

Table S1: Sequencing metrics summary and *Fukatsuia symbiotica* strain comparison. bp, base pairs; CDS, coding sequence; ncRNA, non-coding RNA; rRNA, ribosomal RNA; tRNA, transfer RNA; tmRNA, transfer-messenger RNA; TE, transposable element. Pseudo in parenthesis indicates the number of CDSs, Fragmented CDS = pseudo.

	Fukatsuia Ap5D					Fukatsuia Ci			
	Chromosome	pFS5D.1	pFS5D.2	pFS5D.3	Total	Chromosome	pFSCi.1	pFSCi.3	Total
Contigs	1	1	1	1	4	363	14	4	381
Size (bases)	2,824,275	148,330	91,928	67,451	3,131,984	2,601,933	136,288	56,360	2,794,581
G+C%	43.5	48.3	44.3	45.1	43.8	43.2	48.1	45	43.4
Circularization	Yes	Yes	No	No		No	No	No	
CDS (pseudo)	2,606 (160)	133 (17)	121 (9)	69 (3)	2929 (189)	2,616 (112)	126 (12)	58 (2)	2,800 (126)
Fragmented CDS	0	0	0	0	0	441	18	1	460
ncRNA	53	4	0	1	58	40	4	1	45
tRNA	48	0	0	0	48	41	0	0	41
rRNA	5	0	0	0	5	6	0	0	6
tmRNA	1	0	0	0	1	1	0	0	1
Prophage island (CDS)	33 (489)	0	0	0		(436)			
Plasmid island (CDS)	2 (42)	0	0	0		(68)			
No. of reads	110,204								
N50 read length	27,056								
Mapped read	94,171								
Mean coverage	291								
Mean Read length	11,342								

Table S2:		
A. Reference genomes with NCBI BioProject numbers for sequences used in phylogeny		
No.	Reference genomes	BioProject
1	<i>Pasteurella dagmatis</i> NCTC11617	PRJEB6403
2	<i>Pasteurella multocida</i> Pm70	PRJNA39
3	<i>Escherichia coli</i> str. K-12	PRJNA57779
4	<i>Pantoea agglomerans</i> FDAARGOS 407	PRJNA231221
5	<i>Sodalis pierantonius</i> SOPE	PRJNA34865
6	<i>Pectobacterium carotovorum</i> LMG21371	PRJNA259701
7	<i>Serratia marcescens</i> WW4	PRJNA88659
8	<i>Serratia symbiotica</i> pea aphid Tucson	PRJNA59889
9	<i>Serratia symbiotica</i> black bean aphid	PRJEB6106
10	<i>Hafnia alvei</i> DSM30099	PRJNA236111
11	<i>Edwardsiella tarda</i> LADL99-302	PRJNA450491
12	<i>Xenorhabdus nematophila</i> AN6/1	PRJEB5061
13	<i>Xenorhabdus bovienii</i> SS-2004	PRJNA13399
14	<i>Photorhabdus asymbiotica</i> ATCC 43949	PRJEA30577
15	<i>Photorhabdus temperata</i> Hm	PRJNA282823
16	<i>Yersinia pestis</i> CO92	PRJNA57621
17	<i>Yersinia entomophaga</i> MH96T	PRJNA267025
18	<i>Hamiltonella defensa</i> pea aphid 5AT	PRJNA31259
19	<i>Hamiltonella defensa</i> pea aphid A2C	PRJNA345370
20	<i>Hamiltonella defensa</i> pea aphid ZA17.	PRJNA345370
21	<i>Hamiltonella defensa</i> whitefly MED	PRJNA80993
22	<i>Regiella insecticola</i> pea aphid LSR1	PRJNA39723
23	<i>Regiella insecticola</i> green peach aphid 5.15	PRJNA65437
24	<i>Fukatsuia symbiotica</i> pea aphid 5D	PRJNA388070
25	<i>Fukatsuia symbiotica</i> lachninae aphid Ci	PRJEB15504
B. Models of sequence evolution for each locus used in phylogenetic analysis: JTT+I+G4 for <i>dnaA</i> ; JTT+G4 for <i>rpoS</i> ; LG+I+G4 for <i>accD</i> , <i>gyrB</i> , <i>murE</i> , <i>ptsI</i> and <i>recJ</i> .		

