

Supplementary FIG. 1.

<i>glcK</i> locus	<i>tkt</i> locus	<i>pyrE</i> locus
111112233 34	11222234 45	1222444 45
4034581856 71	2548458946 90	2373369024 91
8683332650 63	2291133233 36	1315175831 89
<i>glk2th</i> GGTCCGAGTG AG	<i>tkt8th</i> TTGGCCTGTC TA	<i>pyr11th</i> AGCGGCGACT TG
<i>glk3th</i> .....T.... ..	<i>tkt10th</i> .....C. .G	<i>pyr13th</i> .TT.....TC C.
<i>glk5th</i> AA..... ..	<i>tkt2th</i> ..... .G	<i>pyr10th</i> .T.....TC C.
<i>glk1th</i> .A..... ..	<i>tkt3th</i> .C.....A.. .G	<i>pyr9th</i> .TT...A.TC C.
<i>glk4th</i> .A.....A ..	<i>tkt11th</i> .....A.. .G	<i>pyr5th</i> ...A....TC C.
<i>glk6th</i> .....A..C. TT	<i>tkt7th</i> .C..T..... .G	<i>pyr4th</i> ...AA...TC C.
<i>glk7th</i> ..CTA..A.. C.	<i>tkt4th</i> .C..... .G	<i>pyr12th</i> G..A....TC C.
<i>glk8th</i> .....A.. C.	<i>tkt5th</i> .C....G... .G	<i>pyr1th</i> .....T..TC C.
	<i>tkt6th</i> .C..... CG	<i>pyr2th</i> .....T.GTC C.
	<i>tkt11th</i> .C.A.T.... .G	<i>pyr6th</i> .....TC C.
	<i>tkt9th</i> CCA.....T .G	<i>pyr3th</i> ....A...TC C.
		<i>pyr7th</i> .....T. C.
		<i>pyr8th</i> .....TC CA
<i>ddlA</i> locus	<i>thrS</i> locus	<i>dnaE</i> locus
1	111	1234
43	7245	3457
01	7902	0902
<i>ddl1th</i> GG	<i>thr1th</i> GGCC	<i>dna3th</i> CCGA
<i>ddl2th</i> T.	<i>thr5th</i> T...	<i>dna2th</i> ...C
<i>ddl3th</i> TA	<i>thr2th</i> ...T	<i>dna1th</i> T..C
	<i>thr4th</i> ..AT	<i>dna4th</i> TT.C
	<i>thr3th</i> .T.T	<i>dna5th</i> T.CC
<i>pepO</i> locus	<i>ilvC</i> locus	
2	1	
673	5	
12980	5	
<i>pep3th</i> CGTAA	<i>ilv1th</i> A	
<i>pep5th</i> T..C.	<i>ilv2th</i> T	
<i>pep1th</i> ...C.		
<i>pep2th</i> ..CC.		
<i>pep6th</i> ...CG		
<i>pep4th</i> .A.C.		

Supplementary FIG. 1. Polymorphic nucleotide sites among MLST alleles of *S. thermophilus*.

Variable sites in each allele are found from 27 *S. thermophilus* isolates for all loci, except *glcK*, which was also analyzed in additional 21 strains. The sites are numbered above in vertical format.

Supplementary FIG. 2.

	111222222	334444445
	1458125588	682456794
	5683685713	858384052
S.th-prtS1 (2)	CAGTACGGAA	GTGGCTGTC
S.th-prtS2 (1)	...CTTTAGG	..T.T.AG.
S.th-prtS3 (1)	....TTTAGG	..T.T.AG.
S.su-prtS1 (12)	TTACTTTAGG	.GT.T.AGA
S.su-prtS2 (11)	T.ACCTTAGG	TGTATC.GA
S.su-prtS3 (1)	TTACTTTAGG	.GTATC.GA
	111111111	2222223333 333334
	2334456	9001245699 0223370112 357880
	1478143831	8162427609 2192874690 763250
S.su-eric6 (6)	GTCTTATTTCG	TTAAGACCCA CCGTCGATCG ATTGCC
S.su-eric1 (4)	.....T.	.....G .....
S.su-eric3 (5)	AC.....T.	.....G .....
S.su-eric4 (1)	AC.....A	..... .....
S.su-eric2 (6)	AC.....	..... .....
S.su-eric5 (1)	AC....C...	.....T.....
S.th-eric1 (3)	..TCCG.A.A	CCTGA.TTGG T.TATCGCTT CCA.TT
S.th-eric2 (1)	..TCCG.A.A	CCTGA.TTGG TATATCGCTT CCA.TT

Supplementary FIG.2. Polymorphic nucleotide sites of *prtS* and *eriC* alleles of *S. thermophilus* (S.th) and *S. suis* (S.su) strains. Sequences of fragments from LMD-9, CNRZ703, CNRZ385 and JIM8232 are shown for *S. thermophilus*. Besides sequences of 20 *S. suis* strains isolated from human and pigs, available sequences of fragments from 98HAH33, 05ZYH33, P1/7 and 89/1591 (only for *prtS*) are shown for *S. suis*. Only the variable sites are shown. The sites are numbered above in vertical format. The number of strains corresponding to each allele is indicated in brackets.