Table S2 - Single nucleotide polymorphisms detected within the *agr* locus

		Prevalence Amongst Collection		
Mutation (Location)[a]	**Predicted Consequence**	***agr* Positive**[b]	***agr* Negative**[b]	**Total**
C-A (2172611)	AgrC $_{\mathrm{R6S}}$	40	16	56
C-T (2173112)	AgrC $_{\mathrm{P24S}}$	0	1	1
T-C (2173535)	AgrC $_{\mathrm{F165L}}$	0	1	1
INS-C (2173719)	AgrC - Frame shift	1	0	1
G-A (2174192)	AgrC $_{\mathrm{E384K}}$	0	1	1
C-T (2174219)	AgrC $_{\mathrm{R393C}}$	0	5	5
T-C (2174754)	AgrA $_{\mathrm{L134S}}$	0	1	1
INS-A (2175059)	AgrA - Frame shift	0	1	1
No mutation		0	27	27
No mutation (excluding AgrC $_{\mathrm{R6S}}$)		39	37	76

[a] Base position in TW20

[b] *agr* activity determined by the visual assessment of delta-haemolysis (present, positive; absent, negative)