

Supplementary file

Supplementary Table S1. Distribution of samples used in this study by cohort, date of collection or DNA extraction (GTEx) and population.

Cohort	Date of collection or DNA extraction	Population		
		European	East Asian	Other
TCGA	2010	37	0	0
GTEx		0	0	0
TCGA	2011	66	7	0
GTEx		22	0	0
TCGA	2012	83	54	0
GTEx		54	0	0
TCGA	2013	36	0	4
GTEx		76	0	0
TCGA	2014	15	4	69
GTEx		12	0	0

Supplementary Table S2. List of bacterial species used in this study based on the species identified by the Human Microbiome [1] and MetaHit [2] projects complemented by species identified by Rajilić-Stojanović and de Vos [3]. Additional species appearing in disease conditions identified by Ferreira et al were also added [4]. One representative strain was chosen for each species.

Species Name	RefSeq assembly accession	Species Name	RefSeq assembly accession
<i>Abiotrophia defectiva</i> ATCC 49176	GCF_000160075.2	<i>Geobacillus stearothermophilus</i> DSM 458	GCF_002300135.1
<i>Absiella dolichum</i> DSM 3991	GCF_000154285.1	<i>Geobacillus vulcani</i> PSS1	GCF_000733845.1
<i>Acetanaerobacterium elongatum</i> CGMCC 1.5012	GCF_900103835.1	<i>Georgenia muralis</i> DSM 14418	GCF_003814705.1
<i>Acetanaerobium sticklandii</i> DSM 519	GCF_000196455.1	<i>Gordonia rubripertincta</i> CWB2	GCF_003568625.1
<i>Acetomicrobium hydrogeniformans</i> ATCC BAA-1850	GCF_000160455.2	<i>Gordonia terrae</i> 3612	GCF_001698225.1
<i>Achromobacter denitrificans</i>	GCF_003812265.1	<i>Gordonibacter pamelaee</i> 7-10-1-b	GCF_000210055.1
<i>Achromobacter piechoudii</i> ATCC 43553	GCF_000164035.1	<i>Granulicatella adiacens</i> ATCC 49175	GCF_000160675.1
<i>Achromobacter</i> sp. MFA1 R4	GCF_900156745.1	<i>Granulicatella elegans</i> ATCC 700633	GCF_000162475.2
<i>Achromobacter xylosoxidans</i> NCTC10807	GCF_001457475.1	<i>Grimontia hollisae</i> ATCC 33564	GCF_001558255.2
<i>Acidaminococcus fermentans</i> DSM 20731	GCF_000025305.1	<i>Haemophilus haemolyticus</i> M19346	GCF_003352385.1
<i>Acidaminococcus intestini</i> RYC-MR95	GCF_000230275.1	<i>Haemophilus influenzae</i> Rd KW20	GCF_000027305.1
<i>Acidaminococcus</i> sp. AM33-14BH	GCF_003603525.1	<i>Haemophilus parainfluenzae</i> T3T1	GCF_000210895.1
<i>Acidipropionibacterium acidipropionici</i> CGMCC 1.2230	GCF_001441165.1	<i>Haemophilus quentini</i> MP1	GCF_001702075.1
<i>Acidipropionibacterium jensenii</i> DSM 20535	GCF_000425285.1	<i>Haemophilus sputorum</i> CCUG 13788	GCF_000238795.1
<i>Acinetobacter baumannii</i> AB030	GCF_000746645.1	<i>Hafnia alvei</i> FB1	GCF_000597785.2
<i>Acinetobacter calcoaceticus</i> CA16	GCF_002055515.1	<i>Helicobacter bilis</i> AAQJH	GCF_001999985.1
<i>Acinetobacter haemolyticus</i> HW-2A	GCF_003323815.1	<i>Helicobacter bizzozeronii</i> CIII-1	GCF_000237285.1
<i>Acinetobacter johnsonii</i> XBB1	GCF_001484935.1	<i>Helicobacter canadensis</i> MIT 98-5491	GCF_000162575.1
<i>Acinetobacter junii</i> 65	GCF_001941805.1	<i>Helicobacter cinaedi</i> CCUG 18818 = ATCC BAA-847	GCF_000349975.1
<i>Acinetobacter lwoffii</i> WJ10621	GCF_000219275.1	<i>Helicobacter hepaticus</i> ATCC 51449	GCF_000007905.1
<i>Acinetobacter pittii</i> PHEA-2	GCF_000191145.1	<i>Helicobacter pullorum</i> MIT 98-5489	GCF_000155495.1
<i>Acinetobacter radioresistens</i> DSM 6976	GCF_000368905.1	<i>Helicobacter pylori</i> 26695	GCF_000008525.1
<i>Actinobacillus pleuropneumoniae</i> serovar 8	GCF_001460855.1	<i>Helicobacter winhamensis</i> ATCC BAA-430	GCF_000158455.1
<i>Actinomyces canis</i> OH770	GCF_003858455.1	<i>Hespellia stercorisuis</i> DSM 15480	GCF_900142165.1

<i>Actinomyces cardiffensis</i> F0333	GCF_000364865.1	<i>Holdemania bififormis</i> DSM 3989	GCF_000156655.1
<i>Actinomyces georgiae</i> DSM 6843	GCF_000429245.1	<i>Holdemania filiformis</i> DSM 12042	GCF_000157995.1
<i>Actinomyces graevenitzi</i> C83	GCF_000239695.1	<i>Holdemania massiliensis</i> AP2	GCF_000327285.1
<i>Actinomyces naeslundii</i> NCTC 10301	GCF_001956585.1	<i>Hungateiclostridium clariflavum</i> DSM 19732	GCF_000237085.1
<i>Actinomyces odontolyticus</i> ATCC 17982	GCF_000154225.1	<i>Hungateiclostridium thermocellum</i> ATCC 27405	GCF_000015865.1
<i>Actinomyces oris</i> T14V	GCF_001553935.1	<i>Hungatella hathewayi</i> WAL-18680	GCF_000235505.1
<i>Actinomyces radingae</i> DSM 9169	GCF_900106055.1	<i>Hydrogenibacillus schlegelii</i> MA 48	GCF_001653195.1
<i>Actinomyces</i> sp. 2129	GCF_003606385.1	<i>Hydrogenoanaerobacterium saccharovorans</i> CGMCC 1.5070	GCF_900110045.1
<i>Actinomyces turicensis</i> ACS-279-V-Col4	GCF_000296505.1	<i>Hymenobacter rigui</i> KCTC 12533	GCF_003944715.1
<i>Actinomyces urogenitalis</i> DSM 15434	GCF_000159035.1	<i>Intestinimonas butyriciproducens</i> AF211	GCF_001454945.1
<i>Actinomyces viscosus</i> NCTC10951	GCF_900637975.1	<i>Janibacter limosus</i> NBRC 16128	GCF_001570985.1
<i>Adlercreutzia equolifaciens</i> DSM 19450	GCF_000478885.1	<i>Kallipyga massiliensis</i> ph2	GCF_000311985.1
<i>Aeribacillus pallidus</i> 8m3	GCF_001629795.1	<i>Kandleria vitulina</i> DSM 20405	GCF_000702065.1
<i>Aerococcus viridans</i> CCUG4311	GCF_001543285.1	<i>Klebsiella aerogenes</i> KCTC 2190	GCF_000215745.1
<i>Aeromicrobium massiliense</i> JC14	GCF_000312105.1	<i>Klebsiella oxytoca</i> CAV1374	GCF_001022195.1
<i>Aeromonas allosaccharophila</i> CECT 4199	GCF_000819685.1	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> HS11286	GCF_000240185.1
<i>Aeromonas bestiarum</i> CECT 4227	GCF_000819745.1	<i>Klebsiella</i> sp. LY	GCF_004010915.1
<i>Aeromonas caviae</i> GSH8M-1	GCF_003925855.1	<i>Klebsiella varicola</i> At-22	GCF_000025465.1
<i>Aeromonas enteropelogenes</i> CECT 4255T	GCF_000820205.1	<i>Kluyvera ascorbata</i> ATCC 33433	GCF_000735365.1
<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ATCC 7966	GCF_000014805.1	<i>Kocuria kristinae</i> NBRC 15354	GCF_001570865.1
<i>Aeromonas jandaei</i> IMET J	GCF_002925765.1	<i>Kocuria marina</i>	GCF_900169805.1
<i>Aeromonas media</i> WS	GCF_000287215.2	<i>Kocuria palustris</i> MU14/1	GCF_001275345.1
<i>Aeromonas tecta</i> CECT 7082	GCF_000820185.1	<i>Kocuria rhizophila</i> DC2201	GCF_000010285.1
<i>Aeromonas veronii</i> B565	GCF_000204115.1	<i>Kocuria rosea</i> NCTC7512	GCF_900638085.1
<i>Agathobaculum desmolans</i> ATCC 43058	GCF_000701665.1	<i>Krasilnikovella flava</i> DSM 21481	GCF_900167525.1
<i>Aggregatibacter aphrophilus</i> ATCC 33389	GCF_900636915.1	<i>Kurthia gibsonii</i> B83	GCF_003660425.1
<i>Aggregatibacter segnis</i> ATCC 33393	GCF_900476035.1	<i>Kurthia massiliensis</i> JC30T	GCF_000285555.1
<i>Agrococcus jejuensis</i> DSM 22002	GCF_900099705.1	<i>Kurthia senegalensis</i> JC8E	GCF_000285595.1
<i>Akkermansia muciniphila</i> ATCC BAA-835	GCF_000020225.1	<i>Kurthia</i> sp. 11kri321	GCF_001534765.1
<i>Alistipes finegoldii</i> DSM 17242	GCF_000265365.1	<i>Kytococcus schroeteri</i> UMB1298	GCF_002847825.1
<i>Alistipes indistinctus</i> YIT 12060	GCF_000231275.1	<i>Kytococcus sedentarius</i> DSM 20547	GCF_000023925.1
<i>Alistipes obesi</i>	GCF_000311925.1	<i>Lachnoanaerobaculum saburreum</i> DSM 3986	GCF_000185385.1
<i>Alistipes onderdonkii</i> WAL 8169 = DSM 19147	GCF_000374505.1	<i>Lachnoanaerobaculum umeaense</i> DSM 23576 = CCUG 58757	GCF_003589745.1
<i>Alistipes putredinis</i> DSM 17216	GCF_000154465.1	<i>Lachnobacterium bovis</i> DSM 14045	GCF_900107245.1
<i>Alistipes senegalensis</i> JC50	GCF_000312145.1	<i>Lachnospira pectinoschiza</i> M83	GCF_900103815.1
<i>Alistipes shahii</i> WAL 8301	GCF_000210575.1	<i>Lachnospiraceae</i> bacterium KH1P17	GCF_900168235.1
<i>Alistipes</i> sp. Marseille-P5997	GCF_900604385.1	<i>Lactobacillus acidophilus</i> NCFM	GCF_000011985.1
<i>Alistipes timonensis</i> JC136	GCF_900107675.1	<i>Lactobacillus alimentarius</i> DSM 20249	GCF_001434745.1
<i>Allisonella histaminiformans</i> DSM 15230	GCF_900103425.1	<i>Lactobacillus amylolyticus</i> L6	GCF_002075105.1
<i>Alloprevotella tannerae</i> ATCC 51259	GCF_000159995.1	<i>Lactobacillus amylovorus</i> 30SC	GCF_000191545.1
<i>Anaerobiospirillum succiniciproducens</i> DSM 6400	GCF_000482845.1	<i>Lactobacillus animalis</i> KCTC 3501 = DSM 20602	GCF_001434535.1
<i>Anaerobiospirillum thomasi</i> NCTC12467	GCF_900445255.1	<i>Lactobacillus antri</i> DSM 16041	GCF_000160835.1
<i>Anaerococcus hydrogenalis</i> UMB0204	GCF_002871895.1	<i>Lactobacillus brevis</i> ATCC 367	GCF_000014465.1
<i>Anaerococcus obesius</i> ph10	GCF_000311745.1	<i>Lactobacillus buchneri</i> CD034	GCF_000298115.2
<i>Anaerococcus octavius</i> UMB0119	GCF_002847745.1	<i>Lactobacillus casei</i> LcY	GCF_000388095.2
<i>Anaerococcus prevotii</i> DSM 20548	GCF_000024105.1	<i>Lactobacillus coleohominis</i> 101-4-CHN	GCF_000161935.1
<i>Anaerococcus senegalensis</i> JC48	GCF_000321005.1	<i>Lactobacillus coryniformis</i> subsp. <i>coryniformis</i> DSM 20001	GCF_001433765.1
<i>Anaerococcus tetradius</i> ATCC 35098	GCF_000159095.1	<i>Lactobacillus crispatus</i> ST1	GCF_000091765.1
<i>Anaerococcus vaginalis</i> PH9	GCF_000307225.1	<i>Lactobacillus curvatus</i> MRS6	GCF_002224425.1
<i>Anaerocolumna aminovalerica</i> DSM 1283	GCF_900115365.1	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> ATCC 11842	GCF_000056065.1
<i>Anaerofustis stercorihominis</i> DSM 17244	GCF_000154825.1	<i>Lactobacillus fermentum</i> IFO 3956	GCF_000010145.1
<i>Anaerorhabdus furcosa</i> ATCC 25662	GCF_900167375.1	<i>Lactobacillus fructivorans</i> ATCC 27394	GCF_001437175.1
<i>Anaerostipes caccae</i> DSM 14662	GCF_000154305.1	<i>Lactobacillus gasseri</i> ATCC 33323 = JCM 1131	GCF_000014425.1
<i>Anaerostipes hadrus</i> BPB5	GCF_001998765.1	<i>Lactobacillus gastricus</i> DSM 16045	GCF_001434365.1
<i>Anaerostipes</i> sp. AF04-45	GCF_003461725.1	<i>Lactobacillus helveticus</i> CAUH18	GCF_001308285.1
<i>Anaerotignum lactatifermentans</i> DSM 14214	GCF_900142265.1	<i>Lactobacillus hilgardii</i> DSM 20176 = ATCC 8290	GCF_0000159315.1
<i>Anaerotruncus colihominis</i> DSM 17241	GCF_000154565.1	<i>Lactobacillus iners</i> DSM 13335	GCF_000160875.1
<i>Aneurinibacillus aneurinilyticus</i> ATCC 12856	GCF_000466385.1	<i>Lactobacillus jensenii</i> SNUV360	GCF_001936235.1
<i>Aneurinibacillus migulanus</i> DSM 2895	GCF_001274715.1	<i>Lactobacillus johnsonii</i> DPC 6026	GCF_000204985.1
<i>Arcanobacterium haemolyticum</i> DSM 20595	GCF_000092365.1	<i>Lactobacillus kalixensis</i> DSM 16043	GCF_001434335.1

