Supplementary Table 1. Origin and characteristics of *Staphylococcus aureus* strains sequenced in this study.

Strain	Host	Geographic origin	Isolation date	Accession Number
J	Rabbit	France	2002	ERS400835
I	Rabbit	Belgium	1997	ERS400834
DL190	Rabbit	Spain	2003	ERS400836
DV602	Rabbit	Italy	2010	ERS400837
DL688	Rabbit	Spain	2007	ERS400838
DL645	Rabbit	Spain	2007	ERS400839
A	Human	France	1981	ERS400826
B	Human	USA	2001	ERS400827
C	Human	Spain	2002	ERS400828
D	Human	Belgium	2003	ERS400829
E	Human	Lesser Antilles	2005	ERS400830
F	Human	UK	2007	ERS400831
G	Human	India	2009	ERS400832
H	Human	Denmark	1957	ERS400833

Supplementary Table 2. Pseudogenes and genes specific to all rabbit *S. aureus* ST121 strains.

Annotation	Position in ED133	Original sequence	New sequence	% CDS affected	Skin model[1]
EssB	279142	AAAATGAAATG	A	97.5	-
MatE	381320	TGGG	TGG	42.9	-
Histidinol-phosphate aminotransferase	786424	TC	TCC	72.5	-
Rot (repressor of toxins)	1849323	T	TA	38.8	+
Lipase precursor	319553	CAG	TAG[2]		-
Conserved hypothetical protein (NADH dehydrogenase superfamily)	914456	CAA	TAA[2]		-
Aspartate kinase II	1444895	CAA	TAA[2]		-
Urease accessory protein	2375137	TCA	TGA[2]		-
Probable oxidoreductase	2413360	GGA	TGA[2]		-
β-toxin gene (*hlb*)[3]					-
Serine protease SplE[4]					-

[1] Role of the mutations in the infectivity of the human or rabbit clones in the skin model. (-): no effect; (+): changes in infectivity.

[2] Stop codon.

[3] Prophage insertion in the human ST121 strains.

[4] Gene located in vSaβ.

Supplementary Table 3. Non-synonymous mutations identified in the rabbit ST121 strains.

Position in ED133	CDS/inter genic	original codon	new codon	original AA	new AA	annotated CDS
11335	CDS	CCA	CTA	P	L	histidine ammonia-lyase
45510	CDS	GCA	ACA	A	T	conserved hypothetical protein
65511	CDS	GAT	GAG	D	E	Na/Pi cotransporter family protein
70555	CDS	GTT	GCT	V	A	L-lactate permease
109775	CDS	ATG	ATA	M	I	5' nucleotidase family protein
118223	CDS	GGT	GAT	G	D	capsular polysaccharide biosynthesis protein CapC
138492	CDS	GAT	GGT	D	G	conserved hypothetical protein
140409	CDS	AGA	AGT	R	S	hypothetical protein
140953	CDS	GTA	GAA	V	E	ABC transporter, permease protein
150450	CDS	CAT	TAT	H	Y	surfactin/siderphore synthesase
165057	CDS	CCT	CTT	P	L	hypothetical protein
166637	CDS	GTA	GCA	V	A	glucokinase regulator-related protein
170974	CDS	CCC	TCC	P	S	type I restriction-modification enzyme, R subunit
178367	CDS	AAG	GAG	K	E	Putative glutathione transporter, permease component
184278	CDS	GAT	AAT	D	N	gamma-glutamyltranspeptidase
199620	CDS	CAG	CGG	Q	R	Two-component sensor histidine kinase family protein
210606	CDS	CTC	TTC	L	F	acetyl-CoA acetyltransferase
213046	CDS	GTA	GGA	V	G	3-hydroxyacyl-CoA dehydrogenase protein
219237	CDS	AAA	AGA	K	R	hypothetical protein
265897	CDS	TCC	TTC	S	F	Choloylglycine hydrolase family protein
283750	CDS	AGT	AAT	S	N	virulence protein EssC
306463	CDS	ACG	GCG	T	A	ABC transporter, ATP-binding protein
370183	CDS	GAT	TAT	D	Y	NADH-dependent flavin oxidoreductase
373801	CDS	GGC	AGC	G	S	hypothetical protein
376156	CDS	TTC	TTA	F	L	transport protein, putative
394015	CDS	GCT	GTT	A	V	hypothetical protein
396787	CDS	GTG	TTG	V	L	conserved hypothetical protein
401320	CDS	CGC	TGC	R	C	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase
408832	CDS	GTA	ATA	V	I	Chromosome partitioning protein ParB
432638	CDS	GCT	GTT	A	V	inosine-5'-monophosphate dehydrogenase
485848	CDS	GCG	GAG	A	E	hypothetical transmembrane protein
497132	CDS	AGC	AAC	S	N	LysM domain protein
503355	CDS	CCT	GCT	P	A	glutamate synthase, large subunit
504891	CDS	CAT	TAT	H	Y	glutamate synthase, large subunit
539424	CDS	GAT	AAT	D	N	UDP-N-acetylglucosamine pyrophosphorylase
572279	CDS	GGA	AGA	G	R	nucleoside permease NupC
586608	CDS	CCA	CTA	P	L	hypothetical protein
586966	CDS	ATG	ATC	M	I	hypothetical protein
592700	CDS	CCA	TCA	P	S	DNA-directed RNA polymerase, beta subunit
599503	CDS	ACA	ATA	T	I	ribosomal L7Ae family protein
609241	CDS	ATT	ACT	I	T	L-ribulokinase, putative
617650	CDS	CGT	CAT	R	H	sdrC protein
635689	CDS	TTC	TTA	F	L	6-phospho-3-hexuloisomerase
650300	CDS	TCA	TTA	S	L	conserved hypothetical protein
654164	CDS	GAA	CAA	E	Q	Diphosphomevalonate decarboxylase
654861	CDS	ATA	ACA	I	T	Diphosphomevalonate decarboxylase
655484	CDS	GCG	ACG	A	T	phosphomevalonate kinase
656295	CDS	GAT	GAG	D	E	conserved hypothetical protein
675435	CDS	GGT	GAT	G	D	hydrolase
678502	CDS	CAT	TAT	H	Y	probable esterase or lipase
689310	CDS	GCA	GTA	A	V	Na+/H+ antiporter
706375	CDS	CGT	TGT	R	C	nucleoside permease NupC, putative
719366	CDS	GAA	aaa	E	K	two-component response regulator

