

Table S1. Characteristics of the reference genomes and of the cgMLST gene sets of the investigated species.

Species	Reference genome		cgMLST schemes		
	Strain ID (NCBI acc. no.)	No. of genes (genome size in bp)	No. of NCBI RefSeq genome sequences available (date)	No. of target genes analyzed (concatenated size in bp; % of genome)	List of target genes
<i>S. aureus</i>	COL (NC_002951)	2,612 (2,809.422)	40 (August 9, 2013)	1,861 (1,694.861; 60.3)	Table S2, from (1)
<i>E. coli</i>	O157:H7 str. Sakai (NC_002695)	5,230 (5,498.450)	60 (July 30, 2013)	2,325 (2,261.241; 41.1)	Table S2
<i>E. faecium</i>	DO (NC_017960)	2,703 (2,698.137)	3 (May 14, 2013)	2,057 (1,838.827; 68.2)	Table S2
<i>P. aeruginosa</i>	PAO1 (NC_002516)	5,570 (6,264.404)	10 (July 18, 2013)	3,842 (3,888.805; 62.1)	Table S2

bp, base pair.

Supplementary References

1. **Leopold SR, Goering RV, Witten A, Harmsen D, Mellmann A.** 2014. Bacterial whole-genome sequencing revisited: portable, scalable, and standardized analysis for typing and detection of virulence and antibiotic resistance genes. J Clin Microbiol **52**:2365-2370.