Prevotella diversity, niches and interactions with the human host

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Abstract

The genus *Prevotella* includes more than fifty characterized species occurring in very different natural habitats, yet the majority have been associated with the human host. In the human microbiome, *Prevotella* species are highly abundant in different body-sites where they are key players in the balance between health and disease. Host factors related with diet, lifestyle, and geography are fundamental in affecting *Prevotella* species- and strain-level diversity in the human microbiome. These factors, along with the ecological relationship of *Prevotella* with other members of the microbiome, likely determine the extent of *Prevotella* contribution to human metabolism and health. Here we review the diversity, prevalence and impact of *Prevotella* spp. in the human host highlighting how genomics has improved, and will further help framing its ecological role. We also provide suggestions for future research to better understand their possible functions and the role of Westernisation in the host-*Prevotella* symbiotic relationship in the context of maintaining human health.

Introduction

Prevotella is a diverse genus of gram negative anaerobic bacteria. The genus was first suggested in 1990 by Shar and Collins as a reclassification of certain oral species based on specific phenotypic traits (moderately saccharolytic capabilities and bile salt sensitivity) and a phylogeny that distinguished them from *Bacteroides,* in which they were originally placed. The name *Prevotella* was given in honour of the pioneering anaerobic microbiologist A. R. Prévot [1]. The type strain for the genus is *P. melaninogenica* isolated by Oliver and Wherry in 1921 from differing human body-sites, so called due to its black colonial pigmentation [1,2]. *Prevotella* are non-spore forming and non-motile short rods that are either saccharolytic or moderately so [3,4]. *Prevotella* now sits in the family *Prevotellaceae*, which comprises three other closely related genera: *Paraprevotella*, *Alloprevotella* and *Hallella*.

Prevotella species have been isolated from a number of animal hosts and even free living in the environment. In comparison to other genera containing members with clear associations with disease or with convenient cultivation protocols, *Prevotella* has received less attention possibly due to potential limitations and confusion in phenotype-based identification of strains [5,6]. Nevertheless, the advent of cultivation-free microbial profiling have shown *Prevotella* species are a common, abundant, and consistent feature of the human- and mammalian-associated microbial community (microbiome) inhabiting multiple body-sites, including skin, oral cavity, vagina and the gastrointestinal tract. These species are not rare, in the oral cavity they represent one of the most dominant genera [7]. In populations that are rural and follow a more pre-industrial traditional lifestyle and diet - the so-called “non-Westernised populations” - *Prevotella* tend to dominate [8–15]. Westernisation is the consequence of industrialization of the past two hundred years. While separating populations into Westernised and non-Westernised demarcates what is best seen as a continuum and is not without its difficulties as previously discussed [14–16], multiple reports have consistently highlighted a decreased prevalence of *Prevotella* in Westernised populations generally compensated by the domination of *Bacteroides* species [8–15]. Our understanding of the human microbiome is skewed towards Western populations and as such *Bacteroides* spp. have received more attention compared to *Prevotella,* although as the number of non-Westernised populations sampled expand, the diversity, dominance and importance of *Prevotella* is becoming increasingly evident. This is particularly true for intestinal *Prevotella* that have been shown to be longstanding key members of our co-evolved microbiome, supporting the hypothesis that modern lifestyle is causal in the loss of *Prevotella* diversity and further raising the question about what are the consequence of their loss from a health perspective [16].

Despite the abundance and prevalence of human associated *Prevotella* species, their involvement in health and disease, their role within the microbiome and in host-microbiome crosstalk is unclear. *Prevotella* contains no known obligate pathogenic species, yet members have been implicated in multiple diseases, including inflammatory autoimmune disease [17], opportunistic infections [18–21], bacterial vaginosis [22] and biofilm formation and oral diseases [23,24], although direct causation of disease is uncertain. Similarly, in the intestine, conflicting reports have been given regarding whether *Prevotella* is beneficial or detrimental to health, particularly in glucose homeostasis [25–27]. Associating *Prevotella* and disease is likely further confounded by the recent discoveries that this genus may be more diverse than previously appreciated [4,16]. In the current view of the human microbiome as an integral part of human biology, *Prevotella* is an exemplar case of a genus likely involved in intricate ecological and human-crosstalk interaction, with indirect but potential major effects on human health.

In light of the open questions regarding these enigmatic bacteria, it is timely to discuss the genus *Prevotella* and its association and distribution on and within the human host, across age,

lifestyles and disease. Using available genomes from cultivated strains as well as genomes recovered directly from thousands of metagenomic samples (**Box 1**), we explore and summarise the overall *Prevotella* diversity in the context of what is currently known, ultimately discussing the role of *Prevotella* species in human health and disease.

Prevotella is a phylogenetically diverse genus with multiple ecological niches

Since their initial isolation from the human oral cavity and respiratory tract, *Prevotella* species have been identified and shown to occupy an ecological diverse number of habitats. Currently, there are 57 named *Prevotella* species isolates publicly available (**Figure 1, Table 1**, **Supplementary Table 1**). By far the largest number of isolates and known species are associated with human hosts, but *Prevotella* species have also been identified in other mammalian species. Of non-human hosts, *Prevotella* spp. are a common and predominant feature of ruminants with *P. bryantii*, *P. ruminicola*, *P. brevis* and *P. albensis* being some of the best known members [28,29]. Collectively, *Prevotella* is integral in the carbohydrate utilisation in the rumen [30] and is a common feature particular of the swine microbiome [31,32]. Other *Prevotellaceae* genomes have been recovered from non-human primates, dogs and mice [33,34] (**Supplementary Table 1**). In non-mammalian environments, sources include the fermentative crop of the avian species *Opisthocomus hoazin* (the hoatzin), and they have also been identified free living in natural habitats including soil [35].

What is distinguishing between human and non-human isolates is their species-level evolutionary history (as inferred by whole-genome phylogenetics, **Fig. 1**), with large subtrees clustering in which human species largely separated from those of non-human origin (**Fig. 1**), and a large multi-species clade comprising *P. ruminicola* and *P. brevis* and numerous unnamed species specific to swine and ruminants. The size of the isolate genomes vary, with the largest (4.26Mb) being a member of *P. copri* complex and the smallest (2.37Mb) from *P. amnii* (**Fig. 1, Table 1**). As comparison, such numbers are lower than the average length of Bacteroides *spp.* (5.46Mb from 1,116 isolate genomes). There is also a considerable spread in G+C content across the genus ranging form 36.4% (*P. amnii*) to 56.1% (*P. dentalis*) (**Table. 1**), further evidence of the remarkable diversity in the *Prevotella* genus. A comparison of the core genome associated with species for which there are multiple independent isolates reveals *Prevotella* spp have a core of ~1200-1900 genes with the core genome accounting for ~50-75% of the genome, which is consistent even for species from different host-types (**Fig. 1**). *Prevotella* is a diverse microbial genus, yet like most isolate collections they are likely biased, increased isolation efforts from animal species and undersampled environments will surely expand the number of hosts and diversity of *Prevotella* species.

The ecological importance of bacteriophages (phages) in shaping the complex host-associated microbiome is undoubted, nevertheless investigation of these phage communities is still in its infancy [36]. Consequently little is also known about *Prevotella*-specific phages, with only a few reports describing those associated with *Prevotella* species in ruminants [37,38]. Recently, metagaenomically-based discovery has identified large “megaphages”, Lak phages, associated with *Prevotella* in humans, non-human primates, other mammalian hosts and also reptiles [39,40]. These phages utilise an alternative genetic code and with a genome size upto ~660 kbp they represent the largest known intestinal phages discovered to date [40]. The identification of these diverse phages raises intriguing questions on their ability, and the implications of modulating *Prevotella* populations in the intestine.

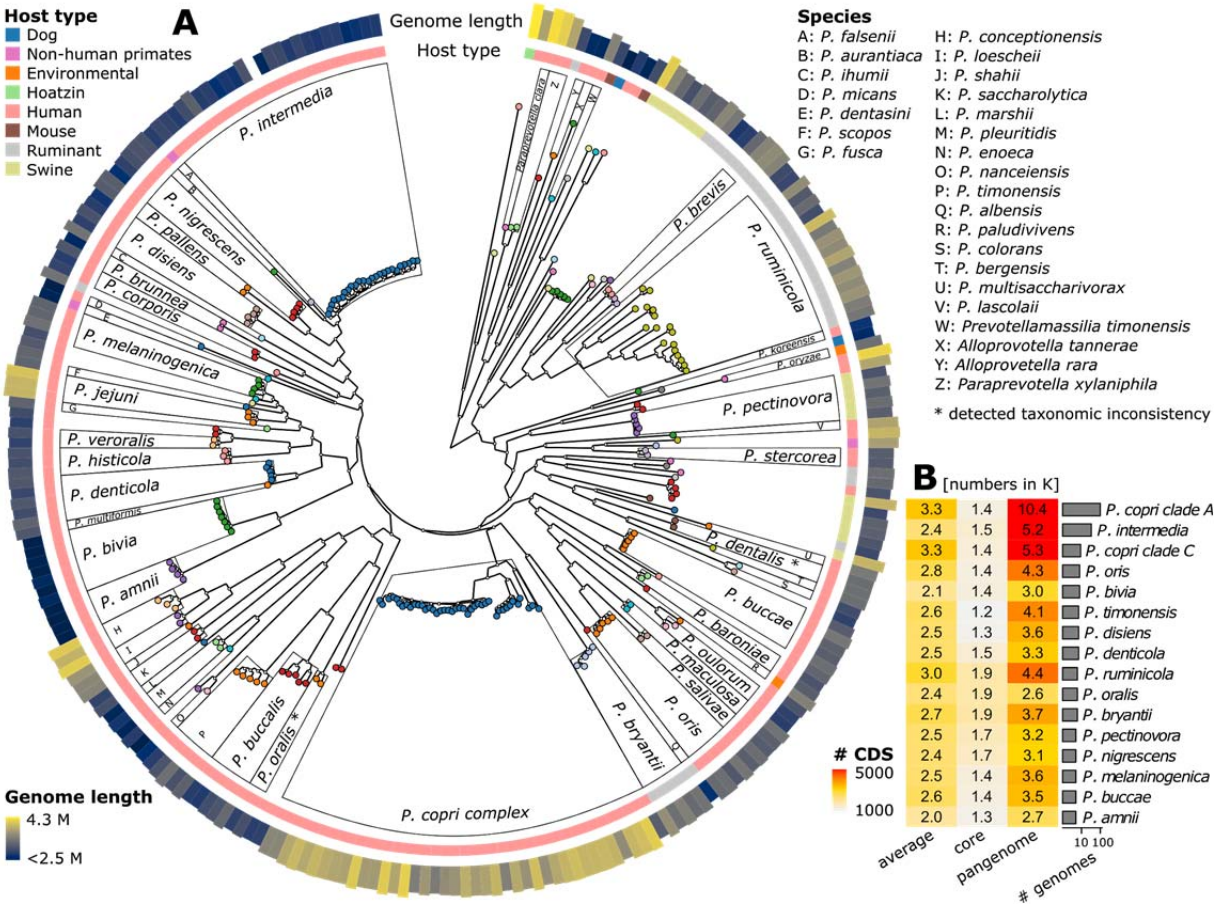

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Fig. 1 - **Genomic overview of the *Prevotella* genus by a whole-genome analysis using all currently available *Prevotella* genomes from isolates in public repositories** (**A**) Phylogenetic tree of reference genomes of strains of *Prevotella* and other *Prevotellaceae* species (**Table 1, Supplementary Table 1**) with an indication of their ecological niches. The largest number of genomes are associated with human hosts, although they are identified also in other seven host types. Species exhibit variable genome length ranging from 4.26Mb for *P. copri* to 2.37Mb for *P. amnii*. Only named species are reported in the tree that was built using a maximum likelihood approach applied on marker genes (Supplementary note). (**B**) Statistics on the number of coding sequences (CDS) for the species with at least five available genomes. The average number of CDS vary between 2,000 and 3,300. The core size (i.e., number of CDSs present in virtually all genomes) is variable from 1,200 to 1,900 genes. The pangenome size varies between 2,600 and 10,400, which is however partially affected by the number of available genomes (Spearman correlation between genome number and pangenome size = 0.64).

Table 1. Main genomic characteristics of *Prevotella* species with at least 3 sequenced genomes. (See **Supplementary Table 1** for the complete list and the genome list)

Species name	# of	Average	GC content	Host(s)	Host site(s)

	genomes	genome length (Mb)	(perc)		
P. copri complex	106	3.65±0.21	44.93±0.23	human	gut
P. intermedia	33	2.79±0.13	43.45±0.15	human	oral,empyema
P. ruminicola	9	3.53±0.3	47.69±0.71	ruminant	rumen
P. bivia	8	2.49±0.08	39.79±0.17	human	vagina
P. denticola	7	3.06±0.11	50.04±0.18	human	vagina,oral
P. disiens	7	2.86±0.13	39.93±0.21	human	vagina,gut,bartholin abscess
P. timonensis	7	3.09±0.16	42.41±0.16	human	vagina,breast abscess
P. bryantii	6	3.41±0.14	38.8±0.19	ruminant	rumen
P. amnii	5	2.4±0.03	36.52±0.08	human	vagina,amniotic fluid
P. melaninogenica	5	3.14±0.12	41.02±0.23	human	vagina,oral,sputum
P. nigrescens	5	2.85±0.16	42.64±0.11	human	oral
P. oralis	5	2.87±0.07	44.54±0.09	human	vagina,gut,oral
P. oris	5	3.18±0.12	43.86±0.09	human	oral,airways
P. pectinovora	5	3.17±0.12	47.74±0.25	swine	gut
P. buccae	4	3.22±0.12	51.15±0.19	human	oral
P. buccalis	4	2.99±0.2	45.5±0.18	human	vagina
P. baroniae	3	3.09±0.06	53.1±0.17	human	oral
P. corporis	3	2.81±0.04	44.1±0.1	human	vagina
P. histicola	3	3.0±0.06	41.2±0.0	human	vagina,oral
P. loescheii	3	3.49±0.02	46.6±0.0	human	oral
P. maculosa	3	3.25±0.09	47.5±0.17	human	oral
P. micans	3	2.45±0.03	45.5±0.0	human	oral
P. oulorum	3	2.82±0.02	46.8±0.0	human	oral
P. pallens	3	3.1±0.04	37.47±0.06	human	oral
P. salivae	3	3.22±0.1	41.5±0.17	human	gut,oral
P. scopos	3	3.23±0.06	40.7±0.0	human	oral
P. stercorea	3	3.11±0.01	48.93±0.06	human	gut
P. veroralis	3	2.89±0.09	41.83±0.06	human	oral

Prevotella **in humans: different key species in different body-sites**

Even within a given host, *Prevotella* species are stratified in different body locations. Specifically in humans and similarly to other genera [41], distinct *Prevotella* species have been identified and isolated from the oral cavity and respiratory tract, vagina, skin and intestine. Surveying the prevalence and abundance of the known characterised *Prevotella* species in over 9,500 individuals from multiple integrated datasets [15], reveals that with the exception of vaginal *Prevotella* species, most species are body-site specific (**Fig. 2A-B**). A previous analysis of human *Prevotella* isolates identified differing functional potential at different body-sites, suggesting niche-specific differentiation and specialism [42]. Further stratification is also observed across lifestyle, with non-Westernised individuals that follow a more traditional lifestyle and diet tending towards a higher prevalence of *Prevotella* [8–13], both in the gut and oral cavity (**Fig. 2C**).

The distribution of *Prevotella* species is also influenced by age, in the gut both *P. copri* and *P. stercorea* show an age-dependent increase in prevalence regardless of Westernisation, although their relative abundance drops from adulthood to seniority (**Fig. 2A-B**). However, some species (*P. bivia*, *P. timonensis*, *P. buccalis, P. disiens* and *P. corporis*) seem to have the highest prevalence in the gut of senior subjects in Westernised populations, and they intriguingly have a correspondingly similar prevalence pattern in the vagina (**Fig. 2A-B**). Sex effects have also been oberved with *Prevotella* being more prevalent in men than women [43,44]. However, female hormones metabolism appears to be linked to the regulation of *Prevotella* spp. in the human body. Hormonal steroids can favour the growth of *P. intermedia* and *P. melaninogenica* from the oral cavity [45,46] and affect oral microbial ecology and occurrence of gingivitis in hormone-driven diseases [47]. Evidently what drives the distribution and prevalence of *Prevotella* species in the human host is multifaceted across body-site, lifestyle, sex and age and it is an area of continued research.

While isolation has been, and continues to be, a stalwart of microbiological research, recently culture-independent methods offer a new complementary approach in microbial discovery. For instance, identifying and recovering genomes directly from mixed environmental samples (metagenomes) has begun to transform our understanding of the true microbial diversity in natural systems [4,15,16,48–51] (**Box 1**), and gives an unprecedented opportunity to characterize the role and ecology of *Prevotella* by exploiting the increasingly available large metagenomic datasets. To assess the *Prevotella* diversity in the human host, we examined 7,480 *Prevotella* assigned metagenome assembled genomes (MAGs) from >9,500 metagenomes covering multiple human geographies, lifestyles and body-sites [15]. In total 56 species-level genomes bins (SGBs; using a 5% nucleotide whole-genome distance threshold to define the bins) were identified with at least twenty genomes reconstructed from human sources. Of these, only 32 were populated with at least one isolate genome with assigned taxonomy (**Fig. 3A**), demonstrating human associated *Prevotella* spp. are far more diverse than appreciable from the current catalogue of *Prevotella* isolates. These unnamed and uncharacterized *Prevotella* SGBs are not all rare metagenomic occurrences, as in some cases hundreds of genomes were recovered from independent metagenomic samples (**Fig. 3A,B**). Of note are nine uncharacterized SGBs being at the boundary of *Prevotella* (**Fig. 3A**, subtree at the root) and comprising only two genomes labelled as "*Prevotellaceae* bacterium".

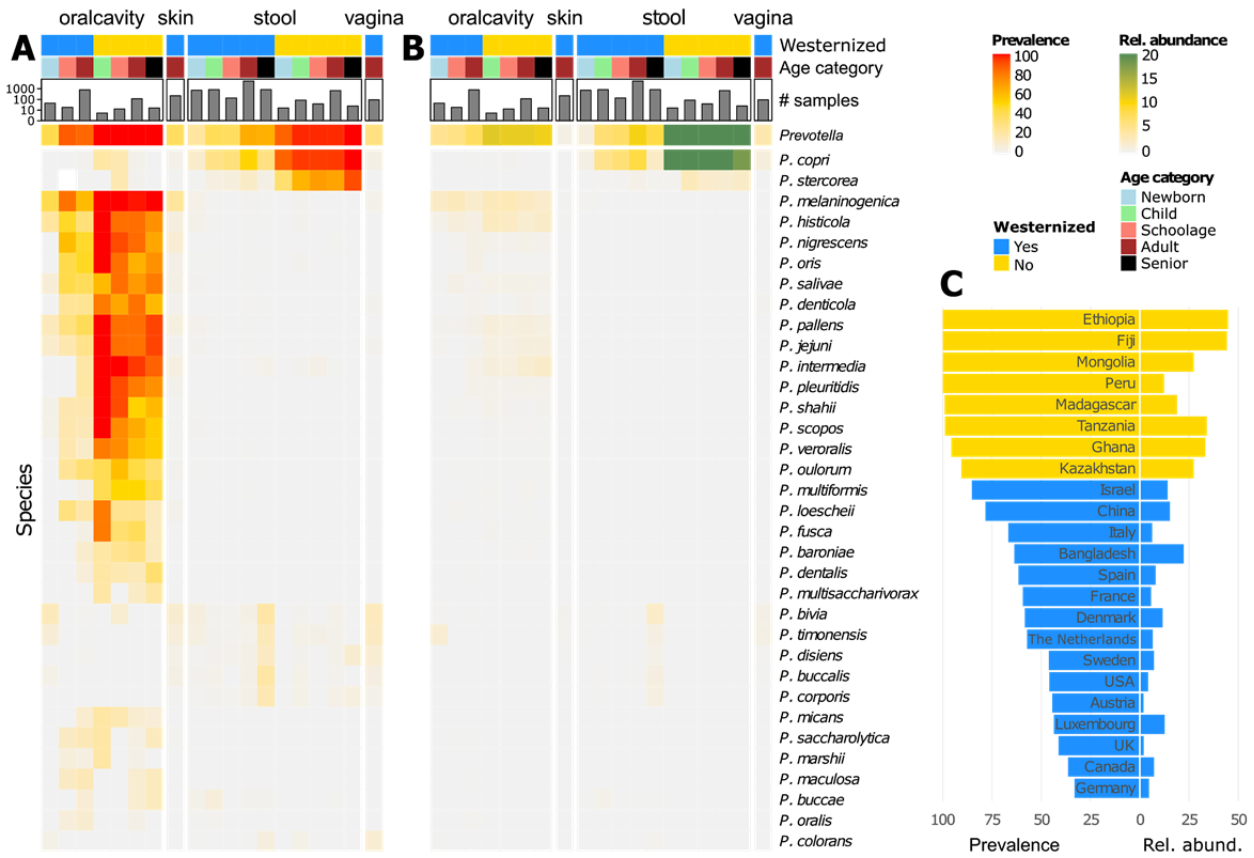

Fig. 2 - Distribution and stratification of *Prevotella* species across human populations and body-sites. (**A**) Prevalence and (**B**) relative abundance of known *Prevotella* species across four main body-sites which are the oral cavity (saliva or oral swabs), the skin (cutaneous swabs), the gut (stool samples), and vagina (vaginal swabs), and across five age categories (i.e., newborn, child, school-age, adult, and senior), and two main lifestyles (i.e., westernized and non-Westernized). These data were obtained by exploiting public integrated repositories of >9,500 profiled human metagenomes. Only named species with prevalence > 0.1% in at least one category are reported. Most species are body-site specific, and further differences are observed across age categories. (**C**) Prevalence and relative abundance of *Prevotella* in the gut are largely influenced by lifestyle. Non-westernized populations (yellow bars) that follow a more traditional diet and lifestyle are enriched in *Prevotella* species, and this is consistently observed across countries (extended heatmaps in **Supplementary Fig. 1**).

Prevotella in the oral cavity: from commensals to pathobionts

The oral cavity is by far the body-site hosting the largest diversity of known human *Prevotella* species (**Fig. 2 and 3**). While the human gut may still harbour many undiscovered *Prevotella* species particularly recalcitrant to cultivation (**Fig. 3B)**, the oral taxa from this genus have been studied long before cultivation-free surveys [52] , owing to their less complex cultivation conditions and their potential - sometimes confirmed - role in oral diseases [53] and systemic infections [54]. The total abundance of the *Prevotella* genus in the oral cavity of healthy individuals exceeds, on average, 10% of the whole microbiome in the saliva (13.0%), tongue (10.3%), tonsils (11.4%), and throat (11.6%) according to the first comprehensive 16S rRNA gene sequencing investigation [7]. Recent microbiome studies confirmed even higher salivary average abundances

(from 12% to 17%) in multiple socioeconomic and age categories [55,56] making *Prevotella* the most abundant oral genus after *Streptococcus*. Slightly lower *Prevotella* abundances are estimated in oral locations with more divergent structural and biochemical conditions such as the dental plaque, the gingiva and the buccal mucosa [7]. The integrative analysis we report in **Fig. 2** collapses all oral body-sites for an overall *Prevotella* prevalence of 85% in Westernised populations and 100% in non-Westernised populations, with average abundances of 7.4% and 11.5% respectively. Our oral metagenomic data for non-Westernized populations is based on a single cohort from Fiji [57], but re-analysis of another work [58] reinforced the intriguing observation of higher prevalence and abundance of *Prevotella* in the oral cavity of individuals not belonging to Western-style industrialized populations. Interestingly, the levels of salivary *P. intermedia* have been shown to decrease upon Mediterranean diet nutritional intervention in obese subjects [59] suggesting a dependency of oral *Prevotella* from lifestyle factors that may include those connected with the Westernization process.

