

## Supplementary Information

**Supplementary Table S1.** Type and origin of samples from which strains were isolated.

Sample Type	Number of Samples	Sample Source Location	Number of Isolates
Raw sheep's milk	74	New Zealand	293
Raw goat's milk	21	New Zealand	174
Raw cow's milk	9	Ireland	130
Other*	8	-	226

\* Unpasteurised sheep, goat, cow and buffalo cheeses, fresh honey, honeycomb, sheep faeces, and canine saliva samples.

**Supplementary Table S2.** Genomes of *Streptococcus equinus* used in pangenome analysis.

Organism Scientific Name	Organism Qualifier	Assembly Name	Assembly Accession	Source	Level	Size
<i>Streptococcus equinus</i>	strain: ATCC 700338	ASM14640v1	GCF_000146405.1	RefSeq	Scaffold	2083084
<i>Streptococcus equinus</i>	strain: ATCC 9812	ASM18726v1	GCF_000187265.1	RefSeq	Scaffold	1741734
<i>Streptococcus equinus</i>	strain: SN033	ASM42142v1	GCF_000421425.1	RefSeq	Contig	1843423
<i>Streptococcus equinus</i>	strain: B315	ASM42404v1	GCF_000424045.1	RefSeq	Scaffold	1786673
<i>Streptococcus equinus</i>	strain: 2B	ASM70210v1	GCF_000702105.1	RefSeq	Scaffold	1919820
<i>Streptococcus equinus</i>	strain: HC5	ASM73108v1	GCF_000731085.1	RefSeq	Scaffold	1846241
<i>Streptococcus equinus</i>	strain: ATCC 33317	ASM74719v1	GCF_000747195.1	RefSeq	Contig	1841890
<i>Streptococcus equinus</i>	strain: JB1	Streptococcus bovis JB1	GCF_000747205.1	RefSeq	Contig	1954216
<i>Streptococcus equinus</i>	strain: AG46	ASM96431v1	GCF_000964315.1	RefSeq	Contig	1930741
<i>Streptococcus equinus</i>	strain: ICDDR-B-NRC-S6	ASM148148v1	GCF_001481485.1	RefSeq	Contig	1849355
<i>Streptococcus equinus</i>	strain: FMD1	ASM452577v1	GCF_004525775.1	RefSeq	Contig	1935083
<i>Streptococcus equinus</i>	strain: NBRC 12057	ASM653894v1	GCF_006538945.1	RefSeq	Contig	1926856
<i>Streptococcus equinus</i>	strain: CNU 77-23	ASM975807v1	GCF_009758075.1	RefSeq	Complete Genome	1911874
<i>Streptococcus equinus</i>	strain: CNU G6	ASM975809v1	GCF_009758095.1	RefSeq	Complete Genome	1997064
<i>Streptococcus equinus</i>	strain: MDC1	ASM1404187v1	GCF_014041875.1	RefSeq	Complete Genome	1936555
<i>Streptococcus equinus</i>	strain: Colony399	ASM1690612v1	GCF_016906125.1	RefSeq	Chromosome	1904424
<i>Streptococcus equinus</i>	strain: C277	IMG-taxon 2623621021 annotated assembly	GCF_900099885.1	RefSeq	Scaffold	1825979
<i>Streptococcus equinus</i>	strain: GA-1	IMG-taxon 2593339267 annotated assembly	GCF_900100035.1	RefSeq	Contig	1799853
<i>Streptococcus equinus</i>	strain: MPR2	IMG-taxon 2651870307 annotated assembly	GCF_900100215.1	RefSeq	Scaffold	1863305

<i>Streptococcus equinus</i> strain: Sb05	IMG-taxon 2654588139 annotated assembly	GCF_900101445.1	RefSeq	Scaffold	1962621
<i>Streptococcus equinus</i> strain: Sb10	IMG-taxon 2654588134 annotated assembly	GCF_900101715.1	RefSeq	Contig	1887161
<i>Streptococcus equinus</i> strain: pGA-7	IMG-taxon 2608642168 annotated assembly	GCF_900102715.1	RefSeq	Scaffold	1797051
<i>Streptococcus equinus</i> strain: Sb09	IMG-taxon 2654588197 annotated assembly	GCF_900103355.1	RefSeq	Scaffold	2042259
<i>Streptococcus equinus</i> strain: Sb04	IMG-taxon 2651870306 annotated assembly	GCF_900104225.1	RefSeq	Contig	1875611
<i>Streptococcus equinus</i> strain: Sb17	IMG-taxon 2654588136 annotated assembly	GCF_900106895.1	RefSeq	Contig	1909978
<i>Streptococcus equinus</i> strain: Ye01	IMG-taxon 2654588209 annotated assembly	GCF_900109105.1	RefSeq	Contig	1931095
<i>Streptococcus equinus</i> strain: pR-5	IMG-taxon 2608642181 annotated assembly	GCF_900109395.1	RefSeq	Scaffold	1820620
<i>Streptococcus equinus</i> strain: H24	IMG-taxon 2654588151 annotated assembly	GCF_900109415.1	RefSeq	Scaffold	1875780
<i>Streptococcus equinus</i> strain: ES1	IMG-taxon 2623620585 annotated assembly	GCF_900110365.1	RefSeq	Scaffold	1827295
<i>Streptococcus equinus</i> strain: Sb18	IMG-taxon 2654588130 annotated assembly	GCF_900110845.1	RefSeq	Contig	1991056
<i>Streptococcus equinus</i> strain: MPR1	IMG-taxon 2651870309 annotated assembly	GCF_900110935.1	RefSeq	Scaffold	1864122
<i>Streptococcus equinus</i> strain: Sb13	IMG-taxon 2654588137 annotated assembly	GCF_900112385.1	RefSeq	Scaffold	1878198

