Figure S1

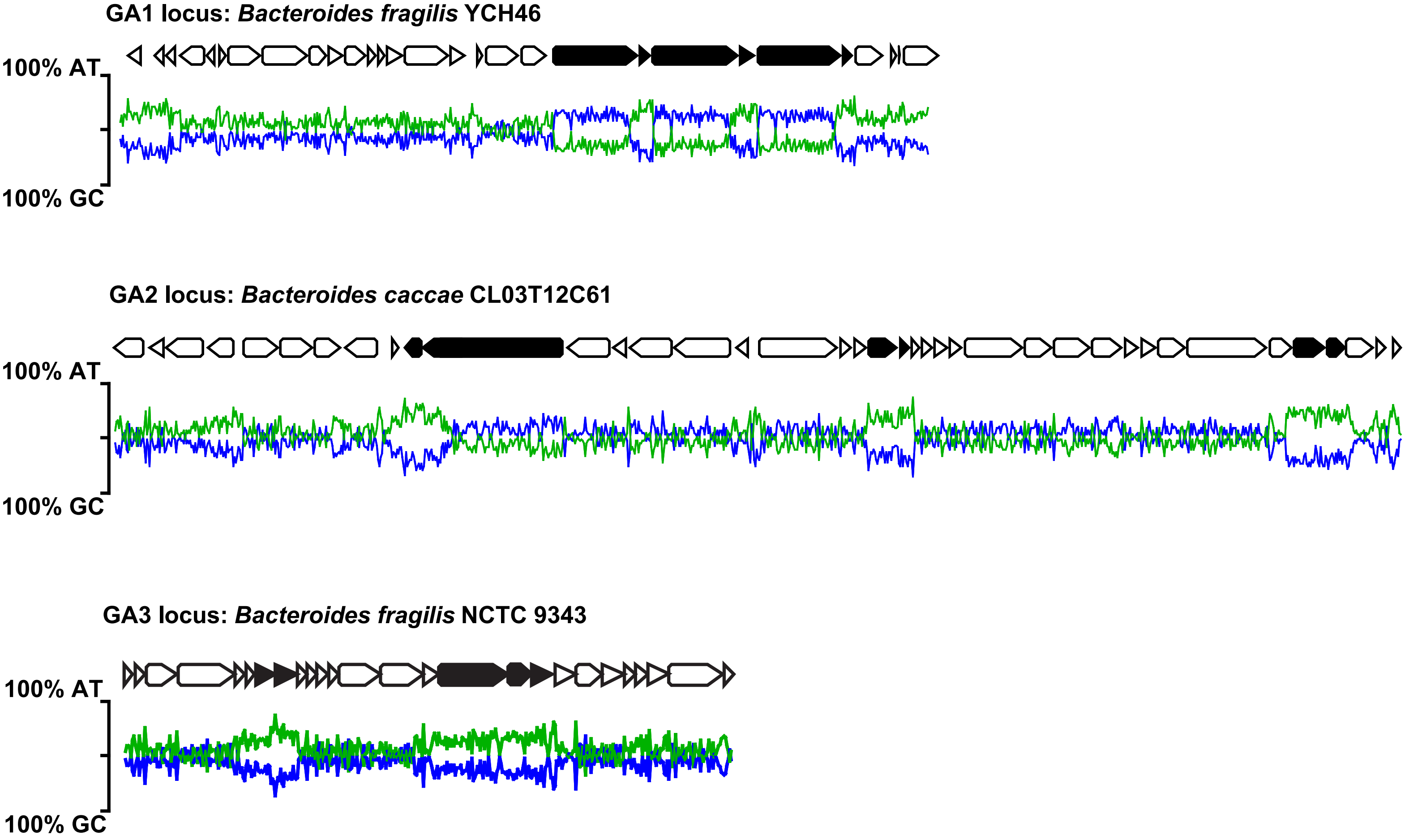

Figure S1. Genetic organization of the GA1-3 loci in Bacteroidales. Related to Figure 1. Schematic of the GA1, GA2, and GA3 loci. E–I genes are filled in with black, while structural genes are outlined. GC and AT content is plotted below the gene diagrams for each locus.

