

Genomic Landscape of Multidrug Resistance and Virulence in *Enterococcus faecalis* IRMC827A from a Long-Term Patient

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Table S1. List of virulence factors in the genome of *E. faecalis* IRMC827A.

S. No	Source	Source ID	SO	Gene	Product	Classification	SC	QC	% Identity	E-Value
1	ResFinder 4.1	CP003726.1	a	<i>ElrA</i>					98.76	
2	ResFinder 4.1 / Victors	CP002491.1 / 29377514	b / c	<i>SrtA</i>	Sortase A, LPXTG specific		100	100	100	1e-134
3	ResFinder 4.1 / VFDB	AF260876.1 / VFG002166	d / c	<i>ace</i>	Collagen adhesin	Adherence, MSCRAMM	78	84	96	1e-296
4	ResFinder 4.1	CP002491.1	b	<i>cCF10</i>					99.76	
5	ResFinder 4.1	295112306	e	<i>cOBI</i>					99.53	
6	ResFinder 4.1	CP002621.1	f	<i>cad</i>					99.89	
7	ResFinder 4.1	AF435439.1	g	<i>camE</i>	Sex pheromone cam373 precursor				99.80	
8	ResFinder 4.1 / VFDB / Victors	CP003726.1 / VFG042976 / 306753329	a / c /	<i>ebpA</i>	Von Willebrand factor type A domain protein	Adherence, Biofilm formation, Sortase-assembled pili	100	74	99	1e-130
9	ResFinder 4.1 / VFDB	CP003726.1 / VFG042977	a / C	<i>ebpB</i>	Cell wall surface anchor family protein	Adherence, Biofilm formation, Sortase-assembled pili	100	100	98	1e-274
10	ResFinder 4.1	AE016830.1	c	<i>efaAfs</i>					99.68	
11	ResFinder 4.1	CP002491.1	b	<i>hylA</i>					98.93	
12	ResFinder 4.1	AE016830.1	c	<i>tpx</i>					99.61	
13	Victors	15676067	h	<i>tufA</i>	Translation elongation factor Tu		98	98	81	1e-189
14	Victors	29376182	c	<i>EF1623</i>	Ethanolamine utilization protein similar to pdua/pduj		100	100	100	7e-46
15	Victors	29376163	c	<i>scrB-1</i>	Sucrose-6-phosphate hydrolase (EC		100	99	98	1e-293
16	Victors / VFDB	29375537	c	<i>bopD</i>	Maltose operon transcriptional repressor malr, lacI family	Biofilm formation	100	100	99	1e-190
17	VFDB	VFG043509	c	<i>fs2</i>	Cell wall surface anchor family protein		25	100	95	1e-231
18	Victors	29375014	c	<i>EF0376</i>	Putative lipoprotein		100	100	100	1e-206
19	VFDB / Victors	VFG001359 / 15903537	i / j	<i>psaA</i>	Manganese ABC transporter, periplasmic-binding protein sita	Manganese uptake, ABC transporter	89	87	82	1e-135
20	Patric / Victors	LMOh7858_1 898 / 116516623	k / l	<i>purB</i>	Adenylosuccinate lyase, SAICAR lyase		94	94	82	1e-200
21	VFDB	VFG002189	c	<i>cpsB</i>	Phosphatidate cytidyltransferase	Antiphagocytosis	100	100	99	1e-147
22	Victors	29377157	c	<i>EF2675</i>	Competence protein coia		99	100	95	1e-226
23	Victors	29376329	c	<i>purL</i>	Phosphoribosylformylglycinamide synthase,		100	100	99	0.0

