

***Staphylococcus edaphicus* sp. nov., isolated in Antarctica, harbours *mecC* gene
and genomic islands with suspected role in adaptation to extreme environment**

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Supplemental material

Table S1. Cellular fatty acid composition (as a percentage of the total) of strains CCM 8730^T, CCM 8731, *Staphylococcus saprophyticus* subsp. *saprophyticus* CCM 883^T, *Staphylococcus saprophyticus* subsp. *bovis* CCM 4410^T, and *Staphylococcus xylosus* CCM 2738^T. All data were obtained in this study. Values of less than 1% are not shown. All strains were cultivated on TSBA agar plates for 24 h at 28±1°C.

Fatty acid	CCM 8730 ^T	CCM 8731	CCM 883 ^T	CCM 4410 ^T	CCM 2738 ^T
C _{13:0} iso	TR	TR	TR	TR	2.2
C _{13:0} anteiso	ND	TR	ND	ND	2.2
C _{14:0} iso	TR	TR	TR	TR	1.4
C _{14:0}	TR	TR	TR	1.0	1.3
C _{15:0} iso	13.3	13.2	13.4	14.8	19.6
C _{15:0} anteiso	51.4	51.0	52.8	45.6	42.0
C _{16:0} iso	1.2	1.2	1.2	1.1	1.3
C _{16:0}	2.5	2.6	1.4	3.30	2.7
C _{17:0} iso	5.6	5.3	6.3	6.0	5.8
C _{17:0} anteiso	12.9	12.8	12.9	9.9	5.9
C _{18:1} ω _{9c}	TR	TR	ND	ND	1.1
C _{18:0}	3.5	3.7	2.4	5.5	4.8
C _{19:0} iso	1.2	1.2	2.3	1.8	2.0
C _{20:1} ω _{9c}	1.0	1.0	ND	ND	1.6
C _{20:0}	5.2	5.6	5.2	8.6	4.9

Legend: TR, trace amounts (< 1%); ND, not detected

Table S2. Statistics of the IonTorrent sequencing and assembly of *Staphylococcus edaphicus* CCM 8730T draft genome sequence (GenBank Accession number MRZN00000000).

Library summary based on predicted per-base quality scores	
Total Number of Bases [Mbp]	1,344.76
Number of Q20 Bases [Mbp]	1,228.63
Total Number of Reads [Count]	3,973,034
Mean Length [bp]	338
Longest Read [bp]	745
Assembly statistics	
contigs (\geq 500 bp) [Count]	45
contigs (\geq 1000 bp) [Count]	38
contigs (\geq 5000 bp) [Count]	36
contigs (\geq 10000 bp) [Count]	36
contigs (\geq 25000 bp) [Count]	30
contigs (\geq 50000 bp) [Count]	18
Largest contig [bp]	275,845
Total length [bp]	2,687,658
Total length (\geq 0 bp) [bp]	2,692,679
Total length (\geq 1000 bp) [bp]	2,682,949
Total length (\geq 5000 bp) [bp]	2,678,026
Total length (\geq 10000 bp) [bp]	2,678,026
Total length (\geq 25000 bp) [bp]	2,572,181
Total length (\geq 50000 bp) [bp]	2,139,734
N50	99,210
N75	69,093
L50 [count]	8
L75 [count]	16
GC [%]	33.25

Table S3. Intergenomic distances between the genomes of *Staphylococcus edaphicus* CCM 8730^T and reference type strains of phylogenetically closest staphylococcal species represented by average nucleotide identity (ANI) and digitally derived genome-to-genome distances (GGD) emulating DNA-DNA hybridization (DDH) values (%).

