

Genomic Insights into Virulence Factors and Multi-Drug Resistance in *Clostridium perfringens* IRLC2505A

Supplementary Table S1: Assembly Details and annotated features of *Clostridium perfringens* IRLC2505A.

General Info	
Genome Name	<i>Clostridium perfringens</i> IRLC2505A
Taxonomy Info	
Taxon ID	1502
Superkingdom	Bacteria
Phylum	Firmicutes
Class	Clostridia
Order	Eubacteriales
Family	Clostridiaceae
Genus	<i>Clostridium</i>
Species	<i>Clostridium perfringens</i>
Status	
Genome Status	WGS
Genome Statistics	
Contigs	108
Genome Length	4322225
GC Content	28.275791
Contig L50	15
Contig N50	91957
Annotation Statistics	
tRNA	80
rRNA	7
CDS	4159
CDS Ratio	0.96223587
Hypothetical CDS	1411
Hypothetical CDS Ratio	0.4308728

PLFAM CDS	3608
PLFAM CDS Ratio	0.8675162
Genome Quality	
Coarse Consistency	99.6
Fine Consistency	94.5
CheckM Completeness	99.9
CheckM Contamination	12.3
Genome Quality	Good

Supplementary Table S2: List of antimicrobial resistance genes identified in the genome of *Clostridium perfringens* IRLC2505A.

	Source	Gene	Product/Function	Classification	Subject Coverage	Query Coverage	Identity	E-value*
1	PATRIC	<i>EF-G</i>	Translation elongation factor G	antibiotic target in susceptible species				
2	NDARO	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)		13	91	95	5e-40
3	PATRIC	<i>S12p</i>	SSU ribosomal protein S12p (S23e)	antibiotic target in susceptible species				
4	PATRIC	<i>EF-Tu</i>	Translation elongation factor Tu	antibiotic target in susceptible species				
5	PATRIC	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein				
6	PATRIC	<i>MurA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species				
7	PATRIC	<i>Alr</i>	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species				
8	PATRIC	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein				
9	PATRIC	<i>gidB</i>	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	gene conferring resistance via absence				
10	PATRIC	<i>gyrB</i>	DNA gyrase subunit B (EC 5.99.1.3)	antibiotic target in susceptible species				
11	PATRIC	<i>Iso-tRNA</i>	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	antibiotic target in susceptible species				
12	PATRIC	<i>Alr</i>	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species				
13	CARD	<i>EF-Tu</i>	Translation elongation factor Tu	antibiotic resistant gene variant or mutant,elfamycin resistance gene	6	96	83	7e-03

14	PATRIC	<i>EF-Tu</i>	Translation elongation factor Tu	antibiotic target in susceptible species				
15	NDARO	<i>TetA(P)</i>	Tetracycline resistance, MFS efflux pump => TetA(P)		100	100	100	1e-237
16	PATRIC	<i>FabK-like</i>	Putative FabK-like enoyl-[acyl-carrier-protein] reductase	protein involved in antibiotic sequestration				
17	CARD	<i>mprF</i>	putative membrane protein	antibiotic target modifying enzyme,peptide antibiotic resistance gene	100	100	95	0.0
18	PATRIC	<i>NimB</i>	Nitroimidazole resistance protein NimB	antibiotic inactivation enzyme				
19	PATRIC	<i>gyrB</i>	DNA gyrase subunit B (EC 5.99.1.3)	antibiotic target in susceptible species				
20	PATRIC	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein				
21	PATRIC	<i>S10p</i>	SSU ribosomal protein S10p (S20e)	antibiotic target in susceptible species				
22	PATRIC	<i>GdpD</i>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	protein altering cell wall charge conferring antibiotic resistance				
23	PATRIC	<i>kasA</i>	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	antibiotic target in susceptible species				
24	CARD	<i>tetA(P)</i>	Tetracycline resistance, MFS efflux pump => TetA(P)	efflux pump conferring antibiotic resistance	100	100	98	1e-234
25	PATRIC	<i>fabV</i>	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	antibiotic target replacement protein				
26	PATRIC	<i>MurA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species				
27	CARD	<i>EF-Tu</i>	Translation elongation factor Tu	antibiotic resistant gene variant or	6	96	83	7e-03

				mutant,elfamycin resistance gene				
28	CARD	<i>tetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein,tetracycline resistance gene	48	99	98	1e-180
29	PATRIC	<i>TetA(P)</i>	Tetracycline resistance, MFS efflux pump => TetA(P)	efflux pump conferring antibiotic resistance				
30	PATRIC	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	antibiotic target in susceptible species				
31	PATRIC	<i>MprF</i>	L-O-lysylphosphatidylglycerol synthase (EC 2.3.2.3)	protein altering cell wall charge conferring antibiotic resistance				
32	NDARO	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)		48	99	98	1e-180
33	PATRIC	<i>rho</i>	Transcription termination factor Rho	antibiotic target in susceptible species				
34	PATRIC	<i>gyrA</i>	DNA gyrase subunit A (EC 5.99.1.3)	antibiotic target in susceptible species				
35	PATRIC	<i>GdpD</i>	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	protein altering cell wall charge conferring antibiotic resistance				
36	PATRIC	<i>PgsA</i>	CDP-diacylglycerol--glycerol-3- phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	protein altering cell wall charge conferring antibiotic resistance				
37	PATRIC	<i>gidB</i>	16S rRNA (guanine(527)-N(7))- methyltransferase (EC 2.1.1.170)	gene conferring resistance via absence				
38	PATRIC	<i>gyrA</i>	DNA gyrase subunit A (EC 5.99.1.3)	antibiotic target in susceptible species				
39	PATRIC	<i>rpoC</i>	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	antibiotic target in susceptible species				
40	PATRIC	<i>TetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein				

