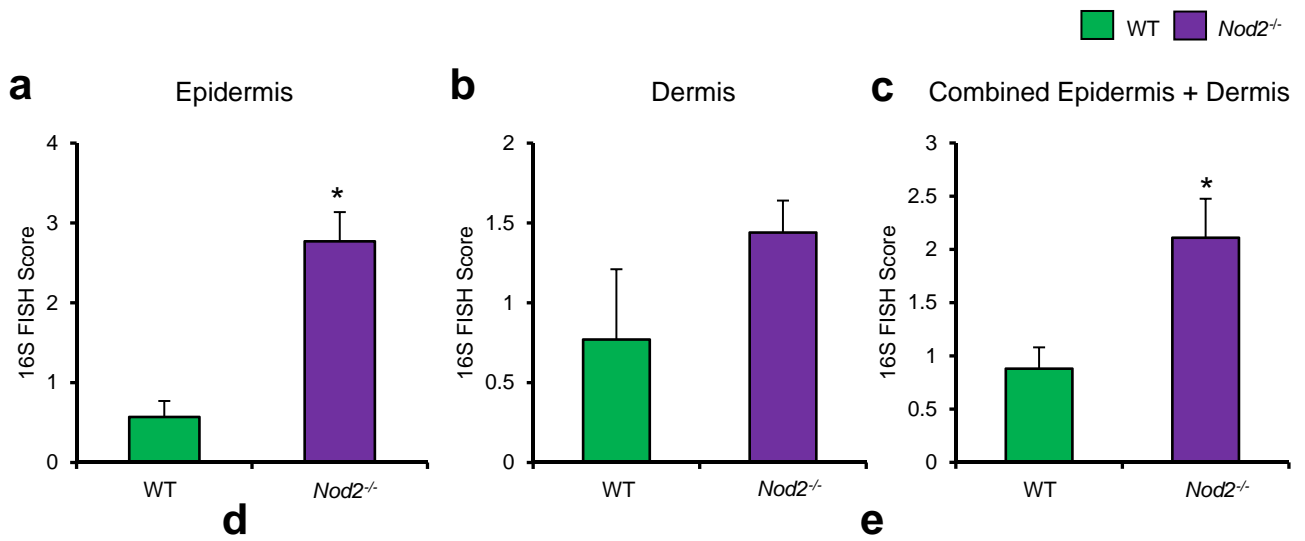


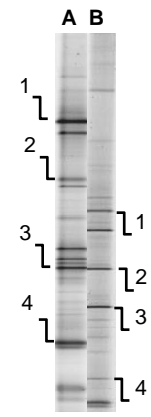
Supplementary Figure S1. Gram-stain quantification. Quantification of Gram-staining showed there was a no significant difference in total eubacterial burden in both WT vs. *Nod2*^{-/-} normal skin (a) epidermis, (b) dermis and (c) combined epidermal and dermal scores. There was, however, a trend towards altered eubacterial abundance in the dermis (b) of *Nod2*^{-/-} normal skin. All data are representative of two independent experiments, with $n = 5$ mice/group. Mean + standard error of the mean. WT, wild type.



d **e**

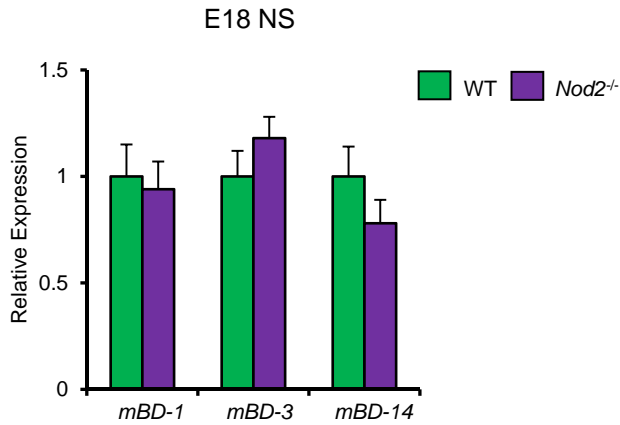
Band	WT	<i>Nod2</i> ^{-/-}
1	<i>Staphylococcus aureus</i> . YP040448	Uncultured actinbacterium. GCP1
2	<i>Staphylococcus epidermidis</i> . D83363	<i>Pseudomonas</i> sp. AF320988
3	<i>Pseudomonas</i> sp. AB013827.	<i>Pseudomonas fragi</i> . AHZY01000001.
4	<i>Actinobacteria</i> sp. cIK1_14b.	<i>Arenibacter certessi</i> . CCUG48006T.

Putative identity of nearest database match and accession number: *ih*, sequence insufficient homology to enable identification;

