Figure S1. OTUs with different relative abundance in health and periodontitis. Graph depicts OTUs with different relative abundance based on LEfSe results. Bars represent linear discriminant analysis scores (LDA). OTUs were named based on the consensus taxonomy for sequences within the OTU. Name in parentheses depicts the oral taxon (OT) from the HOMD with the highest hit (>97%) to the OTU representative sequence, in OTUs with no consensus taxonomy.
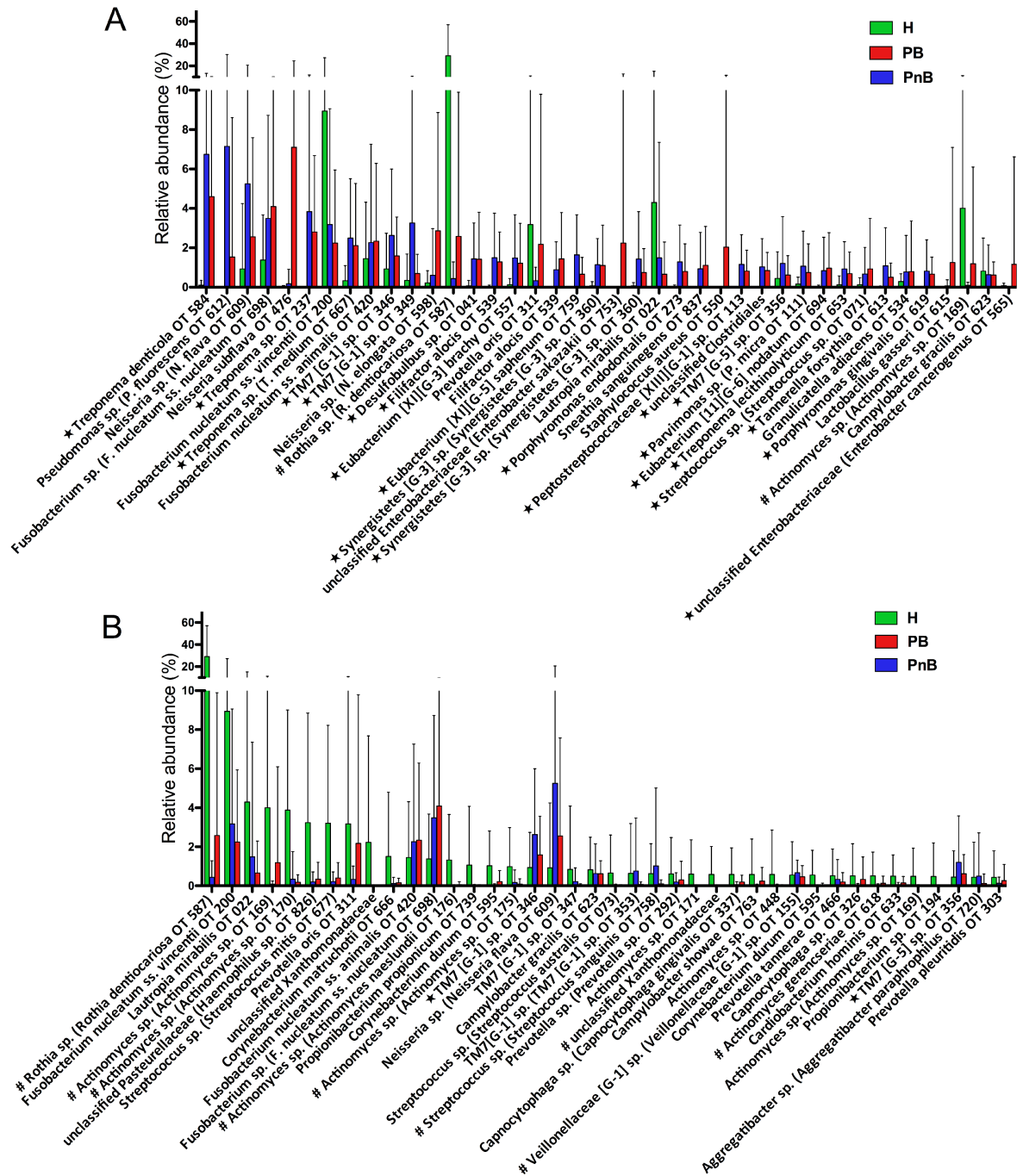
Figure S2. The most abundant OTUs in health and in periodontitis sites with and without bleeding. Graphs depict the 40 most abundant OTUs in health (H) and in communities from subjects with periodontitis (P), in sites with bleeding (PB) or without bleeding (PnB). Panel A shows the most abundant OTUs in periodontitis and panel B the most abundant OTUs in health. Bars represent the mean (±SD) relative abundance of OTUs. OTUs were named based on the consensus taxonomy for sequences within the OTU. Name in parentheses depicts the oral taxon (OT) from the HOMD with

the highest hit (>97%) to the OTU representative sequence, in OTUs with no consensus taxonomy. A black star indicates that the relative abundance of the OTU was higher in periodontitis, according to LEfSe, while a # sign indicates it was higher in health. No differences in OTU abundance were observed between bleeding and non-bleeding sites.