41	PATRIC	<i>MurA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species				
42	CARD	<i>tetB(P)</i>	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein, tetracycline resistance gene	13	91	95	5e-40
43	PATRIC	<i>folP</i>	Dihydropteroate synthase (EC 2.5.1.15)	antibiotic target in susceptible species				
44	PATRIC	<i>Ddl</i>	D-alanine--D-alanine ligase (EC 6.3.2.4)	antibiotic target in susceptible species				
45	PATRIC	<i>Ddl</i>	D-alanine--D-alanine ligase (EC 6.3.2.4)	antibiotic target in susceptible species				
46	PATRIC	<i>Alr</i>	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species				
47	PATRIC	<i>folA, Dfr</i>	Dihydrofolate reductase (EC 1.5.1.3)	antibiotic target in susceptible species				
48	PATRIC	<i>rpoB</i>	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	antibiotic target in susceptible species				

*E-values were available only for CARD (Comprehensive Antibiotic Resistance Database) and NDARO (National Database of Antibiotic Resistant Organisms). PATRIC: Pathosystems Resource Integration Center.

Supplementary Table S3: Functions and classifications of list of antimicrobial resistance genes in the genome of *C. perfringens* IIRC2505A.

Evidence	Property	Source	Genome Name	BRIC ID	RefSeq Tag	Alt Locus Tag	Source ID	Source Organism	Gene	Product	Function	Classification	PubMed	Subject Coverage	Query Coverage	Identity	E-value
BLAT	Transporter	TCDB	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.21			Q08637	Enterococcus hirae		V-type ATP synthase subunit B (EC 3.6.3.14)	the h ⁺ - or na ⁺ -translocating f-type, v-type and a-type atpase (f-atpase) superfamily	3.A.2.2.2	8144530;8157629;8373385	99	99	82	1e-222
BLAT	Virulence Factor	Victors	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.824			15676067	Neisseria meningitidis MC58	tufA	Translation elongation factor Tu			11062540	5	92	86	3e-03
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3739					EF-G	Translation elongation factor G	Translation elongation factor G	antibiotic target in susceptible species	17980694				
BLAT	Antibiotic Resistance	NDARO	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3985			WP_012478245.1	Clostridium perfringens		Tetracycline resistance, ribosomal protection type => TetB(P)	tetracycline resistance ribosomal protection protein TetB(P)			13	91	95	5e-40
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3737					S12p	SSU ribosomal protein S12p (S23e)	SSU ribosomal protein S12p (S23e)	antibiotic target in susceptible species	7934937				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3726					EF-Tu	Translation elongation factor Tu	Translation elongation factor Tu	antibiotic target in susceptible species	364475;9678602				
BLAT	Virulence Factor	VFDB	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.1184			VFG002285	Clostridium perfringens ATCC 13124	nanH			Exoenzyme,Carbohydrate-active enzyme,Sialidase		100	100	98	1e-226
BLAT	Drug Target	TTD	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.824			TTD02058			Translation elongation factor Tu				5	88	86	3e-02
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3987					TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein	8170402;11717269				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.624					MurA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species	8994972				
BLAT	Transporter	TCDB	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.2183			P0C2E9	Clostridium perfringens		Thiol-activated cytolyisin	the thiol-activated cholesterol-dependent cytolyisin (cdc) family.	1.C.12.1.1		92	88	87	1e-243
BLAT	Drug Target	DrugBank	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.4032			Q8XL08	Clostridium perfringens (strain 13 / Type A)	nagJ	Protein O-GlcNAcase (EC 3.2.1.169)	gamma-butyrolactone	Drug target		100	100	98	0.0
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.1488					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3985					TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein	8170402;11717269				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3358					gidB	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	gene conferring resistance via absence	17238915				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3344					gyrB	DNA gyrase subunit B (EC 5.99.1.3)	DNA gyrase subunit B (EC 5.99.1.3)	antibiotic target in susceptible species	21693461;22279180;9293187				
BLAT	Drug Target	TTD	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3726			TTD02058			Translation elongation factor Tu				5	88	86	3e-02
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.1048					Iso-rRNA	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	antibiotic target in susceptible species	7929087				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.1111					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782				
BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.824			WP_009887863.1	Clostridium difficile		Translation elongation factor Tu		antibiotic resistant gene variant or mutant,clfrancycin resistance gene		6	96	83	7e-03
BLAT	Virulence Factor	Victors	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.710			110801372	Clostridium perfringens ATCC 13124	virS	hypothetical protein			8052128	99	100	95	1e-243
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.824					EF-Tu	Translation elongation factor Tu	Translation elongation factor Tu	antibiotic target in susceptible species	364475;9678602				
BLAT	Transporter	TCDB	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3983			Q46305	Clostridium perfringens		Tetracycline resistance, MFS efflux pump => TetA(P)	the major facilitator superfamily (mfs).	2.A.1.21.6	16788202;8170402	100	100	98	1e-234
BLAT	Antibiotic Resistance	NDARO	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3983			WP_003479690.1	Clostridium perfringens		Tetracycline resistance, MFS efflux pump => TetA(P)	tetracycline efflux MFS transporter TetA(P)			100	100	100	1e-237
BLAT	Virulence Factor	Victors	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.2183			18309145	Clostridium perfringens str. 13	pfoA	Thiol-activated cytolyisin			9182756	92	88	87	1e-243
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.1362					FabK-like	Putative FabK-like enoyl-[acyl-carrier-protein] reductase	Putative FabK-like enoyl-[acyl-carrier-protein] reductase	protein involved in antibiotic sequestration	27577999				
BLAT	Virulence Factor	Victors	Clostridium perfringens IIRC2505A	fig1502.2785.pcg.3726			15676067	Neisseria meningitidis MCS8	tufA	Translation elongation factor Tu			11062540	5	92	86	3e-03

BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IRLC2505A	fig1502.2785.psg.812		Q0SSM7	Clostridium perfringens SM101	mpfF	putative membrane protein		antibiotic target modifying enzyme,peptide antibiotic resistance gene		100	100	95	0.0
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.4118				NimB	Nitroimidazole resistance protein NimB	Nitroimidazole resistance protein NimB	antibiotic inactivation enzyme	16338949				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.2790				gyrB	DNA gyrase subunit B (EC 5.99.1.3)	DNA gyrase subunit B (EC 5.99.1.3)	antibiotic target in susceptible species	21693461;22279180;9293187				
BLAT	Transporter	TCDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3028		Q8XME6	Clostridium perfringens (strain 13 / Type A)		Carbon starvation protein A	the putative peptide transporter carbon starvation estA (esta) family.	2.A.114.1.4		100	100	99	1e-277
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.1125		VFG002278	Clostridium perfringens str. 13	nagJ	Protein O-GlcNAcase (EC 3.2.1.169)		Exoenzyme,Carbohydrate-active enzyme,Hyaluronidase		100	100	96	0.0
BLAT	Drug Target	DrugBank	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3726		P60339	Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579)	tufB	Translation elongation factor Tu	Aurodox/Guanosine-5'-Diphosphate	Drug target		5	96	87	9e-04
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3986				TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein	8170402;11717269				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.825				S10p	SSU ribosomal protein S10p (S20c)	SSU ribosomal protein S10p (S20c)	antibiotic target in susceptible species	26124155				
BLAT	Transporter	TCDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.2308		B1V6H1	Clostridium perfringens D str. JGS1721		hypothetical protein	the 11 holin (11 holin) family.	1.E.11.2.2		100	100	87	2e-35
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.314				GdpD	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	protein altering cell wall charge conferring antibiotic resistance	21899450				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.1498				kaaA	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	antibiotic target in susceptible species	10428945				
BLAT	Virulence Factor	Victors	Clostridium perfringens IRLC2505A	fig1502.2785.psg.1147		29376182	Enterococcus faecalis V583	EF1623	Ethanolamine utilization protein similar to PduA/PduJ			17307944	91	91	92	4e-38
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3754		VFG002274	Clostridium perfringens str. 13	plc	Broad-substrate range phospholipase C (EC 3.1.4.3)		Toxin,Zinc-metallophospholipase C		100	100	99	1e-242
BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3983		AAA20116.1	Clostridium perfringens	tetA(P)	Tetracycline resistance, MFS efflux pump => TetA(P)		efflux pump conferring antibiotic resistance		100	100	98	1e-234
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.513				fabV	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	antibiotic target replacement protein	19933806;18032386				
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.2129		VFG002282	Clostridium perfringens str. 13	cloSI	hypothetical protein		Exoenzyme,Cysteine endopeptidase		99	100	97	1e-306
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3718				MurA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species	8994972				
BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3726		WP_009887863.1	Clostridium difficile		Translation elongation factor Tu		antibiotic resistant gene variant or mutant,clfamycin resistance gene		6	96	83	7e-03
BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3987		AAA20117.1	Clostridium perfringens	tetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)		antibiotic target protection protein,tetracycline resistance gene		48	99	98	1e-180
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3983				TetA(P)	Tetracycline resistance, MFS efflux pump => TetA(P)	Tetracycline resistance, MFS efflux pump => TetA(P)	efflux pump conferring antibiotic resistance	8170402;11717269				
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRLC2505A	fig1502.2785.psg.4032		VFG002279	Clostridium perfringens str. 13	nagJ	Protein O-GlcNAcase (EC 3.2.1.169)		Exoenzyme,Carbohydrate-active enzyme,Hyaluronidase		100	100	98	0.0
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.80				dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	antibiotic target in susceptible species	16321944				
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRLC2505A	fig1502.2785.psg.1695				MprF	L-O-lysylphosphatidylglycerol synthase (EC 2.3.2.3)	L-O-lysylphosphatidylglycerol synthase (EC 2.3.2.3)	protein altering cell wall charge conferring antibiotic resistance	19289517;16723576				
BLAT	Drug Target	DrugBank	Clostridium perfringens IRLC2505A	fig1502.2785.psg.399		Q8XJ01	Clostridium perfringens (strain 13 / Type A)	pfbA	Multimodular transpeptidase (strain 13 / Type A)	Cefotam,Cefmenoxime,Flucloracillin; Phenoxymethylpenicillin,Loracarbef,Cefalotin; Oxacillin,Cefaclor,Merzocillin,Cyclacillin; Amoxicillin,Azlocillin,Cefitoren,Cefuroxime; Cefapirin,Cloxacillin,Bacampicillin,Pivampicillin; Pivmecillinam,Degraded Cephaloridine	Drug target		99	81	97	0.0
BLAT	Drug Target	DrugBank	Clostridium perfringens IRLC2505A	fig1502.2785.psg.824		P60339	Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579)	tufB	Translation elongation factor Tu	Aurodox/Guanosine-5'-Diphosphate	Drug target		5	96	87	9e-04
BLAT	Antibiotic Resistance	NDARO	Clostridium perfringens IRLC2505A	fig1502.2785.psg.3987		WP_012478245.1	Clostridium perfringens		Tetracycline resistance, ribosomal protection type => TetB(P)	tetracycline resistance ribosomal protection protein TetB(P)			48	99	98	1e-180