<i>Streptococcus equinus</i> strain: MPR4	IMG-taxon 2654588204 annotated assembly	GCF_900113235.1	RefSeq	Scaffold	1912748
<i>Streptococcus equinus</i> strain: JB1	IMG-taxon 2593339156 annotated assembly	GCF_900114525.1	RefSeq	Scaffold	1967362
<i>Streptococcus equinus</i> strain: SI	IMG-taxon 2654588207 annotated assembly	GCF_900115895.1	RefSeq	Scaffold	1912510
<i>Streptococcus equinus</i> strain: Sb20	IMG-taxon 2654588135 annotated assembly	GCF_900115995.1	RefSeq	Scaffold	1894454
<i>Streptococcus equinus</i> strain: AR3	IMG-taxon 2654588192 annotated assembly	GCF_900199575.1	RefSeq	Contig	2021307
<i>Streptococcus equinus</i> strain: NCTC12969 42197_F02		GCF_900459295.1	RefSeq	Contig	1806069
<i>Streptococcus equinus</i> strain: NCTC10386 42912_H01		GCF_900459945.1	RefSeq	Contig	1759508
<i>Streptococcus equinus</i> strain: NCTC8140 42290_E02		GCF_900636465.1	RefSeq	Complete Genome	1873522
<i>Streptococcus equinus</i> strain: NCTC10389 42880_B01		GCF_900636565.1	RefSeq	Complete Genome	1781995
<i>Streptococcus equinus</i> strain: NCTC8133 42290_D02		GCF_901543475.1	RefSeq	Complete Genome	1867673
<i>Streptococcus equinus</i> isolate: MGYG-HGUT-01308	MGYG-HGUT-01308	GCF_902373735.1	RefSeq	Scaffold	1925187
<i>Streptococcus equinus</i> isolate: MGYG-HGUT-01363	MGYG-HGUT-01363	GCF_902374225.1	RefSeq	Scaffold	1741734

**Supplementary Table S3.** Nisin resistance protein sequences used in pan genome screen.

UniProt Entry	Entry Name	Protein names	Gene Names	Organism	Length
A0A0A0DLE3	A0A0A0DLE3_9STRE	Nisin-resistance protein	SSIN_0444	<i>Streptococcus sinensis</i>	314
A0A0G2Z1C9	A0A0G2Z1C9_STRAG	Nisin-resistance protein, putative	RDF_0967	<i>Streptococcus agalactiae</i>	117
A0A0G2Z5M0	A0A0G2Z5M0_STRAG	Nisin-resistance protein, putative	RDF_0966	<i>Streptococcus agalactiae</i>	179
A0A139P896	A0A139P896_9STRE	Nisin-resistance protein	STRDD11_00955	<i>Streptococcus sp. DD11</i>	315
A0A140UHB6	A0A140UHB6_STRAG	Putative nisin-resistance protein	SAL_1042	<i>Streptococcus agalactiae</i> 515	167
A0A1A9E115	A0A1A9E115_STRAG	Nisin-resistance protein, putative (Peptidase S41)	DK41_05165 NCTC8183_01371	<i>Streptococcus agalactiae</i>	320
A0A2X2M2N2	A0A2X2M2N2_STRAG	Nisin-resistance protein, putative (Peptidase S41)	D5F95_09920 NCTC8181_02301 NCTC8185_02307	<i>Streptococcus agalactiae</i>	320
A0A2X3VPC5	A0A2X3VPC5_STRSA	Nisin resistance protein	NCTC11085_01675	<i>Streptococcus sanguinis</i>	336
A0A2X3YJM2	A0A2X3YJM2_STRSA	Nisin resistance protein	NCTC11086_00744	<i>Streptococcus sanguinis</i>	336
A0A380IMG6	A0A380IMG6_STRAG	Nisin-resistance protein, putative	NCTC6175_01352	<i>Streptococcus agalactiae</i>	320
A0A380JWG9	A0A380JWG9_STRDY	Nisin-resistance protein	nsr NCTC4670_00790	<i>Streptococcus dysgalactiae subsp. dysgalactiae</i>	321
A0A380KH18	A0A380KH18_STREQ	Nisin-resistance protein	nsr NCTC11564_00976	<i>Streptococcus dysgalactiae subsp. equisimilis</i> ( <i>Streptococcus equisimilis</i> )	321
A0A380L0L5	A0A380L0L5_9STRE	Nisin resistance protein	NCTC13765_01951	<i>Streptococcus massiliensis</i>	159
A0A380M477	A0A380M477_9STRE	Putative nisin-resistance protein	NCTC1080_00568	<i>Streptococcus viridans</i>	313
A0A448DKR6	A0A448DKR6_STREQ	Nisin-resistance protein	nsr NCTC6181_01847	<i>Streptococcus dysgalactiae subsp. equisimilis</i> ( <i>Streptococcus equisimilis</i> )	321
A0A4U9YX70	A0A4U9YX70_STREQ	Nisin-resistance protein	nsr NCTC6407_00995	<i>Streptococcus dysgalactiae subsp. equisimilis</i> ( <i>Streptococcus equisimilis</i> )	321
A0A4V0C1Q5	A0A4V0C1Q5_STRCB	Nisin-resistance protein	nsr NCTC6198_01136 TANIYAMA4_0743	<i>Streptococcus canis</i>	320