Figure S2

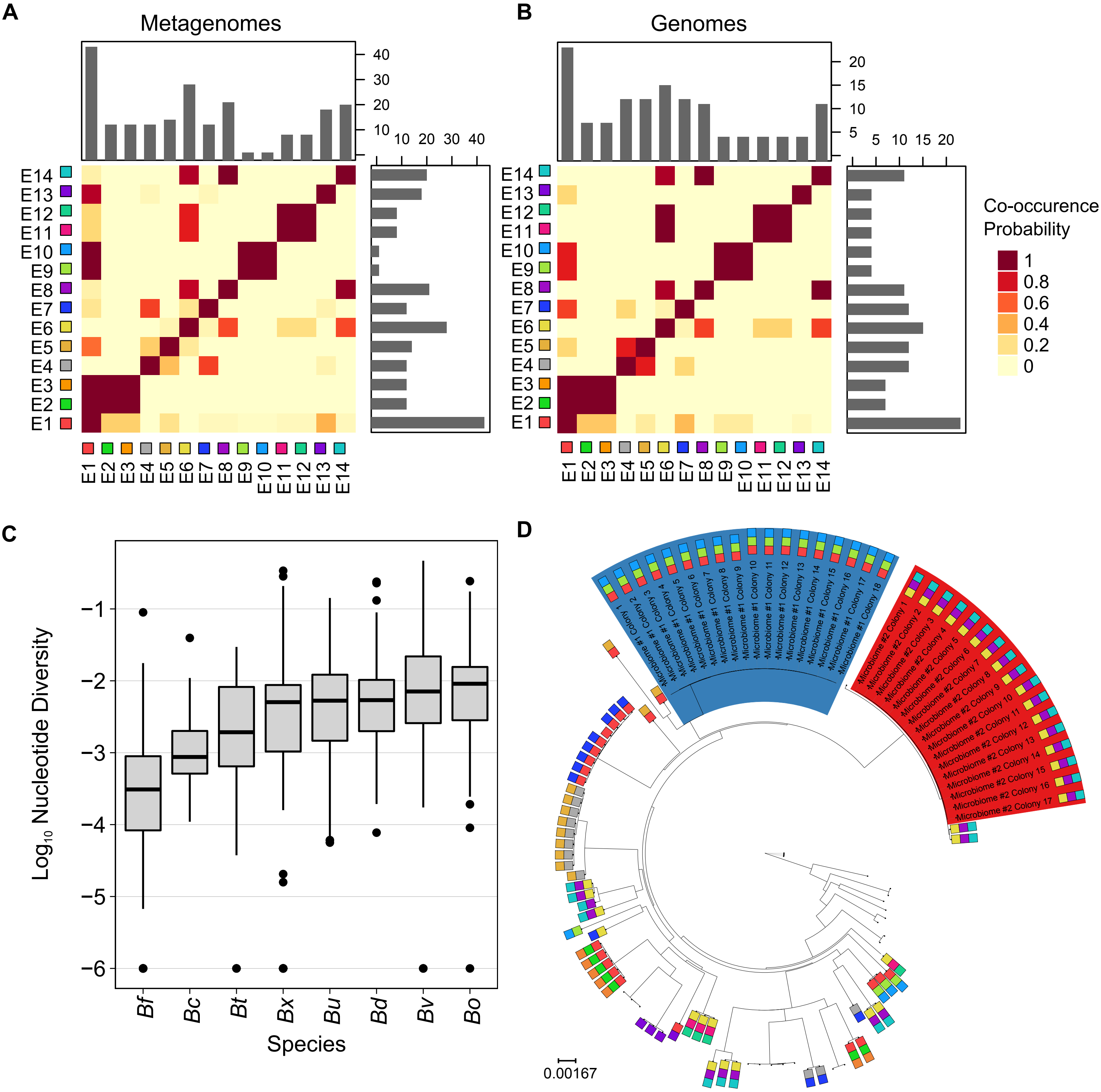

Figure S2. The co-occurrence of GA3 effector genes, and *Bacteroides* nucleotide and strain diversity in the gut microbiome of adults. Related to Figure 2.

(A-B) Each cell in the heatmap, a_{ij}, denotes the probability that effector gene i is detected in a metagenomic sample **(A)** or encoded in a genome **(B)** given that effector gene j was detected/encoded. The barplots on the top and right of each heatmap illustrate the number of metagenomes or genomes in which each effector gene was detected. **(C)** The nucleotide diversity for different Bacteroides spp. in adult samples from the HMP and MetaHIT studies. Nucleotide diversity was calculated based on population variants in species-specific marker genes (Experimental Procedures). Only species with at least 5 genomes in RefSeq were considered. *Bf:B. fragilis; Bc: B. cellulosilyticus; Bt: B. thetaiotaomicron; Bx: B. xylanisolvens; Bu: B. uniformis; Bd: B. dorei; Bv: B. vulgatus; Bo: B. ovatus*. **(D)** A phylogenetic tree linking previously sequenced *B. fragilis* reference genomes with sequenced colonies from two individuals (in red and blue). The effector genes encoded by each reference genome and the new sequenced genomes from stool are represented by colored squares as in Figure 1A.

