



Figure S1 - Compositional biplot, that simultaneously displays the sample clustering, with each point representing a single sample of the healthy sites, and the important taxa identified at phylum level. This plot showed that healthy sites samples were mainly driven by Firmicutes and TM7.

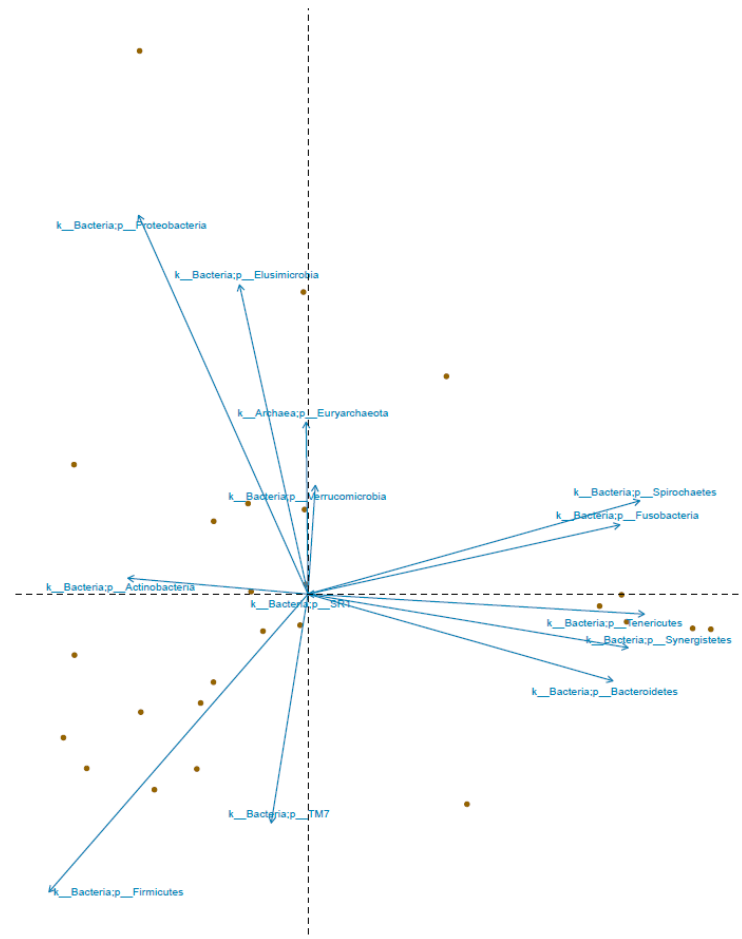


Figure S2 - Compositional biplot, that simultaneously displays the sample clustering, with each point representing a single sample of the healthy sites, and the important taxa identified at phylum level. This plot showed that diseased samples were mainly driven by Synergistetes and Bacteroidetes.

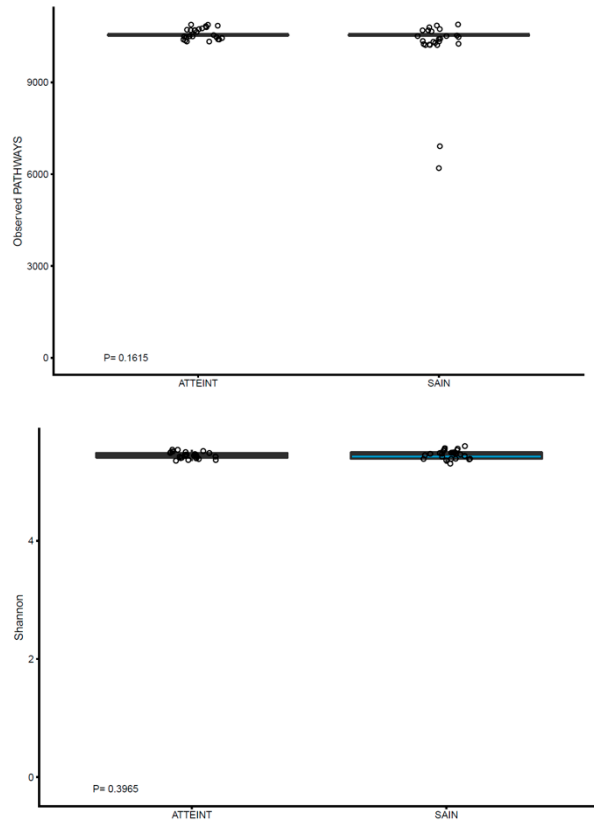


Figure S3 - Alpha diversities of the predict metagenomic functions of the samples collected in periodontitis sites and healthy sites using (A) the total numbers of observed pathways and (B) the shannon index. Whiskers in the boxplot represent the range of minimum and maximum alpha diversity values within a population, excluding outliers. No tests yielded a significant difference.

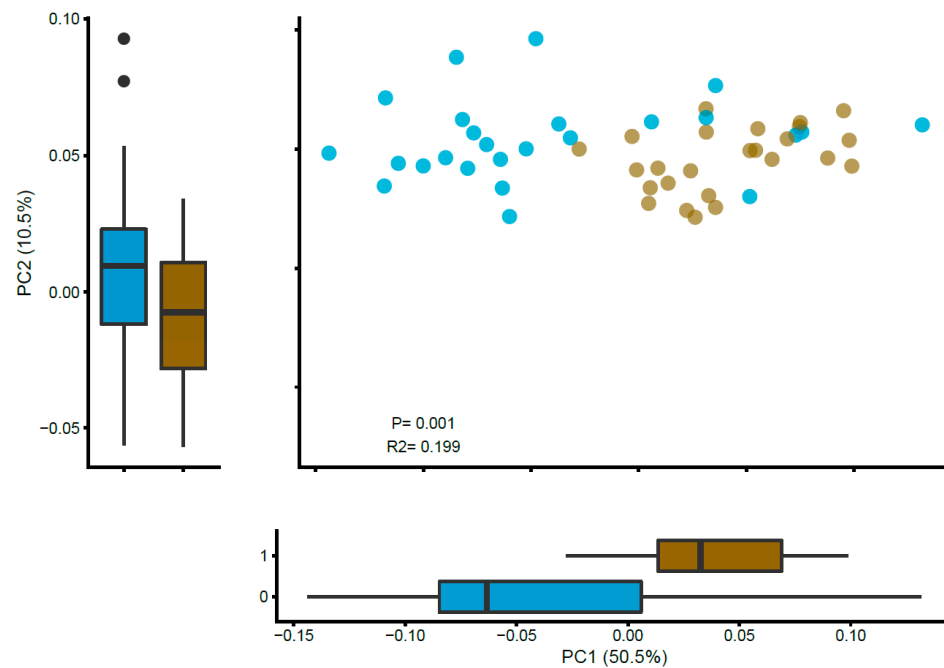


Figure S4 - Functional diversity of the oral microbiomes of the predict metagenomic functions of the samples collected in periodontitis sites and healthy sites. Principal Coordinates Analysis of Bray–Curtis distances generated from pathways table. Proportion of variance explained by each principal coordinate axis is denoted in the corresponding axis label. The PCoA shows clear separation between faecal samples collected before chemotherapy and after chemotherapy.

Feature	P value	FDR corrected P value	mean relative abundance healthy sites	mean relative abundance diseased sites
k_Bacteria;p_Synergistetes	0.0000127963181505418	0.000204741090408669	0.0130342887773651	0.0436740765836695
k_Bacteria;p_Firmicutes	0.0000887786327270478	0.000473486041210921	0.381067316933096	0.223589012028169
k_Bacteria;p_TM7	0.000478348082313356	0.0017440863141694	0.0245489811479369	0.078776742131996
k_Bacteria;p_SR1	0.000545026973177937	0.0017440863141694	0	0.00215848238376248
k_Bacteria;p_Spirochaetes	0.000780787451612888	0.0020820998709677	0.0415370521086175	0.0937275137812838
k_Bacteria;p_Bacteroidetes	0.00280773814974955	0.00641768719942754	0.189027028601388	0.26581083203824
k_Bacteria;p_Proteobacteria	0.0198939507675555	0.0397879015351109	0.198693091678517	0.116957110402858
k_Bacteria;p_Tenericutes	0.0249433697703493	0.044343768480621	0.00237656679120939	0.00412197754699422
k_Bacteria;p_Fusobacteria	0.0378658098717794	0.060585295794847	0.0765980599127453	0.114318718130449
k_Bacteria;p_Actinobacteria	0.0572392612793856	0.0832571073154699	0.0699247819222139	0.0427055644726608

Table S1A. Relative abundance of the most significant phyla in the samples collected in periodontitis sites and healthy sites as assessed by Mann-Whitney U tests with false-discovery-rate correction.

Feature	P value	FDR corrected P value	mean relative abundance healthy sites	mean relative abundance diseased sites
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Schwarztzia	0.0000100791304482579	0.00156341723298603	0.00185557988957733	0.00750991065434733
k_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_TG5	0.0000198867513278845	0.00156341723298603	0.0130342887773651	0.0412271032692709
k_Bacteria;p_TM7;c_TM7-3;o_;f_;g_	0.0000203041199089094	0.00156341723298603	0.010056874230823	0.0661263239468699

k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	0.0000423272928 012977	0.00197192320 788367	0.0611968347072 659	0.0067640458085 4227
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	0.0000539704245 459434	0.00197192320 788367	0.0218921164835 223	0.0017384075274 9208
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__	0.0000715050908 165901	0.00197192320 788367	0.0176239620787 316	0.0020042577319 8034
k__Bacteria;p__TM7;c__TM7-3;o__I025;f__Rs-045;g__	0.0000737874573 352613	0.00197192320 788367	0.0014969570040 4925	0.0062578001646 5631
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas	0.0000744767000 457875	0.00197192320 788367	0.0193267612260 351	0.0728691569606 997
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Filifactor	0.0000768281769 305324	0.00197192320 788367	0.0084088476681 549	0.0208988469218 348
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__	0.0000960631906 447407	0.00205408678 164307	0.0009316035042 0155	0.0032945521519 6643
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolinaceae;g__SHD-231	0.0001053864731 84199	0.00205408678 164307	0.0012735961597 049	0.0081025246077 8169
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__Mogibacterium	0.0001067058068 38601	0.00205408678 164307	0.0050095506772 3661	0.0095038250050 9464
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Blvii28	0.0001176021760 56931	0.00207150644 368834	0.0017592820357 6694	0.0076522742306 1183
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Paraprevotellaceae];g__[Prevotella]	0.0001255458450 72021	0.00207150644 368834	0.0020949178058 4918	0.0183025040253 202
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium	0.0001549090278 28394	0.00238559902 855727	0.0016329210989 8592	0.0003590366130 51911

k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfobulbus	0.0001998637634 31739	0.00288553308 454574	0.0071943045826 5305	0.0235958213627 634
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Dialister	0.0002349559886 19876	0.00319263725 71289	0.0088365817206 8227	0.0234966617440 765
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Pseudoramibacter_Eubacterium	0.0002818016037 47826	0.00361645391 476377	0.0002800764848 04709	0.0008649958203 9246
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Bulleidia	0.0003054348939 43592	0.00371344528 952473	0.0004514636911 67561	0.0021433557929 4333
k__Bacteria;p__SR1;c__o__f__g__	0.0005450269731 77937	0.00608043884 00556	0	0.0021584823837 6248
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;__	0.0005527671672 77782	0.00608043884 00556	0.0544241252642 022	0.0075459491766 2256
k__Bacteria;p__Tenericutes;c__RF3;o__ML615J-28;f__g__	0.0006514536816 05986	0.00663728803 059029	0.0000924755239 1704	0.0005175439970 17256
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__[Exiguobacteraceae];g__	0.0006608555181 97302	0.00663728803 059029	0.0199636232701 272	0.0016985613939 5153
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Selenomonas	0.0007095423142 77409	0.00682934477 492006	0.0089533238781 5447	0.0197580145490 676
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Spirochaetales;f__Spirochaetaceae;g__Treponema	0.0007807874516 12888	0.00721447605 290309	0.0414886629579 744	0.0934090274101 671
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Moryella	0.0008640923260 60033	0.00754700663 591315	0.0002828163602 63572	0.0044839504837 3287
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ethanoligenens	0.0008979875085 12424	0.00754700663 591315	0.0172419272400 075	0.0024192194958 4356

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Acidaminobacteraceae];g__	0.0009147886831	0.00754700663	0.0033612059372	0.0080106682273
—	40988	591315	6106	9141
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__	0.0010385521365	0.00827260494	0.0114692732410	0.0170527643927
	436	970939	886	847
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteraceae;g__Campylobacter	0.0011046476841	0.00850578716	0.0131674572575	0.0282356117550
	6196	804706	732	576
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Slackia	0.0011921558662	0.00888348403	0.0002626946027	0.0011429658822
	2122	539036	75136	502
k__Bacteria;p__TM7;c__TM7-3;o__CW040;f__F16;g__	0.0013940080421	0.01006299555	0.0001346918777	0.0018892255013
	6599	43857	98137	6516
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__;g__	0.0015807595412	0.01106531678	0.0026130982270	0.0069900316041
	5632	87943	1033	4388
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Catonella	0.0017502784754	0.01189159787	0.0007060994077	0.0014405924183
	4265	72721	84039	1715
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus	0.0019166936878	0.01265017833	0.0004023448613	0.0014622964536
	6674	99205	23961	7025
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Olsenella	0.0020803510996	0.01334891955	0.0005493995405	0.0014005042096
	2183	59067	26134	8871
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Clostridium	0.0023676643420	0.01478190440	0.0026176805329	0.0000581791884
	0015	54604	6383	145145
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Sharpea	0.0024888859374	0.01512980661	0	0.0005684948827
	8454	99718		28101
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;__;__	0.0026805463703	0.01571657686	0.0020078803021	0.0075089712819
	1222	4531	7186	7941

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__	0.0027214851713 4736	0.01571657686 4531	0.0000369318181 818182	0.0004035719551 12187
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Oribacterium	0.0028427352957 7778	0.01601638666 64553	0.0005324258302 92538	0.0016301772492 7436
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Tannerella	0.0033646643214 9853	0.01850565376 82419	0.0305468604540 926	0.0534684578600 18
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter	0.0051454660145 2188	0.02764192207 80129	0.0003750032804 78809	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus	0.0087883097542 5357	0.04546152740 49267	0.0031725604308 3474	0.0000761432190 314789
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospira	0.0088561417022 5845	0.04546152740 49267	0.0004055233052 98843	0.0016920908479 6847
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__Alishewanella	0.0099687409280 1338	0.04921678450 35	0.0066798545993 2246	0.0004459040628 55519
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium	0.0100748513880 316	0.04921678450 35	0.0056376593145 4027	0.0006087397387 28708
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Leptotrichia	0.0103298131685 447	0.04921678450 35	0.0021245582723 576	0.0109927700858 195
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Helicobacteraceae;g__Wolinella	0.0104399239855 909	0.04921678450 35	0	0.0001148506406 06329
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Johnsonella	0.0115558775330 482	0.05314215774 01816	0.0041412801111 3663	0.0093872564656 937
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium	0.0117326841764 037	0.05314215774 01816	0.0025350840525 4652	0.0003881255168 00053

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium	0.0122425901229 375	0.05438535227 68955	0.0163768680468 491	0.0020376046720 1337
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Aeromonas	0.0126100379859 645	0.05496073159 92037	0.0115720285190 774	0.0011043133001 5511
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Atopobium	0.0170705259149 819	0.07302391641 40893	0.0007864770501 8408	0.0031893118818 9061
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Paenibacillus	0.0184953149625 019	0.07768032284 2508	0.0033823290074 6662	0.0004438318215 22706
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Chryseobacterium	0.0195039975247 131	0.08045398978 94417	0.0061760336812 1491	0.0003951355080 40151
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__	0.0208570245951 454	0.08306849450 82516	0.0019361149588 7619	0
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__Pyramidobacter	0.0208570245951 454	0.08306849450 82516	0	0.0024469733143 9855
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio	0.0219532861781 437	0.08595269673 13761	0.0003197866640 16445	0.0054972555861 5802

Table S1B. Relative abundance of the most significant genera in the samples collected in periodontitis sites and healthy sites as assessed by Mann-Whitney U tests with false-discovery-rate correction.