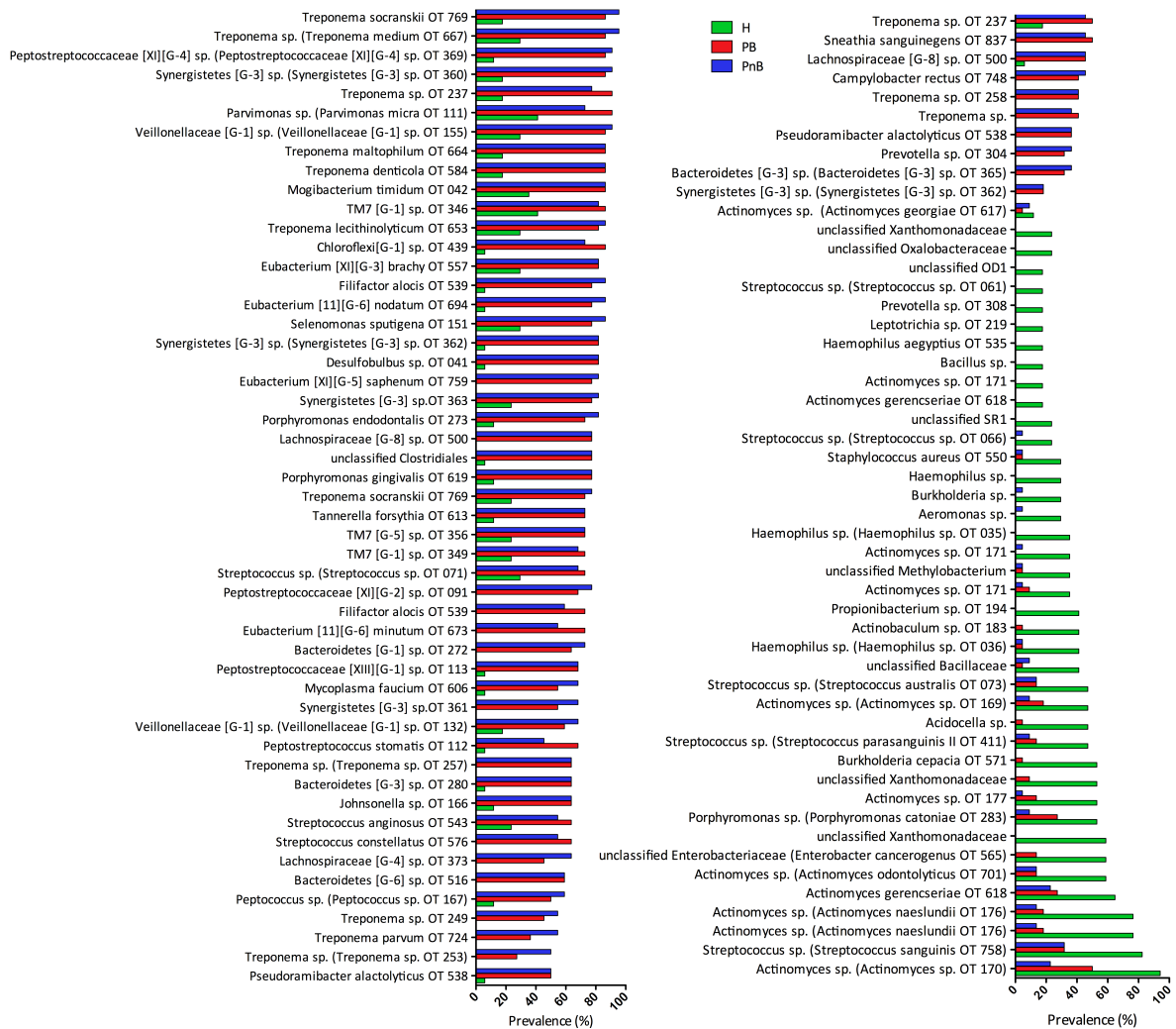
Figure S3. OTUs with different frequency of detection in health and periodontitis. Graph depicts OTUs with different frequency of detection (χ^2). Bars represent percentage of samples in which the OTU was detected. Graph was divided in two for visualization purposes. Top OTUs were more frequently detected in periodontitis (P), while bottom OTUs were more frequently detected in health (H). No differences in frequency of detection of OTUs were observed between bleeding (PB) and non-bleeding sites (PnB). OTUs were named based on the consensus taxonomy for sequences within the OTU. Name in parentheses depicts the oral taxon (OT) from the HOMD with the highest hit (>97%) to the OTU representative sequence, in OTUs with no consensus taxonomy.
