Fig. S2. Genetic relationships among *emm*89 reference strain, with *emm*1 reference strain SF370 used as the rooting outgroup. Shown are genetic relationships among the three *emm*89 reference strains and the seven outlier strains using *emm*1 reference strain SF370 as an outgroup. Relationships were inferred based on 26,371 core SNPs by neighbor-network splits-decomposition. The sequence of branching of the three numerically dominant *emm*89 primary clades along the evolutionary path leading to the contemporary epidemic *emm*89 strains is clade1 (MGAS11027), followed by clade 2 (MGAS23530) and then epidemic clade 3 (MGAS27061).