validation (that is, for each training set) by first calculating the single-feature AUROC and then removing features with an AUROC <0.5, thereby selecting features enriched in PDAC ('enrichment-constrained' model).

In order to combine the predictions from the microbiome-based machine learning models with the CA19-9 marker,

the coded CA19-9 marker (1 for positive, 0 for negative or not available) was added to the mean predictions from the repeated cross-validation runs, resulting in an OR combination. Alternatively, the AND combination was calculated by multiplying the predictions with the CA19-9 marker. ROC curves and AUROC values were calculated for both combinations using the pROC R package v1.15.[78] The 95% CI is shaded in corresponding colour and specified in figure legends for each ROC curve.

The trained ES metagenomic classifiers for PDAC were then applied to the DE dataset after applying a data normalisation routine, which selects the same set of features and uses the same normalisation parameters (for example, the mean of a feature for standardisation by using the frozen normalisation functionality in SIAMCAT) as in the normalisation procedure from the ES pancreatic cancer dataset. For this analysis, the cut-off point for the predictions was set to a false-positive rate of 10% among controls in the initial ES PDAC study population (figure 2).

All steps of data preprocessing (filtering and normalisation), model training, predictions and model evaluation were performed using the SIAMCAT R package v.1.5.0[79] (https://siamcat.embl.de/).

External validation of the metagenomic classifiers

To assess the disease specificity of the trained models, we obtained predictions for samples from other gut metagenomic datasets (online supplemental table S6) for the full list, including accession numbers). We performed a literature search to identify publicly available datasets of faecal metagenomes in case–control or cohort studies for relevant diseases. For a total set of 25 studies covering 5792 samples across nine disease states, raw sequencing data were downloaded from the European Nucleotide Archive and taxonomically profiled as described above.[35–59]

The trained metagenomic classifiers for PDAC were then applied to each external dataset after applying a data normalisation routine which selects the same set of features and uses the same normalisation parameters (for example, the mean of a feature for standardisation by using frozen normalisation functionality in SIAMCAT) as in the normalisation procedure from the pancreatic cancer dataset. Then, predictions were assessed for disease specificity because high prediction scores for samples from other disease samples would indicate that the classifier relies on general features of dysbiosis in contrast to signals specific to pancreatic cancer, which would not result in elevated false-positive rates on samples from other diseases. For this analysis, the cut-off point for the predictions was set at a false-positive rate of 10% among controls in the initial PDAC study population (figure 3). The effect of age, sex and sequencing depth of 25 populations on prediction score were tested by using the cor.test function (Spearman method) in the car R package v3.0–3.

Subspecies and strain-level analyses

Metagenomic reads were mapped against species-representative genomes from the proGenomes v1 database[80] (see above). Microbial single nucleotide variants were called from uniquely mapping reads using metaSNV,[81] and within-species allele distances between samples were calculated as described previously.[82] Associations between allele distance and PDAC disease state were quantified using PERMANOVA after stratifying for potential confounders (including sampled body site).

Oral-intestinal transmission of strains was quantified as described previously.[83] In short, the overlap between microbial single nucleotide variants in salivary and faecal samples within subjects was contrasted with a between-subject background to compute a quantitative oral-faecal transmission score and p value. Associations of species- and subject-specific transmission scores with clinical factors were tested using ANOVA and *post hoc* tests, followed by a Benjamini-Hochberg correction for multiple tests.

Fluorescence *in situ* hybridisation microscopy

FISH analyses were performed using probes specifically targeting the 16S rRNA sequence unique to a particular taxon of bacteria (figure 4). All probes were selected based on a literature search and the corresponding taxa are displayed in online supplemental table S7).

Pancreatic tumour and normal pancreas samples were obtained from the pathology department and immediately frozen in liquid nitrogen within less than 30 min of surgical excision. Sterile material was used to dissect the different samples. The minimum size of tissue for freezing was approximately 0.125 cm^3 (0.5×0.5×0.5 cm). Samples were transferred from the temporary liquid nitrogen transport container and kept in a locked freezer at –80°C. Before analysis they were transported on dry ice, moved to an optimal cutting temperature mould in liquid nitrogen and immediately cut on a cryotome to obtain 10 sections of 3–5 µm each. All material was sterilised with ethanol after each sample handling.

Tissue sections of 5 µm thickness were mounted on positively charged slides (SuperFrost, Thermo Scientific). Briefly, tissues were postfixed in freshly prepared 4% paraformaldehyde. After enhancement of the bacteria wall permeabilisation by lysozyme treatment (10 g/L Tris HCl 6.5M), samples were hybridised for 1 hour at 45°C in the presence of the specific probe in a hybridiser machine (DAKO). Hybridisation was done in 20 µL of hybridisation buffer (20 nM Tris, pH 8.0. 0.9 M NaCl, 0.02% sodium dodecyl sulfate, 30% formamide) added to 100 ng of the probe. Finally, the tissues were washed in washing solution (70% formamide, 10 mM Tris pH7.2 and 01% bovine serum albumin), dehydrated in a series of ethanol samples, air-dried and stained with 0.5 µg/mL DAPI (4',6,-diamidino-2-phenylindole)/antifade solution (Palex Medical). FISH images were captured using a Leica DM5500B microscope with a CCD camera (Photometrics SenSys) connected to a PC running the CytoVision software 7.2 image analysis system (Applied Imaging). Images were analysed blind and scored based on the intensity of the probe signal.

RESULTS

PDAC is associated with moderate shifts in microbiome composition when controlling for confounding factors in shotgun metagenomic data

We studied 57 newly diagnosed, treatment-naïve patients with PDAC, 29 patients with chronic pancreatitis (CP), and 50 controls matched for age, gender and hospital. Participants were prospectively recruited from two hospitals in Barcelona and Madrid, Spain, between 2016 and 2018, using the same standards (see subject characteristics in figure 1A and online supplemental table S1-S3 for the clinical data for each subject). We obtained faecal shotgun metagenomes for all subjects and salivary metagenomes for 45 patients with PDAC, 12 with CP, and 43 controls (see 'Methods'). The

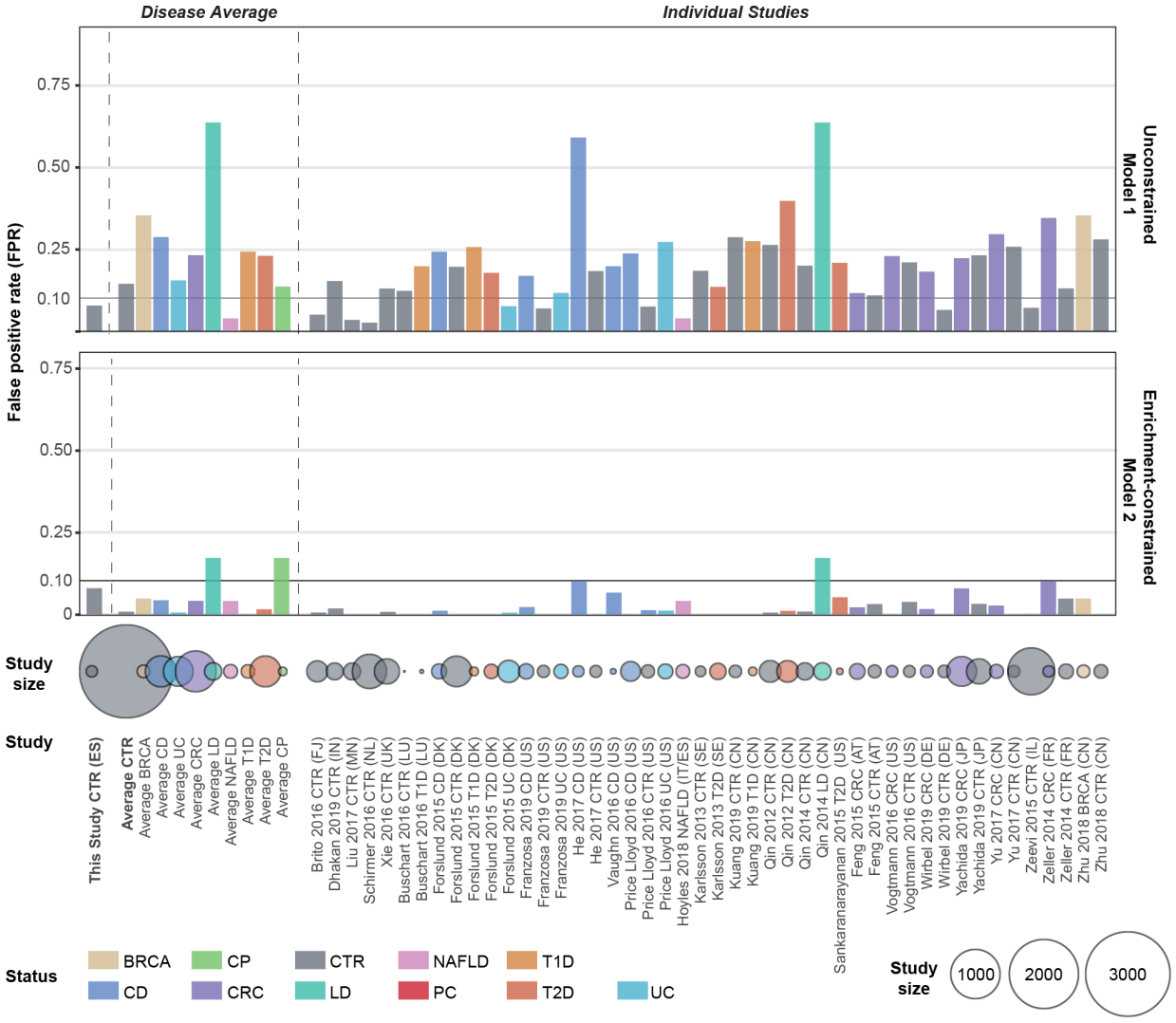

Figure 3 External validation of the disease specificity of pancreatic ductal adenocarcinoma (PDAC) faecal microbiome models. False positive rate (FPR) of metagenomic unconstrained model-1 and enrichment-constrained model-2 in 25 external test sets is shown as a bar plot (see online supplemental table S4 for a list of all studies included). Validation datasets were profiled and normalised in the same way as the initial dataset (see 'Methods'). Each study was stratified according to health status and models were tested to predict in the given group at a 90% specificity cut-off. A low FPR on metagenomes from patients with other disorders and healthy individuals indicates that the model is specific to PDAC. The number of subjects in each group is displayed as colour coded circles below. BRCA, breast cancer; CRC, colorectal cancer; CD, Crohn's disease; CP, chronic pancreatitis;, CTR, controls; LD, liver disease; NAFLD, non-alcoholic fatty liver disease; PC, pancreatic cancer; T1D, type 1 diabetes; T2D, type 2 diabetes; UC, ulcerative colitis; ES, Spanish; DE, German.

analysis workflow is detailed in online supplemental figure 1.

As several PDAC risk factors, such as tobacco smoking, alcohol consumption, obesity or diabetes, are themselves associated with microbiome composition[84], we first sought to establish potential confounders of microbiome signatures in our study population, in order to adjust analyses accordingly. For a total of 26 demographic and clinical variables, we quantified marginal effects on microbiome community-level diversity (online supplemental table S4). Faecal and salivary microbiome richness (as a proxy for alpha diversity) were not univariately associated with any tested variable, or with PDAC status, when accounting for the most common PDAC risk factors and applying a false discovery rate threshold of 0.05 (online supplemental figure 2, online supplemental table S4).

Microbiome community composition, in contrast, varied with age at diagnosis (PERMANOVA on between-sample Bray-Curtis dissimilarities, R2=0.01, Benjamini-Hochberg-corrected p=0.03), diabetes (R2=0.01, p=0.04) and jaundice status (R2=0.02, p=0.009) in faeces, and with aspirin/paracetamol use (R2=0.02, p=0.04) in saliva, albeit at very low effect sizes (online supplemental table S5). Even though cases and controls were matched for age and sex, we included these factors as strata for subsequent analyses. Under such adjustment, subject disease status was mildly but statistically significantly associated with community composition in faeces (R2=0.02, p=0.001), but not in saliva (R2=0.01, p=0.5) (figure 1B, online supplemental figure 3–4, online supplemental table S5). Indeed, the faecal microbiome composition of patients with PDAC differed from that of both controls (R2=0.02, p≤0.0001) and patients with CP

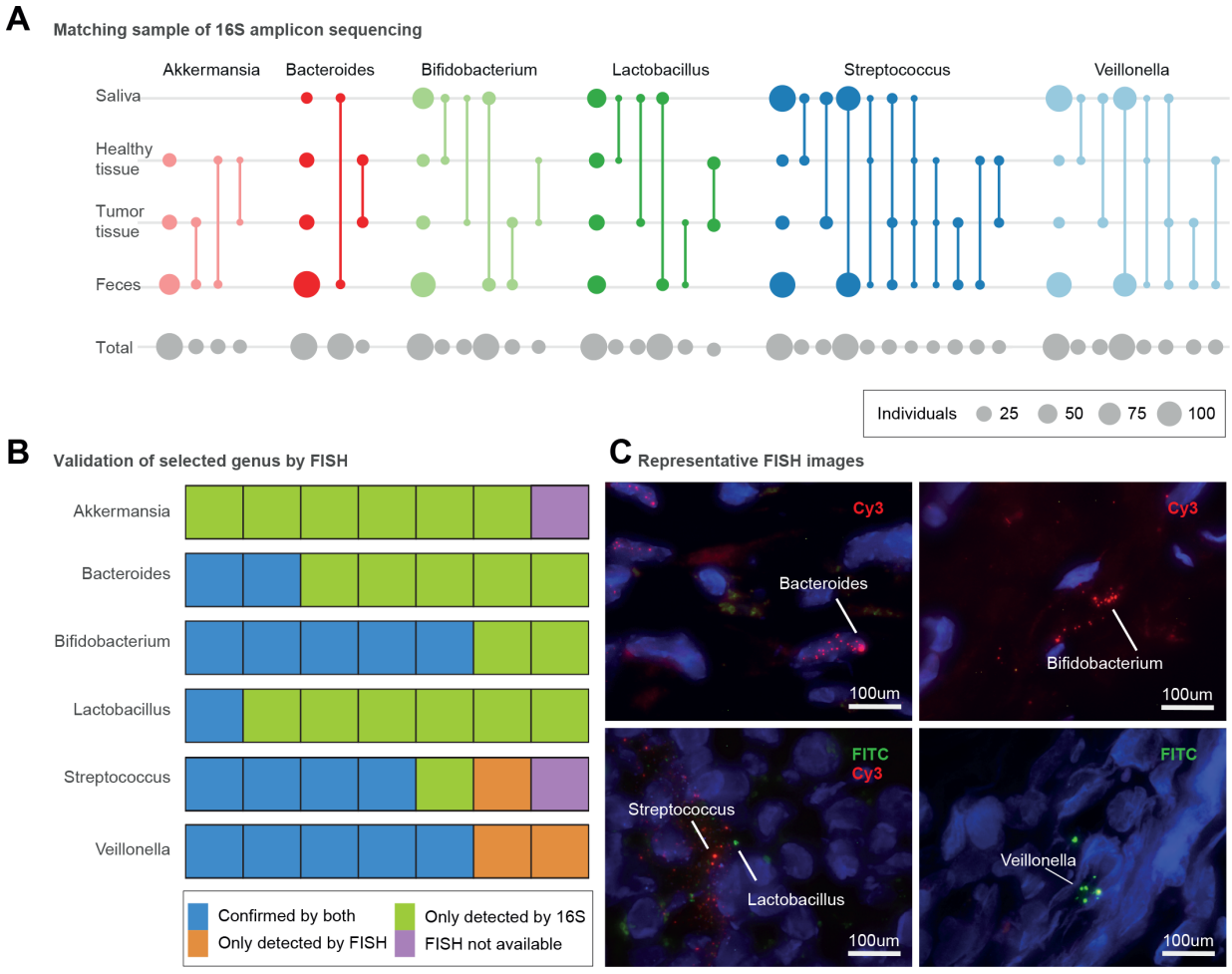

Figure 4 Presence of microbiomes in different sections of the pancreas with different conditions. (A) Presence of different genera in four different body sites including faecal, saliva, pancreatic tumour and healthy tissue samples, as inferred by 16S amplicon data. Circle size corresponds to the total number of subjects available for each comparison (grey, bottom row) or with intra-individually matched amplicon sequence variants (coloured); matched sample types are connected by lines. The first column shows the total number of samples per site in which the genus was detected. (B) Seven selected pancreatic tissue samples (five tumour and two non-tumour) to show bacterial presence/absence with both 16S amplicon and fluorescence *in situ* hybridisation (FISH) methods. Validation of bacterial presence with both 16S amplicon sequencing and FISH is shown in blue. Samples showing bacterial presence according to 16S only are displayed in green. Bacterial presence validated only by FISH is shown in orange, and samples not subjected to FISH validation owing to lack of tissue material are shown in purple. (C) Representative microscopy images for *Bacteroides* (intranuclear, tumour tissue), *Bifidobacterium* (extranuclear, tumour tissue), *Lactobacillus* (extranuclear, non-tumour tissue), *Streptococcus* (extranuclear, non-tumour tissue), *Veillonella* (extranuclear, tumour tissue). Fluorescein isothiocyanate (FITC) and Cy3 fluorescent dyes were used as indicated, and DAPI (4',6,-diamidino-2-phenylindole; blue) was used to label the nucleus.

(R2=0.02, p=0.003), although likewise at very small effect sizes.

High-accuracy metagenomic classifiers capture specific faecal microbiome signatures in patients with PDAC

Having established the presence of a gut microbiome signal for PDAC at the coarse level of overall community composition, we next identified nine species with disease-specific univariate associations (Wilcoxon test of relative abundances in PDAC cases vs controls, Benjamini-Hochberg-corrected p<0.05; see figure 1c). Most prominently, *Veillonella atypica*, *Fusobacterium nucleatum/hwasookii* and *Alloscardovia omnicolens* were enriched in faeces of patients with PDAC, whereas *Romboutsia timonensis, Faecalibacterium prausnitzii, Bacteroides coprocola* and *Bifidobacterium bifidum* species clusters were depleted. In contrast, we did not detect any species with significantly differential abundance in the salivary microbiome when correcting for multiple tests, including previously reported associations, such as *Porphyromonas gingivalis, Aggregatibacter actinomycetemcomitans*,[22] *Neisseria elongata* or *Streptococcus mitis*[18] (online supplemental figure 5).

Among the univariately associated faecal species, several were by themselves moderately predictive of PDAC state (online supplemental figure 5). To coalesce such individual signals into an overarching model, we next built multispecies metagenomic classifiers by fitting LASSO logistic regression models in 10-fold cross-validation (see 'Methods'). When applying no further constraints, the obtained model discriminated between patients with PDAC and controls with high accuracy in our study population ('model-1'; AUROC=0.84; Figure 2). The most prominent positive marker species in the model were *Methanobrevibacter smithii*, *Alloscardovia omnicolens*, *Veillonella atypica* and *Bacteroides finegoldii*. We note that by design, LASSO regression selects representative features among inter-correlated sets;

therefore, these species may be representatives of larger species sets with highly correlated abundances. None of the 26 demographic and epidemiological variables describing our study population were selected as predictive features by the model, and the microbiome signature was more informative than any other feature (see online supplemental figure 6 and 7). Further, none of these variables were individually associated with the microbial species represented in the model, ruling them out as potential confounders. This indicates that the classifier captured a diagnostic gut microbiome signature of PDAC that is probably independent of other disease risk factors and potential confounders.

An analogous model built to differentiate patients with CP from controls had no predictive power (AUROC=0.5; online supplemental figure 8), consistent with the observation that these groups were compositionally largely indistinguishable. Similarly, no robust PDAC signature was detected for the salivary microbiome (AUROC=0.48; online supplemental figure 9). However, a faecal model to distinguish patients with PDAC from those with CP performed better with an AUC of 0.75, but model robustness was limited by the low sample size in the group with CP (online supplemental figure 8). We further explored predictive associations at the higher resolution of functional microbiome profiles. Models based on the abundances of KEGG modules (online supplemental figure 10) achieved an accuracy of up to AUROC=0.74, but feature selection was likewise not robust across validation folds, as a consequence of fitting a high number of variables (modules) against a limited set of samples. We therefore pursued the species-based classifiers, as they provided stable models.

The initial gut microbiome-based classifier included several species depleted in PDAC relative to controls, such as *Faecalibacterium prausnitzii, Bacteroides coprocola, Bifidobacterium bifidum* or *Romboutsia timonensis* (figure 2B). For some of these species, it was previously suggested that depletion is linked to intestinal inflammation, in general, rather than to specific diseases.[85] We therefore retrained a classifier with the constraint that positively associated (enriched) microbial features were exclusively selected in each cross-validation fold. The resulting enrichment-constrained model (model-2) discerned patients with PDAC with an accuracy of AUROC=0.71. The difference with the unconstrained model, model-1, was mostly attributable to a penalty on sensitivity—that is, a decrease in confident detections of patients with PDAC, in line with expectations when training on sparse data.

Combination of metagenomic classifiers with antigen CA19-9 levels increases accuracy

Blood serum levels of the antigen CA19-9 are routinely used to monitor PDAC progress,[86 87] but have also been suggested as a potential marker for early diagnosis of PDAC, although with moderate reported sensitivity (0.80, 95%CI 0.72 to 0.86) and specificity (0.75, 95%CI 0.68 to 0.80).[12] CA19-9 serum levels were available for a subset of 77 individuals (33/50 controls and 44/57 patients with PDAC) in our Spanish population (online supplemental figure S11). Given that CA19-9 is directly secreted by tumours, we hypothesised that the readouts provided by CA19-9 serum levels and by our microbiome classifiers were complementary, and that their combination could improve the accuracy of PDAC prediction. Indeed, accounting for CA19-9 increased the accuracy of our unconstrained model-1 from AUROC=0.84 to 0.94, driven mostly by an increase in sensitivity (figure 2B). More strikingly, when we amended the enrichment-constrained model-2 with CA19-9 information, we observed a large increase in accuracy from AUC=0.71 to 0.89, likewise driven by a significant improvement in sensitivity, thereby essentially abolishing the performance penalty relative to model-1 (figure 2C, online supplemental figure S11). There was no significant bias towards higher CA19-9 levels in later disease stages in either the ES or DE populations (online supplemental figure S11).

Our Spanish study population included 25 patients with PDAC in early disease stages (T1, T2) and 32 subjects in later stages (T3, T4). Disease stage did not affect the performance of either microbiome-based model (figure 2D); in particular, recall was not biased towards later stages.

Performance of metagenome-based classifiers generalises to independent validation cohorts

To test whether the observed microbiome signatures generalise beyond our focal Spanish study population, we next challenged our models in two validation scenarios. First, we tested prediction accuracy in an independent study population of 44 patients with PDAC and 32 matched controls, recruited from two hospitals in Erlangen and Frankfurt am Main, Germany (see figure 1, Methods and online supplemental table S3), with the samples being processed identically to those of the Spanish population. On this DE validation population, both the unconstrained model-1 (figure 2B) and the enrichment-constrained model-2 (figure 2C) performed with comparable or indeed superior accuracies to the training population, both with and without complementation by CA19-9 levels, and with similar trends across disease stages (figure 2D).

Next, to confirm that our metagenomic classifiers captured PDAC-specific signatures, rather than unspecific, more general disease-associated variation, we further validated them against independent, external metagenomic datasets on various health conditions. In total, we classified 5792 publicly available gut metagenomes from 25 studies across 18 countries, including subjects with CP (this study), type 1 or type 2 diabetes, colorectal cancer, breast cancer, liver diseases, non-alcoholic fatty liver disease, including Crohn's disease and ulcerative colitis, as well as healthy controls (figure 3 and online supplemental table S6).

When tuned to 90% specificity (allowing for 10% false positive predictions) in our focal ES study population, the unconstrained model-1 showed a recall of 56% of patients with PDAC in the ES population and 48% in the DE validation population (with 6% false-positive rate), and up to 64% when complemented with information on CA19-9 levels (available for 8/32 controls and 43/44 patients with cases in the DE cohort). The disease specificity of model-1, however, was limited, with predictions of PDAC state for 15% of control subjects on average across all external datasets. Most of these false positive calls were observed in two Chinese populations of patients with Crohn's disease[48] or liver cirrhosis.[44] Crohn's disease has been associated with depletion signatures similar to those observed in our model (in particular of *F. prausnitzii*,[88]) whereas liver diseases share some physiological characteristics with impaired pancreas function. However, all other liver disease and Crohn's disease sets showed lower false detection rates, indicating that the effect was probably attributable, in part, to technical and demographic effects between studies. Indeed, we note that subjects in these two Chinese study populations were significantly younger than our populations (50±11 years for Qin_2014; 28.5±8 years for He_2017; 70±12 y ears for our ES population). This age effect was systematic: across all validation sets, PDAC prediction scores were associated with subject age (ANOVA $p=0.007$; $\rho_{Spearman} = 0.16$), as well as with the sex of the subject ($p<10^{-6;}$) and sequencing depth ($p=0.0008$; $\rho_{Spearman} = 0.1$) (online supplemental figure S12, online supplemental table S6).

The enrichment-constrained model-2 showed lower detection rates in patients with PDAC in both populations, although recall

was reinstated for CA19-9 combined models. Model-2 was highly specific for PDAC with, on average, just 0–5%PDAC predictions in almost all external populations, at a maximum of 17% predictions among the aforementioned[44] population with liver disease. In particular, the detected microbiome signatures were also robust against misclassification of patients with type 2 diabetes (<2%false-positive rate); this is relevant to potential screening applications, as these patients are a major PDAC risk group (figure 3).

PDAC harbours characteristic bacteria, consistent with oral and gut microbiome communities

Alterations in pancreatic secretion, as a consequence of tumour growth in the pancreatic duct, can affect digestive function and may thus plausibly underlie characteristic gut microbiome signatures, such as those described above. This would imply that PDAC progression can indirectly cause microbiome shifts (ie, reverse causation). In addition, the pancreatic duct directly communicates with the duodenum, providing an anatomical link for bacteria[25 30 89] and fungi[34] to colonise the pancreas and contribute to carcinogenesis.[31]

We therefore hypothesised that several gut microbial taxa associated with PDAC should be detectable in pancreatic tumours. We taxonomically profiled all faecal and salivary samples, as well as biopsies of tumours (n=23) and adjacent healthy pancreatic tissue (n=20) of patients with PDAC from our study population using 16S rRNA amplicon sequencing, applying strict filters to exclude putative reagent contaminants often seen in samples of low bacterial biomass[33 90] (see 'Methods'). We observed a surprisingly rich and diverse pancreas microbiome, with at least 13 bacterial genera present in ≥25% of samples, prominently including taxa with characteristic PDAC signatures in the faecal microbiome[91] (figure 4A, online supplemental figure 13). Among these, *Lactobacillus* spp, *Akkermansia muciniphila* and *Bacteroides* spp were enriched in tumours relative to non-tumour pancreatic tissue (Wilcoxon test, false discovery rate-corrected p<0.006).

In a subset of five tumour and two non-tumoral pancreatic tissue samples, we could further verify the prevalence of *Akkermansia* spp, *Lactobacillus* spp, *Bifidobacterium* spp, *Veillonella* spp, *Bacteroides* spp and *Streptococcus* spp using FISH assays with genus-specific primers (online supplemental figure 4, online supplemental table S7). Generally, amplicon and FISH data were concordant, though amplicon-based detection appeared more sensitive probably due to the amount of tissue analysed. Intriguingly, however, *Akkermansia* spp, although observed by amplicon sequencing in 26/30 subjects, were not detectable using FISH in any of the tested samples (figure 4B–C, online supplemental figure 14).

Links between oral, intestinal and pancreatic microbiomes

We next traced exact amplicon sequence variants (ASVs) across salivary, faecal, tumour and healthy tissue samples within subjects (figure 4A), at the highest taxonomic resolution attainable using 16S rRNA data. *Veillonella* spp, characteristically enriched in stool of patients with PDAC, were highly prevalent in both salivary (100% of subjects) and faecal (87.5%) samples across the entire study population, while oral and faecal types also matched tumour and non-tumour tissue ASVs. Interestingly, we found no intraindividual match in *Veillonella* ASVs between tumour and adjacent tissue samples, indicating that tumor-dwelling *Veillonella* spp may be distinct from those in healthy tissue. In addition, our data confirm previous reports that *Lactobacillus* spp[26] and *Bifidobacterium* spp[25] are present in both PDAC tumour and non-tumour tissue. For both genera, we found that tumour types corresponded to either oral or faecal ASVs, but not both, whereas no ASVs from healthy tissue were matched with faecal samples, indicating that distinct pancreatic subpopulations may be linked to the mouth and the gut.

Using paired salivary and faecal shotgun metagenomes, we further confirmed that strains of faecal PDAC-associated microbes may be sourced from the oral cavity (online supplemental results).

DISCUSSION

Early detection of PDAC remains a formidable challenge, at the heart of ongoing efforts to mitigate the burden of this cancer. Currently, the sole FDA-approved biomarker for PDAC is serum CA19-9, mostly used for disease monitoring rather than screening, due to inherent limits of sensitivity and specificity: CA19-9 levels can be elevated in several conditions unrelated to pancreatic cancer, while subjects lacking the Lewis-A antigen do not produce CA19-9 at all.[10–12] Small-scale studies have proposed PDAC markers based on pancreatic tissue,[5] urine[6 7] and blood serum[8 9] with limited applicability. Yet there are currently no screening tools for PDAC in the clinic—in particular, for early disease stages.

In a prospectively recruited study population of newly diagnosed, treatment-naïve patients and matched controls for whom oral, faecal and tissue microbiomes were analysed (figure 1A), we developed metagenomic classifiers that robustly and accurately predict PDAC solely based on characteristic faecal microbial species (figure 2). PDAC signatures captured by our multispecies models were orthogonal to well-established PDAC risk factors (figures 1B and 2A). This suggests that, in practice, the faecal microbiome may be used to screen for PDAC, complementary to other testable markers, with added diagnostic accuracy in combined tests, as has been proposed for colorectal cancer.[39] Indeed, a combination of our microbiome classifiers with CA19-9 data, available for a subset of our population, significantly enhanced the accuracy of PDAC detection (figure 2B–D).

Previous studies have explored links between PDAC and the oral[18–22 26 92 93] or faecal[23 24] microbiome at the limited taxonomic resolution of 16S rRNA sequencing, but provided conflicting reports regarding the association patterns of individual taxa, probably due to heterogeneous experimental and analytical approaches. The non-availability of raw sequence and patient-level clinical data for several PDAC datasets has made comparisons between studies challenging, and thus a consensus on PDAC-associated microbiome signatures has so far failed to emerge. Several previously reported univariate PDAC associations of oral taxa including *P. gingivalis*, *A. actinomycetemcomitans*, *S. thermophilus* and *Fusobacterium* spp were not confirmed in our study population (online supplemental figure 4); we generally did not observe any salivary PDAC signature either for individual species or for multispecies models.

We carefully checked our analyses for demographic, lifestyle, and clinical confounders, as these can show stronger microbiome associations than disease states.[84] We moreover validated our metagenomic classifiers against the independently sampled, yet consistently processed, DE population (figure 2B–D) and against external populations of various health states from 25 different studies (n=5792)[35–59] (figure 3). Both confounder control and external validation are essential when assessing the disease specificity of predictive models, in particular for diseases

like PDAC with low incidence in the general population. This was confirmed in our analyses: among our two metagenomic classifiers, model-1 showed a high accuracy of AUROC=0.84 in our ES study population, driven by a high recall of patients with PDAC. However, model-1 showed only limited disease specificity in external validations, capturing non-specific species depletion signals discriminative between cases and controls in our population, but also shared by subjects with other diseases. These included generic inflammation signatures—for example, a depletion of *F. prausnitzii, E. rectale* or *B. bifidum*. Published metagenomic classifiers for various diseases, and in particular previously reported signatures for PDAC, share similar limitations: highly tuned accuracy on the focal population, but non-specific features shared with other diseases. This lack of specificity limits their translation into clinical practice. In contrast, our model-2, constrained to PDAC-enriched features, achieved only moderate accuracy within our populations (AUC=0.71 on ES, AUC=0.85 on DE) due to a penalty on sensitivity, but was highly PDAC-specific with very low false prediction rates in external populations, including known PDAC risk groups such as those with type 2 diabetes. In particular, PDAC-enriched features in both model-1 and model-2 showed little overlap with characteristic faecal microbiome features for other cancer types, such as colorectal cancer, indicating that a combination of our microbiome models with CA19-9 levels (highly sensitive, but not specific to PDAC) is promising. We note that the residual false positive rate among external populations may partly be due to technical heterogeneity, as all external populations were sampled and processed using independent protocols, and that univariate PDAC associations of individual species may be informative, but not disease-specific (Supplementary Discussion). The panel of PDAC-enriched species in model-2 thus shows potential for microbiome-based PDAC screening, given that a combination with complementary information on serum CA19-9 significantly increased accuracy (AUC=0.89 and 0.92).

Our models showed comparable performance across PDAC disease stages, with no bias towards later stages (figure 2B–D). This indicates that characteristic microbiome signatures emerge early during progression of the disease and that the faecal microbiome can serve for the early detection of PDAC.

Our data are strictly observational and cross-sectional. Nevertheless, there are strong indications that the identified faecal microbiome shifts are not merely a consequence of impaired pancreatic function or systemic effects thereof, although indirect effects cannot be ruled out. Several taxa could be traced between the gut and pancreas, with univariate enrichment in tumours relative to adjacent healthy tissue, indicating direct associations of PDAC with the gut microbiome. We confirmed previous observations[25 30 31 89 91] that the human pancreas harbours a microbiome, both by amplicon sequencing, and by FISH for the most comprehensive panel of taxa to date (figure 4). Pancreatic tissue and tumours contain only low bacterial biomass and are therefore prone to contamination in 16S rRNA amplicon data[33], whereas FISH testing requires specific hypotheses, so a comprehensive cataloguing of the healthy and diseased pancreatic microbiome composition is still emerging. In our study, we carefully filtered our dataset against known kit contaminants and confirmed the presence of various key genera using FISH assays. We moreover observed an intraindividual overlap of exact amplicon sequence variants between oral, faecal and tissue samples, confirming a shared presence across multiple sites for several species at the highest attainable taxonomic resolution for amplicon data.

Faecal populations of characteristic PDAC-associated taxa could thus be traced back to pancreatic tumours. Similarly, we observed significantly increased levels of oral-intestinal strain transmission in patients with PDAC, in particular of PDAC signature taxa, indicating that these may be sourced intraindividually, from the oral cavity (online supplemental results). These findings suggest that the oral, intestinal and pancreatic microbiomes may be intricately linked, and that multibody site study designs such as presented here will be necessary to disentangle their respective roles and interactions in PDAC aetiology.

In summary, the described faecal microbiome signatures enabled robust metagenomic classifiers for PDAC detection at high disease specificity, complementary to existing markers, and with potential towards cost-effective PDAC screening and monitoring. Furthermore, in view of previous reports on microbe-mediated pancreatic carcinogenesis in murine models and humans,[25 30 94] we believe that the presented panel of PDAC-associated bacterial species may be relevant beyond their use for diagnosis, providing promising future entry points for disease prevention and therapeutic intervention.

Author affiliations
[1]Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany
[2]Collaboration for joint PhD degree, European Molecular Biology Laboratory and Heidelberg University, Heidelberg, Germany
[3]Genetic and Molecular Epidemiology Group, Spanish National Cancer Research Centre (CNIO), Madrid, Spain
[4]Centro de Investigación Biomédica en Red de Oncología (CIBERONC), Madrid, Spain
[5]Molecular Cytogenetics Unit, Spanish National Cancer Research Centre (CNIO), Madrid, Spain
[6]Member of the German Center for Lung Research (DZL) and the Universities of Giessen and Marburg Lung School (UGMLC), Philipps University Marburg Faculty of Medicine, Marburg, Germany
[7]Medical Oncology Department of Oncology, Hospital Ramón y Cajal, Madrid, Spain
[8]University of Alcala de Henares, Alcala de Henares, Spain
[9]Translational Hepatology Department of Internal Medicine I, Goethe-Universitat Frankfurt am Main, Frankfurt am Main, Germany
[10]Frankfurt Cancer Institute, Goethe University Frankfurt, Frankfurt am Main, Hessen, Germany
[11]Genomic Core Facility, European Molecular Biology Laboratory, Heidelberg, Germany
[12]Department of Surgery, Erlangen University Hospital, Erlangen, Germany
[13]Department of Surgery, University of Greifswald, Greifswald, Germany
[14]Hospital Universitari Vall d'Hebron, Institut de Recerca (VHIR), Barcelona, Spain
[15]Universitat Autònoma de Barcelona, Barcelona, Spain
[16]Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREHD), Madrid, Spain
[17]EF Clif, European Foundation for the Study of Chronic Liver Failure, Barcelona, Spain
[18]Epithelial Carcinogenesis Group, Spanish National Cancer Research Centre (CNIO), Madrid, Spain
[19]Departament de Ciències Experimentals i de la Salut, Universitat Pompeu Fabra, Barcelona, Spain
[20]Department of Bioinformatics, Biocenter, University of Würzburg, Würzburg, Germany
[21]Yonsei Frontier Lab (YFL), Yonsei University, Seoul, South Korea
[22]Max Delbrück Centre for Molecular Medicine, Berlin, Germany

Twitter Ece Kartal @ps_ecekartal, Thomas S B Schmidt @TSBSchm, Oleksandr M Maistrenko @o__maistrenko, Georg Zeller @ZellerGroup, Jonel Trebicka @JonelTrebicka, Nuria Malats @nmalats and Peer Bork @BorkLab

Acknowledgements We thank members of the Bork, Malats and Zeller groups for inspiring discussions and all contributions. Additionally, we thank the EMBL Genomics Core Facility for sequencing support.