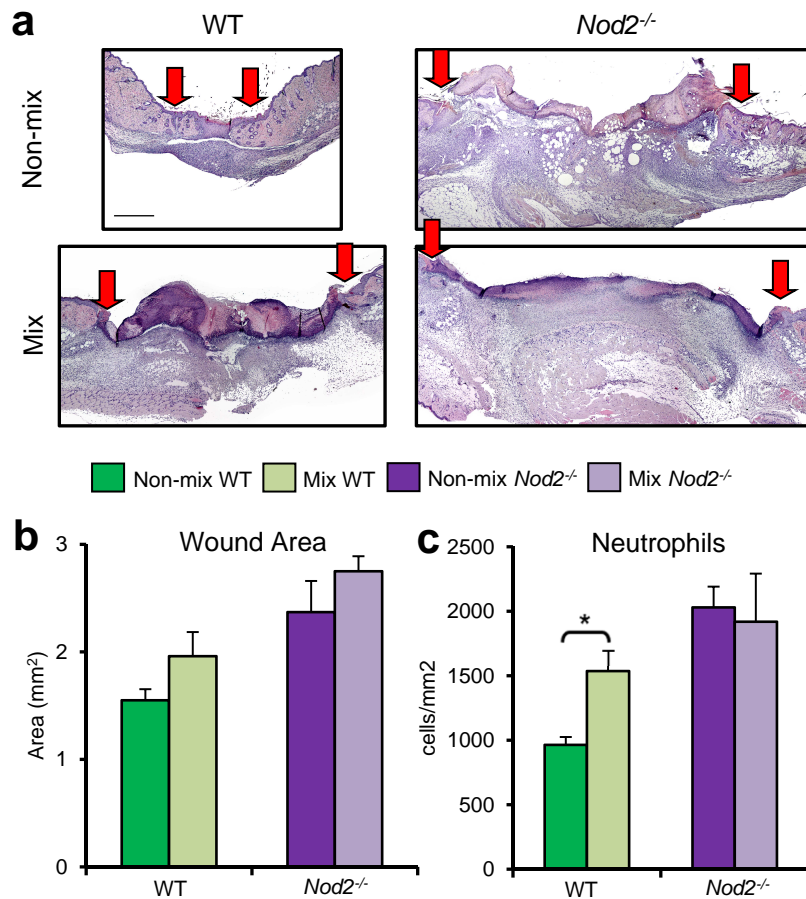


Supplementary Figure S2. Wound microbiome dysbiosis in *Nod2*-deficient mice. (a-c) Quantification of 16S FISH confirmed a significant increase in total eubacterial abundance in *Nod2*^{-/-} day 3 wounds. (d-e) 16S rDNA sequencing of differentially expressed bands from the DGGE fingerprints revealed the bacterial species in wounded WT and *Nod2*^{-/-} mice. All data are representative of two independent experiments, with *n* = 5 mice/group. * *P* < 0.05. Mean + standard error of the mean. FISH, fluorescence in situ hybridization; sp., species; WT, wild type.

a



Supplementary Figure S3. Absence of altered antimicrobial peptide production in *Nod2*-deficient mice obtained via caesarean birth. (a) There was no significant difference in cutaneous *mBD-1*, *-3* or *-14* in *Nod2*^{-/-} mouse skin versus WT from mice born via caesarean section. All data are representative of two independent experiments with $n = 8-10$ mice/group. Mean + standard error of the mean. E, embryonic day; WT, wild type.



Supplementary Figure S4. Co-housing from birth with a WT mother shows the skin microbiome directly influences healing outcome. Newborn WT and *Nod2^{-/-}* litters were mixed from birth with a WT mother, and then wounded in adulthood. (a) Representative H+E stained sections of excisional wounds (day 5) from WT and *Nod2^{-/-}* control (non-mix), and co-housed (mix) cages (arrows denote wound margins). (b) Quantification showed significantly delayed healing in *Nod2^{-/-}* mice co-housed with WT mice, with (c) increased local neutrophil influx. All data are representative of two independent experiments with $n = 6$ mice/non-mix groups and $n = 5$ mice/mix group. * $P < 0.05$. Mean + stand error of the mean. Scale bar = 250 μ M (a). WT, wild type.

Supplementary Table S1. Average proportion of genera for all mapped reads from the 16S Illumina high-throughput sequencing data, including probability values as determined by one-way ANOVA.

