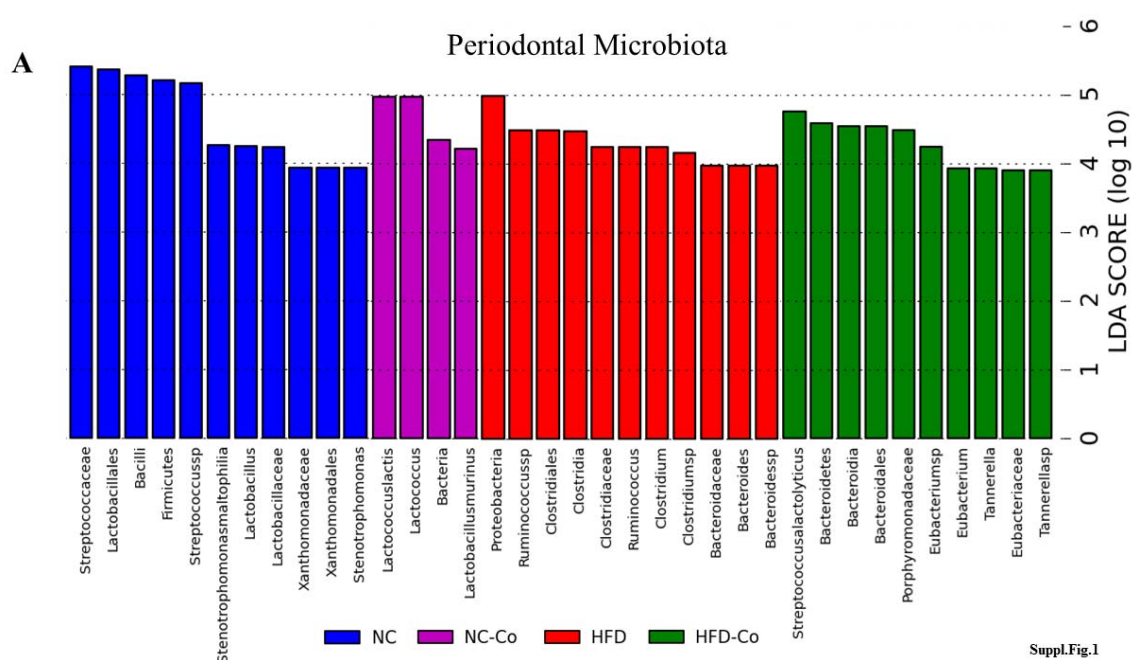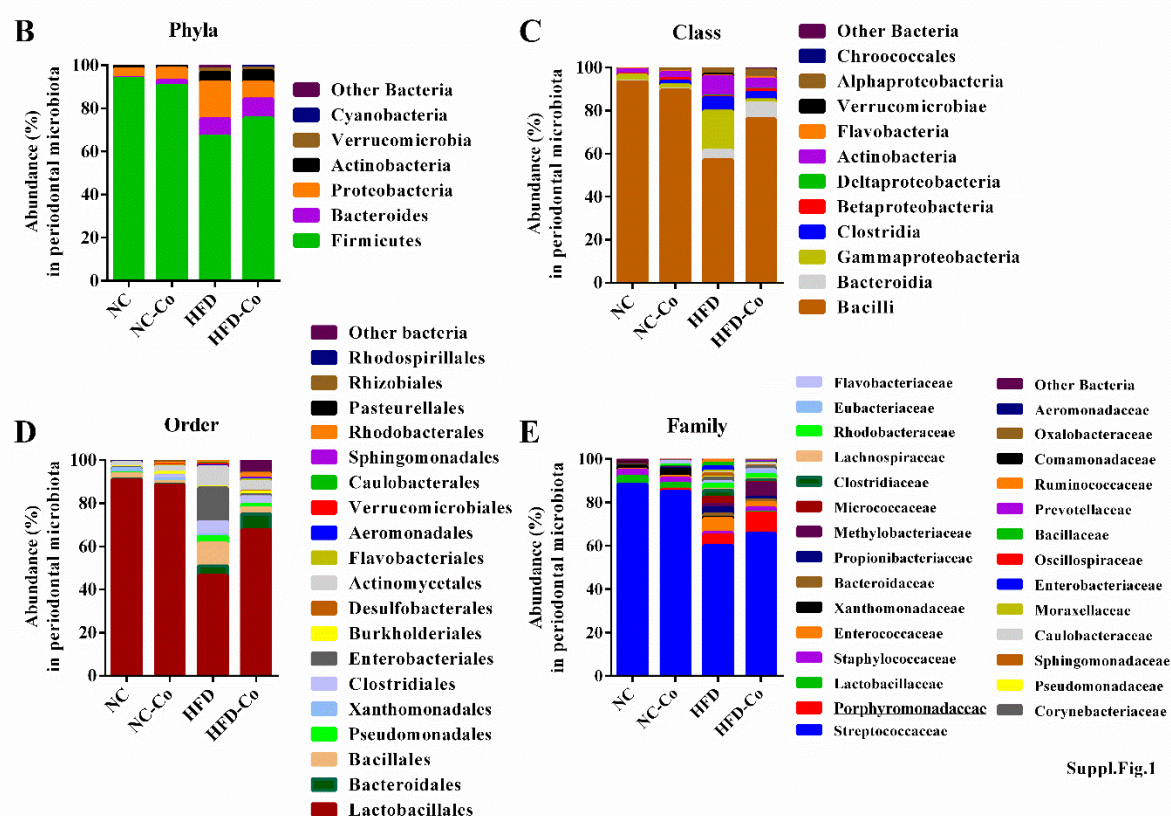**Supplementary Figure 1. *Pg*, *Fn* and *Pi* oral colonization induces periodontitis linked to specific periodontal pathogens.** Periodontal microbiota was explored by Pyrosequencing analysis. A) Linear Discriminant Analysis (LDA) score for discriminating bacteria in each group: NC (normal chow, blue bar, n = 6), NC-Co (normal chow colonized, purple bar, n=6), HFD (high-fat diet, red bar, n=7) and HFD-Co (High-fat diet colonized, green bar, n=10); abundance (% of the total identified sequences per group) at the level of Phylum (B), Class (C), Order (D), Family (E), Genus (F) and Species (G) in each group.

