

Signature of Oral Microbial Dysbiosis in Different Periodontitis Risk Levels

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Supplementary materials and methods

Study population

The detailed diagnostic criteria for periodontitis were as follows (Papapanou et al. 2018): 1) Interdental clinical attachment loss (CAL) is evident at ≥ 2 non-adjacent teeth; or 2) buccal or lingual CAL ≥ 3 mm with probing depth (PD) ≥ 3 mm is detectable at ≥ 2 teeth, excluding the following causes: traumatic gingival recession; dental caries extending to the tooth's cervical area; CAL present on the distal aspect of the second molar associated with malposition or extraction of the third molar; endodontic lesions draining through the marginal periodontium; and vertical root fractures.

Shotgun metagenome analysis

Extraction of microbiome DNA

DNA was extracted from samples using the MagPure Stool DNA KF Kit B (MAGEN, Guangzhou, China) according to the manual instructions. A 100–200 mg sample was transferred into a centrifuge tube with grinding beads. 1 mL of buffer ATL/PVOP-10 was added, and the sample was ground in the grinding machine (Shanghai Jingxin Tech, China) and incubated at 65°C for 20 min. The mixture was centrifuged at 14,000 $\times$ g for 5 min (Eppendorf, Hamburg, Germany). Then, the supernatant was transferred to a new tube. 0.6 mL buffer PCI was added to the sample, and the mixture was then vortexed thoroughly for 15 seconds. The mixture was centrifuged at 18,213 $\times$ g for 10 minutes. The supernatant was transferred to a deep well plate with a magnetic bead binding solution (600 μ L buffer with magnetic beads + 20 μ L Protease K + 5 μ L RNase A; 700 μ L wash 1; 700 μ L wash 2; 700 μ L wash 3; 100 μ L elution buffer). The sample was then transferred to the corresponding position in the deep well plate of the machine (ThermoFisher, Waltham, MA, USA). Then, the corresponding program on the Kingfisher (ThermoFisher, Waltham, MA, USA) was started. The resulting DNA was transferred into a 1.5 mL centrifuge tube for storage after the program finished.

Library construction and sequencing

Library preparation was performed using the MGIEasy Universal DNA Library Prep Set (MGI, Shenzhen, China). A certain amount of genomic DNA was taken and subjected to fragmentation. The fragmented samples were size-selected using magnetic beads. Then, the size-selected DNA fragments were converted to blunt-end DNA via an end-repair reaction. A single adenosine nucleotide was added to the 3' end of the DNA through the A-tailing reaction. Afterwards, library adapters were ligated to both ends of the DNA. Finally, the library products were amplified via polymerase chain reaction (PCR) and subjected to quality control.

Next, the final double-stranded library products were denatured to generate single-stranded library products. A circularization reaction was then set up to obtain single-stranded circular DNA products. Any single-stranded linear DNA was digested and removed. The final single-stranded circular library was amplified with phi29 DNA polymerase via rolling circle amplification (RCA) to generate DNA nanoballs (DNBs), each carrying approximately 300 copies of the initial single-stranded library molecule. The DNBs were loaded onto the patterned nanoarray, and 150-base paired-end (PE150) sequencing reads were generated using the DNBSEQ-T7 platform (BGI, Shenzhen, China).

Data analysis

Human Oral Microbiome Database (HOMD) is a rich information base and reference database devoted to the biology and ecology of oral microbiota, but it is not intended for the fundamental "host removal" procedure in metagenomic research or as the major database for microbial classification and functional annotation. It is ideally suited for result validation, interpretation, and in-depth research of oral microbiota following core analyses in general databases. So, raw data were filtered, screened, and

processed using SOAPnuke v.2.2.1 (Chen et al. 2018). Subsequently, Bowtie2 v.2.4.4 (Langmead and Salzberg 2012) was used to align host sequences and remove aligned sequences, yielding clean data. Next, MEGAHIT v.1.2.9 (Li et al. 2015) was employed for k-mer-based assembly of clean data to generate contigs. MetaGeneMark v.3.38 (Zhu et al. 2010) predicted gene sequences within contigs. Redundancy among the obtained genes was removed using CD-HIT v.4.8.1 (Li et al. 2001). Salmon v.1.6.0 (Patro et al. 2017) was used to calculate relative abundance tables for each gene. For gene function annotation, DIAMOND (Buchfink et al. 2015) was used to align non-redundant genes against databases including Evolutionary Genealogy of Genes: Non-supervised Orthologous Groups (eggNOG) (Huerta-Cepas et al. 2019), Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa and Goto 2000), Antibacterial Biocide and Metal Resistance Genes Database (BacMet) (Pal et al. 2014), Comprehensive Antibiotic Resistance Database (CARD) (Jia et al. 2017), Cluster of Orthologous Groups of proteins (COG) (Galperin et al. 2015), Carbohydrate-Active EnZymes database (CAZy) (Lombard et al. 2014), and Swiss-Prot Protein Sequence Database (Swiss-Prot) (Poux et al. 2017). Kraken2 v.2.1.2 (Wood et al. 2019) and a custom database [filtered from the National Center for Biotechnology Information (NCBI) Nucleotide Database or the Unified Human Gastrointestinal Genome (UHGG) database] were used for alignment to determine the number of species-specific sequences in samples. Bracken2 v.2.6.1 (Lu et al. 2017) was then used to estimate the true species abundance in samples, enabling complete species annotation. Alpha diversity of species was calculated using the Chao1, Shannon, and Simpson indices. Beta diversity among samples or groups was assessed using Bray-Curtis distance (Bray and Curtis 1957). Statistical analysis was performed using the Wilcoxon rank-sum test.

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Perio Exam For _____

Perio Exam Date ____/____/____

Prepared By _____

Smoking

- | | | | |
|---------------------------------------|--|--|--|
| ☐ Never smoked | Smoke(d) | Smoke(d) | Quit |
| | ☐ Less than 10cigs/day | ☐ Less than 10 years | ☐ Less than 10 years ago |
| | ☐ 10 or more cigs/day | ☐ 10 or more years | ☐ 10 or more years ago |

Diabetic Status

	Good Control	Fair Control	Poor Control
HbA1c (%)	Less than 6.5	6.5 - 7.5	Greater than 7.5
All fasting plasma glucose (mg/dl)	90 - 104	105 - 130	Greater than 130

- ☐ Not diabetic or unknown ☐ Good diabetic control ☐ Fair diabetic control ☐ Poor diabetic control

Check all that apply

- | | |
|---|--|
| ☐ Oral hygiene improvement is needed | ☐ Dental care frequency is NOT regular as advised |
| ☐ Scaling and root planing for any tooth has been done | ☐ Peridontal surgery for pockets has been done |
| ☐ Furcation involvements exist | ☐ Subgingival restorations are present |
| ☐ Vertical bone lesions exist | ☐ Subgingival calculus detected by x-ray or exam |

Deepest Pocket per sextant from the gingival margin to the base of the Sulcus

Upper Right

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

Lower Right

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

Upper Anterior

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

Lower Anterior

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

Upper Left

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

Lower Left

- ☐ Less than 5 mm
☐ 5 - 7 mm
☐ Greater than 7 mm
☐ No Teeth
☐ Bleeding

X-ray distance from CEJ to Bone Crest

Measured	Visual
Less than 2 mm	Normal bone height
2-4 mm	Between normal and excessive
Greater than 4 mm	Excessive bone loss

Upper Right

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Upper Anterior

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Upper Left

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Lower Right

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Lower Anterior

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Lower Left

- ☐ Less than 2 mm
- ☐ 2-4 mm
- ☐ Greater than 4 mm
- ☐ No Teeth

Report Settings

☐ Treatment Options

☐ Home Care Report (coming soon)

☐ Clinical Care Plan (coming soon)

Include in Report

☐ AAP, Surgical Emphasis

☐ Do you wish to indicate the use of laser therapy?

