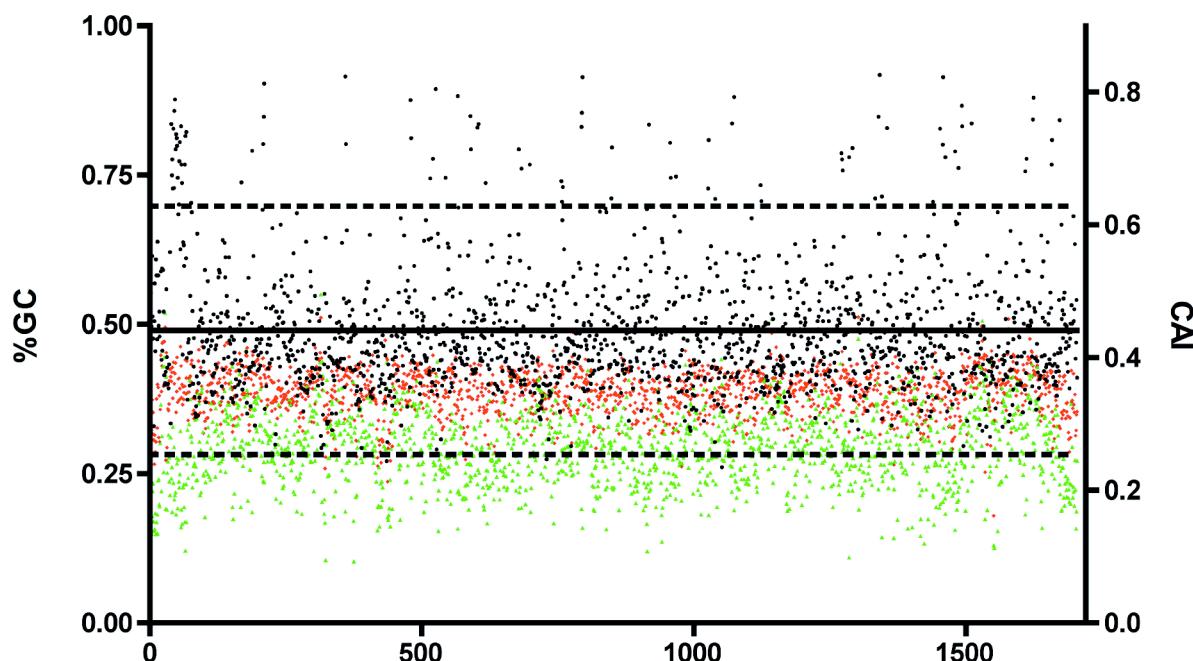


NZ131 – Supplemental Materials

Supplemental Figure 1. Codon adaptation index (CAI) and %G+C analysis of the NZ131 genome. The CAI of each predicted ORF is indicated (black points) with the mean CAI indicated by the solid line. The dotted lines indicated the limits defined by two standard deviations above and below the mean. The percentage %G+C for each predicted ORF is shown for the total coding region (red) and the third base position for each codon (green).



Supplemental Table 1. GAS strains used in these studies. All strains are from the University of Oklahoma collection or were recent clinical isolates.

