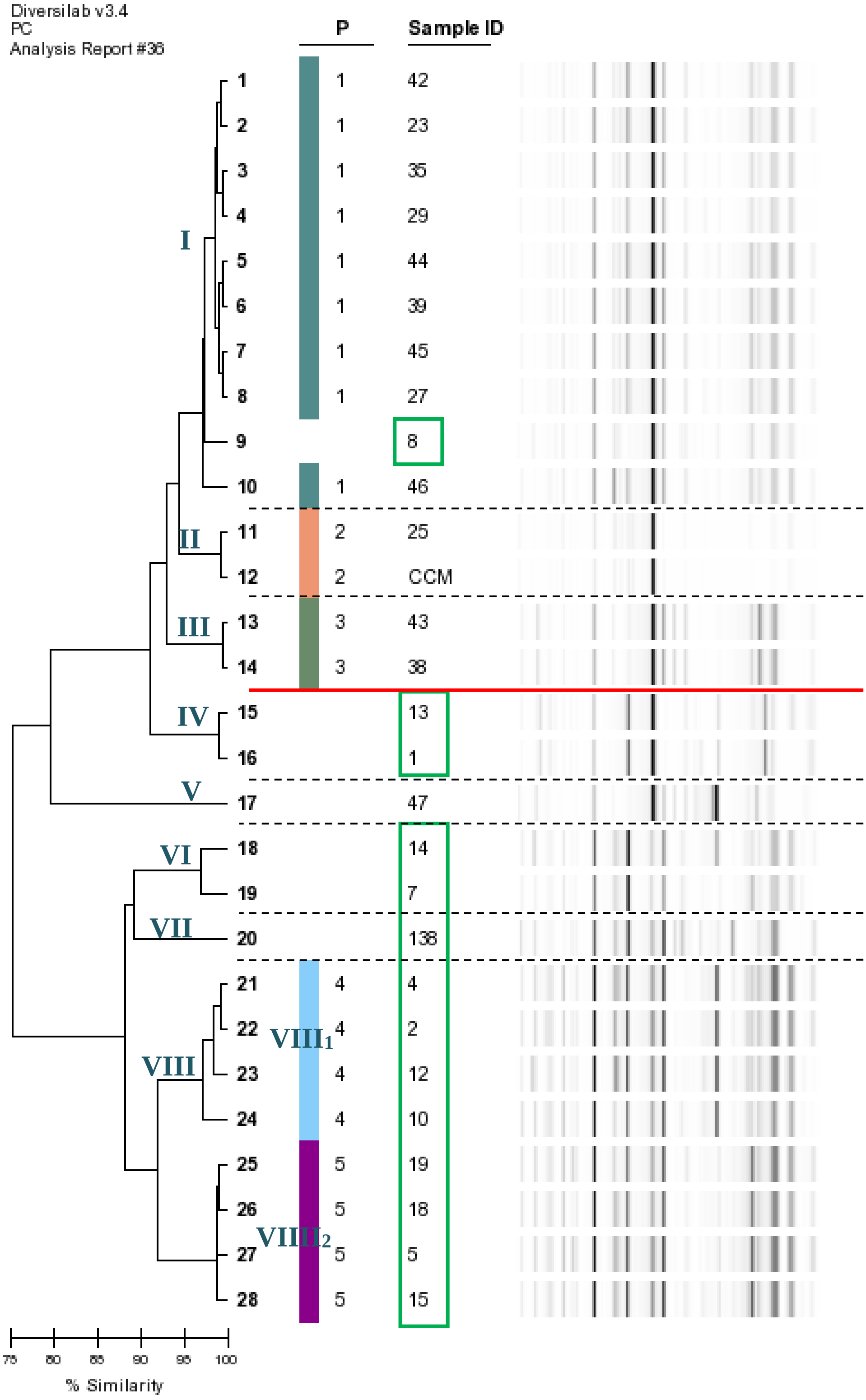
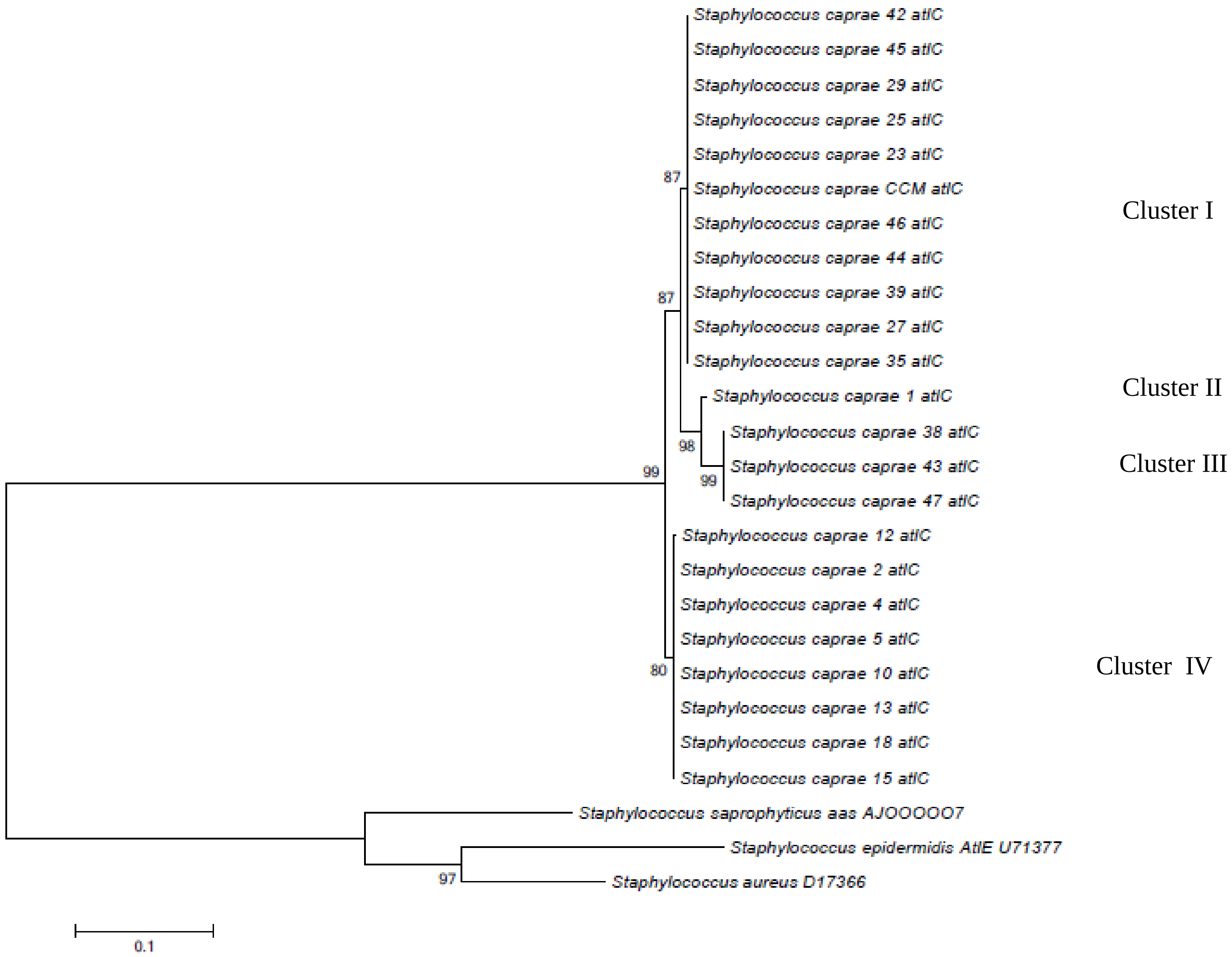