Model this Patient

Save for Later

Finish

Supplementary figures and captions

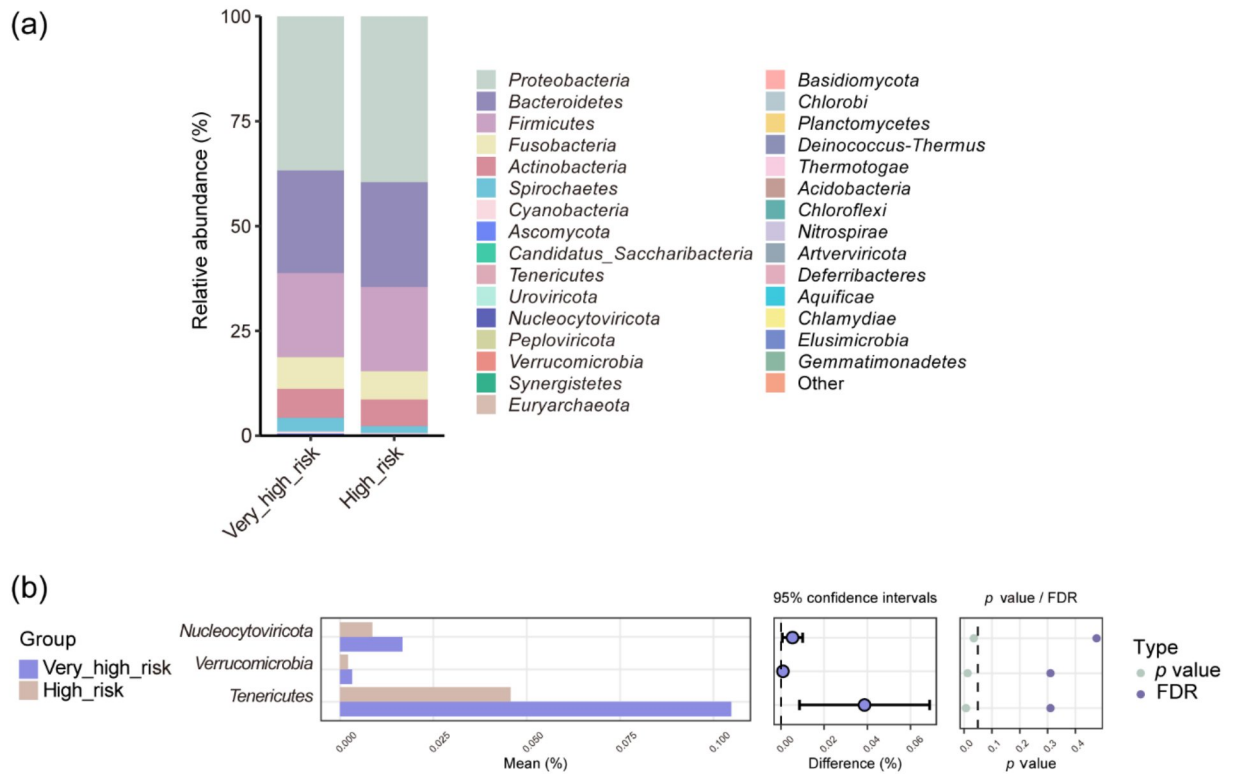


Fig. S1 Differences in the taxonomic composition between groups at the phylum level. (a) Stacked diagram of identified phyla that differ between the very high risk group and the high risk group. (b) The Statistical Analysis of Metagenomic Profiles (STAMP) analysis identifies phyla that differ significantly between the two groups.

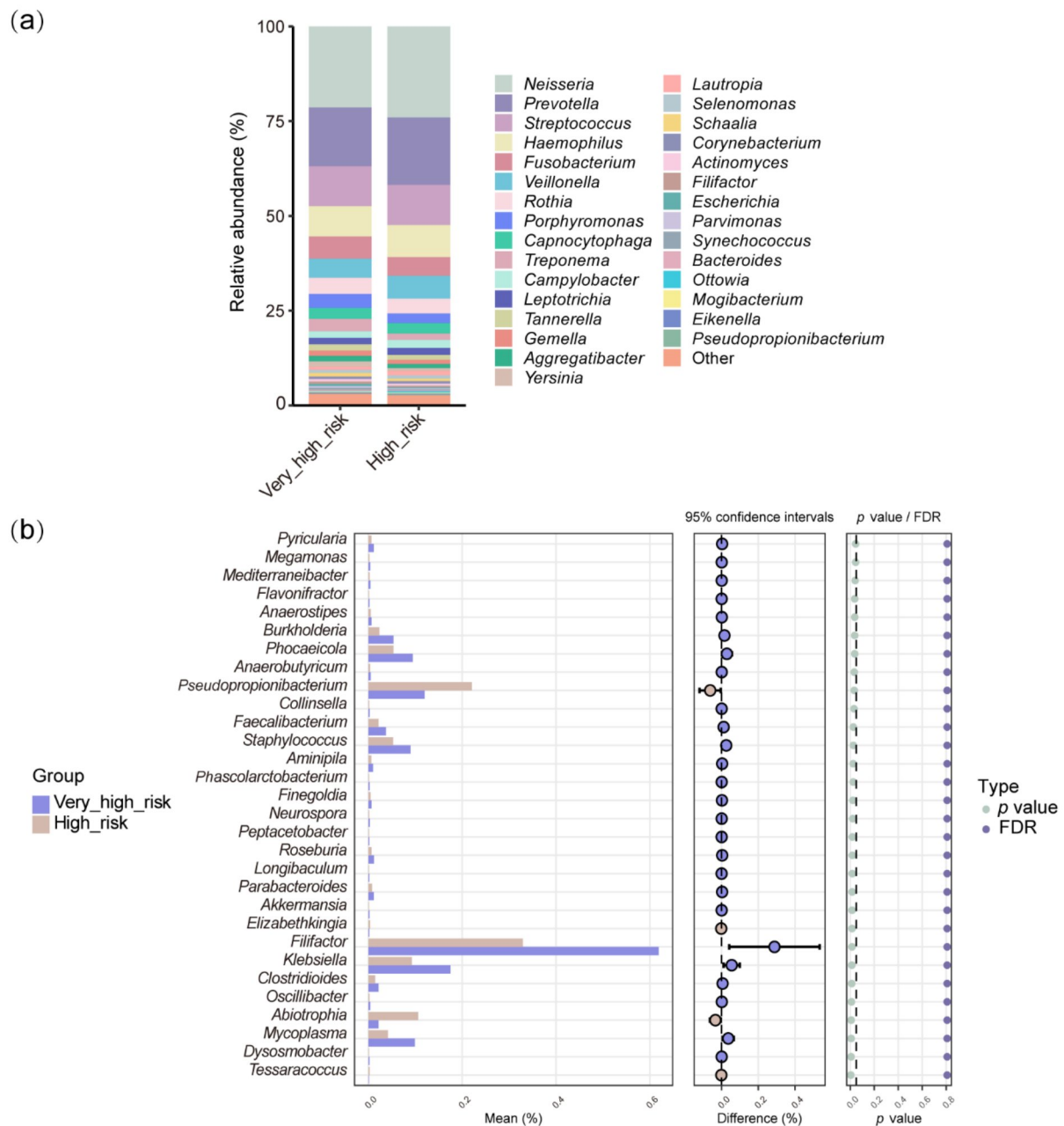


Fig. S2 Differences in the taxonomic composition between groups at the genus level. (a) Stacked diagram of identified genera that differ between the very high risk group and the high risk group. (b) The STAMP analysis identifies genera that differ significantly between the two groups.