Genus-level quantification clearly conceals extensive species-level and inter-individual diversity which is now readily available via shotgun metagenomics [60]. Available metagenomic analyses [61–65] point to the presence of at least 15 known *Prevotella* species in the oral cavity (and a couple of yet-to-be-characterized taxa, **Fig. 3**), however individuals are dominated by *P. melaninogenica* and to a slightly lesser extent *P. histicola* and *P. intermedia* in adult non-Westernised populations (**Fig. 2**). Recent analyses for other oral genera in the context of the healthy oral microbiome such as *Neisseria* [41], *Streptococcus* [66] and others [67,68] revealed extensive strain-level variation hidden at the species level, and that strains within a species are subject-specific except for related individuals such as mother-infant couples in which direct transmission can occur [63,69,70]. Currently such strain level analyses are not available for oral *Prevotella*, and while the degree of within-species genetic and genomic variability is species-specific, it is likely that similar strain level variation and subject specificity would also be observed for *Prevotella* species.

As for other members of the oral microbiome, oral *Prevotella* species have the potential to seed the lower gastrointestinal tract. A systematic metagenomic investigation of oral-to-gut microbial transmission [71] indeed found that all oral *Prevotella* species can occasionally be found in the stool microbiome (**Fig. 2B**), and in most cases the oral and gut strains were the same within a host thus suggesting a direct oral-faecal route in healthy individuals. Interestingly, high enrichment in the gut of oral species has been observed in newly diagnosed colorectal cancer patients [72,73] however, only *P. intermedia* and to a lesser extent *P. nigrescens* are biomarkers of this oncological condition. Oral *Prevotella* seeding of the gut environment appears to be a physiological mechanism, but oral *Prevotella* species have nonetheless been implicated occasionally in systemic infections [74].

In the oral cavity *Prevotella* is also involved in the biofilm-formation process potentially connected with low oral hygiene care [24] as well as in the etiology of oral diseases such as the very prevalent gingivitis and periodontitis [23]. *P. nigrescens* and *P. intermedia* are particularly associated with the plaque microbiome in periodontitis as already established in the pre-sequencing era by Socransky et al. [75] and these two species may promote tissue inflammation by driving Th17-mediated immune responses [23,76]. Complementary FISH-based investigations of the dental plaque [77,78] intriguingly pointed to *Prevotella* as one of the early necessary colonizers for stable biofilm formation. In the complex biofilm formation process, several *Prevotella* species including *P. loescheii*, *P. intermedia*, and *P. denticola* may be functional in early and middle stages in promoting cell-to-cell adhesion and to favour later colonizers [79,80]. The microbial consortia in oral biofilms can be very diverse and *P. intermedia* can for example

mimic streptococcal structures when *Streptococcus* species are not part of the multispecies biofilm [81]. They can also synergistically support *Aggregatibacter actinomycetemcomitans*, a species strongly associated with aggressive periodontitis [82], via molecular inter-species regulation [83]. Although an area of continuous research for many years, the complexity of oral biofilm formation and its intricate interactions with host tissues and immunology remain only partially understood. Moreover, the hypothetical role of low-abundance taxa and of synergistic bacterial interactions [84] further underlines the relevance of biofilm formation both as a model for microbial ecology and as a potential therapeutic target. *Prevotella* is likely one of the most relevant genera in this context as it was found by physical proximity analysis to be, together with *Actinomyces*, the genus with the highest number of interacting oral genera [77].

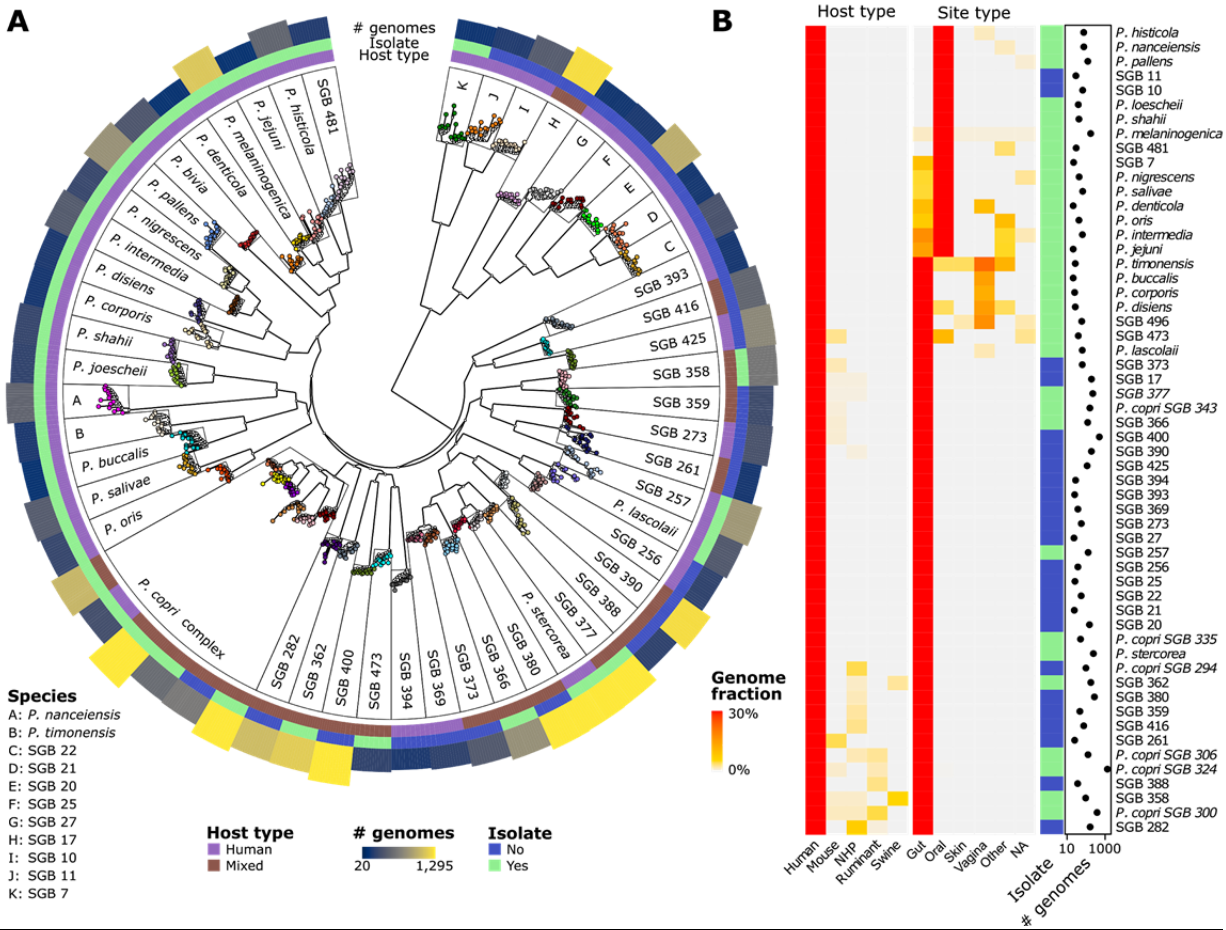

Fig. 3 - Current diversity of known and unknown *Prevotella* species in the human microbiome. (**A**) The large phylogenetic tree spanning the 56 most prevalent (at least twenty genomes retrieved from human microbiomes) *Prevotella* species by integrating isolate sequences with metagenome assembled genomes (MAGs) retrieved from >10,000 metagenomes and >50 human populations. For each species, fifteen randomly selected genomes are reported along with the information on the host type (i.e., human or mixed sources), the public availability of isolate sequences, and the number of retrieved genomes (see **Supplementary Note**). The tree highlights the gap in strain isolation with 24 human-associated species that completely lack isolate genomes, the within-species strain diversity, and the remarkably well-defined taxonomic species based on the inter- vs- intra species diversity. (**B**) The fraction of *Prevotella* genomes retrieved from human and non-human hosts

(both from isolation and MAGs) and different human site type suggest multiple ecological patterns. Along with human-specific species, others are shared across two or more host types. Moreover, we highlight the presence of few species that are ecologically adapted to multiple human body-sites, which is also possibly due to the influx of oral species into the lower gastrointestinal tract [71].

Despite their abundance and role, oral *Prevotella* species are still understudied compared to other oral bacteria. Overall there is a limited body of work particularly in the comparative analysis of oral *Prevotella* [85] , and clearly more studies are required to better understand their characteristics and ecological role in the oral microbiome [86,87].

Prevotella in the female urogenital tract

The human vaginal microbiome has been comprehensively surveyed and *Prevotella* stood out as one the dominant genera [88]. The most prevalent species are *P. bivia*, *P. timonensis*, *P. buccalis, P. disiens* and *P. corporis.* Interestingly, these species belong to separate phylogenetic clusters and none has the urogenital tract as their unique occurrence site, as they also occur either in the oral and gut microbiome (**Fig. 2**). However, it is possible that for these species genomic adaptation to the different body-sites may occur at the sub-species level and is therefore unobservable at the species level. *Prevotella* have a recognized role in bacterial vaginosis (BV), which occurs upon loss of the protective guilds of the normally dominant *Lactobacillus* species and the establishment of strictly anaerobic microbes [22]. They have been shown to be the most heritable vaginal bacteria and also to be associated with increased BMI [22,89]. *P. bivia* is an important source of ammonia, lipopolysaccharide and sialidase activity in vaginal mucus and linked to epithelial cytokine production, identified in infected uterine and placental tissues and amniotic fluid during pregnancy complications [90–92]. *P. bivia* often co-occurs with *Gardnerella vaginalis*, and this is recognized as a clear example of how microbial species can establish synergies in certain environments. The two microbes are co-abundant in the vagina and both are increased in cases of BV [93], although neither induce a robust inflammatory response [94]. Their co-inoculation has no major effect on their growth in mice models of BV, although co-colonization appeared to increase the chances of *P. bivia* ascension to the uterus [90], which is relevant for the recognized association of *Prevotella* with preterm birth [95–97]. Interestingly, a network of other species of *Prevotella* including *P. amnii*, *P. buccalis*, *P. timonensis* can co-occur in other infections such as those caused by *Chlamydia trachomatis* [98] and have a role in BV and increasing predisposition to viral infections such as HIV [99,100]. *P. timonensis* interacts with vaginal dendritic cells determining mucosal inflammation [101] and has also recently been associated with persistence and slower regression of cervical intraepithelial neoplasia [102].

In absence of further evidence elucidating the mechanisms of action of the *Prevotella* species and strains in the development of BV and related diseases, *Prevotella* simply appears as an inhabitant of the female uro-genital tract opportunistically increasing in the cases of impoverishment of the protective vaginal lactobacilli community.

Intestinal *Prevotella* species and the expanded diversity in the *P. copri* complex

The human gut is home to many microbial species mostly belonging to the Firmicutes or Bacteroidetes phyla [61,103]. Of the Bacteroidetes, two genera tend to dominate, *Bacteroides* and *Prevotella* while several genera including *Ruminococcus*, *Blautia*, *Eubacterium*, and *Faecalibacterium* represent the *Firmicutes*. The observation that these groups of taxa drive a subject-specific microbiome type led to the concept of the human gut enterotypes [104]. Since its

introduction almost 10 years ago, this concept has fed further studies and fueled debate within the field, [105] which resulted in a revisited formulation of the enterotypes as non-discrete microbiome types [106]. What is clear is *Prevotella* (particularly members of the *P. copri* complex) appears to be a discrete and well defined feature of the gut microbiome, and their relative abundance is inversely correlated to *Bacteroides,* i.e. the presence of one appears to co-exclude the other [61,104,107]. Nevertheless, quantitative profiling based on absolute abundances have suggested this inverse correlation may simply be an artifact of relative abundance microbiome approaches [108]. In the human gut the prevalence of *Prevotella* varies on average from 20 to 100% depending on the population surveyed [109]. Of the characterised *Prevotella* species, *P. stercorea* and the *P. copri* complex are the two most common. Of note is that these two species despite both being identified in the gut are more phylogenetically distant from each other compared to other *Prevotella* spp. that occupy other niches (**Fig. 1** and **Fig. 2**). Yet, analysis of MAGs suggests that the number of *Prevotella* species in the gut is underestimated, with 22 additional SGBs with at least twenty MAGs reconstructed from gut microbiomes being identified that are not represented by a genome from an isolate (**Fig. 3**).

Of the human intestinal *Prevotella* species, the most recognised and relevant member is *P. copri*. While *P. copri* is not universally present, when identified it tends to be highly abundant [15]. *P. copri* has increasingly become under the spotlight driven by differential accounts on whether it is either positive or detrimental to human health [25–27]. For the latter, it has been implicated with inflammatory conditions including rheumatoid arthritis (RA) [17,110,111], ankylosing spondylitis [112], and HIV infection [113], and in exacerbating pathogen intestinal infection [114]. Amongst these conditions, the association of *Prevotella* and *P. copri* with RA[115] was reported based on its abundance in the fecal microbiome [17,116,117] and presence directly in the synovial fluid [110,118] (see also **Supplementary Table 2**). An increased *Prevotella* abundance has not only been associated with overt RA, but also with a RA-predisposing genotypes before disease onset, and in individuals with a high-risk of RA development [111,119]. In preclinical models, faecal transplantation from early-stage RA patients with increased abundance of *P. copri* induced a proinflammatory Th17 T-cells response and RA phenotype in RA-prone mice [120]. Proinflammatory Th-17/Th-1 immune responses mediated by *P. copri*-specific antibodies have also been reported in RA patients [17,110,111]. Beyond associations with disease, studies have also suggested contrasting diet-dependent effects of *P. copri* on insulin resistance as discussed below. Of note is that studies of *Prevotella* and particularly *P.copri* dietary or disease associations have mostly relied on the type strain DSM18205 [121], although *P. copri* has been observed to display considerable sub-species strain level variation [67,122,123]. Therefore, future mechanistic and intervention studies should better factor in such strain-level diversity as some of the observed host phenotypes could be sub-species dependent.

Recently, two studies expanded the concept of *P. copri* genetic and functional diversity, combining a large-scale meta-analysis of publicly available metagenomes (>6,800) with a targeted isolation and sequencing of human *P. copri* isolates [4,16]. What was evident is that unlike previously assumed, *P. copri* is not monotypic (i.e. not a single species-level lineage) but is actually composed of four genetically distinct clades, which comprise the *P. copri* complex (**Fig. 1**) [16]. These clades (designated A-D) are distinct from each other at an average nucleotide identity (13-21.4%) greater than would be expected within a single species lineage (<5-6%) [124–126]. *Prevotella* spp. have long been associated with non-Westernised populations (i.e. in individuals following more traditional dietary habits and lifestyles) where they tend to predominate [8–13]. Analysing the prevalence of the complex in these populations confirmed *P. copri* is very common (95.4% non-Westernised versus 29.6% Westernised)[16] and a long-standing constituent of the human microbiome, having been identified in ancient faecal and intestinal contents (**Box 2**), but is rapidly being lost due to the process of Westernisation.

Another revelation was the presence of multiple cohabiting *P. copri* clades within an individual. In fact, it was more likely to identify multiple *P. copri* rather than a single clade in a non-Westernised individual (>2 clades 93.5% non-West versus 32.1% Westernised) [16]. This suggests that the members of the *P. copri* complex are niche-separated and potentially complementary as it has also been described in mice studies [127].

Enigmatic links between gut *Prevotella* and diet, lifestyle and health

Intestinal *Prevotella* and the *P. copri* complex in particular are traditionally associated with non-Western diets and to nutritional patterns rich in carbohydrates, resistant starch, and fibre [8,128–132]. In Western-style diets, members of Clostridia (*Ruminococcaceae* and *Lachnospiraceae*) often contribute as fiber degraders [133], although nutritional interventions with fibre-rich foods usually determine an increase in *Prevotella* [131,134–137]. In addition, a loss of members of the *Bacteroidales* order (including *Prevotella*) was observed upon consumption of a diet with low amounts of microbiota-accessible carbohydrates from dietary fibre in a humanized mice trial [138]. The first attempts to develop a microbiome-oriented personalised nutrition, have demonstrated that having subjects stratified based on microbiome composition may be a way to maximize clinical responses to dietary treatments. Indeed, the *Prevotella*-rich subject-type was found to potentiate weight loss [139–142], decrease cholesterol [143] and to limit the bifidogenic effect [144] in individuals following a fiber-rich diet. Improved glucose metabolism upon fibre consumption, has been attributed to a higher *Prevotella/Bacteroides* ratio and succinate metabolism [145,146]. Recently, looking at associations between gut bacteria and postprandial responses in over 1,000 individuals, identified *P. copri* as potentially beneficial in glucose homeostasis and host metabolism [147]. By contrast, it has been associated with insulin resistance [148] and it was recently demonstrated that lower baseline levels of *P. copri* were linked to a reduction in insulin resistance in overweight subjects following a Mediterranean diet intervention [149].

These effects might be explained by *Prevotella's* potential to degrade the complex polysaccharides in individuals with a mixed high-fibre diet. This is relevant to human metabolism: the human genome only encodes enzymes for the degradation of a limited number of carbohydrates including sucrose, lactose and starch [150], therefore, the ability of the gut microorganisms to ferment polysaccharides is critical in human nutrition. *Prevotella* are good propionate producers from arabinoxylans and fructo-oligosaccharides *in vitro* [151], and the efficiency of specific strains to degrade these polysaccharides has been shown to be linked with ecological and dominance patterns of *Prevotella* in mice [127]. In addition, it has been shown that the *P. copri* complex is capable of breaking down only plant polysaccharides and host derived mucin but not dietary derived animal polysaccharides [4,1524]. This may explain the decreased *Prevotella* diversity in industrialized, Westernised populations [153] where a high and diverse plant-based food intake is rarely maintained. A highly specialized enzymatic potential, with remarkable strain-level variations, has been demonstrated *in vitro* to be responsible for complex polysaccharides degradation by different strains of the *P. copri* complex [4]. The diversity and mechanism are driven by the occurrence of different bacterial transmembrane proteins that transport polysaccharides into the periplasm (SusC) that are usually located in polysaccharide utilization loci (PULs) along with degradation enzymes. These genes are selectively overexpressed upon exposure of *P. copri* strains to different plant polysaccharides, with such exposure influencing growth capability [4]. It may therefore be plausible to suggest the higher the *P. copri* diversity in the gut, the greater the number of types of complex polysaccharides that can be potentially utilised. Indeed, strain-level variations in *P. copri* genomes have been found as dependent on different habitual diets [123,154] and such diversity may be simply driven by selective exposure of the individuals to different typologies and amounts of plant polysaccharides. Remarkably, diet-driven selection can have unexpected health implications, as

P. copri strains associated with an omnivore diet had a higher prevalence of the *leuB* gene involved in branched-chain amino acid biosynthesis, a risk factor for glucose intolerance and type 2 diabetes [123].

Overall, there is a remarkable amount of literature pointing to *Prevotella*, and especially the *P. copri* complex as key players in driving individual clinical and metabolic responses to diet variation and to health status. However, the mechanisms of microbial contributions to these responses are far from clear, and this is also cause of the uncertainty on the role of friend or foe of *Prevotella* and *P. copri* in human health, which is debated [26,27,155]. The limitations that contribute to confounding the roles of such microbes in gut health include (i) the species-level and strain-level variability of gut *Prevotella* including how many *P. copri* clades of the complex are present, that can hugely affect the responses to diet; (ii) the variability of the dietary patterns studied, all with very different supply of fibre and/or fibre-rich foods. *Prevotella* arsenal of enzymes to digest polysaccharides represents an invaluable resource for digestion dynamics and gut homeostasis. It is thus the current most likely interpretation that the higher the *Prevotella* (and other fibre degraders) diversity, the more complementary the fermenting ability of the microbiome will be for the benefit of our gut.

Prevotella **as a potential pathogen**

Prevotella spp. have been implied in local and systemic infections, and to appreciate the extent of their involvement we analyzed the available literature through a systematic approach (see **Supplementary Information**). Studies linking *Prevotella* with human infections are mostly observational (43%), but there are also case-reports, retrospective and prospective studies (**Suppl. Fig. 2A, Suppl. Table 2**). The most prevalent *Prevotella*-related infections are found within the oral cavity with periodontal (n=31) and endodontic infections (n=35) being the most reported. Of the non oral infections, musculoskeletal, head-and-neck, low-respiratory-tract (LRTI) and skin infections have been reported (**Suppl. Fig. 2B**). Interestingly, oral infections may cause secondary systemic or organ-related infections [156]. For instance cases of *Prevotella*-related bacteremia after dental extraction [157] or periodontal probing [158] have been documented, as well as a case of liver pyogenic abscess related to dental disease [159]. Further, a relationship between oral infections and cardiac diseases has also been proposed [160]. In other cases, *Prevotella*-related infections occurred secondary to major diseases such as heart failure [161], in individuals with a compromised immune system [162] as well as a complication of surgery [162–166].

P. intermedia, *P. bivia*, *P. nigrescens* and *P. melaninogenica* are the most associated amongst human infections (**Fig. 4A** and **Suppl. Fig. 2D**). However, methodologies routinely used to identify *Prevotella* varied from standard clinical microbiology to molecular low- or high-throughput approaches and species-level identification was only reliably achieved in a fraction of these clinical cases. Bacterial isolation and cultivation were the most prevalent methods (**Fig. 4B** and **Suppl. Fig. 2C**), especially in clinical case-reports. Particular attention must be paid to the "causation" link in clinical cases as mere isolation of *Prevotella* spp. does not indicate causality, but isolation of *Prevotella* spp. from blood or from the infection fluids provides evidence they are the cause of infection especially if the infection is mono-bacterial. However, for oral infections, *Prevotella* can be present in the infection site just as a consequence of its presence in the (healthy) oral microbiome. The causative role of *Prevotella* spp. in infections has rarely been investigated by reproducing the human disease phenotype in animal models. In a bacterial vaginosis mouse model the co-inoculation of *P. bivia* with *Gardenella vaginalis* did reproduce some features of human BV infection, including uterus ascension, epithelial exfoliation and sialidase activity [90]. Overall, only a small percentage of studies addressed the causative role of *Prevotella* spp. (**Figure 4B**) and only for a few infections (e.g. genitourinary infections) or in autoimmunity (e.g. multiple sclerosis and rheumatoid arthritis) further

questioned the pathogenic potentials of *Prevotella* strains. Moreover, in the majority of cases (60%, **Suppl. Fig. 2B**) *Prevotella* spp. tend to co-infect with other microorganisms [167,168]. This suggests that while not obligate pathogens, *Prevotella* spp. may, alone or synergistically with other microorganisms, be opportunistic when the ecological conditions allow.

Anaerobic bacterial infections, such those involving *Prevotella* spp., are usually treated with broad-spectrum antibiotics. However, the insurgence of antibiotic resistance may constitute a major limitation to the infection resolution and poses a major issue for global health but the available information on antibiotic resistance for *Prevotella* is scarce. Indeed, out of the 226 papers we considered here, only 80 studies (35.4%) investigated the antibiotic resistance of the *Prevotella* species through either biochemical or genetic methods. Beta-lactamase resistance, in particular to penicillin and ampicillin, was reported in *Prevotella* isolates from head-and-neck infections [169]. Metronidazole resistance is also possible and has been reported in the clinic [170], more specifically in *P. buccae* [171], and in *P. bivia* [172]. While *Prevotella* does not appear as one of the major resistant infectious threats, antibiotic resistance tests should be carried out whenever possible, especially in critical conditions such as in cystic fibrosis patients [173–177].