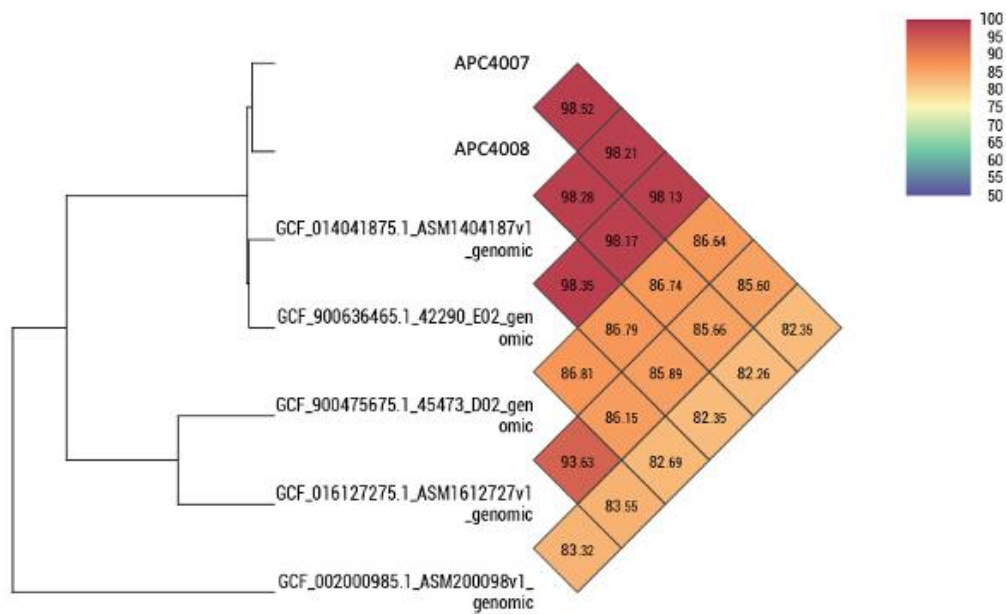
UniProt Entry	Entry Name	Protein names	Gene Names	Organism	Length
A0A4V0CQZ6	A0A4V0CQZ6_STRDY	Nisin-resistance protein	nsr NCTC7982_01632	<i>Streptococcus dysgalactiae</i>	321
A0A509DCT4	A0A509DCT4_9STRE	Nisin-resistance protein	nsr NCTC11567_01111	<i>Streptococcus sp.</i> NCTC 11567	321
A0A8B4IQF1	A0A8B4IQF1_STRUB	Nisin-resistance protein	nsr NCTC3858_01034	<i>Streptococcus uberis</i>	320
A0A8B6LB27	A0A8B6LB27_STREQ	Nisin-resistance protein (Peptidase S41)	nsr BBG08_07485 NCTC11557_01376	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> ( <i>Streptococcus equisimilis</i> )	321
A3CPD7	A3CPD7_STRSV	Nisin resistance protein, putative	SSA_1656	<i>Streptococcus sanguinis</i> (strain SK36)	336
E6J086	E6J086_STRAP	Nisin-resistance protein	nsr HMPREF0813_00656	<i>Streptococcus anginosus</i> F0211	317
F0FC69	F0FC69_STRSA	Nisin-resistance protein	nsr HMPREF9388_0252	<i>Streptococcus sanguinis</i> SK353	336
F0FT01	F0FT01_STRSA	Nisin-resistance protein	nsr HMPREF9392_1733	<i>Streptococcus sanguinis</i> SK678	336
F0I2W2	F0I2W2_STRSA	Nisin resistance protein	HMPREF9381_1502	<i>Streptococcus sanguinis</i> SK72	336
F0I5L0	F0I5L0_STRSA	Nisin resistance protein	HMPREF9382_0164	<i>Streptococcus sanguinis</i> SK115	314
F0IL53	F0IL53_STRSA	Nisin resistance protein	HMPREF9383_0855	<i>Streptococcus sanguinis</i> SK150	336
F0IWA8	F0IWA8_STRSA	Nisin resistance protein	HMPREF9384_2120	<i>Streptococcus sanguinis</i> SK160	336
F2BQW8	F2BQW8_STRSA	Nisin resistance protein	HMPREF9394_0793	<i>Streptococcus sanguinis</i> SK1057	336
F2C524	F2C524_STRSA	Nisin resistance protein	HMPREF9386_0177	<i>Streptococcus sanguinis</i> SK330	336
F2CCD0	F2CCD0_STRSA	Nisin resistance protein	HMPREF9391_0158	<i>Streptococcus sanguinis</i> SK408	336
F3SGA9	F3SGA9_STRSA	Nisin resistance protein	HMPREF9397_0181	<i>Streptococcus sanguinis</i> SK1087	336
F3U958	F3U958_STRSA	Nisin resistance protein	HMPREF9393_0161	<i>Streptococcus sanguinis</i> SK1056	336
F3UTK7	F3UTK7_STRSA	Nisin resistance protein	HMPREF9389_2165	<i>Streptococcus sanguinis</i> SK355	336
F3UW53	F3UW53_STRSA	Nisin resistance protein	HMPREF9380_0741	<i>Streptococcus sanguinis</i> SK49	336
M4YXC9	M4YXC9_STREQ	Putative nisin-resistance protein	GGs_0959	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> RE378	321
Q8DZX2	Q8DZX2_STRAS	Nisin-resistance protein, putative	SAG0973	<i>Streptococcus agalactiae</i> serotype V (strain ATCC BAA-611 / 2603 V/R)	320

