Table S1. The number of *S. pyogenes* MGAS315 IGRs that have homologous sequences in the selected *Streptococcus* genome

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| *Streptococcus* genome (Subjecta) | Numberb of *S. pyogenes* IGRs (Query) that showed up in the BLASTN alignments  | tRNAs and tmRNA of *S. pyogenes* (Query, total 68) that showed up in the BLASTN alignments  |
| *S. equi* *zooepidemicus* MGCS 10565 | 337 | 67 |
| *S. mutans* UA159 | 143 | 68 |
| *S. suis* 05ZYH33 | 101 | 65 |
| *S. sanguinis* SK36 | 93 | 66 |
| *S*. *gordonii str. Challis substr.* CH1 | 92 | 66 |
| *S. pneumoniae* CGSP14 | 96 | 66 |
| *S. agalactiae* NEM316 | 197 | 68 |

a Subject is each genome sequence of the seven selected streptococcal species. Each number in the table represents the number of pairwise alignments after query sequences interrogated each subject species.

b Redundant IGRs were removed, so each IGR represents a unique locus.