Table S1. Strains used in this work.

Strain	Description	Reference
Enterococcus faecalis		
VE14089	*E. faecalis* V583 cured of its plasmids. EfCIV583 positive	(Rigottier-Gois *et al.*, 2011)
E. faecalis JH2-2	Laboratory strain	(Jacob and Hobbs, 1974)
VE18590	*E. faecalis* V583 deriviative. Non-lysogenic, EfCIV583-negative.	(Matos *et al*. 2013)
VE18589	VE18590 (EfCIV583)	(Matos *et al*. 2013)
JP10318	VE14089 EfCIV583 *tet*M	This work
JP10416	JP10318 Δp1	This work
JP10860	JP10318 Δp2	This work
JP10861	JP10318 Δp3	This work
JP10862	JP10318 Δp4	This work
JP10863	JP10318 Δp5	This work
JP10864	JP10318 Δp6	This work
JP10984	VE 18562 (pp1+)	(Matos *et al*. 2013)
JP11211	JP10984 ΔEF0309	This work
JP11028	JP10984 EfCIV583 *tet*M	This work
JP13142	JP11028 ΔEF0309	This work
Bacillus subtilis		
B. subtilis RL-3	Natural competent	Richard Losick lab
Listeria monocytogenes		
L. monocytogenes RN10983	Natural lysogenic strain	Richard Novick lab
Staphylococcus aureus		
S. aureus RN4220	Restriction-defective strain	(Kreiswirth *et al.*, 1983)
JP8546	RN4220 pJP1097	(Mir-Sanchis *et al.*, 2012)
JP8545	RN4220 pJP1096	(Mir-Sanchis *et al.*, 2012)
JP10837	RN4220 pJP1350	This work
JP10838	RN4220 pJP449	This work
JP5267	RN4220 pJP788	This work
JP5266	RN4220 pJP787	This work
JP9991	RN4220 pJP1277	This work
JP9992	RN4220 pJP1278	This work
JP5118	RN4220 pJP782	This work
RN10733	RN4220 pRN9211	(Ubeda *et al.*, 2007)
RN10734	RN4220 pRN9217	(Ubeda *et al.*, 2007)
JP10399	RN4220 pJP1316	This work
JP10739	JP10399 pJP1317	This work
JP10740	JP10399 pJP1318	This work

Strain	Description	Reference
Staphylococcus aureus		
JP10822	JP10399 pJP1330	This work
JP10741	JP10399 pJP1319	This work
JP10742	JP10399 pJP1320	This work
JP10743	JP10399 pJP1321	This work
JP10744	JP10399 pJP1322	This work
JP10745	JP10399 pJP1323	This work
JP10746	JP10399 pJP1324	This work
JP10747	JP10399 pJP1325	This work
JP10748	JP10399 pJP1326	This work
JP10749	JP10399 pJP1327	This work
Escherichia coli		
JP5630	DH5α pJP795/pJP796	This work
JP5631	DH5α pJP795/pJP797	This work
JP5632	DH5α pJP795/pJP798	This work
JP5039	DH5α pJP782	This work
JP4994	DH5α pJP781	This work
JP9821	DH5α pJP1306	This work
JP10488	BL21 (DE3) pJP1328	This work
Lactococcus lactis		
IL1403	Laboratory strain	(Chopin *et al.*, 1984)
JP14198	IL1403 pAGEnt	This work
JP14199	IL1403 pJP1868	This work
JP14203	IL1403 pJP1869	This work

Table S2. Oligonucleotides used in this work.

Plasmid	Oligonucleotides	Sequence (5’-3’)
Excision, circularisation and integration		
EfCI$_{V583}$		
Excision	EfPI-1m	TAAAAACAGCGCCTTCGTCC
	EfPI-2c	AATCGAGTAGTAGCTGAAACG
Circularization	EfPI-8m	CTTCTTCAATCAGGAGTGCC
	EfPI-12c	TATGGTTGGTACTGATAGGCG
In/out	EfPI-8m	CTTCTTCAATCAGGAGTGCC
	EfPI-2c	AATCGAGTAGTAGCTGAAACG
pJP795	EfCI-int-5mH	CCCAAGCTTTTGGCTTAAACCAAGAAAAGC
	EfCI-int-4cB	CGCGGATCCATTATGGGTGTTTTAAATGGC
pJP796	EfCI-int-1mS	ACGCGTCGACCAGTTATAGAAACATCTCTCC
	EfCI-int-3cB	CGCGGATCCAGTGATAATCAGTCAGTTGGC
pJP797	EfCI-int-1mS	ACGCGTCGACCAGTTATAGAAACATCTCTCC
	EfCI-int-4cB	CGCGGATCCATTATGGGTGTTTTAAATGGC
pJP798	EfCI-int-2mS	ACGCGTCGACTGAAACACTTCAAATTATGGC
	EfCI-int-3cB	CGCGGATCCAGTGATAATCAGTCAGTTGGC
pJP1350	SaPIbov-149cB	CGCGGATCCGATCAGTACCTAAATATGCG
	SaPIbov1-243mK	CGGGGTACCTACGACATTAACGTCATTGCG
pJP788	EfPI-16mE	CCGGAATTCGCTTTTTATCAAGCGTATGGC
	EfPI-15cB	CGCGGATCCACATATAGGCGGTTGTACCG
pJP787	EfPI-16mE	CCGGAATTCGCTTTTTATCAAGCGTATGGC
	EfPI-17cB	CGCGGATCCCGTGGAATACCTAACTCCTC
pJP1277	EfPI-56mE	CCGGAATTCGGAAACGCCCTCTACTATCTTC
	EfPI-15cB	CGCGGATCCACATATAGGCGGTTGTACCG
pJP1278	EfPI-56mE	CCGGAATTCGGAAACGCCCTCTACTATCTTC
	EfPI-17cB	CGCGGATCCCGTGGAATACCTAACTCCTC
pJP782	EfPI-7mB	CGCGGATCCAATGACCTCGTGTAAAAGCC
	EfPI-9cS	ACGCGTCGACCAATAGAGAATCCGAGATAGC
pJP781	EfPI-6mB	CGCGGATCCAAGGGATTTGGTCGGTTACC
	EfPI-9cS	ACGCGTCGACCAATAGAGAATCCGAGATAGC
pJP1306	EfPI-7mB	CGCGGATCCAATGACCTCGTGTAAAAGCC
	EfPI-49c	GCATTGGGAGATTTTTTCAGC
	EfPI-50m	GCTGAAAAAATCTCCCAATGCCTCTGGTAGGTACTCCACAAG
	EfPI-9cS	ACGCGTCGACCAATAGAGAATCCGAGATAGC
pJP1312	EfPI-27mXS	GCTCTAGAGCACGCGTCGACTGACAACGTTCCTCTCTTTCC
	EfPI-28cB	CGCGGATCCTCTTAAGGAGTGCTAAAGAGC
	EfPI-29mP	AAAACTGCAGGAAGCGGAAGATTTCATGCCG
	EfPI-30cE	CCGGAATTCCTTACTGAGAATCAGGAGAGC
pJP1313	EFV583phi1-3mBglII	GAAGATCTTTAGGAACACCGCCAGAAACC
	EFV583phi1-4cS	ACGCGTCGACTTTACGACCAGACGAAGAGCC

Plasmid	Oligonucleotides	Sequence (5’-3’)
pJP1351	EFV583phi2-3mB	CGCGGATCCTTAGCCGCAGCAAGTAATGCG
	EFV583phi2-6m	ACAGAATAATCCCTAAATTCCCAAACGATGGCAACGCACAG
	EFV583phi2-5c	GAATTTAGGGATTATTCTGTG
	EFV583phi2-4cS	ACGCGTCGACTAAATCCGACATATGGGCAGG
pJP1352	EFV583phi3-3mB	CGCGGATCCAGTTGAAGCTGATGCGGAAGG
	EFV583phi3-4cS	ACGCGTCGACGAAATTTCGGAAAATTCTCCG
pJP1353	EFV583phi4-3mB	CGCGGATCCTTTATGGCAATATGGAAGGAG
	EFV583phi4-4cS	ACGCGTCGACAATTAACAGCGGTTGATAGCC
pJP1354	EFV583phi5-3mB	CGCGGATCCAATACTCAATGCCATATAGGG
	EFV583phi5-4cS	ACGCGTCGACAGCGTTTTGCTAGTAAAGGGC
pJP1355	EFV583phi6-3mB	CGCGGATCCACAGTACGTTTCCACTGTCGC
	EFV583phi6-4cS	ACGCGTCGACTCCAATACCTTTCCCGATACG
pJP1552	EFV583phi1-5mS	AGCGTCGACTTTGAAACTTTGTGGGAATACG
	EF0309-5c	AACCGGTTTTGGCATACCCC
	EF0309-6m	GGTATGCCAAAACCGGTTAAGAAAAGAAAGGGCGGATAG
	EFV583phi1-6cB	CGCGGATCCTGCCGCTATACGTCTTAATTG
pJP1316	EfPI-15cB	CGCGGATCCACATATAGGCGGTTGTACCG
	TT-1cSp	ACATGCATGCTGTCACTTTGCTTGATATATGAG
pJP1317	EFV583phi1-5mS	ACGCGTCGACTTTGAAACTTTGTGGGAATACG
	EFV583phi1-6cB	CGCGGATCCTGCCGCTATACGTCTTAATTG
pJP1318	EFV583phi1-7mS	ACGCGTCGACAATATCTCAATTTATGAGGTGTAC
	EFV583phi1-8cB	CGCGGATCCTGAATCTGCTTCAATATTTAAATAG
pJP1330	EFV583phi1-9mS	ACGCGTCGACAAAGCGATTTTCAATGTAACAGATG
	EFV583phi1-10cB	CGCGGATCCTGAATTTTTTAAAGTAATCACATGG
pJP1319	EFV583phi1-11mS	ACGCGTCGACGAATTCGGAGATACTAATTTTTATG
	EFV583phi1-12cB	CGCGGATCCTAATTTGATGTTTTTTTCTGGCTG
pJP1320	EFV583phi1-13mS	ACGCGTCGACTATCAAGAAGGATGGCTTGAC
	EFV583phi1-14cB	CGCGGATCCTCTTAGAGTATTCCTGATAGGG
pJP1321	EFV583phi1-15mS	ACGCGTCGACAGCAACGTTACATCCCTATCAG
	EFV583phi1-16cB	CGCGGATCCTAATTTTTGATAGCTGACTAACC
pJP1322	EFV583phi1-17mS	ACGCGTCGACATACCGTATGATGTTAGATTTATATTG
	EFV583phi1-18cB	CGCGGATCCGTCTTCACTAAGTAAAGCTTCC
pJP1323	EFV583phi1-5mS	ACGCGTCGACTTTGAAACTTTGTGGGAATACG
	EFV583phi1-35cB	CGCGGATCCTTCGACAGCTTCCAGATCAAC
pJP1324	EFV583phi1-36mS	ACGCGTCGACGTTACCGATTATGTGGCTGTG
	EFV583phi1-37cB	CGCGGATCCGCATAATATCCACGCTTCTTG
pJP1325	EFV583phi1-38mS	ACGCGTCGACGTGTTTGATGAGTTTGTTCGC
	EFV583phi1-39cB	CGCGGATCCCCTCCTACGGAATTAATCTGT
pJP1326	EFV583phi1-40mS	ACGCGTCGACGTCGTTTAGAAGATAAGAACCG
	EFV583phi1-41cB	CGCGGATCCAAATTCCACGCTAGCCTTTTG
pJP1327	EFV583phi1-42mS	ACGCGTCGACGATGAACGTTTGCCAGAAGCA
	EFV583phi1-6cB	CGCGGATCCTGCCGCTATACGTCTTAATTG