**Supplementary Data S4.** Nisin immunity protein sequences used in pan genome screen.

UniProt Entry	Entry Name	Protein Name	Gene Name	Organism	Length
P42708	NISI_LACLL	Nisin immunity protein	<i>nisI</i>	<i>Lactococcus lactis</i> subsp. <i>lactis</i> ( <i>Streptococcus lactis</i> )	245 AA
Q2QBS6	Q2QBS6_STRUB	NsuI	<i>nsuI</i>	<i>Streptococcus uberis</i>	238 AA
A0A6C0GXF1	A0A6C0GXF1_9STRE	Immunity protein NspI	<i>nspI</i>	<i>Streptococcus gallolyticus</i>	238 AA
B5MEU0	B5MEU0	Immunity protein	<i>niqI</i>	<i>Lactococcus lactis</i>	238 AA
Q45403	Q45403_BACIU	SpaI	<i>spaI</i>	<i>Bacillus subtilis</i>	165 AA
A0A286N5V2	A0A286N5V2_9FIRM	NsoI	<i>nsol</i>	<i>Blautia obeum</i>	278 AA
-	-	NseI	<i>nseI</i>	<i>Streptococcus equinus</i>	245 AA

**Supplementary Table S5.** Nucleotide accessions containing nisin operon sequences

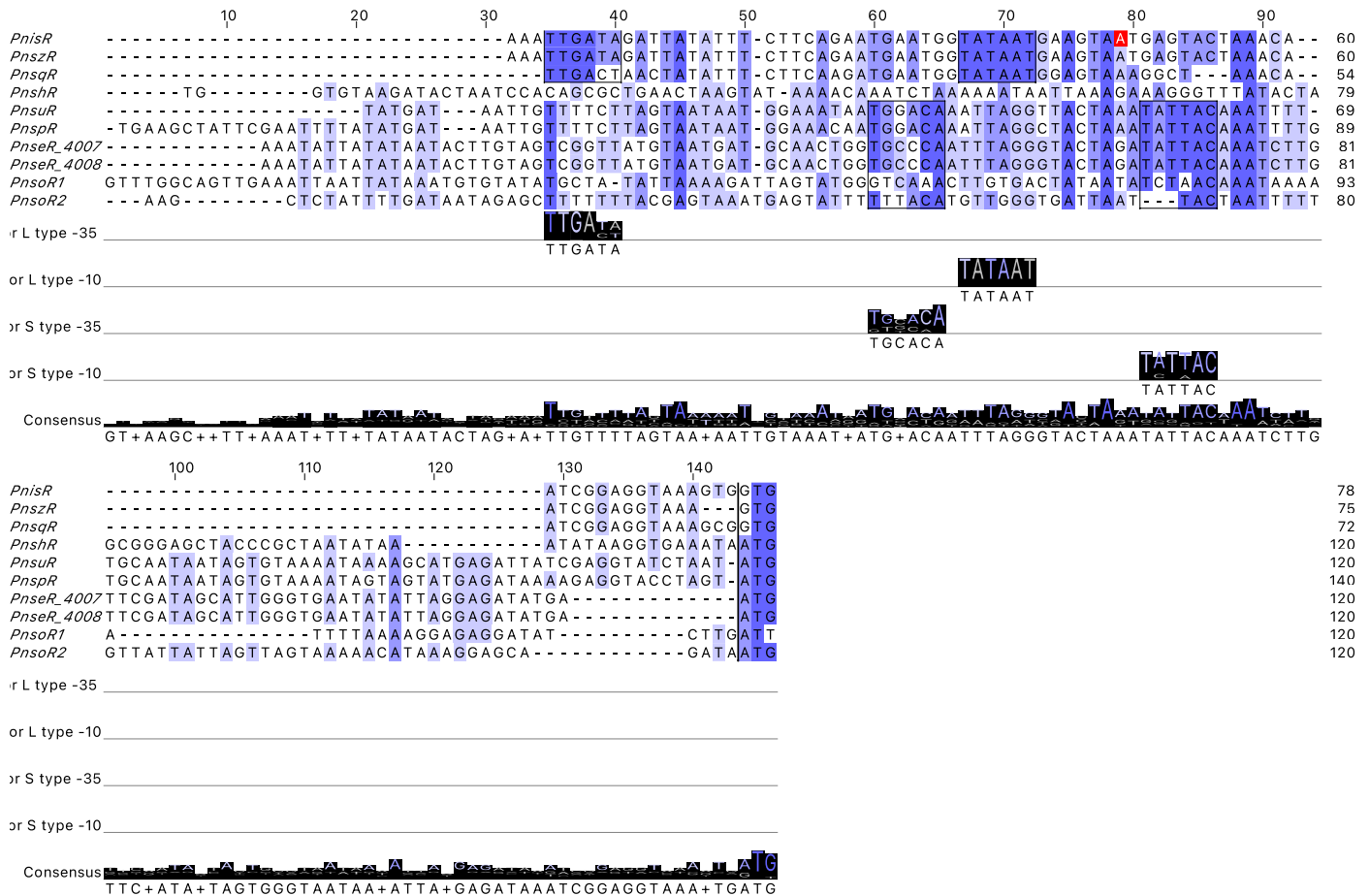
Species	Strain	Nisin Variant	NCBI Genome Accession	Assembly level