Table S3: Energy, carbohydrate metabolism, amino acid and vitamin/cofactor synthesis in aphid symbionts: green = present, white = absent, orange = pseudogene

Symbiont species		<i>H. defensa</i>	<i>R. insecticola</i>		<i>Fukatsuia</i>	
strains		Pan-genome	LSR1	5.15	Ci	Ap5D
Energy metabolism						
NAD phosphorylation	<i>nadK</i>					
	<i>pfkA</i>					
ATP synthase	<i>atpC</i>					
	<i>atpD</i>					
	<i>atpG</i>					
	<i>atpA</i>					
	<i>atpH</i>					
	<i>atpF</i>					
	<i>atpE</i>					
	<i>atpB</i>					
	<i>nuoA</i>					
	<i>nuoB</i>					
	<i>nuoC</i>					
	<i>nuoE</i>					
	<i>nuoF</i>					
	<i>nuoG</i>					
	<i>nuoH</i>					
	<i>nuoI</i>					
	<i>nuoJ</i>					
	<i>nuoK</i>					
	<i>nuoL</i>					
NADH dehydrogenase I	<i>nuoM</i>					
NADH dehydrogenase II	<i>ndh</i>					
Na(+)-translocating NADH-quinone oxidoreductase	<i>nqrA</i>					
	<i>nqrB</i>					
	<i>nqrC</i>					
	<i>nqrD</i>					
	<i>nqrE</i>					
	<i>nxfF</i>					
	<i>rfmA</i>					
	<i>rfmB</i>					
	<i>rfmC</i>					
	<i>rfmD</i>					
	<i>rfmE</i>					
	<i>rfmG</i>					
Electron Transport chain						
Cytochrome <i>b</i> terminal oxidase	<i>cyoA</i>					
	<i>cyoB</i>					
	<i>cyoC</i>					
	<i>cyoD</i>					
	<i>cyoE</i>					
cytochrome bd-I terminal oxidase	<i>cydA</i>					
	<i>cydB</i>					
	<i>cydX</i>					
Metabolism						
Glycolysis	<i>ytjC</i>					
	<i>pyk</i>					
	<i>fbaA</i>					
	<i>eno</i>					
	<i>pgk</i>					
	<i>pfkA</i>					
	<i>pgl</i>					
	<i>fbp</i>					
	<i>tpiA</i>					
	<i>epd</i>					
	<i>gpm</i>					
	<i>gapA</i>					
	Acetate (from acetyl-CoA)	<i>pta</i>				
<i>ackA</i>						
Lactate (from pyruvate)	<i>pykF</i>					
	<i>ldhA</i>					
Pentose phosphate pathway	<i>rpE</i>					
	<i>gndA</i>					
	<i>tal</i>					
	<i>tkt</i>					
	<i>pgl</i>					
	<i>rpiA</i>					
	<i>zwf</i>					
TCA cycle	<i>glfA</i>					
	<i>acn</i>					
	<i>icd</i>					
	<i>sucA</i>					
	<i>sucB</i>					
	<i>sucC</i>					
	<i>sucD</i>					
	<i>sdhA</i>					
	<i>sdhB</i>					
	<i>sdhC</i>					
	<i>sdhD</i>					
	<i>fum</i>					
	<i>mdh</i>					
	<i>mon</i>					

