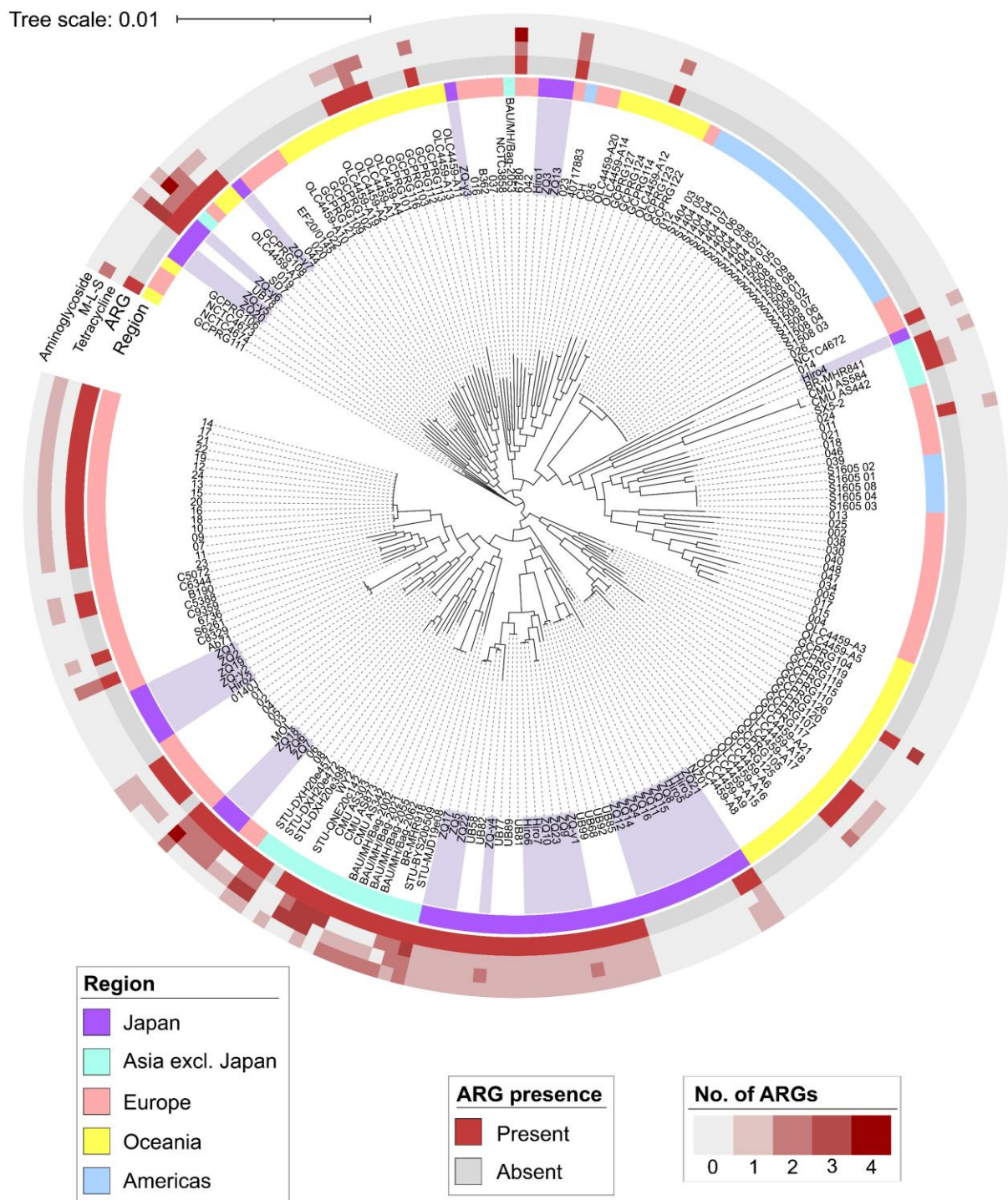
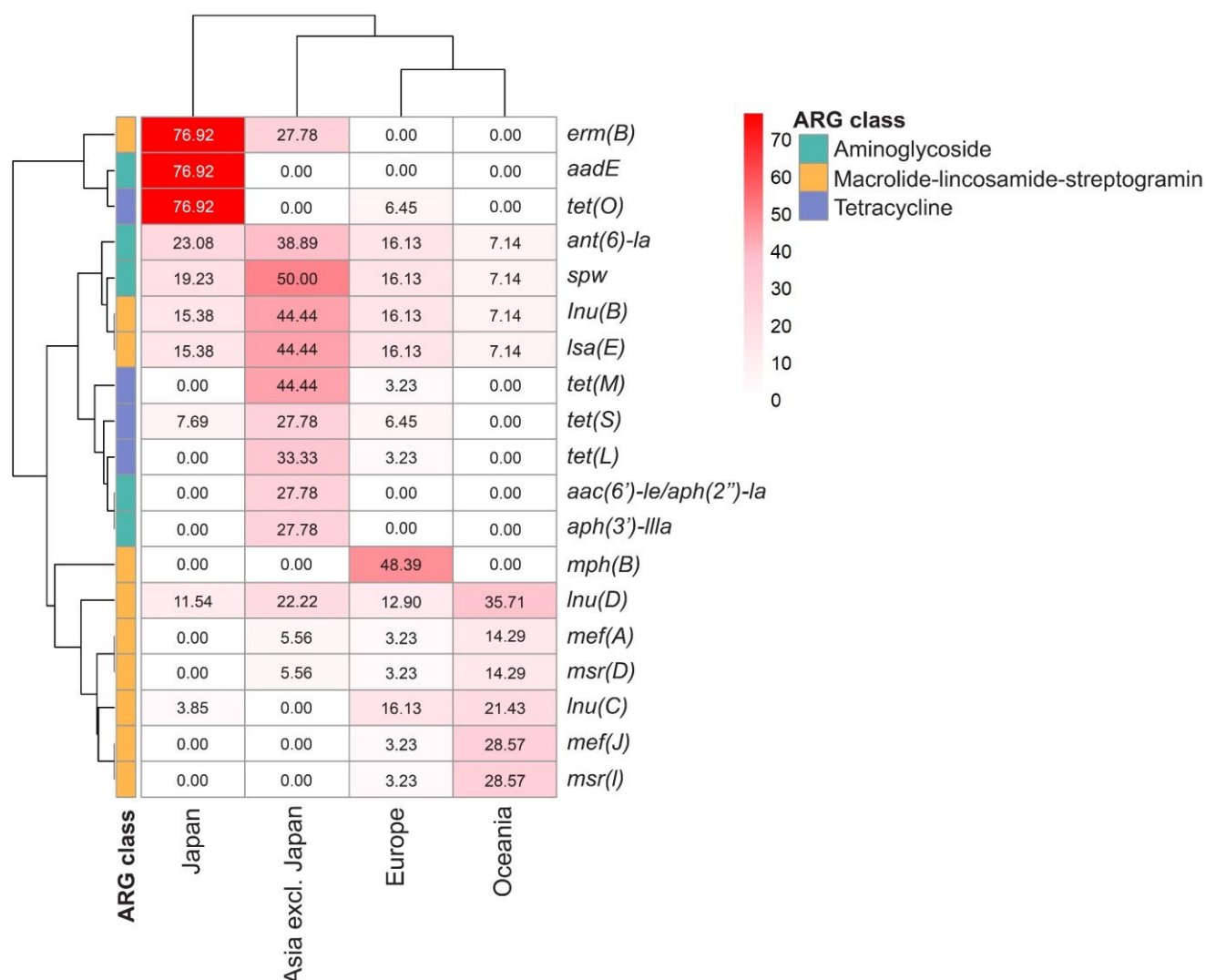
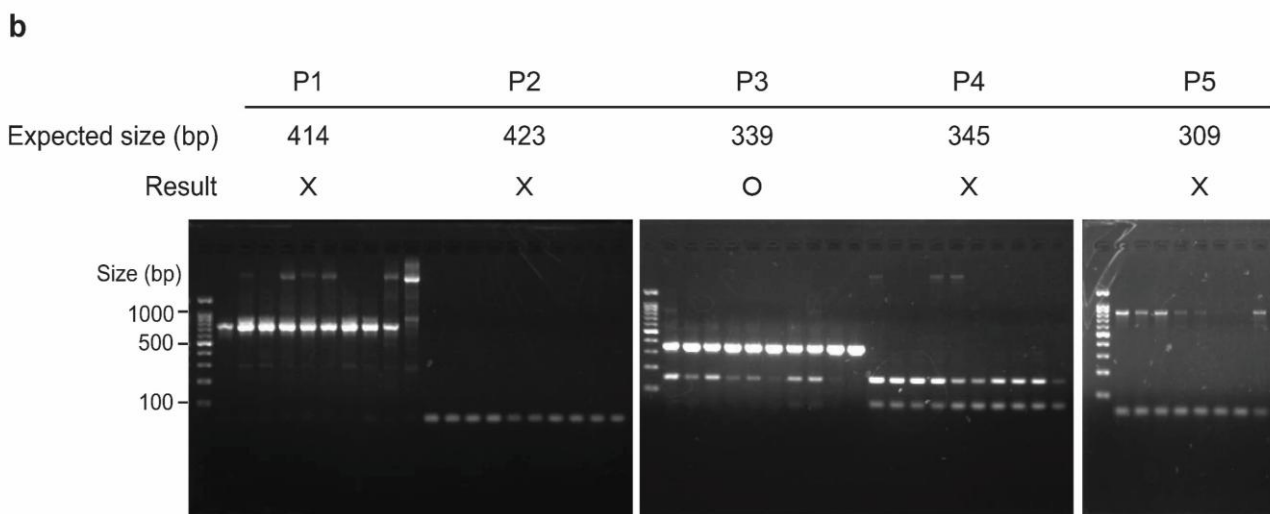
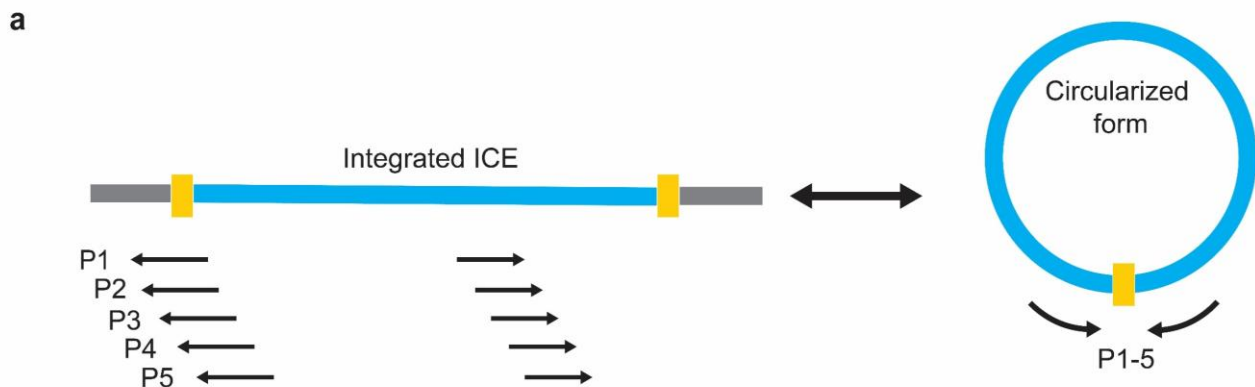




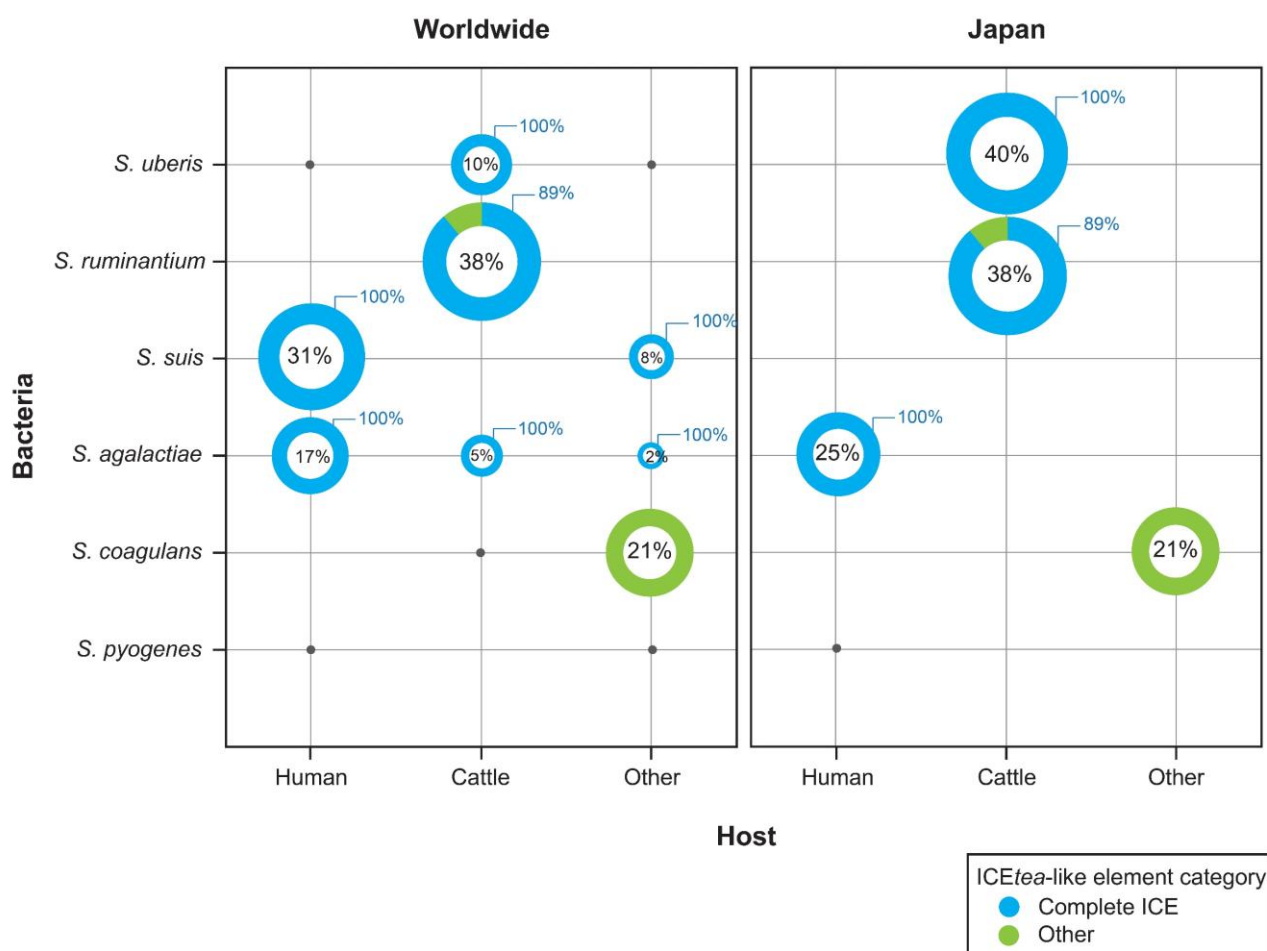
Supplementary Fig. S1 Core-genome phylogeny and distribution of antimicrobial resistance genes in *Streptococcus uberis*. The phylogenetic tree was inferred using FastTree from the concatenated core-gene alignment generated by Roary for 217 *S. uberis* genomes. The 37 isolates newly sequenced in this study are highlighted in purple. Outer rings indicate geographic region, overall ARG presence, and the numbers of detected ARGs belonging to the tetracycline, macrolide–lincosamide–streptogramin (M-L-S), and aminoglycoside resistance classes. ARGs were detected in 55% (26/47) of Japanese isolates, 86% (18/21) of isolates from Asia excluding Japan, 42% (31/74) of European isolates, and 29% (14/49) of Oceanian isolates, whereas no ARGs were detected in isolates from the Americas. Among the 235 ARG detections, 51% (119/235) were associated with macrolide–lincosamide–streptogramin resistance, 29% (69/235) with aminoglycoside resistance, and 20% (47/235) with tetracycline resistance (Supplementary Table S1).



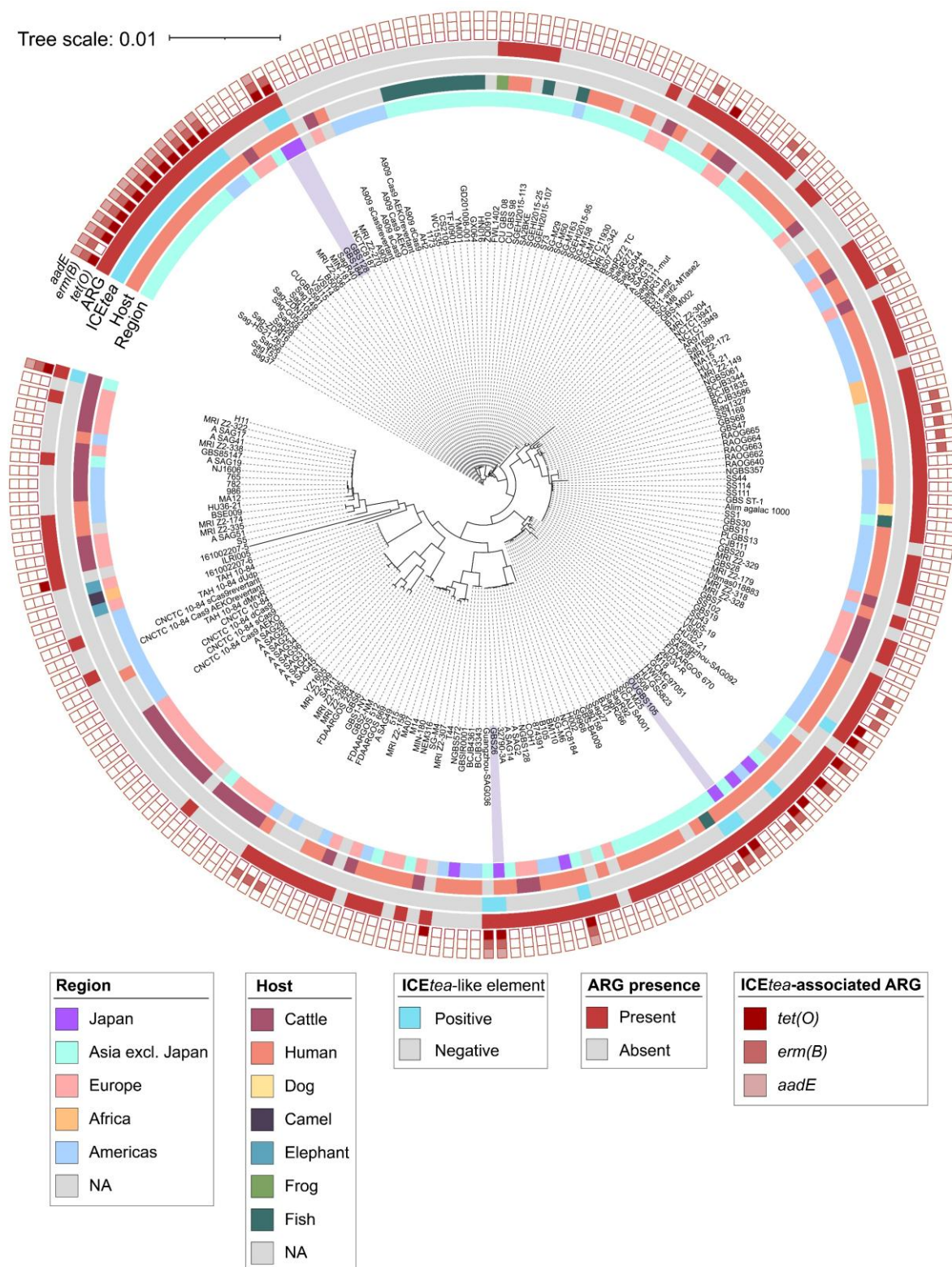
Supplementary Fig. S2 Geographic distribution of ARGs in *S. uberis*. The numerical value in each heatmap cell indicates the percentage of ARG-positive isolates within each geographic region (Japan, $n = 26$; Asia excluding Japan, $n = 18$; Europe, $n = 31$; Oceania, $n = 14$) carrying the corresponding ARG. Isolates from the Americas are not shown because no ARGs were detected. The same percentages are represented by the intensity of the red shading, as indicated by the color scale on the right.



Supplementary Fig. S3 PCR strategy for ICEtea boundary determination and circular-junction detection. **a** Schematic representation of primer sets P1–P5, which were designed to amplify the circular junction of ICEtea and define the terminal sequences of the integrated element. Arrows indicate primer orientations. **b** PCR analysis of 10 ICEtea-positive *S. uberis* isolates using primer sets P1–P5. In the electropherograms, lanes from left to right correspond to *S. uberis* ZQ5, ZQ9, ZQ10, ZQ17, ZQ22, ZQ23, Hiro6, Hiro7, ZQ-y1, and ZQ-y4, respectively. Among the five primer sets, only P3 yielded the expected 339-bp amplicon, consistent with amplification of the ICEtea circular junction. ○, amplicon of the expected size detected; ×, no amplicon of the expected size detected. The P3 amplicon was subsequently subjected to Sanger sequencing to confirm the circular junction.