Plasmid	Oligonucleotides	Sequence (5’-3’)
pJP1328	EfPI-45mB	CGCGGATCCGATGAGAAAGGAGTTTCCTCTGATG
	EfPI-46cE	CCGGAATTCTCATTCTTTAGCTTTTGATTTACG
	EF0309-1mS	ACGCGTCGACTTCACACAGGAAACAGACCATGCCAAAACCGGTTAAGGTT
	EF0309-2cP	AACTGCAGCTATCCGCCCTTTCTTTTCTT
pJP1868	bIL286-cos_mP	TCAGTTCTGCAGATTTTTAATAACCCTCCCCCCGTATCTT
	bIL286-cos_cS	TCTCTTACTAGTTTTTTCTCCTTTCTTTTAGTGTTTTGAC
pJP1869	bIL310-cos_mP	TCAGTTCTGCAGTTTTTAAACACCCCCGCCCGTAT
	bIL310-cos_cS	CTTACTAGTTTTTAGATTTTTGACCCCCCTATATAAAAAT

Southern blot	Oligonucleotides	Sequence (5’-3’)
EfCIV583 probe	EfPI-29mP	AAAACTGCAGGAAGCGGAAGATTTCATGCCG
	EfPI-30cE	CCGGAATTCCTTACTGAGAATCAGGAGAGC
Phage p1 probe	EFV583phi1V-1m	GTGCCTAAATCATAAGGACGG
	EFV583phi1V-2c	AAAGATTCCGTGCGATTATCC

Table S3. Plasmids used in this work.

Plasmid	Description	Reference
pCN41	Ap^r. Used in transcriptional fusions to the staphylococcal β–lactamase *bla*Z	(Charpentier *et al.*, 2004)
pCN33	Ap^r. Cloning vector	(Charpentier *et al.*, 2004)
pCN51	Ap^r. Expression vector	(Charpentier *et al.*, 2004)
pMAK700	Cm^r. Plasmid thermosensitive in *E. coli*	(Hamilton *et al.*, 1989)
pMAD	Vector for efficient allelic replacement	(Arnaud *et al.*, 2004)
pCU1	Cm^r. Cloning vector	(Augustin *et al.*, 1992)
pPROEX HTa	Expression vector	Invitrogen
pAGEnt	Cm^r. Expression vector	(Linares *et al.*, 2014)
pJP795	pMAK700 *att*$_C$ EfCIV583	This work
pJP796	pCN51 *int-att*$_{PI}$ EfCIV583	This work
pJP797	pCN51 *int-att*$_L$ EfCIV583	This work
pJP798	pCN51 Δ*int-att*$_{PI}$ EfCIV583	This work
pJP1097	pCN41 *stl-xis-bla*Z SaPIbov1	(Mir-Sanchis *et al.*, 2012)
pJP1096	pCN41 Δ*stl-xis-bla*Z SaPIbov1	(Mir-Sanchis *et al.*, 2012)
pJP1350	pCN41 *stl-hel-bla*Z SaPIbov1	This work
pJP449	pCN41 Δ*stl-hel-bla*Z SaPIbov1	(Ubeda *et al.*, 2008)
pJP788	pCN41 *stl-xis-bla*Z EfCIV583	This work
pJP787	pCN41 Δ*stl-xis-bla*Z EfCIV583	This work
pJP1277	pCN41 *stl-hel-bla*Z EfCIV583	This work
pJP1278	pCN41 Δ*stl-hel-bla*Z EfCIV583	This work
pJP782	Suicide plasmid. Em^R Δ*stl-pri-hel-ori* EfCIV583	This work
pJP781	Suicide plasmid. Em^R Δ*stl-pri-hel-*Δ*ori* EfCIV583	This work
pJP1306	Suicide plasmid. Em^R Δ*stl-pri-*Δ*hel-ori* EfCIV583	This work
pRN9211	Suicide plasmid. Em^R *pri-hel-ori* SaPIbov1	(Ubeda *et al.*, 2007)
pRN9217	Suicide plasmid. Em^R *pri-hel-ori* SaPI1	(Ubeda *et al.*, 2007)
pJP1312	pMAD derivative. Insertion of *tet*M cassette in EfCIV583	This work
pJP1313	pMAD derivative. Deletion of phage p1 from VE14089	This work
pJP1351	pMAD derivative. Deletion of phage p2 from VE14089	This work
pJP1352	pMAD derivative. Deletion of phage p3 from VE14089	This work
pJP1353	pMAD derivative. Deletion of phage p4 from VE14089	This work
pJP1354	pMAD derivative. Deletion of phage p5 from VE14089	This work
pJP1355	pMAD derivative. Deletion of phage p6 from VE14089	This work
pJP1552	pMAD derivative. Deletion of EF0309 from V583 p1.	This work
pJP1316	Transcriptional analysis of stl EfCIV583, pCU1 β-lactamase *bla*Z	This work
pJP1317	Expression of EF0308 to EF0312, pCN51 derivative	This work
pJP1318	Expression of EF0313 to EF0317, pCN51 derivative	This work
pJP1330	Expression of EF0318 to EF0323, pCN51 derivative	This work
pJP1319	Expression of EF0324 to EF0327, pCN51 derivative	This work
pJP1320	Expression of EF0328 to EF0329, pCN51 derivative	This work
pJP1321	Expression of EF0330, pCN51 derivative	This work

Plasmid	Description	Reference
pJP1322	Expression of EF0331 to EF0333, pCN51 derivative	This work
pJP1323	Expression of EF0308, pCN51 derivative	This work
pJP1324	Expression of EF0309, pCN51 derivative	This work
pJP1325	Expression of EF0310, pCN51 derivative	This work
pJP1326	Expression of EF0311, pCN51 derivative	This work
pJP1327	Expression of EF0312, pCN51 derivative	This work
pJP1328	Expression in *E. coli* of His-Stl EfCIV583 + EF0309, pPROEX HTa derivative	This work
pJP1868	pAGEnt containing phage bIL286 *cos* site	This work
pJP1869	pAGEnt containing LlCIbIL310 putative *cos* site	This work

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Table S4. Description and relationships between the *E. faecalis* PICI elements[a].

EfCIV583[b]	**GenBank acces**		**EfCI918**	**EfCISF105**	**EfCIB16457**	**EfCILA3B-2**
EfCIV583_1	EF2955	*int*	95	93	100	85
EfCIV583_2	EF2954	*rpr*	■	■	100	99
EfCIV583_3	not annotated		85		100	97
EfCIV583_4	EF2953		90	76	100	83
EfCIV583_5	EF2952		90		100	99
EfCIV583_6	EF2951		72	85	99	84
EfCIV583_7	EF2950		80	80	94	95
EfCIV583_8	EF2949		80	98	82	82
EfCIV583_9	EF2948	*pri-rep*	■	■	■	■
EfCIV583_10	EF2947		■	■	■	■
EfCIV583_11	not annotated		83	80	78	77
EfCIV583_12	EF2946		65	65	65	65
EfCIV583_13	EF2945		100	100	100	100
EfCIV583_14	EF2944		94	100	94	91
EfCIV583_15	EF2943		93	100	93	96
EfCIV583_16	EF2942		94	99	94	92
EfCIV583_17	EF2941		88	100	88	100
EfCIV583_18	EF2940		97	100	97	97
EfCIV583_19	EF2939	*csp*	96	100	96	90
EfCIV583_20	EF2938		60	100	60	
EfCIV583_21	EF2937	*uvr*B	100	100	100	
EfCIV583_22	EF2936		97	90	97	
EfCIV583_23	I574_00041		98	98	98	

EfCILA3B-2[b]	**GenBank acces**		**EfCIV583**	**EfCI918**	**EfCISF105**	**EfCIB16457**
EfCILA3B-2_1	D347_01789	*fic*				
EfCILA3B-2_2	D347_01790	*int*	85	84	87	85
EfCILA3B-2_3	D347_01791	*rpr*	99	■	■	99
EfCILA3B-2_4	D347_01792		97	81		97
EfCILA3B-2_5	D347_01793		83	83	70	83
EfCILA3B-2_6	D347_01794		99	90		99
EfCILA3B-2_7	D347_01795		84	84	84	85
EfCILA3B-2_8	D347_01796		95	73	75	94
EfCILA3B-2_9	D347_01797		83	90	81	100
EfCILA3B-2_10	D347_01798	*pri-rep*	■	98	97	96
EfCILA3B-2_11	D347_01799		80	94	97	95
EfCILA3B-2_12	D347_01800		64	64	64	64
EfCILA3B-2_13	D347_01801		100	100	100	100
EfCILA3B-2_14	D347_01802		91	93	91	93
EfCILA3B-2_15	D347_01803		96	92	95	92
EfCILA3B-2_16	D347_01804		92	94	91	94
EfCILA3B-2_17	D347_01805		100	86	100	86
EfCILA3B-2_18	D347_01806		97	97	97	97
EfCILA3B-2_19	D347_01807	*csp*	88	93	88	93
EfCILA3B-2_20	D347_01808					

