Supplementary fig. 1. DNA microarray analysis highlighting the core genome of the non-M1 GAS strains used in this study. Heat map generated from an oligonucleotide microarray with probes representing M1 core ORFeome in addition to ORFs representing various M1, M3, M18, and *S. dysgalactiae subsp. equisimilis* prophages (phage, and corresponding genes, are indicated; see Supplementary table 1). Strains under examination are designated at the top of each column. Red indicates gene present, based on median-normalised fluorescence units exceeding a threshold value, and black indicates gene absent.

- \$\phi 370.1 (SpcC/MF2)
- \$\phi 370.2 (SpcL/H)
- \$\phi 370.3 (MF3)
- \$\phi 370.4 (tr.ncated phage - no toxin)
- \$\phi 5001 (SpcA2)
- \$\phi 5005.3 (Sda1)
- \$\phi 315.1 (Ne toxin)
- \$\phi 315.1 (Spc toxin)
- \$\phi 315.5 (SpcA)
- \$\phi 315.5 (SpcA)
- \$\phi 315.6 (SpcA)
- \$\phi 315.6