

Supplementary Table S1. Relative abundance of taxa identified by 16S rRNA sequencing in semen samples using ONT MinION platform. The mean proportion of each taxon with a minimum relative abundance of 0.05% in whole sample is shown.

	Total (%)	Controls (%)	Idiopathic patients (%)
Phylum			
Firmicutes	66.51	71.90	64.72
Proteobacteria	20.81	17.59	21.88
Bacteroidetes	5.37	5.43	5.35
Actinobacteria	5.33	4.93	5.47
Tenericutes	1.54	0.00	2.05
Fusobacteria	0.31	0.13	0.37
Cyanobacteria	0.08	0.00	0.10
Family			
Peptoniphilaceae	38.79	44.33	36.94
Staphylococcaceae	7.99	15.62	5.45
Campylobacteraceae	6.34	3.14	7.41
Prevotellaceae	5.65	5.95	5.54
Streptococcaceae	4.88	3.86	5.21
Lactobacillaceae	4.46	0.14	5.90
Veillonellaceae	2.92	2.44	3.08
Bacillaceae	2.46	1.11	2.91
Enterococcaceae	2.42	3.84	1.94
Enterobacteriaceae	2.37	0.08	3.13
Corynebacteriaceae	2.17	2.89	1.93
Burkholderiaceae	1.83	1.04	2.09
Propionibacteriaceae	1.64	1.03	1.85
Mycoplasmataceae	1.64	0.00	2.18
Moraxellaceae	1.48	0.03	1.97
Pasteurellaceae	1.45	5.26	0.17
Actinomycetaceae	1.29	1.01	1.38
Caulobacteraceae	1.12	1.68	0.93
Aerococcaceae	1.04	0.74	1.14
Rhodobacteraceae	0.92	2.06	0.53
Porphyromonadaceae	0.88	0.25	1.10
Oxalobacteraceae	0.81	0.14	1.03
Listeriaceae	0.80	0.17	1.01
Bradyrhizobiaceae	0.52	0.04	0.68
Comamonadaceae	0.43	0.46	0.42
Micrococcaceae	0.43	0.10	0.54
Neisseriaceae	0.42	0.00	0.56
Fusobacteriaceae	0.41	0.14	0.50
Pseudomonadaceae	0.24	0.18	0.26
Sphingomonadaceae	0.24	0.74	0.07
Peptostreptococcaceae	0.23	0.28	0.21
Clostridiaceae	0.21	0.01	0.28
Planococcaceae	0.20	0.01	0.26

Paenibacillaceae	0.16	0.00	0.21
Thermoactinomycetaceae	0.12	0.00	0.15
Bifidobacteriaceae	0.11	0.02	0.14
Tissierellaceae	0.10	0.06	0.12
Methylobacteriaceae	0.09	0.35	0.00
Weeksellaceae	0.08	0.14	0.06
Carnobacteriaceae	0.08	0.05	0.09
Eubacteriales	0.06	0.20	0.02

Genera

Peptoniphilus	15.71	15.49	13.31
Finegoldia	14.74	15.64	12.13
Staphylococcus	8.28	14.32	4.96
Anaerococcus	6.63	7.91	5.16
Campylobacter	6.01	2.89	6.10
Prevotella	5.41	5.36	4.58
Streptococcus	5.34	3.68	5.05
Lactobacillus	4.22	0.03	4.95
Ezakiella	3.78	1.53	3.93
Enterococcus	2.59	3.63	1.83
Corynebacterium	2.28	2.78	1.75
Bacillus	2.20	0.69	2.35
Dialister	1.92	1.58	1.73
Ureaplasma	1.80	0.00	2.11
Ralstonia	1.76	0.91	1.77
Cutibacterium	1.37	0.75	1.36
Moraxella	1.35	0.00	1.59
Haemophilus	1.27	4.15	0.12
Brevundimonas	0.97	1.62	0.60
Massilia	0.93	0.09	1.06
Paracoccus	0.89	1.79	0.45
Porphyromonas	0.85	0.22	0.93
Veillonella	0.82	0.60	0.76
Bradyrhizobium	0.71	0.08	0.80
Listeria	0.65	0.14	0.72
Winkia	0.49	0.24	0.50
Gardnerella	0.43	0.00	0.50
Neisseria	0.42	0.00	0.49
Fusobacterium	0.40	0.13	0.43
Rothia	0.33	0.01	0.38
Mobiluncus	0.29	0.21	0.28
Fenollaria	0.25	0.21	0.23
Varibaculum	0.25	0.25	0.21
Gemella	0.25	0.00	0.29
Pseudomonas	0.25	0.18	0.23
Pelomonas	0.23	0.44	0.13
Clostridium	0.22	0.00	0.26
Facklamia	0.21	0.52	0.07

Peptostreptococcus	0.18	0.19	0.15
Methylobacterium	0.18	0.63	0.00
Delftia	0.16	0.00	0.19
Salmonella	0.16	0.07	0.17
Limosilactobacillus	0.15	0.00	0.17
Rummeliibacillus	0.14	0.00	0.17
Brochothrix	0.14	0.00	0.16
Parvimonas	0.13	0.00	0.15
Planifilum	0.12	0.00	0.14
Paenibacillus	0.12	0.00	0.14
Acinetobacter	0.11	0.03	0.12
Methylobacterium	0.09	0.32	0.00
Aerococcus	0.09	0.02	0.10
Sphingobium	0.08	0.28	0.00
Companilactobacillus	0.08	0.00	0.09
Caulobacter	0.08	0.00	0.09
Chryseobacterium	0.07	0.08	0.06
Kocuria	0.07	0.07	0.05
Macrococcus	0.05	0.04	0.05