Figure S3

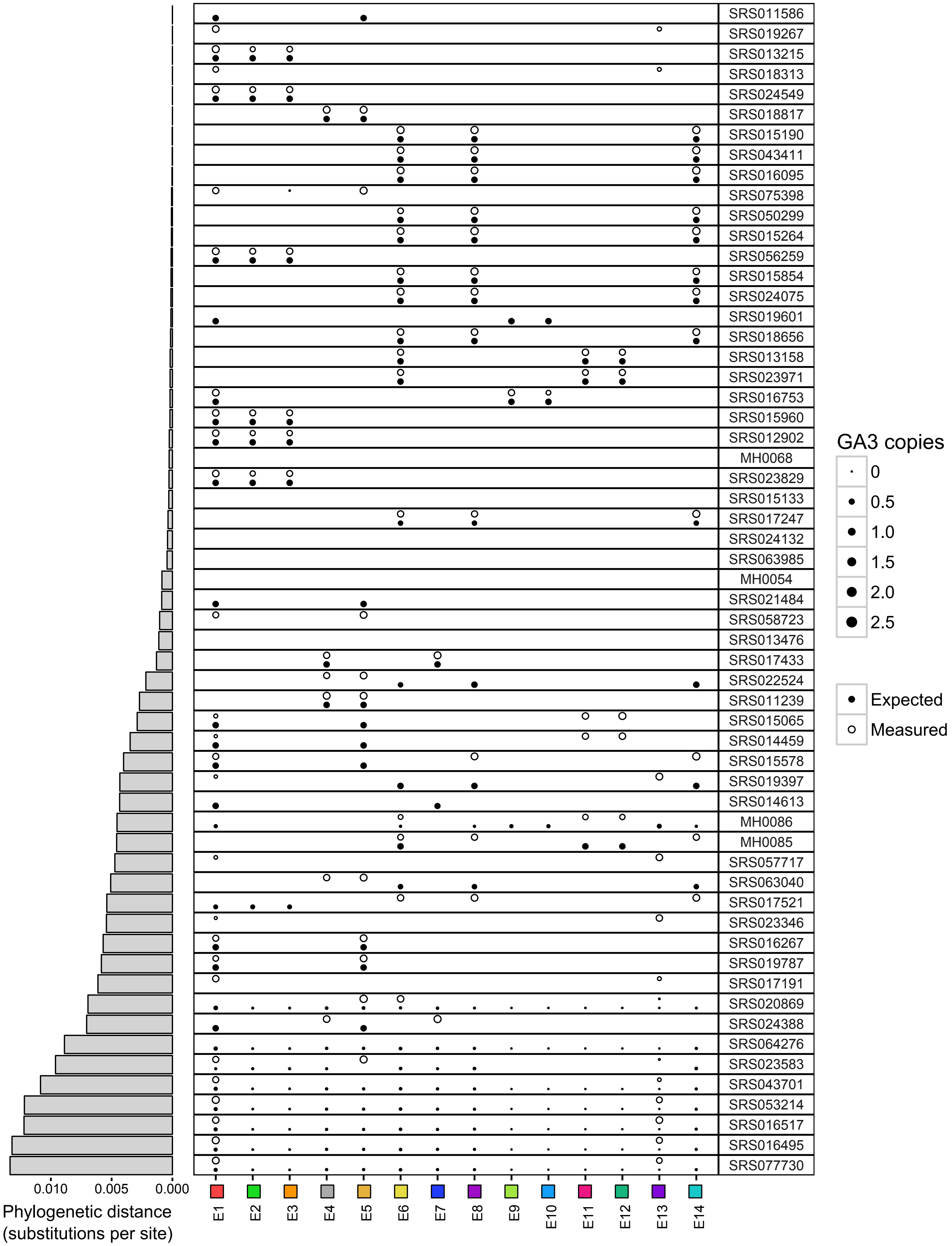

Figure S3. Measured and expected E–I gene abundances in HMP and MetaHIT samples. Related to Figure 2. Measured abundances (hollow circles) are based on short read mapping to effector genes. Expected abundances (filled circles) are based on the reference strains phylogenetically closest to the inferred strain. Point size is scaled to the calculated copy number of each effector. The barplot on the left shows the phylogenetic distance between the inferred strain and its nearest reference strain in the phylogenetic tree.

Figure S4

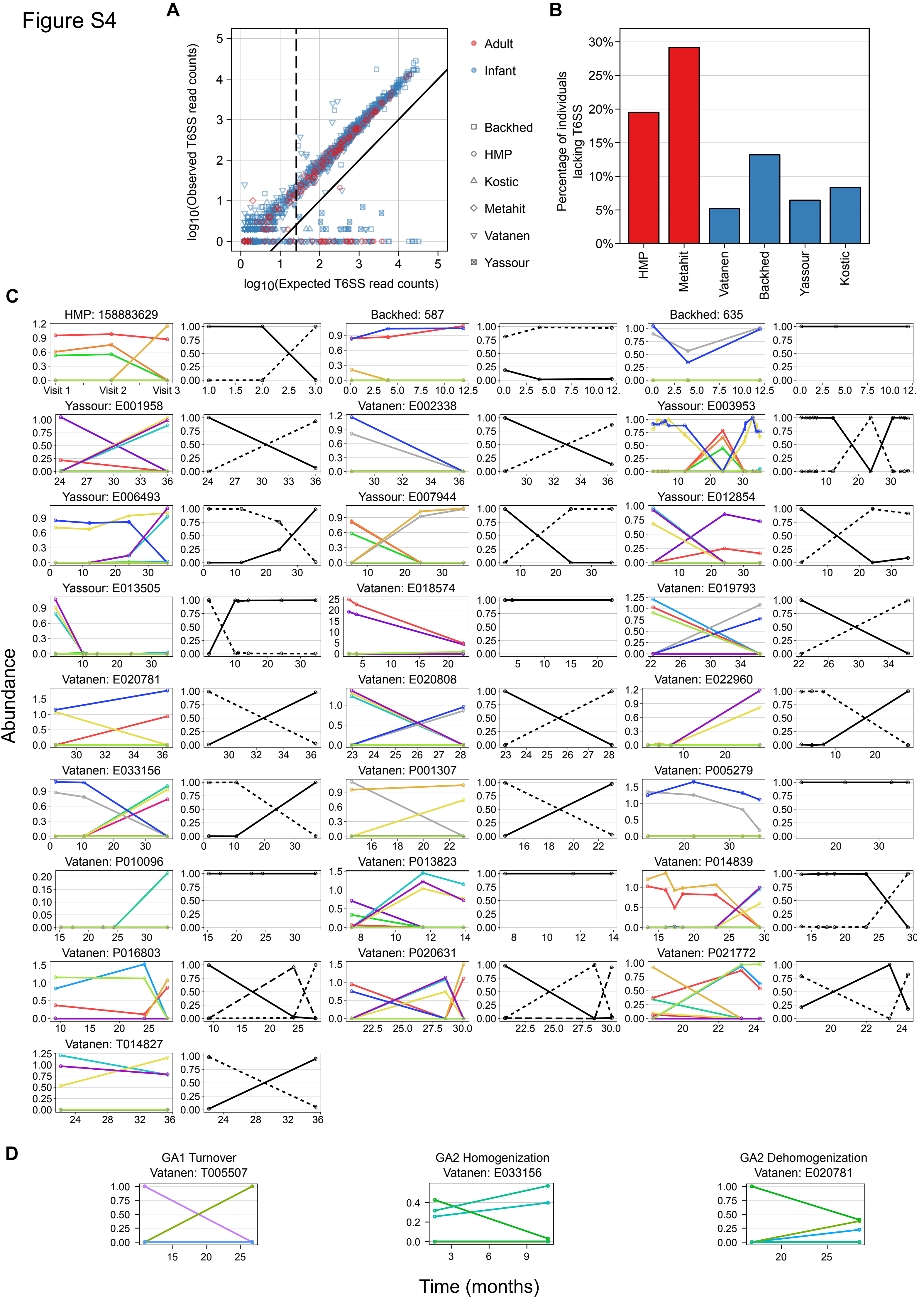
A
log10(Observed T6SS read counts)
log10(Expected T6SS read counts)
0
1
2
3
4
5
Adult
Infant
Backhed
HMP
Kostic
Metahit
Vatanen
Yassour
B
Percentage of individuals lacking T6SS
0%
5%
10%
15%
20%
25%
30%
HMP
Metahit
Vatanen
Backhed
Yassour
Kostic
C
HMP: 158883629
Visit 1
Visit 2
Visit 3
Backhed: 587
Backhed: 635
Yassour: E001958
Vatanen: E002338
Yassour: E003953
Yassour: E006493
Yassour: E007944
Yassour: E012854
Yassour: E013505
Vatanen: E018574
Vatanen: E019793
Vatanen: E020781
Vatanen: E020808
Vatanen: E022960
Vatanen: E033156
Vatanen: P001307
Vatanen: P005279
Vatanen: P010096
Vatanen: P013823
Vatanen: P014839
Vatanen: P016803
Vatanen: P020631
Vatanen: P021772
Vatanen: T014827
Abundance
D
GA1 Turnover
Vatanen: T005507
GA2 Homogenization
Vatanen: E033156
GA2 Dehomogenization
Vatanen: E020781
Time (months)