Feature	P value	FDR corrected P value
c6fe05e0eadde34514f9c0114e4e6217k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__	0.00000067439014384661 4	0.00092327293996751 1
bc5ba73185ee3b14bb2d58b32352573dk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Dialister; s__	0.00000101570180414468	0.00092327293996751 1

551afecd8c6458bbc62c7b8c202333d6k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.00000400970689334508	0.00228806082949444
73185b4ea26a363e443916df0e80da85k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__TG5; s__	0.00000918614206296093	0.00228806082949444
c95baa0e17797184c2babd17b5b602fdk__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__; g__; s__	0.00000947382080970403	0.00228806082949444
f872dd32faa2d1ce555803411d38bd04k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__TG5; s__	0.0000096820260747471	0.00228806082949444
d408960aaa7ed992b378f7b989c83352k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__socranskii	0.0000110861296220094	0.00228806082949444
1b84689077164dbfd545d0166414c410k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.0000129923356289357	0.00228806082949444
f37c1e77018a107cdfb67494ad642c71k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.0000132835669621462	0.00228806082949444
83e17f478f7b8555164930da9d203a1bk__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__	0.0000133431793534294	0.00228806082949444
9564ad66d1862a76320e4f0f0611b951k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__socranskii	0.0000138441524336848	0.00228806082949444
cfe787fd73e7e99342f3795b93c8094ek__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.0000171038818620973	0.00259123810210775
76c67adc9e35b61b046958ca9265cb52k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Megasphaera; s__	0.0000217572629266551	0.00304266953851223
e96068176ed806770bce75b445f52bf0k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Dialister; s__	0.0000302888796290739	0.00384817726949115

144f6dc6ca0a9419a0d4441bd06fded6k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.0000317506375370557	0.00384817726949115
13799ebd90b035f0f87a6cfb4b5b9785k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.0000381319770916692	0.0042425011190912
ac8d1d95775840e7164322beaad96fc3k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Schwartzia; s__	0.0000416942741784366	0.0042425011190912
790fe3b27ec763bb3d21d47ab02eca80k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__TG5; s__	0.0000442632153632012	0.0042425011190912
d4787d376913d382877e5f423dc6fcbfk__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__TG5; s__	0.0000443385705515581	0.0042425011190912
4791c48746fd0d53a6252ab17a4bf90fk__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__; g__; s__	0.0000549134353812854	0.00499163127615884
36839726526cc2fd509378431a87de2ek__Bacteria; p__TM7; c__TM7-3; o__I025; f__Rs-045; g__; s__	0.0000615730442498487	0.00533046640220119
2b18cb213d6dc1f56502ae84e29b4587k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__; g__; s__	0.0000765085487379435	0.00632238825479915
5d23c90c9c9e913dbeeb783b3a965744k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.0000911546603150587	0.00720518141099029
a9dbae538a72ec4456d0c44a3311c9c7k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Megasphaera; s__	0.000104728900671664	0.00758945151231151
4a2c4912f078689e3a3f86781668c24bk__Bacteria; p__TM7; c__TM7-3; o__I025; f__Rs-045; g__; s__	0.000107244448240939	0.00758945151231151
2a0cc23acd500009cb08f6e1e585cec5k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacterales; f__Desulfobulbaceae; g__Desulfobulbus; s__	0.000111161089824584	0.00758945151231151
519cc5eed90752b5ec6f4bf826414be9k__Bacteria; p__TM7; c__TM7-3; o__; f__; g__; s__	0.000112714626420468	0.00758945151231151
5a1ce3b38295597fa289c6d4a87dc931k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__rectus	0.000120306407578308	0.00781132317776301

2bbe980ffbf03d99af48e37a96b846d2k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__ ; g__ ; s__	0.000128731287721336	0.00807012003715134
bf52686b796569563cd1101d06a81652k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter; s__rectus	0.000146463719180786	0.00874760141359196
c857267853fcb382f31c347a4cd18779k__Bacteria; p__TM7; c__TM7-3; o__ ; f__ ; g__ ; s__	0.000149161520253768	0.00874760141359196
a8ccf8547a9588b16888ed0c2965372dk__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.000181665400033847	0.010038407749674
9aefcdd447c21a7e8db1289570b0525ak__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfobacteriales; f__Desulfobulbaceae; g__Desulfobulbus; s__	0.000182499703681771	0.010038407749674
f21b8cc7513de3a8858f616d95aa0ef0k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__	0.000187736998618766	0.010038407749674
69356212695e27fe4c2cf626f17d383ek__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Eubacteriaceae; g__Pseudoramibacter_Eubacterium; s__	0.000195668063425801	0.0101635582659459
a329e9b559532fe253c6ec195ad9bae9k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Schwartzia; s__	0.000204925784795082	0.0103487521321517
2b0da9fcb02a4e7e60c5789761a8e43k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	0.000213921317448761	0.010511052841131
ecdd86b0cb840f683461c6bc18db6ddak__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Schwartzia; s__	0.000252949905360099	0.0118945462630402
bf3651ee44868000213c7da680830495k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.000255163533695581	0.0118945462630402
d45149d997d8a052551e26cf9a001017k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Filifactor; s__	0.000265889676595768	0.0120846858012776
9ac732c08f0112c91f65d27aad0d79a8k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Eubacteriaceae; g__Pseudoramibacter_Eubacterium; s__	0.000280867388149132	0.0124540710159786

a054733fa78e1f68418eb5c25bba3f3ck__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolinaceae; g__SHD-231; s__	0.0003016912358484	0.0130589206374379
8e0097c236b4dcfd96c4f15431283011k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolinaceae; g__SHD-231; s__	0.000315110505774773	0.0133225790581055
a49fd8e92bf0c535490f157c5830220dk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Filifactor; s__	0.000342508115434604	0.0141518125877298
5c3bed3239c2712137b24fe8d30f54e3k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; s__	0.000360530712824447	0.0145023034892892
8d0a25543b5540681c5fa5a24b788d2ck__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.000367302319523396	0.0145023034892892
fe83ceb71e65a2e803c46db3f91c40dbk__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; s__	0.000374922037401866	0.0145023034892892
a79e88579e498b17533d0eb3fbc97097k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae	0.00044095899500005	0.0167013219356269
0914f9d58849b13a1b0e58a9a5aedb52k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.000546275022207647	0.0200832315301099
3be1ebe170fe290f25d50b19bd38e5a3k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.00055234410148817	0.0200832315301099
605e49a560632564826705835a96340ek__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Acidaminobacteraceae]; g__; s__	0.000573818328586224	0.0204549357131325
1c76fdf12e1bc025eb1fd181502e26f8k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Ethanolgenens; s__	0.000591805641901514	0.0206904357110952
5cccbe2d225183bcf86c8550bf6e5663k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.000723300540975533	0.0248105732734626

817f2e9e3d43576ce1ef9a949941568bk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Moryella; s__	0.000914380159238831	0.0307841320277073
a8272bacf2c2f52cf6d6671945f3b8b1k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__Mogibacterium; s__	0.000959971963750901	0.0317314369108934
3215553ee75c244878f20d87fac2ecc4k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.00100993022971941	0.0327866635291052
fd1bf824f51935de4165b38b65de449fk__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Olsenella; s__uli	0.00107495521383502	0.0342854136623169
c35f25a0fbe693b2756952031d032a19k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__endodontalis	0.00114102386582525	0.0357651963460398
eb1b52c186280f228ba2ad84174e2375k__Bacteria; p__SR1; c__; o__; f__; g__; s__	0.00117703007848985	0.0362684861473651
7d9a6febbb1e3dbaf757b457b35793c8k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__	0.00129524337337938	0.0392458742133951
cea3087aa1309826968d10332c43cac2k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Slackia; s__	0.00133493631442647	0.0397854790102841
adb88e338556ef8f64fc2274be474a2bk__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas	0.00140078505921287	0.0410746328653064
f6417b4f09f1d0a99a0f7e3b99b633b6k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.00154894107704419	0.0444766367766848
1566fb11e14dfd6eb34380ea013681b8k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__[Paraprevotellaceae]; g__[Prevotella]; s__tannerae	0.0015657341879581	0.0444766367766848
d3ca912e1fa90614ab126ec80ce08bffk__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Olsenella; s__uli	0.00168808453265172	0.0472144258517049
5150194a19241bd02c775d7141db7a3fk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.00177050160418882	0.0487692714608374

cefd913c459ceb525dea51c11fed8410k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__nigrescens	0.00187595297839018	0.0504736793925543
0e186d0679dd22f725dae36e97f1a419k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.0018879043997215	0.0504736793925543
09b40fa2d19acbe34df3ac8ce140197dk__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__endodontalis	0.00195211154532687	0.0514338954986122
cd719f1457b504943146deec30dfa854k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0.00201376394133013	0.052300326361974
daa0a485041ae3854efb3e3504688f04k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	0.00212724557153839	0.0537309372918934
d4a306d7fca5f9e6600812d9885a8bc5k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Schwartzia; s__	0.00212795791255023	0.0537309372918934
5e0c5fa206b7fd068d72d24ea5d3c1f8k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Peptostreptococcus; s__	0.00223194623139672	0.0552842652974155
8aec1d202d5fef48dcec9784f1fdeb61k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Dialister; s__	0.00225029462706752	0.0552842652974155
24b9b343cc35188986de7591182a1e82k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Moryella; s__	0.00236679140379998	0.055828747033421
9fe5a73817c09ab0936b15f4a9a9e754k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Propionibacteriaceae; g__Propionibacterium; s__	0.0024027594952735	0.055828747033421
caf53c77c1727cd43a2d4425aa7e8149k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Tannerella; s__	0.00242161525786669	0.055828747033421
ec6c428af11dff7772e6d9f5e96194dk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.00245965657343451	0.055828747033421
dfe38c58277aea481171bfe846e3c561k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; s__	0.00247716869537676	0.055828747033421

03c934fdf5c5364a7cd07168f0f14d23k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__; s__	0.00248155867595045	0.055828747033421
4f488ca2f85e46a8cb5f1ff6dbcf4acbk__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__	0.00248741942228114	0.055828747033421
df0fd01e72ffe52482b59a99681dfb89k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__	0.00302033204912169	0.0669629715280883
6d338377a30786cb18feca9a0559ee19k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	0.00317538228601869	0.0695523493491804
2bed993692d7a0d8d6b66cd44a260b05k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__nigrescens	0.00322677132494882	0.0698365508185351
e078ee117330ac196ca272bf18b08f8ck__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0.00346824508287025	0.0741796418900955
3a804f03bb646fdbf7e0573543523525k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__	0.00396001607733144	0.0837128980068438
d4418cb8173f9aa6b7728ef28f2d19a0k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0.00418508846226731	0.0874539175218616
65e7acabb644a37d980ca633c1c26e7dk__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Mogibacteriaceae]; g__Mogibacterium; s__	0.00450842840851339	0.0931400323486062
cf2fa22dcc7fb6803c8159d8a1238e4k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__hyovaginalis	0.00474796962279649	0.0935128324097611
70a6351e6aebc07f4687dbd9f6042625k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__[Exiguobacteraceae]; g__; s__	0.00488784208319431	0.0935128324097611
8f966d7ebee98150bcde5873000e1121k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Tannerella; s__	0.00507718686512873	0.0935128324097611
b5d801665b8a57b7ec8e6d692022f21fk__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.00513371591998184	0.0935128324097611

446b8b9418dd980c65b0193e336d7397k__Bacteria; p__Firmicutes; c__Erysipelotrichi; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Sharpea; s__	0.00513958909533904	0.0935128324097611
388a7ccbe8686fab8f272eac3b2fc879k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; s__	0.00513958909533904	0.0935128324097611
430c12c4272206d85e53713539a8acf4k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Selenomonas; s__	0.005142527086965	0.0935128324097611
41225c8338f999f75b73968518653579k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__	0.005142527086965	0.0935128324097611
1392616d0058071c29c79221e0ecdb90k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__	0.005142527086965	0.0935128324097611
73d339dcc87bbf534c6c9c0592422680k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__; g__; s__	0.005142527086965	0.0935128324097611
a6abe48ab079a4d35a15c59017217bd6k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__	0.005142527086965	0.0935128324097611
b59bd58bd9c78ace8f946f119363b459k__Bacteria; p__SR1; c__; o__; f__; g__; s__	0.00514546601452188	0.0935128324097611
a68bacb3b6b8130e0258cb628daee22k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Tannerella; s__	0.00519515735609784	0.0935128324097611
c3d7a43c6666766f50d4962db19f38e7k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Paludibacter; s__	0.00525406572337695	0.0936459949519539
855a533637bcdd353eb10c47cb021d47k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Acidaminobacteraceae]; g__; s__	0.00530968711219886	0.0937185550483256
e8c5d0c8c25d7174965a425152d8ec9bk__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__	0.00547173019039772	0.0951454983462067
a947d19dd35a6557cc57c114c2d88f6dk__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__[Paraprevotellaceae]; g__[Prevotella]; s__tannerae	0.00549520204969841	0.0951454983462067

Table S1C. Relative abundance of the most significant ASV in the samples collected in periodontitis sites and healthy sites as assessed by Mann-Whitney U tests with false-discovery-rate correction.

Feature	P value	FDR corrected P value	mean relative abundance healthy sites
K01885	0.0000000399649528799859	0.000217329225747356	0.000634224634696454
K02493	0.0000000497502187039539	0.000217329225747356	0.000724771164667135
K09141	0.0000000618408116515288	0.000217329225747356	0.00000988783440930178
K16887	0.000000161650784712705	0.000221432691509016	0.00000837155697961101
K00537	0.000000199327343052566	0.000221432691509016	0.000525176425315405
K11180	0.000000199327343052566	0.000221432691509016	0.00000538596040734554
K11181	0.000000199327343052566	0.000221432691509016	0.00000536093232750798
K05772	0.000000245426793896234	0.000221432691509016	0.000042399115942591
K03388	0.000000272183543826178	0.000221432691509016	0.0000513825081518665
K19116	0.000000272183543826178	0.000221432691509016	0.0000268414419934178
K04070	0.000000370451440882709	0.000221432691509016	0.0000982727445737541
K05773	0.000000370451440882709	0.000221432691509016	0.0000309734365091087
K11782	0.000000370451440882709	0.000221432691509016	0.0000316696425131894
K01922	0.000000410239797767579	0.000221432691509016	0.000139914230566253
K05299	0.000000454136099359966	0.000221432691509016	0.0000254651382345501
K06857	0.000000454136099359966	0.000221432691509016	0.0000290082147274849
K11785	0.000000454136099359966	0.000221432691509016	0.0000221902762310504
K05362	0.000000502546242123424	0.000221432691509016	0.000137951425848812
K11784	0.000000502546242123424	0.000221432691509016	0.0000331599923787385
K09740	0.00000055591428809767	0.000221432691509016	0.00000798772987881901
K16885	0.00000055591428809767	0.000221432691509016	0.00000649002179551631

K03686	0.000000614725854433303	0.000221432691509016	0.0008653370528741
K19419	0.000000614725854433303	0.000221432691509016	0.00000688338225919987
K07404	0.000000679511784310068	0.000221432691509016	0.000214231545047507
K08253	0.000000679511784310068	0.000221432691509016	0.00000479068484855994
K00958	0.000000829380406221231	0.000221432691509016	0.0000355150320958098
K01155	0.000000829380406221231	0.000221432691509016	0.000185955825838931
K02236	0.000000829380406221231	0.000221432691509016	0.00016689777433406
K04077	0.000000829380406221231	0.000221432691509016	0.000797226355907243
K06878	0.000000829380406221231	0.000221432691509016	0.000250837750782942
K07714	0.000000829380406221231	0.000221432691509016	0.0000265633925917191
K03739	0.000000915788332803924	0.000221432691509016	0.000160659868611631
K03740	0.000000915788332803924	0.000221432691509016	0.000161027244416888
K18285	0.000000915788332803924	0.000221432691509016	0.0000429322945767112
K02428	0.00000101083076871153	0.000221432691509016	0.000842237230990787
K03465	0.00000101083076871153	0.000221432691509016	0.000120084822140722
K03933	0.00000101083076871153	0.000221432691509016	0.000070902504465135
K07707	0.00000101083076871153	0.000221432691509016	0.000224329528068607
K16886	0.00000101083076871153	0.000221432691509016	0.00000689897428396655
K00687	0.000001115331189493	0.000221432691509016	0.000131178439329202
K16509	0.000001115331189493	0.000221432691509016	0.00037804819251603
K19710	0.000001115331189493	0.000221432691509016	0.0000857734418361348
K00383	0.00000123018754345587	0.000221432691509016	0.000247106088163256
K02440	0.00000123018754345587	0.000221432691509016	0.000460578997131037
K05593	0.00000123018754345587	0.000221432691509016	0.000119687812289722
K07467	0.00000123018754345587	0.000221432691509016	0.000246051773452677