Symbiont species		H. defensa	R. insecticola		Fukatsuia	
strains		Pan-genome	LSR 1	5.15	Ci	Ap5D
		Vitamin biosynthesis				
Vitamin B1 (Thiamine)	thiL					
	thiK					
	thiE					
	thiC					
	thiH					
	thiG					
	thiM					
	dxs					
	thiD					
	iscS					
thiFS						
Vitamin B2 (Riboflavin)	ribA					
	ribB					
	ribC					
	ribD					
	ribE					
	ribF					
Vitamin B3 (Niacin)	nadB					
	nadA					
	nadC					
	nadD					
	nadE					
Vitamin B6 (Pyridoxal)	Dxs					
	pdxA					
	pdxH					
	pdxJ					
	pdxB					
	Epd					
	serC					
Vitamin B7 (Biotin)	bioC					
	bioD					
	bioH					
	bioF					
	bioB					
	bioA					
	mioC					
Vitamin B9 (Folate)	folA					
	folB					
	folC					
	folD					
	folE					
	folK					
	folP					
	glyA					
	Lpd					
	pabA					
	pabB					
	pabC					
	purN					
		Vitamin transportation				
Vitamin B12 (Cobalamine)						
Vitamin B1 (Thiamine)	thiP					
	thiQ					
	tbpA					
Vitamin B5 (Pantothenic acid)	panF					
		Amino acid biosynthesis				
Chorismate	aroQ					
	aroC					
	aroE					
	aroK					
	aroA					
	aroB					
	aroH					
LYS	thrA					
	Asd					
	dapA					
	dapD					
	dapB					
	dapE					
	dapF					
THR	lysA					
	thrB					
	thrC					
ILE,VAL,LEU	thrA					
	ilvA					
	ilvE					
	ilvH					
	ilvD					
	ilvB					
	ilvC					
	leuA					
	leuB					
	leuC					
	leuD					

Symbiont species		<i>H. defensa</i>		<i>R. insecticola</i>		<i>Fukatsuia</i>	
strains		Pan-genome	LSR1	5.15	Ci	Ap5D	
Amino acid biosynthesis cont'd							
sGLY	glyA						
SER	serA						
	serB						
	serC						
CYS	cysE						
	cysK						
ASP	aspC						
PRO	proC						
ALA	iscS						
ASN	asnB						
GLU	putA						
PHE	pheA						
Amino acid transport							
MET	metI						
	metQ						
	metN						
GLY	glnH						
	glnP						
ARG	glnQ						
	artM						
	artQ						
	artL						
GLU/ASP	artP						
	gltS						
SER	gltL						
	gltJ						
CYS/GSH	cysA						
	cycC						
ILE,VAL,LEU	cycD						
	brnQ						
SER	sdaC						
PRO	putP						
PRO	proY						
LYS	lysP						
TYR	tyrP						
PHE,TYR,TRP	aroP						
Cofactor biosynthesis							
Isoprenoid	Dxs						
	Dxr						
	ispD						
	ispE						
	ispG						
	ispH						
	ispA						
	ispU						
Coenzyme A	ispB						
	coaA						
	coaBC						
	coaD						
	coaE						
Heme	hemB						
	hemH						
	cyoE						
	hemF						
	hemA						
	hemC						
	hemD						
	hemE						
	gltX						
	hemL						
Ubiquinone	hemN						
	hemG						
	ubiF						
	ubiD						
	ubiG						
	ubiA						
	ubiC						
	ubiF						
Spermidine	ubiE						
	ubiH						
	ubiB						
	ubiX						
	speD						
Putrescine	speE						
	aguA						
	aguB						
	speA						
Other transporters	speB						
	tolQ						
Protein	tolR						
	tolA						
	tolB						
	Pal						
Peptide	sapF						
	sapD						
	sapC						
	sapB						
Oligopeptide	sapA						
	oppF						
	oppD						
	oppC						
	oppB						

Symbiont species		H.defensa	R. insecticola		Fukatsuia	
strains		Pan-genome	LSR 1	5.15	Ci	Ap5D
Putresine	potG					
	potH					
	potI					
	potF					
phosphate	pstB					
	pstA					
	pstS					
	pstC					
K+/H+	kefC					
	kefG					
	kefB					
Zinc	znuB					
	znuC					
	znuA					
Iron/ Manganese	sitA					
	sitB					
	sitC					
	sitD					
Siderophore synthesis and transportation						
Aerobactin	iutA					
	iucA/					
	iucB					
	iucC					
Iron hydroxymate transporter	iucD					
	fhuC					
	fhuD					
	fhuE					
Flagella biosynthesis						
	flhA					
	flhB					
	flhR					
	flhQ					
	flhP					
	flhN					
	flhM					
	unk					
	flhE					
	flhF					
	flhG					
	flhH					
	flhI					
	flhJ					
	flgN					
	flgA					
	flgB					
	flgC					
	flgD					
	flgE					
	flgF					
	flgG					
	flgH					
	flgI					
	flgJ					
	flgK					
	flgL					
	flaA					
	flaC					
	lafA					
	flaD					
	flaS					
	lafD					
	fliK					
	flaL					
	flaA					
	motA					
	motB					

TableS4. Annotation file: large, so included as separate document.

