

Table S1. S32 genes that are absent in strain J11-6^T

Gene id	Length (aa)	Predicted function
fig 2034155.4.peg.2	173	UDP-galactopyranose mutase (EC 5.4.99.9)
fig 2034155.4.peg.3	168	Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)
fig 2034155.4.peg.7	162	Thymidine phosphorylase (EC 2.4.2.4)
fig 2034155.4.peg.243	723	FIG035595: Phage protein
fig 2034155.4.peg.298	711	TonB-dependent receptor
fig 2034155.4.peg.302	83	Programmed cell death antitoxin MazE
fig 2034155.4.peg.303	111	Programmed cell death toxin MazF
fig 2034155.4.peg.504	423	Mobile element protein
fig 2034155.4.peg.505	1086	Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)
fig 2034155.4.peg.506	436	Type I restriction-modification system, specificity subunit S
fig 2034155.4.peg.516	175	phage-associated protein
fig 2034155.4.peg.520	193	Uncharacterized protein YmfQ in lambdoid prophage e14 region
fig 2034155.4.peg.521	353	Putative protein JayE from lambdoid prophage e14 region
fig 2034155.4.peg.522	138	Bacteriophage protein GP46
fig 2034155.4.peg.523	180	Prophage baseplate assembly protein V
fig 2034155.4.peg.524	360	FIG003269: Prophage tail protein
fig 2034155.4.peg.525	353	Phage tail/DNA circulation protein
fig 2034155.4.peg.527	90	L33
fig 2034155.4.peg.533	343	Adenine-specific methyltransferase (EC 2.1.1.72)
fig 2034155.4.peg.1773	82	Phage replication protein
fig 2034155.4.peg.1951	194	hypothetical protein; Some similarities with unknown protein
fig 2034155.4.peg.1953	81	hypothetical protein; Some similarities with unknown protein
fig 2034155.4.peg.2016	102	HipB protein @ Antitoxin HigA
fig 2034155.4.peg.2017	445	Toxin HigB / Protein kinase domain of HipA
fig 2034155.4.peg.2023	303	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)
fig 2034155.4.peg.2025	96	Transcriptional regulator
fig 2034155.4.peg.2026	101	FIG022160: hypothetical toxin
fig 2034155.4.peg.2041	373	Lipid carrier: UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-); Putative glycosyltransferase
fig 2034155.4.peg.2042	140	FIG01210424: hypothetical protein
fig 2034155.4.peg.3173	1153	Phage tail fiber protein
fig 2034155.4.peg.3174	207	Phage tail assembly protein I
fig 2034155.4.peg.3175	106	Phage tail assembly protein
fig 2034155.4.peg.3176	165	Phage integrase
fig 2034155.4.peg.3267	160	COG0286: Type I restriction-modification system methyltransferase subunit
fig 2034155.4.peg.3300	180	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)
fig 2034155.4.peg.3307	337	DNA-cytosine methyltransferase (EC 2.1.1.37)
fig 2034155.4.peg.3310	659	Type III restriction-modification system methylation subunit (EC 2.1.1.72)
fig 2034155.4.peg.3311	987	Type III restriction-modification system restriction subunit (EC 3.1.21.5)
fig 2034155.4.peg.3313	301	Chromosome (plasmid) partitioning protein ParB
fig 2034155.4.peg.3314	511	Recombinase
fig 2034155.4.peg.3317	497	hypothetical protein; Some similarities with nicking enzyme (TraA)
fig 2034155.4.peg.3582	164	Transposase
fig 2034155.4.peg.3588	198	CFA/I fimbrial major subunit