Supplementary Fig. S4 Distribution of ICEtea-like elements across Gram-positive bacterial taxa and host origins worldwide and in Japan. The left and right panels show the distributions of ICEtea-like elements worldwide and in Japan, respectively. The bubble size and percentage shown at the center of each bubble indicate the proportion of genomes carrying ICEtea-like elements within each species–host group. Donut segments indicate ICEscreen-based classifications: blue, “Complete ICE”; green, “Other.” External blue labels indicate the proportion of detected ICEtea-like elements classified as “Complete ICE” within each group. Small gray dots indicate species–host groups for which genome data were available, but no ICEtea-like elements were detected, whereas blank positions indicate species–host combinations for which no genome data were available. The left panel shows the overall worldwide dataset, including Japanese genomes, whereas the right panel shows the Japanese subset. The four *S. agalactiae* genomes sequenced after PCR-positive selection in this study were excluded from proportion calculations.



Supplementary Fig. S5 Core-genome phylogeny of *Streptococcus agalactiae* and distribution of ICEtea-like elements and antimicrobial resistance genes. The phylogenetic tree was inferred using FastTree from the concatenated core-gene alignment generated by Roary for 210 *S. agalactiae* genomes. Concentric rings surrounding the tree indicate, from inner to outer, geographic region, host origin, ICEtea-like element presence, overall ARG presence, and presence of the three ICEtea-associated ARGs *tet(O)*, *erm(B)*, and *aadE*. The four *S. agalactiae* isolates characterized in this study—GBS26, GBS128, GBS184, and OUGBS105—are highlighted in purple and were included for phylogenetic context but excluded from comparative proportion calculations. ARGs were detected in 61.9% (130/210) of the genomes.

Supplementary Table S1. Indicator analysis of ARGs associated with geographic regions.

ARG class	Proportion of ARG detections (%) (n = 235)	ARG	Indicator region	Indicator value ^a	P value	FDR-adjusted P value
Aminoglycoside	29	<i>aac(6')-Ie/aph(2'')-Ia</i>	Asia excl. Japan	0.47	0.001	0.003
		<i>aadE</i>	Japan	0.85	0.001	0.003
		<i>ant(6)-Ia</i>	Asia excl. Japan	0.25	0.082	0.104
		<i>aph(3')-IIIa</i>	Asia excl. Japan	0.47	0.002	0.004
		<i>spw</i>	Asia excl. Japan	0.37	0.002	0.004
Macrolide- lincosamide- streptogramin	51	<i>erm(B)</i>	Japan	0.67	0.001	0.003
		<i>lnu(B)</i>	Asia excl. Japan	0.34	0.008	0.012
		<i>lnu(C)</i>	Oceania	0.21	0.143	0.160
		<i>lnu(D)</i>	Oceania	0.22	0.137	0.160
		<i>lsa(E)</i>	Asia excl. Japan	0.34	0.008	0.012
		<i>mef(A)</i>	Oceania	0.21	0.168	0.168
		<i>mef(J)</i>	Oceania	0.44	0.003	0.005
		<i>mph(B)</i>	Europe	0.64	0.001	0.003
		<i>msr(D)</i>	Oceania	0.21	0.168	0.168
		<i>msr(I)</i>	Oceania	0.44	0.003	0.005
Tetracycline	20	<i>tet(L)</i>	Asia excl. Japan	0.48	0.001	0.003
		<i>tet(M)</i>	Asia excl. Japan	0.58	0.001	0.003
		<i>tet(O)</i>	Japan	0.80	0.001	0.003
		<i>tet(S)</i>	Asia excl. Japan	0.33	0.016	0.022

^a, The indicator value represents the strength of association between each ARG and the corresponding geographic region. Indicator values were categorized as strong (>0.70), moderate (0.50–0.70), weak-to-moderate (0.30–0.50), or weak (<0.30).

Supplementary Table S2. Distribution of ICE/IME-related element categories predicted by ICEscreen in *S. uberis* genomes.

Category	Classification scheme based on signature proteins in ICEscreen ^a	Proportion (%; no. of elements/total)
Complete ICE	R + C + V + I	35.4% (242 / 684)
Complete IME	R + I (± C)	37.9% (259 / 684)
Conjugation module	R + C + V	4.2% (29 / 684)
Mobilizable element	R + C	5.7% (39 / 684)
Partial ICE	Incomplete ICE containing V	1.3% (9 / 684)
Other partial element	≥ 2 SPs	15.5% (106 / 684)

^a, R, relaxase; C, coupling protein; V, VirB4; I, integrase; SP, signature protein.

Supplementary Table S3. ICEScreen-predicted features of *ICEtea* in 19 *S. uberis* genomes and circular-junction validation in 10 isolates.

Strain	Prediction by ICEScreen				ICEtea after circular-junction validation		BLASTn analysis ^a		Nucleotide differences relative to ICEtea from <i>S. uberis</i> Hiro6 ^b			
	Category of element	ICE family	Size (bp)	G+C content (%)	Size (bp)	G+C content (%)	Sequence coverage (%)	Sequence identity (%)	19,222 nt	20,423 nt	60,403 nt	63,481 nt
Hiro6	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
Hiro7	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ5	Complete ICE	Tn5252	61,338	37.40	66,280	37.63	100	99.998	A	C	C	-
ZQ9	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ10	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ17	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ22	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ23	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	100	A	C	C	T
ZQ-y1	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	99.997	T	C	T	T
ZQ-y4	Complete ICE	Tn5252	61,339	37.40	66,281	37.62	100	99.998	A	T	C	T
UB58	Complete ICE	Tn5252	61,339	37.40	NA	NA	100	99.998	NA	NA	NA	NA
UB68	Complete ICE	Tn5252	60,688	37.36	NA	NA	99	99.939	NA	NA	NA	NA
UB77	Complete ICE	Tn5252	61,339	37.40	NA	NA	100	99.995	NA	NA	NA	NA
UB78	Complete ICE	Tn5252	61,360	37.40	NA	NA	100	99.964	NA	NA	NA	NA
UB81	Complete ICE	Tn5252	61,339	37.40	NA	NA	100	99.995	NA	NA	NA	NA
UB82	Complete ICE	Tn5252	61,339	37.40	NA	NA	100	99.998	NA	NA	NA	NA
UB85	Complete ICE	Tn5252	60,688	37.36	NA	NA	99	99.939	NA	NA	NA	NA
UB89	Complete ICE	Tn5252	61,339	37.40	NA	NA	100	99.995	NA	NA	NA	NA
UB92	Complete ICE	Tn5252	60,688	37.36	NA	NA	99	99.939	NA	NA	NA	NA

^a, Sequence coverage and nucleotide identity were calculated using BLASTn with the circular-junction-validated *ICEtea* sequence from strain Hiro6 as the query. For isolates with circular-junction validation, the validated *ICEtea* sequence was used as the subject; for the remaining isolates, the ICEScreen-predicted region was used.

^b, Nucleotide positions are based on the *ICEtea* sequence from strain Hiro6. A dash indicates a nucleotide deletion relative to the Hiro6 sequence. Nucleotides differing from the Hiro6 sequence are indicated in red.

^b, NA, not assessed.

Supplementary Table S4. Antimicrobial susceptibility profiles of 37 *S. uberis* isolates.

Antimicrobial agent ^a	MIC (µg/mL) ^b			Resistance rate (%) ^c
	Range	MIC ₅₀	MIC ₉₀	
Penicillin G	≤0.031 – 0.5	0.125	0.25	0
Ampicillin	≤0.031 – 0.5	0.125	0.25	0
Amoxicillin	≤0.031 – 0.5	0.25	0.5	0
Cefazolin	0.125 – 2	0.5	1	0
Cefoperazone	0.25 – 4	2	4	0
Cefquinome	≤0.031 – 0.5	0.125	0.25	0
Ceftiofur	0.125 – 4	1	4	0
Erythromycin	≤0.031 – >64	0.063	>64	27.0
Lincomycin	0.063 – >64	0.25	>64	32.4
Gentamicin	2 – 64	16	32	0
Oxytetracycline	0.125 – 64	0.25	32	35.1
Ciprofloxacin	0.25 – 1	0.5	1	0
Enrofloxacin	0.25 – 2	1	1	0
Sulfamethoxazole/trimethoprim	0.125 – 1	0.25	0.5	0

^a, Antimicrobial agents are ordered according to antibiotic class.

^b, MIC₅₀ and MIC₉₀ represent the MICs at which 50% and 90% of isolates were inhibited, respectively.

^c, Resistance rates were determined using CLSI VET01S interpretive criteria where applicable ⁴⁷; for antimicrobial agents lacking applicable CLSI criteria for *S. uberis*, previously published interpretive criteria were used ^{48,49}.

Supplementary Table S5. Environmental vector fitting (envfit) analysis and comparisons of MICs between ICE*tea* -positive and ICE*tea* -negative *S. uberis* isolates (n = 37).

Antimicrobial agent ^a	envfit analysis ^b		Two-group comparison ^c	
	R^2	<i>P</i> value	<i>P</i> value	FDR-adjusted <i>P</i> value
Lincomycin	0.98	0.001	<0.001	<0.001
Erythromycin	0.95	0.001	<0.001	<0.001
Oxytetracycline	0.69	0.001	<0.001	<0.001
Ampicillin	0.50	0.001	<0.001	<0.001
Amoxicillin	0.391	0.001	0.003	0.007
Cefazolin	0.372	0.001	0.001	0.004
Gentamicin	0.311	0.004	1.000	1.000
Penicillin G	0.299	0.004	0.005	0.010
Cefoperazone	0.210	0.019	0.202	0.313
Cefquinome	0.196	0.030	0.226	0.316
Ceftiofur	0.161	0.046	0.139	0.242
Enrofloxacin	0.070	0.283	0.787	0.848
Sulfamethoxazole/trimethoprim	0.064	0.309	0.322	0.410
Ciprofloxacin	0.017	0.782	0.685	0.799

^a, The antimicrobial agents are listed in descending order of the R^2 values from the envfit

^b, In the envfit analysis, R^2 represents the strength of association between each antimicrobial agent and variation in the PCoA ordination.

^c, Differences in MIC distributions between ICE*tea* -positive and ICE*tea* -negative isolates were assessed using the Mann–Whitney *U* test. *P* values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate method.

Supplementary Table S6. Gene annotation of ICEtea from *S. uberis* strain Hiro6.

CDS	Direction	Start	End	Length (aa)	Predicted function ^a
CDS_01	+	253	426	57	Hypothetical protein
CDS_02	+	423	1,241	272	RepA-like replication initiator protein
CDS_03	+	1,390	2,745	451	DNA cytosine methyltransferase (Dcm)
CDS_04	+	2,729	3,157	142	Hypothetical protein
CDS_05	+	3,168	3,551	127	Transcriptional regulator; thioredoxin-like protein
CDS_06	+	3,560	3,793	77	Hypothetical protein
CDS_07	+	3,796	4,380	194	Rce1-like intramembrane protease
CDS_08	+	4,458	4,946	162	Hypothetical protein
CDS_09	+	4,946	6,763	605	VirD4-like type IV secretion system coupling ATPase
CDS_10	+	6,769	7,023	84	Hypothetical protein
CDS_11	+	7,042	7,896	284	Hypothetical protein
CDS_12	+	7,958	8,311	117	Type IV secretion system-associated PrgI family protein
CDS_13	+	8,289	10,619	776	Type IV secretion system VirB4 ATPase
CDS_14	+	10,621	13,422	933	Cell wall hydrolase with phage tail lysozyme-like domain
CDS_15	-	13,485	14,330	281	Nucleotidyltransferase component of a viral defense system
CDS_16	-	14,327	14,917	196	AbiEi antitoxin component of AbiE toxin-antitoxin system
CDS_17	+	15,087	19,982	1,631	LPXTG-anchored antigen I/II family adhesin
CDS_18	+	19,983	20,174	63	CglD-like lipoprotein
CDS_19	+	20,158	20,709	183	Hypothetical protein
CDS_20	+	20,759	26,200	1,813	Adenine-specific DNA methyltransferase, N12 class
CDS_21	+	26,698	28,476	592	Group II intron-encoded protein LtrA
CDS_22	+	28,614	29,957	447	Adenine-specific DNA methyltransferase, N12 class
CDS_23	+	30,028	30,327	99	Uncharacterized DUF5962 family protein
CDS_24	+	30,726	31,457	243	Hypothetical protein
CDS_25	+	31,397	31,771	124	Uncharacterized transposon-encoded TnpV family protein
CDS_26	+	32,138	34,057	639	Tetracycline resistance ribosomal protection protein Tet(O)
CDS_27	+	34,485	34,655	56	Hypothetical protein
CDS_28	+	34,669	35,286	205	Putative transposon Tn552 DNA-invertase bin3
CDS_29	+	35,286	37,430	714	DNA topoisomerase III
CDS_30	+	37,546	37,779	77	Omega transcriptional repressor
CDS_31	+	38,048	38,785	245	23S rRNA (adenine(2058)-N(6))-methyltransferase Erm(B)
CDS_32	+	38,730	38,921	63	Hypothetical protein
CDS_33	+	39,297	40,193	298	ParA-like partitioning ATPase
CDS_34	+	40,285	40,500	71	Omega transcriptional repressor
CDS_35	+	40,518	40,790	90	Epsilon antitoxin
CDS_36	+	40,792	40,950	52	Toxin zeta
CDS_37	+	41,002	41,547	181	AAA-domain kinase
CDS_38	+	41,723	42,589	288	Aminoglycoside 6-adenylyltransferase AadE
CDS_39	+	43,202	43,828	208	Toxin zeta

^a, Orange shading indicates genes associated with toxin–antitoxin systems potentially involved in element maintenance or anti-phage defense. Green shading indicates genes associated with lantibiotic biosynthesis, regulation, transport, and immunity.

Supplementary Table S6 — Continued .

CDS	Direction	Start	End	Length (aa)	Predicted function ^a
CDS_40	+	43,979	44,470	163	Hypothetical protein
CDS_41	+	44,463	44,624	53	Hypothetical protein
CDS_42	+	44,621	45,628	335	VirD4-like type IV secretion system coupling ATPase
CDS_43	+	45,646	47,442	598	Serine integrase
CDS_44	+	47,506	48,606	366	Bacterial DNA primase/Toprim domain protein
CDS_45	+	48,634	48,861	75	Uncharacterized DUF5965 family protein
CDS_46	+	48,858	49,247	129	Uncharacterized DUF5945 family protein
CDS_47	+	49,298	49,588	96	Hypothetical protein
CDS_48	+	49,640	50,134	164	PezA antitoxin component of type II toxin-antitoxin system
CDS_49	+	50,134	50,901	255	PezT toxin component of type II toxin-antitoxin system
CDS_50	+	50,902	53,445	847	AbiEii-like toxin/ATP-dependent endonuclease
CDS_51	+	53,783	54,145	120	Conjugative relaxosome accessory protein
CDS_52	+	54,148	54,513	121	MobC mobilization protein
CDS_53	+	54,500	56,383	627	SAG1250 family conjugative relaxase
CDS_54	+	56,480	57,853	457	Lantibiotic-specific S8 family serine protease
CDS_55	+	57,894	58,592	232	OmpR family DNA-binding response regulator
CDS_56	+	58,570	59,913	447	Signal transduction histidine kinase
CDS_57	+	60,088	60,804	238	Bacitracin/lantibiotic-associated ABC transporter ATP-binding protein
CDS_58	+	60,782	61,534	250	Lantibiotic immunity ABC transporter permease, MutE/EpiE family
CDS_59	+	61,512	62,198	228	Lantibiotic immunity ABC transporter permease, NisG family
CDS_60	+	62,312	62,635	107	LanC-like lantibiotic cyclase
CDS_61	+	62,637	63,353	238	NisI/SpaI family lantibiotic immunity lipoprotein
CDS_62	+	63,621	64,025	134	Putative sigma factor-related protein
CDS_63	+	64,530	66,281	583	Serine integrase

^a, Orange shading indicates genes associated with toxin–antitoxin systems potentially involved in element maintenance or anti-phage defense. Green shading indicates genes associated with lantibiotic biosynthesis, regulation, transport, and immunity.

Supplementary Table S7. Transfer efficiencies of ICE_{tea} from *S. uberis* donor strains to recipient bacteria in filter-mating assays.

Donor strain	Recipient strain	Number of experimental replicates	Transfer efficiency (mean $\pm$ SD) ^a
<i>S. uberis</i> Hiro6	<i>S. uberis</i> ZQ1	4	$4.63 \times 10^{-7} \pm 2.86 \times 10^{-7}$
<i>S. uberis</i> ZQ9	<i>S. uberis</i> ZQ1	3	$4.63 \times 10^{-6} \pm 1.31 \times 10^{-6}$
<i>S. uberis</i> ZQ22	<i>S. uberis</i> ZQ1	3	$1.75 \times 10^{-5} \pm 6.93 \times 10^{-6}$
<i>S. uberis</i> ZQ-y1	<i>S. uberis</i> ZQ1	3	$2.18 \times 10^{-7} \pm 3.41 \times 10^{-8}$
<i>S. uberis</i> ZQ-y4	<i>S. uberis</i> ZQ1	3	$2.60 \times 10^{-5} \pm 6.19 \times 10^{-6}$
<i>S. uberis</i> Hiro6	<i>S. uberis</i> ZQ12	3	$3.40 \times 10^{-8} \pm 8.54 \times 10^{-9}$
<i>S. uberis</i> Hiro6	<i>S. agalactiae</i> GBS3	3	$6.02 \times 10^{-7} \pm 1.70 \times 10^{-7}$
<i>S. uberis</i> Hiro6	<i>S. agalactiae</i> GBS5	3	$6.00 \times 10^{-8} \pm 2.01 \times 10^{-8}$
<i>S. uberis</i> Hiro6	<i>S. pyogenes</i> GAS5001	3	$3.43 \times 10^{-7} \pm 4.00 \times 10^{-7}$
<i>S. uberis</i> Hiro6	<i>S. pyogenes</i> GAS5006	3	$7.30 \times 10^{-9} \pm 6.00 \times 10^{-9}$
<i>S. uberis</i> Hiro6	<i>S. aureus</i> RN4220	6	$3.94 \times 10^{-11} \pm 8.81 \times 10^{-11}$
<i>S. uberis</i> Hiro6	<i>E. coli</i> DH5 α	6	ND

^a, Transfer efficiency was calculated as the number of transconjugant CFU divided by the number of recipient CFU recovered on recipient-selective media. Values are presented as the mean $\pm$ SD from the indicated number of independent experiments. ND, no transconjugants detected.

Overall differences in transfer efficiency were assessed using the Kruskal–Wallis test (*S. uberis* -to-*S. uberis* : $H = 13.11$, $P < 0.0001$; *S. uberis* -to-other recipients: $H = 20.13$, $P = 0.0026$), followed by Dunn's multiple-comparisons test. Significant pairwise differences were observed only for GBS3 versus RN4220 (adjusted $P = 0.0308$) and GBS3 versus DH5 α (adjusted $P = 0.0141$).

Supplementary Table S8. Attachment-site sequences in recipient strains and corresponding ICE_{tea} transconjugants.

ICE transfer experiment		Recipient bacteria	Transconjugants	
Donor bacteria	Recipient bacteria	<i>attB</i>	<i>attL</i>	<i>attR</i>
<i>S. uberis</i> ZQ9	<i>S. uberis</i> ZQ1	CACGT	CACGT	CACGT
<i>S. uberis</i> ZQ22	<i>S. uberis</i> ZQ1	CACGT	CACGT	CACGT
<i>S. uberis</i> ZQ-y1	<i>S. uberis</i> ZQ1	CACGT	CACGT	CACGT
<i>S. uberis</i> ZQ-y4	<i>S. uberis</i> ZQ1	CACGT	CACGT	CACGT
<i>S. uberis</i> Hiro6	<i>S. uberis</i> ZQ1	CACGT	CACGT	CACGT
<i>S. uberis</i> Hiro6	<i>S. uberis</i> ZQ12	CACGT	CACGT	CACGT
<i>S. uberis</i> Hiro6	<i>S. agalactiae</i> GBS3	CATGT	CACGT	CATGT
<i>S. uberis</i> Hiro6	<i>S. agalactiae</i> GBS5	CATGT	CACGT	CATGT
<i>S. uberis</i> Hiro6	<i>S. pyogenes</i> GAS5001	CACGT	CACGT	CACGT
<i>S. uberis</i> Hiro6	<i>S. pyogenes</i> GAS5006	CACGT	CACGT	CACGT
<i>S. uberis</i> Hiro6	<i>S. aureus</i> RN4220	CATGT	CACGT	CATGT

The attachment-site core sequences were CACGT or CATGT. The central T in the CATGT variant is highlighted in red.

Supplementary Table S9. MICs of parental recipient strains and corresponding ICE*tea* -carrying transconjugants.