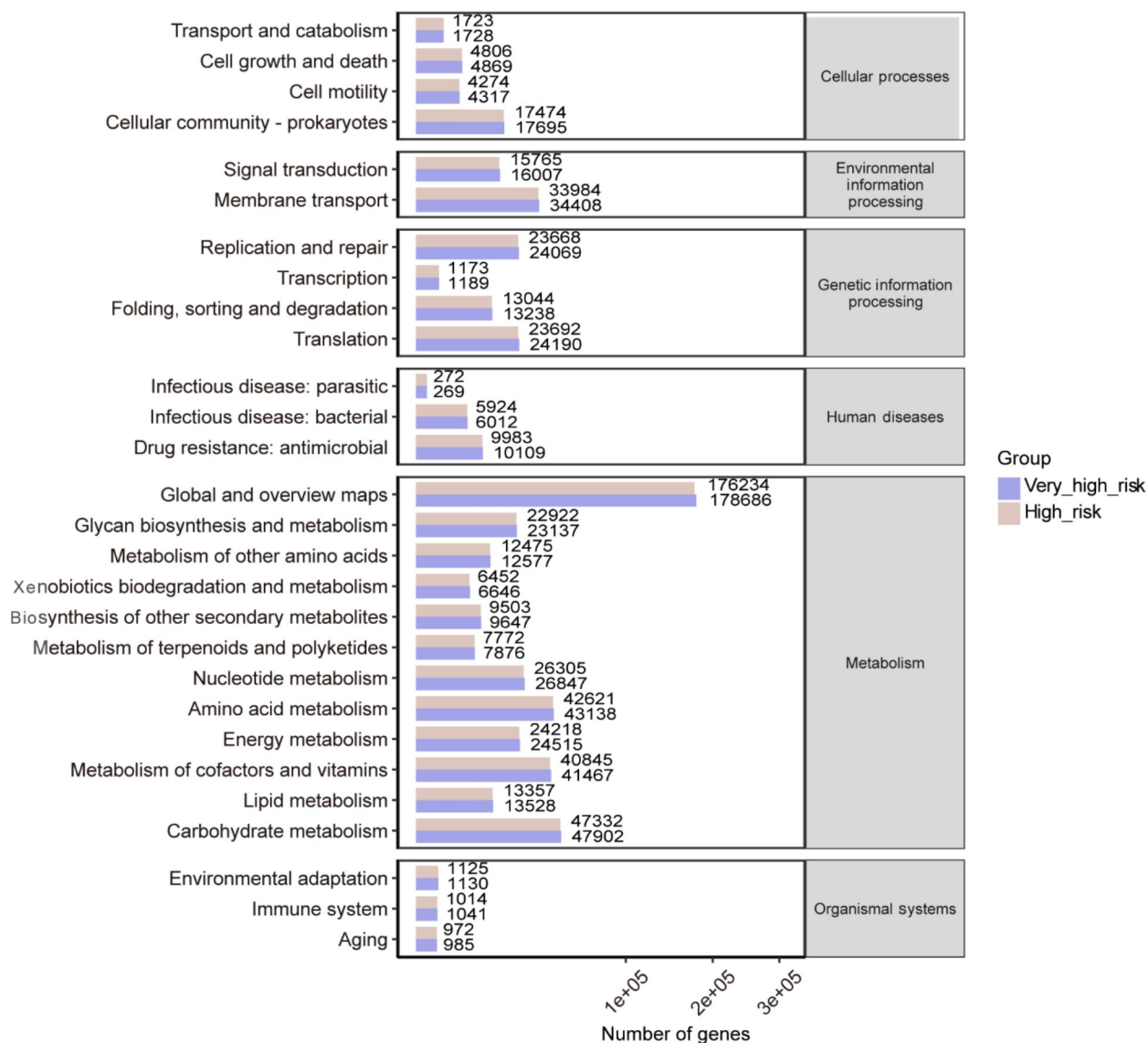


Fig. S3 Kyoto Encyclopedia of Genes and Genomes (KEGG) annotation analysis of functional genes in the two groups

Table S1 Criteria for determining the stage of periodontitis (Cited from Tonetti et al. 2018, Table 3)

Severity	Periodontitis stage		Stage I		Stage II		Stage III		Stage IV	
	Interdental CAL at site of greatest loss		1 to 2 mm		3 to 4 mm		≥5 mm		≥5 mm	
	Radiographic bone loss		Coronal third (<15%)		Coronal third (15% to 33%)		Extending to mid-third of root and beyond		Extending to mid-third of root and beyond	
Tooth loss			No tooth loss due to periodontitis				Tooth loss due to Periodontitis ≤4 teeth		Tooth loss due to Periodontitis ≥5 teeth	
Complexity	Local	Maximum probing depth ≤4 mm Mostly horizontal bone loss		Maximum probing depth ≤5 mm Mostly horizontal bone loss		In addition to stage II complexity: Probing depth ≥6 mm Vertical bone loss ≥3 mm Furcation involvement Class II or III Moderate ridge defect		In addition to stage III complexity: Need for complex rehabilitation due to: Masticatory dysfunction Secondary occlusal trauma (tooth mobility degree ≥2) Severe ridge defect Bite collapse, drifting, faring Less than 20 remaining teeth (10 opposing pairs)		
Extent and distribution	Add to stage as descriptor		For each stage, describe extent as localized (<30% of teeth involved), generalized, or molar/incisor pattern							

Note: CAL clinical attachment loss

Table S2 Criteria for determining the grade of periodontitis (Cited from Tonetti et al. 2018, Table 4)

Periodontitis grade			Grade A: Slow rate of progression	Grade B: Moderate rate of progression	Grade C: Rapid rate of progression
Primary criteria	Direct evidence of progression	Longitudinal data (radiographic bone loss or CAL)	Evidence of no loss over 5 years	<2 mm over 5 years	≥2 mm over 5 years
	Indirect evidence of progression	% bone loss/age	<0.25	0.25 to 1.0	>1.0
		Case phenotype	Heavy biofilm deposits with low levels of destruction	Destruction Commensurate with biofilm deposits	Destruction exceeds expectation given biofilm deposits; specific clinical patterns suggestive of periods of rapid progression and/or early onset disease (e.g., molar/incisor pattern; lack of expected response to standard bacterial control therapies)
Grade modifiers	Risk factors	Smoking	Non-smoker	Smoker <10 cigarettes/day	Smoker ≥10 cigarettes/day
		Diabetes	Normoglycemic/no diagnosis of diabetes	HbA1c <7.0% in patients with diabetes	HbA1c ≥7.0% in patients with diabetes
Risk of systemic impact of periodontitis	Inflammatory burden	High sensitivity CRP (hsCRP)	<1 mg/L	1 to 3 mg/L	>3 mg/L
Biomarkers	Indicators of CAL/bone loss	Saliva, gingival crevicular fluid serum	?	?	?

Note: HbA1c glycated hemoglobin; hsCRP high sensitivity C-reactive protein; CAL clinical attachment loss

Table S3 Taxa distribution of the very high risk group and the high risk group at the phylum level

Note: Only the top 30 phyla in terms of mean relative abundance in the taxonomic units were detailed in the table; the rest were classified as other phyla

Table S4 Taxa differences between the very high risk group and the high risk group at the phylum level

Note: Wilcoxon rank-sum test was performed on the abundance of all phyla involved to screen for phyla with $p < 0.05$, and only the top 30 phyla with the highest relative abundance were detailed in the table if the number of divergent phyla was greater than 30, and all divergent phyla were displayed if the number of divergent phyla was less than 30.

