Fallico et al. Plasmids of raw milk cheese isolate *L. lactis* subsp. *lactis* biovar. diacetylactis DPC3901 suggest a plant-based origin for the strain. Supplementary file_Tables S1-S4

TABLE S1. List of ORFs identified in pVF50 (size 53,876 bps; GC content 34.5%)

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
orf1	518	1243	+	241	30.71	Putative phage transcriptional repressor; Peptidase S24_S26_LexA-like superfamily (cd06462)	putative transcriptional regulator	73/192 (38%)	7e-30	*Streptococcus thermophilus*
repA	1748	3100	+	450	31.18	Initiator Replication protein (pfam01051)	replication protein	448/450 (99%)	0.0	*Lactococcus lactis*, pGdh442
parA	3853	4611	+	252	28.83	ParA domain (cd02042); Soj domain, ATPases involved in chromosome partitioning (COG1192)	partition protein A	250/252 (99%)	1e-178	*Lactococcus lactis*, pGdh442
parB	4616	5344	+	242	33.88	ParB-like nuclease domain (pfam02195)	partition protein B	241/242 (99%)	3e-173	*Lactococcus lactis*, pGdh442
tnp-IS110	6092	7348	+	418	38.03	Transposase belonging to the IS110 family; Transposase_20 domain (pfam02371); Transposase_9 domain (pfam01548)	transposase, IS116/IS110/IS902 family protein	314/419 (75%)	0.0	*Streptococcus pneumoniae* SP19-BS75
orf6	7514	7849	+	111	34.82	Transposase and inactivated derivatives, Tra5 (COG2801); truncated, C-terminus	transposase	106/110 (97%)	1e-58	*L. lactis* subsp. *cremoris* SK11, pSK11P
orf7	7860	8213	+	117	36.75	Transposase and inactivated derivatives, Tra5 (COG2963); Helix-turn-helix domain of Hin and related proteins (cl01116); truncated, C-terminus	IS-LL6 transposase/hypothetical protein fusion	115/115 (100%)	8e-60	*L. lactis* subsp. *cremoris* SK11, pSK11P
tnp-IS3	8171	9070	+	299	38.46	Transposase belonging to the IS3 family; putative transposase OrfB (PHA02517)	unnamed protein product	298/299 (99%)	5e-177	*Lactococcus lactis*
orf9	9329	11191	+	620	40.91	Cation transport ATPase (COG2217); Haloacid Dehalogenase superfamily (TIGR01488); E1-E2 ATPase (pfam00122)	cation transport ATPase	617/620 (99%)	0.0	*L. lactis* subsp. *lactis* KF147, pKF147A
orf10	11894	12121	+	75	37.77	Heavy-metal-associated domain (pfam00403); Copper chaperone [Inorganic ion transport and metabolism] (COG2608)	copper chaperone	75/75 (100%)	3e-34	*L. lactis* subsp. *lactis* KF147, pKF147A
dpsB	12170	12715	+	181	35.91	DPS protein, ferritin-like diiron-binding domain (cd01043)	DNA binding protein	181/181 (100%)	9e-101	*L. lactis* subsp. *lactis* KF147, pKF147A
flp	12801	13490	+	229	38.71	cAMP-binding proteins (COG0664); effector domain of the CAP family of transcription factors (cd00038); Winged helix-turn-helix (WHTH) DNA-binding domain of the GntR family of transcriptional regulators (cl00088)	FNR family transcriptional regulator	225/229 (99%),	5e-129	*L. lactis* subsp. *lactis* KF147, pKF147A
oppD	14464	15480	+	338	37.77	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component, DppD (COG0444); ABC_NikE_OppD_transporters (cd03257)	oligopeptide ABC trasporter ATP binding protein	333/338 (99%)	0.0	*L. lactis* subsp. *lactis* IL1403
oppF	15477	16436	+	319	35.63	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component, DppF (COG0444); ABC_NikE_OppD_transporters (cd03257)	oligopeptide transporter F	316/319 (99%)	0.0	*Lactococcus lactis*, pGdh442
oppB	16417	17376	+	319	38.14	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components (COG0601); Transmembrane subunit found in Periplasmic Binding Protein (PBP)-dependent ATP-Binding Cassette (ABC) transporters (cd06261)	oligopeptide transporter B	316/319 (99%)	0.0	*Lactococcus lactis*, pGdh442
