

**Table S2.** Distribution of the main virulence factor-encoding genes between clonal and non-clonally-related *S. aureus* strains isolated at patient inclusion and follow-up.

	<b>Clonal <i>S. aureus</i> isolated at inclusion and during the follow- up (n=28 strains) (%)</b>	<b>Non-clonal <i>S. aureus</i> isolated at inclusion and during the follow-up (n=82 strains) (%)</b>	<b><i>P</i>-value</b>
<i>sea</i>	6 (21.4)	28 (34.1)	NS
<i>seb</i>	2 (7.1)	3 (3.7)	NS
<i>sec</i>	6 (21.4)	9 (11.0)	NS
<i>sed</i>	5 (17.9)	8 (9.8)	NS
<i>seg</i>	15 (53.6)	42 (51.2)	NS
<i>lukF/S-PV</i>	0 (0)	0 (0)	NS
<i>lukD/E</i>	19 (67.9)	41 (50.0)	NS
<i>hla</i>	28 (100)	82 (100)	NS
<i>hlb</i>	15 (53.6)	56 (68.3)	NS
<i>sak</i>	17 (60.7)	53 (64.6)	NS
<i>chp</i>	19 (67.9)	58 (70.7)	NS
<i>scn</i>	23 (82.1)	73 (89.0)	NS
<i>tst</i>	0 (0)	12 (14.6)	0.034
<i>etA</i>	0 (0)	1 (1.2)	NS
<i>etB</i>	0 (0)	0 (0)	NS
<i>etD</i>	2 (7.1)	3 (3.7)	NS
<i>edinA</i>	0 (0)	0 (0)	NS
<i>edinB</i>	2 (7.1)	3 (3.7)	NS
<i>edinC</i>	0 (0)	0 (0)	NS
<i>splA/B</i>	19 (67.9)	42 (51.2)	NS
<i>agrI</i>	18 (64.3)	49 (59.8)	NS
<i>agrII</i>	10 (35.7)	17 (20.7)	NS
<i>agrIII</i>	0 (0)	14 (17.1)	0.019
<i>agrIV</i>	2 (7.1)	2 (2.4)	NS
<i>cap5</i>	15 (53.6)	49 (59.8)	NS
<i>cap8</i>	13 (46.4)	33 (40.2)	NS
<i>bbp</i>	23 (82.1)	69 (84.1)	NS
<i>clfA/B</i>	28 (100)	82 (100)	NS
<i>fnbpA/B</i>	28 (100)	82 (100)	NS

Statistical analysis was performed using the Fisher's exact test. *P*-values <0.01 were considered as significant. NS, not significant.