Table S5 Differential taxa between the very high risk group and the high risk group identified through Linear Discriminant Analysis Effect Size (LEfSe)

Biomarker_name	Logarithm_value	Group	LDA_value	p_value
Bacteria	5.996936449			
Bacteria.Actinobacteria	4.834506665			
Bacteria.Actinobacteria.Actinobacteria	4.825208614			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales	4.206561042			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae	4.214418094			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes	3.82516509			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_naeslundii	2.833675533			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_oris	2.881068675			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_pacaensis	2.741033078			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_radidentis	1.558472093			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_slackii	1.587388794			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_sp_oral_taxon_169	3.191639407			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_sp_oral_taxon_171	3.005449829			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_sp_oral_taxon_414	3.063982096			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_sp_oral_taxon_897	2.530818774			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes.Actinomycetes_viscosus	2.698287173			0.027925
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Pauljensenia	2.495722205			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Pauljensenia.Pauljensenia_hongkongensis	2.495600138			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Schaalia	3.956129615			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Schaalia.Schaalia_cardiffensis	2.239559875			0.006591
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Schaalia.Schaalia_meyeri	2.570325493			
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Schaalia.Schaalia_odontolytica	3.928819865			
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales	2.250705554			
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae	2.254471746			
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	2.180254956			
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Bifidobacterium_dentium	1.887369843			
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Bifidobacterium_longum	1.727618739			0.04209
Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales	3.828580294			
Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Corynebacteriaceae	3.831131264			
Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Corynebacteriaceae.Corynebacterium	3.825279686			
Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Corynebacteriaceae.Corynebacterium.Corynebacterium_argentoratense	1.813386683			
Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Corynebacteriaceae.Corynebacterium.Corynebacterium_matruchotii	3.81460707			
Bacteria.Actinobacteria.Actinobacteria.Micrococcales	4.624042385			
Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae	4.628931957			
Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Rothia	4.622065359			
Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Rothia.Rothia_aeria	3.81341324			
Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Rothia.Rothia_dentocariosa	3.515302898			

<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Rothia.Rothia_mucilaginosa</i>	4.50620704			
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales</i>	3.41216188	High_risk	2.730015	0.022531
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae</i>	3.413812806	High_risk	2.731078	0.022531
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Cutibacterium</i>	1.922505604			
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Cutibacterium.Cutibacterium_acnes</i>	1.864534762			
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Propionibacterium</i>	2.381181248			
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Propionibacterium.Propionibacterium_acidifaciens</i>	2.359642316			
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Pseudopropionibacterium</i>	3.340550817	High_risk	2.660274	0.027925
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Propionibacteriaceae.Pseudopropionibacterium.Pseudopropionibacterium_propionicum</i>	3.340409396	High_risk	2.660175	0.027925
<i>Bacteria.Actinobacteria.Coriobacteriia</i>	3.248391517			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales</i>	3.239171985			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae</i>	3.237783965			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae.Lancefieldella</i>	3.12603082			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae.Lancefieldella.Lancefieldella_parvula</i>	3.125945679			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae.Olsenella</i>	2.565999184			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae.Olsenella.Olsenella_sp_oral_taxon_807</i>	2.458175594			
<i>Bacteria.Actinobacteria.Coriobacteriia.Coriobacteriales.Atopobiaceae.Olsenella.Olsenella_uli</i>	1.866538289			
<i>Bacteria.Bacteroidetes</i>	5.395009324			
<i>Bacteria.Bacteroidetes.Bacteroidia</i>	5.339416506			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales</i>	5.338179115			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae</i>	3.507138504			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides</i>	3.500528353			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_caccae</i>	1.883890283			0.038088
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_fragilis</i>	2.582207184			0.026482
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_heparinolyticus</i>	3.217756589			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_ovatus</i>	1.950233754			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_sp_A1C1</i>	1.772424652			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_sp_HF_5287</i>	1.823164928			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_thetaiotaomicron</i>	2.013394718			0.042111
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_uniformis</i>	2.141981581			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_xylanisolvans</i>	1.630774477			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Bacteroides_zoogloeiformans</i>	2.516289029			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Barnesiellaceae</i>	1.631899526			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Barnesiellaceae.Barnesiella</i>	1.623216019			
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Barnesiellaceae.Barnesiella.Barnesiella_viscericola</i>	1.623105336			

<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Muribaculaceae</i>	2.087748264
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Muribaculaceae.Muribaculum</i>	1.935931355
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Muribaculaceae.Muribaculum.Muribaculum_intestinale</i>	1.608229034
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Muribaculaceae.Muribaculum.Muribaculum_sp_TLL_A4</i>	1.65788444
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Odoribacteraceae</i>	2.192979032
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Odoribacteraceae.Butyricimonas</i>	1.621649112
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Odoribacteraceae.Butyricimonas.Butyricimonas_faecalis</i>	1.621578801
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Odoribacteraceae.Odoribacter</i>	2.08349085
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Odoribacteraceae.Odoribacter.Odoribacter_splanchnicus</i>	2.083375429
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Paludibacteraceae</i>	1.604559373
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Paludibacteraceae.Paludibacter</i>	1.59287267
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Paludibacteraceae.Paludibacter.Paludibacter_propionici</i>	1.592758259
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae</i>	4.570966358
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonas</i>	4.565093724
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonas.Porphyromonas_asaccharolytica</i>	2.475128847
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonas.Porphyromonas_cangingivalis</i>	2.155147987
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonas.Porphyromonas_crevioricanis</i>	2.326312285
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonas.Porphyromonas_gingivalis</i>	4.557163577
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae</i>	5.251068652
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Alloprevotella</i>	2.163056624
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Alloprevotella.Alloprevotella_sp_E39</i>	2.1629471
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Paraprevotella</i>	2.001939823
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Paraprevotella.Paraprevotella_xylaniphila</i>	2.001823322
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella</i>	5.246157586
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_dentalis</i>	3.074721626
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_denticola</i>	3.731345375
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_enoeca</i>	3.280916136
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_fusca</i>	3.415788368
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_intermedia</i>	4.458316118
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_jejuni</i>	4.603930471
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_melaninogenica</i>	4.924815668
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_oris</i>	3.664645558
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_ruminicola</i>	2.134831092
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_scopos</i>	3.865761843
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Prevotella_sp_oral_taxon_299</i>	3.699026289

<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae</i>	2.440998577	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes</i>	2.410697523	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Alistipes_communis</i>	1.7062972	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Alistipes_finegoldii</i>	1.597854592	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Alistipes_onderdonkii</i>	1.597471036	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Alistipes_shahii</i>	1.680553101	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae</i>	4.225065549	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae.Parabacteroides</i>	2.057539739	0.01708
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae.Parabacteroides.Parabacteroides_distasonis</i>	2.049380679	0.029436
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae.Tannerella</i>	4.215087266	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae.Tannerella.Tannerella_forsythia</i>	4.084908827	
<i>Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Tannerellaceae.Tannerella.Tannerella_sp_oral_taxon_HOT_286</i>	3.721025908	
<i>Bacteria.Bacteroidetes.Flavobacteriia</i>	4.479703596	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales</i>	4.47852826	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Blattabacteriaceae</i>	1.656652018	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Blattabacteriaceae.Blattabacterium</i>	1.650686495	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Blattabacteriaceae.Blattabacterium.Blattabacterium_cuenoti</i>	1.638481155	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae</i>	4.465566116	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga</i>	4.452931972	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_canimorsus</i>	1.791058236	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_endodontalis</i>	3.364475363	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_gingivalis</i>	3.800951978	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_haemolytica</i>	2.255728341	0.007465
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_leadbetteri</i>	3.678893396	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_ochracea</i>	2.781648647	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sp_FDARGOS_737</i>	3.721746042	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sp_oral_taxon_323</i>	2.897790124	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sp_oral_taxon_864</i>	2.898549721	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sp_oral_taxon_878</i>	3.010447382	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sp_oral_taxon_902</i>	3.002063931	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Capnocytophaga_sputigena</i>	3.826394021	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Weeksellaceae</i>	3.23133285	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Weeksellaceae.Bergeyella</i>	3.129883752	
<i>Bacteria.Bacteroidetes.Flavobacteriia.Flavobacteriales.Weeksellaceae.Bergeyella.Bergeyella_cardium</i>	3.1297648	
<i>Bacteria.Candidatus_Saccharibacteria</i>	3.203728297	