					synthetase subunit					
24	VFDB	VFG002196	c	<i>EF3023</i>	Hyaluronate lyase precursor, polysaccharide lyase, family 8	Exoenzyme, Spreading factor	84	78	98	0.0
25	VFDB	VFG043508	c	<i>fssI</i>	Hypothetical protein		99	97	98	0.0
26	Victors	67043736	m	<i>perR</i>	Peroxide stress regulator perr, FUR family		100	100	100	1e-82
27	Victors	29376108	c	<i>recQ-1</i>	ATP-dependent DNA helicase recq		99	99	99	1e-275
28	Victors	29376080	c	<i>EF1513</i>	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)		100	100	99	0.0
29	Victors	29375449	c	<i>EF0861</i>	Acetyltransferase, GNAT family		100	100	99	1e-88
30	Victors / VFDB	16804506 / VFG000077	n	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit clpp		94	94	83	8e-87
31	Victors	29376708	c	<i>map</i>	Methionine aminopeptidase		100	100	100	1e-151
32	Victors	29374885	c	<i>brnQ</i>	Na (+)-dependent branched-chain amino acid transporter		100	100	100	1e-256
33	Victors	29376132	c	<i>psr</i>	Cell envelope-associated transcriptional attenuator lytr-cpsa-Psr, subfamily A1		100	100	99	1e-225
34	VFDB	VFG002190	c	<i>cpsA</i>	Undecaprenyl diphosphate synthase	Antiphagocytosis	100	100	99	1e-156
35	Victors	29375019	c	<i>EF0382</i>	Regulator of polyketide synthase expression		100	100	100	1e-304
36	Victors	29376338	c	<i>EF1792</i>	Hypothetical protein		100	75	98	1e-39
37	Victors	29377421	c	<i>EF2957</i>	Maltose O-acetyltransferase		100	100	100	1e-106
38	Victors	15901058	i	<i>SP 1193</i>	Galactose-6-phosphate isomerase, laca subunit		99	99	83	1e-62
39	VFDB / Victors	VFG002164	c	<i>prgB/asc 10</i>	Aggregation substance Asa1/prgb	Adherence	56	100	97	0.0
40	VFDB	VFG002165	c	<i>efaA</i>	Manganese ABC transporter, periplasmic-binding protein sita	Adherence	100	100	99	1e-178
41	Victors	29376164	c	<i>scrR-1</i>	Sucrose operon repressor scrr, lacI family		100	99	100	1e-183
42	Victors	29376159	c	<i>phrB</i>	Deoxyribodipyrimidine photolyase		100	100	98	1e-286
43	Victors	29376105	c	<i>EF1542</i>	Hypothetical protein		71	100	99	1e-195
44	Victors	29375870	c	<i>EF1302</i>	Transcriptional regulator		100	100	99	1e-167
45	Victors	29377084	c	<i>EF2598</i>	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component		100	100	99	0.0
46	Victors	29377078	c	<i>EF2591</i>	Glyoxalase family protein		100	97	100	1e-156
47	VFDB	VFG042978	c	<i>ebpC</i>	Cell wall surface anchor family protein	Adherence, Biofilm formation, Sortase-assembled pili	100	100	99	0.0
48	VFDB / Victors	VFG042979 / 29375670	c	<i>srtC</i>	Sortase A, LPXTG specific	Adherence, Biofilm formation, Sortase-	99	98	99	1e-160

						assembled pili				
49	Victors	29375331	c	<i>EF0737</i>	Hypothetical protein		100	100	99	1e-298
50	Victors	76788416	o	<i>lepA</i>	Translation elongation factor lepa		99	98	83	1e-302
51	Victors	29376151	c	<i>EF1590</i>	N1-spermidine/spermine acetyltransferase paia		100	100	100	1e-100
52	Victors	29376139	c	<i>thyA</i>	Thymidylate synthase		100	100	99	1e-189

SO: Source organism; a = *E. faecalis* D32; b = *E. faecalis* 62; c = *E. faecalis* V583; d: *E. faecalis* strain MC02152/TX0024; e: *Enterococcus* sp. 7L76; f: *E. faecalis* OG1RF; g: *E. faecalis* strain OG1X; h: *Neisseria meningitidis* MC58; i: *Streptococcus pneumoniae* TIGR4; j: *S. pneumoniae* R6; k: *Listeria monocytogenes* serotype 4b str. H7858; l: *S. pneumoniae* D39; m: *E. faecalis*; n: *Listeria monocytogenes* EGD-e; o: *Streptococcus agalactiae* A909; SC: Subject coverage; QC: Query coverage.

Table S2: Metagenomic read mapping of *E. faecalis* IRMC827A through various database.