EfCISF105[b]	**GenBank acces**		**EfCIV583**	**EfCI918**	**EfCILA3B-2**	**EfCIB16457**
EfCISF105_1	UM9_00916					
EfCISF105_2	UM9_00917	*int*	93	92	87	93
EfCISF105_3	UM9_00918	*rpr*	■	■	■	■
EfCISF105_4	UM9_00919					
EfCISF105_5	UM9_00920		80	81	71	80
EfCISF105_6	UM9_00921					
EfCISF105_7	UM9_00922		85	83	83	84
EfCISF105_8	UM9_00923		100	98	95	96
EfCISF105_9	UM9_00924		99	79	81	81
EfCISF105_10	UM9_00925	*pri-rep*	■	97	97	96
EfCISF105_11	UM9_00926		74	92	88	98
EfCISF105_12	UM9_00927		100	100	100	100
EfCISF105_13	UM9_00928		100	94	91	94
EfCISF105_14	UM9_00929		99	93	95	93
EfCISF105_15	UM9_00930		99	93	91	93
EfCISF105_16	UM9_00931		100	86	100	86
EfCISF105_17	UM9_00932		100	97	97	97
EfCISF105_18	UM9_00933	*csp*	99	94	94	94
EfCISF105_19	UM9_00934		100	60		60
EfCISF105_20	UM9_00935	*uvr*B	100	100		100
EfCISF105_21	UM9_00936		99	98		98
EfCISF105_22	UM9_00937		98	97		97

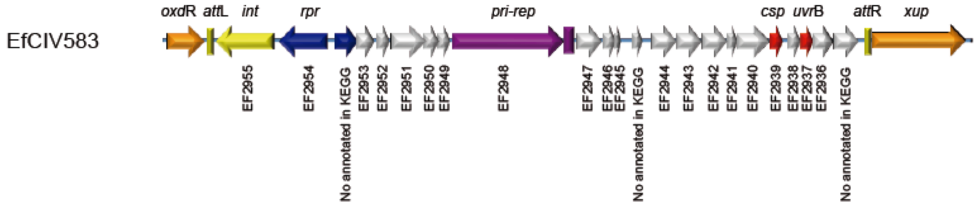
EfCIB16457[b]	**GenBank acces**		**EfCIV583**	**EfCI918**	**EfCILA3B-2**	**EfCISF105**
EfCIB16457_1	Q95_00339	*int*	100	95	85	93
EfCIB16457_2	Q95_00340	*rpr*	100	■	99	■
EfCIB16457_3	Q95_00341		100	100	99	
EfCIB16457_4	Q95_00342		100	94	83	80
EfCIB16457_5	Q95_00343		100	90	99	
EfCIB16457_6	Q95_00344		99	84	84	84
EfCIB16457_7	Q95_00345		94	76	94	78
EfCIB16457_8	Q95_00346		83	90	100	81
EfCIB16457_9	Q95_00347	*pri-rep*	■	96	96	96
EfCIB16457_10	Q95_00348		82	92	84	98
EfCIB16457_11	Q95_00349		100	100	98	100
EfCIB16457_12	Q95_00350		94	100	93	94
EfCIB16457_13	Q95_00351		93	99	92	93
EfCIB16457_14	Q95_00352		94	100	94	93
EfCIB16457_15	Q95_00353		91	100	93	91
EfCIB16457_16	Q95_00354		97	100	97	97
EfCIB16457_17	Q95_00355	*csp*	94	99	93	94
EfCIB16457_18	Q95_00356		73	99		73
EfCIB16457_19	Q95_00357	*uvr*B	100	100		100
EfCIB16457_20	Q95_00358		90	100		90
EfCIB16457_21	Q95_00359		98	100		97

EfCI918[b]	**GenBank acces**		**EfCIV583**	**EfCIB16457**	**EfCILA3B-2**	**EfCISF105**
EfCI918_1	HMPREF2097_00609	*int*	95	95	84	92
EfCI918_2	HMPREF2097_00610	*rpr*	■	■	■	■
EfCI918_3	HMPREF2097_00611		67	67	64	
EfCI918_4	HMPREF2097_00612		99	95	85	82
EfCI918_5	HMPREF2097_00613		88	88	90	
EfCI918_6	HMPREF2097_00614		69	69	94	70
EfCI918_7	HMPREF2097_00615		93	93	93	91
EfCI918_8	HMPREF2097_00616		98	95	100	98
EfCI918_9	HMPREF2097_00617		80	90	90	79
EfCI918_10	HMPREF2097_00618	*pri-rep*	■	96	98	97
EfCI918_11	HMPREF2097_00619		58	78	57	78
EfCI918_12	HMPREF2097_00620		64	64	64	60
EfCI918_13	HMPREF2097_00621		100	100	98	100
EfCI918_14	HMPREF2097_00622		94	100	93	94
EfCI918_15	HMPREF2097_00623		93	99	92	94
EfCI918_16	HMPREF2097_00624		94	100	94	93
EfCI918_17	HMPREF2097_00625		91	100	91	91
EfCI918_18	HMPREF2097_00626		97	100	97	97
EfCI918_19	HMPREF2097_00627	*csp*	94	99	93	94
EfCI918_20	HMPREF2097_00628			100		
EfCI918_21	HMPREF2097_00629		55	100		55
EfCI918_22	HMPREF2097_00630	*uvr*B	100	100		100
EfCI918_23	HMPREF2097_00631		91	100		91
EfCI918_24	HMPREF2097_00632		98	100		97

[a] PICI similarities were determined with BLASTX. Shading: light grey, >90 % similarity to corresponding gene in the PICI element described in the left column; dark grey, 50–90 %; black, <50 %; white, no corresponding gene. Abbreviations: *int*, integrase; *rpr*, PICI represor; *pri-rep*, primase-helicase homologues; *csp*, cold-shock protein.

[b] We have annotated genes in the PICIs according to the following nomenclature: *PICI_ORF number.*

Table S5. EfCIV583 orthologies.



EfCIV583 gene	Function	Orthologs	Species	Length	Similarity (aa)	Overlap	Element	Start	End	Size (kb)	Comments
EF2936		efa:EF2936	*Enterococcus faecalis*	112			EfCIV583				No matches in database (DB)
EF2937		efa:EF2937	*Enterococcus faecalis*	69	1.000	69	EfCIV583				
		efq:DR75_2900	*Enterococcus faecalis*	69	0.492	59	No insert				
		efl:EF62_pB0056	*Enterococcus faecalis*	69	0.475	59	PICI	39611	46683	17.0	
		lpk:LACPI_0388	*Lactococcus piscium*	59	0.475	59	No insert[a]				
		lrg:LRHM_0140	*Lactobacillus rhamnosus*	69	0.491	57	No insert				
		lrh:LGG_00140	*Lactobacillus rhamnosus*	68	0.491	57	No insert				
		lcl:LOCK919_0751	*Lactobacillus casei*	66	0.439	57	No insert				
		lcz:LCAZH_0582	*Lactobacillus casei*	66	0.439	57	No insert				
		lpb:SH83_03640	*Lactobacillus plantarum*	66	0.368	57	No insert				
		lpj:JDM1_0749	*Lactobacillus plantarum*	66	0.368	57	No insert				
		lpl:lp_0899	*Lactobacillus plantarum*	66	0.368	57	No insert				
EF2938		efa:EF2938	*Enterococcus faecalis*	92			EfCIV583				No match in enterococci; no match in DB with less than 2x MW & over 35% similarity
EF2939		efa:EF2939	*Enterococcus faecalis*	67			EfCIV583				Cold-shock protein, has many matches in different species, none in any inserted element
EF2940		efa:EF2940	*Enterococcus faecalis*	190			EfCIV583				No significant match in DB
EF2941		efa:EF2941	*Enterococcus faecalis*	65	1.000	65	EfCIV583				
		spu:576079	*Strongylocentrotus purpuratus*	297	0.358	67	No insert				
		wse:WALSEDRAFT_57668	*Wallemia sebi*	491	0.391	64	No insert				
		bdi:100822641	*Brachypodium distachyon*	1101	0.381	63	No insert				
		ath:AT1G10490	*Arabidopsis thaliana*	1028	0.413	63	No insert				

EfCIV583 gene	Function	Orthologs	Species	Lenght	Similarity	Overlap	Element	Start	End	Size (kb)	Comments
		…									
		wci:WS105_0618	*Weissella ceti*	74	0.429	49	Prophage				
		wct:WS74_0819	*Weissella ceti*	74	0.429	49	Prophage				
EF2942		efa:EF2942	*Enterococcus faecalis*	185			EfCIV583				No match in enterococci; no significant match in DB
EF2943		efa:EF2943	*Enterococcus faecalis*	177			EfCIV583				No match in enterococci; no significant match in DB
EF2944		efa:EF2944	*Enterococcus faecalis*	160			EfCIV583				No match in enterococci; no significant match in DB
EF2945		efa:EF2945	*Enterococcus faecalis*	46			EfCIV583				No match in DB
EF2946		efa:EF2946	*Enterococcus faecalis*	47			EfCIV583				No match in DB
EF2947		efa:EF2947	*Enterococcus faecalis*	136	1.000	136	EfCIV583				
		efc:EFAU004_02137	*Enterococcus faecium*	135	0.406	128	PICI	2159624	2173033	13.4	Has full capsid module
		efu:HMPREF0351_12135	*Enterococcus faecium*	135	0.406	128	PICI				Has full capsid module
		pper:PRUPE_ppa005581mg	*Prunus persica*	453	0.302	96	No insert				
		cts:Ctha_2453	*Chloroherpeton thalassium*	755	0.333	66	No insert				
EF2948	*pri-rep*	efa:EF2948	*Enterococcus faecalis*	794	1.000	794	EfCIV583				
		lmoc:LMOSLCC5850_1262	*Listeria monocytogenes*	780	0.585	482	Prophage				
		lmod:LMON_1266	*Listeria monocytogenes*	780	0.585	482	Prophage				
		lmow:AX10_00090	*Listeria monocytogenes*	780	0.585	482	Prophage				
		lwe:lwe1216	*Listeria welshimeri*	780	0.585	482	Prophage				
		saa:SAUSA300_0809	*Staphylococcus aureus*	790	0.449	637	SaPI	881996	895129	13.1	
		saui:AZ30_04285	*Staphylococcus aureus*	790	0.449	637	SaPI				
		sax:USA300HOU_0861	*Staphylococcus aureus*	790	0.449	637	SaPI				
		bthu:YBT1518_01285 pu	*Bacillus thuringiensis*	797	0.532	477	Prophage				
EF2949		efa:EF2949	*Enterococcus faecalis*	82			EfCIV583				No significant match in DB