Collaborators PanGenEU Study Investigators. Spanish National Cancer Research Centre (CNIO), Madrid, Spain: Núria Malats, Francisco X Real, Evangelina López de Maturana, Paulina Gómez-Rubio, Esther Molina-Montes, Lola Alonso, Mirari Márquez, Roger Milne, Ana Alfaro, Tania Lobato, Lidia Estudillo. Verona University, Italy: Rita Lawlor, Aldo Scarpa, Stefania Beghelli. National Cancer Registry Ireland, Cork, Ireland: Linda Sharp, Damian O'Driscoll. Hospital Madrid-Norte-Sanchinarro,

Madrid, Spain: Manuel Hidalgo, Jesús Rodríguez Pascual. Hospital Ramon y Cajal, Madrid, Spain: Alfredo Carrato, Alejandra Caminoa, Carmen Guillén-Ponce, Mercedes Rodríguez-Garrote, Federico Longo-Muñoz, Reyes Ferreiro, Vanessa Pachón, M Ángeles Vaz. Hospital del Mar, Barcelona, Spain: Mar Iglesias, Lucas Ilzarbe, Cristina Álvarez-Urturi, Xavier Bessa, Felipe Bory, Lucía Márquez, Ignasi Poves, Fernando Burdío, Luis Grande, Javier Gimeno. Hospital Vall dHebron, Barcelona, Spain: Xavier Molero, Luisa Guarner, Joaquin Balcells, Mayte Salcedo. Technical University of Munich, Germany: Christoph Michalski, Irene Esposito, Jörg Kleeff, Bo Kong. Karolinska Institute, Stockholm, Sweden: Matthias Löhr, Jiaqui Huang, Caroline Verbeke, Weimin Ye, Jingru Yu. Hospital 12 de Octubre, Madrid, Spain: José Perea, Pablo Peláez. Hospital de la Santa Creu i Sant Pau, Barcelona, Spain: Antoni Farré, Josefina Mora, Marta Martín, Vicenç Artigas, Carlos Guarner, Francesc J Sancho, Mar Concepción, Teresa Ramón y Cajal. The Royal Liverpool University Hospital, UK: William Greenhalf, Eithne Costello. Queen's University Belfast, UK: Michael O'Rorke, Liam Murray, Marie Cantwell. Laboratorio de Genética Molecular, Hospital General Universitario de Elche, Spain: Víctor M Barberá, Javier Gallego. Instituto Universitario de Oncología del Principado de Asturias, Oviedo, Spain: Adonina Tardón, Luis Barneo. Hospital Clínico Universitario de Santiago de Compostela, Spain: Enrique Domínguez Muñoz, Antonio Lozano, Maria Luaces. Hospital Clínico Universitario de Salamanca, Spain: Luís Muñoz-Bellvís, J.M. Sayagués Manzano, M.L. Gutíerrrez Troncoso, A. Orfao de Matos. University of Marburg, Department of Gastroenterology, Phillips University of Marburg, Germany: Thomas Gress, Malte Buchholz, Albrecht Neesse. Queen Mary University of London, UK: Tatjana Crnogorac-Jurcevic, Hemant M Kocher, Satyajit Bhattacharya, Ajit T Abraham, Darren Ennis, Thomas Dowe, Tomasz Radon. Scientific advisors of the PanGenEU Study: Debra T Silverman (NCI, USA) and Douglas Easton (U. of Cambridge, UK).MAGIC (MicrobiotA-focused German Interdisciplinary Collaboration) Study Investigators. Section for Translational Hepatology, Department of Internal Medicine I, Frankfurt Cancer Institute, Goethe University Frankfurt: Jonel Trebicka, Hans-Peter Erasmus, Fabian Finkelmeier, Robert Schierwagen, Wenyi Gu, Olaf Tyc, Frank Erhard Uschner, Stefan Zeuzem. Department of Surgery, University Greifswald: Stephan Kersting, Melanie Langheinrich. Department of Surgery, University Erlangen: Robert Grützmann, Georg F. Weber, Christian Pilarsky. Department of Internal Medicine, University Erlangen: Stefan Wirtz.

Contributors EK designed the study, conducted experimental work, acquired and analysed data, wrote the first manuscript draft and the revised manuscript.TSBS designed the study, acquired and analysed data, wrote the first manuscript draft and the revised manuscript.EM-M designed the study, contributed to patient recruitment and the collection of biomaterials and clinical data, acquired and analysed data, and wrote the first manuscript draft.SR-P contributed to patient recruitment and the collection of biomaterials and clinical data and conducted experimental work. JW, OMM, WAA, BAA, AC, HP-E, FF, PG-R, SKe, ML, MM, XM, RT-R, JT contributed to patient recruitment and the collection of biomaterials and clinical data. RJA, AF, AMG, KZ contributed to data analysis. LE contributed to patient recruitment and the collection of biomaterials and clinical data and conducted experimental work. RH, FJ, SKa, AT conducted experimental work and acquired data. AO, TvR contributed to data analysis. MSI, PSI contributed to patient recruitment. VB acquired data. GZ designed the study and contributed to data analysis. FXR designed the study and contributed to data analysis and wrote the first manuscript draft. NM conceived the study, designed the study, contributed to patient recruitment and the collection of biomaterials and clinical data and wrote the first manuscript draft. PB conceived of the study, designed the study, contributed to data analysis and wrote the first manuscript draft. All authors reviewed, edited and approved the final version of the manuscript.

Funding We acknowledge funding from EMBL, CNIO, World Cancer Research (#15–0391), the European Research Council (ERC-AdG-669830 MicrobioS), the BMBF-funded Heidelberg CenterCentre for Human Bioinformatics (HD-HuB) within the German Network for Bioinformatics Infrastructure (de.NBI #031A537B), Fondo de Investigaciones Sanitarias (FIS), Instituto de Salud Carlos III-FEDER, Spain (grant numbers PI15/01573, PI18/01347, FIS PI17/02303); Red Temática de Investigación Cooperativa en Cáncer, Spain (grant numbers RD12/0036/0034, RD12/0036/0050, RD12/0036/0073); III beca Carmen Delgado/Miguel Pérez-Mateo de AESPANC-ACANPAN; EU-6FP Integrated Project (#018771-MOLDIAG-PACA); EU-FP7-HEALTH (#259737-CANCERALIA). Funders had no involvement in the study design, patient enrolment, analysis, manuscript writing or reviewing.

Competing interests EK, TSBS, JW, OMM, EM-M, GZ, LE, SR-P, FXR, NM and PB have a pending patent application (application number: EP21382876.7) for early detection of pancreatic cancer based on microbial biomarkers. The other authors declare no conflicts of interest.

Patient consent for publication Not applicable.

Ethics approval Participants were prospectively recruited from the Hospital Ramón y Cajal in Madrid and Hospital Vall dHebron in Barcelona, Spain. Institutional review board ethical approval (CEI PI 26 2015-v7) and written informed consent was obtained from participating centres and study participants, respectively. An independent validation population was recruited at the Department of Surgery, University Hospital of Erlangen (32 PDAC and 32 control samples) and Section for Translational Hepatology, Department of Internal Medicine I, Goethe University Clinic Frankfurt (12 PDAC samples). The study was approved by the local ethics committees (SGI-3-2019, 451_18 B). Clinical data, including disease stage and follow-up data, were retrieved from the clinical records of the hospital charts of the respective patients.

Provenance and peer review Not commissioned; externally peer reviewed.

Data availability statement Data are available in a public, open access repository. All data relevant to the study are included in the article or uploaded as supplementary information. The raw sequencing data for the samples are made available in the European Nucleotide Archive (ENA) under the study identifiers PRJEB38625 and PRJEB42013. Metadata for these samples are available as Supplementary Tables S1 and S2. Filtered taxonomic and functional profiles used as input for the statistical modelling pipeline are available in Supplementary Data S1 and S2. Analysis code and results available under https://github.com/psecekartal/PDAC.git.

ORCID iDs
Ece Kartal http://orcid.org/0000-0002-7720-455X
Thomas S B Schmidt http://orcid.org/0000-0001-8587-4177
Esther Molina-Montes http://orcid.org/0000-0002-0428-2426
Sandra Rodríguez-Perales http://orcid.org/0000-0001-7221-3636
Jakob Wirbel http://orcid.org/0000-0002-4073-3562
Oleksandr M Maistrenko http://orcid.org/0000-0003-1961-7548
Wasiu A Akanni http://orcid.org/0000-0002-2075-2387
Bilal Alashkar Alhamwe http://orcid.org/0000-0002-7120-0013
Renato J Alves http://orcid.org/0000-0002-7212-0234
Alfredo Carrato http://orcid.org/0000-0001-7749-8140
Lidia Estudillo http://orcid.org/0000-0003-3891-3713
Anthony Fullam http://orcid.org/0000-0002-0884-8124
Ferris Jung http://orcid.org/0000-0002-5534-7832
Stefanie Kandels http://orcid.org/0000-0002-4194-4927
Stephan Kersting http://orcid.org/0000-0002-2124-3103
Melanie Langheinrich http://orcid.org/0000-0002-0120-9135
Askarbek Orakov http://orcid.org/0000-0001-6823-5269
Thea Van Rossum http://orcid.org/0000-0002-3598-5001
Raul Torres-Ruiz http://orcid.org/0000-0001-9606-0398
Anja Telzerow http://orcid.org/0000-0001-9855-0809
Konrad Zych http://orcid.org/0000-0001-7426-0516
Vladimir Benes http://orcid.org/0000-0002-0352-2547
Georg Zeller http://orcid.org/0000-0003-1429-7485
Jonel Trebicka http://orcid.org/0000-0002-7028-3881
Francisco X Real http://orcid.org/0000-0001-9501-498X
Nuria Malats http://orcid.org/0000-0003-2538-3784
Peer Bork http://orcid.org/0000-0002-2627-833X

REFERENCES

1 Siegel RL, Miller KD, Jemal A. Cancer statistics, 2018. *CA Cancer J Clin* 2018;68:7–30. doi:10.3322/caac.21442
2 Bray F, Ferlay J, Soerjomataram I, *et al*. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA Cancer J Clin* 2018;68:394–424. doi:10.3322/caac.21492
3 Kamisawa T, Wood LD, Itoi T, *et al*. Pancreatic cancer. *The Lancet* 2016;388:73–85. doi:10.1016/S0140-6736(16)00141-0
4 Park W, Chawla A, O'Reilly EM. Pancreatic cancer: a review. *JAMA* 2021;326. doi:10.1001/jama.2021.13027
5 Wang Y, Li Z, Zheng S, *et al*. Expression profile of long non-coding RNAs in pancreatic cancer and their clinical significance as biomarkers. *Oncotarget* 2015;6:35684–98. doi:10.18632/oncotarget.5533

6 Blyuss O, Zaikin A, Cherepanova V, *et al*. Development of PancRISK, a urine biomarker-based risk score for stratified screening of pancreatic cancer patients. *Br J Cancer* 2020;122:692–6. doi:10.1038/s41416-019-0694-0
7 Debernardi S, Massat NJ, Radon TP, *et al*. Noninvasive urinary miRNA biomarkers for early detection of pancreatic adenocarcinoma. *Am J Cancer Res* 2015;5:3455–66.
8 Seifert AM, Reiche C, Heiduk M, *et al*. Detection of pancreatic ductal adenocarcinoma with galectin-9 serum levels. *Oncogene* 2020;39:3102–13. doi:10.1038/s41388-020-1186-7
9 Melo SA, Luecke LB, Kahlert C, *et al*. Glypican-1 identifies cancer exosomes and detects early pancreatic cancer. *Nature* 2015;523:177–82. doi:10.1038/nature14581
10 Goonetilleke KS, Siriwardena AK. Systematic review of carbohydrate antigen (CA 19-9) as a biochemical marker in the diagnosis of pancreatic cancer. *Eur J Surg Oncol* 2007;33:266–70 http://www.sciencedirect.com/science/article/pii/S0748798306003763 doi:10.1016/j.ejso.2006.10.004
11 Gui J-C, Yan W-L, Liu X-D. CA19-9 and CA242 as tumor markers for the diagnosis of pancreatic cancer: a meta-analysis. *Clin Exp Med* 2014;14:225–33. doi:10.1007/s10238-013-0234-9
12 Xing H, Wang J, Wang Y, *et al*. Diagnostic value of CA 19-9 and carcinoembryonic antigen for pancreatic cancer: a meta-analysis. *Gastroenterol Res Pract* 2018;2018:1–9. doi:10.1155/2018/8704751
13 Hasan S, Jacob R, Manne U, *et al*. Advances in pancreatic cancer biomarkers. *Oncol Rev* 2019;13:410. doi:10.4081/oncol.2019.410
14 Qader G, Aali M, Smail SW, *et al*. Cardiac, hepatic and renal dysfunction and IL-18 polymorphism in breast, colorectal, and prostate cancer patients. *Asian Pac J Cancer Prev* 2021;22:131–7. doi:10.31557/APJCP.2021.22.1.131
15 Rawla P, Sunkara T, Gaduputi V. Epidemiology of pancreatic cancer: global trends, etiology and risk factors. *World J Oncol* 2019;10:10–27. doi:10.14740/wjon1166
16 Wood LD, Yurgelun MB, Goggins MG. Genetics of familial and sporadic pancreatic cancer. *Gastroenterology* 2019;156:2041–55. doi:10.1053/j.gastro.2018.12.039
17 Michaud DS, Lu J, Peacock-Villada AY, *et al*. Periodontal disease assessed using clinical dental measurements and cancer risk in the ARIC study. *J Natl Cancer Inst* 2018;110:843–54. doi:10.1093/jnci/djx278
18 Farrell JJ, Zhang L, Zhou H, *et al*. Variations of oral microbiota are associated with pancreatic diseases including pancreatic cancer. *Gut* 2012;61:582–8. doi:10.1136/gutjnl-2011-300784
19 Michaud DS, Izard J, Wilhelm-Benartzi CS, *et al*. Plasma antibodies to oral bacteria and risk of pancreatic cancer in a large European prospective cohort study. *Gut* 2013;62:1764–70. doi:10.1136/gutjnl-2012-303006
20 Olson SH, Satagopan J, Xu Y, *et al*. The oral microbiota in patients with pancreatic cancer, patients with IPMNs, and controls: a pilot study. *Cancer Causes Control* 2017;28:959–69. doi:10.1007/s10552-017-0933-8
21 Lu H, Ren Z, Li A, *et al*. Tongue coating microbiome data distinguish patients with pancreatic head cancer from healthy controls. *J Oral Microbiol* 2019;11:1563409. doi:10.1080/20002297.2018.1563409
22 Fan X, Alekseyenko AV, Wu J, *et al*. Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. *Gut* 2018;67:120–7. doi:10.1136/gutjnl-2016-312580
23 Ren Z, Jiang J, Xie H, *et al*. Gut microbial profile analysis by MiSeq sequencing of pancreatic carcinoma patients in China. *Oncotarget* 2017;8:95176–91. doi:10.18632/oncotarget.18820
24 Half E, Keren N, Reshef L, *et al*. Fecal microbiome signatures of pancreatic cancer patients. *Sci Rep* 2019;9:16801. doi:10.1038/s41598-019-53041-4
25 Pushalkar S, Hundeyin M, Daley D, *et al*. The pancreatic cancer microbiome promotes oncogenesis by induction of innate and adaptive immune suppression. *Cancer Discov* 2018;8:403–16. doi:10.1158/2159-8290.CD-17-1134
26 Del Castillo E, Meier R, Chung M, *et al*. The microbiomes of pancreatic and duodenum tissue overlap and are highly subject specific but differ between pancreatic cancer and noncancer subjects. *Cancer Epidemiol Biomarkers Prev* 2019;28:370–83. doi:10.1158/1055-9965.EPI-18-0542
27 Mei Q-X, Huang C-L, Luo S-Z, *et al*. Characterization of the duodenal bacterial microbiota in patients with pancreatic head cancer vs. healthy controls. *Pancreatology* 2018;18:438–45. doi:10.1016/j.pan.2018.03.005
28 Geller LT, Barzily-Rokni M, Danino T, *et al*. Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. *Science* 2017;357:1156–60. doi:10.1126/science.aah5043
29 Mitsuhashi K, Nosho K, Sukawa Y, *et al*. Association of *Fusobacterium* species in pancreatic cancer tissues with molecular features and prognosis. *Oncotarget* 2015;6:7209–20. doi:10.18632/oncotarget.3109
30 Thomas RM, Gharaibeh RZ, Gauthier J, *et al*. Intestinal microbiota enhances pancreatic carcinogenesis in preclinical models. *Carcinogenesis* 2018;39:1068–78. doi:10.1093/carcin/bgy073
31 Riquelme E, Zhang Y, Zhang L, *et al*. Tumor microbiome diversity and composition influence pancreatic cancer outcomes. *Cell* 2019;178:795–806. doi:10.1016/j.cell.2019.07.008
32 Gaiser RA, Halimi A, Alkharaan H, *et al*. Enrichment of oral microbiota in early cystic precursors to invasive pancreatic cancer. *Gut* 2019;68:2186–94. doi:10.1136/gutjnl-2018-317458
33 Salter SJ, Cox MJ, Turek EM, *et al*. Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. *BMC Biol* 2014;12:87. doi:10.1186/s12915-014-0087-z
34 Aykut B, Pushalkar S, Chen R, *et al*. The fungal mycobiome promotes pancreatic oncogenesis via activation of MBL. *Nature* 2019;574:264–7. doi:10.1038/s41586-019-1608-2
35 Heintz-Buschart A, May P, Laczny CC, *et al*. Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. *Nat Microbiol* 2017;2:16180.
36 Dhakan DB, Maji A, Sharma AK, *et al*. The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. *Gigascience* 2019;8:giz004. doi:10.1093/gigascience/giz004
37 Feng Q, Liang S, Jia H, *et al*. Gut microbiome development along the colorectal adenoma-carcinoma sequence. *Nat Commun* 2015;6:6528. doi:10.1038/ncomms7528
38 Wirbel J, Pyl PT, Kartal E, *et al*. Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. *Nat Med* 2019;25:679–89. doi:10.1038/s41591-019-0406-6
39 Zeller G, Tap J, Voigt AY, *et al*. Potential of fecal microbiota for early-stage detection of colorectal cancer. *Mol Syst Biol* 2014;10:766. doi:10.15252/msb.20145645
40 Brito IL, Yilmaz S, Huang K, *et al*. Mobile genes in the human microbiome are structured from global to individual scales. *Nature* 2016;535:435–9. doi:10.1038/nature18927
41 Vaughn BP, Vatanen T, Allegretti JR, *et al*. Increased intestinal microbial diversity following fecal microbiota transplant for active Crohn's disease. *Inflamm Bowel Dis* 2016;22:2182–90. doi:10.1097/MIB.0000000000000893
42 Forslund K, Hildebrand F, Nielsen T, *et al*. Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature* 2015;528:262–6. doi:10.1038/nature15766
43 Liu W, Zhang J, Wu C, *et al*. Unique features of ethnic Mongolian gut microbiome revealed by metagenomic analysis. *Sci Rep* 2016;6:34826. doi:10.1038/srep34826
44 Qin N, Yang F, Li A, *et al*. Alterations of the human gut microbiome in liver cirrhosis. *Nature* 2014;513:59–64. doi:10.1038/nature13568
45 Kuang Y-S, Lu J-H, Li S-H, *et al*. Connections between the human gut microbiome and gestational diabetes mellitus. *Gigascience* 2017;6:1–12.
46 Karlsson FH, Tremaroli V, Nookaew I, *et al*. Gut metagenome in European women with normal, impaired and diabetic glucose control. *Nature* 2013;498:99–103. doi:10.1038/nature12198
47 Hoyles L, Fernández-Real J-M, Federici M, *et al*. Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. *Nat Med* 2018;24:1070–80. doi:10.1038/s41591-018-0061-3
48 Quing H, Gao Y, Jie Z, *et al*. Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients. *Gigascience* 2017;6:gix050. doi:10.1093/gigascience/gix050
49 Franzosa EA, Sirota-Madi A, Avila-Pacheco J, *et al*. Gut microbiome structure and metabolic activity in inflammatory bowel disease. *Nat Microbiol* 2019;4:293–305. doi:10.1038/s41564-018-0306-4
50 Yu J, Feng Q, Wong SH, *et al*. Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. *Gut* 2017;66:70–8. doi:10.1136/gutjnl-2015-309800
51 Zeevi D, Korem T, Zmora N, *et al*. Personalized nutrition by prediction of glycemic responses. *Cell* 2015;163:1079–94. doi:10.1016/j.cell.2015.11.001
52 Zhu J, Liao M, Yao Z, *et al*. Breast cancer in postmenopausal women is associated with an altered gut metagenome. *Microbiome* 2018;6:136. doi:10.1186/s40168-018-0515-3
53 Yachida S, Mizutani S, Shiroma H, *et al*. Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer. *Nat Med* 2019;25:968–76. doi:10.1038/s41591-019-0458-7
54 Vogtmann E, Hua X, Zeller G, *et al*. Colorectal cancer and the human gut microbiome: reproducibility with whole-genome shotgun sequencing. *PLoS One* 2016;11:e0155362. doi:10.1371/journal.pone.0155362
55 Sankaranarayanan K, Ozga AT, Warinner C, *et al*. Gut microbiome diversity among Cheyenne and Arapaho individuals from Western Oklahoma. *Curr Biol* 2015;25:3161–9. doi:10.1016/j.cub.2015.10.060
56 Qin J, Li Y, Cai Z, *et al*. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature* 2012;490:55–60. doi:10.1038/nature11450
57 Lloyd-Price J, Mahurkar A, Rahnavard G, *et al*. Strains, functions and dynamics in the expanded human microbiome project. *Nature* 2017;550:61–6.
58 Schirmer M, Smeekens SP, Vlamakis H, *et al*. Linking the human gut microbiome to inflammatory cytokine production capacity. *Cell* 2016;167:1125–36. doi:10.1016/j.cell.2016.10.020
59 Xie H, Guo R, Zhong H, *et al*. Shotgun metagenomics of 250 adult twins reveals genetic and environmental impacts on the gut microbiome. *Cell Syst* 2016;3:572–84. doi:10.1016/j.cels.2016.10.004
60 Stekhoven DJ, Bühlmann P. MissForest--non-parametric missing value imputation for mixed-type data. *Bioinformatics* 2012;28:112–8. doi:10.1093/bioinformatics/btr597

61 Nadkarni MA, Martin FE, Jacques NA, *et al*. Determination of bacterial load by real-time PCR using a broad-range (universal) probe and primers set. *Microbiology* 2002;148:257–66. doi:10.1099/00221287-148-1-257
62 Kramski M, Gaeguta AJ, Lichtfuss GF, *et al*. Novel sensitive real-time PCR for quantification of bacterial 16S rRNA genes in plasma of HIV-infected patients as a marker for microbial translocation. *J Clin Microbiol* 2011;49:3691–3. doi:10.1128/JCM.01018-11
63 Caporaso JG, Lauber CL, Walters WA, *et al*. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proc Natl Acad Sci U S A* 2011;108 Suppl 1:4516–22. doi:10.1073/pnas.1000080107
64 Callahan BJ, McMurdie PJ, Rosen MJ, *et al*. DADA2: high-resolution sample inference from illumina amplicon data. *Nat Methods* 2016;13:581–3. doi:10.1038/nmeth.3869
65 Matias Rodrigues JF, Schmidt TSB, Tackmann J, *et al*. MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. *Bioinformatics* 2017;33:3808–10. doi:10.1093/bioinformatics/btx517
66 Nawrocki EP, Eddy SR. Infernal 1.1: 100-fold faster RNA homology searches. *Bioinformatics* 2013;29:2933–5. doi:10.1093/bioinformatics/btt509
67 Matias Rodrigues JF, von Mering C. HPC-CLUST: distributed hierarchical clustering for large sets of nucleotide sequences. *Bioinformatics* 2014;30:287–8. doi:10.1093/bioinformatics/btt657
68 Schmidt TSB, Matias Rodrigues JF, von Mering C. Limits to robustness and reproducibility in the demarcation of operational taxonomic units. *Environ Microbiol* 2015;17:1689–706. doi:10.1111/1462-2920.12610
69 Coelho LP, Alves R, Monteiro P, *et al*. NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. *Microbiome* 2019;7:84.
70 Mende DR, Letunic I, Maistrenko OM, *et al*. proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. *Nucleic Acids Res* 2020;48:D621-D625. doi:10.1093/nar/gkz1002
71 Milanese A, Mende DR, Paoli L, *et al*. Microbial abundance, activity and population genomic profiling with mOTUs2. *Nat Commun* 2019;10. doi:10.1038/s41467-019-08844-4
72 Coelho LP, Alves R, Del Río Álvaro Rodríguez, del Río Á.R, *et al*. Towards the biogeography of prokaryotic genes. *Nature* 2021. doi:10.1038/s41586-021-04233-4. [Epub ahead of print: 15 Dec 2021].
73 Huerta-Cepas J, Szklarczyk D, Forslund K, *et al*. eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. *Nucleic Acids Res* 2016;44:D286–93. doi:10.1093/nar/gkv1248
74 Schmidt TSB, Matias Rodrigues JF, von Mering C. A family of interaction-adjusted indices of community similarity. *ISME J* 2017;11:791–807.
75 Oksanen J, Blanchet FG, Friendly M. Vegan: community ecology package, 2019. Available: https://CRAN.R-project.org/package=vegan
76 Tibshirani R. Regression shrinkage and selection via the LASSO. *Journal of the Royal Statistical Society: Series B* 1996;58 http://doi.wiley.com/
77 Helleputte T. *LiblineaR: linear predictive models based on the LIBLINEAR C/C++ library, 2015. R package version*, 2015: 1–94.
78 Robin X, Turck N, Hainard A, *et al*. pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics* 2011;12:77. doi:10.1186/1471-2105-12-77
79 Wirbel J, Zych K, Essex M, *et al*. Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. *Genome Biol* 2021;22:93.
80 Mende DR, Letunic I, Huerta-Cepas J, *et al*. proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. *Nucleic Acids Res* 2017;45:D529–34. doi:10.1093/nar/gkw989
81 Costea PI, Munch R, Coelho LP, *et al*. metaSNV: a tool for metagenomic strain level analysis. *PLoS One* 2017;12:e0182392. doi:10.1371/journal.pone.0182392
82 Costea PI, Coelho LP, Sunagawa S, *et al*. Subspecies in the global human gut microbiome. *Mol Syst Biol* 2017;13:960. doi:10.15252/msb.20177589
83 Schmidt TS, Hayward MR, Coelho LP, *et al*. Extensive transmission of microbes along the gastrointestinal tract. *Elife* 2019;8. doi:10.7554/eLife.42693. [Epub ahead of print: 12 02 2019].
84 Schmidt TSB, Raes J, Bork P. The human gut microbiome: from association to modulation. *Cell* 2018;172:1198–215. doi:10.1016/j.cell.2018.02.044
85 Duvallet C, Gibbons SM, Gurry T, *et al*. Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. *Nat Commun* 2017;8:1784. doi:10.1038/s41467-017-01973-8
86 Azizian A, Rühlmann F, Krause T, *et al*. CA19-9 for detecting recurrence of pancreatic cancer. *Sci Rep* 2020;10:1332. doi:10.1038/s41598-020-57930-x
87 Winter JM, Yeo CJ, Brody JR. Diagnostic, prognostic, and predictive biomarkers in pancreatic cancer. *J Surg Oncol* 2013;107:15–22. doi:10.1002/jso.23192
88 Cao Y, Shen J, Ran ZH. Association between Faecalibacterium prausnitzii reduction and inflammatory bowel disease: a meta-analysis and systematic review of the literature. *Gastroenterol Res Pract* 2014;2014:1–7. doi:10.1155/2014/872725
89 Poore GD, Kopylova E, Zhu Q, *et al*. Microbiome analyses of blood and tissues suggest cancer diagnostic approach. *Nature* 2020;579:567–74. doi:10.1038/s41586-020-2095-1
90 de Goffau MC, Lager S, Sovio U, *et al*. Human placenta has no microbiome but can contain potential pathogens. *Nature* 2019;572:329–34. doi:10.1038/s41586-019-1451-5
91 Nejman D, Livyatan I, Fuks G, *et al*. The human tumor microbiome is composed of tumor type-specific intracellular bacteria. *Science* 2020;368:973–80. doi:10.1126/science.aay9189
92 Torres PJ, Fletcher EM, Gibbons SM, *et al*. Characterization of the salivary microbiome in patients with pancreatic cancer. *PeerJ* 2015;3:e1373. doi:10.7717/peerj.1373
93 Vogtmann E, Han Y, Caporaso JG, *et al*. Oral microbial community composition is associated with pancreatic cancer: a case-control study in Iran. *Cancer Med* 2020;9:797–806. doi:10.1002/cam4.2660
94 Sethi V, Kurtom S, Tarique M, *et al*. Gut microbiota promotes tumor growth in mice by modulating immune response. *Gastroenterology* 2018;155:33–7. doi:10.1053/j.gastro.2018.04.001

SUPPLEMENTARY RESULTS & DISCUSSION

Several PDAC-associated species in the gut may be sourced from the oral cavity.

Many microbial species traverse the gastrointestinal tract to form overlapping populations between the oral cavity and intestine, with increased levels of intra-individual strain transmission associated with diseases such as CRC (83). Indeed, several prominent marker taxa showing fecal enrichment in PDAC are common oral commensals, such as *Veillonella sp.*, *Streptococcus sp.* or *Fusobacterium sp..* We hypothesized that intestinal populations of these PDAC-associated species were primarily of oral origin, with generally enhanced levels of autologous oral-intestinal strain exchange in PDAC patients. Therefore, we explored microbiome links between body sites at the highest taxonomic resolution attainable with metagenomic data, at the level of strain populations.

We quantified oral-to-gut transmission based on the intra-individual overlap of microbial Single Nucleotide Variants (SNVs) for species prevalent in both mouth and gut metagenomes, as a proxy for oral and intestinal strain populations (see Methods, **Supplementary Fig. 15**). We found that viewed across all subjects and species, PDAC was associated with increased levels of oral-intestinal strain population overlap (Cohen's d = 0.33; ANOVA $p<10^{-3}$ when adjusting for species-level effects and technical, demographic and clinical variables). This observation extended to individual PDAC-associated species, with enhanced levels of autologous transmission in several *Veillonellaceae sp.* (*V. dispar,* d=0.71; *V. atypica*, d=0.6; *V. parvula*, d=0.2; *Megasphaera micronuciformis*, d=2.47) and *Streptococcus sp.* (*S. salivarius*, d=0.51; *S. vestibularis*, d=0.49; *S. parasanguinis*, d=0.36). The situation was more nuanced among *Bifidobacteriaceae sp.*, with enhanced transmission in *B. longum* (d=2.16) and *A. omnicolens* (d=1.24), but less strain overlap in *B. dentium* (d=-0.89). However, due to limits in metagenomic coverage and species prevalence, our dataset size did not provide sufficient statistical power to significantly discern these trends for

individual species with confidence, in particular when adjusting for putative confounders and correcting for multiple tests. Nevertheless, our data indicates that PDAC patients showed overall enhanced levels of oral-intestinal transmission, and that intestinal strain populations of PDAC signature species may be sourced autologously from the oral cavity.

False positive PDAC detections in external validation populations may be due to technical artefacts.

We note that for both model-1 and model-2, at least some false predictions in external validation sets may be attributable to technical artefacts: technical variation between studies often exceeds biological differences in microbiome composition (96), while shallower metagenomic sequencing depths skew taxonomic profiles and bias against lowly abundant species. Moreover, by design, the external validation sets were matched for neither age nor sex, and information on clinical variables with relevance to PDAC was usually not collected or not publicly available. The highest false detection rates were observed among populations with much younger subjects than would normally be considered a PDAC risk group (**Supplementary Fig. 12**). To overcome such limitations, meta-studies of multiple geographically and ethnically diverse PDAC cohorts will be required to further establish globally consistent PDAC microbiome signatures, as has been successfully shown for colorectal cancer (38,97).

Univariate associations of individual species may be informative, but not specific to PDAC.

Species enriched in PDAC included various *Veillonella sp., Alloscardovia omnicolens,* and *Methanobrevibacter smithii*, among others **(Fig. 1c and Fig. 2a**). We confirmed that these were generally not univariately associated with putative confounding factors (**Supplementary Fig. 7**), yet we note that several among them have previously been linked to both health and disease. For example, *Veillonella sp.* are common oral and gut commensals and have been associated with exercise performance in athletes (98), but also with various disease states including cystic fibrosis

(a PDAC risk factor) (99), several infections including meningitis (100), as well as lung (101) and oral carcinomas (102). The role of *Methanobrevibacter smithii,* a prevalent methanogenic archaeon, in the human gut remains poorly understood (103,104), but the species has likewise been associated with athletic performance (105) and disease states (104) such as anorexia nervosa (106,107) and irritable bowel disease (108). This indicates that individual univariate species associations may be informative, but not specific to PDAC. In contrast, our multi-species classifier model-2, capturing a combined signature of PDAC-enriched species, provided very high disease specificity.

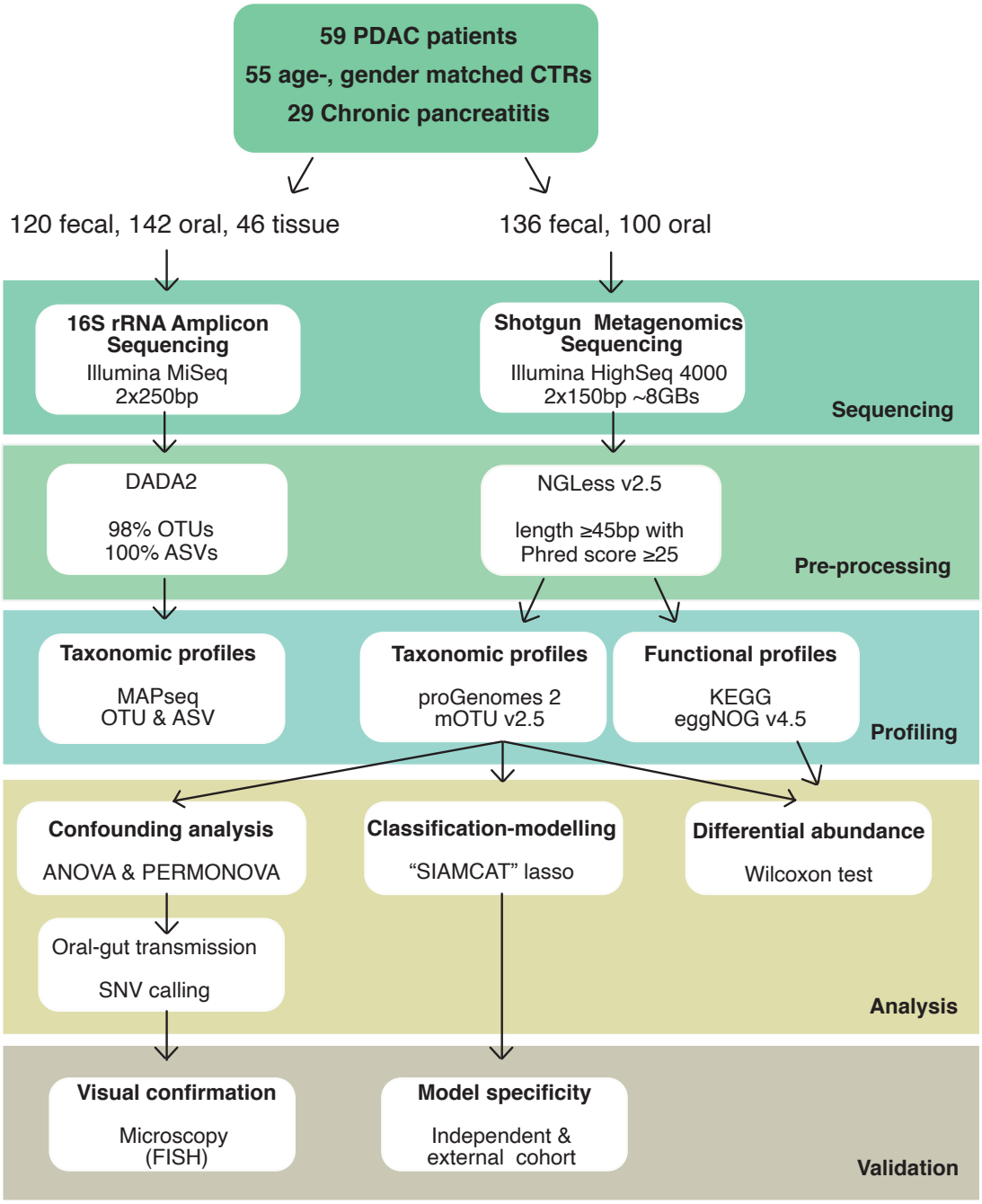

Figure S1. Analysis workflow.
Diagram of analysis steps for 16S rRNA amplicon sequencing data and for shotgun metagenomics sequencing data.

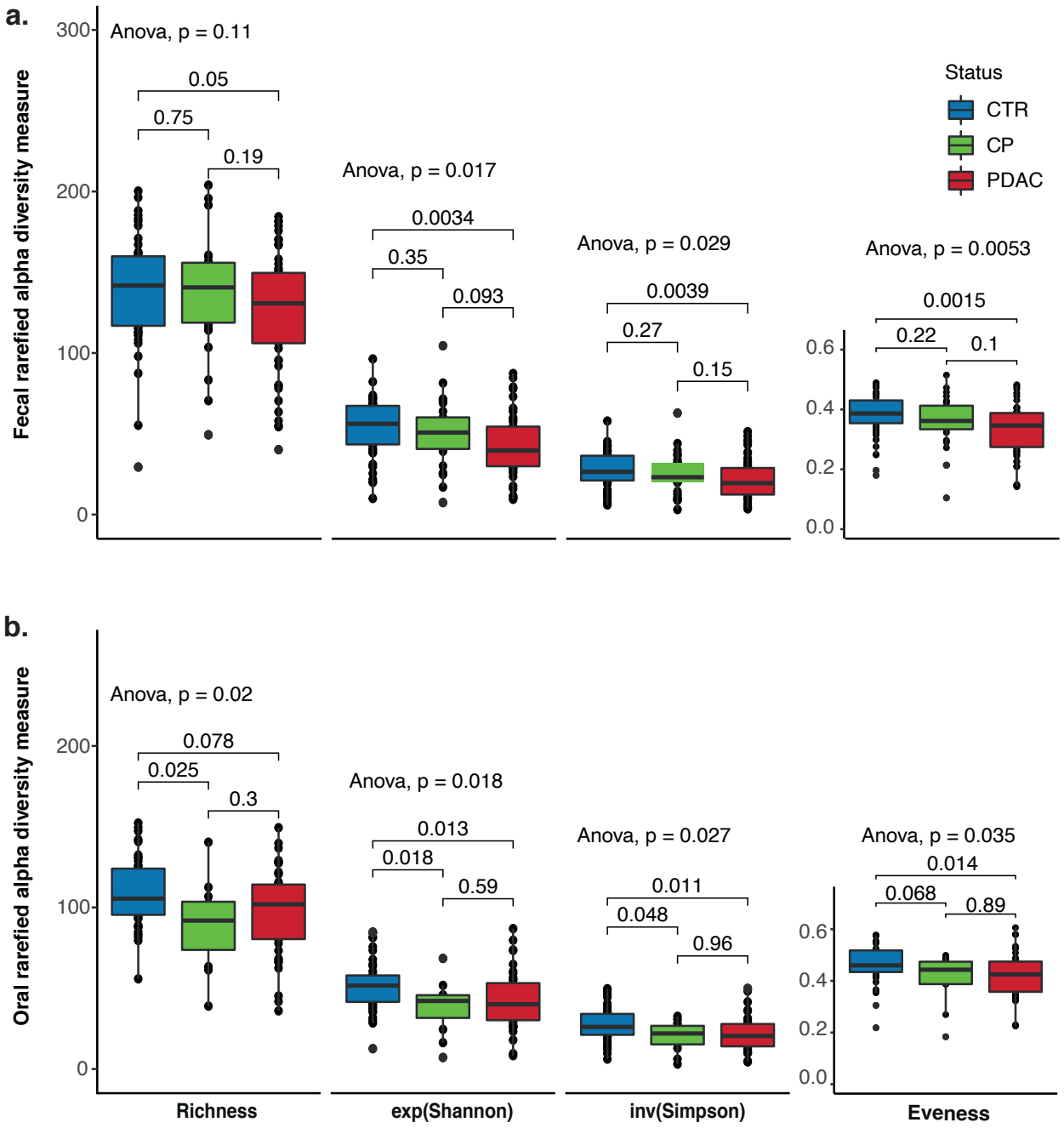

Figure S2. Alpha diversity measurements comparing PDAC and CP patients with controls.
Alpha diversity metrics for (a) fecal and (b) oral samples calculated as richness, exponential Shannon index (exp(Shannon)), inverse Simpson index (inv(Simpson)) and eveness. Colors denote groups, with blue for controls (CTR), green for chronic pancreatitis (CP) patients and red for PDAC cases. Pairwise comparisons were performed using Wilcoxon test and comparisons across all three groups were performed using ANOVA (see Methods).