Template	Function	Genome	GAS	EAS	TL	TI	TC	QI	QC	q value	p value
CARD BAE15963.1	<i>Dfrg</i>	a	501	3	498	100.00	100.00	100.00	100.00	489.79	1.0e-26
CARD NZ_CP018138.1_1692408_1695312	<i>S. pneumoniae</i> 23S rna mutation conferring resistance to macrolides and streptogramins antibiotics	b	1892	20	2904	89.29	100.38	88.95	99.62	1831.46	1.0e-26
CARD CDO61513.1	<i>Efra</i>	c	1394	10	1457	98.63	99.59	99.04	100.41	1362.68	1.0e-26
CARD AAO82601.1	<i>E. faecalis</i> liaf mutant conferring daptomycin resistance	d	711	5	732	98.91	100.00	98.91	100.00	694.70	1.0e-26
CARD AEA93051.1	<i>E. faecalis</i> cls conferring resistance to daptomycin	e	1422	10	1446	99.38	100.00	99.38	100.00	1390.96	1.0e-26
CARD NP_863168.1	<i>E. faecium</i> chloramphenicol acetyltransferase	c	528	4	648	93.67	100.00	93.67	100.00	513.47	1.0e-26
CARD EOD99669.1	<i>Dfre</i>	f	459	3	495	97.37	100.00	97.37	100.00	447.85	1.0e-26
CARD AAO82600.1	<i>E. faecalis</i> lias mutant conferring daptomycin resistance	d	1083	8	1104	99.28	100.00	99.28	100.00	1058.88	1.0e-26
CARD CAJ67339.1	<i>Tetm</i>	g	1617	13	1920	94.69	100.00	94.69	100.00	1576.26	1.0e-26
CARD YP_006374661.1	<i>E. faecium</i> EF-Tu mutants conferring resistance to GE2270A	h	882	9	1272	85.93	99.29	86.54	100.71	854.04	1.0e-26
CARD AAA22851.1	<i>Tet(L)</i>	i	1371	9	1377	99.78	100.00	99.78	100.00	1341.36	1.0e-26
CARD AAT46077.1	<i>Lsaa</i>	j	1443	10	1497	98.73	100.00	98.73	100.00	1410.90	1.0e-26
CARD WP_002389492.1	<i>E. faecalis</i> gshf with mutation conferring daptomycin resistance	k	2232	15	2271	99.38	100.00	99.38	100.00	2185.32	1.0e-26
CARD NP_816529.1	<i>E. faecalis</i> liar mutant conferring daptomycin resistance	d	621	4	633	99.21	100.00	99.21	100.00	606.84	1.0e-26
VFDB VFG002165	Endocarditis specific antigen	d	921	5	927	99.68	100.00	99.68	100.00	904.26	1.0e-26
VFDB VFG002166	Collagen adhesin protein	d	1644	11	2025	91.70	93.04	98.57	107.48	1608.56	1.0e-26
VFDB VFG002189	Phosphatidate cytidyltransferase	d	786	4	801	99.25	100.00	99.25	100.00	771.45	1.0e-26
VFDB VFG002190	Undecaprenyl diphosphate synthase	d	798	4	816	99.14	100.00	99.14	100.00	783.19	1.0e-26
VFDB VFG002196	Polysaccharide lyase, family 8	d	3597	22	4119	98.37	106.99	91.94	93.46	3530.76	1.0e-26
VFDB VFG002197	Sugar-binding transcriptional regulator, lacI family	d	987	6	1011	99.11	100.00	99.11	100.00	968.79	1.0e-26
VFDB VFG042976	Endocarditis and biofilm-associated pilus tip protein <i>ebpa</i>	d	3261	18	3312	99.46	100.00	99.46	100.00	3206.87	1.0e-26
VFDB VFG042977	Endocarditis and biofilm-associated pilus minor subunit <i>ebpb</i>	d	1407	8	1431	99.37	100.00	99.37	100.00	1381.67	1.0e-26
VFDB VFG042978	Endocarditis and biofilm-associated pilus major subunit <i>ebpc</i>	d	1855	10	1878	99.68	100.32	99.36	99.68	1822.37	1.0e-26
VFDB VFG042979	Sortase	d	832	5	855	99.18	100.35	98.83	99.65	816.50	1.0e-26