<i>Arcobacter butzleri</i> RM4018	GCF_000014025.1	<i>Lactobacillus mucosae</i> LM1	GCF_000248095.2
<i>Arcobacter cryaerophilus</i> L406	GCF_001572875.1	<i>Lactobacillus oris</i> F0423	GCF_000221505.1
<i>Arthrobacter castelli</i> DSM 16402	GCF_000430705.1	<i>Lactobacillus parabuchneri</i> FAM21731	GCF_001922025.1
<i>Asaccharobacter celatus</i> AP38TSA	GCF_003340305.1	<i>Lactobacillus paracasei</i> ATCC 334	GCF_000014525.1
<i>Asaccharospora irregularis</i> DSM 2635	GCF_900129815.1	<i>Lactobacillus pentosus</i> KCA1	GCF_000271445.1
<i>Atlantibacter hermannii</i> NBRC 105704	GCF_000248015.1	<i>Lactobacillus plantarum</i> WCFS1	GCF_000203855.3
<i>Atopobium minutum</i> DSM 20586	GCF_001437015.1	<i>Lactobacillus reuteri</i> DSM 20016	GCF_000016825.1
<i>Atopobium parvulum</i> DSM 20469	GCF_000024225.1	<i>Lactobacillus rhamnosus</i> GG	GCF_000026505.1
<i>Atopobium rimae</i> ATCC 49626	GCF_000174015.1	<i>Lactobacillus ruminis</i> ATCC 27782	GCF_000224985.1
<i>Atopobium vaginae</i> DSM 15829	GCF_000159235.2	<i>Lactobacillus sakei</i> FAM18311	GCF_002224565.1
<i>Bacillus altitudinis</i> SGAir0031	GCF_002443015.2	<i>Lactobacillus salivarius</i> UCC118	GCF_000008925.1
<i>Bacillus amyloliquefaciens</i> DSM 7	GCF_000196735.1	<i>Lactobacillus saniviri</i> JCM 17471 = DSM 24301	GCF_001311785.1
<i>Bacillus atrophaeus</i> SRCM101359	GCF_002173495.1	<i>Lactobacillus senioris</i> DSM 24302 = JCM 17472	GCF_001436555.1
<i>Bacillus badius</i> SGD-V-25	GCF_001630115.1	<i>Lactobacillus sharpeae</i> JCM 1186 = DSM 20505	GCF_001436225.1
<i>Bacillus cereus</i> ATCC 14579	GCF_000007825.1	<i>Lactobacillus</i> sp. wkB8	GCF_000761135.1
<i>Bacillus circulans</i> NBRC 13626	GCF_001591585.1	<i>Lactobacillus ultunensis</i> DSM 16047	GCF_000159415.1
<i>Bacillus clausii</i> KSM-K16	GCF_000009825.1	<i>Lactobacillus vaginalis</i> DSM 5837 = ATCC 49540	GCF_000159435.1
<i>Bacillus coagulans</i> DSM 1 = ATCC 7050	GCF_000832905.1	<i>Lactococcus garvieae</i> ATCC 49156	GCF_000269925.1
<i>Bacillus endophyticus</i> DSM 13796	GCF_900115845.1	<i>Lactococcus lactis</i> subsp. <i>lactis</i> Il1403	GCF_000006865.1
<i>Bacillus firmus</i> 14_TX	GCF_003315495.1	<i>Lactococcus plantarum</i> DSM 20686	GCF_002441715.1
<i>Bacillus flexus</i> KLBMP 4941	GCF_002024265.1	<i>Lactococcus raffinolactis</i> WiKim0068	GCF_002310475.1
<i>Bacillus fordii</i> DSM 16014 = CIP 108821	GCF_000374565.1	<i>Lactonifactor longoviformis</i> DSM 17459	GCF_900129135.1
<i>Bacillus halodurans</i> C-125	GCF_000011145.1	<i>Leminorella grimonii</i> ATCC 33999 = DSM 5078	GCF_000439085.1
<i>Bacillus halotolerans</i> ZB201702	GCF_004006435.1	<i>Leminorella richardii</i> NCTC12151	GCF_900478135.1
<i>Bacillus infantis</i> NRRL B-14911	GCF_000473245.1	<i>Leptotrichia buccalis</i> C-1013-b	GCF_000023905.1
<i>Bacillus licheniformis</i> DSM 13 = ATCC 14580	GCF_000011645.1	<i>Leptotrichia hofstadii</i> F0254	GCF_000162955.1
<i>Bacillus marisflavi</i> JCM 11544	GCF_001274775.1	<i>Leuconostoc gelidium</i> subsp. <i>gasicomitatum</i> LMG 18811	GCF_000196855.1
<i>Bacillus massiliolanorexius</i> AP8	GCF_000321185.1	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> ATCC 8293	GCF_000014445.1
<i>Bacillus massiliosenegalensis</i> JC6	GCF_000311725.1	<i>Listeria grayi</i> DSM 20601	GCF_000148995.1
<i>Bacillus megaterium</i> NBRC 15308 = ATCC 14581	GCF_000832985.1	<i>Listeria innocua</i> FSL J1-023	GCF_000183905.1
<i>Bacillus mojavensis</i> RO-H-1 = KCTC 3706	GCF_000507105.1	<i>Listeria monocytogenes</i> EGD-e	GCF_000196035.1
<i>Bacillus mycoides</i> ATCC 6462	GCF_000832605.1	<i>Lysinibacillus fusiformis</i> RB-21	GCF_000724775.3
<i>Bacillus nealsonii</i> AAU1	GCF_000401235.1	<i>Lysinibacillus massiliensis</i> 4400831	GCF_000772965.1
<i>Bacillus niacini</i> NBRC 15566	GCF_001591505.1	<i>Lysinibacillus sphaericus</i> LMG 22257	GCF_001753205.1
<i>Bacillus pseudofirmus</i> OF4	GCF_000005825.2	<i>Lysobacter soli</i> KCTC 22011	GCF_00338285.1
<i>Bacillus pumilus</i> SH-B9	GCF_001578205.1	<i>Marvinbryantia formatexigens</i> DSM 14469	GCF_000173815.1
<i>Bacillus simplex</i> SH-B26	GCF_001578185.1	<i>Megamonas funiformis</i> YIT 11815	GCF_000245775.1
<i>Bacillus smithii</i> DSM 4216	GCF_001050115.1	<i>Megamonas hypermegale</i> DSM 1672	GCF_000423385.1
<i>Bacillus sonorensis</i> SRCM101395	GCF_002202015.1	<i>Megasphaera elsdenii</i> 14-14	GCF_001304715.1
<i>Bacillus</i> sp. FJAT-42376	GCF_003816055.1	<i>Megasphaera micronuciformis</i> F0359	GCF_000165735.1
<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	GCF_000009045.1	<i>Metakosakonia massiliensis</i> JC163	GCF_000321045.1
<i>Bacillus thermoamylovorans</i> 1A1	GCF_000751775.1	<i>Microbacterium aurum</i> KACC 15219	GCF_001974985.1
<i>Bacillus thuringiensis</i> YBT-1518	GCF_000497525.1	<i>Microbacterium chokolatum</i> SJT 101	GCF_001652465.1
<i>Bacillus timonensis</i> MM10403188	GCF_000285535.1	<i>Microbacterium foliorum</i> DSM 12966	GCF_000956415.1
<i>Bacillus vallismortis</i> Bac111	GCF_003667885.1	<i>Microbacterium gubbeenense</i> DSM 15944	GCF_000422745.1
<i>Bacillus velezensis</i> AP183	GCF_000875875.2	<i>Microbacterium hydrocarbonoxydans</i> SA35	GCF_000956475.1
<i>Bacteroides caccae</i> ATCC 43185	GCF_002222615.2	<i>Microbacterium oleivorans</i> NBRC 103075	GCF_001552475.1
<i>Bacteroides cellulosilyticus</i> WH2	GCF_001318345.1	<i>Microbacterium paraoxydans</i> DSM 15019	GCF_900105335.1
<i>Bacteroides clarus</i> YIT 12056	GCF_000195615.1	<i>Microbacterium phyllosphaerae</i> A1.1	GCF_003614915.1
<i>Bacteroides coprocola</i> DSM 17136	GCF_000154845.1	<i>Micrococcus luteus</i> NCTC 2665	GCF_000023205.1
<i>Bacteroides coprophilus</i> DSM 18228 = JCM 13818	GCF_000157915.1	<i>Micrococcus lylae</i> NBRC 15355	GCF_001570885.1
<i>Bacteroides dorei</i> CL03T12C01	GCF_001640865.1	<i>Micromonospora aurantiaca</i> ATCC 27029	GCF_000145235.1
<i>Bacteroides eggerthii</i> DSM 20697	GCF_000155815.1	<i>Mitsuokella jalaludinii</i> 2789STDY5608828	GCF_001404615.1
<i>Bacteroides faecis</i> MAJ27	GCF_900106755.1	<i>Mitsuokella multacida</i> DSM 20544	GCF_000155955.1
<i>Bacteroides finegoldii</i> DSM 17565	GCF_000156195.1	<i>Mobiluncus curtisi</i> ATCC 43063	GCF_000196535.1
<i>Bacteroides fluxus</i> YIT 12057	GCF_000195635.1	<i>Mobiluncus mulieris</i> ATCC 35243	GCF_000160615.1
<i>Bacteroides fragilis</i> YCH46	GCF_000009925.1	<i>Moellerella wisconsinensis</i> ATCC 35017	GCF_001294465.1
<i>Bacteroides graminisolvens</i> DSM 19988 = JCM 15093	GCF_000428125.1	<i>Mogibacterium diversum</i> CCUG 47132	GCF_002998925.1
<i>Bacteroides intestinalis</i> AF31-23	GCF_003475505.1	<i>Mogibacterium timidum</i> ATCC 33093	GCF_000525775.1
<i>Bacteroides massiliensis</i> B84634	GCF_000382445.1	<i>Moraxella catarrhalis</i> BBH18	GCF_000092265.1

<i>Bacteroides nordii</i> CL02T12C05	GCF_000273175.1	<i>Moraxella osloensis</i> CCUG 350	GCF_001553955.1
<i>Bacteroides oleiciplenus</i> YIT 12058	GCF_000315485.1	<i>Morganella morganii</i> subsp. <i>morganii</i> KT	GCF_000286435.2
<i>Bacteroides ovatus</i> ATCC 8483	GCF_001314995.1	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> K-10	GCF_000007865.1
<i>Bacteroides pectinophilus</i> ATCC 43243	GCF_000155855.1	<i>Mycobacterium florentinum</i> DSM 44852	GCF_002101635.1
<i>Bacteroides plebeius</i> DSM 17135	GCF_000187895.1	<i>Mycobacterium tuberculosis</i> H37Rv	GCF_000195955.2
<i>Bacteroides pyogenes</i> JCM 10003	GCF_000511775.1	<i>Mycobacteroides abscessus</i>	GCF_000069185.1
<i>Bacteroides salanitronis</i> DSM 18170	GCF_000190575.1	<i>Mycolicibacterium fortuitum</i> CT6	GCF_001307545.1
<i>Bacteroides salyersiae</i> WAL 10018	GCF_000381365.1	<i>Mycoplasma hominis</i> ATCC 23114	GCF_000085865.1
<i>Bacteroides</i> sp. 4_1_36 TM07-1	GCF_003466325.1	<i>Mycoplasma pneumoniae</i> M129	GCF_000027345.1
<i>Bacteroides stercoris</i> ATCC 43183	GCF_000154525.1	<i>Neisseria cinerea</i> NCTC10294	GCF_900475315.1
<i>Bacteroides thetaiotaomicron</i> VPI-5482	GCF_000011065.1	<i>Neisseria elongata</i> subsp. <i>glycolytica</i> ATCC 29315	GCF_000818035.1
<i>Bacteroides timonensis</i>	GCF_000513195.1	<i>Neisseria flavescens</i> SK114	GCF_000175275.1
<i>Bacteroides uniformis</i> ATCC 8492	GCF_000154205.1	<i>Neisseria macacae</i> ATCC 33926	GCF_000220865.1
<i>Bacteroides vulgatus</i> ATCC 8482	GCF_000012825.1	<i>Neisseria mucosa</i> C102	GCF_000186165.1
<i>Bacteroides xylanisolvens</i> SD CC 2a	GCF_000577955.1	<i>Neisseria perflava</i> UMB0023	GCF_002863305.1
<i>Barnesiella intestinihominis</i> YIT 11860	GCF_000296465.1	<i>Neisseria sicca</i> FDAARGOS_260	GCF_002073715.2
<i>Bhargavaea beijingensis</i> CGMCC 1.6762	GCF_900101985.1	<i>Neisseria subflava</i> M18660	GCF_003351665.1
<i>Bifidobacterium adolescentis</i> ATCC 15703	GCF_000010425.1	<i>Nevskia ramosa</i> DSM 11499	GCF_000420645.1
<i>Bifidobacterium angulatum</i> DSM 20098 = JCM 7096	GCF_001025155.1	<i>Oceanobacillus caeni</i> HM6	GCF_001298135.1
<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> DSM 10140	GCF_000022965.1	<i>Oceanobacillus massiliensis</i> str. <i>N'diop</i>	GCF_000285495.1
<i>Bifidobacterium bifidum</i> PRL2010	GCF_000165905.1	<i>Odoribacter laneus</i> YIT 12061	GCF_000243215.1
<i>Bifidobacterium boum</i> DSM 20432	GCF_000687615.1	<i>Odoribacter splanchnicus</i> DSM 20712	GCF_000190535.1
<i>Bifidobacterium breve</i> DSM 20213 = JCM 1192	GCF_001025175.1	<i>Olsenella profusa</i> F0195	GCF_000468755.1
<i>Bifidobacterium catenulatum</i> DSM 16992	GCF_001025195.1	<i>Olsenella uli</i> DSM 7084	GCF_000143845.1
<i>Bifidobacterium coryneforme</i> LMG18911	GCF_000737865.1	<i>Oribacterium sinus</i> F0268	GCF_000160635.1
<i>Bifidobacterium dentium</i> JCM 1195 = DSM 20436	GCF_001042595.1	<i>Oscillibacter valericigenes</i> Sjm18-20	GCF_000283575.1
<i>Bifidobacterium gallicum</i> DSM 20093 = LMG 11596	GCF_000741205.1	<i>Paenibacillus alvei</i> DSM 29	GCF_000293805.1
<i>Bifidobacterium kashiwanohense</i> PV20-2	GCF_000800455.1	<i>Paenibacillus antibiotrophicus</i> GD11	GCF_000455265.1
<i>Bifidobacterium longum</i> NCC2705	GCF_000007525.1	<i>Paenibacillus barcinonensis</i> CECT 7022	GCF_003217495.1
<i>Bifidobacterium mongoliense</i> DSM 21395	GCF_000741285.1	<i>Paenibacillus barengoltzii</i> G22	GCF_000403375.2
<i>Bifidobacterium pseudocatenulatum</i> DSM 20438	GCF_001025215.1	<i>Paenibacillus daejeonensis</i> DSM 15491	GCF_000378385.1
<i>Bifidobacterium pseudolongum</i> PV8-2	GCF_000800475.2	<i>Paenibacillus durus</i> DSM 1735	GCF_000756615.1
<i>Bifidobacterium ruminantium</i> LMG 21811	GCF_000741365.1	<i>Paenibacillus glucanolyticus</i> 5162	GCF_001632305.1
<i>Bifidobacterium scardovii</i> JCM 12489 = DSM 13734	GCF_001042635.1	<i>Paenibacillus graminis</i> DSM 15220	GCF_000758705.1
<i>Bifidobacterium</i> sp. AGR2158	GCF_000424225.1	<i>Paenibacillus illinoisensis</i> NBRC 15959	GCF_0004000925.1
<i>Bifidobacterium stercoris</i> JCM 15918	GCF_000771705.1	<i>Paenibacillus lactis</i> 154	GCF_000230915.1
<i>Bifidobacterium thermacidophilum</i> subsp. <i>Thermacidophilum</i> LMG 21395	GCF_000741455.1	<i>Paenibacillus lautus</i> E7593-69	GCF_003590055.1
<i>Bifidobacterium thermophilum</i> RBL67	GCF_000347695.1	<i>Paenibacillus rhizosphaerae</i> FSL R5-0378	GCF_001956185.1
<i>Bilophila</i> sp. 4_1_30	GCF_000224655.1	<i>Paenibacillus senegalensis</i> JC66	GCF_000285515.1
<i>Bilophila wadsworthia</i> ATCC 49260	GCF_000701705.1	<i>Paenibacillus</i> sp. RUD330	GCF_002243345.1
<i>Blautia coccoides</i> YL58	GCF_002221555.2	<i>Paenibacillus thiaminolyticus</i> B05	GCF_003591545.1
<i>Blautia hansenii</i> DSM 20583	GCF_000156675.1	<i>Paenoclostridium sordellii</i> CBA7122	GCF_001950115.1
<i>Blautia hydrogenotrophica</i> DSM 10507	GCF_000157975.1	<i>Paenisporosarcina</i> sp. K2R23-3	GCF_003595195.1
<i>Blautia massiliensis</i> GD9	GCF_001487165.1	<i>Pantoea agglomerans</i> C410P1	GCF_001709315.1
<i>Blautia obeum</i> ATCC 29174	GCF_000153905.1	<i>Papillibacter cinnamivorans</i> DSM 12816	GCF_900176335.1
<i>Blautia producta</i> ATCC 27340 = DSM 2950	GCF_000373885.1	<i>Parabacteroides distasonis</i> ATCC 8503	GCF_000012845.1
<i>Blautia wexlerae</i> DSM 19850	GCF_000484655.1	<i>Parabacteroides goldsteinii</i> DSM 19448 = WAL 12034	GCF_000969835.1
<i>Brachybacterium paraconglomeratum</i> LC44	GCF_000233655.1	<i>Parabacteroides gordonii</i> DSM 23371	GCF_000428565.1
<i>Brachyspira pilosicoli</i> P43/6/78	GCF_000325665.1	<i>Parabacteroides johnsonii</i> CL02T12C29	GCF_000307375.1
<i>Brevibacillus agri</i> 5-2	GCF_000612125.1	<i>Parabacteroides merdae</i> ATCC 43184	GCF_000154105.1
<i>Brevibacillus borstelensis</i> AK1	GCF_000353565.1	<i>Parabacteroides</i> sp. CT06	GCF_002257605.1
<i>Brevibacillus brevis</i> NBRC 100599	GCF_000010165.1	<i>Paraclostridium bifermentans</i> ATCC 638	GCF_000452245.2
<i>Brevibacillus massiliensis</i>	GCF_000311785.1	<i>Paraeggerthella hongkongensis</i> RC2/2 A	GCF_003340345.1
<i>Brevibacterium casei</i> S18	GCF_000314575.1	<i>Paraprevotella clara</i> YIT 11840	GCF_000233955.1
<i>Brevibacterium epidermidis</i> EZ-K02	GCF_002573745.1	<i>Paraprevotella xylaniphila</i> YIT 11841	GCF_000205165.1
<i>Brevibacterium iodinum</i> ATCC 49514	GCF_900169265.1	<i>Parasporobacterium paucivorans</i> DSM 15970	GCF_900141895.1
<i>Brevibacterium linens</i> BS258	GCF_001606005.1	<i>Parasutterella excrementihominis</i> YIT 11859	GCF_000205025.1
<i>Brevibacterium ravensturnense</i> 5401308 = CCUG 53855	GCF_000285915.1	<i>Parvimonas micra</i> KCOM 1535; ChDC B708	GCF_000800295.1
<i>Brevibacterium senegalense</i>	GCF_000285835.1	<i>Parvimonas</i> sp. KA00067	GCF_001553085.1

