

Supplementary Information: Tables and Figures

Sequencing, fast and slow: profiling microbiomes in human samples with nanopore sequencing

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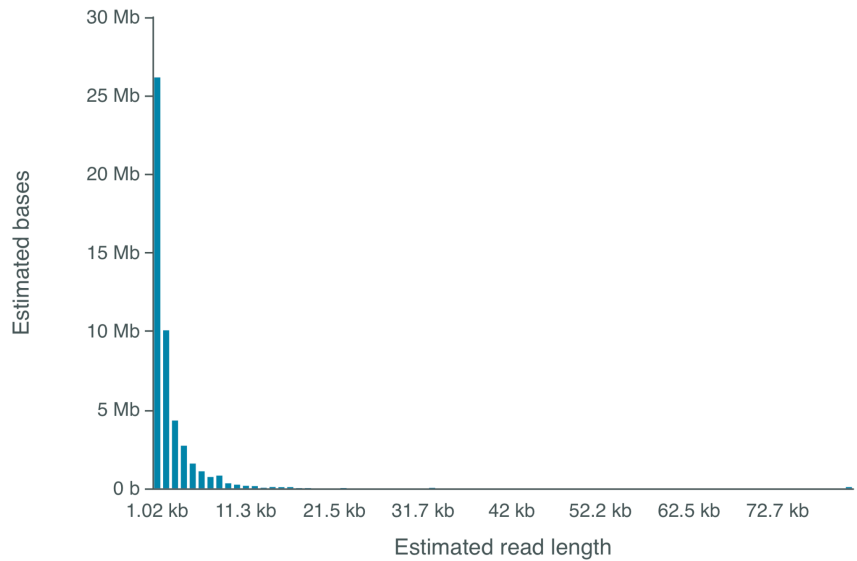
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[†]These authors contributed equally to this work.

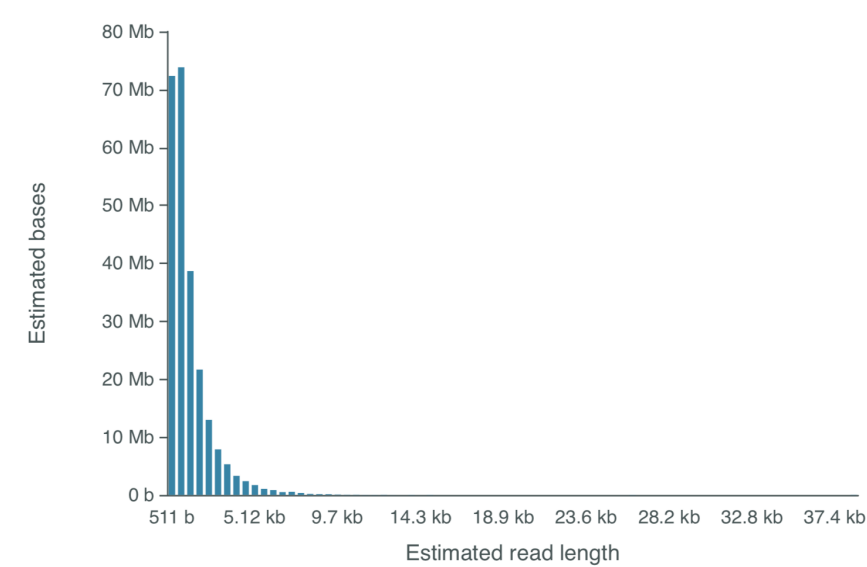
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Figure S1. Read Length Histogram Estimated Bases showing Estimated N50 per microbiome replicate.

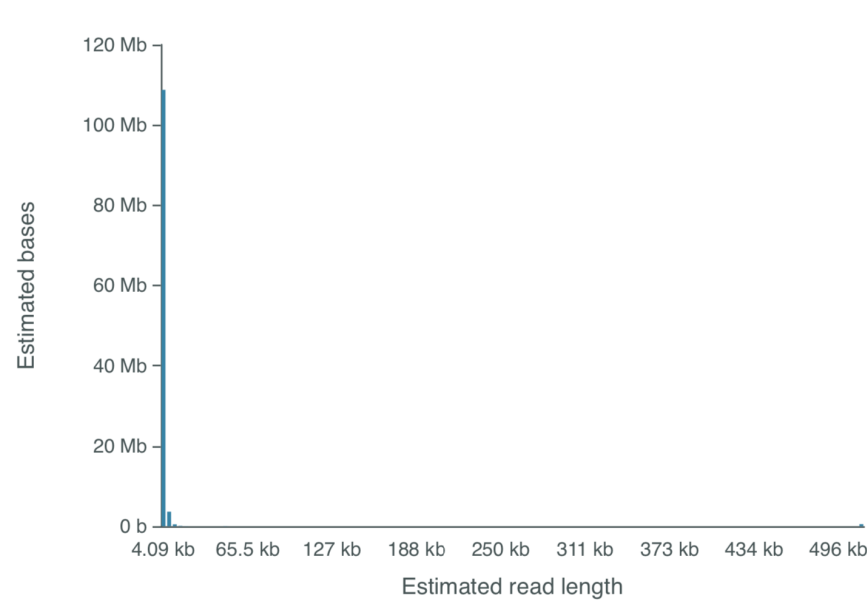
Date of measure: 20220303 - Saliva1 R1



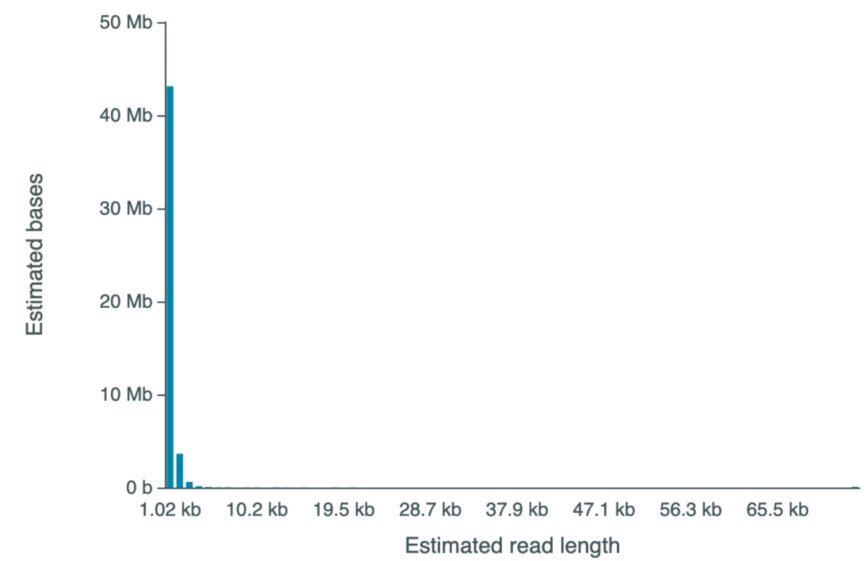
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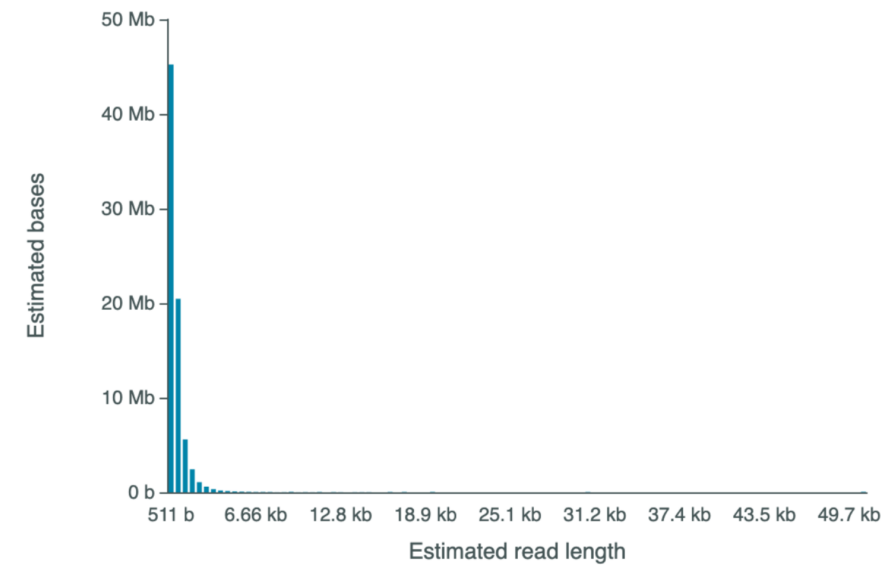
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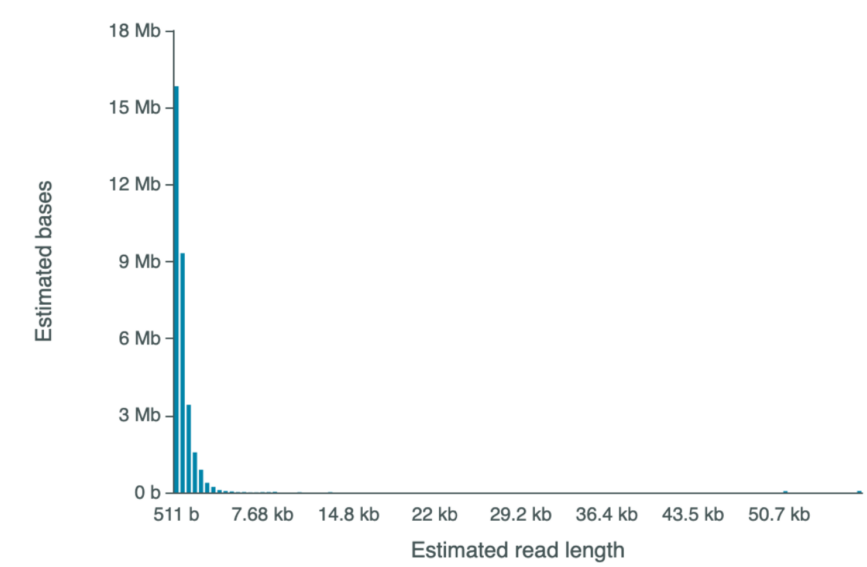
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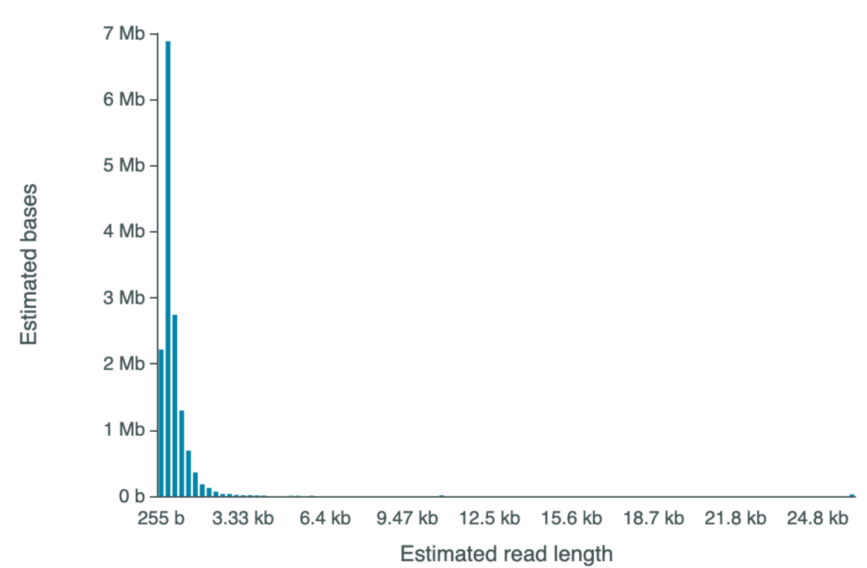
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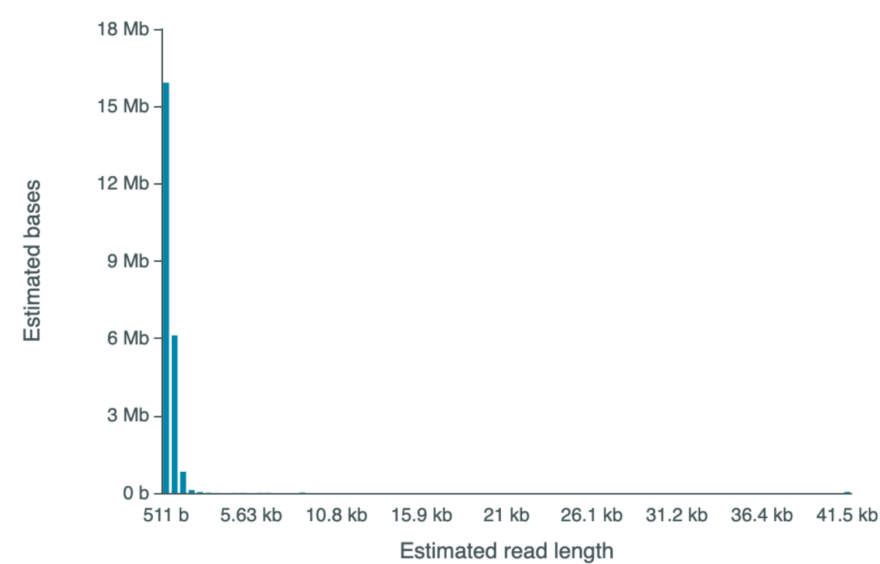
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Date of measure: 20220321 - Saliva3 R2



Date of measure: 20220701 - Stool2 R1



Date of measure: 20220701 - Stool2 R2

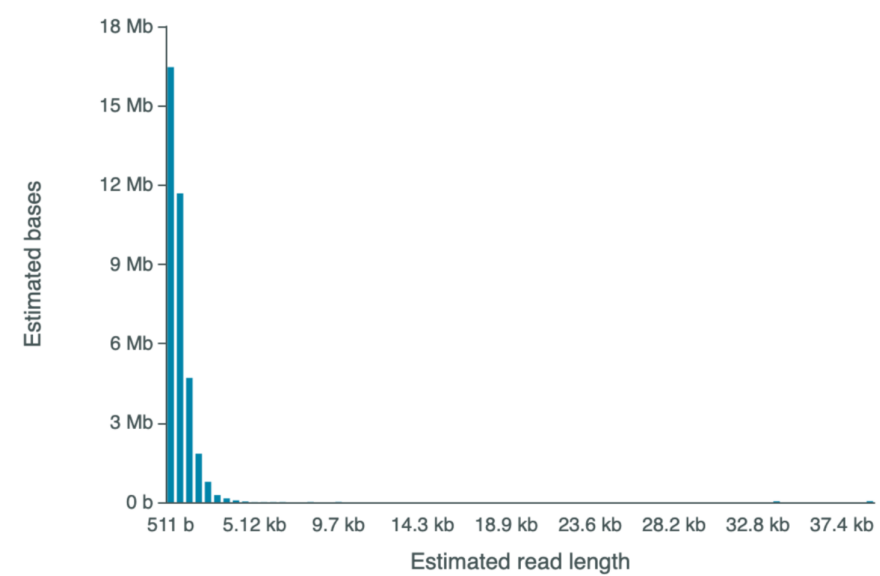
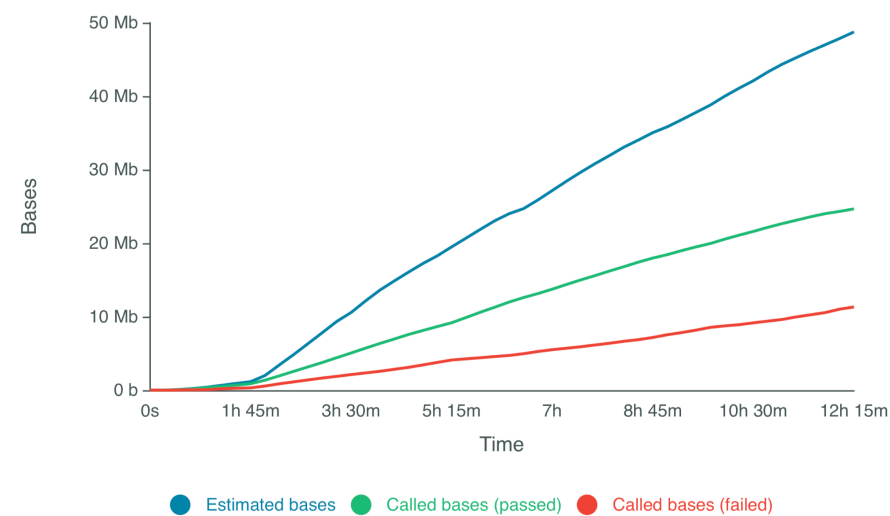
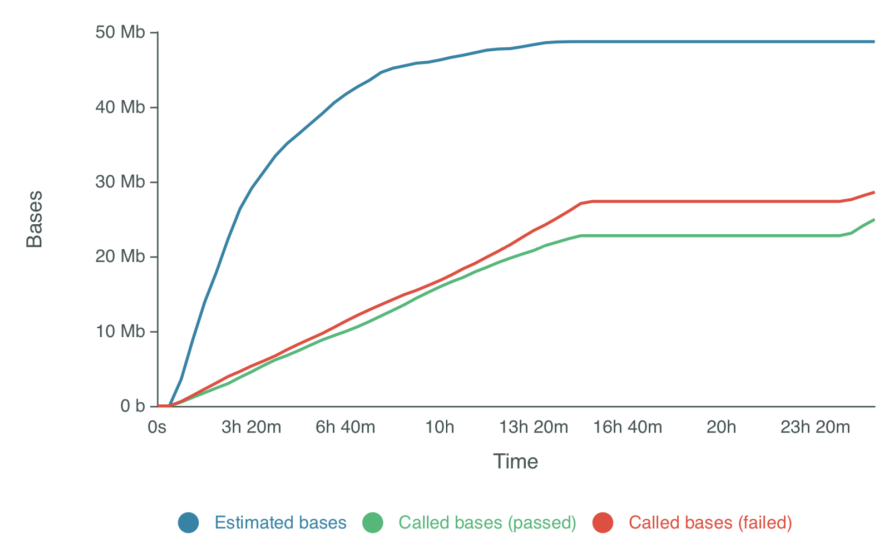


Figure S2. Cumulative Output Bases per microbiome replicate.