K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.646					rho	Transcription termination factor Rho	Transcription termination factor Rho	antibiotic target in susceptible species	8466900					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2791					gyrA	DNA gyrase subunit A (EC 5.99.1.3)	DNA gyrase subunit A (EC 5.99.1.3)	antibiotic target in susceptible species	9293187					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.1881					GdpD	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	protein altering cell wall charge conferring antibiotic resistance	21899450					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.60					PgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	protein altering cell wall charge conferring antibiotic resistance	22238576					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2776					gidB	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	gene conferring resistance via absence	17238915					
BLAT	Virulence Factor	Victors	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3754			18309018	Clostridium perfringens str. 13	nle	Broad-substrate range phospholipase C (EC 3.1.4.3)			7746141	100	100	99	1e-242	
BLAT	Transporter	TCDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3795			Q0SPM4	Clostridium perfringens (strain SM101 / Type A)		bacteriocin UviB	the bhla holin (bhla holin) family.	1.E.27.1.5		95	92	98	3e-26	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3343					gyrA	DNA gyrase subunit A (EC 5.99.1.3)	DNA gyrase subunit A (EC 5.99.1.3)	antibiotic target in susceptible species	9293187					
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.736			VFG002281	Clostridium perfringens str. 13	naaL	hypothetical protein		Exoenzyme,Carbohydrate-active enzyme,Hyaluronidase		100	100	95	0.0	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3735					rpoC	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	antibiotic target in susceptible species	16723576					
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3010			VFG002283	Clostridium perfringens str. 13	nanI	Sialidase (EC 3.2.1.18)		Exoenzyme,Carbohydrate-active enzyme,Sialidase		100	100	99	0.0	
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2195			VFG002276	Clostridium perfringens str. 13	colA	Microbial collagenase (EC 3.4.24.3)		Exoenzyme,Collagenase		100	100	98	0.0	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3984					TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)	antibiotic target protection protein	8170402;11717269					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2868					MurA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	antibiotic target in susceptible species	8994972					
BLAT	Antibiotic Resistance	CARD	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3985			AAA20117.1	Clostridium perfringens	tetB(P)	Tetracycline resistance, ribosomal protection type => TetB(P)		antibiotic target protection protein,tetracycline resistance gene		13	91	95	5e-40	
BLAT	Drug Target	DrugBank	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2494			P54965	Clostridium perfringens (strain 13 / Type A)	cbh	Choloylglycine hydrolase (EC 3.5.1.24)	2-Aminoethanesulfonic Acid;Cholic Acid;Deoxycholic Acid	Drug target		100	100	91	1e-182	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2322					folP	Dihydropteroate synthase (EC 2.5.1.15)	Dihydropteroate synthase (EC 2.5.1.15)	antibiotic target in susceptible species	15673783					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2156					Ddl	D-alanine--D-alanine ligase (EC 6.3.2.4)	D-alanine--D-alanine ligase (EC 6.3.2.4)	antibiotic target in susceptible species	24303782;24033232					
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2700			VFG002284	Clostridium perfringens str. 13	nanJ	Sialidase (EC 3.2.1.18)		Exoenzyme,Carbohydrate-active enzyme,Sialidase		100	100	95	0.0	
BLAT	Transporter	TCDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3198			Q186B7	Clostridium difficile (strain 630)		Sulfite transporter, NirC family	the formate-nitrite transporter (fnt) family.	1.A.16.3.3		62	99	100	1e-85	
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2183			VFG002275	Clostridium perfringens str. 13	pfoA	Thiol-activated cytotoxin		Toxin,Membrane-damaging,Pore-forming,Channel-forming involving beta-sheet-containing toxin (beta-barrel),Cholesterol-dependent cytotoxin		92	88	87	1e-243	
BLAT	Virulence Factor	VFDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2213			VFG002277	Clostridium perfringens str. 13	nagH	Hyaluronoglucosaminidase (EC 3.2.1.35)		Exoenzyme,Carbohydrate-active enzyme,Hyaluronidase		100	100	97	0.0	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.1762					Ddl	D-alanine--D-alanine ligase (EC 6.3.2.4)	D-alanine--D-alanine ligase (EC 6.3.2.4)	antibiotic target in susceptible species	24303782;24033232					
BLAT	Transporter	TCDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2585			P50487	Clostridium perfringens		uracil-xanthine permease	the nucleobase/ascorbate transporter (nat) or nucleobase:cation symporter-2 (nsc2) family.	2.A.40.2.1		11792842;8162194	100	100	99	1e-250
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.2657					Alr	Alanine racemase (EC 5.1.1.1)	Alanine racemase (EC 5.1.1.1)	antibiotic target in susceptible species	19748470;24303782					
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3429					folA, Df	Dihydrofolate reductase (EC 1.5.1.3)	Dihydrofolate reductase (EC 1.5.1.3)	antibiotic target in susceptible species	20169085;25288078					
BLAT	Transporter	TCDB	Clostridium perfringens IRMC2505A	fig1502.2785.psg.1109			H7CZV2	Clostridium perfringens F262		hypothetical protein	the mycobacterial 4 tms phage holin (mp4 holin) family.	1.E.40.4.3		100	100	97	1e-60	
K-mer Search	Antibiotic Resistance	PATRIC	Clostridium perfringens IRMC2505A	fig1502.2785.psg.3734					rpoB	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	antibiotic target in susceptible species	3050121;15047531;16723576					

Supplementary Table S4: Gene families are ranked by alignment score for phylogenetic tree of IRMC2505A genome.