VFDB VFG043508	<i>E. faecalis</i> surface protein Fss1, fibrinogen binding protein	d	5700	29	5964	98.51	100.00	98.51	100.00	5613.26	1.0e-26
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Template: Reference gene sequence; Genome: Genome that contains template gene; a: *Staphylococcus aureus*; b: *Streptococcus pneumoniae*; c: *E. faecium*; d: *E. faecalis* V583; e: *E. faecalis* OG1RF; f: *E. faecalis* EnGen0074; g: *Clostridium difficile* 630; h: *E. faecium* DO; i: *Geobacillus stearothermophilus*; j: *E. faecalis*; k: *Enterococcus*. GAS: Global alignment score of the template; EAS: Expected alignment score; TL: Template gene length in nucleotides; TI: Template Identity in percentage between the template and query, over the length of the matching query; TC: Template coverage in percentage of the template that is covered by the query; QI: Query identity in percentage between the query and template sequence, over the length of the matching query sequence; QC: Query coverage about the length of the matching query divided by the length of template; q value: Quantile from McNemars test, to test whether the current template is a significant hit.; p value: p-value corresponding to the obtained q-value.

Table S3: Antimicrobial resistant phenotype results observed in *Enterococcus faecalis* IRMC827A.

# Antimicrobial	Class	WGS-predicted phenotype	Match	Genetic background
Tetracycline	Tetracycline	Resistant	3	<i>tet(L) (tet(L)_M29725), tet(M) (tet(M) EU182585)</i>
Tigecycline	Tetracycline	No resistance	0	
Doxycycline	Tetracycline	Resistant	3	<i>tet(L) (tet(L)_M29725), tet(M) (tet(M) EU182585)</i>
Minocycline	Tetracycline	Resistant	2	<i>tet(M) (tet(M) EU182585)</i>
Metronidazole	Nitroimidazole	No resistance	0	
Rifampicin	Rifamycin	No resistance	0	
Hydrogen peroxide	Peroxide	No resistance	0	
Cefoxitin	Beta-lactam	No resistance	0	
Ampicillin	Beta-lactam	No resistance	0	
Cefepime	Beta-lactam	No resistance	0	
Ticarcillin	Beta-lactam	No resistance	0	
Amoxicillin	Beta-lactam	No resistance	0	
Ceftazidime	Beta-lactam	No resistance	0	
Ticarcillin+clavulanic acid	Beta-lactam	No resistance	0	
Ceftriaxone	Beta-lactam	No resistance	0	
Meropenem	Beta-lactam	No resistance	0	
Cephalotin	Beta-lactam	No resistance	0	
Unknown beta-lactam	Beta-lactam	No resistance	0	
Aztreonam	Beta-lactam	No resistance	0	
Piperacillin+tazobactam	Beta-lactam	No resistance	0	
Cephalothin	Beta-lactam	No resistance	0	
Cefixime	Beta-lactam	No resistance	0	

Cefotaxime+clavulanic acid	Beta-lactam	No resistance	0	
Penicillin	Beta-lactam	No resistance	0	
Imipenem	Beta-lactam	No resistance	0	
Ampicillin+clavulanic acid	Beta-lactam	No resistance	0	
Ceftazidime+avibactam	Beta-lactam	No resistance	0	
Ertapenem	Beta-lactam	No resistance	0	
Piperacillin	Beta-lactam	No resistance	0	
Amoxicillin+clavulanic acid	Beta-lactam	No resistance	0	
Temocillin	Beta-lactam	No resistance	0	
Piperacillin+clavulanic acid	Beta-lactam	No resistance	0	
Cefotaxime	Beta-lactam	No resistance	0	
Quinupristin+dalfopristin	Streptogramin a	No resistance	0	
Dalfopristin	Streptogramin a	Resistant	2	<i>lsa(A) (lsa(A)_AY737526)</i>
Virginiamycin m	Streptogramin a	Resistant	2	<i>lsa(A) (lsa(A)_AY737526)</i>
Pristinamycin iia	Streptogramin a	Resistant	2	<i>lsa(A) (lsa(A)_AY737526)</i>
Temperature	Heat	No resistance	0	
Fosfomycin	Fosfomycin	No resistance	0	
Fusidic acid	Steroid antibacterial	No resistance	0	
Chloramphenicol	Amphenicol	Resistant	2	<i>cat (cat_U35036)</i>
Florfenicol	Amphenicol	No resistance	0	
Mupirocin	Pseudomonic acid	No resistance	0	
Linezolid	Oxazolidinone	No resistance	0	
Tiamulin	Pleuromutilin	No resistance	0	
Formaldehyde	Aldehyde	No resistance	0	
Ceftiofur	Under_development	No resistance	0	
Spectinomycin	Aminocyclitol	No resistance	0	
Butirosin	Aminoglycoside	No resistance	0	
Isepamicin	Aminoglycoside	No resistance	0	
Arbekacin	Aminoglycoside	No resistance	0	
Kasugamycin	Aminoglycoside	No resistance	0	