<i>Bacteria.Candidatus_Saccharibacteria.Candidatus_Saccharimonia</i>	3.193885344		
<i>Bacteria.Candidatus_Saccharibacteria.Candidatus_Saccharimonia.Candidatus_Nanosynbacterales</i>	3.192788293		
<i>Bacteria.Candidatus_Saccharibacteria.Candidatus_Saccharimonia.Candidatus_Nanosynbacterales.Candidatus_Nanosynbacteraceae</i>	3.197690371		
<i>Bacteria.Candidatus_Saccharibacteria.Candidatus_Saccharimonia.Candidatus_Nanosynbacterales.Candidatus_Nanosynbacteraceae.Candidatus_Nanosynbacter</i>	3.192884969		
<i>Bacteria.Candidatus_Saccharibacteria.Candidatus_Saccharimonia.Candidatus_Nanosynbacterales.Candidatus_Nanosynbacteraceae.Candidatus_Nanosynbacter.Candidatus_Nanosynbacter_lyticus</i>	3.192812302		
<i>Bacteria.Cyanobacteria</i>	3.689986224		
<i>Bacteria.Firmicutes</i>	5.301243811		
<i>Bacteria.Firmicutes.Bacilli</i>	5.085759798		
<i>Bacteria.Firmicutes.Bacilli.Bacillales</i>	4.194209833		
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae</i>	2.571508389		
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Bacillus</i>	2.398794813		
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Bacillus.Bacillus_cereus</i>	1.958797885		
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae</i>	2.960153226	Very_high_risk	2.303059
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus</i>	2.94569302	Very_high_risk	2.299513
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus.Staphylococcus_aureus</i>	2.748234786	Very_high_risk	2.133061
<i>Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus.Staphylococcus_haemolyticus</i>	2.403959155		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales</i>	5.031952422		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae</i>	3.049508239	High_risk	2.537364
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Abiotrophia</i>	3.022544529	High_risk	2.530895
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Abiotrophia.Abiotrophia_defectiva</i>	3.022339484	High_risk	2.530692
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae</i>	2.440684493		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus</i>	2.235832713		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Enterococcus_faecium</i>	1.603835981		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae</i>	2.570457044		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus</i>	2.192693679		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Lactobacillus_delbrueckii</i>	1.932343219		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Lactobacillus_iners</i>	1.548510111		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae</i>	5.030547224		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus</i>	2.037707817		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus.Lactococcus_lactis</i>	1.884392472		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus</i>	5.024438235		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_agalactiae</i>	2.548537708		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_anginosus</i>	3.098402919	Very_high_risk	2.393118
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_australis</i>	3.64959669		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_canis</i>	1.75224773		

<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_constellatus</i>	2.280662521	Very_high_risk	3.078991
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_cristatus</i>	3.626957412		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_dysgalactiae</i>	2.53009941		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_equi</i>	2.318537263		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_equinus</i>	2.191707438		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_gordonii</i>	3.325085598		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_gwangjuense</i>	3.501052995		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_himalayensis</i>	1.642747317		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_intermedius</i>	2.861617526		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_koreensis</i>	3.305983826		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_milleri</i>	2.504775238		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_mitis</i>	4.399295829		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_mutans</i>	2.21537542		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_oralis</i>	4.202933834		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_parasanguinis</i>	3.44078488		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_periodonticum</i>	2.045274151		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_pluranimalium</i>	1.588299202		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_pneumoniae</i>	3.963057281		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_porcinus</i>	1.894944649		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_pseudopneumoniae</i>	3.330909162		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_pseudoporcinus</i>	2.126280253		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_pyogenes</i>	2.644079956		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_salivarius</i>	3.576131647		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sanguinis</i>	3.835279342		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sobrinus</i>	1.598159809		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_116_D4</i>	3.299994156		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_1643</i>	3.099485253		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_A12</i>	3.012109596		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_FDAARGOS_192</i>	2.276002704		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_FDAARGOS_522</i>	2.469282271		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_HSISM1</i>	3.170553686		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_HSISM1</i>	1.855986449		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_HSISS2</i>	2.099190776		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_HSISS3</i>	2.011507391		
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_I_G2</i>	3.327909428		

<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_L_P16</i>				3.380875147
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_KS_6</i>				1.91124462
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_LPB0220</i>				3.203092327
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_NCTC_11567</i>				1.973321796
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_NPS_308</i>				3.474706523
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_NSL_72</i>				2.548871047
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_oral_taxon_061</i>				3.844168421
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_oral_taxon_064</i>				3.056965864
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_sp_oral_taxon_431</i>				3.790237913
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_suis</i>				2.448082175
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_thermophilus</i>				3.131017589
<i>Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Streptococcus_vestibularis</i>				2.386537051
<i>Bacteria.Firmicutes.Clostridia</i>			Very_high_risk	3.349919
<i>Bacteria.Firmicutes.Clostridia.Clostridiales</i>				
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae</i>			Very_high_risk	3.344275
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Clostridium</i>				2.564273729
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Clostridium.Clostridium_botulinum</i>				1.910513532
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiales_Family_XIII_Incertae_Sedis</i>				3.428899099
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiales_Family_XIII_Incertae_Sedis.Mogibacterium</i>				3.40615278
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiales_Family_XIII_Incertae_Sedis.Mogibacterium.Mogibacterium_diversum</i>				3.280407895
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiales_Family_XIII_Incertae_Sedis.Mogibacterium.Mogibacterium_pumilum</i>				2.805937301
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae</i>				3.389179629
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerobutyricum</i>				1.676072434
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerobutyricum.Anaerobutyricum_hallii</i>				1.675942889
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes</i>				1.833639196
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes.Anaerostipes_hadrus</i>				1.733177568
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blauita</i>				2.085998378
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blauita.Blauita_sp_SC05B48</i>				1.63752367
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Enterocloster</i>				1.775602107
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Enterocloster.Enterocloster_clostridioformis</i>				1.575416633
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoanaerobaculum</i>				3.194950992
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoanaerobaculum.Lachnoanaerobaculum_umecaense</i>				3.194865058
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoclostridium</i>				2.080508046
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoclostridium.Lachnoclostridium_sp_Y132</i>				1.722065398
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospira</i>				1.995869861

<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospira.Lachnospira_eligens</i>	1.995718536			0.048815
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Mediterraneibacter</i>	1.597937577			0.046487
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Mediterraneibacter__Ruminococcus__gnavus</i>	1.597799537			0.046487
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia</i>	2.072001187			0.01708
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Roseburia_hominis</i>	1.586480674			0.048815
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Roseburia_intestinalis</i>	1.898737061			0.00794
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae</i>	3.813930211	Very_high_risk	3.206015	0.012822
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridioides</i>	2.327365001			0.012822
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridioides.Clostridioides_difficile</i>	2.327231811			0.012822
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Filifactor</i>	3.785933152	Very_high_risk	3.184356	0.014397
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Filifactor.Filifactor_alocis</i>	3.785805026	Very_high_risk	3.184223	0.014397
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae</i>	2.670591163	Very_high_risk	2.014338	0.022531
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium</i>	2.568327761			0.027925
<i>Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium_prausnitzii</i>	2.568175613			0.027925
<i>Bacteria.Firmicutes.Negativicutes</i>	4.839926959			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales</i>	3.935500564			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae</i>	3.939774119			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas</i>	3.93392188			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sp_Marseille_Q3039</i>	2.922761419			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sp_oral_taxon_126</i>	3.005228345			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sp_oral_taxon_136</i>	3.24280937			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sp_oral_taxon_478</i>	3.276200962			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sp_oral_taxon_920</i>	2.999295477			
<i>Bacteria.Firmicutes.Negativicutes.Selenomonadales.Selenomonadaceae.Selenomonas.Selenomonas_sputigena</i>	3.363516743			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales</i>	4.780779583			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae</i>	4.78516991			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Dialister</i>	2.914604134			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Dialister.Dialister_pneumosintes</i>	2.913094923			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Megasphaera</i>	1.852001268			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Megasphaera.Megasphaera_stantonii</i>	1.633547507			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella</i>	4.777200617			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella.Veillonella_atypica</i>	4.305449718			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella.Veillonella_dispar</i>	4.039181712			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella.Veillonella_parvula</i>	4.206483527			
<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella.Veillonella_rodentium</i>	2.8744343			