Parental recipient	ICE <i>tea</i> -carrying transconjugant	Ampicillin		Erythromycin*		Tetracycline		Streptomycin		Lincomycin*	
		Recipient	Transconjugant	Recipient	Transconjugant	Recipient	Transconjugant	Recipient	Transconjugant	Recipient	Transconjugant
<i>S. uberis</i> ZQ1	<i>S. uberis</i> H6-ZQ1	0.125	0.125	≤0.063	>64	0.25	32	64	>64	0.125	>64
<i>S. uberis</i> ZQ1	<i>S. uberis</i> ZQ-y1-ZQ1	0.125	0.125	≤0.063	>64	0.25	32	64	>64	0.125	>64
<i>S. uberis</i> ZQ1	<i>S. uberis</i> ZQ-y4-ZQ1	0.125	0.125	≤0.063	>64	0.25	32	64	>64	0.125	>64
<i>S. uberis</i> ZQ1	<i>S. uberis</i> ZQ9-ZQ1	0.125	0.125	≤0.063	>64	0.25	32	64	>64	0.125	>64
<i>S. uberis</i> ZQ1	<i>S. uberis</i> ZQ22-ZQ1	0.125	0.125	≤0.063	>64	0.25	32	64	>64	0.125	>64
<i>S. uberis</i> ZQ12	<i>S. uberis</i> H6-ZQ12	0.25	0.25	≤0.063	>64	0.125	64	32	>64	0.125	>64
<i>S. agalactiae</i> GBS3	<i>S. agalactiae</i> H6-GBS3	0.125	0.125	≤0.063	>64	0.5	64	>64	>64	0.25	>64
<i>S. agalactiae</i> GBS5	<i>S. agalactiae</i> H6-GBS5	0.125	0.125	≤0.063	>64	32	32	>64	>64	0.125	>64
<i>S. pyogenes</i> GAS5001	<i>S. pyogenes</i> H6-GAS5001	≤0.063	≤0.063	≤0.063	>64	0.125	64	32	>64	≤0.063	>64
<i>S. pyogenes</i> GAS5006	<i>S. pyogenes</i> H6-GAS5006	≤0.063	≤0.063	≤0.063	>64	0.125	32	16	>64	0.125	>64
<i>Staphylococcus aureus</i> RN4220	<i>Staphylococcus aureus</i> H6-RN4220	≤0.063	0.125	0.25	>64	0.25	8	4	>64	0.5	>64

Statistical analysis: For each antimicrobial agent, changes in MIC following ICE*tea* acquisition were evaluated using a two-sided exact sign test, with each independent recipient background treated as one paired analytical unit. Multiple transconjugants derived from the same *S. uberis* ZQ1 recipient background were counted as a single analytical unit to avoid pseudoreplication. Ties, including values reported at the same censoring limit (e.g., >64 versus >64), were excluded from the sign test. MICs increased in 1/7 recipient backgrounds for ampicillin ($P = 1.000$, adjusted $P = 1.000$), 7/7 for erythromycin ($P = 0.0156$, adjusted $P = 0.0391$), 6/7 for tetracycline ($P = 0.0313$, adjusted $P = 0.0521$), 5/7 for streptomycin ($P = 0.0625$, adjusted $P = 0.0781$), and 7/7 for lincomycin ($P = 0.0156$, adjusted $P = 0.0391$). P values were adjusted for multiple comparisons across the five antimicrobial agents using the Benjamini–Hochberg method; adjusted P values < 0.05 were considered statistically significant and are indicated by an asterisk (*).

Supplementary Table S10. PCR screening for ICE_{tea} -like elements and associated ARGs in human-derived *S. agalactiae* isolates.

Strain	Source	PCR results ^a					Interpretation of PCR results	
		ICE _{tea} circular junction	Integrase gene	<i>tet(O)</i> gene	<i>erm(B)</i> gene	<i>aadE</i> gene	ICE _{tea} -like element ^b	ARGs ^c
GBS4	Vaginal swab	–	–	–	–	–	Negative	None
GBS12	Vaginal swab	–	–	–	–	–	Negative	None
GBS19	Vaginal swab	–	–	–	–	–	Negative	None
GBS26	Vaginal swab	+	+	+	+	+	Positive	<i>tet(O)</i> , <i>erm(B)</i> , <i>aadE</i>
GBS31	Vaginal swab	–	–	–	–	–	Negative	None
GBS38	Vaginal swab	–	–	–	–	–	Negative	None
GBS52	Vaginal swab	–	–	–	–	–	Negative	None
GBS61	Vaginal swab	–	–	–	–	–	Negative	None
GBS87	Vaginal swab	–	–	–	–	–	Negative	None
GBS95	Vaginal swab	–	–	–	–	–	Negative	None
GBS97	Vaginal swab	–	–	–	–	–	Negative	None
GBS100	Vaginal swab	–	–	–	–	–	Negative	None
GBS102	Vaginal swab	–	–	–	–	–	Negative	None
GBS104	Vaginal swab	–	–	–	–	–	Negative	None
GBS113	Vaginal swab	–	–	–	–	–	Negative	None
GBS116	Vaginal swab	–	–	–	–	–	Negative	None
GBS128	Vaginal swab	+	+	+	+	–	Positive	<i>tet(O)</i> , <i>erm(B)</i>
GBS131	Vaginal swab	–	–	–	–	–	Negative	None
GBS150	Vaginal swab	–	–	–	–	–	Negative	None
GBS151	Vaginal swab	–	–	–	–	–	Negative	None
GBS153	Vaginal swab	–	–	–	+	–	Negative	<i>erm(B)</i>
GBS154	Vaginal swab	–	–	–	+	–	Negative	<i>erm(B)</i>
GBS156	Vaginal swab	–	–	–	–	–	Negative	None
GBS159	Vaginal swab	–	–	–	–	–	Negative	None
GBS161	Vaginal swab	–	–	–	–	–	Negative	None
GBS166	Vaginal swab	–	–	–	–	–	Negative	None
GBS173	Vaginal swab	–	–	–	–	–	Negative	None
GBS176	Vaginal swab	–	–	–	–	–	Negative	None
GBS184	Vaginal swab	+	+	+	+	+	Positive	<i>tet(O)</i> , <i>erm(B)</i> , <i>aadE</i>
GBS187	Vaginal swab	–	–	–	+	–	Negative	<i>erm(B)</i>
GBS392	Vaginal swab	–	–	–	–	–	Negative	None
GBS394	Vaginal swab	–	–	–	–	–	Negative	None
GBS396	Vaginal swab	–	–	–	–	–	Negative	None
GBS422	Vaginal swab	–	–	–	–	–	Negative	None
GBS427	Vaginal swab	–	–	–	–	–	Negative	None

^a, +, PCR positive; –, PCR negative.

^b, Isolates positive for both the ICE_{tea} circular junction and integrase were considered presumptively positive for an ICE_{tea} -like element.

^c, ARG profiles were determined by PCR detection of *tet(O)*, *erm(B)*, and *aadE*.

Supplementary Table S10 — *Continued.*

Strain	Source	PCR results ^a					Interpretation of PCR results	
		ICE _{tea} circular junction	Integrase gene	<i>tet(O)</i> gene	<i>erm(B)</i> gene	<i>aadE</i> gene	ICE _{tea} -like element ^b	ARGs ^c
GBS471	Vaginal swab	—	—	—	—	—	Negative	None
OUGBS130	Blood	—	—	+	+	+	Negative	<i>tet(O)</i> , <i>erm(B)</i> , <i>aadE</i>
OUGBS165a	Blood	—	—	—	—	—	Negative	None
OUGBS211	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS244	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS264	Blood	—	—	—	—	—	Negative	None
OUGBS396	Blood	—	—	—	+	+	Negative	<i>erm(B)</i> , <i>aadE</i>
OUGBS165b	Blood	—	—	—	—	—	Negative	None
OUGBS176a	Blood	—	—	—	—	—	Negative	None
OUGBS105	Blood	+	+	+	+	—	Positive	<i>tet(O)</i> , <i>erm(B)</i>
OUGBS554	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS433	Blood	—	—	—	—	—	Negative	None
OUGBS384	Blood	—	—	—	—	—	Negative	None
OUGBS291	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS274	Blood	—	—	—	—	—	Negative	None
OUGBS251	Blood	—	—	—	—	—	Negative	None
OUGBS233	Blood	—	—	—	—	—	Negative	None
OUGBS119	Blood	—	—	—	—	—	Negative	None
OUGBS176b	Blood	—	—	—	—	—	Negative	None
OUGBS232	Blood	—	—	—	—	+	Negative	<i>aadE</i>
OUGBS388	Blood	—	—	—	—	—	Negative	None
OUGBS439	Blood	—	—	—	—	—	Negative	None
OUGBS456	Blood	—	—	—	—	—	Negative	None
OUGBS528	Blood	—	—	—	—	—	Negative	None
OUGBS548	Blood	—	—	—	—	—	Negative	None
OUGBS41	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS43	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS46	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS100	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS492	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS270	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>
OUGBS269	Blood	—	—	—	+	—	Negative	<i>erm(B)</i>

^a, +, PCR positive; -, PCR negative.

^b, Isolates positive for both the ICE_{tea} circular junction and integrase were considered presumptively positive for an ICE_{tea}-like element.

^c, ARG profiles were determined by PCR detection of *tet(O)*, *erm(B)*, and *aadE*.

Supplementary Table S11. Antimicrobial susceptibility profiles of 67 human-derived *S. agalactiae* isolates.

Antimicrobial agent ^a	MIC (µg/mL) ^b			Non-susceptible or resistant rate (%) ^c
	Range	MIC ₅₀	MIC ₉₀	
Penicillin G	≤0.06 – 1	≤0.06	≤0.06	1.5
Ampicillin	≤0.12 – 0.5	≤0.12	≤0.12	1.5
Amoxicillin/clavulanic acid	≤0.25 – 0.5	≤0.25	≤0.25	1.5
Ampicillin/sulbactam	≤0.12 – 0.5	≤0.12	≤0.12	1.5
Cefazolin	≤0.25 – >2	≤0.25	≤0.25	1.5
Cefotaxime	≤0.06 – >2	≤0.06	0.12	3.0
Ceftriaxone	≤0.25 – >2	≤0.25	≤0.25	3.0
Cefepime	≤0.25 – >2	≤0.25	≤0.25	1.5
Imipenem	≤0.12 – 0.5	≤0.12	≤0.12	0
Meropenem	≤0.06 – 2	≤0.06	≤0.06	1.5
Azithromycin	≤0.12 – >4	0.25	>4	37.3
Clarithromycin	≤0.25 – >16	≤0.25	>16	32.8
Erythromycin	≤0.25 – >2	≤0.25	>2	35.8
Clindamycin	≤0.25 – >2	≤0.25	>2	20.9
Erythromycin/clindamycin	≤0.5 – >0.5	≤0.5	>0.5	23.9
Minocycline	≤1 – >4	>4	>4	52.2
Levofloxacin	≤1 – >4	2	>4	35.8
Sulfamethoxazole/trimethoprim	≤0.25 – 1	≤0.5	1	0
Vancomycin	≤0.25 – 1	0.5	0.5	0

^a, Antimicrobial agents are ordered according to antibiotic class.

^b, MIC₅₀ and MIC₉₀ represent the minimum concentrations required to inhibit 50% and 90% of isolates,

^c, Interpretive categories were assigned according to CLSI M100 (36th edition, 2026) where applicable. For penicillin and ampicillin, values above the CLSI susceptible breakpoint were considered nonsusceptible rather than resistant. Antimicrobial agents without applicable CLSI interpretive criteria were not assigned a resistance category.

Supplementary Table S12. Environmental vector fitting (envfit) analysis and comparisons of MICs between ICE_{tea} -like element-positive and -negative human-derived *S. agalactiae* isolates.

Antimicrobial agent ^a	envfit analysis ^b		Two-group comparison ^c	
	<i>R</i> ²	<i>P</i> value	<i>P</i> value	FDR-adjusted <i>P</i> value
Erythromycin	0.919	0.001	0.004	0.021
Azithromycin	0.899	0.001	0.008	0.032
Erythromycin/clindamycin	0.802	0.001	<0.001	0.003
Clarithromycin	0.785	0.001	0.002	0.012
Minocycline	0.763	0.001	0.058	0.183
Clindamycin	0.585	0.001	<0.001	0.003
Levofloxacin	0.402	0.001	0.536	0.897
Vancomycin	0.010	0.760	0.912	0.912
Sulfamethoxazole/trimethoprim	0.010	0.740	0.349	0.829
Amoxicillin/clavulanic acid	0.006	0.909	0.850	0.897
Ampicillin	0.006	0.909	0.850	0.897
Imipenem	0.006	0.909	0.850	0.897
Ampicillin/sulbactam	0.006	0.909	0.850	0.897
Meropenem	0.006	0.909	0.850	0.897
Cefazolin	0.006	0.909	0.850	0.897
Penicillin G	0.006	0.909	0.850	0.897
Cefepime	0.004	0.941	0.629	0.897
Ceftriaxone	0.004	0.936	0.629	0.897
Cefotaxime	0.002	0.965	0.115	0.312

^a, The antimicrobial agents are listed in descending order of the *R*² values from the envfit analysis.

^b, In the envfit analysis, *R*² represents the strength of association between each antimicrobial agent and variation in the PCoA ordination.

^c, Differences in MIC distributions between ICE_{tea} -like element-positive and -negative isolates were assessed using the Mann–Whitney *U* test. *P* values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate method.

Supplementary Table S13. Transfer efficiencies of ICE_{tea}-like elements from *S. agalactiae* donor strains to recipient bacteria in filter-mating assays.

Donor strain	Recipient strain	Number of experimental replicates	Transfer efficiency (mean $\pm$ SD) ^a
<i>S. agalactiae</i> GBS26	<i>S. agalactiae</i> GBS3	3	ND
<i>S. agalactiae</i> GBS26	<i>S. agalactiae</i> GBS5	3	ND
<i>S. agalactiae</i> GBS26	<i>S. uberis</i> ZQ1	3	ND
<i>S. agalactiae</i> GBS26	<i>S. uberis</i> ZQ12	3	ND
<i>S. agalactiae</i> GBS128	<i>S. agalactiae</i> GBS3	3	$3.33 \times 10^{-5} \pm 2.68 \times 10^{-5}$
<i>S. agalactiae</i> GBS128	<i>S. agalactiae</i> GBS5	3	ND
<i>S. agalactiae</i> GBS128	<i>S. uberis</i> ZQ1	3	$4.12 \times 10^{-5} \pm 1.14 \times 10^{-5}$
<i>S. agalactiae</i> GBS128	<i>S. uberis</i> ZQ12	3	ND
<i>S. agalactiae</i> GBS184	<i>S. agalactiae</i> GBS3	3	ND
<i>S. agalactiae</i> GBS184	<i>S. agalactiae</i> GBS5	3	ND
<i>S. agalactiae</i> GBS184	<i>S. uberis</i> ZQ1	3	$2.74 \times 10^{-8} \pm 1.47 \times 10^{-8}$
<i>S. agalactiae</i> GBS184	<i>S. uberis</i> ZQ12	3	ND
<i>S. agalactiae</i> OUGBS105	<i>S. agalactiae</i> GBS3	3	$2.66 \times 10^{-9} \pm 2.58 \times 10^{-9}$
<i>S. agalactiae</i> OUGBS105	<i>S. agalactiae</i> GBS5	3	ND
<i>S. agalactiae</i> OUGBS105	<i>S. uberis</i> ZQ1	3	$1.27 \times 10^{-7} \pm 7.31 \times 10^{-8}$
<i>S. agalactiae</i> OUGBS105	<i>S. uberis</i> ZQ12	3	ND

^a, Transfer efficiency was calculated as the number of transconjugant CFU divided by the number of recipient CFU recovered on recipient-selective media. Values are presented as the mean $\pm$ SD from the indicated number of independent experiments. ND, no transconjugants detected.

Supplementary Table S14. Genome sequencing and assembly statistics for bacterial strains sequenced in this study.

Species	Strain	BioProject	BioSample	Accession number	Sequencer	Read configuration	Mean coverage (×)	Genome size (bp)	No. of contigs	N50 (bp)	G+C (%)
<i>S. uberis</i>	ZQ1	PRJDB35858	SAMD01607660	GCA_054095605.1	Illumina NextSeq 1000	2 × 150 bp	453.2	1,929,685	10	1,050,565	36.4
<i>S. uberis</i>	ZQ2	PRJDB35858	SAMD01607661	GCA_054095585.1	Illumina NextSeq 1000	2 × 150 bp	355.2	1,929,685	10	1,050,565	36.4
<i>S. uberis</i>	ZQ3	PRJDB35858	SAMD01607662	GCA_054095565.1	Illumina NextSeq 1000	2 × 150 bp	446.2	2,105,085	42	365,299	36.0
<i>S. uberis</i>	ZQ4	PRJDB35858	SAMD01607663	GCA_054095545.1	Illumina NextSeq 1000	2 × 150 bp	441.5	2,044,454	11	1,063,137	36.2
<i>S. uberis</i>	ZQ5	PRJDB35858	SAMD01607664	GCA_054095525.1	Illumina NextSeq 1000	2 × 150 bp	458.3	2,038,368	7	1,124,989	36.4
<i>S. uberis</i>	ZQ6	PRJDB35858	SAMD01607665	GCA_054095505.1	Illumina NextSeq 1000	2 × 150 bp	381.3	1,889,066	12	993,352	36.4
<i>S. uberis</i>	ZQ7	PRJDB35858	SAMD01607666	GCA_054095485.1	Illumina NextSeq 1000	2 × 150 bp	415.7	1,918,189	12	1,008,561	36.4
<i>S. uberis</i>	ZQ8	PRJDB35858	SAMD01607667	GCA_054095465.1	Illumina NextSeq 1000	2 × 150 bp	358.5	1,958,511	8	1,073,297	36.3
<i>S. uberis</i>	ZQ9	PRJDB35858	SAMD01607668	GCA_054095445.1	Illumina NextSeq 1000	2 × 150 bp	347.6	2,024,179	7	1,129,365	36.4
<i>S. uberis</i>	ZQ10	PRJDB35858	SAMD01607669	GCA_054095425.1	Illumina NextSeq 1000	2 × 150 bp	441.7	2,055,614	8	1,157,528	36.4
<i>S. uberis</i>	ZQ11	PRJDB35858	SAMD01607670	GCA_054095405.1	Illumina NextSeq 1000	2 × 150 bp	265.3	2,005,101	14	1,073,298	36.3
<i>S. uberis</i>	ZQ12	PRJDB35858	SAMD01607671	GCA_054095385.1	Illumina NextSeq 1000	2 × 150 bp	396.9	2,043,575	8	1,115,882	36.2
<i>S. uberis</i>	ZQ13	PRJDB35858	SAMD01607672	GCA_054095365.1	Illumina NextSeq 1000	2 × 150 bp	258.0	2,109,342	21	365,293	36.0
<i>S. uberis</i>	ZQ14	PRJDB35858	SAMD01607673	GCA_054095345.1	Illumina NextSeq 1000	2 × 150 bp	468.1	2,043,689	8	1,115,882	36.2
<i>S. uberis</i>	ZQ15	PRJDB35858	SAMD01607674	GCA_054095325.1	Illumina NextSeq 1000	2 × 150 bp	286.2	2,004,332	15	1,073,298	36.3
<i>S. uberis</i>	ZQ16	PRJDB35858	SAMD01607675	GCA_054095305.1	Illumina NextSeq 1000	2 × 150 bp	394.2	2,043,470	8	1,115,886	36.2
<i>S. uberis</i>	ZQ17	PRJDB35858	SAMD01607676	GCA_054095285.1	Illumina NextSeq 1000	2 × 150 bp	287.0	2,037,633	9	1,124,995	36.4
<i>S. uberis</i>	ZQ18	PRJDB35858	SAMD01607677	GCA_054095265.1	Illumina NextSeq 1000	2 × 150 bp	343.9	1,902,570	9	1,008,365	36.4
<i>S. uberis</i>	ZQ19	PRJDB35858	SAMD01607678	GCA_054095245.1	Illumina NextSeq 1000	2 × 150 bp	179.5	1,931,445	11	1,050,801	36.4
<i>S. uberis</i>	ZQ20	PRJDB35858	SAMD01607679	GCA_054095225.1	Illumina NextSeq 1000	2 × 150 bp	361.3	1,910,146	9	698,434	36.3
<i>S. uberis</i>	ZQ21	PRJDB35858	SAMD01607680	GCA_054095185.1	Illumina NextSeq 1000	2 × 150 bp	343.9	1,969,158	13	556,892	36.4
<i>S. uberis</i>	ZQ22	PRJDB35858	SAMD01607681	GCA_054095165.1	Illumina NextSeq 1000	2 × 150 bp	384.7	2,038,813	7	1,125,024	36.4
<i>S. uberis</i>	ZQ23	PRJDB35858	SAMD01607682	GCA_054095135.1	Illumina NextSeq 1000	2 × 150 bp	332.4	2,024,079	7	1,129,365	36.4
<i>S. uberis</i>	Hiro1	PRJDB35858	SAMD01607653	GCA_054094905.1	Illumina NextSeq 1000	2 × 150 bp	570.8	1,897,085	6	1,047,454	36.4
<i>S. uberis</i>	Hiro2	PRJDB35858	SAMD01607654	GCA_054094885.1	Illumina NextSeq 1000	2 × 150 bp	456.6	1,884,353	13	1,011,637	36.3

Genome size, number of contigs, N50, and G+C content were calculated using QUAST v5.2.0 with the default minimum contig length of 500 bp.

