

Supplementary Table 2: List of SNPs.

CHR	POS	B1	B2	B3	B4	B5	B6	B7	B8	B9	D1	D2	D3	D4	D5	D6	EFFECT	GENE	PRODUCT
NODE_1	44621	C	C	C	C	T	T	C	C	C	C	T	T	C	T	T	missense_variant c.482G>A p.Gly161Asp	rpIF	50S ribosomal protein L6
NODE_1	182969	C	C	C	C	C	C	T	T	T	T	C	C	T	C	C	missense_variant c.724C>T p.Pro242Ser		hypothetical protein
NODE_1	183464	T	T	G	G	T	T	T	T	T	T	T	T	T	T	T	missense_variant c.1219T>G p.Phe407Val		hypothetical protein
NODE_1	188200	C	C	C	C	C	C	C	C	T	T	C	C	C	C	C	missense_variant c.110C>T p.Thr37Ile	sarZ	HTH-type transcriptional regulator SarZ
NODE_1	457917	T	T	T	T	T	T	T	T	T	T	C	C	T	C	C			
NODE_1	458671	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	synonymous_variant c.258A>G p.Gln86Gln	arcR	HTH-type transcriptional regulator ArcR
NODE_1	525887	T	T	T	T	T	T	T	T	T	T	T	T	A	T	T	synonymous_variant c.60A>T p.Thr20Thr	ykoD_1	Putative HMP/thiamine import ATP-binding protein YkoD
NODE_1	561236	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	synonymous_variant c.660T>C p.Thr220Thr	gyrA	DNA gyrase subunit A
NODE_1	562432	C	C	C	C	T	T	C	C	C	C	T	T	C	T	T	missense_variant c.1856C>T p.Thr619Ile	gyrA	DNA gyrase subunit A

NODE_1	626418	G	G	G	G	G	G	A	A	A	A	G	G	A	G	G	stop_gained c.448C>T p.Gln150*	spa	Immunoglobulin G-binding protein A
NODE_1	628320	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T			
NODE_1	752886	G	G	A	A	G	G	G	G	G	G	G	G	G	G	G	stop_gained c.684G>A p.Trp228*	uhpT	Hexose-6-phosphate:phosphate antiporter
NODE_1	753275	G	G	G	G	T	T	G	G	G	G	T	T	G	T	T	missense_variant c.1073G>T p.Gly358Val	uhpT	Hexose-6-phosphate:phosphate antiporter
NODE_1	755422	A	A	A	A	A	A	T	T	T	T	A	A	T	A	A	stop_gained c.827T>A p.Leu276*		putative sensor-like histidine kinase
NODE_1	887607	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	missense_variant c.478T>C p.Trp160Arg	glpT	Glycerol-3-phosphate transporter
NODE_1	887624	C	C	C	C	T	T	C	C	C	C	T	T	C	T	T	missense_variant c.461G>A p.Gly154Glu	glpT	Glycerol-3-phosphate transporter
NODE_1	960289	A	A	A	A	A	A	A	A	A	A	A	A	A	A	C	synonymous_variant c.216A>C p.Thr72Thr	ssl1	Staphylococcal superantigen-like 1
NODE_1	971750	T	T	T	T	T	T	T	T	T	T	T	T	C	T	T			
NODE_1 1	11467	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	missense_variant c.751G>A p.Val251Met		hypothetical protein
NODE_1 1	16959	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	synonymous_variant c.231A>G p.Ala77Ala	sepA	Multidrug resistance efflux pump SepA
NODE_2	79686	A	A	A	A	A	A	T	T	T	T	A	A	T	A	A			

Supplementary Material

NODE_2	93673	C	C	T	T	C	C	C	C	C	C	C	C	C	C	C	missense_variant c.85C>T p.His29Tyr	cspA_1	Cold shock protein CspA
NODE_2	93766	G	G	G	G	A	A	A	A	A	A	A	A	A	A	A	missense_variant c.178G>A p.Ala60Thr	cspA_1	Cold shock protein CspA
NODE_2	146090	C	C	T	T	C	C	C	C	C	C	C	C	C	C	C	missense_variant c.1411G>A p.Glu471Lys	parE	DNA topoisomerase 4 subunit B
NODE_2	265051	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	missense_variant c.188G>A p.Gly63Asp	topA	DNA topoisomerase 1
NODE_2	408124	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	stop_gained c.994C>T p.Gln332*	pycA	Pyruvate carboxylase
NODE_2	411085	G	C	G	G	G	G	G	G	G	G	G	G	G	G	G			
NODE_2	418613	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G			
NODE_2	515535	G	G	G	G	G	G	T	T	T	T	G	G	G	G	G			
NODE_2	515569	C	C	C	C	C	C	T	T	T	T	C	C	T	C	C			
NODE_2	525857	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	missense_variant c.491C>T p.Ser164Phe		hypothetical protein
NODE_2	530801	T	T	T	T	T	T	C	C	C	C	T	T	C	T	T	missense_variant c.280A>G p.Ile94Val	spxA	Regulatory protein Spx
NODE_2	543962	A	A	G	G	A	A	A	A	A	A	A	A	A	A	A			
NODE_2	643649	A	T	A	A	A	A	A	A	A	A	A	A	A	A	A	stop_gained c.1182T>A p.Tyr394*	clfA	Clumping factor A

NODE_2	801375	G	G	G	G	A	A	G	G	G	G	A	A	G	A	A			
NODE_2	805464	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T			
NODE_2	846956	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	missense_variant c.149A>G p.Lys50Arg		hypothetical protein
NODE_2	907981	G	G	A	A	G	G	G	G	G	G	G	G	G	G	G	missense_variant c.1739C>T p.Ala580Val	fusA	Elongation factor G
NODE_2	917151	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	missense_variant c.1441T>C p.Tyr481His	rpoB	DNA-directed RNA polymerase subunit beta
NODE_2	917179	G	G	G	G	C	C	C	C	C	C	C	C	C	C	C	missense_variant c.1413C>G p.Asp471Glu	rpoB	DNA-directed RNA polymerase subunit beta
NODE_2	917202	A	A	G	G	A	A	A	A	A	A	A	A	A	A	A	missense_variant c.1390T>C p.Ser464Pro	rpoB	DNA-directed RNA polymerase subunit beta
NODE_2	942440	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C			
NODE_2	942452	A	A	A	A	A	A	A	A	A	A	A	G	A	A	A			
NODE_2	942485	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T			
NODE_3	38470	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	synonymous_variant c.516T>C p.Arg172Arg	rlhA	23S rRNA 5- hydroxycytidine synthase
NODE_3	134055	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C	stop_gained c.706C>T p.Gln236*	malL	Oligo-1,6-glucosidase