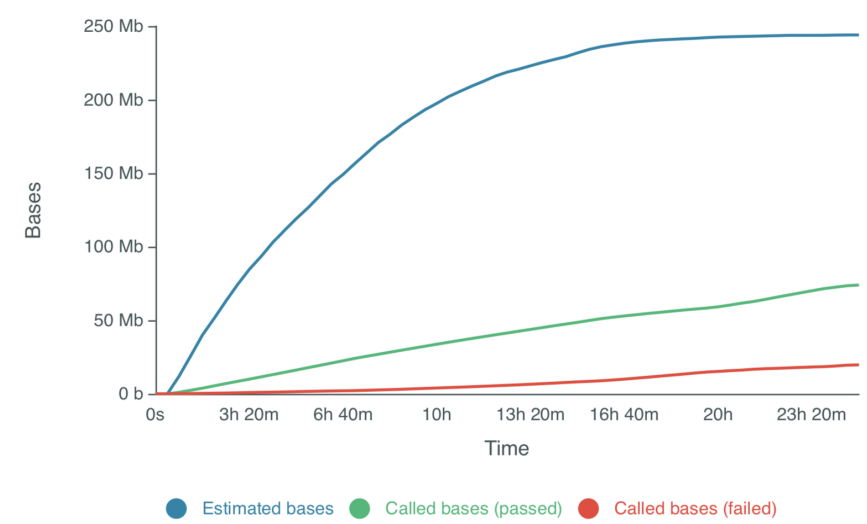
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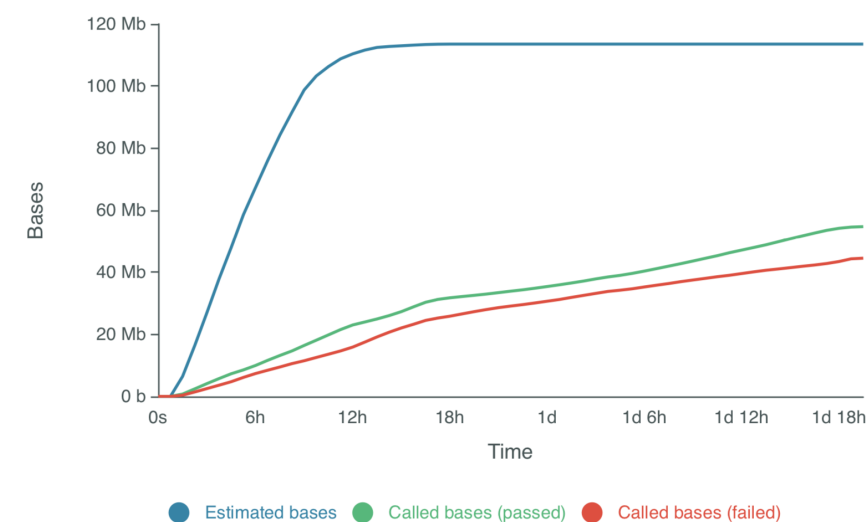
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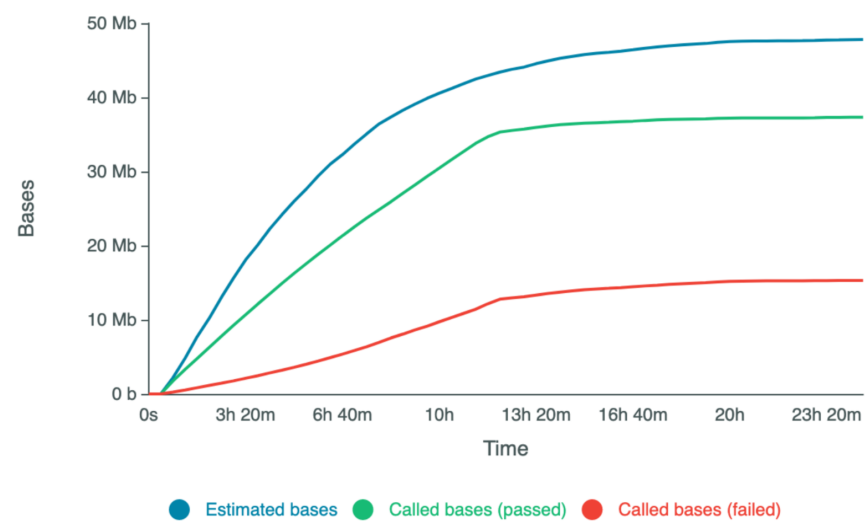
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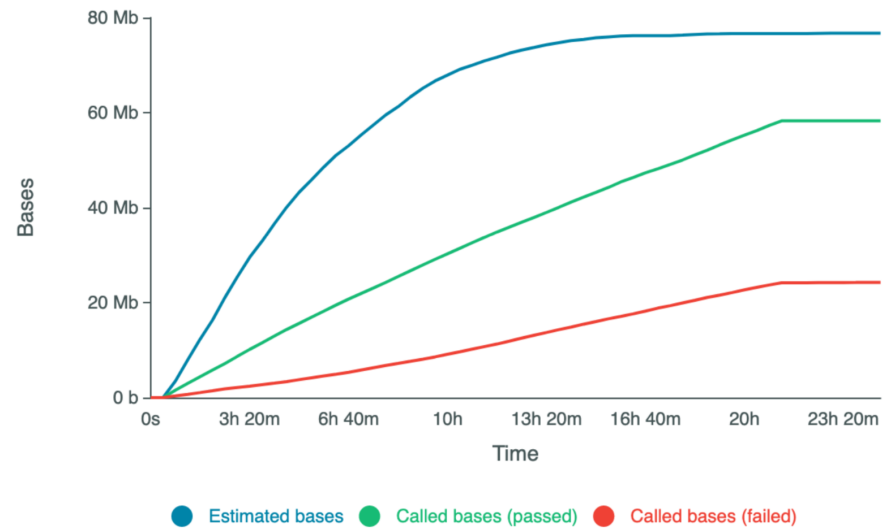
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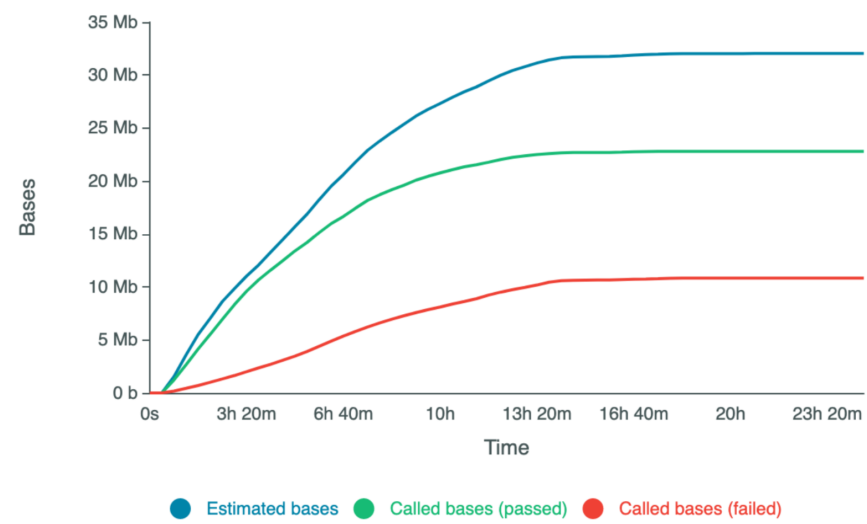
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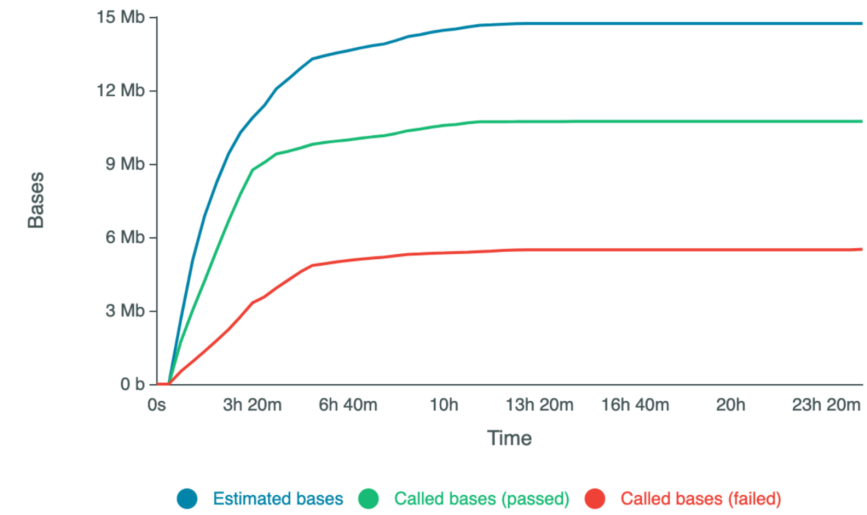
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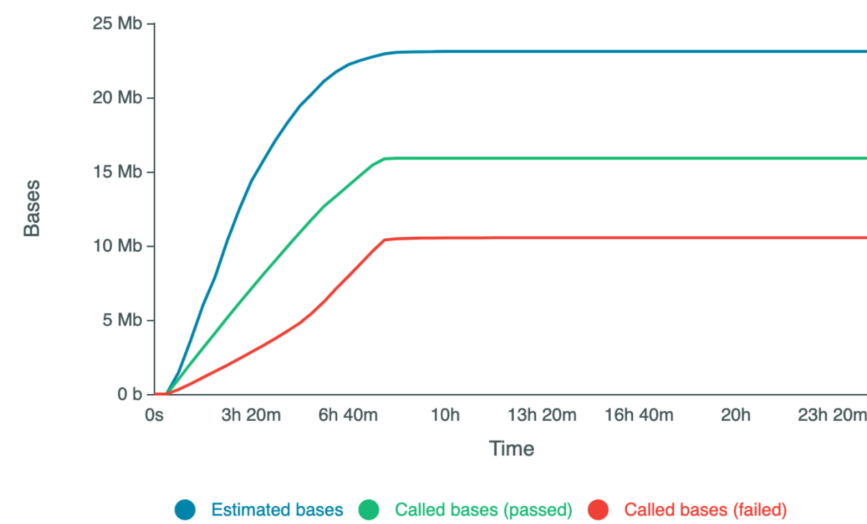
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Date of measure: 20220321 - Saliva3 R2



Date of measure: 20220701 - Stool2 R1



Date of measure: 20220701 - Stool2 R2

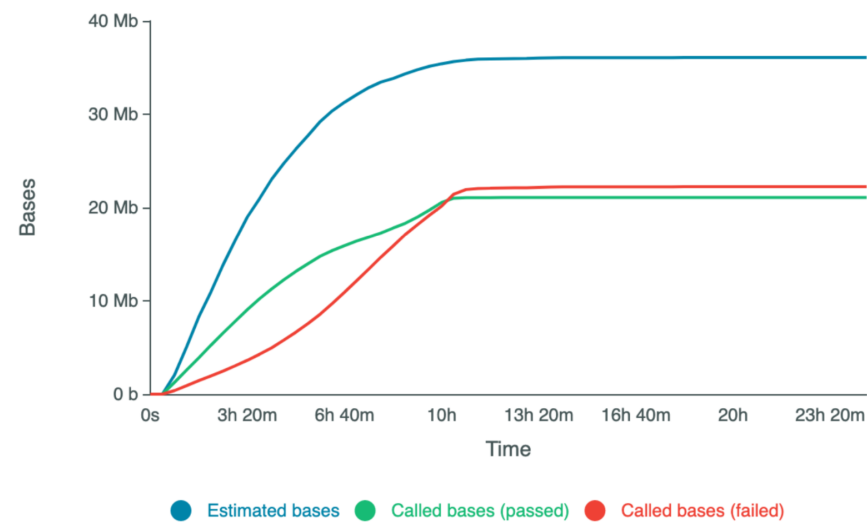
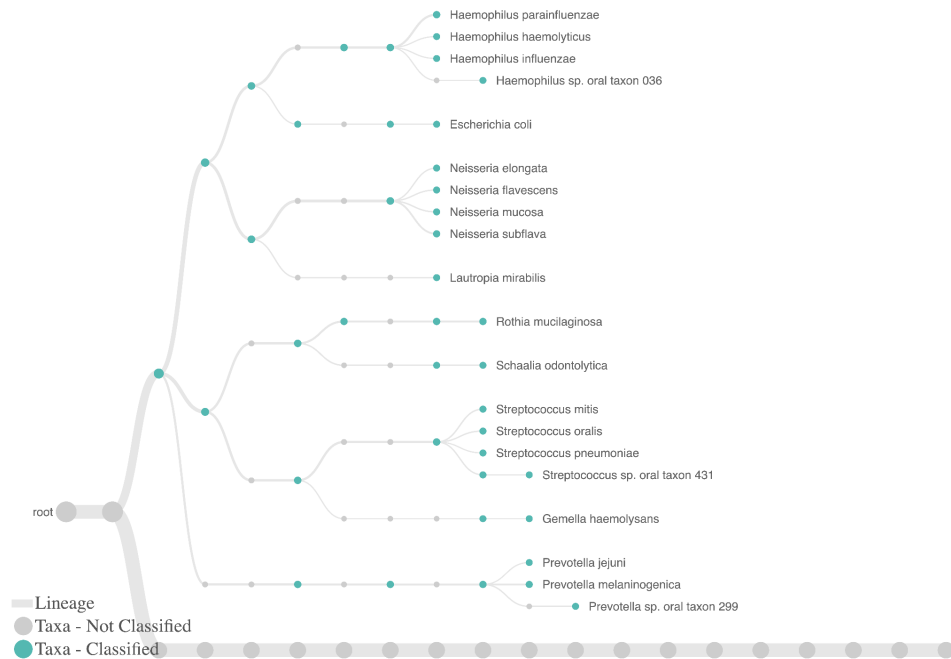
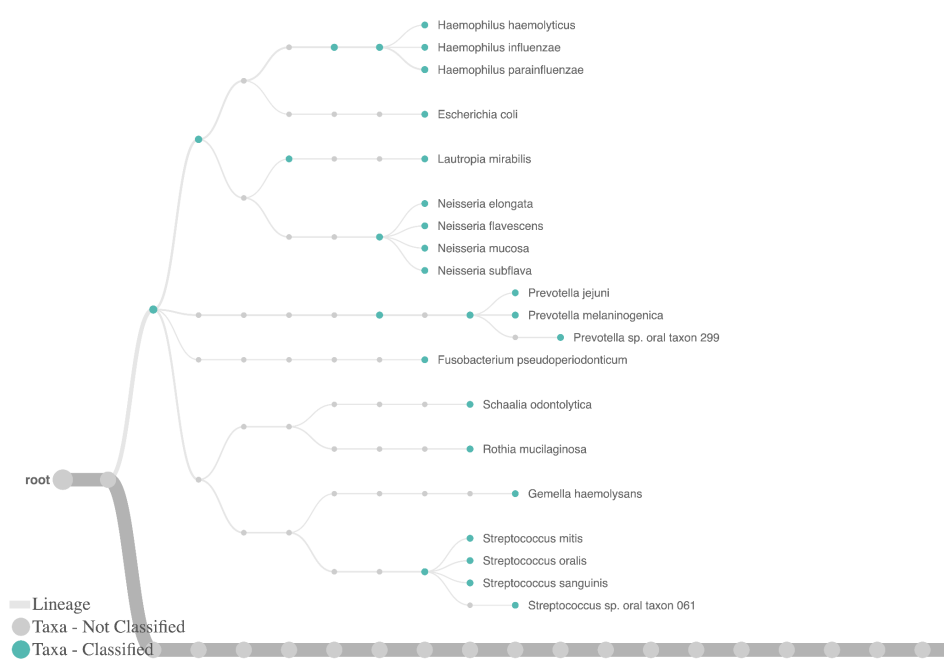


Figure S3. The taxonomy tree showing Top 20 taxa generated by the WIMP data analysis platform from the Centrifuge results, with a score to each taxonomic placement.