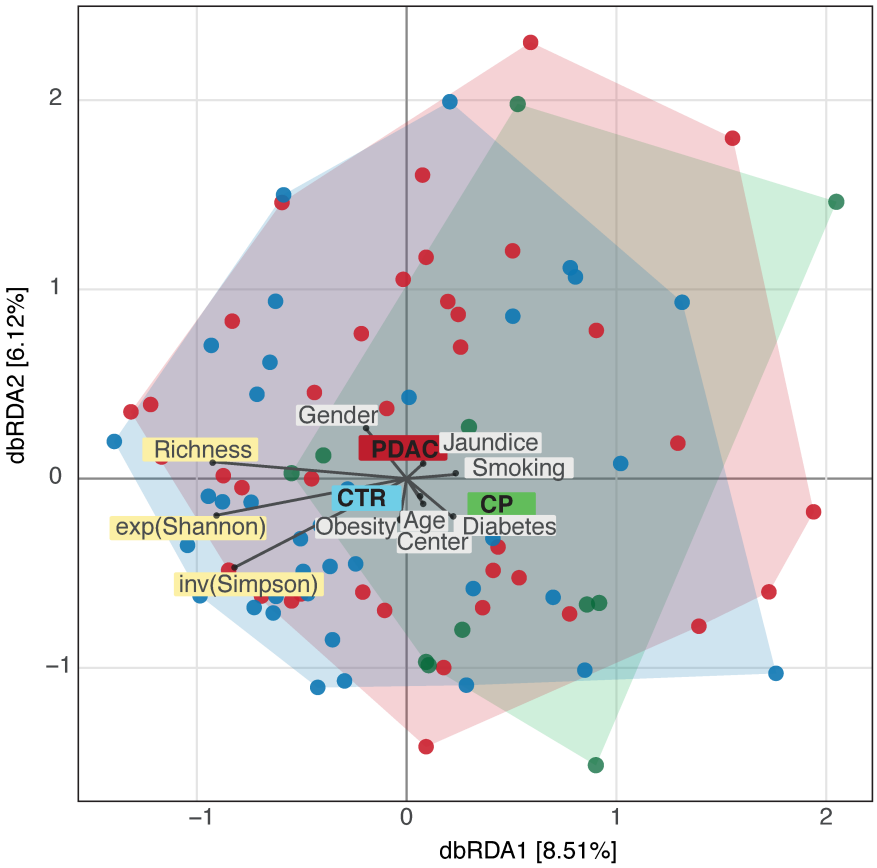

Figure S3. Distance-based redundancy analysis of saliva microbiome.
Bray-Curtis distance-based redundancy analysis (dbRDA) of PDAC, CP and control saliva microbiome data. PDAC samples are shown as red circles, CP patients as green and controls as blue. Association with metadata variables are shown as labeled lines. Richness, exponential Shannon (exp(Shannon)) and inverse Simpson (inv(Simpson)) diversity measures are also visualized with lines and were analysed similarly to metadata variables. The length of the metadata variable line represents the confounding effect size (see Methods).

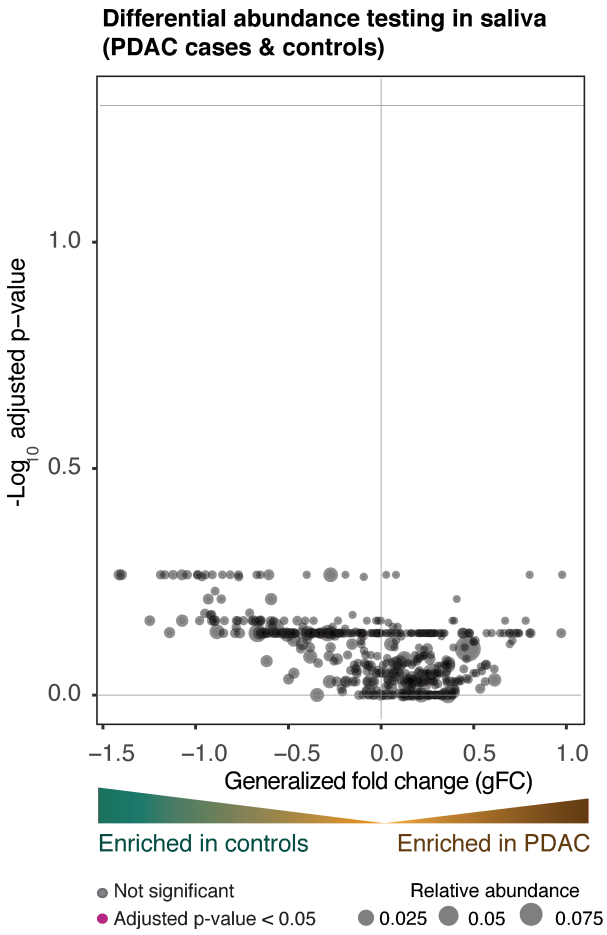

Figure S4. Differential abundance testing of saliva microbiome

Wilcoxon test results of saliva microbiome data to test for enrichment of taxa between PDAC cases and controls (see Methods). Y-axis is log10(FDR corrected p-values), x-axis is generalized fold change and dot size represents the relative abundance of given species and strains. Red dots represent significantly differentially abundant species/strains in either group, while black dots show non-significant species after FDR correction.

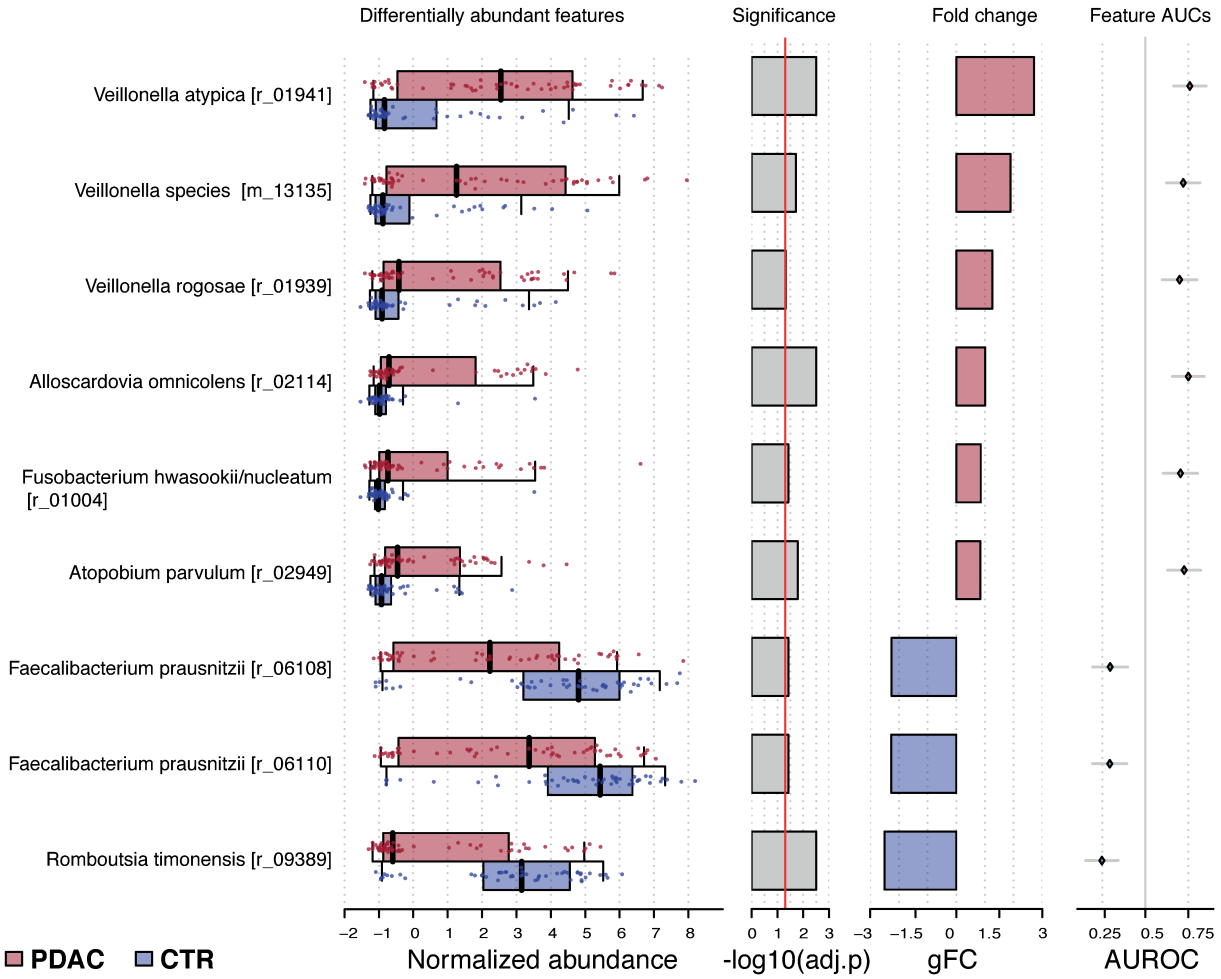

Figure S5. Differentially abundant species in fecal microbiome between PDAC cases and controls.
First column panel shows the differentially abundant species between PDAC cases (red) and controls (blue). Middle panels display the log10(FDR corrected p-values) and generalized fold change for each taxon and the last panel presents the AUC of each feature to distinguish cases from controls. gFC:Generalized fold change.

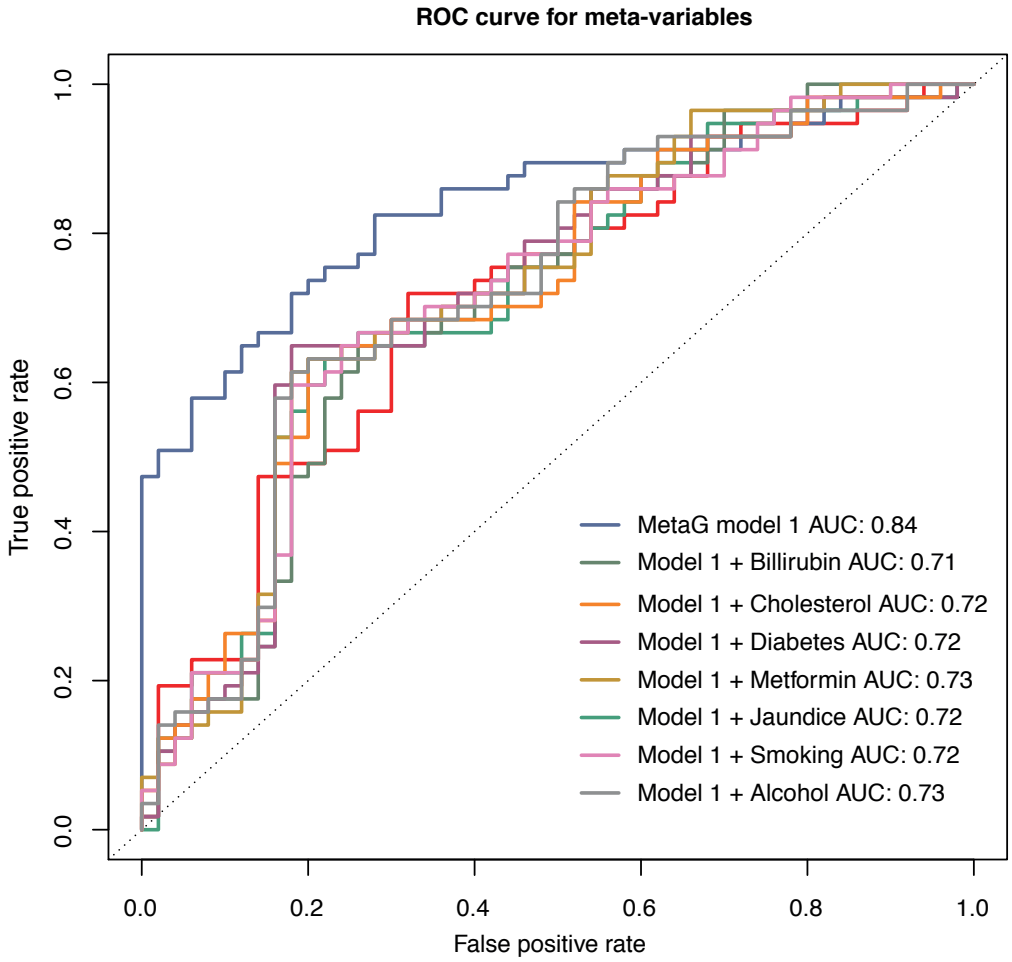

Figure S6. Contribution of confounding factors to the model.
The area under the ROC curve (AUROC) is used to show the performance of lasso_ll model based on fecal microbiome data of PDAC and control samples with 10 times resampling and 10 cross validation (see Methods). Each color corresponds to one specific model based on metagenomics features with an additional metadata variable. Shown metadata variables were added to the metagenomics features table with “add.meta.pred” function from “SIAMCAT” package v1.5.0.

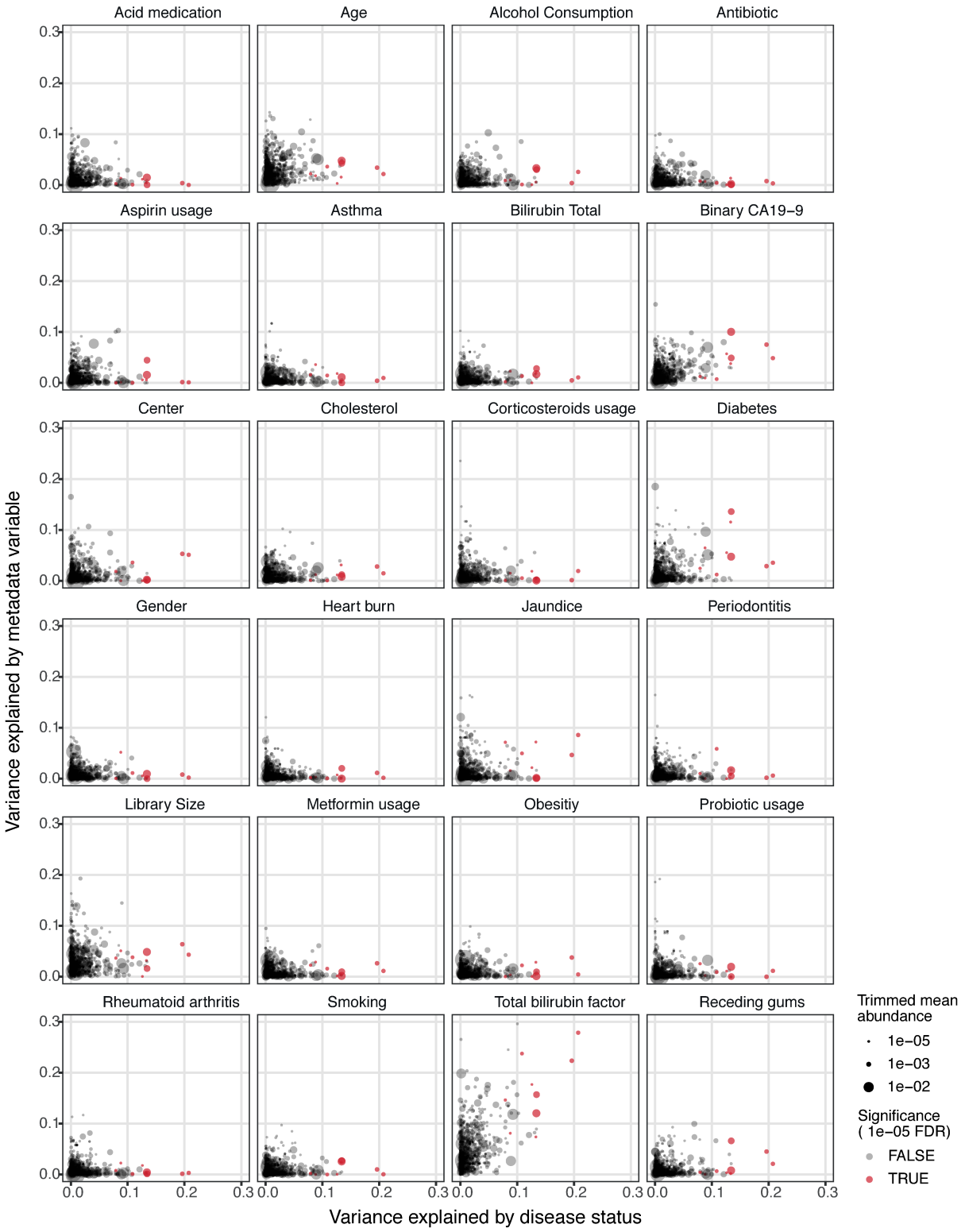

Figure S7. Potential confounder of single species associations by individual demographic and technical variables.

Variance explained by diagnosis is represented against confounding factors for single microbial species. Each circle is a strain or species and is colored red if it is differentially abundant between PDAC cases and controls. The size of each circle represents the mean abundance of that species or strain. Disease status and the tested variables were used as explanatory variables in the linear model for feature abundance.

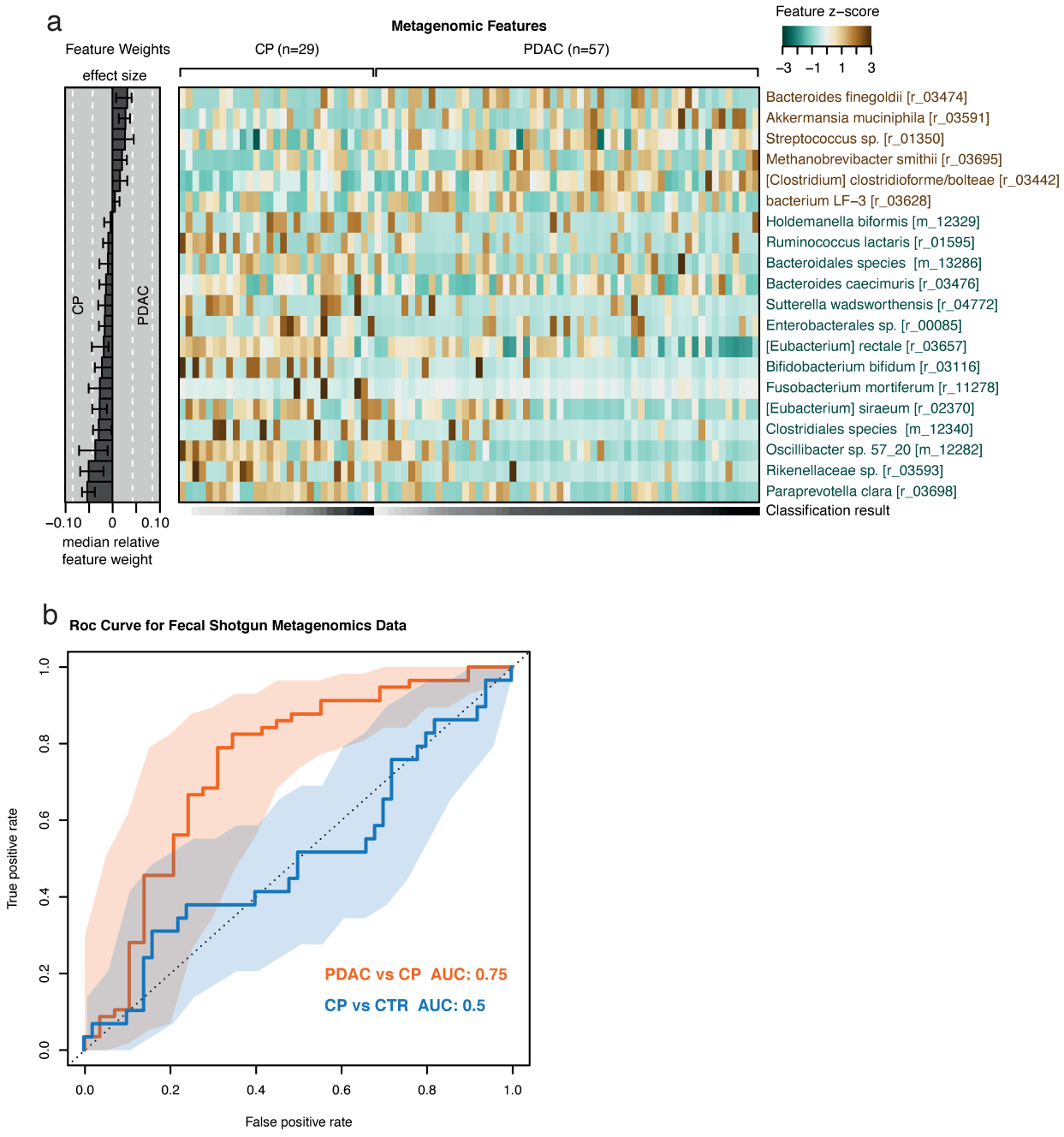

Figure S8. Fecal microbiome-based classifier distinguishes chronic pancreatitis cases from PDAC patients
(a) Heatmap representing the selected metagenomic features in the lasso_ll regression model between PDAC cases and chronic pancreatitis (CP) patients in the fecal microbiome data. (b) ROC curve based on 10 resamplings and 10-fold cross validation (see methods). The blue line represents the model for CP versus controls and the orange line for PDAC vs CP cases. Internal cross validation results are shown as receiver operating characteristic (ROC) curve with a 95% confidence interval shaded in corresponding color.

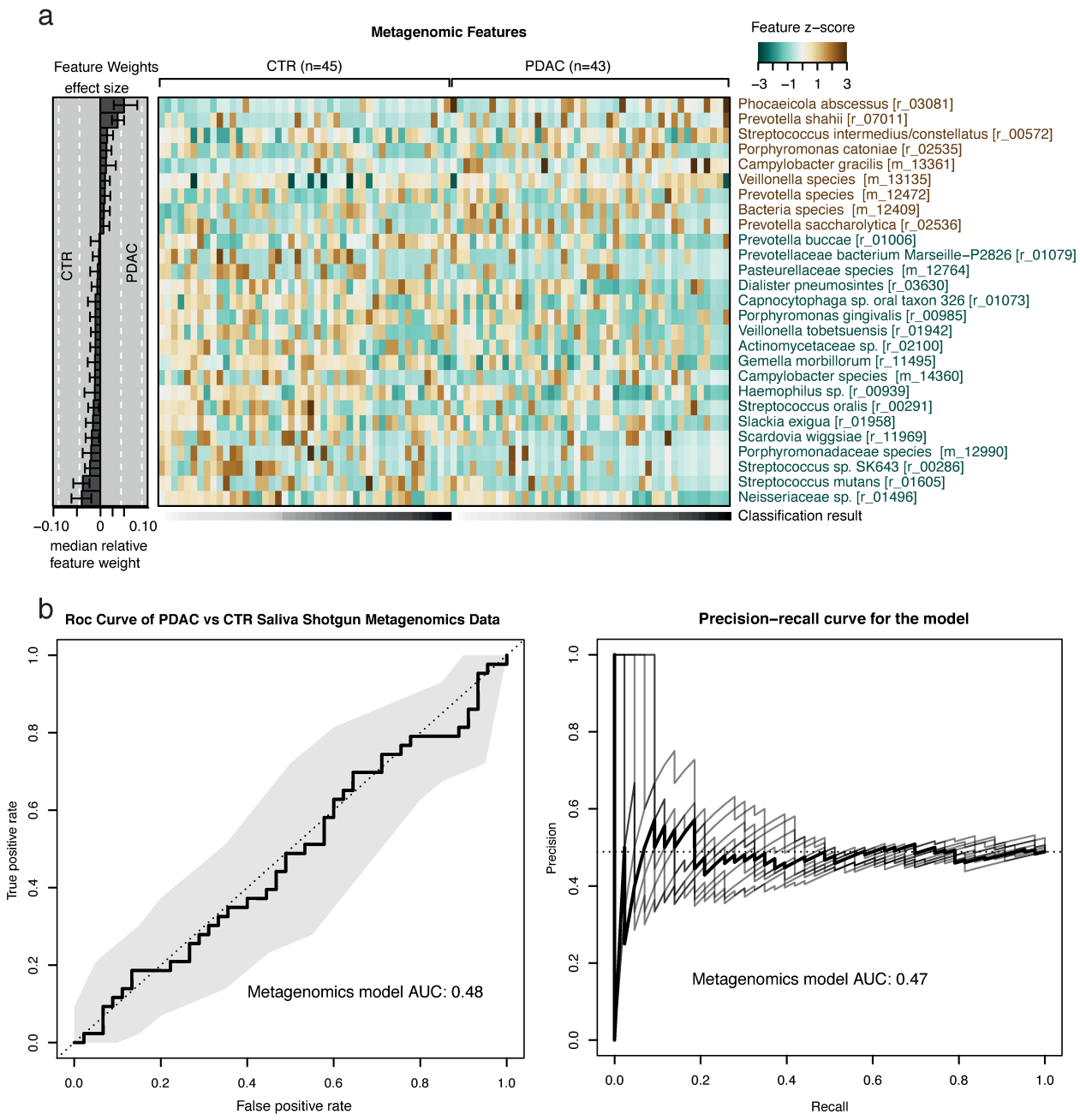

Figure S9. Oral microbiome does not distinguish PDAC samples from control samples.
(a) Heatmap representing the selected metagenomic features in the lasso_ll regression model between cases and controls in the saliva microbiome data. (b) ROC curve based on 10 resamplings and 10-fold cross validation (see methods) and precision recall curve. Internal cross validation results are shown as receiver operating characteristic (ROC) curve with a 95% confidence interval shaded in grey.

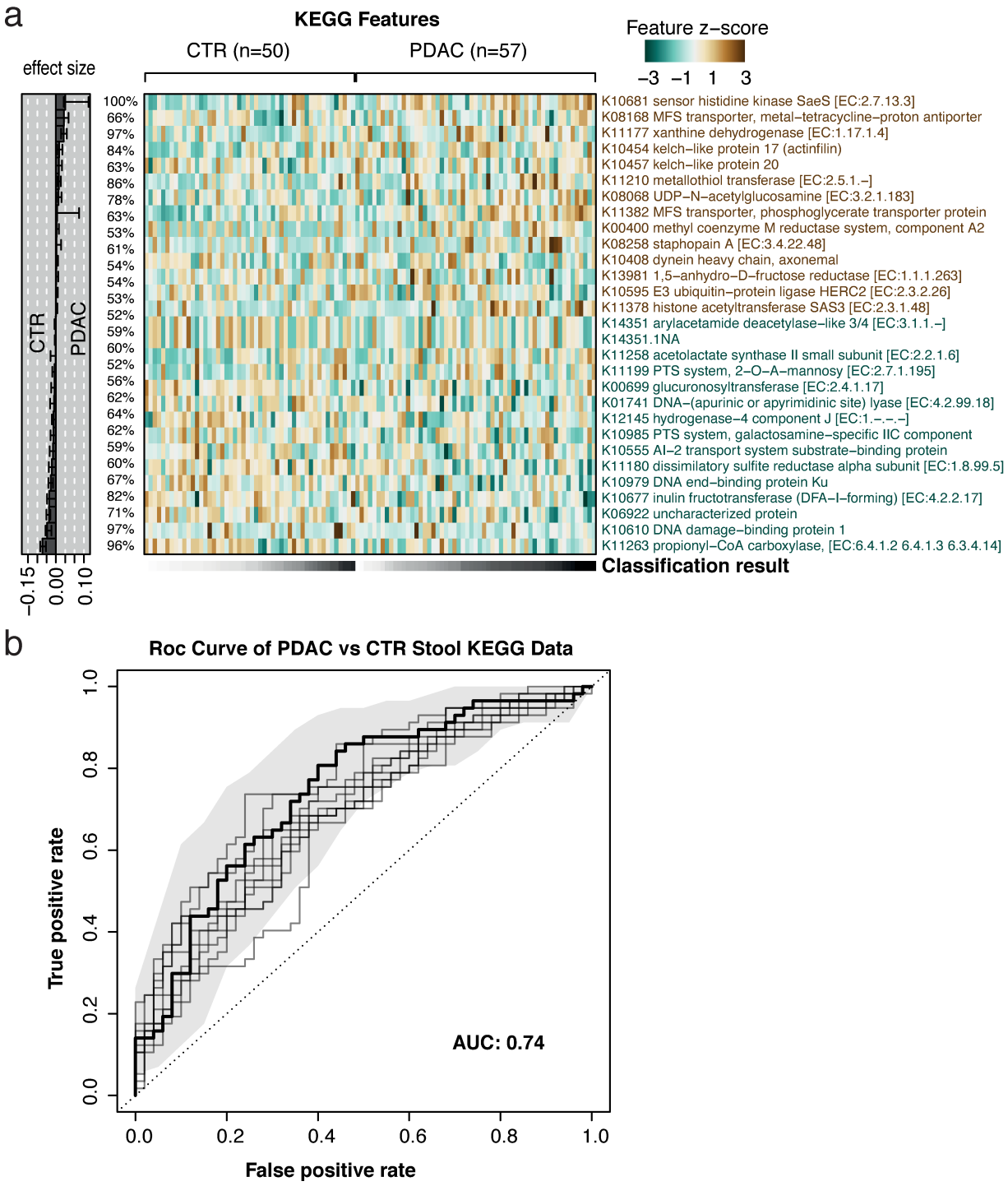

Figure S10. Lasso_ll regression model based on top 200 KEGG modules.
(a) Heatmap representing the selected KEGG modules in the lasso_ll regression model. (b) ROC curve based on 10 resamplings and 10-fold cross validation (see methods).

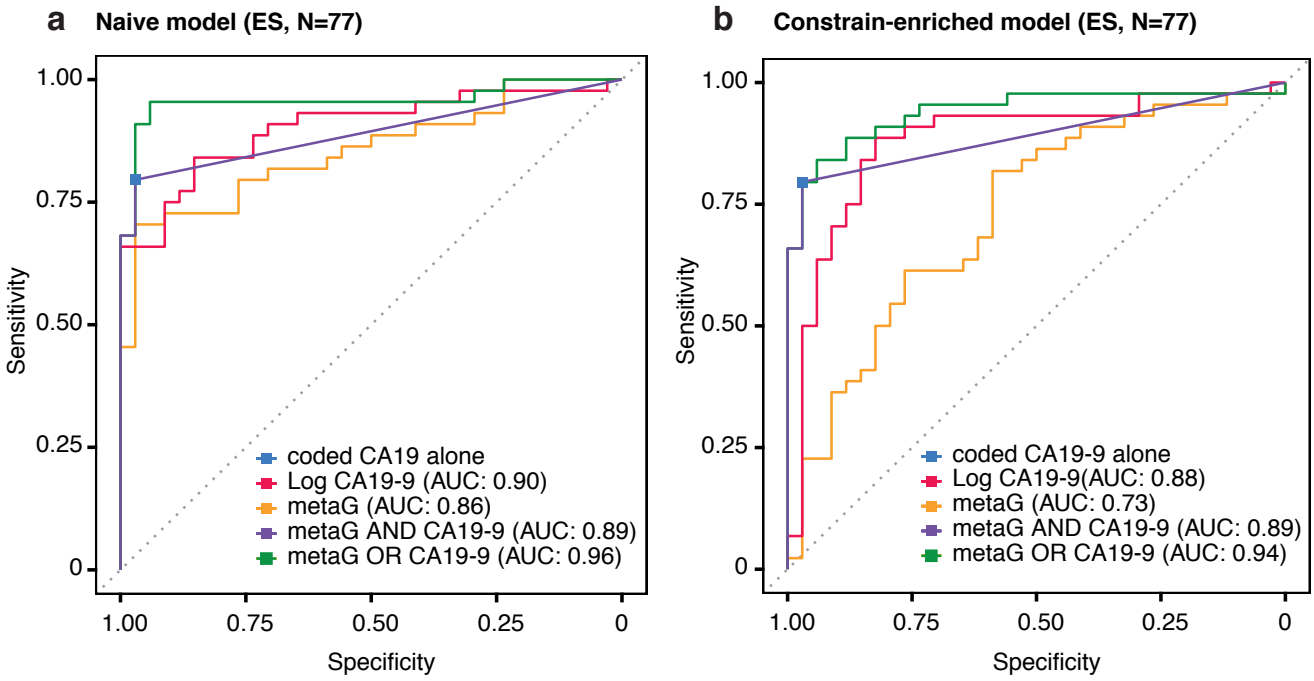

Figure S11. Combination of fecal microbiome data with CA19-9 results increase sensitivity.
77/107 (33/50 CTRs and 44/57 PDAC cases) individuals in Spanish (ES) whom CA19-9 data were available included in the modelling process explicitly. CA19-9 values were converted to binary values (>37ul/ml = 1 & <37ul/ml = 0) **(a)** ROC curve of full feature set. **(b)** ROC curve of enrichment-constrained models based on 77 individual fecal microbiomes. Coded CA19-9 is the binary version of data, which is represented by a blue dot. Log(CA19-9) is displayed with red, while "AND" and "OR" combinations are shown with purple and green respectively. 8/32 CTRs and 43/44 PDAC patients in the German (DE) cohort

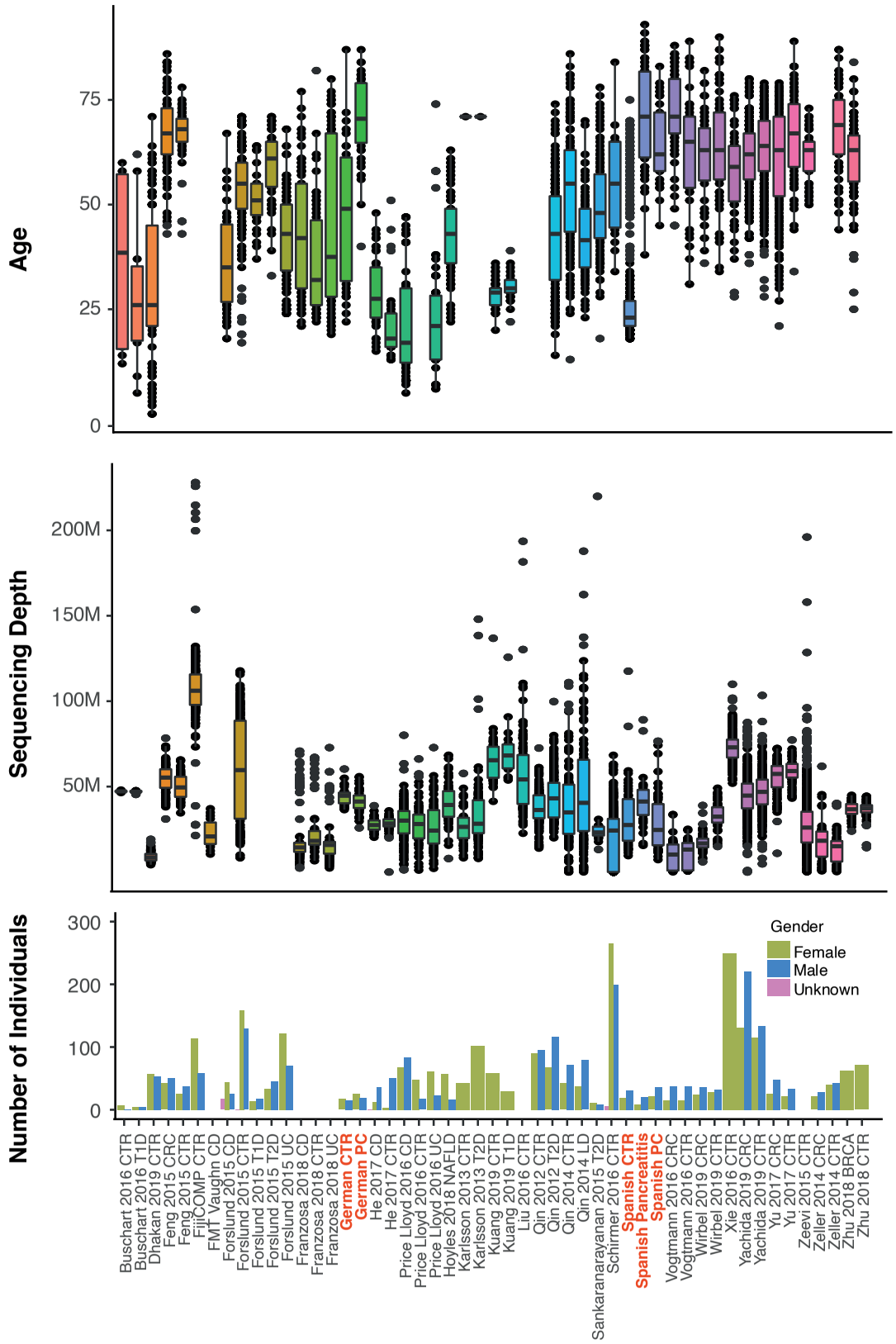

Figure S12. The overview of external validation cohorts.
(a) Age distribution is shown for all external datasets per group. X-axis shows all the studies and y-axis displays the age distribution. **(b)** Sequencing depth is represented across cohorts. **(c)** Gender information is displayed if available as bar plot. Green is used for females while blue is for males for available studies. M:Million.

