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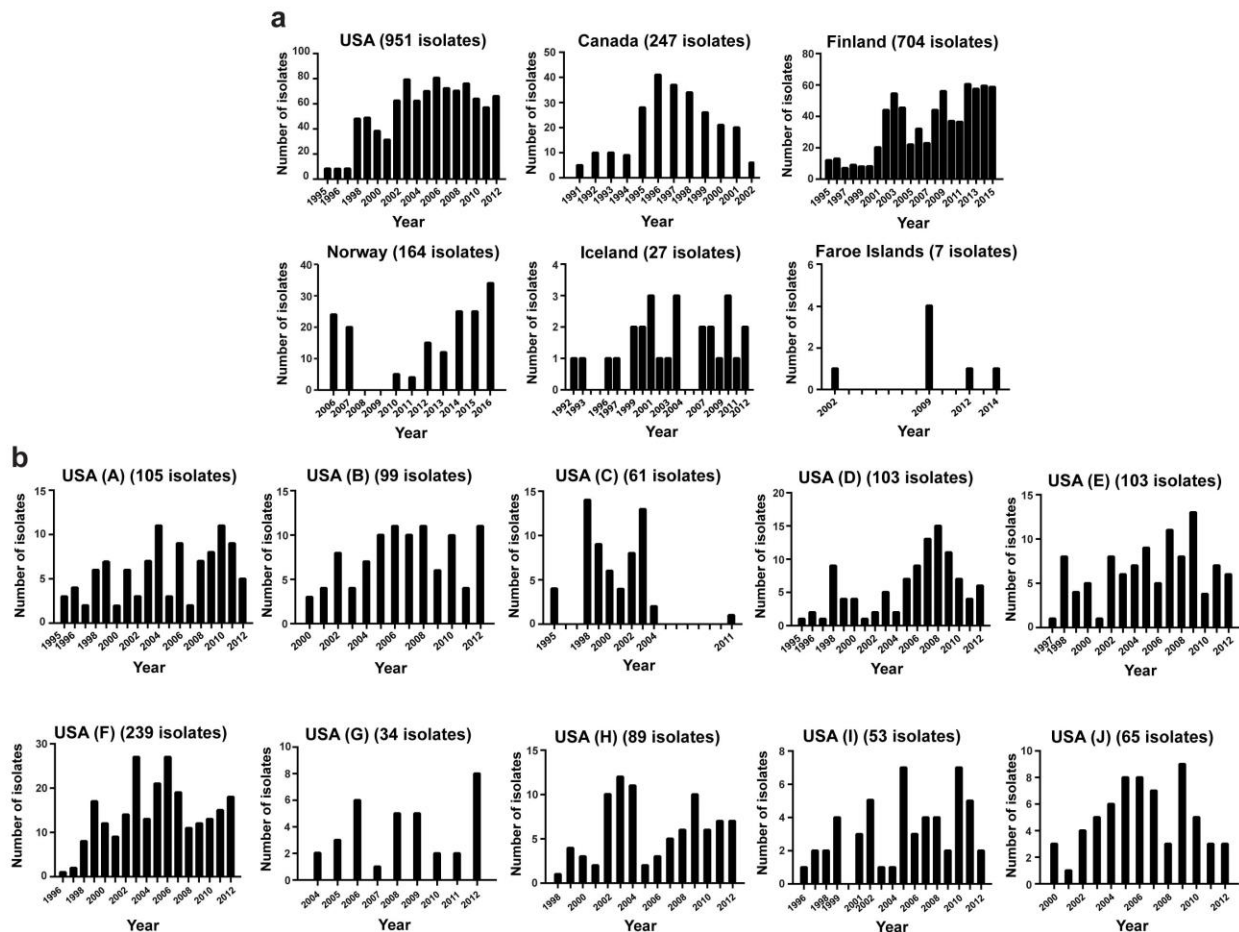
Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into *Streptococcus pyogenes* pathogenesis

Priyanka Kachroo ^{1,20}, Jesus M. Eraso ^{1,20}, Stephen B. Beres ¹, Randall J. Olsen^{1,2,3}, Luchang Zhu¹, Waleed Nasser¹, Paul E. Bernard¹, Concepcion C. Cantu¹, Matthew Ojeda Saavedra¹, María José Arredondo¹, Benjamin Strobe¹, Hackwon Do¹, Muthiah Kumaraswami¹, Jaana Vuopio ^{4,5}, Kirsi Gröndahl-Yli-Hannuksela⁴, Karl G. Kristinsson^{6,7}, Magnus Gottfredsson ^{7,8}, Maiju Pesonen^{9,10}, Johan Pensar⁹, Emily R. Davenport¹¹, Andrew G. Clark¹¹, Jukka Corander^{9,12}, Dominique A. Caugant¹³, Shahin Gaini^{14,15,16,17}, Marita Debess Magnussen^{7,18}, Samantha L. Kubiak¹, Hoang A. T. Nguyen¹, S. Wesley Long¹, Adeline R. Porter¹⁹, Frank R. DeLeo¹⁹ and James M. Musser ^{1,2,3*}

¹Center for Molecular and Translational Human Infectious Diseases Research, Department of Pathology and Genomic Medicine, Houston Methodist Research Institute and Houston Methodist Hospital, Houston, TX, USA. ²Department of Pathology and Laboratory Medicine, Weill Cornell Medical College, New York, NY, USA. ³Department of Microbiology and Immunology, Weill Cornell Medical College, New York, NY, USA. ⁴Institute of Biomedicine, Medical Microbiology and Immunology, University of Turku, Turku, Finland. ⁵National Institute for Health and Welfare, Helsinki, Finland.

⁶Department of Clinical Microbiology, Landspítali University Hospital, Reykjavik, Iceland. ⁷Faculty of Medicine, School of Health Sciences, University of Iceland, Reykjavik, Iceland. ⁸Department of Infectious Diseases, Landspítali University Hospital, Reykjavik, Iceland. ⁹Helsinki Institute of Information Technology, Department of Mathematics and Statistics, University of Helsinki, Helsinki, Finland. ¹⁰Department of Computer Science, Aalto University, Espoo, Finland. ¹¹Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA. ¹²Department of Biostatistics, University of Oslo, Oslo, Norway. ¹³Division for Infection Control and Environmental Health, Norwegian Institute of Public Health, Oslo, Norway. ¹⁴Medical Department, Infectious Diseases Division, National Hospital of the Faroe Islands, Tórshavn, Denmark. ¹⁵Department of Infectious Diseases, Odense University Hospital, Odense, Denmark. ¹⁶Department of Clinical Research, University of Southern Denmark, Odense, Denmark. ¹⁷Department of Science and Technology, Centre of Health Research, University of the Faroe Islands, Tórshavn, Denmark. ¹⁸Thetis, Food and Environmental Laboratory, Tórshavn, Denmark.

¹⁹Laboratory of Bacteriology, Rocky Mountain Laboratories, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, USA. ²⁰These authors contributed equally: Priyanka Kachroo, Jesus M. Eraso. *e-mail: JMMusser@houstonmethodist.org

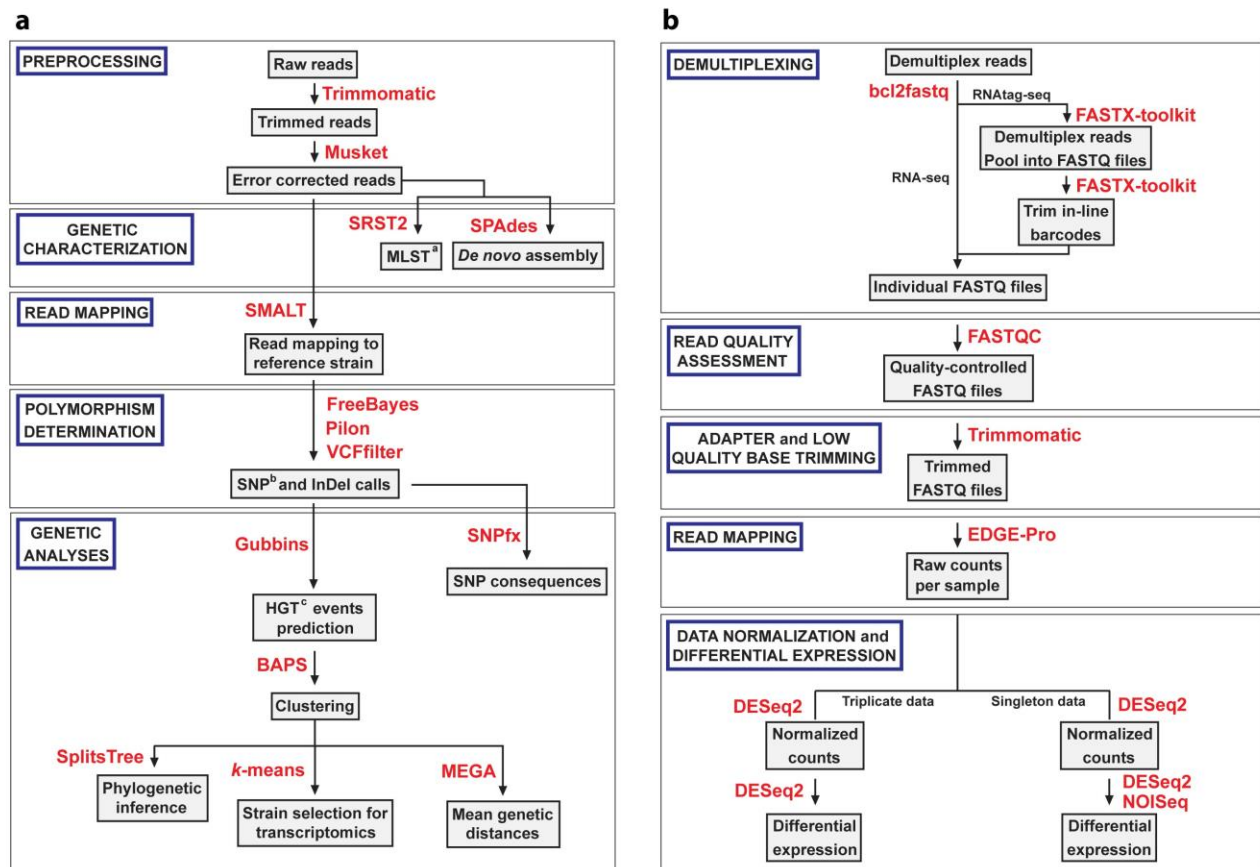


Supplementary Figure 1. Distribution of *emm28* isolates by country and state in the USA

Supplementary Figure 1

Distribution of *emm28* isolates by country and state in the USA.

All strains were isolated during a 26-year period, spanning 1991 through 2016. **(a)** Distribution of strains by country. Vertical black bars indicate the number of isolates per year. The total number of strains isolated in the USA was 952, of which 951 strains were collected as part of the Active Bacterial Core (ABC) surveillance study conducted by the Centers for Disease Control and Prevention (see <https://www.cdc.gov/abcs/index.html> for a complete description of the study). The one additional strain (from Texas) is strain MGAS6180, which is the genome sequence reference strain. Canadian strains are all from Ontario. The Faroe Islands are a self-governing part of Denmark. Regardless of country, all strains were recovered as part of comprehensive, population-based studies. **(b)** Distribution of *emm28* isolates by state in the USA. All strains were isolated during a period of 18 years, spanning 1995 through 2012. Vertical black bars indicate the number of isolates per year. For the U.S. isolates, the states have been coded (A-J) at the request of the Centers for Disease Control.

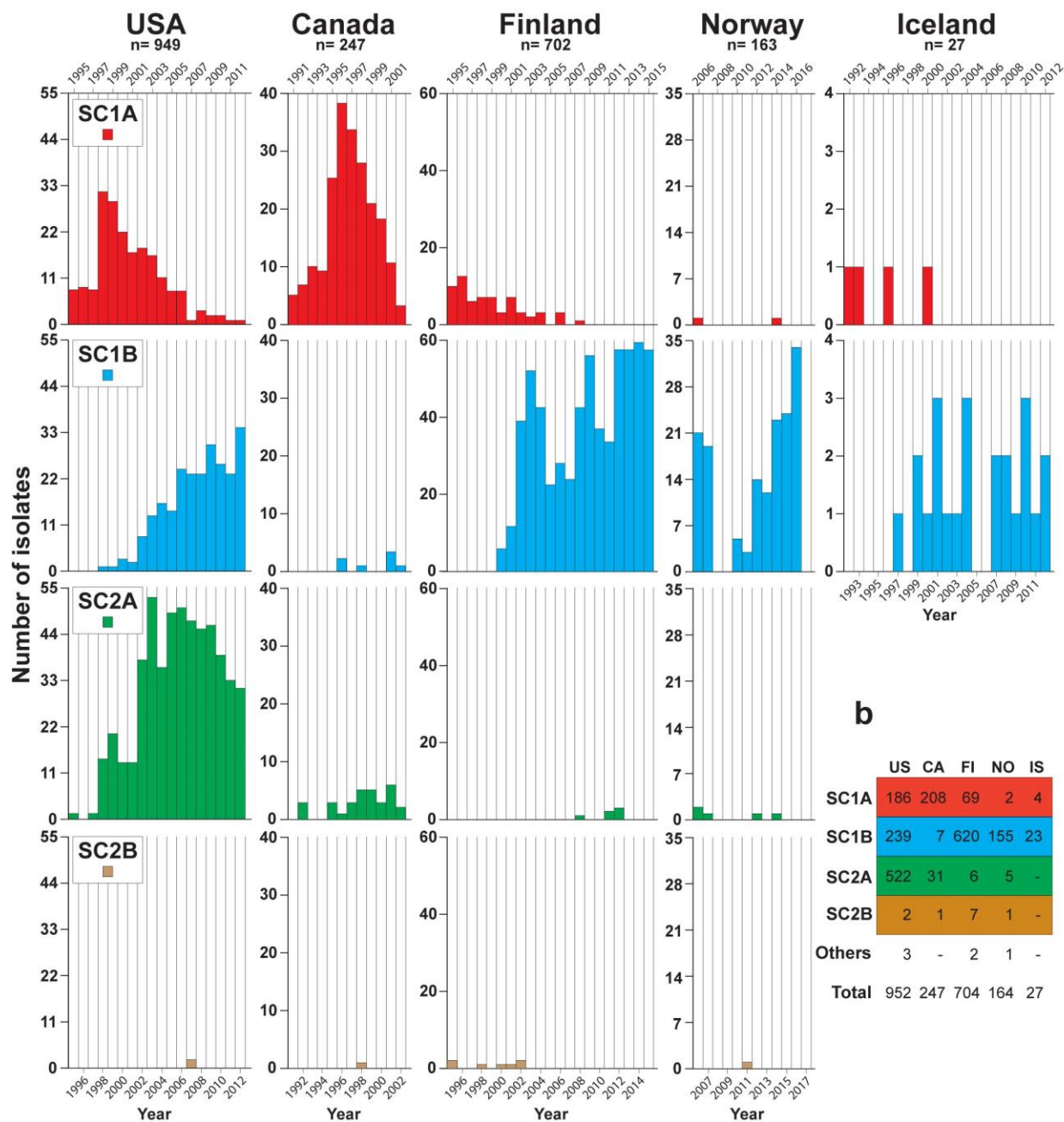


Supplementary Figure 2

Flowcharts depicting bacterial genome and transcriptome data analysis.

(a) Next-generation sequencing data analysis pipeline employed for the preprocessing, read mapping, variant discovery and downstream genomic analyses of whole-genome sequencing data. ^aMLST: Multilocus sequence type, ^bSNP: Single nucleotide polymorphism, ^cHGT: Horizontal gene transfer. (b) Bioinformatics pipeline for demultiplexing, quality assessment, adapter trimming, read mapping, and data normalization and differential expression of transcriptome data.

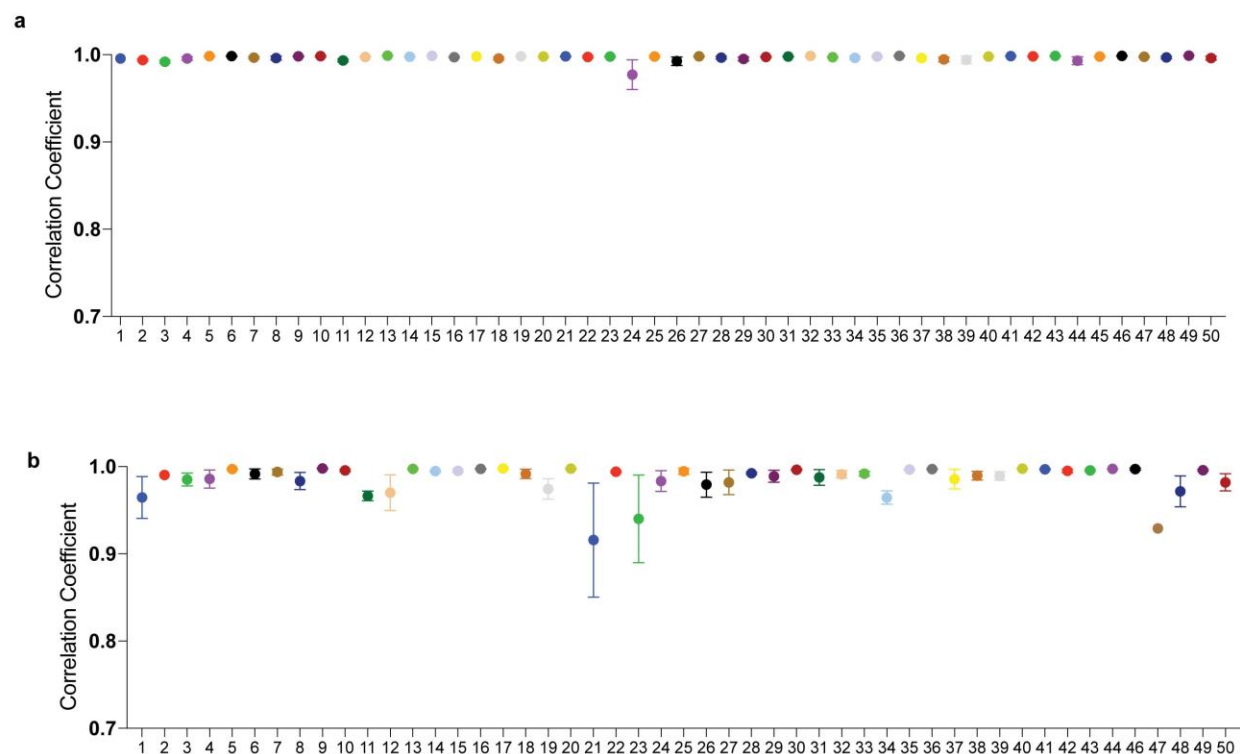
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Supplementary Figure 3

Distribution of *emm28* isolates by genetic subclade, country and year.

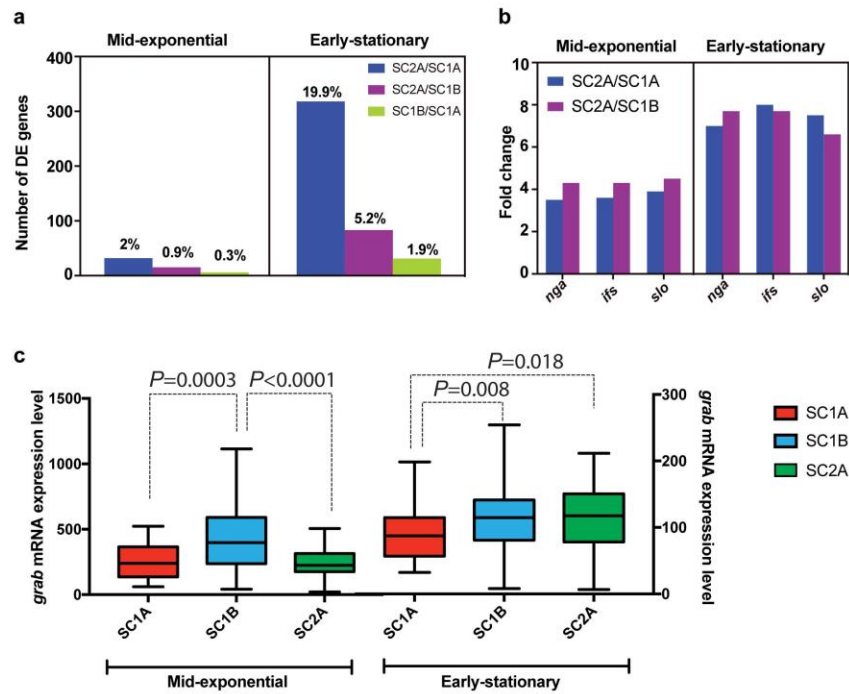
Strains are represented by country and year of isolation. Only strains belonging to subclades 1A (SC1A-red), 1B (SC1B-blue), 2A (SC2A-green), and 2B (SC2B-brown) are shown. **(a)** Vertical bars indicate the number of isolates per year. The number (n) of strains isolated in each country is shown. Six distant outlier strains in the phylogenetic tree and 7 strains from the Faroe Islands are not shown. Thus, the number of strains does not sum to the total sample of 2,101 strains. No strains belonging to subclade SC2A or SC2B were isolated in Iceland. **(b)** Total number of strains belonging to each individual subclade per country. US, United States; CA, Canada (Ontario); FI, Finland; NO, Norway; IS, Iceland. Others refers to 6 distant outlier strains in the phylogenetic tree.



Supplementary Figure 4

Correlation among biological replicates for 50 strains analyzed by RNA-seq.

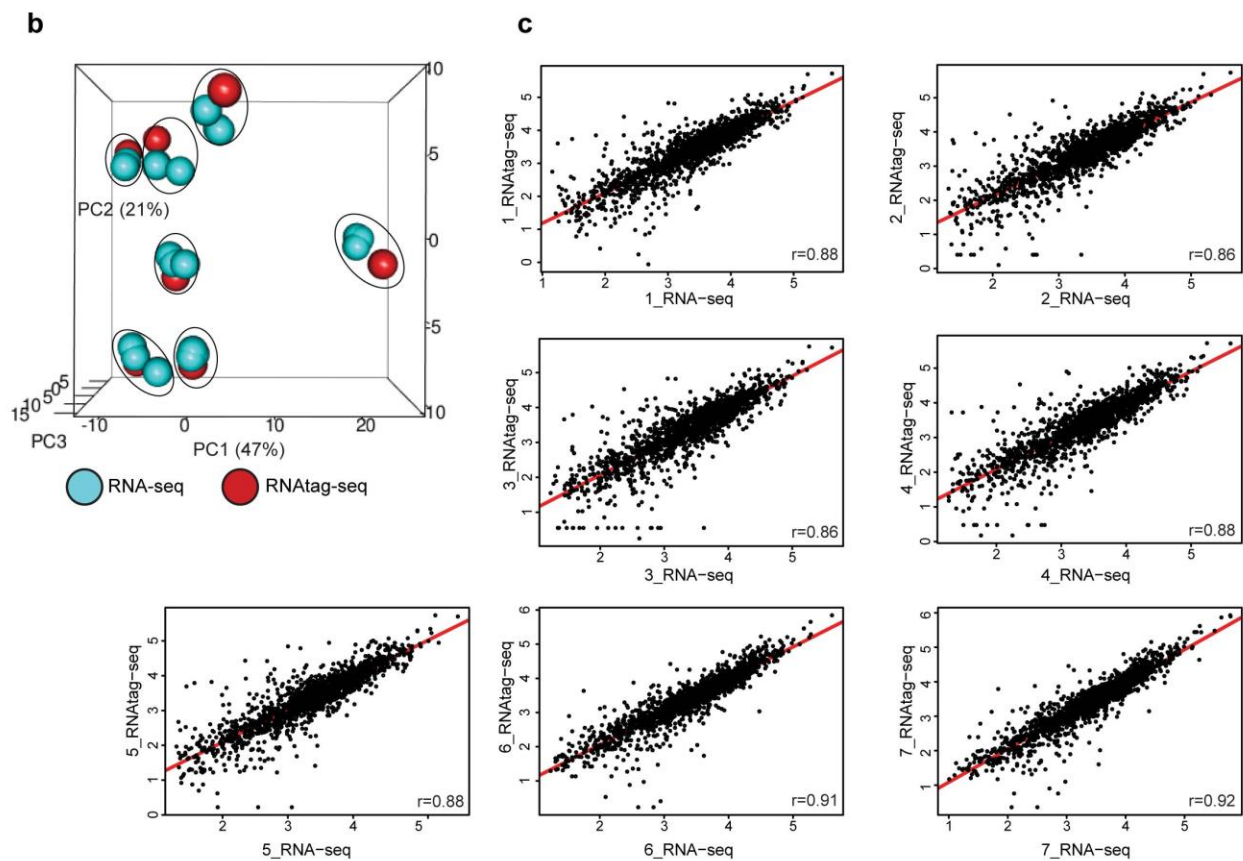
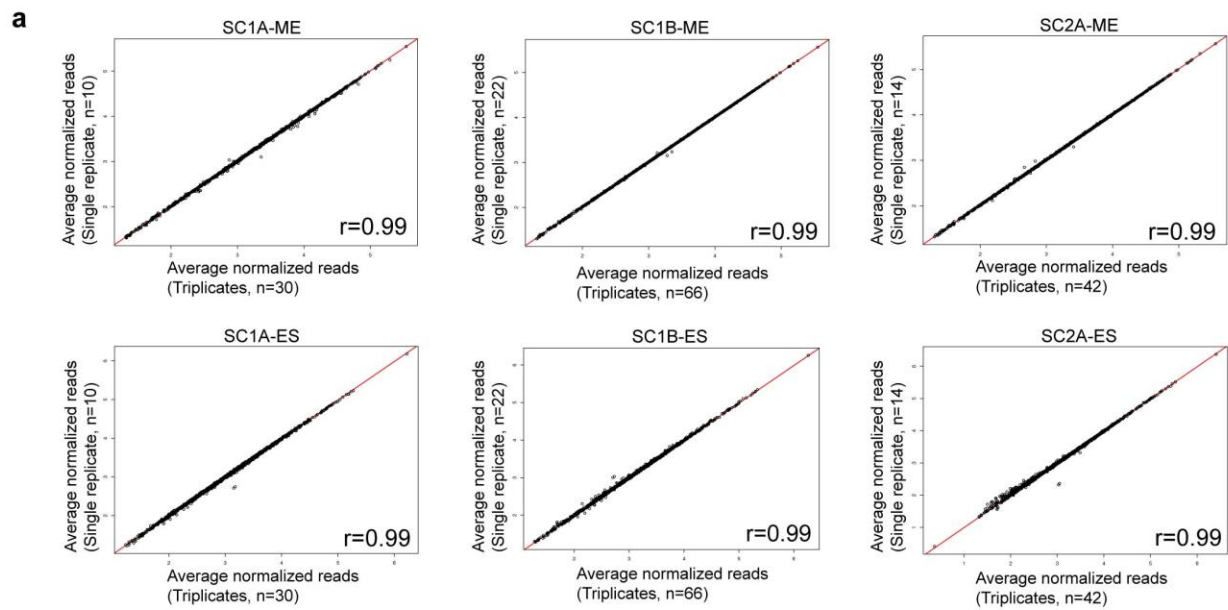
Comparison of biological replicates per strain at mid-exponential (a) and early-stationary phase (b). Mean correlation coefficient (Pearson) and standard deviation of normalized and log-transformed transcript counts for three biological replicates per strain are plotted.



Supplementary Figure 5

Transcriptome alterations and genetic subclades.