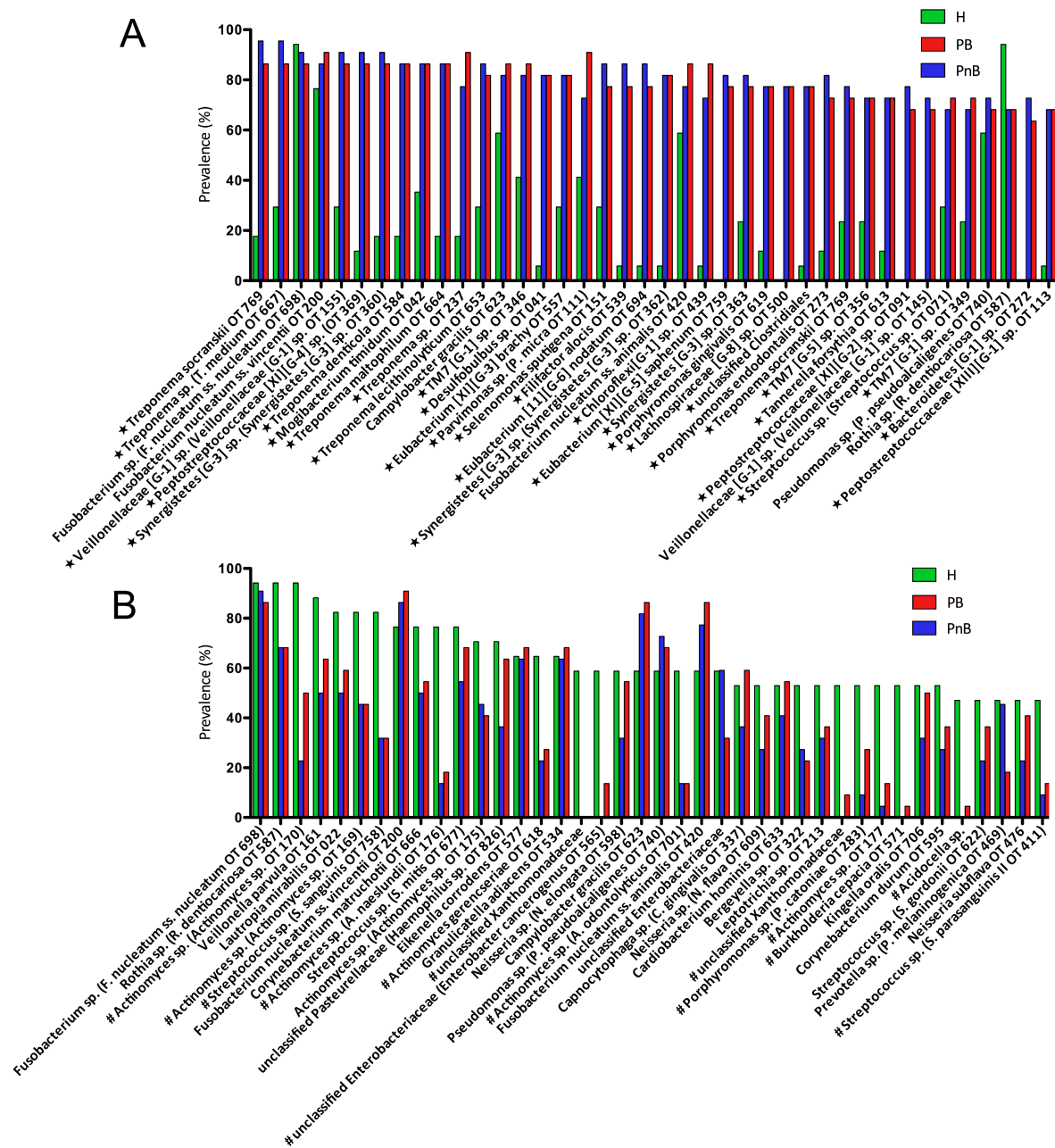
Figure S4. The most prevalent OTUs in health and periodontitis. Panel A shows the most frequently detected OTUs in periodontitis (P), while panel B shows the most frequently detected OTUs in health (H). A black star indicates that the frequency of detection of the OTU was higher in periodontitis, while a # sign indicates it was higher in health. No differences in frequency of detection of OTUs were observed between bleeding (PB) and non-bleeding sites (PnB).