Supplementary Material

NODE_3	167055	T	T	T	T	A	A	T	T	T	T	A	A	T	A	A	missense_variant c.264T>A p.Phe88Leu	der_2	GTPase Der
NODE_4	153708	A	A	A	A	A	A	A	A	A	G	A	A	A	A	A	synonymous_variant c.969A>G p.Val323Val	pepS	Aminopeptidase PepS
NODE_6	18020	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	missense_variant c.361T>C p.Tyr121His		IS1182 family transposase ISSau3
NODE_6	46531	G	G	G	G	G	G	T	T	G	G	G	G	G	G	G	missense_variant c.409G>T p.Val137Phe		hypothetical protein
NODE_9	42869	T	T	T	T	T	T	C	C	C	C	T	T	C	T	T			

Abbr.: For numeration of isolates, see Supplementary Figure 1.

Supplementary Table 3: Accessory genome.

Gene	Annotation	No. of isolates	B 1	B 2	B 3	B 4	B 5	B 6	B 7	B 8	B 9	D 1	D 2	D 3	D 4	D 5	D 6
<i>aceF</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>alsT_1</i>	Amino-acid carrier protein AlsT	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>clfA_1</i>	Clumping factor A	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>clpP_2</i>	ATP-dependent Clp protease proteolytic subunit	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>codY</i>	GTP-sensing transcriptional pleiotropic repressor CodY	14	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
<i>dltD_2</i>	Protein DltD	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>est_2</i>	Carboxylesterase	2	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
<i>glpT_2</i>	Glycerol-3-phosphate transporter	5	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_1</i>	IS1182 family transposase ISSau3	8	0	1	0	0	1	1	1	0	0	0	1	1	1	1	0
<i>group_10</i> <i>0</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0

<i>group_10</i> <i>1</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>2</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>3</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>4</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>5</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>6</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>8</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_10</i> <i>9</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> <i>0</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> <i>1</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> <i>2</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> <i>3</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0

<i>group_11</i> 4	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> 5	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> 6	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> 7	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> 8	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_11</i> 9	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 0	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 1	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 2	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 3	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 5	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 6	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 7	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0

<i>group_12</i> 8	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_12</i> 9	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 0	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 1	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 2	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 3	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 4	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 5	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 6	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 7	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 8	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_13</i> 9	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0

<i>group_14</i> <i>0</i>	hypothetical protein	6	1	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_14</i> <i>1</i>	hypothetical protein	6	1	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_14</i> <i>3</i>	putative autolysin PH	6	1	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_14</i> <i>5</i>	hypothetical protein	14	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
<i>group_14</i> <i>6</i>	IS200/IS605 family transposase ISSep3	5	1	1	0	1	1	0	0	0	0	0	0	0	0	0	1	0
<i>group_14</i> <i>7</i>	hypothetical protein	8	0	1	0	1	1	1	1	1	0	1	0	0	0	1	0	0
<i>group_14</i> <i>8</i>	hypothetical protein	7	0	1	1	1	1	1	0	1	0	0	0	0	0	0	1	0
<i>group_14</i> <i>9</i>	hypothetical protein	9	0	1	0	1	1	1	1	0	0	0	1	1	1	1	1	0
<i>group_15</i> <i>0</i>	hypothetical protein	6	1	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_15</i> <i>1</i>	hypothetical protein	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>group_17</i>	hypothetical protein	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>group_2</i>	IS1182 family transposase ISSau3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>group_21</i>	hypothetical protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

<i>group_22</i>	putative sensor-like histidine kinase	12	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1
<i>group_23</i>	putative sensor-like histidine kinase	8	0	1	1	1	0	0	1	1	1	1	0	0	1	0	0
<i>group_25</i> <i>56</i>	hypothetical protein	14	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>group_25</i> <i>57</i>	hypothetical protein	3	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1
<i>group_3</i>	IS1182 family transposase ISSau3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>group_4</i>	IS1182 family transposase ISSau3	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
<i>group_5</i>	IS1182 family transposase ISSau3	9	0	1	0	1	1	1	1	0	0	0	1	1	1	1	0
<i>group_55</i>	hypothetical protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>group_58</i>	NAD-dependent malic enzyme	7	1	0	0	0	1	1	0	0	0	0	1	1	0	1	1
<i>group_59</i>	NAD-dependent malic enzyme	14	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>group_6</i>	IS1182 family transposase ISSau3	9	0	1	0	1	1	1	1	0	0	0	1	1	1	1	0
<i>group_7</i>	IS1182 family transposase ISSau3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

<i>group_8</i>	IS1182 family transposase ISSau3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>group_83</i>	hypothetical protein	14	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>group_84</i>	hypothetical protein	14	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>group_85</i>	hypothetical protein	14	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>group_87</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_88</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_89</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_9</i>	IS1182 family transposase ISSau3	6	0	0	1	0	0	1	0	0	1	1	0	0	0	1	1
<i>group_90</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_91</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_93</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_94</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_95</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0

<i>group_96</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_97</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_98</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>group_99</i>	hypothetical protein	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>hlb_1</i>	Phospholipase C	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>hpf_2</i>	Ribosome hibernation promotion factor	4	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0
<i>hutH_1</i>	Histidine ammonia-lyase	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>lexA_2</i>	LexA repressor	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>malL</i>	Oligo-1,6-glucosidase	14	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1
<i>malL_2</i>	Oligo-1,6-glucosidase	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
<i>malR</i>	HTH-type transcriptional regulator MalR	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
<i>malR</i>	HTH-type transcriptional regulator MalR	14	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1