EfCIV583 gene	Function	Orthologs	Species	Length	Similarity	Overlap	Element	Start	End	Size (kb)	Comments
EF2950		efa:EF2950	*Enterococcus faecalis*	97	1.000	97	EfCIV583				
		efc:EFAU004_02141	*Enterococcus faecium*	52	0.396	48	PICI	2159624	2174178	14.5	Has full capsid module
		efu:HMPREF0351_12139	*Enterococcus faecium*	52	0.396	48	PICI				Has full capsid module
		efd:EFD32_1868	*Enterococcus faecalis*	84	0.333	72	defective phage?			3.2	
		cpae:CPAST_c11890	*Clostridium pasteurianum*	398	0.457	46	No insert				
		gmx:100776868	*Glycine max (soybean)*	922	0.322	90	No insert				
EF2951		efa:EF2951	*Enterococcus faecalis*	221	1.000	221	EfCIV583				No match in enterococci
		ppen:T256_00520	*Pediococcus pentosaceus*	234	0.471	227	PICI	99518	111337	11.8	
		lbh:Lbuc_0024	*Lactobacillus buchneri*	232	0.416	219	PICI	24658	40308	15.6	
		cpas:Clopa_0076	*Clostridium pasteurianum*	225	0.420	207	PICI	76442	85886	9.4	Defective
		std:SPPN_01200	*Streptococcus pseudopneumoniae*	209	0.421	202	PICI	190041	202462	12.4	Defective
		lbk:LVISKB_0740	*Lactobacillus brevis*	225	0.392	222	PICI	765893	774063	8.1	Defective
		smb:smi_2013	*Streptococcus mitis*	208	0.408	201	PICI	2057587	2068441	10.9	
		snc:HMPREF0837_10280	*Streptococcus pneumoniae*	201	0.399	203	PICI	249288	267373	18.1	
		snd:MYY_0022	*Streptococcus pneumoniae*	201	0.399	203	PICI				Defective
		snt:SPT_0025	*Streptococcus pneumoniae*	201	0.399	203	PICI				Defective
		ssut:TL13_0174	*Streptococcus suis*	206	0.391	202	PICI	131344	143429	12.1	
EF2952		efa:EF2952	*Enterococcus faecalis*	82			EfCIV583				No matches in DB
EF2953		efa:EF2953	*Enterococcus faecalis*	105	1.000	105	EfCIV583				
		xne:XNC1_0454	*Xenorhabdus nematophila*	313	0.300	100	No insert				
		xnm:XNC2_0444	*Xenorhabdus nematophila*	313	0.300	100	No insert				
		rca:Rcas_1163	*Roseiflexus castenholzii*	325	0.323	93	No insert				
		gca:Galf_2037	*Gallionella capsiferriformans*	79	0.316	76	PICI	2192302	2211152	18.8	Integrase backwards, no transcriptional divergence
		…									
		efd:EFD32_2452	*Enterococcus faecalis*	89	0.306	72	Prophage	2470933	2506883	36.0	
		elo:EC042_2423	*Escherichia coli*	63	0.333	54	Prophage	2552120	2559893	7.8	Defective phage

EfCIV583 gene	Function	Orthologs	Species	Length	Similarity	Overlap	Element	Start	End	Size (kb)	Comments
EF2954	*rpr*	efa:EF2954	*Enterococcus faecalis*	316	1.000	316	EfCIV583				No close match in enterococci
		scp:HMPREF0833_11008	*Streptococcus parasanguinis*	175	0.398	118	No insert				
		rto:RTO_22090	*Ruminococcus torques*	138	0.400	110	No insert				
		ssui:T15_0899	*Streptococcus suis*	182	0.412	102	PICI				
		csc:Csac_2097	*Caldicellulosiruptor saccharolyticus*	211	0.318	198	No insert				
		lam:LA2_03865	*Lactobacillus amylovorus*	147	0.540	63	No insert				
		lay:LAB52_03720	*Lactobacillus amylovorus*	241	0.507	71	No insert				
EF2955	*int*	efa:EF2955	*Enterococcus faecalis*	381	1.000	381	EfCIV583				
		efau:EFAU085_00503	*Enterococcus faecium*	393	0.467	379	Genomic island				
		efc:EFAU004_00565	*Enterococcus faecium*	393	0.467	379	Genomic island				
		efl:EF62_2611	*Enterococcus faecalis*	380	0.467	379	Genomic island				
		efu:HMPREF0351_10594	*Enterococcus faecium*	393	0.467	379	Genomic island				
		ehr:EHR_01850	*Enterococcus hirae*	380	0.467	379					
		efq:DR75_1138	*Enterococcus faecalis*	380	0.464	379	Genomic island				
		ecas:ECBG_01612	*Enterococcus casseliflavus*	380	0.488	381					
		crn:CAR_c08850	*Carnobacterium* sp	382	0.448	384	Genomic island				

[a] No insert: The ortholog seems to be chromsomally encoded, not been part of a defined mobile element.

Table S6. Orthology analysis of the 22 ORFs of LlCICV56-1

Abbreviations

ll – *Lactococcus lactis*
lla: IL1403
llc: SK11
lld: KLDS
lli: UC509.9
llm:MG1363
lln: NZ9000
llr: A76
lls: IO-1
llk: KF147
llt: CV56
llw: KW2
llx:NCDO2118

cbr - *Cenorabditis elegans*
cat - *Croceibacter atlanticus*
cdf - *Peptoclostridium difficile* 630
ckl - *Clostridium kluyveri* DSM 555
cso - *Clostridium cf. saccharolyticum* K10
efq - *E. faecalis* ATCC 29212
ehr - *E. hirae*
efm - *Enterococcus faecium* NRRL B-2354
ere - Eubacterium rectale ATCC 33656
evi - *Echinicola vietnamensis*
lpl - *Lactobacillus plantarum* WCFS1
lcb - *Lactobacillus casei*
lpg - Lactobacillus paracasei N1115
lca - *Lactobacillus casei* ATCC 334

lga - *Lactobacillus gasseri* ATCC 33323
lmc - *Listeria monocytogenes* Clip81459
lcn - *Leuconostoc carnosum*
loa - Loa loa (eye worm)
lgr - *Lactococcus garveae* ATCC 49156
lgv - *Lactococcus garveae* Lg2
mar - *Microcystis aeruginosa*
mtr - *Meleagris gallopavo* (turkey): 100539070
myr - *Myroides sp.* A21
mer - *Methanomassiliicoccus sp. Mx1-Issoire*
smb - *S. mitis* B
stk - *S. parauberis*
snu - *S. pneumoniae* A45
stx - *S. pyogenes* MGAS1882

Orthologies

Gene		**length**	**sim**	**OL**	**insert**	**start**	**end**	**size (kb)**	**comment**
llt:CVCAS_0027a*	*ltr*C	107	1.000	107	PICI	36265	50942	14.7	
lla:L35519		107	1.000	107	PICI	35516	50948	15.4	
llm:llmg_2538		107	0.897	107	PICI	2478636	2491949	13.3	
lln:LLNZ_13110		107	0.897	107	PICI	2479452	2492765	13.3	
lld:P620_13395		106	0.796	98	PICI	2530163	2544289	14.2	
lls:lilo_1806		111	0.698	96	PICI	1963199	1976945	13.7	
myr:MYRA21_3441		179	0.344	64	NI**				
llt:CVCAS_0027b*	HP	136	1.000	136	PICI	36265	50942	14.7	
lla:L35867		136	1.000	136	PICI	35516	50948	15.4	
llm:llmg_2537		136	0.949	136	PICI	2478636	2491949	13.3	
lln:LLNZ_13105		136	0.949	136	PICI	2479452	2492765	13.3	
llc:LACR_2255		136	0.904	136	PICI	2111920	2125925	14.0	
:llh_11410		136	0.904	136	PICI	2111920	2125925	14.0	
lgr:LCGT_1117		140	0.530	132	Prophage	1109676	1146622	36.9	
lgv :LCGL_1137		140	0.530	132	Prophage				
lld:P620_10790		140	0.534	133	Prophage	2078353	2118530	40.2	
llt:CVCAS_0027	*terS*	147	1.000	147	PICI	36265	50942	14.7	
lla:L36274		147	1.000	147	PICI	35516	50948	15.4	
llc:LACR_2256		147	0.959	147	PICI	2111920	2125925	14.0	
llr:llh_11415		147	0.959	147	PICI	2111920	2125925	14.0	
llm:llmg_2250		146	0.938	146	PICI	2211673	2228382	16.7	Has phage resistance
lln:llnZ_11610		146	0.938	146	PICI	2211673	2228382	16.7	Has phage resistance
lga:LGAS_0603		173	0.550	120	Prophage	600763	680457	79.7	Probably 2 prophages in tandem
lpl:lp_2423		169	0.530	115	Prophage	2163938	2203818	39.9	
llt:CVCAS_0028	HP	193	1.000	193	PICI	36265	50942	14.7	
lla:L36850		193	0.995	193	PICI	35516	50948	15.4	
llm:llmg_0029		193	0.902	193	PICI	32974	51647	18.7	
lln:llnZ_00140		193	0.902	193	PICI	32974	51647	18.7	
llc:LACR_2257		180	0.631	179	PICI	2116658	2128806	12.1	
llr:llh_11420		180	0.631	179	PICI	2111920	2125925	14.0	