Table S5. Plasmid-associated factors of interest in <i>Fukatsuia</i> Ap5D		
pFS5D.1		
Type IV	CCS41_13650, CCS41_13665, CCS41_13685, CCS41_13700, CCS41_13705, CCS41_13720, CCS41_13725, CCS41_13735, CCS41_13740, CCS41_13745, CCS41_13750, CCS41_13755, CCS41_13770, CCS41_13790, CCS41_13795, CCS41_13800, CCS41_13810	<i>tra</i> and <i>pil</i>
Type I	CCS41_14030, CCS41_14035, CCS41_14040	TolC, HylD
RTX toxin	CCS41_14170, CCS41_14175	
Toxin and antitoxin	CCS41_13670, CCS41_13675, CCS41_13780, CCS41_13825, CCS41_14240, CCS41_13785	VapC/VapB toxin protein, toxin-antitoxin system YhaV, RelB/StbD replicon stabilization protein,
Quorum sensing	CCS41_14095	
Secondary metabolites	CCS41_13860, CCS41_13865, CCS41_13870, CCS41_13875, CCS41_13880, CCS41_13885, CCS41_13900, CCS41_13905, CCS41_13910	Non-ribosomal peptide synthase and transporter
pFS5D.2		
Type IV	CCS41_14395 CCS41_14400 CCS41_14405 CCS41_14410 CCS41_14415 CCS41_14420 CCS41_14425 CCS41_14430 CCS41_14435 CCS41_14440 CCS41_14445 CCS41_14480 CCS41_14490 CCS41_14495 CCS41_14505 CCS41_14510 CCS41_14525 CCS41_14580 CCS41_14585 CCS41_14590 CCS41_14600 CCS41_14805	<i>virB</i> and <i>pil</i>
pFS5D.3		
Type IV	CCS41_15020 CCS41_15035 CCS41_15040 CCS41_15045 CCS41_15050 CCS41_15055 CCS41_15060 CCS41_15065 CCS41_15080 CCS41_15085 CCS41_15090 CCS41_15100 CCS41_15120 CCS41_15125 CCS41_15130	<i>tra</i>