Supplementary Table S14. — *Continued.*

Species	Strain	BioProject	BioSample	Accession number	Sequencer	Read configuration	Mean coverage (×)	Genome size (bp)	No. of contigs	N50 (bp)	G+C (%)
<i>S. uberis</i>	Hiro3	PRJDB35858	SAMD01607655	GCA_054094865.1	Illumina NextSeq 1000	2 × 150 bp	386.2	2,024,579	14	367,023	36.5
<i>S. uberis</i>	Hiro4	PRJDB35858	SAMD01607656	GCA_054094845.1	Illumina NextSeq 1000	2 × 150 bp	420.3	2,066,571	7	1,067,351	36.3
<i>S. uberis</i>	Hiro5	PRJDB35858	SAMD01607657	GCA_054094825.1	Illumina NextSeq 1000	2 × 150 bp	413.7	2,081,050	7	1,122,940	36.4
<i>S. uberis</i>	Hiro6	PRJDB35858	SAMD01607658	GCA_054094805.1	Illumina NextSeq 1000	2 × 150 bp	390.6	2,061,396	8	1,161,468	36.4
<i>S. uberis</i>	Hiro7	PRJDB35858	SAMD01607659	GCA_054094785.1	Illumina NextSeq 1000	2 × 150 bp	267.3	2,061,388	8	1,161,469	36.4
<i>S. uberis</i>	ZQ-y1	PRJDB35858	SAMD01607683	GCA_054095085.1	Illumina NextSeq 1000	2 × 150 bp	1340.1	2,021,459	12	424,341	36.4
<i>S. uberis</i>	ZQ-y2	PRJDB35858	SAMD01607684	GCA_054095065.1	Illumina NextSeq 1000	2 × 150 bp	1512.0	1,966,053	14	1,088,239	36.4
<i>S. uberis</i>	ZQ-y3	PRJDB35858	SAMD01607685	GCA_054095045.1	Illumina NextSeq 1000	2 × 150 bp	1367.7	2,042,058	14	329,545	36.2
<i>S. uberis</i>	ZQ-y4	PRJDB35858	SAMD01607686	GCA_054095025.1	Illumina NextSeq 1000	2 × 150 bp	1294.9	2,099,077	13	1,119,950	36.3
<i>S. uberis</i>	ZQ-y5	PRJDB35858	SAMD01607687	GCA_054095005.1	Illumina NextSeq 1000	2 × 150 bp	1392.9	1,956,004	12	1,059,048	36.3
<i>S. uberis</i>	ZQ-y6	PRJDB35858	SAMD01607688	GCA_054094985.1	Illumina NextSeq 1000	2 × 150 bp	1202.7	1,997,951	9	1,059,139	36.4
<i>S. uberis</i>	ZQ-y7	PRJDB35858	SAMD01607689	GCA_054094965.1	Illumina NextSeq 1000	2 × 150 bp	1364.9	1,947,193	15	1,027,687	36.3
<i>S. agalactiae</i>	GBS26	PRJDB42709	SAMD01942124	BAALRJ000000000.1	DNBSEQ-G400RS	2 × 150 bp	374.96	2,107,944	32	124,073	35.4
<i>S. agalactiae</i>	GBS128	PRJDB42709	SAMD01942125	BAALRK000000000.1	DNBSEQ-G400RS	2 × 150 bp	1124.02	2,107,928	23	265,947	35.4
<i>S. agalactiae</i>	GBS184	PRJDB42709	SAMD01942126	BAALRL000000000.1	DNBSEQ-G400RS	2 × 150 bp	1880.81	2,125,462	26	265,419	35.4
<i>S. agalactiae</i>	OUGBS105	PRJDB42709	SAMD01942127	BAALRM000000000.1	DNBSEQ-G400RS	2 × 150 bp	796.12	2,090,713	51	101,958	35.5
<i>S. uberis</i>	H6-ZQ1	PRJDB42710	SAMD01942128	BAALRN000000000.1	DNBSEQ-G400RS	2 × 150 bp	599.3	1,951,670	11	1,116,483	36.5
<i>S. uberis</i>	ZQ9-ZQ1	PRJDB42710	SAMD01942129	BAALRO000000000.1	DNBSEQ-G400RS	2 × 150 bp	1887.85	1,951,501	12	1,116,484	36.5
<i>S. uberis</i>	ZQ22-ZQ1	PRJDB42710	SAMD01942130	BAALRP000000000.1	DNBSEQ-G400RS	2 × 150 bp	653.02	1,951,758	12	1,116,741	36.5
<i>S. uberis</i>	ZQ-y1-ZQ1	PRJDB42710	SAMD01942131	BAALRQ000000000.1	DNBSEQ-G400RS	2 × 150 bp	1829.73	1,961,225	12	1,126,208	36.5
<i>S. uberis</i>	ZQ-y4-ZQ1	PRJDB42710	SAMD01942132	BAALRR000000000.1	DNBSEQ-G400RS	2 × 150 bp	1388.86	1,992,443	10	1,122,810	36.4
<i>S. uberis</i>	H6-ZQ12	PRJDB42710	SAMD01942133	BAALRS000000000.1	DNBSEQ-G400RS	2 × 150 bp	308.72	2,113,826	9	1,181,929	36.2
<i>S. agalactiae</i>	H6-GBS3	PRJDB42710	SAMD01942134	BAALRT000000000.1	DNBSEQ-G400RS	2 × 150 bp	290.12	2,111,018	13	1,425,923	35.4
<i>S. agalactiae</i>	H6-GBS5	PRJDB42710	SAMD01942135	BAALRU000000000.1	DNBSEQ-G400RS	2 × 150 bp	337.59	2,125,403	20	397,676	35.4
<i>S. pyogenes</i>	H6-GAS5001	PRJDB42710	SAMD01942136	BAALRV000000000.1	DNBSEQ-G400RS	2 × 150 bp	903.74	1,869,582	28	132,256	38.3

Genome size, number of contigs, N50, and G+C content were calculated using QUAST v5.2.0 with the default minimum contig length of 500 bp.

Supplementary Table S14. — *Continued.*

Species	Strain	BioProject	BioSample	Accession number	Sequencer	Read configuration	Mean coverage (×)	Genome size (bp)	No. of contigs	N50 (bp)	G+C (%)
<i>S. pyogenes</i>	H6-GAS5006	PRJDB42710	SAMD01942137	BAALRW000000000.1	DNBSEQ-G400RS	2 × 150 bp	1246.63	1,824,004	14	268,890	38.3
<i>S. aureus</i>	H6-RN4220	PRJDB42710	SAMD01942138	BAALRX000000000.1	DNBSEQ-G400RS	2 × 150 bp	278.56	2,735,695	10	2,221,734	32.8
<i>S. agalactiae</i>	GBS3	PRJDB42710	SAMD01942139	BAALRY000000000.1	DNBSEQ-G400RS	2 × 150 bp	336.42	2,041,400	13	1,425,923	35.3
<i>S. agalactiae</i>	GBS5	PRJDB42710	SAMD01942140	BAALRZ000000000.1	DNBSEQ-G400RS	2 × 150 bp	317.83	2,054,865	18	397,676	35.4
<i>S. pyogenes</i>	GAS5001	PRJDB42710	SAMD01942141	BAALSA000000000.1	DNBSEQ-G400RS	2 × 150 bp	1086.26	1,802,914	27	132,256	38.3
<i>S. pyogenes</i>	GAS5006	PRJDB42710	SAMD01942142	BAALSB000000000.1	DNBSEQ-G400RS	2 × 150 bp	1287.02	1,753,944	12	275,362	38.4
<i>S. aureus</i>	RN4220	PRJDB42710	SAMD01942143	BAALSC000000000.1	DNBSEQ-G400RS	2 × 150 bp	503.62	2,669,884	12	1,351,840	32.7

Genome size, number of contigs, N50, and G+C content were calculated using QUAST v5.2.0 with the default minimum contig length of 500 bp.

Genome sequences have been submitted to DDBJ and are currently being registered in the NCBI Assembly database. The accession numbers shown are DDBJ WGS master accessions and will be updated to the corresponding GCA assembly accession numbers once available.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. uberis</i>	ZQ1	GCA_054095605.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ2	GCA_054095585.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ3	GCA_054095565.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ4	GCA_054095545.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ5	GCA_054095525.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ6	GCA_054095505.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ7	GCA_054095485.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ8	GCA_054095465.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ9	GCA_054095445.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ10	GCA_054095425.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ11	GCA_054095405.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ12	GCA_054095385.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ13	GCA_054095365.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ14	GCA_054095345.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ15	GCA_054095325.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ16	GCA_054095305.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ17	GCA_054095285.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ18	GCA_054095265.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ19	GCA_054095245.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ20	GCA_054095225.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ21	GCA_054095185.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ22	GCA_054095165.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	ZQ23	GCA_054095135.1	Cattle	Milk from mastitic udder	2018	Japan
<i>S. uberis</i>	Hiro1	GCA_054094905.1	Cattle	Milk from mastitic udder	2022	Japan
<i>S. uberis</i>	Hiro2	GCA_054094885.1	Cattle	Milk from mastitic udder	2022	Japan
<i>S. uberis</i>	Hiro3	GCA_054094865.1	Cattle	Milk from mastitic udder	2022	Japan
<i>S. uberis</i>	Hiro4	GCA_054094845.1	Cattle	Milk from mastitic udder	2023	Japan
<i>S. uberis</i>	Hiro5	GCA_054094825.1	Cattle	Milk from mastitic udder	2023	Japan
<i>S. uberis</i>	Hiro6	GCA_054094805.1	Cattle	Milk from mastitic udder	2023	Japan
<i>S. uberis</i>	Hiro7	GCA_054094785.1	Cattle	Milk from mastitic udder	2023	Japan
<i>S. uberis</i>	ZQ-y1	GCA_054095085.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y2	GCA_054095065.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y3	GCA_054095045.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y4	GCA_054095025.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y5	GCA_054095005.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y6	GCA_054094985.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	ZQ-y7	GCA_054094965.1	Cattle	Milk from mastitic udder	2025	Japan
<i>S. uberis</i>	0140J	GCF_000009545.1	Cattle	Bovine mastitis	2009	United Kingdom
<i>S. uberis</i>	S6261	GCF_000975325.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	C9359	GCF_000975335.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	Ab71	GCF_000975345.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	EF20/0145	GCF_000975355.1	Cattle	Milk from an udder	1970	United Kingdom
<i>S. uberis</i>	6780	GCF_000975405.1	Cattle	Milk from an udder	2000	United Kingdom
<i>S. uberis</i>	B362	GCF_000975415.1	Cattle	Milk from an udder	2000	United Kingdom
<i>S. uberis</i>	C6344	GCF_000975435.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	6736	GCF_000975445.1	Cattle	Milk from an udder	1999	United Kingdom
<i>S. uberis</i>	C5072	GCF_000975485.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	C8329	GCF_000975495.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	C5388	GCF_000975505.1	Cattle	Milk from an udder	2002	United Kingdom
<i>S. uberis</i>	B190	GCF_000975545.1	Cattle	Milk from an udder	2000	United Kingdom
<i>S. uberis</i>	NZ01	GCF_002814135.1	Cattle	N/A	2014	New Zealand
<i>S. uberis</i>	OLC4459-A20	GCF_009706695.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A21	GCF_009706705.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A19	GCF_009706755.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A17	GCF_009706785.1	Cattle	Milk	2017	Australia

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. uberis</i>	OLC4459-A14	GCF_009706805.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A18	GCF_009706815.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A16	GCF_009706825.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A15	GCF_009706845.1	Cattle	Milk	2017	Australia
<i>S. uberis</i>	OLC4459-A13	GCF_009706885.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	OLC4459-A12	GCF_009706895.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	OLC4459-A9	GCF_009706905.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	OLC4459-A11	GCF_009706935.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	OLC4459-A8	GCF_009706955.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	OLC4459-A4	GCF_009706985.1	Cattle	Milk	2013	Australia
<i>S. uberis</i>	OLC4459-A7	GCF_009706995.1	Cattle	Milk	2015	Australia
<i>S. uberis</i>	OLC4459-A6	GCF_009707015.1	Cattle	Milk	2014	Australia
<i>S. uberis</i>	OLC4459-A5	GCF_009707035.1	Cattle	Milk	2014	Australia
<i>S. uberis</i>	OLC4459-A3	GCF_009707045.1	Cattle	Milk	2013	Australia
<i>S. uberis</i>	OLC4459-A2	GCF_009707085.1	Cattle	Milk	2013	Australia
<i>S. uberis</i>	OLC4459-A1	GCF_009707105.1	Cattle	Milk	2010	Australia
<i>S. uberis</i>	OLC4459-A10	GCF_009807055.1	Cattle	Milk	2016	Australia
<i>S. uberis</i>	40717883	GCF_016113545.1	Cattle	Milk	2008	Canada
<i>S. uberis</i>	GCPRG127	GCF_016837285.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG125	GCF_016837305.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG126	GCF_016837325.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG124	GCF_016837345.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG123	GCF_016837365.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG121	GCF_016837385.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG120	GCF_016837405.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG122	GCF_016837425.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG118	GCF_016837445.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG115	GCF_016837455.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG114	GCF_016837485.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG113	GCF_016837505.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG112	GCF_016837525.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG110	GCF_016837545.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG111	GCF_016837565.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG101	GCF_016837585.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG119	GCF_016838345.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG117	GCF_016838365.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG116	GCF_016838375.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG109	GCF_016838425.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG108	GCF_016838445.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG106	GCF_016838465.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG107	GCF_016838485.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG105	GCF_016838495.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG104	GCF_016838525.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG103	GCF_016838545.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	GCPRG102	GCF_016838555.1	Cattle	Milk	2019	Australia
<i>S. uberis</i>	WY2	GCF_019794295.1	Cattle	N/A	2018	China
<i>S. uberis</i>	044	GCF_023060715.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	048	GCF_023060725.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	047	GCF_023060755.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	046	GCF_023060795.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	042	GCF_023060805.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	040	GCF_023060825.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	039	GCF_023060855.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	038	GCF_023060875.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	037	GCF_023060895.1	Sheep	Milk	2016	Italy

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. uberis</i>	035	GCF_023060915.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	026	GCF_023061875.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	020	GCF_023061935.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	019	GCF_023061955.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	012	GCF_023061975.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	018	GCF_023062005.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	011	GCF_023062075.1	Sheep	Milk	2014	Italy
<i>S. uberis</i>	002	GCF_023062135.1	Sheep	Milk	2011	Italy
<i>S. uberis</i>	015	GCF_023062215.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	014	GCF_023062235.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	025	GCF_023062295.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	034	GCF_023062315.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	016	GCF_023062355.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	004	GCF_023062395.1	Sheep	Milk	2012	Italy
<i>S. uberis</i>	017	GCF_023062425.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	030	GCF_023062455.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	024	GCF_023062475.1	Sheep	Milk	2016	Italy
<i>S. uberis</i>	005	GCF_023062495.1	Sheep	Milk	2013	Italy
<i>S. uberis</i>	023	GCF_023062515.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	013	GCF_023062535.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	022	GCF_023062555.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	021	GCF_023062565.1	Sheep	Milk	2015	Italy
<i>S. uberis</i>	23	GCF_023504065.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	20	GCF_023504085.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	22	GCF_023504105.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	24	GCF_023504115.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	21	GCF_023504135.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	19	GCF_023504165.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	18	GCF_023504175.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	15	GCF_023504185.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	16	GCF_023504215.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	17	GCF_023504225.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	12	GCF_023504265.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	14	GCF_023504285.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	13	GCF_023504295.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	09	GCF_023504325.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	11	GCF_023504335.1	Cattle	Cow udder	2016	Germany
<i>S. uberis</i>	08	GCF_023504365.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	03	GCF_023504385.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	05	GCF_023504395.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	06	GCF_023504405.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	04	GCF_023504445.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	02	GCF_023504465.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	01	GCF_023504495.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	10	GCF_023507605.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	07	GCF_023507665.1	Cattle	Cow udder	2019	Germany
<i>S. uberis</i>	BAU/MH/Bag-2002	GCF_024655465.1	Cattle	Milk	2019	Bangladesh
<i>S. uberis</i>	BAU/MH/Bag-2021	GCF_024655485.1	Cattle	Milk	2020	Bangladesh
<i>S. uberis</i>	BAU/MH/Bag-2053	GCF_024655505.1	Cattle	Milk	2020	Bangladesh
<i>S. uberis</i>	BAU/MH/Bag-2062	GCF_024655525.1	Cattle	Milk	2020	Bangladesh
<i>S. uberis</i>	BAU/MH/Bag-2055	GCF_024655535.1	Cattle	Milk	2020	Bangladesh
<i>S. uberis</i>	BR-MHR918	GCF_025801985.1	Cattle	Milk	2021	Bangladesh
<i>S. uberis</i>	BR-MHR841	GCF_027533805.1	Cattle	Milk	2021	Bangladesh
<i>S. uberis</i>	MOL	GCF_036348795.1	Cattle	Udder	2021	Russia
<i>S. uberis</i>	CH	GCF_036348975.1	Cattle	Udder	2021	Russia

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. uberis</i>	UB85	GCF_040361825.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB92	GCF_040361975.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB82	GCF_040362065.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB81	GCF_040364165.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB89	GCF_040366625.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB78	GCF_040370765.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB68	GCF_040370885.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB99	GCF_040371295.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB77	GCF_040371825.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	UB58	GCF_040372995.1	Cattle	Milk	2022	Japan
<i>S. uberis</i>	S1605_08	GCF_044430765.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1605_04	GCF_044430895.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1605_03	GCF_044431035.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1605_02	GCF_044431075.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1605_01	GCF_044431115.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_09	GCF_044432345.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_10	GCF_044432365.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_08	GCF_044432375.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_07	GCF_044432455.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_05	GCF_044432545.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_06	GCF_044432555.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_02	GCF_044432585.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_04	GCF_044432605.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_01	GCF_044434405.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1508_03	GCF_044434445.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_08	GCF_044435425.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_09	GCF_044435445.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_10	GCF_044435485.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_06	GCF_044435545.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_07	GCF_044435565.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_05	GCF_044435585.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_04	GCF_044435645.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_03	GCF_044435665.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_01	GCF_044435705.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	S1404_02	GCF_044435735.1	Cattle	Popliteal lymph node of steer	2022	Canada
<i>S. uberis</i>	CMU_AS584	GCF_045794675.1	Cattle	Milk	2019	Thailand
<i>S. uberis</i>	CMU_AS873	GCF_045794695.1	Cattle	Milk	2019	Thailand
<i>S. uberis</i>	CMU_AS303	GCF_045798785.1	Cattle	Milk	2019	Thailand
<i>S. uberis</i>	CMU_AS342	GCF_045987795.1	Cattle	Milk	2020	Thailand
<i>S. uberis</i>	CMU_AS442	GCF_045987885.1	Cattle	Milk	2020	Thailand
<i>S. uberis</i>	SD7	GCF_046098125.1	Cattle	Milk	2020	China
<i>S. uberis</i>	SX5-2	GCF_050606245.1	Cattle	Milk	2020	China
<i>S. uberis</i>	STU-BYS20b509	GCF_050686055.1	Cattle	Breast milk and teat skin	2020	China
<i>S. uberis</i>	STU-DXH20e472	GCF_050686195.1	Cattle	Breast milk and teat skin	2020	China
<i>S. uberis</i>	STU-QNE20c142	GCF_050686235.1	Cattle	Breast milk and teat skin	2020	China
<i>S. uberis</i>	STU-DXH20e457	GCF_050686295.1	Cattle	Breast milk and teat skin	2020	China
<i>S. uberis</i>	STU-MJD19e08	GCF_050686395.1	Cattle	Breast milk and teat skin	2019	China
<i>S. uberis</i>	STU-DXH20e399	GCF_050789305.1	Cattle	Breast milk and teat skin	2020	China
<i>S. uberis</i>	NCTC4673	GCF_900459985.1	Human	N/A	1935	United Kingdom
<i>S. uberis</i>	NCTC4672	GCF_900460135.1	Human	N/A	1935	United Kingdom
<i>S. uberis</i>	NCTC3858	GCF_900475595.1	N/A	N/A	1933	Austria
<i>S. uberis</i>	NCTC4674	GCF_900475695.1	Human	N/A	1932	United Kingdom
<i>S. agalactiae</i>	GBS26	BAALRJ000000000.1	Human	Vagina	2020	Japan
<i>S. agalactiae</i>	GBS128	BAALRK000000000.1	Human	Vagina	2020	Japan
<i>S. agalactiae</i>	GBS184	BAALRL000000000.1	Human	Vagina	2020	Japan