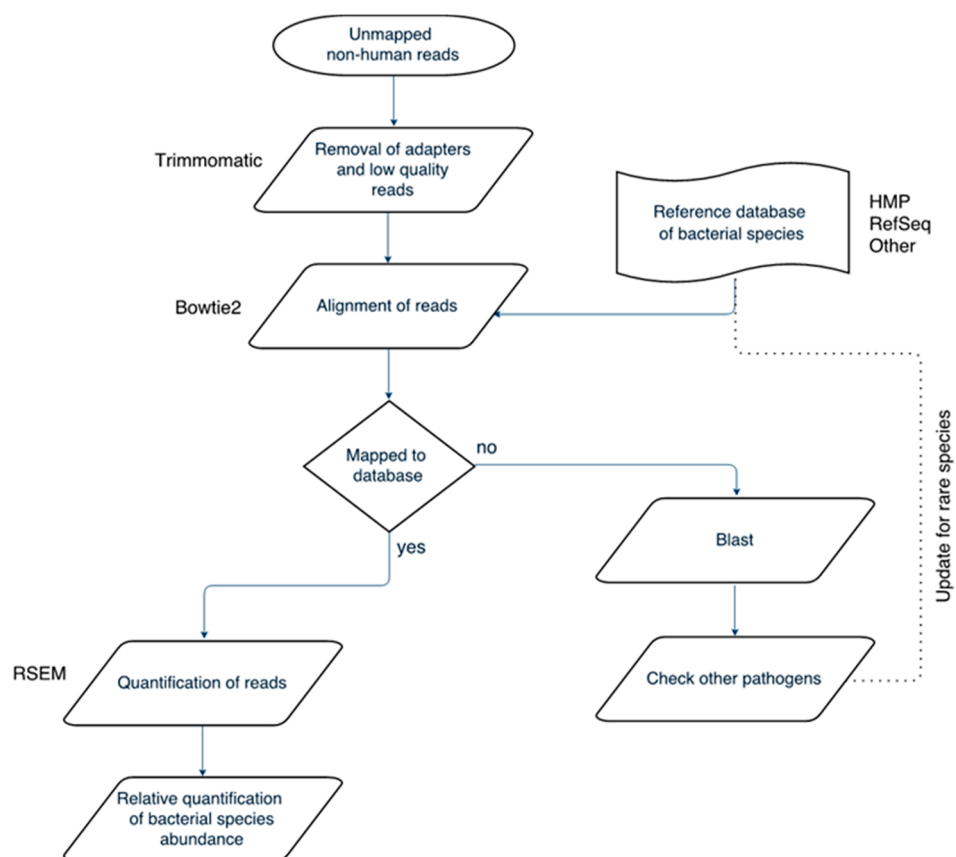
<i>Brochothrix thermosphacta</i> DSM 20171 = FSL F6-1036	GCF_000620985.1	<i>Pediococcus acidilactici</i> ZPA017	GCF_001767275.1
<i>Bulleidia extructa</i> W1219	GCF_000177375.1	<i>Pediococcus damnosus</i> TMW 2.1535	GCF_001611135.1
<i>Burkholderiales bacterium</i> JOSHI_001	GCF_000244995.1	<i>Pediococcus pentosaceus</i> ATCC 25745	GCF_000014505.1
<i>Butyricoccus pullicaecorum</i> 1.2	GCF_000398925.1	<i>Peptococcus niger</i> DSM 20475	GCF_900101835.1
<i>Butyricimonas synergistica</i> DSM 23225	GCF_000379665.1	<i>Peptoniphilus asaccharolyticus</i> DSM 20463	GCF_900176115.1
<i>Butyricimonas virosa</i> DSM 23226	GCF_000519105.1	<i>Peptoniphilus duerdenii</i> ATCC BAA-1640	GCF_000146345.1
<i>Butyrivibrio crossotus</i> DSM 2876	GCF_000156015.1	<i>Peptoniphilus grossensis</i> ph5	GCF_000311825.1
<i>Butyrivibrio fibrisolvens</i> DSM 3071	GCF_900129945.1	<i>Peptoniphilus harei</i> ACS-146-V-Sch2b	GCF_000183565.1
<i>Campylobacter coli</i> aerotolerant OR12	GCF_002024185.1	<i>Peptoniphilus indolicus</i> ATCC 29427	GCF_000227315.1
<i>Campylobacter concisus</i> ATCC 33237	GCF_001298465.1	<i>Peptoniphilus lacrimalis</i> DSM 7455	GCF_000378725.1
<i>Campylobacter curvus</i> 525.92	GCF_000017465.2	<i>Peptoniphilus senegalensis</i> JC140	GCF_000321025.1
<i>Campylobacter fetus</i> subsp. <i>testudinum</i> 03-427	GCF_000495505.1	<i>Peptoniphilus</i> sp. ING2-D16	GCF_000952975.1
<i>Campylobacter gracilis</i> ATCC 33236	GCF_001190745.1	<i>Peptoniphilus timonensis</i> JC401	GCF_000312025.1
<i>Campylobacter hominis</i> ATCC BAA-381	GCF_000017585.1	<i>Peptostreptococcus anaerobius</i> VPI 4330 = DSM 2949	GCF_000381525.1
<i>Campylobacter hyointestinalis</i> subsp. <i>Lawsonii</i> LMG 15993	GCF_001643975.1	<i>Peptostreptococcus stomatis</i> DSM 17678	GCF_000147675.1
<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	GCF_000009085.1	<i>Phascolarctobacterium faecium</i> JCM 30894	GCF_003945365.1
<i>Campylobacter lari</i> RM2100	GCF_000019205.1	<i>Phascolarctobacterium succinatutens</i> YIT 12067	GCF_000188175.1
<i>Campylobacter rectus</i> RM3267	GCF_000174175.1	<i>Phyllobacterium myrsinacearum</i> IAM 13584	GCF_003182235.1
<i>Campylobacter showae</i> CSUNSWCD	GCF_000313615.1	<i>Phyllobacterium</i> sp. UNC302MFC05.2	GCF_000686005.1
<i>Campylobacter</i> sp. 10_1_50	GCF_000238755.1	<i>Planococcus rifietoensis</i> M8	GCF_001465795.2
<i>Campylobacter upsaliensis</i> DSM 5365	GCF_000620965.1	<i>Plesiomonas shigelloides</i> NCTC10360	GCF_900087055.1
<i>Campylobacter ureolyticus</i> RIGS 9880	GCF_001190755.1	<i>Porphyromonas asaccharolytica</i> DSM 20707	GCF_000212375.1
<i>Candidatus Blastococcus massiliensis</i> AP3	GCF_000582785.1	<i>Porphyromonas endodontalis</i> ATCC 35406	GCF_000174815.1
<i>Candidatus Dorea massiliensis</i> AP6	GCF_001282705.1	<i>Porphyromonas gingivalis</i> ATCC 33277	GCF_000010505.1
<i>Candidatus Soleaferrea massiliensis</i> AP7	GCF_000820765.1	<i>Porphyromonas somerae</i> KA00683	GCF_001553215.1
<i>Candidatus Stoquefichus massiliensis</i> AP9	GCF_000455285.1	<i>Porphyromonas uenonis</i> DSM 23387 = JCM 13868	GCF_000482365.1
<i>Capnocytophaga gingivalis</i> ATCC 33624	GCF_000174755.1	<i>Prevotella albensis</i> DSM 11370 = JCM 12258	GCF_000426565.1
<i>Capnocytophaga granulosa</i> ATCC 51502	GCF_000411115.1	<i>Prevotella amnii</i> DSM 23384 = JCM 14753	GCF_000378745.1
<i>Capnocytophaga ochracea</i> DSM 7271	GCF_000023285.1	<i>Prevotella bivia</i> DSM 20514	GCF_000262545.1
<i>Capnocytophaga sputigena</i> NCTC11097	GCF_900638125.1	<i>Prevotella brevis</i> ATCC 19188	GCF_000621725.1
<i>Cardiobacterium hominis</i> ATCC 15826	GCF_000160655.1	<i>Prevotella bryantii</i> B14	GCF_000179055.1
<i>Catabacter hongkongensis</i> HKU16	GCF_000981035.1	<i>Prevotella buccae</i> ATCC 33574	GCF_000184945.1
<i>Catenibacterium mitsuokai</i> DSM 15897	GCF_000173795.1	<i>Prevotella conceptionensis</i> 9403948	GCF_000312305.1
<i>Catonella morbi</i> ATCC 51271	GCF_000160035.2	<i>Prevotella copri</i> DSM 18205	GCF_000157935.1
<i>Cedecea davisae</i> DSM 4568	GCF_000412335.2	<i>Prevotella corporis</i> DSM 18810 = JCM 8529	GCF_000430525.1
<i>Cellulomonas massiliensis</i> JC225	GCF_000312005.1	<i>Prevotella denticola</i> F0289	GCF_000193395.1
<i>Cellulosilyticum lentocellum</i> DSM 5427	GCF_000178835.2	<i>Prevotella disiens</i> JCM 6334 = ATCC 29426	GCF_000613345.1
<i>Cellulosimicrobium cellulans</i> PSBB019	GCF_002162335.1	<i>Prevotella enoeca</i> F0113	GCF_001444445.1
<i>Cetobacterium somerae</i> ATCC BAA-474	GCF_000479045.1	<i>Prevotella intermedia</i> ATCC 25611 = DSM 20706	GCF_001953955.1
<i>Christensenella minuta</i> DSM 22607	GCF_001652705.1	<i>Prevotella loeschei</i> DSM 19665 = JCM 12249 = ATCC 15930	GCF_000378085.1
<i>Chryseobacterium hominis</i> DSM 19326	GCF_900108525.1	<i>Prevotella marshii</i> DSM 16973 = JCM 13450	GCF_000146675.1
<i>Citrobacter amalonaticus</i> Y19	GCF_000981805.1	<i>Prevotella melaninogenica</i> ATCC 25845	GCF_000144405.1
<i>Citrobacter braakii</i> FDAARGOS_290	GCF_002208845.2	<i>Prevotella nanceiensis</i> DSM 19126 = JCM 15639	GCF_000379965.1
<i>Citrobacter farmeri</i> AUSMDU00008141	GCF_002249995.1	<i>Prevotella nigrescens</i> ATCC 33563	GCF_000220235.1
<i>Citrobacter freundii</i> CFNIH1	GCF_000648515.1	<i>Prevotella oralis</i> ATCC 33269	GCF_000185145.2
<i>Citrobacter gillenii</i> C3	GCF_003429605.1	<i>Prevotella oalorum</i> JCM 14966	GCF_000613785.1
<i>Citrobacter koseri</i> ATCC BAA-895	GCF_000018045.1	<i>Prevotella pallens</i> ATCC 700821	GCF_000220255.1
<i>Citrobacter sedlakii</i> NBRC 105722	GCF_000759835.1	<i>Prevotella ruminicola</i> 23	GCF_000025925.1
<i>Citrobacter</i> sp. 92	GCF_900079795.1	<i>Prevotella salivae</i> DSM 15606	GCF_000185845.1
<i>Citrobacter werkmanii</i> UMH18	GCF_003665555.1	<i>Prevotella shahii</i> DSM 15611 = JCM 12083	GCF_000613445.1
<i>Citrobacter youngae</i> NCTC13709	GCF_900638065.1	<i>Prevotella stercorea</i> DSM 18206	GCF_000235885.1
<i>Cloacibacillus evryensis</i> DSM 19522	GCF_000585335.1	<i>Prevotella timonensis</i> 4401737 = DSM 22865 = JCM 15640	GCF_000455445.1
<i>Cloacibacterium normanense</i> DSM 15886	GCF_900104195.1	<i>Prevotella veroralis</i> DSM 19559 = JCM 6290	GCF_000377625.1
<i>Clostridiales bacterium</i> WTE2008	GCF_900176495.1	<i>Propionibacterium freudenreichii</i> subsp. <i>Freudenreichii</i> DSM 20271	GCF_000940845.1
<i>Clostridioides difficile</i> 630	GCF_000009205.2	<i>Propionibacterium</i> sp. <i>oral</i> taxon 193	GCF_001717565.1
<i>Clostridium acetobutylicum</i> ATCC 824	GCF_000008765.1	<i>Proteus mirabilis</i> HI4320	GCF_000069965.1
<i>Clostridium aldenense</i> AM40-2AC	GCF_003467385.1	<i>Proteus penneri</i> ATCC 33519	GCF_003144535.1
<i>Clostridium asparagiforme</i> DSM 15981	GCF_000158075.1	<i>Proteus vulgaris</i> FDAARGOS_556	GCF_003812525.1
<i>Clostridium baratii</i> str. <i>Sullivan</i>	GCF_000789395.1	<i>Providencia alcalifaciens</i> Dmel2	GCF_000314875.2

