



Fig. S6. *hasABC* promoter variants. (A) Illustrated are *hasABC* promoter pattern variants identified among the *emm89* clade 1 and and 2 strains. Patterns A and B account for 99% of the strains. Pattern B has a 38 bp deletion relative to pattern A, which eliminates a putative Rho independent terminator. In M1 strain MGAS2221, deletion of this terminator results in release of *hasABC* from CovR repression resulting in enhanced capsule production. (B) Distribution of *hasABC* promoter variants among the clade 1 and 2 strains. (C) Distribution of *hasABC* promoter variants among the clade 1 and 2 strains. Illustrated is genetic relationships among the *emm89* clade 1 and 2 strains inferred by neighbor-joining based on 5,663 core SNPs filtered using GUBBINS to exclude regions of horizontal gene transfer. Strains are colored by promoter variant as indicated in the index. Clade 1 strains are a nearly equal mix of pattern A (weak/repressed) and pattern B (strong/derepressed) promoter variants, whereas the vast majority of clade 2 strains are pattern A. These findings are consistent with the significantly greater level of *hasABC* transcripts for clade 1 strain MGAS11027 relative to clade 2 strain MGAS23530 determined by RNAseq.