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Supplemental Material to:

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The Ellis Island Effect: A novel mobile element in a multi-drug resistant *Bacteroides fragilis* clinical isolate includes a mosaic of resistance genes from Gram-positive bacteri

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Table S1: Primers used				
Primers used	**Associated locus tag**	**Sequence (5'-3')**	**Use**	**Position**
2377	BF638R_1255	TTTTCGTGTTGCTGTACCTGAAGAATGG	Used in PCR and sequencing	For Left end of CTnHyb
2378	BF615_00026-R	CAAAGTCCTTGCGAAGAACTCTTCTCCG	Used in PCR	For Left end of CTnHyb
2376	BF638R_1258-F	TGGAGACTATCGACGAAACACTGTGGC	Used in PCR	For Right end
2379	BF615_03037-R	CTGACGGATTTCTGCATCCTTACCTACG	Used in PCR	For Right end
2392	615_03040-41-F	GCACGAATCATAATTGCCCTGTAGG	Used in sequencing	For Right end
2378	BF615_00026-R	CAAAGTCCTTGCGAAGAACTCTTCTCCG	Used in PCR and sequencing	For the circle
2379	BF615_03037-R	CTGACGGATTTCTGCATCCTTACCTACG	Used in PCR	For the circle
2384	615_00015-F	GCTGGGGAGCGGACGCACTTGCGAGTGCCC	Used in PCR and sequencing	For popout 1
2385	615_02927-R	GAAGATGCAGTAGCCGAGGATGAAACCCGC	Used in PCR	For popout 1
2386	615_02928-F	CCATCTCGAAAACTCCTTCTCGCGCATGGG	Used in PCR and sequencing	For popout2
2387	615_02946_R	CTCCAGTTCGGGTATCTGCGTCTCCGAGCC	Used in PCR	For popout2

Table S2: Genes contained in CTnHyb

Gene	**Annotation** [1]	**Phyre2**			**RNA-seq Count** [2]	**STD DEV**
Locus Tag (NCBI designation)		**Confidence, Coverage (%)**				
HMPREF1204_00027	**Chaperone protein DnaK**				**6578.5**	**924.2**
HMPREF1204_00026	putative transposase				3.5	0.7
HMPREF1204_00025	tyrosine type site-specific recombinase				21	8.5
HMPREF1204_00024	transferase (monofunctional glycosyltransferase)	60	,	43	1	1.4
HMPREF1204_00023	transferase (monofunctional glycosyltransferase)	99	,	40	1.5	0.7
HMPREF1204_00022	putative excisionase				0	0.0
HMPREF1204_00021	P-loop containing nucleoside triphosphate hydrolases	100	,	64	26.5	6.4
HMPREF1204_00020	DNA primase (EC 2.7.7.-)				76	8.5
HMPREF1204_00019	DNA/RNA-binding 3-helical bundle	98	,	24	93	9.9
HMPREF1204_00018	transferase (lincosamide resistance protein)	95	,	23	73	7.1
HMPREF1204_00017	Ser/Thr protein phosphatase family protein				64	12.7
HMPREF1204_00016	Four-helical up-and-down bundle	10	,	18	4	0.0
HMPREF1204_00015	virus	46	,	26	4	2.8
HMPREF1204_00014	**Conjugative transposon protein TraE**				**9**	**1.4**
HMPREF1204_00013	transport protein	28	,	60	1.5	0.7
HMPREF1204_00012	integrase				64.5	4.9
HMPREF1204_00011	integrase				22	8.5
HMPREF1204_00010	excisionase family DNA binding domain-containing protein				0.5	0.7
HMPREF1204_00009	protein transport	41	,	17	3	4.2
HMPREF1204_00008	Integrase IntN1				9.5	3.5
HMPREF1204_00007	DNA/RNA-binding 3-helical bundle	96	,	17	12.5	0.7
HMPREF1204_00006	dna-binding protein	98	,	36	4	1.4
HMPREF1204_00005	hydrolase (mobilization protein A)	98	,	29	46	11.3
HMPREF1204_00004	membrane protein	52	,	72	122	2.8
HMPREF1204_00003	Maltose O-acetyltransferase (EC 2.3.1.79)				2062	175.4
HMPREF1204_00002	**Pyridoxamine; FMN-binding; nimJ (metronidazole resistance)**				**2979.5**	**306.2**
HMPREF1204_0001	transposase				51.5	7.8
HMPREF1204_02924	DNA-cytosine methyltransferase (EC 2.1.1.37)				35.5	13.4
HMPREF1204_02925	dna-binding protein (excisionase from transposon tn916)	27	,	11	12.5	0.7
HMPREF1204_02926	dna-binding protein	100	,	87	41	2.8
HMPREF1204_02927	transmembrane protein (colicin ia)	12	,	39	9.5	0.7
HMPREF1204_02928	**Conjugative transposon protein TraG**				**12.5**	**4.9**
HMPREF1204_02929	excisionase family DNA binding domain-containing protein				11	2.8
HMPREF1204_02930	mobilizable transposon, int protein				22	8.5
HMPREF1204_02931	excisionase				2	1.4
HMPREF1204_02932	transcriptional regulator	97	,	17	11.5	2.1
HMPREF1204_02933	dna-binding protein	97	,	38	1.5	0.7
HMPREF1204_02934	conserved hypothetical protein with relaxase/mobilization nuclease domain				4.5	2.1