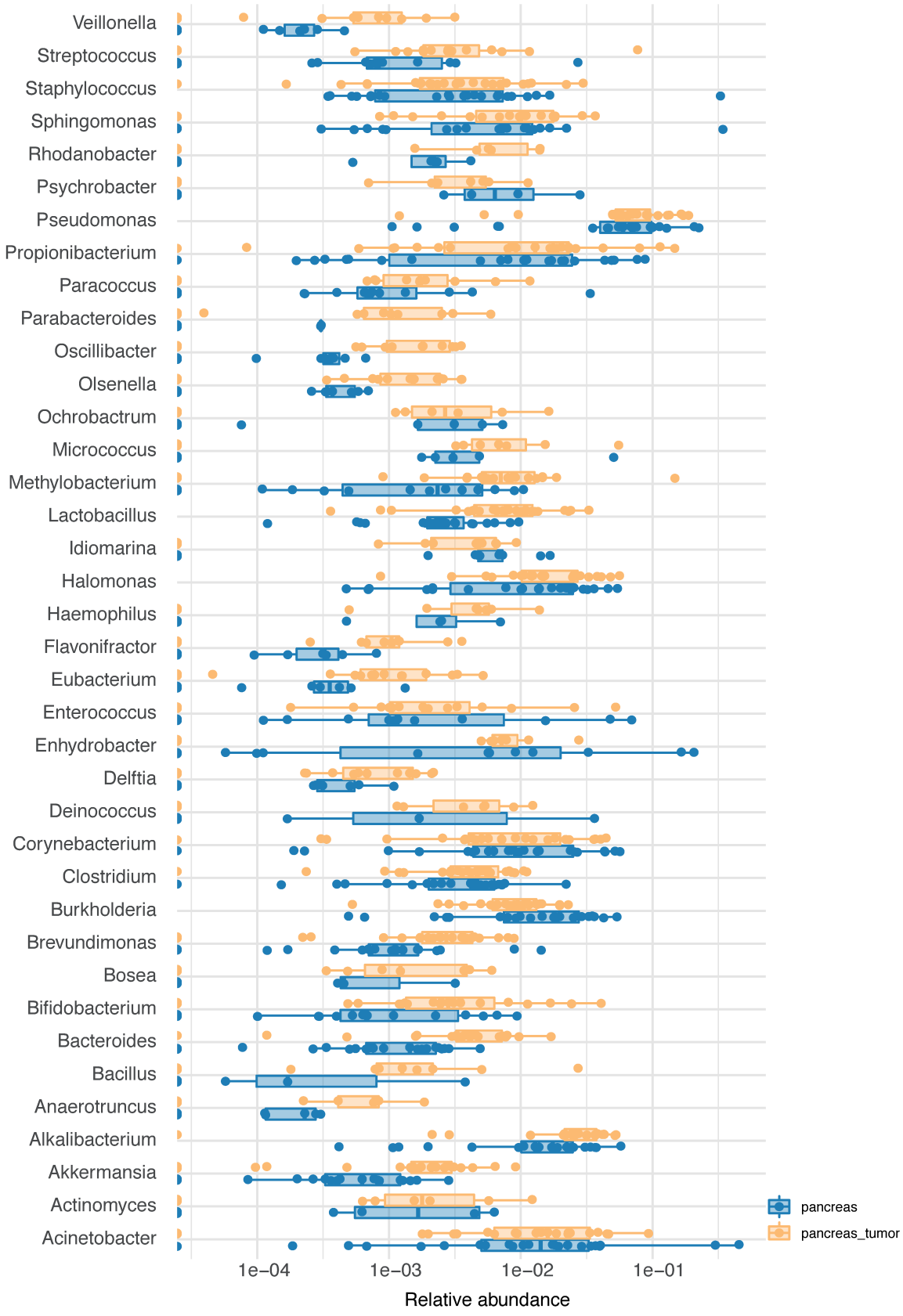

Figure S13. Relative abundance of genera in tumor and non-tumor pancreatic tissue.
Relative abundance of several genera is shown as bar plots. Orange is used to present the pancreatic tumor tissue, while blue is used for non-tumor tissue.

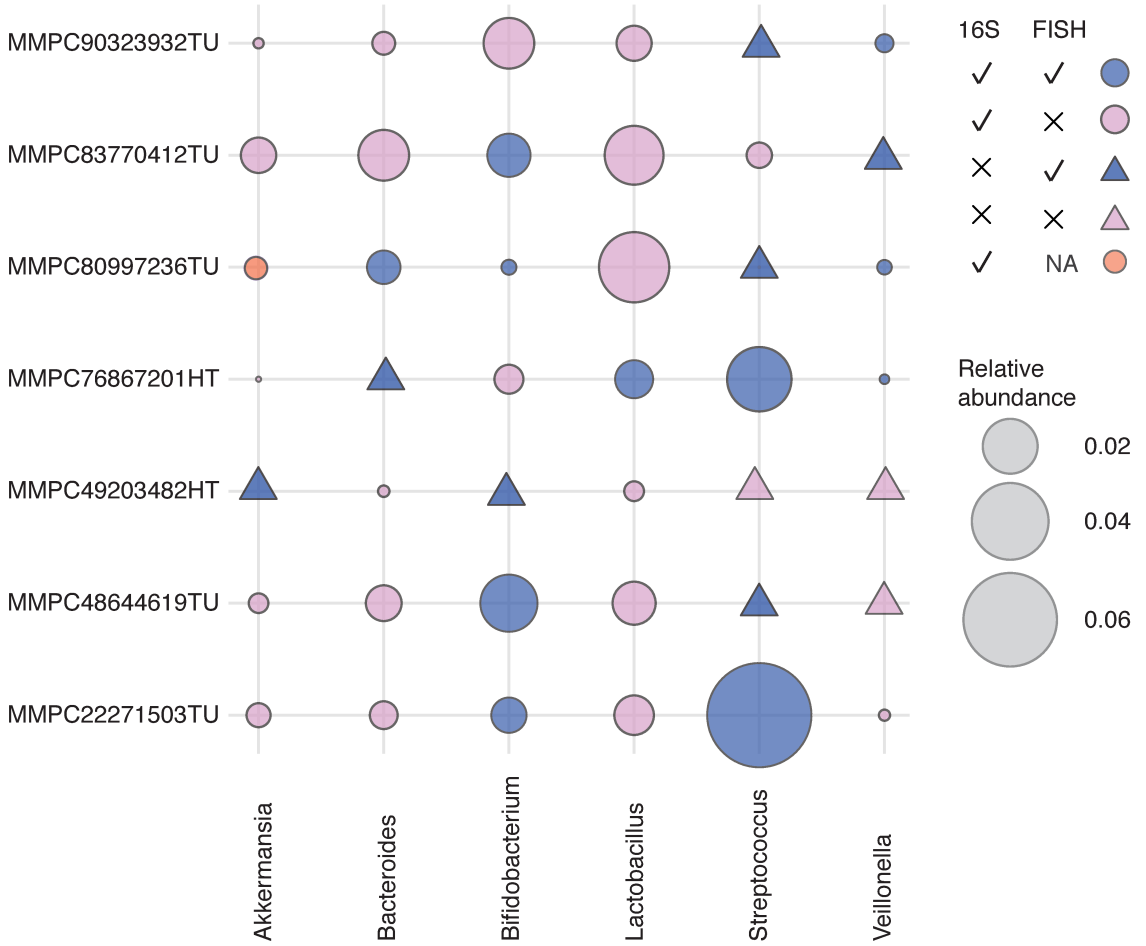

Figure S14. Detailed information of tested samples via in-situ hybridization (FISH).
Rows display the tested samples and columns show the tested genera. The size of the dot represents relative abundance of genus in the given sample. Triangles show that 16S was negative for given samples and color code displays if FISH was positive (blue) or negative (pink). One sample, displayed in orange, did not have enough tissue material for FISH testing.NA: Not available.

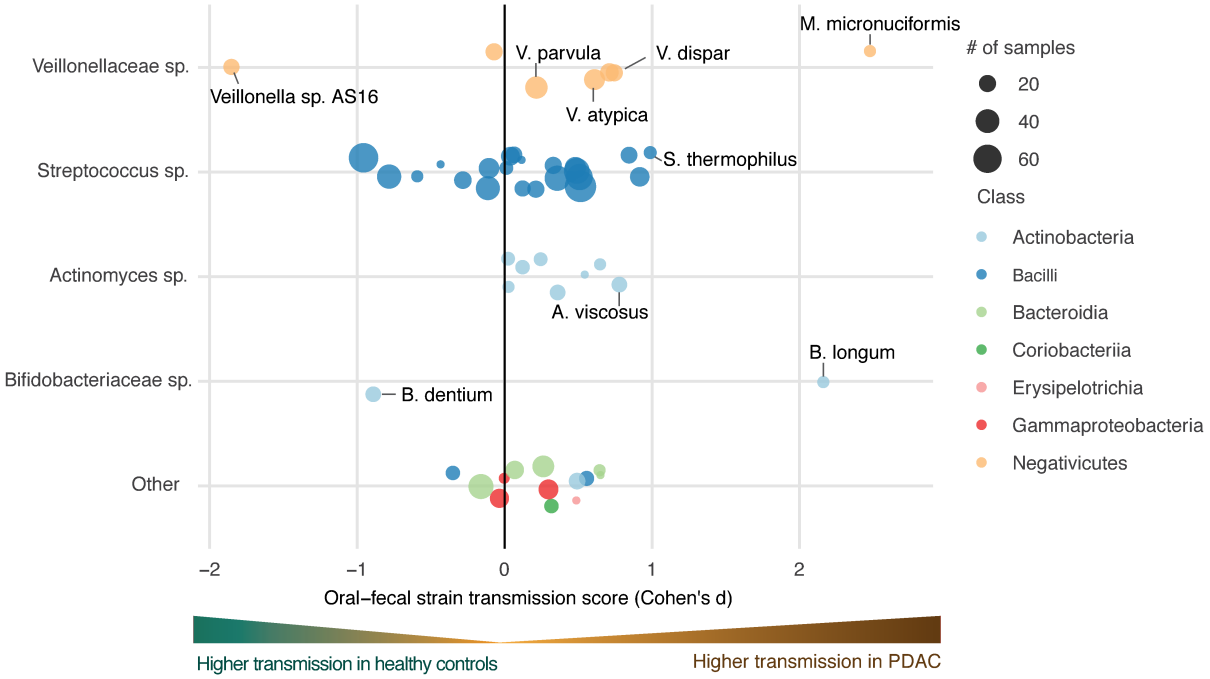

Figure S15. Oral-fecal transmission scores differ between PDAC cases and controls.
Oral-gut transmission scores (y-axis) of each species are displayed grouped by genus (x-axis). The number of subjects is represented by the size of the circle and the color represents the corresponding class group.

Supplementary Table S1: ES Cohort Details

sample_alias	experiment_name	experiment_type	instrument_model	replicate	insert_size	read_length	read_count	environment_material	timepoint
MMPC-3103102-ST-0	MMPC35551931ST	metagenome	Illumina HiSeq 4000	0	350	150	11417135	feces [ENVO:00002003]	0
MMPC-3103103-ST-0	MMPC41376408ST	metagenome	Illumina HiSeq 4000	0	350	150	22532306	feces [ENVO:00002003]	0
MMPC-3103106-ST-0	MMPC59659730ST	metagenome	Illumina HiSeq 4000	0	350	150	22296806	feces [ENVO:00002003]	0
MMPC-3103107-ST-0	MMPC96048560ST	metagenome	Illumina HiSeq 4000	0	350	150	15812641	feces [ENVO:00002003]	0
MMPC-3103107-ST-0	MMPW24306397ST	metagenome	Illumina HiSeq 4000	0	350	150	562381156	feces [ENVO:00002003]	0
MMPC-3103108-ST-0	MMPC42296680ST	metagenome	Illumina HiSeq 4000	0	350	150	12998378	feces [ENVO:00002003]	0
MMPC-3103109-ST-0	MMPC49776422ST	metagenome	Illumina HiSeq 4000	0	350	150	24362813	feces [ENVO:00002003]	0
MMPC-3103109-ST-0	MMPW76972986ST	metagenome	Illumina HiSeq 4000	0	350	150	597499733	feces [ENVO:00002003]	0
MMPC-3103111-ST-0	MMPC19228810ST	metagenome	Illumina HiSeq 4000	0	350	150	15320194	feces [ENVO:00002003]	0
MMPC-3103112-ST-0	MMPW28983031ST	metagenome	Illumina HiSeq 4000	0	350	150	514088417	feces [ENVO:00002003]	0
MMPC-3103112-ST-0	MMPC45272194ST	metagenome	Illumina HiSeq 4000	0	350	150	19734216	feces [ENVO:00002003]	0
MMPC-3103114-ST-0	MMPC36793964ST	metagenome	Illumina HiSeq 4000	0	350	150	12388494	feces [ENVO:00002003]	0
MMPC-3103115-ST-0	MMPC92286162ST	metagenome	Illumina HiSeq 4000	0	350	150	12858226	feces [ENVO:00002003]	0
MMPC-3103116-ST-0	MMPC23673679ST	metagenome	Illumina HiSeq 4000	0	350	150	13475213	feces [ENVO:00002003]	0
MMPC-3103116-ST-0	MMPW31043630ST	metagenome	Illumina HiSeq 4000	0	350	150	540784922	feces [ENVO:00002003]	0
MMPC-3103117-ST-0	MMPW39199901ST	metagenome	Illumina HiSeq 4000	0	350	150	551836962	feces [ENVO:00002003]	0
MMPC-3103117-ST-0	MMPC53747560ST	metagenome	Illumina HiSeq 4000	0	350	150	19414746	feces [ENVO:00002003]	0
MMPC-3103118-ST-0	MMPC76278395ST	metagenome	Illumina HiSeq 4000	0	350	150	23770034	feces [ENVO:00002003]	0
MMPC-3103119-ST-0	MMPC92856474ST	metagenome	Illumina HiSeq 4000	0	350	150	24862116	feces [ENVO:00002003]	0
MMPC-3103120-ST-0	MMPC41385323ST	metagenome	Illumina HiSeq 4000	0	350	150	17450417	feces [ENVO:00002003]	0
MMPC-3103121-ST-0	MMPC12800445ST	metagenome	Illumina HiSeq 4000	0	350	150	20514446	feces [ENVO:00002003]	0
MMPC-3103124-ST-0	MMPC10431544ST	metagenome	Illumina HiSeq 4000	0	350	150	34540047	feces [ENVO:00002003]	0
MMPC-3103124-ST-0	MMPW97100755ST	metagenome	Illumina HiSeq 4000	0	350	150	616136180	feces [ENVO:00002003]	0
MMPC-3103125-ST-0	MMPC29682684ST	metagenome	Illumina HiSeq 4000	0	350	150	29767506	feces [ENVO:00002003]	0
MMPC-3103126-ST-0	MMPC51115713ST	metagenome	Illumina HiSeq 4000	0	350	150	38401273	feces [ENVO:00002003]	0
MMPC-3103127-ST-0	MMPC99615156ST	metagenome	Illumina HiSeq 4000	0	350	150	11813347	feces [ENVO:00002003]	0
MMPC-3103129-ST-0	MMPC45114789ST	metagenome	Illumina HiSeq 4000	0	350	150	43078526	feces [ENVO:00002003]	0
MMPC-3103202-ST-0	MMPC52359973ST	metagenome	Illumina HiSeq 4000	0	350	150	18061157	feces [ENVO:00002003]	0
MMPC-3103203-ST-0	MMPW21548424ST	metagenome	Illumina HiSeq 4000	0	350	150	542893761	feces [ENVO:00002003]	0
MMPC-3103203-ST-0	MMPC73667956ST	metagenome	Illumina HiSeq 4000	0	350	150	18138792	feces [ENVO:00002003]	0
MMPC-3103206-ST-0	MMPC47668641ST	metagenome	Illumina HiSeq 4000	0	350	150	28939256	feces [ENVO:00002003]	0
MMPC-3103207-ST-0	MMPC69211422ST	metagenome	Illumina HiSeq 4000	0	350	150	19540088	feces [ENVO:00002003]	0
MMPC-3103208-ST-0	MMPC78378767ST	metagenome	Illumina HiSeq 4000	0	350	150	18782020	feces [ENVO:00002003]	0
MMPC-3103209-ST-0	MMPC75057555ST	metagenome	Illumina HiSeq 4000	0	350	150	41063683	feces [ENVO:00002003]	0
MMPC-3103211-ST-0	MMPC63233635ST	metagenome	Illumina HiSeq 4000	0	350	150	34235593	feces [ENVO:00002003]	0
MMPC-3103211-ST-0	MMPW67722444ST	metagenome	Illumina HiSeq 4000	0	350	150	577789449	feces [ENVO:00002003]	0
MMPC-3103212-ST-0	MMPC25016485ST	metagenome	Illumina HiSeq 4000	0	350	150	13684247	feces [ENVO:00002003]	0
MMPC-3103214-ST-0	MMPC82779175ST	metagenome	Illumina HiSeq 4000	0	350	150	15530149	feces [ENVO:00002003]	0
MMPC-3103215-ST-0	MMPC64434180ST	metagenome	Illumina HiSeq 4000	0	350	150	28178046	feces [ENVO:00002003]	0
MMPC-3103216-ST-0	MMPC37499694ST	metagenome	Illumina HiSeq 4000	0	350	150	35725071	feces [ENVO:00002003]	0
MMPC-3103217-ST-0	MMPC59151585ST	metagenome	Illumina HiSeq 4000	0	350	150	47396825	feces [ENVO:00002003]	0
MMPC-3103218-ST-0	MMPC12849395ST	metagenome	Illumina HiSeq 4000	0	350	150	48769925	feces [ENVO:00002003]	0
MMPC-3103219-ST-0	MMPC96275284ST	metagenome	Illumina HiSeq 4000	0	350	150	21659974	feces [ENVO:00002003]	0
MMPC-3103220-ST-0	MMPC32834082ST	metagenome	Illumina HiSeq 4000	0	350	150	17111873	feces [ENVO:00002003]	0
MMPC-3103221-ST-0	MMPC69837834ST	metagenome	Illumina HiSeq 4000	0	350	150	9569359	feces [ENVO:00002003]	0
MMPC-3103223-ST-0	MMPC36232351ST	metagenome	Illumina HiSeq 4000	0	350	150	59219214	feces [ENVO:00002003]	0
MMPC-3103224-ST-0	MMPC21449543ST	metagenome	Illumina HiSeq 4000	0	350	150	31704480	feces [ENVO:00002003]	0
MMPC-3103225-ST-0	MMPC63481302ST	metagenome	Illumina HiSeq 4000	0	350	150	38774804	feces [ENVO:00002003]	0
MMPC-3103226-ST-0	MMPC22175846ST	metagenome	Illumina HiSeq 4000	0	350	150	44695903	feces [ENVO:00002003]	0
MMPC-3103227-ST-0	MMPC17251241ST	metagenome	Illumina HiSeq 4000	0	350	150	44644402	feces [ENVO:00002003]	0
MMPC-3103228-ST-0	MMPC16651671ST	metagenome	Illumina HiSeq 4000	0	350	150	45156079	feces [ENVO:00002003]	0
MMPC-3103229-ST-0	MMPC59362655ST	metagenome	Illumina HiSeq 4000	0	350	150	42996294	feces [ENVO:00002003]	0
MMPC-3103302-ST-0	MMPC88343716ST	metagenome	Illumina HiSeq 4000	0	350	150	26171451	feces [ENVO:00002003]	0
MMPC-3103303-ST-0	MMPC67317135ST	metagenome	Illumina HiSeq 4000	0	350	150	41987974	feces [ENVO:00002003]	0
MMPC-3103306-ST-0	MMPC75070829ST	metagenome	Illumina HiSeq 4000	0	350	150	46219614	feces [ENVO:00002003]	0
MMPC-3103307-ST-0	MMPC93358150ST	metagenome	Illumina HiSeq 4000	0	350	150	41266766	feces [ENVO:00002003]	0
MMPC-3103308-ST-0	MMPC95108539ST	metagenome	Illumina HiSeq 4000	0	350	150	51296849	feces [ENVO:00002003]	0
MMPC-3103309-ST-0	MMPC68695449ST	metagenome	Illumina HiSeq 4000	0	350	150	16713617	feces [ENVO:00002003]	0
MMPC-3103311-ST-0	MMPC79169108ST	metagenome	Illumina HiSeq 4000	0	350	150	29917194	feces [ENVO:00002003]	0
MMPC-3103312-ST-0	MMPC95991337ST	metagenome	Illumina HiSeq 4000	0	350	150	40108122	feces [ENVO:00002003]	0
MMPC-3103314-ST-0	MMPC82784238ST	metagenome	Illumina HiSeq 4000	0	350	150	49888210	feces [ENVO:00002003]	0
MMPC-3103315-ST-0	MMPC35131016ST	metagenome	Illumina HiSeq 4000	0	350	150	39883458	feces [ENVO:00002003]	0
MMPC-3103316-ST-0	MMPC52740890ST	metagenome	Illumina HiSeq 4000	0	350	150	33343541	feces [ENVO:00002003]	0
MMPC-3103317-ST-0	MMPC48152369ST	metagenome	Illumina HiSeq 4000	0	350	150	48281105	feces [ENVO:00002003]	0
MMPC-3103318-ST-0	MMPC93983194ST	metagenome	Illumina HiSeq 4000	0	350	150	38098451	feces [ENVO:00002003]	0
MMPC-3103319-ST-0	MMPC11113549ST	metagenome	Illumina HiSeq 4000	0	350	150	40759382	feces [ENVO:00002003]	0
MMPC-3103319-ST-0	MMPC50507232ST	metagenome	Illumina HiSeq 4000	0	350	150	48108766	feces [ENVO:00002003]	0
MMPC-3103320-ST-0	MMPC77686266ST	metagenome	Illumina HiSeq 4000	0	350	150	41439816	feces [ENVO:00002003]	0
MMPC-3103321-ST-0	MMPC56485647ST	metagenome	Illumina HiSeq 4000	0	350	150	55325188	feces [ENVO:00002003]	0
MMPC-3103324-ST-0	MMPC71307280ST	metagenome	Illumina HiSeq 4000	0	350	150	28830324	feces [ENVO:00002003]	0
MMPC-3103325-ST-0	MMPC99058548ST	metagenome	Illumina HiSeq 4000	0	350	150	31073638	feces [ENVO:00002003]	0
MMPC-3103326-ST-0	MMPC16382508ST	metagenome	Illumina HiSeq 4000	0	350	150	34469441	feces [ENVO:00002003]	0
MMPC-3103327-ST-0	MMPC23660755ST	metagenome	Illumina HiSeq 4000	0	350	150	41089562	feces [ENVO:00002003]	0
MMPC-3103329-ST-0	MMPC29268878ST	metagenome	Illumina HiSeq 4000	0	350	150	50747715	feces [ENVO:00002003]	0
MMPC-3103330-ST-0	MMPC96910089ST	metagenome	Illumina HiSeq 4000	0	350	150	15562457	feces [ENVO:00002003]	0
MMPC-3109101-ST-0	MMPC14211565ST	metagenome	Illumina HiSeq 4000	0	350	150	74174779	feces [ENVO:00002003]	0
MMPC-3109101-ST-0	MMPW29397139ST	metagenome	Illumina HiSeq 4000	0	350	150	468087742	feces [ENVO:00002003]	0
MMPC-3109102-ST-0	MMPC20689138ST	metagenome	Illumina HiSeq 4000	0	350	150	42313248	feces [ENVO:00002003]	0
MMPC-3109103-ST-0	MMPW82409611ST	metagenome	Illumina HiSeq 4000	0	350	150	448012729	feces [ENVO:00002003]	0
MMPC-3109103-ST-0	MMPC61634104ST	metagenome	Illumina HiSeq 4000	0	350	150	28553975	feces [ENVO:00002003]	0
MMPC-3109104-ST-0	MMPC53642802ST	metagenome	Illumina HiSeq 4000	0	350	150	12302431	feces [ENVO:00002003]	0
MMPC-3109105-ST-0	MMPC83679680ST	metagenome	Illumina HiSeq 4000	0	350	150	18019953	feces [ENVO:00002003]	0
MMPC-3109106-ST-0	MMPC21059026ST	metagenome	Illumina HiSeq 4000	0	350	150	15660594	feces [ENVO:00002003]	0
MMPC-3109108-ST-0	MMPC29596062ST	metagenome	Illumina HiSeq 4000	0	350	150	15449487	feces [ENVO:00002003]	0
MMPC-3109109-ST-0	MMPC79962166ST	metagenome	Illumina HiSeq 4000	0	350	150	45702011	feces [ENVO:00002003]	0
MMPC-3109110-ST-0	MMPC84979047ST	metagenome	Illumina HiSeq 4000	0	350	150	51915806	feces [ENVO:00002003]	0
MMPC-3109111-ST-0	MMPC54944306ST	metagenome	Illumina HiSeq 4000	0	350	150	9093837	feces [ENVO:00002003]	0
MMPC-3109112-ST-0	MMPC36137610ST	metagenome	Illumina HiSeq 4000	0	350	150	11591475	feces [ENVO:00002003]	0

MMPC-3109114-ST-0	MMPC36075929ST	metagenome	Illumina HiSeq 4000	0	350	150	29343109	feces [ENVO:00002003]	0
MMPC-3109115-ST-0	MMPC40565253ST	metagenome	Illumina HiSeq 4000	0	350	150	24643317	feces [ENVO:00002003]	0
MMPC-3109116-ST-0	MMPC67417777ST	metagenome	Illumina HiSeq 4000	0	350	150	45871936	feces [ENVO:00002003]	0
MMPC-3109117-ST-0	MMPW14699153ST	metagenome	Illumina HiSeq 4000	0	350	150	560238359	feces [ENVO:00002003]	0
MMPC-3109117-ST-0	MMPC49013463ST	metagenome	Illumina HiSeq 4000	0	350	150	23300387	feces [ENVO:00002003]	0
MMPC-3109118-ST-0	MMPC65662501ST	metagenome	Illumina HiSeq 4000	0	350	150	15601130	feces [ENVO:00002003]	0
MMPC-3109119-ST-0	MMPC40914520ST	metagenome	Illumina HiSeq 4000	0	350	150	22964094	feces [ENVO:00002003]	0
MMPC-3109120-ST-0	MMPC47063504ST	metagenome	Illumina HiSeq 4000	0	350	150	49317362	feces [ENVO:00002003]	0
MMPC-3109121-ST-0	MMPC17245919ST	metagenome	Illumina HiSeq 4000	0	350	150	16398595	feces [ENVO:00002003]	0
MMPC-3109123-ST-0	MMPW92389414ST	metagenome	Illumina HiSeq 4000	0	350	150	623483187	feces [ENVO:00002003]	0
MMPC-3109123-ST-0	MMPC68480658ST	metagenome	Illumina HiSeq 4000	0	350	150	13327091	feces [ENVO:00002003]	0
MMPC-3109124-ST-0	MMPC19165288ST	metagenome	Illumina HiSeq 4000	0	350	150	30229110	feces [ENVO:00002003]	0
MMPC-3109125-ST-0	MMPC57469621ST	metagenome	Illumina HiSeq 4000	0	350	150	39790710	feces [ENVO:00002003]	0
MMPC-3109126-ST-0	MMPC79996713ST	metagenome	Illumina HiSeq 4000	0	350	150	45709125	feces [ENVO:00002003]	0
MMPC-3109127-ST-0	MMPC37034483ST	metagenome	Illumina HiSeq 4000	0	350	150	7234175	feces [ENVO:00002003]	0
MMPC-3109128-ST-0	MMPC81211466ST	metagenome	Illumina HiSeq 4000	0	350	150	58854083	feces [ENVO:00002003]	0
MMPC-3109129-ST-0	MMPC24594620ST	metagenome	Illumina HiSeq 4000	0	350	150	76431268	feces [ENVO:00002003]	0
MMPC-3109130-ST-0	MMPC96182596ST	metagenome	Illumina HiSeq 4000	0	350	150	76577158	feces [ENVO:00002003]	0
MMPC-3109132-ST-0	MMPC77094060ST	metagenome	Illumina HiSeq 4000	0	350	150	36697241	feces [ENVO:00002003]	0
MMPC-3109134-ST-0	MMPC19619725ST	metagenome	Illumina HiSeq 4000	0	350	150	69280835	feces [ENVO:00002003]	0
MMPC-3109135-ST-0	MMPC16706723ST	metagenome	Illumina HiSeq 4000	0	350	150	32414314	feces [ENVO:00002003]	0
MMPC-3109136-ST-0	MMPC97506376ST	metagenome	Illumina HiSeq 4000	0	350	150	31971411	feces [ENVO:00002003]	0
MMPC-3109137-ST-0	MMPC54830782ST	metagenome	Illumina HiSeq 4000	0	350	150	38208164	feces [ENVO:00002003]	0
MMPC-3109138-ST-0	MMPC91449240ST	metagenome	Illumina HiSeq 4000	0	350	150	30254506	feces [ENVO:00002003]	0
MMPC-3109139-ST-0	MMPC55161862ST	metagenome	Illumina HiSeq 4000	0	350	150	43855433	feces [ENVO:00002003]	0
MMPC-3109140-ST-0	MMPC83312436ST	metagenome	Illumina HiSeq 4000	0	350	150	33084701	feces [ENVO:00002003]	0
MMPC-3109141-ST-0	MMPC27779234ST	metagenome	Illumina HiSeq 4000	0	350	150	44147402	feces [ENVO:00002003]	0
MMPC-3109201-ST-0	MMPC56144240ST	metagenome	Illumina HiSeq 4000	0	350	150	26869755	feces [ENVO:00002003]	0
MMPC-3109203-ST-0	MMPC13726847ST	metagenome	Illumina HiSeq 4000	0	350	150	21663895	feces [ENVO:00002003]	0
MMPC-3109204-ST-0	MMPC22312907ST	metagenome	Illumina HiSeq 4000	0	350	150	41893983	feces [ENVO:00002003]	0
MMPC-3109205-ST-0	MMPC30948868ST	metagenome	Illumina HiSeq 4000	0	350	150	21480386	feces [ENVO:00002003]	0
MMPC-3109206-ST-0	MMPC30623640ST	metagenome	Illumina HiSeq 4000	0	350	150	13694714	feces [ENVO:00002003]	0
MMPC-3109209-ST-0	MMPC97173638ST	metagenome	Illumina HiSeq 4000	0	350	150	19516074	feces [ENVO:00002003]	0
MMPC-3109210-ST-0	MMPC21135377ST	metagenome	Illumina HiSeq 4000	0	350	150	16258379	feces [ENVO:00002003]	0
MMPC-3109211-ST-0	MMPC19217531ST	metagenome	Illumina HiSeq 4000	0	350	150	53969453	feces [ENVO:00002003]	0
MMPC-3109212-ST-0	MMPC94907966ST	metagenome	Illumina HiSeq 4000	0	350	150	13649260	feces [ENVO:00002003]	0
MMPC-3109213-ST-0	MMPC60840390ST	metagenome	Illumina HiSeq 4000	0	350	150	13085767	feces [ENVO:00002003]	0
MMPC-3109215-ST-0	MMPC37485778ST	metagenome	Illumina HiSeq 4000	0	350	150	35733187	feces [ENVO:00002003]	0
MMPC-3109216-ST-0	MMPC11119852ST	metagenome	Illumina HiSeq 4000	0	350	150	14931356	feces [ENVO:00002003]	0
MMPC-3109217-ST-0	MMPC34174031ST	metagenome	Illumina HiSeq 4000	0	350	150	12765922	feces [ENVO:00002003]	0
MMPC-3109218-ST-0	MMPC52379257ST	metagenome	Illumina HiSeq 4000	0	350	150	50336511	feces [ENVO:00002003]	0
MMPC-3109219-ST-0	MMPC63364113ST	metagenome	Illumina HiSeq 4000	0	350	150	11273985	feces [ENVO:00002003]	0
MMPC-3109221-ST-0	MMPC27749512ST	metagenome	Illumina HiSeq 4000	0	350	150	22832202	feces [ENVO:00002003]	0
MMPC-3109222-ST-0	MMPC44022233ST	metagenome	Illumina HiSeq 4000	0	350	150	22174223	feces [ENVO:00002003]	0
MMPC-3109223-ST-0	MMPW83144761ST	metagenome	Illumina HiSeq 4000	0	350	150	623360223	feces [ENVO:00002003]	0
MMPC-3109223-ST-0	MMPC43926327ST	metagenome	Illumina HiSeq 4000	0	350	150	25244238	feces [ENVO:00002003]	0
MMPC-3109225-ST-0	MMPC12345974ST	metagenome	Illumina HiSeq 4000	0	350	150	85252767	feces [ENVO:00002003]	0
MMPC-3109226-ST-0	MMPC93332686ST	metagenome	Illumina HiSeq 4000	0	350	150	24901051	feces [ENVO:00002003]	0
MMPC-3109227-ST-0	MMPC92143124ST	metagenome	Illumina HiSeq 4000	0	350	150	23379659	feces [ENVO:00002003]	0
MMPC-3109228-ST-0	MMPC34385278ST	metagenome	Illumina HiSeq 4000	0	350	150	57769402	feces [ENVO:00002003]	0
MMPC-3109232-ST-0	MMPC36947286ST	metagenome	Illumina HiSeq 4000	0	350	150	31537988	feces [ENVO:00002003]	0
MMPC-3109233-ST-0	MMPC71968369ST	metagenome	Illumina HiSeq 4000	0	350	150	117568149	feces [ENVO:00002003]	0
MMPC-3109234-ST-0	MMPC74548980ST	metagenome	Illumina HiSeq 4000	0	350	150	35408139	feces [ENVO:00002003]	0
MMPC-3109236-ST-0	MMPC34834469ST	metagenome	Illumina HiSeq 4000	0	350	150	35375340	feces [ENVO:00002003]	0
MMPC-3109237-ST-0	MMPC50966165ST	metagenome	Illumina HiSeq 4000	0	350	150	52246735	feces [ENVO:00002003]	0
MMPC-3109238-ST-0	MMPC99183360ST	metagenome	Illumina HiSeq 4000	0	350	150	37883668	feces [ENVO:00002003]	0
MMPC-3109301-ST-0	MMPC35249031ST	metagenome	Illumina HiSeq 4000	0	350	150	43745786	feces [ENVO:00002003]	0
MMPC-3109305-ST-0	MMPC42290635ST	metagenome	Illumina HiSeq 4000	0	350	150	89100466	feces [ENVO:00002003]	0
MMPC-3109306-ST-0	MMPC42177786ST	metagenome	Illumina HiSeq 4000	0	350	150	22749462	feces [ENVO:00002003]	0
MMPC-3109315-ST-0	MMPC21236273ST	metagenome	Illumina HiSeq 4000	0	350	150	42079811	feces [ENVO:00002003]	0
MMPC-3109319-ST-0	MMPC11597832ST	metagenome	Illumina HiSeq 4000	0	350	150	47040985	feces [ENVO:00002003]	0
MMPC-3109324-ST-0	MMPC81505326ST	metagenome	Illumina HiSeq 4000	0	350	150	82601665	feces [ENVO:00002003]	0
MMPC-3103102-SA-0	MMPC54012223OR	metagenome	Illumina HiSeq 4000	0	350	150	4639773	saliva [ENVO:02000036]	0
MMPC-3103103-SA-0	MMPC71823580OR	metagenome	Illumina HiSeq 4000	0	350	150	10568615	saliva [ENVO:02000036]	0
MMPC-3103106-SA-0	MMPC76793553OR	metagenome	Illumina HiSeq 4000	0	350	150	5174708	saliva [ENVO:02000036]	0
MMPC-3103107-SA-0	MMPC33950978OR	metagenome	Illumina HiSeq 4000	0	350	150	3047069	saliva [ENVO:02000036]	0
MMPC-3103108-SA-0	MMPC72235353OR	metagenome	Illumina HiSeq 4000	0	350	150	24305625	saliva [ENVO:02000036]	0
MMPC-3103109-SA-0	MMPC84070936OR	metagenome	Illumina HiSeq 4000	0	350	150	22754410	saliva [ENVO:02000036]	0
MMPC-3103111-SA-0	MMPC74186942OR	metagenome	Illumina HiSeq 4000	0	350	150	13359112	saliva [ENVO:02000036]	0
MMPC-3103112-SA-0	MMPC51170653OR	metagenome	Illumina HiSeq 4000	0	350	150	9668483	saliva [ENVO:02000036]	0
MMPC-3103114-SA-0	MMPC26639644OR	metagenome	Illumina HiSeq 4000	0	350	150	26536006	saliva [ENVO:02000036]	0
MMPC-3103115-SA-0	MMPC24238465OR	metagenome	Illumina HiSeq 4000	0	350	150	1190050	saliva [ENVO:02000036]	0
MMPC-3103116-SA-0	MMPC48007504OR	metagenome	Illumina HiSeq 4000	0	350	150	27468049	saliva [ENVO:02000036]	0
MMPC-3103117-SA-0	MMPC24667695OR	metagenome	Illumina HiSeq 4000	0	350	150	5172735	saliva [ENVO:02000036]	0
MMPC-3103118-SA-0	MMPC38043539OR	metagenome	Illumina HiSeq 4000	0	350	150	20782971	saliva [ENVO:02000036]	0
MMPC-3103119-SA-0	MMPC11188431OR	metagenome	Illumina HiSeq 4000	0	350	150	25870866	saliva [ENVO:02000036]	0
MMPC-3103120-SA-0	MMPC90304226OR	metagenome	Illumina HiSeq 4000	0	350	150	19302260	saliva [ENVO:02000036]	0
MMPC-3103121-SA-0	MMPC32262645OR	metagenome	Illumina HiSeq 4000	0	350	150	19336162	saliva [ENVO:02000036]	0
MMPC-3103124-SA-0	MMPC36945431OR	metagenome	Illumina HiSeq 4000	0	350	150	2761113	saliva [ENVO:02000036]	0
MMPC-3103125-SA-0	MMPC55889507OR	metagenome	Illumina HiSeq 4000	0	350	150	10636750	saliva [ENVO:02000036]	0
MMPC-3103126-SA-0	MMPC17325940OR	metagenome	Illumina HiSeq 4000	0	350	150	9278513	saliva [ENVO:02000036]	0
MMPC-3103127-SA-0	MMPC81782599OR	metagenome	Illumina HiSeq 4000	0	350	150	1725271	saliva [ENVO:02000036]	0
MMPC-3103129-SA-0	MMPC52574889OR	metagenome	Illumina HiSeq 4000	0	350	150	4074564	saliva [ENVO:02000036]	0
MMPC-3103202-SA-0	MMPC36095950OR	metagenome	Illumina HiSeq 4000	0	350	150	2719346	saliva [ENVO:02000036]	0
MMPC-3103203-SA-0	MMPC28881424OR	metagenome	Illumina HiSeq 4000	0	350	150	22060600	saliva [ENVO:02000036]	0
MMPC-3103206-SA-0	MMPC96912492OR	metagenome	Illumina HiSeq 4000	0	350	150	29036267	saliva [ENVO:02000036]	0
MMPC-3103207-SA-0	MMPC19824023OR	metagenome	Illumina HiSeq 4000	0	350	150	24225787	saliva [ENVO:02000036]	0
MMPC-3103208-SA-0	MMPC90619750OR	metagenome	Illumina HiSeq 4000	0	350	150	3644416	saliva [ENVO:02000036]	0
MMPC-3103209-SA-0	MMPC19288609OR	metagenome	Illumina HiSeq 4000	0	350	150	5173307	saliva [ENVO:02000036]	0
MMPC-3103211-SA-0	MMPC58110896OR	metagenome	Illumina HiSeq 4000	0	350	150	14608140	saliva [ENVO:02000036]	0