<i>Bacteria.Firmicutes.Negativicutes.Veillonellales.Veillonellaceae.Veillonella.Veillonella_sp_T1_7</i>	4.087836626		
<i>Bacteria.Firmicutes.Tissierellia</i>	3.711445705		
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales</i>	3.707734725		
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales.Peptoniphilaceae</i>	3.713332952	Very_high_risk	3.089898
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales.Peptoniphilaceae.Finegoldia</i>	1.83763952		
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales.Peptoniphilaceae.Finegoldia.Finegoldia_magna</i>	1.837517903		
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales.Peptoniphilaceae.Parvimonas</i>	3.694945003		
<i>Bacteria.Firmicutes.Tissierellia.Tissierellales.Peptoniphilaceae.Parvimonas.Parvimonas_micra</i>	3.694831093		
<i>Bacteria.Fusobacteria</i>	4.873861689		
<i>Bacteria.Fusobacteria.Fusobacteriia</i>	4.876078456		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales</i>	4.873914561		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae</i>	4.767926723		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium</i>	4.762377945		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_hwasookii</i>	3.422158745		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_necrophorum</i>	2.451097645		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_nucleatum</i>	4.347922375		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_periodonticum</i>	3.294533381		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_pseudoperiodonticum</i>	4.478052046		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Fusobacterium_sp_oral_taxon_203</i>	2.75492715		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae</i>	4.253867606		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia</i>	4.244388045		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_buccalis</i>	3.368655503		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_hofstadii</i>	3.208531935		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_hongkongensis</i>	3.055221276		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_shahii</i>	2.646450908		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_sp_oral_taxon_212</i>	3.61065796		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_sp_oral_taxon_498</i>	3.176022446		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_sp_oral_taxon_847</i>	2.664324175		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_trevisanii</i>	3.220861726		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Leptotrichia_wadei</i>	3.729714048		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Pseudoleptotrichia</i>	2.10550035		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Pseudoleptotrichia.Pseudoleptotrichia_goodfellowii</i>	2.105395834		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Sneathia</i>	1.631502552		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Sneathia.Sneathia_amnii</i>	1.631392701		
<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Streptobacillus</i>	1.70263545		

<i>Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Streptobacillus.Streptobacillus_moniliformis</i>	1.702516362			
<i>Bacteria.Proteobacteria</i>	5.594883128			
<i>Bacteria.Proteobacteria.Betaproteobacteria</i>	5.413261426			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales</i>	4.188558949			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae</i>	4.045547915			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia</i>	2.720274467	Very_high_risk	2.234147	0.036203
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia.Burkholderia_pseudomallei</i>	2.708639017	Very_high_risk	2.231762	0.038088
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Lautropia</i>	4.029525624			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Lautropia.Lautropia_mirabilis</i>	4.029369142			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Ralstonia</i>	1.675797938			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Ralstonia.Ralstonia_solanacearum</i>	1.670361937			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae</i>	3.644165257			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Ottowia</i>	3.629777906			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Ottowia.Ottowia_sp_oral_taxon_894</i>	3.629294531			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales</i>	5.385255681			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae</i>	5.390180094			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella</i>	3.394914575			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella.Eikenella_corrodens</i>	3.337620426			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella.Eikenella_exigua</i>	2.485790355			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Kingella</i>	2.908746308			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Kingella.Kingella_kingae</i>	2.048352069			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Kingella.Kingella_oralis</i>	2.844073825			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria</i>	5.378876057			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_animalis</i>	2.453066359			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_animaloris</i>	2.243822884			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_bacilliformis</i>	2.71388624			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_brasilensis</i>	2.474501526			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_canis</i>	2.027724928			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_chemvengui</i>	2.486843669			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_cinerea</i>	3.368241782			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_dentiae</i>	2.263474133			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_elongata</i>	4.22059776			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_flavescens</i>	4.406459931			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_gonorrhoeae</i>	3.231350621			
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_lactamica</i>	3.47829824			

<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_meningitidis</i>	4.167345898
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_mucosa</i>	4.752102515
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_musculi</i>	2.203710876
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_polysaccharea</i>	3.149012498
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_shayeganii</i>	1.975897901
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_sicca</i>	4.151481319
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_sp_10022</i>	2.358923828
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_sp_KEM232</i>	2.865060844
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_sp_ZJ785</i>	2.626789684
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_sp_oral_taxon_014</i>	3.934128584
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_subflava</i>	4.970382461
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_wadsworthii</i>	2.102871745
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_weaveri</i>	2.263429932
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_zalophi</i>	2.149917866
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Neisseria_zoodegmatidis</i>	2.191498671
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Simonsiella</i>	2.357300829
<i>Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Simonsiella.Simonsiella_muelleri</i>	2.357217576
<i>Bacteria.Proteobacteria.Deltaproteobacteria</i>	3.132585906
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfobacterales</i>	2.862005254
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfobacterales.Desulfobulbaceae</i>	2.866465739
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfobacterales.Desulfobulbaceae.Desulfobulbus</i>	2.857923313
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfobacterales.Desulfobulbaceae.Desulfobulbus.Desulfobulbus_oralis</i>	2.85742932
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfovibrionales</i>	2.766485696
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfomicrobiaceae</i>	2.695290738
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfomicrobiaceae.Desulfomicrobium</i>	2.688167375
<i>Bacteria.Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfomicrobiaceae.Desulfomicrobium.Desulfomicrobium_orale</i>	2.687910834
<i>Bacteria.Proteobacteria.Epsilonproteobacteria</i>	4.333164014
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales</i>	4.332016921
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae</i>	4.336200075
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter</i>	4.331091066
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_conciscus</i>	4.110845674
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_curvus</i>	2.506565872
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_gracilis</i>	3.037917384
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_hominis</i>	1.689111867
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_jejuni</i>	1.800011809

<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_rectus</i>	3.60942621			
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_showae</i>	3.587569802			
<i>Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Campylobacter_sp_CCUG_57310</i>	1.57317592			
<i>Bacteria.Proteobacteria.Gammaproteobacteria</i>	5.082352136			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Cardionbacteriales</i>	3.212298272			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Cardionbacteriales.Cardionbacteriaceae</i>	3.217962794			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Cardionbacteriales.Cardionbacteriaceae.Cardionbacterium</i>	3.211756167			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Cardionbacteriales.Cardionbacteriaceae.Cardionbacterium_hominis</i>	3.21167441			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales</i>	4.341982789			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae</i>	3.877901145			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Escherichia</i>	3.748110529			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Escherichia.Escherichia_coli</i>	3.747823316			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Klebsiella</i>	3.236053752	Very_high_risk	2.649001	0.012822
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Klebsiella.Klebsiella_pneumoniae</i>	3.232169862	Very_high_risk	2.64764	0.015247
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Salmonella</i>	1.723585563			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Enterobacteriaceae.Salmonella.Salmonella_enterica</i>	1.722889347			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Erviniaceae</i>	1.846984644			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Erviniaceae.Buchnera</i>	1.650234747			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Erviniaceae.Buchnera.Buchnera_aphidicola</i>	1.650104231			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Yersiniaceae</i>	4.166061945			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Yersiniaceae.Yersinia</i>	4.158296333			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacterales.Yersiniaceae.Yersinia.Yersinia_enterocolitica</i>	4.15795271			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales</i>	3.272072924			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Halomonadaceae</i>	3.268431401			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Halomonadaceae.Candidatus_Portiera</i>	3.257424999			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Halomonadaceae.Candidatus_Portiera.Candidatus_Portiera_aleyrodidarum</i>	3.257275011			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales</i>	4.985304451			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae</i>	4.990817933			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Actinobacillus</i>	2.522908628			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Actinobacillus.Actinobacillus_pleuropneumoniae</i>	1.956124502			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Actinobacillus.Actinobacillus_porcitonsillarum</i>	1.898808572			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Aggregatibacter</i>	4.136336166			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Aggregatibacter.Aggregatibacter_actinomycetemcomitans</i>	2.713841921			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Aggregatibacter.Aggregatibacter_apthrophilus</i>	3.65443643			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Aggregatibacter.Aggregatibacter_segnis</i>	3.937172986			