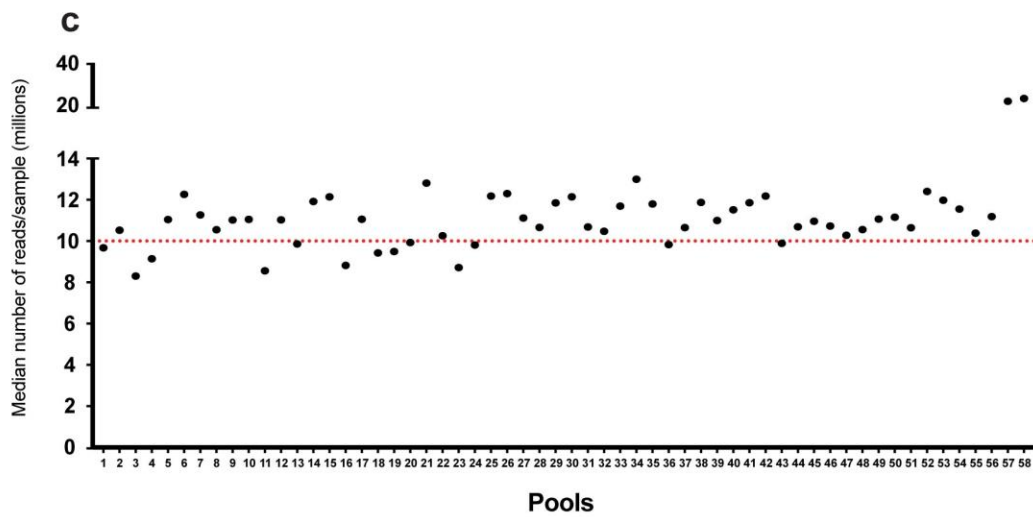
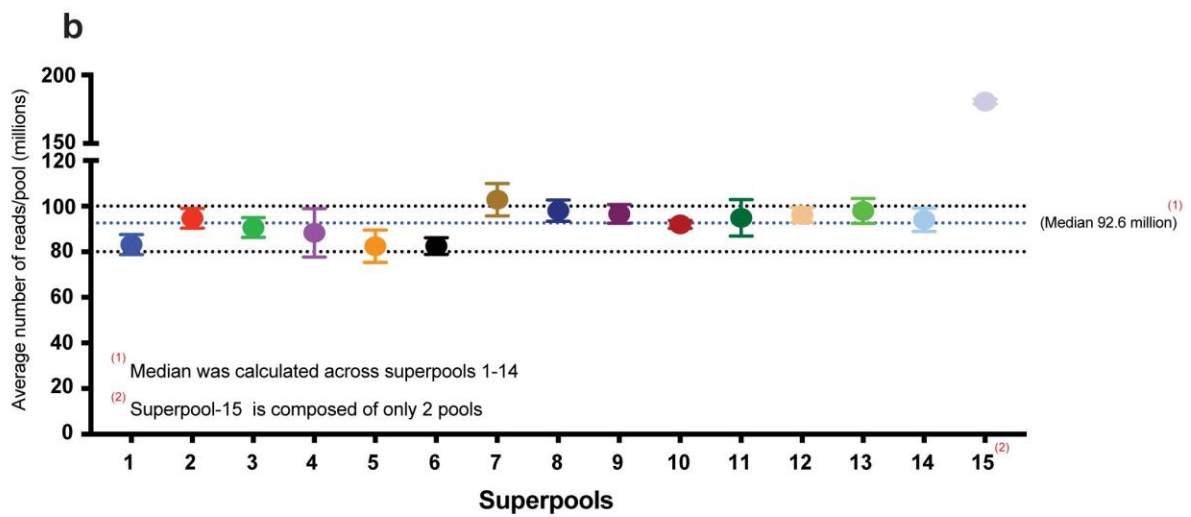
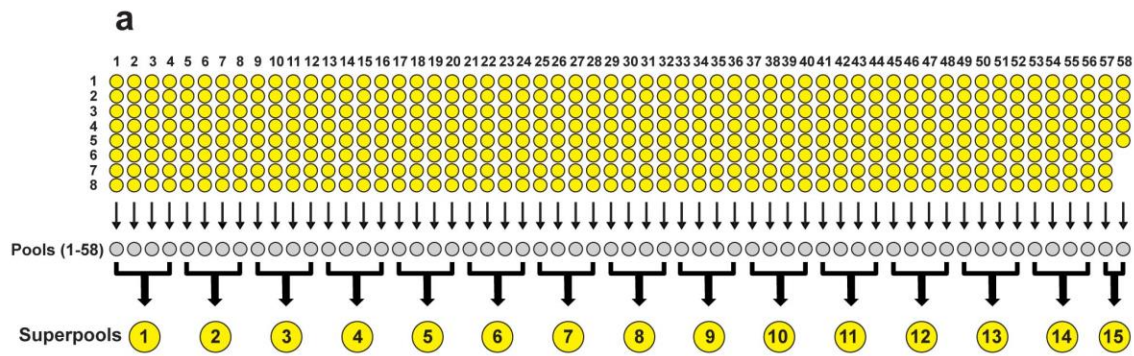
(a) Schematic depicts number of differentially expressed (DE) genes obtained by comparing transcriptome data for strains in the three major genetic subclades at mid-exponential (ME) and early stationary (ES) phases. (b) Fold-increase in *nga-ifs-slo* transcript levels in SC2A (n=15) strains compared to SC1A (n=12) and SC1B (n=23) strains at ME and ES phase. (c) *grab* gene transcript levels (normalized counts) were significantly increased in SC1B (n=23) strains compared to SC1A (n=12) strains at both growth phases (ME and ES). A significant increase in *grab* transcript levels in SC2A (n=15) strains compared to SC1A (n=12) strains was observed at ES phase. Statistical tests were performed using Mann-Whitney (two-tailed) test. Data are presented as box and whisker plots, where whiskers represent the minimum and maximum values. n represents the number of strains; each strain has three independent biological replicates.



Supplementary Figure 6

Comparison of three replicates versus single replicate and RNA-seq versus RNAtag-seq.

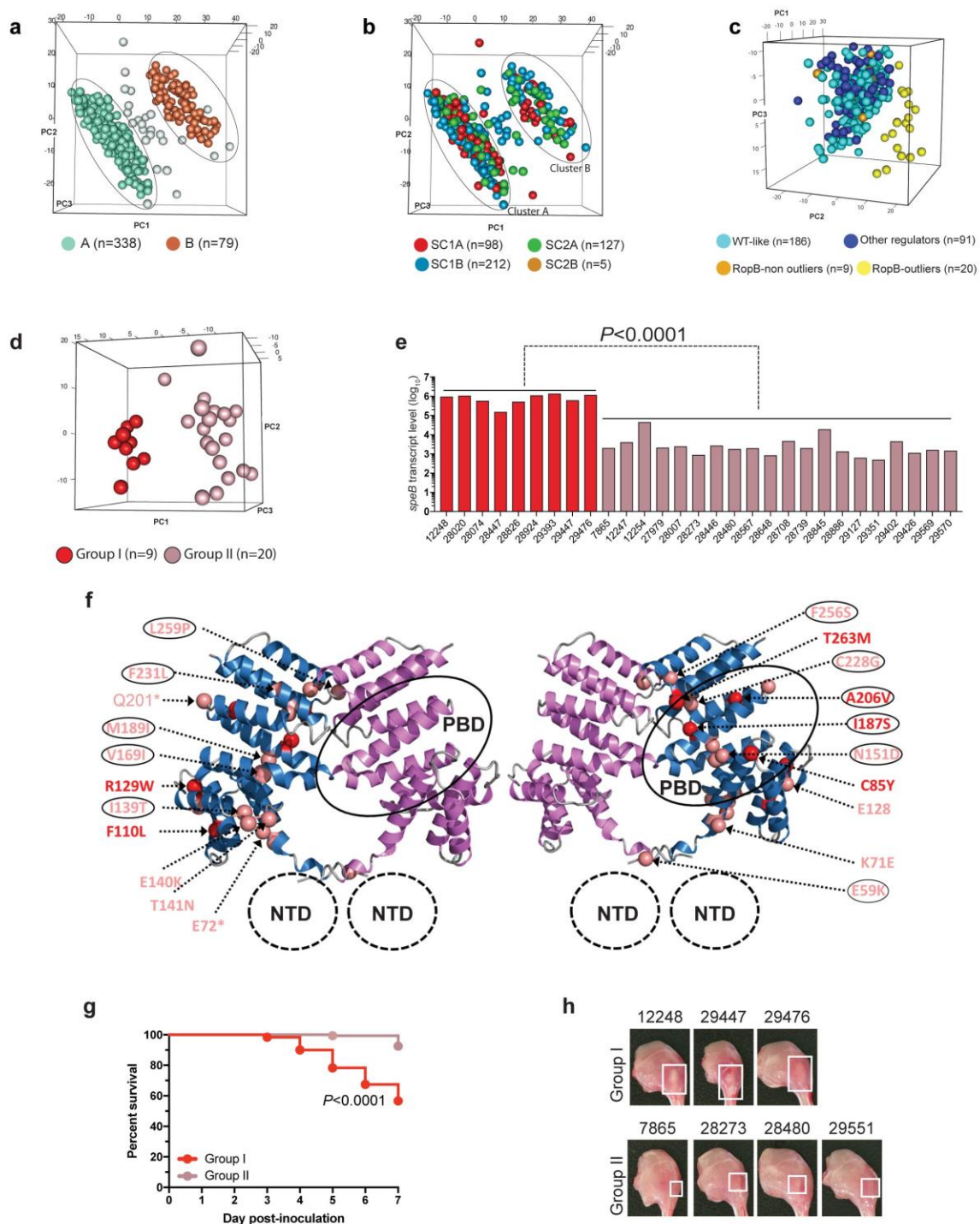
(a) Scatterplots comparing WT-like strains from each of three major subclades (10 SC1A, 22 SC1B, 14 SC2A) using triplicates versus one randomly selected replicate from the 50-strain data. Presence of three biological replicates in the 50-strain data allowed us to simulate comparisons of averaged normalized counts when three versus one replicate were used. Strong correlation ($r=0.99$) was observed for each triplicate versus single-replicate comparison. Pearson correlation coefficient (r) is shown for each comparison. n represents number of samples (number of strains multiplied by number of replicates). **(b)** Seven strains were processed using the two protocols, i.e., RNA-seq (three biological replicates per strain) and RNAtag-seq (singletons, i.e., using single replicates). Principal component analysis of the seven strains processed using RNA-seq (three spheres colored cyan in the PCA plot) and RNAtag-seq (single sphere colored red in the PCA plot) displays overlapping spatial clustering. Expression profile of the 7 strains in the PCA plot is circled and numbered 1 through 7. Strains analyzed: 1-MGAS7888, 2-MGAS29284, 3-MGAS29553, 4-MGAS28746, 5-MGAS7914, 6-MGAS28647, and 7-MGAS28686. **(c)** Scatterplots were generated for the normalized counts (log transformed) from the aforementioned seven strains processed using the two protocols, i.e., RNA-seq and RNAtag-seq. For each strain, normalized transcript counts were averaged over the three biological replicates (RNA-seq protocol) and compared to RNAtag-seq normalized counts (singleton strain samples). Pearson correlation coefficient (r) is shown for each comparison.



Supplementary Figure 7

Strategy used to make pools and superpools and their sequencing read content (millions).

(a) Strategy used to make pools and superpools. Strains (small yellow circles) were grouped to form 58 distinct pools (grey circles) by labeling total RNA extracted from each strain with unique barcoded oligoribonucleotides. RNA from 8 strains was mixed to create one pool, with the exception of pool 58, which contained RNA from only 5 strains. In total there were 58 pools. cDNAs from each pool were individually barcoded with Illumina P7 index oligonucleotides. Four different P7 oligonucleotides were used in this study. Four pools were mixed to form one superpool (large yellow circles). In total there were 15 superpools. Pool 58 contained cDNA from only five strains, and superpool 15 contained only two pools. The original number of strains we performed RNAtag-seq analysis on was 461, and here we present data for 442. Data from 19 strains were not included because of low sequence coverage. **(b)** Average number of sequence reads per pool for each of the 15 superpools is presented. Each circle represents mean and error bars represent standard deviation (SD). Median was calculated using data for superpools 1-14 (each comprised of four pools). Superpool 15 contained only two pools. **(c)** Graph depicts the median number of reads per sample per pool in millions. Median reads per sample for the pools 57 and 58 are larger due to the higher sequencing depth of these pools.

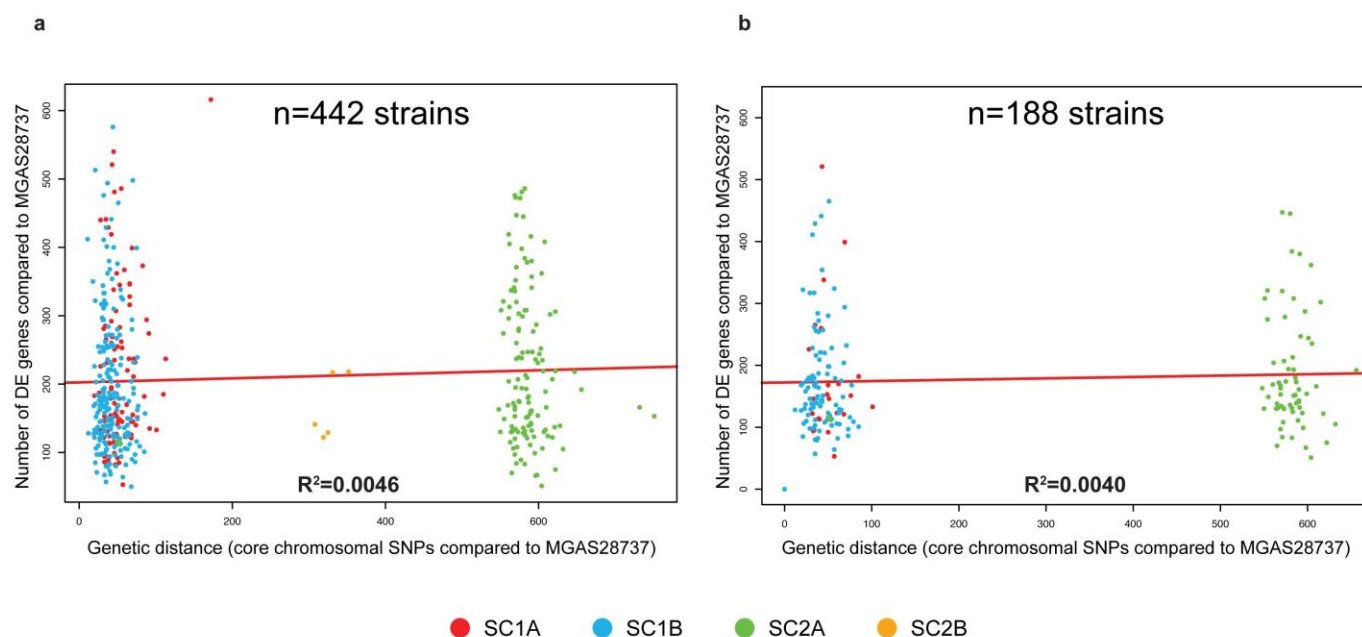


Supplementary Figure 8. PCA plot of singleton strains and analysis of Cluster A *ropB* mutant strains

Supplementary Figure 8

PCA plot of singleton strains and analysis of Cluster A *ropB* mutant strains.

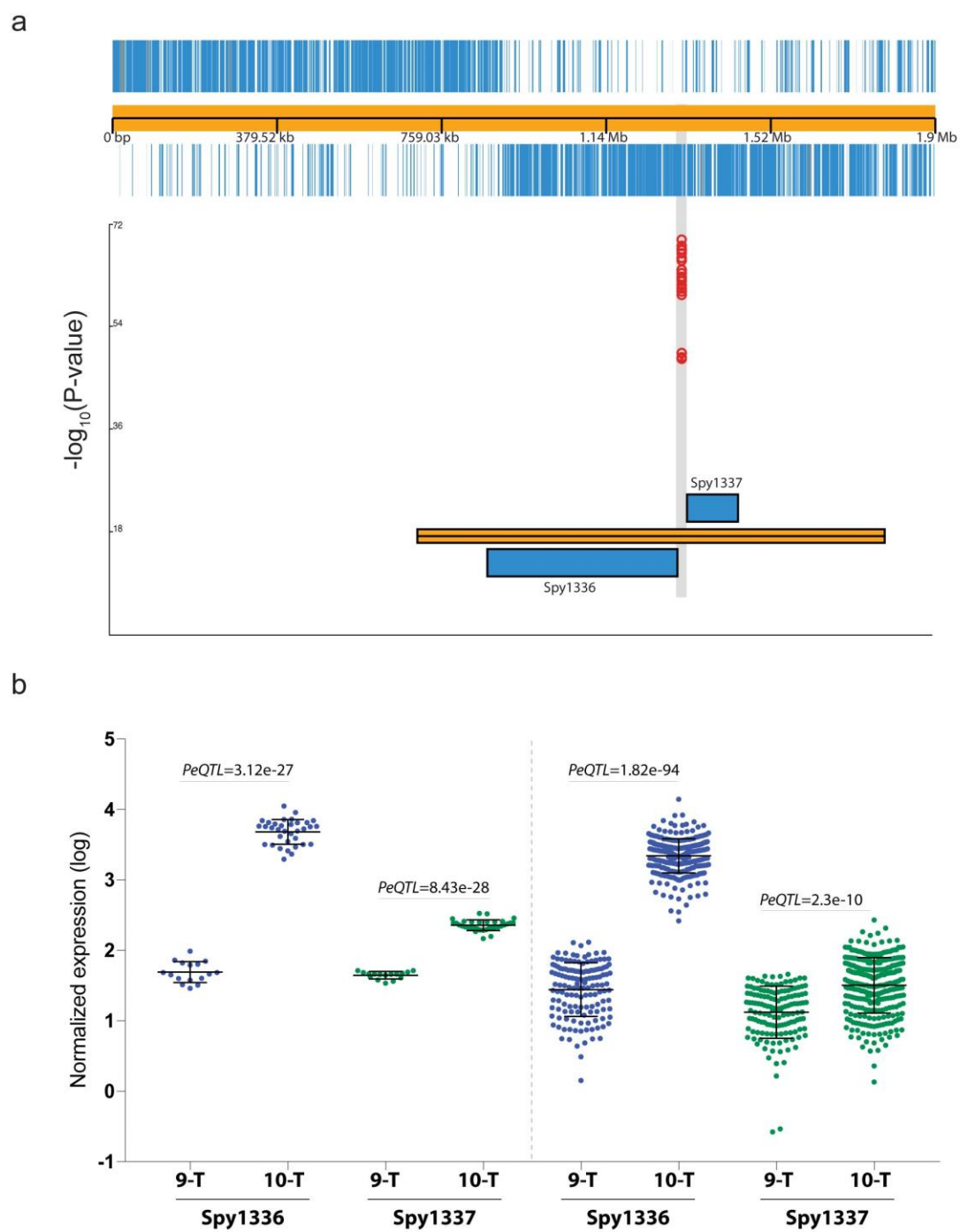
(a) The two major clusters identified by DBSCAN are shown. (b) No subclade-specific clustering was evident within the two clusters. (c) Twenty strains with *ropB* mutations are outliers (colored yellow) and group away from the other strains with *ropB* mutations (colored orange). *ropB*-non-outlier strains cluster with WT-like strains (colored light blue) and strains with mutations in other major regulator genes (colored blue). (d) Cluster A *ropB* mutant strains separated into two groups validated by *k*-means clustering and were designated arbitrarily as Group I and Group II. (e) Group II *ropB* mutant strains had significantly decreased *speB* transcript levels compared to Group I strains (Mann-Whitney, two-tailed, $P < 0.0001$). (f) Mutations were mapped onto the crystal structure of the C-terminal region of the RopB protein. Variant amino acid positions associated with Group I or Group II organisms are labeled in red and pink, respectively. Amino acid residues present in inferred functional domains are demarcated with ovals. Mutations located in RopB functional domains were present at significantly increased frequency (test of proportions-one-tailed, $P < 0.05$) in Group II strains (pink labels within ovals) compared to Group I strains (red labels within ovals). PBD: peptide binding domain, NTD: N-terminal domain. The crystal structure of the NTD has not been solved. (g) Kaplan-Meier curve showing that the Group I ($n=3$) and Group II ($n=4$) strains differ significantly (log-rank test) in virulence in a mouse necrotizing myositis infection model (40 mice per strain). (h) Gross pathology images of infected mouse hindlimbs ($n=5$ mice per strain) reflect the difference in virulence between the Group I (top) and Group II (bottom) strains, and representative images are displayed. Boxed areas demarcated in white illustrate major lesion areas.



Supplementary Figure 9

Lack of significant relationship between extent of transcriptome remodeling (number of DE genes) and genetic distance.

(a) Scatterplot comparing the number of differentially expressed genes (DE) and the genetic distance of the 442 singleton strains. For each of the strains, genes were called differentially expressed compared to reference strain MGAS28737. Genetic distance was measured as the number of core chromosomal SNPs compared to strain MGAS28737. Red line represents the line of regression. No significant correlation was observed between genetic distance and extent of transcriptome remodeling (number of DE genes) with R^2 value of 0.0046. **(b)** No improvement in correlation ($R^2 = 0.0040$) was observed when the analysis was conducted using only data for the 188 strains that have wild-type alleles for all known major regulatory genes. Red, SC1A; blue, SC1B; green, SC2A; yellow, SC2B. R^2 value was calculated by linear regression analysis.



Supplementary Figure 10

Genome-wide association analysis and eQTL analysis of 442 strains

(a) Genome-wide association analysis was performed on 442 strains. Manhattan plot showing statistical significance (y-axis) of each *k-mer* (red circles) positively associated with high transcript expression of genes Spy1336/R28 and Spy1337, and their position along the 1.9 Mb GAS genome. Significant *k-mers* mapped to only one region of the chromosome, corresponding to the intergenic region between the Spy1336/R28 and Spy1337 genes. The top part is a schematic of the GAS genome, with vertical blue lines corresponding to open reading frames (ORFs) encoded by each strand of the chromosome. The bottom part shows an enlargement of the genome location corresponding to Spy1336/R28 and Spy1337, and the intergenic region. *P* values were computed by SEER software (Online Methods) **(b)** eQTL analysis identifies significant association between genotype (9T versus 10T) and expression level of genes Spy1336/R28 and Spy1337 in 50 strains at mid-exponential phase (left panel) and in 442 strains at early-stationary phase (right panel). Horizontal black bars represent mean transcript expression and standard deviation. *PeQTL* refers to q-values (False discovery rate, FDR) as reported by MatrixEQTL package. The threshold used for genome-wide significance was adjusted *P* value < 10e-8.

SUPPLEMENTARY NOTE

Bacterial strains. We analyzed 2,101 *emm28 S. pyogenes* strains (see **Supplementary Table 1** and **Supplementary Fig. 1**). These strains were collected as part of comprehensive population-based public health surveillance studies¹¹⁴⁻¹¹⁷ of *emm28 S. pyogenes* infections conducted in 11 states in the United States, Canada (ON), the Faroe Islands in Denmark, Finland, Iceland, and Norway. For the U.S. isolates, ten states have been coded (A-J) at the request of the Centers for Disease Control. All strains were collected between 1991 and 2016. Statistical analysis of 951 invasive U.S. isolates was performed using the chi-square test (Prism 7.0a, GraphPad Software).

Assessment of mobile genetic element content. The MGE content for each strain was inferred in a three-step process. First, each strain was assigned an MGE-50 genotype based on the presence/absence of alleles for 50 MGE-encoded site-specific integrase ($n = 31$) or secreted virulence factor (VF) ($n = 19$) genes by comparison to the MGE-50 database using SRST2¹¹⁸. The 50-gene clusters of the MGE-50 database encompass the known diversity of *S. pyogenes* phages and ICEs (as described below). This first step clusters strains on the basis of sharing a common set of MGE-encoded genes (*i.e.* having the same MGE-50 genotype). Second, the MGE content of a given MGE-50 genotype was inferred based on the site-specific integrases and virulence factors detected as present. Specifically, the number of phages and ICEs, the VFs they encode, and their site of integration into the core genome was inferred. This inference was also informed by knowledge of the MGEs present in the six complete *emm28*

genomes in Genbank (**Supplementary Tables 3-6**). In the third step, the validity of the inferred MGE content was assessed for consistency with *de novo* assemblies for two or more strains of each MGE-50 genotype by blastn comparison of the detected MGE gene alleles to the assembled contigs and manual inspection using Artemis. If the inferred MGE content was inconsistent with the assemblies, then the inference was adjusted accordingly. In this three-step process all strains of a given MGE-50 genotype are inferred to have the same MGE content.

The MGE-50 database was constructed from all site-specific integrase genes and secreted virulence factor genes encoded by MGEs present in 60 complete *S. pyogenes* reference genomes of 26 *emm* types obtained from GenBank (**Supplementary Table 6**). To account for possible differences in MGE annotation, potential MGEs in 59 query genomes were identified by blastp comparison of their annotated coding sequences (CDSs) to the CDSs of the target *emm89* strain MGAS23530 genome which lacks MGEs. Potential MGEs were identified as regions of contiguous CDSs present in the query genomes but absent in the MGAS23530 genome. Through this comparison, 224 MGEs (202 phages and 22 ICEs, based on the nature of their gene content) were found to be integrated at 26 distinct sites of the *S. pyogenes* core genome. All site-specific integrase and secreted virulence factor genes (super-antigens/streptococcal pyrogenic exotoxins, DNases, phospholipases/Sla, Fic domain proteins, adhesins/AgI-II/R28/R6), were extracted from the MGEs and clustered based on sequence similarity. Unique alleles in each gene cluster were determined using the online tool FaBox (see URLs) and used to generate the MGE-50 database using SRST2 (**Supplementary Tables 3 and 6**).

47
48 **Media preparation and bacterial growth for population transcriptomics.** To
49 minimize the potential for transcriptome variation caused by differences in growth media
50 composition, a single lot of solid media was used, prepared as follows. Todd-Hewitt
51 Broth (6 x 500 grams; lot 6110928) and Bacto™ Yeast Extract (200 grams; lot 6116875;
52 Becton-Dickinson) were combined in a large bowl and mixed manually for 133 sec. with
53 a Le Creuset rubber spatula (2.5 inches wide x 4 inches long) followed by 124 sec. with
54 a Hamilton Beach QuickBurst™ hand-held mixer (power setting of 1). Aliquots of this
55 homogenous powdered medium were dispensed to make broth (32 grams/liter of water)
56 as needed. Typically, 10.5 liters of liquid THY media were made for the growth and
57 collection of approximately 95 to 100 *emm28* strains per week. The 10.5 liters were
58 prepared by autoclaving 3.5 liters in three 5-liter flasks (KIMAX Kimble). The 5-liter
59 flasks were autoclaved for 75 min. using the liquid cycle in a Century SV-1262 Prevac
60 Steam Sterilizer (Steris Life Sciences). The media was removed from the autoclave
61 immediately after the autoclave cycle finished to avoid caramelization due to the
62 presence of glucose in Todd-Hewitt medium.

63 All *emm28* strains (**Supplementary Table 1**) were streaked onto sheep blood
64 agar plates from frozen stocks, inoculated into THY broth from fresh, one-day-old blood
65 agar plates that were refrigerated between the end of growth and inoculation, and
66 grown overnight (O/N) in 10 ml of THY medium with 5% CO₂ at 37°C, for no longer than
67 10 hrs. Aliquots (0.8 ml) from O/N cultures were used to inoculate 40 ml of THY in 50-
68 ml conical tubes (1:50 dilution) prewarmed at 37°C. Fifty strains, weighted to represent
69 the frequency distribution of strains in each of the three major subclades, were grown in

triplicate (3 biological replicates), with 2 technical replicates. These strains were collected at two time points: when the optical density (OD) at 600 nm reached 0.5 and 1.65, corresponding to the mid-exponential (ME) and early stationary (ES) phases of growth, respectively. Additionally, 461 strains were grown as individual biological replicates (singletons), with two technical replicates. Bacteria were collected when the OD at 600 nm reached 1.65, corresponding to the early stationary phase of growth. Two ml of bacteria from the mid-log phase and 1 ml from the early stationary phase were added to 4, and 2 ml of RNAprotect Bacteria Reagent (Qiagen), respectively, incubated at room temperature (R/T) for 20 min, and centrifuged at 4,000 rpm for 15 min. The supernatant was discarded, and the bacterial pellet was frozen in liquid nitrogen and stored at -80°C. RNA extraction for all *emm28* strains was performed as described previously^{119,120}. Ultimately, we used transcriptome data for 442 singletons because data for 19 strains were excluded: genome data for 14 strains did not satisfy %GC and *de novo* assembly criteria after whole genome sequencing, and five singleton strains were excluded due to low read coverage after RNAtag-seq analysis.

Exclusion of low-expressed genes. Differential expression cannot be reliably estimated for genes with low read counts¹²¹⁻¹²³. Hence, low-expression genes (i.e., genes with low normalized read counts) were excluded from subsequent analyses. A gene was assigned to the low-expression group and excluded if it satisfied two criteria, as follows. First, the gene had less than 20 reads in 50% or higher percentage of strains, and second, average read count per gene across 442 strains was less than the lowest 5th percentile of average read counts for all genes. Only genes that satisfied both criteria

were excluded. For the 442 singleton strains, employing this process resulted in exclusion of 80 genes.

Selection of reference strain for transcriptome analysis. To compare each singleton strain to a common reference, we selected one strain among the WT-like singleton strains. The *k*-means method was used¹²⁴ to identify the centroid of the two-dimensional spatial clustering of WT-like strains generated via principal component analysis. The strain MGAS28737 with wild-type major regulatory genes, and located closest to the centroid was chosen as the reference strain.