B Phyla

Abundance (%) in periodontal microbiota

Other Bacteria
Cyanobacteria
Verrucomicrobia
Actinobacteria
Proteobacteria
Bacteroides
Firmicutes

NC, NC-Co, HFD, HFD-Co

C Class

Abundance (%) in periodontal microbiota

Other Bacteria
Chroococcales
Alphaproteobacteria
Verrucomicrobiae
Flavobacteria
Actinobacteria
Deltaproteobacteria
Betaproteobacteria
Clostridia
Gammaproteobacteria
Bacteroidia
Bacilli

NC, NC-Co, HFD, HFD-Co

D Order

Abundance (%) in periodontal microbiota

Other bacteria
Rhodospirillales
Rhizobiales
Pasteurellales
Rhodobacterales
Sphingomonadales
Caulobacterales
Verrucomicrobiales
Aeromonadales
Flavobacteriales
Actinomycetales
Desulfobacterales
Burkholderiales
Enterobacteriales
Clostridiales
Xanthomonadales
Pseudomonadales
Bacillales
Bacteroidales
Lactobacillales

NC, NC-Co, HFD, HFD-Co

E Family

Abundance (%) in periodontal microbiota

Flavobacteriaceae
Eubacteriaceae
Rhodobacteraceae
Lachnospiraceae
Clostridiaceae
Micrococcaceae
Methylobacteriaceae
Propionibacteriaceae
Bacteroidaceae
Xanthomonadaceae
Enterococcaceae
Staphylococcaceae
Lactobacillaceae
Porphyromonadaceae
Streptococcaceae

Other Bacteria
Aeromonadaceae
Oxalobacteraceae
Comamonadaceae
Ruminococcaceae
Prevotellaceae
Bacillaceae
Oscillospiraceae
Enterobacteriaceae
Moraxellaceae
Caulobacteraceae
Sphingomonadaceae
Pseudomonadaceae
Corynebacteriaceae