Kanamycin	Aminoglycoside	No resistance	0	
Netilmicin	Aminoglycoside	No resistance	0	
Paromomycin	Aminoglycoside	No resistance	0	
Apramycin	Aminoglycoside	No resistance	0	
Unknown aminoglycoside	Aminoglycoside	No resistance	0	
Butiromycin	Aminoglycoside	No resistance	0	
Amikacin	Aminoglycoside	No resistance	0	
Astromicin	Aminoglycoside	No resistance	0	
Tobramycin	Aminoglycoside	No resistance	0	
Ribostamycin	Aminoglycoside	No resistance	0	
Neomycin	Aminoglycoside	No resistance	0	
Hygromycin	Aminoglycoside	No resistance	0	
Fortimicin	Aminoglycoside	No resistance	0	
Dibekacin	Aminoglycoside	No resistance	0	
Sisomicin	Aminoglycoside	No resistance	0	
Gentamicin	Aminoglycoside	No resistance	0	
Streptomycin	Aminoglycoside	Resistant	3	<i>str (str_X92946)</i>
Bleomycin	Aminoglycoside	No resistance	0	
Lividomycin	Aminoglycoside	No resistance	0	
Clindamycin	Lincosamide	Resistant	2	<i>lsa(A) (lsa(A)_AY737526)</i>
Lincomycin	Lincosamide	Resistant	2	<i>lsa(A) (lsa(A)_AY737526)</i>
Colistin	Polymyxin	No resistance	0	
Trimethoprim	Folate pathway antagonist	Resistant	3	<i>dfrG (dfrG_AB205645)</i>
Sulfamethoxazole	Folate pathway antagonist	No resistance	0	
Chlorhexidine	Quaternary ammonium compound	No resistance	0	
Benzylkonium chloride	Quaternary ammonium compound	No resistance	0	
Cetylpyridinium chloride	Quaternary ammonium compound	No resistance	0	

Ethidium bromide	Quaternary ammonium compound	No resistance	0	
Carbomycin	Macrolide	No resistance	0	
Azithromycin	Macrolide	No resistance	0	
Telithromycin	Macrolide	No resistance	0	
Erythromycin	Macrolide	No resistance	0	
Oleandomycin	Macrolide	No resistance	0	
Spiramycin	Macrolide	No resistance	0	
Tylosin	Macrolide	No resistance	0	
Virginiamycin s	Streptogramin b	No resistance	0	
Pristinamycin ia	Streptogramin b	No resistance	0	
Quinupristin	Streptogramin b	No resistance	0	
Vancomycin	Glycopeptide	No resistance	0	
Teicoplanin	Glycopeptide	No resistance	0	
Fluoroquinolone	Quinolone	No resistance	0	
Unknown quinolone	Quinolone	No resistance	0	
Nalidixic acid	Quinolone	Resistant	3	<i>gyrA (p.S83Y), parC (p.S80I)</i>
Ciprofloxacin	Quinolone	Resistant	3	<i>gyrA (p.S83Y), parC (p.S80I)</i>

Match: 0: No match found; 1: Match < 100% ID AND match length < ref length; 2: Match = 100% ID AND match length < ref length; 3: Match = 100% ID AND match length = ref length.