Position in ED133	CDS/inter genic	original codon	new codon	original AA	new AA	annotated CDS
729917	CDS	ACT	ATT	T	I	transcriptional regulator, AraC family
730649	CDS	CTT	CAT	L	H	transcriptional regulator, AraC family
732738	CDS	GCG	GTG	A	V	conserved hypothetical protein
761891	CDS	CCT	ACT	P	T	N-acetylglucosamine-6-phosphate deacetylase
813400	CDS	GTC	GCC	V	A	degV family protein
833512	CDS	CAT	CGT	H	R	thioredoxin reductase
837248	CDS	GCT	GTT	A	V	conserved hypothetical protein
839280	CDS	TGT	CGT	C	R	malate dehydrogenase
847351	CDS	TTG	atg	L	M	phosphoglycerate kinase
849950	CDS	GTC	GCC	V	A	enolase 2-phosphoglycerate dehydratase
850259	CDS	GGT	GCT	G	A	enolase 2-phosphoglycerate dehydratase
851714	CDS	GAT	GGT	D	G	probable membrane protein
867101	CDS	GAT	AAT	D	N	staphylococcal thermonuclease precursor
885877	CDS	TAC	CAC	Y	H	conserved hypothetical protein
903320	CDS	ACA	AAA	T	K	D-alanine lipoteichoic acid and wall teichoic acid esterification protein
903730	CDS	TAT	CAT	Y	H	D-alanine lipoteichoic acid and wall teichoic acid esterification protein
904197	CDS	TAA	TAT	*	Y	D-alanine lipoteichoic acid and wall teichoic acid esterification protein
914437	CDS	GGA	GAA	G	E	conserved hypothetical protein
929999	CDS	TTA	ATA	L	I	argininosuccinate lyase
936781	CDS	GAT	AAT	D	N	ATP-dependent nuclease subunit B
937594	CDS	GAT	AAT	D	N	ATP-dependent nuclease subunit B
943586	CDS	GCT	GTT	A	V	fumarylacetoacetate hydrolase family protein
943909	CDS	CGC	TGC	R	C	fumarylacetoacetate hydrolase family protein
946614	CDS	GCG	GTG	A	V	probable hydrolase
948776	CDS	CCA	CTA	P	L	Lipopolysaccharide modification acyltransferase
951585	CDS	TCA	TTA	S	L	putative ATP-dependent protease protein
952545	CDS	TCT	TTT	S	F	putative ATP-dependent protease protein
964210	CDS	GCA	GTA	A	V	oligopeptide transport system ATP-binding protein
964957	CDS	GTA	Cta	V	L	oligopeptide transport system ATP-binding protein
965060	CDS	AAG	ACG	K	T	oligopeptide transport system ATP-binding protein
966215	CDS	GAT	GCT	D	A	oligopeptide binding protein
968210	CDS	ACA	GCA	T	A	oligopeptide ABC transporter, oligopeptide-binding protein
972027	CDS	GAT	TAT	D	Y	oligopeptide ABC transporter, permease protein
976389	CDS	CAA	CCA	Q	P	probable competence-related protein
981313	CDS	TCA	TTA	S	L	conserved hypothetical protein
1001904	CDS	ATG	GTG	M	V	Serine protease
1016199	CDS	ACA	ATA	T	I	Heme ABC type transporter HtsABC, heme-binding protein
1021920	CDS	GAG	AAG	E	K	probable hydrolase
1036100	CDS	ATT	TTT	I	F	probable exported protein
1063044	CDS	GTG	GGG	V	G	conserved hypothetical protein
1065279	CDS	GTA	ATA	V	I	phosphoenolpyruvate-protein phosphatase
1080147	CDS	TCA	TTA	S	L	Spermidine Putrescine transport ATP-binding protein potA
1092356	CDS	CGT	TGT	R	C	conserved hypothetical protein
1102818	CDS	GAT	AAT	D	N	probable exported protein
1180231	CDS	AGC	AGA	S	R	fibrinogen-binding protein
1183493	CDS	GAC	GGC	D	G	alpha-hemolysin precursor
1207772	CDS	TTA	TCA	L	S	cell division protein
1213204	CDS	GAT	GTT	D	V	hypothetical protein
1231095	CDS	AAA	AAT	K	N	orotate phosphoribosyltransferase
1237125	CDS	GGT	AGT	G	S	primosomal protein
1239905	CDS	ACA	GCA	T	A	hypothetical protein
1244241	CDS	ATA	ACA	I	T	conserved hypothetical protein