Reference genome	<i>S. edaphicus</i> CCM 8730 ^T			<i>S. saprophyticus</i> ATCC 15305 ^T		<i>S. xylosus</i> CCM 2783 ^T		<i>S. equorum</i> UMC-CNS-924		<i>S. succinus</i> DSM 14617 ^T		<i>S. gallinarum</i> DSM 20610 ^T	
	ANI (%)	dDDH		ANI (%)	dDDH	ANI (%)	dDDH	ANI (%)	dDDH	ANI (%)	dDDH	ANI (%)	dDDH
	Formula*												
<i>S. edaphicus</i> CCM 8730 ^T GenBank accession number MRZN000000000	-	1	-		63.50% [59.7 - 67.1%]		35.00% [31.7 - 38.6%]		30.10% [26.7 - 33.7%]		26.00% [22.7 - 29.7%]		21.90% [18.7 - 25.6%]
		2 (recom.)	-	84.78	29.00% [26.6 - 31.5%]	80.37	24.00% [21.7 - 26.4%]	79.49	22.90% [20.6 - 25.3%]	78.53	22.20% [19.9 - 24.6%]	76.9	21.30% [19.1 - 23.8%]
		3	-		53.00% [49.9 - 56.1%]		31.20% [28.3 - 34.3%]		27.30% [24.4 - 30.5%]		24.20% [21.3 - 27.3%]		20.90% [18.1 - 23.9%]
<i>S. saprophyticus</i> ATCC 15305 ^T GenBank accession number AP008934	84.78	1	63.50% [59.7 - 67.1%]	-	-	80.61	35.10% [31.7 - 38.6%]	79.71	33.90% [30.5 - 37.4%]	78.72	28.30% [25 - 32%]	77.29	22.60% [19.4 - 26.3%]
		2 (recom.)	29.00% [26.6 - 31.5%]	-	-		24.20% [21.9 - 26.7%]		23.20% [20.9 - 25.7%]		22.60% [20.4 - 25.1%]		21.90% [19.7 - 24.4%]
		3	53.00% [49.9 - 56.1%]	-	-		31.30% [28.4 - 34.4%]		30.10% [27.2 - 33.2%]		26.00% [23.1 - 29.1%]		21.50% [18.7 - 24.6%]
<i>S. xylosus</i> CCM 2783 ^T GenBank accession number MRZO000000000	80.37	1	35.00% [31.7 - 38.6%]	80.61	35.10% [31.7 - 38.6%]	-	-	79.78	31.50% [28.1 - 35.1%]	78.9	28.10% [24.7 - 31.7%]	77.38	22.50% [19.2 - 26.1%]
		2 (recom.)	24.00% [21.7 - 26.4%]		24.20% [21.9 - 26.7%]		-		23.30% [21 - 25.8%]		22.70% [20.4 - 25.1%]		21.70% [19.5 - 24.2%]
		3	31.20% [28.3 - 34.3%]		31.30% [28.4 - 34.4%]		-		28.50% [25.5 - 31.6%]		25.80% [22.9 - 28.9%]		21.40% [18.6 - 24.5%]
<i>S. equorum</i> UMC-CNS-924 GenBank accession number CP013114	79.49	1	30.10% [26.7 - 33.7%]	79.71	33.90% [30.5 - 37.4%]	79.78	31.50% [28.1 - 35.1%]	-	-	79.86	32.70% [29.4 - 36.3%]	77.445	22.60% [19.3 - 26.3%]
		2 (recom.)	22.90% [20.6 - 25.3%]		23.20% [20.9 - 25.7%]		23.30% [21 - 25.8%]		-		23.30% [21 - 25.8%]		21.70% [19.4 - 24.1%]
		3	27.30% [24.4 - 30.5%]		30.10% [27.2 - 33.2%]		28.50% [25.5 - 31.6%]		-		29.40% [26.4 - 32.5%]		21.50% [18.7 - 24.5%]
<i>S. succinus</i> DSM 14617 ^T GenBank accession number LCSH000000000	78.53	1	26.00% [22.7 - 29.7%]	78.72	28.30% [25 - 32%]	78.9	28.10% [24.7 - 31.7%]	79.86	32.70% [29.4 - 36.3%]	-	-	78.19	25.70% [22.4 - 29.4%]
		2 (recom.)	22.20% [19.9 - 24.6%]		22.60% [20.4 - 25.1%]		22.70% [20.4 - 25.1%]		23.30% [21 - 25.8%]		-		22.80% [20.5 - 25.2%]
		3	24.20% [21.3 - 27.3%]		26.00% [23.1 - 29.1%]		25.80% [22.9 - 28.9%]		29.40% [26.4 - 32.5%]		-		24.00% [21.2 - 27.1%]
<i>S. gallinarum</i> DSM 20610 ^T GenBank accession number JXCF000000000	76.9	1	21.90% [18.7 - 25.6%]	77.29	22.60% [19.4 - 26.3%]	77.38	22.50% [19.2 - 26.1%]	77.45	22.60% [19.3 - 26.3%]	78.19	25.70% [22.4 - 29.4%]	-	-
		2 (recom.)	21.30% [19.1 - 23.8%]		21.90% [19.7 - 24.4%]		21.70% [19.5 - 24.2%]		21.70% [19.4 - 24.1%]		22.80% [20.5 - 25.2%]		-
		3	20.90% [18.1 - 23.9%]		21.50% [18.7 - 24.6%]		21.40% [18.6 - 24.5%]		21.50% [18.7 - 24.5%]		24.00% [21.2 - 27.1%]		-

Legend: *, Genome-to-Genome Distance Calculator available at <http://ggdc.dsmz.de/> was used for calculating the digital DDH (dDDH) values with 3 formulas; formula no. 2 is recommended for draft genomes.