fig 2034155.4.peg.3589	232	CFA/I fimbrial auxiliary subunit
fig 2034155.4.peg.3590	833	CFA/I fimbrial subunit C usher protein
fig 2034155.4.peg.3591	530	CFA/I fimbrial minor adhesin
fig 2034155.4.peg.3592	225	CFA/I fimbrial chaperone
fig 2034155.4.peg.3602	73	Mobile element protein
fig 2034155.4.peg.3603	216	Metal-binding protein ZinT
fig 2034155.4.peg.3608	353	Uncharacterized SAM-dependent O-methyltransferase
fig 2034155.4.peg.3609	241	3-oxoacyl-[ACP] synthase
fig 2034155.4.peg.3610	264	FIG018329: 1-acyl-sn-glycerol-3-phosphate acyltransferase
fig 2034155.4.peg.3611	86	Acyl carrier protein (ACP1)
fig 2034155.4.peg.3612	84	Acyl carrier protein (ACP2)
fig 2034155.4.peg.3613	194	FIG017861: hypothetical protein
fig 2034155.4.peg.3614	467	FIGfam138462: Acyl-CoA synthetase, AMP-(fatty) acid ligase
fig 2034155.4.peg.3615	118	(3R)-hydroxymyristoyl-[ACP] dehydratase (EC 4.2.1.-)
fig 2034155.4.peg.3616	568	FIG143263: Glycosyl transferase / Lysophospholipid acyltransferase
fig 2034155.4.peg.3617	141	FIG002571: 4-hydroxybenzoyl-CoA thioesterase domain protein
fig 2034155.4.peg.3618	202	FIG027190: Putative transmembrane protein
fig 2034155.4.peg.3619	773	FIG021862: membrane protein, exporter
fig 2034155.4.peg.3620	196	FIG035331: hypothetical protein
fig 2034155.4.peg.3622	159	3-hydroxydecanoyl-[ACP] dehydratase (EC 4.2.1.59)
fig 2034155.4.peg.3654	83	Transposase
fig 2034155.4.peg.3659	192	putative thioesterase
fig 2034155.4.peg.3661	306	Permease of the drug/metabolite transporter (DMT) superfamily
fig 2034155.4.peg.3662	227	Metal-dependent hydrolase related to alanyl-tRNA synthetase
fig 2034155.4.peg.3663	314	CmaB
fig 2034155.4.peg.3666	113	Mobile element protein
fig 2034155.4.peg.3667	115	Mobile element protein
fig 2034155.4.peg.3745	260	Putative membrane protein precursor
fig 2034155.4.peg.3900	127	Phage replication protein
fig 2034155.4.peg.3995	86	Colicin immunity protein
fig 2034155.4.peg.3996	170	Translation initiation factor 2
fig 2034155.4.peg.4101	403	Mobile element protein
fig 2034155.4.peg.4104	89	Transposase, IS3/IS911 family
fig 2034155.4.peg.4161	98	Transcriptional regulator, ArsR family
fig 2034155.4.peg.4163	182	RNA polymerase sigma factor SigZ
fig 2034155.4.peg.4248	343	Phage integrase
fig 2034155.4.peg.4251	227	Phage exonuclease (EC 3.1.11.3); Putative phage-encoded enzyme involved in integration-recombination
fig 2034155.4.peg.4252	330	Recombinational DNA repair protein RecT (prophage associated)
fig 2034155.4.peg.4253	255	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
fig 2034155.4.peg.4255	79	Phage holin lysis protein S (ACLAME 206)
fig 2034155.4.peg.4256	171	Lysozyme (EC 3.2.1.17)
fig 2034155.4.peg.4318	109	Holin
fig 2034155.4.peg.4320	195	Chitin binding protein
fig 2034155.4.peg.4379	81	FIG01056585: hypothetical protein
fig 2034155.4.peg.4428	83	ISSod13, transposase