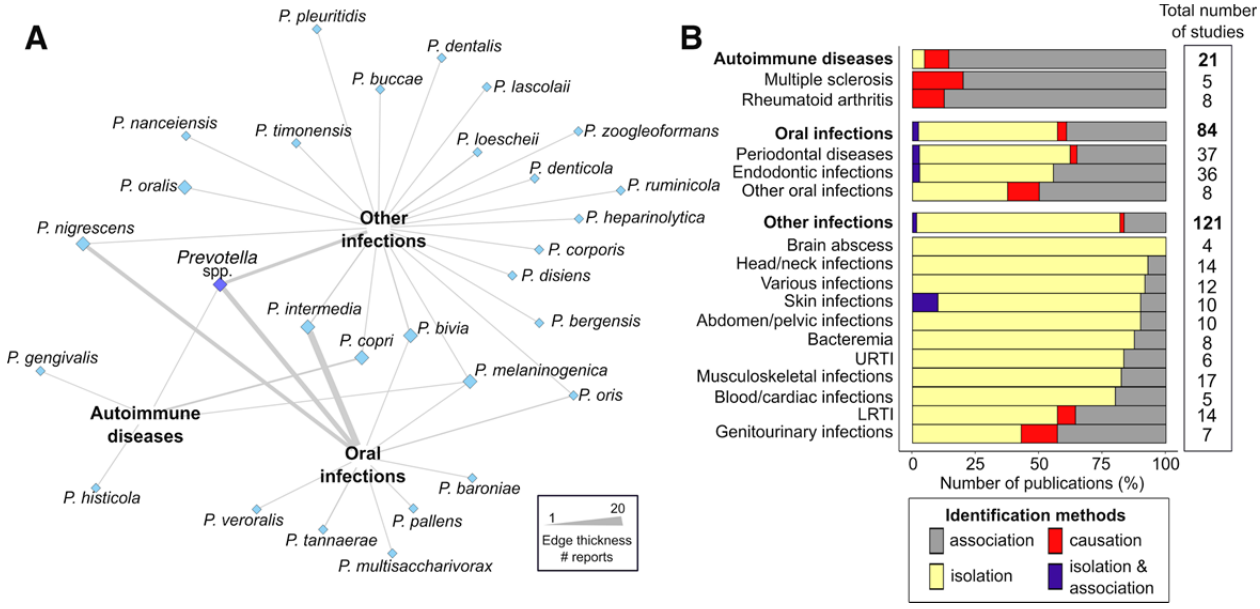

Fig. 4 - Evidence for a role of *Prevotella* species in human infections and autoimmunity. (**A**) Network analysis showing the association of each *Prevotella* species with one or more diseases (grouped into three broad categories: autoimmune diseases, oral infections or other infections) based on a total of 226 studies considered (see **Supplementary Information)**. The thickness of the edges is proportional to the number of papers reporting the involvement of *Prevotella* spp. in diseases. While some species were reported specifically associated with one disease group, few others were shared amongst the three categories. *Prevotella* spp. refers to cases for which species identification was not available. (**B**) Most of the studies providing evidence on the link between *Prevotella* and diseases are isolation-based or merely associative. We report, for each disease with at least 4 studies linking them with *Prevotella* species, the percentage of such studies falling under the categories of "Isolation" (standard microbiology approaches of isolation and cultivation without mechanistic or causative investigations), "Association" (low- or high-input molecular approaches such as species-specific PCR or 16S rRNA gene sequencing that survey the presence of bacteria in a sample), and "Causation" (studies in which the causative role of *Prevotella* spp. in the

infection was proved in animal models). Diseases were ordered based on a descending "isolation" order and the total number of studies considered per disease is also shown.

Outlook on research and translational applications for human *Prevotella* species

Prevotella is the second most abundant genus in the human oral cavity, and when present, it is usually the most abundant in the gut microbiome. As such, it is surprising how little is known about this genus and why other oral and intestinal genera have received much more attention. This can only partially be explained by the substantially non-pathogenic nature of *Prevotella* species and the difficulties in cultivating intestinal *Prevotella* taxa. There are however two main aspects that are starting to fuel the investigation of this genus as described in this review: the advances of (untargeted) metagenomic datasets (**Box 1**) of the human microbiome that can reveal the hidden *Prevotella* diversity across worldwide populations, and the recognition of intestinal *Prevotella* species as key players in host-microbiome interactions especially in relation with nutrition and metabolism.

We outline some of the main questions and research lines that can be most impactful from the scientific and biomedical viewpoints based on the current understanding of *Prevotella* genomics and ecology. First of all, there is now overwhelming evidence that non-Westernised populations have higher abundances of oral and intestinal *Prevotella* [8–13,15,57,58]. Analysing ancient microbiome samples have supported the theory, at least for the *P. copri* complex, that the loss of diversity is associated with - and likely driven by - the process of Westernisation and it is not just a common feature of modern non-industrialized communities [16]. Other microbes may be subject to the same forces, but the link with Western lifestyle is stronger for *Prevotella* based on the observed differential prevalence and within-subject genus-level diversity. Because intestinal *Prevotella* species also tend to be highly abundant, some of the differences observed for other species across populations with different lifestyles could also partially be a statistical artifact due to the compositional data of microbiome profiles as well as the consequence of *Prevotella*-induced ecological effects. Further investigations to understand the genetic and ecological features driving the distinct host-*Prevotella* equilibrium are thus urgently needed and they will be crucial in combination with proper study designs also in assessing which of the multiple lifestyle aspects differentiating Westernized and non-Westernized populations (including diet, availability of antimicrobial drugs, hygiene practices) are the most connected with the differences in *Prevotella* prevalence and diversity. Ultimately, the outstanding question is whether the decreased *Prevotella* prevalence and diversity observed at the population level in modern industrialized society can be a reversible process, and whether reverting this trend would indeed be desirable from a health perspective. In case it is, studies would be necessary to understand whether individual dietary and lifestyle-induced microbiome modulations are sufficient to restore a gut homeostasis or if direct supplementation of *Prevotella* diversity would be required.

The second aspect we believe is crucial to be unravelled by future research is primarily of biomedical relevance. Indeed, while the pathogenic potential of *Prevotella* proved to be limited and mostly connected with opportunistic infections, its role in the onset and development of immune-mediated diseases remains unclear. Initial reports of a link with diseases such as rheumatoid arthritis [17] received only partial confirmation by follow-up studies [110,111,116]. The intricate mucosal immunology properties of *Prevotella* species [23,178] could both substantiate its involvement in auto-immunity as well as increased protection by pathobionts, and strain-level differences are likely responsible for the subject-level variability in immunological phenotypes especially in light of the expanded genomic diversity of the multi-species *Prevotella copri* complex [16]. As such, investigations on larger cohorts, especially including a longitudinal

sampling, and accounting for host population differences, immunological aspects, and strain-level *Prevotella* diversity are needed to clarify this link which has a wide potential translational impact.

A third line that should receive more research focus is the relation between intestinal *Prevotella* species and nutrition. There are multiple and convincing studies associating *Prevotella* spp. with dietary patterns and cardiometabolic health, but such reports are often conflicting [128,130,139–143,145,146,148,149] and, again, subspecies and strain diversity may obscure the consistency of experimental outcomes therefore calling for different study designs and larger clinical and preclinical cohorts. Because of the potential modulability of the gut microbiome, a clear understanding of the role of *Prevotella* in nutritional and human metabolism can have tremendous clinical applications with advanced probiotic and prebiotic options similarly to what is starting to be implemented for other species such as *Akkermansia muciniphila* [179]. In that perspective, isolation efforts of *Prevotella* strains will be pivotal in the coming years. The possibility to characterize strains particularly from individuals with different diets and lifestyles and observe their behaviour *in vitro* or in animal models will be of utmost importance to clarify the role of *Prevotella* in affecting health and also how impactful lifestyle features are in selecting strains with defined features.

Intriguingly, these three open questions could be inter connected in one hypothetical scenario. Considering the clear dietary implications of the Westernization process, the link between *Prevotella* and diet might be driving the decreasing presence in fat-rich/fiber-poor Westernized populations. Such changing equilibrium potentially affects the host-*Prevotella* symbiotic relationship set by hundreds of thousands of years of co-evolution, leading in turn to impaired host-microbe interactions that could make the host more prone to disease. This remains for now an unproven hypothesis, but *Prevotella* appears to be the most promising genus to try to prove (or reject) such hypothesis.

Box 1 - Genomes from metagenomes: uncovering the diversity of *Prevotella* with cultivation-free approaches.

The study of human-associated *Prevotella* species has been hampered by the intrinsic difficulties in cultivating *in vitro* some taxa, especially anaerobic strains in the gut. By surveying the genetic content of complex microbial samples via high-throughput sequencing, i.e. metagenomics [60], it is not only possible to identify and quantify known species but the investigator is given the intriguing opportunity to discover previously uncharacterized "novel" species. This is becoming increasingly effective via metagenomic assembly that first reconstructs relatively long fragments of the genomes (called contigs) [180,181] and then groups contigs into draft genomes - called Metagenome-Assembled Genomes, MAGs - by exploiting reads' coverage and intrinsic genetic features (e.g. tetranucleotide frequency distribution) across contigs [182]. After quality control of the resulting MAGs [183], high-quality sequences can be phylogenetically and taxonomically contextualized [184] revealing in many cases that MAGs do not belong to any previously named or catalogued species. As metagenomic assembly reached its maturity, large collections of MAGs have been built and analyzed [15,49,50]. Currently there are over 200,000 MAGs in such integrative catalogues that are based on many large human metagenomic studies; thousands of these MAGs have expanded the strain-level genetic diversity of known species, while many others define new Species-level Genomes Bins (SGBs, interpretable as yet-to-be cultivated new candidate species). Applied to the *Prevotella* genus, such approaches confirmed additional genetically and functionally distinct clades forming a larger *Prevotella copri* complex [4,16], and a total of 4,886 human associated MAGs assigned to the *Prevotellaceae* family but not belonging to any known *Prevotella* species [15] (**Fig. 3**). While *in vitro* cultivation remains indispensable to understand the physiology of bacterial species and their possible involvement in hosts' diseases, metagenomic assembly is emerging as a key tool to characterize previously overlooked bacterial diversity, drive targeted cultivation efforts, and formulate hypotheses on the biomedical relevance of some taxa.

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Box 2 - Ancient and evolutionary *Prevotella* genomic fossils.

The human microbiome is the result of a continuous interplay and co-evolution with the human host. Understandably, our knowledge of the microbiome relating to human health has been gleaned almost exclusively from biological samples collected from modern contemporary populations. More specifically populations that have undergone the process of Westernisation driven by industrialisation and culminating in dietary and lifestyle changes. Recently, the comparison to contemporary non-Westernised populations, i.e. those following a more traditional lifestyle and diet, has shown a stark difference between the microbiomes of these populations [8–15]. This raises the interesting questions of how reflective is the Westernised microbiome to our long established co-evolved microbiome? And are non-Westernised populations a better proxy of this? Ancient samples have started to give a historical snapshot of the microbes present in our ancestors and how they have evolved, with the help of accurate molecular clocking [185]. These works have primarily focussed on the evolution of human pathogens and from samples where microbial DNA has been preserved, such as dental calculus or pulp and other skeletal remains. Examples include the unravelling of the evolutionary and adaptive trajectories of *Yersinia pestis*, the cause of the Black death [186] , and *Mycobacterium tuberculosis* [187]. For review see Spyrou et al 2019 [188].

While small in number, ancient microbiomes from stool or intestinal samples have become available including those from coprolites (fossilised faeces) and the Iceman (Otzi) [16], a natural ice mummy [189]. These have provided an initial awareness on how our ancestral microbiome compares to contemporary populations. For instance, analysis of the Iceman offered an insight into the historical global spread and evolutionary history of the stomach parasite *Helicobacter pylori* [190]. Ancient samples also revealed the divergence of *P. copri* into four distinct clades may possibly pre-date modern humans, and *P. copri* was almost certainly a core species in the microbiome of populations before human migratory waves out of Africa [16]. The decreased prevalence of *P. copri* in Westernised compared to non-Westernised populations is suggestive that non-Westernised populations are a more historical representative of our co-evolved microbiome. However, efforts to increase the number of ancient samples from differing human populations are needed to definitively answer this question. Nevertheless, the increasing evidence that Westernised microbiomes are not accurate representations of our long-term microbiome raises the question of whether this perturbation is ultimately detrimental to overall health or not, and warrants further investigation.

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Supplementary Information

[Figure 1, Table 1, Supplementary Table 1]: We considered the genomes labelled as "Prevotellaceae" available in the NCBI Reference Sequence Database (RefSeq) as of May 2020 (N = 384, **Table 1**). Metadata information was retrieved directly from the NCBI portal or, when missing, from related publications. Genomes were dereplicated at 0.5% genetic distance based on whole-genome nucleotide similarity estimating using Mash (v. 2.0; option "-s 10000" for sketching) [191]. Dereplicated genomes (N = 254) were considered to build the phylogenetic tree of strains of *Prevotella* and other *Prevotellaceae* species using PhyloPhlAn 3.0 [184] and GraPhlAn [192] (**Figure 1A**). Genomes were annotated with Prokka (v. 1.12) [193] using default parameters. Proteins inferred by Prokka were then functionally annotated with UniRef90 using diamond (v. 0.9.9.110) [194]. Statistics on the coding regions (CDS) were reported for the species with at least five genomes (**Figure 1B**).

[Figure 2]: We considered 9,539 human metagenomes coming from 51 publicly available independent datasets and with curated metadata information available in [109]. Taxonomic profiles were generated using MetaPhlAn 3.0 [195]. Prevalence and relative abundance across multiple host conditions (i.e., age category, body-site, country, and lifestyle) are reported only for named *Prevotella* species with prevalence > 0.1% in at least one category in **Figure 2A-C**. Extended results by including also *Prevotella sp.* species are reported in **Supplementary Figure 1**.

[Figure 3]: We considered 213,635 MAGs that were retrieved from publicly available metagenomes coming from human [15], non-human primate [196], food [197], and other hosts that we retrieved from [198,199] or directly reconstructed from raw reads deposited in NCBI SRA. We kept only MAGs having completeness > 50% and contamination < 5% as estimated by CheckM [183]. Such MAGs were integrated with the set of 384 reference genomes (summarized in **Table 1**) and clustered into SGBs following the procedure proposed in [15]. Genomes were clustered with average linkage at 5% genetic distance based on whole-genome nucleotide similarity estimation using Mash (v. 2.0; option "-s 10000" for sketching) [191]. We identified a total of 10,243 genomes (384 reference genomes and 9,859 MAGs; **Supplementary Table 1**) belonging to *Prevotellaceae* and coming from different sources: dog (N = 2), elephant (N = 1), environmental (N = 4), hoatzin (N = 1) human (N = 7,819), mouse (N = 142), non-human primate (N = 214), ruminant (N = 2,041), and swine (N = 19). Such genomes were grouped into 526 distinct SGBs. We considered the 56 most prevalent human *Prevotella* SGBs (i.e., with at least twenty genomes retrieved from human microbiomes) to build the phylogenetic tree of **Figure 3A**, in which only fifteen randomly selected genomes were considered for each SGB. The same set of SGBs was taken into account in **Figure 3B**.

[Figure 4]: The systematic review of the literature was conducted searching for "*Prevotella* & Infection & Humans" in Pubmed. A total of 2,225 results were initially obtained. Exclusion criteria for study selection were: i) absence of the *Prevotella* spp., ii) healthy conditions, iii) non-infectious specimens, iv) broad reviews citing other main findings. After applying those criteria, 205 infections-related papers were retained and investigated. Another 21 autoimmune diseases, already discussed in other paragraphs, were also surveyed in a similar manner. Infections were initially grouped into broad categories such as "other infections" (accounting for the 54% of the total) or "oral infections" (37%), while the remaining 9% is the autoimmune disease category. **Supplementary Table 2** includes all the data extracted from the 226 papers analysed and used in this work. Statistical analysis and figures were generated in R from the information stored in **Supplementary Table 2**. **Fig. 4A** represents the associations between each *Prevotella* species surveyed and the corresponding disease (represented as broad classifications). The network was created with Cytoscape v3.8.1. and edge thickness represents the number of papers

showing such an association between species and disease. For **Fig. 4B**, the methodology of *Prevotella* spp. identification were surveyed and displayed for each broad-classification category and in the most prevalent diseases observed (i.e. those described in at least 4 studies). "Isolation" refers to standard microbiology approaches. "Association" refers to low- or high-input molecular approaches such as species-specific PCR or through 16S rRNA gene sequencing. "Causation" refers only to studies where the contribution of *Prevotella* spp. was proved in animal models. The number of papers in each category were normalized against the total number of papers surveyed and showed as percentages. In **Suppl. Fig. 2A**, papers were grouped by the type of study they proposed: the majority were observational studies (44%), followed by case-reports (32%), prospective (6%) and retrospective studies (5%). **Suppl. Fig. 2B** shows the total number of papers per disease investigated (black circles) and the number of papers related to a "mono-bacterial" or "poly-microbial" nature of the *Prevotella* spp. infections. Studies that did not clearly state the type of infections were referred to as "not assessed". **Suppl. Fig. 2C** includes the methodology used to identify the *Prevotella* species in each disease, as an extended data for Figure 4B**.** The top-4 most abundant *Prevotella* spp. identified in each disease were included in **Suppl. Fig. 2D**, which included *P. intermedia*, *P. bivia*, *P. nigrescens* and *P. melaninogenica.* Low-abundant species were grouped into "other species", while "*Prevotella* spp." was used when the species was not identified or reported.

Supplementary Figures and Tables

Supplementary Table 1. List of the available isolate genomes and reconstructed MAGs of *Prevotella* and other *Prevotellaceae* strains with their genomic characteristics. For each isolate genome, we report the taxonomy as reported in NCBI, metadata information in terms of host and site types, genome length, and GC content. For each MAG, we report quality scores in terms of estimated completeness, estimated contamination, and number of contigs.

Supplementary Table 2. Results of the systematic literature review on *Prevotella* spp. in autoimmune diseases and opportunistic infections. A total of 226 papers were surveyed on the role of *Prevotella* spp. in diseases and infections. Description of the methodology used for the systematic review literature is available in Supplementary Information:Figure 4.

Supplementary Figure 1. Distribution and stratification of *Prevotella* species across human populations and body-sites. Prevalence and relative abundance of *Prevotella* species across (**A**) body-sites, age and lifestyles, and (**B**) countries by exploiting public integrated repositories of >9,500 profiled human metagenomes. The heatmaps extend the results reported in **Figure 2** by including also unnamed species.

Supplementary Figure 2. An overview of the identified links between *Prevotella* species and human diseases. (**A**) As a result of the systematic literature review (see Supplementary Information for methods) on the role of *Prevotella* spp. in human infections, we surveyed 226 papers that are here classified according to the type of the study proposed (%). (**B**) Total

number of papers per infection or disease surveyed, and number of papers in each disease related to mono-bacterial or poly-microbial infection types. URTI, upper-respiratory tract infections. LRTI, low-respiratory tract infections. NA, not clearly assessed in the study. (**C**) Number of publications per disease according to the methodology used to identify the presence of *Prevotella* spp. Isolation refers to standard microbiology approaches of isolation and cultivation. Association refers to low- or high-input molecular approaches such as species-specific PCR or through 16S rRNA gene sequencing. Causation refers only to studies where the contribution of *Prevotella* spp. was proved in animal models. (**D**) Number of the top-4 most abundant *Prevotella* species identified in each disease investigated. Low-abundant species were grouped into "other species", while *Prevotella* spp. was used when the species was not identified or reported.

