

Table 1. Detection frequency (%) of species identified by culture and characterisation of isolates by comparing 16SrRNA gene sequences with the database HOMD.

	Species isolated	Trauma ^a	Non-trauma ^a	Total ^a	Trauma ^b (%)	Non-trauma ^b (%)
1	<i>Fusobacterium nucleatum</i>	11	7	18	50,000	24,138
2	<i>Slackia exigua</i>	6	10	16	27,273	34,483
3	<i>Dialister invisus</i>	7	7	14	31,818	24,138
4	<i>Parvimonas micra</i>	3	9	12	13,636	31,034
5	<i>Peptostreptococcaceae infirmum / sulci</i>	2	8	10	9,091	27,586
6	<i>Prevotella nigrescens</i>	4	6	10	18,182	20,690
7	<i>Pseudoramibacter alactolyticus</i>	0	10	10	0,000	34,483
8	<i>Prevotella denticola</i>	4	4	8	18,182	13,793
9	<i>Actinomyces georgiae</i>	2	5	7	9,091	17,241
10	<i>Atopobium rimae</i>	2	5	7	9,091	17,241
11	<i>Peptostreptococcus stomatis</i>	2	5	7	9,091	17,241
12	<i>Actinomyces gerencseriae</i>	3	3	6	13,636	10,345
13	<i>Mogibacterium timidum</i>	2	4	6	9,091	13,793
14	<i>Peptostreptococcaceae yurii</i>	5	1	6	22,727	3,448
15	<i>Selenomonas noxia</i>	5	1	6	22,727	3,448
16	<i>Atopobium parvulum</i>	0	5	5	0,000	17,241
17	<i>Olsenella uli</i>	1	4	5	4,545	13,793
18	<i>Parvimonas sp.</i>	1	4	5	4,545	13,793
19	<i>Porphyromonas gingivalis</i>	0	5	5	0,000	17,241
20	<i>Prevotella sp.</i>	2	3	5	9,091	10,345
21	<i>Alloprevotella tannerae</i>	4	0	4	18,182	0,000
22	<i>Anaeroglobus geminatus</i>	1	3	4	4,545	10,345
23	<i>Campylobacter showae</i>	4	0	4	18,182	0,000
24	<i>Dialister pneumosintes</i>	2	2	4	9,091	6,897
25	<i>Enterococcus faecalis</i>	0	4	4	0,000	13,793
26	<i>Filifactor alocis</i>	0	4	4	0,000	13,793
27	<i>Streptococcus sanguinis</i>	2	2	4	9,091	6,897
28	<i>Actinomyces meyeri</i>	1	2	3	4,545	6,897
29	<i>Campylobacter rectus</i>	3	0	3	13,636	0,000
30	<i>Capnocytophaga sp.</i>	3	0	3	13,636	0,000
31	<i>Olsenella sp.</i>	1	2	3	4,545	6,897
32	<i>Peptoniphilus lacrimalis</i>	1	2	3	4,545	6,897
33	<i>Peptostreptococcaceae nodatum</i>	0	3	3	0,000	10,345
34	<i>Porphyromonas catoniae</i>	3	0	3	13,636	0,000
35	<i>Streptococcus constellatus / intermedius</i>	1	2	3	4,545	6,897
36	<i>Aggregatibacter sp.</i>	0	2	2	0,000	6,897
37	<i>Bulleidia extructa</i>	0	2	2	0,000	6,897
38	<i>Capnocytophaga ochracea</i>	0	2	2	0,000	6,897
39	<i>Cutibacterium acnes</i>	1	1	2	4,545	3,448
40	<i>Eikenella corrodens/Kingella denitrificans</i>	0	2	2	0,000	6,897
41	<i>Leptotrichia hongkongensis</i>	1	1	2	4,545	3,448
42	<i>Mogibacterium</i>	1	1	2	4,545	3,448
43	<i>Olsenella profusa</i>	0	2	2	0,000	6,897
44	<i>Paenibacillus glucanolyticus</i>	0	2	2	0,000	6,897
45	<i>Prevotella intermedia</i>	0	2	2	0,000	6,897
46	<i>Prevotella oralis</i>	0	2	2	0,000	6,897
47	<i>Propionibacterium propionicum</i>	1	1	2	4,545	3,448
48	<i>Pyramidobacter pisciolens</i>	0	2	2	0,000	6,897
49	<i>Selenomonas sp.</i>	2	0	2	9,091	0,000
50	<i>Shuttleworthia satellites</i>	1	1	2	4,545	3,448
51	<i>Staphylococcus (trogilgen epidermidis)</i>	2	0	2	9,091	0,000
52	<i>Actinomyces israelii</i>	0	1	1	0,000	3,448
53	<i>Actinomyces johnsonii</i>	1	0	1	4,545	0,000
54	<i>Actinomyces lingnae</i>	1	0	1	4,545	0,000
55	<i>Actinomyces massiliensis</i>	1	0	1	4,545	0,000
56	<i>Bacillus subtilis</i>	1	0	1	4,545	0,000
57	<i>Campylobacter concisus</i>	0	1	1	0,000	3,448
58	<i>Campylobacter gracilis</i>	1	0	1	4,545	0,000