<i>mntA_2</i>	Manganese-binding lipoprotein MntA	5	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>mprF</i>	Phosphatidylglycerol lysyltransferase	14	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
<i>mprF_2</i>	Phosphatidylglycerol lysyltransferase	6	0	0	0	0	0	0	1	1	1	1	0	0	1	0	1
<i>prkC_2</i>	Serine/threonine-protein kinase PrkC	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>pycA_1</i>	Pyruvate carboxylase	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>rsmH_1</i>	Ribosomal RNA small subunit methyltransferase H	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
<i>sak</i>	Staphylokinase	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>scn_3</i>	Staphylococcal complement inhibitor	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>spa_2</i>	Immunoglobulin G-binding protein A	5	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>ssbA_2</i>	Single-stranded DNA-binding protein A	6	1	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>thiI_1</i>	putative tRNA sulfurtransferase	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>uhpT</i>	Hexose-6-phosphate:phosphate antiporter	10	1	1	1	1	1	1	0	0	0	0	1	1	0	1	1
<i>uhpT</i>	Hexose-6-phosphate:phosphate antiporter	8	0	1	1	1	0	0	1	1	1	1	0	0	1	0	0

<i>xerC_3</i>	Tyrosine recombinase XerC	6	1	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0
<i>yic_3</i>	Putative metal chaperone YciC	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0

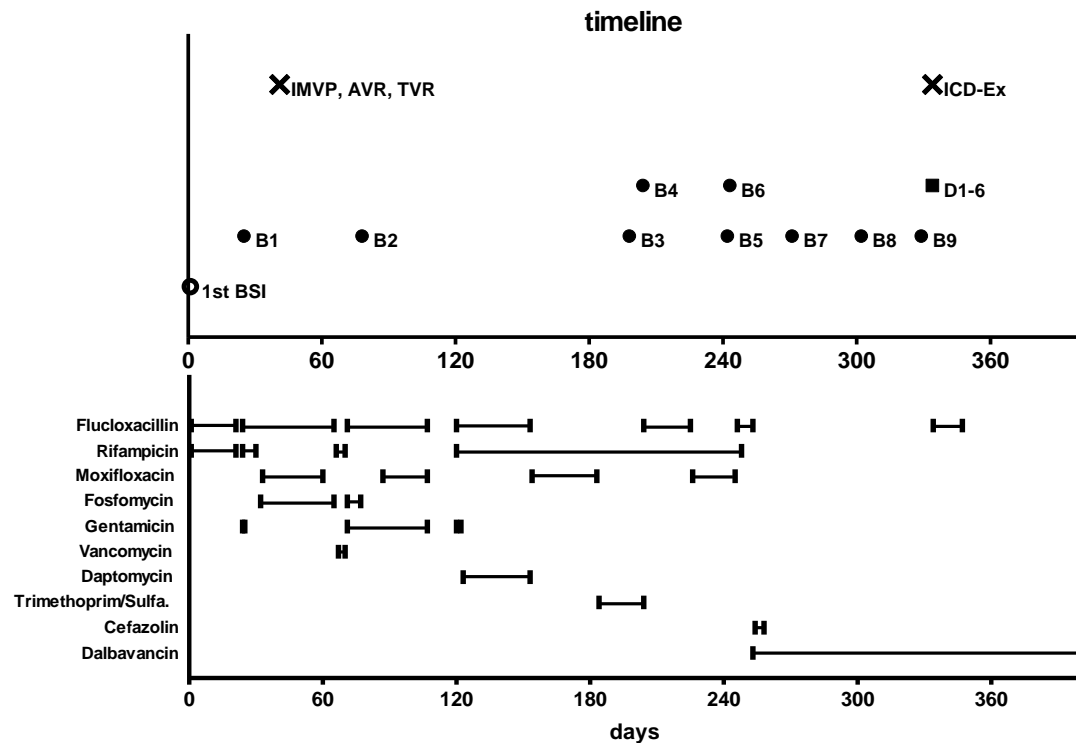
Abbr.: For numeration of isolates, see Supplementary Figure 1. Absence of the respective gene is presented as 0, presence as 1.

Supplementary Table 4: Phenotypic AMR.