Gene		length	sim	OL	insert	start	end	size	comment
llk:llkF_2464		179	0.609	179	PICI	2505047	2520783	15.7	
lld:P620_02915		133	0.568	139	PICI	527748	537492	9.7	Defective; has prohead protease
lgr:LCGT_1791		287	0.328	125	PICI	175594	178604	12.7	Has phage protease
lgv:LCGL_1812		287	0.328	125	PICI	175594	178604	12.7	Has phage protease
Mtr:mgr		1527	0.272	173	NI				
llt:CVCAS_0029	*rep*	542	1.000	542	PICI	36265	50942	14.7	
lla:L37667		542	1.000	542	PICI	35516	50948	15.4	
llm:llmg_0030		542	0.985	542	PICI	32974	51647	18.7	
lln:llnZ_00145		542	0.985	542	PICI	32974	51647	18.7	
lld:P620_13370		542	0.954	542	PICI	2530163	2544289	14.2	
llk:llkF_2463		542	0.941	542	PICI	2505047	2520783	15.7	
llr:llh_12835		544	0.930	542	PICI	2352357	2368410	16.0	
llc:LACR_2258		542	0.917	542	PICI	2111920	2125925	14.0	
llw:kw2_1828		487	0.495	489	Prophage	1878501	1919139	40.6	
smb:smi_0425		534	0.458	509	Prophage	398225	440170	41.9	
stx:MGAS1882_1149		491	0.452	489	Prophage	1099359	1143106	46.7	
llt:CVCAS_0030	*pri*	264	1.000	264	PICI	36265	50942	14.7	
lla:L39306		264	1.000	264	PICI	35516	50948	15.4	
llc:LACR_2259		264	0.962	264	PICI	2111920	2125925	14.0	
llm:llmg_2253		264	0.958	264	PICI	2211673	2228382	16.7	Has phage resistance
lln:llnZ_11625		264	0.958	264	PICI	2211673	2228382	16.7	Has phage resistance
llr:llh_11430		264	0.951	264	PICI	2111920	2125925	14.0	
llk:llkF_2462		264	0.920	264	PICI	2505047	2520783	15.7	
lld:P620_11530		264	0.917	264	PICI	2217535	2230575	13.0	
lcb:LCABL_30870		273	0.323	266	Hybrid	3030347	3044256	13.9	PICI-prophage hybrid, with entire capsid module
llt:CVCAS_0031	HP	109	1.000	109	PICI	36265	50942	14.7	
lla:L40104		109	1.000	109	PICI	35516	50948	14.4	
llm:llmg_2532		109	0.954	109	PICI	2478636	2491949	13.3	
lln:llnZ_13075		109	0.954	109	PICI	2479452	2492765	13.3	
llr:llh_11435		111	0.963	108	PICI	2111920	2125925	14.0	
lld:P620_11535		109	0.944	108	PICI	2217535	2230575	13.0	
llk:llkF_2461		109	0.917	109	PICI	2505047	2520783	15.7	
llc:LACR_2260		111	0.907	108	PICI	2116658	2128806	12.1	
lgr:LCGT_1789		109	0.562	105	PICI	175594	178604	12.7	Has phage protease
lgv:LCGL_1810		109	0.562	105	PICI	75594	178604	12.7	Has phage protease
stk:STP_1275		115	0.321	81	Prophage	1375102	1412591	37.5	
llt:CVCAS_0032	HP	64	1.000	64	PICI	36265	50942	14.7	
lla:L200001		64	1.000	64	PICI	35516	50948	14.4	
llk:llkF_2460		64	0.969	64	PICI	2505047	2520583	15.0	
lld:P620_02875		64	0.953	64	Hybrid	521256	537492	16.2	Has 2 integrases
llr:llh_12820		104	0.344	61	PICI	2352357	2368410	16.0	
llt:CVCAS_0033	HP	79	1.000	79	PICI	36265	50942	14.7	
lla:L40862		79	0.987	79	PICI	35516	50948	14.4	
lld:P620_11550		79	0.949	79	PICI	2217535	2230575	13.0	
llk:llkF_2458		79	0.924	79	PICI	2505047	2520583	15.0	
llc:LACR_2262		79	0.924	79	PICI	2116658	2128806	12.2	
llm:llmg_0034		79	0.911	79	PICI	32974	51647	18.6	
lln:llnZ_00165		79	0.911	79	PICI	32974	51647	18.6	
llr:llh_11440		79	0.848	79	PICI	2111920	2125925	14.0	
lgr:LCGT_1792		59	0.426	61	PICI	1755947	1768604	12.7	
lgv:LCGL_1813		59	0.426	61	PICI	1769776	1782433	12.7	

Gene		**length**	**sim**	**OL**	**insert**	**start**	**end**	**size**	**comment**
evi:Echvi_3649		1172	0.387	75	NI				
llt:CVCAS_0034	HP	173	1.000	173	PICI	36265	50942	14.7	
lla:L41670		173	1.000	173	PICI	35516	50948	14.4	
llm:llmg_2260		173	0.789	171	PICI	2211673	2228382	16.7	Has phage resistance
lln:llnZ_11660		173	0.789	171	PICI	2211673	2228382	16.7	Has phage resistance
lld:P620_01795		173	0.789	171	PICI	321043	333060	12.0	3′ end uncertain
llk:llkF_2456		174	0.759	174	PICI	2505047	2520583	15.0	
llc:LACR_2265		201	0.724	170	PICI	2116658	2128806	12.2	
llr:llh_11460		201	0.679	168	PICI	2111920	2125925	14.0	
mar:MAE_57910		265	0.313	134	NI				
cbr:CBG10226		806	0.312	112	No map				Caenorhabditis
llt:CVCAS_0035	HP	64	1.000	64	PICI	36265	50942	14.7	
lla:L42195		64	1.000	64	PICI	35516	50948	14.4	
lld:P620_02515		64	0.969	64	PICI	453940	463397	9.3	Defective
llr:llh_11465		64	0.953	64	PICI	2111920	2125925	14.0	
lls:lilo_1816		73	0.922	64	PICI	1963199	1976945	13.7	
llk:llkF_2455		64	0.938	64	PICI	2505047	2520583	15.0	
llc:LACR_2266		64	0.938	64	PICI	2116658	2128806	12.2	
llm:llmg_0037		64	0.922	64	PICI	32974	51647	18.6	
lln:llnZ_00180		64	0.922	64	PICI	32974	51647	18.6	
llt:CVCAS_0036	*reg*	246	1.000	246	PICI	36265	50942	14.7	
lla:L42465		246	1.000	245	PICI	35516	50948	14.4	
llm:llmg_2527		230	0.327	196	PICI	2478636	2491949	13.3	
lln:llnZ_13050		230	0.327	196	PICI	2479452	2492765	13.3	
lld:P620_01785		230	0.321	196	PICI	321043	330910	9.9	
llk:llkF_2454		230	0.306	196	PICI	2505047	2520583	15.0	
lgr:LCGT_1785		232	0.298	188	PICI	1755947	1768604	12.7	
lgv:LCGL_1806		232	0.298	188	PICI	1769776	1782433	12.7	
efm:M7W_2070		241	0.367	120	Prophage	1889045	1924864	39.5	
ehr:EHR_09450		241	0.358	120	Prophage	1847859	1882330	34.5	
llt:CVCAS_0037	HP	246	1.000	246	PICI	36265	50942	14.7	
lla:L42465		246	1.000	245	PICI	35516	50948	14.4	
llm:llmg_2527		230	0.327	196	PICI	2478636	2491949	13.3	
lln:llnZ_13050		230	0.327	196	PICI	2479452	2492765	13.3	
lld:P620_01785		230	0.321	196	PICI	321043	330910	9.9	
llk:llkF_2454		230	0.306	196	PICI	2505047	2520583	15.0	
lgr:LCGT_1785		232	0.298	188	PICI	1755947	1768604	12.7	
lgv:LCGL_1806		232	0.298	188	PICI	1769776	1782433	12.7	
efm:M7W_2070		241	0.367	120	Prophage	1889045	1924864	39.5	
ehr:EHR_09450		241	0.358	120	Prophage	1847859	1882330	34.5	
llt:CVCAS_0038	HP	128	1.000	246	PICI	36265	50942	14.7	
lla:L43680		128	1.000	128	PICI	35516	50948	14.4	
llr:llh_12770		128	0.781	128	PICI	2352357	2368410	16.0	
llc:LACR_2269		127	0.701	127	PICI	2116658	2128806	12.2	
llm:llmg_0041		140	0.550	129	PICI	32974	51647	18.6	
lln:llnZ_00200		146	0.550	129	PICI	32974	51647	18.6	
llw:kw2_0886		118	0.505	111	PICI	903732	908883	5.1	Defective PICI? Has lysin gene
lld:P620_12480		141	0.454	130	Prophage	2348850	2374861	26.0	Defective prophage, 2 int genes, no tail
lgr:LCGT_1146		114	0.470	115	Prophage	1110376	1146622	36.2	
lgv:LCGL_1166		114	0.470	115	Prophage				
lli:lli_0637		115	0.461	115	NI				

Gene		**length**	**sim**	**OL**	**insert**	**start**	**end**	**size**	**comment**
efq:DR75_1672		110	0.456	114	Prophage	1660409	1695776	35.4	
llt:CVCAS_0039	reg	184	1.000	184	PICI	36265	50942	14.7	
lla:L44085		184	1.000	184	PICI	35516	49727	14.2	
llm:llmg_0042		184	0.924	184	PICI	32974	51647	18.6	
lln:llnZ_00205		184	0.924	184	PICI	32974	51647	18.6	
llr:llh_12765		184	0.913	184	PICI	2352357	2368410	16.0	
llc:LACR_2270		183	0.799	184	PICI	2116658	2128806	12.2	
lld:P620_12940		98	0.887	97	PICI	2464618	2479987	15.4	
lgr:LCGT_0311		196	0.395	195	NI				
lgv:LCGL_0311		196	0.395	195	NI				
llk:llkF_1033		187	0.343	181	Prophage	1066254	1100809	34.6	
llt:CVCAS_0040	reg	64	1.000	64	PICI	36265	50942	14.7	
lla:L45035		64	1.000	64	PICI	35516	49727	14.2	
llm:llmg_0044		64	0.984	64	PICI	32974	51647	18.6	
lln:llnZ_00215		64	0.984	64	PICI	32974	51647	18.6	
llr:llh_12760		64	0.984	64	PICI	2352357	2368410	16.0	
llc:LACR_2271		64	0.969	64	PICI	2116658	2128806	12.2	
lld:P620_12935		64	0.969	64	PICI	2464618	2479987	15.4	
llk:llkF_2448		64	0.938	64	PICI	2505047	2520583	15.0	
loa:LOAG_08304		788	0.372	43					eye worm gene
llt:CVCAS_0041	reg	53	1.000	53	PICI	36265	50942	14.7	
lla:L45351		80	0.981	53	PICI	35516	49727	14.2	
llm:llmg_0047		80	0.962	53	PICI	32974	51647	18.6	
lln:llnZ_00240		80	0.962	53	PICI	32974	51647	18.6	
cat:CA2559_02645		294	0.368	38	NI				
llt:CVCAS_0042	HP	74	1.000	74	PICI	36265	50942	14.7	
lla:L45702		74	1.000	74	PICI	35516	49727	14.2	
llm:llmg_0048		74	1.000	74	PICI	32974	51647	18.6	
lln:llnZ_00245		70	1.000	70	PICI	32974	51647	18.6	
cso:CLS_07510		55	0.491	53	NI				
ckl:CKL_1132		56	0.446	56	NI				
ere:EUBREC_3588		55	0.462	52					Tiny defective prophage remnant?
mer:H729_05640		69	0.441	59	NI				
cdf:CD630_05860		59	0.453	53	NI				
lmc:Lm4b_00359		62	0.463	54	NI				
llt:CVCAS_0043	HP	108	1.000	108	PICI	36265	50942	14.7	
lld:P620_13295		108	1.000	108	PICI	2530163	2544289	14.1	
llm:llmg_0051		108	1.000	108	PICI	32974	51647	18.6	
lln:llnZ_00260		108	1.000	108	PICI	32974	51647	18.6	
llk:llkF_2449		108	0.963	108	PICI	2505047	2520583	15.0	
llc:LACR_C39		120	0.627	102					Transposon on plasmid
lli:lli_p6024		120	0.627	102					Transposon on plasmid
llr:llh_13780		117	0.618	102					Transposon on plasmid
lpq:AF91_13470		105	0.519	106	NI				
lca:LSEI_2757		105	0.519	106	NI				
llt:CVCAS_0044	HP	54	1.000	54	PICI	36265	50942	14.7	
lla:L200004		54	1.000	54	PICI	35516	50948	14.4	
lld:P620_12920		54	1.000	54	PICI	2463882	2479987	16.1	
llm:llmg_0053		54	1.000	54	PICI	32974	51647	18.6	
lln:llnZ_00265		54	1.000	54	PICI	32974	51647	18.6	