<i>Clostridium beijerinckii</i> NCIMB 14988	GCF_000833105.2	<i>Providencia rettgeri</i> Dmel1	GCF_000314835.2
<i>Clostridium bolteae</i> 90A9	GCF_000371705.1	<i>Providencia rustigianii</i> NCTC8113	GCF_900637755.1
<i>Clostridium botulinum</i> A str. Hall	GCF_000017045.1	<i>Providencia stuartii</i> MRSN 2154	GCF_000259175.1
<i>Clostridium butyricum</i> KNU-L09	GCF_001456065.2	<i>Pseudoclavibacter</i> sp. RFBG4	GCF_002931515.1
<i>Clostridium cadaveris</i> AGR2141	GCF_000424205.1	<i>Pseudoflavonifactor capillosus</i> ATCC 29799	GCF_000169255.2
<i>Clostridium celatum</i> DSM 1785	GCF_000320405.1	<i>Pseudoglutamicibacter albus</i> DNF00011	GCF_000758985.1
<i>Clostridium chauvoei</i> JF4335	GCF_900168365.1	<i>Pseudomonas aeruginosa</i> PAO1	GCF_000006765.1
<i>Clostridium citroniae</i> WAL-17108	GCF_000233455.1	<i>Pseudomonas alcaliphila</i> JAB1	GCF_001941865.1
<i>Clostridium clostridioforme</i> ATCC 25537	GCF_900113155.1	<i>Pseudomonas fluorescens</i> F113	GCF_000237065.1
<i>Clostridium cochlearium</i> NLAE-zl-C224	GCF_900103025.1	<i>Pseudomonas monteilii</i> USDA-ARS-USMARC-56711	GCF_001534745.1
<i>Clostridium cocleatum</i> DSM 1551	GCF_900102365.1	<i>Pseudomonas nitroreducens</i> NBRC 12694	GCF_002091755.1
<i>Clostridium disporicum</i> 2789STDY5834856	GCF_001405015.1	<i>Pseudomonas oleovorans</i> MOIL14HWK12	GCF_000510765.1
<i>Clostridium fallax</i> DSM 2631	GCF_900129365.1	<i>Pseudomonas putida</i> KT2440	GCF_000007565.2
<i>Clostridium felsineum</i> DSM 794	GCF_002006355.1	<i>Pseudomonas</i> sp. 09C 129	GCF_002843625.1
<i>Clostridium glycyrrhizinilyticum</i> JCM 13369	GCF_001311035.1	<i>Pseudomonas stutzeri</i> CGMCC 1.1803	GCF_000219605.1
<i>Clostridium hiranonis</i> DSM 13275	GCF_000156055.1	<i>Pseudopropionibacterium propionicum</i> F0230a	GCF_000277715.1
<i>Clostridium hylemonae</i> DSM 15053	GCF_000156515.1	<i>Pseudoramibacter alactolyticus</i> ATCC 23263	GCF_000185505.1
<i>Clostridium indolis</i> DSM 755	GCF_000526995.1	<i>Pseudoxanthomonas mexicana</i> CCH9-G4	GCF_001556105.1
<i>Clostridium innocuum</i> 2959	GCF_000371425.1	<i>Pyramidobacter piscolens</i> W5455	GCF_000177335.1
<i>Clostridium lavalense</i> NLAE-zl-G277	GCF_900102595.1	<i>Raoultella planticola</i> FDAARGOS_430	GCF_003699975.1
<i>Clostridium leptum</i> DSM 753	GCF_000154345.1	<i>Raoultella terrigena</i> BIGb0267	GCF_003752645.1
<i>Clostridium methoxybenzovorans</i> SR3	GCF_000421505.1	<i>Rhodococcus erythropolis</i> CCM2595	GCF_000454045.1
<i>Clostridium methylpentosum</i> DSM 5476	GCF_000158655.1	<i>Rhodococcus hoagii</i> 1035	GCF_000196695.1
<i>Clostridium neonatale</i> LCDc no.99-A-005	GCF_001458595.1	<i>Rhodococcus rhodochrous</i> EP4	GCF_003004765.2
<i>Clostridium paraputrificum</i> AGR2156	GCF_000424025.1	<i>Rhodococcus</i> sp. PBTS 1	GCF_001620025.1
<i>Clostridium perfringens</i> ATCC 13124	GCF_000013285.1	<i>Robinsoniella peoriensis</i> WT	GCF_000797495.1
<i>Clostridium populeti</i> 743A	GCF_900112775.1	<i>Romboutsia lituseburensis</i> DSM 797	GCF_900103615.1
<i>Clostridium putrefaciens</i> NCTC9836	GCF_900461105.1	<i>Roseburia faecis</i> 2789STDY5608863	GCF_001405615.1
<i>Clostridium saccharogumia</i> DSM 17460	GCF_000686665.1	<i>Roseburia hominis</i> A2-183	GCF_000225345.1
<i>Clostridium saccharolyticum</i> WM1	GCF_000144625.1	<i>Roseburia intestinalis</i> L1-82	GCF_000156535.1
<i>Clostridium saccharoperbutylacetonicum</i> N1-4(HMT)	GCF_000340885.1	<i>Roseburia inulinivorans</i> DSM 16841	GCF_000174195.1
<i>Clostridium sartagoforme</i> AAU1	GCF_000401215.1	<i>Rothia aeria</i> JCM 11412	GCF_002355935.1
<i>Clostridium scindens</i> ATCC 35704	GCF_000154505.1	<i>Rothia dentocariosa</i> ATCC 17931	GCF_000164695.2
<i>Clostridium senegalense</i> JC122	GCF_000285575.1	<i>Rothia mucilaginosa</i> DY-18	GCF_000011025.1
<i>Clostridium septicum</i> DSM 7534	GCF_003606265.1	<i>Rudanella lutea</i> DSM 19387	GCF_000383955.1
<i>Clostridium</i> sp. DL-VIII	GCF_000230835.1	<i>Ruminiclostridium cellobioparum</i> subsp. <i>termitidis</i> CT1112	GCF_000350485.1
<i>Clostridium sphenoides</i> JCM 1415	GCF_900105615.1	<i>Ruminococcaceae</i> bacterium KHP2	GCF_900176545.1
<i>Clostridium spiroforme</i> DSM 1552	GCF_000154805.1	<i>Ruminococcus albus</i> 7 = DSM 20455	GCF_000179635.2
<i>Clostridium sporogenes</i> DSM 795	GCF_001020205.1	<i>Ruminococcus bromii</i> YE282	GCF_900101355.1
<i>Clostridium sporosphaeroides</i> DSM 1294	GCF_000383295.1	<i>Ruminococcus callidus</i> ATCC 27760	GCF_000468015.1
<i>Clostridium symbiosum</i> WAL-14163	GCF_000189595.1	<i>Ruminococcus champanellensis</i> 18P13 = JCM 17042	GCF_000210095.1
<i>Clostridium tertium</i>	GCF_900217175.1	<i>Ruminococcus faecis</i> JCM 15917	GCF_001312505.1
<i>Clostridium tyrobutyricum</i> KCTC 5387	GCF_001642655.1	<i>Ruminococcus flavefaciens</i> MC2020	GCF_000701945.1
<i>Clostridium ventriculi</i> 2789STDY5834858	GCF_001404895.1	<i>Ruminococcus gausvreauii</i> DSM 19829	GCF_000425525.1
<i>Clostridium vincentii</i> DSM 10228	GCF_002995745.1	<i>Ruminococcus gnavus</i> AGR2154	GCF_000526735.1
<i>Clostridium viride</i> DSM 6836	GCF_000620945.1	<i>Ruminococcus lactaris</i> ATCC 29176	GCF_000155205.1
<i>Collinsella aerofaciens</i> ATCC 25986	GCF_000169035.1	<i>Ruminococcus</i> sp. YE71	GCF_900119155.1
<i>Collinsella intestinalis</i> DSM 13280	GCF_000156175.1	<i>Ruminococcus torques</i> ATCC 27756	GCF_000153925.1
<i>Collinsella stercoris</i> DSM 13279	GCF_000156215.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i> str. L72	GCF_000006945.2
<i>Collinsella tanakaei</i> YIT 12063	GCF_000225705.1	<i>Scardovia inopinata</i> JCM 12537	GCF_001042695.1
<i>Coprobacillus cateniformis</i> OF01-6	GCF_003463235.1	<i>Schlesneria paludicola</i> DSM 18645	GCF_000255655.1
<i>Coprobacillus</i> sp. D7	GCF_000158555.2	<i>Selenomonas ruminantium</i> subsp. <i>lactilytica</i> TAM6421	GCF_000284095.1
<i>Coprococcus catus</i> AM28-39	GCF_003434235.1	<i>Selenomonas</i> sp. oral taxon 149 str. 67H29BP	GCF_000146365.1
<i>Coprococcus comes</i> ATCC 27758	GCF_000155875.1	<i>Senegalimassilia anaerobia</i> JC110	GCF_000236865.1
<i>Coprococcus eutactus</i> ATCC 27759	GCF_000154425.1	<i>Serratia ficaria</i> NCTC12148	GCF_900187015.1
<i>Corynebacterium afermentans</i> subsp. <i>Afermentans</i> LCDc880199	GCF_001639025.1	<i>Serratia fonticola</i> DSM 4576	GCF_001006005.1
<i>Corynebacterium ammoniagenes</i> DSM 20306	GCF_001941425.1	<i>Serratia liquefaciens</i> ATCC 27592	GCF_000422085.1
<i>Corynebacterium amycolatium</i> UMB0338	GCF_002861405.1	<i>Serratia marcescens</i> subsp. <i>marcescens</i> Db11	GCF_000513215.1
<i>Corynebacterium appendicis</i> CIP 107643	GCF_900156665.1	<i>Shewanella</i> sp. M2	GCF_003855155.1

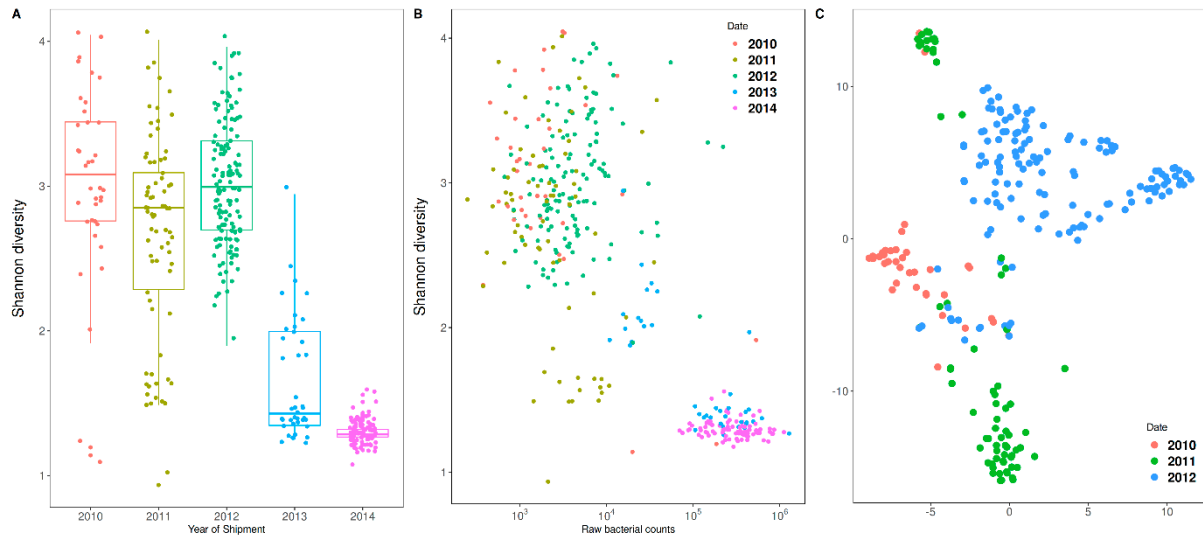
<i>Corynebacterium aurimucosum</i> ATCC 700975	GCF_000022905.1	<i>Shigella boydii</i> G1227	GCF_003336935.1
<i>Corynebacterium coyleae</i> DSM 44184	GCF_900105505.1	<i>Shigella dysenteriae</i> Sd197	GCF_000012005.1
<i>Corynebacterium durum</i> F0235	GCF_000318135.1	<i>Shigella flexneri</i> 2a str. 301	GCF_000006925.2
<i>Corynebacterium freneyi</i> DNF00450	GCF_000758965.1	<i>Shigella sonnei</i> KY 1629	GCF_001261695.1
<i>Corynebacterium glaucum</i> DSM 30827	GCF_002287505.1	<i>Shigella</i> sp. PAMC 28760	GCF_001596115.1
<i>Corynebacterium glucuronolyticum</i> DSM 44120	GCF_900176155.1	<i>Silanimonas lenta</i> DSM 16282	GCF_000429065.1
<i>Corynebacterium kroppenstedtii</i> DSM 44385	GCF_000023145.1	<i>Slackia equolifaciens</i> DSM 24851	GCF_003725995.1
<i>Corynebacterium matruchotii</i> ATCC 14266	GCF_000175375.1	<i>Slackia exigua</i> ATCC 700122	GCF_000162875.1
<i>Corynebacterium minutissimum</i> NCTC10288	GCF_900478045.1	<i>Slackia isoflavoniconvertens</i> OB21 GAM31	GCF_003340315.1
<i>Corynebacterium propinquum</i> DSM 44285	GCF_000375525.1	<i>Slackia piriformis</i> YIT 12062	GCF_000296445.1
<i>Corynebacterium pseudodiphtheriticum</i> DSM 44287	GCF_000688415.1	<i>Sneathia amnii</i> SN35	GCF_000973085.1
<i>Corynebacterium pseudogenitalium</i> ATCC 33035	GCF_000156615.2	<i>Solobacterium moorei</i> DSM 22971	GCF_000425005.1
<i>Corynebacterium simulans</i> PES1	GCF_001586215.1	<i>Sphingobacterium multivorum</i> NCTC11034	GCF_900457115.1
<i>Corynebacterium</i> sp. HFH0082	GCF_000411235.1	<i>Sporosarcina koreensis</i> Q1	GCF_001531445.1
<i>Corynebacterium striatum</i> 216	GCF_002804085.1	<i>Staphylococcus arlettae</i> CVD059	GCF_000295715.1
<i>Corynebacterium tuberculostearicum</i> SK141	GCF_000175635.1	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> NCTC 8325	GCF_000013425.1
<i>Corynebacterium ulcerans</i> FRC11	GCF_000767685.1	<i>Staphylococcus auricularis</i> DSM 20609	GCF_001500315.1
<i>Corynebacterium urelicelerivorans</i> IMMIB RIV-2301	GCF_000747315.1	<i>Staphylococcus capitis</i> subsp. <i>Capitis</i> AYP1020	GCF_001028645.1
<i>Corynebacterium xerosis</i> NBRC 16721	GCF_001552415.1	<i>Staphylococcus caprae</i> JMUB898	GCF_003966625.1
<i>Cronobacter sakazakii</i> ATCC 29544	GCF_000982825.1	<i>Staphylococcus cohnii</i> subsp. <i>Cohnii</i> 532	GCF_000972575.1
<i>Cryptobacterium curtum</i> DSM 15641	GCF_000023845.1	<i>Staphylococcus condimenti</i> DSM 11674	GCF_001618885.1
<i>Curtobacterium flaccumfaciens</i> UCD-AKU	GCF_000349565.1	<i>Staphylococcus epidermidis</i> ATCC 12228	GCF_000007645.1
<i>Cutibacterium acnes</i> KPA171202	GCF_000008345.1	<i>Staphylococcus equorum</i> KS1039	GCF_001432245.1
<i>Cutibacterium avidum</i> 44067	GCF_000367205.1	<i>Staphylococcus haemolyticus</i> JCSC1435	GCF_000009865.1
<i>Cutibacterium granulosum</i> DSM 20700	GCF_000463665.1	<i>Staphylococcus hominis</i> subsp. <i>hominis</i> C80	GCF_000183685.1
<i>Deinococcus radiodurans</i> R1	GCF_000008565.1	<i>Staphylococcus intermedius</i> NCTC 11048	GCF_002902385.1
<i>Dermabacter hominis</i> 1368	GCF_000775415.1	<i>Staphylococcus kloosii</i> ATCC 43959	GCF_003019255.1
<i>Dermabacter</i> sp. HFH0086	GCF_000413375.1	<i>Staphylococcus lugdunensis</i> HKU09-01	GCF_000025085.1
<i>Dermacoccus nishinomiyaensis</i> M25	GCF_000725405.1	<i>Staphylococcus pasteurii</i> SP1	GCF_000494875.1
<i>Desulfitobacterium hafniense</i> DCB-2	GCF_000021925.1	<i>Staphylococcus pettenkoferi</i> FDAARGOS_288	GCF_002208805.2
<i>Desulfovibrio desulfuricans</i> ND132	GCF_000189295.2	<i>Staphylococcus saccharolyticus</i> NCTC 11807	GCF_003970495.1
<i>Desulfovibrio fairfieldensis</i> CCUG 45958	GCF_001553605.1	<i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305	GCF_000010125.1
<i>Desulfovibrio piger</i>	GCF_900116045.1	<i>Staphylococcus schleiferi</i> OT1-1	GCF_004026205.1
<i>Desulfovibrio</i> sp. FW1012B	GCF_000177215.2	<i>Staphylococcus sciuri</i> FDAARGOS_285	GCF_002209165.2
<i>Dialister invisus</i> DSM 15470	GCF_000160055.1	<i>Staphylococcus simulans</i> FDAARGOS_124	GCF_001559115.2
<i>Dialister microaerophilus</i> DSM 19965	GCF_000194985.1	<i>Staphylococcus</i> sp. AntiMn-1	GCF_001663395.1
<i>Dialister microaerophilus</i> UPII 345-E	GCF_000183445.1	<i>Staphylococcus succinus</i> 14BME20	GCF_001902315.1
<i>Dialister pneumosintes</i>	GCF_001717505.1	<i>Staphylococcus vitulinus</i> F1028	GCF_000286335.1
<i>Dialister succinatiphilus</i> YIT 11850	GCF_000242435.1	<i>Staphylococcus warneri</i> SG1	GCF_000332735.1
<i>Dielma fastidiosa</i>	GCF_000313565.1	<i>Staphylococcus xylosus</i> HKUOPL8	GCF_000706685.1
<i>Dietzia cinnamea</i>	GCF_001643175.1	<i>Stenotrophomonas maltophilia</i> K279a	GCF_000072485.1
<i>Dietzia maris</i>	GCF_001630765.1	<i>Stenotrophomonas rhizophila</i> QL-P4	GCF_001704155.1
<i>Dietzia natronolimnaea</i>	GCF_002289575.1	<i>Streptococcus agalactiae</i> 2603V/R	GCF_000007265.1
<i>Dorea formicigenerans</i> ATCC 27755	GCF_000169235.1	<i>Streptococcus anginosus</i> C238	GCF_000463505.1
<i>Dorea longicatena</i> DSM 13814	GCF_000154065.1	<i>Streptococcus australis</i> NCTC13166	GCF_900476055.1
<i>Dyadobacter beijingensis</i> DSM 21582	GCF_000382205.1	<i>Streptococcus constellatus</i> subsp. <i>pharyngis</i> C818	GCF_000463445.1
<i>Dyadobacter fermentans</i> DSM 18053	GCF_000023125.1	<i>Streptococcus cristatus</i> AS 1.3089	GCF_000385925.1
<i>Dysgonomonas gadei</i> ATCC BAA-286	GCF_000213555.1	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> AC-2713	GCF_000317855.1
<i>Dysgonomonas mossii</i> DSM 22836	GCF_000213575.1	<i>Streptococcus equi</i> subsp. <i>Zooepidemicus</i> H70	GCF_000026605.1
<i>Edwardsiella tarda</i> FL6-60	GCF_000146305.1	<i>Streptococcus equinus</i> AG46	GCF_000964315.1
<i>Eggerthella lenta</i> DSM 2243	GCF_000024265.1	<i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> DSM 16831	GCF_002000985.1
<i>Eggerthella</i> sp. YY7918	GCF_000270285.1	<i>Streptococcus gordonii</i> str. <i>Challis</i> substr. CH1	GCF_000017005.1
<i>Eggerthia cateniformis</i> OT 569 = DSM 20559	GCF_000340375.1	<i>Streptococcus infantarius</i> subsp. <i>infantarius</i> CJ18	GCF_000246835.1
<i>Empedobacter falsenii</i>	GCF_003935845.1	<i>Streptococcus infantis</i> ATCC 700779	GCF_000187465.1
<i>Enorma massiliensis</i> phl	GCF_000311845.1	<i>Streptococcus intermedius</i> B196	GCF_000463355.1
<i>Enterobacter asburiae</i>	GCF_001521715.1	<i>Streptococcus lutetiensis</i> 033	GCF_000441535.1
<i>Enterobacter cancerogenus</i>	GCF_002850575.1	<i>Streptococcus mitis</i> B6	GCF_000027165.1
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> ATCC 13047	GCF_000025565.1	<i>Streptococcus mutans</i> UA159	GCF_000007465.2
<i>Enterobacter hormaechei</i> subsp. <i>steigerwaltii</i>	GCF_001729725.1	<i>Streptococcus oralis</i> ATCC 35037	GCF_900637025.1
<i>Enterobacter ludwigii</i>	GCF_001750725.1	<i>Streptococcus parasanguinis</i> ATCC 15912	GCF_000164675.2