	WT	Nod2 ^{-/-}	Mix	P value
k_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Weeksellaceae.g	0.00314	0	0.00018	0.00019
k_Bacteria.p_GN02.c_BD1.5.o_f_g	0.00011	0.00162	0	0.00354
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.g_Micrococcus	4.8E-05	0.00058	0.00176	0.00457
k_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Flavobacteriaceae.g	0.00205	0.00673	0.00203	0.00998
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Legionellales.f_Coxiellaceae.g_Rickettsiella	0	0.00098	0	0.01268
k_Bacteria.p_OD1.c_ZB2.o_f_g	0.00041	0.00294	0.00026	0.01494
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Coproccoccus	0	0	0.00032	0.01507
k_Bacteria.p_Proteobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Campylobacteraceae.g_Campylobacter	0.00143	0	0	0.01603
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Brevibacteriaceae.g_Brevibacterium	0.0082	0.00633	0.0035	0.0169
k_Bacteria.p_TM7.c_SC3.o_f_g	0	0.0006	0	0.01718
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Pasteurellales.f_Pasteurellaceae.g_Actinobacillus	0.00559	0	0.00018	0.01868
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g	0.116	0.12887	0.09599	0.02616
k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae.g_Sphingomonas	0.00049	0.0006	0.00259	0.02692
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Pasteurellales.f_Pasteurellaceae.g_Aggregatibacter	0.00057	0.0017	0.01141	0.02792
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Leuconostocaceae.g	0.00275	0.00105	0.00049	0.02851
k_Bacteria.p_Proteobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Campylobacteraceae.g_Arcobacter	0	0.00077	0	0.03126
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Corynebacteriaceae.g_Corynebacterium	0.08297	0.07383	0.04718	0.0387
k_Bacteria.p_Proteobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Helicobacteraceae.g_Helicobacter	9.57E-06	0	4E-05	0.04988
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae.g	9.6E-05	0	0.00151	0.05335
k_Bacteria.p_Actinobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Campylobacteriaceae.g_Sulfurospirillum	0	0	0.00084	0.05345
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g	0	0.0016	0.0033	0.05784
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g_Paenisporsosarcina	0	0	0.00029	0.05944
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Exiguobacteraceae.g_Exiguobacterium	0.00013	4.8E-05	0.00356	0.06115
k_Bacteria.p_Proteobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Helicobacteraceae.Other	0.00022	0.00087	0.0029	0.063
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g	9.6E-05	0	0.00108	0.07044
k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Phyllobacteriaceae.Other	0.00948	0.00769	0.00511	0.08109
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Bdellovibrionales.f_Bacteriovoraceae.g	0	0.00023	0	0.08894
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Burkholderiaceae.g_Burkholderia	5.74E-05	0.00116	0.00033	0.09309
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Leuconostocaceae.g_Leuconostoc	0	0.0006	0.00221	0.10767
k_Bacteria.p_Actinobacteria.c_Coriobacteriales.f_Coriobacteriaceae.g_Atopobium	0.00337	0.00104	0.00204	0.10879
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Lactococcus	0	0	0.0005	0.11566
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyrinomonadaceae.g_Parabacteroides	0	3.8E-05	0.00076	0.11989
Unassigned.Other.Other.Other.Other	0.0148	0.01508	0.00966	0.12002
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.Other	0.00057	0.00282	0.00121	0.12411
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus	0.08336	0.0631	0.04731	0.13493
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcaceae.g_Enterococcus	0.06768	0.05184	0.04181	0.15836
k_Bacteria.p_Proteobacteria.c_Epsilonproteobacteria.o_Campylobacteriales.f_Helicobacteraceae.g	0	0.00113	6.89E-05	0.17481
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g_vadinHB04	0	0	0.0003	0.17855
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g_Lysinibacillus	0	0.00055	0	0.17906
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Proteus	0.00122	0.00269	0.00085	0.18763
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Staphylococcaceae.g_Staphylococcus	0.30266	0.32254	0.24689	0.18925
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Dehalobacteriaceae.g_Dehalobacterium	0	0.00019	0	0.19852
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Pseudomonadaceae.g	2.9E-05	0.00057	0.00557	0.19956
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.Other	0	0.00011	0.00015	0.19993
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.Other.Other	0.00171	0.00284	0.0011	0.2107
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae.g_Akkermansia	0	0.00088	0.00014	0.21867
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Citrobacter	0	0.00104	0.00281	0.22641
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.Other	9.57E-06	0	2.9E-05	0.23156
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Mycobacteriaceae.g_Mycobacterium	0	0	0.00049	0.23489
k_Bacteria.p_Fusobacteria.c_Fusobacteriales.f_Leptotrichiaceae.g	0.00093	0	0	0.24174
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae.Other	0	0	0.00165	0.24274
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Tepidimonas	0	0	0.00025	0.25053
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Moraxellaceae.g_Acinetobacter	0.00331	0.00874	0.12338	0.25066
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_g	0.02757	0.0244	0.01827	0.26236
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Dermabacteriaceae.g_Dermabacter	0.00097	0.00123	0.00026	0.26966
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.g_Granulicatella	0.00174	2.9E-05	0.00029	0.27766
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Neisseriales.f_Neisseriaceae.g	0.00055	0	0.00015	0.27905
k_Bacteria.Other.Other.Other.Other.Other	0	0	1.1E-05	0.2892
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Dermabacteriaceae.Other	0	9.57E-06	0	0.2892
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Microbacteriaceae.Other	0	9.57E-06	2.3E-05	0.2892
k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Microbacteriaceae.g_Leucobacter	0	0.00031	0	0.2892
k_Bacteria.p_Actinobacteria.c_Coriobacteriales.f_Coriobacteriaceae.g	0.0002	0	0	0.2892
k_Bacteria.p_Armatimonadetes.c_Chthonomonadetes.o_Chthonomonadales.f_Chthonomonadaceae.g_Chthonomonas	0.00054	0	0	0.2892
k_Bacteria.p_Armatimonadetes.c_Fimbrimonadetes.o_Fimbrimonadales.f_Fimbrimonadaceae.g_Fimbrimonas	0	0.00019	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Paraprevotellaceae.g_Prevotella	0.00563	0	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Cryomorphaceae.g_Fluviicola	0	0.00026	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Weeksellaceae.g_Wautersiella	0	9.57E-06	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Sphingobacteriales.f_Sphingobacteriales.f_g	6.7E-05	0	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Saprospirales.f_Chitinophagaceae.g_Sediminibacterium	1.91E-05	0	0	0.2892
k_Bacteria.p_Bacteroidetes.c_Saprospirales.f_Saprospiraceae.g	0	0.0002	0	0.2892
k_Bacteria.p_Cyanobacteria.c_Chloroplast.o_Cryptophyta.f_g	0	0.00013	0	0.2892
k_Bacteria.p_Cyanobacteria.c_Chloroplast.o_Stramenopiles.f_g	4.8E-05	0	0	0.2892
k_Bacteria.p_Cyanobacteria.c_Synechococcales.f_Synechococcaceae.g_Synechococcus	0	0.00059	0	0.2892
k_Bacteria.p_Firmicutes.Other.Other.Other	0	0	1.1E-05	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g_Anoxybacillus	1.91E-05	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g_Geobacillus	0	0.00023	0	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Paenibacillaceae.g_Paenibacillus	0	4.8E-05	0	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Staphylococcaceae.g_Salinococcus	0	9.57E-06	0	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Bacillales.f_Thermoactinomyces.g_Trichococcus	1.91E-05	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.g_Trichococcus	0	0	1.1E-05	0.2892
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Leuconostocaceae.Other	0	9.57E-06	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Oribacterium	0.00041	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptococcaceae.g_Peptococcus	0.00022	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptostreptococcaceae.g_Filifactor	9.57E-06	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptostreptococcaceae.g_Peptostreptococcus	0.00067	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Faecalibacterium	0	4.8E-05	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.Other	9.57E-06	0	0	0.2892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g_Megasphaera	0.00203	0	0	0.2892