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. agalactiae</i>	OUGBS105	BAALRM000000000.1	Human	Blood	2025	Japan
<i>S. agalactiae</i>	2603V-R	GCF_000007265.1	Human	N/A	N/A	N/A
<i>S. agalactiae</i>	A909	GCF_000012705.1	Human	Umbilicus cultures	N/A	N/A
<i>S. agalactiae</i>	NEM316	GCF_000196055.1	Human	N/A	N/A	France
<i>S. agalactiae</i>	GD201008-001	GCF_000299135.1	Fish	Fish organ	2010	China
<i>S. agalactiae</i>	09mas018883	GCF_000427035.1	Cattle	Bovine milk	N/A	Sweden
<i>S. agalactiae</i>	ILRI005	GCF_000427075.1	Camel	Abscess lesion	N/A	Kenya
<i>S. agalactiae</i>	NGBS061	GCF_000730215.1	Human	N/A	2010	Canada
<i>S. agalactiae</i>	NGBS572	GCF_000730255.1	Human	N/A	2012	Canada
<i>S. agalactiae</i>	CNCTC_10-84	GCF_000782855.1	Human	N/A	N/A	USA
<i>S. agalactiae</i>	GBS6	GCF_000831105.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	GBS2-NM	GCF_000831125.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	GBS1-NY	GCF_000831145.1	N/A	Blood	2012	USA
<i>S. agalactiae</i>	SS1	GCF_001026925.1	Human	Blood	1992	USA
<i>S. agalactiae</i>	HN016	GCF_001190805.1	Fish	Brain	2011	China
<i>S. agalactiae</i>	YM001	GCF_001190825.1	Fish	Brain	2011	China
<i>S. agalactiae</i>	GX064	GCF_001190845.1	Fish	Brain	2011	China
<i>S. agalactiae</i>	H002	GCF_001190885.1	Human	Vagina	2011	China
<i>S. agalactiae</i>	GBS85147	GCF_001266635.1	Human	N/A	N/A	Brazil
<i>S. agalactiae</i>	SG-M1	GCF_001275545.2	Human	Blood	2015	Singapore
<i>S. agalactiae</i>	GBS_ST-1	GCF_001448985.1	Dog	Gumline	2015	USA
<i>S. agalactiae</i>	NGBS128	GCF_001552035.1	Human	N/A	2010	Canada
<i>S. agalactiae</i>	CU_GBS_08	GCF_001592385.1	Human	Blood	2008	Hong Kong
<i>S. agalactiae</i>	CU_GBS_98	GCF_001592425.1	Human	Cerebro-spinal fluid	1998	Hong Kong
<i>S. agalactiae</i>	FWL1402	GCF_001683515.1	Frog	N/A	2014	China
<i>S. agalactiae</i>	NGBS357	GCF_001712835.1	Human	N/A	2011	N/A
<i>S. agalactiae</i>	WC1535	GCF_001729925.2	Fish	N/A	2015	China
<i>S. agalactiae</i>	GBS-M002	GCF_001932715.1	Human	Cervix	2014	China
<i>S. agalactiae</i>	Sag158	GCF_002025005.1	Human	N/A	2014	China
<i>S. agalactiae</i>	Sag37	GCF_002025025.1	Human	N/A	2014	China
<i>S. agalactiae</i>	FDAARGOS_254	GCF_002073695.2	Human	Blood	2014	USA
<i>S. agalactiae</i>	CUGBS591	GCF_002197205.1	Human	Joint aspiration	2008	Hong Kong
<i>S. agalactiae</i>	SG-M50	GCF_002197245.1	Human	Blood	2013	Singapore
<i>S. agalactiae</i>	SG-M158	GCF_002197265.1	Human	Blood	2015	Singapore
<i>S. agalactiae</i>	SG-M29	GCF_002197285.1	Human	Blood	2012	Singapore
<i>S. agalactiae</i>	SG-M25	GCF_002197305.1	Human	Blood	2012	Singapore
<i>S. agalactiae</i>	SG-M8	GCF_002197325.1	Human	Blood	2011	Singapore
<i>S. agalactiae</i>	SG-M6	GCF_002197365.1	Human	Blood	2011	Singapore
<i>S. agalactiae</i>	SG-M4	GCF_002197385.1	Human	Blood	2011	Singapore
<i>S. agalactiae</i>	SG-M163	GCF_002197425.1	Human	Blood	2015	Singapore
<i>S. agalactiae</i>	874391	GCF_002289205.1	Human	Vagina	1992	Japan
<i>S. agalactiae</i>	SGEHI2015-107	GCF_002812425.1	N/A	Fish organ	2015	Singapore
<i>S. agalactiae</i>	SGEHI2015-95	GCF_002812445.1	N/A	Fish organ	2015	Singapore
<i>S. agalactiae</i>	SGEHI2015-25	GCF_002812465.1	N/A	Fish organ	2015	Singapore
<i>S. agalactiae</i>	SGEHI2015-113	GCF_002812505.1	N/A	Fish organ	2015	Singapore
<i>S. agalactiae</i>	B509	GCF_003287995.1	Human	Vagina	2016	China
<i>S. agalactiae</i>	B508	GCF_003288015.1	Human	Vagina	2016	China
<i>S. agalactiae</i>	B105	GCF_003288035.1	Human	Blood	2016	China
<i>S. agalactiae</i>	B507	GCF_003288055.1	Human	Vagina	2016	China
<i>S. agalactiae</i>	B111	GCF_003288075.1	Human	Blood	2016	China
<i>S. agalactiae</i>	S73	GCF_003319215.1	Fish	Brain	2016	Brazil
<i>S. agalactiae</i>	Sag27	GCF_003403115.1	Human	Perianal region	2018	China
<i>S. agalactiae</i>	FDAARGOS_512	GCF_003812805.1	Human	Endotracheal aspirate	2016	N/A
<i>S. agalactiae</i>	TFJ0901	GCF_003939065.1	Fish	N/A	2009	China
<i>S. agalactiae</i>	HU-GS5823	GCF_003966545.1	Human	N/A	2017	Japan

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Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. agalactiae</i>	32790-3A	GCF_006716245.1	Human	Blood	2016	China
<i>S. agalactiae</i>	PLGBS13	GCF_006874565.1	Human	Soft tissue wound	1997	Canada
<i>S. agalactiae</i>	FDAARGOS_669	GCF_008693505.1	Human	N/A	N/A	USA
<i>S. agalactiae</i>	FDAARGOS_670	GCF_008693585.1	Human	N/A	N/A	USA
<i>S. agalactiae</i>	BSE009	GCF_009866845.1	Human	N/A	N/A	N/A
<i>S. agalactiae</i>	YZ1605	GCF_009930895.1	Cattle	Bovine milk	2016	China
<i>S. agalactiae</i>	NJ1606	GCF_009930915.1	Cattle	Bovine milk	2016	China
<i>S. agalactiae</i>	ZQ0910	GCF_011383065.1	N/A	N/A	2010	China
<i>S. agalactiae</i>	Sag153	GCF_012222485.1	Human	Vagina	2017	China
<i>S. agalactiae</i>	515	GCF_012593885.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	1173	GCF_013000945.1	Fish	N/A	2001	Kuwait
<i>S. agalactiae</i>	S9968	GCF_013414325.1	Human	Urine	2013	South Korea
<i>S. agalactiae</i>	BJ01	GCF_013786965.1	Human	Blood	2017	China
<i>S. agalactiae</i>	GBS7	GCF_014218075.1	Human	Blood	1987	USA
<i>S. agalactiae</i>	GBS11	GCF_014218095.1	Human	Blood	1989	USA
<i>S. agalactiae</i>	GBS19	GCF_014218115.1	Human	Blood	1993	USA
<i>S. agalactiae</i>	GBS28	GCF_014218135.1	Human	Blood	1994	USA
<i>S. agalactiae</i>	GBS30	GCF_014218155.1	Human	Blood	1995	USA
<i>S. agalactiae</i>	CJB111	GCF_015221735.2	Human	Blood	1990	USA
<i>S. agalactiae</i>	SS1168	GCF_019552345.1	Human	N/A	1997	USA
<i>S. agalactiae</i>	MIN-181	GCF_021460175.1	Human	N/A	2019	United Kingdom
<i>S. agalactiae</i>	MIN-180	GCF_021460195.1	Human	N/A	2019	United Kingdom
<i>S. agalactiae</i>	SS114	GCF_021496805.1	Human	Blood	2007	USA
<i>S. agalactiae</i>	SS102	GCF_021496825.1	Human	Blood	2006	USA
<i>S. agalactiae</i>	SS44	GCF_021496845.1	Human	Blood	1999	USA
<i>S. agalactiae</i>	SS43	GCF_021496865.1	Human	Blood	1998	USA
<i>S. agalactiae</i>	GBS68	GCF_021496885.1	Human	Vagina	1993	Gambia
<i>S. agalactiae</i>	GBS20	GCF_021496905.1	Human	Blood	1993	USA
<i>S. agalactiae</i>	SS111	GCF_021496945.1	Human	Blood	2007	USA
<i>S. agalactiae</i>	GBS47	GCF_021496965.1	Human	Vagina	1993	Gambia
<i>S. agalactiae</i>	GCMC97051	GCF_021655535.1	Human	N/A	2018	Japan
<i>S. agalactiae</i>	AH2	GCF_024502145.1	Fish	Kidney	2000	Saudi Arabia
<i>S. agalactiae</i>	TAH_10-84	GCF_025402735.1	N/A	N/A	2019	USA
<i>S. agalactiae</i>	TAH_10-84_dUdp	GCF_025402755.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	TAH_10-84_dMrvR	GCF_025402775.1	N/A	N/A	2019	USA
<i>S. agalactiae</i>	SA5087	GCF_025808195.1	Human	Urine	2022	China
<i>S. agalactiae</i>	VSI63	GCF_029011195.1	Human	N/A	2021	USA
<i>S. agalactiae</i>	VSI15	GCF_029011635.1	Human	N/A	2020	USA
<i>S. agalactiae</i>	VSI14	GCF_029011675.1	Human	N/A	2020	USA
<i>S. agalactiae</i>	Guangzhou-SAG092	GCF_029278525.1	N/A	Blood	2018	China
<i>S. agalactiae</i>	Guangzhou-SAG036	GCF_029537275.1	N/A	Tryptic soy broth	2018	China
<i>S. agalactiae</i>	S5	GCF_029625255.1	N/A	N/A	2017	N/A
<i>S. agalactiae</i>	S1	GCF_029625275.1	N/A	N/A	2021	N/A
<i>S. agalactiae</i>	CS2108	GCF_029917085.1	Fish	N/A	2021	China
<i>S. agalactiae</i>	CNCTC_10-84_dCas9	GCF_030078235.1	N/A	N/A	2019	USA
<i>S. agalactiae</i>	A909_sCas9	GCF_030078255.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	A909_sCas9revertant	GCF_030078275.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	CNCTC_10-84_sCas9	GCF_030078295.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	CNCTC_10-84_sCas9revertant	GCF_030078315.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	A909_dCas9	GCF_030078335.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	CNCTC_10-84_Cas9_AEKOrevertant	GCF_030078355.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	CNCTC_10-84_Cas9_AEKO	GCF_030078375.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	A909_Cas9_AEKOrevertant	GCF_030078395.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	A909_Cas9_AEKO	GCF_030078415.1	N/A	N/A	2022	USA
<i>S. agalactiae</i>	GBSIR0001	GCF_030323365.1	Human	Spinal Fluid	2022	Japan

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. agalactiae</i>	COH1	GCF_030489705.1	Human	Blood	N/A	USA
<i>S. agalactiae</i>	BCJB4361	GCF_031202875.1	Human	Blood	2018	USA
<i>S. agalactiae</i>	BCJB3586	GCF_031202895.1	Human	Blood	2012	USA
<i>S. agalactiae</i>	BCJB3344	GCF_031203395.1	Human	Bone	2010	USA
<i>S. agalactiae</i>	BCJB3343	GCF_031203445.1	Human	Blood	2010	USA
<i>S. agalactiae</i>	BCJB1835	GCF_031203715.1	Human	Blood	2014	USA
<i>S. agalactiae</i>	Alim_agalac_1000	GCF_031584935.1	Fish	Fish organ	2020	Bangladesh
<i>S. agalactiae</i>	R31-snf2-MTase2	GCF_033798845.1	Human	Urine	2021	China
<i>S. agalactiae</i>	SagR92	GCF_033798865.1	Human	Urine	2021	China
<i>S. agalactiae</i>	SagR31	GCF_033798885.1	Human	Urine	2021	China
<i>S. agalactiae</i>	SagR40	GCF_033798905.1	Human	Urine	2021	China
<i>S. agalactiae</i>	R31-snf2	GCF_033798925.1	Human	Urine	2021	China
<i>S. agalactiae</i>	SagR272_TC	GCF_037242635.1	N/A	N/A	2021	China
<i>S. agalactiae</i>	SagR266	GCF_037248035.1	N/A	N/A	2021	China
<i>S. agalactiae</i>	SA2BKE	GCF_041728555.1	Fish	Fish organ	2009	Malaysia
<i>S. agalactiae</i>	GBS-B4009	GCF_041804565.1	Human	Blood	2022	China
<i>S. agalactiae</i>	HU05-19	GCF_046529645.1	Human	Urine	2019	Brazil
<i>S. agalactiae</i>	MA07	GCF_046529655.1	Human	Anal/vaginal	2021	Brazil
<i>S. agalactiae</i>	HU13-21	GCF_046529665.1	Human	Anal/vaginal	2021	Brazil
<i>S. agalactiae</i>	HU32-21	GCF_046529675.1	Human	Urine	2021	Brazil
<i>S. agalactiae</i>	HU36-21	GCF_046529685.1	Human	Anal/vaginal	2021	Brazil
<i>S. agalactiae</i>	MA15	GCF_046529705.1	Human	Anal/vaginal	2021	Brazil
<i>S. agalactiae</i>	M18	GCF_047783005.1	Human	Vagina	2021	China
<i>S. agalactiae</i>	M14	GCF_047783015.1	Human	Vagina	2021	China
<i>S. agalactiae</i>	161002207-5	GCF_049677795.1	Elephant	Mouth	2016	Germany
<i>S. agalactiae</i>	161002207-6	GCF_049678225.1	Elephant	Vagina	2016	Germany
<i>S. agalactiae</i>	AR977	GCF_049803895.1	Human	N/A	2013	USA
<i>S. agalactiae</i>	T44	GCF_050367445.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	765	GCF_051044175.1	Cattle	Bovine milk	2021	Brazil
<i>S. agalactiae</i>	MA12	GCF_051044185.1	Human	Tracheal aspirate	2021	Brazil
<i>S. agalactiae</i>	782	GCF_051045055.1	Cattle	Bovine milk	2021	Brazil
<i>S. agalactiae</i>	986	GCF_051045085.1	Cattle	Bovine milk	2021	Brazil
<i>S. agalactiae</i>	RAOG665	GCF_051546165.1	Human	Fetal cord blood	2023	Thailand
<i>S. agalactiae</i>	RAOG664	GCF_051546175.1	Human	Amniotic fluid	2023	Thailand
<i>S. agalactiae</i>	RAOG663	GCF_051546185.1	Human	Placenta	2023	Thailand
<i>S. agalactiae</i>	RAOG662	GCF_051546195.1	Human	Placenta	2023	Thailand
<i>S. agalactiae</i>	RAOG640	GCF_051546205.1	Human	Vagina	2024	Thailand
<i>S. agalactiae</i>	Sag105	GCF_052343055.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag149	GCF_052343185.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag28	GCF_052343195.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag58	GCF_052343385.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag56	GCF_052343395.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag-G044	GCF_052343525.1	Human	Vagina	2025	China
<i>S. agalactiae</i>	Sag-G052	GCF_052343535.1	Human	Vagina	2025	China
<i>S. agalactiae</i>	Sag-ZDN16	GCF_052343785.1	Human	Urine	2025	China
<i>S. agalactiae</i>	Sag-HS21-263	GCF_052343795.1	Human	BALF (Bronchoalveolar Lavage Fluid)	2025	China
<i>S. agalactiae</i>	Sag-ZDN19	GCF_052344085.1	Human	Urine	2025	China
<i>S. agalactiae</i>	SagR311-mut	GCF_052783735.1	N/A	N/A	2023	China
<i>S. agalactiae</i>	H11	GCF_053163275.1	Cattle	N/A	2021	China
<i>S. agalactiae</i>	SagR272	GCF_053503135.1	N/A	N/A	2023	China
<i>S. agalactiae</i>	A_SAG51	GCF_054401175.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG49	GCF_054401195.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG48	GCF_054401215.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG45	GCF_054401275.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG42	GCF_054401315.1	Cattle	Bovine milk	N/A	Italy

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Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. agalactiae</i>	A_SAG41	GCF_054401355.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG36	GCF_054401535.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG34	GCF_054401635.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG31	GCF_054401715.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG28	GCF_054401855.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG25	GCF_054401955.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG21	GCF_054402015.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG19	GCF_054402055.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG17	GCF_054402085.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG14	GCF_054402155.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG13	GCF_054402175.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	A_SAG2	GCF_054402495.1	Cattle	Bovine milk	N/A	Italy
<i>S. agalactiae</i>	Saf1689	GCF_054847945.1	Human	N/A	2019	USA
<i>S. agalactiae</i>	Sag1327	GCF_054847965.1	Human	N/A	2019	USA
<i>S. agalactiae</i>	HWI216	GCF_054881775.1	Human	Diabetic foot wound	2021	USA
<i>S. agalactiae</i>	SICAU_SA001	GCF_054952625.1	Fish	Kidney	2019	China
<i>S. agalactiae</i>	SA111	GCF_900078265.1	Cattle	Bovine milk	2013	Portugal
<i>S. agalactiae</i>	BM110	GCF_900155855.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	NCTC11930	GCF_900474905.1	N/A	N/A	1978-1980	Denmark
<i>S. agalactiae</i>	NCTC8187	GCF_900475355.1	N/A	N/A	N/A	N/A
<i>S. agalactiae</i>	NCTC8184	GCF_900636375.1	N/A	N/A	N/A	United Kingdom
<i>S. agalactiae</i>	NCTC13949	GCF_900638415.1	N/A	N/A	1900-2017	N/A
<i>S. agalactiae</i>	NCTC13947	GCF_900638495.1	N/A	N/A	1900-2017	N/A
<i>S. agalactiae</i>	MRI_Z2-336	GCF_947313835.2	Cattle	Bovine milk	2006	Sweden
<i>S. agalactiae</i>	MRI_Z2-265	GCF_949787155.1	Cattle	Bovine milk	1954	Sweden
<i>S. agalactiae</i>	MRI_Z2-329	GCF_949787645.1	Cattle	Bovine milk	2005	Sweden
<i>S. agalactiae</i>	MRI_Z2-322	GCF_949787715.1	Cattle	Bovine milk	2004	Sweden
<i>S. agalactiae</i>	MRI_Z2-174	GCF_949788565.1	Cattle	Bovine milk	2012	Sweden
<i>S. agalactiae</i>	MRI_Z2-286	GCF_949788745.1	Cattle	Bovine milk	1964	Sweden
<i>S. agalactiae</i>	MRI_Z2-335	GCF_949788775.1	Cattle	Bovine milk	2006	Sweden
<i>S. agalactiae</i>	MRI_Z2-318	GCF_949788785.1	Cattle	Bovine milk	2004	Sweden
<i>S. agalactiae</i>	MRI_Z2-304	GCF_949788915.1	Cattle	Bovine milk	1970	Sweden
<i>S. agalactiae</i>	MRI_Z2-179	GCF_949788925.1	Cattle	Bovine milk	2012	Sweden
<i>S. agalactiae</i>	MRI_Z2-328	GCF_949788935.1	Cattle	Bovine milk	2005	Sweden
<i>S. agalactiae</i>	MRI_Z2-158	GCF_949788945.1	Cattle	Bovine milk	2011	Sweden
<i>S. agalactiae</i>	MRI_Z2-299	GCF_949788975.1	Cattle	Bovine milk	1967	Sweden
<i>S. agalactiae</i>	MRI_Z2-342	GCF_949790125.1	Cattle	Bovine milk	2009	Sweden
<i>S. agalactiae</i>	MRI_Z2-172	GCF_949790945.1	Cattle	Bovine milk	2012	Sweden
<i>S. agalactiae</i>	MRI_Z2-307	GCF_949791205.1	Cattle	Bovine milk	1977	Sweden
<i>S. agalactiae</i>	MRI_Z2-338	GCF_949792585.1	Cattle	Bovine milk	2006	Sweden
<i>S. agalactiae</i>	MRI_Z2-149	GCF_949793775.1	Cattle	Bovine milk	2010	Sweden
<i>S. agalactiae</i>	MRI_Z2-270	GCF_951392265.1	Cattle	Bovine milk	1954	Sweden
<i>S. ruminantium</i>	GUT-187	GCF_003609975.1	Cattle	Hard palate (HPAL)	1991	Japan
<i>S. ruminantium</i>	MO492	GCF_009730935.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO505	GCF_009730955.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO533	GCF_009730975.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO402	GCF_009730995.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO430	GCF_009731015.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO449	GCF_009731035.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO498	GCF_009731055.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO512	GCF_009731075.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	MO557	GCF_009731095.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	DTK377	GCF_009731115.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	DAT837	GCF_009731135.1	Cattle	Bovine body	1992	Japan
<i>S. ruminantium</i>	DTK284	GCF_009731155.1	Cattle	Bovine body	2005	Japan

