

Table 6. Characteristics of phages present in the sequenced GAS genomes

Phage	Insertion [*] site	Size kbp	Virulence [†] factor(s)	% G+C	CDS
315.1	1049-1053	39.5	None	37.8	56
315.2	1289-1290	40.1	<i>ssa</i>	38.3	60
315.3	1434-1491	34.4	<i>mf4</i>	38.0	52
315.4	1556-1557	41.8	<i>speK, sla</i>	38.6	64
315.5	1606-1607	38.2	<i>speA3</i>	38.1	55
315.6	1672-1673	40.0	<i>sdn</i>	39.7	51
8232.1	0342-0343	39.0	<i>speA1</i>	37.7	53
8232.2	0654-0713	41.1	<i>speC, mf2</i>	38.2	60
8232.3	1289-1290	46.7	<i>speL, speM</i>	37.6	69
8232.4	1434-1491	35.4	<i>mf3</i>	37.7	56
8232.5	1736-1737	41.8	<i>sda</i>	38.5	56
370.1	0654-0713	40.9	<i>speC, mf2</i>	39.3	49
370.2	0936-1010	42.5	<i>speI, speH</i>	38.0	57
370.3	1434-1491	33.5	<i>mf3</i>	38.0	48
370.4	2121-2148	13.5	None	36.8	18

^{*}SPy gene numbers from the M1 SF370 genome are given for CDSs flanking the phages.

[†]Only the putative secreted virulence factors encoded at the phage ends are listed.