k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Selenomonas	0.00113	0	0	0.2892
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Mogibacteriaceae_g	0.00063	0	0	0.2892
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Tissierellaceae_g	7.7E-05	0	0	0.2892
k_Bacteria_p_Fusobacteria_c_Fusobacteria_o_Fusobacteriales_f_Fusobacteriaceae_g_Cetobacterium	0	0.00011	0	0.2892
k_Bacteria_p_GN02_c_3BR.5F_o_f_g	0	9.57E-06	0	0.2892
k_Bacteria_p_Planctomycetes_c_Planctomycetia_o_Gemmatales_f_Gemmataceae_g_Gemmata	0	0.00013	0	0.2892
k_Bacteria_p_Planctomycetes_c_Planctomycetia_o_Gemmatales_f_Isosphaeraceae_g	0	0.0002	0	0.2892
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Ellin329.f_g	0	9.57E-06	0	0.2892
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhodobacteriales_f_Rhodobacteraceae_g_Rhodobacter	0	7.7E-05	0	0.2892
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales_f_g	0	0.00039	0	0.2892
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales_f_Rickettsiaceae_g	0	0.00023	0	0.2892
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Sphingomonadales_f_g	0	0.00032	0	0.2892
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Alcaligenaceae_g_Sutterella	0	0.00011	0	0.2892
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g_Ramlibacter	0	9.57E-06	0	0.2892
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Rhodocyclales_f_Rhodocyclaceae_g_Propionivibrio	9.57E-06	0	0	0.2892
k_Bacteria_p_Proteobacteria_c_Deltaproteobacteria_o_Myxococcales_f_Polyangiaceae_Other	6.7E-05	0	0	0.2892
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Xanthomonadales_f_Xanthomonadaceae_Other	2.9E-05	0	0	0.2892
k_Bacteria_p_Synergistetes_c_Synergistia_o_Synergistales_f_Dethiosulfonitrilobacteraceae_g_TG5	1.91E-05	0	0	0.2892
k_Bacteria_p_TM7_c_o_f_g	0.00011	0	0	0.2892
k_Bacteria_p_TM7_c_TM7.3_o_CW040.f_g	0.00055	0	0	0.2892
k_Bacteria_p_Verrucomicrobia_c_Opitutae_o_Opitutales_f_Opitutaceae_g_Opitutus	9.57E-06	0	0	0.2892
k_Bacteria_p_Verrucomicrobia_c_Spartobacteria_o_Chthoniobacterales_f_Chthoniobacteraceae_g	0	0.00027	0	0.2892
k_Bacteria_p_Verrucomicrobia_c_Spartobacteria_o_Chthoniobacterales_f_Chthoniobacteraceae_g_Candidatus.Xiphinematobacter	0	0.00036	0	0.2892
k_Bacteria_p_ZB3_c_BS119.o_f_g	0	0.00015	0	0.2892
k_Bacteria_p_Cyanobacteria_c_Chloroplast.o_Streptophyta_f_g	0.00602	0.0263	0.03198	0.29009
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Nocardiaceae_g_Rhodococcus	0	0	8.6E-05	0.29148
k_Bacteria_p_Verrucomicrobia_c_Opitutae_o_HA64.f_g	0	0	0.00014	0.29276
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_g	0.0002	0.00126	0.00055	0.29354
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_g	0	0.0004	5.7E-06	0.29491
k_Bacteria_p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Bulleidia	0.00039	0	5.7E-06	0.29505
k_Bacteria_p_Cyanobacteria_c_4C0d.2_o_YS2.f_g	0	0	0.00015	0.29551
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g_Delftia	0.00032	0.00019	4.59E-05	0.29572
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Nocardiodiaceae_g_Aeromicrobium	9.6E-05	0.00072	0	0.29659
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Leionellales_f_Leionellaceae_g	0	0.00045	4.59E-05	0.29857
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Actinomycetaceae_Other	0	0.00044	1.1E-05	0.29948
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhodospirillales_f_Rhodospirillaceae_g_Azospirillum	0	0	8.04E-05	0.29958
k_Bacteria_p_Acidobacteria_c_Chloracidobacteria_o_RB41.f_Ellin6075_g	9.57E-06	0.00016	0	0.30317
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Sphingomonadales_f_Sphingomonadaceae_g_Sphingobium	0	0	0.00063	0.30456
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Micrococcales_g_Renibacterium	0.00013	9.57E-06	0	0.30625
k_Bacteria_p_Actinobacteria_c_Rubrobacteria_o_Rubrobacteriales_f_Rubrobacteraceae_g_Rubrobacter	0.00036	0	1.7E-05	0.30962
k_Bacteria_p_Actinobacteria_c_Alphaproteobacteria_o_f_g	0.0004	3.8E-05	0	0.31211
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Micrococcales_g_Kocuria	9.57E-06	0	0.00053	0.31422
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Leionellales_f_Leionellaceae_g_Legionella	0	8.6E-05	5.7E-06	0.31915
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Clostridium	0.00273	0.00136	0.00161	0.32116
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Dermacoccaceae_g_Dermacoccus	0.00066	0.00019	0.00018	0.32335
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Veillonella	0.02822	0.00474	0.00191	0.32897
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Sphingomonadales_f_Erythrobacteraceae_g	0	6.7E-05	5.7E-06	0.32921
k_Bacteria_p_Cyanobacteria_c_ML635J.21.o_f_g	0.00046	0	4.02E-05	0.33019