K12556	0.00000123018754345587	0.000221432691509016	0.000129370769158944
K13929	0.00000123018754345587	0.000221432691509016	0.0000705607513162033
K00105	0.00000135637858311105	0.000221432691509016	0.000123944049011046
K02082	0.00000135637858311105	0.000221432691509016	0.000105441729170464
K03697	0.00000135637858311105	0.000221432691509016	0.000125655168874951
K08982	0.00000135637858311105	0.000221432691509016	0.0000290986054794242
K11706	0.00000135637858311105	0.000221432691509016	0.000173865052712788
K13038	0.00000135637858311105	0.000221432691509016	0.000566034037628397
K13932	0.00000135637858311105	0.000221432691509016	0.000070551422586573
K02008	0.00000149497069640244	0.000221432691509016	0.00012413312264324
K02779	0.00000149497069640244	0.000221432691509016	0.000210151016685277
K03346	0.00000149497069640244	0.000221432691509016	0.000155545241516348
K03367	0.00000149497069640244	0.000221432691509016	0.000167386518347016
K03930	0.00000149497069640244	0.000221432691509016	0.00013070266246237
K06198	0.00000149497069640244	0.000221432691509016	0.0001340217136928
K09116	0.00000149497069640244	0.000221432691509016	0.000011465004234231
K13930	0.00000149497069640244	0.000221432691509016	0.0000688822644991053
K13934	0.00000149497069640244	0.000221432691509016	0.0000703352069383497
K14188	0.00000149497069640244	0.000221432691509016	0.000163766911345833
K19115	0.00000149497069640244	0.000221432691509016	0.000030936585683141
K03095	0.00000164712527365909	0.000221432691509016	0.000121767806338998
K07660	0.00000164712527365909	0.000221432691509016	0.0000418933060031735
K10013	0.00000164712527365909	0.000221432691509016	0.0000179433266251694
K13931	0.00000164712527365909	0.000221432691509016	0.0000702239477037776
K15342	0.00000164712527365909	0.000221432691509016	0.000485859262751768

K03825	0.00000181410664848461	0.000221432691509016	0.0000341198303740731
K06990	0.00000181410664848461	0.000221432691509016	0.00004681579704887
K11704	0.00000181410664848461	0.000221432691509016	0.000174969588977242
K12525	0.00000181410664848461	0.000221432691509016	0.0000223299820146314
K18237	0.00000181410664848461	0.000221432691509016	0.0000012342130391443
K00762	0.00000199729065319521	0.000221432691509016	0.000710986907146674
K01484	0.00000199729065319521	0.000221432691509016	0.0000507888826998622
K02819	0.00000199729065319521	0.000221432691509016	0.000181366184723605
K03389	0.00000199729065319521	0.000221432691509016	0.0000362234729353292
K03564	0.00000199729065319521	0.000221432691509016	0.000417682317216159
K06286	0.00000199729065319521	0.000221432691509016	0.000141696387831016
K07533	0.00000199729065319521	0.000221432691509016	0.000262179955413911
K13935	0.00000199729065319521	0.000221432691509016	0.0000616178217408233
K15723	0.00000199729065319521	0.000221432691509016	0.0000221212956593237
K19005	0.00000199729065319521	0.000221432691509016	0.000173951700630612
K00395	0.00000219817383193646	0.000221432691509016	0.0000218333752598138
K00486	0.00000219817383193646	0.000221432691509016	0.0000113240452980504
K00800	0.00000219817383193646	0.000221432691509016	0.000712836635130302
K01215	0.00000219817383193646	0.000221432691509016	0.000153412927819654
K03184	0.00000219817383193646	0.000221432691509016	0.0000319562390178917
K03531	0.00000219817383193646	0.000221432691509016	0.000753254546414493
K07136	0.00000219817383193646	0.000221432691509016	0.0000422606081954548
K07146	0.00000219817383193646	0.000221432691509016	0.000272500127677366
K07345	0.00000219817383193646	0.000221432691509016	0.0000526643309434323
K11085	0.00000219817383193646	0.000221432691509016	0.000454525192367247

K01261	0.00000241838335725486	0.000221432691509016	0.000140204738454209
K01844	0.00000241838335725486	0.000221432691509016	0.0000646222545065438
K02086	0.00000241838335725486	0.000221432691509016	0.000143669586285372
K05910	0.00000241838335725486	0.000221432691509016	0.0000660184919838832
K07070	0.00000241838335725486	0.000221432691509016	0.0000318380543479259
K07706	0.00000241838335725486	0.000221432691509016	0.000203367977421999
K12293	0.00000241838335725486	0.000221432691509016	0.0000456787060642847
K13057	0.00000241838335725486	0.000221432691509016	0.0000338236503877647
K16169	0.00000241838335725486	0.000221432691509016	0.000139598652582366
K16693	0.00000241838335725486	0.000221432691509016	0.00000605614942943825
K18011	0.00000241838335725486	0.000221432691509016	0.0000646927101520438
K10461	0.00000265822105024469	0.000221432691509016	0.0000000619148521904013
K00864	0.00000265968769867704	0.000221432691509016	0.000527740032125822
K01146	0.00000265968769867704	0.000221432691509016	0.0000210663748555657
K02248	0.00000265968769867704	0.000221432691509016	0.0000950209182044395
K02853	0.00000265968769867704	0.000221432691509016	0.00000581160401234306
K03761	0.00000265968769867704	0.000221432691509016	0.0000631019930908956
K05368	0.00000265968769867704	0.000221432691509016	0.0000210667026246272
K06169	0.00000265968769867704	0.000221432691509016	0.0000428975647412542
K06858	0.00000265968769867704	0.000221432691509016	0.0000281048541657316
K08351	0.00000265968769867704	0.000221432691509016	0.0000184561590858417
K12292	0.00000265968769867704	0.000221432691509016	0.0000488083430507733
K12582	0.00000265968769867704	0.000221432691509016	0.00000581008052617097
K12961	0.00000265968769867704	0.000221432691509016	0.0000210664027534748
K17999	0.0000029224084863488	0.000221432691509016	0.000000372880151436163

K00394	0.00000292400809476094	0.000221432691509016	0.0000224924263697255
K01598	0.00000292400809476094	0.000221432691509016	0.000146102660748014
K02043	0.00000292400809476094	0.000221432691509016	0.0000275542987424163
K02859	0.00000292400809476094	0.000221432691509016	0.0000488559787078402
K03390	0.00000292400809476094	0.000221432691509016	0.0000388969436833685
K03713	0.00000292400809476094	0.000221432691509016	0.000143704207602345
K03807	0.00000292400809476094	0.000221432691509016	0.0000270860008519012
K05827	0.00000292400809476094	0.000221432691509016	0.0000140197716273457
K06168	0.00000292400809476094	0.000221432691509016	0.000574167759307935
K08352	0.00000292400809476094	0.000221432691509016	0.000024028993465286
K08994	0.00000292400809476094	0.000221432691509016	0.000113220757999262
K09976	0.00000292400809476094	0.000221432691509016	0.000147116715544744
K11391	0.00000292400809476094	0.000221432691509016	0.00002085283963972
K11617	0.00000292400809476094	0.000221432691509016	0.000143375308480172
K18692	0.00000292400809476094	0.000221432691509016	0.000146102974227502
K18891	0.00000292400809476094	0.000221432691509016	0.0000949190201370871
K18892	0.00000292400809476094	0.000221432691509016	0.0000948983112071306
K19049	0.00000292400809476094	0.000221432691509016	0.000021853925658448
K00138	0.00000321343088313378	0.000221432691509016	0.0000919247955116601
K00158	0.00000321343088313378	0.000221432691509016	0.000108699817415545
K01892	0.00000321343088313378	0.000221432691509016	0.000749977430425447
K02006	0.00000321343088313378	0.000221432691509016	0.000130217065588193
K02243	0.00000321343088313378	0.000221432691509016	0.000145876168854405
K03472	0.00000321343088313378	0.000221432691509016	0.0000317800142013612
K09916	0.00000321343088313378	0.000221432691509016	0.0000313859008381164

K12308	0.00000321343088313378	0.000221432691509016	0.000374547261125537
K14982	0.00000321343088313378	0.000221432691509016	0.00011431090516968
K16869	0.00000321343088313378	0.000221432691509016	0.0000808234232535075
K17759	0.00000321343088313378	0.000221432691509016	0.000352466081458749
K18014	0.00000321343088313378	0.000221432691509016	0.0000757838530340061
K18954	0.00000321343088313378	0.000221432691509016	0.0000553322730329956
K19000	0.00000321343088313378	0.000221432691509016	0.0000224867475146454
K00452	0.0000035302207462238	0.000228338143113114	0.0000121020123445711
K01482	0.0000035302207462238	0.000228338143113114	0.0000209455030132888
K02244	0.0000035302207462238	0.000228338143113114	0.000156320856777631
K04485	0.0000035302207462238	0.000228338143113114	0.000750338651229583
K06447	0.0000035302207462238	0.000228338143113114	0.0000708742341944725
K07012	0.0000035302207462238	0.000228338143113114	0.000319549999610333
K11705	0.0000035302207462238	0.000228338143113114	0.000169820370595564
K12555	0.0000035302207462238	0.000228338143113114	0.000143621963506434
K13938	0.0000035302207462238	0.000228338143113114	0.0000307461039037346
K14983	0.0000035302207462238	0.000228338143113114	0.000134216478985991
K00839	0.00000387683493373189	0.000230104409659428	0.0000349136931858627
K01678	0.00000387683493373189	0.000230104409659428	0.000119552688881619
K01825	0.00000387683493373189	0.000230104409659428	0.0000313711025563649
K01883	0.00000387683493373189	0.000230104409659428	0.000739925987241459
K02245	0.00000387683493373189	0.000230104409659428	0.000139760919804379
K02362	0.00000387683493373189	0.000230104409659428	0.0000297775104890175
K02761	0.00000387683493373189	0.000230104409659428	0.000799576012789424
K03525	0.00000387683493373189	0.000230104409659428	0.000353255625987404

K07225	0.00000387683493373189	0.000230104409659428	0.0000253165377280844
K07570	0.00000387683493373189	0.000230104409659428	0.000147598433040097
K07637	0.00000387683493373189	0.000230104409659428	0.0000409814089119894
K09984	0.00000387683493373189	0.000230104409659428	0.0000334466329326113
K11473	0.00000387683493373189	0.000230104409659428	0.0000704515735593315
K00563	0.0000042559385263766	0.000230104409659428	0.000195169200086045
K01590	0.0000042559385263766	0.000230104409659428	0.0000118251037873293
K01868	0.0000042559385263766	0.000230104409659428	0.000740108742467166
K02240	0.0000042559385263766	0.000230104409659428	0.000147126805436559
K03664	0.0000042559385263766	0.000230104409659428	0.000726770495075672
K03693	0.0000042559385263766	0.000230104409659428	0.000143848403086787
K05340	0.0000042559385263766	0.000230104409659428	0.000154956380461052
K05812	0.0000042559385263766	0.000230104409659428	0.0000359156963784232
K06222	0.0000042559385263766	0.000230104409659428	0.0000389152432912445
K07284	0.0000042559385263766	0.000230104409659428	0.000787193089330358
K07577	0.0000042559385263766	0.000230104409659428	0.0000539912766740487
K07740	0.0000042559385263766	0.000230104409659428	0.0000302507571245606
K09945	0.0000042559385263766	0.000230104409659428	0.0000193831625631935
K11144	0.0000042559385263766	0.000230104409659428	0.00015289548992259
K14287	0.0000042559385263766	0.000230104409659428	0.000061544371058561
K17737	0.0000042559385263766	0.000230104409659428	0.0000147261729241386
K18888	0.0000042559385263766	0.000230104409659428	0.000090988227547257
K19050	0.0000042559385263766	0.000230104409659428	0.0000095925114380838
K19135	0.0000042559385263766	0.000230104409659428	0.00000210421542710367
K03278	0.00000467042080908701	0.00024137375779512	0.00000133080184589096

K05526	0.00000467042080908701	0.00024137375779512	0.0000345323114594561
K05979	0.00000467042080908701	0.00024137375779512	0.0000846532356428955
K07777	0.00000467042080908701	0.00024137375779512	0.000030090793891745
K08317	0.00000467042080908701	0.00024137375779512	0.0000791871233568476
K09024	0.00000467042080908701	0.00024137375779512	0.0000386054854378461
K09458	0.00000467042080908701	0.00024137375779512	0.000874742083693158
K09918	0.00000467042080908701	0.00024137375779512	0.0000300340568515956
K18887	0.00000467042080908701	0.00024137375779512	0.0000910361856641152
K03566	0.00000512341282561339	0.000254793119907745	0.00023786938508113
K05836	0.00000512341282561339	0.000254793119907745	0.0000911633268122536
K07251	0.00000512341282561339	0.000254793119907745	0.0000180143391291408
K09778	0.00000512341282561339	0.000254793119907745	0.0000536414495927658
K09959	0.00000512341282561339	0.000254793119907745	0.0000485352173610371
K18012	0.00000512341282561339	0.000254793119907745	0.0000698947395589224
K18013	0.00000512341282561339	0.000254793119907745	0.0000648812845512964
K19114	0.00000512341282561339	0.000254793119907745	0.0000206165416847346
K00793	0.00000561830619048016	0.0002586628915556	0.000544024528336537
K00842	0.00000561830619048016	0.0002586628915556	0.000033485549471243
K00867	0.00000561830619048016	0.0002586628915556	0.000297622963503846
K00892	0.00000561830619048016	0.0002586628915556	0.0000215710158805016
K02007	0.00000561830619048016	0.0002586628915556	0.000131508072620668
K02509	0.00000561830619048016	0.0002586628915556	0.0000441812444912146
K03046	0.00000561830619048016	0.0002586628915556	0.000748284310219433
K04064	0.00000561830619048016	0.0002586628915556	0.0000132309909810626
K05826	0.00000561830619048016	0.0002586628915556	0.0000123348327892269

K05828	0.00000561830619048016	0.0002586628915556	0.0000123664721942235
K05829	0.00000561830619048016	0.0002586628915556	0.0000123210061616346
K07075	0.00000561830619048016	0.0002586628915556	0.000236625385341313
K07497	0.00000561830619048016	0.0002586628915556	0.000865151746566149
K07652	0.00000561830619048016	0.0002586628915556	0.000155403393768606
K11358	0.00000561830619048016	0.0002586628915556	0.0000831927961125175
K15536	0.00000561830619048016	0.0002586628915556	0.0000216591858331036
K15726	0.00000561830619048016	0.0002586628915556	0.000272120079471343
K00566	0.00000615877323832001	0.000265028352047379	0.000805202678464795
K00794	0.00000615877323832001	0.000265028352047379	0.000550621694380596
K01159	0.00000615877323832001	0.000265028352047379	0.000565675691146629
K01715	0.00000615877323832001	0.000265028352047379	0.000162265385963479
K03119	0.00000615877323832001	0.000265028352047379	0.0001072157053571
K03738	0.00000615877323832001	0.000265028352047379	0.000087007237700443
K04952	0.00000615877323832001	0.000265028352047379	0.000000547801071839679
K07082	0.00000615877323832001	0.000265028352047379	0.000722951068502611
K07498	0.00000615877323832001	0.000265028352047379	0.000514791335323759
K07709	0.00000615877323832001	0.000265028352047379	0.0000179377953769682
K08995	0.00000615877323832001	0.000265028352047379	0.0000529002997967185
K11208	0.00000615877323832001	0.000265028352047379	0.0000106769954158175
K11741	0.00000615877323832001	0.000265028352047379	0.000189808905035565
K12983	0.00000615877323832001	0.000265028352047379	0.00000584331108482591
K13626	0.00000615877323832001	0.000265028352047379	0.000101117334590232
K18824	0.00000615877323832001	0.000265028352047379	0.00000442411567964187
K01118	0.00000674878859490549	0.000279029326102308	0.000300820151128754

K02356	0.00000674878859490549	0.000279029326102308	0.000753620536916892
K03381	0.00000674878859490549	0.000279029326102308	0.0000716796241881149
K03470	0.00000674878859490549	0.000279029326102308	0.000735955927621513
K03488	0.00000674878859490549	0.000279029326102308	0.000439989769848326
K09143	0.00000674878859490549	0.000279029326102308	0.0000102397004713271
K10040	0.00000674878859490549	0.000279029326102308	0.000281918976343094
K14127	0.00000674878859490549	0.000279029326102308	0.00000971767413503127
K16850	0.00000674878859490549	0.000279029326102308	0.0000217669755046713
K19776	0.00000674878859490549	0.000279029326102308	0.00000688905021521602
K00117	0.00000739265225863569	0.000287604179936517	0.0000710305520430623
K00673	0.00000739265225863569	0.000287604179936517	0.0000871629007011518
K01338	0.00000739265225863569	0.000287604179936517	0.000656068073552144
K01923	0.00000739265225863569	0.000287604179936517	0.000741141114062021
K02996	0.00000739265225863569	0.000287604179936517	0.000731852264182725
K03330	0.00000739265225863569	0.000287604179936517	0.00000292340283777933
K03812	0.00000739265225863569	0.000287604179936517	0.0000236896417405213
K04080	0.00000739265225863569	0.000287604179936517	0.00008400772992976
K06183	0.00000739265225863569	0.000287604179936517	0.000515588804212296
K06445	0.00000739265225863569	0.000287604179936517	0.0000477843873381176
K07277	0.00000739265225863569	0.000287604179936517	0.000464461828981235
K07483	0.00000739265225863569	0.000287604179936517	0.00117728829491248
K10039	0.00000739265225863569	0.000287604179936517	0.00014106461271107
K11935	0.00000739265225863569	0.000287604179936517	0.0000149432792662228
K13479	0.00000739265225863569	0.000287604179936517	0.0000391624952788118
K16704	0.00000739265225863569	0.000287604179936517	0.00000642752987733899