Supplementary Figure 1: Cluster analysis (dendrogram) and virtual gel image from DiversiLab® generated fingerprints of the 28 stains analyzed after rep-PCR. Human strains are in square and reference strain *S. caprae* CCM3573 was included in this analysis.

Supplementary Figure 2 :

Neighbor-Joining method tree showing the phylogenetic distribution of *Staphylococcus caprae atlC* sequences. Twenty six gene sequences including 23 available from this study were aligned by using MEGA6 (www.megasoftware.net). The figures shows the optimal tree, the sum of branch length for *atl* genes was 1.29853053. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. The analysis involved 26 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 829 positions in the final dataset. Evolutionary analyses were conducted in MEGA6.Scale bar indicates substitutions per nucleotide position.



Clusters I and III = animal origin and clusters II and IV = human origin

Supplementary Table 1: Comparison of identification results by using phenotypic, genotypic and spectrometric methods

	Vitek2® ID-GP identification (probability %)	***tuf* sequencing identification**	**MALDI-TOF identification**
Human strains			
1	***S. caprae*** (92 %)	***S. caprae***	***S. caprae***
2	***S. caprae*** (94 %)	***S. caprae***	***S. caprae***
4	***S. caprae*** (93 %)	***S. caprae***	***S. caprae***
5	***S. caprae*** (93 %)	***S. caprae***	***S. caprae***
7	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
8	***S. caprae*** (85 %)	No identification	***S. caprae***
10	***S. caprae*** (95 %)	***S. caprae***	***S. caprae***
12	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
13	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
14	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
15	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
18	*S. warneri/S. hominis*	***S. caprae***	***S. caprae***
19	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
138	***S. caprae*** (96 %)	***S. caprae***	***S. caprae***
Animal strains			
23	*S. hominis hominis* (90 %)	***S. caprae***	***S. caprae***
25	*S. hominis hominis* (88 %)	***S. caprae***	***S. caprae***
27	***S. caprae*** (95 %)	***S. caprae***	***S. caprae***
29	*S. capitis/****S. caprae***	***S. caprae***	***S. caprae***
35	***S. caprae*** (98 %)	***S. caprae***	***S. caprae***
38	*S. epidermidis*	***S. caprae***	***Staphylococcaceae***
39	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
42	*S. capitis/****S. caprae***	***S. caprae***	***S. caprae***
43	No identification	***S. caprae***	***S. caprae***
44	*S.capitis/****S. caprae***	***S. caprae***	***S. caprae***
45	***S. caprae***	***S. caprae***	***S. caprae***
46	***S. caprae*** (99 %)	***S. caprae***	***S. caprae***
47	***S. caprae****/S.simulans*	***S. caprae***	***S. caprae***
CCM3573	***S. caprae***	***S. caprae***	***S. caprae***