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_g_Janthinobacterium	0	9.57E-06	0.00086	0.33168
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g_Prevotella	0.02799	0.00159	0.00454	0.33181
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_Gemellaceae_g_Gemella	0.00521	0.04544	0.00592	0.33343
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Streptococcaceae_g	5.74E-05	0.00014	5.7E-06	0.33362
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g	0.00012	0.00124	0.00051	0.33768
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Erwinia	2.9E-05	1.91E-05	0.0007	0.33859
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Methylophilales_f_Methylophilaceae_g	1.91E-05	0.0002	1.1E-05	0.33964
k_Bacteria_p_Bacteroidetes_c_Flavobacteria_o_Flavobacteriales_f_Flavobacteriaceae_g_Flavobacterium	4.8E-05	0.00035	5.17E-05	0.34026
k_Bacteria_p_Proteobacteria_c_Deltaproteobacteria_o_Desulfonitrilobacteriales_f_Desulfonitrilobacteraceae_g	0	0.00042	5.17E-05	0.34084
k_Bacteria_p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Leuconostocaceae_g_Weissella	0	0	3.44E-05	0.34288
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pseudomonadales_f_Moraxellaceae_g_Enhydrobacter	0.002	0.00036	0.00157	0.34575
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Butyrvibrio	4.8E-05	0	5.7E-06	0.34886
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_g_Polynucleobacter	0	9.6E-05	1.1E-05	0.34886
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Dietziaceae_Other	0	0.00037	5.17E-05	0.34919
k_Bacteria_p_Deferribacteres_c_Deferribacteres_o_Deferribacterales_f_Deferribacteraceae_g_Mucispirillum	0	0	0.00032	0.35307
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Rhizobiaceae_g_Agrobacterium	0.00058	0.00104	0.00135	0.35625
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Hyphomicrobiaceae_g_Devesia	0	8.6E-05	1.1E-05	0.35699
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhodospirillales_f_Acetobacteraceae_g	0	2.9E-05	1.1E-05	0.35699
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g_Comamonas	0	0	0.00119	0.36243
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Bogoriellaceae_g_Georginia	2.9E-05	3.83E-05	0.00012	0.36246
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Neisseriales_f_Neisseriaceae_g_Neisseria	0.00401	6.7E-05	0.00083	0.3691
k_Bacteria_p_TM7_c_TM7.3.o_f_g	0.00139	0	0.00028	0.37334
k_Bacteria_p_Proteobacteria_Other_Other_Other_Other	9.57E-06	6.7E-05	5.7E-06	0.37438
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Serratia	0.00013	4.8E-05	0	0.37575
k_Bacteria_p_Proteobacteria_c_Deltaproteobacteria_o_Desulfonitrilobacteriales_f_Desulfonitrilobacteraceae_g_Desulfovibrio	0	0	0.00033	0.37799
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Ruminococcus	4.8E-05	0.00065	0.0001	0.38082
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pasteurellales_f_Pasteurellaceae_Other	3.8E-05	0	6.89E-05	0.38149
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Actinomycetaceae_g_Actinomycetes	0.00389	0.00209	0.00069	0.38492
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Caulobacteriales_f_Caulobacteraceae_g	0.00042	0.00034	0.00087	0.38534
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_Gemellaceae_g	0.0017	0.00286	0.00362	0.38795
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae_g	0	9.57E-06	0.00046	0.3914
k_Bacteria_p_Firmicutes_c_Bacilli_o_Gemellales_f_g	9.57E-06	0.00034	0.00057	0.40063
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Leionellales_f_g	0	5.7E-05	1.1E-05	0.40095
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_Other_Other_Other	0	0	2.3E-05	0.40095
k_Bacteria_p_Proteobacteria_c_Gammaproteobacteria_o_Pasteurellales_f_Pasteurellaceae_g	2.9E-05	0	5.7E-06	0.40095
k_Bacteria_p_Actinobacteria_c_Betaproteobacteria_o_Methylophilales_f_Methylophilaceae_g_Methylotenera	0	0	6.89E-05	0.40096
k_Bacteria_p_Bacteroidetes_c_Sphingobacteria_o_Sphingobacteriales_f_Sphingobacteriaceae_g	9.57E-06	1.91E-05	0	0.4037
k_Bacteria_p_Planctomycetes_c_Phycisphaerae_o_Phycisphaerales_f_g	1.91E-05	9.57E-06	0	0.4037
k_Bacteria_p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrmonadaceae_g	0	0	0.00151	0.40662
k_Bacteria_p_Firmicutes_c_Clostridia_o_Clostridiales_f_Tissierellaceae_g_Helcococcus	0.013	0.01404	0.00876	0.41212
k_Bacteria_p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_g_Ralstonia	8.6E-05	6.7E-05	0.00033	0.41857
k_Bacteria_p_Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Phylobacteriaceae_g	0.00218	0.00164	0.00137	0.41942
k_Bacteria_p_Fusobacteria_c_Fusobacteria_o_Fusobacteriales_f_Leptotrichiaceae_g_Leptotrichia	0.00098	0	0.00022	0.42161
k_Bacteria_p_Actinobacteria_c_Actinobacteria_o_Bifidobacteriales_f_Bifidobacteriaceae_g_Bifidobacterium	7.7E-05	0.00011	0	0.42604

