feature_Taxon	T5161	T54	T55	T64	T65	T74	T75	T84	T85
ASV_16942__sum_of_decays_for_non−surrounding/distant_teeth	3	2	1	1	3	3	3	3	3
ASV_16943__sum_of_decays_for_surrounding_teeth			1	4	4	4	4	4	4
ASV_7424__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces	98	135	25	77	2878	93	273	88	58
ASV_7315__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__Actinomyces_naeslundii	104	94	39	372	2888	81	220	10	116
ASV_10606__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cardiobacteriales; f__Cardiobacteriaceae; g__Cardiobacterium	76	134	15	2535	27	24	23	34	336
ASV_7774__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium_matruchotii	333	152	290	355	139	482	421	238	13
ASV_16939__spatial−distance−weighted_mean_of_dmfs_of_all_remaining_teeth	2	3	3	2	2	2	2	2	1
ASV_1938__d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Gemellaceae; g__Gemella	130	32	602	30	2843	98	14	25	158
ASV_4823__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Tannerellaceae; g__Tannerella; s__Tannerella_sp.	3812	37	209	11	56	86	11	66	121
ASV_6949__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Rothia	3851	27	40	84	6	359	87	78	93
ASV_15378__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	152	21	78	78	25	467	201	205	112
ASV_15840__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Comamonas; s__Ottowia_sp.	381	155	3467	254	61	71	212	21	113
ASV_7543__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium_durum	66	9	75	64	8	2440	297	285	36
ASV_1504__d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus	325	76	312	10	276	2372	127	104	166
ASV_7489__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces	3784	111	50	65	264	144	18	143	25
ASV_12257__d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales−Selenomonadales; f__Veillonellaceae; g__Veillonella	10	47	3473	73	91	17	26	158	38
ASV_3643__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Capnocytophaga	120	179	97	37	14	94	149	28	160
ASV_1989__d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Gemellaceae; g__Gemella	37	120	32	42	24	85	130	99	34
ASV_10960__d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__Leptotrichia_sp.	273	43	101	18	53	70	89	65	66
ASV_4653__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella_7; s__Prevotella_histicola	32	48	21	27	29	16	46	174	3665
ASV_16931__average_microbiome_distance_based_on_all_ASVs_between_a_focal_tooth_and_all_healthy_teeth_at_position_54	46	24	60	14	135	252	52	130	102
ASV_14190__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Lautropia	5	2640	6	112	11	36	22	30	103
ASV_4904__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	7	26	98	26	57	29	7	5	22
ASV_5959__d__Bacteria; p__Patescibacteria; c__Saccharimonadia; o__Saccharimonadales; f__Saccharimonadaceae; g__Saccharimonadaceae; s__uncultured_bacterium	168	25	72	217	169	127	641	128	4032
ASV_7121__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces	119	29	23	24	2556	12	73	15	15
ASV_7597__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium_durum	111	116	105	75	22	25	29	45	27
ASV_2160__d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus_mutans	4	5	5	5	5	5	5	6	5
ASV_11264__d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__uncultured_bacterium	24	71	3431	118	203	90	153	159	606
ASV_5306__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella_7	27	96	43	245	381	8	10	13	12
ASV_5726__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Capnocytophaga; s__Capnocytophaga_granulosa	23	30	22	35	88	190	13	85	7
ASV_7510__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Scardovia; s__Scardovia_wiggsiae	189	18	14	6	201	7	17	48	11
ASV_7755__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium_matruchotii	174	17	77	21	48	188	108	95	161
ASV_16756__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces	25	10	7	152	36	9	57	117	19
ASV_5039__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	122	2594	59	286	278	42	112	18	53
ASV_1443__d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Ligilactobacillus	3791	113	30	12	65	136	184	22	410
ASV_16934__average_microbiome_distance_based_on_all_ASVs_between_a_focal_tooth_and_all_healthy_teeth_at_position_65	135	40	65	23	30	104	122	77	107
ASV_7965__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__Actinomyces_gerencseriae	146	161	132	179	510	155	9	348	45
ASV_6301__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Pseudopropionibacterium; s__uncultured_bacterium	261	267	229	172	21	240	3864	126	154
ASV_7149__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces	29	53	41	16	7	32	8	183	44
ASV_8226__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Pasteurellaceae; g__Actinobacillus	38	83	37	36	2882	35	54	16	29
ASV_12302__d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales−Selenomonadales; f__Veillonellaceae; g__Veillonella	187	39	9	17	166	477	163	94	202
ASV_4983__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	16	14	69	465	277	110	51	58	16
ASV_4847__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	138	102	129	43	31	260	103	3484	35
ASV_16941__sum_of_dmfs_for_all_other_teeth	1	4	2	3	1	1	1	1	2
ASV_6531__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__Schaalia_odontolytica	54	8	19	13	17	68	16	47	150
ASV_7886__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Propionibacterium	11	7	45	9	15	6	12	91	8
ASV_3559__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Capnocytophaga; s__Capnocytophaga_sputigena	33	473	157	95	89	2437	72	122	10
ASV_1822__d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Carnobacteriaceae; g__Granulicatella	77	35	52	34	10	34	25	50	46
ASV_11671__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cardiobacteriales; f__Cardiobacteriaceae; g__Cardiobacterium; s__uncultured_bacterium	3759	404	104	478	108	124	30	49	18
ASV_6951__d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Rothia	105	6	11	141	18	31	21	3576	6
ASV_1665__d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	44	13	36	2320	34	14	6	9	17
ASV_5650__d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Capnocytophaga	14	145	56	98	70	143	45	156	3972
ASV_12878__d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Atopobiaceae; g__Atopobium	269	81	593	25	2851	55	59	42	197
ASV_9466__d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	26	56	12	20	16	18	15	60	123
ASV_9253__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Pasteurellaceae	3827	12	87	19	84	23	246	7	119
ASV_8766__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Pasteurellaceae; g__Haemophilus	89	77	38	28	93	158	38	204	80
ASV_8872__d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Pasteurellaceae; g__Aggregatibacter	9	44	26	38	12	10	177	11	114

rf_imps_rank: 4000, 3000, 2000, 1000