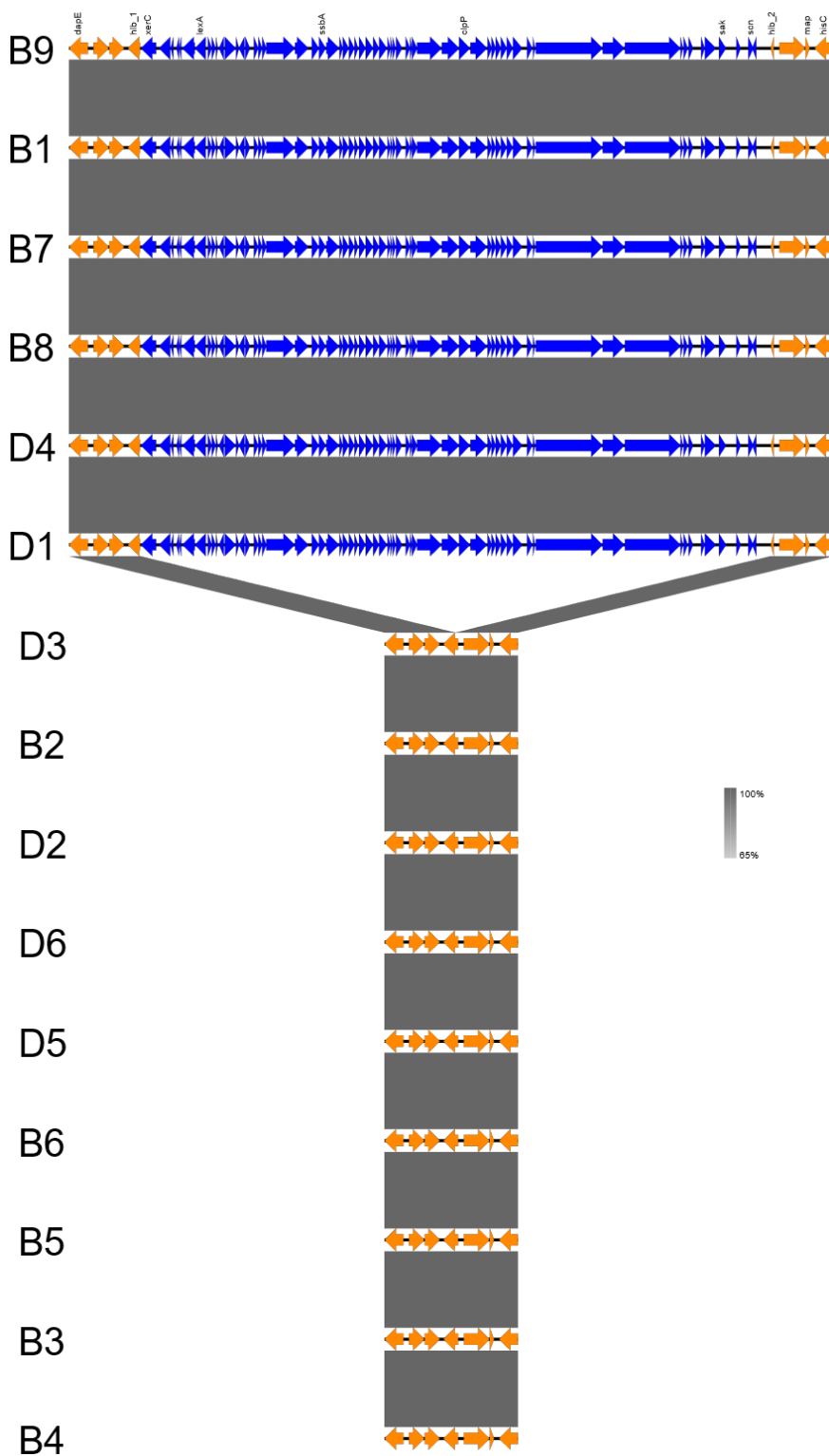
	IEC ⁺												IEC ⁻																	
	B1		B7		B8		B9		D1		D4		B2		B3		B4		B5		B6		D2		D3		D5		D6	
	MIC	Int	MIC	Int	MIC	In.	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int	MIC	Int
OXA	≤0.25	S	≤0.25	S	0,5	S	1	S	0,5	S	≤0.25	S	≤0.25	S	0,5	S	0,5	S	1*	S	1*	S	0,5	S	16*	R	12*	R	1	S
PEN	≤0.03	S	≤0.03	S	≤0.03	S	0,12	S	≤0.03	S	≤0.03	S	≤0.03	S	0,12	S	0,12	S	0,06	S	0,12	S	≤0.03	S	0,25	S	0,25	S	0,12	S
LVX	≤0.12	S	0,25	S	0,5	S	0,5	S	0,25	S	0,5	S	0,5	S	1	S	1	S	0,25	S	1	S	0,5	S	0,25	S	0,25	S	0,25	S
SXT	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S	≤10	S
GEN	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S
CLI	0,25	S	0,25	S	0,25	S	0,25	S	0,25	S	0,25	S	0,25	S	0,25	S	≤0.12	S	≤0.12	S	≤0.12	S	0,25	S	≤0.12	S	≤0.12	S	0,25	S
ERY	1	S	0,5	S	0,5	S	0,5	S	≤0.25	S	≤0.25	S	1	S	0,5	S	1	S	0,5	S	≤0.25	S	≤0.25	S	0,5	S	0,5	S	0,5	S
VAN	1	S	≤0.5	S	1	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S
TEC	2	S	≤0.5	S	1	S	≤0.5	S	≤0.5	S	1	S	≤0.5	S	2	S	≤0.5	S	≤0.5	S	≤0.5	S	1	S	≤0.5	S	≤0.5	S	≤0.5	S
RIF	>32*	R	0,064*	S	0,064*	S	0,064*	S	0,125*	S	0,094*	S	0,012*	S	16*	R	6*	R	0,125*	S	0,25*	S	0,094*	S	0,19*	S	0,19*	S	0,19*	S
LZD	2	S	4	S	4	S	2	S	4	S	2	S	2	S	2	S	1	S	4	S	4	S	4	S	4	S	4	S	4	S
TET	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S	2	S	≤1	S	≤1	S	≤1	S	≤1	S	≤1	S
TGC	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S
FOF	≤8	S	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R	≥128	R
FA	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S	≤0.5	S
DAP	0,25	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	≤0.12	S	1	S	1	S	0,5	S	≤0.12	S	≤0.12	S	0,5	S	0,5	S	0,5	S	0,5	S

Abbr.: OXA oxacillin, PEN penicillin, LVX levofloxacin, SXT trimethoprim-sulfamethoxazole, GEN gentamicin, CLI clindamycin, ERY erythromycin, VAN vancomycin, TEC teicoplanin, RIF rifampicin, LZD linezolid, TET tetracycline, TGC tigecycline, FOF Fosfomycin, FA fusidic acid, DAP daptomycin, IEC immune evasion cluster, MIC minimal inhibitory concentration, Int interpretation. For enumeration of isolates, please see Supplementary Figure 1. *MIC determined by MIC test strip.