NC, NC-Co, HFD, HFD-Co

Suppl.Fig.1

2

F

Genus

Abundance (%) in periodontal microbiota

NC, NC-Co, HFD, HFD-Co

Legend:
- Oscillibacter
- Bacteroides
- Pseudomonas
- Prevotella
- Clostridium
- Bacillus
- Escherichia
- Eubacterium
- Stenotrophomonas
- Enterococcus
- Staphylococcus
- Lactobacillus
- Tannerella
- Lactococcus
- Streptococcus
- Pasteurella
- Comamonas
- Nesterenkonia
- Thermicanus
- Ralstonia
- Paracoccus
- Brevundimonas
- Porphyromonas
- Shigella
- Enhydrobacter
- Corynebacterium
- Butyrivibrio
- Ruminococcus
- Acidovorax
- Alistipes
- Other Bacteria
- Leuconostoc
- Hydrogenophilus
- Psychrobacter
- Blastococcus
- Methylobacterium
- Micrococcus
- Faecalibacterium
- Roseburia
- Propionibacterium
- Flavobacterium
- Akkermansia
- Aeromonas

G

Species

Relative abundance (%) in periodontal microbiota

NC, NC-Co, HFD, HFD-Co

Legend:
- Micrococcus sp
- Corynebacterium accolens
- Micrococcus luteus
- Streptococcus sanguinis
- Aeromonas caviae
- Faecalibacterium sp
- Corynebacterium sp
- Propionibacterium sp
- Bacillus sp
- Akkermansia muciniphila
- Aeromonas sp
- Delftia sp
- Staphylococcus lugdunensis
- Enhydrobacter aerosaccus
- Streptococcus mitis
- Ruminococcus sp
- Pseudomonas aeruginosa
- Alistipes sp
- Bacteroides sp
- Staphylococcus epidermidis
- Prevotella sp
- Staphylococcus sp