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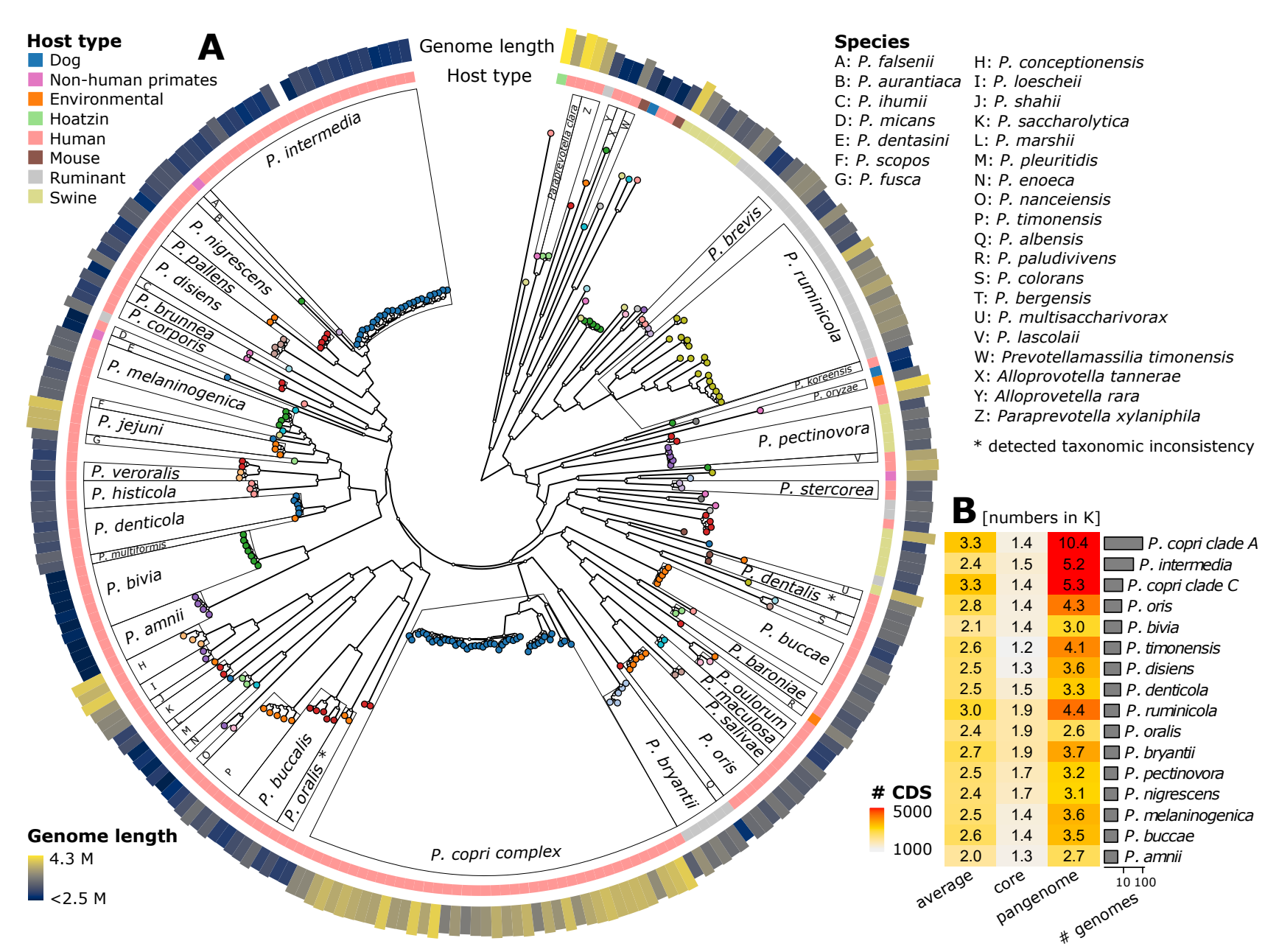
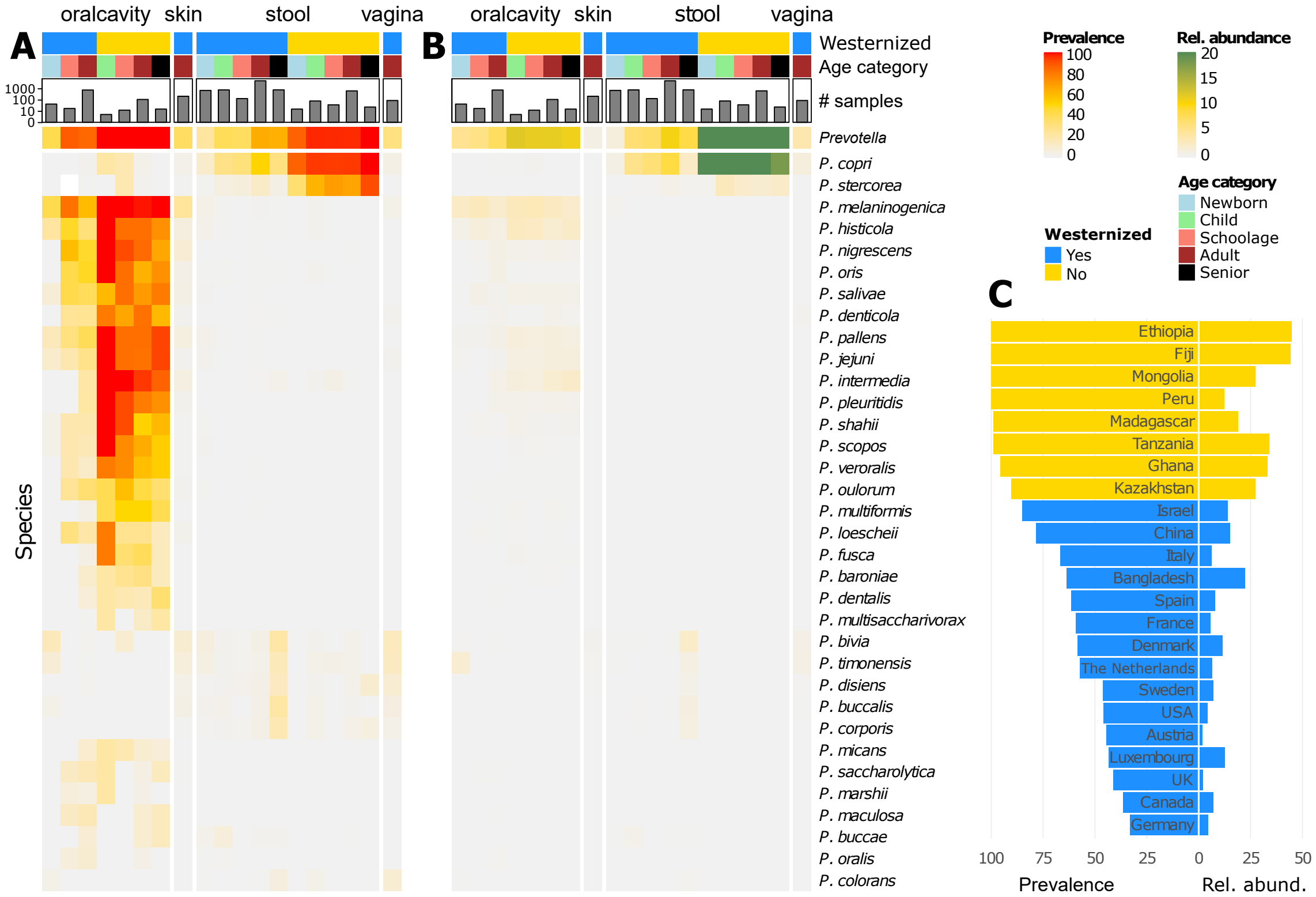
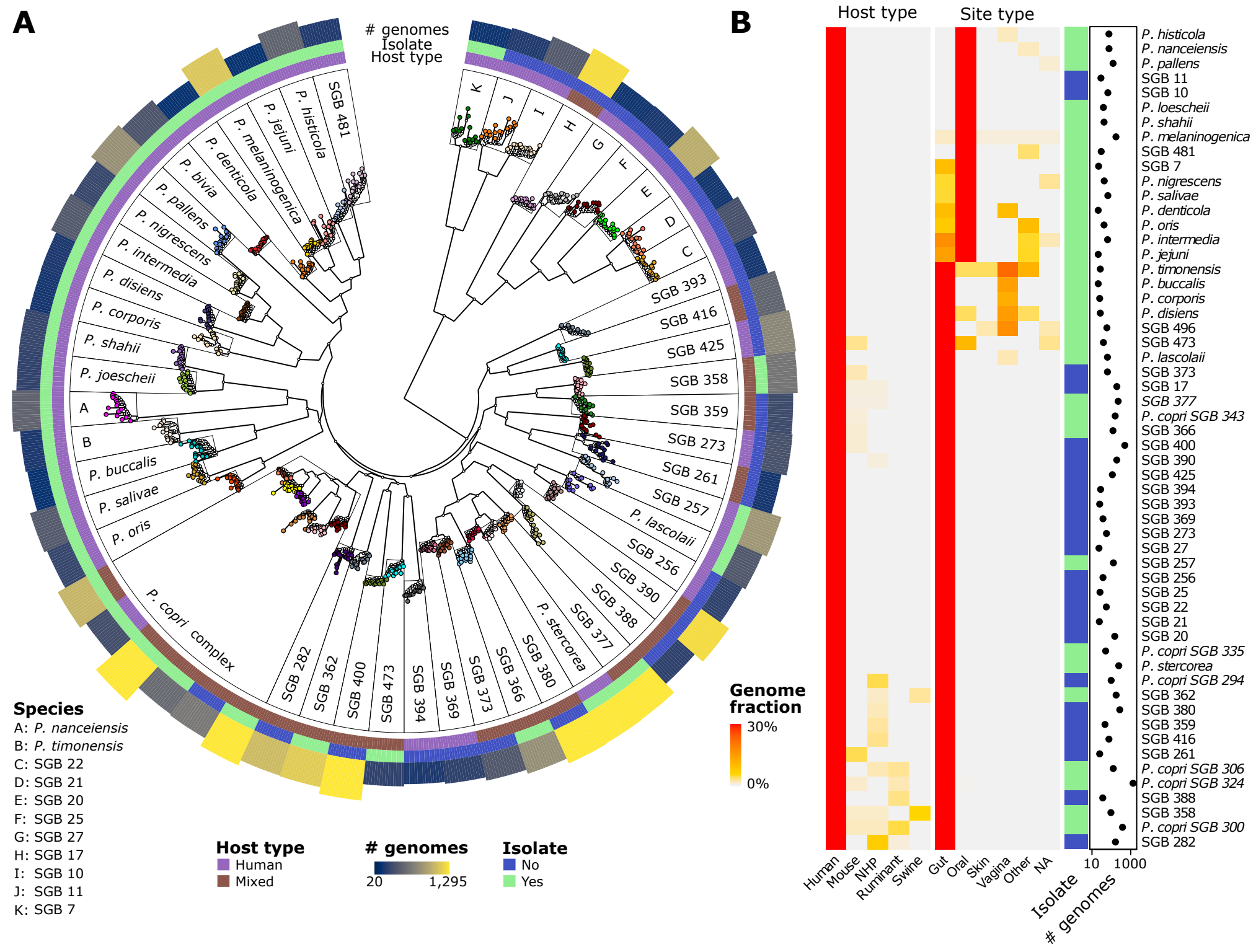
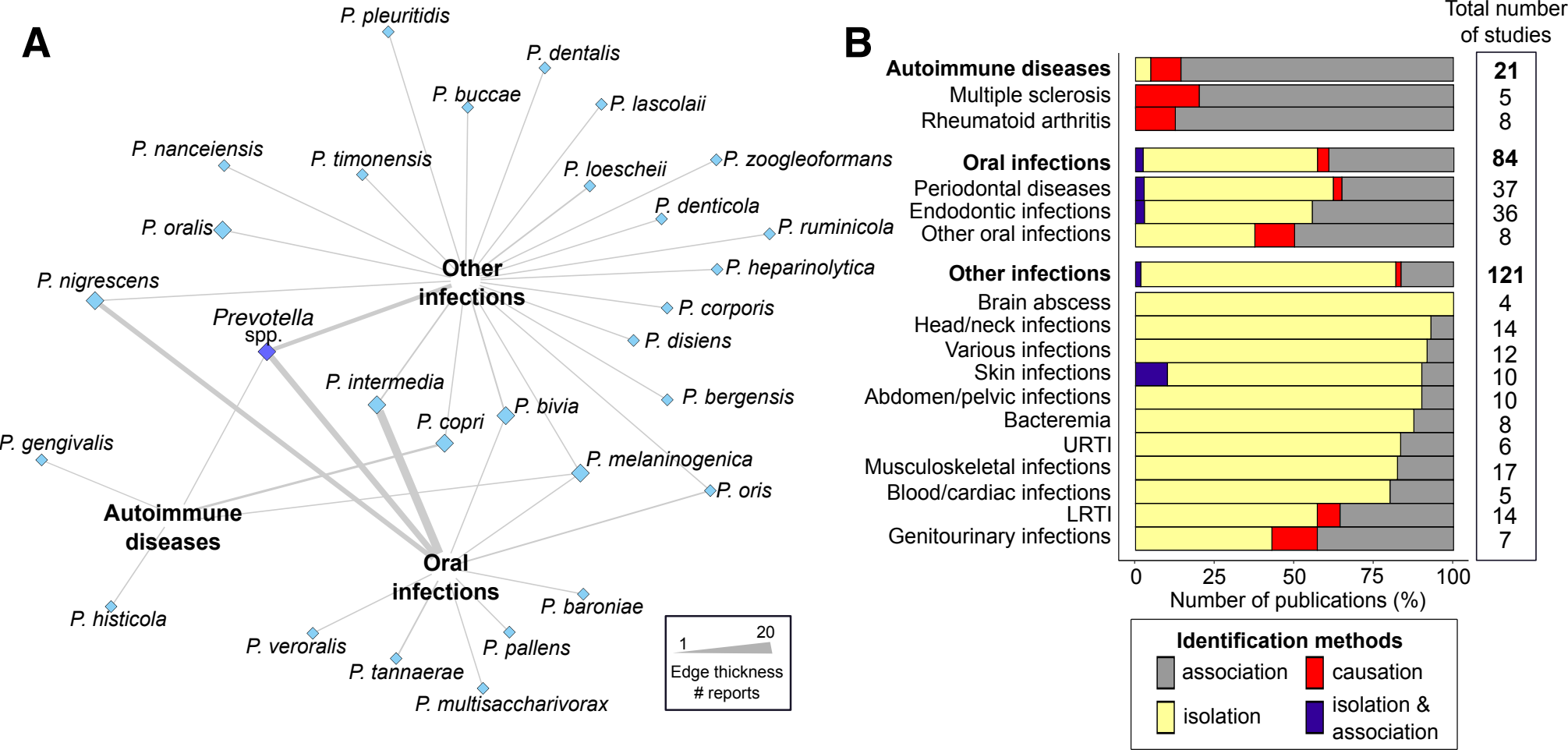
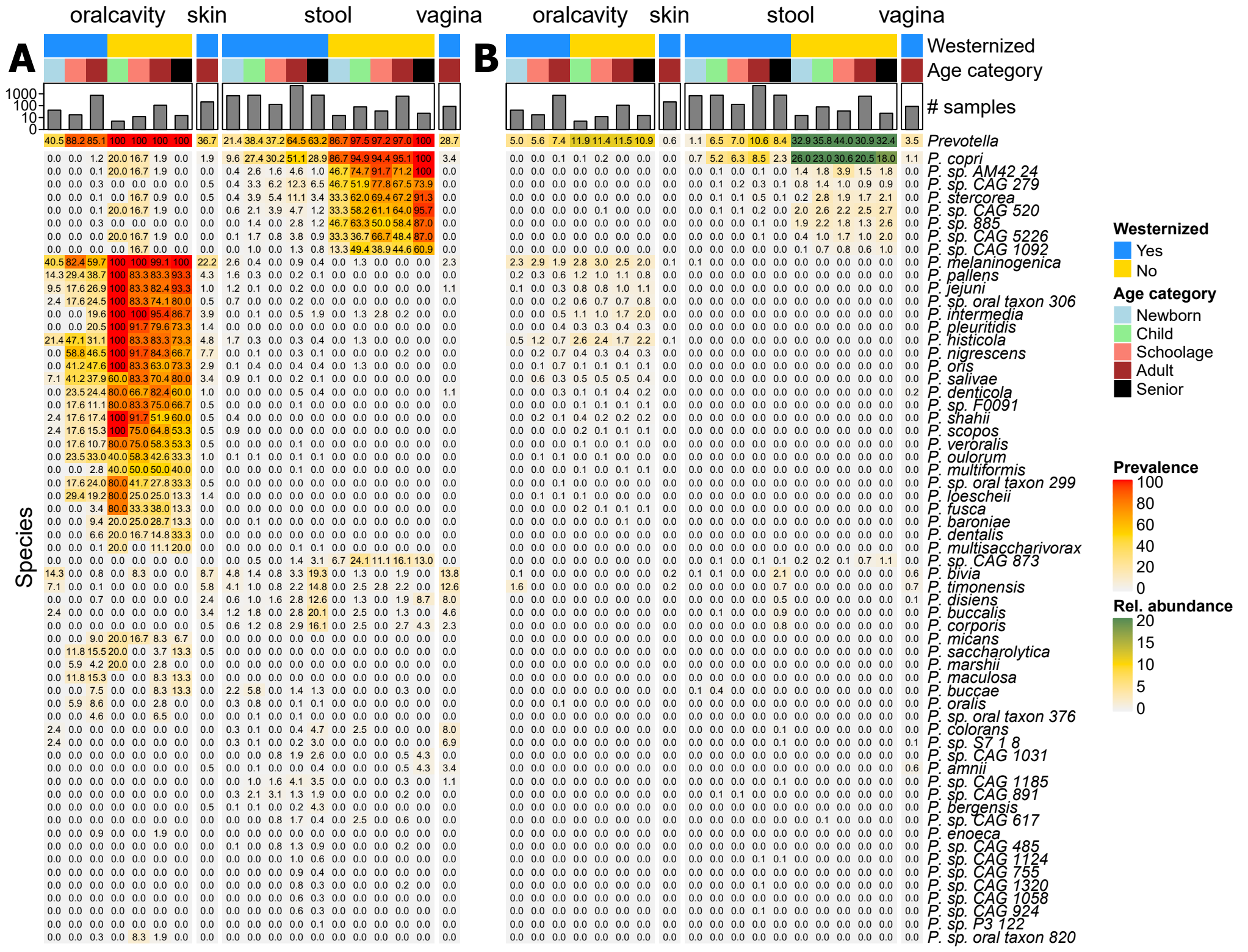


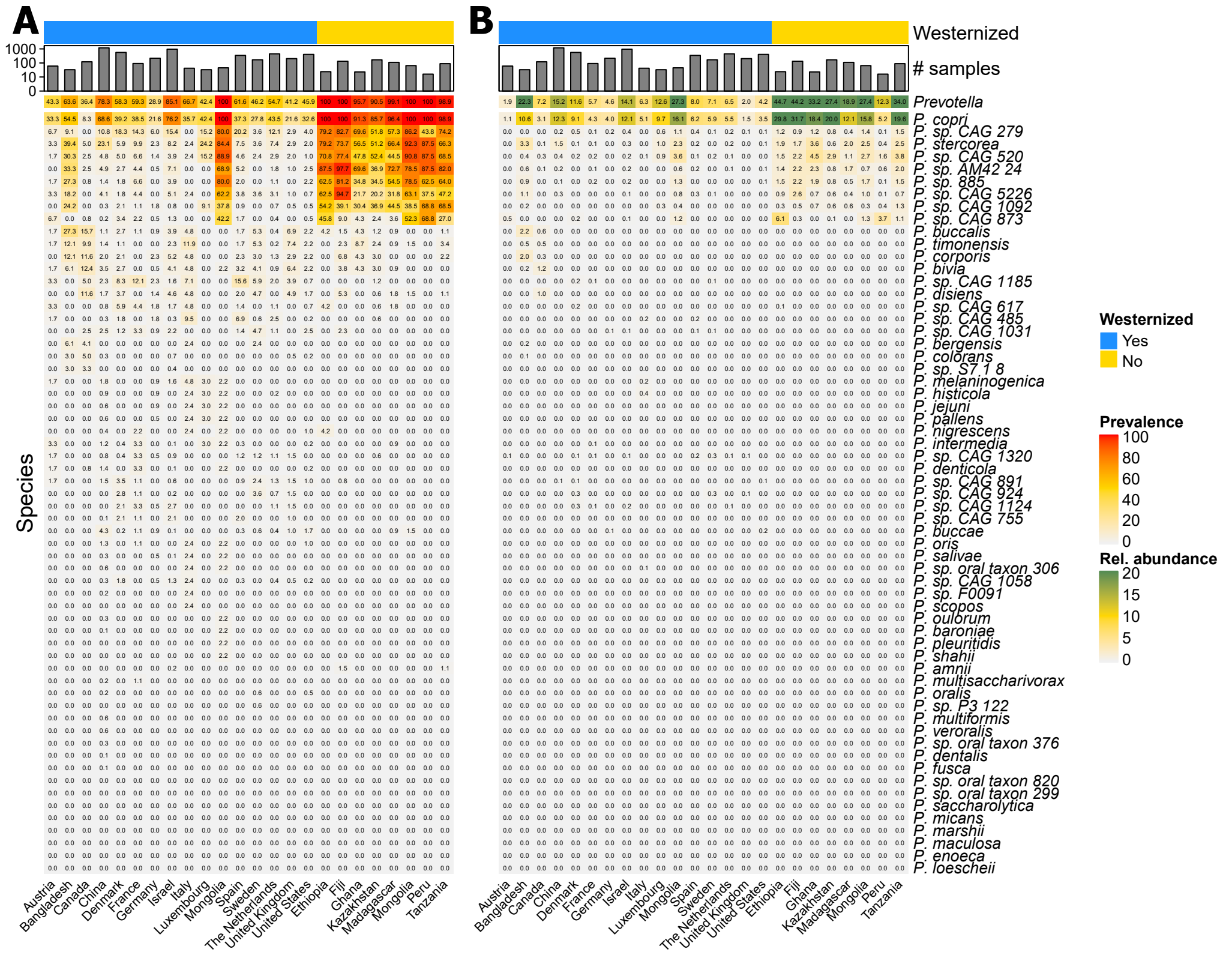
average	core	pangenome	
3.3	1.4	10.4	*P. copri clade A*
2.4	1.5	5.2	*P. intermedia*
3.3	1.4	5.3	*P. copri clade C*
2.8	1.4	4.3	*P. oris*
2.1	1.4	3.0	*P. bivia*
2.6	1.2	4.1	*P. timonensis*
2.5	1.3	3.6	*P. disiens*
2.5	1.5	3.3	*P. denticola*
3.0	1.9	4.4	*P. ruminicola*
2.4	1.9	2.6	*P. oralis*
2.7	1.9	3.7	*P. bryantii*
2.5	1.7	3.2	*P. pectinovora*
2.4	1.7	3.1	*P. nigrescens*
2.5	1.4	3.6	*P. melaninogenica*
2.6	1.4	3.5	*P. buccae*
2.0	1.3	2.7	*P. amnii*

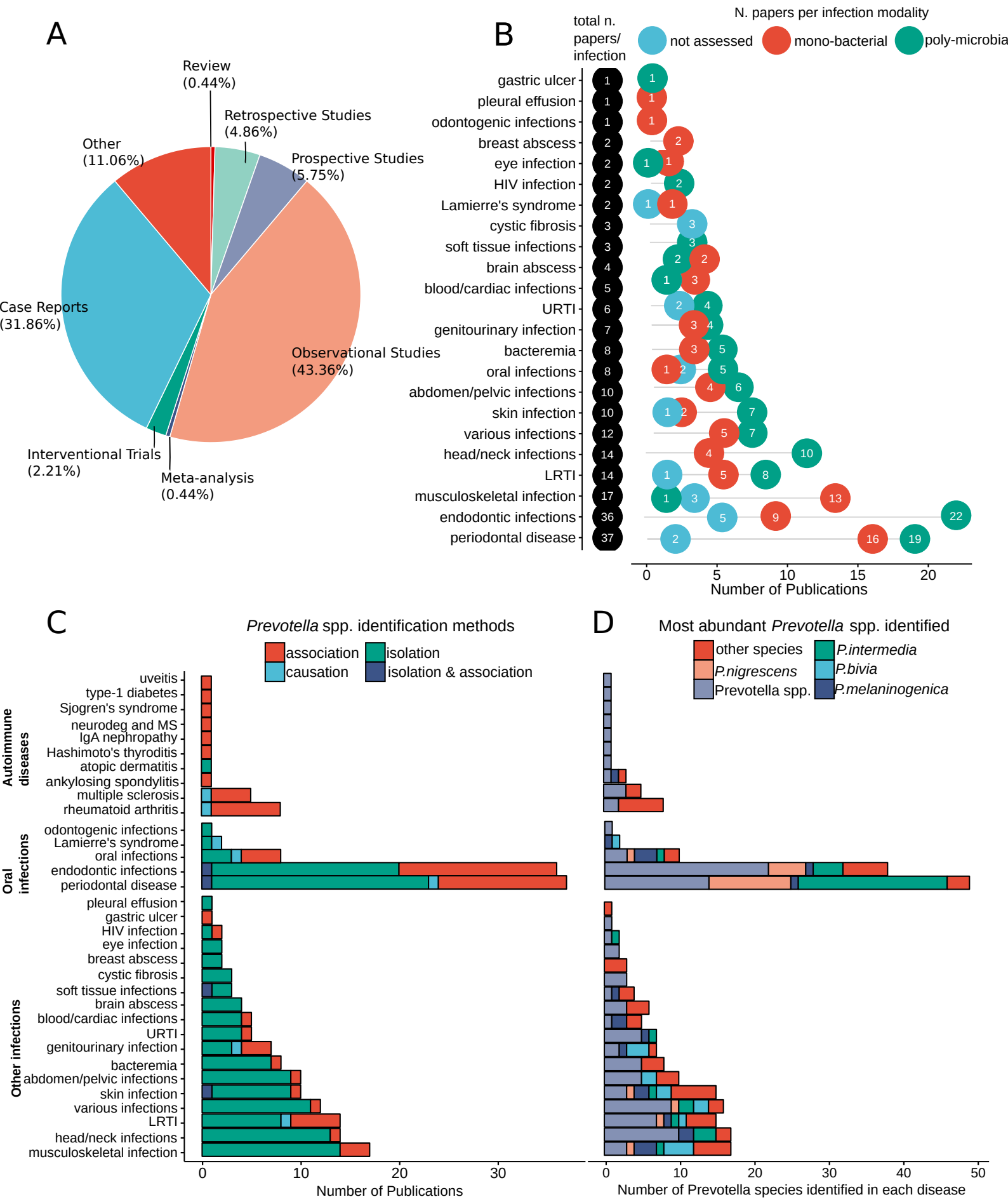

A
B
C
oralcavity
skin
stool
vagina
Westernized
Age category
samples
1000
100
10
0
Species
Prevotella
P. copri
P. stercorea
P. melaninogenica
P. histicola
P. nigrescens
P. oris
P. salivae
P. denticola
P. pallens
P. jejuni
P. intermedia
P. pleuritidis
P. shahii
P. scopos
P. veroralis
P. oulorum
P. multiformis
P. loescheii
P. fusca
P. baroniae
P. dentalis
P. multisaccharivorax
P. bivia
P. timonensis
P. disiens
P. buccalis
P. corporis
P. micans
P. saccharolytica
P. marshii
P. maculosa
P. buccae
P. oralis
P. colorans
Prevalence
100
80
60
40
20
0
Rel. abundance
20
15
10
5
0
Age category
Newborn
Child
Schoolage
Adult
Senior
Westernized
Yes
No
Ethiopia
Fiji
Mongolia
Peru
Madagascar
Tanzania
Ghana
Kazakhstan
Israel
China
Italy
Bangladesh
Spain
France
Denmark
The Netherlands
Sweden
USA
Austria
Luxembourg
UK
Canada
Germany
100
75
50
25
0
25
50
Prevalence
Rel. abund.