K00564	0.00000809501428584255	0.00030372147905921	0.000278950296074834
K00887	0.00000809501428584255	0.00030372147905921	0.000181770280046699
K01826	0.00000809501428584255	0.00030372147905921	0.0000407231502447601
K03086	0.00000809501428584255	0.00030372147905921	0.000952123092120031
K05549	0.00000809501428584255	0.00030372147905921	0.0000293245848464961
K06981	0.00000809501428584255	0.00030372147905921	0.00000173385359305205
K08993	0.00000809501428584255	0.00030372147905921	0.0000230399952196327
K09482	0.00000809501428584255	0.00030372147905921	0.00000290692360118262
K10014	0.00000809501428584255	0.00030372147905921	0.0000279139259242503
K11535	0.00000809501428584255	0.00030372147905921	0.0000598846400703464
K02281	0.00000886090117805434	0.000312443080669655	0.00002764785522113
K02798	0.00000886090117805434	0.000312443080669655	0.000175208877933834
K02906	0.00000886090117805434	0.000312443080669655	0.000719067348104738
K03826	0.00000886090117805434	0.000312443080669655	0.000135996064628144
K07080	0.00000886090117805434	0.000312443080669655	0.000229547745296157
K07348	0.00000886090117805434	0.000312443080669655	0.00000712847177618927
K07702	0.00000886090117805434	0.000312443080669655	0.0000117034671624246
K07713	0.00000886090117805434	0.000312443080669655	0.0000729203691661377
K07803	0.00000886090117805434	0.000312443080669655	0.0000161799759901081
K09122	0.00000886090117805434	0.000312443080669655	0.0000107597583998055
K10041	0.00000886090117805434	0.000312443080669655	0.000139977091514839
K11618	0.00000886090117805434	0.000312443080669655	0.000150427346177727
K12952	0.00000886090117805434	0.000312443080669655	0.00030561044205032
K13638	0.00000886090117805434	0.000312443080669655	0.0000265925327391067
K14056	0.00000886090117805434	0.000312443080669655	0.0000133375782906298

K16511	0.00000886090117805434	0.000312443080669655	0.000163716321489529
K18581	0.00000886090117805434	0.000312443080669655	0.000159666811482601
K18765	0.00000886090117805434	0.000312443080669655	0.0000188476627054137
K01223	0.00000969574407429318	0.000326588593531224	0.00100954108253861
K01631	0.00000969574407429318	0.000326588593531224	0.0000475388884566752
K01729	0.00000969574407429318	0.000326588593531224	0.0000184143999556845
K01756	0.00000969574407429318	0.000326588593531224	0.00075345791749239
K02469	0.00000969574407429318	0.000326588593531224	0.000817990006787293
K03543	0.00000969574407429318	0.000326588593531224	0.000290909529772215
K06928	0.00000969574407429318	0.000326588593531224	0.00000946213946487025
K07013	0.00000969574407429318	0.000326588593531224	0.0000123491943233929
K07464	0.00000969574407429318	0.000326588593531224	0.000231378166999526
K09018	0.00000969574407429318	0.000326588593531224	0.0000295013678104104
K13633	0.00000969574407429318	0.000326588593531224	0.0000118985456843768
K14260	0.00000969574407429318	0.000326588593531224	0.000242077137098231
K16079	0.00000969574407429318	0.000326588593531224	0.0000664416301506332
K16849	0.00000969574407429318	0.000326588593531224	0.0000196014185990979
K00150	0.0000106054088565888	0.000331788799925862	0.0000217162476456483
K01730	0.0000106054088565888	0.000331788799925862	0.0000149626204911278
K01929	0.0000106054088565888	0.000331788799925862	0.000738261283936431
K02066	0.0000106054088565888	0.000331788799925862	0.000438238177227368
K02167	0.0000106054088565888	0.000331788799925862	0.0000263718529299944
K02340	0.0000106054088565888	0.000331788799925862	0.000715836249567066
K02345	0.0000106054088565888	0.000331788799925862	0.0000169214573671261
K02933	0.0000106054088565888	0.000331788799925862	0.000719656792412375

K03489	0.0000106054088565888	0.000331788799925862	0.0000111775407914602
K03863	0.0000106054088565888	0.000331788799925862	0.000069098014409675
K05830	0.0000106054088565888	0.000331788799925862	0.0000111645857108933
K05831	0.0000106054088565888	0.000331788799925862	0.0000112614186895884
K06191	0.0000106054088565888	0.000331788799925862	0.000217418371114052
K07104	0.0000106054088565888	0.000331788799925862	0.000176885083654664
K07639	0.0000106054088565888	0.000331788799925862	0.0000281783492488851
K07823	0.0000106054088565888	0.000331788799925862	0.000015935795742911
K08219	0.0000106054088565888	0.000331788799925862	0.00000634089504204356
K09958	0.0000106054088565888	0.000331788799925862	0.0000521820277122363
K13069	0.0000106054088565888	0.000331788799925862	0.0000297022070892575
K13819	0.0000106054088565888	0.000331788799925862	0.0000341554188689528
K13933	0.0000106054088565888	0.000331788799925862	0.0000336814679026749
K14128	0.0000106054088565888	0.000331788799925862	0.0000100475017318177
K19267	0.0000106054088565888	0.000331788799925862	0.000197020939364253
K19788	0.0000106054088565888	0.000331788799925862	0.00000000141073816169145
K00441	0.0000115962282821611	0.000344391647264295	0.000012017021573745
K01244	0.0000115962282821611	0.000344391647264295	0.000000861537350084845
K01467	0.0000115962282821611	0.000344391647264295	0.000110831028637443
K01783	0.0000115962282821611	0.000344391647264295	0.000774608915890132
K02226	0.0000115962282821611	0.000344391647264295	0.000398869978836124
K02234	0.0000115962282821611	0.000344391647264295	0.0000453836994079536
K02470	0.0000115962282821611	0.000344391647264295	0.000824168098984171
K03491	0.0000115962282821611	0.000344391647264295	0.000273570626937153
K05515	0.0000115962282821611	0.000344391647264295	0.00055562371977983

K05550	0.0000115962282821611	0.000344391647264295	0.0000292785600193415
K06320	0.0000115962282821611	0.000344391647264295	0.0000324471978265274
K07303	0.0000115962282821611	0.000344391647264295	0.0000991707986035795
K07336	0.0000115962282821611	0.000344391647264295	0.0000497952601201465
K07469	0.0000115962282821611	0.000344391647264295	0.0000213089101043945
K07576	0.0000115962282821611	0.000344391647264295	0.000141449890845972
K09797	0.0000115962282821611	0.000344391647264295	0.000111452977697599
K09880	0.0000115962282821611	0.000344391647264295	0.0000213881067886734
K13016	0.0000115962282821611	0.000344391647264295	0.0000353772788853416
K00952	0.0000126689588526414	0.000363132900275518	0.00000153827610320855
K02233	0.0000126750362611582	0.000363132900275518	0.000354818599523611
K02297	0.0000126750362611582	0.000363132900275518	0.0000796108064866804
K02298	0.0000126750362611582	0.000363132900275518	0.0000795113059954364
K02931	0.0000126750362611582	0.000363132900275518	0.00072000788834864
K03328	0.0000126750362611582	0.000363132900275518	0.000264130825705993
K05359	0.0000126750362611582	0.000363132900275518	0.00000107021985813402
K09912	0.0000126750362611582	0.000363132900275518	0.0000314403481074507
K09948	0.0000126750362611582	0.000363132900275518	0.0000375527799885784
K10017	0.0000126750362611582	0.000363132900275518	0.0000244136585180085
K10775	0.0000126750362611582	0.000363132900275518	0.00000372750679556838
K11209	0.0000126750362611582	0.000363132900275518	0.000160860995637521
K18149	0.0000126750362611582	0.000363132900275518	0.0000847947285074745
K00932	0.0000138492044044299	0.000379252368924427	0.00000889499234709152
K01007	0.0000138492044044299	0.000379252368924427	0.000251464165385389
K01071	0.0000138492044044299	0.000379252368924427	0.000153444919621026

K01807	0.0000138492044044299	0.000379252368924427	0.000353993438504064
K01838	0.0000138492044044299	0.000379252368924427	0.000224056267898532
K02224	0.0000138492044044299	0.000379252368924427	0.000308172205312487
K02994	0.0000138492044044299	0.000379252368924427	0.000720527000171368
K03112	0.0000138492044044299	0.000379252368924427	0.0000262923041804544
K03919	0.0000138492044044299	0.000379252368924427	0.000033225962554988
K06603	0.0000138492044044299	0.000379252368924427	0.0000858648792964261
K07092	0.0000138492044044299	0.000379252368924427	0.00000329072965352635
K07350	0.0000138492044044299	0.000379252368924427	0.00000855467864925211
K09129	0.0000138492044044299	0.000379252368924427	0.0000236281979023169
K09920	0.0000138492044044299	0.000379252368924427	0.0000399774393033405
K11735	0.0000138492044044299	0.000379252368924427	0.0000534345626715744
K13583	0.0000138492044044299	0.000379252368924427	0.0000364707920856086
K18231	0.0000138492044044299	0.000379252368924427	0.0000543484971327194
K00123	0.0000151266809715721	0.000388030650810912	0.000387653898657604
K00840	0.0000151266809715721	0.000388030650810912	0.0000120184145330233
K01575	0.0000151266809715721	0.000388030650810912	0.000184374588637368
K01912	0.0000151266809715721	0.000388030650810912	0.000252653586557174
K02617	0.0000151266809715721	0.000388030650810912	0.0000123978396779613
K02623	0.0000151266809715721	0.000388030650810912	0.0000200428122948719
K03519	0.0000151266809715721	0.000388030650810912	0.0000720693697350265
K03569	0.0000151266809715721	0.000388030650810912	0.000681405966663967
K04069	0.0000151266809715721	0.000388030650810912	0.00081655485521012
K04078	0.0000151266809715721	0.000388030650810912	0.000748691276548971
K06208	0.0000151266809715721	0.000388030650810912	0.0000664820131041233

K07156	0.0000151266809715721	0.000388030650810912	0.0000845262770334356
K08170	0.0000151266809715721	0.000388030650810912	0.0000103562447262294
K08348	0.0000151266809715721	0.000388030650810912	0.0000152112131136482
K08484	0.0000151266809715721	0.000388030650810912	0.0000578057696616347
K10015	0.0000151266809715721	0.000388030650810912	0.0000261151480747806
K11178	0.0000151266809715721	0.000388030650810912	0.0000675693094660973
K12972	0.0000151266809715721	0.000388030650810912	0.0000805969894398574
K12973	0.0000151266809715721	0.000388030650810912	0.0000138690983744098
K13255	0.0000151266809715721	0.000388030650810912	0.0000156903463683582
K14052	0.0000151266809715721	0.000388030650810912	0.0000053224457134097
K15727	0.0000151266809715721	0.000388030650810912	0.000203808962515939
K17754	0.0000151266809715721	0.000388030650810912	0.00000255918166992185
K18456	0.0000151266809715721	0.000388030650810912	0.0000108859302545805
K19165	0.0000151266809715721	0.000388030650810912	0.000016230144846067
K19775	0.0000151266809715721	0.000388030650810912	0.00000680304357120389
K02499	0.00001651603235538	0.000407795150170425	0.00016150781774891
K04061	0.00001651603235538	0.000407795150170425	0.000117309490298274
K05790	0.00001651603235538	0.000407795150170425	0.00000583258338506558
K07110	0.00001651603235538	0.000407795150170425	0.0000764806906863028
K07460	0.00001651603235538	0.000407795150170425	0.000582210624095478
K13483	0.00001651603235538	0.000407795150170425	0.0000608236598444248
K14057	0.00001651603235538	0.000407795150170425	0.00000440070555995493
K14126	0.00001651603235538	0.000407795150170425	0.00000937125115721473
K15011	0.00001651603235538	0.000407795150170425	0.0000640598319333635
K15012	0.00001651603235538	0.000407795150170425	0.0000693286230028852

K15540	0.00001651603235538	0.000407795150170425	0.0000199718231482291
K16149	0.00001651603235538	0.000407795150170425	0.0000443203180289876
K17870	0.00001651603235538	0.000407795150170425	0.00000875453021234548
K17992	0.00001651603235538	0.000407795150170425	0.0000371355497339552
K18335	0.00001651603235538	0.000407795150170425	0.0000334272133410127
K18551	0.00001651603235538	0.000407795150170425	0.000000856733009043173
K00177	0.0000180264872449071	0.000420471803148352	0.00026172417951662
K00442	0.0000180264872449071	0.000420471803148352	0.00000335879534561359
K00691	0.0000180264872449071	0.000420471803148352	0.000152636824356979
K00927	0.0000180264872449071	0.000420471803148352	0.000738797166490075
K01453	0.0000180264872449071	0.000420471803148352	0.0000350370477514483
K02246	0.0000180264872449071	0.000420471803148352	0.000108062104888173
K02863	0.0000180264872449071	0.000420471803148352	0.000710247144803156
K03518	0.0000180264872449071	0.000420471803148352	0.0002223819881757
K05358	0.0000180264872449071	0.000420471803148352	0.0000233823610641466
K05804	0.0000180264872449071	0.000420471803148352	0.0000135155516136618
K05835	0.0000180264872449071	0.000420471803148352	0.00000658892179607379
K06898	0.0000180264872449071	0.000420471803148352	0.000127998190379845
K07391	0.0000180264872449071	0.000420471803148352	0.000614311273511779
K07689	0.0000180264872449071	0.000420471803148352	0.0000254222182504167
K08350	0.0000180264872449071	0.000420471803148352	0.00000687773337385296
K09457	0.0000180264872449071	0.000420471803148352	0.000290092355019761
K09965	0.0000180264872449071	0.000420471803148352	0.0000277184696210493
K10530	0.0000180264872449071	0.000420471803148352	0.0000539939061731264
K11752	0.0000180264872449071	0.000420471803148352	0.000544794216096077

K13979	0.0000180264872449071	0.000420471803148352	0.000121774676275249
K13993	0.0000180264872449071	0.000420471803148352	0.000394834968556199
K16845	0.0000180264872449071	0.000420471803148352	0.00000409868694610295
K17329	0.0000180264872449071	0.000420471803148352	0.0000136486982179722
K18007	0.0000180264872449071	0.000420471803148352	0.0000153670278209028
K18023	0.0000180264872449071	0.000420471803148352	0.00000924223962943736
K13048	0.0000196589501226216	0.000435629309366497	0.000000117008755371978
K16956	0.0000196589501226216	0.000435629309366497	0.0000000737745477249731
K00176	0.0000196679836155224	0.000435629309366497	0.000223608416557795
K01775	0.0000196679836155224	0.000435629309366497	0.000837065443941745
K02300	0.0000196679836155224	0.000435629309366497	0.0000780026098263392
K02956	0.0000196679836155224	0.000435629309366497	0.000710133899974932
K02982	0.0000196679836155224	0.000435629309366497	0.000720126337775033
K04720	0.0000196679836155224	0.000435629309366497	0.000277599364037432
K05587	0.0000196679836155224	0.000435629309366497	0.00000396115886357909
K06876	0.0000196679836155224	0.000435629309366497	0.000064363357227882
K07458	0.0000196679836155224	0.000435629309366497	0.000128867375263827
K07644	0.0000196679836155224	0.000435629309366497	0.0000795185414890839
K07739	0.0000196679836155224	0.000435629309366497	0.00000842862897279458
K10748	0.0000196679836155224	0.000435629309366497	0.0000162411940344081
K11041	0.0000196679836155224	0.000435629309366497	0.000100454446813508
K11811	0.0000196679836155224	0.000435629309366497	0.0000311217429191637
K13060	0.0000196679836155224	0.000435629309366497	0.0000286657199208909
K15532	0.0000196679836155224	0.000435629309366497	0.000172093896620253
K15780	0.0000196679836155224	0.000435629309366497	0.0000779018929100923

K16846	0.0000196679836155224	0.000435629309366497	0.00000367677986059957
K17240	0.0000196679836155224	0.000435629309366497	0.00000741222339700479
K18299	0.0000196679836155224	0.000435629309366497	0.00000921142364555291
K18932	0.0000196679836155224	0.000435629309366497	0.00000000384988425045645
K19714	0.0000196679836155224	0.000435629309366497	0.0000078206710054425
K19737	0.0000214414515912223	0.000446956914548294	0.00000000637949509570311
K00174	0.0000214512187006959	0.000446956914548294	0.000446048194045338
K00215	0.0000214512187006959	0.000446956914548294	0.000714135206113125
K00500	0.0000214512187006959	0.000446956914548294	0.0000672973770802796
K00627	0.0000214512187006959	0.000446956914548294	0.000518089766260736
K00694	0.0000214512187006959	0.000446956914548294	0.0000984811172832143
K00891	0.0000214512187006959	0.000446956914548294	0.000704633038525815
K01358	0.0000214512187006959	0.000446956914548294	0.000907768963529624
K01829	0.0000214512187006959	0.000446956914548294	0.0000286973914765697
K01950	0.0000214512187006959	0.000446956914548294	0.000356264566422878
K02225	0.0000214512187006959	0.000446956914548294	0.0000474246778649206
K02385	0.0000214512187006959	0.000446956914548294	0.0000896946329119102
K02600	0.0000214512187006959	0.000446956914548294	0.000749668799301328
K03647	0.0000214512187006959	0.000446956914548294	0.000236433825338674
K05800	0.0000214512187006959	0.000446956914548294	0.000119171252084568
K05919	0.0000214512187006959	0.000446956914548294	0.000186100237417565
K06937	0.0000214512187006959	0.000446956914548294	0.0000326594124072282
K07065	0.0000214512187006959	0.000446956914548294	0.0000184682464292047
K07217	0.0000214512187006959	0.000446956914548294	0.00008970838127682
K07233	0.0000214512187006959	0.000446956914548294	0.0000519846909634965

K07477	0.0000214512187006959	0.000446956914548294	0.00000502905275253772
K07506	0.0000214512187006959	0.000446956914548294	0.0000967298625243613
K07700	0.0000214512187006959	0.000446956914548294	0.0000120648699085585
K09951	0.0000214512187006959	0.000446956914548294	0.000532204794476112

Table S1D. Relative abundance of the most significant KEGG metabolic pathways in the samples collected in periodontitis sites and healthy sites as assessed by Mann-Whitney U tests with false-discovery-rate correction.