<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC11454	A	*	Contig
<i>Lactococcus lactis</i> subsp. <i>lactis</i>	IO-1	Z	AP012281	Complete genome
<i>Lactococcus lactis</i>	61-64	Q	AB362350	Contig
<i>Streptococcus hyointestinalis</i>	DPC6484	H	KP793707	Contig
<i>Streptococcus agalactiae</i>	DPC7040	P	WIDP01000009	Contig
<i>Streptococcus uberis</i>	42	U	DQ146939	Contig
<i>Staphylococcus capitis</i>	APC2923	J	MN602039	Contig
<i>Blautia obeum</i>	A2-162	O	KY914474	Contig
<i>Streptococcus equinus</i>	APC4007	E	JANHMF000000000	Contig
<i>Streptococcus equinus</i>	APC4008	E	JANHME000000000	Contig
*Accessed from <a href="http://genomes.atcc.org/">genomes.atcc.org/</a>				



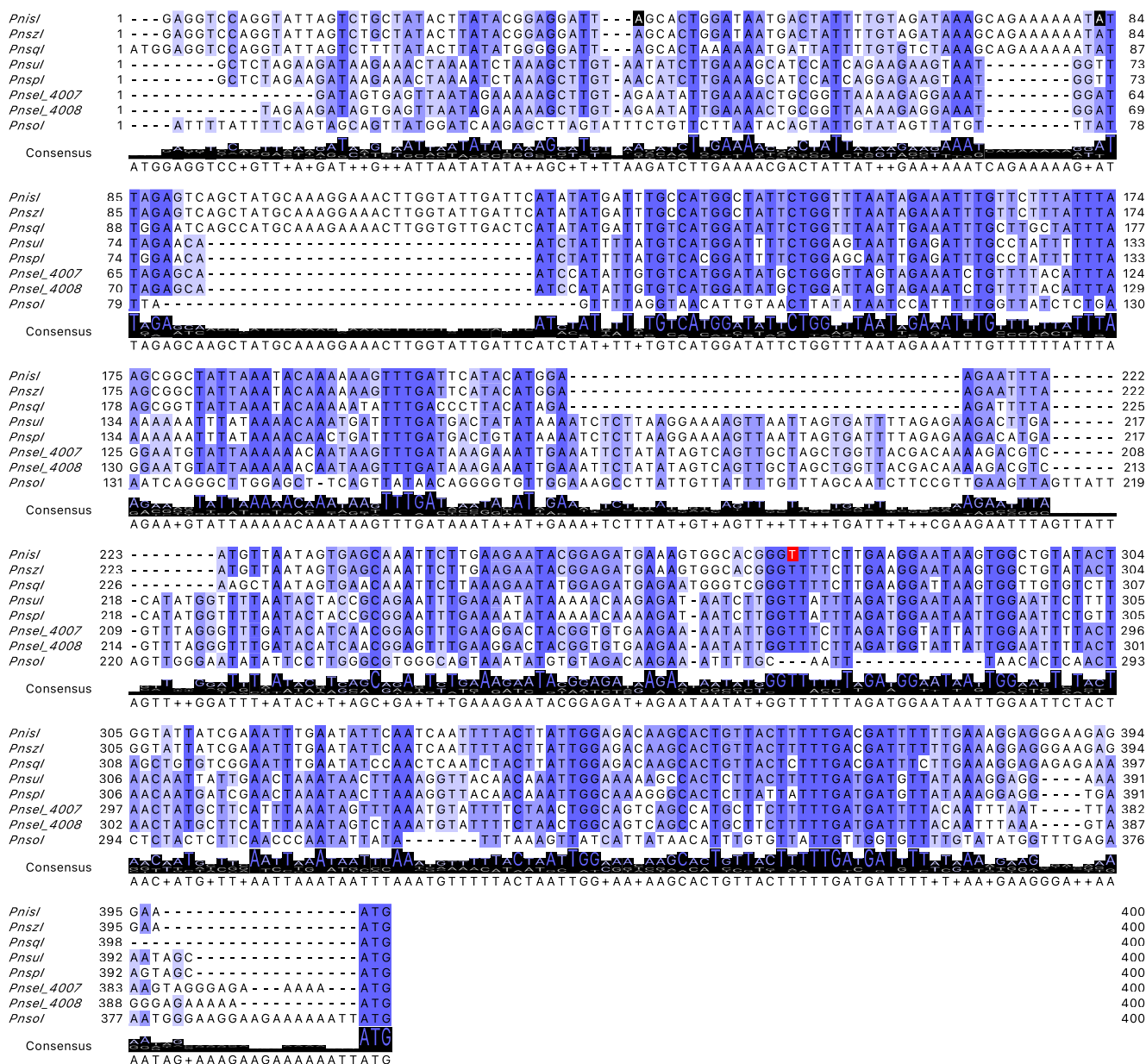
**Supplementary Figure S1.** Phylogram and genome average nucleotide identity (ANI) *S. equinus* APC4007 and *S. equinus* APC4008 compared with related *Streptococcus* spp. of the SBSEC. ANI values were calculated and visualised using OrthoANI<sup>1</sup>.