oppC	17386	18270	+	294	36.39	ABC-type uncharacterized transport system, permease component (COG4239); Transmembrane subunit found in Periplasmic Binding Protein (PBP)-dependent ATP-Binding Cassette (ABC) transporters (cd06261)	oligopeptide transporter C	289/294 (99%)	1e-164	*Lactococcus lactis*, pGdh442
oppA	18375	20177	+	600	37.37	PBP2_Lactococcal_OppA_like transport system, substrate binding domain (cd08510)	oligopeptide transporter A	576/599 (97%)	0.0	*Lactococcus lactis*, pGdh442
pepO	20302	22185	+	627	35.17	Predicted metalloendopeptidase PepO (COG3590); Peptidase family M13 (pfam01431)	oligoendopeptidase O	623/626 (99%)	0.0	*L. lactis* subsp. *lactis* KF147, pKF147A
tnp-IS946	23487	22849	-	212	39.93	rve, Integrase core domain (pfam00665); Transposase and inactivated derivatives (COG3316)	transposase	201/213 (95%)	3e-113	*Lactococcus lactis*, pTR2030
nah	24387	25532	+	381	30.44	Sodium/hydrogen exchanger family (pfam00999); Kef-type K+ transport systems, membrane components (COG0475)	Na+/H+ antiporter	374/374 (100%)	0.0	*Lactococcus lactis*, pGdh442
orf21	25545	26882	+	445	34.23	potassium uptake protein, TrkH family (TIGR00933); Trk-type K+ transport systems, membrane components, TrkG (COG0168)	putative K+ transporter	443/445 (99%)	0.0	*Lactococcus lactis*, pGdh442

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
orf22	26902	27573	+	223	32.88	K+ transport systems, NAD-binding component, TrkA (COG0569); Anion permease ArsB/NhaD (cl09110); Rossmann-fold NAD(P)(+)-binding proteins (cl09931)	putative K+ transport system TrkA	213/214 (99%)	5e-118	*Lactococcus lactis*, pGdh442
orf23	28408	27952	-	152	39.6	transposase IS1216E belonging to IS6 family; truncated, C-terminus	transposase	151/152 (99%)	8e-84	*L. lactis* subsp. *lactis* K214, pK214
orf24	29250	28969	-	93	33.69	hypothetical protein	hypothetical protein pGdh442_p07	92/93 (99%)	2e-47	*Lactococcus lactis*, pGdh442
orf25	29314	29685	+	124	33.81	Protein family of unknown function, DUF322 (PFAM03780); may be involved in stress response; truncated, C-terminus	General stress protein, Gls24 family	123/125 (99%)	3e-60	*L. lactis* subsp. *lactis* KF147, pKF147A
cspA	30661	30861	+	66	33.33	putative cold shock protein	cold shock protein	66/66 (100%)	3e-29	*L. lactis* subsp. *lactis* CV56
cspC	30992	31192	+	66	32.82	Cold-shock' DNA-binding domain (pfam00313); Ribosomal protein S1-like RNA-binding domain (cl09927)	cold shock protein	64/66 (97%)	1e-29	*L. lactis* subsp. *lactis* KF147
cspB	31397	31672	+	91	32.6	Cold-shock' DNA-binding domain (pfam00313); Ribosomal protein S1-like RNA-binding domain (cl09927)	cold shock protein	90/91 (99%)	9e-46	*L. lactis* subsp. *lactis* KF147
orf29	32168	32761	+	197	31.47	Helix-turn-helix XRE-family like proteins (cd00093)	XRE family transcriptional regulator	169/179 (95%)	1e-85	*L. lactis* subsp. *lactis* KF147, pKF147A
mobC	33951	34397	+	148	26.8	Bacterial mobilisation protein, MobC (pfam05713)	ORF57	104/122 (86%)	4e-52	Lactococcus lactis, pNP40
mobD	34324	34836	+	170	32.15	Relaxase/Mobilisation nuclease domain (pfam03432)	relaxase	160/168 (95%)	5e-92	*L. lactis* subsp. *lactis* CV56
tnp-ISLpl1	35165	34743	+	140	36.19	Transposase and inactivated derivatives, IS30 family (COG2826)	putative transposase of ISLpl1	139/140 (99%)	1e-75	*Lactococcus lactis*, pGdh442