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. ruminantium</i>	DTK366	GCF_009731175.1	Cattle	Bovine body	2009	Japan
<i>S. ruminantium</i>	DTK285	GCF_009731195.1	Cattle	Bovine body	2011	Japan
<i>S. ruminantium</i>	MO591	GCF_009731215.1	Cattle	Bovine body	2013	Japan
<i>S. ruminantium</i>	DTK360	GCF_009731235.1	Cattle	Bovine body	2012	Japan
<i>S. ruminantium</i>	DTK397	GCF_009731255.1	Cattle	Bovine body	2014	Japan
<i>S. ruminantium</i>	DTK364	GCF_009731275.1	Cattle	Bovine body	2008	Japan
<i>S. ruminantium</i>	DAT741	GCF_009731295.1	Cattle	Bovine body	2011	Japan
<i>S. ruminantium</i>	DTK390	GCF_009731315.1	Cattle	Bovine body	2014	Japan
<i>S. ruminantium</i>	GUT-183	GCF_021654515.1	Cattle	N/A	2001	Japan
<i>S. ruminantium</i>	GUT-184	GCF_021654535.1	Cattle	N/A	2003	Japan
<i>S. ruminantium</i>	GUT-189	GCF_021654555.1	Cattle	N/A	N/A	Japan
<i>S. suis</i>	GZ1	GCF_000018185.1	Human	N/A	2005	China
<i>S. suis</i>	SC84	GCF_000026725.1	Human	N/A	2005	China
<i>S. suis</i>	BM407	GCF_000026745.1	Human	N/A	2004	Vietnam
<i>S. suis</i>	P1-7	GCF_000091905.1	Pig	Ante-mortem blood culture	N/A	N/A
<i>S. suis</i>	05HAS68	GCF_000168355.3	Pig	Tonsil of a healthy pig	2005	China
<i>S. suis</i>	JS14	GCF_000186405.1	Pig	Articulation of a diseased pig	N/A	China
<i>S. suis</i>	ST3	GCF_000204625.1	Pig	N/A	N/A	China
<i>S. suis</i>	SS12	GCF_000231865.1	N/A	N/A	N/A	China
<i>S. suis</i>	D9	GCF_000231885.1	N/A	N/A	N/A	China
<i>S. suis</i>	D12	GCF_000231905.1	N/A	N/A	N/A	China
<i>S. suis</i>	ST1	GCF_000231925.1	N/A	N/A	N/A	China
<i>S. suis</i>	A7	GCF_000233575.1	N/A	N/A	N/A	China
<i>S. suis</i>	S735	GCF_000294495.1	Pig	Pneumonia	N/A	Netherlands
<i>S. suis</i>	SC070731	GCF_000344765.1	Pig	Meningitis	2007	China
<i>S. suis</i>	TL13	GCF_000390245.1	Pig	N/A	N/A	China
<i>S. suis</i>	YB51	GCF_000471985.1	Pig	N/A	N/A	China
<i>S. suis</i>	6407	GCF_000732355.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	ZY05719	GCF_000993745.1	Pig	N/A	2005	China
<i>S. suis</i>	NSUI002	GCF_001272635.1	Pig	N/A	2008	Canada
<i>S. suis</i>	NSUI060	GCF_001572685.1	Pig	N/A	2008	Canada
<i>S. suis</i>	90-1330	GCF_001610935.1	Pig	N/A	1990	Canada
<i>S. suis</i>	DN13	GCF_001640765.1	Pig	N/A	2013	China
<i>S. suis</i>	GZ0565	GCF_001721625.1	Pig	Brain	2005	China
<i>S. suis</i>	SS2-1	GCF_001936415.1	N/A	N/A	1998	China
<i>S. suis</i>	SC19	GCF_002111405.1	Pig	N/A	2005	China
<i>S. suis</i>	LSM102	GCF_002189695.1	Human	N/A	2014	China
<i>S. suis</i>	SRD478	GCF_002285535.2	Pig	Nasal cavity	2011	USA
<i>S. suis</i>	ISU2812	GCF_002285735.2	Pig	Respiratory tract	2012	USA
<i>S. suis</i>	CS100322	GCF_002688665.1	Pig	N/A	2010	China
<i>S. suis</i>	HA0609	GCF_002736265.1	Pig	N/A	2006	China
<i>S. suis</i>	CZ130302	GCF_002803825.1	Pig	N/A	2013	China
<i>S. suis</i>	AH681	GCF_002812525.1	Pig	N/A	2007	China
<i>S. suis</i>	HN105	GCF_003144175.1	Pig	N/A	2016	N/A
<i>S. suis</i>	61	GCF_003285225.1	Pig	Tonsil scrape	2013	China
<i>S. suis</i>	1081	GCF_003285245.1	Pig	Tonsil scrape	2013	China
<i>S. suis</i>	SH0104	GCF_003288175.1	Pig	Lung	2016	China
<i>S. suis</i>	HA1003	GCF_003352205.1	Pig	Tonsil	2010	China
<i>S. suis</i>	SH1510	GCF_003352225.1	Pig	Lung	2015	China
<i>S. suis</i>	WUSS351	GCF_004843685.1	Pig	Tonsil	2017	China
<i>S. suis</i>	INT-01	GCF_007724845.1	Pig	N/A	2018	South Korea
<i>S. suis</i>	ISU1606	GCF_013488085.1	Pig	N/A	2010	USA
<i>S. suis</i>	ISU2514	GCF_013488105.1	Pig	Brain	2014	USA
<i>S. suis</i>	ISU2714	GCF_013488125.1	Pig	Brain	2014	USA
<i>S. suis</i>	ISU2414	GCF_013488145.1	Pig	Pericardium	2014	USA

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			Host	Isolation source	Year	Country
<i>S. suis</i>	ISU2614	GCF_013488165.1	Pig	Brain	2014	USA
<i>S. suis</i>	DAT299	GCF_014192345.1	Pig	N/A	N/A	N/A
<i>S. suis</i>	DAT300	GCF_014192525.1	Pig	N/A	N/A	N/A
<i>S. suis</i>	13-00283-02	GCF_014843075.1	Pig	Brain	2013	Germany
<i>S. suis</i>	LSM178	GCF_014874555.1	Human	N/A	2016	China
<i>S. suis</i>	YZDH1	GCF_015908885.1	Pig	N/A	2018	China
<i>S. suis</i>	YP20190405	GCF_015908985.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	ID33329	GCF_016774475.1	Human	Blood	2010	Thailand
<i>S. suis</i>	ID32098	GCF_016887735.2	Human	Blood	2010	Thailand
<i>S. suis</i>	1112S	GCF_017372155.1	Pig	N/A	2016	China
<i>S. suis</i>	39565	GCF_018885285.1	Human	Blood	2012	Thailand
<i>S. suis</i>	Colony132	GCF_019265165.1	N/A	Hemoculture	2019	Thailand
<i>S. suis</i>	Colony29	GCF_019265185.1	N/A	Rectal Swab	N/A	Thailand
<i>S. suis</i>	Colony133	GCF_019265205.1	N/A	Hemoculture	2019	Thailand
<i>S. suis</i>	ID41570	GCF_019297755.1	Human	Blood	2020	Thailand
<i>S. suis</i>	SS389	GCF_019856275.1	Pig	N/A	2018	China
<i>S. suis</i>	NJ3	GCF_019856315.1	Pig	N/A	2005	China
<i>S. suis</i>	FJSM5	GCF_019856335.1	Pig	N/A	2018	China
<i>S. suis</i>	Transconjugant_cNJ3	GCF_019856355.1	Laboratory	N/A	2020	China
<i>S. suis</i>	Transconjugant_cFJSM5	GCF_019856375.1	Laboratory	N/A	2020	China
<i>S. suis</i>	Transconjugant_cSS389	GCF_019856395.1	Laboratory	N/A	2020	China
<i>S. suis</i>	Transconjugant_cDY107	GCF_019856415.1	Laboratory	N/A	2020	China
<i>S. suis</i>	AKJ18	GCF_019856455.1	Pig	N/A	2016	China
<i>S. suis</i>	Transconjugant_cAKJ18	GCF_019856475.1	Laboratory	N/A	2020	China
<i>S. suis</i>	SZ1908	GCF_019967855.1	Human	Intestinal	2019	China
<i>S. suis</i>	GX69	GCF_020462325.1	Human	N/A	2016	China
<i>S. suis</i>	Ssuis_MA8	GCF_020541945.1	Pig	Tonsil	2016	Canada
<i>S. suis</i>	Ssuis_MA6	GCF_020541965.1	Pig	Brain/blood	2017	Netherlands
<i>S. suis</i>	Ssuis_MA2	GCF_020542025.1	Pig	Tonsil	2016	Canada
<i>S. suis</i>	Ssuis_MA1	GCF_020542045.1	Pig	Brain/blood	2014	Canada
<i>S. suis</i>	LSM29	GCF_021729385.1	Human	N/A	2013	China
<i>S. suis</i>	LSM157	GCF_021729405.1	Human	N/A	2016	China
<i>S. suis</i>	TJS75	GCF_022964955.1	Pig	N/A	2015	China
<i>S. suis</i>	TJS56	GCF_023023005.1	Pig	N/A	2014	China
<i>S. suis</i>	STC78	GCF_024206595.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC80	GCF_024206615.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC84	GCF_024206635.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC83	GCF_024206655.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC81	GCF_024206675.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC90	GCF_024206695.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC86	GCF_024206715.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC85	GCF_024206735.1	Human	Blood	2021	Thailand
<i>S. suis</i>	STC104	GCF_024206755.1	Human	Blood and CSF	2021	Thailand
<i>S. suis</i>	1521251	GCF_024220075.1	Pig	N/A	2013	Canada
<i>S. suis</i>	LSS42	GCF_024220115.1	Pig	N/A	2011	United Kingdom
<i>S. suis</i>	T15	GCF_024220135.1	N/A	N/A	N/A	Netherlands
<i>S. suis</i>	2018WUSS151	GCF_024498155.1	Pig	N/A	2018	China
<i>S. suis</i>	DE609B	GCF_024509515.2	Pig	Brain	2020	Germany
<i>S. suis</i>	12RC1	GCF_024582755.1	Pig	Tonsil swab	2018	Spain
<i>S. suis</i>	DNC49	GCF_024582915.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	M106471_S40	GCF_024582935.1	Pig	N/A	N/A	Spain
<i>S. suis</i>	M104300_S20	GCF_024582955.1	Pig	N/A	N/A	Spain
<i>S. suis</i>	M105052_S26	GCF_024582975.1	Pig	N/A	N/A	Spain
<i>S. suis</i>	M102942_S11	GCF_024582995.1	Pig	N/A	N/A	Spain
<i>S. suis</i>	DNR43	GCF_024583015.1	Pig	N/A	N/A	Denmark

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. suis</i>	DNR48	GCF_024583035.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	DNS20	GCF_024583055.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	DNC15	GCF_024583075.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	DNS11	GCF_024583115.1	Pig	N/A	N/A	Denmark
<i>S. suis</i>	SS15055_N2_C15	GCF_024583135.1	Pig	N/A	N/A	Spain
<i>S. suis</i>	89-1591	GCF_025723185.1	Pig	N/A	1989	Canada
<i>S. suis</i>	ID36054	GCF_025946865.1	Human	Blood	2011	Thailand
<i>S. suis</i>	TRG6	GCF_025946885.1	Pig	Lung	2010	Thailand
<i>S. suis</i>	ID38828	GCF_025946905.1	Human	Blood	2011	Thailand
<i>S. suis</i>	ID34572	GCF_025946925.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	ID35541	GCF_025946945.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	WUSS030	GCF_025980045.1	Pig	N/A	2017	China
<i>S. suis</i>	3112	GCF_029203915.2	Fish	Head kidney of the diseased fish	2021	Thailand
<i>S. suis</i>	Transconjugant_cAKJ47-2	GCF_029542025.1	N/A	N/A	2020	China
<i>S. suis</i>	Transconjugant_cSFJ45	GCF_029542065.1	N/A	N/A	2020	China
<i>S. suis</i>	SS-UPM-MY-F001	GCF_029542385.1	Cat	Oral cavity	2020	Malaysia
<i>S. suis</i>	NLS50	GCF_031767395.1	Pig	Brain	2017	Netherlands
<i>S. suis</i>	NLS40	GCF_031767605.1	Pig	Brain	2017	Netherlands
<i>S. suis</i>	1522228	GCF_031767625.1	Pig	Brain	2013	Canada
<i>S. suis</i>	TMW_SS028	GCF_031767645.1	Pig	Lungs	2013	United Kingdom
<i>S. suis</i>	PH2016-081	GCF_031875385.1	Pig	Lungs	2016	Germany
<i>S. suis</i>	M104170_C2	GCF_031875405.1	Pig	Tonsils	2017	Spain
<i>S. suis</i>	ID32563	GCF_032147025.1	Human	Blood	2010	Thailand
<i>S. suis</i>	ID24665	GCF_032147105.1	Human	Ascitic fluid	2007	Thailand
<i>S. suis</i>	ID26102	GCF_032230435.1	Pig	Tonsil	2008	Thailand
<i>S. suis</i>	ID34567	GCF_032230945.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	ID48908	GCF_032230965.1	Human	CSF	2014	Thailand
<i>S. suis</i>	1652329	GCF_032230985.1	Human	CSF	2014	Argentina
<i>S. suis</i>	1547095	GCF_032231005.1	Human	Joint fluid	2014	USA
<i>S. suis</i>	cnzyss2-311	GCF_034047115.1	Pig	Lung	2023	China
<i>S. suis</i>	Ss_134	GCF_034423895.1	Pig	N/A	2019	Spain
<i>S. suis</i>	Ss_109	GCF_034423915.1	Pig	N/A	2018	Spain
<i>S. suis</i>	Ss_48	GCF_034423935.1	Pig	Valencia	2018	Spain
<i>S. suis</i>	Ss_46	GCF_034423955.1	Pig	Murcia	2019	Spain
<i>S. suis</i>	Ss_45	GCF_034423975.1	Pig	N/A	2018	Spain
<i>S. suis</i>	Ss_22	GCF_034423995.1	Pig	Alava	2019	Spain
<i>S. suis</i>	Ss_21	GCF_034424015.1	Pig	N/A	2020	Spain
<i>S. suis</i>	Ss_08	GCF_034424035.1	Pig	N/A	2019	Spain
<i>S. suis</i>	2022WUSS148	GCF_034440185.1	Pig	Brain tissue	2022	China
<i>S. suis</i>	8324	GCF_035658235.1	Human	N/A	2023	Italy
<i>S. suis</i>	HB18	GCF_036320595.1	Pig	Throat swab	2023	China
<i>S. suis</i>	YA	GCF_037940715.1	Pig	Tissue	2022	China
<i>S. suis</i>	Ss2301	GCF_038650695.1	Human	N/A	2023	China
<i>S. suis</i>	MY1C3_3B	GCF_044361715.1	Pig	Tonsils	2016	Canada
<i>S. suis</i>	65555	GCF_045689715.1	Human	Cerebrospinal fluid	2023	Italy
<i>S. suis</i>	KKAHC02	GCF_046245185.1	Cattle	Placenta	2021	Canada
<i>S. suis</i>	HBXY-SL	GCF_048213105.1	Human	N/A	2020	China
<i>S. suis</i>	34391	GCF_049163785.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34410	GCF_049163795.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34550	GCF_049164385.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34558	GCF_049164415.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34562	GCF_049164905.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34566	GCF_049164955.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34684	GCF_049165385.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	34692	GCF_049165415.1	Pig	Tonsil	2011	Thailand

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Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. suis</i>	35538	GCF_049165925.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35539	GCF_049165935.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35540	GCF_049166465.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35542	GCF_049166495.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35543	GCF_049166525.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35544	GCF_049166535.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	35545	GCF_049166545.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	STC501	GCF_049166555.1	Pig	Oral	2022	Thailand
<i>S. suis</i>	STC516	GCF_049166565.1	Pig	Oral	2022	Thailand
<i>S. suis</i>	SC2022MYS167	GCF_051425555.1	Human	Blood	2022	China
<i>S. suis</i>	SS2413	GCF_052537815.1	Pig	Lung	2024	China
<i>S. suis</i>	SS2401	GCF_052537835.1	Pig	Lung	2024	China
<i>S. suis</i>	SS2422	GCF_052544955.1	Pig	Lung	2024	China
<i>S. suis</i>	SS2404	GCF_052625925.1	Pig	Lung	2024	China
<i>S. suis</i>	3453	GCF_053215895.1	Pig	Tonsil	2011	Thailand
<i>S. suis</i>	H CJ3	GCF_054906175.1	N/A	N/A	2021	China
<i>S. suis</i>	cH CJ3-PP1	GCF_054909155.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cH CJ3-PP2	GCF_054909585.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cH CJ3-PP3	GCF_054909595.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cH CJ3-PP4	GCF_054910245.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cSS389-2	GCF_054910295.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cSS389-3	GCF_054910945.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	cSS389-4	GCF_054910955.1	Laboratory	Laboratory	2023	China
<i>S. suis</i>	SC19_PBS1	GCF_054922615.1	Pig	N/A	2023	N/A
<i>S. suis</i>	SC19_Lys0859R1	GCF_054922755.1	Pig	N/A	2023	N/A
<i>S. suis</i>	1704A	GCF_055686205.1	Pig	Tonsil	2020	China
<i>S. suis</i>	1703A	GCF_055686225.1	Pig	Tonsil	2019	China
<i>S. suis</i>	1702I	GCF_055686245.1	Pig	Brain	2018	China
<i>S. suis</i>	1701V	GCF_055686265.1	Pig	Brain	2017	China
<i>S. suis</i>	LS9N	GCF_900143575.1	Human	Nasal Swabs	2021	USA
<i>S. suis</i>	NCTC10234	GCF_900475585.1	Pig	N/A	1961	United Kingdom
<i>S. suis</i>	NCTC10237	GCF_901543625.1	Pig	N/A	N/A	United Kingdom
<i>S. suis</i>	861160	GCF_902702745.1	Human	CSF or blood culture	1986	Netherlands
<i>S. suis</i>	S10	GCF_902702755.1	Pig	Tonsil	1982	Netherlands
<i>S. suis</i>	GD-0088	GCF_902702765.1	Pig	CSF or blood culture	2006	Netherlands
<i>S. suis</i>	9401240	GCF_902702775.1	Pig	CSF or blood culture	2006	Netherlands
<i>S. suis</i>	GD-0001	GCF_902702785.1	Pig	CSF or blood culture	1996	Netherlands
<i>S. suis</i>	861160_d xerD_hsdSA	GCF_947096915.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	861160_d xerD_hsdSE	GCF_947097575.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	861160_LM_H	GCF_947098765.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	861160_LM_A	GCF_947098835.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	861160_WT	GCF_947098855.1	N/A	N/A	N/A	N/A
<i>S. suis</i>	861160_d hsdS	GCF_947099305.1	N/A	N/A	N/A	N/A
<i>S. coagulans</i>	TA91	GCF_050328415.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	TA85	GCF_050328505.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	TA94	GCF_050328525.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	TA84	GCF_050328605.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	TA79	GCF_050328665.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	SI86	GCF_050328675.1	Dog	N/A	2018	Japan
<i>S. coagulans</i>	TA81	GCF_050328695.1	Dog	N/A	2019	Japan
<i>S. coagulans</i>	SI78	GCF_050328785.1	Dog	N/A	2018	Japan
<i>S. coagulans</i>	SI76	GCF_050328795.1	Dog	N/A	2018	Japan
<i>S. coagulans</i>	SI82	GCF_050328805.1	Dog	N/A	2018	Japan
<i>S. coagulans</i>	942	GCF_050328905.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	943	GCF_050328915.1	Dog	N/A	2020	Japan