- Escherichia sp
- Stenotrophomonas sp
- Staphylococcus aureus
- Tannerella sp
- Streptococcus sp
- Brevundimonas nasdae
- Paracoccus sp
- Corynebacterium macginleyi
- Butyrivibrio crossotus
- Pasteurella pneumotropica
- Rubellimicrobium sp
- Nesterenkonia flava
- Clostridium leptum
- Flavobacterium sp
- Dorea sp
- Finegoldia magna
- Shigella sp
- Escherichia coli
- Corynebacterium bovis
- Clostridium nexile
- Acidovorax sp
- Pseudomonas sp
- Oscillibacter valericigenes
- Stenotrophomonas maltophilia
- Streptococcus alactolyticus
- Clostridium sp
- Enterococcus faecalis
- Eubacterium sp
- Staphylococcus warneri
- Lactobacillus murinus
- Lactococcus lactis
- Hydrogenophilus sp
- Clostridium bartlettii
- Psychrobacter sp
- Thermicanus aegyptius
- C. pseudogenitalium
- Ralstonia sp
- Other Bacteria
- Streptosporangium sp
- Micrococcus lylae
- Comamonas sp
- Massilia timonae
- Sphingomonas sp
- Lactobacillus johnsonii
- Massilia sp
- Desulforegula sp
- Cyanothece sp
- Brevundimonas sp
- Aerococcus sp
- Roseburia sp
- Planktoluna difficilis
- Clostridium herbivorans
- Porphyromonas gingivalis
- Clostridium bolteae
- Blastococcus sp
- Roseomonas mucosa
- Methylobacterium sp
- Lactobacillus reuteri
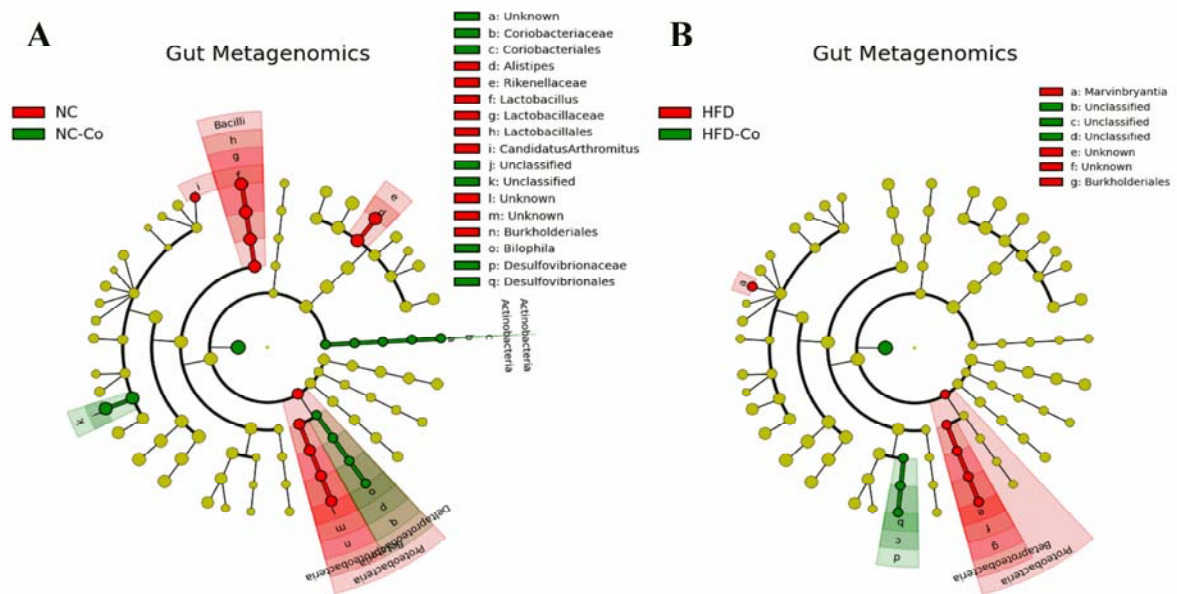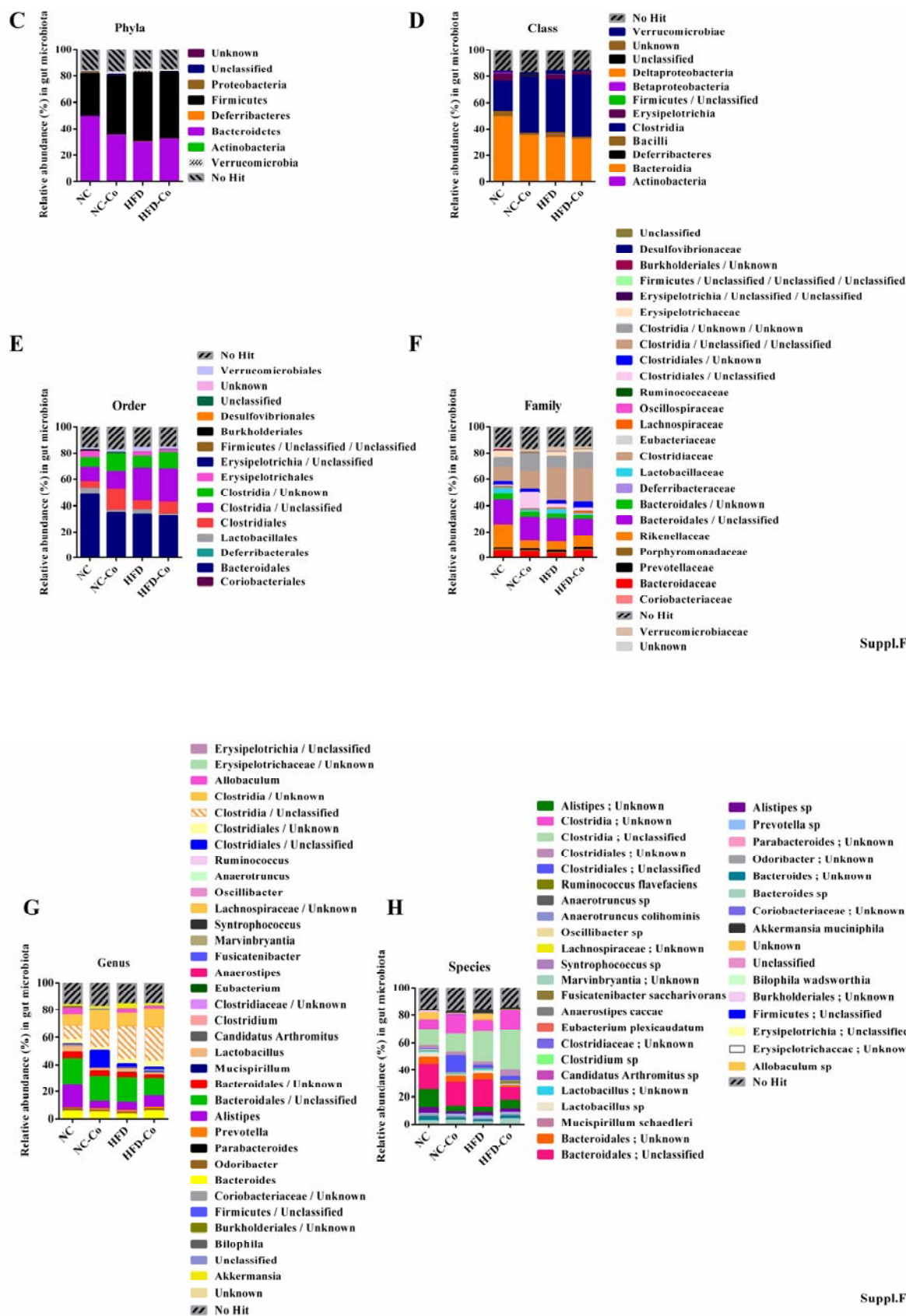
Suppl.Fig.1