Validation of singleton RNAtag-seq analysis. We hypothesized, based on the negligible variance we obtained between biologic triplicates using the 50 closely genetically related strains, that a large-scale population transcriptomic analysis performed without-replicates, could accurately identify significantly differentially expressed gene patterns. As a preliminary assessment of the reliability of using singleton data, we simulated comparisons of the transcriptome of strains from the same genetic subclade when three biological replicates versus only one randomly selected replicate were used. Regardless of genetic subclade or growth phase, the transcriptomes of strains within the same genetic subclades were highly correlated ($r = 0.99$), even without replication (**Supplementary Fig. 6a**). These results gave us confidence in the technical and biological reproducibility of the transcriptome data. Next, we compared transcriptome data generated for 7 of the 50 strains analyzed in triplicate with data generated for the same 7 strains by RNAtag-seq (singleton cultures without

replicates). Importantly, there was very strong correlation in the global expression profile of the same 7 strains with and without replicates, irrespective of the library preparation method used (RNAseq or RNAtag-seq) (**Supplementary Fig. 6b,c**). Taken together, these analyses indicated that the RNAtag-seq (singleton) strategy yielded accurate transcript data. Thus, we proceeded with population transcriptome analysis of 442 genetically representative and diverse strains (**Supplementary Table 10** and **Supplementary Fig. 7**) chosen by *k*-means clustering statistical strategy.

Use of distance-based clustering to find additional substructure in Cluster B

strains. We used distance-based clustering to test the hypothesis that additional substructure not evident by the visual representation of the PCA (**Fig. 5a**) was present in the transcriptome data (**Fig. 5b**). Consistent with this hypothesis, Cluster B strains were further subdivided into subclusters B.1 (*n*=17 strains) and B.2 (*n*=66) (**Fig. 5b**). Overall, strains in these two subclusters differed by 147 DE genes, and 8.8% of genes had expression changes greater than 5-fold (**Supplementary Table 12**). Subcluster B.2 strains have significantly increased levels of CovRS regulated virulence gene transcripts, including the *rofA* regulator, the pilus-encoding operon, and the *sag* operon whereas *speB* transcript levels were decreased. Subcluster B.2 strains further differentiated into B.2.1 and B.2.2 (**Fig. 5b**), which differed from one another by 14 DE genes.

Different mutations in *ropB* variably affect the expression and activity of the SpeB cysteine protease virulence factor. We also studied strains in Cluster A (**Fig. 5a**) that

lack mutations in *covR* or *covS* ($n=306$) but have mutations in *ropB* ($n=29$), a gene that also encodes a major regulatory protein. By PCA 31% of the strains with *ropB* mutations are in close proximity with other Cluster A strains, but 69% of *ropB* mutants were more distant (**Supplementary Fig. 8c, yellow**). PCA of the 29 *ropB* mutant strains separated into two populations, arbitrarily designated Group I (9 non-outliers) and Group II (20 outliers) (**Supplementary Fig. 8d**). *k*-means clustering verified the grouping of strains identified by the PCA (**Supplementary Fig. 8d**).

RopB is a direct positive regulator of the *speB* gene encoding a secreted cysteine protease virulence factor^{125,126}. Thus, we tested the hypothesis that the two strain groups differed significantly in *speB* transcript level. We discovered that Group II strains expressed significantly less *speB* transcript than Group I organisms ($P < 0.0001$, Mann-Whitney test) (**Supplementary Fig. 8e**). Consistent with this finding, Group II strains produced significantly less protease activity as measured by a standard casein hydrolysis assay¹²⁷ ($P < 0.0007$, Fisher exact test, two-tailed) (**Supplementary Table 13**). Differential gene expression analysis of Group II compared to Group I strains revealed significantly decreased transcripts of the *ropB* core regulon that is comprised of seven genes (*sip*, *spy1723*, *spy1722*, *speB*, *spi*, *spy1719* and *prsA*) (**Supplementary Table 14**). The *sip* gene encodes an 8-amino acid leaderless peptide (SpeB-inducing peptide, SIP) and was recently discovered to be critical for SpeB expression. SIP binds to RopB, resulting in SIP-dependent modulation of DNA binding and regulatory activity of RopB¹²⁷.

Based on these findings, we hypothesized that polymorphisms in Group II strains are more likely to be function-altering mutations that substantially change RopB

regulatory activity. Therefore, we mapped the variant amino acid positions onto the recently solved crystal structure¹²⁸ (PDB: 5DL2) of the RopB C-terminal region (amino acids 56-280; **Supplementary Fig. 8f**). This region is comprised of a tetratricopeptide repeat (TPR) domain containing 5 individual TPR motifs. Interactions between individual motifs of the TPR domain are crucial for proper folding of TPR, the architecture of the ligand (peptide)-binding pocket and RopB dimerization¹²⁸. The vast majority of amino acid replacements in Group II strains mapped onto the critical functional elements of RopB such as (i) interaction between TPR motifs, (ii) RopB dimerization area, and (iii) putative peptide binding pocket. In contrast, most of the amino acid replacements in Group I strains were surface exposed, resulting in no predicted alteration in RopB function ($P = 0.04$, test of proportions-one-tailed) (**Supplementary Fig. 8f** and **Supplementary Table 13**). Based on structure-function predictions, we next hypothesized that Group I strains are significantly more virulent than Group II strains. To test this hypothesis, the virulence of three Group I strains and four Group II strains were compared using a mouse model of necrotizing myositis. These strains were selected based on an absence of mutations in other major gene regulators, the location of the RopB mutation, SpeB activity phenotype, and predicted nature of the mutation (**Supplementary Table 13**). Consistent with the hypothesis, compared to group II organisms, Group I strains caused significantly higher mortality (**Supplementary Fig. 8g**) and larger lesions with more tissue destruction (**Supplementary Fig. 8h**).

Transcriptome variation with respect to genome differentiation. Due to the

magnitude of our dataset we decided to study the relationship between changes in the transcriptome and genome differentiation. This relationship, which has not been previously studied to this extent in any bacterium, bears on the fundamental evolutionary genetics of microbes. We tested the hypothesis that a significant relationship exists between the number of DE genes and the genetic distance between the 442 singleton strains based on core chromosomal SNPs. For this analysis we used core chromosomal SNPs, and excluded polymorphisms within MGEs, as MGEs can be readily acquired and lost independently and repeatedly, potentially obscuring phylogenetic relationships based on core chromosomal SNPs. No significant correlation ($R^2 = 0.0046$) was found between genetic distance and extent of transcriptome remodeling, as assessed by the number of DE genes (**Supplementary Fig. 9a**). We also conducted the analysis using only data for the 188 strains that had wild-type alleles for all known major regulatory genes, but there was no improvement in correlation ($R^2 = 0.0040$) (**Supplementary Fig. 9b**). This lack of correlation suggests that the nature of the polymorphisms between any two strains can have more transcriptional consequences than simply the number of polymorphisms. This is consistent with mutations in major regulatory genes driving extensive changes in the transcriptome, even between two otherwise closely genetically related strains.

Construction of isogenic mutant strains. The isogenic mutant strain MGAS27961-10T, with a 10-T homopolymeric tract, was generated using allelic exchange as described previously¹²⁹. Briefly, primers HPN-1 and HPN-2 (all primers are shown in **Supplementary Table 18**) were used to amplify a 2,690-bp fragment using genomic DNA of MGAS28085, an

208 *emm28* clinical isolate with the naturally occurring 10-T variant region. The amplicon
209 encompasses the homopolymeric tract present in the upstream region of Spy1336/R28 and
210 Spy1337. The resulting PCR product was cloned into suicide plasmid pBBL740 and
211 transformed into the parental strain MGAS27961. The plasmid integrant was used for allelic
212 exchange. The Spy1336-Spy1337 upstream region of putative candidates was sequenced
213 using primer HPN-seq.

214 Isogenic mutant strain MGAS27961-SC1A-*nga*-promoter was generated by
215 replacing its *nga* upstream region with the analogous region from strain MGAS6180.
216 Briefly, primers nga-1 and nga-2 were used to amplify a 1,177-bp fragment (fragment A)
217 located upstream of the *nusG-nga* intergenic region using MGAS27961 genomic DNA.
218 Primers nga-3 and nga-4 were used to amplify the *nusG-nga* intergenic region
219 (fragment B) from MGAS6180 genomic DNA . Primers nga-5 and nga-6 were used to
220 amplify a 1,131-bp fragment (fragment C) that is downstream of the *nusG-nga*
221 intergenic region from MGAS27961. Fragments A, B, and C were ligated consecutively
222 using overlap extension PCR. The combined fragment was ligated into the BamHI site
223 of suicide plasmid pBBL740 and then transformed into parental strain MGAS27961 for
224 allelic exchange. Whole genome sequencing of all mutant strains confirmed the
225 absence of spurious mutations.

226

227 ***S. pyogenes*-human polymorphonuclear leukocyte (PMN) killing assays.** Human
228 PMNs were isolated from heparinized venous blood of healthy human volunteers as
229 described¹³⁰. All studies with human blood and blood components were performed in
230 accordance with a protocol (01-I-N055) approved by the Institutional Review Board for

231 human subjects, National Institute of Allergy and Infectious Diseases. All study
232 volunteers gave written informed consent. GAS strains were cultured to $OD_{600} = 0.182 -$
233 0.302 in THY broth, washed once with phosphate buffered saline, and resuspended in
234 phosphate buffered saline and kept at 4°C until used. Bacteria were diluted 1:10 in
235 HEPES-buffered RPMI 1640 medium, and GAS ($\sim 10^6$ CFUs) and PMNs (10^6) were
236 combined in a 1.5-ml tube containing 10% autologous human serum in HEPES-buffered
237 RPMI 1640 medium (600 μl). Assay tubes were rotated gently for 3 h at 37°C . At the
238 designated time point, assay tubes were placed on ice and an aliquot from each tube
239 was diluted in water (pH 11) and incubated at ambient temp for 20 min to lyse PMNs.
240 Following dilution, aliquots from each assay tube were cultured overnight on THY agar
241 and CFUs were enumerated the following day. Percent bacterial survival was
242 determined by comparing CFUs from assays with PMNs to CFUs from control assays
243 without PMNs (time-matched). Data were analyzed with a paired t-test (Prism 7.03,
244 GraphPad Software).

245

246 **Western immunoblot analysis.** Cells were collected at $OD=0.5$ (ME) and $OD=1.6$ (ES),
247 centrifuged for 1 min, and the resulting pellets were suspended in 100 μl PBS.
248 Supernatants were filtered-sterilized with a 0.22 μm filter to make them cell-free. Whole
249 cells and supernatants were suspended in 1x Laemmli buffer containing 10% β -
250 mercaptoethanol and boiled immediately for 10 min. Proteins in the lysates and
251 supernatants were separated by 12% SDS-PAGE and transferred to a nitrocellulose
252 membrane. Transfer was done for 80-min at 120 volts. The blocking conditions used
253 were PBST (PBS with 0.05% Tween-20) with 5% nonfat dry milk. Immunoblot analysis

was performed with an affinity-purified rabbit anti-R28 antibody (GenScript, Piscataway, NJ) and anti-rabbit (HRP) (Abcam, Cambridge, MA). The anti-R28 antibody was custom-made against an R28 internal peptide with the sequence VVDPRTDADKNDPA. Primary antibody was diluted to 1: 1,000 in PBS-T with 5% nonfat dry milk, and the secondary antibody was diluted 1:10,000. Membranes were incubated with anti-R28 antibody for 1 hour at 4° C followed by 3 10-min washes with PBST, and with the secondary antibody for 1 h. at 4 °C, followed by 5 10-min washes with PBST, imaged using SuperSignal™ West Pico (34080) from ThermoFisher Scientific, and visualized using an SRX-101A medical film processor from Konica Minolta Medical & Graphic, Inc. (China).

NAD⁺-glycohydrolase enzyme activity assay. The NADase activity present in culture supernatants of the wild-type-like isolates chosen for analysis was assayed as described previously^{131,132}, with the modification that incubation in the presence of exogenous NAD⁺ was performed for 3 hours at 37°C.

qRT-PCR analysis. Isogenic mutant strains MGAS27961-10T, MGAS27961-9T (low expresser parental strain), and MGAS28085-10T (high expresser strain) were grown to mid-exponential phase (OD₆₀₀~0.5). Similarly, cell pellets were harvested from isogenic mutant strains 27961-SC1A-*nga*-promoter, parental strain (MGAS27961; SC2A), and a representative SC1A strain (MGAS7868) at mid-exponential phase. RNA was extracted using a RNeasy mini kit (Qiagen) and converted into cDNA using Superscript III reverse Transcriptase (ThermoFisher Scientific). Quantitative RT-PCR (qRT-PCR) was

performed with an ABI 7500 Fast System instrument (Life Technologies). The sequences of primers and probes used in the qRT-PCR experiments are listed in the **Supplementary Table 18**. Each experiment was performed with two biological and three technical replicates. Comparisons of transcript levels were performed relative to *tufA* gene (encoding elongation factor EF-Tu) as the endogenous control and statistical analyses were performed using the Mann-Whitney test.

SUPPLEMENTARY NOTE REFERENCES

114. Nelson, G.E. *et al.* Epidemiology of Invasive Group A Streptococcal Infections in the United States, 2005-2012. *Clin Infect Dis* **63**, 478-86 (2016).
115. Chochua, S. *et al.* Population and Whole Genome Sequence Based Characterization of Invasive Group A Streptococci Recovered in the United States during 2015. *MBio* **8**(2017).
116. Smeesters, P.R., Laho, D., Beall, B., Steer, A.C. & Van Beneden, C.A. Seasonal, Geographic, and Temporal Trends of emm Clusters Associated With Invasive Group A Streptococcal Infections in US Multistate Surveillance. *Clin Infect Dis* **64**, 694-695 (2017).
117. Case definitions for infectious conditions under public health surveillance. Centers for Disease Control and Prevention. *MMWR Recomm Rep* **46**, 1-55 (1997).
118. Inouye, M. *et al.* SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. *Genome Med* **6**, 90 (2014).
119. Beres, S.B. *et al.* Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen *Streptococcus pyogenes*. *MBio* **7**(2016).
120. Eraso, J.M. *et al.* Genomic Landscape of Intrahost Variation in Group A Streptococcus: Repeated and Abundant Mutational Inactivation of the *fabT* Gene Encoding a Regulator of Fatty Acid Synthesis. *Infect Immun* **84**, 3268-3281 (2016).
121. Labaj, P.P. & Kreil, D.P. Sensitivity, specificity, and reproducibility of RNA-Seq differential expression calls. *Biol Direct* **11**, 66 (2016).
122. Tarazona, S. *et al.* Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. *Nucleic Acids Res* **43**, e140 (2015).
123. Conesa, A. *et al.* A survey of best practices for RNA-seq data analysis. *Genome Biol* **17**, 13 (2016).
124. Bishop, C. *Pattern Recognition and Machine Learning* (Springer, New York, 2006).
125. Chaussee, M.S., Ajdic, D. & Ferretti, J.J. The *rgg* gene of *Streptococcus pyogenes* NZ131 positively influences extracellular SPE B production. *Infect Immun* **67**, 1715-22 (1999).

126. Lyon, W.R., Gibson, C.M. & Caparon, M.G. A role for trigger factor and an rgg-like regulator in the transcription, secretion and processing of the cysteine proteinase of *Streptococcus pyogenes*. *EMBO J* **17**, 6263-75 (1998).
127. Do, H. *et al.* Leaderless secreted peptide signaling molecule alters global gene expression and increases virulence of a human bacterial pathogen. *Proc Natl Acad Sci U S A* **114**, E8498-E8507 (2017).
128. Makthal, N. *et al.* Structural and functional analysis of RopB: a major virulence regulator in *Streptococcus pyogenes*. *Mol Microbiol* **99**, 1119-33 (2016).
129. Zhu, L. *et al.* A molecular trigger for intercontinental epidemics of group A *Streptococcus*. *J Clin Invest* **125**, 3545-59 (2015).
130. Kobayashi, S.D., Voyich, J.M., Buhl, C.L., Stahl, R.M. & DeLeo, F.R. Global changes in gene expression by human polymorphonuclear leukocytes during receptor-mediated phagocytosis: cell fate is regulated at the level of gene expression. *Proc Natl Acad Sci U S A* **99**, 6901-6 (2002).
131. Bricker, A.L., Cywes, C., Ashbaugh, C.D. & Wessels, M.R. NAD⁺-glycohydrolase acts as an intracellular toxin to enhance the extracellular survival of group A streptococci. *Mol Microbiol* **44**, 257-69 (2002).
132. Sumby, P. *et al.* Evolutionary origin and emergence of a highly successful clone of serotype M1 group a *Streptococcus* involved multiple horizontal gene transfer events. *J Infect Dis* **192**, 771-82 (2005).

Supplementary Table 1. List of *emm28* invasive strains used in this study

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1	6180 ⁶	1990s	USA (TX) ⁷	SC1A	Invasive ⁸	162	99.95	2
2	7865	1991	Canada ⁹	SC1A	Invasive	45	96.42	11
3	7866	1991	Canada	SC1A	Invasive	246	98.44	142
4	7867	1991	Canada	SC1A	Invasive	75	98.36	4
5	7868	1991	Canada	SC1A	Invasive	290	98.53	109
6	7869	1991	Canada	SC1A	Invasive	206	99.96	1
7	7870	1992	Canada	SC1A	Invasive	179	99.95	1
8	7873	1992	Canada	SC1A	Invasive	280	96.26	189
9	7874	1992	Canada	SC1A	Invasive	264	99.94	1
10	7876	1992	Canada	SC1A	Invasive	202	96.8	91
11	7877	1993	Canada	SC1A	Invasive	211	99.96	1
12	7878	1993	Canada	SC1A	Invasive	234	99.95	1
13	7879	1993	Canada	SC1A	Invasive	26	97.01	80
14	7880	1993	Canada	SC1A	Invasive	295	99.95	1
15	7881	1993	Canada	SC1A	Invasive	258	99.96	1
16	7882	1993	Canada	SC1A	Invasive	161	99.86	1
17	7883	1994	Canada	SC1A	Invasive	147	99.86	1
18	7884	1994	Canada	SC1A	Invasive	168	99.86	1
19	7885	1994	Canada	SC1A	Invasive	201	99.96	1
20	7886	1994	Canada	SC1A	Invasive	162	99.79	1
21	7887	1994	Canada	SC1A	Invasive	37	97.48	15
22	7888	1994	Canada	SC1A	Invasive	187	96.31	93
23	7889	1994	Canada	SC1A	Invasive	35	95.13	136
24	7890	1994	Canada	SC1A	Invasive	199	96.7	88
25	7891	1994	Canada	SC1A	Invasive	163	99.95	1
26	7892	1995	Canada	SC1A	Invasive	206	95.8	147
27	7893	1995	Canada	SC1A	Invasive	239	97.66	86
28	7894	1995	Canada	SC1A	Invasive	239	93.53	20
29	7895	1995	Canada	SC1A	Invasive	305	95.61	201
30	7896	1995	Canada	SC1A	Invasive	129	99.87	1
31	7897	1995	Canada	SC1A	Invasive	192	99.76	1
32	7898	1995	Canada	SC1A	Invasive	337	95.86	16
33	7899	1995	Canada	SC1A	Invasive	172	96.44	30

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
34	7900	1995	Canada	SC1A	Invasive	319	98.23	16
35	7901	1995	Canada	SC1A	Invasive	287	98.2	16
36	7902	1995	Canada	SC1A	Invasive	175	99.88	1
37	7903	1995	Canada	SC1A	Invasive	92	96.15	53
38	7904	1995	Canada	SC1A	Invasive	52	93.77	43
39	7905	1995	Canada	SC1A	Invasive	246	97.98	16
40	7906	1995	Canada	SC1A	Invasive	139	97.83	146
41	7907	1995	Canada	SC1A	Invasive	234	97.67	133
42	7908	1995	Canada	SC1A	Invasive	393	96.25	53
43	7909	1995	Canada	SC1A	Invasive	265	96.61	43
44	7910	1995	Canada	SC1A	Invasive	217	98.15	117
45	7912	1995	Canada	SC1A	Invasive	170	98.94	5
46	7913	1995	Canada	SC1A	Invasive	171	99.9	1
47	7914	1995	Canada	SC1A	Invasive	150	97.84	1
48	7916	1995	Canada	SC1A	Invasive	181	98.2	16
49	7919	1995	Canada	SC1A	Invasive	312	96.35	30
50	7920	1996	Canada	SC1A	Invasive	178	99.9	2
51	7921	1996	Canada	SC1A	Invasive	205	98.22	16
52	7922	1996	Canada	SC1A	Invasive	219	95.89	16
53	7924	1993	Canada	SC1A	Invasive	175	99.96	1
54	7927	1996	Canada	SC1A	Invasive	197	99.96	1
55	7928	1996	Canada	SC1A	Invasive	452	95.48	192
56	7929	1996	Canada	SC1A	Invasive	402	98.16	183
57	7930	1996	Canada	SC1A	Invasive	152	99.76	1
58	7931	1996	Canada	SC1A	Invasive	103	96.43	56
59	7932	1996	Canada	SC1A	Invasive	260	97.42	34
60	7933	1996	Canada	SC1A	Invasive	167	96.58	34
61	7934	1996	Canada	SC1A	Invasive	252	98.07	44
62	7935	1996	Canada	SC1A	Invasive	213	99.97	2
63	7936	1996	Canada	SC1A	Invasive	161	99.96	2
64	7937	1996	Canada	SC1A	Invasive	203	99.96	2
65	7938	1996	Canada	SC1A	Invasive	224	99.96	2
66	7939	1996	Canada	SC1A	Invasive	234	96.43	69
67	7940	1996	Canada	SC1A	Invasive	309	96.59	69
68	7941	1996	Canada	SC1A	Invasive	193	99.58	8
69	7942	1996	Canada	SC1A	Invasive	145	99.85	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
70	7943	1996	Canada	SC1A	Invasive	165	99.9	2
71	7944	1996	Canada	SC1A	Invasive	279	96.65	17
72	7945	1996	Canada	SC1A	Invasive	230	95.61	206
73	7946	1996	Canada	SC1A	Invasive	226	99.86	1
74	7947	1996	Canada	SC1A	Invasive	215	99.97	2
75	7948	1996	Canada	SC1A	Invasive	211	99.96	2
76	7949	1996	Canada	SC1A	Invasive	261	95.69	6
77	7950	1996	Canada	SC1A	Invasive	194	99.96	1
78	7951	1996	Canada	SC1A	Invasive	233	97.04	14
79	7952	1996	Canada	SC1A	Invasive	223	99.78	1
80	7953	1996	Canada	SC1A	Invasive	164	99.09	2
81	7956	1996	Canada	SC1A	Invasive	159	99.94	97
82	7957	1996	Canada	SC1A	Invasive	242	97.12	14
83	7958	1996	Canada	SC1A	Invasive	207	96.79	15
84	7959	1996	Canada	SC1A	Invasive	169	99.32	159
85	7960	1996	Canada	SC1A	Invasive	226	99.9	126
86	7961	1996	Canada	SC1A	Invasive	210	99.96	1
87	7962	1996	Canada	SC1A	Invasive	180	99.83	1
88	7963	1997	Canada	SC1A	Invasive	388	98.04	138
89	7964	1997	Canada	SC1A	Invasive	233	97.57	1
90	7966	1997	Canada	SC1A	Invasive	331	95.45	179
91	7967	1997	Canada	SC1A	Invasive	413	95.49	173
92	7968	1997	Canada	SC1A	Invasive	174	99.87	1
93	7969	1997	Canada	SC1A	Invasive	143	99.96	5
94	7970	1997	Canada	SC1A	Invasive	164	99.83	134
95	7971	1997	Canada	SC1A	Invasive	247	98.1	6
96	7972	1997	Canada	SC1A	Invasive	134	96.88	156
97	7973	1997	Canada	SC1A	Invasive	312	95.92	16
98	7975	1997	Canada	SC1A	Invasive	163	97.86	1
99	7976	1997	Canada	SC1A	Invasive	123	93.86	16
100	7977	1997	Canada	SC1A	Invasive	178	97.63	15
101	7978	1997	Canada	SC1A	Invasive	393	97.19	135
102	7979	1997	Canada	SC1A	Invasive	170	99.7	4
103	7981	1997	Canada	SC1A	Invasive	146	99.91	104
104	7982	1997	Canada	SC1A	Invasive	198	99.21	9
105	7983	1997	Canada	SC1A	Invasive	114	99.87	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
106	7984	1997	Canada	SC1A	Invasive	191	99.87	1
107	7985	1997	Canada	SC1A	Invasive	152	99.75	1
108	7986	1997	Canada	SC1A	Invasive	23	91.98	6
109	7987	1997	Canada	SC1A	Invasive	207	99.97	2
110	7988	1997	Canada	SC1A	Invasive	527	96.34	30
111	7989	1997	Canada	SC1A	Invasive	161	99.96	1
112	7990	1997	Canada	SC1A	Invasive	202	99.77	2
113	7991	1997	Canada	SC1A	Invasive	180	99.66	1
114	7994	1997	Canada	SC1A	Invasive	191	97.61	4
115	7995	1997	Canada	SC1A	Invasive	386	95.17	172
116	7996	1997	Canada	SC1A	Invasive	144	95.53	14
117	7997	1997	Canada	SC1A	Invasive	201	97.06	14
118	7999	1997	Canada	SC1A	Invasive	160	99.93	39
119	8000	1997	Canada	SC1A	Invasive	127	97.87	1
120	8001	1997	Canada	SC1A	Invasive	103	97.88	1
121	8002	1999	Canada	SC1A	Invasive	126	98.05	6
122	8003	1999	Canada	SC1A	Invasive	120	97.04	73
123	8004	1999	Canada	SC1A	Invasive	145	99.88	1
124	8005	1999	Canada	SC1A	Invasive	169	96.82	18
125	8006	1999	Canada	SC1A	Invasive	221	98.07	6
126	8007	1999	Canada	SC1A	Invasive	163	97.68	1
127	8008	1999	Canada	SC1A	Invasive	148	97.82	1
128	8009	1999	Canada	SC1A	Invasive	357	98.05	6
129	8010	1999	Canada	SC1A	Invasive	116	96.38	49
130	8011	1999	Canada	SC1A	Invasive	285	97.18	114
131	8013	1999	Canada	SC1A	Invasive	164	96.86	1
132	8014	1999	Canada	SC1A	Invasive	144	99.96	1
133	8015	1999	Canada	SC1A	Invasive	150	99.94	1
134	8016	1999	Canada	SC1A	Invasive	175	99.96	2
135	8018	1999	Canada	SC1A	Invasive	236	98.14	181
136	8020	1999	Canada	SC1A	Invasive	169	98.23	196
137	8342	1995	Finland ¹⁰	SC1A	Blood	167	99.78	2
138	8345	1995	Finland	SC1A	Blood	182	96.93	1
139	8346	1995	Finland	SC1A	Blood	124	99.96	1
140	8347	1995	Finland	SC1A	Blood	146	98.11	36
141	8349	1995	Finland	SC1A	Blood	145	99.79	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
142	8350	1995	Finland	SC1A	Blood	307	99.21	9
143	8351	1995	Finland	SC1A	Blood	161	99.61	1
144	8353	1995	Finland	SC1A	Blood	248	99.2	9
145	8354	1995	Finland	SC1A	Blood	295	99.21	9
146	8355	1995	Finland	SC1A	Blood	237	99.96	1
147	8356	1996	Finland	SC1A	Blood	224	97.62	9
148	8357	1996	Finland	SC1A	Blood	180	99.91	2
149	8358	1996	Finland	SC1A	Blood	147	99.79	2
150	8359	1996	Finland	SC1A	Blood	121	95.01	24
151	8360	1996	Finland	SC1A	Blood	217	97.33	20
152	8361	1996	Finland	SC1A	Blood	147	99.7	44
153	8362	1996	Finland	SC1A	Blood	235	97.93	37
154	8363	1996	Finland	SC1A	Blood	261	97	115
155	8364	1996	Finland	SC1A	Blood	120	99.96	1
156	8365	1996	Finland	SC1A	Blood	130	99.96	1
157	8366	1996	Finland	SC1A	Blood	201	99.11	9
158	8374	1996	Finland	SC1A	Blood	176	98.05	36
159	8375	1996	Finland	SC1A	Blood	264	99.23	9
160	8376	1997	Finland	SC1A	Blood	369	96.98	17
161	8379	1997	Finland	SC1A	Blood	116	99.96	1
162	8381	1997	Finland	SC1A	Blood	120	99.87	1
163	8383	1997	Finland	SC1A	Blood	110	97.14	107
164	8385	1997	Finland	SC1A	Blood	162	98.25	1
165	8387	1997	Finland	SC1A	Blood	231	98.24	1
166	8389	1997	Finland	SC1A	Blood	203	97.55	1
167	8394	1998	Finland	SC1A	Blood	165	99.79	2
168	8405	1998	Finland	SC1A	Blood	271	99.8	2
169	8406	1998	Finland	SC1A	Blood	457	95.86	6
170	8408	1998	Finland	SC1A	Blood	227	96.73	17
171	8410	1998	Finland	SC1A	Blood	223	99.96	5
172	8415	1998	Finland	SC1A	Blood	211	99.96	1
173	8417	1998	Finland	SC1A	Blood	231	97.07	17
174	8423	1998	Finland	SC1A	Blood	244	97.08	17
175	8432	1999	Finland	SC1A	Blood	206	95.52	215
176	8438	1999	Finland	SC1A	Blood	251	99.2	9
177	8439	1999	Finland	SC1A	Blood	176	98.25	105

