

Additional file 1: Program versions and parameters for bioinformatic analysis

Sample reads were trimmed with Trimmomatic [1] and checked for contamination with Kraken2 [2]. For whole genome assembly the reads were normalized with the BBNorm tool from the BBTools suite [3] and assembled with Unicycler [4]. The assembly was then used for multi-locus sequence typing (MLST) using PubMLST schemes [5-9] and resistance gene identification with ResFinder [10-12]. Samples with the same sequence type or allele combination were compared with single nucleotide polymorphism (SNP)-analysis. SNP-analysis was performed for all *S. capitis* samples since there is no MLST scheme available for this species. For the SNP-analysis reads were downsampled using the reformat tool from BBTools [3] and mapped to reference genomes (Accession nrs. [GCA_020740065.1](#), [GCF_006094375.1](#), [GCF_003812505.1](#), [GCF_016126715.1](#)) with Bowtie2 [13] and SAMTools [14]. SNPs were called and filtered with BCFTools [14] and an in-house python script [15].

Program	Use	Version	Parameters	References
FastQC	Quality check of raw, trimmed, normalized and downsampled reads	0.11.9	NA	16
Trimmomatic PE	Read trimming	0.39	ILLUMINACLIP:NexteraPE-PE.fa:2:30:10:2:true SLIDINGWINDOW:4:20 MINLEN:36	1
BBTools - BBNorm	Read normalising for assembly	38.79	target=100	3
Kraken2	Contamination check	2.1.2 Database: MiniKraken v2 8GB 2019-04-23	--paired	2
Unicycler	Whole genome assembly	0.4.8	--mode normal	4
mlst	Multi-locus sequence typing	2.19.0 Database downloaded 2022-02-14	--minid 95 --mincov 10 --minscore 50	17

ResFinder	Identification of resistance genes	Software: 4.1.10 Database: 2022-02-04	ID threshold: 90 % Min. length: 60 % Species database “Staphylococcus aureus” for <i>S. aureus</i> samples, “Other” for other samples.	10-12
BBTools - reformat	Downsampling of reads for SNP analysis	38.79	sbt=250000000 for <i>S. capitis</i> and <i>S. epidermis</i> sbt=230000000 for <i>S. hominis</i> sbt=270000000 for <i>S. pseudointermedius</i> sbt=290000000 for <i>S. aureus</i>	3
Bowtie2	Mapping of reads to reference sequence	2.4.4	-X 1000	13
SAMTools	BCF file conversion and sorting	1.14	NA	14
BCFTools	Mpileup generation	1.14	-O u -d 1000	14
	SNP calling	1.14	-m -v -O v --ploidy 1	
	SNP filtering	1.14	-O v -i 'QUAL > 30 && DP > N_SAMPLES*10 && INDEL = 0 && COUNT(GT[*] = ".") = 0 && COUNT(GT[*] = "1") < N_SAMPLES'	
Python script	SNP filtering based on phred-scaled genotype likelihood (PL) values	3.7.6	max(PL) – min(PL) > 100	15

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