A
genomes
Isolate
Host type
SGB 481
P. histicola
P. jejuni
P. melaninogenica
P. denticola
P. bivia
P. pallens
P. nigrescens
P. intermedia
P. disiens
P. corporis
P. shahii
P. joescheii
A
B
P. buccalis
P. salivae
P. oris
P. copri complex
SGB 282
SGB 362
SGB 400
SGB 473
SGB 394
SGB 369
SGB 373
SGB 366
SGB 380
P. stercorea
SGB 377
SGB 388
SGB 390
SGB 256
P. lascolaii
SGB 257
SGB 261
SGB 273
SGB 359
SGB 358
SGB 425
SGB 416
SGB 393
C
D
E
F
G
H
I
J
K
Species
A: P. nanceiensis
B: P. timonensis
C: SGB 22
D: SGB 21
E: SGB 20
F: SGB 25
G: SGB 27
H: SGB 17
I: SGB 10
J: SGB 11
K: SGB 7
Host type
Human
Mixed
genomes
20
1,295
Isolate
No
Yes
B
Host type
Site type
Genome fraction
30%
0%
P. histicola
P. nanceiensis
P. pallens
SGB 11
SGB 10
P. loescheii
P. shahii
P. melaninogenica
SGB 481
SGB 7
P. nigrescens
P. salivae
P. denticola
P. oris
P. intermedia
P. jejuni
P. timonensis
P. buccalis
P. corporis
P. disiens
SGB 496
SGB 473
P. lascolaii
SGB 373
SGB 17
SGB 377
P. copri SGB 343
SGB 366
SGB 400
SGB 390
SGB 425
SGB 394
SGB 393
SGB 369
SGB 273
SGB 27
SGB 257
SGB 256
SGB 25
SGB 22
SGB 21
SGB 20
P. copri SGB 335
P. stercorea
P. copri SGB 294
SGB 362
SGB 380
SGB 359
SGB 416
SGB 261
P. copri SGB 306
P. copri SGB 324
SGB 388
SGB 358
P. copri SGB 300
SGB 282
Human
Mouse
NHP
Ruminant
Swine
Gut
Oral
Skin
Vagina
Other
NA
Isolate
10
1000
genomes


A
P. pleuritidis
P. dentalis
P. buccae
P. lascolaii
P. nanceiensis
P. timonensis
P. loescheii
P. zoogleoformans
P. denticola
P. oralis
P. ruminicola
P. heparinolytica
P. nigrescens
Other infections
P. corporis
Prevotella spp.
P. disiens
P. intermedia
P. bergensis
P. bivia
P. copri
P. gengivalis
P. melaninogenica
P. oris
Autoimmune diseases
Oral infections
P. baroniae
P. histicola
P. veroralis
P. pallens
P. tannaerae
P. multisaccharivorax
1
20
Edge thickness
reports
B
Total number of studies
Autoimmune diseases
21
Multiple sclerosis
5
Rheumatoid arthritis
8
Oral infections
84
Periodontal diseases
37
Endodontic infections
36
Other oral infections
8
Other infections
121
Brain abscess
4
Head/neck infections
14
Various infections
12
Skin infections
10
Abdomen/pelvic infections
10
Bacteremia
8
URTI
6
Musculoskeletal infections
17
Blood/cardiac infections
5
LRTI
14
Genitourinary infections
7
0
25
50
75
100
Number of publications (%)
Identification methods
association
causation
isolation
isolation & association


A
B
oralcavity
skin
stool
vagina
Westernized
Age category
samples
1000
100
10
0
Species
Prevotella
P. copri
P. sp. AM42 24
P. sp. CAG 279
P. stercorea
P. sp. CAG 520
P. sp. 885
P. sp. CAG 5226
P. sp. CAG 1092
P. melaninogenica
P. pallens
P. jejuni
P. sp. oral taxon 306
P. intermedia
P. pleuritidis
P. histicola
P. nigrescens
P. oris
P. salivae
P. denticola
P. sp. F0091
P. shahii
P. scopos
P. veroralis
P. oulorum
P. multiformis
P. sp. oral taxon 299
P. loescheii
P. fusca
P. baroniae
P. dentalis
P. multisaccharivorax
P. sp. CAG 873
P. bivia
P. timonensis
P. disiens
P. buccalis
P. corporis
P. micans
P. saccharolytica
P. marshii
P. maculosa
P. buccae
P. oralis
P. sp. oral taxon 376
P. colorans
P. sp. S7 1 8
P. sp. CAG 1031
P. amnii
P. sp. CAG 1185
P. sp. CAG 891
P. bergensis
P. sp. CAG 617
P. enoeca
P. sp. CAG 485
P. sp. CAG 1124
P. sp. CAG 755
P. sp. CAG 1320
P. sp. CAG 1058
P. sp. CAG 924
P. sp. P3 122
P. sp. oral taxon 820
Westernized
Yes
No
Age category
Newborn
Child
Schoolage
Adult
Senior
Prevalence
100
80
60
40
20
0
Rel. abundance
20
15
10
5
0


A
B
Westernized
samples
1000
100
10
0
Species
Prevotella
P. copri
P. sp. CAG 279
P. stercorea
P. sp. CAG 520
P. sp. AM42 24
P. sp. 885
P. sp. CAG 5226
P. sp. CAG 1092
P. sp. CAG 873
P. buccalis
P. timonensis
P. corporis
P. bivia
P. sp. CAG 1185
P. disiens
P. sp. CAG 617
P. sp. CAG 485
P. sp. CAG 1031
P. bergensis
P. colorans
P. sp. S7 1 8
P. melaninogenica
P. histicola
P. jejuni
P. pallens
P. nigrescens
P. intermedia
P. sp. CAG 1320
P. denticola
P. sp. CAG 891
P. sp. CAG 924
P. sp. CAG 1124
P. sp. CAG 755
P. buccae
P. oris
P. salivae
P. sp. oral taxon 306
P. sp. CAG 1058
P. sp. F0091
P. scopos
P. oulorum
P. baroniae
P. pleuritidis
P. shahii
P. amnii
P. multisaccharivorax
P. oralis
P. sp. P3 122
P. multiformis
P. veroralis
P. sp. oral taxon 376
P. dentalis
P. fusca
P. sp. oral taxon 820
P. sp. oral taxon 299
P. saccharolytica
P. micans
P. marshii
P. maculosa
P. enoeca
P. loescheii
Austria
Bangladesh
Canada
China
Denmark
France
Germany
Israel
Italy
Luxembourg
Mongolia
Spain
Sweden
The Netherlands
United Kingdom
United States
Ethiopia
Fiji
Ghana
Kazakhstan
Madagascar
Mongolia
Peru
Tanzania
Westernized
Yes
No
Prevalence
100
80
60
40
20
0
Rel. abundance
20
15
10
5
0


A
Review
(0.44%)
Retrospective Studies
(4.86%)
Other
(11.06%)
Prospective Studies
(5.75%)
Case Reports
(31.86%)
Observational Studies
(43.36%)
Interventional Trials
(2.21%)
Meta-analysis
(0.44%)
B
total n.
papers/
infection
N. papers per infection modality
not assessed
mono-bacterial
poly-microbia
gastric ulcer
pleural effusion
odontogenic infections
breast abscess
eye infection
HIV infection
Lamierre's syndrome
cystic fibrosis
soft tissue infections
brain abscess
blood/cardiac infections
URTI
genitourinary infection
bacteremia
oral infections
abdomen/pelvic infections
skin infection
various infections
head/neck infections
LRTI
musculoskeletal infection
endodontic infections
periodontal disease
Number of Publications
C
Prevotella spp. identification methods
association
causation
isolation
isolation & association
Autoimmune diseases
uveitis
type-1 diabetes
Sjogren's syndrome
neurodeg and MS
IgA nephropathy
Hashimoto's thyroiditis
atopic dermatitis
ankylosing spondylitis
multiple sclerosis
rheumatoid arthritis
Oral infections
odontogenic infections
Lamierre's syndrome
oral infections
endodontic infections
periodontal disease
Other infections
pleural effusion
gastric ulcer
HIV infection
eye infection
breast abscess
cystic fibrosis
soft tissue infections
brain abscess
blood/cardiac infections
URTI
genitourinary infection
bacteremia
abdomen/pelvic infections
skin infection
various infections
LRTI
head/neck infections
musculoskeletal infection
Number of Publications
D
Most abundant Prevotella spp. identified
other species
P.nigrescens
Prevotella spp.
P.intermedia
P.bivia
P.melaninogenica
Number of Prevotella species identified in each disease

GenomeID	Estimated completeness
AmatoKR_2018__qiita_sid_11212:11212.Gor2__bin.7	90.15003975
AmatoKR_2018__qiita_sid_11212:11212.Gor3__bin.30	63.79310345
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CM_cf__CF_TNFC022IS_t2M15__bin.19	96.25
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CM_cf__CF_TNFC022IS_t3M16__bin.23	79.99470058
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CM_cf__CF_TNFC038SA_t1M16__bin.14	98.14189189
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CM_cf__CF_TNFC039IS_t2M15__bin.7	96.95945946
CM_cf__CF_TNFC039IS_t2M15__bin.9	94.95495495
CM_cf__CF_TNFC039IS_t5M16__bin.2	89.40376038
CM_cf__CF_TNFC039SA_t1M16__bin.16	64.64891362
CM_cf__CF_TNFC039SA_t1M16__bin.24	98.31081081
CM_cf__CF_TNFC040IS_t1M15__bin.7	71.94078532
CM_cf__CF_TNFC040IS_t2M15__bin.2	93.51897854
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CM_cf__CF_TNFC041IS_t1M15__bin.7	85.3410238
CM_cf__CF_TNFC041IS_t2M15__bin.15	95.32657658
CM_cf__CF_TNFC041IS_t3M15__bin.7	76.89655172
CM_cf__CF_TNFC041IS_t4M16__bin.1	66.52927612
CM_cf__CF_TNFC041IS_t4M16__bin.13	97.21283784

CM_cf__CF_TNFC041IS_t4M16__bin.21	66.84952978
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CM_trypto__HFD_DIET_76_CA__bin.12	51.18
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CM_vacci__GG_VPP_849_T2_STL_s__bin.37	81.93
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GhensiP_2020__SP_133SPT_T016__bin.2	57.80298155
GhensiP_2020__SP_143SPI_T016__bin.22	64.90603057
GhensiP_2020__SP_143SPI_T016__bin.31	95.60678325
GhensiP_2020__SP_143SPI_T016__bin.33	96.38866808
GhensiP_2020__SP_143SPI_T016__bin.7	93.90920332
GhensiP_2020__SP_162SPI_T016__bin.16	56.89655172
GhensiP_2020__SP_162SPI_T016__bin.17	90.12817965
GhensiP_2020__SP_162SPI_T016__bin.5	98.02265501
GhensiP_2020__SP_163SPI_T016__bin.16	93.53322072
GhensiP_2020__SP_163SPT_T016__bin.32	53.44827586
GhensiP_2020__SP_163SPT_T016__bin.34	95.34346847
GhensiP_2020__SP_163SPT_T016__bin.40	72.2721598
GhensiP_2020__SP_184SPT_T016__bin.11	94.85347803
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GhensiP_2020__SP_184SPT_T016__bin.15	76.6284667
GhensiP_2020__SP_184SPT_T016__bin.24	93.5766649
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GhensiP_2020__SP_186SPI_T016_R__bin.12	80.18081157
GhensiP_2020__SP_187SPT_T016_R__bin.9	67.20074066
GhensiP_2020__SP_189SPI_T016__bin.12	80.18393393
GhensiP_2020__SP_189SPI_T016__bin.28	90.68075428
GhensiP_2020__SP_189SPI_T016__bin.34	96.21621622
GhensiP_2020__SP_189SPI_T016__bin.5	88.02442148
GhensiP_2020__SP_201SPI_T016__bin.3	96.79054054
GhensiP_2020__SP_264SPI_T016__bin.3	97.81813063
GhensiP_2020__SP_281SPI_T016__bin.18	77.80676685
GhensiP_2020__SP_281SPI_T016__bin.22	96.20815669
GhensiP_2020__SP_281SPI_T016__bin.25	97.63513514
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GhensiP_2020__SP_283SPT_T016__bin.32	85.81279809
GhensiP_2020__SP_285SPI_T016__bin.4	87.97805158
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GhensiP_2020__SP_287SPT_T016__bin.27	66.02996255
GhensiP_2020__SP_287SPT_T016__bin.3	76.52671316
GhensiP_2020__SP_287SPT_T016__bin.35	72.38450816
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PasolliE_2019__A07_01_1FE__bin.36	68.44827586
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PasolliE_2019__A08_01_1FE__bin.11	78.30246914
PasolliE_2019__A08_01_1FE__bin.43	52.5862069
PasolliE_2019__A08_01_1FE__bin.63	85.33220721
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PasolliE_2019__A20_03_1FE__bin.19	75.15673981
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PasolliE_2019__A22_01_1FE__bin.9	51.6047088
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StewartRD_2018__10675_0019_idba__bin.65	98.23
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StewartRD_2018__10676_0022_idba__bin.29	94.81
StewartRD_2018__10676_0022_idba__bin.38	57.24
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TettAJ_2019_a__C16-20237-TZ__bin.18	51.72
TettAJ_2019_a__C16-20237-TZ__bin.31	85.45
TettAJ_2019_a__C16-20237-TZ__bin.34	79.04
TettAJ_2019_a__C16-20237-TZ__bin.4	84.13
TettAJ_2019_a__C16-20237-TZ__bin.40	82.03
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TettAJ_2019_a__C16-20237-TZ__bin.65	93.97
TettAJ_2019_a__C16-20238-TZ__bin.16	91.33
TettAJ_2019_a__C16-20238-TZ__bin.22	94.49
TettAJ_2019_a__C16-20238-TZ__bin.24	86.86
TettAJ_2019_a__C16-20238-TZ__bin.26	92.07
TettAJ_2019_a__C16-20238-TZ__bin.33	96.06
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TettAJ_2019_a__C16-20246-TZ__bin.34	94.18
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TettAJ_2019_a__C16-20248-TZ__bin.9	96.78
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TettAJ_2019_a__C16-20371-TZ__bin.33	94.9
TettAJ_2019_a__C16-20372-TZ__bin.10	95.65
TettAJ_2019_a__C16-20372-TZ__bin.30	85.24
TettAJ_2019_a__C16-20372-TZ__bin.32	94.65
TettAJ_2019_a__C16-20372-TZ__bin.33	51.72
TettAJ_2019_a__C16-20372-TZ__bin.44	69.12
TettAJ_2019_a__C16-20372-TZ__bin.50	77.59
TettAJ_2019_a__C16-20372-TZ__bin.51	66.58
TettAJ_2019_a__C16-20373-TZ__bin.11	93.69
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TettAJ_2019_a__C16-20440-TZ__bin.30	86.66
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TettAJ_2019_a__C16-20474-TZ__bin.10	91.31
TettAJ_2019_a__C16-20474-TZ__bin.39	88.92
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TettAJ_2019_b__C16-20274-GH__bin.20	70.14
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TettAJ_2019_b__C16-20275-GH__bin.24	53.86
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TettAJ_2019_b__C16-20362-GH__bin.39	81.15
TettAJ_2019_b__C16-20363-GH__bin.24	71.71
TettAJ_2019_b__C16-20363-GH__bin.25	92.8
TettAJ_2019_b__C16-20363-GH__bin.26	70.85
TettAJ_2019_b__C16-20363-GH__bin.37	54.64
TettAJ_2019_b__C16-20363-GH__bin.46	65.44
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TettAJ_2019_b__C16-20374-GH__bin.41	75.86
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TettAJ_2019_c__CM_A04_M0_18__bin.12	72.41
TettAJ_2019_c__CM_A04_M0_18__bin.23	58.62
TettAJ_2019_c__CM_A04_M0_18__bin.31	59.69
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VincentC_2016__MM012.2__bin.5	67.95366795
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VincentC_2016__MM013.2__bin.2	58.23519949
VincentC_2016__MM014__bin.3	68.63095238
VincentC_2016__MM015.1__bin.7	50.24294515
VincentC_2016__MM016.1__bin.17	97.40990991
VincentC_2016__MM016.2__bin.2	76.29845181
VincentC_2016__MM017__bin.1	93.73807631
VincentC_2016__MM017__bin.22	95.85431019
VincentC_2016__MM017__bin.4	91.97932668
VincentC_2016__MM018__bin.14	50
VincentC_2016__MM019.2__bin.2	90.37162162
VincentC_2016__MM019.2__bin.5	61.7280786
VincentC_2016__MM019.3__bin.15	98.47972973
VincentC_2016__MM019.3__bin.21	51.72413793
VincentC_2016__MM020.1__bin.2	53.44827586
VincentC_2016__MM020.2__bin.2	60.34482759
VincentC_2016__MM020.3__bin.9	53.82043651
VincentC_2016__MM021.1__bin.6	97.09389401
VincentC_2016__MM022.1__bin.3	97.55785197
VincentC_2016__MM022.1__bin.7	63.79310345
VincentC_2016__MM022.3__bin.12	93.74599389
VincentC_2016__MM023.1__bin.6	73.06694828
VincentC_2016__MM023.2__bin.1	82.0781893
VincentC_2016__MM027.1__bin.29	96.140553
VincentC_2016__MM027.1__bin.6	95.69444444
VincentC_2016__MM027.2__bin.35	95.01413178
VincentC_2016__MM027.3__bin.24	71.08957373
VincentC_2016__MM027.3__bin.7	93.46846847
VincentC_2016__MM028.2__bin.5	96.75675676
VincentC_2016__MM029.1__bin.7	90.99938173
VincentC_2016__MM029.2__bin.9	97.00582936
VincentC_2016__MM030.1__bin.11	87.68810804
VincentC_2016__MM030.1__bin.28	92.63677543
VincentC_2016__MM030.1__bin.9	90.80882353

VincentC_2016__MM032.1__bin.26	96.23078961
VincentC_2016__MM032.1__bin.32	58.88437019
VincentC_2016__MM032.1__bin.4	86.22041159
VincentC_2016__MM032.4__bin.9	97.31606607
VincentC_2016__MM033.1__bin.5	55.17241379
VincentC_2016__MM033.3__bin.14	62.06896552
VincentC_2016__MM033.3__bin.3	70.19786866
VincentC_2016__MM034.1__bin.2	93.03174603
VincentC_2016__MM037.2__bin.5	80.83333333
VincentC_2016__MM038__bin.1	58.62068966
VincentC_2016__MM038__bin.15	60.69958848
VincentC_2016__MM038__bin.22	90.29166667
VincentC_2016__MM039__bin.5	65.30604134
VincentC_2016__MM039__bin.6	63.79310345
VincentC_2016__MM041.1__bin.6	72.18468468
VincentC_2016__MM041.1__bin.9	71.69278997
VincentC_2016__MM041.2__bin.10	90.90143715
VincentC_2016__MM041.2__bin.15	62.02194357
VincentC_2016__MM043.1__bin.11	94.08783784
VincentC_2016__MM043.1__bin.14	70.84639498
VincentC_2016__MM043.2__bin.16	82.30920379
VincentC_2016__MM044.1__bin.1	95.38210445
VincentC_2016__MM044.1__bin.2	91.96641494
VincentC_2016__MM045.1__bin.7	95.67300307
VincentC_2016__MM048.1__bin.1	53.21690388
VincentC_2016__MM048.2__bin.10	89.57670906
VincentC_2016__MM048.2__bin.8	53.57142857
VincentC_2016__MM049.1__bin.3	69.30501931
VincentC_2016__MM049.2__bin.1	61.87258687
VincentC_2016__MM050.4__bin.33	67.45718837
VincentC_2016__MM051__bin.2	58.62068966
VincentC_2016__MM052.1__bin.10	94.46100512
VincentC_2016__MM052.1__bin.16	89.02358241
VincentC_2016__MM052.1__bin.4	96.54516649
VincentC_2016__MM052.2__bin.3	93.64069952
VincentC_2016__MM054.1__bin.3	98.78941441
VincentC_2016__MM056.2__bin.2	96.05855856
VincentC_2016__MM057.2__bin.1	91.65673026
VincentC_2016__MM058.1__bin.32	97.85714286
VincentC_2016__MM059.2__bin.8	52.89968652
VincentC_2016__MM060.1__bin.6	89.0327381
VincentC_2016__MM060.2__bin.10	98.27586207
VincentC_2016__MM060.2__bin.7	95.70636813
VincentC_2016__MM061__bin.16	94.56835637
VincentC_2016__MM062.2__bin.1	78.62068966
VincentC_2016__MM064.1__bin.15	54.43021803
VincentC_2016__MM064.1__bin.2	87.76984127

VincentC_2016__MM064.2__bin.6	62.88610039
VincentC_2016__MM065__bin.13	63.79310345
VincentC_2016__MM069__bin.4	95.15765766
VincentC_2016__MM071.2__bin.4	80.17241379
VincentC_2016__MM072.2__bin.1	98.04142378
VincentC_2016__MM072.2__bin.11	95.66496644
VincentC_2016__MM074.1__bin.4	95
VincentC_2016__MM075.2__bin.1	92.17933948
VincentC_2016__MM075.2__bin.15	94.95561738
VincentC_2016__MM077__bin.1	63.078085
VincentC_2016__MM077__bin.5	75.44146825
VincentC_2016__MM079.1__bin.3	64.61060325
VincentC_2016__MM079.2__bin.10	93.36248013
VincentC_2016__MM079.2__bin.11	82.80645161
VincentC_2016__MM079.2__bin.8	67.70525778
VincentC_2016__MM081__bin.6	91.89189189
VincentC_2016__MM083.1__bin.14	93.44197138
VincentC_2016__MM083.2__bin.1	97.21780604
VincentC_2016__MM083.2__bin.15	89.69034818
VincentC_2016__MM083.3__bin.4	97.97297297
VincentC_2016__MM083.4__bin.10	92.50206526
VincentC_2016__MM086.2__bin.3	97.63513514
VincentC_2016__MM086.3__bin.4	94.38813814
VincentC_2016__MM086.5__bin.7	91.89189189
VincentC_2016__MM086.6__bin.4	92.98986486
VincentC_2016__MM086.6__bin.5	58.62068966
VincentC_2016__MM087.1__bin.10	79.46166755
VincentC_2016__MM088__bin.11	95.02265745
VincentC_2016__MM088__bin.20	62.06896552
VincentC_2016__MM089.1__bin.18	95.17857143
VincentC_2016__MM089.1__bin.7	97.31606607
VincentC_2016__MM089.2__bin.5	95.14362519
VincentC_2016__MM089.2__bin.7	96.64480657
VincentC_2016__MM091.1__bin.6	92.36111111
VincentC_2016__MM091.3__bin.5	94.1380719
VincentC_2016__MM092__bin.3	97.96466974
VincentC_2016__MM094.1__bin.2	86.04761905
VincentC_2016__MM094.2__bin.11	76.97480569
VincentC_2016__MM096__bin.12	98.57142857
VincentC_2016__MM098.10__bin.2	76.3322884
VincentC_2016__MM099.1__bin.2	76.62783751
VincentC_2016__MM100.1__bin.32	88.66067741
VincentC_2016__MM101.1__bin.1	90.76576577
VincentC_2016__MM101.2__bin.3	91.89189189
VincentC_2016__MM103.1__bin.14	60.34482759
VincentC_2016__MM103.2__bin.14	58.01886971
VincentC_2016__MM103.2__bin.30	97.83761703

VincentC_2016__MM103.2__bin.35	82.77777778
VincentC_2016__MM103.2__bin.38	69.83240527
VincentC_2016__MM103.3__bin.14	75.49682035
VincentC_2016__MM103.3__bin.6	86.22461171
VogtmannE_2016__MMRS11288076ST-27-0-0__bin.5	92.56505576
VogtmannE_2016__MMRS12272136ST-27-0-0__bin.50	69.91734588
VogtmannE_2016__MMRS15137911ST-27-0-0__bin.42	96.60773734
VogtmannE_2016__MMRS18295921ST-27-0-0__bin.55	85.02478315
VogtmannE_2016__MMRS18295921ST-27-0-0__bin.62	97.91408509
VogtmannE_2016__MMRS20257302ST-27-0-0__bin.36	98.38909542
VogtmannE_2016__MMRS20257302ST-27-0-0__bin.51	50.42750929
VogtmannE_2016__MMRS34525504ST-27-0-0__bin.17	75.10288066
VogtmannE_2016__MMRS34525504ST-27-0-0__bin.46	96.56133829
VogtmannE_2016__MMRS34525504ST-27-0-0__bin.5	62.06896552
VogtmannE_2016__MMRS34569532ST-27-0-0__bin.36	60.34482759
VogtmannE_2016__MMRS34569532ST-27-0-0__bin.39	69.29938272
VogtmannE_2016__MMRS34569532ST-27-0-0__bin.48	81.03448276
VogtmannE_2016__MMRS35808664ST-27-0-0__bin.45	58.62068966
VogtmannE_2016__MMRS35808664ST-27-0-0__bin.48	97.0260223
VogtmannE_2016__MMRS36405092ST-27-0-0__bin.37	91.09172311
VogtmannE_2016__MMRS39582183ST-27-0-0__bin.29	97.39776952
VogtmannE_2016__MMRS39582183ST-27-0-0__bin.48	96.62162162
VogtmannE_2016__MMRS39582183ST-27-0-0__bin.74	62.06896552
VogtmannE_2016__MMRS43563715ST-27-0-0__bin.17	53.88513514
VogtmannE_2016__MMRS44197125ST-27-0-0__bin.36	55.62421973
VogtmannE_2016__MMRS44587603ST-27-0-0__bin.11	98.31081081
VogtmannE_2016__MMRS44587603ST-27-0-0__bin.55	96.96360923
VogtmannE_2016__MMRS47662059ST-27-0-0__bin.8	93.18247044
VogtmannE_2016__MMRS51737257ST-27-0-0__bin.21	85.76131687
VogtmannE_2016__MMRS51737257ST-27-0-0__bin.34	95.44609665
VogtmannE_2016__MMRS51737257ST-27-0-0__bin.39	97.17265593
VogtmannE_2016__MMRS51737257ST-27-0-0__bin.40	59.89711934
VogtmannE_2016__MMRS51737257ST-27-0-0__bin.53	64.61751626
VogtmannE_2016__MMRS54246132ST-27-0-0__bin.60	96.54068567
VogtmannE_2016__MMRS54246132ST-27-0-0__bin.63	94.08783784
VogtmannE_2016__MMRS54316675ST-27-0-0__bin.38	95.17421834
VogtmannE_2016__MMRS54316675ST-27-0-0__bin.63	73.54399009
VogtmannE_2016__MMRS56137463ST-27-0-0__bin.12	69.73940994
VogtmannE_2016__MMRS57276462ST-27-0-0__bin.17	64.9382716
VogtmannE_2016__MMRS57276462ST-27-0-0__bin.34	98.53366378
VogtmannE_2016__MMRS57276462ST-27-0-0__bin.49	97.36111111
VogtmannE_2016__MMRS57276462ST-27-0-0__bin.73	96.78567329
VogtmannE_2016__MMRS62376181ST-27-0-0__bin.5	68.49385834
VogtmannE_2016__MMRS62666492ST-27-0-0__bin.48	55.17241379
VogtmannE_2016__MMRS64281551ST-27-0-0__bin.15	94.59459459
VogtmannE_2016__MMRS65742083ST-27-0-0__bin.24	97.97297297
VogtmannE_2016__MMRS65742083ST-27-0-0__bin.37	96.07392951