MMPC-3103212-SA-0	MMPC73162206OR	metagenome	Illumina HiSeq 4000	0	350	150	13760338	saliva [ENVO:02000036]	0
MMPC-3103214-SA-0	MMPC93850203OR	metagenome	Illumina HiSeq 4000	0	350	150	23079043	saliva [ENVO:02000036]	0
MMPC-3103215-SA-0	MMPC24307334OR	metagenome	Illumina HiSeq 4000	0	350	150	24381582	saliva [ENVO:02000036]	0
MMPC-3103216-SA-0	MMPC19845294OR	metagenome	Illumina HiSeq 4000	0	350	150	586889	saliva [ENVO:02000036]	0
MMPC-3103217-SA-0	MMPC34133423OR	metagenome	Illumina HiSeq 4000	0	350	150	11088793	saliva [ENVO:02000036]	0
MMPC-3103218-SA-0	MMPC71556090OR	metagenome	Illumina HiSeq 4000	0	350	150	23124397	saliva [ENVO:02000036]	0
MMPC-3103219-SA-0	MMPC91688118OR	metagenome	Illumina HiSeq 4000	0	350	150	3228394	saliva [ENVO:02000036]	0
MMPC-3103220-SA-0	MMPC62647302OR	metagenome	Illumina HiSeq 4000	0	350	150	21615248	saliva [ENVO:02000036]	0
MMPC-3103221-SA-0	MMPC65407889OR	metagenome	Illumina HiSeq 4000	0	350	150	9669442	saliva [ENVO:02000036]	0
MMPC-3103223-SA-0	MMPC31969297OR	metagenome	Illumina HiSeq 4000	0	350	150	10392474	saliva [ENVO:02000036]	0
MMPC-3103224-SA-0	MMPC56597853OR	metagenome	Illumina HiSeq 4000	0	350	150	6055196	saliva [ENVO:02000036]	0
MMPC-3103225-SA-0	MMPC56843559OR	metagenome	Illumina HiSeq 4000	0	350	150	7623136	saliva [ENVO:02000036]	0
MMPC-3103226-SA-0	MMPC64507639OR	metagenome	Illumina HiSeq 4000	0	350	150	19496040	saliva [ENVO:02000036]	0
MMPC-3103227-SA-0	MMPC64423720OR	metagenome	Illumina HiSeq 4000	0	350	150	6255265	saliva [ENVO:02000036]	0
MMPC-3103228-SA-0	MMPC60219907OR	metagenome	Illumina HiSeq 4000	0	350	150	15063547	saliva [ENVO:02000036]	0
MMPC-3103229-SA-0	MMPC71889536OR	metagenome	Illumina HiSeq 4000	0	350	150	5309775	saliva [ENVO:02000036]	0
MMPC-3103302-SA-0	MMPC68638114OR	metagenome	Illumina HiSeq 4000	0	350	150	21593638	saliva [ENVO:02000036]	0
MMPC-3103303-SA-0	MMPC85565182OR	metagenome	Illumina HiSeq 4000	0	350	150	27146282	saliva [ENVO:02000036]	0
MMPC-3103307-SA-0	MMPC78869687OR	metagenome	Illumina HiSeq 4000	0	350	150	2896177	saliva [ENVO:02000036]	0
MMPC-3103309-SA-0	MMPC52849207OR	metagenome	Illumina HiSeq 4000	0	350	150	4140770	saliva [ENVO:02000036]	0
MMPC-3103315-SA-0	MMPC83526018OR	metagenome	Illumina HiSeq 4000	0	350	150	3405407	saliva [ENVO:02000036]	0
MMPC-3103318-SA-0	MMPC57142773OR	metagenome	Illumina HiSeq 4000	0	350	150	21599119	saliva [ENVO:02000036]	0
MMPC-3103319-SA-0	MMPC54160426OR	metagenome	Illumina HiSeq 4000	0	350	150	15712615	saliva [ENVO:02000036]	0
MMPC-3103330-SA-0	MMPC75414130OR	metagenome	Illumina HiSeq 4000	0	350	150	13142288	saliva [ENVO:02000036]	0
MMPC-3109101-SA-0	MMPC49718201OR	metagenome	Illumina HiSeq 4000	0	350	150	10271280	saliva [ENVO:02000036]	0
MMPC-3109102-SA-0	MMPC95809433OR	metagenome	Illumina HiSeq 4000	0	350	150	2270393	saliva [ENVO:02000036]	0
MMPC-3109103-SA-0	MMPC16794525OR	metagenome	Illumina HiSeq 4000	0	350	150	9038542	saliva [ENVO:02000036]	0
MMPC-3109104-SA-0	MMPC19392645OR	metagenome	Illumina HiSeq 4000	0	350	150	3568912	saliva [ENVO:02000036]	0
MMPC-3109105-SA-0	MMPC90169023OR	metagenome	Illumina HiSeq 4000	0	350	150	7204089	saliva [ENVO:02000036]	0
MMPC-3109106-SA-0	MMPC86976445OR	metagenome	Illumina HiSeq 4000	0	350	150	10768021	saliva [ENVO:02000036]	0
MMPC-3109107-SA-0	MMPC44731247OR	metagenome	Illumina HiSeq 4000	0	350	150	8048004	saliva [ENVO:02000036]	0
MMPC-3109108-SA-0	MMPC65660081OR	metagenome	Illumina HiSeq 4000	0	350	150	21617221	saliva [ENVO:02000036]	0
MMPC-3109109-SA-0	MMPC41147837OR	metagenome	Illumina HiSeq 4000	0	350	150	6344692	saliva [ENVO:02000036]	0
MMPC-3109110-SA-0	MMPC41118143OR	metagenome	Illumina HiSeq 4000	0	350	150	4560687	saliva [ENVO:02000036]	0
MMPC-3109111-SA-0	MMPC66171614OR	metagenome	Illumina HiSeq 4000	0	350	150	3102631	saliva [ENVO:02000036]	0
MMPC-3109112-SA-0	MMPC96133527OR	metagenome	Illumina HiSeq 4000	0	350	150	2593028	saliva [ENVO:02000036]	0
MMPC-3109113-SA-0	MMPC93366499OR	metagenome	Illumina HiSeq 4000	0	350	150	1364850	saliva [ENVO:02000036]	0
MMPC-3109114-SA-0	MMPC65022621OR	metagenome	Illumina HiSeq 4000	0	350	150	16802842	saliva [ENVO:02000036]	0
MMPC-3109115-SA-0	MMPC78563626OR	metagenome	Illumina HiSeq 4000	0	350	150	10555862	saliva [ENVO:02000036]	0
MMPC-3109116-SA-0	MMPC53407274OR	metagenome	Illumina HiSeq 4000	0	350	150	5335597	saliva [ENVO:02000036]	0
MMPC-3109117-SA-0	MMPC53148798OR	metagenome	Illumina HiSeq 4000	0	350	150	3146036	saliva [ENVO:02000036]	0
MMPC-3109118-SA-0	MMPC56085636OR	metagenome	Illumina HiSeq 4000	0	350	150	8008994	saliva [ENVO:02000036]	0
MMPC-3109119-SA-0	MMPC90053642OR	metagenome	Illumina HiSeq 4000	0	350	150	12510374	saliva [ENVO:02000036]	0
MMPC-3109121-SA-0	MMPC60116897OR	metagenome	Illumina HiSeq 4000	0	350	150	9130757	saliva [ENVO:02000036]	0
MMPC-3109122-SA-0	MMPC21941683OR	metagenome	Illumina HiSeq 4000	0	350	150	1074483	saliva [ENVO:02000036]	0
MMPC-3109123-SA-0	MMPC32965142OR	metagenome	Illumina HiSeq 4000	0	350	150	5930486	saliva [ENVO:02000036]	0
MMPC-3109201-SA-0	MMPC95669500OR	metagenome	Illumina HiSeq 4000	0	350	150	8322995	saliva [ENVO:02000036]	0
MMPC-3109202-SA-0	MMPC31897883OR	metagenome	Illumina HiSeq 4000	0	350	150	26509835	saliva [ENVO:02000036]	0
MMPC-3109203-SA-0	MMPC46886173OR	metagenome	Illumina HiSeq 4000	0	350	150	24073587	saliva [ENVO:02000036]	0
MMPC-3109204-SA-0	MMPC55860177OR	metagenome	Illumina HiSeq 4000	0	350	150	6325821	saliva [ENVO:02000036]	0
MMPC-3109205-SA-0	MMPC39189434OR	metagenome	Illumina HiSeq 4000	0	350	150	14245117	saliva [ENVO:02000036]	0
MMPC-3109206-SA-0	MMPC54555576OR	metagenome	Illumina HiSeq 4000	0	350	150	7426412	saliva [ENVO:02000036]	0
MMPC-3109207-SA-0	MMPC76436299OR	metagenome	Illumina HiSeq 4000	0	350	150	15891919	saliva [ENVO:02000036]	0
MMPC-3109208-SA-0	MMPC485551150R	metagenome	Illumina HiSeq 4000	0	350	150	1067722	saliva [ENVO:02000036]	0
MMPC-3109208-SA-0	MMPC95862719OR	metagenome	Illumina HiSeq 4000	0	350	150	3806358	saliva [ENVO:02000036]	0
MMPC-3109209-SA-0	MMPC61999432OR	metagenome	Illumina HiSeq 4000	0	350	150	1080307	saliva [ENVO:02000036]	0
MMPC-3109210-SA-0	MMPC92345363OR	metagenome	Illumina HiSeq 4000	0	350	150	8191798	saliva [ENVO:02000036]	0
MMPC-3109210-SA-0	MMPC87948870OR	metagenome	Illumina HiSeq 4000	0	350	150	9477616	saliva [ENVO:02000036]	0
MMPC-3109211-SA-0	MMPC31618027OR	metagenome	Illumina HiSeq 4000	0	350	150	3968655	saliva [ENVO:02000036]	0
MMPC-3109212-SA-0	MMPC14824749OR	metagenome	Illumina HiSeq 4000	0	350	150	13866065	saliva [ENVO:02000036]	0
MMPC-3109213-SA-0	MMPC15910261OR	metagenome	Illumina HiSeq 4000	0	350	150	6374672	saliva [ENVO:02000036]	0
MMPC-3109214-SA-0	MMPC27383418OR	metagenome	Illumina HiSeq 4000	0	350	150	10627159	saliva [ENVO:02000036]	0
MMPC-3109215-SA-0	MMPC12870707OR	metagenome	Illumina HiSeq 4000	0	350	150	2480791	saliva [ENVO:02000036]	0
MMPC-3109216-SA-0	MMPC15441403OR	metagenome	Illumina HiSeq 4000	0	350	150	5975117	saliva [ENVO:02000036]	0
MMPC-3109217-SA-0	MMPC73436744OR	metagenome	Illumina HiSeq 4000	0	350	150	1084350	saliva [ENVO:02000036]	0
MMPC-3109218-SA-0	MMPC63628582OR	metagenome	Illumina HiSeq 4000	0	350	150	5800566	saliva [ENVO:02000036]	0
MMPC-3109219-SA-0	MMPC13132715OR	metagenome	Illumina HiSeq 4000	0	350	150	9675003	saliva [ENVO:02000036]	0
MMPC-3109220-SA-0	MMPC23272164OR	metagenome	Illumina HiSeq 4000	0	350	150	4438841	saliva [ENVO:02000036]	0
MMPC-3109221-SA-0	MMPC32315383OR	metagenome	Illumina HiSeq 4000	0	350	150	19454442	saliva [ENVO:02000036]	0
MMPC-3109222-SA-1	MMPC57477276OR	metagenome	Illumina HiSeq 4000	0	350	150	10220171	saliva [ENVO:02000036]	1
MMPC-3109222-SA-1	MMPC33706732OR	metagenome	Illumina HiSeq 4000	0	350	150	4735876	saliva [ENVO:02000036]	1
MMPC-3109223-SA-0	MMPC41357154OR	metagenome	Illumina HiSeq 4000	0	350	150	38849239	saliva [ENVO:02000036]	0
MMPC-3109301-SA-0	MMPC93150325OR	metagenome	Illumina HiSeq 4000	0	350	150	16728492	saliva [ENVO:02000036]	0
MMPC-3109315-SA-0	MMPC96783701OR	metagenome	Illumina HiSeq 4000	0	350	150	11039995	saliva [ENVO:02000036]	0
MMPC-3109319-SA-0	MMPC96263337OR	metagenome	Illumina HiSeq 4000	0	350	150	6969069	saliva [ENVO:02000036]	0
MMPC-3103106129-DU-0	MMPC89983827DU	16S	Illumina MiSeq	0	292	292	54547	duodenum [UBERON:0002114]	0
MMPC-3103107129-DU-0	MMPC73658283DU	16S	Illumina MiSeq	0	292	292	64250	duodenum [UBERON:0002114]	0
MMPC-3103108129-DU-0	MMPC33709560DU	16S	Illumina MiSeq	0	292	292	96936	duodenum [UBERON:0002114]	0
MMPC-3103111129-DU-0	MMPC57647850DU	16S	Illumina MiSeq	0	292	292	73326	duodenum [UBERON:0002114]	0
MMPC-3103118129-DU-0	MMPC69746296DU	16S	Illumina MiSeq	0	292	292	120850	duodenum [UBERON:0002114]	0
MMPC-3103119129-DU-0	MMPC80849866DU	16S	Illumina MiSeq	0	292	292	130442	duodenum [UBERON:0002114]	0
MMPC-3103119129-DU-c	MMPC43438216DU	16S	Illumina MiSeq	0	292	292	112252	duodenum [UBERON:0002114]	0
MMPC-3103120129-DU-0	MMPC72924201DU	16S	Illumina MiSeq	0	292	292	86565	duodenum [UBERON:0002114]	0
MMPC-3103120129-DU-c	MMPC14537843DU	16S	Illumina MiSeq	0	292	292	86185	duodenum [UBERON:0002114]	0
MMPC-3103121129-DU-0	MMPC36189783DU	16S	Illumina MiSeq	0	292	292	37643	duodenum [UBERON:0002114]	0
MMPC-3103125129-DU-0	MMPC80414181DU	16S	Illumina MiSeq	0	292	292	39130	duodenum [UBERON:0002114]	0
MMPC-3103129129-DU-0	MMPC53972105DU	16S	Illumina MiSeq	0	292	292	85409	duodenum [UBERON:0002114]	0
MMPC-3103302129-DU-0	MMPC19587595DU	16S	Illumina MiSeq	0	292	292	104839	duodenum [UBERON:0002114]	0
MMPC-3103307129-DU-0	MMPC68318389DU	16S	Illumina MiSeq	0	292	292	71624	duodenum [UBERON:0002114]	0
MMPC-3103307129-DU-0	MMPC71903222DU	16S	Illumina MiSeq	0	292	292	58134	duodenum [UBERON:0002114]	0

MMPC-3103102-ST-0	MMPC94299916ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103103-ST-0	MMPC24623808ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103106-ST-0	MMPC64014581ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103107-ST-0	MMPC82135016ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103108-ST-0	MMPC45547467ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103109-ST-0	MMPC66174878ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103111-ST-0	MMPC91082775ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103112-ST-0	MMPC29677848ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103114-ST-0	MMPC39575354ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103115-ST-0	MMPC50889135ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103116-ST-0	MMPC50185623ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103117-ST-0	MMPC85685924ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103118-ST-0	MMPC59183318ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103119-ST-0	MMPC71791865ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103120-ST-0	MMPC21711187ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103121-ST-0	MMPC21060483ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103124-ST-0	MMPC82177922ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103125-ST-0	MMPC54152785ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103126-ST-0	MMPC84720270ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103127-ST-0	MMPC61075350ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103129-ST-0	MMPC76947975ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103202-ST-0	MMPC17827720ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103203-ST-0	MMPC43730151ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103206-ST-0	MMPC62596168ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103207-ST-0	MMPC62530950ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103208-ST-0	MMPC57166568ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103209-ST-0	MMPC15725313ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103211-ST-0	MMPC84441239ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103212-ST-0	MMPC56144255ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103214-ST-0	MMPC99601038ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103215-ST-0	MMPC75618331ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103216-ST-0	MMPC16095290ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103217-ST-0	MMPC87962373ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103218-ST-0	MMPC99264450ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103219-ST-0	MMPC66473877ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103220-ST-0	MMPC80434434ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103221-ST-0	MMPC47628612ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103223-ST-0	MMPC12333772ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103224-ST-0	MMPC50116517ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103225-ST-0	MMPC44968505ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103226-ST-0	MMPC52586872ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103227-ST-0	MMPC32976245ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103228-ST-0	MMPC95231866ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103229-ST-0	MMPC68831667ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103302-ST-0	MMPC60182036ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103303-ST-0	MMPC45406530ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103306-ST-0	MMPC99577153ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103307-ST-0	MMPC93314562ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103309-ST-0	MMPC85038078ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103311-ST-0	MMPC11696984ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103312-ST-0	MMPC41061772ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103314-ST-0	MMPC45116274ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103315-ST-0	MMPC86671846ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103316-ST-0	MMPC66358697ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103317-ST-0	MMPC34674582ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103318-ST-0	MMPC22518056ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103319-ST-0	MMPC65945502ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103319-ST-0	MMPC80934998ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103321-ST-0	MMPC48683862ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103324-ST-0	MMPC83668164ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103325-ST-0	MMPC55570441ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103326-ST-0	MMPC43042571ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103329-ST-0	MMPC60345757ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103330-ST-0	MMPC29021039ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109101-ST-0	MMPC24977504ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109102-ST-0	MMPC62392110ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109103-ST-0	MMPC45287801ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109104-ST-0	MMPC40826089ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109105-ST-0	MMPC80964294ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109106-ST-0	MMPC78341196ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109108-ST-0	MMPC62146737ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109109-ST-0	MMPC69770767ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109110-ST-0	MMPC31154145ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109111-ST-0	MMPC76934936ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109112-ST-0	MMPC91853026ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109114-ST-0	MMPC31444727ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109115-ST-0	MMPC73932880ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109116-ST-0	MMPC59288570ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109117-ST-0	MMPC36926728ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109118-ST-0	MMPC96496937ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109119-ST-0	MMPC74128230ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109120-ST-0	MMPC74940396ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109121-ST-0	MMPC30256497ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109122-ST-0	MMPC21699325ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109122-ST-0	## MMPC46833664ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109123-ST-0	MMPC91722361ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109124-ST-0	MMPC94188621ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109125-ST-0	MMPC91811211ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109126-ST-0	MMPC90395905ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109136-ST-0	MMPC22960059ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0

MMPC-3109137-ST-0	MMPC61697353ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109138-ST-0	MMPC82855966ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109139-ST-0	MMPC29844214ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109140-ST-0	MMPC50483831ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109141-ST-0	MMPC48709788ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109201-ST-0	MMPC84981989ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109203-ST-0	MMPC94959046ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109204-ST-0	MMPC30552564ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109205-ST-0	MMPC80314763ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109206-ST-0	MMPC99362803ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109209-ST-0	MMPC74755332ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109210-ST-0	MMPC94006070ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109211-ST-0	MMPC61453521ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109212-ST-0	MMPC13718212ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109213-ST-0	MMPC29098777ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109215-ST-0	MMPC31684537ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109216-ST-0	MMPC52834855ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109217-ST-0	MMPC45463255ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109218-ST-0	MMPC66427657ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109219-ST-0	MMPC83101778ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109221-ST-0	MMPC45481781ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109222-ST-0	MMPC28617437ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109223-ST-0	MMPC49582267ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109226-ST-0	MMPC57772499ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109232-ST-0	MMPC92950288ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109234-ST-0	MMPC35779891ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109236-ST-0	MMPC19331607ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109237-ST-0	MMPC55213614ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109238-ST-0	MMPC25677890ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109301-ST-0	MMPC43182434ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109315-ST-0	MMPC38663896ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3109319-ST-0	MMPC66201737ST	16S	Illumina MiSeq	0	292	292	NA	feces [ENVO:00002003]	0
MMPC-3103102-SA-0	MMPC68158800OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103103-SA-0	MMPC55436260OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103106-SA-0	MMPC88921841OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103107-SA-0	MMPC71486420OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103108-SA-0	MMPC46739872OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103109-SA-0	MMPC31622432OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103111-SA-0	MMPC51692793OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103112-SA-0	MMPC12922693OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103114-SA-0	MMPC22137064OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103115-SA-0	MMPC67978674OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103116-SA-0	MMPC65303959OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103117-SA-0	MMPC63118595OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103118-SA-0	MMPC11179595OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103119-SA-0	MMPC20954519OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103120-SA-0	MMPC21775404OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103121-SA-0	MMPC23514621OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103124-SA-0	MMPC42192127OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103125-SA-0	MMPC45339999OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103126-SA-0	MMPC68048817OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103127-SA-0	MMPC62601303OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103129-SA-0	MMPC31367206OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103202-SA-0	MMPC42991028OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103203-SA-0	MMPC74059481OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103206-SA-0	MMPC74490281OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103207-SA-0	MMPC53231545OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103208-SA-0	MMPC48136943OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103209-SA-0	MMPC20195220OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103211-SA-0	MMPC45318061OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103212-SA-0	MMPC37399343OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103214-SA-0	MMPC38394840OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103215-SA-0	MMPC84970403OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103216-SA-0	MMPC56379457OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103217-SA-0	MMPC40967934OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103218-SA-0	MMPC73927114OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103219-SA-0	MMPC97872292OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103220-SA-0	MMPC68758730OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103221-SA-0	MMPC54458294OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103223-SA-0	MMPC55525481OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103224-SA-0	MMPC90470189OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103225-SA-0	MMPC85390604OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103226-SA-0	MMPC87516576OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103227-SA-0	MMPC50847145OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103228-SA-0	MMPC24608714OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103229-SA-0	MMPC58829082OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103302-SA-0	MMPC63553475OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103303-SA-0	MMPC27266285OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103306-SA-0	MMPC85705244OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103307-SA-0	MMPC57892266OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103308-SA-0	MMPC58558599OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103309-SA-0	MMPC55133623OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103311-SA-0	MMPC37416843OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103312-SA-0	MMPC50998073OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103314-SA-0	MMPC35036620OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103315-SA-0	MMPC79959139OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103316-SA-0	MMPC65969751OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103317-SA-0	MMPC85634415OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103318-SA-0	MMPC93112149OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103319-SA-0	MMPC12461225OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0

MMPC-3103320-SA-0	MMPC34498596OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103321-SA-0	MMPC56325888OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103324-SA-0	MMPC99338054OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103325-SA-0	MMPC96167252OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103326-SA-0	MMPC55035531OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103327-SA-0	MMPC81837161OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103329-SA-0	MMPC42646817OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3103330-SA-0	MMPC16231550OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109101-SA-0	MMPC91896521OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109102-SA-0	MMPC91354261OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109103-SA-0	MMPC49489785OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109104-SA-0	MMPC78236242OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109105-SA-0	MMPC46123748OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109106-SA-0	MMPC95372332OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109107-SA-0	MMPC42247540OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109108-SA-0	MMPC22594900OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109109-SA-0	MMPC42369256OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109110-SA-0	MMPC52559088OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109111-SA-0	MMPC48186797OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109112-SA-0	MMPC35162108OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109113-SA-0	MMPC77190173OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109114-SA-0	MMPC91664155OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109115-SA-0	MMPC86145124OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109116-SA-0	MMPC28815814OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109117-SA-0	MMPC55730016OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109118-SA-0	MMPC73361074OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109119-SA-0	MMPC99082893OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109120-SA-0	MMPC34568026OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109121-SA-0	MMPC91033830OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109122-SA-0	MMPC75634766OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109123-SA-0	MMPC78765773OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109124-SA-0	MMPC42978442OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109125-SA-0	MMPC13169976OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109126-SA-0	MMPC21250627OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109127-SA-0	MMPC89348908OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109128-SA-0	MMPC41437470OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109129-SA-0	MMPC68946435OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109130-SA-0	MMPC10578010OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109132-SA-0	MMPC58837755OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109134-SA-0	MMPC42441792OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109135-SA-0	MMPC880955400R	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109136-SA-0	MMPC67321556OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109137-SA-0	MMPC25056624OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109138-SA-0	MMPC29668362OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109139-SA-0	MMPC80846477OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109140-SA-0	MMPC92702195OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109141-SA-0	MMPC42107863OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109201-SA-0	MMPC85802458OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109202-SA-0	MMPC27037046OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109203-SA-0	MMPC42326903OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109204-SA-0	MMPC96578111OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109205-SA-0	MMPC67377108OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109206-SA-0	MMPC24821675OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109207-SA-0	MMPC60572150OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109208-SA-0	MMPC27025376OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109208-SA-0	MMPC62405084OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109209-SA-0	MMPC19177783OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109210-SA-0	MMPC24845793OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109210-SA-0	MMPC47372291OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109211-SA-0	MMPC89522066OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109212-SA-0	MMPC73773857OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109213-SA-0	MMPC37783467OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109214-SA-0	MMPC39636267OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109215-SA-0	MMPC40536708OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109216-SA-0	MMPC43503506OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109217-SA-0	MMPC22439119OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109218-SA-0	MMPC93571858OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109219-SA-0	MMPC45008410OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109220-SA-0	MMPC29277640OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109221-SA-0	MMPC32291597OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109222-SA-1	MMPC99658636OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	1
MMPC-3109222-SA-1	MMPC13427371OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	1
MMPC-3109223-SA-0	MMPC48873249OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109225-SA-0	MMPC37580697OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109226-SA-0	MMPC61992937OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109227-SA-0	MMPC67918047OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109228-SA-0	MMPC35478733OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109232-SA-0	MMPC54640065OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109233-SA-0	MMPC94081974OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109234-SA-0	MMPC29658279OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109236-SA-0	MMPC40797909OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109237-SA-0	MMPC47432795OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109238-SA-0	MMPC81538982OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109301-SA-0	MMPC62882996OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109305-SA-0	MMPC59454227OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109305-SA-0	MMPC63021713OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109306-SA-0	MMPC33663665OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109315-SA-0	MMPC59175809OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109319-SA-0	MMPC52031211OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0
MMPC-3109324-SA-0	MMPC11599193OR	16S	Illumina MiSeq	0	292	292	NA	saliva [ENVO:02000036]	0

MMPC-3103102123-TU-0	MMPC52294238TU	16S	Illumina MiSeq	0	292	292	16762	pancreas [UBERON:0001264]	0
MMPC-3103102125-HT-0	MMPC96437096HT	16S	Illumina MiSeq	0	292	292	118983	pancreas [UBERON:0001264]	0
MMPC-3103106123-TU-0	MMPC22271503TU	16S	Illumina MiSeq	0	292	292	27346	pancreas [UBERON:0001264]	0
MMPC-3103107123-TU-0	MMPC87955180TU	16S	Illumina MiSeq	0	292	292	50932	pancreas [UBERON:0001264]	0
MMPC-3103108123-TU-0	MMPC54922715TU	16S	Illumina MiSeq	0	292	292	31245	pancreas [UBERON:0001264]	0
MMPC-3103108125-HT-0	MMPC24466339HT	16S	Illumina MiSeq	0	292	292	127835	pancreas [UBERON:0001264]	0
MMPC-3103111125-HT-0	MMPC80734101HT	16S	Illumina MiSeq	0	292	292	95924	pancreas [UBERON:0001264]	0
MMPC-3103112123-TU-0	MMPC83770412TU	16S	Illumina MiSeq	0	292	292	21764	pancreas [UBERON:0001264]	0
MMPC-3103112125-HT-0	MMPC40334378HT	16S	Illumina MiSeq	0	292	292	91218	pancreas [UBERON:0001264]	0
MMPC-3103114123-TU-0	MMPC48644619TU	16S	Illumina MiSeq	0	292	292	17849	pancreas [UBERON:0001264]	0
MMPC-3103114125-HT-0	MMPC35209818HT	16S	Illumina MiSeq	0	292	292	114214	pancreas [UBERON:0001264]	0
MMPC-3103116123-TU-0	MMPC75019385TU	16S	Illumina MiSeq	0	292	292	38264	pancreas [UBERON:0001264]	0
MMPC-3103116125-HT-0	MMPC89754577HT	16S	Illumina MiSeq	0	292	292	84488	pancreas [UBERON:0001264]	0
MMPC-3103116125-HT-c	MMPC76929964HT	16S	Illumina MiSeq	0	292	292	99306	pancreas [UBERON:0001264]	0
MMPC-3103118123-TU-0	MMPC53213093TU	16S	Illumina MiSeq	0	292	292	19403	pancreas [UBERON:0001264]	0
MMPC-3103119123-TU-0	MMPC77465766TU	16S	Illumina MiSeq	0	292	292	35083	pancreas [UBERON:0001264]	0
MMPC-3103119123-TU-c	MMPC24078588TU	16S	Illumina MiSeq	0	292	292	71331	pancreas [UBERON:0001264]	0
MMPC-3103119125-HT-0	MMPC37714156HT	16S	Illumina MiSeq	0	292	292	85195	pancreas [UBERON:0001264]	0
MMPC-3103119125-HT-c	MMPC49102349HT	16S	Illumina MiSeq	0	292	292	111138	pancreas [UBERON:0001264]	0
MMPC-3103120125-HT-0	MMPC36983914HT	16S	Illumina MiSeq	0	292	292	73461	pancreas [UBERON:0001264]	0
MMPC-3103121123-TU-0	MMPC90323932TU	16S	Illumina MiSeq	0	292	292	32825	pancreas [UBERON:0001264]	0
MMPC-3103121123-TU-c	MMPC58485046TU	16S	Illumina MiSeq	0	292	292	140836	pancreas [UBERON:0001264]	0
MMPC-3103125123-TU-0	MMPC49164313TU	16S	Illumina MiSeq	0	292	292	50097	pancreas [UBERON:0001264]	0
MMPC-3103125127-HT-0	MMPC86673187HT	16S	Illumina MiSeq	0	292	292	96102	pancreas [UBERON:0001264]	0
MMPC-3103129123-TU-0	MMPC80997236TU	16S	Illumina MiSeq	0	292	292	64881	pancreas [UBERON:0001264]	0
MMPC-3103129125-HT-0	MMPC49203482HT	16S	Illumina MiSeq	0	292	292	110366	pancreas [UBERON:0001264]	0
MMPC-3103302125-HT-0	MMPC25083626HT	16S	Illumina MiSeq	0	292	292	87920	pancreas [UBERON:0001264]	0
MMPC-3103302127-HT-0	MMPC02321546HT	16S	Illumina MiSeq	0	292	292	94815	ncreatic duct [UBERON:000732	0
MMPC-3103307123-TU-0	MMPC84306689TU	16S	Illumina MiSeq	0	292	292	35125	pancreas [UBERON:0001264]	0
MMPC-3103307123-TU-c	MMPC63721423TU	16S	Illumina MiSeq	0	292	292	101573	pancreas [UBERON:0001264]	0
MMPC-3103307125-HT-0	MMPC74146850HT	16S	Illumina MiSeq	0	292	292	87273	pancreas [UBERON:0001264]	0
MMPC-3103309123-TU-0	MMPC53390762TU	16S	Illumina MiSeq	0	292	292	25942	pancreas [UBERON:0001264]	0
MMPC-3103309125-HT-0	MMPC33872709HT	16S	Illumina MiSeq	0	292	292	93994	pancreas [UBERON:0001264]	0
MMPC-3103330125-HT-0	MMPC35081045HT	16S	Illumina MiSeq	0	292	292	75059	pancreas [UBERON:0001264]	0
MMPC-3109101123-TU-0	MMPC82234530TU	16S	Illumina MiSeq	0	292	292	63990	pancreas [UBERON:0001264]	0
MMPC-3109102123-TU-0	MMPC26308927TU	16S	Illumina MiSeq	0	292	292	63118	pancreas [UBERON:0001264]	0
MMPC-3109102125-HT-0	MMPC83100372HT	16S	Illumina MiSeq	0	292	292	97384	pancreas [UBERON:0001264]	0
MMPC-3109103123-TU-0	MMPC79418921TU	16S	Illumina MiSeq	0	292	292	92173	pancreas [UBERON:0001264]	0
MMPC-3109105123-TU-0	MMPC96387591TU	16S	Illumina MiSeq	0	292	292	86922	pancreas [UBERON:0001264]	0
MMPC-3109105125-HT-0	MMPC33126922HT	16S	Illumina MiSeq	0	292	292	96057	pancreas [UBERON:0001264]	0
MMPC-3109107123-TU-0	MMPC80047993TU	16S	Illumina MiSeq	0	292	292	78692	pancreas [UBERON:0001264]	0
MMPC-3109107125-HT-0	MMPC65170291HT	16S	Illumina MiSeq	0	292	292	66822	pancreas [UBERON:0001264]	0
MMPC-3109111123-TU-0	MMPC23067667TU	16S	Illumina MiSeq	0	292	292	8	pancreas [UBERON:0001264]	0
MMPC-3109111125-HT-0	MMPC80978814HT	16S	Illumina MiSeq	0	292	292	150064	pancreas [UBERON:0001264]	0
MMPC-3109111125-HT-c	MMPC42159796HT	16S	Illumina MiSeq	0	292	292	116464	pancreas [UBERON:0001264]	0
MMPC-3109113123-TU-0	MMPC42025082TU	16S	Illumina MiSeq	0	292	292	91603	pancreas [UBERON:0001264]	0
MMPC-3109113125-HT-0	MMPC93630826HT	16S	Illumina MiSeq	0	292	292	93581	pancreas [UBERON:0001264]	0
MMPC-3109117123-TU-0	MMPC44512561TU	16S	Illumina MiSeq	0	292	292	101695	pancreas [UBERON:0001264]	0
MMPC-3109117125-HT-0	MMPC58544120HT	16S	Illumina MiSeq	0	292	292	76970	pancreas [UBERON:0001264]	0
MMPC-3109117127-HT-0	MMPC66546739HT	16S	Illumina MiSeq	0	292	292	72952	ncreatic duct [UBERON:000732	0
MMPC-3109140123-TU-0	MMPC57986041TU	16S	Illumina MiSeq	0	292	292	137586	pancreas [UBERON:0001264]	0

gender	age_years	ollection_dat	ct_disease_s	tax_id	smoker	center	alcohol_statu	alldiab	diabcat	obese	panctype	asthma	allacid
male	79	2015-2018	PC	408170	smoker	2	0	0	0	0	0	0	0
male	62	2015-2018	PC	408170	ex-smoker	2	1	0	0	0	0	0	0
female	69	2015-2018	PC	408170	smoker	2	0	0	0	0	0	0	1
male	54	2015-2018	PC	408170	non-smoker	2	1	0	0	0	0	0	0
male	54	2015-2018	PC	408170	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	PC	408170	non-smoker	2	1	0	0	NA	0	0	0
male	68	2015-2018	PC	408170	ex-smoker	2	1	1	1	0	0	0	0
male	68	2015-2018	PC	408170	ex-smoker	2	1	1	1	0	0	0	0
male	71	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	0	0
male	84	2015-2018	PC	408170	non-smoker	2	1	1	1	0	0	0	0
male	84	2015-2018	PC	408170	non-smoker	2	1	1	1	0	0	0	0
female	69	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	1	1
male	66	2015-2018	PC	408170	smoker	2	1	0	0	0	0	0	1
male	82	2015-2018	PC	408170	ex-smoker	2	1	1	2	0	0	0	0
male	82	2015-2018	PC	408170	ex-smoker	2	1	1	2	0	0	0	0
male	70	2015-2018	PC	408170	non-smoker	2	1	1	2	1	0	0	0
male	70	2015-2018	PC	408170	non-smoker	2	1	1	2	1	0	0	0
male	60	2015-2018	PC	408170	smoker	2	1	0	0	0	2	0	0
male	63	2015-2018	PC	408170	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2018	PC	408170	ex-smoker	2	1	0	0	0	NA	1	0
female	73	2015-2018	PC	408170	non-smoker	2	1	0	0	1	0	0	0
female	67	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	0	0
female	67	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	0	0
male	66	2015-2018	PC	408170	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2018	PC	408170	smoker	2	1	1	1	0	0	0	0
male	52	2015-2018	PC	408170	smoker	2	1	0	0	1	0	0	1
male	68	2015-2018	PC	408170	non-smoker	2	1	0	0	0	0	0	0
male	83	2015-2018	CTR	408170	ex-smoker	2	1	0	0	NA	0	0	0
male	57	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
male	57	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
female	70	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	1	0	1
male	54	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
female	72	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	76	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	1	2	0	0
male	67	2015-2018	CTR	408170	non-smoker	2	1	1	2	0	0	0	0
male	67	2015-2018	CTR	408170	non-smoker	2	1	1	2	0	0	0	0
male	82	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	0	0	0
female	64	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	1
male	84	2015-2018	CTR	408170	ex-smoker	2	1	1	2	1	0	0	0
male	61	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	53	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
male	57	2015-2018	CTR	408170	non-smoker	2	1	0	0	1	0	0	1
male	38	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
female	81	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	1
female	65	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
male	61	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	0	0	0
male	59	2015-2018	CTR	408170	ex-smoker	2	1	0	0	1	0	0	0
male	56	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	1
male	63	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	79	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
female	62	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	1	2	1	0
male	54	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
female	58	2015-2018	Pancreatitis	408170	smoker	2	1	1	1	0	2	0	1
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
male	67	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
male	76	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
female	72	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	1	2	0	0
male	78	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	60	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	1
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	1	1	2	0	1
male	64	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	1	1	2	0	1
male	45	2015-2018	Pancreatitis	408170	ex-smoker	2	1	0	0	0	2	0	1
female	83	2015-2018	Pancreatitis	408170	smoker	2	0	1	2	0	2	0	0
female	71	2015-2018	Pancreatitis	408170	non-smoker	2	0	0	0	0	2	1	0
male	64	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	61	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	55	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	62	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
female	55	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	1	2	0	0
female	78	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
female	78	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
female	67	2015-2018	PC	408170	smoker	8	0	0	0	0	0	1	1
female	74	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
female	74	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	85	2015-2018	PC	408170	ex-smoker	8	0	0	0	0	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	0	1	1	1	0	0	1
female	68	2015-2018	PC	408170	non-smoker	8	1	1	1	0	0	0	0
female	81	2015-2018	PC	408170	non-smoker	8	1	1	1	1	0	0	0
male	86	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	1	0	0	0	0	0	1
male	85	2015-2018	PC	408170	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	1