<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Glaesserella</i>	1.996858322			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Glaesserella.Glaesserella_parasuis</i>	1.815241991			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Glaesserella.Glaesserella_sp_15_184</i>	1.561279117			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus</i>	4.925120817			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_aegyptius</i>	1.78313417			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_haemolyticus</i>	3.704982361			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_influenzae</i>	3.579952746			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_paraahaemolyticus</i>	3.624831346			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_parainfluenzae</i>	4.837591317			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_pittmaniae</i>	2.960562854			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Haemophilus_sp_oral_taxon_036</i>	3.088984069			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus_Haemophilus__ducreyi</i>	1.731250866			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Histophilus</i>	1.778602699			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Histophilus.Histophilus_somni</i>	1.778480546			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Mannheimia</i>	2.554535529			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Mannheimia.Mannheimia_granulomatis</i>	1.913521414			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Mannheimia.Mannheimia_haemolytica</i>	1.868068872			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Mannheimia.Mannheimia_varigena</i>	1.825406652			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurella</i>	2.840145045			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurella.Pasteurella_multocida</i>	2.824945533	Very_high_risk	2.228989	0.048815
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Rodentibacter</i>	2.285593176			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Rodentibacter.Rodentibacter_heylii</i>	1.830462785			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Rodentibacter.Rodentibacter_pneumotropicus</i>	1.805568058			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Rodentibacter.Rodentibacter_sp_DSM_111151</i>	1.786261885			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales</i>	2.615658876			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae</i>	2.425839963			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter</i>	2.072504771			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter.Acinetobacter_baumannii</i>	1.587714443			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae</i>	2.220882394			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas</i>	2.209306058			
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas.Pseudomonas_aeruginosa</i>	1.798433589			
<i>Bacteria.Spirochaetes</i>	4.511025992			
<i>Bacteria.Spirochaetes.Spirochaetia</i>	4.514119743			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales</i>	4.510879065			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae</i>	4.516643973			

<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema</i>	4.510757633			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_denticola</i>	4.187462544			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_pedis</i>	2.500498998			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_phagedenis</i>	2.098994858			0.012822
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_putidum</i>	3.280377341			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_socranskii</i>	3.005376288			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_sp_Marseille_Q4132</i>	2.825422129			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_sp_OMZ_804</i>	3.865081144			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_sp_OMZ_838</i>	3.739469227			
<i>Bacteria.Spirochaetes.Spirochaetia.Spirochaetales.Spirochaetaceae.Treponema.Treponema_succinifaciens</i>	2.018289291			
<i>Bacteria.Tenericutes</i>	3.015380668	Very_high_risk	2.407548	0.007465
<i>Bacteria.Tenericutes.Mollicutes</i>	3.017170322	Very_high_risk	2.412211	0.00619
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales</i>	2.996598017	Very_high_risk	2.398727	0.007016
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae</i>	3.002929896	Very_high_risk	2.40543	0.006591
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma</i>	2.990079233	Very_high_risk	2.394081	0.00794
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma.Mycoplasma_hyosynoviae</i>	1.72391448			
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma.Mycoplasma_orale</i>	2.455646807			
<i>Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma.Mycoplasma_salivarium</i>	2.52484003			
<i>Bamfordvirae.Nucleocytoviricota</i>	2.215617778			0.034397
<i>Bamfordvirae.Nucleocytoviricota.Pokkesviricetes</i>	2.217802138			0.036203
<i>Bamfordvirae.Nucleocytoviricota.Pokkesviricetes.Chitovirales</i>	2.214554125			0.036203
<i>Bamfordvirae.Nucleocytoviricota.Pokkesviricetes.Chitovirales.Poxviridae</i>	2.220998626			0.036203
<i>Fungi.Ascomycota</i>	3.290479386			
<i>Fungi.Ascomycota.Leotiomycetes</i>	2.152348451			
<i>Fungi.Ascomycota.Leotiomycetes.Helotiales</i>	2.149009181			
<i>Fungi.Ascomycota.Leotiomycetes.Helotiales.Sclerotiniaceae</i>	2.156425056			
<i>Fungi.Ascomycota.Leotiomycetes.Helotiales.Sclerotiniaceae.Botrytis</i>	2.149194336			
<i>Fungi.Ascomycota.Leotiomycetes.Helotiales.Sclerotiniaceae.Botrytis.Botrytis_cinerea</i>	2.149039269			
<i>Fungi.Ascomycota.Saccharomycetes</i>	2.709972991			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales</i>	2.706688567			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Deбaryomycetaceae</i>	2.453602527			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Deбaryomycetaceae.Candida</i>	2.445460724			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Deбaryomycetaceae.Candida.Candida_dubliniensis</i>	2.41750741			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Saccharomycetaceae</i>	2.305843917			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Saccharomycetaceae.Kluyveromyces</i>	1.727315627			

<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Saccharomycetaceae.Kluyveromyces.Kluyveromyces_marxianus</i>	1.660701814			0.036203
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Saccharomycetaceae.Naumovozyma</i>	1.670485846			
<i>Fungi.Ascomycota.Saccharomycetes.Saccharomycetales.Saccharomycetaceae.Naumovozyma.Naumovozyma_dairenensis</i>	1.666733371			
<i>Fungi.Ascomycota.Sordariomycetes</i>	3.106327863			
<i>Fungi.Ascomycota.Sordariomycetes.Glomerellales</i>	1.705695112			
<i>Fungi.Ascomycota.Sordariomycetes.Glomerellales.Glomerellaceae</i>	1.71254858			
<i>Fungi.Ascomycota.Sordariomycetes.Glomerellales.Glomerellaceae.Colletotrichum</i>	1.705882489			
<i>Fungi.Ascomycota.Sordariomycetes.Glomerellales.Glomerellaceae.Colletotrichum.Colletotrichum_higginsianum</i>	1.705722405			
<i>Fungi.Ascomycota.Sordariomycetes.Hypocreales</i>	3.015441702			
<i>Fungi.Ascomycota.Sordariomycetes.Hypocreales.Nectriaceae</i>	3.021643673			
<i>Fungi.Ascomycota.Sordariomycetes.Hypocreales.Nectriaceae.Fusarium</i>	3.014636131			
<i>Fungi.Ascomycota.Sordariomycetes.Hypocreales.Fusarium.Fusarium_oxysporum</i>	3.005530202			
<i>Fungi.Ascomycota.Sordariomycetes.Magnaporthales</i>	2.056821436			0.046487
<i>Fungi.Ascomycota.Sordariomycetes.Magnaporthales.Pyriculariaceae</i>	2.063669521			0.046487
<i>Fungi.Ascomycota.Sordariomycetes.Magnaporthales.Pyriculariaceae.Pyricularia</i>	2.057010198			0.046487
<i>Fungi.Ascomycota.Sordariomycetes.Magnaporthales.Pyriculariaceae.Pyricularia.Pyricularia_pennisetigena</i>	1.79523275			
<i>Viruses</i>	2.70798843			
<i>Viruses.Peploviricota</i>	2.003246529			
<i>Viruses.Peploviricota.Herviviricetes</i>	2.006664887			
<i>Viruses.Peploviricota.Herviviricetes.Herpesvirales</i>	2.003313668			
<i>Viruses.Peploviricota.Herviviricetes.Herpesvirales.Herpesviridae</i>	2.019625161			
<i>Viruses.Peploviricota.Herviviricetes.Herpesvirales.Herpesviridae.Roseolovirus</i>	1.774440502			
<i>Viruses.Peploviricota.Herviviricetes.Herpesvirales.Herpesviridae.Roseolovirus.Human_betaherpesvirus_7</i>	1.774321203			
<i>Viruses.Uroviricota</i>	2.44077235			
<i>Viruses.Uroviricota.Caudoviricetes</i>	2.442092245			
<i>Viruses.Uroviricota.Caudoviricetes.Caudovirales</i>	2.440815465			
<i>Viruses.Uroviricota.Caudoviricetes.Caudovirales.Siphoviridae</i>	2.355120507			
<i>Bamfordvirae</i>	2.819310155	Very_high_risk	2.247017	0.036203
<i>Fungi</i>	4.038351074			

Note: LDA Linear Discriminant Analysis.