dld	35423	37102	+	559	38.87	D-lactate dehydrogenase, membrane binding (pfam09330); FAD/FMN-containing dehydrogenases (COG0277)	D-lactate dehydrogenase	558/559 (99%)	0.0	*Enterococcus faecalis* TX1322
tnp1-IS150	37206	37757	+	183	36.24	Transposase and inactivated derivatives, IS3 family (COG2963)	transposase	182/183 (99%)	6e-103	*L. lactis* subsp. *cremoris* SK11
tnp2-IS150	37760	38581	+	273	34.67	Integrase core domain (pfam00665); Transposase and inactivated derivatives, IS3 family (COG2801)	transposase	269/273 (99%)	2e-158	*Enterococcus faecalis* T1
orf36	38592	38942	+	117	36.75	Transposase and inactivated derivatives, IS3 family (COG2963); Helix-turn-helix DNA-binding domain of Hin and related proteins (cl01116)	IS-LL6 transposase/hypothetical protein fusion	115/115 (100%)	8e-60	*L. lactis* subsp. *cremoris* SK11, pSK11P
orf37	38915	39799	+	295	38.75	Transposase and inactivated derivatives, IS3 family (COG2963); Helix-turn-helix DNA-binding domain of Hin and related proteins (cl01116)	unnamed protein product	294/295 (99%)	8e-175	*Lactococcus lactis*, pGdh442
orf38	39944	40387	-	148	36.93	Integrase core domain (pfam00665); Transposase and inactivated derivatives, IS3 family (COG2801); truncated	IS981 transposase B	92/136 (68%)	3e-42	*L. lactis* subsp. *lactis* KF147
pepF	40372	42177	-	601	33.94	Oligoendopeptidase F (COG1164); Peptidase family M3B Oligopeptidase F (cd06459)	oligopeptidase F	597/602 (99%)	0.0	*L. lactis* subsp. *cremoris* SK11, pSK11P
tnp-IS1297	43658	44335	+	225	34.36	transposase, IS1297 family	integrase core domain protein	166/226 (73%)	1e-110	*Enterococcus faecalis* TX1302
lacX	44397	45296	-	299	37.44	Aldose 1-epimerase, similar to Lactococcus lactis lacX (cd09024); Galactose mutarotase and related enzymes (COG2017); truncated, N-terminus	galactose mutarotase-like protein	257/299 (86%)	0.0	*L. lactis*, pLP712
lacG	45588	47021	-	477	38.15	Glycosyl hydrolase family (pfam00232); 6-phospho-beta-galactosidase (TIGR01233)	6-phospho-beta-galactosidase	475/477 (99%)	0.0	*Lactobacillus sakei*
lacE	47132	48838	-	568	41	phosphotransferase system, lactose specific, IIC component (TIGR00394); PTS_IIB_lactose (cd05565)	PTS family lactose porter IICB component	557/568 (98%)	0.0	*Enterococcus casseliflavus* ATCC 12755
lacF	48838	49155	-	105	42.53	PTS_IIA, PTS system, lactose/cellobiose specific IIA subunit (cd00215)	PTS family lactose-N,N-diacetylchitobiose-beta-glucoside porter component IIA	105/105 (100%)	3e-54	*Enterococcus faecium* TX1330

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
lacD	49183	50163	-	326	39.05	Tagatose 1,6-diphosphate aldolase (TIGR01232)	tagatose 1,6-diphosphate aldolase	322/326 (99%)	0.0	*Enterococcus faecium* TX1330
lacC	50167	51099	-	310	36.66	1-phosphofructokinase (FruK), minor 6-phosphofructokinase (pfkB) and related sugar kinases (cd01164); tagatose-6-phosphate kinase, lacC (TIGR01231)	tagatose-6-phosphate kinase	307/310 (99%)	2e-176	*Enterococcus faecium* TX1330
lacB	51110	51625	-	171	39.76	Galactose-6-phosphate isomerase subunit LacB (TIGR01119)	galactose-6-phosphate isomerase, subunit LacB	170/171 (99%)	2e-95	*Lactobacillus sakei*
lacA	51642	52067	-	141	39.0	Galactose-6-phosphate isomerase subunit LacA (TIGR01118)	galactose-6-phosphate isomerase, subunit LacA	140/141 (99%)	1e-74	*Lactococcus lactis*, pLP712