female	84	2015-2018	PC	408170	non-smoker	8	1	1	1	1	0	0	1
male	74	2015-2018	PC	408170	non-smoker	8	1	0	0	1	0	0	1
male	88	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	1
female	79	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	1
female	79	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	1
male	80	2015-2018	PC	408170	non-smoker	8	1	1	2	0	0	0	1
male	49	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	1	1
male	79	2015-2018	PC	408170	smoker	8	1	0	0	0	0	0	0
female	80	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	86	2015-2018	PC	408170	NA	8	1	0	0	1	0	0	0
male	86	2015-2018	PC	408170	NA	8	1	0	0	1	0	0	0
male	70	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	PC	408170	non-smoker	8	1	0	0	1	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	1	0	0	0	0	0	0
male	67	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
male	69	2015-2018	PC	408170	ex-smoker	8	1	1	2	1	0	0	0
female	75	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
female	79	2015-2018	PC	408170	non-smoker	8	0	0	0	1	0	0	0
female	74	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	62	2015-2018	PC	408170	ex-smoker	8	1	1	2	0	1	0	1
male	83	2015-2018	PC	408170	ex-smoker	8	1	1	2	0	0	0	0
female	65	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
male	56	2015-2018	PC	408170	ex-smoker	8	1	0	0	1	0	0	1
male	78	2015-2018	PC	408170	ex-smoker	8	1	0	0	1	0	0	0
male	45	2015-2018	PC	408170	smoker	8	1	0	0	1	0	0	1
male	81	2015-2018	PC	408170	non-smoker	8	1	1	2	1	0	0	0
male	64	2015-2018	PC	408170	smoker	8	1	1	1	0	0	0	0
female	88	2015-2018	CTR	408170	non-smoker	8	1	0	0	NA	0	0	0
female	80	2015-2018	CTR	408170	non-smoker	8	0	1	2	1	0	1	1
male	88	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
female	79	2015-2018	CTR	408170	non-smoker	8	1	0	0	1	0	0	0
female	59	2015-2018	CTR	408170	non-smoker	8	0	0	0	1	0	0	0
male	91	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	1
female	62	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	0
male	81	2015-2018	CTR	408170	ex-smoker	8	1	1	2	0	0	0	0
male	81	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	1
female	76	2015-2018	CTR	408170	non-smoker	8	0	0	0	0	0	0	0
male	71	2015-2018	CTR	408170	non-smoker	8	1	0	0	1	0	0	0
male	93	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	1	0
female	85	2015-2018	CTR	408170	smoker	8	0	0	0	0	0	0	0
male	72	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	0	0
male	49	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	1
female	87	2015-2018	CTR	408170	non-smoker	8	0	1	2	1	0	0	0
male	87	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	78	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	0	0
male	78	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	0	0
female	88	2015-2018	CTR	408170	non-smoker	8	0	0	0	0	0	0	0
female	69	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	73	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	77	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	CTR	408170	non-smoker	8	0	0	0	0	0	0	0
female	89	2015-2018	CTR	408170	non-smoker	8	1	NA	NA	0	0	1	0
male	69	2015-2018	CTR	408170	ex-smoker	8	1	0	0	1	0	0	1
female	58	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	59	2015-2018	CTR	408170	ex-smoker	8	0	0	0	0	0	0	0
male	71	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	1	0
female	77	2015-2018	Pancreatitis	408170	non-smoker	8	1	0	0	0	2	0	1
female	51	2015-2018	Pancreatitis	408170	ex-smoker	8	1	0	0	0	2	0	1
female	56	2015-2018	Pancreatitis	408170	non-smoker	8	1	0	0	0	2	0	1
male	74	2015-2018	Pancreatitis	408170	ex-smoker	8	1	0	0	1	2	0	0
male	54	2015-2018	Pancreatitis	408170	non-smoker	8	1	1	2	0	2	0	0
male	68	2015-2018	Pancreatitis	408170	smoker	8	0	1	2	1	2	0	0
male	79	2015-2018	PC	1679718	smoker	2	0	0	0	0	0	0	0
male	62	2015-2018	PC	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	69	2015-2018	PC	1679718	smoker	2	0	0	0	0	0	0	1
male	54	2015-2018	PC	1679718	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	PC	1679718	non-smoker	2	1	0	0	NA	0	0	0
male	68	2015-2018	PC	1679718	ex-smoker	2	1	1	1	0	0	0	0
male	71	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	0	0
male	84	2015-2018	PC	1679718	non-smoker	2	1	1	1	0	0	0	0
female	69	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	1	1
male	66	2015-2018	PC	1679718	smoker	2	1	0	0	0	0	0	1
male	82	2015-2018	PC	1679718	ex-smoker	2	1	1	2	0	0	0	0
male	70	2015-2018	PC	1679718	non-smoker	2	1	1	2	1	0	0	0
male	60	2015-2018	PC	1679718	smoker	2	1	0	0	0	2	0	0
male	63	2015-2018	PC	1679718	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2018	PC	1679718	ex-smoker	2	1	0	0	0	NA	1	0
female	73	2015-2018	PC	1679718	non-smoker	2	1	0	0	1	0	0	0
female	67	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	0	0
male	66	2015-2018	PC	1679718	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2018	PC	1679718	smoker	2	1	1	1	0	0	0	0
male	52	2015-2018	PC	1679718	smoker	2	1	0	0	1	0	0	1
male	68	2015-2018	PC	1679718	non-smoker	2	1	0	0	0	0	0	0
male	83	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	NA	0	0	0
male	57	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
female	70	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	1	0	1
male	54	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
female	72	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	76	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	1	2	0	0
male	67	2015-2018	CTR	1679718	non-smoker	2	1	1	2	0	0	0	0

male	82	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	0	0	0
female	64	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	1
male	84	2015-2018	CTR	1679718	ex-smoker	2	1	1	2	1	0	0	0
male	61	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	53	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
male	57	2015-2018	CTR	1679718	non-smoker	2	1	0	0	1	0	0	1
male	38	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	81	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	1
female	65	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
male	61	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	0	0	0
male	59	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	1	0	0	0
male	56	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	1
male	63	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	79	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	54	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	0	2	0	0
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	0	2	0	0
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	1	2	0	0
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	1	1	2	0	1
female	55	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	1	2	0	0
female	78	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
female	67	2015-2018	PC	1679718	smoker	8	0	0	0	0	0	1	1
female	74	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	85	2015-2018	PC	1679718	ex-smoker	8	0	0	0	0	0	0	0
female	71	2015-2018	PC	1679718	non-smoker	8	0	1	1	1	0	0	1
female	68	2015-2018	PC	1679718	non-smoker	8	1	1	1	0	0	0	0
female	81	2015-2018	PC	1679718	ex-smoker	8	0	1	2	1	0	0	0
female	81	2015-2018	PC	1679718	non-smoker	8	1	1	1	1	0	0	0
male	86	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	71	2015-2018	PC	1679718	non-smoker	8	1	0	0	0	0	0	1
male	85	2015-2018	PC	1679718	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	78	2015-2018	PC	1679718	non-smoker	8	0	0	0	1	0	0	0
female	84	2015-2018	PC	1679718	non-smoker	8	1	1	1	1	0	0	1
male	74	2015-2018	PC	1679718	non-smoker	8	1	0	0	1	0	0	1
male	88	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	79	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	1
male	80	2015-2018	PC	1679718	non-smoker	8	1	1	2	0	0	0	1
male	49	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	1	1
female	80	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	81	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	86	2015-2018	PC	1679718	NA	8	1	0	0	1	0	0	0
female	88	2015-2018	CTR	1679718	non-smoker	8	1	0	0	NA	0	0	0
female	68	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	80	2015-2018	CTR	1679718	non-smoker	8	0	1	2	1	0	1	1
male	88	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	79	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
female	59	2015-2018	CTR	1679718	non-smoker	8	0	0	0	1	0	0	0
female	77	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
female	84	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	84	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
male	91	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	1
female	62	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	0
female	62	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	0
male	81	2015-2018	CTR	1679718	ex-smoker	8	1	1	2	0	0	0	0
male	81	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	76	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	78	2015-2018	CTR	1679718	non-smoker	8	0	1	2	0	0	0	1
male	71	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
male	93	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	1	0
female	85	2015-2018	CTR	1679718	smoker	8	0	0	0	0	0	0	0
male	72	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	0	0
male	49	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	1
female	78	2015-2018	CTR	1679718	smoker	8	1	NA	0	0	0	0	0
female	87	2015-2018	CTR	1679718	non-smoker	8	0	1	2	1	0	0	0
male	87	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	87	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	78	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	0	0
female	77	2015-2018	Pancreatitis	1679718	non-smoker	8	1	0	0	0	2	0	1
male	74	2015-2018	Pancreatitis	1679718	ex-smoker	8	1	0	0	1	2	0	0
male	54	2015-2018	Pancreatitis	1679718	non-smoker	8	1	1	2	0	2	0	0
female	68	2015-2017	PC	646099	smoker	2	0	0	0	0	0	0	1
male	54	2015-2017	PC	646099	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
male	71	2015-2017	PC	646099	non-smoker	2	0	0	0	0	0	0	0
male	60	2015-2017	PC	646099	smoker	2	1	0	0	0	2	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2017	PC	646099	ex-smoker	2	1	0	0	0	0	1	0
male	45	2015-2017	PC	646099	ex-smoker	2	1	0	0	0	0	1	0
female	73	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
male	66	2015-2017	PC	646099	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2017	PC	646099	non-smoker	2	1	0	0	0	0	0	0
male	79	2015-2017	Pancreatitis	646099	ex-smoker	2	1	1	2	0	2	0	0
male	54	2015-2017	Pancreatitis	646099	NA	2	1	0	0	0	1	0	0
male	54	2015-2017	Pancreatitis	646099	NA	2	1	0	0	0	1	0	0

male	79	2015-2018	PC	408170	smoker	2	0	0	0	0	0	0	0
male	62	2015-2018	PC	408170	ex-smoker	2	1	0	0	0	0	0	0
female	69	2015-2018	PC	408170	smoker	2	0	0	0	0	0	0	1
male	54	2015-2018	PC	408170	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	PC	408170	non-smoker	2	1	0	0	NA	0	0	0
male	68	2015-2018	PC	408170	ex-smoker	2	1	1	1	0	0	0	0
male	71	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	0	0
male	84	2015-2018	PC	408170	non-smoker	2	1	1	1	0	0	0	0
female	69	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	1	1
male	66	2015-2018	PC	408170	smoker	2	1	0	0	0	0	0	1
male	82	2015-2018	PC	408170	ex-smoker	2	1	1	2	0	0	0	0
male	70	2015-2018	PC	408170	non-smoker	2	1	1	2	1	0	0	0
male	60	2015-2018	PC	408170	smoker	2	1	0	0	0	2	0	0
male	63	2015-2018	PC	408170	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2018	PC	408170	ex-smoker	2	1	0	0	0	NA	1	0
female	73	2015-2018	PC	408170	non-smoker	2	1	0	0	1	0	0	0
female	67	2015-2018	PC	408170	non-smoker	2	0	0	0	0	0	0	0
male	66	2015-2018	PC	408170	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2018	PC	408170	smoker	2	1	1	1	0	0	0	0
male	52	2015-2018	PC	408170	smoker	2	1	0	0	1	0	0	1
male	68	2015-2018	PC	408170	non-smoker	2	1	0	0	0	0	0	0
male	83	2015-2018	CTR	408170	ex-smoker	2	1	0	0	NA	0	0	0
male	57	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
female	70	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	1	0	1
male	54	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
female	72	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	76	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	1	2	0	0
male	67	2015-2018	CTR	408170	non-smoker	2	1	1	2	0	0	0	0
male	82	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	0	0	0
female	64	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	1
male	84	2015-2018	CTR	408170	ex-smoker	2	1	1	2	1	0	0	0
male	61	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	53	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
male	57	2015-2018	CTR	408170	non-smoker	2	1	0	0	1	0	0	1
male	38	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	CTR	408170	ex-smoker	2	1	0	0	0	0	0	0
female	81	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	1
female	65	2015-2018	CTR	408170	non-smoker	2	1	0	0	0	0	0	0
male	61	2015-2018	CTR	408170	non-smoker	2	0	0	0	0	0	0	0
male	59	2015-2018	CTR	408170	ex-smoker	2	1	0	0	1	0	0	0
male	56	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	1
male	63	2015-2018	CTR	408170	smoker	2	1	0	0	0	0	0	0
male	79	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
female	62	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	1	2	1	0
male	54	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
male	67	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	0	2	0	0
male	76	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
female	72	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	1	2	0	0
male	78	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	0
male	60	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	2	0	2	0	1
male	58	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	1	1	2	0	1
male	64	2015-2018	Pancreatitis	408170	ex-smoker	2	1	1	1	1	2	0	1
female	83	2015-2018	Pancreatitis	408170	smoker	2	0	1	2	0	2	0	0
female	71	2015-2018	Pancreatitis	408170	non-smoker	2	0	0	0	0	2	1	0
male	64	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	61	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
male	62	2015-2018	Pancreatitis	408170	smoker	2	1	1	2	0	2	0	0
female	55	2015-2018	Pancreatitis	408170	smoker	2	1	0	0	1	2	0	0
female	78	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
female	67	2015-2018	PC	408170	smoker	8	0	0	0	0	0	1	1
female	74	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	85	2015-2018	PC	408170	ex-smoker	8	0	0	0	0	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	0	1	1	1	0	0	1
female	68	2015-2018	PC	408170	non-smoker	8	1	1	1	0	0	0	0
female	81	2015-2018	PC	408170	non-smoker	8	1	1	1	1	0	0	0
male	86	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	1	0	0	0	0	0	1
male	85	2015-2018	PC	408170	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	1
female	84	2015-2018	PC	408170	non-smoker	8	1	1	1	1	0	0	1
male	74	2015-2018	PC	408170	non-smoker	8	1	0	0	1	0	0	1
male	88	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	1
female	79	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	1
male	80	2015-2018	PC	408170	non-smoker	8	1	1	2	0	0	0	1
male	49	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	1	1
male	79	2015-2018	PC	408170	smoker	8	1	0	0	0	0	0	0
female	80	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	81	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	81	2015-2018	PC	408170	non-smoker	8	0	0	0	0	0	0	0
male	86	2015-2018	PC	408170	NA	8	1	0	0	1	0	0	0
male	70	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	PC	408170	non-smoker	8	1	0	0	1	0	0	0
female	71	2015-2018	PC	408170	non-smoker	8	1	0	0	0	0	0	0
female	65	2015-2018	PC	408170	ex-smoker	8	1	0	0	0	0	0	0

male	56	2015-2018	PC	408170	ex-smoker	8	1	0	0	1	0	0	1
male	78	2015-2018	PC	408170	ex-smoker	8	1	0	0	1	0	0	0
male	45	2015-2018	PC	408170	smoker	8	1	0	0	1	0	0	1
male	81	2015-2018	PC	408170	non-smoker	8	1	1	2	1	0	0	0
male	64	2015-2018	PC	408170	smoker	8	1	1	1	0	0	0	0
female	88	2015-2018	CTR	408170	non-smoker	8	1	0	0	NA	0	0	0
female	80	2015-2018	CTR	408170	non-smoker	8	0	1	2	1	0	1	1
male	88	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
female	79	2015-2018	CTR	408170	non-smoker	8	1	0	0	1	0	0	0
female	59	2015-2018	CTR	408170	non-smoker	8	0	0	0	1	0	0	0
male	91	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	1
female	62	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	0
male	81	2015-2018	CTR	408170	ex-smoker	8	1	1	2	0	0	0	0
male	81	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	1
female	76	2015-2018	CTR	408170	non-smoker	8	0	0	0	0	0	0	0
male	71	2015-2018	CTR	408170	non-smoker	8	1	0	0	1	0	0	0
male	93	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	1	0
female	85	2015-2018	CTR	408170	smoker	8	0	0	0	0	0	0	0
male	72	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	0	0
male	49	2015-2018	CTR	408170	non-smoker	8	1	0	0	0	0	0	1
female	87	2015-2018	CTR	408170	non-smoker	8	0	1	2	1	0	0	0
male	87	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	78	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	0	0
female	69	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	CTR	408170	non-smoker	8	0	0	0	0	0	0	0
male	69	2015-2018	CTR	408170	ex-smoker	8	1	0	0	1	0	0	1
female	58	2015-2018	CTR	408170	ex-smoker	8	1	0	0	0	0	0	0
male	59	2015-2018	CTR	408170	ex-smoker	8	0	0	0	0	0	0	0
male	71	2015-2018	CTR	408170	smoker	8	1	0	0	1	0	1	0
female	77	2015-2018	Pancreatitis	408170	non-smoker	8	1	0	0	0	2	0	1
male	74	2015-2018	Pancreatitis	408170	ex-smoker	8	1	0	0	1	2	0	0
male	54	2015-2018	Pancreatitis	408170	non-smoker	8	1	1	2	0	2	0	0
male	79	2015-2018	PC	1679718	smoker	2	0	0	0	0	0	0	0
male	62	2015-2018	PC	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	69	2015-2018	PC	1679718	smoker	2	0	0	0	0	0	0	1
male	54	2015-2018	PC	1679718	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	PC	1679718	non-smoker	2	1	0	0	NA	0	0	0
male	68	2015-2018	PC	1679718	ex-smoker	2	1	1	1	0	0	0	0
male	71	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	0	0
male	84	2015-2018	PC	1679718	non-smoker	2	1	1	1	0	0	0	0
female	69	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	1	1
male	66	2015-2018	PC	1679718	smoker	2	1	0	0	0	0	0	1
male	82	2015-2018	PC	1679718	ex-smoker	2	1	1	2	0	0	0	0
male	70	2015-2018	PC	1679718	non-smoker	2	1	1	2	1	0	0	0
male	60	2015-2018	PC	1679718	smoker	2	1	0	0	0	2	0	0
male	63	2015-2018	PC	1679718	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2018	PC	1679718	ex-smoker	2	1	0	0	0	NA	1	0
female	73	2015-2018	PC	1679718	non-smoker	2	1	0	0	1	0	0	0
female	67	2015-2018	PC	1679718	non-smoker	2	0	0	0	0	0	0	0
male	66	2015-2018	PC	1679718	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2018	PC	1679718	smoker	2	1	1	1	0	0	0	0
male	52	2015-2018	PC	1679718	smoker	2	1	0	0	1	0	0	1
male	68	2015-2018	PC	1679718	non-smoker	2	1	0	0	0	0	0	0
male	83	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	NA	0	0	0
male	57	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
female	70	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	1	0	1
male	54	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
female	72	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	76	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	1	2	0	0
male	67	2015-2018	CTR	1679718	non-smoker	2	1	1	2	0	0	0	0
male	82	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	0	0	0
female	64	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	1
male	84	2015-2018	CTR	1679718	ex-smoker	2	1	1	2	1	0	0	0
male	61	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	53	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
male	57	2015-2018	CTR	1679718	non-smoker	2	1	0	0	1	0	0	1
male	38	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	68	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	0	0	0	0
female	81	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	1
female	65	2015-2018	CTR	1679718	non-smoker	2	1	0	0	0	0	0	0
male	61	2015-2018	CTR	1679718	non-smoker	2	0	0	0	0	0	0	0
male	59	2015-2018	CTR	1679718	ex-smoker	2	1	0	0	1	0	0	0
male	56	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	63	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	1
male	63	2015-2018	CTR	1679718	smoker	2	1	0	0	0	0	0	0
male	79	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
female	62	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	1	2	1	0
male	54	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	0	2	0	0
female	58	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	1
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	0	2	0	0
male	67	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	0	2	0	0
male	76	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	2	0	0
female	72	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	2	0	0
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	1	2	0	0
male	78	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	2	0	0
male	60	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	2	0	1	0	1
male	58	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	64	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	1	1	1	2	0	1

male	45	2015-2018	Pancreatitis	1679718	ex-smoker	2	1	0	0	0	2	0	1
female	83	2015-2018	Pancreatitis	1679718	smoker	2	0	1	2	0	2	0	0
female	71	2015-2018	Pancreatitis	1679718	non-smoker	2	0	0	0	0	2	1	0
male	64	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	61	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	55	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
male	62	2015-2018	Pancreatitis	1679718	smoker	2	1	1	2	0	2	0	0
female	55	2015-2018	Pancreatitis	1679718	smoker	2	1	0	0	1	2	0	0
female	78	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
female	67	2015-2018	PC	1679718	smoker	8	0	0	0	0	0	1	1
female	74	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	85	2015-2018	PC	1679718	ex-smoker	8	0	0	0	0	0	0	0
female	71	2015-2018	PC	1679718	non-smoker	8	0	1	1	1	0	0	1
female	68	2015-2018	PC	1679718	non-smoker	8	1	1	1	0	0	0	0
female	81	2015-2018	PC	1679718	ex-smoker	8	0	1	2	1	0	0	0
female	81	2015-2018	PC	1679718	non-smoker	8	1	1	1	1	0	0	0
male	86	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	71	2015-2018	PC	1679718	non-smoker	8	1	0	0	0	0	0	1
male	85	2015-2018	PC	1679718	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	78	2015-2018	PC	1679718	non-smoker	8	0	0	0	1	0	0	0
female	84	2015-2018	PC	1679718	non-smoker	8	1	1	1	1	0	0	1
male	74	2015-2018	PC	1679718	non-smoker	8	1	0	0	1	0	0	1
male	88	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	79	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	1
male	80	2015-2018	PC	1679718	non-smoker	8	1	1	2	0	0	0	1
male	49	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	1	1
male	79	2015-2018	PC	1679718	smoker	8	1	0	0	0	0	0	0
female	80	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	81	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	86	2015-2018	PC	1679718	NA	8	1	0	0	1	0	0	0
male	70	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	PC	1679718	non-smoker	8	1	0	0	1	0	0	0
female	71	2015-2018	PC	1679718	non-smoker	8	1	0	0	0	0	0	0
male	67	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	69	2015-2018	PC	1679718	ex-smoker	8	1	1	2	1	0	0	0
female	75	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
female	79	2015-2018	PC	1679718	non-smoker	8	0	0	0	1	0	0	0
female	74	2015-2018	PC	1679718	non-smoker	8	0	0	0	0	0	0	0
male	62	2015-2018	PC	1679718	ex-smoker	8	1	1	2	0	1	0	1
male	83	2015-2018	PC	1679718	ex-smoker	8	1	1	2	0	0	0	0
female	65	2015-2018	PC	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	56	2015-2018	PC	1679718	ex-smoker	8	1	0	0	1	0	0	1
male	78	2015-2018	PC	1679718	ex-smoker	8	1	0	0	1	0	0	0
male	45	2015-2018	PC	1679718	smoker	8	1	0	0	1	0	0	1
male	81	2015-2018	PC	1679718	non-smoker	8	1	1	2	1	0	0	0
male	64	2015-2018	PC	1679718	smoker	8	1	1	1	0	0	0	0
female	88	2015-2018	CTR	1679718	non-smoker	8	1	0	0	NA	0	0	0
female	68	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	80	2015-2018	CTR	1679718	non-smoker	8	0	1	2	1	0	1	1
male	88	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
female	79	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
female	59	2015-2018	CTR	1679718	non-smoker	8	0	0	0	1	0	0	0
female	77	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
female	84	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	84	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
male	91	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	1
female	62	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	0
female	62	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	0
male	81	2015-2018	CTR	1679718	ex-smoker	8	1	1	2	0	0	0	0
male	81	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	1
female	76	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	78	2015-2018	CTR	1679718	non-smoker	8	0	1	2	0	0	0	1
male	71	2015-2018	CTR	1679718	non-smoker	8	1	0	0	1	0	0	0
male	93	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	1	0
female	85	2015-2018	CTR	1679718	smoker	8	0	0	0	0	0	0	0
male	72	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	0	0
male	49	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	1
female	78	2015-2018	CTR	1679718	smoker	8	1	NA	0	0	0	0	0
female	87	2015-2018	CTR	1679718	non-smoker	8	0	1	2	1	0	0	0
male	87	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	87	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	78	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	0	0
female	88	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	69	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	73	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	77	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	0	0
female	85	2015-2018	CTR	1679718	non-smoker	8	0	0	0	0	0	0	0
female	89	2015-2018	CTR	1679718	non-smoker	8	1	0	0	0	0	1	0
male	69	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	1	0	0	1
female	58	2015-2018	CTR	1679718	ex-smoker	8	1	0	0	0	0	0	0
male	59	2015-2018	CTR	1679718	ex-smoker	8	0	0	0	0	0	0	0
male	71	2015-2018	CTR	1679718	smoker	8	1	0	0	1	0	1	0
female	77	2015-2018	Pancreatitis	1679718	non-smoker	8	1	0	0	0	2	0	1
female	51	2015-2018	Pancreatitis	1679718	ex-smoker	8	1	0	0	0	2	0	1
female	51	2015-2018	Pancreatitis	1679718	ex-smoker	8	1	0	0	0	2	0	1
female	56	2015-2018	Pancreatitis	1679718	non-smoker	8	1	0	0	0	2	0	1
male	74	2015-2018	Pancreatitis	1679718	ex-smoker	8	1	0	0	1	2	0	0
male	54	2015-2018	Pancreatitis	1679718	non-smoker	8	1	1	2	0	2	0	0
male	68	2015-2018	Pancreatitis	1679718	smoker	8	0	1	2	1	2	0	0

male	79	2015-2017	PC	646099	smoker	2	0	0	0	0	0	0	0
male	79	2015-2017	PC	646099	smoker	2	0	0	0	0	0	0	0
female	68	2015-2017	PC	646099	smoker	2	0	0	0	0	0	0	1
male	54	2015-2017	PC	646099	non-smoker	2	1	0	0	0	0	0	0
female	68	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
female	68	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
male	71	2015-2017	PC	646099	non-smoker	2	0	0	0	0	0	0	0
male	84	2015-2017	PC	646099	non-smoker	2	1	1	1	0	0	0	0
male	84	2015-2017	PC	646099	non-smoker	2	1	1	1	0	0	0	0
female	69	2015-2017	PC	646099	non-smoker	2	0	0	0	0	0	1	1
female	69	2015-2017	PC	646099	non-smoker	2	0	0	0	0	0	1	1
male	82	2015-2017	PC	646099	ex-smoker	2	1	1	2	0	0	0	0
male	82	2015-2017	PC	646099	ex-smoker	2	1	1	2	0	0	0	0
male	82	2015-2017	PC	646099	ex-smoker	2	1	1	2	0	0	0	0
male	60	2015-2017	PC	646099	smoker	2	1	0	0	0	2	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	63	2015-2017	PC	646099	ex-smoker	2	1	0	0	1	0	0	0
male	45	2015-2017	PC	646099	ex-smoker	2	1	0	0	0	0	1	0
female	73	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
female	73	2015-2017	PC	646099	non-smoker	2	1	0	0	1	0	0	0
male	66	2015-2017	PC	646099	non-smoker	2	0	1	2	0	0	0	0
male	66	2015-2017	PC	646099	non-smoker	2	0	1	2	0	0	0	0
male	68	2015-2017	PC	646099	non-smoker	2	1	0	0	0	0	0	0
male	68	2015-2017	PC	646099	non-smoker	2	1	0	0	0	0	0	0
male	79	2015-2017	Pancreatitis	646099	ex-smoker	2	1	1	2	0	2	0	0
male	79	2015-2017	Pancreatitis	646099	ex-smoker	2	1	1	2	0	2	0	0
male	54	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	0	1	0	0
male	54	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	0	1	0	0
male	54	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	0	1	0	0
male	58	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	0	0	0	0
male	58	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	0	0	0	0
female	55	2015-2017	Pancreatitis	646099	smoker	2	1	0	0	1	0	0	0
female	78	2015-2017	PC	646099	non-smoker	8	0	0	0	0	0	0	0
female	67	2015-2017	PC	646099	smoker	8	0	0	0	0	0	1	1
female	67	2015-2017	PC	646099	smoker	8	0	0	0	0	0	1	1
female	74	2015-2017	PC	646099	non-smoker	8	0	0	0	0	0	0	0
female	71	2015-2017	PC	646099	non-smoker	8	0	1	1	1	0	0	1
female	71	2015-2017	PC	646099	non-smoker	8	0	1	1	1	0	0	1
female	81	2015-2017	PC	646099	ex-smoker	8	0	1	2	1	0	0	0
female	81	2015-2017	PC	646099	ex-smoker	8	0	1	2	1	0	0	0
male	85	2015-2017	PC	646099	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2017	PC	646099	ex-smoker	8	1	1	2	0	0	0	0
male	85	2015-2017	PC	646099	ex-smoker	8	1	1	2	0	0	0	0
female	78	2015-2017	PC	646099	non-smoker	8	0	0	0	1	0	0	0
female	78	2015-2017	PC	646099	non-smoker	8	0	0	0	1	0	0	0
female	79	2015-2017	PC	646099	non-smoker	8	0	0	0	0	0	0	1
female	79	2015-2017	PC	646099	non-smoker	8	0	0	0	0	0	0	1
female	79	2015-2017	PC	646099	non-smoker	8	0	0	0	0	0	0	1
male	81	2015-2017	PC	646099	non-smoker	8	1	1	2	1	0	0	0

allhburn	allrheum	allhbp	cholesterol	abmedicatior	antibiotic	asparmed	salicylic.ever	racetamol.ev	holmedicatio	cortmed	diabdiet	diabin	diabmed
0	0	1	0	0	1	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	1	1	1	1	0	NA	0	1	1	1
0	0	1	0	1	1	1	1	0	NA	0	1	1	1
1	0	1	1	1	1	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	1	0	NA	0	2	2	1
0	0	1	0	0	0	1	1	0	NA	0	2	2	1
0	0	1	1	0	1	0	0	0	1	0	1	2	1
0	0	1	1	0	1	0	0	0	1	0	1	2	1
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	1	2	1
0	0	1	1	1	0	1	0	0	1	0	1	1	2
1	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	1	1	NA	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	1	0	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	2	1	2
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	1	1	0	0	0	NA	0	1	2	1
0	0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	1	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	1	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	0	1	1	1	0	0	0	0	0	0
1	0	0	1	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	2	2	1
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
1	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
1	0	0	1	1	0	1	0	0	1	1	2	1	2
0	0	1	0	0	1	1	0	1	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	1	1	1
0	0	1	1	1	1	1	0	0	1	0	1	1	1
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	1	0	0	0	0	0	0	0	0	1	2	1
1	0	0	1	1	1	0	0	0	1	0	1	1	2
0	0	1	1	1	1	0	0	0	1	0	1	1	1
1	0	0	1	1	1	0	0	0	0	0	1	2	2
1	0	0	1	1	1	0	0	0	0	0	1	2	2
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	0	1	1	1	1	0	1	1	0	0	0	0
1	0	0	0	1	1	1	0	1	0	0	2	1	1
0	0	0	1	1	0	0	0	0	1	0	1	1	1
0	0	0	0	1	1	1	0	1	NA	0	2	1	2
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	1	0	1	1	1	1	1	NA	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	1	1	1	0	1	1	1	1	1	0	0	0	0
0	1	1	1	NA	1	1	0	1	1	0	0	0	0
0	1	1	1	NA	1	1	0	1	1	0	0	0	0
0	0	1	1	0	1	1	0	1	1	0	0	0	0
1	1	0	1	0	1	0	0	0	0	0	1	2	2
0	0	0	1	0	1	0	0	0	1	0	1	2	1
0	0	1	1	0	NA	0	0	0	1	0	2	2	1
0	0	NA	1	0	0	1	0	1	0	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
1	0	1	0	1	1	0	0	0	NA	0	2	2	1
1	0	1	1	1	0	0	0	0	1	0	0	0	0

1	0	1	0	1	1	1	0	1	0	1	2	1	2
1	0	1	NA	1	1	0	0	0	1	0	0	0	0
0	0	1	1	0	0	1	1	1	1	1	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	0	1	1	1
0	1	0	1	1	0	1	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	1	0	0	0	0	0
NA	0	0	0	0	0	1	1	1	0	0	0	0	0
NA	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	NA	0	0	1	0	1	1	0	0	0	0
0	0	1	1	1	1	1	0	0	1	0	0	0	0
0	0	0	NA	1	1	1	1	0	0	0	0	0	0
0	0	1	0	1	0	0	0	0	1	0	1	2	1
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0	0	0	1	0	0	0
1	0	0	1	0	1	1	0	0	1	0	1	1	1
0	0	0	NA	NA	1	1	0	1	NA	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	1	0	1	0	0	0	1	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	0	1	1	1	1	1	1	0	0	0	0	0
1	0	1	1	0	0	0	0	0	1	0	2	2	1
0	0	0	0	0	1	0	0	0	0	0	1	1	2
0	1	0	0	NA	0	1	0	0	NA	NA	0	0	0
1	0	1	1	0	1	1	0	1	1	1	1	1	2
0	0	1	0	1	1	1	1	1	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	1	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	1	1	0	0	0	0	0
0	1	0	1	0	1	0	0	0	1	0	1	2	2
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	1	1	0	1	0	0	0	0
0	0	1	0	NA	1	0	0	0	NA	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
0	1	0	0	1	1	1	0	0	0	1	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	1	0	1	1	1	0	0	1	2	1
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	0	0	0
0	1	1	0	1	1	1	0	1	1	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	1	1	NA	0	1	0	0	0	1	0	0	0	0
0	0	1	0	0	1	1	NA	NA	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	NA	NA	NA
0	0	0	0	1	1	1	0	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
1	1	1	0	0	0	1	0	0	NA	0	0	0	0
0	1	0	0	1	1	1	0	0	NA	0	0	0	0
1	0	0	NA	1	1	1	NA	NA	0	1	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
1	0	0	0	1	1	1	0	0	0	0	2	1	2
0	0	0	0	1	1	1	1	0	0	0	1	2	1
0	0	1	0	0	1	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	1	1	1	1	0	NA	0	1	1	1
1	0	1	1	1	1	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	1	0	NA	0	2	2	1
0	0	1	1	0	1	0	0	0	1	0	1	2	1
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	1	2	1
0	0	1	1	1	0	1	0	0	1	0	1	1	2
1	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	1	1	NA	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	1	0	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	2	1	2
0	0	0	0	0	0	0	0	0	NA	0	1	2	1

0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	1	1	0	0	0	NA	0	1	2	1
0	0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	1	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	1	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	0	1	1	1	0	0	0	0	0	0
1	0	0	1	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	2	2	1
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	1	0	1	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	1	1	1	1	0	0	0	1	0	1	1	1
1	0	0	1	1	1	0	0	0	0	0	1	2	2
0	0	1	0	1	1	1	1	1	NA	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	1	1	1	0	1	1	1	1	1	0	0	0	0
0	1	1	1	NA	1	1	0	1	1	0	0	0	0
0	0	1	1	0	1	1	0	1	1	0	0	0	0
1	1	0	1	0	1	0	0	0	0	0	1	2	2
0	0	0	1	0	1	0	0	0	1	0	1	2	1
0	NA	1	1	0	1	1	0	0	1	0	1	1	1
0	0	1	1	0	NA	0	0	0	1	0	2	2	1
0	0	NA	1	0	0	1	0	1	0	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
1	0	1	0	1	1	0	0	0	NA	0	2	2	1
1	0	1	1	1	0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	0	1	0	1	2	1	2
1	0	1	NA	1	1	0	0	0	1	0	0	0	0
0	0	1	1	0	0	1	1	1	1	1	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	0	1	1	1
0	1	0	1	1	0	1	0	1	0	1	0	0	0
0	0	1	0	1	1	1	0	1	0	0	0	0	0
0	0	0	1	0	1	0	0	0	1	0	0	0	0
NA	0	0	0	0	0	1	1	1	0	0	0	0	0
0	1	0	0	NA	0	1	0	0	NA	NA	0	0	0
0	1	1	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	1	0	1	1	0	1	1	1	1	1	2
0	0	1	0	1	1	1	1	1	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	1	0	0	0
0	0	1	0	0	0	1	0	1	NA	1	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	1	1	0	0	0	0	0
0	1	1	0	1	0	1	1	1	0	0	0	0	0
0	1	0	1	0	1	0	0	0	1	0	1	2	2
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	1	1	0	1	0	0	0	0
0	0	1	1	1	1	1	1	1	0	NA	1	1	1
0	0	1	0	NA	1	0	0	0	NA	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
0	1	0	0	1	1	1	0	0	0	1	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	NA	NA	0	0	0	0	0
0	0	1	0	1	0	1	1	1	0	0	1	2	1
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	0	0	0
1	1	1	0	0	0	1	0	0	NA	0	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
1	0	0	0	1	1	1	0	0	0	0	2	1	2
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	1	2	1
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	1	0	0	2	2	1
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0

0	0	1	0	0	1	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	1	1	1	1	0	NA	0	1	1	1
1	0	1	1	1	1	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	1	0	NA	0	2	2	1
0	0	1	1	0	1	0	0	0	1	0	1	2	1
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	1	2	1
0	0	1	1	1	0	1	0	0	1	0	1	1	2
1	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	1	1	NA	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	1	0	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	2	1	2
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	1	1	0	0	0	NA	0	1	2	1
0	0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	1	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	1	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	0	1	1	1	0	0	0	0	0	0
1	0	0	1	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	2	2	1
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
1	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	1	0	1	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	0	0	0	1	1	1
0	0	1	1	1	1	1	0	0	1	0	1	1	1
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	1	0	0	0	0	0	0	0	0	1	2	1
1	0	0	1	1	1	0	0	0	1	0	1	1	2
0	0	1	1	1	1	0	0	0	1	0	1	1	1
1	0	0	1	1	1	0	0	0	0	0	1	2	2
1	0	0	1	1	1	0	0	0	0	0	1	2	2
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	0	1	1	1	1	0	1	1	0	0	0	0
1	0	0	0	1	1	1	0	1	0	0	2	1	1
0	0	0	1	1	0	0	0	0	1	0	1	1	1
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	1	0	1	1	1	1	1	NA	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	1	1	1	0	1	1	1	1	1	0	0	0	0
0	1	1	1	NA	1	1	0	1	1	0	0	0	0
0	0	1	1	0	1	1	0	1	1	0	0	0	0
1	1	0	1	0	1	0	0	0	0	0	1	2	2
0	0	0	1	0	1	0	0	0	1	0	1	2	1
0	0	1	1	0	NA	0	0	0	1	0	2	2	1
0	0	NA	1	0	0	1	0	1	0	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
1	0	1	0	1	1	0	0	0	NA	0	2	2	1
1	0	1	1	1	0	0	0	0	1	0	0	0	0
1	0	1	0	1	1	1	0	1	0	1	2	1	2
1	0	1	NA	1	1	0	0	0	1	0	0	0	0
0	0	1	1	0	0	1	1	1	1	1	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	0	1	1	1
0	1	0	1	1	0	1	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	1	0	0	0	0	0
0	0	0	1	0	1	0	0	0	1	0	0	0	0
0	0	0	1	0	1	0	0	0	1	0	0	0	0
NA	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	NA	0	0	1	0	1	1	0	0	0	0
0	0	1	1	1	1	1	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0