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
178	8444	1999	Finland	SC1A	Blood	166	98.17	1
179	8446	1999	Finland	SC1A	Blood	299	95.96	6
180	8447	1999	Finland	SC1A	Blood	209	98.38	2
181	8448	1999	Finland	SC1A	Blood	292	98.17	81
182	10751	1992	Canada	SC1A	Invasive	172	93.68	17
183	10752	1992	Canada	SC1A	Invasive	207	96.69	75
184	10753	1993	Canada	SC1A	Invasive	247	96.97	106
185	10754	1993	Canada	SC1A	Invasive	177	98	83
186	10755	1993	Canada	SC1A	Invasive	207	99.21	9
187	10756	1998	Canada	SC1A	Invasive	138	98.28	49
188	10757	1998	Canada	SC1A	Invasive	185	99.87	1
189	10758	1998	Canada	SC1A	Invasive	167	97.84	1
190	10760	1998	Canada	SC1A	Invasive	144	98.55	1
191	10761	1998	Canada	SC1A	Invasive	324	96.42	30
192	10762	1998	Canada	SC1A	Invasive	169	99.88	1
193	10763	1998	Canada	SC1A	Invasive	269	99.96	1
194	10764	1998	Canada	SC1A	Invasive	180	99.87	1
195	10765	1998	Canada	SC1A	Invasive	275	97.23	`
196	10766	1998	Canada	SC1A	Invasive	191	97.94	6
197	10767	1998	Canada	SC1A	Invasive	341	98.06	6
198	10769	1998	Canada	SC1A	Invasive	204	99.88	1
199	10770	1998	Canada	SC1A	Invasive	194	97.75	1
200	10771	1998	Canada	SC1A	Invasive	190	99.96	1
201	10774	1998	Canada	SC1A	Invasive	152	99.88	1
202	10776	1998	Canada	SC1A	Invasive	193	96.52	11
203	10777	1998	Canada	SC1A	Invasive	248	95.54	158
204	10779	1998	Canada	SC1A	Invasive	202	99.95	1
205	10780	1998	Canada	SC1A	Invasive	228	99.96	1
206	10782	1998	Canada	SC1A	Invasive	199	97.53	11
207	10784	1998	Canada	SC1A	Invasive	168	99.88	1
208	10785	1998	Canada	SC1A	Invasive	129	98.04	4
209	10786	1998	Canada	SC1A	Invasive	192	97.64	157
210	10787	1998	Canada	SC1A	Invasive	272	99.88	1
211	10788	1998	Canada	SC1A	Invasive	317	99.71	1
212	10789	1998	Canada	SC1A	Invasive	206	97.74	1
213	10790	1998	Canada	SC1A	Invasive	134	99.88	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
214	10794	1999	Canada	SC1A	Invasive	233	99.97	1
215	10795	1999	Canada	SC1A	Invasive	207	99.72	1
216	10797	1999	Canada	SC1A	Invasive	197	99.86	1
217	10799	1999	Canada	SC1A	Invasive	283	99.88	1
218	10800	1999	Canada	SC1A	Invasive	292	99.96	1
219	10802	1992	Canada	SC1A	Invasive	257	99.97	1
220	10803	1995	Canada	SC1A	Invasive	248	96.27	30
221	10804	1996	Canada	SC1A	Invasive	126	99.86	1
222	10806	1997	Canada	SC1A	Invasive	150	99.87	1
223	10807	2000	Canada	SC1A	Invasive	213	97.75	1
224	10809	2000	Canada	SC1A	Invasive	319	98.06	6
225	10811	2000	Canada	SC1A	Invasive	341	98.01	6
226	10812	2000	Canada	SC1A	Invasive	243	99.94	1
227	10813	2000	Canada	SC1A	Invasive	232	99.9	1
228	10815	2000	Canada	SC1A	Invasive	170	99.12	74
229	10816	2000	Canada	SC1A	Invasive	304	96.88	20
230	10817	2000	Canada	SC1A	Invasive	240	99.96	1
231	10818	2000	Canada	SC1A	Invasive	145	97.77	1
232	10819	2000	Canada	SC1A	Invasive	218	95.59	1
233	10820	2000	Canada	SC1A	Invasive	283	96.8	66
234	10821	2000	Canada	SC1A	Invasive	217	99.88	160
235	10823	2000	Canada	SC1A	Invasive	170	99.12	1
236	10824	2000	Canada	SC1A	Invasive	266	97.08	14
237	10825	2000	Canada	SC1A	Invasive	210	99.84	1
238	10826	2000	Canada	SC1A	Invasive	221	99.87	1
239	10827	2000	Canada	SC1A	Invasive	310	98.03	6
240	10828	2000	Canada	SC1A	Invasive	225	99.87	1
241	11050	1999	Finland	SC1A	Blood	252	96.2	6
242	11053	2000	Finland	SC1A	Blood	261	96.66	108
243	11063	2000	Finland	SC1A	Blood	227	98.49	6
244	11067	2000	Finland	SC1A	Blood	265	96.95	73
245	11081	2001	Finland	SC1A	Blood	236	99.79	2
246	11083	2001	Finland	SC1A	Blood	216	97.67	36
247	11084	2001	Finland	SC1A	Blood	209	95.6	6
248	11090	2001	Finland	SC1A	Blood	285	99.74	2
249	11097	2001	Finland	SC1A	Blood	157	97.89	6

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
250	11102	2001	Finland	SC1A	Blood	236	96.12	6
251	11103	2001	Finland	SC1A	Blood	229	97.88	6
252	11110	2001	Finland	SC1A	Blood	240	99.76	2
253	11116	2002	Finland	SC1A	Blood	180	97.73	6
254	11154	2002	Finland	SC1A	Blood	140	97.63	2
255	11155	2002	Finland	SC1A	Blood	236	97.62	2
256	12226	2001	Canada	SC1A	Invasive	244	99.91	120
257	12227	2001	Canada	SC1A	Invasive	227	98.43	127
258	12228	2001	Canada	SC1A	Invasive	257	98.06	6
259	12230	2001	Canada	SC1A	Invasive	208	96.11	194
260	12231	2001	Canada	SC1A	Invasive	257	97.5	53
261	12233	2001	Canada	SC1A	Invasive	178	99.96	1
262	12236	2001	Canada	SC1A	Invasive	217	99.93	13
263	12242	2001	Canada	SC1A	Invasive	174	99.79	1
264	12245	2001	Canada	SC1A	Invasive	201	99.96	1
265	12247	2001	Canada	SC1A	Invasive	237	98.04	56
266	12248	2001	Canada	SC1A	Invasive	269	97.45	75
267	12250	2002	Canada	SC1A	Invasive	226	97.02	205
268	12252	2002	Canada	SC1A	Invasive	304	97.07	14
269	12253	2002	Canada	SC1A	Invasive	226	97.71	13
270	27720	1992	Iceland	SC1A	Invasive	144	98.24	11
271	27737	1993	Iceland	SC1A	Invasive	225	96.21	185
272	27745	1996	Iceland	SC1A	Invasive	214	95.55	17
273	27776	2000	Iceland	SC1A	Invasive	213	99.56	39
274	27935	1995	USA (D)	SC1A	Bacteremia	189	99.57	8
275	27936	1995	USA (A)	SC1A	Pneumonia	347	96.52	21
276	27940	1995	USA (A)	SC1A	Septic arthritis	264	99.96	1
277	27941	1995	USA (C)	SC1A	Septic arthritis	269	99.91	13
278	27942	1995	USA (C)	SC1A	Bacteremia	209	98.85	42
279	27943	1995	USA (C)	SC1A	Bacteremia	269	99.89	13
280	27944	1995	USA (C)	SC1A	Osteomyelitis	179	97.98	15
281	27945	1996	USA (A)	SC1A	Bacteremia	196	94.79	1
282	27946	1996	USA (A)	SC1A	Bacteremia	299	99.11	12
283	27947	1996	USA (D)	SC1A	Septic arthritis	200	94.54	199
284	27948	1996	USA (D)	SC1A	Bacteremia	318	94.59	11
285	27949	1996	USA (I)	SC1A	Bacteremia	284	99.77	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
286	27950	1996	USA (A)	SC1A	Bacteremia	380	99.93	5
287	27951	1996	USA (A)	SC1A	Septic arthritis	306	94.19	1
288	27952	1996	USA (F)	SC1A	Bacteremia	277	99.66	1
289	27960	2005	USA (F)	SC1A	Cellulitis	138	93.25	54
290	27962	2005	USA (D)	SC1A	Septic arthritis	103	96.78	116
291	27982	2005	USA (D)	SC1A	Pneumonia	114	97.93	6
292	27983	2005	USA (F)	SC1A	Septic arthritis	167	96.47	59
293	28006	2005	USA (E)	SC1A	Bacteremia	178	98.9	103
294	28009	2005	USA (F)	SC1A	Pneumonia	195	96.03	164
295	28015	2006	USA (F)	SC1A	Bacteremia	188	95.38	6
296	28016	2005	USA (F)	SC1A	Bacteremia	155	97.04	14
297	28035	2006	USA (F)	SC1A	Necrotizing fasciitis	214	94.95	20
298	28041	2009	USA (J)	SC1A	Abscess	173	92.9	54
299	28053	2009	USA (F)	SC1A	Septic arthritis	122	97	20
300	28109	2001	USA (H)	SC1A	Bacteremia	226	97.1	14
301	28112	2001	USA (A)	SC1A	Cellulitis	139	99.77	1
302	28113	2001	USA (A)	SC1A	Abscess	142	99.95	1
303	28116	2001	USA (A)	SC1A	Bacteremia	221	96.78	197
304	28118	2002	USA (B)	SC1A	Cellulitis	331	96.45	184
305	28122	1999	USA (D)	SC1A	Bacteremia	117	96.86	218
306	28132	1998	USA (H)	SC1A	Bacteremia	176	95.52	118
307	28133	1998	USA (D)	SC1A	Bacteremia	205	99.79	1
308	28136	2001	USA (C)	SC1A	Cellulitis	223	98.08	6
309	28137	2001	USA (C)	SC1A	Bacteremia	260	97.05	14
310	28138	2001	USA (E)	SC1A	Cellulitis	239	97.46	180
311	28152	1998	USA (C)	SC1A	Cellulitis	234	99.91	13
312	28154	1998	USA (C)	SC1A	Bacteremia	190	96.8	17
313	28155	1998	USA (C)	SC1A	Bacteremia	246	99.94	1
314	28157	2002	USA (C)	SC1A	Cellulitis	233	96.99	167
315	28162	1998	USA (F)	SC1A	Pneumonia	181	99.95	1
316	28164	1998	USA (F)	SC1A	Cellulitis	174	99.96	1
317	28165	1998	USA (D)	SC1A	Septic arthritis	168	99.14	46
318	28166	1998	USA (D)	SC1A	Bacteremia	167	99.94	1
319	28176	2002	USA (H)	SC1A	Bacteremia	243	96.91	14
320	28177	2001	USA (C)	SC1A	Abscess	145	94.88	14

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
321	28182	1998	USA (C)	SC1A	Bacteremia	125	97.27	20
322	28183	1998	USA (C)	SC1A	Abscess	138	97.18	113
323	28185	1999	USA (H)	SC1A	Bacteremia	118	98.86	38
324	28186	1999	USA (D)	SC1A	Bacteremia	142	99.94	5
325	28189	1999	USA (F)	SC1A	Bacteremia	245	99.94	1
326	28190	1999	USA (F)	SC1A	Bacteremia	295	98.3	140
327	28200	1999	USA (F)	SC1A	Bacteremia	234	95.55	18
328	28201	1999	USA (F)	SC1A	Pneumonia	272	99.93	5
329	28203	1999	USA (F)	SC1A	Unknown	417	99.05	8
330	28204	1999	USA (I)	SC1A	Pneumonia	213	99.96	5
331	28213	1999	USA (H)	SC1A	Bacteremia	184	98.07	6
332	28216	1999	USA (C)	SC1A	Septic arthritis	198	97.93	6
333	28217	1999	USA (C)	SC1A	Bacteremia	183	98.03	6
334	28218	1999	USA (C)	SC1A	Bacteremia	189	98.02	6
335	28219	1998	USA (F)	SC1A	Cellulitis	174	99.45	8
336	28220	1998	USA (F)	SC1A	Bacteremia	162	99.96	1
337	28221	1999	USA (F)	SC1A	Cellulitis	363	99.94	1
338	28222	1999	USA (F)	SC1A	Septic arthritis	303	95.19	15
339	28223	2002	USA (F)	SC1A	Cellulitis	163	99.95	1
340	28225	2002	USA (F)	SC1A	Bacteremia	156	99.95	1
341	28233	1998	USA (C)	SC1A	Cellulitis	189	98.03	6
342	28234	1998	USA (C)	SC1A	Bacteremia	110	94.92	18
343	28235	2002	USA (C)	SC1A	STSS ¹¹	180	97.06	14
344	28236	2002	USA (C)	SC1A	Bacteremia	154	94.85	20
345	28238	2002	USA (C)	SC1A	STSS	185	98.04	6
346	28240	2002	USA (E)	SC1A	Cellulitis	183	97.05	14
347	28243	2002	USA (B)	SC1A	Bacteremia	269	99.96	13
348	28245	1998	USA (D)	SC1A	Bacteremia	304	99.96	1
349	28246	2002	USA (H)	SC1A	Cellulitis	310	95.49	89
350	28247	1998	USA (D)	SC1A	Bacteremia	315	99.96	5
351	28254	2010	USA (F)	SC1A	Bacteremia	174	97.27	198
352	28257	2002	USA (D)	SC1A	Cellulitis	307	96.69	18
353	28276	2001	USA (B)	SC1A	Cellulitis	199	99.96	1
354	28285	2001	USA (I)	SC1A	Cellulitis	269	90.11	18
355	28286	2002	USA (E)	SC1A	Bacteremia	306	96.89	14
356	28287	2002	USA (E)	SC1A	Pneumonia	102	96.97	14

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
357	28290	2001	USA (B)	SC1A	Bacteremia	261	98.71	12
358	28292	2002	USA (H)	SC1A	Bacteremia	251	97.52	6
359	28298	2002	USA (F)	SC1A	Bacteremia	114	99.83	5
360	28303	2000	USA (C)	SC1A	Pneumonia	533	97.96	6
361	28309	1998	USA (D)	SC1A	Septic arthritis	167	98.05	10
362	28315	1998	USA (E)	SC1A	Cellulitis	142	99.68	1
363	28317	2001	USA (D)	SC1A	Cellulitis	138	96.65	18
364	28318	2001	USA (F)	SC1A	Cellulitis	181	95.58	18
365	28319	2001	USA (F)	SC1A	Bacteremia	401	96.19	50
366	28323	2001	USA (F)	SC1A	Bacteremia	113	97.97	10
367	28324	2001	USA (F)	SC1A	Pneumonia	135	99.83	1
368	28328	1998	USA (E)	SC1A	Bacteremia	104	96.71	14
369	28329	1998	USA (E)	SC1A	Bacteremia	101	97.2	1
370	28330	1998	USA (E)	SC1A	Cellulitis	110	98.69	38
371	28333	2000	USA (F)	SC1A	Bacteremia	549	97.86	6
372	28334	2000	USA (F)	SC1A	Cellulitis	894	99.88	5
373	28336	2000	USA (F)	SC1A	Cellulitis	984	98.99	46
374	28338	2000	USA (F)	SC1A	Cellulitis	129	95.04	50
375	28339	2000	USA (E)	SC1A	Bacteremia	120	97.98	203
376	28353	2003	USA (C)	SC1A	Septic arthritis	124	99.86	1
377	28355	2003	USA (C)	SC1A	Cellulitis	178	97.8	37
378	28357	2003	USA (F)	SC1A	Unknown	124	97.88	6
379	28360	2000	USA (H)	SC1A	Bacteremia	105	97.88	10
380	28361	2000	USA (F)	SC1A	Bacteremia	375	99.89	1
381	28367	2003	USA (J)	SC1A	Septic arthritis	191	98.6	21
382	28374	1998	USA (D)	SC1A	Bacteremia	159	99.87	5
383	28376	1997	USA (E)	SC1A	Bacteremia	909	99.8	2
384	28380	2003	USA (D)	SC1A	Septic arthritis	186	97.9	6
385	28385	2002	USA (F)	SC1A	Cellulitis	96	96.03	50
386	28387	1998	USA (C)	SC1A	Bacteremia	105	96.41	27
387	28389	1998	USA (E)	SC1A	Cellulitis	451	97.92	6
388	28390	1998	USA (E)	SC1A	Bacteremia	96	98.1	1
389	28391	1998	USA (F)	SC1A	Pneumonia	129	99.49	8
390	28397	1998	USA (C)	SC1A	STSS	94	96.62	17
391	28398	1998	USA (C)	SC1A	Cellulitis	144	97.46	1
392	28400	1998	USA (D)	SC1A	Cellulitis	192	99.74	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
393	28403	1997	USA (F)	SC1A	Unknown	171	99.88	5
394	28404	1998	USA (F)	SC1A	Bacteremia	130	99.88	1
395	28409	1997	USA (A)	SC1A	Bacteremia	116	99.29	1
396	28410	1997	USA (I)	SC1A	Osteomyelitis	124	99.87	13
397	28411	1997	USA (I)	SC1A	Endometritis	138	95.24	131
398	28412	1997	USA (F)	SC1A	Septic arthritis	162	96.78	195
399	28414	1997	USA (D)	SC1A	Bacteremia	139	98.77	139
400	28415	2003	USA (C)	SC1A	Bacteremia	179	97.52	1
401	28420	2003	USA (H)	SC1A	Cellulitis	93	96.26	122
402	28422	1999	USA (H)	SC1A	Cellulitis	96	96.72	14
403	28425	1999	USA (I)	SC1A	Cellulitis	142	99.75	2
404	28426	1999	USA (F)	SC1A	Bacteremia	299	99.94	1
405	28430	2003	USA (C)	SC1A	Cellulitis	132	96.92	16
406	28433	2003	USA (E)	SC1A	Cellulitis	201	99.62	1
407	28448	2003	USA (H)	SC1A	Bacteremia	157	97.39	6
408	28449	2000	USA (D)	SC1A	Unknown	149	99.88	98
409	28452	1999	USA (C)	SC1A	Cellulitis	91	96.66	16
410	28477	2006	USA (B)	SC1A	Cellulitis	142	91.9	6
411	28486	2006	USA (B)	SC1A	Cellulitis	87	96.6	18
412	28491	2006	USA (B)	SC1A	Necrotizing fasciitis	85	96.97	14
413	28509	2010	USA (F)	SC1A	Pneumonia	104	94.53	18
414	28532	2006	USA (E)	SC1A	Septic arthritis	107	96.93	16
415	28539	2006	USA (F)	SC1A	Septic arthritis	98	96.56	18
416	28601	2007	USA (H)	SC1A	Osteomyelitis	199	97.94	6
417	28640	2008	USA (G)	SC1A	Bacteremia	112	93.06	54
418	28648	2008	USA (A)	SC1A	Cellulitis	313	98.18	155
419	28690	2008	USA (G)	SC1A	Bacteremia	157	99.77	2
420	28708	2011	USA (G)	SC1A	Cellulitis	255	91.55	6
421	28739	2012	USA (H)	SC1A	Osteomyelitis	240	94.66	6
422	28789	2000	USA (A)	SC1A	Bacteremia	217	99.73	1
423	28792	2000	USA (B)	SC1A	Cellulitis	205	99.11	46
424	28796	2003	USA (C)	SC1A	Cellulitis	188	96.96	16
425	28804	1999	USA (H)	SC1A	Pneumonia	260	95.51	188
426	28806	2000	USA (C)	SC1A	Cellulitis	206	96.9	17
427	28808	2003	USA (J)	SC1A	Cellulitis	174	96.73	20

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
428	28812	2003	USA (F)	SC1A	Cellulitis	163	96.67	18
429	28828	2000	USA (J)	SC1A	Pneumonia	189	97.03	14
430	28829	2000	USA (F)	SC1A	Abscess	222	97.43	34
431	28835	2004	USA (H)	SC1A	Pneumonia	186	96.7	16
432	28837	2004	USA (F)	SC1A	Pneumonia	204	95.38	214
433	28838	2004	USA (F)	SC1A	Cellulitis	207	99.9	5
434	28840	2004	USA (C)	SC1A	Bacteremia	256	93.46	6
435	28843	2000	USA (H)	SC1A	Bacteremia	167	97.01	44
436	28844	2000	USA (C)	SC1A	Abscess	113	96.6	18
437	28845	2000	USA (C)	SC1A	Septic arthritis	133	98.04	5
438	28846	2000	USA (C)	SC1A	Cellulitis	123	97.97	6
439	28848	2000	USA (H)	SC1A	Septic arthritis	185	97.04	14
440	28849	2000	USA (E)	SC1A	Bacteremia	194	98.22	163
441	28853	2000	USA (J)	SC1A	Cellulitis	198	97.2	37
442	28859	2004	USA (A)	SC1A	Bacteremia	83	96.93	14
443	28868	2004	USA (J)	SC1A	Bacteremia	283	98.4	5
444	28879	2004	USA (F)	SC1A	Bacteremia	232	97.97	6
445	28894	2004	USA (F)	SC1A	Cellulitis	192	99.17	1
446	28900	2004	USA (H)	SC1A	sepsis	218	93.08	6
447	28907	2004	USA (E)	SC1A	STSS	166	99.96	1
448	28909	2004	USA (B)	SC1A	peritonitis	156	99.91	2
449	28936	2003	USA (F)	SC1A	Bacteremia	198	99.95	5
450	28937	2003	USA (F)	SC1A	Endometritis	209	99.95	1
451	28939	1999	USA (F)	SC1A	Cellulitis	264	96.75	8
452	28941	1999	USA (F)	SC1A	Cellulitis	346	99.93	1
453	28943	1999	USA (F)	SC1A	Bacteremia	291	97.3	87
454	28944	1999	USA (F)	SC1A	Bacteremia	259	98.48	19
455	28946	1999	USA (F)	SC1A	Unknown	312	99.93	1
456	28947	2000	USA (F)	SC1A	Bacteremia	184	98.21	15
457	28949	1999	USA (E)	SC1A	Cellulitis	187	96.22	6
458	28950	1999	USA (E)	SC1A	Bacteremia	198	99.94	5
459	29393	2008	Finland	SC1A	Blood	269	99.74	2
460	29472	2006	Finland	SC1A	Blood	196	99.73	2
461	29496	2006	Finland	SC1A	Blood	435	94.58	90
462	29498	2006	Finland	SC1A	Blood	414	99.22	9
463	29538	2004	Finland	SC1A	Blood	181	99.73	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
464	29547	2004	Finland	SC1A	Blood	161	99.19	9
465	29563	2004	Finland	SC1A	Blood	142	96.96	17
466	29575	2003	Finland	SC1A	Blood	174	94.76	20
467	29608	2003	Finland	SC1A	Blood	191	99.74	2
468	31882	2006	Norway	SC1A	Invasive	108	97.99	16
469	31963	2014	Norway	SC1A	Invasive	119	94.56	20
470	32199	2002	Faroe Islands	SC1A	Invasive	107	96.04	112
471	7925	1996	Canada	SC1B	Invasive	229	99.96	2
472	7926	1996	Canada	SC1B	Invasive	181	99.95	2
473	10783	1998	Canada	SC1B	Invasive	202	99.95	2
474	11052	2000	Finland	SC1B	Blood	250	97.93	3
475	11055	2000	Finland	SC1B	Blood	329	99.96	1
476	11076	2000	Finland	SC1B	Blood	304	98.27	2
477	11080	2000	Finland	SC1B	Blood	198	99.94	2
478	11082	2001	Finland	SC1B	Blood	163	97.07	2
479	11085	2001	Finland	SC1B	Blood	222	97.3	1
480	11086	2001	Finland	SC1B	Blood	193	99.95	2
481	11087	2001	Finland	SC1B	Blood	337	99.95	2
482	11091	2001	Finland	SC1B	Blood	239	99.95	2
483	11092	2001	Finland	SC1B	Blood	209	99.96	1
484	11093	2001	Finland	SC1B	Blood	180	99.95	1
485	11098	2001	Finland	SC1B	Blood	147	99.94	1
486	11100	2001	Finland	SC1B	Blood	179	99.96	1
487	11107	2001	Finland	SC1B	Blood	211	99.94	1
488	11108	2001	Finland	SC1B	Blood	171	99.95	1
489	11112	2002	Finland	SC1B	Blood	34	96.48	3
490	11113	2002	Finland	SC1B	Blood	417	99.97	1
491	11114	2002	Finland	SC1B	Blood	188	99.96	1
492	11115	2002	Finland	SC1B	Blood	155	99.96	1
493	11118	2002	Finland	SC1B	Blood	229	99.95	1
494	11119	2002	Finland	SC1B	Blood	337	97.75	29
495	11120	2002	Finland	SC1B	Blood	260	97.61	3
496	11121	2002	Finland	SC1B	Blood	173	98.09	3
497	11122	2002	Finland	SC1B	Blood	272	97.2	3
498	11123	2002	Finland	SC1B	Blood	219	96.97	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
499	11124	2002	Finland	SC1B	Blood	368	96.32	1
500	11127	2002	Finland	SC1B	Blood	356	96.85	3
501	11128	2002	Finland	SC1B	Blood	402	97.86	1
502	11129	2002	Finland	SC1B	Blood	356	97.57	3
503	11132	2002	Finland	SC1B	Blood	391	99.96	1
504	11133	2002	Finland	SC1B	Blood	305	99.95	1
505	11135	2002	Finland	SC1B	Blood	238	98.17	3
506	11136	2002	Finland	SC1B	Blood	239	99.96	1
507	11138	2002	Finland	SC1B	Blood	143	99.95	1
508	11140	2002	Finland	SC1B	Blood	244	95.27	3
509	11141	2002	Finland	SC1B	Blood	232	94.84	3
510	11142	2002	Finland	SC1B	Blood	260	96.93	3
511	11143	2002	Finland	SC1B	Blood	259	97.29	3
512	11144	2002	Finland	SC1B	Blood	450	94.41	3
513	11145	2002	Finland	SC1B	Blood	350	99.96	2
514	11149	2002	Finland	SC1B	Blood	152	99.95	2
515	11152	2002	Finland	SC1B	Blood	136	99.94	2
516	11153	2002	Finland	SC1B	Blood	130	99.95	2
517	11156	2002	Finland	SC1B	Blood	316	97.43	3
518	11158	2002	Finland	SC1B	Blood	303	99.95	1
519	12232	2001	Canada	SC1B	Invasive	203	99.96	2
520	12237	2001	Canada	SC1B	Invasive	195	93.44	68
521	12249	2001	Canada	SC1B	Invasive	238	99.96	1
522	12251	2002	Canada	SC1B	Invasive	276	99.96	1
523	27754	1997	Iceland	SC1B	Invasive	329	95.41	1
524	27766	1999	Iceland	SC1B	Invasive	328	97.41	95
525	27767	1999	Iceland	SC1B	Invasive	207	97.46	1
526	27775	2000	Iceland	SC1B	Invasive	225	97.48	1
527	27784	2001	Iceland	SC1B	Invasive	194	96.8	1
528	27785	2001	Iceland	SC1B	Invasive	233	97.01	1
529	27787	2001	Iceland	SC1B	Invasive	276	97.4	1
530	27798	2002	Iceland	SC1B	Invasive	154	97.56	1
531	27808	2003	Iceland	SC1B	Invasive	240	97.39	1
532	27809	2004	Iceland	SC1B	Invasive	112	97.48	1
533	27813	2004	Iceland	SC1B	Invasive	131	96.51	1
534	27814	2004	Iceland	SC1B	Invasive	303	97.4	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
535	27843	2007	Iceland	SC1B	Invasive	227	97.27	1
536	27844	2007	Iceland	SC1B	Invasive	290	97.31	1
537	27846	2008	Iceland	SC1B	Invasive	270	97.35	1
538	27848	2008	Iceland	SC1B	Invasive	219	97.35	1
539	27859	2009	Iceland	SC1B	Invasive	302	96.42	208
540	27864	2010	Iceland	SC1B	Invasive	279	99.94	2
541	27865	2010	Iceland	SC1B	Invasive	226	97.49	48
542	27866	2010	Iceland	SC1B	Invasive	214	99.95	2
543	27876	2011	Iceland	SC1B	Invasive	120	99.96	1
544	27893	2012	Iceland	SC1B	Invasive	244	96.63	71
545	27895	2012	Iceland	SC1B	Invasive	221	96.64	71
546	27954	2010	USA (E)	SC1B	Endometritis	204	99.69	1
547	27955	2010	USA (H)	SC1B	Pneumonia	156	97.96	125
548	27956	2004	USA (J)	SC1B	Bacteremia	120	99.94	2
549	27957	2005	USA (J)	SC1B	Bacteremia	167	99.95	1
550	27964	2005	USA (A)	SC1B	Cellulitis	243	97.33	2
551	27967	2005	USA (J)	SC1B	Cellulitis	177	99.96	1
552	27970	2005	USA (B)	SC1B	Cellulitis	185	99.95	2
553	27972	2005	USA (G)	SC1B	Endometritis	180	99.94	2
554	27974	2005	USA (F)	SC1B	Bacteremia	172	99.94	2
555	27984	2005	USA (F)	SC1B	Necrotizing fasciitis	183	98.03	15
556	27990	2005	USA (F)	SC1B	Cellulitis	176	98.07	15
557	27995	2005	USA (J)	SC1B	Cellulitis	188	99.95	2
558	27997	2005	USA (J)	SC1B	STSS	174	99.95	2
559	27998	2005	USA (E)	SC1B	septic shock	163	99.77	1
560	28003	2005	USA (D)	SC1B	Cellulitis	185	99.96	1
561	28012	2005	USA (F)	SC1B	Bacteremia	224	99.94	2
562	28027	2006	USA (E)	SC1B	Cellulitis	162	99.89	1
563	28032	2005	USA (E)	SC1B	Necrotizing fasciitis	184	99.96	1
564	28036	2009	USA (H)	SC1B	Cellulitis	220	97.93	10
565	28040	2009	USA (D)	SC1B	Pneumonia	149	97.59	29
566	28042	2009	USA (B)	SC1B	Bacteremia	151	99.94	2
567	28043	2009	USA (E)	SC1B	Cellulitis	301	99.95	1
568	28044	2009	USA (E)	SC1B	Abscess	269	98.01	1
569	28046	2009	USA (E)	SC1B	Bacteremia	191	99.77	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
570	28048	2009	USA (J)	SC1B	Cellulitis	174	99.95	1
571	28049	2009	USA (J)	SC1B	Cellulitis	172	99.69	1
572	28052	2009	USA (H)	SC1B	Bacteremia	122	97.93	10
573	28056	2009	USA (F)	SC1B	Bacteremia	144	96.9	2
574	28059	2009	USA (D)	SC1B	Bacteremia	154	98.09	3
575	28061	2009	USA (H)	SC1B	Necrotizing fasciitis/STSS	205	97.75	10
576	28066	2009	USA (J)	SC1B	Pneumonia	137	99.95	1
577	28068	2009	USA (E)	SC1B	Necrotizing fasciitis	137	99.68	1
578	28070	2009	USA (H)	SC1B	STSS	139	98.05	10
579	28072	2009	USA (F)	SC1B	Cellulitis	167	99.95	2
580	28073	2009	USA (A)	SC1B	Necrotizing fasciitis	162	99.95	2
581	28075	2009	USA (H)	SC1B	Necrotizing fasciitis	168	96.35	10
582	28079	2009	USA (E)	SC1B	Cellulitis	192	99.95	2
583	28081	2009	USA (E)	SC1B	Cellulitis	169	99.69	1
584	28087	2010	USA (H)	SC1B	Osteomyelitis	185	98.03	10
585	28093	2009	USA (E)	SC1B	Cellulitis	245	97.48	141
586	28096	2009	USA (G)	SC1B	Necrotizing fasciitis	257	99.96	1
587	28098	2009	USA (H)	SC1B	Bacteremia	318	99.96	1
588	28101	2009	USA (A)	SC1B	Cellulitis	185	99.95	2
589	28103	2009	USA (D)	SC1B	Cellulitis	171	99.94	2
590	28104	2009	USA (H)	SC1B	Abscess	206	98.08	10
591	28106	2009	USA (D)	SC1B	Pneumonia	206	99.95	1
592	28108	2009	USA (B)	SC1B	Septic arthritis	238	93.16	2
593	28123	2002	USA (E)	SC1B	Cellulitis	245	99.95	2
594	28141	2010	USA (A)	SC1B	Meningitis	329	98.13	10
595	28142	2010	USA (E)	SC1B	Cellulitis	333	99.96	1
596	28167	2010	USA (G)	SC1B	Meningitis	160	99.94	2
597	28174	2002	USA (J)	SC1B	Pneumonia	214	99.95	2
598	28208	2010	USA (F)	SC1B	Bacteremia	190	99.95	2
599	28224	2002	USA (F)	SC1B	Cellulitis	152	98.26	2
600	28226	2002	USA (F)	SC1B	Bacteremia	170	99.95	2
601	28241	2002	USA (E)	SC1B	peritonitis	248	99.96	1
602	28250	2010	USA (A)	SC1B	Septic shock	253	99.95	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
603	28251	2010	USA (A)	SC1B	Bacteremia	234	99.94	2
604	28252	2010	USA (A)	SC1B	Septic arthritis	200	99.95	2
605	28253	2010	USA (F)	SC1B	Cellulitis	196	99.42	1
606	28256	2010	USA (F)	SC1B	Bacteremia	207	99.94	2
607	28260	2011	USA (A)	SC1B	Endometritis	241	97.91	8
608	28264	2011	USA (H)	SC1B	STSS	212	96.51	128
609	28266	2011	USA (F)	SC1B	Bacteremia	188	97.26	85
610	28268	2011	USA (F)	SC1B	Pneumonia	188	97.87	24
611	28273	2011	USA (E)	SC1B	Cellulitis	203	99.88	2
612	28275	2011	USA (B)	SC1B	Bacteremia	247	99.93	1
613	28277	2011	USA (E)	SC1B	Cellulitis	140	99.54	2
614	28278	2011	USA (H)	SC1B	Necrotizing fasciitis	149	98.03	10
615	28282	2002	USA (F)	SC1B	Cellulitis	237	99.95	2
616	28295	2011	USA (F)	SC1B	Cellulitis	144	99.87	1
617	28308	1998	USA (A)	SC1B	Bacteremia	136	99.88	1
618	28311	2011	USA (H)	SC1B	Abscess	101	97.78	10
619	28320	2001	USA (F)	SC1B	Cellulitis	1472	99.86	24
620	28327	2001	USA (F)	SC1B	Bacteremia	95	99.85	2
621	28359	2003	USA (F)	SC1B	Bacteremia	361	99.88	2
622	28368	2003	USA (F)	SC1B	Cellulitis	327	99.88	2
623	28373	2010	USA (D)	SC1B	Cellulitis	1093	98.42	2
624	28381	2003	USA (D)	SC1B	Cellulitis	169	99.87	2
625	28382	2002	USA (J)	SC1B	Cellulitis	189	99.87	2
626	28423	2010	USA (E)	SC1B	Cellulitis	116	99.86	1
627	28437	2003	USA (B)	SC1B	Bacteremia	112	99.87	2
628	28455	2010	USA (I)	SC1B	Septic arthritis	151	97.39	2
629	28456	2010	USA (I)	SC1B	Cellulitis	246	98.97	38
630	28458	2010	USA (J)	SC1B	Abscess	126	99.88	2
631	28464	2010	USA (B)	SC1B	Septic shock	169	93.83	177
632	28468	2006	USA (J)	SC1B	Bacteremia	171	99.87	2
633	28470	2006	USA (A)	SC1B	Bacteremia	124	95.15	3
634	28472	2006	USA (F)	SC1B	Bacteremia	105	99.84	2
635	28473	2006	USA (F)	SC1B	Septic arthritis	125	98.14	2
636	28474	2006	USA (B)	SC1B	Osteomyelitis	112	99.85	2
637	28478	2006	USA (B)	SC1B	Bacteremia	180	98.09	57