Gene		length	sim	OL	insert	start	end	size	comment
llk:llkF_2446		54	0.926	54	PICI	2505047	2520583	15.0	
llw:kw2_2347		53	0.731	52	NI				
llc:LACR_2598		53	0.712	52	NI				
lli:lli_2241		53	0.712	52	NI				
llr:llh_13190		53	0.712	52	NI				
lls:lilo_0576		66	0.558	52	NI				
lgr:LCGT_1418		64	0.560	50	NI				
lgv:LCGL_1439		64	0.560	50	NI				
llt:CVCAS_0045	HP	101	1.000	101	PICI	36265	50942	14.7	
lla:L47979		101	1.000	101	PICI	35516	50948	14.4	
llm:llmg_0054		101	1.000	101	PICI	32974	51647	18.6	
lln:llnZ_00270		101	1.000	101	PICI	32974	51647	18.6	
llk:llkF_2445		101	0.990	101	PICI	2505047	2520583	15.0	
lgr:LCGT_1323		99	0.494	87	NI				
lgv:LCGL_1344		99	0.494	87	NI				
lcn:C270_07595		99	0.354	99	NI				
llt:CVCAS_0046	*int*	394	1.000	394	PICI	36265	50942	14.7	
lla:L48477		394	0.997	394	PICI	35516	50948	14.4	
llm:llmg_0055		394	0.997	394	PICI	32974	51647	18.6	
lln:llnZ_00275		394	0.997	394	PICI	32974	51647	18.6	
lld:P620_01770		398	0.515	396	PICI	321043	333060	12.0	3’end uncertain
llc:LACR_0301		398	0.513	396	PICI	278489	289370	10.9	3’end uncertain
llk:llkF_2008		399	0.477	396	PICI	2063071	2074196	11.1	
lls:lilo_1819		410	0.470	396	PICI	1963199	1976945	13.7	
llr:llh_10885		393	0.471	397	Prophage	1973375	2011192	37.8	
lgr:LCGT_1777		396	0.415	393	PICI	1755947	1768604	12.5	
lgv:LCGL_1798		396	0.415	393	PICI	1769776	1782433	12.6	
lli:lli_1862		343	0.444	347	Prophage	1846819	1857113	10.9	Defective. Has *dut*
snu:SPNA45_01857		388	0.414	391	PICI	1886061	1902018	15.9	
smb:smi_2017		388	0.376	391	PICI	2057587	2070717	13.1	

*ORFs that are not annotated in LlCICV56-1 but are annotated in LlCIIL1403-1, which has the identical sequence in that region.

Table S7. Putative phage-inducible chromosomal islands of Gram-positive cocci.

PICI	Strain	Accession number (Genomic location)	Size (kb)	*att* site core	Accessory genes[b]
EfCIV583	*E. faecalis* V583	AE016830 (2816732-2829670)	12.9	TATTAATGAAACAACGTG	UvrB protein; Cold-shock protein
EfCILA3B-2	*E. faecalis* LA3B-2	ATJC01000082 (5397-18340)	12.9	TAAACTGTAAGTTTAGT	Cold-shock protein
EfCI918	*E. faecalis* 918	AVNY01000040 (1-12614)	12.6	TATTAATGAAACAACGTG	UvrB protein; Cold-shock protein
EfCIB16457	*E. faecalis* B16457	AIIL01000003 (236044-248787)	12.7	TATTAATGAAACAACGTG	UvrB protein; Cold-shock protein
EfCISF105	*E. faecalis* SF105	AJEE01000013 (53058- 65413)	12.3	TATTAATGAAACAACGTG	UvrB protein; Cold-shock protein
LlCIbIL310	*L. lactis* IL1403	AE005176 (34907-49863)	14.9	CAAAAAAACACTGATTGAATGCCGTATG	Enterocin immunity (EntA); LtrA
LlCIbIL312	*L. lactis* IL1403	AE005176 (502595-517773)	15.1	GAAAGACGCAGTTAAATAATTATAGCTAT	Peptidase_M48; Cold shock protein
LlCINZ9000-1	*L lactis* - cremoris NZ9000	CP002094 (32370-51783)	19.4	CAAAAAAACACTGATTGAATGCCGT	*bcn*A; IS712A; Non-specific endonuclease
LlCINZ9000-2	*L. lactis* - cremoris NZ9000	CP002094 (2210232-2228483)	18.3	TAGAACTATGTTAAAA	Abortive phage resistance
LlCI-NZ9000-3	*L lactis* - cremoris NZ9000	CP002094 (2482743-2492765)	10.3	ATTCACTTGAGCAATGAATATA	LtrA
LlCISK11	*L. lactis* - cremoris SK11	CP000425 (2115981-2128907)	12.9	TAGAACTATGTTAAAA	DNA/RNA non-specific endonuclease
LlCICV56-1	*L. lactis* - lactis CV56	CP002365 (36265-50942)	14.7	CAAAAAAACACTGATTGAATGCCGTATG	Enterocin immunity (EntA); LtrA
LlCI-CV56-2	*L. lactis* - lactis CV56	CP002365 (1723782-1733895)	10.1	J_LTAAAAAATAGGACCTAAGACTGATGA J_RTAAAAAATCAGACCTAAGACTTATGA	Cold shock protein
LlCIKLDS-2	*L. lactis* - *lactis* KLDS 4.0325	CP006766 (1903120-1915186)	12.1	TCAGACCTAAGACTGATGATATAAAG	
LlCI-KLDS-3	*L. lactis* – *lactis* KLDS 4.0325	CP006766 2464508-2479769	15.2	GCTATAATAAAACTATAT	Prohead protease
LlCIA76-1	*L. lactis* - cremoris A76	CP003132 (2111244-2126036)	14.8	TTTTAACATAGTTCTATTTTATCACA	
LlCIA76-2	*L. lactis* - cremoris A76	CP003132 (2352993- 2368188)	15,2	TAAAACTATA	
LlCIKF147	*L. lactis* - lactis KF147	CP001834 (2505680- 2520561)	14.9	TAAAACTATA	BcnA-imm; Pyrimidine dimer DNA glycosylases
MG1363-1	*L. lactis* - lactis MG1363	AM406671 (32370-51783)	19.4	CAAAAAAACACTGATTGAATGCCGT	*bcn*A; IS712A; Non-specific endonuclease

PICI	Strain	Accession number (Genomic location)	Size (kb)	*att* site core	Accessory genes[b]
SpnCI-Taiwan-0.03	*S. pneumoniae* Taiwan	NC_012469 3563-23357	19.8	CCCTTTTTGTGTTA	
SpnCI-ST556-0.03	*S. pneumoniae* ST556	CP003357 3563-21646	18.1	CCCTTTTTGTGTTA	
SpnCI-Taiwan-0.2	*S. pneumoniae* Taiwan	NC_012469 197987-210888	12.9	TACAAAATCGGCTTTTTT	
SpnCI-Tigr4-1.06	*S. pneumoniae* Tigr4	NC_003028 1063231-1073321	10.1	CCTAACAAAAC	TA system
SpnCI-INV104-1.06	*S. pneumoniae* INV104	FQ312030 1070841-1079518	8.7	CCTTAAAAAAATAA	
SpnCI-A45-1.9	*S. pneumoniae* A45	NC_018594.1 1887286-1902018	14.7	GCCCATACAAACCCCATA	DNA-damage-inducible protein D
SsuCI-TL13	*S. suis* TL-13	CP003993 1339840-1351861	12.0	CTTGAAAAAAATAA	
SolCI-AS1.3089-0.6	*S. oligofermentans* AS1.3089	CP004409.1 602331`- 612649	10.3	CTTGAAAAAAATAA	TA system
SpnCI-TCH8341-0.45	*S. pneumoniae* TCH8431/19A	CP001993 (440193-453094)	12.9	ATTATACTACAAAATCGGC	
SpnCI-TCH8341-0.25	*S. pneumoniae* TCH8431/19A	CP001993 (248868-267453)	18.6	TAACACAAAAAGGG	DNA-damage-inducible protein D Inserted plasmid

[a] NI: Not identified.

[b] The identities of the accessory genes are based on annotations; none has been tested experimentally.

Table S8. Role of the cloned *cos* site in pAGEnt transfer[a].

Donor strain	Cloned site *cos*	Plasmid titre[b]
JP14198	Empty vector	< 10
JP14199	Phage bIL286	4.5×10^2
JP14203	LlCI-bIL310	1.2×10^2

[a] The means of results from three independent experiments are shown. Variation was within ±5% in all cases.

[b] No. of transductants/ml induced culture, using IL1403 as recipient strain.