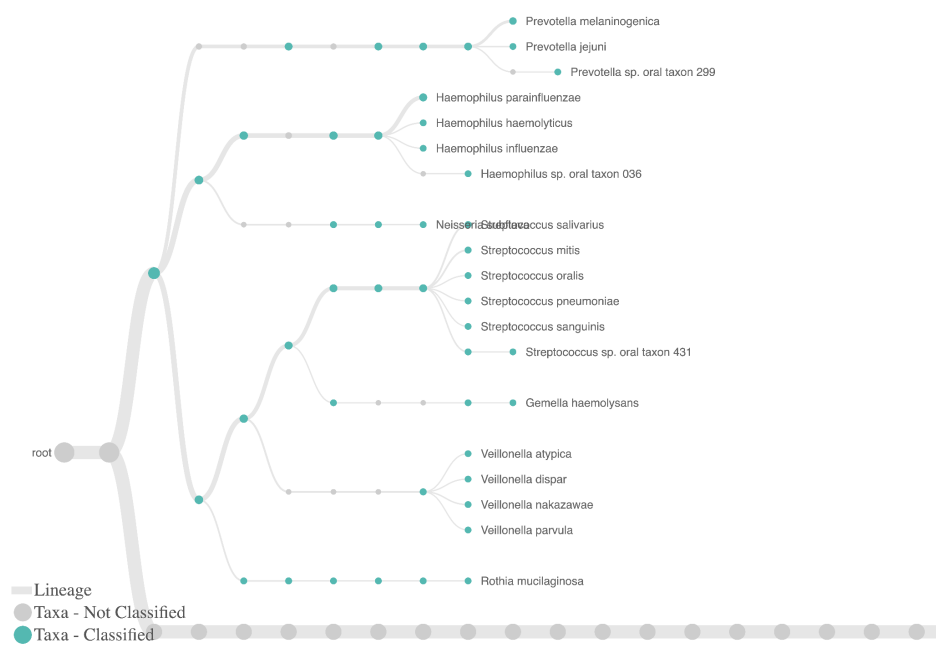
Date of measure: 20220303 - Saliva1 R1



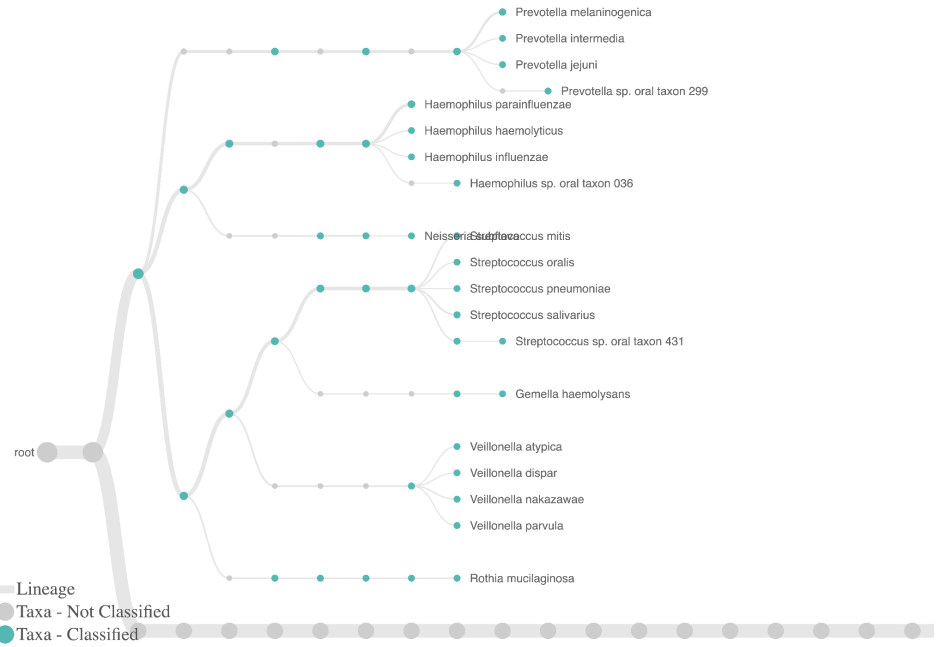
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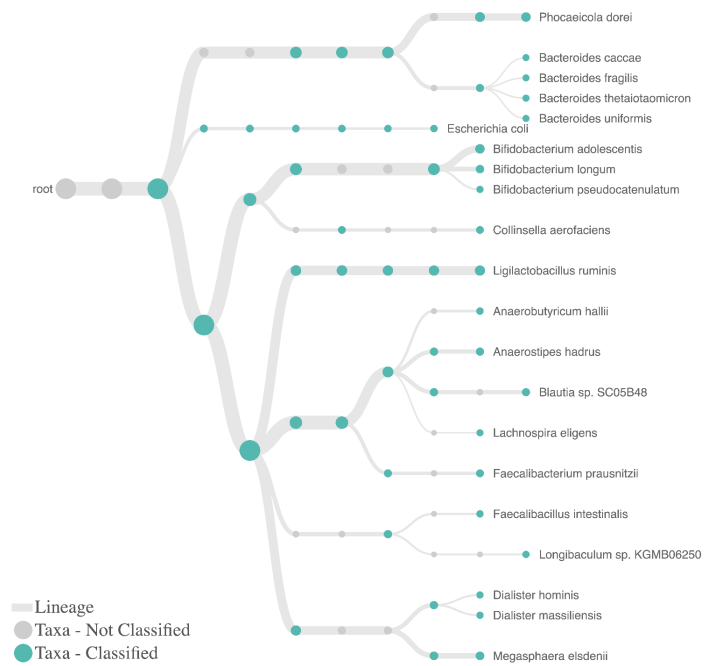
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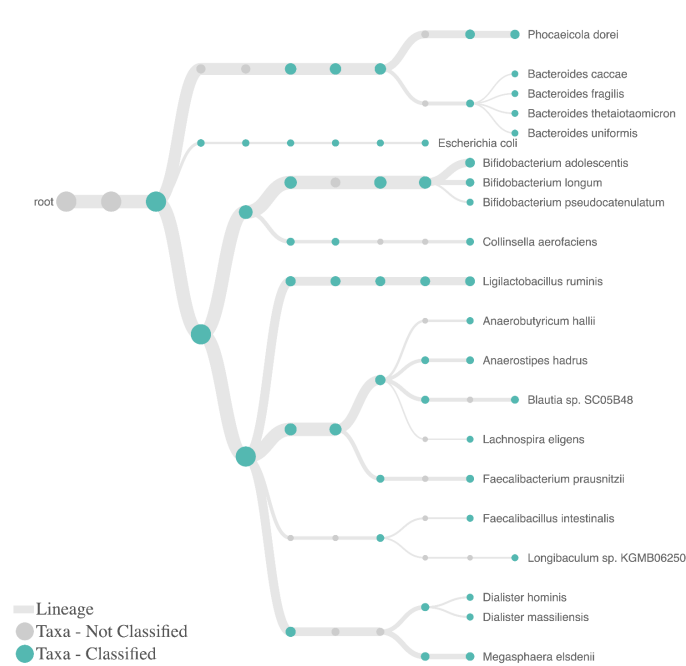
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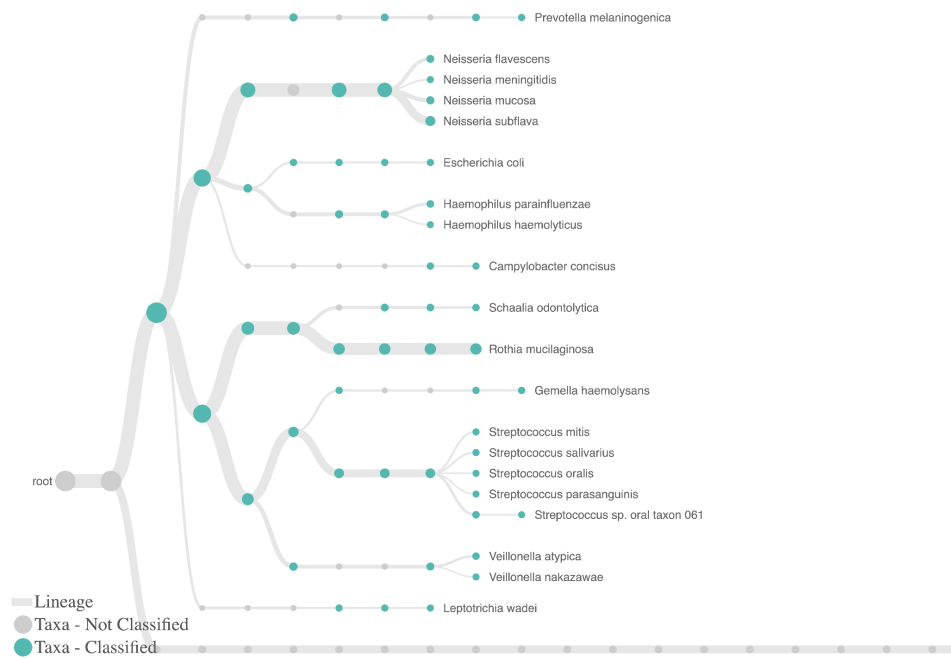
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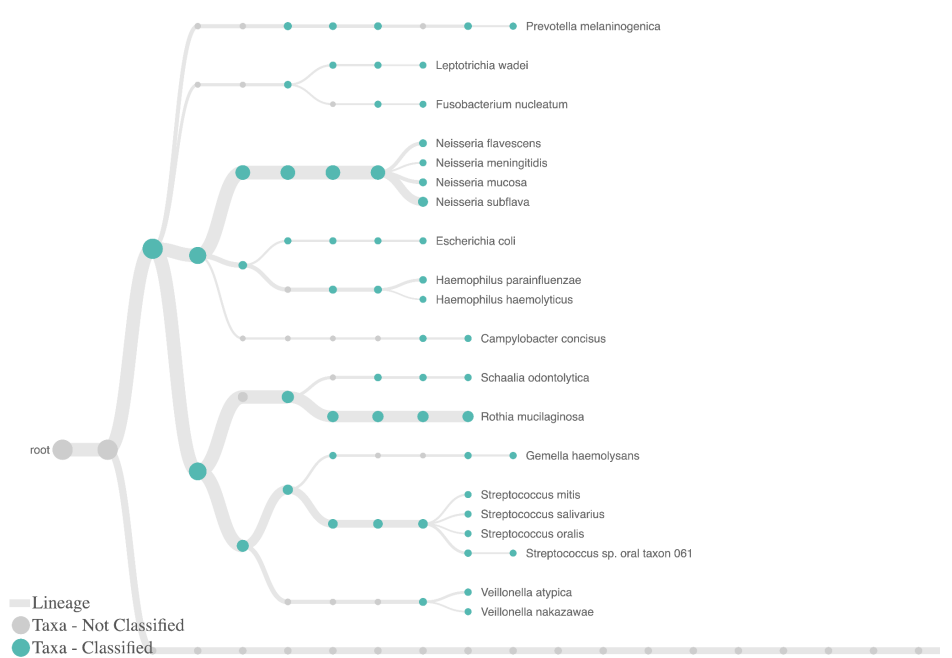
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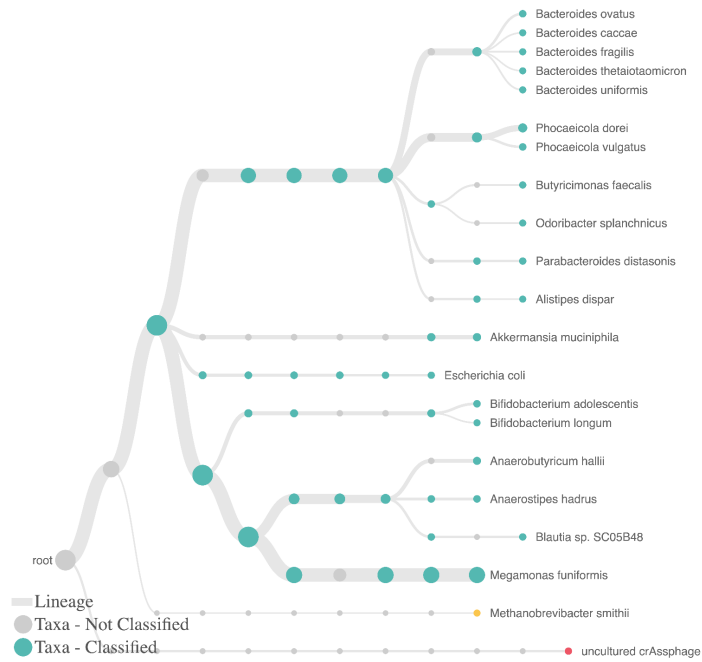
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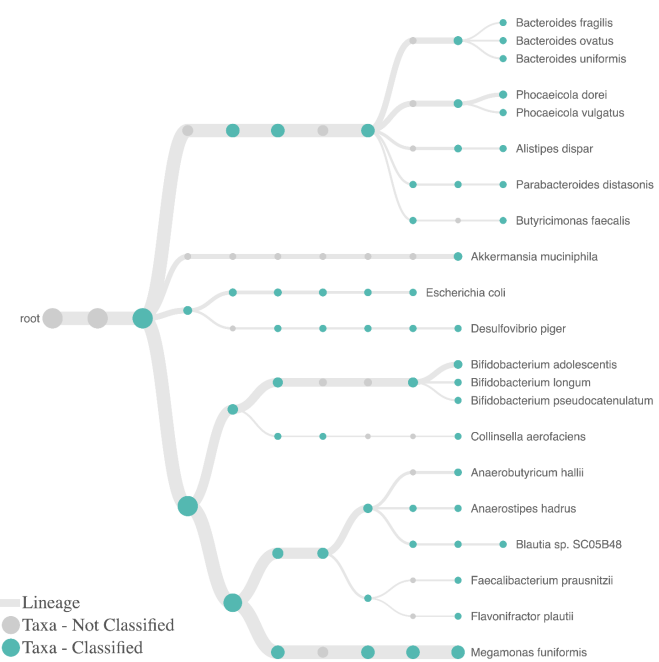


Figure S5. The Comprehensive Antibiotic Resistance Database (CARD) model conferring resistance to antibiotics in each microbiome replicate.

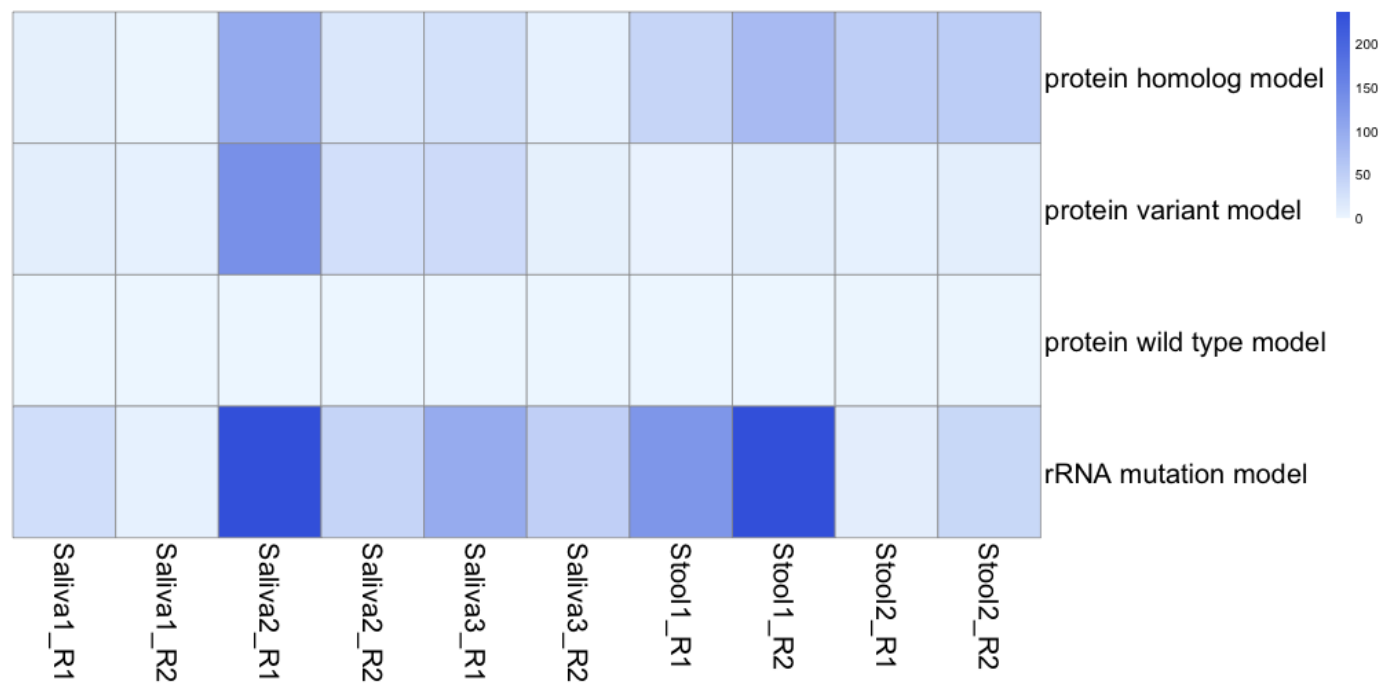
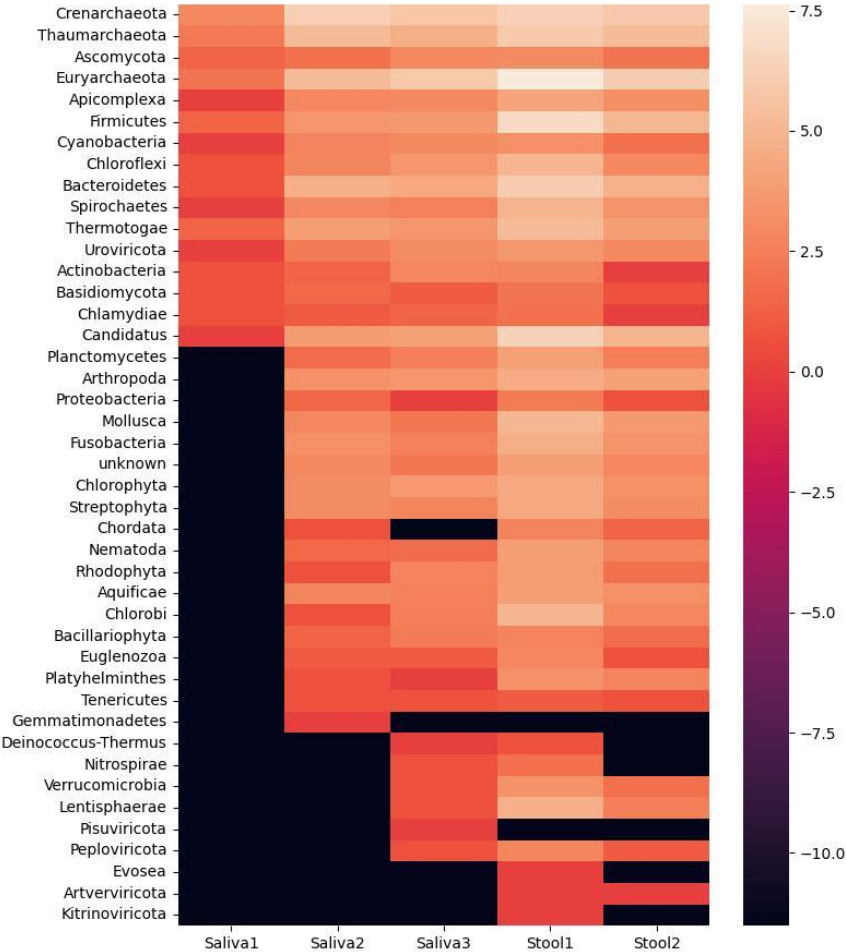
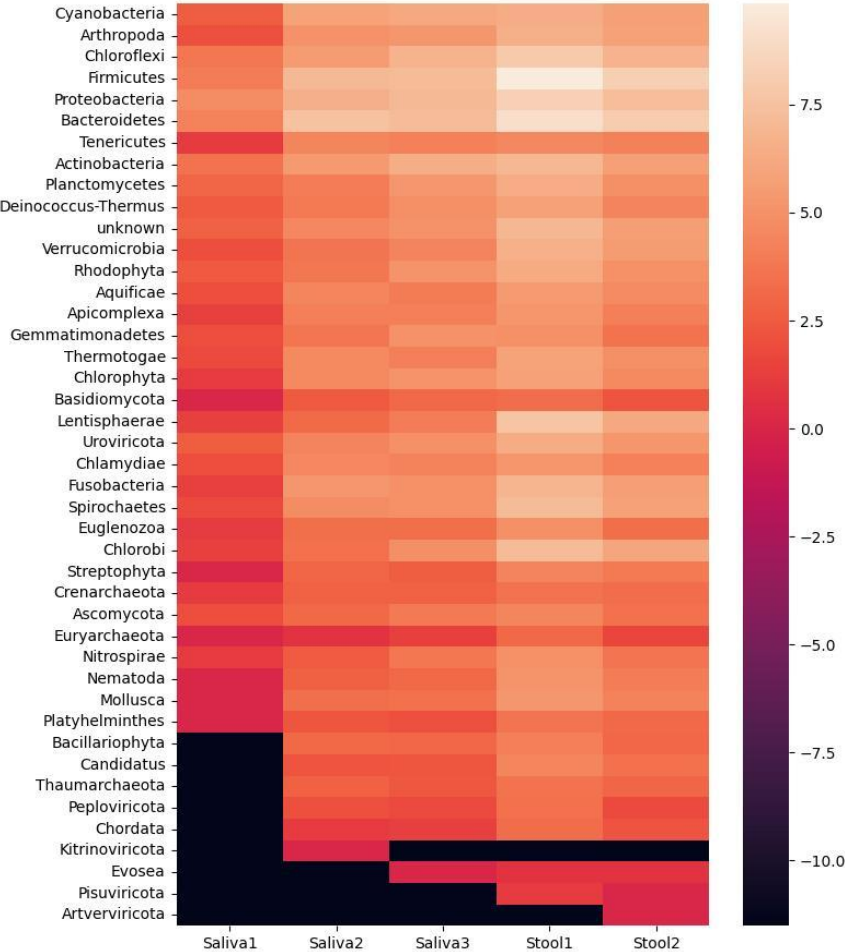


Figure S6. Phylum predicted by BERTax of unclassified reads belonging to (a) archaea, (b) bacteria, (c) eukaryota, and (d) virus.

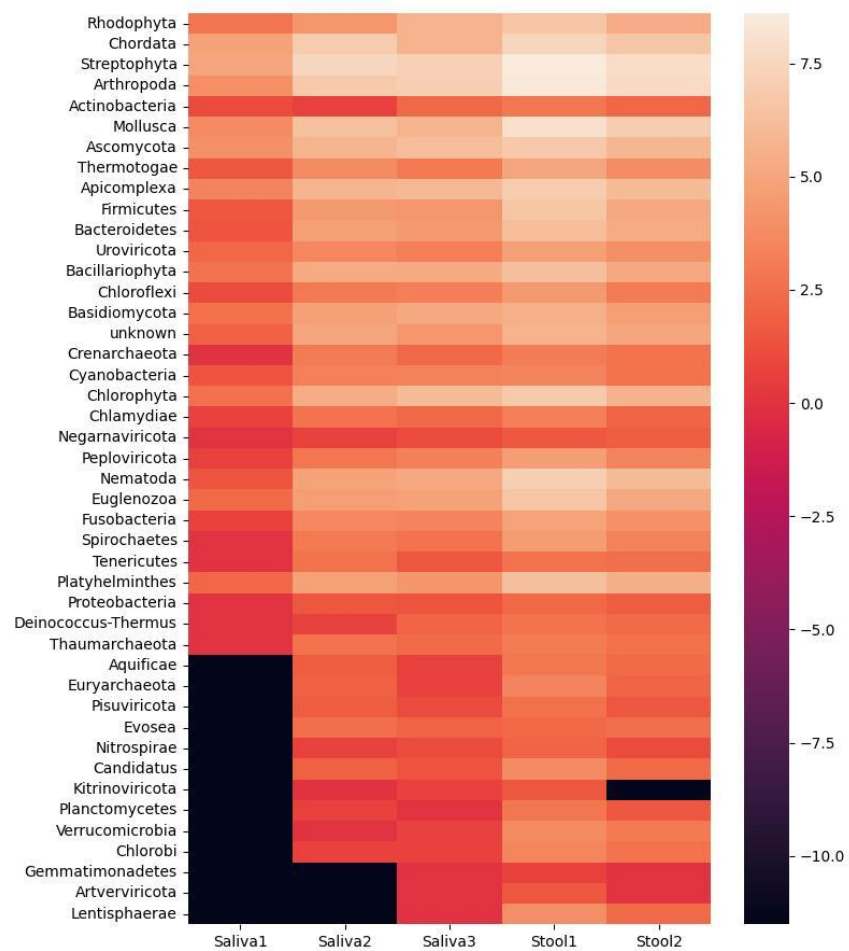
a.



b.



c.



d.