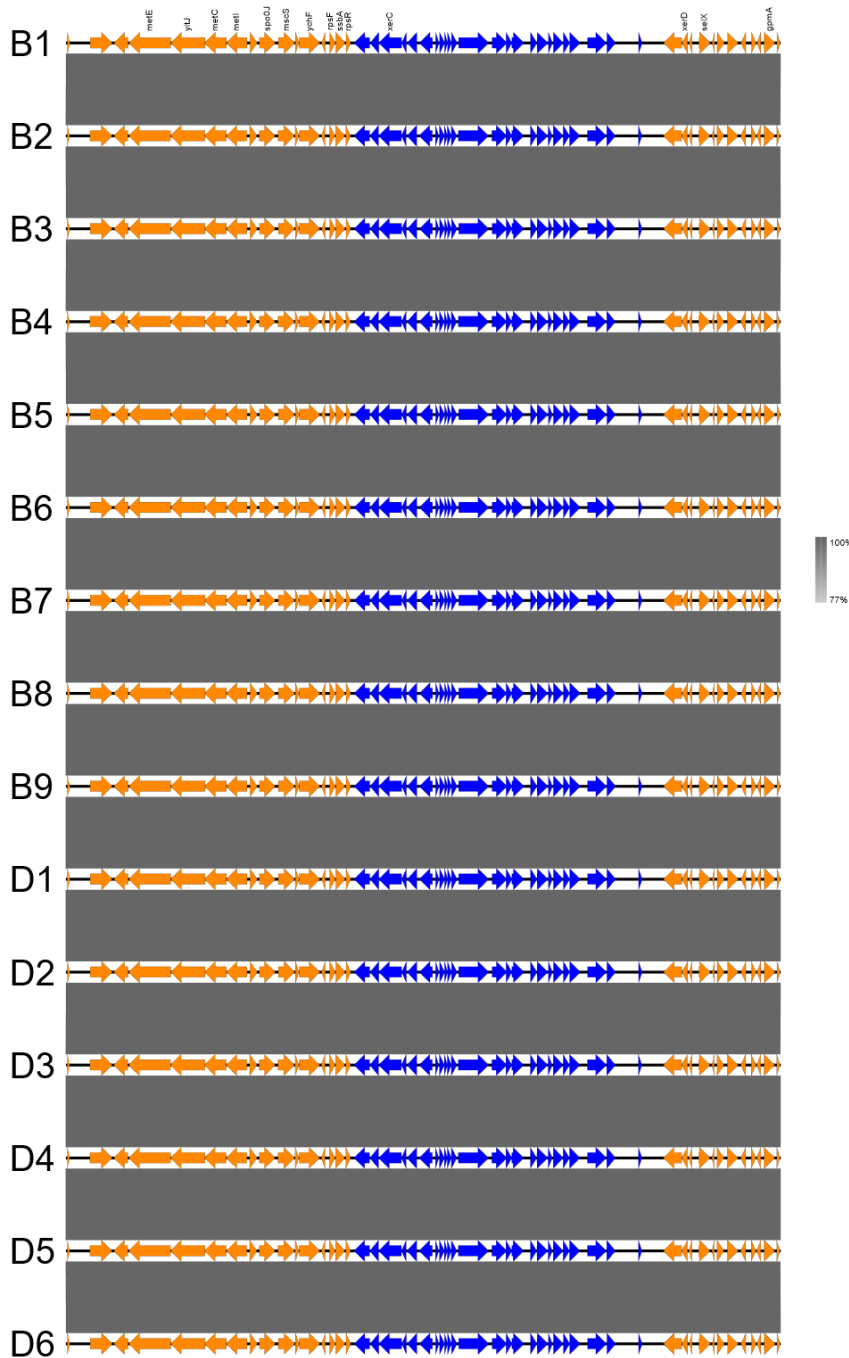
3 Supplementary Figures



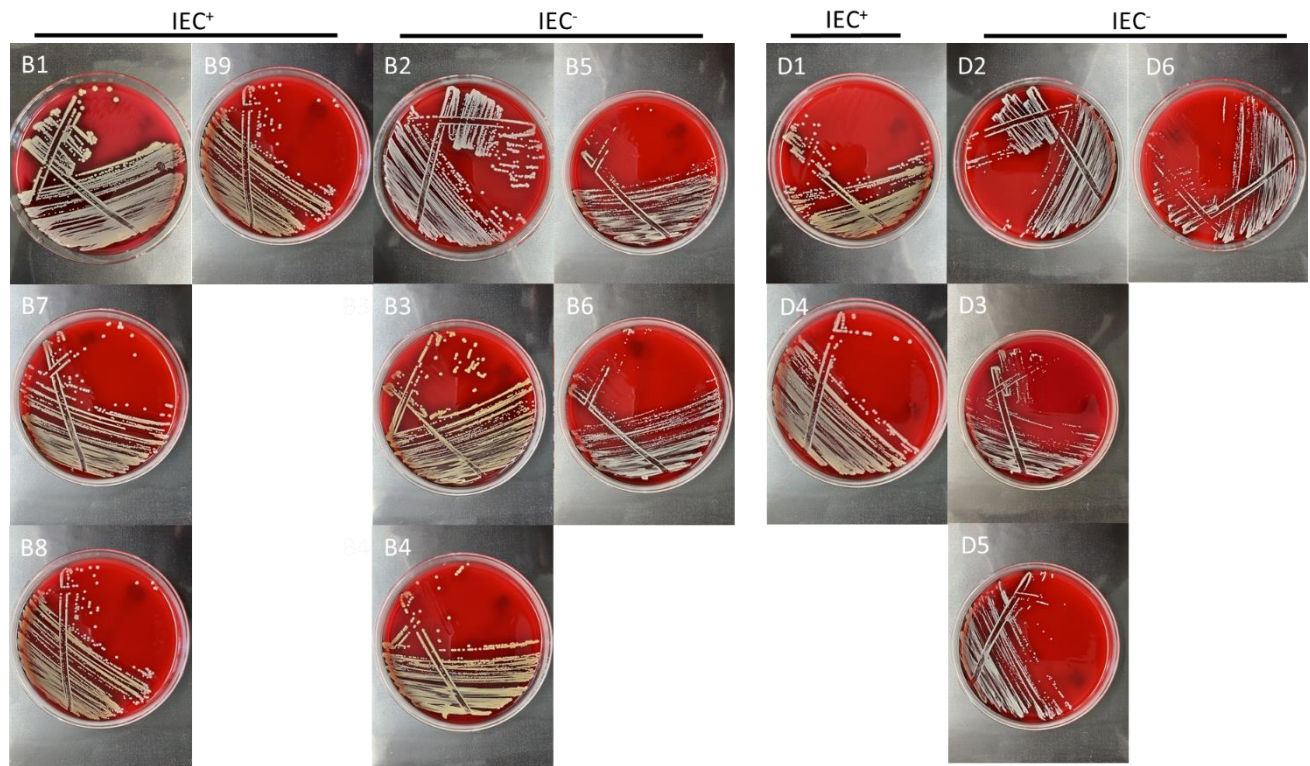
Supplementary Figure 1. Timeline of events and antibiotic therapy. Upper panel: Timeline of events. Day 0 is defined as the day of the first BSI episode (1st BSI). The *S. aureus* isolate of the first BSI was not available for analyses. B1-B9: Blood culture isolates of following BSI episodes. D1-D6: *S. aureus* isolates from the Device (implantable cardioverter-defibrillator, ICD). Abbr.: IMVP: Inspection of mitral valve prosthesis; AVR: Aortic valve replacement; TVR: Tricuspidal valve replacement; ICD-Ex: ICD explantation. There were no episodes of BSI after explantation of the ICD. Lower panel: Overview over antimicrobial therapy. The timespan an antibiotic was given is visible as black line. Dosages: Flucloxacillin 2 g every 4 h or 3 g every 6 h; rifampicin 450 mg every 12 h or 600 mg every 24h; moxifloxacin 400 mg every 24 h; fosfomycin 4 g or 5 g every 24 h adjusted to current renal function; gentamicin 240 mg, 200 mg, 160 mg or 80 mg every 2 h according to drug monitoring results; vancomycin 1000mg on the first day, then 500mg according to drug monitoring results; daptomycin 500 mg or 700 mg every 24 h; trimethoprim/sulfamethoxazole 960 mg every 12h; cefazolin 2 g every 8 h; dalbavancin 1500 mg every 7 days.



