

**Table 5. BLAST comparisons of sequenced GAS genomes CDSs**

CDS	M3 vs. M1 (TBLASTN)	M1 vs. M3 (BLASTP)	M3 vs. M18 (TBLASTN)	M18 vs. M3 (BLASTP)
Common <sup>*</sup>	1641/1865 88.0%	1607/1752 91.7%	1753/1894 92.6%	1761/1889 93.2%
Unique <sup>†</sup>	224/1865 12.0%	145/1752 8.3%	141/1894 7.4%	128/1889 6.8%
Phage and unique	201/224 89.7%	71/145 49.0%	112/141 79.4%	71/128 55.5%

<sup>\*</sup>A CDS was defined “common” if it had a homologue in the comparison genome sharing greater than 50% positive (identical plus similar) amino acids across its complete sequence.

<sup>†</sup>A CDS was defined “unique” if it lacked a homologue in the comparison genome sharing greater than 50% positive (identical plus similar) amino acids across its complete sequence.