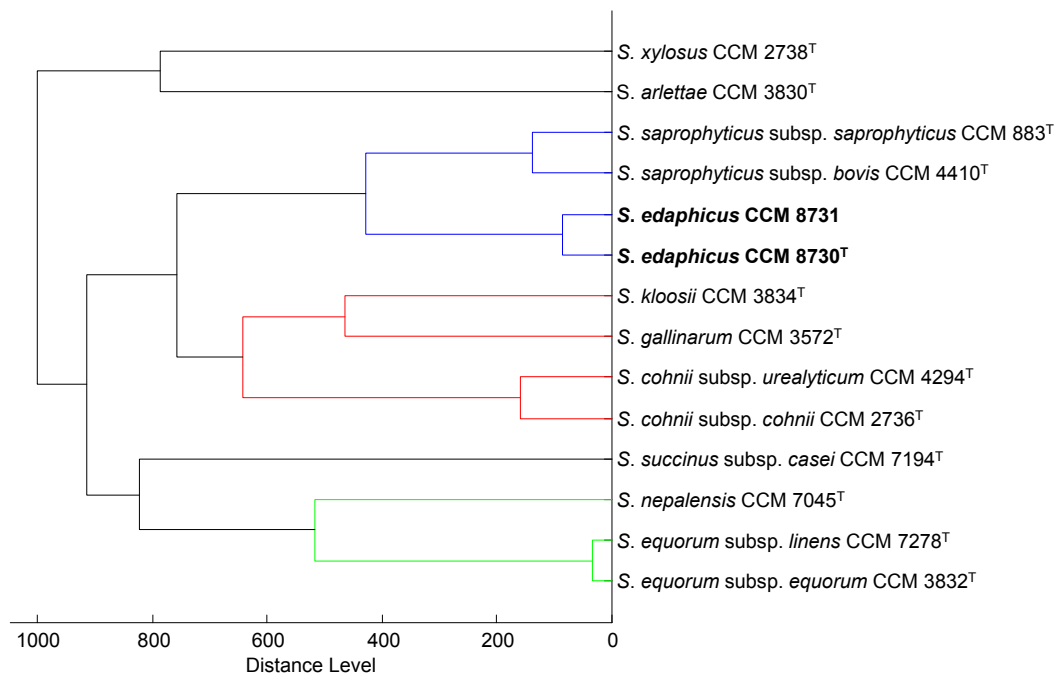


Fig. S1. Dendrogram based on MALDI-TOF MS profiles of *Staphylococcus edaphicus* sp. nov. and other phylogenetically related species. The MALDI-TOF MS profiles were acquired using a Microflex instrument (Bruker Daltonik) and the dendrogram was generated using the correlation distance measure with the average linkage algorithm (UPGMA).

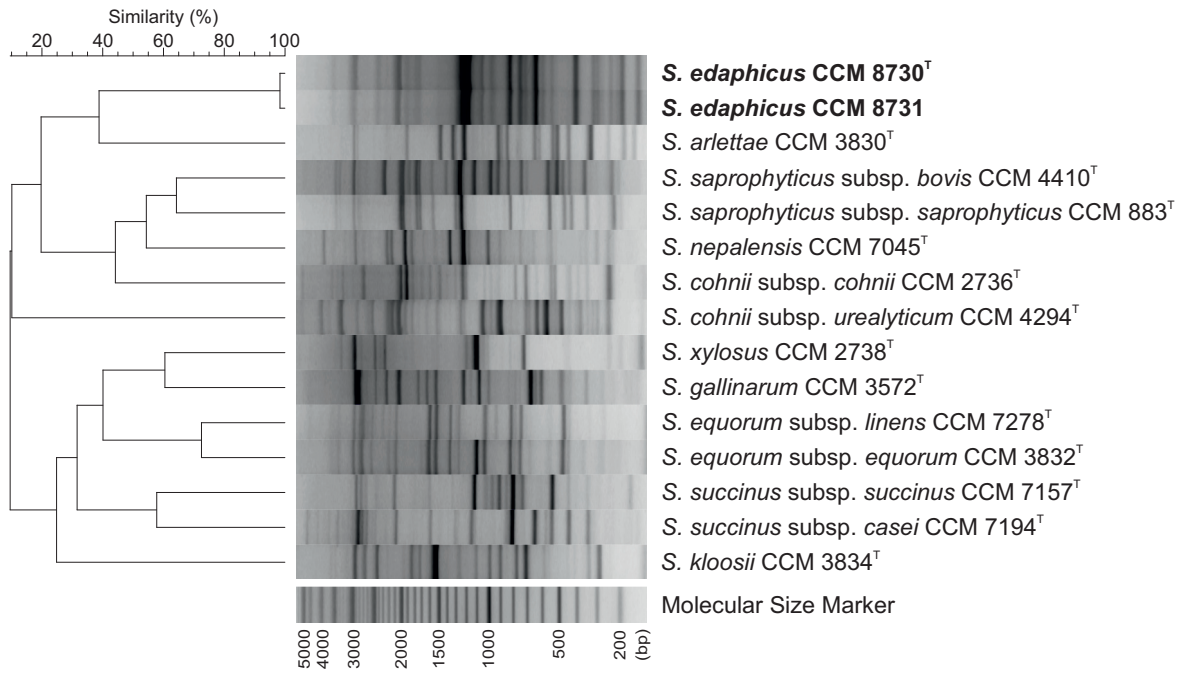


Fig. S2. Dendrogram based on cluster analysis of rep-PCR fingerprints obtained with (GTG)₅ primer from novel *Staphylococcus* strains and the type strains of the phylogenetically closely related species. The dendrogram was calculated with Pearson's correlation coefficients with UPGMA clustering method (r , expressed as percentage similarity values).