VogtmannE_2016__MMRS65742083ST-27-0-0__bin.40	94.83439533
VogtmannE_2016__MMRS65742083ST-27-0-0__bin.52	59.48275862
VogtmannE_2016__MMRS65862658ST-27-0-0__bin.40	98.11648079
VogtmannE_2016__MMRS68910755ST-27-0-0__bin.5	57.82921811
VogtmannE_2016__MMRS72802364ST-27-0-0__bin.35	98.31081081
VogtmannE_2016__MMRS77018926ST-27-0-0__bin.15	67.9574556
VogtmannE_2016__MMRS77018926ST-27-0-0__bin.35	73.39506173
VogtmannE_2016__MMRS77018926ST-27-0-0__bin.69	84.1503268
VogtmannE_2016__MMRS77018926ST-27-0-0__bin.73	97.675353
VogtmannE_2016__MMRS77487595ST-27-0-0__bin.43	63.68958788
VogtmannE_2016__MMRS77487595ST-27-0-0__bin.79	93.64931846
VogtmannE_2016__MMRS78791111ST-27-0-0__bin.16	96.62162162
VogtmannE_2016__MMRS78791111ST-27-0-0__bin.54	97.39776952
VogtmannE_2016__MMRS79893829ST-27-0-0__bin.11	80.43370508
VogtmannE_2016__MMRS81135225ST-27-0-0__bin.51	71.133829
VogtmannE_2016__MMRS81135225ST-27-0-0__bin.63	97.61462206
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VogtmannE_2016__MMRS81194191ST-27-0-0__bin.33	59.61844197
VogtmannE_2016__MMRS81194191ST-27-0-0__bin.38	95.67655891
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VogtmannE_2016__MMRS84085284ST-27-0-0__bin.14	67.24137931
VogtmannE_2016__MMRS84159866ST-27-0-0__bin.24	94.11663414
VogtmannE_2016__MMRS86168210ST-27-0-0__bin.6	83.51126928
VogtmannE_2016__MMRS88581325ST-27-0-0__bin.58	96.95945946
VogtmannE_2016__MMRS92546335ST-27-0-0__bin.28	97.74774775
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VogtmannE_2016__MMRS93508324ST-27-0-0__bin.18	92.03703704
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VogtmannE_2016__MMRS93508324ST-27-0-0__bin.68	97.2972973
VogtmannE_2016__MMRS93621581ST-27-0-0__bin.45	95.16728625
VogtmannE_2016__MMRS94549160ST-27-0-0__bin.58	95.7957958
VogtmannE_2016__MMRS94549160ST-27-0-0__bin.64	86.51877981
VogtmannE_2016__MMRS95479054ST-27-0-0__bin.12	96.25186546
VogtmannE_2016__MMRS95479054ST-27-0-0__bin.67	56.19369369
VogtmannE_2016__MMRS95674036ST-27-0-0__bin.5	98.09995869
VogtmannE_2016__MMRS96422329ST-27-0-0__bin.16	87.22222222
VogtmannE_2016__MMRS97327636ST-27-0-0__bin.49	94.82837791
WenC_2017__N009__bin.3	87.59259259
WenC_2017__N010__bin.1	58.51851852
WenC_2017__N010__bin.27	97.70551802
WenC_2017__N014__bin.13	95.47562268
WenC_2017__N018__bin.60	97.63513514
WenC_2017__N021__bin.17	95.4954955
WenC_2017__N021__bin.24	59.81481481
WenC_2017__N023__bin.27	97.97297297
WenC_2017__N025__bin.23	72.45456423
WenC_2017__N025__bin.27	50

WenC_2017__N025__bin.29	69.93243243
WenC_2017__N025__bin.52	94.85065711
WenC_2017__N025__bin.57	64.94650206
WenC_2017__N027__bin.30	97.04667493
WenC_2017__N030__bin.46	84.36080132
WenC_2017__N031__bin.1	71.09665428
WenC_2017__N031__bin.52	57.67141677
WenC_2017__N032__bin.7	97.63513514
WenC_2017__N035__bin.84	95.503924
WenC_2017__N037__bin.3	95.27027027
WenC_2017__N040__bin.22	73.41563786
WenC_2017__N040__bin.46	87.16216216
WenC_2017__N041__bin.14	51.72413793
WenC_2017__N219__bin.1	96.87242798
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WenC_2017__N233__bin.2	56.19122257
WenC_2017__N233__bin.4	92.22972973
WenC_2017__N235__bin.4	94.56422966
WenC_2017__N237__bin.3	93.58116481
WenC_2017__N237__bin.41	96.50900901
WenC_2017__N237__bin.5	97.15613383
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WenC_2017__N243__bin.48	96.32899628
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WenC_2017__N244__bin.41	97.76125568
WenC_2017__N252__bin.26	91.4291615
WenC_2017__N252__bin.8	94.14414414
WenC_2017__N253__bin.119	60.55865345
WenC_2017__N253__bin.65	63.79310345
WenC_2017__N263__bin.11	75.45045045
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WenC_2017__N266__bin.14	93.51320855
WenC_2017__N266__bin.21	97.97297297
WenC_2017__N267__bin.33	97.89348172
WenC_2017__N267__bin.36	89.8409748
WenC_2017__N274__bin.52	65
WenC_2017__N277__bin.49	72.4137931
WenC_2017__N279__bin.29	75.86206897
WenC_2017__N279__bin.61	93.55638166
WenC_2017__N283__bin.37	85.69256757
WenC_2017__N285__bin.18	78.71621622
WenC_2017__N286__bin.2	86.88558447
WenC_2017__N287__bin.35	96.62162162
WenC_2017__N295__bin.38	91.61916563
WenC_2017__N306__bin.38	93.04617117
WenC_2017__N306__bin.5	92.87534847
WenC_2017__N308__bin.19	71.76579926

WenC_2017__N308__bin.28	61.0212722
WenC_2017__N308__bin.30	53.05642633
WenC_2017__N308__bin.34	64.48275862
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WenC_2017__N314__bin.25	67.88065844
WenC_2017__N314__bin.29	67.38744321
WenC_2017__N314__bin.31	93.98142833
WenC_2017__N314__bin.32	79.37698413
WenC_2017__N315__bin.2	83.79310345
WenC_2017__N315__bin.53	94.8292042
WenC_2017__N315__bin.60	53.58934169
WenC_2017__N316__bin.50	96.21643949
WenC_2017__RA002__bin.36	58.62068966
WenC_2017__RA005__bin.33	58.62068966
WenC_2017__RA005__bin.37	95.00631386
WenC_2017__RA007__bin.14	86.97232549
WenC_2017__RA009__bin.29	72.74193548
WenC_2017__RA009__bin.36	67.16026435
WenC_2017__RA012__bin.2	97.31928955
WenC_2017__RA013__bin.19	87.5
WenC_2017__RA013__bin.27	59.27983539
WenC_2017__RA016__bin.24	93.83445946
WenC_2017__RA016__bin.28	98.88475836
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WenC_2017__RA017__bin.5	60.81504702
WenC_2017__RA018__bin.29	62.06896552
WenC_2017__RA019__bin.12	95.94594595
WenC_2017__RA020__bin.12	93.75750751
WenC_2017__RA023__bin.17	50.86206897
WenC_2017__RA024__bin.11	70.68965517
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WenC_2017__RA025__bin.59	80.03614209
WenC_2017__RA029__bin.9	94.75629905
WenC_2017__RA035__bin.15	96.06269873
WenC_2017__RA042__bin.15	95.93143329
WenC_2017__RA042__bin.91	61.20689655
WenC_2017__RA045__bin.49	81.03448276
WenC_2017__RA047__bin.27	79.79423868
WenC_2017__RA047__bin.47	96.69558034
WenC_2017__RA049__bin.2	98.31081081
WenC_2017__RA049__bin.5	94.49401074
WenC_2017__RA052__bin.30	96.03056588
WenC_2017__RA053__bin.12	57.5862069
WenC_2017__RA053__bin.14	51.72413793
WenC_2017__RA053__bin.30	55.43887147

WenC_2017__RA065__bin.11	90.2027027
WenC_2017__RA076__bin.21	88.6802974
WenC_2017__RA076__bin.57	82.55144033
WenC_2017__RA082__bin.11	96.26187526
WenC_2017__RA085__bin.14	55.51724138
WenC_2017__RA085__bin.8	83.82796365
WenC_2017__RA088__bin.23	96.84684685
WenC_2017__RA089__bin.10	92.19992051
WenC_2017__RA089__bin.25	55.30864198
WenC_2017__RA091__bin.4	75.86206897
WenC_2017__RA091__bin.79	85.18518519
WenC_2017__RA094__bin.25	95.77702703
WenC_2017__RA097__bin.15	98.81756757
WenC_2017__RA098__bin.3	73.90437836
WenC_2017__RA0X1__bin.9	53.55741429
WenC_2017__RA100__bin.18	93.24831949
WenC_2017__RA103__bin.16	57.75862069
WenC_2017__RA105__bin.21	96.43581081
WenC_2017__RA110__bin.24	50.86206897
WenC_2017__RA110__bin.8	75
WenC_2017__RA111__bin.5	77.5862069
WenC_2017__RA118__bin.26	91.18546055
WenC_2017__RA118__bin.4	77.77777778
WenC_2017__RA120__bin.38	55.00149343
WenC_2017__RA130__bin.24	93.37462462
XiaoL_2015__SAMEA3134506__bin.64	64.75
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XiaoL_2015__SAMEA3134525__bin.23	58.62
XiaoL_2015__SAMEA3134526__bin.17	66.46
XiaoL_2015__SAMEA3134529__bin.17	59.44
XieH_2016__YSZC12003_35387__bin.35	75.17241379
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XieH_2016__YSZC12003_35390__bin.29	55.17241379
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XieH_2016__YSZC12003_35392__bin.95	91.07806691
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XieH_2016__YSZC12003_35519__bin.52	68.87758226
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XieH_2016__YSZC12003_35549__bin.89	57.93918919
XieH_2016__YSZC12003_35550__bin.136	99.13258984
XieH_2016__YSZC12003_35550__bin.16	86.90878378
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XieH_2016__YSZC12003_35561__bin.36	70.74074074
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XieH_2016__YSZC12003_35563__bin.40	98.51301115
XieH_2016__YSZC12003_35563__bin.41	80.1425031
XieH_2016__YSZC12003_35564__bin.81	96.28378378
XieH_2016__YSZC12003_35658__bin.76	98.64864865
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XieH_2016__YSZC12003_35740__bin.4	53.44827586
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XieH_2016__YSZC12003_35989__bin.116	59.48275862
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ZeeviD_2015__PNP_Main_16__bin.48	63.79310345
ZeeviD_2015__PNP_Main_161__bin.14	83.22072072
ZeeviD_2015__PNP_Main_162__bin.38	53.44827586
ZeeviD_2015__PNP_Main_163__bin.3	81.03448276
ZeeviD_2015__PNP_Main_163__bin.36	81.66666667
ZeeviD_2015__PNP_Main_163__bin.44	56.89655172
ZeeviD_2015__PNP_Main_163__bin.47	93.8692689
ZeeviD_2015__PNP_Main_163__bin.61	80.04249872
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ZeeviD_2015__PNP_Main_165__bin.43	66.55172414
ZeeviD_2015__PNP_Main_165__bin.55	69.27899687
ZeeviD_2015__PNP_Main_165__bin.60	56.89655172
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ZeeviD_2015__PNP_Main_166__bin.42	62.82011565
ZeeviD_2015__PNP_Main_166__bin.53	75.18518519
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ZeeviD_2015__PNP_Main_170__bin.64	61.12852665
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ZeeviD_2015__PNP_Main_177__bin.55	53.44827586
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ZeeviD_2015__PNP_Main_182__bin.35	95.60810811
ZeeviD_2015__PNP_Main_183__bin.12	56.89655172
ZeeviD_2015__PNP_Main_185__bin.14	80.34482759
ZeeviD_2015__PNP_Main_185__bin.17	96.85185185
ZeeviD_2015__PNP_Main_185__bin.24	97.67657993
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ZeeviD_2015__PNP_Main_189__bin.45	91.88271254

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ZeeviD_2015__PNP_Main_207__bin.3	64.65517241
ZeeviD_2015__PNP_Main_207__bin.4	55.48430401
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ZeeviD_2015__PNP_Main_253__bin.34	94.59459459
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ZeeviD_2015__PNP_Main_514__bin.3	51.72413793
ZeeviD_2015__PNP_Main_515__bin.30	99.25650558
ZeeviD_2015__PNP_Main_517__bin.15	95.77702703
ZeeviD_2015__PNP_Main_517__bin.33	87.5299463
ZeeviD_2015__PNP_Main_518__bin.6	94.42379182

ZeeviD_2015__PNP_Main_520__bin.53	90.73585122
ZeeviD_2015__PNP_Main_520__bin.77	92.32032218
ZeeviD_2015__PNP_Main_521__bin.1	70.66294919
ZeeviD_2015__PNP_Main_526__bin.25	78.39012805
ZeeviD_2015__PNP_Main_527__bin.13	78.7732342
ZeeviD_2015__PNP_Main_529__bin.14	94.38813814
ZeeviD_2015__PNP_Main_529__bin.19	96.07392951
ZeeviD_2015__PNP_Main_53__bin.21	95.60810811
ZeeviD_2015__PNP_Main_530__bin.28	89.52459813
ZeeviD_2015__PNP_Main_530__bin.9	93.57865218
ZeeviD_2015__PNP_Main_532__bin.13	99.25650558
ZeeviD_2015__PNP_Main_532__bin.20	95.87837838
ZeeviD_2015__PNP_Main_532__bin.8	91.38270624
ZeeviD_2015__PNP_Main_535__bin.26	94.25925926
ZeeviD_2015__PNP_Main_535__bin.33	80.46447182
ZeeviD_2015__PNP_Main_535__bin.36	96.07392951
ZeeviD_2015__PNP_Main_536__bin.30	58.7037037
ZeeviD_2015__PNP_Main_537__bin.1	87.83801274
ZeeviD_2015__PNP_Main_537__bin.11	84.63949843
ZeeviD_2015__PNP_Main_537__bin.13	97.40740741
ZeeviD_2015__PNP_Main_537__bin.15	65
ZeeviD_2015__PNP_Main_537__bin.17	90.91697598
ZeeviD_2015__PNP_Main_537__bin.19	79.62382445
ZeeviD_2015__PNP_Main_537__bin.22	71.63362247
ZeeviD_2015__PNP_Main_537__bin.4	96.28378378
ZeeviD_2015__PNP_Main_538__bin.16	51.72413793
ZeeviD_2015__PNP_Main_538__bin.2	67.6293941
ZeeviD_2015__PNP_Main_538__bin.7	92.98503252
ZeeviD_2015__PNP_Main_539__bin.55	94.98141264
ZeeviD_2015__PNP_Main_542__bin.10	64.80286738
ZeeviD_2015__PNP_Main_542__bin.15	95.60810811
ZeeviD_2015__PNP_Main_543__bin.7	85.97972973
ZeeviD_2015__PNP_Main_544__bin.11	96.11243597
ZeeviD_2015__PNP_Main_545__bin.38	94.25675676
ZeeviD_2015__PNP_Main_546__bin.10	75.21685254
ZeeviD_2015__PNP_Main_548__bin.16	74.53428335
ZeeviD_2015__PNP_Main_548__bin.27	60.30405405
ZeeviD_2015__PNP_Main_549__bin.12	64.83890954
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ZeeviD_2015__PNP_Main_55__bin.7	59.77499713
ZeeviD_2015__PNP_Main_550__bin.13	89.31236368
ZeeviD_2015__PNP_Main_551__bin.17	67.22972973
ZeeviD_2015__PNP_Main_553__bin.37	75.21757293
ZeeviD_2015__PNP_Main_553__bin.8	97.2972973
ZeeviD_2015__PNP_Main_557__bin.9	93.41216216
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ZeeviD_2015__PNP_Main_559__bin.17	50.8045977

ZeeviD_2015__PNP_Main_559__bin.26	84.48275862
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ZeeviD_2015__PNP_Main_560__bin.55	94.73251029
ZeeviD_2015__PNP_Main_560__bin.6	94.63213213
ZeeviD_2015__PNP_Main_561__bin.37	67.70342834
ZeeviD_2015__PNP_Main_562__bin.18	80.74324324
ZeeviD_2015__PNP_Main_563__bin.16	52.96296296
ZeeviD_2015__PNP_Main_567__bin.18	86.78918414
ZeeviD_2015__PNP_Main_567__bin.36	83.22593969
ZeeviD_2015__PNP_Main_568__bin.27	65.12345679
ZeeviD_2015__PNP_Main_57__bin.39	63.27586207
ZeeviD_2015__PNP_Main_57__bin.42	62.47211896
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ZeeviD_2015__PNP_Main_570__bin.7	91.99074074
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ZeeviD_2015__PNP_Main_575__bin.12	67.37654321
ZeeviD_2015__PNP_Main_575__bin.3	73.51851852
ZeeviD_2015__PNP_Main_575__bin.30	96.62162162
ZeeviD_2015__PNP_Main_578__bin.29	95.77702703
ZeeviD_2015__PNP_Main_579__bin.38	83.8992152
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ZeeviD_2015__PNP_Main_584__bin.10	93.95910781
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ZeeviD_2015__PNP_Main_590__bin.7	67.24137931
ZeeviD_2015__PNP_Main_591__bin.17	53.44827586
ZeeviD_2015__PNP_Main_593__bin.12	62.38244514
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ZeeviD_2015__PNP_Main_596__bin.63	69.48275862
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ZeeviD_2015__PNP_Main_601__bin.5	93.16816817

ZeeviD_2015__PNP_Main_603__bin.31	55.17241379
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ZeeviD_2015__PNP_Main_606__bin.2	90.8983891
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ZeeviD_2015__PNP_Main_614__bin.7	85.92592593
ZeeviD_2015__PNP_Main_614__bin.8	51.28562577
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ZeeviD_2015__PNP_Main_617__bin.2	99.13258984
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ZeeviD_2015__PNP_Main_618__bin.8	64.83271375
ZeeviD_2015__PNP_Main_618__bin.9	65.74507146
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ZeeviD_2015__PNP_Main_623__bin.10	54.69667069
ZeeviD_2015__PNP_Main_623__bin.12	97.32710652
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ZeeviD_2015__PNP_Main_626__bin.7	88.42592593
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ZeeviD_2015__PNP_Main_669__bin.20	90.87837838
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Estimated contamination	# of contigs
1.811186186	463
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2.083333333	508
4.23048048	527
0	557
1.724137931	452
1.983858859	301
2.470238095	411
1.724137931	543
3.023648649	454
1.70045045	340
4.05	544
1.724137931	270
0	218
0.675675676	74
0.743494424	357
0.844594595	122
2.263513514	350
0	486
0.49382716	101
0	317
0.800477897	481
1.512226512	232
0	84
0.912162162	115
0	216
1.889714994	306
0.337837838	209
0.743494424	181
1.013513514	97
0.675675676	161
1.724137931	267
0.844594595	242
0	53
0.281531532	134
0	283
0.506756757	132
1.182432432	108
0	131
0.755885998	151
0	40
0.975836431	641
0.046468401	91
1.013513514	75
0.37037037	70
0.817843866	199

0	490
0	95
0.844594595	89
2.857142857	183
2.432432432	234
1.576576577	58
0	34
0.506756757	64
0.844594595	205
2.0755886	445
0	20
0.666047088	135
0.092936803	83
0.675675676	222
1.182432432	117
2.865551425	273
0	64
0	109
0.714285714	176
0.907682776	574
1.430407276	341
0	207
0.650557621	394
1.182432432	198
0.787037037	265
0	73
3.43866171	702
0.675675676	160
0.418215613	106
0	87
0.957207207	198
0.371747212	126
0.49382716	34
1.632882883	129
0.37037037	89
1.672862454	150
0.050838841	284
1.202305246	154
2.103174603	494
1.013513514	126
1.824324324	139
0.418215613	112
1.013513514	93
0.711743772	247
2.524399399	284
0.844594595	47
3.43866171	498

0	527
1.407657658	66
0	41
1.013513514	56
3.378378378	55
0.37037037	28
0	27
2.871621622	47
0	27
0.260223048	168
0	49
1.745495495	103
1.301115242	197
0	95
1.295045045	45
0	178
0	33
0.185873606	65
2.111486486	258
0	20
0	141
0.86470399	220
0	118
0	47
0.442406692	122
0	88
0.074349442	106
0	62
0.844594595	83
0	56
0	82
0	46
0	47
0	69
0.355871886	35
0	31
0	52
0.557620818	53
0	37
0	57
0	75
0	42
0.533807829	94
0	51
0	40
0.371747212	55
1.486988848	64

0.711743772	60
0	39
0.82094176	482
1.703465605	347
0.177935943	40
0.337837838	46
2.131350682	321
0	50
2.397769517	289
0.394144144	117
0	48
0	143
1.21	242
1.45	431
2.47	328
0	120
0.19	201
0	382
0	437
2.2	131
0	388
0.9	257
0.19	151
0.16	345
0.77	424
0	403
0	91
0	384
0	157
2.03	405
1.01	168
0	85
1.53	380
0.862068966	369
0	51
0.864197531	106
2.213961173	327
0	76
1.724137931	341
0	206
0.555019305	54
2.142857143	177
0.617283951	252
0	129
0	131
0.355871886	51
0.825825826	148

3.055555556	215
0.37037037	69
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0	182

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0.86	135
0	285
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0	203
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1.01	96
0.11	273
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0.675675676	93
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0	169
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0	50
0	73
0	115
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0.53490991	352
0	68
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1.410969793	356
0.668720191	478
1.017267267	481
0.862068966	744
1.644144144	114
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0.084459459	103
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0.247831475	185
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1.745495495	373
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0.827757905	431
0.337837838	416
0.371747212	22
0	66
0	21
0	63
1.554054054	477
0	73

0.822072072	414
0.337837838	233
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0.337837838	184
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0	255
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1.402027027	292
3.354231975	68
0.309684685	182
0.156739812	345
4.448198198	413
0	233
0.731981982	186
0	33
4.19481982	473
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4.812643526	756
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0.743494424	98
0	44
0	30
1.144894895	207
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0.123915737	17
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0.892857143	309
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0.260223048	58
0	26