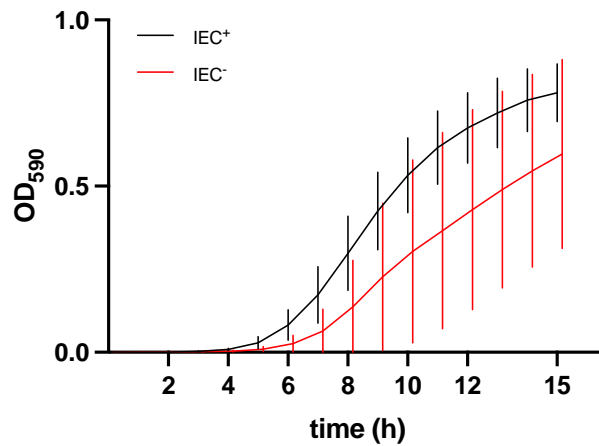
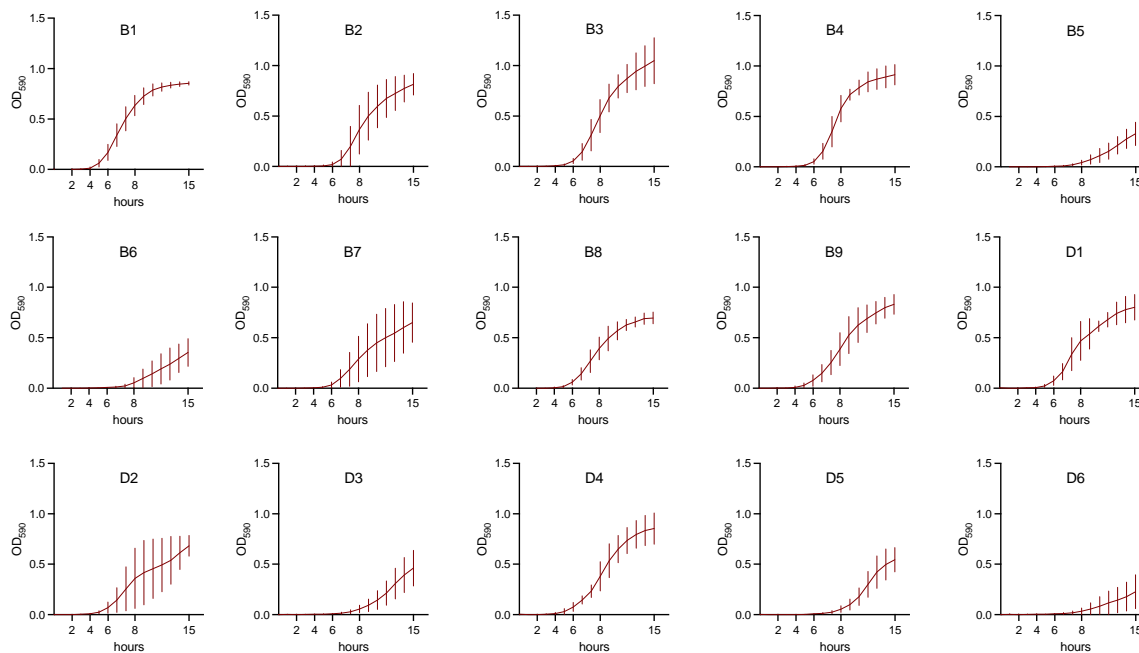
Supplementary Figure 2. Genetic context of the prophage inserted in the *hlb* gene. Abbr.: *dapE* probable succinyl-diaminopimelate desuccinylase; *hlb* hemolysin b; *xerC* tyrosine recombinase; *lexA* LexA repressor; *ssbA* *Staphylococcus aureus* single-stranded DNA-binding protein; *clpP* ATP-dependent Clp protease proteolytic subunit; *sak* staphylokinase; *scn* staphylococcal complement inhibitor; *map* Major histocompatibility complex class II analogue protein; *hisC* Histidinol-phosphate aminotransferase.