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Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. coagulans</i>	938	GCF_050328985.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	937	GCF_050329025.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	936	GCF_050329035.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	908	GCF_050329105.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	907	GCF_050329145.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	906	GCF_050329185.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	905	GCF_050329235.1	Dog	N/A	2020	Japan
<i>S. coagulans</i>	DSM_6628	GCF_002901995.1	Dog	External auditory meatus with external ear otitis	1990	Germany
<i>S. coagulans</i>	1031373	GCF_022557115.1	Dog	Pus swab	2017	India
<i>S. coagulans</i>	1031336	GCF_022557135.1	Dog	Pus swab	2017	India
<i>S. coagulans</i>	NN-2474	GCF_031344205.1	Cat	N/A	2022	Russia
<i>S. coagulans</i>	NNSsch_2520	GCF_031583935.1	Dog	N/A	2022	Russia
<i>S. pyogenes</i>	MGAS8232	GCF_000007285.1	Human	N/A	1980	N/A
<i>S. pyogenes</i>	MGAS315	GCF_000007425.1	Human	N/A	1952	USA
<i>S. pyogenes</i>	Manfredo	GCF_000009385.1	Human	N/A	1994	USA
<i>S. pyogenes</i>	SSI-1	GCF_000011285.1	Human	N/A	N/A	Japan
<i>S. pyogenes</i>	MGAS10394	GCF_000011665.1	Human	N/A	1996	USA
<i>S. pyogenes</i>	MGAS5005	GCF_000011765.3	Human	N/A	1998	Canada
<i>S. pyogenes</i>	MGAS6180	GCF_000012165.2	Human	N/A	N/A	USA
<i>S. pyogenes</i>	MGAS9429	GCF_000013485.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	M49_591	GCF_000167435.2	Human	Skin infection	1986	N/A
<i>S. pyogenes</i>	Alab49	GCF_000230295.1	Human	Impetigo lesion	2008	USA
<i>S. pyogenes</i>	MGAS15252	GCF_000250905.1	Human	Soft tissue infection	N/A	Canada
<i>S. pyogenes</i>	MGAS1882	GCF_000250925.1	Human	N/A	2011	USA
<i>S. pyogenes</i>	HKU_QMH11M0907901	GCF_000275625.1	Human	Blood from scarlet fever outbreak	N/A	China
<i>S. pyogenes</i>	A20	GCF_000307535.1	Human	N/A	1994	Taiwan
<i>S. pyogenes</i>	M1_476	GCF_000349925.2	Human	N/A	N/A	Japan
<i>S. pyogenes</i>	HSC5	GCF_000422045.1	Human	N/A	N/A	USA
<i>S. pyogenes</i>	STAB1102	GCF_000732345.1	Human	N/A	N/A	France
<i>S. pyogenes</i>	STAB902	GCF_000732425.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	ATCC_19615	GCF_000743015.1	N/A	N/A	2012	N/A
<i>S. pyogenes</i>	M23ND	GCF_000756485.1	Human	N/A	2011	Japan
<i>S. pyogenes</i>	7F7	GCF_000767505.1	Human	N/A	2011	France
<i>S. pyogenes</i>	HKU360	GCF_000772185.1	Human	Throat swab	2009	Hong Kong
<i>S. pyogenes</i>	1E1	GCF_000772245.1	Human	N/A	N/A	France
<i>S. pyogenes</i>	AP1	GCF_000993765.1	Human	Blood	1971	Czech Republic
<i>S. pyogenes</i>	JRS4	GCF_001014285.1	Human	N/A	1971	N/A
<i>S. pyogenes</i>	D471	GCF_001014305.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NGAS743	GCF_001019635.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NGAS596	GCF_001019675.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NGAS327	GCF_001019695.1	Human	N/A	2009	N/A
<i>S. pyogenes</i>	M28PF1	GCF_001020185.2	Human	Vaginal swab	2010	France
<i>S. pyogenes</i>	STAB10015	GCF_001023495.1	Human	N/A	1995	N/A
<i>S. pyogenes</i>	H293	GCF_001039695.1	Human	N/A	2012	United Kingdom
<i>S. pyogenes</i>	HKU488	GCF_001051095.1	Human	N/A	N/A	Hong Kong
<i>S. pyogenes</i>	NGAS322	GCF_001267805.1	N/A	N/A	N/A	N/A
<i>S. pyogenes</i>	NGAS638	GCF_001267845.1	N/A	N/A	2014	N/A
<i>S. pyogenes</i>	FDAARGOS_149	GCF_001559175.2	Human	Peripheral blood	1967	USA
<i>S. pyogenes</i>	AP53	GCF_001620285.1	Human	Skin	2002	USA
<i>S. pyogenes</i>	MGAS11027	GCF_001635895.1	Human	Pharynx	1997	USA
<i>S. pyogenes</i>	MGAS23530	GCF_001635935.1	Human	Throat swab	2008	Italy
<i>S. pyogenes</i>	MGAS27061	GCF_001635975.1	Human	N/A	1990	USA
<i>S. pyogenes</i>	NS53	GCF_001638845.2	Human	Nonsterile tissues such as skin	2013	Australia
<i>S. pyogenes</i>	STAB13021	GCF_001640945.2	Human	N/A	2009	France

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	STAB09014	GCF_001678885.1	Human	N/A	1950	N/A
<i>S. pyogenes</i>	NCTC8198	GCF_002055535.1	Human	Throat	2014	United Kingdom
<i>S. pyogenes</i>	STAB14018	GCF_002163545.1	Human	Blood	2011	France
<i>S. pyogenes</i>	GURSA1	GCF_002236855.1	Human	N/A	1938	Russia
<i>S. pyogenes</i>	GUR	GCF_002236875.1	Human	N/A	2009	Russia
<i>S. pyogenes</i>	STAB090229	GCF_002238295.1	Human	N/A	2012	France
<i>S. pyogenes</i>	STAB120304	GCF_002238315.1	Human	Throat	1994	France
<i>S. pyogenes</i>	M3-b	GCF_002355175.1	Human	Human blood	2016	Japan
<i>S. pyogenes</i>	JMUB1235	GCF_002355815.1	Human	N/A	2017	Japan
<i>S. pyogenes</i>	HarveyGAS	GCF_002557755.1	Human	Wound	1997	USA
<i>S. pyogenes</i>	JS12	GCF_002844355.1	Human	CSF	2011	Israel
<i>S. pyogenes</i>	TJ11-001	GCF_003025365.1	Human	Swab throat	2016	China
<i>S. pyogenes</i>	NGAS979	GCF_003203475.1	Human	N/A	2014	N/A
<i>S. pyogenes</i>	DMG1800716	GCF_003352145.1	Human	Blood	2017	New Zealand
<i>S. pyogenes</i>	KS030	GCF_003609955.1	Human	Saliva	N/A	Japan
<i>S. pyogenes</i>	SASM4-Duke	GCF_003640605.1	Human	Blood	2011	USA
<i>S. pyogenes</i>	ABC020055975	GCF_003698205.1	Human	N/A	2016	N/A
<i>S. pyogenes</i>	FDAARGOS_534	GCF_003812645.1	Human	Endotracheal aspirate	2016	N/A
<i>S. pyogenes</i>	FDAARGOS_514	GCF_003812725.1	Human	Clinical isolate	N/A	N/A
<i>S. pyogenes</i>	Duke-Large	GCF_003814365.1	Human	Blood	N/A	USA
<i>S. pyogenes</i>	RLGH	GCF_003814385.1	Human	N/A	2005	USA
<i>S. pyogenes</i>	MGAS27961	GCF_004010855.1	Human	Normally sterile site	2009	USA
<i>S. pyogenes</i>	MGAS28085	GCF_004010875.1	Human	Normally sterile site	N/A	USA
<i>S. pyogenes</i>	CCUG_4207	GCF_004028355.1	Human	Throat swab	2013	United Kingdom
<i>S. pyogenes</i>	TSPY155	GCF_004123995.1	Human	Abscess (retropharyngeal)	2015	USA
<i>S. pyogenes</i>	TSPY556	GCF_004124015.1	Human	Abscess (lymph node)	2014	USA
<i>S. pyogenes</i>	TSPY453	GCF_004124075.1	Human	Cellulitis	2014	USA
<i>S. pyogenes</i>	TSPY208	GCF_004124115.1	Human	Pharyngeal	2013	USA
<i>S. pyogenes</i>	TSPY165	GCF_004124135.1	Human	Otitis media	2011	USA
<i>S. pyogenes</i>	M75	GCF_004135875.1	Human	Throat	1995	Australia
<i>S. pyogenes</i>	MGAS8347	GCF_004153945.1	Human	Normally sterile site	1998	Finland
<i>S. pyogenes</i>	MGAS10786	GCF_004153965.1	Human	Normally sterile site	1995	Canada
<i>S. pyogenes</i>	MGAS7914	GCF_004153985.1	Human	Normally sterile site	1994	Canada
<i>S. pyogenes</i>	MGAS7888	GCF_004154005.1	Human	Normally sterile site	2008	Canada
<i>S. pyogenes</i>	MGAS29409	GCF_004154025.1	Human	Normally sterile site	2010	Finland
<i>S. pyogenes</i>	MGAS29326	GCF_004154045.1	Human	Normally sterile site	2011	Finland
<i>S. pyogenes</i>	MGAS29284	GCF_004154065.1	Human	Normally sterile site	2012	Finland
<i>S. pyogenes</i>	MGAS28746	GCF_004154085.1	Human	Normally sterile site	2008	USA
<i>S. pyogenes</i>	MGAS28686	GCF_004154105.1	Human	Normally sterile site	2008	USA
<i>S. pyogenes</i>	MGAS28669	GCF_004154125.1	Human	Normally sterile site	2008	USA
<i>S. pyogenes</i>	MGAS28650	GCF_004154145.1	Human	Normally sterile site	2006	USA
<i>S. pyogenes</i>	MGAS28533	GCF_004154165.1	Human	Normally sterile site	2000	USA
<i>S. pyogenes</i>	MGAS28360	GCF_004154185.1	Human	Normally sterile site	1998	USA
<i>S. pyogenes</i>	MGAS28330	GCF_004154205.1	Human	Normally sterile site	2011	USA
<i>S. pyogenes</i>	MGAS28278	GCF_004154225.1	Human	Normally sterile site	2011	USA
<i>S. pyogenes</i>	MGAS28271	GCF_004154245.1	Human	Normally sterile site	1999	USA
<i>S. pyogenes</i>	MGAS28191	GCF_004154265.1	Human	Normally sterile site	2002	USA
<i>S. pyogenes</i>	MGAS11115	GCF_004154285.1	Human	Normally sterile site	2001	Finland
<i>S. pyogenes</i>	MGAS11108	GCF_004154305.1	Human	Normally sterile site	2015	Finland
<i>S. pyogenes</i>	MGAS29064	GCF_004154325.1	Human	Normally sterile site	2002	Finland
<i>S. pyogenes</i>	MGAS28386	GCF_004154345.1	Human	Normally sterile site	2010	USA
<i>S. pyogenes</i>	MGAS28078	GCF_004154365.1	Human	Normally sterile site	2000	USA
<i>S. pyogenes</i>	MGAS11052	GCF_004154385.1	Human	Normally sterile site	2000	Finland
<i>S. pyogenes</i>	MGAS10826	GCF_004154405.1	Human	Normally sterile site	2017	Canada
<i>S. pyogenes</i>	SP1336	GCF_004193935.1	Human	Throat	2006	Australia

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	emm57	GCF_005160445.1	Human	Skin	2014	Fiji
<i>S. pyogenes</i>	emm74	GCF_005160565.1	Human	Throat	2005	New Zealand
<i>S. pyogenes</i>	emmSTG866.1	GCF_005160785.1	Human	Soft tissue	2005	Kenya
<i>S. pyogenes</i>	emm55	GCF_005160925.1	Human	Skin	2006	Australia
<i>S. pyogenes</i>	emm105	GCF_005161125.1	Human	Skin	2003	Fiji
<i>S. pyogenes</i>	emm64.3	GCF_005161325.1	Human	Throat	2002	Brazil
<i>S. pyogenes</i>	emm78.3	GCF_005161465.1	Human	Throat	N/A	New Zealand
<i>S. pyogenes</i>	emm22.8	GCF_005161605.1	Human	Skin	1997	India
<i>S. pyogenes</i>	emm124	GCF_005161825.1	Human	Throat	1995	Australia
<i>S. pyogenes</i>	emm58	GCF_005161985.1	Human	Blood	2007	Australia
<i>S. pyogenes</i>	emm97.1	GCF_005162245.1	Human	Soft tissue	2005	Kenya
<i>S. pyogenes</i>	emm56	GCF_005162405.1	Human	Skin	2006	Australia
<i>S. pyogenes</i>	emm70	GCF_005162565.1	Human	Skin	2006	Fiji
<i>S. pyogenes</i>	emm93.4	GCF_005162725.1	Human	Skin	2005	Fiji
<i>S. pyogenes</i>	emm230	GCF_005162865.1	Human	Skin	2006	Australia
<i>S. pyogenes</i>	emm123	GCF_005163085.1	Human	Skin	1994	Fiji
<i>S. pyogenes</i>	emm54	GCF_005163245.1	Human	Skin	1999	Australia
<i>S. pyogenes</i>	emmNA	GCF_005163385.1	Human	Throat	2011	Australia
<i>S. pyogenes</i>	emm11	GCF_005163565.1	Human	Throat	1998	New Zealand
<i>S. pyogenes</i>	emm65	GCF_005163705.1	Human	Blood	1991	Kenya
<i>S. pyogenes</i>	emm75.1	GCF_005163865.1	Human	Skin	2006	Australia
<i>S. pyogenes</i>	emm89.14	GCF_005164025.1	Human	Skin	2005	Fiji
<i>S. pyogenes</i>	emm77	GCF_005164305.1	Human	Throat	N/A	Australia
<i>S. pyogenes</i>	emm1	GCF_005164585.1	Human	Blood	2006	India
<i>S. pyogenes</i>	emm25	GCF_005164705.1	Human	Skin	2014	Fiji
<i>S. pyogenes</i>	emm90.5	GCF_005164885.1	Human	Blood	2006	New Zealand
<i>S. pyogenes</i>	emm92	GCF_005165045.1	Human	Throat	2006	Fiji
<i>S. pyogenes</i>	emm100	GCF_005165265.1	Human	Blood	2013	Fiji
<i>S. pyogenes</i>	emm197	GCF_005165385.1	Human	Throat	2004	New Zealand
<i>S. pyogenes</i>	emm68.2	GCF_005222545.1	Human	Throat	N/A	Brazil
<i>S. pyogenes</i>	FDAARGOS_774	GCF_006364235.1	N/A	ATCC isolate	2010	USA
<i>S. pyogenes</i>	10-85	GCF_006740645.1	Human	Keratinized gingiva	N/A	Japan
<i>S. pyogenes</i>	FDAARGOS_668	GCF_008694005.1	Human	Clinical isolate	2013	USA
<i>S. pyogenes</i>	AUSMDU00010539	GCF_009664495.1	Human	N/A	2009	Australia
<i>S. pyogenes</i>	STAB09023	GCF_009738475.1	Human	Genital	2010	France
<i>S. pyogenes</i>	STAB10048	GCF_009738495.1	Human	Facial cutaneous	2008	France
<i>S. pyogenes</i>	1085	GCF_009832845.1	Human	Blood	2008	India
<i>S. pyogenes</i>	1040	GCF_011290565.1	Human	Throat	1988	India
<i>S. pyogenes</i>	MGAS2221	GCF_012572265.1	Human	N/A	2005	Australia
<i>S. pyogenes</i>	4063-05	GCF_013306985.1	Human	N/A	N/A	USA
<i>S. pyogenes</i>	NIH34	GCF_014191695.1	Human	N/A	N/A	Japan
<i>S. pyogenes</i>	NIH35	GCF_014191835.1	Human	N/A	2007	Japan
<i>S. pyogenes</i>	KUN-0012590	GCF_014192005.1	Human	N/A	2009	Japan
<i>S. pyogenes</i>	KUN-0014944	GCF_014192175.1	Human	N/A	1997	Japan
<i>S. pyogenes</i>	37-97S	GCF_014218015.1	Human	Oropharynx	1997	Brazil
<i>S. pyogenes</i>	37-97P	GCF_014218035.1	Human	Oropharynx	2001	Brazil
<i>S. pyogenes</i>	BSAC_bs192	GCF_014495925.1	Human	Blood	2006	United Kingdom
<i>S. pyogenes</i>	BSAC_bs1388	GCF_014495945.1	Human	Blood	2008	United Kingdom
<i>S. pyogenes</i>	BSAC_bs1802	GCF_014495965.1	Human	Blood	2002	United Kingdom
<i>S. pyogenes</i>	BSAC_bs472	GCF_014495985.1	Human	Blood	2020	United Kingdom
<i>S. pyogenes</i>	emm9ST603	GCF_016126835.1	Human	Bone	2015	Australia
<i>S. pyogenes</i>	iGAS426	GCF_016549335.1	Human	Blood	2018	United Kingdom
<i>S. pyogenes</i>	iGAS376	GCF_016549355.1	Human	Blood	2019	United Kingdom
<i>S. pyogenes</i>	iGAS391	GCF_016549375.1	Human	Blood	2018	United Kingdom
<i>S. pyogenes</i>	M11318	GCF_017132795.1	Human	Tissue	2020	Australia

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Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	M08500	GCF_017638465.1	Human	Blood culture	2018	Australia
<i>S. pyogenes</i>	TSPY1687	GCF_018140985.1	Human	Pharyngeal	2016	USA
<i>S. pyogenes</i>	TSPY806	GCF_019342845.1	Human	Cellulitis	2015	USA
<i>S. pyogenes</i>	TSPY637	GCF_019342865.1	Human	Throat	2014	USA
<i>S. pyogenes</i>	TSPY515	GCF_019342885.1	Human	Abscess (skin)	2006	USA
<i>S. pyogenes</i>	ABC245	GCF_019342905.1	Human	N/A	2006	USA
<i>S. pyogenes</i>	ABC221	GCF_019342925.1	Human	N/A	2005	USA
<i>S. pyogenes</i>	ABC208	GCF_019342945.1	Human	N/A	2005	USA
<i>S. pyogenes</i>	ABC199	GCF_019342965.1	Human	N/A	2004	USA
<i>S. pyogenes</i>	ABC157	GCF_019342985.1	Human	N/A	2004	USA
<i>S. pyogenes</i>	ABC155	GCF_019343005.1	Human	N/A	2003	USA
<i>S. pyogenes</i>	ABC122	GCF_019343025.1	Human	N/A	2000	USA
<i>S. pyogenes</i>	ABC76	GCF_019343045.1	Human	N/A	1998	USA
<i>S. pyogenes</i>	ABC25	GCF_019343065.1	Human	N/A	1997	USA
<i>S. pyogenes</i>	ABC3	GCF_019343085.1	Human	N/A	2015	USA
<i>S. pyogenes</i>	TSPY767	GCF_019448315.1	Human	Throat	2013	USA
<i>S. pyogenes</i>	TSPY141	GCF_020826915.1	Human	Throat	2013	USA
<i>S. pyogenes</i>	TSPY153	GCF_020826935.1	Human	Throat	2015	USA
<i>S. pyogenes</i>	TSPY764	GCF_020826955.1	Human	Throat	2014	USA
<i>S. pyogenes</i>	TSPY210	GCF_020826975.1	Human	Blood	2017	USA
<i>S. pyogenes</i>	TSPY1312	GCF_020826995.1	Human	Throat	2014	USA
<i>S. pyogenes</i>	TSPY416	GCF_020827015.1	Human	Skin	2017	USA
<i>S. pyogenes</i>	TSPY1309	GCF_020827035.1	Human	Skin	2017	USA
<i>S. pyogenes</i>	TSPY1349	GCF_020827055.1	Human	Throat	2016	USA
<i>S. pyogenes</i>	TSPY1026	GCF_020827075.1	Human	Skin	2013	USA
<i>S. pyogenes</i>	TSPY136	GCF_020827095.1	Human	Throat	2014	USA
<i>S. pyogenes</i>	TSPY383	GCF_020827115.1	Human	Throat	2014	USA
<i>S. pyogenes</i>	TSPY270	GCF_020827135.1	Human	Skin	2018	USA
<i>S. pyogenes</i>	SHZ-1	GCF_022494495.1	Human	Secretion	N/A	China
<i>S. pyogenes</i>	PartK-Spyogenes-RM8376	GCF_022869605.1	N/A	N/A	N/A	N/A
<i>S. pyogenes</i>	52SS1	GCF_022869745.1	Human	Oropharynx	1986	Saudi Arabia
<i>S. pyogenes</i>	MGAS270	GCF_023278205.1	Human	N/A	2021	USA
<i>S. pyogenes</i>	21SPY7071	GCF_023380045.1	Human	Cerebral abscess pus	2008	China
<i>S. pyogenes</i>	1095	GCF_028215815.1	N/A	Invasive	2019	India
<i>S. pyogenes</i>	SP1451	GCF_028370195.1	Human	Blood	2019	Australia
<i>S. pyogenes</i>	SP1450	GCF_028370215.1	Human	Blood	2019	Australia
<i>S. pyogenes</i>	SP1448	GCF_028370235.1	Human	Blood	2019	Australia
<i>S. pyogenes</i>	SP1426	GCF_028370255.1	Human	Throat	2019	Australia
<i>S. pyogenes</i>	SP1384	GCF_028370275.1	Human	Throat	2019	Australia
<i>S. pyogenes</i>	SP1380	GCF_028370295.1	Human	Throat	N/A	Australia
<i>S. pyogenes</i>	MGAS10870	GCF_028867825.1	N/A	N/A	2008	N/A
<i>S. pyogenes</i>	1039	GCF_029280505.1	Human	Throat	2000/2008	India
<i>S. pyogenes</i>	1042	GCF_029280565.1	Human	Skin sample	2008	India
<i>S. pyogenes</i>	1133	GCF_029280585.1	Human	Throat	2008	India
<i>S. pyogenes</i>	1004	GCF_029323775.1	Human	Skin	2002/2007	India
<i>S. pyogenes</i>	1044	GCF_029637645.1	Human	Skin sample	N/A	India
<i>S. pyogenes</i>	NV28	GCF_034430055.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NV27	GCF_034432415.1	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NV1	GCF_034434355.2	Human	N/A	N/A	N/A
<i>S. pyogenes</i>	NV6	GCF_034436135.1	Human	N/A	1942	N/A
<i>S. pyogenes</i>	11RS100	GCF_035918415.1	Human	N/A	1997	USA
<i>S. pyogenes</i>	SS1445	GCF_035918435.1	Human	N/A	1995	Brazil
<i>S. pyogenes</i>	SS1366	GCF_035918455.1	Human	N/A	1997	USA
<i>S. pyogenes</i>	2907-97	GCF_035918475.1	Human	N/A	1972	Brazil
<i>S. pyogenes</i>	D641	GCF_035918495.1	Human	N/A	1999	Trinidad and Tobago