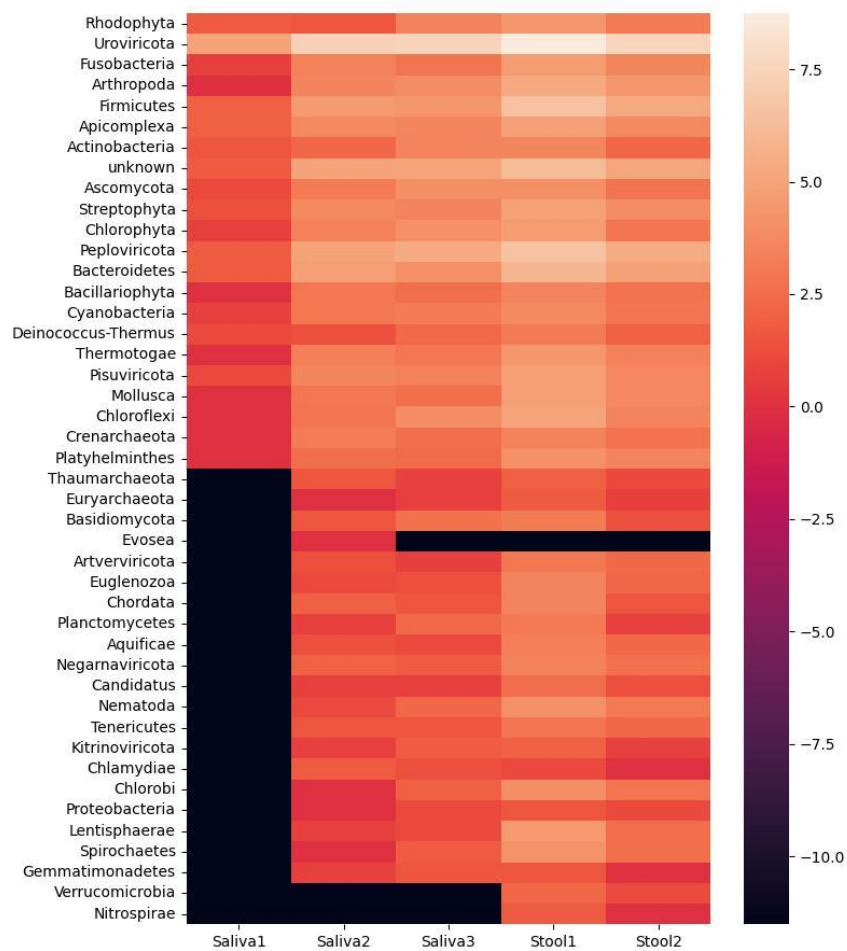
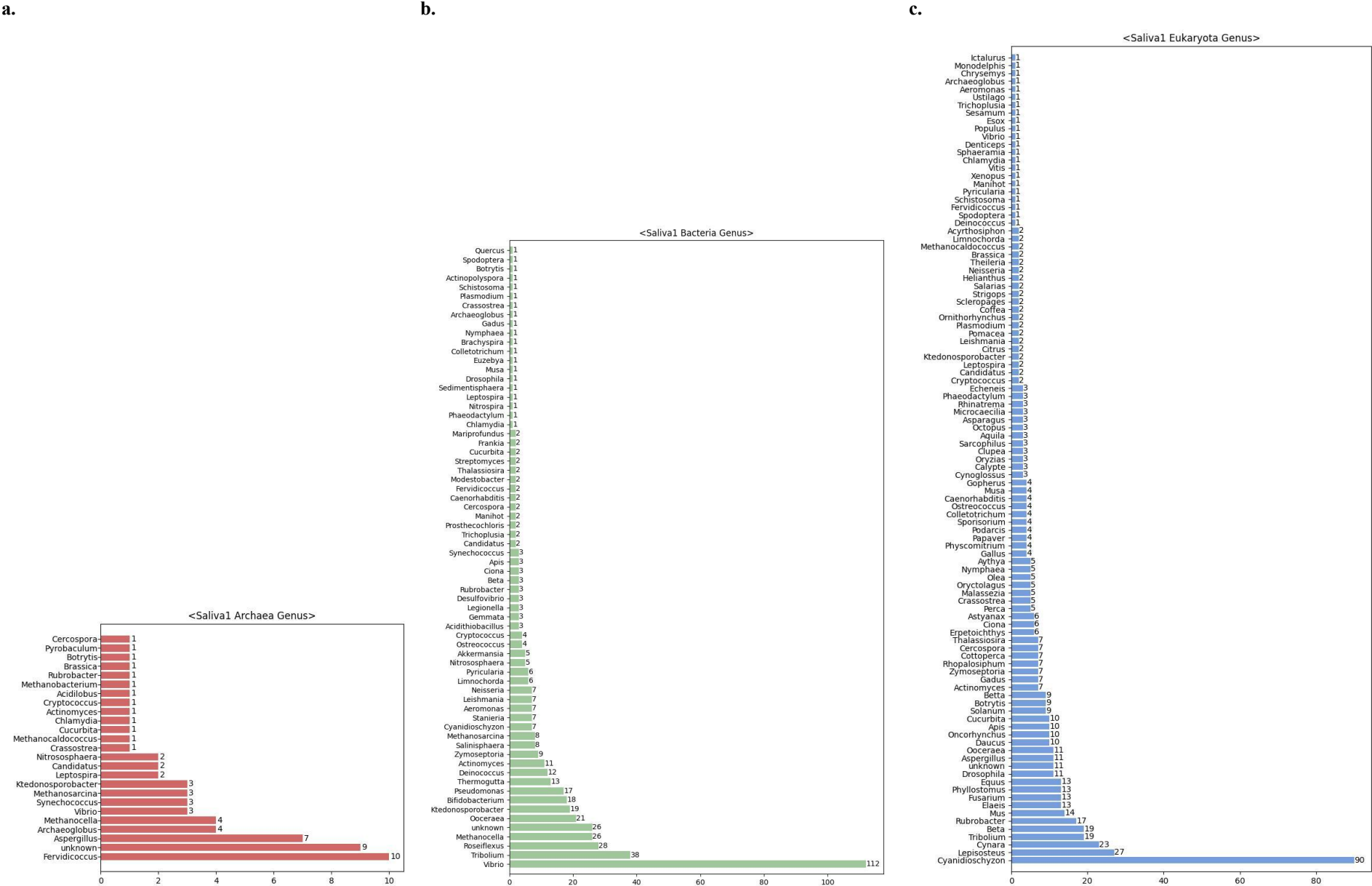


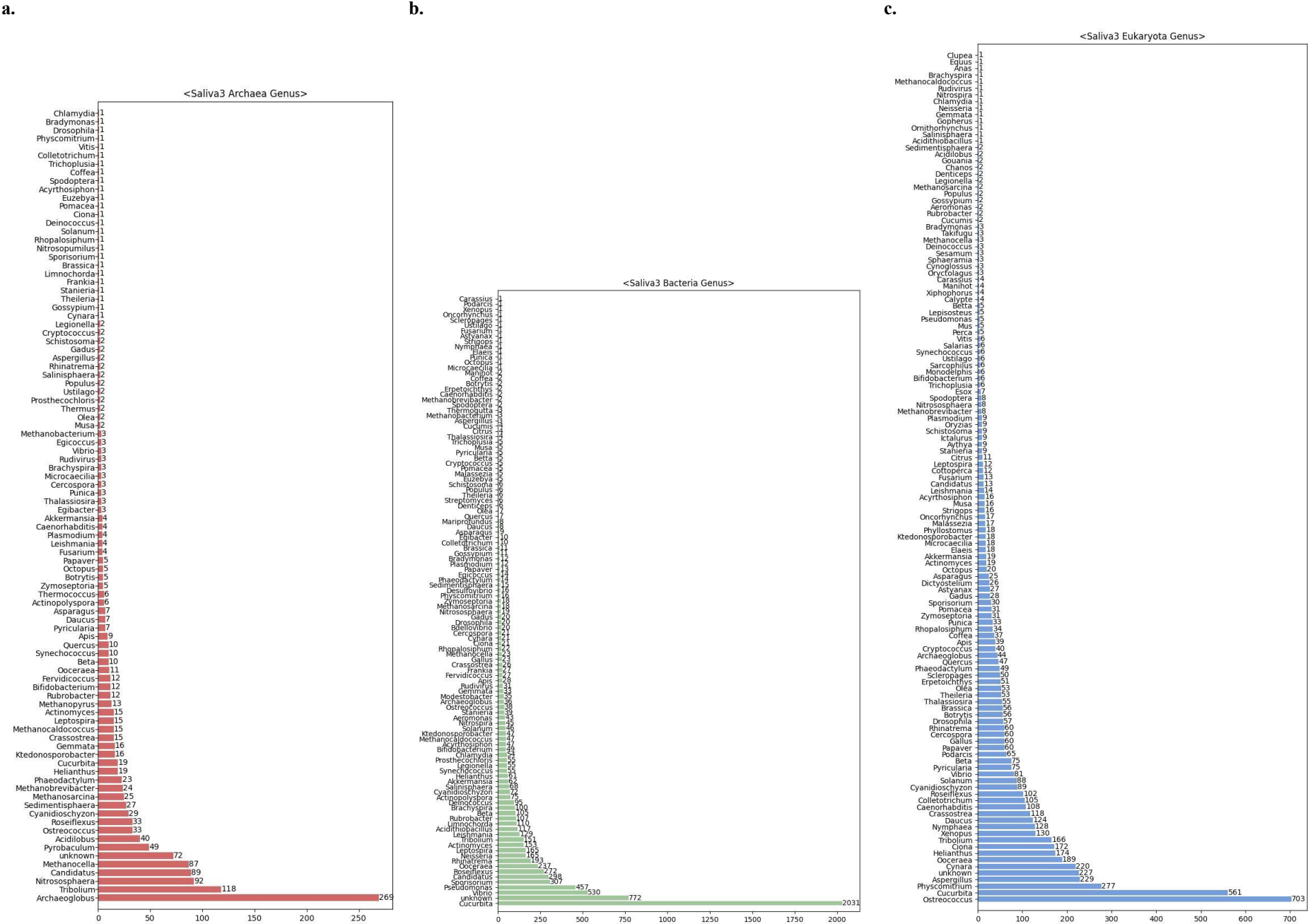
Figure S7. Genus predicted by BERTax of unclassified reads in Saliva1 belonging to (a) Archaea, (b) Bacteria, and (c) Eukaryota.



a.



Figure S9. Genus predicted by BERTax of unclassified reads in Saliva3 belonging to (a) Archaea, (b) Bacteria, and (c) Eukaryota.



a.

c.

a.

c.

Figure S12. Virus host genus predicted by BERTax of unclassified reads in (a) Saliva1, (b) Saliva2, (c) Saliva3, (d) Stool1, and (e) Stool2.

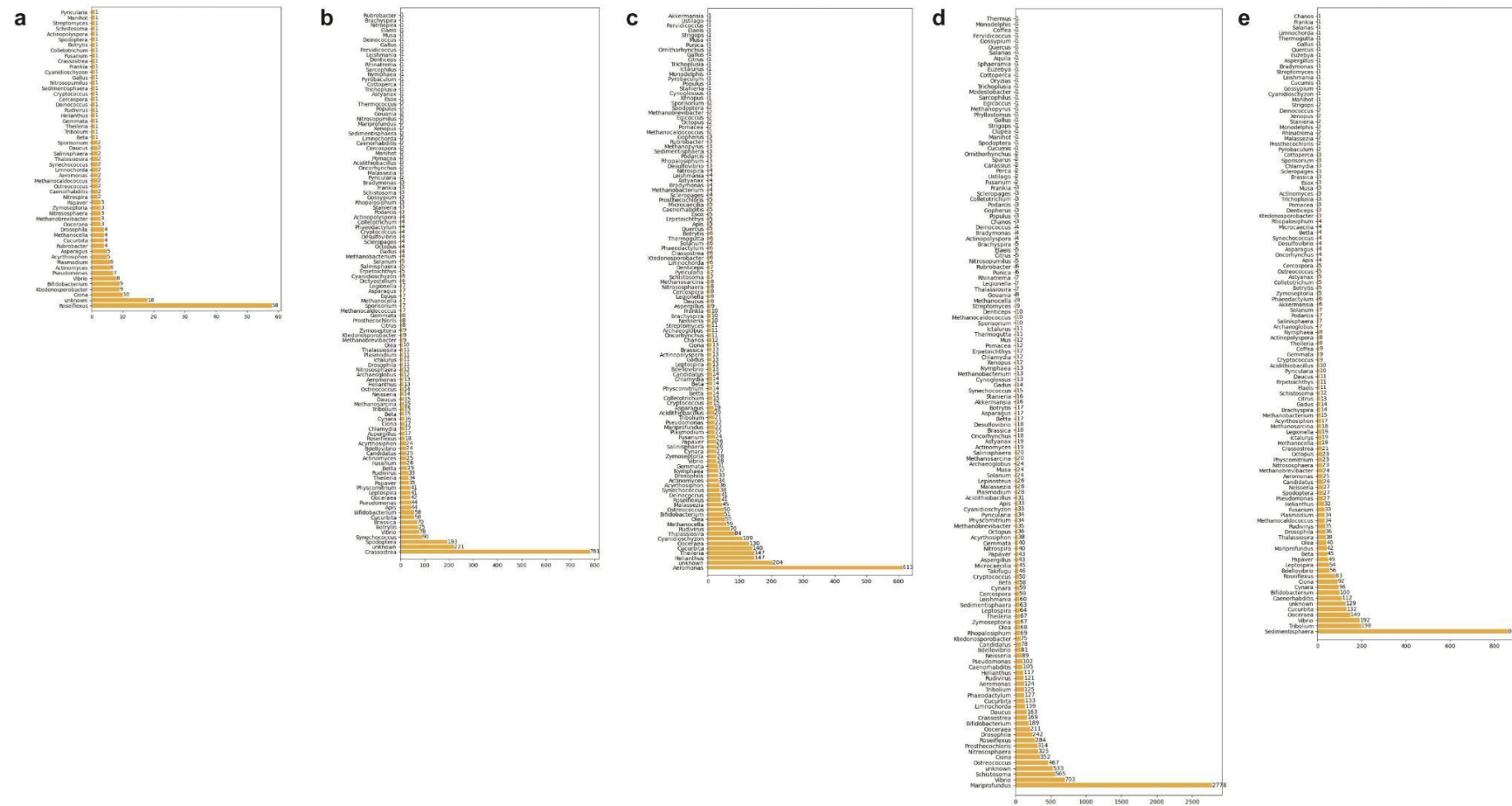


Table S1. Nanodrop results on DNA quantity and quality extracted from the human samples.

Sample_Replicate	DNA concentration (ng/μl)	A260 (10 mm path)	A280 (10 mm path)	260/280	260/230
Saliva1_R1	143.8	2.877	1.261	2.28	3.20
Saliva1_R2	20.5	0.409	0.125	3.29	0.72
Saliva2_R1	60.4	1.208	0.559	2.16	1.42
Saliva2_R2	119.7	2.395	1.264	1.89	2.20
Saliva3_R1	42.5	0.850	0.429	1.98	1.49
Saliva3_R2	103.7	2.074	1.011	2.05	1.90
Stool1_R1	66.6	1.332	0.641	2.08	1.59
Stool1_R2	102.6	2.053	1.020	2.01	1.28
Stool2_R1	101.5	2.030	1.132	1.79	0.96
Stool2_R2	95.2	1.904	1.010	1.88	0.93
Nasal1_R1	0.2	0.004	-0.012	-0.36	0.03
Nasal1_R2	1.0	0.020	0.002	9.41	0.04
Urine1_R1	1.1	0.023	-0.005	-4.44	0.13
Urine1_R2	1.3	0.026	0.004	7.30	0.17
Vaginal1_R1	0.0	0.000	0.017	-0.02	0.00
Vaginal1_R2	-0.8	-0.017	-0.007	2.56	-0.05

Table S2. Nanopore raw output summary per microbiome replicate (run length > 12 hours; Read filtering min_qscore = 9).

Sample_Replicate	Passed Bases	Failed Bases	Total Bases	Reads Generated	Estimated N50 (Estimated Bases)
Saliva1_R1	24.69 Mb	11.36 Mb	36.05 Mb	66.54 k	925 b
Saliva1_R2	24.95 Mb	28.59 Mb	53.54 Mb	59.12 k	1,090 b
Saliva2_R1	73.93 Mb	19.68 Mb	93.61 Mb	381.96 k	816 b
Saliva2_R2	54.72 Mb	44.52 Mb	99.24 Mb	180.56 k	769 b
Saliva3_R1	22.80 Mb	10.84 Mb	33.64 Mb	68.37 k	518 b
Saliva3_R2	10.73 Mb	5.5 Mb	16.23 Mb	36.6 k	412 b
Stool1_R1	37.33 Mb	15.31 Mb	52.64 Mb	123.11 k	384 b
Stool1_R2	58.27 Mb	24.26 Mb	82.53 Mb	182.84 k	434 b
Stool2_R1	15.90 Mb	10.53 Mb	26.43 Mb	61.29 k	378 b
Stool2_R2	21.07 Mb	22.23 Mb	43.30 Mb	74.28 k	558 b

Table S3. Classification of each nanopore read to the microbe species or strain.
(refer to CSV files)

Table S4. Ten most abundant species in each microbiome replicate, with the host-microbe interaction type assessment as beneficial, harmful, or commensal.

Saliva1_R1: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	650	1462.15	1524.83	1523.65	857.50	10.67	1.38	1.37	10
<i>Schaalia odontolytica</i>	84	2068.08	2003.65	1991.69	1631.00	10.18	1.05	1.05	10
<i>Gemella haemolysans</i>	48	2161.42	2272.39	2248.60	1154.00	10.88	1.58	1.56	10.5
<i>Haemophilus parainfluenzae T3T1</i>	40	1195.28	833.68	823.19	959.50	10.78	1.19	1.17	11
<i>Actinomyces sp. oral taxon 169</i>	35	2203.29	2684.60	2645.97	1068.00	10.29	1.23	1.21	10
<i>Streptococcus sanguinis</i>	29	1609.66	1666.50	1637.51	837.00	10.97	1.66	1.63	11
<i>Streptococcus salivarius</i>	27	1610.89	1511.01	1482.77	898.00	10.56	1.40	1.37	10
<i>Actinomyces naeslundii</i>	19	2365.26	2523.48	2456.18	1617.00	10.37	1.01	0.98	10
<i>Actinomyces oris</i>	16	1693.94	1655.18	1602.62	956.00	10.31	1.20	1.16	10
<i>Actinomyces sp. HMT 175</i>	11	1589.27	1704.39	1625.08	1162.00	10.45	1.13	1.08	11
Saliva1_R1: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Actinomyces sp. oral taxon 169</i>	35	2203.29	2684.60	2645.97	1068.00	10.29	1.23	1.21	10
<i>Cardiobacterium hominis</i>	25	1671.84	1449.06	1419.78	1054.00	10.16	1.14	1.12	10
<i>Aggregatibacter aphrophilus</i>	24	1497.33	2085.09	2041.18	785.50	10.83	1.17	1.14	11
<i>Capnocytophaga sputigena</i>	19	1795.79	1654.65	1610.51	1042.00	10.00	1.11	1.08	10
<i>Actinomyces oris</i>	16	1693.94	1655.18	1602.62	956.00	10.31	1.20	1.16	10
<i>Capnocytophaga gingivalis</i>	13	1567.31	1277.39	1227.27	921.00	10.15	0.90	0.86	10
<i>Actinomyces sp. HMT 175</i>	11	1589.27	1704.39	1625.08	1162.00	10.45	1.13	1.08	11
<i>Actinomyces sp. oral taxon 171 str. F0337</i>	9	1606.78	1050.72	990.63	1216.00	10.44	0.73	0.68	10
<i>Gemella sanguinis</i>	9	2937.33	2717.33	2561.93	2262.00	10.56	1.81	1.71	10
<i>Eikenella corrodens</i>	7	3405.29	3672.37	3399.95	2337.00	10.14	1.46	1.36	9
Saliva1_R1: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Neisseria subflava</i>	435	2127.49	2083.72	2081.32	1478.00	10.46	1.19	1.19	10
<i>Rothia mucilaginosa</i>	402	1470.37	1648.10	1646.05	900.50	10.16	1.06	1.05	10
<i>Prevotella melaninogenica</i>	360	1194.75	1370.90	1369.00	739.00	10.55	1.31	1.31	10
<i>Streptococcus mitis</i>	181	2382.03	2388.87	2382.26	1643.00	10.57	1.26	1.25	11
<i>Neisseria mucosa</i>	177	2150.41	2016.20	2010.50	1461.00	10.44	1.17	1.16	10
<i>Rothia mucilaginosa DY-18</i>	143	1577.58	1451.70	1446.62	1021.00	10.24	1.05	1.05	10
<i>Prevotella sp. oral taxon 299 str. F0039</i>	141	1141.89	1345.37	1340.59	689.00	10.70	1.36	1.35	10

<i>Neisseria flavescens</i>	132	1738.63	1783.62	1776.85	1149.50	10.40	1.23	1.22	10
<i>Lautropia mirabilis</i>	125	1815.30	1719.66	1712.76	1326.00	10.31	0.98	0.98	10
<i>Neisseria elongata</i>	87	2051.25	1772.53	1762.32	1287.00	10.37	1.14	1.14	10