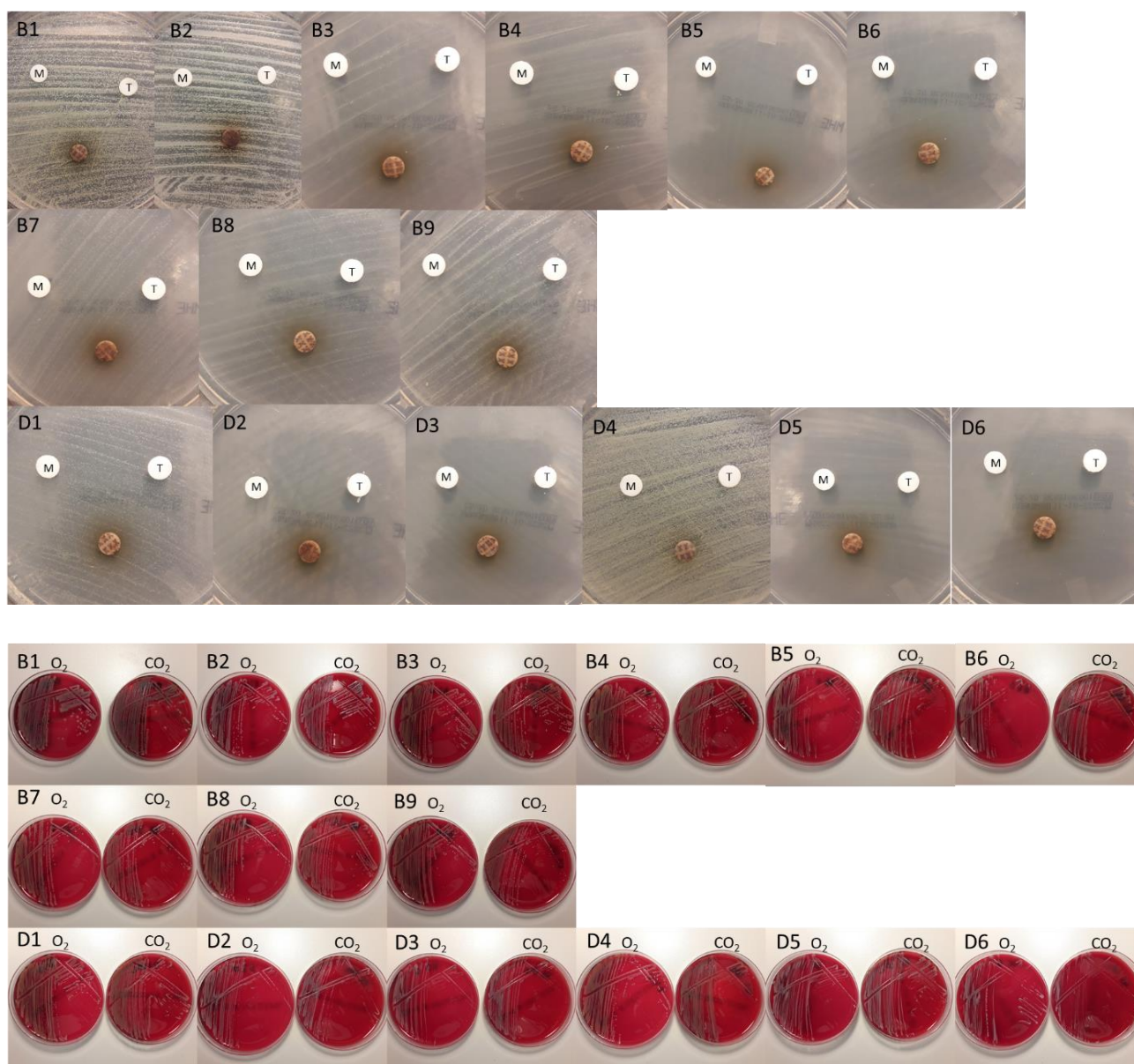
Supplementary Figure 3. Genetic context of the second mobile genetic element inserted after the gene *ychF*. Abbr.: *metE* 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase; *yitJ* 5,10-methylenetetrahydrofolate reductase; *metC* aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme; *metI* Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme; *spoOJ* SpoOJ protein; *mscS* mechanosensitive ion channel family protein; *ychF* ribosome-binding ATPase YchF; *rpsF* 30S ribosomal protein S6; *ssbA* single-stranded DNA-binding protein; *rpsR* 30S ribosomal protein S18; *xerC* Tyrosine recombinase XerC; *xerD* Tyrosine recombinase XerD; *selX* Enterotoxin-like toxin X; *gpmA* 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase.



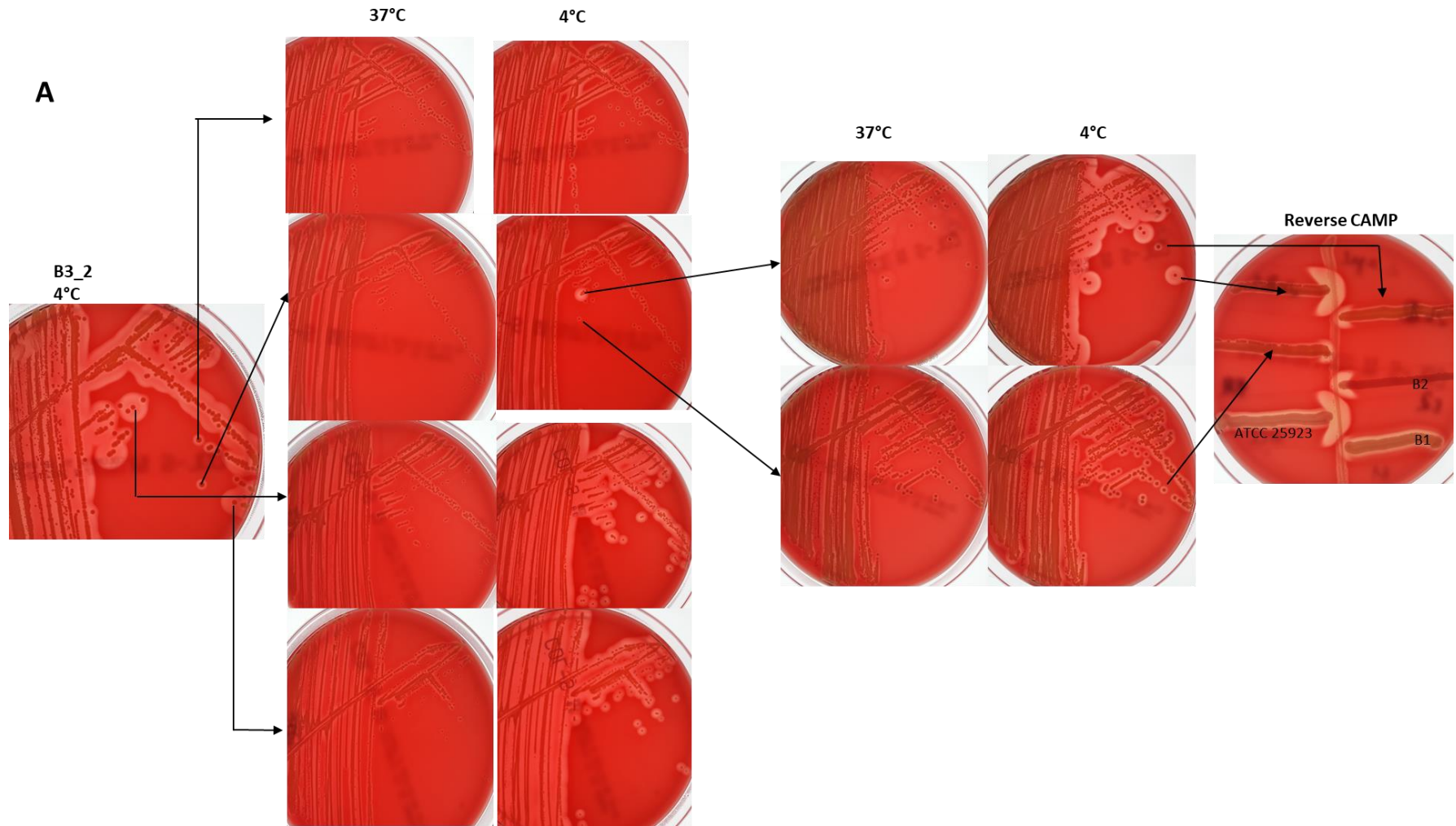
Supplementary Figure 4. Macromorphology of *S. aureus* isolates on Columbia blood agar. Morphology of isolates on Columbia blood agar following 24h cultivation. For numbering of isolates, see Supplementary Figure 1.