Table S9. Orthology analysis of SpnCI6706B

Abbreviations

spn: SPN TIGR4
std: SPPN
snb: SPN 670-6B
snc: SPN TCH8431/19A
snd: SPN ST556
sni: SPN INV104
snt: SPN Taiwan19f-14
snu: SPN A45
spi: SPY MGAS10750
smb: SMB
scp: SPS ATCC 15912
stc: STH CNRZ1066
ste: STH LMD-9
stn: STH ND03
stw: STH MN-ZLW-002
spv: SPN Hungary19A 6
stk: SPU
*sthe:*STH ASCC 1725
sga: SGL UCN34
sgg: SGL ATCC BAA-2069
sgt: SGL ATCC 43143
sjj: SPN JJA
sagm:SAG 09mas018883
sub: SUB
sui: SSU T15
ssut: SSU TL-13
sst: SSU ST3
ssuy: SSU YB51
slu: SLT KE3
sak: SAG A909
sagt:SAG COH1
nce: NCE
stx: SPY MGAS1882
spnn:SPN A026
lmn: LMO 08-5778
fsc: FSU
pph: PPH
drs: =Dehalobacter restrictus
dec: =Dehalobacter sp. CF
ded: =Dehalobacter sp. DCA
rbr: =Ruminococcus bromii

SPN = *Streptococcus pneumoniae*

SPNN = *S. pseudopneumoniae*

SMB = *S. mitisB*
SPS = *S. parasanguinis*

STH = *S. thermophilus*

SPU = *S. parauberis*

SGL = *S. galactiae*

SUB = *S. uberis*
SSU = S. suis

SLT = *S lutetiensis*
SAG = *S. agalactiae*

NCE = *Nocema seranae*
SPY = *S. pyogenes*

LMO = *Listeria monocytogenes*
FSU = Fibrinobacter succinogenes
PPH = Pelodictyon phaeoclathratiforme

Orthologs

Gene		**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**
snb:SP670_0026 (388 a.a.)	*int*							
snc:HMPREF0837_10291		388	0.874	388	PICI	0.25	14.9	*dna*A
snd:MYY_0032		398	0.874	388	PICI	0.01	16.1	*dna*A
snt:SPT_0037		388	0.874	388	PICI	0.01	14.9	*dna*A
smb:smi_2017		388	0.546	388	PICI	2.05	12.2	sugar hydrolase
scp:S. parasangui:HMPREF0833_11010		388	0.549	388	PICI	1.02	10.6	*cna*
ste:STER_0829		388	0.531	388	PICI	0.74	9.4	*pab*B
stc:str0783		388	0.531	388	PICI	0.73	8.1	*pab*B
sthe:T303_05120		388	0.531	388	PICI	0.93	7.7	*dlt*D
stn:STND_0774		388	0.531	388	PICI	0.75	10.2	*uvr*A
stw:Y1U_C0751		388	0.531	388	PICI	0.73	6.5	*pab*B
spv:SPH_0289		388	0.536	388	PICI	0.26	12.4	*uvr*A
stkpara:STP_1346		386	0.525	387	PICI	1.48	11	SAM
sga:GALLO_2149		388	0.525	387	PICI	2.2	11.9	*gsh*A
sgg:SGGBAA2069_c21460		388	0.525	387	PICI	2.2	11.8	*gsh*A
sgt:S GGB_2132		388	0.525	387	PICI	2.2	11.9	*gsh*A
sagm:BSA_21480		388	0.503	388	PICI	2.1	14.6	*rps*D
sub:SUB1840		388	0.505	388	PICI	1.8	12.6	*rps*D
slu:KE3_0026		381	0.518	388	PICI	0.03	11.0	*tyr*S
sak:SAK_2094		388	0.508	388	PICI	2.06	15.6	*rps*D
snb:SP670_0025 (284 a.a.)	*din*D							
snu:SPNA45_01858		274	0.993	271	PICI	1.9	14.7	*yes*MN
drs:DEHRE_03560		278	0.598	276	NI*			
dec:DCF50_p2453		278	0.583	276	NI			
ded:DHBDCA_p2442		278	0.583	276	NI			
rbr:RBR_05470		280	0.561	278	NI			
snc:HMPREF0837_10290		186	0.987	155	PICI	0.25	14.9	*dna*A
snd:MYY_0031		186	0.987	155	PICI	0.01	14.9	*dna*A
snt:SPT_0036		186	0.987	155	PICI	0.01	14.9	*dna*A
fsc:FSU_1649		279	0.570	270	NI			
fsu:Fisuc_1187		279	0.570	270	NI			
pph:Ppha_0973		362	0.525	276	NI			
xne:XNC1_0195		271	0.549	266	defective and rearranged PICI-like fragment xne:XNE =Xenorabdus nematophila			
snb:SP670_0024 (238 a.a.)	*rpr*							
snc:HMPREF0837_10283		246	0.983	237	PICI	0.25	18.1	*dna*N
snd:MYY_0025		246	0.983	237	PICI	0.01	16.1	*dna*A
snt:SPT_0029		238	0.983	237	PICI	0.01	14.9	*dna*A
snu:SPNA45_01863		255	0.745	239	PICI	1.9	15.4	*yes*MN
sjj:SPJ_1901		250	0.626	246	prophage			

Gene		**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**
snb:SP670_0023 (50 a.a.)	*reg*							
snc:HMPREF0837_10282		50	1.000	50	PICI	0.25	18.1	*dna*N
snd:MYY_0024		50	1.000	50	PICI	0.01	16.1	*dna*A
snt:SPT_0028		50	1.000	50	PICI	0.01	14.9	*dna*A
saua:SAAG_02514		73	0.460	50	Proph	2.0	43.4	*hlb*
snb:SP670_0022 (194 a.a.)	*ant*R							
ssq:SSUD9_2185		248	0.568	192	PICI	2.1		*rec*F
sst:SSUST3_2012		248	0.568	192	PICI	2.0	10.7	*rec*F
ssuy:YB51_9970		248	0.568	192	PICI	2.0	10.7	*rec*F
spy:SPy_2127		255	0.457	184	PICI	1.8	12.9	*mut*S/L
stz:SPYALAB49_001792		193	0.457	184	PICI	1.7	13.2	*mut*S/L
sdq:SDSE167_2198		255	0.446	184	PICI	2.0	19.6	*mut*S/L
sdg:SDE12394_10830		187	0.415	183	PICI	2.1	14.8	*rps*D
sds:SDEG_2138		187	0.415	183	PICI	2.1	11.2	*rps*D
ssui:T15_1236		261	0.425	153	proph	1.2	33.0	*rps*A
spb:M28_Spy1861		188	0.416	185	PICI	1.8	10.8	*rps*D
sph:MGAS10270_Spy1948		188	0.416	185	PICI	1.8	10.7	*rps*d
stg:MGAS15252_1718		188	0.416	185	PICI	1.7	12.2	*rps*D
clb:Clo1100_2443		239	0.453	148	proph	2.7	26.3	defective
ctc:CTC01071		270	0.484	126	proph	1.3	36.2	
snb:SP670_0021 (208 a.a.)								
snc:HMPREF0837_10490		208	0.952	208	PICI	0.44	15.4	*uvr*A
snt:SPT_0226		208	0.952	208	PICI	0.2	12.4	*uvr*A
spnn:T308_00870		208	0.952	208	PICI	1.6	12.4	*uvr*A
spv:SPH_0293		208	0.952	208	PICI	0.26	12.4	*uvr*A
snd:MYY_0262		203	0.951	203	PICI	0.24	12.4	*uvr*A
smb:smi_2013		208	0.841	208	PICI	2.1	10.9	sugar hydrolase
std:SPPN_01200		209	0.833	209	PICI	0.2	12.4	*mnm*A
scp:HMPREF0833_11006		208	0.812	208	PICI	1.02	10.6	*cna*
snu:SPNA45_01864		200	0.779	199	PICI	1.9	15.4	*yes*MN
ssut:TL13_1976		208	0.721	208	PICI	2.0	15.1	*rec*F
spn:SP_1134		205	0.744	203	PICI	1.1	10.1	enolase
ssui:T15_1587		206	0.677	201	PICI	1.60	10.0	*fab*G
snb:SP670_0020 (55 a.a.)								
ssui:T15_1694		54	0.698	53	proph	1.7	34.5	*hup*B
spy:SPy_0978		56	0.472	53	proph	0.8	40.2	*cps*FQ/*mut*X
stz:SPYALAB49_001012		56	0.472	53	proph	1.0	47.3	*glg*P
lld:P620_11580		61	0.412	51	PICI	2.2	13.0	*cut*C
spb:M28_Spy1797		64	0.491	55	PICI	1.8	13.3	*mut*S/L
sph:MGAS10270_Spy1881		64	0.491	55	PICI	1.8	13.9	*mut*S/L
sagm:BSA_21410		57	0.439	57	PICI	2.1	14.6	*rps*D
snc:HMPREF0837_10278		77	0.473	55	PICI	0.25	18.1	*dna*N
snd:MYY_0020		57	0.473	55	PICI	0.01	16.1	*dna*A
snt:SPT_0023		57	0.473	55	PICI	0.01	14.9	*dna*A
snu:SPNA45_01866		57	0.473	55	PICI	1.9	15.4	*yes*MN
aoe:Clos_1887		60	0.357	56	NI			