lacR	52567	53334	-	255	34.63	Winged helix-turn-helix DNA-binding domain of the GntR family of transcriptional regulators (cd07377); Bacterial regulatory proteins, deoR family (pfam00455); truncated, N-terminus	lactose phosphotransferase system repressor	238/254 (94%)	2e-160	*L. lactis*, pLP712

TABLE S2. List of ORFs identified in pVF22 (size 22,166 bp; GC content 35.14%)

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
repB	241	1566	+	441	36.58	hypothetical protein	replication protein B	344/383 (90%)	0.0	*L. lactis* subsp. *lactis* CV56
orfX	1559	2596	+	345	39.9	replication-associated protein, similar to OrfX	hypothetical protein pDB0R0p06	191/202 (94%)	8e-103	*L. lactis* subsp. *lactis* bv. *diacetylactis*
hsdR	2607	3254	+	215	36.43	type I restriction-modification system restriction subunit, N-terminus; hsdS domain, C-terminus	restriction subunit	135/181 (74%)	7e-66	*L. lactis* subsp. *lactis* bv. *diacetylactis*
corA1	3440	4390	+	316	31.96	Mg2+ and Co2+ transport protein, CorA superfamily	CorA like magnesium and cobalt transport protein	316/316 (100%)	0.0	*L. lactis* subsp. *cremoris* MG1363
orf5	4772	5032	+	86	33.33	hypothetical protein; similar to repA	hypothetical protein pAH33_04	85/86 (98%)	2e-42	*L. lactis*
corA2	5126	6034	+	302	43.15	Mg2+ and Co2+ transport protein, CorA superfamily	hypothetical protein pNZ4000_44	300/302 (99%)	4e-174	*L. lactis* subsp. *cremoris*
orf7	7044	9158	+	704	40.29	ATP-dependent Clp protease, ATP-binding subunit ClpL	ATP-dependent Clp protease, ATP-binding subunit ClpL	698/704 (99%)	0.0	*Enterococcus casseliflavus ATCC 12755*
orf8	9346	9822	+	158	40.04	truncated transposase	integrase core domain protein	148/158 (94%)	5e-82	*Enterococcus faecalis* TX4244
orf9	9917	10492	+	191	35.07	putative glycopeptide antibiotics resistance protein	hypothetical protein	189/191 (98%)	1e-101	*Streptococcus salivarius*
pinR	10866	11420	+	184	34.78	Site-specific Serine Recombinase	resolvase	182/184 (99%)	2e-103	*L. lactis* subsp. *lactis* KF147
orf11	12130	11594	–	178	32.95	putative acetyltransferase, GNAT family	Acetyltransferase	87/177 (49%)	2e-40	*Streptococcus suis* 05ZYH33
tnp1-IS1216	12937	12293	–	214	38	transposase, IS1216 family	IS1216 transposase	212/214 (99%)	1e-120	*Enterococcus faecalis* V583
orf13	12971	13216	+	81	27.98	hypothetical protein	hypothetical protein pLK0018_p17	80/81 (99%)	9e-38	*Lactococcus garvieae*, pLK0018
orf14	14046	15986	+	646	33.38	tetracycline resistance protein	tetracycline resistance protein	646/646 (100%)	0.0	*Lactococcus garvieae*, pLK0018
orf15	16074	16241	+	55	35.75	hypothetical protein	hypothetical protein pK214_p31	54/55 (98%)	2e-23	*L. lactis* subsp. *lactis*, pK214
tnp2-IS1216	17252	16566	–	228	37.71	transposase, IS1216 family	IS1216 transposase	228/228 (100%)	5e-131	*Enterococcus faecalis*, pEF-01
orf17	18401	18658	+	85	38.43	DNA recombinase, C-terminal fragment	DNA recombinase	82/85 (96%)	8e-42	*L. lactis* subsp. *lactis*
orf18	18787	19110	+	107	34.26	conserved hypothetical protein	cytochrome B	104/107 (97%)	1e-47	*L. lactis* subsp. *lactis* CV56
mobC1	19082	19576	+	164	34.34	MobC-like mobilization protein	conserved hypothetical protein	163/164 (98%)	3e-88	*Enterococcus faecalis* TX2141
mobA	19555	20787	+	410	40.4	MobA-like mobilization protein	Relaxase/Mobilisation nuclease domain	406/410 (99%)	0.0	*Enterococcus* sp. 7L76
mobB	20784	21407	+	207	37.35	MobB-like mobilization protein	putative mobilization protein	184/207 (88%)	3e-104	*L. lactis* subsp. *cremoris*
mobC2	21424	22026	+	200	32	MobC-like mobilization protein	putative mobilization protein	198/200 (99%)	5e-111	*L. lactis* subsp. *cremoris*