Saliva1_R2: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	276	2314.18	3157.86	3152.13	1051.00	9.96	1.01	1.01	10
<i>Schaalia odontolytica</i>	19	5007.16	4750.45	4623.75	3668.00	10.00	0.82	0.79	10
<i>Haemophilus parainfluenzae T3T1</i>	17	3735.18	5018.24	4868.41	1421.00	9.76	0.75	0.73	10
<i>Gemella haemolysans</i>	16	4301.31	4544.72	4400.40	2732.50	9.88	0.96	0.93	10
<i>Streptococcus sanguinis</i>	13	2803.54	3092.82	2971.48	1416.00	10.00	0.82	0.78	10
<i>Actinomyces sp. oral taxon 169</i>	9	2534.00	4237.09	3994.77	848.00	10.33	0.87	0.82	10
<i>Streptococcus salivarius</i>	4	3279.50	4337.62	3756.49	1497.50	9.75	0.96	0.83	9.5
<i>Streptococcus sanguinis SK36</i>	3	898.00	805.40	657.61	433.00	10.00	1.00	0.82	10
<i>Actinomyces sp. HMT 175</i>	3	6489.00	10513.68	8584.39	472.00	9.33	0.58	0.47	9
<i>Streptococcus cristatus ATCC 51100</i>	2	1557.00	1613.62	1141.00	1557.00	9.50	0.71	0.50	9.5
Saliva1_R2: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Actinomyces sp. oral taxon 169</i>	9	2534.00	4237.09	3994.77	848.00	10.33	0.87	0.82	10
<i>Cardiobacterium hominis</i>	6	8475.67	7276.41	6642.43	6918.50	9.67	0.52	0.47	10
<i>Capnocytophaga sputigena</i>	6	3853.83	4137.45	3776.96	1763.00	9.33	0.52	0.47	9
<i>Gemella sanguinis</i>	4	2815.00	2159.66	1870.32	2175.50	9.50	0.58	0.50	9.5
<i>Aggregatibacter segnis</i>	3	483.33	284.61	232.38	376.00	9.67	0.58	0.47	10
<i>Pseudopropionibacterium propionicum</i>	3	3725.33	4271.58	3487.73	1333.00	9.00	0.00	0.00	9
<i>Actinomyces sp. HMT 175</i>	3	6489.00	10513.68	8584.39	472.00	9.33	0.58	0.47	9
<i>Aggregatibacter aphrophilus</i>	2	1479.00	1206.32	853.00	1479.00	10.50	0.71	0.50	10.5
<i>Aggregatibacter aphrophilus ATCC 33389</i>	2	4183.50	1784.03	1261.50	4183.50	9.00	0.00	0.00	9
<i>Aggregatibacter segnis ATCC 33393</i>	2	5609.50	5370.48	3797.50	5609.50	11.00	0.00	0.00	11
Saliva1_R2: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Prevotella melaninogenica</i>	147	1216.85	827.82	825.00	984.00	9.78	0.89	0.89	10
<i>Rothia mucilaginosa</i>	105	3040.09	4526.26	4504.66	1501.00	9.51	0.67	0.66	9
<i>Prevotella sp. oral taxon 299 str. F0039</i>	86	1216.74	1125.06	1118.50	884.50	9.74	0.88	0.88	9.5
<i>Neisseria subflava</i>	73	5632.60	6247.08	6204.14	2897.00	9.64	0.73	0.73	10

<i>Streptococcus mitis</i>	50	5764.28	6388.25	6324.05	2841.00	9.64	0.98	0.97	9
<i>Neisseria flavescens</i>	32	3936.75	4905.76	4828.50	1901.00	9.94	0.91	0.90	10
<i>Neisseria mucosa</i>	26	4059.19	4307.23	4223.59	2335.50	9.92	0.98	0.96	10
<i>Rothia mucilaginosa</i> DY-18	25	2371.88	2108.30	2065.70	1939.00	9.48	0.59	0.57	9
<i>Lautropia mirabilis</i>	23	4998.96	5468.15	5347.95	2138.00	9.74	0.81	0.79	10
<i>Prevotella jejuni</i>	22	2664.64	2799.04	2734.69	1705.50	9.64	0.90	0.88	9

Saliva2_R1: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	13348	768.04	827.26	827.23	474.00	11.68	1.80	1.80	12
<i>Streptococcus salivarius</i>	3034	840.50	922.37	922.22	521.50	11.64	1.77	1.77	11
<i>Haemophilus parainfluenzae</i> T3T1	642	772.97	695.25	694.71	534.50	11.94	1.72	1.72	12
<i>Gemella haemolysans</i>	599	783.52	905.28	904.52	487.00	11.99	1.95	1.95	12
<i>Streptococcus sanguinis</i>	473	753.59	785.80	784.97	462.00	11.55	1.71	1.71	11
<i>Schaalia odontolytica</i>	405	962.52	1218.66	1217.16	557.00	11.40	1.56	1.56	11
<i>Streptococcus salivarius</i> JIM8777	151	914.30	794.71	792.08	607.00	11.89	1.83	1.83	12
<i>Streptococcus salivarius</i> CCHSS3	145	834.17	724.99	722.48	575.00	12.23	1.83	1.83	12
<i>Actinomyces</i> sp. oral taxon 169	91	999.13	989.38	983.93	541.00	11.38	1.42	1.41	11
<i>Streptococcus sanguinis</i> SK36	65	802.49	603.50	598.84	601.00	12.11	1.71	1.69	12
Saliva2_R1: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Aggregatibacter aphrophilus</i>	249	848.16	1045.68	1043.57	482.00	11.62	1.77	1.77	12
<i>Gemella sanguinis</i>	217	753.69	705.51	703.89	505.00	12.21	1.97	1.96	12
<i>Capnocytophaga sputigena</i>	145	826.92	908.91	905.77	475.00	11.48	1.66	1.65	11
<i>Capnocytophaga gingivalis</i>	112	796.21	877.12	873.20	420.50	11.63	1.67	1.66	11
<i>Cardiobacterium hominis</i>	96	942.53	1135.61	1129.68	485.50	11.66	1.51	1.50	12
<i>Actinomyces</i> sp. oral taxon 169	91	999.13	989.38	983.93	541.00	11.38	1.42	1.41	11
<i>Capnocytophaga endodontalis</i>	60	889.93	858.65	851.46	518.00	11.63	2.11	2.09	11
<i>Aggregatibacter aphrophilus</i> ATCC 33389	59	725.76	544.28	539.65	522.00	11.20	1.68	1.66	11
<i>Actinomyces oris</i>	54	1108.11	1967.81	1949.50	557.50	11.11	1.66	1.64	11
<i>Capnocytophaga leadbetteri</i>	49	922.88	1097.81	1086.55	429.00	11.31	1.56	1.54	11
Saliva2_R1: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Prevotella melaninogenica</i>	7865	737.65	759.79	759.74	472.00	11.61	1.74	1.74	11

<i>Streptococcus mitis</i>	2644	739.69	784.16	784.02	453.00	11.67	1.75	1.75	12
<i>Prevotella jejuni</i>	1314	749.44	759.66	759.37	471.00	11.57	1.75	1.75	11
<i>Rothia mucilaginosa</i>	1076	829.42	929.18	928.74	505.00	11.02	1.50	1.50	11
<i>Neisseria subflava</i>	1029	830.48	915.82	915.37	482.00	11.51	1.67	1.67	11
<i>Haemophilus haemolyticus</i>	1026	725.07	699.35	699.01	475.00	11.79	1.75	1.75	12
<i>Prevotella sp. oral taxon 299 str. F0039</i>	924	669.96	645.53	645.18	450.00	11.76	1.74	1.74	12
<i>Haemophilus sp. oral taxon 036</i>	836	838.95	984.23	983.64	487.50	11.81	1.78	1.78	12
<i>Haemophilus influenzae</i>	648	663.48	695.86	695.32	441.50	11.62	1.78	1.77	11.5
<i>Prevotella intermedia</i>	498	726.08	773.61	772.83	457.50	11.66	1.79	1.78	12

Saliva2_R2: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	2890	836.46	900.82	900.67	562.00	10.11	1.09	1.09	10
<i>Streptococcus salivarius</i>	794	856.61	1017.57	1016.93	558.00	10.09	1.07	1.07	10
<i>Gemella haemolysans</i>	132	818.05	796.73	793.70	580.00	10.49	1.24	1.23	10
<i>Haemophilus parainfluenzae T3T1</i>	117	837.78	722.06	718.97	583.00	9.94	0.94	0.94	10
<i>Schaalia odontolytica</i>	117	750.74	822.20	818.68	472.00	9.71	0.82	0.82	10
<i>Streptococcus sanguinis</i>	108	911.94	1153.83	1148.48	565.00	10.05	1.06	1.06	10
<i>Streptococcus salivarius CCHSS3</i>	36	1015.25	1395.53	1376.01	565.00	10.17	1.18	1.17	10
<i>Streptococcus salivarius JIM8777</i>	33	932.33	966.26	951.51	652.00	10.27	1.38	1.35	10
<i>Actinomyces sp. oral taxon 169</i>	24	801.79	727.54	712.22	536.50	9.96	1.27	1.24	10
<i>Streptococcus sanguinis SK36</i>	21	571.38	315.73	308.12	475.00	10.38	1.24	1.21	10
Saliva2_R2: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Gemella sanguinis</i>	65	977.71	1267.49	1257.70	539.00	10.31	1.16	1.15	10
<i>Aggregatibacter aphrophilus</i>	54	803.74	795.97	788.56	589.00	9.98	1.22	1.21	10
<i>Capnocytophaga sputigena</i>	28	1004.68	826.50	811.60	784.50	9.75	0.93	0.91	9.5
<i>Actinomyces sp. oral taxon 169</i>	24	801.79	727.54	712.22	536.50	9.96	1.27	1.24	10
<i>Capnocytophaga gingivalis</i>	23	703.39	756.98	740.34	418.00	10.13	1.14	1.12	10
<i>Cardiobacterium hominis</i>	16	682.88	779.24	754.50	508.50	10.75	0.93	0.90	11
<i>Actinomyces oris</i>	15	922.00	1203.91	1163.09	590.00	9.93	0.70	0.68	10
<i>Aggregatibacter aphrophilus NJ8700</i>	13	447.00	304.14	292.21	370.00	10.77	1.17	1.12	11
<i>Aggregatibacter aphrophilus ATCC 33389</i>	12	692.08	334.76	320.51	580.00	10.50	1.17	1.12	10
<i>Capnocytophaga</i>	12	668.00	567.90	543.72	492.50	9.33	0.49	0.47	9

Saliva2_R2: Harmful Bacteria

	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Prevotella melaninogenica</i>	1890	733.59	745.74	745.55	513.00	10.07	1.07	1.07	10
<i>Streptococcus mitis</i>	676	803.39	756.15	755.59	553.50	10.08	1.04	1.03	10
<i>Prevotella jejuni</i>	305	777.83	890.30	888.84	525.00	9.95	1.05	1.05	10
<i>Rothia mucilaginosa</i>	279	837.38	953.87	952.16	522.00	9.76	0.88	0.87	10
<i>Neisseria subflava</i>	207	888.38	1164.29	1161.47	618.00	10.01	1.01	1.00	10
<i>Haemophilus haemolyticus</i>	199	1043.96	1429.08	1425.48	546.00	10.17	1.03	1.03	10
<i>Prevotella sp. oral taxon 299 str. F0039</i>	176	621.89	583.03	581.37	458.50	10.31	1.13	1.13	10
<i>Haemophilus sp. oral taxon 036</i>	164	1017.40	1340.87	1336.78	562.50	10.23	1.11	1.11	10
<i>Prevotella intermedia</i>	139	700.46	583.69	581.58	498.00	10.14	1.21	1.20	10
<i>Haemophilus influenzae</i>	136	772.99	809.02	806.04	569.00	9.92	1.01	1.01	10

Saliva3_R1: Beneficial Bacteria

	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	883	549.92	443.45	443.20	385.00	10.91	1.53	1.53	11
<i>Schaalia odontolytica</i>	802	589.87	474.56	474.26	421.50	10.77	1.31	1.31	11
<i>Gemella haemolysans</i>	526	535.10	444.80	444.38	398.00	11.21	1.68	1.67	11
<i>Streptococcus salivarius</i>	455	567.61	423.89	423.43	418.00	10.93	1.49	1.48	11
<i>Schaalia meyeri</i>	112	478.91	275.72	274.48	385.50	10.80	1.31	1.31	11
<i>Actinomyces pacaensis</i>	70	532.91	455.08	451.82	381.00	10.59	1.40	1.39	10
<i>Haemophilus parainfluenzae T3T1</i>	64	571.73	384.99	381.97	461.50	10.86	1.52	1.51	11
<i>Actinomyces oris</i>	52	659.13	583.83	578.19	423.00	10.77	1.26	1.25	11
<i>Streptococcus gordonii</i>	45	410.56	163.73	161.90	333.00	10.78	1.46	1.44	11
<i>Streptococcus sanguinis</i>	44	522.61	307.75	304.24	442.50	10.52	1.41	1.39	10

Saliva3_R1: Commensal Bacteria

	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Capnocytophaga sputigena</i>	85	546.06	354.50	352.41	412.00	11.20	1.45	1.45	11
<i>Eikenella corrodens</i>	80	558.41	430.59	427.89	405.50	10.59	1.26	1.25	11
<i>Actinobacteria</i>	78	418.92	217.53	216.13	352.00	10.59	1.31	1.31	10
<i>Actinomyces pacaensis</i>	70	532.91	455.08	451.82	381.00	10.59	1.40	1.39	10
<i>Abiotrophia defectiva</i>	64	559.63	284.21	281.98	464.50	10.72	1.36	1.35	11
<i>Actinomyces oris</i>	52	659.13	583.83	578.19	423.00	10.77	1.26	1.25	11
<i>Aggregatibacter segnis</i>	47	666.47	570.71	564.61	426.00	10.98	1.41	1.39	11

<i>Kingella denitrificans</i>	43	494.91	300.81	297.29	351.00	11.05	1.33	1.31	11
<i>Ottowia sp. oral taxon 894</i>	40	494.33	381.04	376.25	356.50	10.43	1.11	1.09	10
<i>Pseudopropionibacterium propionicum</i>	39	589.03	448.11	442.33	357.00	10.74	1.39	1.37	11
Saliva3_R1: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Rothia mucilaginosa</i>	4232	553.26	442.13	442.08	397.00	10.60	1.28	1.28	10
<i>Neisseria subflava</i>	3905	591.99	494.60	494.53	418.00	10.86	1.39	1.39	11
<i>Neisseria mucosa</i>	1614	567.27	444.96	444.82	411.50	10.82	1.39	1.39	11
<i>Neisseria flavescens</i>	1385	580.08	488.01	487.84	409.00	10.80	1.44	1.44	11
<i>Rothia mucilaginosa</i> DY-18	1337	598.71	466.08	465.91	437.00	10.73	1.36	1.36	11
<i>Neisseria</i>	1307	408.89	256.45	256.35	318.00	10.35	1.25	1.25	10
<i>Prevotella melaninogenica</i>	530	510.59	351.14	350.81	385.00	10.84	1.46	1.46	11
<i>Campylobacter concisus</i>	482	497.64	350.14	349.78	370.00	10.61	1.33	1.33	10
<i>Escherichia coli</i>	472	577.41	430.56	430.11	420.00	10.85	1.47	1.47	11
<i>Streptococcus mitis</i>	451	525.09	385.66	385.23	396.00	11.10	1.54	1.54	11

Saliva3_R2: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Haemophilus parainfluenzae</i>	494	469.70	267.78	267.51	371.00	10.96	1.45	1.45	11
<i>Schaalia odontolytica</i>	363	467.12	272.84	272.46	373.00	10.91	1.32	1.32	11
<i>Gemella haemolysans</i>	319	492.47	340.36	339.82	389.00	11.61	1.83	1.83	11
<i>Streptococcus salivarius</i>	229	513.80	373.04	372.23	385.00	11.01	1.48	1.47	11
<i>Schaalia meyeri</i>	49	463.98	257.46	254.82	380.00	10.86	1.26	1.25	11
<i>Haemophilus parainfluenzae</i> T3T1	37	440.27	206.49	203.68	396.00	10.86	1.36	1.34	11
<i>Streptococcus sanguinis</i>	23	468.17	270.00	264.06	390.00	11.04	1.80	1.76	11
<i>Actinomyces oris</i>	20	475.70	265.35	258.63	369.50	10.75	1.12	1.09	11
<i>Streptococcus cristatus</i> ATCC 51100	17	429.59	237.68	230.59	347.00	11.76	1.35	1.31	12
<i>Actinomyces pacaensis</i>	17	462.18	231.06	224.16	380.00	10.76	1.25	1.21	11
Saliva3_R2: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Capnocytophaga sputigena</i>	51	539.53	377.16	373.45	388.00	11.14	1.33	1.31	11
<i>Eikenella corrodens</i>	37	389.27	164.53	162.29	360.00	11.08	1.19	1.17	11
<i>Actinobacteria</i>	30	399.20	166.92	164.11	334.00	10.80	1.42	1.40	10
<i>Kingella denitrificans</i>	25	516.20	371.32	363.82	404.00	10.88	1.36	1.34	11

<i>Abiotrophia defectiva</i>	22	408.55	193.89	189.44	386.50	10.91	1.19	1.16	11
<i>Gemella sanguinis</i>	21	559.48	319.29	311.59	443.00	11.05	1.66	1.62	11
<i>Actinomyces oris</i>	20	475.70	265.35	258.63	369.50	10.75	1.12	1.09	11
<i>Proteobacteria</i>	20	354.05	139.59	136.05	274.50	10.25	1.16	1.13	10
<i>Actinomyces pacaensis</i>	17	462.18	231.06	224.16	380.00	10.76	1.25	1.21	11
<i>Gemella morbillorum</i>	17	465.06	181.87	176.44	380.00	11.65	1.77	1.71	12
Saliva3_R2: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Rothia mucilaginosa</i>	2244	472.15	299.05	298.98	374.50	10.72	1.30	1.30	11
<i>Neisseria subflava</i>	2118	510.45	362.07	361.98	392.00	11.06	1.44	1.44	11
<i>Neisseria mucosa</i>	781	495.98	349.50	349.27	381.00	11.01	1.43	1.42	11
<i>Neisseria flavescens</i>	726	493.27	304.91	304.70	383.50	11.02	1.47	1.47	11
<i>Neisseria</i>	673	385.08	200.80	200.65	321.00	10.67	1.35	1.35	10
<i>Rothia mucilaginosa</i> DY-18	672	507.59	351.63	351.37	388.00	10.85	1.33	1.33	11
<i>Prevotella melaninogenica</i>	302	444.28	247.47	247.06	363.50	11.03	1.61	1.61	11
<i>Campylobacter concisus</i>	268	456.25	278.83	278.31	372.50	10.86	1.38	1.38	11
<i>Escherichia coli</i>	253	519.11	338.61	337.94	399.00	11.13	1.43	1.43	11
<i>Streptococcus mitis</i>	241	519.20	314.38	313.72	413.00	11.12	1.43	1.43	11

Stool1_R1: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Lactobacillus ruminis</i> ATCC 27782	6066	462.83	317.60	317.57	357.00	11.46	1.66	1.66	11
<i>Bifidobacterium adolescentis</i>	4637	440.23	299.16	299.13	339.00	11.08	1.48	1.48	11
<i>Bifidobacterium longum</i>	2397	420.21	281.57	281.51	329.00	10.95	1.44	1.44	11
<i>Collinsella aerofaciens</i>	1391	431.13	294.24	294.14	335.00	10.93	1.41	1.41	11
<i>Bifidobacterium pseudocatenulatum</i>	483	417.66	223.81	223.58	338.00	11.09	1.49	1.49	11
<i>Bacteroides thetaiotaomicron</i>	384	419.05	227.59	227.29	348.00	11.12	1.58	1.58	11
<i>Bacteroides uniformis</i>	301	479.55	318.46	317.93	374.00	11.27	1.71	1.71	11
<i>Collinsella aerofaciens</i> ATCC 25986	288	461.43	306.02	305.49	357.50	11.07	1.39	1.39	11
<i>Bacteroides dorei</i> CL03T12C01	275	463.63	255.95	255.49	374.00	11.52	1.56	1.56	11
<i>Bacteroides fragilis</i>	269	440.92	258.41	257.93	367.00	11.29	1.67	1.67	11
Stool1_R1: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Phocaeicola dorei</i>	4519	428.32	263.54	263.51	352.00	11.27	1.65	1.65	11

<i>Anaerostipes hadrus</i>	2431	465.11	312.70	312.64	365.00	11.48	1.75	1.75	11
<i>Blautia</i> sp. SC05B48	2214	461.25	320.66	320.59	363.00	11.27	1.62	1.62	11
<i>Faecalibacterium prausnitzii</i>	1676	445.64	309.44	309.35	346.00	11.10	1.44	1.44	11
<i>Escherichia coli</i>	1063	524.94	334.07	333.91	411.00	11.23	1.57	1.57	11
<i>Anaerobutyricum hallii</i>	1048	527.96	446.95	446.74	387.50	11.51	1.75	1.75	11
<i>Faecalibacillus intestinalis</i>	848	522.90	333.70	333.50	406.00	11.90	1.91	1.91	12
<i>Dialister hominis</i>	644	508.46	341.92	341.66	398.00	11.22	1.46	1.46	11
<i>Bacteroides</i>	530	395.00	218.77	218.56	328.50	11.11	1.53	1.53	11
<i>Bifidobacterium</i>	409	357.18	188.46	188.23	297.00	10.73	1.47	1.47	10