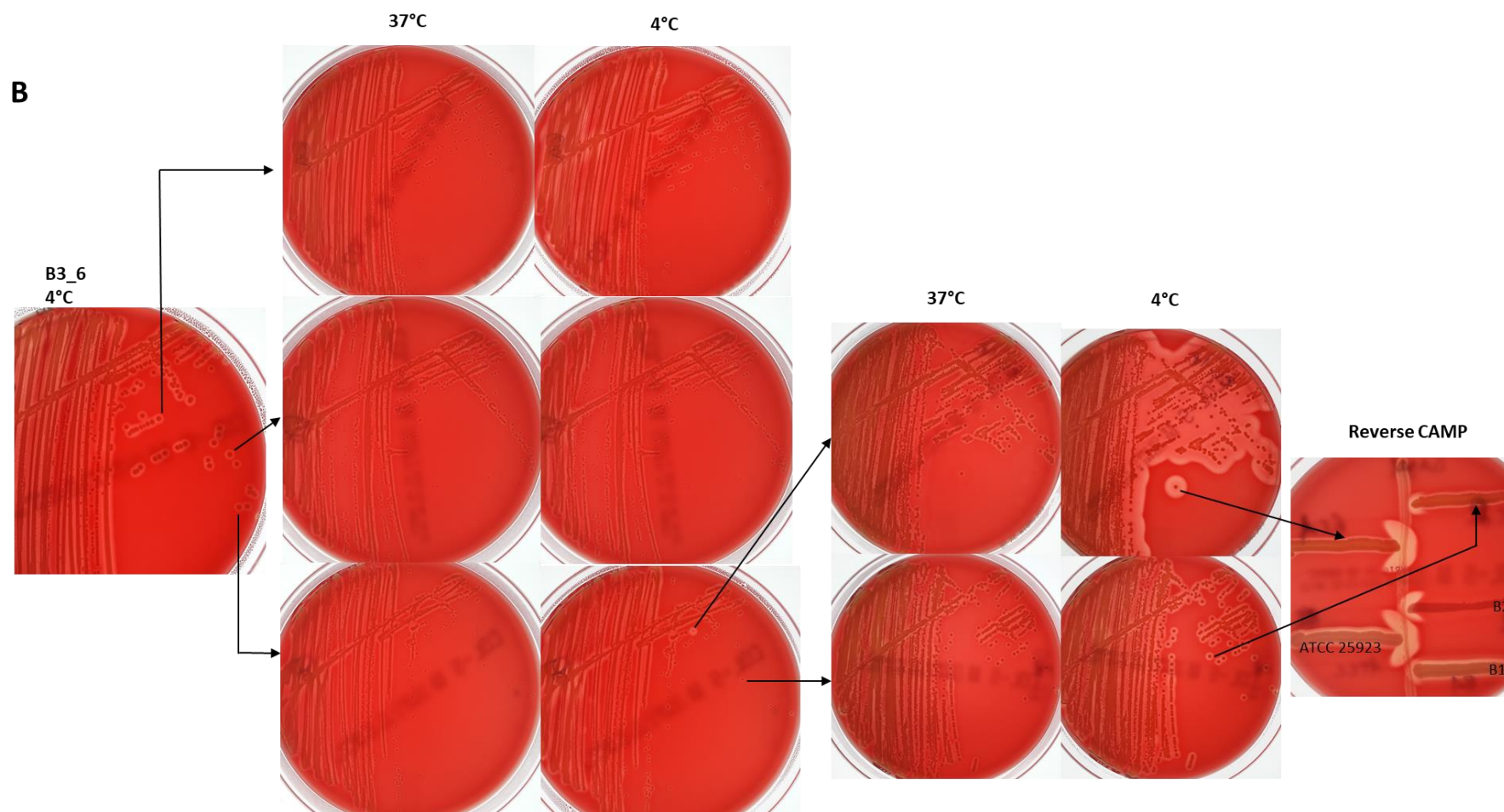
A**B**

Supplementary Figure 5. Growth characteristics of bacterial isolates. Growth was determined by measuring the OD at 590nm every 5 min at 37°C for 15 hours in total. (A) There was no significant association between the growth characteristics of IEC⁻ and IEC⁺ isolates. Growth curve of all study isolates (performed as three independent experiments with technical triplicates each) in tryptic soy broth at 37° C, grouped by the IEC genotype. Data points of isolates belonging to the IEC⁻ group were nudged on the x-axis by 10 data points for better visibility of standard deviations (only shown at full hours). (B) Individual growth curves of all study isolates (mean of three biological triplicates shown with standard deviation at full hours).



Supplementary Figure 6. Testing for auxotrophy. Upper panel: Testing for auxotrophy on Mueller-Hinton agar with impregnated discs with menadione (M), thymidine (T) and hemin (dark discs; X). Lower panel: Overnight culture on Columbia blood sheep agar with or without 5% CO₂. For enumeration of isolates, see Supplementary Figure 1.





Supplementary Figure 7. Testing for β -hemolysis. Single colonies of isolate B3 were subcultured on 5% sheep blood agar at 37°C overnight, then imaged (named 37°C), incubated at 4°C overnight and then imaged again (named 4°C). Enlargement of the hemolysis zone following incubation for 4°C is indicating β -hemolysin production (hot-cold effect). For the reverse CAMP test, the tested colonies were streaked perpendicularly to a *Streptococcus agalactiae* ATCC 27956 reference strain in the middle of a 5% sheep blood agar plate. Enlargement of the hemolysis zone near to the *S. agalactiae*, so called “arrowhead”, indicated β -hemolysin production. *S. aureus* ATCC 25923 was used as positive control and isolates B1 and B2 for comparison. (A) Subcultures of B3_2, (B) subcultures of B3_6.