Supplementary Figure 2. Oral colonization with *Pg*, *Fn* and *Pi* did not affect gut microbiota in HFD- and NC Diet-fed mice. A-B) Cladograms on gut microbiota explored by MiSeq analysis for NC (normal chow, red bar, n = 4), NC-Co (normal chow colonized, green bar, n=3), HFD (high-fat diet, red bar, n=6) and HFD-Co (High-fat diet colonized, green bar, n=7). Abundance (% of the total identified sequences per group) at the level of Phylum (C), Class (D), Order (E), Family (F), Genus (G) and Species (H) in each group.

C

Phyla

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- Unknown
- Unclassified
- Proteobacteria
- Firmicutes
- Deferribacteres
- Bacteroidetes
- Actinobacteria
- Verrucomicrobia
- No Hit

D

Class

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- No Hit
- Verrucomicrobiae
- Unknown
- Unclassified
- Deltaproteobacteria
- Betaproteobacteria
- Firmicutes / Unclassified
- Erysipelotrichia
- Clostridia
- Bacilli
- Deferribacteres
- Bacteroidia
- Actinobacteria

E

Order

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- No Hit
- Verrucomicrobiales
- Unknown
- Unclassified
- Desulfovibrionales
- Burkholderiales
- Firmicutes / Unclassified / Unclassified
- Erysipelotrichia / Unclassified
- Erysipelotrichales
- Clostridia / Unknown
- Clostridia / Unclassified
- Clostridiales
- Lactobacillales
- Deferribacterales
- Bacteroidales
- Coriobacteriales

F

Family

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- Unclassified
- Desulfovibrionaceae
- Burkholderiales / Unknown
- Firmicutes / Unclassified / Unclassified / Unclassified
- Erysipelotrichia / Unclassified / Unclassified
- Erysipelotrichaceae
- Clostridia / Unknown / Unknown
- Clostridia / Unclassified / Unclassified
- Clostridiales / Unknown
- Clostridiales / Unclassified
- Ruminococcaceae
- Oscillospiraceae
- Lachnospiraceae
- Eubacteriaceae
- Clostridiaceae
- Lactobacillaceae
- Deferribacteraceae
- Bacteroidales / Unknown
- Bacteroidales / Unclassified
- Rikenellaceae
- Porphyromonadaceae
- Prevotellaceae
- Bacteroidaceae
- Coriobacteriaceae
- No Hit
- Verrucomicrobiaceae
- Unknown