Table S6: Summary of phage and plasmid islands in *Fukatsuia* Ap5D

		start	stop	length	G+C	total CDS	Description
Phage island on chromosome							
group 1	Lambda-like viruses	73103	90769	17667	43.8	27	Phage protein, integrase, exonuclease, transcription regulator, antiterminator, primosomal protein, LexA family transcriptional repressor
group 2	Unclassified	102549	102818	270	41.9	1	Phage, capsid and scaffold
group 3	Unclassified	222522	222943	425	46.8	2	Phage integrase, hypothetical protein
group 4	Myoviridae	310569	332339	21770	48.6	31	lysozyme, phage structural proteins, phage replication proteins, antitoxin, terminase, transcription regulator
group 5	Unclassified	363084	365578	2458	43.6	4	Repressor protein, primosomal protein, hypothetical proteins
group 6	Unclassified	370123	370524	401	42.8	1	Repressor protein
group 7	Lamda like HK639	386018	410341	24447	49	29	structural proteins cold shock protein, Phage protein, terminase, lysozyme, transcription regulator, DNA binding proteins, 62kDa structural proteins
group 8	Unclassified	421839	424376	2537	43.2	5	Phage protein, phage lysin, antitermination, putative membrane proteins
group 9	Unclassified	493073	496897	3824	41.4	5	Excisionase, integrase, phage antirepressor transcriptional regulator
group 10	Unclassified	510823	515038	4215	41.5	6	Excisionase, integrase, phage antirepressor, transcription regulator
group 11	Unclassified	521865	527759	5894	42.4	7	Excisionase, integrase, phage antirepressor, transcription regulator
group 12	Lambda-like HK639	535585	563526	27941	45.8	39	Excisionase, integrase, phage antirepressor, transcription regulator, P22 coat protein, excisionase, integrase
group 13	Unclassified	605374	609695	4321	41.8	7	Excisionase, integrase, phage antirepressor, transcription regulator
group 14	Siphoviridae	664601	682850	18250	47.4	27	Repressor protein, primosomal protein, excisionase, integrase, transcription regulator, toxin HlgB2, lysozyme, terminase, VapC toxin
group 15	Myoviridae like phages	705548	731665	26117	44.8	28	Tail proteins, excisionase, integrase, phage antirepressor, transcription regulator
group 16	Lambdavirus HK97	867733	883743	16010	44.6	19	Excisionase, integrase, transcription regulator
group 17	Unclassified	914375	915352	977	43.1	2	Lysozyme, phage out membrane protein
group 18	Unclassified	989946	997856	7910	41.7	10	Excisionase, integrase, phage antirepressor, transcription regulator
group 19	Unclassified	1005756	1008444	2688	50.1	2	Tail fiber protein
group 20	unclassified Siphoviridae	1141404	1166263	24859	45.8	34	Excisionase, integrase, phage antirepressor, transcription regulator, phage lysin
group 21	Unclassified	1192000	1192291	291	39.9	1	Prophage integrase
group 22	Unclassified	1203969	1210639	6670	43.3	10	Antiterminator, antitoxin YoeB, Orf33, transcription regulator
group 23	Lambda-like viruses HK639	1217744	1261059	43315	45.8	59	Repressor protein, phage lysin, transcription regulator, primosomal protein, Phage DNA binding Protein, antitermination, integrase,
group 24	Unclassified	1268782	1273173	4391	42.2	6	integrase, phage antirepressor, transcription regulator
group 25	Lambda-like viruses HK639	1299078	1318368	19288	49.7	26	Tail protein, phage protein, P22 coat protein
group 26	Unclassified	1329452	1332208	2756	44.5	4	Integrase, transcription regulator
group 27	Unclassified	1380171	1382511	2340	41.7	3	transcription regulator, Prophage integrase
group 28	Unclassified	1647826	1648530	706	44.7	1	Phage antitermination Q
group 29		1808728	1824855	16127	43.3	15	Tail protein, transcription regulator
group 30	Unclassified	2098739	2099797	1058	48	3	Phage lysin
group 31	Myoviridae_ ELPhiS	2116097	2148655	32558	46.8	45	Tail protein, tail protein, terminase, capsid protein, integrase,
group 32	Lambdavirus	2486434	2497888	11454	42.6	17	Phage replication, Prophage CP4-57, Transcription regulator
group 33	Myoviridae_partial	2580762	2597519	16757	45.6	15	Phage tail protein, baseplate protein, Phage protein
Plasmid island on chromosome							
group A	pS68-1 like plasmid (<i>A. salmonicida</i> strain S68)	2623403	2656289	32886	47.3	30	TraI, TraD, TraG, TraH, TraB, TrbC, TraU, TraW, TraC, TraV, TraK, TraL, AbrB family transcriptional regulator, addiction module toxin RelE, VapC toxin
group B	pXF-De_Donno like plasmid (<i>X. fastidiosa</i> subsp. pauca strain De Donno)	2543190	2555222	12032	45.6	12	TrbL, TrbB, TrbD, TrbE, TrbF, TrbG, TrbI, TrbJ, TrbL, RecA protein, C-terminal domain of Cin type S

Table S7: IS families in <i>Fukatsuia</i> Ap5D.					
IS families	Chromosome	pFS5D.1	pFS5D.2	pFS5D.3	All
IS630	139	8	1	3	151
IS5	42	3	2	0	47
IS4	21	3	0	3	27
Retron-type RNA-directed DNA polymerase	21	0	0	0	21
Tn3	21	7	11	5	44
IS481	18	0	0	1	19
ISNCY	13	0	0	0	13
IS110	12	0	1	1	14
IS200/IS605	12	2	0	0	14
IS701	11	1	0	0	12
IS21	10	0	0	0	10
Transposase	10	8	0	0	18
IS982	9	0	0	0	9
ISAs1	8	1	2	0	11
IS1	7	0	0	0	7
IS3	5	2	1	0	8
IS91	5	0	2	0	7
Mobile element protein	2	0	0	9	11
IS256	1	0	0	0	1
ISKra4	0	0	1	1	2