59	Capnocytophaga sputigena	0	1	1	0,000	3,448
60	Catonella morbi	1	0	1	4,545	0,000
61	Fusobacterium necrophorum	1	0	1	4,545	0,000
62	Gemella bergeri	1	0	1	4,545	0,000
63	Granulicatella adiacens	0	1	1	0,000	3,448
64	Lactobacillus	0	1	1	0,000	3,448
65	Peptoniphilus asaccharolyticus	0	1	1	0,000	3,448
66	Peptostreptococcaceae [XI][G-5] bacterium	1	0	1	4,545	0,000
67	Peptostreptococcaceae [XI][G-7] yurii subsp. yurii & margaretiae	1	0	1	4,545	0,000
68	Prevotella baroniae	0	1	1	0,000	3,448
69	Prevotella buccae	0	1	1	0,000	3,448
70	Prevotella melaniogenica	0	1	1	0,000	3,448
71	Prevotella oulorum	1	0	1	4,545	0,000
72	Propionibacterium acidifaciens	0	1	1	0,000	3,448
73	Propionibacterium avidum	0	1	1	0,000	3,448
74	Staphylococcus epidermidis / caprae	0	1	1	0,000	3,448
75	Staphylococcus pasteurii	1	0	1	4,545	0,000
76	Staphylococcus warneri	1	0	1	4,545	0,000
77	Streptococcus intermedius	0	1	1	0,000	3,448
78	Streptococcus anginosus	0	1	1	0,000	3,448
79	Veillonella dispar / parvulva	0	1	1	0,000	3,448

Table 2. Bacterial association to trauma and non-trauma teeth presented at species level.

Phylum	Genus	Species	log2Fold Change	p-adj
Firmicutes	Mogibacterium	timidum	-7.733251	0.0000000
Firmicutes	Stomatobaculum	sp._HMT_910	-9.750942	0.0000000
Firmicutes	Selenomonas	noxia	9.230914	0.0000015
Firmicutes	Lactobacillus	casei	-8.647475	0.0000000
Firmicutes	Veillonellaceae_[G-1]	bacterium_HMT_132	6.311425	0.0001167
Firmicutes	Selenomonas	sputigena	-5.713459	0.0000573
Firmicutes	Peptostreptococcaceae_[XI] [G-7]	yurii_subsp._yurii_& margaretiae	13.193901	0.0000000
Firmicutes	Peptoniphilus	lacrimalis	5.684783	0.0006669
Firmicutes	Peptostreptococcaceae_[XI] [G-9]	brachy	6.487365	0.0001905
Firmicutes	Streptococcus	vestibularis	-6.739119	0.0000000
Firmicutes	Mycoplasma	salivarium	-6.612241	0.0000005
Firmicutes	Johnsonella	ignava	7.926672	0.0000125
Firmicutes	Paenibacillus	glucanolyticus	-13.882510	0.0000000
Firmicutes	Veillonella	dispar	-4.289847	0.0052933
Firmicutes	Peptostreptococcaceae_[XI] [G-4]	bacterium_HMT_369	7.587072	0.0000274
Spirochaetes	Treponema	maltophilum	8.758014	0.0000002
Bacteroidetes	Porphyromonas	endodontalis	-8.874290	0.0000000
Bacteroidetes	Bacteroidetes_[G-3]	bacterium_HMT_365	-9.573662	0.0000000
Bacteroidetes	Prevotella	sp._HMT_317	-6.935651	0.0000443
Bacteroidetes	Porphyromonas	sp._HMT_275	6.074244	0.0003361
Bacteroidetes	Bacteroidales_[G-2]	bacterium_HMT_24	5.888751	0.0001110
Bacteroidetes	Bacteroidetes_[G-5]	bacterium_HMT_51	8.562230	0.0000055
Bacteroidetes	Prevotella	nanceiensis	-6.682456	0.0000000
Bacteroidetes	Porphyromonas	gingivalis	-6.900814	0.0000000
Bacteroidetes	Prevotella	sp._HMT_313	-7.537308	0.0000000
Bacteroidetes	Prevotella	sp._HMT_292	-4.873577	0.0005656
Bacteroidetes	Prevotella	nigrescens	4.470768	0.0048599
Bacteroidetes	Prevotella	intermedia	-11.970001	0.0000000
Bacteroidetes	Alloprevotella	sp._HMT_473	-7.560106	0.0000000
Bacteroidetes	Prevotella	melaninogenica	-10.595443	0.0000000
Actinobacteria	Rothia	dentocariosa	-4.342347	0.0037499
Actinobacteria	Actinomyces	oris	6.913926	0.0000188
Actinobacteria	Corynebacterium	matruchotii	4.342142	0.0056922
Actinobacteria	Rothia	mucilaginosa	-6.811720	0.0000001
Actinobacteria	Atopobium	sp._HMT_199	-10.051236	0.0000000
Actinobacteria	Olsenella	uli	-5.396915	0.0001584
Proteobacteria	Escherichia	coli	-8.420180	0.0000000
Proteobacteria	Haemophilus	parainfluenzae	-4.978336	0.0001306
Proteobacteria	Yersinia	pestis	-9.918709	0.0000000
Proteobacteria	Pseudomonas	fluorescens	-5.958878	0.0000017
Proteobacteria	Campylobacter	showae	6.682366	0.0000230
Proteobacteria	Campylobacter	concisus	-10.118541	0.0000000
Proteobacteria	Cardiobacterium	hominis	5.582932	0.0010912
Fusobacteria	Fusobacterium	nucleatum_subsp._ polymorphum	5.423556	0.0026090
Fusobacteria	Fusobacterium	hwasookii	-6.694746	0.0000045
Fusobacteria	Fusobacterium	sp._HMT_203	6.654830	0.0000787
Synergistetes	Pyramidobacter	piscolens	-8.983015	0.0000000

Synergistetes	Fretibacterium	fastidiosum	-4.666563	0.0053617
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Different HMT sorted based on the Phylum to find a specific organism easily. The color differences to easily separate the high abundant from the low abundant in Trauma samples. If the log2FoldChange is above ZERO (blue), meaning that the HMTs were more abundant in Trauma samples and below ZERO (orange) HMTs were more abundant in Non-Trauma samples.