Table S4: Antimicrobial resistant phenotype specific for *Enterococcus faecalis* results observed in *E. faecalis* IRMC827A.

# Antimicrobial	Class	WGS-predicted phenotype	Match	Genetic background
Tetracycline	Tetracycline	Resistant	3	<i>tet(L) (tet(L)_M29725), tet(M) (tet(M)_EU182585)</i>
Tigecycline	Tetracycline	No resistance	0	
Teicoplanin	Glycopeptide	No resistance	0	
Ciprofloxacin	Quinolone	Resistant	3	<i>gyrA (p.S83Y), parC (p.S80I)</i>
Erythromycin	Macrolide	No resistance	0	
Vancomycin	Glycopeptide	No resistance	0	
Linezolid	Oxazolidinone	No resistance	0	
Fosfomycin	Fosfomycin	No resistance	0	
Chloramphenicol	Amphenicol	Resistant	2	<i>cat (cat_U35036)</i>
Gentamicin	Aminoglycoside	No resistance	0	

Match: 0: No match found; 1: Match < 100% ID AND match length < ref length; 2: Match = 100% ID AND match length < ref length; 3: Match = 100% ID AND match length = ref length.

Table S5: List of pathogenic protein families of the IRMC827A.

	Organism	Class	Protein function	Protein ID	Identity
1	<i>Enterococcus faecalis</i> V583	Lactobacillales	sigma-54 interaction domain protein	AAO80815	100%
2	<i>Enterococcus faecalis</i> V583	Lactobacillales	lipoprotein, putative	AAO79950	99.61%
3	<i>Enterococcus faecalis</i> V583	Lactobacillales	pheromone binding protein, putative	AAO79943	100%
4	<i>Enterococcus faecalis</i> V583	Lactobacillales	peptide ABC transporter, peptide-binding protein	AAO80715	99.82%
5	<i>Enterococcus faecalis</i> V583	Lactobacillales	pheromone binding protein	AAO82723	100%
6	<i>Enterococcus faecalis</i> V583	Lactobacillales	membrane protein, putative	AAO81879	99.6%
7	<i>Enterococcus faecalis</i> V583	Lactobacillales	DNA-binding response regulator, AraC family	AAO81949	99.59%
8	<i>Enterococcus faecalis</i> V583	Lactobacillales	C4-dicarboxylate transporter, putative	AAO79983	100%
9	<i>Enterococcus faecalis</i> V583	Lactobacillales	D-alanyl-D-alanine carboxypeptidase	AAO82807	99.59%
10	<i>Enterococcus faecalis</i> V583	Lactobacillales	ribonuclease PH/Ham1 protein	AAO80922	99.75%
11	<i>Enterococcus faecalis</i> V583	Lactobacillales	FolC family protein	AAO82616	100%
12	<i>Enterococcus faecalis</i> V583	Lactobacillales	regulatory protein pfoR, putative	AAO79972	99.73%
13	<i>Enterococcus faecalis</i> V583	Lactobacillales	transposase, putative	AAO80721	99.72%
14	<i>Enterococcus faecalis</i> V583	Lactobacillales	carbohydrate kinase, pfkB family	AAO80652	99.70%
15	<i>Enterococcus faecalis</i> V583	Lactobacillales	sugar-binding transcriptional regulator,	AAO80046	100%
16	<i>Enterococcus faecalis</i> V583	Lactobacillales	iron compound ABC transporter, iron compound-binding protein	AAO81420	100%
17	<i>Enterococcus faecalis</i> V583	Lactobacillales	aminoglycoside 6-adenylyltransferase	AAO82553	99.65%
18	<i>Enterococcus faecalis</i> V583	Lactobacillales	MutT/nudix family protein	AAO82404	100%
19	<i>Enterococcus faecalis</i> V583	Lactobacillales	PTS system, IIC component	AAO82884	100%
20	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO80309	99.61%