Table S8: Secretory systems in <i>Fukatsuia</i> Ap5D				<i>Fukatsuia</i>	
	Location	Locus tag	gene	Ci	Ap5D
Type I Secretory System					
T1SS	pFS5D.1	CCS41_14040	lapB	Pseudo	Pseudo
	Chromosome	CCS41_07385	rtxB		
	Chromosome	CCS41_07390	rtxD		
	Chromosome	CCS41_07395	rtxE		
Putative T1SS	pFS5D.1	CCS41_14020	Inner/exported protein		
	pFS5D.1	CCS41_14025	Membrane protein		
	pFS5D.1	CCS41_14030	lapE		
	pFS5D.1	CCS41_14035	lapC		
Putative ABC-TS	Chromosome	CCS41_12150	YrbA		
	Chromosome	CCS41_12155	YrbB		
	Chromosome	CCS41_12160	YrbC		
	Chromosome	CCS41_12165	YrbD		
	Chromosome	CCS41_12170	yrdE		
	Chromosome	CCS41_12175	yrdF		
Type II Secretory system					
	Chromosome	CCS41_12845	gspD	Pseudo	
	Chromosome	CCS41_12850	gspE		
	Chromosome	CCS41_12855	gspF		
	Chromosome	CCS41_12860	gspG		
	Chromosome	CCS41_12865	gspH		
	Chromosome	CCS41_12870	gspI		
	Chromosome	CCS41_12875	gspJ		
	Chromosome	CCS41_12880	gspK		
	Chromosome	CCS41_12885	gspL		
Type III Secretory System					
SPI	Chromosome	CCS41_07190	spaS		
	Chromosome	CCS41_07195	spaR		
	Chromosome	CCS41_07200	spaQ		
	Chromosome	CCS41_07205	spaP		
	Chromosome	CCS41_07210	spaO		
	Chromosome	CCS41_07215	spaN		
	Chromosome	CCS41_07220	spaM		
	Chromosome	CCS41_07225	speL/fliL		
	Chromosome	CCS41_07230	InvB/spaK		
	Chromosome	CCS41_07235	InvA		
	Chromosome	CCS41_07240	invF/Arc		
	Chromosome	CCS41_07245	invG		
	Chromosome	CCS41_07250	InvE		
	Chromosome	CCS41_07255	sicA		
	Chromosome	CCS41_07260	sipB		
	Chromosome	CCS41_07265	sipC		
	Chromosome	CCS41_07270	sipD		
	Chromosome	CCS41_08985	iagA		
	Chromosome	CCS41_08990	iagB		
	Chromosome	CCS41_08995	prgH		
	Chromosome	CCS41_09000	prgH		
	Chromosome	CCS41_09005	prgI		
	Chromosome	CCS41_09010	prgJ		
	Chromosome	CCS41_09015	orgB		
	Chromosome	CCS41_04400	orgA		

	Chromosome	CCS41_04405	prgK
	Chromosome	CCS41_04395	prgH
	Chromosome	CCS41_04980	SsaC
	Chromosome	CCS41_04985	SsaD
SPII	Chromosome	CCS41_05000	sseB
	Chromosome	CCS41_05005	SscA
	Chromosome	CCS41_05010	SscC
	Chromosome	CCS41_05015	HP
	Chromosome	CCS41_05020	SseE
	Chromosome	CCS41_05025	SscB
	Chromosome	CCS41_05030	HP
	Chromosome	CCS41_05035	CesD type/SscB
	Chromosome	CCS41_05040	SseF/HP
	Chromosome	CCS41_05045	SsaI
	Chromosome	CCS41_05050	SsaG
	Chromosome	CCS41_05055	SsaH
	Chromosome	CCS41_05060	EscI
	Chromosome	CCS41_05065	EscJ/SsaJ
	Chromosome	CCS41_05070	SsaL
	Chromosome	CCS41_05075	SsaK
	Chromosome	CCS41_05080	SsaO
	Chromosome	CCS41_05085	SsaM
	Chromosome	CCS41_05090	SsaV
	Chromosome	CCS41_05095	ssaN
	Chromosome	CCS41_05100	YscO
	Chromosome	CCS41_05105	Hp
	Chromosome	CCS41_05110	SsaQ
	Chromosome	CCS41_05115	SsaR
	Chromosome	CCS41_05120	SsaS
	Chromosome	CCS41_05125	SsaT
	Chromosome	CCS41_05130	SsaU
Type III effectors			
	Chromosome	CCS41_07400	Tir
	Chromosome	CCS41_02100	sifA
	Chromosome	CCS41_04975	ssaB(spiC)
	Chromosome	CCS41_04990	ssaE
Type IV Secretory System			
T4SS_F	Plasmid_island_2	CCS41_12705	traV
	Plasmid_island_2	CCS41_12710	traB
	Plasmid_island_2	CCS41_12715	traK
	Plasmid_island_2	CCS41_12720	traE
	Plasmid_island_2	CCS41_12725	traL
	Plasmid_island_2	CCS41_12650	traG
	Plasmid_island_2	CCS41_12655	traH
	Plasmid_island_2	CCS41_12665	traF
	Plasmid_island_2	CCS41_12680	trbC
	Plasmid_island_2	CCS41_12690	traW
T4SS_I	pFS5D.1	CCS41_13725	traR
	pFS5D.1	CCS41_13730	traQ
	pFS5D.1	CCS41_13735	traP
	pFS5D.1	CCS41_13740	traO
	pFS5D.1	CCS41_13745	traN
	pFS5D.1	CCS41_13770	traK