Position in ED133	CDS/inter genic	original codon	new codon	original AA	new AA	annotated CDS
1256899	CDS	GCT	ACT	A	T	fatty acid/phospholipid synthesis protein
1261572	CDS	GAT	AAT	D	N	chromosome segregation SMC protein
1271122	CDS	CGT	TGT	R	C	hypothetical protein
1285909	CDS	GAA	GAC	E	D	ATP-dependent protease ATP-binding subunit of heat shock protein
1295264	CDS	GAG	AAG	E	K	prolyl-tRNA synthetase
1300223	CDS	ACA	ATA	T	I	DNA polymerase III, alpha subunit
1302552	CDS	GAT	GAA	D	E	N utilization substance protein A, putative
1310157	CDS	GAT	AAT	D	N	polyribonucleotide nucleotidyltransferase
1317257	CDS	ATT	ATG	I	M	zinc protease
1319722	CDS	GTG	CTG	V	L	acetoacetyl-CoA reductase, putative
1341913	CDS	CCG	TCG	P	S	glycerol kinase
1345777	CDS	GTT	GCT	V	A	tRNA delta(2)-isopentenylpyrophosphate transferase
1349126	CDS	ACG	ATG	T	M	aluminum resistance protein
1373590	CDS	GAT	GAG	D	E	threonine synthase
1395375	CDS	CAT	TAT	H	Y	aconitate hydratase
1416114	CDS	ACT	ATT	T	I	prephenate dehydrogenase
1422196	CDS	CAA	CTA	Q	L	indole-3-glycerol phosphate synthase
1432102	CDS	GAT	AAT	D	N	probable oligopeptide membrane permease
1447050	CDS	CCA	TCA	P	S	dihydrodipicolinate synthase
1450422	CDS	CTA	GTA	L	V	probable alanine racemase
1456935	CDS	CAA	AAA	Q	K	probable toxic ion resistance protein
1462261	CDS	CTC	TTC	L	F	conserved hypothetical protein
1480187	CDS	TTA	ATA	L	I	conserved hypothetical protein
1480834	CDS	CAT	CGT	H	R	conserved hypothetical protein
1482778	CDS	GTA	ATA	V	I	probable membrane protein
1523689	CDS	CCA	TCA	P	S	probable membrane protein
1527206	CDS	AAT	AGT	N	S	conserved hypothetical protein
1544426	CDS	ATT	CTT	I	L	conserved hypothetical protein
1556783	CDS	GAC	TAC	D	Y	30S ribosomal protein S1
1559039	CDS	ATC	AAC	I	N	L-asparaginase
1562624	CDS	CGC	TGC	R	C	cell surface elastin binding protein
1573416	CDS	ATG	ATA	M	I	site-specific recombinase
1584325	CDS	CCT	TCT	P	S	maltose operon repressor
1597515	CDS	TTG	GTG	L	V	Arginine pathway regulatory protein ArgR
1608787	CDS	GGT	GAT	G	D	glycine dehydrogenase subunit 2
1615420	CDS	GAT	TAT	D	Y	Late competence protein, putative
1616237	CDS	AAT	GAT	N	D	probable late competence protein
1624452	CDS	GAT	GTT	D	V	zinc-specific metalloregulator
1637719	CDS	GGT	gcT	G	A	probable recombination protein
1643482	CDS	ATT	TTT	I	F	probable membrane protein
1647581	CDS	GGA	GAA	G	E	probable methyltransferase
1655981	CDS	ATT	ACT	I	T	GTP binding protein protein
1656757	CDS	GCT	GTT	A	V	conserved hypothetical protein
1661261	CDS	ACA	ATA	T	I	conserved hypothetical protein
1682767	CDS	GGC	AGC	G	S	alanyl-tRNA synthetase
1688662	CDS	GAC	AAC	D	N	5-methylaminomethyl-2-thiouridylate-methyltransferase tRNA
1701330	CDS	TTC	CTC	F	L	GTP pyrophosphokinase
1710165	CDS	GGC	TGC	G	C	queuine tRNA-ribosyltransferase
1716935	CDS	GAC	ggc	D	G	probable membrane protein
1725221	CDS	CTT	TTT	L	F	valyl-tRNA synthetase
1731787	CDS	CGT	TGT	R	C	Porphobilinogen deaminase
1737022	CDS	GAC	GAG	D	E	trigger factor prolyl isomerase
1741714	CDS	GTT	GGT	V	G	lysine specific permease
1742444	CDS	GGA	AGA	G	R	lysine specific permease