Figure S4. The prevalence of T6SS- samples and patterns of E-I turnover. Related to Figure 3.

(A) The prevalence of T6SS- samples in infants and adults as ascertained through the relationship between the number of reads expected and measured to map to the GA3 T6SS structural genes, from each adult (red) and infant (blue) gut microbiome sample. The expected number is based on the number of reads mapping to *B. fragilis*-specific marker genes, normalized by gene lengths. The dotted line represents the cutoff used for determining that *B. fragilis* is present in a sample. The solid line represents an observed number of reads that is 10% of expected, and was used to distinguish T6SS+ from T6SS- samples. As evident by this plot, T6SS+ and T6SS- samples can be clearly defined. Different shapes correspond to different datasets, with adult samples colored in red and infant samples in blue. **(B)** The percentage of individuals of those harboring B. fragilis, that lack the GA3 T6SS across different adult (red) and infant (blue) datasets. Individuals that were not consistent in terms of T6SS+/- classification across different time points were not included. **(C)** E–I turnover and strain replacement for GA3. Details and format are as in Figure 3C-E (top plots). Each pair of plots is labeled with the individual code and the dataset it comes from. **(D)** Analysis of GA1 and GA2 over time has demonstrated similar patterns to those observed for GA3, with most individuals exhibiting a conserved effector profile over time. Among the few individuals that exhibited different E-I profiles at different time points, we can observe examples of E-I turnover, E–I genotype homogenization (a decrease in diversity over time), and E-I genotype dehomogenization. Here the abundance on the y-axis refers to the relative abundance of GA1 or GA2 effector genes.

Table S1. Genus-level differential abundance in T6SS+ vs. T6SS- samples. Related to Figure 4.
Abundances are based on a 16S rRNA survey and only genera which are sufficiently abundant across T6SS+ vs. T6SS- samples are listed.

Genus	**Median Abundance T6SS+ (%)**	**Median Abundance T6SS- (%)**	**p-value**	**FDR Adjusted p-value**	**Passes FDR**
Faecalibacterium	3.8	10.6	8.30E-04	1.70E-02	TRUE
Bacteroides	57.9	37.5	3.10E-03	1.90E-02	TRUE
Ruminococcus	1.5	3.5	3.10E-03	1.90E-02	TRUE
Oscillospira	1.8	3.5	3.60E-03	1.90E-02	TRUE
Eubacterium	0.3	0.4	1.70E-02	7.20E-02	FALSE
Odoribacter	0.4	0.8	2.80E-02	9.80E-02	FALSE
Subdoligranulum	1.9	3.3	3.50E-02	1.10E-01	FALSE
Sutterella	2.4	0.1	7.60E-02	2.00E-01	FALSE
Dialister	1.2	0.7	1.10E-01	2.50E-01	FALSE
Clostridium	1.5	0.9	1.60E-01	3.20E-01	FALSE
Alistipes	5.7	6.7	1.80E-01	3.20E-01	FALSE
Coprococcus	0.5	0.6	1.80E-01	3.20E-01	FALSE
Akkermansia	0.1	0.3	2.20E-01	3.50E-01	FALSE
Lachnospira	0.7	0.7	2.60E-01	3.90E-01	FALSE
Parabacteroides	4.5	2.1	3.00E-01	4.20E-01	FALSE
Roseburia	1.5	2.7	4.50E-01	5.70E-01	FALSE
Blautia	0.9	0.5	4.60E-01	5.70E-01	FALSE
Megamonas	0.2	0	5.30E-01	6.20E-01	FALSE
Prevotella	0.1	0.3	6.00E-01	6.60E-01	FALSE
Phascolarctobacterium	0.8	0.8	8.00E-01	8.40E-01	FALSE
Escherichia	0.1	0.1	8.50E-01	8.50E-01	FALSE

Table S2. E–I gene catalog and reference strains used. Related to STAR Methods.