HMPREF1204_02935	protein binding	78	,	65	1	0.0
HMPREF1204_02936	protein transport (synaptosomal-associated protein 23)	45	,	18	0.5	0.7
HMPREF1204_02937	recombination	100	,	93	25.5	6.4
HMPREF1204_02938	dna binding protein	100	,	58	26	1.4
HMPREF1204_02939	hydrolase	100	,	37	72.5	4.9
HMPREF1204_02940	hydrolase	67	,	6	138	11.3
HMPREF1204_02941	DNA-binding domain of Mlu1-box binding protein MBP1	98	,	31	68	12.7
HMPREF1204_02942	5-methylcytosine-specific restriction related enzyme				154	33.9
HMPREF1204_02943	Modification methylase HgaIA (Cytosine-specific methyltransferase HgaIA)				68	5.7
HMPREF1204_02944	Modification methylase HgaIA (Cytosine-specific methyltransferase HgaIA)				84.5	3.5
HMPREF1204_02945	dna binding protein	100	,	86	43.5	14.8
HMPREF1204_02946	**Conjugative transposon protein TraG**				**5**	**1.4**
HMPREF1204_02947	hypothetical protein				15.5	0.7
HMPREF1204_02948	alpha-Amylase inhibitor tendamistat	39	,	5	3	4.2
HMPREF1204_02949	transcription	36	,	41	3.5	2.1
HMPREF1204_02950	putative antirepressor				5.5	0.7
HMPREF1204_02951	ribosome	40	,	14	0.5	0.7
HMPREF1204_02952	ribosome	20	,	8	7.5	0.7
HMPREF1204_02953	ribosome	28	,	14	3	0.0
HMPREF1204_02954	**Conjugative transposon protein TraK**				**3.5**	**2.1**
HMPREF1204_02955	Mitochondrial import receptor subunit Tom20	44	,	29	3.5	2.1
HMPREF1204_02956	**Conjugative transposon protein TraM**				**13**	**1.4**
HMPREF1204_02957	**Conjugative transposon protein TraN**				**17**	**4.2**
HMPREF1204_02958	transferase	59	,	12	5.5	0.7
HMPREF1204_02959	structural genomics, unknown function	100	,	87	14.5	3.5
HMPREF1204_02960	structural genomics, unknown function	100	,	78	19.5	6.4
HMPREF1204_02961	Putative mobilization protein BF0133				32.5	2.1
HMPREF1204_02962	lysozyme - like/ phage lysozyme family	100	,	91	2	0.0
HMPREF1204_02963	Integrase	100	,	80	6	2.8
HMPREF1204_02964	**transposase**				**332**	**36.8**
HMPREF1204_02965	**Macrolide-efflux protein, *mefA***				**666.5**	**103.9**
HMPREF1204_02966	signaling protein	5	,	43	74	14.1
HMPREF1204_02967	hydrolase	32	,	17	236	9.9
HMPREF1204_02968	Transcriptional regulator, MerR family				8.5	2.1
HMPREF1204_02969	**APH phosphotransferases (kanamycin resistance)**	**100**	,	**100**	**38**	**9.9**
HMPREF1204_02970	transcriptional regulator, putative				3	2.8
HMPREF1204_02971	DNA/RNA-binding 3-helical bundle	100	,	75	21	4.2
HMPREF1204_02972	ABC transporter, ATP-binding protein				2.5	2.1
HMPREF1204_02973	membrane protein, putative				4	1.4
HMPREF1204_02974	hydrolase/ mobilization protein a	99	,	34	22	4.2
HMPREF1204_02975	Adenylate cyclase				17.5	6.4
HMPREF1204_02976	transcription regulator	99	,	42	69.5	2.1
HMPREF1204_02977	dna binding protein /dna / integrase	100	,	74	67.5	4.9
HMPREF1204_02978	Spectinomycin 9-O-adenylyltransferase				3	1.4
HMPREF1204_02979	transferase/ kanamycin nucleotidyltransferase	96	,	54	0.5	0.7
HMPREF1204_02980	Ubiquinone/menaquinone biosynthesis methyltransferase				3	1.4
HMPREF1204_02981	HD superfamily hydrolase				2	1.4
HMPREF1204_02982	transposase				607	21.2