TABLE S3. List of ORFs identified in pVF21 (size 21,728 bp; GC content 33.59%)

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
orf1	1506	1	–	501	28.03	Primosomal protein N' (replication factor Y), superfamily II helicase (COG1198)	hypothetical protein HMPREF9397_2038	214/510 (42%)	6e-92	*Streptococcus sanguinis* SK1087
tnp1A-IS981	2179	1679	–	166	35.14	transposase, IS981 family; C-terminus, frame shift	transposase	148/163 (90%)	3e-85	*L. lactis* subsp. *cremoris* SK11
tnp1B-IS981	2502	2161	–	119	40.33	transposase, IS981 family; N-terminus, frame shift	transposase	100/117 (85%)	2e-53	*L. lactis* subsp. *cremoris* SK11
tnp2-IS981	2774	2514	–	86	37.98	transposase of IS981, IS3 family	transposase	85/86 (99%)	8e-42	*L. lactis* subsp. *lactis* KF147
orf5	4964	3867	–	365	26.48	hypothetical protein containing the DGQHR domain (TIGR03187)	hypothetical protein HMPREF9382_0017	140/362 (39%)	5e-46	*Streptococcus sanguinis* SK115
repB	6967	8118	+	383	33.5	replication protein RepB	replication protein	378/383 (98%)	0.0	*L. lactis* subsp. c*remoris*, pNZ4000
orfX	8118	8747	+	209	33.33	replication-associated protein, similar to OrfX	hypothetical protein LACR_E7	126/222 (56%)	1e-50	*L. lactis* subsp. *cremoris* SK11
hsdR	8758	11835	+	1025	37.91	type I restriction-modification system, restriction subunit	hypothetical protein pAH82_p15	1017/1025 (99%)	0.0	*L. lactis* subsp. *lactis*
hsdM	11817	13430	+	537	39.78	type I restriction-modification system, modification subunit	putative type I site-specific deoxyribonuclease	534/537 (99%)	0.0	*L. lactis* subsp. *cremoris* MG1363
hsdS	13420	14644	+	414	36.47	type I restriction-modification system, specificity subunit	type I R/M system specificity subunit	159/430 (36%)	3e-58	*L. lactis* subsp. *lactis* bv. *diacetylactis*
gdh	15048	16394	+	448	44.27	NADP-dependent glutamate dehydrogenase	glutamate dehydrogenase	447/448 (99%)	0.0	*Lactococcus lactis*, pGdh442
tnp-IS1216	17201	16515	–	228	39.32	transposase for insertion sequence-like element IS1216	hypothetical protein pGdh442_02	227/228 (99%)	7e-131	*Lactococcus lactis*, pGdh442
cadA	19475	17358	–	705	37.16	cadmium efflux ATPase CadA	cadmium efflux ATPase CadA	705/705 (100%)	0.0	*L. lactis* subsp. *lactis*
cadC	19472	19831	–	119	31.37	cadmium resistance regulator CadC	cadmium resistance regulator CadC	119/119 (100%)	1e-61	*L. lactis* subsp. *lactis*
orf15	20550	20227	–	107	20.87	putative cation efflux system protein	hypothetical protein LLKF_p0013	106/107 (99%)	8e-53	*L. lactis* subsp. *lactis* KF147, pKF147A
entA-imm	21163	20825	–	111	33.33	enterocin A Immunity domain (pfam08951)	ORF13	96/107 (90%)	9e-45	*Lactococcus lactis*, pNP40

Table S4. List of ORFs identified in pVF18 (size 18,977 bp; GC content 33.9%)

Gene name	Start (bp)	End (bp)	Strand	Length (aa)	G+C (%)	Product / Predicted function / Conserved domain(s)	Highest homology protein	aa identity (%)	E-value	Organism, plasmid
orf1	834	7	-	275	30.30	putative membrane protein	hypothetical protein llmg_0710	271/275 (99%)	1e-151	*L. lactis* subsp. *cremoris* MG1363
orf2	1175	831	-	114	31.87	transcriptional regulator, PadR-like family	hypothetical protein pMRC01_047	114/114 (100%)	2e-58	*Lactococcus lactis*, pMRC01
tnp1-1216	1355	2005	+	216	37.25	transposase, IS1216 family	integrase core domain protein	201/202 (99%)	2e-112	*Streptococcus parauberis* NCFD2020