PGFam	Align. Score	Align. Length	Num Seqs	Mean Sqr Freq	Prop Gaps	Used In Analysis	Product
PGF_02797402	27.70	1333	22	0.759	0.070	True	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)
PGF_02704551	27.20	1269	22	0.764	0.071	True	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)
PGF_05171623	22.81	1088	22	0.692	0.045	True	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
PGF_05500127	21.83	903	22	0.726	0.024	True	Valyl-tRNA synthetase (EC 6.1.1.9)
PGF_00950554	19.48	674	22	0.750	0.022	True	Excinuclease ABC subunit B
PGF_02906681	19.10	732	22	0.706	0.016	True	Transcription accessory protein (S1 RNA-binding domain)
PGF_03104485	18.87	752	22	0.688	0.062	True	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)
PGF_00033095	18.36	817	22	0.642	0.029	True	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)
PGF_10300474	18.13	714	22	0.679	0.025	True	DNA topoisomerase I (EC 5.99.1.2)
PGF_00030643	17.91	541	22	0.770	0.019	True	Peptide chain release factor 3
PGF_06776852	17.37	804	22	0.612	0.022	True	Recombination inhibitory protein MutS2
PGF_00057270	17.26	1020	22	0.541	0.076	True	DNA topoisomerase IV subunit A (EC 5.99.1.3)
PGF_09950730	17.26	1197	22	0.499	0.009	True	Chromosome partition protein smc
PGF_03752158	17.00	635	22	0.674	0.027	True	FIG092679: Fe-S oxidoreductase
PGF_00047095	16.34	811	22	0.574	0.081	True	RecD-like DNA helicase YrrC
PGF_00021217	16.31	518	22	0.716	0.013	True	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)
PGF_10525419	16.23	923	22	0.534	0.243	True	Translation initiation factor 2
PGF_00075770	16.17	454	22	0.759	0.006	True	FIG00519347: Ribonucleotide reductase-like protein
PGF_00066502	15.95	467	22	0.738	0.010	True	Asparaginyl-tRNA synthetase (EC 6.1.1.22)
PGF_02277678	15.78	406	22	0.783	0.023	True	Phosphoglycerate kinase (EC 2.7.2.3)
PGF_00025600	15.78	500	22	0.706	0.017	True	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)
PGF_00007024	15.60	442	22	0.742	0.008	True	GTP-binding protein EngA
PGF_00052238	15.24	474	22	0.700	0.049	True	Signal recognition particle protein Ffh
PGF_01137124	14.94	465	22	0.693	0.033	True	Phosphoglucosamine mutase (EC 5.4.2.10)

PGF_00007012	14.89	371	22	0.773	0.016	True	GTP-binding and nucleic acid-binding protein YchF
PGF_02226715	14.86	705	22	0.560	0.036	True	ATP-dependent DNA helicase RecG (EC 3.6.4.12)
PGF_00030640	14.55	363	22	0.763	0.012	True	Peptide chain release factor 1
PGF_00011081	14.47	853	22	0.495	0.134	True	Helicase PriA essential for oriC/DnaA-independent DNA replication
PGF_01281052	14.45	856	22	0.494	0.086	True	Uncharacterized protease CPF_2136
PGF_02029783	14.40	443	22	0.684	0.036	True	GTP-binding protein Obg
PGF_00422271	14.39	320	22	0.805	0.015	True	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)
PGF_00060120	14.24	467	22	0.659	0.027	True	SCIIF radical SAM maturase
PGF_00024314	14.20	571	22	0.594	0.064	True	NAD(FAD)-utilizing dehydrogenase, sll0175 homolog
PGF_02019462	13.89	341	22	0.752	0.006	True	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
PGF_00019248	13.68	553	22	0.582	0.012	True	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)
PGF_08562657	13.67	512	22	0.604	0.118	True	tRNA-i(6)A37 methylthiotransferase (EC 2.8.4.3)
PGF_00063999	13.67	464	22	0.634	0.012	True	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
PGF_05049118	13.56	358	22	0.717	0.039	True	Holliday junction ATP-dependent DNA helicase RuvB (EC 3.6.4.12)
PGF_03520151	13.54	419	22	0.661	0.102	True	Cell division protein FtsZ
PGF_00016393	13.49	281	22	0.804	0.015	True	LSU ribosomal protein L2p (L8e)
PGF_00007028	13.30	626	22	0.531	0.086	True	Ribosome LSU-associated GTP-binding protein HflX
PGF_09111052	13.25	407	22	0.657	0.028	True	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)
PGF_09945387	13.13	600	22	0.536	0.038	True	Fibronectin/fibrinogen-binding protein
PGF_00426236	13.08	359	22	0.690	0.027	True	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase (flavodoxin) (EC 1.17.7.3)
PGF_02620298	13.03	472	22	0.600	0.042	True	Argininosuccinate lyase (EC 4.3.2.1)
PGF_00048846	12.91	470	22	0.596	0.046	True	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase (EC 2.8.4.4)
PGF_09019918	12.77	438	22	0.610	0.025	True	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)
PGF_00421796	12.71	579	22	0.528	0.025	True	DNA repair protein RecN
PGF_00413298	12.64	487	22	0.573	0.087	True	tRNA t(6)A37-methylthiotransferase (EC 2.8.4.5)
PGF_00033444	12.61	716	22	0.471	0.087	True	Cyclic-di-AMP phosphodiesterase GdpP
PGF_07063065	12.50	436	22	0.598	0.158	True	Transcription termination protein NusA
PGF_04505269	12.38	246	22	0.790	0.050	True	SSU ribosomal protein S2p (SAe)