| Strain | M serotype | Origin | Case |
|----------------------|------------|-------------|-------------------|
| Non invasive GAS M49 | | | |
| NZ131 | 49 | New Zealand | APSAGN |
| 2 | 49 | New Zealand | APSAGN |
| 3 | 49 | New Zealand | Scarlet fever |
| 4 | 49 | New Zealand | Scarlet fever |
| 5 | 49 | England | Scarlet fever |
| 6 | 49 | England | Scarlet fever |
| 7 | 49 | England | Scarlet fever |
| 8 | 49 | New Zealand | Scarlet fever |
| 9 | 49 | New Zealand | Scarlet fever |
| 10 | 49 | New Zealand | Scarlet fever |
| 11 | 49 | New Zealand | Pharyngitis |
| 12 | 49 | New Zealand | Scarlet fever |
| 13 | 49 | Denmark | Pharyngitis |
| 14 | 49 | Japan | Pharyngitis |
| 15 | 49 | Japan | Pharyngitis |
| 16 | 49 | USSR | Scarlet fever |
| 17 | 49 | Thailand | Scarlet fever |
| Invasive GAS M49* | | | |
| 1 | 49 | CA | Sepsis |
| 2 | 49 | CA | Sepsis |
| 3 | 49 | CA | Sepsis |
| 4 | 49 | CA | Sepsis |
| 5 | 49 | CA | Sepsis |
| 6 | 49 | Minnesota | Sepsis |
| 7 | 49 | CA | Sepsis |
| 8 | 49 | CA | Sepsis |
| 9 | 49 | CA | Sepsis |
| 10 | 49 | CA | Sepsis |
| 11 | 49 | CA | Sepsis |
| 12 | 49 | CA | Sepsis |
| 13 | 49 | Minnesota | Sepsis |
| 14 | 49 | CA | Sepsis |
| 15 | 49 | Oregon | Sepsis |
| 16 | 49 | Minnesota | Sepsis |
| 17 | 49 | CA | Surgical material |
| 18 | 49 | CA | Sepsis |
| 19 | 49 | CA | Sepsis |

| | | | |
|---------------------|----|-------------|-------------|
| 20 | 49 | CA | Sepsis |
| 21 | 49 | CA | Sepsis |
| 22 | 49 | CA | Sepsis |
| Other GAS Strains** | | | |
| SF370 | 1 | USA | Wound (41) |
| 287 | 1 | New Zealand | Tonsillitis |
| | 2 | USA | |
| 587 | 3 | USA | Skin lesion |
| | 3 | USA | |
| | 4 | USA | |
| | 4 | USA | |
| | 6 | USA | |
| | 9 | USA | |
| | 9 | USA | |
| | 11 | USA | |
| | 11 | USA | |
| 365 | 12 | USA | Pharyngitis |
| | 12 | USA | |
| | 22 | USA | |
| | 22 | USA | |
| | 22 | USA | |
| | 25 | USA | |
| | 25 | USA | |
| 785 | 28 | Trinidad | |
| | 28 | USA | |
| | 29 | USA | |
| 120 | 49 | England | |
| D914 | 53 | Germany | |
| 291 | 58 | USA | |
| | 58 | USA | |
| 260 | 60 | New Zealand | APSGN |
| 261 | 60 | New Zealand | Tonsillitis |
| | 80 | USA | |
| | 80 | USA | |
| 5082-01 | 82 | USA | |
| 5082-02 | 82 | USA | |
| 5082-03 | 82 | USA | |
| 5082-04 | 82 | USA | |
| 5082-05 | 82 | USA | |
| 5082-06 | 82 | USA | |
| 5082-07 | 82 | USA | |
| 5082-08 | 82 | USA | |
| 5082-09 | 82 | USA | |
| 5082-10 | 82 | USA | |

| | | |
|---------|-----|-----|
| | 87 | USA |
| | 87 | USA |
| | 103 | USA |
| | 103 | USA |
| | 107 | USA |
| | 111 | USA |
| 3602-00 | 118 | USA |
| | 118 | USA |

*Provided by Bernard Beale from the CDC collection of invasive strains collected in the USA during a six-year period from 2000 to 2006

**Strains with no associated strain number were recent clinical isolates. The *emm* type was confirmed by DNA sequencing.