Feature	Feature	P value	FDR corrected P value	mean relative abundance healthy sites	mean relative abundance diseased sites
reductive acetyl coenzyme A pathway	CODH-PWY	0.0000002212196270 49992	0.000065736864567 5495	0.000494926518447 968	0.001350693672150 16
1,4-dihydroxy-6-naphthoate biosynthesis I	PWY-7374	0.0000003017472761 84077	0.000065736864567 5495	0.000134879291272 032	0.000400221748031 889
superpathway of menaquinol-8 biosynthesis II	PWY-6263	0.0000005025462421 23424	0.000065736864567 5495	0.000674538621947 707	0.001669745111229 18
1,4-dihydroxy-6-naphthoate biosynthesis II	PWY-7371	0.0000005559142880 9767	0.000065736864567 5495	0.000291510171363 232	0.000796956753344 786
peptidoglycan biosynthesis IV (Enterococcus faecium)	PWY-6471	0.0000035302207462 238	0.000203749213739 465	0.003535550120348 55	0.002062847677681 24
L-arginine degradation II (AST pathway)	AST-PWY	0.0000038768349337 3189	0.000203749213739 465	0.000368631543101 274	0.000047653540455 56
NAD biosynthesis II (from tryptophan)	NADSYN-PWY	0.0000038768349337 3189	0.000203749213739 465	0.000274024987771 599	0.000054805736821 6869

incomplete reductive TCA cycle	P42-PWY	0.0000038768349337 3189	0.000203749213739 465	0.005331603452304 98	0.006524192416652 13
L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde	PWY-5651	0.0000038768349337 3189	0.000203749213739 465	0.000181033735836 268	0.000034518417660 6504
superpathway of demethylmenaquinol-6 biosynthesis II	PWY-7373	0.0000051234128256 1339	0.000242337426651 513	0.000161722777380 462	0.000472951615195 553
peptidoglycan biosynthesis V (β-lactam resistance)	PWY-6470	0.0000067487885949 0549	0.000268978809102 668	0.002181479521691 14	0.001029974210554 83
L-methionine salvage cycle I (bacteria and plants)	PWY-7528	0.0000073926522586 3569	0.000268978809102 668	6.94805810427789 E-06	0.000033947041590 1102
superpathway of thiamin diphosphate biosynthesis I	THISYN-PWY	0.0000073926522586 3569	0.000268978809102 668	0.003642901451803 92	0.004678175277005 94
L-lysine fermentation to acetate and butanoate	P163-PWY	0.0000080950142858 4255	0.000273495839800 252	0.001116284247366 02	0.002607149007282 7
pyrimidine deoxyribonucleotides de novo biosynthesis III	PWY-6545	0.0000096957440742 9318	0.000288685051445 38	0.002396034297873 42	0.003451529141881 92
L-glutamate degradation V (via hydroxyglutarate)	P162-PWY	0.0000106054088565 888	0.000288685051445 38	0.001184128832841 25	0.002182860844402 45
thiazole biosynthesis I (E. coli)	PWY-6892	0.0000106054088565 888	0.000288685051445 38	0.002761414516625 97	0.004172891609622 33
enterobacterial common antigen biosynthesis	ECASYN-PWY	0.0000115962282821 611	0.000288685051445 38	0.000108454862303 882	0.000022766753323 8225
superpathway of L-alanine biosynthesis	PWY0-1061	0.0000115962282821 611	0.000288685051445 38	0.003894059233443 01	0.001838385417548 24

hexitol fermentation to lactate, formate, ethanol and acetate	P461-PWY	0.0000180264872449 071	0.000387569475765 502	0.002085354793031 14	0.000943572517046 8
pyrimidine deoxyribonucleotides de novo biosynthesis IV	PWY-7198	0.0000180264872449 071	0.000387569475765 502	0.000260986553566 879	0.000623906169274 919
pyrimidine deoxyribonucleotides biosynthesis from CTP	PWY-7210	0.0000180264872449 071	0.000387569475765 502	0.000362884524019 541	0.000824782073742 826
chorismate biosynthesis II (archaea)	PWY-6165	0.0000196589501226 216	0.000387623177089 254	0.000010555787606 0832	0.000052968195195 632
acetylene degradation	P161-PWY	0.0000196679836155 224	0.000387623177089 254	0.003711646978116 5	0.002002718124899 83
pyruvate fermentation to acetone	PWY-6588	0.0000214512187006 959	0.000390247170978 044	0.002505706017967 52	0.004521814493671
superpathway of thiamin diphosphate biosynthesis II	PWY-6895	0.0000214512187006 959	0.000390247170978 044	0.002976053268217 61	0.004176780592580 7
flavin biosynthesis I (bacteria and plants)	RIBOSYN2-PWY	0.0000233877021067 009	0.000409717892461 834	0.005238535584218 13	0.006326352726204 2
adenosylcobalamin salvage from cobinamide I	COBALSYN-PWY	0.0000277708562078 396	0.000444998440217 873	0.003251347386102 32	0.005133876132325 05
superpathway of demethylmenaquinol-6 biosynthesis I	PWY-5860	0.0000302451334151 159	0.000444998440217 873	0.000886221846684 19	0.000392196498902 103
adenosylcobalamin biosynthesis from cobyrate a,c-diamide I	PWY-5509	0.0000329280029759 525	0.000444998440217 873	0.003159967834882 4	0.004998906667595 5
5-aminoimidazole ribonucleotide biosynthesis II	PWY-6122	0.0000329280029759 525	0.000444998440217 873	0.006821464334067 57	0.007642417896236 89

CMP-pseudamate biosynthesis	PWY-6143	0.0000329280029759 525	0.000444998440217 873	0.000098116799923 0143	0.000349141463134 474
superpathway of salicylate degradation	PWY-6182	0.0000329280029759 525	0.000444998440217 873	0.000345040490450 165	0.000063104754688 6317
adenosylcobalamin salvage from cobinamide II	PWY-6269	0.0000329280029759 525	0.000444998440217 873	0.003181458702601 26	0.005042991249833 3
superpathway of 5-aminoimidazole ribonucleotide biosynthesis	PWY-6277	0.0000329280029759 525	0.000444998440217 873	0.006821464334067 57	0.007642417896236 89
superpathway of menaquinol-6 biosynthesis I	PWY-5850	0.0000358359552047 385	0.000446063337153 719	0.001144291169854 53	0.000554685863628 255
superpathway of menaquinol-10 biosynthesis	PWY-5896	0.0000358359552047 385	0.000446063337153 719	0.001144291169854 53	0.000554685863628 255
inosine-5'-phosphate biosynthesis III	PWY-7234	0.0000358359552047 385	0.000446063337153 719	0.004242155109390 54	0.002648928825015 15
ADP-L-glycero-β-D-manno-heptose biosynthesis	PWY0-1241	0.0000460938008457 867	0.000515080102564 18	0.001341097398107 31	0.002079235277056 3
1,3-propanediol biosynthesis (engineered)	PWY-7385	0.0000500714942768 574	0.000515080102564 18	2.76734628774204 E-06	0.000010161176861 0968
Calvin-Benson-Bassham cycle	CALVIN-PWY	0.0000500923566975 736	0.000515080102564 18	0.000452735549021 858	0.000092660348363 4548
catechol degradation III (ortho-cleavage pathway)	PWY-5417	0.0000500923566975 736	0.000515080102564 18	0.000452735549021 858	0.000092660348363 4548
aromatic compounds degradation via β-ketoadipate	PWY-5431	0.0000500923566975 736	0.000515080102564 18	0.000886221846684 19	0.000417487467232 591

superpathway of demethylmenaquinol-9 biosynthesis	PWY-5862	0.0000500923566975 736	0.000515080102564 18	0.000021718653711 8378	0.000119794532606 461
mevalonate pathway II (archaea)	PWY-6174	0.0000500923566975 736	0.000515080102564 18	0.003423803854950 24	0.002357050633398 75
superpathway of purine deoxyribonucleosides degradation	PWY0-1297	0.0000544182261240 23	0.000527407858959 796	0.001304535739349 3	0.000648967651360 971
superpathway of chorismate metabolism	ALL-CHORISMATE-PWY	0.0000544182261240 23	0.000527407858959 796	0.006795227707430 61	0.007504576913830 69
5-aminoimidazole ribonucleotide biosynthesis I	PWY-6121	0.0000590722747866 476	0.000527407858959 796	4.44347617111497 E-06	0.000018541049117 9205
L-lysine biosynthesis V	PWY-3081	0.0000590964408559 603	0.000527407858959 796	0.004857920864607 14	0.005452206222990 64
pantothenate and coenzyme A biosynthesis I	PANTOSYN-PWY	0.0000590964408559 603	0.000527407858959 796	0.001144291169854 53	0.000590964833435 688
superpathway of menaquinol-9 biosynthesis	PWY-5845	0.0000590964408559 603	0.000527407858959 796	0.007343647530859 83	0.008409692388125 07
adenosine ribonucleotides de novo biosynthesis	PWY-7219	0.0000590964408559 603	0.000527407858959 796	0.003475836222835 14	0.004630964208044 77
superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis	PWY-7323	0.0000641537954385 207	0.000551722640771 278	0.000302161805093 1	0.000063461719595 6713
gallate degradation I	GALLATE-DEGRADATION-II-PWY	0.0000641537954385 207	0.000551722640771 278	0.006535827545355 98	0.007147096633107 39
UMP biosynthesis	PWY-5686	0.0000696189589734 684	0.000588031564186 617	0.002608951716165 4	0.001349327067353 47

heterolactic fermentation	P122-PWY	0.0000755225929815 156	0.000605460787800 964	0.001217296164478 53	0.001724013777542 31
superpathway of polyamine biosynthesis I	POLYAMSYN-PWY	0.0000755225929815 156	0.000605460787800 964	0.002164420448486 64	0.001054545425885 9
sucrose degradation IV (sucrose phosphorylase)	PWY-5384	0.0000755225929815 156	0.000605460787800 964	0.006274625175349 12	0.007039778701250 12
chorismate biosynthesis from 3-dehydroquinate	PWY-6163	0.0000818974756486 839	0.000635041081669 303	0.001089023998172 97	0.002141663020919 3
succinate fermentation to butanoate	PWY-5677	0.0000818974756486 839	0.000635041081669 303	0.002989507239422 21	0.003952612480484 11
preQ0 biosynthesis	PWY-6703	0.0000887786327270 478	0.000666544337776 089	0.001659254979820 06	0.002751937104494 13
thiazole biosynthesis II (Bacillus)	PWY-6891	0.0000887786327270 478	0.000666544337776 089	0.001612313332972 03	0.002537682921090 67
cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion)	PWY-7377	0.0000962034753662 64	0.000711003810128 795	0.004294657117873 03	0.002878424807340 86
peptidoglycan maturation (meso-diaminopimelate containing)	PWY0-1586	0.0001042119451580 89	0.000724886030290 826	0.002793894354953 1	0.001908055431992 63
superpathway of hexitol degradation (bacteria)	HEXITOLDEGSUPER-PWY	0.0001042119451580 89	0.000724886030290 826	0.002929841340427 14	0.001498210726861 97
TCA cycle IV (2-oxoglutarate decarboxylase)	P105-PWY	0.0001042119451580 89	0.000724886030290 826	0.001369246380659 44	0.000602116711329 558
superpathway of heme biosynthesis from glycine	PWY-5920	0.0001042119451580 89	0.000724886030290 826	0.000226133078153 31	0.000048078193060 7917

4-methylcatechol degradation (ortho cleavage)	PWY-6185	0.0001128038495411 05	0.000762521047719 722	3.04366974181011 E-08	2.80787774947345 E-07
L-selenocysteine biosynthesis II (archaea and eukaryotes)	PWY-6281	0.0001128466666815 66	0.000762521047719 722	0.004049362198995 96	0.003168706239818 94
mixed acid fermentation	FERMENTATION-PWY	0.0001221072001851 48	0.000780789459582 707	1.45616335305813 E-06	5.30836934777156 E-06
3-hydroxypropanoate cycle	PWY-5743	0.0001221072001851 48	0.000780789459582 707	1.19564269925353 E-08	3.25897680512628 E-07
superpathway of methanogenesis	PWY-6830	0.0001221531078416 92	0.000780789459582 707	0.005149107853069 92	0.006377261927975 03
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	PWY-5121	0.0001221531078416 92	0.000780789459582 707	0.004953128916303 58	0.004329351621346 97
pyrimidine deoxyribonucleotides de novo biosynthesis I	PWY-7184	0.0001321305468372 05	0.000791405328423 846	1.20480619307481 E-07	6.50001136954347 E-07
3-hydroxypropanoate/4-hydroxybutanate cycle	PWY-5789	0.0001321797482991 2	0.000791405328423 846	0.000201881166475 196	0.000047185480036 3959
4-hydroxyphenylacetate degradation	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY	0.0001321797482991 2	0.000791405328423 846	0.002916240463440 08	0.001653361924537 42
Bifidobacterium shunt	P124-PWY	0.0001321797482991 2	0.000791405328423 846	0.000309962543127 924	0.000070636319115 5441
toluene degradation III (aerobic) (via p-cresol)	PWY-5181	0.0001321797482991 2	0.000791405328423 846	0.000758744201622 007	0.000328781796233 62