1	0	1	0	1	0	1	0	0	0	1	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	0	1	1	1	1	1	1	0	0	0	0	0
1	0	1	1	0	0	0	0	0	1	0	2	2	1
0	0	0	0	0	1	0	0	0	0	0	1	1	2
0	1	0	0	NA	0	1	0	0	NA	NA	0	0	0
1	0	1	1	0	1	1	0	1	1	1	1	1	2
0	0	1	0	1	1	1	1	1	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	1	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	1	1	0	0	0	0	0
0	1	0	1	0	1	0	0	0	1	0	1	2	2
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	1	1	0	1	0	0	0	0
0	0	1	0	NA	1	0	0	0	NA	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
0	1	0	0	1	1	1	0	0	0	1	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	1	0	1	1	1	0	0	1	2	1
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
1	1	1	0	0	0	1	0	0	NA	0	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
1	0	0	0	1	1	1	0	0	0	0	2	1	2
0	0	1	0	0	1	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	1	1	1	1	0	NA	0	1	1	1
1	0	1	1	1	1	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	1	0	NA	0	2	2	1
0	0	1	1	0	1	0	0	0	1	0	1	2	1
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	1	2	1
0	0	1	1	1	0	1	0	0	1	0	1	1	2
1	0	1	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	1	1	NA	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	1	0	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	2	1	2
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	0	1	1	0	0	0	NA	0	1	2	1
0	0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
1	0	0	0	1	1	0	0	0	NA	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	1	0	NA	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	0	1	0	1	1	1	0	0	0	0	0	0
1	0	0	1	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	1	0	0	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	NA	0	0	0	0
0	0	1	0	0	0	1	0	1	NA	0	2	2	1
0	0	1	0	0	1	0	0	0	NA	0	1	1	2
1	0	1	0	1	0	0	0	0	NA	0	1	1	1
0	0	1	0	0	1	0	0	0	NA	0	0	0	0
1	0	0	1	1	0	1	0	0	1	1	2	1	2
0	0	1	0	0	1	1	0	1	NA	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	0	0	0	1	1	1
0	0	1	1	1	1	1	0	0	1	0	1	1	1
0	0	0	0	0	0	0	0	0	NA	0	1	2	1
0	0	1	0	0	0	0	0	0	0	0	1	2	1
1	0	0	1	1	1	0	0	0	1	0	1	1	2
0	0	1	1	1	1	0	0	0	1	0	1	1	1
1	0	0	1	1	1	0	0	0	0	0	1	2	2

0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	0	1	1	1	1	0	1	1	0	0	0	0
1	0	0	0	1	1	1	0	1	0	0	2	1	1
0	0	0	1	1	0	0	0	0	1	0	1	1	1
0	0	0	0	1	1	1	0	1	0	0	2	1	2
0	0	1	0	1	0	0	0	0	0	0	1	1	1
0	0	1	0	1	1	1	1	1	NA	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	1	1	1	0	1	1	1	1	1	0	0	0	0
0	1	1	1	NA	1	1	0	1	1	0	0	0	0
0	0	1	1	0	1	1	0	1	1	0	0	0	0
1	1	0	1	0	1	0	0	0	0	0	1	2	2
0	0	0	1	0	1	0	0	0	1	0	1	2	1
0	NA	1	1	0	1	1	0	0	1	0	1	1	1
0	0	1	1	0	NA	0	0	0	1	0	2	2	1
0	0	NA	1	0	0	1	0	1	0	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
1	0	1	0	1	1	0	0	0	NA	0	2	2	1
1	0	1	1	1	0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	0	1	1	1	0	1	0	1	2	1	2
1	0	1	NA	1	1	0	0	0	1	0	0	0	0
0	0	1	1	0	0	1	1	1	1	1	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	0	1	1	1
0	1	0	1	1	0	1	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	1	0	0	0	0	0
0	0	0	1	0	1	0	0	0	1	0	0	0	0
NA	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	1	0	0	1	0	1	1	0	0	0	0
0	0	1	1	1	1	1	0	0	1	0	0	0	0
0	0	0	0	1	1	1	1	0	0	0	0	0	0
0	0	1	0	1	0	0	0	0	1	0	1	2	1
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0	0	0	1	0	0	0
1	0	0	1	0	1	1	0	0	1	0	1	1	1
0	0	0	0	1	1	1	0	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	1	0	1	0	0	0	1	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	0	1	1	1	1	1	1	0	0	0	0	0
1	0	1	1	0	0	0	0	0	1	0	2	2	1
0	0	0	0	0	1	0	0	0	0	0	1	1	2
0	1	0	0	NA	0	1	0	0	NA	NA	0	0	0
0	1	1	0	0	1	0	0	0	NA	0	0	0	0
1	0	1	1	0	1	1	0	1	1	1	1	1	2
0	0	1	0	1	1	1	1	1	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	1	0	1	0	0	0
0	0	1	0	0	0	1	0	1	NA	1	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	0	0	0	0
0	1	1	0	1	0	1	1	1	0	0	0	0	0
0	1	0	1	0	1	0	0	0	1	0	1	2	2
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	1	1	0	1	0	0	0	0
0	0	1	1	1	1	1	1	0	1	NA	1	1	1
0	0	1	0	NA	1	0	0	0	NA	0	0	0	0
1	0	0	1	0	1	0	0	0	1	0	0	0	0
0	1	0	0	1	1	1	0	0	0	1	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	NA	NA	0	0	0	0	0
0	0	1	0	1	0	1	1	1	0	0	1	2	1
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	0	0	0	0	1	1	1	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	0	0	0
0	1	1	0	1	1	1	0	1	1	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	0	0	1	1	0	1	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0	0	1	0	0	0	0
1	1	1	0	0	0	1	0	0	NA	0	0	0	0
0	1	0	0	1	1	1	0	0	0	0	0	0	0
0	1	0	0	1	1	1	0	0	0	0	0	0	0
1	0	0	0	1	1	1	0	1	0	1	0	0	0
0	0	0	0	1	1	1	0	1	0	0	0	0	0
1	0	0	0	1	1	1	0	0	0	0	2	1	2
0	0	0	0	1	1	1	1	0	0	0	1	2	1

0	0	1	0	0	1	1	0	0	0	0	0	0	0
0	0	1	0	0	1	1	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	0	1	1	0	0	0	0
0	0	1	0	1	1	1	1	0	0	0	1	1	1
0	0	1	0	1	1	1	1	0	0	0	1	1	1
1	0	1	1	1	1	0	0	0	0	0	0	0	0
1	0	1	1	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	1	0	0	0	2	2	1
0	0	1	0	0	0	1	1	0	0	0	2	2	1
0	0	1	0	0	0	1	1	0	0	0	2	2	1
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
0	0	1	1	0	1	0	0	0	1	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	1	2	1
0	0	0	0	0	1	0	0	0	0	0	1	2	1
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	1	0	0	2	2	1
0	0	1	0	0	0	1	0	1	0	0	2	2	1
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	1	1	0	1	0	0	0	0	0
0	0	1	0	0	1	1	0	1	0	0	0	0	0
0	0	1	0	1	1	1	1	1	0	0	0	0	0
1	0	0	1	1	1	0	0	0	1	0	0	0	0
1	1	1	1	0	1	1	1	0	1	0	0	0	0
1	1	1	1	0	1	1	1	0	1	0	0	0	0
0	1	1	1	1	1	1	0	1	1	0	0	0	0
1	1	0	1	0	1	0	0	0	0	0	1	2	2
1	1	0	1	0	1	0	0	0	0	0	1	2	2
0	0	1	1	0	1	1	0	0	1	0	1	1	1
0	0	1	1	0	1	1	0	0	1	0	1	1	1
1	0	1	0	1	1	0	0	0	0	0	2	2	1
1	0	1	0	1	1	0	0	0	0	0	2	2	1
1	0	1	0	1	1	0	0	0	0	0	2	2	1
0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
1	0	1	1	0	0	0	0	0	1	0	2	2	1

ıetformin.eve	probiot	periodontitis	recession	FHPDAC	pack/year	ınctype_patie	nasal	CA19	coded_ca19	PDAC_stage
0	0	1	NA	0	3	0	0	18	-1	2
0	0	0	0	0	1	0	0	133	1	4
0	0	0	1	0	2	0	0	126	1	2
0	0	1	1	0	0	0	1	124	1	2
0	0	1	1	0	0	0	1	124	1	2
0	0	0	0	0	0	0	0	5170	1	2
0	0	1	0	0	3	0	0	NA	0	1
0	0	1	0	0	3	0	0	NA	0	1
0	0	NA	0	0	0	0	0	0	-1	2
2	0	0	0	NA	0	0	0	55	1	2
2	0	0	0	NA	0	0	0	55	1	2
0	0	1	1	0	0	0	0	2572	1	2
0	0	1	1	0	3	0	1	151	1	3
1	0	0	0	0	1	0	0	25	-1	2
1	0	0	0	0	1	0	0	25	-1	2
1	0	0	0	0	0	0	0	629	1	4
1	0	0	0	0	0	0	0	629	1	4
0	0	0	0	1	3	2	0	90	1	2
0	0	0	0	0	3	0	0	326	1	2
0	0	1	1	0	2	NA	1	319	1	2
0	0	1	0	0	0	0	0	143	1	2
0	0	0	0	0	0	0	0	0	-1	3
0	0	0	0	0	0	0	0	0	-1	3
1	0	0	0	0	0	0	0	1049	1	2
0	0	1	0	0	3	0	0	2219	1	4
0	0	0	1	0	1	0	0	449	1	4
0	1	1	1	0	0	0	1	1	-1	1
0	0	NA	NA	0	3	0	0	74	1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	0	0	0	0	0	1	0	1	-1	NA
0	0	1	1	0	0	0	0	4	-1	NA
0	0	1	0	0	2	0	0	1	-1	NA
0	0	0	1	0	3	2	0	NA	0	NA
2	0	NA	0	0	0	0	0	11	-1	NA
2	0	NA	0	0	0	0	0	11	-1	NA
0	0	0	1	0	0	0	0	17	-1	NA
0	0	0	0	1	0	0	0	12	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
1	0	NA	0	0	2	0	0	NA	0	NA
0	0	0	0	0	3	0	1	NA	0	NA
0	0	0	0	0	3	0	0	8	-1	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	1	0	0	9	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
0	0	0	0	0	0	0	1	NA	0	NA
0	0	0	0	0	0	0	0	15	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	0	0	0	1	3	0	0	NA	0	NA
0	0	1	1	0	3	0	0	6	-1	NA
0	0	NA	0	0	2	0	1	NA	0	NA
0	0	0	0	0	3	0	1	0	-1	NA
1	0	0	0	NA	2	NA	0	NA	0	NA
0	0	0	0	0	3	2	0	NA	0	NA
2	0	0	1	0	3	NA	1	NA	0	NA
0	0	1	0	0	3	1	0	NA	0	NA
0	0	1	1	0	2	2	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	0	0	3	NA	0	NA	0	NA
2	0	0	0	0	3	NA	0	NA	0	NA
1	0	1	1	0	2	NA	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	0	NA
0	0	0	1	0	2	1	0	NA	0	NA
2	0	1	1	0	3	2	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA
0	0	0	0	0	1	2	0	NA	0	NA
2	0	0	0	0	2	NA	0	NA	0	NA
0	0	1	0	0	0	NA	0	NA	0	NA
1	0	0	1	0	2	NA	0	NA	0	NA
2	0	0	0	0	2	NA	0	NA	0	NA
0	0	1	0	0	3	2	0	NA	0	NA
1	0	0	0	0	2	NA	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	1	0	0	0	0	1033	1	2
0	0	1	1	0	0	0	0	1033	1	2
0	1	0	0	0	2	0	1	495	1	2
0	0	NA	1	0	0	0	0	4862	1	4
0	0	NA	1	0	0	0	0	4862	1	4
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	1	0	0	0	1	3537	1	2
1	0	0	1	0	0	0	0	72	1	4
1	0	0	1	0	0	0	0	NA	0	1
0	0	0	0	0	1	0	0	NA	0	2
0	0	0	1	0	0	0	0	760	1	3
1	0	0	1	1	3	0	1	19	-1	1
0	0	0	0	0	1	0	0	NA	0	1

0	0	0	0	0	0	0	0	9810	1	3
0	0	0	0	0	0	0	0	348	1	3
0	0	0	0	0	1	0	0	13617	1	4
0	0	0	1	0	0	0	0	419	1	2
0	0	0	1	0	0	0	0	419	1	2
1	0	0	1	0	0	0	1	34	-1	4
0	0	0	0	0	0	0	0	351	1	3
0	0	0	0	0	1	NA	0	NA	0	3
0	0	0	0	0	0	0	0	455	1	4
0	0	1	0	0	1	0	0	NA	0	2
0	0	1	0	0	1	0	0	NA	0	2
0	0	1	1	1	3	NA	0	36	-1	4
0	0	0	1	NA	0	0	NA	0	-1	3
0	0	0	0	0	0	NA	0	5459	1	4
0	0	0	0	NA	3	0	0	17031	1	3
1	0	0	0	NA	2	0	0	192	1	4
0	0	1	1	NA	0	0	0	489	1	4
0	0	0	NA	NA	0	0	0	1505	1	3
0	0	1	0	NA	0	0	0	26511	1	4
1	0	1	1	NA	1	1	1	208	1	3
NA	0	0	0	NA	1	0	0	NA	0	4
0	0	0	0	0	2	NA	0	NA	0	4
0	0	1	1	0	1	NA	0	NA	0	3
0	0	1	1	0	1	NA	0	98	1	4
0	0	0	0	0	1	NA	0	NA	0	4
1	0	0	0	1	0	NA	0	NA	0	3
0	0	0	1	0	3	NA	0	NA	0	4
0	0	0	0	0	0	0	0	1	-1	NA
0	0	0	1	0	0	0	0	30	-1	NA
0	0	0	0	0	3	0	0	NA	0	NA
0	NA	0	0	0	0	0	0	NA	0	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	0	0	0	0	3	0	0	15	-1	NA
0	0	0	0	0	1	0	1	NA	0	NA
0	0	1	1	0	0	0	0	0	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	1	0	0	0	2	0	0	13	-1	NA
0	0	0	0	0	1	0	0	28	-1	NA
0	0	1	0	0	3	0	1	15	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
1	0	1	0	0	0	0	0	NA	0	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	1	0	0	NA	0	NA
0	0	0	0	0	1	0	0	NA	0	NA
0	0	1	1	0	0	0	0	17	-1	NA
0	0	1	1	0	1	NA	0	4	-1	NA
0	0	1	0	0	1	0	0	0	-1	NA
0	0	0	1	0	0	0	0	6	-1	NA
0	0	0	0	0	0	NA	0	13	-1	NA
NA	0	1	0	0	0	0	0	NA	0	NA
0	0	0	1	0	3	NA	0	8	-1	NA
0	1	1	1	0	1	NA	0	NA	0	NA
0	0	0	0	0	3	NA	0	NA	0	NA
0	0	0	0	1	1	NA	0	0	-1	NA
0	0	1	0	0	0	1	0	NA	0	NA
0	0	0	0	1	1	2	0	NA	0	NA
0	0	0	0	1	0	NA	0	NA	0	NA
0	0	1	0	0	1	2	0	NA	0	NA
0	0	1	1	0	0	2	0	NA	0	NA
1	0	0	0	0	2	2	0	NA	0	NA
0	0	1	NA	0	3	0	0	18	-1	2
0	0	0	0	0	1	0	0	133	1	4
0	0	0	1	0	2	0	0	126	1	2
0	0	1	1	0	0	0	1	124	1	2
0	0	0	0	0	0	0	0	5170	1	2
0	0	1	0	0	3	0	0	NA	0	1
0	0	NA	0	0	0	0	0	0	-1	2
2	0	0	0	NA	0	0	0	55	1	2
0	0	1	1	0	0	0	0	2572	1	2
0	0	1	1	0	3	0	1	151	1	3
1	0	0	0	0	1	0	0	25	-1	2
1	0	0	0	0	0	0	0	629	1	4
0	0	0	0	1	3	2	0	90	1	2
0	0	0	0	0	3	0	0	326	1	2
0	0	1	1	0	2	NA	1	319	1	2
0	0	1	0	0	0	0	0	143	1	2
0	0	0	0	0	0	0	0	0	-1	3
1	0	0	0	0	0	0	0	1049	1	2
0	0	1	0	0	3	0	0	2219	1	4
0	0	0	1	0	1	0	0	449	1	4
0	1	1	1	0	0	0	1	1	-1	1
0	0	NA	NA	0	3	0	0	74	1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	0	0	0	0	0	1	0	1	-1	NA
0	0	1	1	0	0	0	0	4	-1	NA
0	0	1	0	0	2	0	0	1	-1	NA
0	0	0	1	0	3	2	0	NA	0	NA
2	0	NA	0	0	0	0	0	11	-1	NA

0	0	0	1	0	0	0	0	17	-1	NA
0	0	0	0	1	0	0	0	12	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
1	0	NA	0	0	2	0	0	NA	0	NA
0	0	0	0	0	3	0	1	NA	0	NA
0	0	0	0	0	3	0	0	8	-1	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	1	0	0	9	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
0	0	0	0	0	0	0	1	NA	0	NA
0	0	0	0	0	0	0	0	15	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	0	0	0	1	3	0	0	NA	0	NA
0	0	1	1	0	3	0	0	6	-1	NA
0	0	NA	0	0	2	0	1	NA	0	NA
0	0	0	0	0	3	0	1	0	-1	NA
1	0	0	0	NA	2	NA	0	NA	0	NA
0	0	0	0	0	3	2	0	NA	0	NA
0	0	1	0	0	3	1	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	0	NA
2	0	1	1	0	3	2	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	1	0	0	0	0	1033	1	2
0	1	0	0	0	2	0	1	495	1	2
0	0	NA	1	0	0	0	0	4862	1	4
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	1	0	0	0	1	3537	1	2
1	0	0	1	0	0	0	0	72	1	4
1	0	0	0	0	1	0	0	82	1	2
1	0	0	1	0	0	0	0	NA	0	1
0	0	0	0	0	1	0	0	NA	0	2
0	0	0	1	0	0	0	0	760	1	3
1	0	0	1	1	3	0	1	19	-1	1
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	0	0	0	0	0	525	1	1
0	0	0	0	0	0	0	0	9810	1	3
0	0	0	0	0	0	0	0	348	1	3
0	0	0	0	0	1	0	0	13617	1	4
0	0	0	1	0	0	0	0	419	1	2
1	0	0	1	0	0	0	1	34	-1	4
0	0	0	0	0	0	0	0	351	1	3
0	0	0	0	0	0	0	0	455	1	4
0	0	0	0	0	0	0	0	25	-1	4
0	0	1	0	0	1	0	0	NA	0	2
0	0	0	0	0	0	0	0	1	-1	NA
0	1	0	1	0	2	0	0	7	-1	NA
0	0	0	1	0	0	0	0	30	-1	NA
0	0	0	0	0	3	0	0	NA	0	NA
0	NA	0	0	0	0	0	0	NA	0	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
0	0	1	1	0	0	0	0	NA	0	NA
0	0	1	1	0	0	0	0	NA	0	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	0	0	0	0	3	0	0	15	-1	NA
0	0	0	0	0	1	0	1	NA	0	NA
0	0	1	1	0	0	0	0	0	-1	NA
1	0	0	NA	0	0	0	0	22	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	1	0	0	0	2	0	0	13	-1	NA
0	0	0	0	0	1	0	0	28	-1	NA
0	0	1	0	0	3	0	1	15	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
0	0	0	0	0	1	NA	0	NA	0	NA
1	0	1	0	0	0	0	0	NA	0	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	1	0	0	NA	0	NA
0	0	1	0	0	0	1	0	NA	0	NA
0	0	1	0	0	1	2	0	NA	0	NA
0	0	1	1	0	0	2	0	NA	0	NA
0	0	0	1	0	2	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	0	1	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	2	NA	NA	NA	NA	NA
0	0	1	1	0	2	NA	NA	NA	NA	NA
0	0	1	0	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	0	NA	NA	NA	NA	NA
0	1	1	1	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	2	NA	NA	NA	NA	NA
0	0	1	0	0	3	NA	NA	NA	NA	NA
0	0	1	0	0	3	NA	NA	NA	NA	NA

0	0	1	NA	0	3	0	0	18	-1	2
0	0	0	0	0	1	0	0	133	1	4
0	0	0	1	0	2	0	0	126	1	2
0	0	1	1	0	0	0	1	124	1	2
0	0	0	0	0	0	0	0	5170	1	2
0	0	1	0	0	3	0	0	NA	0	1
0	0	NA	0	0	0	0	0	0	-1	2
2	0	0	0	NA	0	0	0	55	1	2
0	0	1	1	0	0	0	0	2572	1	2
0	0	1	1	0	3	0	1	151	1	3
1	0	0	0	0	1	0	0	25	-1	2
1	0	0	0	0	0	0	0	629	1	4
0	0	0	0	1	3	2	0	90	1	2
0	0	0	0	0	3	0	0	326	1	2
0	0	1	1	0	2	NA	1	319	1	2
0	0	1	0	0	0	0	0	143	1	2
0	0	0	0	0	0	0	0	0	-1	3
1	0	0	0	0	0	0	0	1049	1	2
0	0	1	0	0	3	0	0	2219	1	4
0	0	0	1	0	1	0	0	449	1	4
0	1	1	1	0	0	0	1	1	-1	1
0	0	NA	NA	0	3	0	0	74	1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	0	0	0	0	0	1	0	1	-1	NA
0	0	1	1	0	0	0	0	4	-1	NA
0	0	1	0	0	2	0	0	1	-1	NA
0	0	0	1	0	3	2	0	NA	0	NA
2	0	NA	0	0	0	0	0	11	-1	NA
0	0	0	1	0	0	0	0	17	-1	NA
0	0	0	0	1	0	0	0	12	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
1	0	NA	0	0	2	0	0	NA	0	NA
0	0	0	0	0	3	0	1	NA	0	NA
0	0	0	0	0	3	0	0	8	-1	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	1	0	0	9	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
0	0	0	0	0	0	0	1	NA	0	NA
0	0	0	0	0	0	0	0	15	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	0	0	0	1	3	0	0	NA	0	NA
0	0	1	1	0	3	0	0	6	-1	NA
0	0	NA	0	0	2	0	1	NA	0	NA
0	0	0	0	0	3	0	1	0	-1	NA
1	0	0	0	NA	2	NA	0	NA	0	NA
0	0	0	0	0	3	2	0	NA	0	NA
2	0	0	1	0	3	NA	1	NA	0	NA
0	0	1	0	0	3	1	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	0	0	3	NA	0	NA	0	NA
2	0	0	0	0	3	NA	0	NA	0	NA
1	0	1	1	0	2	NA	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	0	NA
0	0	0	1	0	2	1	0	NA	0	NA
2	0	1	1	0	3	2	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA
2	0	0	0	0	2	NA	0	NA	0	NA
0	0	1	0	0	0	NA	0	NA	0	NA
1	0	0	1	0	2	NA	0	NA	0	NA
2	0	0	0	0	2	NA	0	NA	0	NA
1	0	0	0	0	2	NA	0	NA	0	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	1	0	0	0	0	1033	1	2
0	1	0	0	0	2	0	1	495	1	2
0	0	NA	1	0	0	0	0	4862	1	4
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	1	0	0	0	1	3537	1	2
1	0	0	1	0	0	0	0	72	1	4
1	0	0	1	0	0	0	0	NA	0	1
0	0	0	0	0	1	0	0	NA	0	2
0	0	0	1	0	0	0	0	760	1	3
1	0	0	1	1	3	0	1	19	-1	1
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	0	0	0	0	0	9810	1	3
0	0	0	0	0	0	0	0	348	1	3
0	0	0	0	0	1	0	0	13617	1	4
0	0	0	1	0	0	0	0	419	1	2
1	0	0	1	0	0	0	1	34	-1	4
0	0	0	0	0	0	0	0	351	1	3
0	0	0	0	0	1	NA	0	NA	0	3
0	0	0	0	0	0	0	0	455	1	4
0	0	0	0	0	0	0	0	NA	NA	NA
0	0	0	0	0	0	0	0	NA	NA	NA
0	0	1	0	0	1	0	0	NA	0	2
0	0	1	1	1	3	NA	0	36	-1	4
0	0	0	1	NA	0	0	NA	0	-1	3
0	0	0	0	0	0	NA	0	5459	1	4
0	0	0	0	0	2	NA	0	NA	0	4

0	0	1	1	0	1	NA	0	NA	0	3
0	0	1	1	0	1	NA	0	98	1	4
0	0	0	0	0	1	NA	0	NA	0	4
1	0	0	0	1	0	NA	0	NA	0	3
0	0	0	1	0	3	NA	0	NA	0	4
0	0	0	0	0	0	0	0	1	-1	NA
0	0	0	1	0	0	0	0	30	-1	NA
0	0	0	0	0	3	0	0	NA	0	NA
0	NA	0	0	0	0	0	0	NA	0	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	0	0	0	0	3	0	0	15	-1	NA
0	0	0	0	0	1	0	1	NA	0	NA
0	0	1	1	0	0	0	0	0	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	1	0	0	0	2	0	0	13	-1	NA
0	0	0	0	0	1	0	0	28	-1	NA
0	0	1	0	0	3	0	1	15	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
1	0	1	0	0	0	0	0	NA	0	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	1	0	0	NA	0	NA
0	0	1	1	0	1	NA	0	4	-1	NA
0	0	0	0	0	0	NA	0	13	-1	NA
0	0	0	1	0	3	NA	0	8	-1	NA
0	1	1	1	0	1	NA	0	NA	0	NA
0	0	0	0	0	3	NA	0	NA	0	NA
0	0	0	0	1	1	NA	0	0	-1	NA
0	0	1	0	0	0	1	0	NA	0	NA
0	0	1	0	0	1	2	0	NA	0	NA
0	0	1	1	0	0	2	0	NA	0	NA
0	0	1	NA	0	3	0	0	18	-1	2
0	0	0	0	0	1	0	0	133	1	4
0	0	0	1	0	2	0	0	126	1	2
0	0	1	1	0	0	0	1	124	1	2
0	0	0	0	0	0	0	0	5170	1	2
0	0	1	0	0	3	0	0	NA	0	1
0	0	NA	0	0	0	0	0	0	-1	2
2	0	0	0	NA	0	0	0	55	1	2
0	0	1	1	0	0	0	0	2572	1	2
0	0	1	1	0	3	0	1	151	1	3
1	0	0	0	0	1	0	0	25	-1	2
1	0	0	0	0	0	0	0	629	1	4
0	0	0	0	1	3	2	0	90	1	2
0	0	0	0	0	3	0	0	326	1	2
0	0	1	1	0	2	NA	1	319	1	2
0	0	1	0	0	0	0	0	143	1	2
0	0	0	0	0	0	0	0	0	-1	3
1	0	0	0	0	0	0	0	1049	1	2
0	0	1	0	0	3	0	0	2219	1	4
0	0	0	1	0	1	0	0	449	1	4
0	1	1	1	0	0	0	1	1	-1	1
0	0	NA	NA	0	3	0	0	74	1	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	0	0	0	0	0	1	0	1	-1	NA
0	0	1	1	0	0	0	0	4	-1	NA
0	0	1	0	0	2	0	0	1	-1	NA
0	0	0	1	0	3	2	0	NA	0	NA
2	0	NA	0	0	0	0	0	11	-1	NA
0	0	0	1	0	0	0	0	17	-1	NA
0	0	0	0	1	0	0	0	12	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
1	0	NA	0	0	2	0	0	NA	0	NA
0	0	0	0	0	3	0	1	NA	0	NA
0	0	0	0	0	3	0	0	8	-1	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	1	0	0	9	-1	NA
0	0	0	0	0	2	0	0	NA	0	NA
0	0	0	0	0	0	0	1	NA	0	NA
0	0	0	0	0	0	0	0	15	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	0	0	0	1	3	0	0	NA	0	NA
0	0	1	1	0	3	0	0	6	-1	NA
0	0	NA	0	0	2	0	1	NA	0	NA
0	0	0	0	0	3	0	1	0	-1	NA
1	0	0	0	NA	2	NA	0	NA	0	NA
0	0	0	0	0	3	2	0	NA	0	NA
2	0	0	1	0	NA	NA	1	NA	NA	NA
0	0	1	0	0	3	1	0	NA	0	NA
0	0	1	1	0	2	NA	0	NA	NA	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	0	0	3	NA	0	NA	NA	NA
2	0	0	0	0	3	NA	0	NA	NA	NA
1	0	1	1	0	2	NA	0	NA	NA	NA
1	0	0	0	0	1	NA	0	NA	0	NA
1	0	0	0	0	1	NA	0	NA	NA	NA
0	0	0	1	0	2	NA	0	NA	NA	NA
2	0	1	1	0	3	2	0	NA	0	NA
0	0	1	NA	0	3	1	0	NA	0	NA

0	0	0	0	0	1	NA	0	NA	NA	NA
2	0	0	0	0	2	NA	0	NA	NA	NA
0	0	1	0	0	0	NA	0	NA	NA	NA
1	0	0	1	0	2	NA	0	NA	NA	NA
2	0	0	0	0	2	NA	0	NA	NA	NA
0	0	1	0	0	3	NA	0	NA	NA	NA
1	0	0	0	0	2	NA	0	NA	NA	NA
0	0	1	1	0	3	0	0	NA	0	NA
0	0	1	1	0	0	0	0	1033	1	2
0	1	0	0	0	2	0	1	495	1	2
0	0	NA	1	0	0	0	0	4862	1	4
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	1	0	0	0	1	3537	1	2
1	0	0	1	0	0	0	0	72	1	4
1	0	0	0	0	1	0	0	82	1	2
1	0	0	1	0	0	0	0	NA	0	1
0	0	0	0	0	1	0	0	NA	0	2
0	0	0	1	0	0	0	0	760	1	3
1	0	0	1	1	3	0	1	19	-1	1
0	0	0	0	0	1	0	0	NA	0	1
0	0	0	0	0	0	0	0	525	1	1
0	0	0	0	0	0	0	0	9810	1	3
0	0	0	0	0	0	0	0	348	1	3
0	0	0	0	0	1	0	0	13617	1	4
0	0	0	1	0	0	0	0	419	1	2
1	0	0	1	0	0	0	1	34	-1	4
0	0	0	0	0	0	0	0	351	1	3
0	0	0	0	0	1	NA	0	NA	NA	NA
0	0	0	0	0	0	0	0	455	1	4
0	0	0	0	0	0	0	0	25	-1	4
0	0	1	0	0	1	0	0	NA	0	2
0	0	1	1	1	3	NA	0	NA	NA	NA
0	0	0	1	0	0	NA	0	NA	NA	NA
0	0	0	0	0	0	NA	0	NA	NA	NA
0	0	0	0	0	3	NA	0	NA	NA	NA
1	0	0	0	1	2	NA	0	NA	NA	NA
0	0	1	1	0	0	NA	0	NA	NA	NA
0	0	0	0	1	0	NA	0	NA	NA	NA
0	0	1	0	0	0	NA	0	NA	NA	NA
1	0	1	1	0	1	NA	1	NA	NA	NA
1	0	0	0	0	1	NA	0	NA	NA	NA
0	0	0	0	0	2	NA	0	NA	NA	NA
0	0	1	1	0	1	NA	0	NA	NA	NA
0	0	1	1	0	1	NA	0	NA	NA	NA
0	0	0	0	0	1	NA	0	NA	NA	NA
1	0	0	0	1	0	NA	0	NA	NA	NA
0	0	0	1	0	3	NA	0	NA	NA	NA
0	0	0	0	0	0	0	0	1	-1	NA
0	1	0	1	0	2	0	0	7	-1	NA
0	0	0	1	0	0	0	0	30	-1	NA
0	0	0	0	0	3	0	0	NA	0	NA
0	NA	0	0	0	0	0	0	NA	0	NA
0	0	0	0	0	0	0	0	5	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
0	0	1	1	0	0	0	0	NA	0	NA
0	0	1	1	0	0	0	0	NA	0	NA
0	0	0	1	0	0	0	1	NA	0	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	1	0	1	0	0	0	0	8	-1	NA
0	0	0	0	0	3	0	0	15	-1	NA
0	0	0	0	0	1	0	1	NA	0	NA
0	0	1	1	0	0	0	0	0	-1	NA
1	0	0	NA	0	0	0	0	22	-1	NA
0	0	0	0	0	0	0	0	6	-1	NA
0	1	0	0	0	2	0	0	13	-1	NA
0	0	0	0	0	1	0	0	28	-1	NA
0	0	1	0	0	3	0	1	15	-1	NA
0	0	0	0	0	0	0	0	7	-1	NA
0	0	0	0	0	1	NA	0	NA	0	NA
1	0	1	0	0	0	0	0	NA	0	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	3	0	0	11	-1	NA
0	0	0	0	0	1	0	0	NA	0	NA
0	0	1	1	0	0	NA	0	NA	NA	NA
0	0	1	1	0	1	NA	0	NA	NA	NA
0	0	1	0	0	1	NA	0	NA	NA	NA
0	0	0	1	0	0	NA	0	NA	NA	NA
0	0	0	0	0	0	NA	0	NA	NA	NA
0	0	1	0	0	0	NA	0	NA	NA	NA
0	0	0	1	0	3	NA	0	NA	NA	NA
0	1	1	1	0	1	NA	0	NA	NA	NA
0	0	0	0	0	3	NA	0	NA	NA	NA
0	0	0	0	1	1	NA	0	NA	NA	NA
0	0	1	0	0	0	1	0	NA	0	NA
0	0	0	0	1	1	NA	0	NA	NA	NA
0	0	0	0	1	1	NA	0	NA	NA	NA
0	0	0	0	1	0	NA	0	NA	NA	NA
0	0	1	0	0	1	2	0	NA	0	NA
0	0	1	1	0	0	2	0	NA	0	NA
1	0	0	0	0	2	NA	0	NA	NA	NA

0	0	1	1	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	3	NA	NA	NA	NA	NA
0	0	0	1	0	2	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
2	0	0	0	0	0	NA	NA	NA	NA	NA
2	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	1	NA	NA	NA	NA	NA
1	0	0	0	0	1	NA	NA	NA	NA	NA
1	0	0	0	0	1	NA	NA	NA	NA	NA
0	0	0	0	1	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	0	0	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	2	NA	NA	NA	NA	NA
0	0	1	0	0	0	NA	NA	NA	NA	NA
0	0	1	0	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	0	NA	NA	NA	NA	NA
0	1	1	1	0	0	NA	NA	NA	NA	NA
0	1	1	1	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	2	NA	NA	NA	NA	NA
1	0	0	0	0	2	NA	NA	NA	NA	NA
0	0	1	0	0	3	NA	NA	NA	NA	NA
0	0	1	0	0	3	NA	NA	NA	NA	NA
0	0	1	0	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	3	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
0	1	0	0	0	2	NA	NA	NA	NA	NA
0	1	0	0	0	2	NA	NA	NA	NA	NA
0	0	1	1	0	0	NA	NA	NA	NA	NA
0	0	0	1	0	0	NA	NA	NA	NA	NA
0	0	0	1	0	0	NA	NA	NA	NA	NA
1	0	0	0	0	1	NA	NA	NA	NA	NA
1	0	0	0	0	1	NA	NA	NA	NA	NA
1	0	0	1	1	3	NA	NA	NA	NA	NA
1	0	0	1	1	3	NA	NA	NA	NA	NA
1	0	0	1	1	3	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	0	0	0	NA	NA	NA	NA	NA
0	0	0	1	0	0	NA	NA	NA	NA	NA
0	0	0	1	0	0	NA	NA	NA	NA	NA
0	0	0	1	0	0	NA	NA	NA	NA	NA
1	0	0	0	1	0	NA	NA	NA	NA	NA