k_Bacteria_p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Odoribacteraceae.g_Odoribacter	4.8E-05	0	1.1E-05	0.42915
k_Bacteria_p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_S24.7.g	0.00111	0.00075	0.00201	0.42928
k_Bacteria_p_Firmicutes.c_Bacilli.o_Gemellales.Other.Other	9.57E-06	4.78E-05	2.9E-05	0.42946
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.Other	0.0005	0.00139	0.00109	0.43014
k_Bacteria_p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Porphyromonas	0.00036	0.00011	3.44E-05	0.43517
k_Bacteria_p_Proteobacteria.c_Deltaproteobacteria.o_Bdellovibrionales.f_Bdellovibrionaceae.g_Bdellovibrio	0	0.00011	2.9E-05	0.43632
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Tissierellaceae.g_Parvimonas	0.00021	0.00025	0	0.4381
k_Bacteria_p_Firmicutes.c_Erysipelotrichi.o_Erysipelotrichales.f_Erysipelotrichaceae.g	0	0	0.00014	0.44079
k_Bacteria_p_Actinobacteria.c_Coriobacteriales.f_Coriobacteriaceae.g_Adlercreutzia	0.00019	0	0.00023	0.44314
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcaceae.g	0.00022	0.00012	5.2E-05	0.44435
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rickettsiales.f_mitochondria.Other	0.00448	0.01322	0.01467	0.4464
k_Bacteria_p_Bacteroidetes.c_Flavobacteriales.f_Flavobacteriales.f_Weeksellaceae.g_Cloacibacterium	0	9.57E-06	0.00019	0.4476
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Phyllobacteriaceae.g_Aminobacter	0	1.91E-05	1.7E-05	0.44761
k_Bacteria_p_TM6.c_SJA.4.o_f.g	0	0	0.00026	0.45312
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.Other	0.00011	9.57E-06	2.30E-05	0.45322
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Actinomycetaceae.g_Arcanobacterium	0.02861	0.03215	0.02287	0.45508
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pasteurellales.f_Pasteurellaceae.g_Haemophilus	0.00281	0.00037	0.00105	0.45696
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Trabulsilla	2.9E-05	7.65E-05	4.02E-05	0.46045
k_Bacteria_p_Proteobacteria.c_Sphingobacteria.o_Sphingobacteriales.f_Sphingobacteriaceae.g_Pedobacter	0	0	0.00045	0.46203
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Brucellaceae.g_Ochrobactrum	0.00034	0.00066	0.00028	0.46422
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.Other	0	0	3.4E-05	0.46822
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g_Anaerobacillus	0	1.91E-05	5.7E-06	0.47227
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Enterobacter	1.91E-05	0	5.7E-06	0.47227
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.g	0.00608	0.00809	0.00925	0.48016
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g	0.00011	0.00077	0.00047	0.49121
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Aerococcaceae.Other	0	0	0.0004	0.49964
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g_Sporosarcina	0.00044	0	0.00015	0.49997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylobacteriaceae.g	0	0	0.00045	0.50127
k_Bacteria_p_Fusobacteria.c_Fusobacteriales.f_Fusobacteriaceae.g_Fusobacterium	0.00126	0	0.00051	0.50685
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_g	0.00264	0.00634	0.0068	0.52194
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Shewanellaceae.g_Shewanella	0.00044	4.8E-05	0.0002	0.52602
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Microbacteriaceae.g_Pseudoclavibacter	0.00267	0.00136	0.00242	0.53026
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.g_Rothia	0.00276	0.00056	0.00121	0.54166
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g_Bacillus	0.00057	6.70E-05	0.00039	0.54293
k_Bacteria_p_Bacteroidetes.c_Saprosirales.o_Saprosirales.f_Chitinophagaceae.g_Flavisolobacter	3.8E-05	0	0.00042	0.54371
k_Bacteria_p_Spirochaetes.c_Spirochaetes.o_Spirochaetales.f_Spirochaetaceae.g_Treponema	0.00059	0	0.00024	0.54514
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Acetobacteraceae.g_Acetobacter	0.00144	0.00123	0.0007	0.55039
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Moglibacteriaceae.g_Anaerovorax	0	0	0.00026	0.55061
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g_Dialister	0	0.00045	0.00019	0.55449
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Rhizobiaceae.Other	0	0	0.00011	0.56243
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Aerococcaceae.g_Facklamia	0.0029	0.00413	0.0017	0.56891
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Oscillospira	0.0002	0.00112	0.00145	0.57637
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.g_Arthrobacter	9.57E-06	0.00011	0.00042	0.57831
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Staphylococcaceae.Other	2.9E-05	9.57E-06	1.1E-05	0.57838
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptostreptococcaceae.g	0	0	0.00025	0.58267
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Pseudomonadaceae.g_Pseudomonas	0.01004	0.00351	0.00491	0.58696
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Moraxellaceae.g_Psychrobacter	0	9.57E-06	0.00021	0.59287
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Aerococcaceae.g_Aerococcus	0.00027	0	0.00013	0.59592
k_Bacteria_p_Acidobacteria.c_Acidobacteria.6.o_iii1.15.f.g	0	0	0.00013	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Dermabacteraceae.g_Brachybacterium	0	0	0.0002	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Intrasporangiaceae.g_Janibacter	0	0	0.00018	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Microbacteriaceae.g	0	0	5.17E-05	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Micrococcaceae.g_Nesteronkia	0	0	5.7E-06	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Nocardioideae.g_Nocardioides	0	0	3.44E-05	0.5997
k_Bacteria_p_Actinobacteria.c_Thermoleophilina.o_Solirubrobacterales.Other.Other	0	0	4.59E-05	0.5997
k_Bacteria_p_Armatimonadetes.c_Armatimonadia.o_Armatimonadales.f_Armatimonadaceae.g	0	0	0.00013	0.5997
k_Bacteria_p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_AF12	0	0	0.00021	0.5997
k_Bacteria_p_Bacteroidetes.c_Cytophagia.o_Cytophagales.f_Cytophagaceae.g	0	0	5.17E-05	0.5997
k_Bacteria_p_Bacteroidetes.c_Cytophagia.o_Cytophagales.f_Cytophagaceae.g_Hymenobacter	0	0	5.7E-05	0.5997
k_Bacteria_p_Bacteroidetes.c_Rhodothermiales.o_Rhodothermiales.f_Balneolaceae.g_KSA1	0	0	0.00018	0.5997
k_Bacteria_p_Chlamydiae.c_Chlamydia.o_Chlamydiales.f_g	0	0	5.7E-05	0.5997
k_Bacteria_p_Chlamydiae.c_Chlamydia.o_Chlamydiales.f_Parachlamydiaceae.Other	0	0	5.7E-06	0.5997
k_Bacteria_p_Cyanobacteria.c_Oscillatoriothycideae.o_Chroococcales.f_Xenococcaceae.g	0	0	6.89E-05	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g_Planomicrobium	0	0	5.7E-06	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Exiguobacteraceae.g	0	0	1.1E-05	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.g	0	0	0.00013	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcaceae.g_Melissococcus	0	0	1.1E-05	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g	0	0	0.00025	0.5997
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.Other	0	0	5.7E-06	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Christensenellaceae.g	0	0	1.1E-05	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae.g	0	0	1.7E-05	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Acetobacterium	0	0	1.1E-05	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.Other	0	0	1.7E-05	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptococcaceae.g	0	0	1.1E-05	0.5997
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g_Anaeromusa	0	0	0.0004	0.5997
k_Bacteria_p_Gemmatimonadetes.c_Gemmatimonadetes.o_f.g	0	0	5.17E-05	0.5997
k_Bacteria_p_OD1.c_o_f.g	0	0	7.46E-05	0.5997
k_Bacteria_p_OD1.c_SM2F11.o_f.g	0	0	8.6E-05	0.5997
k_Bacteria_p_Planctomycetes.c_Planctomycetia.o_Pirellulales.f_Pirellulaceae.g	0	0	2.9E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacteriales.f_Caulobacteraceae.g_Brevundimonas	0	0	0.0001	0.5997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae.g	0	0	0.00017	0.5997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Acetobacteraceae.g_Gluconobacter	0	0	0.0002	0.5997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Rhodospirillaceae.g	0	0	0.00025	0.5997
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae.g_Sphingopyxis	0	0	5.7E-06	0.5997
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.Other.Other.Other	0	0	1.1E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Curvibacter	0	0	8.6E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae.g_Cupriavidus	0	0	1.1E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Deltaproteobacteria.o_MIZ46.f.g	0	0	1.7E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Cardiobacteriales.f_Cardiobacteriaceae.g_Cardiobacterium	0	0	0.00015	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Chromatiales.f_g	0	0	0.00021	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.Other.Other	0	0	1.1E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Moraxellaceae.g	0	0	1.1E-05	0.5997