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
638	28480	2006	USA (F)	SC1B	Bacteremia	186	98.12	2
639	28481	2006	USA (F)	SC1B	Bacteremia	175	99.87	2
640	28490	2006	USA (J)	SC1B	Cellulitis	109	99.86	2
641	28496	2006	USA (A)	SC1B	Bacteremia	139	99.88	1
642	28498	2006	USA (F)	SC1B	Septic arthritis	106	98.17	15
643	28499	2006	USA (F)	SC1B	Necrotizing fasciitis	162	98.14	15
644	28505	2006	USA (D)	SC1B	Cellulitis	169	97.79	150
645	28506	2006	USA (D)	SC1B	Cellulitis	168	97.79	3
646	28508	2010	USA (F)	SC1B	Bacteremia	161	99.87	2
647	28511	2010	USA (H)	SC1B	Septic shock	86	97.81	124
648	28517	2006	USA (F)	SC1B	Cellulitis	142	99.87	2
649	28527	2006	USA (I)	SC1B	Cellulitis	158	97.62	15
650	28530	2006	USA (E)	SC1B	Septic arthritis	136	99.87	1
651	28531	2006	USA (E)	SC1B	Cellulitis	111	99.86	1
652	28535	2007	USA (D)	SC1B	Pneumonia	133	96.56	1
653	28538	2006	USA (F)	SC1B	Bacteremia	123	99.86	2
654	28542	2006	USA (A)	SC1B	Cellulitis	129	97.77	3
655	28544	2006	USA (J)	SC1B	Bacteremia	149	99.87	2
656	28545	2006	USA (J)	SC1B	Meningitis	133	99.87	2
657	28546	2006	USA (J)	SC1B	Cellulitis	126	99.87	1
658	28548	2007	USA (B)	SC1B	Cellulitis	142	99.89	5
659	28557	2007	USA (F)	SC1B	Pneumonia	110	99.85	2
660	28558	2007	USA (F)	SC1B	Abscess	126	98.14	2
661	28559	2007	USA (B)	SC1B	Unknown	122	99.88	1
662	28560	2007	USA (B)	SC1B	Bacteremia	107	99.86	1
663	28565	2007	USA (F)	SC1B	Puerperal sepsis	130	98.1	2
664	28566	2007	USA (F)	SC1B	Endometritis	101	99.84	2
665	28569	2007	USA (B)	SC1B	Cellulitis	136	97.66	3
666	28570	2007	USA (E)	SC1B	Bacteremia	94	96.56	4
667	28573	2007	USA (E)	SC1B	Necrotizing fasciitis	110	98.49	70
668	28580	2007	USA (J)	SC1B	Pneumonia	106	99.85	1
669	28582	2007	USA (D)	SC1B	Bacteremia	99	99.85	1
670	28583	2007	USA (I)	SC1B	Necrotizing fasciitis	110	99.8	2
671	28594	2007	USA (D)	SC1B	Cellulitis	271	99.21	9
672	28598	2007	USA (J)	SC1B	Bacteremia	208	98.41	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
673	28599	2007	USA (H)	SC1B	Bacteremia	143	94.89	2
674	28600	2007	USA (H)	SC1B	Bacteremia	195	97.84	10
675	28615	2008	USA (D)	SC1B	Bacteremia	157	95.53	43
676	28616	2008	USA (D)	SC1B	Cellulitis	175	99.88	1
677	28621	2007	USA (J)	SC1B	lymph node	285	99.9	1
678	28622	2007	USA (J)	SC1B	Bacteremia	177	99.87	1
679	28623	2007	USA (J)	SC1B	Bacteremia	218	98.09	1
680	28625	2008	USA (D)	SC1B	septic shock	199	99.9	1
681	28629	2007	USA (E)	SC1B	Bacteremia	148	98.53	25
682	28631	2008	USA (E)	SC1B	Pneumonia	62	99.56	1
683	28637	2008	USA (H)	SC1B	Septic arthritis	163	97.92	10
684	28639	2008	USA (A)	SC1B	Pneumonia	87	99.86	2
685	28645	2007	USA (B)	SC1B	Cellulitis	168	99.88	1
686	28646	2008	USA (B)	SC1B	Bacteremia	216	99.9	1
687	28650	2008	USA (I)	SC1B	Pneumonia	404	99.9	1
688	28652	2008	USA (A)	SC1B	lymph node	158	98	22
689	28653	2008	USA (A)	SC1B	Bacteremia	174	99.89	1
690	28654	2008	USA (F)	SC1B	Pneumonia	137	98.18	2
691	28656	2008	USA (G)	SC1B	Pneumonia	101	99.88	1
692	28657	2008	USA (G)	SC1B	Cellulitis	211	99.89	1
693	28661	2008	USA (H)	SC1B	STSS	186	97.93	10
694	28666	2008	USA (D)	SC1B	Cellulitis	117	99.17	9
695	28667	2008	USA (H)	SC1B	Septic arthritis	114	97.8	15
696	28668	2008	USA (H)	SC1B	Cellulitis	135	97.95	10
697	28673	2008	USA (A)	SC1B	Bacteremia	195	98.37	1
698	28683	2008	USA (B)	SC1B	Empyema	167	99.87	1
699	28684	2008	USA (B)	SC1B	Bacteremia	124	99.86	2
700	28685	2008	USA (D)	SC1B	Bacteremia	190	97.7	3
701	28688	2009	USA (D)	SC1B	Cellulitis	185	98.24	32
702	28693	2008	USA (F)	SC1B	Cellulitis	203	97.58	24
703	28696	2008	USA (F)	SC1B	Cellulitis	294	97.52	2
704	28702	2011	USA (F)	SC1B	Necrotizing fasciitis	240	99.89	2
705	28706	2011	USA (A)	SC1B	Empyema	281	99.91	2
706	28707	2011	USA (J)	SC1B	Cellulitis	262	99.91	1
707	28709	2011	USA (G)	SC1B	Cellulitis	249	98.34	25

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
708	28710	2011	USA (H)	SC1B	Cellulitis	210	97.93	10
709	28711	2011	USA (H)	SC1B	Necrotizing fasciitis/STSS	248	99.91	1
710	28712	2011	USA (H)	SC1B	Bacteremia	216	97.93	10
711	28714	2011	USA (E)	SC1B	Bacteremia	278	99.69	1
712	28716	2011	USA (A)	SC1B	Pneumonia	428	99.93	1
713	28718	2011	USA (F)	SC1B	Cellulitis	275	98.19	15
714	28721	2012	USA (H)	SC1B	Cellulitis	284	98.54	42
715	28723	2012	USA (B)	SC1B	Pneumonia	138	98.15	10
716	28724	2012	USA (G)	SC1B	Bacteremia	153	99.89	1
717	28725	2012	USA (G)	SC1B	Cellulitis	194	99.9	1
718	28730	2012	USA (H)	SC1B	Septic arthritis	361	97.68	10
719	28732	2012	USA (G)	SC1B	Cellulitis	196	99.85	2
720	28733	2012	USA (D)	SC1B	Cellulitis	303	99.91	1
721	28735	2012	USA (H)	SC1B	Pneumonia	385	97.87	10
722	28737	2012	USA (H)	SC1B	Septic arthritis	238	97.8	10
723	28738	2012	USA (H)	SC1B	Cellulitis	256	99.93	1
724	28742	2012	USA (F)	SC1B	Necrotizing fasciitis	274	99.93	2
725	28746	2012	USA (G)	SC1B	Pneumonia	120	99.89	1
726	28747	2012	USA (G)	SC1B	Bacteremia	140	97.9	15
727	28749	2012	USA (D)	SC1B	Unknown	167	99.9	5
728	28750	2012	USA (E)	SC1B	Bacteremia	164	99.73	1
729	28756	2012	USA (F)	SC1B	Septic shock	250	99.93	1
730	28757	2012	USA (A)	SC1B	Pneumonia	334	98.12	1
731	28758	2012	USA (A)	SC1B	Cellulitis	340	99.92	1
732	28759	2012	USA (J)	SC1B	Septic arthritis	377	95.54	174
733	28762	2012	USA (F)	SC1B	Abscess	335	99.94	1
734	28763	2012	USA (F)	SC1B	Bacteremia	284	98.11	2
735	28764	2012	USA (B)	SC1B	Bacteremia	404	98.22	10
736	28765	2012	USA (A)	SC1B	Bacteremia	284	99.91	1
737	28766	2012	USA (E)	SC1B	Necrotizing fasciitis	211	99.9	1
738	28767	2012	USA (F)	SC1B	Septic arthritis	223	97.47	10
739	28768	2012	USA (F)	SC1B	Cellulitis	200	99.92	2
740	28770	2012	USA (B)	SC1B	Pneumonia	196	99.91	1
741	28772	2012	USA (D)	SC1B	Bacteremia	229	99.91	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
742	28773	2012	USA (D)	SC1B	STSS	168	99.9	2
743	28774	2012	USA (E)	SC1B	Endometritis	269	99.78	1
744	28779	2012	USA (B)	SC1B	Bacteremia	204	99.9	2
745	28780	2012	USA (F)	SC1B	Abscess	183	94.87	2
746	28782	2012	USA (G)	SC1B	Cellulitis	171	99.89	1
747	28783	2012	USA (B)	SC1B	Cellulitis	132	98.7	1
748	28794	2003	USA (A)	SC1B	Bacteremia	232	99.88	2
749	28799	2003	USA (J)	SC1B	Cellulitis	209	99.88	2
750	28811	2003	USA (F)	SC1B	Bacteremia	171	99.89	61
751	28814	2003	USA (C)	SC1B	Pneumonia	180	99.9	1
752	28817	2003	USA (F)	SC1B	Bacteremia	188	99.89	2
753	28818	2003	USA (F)	SC1B	Cellulitis	266	99.9	1
754	28821	2004	USA (F)	SC1B	Bacteremia	180	99.82	2
755	28822	2003	USA (B)	SC1B	Necrotizing fasciitis	274	99.89	2
756	28823	2004	USA (F)	SC1B	Septic arthritis	207	99.88	2
757	28824	2004	USA (H)	SC1B	Bacteremia	204	97.61	191
758	28825	2004	USA (H)	SC1B	Bacteremia	179	99.89	1
759	28830	2000	USA (F)	SC1B	Cellulitis	247	99.89	2
760	28839	2004	USA (C)	SC1B	Pneumonia	206	99.89	1
761	28850	2000	USA (E)	SC1B	Bacteremia	173	99.89	2
762	28858	2004	USA (A)	SC1B	lymph node	228	98.2	15
763	28869	2004	USA (J)	SC1B	Bacteremia	259	99.89	28
764	28871	2004	USA (G)	SC1B	Cellulitis	155	97.74	29
765	28876	2004	USA (E)	SC1B	Meningitis	192	99.68	1
766	28880	2004	USA (F)	SC1B	Cellulitis	193	99.89	2
767	28882	2004	USA (B)	SC1B	Cellulitis	216	99.89	2
768	28884	2004	USA (B)	SC1B	Cellulitis	184	99.08	1
769	28889	2010	USA (J)	SC1B	Bacteremia	208	99.79	8
770	28891	2010	USA (D)	SC1B	Bacteremia	226	98.92	2
771	28899	2004	USA (B)	SC1B	Septic arthritis	195	99.88	2
772	28904	2004	USA (A)	SC1B	Bacteremia	258	97.87	3
773	28908	2004	USA (E)	SC1B	Cellulitis	217	99.96	1
774	28916	2010	USA (J)	SC1B	Cellulitis	236	99.96	2
775	28920	2010	USA (F)	SC1B	Bacteremia	211	99.96	2
776	28921	2011	USA (D)	SC1B	Cellulitis	181	98.99	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
777	28924	2011	USA (A)	SC1B	Osteomyelitis	232	99.95	2
778	28927	2011	USA (I)	SC1B	Pneumonia	217	97.65	3
779	28930	2010	USA (E)	SC1B	Cellulitis	173	94.58	216
780	28932	2002	USA (J)	SC1B	Bacteremia	151	99.96	1
781	28934	2003	USA (F)	SC1B	Bacteremia	176	99.97	1
782	28935	2003	USA (F)	SC1B	Abscess	225	99.95	2
783	28945	1999	USA (F)	SC1B	Bacteremia	218	99.93	1
784	28953	2000	USA (J)	SC1B	Pneumonia	173	99.96	2
785	29041	2015	Finland	SC1B	Blood	133	97.61	4
786	29042	2015	Finland	SC1B	Blood	152	96.4	67
787	29043	2015	Finland	SC1B	Blood	103	99.84	5
788	29044	2015	Finland	SC1B	Blood	115	97.78	4
789	29045	2015	Finland	SC1B	Blood	103	99.86	5
790	29046	2015	Finland	SC1B	Blood	94	99.85	1
791	29047	2015	Finland	SC1B	Blood	126	99.85	1
792	29048	2015	Finland	SC1B	Blood	111	97.77	4
793	29049	2015	Finland	SC1B	Blood	148	96.48	3
794	29050	2015	Finland	SC1B	Blood	126	98.14	1
795	29051	2015	Finland	SC1B	Blood	106	99.86	1
796	29052	2015	Finland	SC1B	Blood	114	99.85	1
797	29053	2015	Finland	SC1B	Blood	109	99.86	1
798	29054	2015	Finland	SC1B	Blood	107	99.27	1
799	29055	2015	Finland	SC1B	Blood	102	99.86	1
800	29056	2015	Finland	SC1B	Blood	138	98.05	1
801	29057	2015	Finland	SC1B	Blood	147	97.76	4
802	29058	2015	Finland	SC1B	Blood	211	98.1	1
803	29059	2015	Finland	SC1B	Blood	185	95.47	3
804	29060	2015	Finland	SC1B	Blood	141	99.87	1
805	29061	2015	Finland	SC1B	Blood	109	97.93	1
806	29062	2015	Finland	SC1B	Blood	135	97.68	4
807	29063	2015	Finland	SC1B	Blood	131	99.88	5
808	29064	2015	Finland	SC1B	Blood	118	99.87	5
809	29065	2015	Finland	SC1B	Blood	101	99.85	5
810	29066	2015	Finland	SC1B	Blood	113	99.86	1
811	29067	2015	Finland	SC1B	Blood	103	97.9	1
812	29068	2015	Finland	SC1B	Blood	211	98.07	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
813	29069	2015	Finland	SC1B	Blood	544	97.84	3
814	29070	2015	Finland	SC1B	Blood	169	99.87	1
815	29071	2015	Finland	SC1B	Blood	135	99.86	1
816	29072	2015	Finland	SC1B	Blood	212	96.98	76
817	29073	2015	Finland	SC1B	Blood	88	97.82	1
818	29074	2015	Finland	SC1B	Blood	145	93.68	3
819	29075	2015	Finland	SC1B	Blood	116	97.68	4
820	29076	2015	Finland	SC1B	Blood	155	99.88	1
821	29077	2015	Finland	SC1B	Blood	170	97.73	4
822	29078	2015	Finland	SC1B	Blood	173	94.54	3
823	29079	2015	Finland	SC1B	Blood	118	99.86	1
824	29080	2015	Finland	SC1B	Blood	153	97.35	4
825	29081	2015	Finland	SC1B	Blood	564	99.89	1
826	29082	2015	Finland	SC1B	Blood	710	99.88	1
827	29083	2014	Finland	SC1B	Blood	267	97.66	4
828	29084	2014	Finland	SC1B	Blood	646	99.88	1
829	29085	2014	Finland	SC1B	Blood	203	99.88	1
830	29086	2014	Finland	SC1B	Blood	230	97.99	6
831	29087	2014	Finland	SC1B	Blood	169	99.88	1
832	29088	2014	Finland	SC1B	Blood	183	99.97	1
833	29089	2014	Finland	SC1B	Blood	123	99.86	5
834	29090	2014	Finland	SC1B	Blood	112	99.86	1
835	29091	2014	Finland	SC1B	Blood	171	99.88	1
836	29092	2014	Finland	SC1B	Blood	113	99.15	52
837	29093	2014	Finland	SC1B	Blood	173	98.03	1
838	29094	2014	Finland	SC1B	Blood	268	97.13	3
839	29095	2014	Finland	SC1B	Blood	146	95.93	4
840	29096	2014	Finland	SC1B	Blood	262	99.89	1
841	29097	2014	Finland	SC1B	Blood	656	93.53	4
842	29098	2014	Finland	SC1B	Blood	326	93.63	3
843	29099	2014	Finland	SC1B	Blood	215	95.88	3
844	29100	2014	Finland	SC1B	Blood	129	99.88	1
845	29101	2014	Finland	SC1B	Blood	58	97.58	4
846	29102	2014	Finland	SC1B	Blood	159	97.94	3
847	29103	2014	Finland	SC1B	Blood	217	99.89	1
848	29104	2014	Finland	SC1B	Blood	164	99.89	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
849	29105	2014	Finland	SC1B	Blood	170	99.88	1
850	29106	2014	Finland	SC1B	Blood	529	99.88	1
851	29107	2014	Finland	SC1B	Blood	190	99.9	1
852	29108	2014	Finland	SC1B	Blood	139	97.72	65
853	29109	2014	Finland	SC1B	Blood	168	97.79	1
854	29110	2014	Finland	SC1B	Blood	235	94.15	4
855	29111	2014	Finland	SC1B	Blood	169	95.86	3
856	29112	2014	Finland	SC1B	Blood	155	97.91	1
857	29114	2014	Finland	SC1B	Blood	174	99.87	1
858	29115	2014	Finland	SC1B	Blood	202	99.88	1
859	29116	2014	Finland	SC1B	Blood	334	97.22	3
860	29117	2014	Finland	SC1B	Blood	139	99.86	1
861	29118	2014	Finland	SC1B	Blood	344	97.23	4
862	29119	2014	Finland	SC1B	Blood	625	99.86	1
863	29120	2014	Finland	SC1B	Blood	238	97.14	4
864	29121	2014	Finland	SC1B	Blood	140	99.96	1
865	29122	2014	Finland	SC1B	Blood	815	95.11	3
866	29123	2014	Finland	SC1B	Blood	161	97.83	1
867	29124	2014	Finland	SC1B	Blood	158	99.88	5
868	29125	2014	Finland	SC1B	Blood	749	97.98	1
869	29126	2014	Finland	SC1B	Blood	169	99.96	1
870	29127	2014	Finland	SC1B	Blood	146	97.6	1
871	29128	2014	Finland	SC1B	Blood	195	98.21	1
872	29129	2014	Finland	SC1B	Blood	129	98.14	7
873	29130	2014	Finland	SC1B	Blood	166	97.62	4
874	29131	2014	Finland	SC1B	Blood	91	99.85	1
875	29133	2014	Finland	SC1B	Blood	199	99.88	1
876	29135	2014	Finland	SC1B	Blood	139	99.86	1
877	29136	2014	Finland	SC1B	Blood	101	95.98	4
878	29137	2014	Finland	SC1B	Blood	89	97.65	4
879	29138	2014	Finland	SC1B	Blood	123	99.9	1
880	29139	2014	Finland	SC1B	Blood	256	98.1	4
881	29140	2014	Finland	SC1B	Blood	98	99.86	1
882	29141	2014	Finland	SC1B	Blood	452	98.2	1
883	29142	2014	Finland	SC1B	Blood	137	96.75	68
884	29143	2014	Finland	SC1B	Blood	116	92.77	200