Suppl.Fig.2

G

Genus

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- Erysipelotrichia / Unclassified
- Erysipelotrichaceae / Unknown
- Allobaculum
- Clostridia / Unknown
- Clostridia / Unclassified
- Clostridiales / Unknown
- Clostridiales / Unclassified
- Ruminococcus
- Anaerotruncus
- Oscillibacter
- Lachnospiraceae / Unknown
- Syntrophococcus
- Marvinbryantia
- Fusicatenibacter
- Anaerostipes
- Eubacterium
- Clostridiaceae / Unknown
- Clostridium
- Candidatus Arthromitus
- Lactobacillus
- Mucispirillum
- Bacteroidales / Unknown
- Bacteroidales / Unclassified
- Alistipes
- Prevotella
- Parabacteroides
- Odoribacter
- Bacteroides
- Coriobacteriaceae / Unknown
- Firmicutes / Unclassified
- Burkholderiales / Unknown
- Bilophila
- Unclassified
- Akkermansia
- Unknown
- No Hit

H

Species

Relative abundance (%) in gut microbiota

NC NC-Co HFD HFD-Co

- Alistipes ; Unknown
- Clostridia ; Unknown
- Clostridia ; Unclassified
- Clostridiales ; Unknown
- Clostridiales ; Unclassified
- Ruminococcus flavefaciens
- Anaerotruncus sp
- Anaerotruncus colihominis
- Oscillibacter sp
- Lachnospiraceae ; Unknown
- Syntrophococcus sp
- Marvinbryantia ; Unknown
- Fusicatenibacter saccharivorans
- Anaerostipes caccae
- Eubacterium plexicaudatum
- Clostridiaceae ; Unknown
- Clostridium sp
- Candidatus Arthromitus sp
- Lactobacillus ; Unknown
- Lactobacillus sp
- Mucispirillum schaedleri
- Bacteroidales ; Unknown
- Bacteroidales ; Unclassified