k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Pseudomonadaceae.Other	0	0	5.7E-06	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Xanthomonadales.f_Xanthomonadaceae.g_Luteibacter	0	0	2.30E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Xanthomonadales.f_Xanthomonadaceae.g_Lysobacter	0	0	4.02E-05	0.5997
k_Bacteria_p_TM7.c_TM7.3.o_CW040.f_F16.g	0	0	0.00025	0.5997
k_Bacteria_p_Thermi.c_Deinococci.o_Deinococcales.f_Deinococcaceae.g_Deinococcus	0	0	7.46E-05	0.5997
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Beutenbergiaceae.g_Salana	0	0	3.44E-05	0.5997
k_Bacteria_p_Armatimonadetes.c_Armatimonadia.o_Armatimonadales.f_Armatimonadaceae.g_Armatimonas	0	0	3.44E-05	0.5997
k_Bacteria_p_Chlamydiae.c_Chlamydia.o_Chlamydiales.f_Rhabdochlamydiaceae.g_Candidatus.Rhabdochlamydia	0	0	3.44E-05	0.5997
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Salinisphaerales.f_Salinisphaeraceae.g_Salinisphaera	0	9.57E-06	0.00136	0.60172
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g	0.00105	0.00239	0.00126	0.61075
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Aerococcaceae.g	0	0.00022	0.00011	0.61076
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Staphylococcaceae.g_jeotgaliococcus	0	9.57E-06	0.00018	0.61451
k_Bacteria_p_Proteobacteria.c_Deltaproteobacteria.o_Myxococcales.f_g	0	9.57E-06	0.00013	0.62019
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g	0.00383	0.0048	0.00358	0.6202
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Bradyrhizobiaceae.Other	0	5.7E-05	0.00011	0.62142
k_Bacteria_p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Flavobacteriaceae.g_Capnocytophaga	0.00049	0	0.00073	0.62412
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Gordoniaceae.g_Gordonia	1.91E-05	0.00016	0.00013	0.63502
k_Bacteria_p_Firmicutes.c_Bacilli.Other.Other	0	9.57E-06	5.7E-06	0.64537
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_f_g	0	0.00014	8.6E-05	0.64537
k_Bacteria_p_TM7.c_TM7.1.o_f_g	2.9E-05	0	0.00015	0.65006
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae.Other	9.57E-06	0	4.59E-05	0.65579
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Dietziaceae.g_Dietzia	0	4.8E-05	0.00022	0.65709
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae.Other	9.57E-06	2.9E-05	0.00019	0.65842
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Nocardioideaceae.g	0	1.91E-05	8.04E-05	0.66292
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Aerococcaceae.g_Alloiooccus	1.91E-05	0	7.46E-05	0.66717
k_Bacteria_p_SR1.c_o_f_g	5.7E-05	0	5.17E-05	0.66736
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Xanthomonadales.f_Xanthomonadaceae.g	0.0002	0	0.00025	0.66771
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Actinomycetaceae.g_Actinobaculum	0	4.8E-05	0.00017	0.6741
k_Bacteria_p_Cyanobacteria.c_4C0d.2.o_MLE1.12.f_g	0	4.8E-05	0.00015	0.68113
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales.f_Aeromonadaceae.g	0.00081	0.00031	0.00038	0.6938
k_Bacteria_p_Firmicutes.c_Bacilli.o_Gemellales.f_Gemellaceae.Other	0	9.57E-06	2.30E-05	0.69912
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcaceae.g_Vagococcus	0.00015	9.57E-06	0.00015	0.70622
k_Bacteria_p_Planctomycetes.c_Planctomycetia.o_Gemmatales.f_Gemmataceae.g	0	8.6E-05	7.46E-05	0.71157
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Planococcaceae.g_Rummeliibacillus	0.00012	0	0.00015	0.71357
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Intrasporangiaceae.Other	0	1.91E-05	1.7E-05	0.71569
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Acetobacteraceae.Other	9.57E-06	2.9E-05	1.1E-05	0.71569
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae.g	7.7E-05	9.57E-06	0.00015	0.71782
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Klebsiella	0.00021	0.00068	0.00042	0.71813
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.Other.Other	0	9.57E-06	1.7E-05	0.71816
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Tissierellaceae.g_Anaerococcus	0.03449	0.0322	0.02871	0.72006
k_Bacteria_p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.Other	2.9E-05	0	4.59E-05	0.72446
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Alcaldigenaceae.g_Achromobacter	0	0.00011	0.00018	0.72446
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacteriales.f_Rhodobacteraceae.g_Amaricoccus	7.7E-05	0	8.04E-05	0.72722
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.g_Zoogloea	0.0002	0	0.00022	0.72866
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacteriales.f_Rhodobacteraceae.g_Paracoccus	0	0.0002	0.00026	0.73095
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Microbacteriaceae.g_Microbacterium	0.00016	0.00032	0.00021	0.75145
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.Other	7.65E-05	3.83E-05	0.00019	0.7577
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcaceae.Other	0.00116	0.00172	0.00098	0.76476
k_Bacteria_p_Firmicutes.c_Bacilli.o_Bacillales.Other.Other	0.00061	0.00037	0.0005	0.76886
k_Bacteria_p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus	0.00108	0.00072	0.00062	0.76961
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Ruminococcus	0.00011	0.00033	0.00037	0.77236
k_Bacteria_p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Burkholderiaceae.g_Lautropia	0.00018	2.9E-05	0.00017	0.79238
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Tissierellaceae.g_Peptoniphilus	0.00599	0.00718	0.00749	0.79388
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.Other.Other	0.00034	0.00077	0.00055	0.80237
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Bradyrhizobiaceae.g	8.6E-05	3.8E-05	0.00014	0.84204
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Moryella	0.00221	0.00162	0.00163	0.8713
k_Bacteria_p_Bacteroidetes.c_Sphingobacteriales.f_Sphingobacteriaceae.g_Sphingobacterium	0.00052	0.00094	0.0006	0.88634
k_Bacteria_p_Firmicutes.c_Clostridia.o_Clostridiales.f_Tissierellaceae.g_Finogoldia	0.00685	0.00569	0.00666	0.91703
k_Bacteria_p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides	0.00154	0.00213	0.00154	0.92707
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylobacteriaceae.g_Methylobacterium	0.00033	0.00028	0.00024	0.9394
k_Bacteria_p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Propionibacteriaceae.g_Propionibacterium	0.00124	0.00126	0.00142	0.94828
k_Bacteria_p_Proteobacteria.c_Gammaproteobacteria.o_Xanthomonadales.f_Xanthomonadaceae.g_Stenotrophomonas	0.00205	0.00242	0.00219	0.96167
k_Bacteria_p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Phyllobacteriaceae.g_Phyllobacterium	0.00022	0.00024	0.00028	0.9742
k_Bacteria_p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Weeksellaceae.g_Chryseobacterium	0.00079	0.00068	0.00086	0.97589