T6SS E–I accession numbers and locus tags are listed by genetic architecture subtype.
Reference strains used the study are listed in a separate sheet.

GA1

Effector #	Genome	Effector locus tag	Effector accession	Immunity #	Immunity locus tag	Immunity accesion
GA1_E1	*Bacteroides cellulosilyticus* CL02T12C19	HMPREF1062_03920	WP_007857070.1	GA1_I1	HMPREF1062_03918	WP_004323409.1
GA1_E2	*Parabacteroides* sp. D25	HMPREF0999_RS10520	WP_008669247.1	GA1_I2	HMPREF0999_RS10515	WP_008669248.1
GA1_E3	*Bacteroides coprophilus* DSM 18228	BACCOPRO_01421	WP_008141979.1	GA1_I3	BACCOPRO_01420	WP_008141977.1
GA1_E4	*Bacteroides fragilis* YCH46	BF2847	YP_100131.1	GA1_I4	BF2849	YP_100132.1
GA1_E5	*Bacteroides fragilis* YCH46	BF2850	YP_100133.1	GA1_I5	BF2851	YP_100134.1
GA1_E6	*Bacteroides fragilis* YCH46	BF2852	YP_100135.1	GA1_I6	BF2853	YP_100136.1
GA1_E7	*Bacteroides* sp. 3_2_5	BSHG_RS0220345	WP_007857070.1	GA1_I7	BSHG_4301	WP_008659502.1
GA1_E8	*Bacteroides uniformis* CL03T00C23	HMPREF1072_RS17450	WP_005836806.1	GA1_I8	HMPREF1072_RS17445	WP_005836803.1
GA1_E9	*Bacteroides vulgatus* 3775 SL(B) 10 (iv)	M097_RS18140	WP_011203027.1	GA1_I9	M097_RS18145	WP_008776200.1

GA2

Effector #	Genome	Effector locus tag	Effector accession	Immunity #	Immunity locus tag	Immunity accession
GA2_E1	*Parabacteroides distasonis* CL03T12C09	HMPREF1075_RS12295	WP_036629059.1	GA2_I1	HMPREF1075_RS12300	WP_005858631.1
GA2_E2	*Bacteroides fragilis* CL05T00C42	HMPREF1079_RS08215	WP_005802593.1	GA2_I2	HMPREF1079_RS08220	WP_005802592.1
GA2_E3	*Bacteroides eggerthi* DSM 20697	BACEGG_RS01920	WP_004288712.1	GA2_I3	BACEGG_RS01915	WP_039953011.1
GA2_E4	*Bacteroides caccae* CL03T12C61	HMPREF1061_RS00705	WP_005682920.1	GA2_I4	HMPREF1061_RS00700	WP_005682921.1
GA2_E5	*Bacteroides caccae* CL03T12C61	HMPREF1061_RS00780	WP_005682903.1	GA2_I5	HMPREF1061_RS00775	WP_005682904.1
GA2_E6	*Bacteroides vulgatus* dnLKV7	C800_RS02355	WP_016271567.1	GA2_I6	C800_RS02360	WP_016271566.1
GA2_E7	*Bacteroides vulgatus* dnLKV7	C800_RS02310	WP_016271575.1	GA2_I7	C800_RS02305	WP_016271576.1
GA2_E8	*Bacteroides dorei* DSM17855	BACDOR_RS16910	WP_007832792.1	GA2_I8	BACDOR_RS16905	WP_007832794.1
GA2_E9	*Parabacteroides* sp. 20_3	HMPREF9008_RS04985	WP_007832792.1	GA2_I9	HMPREF9008_RS04990	WP_005858575.1
GA2_E10	*Parabacteroides* sp. 20_3	HMPREF9008_RS04905	WP_008778001.1	GA2_I10	HMPREF9008_RS04900	WP_008778000.1
GA2_E11	*Parabacteroides* sp. 20_3	HMPREF9008_RS23040	WP_008778764.1	GA2_I11	HMPREF9008_RS23045	WP_005942723.1
GA2_E12	*Parabacteroides* sp. 20_3	HMPREF9008_RS22995	WP_005942780.1	GA2_I12	HMPREF9008_RS22990	WP_005942781.1
GA2_E13	*Bacteroides vulgatus* dnLKV7	C800_RS02240	WP_016271588.1	GA2_I13	C800_RS02360	WP_016271589.1
GA2_E14	*Bacteroides dorei* DSM17855	BACDOR_RS22955	WP_007832756.1	GA2_I14	BACDOR_RS17020	WP_032935744.1
GA2_E15	*Parabacteroides distasonis* CL03T12C09	HMPREF1075_RS12175	WP_007832792.1	GA2_I15	HMPREF1075_RS12170	WP_005858587.1
GA2_E16	*Bacteroides caccae* CL03T12C61	HMPREF1061_RS00825	WP_005682893.1	GA2_I16	HMPREF1061_RS00830	WP_050554721.1
GA2_E17	*Bacteroides dorei* DSM17855	BACDOR_RS16955	WP_007832774.1	GA2_I17	BACDOR_RS16960	WP_032935753.1
GA2_E18	*Bacteroides fragilis* CL05T00C42	HMPREF1079_RS08170	WP_005802603.1	GA2_I18	HMPREF1079_RS08165	WP_005802605.1