<i>Enterobacteriaceae bacterium w6</i>	GCF_003336345.1	<i>Streptococcus parauberis</i> KCTC 11537	GCF_000213825.1
<i>Enterococcus asini</i> ATCC 700915	GCF_000407365.1	<i>Streptococcus pasteurianus</i> ATCC 43144	GCF_000270165.1
<i>Enterococcus avium</i> ATCC 14025	GCF_000407245.1	<i>Streptococcus peroris</i> ATCC 700780	GCF_000187585.1
<i>Enterococcus caccae</i> ATCC BAA-1240	GCF_000407145.1	<i>Streptococcus pneumoniae</i> R6	GCF_000007045.1
<i>Enterococcus casseliflavus</i> EC20	GCF_000157355.2	<i>Streptococcus pseudopneumoniae</i> IS7493	GCF_000221985.1
<i>Enterococcus cecorum</i>	GCF_001318405.1	<i>Streptococcus pyogenes</i> M1 GAS	GCF_000006785.2
<i>Enterococcus dispar</i> ATCC 51266	GCF_000406945.1	<i>Streptococcus salivarius</i> NCTC 8618	GCF_000785515.1
<i>Enterococcus durans</i>	GCF_001267865.1	<i>Streptococcus sanguinis</i> SK36	GCF_000014205.1
<i>Enterococcus faecalis</i> V583	GCF_000007785.1	<i>Streptococcus</i> sp. oral taxon 064	GCF_001683375.1
<i>Enterococcus faecium</i> DO	GCF_000174395.2	<i>Streptococcus thermophilus</i> JIM 8232	GCF_000253395.1
<i>Enterococcus gallinarum</i> FDAARGOS_163	GCF_001558875.2	<i>Streptococcus thoraltensis</i> DSM 12221	GCF_000380145.1
<i>Enterococcus hirae</i> ATCC 9790	GCF_000271405.2	<i>Streptococcus uberis</i> 0140J	GCF_000009545.1
<i>Enterococcus phenicolicola</i> ATCC BAA-412	GCF_000407505.1	<i>Streptococcus vestibularis</i> NCTC12167	GCF_900636445.1
<i>Enterococcus pseudoavium</i> NBRC 100491	GCF_001544295.1	<i>Streptococcus viridans</i> NCTC3166	GCF_900636365.1
<i>Enterococcus saccharolyticus</i> subsp. <i>saccharolyticus</i> ATCC 43076	GCF_000407285.1	<i>Streptomyces misionensis</i> DSM 40306	GCF_900104815.1
<i>Enterococcus</i> sp. FDAARGOS_553	GCF_003812305.1	<i>Streptomyces thermovulgaris</i> NRRL B-12375	GCF_002155915.1
<i>Erysipelatoclostridium ramosum</i> DSM 1402	GCF_000154485.1	<i>Subdoligranulum</i> sp. 4_3_54A2FAA	GCF_000238635.1
<i>Erysipelotrichaceae bacterium</i> SG0102	GCF_003925875.1	<i>Subdoligranulum variabile</i> DSM 15176	GCF_000157955.1
<i>Escherichia albertii</i> NCTC 9362	GCF_003864095.1	<i>Succinatimonas hippei</i> YIT 12066	GCF_000188195.1
<i>Escherichia coli</i> O157:H7 str. Sakai	GCF_000008865.2	<i>Succinivibrio dextrinosolvens</i> DSM 3072	GCF_900167015.1
<i>Escherichia fergusonii</i> ECD227	GCF_000191665.1	<i>Sutterella parvivruba</i> YIT 11816	GCF_000250875.1
<i>Escherichia</i> sp. 1_1_43	GCF_000159895.2	<i>Sutterella wadsworthensis</i> HGA0223	GCF_000411515.1
<i>Eubacterium barkeri</i> VPI 5359	GCF_900107125.1	<i>Synergistes</i> sp. 3_1_syn1	GCF_000238615.1
<i>Eubacterium brachy</i> ATCC 33089	GCF_000488855.1	<i>Tannerella forsythia</i> 92A2	GCF_000238215.1
<i>Eubacterium callanderi</i> KIST612	GCF_000152245.2	<i>Tannerella</i> sp. oral taxon HOT-286	GCF_003033925.1
<i>Eubacterium cellulosolvens</i> 6	GCF_000183525.2	<i>Tatumella ptyseos</i> NCTC11468	GCF_900478715.1
<i>Eubacterium eligens</i> ATCC 27750	GCF_000146185.1	<i>Terrisporobacter glycolicus</i> ATCC 14880 = DSM 1288	GCF_000439105.1
<i>Eubacterium hallii</i> DSM 3353	GCF_000173975.1	<i>Tetragenococcus solitarius</i> NBRC 100494	GCF_001544195.1
<i>Eubacterium limosum</i> ATCC 8486	GCF_000807675.2	<i>Timonella senegalensis</i> JC301	GCF_000312125.1
<i>Eubacterium ramulus</i> ATCC 29099	GCF_000469345.1	<i>Tissierella praeacuta</i> DSM 18095	GCF_900128955.1
<i>Eubacterium rectale</i> ATCC 33656	GCF_000020605.1	<i>Trabulsiella guamensis</i> ATCC 49490	GCF_000734965.1
<i>Eubacterium ruminantium</i> ATCC 17233	GCF_900167085.1	<i>Treponema berlinense</i> ATCC BAA-909	GCF_900167025.1
<i>Eubacterium saphenum</i> ATCC 49989	GCF_000161975.1	<i>Tropheryma whipplei</i> str. Twist	GCF_000007485.1
<i>Eubacterium siraeum</i> DSM 15702	GCF_000382085.1	<i>Trueperella bernardiae</i> LCDC 89-0504	GCF_001469025.1
<i>Eubacterium</i> sp. 3_1_31	GCF_000242955.1	<i>Trueperella pyogenes</i> TP6375	GCF_000612055.1
<i>Eubacterium sulci</i> ATCC 35585	GCF_001189495.1	<i>Tumebacillus permanentifrigoris</i> DSM 18773	GCF_003148565.1
<i>Eubacterium ventriosum</i> ATCC 27560	GCF_000153885.1	<i>Turicibacter sanguinis</i> 2789STDY5834851	GCF_001406595.1
<i>Eubacterium yurii</i> subsp. <i>margaretiae</i> ATCC 43715	GCF_000146855.1	<i>Turicibacter</i> sp. H121	GCF_001543345.1
<i>Exiguobacterium aurantiacum</i> DSM 6208	GCF_000702585.1	<i>Tyzzerella nexilis</i> DSM 1787	GCF_000156035.2
<i>Exiguobacterium</i> sp. N4-1P	GCF_002214325.1	<i>Ureaplasma parvum</i> serovar 3 str. ATCC 27815	GCF_000019345.1
<i>Faecalibacterium cf. prausnitzii</i> KLE1255	GCF_000166035.1	<i>Ureaplasma urealyticum</i> serovar 10 str. ATCC 33699	GCF_000021265.1
<i>Faecalibacterium prausnitzii</i> A2-165	GCF_000162015.1	<i>Ureibacillus thermosphaericus</i> str. Thermo-BF	GCF_000284835.1
<i>Faecalicoccus pleomorphus</i> DSM 20574	GCF_000420345.1	<i>Varibaculum cambriense</i> DSM 15806	GCF_000420065.1
<i>Faecalitalea cylindroides</i> T2-87	GCF_000210615.1	<i>Veillonella atypica</i> KON	GCF_000318355.2
<i>Fictibacillus arsenicus</i> G25-54	GCF_001642935.1	<i>Veillonella dispar</i> NCTC11831	GCF_900637515.1
<i>Filifactor alocis</i> ATCC 35896	GCF_000163895.2	<i>Veillonella parvula</i> DSM 2008	GCF_000024945.1
<i>Fingoldia magna</i> ATCC 29328	GCF_000010185.1	<i>Veillonella ratti</i> ATCC 17746	GCF_003992115.1
<i>Flavobacterium lindanitolerans</i> DSM 21886	GCF_003663835.1	<i>Veillonella rogosa</i> JCM 15642	GCF_002959775.1
<i>Flavobacterium oncorhynchi</i> CCUG 59446	GCF_002217355.1	<i>Veillonella</i> sp. AF13-2	GCF_003603295.1
<i>Flavobacterium</i> sp. CJ74	GCF_003403075.1	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961	GCF_000006745.1
<i>Flavonifractor plautii</i> YL31	GCF_001688625.2	<i>Vibrio fluvialis</i> ATCC 33809	GCF_001558415.2
<i>Fusicatenibacter saccharivorans</i> 2789STDY5608849	GCF_001405555.1	<i>Vibrio furnissii</i> NCTC 11218	GCF_000184325.1
<i>Fusobacterium gonidiaformans</i> ATCC 25563	GCF_003019695.1	<i>Vibrio mimicus</i> ATCC 33654	GCF_001558475.2
<i>Fusobacterium mortiferum</i> ATCC 9817	GCF_000158195.2	<i>Vibrio parahaemolyticus</i> RIMD 2210633	GCF_000196095.1
<i>Fusobacterium naviforme</i> ATCC 25832	GCF_003014445.1	<i>Vibrio</i> sp. HBUAS61001	GCF_003716875.1
<i>Fusobacterium necrogenes</i> NCTC10723	GCF_900450765.1	<i>Victivallis vadensis</i> DSM 14823	GCF_003096415.1
<i>Fusobacterium necrophorum</i> subsp. <i>funduliforme</i> ATCC 51357	GCF_000262225.1	<i>Virgibacillus proomii</i> V-P	GCF_900162615.1
<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586	GCF_000007325.1	<i>Weissella cibaria</i> CH2	GCF_001308145.2
<i>Fusobacterium periodonticum</i> 2_1_31	GCF_000158215.3	<i>Weissella confusa</i> DSM 20196	GCF_001436895.1

<i>Fusobacterium russii</i> ATCC 25533	GCF_000381725.1	<i>Weissella paramesenteroides</i> ATCC 33313	GCF_000160575.1
<i>Fusobacterium</i> sp. oral taxon 203 W7671	GCF_002243405.1	<i>Xenorhabdus nematophila</i> AN6/1	GCF_000953355.1
<i>Fusobacterium ulcerans</i> ATCC 49185	GCF_000158315.2	<i>Yersinia aleksiciae</i> 159	GCF_001047675.1
<i>Fusobacterium varium</i> ATCC 27725	GCF_003019655.1	<i>Yersinia bercovieri</i> 127/84	GCF_001131685.1
<i>gamma proteobacterium</i> HdN1	GCF_000198515.1	<i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081	GCF_000009345.1
<i>Gardnerella vaginalis</i> ATCC 14019	GCF_000159155.2	<i>Yersinia frederiksenii</i> Y225	GCF_000834215.1
<i>Gemella haemolysans</i> ATCC 10379	GCF_000173915.1	<i>Yersinia kristensenii</i> ATCC BAA-2637	GCF_003600645.1
<i>Gemella morbillorum</i> NCTC11323	GCF_900476045.1	<i>Yersinia pseudotuberculosis</i> str. PA3606	GCF_000834945.1
<i>Gemella sanguinis</i> ATCC 700632	GCF_000701685.1	<i>Yersinia rohdei</i> YRA	GCF_000834455.1
<i>Gemmiger formicilis</i> ATCC 27749	GCF_900167555.1	<i>Yokenella regensburgei</i> ATCC 49455	GCF_000735455.1



Supplementary Figure S1. Schematic representation of the QmihR pipeline [5].



Supplementary Figure S2. Quality control assessment of the TCGA stomach adenocarcinoma samples based on the raw bacterial counts and alpha diversity (Shannon). (A) Boxplot distribution of the alpha diversity based on shipment year. (B) scatterplot of the distribution of raw reads according to the Shannon diversity index throughout the different shipment years. (C) T-distributed Stochastic Neighbour Embedding (t-SNE) plot based on the Weighted Unifrac distance between samples.

Supplementary Table S3. Percentage of abundance per sample of *Helicobacter* and of genera that reach a value of 90% (*Escherichia*, *Lactobacillus* and *Pseudomonas*), with information of country of origin and year of shipment.

Sample	Country	Date	<i>Escherichia</i>	<i>Helicobacter</i>	<i>Lactobacillus</i>	<i>Pseudomonas</i>
TCGA-CG-4301-01A	Germany	2010	25.34	0.00	0.00	19.83
TCGA-CG-4304-01A	Germany	2010	23.14	0.32	0.65	43.38
TCGA-CG-4305-01A	Germany	2010	31.16	0.00	0.12	9.88
TCGA-CG-4306-01A	Germany	2010	1.55	0.37	86.15	0.37
TCGA-CG-4436-01A	Germany	2010	9.39	0.03	1.25	2.28
TCGA-CG-4438-01A	Germany	2010	32.83	0.00	0.00	2.87
TCGA-CG-4440-01A	Germany	2010	26.78	0.00	0.08	32.44
TCGA-CG-4442-01A	Germany	2010	2.02	0.00	10.44	0.49
TCGA-CG-4443-01A	Germany	2010	33.39	0.00	3.15	4.37
TCGA-CG-4444-01A	Germany	2010	49.33	0.00	0.00	3.96
TCGA-CG-4460-01A	Germany	2010	15.61	0.00	0.18	5.32
TCGA-CG-4462-01A	Germany	2010	16.49	0.00	0.37	1.73
TCGA-CG-4465-01A	Germany	2010	11.52	0.00	0.05	3.92
TCGA-CG-4466-01A	Germany	2010	6.58	0.00	0.46	1.76
TCGA-CG-4469-01A	Germany	2010	16.19	0.00	0.34	15.52
TCGA-CG-4475-01A	Germany	2010	40.36	0.00	0.00	4.61
TCGA-CG-4476-01A	Germany	2010	36.24	0.00	0.10	4.80

TCGA-CG-4477-01A	Germany	2010	36.01	0.00	0.00	9.65
TCGA-BR-4187-01A	Russia	2010	1.68	3.25	22.33	7.18
TCGA-BR-4191-01A	Russia	2010	19.51	0.00	6.04	1.42
TCGA-BR-4201-01A	Russia	2010	20.26	0.00	0.22	3.10
TCGA-BR-4253-01A	Russia	2010	0.00	0.00	1.85	82.24
TCGA-BR-4256-01A	Russia	2010	34.63	0.00	1.23	16.93
TCGA-BR-4257-01A	Russia	2010	1.32	0.00	3.07	12.06
TCGA-BR-4267-01A	Russia	2010	0.05	0.00	0.05	0.50
TCGA-BR-4279-01A	Russia	2010	3.24	4.59	3.13	18.53
TCGA-BR-4280-01A	Russia	2010	19.31	0.85	0.35	2.56
TCGA-BR-4294-01A	Russia	2010	49.86	0.00	0.21	4.97
TCGA-BR-4357-01A	Russia	2010	56.73	1.06	0.00	5.28
TCGA-BR-4361-01A	Russia	2010	16.01	0.19	48.66	1.56
TCGA-BR-4363-01A	Russia	2010	0.00	0.00	0.07	97.51
TCGA-BR-4366-01A	Russia	2010	23.18	0.00	0.18	6.75
TCGA-BR-4367-01A	Russia	2010	16.53	0.27	0.23	3.13
TCGA-BR-4368-01A	Russia	2010	26.60	0.00	39.03	1.55
TCGA-BR-4369-01A	Russia	2010	25.20	0.05	0.38	8.28
TCGA-BR-4370-01A	Russia	2010	20.84	0.00	3.94	9.78
TCGA-BR-4371-01A	Russia	2010	13.81	0.03	0.86	14.29
TCGA-HF-7131-01A	Canada	2011	0.00	0.00	0.00	88.86
TCGA-HF-7132-01A	Canada	2011	0.00	0.00	0.20	92.82
TCGA-HF-7133-01A	Canada	2011	0.03	0.00	0.05	92.61
TCGA-HF-7134-01A	Canada	2011	0.05	0.19	0.05	81.13
TCGA-CG-4437-01A	Germany	2011	0.75	0.14	1.08	1.55
TCGA-CG-4441-01A	Germany	2011	0.27	0.00	2.86	2.59
TCGA-CG-5716-01A	Germany	2011	0.00	0.28	0.76	1.42
TCGA-CG-5717-01A	Germany	2011	0.16	0.00	0.54	6.70
TCGA-CG-5718-01A	Germany	2011	0.32	0.00	7.51	0.45
TCGA-CG-5719-01A	Germany	2011	2.17	0.12	0.82	5.89
TCGA-CG-5720-01A	Germany	2011	0.35	19.60	1.21	1.47
TCGA-CG-5721-01A	Germany	2011	1.68	0.00	14.40	1.56
TCGA-CG-5722-01A	Germany	2011	0.80	0.43	1.47	1.49
TCGA-CG-5723-01A	Germany	2011	0.03	0.06	0.25	0.15
TCGA-CG-5724-01A	Germany	2011	0.30	0.03	3.28	3.51
TCGA-CG-5725-01A	Germany	2011	0.93	0.12	1.86	2.21
TCGA-CG-5726-01A	Germany	2011	0.60	0.00	0.95	1.19
TCGA-CG-5732-01A	Germany	2011	0.08	0.00	0.16	43.30
TCGA-CG-5734-01A	Germany	2011	0.25	0.00	1.27	1.25
TCGA-D7-5577-01A	Poland	2011	0.32	0.00	0.83	5.47
TCGA-D7-5578-01A	Poland	2011	0.94	0.00	1.94	1.17
TCGA-D7-6519-01A	Poland	2011	0.00	0.00	0.00	1.41
TCGA-D7-6520-01A	Poland	2011	0.24	0.00	0.39	0.49
TCGA-D7-6521-01A	Poland	2011	0.63	0.50	1.64	1.39
TCGA-D7-6522-01A	Poland	2011	0.61	2.14	0.73	2.25
TCGA-D7-6524-01A	Poland	2011	0.00	0.00	8.46	1.30
TCGA-D7-6525-01A	Poland	2011	0.00	1.02	6.76	2.46
TCGA-D7-6526-01A	Poland	2011	0.57	0.00	66.48	0.98