L-tyrosine degradation I	TYRFUMCAT-PWY	0.0001429255459067 15	0.000834922410203 152	1.21151273398591 E-07	7.02005064091424 E-07
6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (archaea)	PWY-6797	0.0001429782562927 17	0.000834922410203 152	0.006205907413728 07	0.007140226800801 1
inosine-5'-phosphate biosynthesis I	PWY-6123	0.0001546036741606 26	0.000881054673228 626	0.001406022806689 83	0.000927340729964 588
urea cycle	PWY-4984	0.0001546036741606 26	0.000881054673228 626	0.000192903431835 602	0.000051802168080 9586
superpathway of L-threonine metabolism	THREOCAT-PWY	0.0001671146128687 12	0.000929943669257 658	0.005300247373341 59	0.006819755569489 46
methylerythritol phosphate pathway I	NONMEVIPP-PWY	0.0001671146128687 12	0.000929943669257 658	0.005300247373341 59	0.006819755569489 46
methylerythritol phosphate pathway II	PWY-7560	0.0001805088009572 56	0.000981738443917 436	2.68220849050142 E-08	9.21655931886056 E-08
crotonate fermentation (to acetate and cyclohexane carboxylate)	PWY-7401	0.0001805734558579 64	0.000981738443917 436	0.001808234695354 15	0.000704707162546 314
superpathway of glyoxylate bypass and TCA	TCA-GLYOX-BYPASS	0.0001949774181429 69	0.000995587853151 743	1.89432139758495 E-06	6.20941805230835 E-06
starch biosynthesis	PWY-622	0.0001949774181429 69	0.000995587853151 743	2.30508564704392 E-09	7.9216332100888E- 09
superpathway of seleno-compound metabolism	PWY-6395	0.0001950465725243 99	0.000995587853151 743	0.000455240403643 121	0.000933076537645 966
UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronate biosynthesis	PWY-7090	0.0002105306045027 51	0.000995587853151 743	2.60144256214352 E-09	8.97035058734885 E-09

paromamine biosynthesis II	PWY-7022	0.0002106045416463 89	0.000995587853151 743	0.000306421898856 591	0.000067772836132 9049
gallate degradation II	GALLATE- DEGRADATION-I-PWY	0.0002106045416463 89	0.000995587853151 743	0.000373276964935 33	0.000084489005673 5354
methylgallate degradation	METHYLGALLATE- DEGRADATION-PWY	0.0002106045416463 89	0.000995587853151 743	0.003353947336030 82	0.005036913265127 18
pyruvate fermentation to propanoate I	P108-PWY	0.0002106045416463 89	0.000995587853151 743	6.03840578967739 E-06	0.000019844304800 106
Entner-Doudoroff pathway III (semi- phosphorylative)	PWY-2221	0.0002106045416463 89	0.000995587853151 743	0.000134159803271 314	0.000040220645763 7073
L-tryptophan degradation IX	PWY-5655	0.0002106045416463 89	0.000995587853151 743	2.09422088531732 E-06	7.00047819959841 E-06
nitrifier denitrification	PWY-7084	0.0002272433663114 67	0.000995587853151 743	1.74636271801509 E-07	5.76644842922751 E-07
L-isoleucine degradation I	ILEUDEG-PWY	0.0002272433663114 67	0.000995587853151 743	2.0850185050627E- 08	6.94046875171908 E-08
Entner-Doudoroff pathway II (non- phosphorylative)	NPGLUCAT-PWY	0.0002272433663114 67	0.000995587853151 743	1.72851935930711 E-07	5.70728827104619 E-07
folate transformations I	PWY-2201	0.0002272433663114 67	0.000995587853151 743	4.67378867689059 E-07	1.54328170558121 E-06
nitrate reduction V (assimilatory)	PWY-5675	0.0002272433663114 67	0.000995587853151 743	1.20570185027976 E-06	4.00490875696286 E-06
glyoxylate assimilation	PWY-5744	0.0002272433663114 67	0.000995587853151 743	1.73388722699059 E-06	5.70533367140109 E-06

superpathway of the 3-hydroxypropanoate cycle	PWY-7024	0.0002273223850748 17	0.000995587853151 743	0.000474847331259 4	0.000107777258035 632
catechol degradation to β-ketoadipate	CATECHOL-ORTHO-CLEAVAGE-PWY	0.0002273223850748 17	0.000995587853151 743	0.008452941117151 22	0.009367625596758 67
pentose phosphate pathway (non-oxidative branch)	NONOXIPENT-PWY	0.0002273223850748 17	0.000995587853151 743	0.004734227702030 15	0.003873220913991 36
pentose phosphate pathway	PENTOSE-P-PWY	0.0002273223850748 17	0.000995587853151 743	0.002396004825811 23	0.003856563036054 31
L-glutamate and L-glutamine biosynthesis	PWY-5505	0.0002273223850748 17	0.000995587853151 743	0.000053044200867 461	0.000137298737668 777
ergothioneine biosynthesis I (bacteria)	PWY-7255	0.0002368537321988 21	0.001027814819541 67	9.9692796286453E- 09	4.51017892271445 E-08
superpathway of sialic acids and CMP-sialic acids biosynthesis	PWY-6145	0.0002449422769961 76	0.001035869206041 04	1.15410793860225 E-09	3.8205156369048E- 09
streptomycin biosynthesis	PWY-5940	0.0002452798120012 6	0.001035869206041 04	0.003582118609112 61	0.004451133040720 93
colanic acid building blocks biosynthesis	COLANSYN-PWY	0.0002452798120012 6	0.001035869206041 04	0.002433376859815 69	0.001253957838792 2
superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass	GLYCOLYSIS-TCA-GLYOX-BYPASS	0.0002642010304470 92	0.001078772217740 65	1.50446121613556 E-09	4.97239979173245 E-09
neopentalenoketolactone and pentalenate biosynthesis	PWY-6919	0.0002645614741182 16	0.001078772217740 65	0.001814168220188 96	0.000656436963263 688
fatty acid β-oxidation I	FAO-PWY	0.0002645614741182 16	0.001078772217740 65	0.004938889190693 76	0.003196052157252 18

sucrose degradation III (sucrose invertase)	PWY-621	0.0002645614741182 16	0.001078772217740 65	0.000250567711947 11	0.000078054088198 5392
phenylacetate degradation I (aerobic)	PWY0-321	0.0002842960576832 84	0.001124388922734 16	3.30367704639228 E-10	9.76059061916559 E-10
ribostamycin biosynthesis	PWY-7015	0.0002852572319832 96	0.001124388922734 16	0.000122397462020 045	0.000030898002752 7626
superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation	ARGDEG-PWY	0.0002852572319832 96	0.001124388922734 16	0.003362234228290 96	0.004549630936760 35
lipid IVA biosynthesis	NAGLIPASYN-PWY	0.0002852572319832 96	0.001124388922734 16	0.000122397462020 045	0.000030898002752 7626
superpathway of L-arginine and L-ornithine degradation	ORNARGDEG-PWY	0.0003070519008775 7	0.001163437846079 39	6.49140647224054 E-10	2.13605215297629 E-09
paromamine biosynthesis I	PWY-7014	0.0003070519008775 7	0.001163437846079 39	6.78411456715374 E-10	2.23725197709979 E-09
mevalonate pathway III (archaea)	PWY-7524	0.0003074624328962 44	0.001163437846079 39	0.006136237285293 22	0.006509163651255 1
chorismate biosynthesis I	ARO-PWY	0.0003074624328962 44	0.001163437846079 39	0.006034647919069 58	0.006703420152404 73
coenzyme A biosynthesis I	COA-PWY	0.0003074624328962 44	0.001163437846079 39	0.005699099823389 72	0.005149274081541 13
superpathway of guanosine nucleotides de novo biosynthesis I	PWY-7228	0.0003312782005934 18	0.001243607848259 42	0.000236153759226 996	0.000113510296564 178
superpathway of glycerol degradation to 1,3-propanediol	GOLPDLCAT-PWY	0.0003568117370591 08	0.001328913004952 43	0.006383384369405 38	0.007293953935872 46

tRNA charging	TRNA-CHARGING-PWY	0.0003840522194053 84	0.001419192967021 46	0.000017494539490 3833	0.000060790945975 3789
reductive TCA cycle II	PWY-5392	0.0004133606754619 39	0.001515655810027 11	1.98306250228997 E-06	4.98606794753847 E-06
sitosterol degradation to androstenedione	PWY-6948	0.0004448888404089 26	0.001618710934718 63	0.007380978762816 3	0.008224659747450 94
superpathway of adenosine nucleotides de novo biosynthesis I	PWY-7229	0.0004778976192952 92	0.001689027591915 16	4.9196137027867E- 10	1.45076198432908 E-09
superpathway of butirocin biosynthesis	PWY-7020	0.0004783480823133 56	0.001689027591915 16	0.000022925997033 2246	0.000116587897573 188
coenzyme B biosynthesis	P241-PWY	0.0004784983029949 93	0.001689027591915 16	0.007025934307087 91	0.007864307674577 63
superpathway of adenosine nucleotides de novo biosynthesis II	PWY-6126	0.0004784983029949 93	0.001689027591915 16	0.000104846795875 007	0.000275275512326 133
protein N-glycosylation (bacterial)	PWY-7031	0.0005144641657591 73	0.001802530002993 25	0.003474025306223 2	0.004355091942958 18
CMP-3-deoxy-D-manno-octulosonate biosynthesis I	PWY-1269	0.0005529371525551 78	0.001895212124337 67	0.000185460208450 963	0.000059885351598 1832
toluene degradation IV (aerobic) (via catechol)	PWY-5178	0.0005529371525551 78	0.001895212124337 67	0.006265080557708 58	0.006842015741013 12
peptidoglycan biosynthesis III (mycobacteria)	PWY-6385	0.0005529371525551 78	0.001895212124337 67	0.001297793710215 05	0.000603241493661 769
mevalonate pathway I	PWY-922	0.0005940765408778 92	0.001978860590389 04	1.99956857664599 E-06	6.11725390593094 E-06

benzoyl-CoA degradation II (anaerobic)	CENTBENZCOA-PWY	0.0005940765408778 92	0.001978860590389 04	0.000041359410604 9813	0.000173335810038 483
coenzyme M biosynthesis I	P261-PWY	0.0005940765408778 92	0.001978860590389 04	0.000063665446868 6651	0.000180301416251 358
sucrose degradation II (sucrose synthase)	PWY-3801	0.0005940765408778 92	0.001978860590389 04	0.000173821777935 861	0.000028981499525 3523
polymyxin resistance	PWY0-1338	0.0006380505703199 59	0.002039175133522 57	0.000138715181270 575	0.000272273754638 336
glycolysis V (Pyrococcus)	P341-PWY	0.0006380505703199 59	0.002039175133522 57	0.002011826525660 81	0.002933232367552 88
acetyl-CoA fermentation to butanoate II	PWY-5676	0.0006380505703199 59	0.002039175133522 57	0.001623829337754 1	0.000814694516367 718
superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)	PWY-5910	0.0006380505703199 59	0.002039175133522 57	0.000915605345681 968	0.000500044739134 92
superpathway of 2,3-butanediol biosynthesis	PWY-6396	0.0006380505703199 59	0.002039175133522 57	0.000450023320672 417	0.000148688406627 122
2-methylcitrate cycle I	PWY0-42	0.0006380505703199 59	0.002039175133522 57	0.003278747300273 66	0.002359998213569 19
TCA cycle VIII (helicobacter)	REDCITCYC	0.0006848328775735 56	0.002104041800807 62	1.19688490564676 E-06	0.000041279683258 374
CDP-archaeol biosynthesis	PWY-6349	0.0006848328775735 56	0.002104041800807 62	1.41134924073927 E-06	0.000042281106314 2697
archaetidylinositol biosynthesis	PWY-6350	0.0006850368653792 26	0.002104041800807 62	0.005922180757638 72	0.006359802634954 48

gluconeogenesis I	GLUCONEO-PWY	0.0006850368653792 26	0.002104041800807 62	0.006335235869553 55	0.006903771047022 1
peptidoglycan biosynthesis I (meso-diaminopimelate containing)	PEPTIDOGLYCANSYN-PWY	0.0006850368653792 26	0.002104041800807 62	0.000490731411246 94	0.000109406480177 776
syringate degradation	PWY-6339	0.0006850368653792 26	0.002104041800807 62	0.000461391772241 657	0.000790878588739 43
methylaspartate cycle	PWY-6728	0.0007352228727858 61	0.002243615605340 08	0.006308113499245 82	0.006670945249369 86
superpathway of aromatic amino acid biosynthesis	COMPLETE-ARO-PWY	0.0007885764281363 76	0.002346574756499 65	0.000015727553820 2767	0.000110121816706 357
methanogenesis from H2 and CO2	METHANOGENESIS-PWY	0.0007888063134956 55	0.002346574756499 65	0.001798273307763 77	0.002250290033224 4
superpathway of arginine and polyamine biosynthesis	ARG+POLYAMINE-SYN	0.0007888063134956 55	0.002346574756499 65	0.004018257255433 51	0.003322150349412 89
L-methionine biosynthesis III	HSERMETANA-PWY	0.0007888063134956 55	0.002346574756499 65	0.000101583735116 364	0.000038663076768 8974
superpathway of aerobic toluene degradation	PWY-5183	0.0008435588712467 08	0.002454944430675 96	4.46387012303079 E-10	1.22426394584108 E-09
butirosin biosynthesis	PWY-7019	0.0008459956494718 41	0.002454944430675 96	0.000780594205900 617	0.000306705620093 583
protocatechuate degradation II (ortho-cleavage pathway)	PROTocatechuate-ORTHO-CLEAVAGE-PWY	0.0008459956494718 41	0.002454944430675 96	0.000193496035140 351	0.000067457727100 6742
superpathway of phenylethylamine degradation	PWY-6071	0.0008459956494718 41	0.002454944430675 96	0.001601291422059 48	0.000740415498396 242

fatty acid salvage	PWY-7094	0.0009067519189974 68	0.002568958068331 11	1.27331214377164 E-06	0.000055200051953 2944
tetrahydromethanopterin biosynthesis	PWY-6148	0.0009070105653515 74	0.002568958068331 11	0.004609394186368 55	0.003904695603224 84
superpathway of histidine, purine, and pyrimidine biosynthesis	PRPP-PWY	0.0009070105653515 74	0.002568958068331 11	0.000086071309960 2577	0.000025677165955 4684
2-nitrobenzoate degradation I	PWY-5647	0.0009070105653515 74	0.002568958068331 11	0.004337451619855 92	0.003554845323258 13
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	PWY-7211	0.0009262748738811 01	0.002592473463584 38	2.260001962782E- 11	9.96325569585817 E-11
superpathway of erythromycin biosynthesis	PWY-6977	0.0009262748738811 01	0.002592473463584 38	2.260001962782E- 11	9.68681852649075 E-11
superpathway of megalomicin A biosynthesis	PWY-7110	0.0009718082846448 13	0.002688859684068 64	3.39140096368807 E-07	8.50700969741689 E-07
cholesterol degradation to androstenedione II (cholesterol dehydrogenase)	PWY-6946	0.0009720824650649 83	0.002688859684068 64	0.004374087699778 67	0.003909779679593 06
pyrimidine deoxyribonucleotide phosphorylation	PWY-7197	0.0010414549834444	0.002847446284215 04	0.001463744675172 56	0.000669333821834 835
glyoxylate cycle	GLYOXYLATE-BYPASS	0.0010414549834444	0.002847446284215 04	0.006440898686224 17	0.006998487076626 69
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	PWY-6387	0.0011150767892177 4	0.002997595878227 72	1.15876115842117 E-06	0.000059492535540 6848
phosphopantothenate biosynthesis III	PWY-6654	0.0011153845128289 2	0.002997595878227 72	0.000242177654701 391	0.000433537656095 744

methanogenesis from acetate	METH-ACETATE-PWY	0.0011153845128289 2	0.002997595878227 72	0.003272384310588 66	0.002531711128828 13
superpathway of pyrimidine deoxyribonucleosides degradation	PWY0-1298	0.0011332192423981 2	0.003028320348329 45	6.36551430173179 E-12	4.61114511692195 E-11
erythromycin D biosynthesis	PWY-7106	0.0011941407446348	0.003137936512290 33	0.001162059179528 99	0.000579965596822 105
lactose and galactose degradation I	LACTOSECAT-PWY	0.0011941407446348	0.003137936512290 33	1.19027733081359 E-06	2.74649239934819 E-06
toluene degradation VI (anaerobic)	PWY-5184	0.0011941407446348	0.003137936512290 33	0.000581408764737 014	0.000189062833531 447
2-methylcitrate cycle II	PWY-5747	0.0012766283845406 8	0.003215411796890 53	1.32573724435626 E-06	1.36789989450808 E-09
superpathway of mycolyl-arabinogalactan-peptidoglycan complex biosynthesis	PWY-6404	0.0012776624239361	0.003215411796890 53	0.000036910242831 6905	0.000118421336375 411
gluconeogenesis II (Methanobacterium thermoautotrophicum)	PWY-6142	0.0012776624239361	0.003215411796890 53	1.03307648511157 E-06	0.000093212668037 4041
flavin biosynthesis II (archaea)	PWY-6167	0.0012776624239361	0.003215411796890 53	3.49758151579925 E-07	0.000039966421649 4431
7-(3-amino-3-carboxypropyl)-wyosine biosynthesis	PWY-7286	0.0012780072258254 1	0.003215411796890 53	0.006657330541289 03	0.007128338038021 95
glycolysis I (from glucose 6-phosphate)	GLYCOLYSIS	0.0012780072258254 1	0.003215411796890 53	0.006334699289531 58	0.006882869158844 99
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	PWY-6386	0.0012780072258254 1	0.003215411796890 53	0.000581482203621 785	0.001021805213359 13