Position in ED133	CDS/intergenic	original codon	new codon	original AA	new AA	annotated CDS
1781264	CDS	CAT	TAT	H	Y	acetate kinase
1788714	CDS	GAT	TAT	D	Y	conserved hypothetical protein
1803503	CDS	GAT	GGT	D	G	Cell surface receptor IsdH for hemoglobin-haptoglobin complexes
1804318	CDS	AAG	AAT	K	N	Cell surface receptor IsdH for hemoglobin-haptoglobin complexes
1808304	CDS	GGT	AGT	G	S	acetyl-CoA synthetase
1821381	CDS	CAA	CCA	Q	P	SpoIIIE family cell division protein
1821514	CDS	CCT	TCT	P	S	SpoIIIE family cell division protein
1838939	CDS	GAT	GGT	D	G	cell wall surface anchor family protein
1855437	CDS	CCA	CAA	P	Q	riboflavin specific deaminase
1880131	CDS	CCA	TCA	P	S	probable lipoprotein
1908851	CDS	AAT	gat	N	D	leukotoxin D subunit
1920198	CDS	GAT	AAT	D	N	signal transduction protein
1925410	CDS	CAC	TAC	H	Y	probable peptidyl-prolyl cis-isomerase
1929559	CDS	ATC	ACC	I	T	conserved hypothetical protein
1943526	CDS	TTA	TTT	L	F	glutamate ATP-binding ABC transporter
2024806	CDS	ACA	ATA	T	I	two-component response regulator
2039791	CDS	GGC	AGC	G	S	glutamyl-tRNA amidotransferase subunit B
2048130	CDS	CCT	CTT	P	L	DNA ligase
2048649	CDS	GCA	GTA	A	V	DNA ligase
2051736	CDS	TCT	TTT	S	F	ATP-dependent DNA helicase
2059268	CDS	CCA	TCA	P	S	nicotinate phosphoribosyltransferase
2059610	CDS	CGT	TGT	R	C	nicotinate phosphoribosyltransferase
2060995	CDS	CGT	CTT	R	L	probable nitric oxide synthase
2084165	CDS	TTA	ATA	L	I	beta-hemolysin
2086394	CDS	GAA	AAA	E	K	probable leukocidin F subunit
2088466	CDS	GTC	GCC	V	A	probable succinyldiaminopimelate desuccinylase
2090243	CDS	ATA	ATG	I	M	Permease of the drug/metabolite transporter (DMT) superfamily
2110581	CDS	CGT	TGT	R	C	60 kDa chaperonin protein
2121935	CDS	GGT	gct	G	A	sucrose-6-phosphate hydrolase
2134100	CDS	GCA	GTA	A	V	probable glycoprotein endopeptidase
2134380	CDS	ACA	GCA	T	A	probable glycoprotein endopeptidase
2142489	CDS	GTC	ATC	V	I	3-isopropylmalate dehydrogenase
2159939	CDS	GAT	GGT	D	G	alanine racemase 1
2162049	CDS	CAA	GAA	Q	E	probable membrane protein
2164340	CDS	ACC	GCT	T	A	potassium-transporting ATPase C chain
2174923	CDS	GAT	AAT	D	N	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanine ligase
2186457	CDS	CCA	TCA	P	S	hypothetical protein
2215378	CDS	ATT	ACT	I	T	CTP synthase
2245709	CDS	GGC	GAC	G	D	glucosamine-fructose-6-phosphate aminotransferase
2247099	CDS	CAA	AAA	Q	K	glucosamine-fructose-6-phosphate aminotransferase
2249215	CDS	ACA	AAA	T	K	PTS system mannitol-specific IIBC component
2276085	CDS	GGA	GTA	G	V	probable hemolysin
2278165	CDS	TCG	TGG	S	W	probable membrane protein
2282243	CDS	CAT	TAT	H	Y	ferrichrome ABC transporter
2283319	CDS	AAA	GAA	K	E	ferrichrome ABC transporter lipoprotein
2300522	CDS	CGT	TGT	R	C	PTS system, lactose-specific IIA component
2315823	CDS	GCT	GTT	A	V	alpha-acetolactate synthase
2325198	CDS	AAT	GAT	N	D	DNA-directed RNA polymerase alpha chain
2338068	CDS	AAG	ATG	K	M	30S ribosomal protein S10
2346432	CDS	TCC	TTC	S	F	conserved hypothetical protein
2349214	CDS	ATT	GTT	I	V	multidrug efflux transporter
2374530	CDS	GGT	AGT	G	S	urease alpha subunit
2384488	CDS	GCG	ACG	A	T	Na+/H+ antiporter NhaC