Stool1_R1: Harmful Bacteria

	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Acidaminococcus intestini</i> RyC-MR95	179	452.55	359.02	358.01	357.00	11.17	1.56	1.55	11
<i>Alistipes onderdonkii</i> subsp. <i>vulgaris</i>	134	410.01	267.03	266.03	328.00	10.80	1.38	1.37	11
<i>Roseburia hominis</i>	127	448.18	232.10	231.18	361.00	11.40	1.64	1.64	11
<i>Clostridioides difficile</i>	118	471.91	284.48	283.27	394.00	11.45	1.59	1.58	11
<i>Eggerthella lenta</i>	61	425.75	274.23	271.97	356.00	10.79	1.20	1.19	11
<i>[Clostridium]</i> <i>innocuum</i>	59	449.56	226.44	224.51	406.00	11.17	1.53	1.52	11
<i>Eggerthella lenta</i> DSM 2243	39	480.18	279.86	276.25	370.00	11.00	1.50	1.48	11
<i>Enterococcus faecium</i>	25	460.60	187.60	183.81	396.00	10.96	1.65	1.61	11
<i>Escherichia</i>	25	354.64	119.56	117.14	330.00	10.68	1.46	1.43	10
<i>Shigella flexneri</i>	23	524.30	281.94	275.74	439.00	11.13	1.71	1.68	11

Stool1_R2: Beneficial Bacteria

	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Lactobacillus ruminis</i> ATCC 27782	8599	503.68	374.49	374.47	379.00	11.38	1.63	1.63	11
<i>Bifidobacterium adolescentis</i>	8183	470.76	366.08	366.05	353.00	11.05	1.49	1.49	11
<i>Bifidobacterium longum</i>	4170	454.32	342.44	342.40	341.00	10.92	1.47	1.47	11
<i>Collinsella aerofaciens</i>	2425	454.79	329.75	329.69	347.00	10.83	1.39	1.39	11
<i>Bifidobacterium pseudocatenulatum</i>	811	464.19	367.53	367.31	342.00	11.11	1.50	1.50	11
<i>Bacteroides thetaiotaomicron</i>	563	438.54	271.86	271.62	340.00	11.06	1.64	1.64	11
<i>Collinsella aerofaciens</i> ATCC 25986	474	508.71	369.94	369.55	392.00	11.12	1.47	1.47	11
<i>Bacteroides uniformis</i>	473	472.65	321.57	321.23	371.00	11.25	1.56	1.56	11
<i>Bacteroides dorei</i> CL03T12C01	470	545.58	461.99	461.50	403.50	11.51	1.68	1.67	11
<i>Bacteroides fragilis</i>	392	495.52	377.30	376.82	363.00	11.17	1.58	1.58	11

Stool1_R2: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Phocaeicola dorei</i>	6733	458.05	322.07	322.05	357.00	11.25	1.65	1.65	11
<i>Blautia</i> sp. SC05B48	3258	479.36	338.52	338.47	369.00	11.25	1.63	1.63	11
<i>Faecalibacterium prausnitzii</i>	3006	469.80	343.97	343.91	360.00	11.12	1.54	1.54	11
<i>Anaerostipes hadrus</i>	2943	483.59	329.20	329.14	378.00	11.39	1.72	1.72	11
<i>Anaerobutyricum hallii</i>	1468	535.35	409.27	409.13	400.00	11.49	1.72	1.72	11
<i>Dialister hominis</i>	1100	549.49	394.54	394.36	417.00	11.21	1.56	1.56	11
<i>Escherichia coli</i>	1041	576.95	460.12	459.90	431.00	11.14	1.55	1.55	11
<i>Faecalibacillus intestinalis</i>	943	629.74	526.85	526.57	461.00	11.95	1.88	1.88	12
<i>Bacteroides</i>	797	421.97	297.40	297.21	333.00	11.07	1.58	1.58	11
<i>Bifidobacterium</i>	731	378.85	264.77	264.58	292.00	10.71	1.45	1.44	10
Stool1_R2: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Acidaminococcus intestini</i> RyC-MR95	268	485.40	331.75	331.13	382.00	11.09	1.55	1.55	11
<i>Alistipes onderdonkii</i> subsp. <i>vulgaris</i>	205	434.98	297.16	296.44	338.00	10.93	1.51	1.51	11
<i>Roseburia hominis</i>	189	494.42	359.76	358.80	381.00	11.22	1.54	1.53	11
<i>Clostridioides difficile</i>	161	541.77	400.33	399.09	414.00	11.06	1.58	1.57	11
<i>Eggerthella lenta</i>	103	423.83	304.39	302.91	324.00	10.75	1.53	1.52	11
<i>[Clostridium]</i> <i>innocuum</i>	101	508.01	404.30	402.29	354.00	11.33	1.86	1.85	11
<i>Eggerthella lenta</i> DSM 2243	84	483.75	295.71	293.95	408.00	10.77	1.33	1.32	11
<i>Enterococcus faecium</i>	40	581.38	346.18	341.83	448.00	11.48	1.58	1.57	11
<i>Escherichia</i>	36	507.50	412.37	406.61	382.00	10.50	1.25	1.24	10
<i>Hungatella hathewayi</i> WAL-18680	27	488.74	267.84	262.83	385.00	11.00	1.41	1.39	11

Stool2_R1: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Akkermansia muciniphila</i>	1177	461.73	232.01	231.91	395.00	10.44	1.25	1.25	10
<i>Bifidobacterium adolescentis</i>	552	467.99	230.85	230.64	400.50	10.53	1.22	1.22	10
<i>Bacteroides ovatus</i>	498	487.73	252.59	252.33	410.50	10.76	1.42	1.41	11
<i>Bacteroides uniformis</i>	225	470.24	220.60	220.11	409.00	10.60	1.25	1.25	10
<i>Odoribacter splanchnicus</i>	204	478.44	252.48	251.86	400.50	10.74	1.23	1.23	11
<i>Bacteroides fragilis</i>	203	445.21	216.84	216.31	389.00	10.83	1.50	1.50	11
<i>Bacteroides vulgatus</i> ATCC 8482	184	514.80	289.49	288.70	415.50	10.55	1.35	1.35	10

<i>Bacteroides thetaiotaomicron</i>	160	456.83	212.97	212.30	391.50	10.55	1.22	1.21	10
<i>Bifidobacterium longum</i>	157	463.53	274.60	273.72	390.00	10.55	1.33	1.32	10
<i>Bifidobacterium pseudocatenulatum</i>	102	459.66	217.31	216.24	393.50	10.44	1.13	1.13	10
Stool2_R1: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Megamonas funiformis</i>	7697	468.75	249.06	249.05	388.00	10.96	1.54	1.54	11
<i>Phocaeicola dorei</i>	1744	465.77	231.13	231.07	387.00	10.76	1.41	1.41	11
<i>Anaerobutyricum hallii</i>	999	464.27	243.42	243.30	391.00	10.83	1.44	1.44	11
<i>Anaerostipes hadrus</i>	578	469.46	238.25	238.04	389.00	10.77	1.36	1.36	11
<i>Blautia</i> sp. SC05B48	413	478.95	233.21	232.93	410.00	10.74	1.35	1.35	11
<i>Bacteroides</i>	410	433.59	189.20	188.97	374.00	10.63	1.32	1.32	10
<i>Parabacteroides distasonis</i>	363	487.75	257.11	256.75	398.00	10.74	1.30	1.29	11
<i>Escherichia coli</i>	349	486.87	234.01	233.68	417.00	10.62	1.39	1.39	10
<i>Phocaeicola vulgatus</i>	307	456.73	209.30	208.96	398.00	10.72	1.41	1.41	10
<i>Bacteroides caccae</i>	191	449.29	237.29	236.67	360.00	10.66	1.41	1.40	10
Stool2_R1: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Desulfovibrio piger</i>	128	447.03	241.42	240.47	376.50	10.44	1.22	1.22	10
<i>Alistipes onderdonkii</i> subsp. <i>vulgaris</i>	71	454.30	258.26	256.43	394.00	10.51	1.12	1.11	10
<i>Roseburia hominis</i>	60	436.72	172.11	170.67	370.00	10.53	1.24	1.23	10
<i>Escherichia</i>	35	504.94	230.46	227.15	484.00	10.57	1.20	1.18	11
<i>Clostridioides difficile</i>	25	429.44	236.08	231.31	386.00	11.04	1.06	1.04	11
<i>Enterococcus faecium</i>	15	447.93	198.94	192.20	424.00	10.93	1.94	1.88	10
<i>[Clostridium]</i> <i>innocuum</i>	9	422.44	164.43	155.03	373.00	11.11	1.62	1.52	11
<i>Escherichia fergusonii</i>	9	587.33	368.29	347.22	396.00	10.67	1.50	1.41	11
<i>Escherichia albertii</i>	7	370.71	202.41	187.40	272.00	9.86	1.21	1.12	9
<i>Shigella flexneri</i>	7	566.71	293.55	271.78	502.00	10.43	1.13	1.05	11

Stool2_R2: Beneficial Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Bifidobacterium adolescentis</i>	1618	716.99	508.65	508.49	556.00	10.37	1.16	1.16	10
<i>Akkermansia muciniphila</i>	1488	701.04	483.62	483.46	556.00	10.29	1.17	1.17	10
<i>Bifidobacterium longum</i>	453	671.97	460.27	459.76	498.00	10.42	1.23	1.22	10
<i>Bacteroides ovatus</i>	314	608.07	446.84	446.13	448.00	10.62	1.40	1.39	10

<i>Bacteroides uniformis</i>	295	703.01	461.31	460.52	529.00	10.58	1.28	1.28	10
<i>Bifidobacterium pseudocatenulatum</i>	222	760.96	551.05	549.81	571.00	10.48	1.23	1.23	10
<i>Bacteroides fragilis</i>	217	655.82	476.09	474.99	462.00	10.56	1.33	1.33	10
<i>Odoribacter splanchnicus</i>	149	602.55	458.56	457.02	441.00	10.69	1.34	1.34	11
<i>Collinsella aerofaciens</i>	141	669.09	435.97	434.42	536.00	10.29	1.19	1.18	10
<i>Bacteroides thetaiotaomicron</i>	134	640.90	430.60	428.99	467.00	10.65	1.31	1.30	11
Stool2_R2: Commensal Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Megamonas funiformis</i>	5585	575.21	408.21	408.17	431.00	10.81	1.52	1.52	11
<i>Phocaeicola dorei</i>	1057	599.10	413.97	413.77	463.00	10.64	1.38	1.38	10
<i>Anaerobutyricum hallii</i>	728	574.80	451.33	451.02	427.00	10.75	1.38	1.38	11
<i>Escherichia coli</i>	527	735.91	516.82	516.33	578.00	10.47	1.24	1.24	10
<i>Blautia sp. SC05B48</i>	442	614.80	509.33	508.75	454.00	10.60	1.36	1.36	10
<i>Anaerostipes hadrus</i>	428	546.94	376.15	375.71	416.00	10.80	1.48	1.48	11
<i>Bacteroides</i>	391	568.01	438.39	437.83	428.00	10.53	1.35	1.35	10
<i>Alistipes dispar</i>	369	693.61	458.29	457.67	567.00	10.51	1.23	1.23	10
<i>Parabacteroides distasonis</i>	290	649.74	522.10	521.20	467.50	10.49	1.14	1.13	10
<i>Phocaeicola vulgatus</i>	219	574.89	369.38	368.54	429.00	10.54	1.39	1.39	10
Stool2_R2: Harmful Bacteria									
	reads	seqlen_mean	seqlen_stdev	seqlen_pstdev	seqlen_median	qscore_mean	qscore_stdev	qscore_pstdev	qscore_median
<i>Desulfovibrio piger</i>	400	753.98	556.40	555.71	596.50	10.37	1.16	1.16	10
<i>Alistipes onderdonkii subsp. vulgaris</i>	121	671.40	485.84	483.83	575.00	10.40	1.17	1.16	10
<i>Roseburia hominis</i>	70	660.54	488.84	485.34	539.00	10.70	1.30	1.29	11
<i>Clostridioides difficile</i>	45	558.36	349.05	345.15	416.00	10.33	1.45	1.43	10
<i>Escherichia</i>	38	601.13	431.03	425.32	430.50	10.55	1.27	1.25	10.5
<i>Escherichia fergusonii</i>	14	713.86	413.06	398.04	654.50	10.07	1.21	1.16	10
<i>Eggerthella lenta</i>	13	706.00	581.62	558.80	587.00	10.85	1.28	1.23	11
<i>[Clostridium] innocuum</i>	12	436.08	170.39	163.13	401.00	10.58	1.16	1.11	10.5
<i>Enterococcus faecium</i>	12	761.25	492.94	471.95	655.00	10.67	0.78	0.75	11
<i>Escherichia albertii</i>	8	620.88	375.32	351.08	439.50	10.38	1.30	1.22	10

Table S5. Microbiome assessment by human expert for each replicate.
(refer to Excel files)

Table S6. EPI2ME analysis of antimicrobial resistance. The alignment column shows the number of reads aligned to the known antimicrobial resistance genes.

Saliva1_R1								
Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	12	86.8	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1,551	1,551	100.0
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	5	89.5	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1544	100.0
RlmA(II)	2	80.1	Streptococcus pneumoniae	protein homolog model	macrolide resistance gene, gene involved in self resistance to antibiotic, antibiotic target modifying enzyme	849	842	99.2
Haemophilus parainfluenzae gyrA conferring resistance to fluoroquinolones	2	90.7	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2646	2646	100.0
Haemophilus parainfluenzae parC conferring resistance to fluoroquinolones	2	90.3	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2256	1858	82.4
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	2	93.5	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	428	18.6
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to hygromycin B	2	74.5	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1528	100.0
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	2	80	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	558	36.3
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	2	86.1	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	226	14.6
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	2	79.6	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1246	81.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to	2	80	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1265	82.8

neomycin								
ErmB	1	90.2	Enterococcus faecium	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	748	387	51.7
mtrE	1	74.2	Neisseria gonorrhoeae	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	1405	875	62.3
mel	1	85.9	Streptococcus pneumoniae Taiwan19F-14	protein homolog model	efflux pump conferring antibiotic resistance	1465	379	25.9
tetM	1	85.7	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	1821	94.8
catS	1	89	Streptococcus pyogenes	protein homolog model	antibiotic inactivation enzyme, chloramphenicol resistance gene	492	492	100.0
tetQ	1	86.7	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1974	100.0
Neisseria gonorrhoeae gyrA conferring resistance to fluoroquinolones	1	81.1	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2751	2694	97.9
Staphylococcus aureus rpoC conferring resistance to daptomycin	1	66.1	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	918	25.3
Escherichia coli EF-Tu mutants conferring resistance to kirromycin	1	84.1	Escherichia coli	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1185	436	36.8
rpsJ	1	86.9	Neisseria gonorrhoeae FA 1090	protein variant model	tetracycline resistance gene, antibiotic target protection protein	312	311	99.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	1	75.5	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	526	34.1
Chlamydomphila psittaci 16S rRNA mutation conferring resistance to spectinomycin	1	74.8	Chlamydia psittaci 6BC	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1507	562	37.3
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	1	82.7	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	371	25.0
Mycobacterium abscessus 16S rRNA mutation conferring	1	77.8	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	742	49.3

resistance to amikacin								
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Saliva1_R2

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	3	77.1	Escherichia coli CFT073	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1230	1172	95.3
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	3	87.9	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1544	100.0
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	2	72.1	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1156	74.9
Bifidobacteria intrinsic ileS conferring resistance to mupirocin	1	70.4	Bifidobacterium bifidum PRL2010	protein homolog model	mupirocin resistance gene	3324	1993	60.0
Staphylococcus aureus rpoC conferring resistance to daptomycin	1	79.9	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	190	5.2
Haemophilus parainfluenzae gyrA conferring resistance to fluoroquinolones	1	88.3	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2646	2646	100.0
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	1	82.6	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	1967	85.4
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to streptomycin	1	75	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	882	57.2
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	1	83.5	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	1551	100.0

Saliva2_R1

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	106	88.6	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	1551	100.0
Haemophilus parainfluenzae parC conferring resistance to fluoroquinolones	30	89.1	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2256	2256	100.0
Haemophilus parainfluenzae gyrA conferring resistance to fluoroquinolones	29	92.2	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2646	2646	100.0
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	20	84.4	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1544	100.0
Streptococcus pneumoniae parC conferring resistance to fluoroquinolone	18	86.2	Streptococcus pneumoniae TIGR4	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant, gene involved in self resistance to antibiotic	2473	2453	99.2
tetQ	17	93.7	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1974	100.0
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	11	76.8	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	1224	96.2
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	11	84.6	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1544	100.0
RlmA(II)	10	87	Streptococcus pneumoniae	protein homolog model	macrolide resistance gene, gene involved in self resistance to antibiotic, antibiotic target modifying enzyme	849	842	99.2
Escherichia coli rpoB mutants conferring resistance to rifampicin	10	73.5	Escherichia coli O157:H7 str. Sakai	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	4030	3696	91.7
Staphylococcus aureus rpoC conferring resistance to daptomycin	9	77	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	1759	48.5
Helicobacter pylori 16S rRNA mutation conferring resistance to tetracycline	9	78	Helicobacter pylori 26695	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1501	1497	99.7
mefA	8	90.6	Exiguobacterium sp.	protein homolog	efflux pump conferring antibiotic resistance	1219	923	75.7

			S3-2	model				
tetM	8	86.7	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	1889	98.3
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	8	83.3	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	819	53.0
CfxA2	7	94.7	Prevotella intermedia	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	967	100.0
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	7	89.4	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	1724	74.8
patB	6	87.1	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1167	973	83.4
mel	6	94.2	Streptococcus pneumoniae Taiwan19F-14	protein homolog model	efflux pump conferring antibiotic resistance	1465	1166	79.6
Escherichia coli EF-Tu mutants conferring resistance to Enacyloxin IIa	6	81.7	Escherichia coli str. K-12 substr. MG1655	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1185	1175	99.2
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to hygromycin B	6	84.2	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1528	100.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	5	81	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1520	99.5
hmrM	4	86.3	Haemophilus influenzae	protein homolog model	efflux pump conferring antibiotic resistance	1395	1333	95.6
CfxA5	4	89.8	Parabacteroides distasonis	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	914	94.5
CfxA3	4	97.6	Capnocytophaga ochracea	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	489	50.6
IsaC	4	89.2	Streptococcus agalactiae	protein homolog model	efflux pump conferring antibiotic resistance	1480	1124	75.9
Neisseria gonorrhoeae gyrA conferring resistance to fluoroquinolones	4	87.2	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2751	1095	39.8
Escherichia coli EF-Tu mutants conferring resistance to	4	83.2	Escherichia coli CFT073	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1230	1149	93.4

Pulvomycin								
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to spectinomycin	4	79.1	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	715	46.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to neomycin	4	82.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	806	52.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to viomycin	4	78	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	1283	84.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	4	83.2	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1211	79.3
tetW	3	93.1	Bifidobacterium longum	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	971	50.6
pmrA efflux pump	3	89.8	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1220	876	71.8
CfxA4	3	91.8	Bacteroides fragilis	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	788	81.5
PBP2x	3	83.6	Streptococcus pneumoniae	protein variant model	beta-lactam resistance gene, antibiotic resistant gene variant or mutant	2253	2091	92.8
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	3	87.3	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	679	44.2
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	3	75.1	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	1528	99.4
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	3	75.1	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1533	99.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to gentamicin C	3	89.8	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	495	32.1
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	3	79.2	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	1400	94.2

Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	3	76.8	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	1062	70.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tobramycin	3	77.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1175	76.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to tobramycin	3	83.7	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	886	58.9
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	3	81.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	749	49.0
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to paromomycin	3	76.8	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1093	70.9
macB	2	83.1	Neisseria gonorrhoeae	protein homolog model	efflux pump conferring antibiotic resistance	1935	509	26.3
catS	2	91.5	Streptococcus pyogenes	protein homolog model	antibiotic inactivation enzyme, chloramphenicol resistance gene	492	277	56.3
mtrD	2	81.7	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	3205	3178	99.2
PBP2b	2	85.4	Streptococcus pneumoniae R6	protein variant model	beta-lactam resistance gene, antibiotic resistant gene variant or mutant	2058	502	24.4
PBP1a	2	74.9	Streptococcus pneumoniae	protein variant model	beta-lactam resistance gene, antibiotic resistant gene variant or mutant	2160	1257	58.2
Staphylococcus aureus rpoB mutants conferring resistance to rifampicin	2	77.8	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	3553	817	23.0
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	2	81.9	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	564	36.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to G418	2	74.5	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	552	35.8
Mycobacterium abscessus 16S rRNA mutation conferring resistance to neomycin	2	78.2	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	771	51.3

Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	2	85	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	893	57.9
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	2	88.6	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	465	30.4
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to spectinomycin	2	85.6	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	393	25.5
Escherichia coli 16S rRNA mutation in the rrsC gene conferring resistance to kasugamicin	2	78.3	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	453	29.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to viomycin	2	91.9	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	609	39.9
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to kanamycin	2	78.1	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	817	53.2
Streptomyces cinnamoneus EF-Tu mutants conferring resistance to elfamycin	1	74.2	Streptomyces cinnamoneus	protein homolog model	elfamycin resistance gene, antibiotic resistant gene variant or mutant, gene involved in self resistance to antibiotic	1194	232	19.4
lnuC	1	97.3	Streptococcus agalactiae	protein homolog model	antibiotic inactivation enzyme, lincosamide resistance gene	495	294	59.4
Bifidobacteria intrinsic ileS conferring resistance to mupirocin	1	76.5	Bifidobacterium bifidum PRL2010	protein homolog model	mupirocin resistance gene	3324	611	18.4
macA	1	80.2	Neisseria gonorrhoeae	protein homolog model	efflux pump conferring antibiotic resistance	1179	496	42.1
TEM-4	1	94	Klebsiella pneumoniae	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	1061	580	54.7
Streptomyces rishiriensis parY mutant conferring resistance to aminocoumarin	1	76	Streptomyces rishiriensis	protein homolog model	gene involved in self resistance to antibiotic, antibiotic resistant gene variant or mutant, aminocoumarin resistance gene	2112	365	17.3
CfxA	1	92.7	Bacteroides vulgatus	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	180	18.6
cat-TC	1	96.1	Lactobacillus reuteri	protein homolog	antibiotic inactivation enzyme,	717	76	10.6

				model	chloramphenicol resistance gene			
mtrR	1	76.7	Neisseria gonorrhoeae NCCP11945	protein homolog model	gene modulating antibiotic efflux	634	366	57.7
Escherichia coli EF-Tu mutants conferring resistance to kirromycin	1	86.3	Escherichia coli	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1185	162	13.7
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to streptomycin	1	94.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	56	3.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	1	77.3	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	211	13.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tetracycline	1	94.2	Escherichia coli K-12	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1542	107	6.9
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	1	80.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	322	20.9
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	1	81.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	506	33.1
Mycobacterium chelonae 16S rRNA mutation conferring resistance to kanamycin A	1	76.6	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	301	20.9
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to tetracycline	1	77.2	Escherichia coli K-12	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1542	284	18.4
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	1	96.7	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	159	10.6

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	21	88.4	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	1551	100.0
tetQ	5	89.8	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1204	61.0
Haemophilus parainfluenzae parC conferring resistance to fluoroquinolones	5	89.5	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2256	1338	59.3
Haemophilus parainfluenzae gyrA conferring resistance to fluoroquinolones	4	89	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2646	1105	41.8
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	4	73.4	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	1194	93.9
pmrA efflux pump	3	87.1	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1200	1103	91.9
PBP2b	3	86	Streptococcus pneumoniae R6	protein variant model	beta-lactam resistance gene, antibiotic resistant gene variant or mutant	2058	671	32.6
Streptococcus pneumonia parC conferring resistance to fluoroquinolone	3	82.4	Streptococcus pneumoniae TIGR4	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant, gene involved in self resistance to antibiotic	2473	1295	52.4
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	3	78.3	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1145	74.5
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	3	73.4	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1102	71.7
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	3	84.5	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	718	46.5
Helicobacter pylori 16S rRNA mutation conferring resistance to tetracycline	3	76.7	Helicobacter pylori 26695	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1501	1501	100.0
CfxA2	2	92.2	Prevotella intermedia	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	537	55.5
mefA	2	91.2	Exiguobacterium sp.	protein homolog	efflux pump conferring antibiotic resistance	1219	481	39.5

			S3-2	model				
mel	2	90.1	Streptococcus pneumoniae Taiwan19F-14	protein homolog model	efflux pump conferring antibiotic resistance	1465	579	39.5
CfxA3	2	93	Capnocytophaga ochracea	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	607	62.8
Neisseria gonorrhoeae gyrA conferring resistance to fluoroquinolones	2	81.6	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2751	1765	64.2
Staphylococcus aureus rpoC conferring resistance to daptomycin	2	73	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	1087	30.0
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	2	76.5	Escherichia coli CFT073	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1230	1198	97.4
PBP2x	2	81.8	Streptococcus pneumoniae	protein variant model	beta-lactam resistance gene, antibiotic resistant gene variant or mutant	2253	1493	66.3
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to spectinomycin	2	86.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	278	18.0
patB	1	88.4	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1167	326	27.9
RlmA(II)	1	82.7	Streptococcus pneumoniae	protein homolog model	macrolide resistance gene, gene involved in self resistance to antibiotic, antibiotic target modifying enzyme	849	494	58.2
mtrD	1	68	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	3205	2976	92.9
CfxA4	1	91.7	Bacteroides fragilis	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	133	13.8
Mycobacterium tuberculosis rpoB mutants conferring resistance to rifampicin	1	72.2	Mycobacterium tuberculosis H37Rv	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	3520	1529	43.4
Escherichia coli rpoB mutants conferring resistance to rifampicin	1	70.7	Escherichia coli O157:H7 str. Sakai	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	4030	1681	41.7
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	1	86.8	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	454	19.7
Mycobacterium smegmatis 16S	1	80.3	Mycobacterium	rRNA mutation	aminoglycoside resistance gene, antibiotic	1528	204	13.4

rRNA mutation in the rrsB gene conferring resistance to hygromycin B			smegmatis str. MC2 155	model	resistant gene variant or mutant			
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to streptomycin	1	73.3	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	456	29.6
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	1	74.6	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	1287	83.7
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	1	90	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	389	25.2
Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	1	89.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	203	13.2
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	1	78.7	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	300	20.2
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	1	88.2	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	441	28.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tobramycin	1	81.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	185	12.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	1	98.4	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	69	4.5
Borrelia burgdorferi 16S rRNA mutation conferring resistance to gentamicin	1	80.9	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	206	13.9

Saliva3_R1

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Neisseria meningitidis 16S	36	90.8	Neisseria	rRNA mutation	aminoglycoside resistance gene, antibiotic	1544	1452	94.0

rRNA mutation conferring resistance to spectinomycin			meningitidis	model	resistant gene variant or mutant			
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	15	88.1	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	1958	85.0
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	13	91.3	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	1099	71.1
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	12	88.9	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	1551	100.0
tetM	8	89.2	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	1552	80.8
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	4	80.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1519	99.4
Helicobacter pylori 16S rRNA mutation conferring resistance to tetracycline	4	84.6	Helicobacter pylori 26695	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1501	1519	101.2
macB	3	79.8	Neisseria gonorrhoeae	protein homolog model	efflux pump conferring antibiotic resistance	1935	828	42.8
mtrD	3	81.4	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	3205	990	30.9
Neisseria gonorrhoeae gyrA conferring resistance to fluoroquinolones	3	83.4	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2751	1201	43.7
Haemophilus parainfluenzae gyrA conferring resistance to fluoroquinolones	3	93.7	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2646	1162	43.9
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	3	81	Escherichia coli CFT073	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1230	1007	81.9
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	3	87	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1519	99.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	3	83.4	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	527	34.5

tet32	2	96.3	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	441	23.0
mtrE	2	84.2	Neisseria gonorrhoeae	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	1405	482	34.3
Haemophilus parainfluenzae parC conferring resistance to fluoroquinolones	2	87.4	Haemophilus parainfluenzae	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2256	895	39.7
Escherichia coli rpoB mutants conferring resistance to rifampicin	2	80.3	Escherichia coli O157:H7 str. Sakai	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	4030	913	22.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to hygromycin B	2	88.5	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	393	25.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	2	92.8	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	235	15.3
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to neomycin	2	85.3	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	996	65.2
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	2	75.8	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	514	34.6
Escherichia coli 16S rRNA mutation conferring resistance to edeine	2	78.2	Escherichia coli K-12	rRNA mutation model	polyamine resistance gene, antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1542	315	20.4
Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	2	88.5	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	528	35.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	2	84.9	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	506	33.1
patB	1	87.3	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1167	284	24.3
lnuC	1	96.6	Streptococcus agalactiae	protein homolog model	antibiotic inactivation enzyme, lincosamide resistance gene	495	230	46.5
RlmA(II)	1	82.4	Streptococcus pneumoniae	protein homolog model	macrolide resistance gene, gene involved in self resistance to antibiotic, antibiotic target modifying enzyme	849	277	32.6

TEM-54	1	88.4	Escherichia coli	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	861	407	47.3
mtrC	1	79.2	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	1240	755	60.9
mefA	1	85	Exiguobacterium sp. S3-2	protein homolog model	efflux pump conferring antibiotic resistance	1219	228	18.7
farA	1	74.3	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	1155	324	28.1
IsaC	1	80.8	Streptococcus agalactiae	protein homolog model	efflux pump conferring antibiotic resistance	1480	579	39.1
tetQ	1	93.8	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	179	9.1
pmrA efflux pump	1	94.4	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1200	1108	92.3
Mycobacterium leprae rpoB mutants conferring resistance to rifampicin	1	71.1	Mycobacterium leprae TN	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	3538	1694	47.9
Clostridium difficile EF-Tu mutants conferring resistance to elfamycin	1	76.6	Clostridium difficile	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1194	859	71.9
Staphylococcus aureus rpoC conferring resistance to daptomycin	1	87.4	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	102	2.8
Escherichia coli gyrB conferring resistance to aminocoumarin	1	68.6	Escherichia coli str. K-12 substr. W3110	protein variant model	antibiotic resistant gene variant or mutant, aminocoumarin resistance gene	2416	603	25.0
Mycobacterium tuberculosis rpsL mutations conferring resistance to Streptomycin	1	78.6	Mycobacterium tuberculosis CDC1551	protein variant model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	376	220	58.5
rpsJ	1	84.3	Neisseria gonorrhoeae FA 1090	protein variant model	tetracycline resistance gene, antibiotic target protection protein	312	310	99.4
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	1	78	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	238	18.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	1	81	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	118	7.7
Mycobacterium tuberculosis 16S rRNA mutation conferring	1	86.4	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	218	14.2

resistance to amikacin								
Borrelia burgdorferi 16S rRNA mutation conferring resistance to kanamycin	1	78.9	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	373	25.3
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to gentamicin C	1	78.1	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	411	26.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to spectinomycin	1	82.5	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	262	17.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	1	86.8	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	241	15.6
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	1	78	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	241	15.6
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	1	85.9	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	350	23.3
Mycobacterium abscessus 16S rRNA mutation conferring resistance to kanamycin	1	84.5	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	166	11.0
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to kanamycin	1	80.9	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	449	29.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to tobramycin	1	93.1	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	217	14.4

Saliva3_R2

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Neisseria meningitidis 16S rRNA mutation conferring	12	91.9	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1318	85.4

resistance to spectinomycin								
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	8	93	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	460	29.8
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	6	87.2	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	716	46.2
Neisseria gonorrhoeae parC conferring resistance to fluoroquinolone	4	92.3	Neisseria gonorrhoeae FA 1090	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2304	849	36.8
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	3	78.8	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	829	65.2
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	3	82.7	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	750	50.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	3	86	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	874	57.2
mel	2	98.5	Streptococcus pneumoniae Taiwan19F-14	protein homolog model	efflux pump conferring antibiotic resistance	1465	427	29.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	2	86.2	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	251	16.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to neomycin	2	85.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	329	21.5
tet32	1	86.7	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	331	17.2
tetM	1	85.8	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	338	17.6
pmrA efflux pump	1	91.5	Streptococcus pneumoniae R6	protein homolog model	efflux pump conferring antibiotic resistance	1200	225	18.8
mtrD	1	76	Neisseria meningitidis MC58	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	3205	464	14.5
Haemophilus parainfluenzae	1	93	Haemophilus	protein variant	fluoroquinolone resistance gene, antibiotic	2256	513	22.7

parC conferring resistance to fluoroquinolones			parainfluenzae	model	resistant gene variant or mutant			
Mycobacterium abscessus 16S rRNA mutation conferring resistance to neomycin	1	81.2	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	508	33.8
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	1	91.7	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	65	4.2
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	1	83.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	193	12.5
Borrelia burgdorferi 16S rRNA mutation conferring resistance to spectinomycin	1	74.7	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	370	25.1
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	1	84.5	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	166	10.8
Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	1	74.9	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	202	13.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	1	89	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	193	12.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to spectinomycin	1	80.8	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	221	14.3
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	1	83.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	154	10.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to viomycin	1	84.3	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	523	34.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	1	85	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	255	17.0

Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to viomycin	1	85.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	252	16.5
Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	1	84.1	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	161	10.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	1	92.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	111	7.3

Stool1_R1

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	11	81.5	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	1080	69.9
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	11	82	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1410	91.3
tetQ	9	89.4	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1670	84.6
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	7	80.4	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1146	74.2
tetM	6	90.9	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	1514	78.8
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	6	82.8	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	887	57.7
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	6	80.4	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	832	56.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to	6	81.3	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	921	60.3

viomycin								
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to kanamycin	6	84	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1095	71.2
tetO	5	90.6	Campylobacter jejuni	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	935	48.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	5	77	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	976	63.5
Chlamydomphila psittaci 16S rRNA mutation conferring resistance to spectinomycin	5	79	Chlamydia psittaci 6BC	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1507	844	56.0
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	5	83.8	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1323	86.6
Helicobacter pylori 16S rRNA mutation conferring resistance to tetracycline	5	83.4	Helicobacter pylori 26695	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1501	801	53.4
tet32	4	94.3	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	733	38.2
Bifidobacteria intrinsic ileS conferring resistance to mupirocin	4	85.1	Bifidobacterium bifidum PRL2010	protein homolog model	mupirocin resistance gene	3324	989	29.8
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	4	77.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1538	99.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to viomycin	4	82.6	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	882	57.7
tet40	3	93.5	Streptococcus suis	protein homolog model	efflux pump conferring antibiotic resistance	1222	663	54.3
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	3	82.1	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1152	75.0
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	3	80.1	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	481	31.0

Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	3	78.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	563	36.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to neomycin	3	82.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	890	58.2
Escherichia coli 16S rRNA mutation in the rrsC gene conferring resistance to kasugamicin	3	79.9	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	360	23.3
Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	3	80.6	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	796	52.9
Mycobacterium chelonae 16S rRNA mutation conferring resistance to tobramycin	3	81	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	612	42.5
Mycobacterium tuberculosis rpoB mutants conferring resistance to rifampicin	2	78.6	Mycobacterium tuberculosis H37Rv	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	3520	720	20.5
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	2	86.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	343	22.2
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	2	80.5	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	434	28.4
Borrelia burgdorferi 16S rRNA mutation conferring resistance to kanamycin	2	82	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	233	15.8
Mycobacterium chelonae 16S rRNA mutation conferring resistance to amikacin	2	87.1	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	434	30.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	2	79.4	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	925	60.5
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to	2	83.2	Escherichia coli K-12	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1542	248	16.1

tetracycline								
Escherichia coli 16S rRNA mutation conferring resistance to edeine	2	89.8	Escherichia coli K-12	rRNA mutation model	polyamine resistance gene, antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1542	392	25.4
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tobramycin	2	79.1	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	604	39.2
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	2	83.3	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1470	96.2
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	2	77.6	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	742	48.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to paromomycin	2	78.9	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	906	58.8
sul2	1	94.3	Vibrio cholerae	protein homolog model	sulfonamide resistance gene, antibiotic target replacement protein	817	105	12.9
PmrF	1	94.1	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene altering cell wall charge conferring antibiotic resistance, polymyxin resistance gene	970	201	20.7
ANT(6)-Ib	1	94.8	Campylobacter jejuni	protein homolog model	aminoglycoside resistance gene, antibiotic inactivation enzyme	867	363	41.9
dfrF	1	92	Enterococcus faecalis	protein homolog model	trimethoprim resistance gene, antibiotic target replacement protein	496	164	33.1
ErmB	1	90.5	Enterococcus faecium	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	748	157	21.0
tetW	1	94.5	Bifidobacterium longum	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	404	21.0
ErmF	1	96.7	Bacteroides fragilis	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	801	332	41.4
mefA	1	100	Exiguobacterium sp. S3-2	protein homolog model	efflux pump conferring antibiotic resistance	1219	53	4.3

mdtE	1	89.2	Escherichia coli str. K-12 substr. W3110	protein homolog model	antibiotic resistance gene cluster, cassette, or operon, efflux pump conferring antibiotic resistance	1159	379	32.7
YojI	1	92.9	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1644	168	10.2
AAC(6')-Ie-APH(2'')-Ia	1	95.8	Staphylococcus aureus	protein homolog model	aminoglycoside resistance gene, antibiotic inactivation enzyme	1441	261	18.1
PmrB	1	91.2	Escherichia coli str. K-12 substr. W3110	protein homolog model	gene altering cell wall charge conferring antibiotic resistance, polymyxin resistance gene	1093	300	27.4
Clostridium difficile EF-Tu mutants conferring resistance to elfamycin	1	73.7	Clostridium difficile	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1194	862	72.2
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	1	71.8	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	925	72.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to hygromycin B	1	96.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	58	3.8
Mycobacterium abscessus 16S rRNA mutation conferring resistance to neomycin	1	74.5	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	486	32.3
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to streptomycin	1	90.3	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	133	8.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to gentamicin C	1	76	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	324	21.0
Mycobacterium chelonae 16S rRNA mutation conferring resistance to kanamycin A	1	78.8	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	548	38.0
Mycobacterium abscessus 16S rRNA mutation conferring resistance to kanamycin	1	79.5	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	424	28.2

Stool1_R2

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
Salmonella enterica serovar Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin	19	80.4	Salmonella enterica subsp. salamae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1421	92.0
Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	18	80.8	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	1415	95.2
tetQ	17	89.4	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1915	97.0
Helicobacter pylori 16S rRNA mutation conferring resistance to tetracycline	17	82.9	Helicobacter pylori 26695	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1501	935	62.3
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	14	81.5	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	1544	100.0
tetM	12	88.4	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	1841	95.8
tetO	11	93.6	Campylobacter jejuni	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	1920	100.0
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	11	79.3	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	1307	84.6
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	10	82.1	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1231	80.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	10	84.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1324	86.6
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to neomycin	9	82.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1338	87.6
tet32	8	93.5	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	1407	73.3

Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	8	79.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1441	93.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to viomycin	8	84.2	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	1097	71.8
Bifidobacteria intrinsic ileS conferring resistance to mupirocin	7	85.1	Bifidobacterium bifidum PRL2010	protein homolog model	mupirocin resistance gene	3324	1963	59.1
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	7	86.2	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1374	89.9
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	6	78.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1490	96.6
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	6	79.7	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	894	58.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to kanamycin	6	80.8	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	1061	70.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	6	81.5	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1324	86.6
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to streptomycin	5	82.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	645	41.8
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	5	81.9	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1040	67.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to kanamycin	5	83	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	611	39.8
tetW	4	95	Bifidobacterium longum	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	1140	59.4