21	<i>Enterococcus faecalis</i> V583	Lactobacillales	phosphosugar-binding transcriptional regulator, RpiR family, putative	AAO82731	100%
22	<i>Enterococcus faecalis</i> V583	Lactobacillales	hydrolase, haloacid dehalogenase-like family	AAO82386	99.58%
23	<i>Enterococcus faecalis</i> V583	Lactobacillales	cell division protein DivIVA	AAO80808	100%
24	<i>Enterococcus faecalis</i> V583	Lactobacillales	MgtC family protein	AAO80322	100%
25	<i>Enterococcus faecalis</i> V583	Lactobacillales	transcriptional regulator, Crp/Fnr family	AAO79952	100%
26	<i>Enterococcus faecalis</i> V583	Lactobacillales	nitroreductase family protein, putative	AAO80478	100%
27	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO82554	100%
28	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO82735	100%
29	<i>Enterococcus faecalis</i> V583	Lactobacillales	transcriptional regulator, TetR family	AAO82741	100%
30	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO81470	100%
31	<i>Enterococcus faecalis</i> V583	Lactobacillales	signal peptidase I	AAO81456	100%
32	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO80229	100%
33	<i>Enterococcus faecalis</i> V583	Lactobacillales	PTS system, IIB component	AAO82883	100%
34	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO82774	100%
35	<i>Enterococcus faecalis</i> V583	Lactobacillales	transcriptional regulator SrlR	AAO82973	100%
36	<i>Enterococcus faecalis</i> V583	Lactobacillales	PTS system, IIA component	AAO80516	100%
37	<i>Enterococcus faecalis</i> V583	Lactobacillales	transcriptional regulator, MarR family	AAO81446	100%
38	<i>Enterococcus faecalis</i> V583	Lactobacillales	PTS system, IIA component, putative	AAO82882	100%
39	<i>Enterococcus faecalis</i> V583	Lactobacillales	PTS system, IIA component	AAO80316	100%
40	<i>Enterococcus faecalis</i> V583	Lactobacillales	nrdI protein	AAO80327	100%
41	<i>Enterococcus faecalis</i> V583	Lactobacillales	Conserved hypothetical protein	AAO81798	100%
42	<i>Enterococcus faecalis</i> V583	Lactobacillales	Conserved hypothetical protein	AAO82991	100%

43	<i>Enterococcus faecalis</i> V583	Lactobacillales	competence protein	AAO81779	100%
44	<i>Enterococcus faecalis</i> V583	Lactobacillales	ferredoxin	AAO81330	100%
45	<i>Enterococcus faecalis</i> V583	Lactobacillales	conserved hypothetical protein	AAO80806	100%
46	<i>Enterococcus faecalis</i> V583	Lactobacillales	ribosomal protein L29	AAO80083	100%
47	<i>Enterococcus faecalis</i> V583	Lactobacillales	hypothetical protein	AAO81074	100%
48	<i>Enterococcus faecalis</i> V583 plasmid pTEF1	Lactobacillales	conserved domain protein	AAO83066	100%
49	<i>Enterococcus faecalis</i> V583 plasmid pTEF1	Lactobacillales	site-specific recombinase, resolvase family	AAO83065	100%
50	<i>Enterococcus faecalis</i> V583 plasmid pTEF1	Lactobacillales	mpB/MucB/SamB family protein	AAO83069	99.77%
51	<i>Streptococcus pneumoniae</i> G54	Lactobacillales	Tn5251 transcriptional regulator Cro/CI family	ACF55955	100%
52	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu3 DNA	Bacillales	plasmid recombination enzyme	BAF76914	100%
53	<i>Streptococcus suis</i> 05ZYH33	Lactobacillales	Tn916, transposase	ABP89883	100%
54	<i>Streptococcus agalactiae</i> 2603V/R	Lactobacillales	Tn916, hypothetical protein	AAM99805	100%
55	<i>Streptococcus pneumoniae</i> Hungary19A-6	Lactobacillales	conserved hypothetical protein	ACA36408	100%

Table S6: List of mobile genetic elements associated with antibiotic resistance of the IRMC827A.