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
885	29144	2013	Finland	SC1B	Blood	254	99.89	1
886	29145	2013	Finland	SC1B	Blood	114	97.73	4
887	29146	2013	Finland	SC1B	Blood	106	99.86	5
888	29147	2013	Finland	SC1B	Blood	201	96.95	3
889	29148	2013	Finland	SC1B	Blood	206	97.48	4
890	29149	2013	Finland	SC1B	Blood	339	97.83	4
891	29150	2013	Finland	SC1B	Blood	90	97.69	3
892	29151	2013	Finland	SC1B	Blood	88	93.97	4
893	29152	2013	Finland	SC1B	Blood	112	98.06	1
894	29153	2013	Finland	SC1B	Blood	234	97.59	1
895	29154	2013	Finland	SC1B	Blood	122	96.79	3
896	29155	2013	Finland	SC1B	Blood	150	96.85	3
897	29156	2013	Finland	SC1B	Blood	146	97.72	3
898	29157	2013	Finland	SC1B	Blood	120	96.58	12
899	29158	2013	Finland	SC1B	Blood	150	94.87	67
900	29159	2013	Finland	SC1B	Blood	151	97.58	4
901	29160	2013	Finland	SC1B	Blood	116	97.89	4
902	29161	2013	Finland	SC1B	Blood	131	99.88	1
903	29162	2013	Finland	SC1B	Blood	205	99.89	1
904	29163	2013	Finland	SC1B	Blood	176	98.18	1
905	29164	2013	Finland	SC1B	Blood	179	99.88	1
906	29166	2013	Finland	SC1B	Blood	176	99.88	1
907	29167	2013	Finland	SC1B	Blood	116	99.88	1
908	29168	2013	Finland	SC1B	Blood	169	96.35	4
909	29169	2013	Finland	SC1B	Blood	140	98.12	1
910	29170	2013	Finland	SC1B	Blood	138	97.68	4
911	29171	2013	Finland	SC1B	Blood	194	97.07	3
912	29172	2013	Finland	SC1B	Blood	149	99.88	1
913	29173	2013	Finland	SC1B	Blood	184	98.09	1
914	29174	2013	Finland	SC1B	Blood	237	97.29	12
915	29175	2013	Finland	SC1B	Blood	276	98.43	5
916	29176	2013	Finland	SC1B	Blood	175	98.13	1
917	29177	2013	Finland	SC1B	Blood	160	99.88	1
918	29178	2013	Finland	SC1B	Blood	201	98.17	1
919	29179	2013	Finland	SC1B	Blood	159	99.88	1
920	29180	2013	Finland	SC1B	Blood	186	99.88	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
921	29181	2013	Finland	SC1B	Blood	91	99.87	1
922	29182	2013	Finland	SC1B	Blood	117	99.87	1
923	29183	2013	Finland	SC1B	Blood	162	98.11	11
924	29184	2013	Finland	SC1B	Blood	137	97.83	4
925	29185	2013	Finland	SC1B	Blood	177	99.92	2
926	29186	2013	Finland	SC1B	Blood	150	96.56	3
927	29187	2013	Finland	SC1B	Blood	157	97.65	4
928	29188	2013	Finland	SC1B	Blood	159	99.88	1
929	29189	2013	Finland	SC1B	Blood	154	97.88	3
930	29190	2013	Finland	SC1B	Blood	216	98.24	1
931	29191	2013	Finland	SC1B	Blood	182	96.28	152
932	29192	2013	Finland	SC1B	Blood	388	97.33	4
933	29193	2013	Finland	SC1B	Blood	433	97.63	4
934	29194	2013	Finland	SC1B	Blood	305	99.91	1
935	29195	2013	Finland	SC1B	Blood	394	98.23	7
936	29196	2013	Finland	SC1B	Blood	262	97.71	4
937	29197	2013	Finland	SC1B	Blood	204	96.42	59
938	29198	2013	Finland	SC1B	Blood	330	99.91	1
939	29199	2013	Finland	SC1B	Blood	267	97.16	76
940	29200	2013	Finland	SC1B	Blood	275	96.81	3
941	29201	2013	Finland	SC1B	Blood	125	97.36	1
942	29202	2012	Finland	SC1B	Blood	235	96.99	3
943	29203	2012	Finland	SC1B	Blood	174	96.04	4
944	29204	2012	Finland	SC1B	Blood	493	97	3
945	29205	2012	Finland	SC1B	Blood	183	99.89	1
946	29208	2012	Finland	SC1B	Blood	343	95.97	4
947	29209	2012	Finland	SC1B	Blood	180	99.89	1
948	29210	2012	Finland	SC1B	Blood	305	97.17	3
949	29211	2012	Finland	SC1B	Blood	127	99.89	1
950	29212	2012	Finland	SC1B	Blood	172	94.65	3
951	29213	2012	Finland	SC1B	Blood	202	99.9	1
952	29214	2012	Finland	SC1B	Blood	176	99.34	1
953	29215	2012	Finland	SC1B	Blood	409	98.05	1
954	29217	2012	Finland	SC1B	Blood	144	97.85	4
955	29218	2012	Finland	SC1B	Blood	166	99.88	1
956	29219	2012	Finland	SC1B	Blood	392	97.84	4

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
957	29220	2012	Finland	SC1B	Blood	258	99.9	1
958	29221	2012	Finland	SC1B	Blood	233	97.99	3
959	29222	2012	Finland	SC1B	Blood	136	97.79	4
960	29223	2012	Finland	SC1B	Blood	229	99.88	1
961	29224	2012	Finland	SC1B	Blood	171	94.67	3
962	29226	2012	Finland	SC1B	Blood	188	99.88	1
963	29228	2012	Finland	SC1B	Blood	128	97.85	4
964	29229	2012	Finland	SC1B	Blood	127	99.88	1
965	29230	2012	Finland	SC1B	Blood	156	95.65	5
966	29232	2012	Finland	SC1B	Blood	314	98.11	4
967	29233	2012	Finland	SC1B	Blood	133	99.79	2
968	29234	2012	Finland	SC1B	Blood	119	99.86	1
969	29235	2012	Finland	SC1B	Blood	135	97.76	1
970	29236	2012	Finland	SC1B	Blood	107	98.33	1
971	29237	2012	Finland	SC1B	Blood	108	96.15	4
972	29238	2012	Finland	SC1B	Blood	114	99.86	1
973	29239	2012	Finland	SC1B	Blood	594	96.8	3
974	29240	2012	Finland	SC1B	Blood	332	98.18	1
975	29241	2012	Finland	SC1B	Blood	124	96.66	3
976	29242	2012	Finland	SC1B	Blood	134	99.49	8
977	29243	2012	Finland	SC1B	Blood	134	99.88	1
978	29244	2012	Finland	SC1B	Blood	149	99.88	1
979	29245	2012	Finland	SC1B	Blood	124	98.06	8
980	29246	2012	Finland	SC1B	Blood	156	99.88	1
981	29247	2012	Finland	SC1B	Blood	218	94.36	4
982	29248	2012	Finland	SC1B	Blood	176	96.52	3
983	29249	2012	Finland	SC1B	Blood	176	99.89	1
984	29250	2012	Finland	SC1B	Blood	197	94.92	3
985	29251	2012	Finland	SC1B	Blood	155	97.43	45
986	29253	2012	Finland	SC1B	Blood	194	99.89	1
987	29254	2012	Finland	SC1B	Blood	151	99.89	1
988	29255	2012	Finland	SC1B	Blood	159	99.89	1
989	29256	2012	Finland	SC1B	Blood	179	99.87	1
990	29257	2012	Finland	SC1B	Blood	437	99.91	1
991	29258	2012	Finland	SC1B	Blood	98	99.86	1
992	29259	2012	Finland	SC1B	Blood	161	96.06	4

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
993	29260	2012	Finland	SC1B	Blood	191	97.35	4
994	29261	2012	Finland	SC1B	Blood	439	96.11	4
995	29262	2012	Finland	SC1B	Blood	177	97.46	45
996	29263	2012	Finland	SC1B	Blood	203	99.89	1
997	29264	2012	Finland	SC1B	Blood	182	97.86	4
998	29265	2011	Finland	SC1B	Blood	151	97.73	1
999	29266	2011	Finland	SC1B	Blood	195	99.96	1
1000	29267	2011	Finland	SC1B	Blood	146	97.88	4
1001	29268	2011	Finland	SC1B	Blood	175	99.88	1
1002	29269	2011	Finland	SC1B	Blood	180	97.79	3
1003	29272	2011	Finland	SC1B	Blood	675	97.52	3
1004	29273	2011	Finland	SC1B	Blood	419	99.9	1
1005	29274	2011	Finland	SC1B	Blood	272	99.53	8
1006	29275	2011	Finland	SC1B	Blood	392	97.73	4
1007	29276	2011	Finland	SC1B	Blood	159	97.31	12
1008	29277	2011	Finland	SC1B	Blood	153	99.89	1
1009	29278	2011	Finland	SC1B	Blood	135	97.7	4
1010	29279	2011	Finland	SC1B	Blood	91	98.37	1
1011	29280	2011	Finland	SC1B	Blood	156	96.15	154
1012	29281	2011	Finland	SC1B	Blood	218	97.93	4
1013	29282	2011	Finland	SC1B	Blood	135	98.16	7
1014	29283	2011	Finland	SC1B	Blood	142	97.81	4
1015	29284	2011	Finland	SC1B	Blood	360	97.31	119
1016	29285	2011	Finland	SC1B	Blood	287	99.9	1
1017	29286	2011	Finland	SC1B	Blood	256	95.67	3
1018	29287	2011	Finland	SC1B	Blood	175	99.91	1
1019	29289	2011	Finland	SC1B	Blood	147	98.13	1
1020	29290	2011	Finland	SC1B	Blood	179	99.89	1
1021	29291	2011	Finland	SC1B	Blood	226	96.63	3
1022	29292	2011	Finland	SC1B	Blood	308	96.89	3
1023	29293	2011	Finland	SC1B	Blood	195	99.89	1
1024	29294	2011	Finland	SC1B	Blood	417	97.73	3
1025	29295	2011	Finland	SC1B	Blood	264	99.9	5
1026	29296	2011	Finland	SC1B	Blood	191	99.96	1
1027	29297	2011	Finland	SC1B	Blood	637	94.13	3
1028	29298	2011	Finland	SC1B	Blood	343	99.91	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1029	29299	2011	Finland	SC1B	Blood	306	93.59	3
1030	29300	2010	Finland	SC1B	Blood	219	97.42	11
1031	29301	2010	Finland	SC1B	Blood	116	99.58	1
1032	29302	2010	Finland	SC1B	Blood	76	97.99	4
1033	29303	2010	Finland	SC1B	Blood	89	97.46	3
1034	29304	2010	Finland	SC1B	Blood	150	99.88	1
1035	29305	2010	Finland	SC1B	Blood	162	98.04	1
1036	29306	2010	Finland	SC1B	Blood	332	95.78	17
1037	29307	2010	Finland	SC1B	Blood	162	99.82	101
1038	29308	2010	Finland	SC1B	Blood	214	97.81	4
1039	29310	2010	Finland	SC1B	Blood	248	99.89	1
1040	29311	2010	Finland	SC1B	Blood	142	95.68	1
1041	29312	2010	Finland	SC1B	Blood	167	99.96	1
1042	29313	2010	Finland	SC1B	Blood	160	99.86	2
1043	29314	2010	Finland	SC1B	Blood	155	97.66	4
1044	29315	2010	Finland	SC1B	Blood	147	98.44	8
1045	29316	2010	Finland	SC1B	Blood	74	99.86	1
1046	29317	2010	Finland	SC1B	Blood	57	96.16	4
1047	29318	2010	Finland	SC1B	Blood	84	99.87	1
1048	29319	2010	Finland	SC1B	Blood	61	99.85	1
1049	29320	2010	Finland	SC1B	Blood	86	94.38	22
1050	29321	2010	Finland	SC1B	Blood	190	98.31	1
1051	29322	2010	Finland	SC1B	Blood	324	97.63	1
1052	29323	2010	Finland	SC1B	Blood	139	99.88	1
1053	29324	2010	Finland	SC1B	Blood	79	98.99	12
1054	29325	2010	Finland	SC1B	Blood	60	99.85	1
1055	29326	2010	Finland	SC1B	Blood	43	95.02	3
1056	29327	2010	Finland	SC1B	Blood	105	99.85	1
1057	29328	2010	Finland	SC1B	Blood	152	98.16	1
1058	29329	2010	Finland	SC1B	Blood	161	99.9	1
1059	29330	2010	Finland	SC1B	Blood	160	98.51	27
1060	29331	2010	Finland	SC1B	Blood	141	96.54	3
1061	29332	2010	Finland	SC1B	Blood	108	99.87	1
1062	29333	2010	Finland	SC1B	Blood	292	99.89	1
1063	29334	2010	Finland	SC1B	Blood	133	99.87	1
1064	29335	2010	Finland	SC1B	Blood	148	95.53	4

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1065	29336	2010	Finland	SC1B	Blood	143	96.75	60
1066	29337	2010	Finland	SC1B	Blood	157	99.88	1
1067	29338	2009	Finland	SC1B	Blood	625	98.44	1
1068	29339	2009	Finland	SC1B	Blood	118	98.29	1
1069	29340	2009	Finland	SC1B	Blood	159	94.64	153
1070	29341	2009	Finland	SC1B	Blood	209	97.78	3
1071	29342	2009	Finland	SC1B	Blood	102	98.36	1
1072	29343	2009	Finland	SC1B	Blood	107	98.39	1
1073	29344	2009	Finland	SC1B	Blood	101	99.87	5
1074	29345	2009	Finland	SC1B	Blood	181	99.89	1
1075	29346	2009	Finland	SC1B	Blood	212	99.89	1
1076	29347	2009	Finland	SC1B	Blood	140	99.09	21
1077	29348	2009	Finland	SC1B	Blood	116	99.88	1
1078	29349	2009	Finland	SC1B	Blood	120	98.8	31
1079	29350	2009	Finland	SC1B	Blood	414	99.06	12
1080	29351	2009	Finland	SC1B	Blood	150	95.3	48
1081	29352	2009	Finland	SC1B	Blood	189	99.88	1
1082	29353	2009	Finland	SC1B	Blood	169	98.06	1
1083	29354	2009	Finland	SC1B	Blood	216	94.43	3
1084	29355	2009	Finland	SC1B	Blood	146	97.91	4
1085	29356	2009	Finland	SC1B	Blood	222	98.23	11
1086	29357	2009	Finland	SC1B	Blood	429	99.9	1
1087	29358	2009	Finland	SC1B	Blood	268	99.88	1
1088	29359	2009	Finland	SC1B	Blood	235	97.54	23
1089	29360	2009	Finland	SC1B	Blood	146	96.55	3
1090	29361	2009	Finland	SC1B	Blood	124	97.83	3
1091	29362	2009	Finland	SC1B	Blood	142	97.9	4
1092	29363	2009	Finland	SC1B	Blood	139	99.88	1
1093	29364	2009	Finland	SC1B	Blood	159	99.88	1
1094	29365	2009	Finland	SC1B	Blood	165	95.9	17
1095	29366	2009	Finland	SC1B	Blood	163	97.94	4
1096	29367	2009	Finland	SC1B	Blood	241	99.88	1
1097	29368	2009	Finland	SC1B	Blood	196	99.89	1
1098	29369	2009	Finland	SC1B	Blood	306	97.93	4
1099	29370	2009	Finland	SC1B	Blood	127	97.87	4
1100	29371	2009	Finland	SC1B	Blood	286	97.54	3

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1101	29372	2009	Finland	SC1B	Blood	255	97.49	4
1102	29373	2009	Finland	SC1B	Blood	229	97.75	3
1103	29374	2009	Finland	SC1B	Blood	184	98.72	31
1104	29375	2009	Finland	SC1B	Blood	84	97.73	4
1105	29376	2009	Finland	SC1B	Blood	112	98.72	31
1106	29377	2009	Finland	SC1B	Blood	161	99.87	1
1107	29378	2009	Finland	SC1B	Blood	177	99.88	1
1108	29379	2009	Finland	SC1B	Blood	179	98.38	1
1109	29380	2009	Finland	SC1B	Blood	179	98.82	42
1110	29381	2009	Finland	SC1B	Blood	164	93.69	3
1111	29382	2009	Finland	SC1B	Blood	161	99.87	1
1112	29383	2009	Finland	SC1B	Blood	499	92.84	3
1113	29384	2009	Finland	SC1B	Blood	155	99.53	8
1114	29385	2009	Finland	SC1B	Blood	117	97.72	4
1115	29386	2009	Finland	SC1B	Blood	108	98.35	1
1116	29387	2009	Finland	SC1B	Blood	129	97.99	4
1117	29388	2009	Finland	SC1B	Blood	138	99.38	1
1118	29389	2009	Finland	SC1B	Blood	281	99.91	1
1119	29390	2009	Finland	SC1B	Blood	364	97.47	3
1120	29391	2008	Finland	SC1B	Blood	299	99.9	1
1121	29392	2008	Finland	SC1B	Blood	271	99.91	1
1122	29394	2008	Finland	SC1B	Blood	414	99.54	8
1123	29395	2008	Finland	SC1B	Blood	320	97.33	17
1124	29396	2008	Finland	SC1B	Blood	390	99.91	5
1125	29397	2008	Finland	SC1B	Blood	249	97.9	4
1126	29398	2008	Finland	SC1B	Blood	212	98.09	1
1127	29399	2008	Finland	SC1B	Blood	110	97.99	1
1128	29400	2008	Finland	SC1B	Blood	185	99.89	1
1129	29402	2008	Finland	SC1B	Blood	174	98.1	1
1130	29403	2008	Finland	SC1B	Blood	313	99.89	1
1131	29404	2008	Finland	SC1B	Blood	347	98.02	8
1132	29406	2008	Finland	SC1B	Blood	224	99.89	5
1133	29407	2008	Finland	SC1B	Blood	325	95.99	3
1134	29408	2008	Finland	SC1B	Blood	277	99.01	12
1135	29409	2008	Finland	SC1B	Blood	270	97.94	4
1136	29410	2008	Finland	SC1B	Blood	251	97.42	3

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1137	29411	2008	Finland	SC1B	Blood	276	96.47	3
1138	29412	2008	Finland	SC1B	Blood	117	98.46	1
1139	29413	2008	Finland	SC1B	Blood	269	99.9	1
1140	29414	2008	Finland	SC1B	Blood	211	97.36	3
1141	29415	2008	Finland	SC1B	Blood	181	97.78	3
1142	29416	2008	Finland	SC1B	Blood	237	97.55	3
1143	29417	2008	Finland	SC1B	Blood	239	99.89	1
1144	29418	2008	Finland	SC1B	Blood	363	99.9	1
1145	29419	2008	Finland	SC1B	Blood	261	99.89	1
1146	29420	2008	Finland	SC1B	Blood	299	99.89	2
1147	29421	2008	Finland	SC1B	Blood	150	97.62	4
1148	29422	2008	Finland	SC1B	Blood	158	99.96	1
1149	29423	2008	Finland	SC1B	Blood	173	99.89	1
1150	29424	2008	Finland	SC1B	Blood	441	99.91	1
1151	29425	2008	Finland	SC1B	Blood	145	95.88	1
1152	29426	2008	Finland	SC1B	Blood	201	99.06	12
1153	29427	2008	Finland	SC1B	Blood	173	98.73	31
1154	29428	2008	Finland	SC1B	Blood	154	97.78	3
1155	29429	2008	Finland	SC1B	Blood	176	96.74	3
1156	29430	2008	Finland	SC1B	Blood	126	97.89	4
1157	29432	2008	Finland	SC1B	Blood	474	99.02	12
1158	29433	2008	Finland	SC1B	Blood	156	97.85	4
1159	29434	2008	Finland	SC1B	Blood	87	97.77	4
1160	29435	2008	Finland	SC1B	Blood	122	97.62	3
1161	29436	2008	Finland	SC1B	Blood	407	98	4
1162	29439	2007	Finland	SC1B	Blood	123	99.88	1
1163	29440	2007	Finland	SC1B	Blood	118	99.88	1
1164	29441	2014	Finland	SC1B	Blood	336	99.9	1
1165	29442	2012	Finland	SC1B	Blood	193	99.88	1
1166	29443	2011	Finland	SC1B	Blood	185	99.89	1
1167	29444	2011	Finland	SC1B	Blood	204	96.55	3
1168	29445	2009	Finland	SC1B	Blood	178	97.17	3
1169	29446	2009	Finland	SC1B	Blood	146	99.83	24
1170	29447	2009	Finland	SC1B	Blood	208	96.89	60
1171	29448	2007	Finland	SC1B	Blood	187	96.5	22
1172	29450	2007	Finland	SC1B	Blood	175	97.84	3

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1173	29451	2007	Finland	SC1B	Blood	203	95.25	1
1174	29452	2007	Finland	SC1B	Blood	217	97.82	3
1175	29453	2007	Finland	SC1B	Blood	77	99.86	1
1176	29454	2007	Finland	SC1B	Blood	296	99.91	1
1177	29455	2007	Finland	SC1B	Blood	176	97.76	3
1178	29456	2007	Finland	SC1B	Blood	218	99.87	1
1179	29457	2007	Finland	SC1B	Blood	247	99.89	1
1180	29458	2007	Finland	SC1B	Blood	263	98.42	1
1181	29459	2007	Finland	SC1B	Blood	180	97.79	3
1182	29460	2007	Finland	SC1B	Blood	241	99.9	1
1183	29461	2007	Finland	SC1B	Blood	290	95.41	1
1184	29462	2007	Finland	SC1B	Blood	194	99.89	1
1185	29463	2007	Finland	SC1B	Blood	191	97.75	3
1186	29464	2007	Finland	SC1B	Blood	194	97.81	3
1187	29465	2007	Finland	SC1B	Blood	248	99.58	5
1188	29466	2007	Finland	SC1B	Blood	205	95.82	1
1189	29467	2007	Finland	SC1B	Blood	281	97.9	3
1190	29468	2007	Finland	SC1B	Blood	146	94.73	1
1191	29469	2007	Finland	SC1B	Blood	180	94.52	3
1192	29470	2006	Finland	SC1B	Blood	328	99.91	1
1193	29471	2006	Finland	SC1B	Blood	215	99.88	1
1194	29473	2006	Finland	SC1B	Blood	218	97.82	3
1195	29474	2006	Finland	SC1B	Blood	214	99.88	1
1196	29475	2006	Finland	SC1B	Blood	164	97.5	1
1197	29476	2006	Finland	SC1B	Blood	208	98.09	1
1198	29477	2006	Finland	SC1B	Blood	202	99.88	2
1199	29478	2006	Finland	SC1B	Blood	248	99.91	2
1200	29479	2006	Finland	SC1B	Blood	58	92.85	3
1201	29480	2006	Finland	SC1B	Blood	184	99.88	1
1202	29481	2006	Finland	SC1B	Blood	206	99.89	1
1203	29483	2006	Finland	SC1B	Blood	260	98.22	1
1204	29484	2006	Finland	SC1B	Blood	236	97.73	3
1205	29485	2006	Finland	SC1B	Blood	249	99.51	8
1206	29486	2006	Finland	SC1B	Blood	247	99.88	1
1207	29487	2006	Finland	SC1B	Blood	306	99.9	1
1208	29488	2006	Finland	SC1B	Blood	223	94.47	32

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1209	29489	2006	Finland	SC1B	Blood	212	95.37	3
1210	29490	2006	Finland	SC1B	Blood	203	97.71	3
1211	29491	2006	Finland	SC1B	Blood	500	99.92	1
1212	29492	2006	Finland	SC1B	Blood	213	97.99	11
1213	29493	2006	Finland	SC1B	Blood	194	99.85	1
1214	29494	2006	Finland	SC1B	Blood	219	97.64	3
1215	29495	2006	Finland	SC1B	Blood	188	99.91	1
1216	29497	2006	Finland	SC1B	Blood	326	99.92	1
1217	29500	2006	Finland	SC1B	Blood	199	99.9	1
1218	29501	2006	Finland	SC1B	Blood	230	99.89	1
1219	29502	2006	Finland	SC1B	Blood	242	98.11	1
1220	29503	2005	Finland	SC1B	Blood	181	99.9	1
1221	29504	2005	Finland	SC1B	Blood	136	99.89	2
1222	29505	2005	Finland	SC1B	Blood	145	99.89	1
1223	29506	2005	Finland	SC1B	Blood	145	99.89	1
1224	29507	2005	Finland	SC1B	Blood	198	97.79	3
1225	29508	2005	Finland	SC1B	Blood	214	99.9	1
1226	29509	2005	Finland	SC1B	Blood	248	99.9	2
1227	29510	2005	Finland	SC1B	Blood	312	98.12	1
1228	29511	2005	Finland	SC1B	Blood	215	99.88	1
1229	29512	2005	Finland	SC1B	Blood	209	97.68	3
1230	29513	2005	Finland	SC1B	Blood	186	99.9	1
1231	29514	2005	Finland	SC1B	Blood	243	99.91	1
1232	29515	2005	Finland	SC1B	Blood	198	99.91	1
1233	29516	2005	Finland	SC1B	Blood	174	99.88	2
1234	29517	2005	Finland	SC1B	Blood	149	99.88	1
1235	29518	2005	Finland	SC1B	Blood	158	97.8	3
1236	29519	2005	Finland	SC1B	Blood	164	97.85	3
1237	29520	2005	Finland	SC1B	Blood	247	99.91	1
1238	29521	2005	Finland	SC1B	Blood	209	97.44	1
1239	29522	2005	Finland	SC1B	Blood	241	93.48	3
1240	29523	2005	Finland	SC1B	Blood	219	97.82	3
1241	29524	2005	Finland	SC1B	Blood	312	94.75	3
1242	29525	2004	Finland	SC1B	Blood	296	99.55	8
1243	29526	2004	Finland	SC1B	Blood	222	99.9	1
1244	29527	2004	Finland	SC1B	Blood	296	97.85	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1245	29528	2004	Finland	SC1B	Blood	141	97.48	1
1246	29529	2004	Finland	SC1B	Blood	144	97.7	3
1247	29530	2004	Finland	SC1B	Blood	173	99.89	1
1248	29531	2004	Finland	SC1B	Blood	140	99.81	2
1249	29532	2004	Finland	SC1B	Blood	164	99.88	2
1250	29533	2004	Finland	SC1B	Blood	169	97.77	3
1251	29534	2004	Finland	SC1B	Blood	144	97.76	3
1252	29536	2004	Finland	SC1B	Blood	136	99.81	1
1253	29537	2004	Finland	SC1B	Blood	182	99.92	1
1254	29539	2004	Finland	SC1B	Blood	372	98.94	12
1255	29540	2004	Finland	SC1B	Blood	255	97.86	3
1256	29541	2004	Finland	SC1B	Blood	132	98.03	1
1257	29542	2004	Finland	SC1B	Blood	164	97.86	3
1258	29543	2004	Finland	SC1B	Blood	121	99.86	2
1259	29544	2004	Finland	SC1B	Blood	106	97.55	3
1260	29545	2004	Finland	SC1B	Blood	122	99.88	1
1261	29546	2004	Finland	SC1B	Blood	146	97.31	209
1262	29548	2004	Finland	SC1B	Blood	131	98.46	57
1263	29549	2004	Finland	SC1B	Blood	164	95.42	3
1264	29550	2004	Finland	SC1B	Blood	156	97.61	3
1265	29551	2004	Finland	SC1B	Blood	112	97.32	3
1266	29552	2004	Finland	SC1B	Blood	208	99.89	1
1267	29553	2004	Finland	SC1B	Blood	110	99.88	28
1268	29554	2004	Finland	SC1B	Blood	125	97.25	94
1269	29555	2004	Finland	SC1B	Blood	175	97.39	1
1270	29556	2004	Finland	SC1B	Blood	118	97.71	3
1271	29557	2004	Finland	SC1B	Blood	127	99.86	1
1272	29558	2004	Finland	SC1B	Blood	123	98.1	1
1273	29559	2004	Finland	SC1B	Blood	149	98.08	22
1274	29560	2004	Finland	SC1B	Blood	164	99.88	1
1275	29561	2004	Finland	SC1B	Blood	133	97.25	3
1276	29562	2004	Finland	SC1B	Blood	133	98.5	12
1277	29564	2004	Finland	SC1B	Blood	196	97.77	3
1278	29565	2004	Finland	SC1B	Blood	156	99.88	1
1279	29566	2004	Finland	SC1B	Blood	190	95.53	3
1280	29567	2004	Finland	SC1B	Blood	276	98.37	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1281	29568	2004	Finland	SC1B	Blood	226	99.88	2
1282	29569	2004	Finland	SC1B	Blood	199	97.98	3
1283	29570	2004	Finland	SC1B	Blood	133	99.86	1
1284	29571	2003	Finland	SC1B	Blood	148	99.05	12
1285	29572	2003	Finland	SC1B	Blood	230	99.89	1
1286	29573	2003	Finland	SC1B	Blood	235	99.89	1
1287	29576	2003	Finland	SC1B	Blood	157	97.85	3
1288	29577	2003	Finland	SC1B	Blood	121	98.27	1
1289	29578	2003	Finland	SC1B	Blood	165	99.9	1
1290	29579	2003	Finland	SC1B	Blood	150	97.78	3
1291	29580	2003	Finland	SC1B	Blood	129	99.88	1
1292	29581	2003	Finland	SC1B	Blood	124	98.27	1
1293	29582	2003	Finland	SC1B	Blood	126	99.86	2
1294	29583	2003	Finland	SC1B	Blood	149	97.01	1
1295	29584	2003	Finland	SC1B	Blood	267	99.96	2
1296	29585	2003	Finland	SC1B	Blood	264	97.47	1
1297	29586	2003	Finland	SC1B	Blood	226	99.89	1
1298	29587	2003	Finland	SC1B	Blood	175	96.72	3
1299	29588	2003	Finland	SC1B	Blood	162	99.88	1
1300	29589	2003	Finland	SC1B	Blood	164	97.72	3
1301	29590	2003	Finland	SC1B	Blood	137	99.87	2
1302	29591	2003	Finland	SC1B	Blood	226	99.9	1
1303	29592	2003	Finland	SC1B	Blood	149	99.89	1
1304	29593	2003	Finland	SC1B	Blood	261	99.89	2
1305	29594	2003	Finland	SC1B	Blood	148	99.88	2
1306	29596	2003	Finland	SC1B	Blood	330	99.96	1
1307	29597	2003	Finland	SC1B	Blood	204	99.89	1
1308	29598	2003	Finland	SC1B	Blood	177	97.38	2
1309	29599	2003	Finland	SC1B	Blood	246	97.3	22
1310	29600	2003	Finland	SC1B	Blood	309	99.9	2
1311	29601	2003	Finland	SC1B	Blood	226	99.89	2
1312	29602	2003	Finland	SC1B	Blood	187	99.89	1
1313	29603	2003	Finland	SC1B	Blood	167	99.89	1
1314	29604	2003	Finland	SC1B	Blood	155	99.89	1
1315	29605	2003	Finland	SC1B	Blood	153	91.44	3
1316	29606	2003	Finland	SC1B	Blood	211	95.5	210

