

Fig S1. Flowchart depicting the 62 CoNS PJI patients included in the study and the 16 *S. epidermidis* prosthetic joint infections with multiple isolates analyzed by WGS

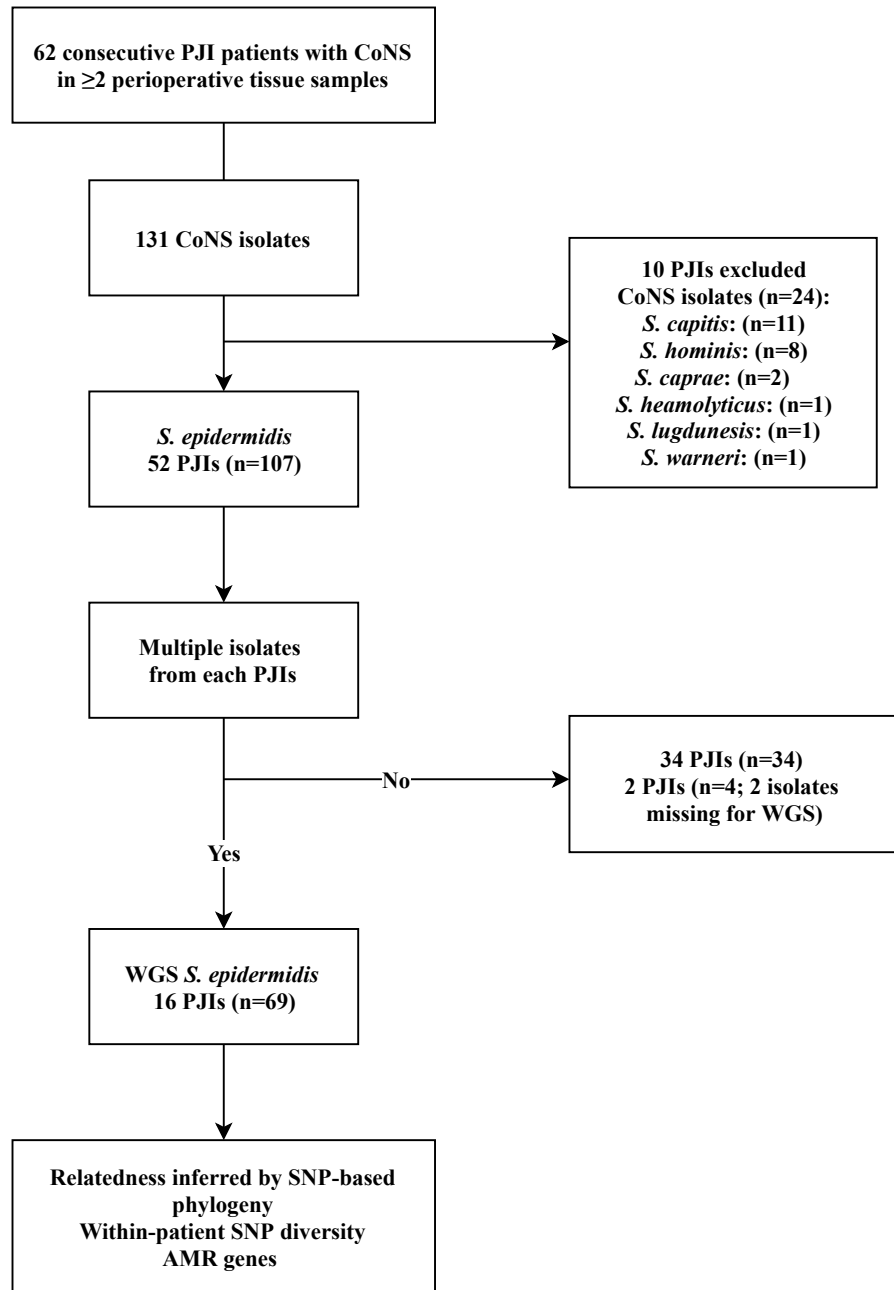


Fig. S2. Dendrogram cluster analysis of the genetic similarity of 131 CoNS isolates using pulsed-field gel electrophoresis (PFGE). The horizontal upper bar indicates genetic similarity (per cent). The dotted lines in the centre of the diagram represent digitalized transformation of the PFGE DNA pattern. The columns to the right present the following: patient ID, PFGE type or non-*S. epidermidis* species and sequence type (ST).