Gene	**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**
snb:SP670_0019 (142 a.a.)							
snc:HMPREF0837_10277	142	0.993	142	PICI	0.25	18.1	*dna*N
snd:MYY_0019	142	0.993	142	PICI	0.01	16.1	*dna*A site
snt:SPT_0022	142	0.993	142	PICI	0.01	14.9	*dna*A
spb:M28_Spy1799	189	0.384	138	PICI	1.80	14.0	*mut*S/L
snb:SP670_0018 (48 a.a.) HP (4 hits only)							
snc:HMPREF0837_10276	48	1.000	48	PICI	0.25	18.1	*dna*N
snd:MYY_0018 hypothet	48	1.000	48	PICI	0.01	16.1	*dna*A
snt:SPT_0021 hypothet	48	1.000	48	PICI	0.01	14.9	*dna*A
rdn:HMPREF0733_10312	1301	0.396	48	NI			*rpo*C
snb:SP670_0017							
snc:HMPREF0837_10275	49	0.980	49	PICI	0.25	18.1	*dna*N
snb:SP670_0016 (38 a.a.) (4 hits only)							
snc:HMPREF0837_10274	46	1.000	29	PICI	0.25	18.1	*dna*N
snd:MYY_0017	46	1.000	29	PICI	0.01	16.1	*dna*A
snt:SPT_0020	46	1.000	29	PICI	0.01	14.9	*dna*A
ssk:SSUD12_0495	155	0.862	29	PICI	0.5	11.6	*lys*S
snb:SP670_0015 (166 a.a.)							
snc:HMPREF0837_10273	170	0.910	166	PICI	0.25	18.1	*dna*N
snd:MYY_0016	170	0.910	166	PICI	0.03	13.2	*dna*A
snt:SPT_0019	166	0.910	166	PICI	0.01	14.9	*dna*A
std:SPPN_01215	169	0.800	165	PICI	0.2	12.4	*mnm*A
eol:Emtol_1450	514	0.342	73	NI			
snb:SP670_0014 (46 a.a.)							
snc:HMPREF0837_10272	46	0.913	46	PICI	0.25	18.1	*dna*N
snt:SPT_0018	46	0.913	46	PICI	0.01	14.9	*dna*A
smb:smi_2011	66	0.826	46	PICI	2.1	10.9	sugar hydrolase
snd:MYY_0015	39	0.923	39	PICI	0.01	16.1	*dna*A
spnn:T308_00880	66	0.674	46	PICI	1.6	12.4	*uvr*A
spv:SPH_0295	66	0.674	46	PICI	0.26	12.4	*uvr*A
spn:SP_1136	148	0.630	46	PICI	1.1	11.5	enolase
scp:HMPREF0833_11005	66	0.630	46	PICI	1.02	10.6	*cna*
sni:INV104_09830	59	0.590	39	PICI	1.1	8.2	enloase
ssui:T15_1589	63	0.571	42	PICI	1.60	10.0	*fab*G
snb:SP670_0013 (71 a.a.)							
snc:HMPREF0837_10270	71	0.986	71	PICI	0.25	18.1	*dna*N
snt:SPT_0016	71	0.986	71	PICI	0.01	14.9	*dna*N
std:SPPN_01220	71	0.901	71	PICI	0.2	13.2	*dna*N
scp:HMPREF0833_11004	71	0.859	71	PICI	1.02	12.4	*mnm*A
smb:smi_2010	71	0.845	71	PICI	2.1	10.9	sugar hydrolase
spnn:T308_00885	71	0.789	71	PICI	1.6	12.4	*mnm*A
spv:SPH_0296	71	0.789	71	PICI	0.26	12.4	*uvr*A
dav:DESACE_04385	580	0.319	69	NI			
scg:SCI_1442	64	0.349	63	PICI		10.5	*gpm*A

Gene	**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**	
scon:SCRE_1399	64	0.349	63	PICI		10.5	*gpm*A	
scos:SCR2_1399	64	0.349	63	PICI		0.5	*gpm*A	
bvu:BVU_2093	583	0.432	37	NI				
snb:SP670_0012 (97 a.a.)								
snc:HMPREF0837_10269	97	0.959	97	PICI	0.25	18.1	*dna*N	
std:SPPN_01225	98	0.928	97	PICI	0.2	12.4	*mnm*A	
snu:SPNA45_01869	94	0.957	93	PICI	1.9	14.7	*yes*MN	has dinD
smb:smi_2009	97	0.856	97	PICI	2.1	10.9	sugar hydrolase	
snd:MYY_0013	68	0.956	68	PICI	0.01	16.1	*dna*A	
snt:SPT_0015	58	0.948	58	PICI	0.01	14.9	*dna*A	
nce:NCER_100853	221	0.302	96	NI				
snb:SP670_0011 (113 a.a.)								
snc:HMPREF0837_10268	113	1.000	113	PICI	0.25	18.1	*dna*N	
snd:MYY_0012	113	1.000	113	PICI	0.01	16.1	*dna*A	
snt:SPT_0014	113	1.000	113	PICI	0.01	14.9	*dna*N	
snu:SPNA45_01870	113	1.000	113	PICI	1.9	15.4	*yes*MN	
std:SPPN_01230	113	1.000	113	PICI	0.2	12.4	*mnm*A	
smb:smi_2008	113	0.841	113	PICI	2.1	10.9	sugar hydrolase	
spnn:T308_00890	113	0.841	113	PICI	1.6	12.4	*uvr*A	
spv:SPH_0297	113	0.841	113	PICI	0.26	12.4	*uvr*A	
scp:HMPREF0833_11003	113	0.735	113	PICI	1.02	10.6	*cna*	
sdq:SDSE167_2216	109	0.667	111	PICI	2.0	19.6	*mut*L/S	
spa:M6_Spy1814	109	0.667	111	PICI	1.8	13.3	*mut*L/S	
stg:MGAS15252_1660	109	0.667	111	PICI	1.7	12.2	*rps*D	
snb:SP670_0010 (90 a.a.)								
snc:HMPREF0837_10267	90	1.000	90	PICI	0.25	18.1	*dna*N	
snt:SPT_0013	90	1.000	90	PICI	0.01	14.9	*dna*N	
std:SPPN_01235	90	0.967	90	PICI	0.2	12.4	*mnm*A	
snd:MYY_0266	93	0.708	89	PICI	0.24	12.4	*uvr*A	
spnn:T308_00895	93	0.708	89	PICI	1.6	12.4	*uvr*A	
spv:SPH_0298	93	0.708	89	PICI	0.26	12.4	*uvr*A	
smb:smi_2007	91	0.674	89	PICI	2.1	10.9	sugar hydrolase site	
scp:HMPREF0833_11002	91	0.607	89	PICI	1.02	10.6	*cna*	
ssut:TL13_0170	92	0.539	89	PICI	0.14	13.1	*ack*A	
sagt:GBSCOH1_1946	90	0.556	90	PICI	2.0	14.8	*rps*D	
sst:SSUST3_2006	94	0.570	86	PICI	2.0	13.5	*rec*F	
snb:SP670_0009 (286 a.a.) *pri*								
snc:HMPREF0837_10266	286	0.965	286	PICI	0.25	18.1	*dna*N	
snd:MYY_0011	286	0.965	286	PICI	0.01	16.1	*dna*A	
snt:SPT_0012	286	0.965	286	PICI	0.01	14.9	*dna*N	
smb:smi_2006	286	0.930	286	PICI	2.1	10.9	sugar hydrolase	
spnn:T308_00905	288	0.907	289	PICI	1.6	12.4	*uvr*A	
spv:SPH_0299	288	0.907	289	PICI	0.26	12.4	*uvr*A	
sagi:MSA_22030	289	0.810	289	PICI	2.1	17.4	*rps*D	
spf:SpyM51773	288	0.741	290	PICI	1.8	11.9	*mut*S/L	
spy:SPy_2135	285	0.718	287	PICI	1.8	12.9	*mut*S/L	

Gene	**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**
stz:SPYALAB49_001801	285	0.718	287	PICI	1.8	14.3	*mut*S/L
spa:M6_Spy1816	285	0.718	287	PICI	1.8	13.3	*mut*S/L
sak:SAK_2084	285	0.725	287	PICI	2.1	15.6	*rps*D
snb:SP670_0008 (492 a.a.) *rep*							
spf:SpyM51774	500	0.915	492	PICI	1.8	11.9	*mut*S/L
spv:SPH_0300	489	0.918	488	PICI	0.26	12.4	*uvr*A
snc:HMPREF0837_10498	489	0.916	488	PICI	0.44	15.4	*uvr*A
snd:MYY_0268	489	0.916	488	PICI	0.26	12.4	*uvr*A
snt:SPT_0233	489	0.916	488	PICI	0.2	12.4	*uvr*A
spnn:T308_00910	489	0.916	488	PICI	1.6	12.4	*uvr*A
sagi:MSA_22020	498	0.897	485	PICI	2.1	17.4	*rps*D
sak:SAK_2083	480	0.900	480	PICI	2.1	15.6	*rps*D
sthe:T303_05075	501	0.758	483	PICI	0.93	7.7	*dlt*D
stc:str0775	500	0.754	483	PICI	0.73	8.1	*pab*B
ste:STER_0819	501	0.754	483	PICI	0.74	9.4	*pab*B
stn:STND_0765	501	0.754	483	PICI	0.75	10.2	*uvr*A
ssui:T15_1593	507	0.484	494	PICI	1.60	10	*fab*G
spi:MGAS10750_Spy1910	498	0.474	485	PICI	1.87	13.5	*mut*S/L
Snb:SP670_0007 (167aa)							
snc:HMPREF0837_10500	176	0.889	162	PICI	0.44	15.4	*uvr*A
snd:MYY_0270	176	0.889	162	PICI	0.26	12.4	*uvr*A
snt:SPT_0235	176	0.889	162	PICI	0.2	12.4	*uvr*A
spnn:T308_00920	176	0.889	162	PICI	1.6	12.4	*uvr*A
spv:SPH_0302	176	0.889	162	PICI	0.25		*uvr*A
snu:SPNA45_01874	142	0.923	142	PICI	1.88		*yes*MN
smb:smi_2003	153	0.865	141	PICI	2.05		fucosidase
ssq:SSUD9_2176	204	0.529	172	PICI	2.16		*rec*F
sn:SSUST3_2003	182	0.529	172	PICI	2.00		*rec*F
sagi:MSA_21990	231	0.537	164	PICI	2.05		*rps*D
ssuy:YB51_9925	150	0.500	148	PICI	2.02		*rec*F
sub:SUB1829	205	0.426	162	PICI	2.01		*rps*D
Snb:SP670_0006 (167aa)							
snu:SPNA45_01875	167	1.000	167	PICI	1.88		*yes*MN
smb:smi_2002	167	0.934	167	PICI	2.05		fucosidase
snc:HMPREF0837_10501	169	0.879	165	PICI	0.44		*uvr*A
spnn:T308_00925	169	0.879	165	PICI	1.6		*uvr*A
spv:SPH_0303	169	0.879	165	PICI	0.25		*uvr*A
sagi:MSA_21980	163	0.722	162	PICI	2.05		*rps*D
ssui:T15_1595	166	0.548	166	PICI	1.60	10	*fab*G
sagm:BSA_21300	162	0.525	162	PICI	2.08	14.6	*rps*D
sak:SAK_2081	162	0.519	162	PICI	2.07	15.7	*rps*D
spa:M6_Spy1821	162	0.512	162	NI			

Gene	**length**	**sim**	**OL**	**insert**	**site**	**size**	**site**
Snb:SP670_0005 (130aa)							
smb:smi_2000	130	0.946	130	PICI	0.19	12.4	*mnm*N
std:SPPN_01285	140	0.311	132	PICI?	1.94	12.6	very poor annot
slu:KE3_2016	140	0.311	132	PICI	1.94	14.1	pgp
sga:GALLO_2136	140	0.303	132	PICI	2.23	11.4	
sgg:SGGBAA2069_c21340	140	0.303	132	PICI	2.18	11.8	
sgt:SGGB_2119	140	0.303	132	PICI	2.18	11.2	
lsa:LSA0600	113	0.350	80	PICI	0.60	8.1	

snb:SP670_0004 (52 a.a.) no matching protein in DB