GA3

Effector #	Genome	Effector locus tag	Effector accession	Immunity #	Immunity locus tag	Immunity accession
GA3_E1	*Bacteroides fragilis* 3774_T13	M117_RS11205	WP_008659774.1	GA3_I1	M117_RS0122600	WP_008659772.1
GA3_E2	*Bacteroides fragilis* 3774_T13	M117_RS11240	WP_008659750.1	GA3_I2	M117_RS11245	WP_008659758.1
GA3_E3	*Bacteroides fragilis* 3774_T13	M117_RS23385	WP_050444646.1	GA3_I3	M117_RS11255	WP_008659747.1
GA3_E4	*Bacteroides fragilis* DS-166	M074_RS10745	WP_025814153.1	GA3_I4	M074_RS10750	WP_025814152.1
GA3_E5	*Bacteroides fragilis* DS-166	M074_RS10800	WP_011202656.1	GA3_I5	M074_RS10805	WP_011202655.1
GA3_E6	*Bacteroides fragilis* NCTC 9343	BF9343_1937	WP_010992803.1	GA3_I6	BF9343_1936	WP_005787090.1
GA3_E7	*Bacteroides fragilis* NCTC 9343	BF9343_1928	WP_010992798.1	GA3_I7	BF9343_1927	WP_010992797.1
GA3_E8	*Bacteroides fragilis* J38-1	M068_RS11120	WP_032561265.1	GA3_I8	M068_2000	WP_005787075.1
GA3_E9	*Bacteroides fragilis* Korea_419	M065_RS13210	WP_032600880.1	GA3_I9	M065_2764	WP_005794673.1
GA3_E10	*Bacteroides fragilis* Korea_419	M065_RS13185	WP_005794682.1	GA3_I10	M065_2759	WP_005794684.1
GA3_E11	*Bacteroides fragilis* B1_(UDC16-1)	M069_RS16890	WP_009292151.1	GA3_I11	M069_2106	WP_009292150.1
GA3_E12	*Bacteroides fragilis* B1_(UDC16-1)	M069_RS31145	WP_050446922.1	GA3_I12	M069_2103	WP_032571500.1
GA3_E13	*Bacteroides fragilis* DS-71	M073_RS11420	WP_032589942.1	GA3_I13	M073_1832	WP_032562840.1
GA3_E14	*Bacteroides fragilis* HMW616	HMPREF1205_RS15360	WP_005819888.1	GA3_I14	HMPREF1205_03575	WP_005819890.1