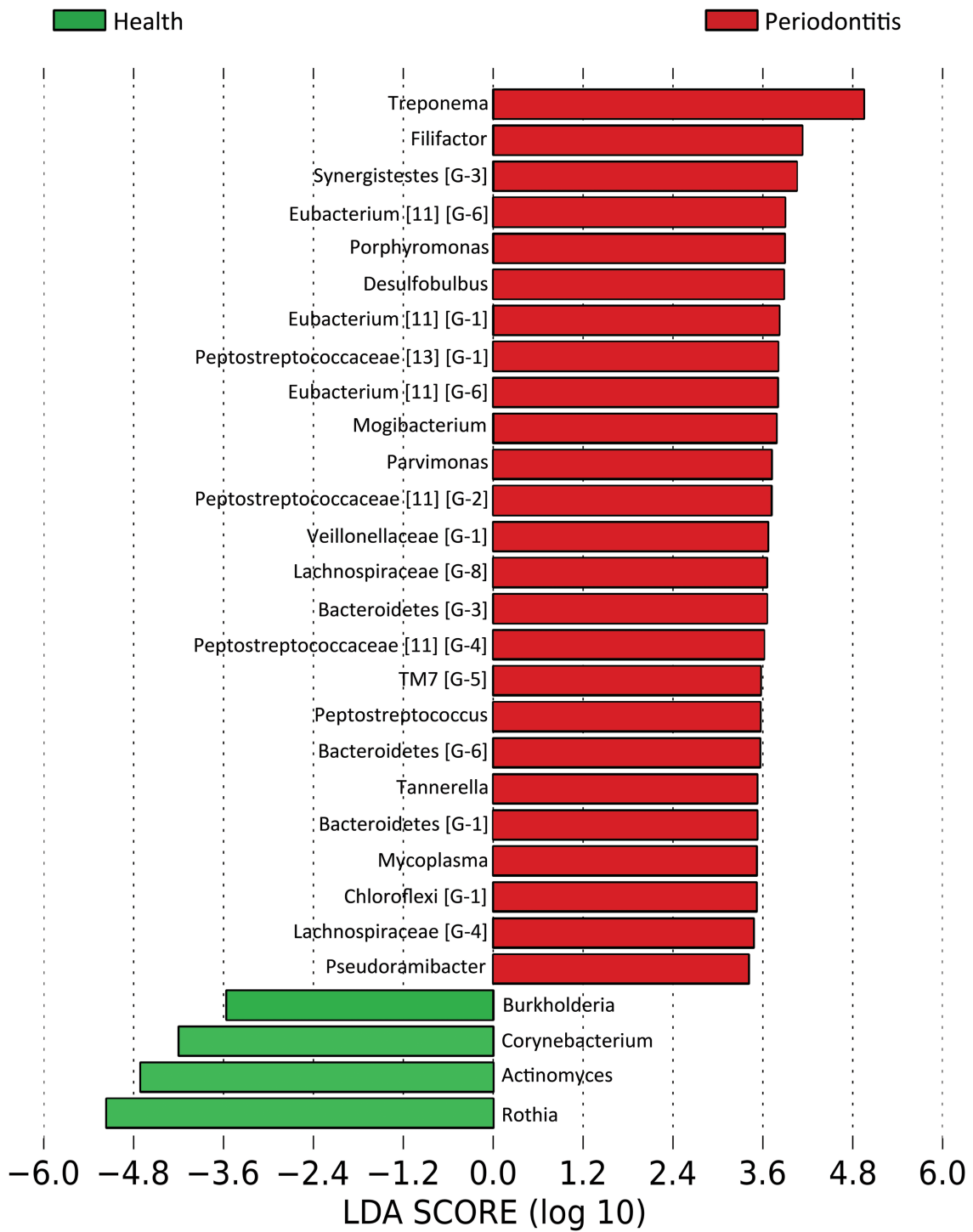
Figure S5. Genera with different abundance in health and periodontitis. Graph depicts genera with different abundance based on LEfSe results. Bars represent linear discriminant analysis scores (LDA).
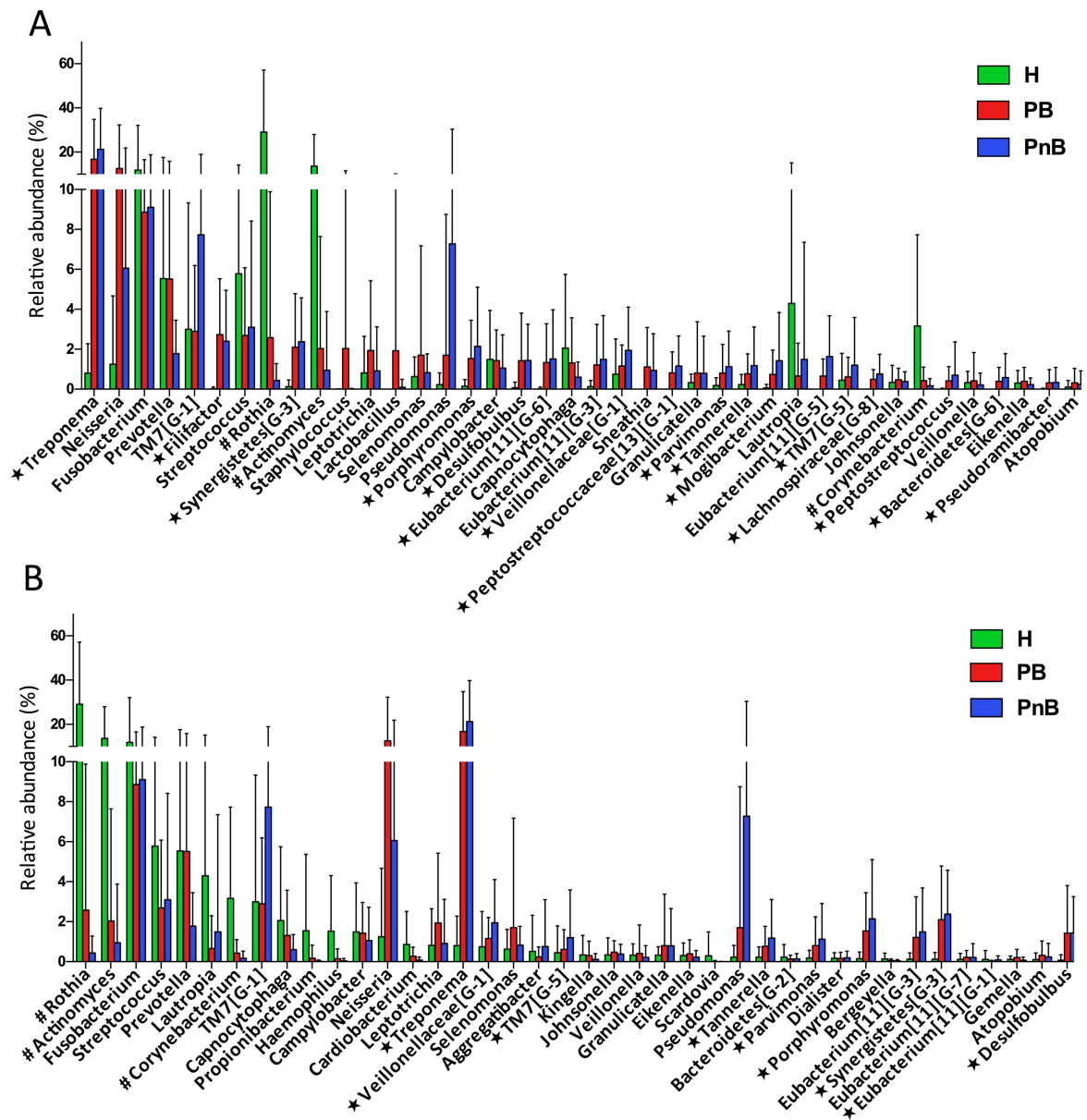
Figure S6. The most abundant genera in health and periodontitis. Graphs depict the 40 most abundant genera in health (H) and in periodontitis sites with bleeding (PB) or without bleeding (PnB). Panel A shows the most abundant genera in periodontitis and panel B the most abundant genera in health. Bars represent the mean (±SD) relative abundance of genera. A