MGE no	name	prediction method	type	allele_len	e_value	identity	coverage	gaps	substitution	contig	start	stop	cigar
1	Tn6009	alignment to reference	Integrative Conjugative Element	1889	0	0.999471	1	0	1	Scaffold2	31342	33230	M1889
6	ISS1N	alignment to reference	Insertion sequence	808	0	0.985149	1	0	12	Scaffold22	16162	16969	M808

dfrG gene

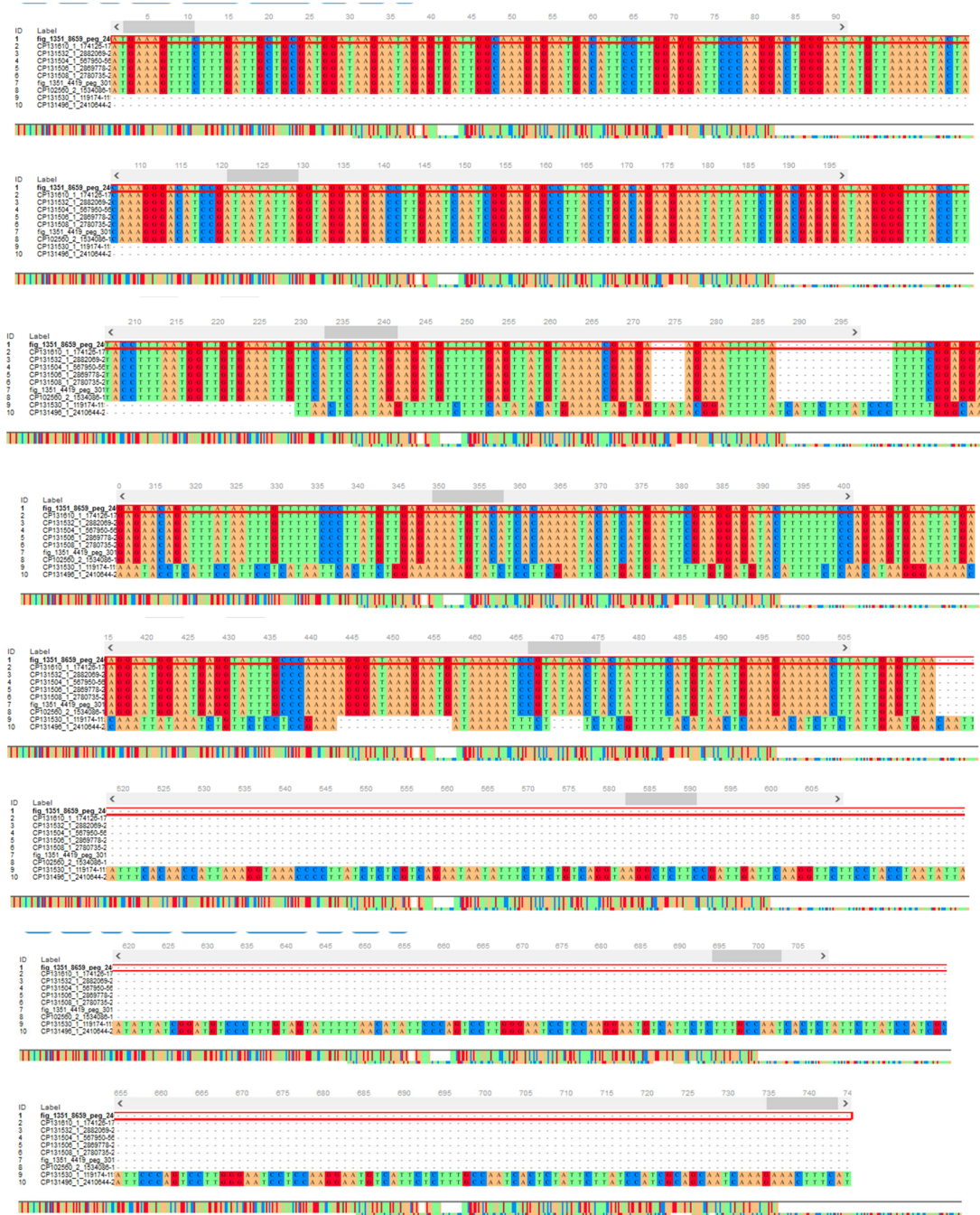


Figure S1: Multiple sequence alignment of *dfrG* gene from *Enterococcus faecalis* IRMC827A.