Genome	Strain	Assembly	GenBank FTP
Bacteroides cellulosilyticus	WH2	GCA_001318345.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001318345.1_ASM131834v1
Bacteroides cellulosilyticus	DSM 14838	GCA_000158035.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000158035.1_ASM15803v1
Bacteroides cellulosilyticus	CL02T12C19	GCA_000273015.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273015.1_Bact_cell_CL02T12C19_V1
Bacteroides cellulosilyticus	WH2	GCA_000463315.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000463315.1_B_cell_WH2_1.0
Bacteroides cellulosilyticus	CL09T06C25	GCA_001535595.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001535595.1_ASM153559v1
Bacteroides dorei	DSM 17855	GCA_000156075.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000156075.1_ASM15607v1
Bacteroides dorei	5_1_36/D4	GCA_000158335.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000158335.2_Bact_dorei_5_1_36_D4_V2
Bacteroides dorei	CL02T00C15	GCA_000273035.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273035.1_Bact_dore_CL02T00C15_V1
Bacteroides dorei	CL02T12C06	GCA_000273055.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273055.1_Bact_dore_CL02T12C06_V1
Bacteroides dorei	CL03T12C01	GCA_000273075.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273075.1_Bact_dore_CL03T12C01_V1
Bacteroides dorei		GCA_000738045.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000738045.1_ASM73804v1
Bacteroides dorei		GCA_000738065.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000738065.1_ASM73806v1
Bacteroides dorei		GCA_001274835.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001274835.1_ASM127483v1
Bacteroides ovatus	ATCC 8483	GCA_001314995.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001314995.1_ASM131499v1
Bacteroides ovatus	ATCC 8483	GCA_000154125.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000154125.1_ASM15412v1
Bacteroides ovatus	3_8_47FAA	GCA_000218325.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000218325.1_Bact_ovat_3_8_47FAA_V1
Bacteroides ovatus	CL02T12C04	GCA_000273195.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273195.1_Bact_ovat_CL02T12C04_V1
Bacteroides ovatus	CL03T12C18	GCA_000273215.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273215.1_Bact_ovat_CL03T12C18_V1
Bacteroides ovatus	KLE1656	GCA_001578575.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001578575.1_ASM157857v1
Bacteroides ovatus	SD CMC 3f	GCA_000178275.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000178275.1_ASM17827v1
Bacteroides ovatus	3725 D9 iii	GCA_000699665.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699665.1_ASM69966v1
Bacteroides ovatus	3725 D1 iv	GCA_000699725.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699725.1_ASM69972v1
Bacteroides ovatus	CL09T03C03	GCA_001535615.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001535615.1_ASM153561v1
Bacteroides thetaiotaomicron	VPI-5482	GCA_000011065.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000011065.1_ASM1106v1
Bacteroides thetaiotaomicron	7330	GCA_001314975.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001314975.1_ASM131497v1
Bacteroides thetaiotaomicron	dnLKV9	GCA_000403155.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000403155.2_Bact_thet_dnLKV9_V1
Bacteroides thetaiotaomicron	KLE1254	GCA_001578565.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001578565.1_ASM157856v1
Bacteroides thetaiotaomicron	2e6A	GCA_001373135.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001373135.1_2e6A_assembly
Bacteroides thetaiotaomicron	19_BTHE	GCA_001055755.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001055755.1_ASM105575v1
Bacteroides thetaiotaomicron	3a5B	GCA_000937835.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000937835.1_3a5B_assembly
Bacteroides thetaiotaomicron		GCA_001049535.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001049535.1_3731
Bacteroides thetaiotaomicron		GCA_001049555.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001049555.1_7330
Bacteroides uniformis	CL03T00C23	GCA_000273785.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273785.1_Bact_unif_CL03T00C23_V1
Bacteroides uniformis	ATCC 8492	GCA_000154205.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000154205.1_ASM15420v1
Bacteroides uniformis	CL03T12C37	GCA_000273275.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273275.1_Bact_unif_CL03T12C37_V1
Bacteroides uniformis	dnLKV2	GCA_000403175.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000403175.2_Bact_unif_dnLKV2_V1
Bacteroides uniformis	KLE1607	GCA_001578555.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001578555.1_ASM157855v1
Bacteroides uniformis	3978 T3 ii	GCA_000699825.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699825.1_ASM69982v1
Bacteroides uniformis	3978 T3 i	GCA_000699885.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699885.1_ASM69988v1
Bacteroides uniformis	2a7B	GCA_000939155.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000939155.1_2a7B_assembly3
Bacteroides uniformis	2a3A	GCA_001403955.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001403955.1_2a7B_assembly2
Bacteroides vulgatus	ATCC 8482	GCA_000012825.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000012825.1_ASM1282v1
Bacteroides vulgatus	mpk	GCA_001412315.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001412315.1_ASM141231v1
Bacteroides vulgatus	CL09T03C04	GCA_000273295.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273295.1_Bact_vulg_CL09T03C04_V1
Bacteroides vulgatus	dnLKV7	GCA_000403235.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000403235.2_Bact_vulg_dnLKV7_V1
Bacteroides vulgatus	PC510	GCA_000178195.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000178195.1_ASM17819v1
Bacteroides vulgatus	3775 SL(B) 10 (iv	GCA_000699705.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699705.1_ASM69970v1
Bacteroides vulgatus	3775 SR(B) 19	GCA_000699845.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699845.1_ASM69984v1
Bacteroides vulgatus	3975 RP4	GCA_000699865.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000699865.1_ASM69986v1
Bacteroides xylanisolvens	CL03T12C04	GCA_000273315.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273315.1_Bact_xyla_CL03T12C04_V1
Bacteroides xylanisolvens	SD CC 1b	GCA_000178215.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000178215.1_ASM17821v1
Bacteroides xylanisolvens	SD CC 2a	GCA_000178295.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000178295.1_ASM17829v1
Bacteroides xylanisolvens		GCA_000577295.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000577295.1_SD_CC_1b
Bacteroides xylanisolvens		GCA_000577955.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000577955.1_SD_CC_2a
Bacteroides xylanisolvens	XB1A	GCA_000210075.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000210075.1_ASM21007v1
Bacteroides fragilis	YCH46	GCA_000009925.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000009925.1_ASM992v1
Bacteroides fragilis	638R	GCA_000210835.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000210835.1_ASM21083v1
Bacteroides fragilis	BOB25	GCA_000965785.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000965785.1_ASM96578v1
Bacteroides fragilis	BE1	GCA_001286525.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_001286525.1_BFBE1.1
Bacteroides fragilis	CL07T00C01	GCA_000263115.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000263115.1_Bact_frag_CL07T00C01_V1
Bacteroides fragilis	CL03T00C08	GCA_000273095.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273095.1_Bact_frag_CL03T00C08_V1
Bacteroides fragilis	CL03T12C07	GCA_000273115.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273115.1_Bact_frag_CL03T12C07_V1
Bacteroides fragilis	CL05T12C13	GCA_000273135.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273135.1_Bact_frag_CL05T12C13_V1
Bacteroides fragilis	CL07T12C05	GCA_000273155.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273155.1_Bact_frag_CL07T12C05_V1
Bacteroides fragilis	CL05T00C42	GCA_000273765.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000273765.1_Bact_frag_CL05T00C42_V1
Bacteroides fragilis	HMW 615	GCA_000297735.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000297735.1_Bact_frag_HMW_615_V1
Bacteroides fragilis	DCMOUH0042B	GCA_000724795.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000724795.1_DCMOUH0042B1.0
Bacteroides fragilis	2-F-2 #7	GCA_000598145.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598145.1_ASM59814v1