HMPREF1204_02983	**GTP-binding protein TypA/BipA (tetracycline resistance)**			**607.5**	**29.0**
HMPREF1204_02984	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (rteA like)			53	4.2
HMPREF1204_02985	**multidrug efflux protein**			**296**	**76.4**
HMPREF1204_02986	**RND efflux system, inner membrane transporter CmeB**			**639**	**151.3**
HMPREF1204_02987	**outer membrane protein oprM precursor**			**178**	**31.1**
HMPREF1204_02988	Glucosamine--fructose-6-phosphate aminotransferase			38.5	4.9
HMPREF1204_02989	Magnesium transport protein CorA, transmembrane region	47	61	2	1.4
HMPREF1204_02990	gene regulation (zinc peptidase site)	100	40	1012.5	137.9
HMPREF1204_02991	Bacillus chorismate mutase-like/ L30e-like	66	37	208	8.5
HMPREF1204_02992	Cell wall endopeptidase, family M23/M37			16.5	4.9
HMPREF1204_02993	structural genomics, unknown function	61	24	15	1.4
HMPREF1204_02994	PEP carboxykinase N-terminal domain	80	68	1	0.0
HMPREF1204_02995	lyase	73	15	26	8.5
HMPREF1204_02996	transferase/ dna primase	100	89	10.5	0.7
HMPREF1204_02997	PH domain-like barrel	95	48	2.5	2.1
HMPREF1204_02998	Spectrin repeat-like/ PhoU-like	73	70	3.5	0.7
HMPREF1204_02999	viral protein/ fusion glycoprotein	43	48	3.5	3.5
HMPREF1204_03000	antimicrobial protein/ plnj	38	6	1.5	0.7
HMPREF1204_03001	putative cell wall endopeptidase family protein			8.5	0.7
HMPREF1204_03002	4-helical cytokines	63	11	16	4.2
HMPREF1204_03003	DNA mismatch repair protein MutS			23.5	9.2
HMPREF1204_03004	**putative hemagglutinin**			**13.5**	**6.4**
HMPREF1204_03005	transferase	17	18	0.5	0.7
HMPREF1204_03006	dna binding protein	99	87	8	2.8
HMPREF1204_03007	hydrolase/ probable dipeptidyl-peptidase 3	97	11	16	1.4
HMPREF1204_03008	structural genomics, unknown function	37	11	0	0.0
HMPREF1204_03009	Ribosomal protein S5 domain 2-like	17	22	1	1.4
HMPREF1204_03010	ATPase			70.5	0.7
HMPREF1204_03011	membrane protein	100	29	9	0.0
HMPREF1204_03012	transmembrane protein	98	76	7.5	0.7
HMPREF1204_03013	transcription, dna/ putative marr-family transcriptional repressor	94	31	2.5	2.1
HMPREF1204_03014	MHC antigen-recognition domain	36	20	1.5	0.7
HMPREF1204_03015	transcription regulator	42	20	3.5	2.1
HMPREF1204_03016	oxidoreductase (aldehyde(d)-nad(a))	41	47	2	2.8
HMPREF1204_03017	replication	48	14	17.5	0.7
HMPREF1204_03018	Serine type site-specific recombinase			79	22.6
HMPREF1204_03019	hydrolase	59	46	34.5	2.1
HMPREF1204_03020	Class II aaRS and biotin synthetases	30	34	41.5	16.3
HMPREF1204_03021	**Thioredoxin**			**13**	**8.5**
HMPREF1204_03022	cell cycle	94	62	18.5	7.8
HMPREF1204_03023	lyase/ fructose-bisphosphate aldolase class 1	50	51	9.5	4.9
HMPREF1204_03024	structural genomics, unknown function	81	18	12	4.2
HMPREF1204_03025	DNA/RNA-binding 3-helical bundle	51	50	3	1.4
HMPREF1204_03026	oxireductase/ thioredoxin h-type	43	41	5	1.4
HMPREF1204_03027	DNA/RNA-binding 3-helical bundle / "Winged helix" DNA-binding domain	97	95	5.5	3.5
HMPREF1204_03028	dna-binding protein	54	70	1.5	0.7
HMPREF1204_03029	MCP/YpsA-like	100	94	6.5	0.7

HMPREF1204_03030	putative ribose phosphate pyrophosphokinase				1	1.4
HMPREF1204_03031	dna-binding protein	96		46	1.5	0.7
HMPREF1204_03032	Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein				3	0.0
HMPREF1204_03033	Single-stranded DNA-binding protein				1.5	0.7
HMPREF1204_03034	viral protein/ superfamily gp37	99		58	0.5	0.7
HMPREF1204_03035	beta-Prism II / alpha-D-mannose-specific plant lectins	33		8	0.5	0.7
HMPREF1204_03036	metal binding protein (archaeal protein sso6904)	19		23	1.5	2.1
HMPREF1204_03037	Single-stranded DNA-binding protein				0	0.0
HMPREF1204_03038	virus (capsid protein gamma)	8		20	1.5	2.1
HMPREF1204_03039	SH3-like barrel	61		68	1.5	0.7
HMPREF1204_03040	viral protein (upper collar protein)	59		23	5	2.8

[1] Annotation in black is from the RAST server and in red from the Phyre2 fold recognition server. If the annotation is derived from Phyre2, the percent confidence and percent coverage are listed to the right.

[2] Average of two biological replicates