**Supplementary Figure S3.** Nucleotide sequence alignment of intergenic region upstream of *nisR* and homologous genes. Putative *Lactococcus* (L type) and *Streptococcus* (S type)-35 and -10 signals, ribosome binding sites and start codons are boxed with consensus sequences displayed below the alignment. Previously identified transcription start site (+1) highlighted in red. Nucleotides coloured by conservation.



**Supplementary Figure S4.** Nucleotide sequence alignment of 400bp region upstream of *nisI* and homologous genes. Nucleotides coloured by conservation. Previously identified transcription start site (+1) highlighted in red. -234 and -194 nucleotides are highlighted in black.

**Supplementary Table S6.** ARNold predicted forward strand terminators from nisin variant operons.

#### Nisin A

Total number of predicted transcription terminators: 8

- 173 Both + AACCAAATCAAAGGATAGTATTTTGTAGTTCAGACATGGATACTATCCTaTTTTTATAAGTTA -7.90
- 3773 Rnamotif + CATGGAACATTGGGGTAGCAATTTTACTCCTTATTGTTCCAG -6.70
- 11173 Both + AAAAAATAAAAAAGTAATTTAGTAATCTCTAAGGATTACTTTTTTTGTTTCTG -3.40
- 13661 Erpin + ACAATGAAAAATCCAAGTATAAATACTTGGATTTTTCATTATTT -8.90

#### Nisin Z

Total number of predicted transcription terminators: 8

173 Both + AACCAAATCAAAGGATAGTATTTTGTAGTTCAGACATGGATACTATCCTaTTTTTATAAGTTA -7.90  
 3773 Rnamotif + CATGGAACATTGGGGTAGCAATTTTACTCCTTATTGTTCCAG -6.70  
 11173 Both + AAAAATAAAAAAGTAATTTAGTAATCTCTAAGGATTACTTTTTTTGTTTCTG -3.40  
 13661 Erpin + ACAATGAAAAATCCAAGTATAAATACTTGGATTTTTCATTATTT -8.90

#### Nisin Q

Total number of predicted transcription terminators: 2

344 Both + AACCAAATCAAAGGATAGTATTTTGTGACTTAGGTAAAGATACTATCCTaTTTTTATAAGTTA -7.90  
 3943 Rnamotif + CATGGAACATTGGAGTAGCATTTTTACTCCTTATTGTTCCAA -7.60

#### Nisin U

Total number of predicted transcription terminators: 7

1591 Rnamotif + TCCATTTCAACTCCTAAAGTCTCTGCAGCTTTGGGATTGATTATAGAA -7.70  
 3810 Erpin + AAAATTTTCAGAGGTAGCAACTAGAAAGTAATGCTACCTTTTTTCTGAACAA -10.30  
 6053 Both + ACAAGCAAAACACTTCTGTTGAAATCTAGTAAACTAGAAACAGGAGTaTTTTGTTATGGTC -6.80  
 7070 Rnamotif + GTTAAAATAAAGGTAGTGGATAGATAGCTTGCTACCTTTATTTTTATA -6.70  
 13995 Both + AATTTAGAACAGCAAGTTCAGGAGAGTTTGCTATTTTTTTGTCA -5.60  
 14922 Erpin + TTCATACAAACTGCCCTCCTATTATTAGATTTTATGTCTAACAATAGGAGGGCagTTCAAAGTGAATT -13.90