Mycobacterium tuberculosis rpoB mutants conferring resistance to rifampicin	4	77.1	Mycobacterium tuberculosis H37Rv	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	3520	1765	50.1
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	4	78.1	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1163	75.4
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	4	77.6	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	540	35.0
Chlamydomophila psittaci 16S rRNA mutation conferring resistance to spectinomycin	4	77.2	Chlamydia psittaci 6BC	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1507	993	65.9
Escherichia coli 16S rRNA mutation in the rrsC gene conferring resistance to kasugamicin	4	78.1	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	1304	84.6
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to tetracycline	4	82.8	Escherichia coli K-12	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1542	663	43.0
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	4	83.7	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	941	62.6
ANT(6)-Ib	3	90.6	Campylobacter jejuni	protein homolog model	aminoglycoside resistance gene, antibiotic inactivation enzyme	867	741	85.5
dfrF	3	95.2	Enterococcus faecalis	protein homolog model	trimethoprim resistance gene, antibiotic target replacement protein	496	293	59.1
Mycobacterium chelonae 16S rRNA mutation conferring resistance to neomycin	3	85.6	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	483	33.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to hygromycin B	3	82	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1224	80.1
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to G418	3	77.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	837	54.3
Escherichia coli 16S rRNA mutation in the rrnB gene	3	78.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	709	46.0

conferring resistance to spectinomycin								
Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin	3	82	Pasteurella multocida 36950	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1551	520	33.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to hygromycin B	3	82.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	508	33.2
Borrelia burgdorferi 16S rRNA mutation conferring resistance to gentamicin	3	79.4	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	377	25.5
mefA	2	91.3	Exiguobacterium sp. S3-2	protein homolog model	efflux pump conferring antibiotic resistance	1219	430	35.3
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	2	79.3	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	1004	78.9
Borrelia burgdorferi 16S rRNA mutation conferring resistance to kanamycin	2	84.3	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	215	14.6
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	2	90.3	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	285	18.7
Mycobacterium chelonae 16S rRNA mutation conferring resistance to gentamicin C	2	84.4	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	611	42.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to viomycin	2	90.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	213	13.9
Escherichia coli 16S rRNA mutation conferring resistance to edeine	2	88.4	Escherichia coli K-12	rRNA mutation model	polyamine resistance gene, antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1542	353	22.9
Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	2	84.4	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	758	50.4
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tobramycin	2	76.6	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	641	41.6

Streptomyces cinnamoneus EF-Tu mutants conferring resistance to elfamycin	1	72.8	Streptomyces cinnamoneus	protein homolog model	elfamycin resistance gene, antibiotic resistant gene variant or mutant, gene involved in self resistance to antibiotic	1194	766	64.2
emrK	1	95.3	Escherichia coli	protein homolog model	efflux pump conferring antibiotic resistance	1057	173	16.4
tet40	1	94.3	Streptococcus suis	protein homolog model	efflux pump conferring antibiotic resistance	1222	141	11.5
ErmB	1	93.1	Plasmid pAM77	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	739	88	11.9
ErmB	1	88.8	Streptococcus pyogenes	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	739	289	39.1
ErmF	1	91.6	Bacteroides fragilis	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	801	354	44.2
mfd	1	93.8	Escherichia coli str. K-12 substr. MG1655	protein homolog model	antibiotic resistance gene cluster, cassette, or operon, efflux pump conferring antibiotic resistance	3115	943	30.3
CfxA3	1	97.6	Capnocytophaga ochracea	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	336	34.7
mdtF	1	93.6	Escherichia coli str. K-12 substr. MG1655	protein homolog model	fluoroquinolone resistance gene, antibiotic target protection protein	3447	603	17.5
APH(6)-Id	1	91.2	Pseudomonas aeruginosa	protein homolog model	aminoglycoside resistance gene, antibiotic inactivation enzyme	838	271	32.3
CfxA	1	96.4	Bacteroides vulgatus	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	304	31.4
YojI	1	95.7	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1644	141	8.6
Clostridium difficile EF-Tu mutants conferring resistance to elfamycin	1	73.1	Clostridium difficile	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1194	921	77.1
Staphylococcus aureus rpoC conferring resistance to daptomycin	1	79.1	Staphylococcus aureus subsp. aureus MRSA252	protein variant model	lipopeptide antibiotic resistance gene, antibiotic resistant gene variant or mutant	3625	387	10.7

Escherichia coli mutant murA conferring resistance to fosfomycin	1	95.7	Escherichia coli ATCC 25922	protein variant model	fosfomycin resistance gene, antibiotic resistant gene variant or mutant	1260	374	29.7
Escherichia coli ompF mutants	1	97.9	Escherichia coli str. K-12 substr. W3110	protein variant model	gene modulating permeability to antibiotic, beta-lactam resistance gene, antibiotic resistant gene variant or mutant	1090	246	22.6
Mycobacterium abscessus 16S rRNA mutation conferring resistance to neomycin	1	74.6	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	687	45.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to tetracycline	1	86.9	Escherichia coli K-12	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1542	165	10.7
Borrelia burgdorferi 16S rRNA mutation conferring resistance to spectinomycin	1	80.4	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	163	11.0
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to gentamicin C	1	77.8	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	528	34.2
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to spectinomycin	1	72	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	496	32.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to tobramycin	1	90.6	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	133	8.8
Mycobacterium chelonae 16S rRNA mutation conferring resistance to tobramycin	1	80.6	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	471	32.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to paromomycin	1	77.7	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	514	33.3

Stool2_R1

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
tetL	12	94.8	Geobacillus	protein homolog	efflux pump conferring antibiotic resistance	1377	1216	88.3

			stearothermophilus	model				
tetQ	12	93.3	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1744	88.3
tetM	5	89.6	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	806	42.0
InuC	4	89.5	Streptococcus agalactiae	protein homolog model	antibiotic inactivation enzyme, lincosamide resistance gene	495	367	74.1
tolC	3	93.3	Escherichia coli	protein homolog model	efflux pump conferring antibiotic resistance	1488	736	49.5
ErmF	2	90.4	Bacteroides fragilis	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	801	331	41.3
cat	1	90	Campylobacter coli	protein homolog model	antibiotic inactivation enzyme, chloramphenicol resistance gene	624	193	30.9
tet32	1	86.4	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	342	17.8
arnA	1	97.8	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene altering cell wall charge conferring antibiotic resistance, polymyxin resistance gene	1984	320	16.1
OXA-209	1	95.9	Riemerella anatipestifer	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	826	247	29.9
mdtD	1	94.9	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1417	179	12.6
leuO	1	96	Escherichia coli str. K-12 substr. MG1655	protein homolog model	sulfonamide resistance gene, gene modulating antibiotic efflux	945	158	16.7
tetW	1	86.8	Bifidobacterium longum	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	232	12.1
ErmG	1	100	Bacteroides thetaiotaomicron	protein homolog model	antibiotic target modifying enzyme, macrolide resistance gene, streptogramin resistance gene, lincosamide resistance gene	736	131	17.8
CfxA3	1	90.5	Capnocytophaga ochracea	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	277	28.6
baeR	1	93.5	Escherichia coli str. K-12 substr. W3110	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	724	174	24.0
YojI	1	95.8	Escherichia coli str.	protein homolog	efflux pump conferring antibiotic resistance	1644	151	9.2

			K-12 substr. MG1655	model				
gadX	1	97.9	Escherichia coli str. K-12 substr. W3110	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	826	95	11.5
adiY	1	96	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	762	280	36.7
CfxA4	1	91.9	Bacteroides fragilis	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	117	12.1
Escherichia coli mutant UhpT conferring resistance to fosfomycin	1	94.8	Escherichia coli str. K-12 substr. MC4100	protein variant model	fosfomycin resistance gene, antibiotic resistant gene variant or mutant	1392	168	12.1
Escherichia coli EF-Tu mutants conferring resistance to kirromycin	1	100	Escherichia coli	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1185	109	9.2
Shigella flexneri gyrA conferring resistance to fluoroquinolones	1	97.7	Shigella flexneri 2a str. 301	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	2628	91	3.5
Escherichia coli parE conferring resistance to fluoroquinolones	1	91.7	Escherichia coli str. K-12 substr. W3110	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant	1894	218	11.5
Enterococcus faecium EF-Tu mutants conferring resistance to GE2270A	1	78.9	Enterococcus faecium DO	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1272	227	17.8
Escherichia coli rpoB mutants conferring resistance to rifampicin	1	95.9	Escherichia coli O157:H7 str. Sakai	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	4030	190	4.7
fosfomycin sensitive pyruvyl transferase (murA)	1	93.3	Escherichia coli O157:H7 str. Sakai	protein wild type model	NA	1282	98	7.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	1	80.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	163	10.6
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to G418	1	96.9	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	72	4.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	1	82.7	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	199	12.9
Neisseria gonorrhoeae 16S	1	78.9	Neisseria	rRNA mutation	aminoglycoside resistance gene, antibiotic	1545	237	15.3

rRNA mutation conferring resistance to spectinomycin			gonorrhoeae	model	resistant gene variant or mutant			
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to gentamicin C	1	84.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	254	16.5
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	1	97	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	72	4.7
Mycobacterium chelonae 16S rRNA mutation conferring resistance to gentamicin C	1	79.8	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	364	25.3
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to viomycin	1	100	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	54	3.5
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	1	95.4	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	88	5.9
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	1	88.4	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	173	11.2
Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to viomycin	1	86.4	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	252	16.5

Stool2_R2

Gene	Alignments	Average Accuracy (%)	Taxon	CARD Model	CARD category	Gene length (base pairs)	Covered length	Gene coverage (100%)
tetQ	9	90.8	Bacteroides fragilis	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1974	1684	85.3
Bifidobacteria intrinsic ileS conferring resistance to mupirocin	4	79.3	Bifidobacterium bifidum PRL2010	protein homolog model	mupirocin resistance gene	3324	1936	58.2
tetW	4	87	Bifidobacterium longum	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	768	40.0

Propionibacterium acnes 16S rRNA mutation conferring resistance to tetracycline	4	75.5	Propionibacterium acnes	rRNA mutation model	tetracycline resistance gene, antibiotic resistant gene variant or mutant	1486	857	57.7
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to kanamycin	4	80.8	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1112	72.3
Escherichia coli rpoB mutants conferring resistance to rifampicin	3	93.9	Escherichia coli O157:H7 str. Sakai	protein variant model	antibiotic resistant gene variant or mutant, rifampin resistance gene	4030	201	5.0
Escherichia coli 16S rRNA mutation in the rrsH gene conferring resistance to spectinomycin	3	90.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	553	35.9
InuC	2	94.3	Streptococcus agalactiae	protein homolog model	antibiotic inactivation enzyme, lincosamide resistance gene	495	373	75.4
gadE	2	96.6	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene modulating antibiotic efflux, antibiotic resistance gene cluster, cassette, or operon, efflux pump conferring antibiotic resistance	528	388	73.5
mdtO	2	91.2	Escherichia coli str. K-12 substr. W3110	protein homolog model	efflux pump conferring antibiotic resistance	2052	350	17.1
tetM	2	92.4	Clostridium difficile 630	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1921	452	23.5
Escherichia coli parC conferring resistance to fluoroquinolone	2	94.5	Escherichia coli str. K-12 substr. MG1655	protein variant model	fluoroquinolone resistance gene, antibiotic resistant gene variant or mutant, gene involved in self resistance to antibiotic	2260	612	27.1
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	2	80.6	Escherichia coli CFT073	protein variant model	elfamycin resistance gene, antibiotic resistant gene variant or mutant	1230	730	59.3
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to streptomycin	2	78.6	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1537	100.0
Neisseria gonorrhoeae 16S rRNA mutation conferring resistance to spectinomycin	2	81	Neisseria gonorrhoeae	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1545	981	63.5
Chlamydomphila psittaci 16S rRNA mutation conferring resistance to spectinomycin	2	77.5	Chlamydia psittaci 6BC	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1507	452	30.0
Mycobacterium chelonae 16S rRNA mutation conferring resistance to amikacin	2	78.1	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	543	37.7

Mycobacterium smegmatis 16S rRNA mutation in the rrsA gene conferring resistance to kanamycin A	2	80.7	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	1276	83.5
Borrelia burgdorferi 16S rRNA mutation conferring resistance to gentamicin	2	79.3	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	373	25.3
bacA	1	88.4	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene conferring antibiotic resistance via molecular bypass, peptide antibiotic resistance gene	823	305	37.1
tetL	1	97	Geobacillus stearothermophilus	protein homolog model	efflux pump conferring antibiotic resistance	1377	139	10.1
emrA	1	91.5	Escherichia coli str. K-12 substr. W3110	protein homolog model	efflux pump conferring antibiotic resistance	1174	181	15.4
cat	1	90.7	Campylobacter coli	protein homolog model	antibiotic inactivation enzyme, chloramphenicol resistance gene	624	240	38.5
mdtG	1	91.3	Escherichia coli str. K-12 substr. W3110	protein homolog model	efflux pump conferring antibiotic resistance	1228	356	29.0
tet32	1	79.7	Clostridiaceae bacterium K10	protein homolog model	tetracycline resistance gene, antibiotic target protection protein	1920	386	20.1
msbA	1	94.4	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1749	212	12.1
arnA	1	82.8	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene altering cell wall charge conferring antibiotic resistance, polymyxin resistance gene	1984	552	27.8
fyuA	1	98.5	Escherichia coli	protein homolog model	aminoglycoside resistance gene, tetracycline resistance gene	2022	137	6.8
CfxA2	1	90.1	Prevotella intermedia	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	967	113	11.7
tet40	1	93.2	Streptococcus suis	protein homolog model	efflux pump conferring antibiotic resistance	1222	774	63.3
mdtM	1	98	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1234	155	12.6
acrF	1	94.7	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	3106	327	10.5
mdtP	1	95.7	Escherichia coli str. K-12 substr. W3110	protein homolog model	efflux pump conferring antibiotic resistance	1467	1467	100.0

mel	1	90.9	Streptococcus pneumoniae Taiwan19F-14	protein homolog model	efflux pump conferring antibiotic resistance	1465	99	6.8
TEM-4	1	90.9	Klebsiella pneumoniae	protein homolog model	beta-lactam resistance gene, antibiotic inactivation enzyme	1061	516	48.6
mdtE	1	93.6	Escherichia coli str. K-12 substr. W3110	protein homolog model	antibiotic resistance gene cluster, cassette, or operon, efflux pump conferring antibiotic resistance	1159	577	49.8
tolC	1	89.7	Escherichia coli	protein homolog model	efflux pump conferring antibiotic resistance	1488	605	40.7
H-NS	1	98.7	Escherichia coli O157:H7 str. Sakai	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	415	79	19.0
mdtA	1	94.3	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1249	245	19.6
mdtF	1	94.6	Escherichia coli str. K-12 substr. MG1655	protein homolog model	antibiotic resistance gene cluster, cassette, or operon, efflux pump conferring antibiotic resistance	3115	262	8.4
gadW	1	90.8	Escherichia coli O25b:H4	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	729	261	35.8
APH(6)-Id	1	94.5	Pseudomonas aeruginosa	protein homolog model	aminoglycoside resistance gene, antibiotic inactivation enzyme	838	693	82.7
baeR	1	90.4	Escherichia coli str. K-12 substr. W3110	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	724	724	100.0
YojI	1	96	Escherichia coli str. K-12 substr. MG1655	protein homolog model	efflux pump conferring antibiotic resistance	1644	279	17.0
emrD	1	90.8	Escherichia coli B185	protein homolog model	efflux pump conferring antibiotic resistance	1191	211	17.7
kdpE	1	98.2	Escherichia coli str. K-12 substr. MG1655	protein homolog model	aminoglycoside resistance gene	678	221	32.6
evgS	1	91.9	Escherichia coli str. K-12 substr. MG1655	protein homolog model	gene modulating antibiotic efflux, efflux pump conferring antibiotic resistance	3595	628	17.5
Escherichia coli soxR mutants	1	89.6	Escherichia coli str. K-12 substr. MG1655	protein variant model	gene modulating antibiotic efflux, antibiotic resistant gene variant or mutant, efflux pump conferring antibiotic resistance	466	464	99.6
Escherichia coli acrR mutants resulting in antibiotic resistance	1	95	Escherichia coli str. K-12 substr.	protein variant model	gene modulating antibiotic efflux, antibiotic resistant gene variant or mutant, efflux	648	280	43.2

			MG1655		pump conferring antibiotic resistance			
Escherichia coli mutant GlpT conferring resistance to fosfomycin	1	88.1	Escherichia coli str. K-12 substr. MC4100	protein variant model	fosfomycin resistance gene, antibiotic resistant gene variant or mutant	1359	417	30.7
fosfomycin sensitive pyruvyl transferase (murA)	1	87.3	Escherichia coli str. K-12 substr. W3110	protein wild type model	NA	1282	396	30.9
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to G418	1	82.6	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	358	23.2
Mycobacterium abscessus 16S rRNA mutation conferring resistance to neomycin	1	89.2	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	150	10.0
Escherichia coli 16S rRNA mutation in the rrnB gene conferring resistance to spectinomycin	1	77	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	319	20.7
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to kanamycin A	1	79.2	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	330	21.4
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to viomycin	1	72.4	Mycobacterium tuberculosis H37Rv	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1537	1192	77.6
Borrelia burgdorferi 16S rRNA mutation conferring resistance to spectinomycin	1	76.6	Borrelia burgdorferi	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1477	317	21.5
Mycobacterium tuberculosis 16S rRNA mutation conferring resistance to amikacin	1	74.9	Mycobacterium tuberculosis H37Rv	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1537	1434	93.3
Escherichia coli 16S rRNA mutation in the rrsB gene conferring resistance to streptomycin	1	73.4	Escherichia coli K-12	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1542	496	32.2
Mycobacterium chelonae 16S rRNA mutation conferring resistance to gentamicin C	1	78.9	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	269	18.7
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to viomycin	1	82.1	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1528	202	13.2
Salmonella enterica serovar	1	70.6	Salmonella enterica	rRNA mutation	aminoglycoside resistance gene, antibiotic	1544	311	20.1

Typhimurium 16S rRNA mutation in the rrsD gene conferring resistance to spectinomycin			subsp. salamae	model	resistant gene variant or mutant			
Mycobacterium abscessus 16S rRNA mutation conferring resistance to gentamicin	1	79.3	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	439	29.2
Neisseria meningitidis 16S rRNA mutation conferring resistance to spectinomycin	1	82.3	Neisseria meningitidis	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1544	238	15.4
Escherichia coli 16S rRNA mutation conferring resistance to edeine	1	80.4	Escherichia coli K-12	rRNA mutation model	polyamine resistance gene, antibiotic resistant gene variant or mutant, peptide antibiotic resistance gene	1542	231	15.0
Mycobacterium abscessus 16S rRNA mutation conferring resistance to amikacin	1	74.9	Mycobacterium abscessus	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1504	551	36.6
Mycobacterium chelonae 16S rRNA mutation conferring resistance to tobramycin	1	79.5	Mycobacterium	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1441	323	22.4
Mycobacterium smegmatis 16S rRNA mutation in the rrsB gene conferring resistance to neomycin	1	83.4	Mycobacterium smegmatis str. MC2 155	rRNA mutation model	aminoglycoside resistance gene, antibiotic resistant gene variant or mutant	1528	167	10.9

Table S7. Antibiotics and related resistance genes and mechanisms against them.

Antibiotics	Mechanisms	Target	Effective	Resistance genes
Beta-lactam	Inhibit Cell wall synthesis	Peptidoglycan cross-linking	Gram-positive	PBP2x, PBP1a, PBP2b, etc
Fosfomycin	Inhibit Cell wall synthesis	MurA	Broad-spectrum	murA, etc
Aminoglycoside	Inhibit Protein synthesis	30S ribosomal subunit	Gram-negative	16S rRNA, etc
Tetracycline	Inhibit Protein synthesis	30S ribosomal subunit	Broad-spectrum	tetM, tetQ, tetW, etc
Macrolide	Inhibit Protein synthesis	50S ribosomal subunit	Gram-positive	ErmF, ErmG, RlmA(II), etc
Streptogramin	Inhibit Protein synthesis	50S ribosomal subunit	Gram-positive	ErmF, ErmG, etc
Mupirocin	Inhibit Protein synthesis	tRNA	Gram-positive	ileS
Fluoroquinolone	Inhibit nucleic acid synthesis	DNA	Broad-spectrum	gyrA, parC
Sulfonamide	Inhibit nucleic acid synthesis	Folic acid	Broad-spectrum	leuO, sul2
Trimethoprim	Inhibit nucleic acid synthesis	Folic acid	Gram-positive	dfrF

Table S8. Statistics and host-microbe interaction type assessment of unclassified reads predicted by BERTax.

Samples	Number of Archaea	Number of Viruses	Number of Eukaryota	Number of Bacteria	Harmful Bacteria	Number of Harmful Bacteria
Saliva1	65	218	612	504	NA	NA
Saliva2	1435	2595	6717	6354	NA	NA
Saliva3	1393	2952	5921	8253	Proteobacteria	1120
					Bacteroidetes	1633
Stool1	6690	10623	24300	49560	Firmicutes	21152
					Bacteroidetes	10244
Stool2	1873	3354	10014	13594	Bacteroidetes	3546