Position in ED133	**CDS/inter genic**	**original codon**	**new codon**	**original AA**	**new AA**	**annotated CDS**
2395287	CDS	CCA	TCA	P	S	formate dehydrogenase alpha subunit
2397406	CDS	TAC	TGC	Y	C	probable extragenic supressor protein
2404764	CDS	GAT	AAT	D	N	conserved hypothetical protein
2416509	CDS	GGA	GAA	G	E	imidazolonepropionase
2419255	CDS	GTT	ATT	V	I	LysR family regulatory protein
2424939	CDS	GCG	GTG	A	V	probable epimerase
2429121	CDS	CGT	CAT	R	H	probable membrane protein
2431024	CDS	ACA	CCA	T	P	sodium/glutamate symporter
2442856	CDS	AGA	AAA	R	K	bicyclomycin and teicoplanin resistance protein
2457670	CDS	TAT	GAT	Y	D	hypothetical protein
2468732	CDS	GTA	ATA	V	I	truncated conserved hypothetical protein
2478422	CDS	CCA	GCA	P	A	nitrite extrusion protein
2478884	CDS	AAA	AGA	K	R	conserved hypothetical protein
2482344	CDS	TCT	TGT	S	C	two component sensor histidine kinase
2485258	CDS	CAA	CAC	Q	H	nitrate reductase beta chain
2498449	CDS	GAT	aAT	D	N	probable zinc-binding lipoprotein
2502411	CDS	CAT	CGT	H	R	fmhA protein
2510648	CDS	GTT	GCT	V	A	immunoglobulin G-binding protein
2528037	CDS	ACC	AGC	T	S	probable transporter protein
2540458	CDS	GCA	ACA	A	T	probable 2-dehydropantoate 2-reductase
2544472	CDS	GAT	AAT	D	N	betaine-carnitine-choline ABC transporter
2554534	CDS	GAG	GAT	E	D	ATP-binding ABC transporter
2564514	CDS	GAT	GGT	D	G	oligopeptide transporter putative membrane permease domain protein
2638247	CDS	GTA	GCA	V	A	pyruvate oxidase
2668994	CDS	GGA	GAA	G	E	probable phytoene dehydrogenase
2675690	CDS	GGT	AGT	G	S	probable membrane-embedded regulatory protein
2683784	CDS	CCA	CTA	P	L	probable cobalmin synthesis protein
2687285	CDS	TTC	CTC	F	L	hypothetical protein
2732696	CDS	GGC	GAC	G	D	alkaline phosphatase III precursor
2745714	CDS	GAC	GAA	D	E	zinc metalloproteinase aureolysin
2753259	CDS	CGT	TGT	R	C	mannose-6-phosphate isomerase
2764923	CDS	CAT	TAT	H	Y	conserved hypothetical protein
2776821	CDS	GAA	AAA	E	K	LPXTG cell wall surface anchor family protein
2780361	CDS	CGC	TGC	R	C	LPXTG cell wall surface anchor family protein
2817525	CDS	GTC	GGC	V	G	high-affinity nickel-transport protein
2827683	CDS	GTT	ATT	V	I	glucose-inhibited division protein B

Supplementary Table 4. Mutant *S. aureus* strains analysed in this work.

Strain	Previous name	Description	Reference
J	DV3 (JP3934)	ST121 rabbit strain.	(14)
I	KH119 (JP311)	ST121 rabbit strain.	(14)
DL190	DL190	ST121 rabbit strain.	This work
JP7966	DV602	ST121 rabbit strain.	This work
DL688	DL688	ST121 rabbit strain.	This work
DL645	DL645	ST121 rabbit strain.	This work
A	A4599 (JP7687)	ST121 human strain.	This work
B	ST20070579 (JP7690)	ST121 human strain.	This work
C	HT20020235 (JP7692)	ST121 human strain.	This work
D	HT20030134 (JP7696)	ST121 human strain.	This work
E	HT20050331 (JP7700)	ST121 human strain.	This work
F	HT20070227 (JP7705)	ST121 human strain.	This work
G	ST20101201 (JP7707)	ST121 human strain.	This work
H	E269 (JP3929)	ST121 human strain.	This work
JP8795		J *ess*B+ (*ess*B^h)	This work
JP8779		J *mat*E+ (*mat*E^h)	This work
JP8796		J histidinol+ (histidinol^h)	This work
JP8348		J *rot*+ (*rot*^{h})	This work
JP8974		J lipase+ (lipase^h)	This work
JP8780		J NADH+ (NADH^h)	This work
JP8853		J aspartate+ (aspartate^h)	This work
JP8816		J urease+ (urease^h)	This work
JP8750		J oxidoreductase+ (oxidoreductase^h)	This work
JP8613		J Δ*hlb*	This work
JP9548		J *dlt*B^h	This work
JP8781		J Δ*rot*	This work
JP9982		J Δ*dlt*B	This work
JP11398		J Δ*spl*E	This work
JP11125		I *ess*B+ (*ess*B^h)	This work
JP11126		I *mat*E+ (*mat*E^h)	This work
JP11127		I histidinol+ (histidinol^h)	This work
JP8350		I *rot*+ (*rot*^{h})	This work
JP11128		I lipase+ (lipase^h)	This work
JP11129		I NADH+ (NADH^h)	This work
JP11130		I aspartate+ (aspartate^h)	This work
JP11131		I urease+ (urease^h)	This work
JP11132		I oxidoreductase + (oxidoreductase^h)	This work
JP9014		I Δ*hlb*	This work
JP10035		I *dlt*B^h	This work