	pFS5D.1	CCS41 13795	traI	Pseudo
	pFS5D.1	CCS41 13755	traL	
	pFS5D.3	CCS41 15060	traR	
	pFS5D.3	CCS41 15085	traW	
	pFS5D.3	CCS41 15100	traY	
	pFS5D.3	CCS41 15040	traN	
	pFS5D.3	CCS41 15045	traO	
	pFS5D.3	CCS41 15050	traP	
	pFS5D.3	CCS41 15120	trbA	
	pFS5D.3	CCS41 15125	trbB	
T4SS_T	Plasmid island 1	CCS41 12190	virB11	Absent
	Plasmid island 1	CCS41 12195	virB2	
	Plasmid island 1	CCS41 12200	virB3	
	Plasmid island 1	CCS41 12210	virB8	
	Plasmid island 1	CCS41 12215	virB9	
	Plasmid island 1	CCS41 12230	virB5	
	Plasmid island 1	CCS41 12235	virB6	
	pFS5D.2	CCS41 14590	virB3	
T4P_putative	Chromosome	CCS41 09440	pilM	Pseudo
	Chromosome	CCS41 10570	pilAE	
	Chromosome	CCS41 11040	pilQ	
	Chromosome	CCS41 11205	pilT pilU	
	Chromosome	CCS41 11310	pilC	
	Chromosome	CCS41 11315	pilB	
	Chromosome	CCS41 11320	pilAE	
	Chromosome	CCS41 12895	pilD	
	pFS5D.1	CCS41 13650	pilT pilU	
	pFS5D.1	CCS41 13790	pilT pilU	
	pFS5D.2	CCS41 14505	pilT pilU	
	pFS5D.2	CCS41 14600	(VirB1)	Absent
Other T4SS	pFS5D.2	CCS41 14405	PilM	Absent
	pFS5D.2	CCS41 14480	PilN	Absent
	pFS5D.2	CCS41 14445	PilO	Absent
	pFS5D.2	CCS41 14440	PilP	Absent
	pFS5D.2	CCS41 14430	PilR	Absent
	pFS5D.2	CCS41 14420	PilS	Absent
	pFS5D.2	CCS41 14415	PilT	Absent
	pFS5D.2	CCS41 14805	PilT	Absent
	pFS5D.2	CCS41 14410	PilV	Absent
	pFS5D.2	CCS41 14495	VirD4	Absent
	pFS5D.2	CCS41 14510	(VirB10)	Absent
	pFS5D.2	CCS41 14585	(VirB4)	Absent
	pFS5D.2	CCS41 14580	(VirB5)	Absent
	pFS5D.2	CCS41 14535	(VirB6)	Absent
	pFS5D.2	CCS41 14530	(VirB8)	Absent
	pFS5D.2	CCS41 14525	(VirB9)	Absent
	Chromosome	CCS41 11320	PilA C;	Absent
	pFS5D.2	CCS41 14395	PilT	
	pFS5D.1	CCS41 13810	PilV	Absent
	pFS5D.2	CCS41 14400	prepilin peptidase	
	Plasmid island 2	CCS41 12700	traC	
	Plasmid island 2	CCS41 12605	traD	
	Plasmid island 2	CCS41 12600	traI	