Table S7 Taxa differences between the very high risk group and the high risk group at the genus level

[illegible]

Note: Wilcoxon rank-sum test was performed on the abundance of all genera involved to screen for genera with $p < 0.05$, and only the top 30 genera with the highest relative abundance were detailed in the table if the number of divergent genera was greater than 30, and all divergent genera were displayed if the number of divergent genera was less than 30.

Table S8 Taxa distribution of the very high risk group and the high risk group at the species level

Note: Only the top 30 species in terms of mean relative abundance in the taxonomic units were detailed in the table; the rest were classified as other species.

Table S9 Taxa differences between the very high risk group and the high risk group at the species level

[illegible]

Note: Wilcoxon rank-sum test was performed on the abundance of all species involved to screen for species with $p < 0.05$, and only the top 30 species with the highest relative abundance were detailed in the table if the number of divergent species was greater than 30, and all divergent species were displayed if the number of divergent species was less than 30

Table S10 The results of the Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) values of the top 30 differential species between the very high risk group and the high risk group

Predictor variables	AUC	CI	Cut-off	Sensitivity	Specificity	Accuracy	Positive predictive value	Negative predictive value	Youden index
<i>Filifactor_alocis</i>	0.711	0.560 – 0.863	0.56654	0.88889	0.48387	0.63265	0.5	0.88235	0.37276
<i>Streptococcus_cristatus</i>	0.738	0.594 – 0.883	0.2866	0.83333	0.58065	0.67347	0.53571	0.85714	0.41398
<i>Pseudopropionibacterium_propionicum</i>	0.685	0.535 – 0.834	0.069568	0.83333	0.51613	0.63265	0.5	0.84211	0.34946
<i>Klebsiella_pneumoniae</i>	0.71	0.564 – 0.856	0.13339	0.94444	0.6129	0.73469	0.58621	0.95	0.55735
<i>Streptococcus_anginosus</i>	0.708	0.563 – 0.852	0.1355	1	0.3871	0.61224	0.48649	1	0.3871
<i>Abiotrophia_defectiva</i>	0.729	0.570 – 0.889	0.006519	0.88889	0.54839	0.67347	0.53333	0.89474	0.43728
<i>Phocaeicola_vulgatus</i>	0.692	0.544 – 0.840	0.054607	0.88889	0.51613	0.65306	0.51613	0.88889	0.40502
<i>Staphylococcus_aureus</i>	0.683	0.534 – 0.832	0.042672	0.88889	0.58065	0.69388	0.55172	0.9	0.46953
<i>Burkholderia_pseudomallei</i>	0.679	0.526 – 0.833	0.03165	0.94444	0.58065	0.71429	0.56667	0.94737	0.52509
<i>Actinomyces_viscosus</i>	0.69	0.529 – 0.851	0.043512	0.55556	0.87097	0.7551	0.71429	0.77143	0.42652
<i>Bacteroides_fragilis</i>	0.69	0.540 – 0.840	0.030784	0.77778	0.64516	0.69388	0.56	0.83333	0.42294
<i>Streptococcus_agalactiae</i>	0.674	0.504 – 0.844	0.028098	0.72222	0.77419	0.7551	0.65	0.82759	0.49642
<i>Faecalibacterium_prausnitzii</i>	0.694	0.536 – 0.851	0.018883	0.55556	0.80645	0.71429	0.625	0.75758	0.36201
<i>Streptococcus_dysgalactiae</i>	0.697	0.523 – 0.872	0.021742	0.66667	0.80645	0.7551	0.66667	0.80645	0.47312
<i>Streptococcus_sp_NSJ-72</i>	0.722	0.578 – 0.867	0.014395	0.61111	0.77419	0.71429	0.61111	0.77419	0.3853
<i>Fusobacterium_necrophorum</i>	0.672	0.520 – 0.824	0.023846	0.83333	0.51613	0.63265	0.5	0.84211	0.34946
<i>Staphylococcus_haemolyticus</i>	0.697	0.549 – 0.845	0.020433	0.94444	0.54839	0.69388	0.54839	0.94444	0.49283
<i>Clostridioides_difficile</i>	0.717	0.568 – 0.865	0.015833	0.66667	0.70968	0.69388	0.57143	0.78571	0.37634
<i>Streptococcus_equi</i>	0.71	0.562 – 0.857	0.018335	0.83333	0.6129	0.69388	0.55556	0.86364	0.44624
<i>BeAn_58058_virus</i>	0.681	0.530 – 0.832	0.012298	0.88889	0.6129	0.71429	0.57143	0.90476	0.50179
<i>Schaalia_cardiffensis</i>	0.735	0.588 – 0.881	0.004858	0.66667	0.83871	0.77551	0.70588	0.8125	0.50538
<i>Streptococcus_pseudoporcinus</i>	0.749	0.608 – 0.890	0.012737	0.94444	0.45161	0.63265	0.5	0.93333	0.39606
<i>Capnocytophaga_haemolytica</i>	0.731	0.591 – 0.871	0.004905	0.88889	0.51613	0.65306	0.51613	0.88889	0.40502
<i>Treponema_phagedenis</i>	0.713	0.569 – 0.857	0.012264	0.94444	0.45161	0.63265	0.5	0.93333	0.39606
<i>Parabacteroides_distasonis</i>	0.69	0.535 – 0.845	0.008597	0.66667	0.74194	0.71429	0.6	0.7931	0.4086
<i>Bacteroides_thetaiotaomicron</i>	0.677	0.524 – 0.831	0.007566	0.66667	0.67742	0.67347	0.54545	0.77778	0.34409
<i>Streptococcus_sp_NCTC_11567</i>	0.692	0.543 – 0.841	0.009582	0.94444	0.58065	0.71429	0.56667	0.94737	0.52509
<i>Streptococcus_porcinus</i>	0.717	0.558 – 0.876	0.007375	0.88889	0.58065	0.69388	0.55172	0.9	0.46953
<i>Bacteroides_caccae</i>	0.679	0.518 – 0.840	0.00553	0.77778	0.6129	0.67347	0.53846	0.82609	0.39068
<i>Roseburia_intestinalis</i>	0.735	0.591 – 0.879	0.005009	0.66667	0.70968	0.69388	0.57143	0.78571	0.37634

Note: CI Confidence Interval.

Table S12 Differential functional KEGG pathways between the very high risk group and the high risk group

Pathway_id	Level 2	Description	Reportscore	Remain_or_delete
map00290	Amino acid metabolism	Valine, leucine and isoleucine biosynthesis	-3.725266794	remain
map00480	Metabolism of other amino acids	Glutathione metabolism	-2.076730382	remain
map00061	Lipid metabolism	Fatty acid biosynthesis	-2.445456894	remain
map00770	Metabolism of cofactors and vitamins	Pantothenate and CoA biosynthesis	-2.739604711	remain
map00190	Energy metabolism	Oxidative phosphorylation	-3.692320229	remain
map00400	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	-1.893020755	remain
map00300	Amino acid metabolism	Lysine biosynthesis	-3.275681378	remain
map00720	Energy metabolism	Carbon fixation pathways in prokaryotes	-1.668956637	remain
map00650	Carbohydrate metabolism	Butanoate metabolism	3.996656607	remain
map00571	Glycan biosynthesis and metabolism	Lipoarabinomannan (LAM) biosynthesis	1.68749544	remain
map00020	Carbohydrate metabolism	Citrate cycle (TCA cycle)	-2.522014353	remain
map00051	Carbohydrate metabolism	Fructose and mannose metabolism	2.705069985	remain
map00130	Metabolism of cofactors and vitamins	Ubiquinone and other terpenoid-quinone biosynthesis	-2.757697456	remain
map00470	Metabolism of other amino acids	D-Amino acid metabolism	2.562357627	remain
map00540	Glycan biosynthesis and metabolism	Lipopolysaccharide biosynthesis	-3.198859895	remain

Note: Only the pathways with a Reporter Score>1.65 or <-1.65 were displayed.