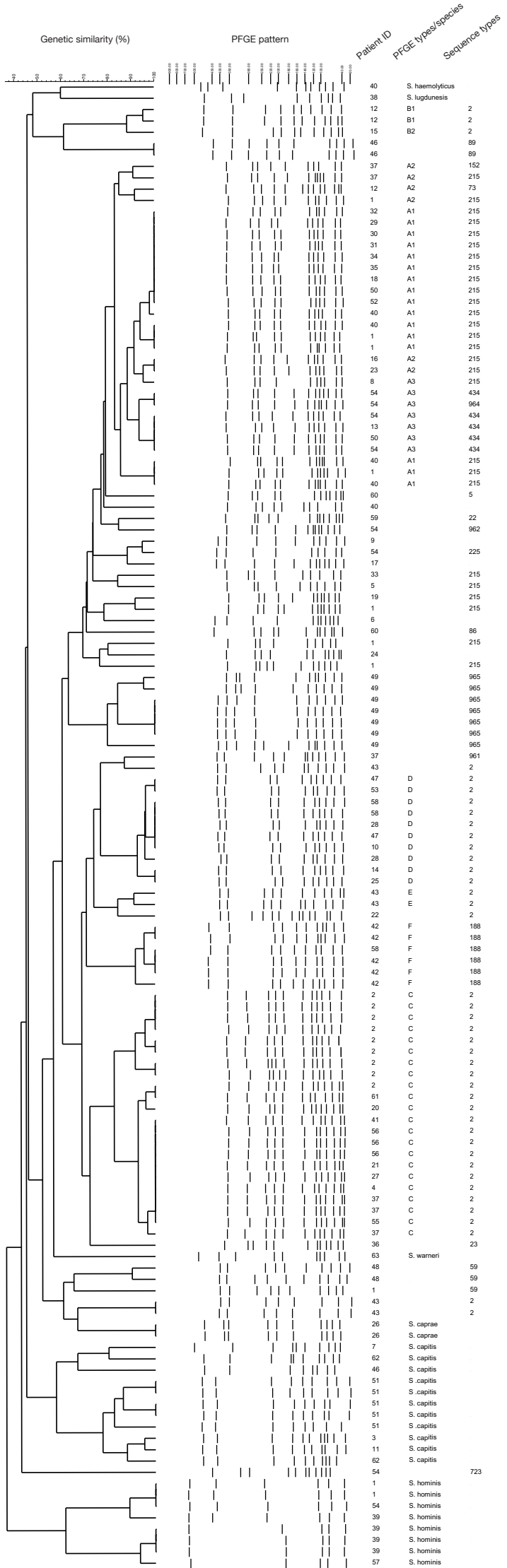


Fig S3. Intra-lineage pairwise SNP diversity among *S. epidermidis* STs within each patient with PJI related to time since primary surgery