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1317	29607	2003	Finland	SC1B	Blood	202	99.9	2
1318	29609	2003	Finland	SC1B	Blood	148	97.67	3
1319	29610	2003	Finland	SC1B	Blood	168	97.55	3
1320	29611	2003	Finland	SC1B	Blood	213	99.88	2
1321	29612	2003	Finland	SC1B	Blood	149	96.99	3
1322	29613	2003	Finland	SC1B	Blood	173	99.89	1
1323	29614	2003	Finland	SC1B	Blood	178	97.67	3
1324	29615	2003	Finland	SC1B	Blood	205	99.89	1
1325	29616	2003	Finland	SC1B	Blood	149	99.9	1
1326	29617	2003	Finland	SC1B	Blood	162	96.18	3
1327	29618	2003	Finland	SC1B	Blood	156	97.69	3
1328	29619	2003	Finland	SC1B	Blood	242	97.85	3
1329	29620	2003	Finland	SC1B	Blood	262	97.73	1
1330	29621	2003	Finland	SC1B	Blood	166	99.88	1
1331	29622	2003	Finland	SC1B	Blood	198	99.89	1
1332	29623	2003	Finland	SC1B	Blood	226	99.89	1
1333	29625	2003	Finland	SC1B	Blood	212	99.88	2
1334	29626	2003	Finland	SC1B	Blood	153	99.87	2
1335	29627	2003	Finland	SC1B	Blood	155	99.89	2
1336	29628	2002	Finland	SC1B	Blood	140	98.35	1
1337	29629	2002	Finland	SC1B	Blood	127	99.84	2
1338	29630	2002	Finland	SC1B	Blood	106	99.88	1
1339	29631	2002	Finland	SC1B	Blood	205	99.89	2
1340	29632	2002	Finland	SC1B	Blood	99	97.57	3
1341	29633	2002	Finland	SC1B	Blood	247	97.96	3
1342	29634	2002	Finland	SC1B	Blood	243	97.94	3
1343	29635	2002	Finland	SC1B	Blood	194	99.89	1
1344	29636	2002	Finland	SC1B	Blood	200	99.89	1
1345	30066	2015	Finland	SC1B	Blood	251	98.25	23
1346	30067	2015	Finland	SC1B	Blood	235	99.96	1
1347	30068	2015	Finland	SC1B	Blood	198	98.1	1
1348	30069	2015	Finland	SC1B	Blood	216	99.97	1
1349	30070	2015	Finland	SC1B	Blood	200	97.89	4
1350	30071	2015	Finland	SC1B	Blood	187	94.8	3
1351	30072	2015	Finland	SC1B	Blood	167	99.96	1
1352	30073	2015	Finland	SC1B	Blood	175	97.55	4

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1353	30074	2015	Finland	SC1B	Blood	182	97.39	4
1354	30076	2015	Finland	SC1B	Blood	190	97.91	4
1355	30077	2015	Finland	SC1B	Blood	169	97.61	5
1356	30078	2015	Finland	SC1B	Blood	213	99.97	1
1357	30080	2015	Finland	SC1B	Blood	246	99.97	1
1358	30081	2015	Finland	SC1B	Blood	207	97.78	4
1359	30084	2015	Finland	SC1B	Blood	159	99.96	1
1360	31876	2006	Norway	SC1B	Invasive	202	99.95	2
1361	31877	2006	Norway	SC1B	Invasive	169	99.96	2
1362	31878	2006	Norway	SC1B	Invasive	92	99.92	2
1363	31879	2006	Norway	SC1B	Invasive	99	97.42	3
1364	31880	2006	Norway	SC1B	Invasive	91	99.93	1
1365	31881	2006	Norway	SC1B	Invasive	336	99.96	1
1366	31883	2006	Norway	SC1B	Invasive	135	98.08	22
1367	31884	2006	Norway	SC1B	Invasive	145	99.94	2
1368	31885	2006	Norway	SC1B	Invasive	143	99.94	2
1369	31887	2006	Norway	SC1B	Invasive	167	98.18	92
1370	31888	2006	Norway	SC1B	Invasive	148	99.94	1
1371	31890	2006	Norway	SC1B	Invasive	254	96.36	12
1372	31891	2006	Norway	SC1B	Invasive	335	99.92	1
1373	31892	2006	Norway	SC1B	Invasive	192	97.16	29
1374	31893	2006	Norway	SC1B	Invasive	229	99.96	1
1375	31894	2006	Norway	SC1B	Invasive	137	97.5	24
1376	31895	2006	Norway	SC1B	Invasive	142	97.23	11
1377	31896	2006	Norway	SC1B	Invasive	384	99.96	1
1378	31897	2006	Norway	SC1B	Invasive	115	98.31	23
1379	31898	2006	Norway	SC1B	Invasive	134	99.94	1
1380	31899	2006	Norway	SC1B	Invasive	190	99.96	1
1381	31901	2007	Norway	SC1B	Invasive	118	99.95	1
1382	31902	2007	Norway	SC1B	Invasive	95	99.94	63
1383	31903	2007	Norway	SC1B	Invasive	128	99.94	2
1384	31904	2007	Norway	SC1B	Invasive	108	99.94	1
1385	31905	2007	Norway	SC1B	Invasive	129	99.94	2
1386	31906	2007	Norway	SC1B	Invasive	149	99.95	1
1387	31907	2007	Norway	SC1B	Invasive	125	99.95	1
1388	31908	2007	Norway	SC1B	Invasive	109	99.95	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1389	31909	2007	Norway	SC1B	Invasive	137	98.31	23
1390	31910	2007	Norway	SC1B	Invasive	139	95.03	77
1391	31911	2007	Norway	SC1B	Invasive	170	97.71	1
1392	31912	2007	Norway	SC1B	Invasive	158	99.95	1
1393	31913	2007	Norway	SC1B	Invasive	106	92.78	213
1394	31914	2007	Norway	SC1B	Invasive	141	98	22
1395	31915	2007	Norway	SC1B	Invasive	251	99.95	2
1396	31916	2007	Norway	SC1B	Invasive	307	99.95	1
1397	31917	2007	Norway	SC1B	Invasive	248	97.83	22
1398	31918	2007	Norway	SC1B	Invasive	366	99.97	1
1399	31919	2007	Norway	SC1B	Invasive	137	97.09	2
1400	31920	2010	Norway	SC1B	Invasive	121	97.66	3
1401	31921	2010	Norway	SC1B	Invasive	117	99.94	2
1402	31922	2010	Norway	SC1B	Invasive	140	99.95	1
1403	31923	2010	Norway	SC1B	Invasive	155	99.94	2
1404	31924	2010	Norway	SC1B	Invasive	72	99.53	41
1405	31925	2011	Norway	SC1B	Invasive	145	99.95	2
1406	31927	2011	Norway	SC1B	Invasive	153	96.96	51
1407	31928	2011	Norway	SC1B	Invasive	118	98.13	15
1408	31929	2012	Norway	SC1B	Invasive	160	99.57	8
1409	31930	2012	Norway	SC1B	Invasive	200	98.07	96
1410	31931	2012	Norway	SC1B	Invasive	129	99.9	2
1411	31932	2012	Norway	SC1B	Invasive	120	99.94	1
1412	31933	2012	Norway	SC1B	Invasive	110	99.95	1
1413	31934	2012	Norway	SC1B	Invasive	139	97.35	29
1414	31935	2012	Norway	SC1B	Invasive	161	94.72	212
1415	31936	2012	Norway	SC1B	Invasive	182	97.72	24
1416	31938	2012	Norway	SC1B	Invasive	133	99.95	1
1417	31939	2012	Norway	SC1B	Invasive	189	99.95	1
1418	31940	2012	Norway	SC1B	Invasive	109	99.88	2
1419	31941	2012	Norway	SC1B	Invasive	134	99.95	1
1420	31942	2012	Norway	SC1B	Invasive	164	99.95	2
1421	31943	2012	Norway	SC1B	Invasive	160	99.92	2
1422	31944	2013	Norway	SC1B	Invasive	139	99.95	1
1423	31945	2013	Norway	SC1B	Invasive	132	98.14	1
1424	31946	2013	Norway	SC1B	Invasive	115	99.94	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1425	31947	2013	Norway	SC1B	Invasive	141	99.88	2
1426	31948	2013	Norway	SC1B	Invasive	98	99.94	1
1427	31949	2013	Norway	SC1B	Invasive	131	99.96	1
1428	31950	2013	Norway	SC1B	Invasive	109	99.59	8
1429	31951	2013	Norway	SC1B	Invasive	122	94.36	10
1430	31952	2013	Norway	SC1B	Invasive	109	99.59	8
1431	31953	2013	Norway	SC1B	Invasive	119	99.89	2
1432	31954	2013	Norway	SC1B	Invasive	118	98.25	15
1433	31955	2013	Norway	SC1B	Invasive	119	99.91	2
1434	31956	2014	Norway	SC1B	Invasive	123	97.64	48
1435	31957	2014	Norway	SC1B	Invasive	137	95.49	77
1436	31958	2014	Norway	SC1B	Invasive	95	99.9	2
1437	31959	2014	Norway	SC1B	Invasive	302	99.9	2
1438	31960	2014	Norway	SC1B	Invasive	83	99.94	1
1439	31961	2014	Norway	SC1B	Invasive	100	99.54	8
1440	31962	2014	Norway	SC1B	Invasive	153	98.11	2
1441	31964	2014	Norway	SC1B	Invasive	104	99.89	2
1442	31965	2014	Norway	SC1B	Invasive	76	99.9	2
1443	31966	2014	Norway	SC1B	Invasive	230	99.16	12
1444	31967	2014	Norway	SC1B	Invasive	74	96.86	207
1445	31968	2014	Norway	SC1B	Invasive	123	99.95	1
1446	31969	2014	Norway	SC1B	Invasive	134	98.24	1
1447	31970	2014	Norway	SC1B	Invasive	118	98.29	23
1448	31971	2014	Norway	SC1B	Invasive	141	99.95	1
1449	31973	2014	Norway	SC1B	Invasive	136	98.38	2
1450	31974	2014	Norway	SC1B	Invasive	135	99.94	2
1451	31975	2014	Norway	SC1B	Invasive	158	99.53	8
1452	31976	2014	Norway	SC1B	Invasive	128	99.88	2
1453	31977	2014	Norway	SC1B	Invasive	127	98.04	4
1454	31978	2014	Norway	SC1B	Invasive	139	96.23	19
1455	31979	2014	Norway	SC1B	Invasive	126	99.88	2
1456	31980	2014	Norway	SC1B	Invasive	188	96.2	65
1457	31981	2015	Norway	SC1B	Invasive	97	97.77	8
1458	31982	2015	Norway	SC1B	Invasive	106	98.1	8
1459	31983	2015	Norway	SC1B	Invasive	135	99.37	1
1460	31984	2015	Norway	SC1B	Invasive	127	99.56	8

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1461	31985	2015	Norway	SC1B	Invasive	173	99.81	2
1462	31986	2015	Norway	SC1B	Invasive	148	99.9	2
1463	31987	2015	Norway	SC1B	Invasive	160	97.35	3
1464	31988	2015	Norway	SC1B	Invasive	131	97.88	2
1465	31989	2015	Norway	SC1B	Invasive	170	99.94	2
1466	31990	2015	Norway	SC1B	Invasive	161	98.71	1
1467	31991	2015	Norway	SC1B	Invasive	170	99.17	9
1468	31992	2015	Norway	SC1B	Invasive	144	98.05	2
1469	31993	2015	Norway	SC1B	Invasive	100	97.41	2
1470	31994	2015	Norway	SC1B	Invasive	116	98.04	4
1471	31995	2015	Norway	SC1B	Invasive	105	98.27	15
1472	31996	2015	Norway	SC1B	Invasive	116	97.41	32
1473	31997	2015	Norway	SC1B	Invasive	144	97.13	12
1474	31998	2015	Norway	SC1B	Invasive	116	96.4	66
1475	31999	2015	Norway	SC1B	Invasive	122	98.08	8
1476	32001	2015	Norway	SC1B	Invasive	192	97.7	2
1477	32002	2015	Norway	SC1B	Invasive	163	99.89	2
1478	32003	2015	Norway	SC1B	Invasive	179	99.89	2
1479	32004	2015	Norway	SC1B	Invasive	163	95.28	1
1480	32005	2015	Norway	SC1B	Invasive	141	98.71	23
1481	32007	2016	Norway	SC1B	Invasive	161	97.56	45
1482	32008	2016	Norway	SC1B	Invasive	131	99.93	1
1483	32009	2016	Norway	SC1B	Invasive	116	97.62	1
1484	32010	2016	Norway	SC1B	Invasive	121	99.9	2
1485	32011	2016	Norway	SC1B	Invasive	144	96.16	4
1486	32012	2016	Norway	SC1B	Invasive	182	99.9	2
1487	32013	2016	Norway	SC1B	Invasive	288	99.96	1
1488	32014	2016	Norway	SC1B	Invasive	276	99.96	1
1489	32015	2016	Norway	SC1B	Invasive	170	99.9	2
1490	32016	2016	Norway	SC1B	Invasive	174	99.95	2
1491	32017	2016	Norway	SC1B	Invasive	108	99.95	2
1492	32018	2016	Norway	SC1B	Invasive	122	98.06	2
1493	32019	2016	Norway	SC1B	Invasive	121	99.95	1
1494	32020	2016	Norway	SC1B	Invasive	133	99.95	1
1495	32021	2016	Norway	SC1B	Invasive	138	99.93	2
1496	32022	2016	Norway	SC1B	Invasive	77	95.46	52

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1497	32023	2016	Norway	SC1B	Invasive	153	93.97	211
1498	32024	2016	Norway	SC1B	Invasive	174	98.09	2
1499	32025	2016	Norway	SC1B	Invasive	261	99.9	61
1500	32026	2016	Norway	SC1B	Invasive	295	99.9	63
1501	32027	2016	Norway	SC1B	Invasive	213	97.69	2
1502	32029	2016	Norway	SC1B	Invasive	123	95.42	2
1503	32030	2016	Norway	SC1B	Invasive	120	98.07	2
1504	32031	2016	Norway	SC1B	Invasive	141	98.12	1
1505	32032	2016	Norway	SC1B	Invasive	107	99.19	52
1506	32033	2016	Norway	SC1B	Invasive	134	99.95	1
1507	32034	2016	Norway	SC1B	Invasive	144	99.95	2
1508	32035	2016	Norway	SC1B	Invasive	131	99.89	2
1509	32036	2016	Norway	SC1B	Invasive	131	99.91	2
1510	32037	2016	Norway	SC1B	Invasive	192	99.9	2
1511	32038	2016	Norway	SC1B	Invasive	228	98.13	2
1512	32039	2016	Norway	SC1B	Invasive	205	99.9	2
1513	32040	2016	Norway	SC1B	Invasive	152	99.89	2
1514	32041	2016	Norway	SC1B	Invasive	114	99.91	2
1515	32053	2009	Faroe Islands	SC1B	Invasive	220	99.91	1
1516	32094	2009	Faroe Islands	SC1B	Invasive	163	97.68	2
1517	32120	2009	Faroe Islands	SC1B	Invasive	211	97.63	2
1518	32179	2009	Faroe Islands	SC1B	Invasive	147	99.94	2
1519	32182	2014	Faroe Islands	SC1B	Invasive	145	99.9	2
1520	32194	2012	Faroe Islands	SC1B	Invasive	112	99.82	2
1521	7871	1992	Canada	SC2A	Invasive	189	92.45	143
1522	7872	1992	Canada	SC2A	Invasive	179	90.91	8
1523	7911	1995	Canada	SC2A	Invasive	170	97.41	190
1524	7917	1995	Canada	SC2A	Invasive	198	99.24	9
1525	7918	1995	Canada	SC2A	Invasive	242	99.26	9
1526	7923	1996	Canada	SC2A	Invasive	229	99.25	9
1527	7965	1997	Canada	SC2A	Invasive	215	99.93	1
1528	7980	1997	Canada	SC2A	Invasive	228	99.94	1
1529	7993	1997	Canada	SC2A	Invasive	212	99.94	1

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1530	8012	1999	Canada	SC2A	Invasive	166	96.36	182
1531	8017	1999	Canada	SC2A	Invasive	141	99.86	2
1532	8019	1999	Canada	SC2A	Invasive	190	99.92	5
1533	10759	1998	Canada	SC2A	Invasive	146	96.46	148
1534	10772	1998	Canada	SC2A	Invasive	177	99.03	204
1535	10778	1998	Canada	SC2A	Invasive	185	96.67	168
1536	10781	1998	Canada	SC2A	Invasive	184	99.23	9
1537	10791	1998	Canada	SC2A	Invasive	195	99.23	9
1538	10793	1999	Canada	SC2A	Invasive	183	98.4	49
1539	10798	1999	Canada	SC2A	Invasive	205	98.24	7
1540	10801	1992	Canada	SC2A	Invasive	308	80.44	8
1541	10808	2000	Canada	SC2A	Invasive	201	99.95	1
1542	10810	2000	Canada	SC2A	Invasive	212	99.22	9
1543	10814	2000	Canada	SC2A	Invasive	229	99.95	1
1544	12229	2001	Canada	SC2A	Invasive	185	98.02	1
1545	12234	2001	Canada	SC2A	Invasive	207	98.61	25
1546	12238	2001	Canada	SC2A	Invasive	214	99.96	2
1547	12240	2001	Canada	SC2A	Invasive	281	97.62	4
1548	12241	2001	Canada	SC2A	Invasive	175	99.96	1
1549	12246	2001	Canada	SC2A	Invasive	228	98.31	7
1550	12254	2002	Canada	SC2A	Invasive	222	98.28	7
1551	12256	2002	Canada	SC2A	Invasive	120	98.27	33
1552	27937	1995	USA (A)	SC2A	Pneumonia	297	99.96	1
1553	27958	2005	USA (D)	SC2A	Necrotizing fasciitis	151	98.27	11
1554	27959	2005	USA (B)	SC2A	Bacteremia	124	99.94	1
1555	27961	2005	USA (F)	SC2A	Bacteremia	96	99.92	1
1556	27963	2005	USA (D)	SC2A	Necrotizing fasciitis	291	95	1
1557	27965	2005	USA (A)	SC2A	Endometritis	197	99.95	1
1558	27966	2005	USA (H)	SC2A	Bacteremia	137	98.32	7
1559	27968	2004	USA (J)	SC2A	Necrotizing fasciitis	175	99.95	1
1560	27969	2005	USA (J)	SC2A	Necrotizing fasciitis	170	98.07	121
1561	27973	2005	USA (H)	SC2A	Endometritis	189	98.45	11
1562	27975	2005	USA (F)	SC2A	Cellulitis	142	98.08	4
1563	27976	2005	USA (I)	SC2A	Bacteremia	141	99.94	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1564	27977	2005	USA (B)	SC2A	Pneumonia	169	99.91	2
1565	27978	2005	USA (B)	SC2A	Bacteremia	247	99.95	1
1566	27979	2005	USA (B)	SC2A	Cellulitis	211	99.95	1
1567	27980	2005	USA (B)	SC2A	Endometritis	198	99.95	1
1568	27981	2005	USA (I)	SC2A	Bacteremia	182	99.95	1
1569	27985	2005	USA (F)	SC2A	Cellulitis	301	99.96	1
1570	27986	2005	USA (F)	SC2A	Septic arthritis	185	99.95	1
1571	27987	2005	USA (F)	SC2A	Cellulitis	149	99.94	1
1572	27988	2005	USA (G)	SC2A	Bacteremia	207	99.95	5
1573	27989	2005	USA (A)	SC2A	STSS	118	98.75	34
1574	27991	2005	USA (F)	SC2A	Septic arthritis	156	99.95	5
1575	27992	2005	USA (F)	SC2A	Cellulitis	167	99.95	5
1576	27993	2005	USA (F)	SC2A	Bacteremia	130	99.95	1
1577	27994	2005	USA (J)	SC2A	Septic arthritis	158	99.95	1
1578	27996	2005	USA (J)	SC2A	Pneumonia	180	96.54	64
1579	27999	2005	USA (E)	SC2A	Pneumonia	155	99.93	1
1580	28000	2005	USA (I)	SC2A	Bacteremia	208	99.89	8
1581	28001	2005	USA (I)	SC2A	Endometritis	200	98.37	130
1582	28002	2005	USA (D)	SC2A	Bacteremia	191	99.95	1
1583	28004	2005	USA (D)	SC2A	Bacteremia	207	95.46	12
1584	28005	2005	USA (E)	SC2A	Bacteremia	189	99.93	1
1585	28007	2005	USA (E)	SC2A	Cellulitis	222	99.95	5
1586	28008	2006	USA (H)	SC2A	Bacteremia	224	97.74	4
1587	28010	2005	USA (F)	SC2A	Cellulitis	270	99.94	1
1588	28011	2005	USA (F)	SC2A	Necrotizing fasciitis	174	99.94	1
1589	28013	2006	USA (F)	SC2A	Bacteremia	180	99.94	5
1590	28014	2006	USA (F)	SC2A	Cellulitis	176	99.95	1
1591	28018	2005	USA (F)	SC2A	Necrotizing fasciitis/STSS	162	99.95	1
1592	28019	2005	USA (E)	SC2A	Cellulitis	163	94.37	151
1593	28020	2005	USA (G)	SC2A	Necrotizing fasciitis/STSS	186	98.48	5
1594	28021	2005	USA (I)	SC2A	Bacteremia	243	99.95	1
1595	28022	2005	USA (I)	SC2A	Bacteremia	186	99.95	1
1596	28023	2005	USA (J)	SC2A	Bacteremia	318	98.66	19
1597	28024	2006	USA (D)	SC2A	Necrotizing fasciitis	214	99.21	186

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1598	28025	2006	USA (D)	SC2A	Bacteremia	194	98.22	11
1599	28026	2006	USA (E)	SC2A	Bacteremia	174	98.27	7
1600	28028	2006	USA (B)	SC2A	Septic arthritis	181	99.95	5
1601	28029	2006	USA (B)	SC2A	Bacteremia	166	99.92	2
1602	28030	2006	USA (I)	SC2A	Cellulitis	174	99.95	1
1603	28031	2004	USA (E)	SC2A	Cellulitis	222	99.92	1
1604	28033	2005	USA (E)	SC2A	Cellulitis	215	99.95	1
1605	28034	2006	USA (F)	SC2A	Necrotizing fasciitis	219	99.96	5
1606	28037	2009	USA (H)	SC2A	Bacteremia	209	99.91	1
1607	28038	2009	USA (A)	SC2A	Endometritis	212	99.06	9
1608	28039	2009	USA (A)	SC2A	Bacteremia	198	99.89	13
1609	28045	2009	USA (E)	SC2A	Cellulitis	202	98.22	11
1610	28047	2009	USA (D)	SC2A	STSS	214	99.94	1
1611	28050	2009	USA (J)	SC2A	Bacteremia	233	99.95	1
1612	28051	2009	USA (J)	SC2A	Pneumonia	157	97.87	11
1613	28054	2009	USA (F)	SC2A	Necrotizing fasciitis	157	99.95	5
1614	28055	2009	USA (F)	SC2A	Pneumonia	125	99.83	1
1615	28057	2009	USA (F)	SC2A	Pneumonia	145	99.94	1
1616	28058	2009	USA (D)	SC2A	STSS	146	99.95	1
1617	28060	2009	USA (A)	SC2A	Cellulitis	152	99.93	1
1618	28062	2009	USA (G)	SC2A	Cellulitis	205	99.95	1
1619	28063	2009	USA (A)	SC2A	STSS	112	99.03	9
1620	28064	2009	USA (J)	SC2A	Bacteremia	173	99.95	5
1621	28065	2009	USA (J)	SC2A	Cellulitis	120	99.95	1
1622	28067	2009	USA (D)	SC2A	Cellulitis	155	99.7	1
1623	28069	2009	USA (I)	SC2A	Puerperal sepsis	127	98.31	7
1624	28071	2009	USA (F)	SC2A	Cellulitis	130	96.07	1
1625	28074	2009	USA (G)	SC2A	Endometritis	172	99.95	5
1626	28076	2009	USA (B)	SC2A	Septic shock	143	99.95	1
1627	28077	2009	USA (J)	SC2A	Bacteremia	139	98.3	1
1628	28078	2010	USA (D)	SC2A	Endometritis	151	99.15	74
1629	28082	2009	USA (E)	SC2A	Septic shock	211	99.95	1
1630	28083	2009	USA (E)	SC2A	Septic arthritis	191	99.95	5
1631	28084	2009	USA (G)	SC2A	Bacteremia	184	99.95	13
1632	28085	2009	USA (G)	SC2A	Cellulitis	220	99.95	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1633	28086	2010	USA (H)	SC2A	Cellulitis	233	99.95	1
1634	28088	2010	USA (H)	SC2A	Cellulitis	152	99.89	1
1635	28089	2009	USA (F)	SC2A	Septic arthritis	222	98.24	7
1636	28090	2009	USA (F)	SC2A	Bacteremia	234	95.51	1
1637	28091	2009	USA (B)	SC2A	Unknown	226	99.95	1
1638	28092	2009	USA (B)	SC2A	Septic shock	242	99.96	1
1639	28094	2009	USA (E)	SC2A	Cellulitis	251	95.87	202
1640	28095	2009	USA (E)	SC2A	Bacteremia	245	99.89	13
1641	28097	2009	USA (H)	SC2A	Cellulitis	213	99.95	1
1642	28099	2009	USA (A)	SC2A	STSS	192	99.92	1
1643	28100	2009	USA (A)	SC2A	Cellulitis	181	99.94	1
1644	28102	2009	USA (H)	SC2A	Bacteremia	178	98.3	7
1645	28105	2009	USA (I)	SC2A	Cellulitis	225	99.95	1
1646	28107	2009	USA (F)	SC2A	Septic arthritis	162	99.94	5
1647	28111	2001	USA (C)	SC2A	Abscess	159	97.99	4
1648	28114	2001	USA (A)	SC2A	Cellulitis	167	99.95	1
1649	28115	2001	USA (A)	SC2A	Pneumonia	287	99.95	1
1650	28117	2001	USA (A)	SC2A	Septic arthritis	246	99.95	1
1651	28119	2002	USA (B)	SC2A	Bacteremia	286	99.94	1
1652	28121	2002	USA (I)	SC2A	Cellulitis	424	99.96	1
1653	28127	2002	USA (H)	SC2A	Necrotizing fasciitis	320	99.92	1
1654	28128	2002	USA (H)	SC2A	Cellulitis	262	99.89	1
1655	28129	2002	USA (H)	SC2A	Cellulitis	251	99.91	1
1656	28130	2002	USA (B)	SC2A	Cellulitis	194	97.98	25
1657	28131	2002	USA (B)	SC2A	Bacteremia	140	99.95	1
1658	28140	2010	USA (D)	SC2A	Cellulitis	272	97.49	11
1659	28143	2010	USA (I)	SC2A	Empyema	229	99.23	9
1660	28144	2010	USA (I)	SC2A	STSS	160	97.7	1
1661	28145	2010	USA (I)	SC2A	Osteomyelitis	239	99.95	1
1662	28148	1999	USA (E)	SC2A	Cellulitis	220	98.28	1
1663	28156	2002	USA (C)	SC2A	Bacteremia	184	98.29	7
1664	28158	2002	USA (C)	SC2A	Cellulitis	242	99.96	1
1665	28159	2002	USA (A)	SC2A	Cellulitis	270	97.01	58
1666	28160	2002	USA (F)	SC2A	Abscess	177	99.95	5
1667	28161	2002	USA (F)	SC2A	Necrotizing fasciitis	172	99.95	5