Table S2. J11-6^T genes that are absent in strain S32

Gene id	Length (aa)	Predicted function
fig 2034155.5.peg.144	464	DNA helicase (EC 3.6.4.12), phage-associated
fig 2034155.5.peg.146	270	Roi protein
fig 2034155.5.peg.155	182	Phage protein
fig 2034155.5.peg.156	440	Phage protein
fig 2034155.5.peg.161	220	Phage repressor
fig 2034155.5.peg.162	70	Phage Cro-like repressor protein
fig 2034155.5.peg.168	84	Probable mRNA interferase HicA
fig 2034155.5.peg.170	118	Phage holin, lambda family
fig 2034155.5.peg.175	208	Phage terminase small subunit
fig 2034155.5.peg.176	441	terminase B protein, putative
fig 2034155.5.peg.177	470	FIG01046817: hypothetical protein
fig 2034155.5.peg.178	259	FIG01047789: hypothetical protein
fig 2034155.5.peg.181	343	FIG01048949: hypothetical protein
fig 2034155.5.peg.185	314	FIG01045937: hypothetical protein
fig 2034155.5.peg.187	147	FIG01049053: hypothetical protein
fig 2034155.5.peg.190	221	FIG00644104: hypothetical protein
fig 2034155.5.peg.193	230	FIG01046179: hypothetical protein
fig 2034155.5.peg.194	115	FIG01047481: hypothetical protein
fig 2034155.5.peg.400	222	HD domain protein
fig 2034155.5.peg.674	65	DNA helicase
fig 2034155.5.peg.677	106	Mobile element protein
fig 2034155.5.peg.1080	156	Transcriptional regulator, MarR family
fig 2034155.5.peg.1110	75	Fatty acid desaturase
fig 2034155.5.peg.1187	77	4-oxalocrotonate tautomerase
fig 2034155.5.peg.1200	182	D-lyxose isomerase (EC 5.3.1.15)
fig 2034155.5.peg.1231	154	D-serine/D-alanine/glycine transporter
fig 2034155.5.peg.1424	120	Transcriptional regulator, LysR family
fig 2034155.5.peg.1426	304	Flavohemoglobin / Nitric oxide dioxygenase (EC 1.14.12.17)
fig 2034155.5.peg.1514	95	CRISPR-associated protein Cas2
fig 2034155.5.peg.1515	305	CRISPR-associated protein Cas1
fig 2034155.5.peg.1516	209	CRISPR-associated protein, Cse3 family
fig 2034155.5.peg.1517	216	CRISPR-associated protein, Cas5e family
fig 2034155.5.peg.1518	379	CRISPR-associated protein, Cse4 family
fig 2034155.5.peg.1520	509	CRISPR-associated protein, Cse1 family
fig 2034155.5.peg.1521	904	CRISPR-associated helicase Cas3
fig 2034155.5.peg.1534	692	Putative lipase
fig 2034155.5.peg.1560	230	Putative intergenic transcriptional regulator
fig 2034155.5.peg.1943	363	Prophage Lp2 protein 6
fig 2034155.5.peg.1948	585	Uncharacterized protein YfaA
fig 2034155.5.peg.1949	218	Uncharacterized protein YfaT
fig 2034155.5.peg.1951	539	Uncharacterized protein YfaQ
fig 2034155.5.peg.1952	268	Uncharacterized protein YfaP
fig 2034155.5.peg.1953	422	Putative monooxygenase