PGF_05507938	12.36	794	22	0.439	0.184	True	DNA mismatch repair protein MutL
PGF_00004169	12.26	711	22	0.460	0.205	True	Fe-S oxidoreductase
PGF_02923127	12.17	240	22	0.785	0.014	True	Uridylate kinase (EC 2.7.4.22)
PGF_03788368	12.02	296	22	0.699	0.008	True	RNase adapter protein RapZ
PGF_00618776	11.89	361	22	0.626	0.038	True	23S rRNA (adenine(2503)-C(2))-methyltransferase @ tRNA (adenine(37)-C(2))-methyltransferase (EC 2.1.1.192)
PGF_00007027	11.84	306	22	0.677	0.034	True	GTP-binding protein Era
PGF_03295331	11.80	374	22	0.610	0.044	True	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)
PGF_00415407	11.77	392	22	0.595	0.032	True	23S rRNA (guanine(2445)-N(2))-methyltransferase (EC 2.1.1.173)
PGF_00049889	11.74	230	22	0.774	0.035	True	SSU ribosomal protein S3p (S3e)
PGF_00057483	11.63	819	22	0.406	0.385	True	Transcription termination factor Rho
PGF_06936561	11.47	313	22	0.648	0.038	True	Translation elongation factor Ts
PGF_00769755	11.37	456	22	0.532	0.033	True	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)
PGF_00403095	11.34	211	22	0.781	0.009	True	Uracil phosphoribosyltransferase (EC 2.4.2.9)
PGF_00426877	11.24	299	22	0.650	0.052	True	LSU ribosomal maturation GTPase RbgA (B. subtilis YlqF)
PGF_00016443	11.14	181	22	0.828	0.008	True	LSU ribosomal protein L5p (L11e)
PGF_05767868	11.09	250	22	0.701	0.020	True	Probable transcriptional regulatory protein YebC
PGF_00011463	11.05	286	22	0.654	0.053	True	RNA binding methyltransferase FtsJ like
PGF_00418291	11.02	266	22	0.676	0.049	True	Cobalt-precorrin-4 C(11)-methyltransferase (EC 2.1.1.271)
PGF_00007045	10.72	304	22	0.615	0.145	True	GTP-sensing transcriptional pleiotropic repressor CodY
PGF_04807486	10.62	335	22	0.580	0.070	True	tRNA dimethylallyltransferase (EC 2.5.1.75)
PGF_00049896	10.59	169	22	0.814	0.022	True	SSU ribosomal protein S5p (S2e)
PGF_00049904	10.59	156	22	0.848	0.000	True	SSU ribosomal protein S7p (S5e)
PGF_04512522	10.58	208	22	0.734	0.017	True	LSU ribosomal protein L4p (L1e)
PGF_06230969	10.48	553	22	0.446	0.092	True	NAD(P)H-hydrate epimerase (EC 5.1.99.6) / ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136)
PGF_00425024	10.41	433	22	0.500	0.075	True	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
PGF_00286985	10.39	462	22	0.483	0.111	True	[FeFe]-hydrogenase maturation protein HydF
PGF_09155108	10.32	444	22	0.490	0.092	True	Exonuclease SbcD

PGF_00413208	10.25	269	22	0.625	0.107	True	tRNA (guanine(37)-N(1))-methyltransferase (EC 2.1.1.228)
PGF_06461498	10.20	318	22	0.572	0.087	True	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
PGF_00046555	10.14	234	22	0.663	0.089	True	RNA polymerase sporulation specific sigma factor SigH
PGF_07695531	10.08	141	22	0.849	0.000	True	LSU ribosomal protein L11p (L12e)
PGF_00047155	10.07	217	22	0.684	0.029	True	Redox-sensing transcriptional repressor Rex
PGF_04244475	10.07	234	22	0.659	0.074	True	Adenylate kinase (EC 2.7.4.3)
PGF_00016444	10.02	181	22	0.745	0.008	True	LSU ribosomal protein L6p (L9e)
PGF_01212500	9.90	307	22	0.565	0.088	True	Diadenylate cyclase spyDAC; Bacterial checkpoint controller DisA with nucleotide-binding domain
PGF_00423533	9.90	316	22	0.557	0.104	True	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
PGF_02746079	9.88	326	22	0.547	0.092	True	Transcription regulator [contains diacylglycerol kinase catalytic domain]
PGF_01867628	9.86	392	22	0.498	0.116	True	Heat-inducible transcription repressor HrcA
PGF_00000196	9.77	446	22	0.462	0.091	True	UPF0348 protein family
PGF_02472178	9.71	277	22	0.583	0.068	True	Uncharacterized metal-dependent hydrolase YcfH
PGF_00049909	9.66	131	22	0.844	0.007	True	SSU ribosomal protein S9p (S16e)
PGF_06784545	9.64	304	22	0.553	0.053	True	(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)
PGF_00689961	9.63	237	22	0.626	0.110	True	Guanylate kinase (EC 2.7.4.8)
PGF_06941403	9.59	139	22	0.814	0.091	True	SSU ribosomal protein S12p (S23e)
PGF_00418285	9.56	287	22	0.565	0.151	True	Cobalt-precorrin-3 C(17)-methyltransferase (EC 2.1.1.272)
PGF_10396914	9.55	319	22	0.535	0.072	True	Similar to ribosomal large subunit pseudouridine synthase D, Bacillus subtilis YjbO type
PGF_08582746	9.49	318	22	0.532	0.128	True	23S rRNA (guanosine(2251)-2'-O)-methyltransferase (EC 2.1.1.185)
PGF_06377994	9.45	544	22	0.405	0.265	True	FtsW-like cell division membrane protein CA_C0505
PGF_07102049	9.42	309	22	0.536	0.050	False	UPF0701 protein YicC
PGF_02623406	9.31	318	22	0.522	0.026	False	FMN adenylyltransferase (EC 2.7.7.2) / Riboflavin kinase (EC 2.7.1.26)
PGF_03174068	9.28	186	22	0.680	0.062	False	Transcription antitermination protein NusG
PGF_00035334	9.22	342	22	0.498	0.066	False	Adenosylcobinamide-phosphate synthase (EC 6.3.1.10)
PGF_03790040	9.07	256	22	0.567	0.083	False	Ribonuclease III (EC 3.1.26.3)
PGF_00049906	9.07	133	22	0.786	0.008	False	SSU ribosomal protein S8p (S15Ae)

