



The *S. pyogenes emm* gene is generally associated between between the *mga* and *scpA* genes in 3 different arrangements (listed 1-3 above). Primers 1 and 2 used in the CDC *emm* typing protocol generally generate the “true” *emm* types shown in black font above, however in a minority of isolates, primers 1 and 2 generate the *emm* like gene sequences shown in red. The instances where multiple *emm* types have been deduced from whole genome sequence data in the Fittipaldi Laboratory are shown above (data taken from “Athey TB, Teatero S, Li A, Marchand-Austin A, Beall BW, Fittipaldi N. J Clin Microbiol. 2014 Mar 19. [Epub ahead of print]. Deriving Group A Streptococcus Typing Information from Short-Read Whole Genome Sequencing Data. We will be adding additional corresponding data documenting additional instances such as the ones listed here.