fig 2034155.5.peg.1956	147	RidA/YER057c/UK114 superfamily protein
fig 2034155.5.peg.1957	225	Protein of unknown function PA5391, DUF1028 family
fig 2034155.5.peg.1971	329	FIG01220208: hypothetical protein
fig 2034155.5.peg.1989	476	Phage integrase
fig 2034155.5.peg.1991	360	FIG00639870: hypothetical protein
fig 2034155.5.peg.1995	583	Zinc binding domain / DNA primase (EC 2.7.7.-), Phage P4-associated / Replicative helicase RepA, Phage P4-associated
fig 2034155.5.peg.1998	393	Phage major capsid protein
fig 2034155.5.peg.1999	184	Phage head maturation protease
fig 2034155.5.peg.2000	404	Phage portal protein
fig 2034155.5.peg.2001	100	FIG00639228: hypothetical protein
fig 2034155.5.peg.2002	149	Phage holin
fig 2034155.5.peg.2004	119	FIG00641869: hypothetical protein
fig 2034155.5.peg.2005	554	Phage terminase, large subunit
fig 2034155.5.peg.2072	347	Transcriptional regulator, LacI family
fig 2034155.5.peg.2073	430	Multiple sugar ABC transporter, substrate-binding protein
fig 2034155.5.peg.2077	352	FIG01423360: glycoside hydrolase
fig 2034155.5.peg.2079	373	Putative exported protein precursor
fig 2034155.5.peg.2080	425	Putative exported protein precursor
fig 2034155.5.peg.2134	101	Urease gamma subunit (EC 3.5.1.5)
fig 2034155.5.peg.2135	143	Urease beta subunit (EC 3.5.1.5)
fig 2034155.5.peg.2136	573	Urease alpha subunit (EC 3.5.1.5)
fig 2034155.5.peg.2137	207	Urease accessory protein UreE
fig 2034155.5.peg.2138	238	Urease accessory protein UreF
fig 2034155.5.peg.2140	317	Urease accessory protein UreD
fig 2034155.5.peg.2141	332	Eukaryotic-type low-affinity urea transporter
fig 2034155.5.peg.2142	353	HoxN/HupN/NixA family nickel/cobalt transporter
fig 2034155.5.peg.2145	136	late embryogenesis abundant (LEA) domain- containing protein
fig 2034155.5.peg.2156	345	alpha-L-arabinofuranosidase II (EC 3.2.1.55)
fig 2034155.5.peg.2158	169	lipoprotein, putative
fig 2034155.5.peg.2170	169	Uncharacterized protein YegL
fig 2034155.5.peg.2172	457	Integrase
fig 2034155.5.peg.2470	275	Glycosyltransferase
fig 2034155.5.peg.2477	477	Lipopolysaccharide biosynthesis protein
fig 2034155.5.peg.2492	196	Mobile element protein
fig 2034155.5.peg.2824	71	Channel-forming transporter/cytolysins activator of TpsB family
fig 2034155.5.peg.2830	439	ATP/GTP-binding protein
fig 2034155.5.peg.2831	732	ATP-dependent helicase
fig 2034155.5.peg.2832	979	Putative helicase
fig 2034155.5.peg.3093	435	FIG00775401: hypothetical protein
fig 2034155.5.peg.3095	120	RelE-like translational repressor toxin
fig 2034155.5.peg.3215	84	Octaprenyl diphosphate synthase (EC 2.5.1.90)
fig 2034155.5.peg.3301	352	Uncharacterized protein ImpA
fig 2034155.5.peg.3399	384	Putative tail fiber protein
fig 2034155.5.peg.3682	104	Mobile element protein
fig 2034155.5.peg.3683	102	Putative transposase
fig 2034155.5.peg.3707	413	COG3547: Transposase and inactivated derivatives

fig 2034155.5.peg.3984	577	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.3989	414	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4424	206	FIG00613801: hypothetical protein
fig 2034155.5.peg.4517	413	COG3547: Transposase and inactivated derivatives
fig 2034155.5.peg.4545	75	FIG131328: Predicted ATP-dependent endonuclease of the OLD family
fig 2034155.5.peg.4561	289	Chromosome partitioning ATPase in PFGI-1-like cluster, ParA-like
fig 2034155.5.peg.4564	577	Protein with ParB-like nuclease domain in PFGI-1-like cluster
fig 2034155.5.peg.4566	190	FIG004780: hypothetical protein in PFGI-1-like cluster
fig 2034155.5.peg.4567	399	FIG141751: hypothetical protein in PFGI-1-like cluster
fig 2034155.5.peg.4568	179	Heat shock protein C
fig 2034155.5.peg.4577	811	Clamp-binding protein CrfC
fig 2034155.5.peg.4581	72	Transcriptional regulator, XRE family
fig 2034155.5.peg.4598	75	cellular communication/signal transduction
fig 2034155.5.peg.4601	91	Uncharacterized protein YrhB
fig 2034155.5.peg.4657	110	Arginine/ornithine antiporter ArcD
fig 2034155.5.peg.4661	152	FIG00208745: hypothetical protein
fig 2034155.5.peg.4666	68	Channel-forming transporter/cytolysins activator of TpsB family
fig 2034155.5.peg.4676	331	FIG00613801: hypothetical protein
fig 2034155.5.peg.4678	202	FIG00613801: hypothetical protein
fig 2034155.5.peg.4687	430	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4698	432	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4699	432	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4700	423	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4708	293	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4709	289	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4710	282	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4713	219	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4722	171	Putative large exoprotein involved in heme utilization or adhesion of ShIA/HecA/FhaA family
fig 2034155.5.peg.4723	167	FIG00613801: hypothetical protein