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0.009936407	174
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0.337837838	83
1.724137931	287
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1.081081081	228
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1.914414414	322
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1.70045045	334
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0.371747212	21
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0.168918919	109
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1.282527881	364
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1.880877743	200
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0.506756757	77
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0	108
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2.027027027	281
1.724137931	571
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0	104
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0	115
0	91
0	148
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1.013513514	487
1.135510511	589
1.933183183	181
0.900900901	48
2.919481982	522
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1.337274775	330
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0.337837838	137
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0.371747212	145
0.337837838	154
0	47
1.435810811	207
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1.325075075	293
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0	39
1.638513514	214
0.084459459	68
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0.743243243	206
1.174388674	264
0.563063063	221
2.797650592	247
0.168918919	74
0.966591592	293
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0.326215896	184
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0.957207207	97
1.724137931	185
1.858108108	183

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0.862068966	281
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0.185873606	273
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1.435810811	195
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0.337837838	105
0.394144144	51
0.337837838	104
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0.253378378	148
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0	117
0.506756757	131
0.371747212	159
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0.798224695	282

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0.371747212	43
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0.675675676	202
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1.182432432	143
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2.759009009	117
0.422297297	97
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0.762012012	147
0.337837838	94
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0.743494424	71
1.724137931	629
0.337837838	48
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0.337837838	125
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0.112612613	147
0.185873606	178
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0.084459459	88
0.53490991	353
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2.149576047	272
0.957207207	343
0.675675676	174
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0.557620818	194
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0	71
3.442192192	120
1.351351351	115
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0.882899628	210

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0.557620818	162
0.281531532	351
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2.14527027	234
3.448275862	411
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1.163127413	569
1.981981982	265
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0.433558559	249
0.337837838	51
0.844594595	118
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0.459834835	183
0.355871886	72
1.351351351	113
1.889714994	497
1.259384384	222
0.478603604	158
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0.743494424	261
0.168918919	68
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0.377583466	195
0.257018584	193
0.619369369	111
1.801801802	161
0.495662949	64
0.533807829	149
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3.885135135	513
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0.168918919	205
0.177935943	83

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1.070371842	165
0.506756757	140
0.448161917	31
1.689189189	181
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0.417329094	100
0.371747212	42
2.13963964	464
0.619369369	131
1.724137931	220
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0.506756757	272
1.013513514	70
0.446096654	185
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0.12345679	90
1.52027027	66
0.371747212	59
0	115
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0.557620818	225
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0	91
0	122
0.355871886	50
0	169
0	85
2.13963964	238

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0.371747212	55
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1.661036036	437
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0.018768769	47
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0.581831832	225
0.816441441	253
0.520005299	208
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1.341966967	444
0.112612613	176
1.136062533	441
1.013513514	167
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0	195
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1.644144144	160
1.724137931	336
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0.506756757	480
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1.418918919	250
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0.760135135	120
0.92936803	218
1.690391459	248
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4.702194357	325
1.511989931	653
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0.337837838	138
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0.337837838	58
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0.788288288	122
0.945945946	215
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0.422297297	167
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0.337837838	86
1.756756757	328
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0	62
0	82
0	142
1.914414414	276
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0	22
0.743243243	213
0.585585586	162
0.422297297	291

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0.371747212	129
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0.197072072	173
0.371747212	19
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0.506756757	137
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1.220570012	266
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1.418918919	261
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0.563063063	191
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0.512276983	111
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0.337837838	265
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1.52027027	176
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1.998141264	549
1.351351351	91
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0.675675676	107
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0	370
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1.334519573	280
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1.435810811	349
3.265765766	547
0.844594595	52

1.970720721	54
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0.544294294	150
0.355871886	347
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0.12345679	62
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0.371747212	248
0.12345679	50
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0.864197531	131
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1.013513514	160
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0.506756757	181
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0	40
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0.844594595	79
0.652431791	231
1.576576577	380
0	210
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1.067615658	245
0.506756757	122
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0.619369369	143
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0.675675676	124
1.197852127	405
0.355871886	175
0.892857143	91
0.675675676	245
0.371747212	37
0.177935943	52
0.844594595	64
0.123915737	331
0	36
0	212
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3.448275862	92
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0.844594595	126
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1.858736059	327
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0.787037037	239
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1.982651797	369
1.755431902	178
0.844594595	63
0.168918919	54
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3.928571429	170
0	265
0	113
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1.724137931	265
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0.663580247	136
0.49382716	163
1.182432432	177
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0.355871886	87
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0.574324324	106
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0.337837838	249
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1.689189189	52
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0.675675676	79
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0.046468401	64
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0.944857497	285
0.711743772	124
0.929054054	328
1.689189189	76
0	38
0.892857143	293
0.711743772	62
0.506756757	83
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1.321767865	37
0.371747212	56
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0	56
0	102
0.123915737	104
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0.975836431	180
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0.675675676	175
0.619369369	195
0.092936803	42
0.675675676	60
0.371747212	75
1.724137931	110
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0.675675676	112
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1.510885886	133
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0.355871886	93
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3.448275862	116
1.082443654	298

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0.889679715	209
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0.557620818	22
0	48
0.371747212	158
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0.675675676	188
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0.12345679	56
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0	134
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0	118

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1.683330509	276
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0	159
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0.675675676	93
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1.689189189	173
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0	52
0	88
0	106

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0.371747212	179
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1.689189189	219
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0	184
1.388888889	106
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0.675675676	52
0.185873606	72
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0.679012346	384
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0	82
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0.49382716	105
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0.844594595	95
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0	29
0	34

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0.675675676	72
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1.52027027	71
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0	190
0.675675676	73
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0.506756757	63
0	110
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3.448275862	335

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1.587837838	85
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0.371747212	52
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0.675675676	52
0.337837838	92
0	63
0.12345679	366
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0	183
0	73
0.844594595	151
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0	236
0	347
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0.337837838	71
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0.675675676	123
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0.844594595	75
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0.092592593	101
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0.92936803	306
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0.185873606	152
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0.557620818	175
0.681536555	368
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2.702702703	35
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2.871621622	35
0.446096654	204
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0.355871886	42

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1.52027027	113
0.506756757	110
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0.12345679	358
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0	186
0	347
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3.526645768	449
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1.619217082	268
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0	332
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0	268

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1.486988848	261
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0.864197531	260
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0.679012346	286
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0	274
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0	175
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0.555555556	142
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0	137
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3.84	315
1.72	215
1.7	130
1.16	84
0.86	158
0.37	130
0.43	122
0.93	143
0.73	201
2.59	345
1.48	182
0.93	112
3.45	217
0.54	66

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0	126
0.19	64
4.31	450
0	139
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1.72	113
0	42
0.16	91
0.37	124
0.25	62
0.86	538
0.28	75
3.58	324
0	64
4.08	181
3.24	497
2.35	251
0.19	85
0	259
0.47	359
1.18	157
0.37	210
0.96	92
0.26	353
0.49	183
0.86	443
0.79	75
2.52	473
1.3	156
0.62	253
3.45	242
3.45	394
0.56	153
4.78	432
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3.45	278
0	346
3.45	341
0	186
4.31	137
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1.72	191
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0.56	83
0	153
3.45	484

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1.72	370
2.59	119
0	77
1.3	162
2.04	242
2.18	287
1.75	134
1.88	118
2.13	363
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3.45	734
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0.371747212	189
0.92936803	89
0.371747212	103
0	83
0	411
1.475225225	194
0.844594595	92
0.711743772	235
0.039541321	162
0.337837838	68
0	103
0.19	33
1.53	184
0.94	221
0.12	147
0.56	35
0.12	18
0.19	39
4.31	590
2.87	90
0	301
0.49	122
1.99	374
1.01	87

1.85	320
0.75	144
2.23	204
0	42
0.65	382
0	40
2.16	283
0.37	73
4.19	137
0.87	77
2.03	103
2.03	142
0	30
1.46	99
2.7	122
2.62	208
1.35	77
1.34	381
0.49	119
2.03	77
0	16
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1.72	150
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0	170
0	82
1.18	108
0.68	80
0.53	147
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1.36	102
0.6	314
2.78	99
1.63	104
1.01	156

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0.74	71
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0	190
0.19	120
0	239
0	239
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1.15	105
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1.3	310
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0.56	29
0.86	194
0.49	25
0.56	27
0	86
0.25	104
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2.19	428

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0.19	67
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1.18	97
1.06	370
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1.72	445
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0	339
0.34	264
0.37	99

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0.68	297
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0.685612083	153
1.165540541	270
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2.487413884	189
0	415
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2.195945946	264
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1.192368839	187
1.724137931	357
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2.13963964	127
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0.675675676	71
1.858108108	170
2.038413879	466
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1.502478315	800
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1.52027027	216
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0	27
0	16
0	58
0	23
0	69
1.72	100
0	26
0.46	242
0	14
0.37	7
0.31	69
0	59
4.31	430
0.37	66
0	61
0.19	68
0	52
0	5
0.39	113
0	43
0	33
0	26
0	12
0.37	21
0	27
1.12	19
0	66
0	18
0	66
0.49	116
0.37	35
0	23
0	10
0.19	32
0	60
0	23
0	34
0	65
0.37	38

0	19
0	10
0	28
0	62
0	37
0	154
0	22
0	11
0	59
0.56	23
0	64
0.65	144
0	31
0	29
0	29
0	15
0	64
0	32
0	28
0	21
1.72	181
2.586206897	583
0	544
1.724137931	840
0	484
1.640946502	422
1.52	139
0.31	75
2.04	121
6.9	165
0	138
5.48	249
0.05	51
0	267
7.47	418
2.73	100
8.62	227
4.58	207
7.76	229
0	35
1.34	304
3.24	376
1.72	173
6.88	380
6.9	153
3.58	108
0.93	54

5.64	288
2.65	75
0	88
2.06	96
2.71	91
2.65	245
2.59	446
1.89	75
1.72	380
2.35	189
0	50
0.56	69
0.57	139
0.42	168
0.8	58
1.17	47
2.9	91
5.17	323
5.08	376
0.37	260
0.74	116
0.34	74
3.45	340
0.56	90
1.07	336
0.11	78
1.72	85
1.72	371
1.4	66
1.26	57
0.49	50
0.31	75
6.03	273
9.66	162
0	53
3.3	297
9.08	209
1.52	110
0.21	89
3.45	397
0	78
0.25	78
0.68	105
5.79	382
0.39	223
3.79	520
0.07	48

5.73	392
1.72	255
1	61
1.01	217
0.19	51
4.7	111
0.45	124
1.72	231
1.3	220
2.35	80
9.48	337
0	176
1.85	65
2.28	302
3.45	345
2.99	403
0	140
6.9	290
5.17	328
2.14	70
2.16	254
0	28
1.36	104
0.68	274
3.45	309
0	26
5.17	274
0.98	133
4.54	288
1.02	278
3.98	306
0.62	294
1.36	167
3.45	67
2.07	113
1.57	346
1.72	427
5.17	301
3.45	191
4.06	268
2.05	121
0.56	250
0.37	31
0.65	343
5.17	267
2.35	278
0	130

1.31	301
6.9	247
6.99	533
8.62	268
1.72	178
6.66	546
1.6	383
1.4	75
6.43	398
1.72	277
0.56	253
4.31	248
0	217
1.72	265
1.65	386
1.7	442
1.06	147
0	336
0.86	375
0	286
0	220
3.4	389
1.36	282
0	231
2.59	526
1.72	394
0	356
1.23	73
1.72	365
7.78	380
1.72	314
1.72	308
0	240
1.87	364
1.72	64
0.14	81
0	83
2.15	291
1.76	238
1.79	263
0	86
1.57	219
1.6	101
2.72	340
2.98	76
0	84
0.19	159

8.62	330
0.74	51
2.31	135
4.38	371
1.72	137
4.38	159
0	71
1.97	191
2.59	104
3.38	134
8.62	225
1.86	359
0	28
2.95	112
2.72	113
1.42	51
1.72	86
0	105
8.46	175
2.59	295
2.76	235
3.95	269
0	80
2.73	129
2.82	104
1.17	90
2.16	114
4.95	208
4.84	140
5.17	312
6.5	214
0	262
0	167
1.94	208
4.24	343
0.91	107
6.3	156
0.19	107
4.71	104
0.88	136
1.21	250
0	312
3.45	233
0	331
0	63
1.72	164
0.97	83

0.34	66
0	57
2.59	141
3.82	147
6.05	344
3.73	409
0	229
0.37	40
2.44	328
0.74	103
0	98
1.82	200
3.18	275
0.37	42
1.58	125
1.11	78
0.05	74
6.9	297
2.35	165
2.07	106
1.43	120
0.99	101
0.68	54
3.91	387
3.45	331
1.56	114
1.72	248
6.9	438
7.04	73
8.28	57
1.37	271
1.82	115
0.37	31
2.35	81
6.19	209
1.73	242
0.37	56
2.73	181
1.72	240
6.9	224
0	284
0	133
2.03	279
1.72	107
2.36	93
0	86
2.98	149

7.21	256
1.72	88
0.74	38
4.91	336
2.25	262
0.37	46
2.12	132
0.41	125
0	66
0.49	88
2.98	204
0	50
4.05	424
0.05	97
0.96	77
2.75	166
1.07	110
2.27	134
2.81	178
8.53	257
5.37	423
1.2	204
3.97	119
0.02	50
0.86	51
0	270
0.46	61
1.5	228
2.47	108
0	191
1.3	57
2.59	327
2.31	137
1.3	74
1.98	111
0.37	46
8.62	239
3.24	200
3.98	362
5.64	125
3.45	307
2.82	217
3.99	151
1.72	280
5.33	135
0.56	271
0.09	89

0	70
6.07	146
0.86	131
4.31	154
0.93	62
0.37	48
0.37	61
5.35	299
0.37	37
2.59	637
2.25	123
1.66	314
0	287
2.59	325
0.74	76
0	191
0.94	85
1.11	144
7.01	448
0	101
0.17	46
1.36	83
0.37	51
1.18	201
0.28	159
0.93	115
0	51
2.65	83
1.72	143
6.9	328
0.98	296
7.93	150
1.01	171
1.97	229
0.86	73
0.34	69
2.39	384
2.96	62
4.07	62
7.84	149
1.62	202
0.37	51
0.74	67
0.86	127
1.23	169
0	126
0.05	119

4.67	223
0.37	43
8.62	305
0.37	94
3.48	309
6.04	194
0.05	106
1.63	75
2.01	287
0.37	42
4.54	149
2.78	105
2.41	299
1.62	372
0.05	107
0.62	108
8.62	287
0.77	82
1.05	118
5.17	216
3.4	112
6.9	295
2.27	276
4.62	372
8.7	382
0.74	73
0	182
2.16	181
0.74	56
1.28	365
0.37	45
2.44	263
1.22	292
1.48	159
1.13	145
1.71	295
0.56	87
3.57	121
1.72	37
4.31	170
0.74	62
0.37	70
0.95	153
2.24	64
3.1	169
1.3	128
1.52	316

7.24	490
0.74	47
0.56	79
2.41	141
1.08	245
7.76	307
0	275
0.74	156
0	427
1.79	275
2.59	257
1	179
0.87	310
1.23	132
1.72	223
5.82	497
0.86	364
3.45	433
4.31	214
0.37	114
0	131
1.72	243
2.25	157
0.71	253
1.72	236
1.41	263
0	213
0	326
0.68	330
3.45	423
0	124
0.41	130
1.72	214
0	253
3.13	368
3.45	388
1.85	208
1.72	157
0	173
1.72	206
6.9	193
1.1	394
3.67	262
0.79	200
1.6	197
0.93	83
1.6	67

1.08	232
0	271
5.36	399
1.72	83
1.88	311
1.3	202
0.74	73
0.31	197
6.03	312
0.94	44
0.74	80
4.26	148
1.3	281
1.64	205
9.94	122
8.62	77
3.45	163
3.03	306
0	61
1.83	212
2.72	108
0.74	90
1.67	93
3.05	394
1.67	344
1.05	92
3.21	86
0	135
1.99	186
1.42	114
2.96	83
5.17	228
8.1	199
3.91	256
0.78	100
0	83
1.67	131
1.72	291
5.64	176
1.51	188
3.45	267
1.92	246
1.2	215
1.72	307
5.99	316
0	72
0	99

1.23	84
1.91	156
2.59	426
4.91	235
1.3	43
1.11	145
2.62	334
5	426
0	63
4.75	75
8.37	103
1.72	342
1.73	205
0	32
3.02	220
0.56	250
2.43	359
3.15	308
1.68	45
5.17	371
0.34	95
1.67	208
0.28	212
0.39	41
0.8	349
0.68	137
0.68	116
1.3	59
1.52	115
3.29	190
8.12	349
1.57	152
1.67	246
1.54	81
0	288
1.3	244
3.36	171
0.96	95
6.94	189
0.83	235
0.37	75
1.72	102
2.53	213
0	312
1.71	187
0.86	136
0.37	236

3.33	265
0.93	344
1.68	98
4.63	180
2.78	101
0	297
3.8	223
1.23	201
1.17	271
1.72	335
0.56	235
1.33	143
1.38	432
0	70
0.49	50
0.7	98
2.59	238
3.45	136
2.53	124
8.62	281
6.9	243
3.15	179
1.72	280
1.9	221
5.18	371
0.74	225
3.45	75
0.86	304
4.57	250
2.59	94
3.64	116
2.96	276
0.83	102
1.27	112
0	141
4.31	245
1.33	112
0	359
4.26	37
1.94	160
0	102
4.17	461
0.56	66
1.68	83
1.48	266
1.53	283
4.16	400

1.72	157
0.86	108
2.04	220
1.48	134
9.25	240
0.37	205
0.93	271
1.05	188
2.35	295
2.62	232
0	79
1.97	263
5.67	120
9.48	179
0	157
1.42	306
0.86	61
0.93	77
0.16	353
5.52	290
1.72	352
0.12	37
2.35	134
1.98	293
0.45	252
2.35	66
0	306
2.59	238
0.09	50
1.2	226
3.21	156
0	58
1.84	285
0.56	70
2.61	240
0.56	152
1.27	109
1.32	153
1.72	340
0.74	125
0.68	83
1.72	123
1.01	98
9.09	228
1.6	84
3.45	304
0.74	107

0.84	110
0.27	117
1.13	110
3.43	120
0.56	148
3.27	334
0	98
2.07	207
0.8	294
1.72	247
1.6	213
5.17	251
2.59	183
6.79	235
3.9	189
3.45	272
1.81	236
2.45	352
4.31	190
2.04	101
3.97	365
1.73	238
0.18	31
2.42	355
1.39	262
0.74	45
1.72	308
1.62	196
0.81	142
7.35	369
1.18	172
0.56	78
0.74	98
4.69	154
0	342
0.84	177
3.45	321
1.65	266
5.17	430
1.54	508
3.45	455
8.62	444
1.72	403
6.9	459
9.48	288
0	424
1.72	226

0	416
3.45	306
1.91	307
0	476
1.72	267
0	261
4.36	495
3.45	332
1.25	191
0	525
0	259
3.45	554
4.66	423
1.72	398
0.65	337
3.45	83
2.5	211
5.93	291
1.85	147
1.88	243
0.56	64
2.28	305
0	225
2.48	251
1.3	110
1.69	120
1.48	130
0.93	116
0.86	84
2.59	379
0	38
2.31	109
3.45	327
0.05	102
8.62	211
4.39	185
0	42
0	51
0.93	226
6.9	413
0.83	151
2.04	289
4.31	117
0.46	237
0	76
1.71	218
1.12	268

0.16	151
1.72	145
0.56	107
4.9	186
1.72	406
0.37	43
0.04	107
0.19	55
6.67	47
7.76	116
1.72	109
5.35	117
2.61	211
2.99	232
3.45	234
0.81	79
2.54	157
2.5	95
0.37	46
6.9	237
1.77	367
0.94	68
1.79	89
0.37	63
3.77	125
1.3	104
0.49	71
1.85	199
2.01	363
3.29	412
0.93	159
0.93	114
2.72	99
3.38	283
0.46	48
4.44	241
2.18	278
0.93	100
1.7	166
0.37	45
1.15	50
0.42	260
1.98	76
1.41	317
1.06	145
0.93	151
8.62	153

0.46	61
0.94	90
3.35	100
1.81	75
0.74	40
1.48	44
0.12	71
0.17	141
1.2	260
0.36	41
0.56	180
0	73
5.25	57
1.67	272
0	311
1.86	311
1.14	407
6.9	113
3.5	88
0	102
1.74	178
5.17	98
0	257
0.19	38
1.3	61
1.72	238
0	40
6.23	62
5.75	159
5.83	65
7.76	298
0.37	56
1.66	148
2.65	144
0	68
3.92	332
3.3	168
1.68	70
0	42
0	270
0.17	219
9.48	353
0.78	76
8.96	146
0	204
1.72	160
0.37	45

1.64	462
5.17	146
8.64	164
8.62	417
0.74	67
2.98	151
0.68	85
5.25	79
2.13	236
3.73	182
0.37	48
0.41	107
4.31	243
0	70
6.25	92
0	320
0	182
0.37	42
1.73	126
0	34
2.41	105
0.37	50
1.97	276
1.48	175
5.6	173
4.57	158
0.78	59
0.28	104
6.9	194
0	217
6.7	211
6.76	188
7.76	148
4.62	425
5.19	138
4.21	202
0.84	93
3.15	103
0.41	126
3	205
0.37	46
0.86	329
7.25	170
3.8	250
2.53	322
0.37	46
2.93	336

1.72	302
2.65	148
0.22	52
1.91	94
1.85	108
5.17	401
4.44	121
2.22	144
4.53	108
0	50
0	114
1.88	116
0	308
0	208
0.74	50
2.07	317
0.83	79
0.19	105
3.02	222
0.86	256
5.17	279
0.56	102
2.87	319
0.62	137
3.1	293
2.61	167
0	452
1.35	99
1.23	110
3.45	161
7.66	278
8.62	237
7.35	396
0.5	111
1.73	106
4.31	97
0.41	155
4.1	168
0.37	235
0	38
0.37	49
7.72	390
0.37	62
0	22
3.45	388
2.05	148
0.37	94

6.9	193
2.96	72
0.68	56
3.75	195
6.43	228
1.37	86
0.05	111
2.04	372
5.17	229
2.9	345
3.81	127
2.75	195
0.11	140
0.93	49
1.85	91
7.5	315
2.9	365
0.04	36
1.85	80
1.69	135
1.58	153
2.21	108
0.68	149
0	333
3.45	340
3.45	726
4.58	316
6.9	142
0.43	98
1.11	110
1.11	248
0.04	52
8.63	245
1.72	95
0.93	83
3.45	103
1.85	71
8.15	231
8.62	287
1.72	355
4.01	55
1.49	210
3.92	154
0.86	73
1.85	254
1.72	401
0.86	117

5.56	120
6.9	263
8.54	396
5.02	264
0.68	87
0.53	98
0	390
0	284
1.16	147
0	45
0.71	137
1.72	296
3.15	110
1.83	236
1.59	73
1.35	219
0.04	48
3.14	99
0.74	62
3.21	184
0.31	63
0.82	57
0.56	68
0.12	33
0.38	67
3.56	261
1.72	267
1.72	257
1.11	196
7.22	325
0	262
3.45	271
4.23	384
1.98	406
1.42	110
0.37	40
0.33	50
3.45	56
1	177
0	47
0.97	219
0.56	54
0.56	32
1.42	165
2.62	182
3.45	232
0	197

3.45	216
3.18	147
0	41
1.72	272
8.35	226
2.93	244
4.07	127
2.62	354
1.36	162
0.6	212
1.67	69
2.25	125
0.37	48
4.44	109
0.68	91
9.37	101
7.84	114
2.22	222
0	308
2.9	348
5.45	159
1.25	269
0	73
2.04	116
7.78	108
0	46
0.31	85
0.16	67
0.93	75
4.71	137
5.22	213
2.39	262
3.64	103
4.06	204
0	41
9.28	406
2.92	364
4.51	92
0.83	50
0.12	51
3.19	86
0.74	62
0.68	64
2.61	79
0.56	88
7.1	174
0.86	85