TCGA-D7-6527-01A	Poland	2011	0.35	3.79	0.77	2.74
TCGA-D7-6528-01A	Poland	2011	0.72	0.00	3.61	1.59
TCGA-D7-6815-01A	Poland	2011	1.06	0.00	2.38	1.06
TCGA-D7-6818-01A	Poland	2011	0.21	0.00	5.91	0.28
TCGA-D7-6822-01A	Poland	2011	1.73	0.00	2.02	0.86
TCGA-B7-5818-01A	Russia	2011	0.02	0.21	6.77	0.07
TCGA-BR-6452-01A	Russia	2011	0.80	6.00	2.00	1.20
TCGA-BR-6453-01A	Russia	2011	0.89	0.74	0.98	1.42
TCGA-BR-6454-01A	Russia	2011	0.00	0.00	0.85	3.05
TCGA-BR-6455-01A	Russia	2011	0.00	0.12	0.33	7.66
TCGA-BR-6456-01A	Russia	2011	0.00	0.00	1.27	1.27
TCGA-BR-6563-01A	Russia	2011	0.00	0.23	0.05	89.61
TCGA-BR-6564-01A	Russia	2011	0.18	0.00	1.60	1.51
TCGA-BR-6565-01A	Russia	2011	0.00	0.00	0.24	0.72
TCGA-BR-6566-01A	Russia	2011	1.16	0.12	1.40	1.40
TCGA-BR-6801-01A	Russia	2011	0.21	0.02	27.06	0.24
TCGA-BR-6802-01A	Russia	2011	0.00	0.00	1.81	0.79
TCGA-BR-6803-01A	Russia	2011	0.62	64.67	0.00	0.97
TCGA-BR-7704-01A	Russia	2011	0.06	0.02	0.02	91.80
TCGA-BR-7707-01A	Russia	2011	0.08	0.00	1.13	89.03
TCGA-BR-7715-01A	Russia	2011	0.20	0.13	4.48	62.96
TCGA-BR-7716-01A	Russia	2011	0.10	0.18	0.04	77.14
TCGA-BR-7717-01A	Russia	2011	0.00	0.00	37.82	44.73
TCGA-BR-6457-01A	Ukraine	2011	0.00	0.00	2.42	1.16
TCGA-BR-6458-01A	Ukraine	2011	0.00	0.00	1.66	1.96
TCGA-BR-6705-01A	Ukraine	2011	0.34	0.00	0.23	1.02
TCGA-BR-6707-01A	Ukraine	2011	0.82	0.00	0.23	1.99
TCGA-BR-6709-01A	Ukraine	2011	0.00	0.35	1.05	5.07
TCGA-BR-6710-01A	Ukraine	2011	0.00	84.20	0.28	0.66
TCGA-BR-6852-01A	Ukraine	2011	0.00	0.00	0.52	0.34
TCGA-BR-7196-01A	Ukraine	2011	0.01	0.01	0.00	88.18
TCGA-BR-7723-01A	Ukraine	2011	0.10	0.00	0.10	88.97
TCGA-F1-6177-01A	United States	2011	0.01	0.00	3.73	0.09
TCGA-F1-6874-01A	United States	2011	0.29	0.10	9.47	0.39
TCGA-F1-6875-01A	United States	2011	0.17	0.00	0.04	88.40
TCGA-FP-7735-01A	United States	2011	0.05	0.00	0.07	90.71
TCGA-FP-7829-01A	United States	2011	0.29	0.00	0.04	84.61
TCGA-IN-7806-01A	United States	2011	0.08	0.00	0.02	91.70
TCGA-CD-5798-01A	Vietnam	2011	0.92	0.00	1.44	1.48
TCGA-CD-5799-01A	Vietnam	2011	0.75	0.00	1.67	0.75
TCGA-CD-5800-01A	Vietnam	2011	0.55	0.00	1.04	1.42
TCGA-CD-5801-01A	Vietnam	2011	0.00	0.00	1.80	1.67
TCGA-CD-5803-01A	Vietnam	2011	0.49	0.00	11.91	1.42
TCGA-CD-5804-01A	Vietnam	2011	0.03	0.00	0.01	88.47
TCGA-CD-5813-01A	Vietnam	2011	0.07	0.18	0.71	29.30
TCGA-D7-8570-01A	Poland	2012	0.00	0.00	0.00	35.94
TCGA-D7-8572-01A	Poland	2012	0.28	0.31	0.65	12.27
TCGA-D7-8573-01A	Poland	2012	0.56	2.92	0.31	29.56

TCGA-D7-8574-01A	Poland	2012	1.00	0.00	0.28	30.80
TCGA-D7-8575-01A	Poland	2012	3.54	0.00	0.87	23.96
TCGA-D7-8576-01A	Poland	2012	0.77	0.00	0.19	35.40
TCGA-D7-8578-01A	Poland	2012	3.28	0.03	12.00	26.36
TCGA-D7-8579-01A	Poland	2012	1.15	1.68	1.63	41.83
TCGA-D7-A4YU-01A	Poland	2012	0.65	0.00	0.39	10.59
TCGA-D7-A4YX-01A	Poland	2012	0.53	0.00	0.42	10.14
TCGA-D7-A4Z0-01A	Poland	2012	0.21	0.04	1.63	8.79
TCGA-BR-7851-01A	Russia	2012	0.03	0.02	11.52	5.85
TCGA-BR-7957-01A	Russia	2012	0.00	0.06	0.18	36.01
TCGA-BR-7958-01A	Russia	2012	1.07	0.00	0.23	27.81
TCGA-BR-7959-01A	Russia	2012	0.04	0.00	0.00	50.44
TCGA-BR-8058-01A	Russia	2012	1.63	0.00	0.19	33.27
TCGA-BR-8059-01A	Russia	2012	0.54	0.00	12.40	22.11
TCGA-BR-8060-01A	Russia	2012	0.02	0.00	0.42	1.94
TCGA-BR-8077-01A	Russia	2012	0.15	0.01	0.21	28.65
TCGA-BR-8080-01A	Russia	2012	1.20	0.02	0.29	24.90
TCGA-BR-8081-01A	Russia	2012	0.52	0.00	0.69	20.69
TCGA-BR-8284-01A	Russia	2012	0.00	0.00	0.14	36.71
TCGA-BR-8286-01A	Russia	2012	0.76	0.08	0.21	25.48
TCGA-BR-8289-01A	Russia	2012	0.08	0.00	0.06	15.92
TCGA-BR-8291-01A	Russia	2012	0.35	0.00	0.09	30.63
TCGA-BR-8295-01A	Russia	2012	0.15	0.00	0.15	32.90
TCGA-BR-8296-01A	Russia	2012	0.67	0.06	0.12	34.74
TCGA-BR-8297-01A	Russia	2012	0.00	0.07	0.14	24.15
TCGA-BR-8361-01A	Russia	2012	0.00	0.00	1.59	34.44
TCGA-BR-8364-01A	Russia	2012	0.00	0.38	0.00	24.74
TCGA-BR-8372-01A	Russia	2012	0.91	0.00	1.26	30.36
TCGA-BR-8484-01A	Russia	2012	0.00	0.00	0.34	31.54
TCGA-BR-8485-01A	Russia	2012	1.39	1.04	0.00	28.06
TCGA-BR-8486-01A	Russia	2012	0.06	3.98	0.67	10.04
TCGA-BR-8588-01A	Russia	2012	0.43	0.00	0.09	24.33
TCGA-BR-8589-01A	Russia	2012	0.11	0.00	0.91	25.27
TCGA-BR-8590-01A	Russia	2012	0.18	0.01	0.71	6.15
TCGA-BR-8591-01A	Russia	2012	1.72	0.00	60.26	9.55
TCGA-BR-8592-01A	Russia	2012	1.26	0.00	0.24	26.84
TCGA-BR-8678-01A	Russia	2012	1.36	0.05	0.50	15.33
TCGA-BR-8679-01A	Russia	2012	0.87	0.00	0.48	32.30
TCGA-BR-8687-01A	Russia	2012	0.47	0.47	0.24	28.35
TCGA-BR-A4CR-01A	Russia	2012	2.98	0.00	38.43	1.50
TCGA-BR-A4CS-01A	Russia	2012	0.58	0.02	0.35	9.14
TCGA-BR-A4PF-01A	Russia	2012	0.14	1.60	1.37	14.17
TCGA-HU-8238-01A	South Korea	2012	0.68	0.98	0.17	21.69
TCGA-HU-8244-01A	South Korea	2012	0.67	0.04	0.21	25.47
TCGA-HU-8602-01A	South Korea	2012	0.22	0.03	1.90	6.18
TCGA-HU-8604-01A	South Korea	2012	0.00	0.01	89.82	0.35
TCGA-HU-8608-01A	South Korea	2012	0.88	0.13	0.38	19.32
TCGA-HU-8610-01A	South Korea	2012	0.00	0.01	31.73	0.18

TCGA-HU-A4G2-01A	South Korea	2012	0.17	0.21	0.38	9.17
TCGA-HU-A4G3-01A	South Korea	2012	0.00	0.00	0.09	13.15
TCGA-HU-A4G8-01A	South Korea	2012	1.25	0.00	0.50	13.30
TCGA-HU-A4G9-01A	South Korea	2012	0.28	0.00	0.28	4.52
TCGA-HU-A4GC-01A	South Korea	2012	0.82	0.00	0.30	6.93
TCGA-HU-A4GF-01A	South Korea	2012	0.52	1.44	0.16	12.00
TCGA-HU-A4GH-01A	South Korea	2012	1.35	0.00	0.09	11.35
TCGA-HU-A4GJ-01A	South Korea	2012	0.34	6.11	0.20	8.88
TCGA-HU-A4GP-01A	South Korea	2012	0.35	0.00	0.76	7.47
TCGA-HU-A4GT-01A	South Korea	2012	0.71	0.00	2.00	7.48
TCGA-HU-A4GU-01A	South Korea	2012	0.18	0.00	19.99	2.54
TCGA-HU-A4GX-01A	South Korea	2012	0.60	0.00	0.75	10.93
TCGA-HU-A4GY-01A	South Korea	2012	1.35	0.03	0.21	16.57
TCGA-HU-A4H0-01A	South Korea	2012	1.14	0.00	0.08	8.17
TCGA-HU-A4H2-01A	South Korea	2012	0.23	0.20	60.80	4.06
TCGA-HU-A4H3-01A	South Korea	2012	0.02	0.15	38.21	0.20
TCGA-HU-A4H4-01A	South Korea	2012	1.78	0.07	0.37	14.17
TCGA-HU-A4H5-01A	South Korea	2012	0.51	0.11	0.81	8.77
TCGA-HU-A4H6-01A	South Korea	2012	0.35	0.12	50.55	4.36
TCGA-HU-A4H8-01A	South Korea	2012	1.23	0.06	0.12	17.46
TCGA-HU-A4HB-01A	South Korea	2012	1.13	0.27	7.35	17.80
TCGA-HU-A4HD-01A	South Korea	2012	0.32	5.49	0.29	7.35
TCGA-BR-7197-01A	Ukraine	2012	0.77	0.15	0.08	30.22
TCGA-BR-7722-01A	Ukraine	2012	0.00	0.00	0.27	32.73
TCGA-BR-7901-01A	Ukraine	2012	1.73	0.00	0.14	29.42
TCGA-BR-8365-01A	Ukraine	2012	0.00	0.00	0.16	34.00
TCGA-BR-8366-01A	Ukraine	2012	0.05	0.00	0.52	25.66
TCGA-BR-8367-01A	Ukraine	2012	0.16	0.00	0.49	27.95
TCGA-BR-8368-01A	Ukraine	2012	0.00	0.00	0.05	37.90
TCGA-BR-8369-01A	Ukraine	2012	1.23	0.29	0.51	40.20
TCGA-BR-8371-01A	Ukraine	2012	0.51	0.00	0.23	31.26
TCGA-BR-8373-01A	Ukraine	2012	3.74	0.90	0.00	34.53
TCGA-BR-8380-01A	Ukraine	2012	0.00	0.00	1.04	26.00
TCGA-BR-8381-01A	Ukraine	2012	0.79	0.04	0.25	21.30
TCGA-BR-8382-01A	Ukraine	2012	3.87	0.00	6.35	14.42
TCGA-BR-8384-01A	Ukraine	2012	0.43	0.11	0.05	14.42
TCGA-BR-8483-01A	Ukraine	2012	0.55	0.00	3.14	33.02
TCGA-BR-8487-01A	Ukraine	2012	1.08	0.00	1.97	20.83
TCGA-BR-8676-01A	Ukraine	2012	0.02	0.00	14.10	3.94
TCGA-BR-8677-01A	Ukraine	2012	0.05	0.00	0.61	16.36
TCGA-BR-8690-01A	Ukraine	2012	0.31	0.03	0.12	22.68
TCGA-BR-A44T-01A	Ukraine	2012	0.59	0.61	0.46	9.03
TCGA-BR-A4J6-01A	Ukraine	2012	0.24	0.00	0.13	6.61
TCGA-BR-A4J8-01A	Ukraine	2012	0.76	0.00	0.08	13.30
TCGA-BR-A4J9-01A	Ukraine	2012	0.61	0.00	0.27	9.49
TCGA-BR-A4QL-01A	Ukraine	2012	0.29	0.03	4.42	6.08
TCGA-EQ-8122-01A	United States	2012	1.14	0.03	0.13	38.66
TCGA-F1-A448-01A	United States	2012	2.08	0.00	1.53	14.41