- Alistipes sp
- Prevotella sp
- Parabacteroides ; Unknown
- Odoribacter ; Unknown
- Bacteroides ; Unknown
- Bacteroides sp
- Coriobacteriaceae ; Unknown
- Akkermansia muciniphila
- Unknown
- Unclassified
- Bilophila wadsworthia
- Burkholderiales ; Unknown
- Firmicutes ; Unclassified
- Erysipelotrichia ; Unclassified
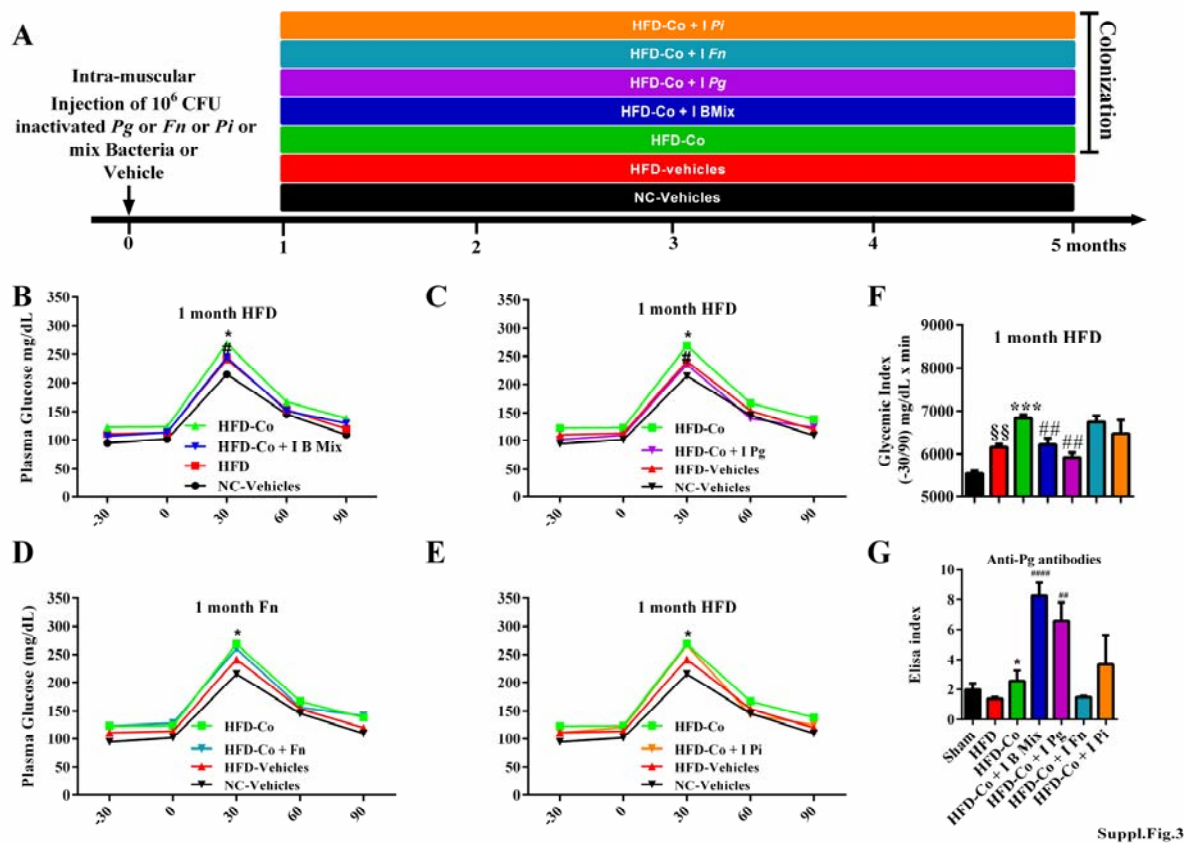- Erysipelotrichaccac ; Unknown
- Allobaculum sp
- No Hit

Suppl.Fig.2

5

Supplementary Figure 3. Pre-treatment with inactivated *Porphyromonas gingivalis* induced production of antibodies against *Porphyromonas gingivalis* A) Mice were injected by 10^6 CFU of inactivated *Porphyromonas gingivalis* or inactivated *Fusobacterium nucleatum* or inactivated *Prevotella intermedia* or a mix of all inactivated bacteria or vehicle solution. 1 month later, mice were colonized by *Pg, Fn, Pi* and or by vehicle solution for one month and then randomized in 7 groups: Sham (vehicle + normal chow, black bar, n = 4), HFD (vehicle + HFD, red bar, n=4), HFD-Co (vehicle + HFD + colonization, green bar, n=4), HFD-Co + I B mix (inactivated mix bacteria + colonization + HFD, black blue bar, n=4), HFD-Co + I *Pg* (inactivated *Porphyromonas gingivalis* + colonization + HFD, purple bar, n= 4), HFD-Co + I *Fn* (inactivated *Fusobacterium nucleatum* + colonization + HFD, light blue bar, n= 4) and HFD-Co + inactivated *Pi* (inactivated *Prevotella intermedia* + colonization + HFD, orange bar, n= 4). Intraperitoneal Glucose-Tolerance Test (IpGTT) and glycaemic index were assessed for each group after 1 month of HFD (B-F); G) Measurement of Immunoglobulin G antibodies specific to LPS of *Porphyromonas* gingivalis in blood. Data are mean ± SEM. Significant results when: $**P<0.01$, $***P<0.001$ and $****P<0.0001$ when compared to HFD-vehicles, $^§P<0.05$ and $^{§§§§}P<0.0001$ when compared to NC-vehicles and $^#P<0.05$ and $^{####}P<0.0001$ when compared to HFD-Co as determined by Two-Way ANOVA with Bonferroni's post-test for B, C,D and E and one-way ANOVA followed by Tukey's post-test for F and G.