GDP-D-glycero-α-D-manno-heptose biosynthesis	PWY-6478	0.0012780072258254 1	0.003215411796890 53	0.001535638385315 18	0.000983332468582 862
superpathway of heme biosynthesis from uroporphyrinogen-III	PWY0-1415	0.0013672819301753 2	0.003333630685427 45	0.003533490244285 3	0.002905321645198 93
L-ornithine biosynthesis	GLUTORN-PWY	0.0013672819301753 2	0.003333630685427 45	0.001300899092979 54	0.001945293541414 76
photorespiration	PWY-181	0.0013672819301753 2	0.003333630685427 45	0.005891007029663 12	0.006711754145657 85
pyruvate fermentation to acetate and lactate II	PWY-5100	0.0013672819301753 2	0.003333630685427 45	0.006679625456439 52	0.007117815057383 64
guanosine ribonucleotides de novo biosynthesis	PWY-7221	0.0013672819301753 2	0.003333630685427 45	0.003423441092325 44	0.002508031919726 99
purine ribonucleosides degradation	PWY0-1296	0.0013672819301753 2	0.003333630685427 45	0.000504697760101 567	0.000243729282167 928
methylphosphonate degradation I	PWY0-1533	0.0014618921337408 5	0.003528864389275 17	0.000007501436569 4816	0.000019783689572 111
mannosylglycerate biosynthesis I	PWY-5656	0.0014622778441816 8	0.003528864389275 17	0.007205518676445 22	0.007920207249719 01
superpathway of pyrimidine nucleobases salvage	PWY-7208	0.0015633235674326 4	0.003753563692363 64	0.000211037286996 612	0.000063112499553 0554
3-phenylpropanoate degradation	P281-PWY	0.0017845056700623 5	0.004262985767371 18	0.000001334368720 2148	0.000047098875999 9314
Methanobacterium thermoautotrophicum biosynthetic metabolism	PWY-6146	0.0020346509993927 4	0.004813148214213 37	3.13100494043165 E-07	0.000036251759846 2128

archaetidylserine and archaetidylethanolamine biosynthesis	PWY-6141	0.0020351578072783 8	0.004813148214213 37	0.000844661919010 2	0.000458072265419 947
myo-inositol degradation I	P562-PWY	0.0021719718205802 3	0.005085854807596 28	0.002682277276022 28	0.003653849906900 34
L-histidine degradation I	HISDEG-PWY	0.0021719718205802 3	0.005085854807596 28	0.000018251440465 5821	0.000048309824721 7487
androstenedione degradation	PWY-6944	0.0022801231740872 8	0.005269334811165 85	2.51504915343216 E-12	6.65411457118316 E-11
pentalenolactone biosynthesis	PWY-6915	0.0022809798815085	0.005269334811165 85	6.36551430173179 E-12	4.36311252483613 E-11
tylosin biosynthesis	PWY-7415	0.0023171704877854	0.005269334811165 85	0.000259634405577 346	0.000076552488488 7063
superpathway of ornithine degradation	ORNDEG-PWY	0.0023171704877854	0.005269334811165 85	0.004157747039846 64	0.003788849209701 59
superpathway of pyrimidine deoxyribonucleoside salvage	PWY-7200	0.0023171704877854	0.005269334811165 85	0.003272788563132 04	0.002183391700192 51
D-fructuronate degradation	PWY-7242	0.0023171704877854	0.005269334811165 85	0.004209276597927 34	0.003634104216803 13
anhydromuropeptides recycling	PWY0-1261	0.0024706156084006 8	0.005539725925949 05	5.07689144000859 E-07	1.45293313814208 E-06
xylose degradation III	PWY-6760	0.0024712096625269 6	0.005539725925949 05	0.001279960535716 64	0.000570395524344 194
enterobactin biosynthesis	ENTBACSYN-PWY	0.0024712096625269 6	0.005539725925949 05	0.000146768228148 806	0.000057909834533 3786

meta cleavage pathway of aromatic compounds	PWY-5430	0.0026345660958435 1	0.005878064921386 69	0.000015175116716 4381	0.000094950322500 6425
factor 420 biosynthesis	PWY-5198	0.0028077381497495 5	0.006235024154138 66	0.006550523917395 86	0.005162054410889 17
pyruvate fermentation to isobutanol (engineered)	PWY-7111	0.0031514884004469 2	0.006965672959866 32	2.31381551423029 E-07	4.64326610558964 E-07
anaerobic aromatic compound degradation (Thauera aromatica)	BENZCOA-PWY	0.0031856349704060 2	0.007008396934893 24	0.004485124629243 32	0.004950249541937 45
phosphopantothenate biosynthesis I	PANTO-PWY	0.0033914710682818 1	0.007258668847499 07	0.004125615597824 29	0.005091236519124 86
superpathway of L-aspartate and L-asparagine biosynthesis	ASPASN-PWY	0.0033914710682818 1	0.007258668847499 07	0.003651015175223 08	0.003032874838263 43
L-methionine biosynthesis I	HOMOSER-METSYN-PWY	0.0033914710682818 1	0.007258668847499 07	0.000319278912712 47	0.000075827264533 2694
protocatechuate degradation I (meta-cleavage pathway)	P184-PWY	0.0033914710682818 1	0.007258668847499 07	0.004910988657010 1	0.005464689335814 1
polyisoprenoid biosynthesis (E. coli)	POLYISOPRENSYN-PWY	0.0033914710682818 1	0.007258668847499 07	0.000031726347803 5459	0.000004087596314 3231
chlorosalicylate degradation	PWY-6107	0.0033914710682818 1	0.007258668847499 07	0.005654081899648 85	0.005308760286282 89
superpathway of guanosine nucleotides de novo biosynthesis II	PWY-6125	0.0038398800013550 5	0.008108318038575 61	0.006673781613904 85	0.007177822455658 57
glycolysis III (from glucose)	ANAGLYCOLYSIS-PWY	0.0038398800013550 5	0.008108318038575 61	5.78173296735349 E-06	0.000014259904223 538

toluene degradation V (aerobic) (via toluene-cis-diol)	PWY-5179	0.0038398800013550 5	0.008108318038575 61	0.003570370353935 53	0.004288545216944 55
NAD salvage pathway I	PYRIDNUCSAL-PWY	0.0040837137563018 55	0.008546887640401 55	0.000368152318422 296	0.000121760365503 336
L-histidine degradation II	PWY-5028	0.0040837137563018 55	0.008546887640401 55	0.006547612337898 87	0.007477500712943 53
urate biosynthesis/inosine 5'-phosphate degradation	PWY-5695	0.0043415185177975 6	0.009046424048098	0.005017139052493 8	0.005589043840484 59
6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia)	PWY-7539	0.0046139921918485 9	0.009572010117299 92	0.004695901220142 99	0.004099627800468 88
galactose degradation I (Leloir pathway)	PWY-6317	0.0050323791136614 9	0.010394390046994 9	2.51504915343216 E-12	2.6321529524165E- 11
dTDP-6-deoxy-α-D-allose biosynthesis	PWY-7413	0.0052048005704251 8	0.010568160711701	2.39126003547435 E-06	6.38660577585327 E-06
D-arabinose degradation III	PWY-5519	0.0052058804351508 3	0.010568160711701	0.004116340490989 8	0.003705744937562 99
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	P4-PWY	0.0052058804351508 3	0.010568160711701	0.002067472635621 78	0.001314940407340 45
TCA cycle VII (acetate-producers)	PWY-7254	0.0052058804351508 3	0.010568160711701	0.001962631637747 65	0.002888193140320 69
superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis	PWY-7332	0.0055268356413798 8	0.010984005287280 2	0.004367151859767 38	0.003841126499904 86
L-lysine biosynthesis I	DAPLYSINESYN-PWY	0.0055268356413798 8	0.010984005287280 2	0.000236726298533 631	0.000059136397771 8484

ketogluconate metabolism	KETOGLUCONMET-PWY	0.0055268356413798 8	0.010984005287280 2	0.000394475154321 69	0.000685801202271 18
biotin biosynthesis II	PWY-5005	0.0055268356413798 8	0.010984005287280 2	0.004913621314567 9	0.005459648335026 04
GDP-mannose biosynthesis	PWY-5659	0.0055268356413798 8	0.010984005287280 2	0.002848368120092 02	0.003573767725830 43
Kdo transfer to lipid IVA III (Chlamydia)	PWY-6467	0.0056548853126238 4	0.011191467585234 6	6.36551430173179 E-12	3.85322076834987 E-11
superpathway of erythromycin biosynthesis (without sugar biosynthesis)	PWY-6975	0.00622284847119	0.012112787353386 3	0.001067520979861 78	0.000661893528028 138
L-leucine degradation I	LEU-DEG2-PWY	0.00622284847119	0.012112787353386 3	0.004532978772422 78	0.004074117014777 77
superpathway of S-adenosyl-L-methionine biosynthesis	MET-SAM-PWY	0.00622284847119	0.012112787353386 3	0.004079028325147 36	0.003715644109330 75
aspartate superpathway	PWY0-781	0.00622284847119	0.012112787353386 3	0.001612984705313 03	0.000979327178303 137
superpathway of ubiquinol-8 biosynthesis (prokaryotic)	UBISYN-PWY	0.0065996328213927	0.012741331936811 2	0.001370171166222 32	0.000832052906329 567
glucose and glucose-1-phosphate degradation	GLUCOSE1PMETAB-PWY	0.0065996328213927	0.012741331936811 2	0.002035053858334 26	0.001408929787049 24
superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis	PWY-7328	0.0069968079197863 2	0.013237960584235 7	0.003073876825527 12	0.003803087400402 64
biotin biosynthesis I	BIOTIN-BIOSYNTHESIS-PWY	0.0069968079197863 2	0.013237960584235 7	0.001636174682751 26	0.000985281125366 759

ubiquinol-7 biosynthesis (prokaryotic)	PWY-5855	0.0069968079197863 2	0.013237960584235 7	0.001636174682751 26	0.000985281125366 759
ubiquinol-9 biosynthesis (prokaryotic)	PWY-5856	0.0069968079197863 2	0.013237960584235 7	0.001636174682751 26	0.000985281125366 759
ubiquinol-10 biosynthesis (prokaryotic)	PWY-5857	0.0069968079197863 2	0.013237960584235 7	0.001636174682751 26	0.000985281125366 759
ubiquinol-8 biosynthesis (prokaryotic)	PWY-6708	0.0078561483669862 4	0.014687581729583	0.000429280537302 05	0.000105316344867 547
glycine betaine degradation I	PWY-3661	0.0078561483669862 4	0.014687581729583	4.95707006065288 E-06	8.06521695039678 E-06
D-galacturonate degradation II	PWY-6486	0.0078561483669862 4	0.014687581729583	0.004273205832675 01	0.004736203994137 73
thiamin salvage II	PWY-6897	0.0083203092261884	0.015313253945475 2	0.000271232003602 766	0.000059062476488 5813
superpathway of vanillin and vanillate degradation	PWY-6338	0.0083203092261884	0.015313253945475 2	0.000271232003602 766	0.000059062476488 5813
vanillin and vanillate degradation I	PWY-7097	0.0083203092261884	0.015313253945475 2	0.000299731197001 97	0.000065101179224 8229
vanillin and vanillate degradation II	PWY-7098	0.0083203092261884	0.015313253945475 2	0.005488692048512 63	0.006102242075338 07
superpathway of L-serine and glycine biosynthesis I	SER-GLYSYN-PWY	0.0093228677519123 6	0.017091924211839 3	0.001128336770101 33	0.000555962374886 31
superpathway of (Kdo)2-lipid A biosynthesis	KDO-NAGLIPASYN-PWY	0.0098634771274733 7	0.017943941081903 5	0.000120722394449 442	0.000016447504102 8527

starch degradation III	PWY-6731	0.0098634771274733 7	0.017943941081903 5	0.001416540420739 15	0.001813873665806 58
glycerol degradation to butanol	PWY-7003	0.0100407217538355	0.018196403791433 6	4.5068627682329E- 11	1.21607612640207 E-10
superpathway of atrazine degradation	PWY-5724	0.0104299968962077	0.018704863807517 1	1.67884072650417 E-06	2.62186874022481 E-06
vitamin E biosynthesis (tocopherols)	PWY-1422	0.0104318433642815	0.018704863807517 1	0.003598899618647 91	0.004169650639066 03
NAD biosynthesis I (from aspartate)	PYRIDNUCSYN-PWY	0.0104399239855909	0.018704863807517 1	0	1.68766610408278 E-11
aclacinomycin biosynthesis	PWY-7354	0.0110291666911012	0.019612014454476 9	0.006959096255425 13	0.007768675367864 27
adenosine deoxyribonucleotides de novo biosynthesis II	PWY-7220	0.0110291666911012	0.019612014454476 9	0.006959096255425 13	0.007768675367864 27
guanosine deoxyribonucleotides de novo biosynthesis II	PWY-7222	0.0116566861323972	0.020573181121730 9	0.000079607597171 2189	7.69352637543703 E-06
glucose degradation (oxidative)	DHGLUCONATE-PYR-CAT-PWY	0.0116566861323972	0.020573181121730 9	4.41359101503416 E-06	0.000012260356875 3206
superpathway of CDP-glucose-derived O-antigen building blocks biosynthesis	PWY-5823	0.0130074666079587	0.022703069024223 1	0.000636887179887 407	0.001060472628018 99
superpathway of sulfur oxidation (Acidianus ambivalens)	PWY-5304	0.0130074666079587	0.022703069024223 1	0.005067690537566 52	0.005632000142993 92
6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	PWY-6147	0.0130074666079587	0.022703069024223 1	0.000235203943838 664	0.000330577318135 843

allantoin degradation IV (anaerobic)	PWY0-41	0.0137334043088943	0.023621455411298 2	0.002154572631272 71	0.001533512078240 26
L-lysine biosynthesis II	PWY-2941	0.0137334043088943	0.023621455411298 2	0.004474604079763 76	0.003865532543361 67
S-adenosyl-L-methionine cycle I	PWY-6151	0.0137334043088943	0.023621455411298 2	0.001022779939919 84	0.001328544728246 27
superpathway of Clostridium acetobutylicum acidogenic fermentation	PWY-6590	0.0137334043088943	0.023621455411298 2	0.000065117088412 2546	0.000024672901324 0846
mandelate degradation to acetyl-CoA	PWY-6957	0.0144948923475206	0.024751206066343 9	0.000009750945203 477	0.000031311734278 0283
sucrose biosynthesis III	PWY-7347	0.0144948923475206	0.024751206066343 9	0.000031966965126 7898	0.000094933900569 4245
sucrose biosynthesis I (from photosynthesis)	SUCSYN-PWY	0.0152933710301989	0.025927471316430 5	0.007092388350018 34	0.007556836031111 97
superpathway of phospholipid biosynthesis I (bacteria)	PHOSLIPSYN-PWY	0.0152933710301989	0.025927471316430 5	0.005534305541490 47	0.005948687756377 92
superpathway of L-threonine biosynthesis	THRESYN-PWY	0.0161303221067591	0.027248722701775 2	0.000836237903661 83	0.001092299315686 27
pyruvate fermentation to butanoate	CENTFERM-PWY	0.0170072690620831	0.028425576912951 6	0.000296199557242 843	0.000083770631517 7688
chlorophyllide a biosynthesis II (anaerobic)	PWY-5531	0.0170072690620831	0.028425576912951 6	0.005190578688634 09	0.006154874700344 51
starch degradation V	PWY-6737	0.0170072690620831	0.028425576912951 6	0.000296199557242 843	0.000083770631517 7688

chlorophyllide a biosynthesis III (aerobic, light independent)	PWY-7159	0.0179257773574065	0.029543180104715 2	0.000026181072458 5547	0.000050361113598 3581
superpathway of lipopolysaccharide biosynthesis	LPSSYN-PWY	0.0179257773574065	0.029543180104715 2	0.005891021518874 57	0.004472946539398 6
aerobic respiration I (cytochrome c)	PWY-3781	0.0179257773574065	0.029543180104715 2	0.006795904901447 99	0.007314406544602 14
phosphatidylglycerol biosynthesis I (plastidic)	PWY4FS-7	0.0179257773574065	0.029543180104715 2	0.006795904901447 99	0.007314406544602 14
phosphatidylglycerol biosynthesis II (non-plastidic)	PWY4FS-8	0.0198939507675555	0.032673051086992 1	0.002166172071003 63	0.001583614787026 65
superpathway of β-D-glucuronide and D-glucuronate degradation	GLUCUROCAT-PWY	0.0209469580967318	0.034283429687730 6	0.000051716774181 3151	0.000058886114903 5589
1,5-anhydrofructose degradation	PWY-6992	0.0220450213562389	0.035715081969122 3	1.79749253119433 E-06	5.95551385308433 E-06
dTDP-D-desosamine biosynthesis	PWY-6942	0.0220482112790353	0.035715081969122 3	0.001765489217863 43	0.001323201887339 32
superpathway of hexuronide and hexuronate degradation	GALACT- GLUCUROCAT-PWY	0.0220482112790353	0.035715081969122 3	0.000855496890496 1	0.000506783469443 296
cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation)	PWY-7376	0.0256558807787127	0.041282002967475	3.73508044084929 E-07	0.000012875991869 7528
superpathway of pyrimidine ribonucleosides degradation	PWY-7209	0.0256594267916229	0.041282002967475	0.004076160449720 98	0.003379610938998 73
L-tryptophan biosynthesis	TRPSYN-PWY	0.0269718544263195	0.042955175567842 1	0.007589430984892 38	0.007912629486614 03