Bacteroides fragilis	3976T7	GCA_000598165.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598165.1_ASM59816v1
Bacteroides fragilis	3986T(B)10	GCA_000598185.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598185.2_ASM59818v2
Bacteroides fragilis	3988 T1	GCA_000598205.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598205.1_ASM59820v1
Bacteroides fragilis	3996 N(B) 6	GCA_000598225.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598225.1_ASM59822v1
Bacteroides fragilis	DS-166	GCA_000598245.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598245.1_ASM59824v1
Bacteroides fragilis	1007-1-F #8	GCA_000598265.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598265.1_ASM59826v1
Bacteroides fragilis	2-F-2 #5	GCA_000598285.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598285.1_ASM59828v1
Bacteroides fragilis	3774 T13	GCA_000598305.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598305.1_ASM59830v1
Bacteroides fragilis	3783N1-2	GCA_000598325.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598325.1_ASM59832v1
Bacteroides fragilis	3783N2-1	GCA_000598345.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598345.1_ASM59834v1
Bacteroides fragilis	3988T(B)14	GCA_000598365.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598365.1_ASM59836v1
Bacteroides fragilis	3998 T(B) 4	GCA_000598385.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598385.1_ASM59838v1
Bacteroides fragilis	34-F-2 #13	GCA_000598425.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598425.1_ASM59842v1
Bacteroides fragilis	3986 N(B)19	GCA_000598445.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598445.1_ASM59844v1
Bacteroides fragilis	3986 T(B)9	GCA_000598465.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598465.1_ASM59846v1
Bacteroides fragilis	3998T(B)3	GCA_000598485.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598485.1_ASM59848v1
Bacteroides fragilis	DS-208	GCA_000598505.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598505.1_ASM59850v1
Bacteroides fragilis	J-143-4	GCA_000598525.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598525.1_ASM59852v1
Bacteroides fragilis	1007-1-F #4	GCA_000598545.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598545.2_ASM59854v2
Bacteroides fragilis	3397 N2	GCA_000598565.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598565.1_ASM59856v1
Bacteroides fragilis	3725 D9(v)	GCA_000598585.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598585.1_ASM59858v1
Bacteroides fragilis	3783N1-8	GCA_000598605.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598605.1_ASM59860v1
Bacteroides fragilis	B1 (UDC16-1)	GCA_000598625.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598625.1_ASM59862v1
Bacteroides fragilis	J38-1	GCA_000598645.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598645.1_ASM59864v1
Bacteroides fragilis	S23 R14	GCA_000598665.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598665.1_ASM59866v1
Bacteroides fragilis	1007-1-F #10	GCA_000598685.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598685.2_ASM59868v2
Bacteroides fragilis	1009-4-F #10	GCA_000598705.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598705.1_ASM59870v1
Bacteroides fragilis	3719 T6	GCA_000598725.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598725.1_ASM59872v1
Bacteroides fragilis	S24L26	GCA_000598745.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598745.1_ASM59874v1
Bacteroides fragilis	S38L3	GCA_000598765.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598765.2_ASM59876v2
Bacteroides fragilis	I1345	GCA_000598785.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598785.2_ASM59878v2
Bacteroides fragilis	Ds-233	GCA_000598805.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598805.1_ASM59880v1
Bacteroides fragilis	2-F-2 #4	GCA_000598825.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598825.1_ASM59882v1
Bacteroides fragilis	3719 A10	GCA_000598845.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598845.1_ASM59884v1
Bacteroides fragilis	3-F-2 #6	GCA_000598865.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598865.1_ASM59886v1
Bacteroides fragilis	1007-1-F #9	GCA_000598885.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598885.1_ASM59888v1
Bacteroides fragilis	20793-3	GCA_000598905.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598905.1_ASM59890v1
Bacteroides fragilis	3397 N3	GCA_000598925.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598925.1_ASM59892v1
Bacteroides fragilis	3986 N(B)22	GCA_000598945.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598945.1_ASM59894v1
Bacteroides fragilis	3986 T(B)13	GCA_000598965.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598965.1_ASM59896v1
Bacteroides fragilis	A7 (UDC12-2)	GCA_000598985.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000598985.1_ASM59898v1
Bacteroides fragilis	S24L15	GCA_000599005.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599005.1_ASM59900v1
Bacteroides fragilis	S36L5	GCA_000599025.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599025.1_ASM59902v1
Bacteroides fragilis	S6R5	GCA_000599045.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599045.1_ASM59904v1
Bacteroides fragilis	3783N1-6	GCA_000599065.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599065.2_ASM59906v2
Bacteroides fragilis	DS-71	GCA_000599085.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599085.1_ASM59908v1
Bacteroides fragilis	S13 L11	GCA_000599105.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599105.1_ASM59910v1
Bacteroides fragilis	S36L11	GCA_000599125.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599125.1_ASM59912v1
Bacteroides fragilis	1007-1-F #7	GCA_000599145.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599145.2_ASM59914v2
Bacteroides fragilis	3397 T14	GCA_000599165.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599165.2_ASM59916v2
Bacteroides fragilis	3976T8	GCA_000599185.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599185.2_ASM59918v2
Bacteroides fragilis	Korea 419	GCA_000599205.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599205.1_ASM59920v1
Bacteroides fragilis	S6L3	GCA_000599225.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599225.1_ASM59922v1
Bacteroides fragilis	S6R6	GCA_000599245.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599245.1_ASM59924v1
Bacteroides fragilis	1007-1-F #3	GCA_000599265.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599265.1_ASM59926v1
Bacteroides fragilis	1009-4-F #7	GCA_000599285.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599285.2_ASM59928v2
Bacteroides fragilis	S23L24	GCA_000599305.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599305.1_ASM59930v1
Bacteroides fragilis	S24L34	GCA_000599325.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599325.1_ASM59932v1
Bacteroides fragilis	S36L12	GCA_000599345.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599345.1_ASM59934v1
Bacteroides fragilis	S38L5	GCA_000599365.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599365.1_ASM59936v1
Bacteroides fragilis	S6L8	GCA_000599385.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000599385.1_ASM59938v1
Bacteroides fragilis	1007-1-F #5	GCA_000601035.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000601035.1_ASM60103v1
Bacteroides fragilis	S23L17	GCA_000601055.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000601055.1_ASM60105v1
Bacteroides fragilis	S6R8	GCA_000601075.2	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000601075.2_ASM60107v2
Bacteroides fragilis	1007-1-F #6	GCA_000601095.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000601095.1_ASM60109v1
Bacteroides fragilis	3986 N3	GCA_000601115.1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA_000601115.1_ASM60111v1