#### Nisin P

Total number of predicted transcription terminators: 5

1263 Both + CAATTTGACTCCTAAAGTCTCTGCAGCTTTAGGaTTGATTATAGAA -8.80  
 3514 Erpin + ATAAACAAAACCGCATGAAATCTTTCATTAAAAACGTTGATTTTATGCGaTTTTTTATTTCTGA -6.80  
 6429 Both + GCTAAAATAAAGGTAGTGGATAGTAGTCTACTACCTTTATTTTTATA -11.20  
 7044 Rnamotif + AGTTCATAAAGTTTATCAACTTATTGATGAGCTTTGTTGTGATA -7.10  
 13361 Both + AAAATATAGATCAGCAAGTTCAGAAGAGCTTGCTGTTTTTTGGTACA -10.60

#### Nisin E

Total number of predicted transcription terminators: 11

2184 Both + TATTCGGTTAACCAGCAGAGAATATGATTTGCTGGaTTTGCTATCAGC -11.70  
 3821 Both + AATTATATGAAGAGGTTGAGTTTAAAAGTGTTCAACCTCtTTGTTTATTTTGC -10.20  
 3963 Both + TGCCAAAAAGATGGCTTTAAATAGGCCATTTTAGGTCAGT -6.80  
 4338 Both + ATTAGGTGAAATAGCATCTTTTTAGATGCTATTTTCTTTTTTTC -9.90  
 4589 Rnamotif + TTAGAAGAAGCTGACAGTGGTGCTGTTGTTTTTAATGGTG -4.30  
 5020 Rnamotif + TGCTGACCACATTGTCATTTTACATGATGGCGAaaTTTTTTATGATG -7.00  
 5264 Rnamotif + TTCGTTTATTGGTGGGAAGCTATCTTTTTGTACACT -3.80  
 6618 Rnamotif + AAGTTGGAAGGTAGTATATAAAATAGCTACCTTTATTTTTATA -6.40  
 13497 Both + AATTAAATCAACCAGACAATCTATTTTTGTCTGGgTTTTATTTGTCA -11.90

#### Nisin O

Total number of predicted transcription terminators: 6

635 Rnamotif + ATGTGGAGAAGGATAGGACCTTACAAGTTCTATCTTTTTTGTATG -7.90  
 5587 Rnamotif + CCGTAGATCATTCTCCTACACATGGGGAGATTATTTTAAACG -7.20

5871 Rnamotif + GTTCAGGTTAGCTCTGGTGAATACACCAGAGTTTTTTTACTTT -14.20  
5913 Both + TTATAGGATTAGGGTGTCAAAAGCCCaTTTTAATATTTG -5.50  
7132 Erpin + ATACATAAAAAAGCTCTATTTTGATAATAGAGCTTTTTTTACGAGTA -8.90