PGF_00413295	8.98	339	22	0.488	0.135	False	tRNA pseudouridine(55) synthase (EC 5.4.99.25)
PGF_00418309	8.89	238	22	0.576	0.121	False	Cobalt-precorrin-8 methylmutase (EC 5.4.99.60)
PGF_00049840	8.88	126	22	0.791	0.028	False	SSU ribosomal protein S13p (S18e)
PGF_00413554	8.83	159	22	0.700	0.019	False	tmRNA-binding protein SmpB
PGF_03295678	8.81	199	22	0.624	0.041	False	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
PGF_01833449	8.68	343	22	0.468	0.074	False	3'-to-5' oligoribonuclease A, Bacillus type
PGF_00016445	8.58	126	22	0.764	0.036	False	LSU ribosomal protein L7p/L12p (P1/P2)
PGF_06530721	8.57	228	22	0.567	0.058	False	tRNA (guanine(46)-N(7))-methyltransferase (EC 2.1.1.33)
PGF_02455692	8.56	237	22	0.556	0.072	False	Cytidylate kinase (EC 2.7.4.25)
PGF_04486278	8.34	340	22	0.452	0.057	False	Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)
PGF_00717752	8.31	250	22	0.526	0.105	False	Cobalt-precorrin-2 C(20)-methyltransferase (EC 2.1.1.151)
PGF_01213071	8.30	187	22	0.607	0.104	False	LSU ribosomal protein L10p (P0)
PGF_04788810	8.30	206	22	0.578	0.079	False	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
PGF_00048556	8.28	299	22	0.479	0.107	False	Ribonuclease HII (EC 3.1.26.4)
PGF_00016385	8.24	101	22	0.820	0.018	False	LSU ribosomal protein L27p
PGF_04845029	8.18	120	22	0.747	0.039	False	LSU ribosomal protein L19p
PGF_07411046	8.16	290	22	0.479	0.116	False	Uncharacterized RNA methyltransferase YsgA
PGF_00016452	8.11	149	22	0.665	0.011	False	LSU ribosomal protein L9p
PGF_00007026	8.09	250	22	0.512	0.200	False	GTP-binding protein EngB
PGF_01382519	8.08	190	22	0.586	0.077	False	Ribosome hibernation promoting factor Hpf
PGF_03021159	8.05	94	22	0.830	0.045	False	UPF0296 protein YlzA
PGF_04762552	7.97	169	22	0.613	0.040	False	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)
PGF_03189552	7.93	223	22	0.531	0.109	False	Holliday junction ATP-dependent DNA helicase RuvA (EC 3.6.4.12)
PGF_03753407	7.85	164	22	0.613	0.068	False	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE
PGF_00049854	7.82	85	22	0.849	0.011	False	SSU ribosomal protein S17p (S11e)
PGF_04978890	7.82	104	22	0.767	0.008	False	LSU ribosomal protein L21p
PGF_00020361	7.81	170	22	0.599	0.026	False	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly
PGF_00413203	7.81	184	22	0.576	0.147	False	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)

PGF_00060431	7.71	72	22	0.909	0.000	False	Translation initiation factor 1
PGF_07504595	7.58	153	22	0.613	0.066	False	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)
PGF_00413189	7.56	244	22	0.484	0.061	False	tRNA (adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)
PGF_05579323	7.53	444	22	0.357	0.185	False	L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)
PGF_00049860	7.42	102	22	0.735	0.083	False	SSU ribosomal protein S19p (S15e)
PGF_00422085	7.39	101	22	0.735	0.071	False	DNA-binding protein SpoVG
PGF_05636025	7.33	119	22	0.672	0.028	False	FIG001802: Putative alkaline-shock protein
PGF_00049847	7.33	88	22	0.781	0.011	False	SSU ribosomal protein S15p (S13e)
PGF_06649360	7.23	230	22	0.477	0.155	False	Segregation and condensation protein B
PGF_00016377	7.19	108	22	0.691	0.032	False	LSU ribosomal protein L24p (L26e)
PGF_00049901	7.13	97	22	0.724	0.019	False	SSU ribosomal protein S6p
PGF_00418278	7.13	498	22	0.319	0.310	False	Cobalt-precorrin 5A hydrolase (EC 3.7.1.12)
PGF_03990071	6.84	105	22	0.667	0.069	False	LSU ribosomal protein L23p (L23Ae)
PGF_00049842	6.79	61	22	0.870	0.000	False	SSU ribosomal protein S14p (S29e) @ SSU ribosomal protein S14p (S29e), zinc-dependent
PGF_08421732	6.75	343	22	0.365	0.179	False	NAD kinase (EC 2.7.1.23)
PGF_00178044	6.66	86	22	0.718	0.043	False	SSU ribosomal protein S16p
PGF_03818138	6.61	65	22	0.820	0.001	False	LSU ribosomal protein L35p
PGF_01135236	6.58	236	22	0.428	0.144	False	Dephospho-CoA kinase (EC 2.7.1.24)
PGF_02454577	6.58	88	22	0.701	0.009	False	SSU ribosomal protein S20p
PGF_00013347	6.46	97	22	0.656	0.128	False	UPF0297 protein YrzL
PGF_05770273	6.41	70	22	0.766	0.019	False	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-dependent
PGF_06948903	6.40	95	22	0.656	0.116	False	SSU ribosomal protein S18p @ SSU ribosomal protein S18p, zinc-dependent
PGF_00415631	6.32	93	22	0.656	0.046	False	COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination
PGF_02899131	6.27	72	22	0.739	0.037	False	LSU ribosomal protein L29p (L35e)
PGF_00598888	6.19	160	22	0.489	0.128	False	Mini-ribonuclease III
PGF_00011792	5.99	127	22	0.531	0.194	False	His repressor

PGF_06609275	5.83	49	22	0.833	0.000	False	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-dependent
PGF_04457297	5.83	209	22	0.403	0.099	False	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)
PGF_00016424	5.73	37	22	0.941	0.000	False	LSU ribosomal protein L36p @ LSU ribosomal protein L36p, zinc-dependent
PGF_00016395	5.60	60	22	0.724	0.020	False	LSU ribosomal protein L30p (L7e)
PGF_00016404	5.58	62	22	0.709	0.031	False	LSU ribosomal protein L32p @ LSU ribosomal protein L32p, zinc-dependent
PGF_00662997	5.44	266	22	0.334	0.073	False	Cobalamin synthase (EC 2.7.8.26)
PGF_10450086	5.31	165	22	0.414	0.161	False	Transcription termination protein NusB
PGF_10097367	5.31	834	22	0.184	0.623	False	Porphobilinogen deaminase (EC 2.5.1.61)
PGF_06632167	5.14	128	22	0.455	0.118	False	Signal recognition particle associated protein
PGF_08432396	4.99	445	22	0.237	0.522	False	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)