Strain	**Previous name**	**Description**	**Reference**
JP11400		I Δ*spl*E	This work
JP11133		F *ess*B- (*ess*B^r)	This work
JP11134		F *mat*E- (*mat*E^r)	This work
JP11135		F histidinol- (histidinol^r)	This work
JP8569		F *rot*- (*rot*^{r})	This work
JP11136		F lipase- (lipase^r)	This work
JP11137		F NADH- (NADH^r)	This work
JP11138		F aspartate- (aspartate^r)	This work
JP11139		F urease- (urease^r)	This work
JP11140		F oxidoreductase - (oxidoreductase^r)	This work
JP10310		F *dlt*B^r	This work
JP8897		F Δ converting-phage (*hlb*+)	This work
JP10770		F DltB T113K	This work
JP10500		F DltB Y260H	This work
JP9692		F DltB *405Y	This work
JP10311		F *dlt*B^r *rot*-	This work
JP11399		JP10770 K113T	This work
JP12370		J *dlt*B rabbit ST96	This work

Supplementary Table 5. pMAD derivative plasmids used in this work.

Plasmid	Description	Reference
pJP1486	Restoration of the *ess*B gene mutation (*ess*B^{h})	This work
pJP1487	Restoration of the *mat*E gene mutation (*mat*E^{h})	This work
pJP1488	Restoration of the histidinol-phosphate aminotransferase gene mutation (histidinol-phosphate aminotransferase^{h})	This work
pJP1478	Restoration of the *rot* mutation (*rot*^{h})	This work
pJP1490	Restoration of the lipase gene mutation (lipase^{h})	This work
pJP1483	Restoration of the NADH dehydrogenase gene mutation (NADH^{h})	This work
pJP1485	Restoration of the aspartate kinase gene mutation (aspartate kinase^{h})	This work
pJP1489	Restoration of the urease gene mutation (urease^{h})	This work
pJP1484	Restoration of the oxidoreductase gene mutation (oxidoreductase^{h})	This work
pJP5486	Mutation of the *ess*B gene (*ess*B^{r})	This work
pJP5487	Mutation of the *mat*E gene (*mat*E^{r})	This work
pJP5488	Mutation of the histidinol-phosphate aminotransferase gene (histidinol-phosphate aminotransferase^{r})	This work
pJP5490	Mutation of the lipase gene (lipase^{r})	This work
pJP5483	Mutation of the NADH dehydrogenase gene (NADH^{r})	This work
pJP5485	Mutation of the aspartate kinase gene (aspartate kinase^{r})	This work
pJP5489	Mutation of the urease gene (urease^{r})	This work
pJP5484	Mutation of the oxidoreductase gene (oxidoreductase^{r})	This work
pJP1482	Deletion of *hlb* (Δ*hlb*)	This work
pJP1492	Introduction of the human *dlt*B sequence in the rabbit clones (DltB^{h}; K113T, H250Y, Y405*)	This work
pJP1480	Introduction of the rabbit *rot* mutation in the human clones (*rot*^{r})	This work
pJP1496	Introduction of the rabbit *dlt*B sequence in the human clones (DltB^{r}; T113K, Y250H, *405Y)	This work
pJP1481	Restoration of human *hlb* mutation (phage deletion)	This work
pJP1497	Generation of DltB T113K	This work
pJP1498	Generation of DltB Y250H	This work
pJP1493	Generation of DltB *405Y	This work
pJP1491	Deletion of *rot*	This work
pJP1495	Deletion of *dlt*B	This work
pJP1494	Generation of DltB Y405*	This work
pJP1499	Deletion of *spl*E	This work
pJP1500	Introduction of the rabbit ST96 *dlt*B sequence in the rabbit ST121 clones	This work

Supplementary Table 6. Oligonucleotides used in this work.