black star indicates that the relative abundance of the genus was higher in periodontitis, according to LEfSe, while a # sign indicates it was higher in health. No differences in genus abundance were observed between bleeding and non-bleeding sites.
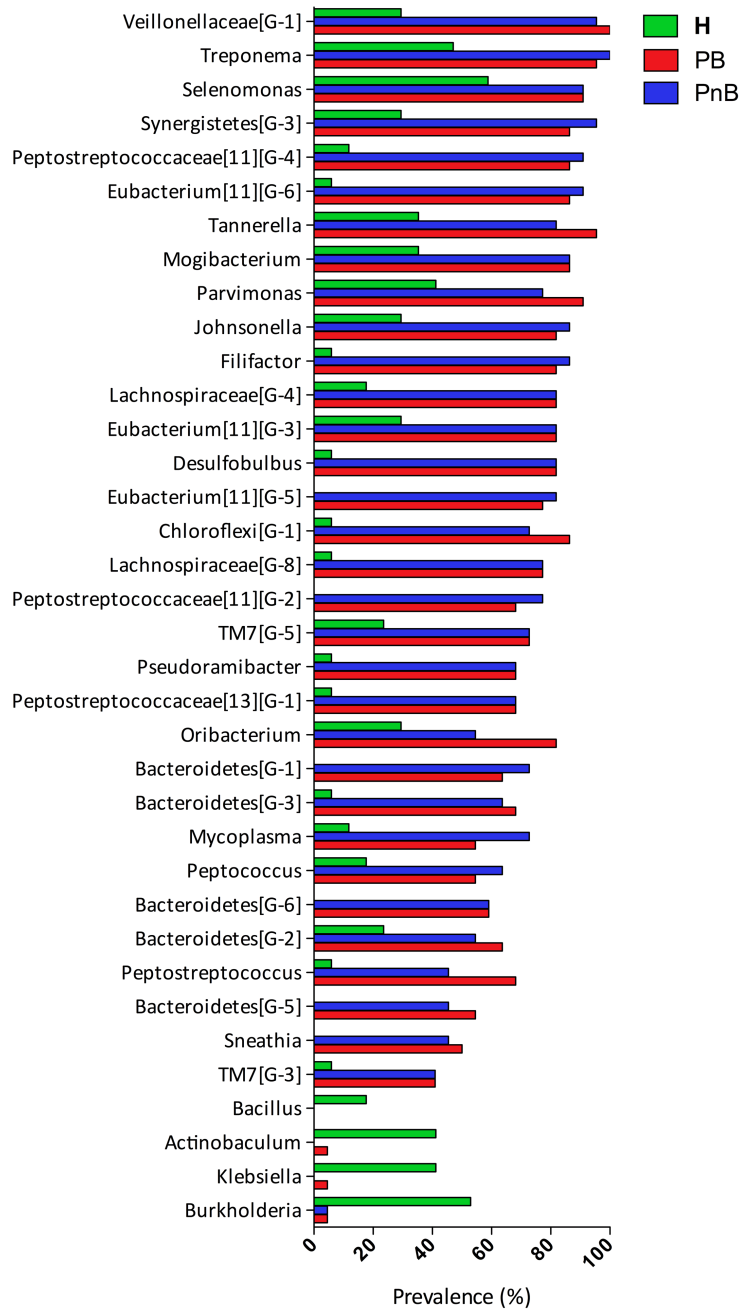
Figure S7. Genera with different frequency of detection in health and periodontitis. Graph depicts genera with different frequency of detection (χ^2). Bars represent percentage of samples in which the genus was detected. Top genera were more frequently detected in periodontitis (P), while bottom genera were more frequently detected in health (H). No differences in frequency of detection of genera were observed between bleeding (PB) and non-bleeding sites (PnB).
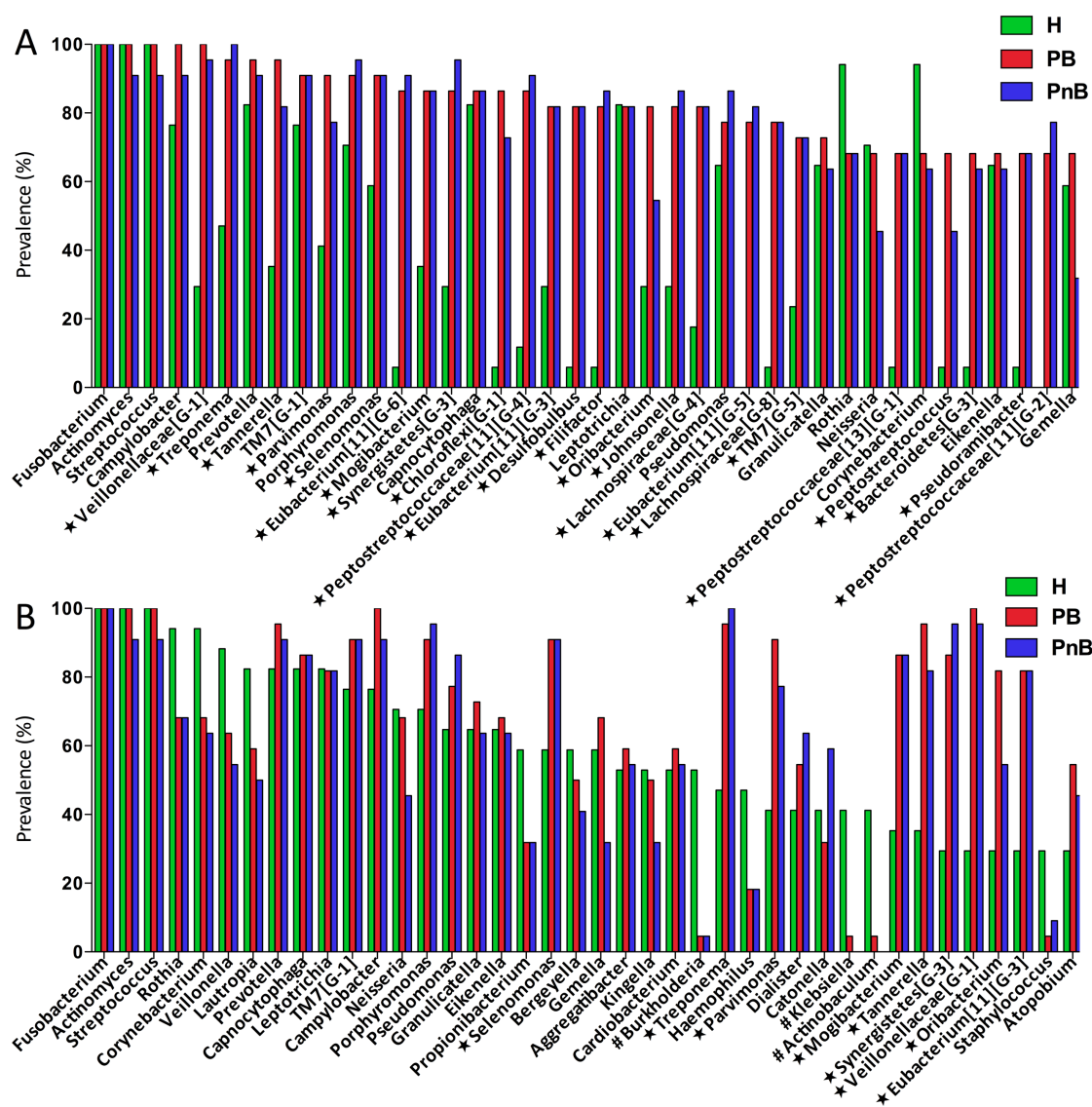
Figure S8. The most prevalent genera in health and periodontitis. Panel A shows the most frequently detected genera in periodontitis (P), while panel B shows the most frequently detected genera in health (H). A black star indicates that the frequency of detection of the genus was higher in periodontitis, while a # sign indicates it was higher in health. No differences in frequency of detection of genera were observed between bleeding (PB) and non-bleeding sites (PnB).