orf4	2230	2469	+	79	40.75	integral membrane protein; putative transglycosylase associated proteins, cl00978	hypothetical protein llmg_1257	78/79 (98%)	6e-26	*L. lactis* subsp. *cremoris* MG1363
orf5	2499	3059	+	186	32.61	putative membrane protein	hypothetical protein LLKF_2283	181/186 (98%)	6e-87	*L. lactis* subsp. *lactis* KF147
orf6	3069	3257	+	62	30.64	small integral membrane protein of unknown function, COG5547	hypothetical protein llmg_1259	62/62 (100%)	2e-07	*L. lactis* subsp. *cremoris* MG1363
orf7	3278	3829	+	183	35.15	general stress protein, Gls24 family	putative 20-kDa protein	183/183 (100%)	6e-80	*Lactococcus lactis*
orf8	4087	4548	+	153	28.32	putative acetyltransferase, GNAT family, cd04301	hypothetical protein pJB01p2	149/153 (97%)	2e-81	*Enterococcus faecium*
orf9	4884	5120	+	74	33.33	putative DNA polymerase III subunit epsilon, PRK06195; truncated, N-terminus	conserved hypothetical protein	73/74 (99%)	1e-34	*Enterococcus faecalis* E1Sol
tnp2-IS1216	7119	6439	-	226	36.57	transposase, IS1216 family	ORF-W2 protein	221/226 (97%)	2e-121	*Lactococcus lactis*
orf11	7288	8586	+	432	36.11	putative hydrolase; polysaccharide deacetylase domain, PFAM01522	conserved hypothetical protein	431/432 (99%)	0.0	*Enterococcus faecium* PC4.1
orf12	8743	8934	+	63	37.56	DNA integrase/recombinase, C-terminal fragment	DNA recombinase	61/63 (96%)	1e-28	*L. lactis* subsp. *lactis*
orf13	9066	9383	+	105	34.06	conserved hypothetical protein; putative cytochrome B-like	unknown	85/91 (94%)	4e-42	*L. lactis* subsp. *cremoris*
repB	10408	11565	+	385	33.93	replication protein RepB	replication protein	305/385 (79%)	2e-178	*L. lactis* subsp. *lactis*
orf15	11579	12106	+	175	27.04	hypothetical protein	hypothetical protein LACR_B7	165/175 (94%)	1e-84	*L. lactis* subsp. *cremoris* SK11
orfX	12103	12735	+	210	31.90	replication-associated protein, similar to OrfX	hypothetical protein pCI305_p2	186/210 (88%)	3e-99	*L. lactis* subsp. *lactis*, pCI305
hsdS	12711	13979	+	422	34.91	type I restriction-modification system, specificity subunit	type I R/M system specificity subunit	172/415 (41%)	4e-70	*L. lactis* subsp. *lactis* CV56
orf18	14113	14649	+	178	30.95	transcriptional regulator, Xre family	putative transcriptional regulator	53/130 (41%)	1e-24	*Leuconostoc kimchii* IMSNU11154
orf19	14793	15020	+	75	40.44	hypothetical protein	hypothetical protein LKI_10701	72/79 (92%)	6e-32	*Leuconostoc kimchii* IMSNU11154
orf20	15017	15667	+	216	44.13	ABC_cobalt_CbiO domain; cl09099: P-loop NTPase	ABC transporter, ATP-binding protein	215/216 (99%)	4e-123	*Leuconostoc kimchii* IMSNU11154
orf21	15664	16419	+	251	46.08	ABC-type uncharacterized transport system, permease component, COG0390; putative YbbM family protein	ABC-type uncharacterized transport system, permease component	251/251 (99%)	9e-139	*Leuconostoc citreum* KM20
orf22	16597	16902	+	102	40.84	DNA integrase/recombinase, N-terminal fragment	integrase/recombinase plasmid associated, putative	101/102 (99%)	2e-51	*Leuconostoc kimchii* IMSNU11154
orf23	16961	17371	+	136	29.13	putative acetyltransferase, GNAT family, cd04301	GNAT family acetyltransferase	134/136 (99%)	6e-70	*L. lactis* subsp. *lactis* CV56
tnp-IS6770	17986	17597	-	130	35.64	transposase, IS30 family, COG2826; N-terminal fragment	transposase	130/130 (100%)	6e-71	*Enterococcus faecalis* TUSoD Ef11
orf25	18201	18623	+	140	35.95	protein containing cupin 2 domain, PFAM07883	hypothetical protein LargK3_07881	140/140 (100%)	2e-76	*Streptococcus parauberis* KCTC11537