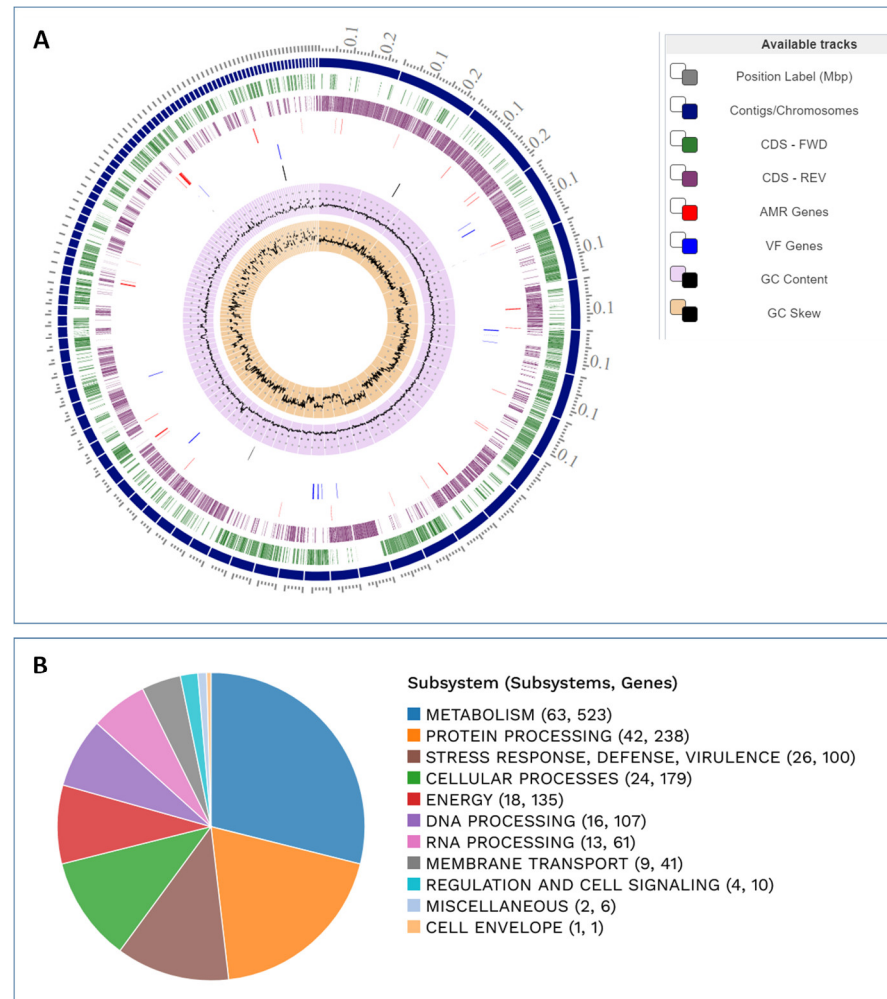


Figure S1: A: A circular graphical display of the distribution of the genome annotations in IRMC2505A. **B:** An overview of the subsystems of genes for the genome IRMC2505A.

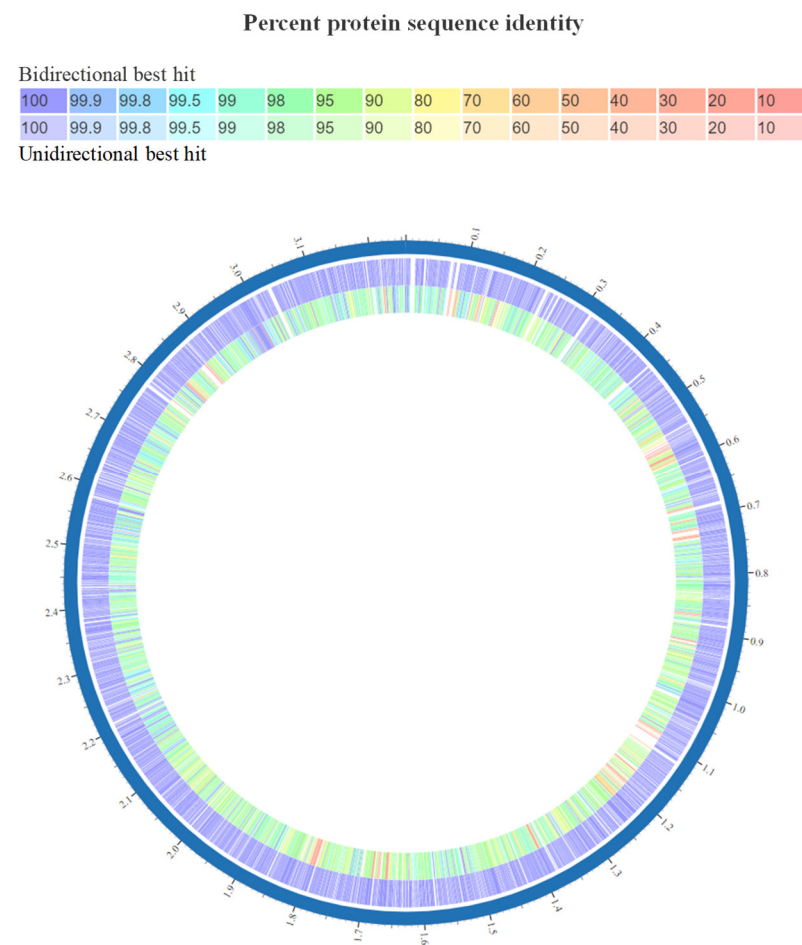


Figure S2: Proteome comparison. List of tracks, from outside to inside: *Clostridium perfringens* ATCC 13124 (195103.10) and *Clostridium perfringens* IRMC2505A (1502.2785).