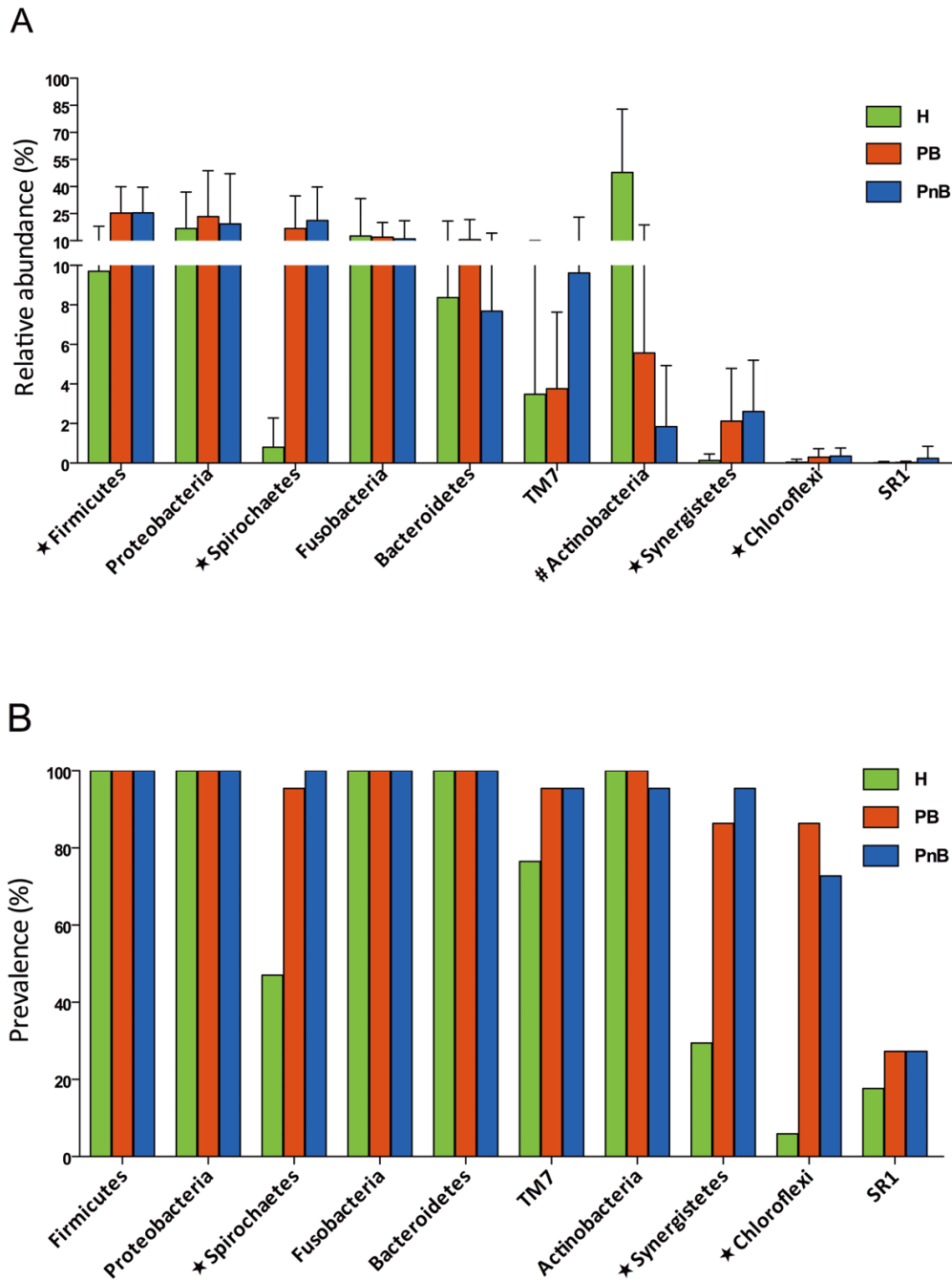
Figure S9. Abundance and frequency of detection of bacterial phyla in health and periodontitis.