CDP-diacylglycerol biosynthesis I	PWY-5667	0.0269718544263195	0.042955175567842 1	0.007589430984892 38	0.007912629486614 03
CDP-diacylglycerol biosynthesis II	PWY0-1319	0.0269718544263195	0.042955175567842 1	0.002975157825821 99	0.002461966770395 23
superpathway of sulfate assimilation and cysteine biosynthesis	SULFATE-CYS-PWY	0.0283418326973812	0.044985526395507 8	0.002059876154287 26	0.001507743212804 64
sulfate reduction I (assimilatory)	SO4ASSIM-PWY	0.029771346975724	0.046783545247566 3	0.004574336167253 65	0.004321568883191 65
superpathway of L-methionine biosynthesis (transsulfuration)	PWY-5347	0.029771346975724	0.046783545247566 3	0.000022705440704 335	0.000033821443028 6905
adenosine nucleotides degradation IV	PWY-5532	0.029771346975724	0.046783545247566 3	0.001787700243049 96	0.002140212354922 37
pyridoxal 5'-phosphate biosynthesis I	PYRIDOXYN-PWY	0.0312624231206811	0.048482380774039 9	0.000013141305993 4326	1.55594470027178 E-06
phospholipases	LIPASYN-PWY	0.0312624231206811	0.048482380774039 9	0.002341913279563 7	0.002892400204965 3
purine nucleobases degradation I (anaerobic)	P164-PWY	0.0312624231206811	0.048482380774039 9	0.001357052008411	0.000847905237538 174
1,4-dihydroxy-2-naphthoate biosynthesis I	PWY-5837	0.0312624231206811	0.048482380774039 9	0.000093592178287 4719	0.000122332535114 439

Table S1E. Relative abundance of the most significant MetaCyc metabolic pathways in the samples collected in periodontitis sites and healthy sites as assessed by Mann-Whitney U tests with false-discovery-rate correction.

cytokines	genus	Correlation	FDR corrected P value
IL-6	k__Bacteria_p__Actinobacteria_c__Actinobacteria_o__Actinomycetales_f__Microbacteriaceae_g__Salinibacterium	0.781058141470492	0.00391896335277532
IL-6	k__Bacteria_p__Actinobacteria_c__Actinobacteria_o__Actinomycetales_f__Nocardoidaceae_g__Propionicimonas	0.77387261365315	0.00391896335277532
IL-6	k__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Ancylobacter	0.781058141470492	0.00391896335277532
TNF_alpha	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Pseudomonadales_f__Moraxellaceae_g__Psychrobacter	0.743367104494179	0.0080953860942272
TNF_alpha	k__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Xanthomonadales_f__Xanthomonadaceae_g__Pseudoxanthomonas	0.743367104494178	0.0080953860942272
TNF_alpha	k__Bacteria_p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Carnobacteriaceae_g__Carnobacterium	0.704471475170114	0.0260357377017787
IL-6	k__Bacteria_p__Fusobacteria_c__Fusobacteriia_o__Fusobacteriales_f__g__	0.682403924137123	0.0438746482692848

Table S2A. Most significant correlations between cytokines and oral microbiome collapsed at genus level in the samples collected in healthy sites as assessed by Pearson correlation with false-discovery-rate correction.

cytokines	genus	Correlation	FDR corrected P value
IL-4	k__Bacteria_p__Actinobacteria_c__Actinobacteria_o__Actinomycetales_f__Actinomycetaceae_g__	0.913181895820066	2.80808337152153e-07
IL-4	k__Bacteria_p__Actinobacteria_c__Coriobacteriia_o__Coriobacteriales_f__Coriobacteriaceae_g__Atopobium	0.917147889369325	2.80808337152153e-07
IL-4	k__Bacteria_p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Lachnoanaerobaculum	0.866304124952008	1.72575647575241e-05

IL-4	k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_B radyrhizobiaceae	0.840219451 283567	8.09320296113803e-05
IL-10	k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Pr opionibacteriaceae g_Propionibacterium	0.799843625 509915	0.000631656205793434
IL-10	k_Bacteria_p_Firmicutes_c_Bacilli_o_Bacillales_f_Staphylococcaceae_ g_Staphylococcus	0.788520300 439248	0.000910949715131011
IL-10	k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_C ellulomonadaceae g_Actinotalea	0.782716791 377285	0.00102134432047806
IL-4	k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Pr opionibacteriaceae g_	0.708536604 395631	0.0154468691733736
IL-6	k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhodobacterales_ f_Rhodobacteraceae	0.696710762 528417	0.019988306088363
TNF_a lpha	k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_A ctinomycetaceae g_Actinomyces	0.668454807 635251	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Carnobacteriac eae g_	0.663662633 943241	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae	0.671428752 259426	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospirace ae g_Clostridium	0.664095655 949535	0.0277109389384337
IL- 17A	k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellacea e g_Acidaminococcus	0.673094496 22526	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Fusobacteria_c_Fusobacteriia_o_Fusobacteriales_f_Fusob acteriaceae g_Fusobacterium	0.664333340 860748	0.0277109389384337
IL-6	k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Neisseriales_f_Ne isseriaceae	0.663890432 48005	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Rhodocyclales_f_ Rhodocyclaceae g_Propionivibrio	0.679586299 145746	0.0277109389384337
TNF_a lpha	k_Bacteria_p_Bacteroidetes_c_Sphingobacteriia_o_Sphingobacteriales_f_ Sphingobacteriaceae g_Sphingobacterium	0.655905782 117121	0.0322653625660387
TNF_a lpha	k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhodobacterales_ f_Rhodobacteraceae g_Amaricoccus	0.646276811 080073	0.0373568106369682

IL-17A	k__Bacteria_p__Proteobacteria_c__Betaproteobacteria_o__Rhodocyclales_f__Rhodocyclaceae_g__Propionivibrio	0.647084788 419367	0.0373568106369682
TNF_alpha	k__Bacteria_p__Actinobacteria_c__Actinobacteria_o__Actinomycetales_f__Microbacteriaceae_g__Microbacterium	0.639484638 392383	0.041842599521803
IL-17A	k__Bacteria_p__Proteobacteria_c__Betaproteobacteria_o__Neisseriales_f__Neisseriaceae	0.638043099 536067	0.041842599521803

Table S2B. Most significant correlations between cytokines and oral microbiome collapsed at genus level in the samples collected in periodontitis sites as assessed by Pearson correlation with false-discovery-rate correction.

cytokines	PATHWAYS	Correlation	FDR corrected P value
IL-6	PWY-1882 superpathway of C1 compounds oxidation to CO2	0.778140117786349	0.0215331440046045
IL-10	PWY-1861 formaldehyde assimilation II (RuMP Cycle)	-0.74049363300693	0.0498192403823827
IL-10	RUMP-PWY formaldehyde oxidation I	- 0.725846352984813	0.0563313324492285

Table S2C. Most significant correlations between cytokines and predicted metagenomic functions (KEGG pathways) in the samples collected in healthy sites as assessed by Pearson correlation with false-discovery-rate correction.

cytokines	PATHWAYS	Correlation	FDR corrected P value
IL-17A	BENZCOA-PWY anaerobic aromatic compound degradation (Thauera aromatica)	0.752822764264593	0.0606265156466369
IL-6	PWY-5499 vitamin B6 degradation	0.735332831719876	0.0606265156466369
IL-6	PWY-7402: benzoate fermentation (to acetate and cyclohexanecarboxylate)	benzoate fermentation (to acetate and cyclohexanecarboxylate)	0.0622478814555644

IL-17A	DENITRIFICATION-PWY nitrate reduction I (denitrification)	0.704120083027345	0.0702784389741
IL-17A	PWY-7402 benzoate fermentation (to acetate and cyclohexane carboxylate)	0.705471289009918	0.0702784389741

Table S2D. Most significant correlations between cytokines and predicted metagenomic functions (KEGG pathways) in the samples collected in periodontitis sites as assessed by Pearson correlation with false-discovery-rate correction.

ENZYMES	ENZYMES names	cytokines	Correlation	FDR corrected P value
1.1.2.7	Methanol dehydrogenase (cytochrome c)	IL-6	0.773298386832442	0.0602654641172393
1.14.19.4	Delta(8)-fatty-acid desaturase	IL-6	0.759263905392162	0.0602654641172393
3.4.23.49	Omptin	IL-6	0.779864140905324	0.0602654641172393
4.1.2.55	aldolase	IL-6	0.758808375620779	0.0602654641172393
4.2.1.66	Cyanide hydratase	IL-6	0.759263905392162	0.0602654641172393

Table S2E. Most significant correlations between cytokines and predicted metagenomic functions (Enzyme Commission) in the samples collected in healthy sites as assessed by Pearson correlation with false-discovery-rate correction.

ENZYMES	ENZYMES names	cytokines	Correlation	FDR corrected P value
1.1.1.105	All-trans-retinol dehydrogenase (NAD(+))	IL-4	0.869243233182877	0.000310357115539233
2.3.2.17	glycyltransferase	IL-4	0.875337744439791	0.000310357115539233
3.5.3.25	N(omega)-hydroxy-L-arginine amidinohydrolase	IL-4	0.83548087667382	0.0021944621149222
1.14.16.1	Phenylalanine 4-monooxygenase	IL-17A	0.826476037589159	0.00282911021140912
1.3.1.75	Divinyl chlorophyllide a 8-vinyl-reductase	IL-6	0.797171936216008	0.0108841160838587
1.14.13.9	Kynurenine 3-monooxygenase	TNF_alpha	0.777746252700735	0.0182933718653553
1.3.8.2	4,4'-diapophytoene desaturase (4,4'-diapolycopene-forming)	IL-10	0.768546994701519	0.0182933718653553

1.8.1.14	CoA-disulfide reductase	IL-10	0.768546993690475	0.0182933718653553
2.3.2.18	glycyltransferase	IL-4	0.773350766173424	0.0182933718653553
2.5.1.96	4,4'-diapophytoene synthase	IL-10	0.768546994552137	0.0182933718653553
3.1.27.6	Enterobacter ribonuclease	IL-6	0.778650981191651	0.0182933718653553
1.10.2.2	Quinol--cytochrome-c reductase	IL-17A	0.75088023364689	0.0242933073163435
1.5.1.36	Flavin reductase (NADH)	IL-6	0.753389316525921	0.0242933073163435
1.7.2.4	Nitrous-oxide reductase	IL-17A	0.751903404506183	0.0242933073163435
2.3.1.207	Beta-ketodecanoyl-[acyl-carrier-protein] synthase	TNF_alpha	0.756946660085144	0.0242933073163435
2.8.3.21	L-carnitine CoA-transferase	IL-4	0.75236649952096	0.0242933073163435
4.2.1.12	Phosphogluconate dehydratase	IL-6	0.752089958274913	0.0242933073163435
3.4.21.72	IgA-specific serine endopeptidase	IL-6	0.74458192422656	0.0292351909194497
1.17.1.1	CDP-4-dehydro-6-deoxyglucose reductase	IL-6	0.734277826214766	0.0405800309771708
1.2.1.68	Coniferyl-aldehyde dehydrogenase	TNF_alpha	0.725785181933035	0.0521493291506078
2.3.2.5	Glutaminy-peptide cyclotransferase	TNF_alpha	0.718330708180412	0.0599002396009973
2.4.1.5	Dextranucrase	TNF_alpha	0.717679891195155	0.0599002396009973
4.2.1.53	Oleate hydratase	TNF_alpha	0.718342687694091	0.0599002396009973
4.2.1.57	Isohexenylglutaconyl-CoA hydratase	TNF_alpha	0.711890489569407	0.0696334110066253
1.1.5.8	Quinate dehydrogenase (quinone)	TNF_alpha	0.703355626100141	0.0816112171008318
3.3.2.1	Isochorismatase	TNF_alpha	0.704536885969368	0.0816112171008318
3.5.1.96	Succinylglutamate desuccinylase	TNF_alpha	0.703558895079998	0.0816112171008318
2.1.1.67	Thiopurine S-methyltransferase	TNF_alpha	0.700895777046166	0.0850759035649384
1.1.3.12	Pyridoxine 4-oxidase	IL-6	0.694091396743781	0.0905060814470634
1.14.13.131	Dimethyl-sulfide monooxygenase	IL-6	0.694688764899713	0.0905060814470634
1.2.1.72	Erythrose-4-phosphate dehydrogenase	TNF_alpha	0.695793119570367	0.0905060814470634
2.1.3.1	Methylmalonyl-CoA carboxytransferase	IL-6	0.692642965310999	0.0905060814470634

5.3.1.26	Galactose-6-phosphate isomerase	IL-6	0.696249620980044	0.0905060814470634
5.3.3.8	Dodecenoyl-CoA isomerase	TNF_alpha	0.692893829833396	0.0905060814470634
1.1.1.67	Mannitol 2-dehydrogenase	TNF_alpha	0.688250398965159	0.0925809501551899
1.14.11.19	Leucocyanidin oxygenase	TNF_alpha	0.673481630066119	0.0925809501551899
1.14.12.14	2-aminobenzenesulfonate 2,3-dioxygenase	TNF_alpha	0.673481630066139	0.0925809501551899
1.14.15.9	Spheroidene monooxygenase	IL-6	0.68784471866614	0.0925809501551899
1.16.1.3	Aquacobalamin reductase	TNF_alpha	0.687012423909958	0.0925809501551899
1.17.5.1	Phenylacetyl-CoA dehydrogenase	TNF_alpha	0.673461370768913	0.0925809501551899
1.18.1.6	Adrenodoxin-NADP(+) reductase	TNF_alpha	0.673482137546604	0.0925809501551899
1.3.1.19	Cis-1,2-dihydrobenzene-1,2-diol dehydrogenase	TNF_alpha	0.681887070958801	0.0925809501551899
1.3.1.62	Pimeloyl-CoA dehydrogenase	TNF_alpha	0.674271020293024	0.0925809501551899
1.4.9.2	Aralkylamine dehydrogenase (azurin)	TNF_alpha	0.673480929371479	0.0925809501551899
1.5.1.37	FAD reductase (NADH)	TNF_alpha	0.673481620408504	0.0925809501551899
1.5.1.41	Riboflavin reductase (NAD(P)H)	TNF_alpha	0.687012423909958	0.0925809501551899
2.1.1.174	23S rRNA (guanine(1835)-N(2))-methyltransferase	TNF_alpha	0.68424502819233	0.0925809501551899
2.1.1.187	23S rRNA (guanine(745)-N(1))-methyltransferase	TNF_alpha	0.685403930557047	0.0925809501551899
2.3.1.230	2-heptyl-4(1H)-quinolone synthase	TNF_alpha	0.674479269437082	0.0925809501551899
2.5.1.39	4-hydroxybenzoate polyprenyltransferase	IL-6	0.680331190099643	0.0925809501551899
2.7.1.89	Thiamine kinase	TNF_alpha	0.680626041302477	0.0925809501551899
2.7.11.5	[Isocitrate dehydrogenase (NADP(+))] kinase	TNF_alpha	0.682515078565384	0.0925809501551899
2.7.7.58	(2,3-dihydroxybenzoyl)adenylate synthase	TNF_alpha	0.688588475577676	0.0925809501551899
3.1.1.56	Methylumbelliferyl-acetate deacetylase	TNF_alpha	0.67313064148987	0.0925809501551899
3.1.1.84	Cocaine esterase	TNF_alpha	0.67313064148987	0.0925809501551899
3.1.2.21	Dodecanoyl-[acyl-carrier-protein] hydrolase	TNF_alpha	0.680514697309054	0.0925809501551899
3.1.2.25	Phenylacetyl-CoA hydrolase	TNF_alpha	0.673461370768913	0.0925809501551899

3.11.1.3	Phosphonopyruvate hydrolase	TNF_alpha	0.67348150156595	0.0925809501551899
4.1.3.45	3-hydroxybenzoate synthase	TNF_alpha	0.677704069620328	0.0925809501551899
3.6.3.33	Vitamin B12-transporting ATPase	TNF_alpha	0.672457923991846	0.0927878998168351
2.6.1.87	UDP-4-amino-4-deoxy-L-arabinose aminotransferase	TNF_alpha	0.670344055081281	0.0937888980299378
2.7.1.13	Dehydrogluconokinase	TNF_alpha	0.670492432188585	0.0937888980299378
2.7.11.26	[Tau protein] kinase	TNF_alpha	0.671428167068617	0.0937888980299378
2.7.1.73	Inosine kinase	TNF_alpha	0.669243977655225	0.0939098900666312
3.5.1.38	Glutamin-(asparagin-)ase	TNF_alpha	0.669181301430355	0.0939098900666312
2.7.1.8	Glucosamine kinase	TNF_alpha	0.66778349651648	0.0955178620089822
4.2.2.3	Poly(beta-D-mannuronate) lyase	TNF_alpha	0.667482893520241	0.0955178620089822
1.1.1.43	Phosphogluconate 2-dehydrogenase	TNF_alpha	0.664517950891738	0.099221005104641
3.1.1.74	Cutinase	IL-10	0.665054152486899	0.099221005104641
3.4.24.20	Peptidyl-Lys metalloendopeptidase	TNF_alpha	0.664636714155371	0.099221005104641

Table S2F. Most significant correlations between cytokines and predicted metagenomic functions (Enzyme Commission) in the samples collected in periodontitis sites as assessed by Pearson correlation with false-discovery-rate correction.