Supplementary Table S2

Variable Description	Variable Name	QES Column	Full Definition	Categories
Alcohol consumption status	alcohol_status		Ever drunk alcohol regularly, that is at least once per month for 6 months or more	NA = Missing or Don´t know 0=Never drinker 1=Ever drinker
Alcohol consumption	alc_dd		Drinks/day of total alcohol in lifetime. Weighted average of the alcohol intakes at different ages, with weights equal to the total subject-specific time of investigation Formula: F/(age-20) F= ((mean (beer_st1, beer_s2,..,spirits_st5) * (Min(age_last, age)-20))	**Continuous** **NA = Missing or Don´t know** **0=Never drinker**
Have been diagnosed with diabetes	alldiab	G19A11, G19AIreland11	Subjects report if they have ever been diagnosed with diabetes.	NA=Missing or Don´t Know 0= No 1=Yes
Have been diagnosed with diabetes categorical by time of diagnosis	diabcat	G19A11, G19B11, agec	Subjects that report having been diagnosed with diabetes are categorized by being diagnosed more or less than 2 years before the time of recruitment in the study	NA=Missing or Don´t Know 1 = less than 3years 2 = more or equal to 3 years
BMI at two years prior recruitment >=30	obese	A7-1-1 and A61-1	Subjects that have BMI >=30 two years before study recruitment	NA=Missing or Don't know 0 = BMI <30 1= BMI>=30
Type of pancreatitis	panctype	G20B11	Subjects report if their type of pancreatitis if they have been diagnosed with it. è **Use this variable for analyses** ***Pancreatitis cases forced all into the 'chornic' category***	NA=Missing or Don't know 0= No pancreatitis 1 = Acute 2 = Chronic
Type of pancreatitis	Panctype_patient	G20B11	Subjects report if their type of pancreatitis if they have been diagnosed with it. Variable exactly as reported by the patient	**NA=Missing or Don't know** **0= No pancreatitis** **1 = Acute** **2 = Chronic**
Have had asthma	asthma	G5-1-1	Subjects that report ever having asthma.	NA=Missing or Don't know 0= No 1=Yes
Have had nasal allergies (Rhinitis)	nasal	G11-1-1	Subjects that report having had nasal allergies including hay fever	NA=Missing or Don't know 0= No 1=Yes
Ever been diagnosed with heartburn	allhburn	G42A11, G42AIreland11	Subjects report if they have ever been diagnosed with Heartburn.	NA=Missing or Don't know 0= No 1=Yes
Ever been diagnosed with acid regurgitation	allacid	G42B11, G42BIreland11	Subjects report if they have ever been diagnosed with Acid regurgitation	NA=Missing or Don't know 0= No 1=Yes
Have been diagnosed with Rheumatoid arthritis	allrheum	G2311, G23Ireland11	Subjects report if they have ever been diagnosed with Rheumatoid arthritis	NA=Missing or Don't know 0= No 1=Yes
Ever been diagnosed with High blood pressure	allhbp	G4011, G40Ireland11	Subjects report if they have ever been diagnosed with High blood pressure	NA=Missing or Don't know 0= No 1=Yes
Ever been diagnosed with high blood pressure	cholesterol	G4311	Subjects report if they have ever been diagnosed with High cholesterol	NA=Missing or Don't know 0= No 1=Yes
Have had periodontitis	periodontitis	J7-1-1	Subjects that report, excluding the last two years, to been told by a dentist that they have	NA=Missing or Don't know 1=Yes

			periodontitis	0 = No
Have had receding gums	recession	J6-1-1	Subjects report having receding gums	NA=Missing or Don't know 1=Yes 0 = No
PDAC in a relative	FHPDAC	All K25 variables and all cancer location variables K26	History of PDAC (pancreatic ductal adenocarcinoma) in a relative. Subjects reported if any first degree relative had ever been diagnosed with PDAC. "Yes" was considered if any K25* variables was reported as yes and if location (any k26*variable) was reported to be PDAC. Diagnoses of other cancers, other than PDAC, in first degree relatives was considered as NO FHPDAC	NA=Missing or Don't know 0=no FHPDAC 1=yes FHPDAC
Diabetes control with diet	diabdiet	cdiabtmodifdieta	Subjects reported if their diabetes is controlled with dietary changes	NA= Missing or Don't know 0= Answered No to alldiab 1 = Yes 2 = No
Diabetes control with insulin	diabin	diabetinsulina	Subjects reported if their diabetes is controlled with insulin pump or injections	NA= Missing or Don't know 0= Answered No to alldiab 1 = Yes 2 = No
Diabetes control with medication	diabmed	diabetmedoral	Subjects reported if their diabetes is controlled with oral medication	NA= Missing or Don't know 0= Answered No to alldiab 1 = Yes 2 = No
Metformin	metformin.ever		Subjects report if ever taking metformin regularly, that is 3 months or more during the last five years	**NA= Don´t know** **0 =No diabetes & no oral medication** **1= Metformin use** **2=No metformin use**
Any acid regurgitation/Heartburn medication	abmedication	tratampirosregur	The subject reports at least one medication of this class (regardless of their report on the disease status)	NA= Missing or Don't know 0= No medication 1= Medication
Cholesterol medication	cholmedication	g37ttocolestalto	The subject reports at least one medication of this class (regardless of their report on the disease status)	NA= Missing or Don't know 0= No medication 1= Medication
Aspirin/Paracetamol medication	asparmed	tomadoantiinflamt	Subjects reported if they ever took aspirin or paracetamol or other ainti-inflammatory medication regularly	NA = Don't know 0 = No 1 = Yes
salicylic	salicylic.ever		Subjects report if they ever took aspirin (irrespective of reportin other anti-inflammatory medication)	NA = Don't know 0 = No 1 = Yes
paracetamol	paracetamol.ever		Subjects report if they ever took paracetamol (irrespective of reportin other anti-inflammatory medication)	NA = Don't know 0 = No 1 = Yes
Corticosteroids medication	cortmed	H3-1-1ttocorticoides	Subjects reported if they ever took corticoids regularly	NA = Missing or Don't know 0 = No 1 = Yes
NSAIDs medication	nsaidmed	H2-1-1	Subjects reported if they ever took nsaids regularly *Answer from Sweden was based on variable H2B_1EU, if nsaids reported then a number 1 was given for this variable	**NA = missing or Don't know** **0 = No** **1 = Yes**
Antibiotics	antibiotic	h3attoantibiot	Subjects reported if they ever took antibiotics during the past five years	**NA = Don't know** **0 = No** **1 = Yes**
Pro/prebiotics	probiot	h4attoprobiotiprebiot	Subjects reported if they ever took **prebiotics or probiotics** regularly during the past five years	**NA = Don't know** **0 = No** **1 = Yes**

Supplementary Table S3: DE Cohort Details

sample_alias	instrument_model	replicate	insert_size	read_length	read_count	ronment_mat	timepoint	gender	age_years	ollection_dat	ct_disease_s
MBJT10257157ST	Illumina HiSeq 4000	0	300	150	47393312	[ENVO:0000	0	female	65	2014-2020	PC
MBJT13029530ST	Illumina HiSeq 4000	0	300	150	44500100	[ENVO:0000	0	male	34	2014-2020	CTR
MBJT13966914ST	Illumina HiSeq 4000	0	300	150	55422086	[ENVO:0000	0	male	66	2014-2020	PC
MBJT14741058ST	Illumina HiSeq 4000	0	300	150	54925804	[ENVO:0000	0	male	29	2014-2020	CTR
MBJT18793872ST	Illumina HiSeq 4000	0	300	150	48908442	[ENVO:0000	0	female	66	2014-2020	PC
MBJT19172978ST	Illumina HiSeq 4000	0	300	150	36491564	[ENVO:0000	0	female	54	2014-2020	CTR
MBJT19739988ST	Illumina HiSeq 4000	0	300	150	43913396	[ENVO:0000	0	male	59	2014-2020	PC
MBJT22022613ST	Illumina HiSeq 4000	0	300	150	37301894	[ENVO:0000	0	male	61	2014-2020	CTR
MBJT22320456ST	Illumina HiSeq 4000	0	300	150	39863688	[ENVO:0000	0	male	74	2014-2020	PC
MBJT23133014ST	Illumina HiSeq 4000	0	300	150	44285414	[ENVO:0000	0	female	40	2014-2020	CTR
MBJT24075712ST	Illumina HiSeq 4000	0	300	150	38908806	[ENVO:0000	0	male	65	2014-2020	PC
MBJT24417068ST	Illumina HiSeq 4000	0	300	150	46462326	[ENVO:0000	0	male	49	2014-2020	CTR
MBJT24770375ST	Illumina HiSeq 4000	0	300	150	41886800	[ENVO:0000	0	female	73	2014-2020	PC
MBJT25397146ST	Illumina HiSeq 4000	0	300	150	38837880	[ENVO:0000	0	female	68	2014-2020	CTR
MBJT26681707ST	Illumina HiSeq 4000	0	300	150	39728784	[ENVO:0000	0	female	57	2014-2020	PC
MBJT28436807ST	Illumina HiSeq 4000	0	300	150	43156950	[ENVO:0000	0	male	63	2014-2020	PC
MBJT28723736ST	Illumina HiSeq 4000	0	300	150	34666406	[ENVO:0000	0	female	79	2014-2020	PC
MBJT30331144ST	Illumina HiSeq 4000	0	300	150	31449568	[ENVO:0000	0	female	76	2014-2020	PC
MBJT32951253ST	Illumina HiSeq 4000	0	300	150	42555236	[ENVO:0000	0	female	78	2014-2020	PC
MBJT34036667ST	Illumina HiSeq 4000	0	300	150	41733736	[ENVO:0000	0	male	55	2014-2020	CTR
MBJT34220088ST	Illumina HiSeq 4000	0	300	150	48977086	[ENVO:0000	0	male	80	2014-2020	PC
MBJT35001732ST	Illumina HiSeq 4000	0	300	150	45479874	[ENVO:0000	0	female	40	2014-2020	CTR
MBJT35016775ST	Illumina HiSeq 4000	0	300	150	47763580	[ENVO:0000	0	female	81	2014-2020	PC
MBJT35058600ST	Illumina HiSeq 4000	0	300	150	51795444	[ENVO:0000	0	female	71	2014-2020	PC
MBJT40306752ST	Illumina HiSeq 4000	0	300	150	46477424	[ENVO:0000	0	female	24	2014-2020	CTR
MBJT40435704ST	Illumina HiSeq 4000	0	300	150	45919556	[ENVO:0000	0	male	63	2014-2020	PC
MBJT40701160ST	Illumina HiSeq 4000	0	300	150	50045710	[ENVO:0000	0	female	26	2014-2020	CTR
MBJT40707177ST	Illumina HiSeq 4000	0	300	150	40242120	[ENVO:0000	0	female	82	2014-2020	PC
MBJT41036209ST	Illumina HiSeq 4000	0	300	150	42245120	[ENVO:0000	0	male	67	2014-2020	PC
MBJT41854002ST	Illumina HiSeq 4000	0	300	150	40271702	[ENVO:0000	0	male	46	2014-2020	CTR
MBJT42733650ST	Illumina HiSeq 4000	0	300	150	35444906	[ENVO:0000	0	male	80	2014-2020	PC
MBJT42917972ST	Illumina HiSeq 4000	0	300	150	40122088	[ENVO:0000	0	female	72	2014-2020	CTR
MBJT44556531ST	Illumina HiSeq 4000	0	300	150	53434320	[ENVO:0000	0	female	50	2014-2020	PC
MBJT46290466ST	Illumina HiSeq 4000	0	300	150	37640290	[ENVO:0000	0	female	49	2014-2020	CTR
MBJT47281689ST	Illumina HiSeq 4000	0	300	150	55830262	[ENVO:0000	0	female	76	2014-2020	PC
MBJT47376024ST	Illumina HiSeq 4000	0	300	150	38754652	[ENVO:0000	0	female	66	2014-2020	PC
MBJT47759212ST	Illumina HiSeq 4000	0	300	150	31813116	[ENVO:0000	0	male	70	2014-2020	PC
MBJT47974019ST	Illumina HiSeq 4000	0	300	150	38234074	[ENVO:0000	0	female	81	2014-2020	PC
MBJT54042978ST	Illumina HiSeq 4000	0	300	150	51374756	[ENVO:0000	0	female	50	2014-2020	CTR
MBJT54598736ST	Illumina HiSeq 4000	0	300	150	46583366	[ENVO:0000	0	male	28	2014-2020	CTR
MBJT54773511ST	Illumina HiSeq 4000	0	300	150	45819402	[ENVO:0000	0	male	31	2014-2020	CTR
MBJT55041082ST	Illumina HiSeq 4000	0	300	150	25828972	[ENVO:0000	0	male	80	2014-2020	PC
MBJT55763017ST	Illumina HiSeq 4000	0	300	150	37164202	[ENVO:0000	0	female	73	2014-2020	PC
MBJT56486370ST	Illumina HiSeq 4000	0	300	150	60275548	[ENVO:0000	0	male	87	2014-2020	CTR
MBJT57869938ST	Illumina HiSeq 4000	0	300	150	36431696	[ENVO:0000	0	female	61	2014-2020	PC
MBJT58818096ST	Illumina HiSeq 4000	0	300	150	42617446	[ENVO:0000	0	female	69	2014-2020	PC
MBJT59111766ST	Illumina HiSeq 4000	0	300	150	39629386	[ENVO:0000	0	female	55	2014-2020	CTR
MBJT61614909ST	Illumina HiSeq 4000	0	300	150	32278494	[ENVO:0000	0	female	56	2014-2020	PC
MBJT61989978ST	Illumina HiSeq 4000	0	300	150	44899094	[ENVO:0000	0	male	67	2014-2020	CTR
MBJT63497322ST	Illumina HiSeq 4000	0	300	150	41550048	[ENVO:0000	0	female	65	2014-2020	PC
MBJT64178099ST	Illumina HiSeq 4000	0	300	150	45792268	[ENVO:0000	0	female	28	2014-2020	CTR
MBJT64323881ST	Illumina HiSeq 4000	0	300	150	51879638	[ENVO:0000	0	female	87	2014-2020	PC
MBJT65314632ST	Illumina HiSeq 4000	0	300	150	40100360	[ENVO:0000	0	male	77	2014-2020	PC
MBJT66677231ST	Illumina HiSeq 4000	0	300	150	38271172	[ENVO:0000	0	male	59	2014-2020	CTR
MBJT69789353ST	Illumina HiSeq 4000	0	300	150	37463630	[ENVO:0000	0	female	79	2014-2020	PC
MBJT71206045ST	Illumina HiSeq 4000	0	300	150	37446348	[ENVO:0000	0	male	64	2014-2020	PC
MBJT73212715ST	Illumina HiSeq 4000	0	300	150	29746146	[ENVO:0000	0	male	81	2014-2020	PC
MBJT73621698ST	Illumina HiSeq 4000	0	300	150	46013560	[ENVO:0000	0	male	22	2014-2020	CTR
MBJT75354344ST	Illumina HiSeq 4000	0	300	150	42836122	[ENVO:0000	0	male	84	2014-2020	PC
MBJT75856433ST	Illumina HiSeq 4000	0	300	150	38763576	[ENVO:0000	0	female	60	2014-2020	PC
MBJT76001019ST	Illumina HiSeq 4000	0	300	150	41432142	[ENVO:0000	0	female	36	2014-2020	CTR
MBJT77767153ST	Illumina HiSeq 4000	0	300	150	51551804	[ENVO:0000	0	female	70	2014-2020	CTR
MBJT79123647ST	Illumina HiSeq 4000	0	300	150	40277574	[ENVO:0000	0	female	72	2014-2020	PC
MBJT82870648ST	Illumina HiSeq 4000	0	300	150	47315674	[ENVO:0000	0	male	30	2014-2020	CTR
MBJT83133832ST	Illumina HiSeq 4000	0	300	150	40995200	[ENVO:0000	0	male	67	2014-2020	PC
MBJT83294902ST	Illumina HiSeq 4000	0	300	150	37680998	[ENVO:0000	0	male	64	2014-2020	CTR
MBJT85450199ST	Illumina HiSeq 4000	0	300	150	47792460	[ENVO:0000	0	male	76	2014-2020	PC
MBJT85948313ST	Illumina HiSeq 4000	0	300	150	44611384	[ENVO:0000	0	male	49	2014-2020	CTR
MBJT87587928ST	Illumina HiSeq 4000	0	300	150	43175984	[ENVO:0000	0	female	62	2014-2020	CTR
MBJT89319187ST	Illumina HiSeq 4000	0	300	150	43302384	[ENVO:0000	0	female	40	2014-2020	PC
MBJT90536787ST	Illumina HiSeq 4000	0	300	150	44711476	[ENVO:0000	0	female	64	2014-2020	CTR
MBJT92561737ST	Illumina HiSeq 4000	0	300	150	40739728	[ENVO:0000	0	female	32	2014-2020	CTR
MBJT92636570ST	Illumina HiSeq 4000	0	300	150	36248620	[ENVO:0000	0	male	57	2014-2020	PC
MBJT93071877ST	Illumina HiSeq 4000	0	300	150	45583612	[ENVO:0000	0	female	56	2014-2020	CTR
MBJT94530819ST	Illumina HiSeq 4000	0	300	150	44454590	[ENVO:0000	0	female	84	2014-2020	PC
MBJT97792954ST	Illumina HiSeq 4000	0	300	150	42824760	[ENVO:0000	0	male	68	2014-2020	PC

bmi	smoker	medication	stage	stage_detailed	metastasis (he	Treatment	ıy_of_operati	erapy_after_G	_of_last_foll	date_of follo	Ca_19_9
27	smoker	NA	2	2b	0	1	27.02.20	1	0	May 20	1702
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
23,8	non-smoker	NA	2	2b	0	1	21.02.20	1	0	02.06.20	2
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
29,7	non-smoker	NA	2	2a	0	4	31.01.20	3	0	03.06.20	1172
NA	NA	L-Thyrox	NA	NA	NA	NA	NA	NA	NA	NA	NA
21,47	non-smoker	NA	4	4	0	6	NA	3	NA	NA	1066
27,78	smoker	NA	NA	NA	0	1	01.04.19	NA	NA	NA	1575
26,01	non-smoker	NA	1	1b	0	1	08.01.19	2	0	19.06.20	17081
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
29,54	smoker	NA	2	2b	0	1	04.07.19	2	0	06.03.20	2
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
28,2	smoker	NA	4	4	NA	8	NA	0	0	16.09.20	4
20,2	non-smoker	NA	NA	NA	0	7	09.07.19	2	0	08.05.20	1412
39,68	smoker	NA	3	3	0	4	08.01.19	3	1	08.11.19	1000
30,37	smoker	NA	3	3	0	2	26.01.19	2	0	15.06.20	71091
22,1	non-smoker	NA	4	4	0	1	04.11.19	1	0	10.08.20	5097
32,8	non-smoker	NA	4	4	0	1	10.02.20	0	0	23.04.20	2183
22,68	non-smoker	NA	4	4	1	4	06.05.19	4	1	17.06.20	2
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
32,3	non-smoker	NA	2	2a	0	1	20.08.19	2	0	14.07.20	164583
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
19,7	smoker	NA	3	3	0	1	03.03.20	1	0	30.03.20	2346
29,76	smoker	NA	4	4	1	4	04.02.19	3	1	17.03.20	3447
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
27,1	non-smoker	NA	2	2b	1	3	NA	2, 3	1	04.05.20	379
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
24,22	smoker	NA	4	4	0	8	NA	NA	0	16.09.20	138
23,26	non-smoker	NA	4	4	0	1	30.07.19	0	0	10.09.20	906
NA	smoker	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
26,8	non-smoker	NA	2	2b	0	3	16.04.19	0	1	13.07.19	160969
31,24	smoker	NA	NA	NA	0	1	17.04.19	NA	NA	NA	834
18,73	non-smoker	NA	3	3	0	1, 7	30.09.19	5	0	unknown	2
NA	NA	L-Thyrox	NA	NA	NA	NA	NA	NA	NA	NA	NA
22,7	non-smoker	NA	3	3	0	2	04.02.20	2	0	04.06.20	6021
22,39	non-smoker	NA	4	4	0	5	03.06.19	0	1	03.07.19	118805
27,13	non-smoker	NA	1	1a	0	1, 3	1.2016-01.07.	0	0	19.07.20	4
19,38	smoker	NA	3	3	NA	1	23.01.20	3	NA	16.09.20	985
28,9	non-smoker	NA	NA	NA	0	4	14.11.19	NA	NA	NA	76814
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
33,03	non-smoker	NA	2	2a	0	3	02.08.19	2	1	Jan 20	611609
25,64	non-smoker	NA	4	4	1	4	30.01.19	3	1	09.04.19	42
21,5	non-smoker	NA	NA	NA	1	2	18.02.20	2	0	11.09.20	239
32,87	non-smoker	NA	2	2a	0	1	12.04.19	2	0	20.05.20	19635
25,35	non-smoker	NA	3	3	0	1	14.02.19	2	1	24.01.20	130723
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
23,92	smoker	NA	2	2b	0	1	20.03.19	2	0	08.06.20	27812
27,47	non-smoker	NA	NA	NA	0	1	13.02.19	NA	NA	NA	16658
30,4	smoker	NA	1	1b	0	3	10.07.19	NA	NA	NA	222
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
24,14	non-smoker	NA	2	2b	0	1	29.01.19	0	1	30.01.19	7009
28,73	non-smoker	NA	2	2a	0	2	24.01.19	0	1	29.03.19	7212
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
27,8	non-smoker	NA	4	4	0	1	20.12.19	2	0	06.08.20	87632
NA	smoker	NA	NA	NA	0	NA	NA	4	NA	NA	12779
26,9	non-smoker	NA	3	3	0	3	20.02.20	NA	NA	NA	3464
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
28,04	non-smoker	NA	1	1b	NA	8	NA	0	0	16.09.20	379
25,9	non-smoker	NA	4	4	1	4	16.01.19	0	1	07.03.19	978
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
25,83	non-smoker	NA	NA	NA	0	2	13.03.19	NA	NA	NA	1865
29,76	non-smoker	NA	3	3	0	3	02.05.19	2	0	12.05.20	2498
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
22,58	non-smoker	NA	3	3	1	7	01.10.14	2	0	16.09.20	451
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
24,61	non-smoker	NA	3	3	0	3	18.07.19	NA	NA	NA	55435
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
26,29	non-smoker	NA	NA	NA	0	6	NA	NA	0	18.03.20	380838
24,22	smoker	NA	3	3	0	2	21.02.19	2	0	04.05.20	140631
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	no	NA	NA	NA	NA	NA	NA	NA	NA	NA
22,9	non-smoker	NA	3	3	0	1	19.12.19	2	0	Aug 20	1146
NA	NA	L-Thyrox	NA	NA	NA	NA	NA	NA	NA	NA	NA
19,92	non-smoker	NA	3	3	1	1	06.09.18	2	1	21.08.19	NA
23,84	non-smoker	NA	2	2a	NA	8	NA	3	1	.04.2020 and	142

alcohol	lcohol_amour	medication.1	ntibiotics <28	PPI	recent_medi	clities_other_t	rbidities_dia	coded_ca19	talogical_sta	ampling_time
1	3-4 per week	1	0	1	NA	1	0	1	:N1L0V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	1	NA	1	0	-1	N0L0V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	1 per week	1	0	1	NA	1	0	1	N0L0V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	-	1	0	0	7	2	0	1	IV	single sample
1	daily	1	0	1	NA	1	0	-1	NA	ay before operation
1	ex abusus	1	1	0	NA	1	1	1	:N0LV0Pn1G3	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	0	NA	1	1	-1	_0V0Pn1G3R	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	-	1	1	1	1, 3, 4, 5, 7	1, 4	0	-1	IV	single sample
1	3-4 per week	1	0	0	NA	1	0	1	NA	ay before operation
0	-	1	0	1	2, 3, 4, 5, 7	1	0	1	III	single sample
1	daily	1	0	0	NA	0	1	1	N2L0V0Pn1G	ay before operation
1	1-2 per week	1	1	1	NA	1	0	1	NA	ay before operation
0	NA	1	0	1	NA	1	0	-1	l1(hep)L0V0P	ay before operation
1	1-2 per week	1	0	0	NA	3	0	-1	NA	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	1	1	NA	1	0	1	aG2; pT3bN0L	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	1 per week	1	0	0	NA	1	0	1	N2L0V1Pn1G	ay before operation
0	NA	1	1	1	NA	2	0	-1	NA	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	occasionally	1	0	1	6, 7	1	0	1	pN1 (2/18), L0	single sample
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	-	1	1	1	NA	1	0	1	IV	single sample
1	daily	1	1	1	NA	1	0	-1	M1(lym)L0V0P	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	0	NA	1	0	1	N1L0V0Pn1G	ay before operation
1	daily	0	0	0	NA	0	0	-1	NA	ay before operation
1	onsumption sir	1	0	1	2, 5, 6, 7	1	1	-1	III	single sample
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	0	NA	1	0	1	N2L0V0Pn1G	ay before operation
0	NA	1	0	0	NA	1, 4	1	1	NA	uvant radiochemotherapy
0	-	1	0	1	2, 4, 5, 7	6	1	-1	IA	single sample
0	-	1	1	0	2, 6, 2007	6	0	1	III	single sample
0	NA	1	0	0	NA	1, 3	1	1	NA	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	1	1	NA	1	1	1	N0L0V0Pn1G	ay before operation
0	NA	1	0	1	NA	1	1	1	NA	ay before operation
0	NA	1	0	0	NA	1	0	-1	NA	ay before operation
0	NA	1	0	1	NA	1	1	1	N0L0V0Pn1G	ay before operation
0	NA	0	0	0	NA	0	0	1	N2L0V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	daily	1	0	0	NA	1	0	1	N1L0V0Pn1G	ay before operation
1	daily	1	1	1	NA	1	1	1	NA	ay before operation
0	NA	1	0	0	NA	1	0	-1	N0L0V0Pn0G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	1 per week	1	0	0	NA	1	0	1	N1L0V0Pn1G	ay before operation
0	NA	1	0	1	NA	1	0	1	N0L0V1Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	0	NA	1	0	1	NA	ay before operation
1	daily	1	0	1	NA	3	0	1	NA	djuvant chemotherapy
0	NA	1	0	0	NA	1	0	-1	N2L1V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	-	1	1	0	1, 2, 3, 5, 7	1	1	1	Ib	single sample
1	1 per week	0	1	0	NA	0	0	-1	NA	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	1 per month	1	0	0	NA	2	0	-1	NA	ay before operation
0	NA	1	0	0	NA	1	0	1	N1L0V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	lcohol since 2	1	0	1	2, 5, 2007	5	1	1	1 (1/12), L1, V	single sample
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	1 per month	1	0	0	NA	1	0	1	N2L1V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	NA	1	0	1	NA	1	0	1	NA	ay before operation
0	NA	1	0	0	NA	5	0	1	N2L0V1Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
1	daily	1	1	0	NA	1	0	1	N2L1V0Pn1G	ay before operation
NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA
0	-	1	0	1	1, 7	1, 6	0	-1	III	single sample
1	lay in the last	1	0	1	1, 7	1	1	1	IIA	single sample

Supplementary Table S4

	Stool			Saliva		
Meta variable	**Sum sq**	**p value**	**adj p**	**Sum sq**	**p value**	**adj p**
abmedication	7,40E+08	0.434882370	1.0	7,26E+07	0.726039062	1.0
Age	5,57E+10	0.348999552	1.0	1,43E+10	0.992133250	1.0
Alcohol consumption	3,28E+09	0.105017752	1.0	4,22E+07	0.796587916	1.0
Acid regurgitation	1,92E+09	0.215874045	1.0	2,05E+07	0.857472013	1.0
Diabetes	1,47E+07	0.914256854	1.0	4,78E+08	0.387311299	1.0
Heart burn	7,20E+08	0.445550072	1.0	2,11E+09	0.059764110	1.0
High blood pressure	8,65E+06	0.934099012	1.0	4,70E+06	0.931832163	1.0
Rheumatoid arthritis	7,36E+08	0.444113445	1.0	3,28E+07	0.821293457	1.0
Antibiotic	6,18E+07	0.825159237	1.0	3,55E+08	0.455050912	1.0
Aspirin/paracetamol	1,36E+09	0.297843618	1.0	1,12E+09	0.181428572	1.0
Asthma	1,76E+09	0.236597169	1.0	4,57E+08	0.395506158	1.0
Center	4,90E+09	0.046953480	1.0	2,76E+06	0.947458361	1.0
Cholesterol	1,72E+09	0.246154381	1.0	2,93E+08	0.493014836	1.0
Cholmedication	6,33E+05	0.982226159	1.0	1,48E+08	0.663216095	1.0
Corticosteroids	2,24E+09	0.179684582	1.0	4,11E+08	0.406201881	1.0
cpy1	7,16E+10	0.825078663	1.0	2,39E+10	0.800141666	1.0
Bilirirubin direct	1,32E+11	0.543089087	1.0	5,08E+10	0.857634747	1.0
Bilirubin lab	1,30E+11	0.455465155	1.0	4,85E+10	0.802784617	1.0
FHPDAC	2,40E+06	0.964420558	1.0	4,78E+08	0.383616587	1.0
Gender	1,04E+09	0.362627665	1.0	5,98E+08	0.330808453	1.0
Jaundice	9,45E+09	0.004406831	0.3437328	4,30E+08	0.412200163	1.0
Jaundice imputed	8,32E+09	0.009192609	0.7078309	4,41E+08	0.403644362	1.0
Library_size	8,15E+09	0.086373435	1.0	1,55E+09	0.487294778	1.0
Metformin usage	3,98E+09	0.205930855	1.0	3,12E+08	0.783170829	1.0
Obesity	8,37E+08	0.415414037	1.0	3,49E+08	0.450252695	1.0
Paracetamol	4,49E+09	0.058802839	1.0	2,03E+09	0.072918539	1.0
Periodontitis	1,73E+08	0.710712567	1.0	1,31E+09	0.136666489	1.0
Probiotic	1,11E+07	0.925379621	1.0	1,09E+07	0.894062783	1.0
Receding gums	8,17E+08	0.415025012	1.0	2,69E+08	0.508708572	1.0
Salicylic acid	1,85E+09	0.227061461	1.0	1,94E+08	0.582723500	1.0
Salicylic acid	1,85E+09	0.227061461	1.0	1,94E+08	0.582723500	1.0
Smoking	9,62E+07	0.782721018	1.0	2,24E+09	0.059311754	1.0
Direct Bilirubin	2,75E+09	0.138132461	1.0	1,71E+09	0.102796407	1.0
Total Bilirubin	7,13E+08	0.440177205	1.0	2,87E+09	0.031822359	1.0

Supplementary Table S5

	Stool		Saliva	
Meta variable	**R2 Bray-Curtis**	**p value**	**R2 Bray-Curtis**	**p value**
status	0.023120267	0.0001	0.010468749	0.6507
center	0.011138008	0.2069	0.016751291	0.1285
age	0.013765355	0.0320	0.018667727	0.0680
gender	0.010546251	0.2884	0.017940759	0.0884
jaundice_imp	0.015980165	0.0087	0.007371362	0.9560
diabetes	0.013610607	0.0396	0.008990599	0.8264
obesity	0.008734297	0.6915	0.016455787	0.1449
smoking	0.008943945	0.6466	0.015490596	0.1926
alcohol_con	0.009730450	0.4545	0.017867998	0.0929
periodontitis	0.009018863	0.6237	0.009449706	0.7709
cholesterol	0.007848892	0.8750	0.010637989	0.6368
metformin	0.008315828	0.7739	0.018288711	0.0898
salicylic	0.009192529	0.5749	0.008768629	0.8462
antibiotic	0.007858670	0.8685	0.006825246	0.9740
aspirin/paracetamol	0.012544261	0.0847	0.020375695	0.0432
corticosteroids	0.010196054	0.3492	0.017140805	0.1277
asthma	0.008577892	0.7244	0.014670641	0.2412
acid regurgitation	0.011797158	0.1335	0.006447749	0.9801
rheumatoid arthritis	0.008798014	0.6747	0.011646596	0.5123
probiotic	0.009681840	0.4578	0.011088990	0.5759
paracetamol	0.010198223	0.3573	0.009887242	0.7242
heartburn	0.008810470	0.6760	0.013602585	0.3241
high blood pressure	0.007920655	0.8614	0.010496978	0.6491
receding gums	0.008765518	0.6873	0.007806693	0.9229
FHPDAC	0.010506425	0.2887	0.012944276	0.3752
acid med	0.010032433	0.3870	0.007517951	0.9390

Supplementary Table S6

Study	Diagnosis	Cohort siz	Pred.pos	Pred.neg	FPR	Model	Accession number
Average BRCA	BRCA	62			0,35	Model 1	
Average BRCA	BRCA	62			0,05	Model 2	
Average CD	CD	340			0,35	Model 1	
Average CD	CD	340			0,05	Model 2	
Average CRC	CRC	679			0,25	Model 1	
Average CRC	CRC	679			0,04	Model 2	
Average CTR	CTR	3872			0,17	Model 1	
Average CTR	CTR	3872			0,01	Model 2	
Average LD	LD	237			0,26	Model 1	
Average LD	LD	237			0,07	Model 2	
Average T1D	T1D	87			0,29	Model 1	
Average T1D	T1D	87			0,00	Model 2	
Average T2D	T2D	382			0,23	Model 1	
Average T2D	T2D	382			0,02	Model 2	
Average UC	UC	352			0,18	Model 1	
Average UC	UC	352			0,01	Model 2	
Buschart 2016	CTR	26	5	21	0,19	Model 1	
Buschart 2016	T1D	27	8	19	0,30	Model 1	PRJNA289586
Buschart 2016	CTR	26	0	26	0,00	Model 2	
Buschart 2016	T1D	27	0	27	0,00	Model 2	
Dhakan 2019	CTR	110	19	91	0,17	Model 1	PRJNA397112
Dhakan 2019	CTR	110	2	108	0,02	Model 2	
Feng 2015	CTR	63	7	56	0,11	Model 1	
Feng 2015	CRC	93	11	82	0,12	Model 1	PRJEB7774
Feng 2015	CTR	63	2	61	0,03	Model 2	
Feng 2015	CRC	93	2	91	0,02	Model 2	
FijiCOMP	CTR	172	14	158	0,08	Model 1	PRJNA217052
FijiCOMP	CTR	172	1	171	0,01	Model 2	
FMT Vaughn	CD	15	4	11	0,27	Model 1	PRJNA321058
FMT Vaughn	CD	15	1	14	0,07	Model 2	
Franzosa 2018	CTR	56	5	51	0,09	Model 1	
Franzosa 2018	UC	76	10	66	0,13	Model 1	
Franzosa 2018	CD	88	19	69	0,22	Model 1	PRJNA400072
Franzosa 2018	CTR	56	0	56	0,00	Model 2	
Franzosa 2018	UC	76	0	76	0,00	Model 2	
Franzosa 2018	CD	88	2	86	0,02	Model 2	
He 2017	CTR	54	11	43	0,20	Model 1	
He 2017	CD	49	33	16	0,67	Model 1	PRJEB15371
He 2017	CTR	54	0	54	0,00	Model 2	
He 2017	CD	49	5	44	0,10	Model 2	
Price-Lloyd 2019	UC	84	26	58	0,31	Model 1	
Price-Lloyd 2019	CD	151	38	113	0,25	Model 1	
Price-Lloyd 2019	CTR	65	5	60	0,08	Model 1	PRJNA398089
Price-Lloyd 2019	UC	84	1	83	0,01	Model 2	
Price-Lloyd 2019	CD	151	2	149	0,01	Model 2	
Price-Lloyd 2019	CTR	65	0	65	0,00	Model 2	

Hoyles 2018	LD	73	3	70	0,04	Model 1	PRJEB14215
Hoyles 2018	LD	73	3	70	0,04	Model 2	
Karlsson 2013	CTR	43	8	35	0,19	Model 1	
Karlsson 2013	T2D	102	14	88	0,14	Model 1	PRJEB1786
Karlsson 2013	CTR	43	0	43	0,00	Model 2	
Karlsson 2013	T2D	102	0	102	0,00	Model 2	
Kuang 2019	CTR	59	18	41	0,31	Model 1	
Kuang 2019	T1D	29	9	20	0,31	Model 1	PRJEB18755
Kuang 2019	CTR	59	0	59	0,00	Model 2	
Kuang 2019	T1D	29	0	29	0,00	Model 2	
Liu 2016	CTR	110	5	105	0,05	Model 1	PRJNA328899
Liu 2016	CTR	110	0	110	0,00	Model 2	
Mardinoglu 2018	LD	48	4	44	0,08	Model 1	PRJNA420817
Mardinoglu 2018	LD	48	0	48	0,00	Model 2	
Forslund 2015	CTR	372	85	287	0,23	Model 1	
Forslund 2015	T2D	78	16	62	0,21	Model 1	
Forslund 2015	T1D	31	8	23	0,26	Model 1	
Forslund 2015	UC	192	20	172	0,10	Model 1	
Forslund 2015	CD	37	13	24	0,35	Model 1	224, PRJEB1220, PRJ
Forslund 2015	CTR	372	0	372	0,00	Model 2	
Forslund 2015	T2D	78	0	78	0,00	Model 2	
Forslund 2015	T1D	31	0	31	0,00	Model 2	
Forslund 2015	UC	192	1	191	0,01	Model 2	
Forslund 2015	CD	37	1	36	0,03	Model 2	
Qin 2012	CTR	185	51	134	0,28	Model 1	
Qin 2012	T2D	183	76	107	0,42	Model 1	PRJNA422434
Qin 2012	CTR	185	1	184	0,01	Model 2	
Qin 2012	T2D	183	2	181	0,01	Model 2	
Qin 2014	LD	116	77	39	0,66	Model 1	
Qin 2014	CTR	114	25	89	0,22	Model 1	PRJEB6337
Qin 2014	LD	116	20	96	0,17	Model 2	
Qin 2014	CTR	114	1	113	0,01	Model 2	
Sankaranarayanan 2015	T2D	19	3	16	0,16	Model 1	PRJNA299502
Sankaranarayanan 2015	T2D	19	1	18	0,05	Model 2	
Schirmer 2016	CTR	471	14	457	0,03	Model 1	
Schirmer 2016	CTR	471	0	471	0,00	Model 2	PRJNA319574
Spanish	CP	29	4	25	0,14	Model 1	
Spanish	CP	29	5	24	0,17	Model 2	
Vogtmann 2016	CRC	51	13	38	0,25	Model 1	
Vogtmann 2016	CTR	52	11	41	0,21	Model 1	PRJEB12449
Vogtmann 2016	CRC	51	0	51	0,00	Model 2	
Vogtmann 2016	CTR	52	2	50	0,04	Model 2	
Wirbel 2019	CRC	60	12	48	0,20	Model 1	
Wirbel 2019	CTR	60	4	56	0,07	Model 1	ERP005534 PRJEB27
Wirbel 2019	CRC	60	1	59	0,02	Model 2	
Wirbel 2019	CTR	60	0	60	0,00	Model 2	
Xie 2016	CTR	250	35	215	0,14	Model 1	PRJEB9576
Xie 2016	CTR	250	2	248	0,01	Model 2	

Yachida 2019	CRC	352	88	264	0,25	Model 1	
Yachida 2019	CTR	289	76	213	0,26	Model 1	PRJDB4176
Yachida 2019	CRC	352	28	324	0,08	Model 2	
Yachida 2019	CTR	289	8	281	0,03	Model 2	
Yassour 2018	CTR	42	3	39	0,07	Model 1	PRJNA290381
Yassour 2018	CTR	42	0	42	0,00	Model 2	
Yu 2017	CRC	74	25	49	0,34	Model 1	
Yu 2017	CTR	54	14	40	0,26	Model 1	PRJEB10878
Yu 2017	CRC	74	2	72	0,03	Model 2	
Yu 2017	CTR	54	0	54	0,00	Model 2	
Zeevi 2015	CTR	900	81	819	0,09	Model 1	PRJEB11532
Zeevi 2015	CTR	900	1	899	0,00	Model 2	
Zeller 2014	CTR	83	10	73	0,12	Model 1	
Zeller 2014	CRC	49	18	31	0,37	Model 1	PRJEB6070, PRJEB2
Zeller 2014	CTR	83	4	79	0,05	Model 2	
Zeller 2014	CRC	49	5	44	0,10	Model 2	
Zhu 2018	BRCA	62	22	40	0,35	Model 1	
Zhu 2018	CTR	71	25	46	0,35	Model 1	PRJNA453965
Zhu 2018	BRCA	62	3	59	0,05	Model 2	
Zhu 2018	CTR	71	0	71	0,00	Model 2	

Supplementary Table S7

Target species/genus	Sequence	Probe	Dye	Reference
Bifidobacterium (genus)	5'- GATAGGACGCGACCCCAT -3'	Bif228	Cy3	http://probebase.csb.univie.ac.at/pb_report/probe/3959
Veillonella (genus)	5'- AGACGCAATCCCCTCCTT -3'	Veil223	FITC	http://probebase.csb.univie.ac.at/pb_report/probe/553
Akkermansia (genus/species)	5'- CCTTGCGGTTGGCTTCAGAT -3'	MUC-1437	FITC	http://probebase.csb.univie.ac.at/pb_report/probe/3898
Lactobacillus (genus)	5'- ACATGGAGTTCCACT -3'	Lact663	FITC	https://repositorium.sdum.uminho.pt/bitstream/1822/24334/1/pp.pdf
Bacteroides (genus)	5'- CCAATGTGGGGGACCTT -3'	Bac303	Cy3	https://onlinelibrary.wiley.com/doi/pdf/10.1111/j.1365-2672.2011.05039.x
Streptococcus (genus)	5'-TTTAGCCGTCCCTTTCTGG -3'	Strc493	Cy3	http://probebase.csb.univie.ac.at/pb_report/probe/964