TCGA-FP-7916-01A	United States	2012	0.62	0.00	0.22	30.29
TCGA-FP-7998-01A	United States	2012	0.90	0.00	0.00	38.72
TCGA-FP-8099-01A	United States	2012	0.97	0.00	0.04	32.04
TCGA-FP-8209-01A	United States	2012	0.42	0.00	0.15	33.22
TCGA-FP-8210-01A	United States	2012	0.86	0.00	0.23	34.07
TCGA-FP-8211-01A	United States	2012	0.00	0.00	0.13	25.21
TCGA-FP-8631-01A	United States	2012	1.12	0.00	0.00	27.56
TCGA-HJ-7597-01A	United States	2012	0.03	0.00	1.08	3.09
TCGA-IN-7808-01A	United States	2012	0.10	0.00	0.25	26.23
TCGA-IN-8462-01A	United States	2012	0.71	0.01	0.09	29.63
TCGA-IN-8663-01A	United States	2012	0.74	0.00	0.46	24.05
TCGA-IP-7968-01A	United States	2012	1.23	0.00	0.05	28.06
TCGA-BR-8680-01A	Vietnam	2012	0.68	0.00	0.19	51.06
TCGA-BR-8682-01A	Vietnam	2012	0.52	1.44	0.13	14.92
TCGA-BR-8683-01A	Vietnam	2012	0.05	0.00	13.31	6.77
TCGA-BR-8686-01A	Vietnam	2012	2.43	3.88	0.16	30.18
TCGA-BR-A4IV-01A	Vietnam	2012	0.51	0.02	0.37	9.99
TCGA-BR-A4J4-01A	Vietnam	2012	0.46	0.02	1.29	13.43
TCGA-BR-A4J5-01A	Vietnam	2012	0.09	0.01	0.18	5.25
TCGA-BR-A4J7-01A	Vietnam	2012	0.09	0.00	0.06	12.72
TCGA-CD-8524-01A	Vietnam	2012	0.28	0.00	1.36	33.13
TCGA-CD-8525-01A	Vietnam	2012	0.00	0.00	0.28	26.17
TCGA-CD-8526-01A	Vietnam	2012	0.33	0.00	0.37	28.56
TCGA-CD-8527-01A	Vietnam	2012	0.10	0.01	0.30	17.79
TCGA-CD-8528-01A	Vietnam	2012	0.97	0.06	0.19	40.91
TCGA-CD-8529-01A	Vietnam	2012	0.09	0.00	1.04	30.37
TCGA-CD-8530-01A	Vietnam	2012	0.08	0.00	0.10	32.51
TCGA-CD-8531-01A	Vietnam	2012	0.22	0.00	0.07	30.21
TCGA-CD-8532-01A	Vietnam	2012	0.30	0.00	0.09	11.78
TCGA-CD-8533-01A	Vietnam	2012	0.00	0.00	0.16	34.65
TCGA-CD-8534-01A	Vietnam	2012	0.35	0.00	0.26	38.55
TCGA-CD-8535-01A	Vietnam	2012	0.00	0.00	1.28	31.06
TCGA-CD-A486-01A	Vietnam	2012	0.00	0.19	1.78	11.96
TCGA-CD-A487-01A	Vietnam	2012	0.46	0.15	0.36	14.62
TCGA-CD-A489-01A	Vietnam	2012	0.64	0.00	0.42	11.46
TCGA-CD-A48C-01A	Vietnam	2012	0.33	0.00	11.63	12.82
TCGA-CD-A4MG-01A	Vietnam	2012	0.07	0.01	0.57	11.03
TCGA-CD-A4MH-01A	Vietnam	2012	0.80	0.05	0.10	11.39
TCGA-RD-A7BS-01A	Australia	2013	0.02	0.00	0.00	95.52
TCGA-RD-A7BT-01A	Australia	2013	0.02	0.00	0.00	96.67
TCGA-RD-A7BW-01A	Australia	2013	0.03	0.00	0.00	95.94
TCGA-RD-A7C1-01A	Australia	2013	0.02	0.00	0.00	97.07
TCGA-HF-A5NB-01A	Canada	2013	0.00	0.01	0.42	77.46
TCGA-KB-A6F7-01A	Canada	2013	0.00	0.00	0.00	96.67
TCGA-SW-A7EA-01A	Moldova	2013	0.04	0.00	0.00	95.85
TCGA-SW-A7EB-01A	Moldova	2013	0.00	0.00	0.00	94.84
TCGA-D7-A6EV-01A	Poland	2013	0.06	0.00	0.25	59.97
TCGA-D7-A6EX-01A	Poland	2013	0.02	0.00	0.03	79.56

TCGA-D7-A6EY-01A	Poland	2013	0.08	0.00	0.01	83.16
TCGA-D7-A6EZ-01A	Poland	2013	0.08	0.21	0.16	46.59
TCGA-D7-A6F0-01A	Poland	2013	0.27	0.00	0.01	83.57
TCGA-D7-A6F2-01A	Poland	2013	0.02	0.25	0.00	73.45
TCGA-D7-A747-01A	Poland	2013	0.00	0.00	0.00	96.03
TCGA-D7-A748-01A	Poland	2013	0.01	0.00	0.01	96.56
TCGA-D7-A74A-01A	Poland	2013	0.00	0.04	0.01	96.65
TCGA-B7-A5TI-01A	Russia	2013	0.04	0.02	0.20	73.94
TCGA-B7-A5TJ-01A	Russia	2013	0.19	0.00	0.07	79.61
TCGA-B7-A5TN-01A	Russia	2013	0.11	0.00	0.02	79.04
TCGA-F1-A72C-01A	United States	2013	0.01	0.00	0.00	97.73
TCGA-IN-A6RI-01A	United States	2013	0.01	0.00	0.00	97.19
TCGA-IN-A6RJ-01A	United States	2013	0.01	0.00	0.00	97.91
TCGA-IN-A6RL-01A	United States	2013	0.00	0.00	0.00	97.13
TCGA-IN-A6RN-01A	United States	2013	0.00	0.00	0.00	94.50
TCGA-IN-A6RO-01A	United States	2013	0.01	0.00	0.00	97.99
TCGA-IN-A6RR-01A	United States	2013	0.01	0.00	0.47	95.64
TCGA-IN-A6RS-01A	United States	2013	0.02	0.00	0.00	82.46
TCGA-IN-A7NR-01A	United States	2013	0.01	0.00	0.00	95.75
TCGA-IN-A7NT-01A	United States	2013	0.00	0.00	0.00	97.32
TCGA-IN-A7NU-01A	United States	2013	0.00	0.00	0.03	95.35
TCGA-MX-A5UG-01A	United States	2013	0.07	0.03	0.02	78.98
TCGA-MX-A5UJ-01A	United States	2013	0.12	0.00	0.00	79.10
TCGA-MX-A663-01A	United States	2013	0.01	0.00	0.04	81.42
TCGA-MX-A666-01A	United States	2013	0.13	0.00	0.02	83.79
TCGA-R5-A7O7-01A	United States	2013	0.00	0.00	0.11	95.11
TCGA-R5-A7ZE-01B	United States	2013	0.03	0.00	0.01	93.52
TCGA-R5-A7ZF-01A	United States	2013	0.01	0.00	0.09	96.53
TCGA-R5-A7ZI-01A	United States	2013	0.01	0.00	0.03	97.08
TCGA-R5-A7ZR-01A	United States	2013	0.02	0.00	0.00	94.70
TCGA-RD-A8MV-01A	Australia	2014	0.01	0.00	0.01	97.68
TCGA-RD-A8MW-01A	Australia	2014	0.01	0.00	0.00	97.99
TCGA-RD-A8N0-01A	Australia	2014	0.00	0.04	0.00	97.58
TCGA-RD-A8N1-01A	Australia	2014	0.02	0.00	0.02	98.02
TCGA-RD-A8N2-01A	Australia	2014	0.01	0.00	0.00	96.34
TCGA-RD-A8N4-01A	Australia	2014	0.01	0.00	0.00	97.19
TCGA-RD-A8N5-01A	Australia	2014	0.04	0.02	0.01	95.88
TCGA-RD-A8N6-01A	Australia	2014	0.03	0.00	0.00	97.55
TCGA-RD-A8N9-01A	Australia	2014	0.00	0.06	0.00	98.24
TCGA-RD-A8NB-01A	Australia	2014	0.01	0.00	0.00	97.98
TCGA-VQ-A8DT-01A	Brazil	2014	0.00	0.04	0.00	97.47
TCGA-VQ-A8DU-01A	Brazil	2014	0.01	0.00	0.00	97.17
TCGA-VQ-A8DV-01A	Brazil	2014	0.00	0.00	0.00	97.97
TCGA-VQ-A8DZ-01A	Brazil	2014	0.00	0.00	0.00	97.52
TCGA-VQ-A8E0-01A	Brazil	2014	0.01	0.00	0.07	98.04
TCGA-VQ-A8E2-01A	Brazil	2014	0.00	0.00	0.00	98.47
TCGA-VQ-A8E3-01A	Brazil	2014	0.00	0.00	0.00	97.74
TCGA-VQ-A8E7-01B	Brazil	2014	0.00	0.00	0.03	96.94

TCGA-VQ-A8P2-01A	Brazil	2014	0.04	0.00	0.01	96.49
TCGA-VQ-A8P3-01A	Brazil	2014	0.00	0.00	0.00	97.49
TCGA-VQ-A8P5-01A	Brazil	2014	0.00	0.00	0.00	95.21
TCGA-VQ-A8P8-01A	Brazil	2014	0.00	0.01	0.00	98.41
TCGA-VQ-A8PB-01A	Brazil	2014	0.07	0.00	0.24	97.72
TCGA-VQ-A8PC-01A	Brazil	2014	0.01	0.00	0.01	97.33
TCGA-VQ-A8PD-01A	Brazil	2014	0.00	0.00	0.12	98.46
TCGA-VQ-A8PE-01A	Brazil	2014	0.01	0.01	0.00	98.07
TCGA-VQ-A8PF-01A	Brazil	2014	0.00	0.00	0.01	97.96
TCGA-VQ-A8PH-01A	Brazil	2014	0.00	0.00	0.24	97.74
TCGA-VQ-A8PJ-01A	Brazil	2014	0.01	0.00	0.00	97.60
TCGA-VQ-A8PK-01A	Brazil	2014	0.00	0.00	0.01	96.55
TCGA-VQ-A8PM-01A	Brazil	2014	0.00	0.00	0.00	97.92
TCGA-VQ-A8PO-01A	Brazil	2014	0.02	0.00	0.02	96.89
TCGA-VQ-A8PP-01A	Brazil	2014	0.03	0.00	0.01	98.21
TCGA-VQ-A8PQ-01A	Brazil	2014	0.00	0.00	0.00	97.73
TCGA-VQ-A8PU-01A	Brazil	2014	0.01	0.00	0.00	97.14
TCGA-VQ-A8PX-01A	Brazil	2014	0.00	0.00	0.00	97.20
TCGA-VQ-A91A-01A	Brazil	2014	0.00	0.00	0.00	98.56
TCGA-VQ-A91D-01A	Brazil	2014	0.00	0.00	0.16	92.58
TCGA-VQ-A91E-01A	Brazil	2014	0.01	0.00	0.36	97.96
TCGA-VQ-A91K-01A	Brazil	2014	0.00	0.00	0.01	97.36
TCGA-VQ-A91N-01A	Brazil	2014	0.00	0.00	0.00	98.17
TCGA-VQ-A91Q-01A	Brazil	2014	0.00	0.00	0.00	97.91
TCGA-VQ-A91S-01A	Brazil	2014	0.00	0.00	0.00	98.12
TCGA-VQ-A91U-01A	Brazil	2014	0.00	0.39	0.03	97.69
TCGA-VQ-A91V-01A	Brazil	2014	0.00	0.00	0.00	98.40
TCGA-VQ-A91X-01A	Brazil	2014	0.00	0.01	0.00	98.56
TCGA-VQ-A91Y-01A	Brazil	2014	0.01	0.00	0.02	95.74
TCGA-VQ-A91Z-01A	Brazil	2014	0.00	0.00	0.00	97.18
TCGA-VQ-A922-01A	Brazil	2014	0.00	0.00	0.02	97.68
TCGA-VQ-A923-01A	Brazil	2014	0.00	0.02	0.01	97.29
TCGA-VQ-A924-01A	Brazil	2014	0.00	0.00	0.00	97.64
TCGA-VQ-A925-01A	Brazil	2014	0.00	0.00	0.01	98.09
TCGA-VQ-A927-01A	Brazil	2014	0.00	0.00	0.02	98.13
TCGA-VQ-A928-01A	Brazil	2014	0.01	0.00	0.11	97.67
TCGA-VQ-A92D-01A	Brazil	2014	0.02	0.00	0.00	97.40
TCGA-VQ-A94O-01A	Brazil	2014	0.01	0.00	0.00	97.85
TCGA-VQ-A94P-01A	Brazil	2014	0.00	0.00	0.34	97.57
TCGA-VQ-A94R-01A	Brazil	2014	0.00	0.00	0.32	96.56
TCGA-VQ-A94T-01A	Brazil	2014	0.01	0.04	0.00	98.11
TCGA-VQ-A94U-01A	Brazil	2014	0.00	0.00	0.00	98.36
TCGA-VQ-AA64-01A	Brazil	2014	0.01	0.00	0.00	97.67
TCGA-VQ-AA68-01A	Brazil	2014	0.02	0.00	0.00	97.92
TCGA-VQ-AA69-01A	Brazil	2014	0.00	0.00	0.00	93.26
TCGA-VQ-AA6A-01A	Brazil	2014	0.00	0.02	0.00	97.24
TCGA-VQ-AA6D-01A	Brazil	2014	0.00	0.00	0.00	96.80
TCGA-VQ-AA6F-01A	Brazil	2014	0.00	0.00	0.01	97.14

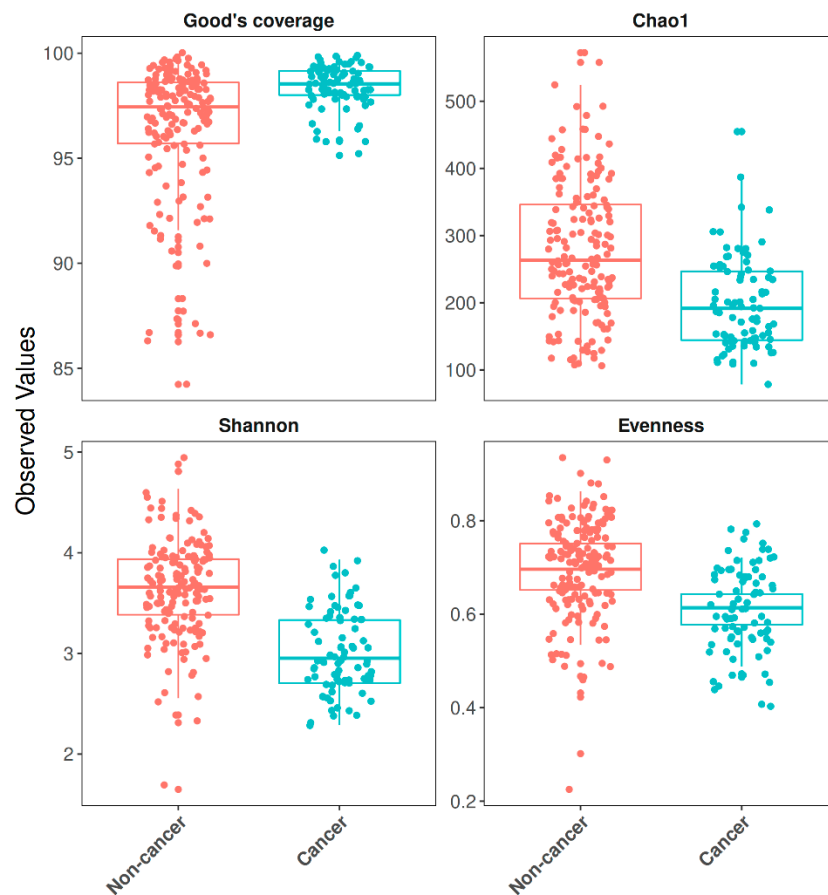
TCGA-VQ-AA6G-01A	Brazil	2014	0.00	0.00	0.00	97.79
TCGA-VQ-AA6J-01A	Brazil	2014	0.00	0.04	0.00	98.48
TCGA-VQ-AA6K-01A	Brazil	2014	0.00	0.00	0.00	97.60
TCGA-KB-A93G-01A	Canada	2014	0.00	0.00	0.00	97.64
TCGA-KB-A93H-01A	Canada	2014	0.00	0.00	0.01	96.91
TCGA-KB-A93J-01A	Canada	2014	0.01	0.00	0.03	97.32
TCGA-B7-A5TK-01A	Russia	2014	0.00	0.00	0.01	96.44
TCGA-HU-8249-01A	South Korea	2014	0.00	0.00	0.00	98.00
TCGA-HU-A4GD-01A	South Korea	2014	0.01	0.00	0.00	98.62
TCGA-HU-A4GQ-01A	South Korea	2014	0.00	0.00	0.03	96.92
TCGA-BR-A44U-01A	Ukraine	2014	0.01	0.00	0.00	97.51
TCGA-ZQ-A9CR-01A	United Kingdom	2014	0.00	0.00	0.00	97.58
TCGA-3M-AB46-01A	United States	2014	0.01	0.00	0.11	98.09
TCGA-3M-AB47-01A	United States	2014	0.00	0.00	0.00	98.67
TCGA-FP-A4BF-01A	United States	2014	0.00	0.00	0.00	97.63
TCGA-FP-A8CX-01A	United States	2014	0.01	0.00	0.21	95.08
TCGA-FP-A9TM-01A	United States	2014	0.01	0.00	0.00	98.22
TCGA-IN-AB1V-01A	United States	2014	0.01	0.00	0.00	97.20
TCGA-IN-AB1X-01A	United States	2014	0.01	0.00	0.00	97.08
TCGA-R5-A805-01A	United States	2014	0.01	0.00	0.00	95.24
TCGA-ZA-A8F6-01A	United States	2014	0.00	0.00	0.00	97.95
TCGA-CD-A48A-01A	Vietnam	2014	0.00	0.00	0.00	97.85
GTEX-O5YW-1526-SM-3MJGL	United States	2011	1.99	0.00	2.52	14.79
GTEX-O1ZH-1526-SM-3NB1J	United States	2011	2.14	0.00	0.00	22.39
GTEX-OXRK-1626-SM-3NB17	United States	2011	3.33	0.00	0.00	13.58
GTEX-P4PP-1526-SM-3P61M	United States	2011	0.43	0.02	0.33	10.35
GTEX-P4PQ-1526-SM-3NMCK	United States	2011	14.08	0.00	2.68	12.82
GTEX-P4QT-1526-SM-3NMCT	United States	2011	14.98	0.00	0.80	31.19
GTEX-P78B-1826-SM-3P5YX	United States	2011	1.42	0.00	0.14	10.91
GTEX-PLZ6-0826-SM-3P61K	United States	2011	2.08	0.06	1.83	24.28
GTEX-PW2O-1226-SM-48TCH	United States	2011	6.63	0.00	3.54	25.39
GTEX-PWCY-0926-SM-48TD7	United States	2011	1.20	0.00	1.64	30.12
GTEX-PWN1-1526-SM-48TDA	United States	2011	1.91	0.00	2.11	29.05
GTEX-PWOO-1226-SM-48TCO	United States	2011	2.26	0.45	1.76	22.32
GTEX-PX3G-1526-SM-48U11	United States	2011	3.14	0.00	0.16	32.59
GTEX-Q2AI-0826-SM-48TZO	United States	2011	0.43	0.01	0.46	15.83
GTEX-Q734-1026-SM-48U16	United States	2011	0.76	0.00	0.04	18.94
GTEX-QCQG-0526-SM-48U2A	United States	2011	1.60	0.05	1.46	21.03
GTEX-QDVJ-1426-SM-48U1Y	United States	2011	2.40	0.00	1.39	45.66
GTEX-QDVN-1226-SM-48TZ5	United States	2011	2.11	0.00	1.62	20.79
GTEX-QMRM-1126-SM-447BN	United States	2011	0.50	0.02	0.13	5.16
GTEX-QV31-0626-SM-447C5	United States	2011	0.85	0.00	0.20	29.23
GTEX-QV44-1226-SM-4R1KE	United States	2011	35.91	0.00	5.73	5.61
GTEX-QXCU-1926-SM-48FE4	United States	2011	0.45	0.00	20.59	7.51
GTEX-R53T-1226-SM-48FCT	United States	2012	0.75	0.00	22.95	6.09
GTEX-R55C-1026-SM-48FCM	United States	2012	0.07	0.00	15.91	4.04
GTEX-R55G-1126-SM-48FDG	United States	2012	0.28	0.00	17.01	5.83