Supplemental Table 2. Oligonucleotide primers used for PCR analysis.

| Sequence (5' – 3') | Gene Target | Product Size (bp) |
|--------------------------|-----------------------|-------------------|
| ACTTGCTACTGGTTGCCGATT | Prophage NZ131.1 int | 354 |
| CGGAAAGCGTGAAAGGTAAAT | | |
| GCCACGAATAACCAAAAGAAC | Prophage NZ131.2 int | 323 |
| AAGCGATAGCGTAGTCGAAGG | | |
| TCTGTTAAGAACGACGGCTCA | Prophage NZ131.3 int | 303 |
| ATTGACATCAGTGTGCCAAC | | |
| GGGCTTGCTGTTCCCTGACTAT | nudA | 303 |
| CACACGAGATGGTGCTAAGTCC | | |
| CGTCCTTCCAAACTCCCATAGA | nudB | 355 |
| CCCTTGAAATGTGTGCAACGTG | | |
| ACGCTATTAAATTCAAGAACCTTC | nudC | 626 |
| ATTTACGATTTTCCAGCTATCT | | |
| GCGAAGTGACCCAAGATGAT | Spy1989-1988 junction | 480 |
| GATAGCAACCCCTTGACTGC | | |
| AAGCGGATGTGATTGTAGCC | Spy1988-1987 junction | 461 |
| CAGGCAATTCCACCTGATCT | | |

Supplemental Table 3. Transcript mapping of the nudABC region. The PCR primers shown were used to map the presence of genes on a cDNA created from a polycistronic mRNA from strain SF370 (*nudABC*-) or NZ131 (*nudABC*+). The results show that *nudABC* is an addition to an operon common to all GAS genomes. The specificity of all amplified products was confirmed by DNA sequencing (not shown).

| Primer | Sequence | cDNA Region Amplified | |
|----------|-------------------------|-----------------------|-------|
| | | SF370 | NZ131 |
| 89b88.L | GCGAAGTGACCCAAGATGAT | + | - |
| 89b88.R | GATAGCAACCCCTTGACTGC | | |
| 88b87.L | AAGCGGATGTGATTGTAGCC | + | + |
| 88b87.R | CAGGCAATTCCACCTGATCT | | |
| 89bO1.L | ACGATAGTGGCGAAATGA | - | + |
| 89bO1.R | GGCATCATCAACTTGGACCT | | |
| O1bNDX.L | TGCGTCTGAATGACGAGAAG | - | + |
| O1bNDX.R | CCAGGTGTCAGGAAAAGGAA | | |
| NDXbO3.L | GCGATTCGCAAGATATGGT | - | + |
| NDXbO3.R | CCCACTGAGATATAGGAAGCTTA | | |

Supplemental Table 4. Survey of NZ131 prophage integrases in M49 strains.

| Non-Invasive M49 GAS | | | |
|----------------------|--------------------|--------------------|--------------------|
| | NZ131.1 <i>int</i> | NZ131.2 <i>int</i> | NZ131.3 <i>int</i> |
| 1 | + | + | + |
| 2 | + | + | + |
| 3 | - | + | - |
| 4 | - | + | - |
| 5 | + | - | - |
| 6 | + | - | - |
| 7 | - | - | - |
| 8 | - | + | - |
| 9 | - | + | - |
| 10 | - | + | - |
| 11 | - | - | - |
| 12 | - | - | - |
| 13 | - | + | - |
| 14 | - | + | - |
| 15 | - | - | - |
| 16 | - | - | - |
| Invasive M49 GAS | | | |
| | | | |
| 1 | - | + | - |
| 2 | - | + | - |
| 3 | - | + | - |
| 4 | - | + | - |
| 5 | - | + | - |
| 6 | - | - | - |
| 7 | - | + | - |
| 8 | - | + | - |
| 9 | - | + | - |
| 10 | - | - | - |
| 11 | - | + | - |
| 12 | + | + | - |
| 13 | - | - | + |
| 14 | - | - | - |
| 15 | - | - | - |
| 16 | + | - | - |
| 17 | - | + | - |
| 18 | - | + | - |
| 19 | - | + | - |
| 20 | - | + | - |
| 21 | - | + | - |
| 22 | - | - | - |