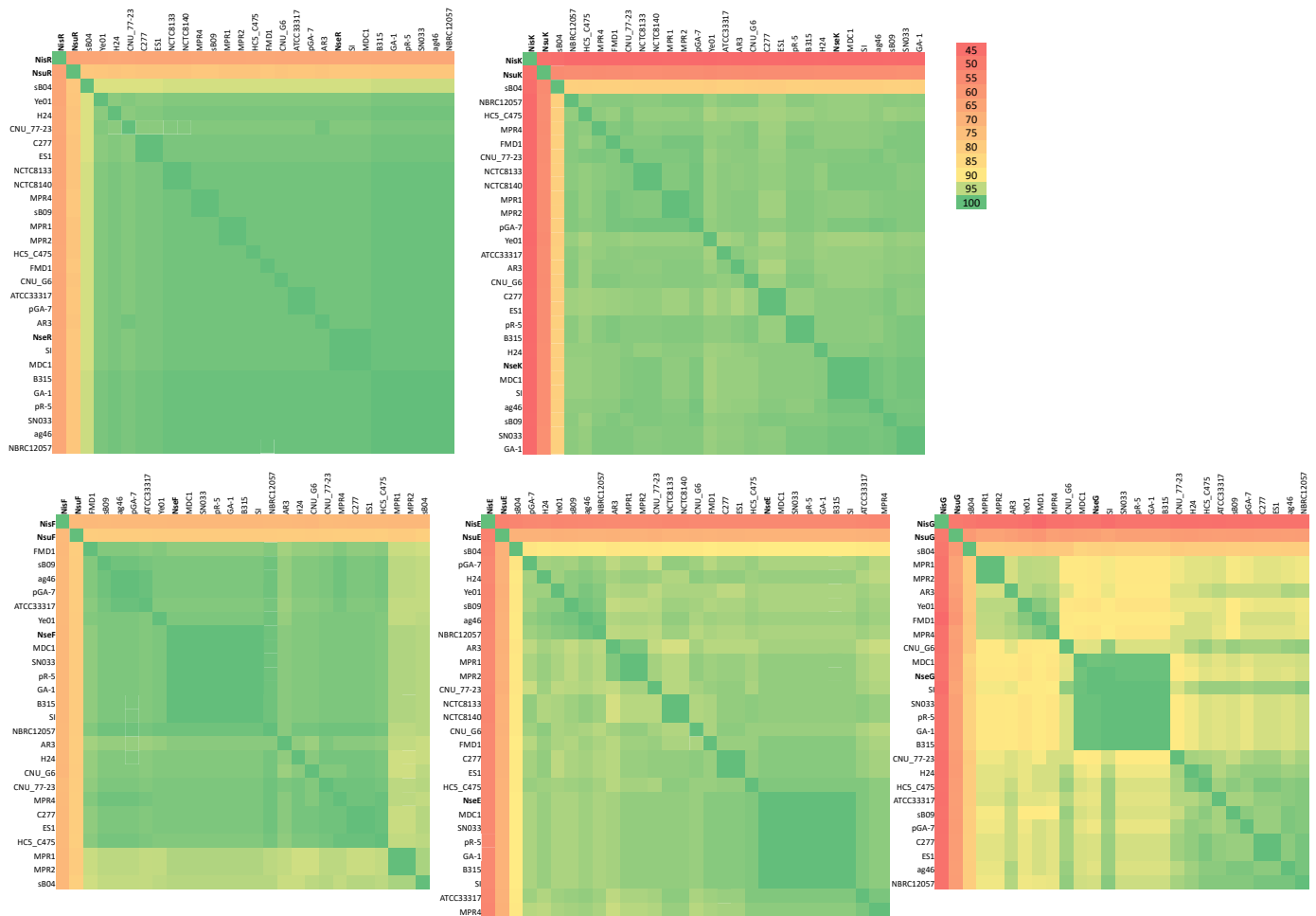
Nisin J

Total number of predicted transcription terminators: 2

2136 Rnamotif + TTATTGTAAATTTTATTGTTGATAGCAGTAGATATTATTTAAT -4.60  
6650 Rnamotif + TACTTTTAGACGAGCCTAGTTCGGCTCTTGATTAGAAT -8.60

**Supplementary Table S7.** *Streptococcus equinus* genomes encoding *nse* genes.

Strain	Recorded Source	Genome Assembly Accession	Encodes
APC4007	Sheep milk		<i>nsePRKAFEGBTCI</i>
APC4008	Sheep milk		<i>nsePRKAFEGBTCI</i>
SI	-	GCA_900115895.1	<i>nsePRKAFEGBTCI</i>
MDC1	Canine oral cavity	GCA_014041875.1	<i>nsePRKAFEGBTCI</i>
GA-1	-	GCA_900100035.1	<i>nsePRKAFEGBTCI</i>
SN033 G637	-	GCA_000421425.1	<i>nsePRKAFEGBTCI</i>
B315 G597	-	GCA_000424045.1	<i>nsePRKAFEGBTCI</i>
pR-5	-	GCA_900109395.1	<i>nsePRKAFEGBTCI</i>
AG46	Sheep rumen	GCA_000964315.1	<i>nseRKFEG</i>
AR3	-	GCA_900199575.1	<i>nseRKFEG</i>
ATCC33317	Cow dung	GCA_000747195.1	<i>nseRKFEG</i>
C277	-	GCA_900099885.1	<i>nseRKFEG</i>
CNU 77-23	<i>Bos taurus</i> rumen fluid	GCA_009758075.1	<i>nseRKFEG</i>
CNU G6	<i>Bos taurus coreanae</i> rumen fluid	GCA_009758095.1	<i>nseRKFEG</i>
ES1	-	GCA_900110365.1	<i>nseRKFEG</i>
FMD1	Forest musk deer	GCA_004525775.1	<i>nseRKFEG</i>
H24	-	GCA_900109415.1	<i>nseRKFEG</i>
HC5	Cow rumen	GCA_000731085.1	<i>nseRKFEG</i>
MPR1	-	GCA_900110935.1	<i>nseRKFEG</i>
MPR2	-	GCA_900100215.1	<i>nseRKFEG</i>
MPR4	-	GCA_900113235.1	<i>nseRKFEG</i>
NBRC12057	Bovine rumen contents	GCA_006538945.1	<i>nseRKFEG</i>
NCTC8133	Infant faeces	GCA_901543475.1	<i>nseRKFEG</i>
NCTC8140	-	GCA_900636465.1	<i>nseRKFEG</i>
pGA-7	-	GCA_900102715.1	<i>nseRKFEG</i>
Sb04	-	GCA_900104225.1	<i>nseRKFEG</i>
Sb09	-	GCA_900103355.1	<i>nseRKFEG</i>
Ye01	-	GCA_900109105.1	<i>nseRKFEG</i>



**Supplementary Figure S5.** Amino acid percent identity heatmaps of NseRKFEF proteins encoded in *S. equinus* genomes compared with *S. uberis* 42 nisin U (NsuRKFEF), and *Lactococcus lactis* ssp. *lactis* ATCC11454 nisin A (NisRKFEF) sequences.