GTEX-RM2N-0826-SM-48FD3	United States	2012	0.27	0.00	20.75	7.05
GTEX-RTLS-2626-SM-46MUJ	United States	2012	1.71	0.00	0.15	21.91
GTEX-RWS6-0926-SM-47JXE	United States	2012	0.45	0.00	51.53	5.37
GTEX-S3XE-1026-SM-4AD4O	United States	2012	0.71	0.12	16.44	9.41
GTEX-S4P3-0726-SM-4AD57	United States	2012	0.56	0.01	4.56	2.65
GTEX-S4Q7-0726-SM-4AD5F	United States	2012	0.37	0.01	25.42	8.24
GTEX-S4UY-1626-SM-4AD55	United States	2012	0.24	0.11	13.8	10.26
GTEX-S4Z8-1226-SM-4AD6W	United States	2012	0.40	0.00	20.38	8.17
GTEX-S7SF-0626-SM-4AD4V	United States	2012	0.18	0.03	8.53	9.82
GTEX-S9S5-0826-SM-4B64N	United States	2012	0.22	0.05	3.97	14.03
GTEX-SIU7-1426-SM-4BRWT	United States	2012	0.61	0.00	5.47	7.52
GTEX-SNMC-0626-SM-4DM6H	United States	2012	1.87	0.00	8.34	9.78
GTEX-SUCS-0926-SM-4DM4Z	United States	2012	0.16	0.01	5.89	8.79
GTEX-T5JC-1926-SM-4DM6Q	United States	2012	0.57	0.00	7.64	9.51
GTEX-T5JW-0926-SM-4DM5K	United States	2012	0.52	0.00	10.88	12.69
GTEX-T6MO-0726-SM-4DM58	United States	2012	0.63	0.00	7.08	7.68
GTEX-T8EM-1226-SM-4DM5J	United States	2012	1.18	0.00	8.54	10.38
GTEX-TKQ2-0926-SM-4DXU5	United States	2012	1.11	0.00	4.70	17.44
GTEX-TMMY-1626-SM-4DXTY	United States	2012	1.53	0.00	6.98	14.96
GTEX-U3ZN-2026-SM-4DXUC	United States	2012	0.74	0.00	2.71	12.35
GTEX-U4B1-1026-SM-4DXT1	United States	2012	0.31	0.01	1.75	2.85
GTEX-U8T8-1226-SM-4E3IH	United States	2012	3.64	0.00	1.25	2.10
GTEX-UPIC-1826-SM-4IHKC	United States	2012	25.64	0.00	0.98	9.16
GTEX-UPK5-2126-SM-4JBKJ	United States	2012	26.96	0.00	1.98	9.67
GTEX-V1D1-1726-SM-4JBHB	United States	2012	30.15	0.00	0.81	12.16
GTEX-V955-1326-SM-4JBHR	United States	2012	27.25	0.00	0.87	8.86
GTEX-W5WG-1726-SM-4LMI5	United States	2012	23.26	0.00	0.53	4.90
GTEX-WEY5-1226-SM-4LMIQ	United States	2012	17.26	0.03	0.14	4.38
GTEX-WFG7-1326-SM-4LMK1	United States	2012	14.20	0.00	0.08	3.89
GTEX-WFG8-1326-SM-4LVN3	United States	2012	38.90	0.00	0.08	9.98
GTEX-WFJO-1126-SM-4LVLZ	United States	2012	27.59	0.06	0.67	6.78
GTEX-WFON-1126-SM-4LVMA	United States	2012	6.34	0.01	0.45	2.79
GTEX-WH7G-1526-SM-4LVMX	United States	2012	26.80	0.00	0.74	7.20
GTEX-WHPG-0426-SM-4M1XW	United States	2012	26.88	0.22	1.08	6.51
GTEX-WHSB-1226-SM-4M1XR	United States	2012	26.93	0.06	1.60	6.24
GTEX-WHWD-1426-SM-4OORU	United States	2012	27.99	0.00	1.07	7.64
GTEX-WRHK-0626-SM-4MVOE	United States	2012	24.05	0.00	0.19	4.94
GTEX-WY7C-1726-SM-4ONCC	United States	2012	44.27	0.00	0.19	9.49
GTEX-WYJK-2526-SM-4ONDF	United States	2012	45.66	0.00	0.04	8.75
GTEX-WYVS-1326-SM-4ONCQ	United States	2012	46.70	0.00	0.04	9.40
GTEX-WZTO-2126-SM-4PQYW	United States	2012	16.81	0.00	5.26	3.97
GTEX-X15G-1126-SM-4PQZG	United States	2012	26.87	0.00	5.64	5.14
GTEX-XAJ8-0326-SM-47JYI	United States	2012	0.45	0.00	46.82	5.17
GTEX-XBED-1226-SM-4AT5V	United States	2012	0.46	0.00	11.28	7.46
GTEX-XBEW-1826-SM-4RTWX	United States	2012	16.79	0.03	2.39	4.06
GTEX-XPVG-1526-SM-4B66C	United States	2012	0.10	0.02	2.05	10.05

GTEX-XQ8I-2026-SM-4BOOL	United States	2012	0.77	0.00	3.29	8.36
GTEX-XUJ4-1226-SM-4BOPD	United States	2012	0.60	0.81	4.79	10.47
GTEX-XUZC-0726-SM-4BOPH	United States	2012	0.07	0.01	13.49	2.27
GTEX-XV7Q-1326-SM-4BRWM	United States	2012	1.95	0.00	8.38	7.84
GTEX-XXEK-0826-SM-4BRWG	United States	2012	0.39	0.01	7.10	4.71
GTEX-111CU-0926-SM-5EGIK	United States	2013	4.52	0.00	0.25	11.06
GTEX-111YS-1126-SM-5GZYQ	United States	2013	1.26	0.00	0.46	7.69
GTEX-1122O-1926-SM-5EGIQ	United States	2013	1.20	0.00	0.06	18.69
GTEX-117YW-2226-SM-5N9DB	United States	2013	1.00	0.00	1.25	5.99
GTEX-11DXX-1326-SM-5GIDZ	United States	2013	1.97	4.82	0.11	12.50
GTEX-11EM3-1026-SM-5A5KL	United States	2013	3.00	0.00	1.67	10.00
GTEX-11EQ9-1226-SM-5987E	United States	2013	17.17	0.00	0.20	8.82
GTEX-11GSP-2126-SM-5HL5E	United States	2013	2.27	0.00	2.51	13.96
GTEX-11I78-1726-SM-5A5M3	United States	2013	2.22	0.00	3.39	9.66
GTEX-11NSD-1426-SM-5HL67	United States	2013	0.00	4.88	6.26	2.39
GTEX-11NUK-2426-SM-5BC4U	United States	2013	10.63	0.00	1.02	6.19
GTEX-11TT1-0726-SM-5GU5A	United States	2013	0.03	0.05	9.03	5.26
GTEX-11VI4-0326-SM-5EQ6L	United States	2013	0.62	0.00	0.35	15.85
GTEX-11WQK-2626-SM-5EQ4K	United States	2013	6.06	0.00	1.18	12.96
GTEX-1211K-1426-SM-5FQTF	United States	2013	1.34	0.00	0.33	7.31
GTEX-12696-1726-SM-5EQLH	United States	2013	0.37	0.12	0.33	6.66
GTEX-12BJ1-1726-SM-5HL9B	United States	2013	1.27	0.00	0.84	8.28
GTEX-12C56-0526-SM-5FQST	United States	2013	0.34	0.10	0.34	4.85
GTEX-12WS9-1426-SM-5FQT3	United States	2013	3.65	0.00	0.24	4.81
GTEX-12WSG-2026-SM-5FQUU	United States	2013	0.87	0.14	0.09	9.04
GTEX-12WSJ-0926-SM-5P9JD	United States	2013	0.36	0.00	0.57	4.91
GTEX-12WSK-1426-SM-5CVNN	United States	2013	3.89	0.00	1.37	10.98
GTEX-13111-1226-SM-5GCNC	United States	2013	1.81	0.00	2.09	13.25
GTEX-131XG-1226-SM-5EGH9	United States	2013	0.00	0.00	0.39	16.80
GTEX-132AR-2426-SM-5IFFD	United States	2013	1.72	0.00	0.94	10.47
GTEX-1339X-1426-SM-5K7YO	United States	2013	0.44	0.05	3.93	2.57
GTEX-133LE-1326-SM-5IFGO	United States	2013	1.52	0.00	0.51	18.73
GTEX-1399R-1126-SM-5IFIO	United States	2013	0.27	0.00	19.48	11.88
GTEX-139D8-2326-SM-5IFGE	United States	2013	1.69	0.02	0.37	8.02
GTEX-139YR-1926-SM-5LZXM	United States	2013	2.99	0.06	10.19	8.44
GTEX-13CF3-1926-SM-5K7WF	United States	2013	0.15	0.04	3.09	3.01
GTEX-13D11-2126-SM-5IFH2	United States	2013	0.54	0.00	0.31	3.99
GTEX-13FH7-1026-SM-5IJGF	United States	2013	0.25	0.00	1.41	3.03
GTEX-13FTW-1726-SM-5KM2B	United States	2013	0.34	0.00	0.67	4.32
GTEX-13FTX-0726-SM-5N9BI	United States	2013	0.62	0.00	0.00	7.37
GTEX-13N1W-2026-SM-5K7YU	United States	2013	0.28	0.11	2.79	4.29
GTEX-13O21-0926-SM-5IFGT	United States	2013	3.09	0.00	1.36	13.47
GTEX-13O3Q-2126-SM-5KM4C	United States	2013	1.71	0.04	1.67	9.77
GTEX-13OW6-2526-SM-5IJEC	United States	2013	1.01	0.00	0.19	13.67
GTEX-13PVQ-2126-SM-5L3FW	United States	2013	3.36	1.53	1.53	22.63
GTEX-13QBU-1126-SM-5LU44	United States	2013	0.32	0.00	1.68	17.92

GTEX-13U4I-2526-SM-5SI8Z	United States	2013	0.00	0.00	0.41	15.20
GTEX-144GM-1726-SM-5O9AS	United States	2013	0.12	0.01	0.15	4.74
GTEX-144GN-1226-SM-5O991	United States	2013	0.26	0.00	0.34	41.93
GTEX-145LT-1426-SM-5O9B3	United States	2013	1.6	0.00	0.40	6.82
GTEX-146FH-2126-SM-5SI9U	United States	2013	2.51	0.00	1.01	18.09
GTEX-146FR-2026-SM-5NQAI	United States	2013	0.07	0.00	2.00	13.99
GTEX-Y3I4-1626-SM-4TT7W	United States	2013	30.24	0.00	1.41	9.25
GTEX-Y5V6-1326-SM-4VDTF	United States	2013	29.96	0.00	0.27	6.37
GTEX-Y8E4-1526-SM-4WWDI	United States	2013	32.66	0.00	0.35	8.28
GTEX-Y8LW-0826-SM-4WWDO	United States	2013	39.93	0.00	0.30	9.40
GTEX-Y9LG-1026-SM-5IFJN	United States	2013	0.28	0.00	12.54	3.10
GTEX-YEC3-1426-SM-5PNXW	United States	2013	0.00	0.00	2.32	3.26
GTEX-YEC4-1426-SM-5IFHS	United States	2013	0.25	0.00	32.31	4.62
GTEX-YJ8A-1526-SM-5P9FT	United States	2013	1.09	0.00	1.00	15.40
GTEX-ZA64-0826-SM-5HL9U	United States	2013	1.11	0.00	1.82	7.66
GTEX-ZAB4-1526-SM-5CVN7	United States	2013	4.59	0.00	0.53	18.55
GTEX-ZDYS-1926-SM-5HL59	United States	2013	1.09	0.00	1.63	17.98
GTEX-ZE7O-3026-SM-51MS4	United States	2013	5.84	0.00	11.72	1.87
GTEX-ZEX8-1626-SM-4WKG7	United States	2013	38.71	0.00	0.16	9.35
GTEX-ZF29-1526-SM-4WK7	United States	2013	22.01	0.00	0.15	7.37
GTEX-ZF2S-1426-SM-57WET	United States	2013	26.57	0.00	6.34	7.35
GTEX-ZLV1-0826-SM-4WWEQ	United States	2013	27.25	0.04	1.16	8.10
GTEX-ZP4G-1226-SM-4WWCJ	United States	2013	32.02	0.00	0.44	7.72
GTEX-ZPIC-2026-SM-57WG3	United States	2013	32.86	0.00	0.79	8.28
GTEX-ZT9W-1526-SM-4YCDE	United States	2013	30.14	0.10	1.03	8.19
GTEX-ZV6S-0926-SM-57WGB	United States	2013	11.29	0.00	0.64	4.07
GTEX-ZVT2-1626-SM-51MRC	United States	2013	40.52	0.00	0.22	9.23
GTEX-ZVT3-2126-SM-59HL2	United States	2013	19.02	0.00	3.84	15.75
GTEX-ZVZP-1726-SM-5GZWY	United States	2013	0.01	0.00	0.07	75.41
GTEX-ZXES-1426-SM-5NQ8S	United States	2013	0.93	0.00	1.04	9.11
GTEX-ZYFG-1326-SM-5GICJ	United States	2013	5.14	0.00	0.00	24.90
GTEX-ZYVF-2726-SM-5GID4	United States	2013	1.23	0.00	0.24	17.02
GTEX-ZYY3-1726-SM-5EGH3	United States	2013	1.51	0.00	0.39	5.20
GTEX-ZZ64-0426-SM-5E43F	United States	2013	1.37	0.00	0.29	10.45
GTEX-ZZPU-1426-SM-5GZZ6	United States	2013	0.00	0.00	0.61	12.84
GTEX-11EI6-2426-SM-5PNVS	United States	2014	0.32	0.00	2.90	3.75
GTEX-11P82-0726-SM-5PNYL	United States	2014	0.05	0.00	0.50	2.57
GTEX-1399S-1626-SM-5P9GI	United States	2014	1.70	0.00	0.01	9.48
GTEX-1399U-1626-SM-5P9J3	United States	2014	0.03	0.00	0.35	78.50
GTEX-13QJ3-2726-SM-5SI6L	United States	2014	0.65	0.01	0.80	7.43
GTEX-13RTK-0226-SM-5RQHR	United States	2014	5.62	0.00	1.18	30.18
GTEX-13S7M-1826-SM-5RQK6	United States	2014	0.92	0.00	1.37	16.59
GTEX-13X6H-1626-SM-5Q5CT	United States	2014	1.13	0.00	0.97	8.95
GTEX-145MO-2226-SM-5Q5BN	United States	2014	0.32	0.00	0.28	2.40
GTEX-14BMU-1126-SM-5RQJ8	United States	2014	2.66	0.00	0.35	17.91
GTEX-14BMV-2226-SM-5RQHx	United States	2014	0.16	0.02	0.29	14.71

GTEX-Y5LM-1326-SM-5RQIS	United States	2014	1.11	0.00	3.33	21.67
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Supplementary Figure S3. Genus richness in the inferred microbiome patterns between the GTEx non-cancer samples and the TCGA cancer samples from the sample ancestral background (European and United states). A- Good's coverage, Chao1, Shannon and evenness in inferred microbiome patterns.

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