1.19	203
0.76	89
1.05	60
1.57	249
2.16	86
3.45	497
2.06	204
8.62	288
0	231
0.42	254
0.7	74
0	80
1.97	85
1.63	196
0.37	39
0.74	62
5.08	181
1.17	263
0.96	105
1.39	129
1.67	202
0	309
5.66	199
2.59	358
3.77	158
5.66	360
1.65	253
0.4	136
1.02	298
2.62	183
0	202
2.44	154
1.67	239
8.78	276
1.72	110
2.31	73
1.85	91
0.37	62
2.9	307
1.92	73
9.48	163
1.3	163
2.31	218
0.37	43
6.9	153
0	38
3.45	290

0	45
3.14	253
0.71	206
0	260
1.16	292
0.86	381
0	292
0	238
1.72	270
3.24	177
0.43	172
0.37	139
0	208
0.05	150
0	87
1.72	224
0	149
1.72	323
0	242
0.86	205
0.58	111
4.51	119
2.66	265
3.52	188
0	250
3.45	190
0	319
1.31	148
6.36	165
3.45	458
1.72	117
1	103
1.39	269
1.67	107
4.31	204
3.5	290
1.93	242
6.9	321
9.68	306
0.14	90
1.11	56
8.62	306
8.09	132
3.8	120
2.78	304
3.3	215
6.03	270

2.25	73
6.84	284
3.6	302
4.31	210
8.62	238
2.18	54
0.68	158
5.17	603
0.44	55
0.74	143
6.88	200
0	58
1.71	256
0	74
1.6	243
1.67	121
0	238
2.96	291
0.93	64
0.09	55
1.72	160
1.72	137
0	220
4.79	178
1.79	116
0.49	71
3.08	351
5	151
0.31	67
0.68	84
9.09	280
3.45	118
3.7	159
0.8	87
0	47
1.72	245
0.31	82
0	100
0.88	217
0.43	125
0.37	42
1.63	129
3.32	389
1.06	127
0.45	90
0.74	257
0.19	45

1.02	105
3.45	193
5.17	176
1.94	66
0.56	29
0.17	151
0.47	210
2.78	382
0.26	71
0.31	56
1.96	190
4.72	176
3.28	157
1.25	68
6.36	290
3.64	158
3.1	104
3.14	232
2.9	215
0.56	63
1.86	91
7.74	186
0.31	93
8.8	79
0.68	72
0.37	91
1.98	70
2.78	105
4.12	135
4.31	264
1.42	215
0.28	135
1.06	255
3.61	332
5.19	172
0.74	132
0.05	98
0.12	277
9.28	378
0.19	185
1.3	96
0.17	85
1.05	56
2.82	75
1.73	124
1.98	64
1.56	72

0.81	176
0.37	48
5.34	99
0	24
0.86	239
1.9	152
4.1	408
0	59
0	62
1.3	49
0	62
0	253
5.17	103
1.6	295
0	34
3.45	337
5.29	443
1.54	74
0	229
0.65	52
0.37	73
3.52	143
0	65
6.43	83
1.72	452
0.72	97
3.83	177
0.52	53
0	57
2.28	135
2.28	80
0.79	209
0	393
0	226
1.31	243
1.98	72
0.42	52
7.95	107
1.91	100
6.69	189
3.64	86
1.54	135
1.59	243
0.12	93
5.17	425
1.72	303
4.29	131

0.05	95
5.17	230
1.72	197
1.23	102
8.83	134
0.93	60
2.31	84
1.11	63
1.05	103
6.82	62
0.12	158
4.32	148
6.08	332
4.8	168
0.05	106
3.59	372
0	183
1.72	236
0.12	95
2.33	297
2.73	120
0.76	109
4.22	78
0	66
0.05	24
5.23	456
1.72	294
8.11	138
0	304
8.95	135
0.37	51
3.11	207
0.51	93
3.45	452
1.54	75
2.22	228
0	81
2.88	232
0.19	125
9.75	319
3.26	193
2.35	68
1.01	83
2.16	91
1.23	52
4.11	211
4.48	117

1.48	81
6.9	258
0.46	71
2.44	122
1.46	216
8.53	154
0.22	51
0.28	161
0.05	110
2.48	124
1.65	96
0.05	103
5.17	307
1.6	283
0.57	75
4.26	30
0.31	68
1.48	52
2.29	234
4.31	284
1.54	77
4.94	142
1.8	112
3.33	116
0.86	52
3.24	350
0.31	61
0.93	80
5.52	69
2.39	132
0.76	107
1.86	143
3.18	355
3.14	152
8.42	296
2.31	268
1.49	123
1.72	224
5.02	336
0.96	124
0.94	57
5.17	399
0.09	76
2.65	263
1.06	135
4.78	306
3	121

2.72	88
2.62	116
1.48	90
1.05	112
9.85	158
1.48	35
3.45	47
1.8	84
4.28	101
2.12	341
1.72	176
0	295
0.98	384
0	46
1.29	277
0.45	114
2.18	227
7.44	92
0.93	81
1.72	199
2.24	348
3.84	126
1.46	80
2.78	44
1.14	195
2.62	250
3.45	314
0.71	169
0.19	122
1.72	243
0	198
3.26	59
3.45	216
4.4	267
1.66	36
2.16	281
0.86	94
0.37	259
0.09	157
1.27	63
0.93	77
4.96	304
1.85	128
0.51	91
0.05	47
0	271
8.09	158

5.17	268
0	86
0.74	71
3.45	315
3.45	336
0.37	73
0.49	80
3.45	288
0	154
0.97	180
0.56	48
0	150
0.31	80
5.17	461
1.48	206
6.9	63
1.3	91
1.9	253
3.09	114
0.86	167
1.48	200
8.87	380
0	85
0.46	61
9.72	141
1.23	62
0.06	107
0.37	161
0.12	50
0.26	51
6.9	209
0	247
2.16	91
1.13	329
1.48	109
0.68	83
0.77	162
0.93	74
0.19	69
2.92	181
4.31	303
7.76	293
1.72	206
0.94	95
0.05	109
6.25	351
0.62	100

1.72	349
0.34	146
0.68	52
0	68
0.56	42
1.21	91
0	299
0.68	80
9.3	279
0.19	50
1.35	106
0	35
1.37	154
3.45	328
5.17	73
1	176
1.72	177
5.17	518
1.72	402
2.13	128
0.17	310
0	267
1.72	335
6.9	279
1.05	215
2.59	345
0	260
3.45	228
2.73	261
3.45	180
0	261
7.28	183
2.45	340
3.45	242
6.9	404
2.11	395
6.9	636
0	74
6.9	308
0.86	325
0.93	410
0	232
0	219
0	246
2.12	341
3.45	297
0	208

1.72	398
0	273
1.42	368
1.72	232
1.72	425
0.12	132
0.68	116
3.45	215
5.62	89
3.45	185
3.33	58
2.87	189
8.62	236
4.46	137
0.34	72
1.88	142
0.68	63
2.22	241
5.22	305
0.56	64
1.39	214
5.17	155
5.88	314
8.97	878
2.34	190
1.72	217
5.96	213
3.45	212
1.3	85
0	73
5.17	238
3.45	63
2.22	87
0	48
1.35	200
2.22	137
0	65
0.74	40
1.11	56
1.36	70
0	77
1.72	255
6.6	470
1.33	199
1.34	185
0	26
0.19	52

3.83	87
6.85	75
2.36	87
1.11	48
0.74	68
2.16	88
0.54	100
0.37	49
8.49	230
1.69	406
0.62	136
0	44
3.33	78
5.17	239
8.15	124
8.26	483
0.37	102
3.45	477
3.45	353
1.23	60
4.17	417
0.86	113
0.74	84
1.72	346
4.35	192
2.25	53
8.62	213
4.25	300
0.05	108
1.42	81
1.85	52
0.37	43
0.83	63
8.65	407
0.74	46
2.16	94
2.9	313
6.33	131
1.72	254
2.35	159
0.49	98
5.65	216
1.54	60
4.43	276
0	156
2.9	129
0.37	69

5.8	279
0.83	92
8.17	77
7.76	355
0	301
4.49	231
1.85	81
3.45	133
2.31	143
0	84
0.25	69
2.41	58
1.49	94
8.62	69
1.72	290
5.52	244
0.62	105
1.46	98
0	42
1.51	210
0	39
0.52	55
9.45	103
6.53	136
3.72	90
0.56	145
0.86	128
1.72	271
4.21	315
1.72	397
1.23	106
1.48	79
7.96	198
4.32	370
1.59	101
4.07	118
1.51	537
0.49	77
5.17	446
6.9	277
0.62	130
3.45	316
1.42	98
0.65	99
0.97	208
1.46	133
1.84	290

2.59	104
0	172
0.31	67
3.55	430
1.48	98
2.84	123
8.62	391
2.96	324
0.84	100
5.17	134
0.37	66
0.74	257
0.56	76
0.56	225
0.37	41
0.66	143
0	284
1.8	118
0.56	75
1.87	71
0	267
1.42	78
0.31	54
0.45	181
5.72	325
0.95	111
3.07	185
0.46	60
0.37	53
8.62	262
5.98	153
3.45	221
1.6	114
7.76	120
2.04	42
2.97	146
1.42	56
6.9	80
0	191
3.45	168
0	86
0	153
1.54	72
2.59	70
1.72	235
2.35	152
0	36

8.59	180
3.45	152
0.31	21
0	56
0.74	104
1.72	229
2.82	177
0	43
0	190
0.88	63
1.72	88
0.83	117
0.19	66
2.22	93
0	46
0.19	92
0	135
0	27
0.68	53
1.6	91
0	184
0	89
2.59	198
0	52
0	158
4.44	90
1.67	77
1.72	148
6.9	197
0.63	72
8.69	287
9.74	93
2.16	106
0.97	231
1.67	98
1.29	217
0	79
4.39	296
1.48	70
3.16	384
5.09	196
8.62	326
6.08	362
2	230
3.2	274
4.54	145
4.81	175

1.33	60
0	179
4.42	240
0.37	47
4.43	154
5.35	298
1.39	81
0	127
0.65	79
1.51	91
2.65	233
5.17	287
1.3	466
2.29	338
0.86	326
1.72	369
1.2	188
2.71	148
2.06	316
8.62	537
1.72	221
2.59	325
3.45	333
0	183
0	248
0	213
0	112
1.42	216
0	212
1.72	309
0.56	160
1.72	362
0.86	127
1.72	221
1.05	322
1.46	282
1.49	207
0	259
8.62	275
0	458
3.45	328
1.32	180
0.68	166
0.56	127
1.01	121
0.44	280
0.68	46

0.31	64
0.56	49
1.32	51
0.05	101
0.46	123
0.7	88
1.6	86
0	59
4.11	175
3.59	147
0.31	83
0.58	73
0.05	58
0.14	42
0.46	102
2.5	172
0	40
2.04	141
1.94	154
2.17	79
0	42
5.18	184
2.88	153
1.3	44
0	57
2.55	94
0.79	66
0.02	39
1.88	137
0.12	84
1.48	58
1.06	101
2.65	63
4.9	144
2.16	116
1.02	162
4.27	171
3.83	135
1.06	156
0.74	71
0.99	64
3.13	181
1.91	112
3.18	198
1.52	86
1.91	327
1.23	58

3.33	133
1.23	176
1.23	135
0.93	90
3.64	83
1.18	99
7.39	369
0.74	67
0.93	72
2.79	279
1.7	133
1.02	90
3.77	188
2.2	110
0.74	109
1.83	231
1.3	278
1.3	166
1.67	71
2.59	193
1	158
1.3	67
0.44	77
1.25	205
5.8	340
1.23	168
1.11	69
2.07	263
0.37	93
1.36	54
2.77	223
0.49	119
2.3	292
5.4	129
0.14	296
1.39	68
1.67	304
2.78	92
5.04	294
1.8	126
1.72	247
2.3	130
2.07	391
1.11	85
0.62	90
5.2	195
0.43	26

2.59	76
0	50
0.37	297
0.12	120
0.22	131
0.18	147
1.72	123
0.56	204
0.73	50
3.11	408
2.67	395
1.35	105
0.59	76
0	94
1.3	75
0	207
2.65	303
0	42
1.3	85
0	223
0.74	228
0	50
0	75
0.31	417
1.01	78
0	164
0	24
1.69	220
0.93	394
0	30
1.72	156
0	344
0	90
0.68	238
0	250
0	177
0	112
0.37	79
3.61	146
0	95
1.72	417
1.72	194
0.86	335
1.72	180
4.26	157
2.78	240
0.36	101

0.49	92
0	118
2.92	311
0	94
0	129
0.56	74
1.46	191
0	85
1.93	354
0.74	172
1.14	306
0	157
0	224
0	378
0.46	160
0	117
2.59	191
2.45	205
1.49	322
3.34	150
0	67
0	111
0.37	124
0.68	38
0	166
0.19	120
0.74	61
0	141
1.18	71
0	151
0	282
0.86	329
0.68	85
1.9	311
1.42	177
2.34	229
1.41	323
1.23	129
0	136
3.45	220
0	60
0	68
3.15	251
0	197
1.72	135
0.86	198
2.35	595

1.7	179
0.12	55
0.45	99
0	22
1.72	247
1.83	346
0.05	310
3.45	565
2.7	81
1.05	136
0.31	537
1.86	122
0	86
2.26	145
0	74
0.74	273
0	75
0.74	115
1.42	203
2.19	316
0	105
0.42	102
0.19	124
0	198
3.45	346
0.86	56
0.47	60
0.49	150
0	473
0	43
0.45	256
1.23	66
1.33	106
1.03	148
1.72	290
0.37	452
3.34	393
0	191
0.23	305
0	96
0.91	262
0.37	79
0.49	94
0	37
0.37	77
0	127
3.45	193

0	82
0	169
0	152
2.07	518
0.71	52
3.33	118
0	184
0.25	48
0.93	90
4.51	167
0	122
0.12	104
4.15	110
1.01	79
0.34	52
0	222
0.77	119
2.03	98
0	214
0	102
0.37	132
4.48	136
1.72	224
0	81
0	171
0.36	87
1.72	444
1.72	106
1.27	143
3.62	281
1.72	304
2.59	304
0.39	41
0	201
1.72	345
0	333
0	351
3.45	486
1.72	105
0	213
2.59	182
1.18	251
2.59	387
0	76
0	62
1.11	147
0.71	232

0	100
0	81
0.86	167
0.31	121
0.12	193
3.92	603
2.02	355
0	143
1.72	293
0.51	252
1.88	86
2.69	229
0	233
0.68	57
0	83
3.45	386
0.93	298
1.72	344
0	54
0	418
1.23	77
0.31	126
0	125
0.19	88
0	430
0.86	120
0.5	258
0	137
1.87	320
1.72	290
1.35	95
0	141
1.11	176
0.98	151
2.98	425
0	71
0	349
0	100
0	58
1.6	139
0	131
1.72	127
1.88	463
2.75	86
2.25	245
4.59	245
0.73	82

3.45	300
2.49	226
2.94	225
1.72	337
2.01	139
0.74	162
1.72	199
0	216
1.72	544
1.36	213
0.65	82
1.43	453
2.32	226
0.74	98
2.14	173
0.37	71
0	42
1.43	236
0.74	163
0	49
0.09	135
0.56	218
0	75
1.72	281
0	128
1.72	273
0.74	135
0.71	50
0	97
0.68	85
0	117
0.49	95
0.28	216
0	391
0	182
2.16	168
3.45	144
0	106
3.55	146
1.33	212
0	236
0	163
0	188
1.72	228
0.8	390
2.84	182
4.78	99

2.48	70
1.72	612
0	197
0.96	117
0.86	120
1.72	265
0.65	129
0.86	57
4.31	313
2.03	93
0.19	94
0.49	107
0.6	81
1.08	134
0	121
1.57	291
0.37	107
0	113
0.37	73
1.75	476
0	179
0.79	93
0.71	148
3.45	214
1.29	293
0	478
0.56	172
1.79	147
0	135
0	69
0	27
0	93
0	286
0	245
2.7	138
0	46
0	104
2.2	60
0.95	153
4.93	217
0.87	109
1.48	151
0.51	266
0	167
0	412
1.86	137
0	92

3.45	254
0	466
0.93	154
0	44
0.12	98
0.68	72
2.41	62
0	92
4.82	75
4.22	183
0.68	133
1.3	390
0	159
1.72	251
0.76	139
0.02	72
4.45	166
0.63	129
5	117
0	125
0	160
0.31	150
0.39	67
0.43	83
0	72
0.09	121
1.72	259
0	178
3.45	163
1.72	264
1.72	165
1.72	258
2.14	481
0.46	78
0.93	121
0.4	84
0	68
1.72	113
0	46
0	212
1.72	79
2.49	115
0.12	86
0	384
0	164
0	136
0.51	155

0	136
1.72	162
0.46	198
0	79
1.01	52
0.09	159
2.49	330
0.68	86
0	53
0.34	44
0.37	61
2.59	99
1.57	62
1.72	308
0	201
0.72	339
1.72	356
0.49	180
0.16	260
3.45	219
1.72	435
0	255
1.72	194
0.05	151
0	224
0	76
0	269
2.43	279
0.52	158
0	51
0.74	101
1.01	96
0.47	277
1.72	295
1.35	145
0	149
0	288
0.5	42
0	64
0	200
3.45	373
0.46	449
0.37	112
0	90
0	197
1.3	329
0	297

0.37	130
0	38
3.45	449
0.56	222
0.56	78
2.85	210
0.56	74
0	450
0	289
0	84
0	203
1.11	124
0.79	166
0	291
0	24
0.51	80
0	182
0	205
0.89	66
0	134
0	38
0	42
0	67
1.07	80
1.31	373
0	175
0	36
2.47	84
0	269
0.56	119
0	313
2.11	289
1.72	122
0	102
0	101
0.87	279
1.72	378
0.74	188
0.37	98
0	82
2.28	356
1.09	162
2.26	113
4.46	412
0	68
0.53	59
0	43

0.74	187
0	211
2.78	454
1.34	51
0	92
0	31
2.59	321
0.62	118
1.07	270
3.45	283
1.3	192
1.76	215
1.21	116
2.82	367
0.37	87
0	138
3.58	256
0.67	55
0.74	199
1.72	312
1.39	295
0	136
0	143
0.19	182
0.86	306
2.51	318
0	72
1.72	334
3.16	333
0.86	329
1.33	317
1.81	275
0.89	76
1.72	292
4.81	289
0	24
0	96
0.37	107
0.74	248
0	233
0.19	121
0.02	94
0	102
0	149
0.74	150
1.69	150
1.72	160

0	65
1.46	64
0.09	108
0.9	44
0	180
1.75	281
1.35	159
0	98
0	203
0.37	102
0	271
1.11	372
2.87	137
2.03	146
0	141
1.46	82
1.01	246
0	37
2.05	338
1.72	369
0	109
0	61
1.18	137
1.72	214
1.6	296
0.19	153
0	84
1.44	362
0	115
0	16
1.91	78
0	147
4.09	295
3.32	189
0	81
0.74	167
0	543
0.93	132
1.01	157
1.58	169
0.56	337
1.64	486
2.14	209
1.78	219
0.79	131
1.75	273
1.36	488

0.34	154
0.91	187
4.01	232
0	71
1.72	542
0.93	117
1.45	246
0	560
3.93	825
0.81	317
2.09	381
3.7	429
0	411
0	455
2.59	378
1.72	577
3.85	516
1.33	352
0.68	146
0.68	139
2.13	380
0.93	328
1.95	382
1.01	143
0	408
0.93	143
0.68	155
0	130
1.75	238
0.93	172
0.34	118
0	276
4.22	261
2.31	160
0.37	235
0.34	137
1.74	257
1.72	75
1.76	217
0	413
1.55	323
1.08	176
1.3	74
1.67	198
0.68	119
2.44	232
0.94	68

0.79	111
2.87	232
1.46	223
2.61	401
2.17	339
1.3	261
3.47	747
1.72	558
0	443
1.01	137
1.72	494
1.7	185
0.68	114
0.93	107
1.01	146
0	505
0.93	199
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4.310344828	241
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1.689189189	176
1.418918919	126
1.689189189	293
1.053283767	482
1.724137931	318
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0.337837838	61
1.801801802	346
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2.195945946	113
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1.047297297	109
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0.123915737	171
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1.689189189	82
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1.071428571	299
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1.351351351	62

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0	51

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0	216
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0.696915777	225
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1.632882883	102
0.371747212	116
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1.189591078	248
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1.801801802	115
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0.836431227	160
0.371747212	146
0	124
0	52
0.557620818	189
0	144
0	109
0.844594595	39
1.604938272	155
2.66626921	531
0	143
3.448275862	233
4.310344828	348
0.555555556	123
1.724137931	258
0	203
0.355871886	64
1.724137931	311
3.333333333	88
0.654761905	257
1.923798799	132
0	329
1.327160494	254
4.310344828	182
0	241
1.672862454	275
0.37037037	68
0.308641975	76
2.149024024	675
0.462962963	145

0.711743772	91
0	93
0.355871886	37
0.337837838	46
1.724137931	461
0.506756757	124
0	45
1.013513514	118
0	259
1.351351351	183
0.828033916	77
1.716232962	492
1.131870304	298
0.277777778	111
1.765799257	492
0	351
2.909159159	270
0.516315572	372
0	196
1.342592593	186
0.357142857	234
1.067615658	81
1.351351351	347
0.925925926	53
0	48
1.118082368	134
0.675675676	75
0.506756757	111
0.87329977	149
1.551724138	557
3.448275862	291
2.59009009	75
0.061728395	112
2.027027027	157
0.711743772	172
0	213
2.225320116	598
0.462962963	33
0	80
0	100
0.371747212	141
2.469433719	135
0.37037037	53
0	411
0.743494424	161
0.371747212	174
0.092592593	255

1.234567901	101
1.294642857	294
0.123915737	156
1.013513514	220
0	163
0.533807829	56
1.717342342	236
0.12345679	423
1.067615658	75
0	135
2.195945946	122
1.750309789	381
0.771604938	94
0.37037037	271
0	382
2.59913259	703
0.49382716	228
0.788288288	300
0.862068966	371
1.334519573	352
1.717342342	75
0	272
0.37037037	35
0	103
0.788288288	314
1.724137931	188
1.512455516	194
3.322072072	193
0.763683852	113
0	171
0.682087782	239
0	540
1.783353986	483
1.621621622	106
0	202
0.675675676	238
1.724137931	296
1.463963964	261
0.37037037	27
0	170
1.364175563	335
0	188
2.233483483	306
0	273
0	308
0.432098765	136
1.14622057	224

1.295045045	183
0	117
1.013513514	87
2.50929368	446
0	37
0	68
3.322072072	93
1.724137931	125
0.675675676	75
0.386100386	36
0.711743772	54
1.724137931	305
0.675675676	112
0	70
1.764264264	136
2.195945946	155
0	59
0.355871886	150
0.355871886	322
0	383
0.12345679	96
0	63
0.889679715	67
0	173
0.557620818	81
0.337837838	33
1.239157373	166
0	545
2.29244114	470
0.351453604	276
0	53
0.185873606	92
1.724137931	356
0	109
0	104
0.844594595	130
0	35

Broad classification	Disease	Mode	Prevotella species	article type
		isolation: if bacteria is isolated and cultured from the sample association: if detected via PCR or sequencing causation: if the causative role of the bacteria is clearly recapitulated		

PubMedID	Year	Note	age cohort	Sampling
			NS: not specified in the original paper	NA: not assessed
			NA: not assessed	NS: not specified in the original paper
			newborn: 0-2 y.o.	
			Children: 3 - 12 y.o.	
			Adolescent: 13-18 y.o.	
			Young adult: 19-27y.o.	
			Adult: 28-60 y.o. Elderly: >60 y.o.	

Methodology	Antibiogram	infection type	Related to oral b	from intestine?
NA: not assessed	NA: not assessed	NA: not assessed	ND: not discussed in the original paper	ND: not discussed in the original paper
NS: not specified in the original paper	no: clearly stated or empirical antibiotics were used		NA: not assessed	NA: not assessed
			discussed: mentioned and literature cited	discussed: mentioned and literature cited
			possible: only hypothesis	possible: only hypothesis
			yes: clearly stated/proved	yes: clearly stated/proved
			no: clearly not related	no: clearly not related

Direction of association

only for association studies:
presence/abscence or increased/decreased