	Plasmid island 2	CCS41 12670	TraN	Pseudo	
	pFS5D.1	CCS41 13695	TraX		
	pFS5D.3	CCS41 15090	TraX		
	Plasmid island 2	CCS41 12660	trbB		
	Chromosome	CCS41 12895	pilD		
	pFS5D.3	CCS41 15130	TrbC		
	Plasmid island 1	CCS41 12205	TrbE		
	Plasmid island 2	CCS41 12695	trbI		
	Plasmid island 1	CCS41 12225	TrbI		
T5aSS	Chromosome	CCS41 01380	T5aSS PF03797	Pseudo	Pseudo
	Chromosome	CCS41 10430	T5aSS PF03797		
	Chromosome	CCS41 02925	T5cSS PF03895		
	Chromosome	CCS41 10315	T5cSS PF03895		
T6SSi	Chromosome	CCS41 04625	T6SSi tssH		
T6SSii	Prophage island 33	CCS41 12435	T6SSiii tssE		
Tad	Chromosome	CCS41 11150	Tad tadZ		

Table S9: RTX toxins		<i>Fukatsuia</i>	
Location	Locus tag	Ci	Ap5D
Chromosome	CCS41_01045	Absent	
Chromosome	CCS41_02060		
Chromosome	CCS41_02070		
Chromosome	CCS41_02075		
Chromosome	CCS41_02080		
Chromosome	CCS41_02085		
Chromosome	CCS41_02090		
Chromosome	CCS41_02885	Pseudo	Pseudo
Chromosome	CCS41_02890		
Chromosome	CCS41_02905		
Chromosome	CCS41_03265		
Chromosome	CCS41_05135		
Chromosome	CCS41_06415		
Chromosome	CCS41_06860		
Chromosome	CCS41_06950	Pseudo	
Chromosome	CCS41_07175		
Chromosome	CCS41_07180		
Chromosome	CCS41_07860		
Chromosome	CCS41_07865		
Chromosome	CCS41_08760		
Chromosome	CCS41_08765		
Chromosome	CCS41_08855	Pseudo	
Chromosome	CCS41_08880		
Chromosome	CCS41_08885	Pseudo	
Chromosome	CCS41_08890		
Chromosome	CCS41_09875		
pFS5D.1	CCS41_14075		
pFS5D.1	CCS41_14170		

Table S10: Pathogenicity loci on main chromosome		<i>Fukatsuia</i>	
	Locus tag	Ci	Ap5D
Two-component system response regulator	CCS41_07825	Pseudo	Pseudo
	CCS41_07830		
Twin-arginine translocation pathway	CCS41_09075		
	CCS41_09080		
	CCS41_09085		
	CCS41_00505		
O antigen biosynthesis	CCS41_11820		
	CCS41_11825		
	CCS41_11830		
	CCS41_11835		
	CCS41_02025		
Tcc-tcd toxin complex	CCS41_02030		
	CCS41_02040		
	CCS41_02045		
	CCS41_05440		
MCf cytotoxin	CCS41_01725		
Toxin A	CCS41_01785		
Peptidase C80	CCS41_11685		
Peptidase C80	CCS41_11685		
Toxin B	CCS41_01670		
Toxin B	CCS41_01685		
CDT subunit B	CCS41_12575		
Peptidase	CCS41_10570		
	CCS41_10575		

Table S11: Methylated motifs detected in <i>Fukatsuia</i> Ap5D					
Motif	# Motifs in Genome	# Motifs Modified	% Motifs Modified	Type	Putative gene (REBASE)
G ^{m6} A <u>T</u> C	26436	25320	95.78%	Orphan	CCS41_11020 = N6-adenine DNA methyltransferase recognizing GATC
<u>T</u> GGCC ^{m6} A	1186	1073	90.47%	IIG (fused)	CCS41_07300 = Type IIG restriction enzyme/N6-adenine DNA methyltransferase recognizing TGGCCA