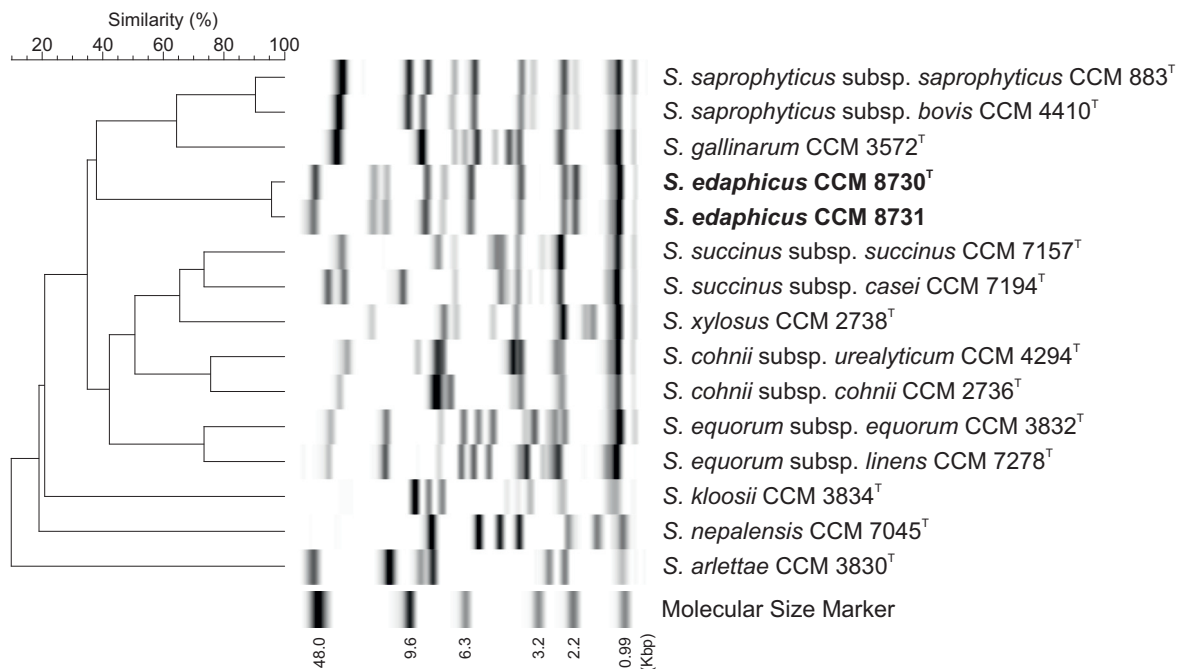


Fig. S3. Dendrogram based on cluster analysis of *EcoRI* ribotype patterns obtained using the RiboPrinter system from novel *Staphylococcus* strains and the type strains of phylogenetically closely related species. The dendrogram was calculated with Pearson's correlation coefficients with the UPGMA clustering method (r , expressed as percentage similarity values).

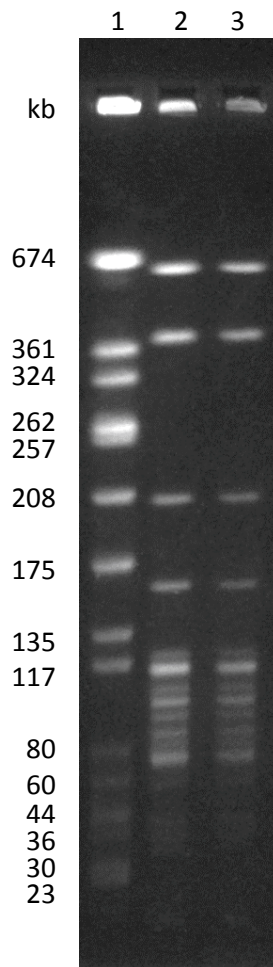


Fig. S4. Pulsed-field gel electrophoresis showing identical *Sma*I macrorestriction patterns of *Staphylococcus edaphicus* sp. nov. strains CCM 8730^T (lane 2) and CCM 8731 (lane 3). *Staphylococcus aureus* NCTC 8325 was used as a size marker (lane 1).