Supplementary Table S2. Primer sequences for DGGE, 16S Illumina high-throughput sequencing and qPCR-amplified genes.

Target Gene	Forward primer sequence (5' - 3')	Reverse primer sequence (5' - 3')
16S rRNA gene (PCR - DGGE)	(P3_GC-341F) 5'-CGC CCG CCG GGC GCG GCG GGC GGG GCG GGG GCA CGG GGG GCC TAC GGG AGG CAG CAG-3'	(P2_518R) 5'-ATT ACC GCG GCT GCT GG-3'
16S rRNA gene (PCR - Illumina)	5'-TCG TCG GCA GCG TCA GAT GTC TAT AAG AGA CAG CCT ACG GGN GGC WGC AG-3'	5'-GTC TCG TGG GCT CGG AGA TGT GTA TAA GAG ACA GGA CTA CHV GGG TAT CTA ATC C-3'
Eubacterial Universal 16S	5'-ACT CCT ACG GGA GGC AGC AGT-3'	5'-ATT ACC GCG GCTGCT GGC-3'
<i>P. aeruginosa</i>	5'-TTC CCT TGA TCA GGT CGA TCT-3'	5'-CCT GGT TGA TCA GGT CGA TCT-3'
<i>P. acnes</i>	5'-ATA CGT AGG GTG CGA GCG TTG TCC-3'	5'-TGG TGT TCC TCC TGA TAT CTG CGC-3'
<i>S. aureus</i>	5'-GCG ATT GAT GGT GAT ACG GTT-3'	5'-AGC CAA GCC TTG ACG AAC TAA-3'
<i>S. epidermidis</i>	5'-TCA GCA GTT GAA GGG ACA GAT-3'	5'-CCA GAA CAA TGA ATG GTT AAG G-3'
<i>mBD-1</i>	5'-TTT CAC ATC CTC TCT GCA CT-3'	5'-ACC TGG CTC CAT CTG GGA GA-3'
<i>mBD-3</i>	5'-CTC TTT GCA TTT CTC CTG GTG CTG CTG-3'	5'-CAT CTT CAT GGA GGA GCA AAT TCT G-3'
<i>mBD-14</i>	5'-ATC CAG ATC TGG GTA CCG ACG ACG ACG ACA ACT TCC TAC CAA AAA CCC TCC- 3'	5'-ATT TGC GGG CGC CTA CTT CTT CTT TCG GCA GC-3'
<i>mIL-22</i>	5'-AGC TTG AGG TGT CCA ACT TC-3'	5'-GGT AGC ACT CAT CCT TAG CAC TG-3'