Plasmid	Oligonucleotides	SEQUENCE (5'-3')
pJP1478	Rot-1mB	CGCGGATCCCTTGAAAAATAACCAATTTAGCC
	Rot-2c	GTTCTTTCATCGTCGACAGGACGCTCTTTTGTAAATCCATTC
	Rot-3m	GAATGGATTTACTAAAGAGCGTCCTGTCGACGATGAAAGAAC
	Rot-4cE	CCGGAATTCGATTTAGCTTTGGAAAATACACG
pJP1480	Rot-1mB	CGCGGATCCCTTGAAAAATAACCAATTTAGCC
	Rot-5c	GTTCTTTCATCGTCGACAGGACGCTCTTT GTAAATCCATTC
	Rot-6m	GAATGGATTTAC AAAGAGCGTCCTGTCGACGATGAAAGAAC
	Rot-4cE	CCGGAATTCGATTTAGCTTTGGAAAATACACG
pJP1481	hlb-1mB	CGCGGATCCCAGTATATTTCGCTTGCTTCG
	hlb-4cE	GGAATTCGCCTGTAACTGTGTCTGAAGG
pJP1482	hlb-1mB	CGCGGATCCCAGTATATTTCGCTTGCTTCG
	hlb-2c	TTTCACCATCATTATCACTCC
	hlb-3m	GGAGTGATAATGATGGTGAAAGATCATTACCCAATCAAAGCC
	hlb-4cE	GGAATTCGCCTGTAACTGTGTCTGAAGG
pJP1483	NADH-1mBglII	GAAGATCTAAGCGGATTAACAACAGACCG
	NADH-2c	CGTGAGGCATGGATCCTTTATGACGTTCACGTTGTACAATGG
	NADH-3m	CCATTGTACAACGTGAACGTCATAAAGGATCCATGCCTCACG
	NADH-4cE	GGAATTCGTGAAACAGCATGTTCATTAGG
pJP1484	oxidoreductase-1mB	CGCGGATCCTAAGTTCCTAGGAAGATTGGG
	oxidoreductase-2c	GCTACACAGTTCACTCGAATTCCTTTTGGTCCTAATTC
	oxidoreductase-3m	GAATTAGGACCAAAAGGAATTCGAGTGAACTGTGTAGC
	oxidoreductase-4cS	ACGCGTCGACATCAGTACTTCTACGGGCAGC
pJP1485	Aspartate-1mS	ACGCGTCGACAGATTACTGTCTGCTAACAGC
	Aspartate-2c	CACAAGGTATTTGATTACTAACAGCAAGTGCCACAGCGGTCGTATCGGATCCACCTCTGCC
	Aspartate-3m	GGCAGAGGTGGATCCGATACGACCGCTGTGGCACTTGCTGTTAGTAATCAAATACCTTGTG
	Aspartate-4cE	GGAATTCTTTTTCTACCGCTTGTTGCCC
pJP1486	essB-1mB	CGCGGATCCGCGGACTTAATATTGATGTGC
	essB-2c	CCATCAGCGATTTGATAATCGATGAGTCGATCATTTTCAAC
	essB-3m	GTTGAAAATGATCGACTCATCGATTATCAAATCGCTGATGG
	essB-4cE	GGAATTCGTTGTCATACCGATAGCAACC
pJP1487	MatE-1mS	ACGCGTCGACGTTGTTGTGTTGATTCAACGC
	MatE-2c	GTGAATCCCATTAAGATACTCATTAAAAATGCAGGGATCCCTATTTTAAAG
	MatE-3m	CTTTAAAATAGGGATCCCTGCATTTTTAATGAGTATCTTAATGGGATTCAC
	MatE-4cE	GGAATTCACCATAATCTACGCGACCACC
pJP1488	histidinol-1mB	CGCGGATCCAACATCCAGAAATTAAGAAACCG
	histidinol-2c	CTGCTCTAGAAATCATTAATATAAC
	histidinol-3m	GTTATATTAATGATTTCTAGAGCAG
	histidinol-4cE	GGAATTCAATTGTAATTCTAACACCAGTTGG
pJP1489	urease-1mB	CGCGGATCCGTTCCGATTCACAGGCAATGG
	urease-2c	GCTTTTGTTTTTCTGAATTCGACAAATTGGCAATATTGCC
	urease-3m	GGCAATATTGCCAATTTGTCGAATTCAGAAAAACAAAAGC
	urease-4cS	ACGCGTCGACGATACCAAGCAATCCATGGGC
pJP1490	lipase-1mS	ACGCGTCGACGTTGTTGTGTTGATTCAACGC
	lipase-2c	CGTTGTCGATTGGGATCCATTACGTTCAGCATGACGGGTATTTTGAACCTGATCATTTTGG
	lipase-3m	CCAAAATGATCAGGTTCAAAATACCCGTCATGCTGAACGTAATGGATCCCAATCGACAACG
	lipase-4cE	GGAATTCACCATAATCTACGCGACCACC

