

Supplementary Information

Proteome-wide selected reaction monitoring assays for the human pathogen *Streptococcus pyogenes*

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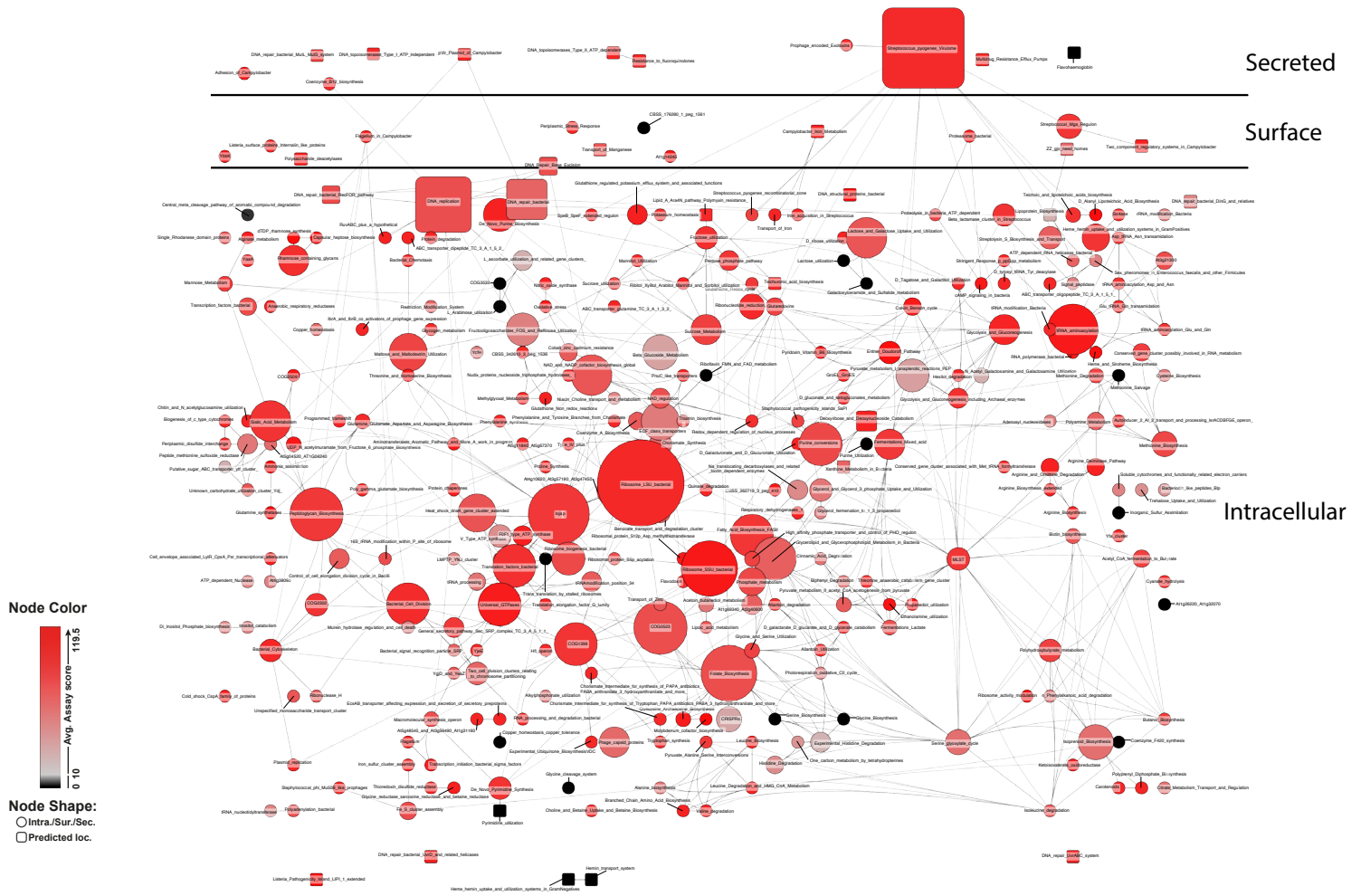
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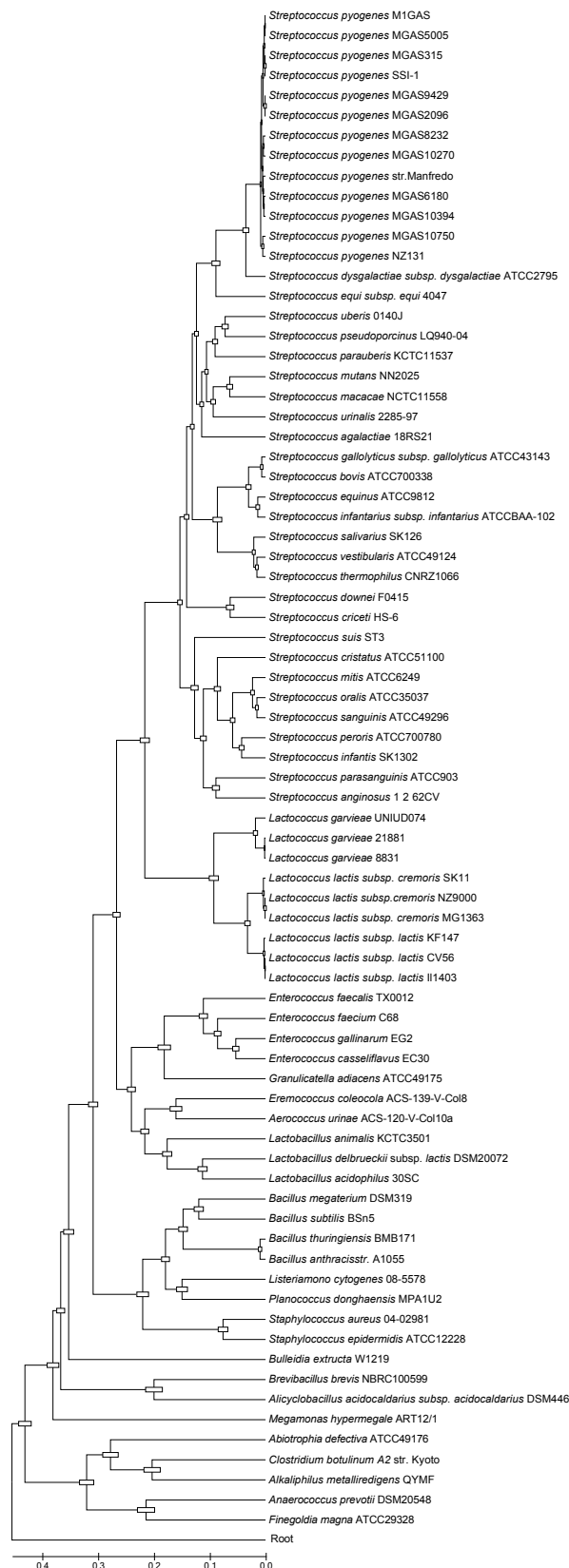
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Supplementary Figure S1 | Outline of the GAS proteome network topology and assay score.