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	6745-99	GCF_035918515.1	Human	N/A	1971	Brazil
<i>S. pyogenes</i>	A946	GCF_035918535.1	Human	N/A	1995	Trinidad and Tobago
<i>S. pyogenes</i>	CT95-157	GCF_035918555.1	Human	N/A	1990	USA
<i>S. pyogenes</i>	AW-534	GCF_035918575.1	Human	N/A	1999	Ethiopia
<i>S. pyogenes</i>	6702-99	GCF_035918595.1	Human	N/A	2022	USA
<i>S. pyogenes</i>	Spyo01	GCF_036347555.1	Human	Venous	2022	USA
<i>S. pyogenes</i>	Spyo06	GCF_036347575.1	Human	Venous	2023	USA
<i>S. pyogenes</i>	Spyo09	GCF_036347595.1	Human	Finger Flexor Tendon Sheath	2023	USA
<i>S. pyogenes</i>	Isolate_21	GCF_036353505.2	Human	oropharynx of 28-years-old male	2023	Italy
<i>S. pyogenes</i>	MGAS37856	GCF_038385395.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37835	GCF_038386885.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37830	GCF_038388625.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37827	GCF_038390225.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37824	GCF_038390915.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	318231	GCF_039619335.1	Human	Pleural aspirate	2017	Germany
<i>S. pyogenes</i>	8373-17	GCF_041071735.1	Human	Respiratory tract	2015	Poland
<i>S. pyogenes</i>	4958-15	GCF_041071845.1	Human	Respiratory tract	2014	Poland
<i>S. pyogenes</i>	1966-14	GCF_041072535.1	Human	Invasive	2011	Poland
<i>S. pyogenes</i>	9606-11	GCF_041072725.1	Human	Respiratory tract	2008	Poland
<i>S. pyogenes</i>	1510-08	GCF_041072835.1	Human	Respiratory tract	2008	Poland
<i>S. pyogenes</i>	997-08	GCF_041073745.1	Human	Respiratory tract	2003	Poland
<i>S. pyogenes</i>	1851-03	GCF_041074175.1	Human	Respiratory tract	2003	Poland
<i>S. pyogenes</i>	400-03	GCF_041074825.1	Human	Respiratory tract	2023	Poland
<i>S. pyogenes</i>	Isolate_34	GCF_041429915.1	Human	Pus from 33-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_35	GCF_041429935.1	Human	Blood from 34-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_31	GCF_041430105.1	Human	Pus from 39-years-old male	2024	Italy
<i>S. pyogenes</i>	Isolate_30	GCF_041430535.1	Human	Blood from 57-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_29	GCF_041430835.1	Human	Blood from 77-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_28	GCF_041430845.1	Human	CSF from 4-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_27	GCF_041430855.1	Human	Wound from 62-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_26	GCF_041430865.1	Human	Wound from 13-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_23	GCF_041430875.1	Human	Blood from 90-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_24	GCF_041430885.1	Human	Blood from 60-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_22	GCF_041430895.1	Human	Oropharynx from 51-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_20	GCF_041430905.1	Human	Blood from 76-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_17	GCF_041430925.1	Human	Blood from 40-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_16	GCF_041430935.1	Human	Blood from 67-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_11	GCF_041430945.1	Human	Wound from 83-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_10	GCF_041430965.1	Human	Genital from 30-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_9	GCF_041430975.1	Human	Genital from 59-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_8	GCF_041430985.1	Human	Oropharynx from 7-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_7	GCF_041430995.1	Human	Oropharynx from 24-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_6	GCF_041431005.1	Human	Blood from 41-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_4	GCF_041431015.1	Human	Oropharynx from 6-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_5	GCF_041431025.1	Human	Pus from 35-years-old male	2023	Italy

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Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	Isolate_3	GCF_041431035.1	Human	Oropharynx from 3-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_2	GCF_041431045.1	Human	Blood from 71-years-old female	2023	Italy
<i>S. pyogenes</i>	Isolate_1	GCF_041431055.1	Human	Pus from 21-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_32	GCF_041447185.1	Human	Wound from 6-years-old male	2023	Italy
<i>S. pyogenes</i>	Isolate_13	GCF_041447195.1	Human	Blood from 54-years-old male	2023	Italy
<i>S. pyogenes</i>	SF370	GCF_043231225.1	Human	N/A	2015	Germany
<i>S. pyogenes</i>	20154608	GCF_044360805.1	Human	Nonsterile wound	2021	USA
<i>S. pyogenes</i>	20200554	GCF_044360885.1	Human	Blood	2019	USA
<i>S. pyogenes</i>	20203206	GCF_044360945.1	Human	Blood	2018	USA
<i>S. pyogenes</i>	20192362	GCF_044361035.1	Human	Blood	2015	USA
<i>S. pyogenes</i>	20154051	GCF_044361075.1	Human	Nonsterile wound	2015	USA
<i>S. pyogenes</i>	20164915	GCF_044361135.1	Human	Deep tissue	2017	USA
<i>S. pyogenes</i>	20181688	GCF_044361195.1	Human	Blood	2018	USA
<i>S. pyogenes</i>	20185322	GCF_044361245.1	Human	Blood	2015	USA
<i>S. pyogenes</i>	20160179	GCF_044361285.1	Human	Blood	2023	USA
<i>S. pyogenes</i>	MGAS37817	GCF_045290375.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37822	GCF_045290385.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37823	GCF_045290395.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37829	GCF_045290405.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37837	GCF_045290415.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37843	GCF_045290435.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37844	GCF_045290545.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37850	GCF_045290615.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37857	GCF_045290705.1	Human	N/A	N/A	Iceland
<i>S. pyogenes</i>	MGAS38345	GCF_045290995.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	EMM113	GCF_045345455.1	Human	N/A	2023	N/A
<i>S. pyogenes</i>	MGAS37826	GCF_045690025.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37828	GCF_045690035.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37831	GCF_045690045.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37832	GCF_045690055.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37833	GCF_045690065.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37834	GCF_045690075.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37836	GCF_045690085.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37839	GCF_045690095.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37842	GCF_045690105.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37847	GCF_045690115.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37848	GCF_045690125.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37849	GCF_045690135.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37853	GCF_045690145.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37854	GCF_045690155.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37859	GCF_045690165.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37861	GCF_045690175.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37637	GCF_045690185.1	Human	N/A	2022	United Kingdom
<i>S. pyogenes</i>	MGAS37641	GCF_045690195.1	Human	N/A	2022	United Kingdom
<i>S. pyogenes</i>	MGAS37642	GCF_045690205.1	Human	N/A	2022	United Kingdom
<i>S. pyogenes</i>	MGAS37644	GCF_045690215.1	Human	N/A	2023	United Kingdom
<i>S. pyogenes</i>	MGAS37674	GCF_045690225.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	MGAS38289	GCF_045690235.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	MGAS38337	GCF_045690245.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	MGAS38343	GCF_045690255.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	MGAS38362	GCF_045690265.1	Human	N/A	2022	United Kingdom
<i>S. pyogenes</i>	DMG2301705	GCF_050823505.1	Human	Blood	2020	Australia
<i>S. pyogenes</i>	DMG2211972	GCF_050823515.1	Human	Blood	2021	Australia
<i>S. pyogenes</i>	DMG2301723	GCF_050824005.1	Human	Blood	2023	Australia

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	MGAS37816	GCF_051530245.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37815	GCF_051530255.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37814	GCF_051530265.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37813	GCF_051530275.1	Human	N/A	2023	Iceland
<i>S. pyogenes</i>	MGAS37812	GCF_051530285.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37810	GCF_051530295.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37809	GCF_051530305.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37808	GCF_051530315.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37807	GCF_051530325.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37806	GCF_051530335.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37805	GCF_051530345.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37804	GCF_051530355.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37803	GCF_051530365.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37802	GCF_051530375.1	Human	N/A	2022	Iceland
<i>S. pyogenes</i>	MGAS37800	GCF_051530385.1	Human	N/A	2010	Iceland
<i>S. pyogenes</i>	M5	GCF_051628085.1	Human	N/A	2025	Belgium
<i>S. pyogenes</i>	DJR5XW	GCF_055179635.1	Human	vulva	2014	USA
<i>S. pyogenes</i>	Carrier10	GCF_055361585.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier9	GCF_055361625.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier8	GCF_055361645.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier7	GCF_055361665.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier6	GCF_055361685.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier3	GCF_055361705.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier5	GCF_055361715.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier2	GCF_055361745.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Carrier1	GCF_055361765.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute43	GCF_055361785.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute37	GCF_055361805.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute27	GCF_055361825.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute26	GCF_055361835.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute25	GCF_055361865.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute21	GCF_055361885.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute17	GCF_055361905.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute15	GCF_055361925.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute14	GCF_055361945.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute12	GCF_055361965.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute11	GCF_055361975.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute9	GCF_055362005.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute8	GCF_055362025.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute6	GCF_055362045.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute5	GCF_055362065.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute2	GCF_055362085.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute4	GCF_055362105.1	Human	Throat swab	2014	USA
<i>S. pyogenes</i>	Acute1	GCF_055362125.1	Human	Throat swab	2023	USA
<i>S. pyogenes</i>	D58	GCF_055378755.1	Human	N/A	1951	USA
<i>S. pyogenes</i>	NCTC8225	GCF_900474455.1	N/A	N/A	1937	USA
<i>S. pyogenes</i>	NCTC5163	GCF_900474645.1	N/A	N/A	1974	United Kingdom
<i>S. pyogenes</i>	NCTC12059	GCF_900474745.1	N/A	N/A	1950	N/A
<i>S. pyogenes</i>	NCTC8314	GCF_900474765.1	N/A	N/A	1979	N/A
<i>S. pyogenes</i>	NCTC12066	GCF_900474775.1	N/A	N/A	1937	United Kingdom
<i>S. pyogenes</i>	NCTC5164	GCF_900474795.1	N/A	N/A	1950	United Kingdom
<i>S. pyogenes</i>	NCTC8300	GCF_900474815.1	Human	Throat	1988	N/A
<i>S. pyogenes</i>	NCTC12045	GCF_900474825.1	N/A	N/A	1981	N/A
<i>S. pyogenes</i>	NCTC12069	GCF_900474835.1	N/A	N/A	1972	United Kingdom
<i>S. pyogenes</i>	NCTC12057	GCF_900474845.1	N/A	N/A	1932	United Kingdom

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S15. List of bacterial genomes used in this study.

Species	Strain	Accession number	Description			
			Host	Isolation source	Year	Country
<i>S. pyogenes</i>	NCTC8328	GCF_900474855.1	Human	N/A	1972	N/A
<i>S. pyogenes</i>	NCTC12058	GCF_900474865.1	N/A	N/A	1986	United Kingdom
<i>S. pyogenes</i>	NCTC12046	GCF_900474885.1	N/A	N/A	1992	USA
<i>S. pyogenes</i>	NCTC12696	GCF_900474895.1	Human	Pharynx	1974	N/A
<i>S. pyogenes</i>	NCTC12048	GCF_900474915.1	N/A	N/A	1974	N/A
<i>S. pyogenes</i>	NCTC12050	GCF_900474925.1	N/A	N/A	1974	N/A
<i>S. pyogenes</i>	NCTC12047	GCF_900474935.1	N/A	N/A	1935	N/A
<i>S. pyogenes</i>	NCTC8316	GCF_900474945.1	Human	N/A	1950	N/A
<i>S. pyogenes</i>	NCTC8332	GCF_900474955.1	Human	N/A	1927	United Kingdom
<i>S. pyogenes</i>	NCTC8231	GCF_900474965.1	N/A	N/A	1965	N/A
<i>S. pyogenes</i>	NCTC12052	GCF_900474975.1	N/A	N/A	1972	N/A
<i>S. pyogenes</i>	NCTC12062	GCF_900475005.1	N/A	N/A	1982	United Kingdom
<i>S. pyogenes</i>	NCTC12064	GCF_900475035.1	N/A	N/A	1950	United Kingdom
<i>S. pyogenes</i>	NCTC8195	GCF_900475075.1	Human	N/A	1932	N/A
<i>S. pyogenes</i>	NCTC8324	GCF_900475085.1	Human	N/A	1933	United Kingdom
<i>S. pyogenes</i>	NCTC4001	GCF_900475105.1	N/A	N/A	1950	N/A
<i>S. pyogenes</i>	NCTC8326	GCF_900475115.1	N/A	N/A	1980	United Kingdom
<i>S. pyogenes</i>	NCTC12067	GCF_900475135.1	N/A	N/A	1981	N/A
<i>S. pyogenes</i>	NCTC12068	GCF_900475155.1	N/A	N/A	1951	N/A
<i>S. pyogenes</i>	NCTC8230	GCF_900475165.1	N/A	N/A	1967	USA
<i>S. pyogenes</i>	NCTC10876	GCF_900475175.1	Human	Foot Lesion	1973	N/A
<i>S. pyogenes</i>	NCTC10874	GCF_900475425.1	Human	N/A	1951	USA
<i>S. pyogenes</i>	NCTC8224	GCF_900475465.1	N/A	N/A	2015	N/A
<i>S. pyogenes</i>	NCTC13738	GCF_900475475.1	Human	Blood culture	1931	United Kingdom
<i>S. pyogenes</i>	NCTC8320	GCF_900475485.1	Human	N/A	2015	N/A
<i>S. pyogenes</i>	NCTC13742	GCF_900475495.1	Human	Blood culture	2015	United Kingdom
<i>S. pyogenes</i>	NCTC13743	GCF_900475525.1	Human	Blood culture	1966	United Kingdom
<i>S. pyogenes</i>	NCTC10880	GCF_900475565.1	Human	Throat	1942	Netherlands
<i>S. pyogenes</i>	NCTC8227	GCF_900475615.1	Human	Upper Respiratory Tract	1953	N/A
<i>S. pyogenes</i>	NCTC10085	GCF_900475645.1	Human	Throat	2013	United Kingdom
<i>S. pyogenes</i>	NCTC13744	GCF_900475705.1	Human	Blood culture	2015	United Kingdom
<i>S. pyogenes</i>	NCTC13736	GCF_900475765.1	Human	Blood culture	1968	United Kingdom
<i>S. pyogenes</i>	NCTC10877	GCF_900475785.1	Human	N/A	1931	USA
<i>S. pyogenes</i>	NCTC8304	GCF_900475795.1	N/A	Throat	2014	N/A
<i>S. pyogenes</i>	NCTC13739	GCF_900475865.1	Human	Blood culture	2012	United Kingdom
<i>S. pyogenes</i>	NCTC13737	GCF_900475875.1	Human	Knee aspirate	1981	United Kingdom
<i>S. pyogenes</i>	NCTC12044	GCF_900475925.1	N/A	N/A	2015	United Kingdom
<i>S. pyogenes</i>	NCTC13745	GCF_900475955.1	N/A	Blood culture	2015	United Kingdom
<i>S. pyogenes</i>	NCTC13751	GCF_900475985.1	Human	Blood culture	1952	United Kingdom
<i>S. pyogenes</i>	NCTC8370	GCF_900476015.1	N/A	N/A	2008	N/A
<i>S. pyogenes</i>	S119	GCF_900608505.1	Human	Blood culture	1994	France
<i>S. pyogenes</i>	5448	GCF_900619585.1	Human	Blood	2008	Canada
<i>S. pyogenes</i>	SP444	GCF_900619595.1	Human	Blood	2012	Australia
<i>S. pyogenes</i>	HKU419	GCF_900619605.1	Human	Throat	2010	China
<i>S. pyogenes</i>	PS003	GCF_900619615.1	Human	Urine	2010	Australia
<i>S. pyogenes</i>	PS006	GCF_900619625.1	Human	Urine	1934	Australia
<i>S. pyogenes</i>	NCTC8232	GCF_900636485.1	Human	N/A	1918	United Kingdom
<i>S. pyogenes</i>	NCTC8302	GCF_900636725.1	Human	Throat	1950	USA
<i>S. pyogenes</i>	NCTC8193	GCF_901472475.1	Human	N/A	N/A	United Kingdom
<i>S. pyogenes</i>	NCTC8318	GCF_901482645.1	Human	N/A	N/A	United Kingdom

Bacterial genomes sequenced in this study are indicated in red.

N/A. Data not available in the NCBI record.

Supplementary Table S16. Antimicrobial agents used in this study.

Antimicrobial agent ^a	Antimicrobial susceptibility testing		
	<i>S. uberis</i> isolates	Human-derived <i>S. agalactiae</i> isolates	Transconjugants
Penicillin G	Yes	Yes	-
Ampicillin	Yes	Yes	Yes
Amoxicillin	Yes	-	-
Amoxicillin/clavulanic acid	-	Yes	-
Ampicillin/sulbactam	-	Yes	-
Cefazolin	Yes	Yes	-
Cefotaxime	-	Yes	-
Ceftriaxone	-	Yes	-
Cefepime	-	Yes	-
Cefoperazone	Yes	-	-
Cefquinome	Yes	-	-
Ceftiofur	Yes	-	-
Imipenem	-	Yes	-
Meropenem	-	Yes	-
Azithromycin	-	Yes	-
Clarithromycin	-	Yes	-
Erythromycin	Yes	Yes	Yes
Clindamycin	-	Yes	-
Lincomycin	Yes	-	Yes
Erythromycin/clindamycin	-	Yes	-
Gentamicin	Yes	-	-
Streptomycin	-	-	Yes
Minocycline	-	Yes	-
Oxytetracycline	Yes	-	-
Tetracycline	-	-	Yes
Ciprofloxacin	Yes	-	-
Enrofloxacin	Yes	-	-
Levofloxacin	-	Yes	-
Sulfamethoxazole/trimethoprim	Yes	Yes	-
Vancomycin	-	Yes	-

^a, Antimicrobial agents are ordered according to antibiotic class.

“Yes” indicates that the antimicrobial agent was included in the corresponding antimicrobial susceptibility testing panel; “-” indicates that the antimicrobial agent was not tested.

Supplementary Table S17. PCR primers and cycling conditions used in this study.

Primer set	Primer name	Sequence (5'–3')	PCR target	Expected product size (bp)
P1	P1_cirICE_F	GTAGGTGGAGTTAATAGCGACGG	ICEtea circular junction	414
	P1_cirICE_R	CCCAAGGATAAAGGCAAGAAGAG		
P2	P2_cirICE_F	CCTGTTAATATGATCCTAGAAATTGGG	ICEtea circular junction	423
	P2_cirICE_R	GCGGTAATTCGTTTCATGATTGTCC		
P3	P1_cirICE_F	GTAGGTGGAGTTAATAGCGACGG	ICEtea circular junction	339
	P3_cirICE_R	GTCTACGCAGTCGACATCCAAAC		
P4	P4_cirICE_F	GGGAGATAGTGTGTTGGGAAGCAA	ICEtea circular junction	345
	P3_cirICE_R	GTCTACGCAGTCGACATCCAAAC		
P5	P5_cirICE_F	CCCTAGAAGAAGATGGTCAAATGATTA	ICEtea circular junction	309
	P3_cirICE_R	GTCTACGCAGTCGACATCCAAAC		
Pint	integrase_F	GGAACACAAGTAGGAAAGAGACAAG	Integrase gene	349
	integrase_R	CTACATCATAGTCATACCCCAAGC		
Pt	tetO_F	TGAAGCAAAAGGTTGGGCAGCAT	<i>tet(O)</i> gene	478
	tetO_R	ATATCACCAGAGCAGGCTGTATC		
Pe	ermB_F	CAGGTAACGTCTATTGAATTAGACAGT	<i>erm(B)</i> gene	247
	ermB_R	AGGTACGCTTGTAGAATCCTTCTTC		
Pa	aadE_F	CGGATATGGACAGCTTCACAAGT	<i>aadE</i> gene	361
	aadE_R	CGGCATAAGCCCTTTACTACATATG		

PCR cycling conditions were as follows: 40 cycles of denaturation at 98 °C for 10 s, annealing at 55 °C for 30 s, and extension at 72 °C for 40 s.