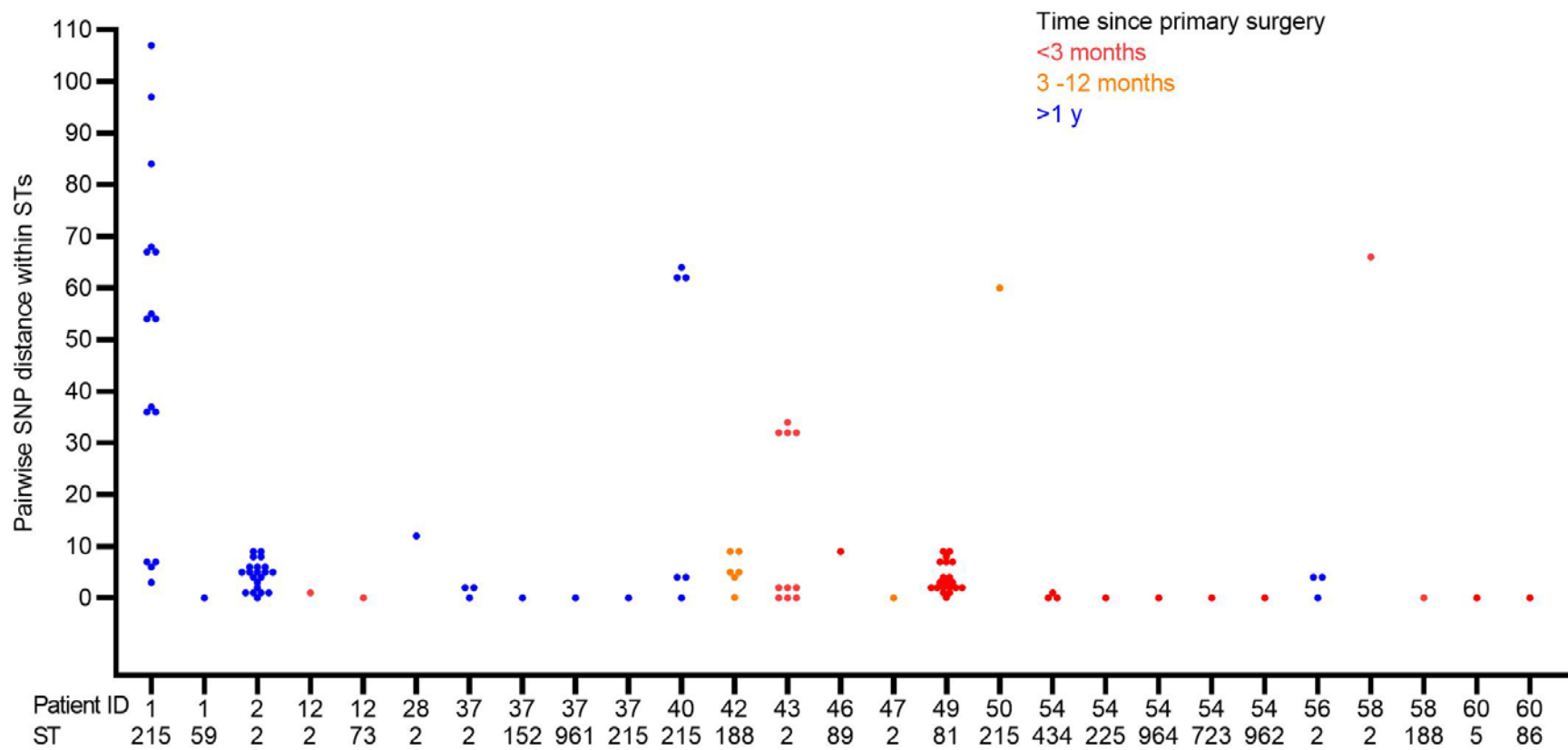


Table S2. Antimicrobial susceptibility pattern among 107 consecutive *S. epidermidis* isolates identified in 62 patients with prosthetic joint infections identified in two Swedish hospitals between 2009 and 2011

		Antimicrobial phenotypic resistance (%)								
	<i>n</i>	GEN	CLI	ERY	FUS	FOX	NOR	RIF	SXT	MDR
<i>S. epidermidis</i>	107	96 (90)	67 (63)	72 (67)	45 (42)	86 (80)	85 (79)	35 (33)	80 (75)	87 (81)
ST2/ST188	47	45 (96)	38 (81)	39 (83)	10 (21)	45 (96)	47 (100)	27 (57)	46 (98)	47 (100)
ST215/ST434	32	32 (100)	24 (75)	24 (75)	32 (100)	26 (81)	32 (100)	5 (16)	31 (97)	32 (100)
Non ST2/ST215 ^a	28	19 (68)	5 (18)	9 (32)	3 (11)	15 (54)	6 (21)	2 (7)	4 (14)	8 (29)

GEN= gentamicin; CLI=clindamycin; ERY=erythromycin; FUS=fusidic acid; FOX=cefoxitin; NOR=norfloxacin; RIF=rifampicin; SXT=trimethoprim-sulfamethoxazole. MDR=multidrug-resistant, defined as resistance towards ≥ 3 antimicrobial categories

^aST5, ST22, ST23, ST86, ST89, ST152, ST225, ST723, ST961, ST962, ST964, ST965

Table S3. Distribution of *S. epidermidis* lineages in 52 consecutive patients with monomicrobial or polymicrobial prosthetic joint infections

Lineage	Monomicrobial (%)	Polymicrobial (%)	Total (%)
ST215 ^c	9 (27)	9 (47)	18 (35)
ST2 ^c	16 (49)	6 (32)	22 (42)
Non-ST215/ST2 ^d	8 (24)	4 (21)	12 (23)
Total	33	19	52

^cIn patient 37, several STs were detected: ST2 ($n=3$), ST215 ($n=1$), ST152 ($n=1$) and ST961 ($n=1$). Patient 37 is included among ST2/188 cases due to several isolates of ST2

^dST5, ST22, ST23, ST86, ST89, ST152, ST225, ST723, ST961, ST962, ST964, ST965

Table S4. Agreement between genomic presence/absence of a gene or a gene mutation encoding antimicrobial resistance and a phenotypical antimicrobial resistance/susceptibility trait

Gene	Antimicrobial resistance		Agent	Agreement (%)
	<i>n</i>	phenotypic R S		
<i>mecA</i> +	51/69	51/51	cefoxitin	100
<i>mecA</i> -	18/69	0/18		100
<i>emrC</i> +	34/69	33/34	erythromycin	97
<i>emrC</i> -	35/69	27/35		77
<i>emrC</i> +	34/69	33/34	clindamycin	97
<i>emrC</i> -	35/69	30/35		86
<i>fosB</i> +	22/69	22/22	fusidic acid	100
<i>fosB</i> -	47/69	44/47		94
<i>aac(6')-aph(2'')</i> +	58/69	58/58	gentamicin	100
<i>aac(6')-aph(2'')</i> -	11/69	8/11		73
Point mutation^a				
<i>gyrA</i> ^b +	50/69	50/50	norfloxacin	100
<i>gyrA</i> ^b -	19/69	19/19		100
<i>rpoB</i> ^c +	23/69	23/23	rifampicin	100
<i>rpoB</i> ^c -	46/69	45/46		98
<i>folA</i> ^d +	40/69	40/69	trimethoprim-sulfamethoxazole	100
<i>folA</i> ^d -	29/69	19/29 ^b		66

^a+ = presence; - = absence

^bS84F (*n*=36); S84Y (*n*=14)

^cD471E, I527M (*n*=17); H481N (*n*=4); S486F (*n*=1); S486Y (*n*=1)

^dF99Y (*n*=40)