Circles represent NMPDR subsystems where all proteins predominantly have the same subcellular location, secreted, surface associated or intracellular, according to the subcellular protein profiles in Figure 4a-d. Rectangles represent NMPDR subsystems where an equal number of members have opposing subcellular location profiles. The localization of the rectangles in the network is influenced by the edges, which represent protein members that belong to more than one NMPDR subsystem. Increasing node size represents increasing number of member proteins. The color represents average SRM assay score, where red indicates NMPDR subsystems with high-average SRM assay score and black indicating NMPDR subsystems with low average SRM assays score.

Supplementary Figure S2 | Phylogenetic relationships among selected species in the Firmicutes phylum



A maximum likelihood phylogenetic tree for selected bacterial species based on the Tamura-Nei model⁴⁹ was built upon an alignment of nucleotide sequences of *rpoB*⁵⁰ extracted from respective genome (downloaded from PATRIC Bacterial Bioinformatics Resource Center²⁸). The tree with the highest log likelihood (-76672.8395) is shown. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 76 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 2323 positions in the final dataset. Evolutionary analyses were conducted in MEGA5⁵¹.

Supplementary Table S1 | Genome sequenced GAS strains used in this work.

| PATRIC Genome Info Id²⁸ | Genome Name | Serotype | CDS† | Publication‡ |
|---|--|-----------------|-------------|------------------------|
| 79812 | <i>Streptococcus pyogenes</i> M1 GAS (SF370) | M1 | 1919 | 11296296 ⁵² |
| 7871 | <i>Streptococcus pyogenes</i> MGAS5005 | M1 | 1931 | 16088826 ³¹ |
| 120482 | <i>Streptococcus pyogenes</i> MGAS10270 | M2 | 2024 | 16636287 ³⁰ |
| 110589 | <i>Streptococcus pyogenes</i> SSI-1 | M3 | 2009 | 12799345 ⁵³ |
| 96585 | <i>Streptococcus pyogenes</i> MGAS315 | M3 | 2010 | 12122206 ⁵⁴ |
| 25933 | <i>Streptococcus pyogenes</i> MGAS10750 | M4 | 2030 | 16636287 ³⁰ |
| 41547 | <i>Streptococcus pyogenes</i> str. Manfredo | M5 | 1935 | 17012393 ⁵⁵ |
| 30273 | <i>Streptococcus pyogenes</i> MGAS10394 | M6 | 1960 | 15272401 ⁵⁶ |
| 37061 | <i>Streptococcus pyogenes</i> MGAS9429 | M12 | 1893 | 16636287 ³⁰ |
| 133020 | <i>Streptococcus pyogenes</i> MGAS2096 | M12 | 1953 | 16636287 ³⁰ |
| 4396 | <i>Streptococcus pyogenes</i> MGAS8232 | M18 | 2007 | 11917108 ⁵⁷ |
| 35950 | <i>Streptococcus pyogenes</i> MGAS6180 | M28 | 1956 | 16088825 ⁵⁸ |
| 129711 | <i>Streptococcus pyogenes</i> NZ131 | M49 | 1876 | 18820018 ³² |

† Coding sequences from PATRIC annotation source

‡ PUBMED identifier

Supplementary References

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