Plasmid	Oligonucleotides	SEQUENCE (5’-3’)
pJP1491	Rot-12mB	CGCGGATCCACGATGGCTCATATTCATGAC
	Rot-13c	AACAAACATCCCAACAATCCC
	Rot-14m	GATTGTTGGGATGTTTGTT ATTGCTGTGTAAGTTTAATAGC
	Rot-15cE	GGAATTCGAAATTCTTATCAAGGCTTGCG
pJP1492	Lipoteichoic-1mB	CGCGGATCCGGCTACAGAATGGAATTAGAAG
	Lipoteichoic-2c	CTTTGTAACACTTTCACTAGTGCTAATGGCAATATTG
	Lipoteichoic-3m	CAATATTGCCATTAGCACTAGTGAAAGTGTTACAAAG
	Lipoteichoic-6c	CTCCTTTATTATATAAGCTTACCTGAGAAGATTAAAAAGC
	Lipoteichoic-5m	GCTTTTTAATCTTCTCAGGTAAGCTTATATAATAAAGGAG
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC
pJP1493	lipoteichoic-11mB	CGCGGATCCAATTCAATTTATTTCATTCTTCCC
	lipoteichoic-13c	CTCCTTTAATATATAAGCTTACCTGAGAAGATTAAAAAGC
	lipoteichoic-12m	GCTTTTTAATCTTCTCAGGTAAGCTTATATATTAAAGGAG
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC
pJP1494	lipoteichoic-11mB	CGCGGATCCAATTCAATTTATTTCATTCTTCCC
	Lipoteichoic-6c	CTCCTTTATTATATAAGCTTACCTGAGAAGATTAAAAAGC
	Lipoteichoic-5m	GCTTTTTAATCTTCTCAGGTAAGCTTATATAATAAAGGAG
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC
pJP1495	DltB-1mS	ACGCGTCGACCGCTTAATGAAGAACAGTATGG
	DltB-2c	CTGAGAAGATTAAAAAGCCAACCGTTAATTACCTCTGCAATTT
	DltB-3m	TTGGCTTTTTAATCTTCTCAGG
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC
pJP1496	Lipoteichoic-1mB	CGCGGATCCGGCTACAGAATGGAATTAGAAG
	lipoteichoic-22c	CCTAACCATTTACTTTGTAACACTTTCACTAGTGCTAATGGCAATATTG
	lipoteichoic-21m	CAATATTGCCATTAGCACTAGTGAAAGTGTTACAAAGTAAATGGTTAGG
	lipoteichoic-13c	CTCCTTTAATATATAAGCTTACCTGAGAAGATTAAAAAGC
	lipoteichoic-12m	GCTTTTTAATCTTCTCAGGTAAGCTTATATATTAAAGGAG
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC
pJP1497	Lipoteichoic-1mB	CGCGGATCCGGCTACAGAATGGAATTAGAAG
	lipoteichoic-22c	CCTAACCATTTACTTTGTAACACTTTCACTAGTGCTAATGGCAATATTG
	lipoteichoic-21m	CAATATTGCCATTAGCACTAGTGAAAGTGTTACAAAGTAAATGGTTAGG
	lipoteichoic-20cE	CCGGAATTCTCGATACCATGCCAAATTCCC
pJP1498	lipoteichoic-16mB	CGCGGATCCAACGGATGATTCCATATGGTG
	lipoteichoic-18c	GTCAAAGAATAAATGTAAGCTGTATGCGTACATATATAACCACAAATTGACAAAGCCATGGAAGTCTAATTGTAA
	lipoteichoic-17m	TTACAATTAGACTTCCATGGCTTTGTCAATTTGTGGTTATATATGTACGCATACAGCTTACATTTATTCTTTGAC
	lipoteichoic-19cE	CCGGAATTCCTTCAAAAATTTCTACGTCTGG
pJP1499	SplE-1mB	CGCGGATCCAGCATCATGAATAAACAGAGG
	SplE-2c	ATGTGCAATGATATGTGCGCC
	SplE-3m	GCGCACATATCATTGCACATTGTTCACTTTGGTGGTAACGG
	SplE-4cE	CCGGAATTCAGGATTGGGTGAATGTCTAAG
pJP1500	Lipoteichoic-1mB	CGCGGATCCGGCTACAGAATGGAATTAGAAG
	Lipoteichoic-2c	CTTTGTAACACTTTCACTAGTGCTAATGGCAATATTG
	Lipoteichoic-3m	CAATATTGCCATTAGCACTAGTGAAAGTGTTACAAAG
	Lipoteichoic-23m	GCTTTTTAATCTTCTCAGGT**C**GACTTATACAATAAAGGAG
	Lipoteichoic-24c	CTCCTTTATTGTATAAGTC**G**ACCTGAGAAGATTAAAAAGC
	Lipoteichoic-4cE	CCGGAATTCGAAACTGTAATAAACGTTGTGC

Sequences recognized by the restriction enzymes used in cloning are underlined.