Graphs depict the relative abundance and prevalence of phyla in health (H) and in subjects with periodontitis in sites with bleeding (PB) or no bleeding (PnB). Panel A shows the relative abundance of each phylum in periodontitis and health, bars represent the mean (±SD) relative abundance of phylla. Panel B shows the prevalence of each phylum in periodontitis and health. A black star indicates that the relative abundance or prevalence of the phylum was higher in periodontitis, according to LEfSe or chi-square test, respectively, while a # sign indicates it was higher in health. No differences in phylum abundance or prevalence were observed between bleeding and non-bleeding sites.
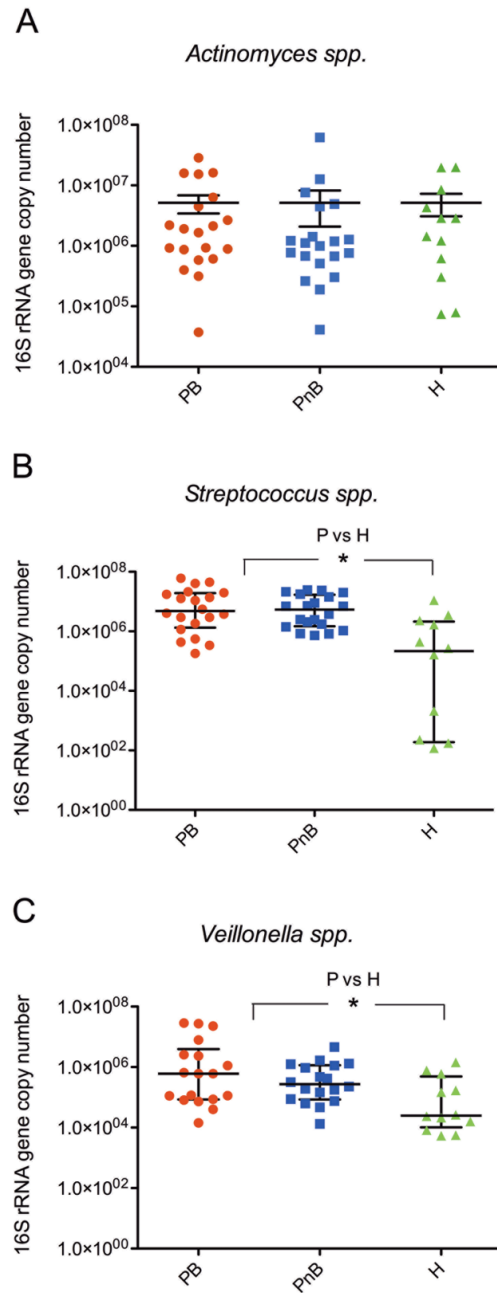
Figure S10. Total abundance of *Actinomyces, Streptococcus* and *Veillonella* in health and periodontitis. Panels show total abundance, measured via real time qPCR of *Actinomyces* (A), *Streptococcus* (B) and *Veillonella* (C) in periodontitis (P) sites with bleeding (PB) or without bleeding (PnB) and in health (H). To compare P and H, communities from bleeding and non-bleeding sites were combined, * indicates a $P < 0.05$. No differences in total abundance were observed between bleeding and non-bleeding sites.

Selenomonas noxia OT 130 (23.0%)
Streptococcus sp. (*S. australis* OT 073) (23.0%)
TM7 [G-1] sp. OT 348 (21.3%)
Treponema sp. (*Treponema* sp. OT 258) (21.3%)
unclassified *Enterobacteriaceae* (*Enterobacter cancerogenus* OT 565) (21.3%)
unclassified *Xanthomonadaceae* (18.0%)
Actinomyces sp. OT 448 (18.0%)
Aggregatibacter sp. (*A. paraphrophilus* OT 720) (18.0%)
unclassified *Xanthomonadaceae* (16.4%)
unclassified *Clostridiales* (16.4%)
Actinomyces sp. (*Actinomyces* sp. OT 169)(16.4%)
Lactobacillus gasseri OT 615 (14.8%)
Pseudomonas sp. (*Pseudomonas fluorescens* OT 612)(14.8%)
Propionibacterium sp. OT 194 (11.5%)
Actinomyces sp. OT 171 (11.5%)
Selenomonas noxia OT 130 (11.5%)
Staphylococcus aureus OT 550 (11.5%)
Prevotella nigrescens OT 693 (4.9%)
Pyramidobacter piscolens OT 357 (4.9%)
Lactobacillus sp. (*Lactobacillus acidophilus* OT 529) (3.3%)
unclassified *Enterobacteriaceae*
(*Enterobacter sakazakii* OT 753) (1.6%)

Figure S11. Endemic but locally abundant OTUs in subgingival communities. Graph depicts endemic but locally abundant OTUs, defined as those which appeared in less than 25% of samples but were at least 5% of sequence reads in at least one sample. OTUs were organized in decreasing order based on their prevalence (in parentheses).