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1668	28163	1998	USA (F)	SC2A	Bacteremia	202	99.95	1
1669	28168	2010	USA (A)	SC2A	Bacteremia	192	97.51	9
1670	28172	2010	USA (F)	SC2A	Cellulitis	209	98.53	25
1671	28173	2010	USA (F)	SC2A	Bacteremia	233	95.27	1
1672	28175	2002	USA (H)	SC2A	Bacteremia	316	98.14	7
1673	28184	1998	USA (C)	SC2A	Pneumonia	140	98.26	7
1674	28188	1999	USA (A)	SC2A	peritonitis	132	95.68	7
1675	28191	1999	USA (C)	SC2A	Cellulitis	170	98.29	7
1676	28192	1999	USA (C)	SC2A	Bacteremia	226	98.29	7
1677	28195	1999	USA (A)	SC2A	Cellulitis	155	99.95	2
1678	28196	1999	USA (A)	SC2A	peritonitis	159	97.97	7
1679	28197	1999	USA (A)	SC2A	Bacteremia	176	99.95	1
1680	28202	1999	USA (F)	SC2A	Cellulitis	318	99.93	2
1681	28206	2010	USA (A)	SC2A	Pneumonia	247	99.23	9
1682	28207	2010	USA (D)	SC2A	Cellulitis	267	98.1	1
1683	28209	2010	USA (F)	SC2A	Cellulitis	359	99.95	1
1684	28210	2002	USA (E)	SC2A	Bacteremia	197	99.95	1
1685	28211	2002	USA (I)	SC2A	Bacteremia	241	99.95	1
1686	28212	2002	USA (I)	SC2A	Bacteremia	249	99.95	1
1687	28214	1998	USA (E)	SC2A	Bacteremia	167	97.67	1
1688	28215	1999	USA (C)	SC2A	Pneumonia	212	98.27	7
1689	28227	2002	USA (B)	SC2A	Bacteremia	197	99.91	1
1690	28228	2002	USA (C)	SC2A	Cellulitis	177	99.95	1
1691	28229	2002	USA (B)	SC2A	Bacteremia	224	99.95	1
1692	28230	2002	USA (B)	SC2A	Bacteremia	307	99.51	8
1693	28231	2002	USA (A)	SC2A	Cellulitis	291	98.14	9
1694	28232	1998	USA (A)	SC2A	Cellulitis	294	97.46	110
1695	28237	2002	USA (C)	SC2A	Cellulitis	145	99.95	1
1696	28239	2002	USA (E)	SC2A	Cellulitis	270	99.96	2
1697	28244	1998	USA (A)	SC2A	Bacteremia	348	99.64	9
1698	28248	2010	USA (A)	SC2A	Cellulitis	321	99.95	1
1699	28249	2010	USA (H)	SC2A	Septic arthritis	276	99.95	1
1700	28255	2010	USA (F)	SC2A	Bacteremia	197	99.95	5
1701	28258	2002	USA (D)	SC2A	Septic arthritis	321	97.44	1
1702	28259	2010	USA (A)	SC2A	Bacteremia	256	99.93	1
1703	28261	2009	USA (B)	SC2A	Septic arthritis	265	98.3	7

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1704	28263	2011	USA (B)	SC2A	Septic arthritis	172	99.95	5
1705	28265	2011	USA (F)	SC2A	Cellulitis	179	99.95	1
1706	28267	2011	USA (F)	SC2A	Pneumonia	222	99.86	5
1707	28269	1998	USA (A)	SC2A	Bacteremia	257	96.49	27
1708	28270	2011	USA (A)	SC2A	Bacteremia	214	99.96	1
1709	28271	2011	USA (F)	SC2A	Pneumonia	183	98.53	19
1710	28272	2011	USA (F)	SC2A	Cellulitis	236	99.95	1
1711	28274	2011	USA (C)	SC2A	Cellulitis	162	99.95	1
1712	28279	2011	USA (A)	SC2A	Septic arthritis	183	99.92	1
1713	28280	2011	USA (D)	SC2A	Necrotizing fasciitis	222	99.89	13
1714	28281	2011	USA (I)	SC2A	Cellulitis	229	99.96	1
1715	28283	2002	USA (F)	SC2A	Cellulitis	246	95.59	4
1716	28284	2001	USA (I)	SC2A	Cellulitis	107	99.51	8
1717	28288	2002	USA (E)	SC2A	Cellulitis	251	98.55	1
1718	28291	2002	USA (H)	SC2A	Bacteremia	351	96.91	171
1719	28294	2011	USA (F)	SC2A	Abscess	125	99.85	1
1720	28296	2002	USA (F)	SC2A	Cellulitis	128	98.76	187
1721	28297	2002	USA (F)	SC2A	Necrotizing fasciitis	184	99.88	2
1722	28299	2001	USA (B)	SC2A	Bacteremia	109	99.85	1
1723	28300	2001	USA (B)	SC2A	Cellulitis	109	99	21
1724	28302	2001	USA (I)	SC2A	Cellulitis	99	99.84	1
1725	28304	2011	USA (A)	SC2A	Cellulitis	125	99.87	82
1726	28305	2011	USA (B)	SC2A	Cellulitis	172	99.86	1
1727	28306	1998	USA (A)	SC2A	Septic arthritis	164	98.27	7
1728	28307	1998	USA (A)	SC2A	Bacteremia	102	99.85	1
1729	28310	2011	USA (H)	SC2A	Bacteremia	147	97.43	4
1730	28312	2011	USA (E)	SC2A	Cellulitis	103	97.53	1
1731	28313	2011	USA (E)	SC2A	Cellulitis	109	99.85	2
1732	28314	2001	USA (H)	SC2A	Bacteremia	62	99.81	1
1733	28316	2002	USA (H)	SC2A	Cellulitis	286	99.93	1
1734	28321	2001	USA (F)	SC2A	Bacteremia	107	97.46	1
1735	28322	2001	USA (F)	SC2A	Pneumonia	92	99.85	1
1736	28325	2001	USA (F)	SC2A	Bacteremia	97	98.17	7
1737	28331	2000	USA (D)	SC2A	Bacteremia	195	97.27	33
1738	28332	2000	USA (F)	SC2A	Bacteremia	140	99.03	9

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1739	28335	2000	USA (F)	SC2A	STSS	129	97.46	1
1740	28337	2000	USA (F)	SC2A	Cellulitis	133	98.99	21
1741	28340	2000	USA (E)	SC2A	Bacteremia	101	98.18	1
1742	28341	2003	USA (A)	SC2A	Cellulitis	167	99.88	1
1743	28342	2003	USA (A)	SC2A	Bacteremia	178	99.89	1
1744	28343	2003	USA (H)	SC2A	Bacteremia	124	96.03	7
1745	28345	2003	USA (E)	SC2A	Bacteremia	272	99.22	9
1746	28346	2003	USA (J)	SC2A	Bacteremia	75	99.82	2
1747	28347	2000	USA (D)	SC2A	Cellulitis	272	99.87	8
1748	28348	1999	USA (A)	SC2A	Bacteremia	550	99.87	1
1749	28350	1999	USA (A)	SC2A	Endometritis	481	98.58	1
1750	28351	1999	USA (A)	SC2A	Meningitis	291	99.22	9
1751	28354	2003	USA (C)	SC2A	Cellulitis	112	98.14	7
1752	28356	2003	USA (F)	SC2A	Bacteremia	128	99.88	1
1753	28358	2003	USA (F)	SC2A	Bacteremia	2086	99.86	1
1754	28362	1999	USA (D)	SC2A	Cellulitis	106	98.16	7
1755	28363	2003	USA (H)	SC2A	Cellulitis	85	99.85	1
1756	28364	2003	USA (D)	SC2A	Bacteremia	153	99.87	13
1757	28365	2001	USA (J)	SC2A	Bacteremia	92	98.07	7
1758	28366	2005	USA (E)	SC2A	Pneumonia	207	99.87	1
1759	28369	2003	USA (F)	SC2A	Cellulitis	162	95.78	1
1760	28370	2003	USA (F)	SC2A	Necrotizing fasciitis	3431	99.72	1
1761	28371	2003	USA (F)	SC2A	Bacteremia	2831	99.88	5
1762	28372	2003	USA (H)	SC2A	Bacteremia	145	98.34	11
1763	28375	1998	USA (D)	SC2A	Bacteremia	97	97.17	7
1764	28378	2002	USA (A)	SC2A	cellulitis	115	96.97	58
1765	28379	2002	USA (H)	SC2A	Septic arthritis	264	99.93	1
1766	28383	2002	USA (J)	SC2A	Osteomyelitis	85	99.83	2
1767	28384	2002	USA (F)	SC2A	Bacteremia	882	99.86	2
1768	28386	2002	USA (F)	SC2A	Puerperal sepsis	112	99.85	5
1769	28388	1998	USA (E)	SC2A	Cellulitis	92	98.26	1
1770	28392	2003	USA (D)	SC2A	Bacteremia	131	99.88	1
1771	28393	1998	USA (F)	SC2A	Cellulitis	118	99.85	1
1772	28394	1998	USA (C)	SC2A	Puerperal sepsis	105	97.95	4
1773	28395	1998	USA (C)	SC2A	Osteomyelitis	116	96.11	178

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1774	28396	1998	USA (C)	SC2A	Cellulitis	150	98.2	7
1775	28401	2003	USA (F)	SC2A	Abscess	144	99.86	5
1776	28402	2003	USA (E)	SC2A	Bacteremia	166	98	123
1777	28406	1997	USA (A)	SC2A	Endometritis	133	99.83	8
1778	28416	2003	USA (C)	SC2A	Cellulitis	156	99.88	1
1779	28417	2003	USA (H)	SC2A	Pneumonia	122	97.23	4
1780	28418	2003	USA (H)	SC2A	Bacteremia	142	99.88	1
1781	28419	2003	USA (H)	SC2A	Bacteremia	135	99.87	1
1782	28421	2002	USA (I)	SC2A	Bacteremia	144	99.87	1
1783	28424	1999	USA (I)	SC2A	Bacteremia	191	99.88	1
1784	28428	2003	USA (H)	SC2A	Cellulitis	122	99.87	1
1785	28429	2003	USA (C)	SC2A	Cellulitis	193	99.87	2
1786	28431	2003	USA (C)	SC2A	Bacteremia	161	99.48	41
1787	28434	2003	USA (E)	SC2A	Pneumonia	165	97.34	2
1788	28435	2003	USA (E)	SC2A	Pneumonia	99	98.17	7
1789	28436	2003	USA (B)	SC2A	Osteomyelitis	215	96.6	1
1790	28438	2003	USA (F)	SC2A	Bacteremia	157	97.39	27
1791	28439	2003	USA (F)	SC2A	Septic arthritis	149	99.88	5
1792	28440	2003	USA (F)	SC2A	Necrotizing fasciitis	142	97.4	27
1793	28441	2003	USA (F)	SC2A	Bacteremia	122	99.81	2
1794	28442	2003	USA (I)	SC2A	Cellulitis	210	95.74	1
1795	28443	2010	USA (B)	SC2A	Septic shock	103	96.9	4
1796	28444	2010	USA (B)	SC2A	Bacteremia	224	99.89	1
1797	28445	2010	USA (B)	SC2A	Cellulitis	252	98.59	19
1798	28446	2010	USA (B)	SC2A	Cellulitis	193	98.71	12
1799	28447	2010	USA (F)	SC2A	Cellulitis	118	97.26	144
1800	28450	2000	USA (A)	SC2A	Bacteremia	106	99.87	1
1801	28451	1999	USA (C)	SC2A	Cellulitis	96	97.87	4
1802	28453	2003	USA (B)	SC2A	Cellulitis	100	99.8	13
1803	28454	2010	USA (A)	SC2A	Cellulitis	135	99.85	1
1804	28457	2010	USA (D)	SC2A	Cellulitis	160	96.15	25
1805	28459	2006	USA (F)	SC2A	Bacteremia	114	99.88	1
1806	28460	2006	USA (F)	SC2A	Cellulitis	181	97.54	2
1807	28461	2006	USA (F)	SC2A	Cellulitis	139	99.86	1
1808	28462	2005	USA (F)	SC2A	Osteomyelitis	151	99.88	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1809	28463	2010	USA (B)	SC2A	Cellulitis	148	98.82	193
1810	28465	2006	USA (B)	SC2A	Abscess	409	99.88	1
1811	28466	2006	USA (B)	SC2A	Cellulitis	160	96.42	176
1812	28467	2006	USA (D)	SC2A	Osteomyelitis	205	96.29	1
1813	28469	2006	USA (G)	SC2A	Septic arthritis	116	96.66	9
1814	28471	2006	USA (F)	SC2A	Bacteremia	138	97.98	4
1815	28475	2006	USA (D)	SC2A	Endometritis	164	98.21	1
1816	28476	2006	USA (H)	SC2A	Cellulitis	179	95.69	166
1817	28479	2006	USA (F)	SC2A	Bacteremia	127	98.05	7
1818	28482	2006	USA (G)	SC2A	Necrotizing fasciitis	147	99.86	5
1819	28483	2006	USA (G)	SC2A	Pneumonia	144	96.87	9
1820	28484	2010	USA (B)	SC2A	Septic arthritis	160	99.88	1
1821	28485	2010	USA (B)	SC2A	Osteomyelitis	89	99.75	13
1822	28487	2006	USA (G)	SC2A	Pneumonia	117	99.87	1
1823	28492	2006	USA (A)	SC2A	Cellulitis	138	99.87	1
1824	28493	2006	USA (A)	SC2A	Bacteremia	134	99.88	1
1825	28494	2006	USA (A)	SC2A	Cellulitis	114	99.86	2
1826	28495	2006	USA (A)	SC2A	Necrotizing fasciitis	131	98.51	19
1827	28500	2006	USA (F)	SC2A	Bacteremia	113	99.85	1
1828	28501	2006	USA (J)	SC2A	Bacteremia	107	98.08	137
1829	28502	2006	USA (J)	SC2A	Cellulitis	126	98.1	7
1830	28503	2006	USA (D)	SC2A	Bacteremia	116	99.75	1
1831	28504	2006	USA (H)	SC2A	Bacteremia	160	99.4	21
1832	28507	2006	USA (B)	SC2A	Bacteremia	130	97.33	27
1833	28510	2010	USA (F)	SC2A	Abscess	161	99.86	2
1834	28512	2010	USA (A)	SC2A	Cellulitis	127	98.36	1
1835	28513	2010	USA (A)	SC2A	Bacteremia	109	99.14	9
1836	28514	2010	USA (I)	SC2A	Necrotizing fasciitis/STSS	149	99.87	2
1837	28515	2006	USA (D)	SC2A	Cellulitis	125	97.09	51
1838	28516	2006	USA (F)	SC2A	Bacteremia	96	99.08	47
1839	28518	2006	USA (F)	SC2A	Bacteremia	110	99.87	5
1840	28519	2006	USA (F)	SC2A	Endometritis	156	99.88	1
1841	28520	2006	USA (A)	SC2A	Bacteremia	143	99.87	1
1842	28521	2006	USA (F)	SC2A	Cellulitis	133	99.87	5

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1843	28522	2006	USA (F)	SC2A	Septic arthritis	121	99.87	5
1844	28523	2006	USA (F)	SC2A	Bacteremia	141	97.39	5
1845	28524	2010	USA (G)	SC2A	Septic arthritis	100	99.07	12
1846	28525	2007	USA (D)	SC2A	Cellulitis	96	99.9	1
1847	28528	2006	USA (I)	SC2A	Endometritis	175	99.87	1
1848	28529	2007	USA (B)	SC2A	Cellulitis	103	99.85	2
1849	28533	2006	USA (G)	SC2A	Cellulitis	131	99.81	28
1850	28534	2006	USA (G)	SC2A	Septic arthritis	99	99.84	1
1851	28536	2006	USA (B)	SC2A	Bacteremia	105	99.87	1
1852	28537	2007	USA (I)	SC2A	Cellulitis	147	99.85	8
1853	28540	2006	USA (F)	SC2A	Pneumonia	132	93.75	5
1854	28543	2006	USA (A)	SC2A	STSS	141	99.87	1
1855	28547	2006	USA (J)	SC2A	Cellulitis	126	96.3	70
1856	28549	2007	USA (H)	SC2A	Bacteremia	152	99.88	1
1857	28550	2007	USA (D)	SC2A	Septic arthritis	110	99.87	1
1858	28551	2007	USA (D)	SC2A	STSS	115	99.77	2
1859	28552	2007	USA (D)	SC2A	Cellulitis	124	96.95	51
1860	28553	2007	USA (F)	SC2A	Bacteremia	110	99.87	1
1861	28554	2007	USA (F)	SC2A	Bacteremia	119	99.08	47
1862	28555	2007	USA (F)	SC2A	Cellulitis	97	99.15	2
1863	28556	2007	USA (F)	SC2A	Septic arthritis	145	99.87	1
1864	28561	2007	USA (G)	SC2A	Cellulitis	101	97.38	12
1865	28562	2007	USA (J)	SC2A	Bacteremia	107	95.43	12
1866	28563	2007	USA (A)	SC2A	Cellulitis	105	99.84	1
1867	28564	2007	USA (F)	SC2A	Cellulitis	104	99.82	1
1868	28567	2007	USA (I)	SC2A	Cellulitis	127	99.86	1
1869	28568	2007	USA (B)	SC2A	Bacteremia	129	99.85	1
1870	28571	2007	USA (H)	SC2A	Pneumonia	104	99.84	1
1871	28572	2007	USA (I)	SC2A	Bacteremia	185	94.74	149
1872	28574	2007	USA (E)	SC2A	Bacteremia	123	99.86	1
1873	28576	2007	USA (E)	SC2A	Bacteremia	102	98.14	7
1874	28578	2007	USA (E)	SC2A	Cellulitis	91	99.84	5
1875	28579	2007	USA (J)	SC2A	Bacteremia	95	98.19	7
1876	28581	2007	USA (F)	SC2A	Bacteremia	113	99.84	1
1877	28584	2007	USA (B)	SC2A	Bacteremia	140	99.86	1
1878	28585	2007	USA (D)	SC2A	Septic arthritis	189	95.58	170

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1879	28586	2007	USA (E)	SC2A	Cellulitis	275	99.89	1
1880	28587	2007	USA (E)	SC2A	Bacteremia	117	98.23	7
1881	28588	2007	USA (F)	SC2A	Cellulitis	210	99.44	41
1882	28589	2007	USA (F)	SC2A	Bacteremia	123	99.88	5
1883	28591	2007	USA (F)	SC2A	Bacteremia	205	98.53	39
1884	28592	2007	USA (F)	SC2A	Pneumonia	133	97.17	62
1885	28593	2007	USA (F)	SC2A	Bacteremia	137	97.17	62
1886	28595	2007	USA (D)	SC2A	Cellulitis	182	98.14	11
1887	28596	2007	USA (A)	SC2A	Bacteremia	228	99.89	1
1888	28597	2007	USA (D)	SC2A	Cellulitis	456	99.84	19
1889	28602	2006	USA (D)	SC2A	Abscess	201	97.5	21
1890	28603	2007	USA (D)	SC2A	Abscess	238	96.7	1
1891	28604	2007	USA (F)	SC2A	Pneumonia	136	99.87	1
1892	28605	2007	USA (F)	SC2A	Bacteremia	179	96.28	1
1893	28606	2007	USA (F)	SC2A	Cellulitis	131	99.88	1
1894	28607	2007	USA (D)	SC2A	Bacteremia	129	96.2	64
1895	28609	2007	USA (D)	SC2A	Necrotizing fasciitis	227	96.68	11
1896	28612	2007	USA (F)	SC2A	Bacteremia	169	99.88	5
1897	28613	2008	USA (F)	SC2A	Septic arthritis	308	99.89	1
1898	28614	2008	USA (D)	SC2A	Osteomyelitis	146	99.82	19
1899	28617	2008	USA (D)	SC2A	Cellulitis	142	99.87	13
1900	28618	2008	USA (D)	SC2A	Abscess	161	99.87	1
1901	28619	2007	USA (B)	SC2A	Septic abortion	128	99.49	8
1902	28620	2007	USA (B)	SC2A	Pneumonia	224	99.88	1
1903	28626	2008	USA (D)	SC2A	Pneumonia	190	99.9	1
1904	28627	2007	USA (E)	SC2A	Bacteremia	172	98.23	7
1905	28630	2008	USA (E)	SC2A	Cellulitis	99	98.02	11
1906	28632	2008	USA (E)	SC2A	septic shock	154	99.83	2
1907	28633	2008	USA (D)	SC2A	Puerperal sepsis	145	99.88	1
1908	28634	2008	USA (F)	SC2A	Septic arthritis	333	99.89	1
1909	28635	2008	USA (F)	SC2A	Bacteremia	138	99.03	12
1910	28636	2008	USA (F)	SC2A	Necrotizing fasciitis	103	97.87	145
1911	28638	2008	USA (A)	SC2A	Pneumonia	141	98.51	19
1912	28641	2008	USA (J)	SC2A	Cellulitis	122	95.33	7
1913	28642	2008	USA (B)	SC2A	Cellulitis	158	99.82	2

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1914	28643	2008	USA (B)	SC2A	Cellulitis	157	99.87	1
1915	28644	2008	USA (B)	SC2A	Pneumonia	240	99.83	2
1916	28647	2008	USA (B)	SC2A	Bacteremia	505	99.85	1
1917	28649	2008	USA (D)	SC2A	Necrotizing fasciitis	265	97.52	1
1918	28651	2008	USA (I)	SC2A	Cellulitis	139	99.87	1
1919	28655	2008	USA (J)	SC2A	Bacteremia	132	99.88	1
1920	28658	2008	USA (I)	SC2A	Septic shock	145	99.88	1
1921	28659	2008	USA (D)	SC2A	Bacteremia	371	99.85	13
1922	28660	2008	USA (H)	SC2A	Abscess	508	97.74	11
1923	28662	2008	USA (E)	SC2A	Necrotizing fasciitis	164	99.88	1
1924	28664	2008	USA (F)	SC2A	Cellulitis	144	99.43	1
1925	28665	2008	USA (F)	SC2A	Cellulitis	120	99.86	5
1926	28669	2008	USA (E)	SC2A	Cellulitis	133	98.16	7
1927	28670	2008	USA (E)	SC2A	Bacteremia	180	99.88	5
1928	28671	2008	USA (E)	SC2A	Bacteremia	119	99.85	1
1929	28674	2008	USA (B)	SC2A	Bacteremia	238	99.87	1
1930	28675	2008	USA (B)	SC2A	Cellulitis	113	98.26	1
1931	28677	2008	USA (D)	SC2A	Cellulitis	118	99.86	1
1932	28678	2008	USA (H)	SC2A	Necrotizing fasciitis	133	99.86	1
1933	28679	2008	USA (I)	SC2A	Bacteremia	117	97.61	1
1934	28680	2008	USA (D)	SC2A	Cellulitis	125	98	11
1935	28681	2008	USA (B)	SC2A	Bacteremia	125	99.81	2
1936	28682	2008	USA (J)	SC2A	Cellulitis	160	98.02	11
1937	28686	2008	USA (G)	SC2A	Cellulitis	128	99.85	28
1938	28687	2008	USA (D)	SC2A	Cellulitis	186	99.87	13
1939	28689	2009	USA (D)	SC2A	Bacteremia	146	99.53	12
1940	28691	2009	USA (D)	SC2A	Septic shock	134	99.88	5
1941	28692	2008	USA (A)	SC2A	Cellulitis	189	99.13	12
1942	28694	2008	USA (F)	SC2A	Bacteremia	214	99.91	1
1943	28695	2008	USA (F)	SC2A	Endometritis	210	99.9	13
1944	28697	2008	USA (B)	SC2A	Cellulitis	228	98.56	19
1945	28698	2009	USA (D)	SC2A	Cellulitis	226	99.9	1
1946	28699	2009	USA (F)	SC2A	Bacteremia	143	99.88	28
1947	28700	2008	USA (E)	SC2A	Pneumonia	214	99.9	1
1948	28701	2009	USA (E)	SC2A	ovary	215	99.9	5

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1949	28703	2011	USA (F)	SC2A	Bacteremia	332	98.55	19
1950	28704	2011	USA (F)	SC2A	Cellulitis	259	98.37	5
1951	28705	2011	USA (F)	SC2A	Cellulitis	245	99.9	1
1952	28713	2011	USA (F)	SC2A	Bacteremia	264	98.08	5
1953	28715	2011	USA (A)	SC2A	Septic arthritis	308	96.52	102
1954	28717	2011	USA (F)	SC2A	Bacteremia	333	99.91	1
1955	28719	2012	USA (F)	SC2A	Cellulitis	355	99.93	1
1956	28720	2012	USA (F)	SC2A	Osteomyelitis	342	99.89	1
1957	28722	2011	USA (B)	SC2A	Bacteremia	96	99.89	5
1958	28726	2011	USA (E)	SC2A	Cellulitis	66	99.88	1
1959	28727	2011	USA (E)	SC2A	Cellulitis	194	99.9	1
1960	28728	2011	USA (J)	SC2A	Abscess	299	99.9	1
1961	28729	2012	USA (J)	SC2A	Osteomyelitis	160	99.82	13
1962	28731	2012	USA (F)	SC2A	Pneumonia	412	99.9	1
1963	28734	2012	USA (B)	SC2A	Bacteremia	267	99.9	1
1964	28736	2012	USA (H)	SC2A	Septic arthritis	380	96.64	1
1965	28740	2012	USA (D)	SC2A	Cellulitis	279	98.1	11
1966	28741	2012	USA (D)	SC2A	Puerperal sepsis	260	99.91	1
1967	28743	2012	USA (F)	SC2A	Bacteremia	274	99.9	5
1968	28744	2012	USA (F)	SC2A	Endometritis	289	97.93	1
1969	28745	2012	USA (F)	SC2A	Cellulitis	298	99.92	5
1970	28748	2012	USA (B)	SC2A	Bacteremia	113	95.38	165
1971	28751	2012	USA (B)	SC2A	Pneumonia	311	99.9	1
1972	28752	2012	USA (B)	SC2A	Osteomyelitis	234	99.9	1
1973	28753	2012	USA (F)	SC2A	Cellulitis	379	99.87	1
1974	28754	2012	USA (F)	SC2A	Bacteremia	309	99.13	9
1975	28755	2012	USA (F)	SC2A	Cellulitis	217	99.91	5
1976	28760	2012	USA (J)	SC2A	Bacteremia	246	99.84	84
1977	28761	2012	USA (F)	SC2A	Cellulitis	353	99.92	1
1978	28769	2012	USA (F)	SC2A	Abscess	187	99.91	5
1979	28771	2012	USA (B)	SC2A	Cellulitis	175	99.86	1
1980	28775	2012	USA (A)	SC2A	Bacteremia	231	98.31	23
1981	28776	2012	USA (A)	SC2A	Septic shock	404	97.39	5
1982	28777	2012	USA (I)	SC2A	Bacteremia	471	99.92	1
1983	28778	2012	USA (B)	SC2A	Bacteremia	253	99.88	1
1984	28781	2012	USA (G)	SC2A	Abscess	146	98.21	1

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
1985	28784	2012	USA (E)	SC2A	Necrotizing fasciitis	113	97.16	40
1986	28785	2012	USA (E)	SC2A	Necrotizing fasciitis	177	97.38	40
1987	28786	2012	USA (E)	SC2A	Necrotizing fasciitis	214	96.96	40
1988	28787	2012	USA (G)	SC2A	Cellulitis	164	98.27	1
1989	28788	2012	USA (I)	SC2A	Bacteremia	221	93.99	33
1990	28791	2000	USA (B)	SC2A	Bacteremia	253	99.9	1
1991	28793	2003	USA (A)	SC2A	Necrotizing fasciitis	285	99.9	1
1992	28795	2003	USA (A)	SC2A	Bacteremia	185	99.74	1
1993	28797	2003	USA (C)	SC2A	Bacteremia	180	97.78	16
1994	28798	2003	USA (C)	SC2A	Septic arthritis	195	99.89	1
1995	28801	2003	USA (H)	SC2A	Necrotizing fasciitis	172	99.88	1
1996	28802	2003	USA (H)	SC2A	Cellulitis	209	98.21	7
1997	28803	2003	USA (H)	SC2A	Pneumonia	249	99.44	21
1998	28805	1999	USA (C)	SC2A	peritonitis	222	99.85	111
1999	28807	2000	USA (C)	SC2A	Cellulitis	222	98.01	4
2000	28809	2003	USA (E)	SC2A	chorioamnionitis	154	99.9	1
2001	28810	2003	USA (D)	SC2A	Cellulitis	81	95.49	175
2002	28813	2003	USA (F)	SC2A	Bacteremia	120	99.88	1
2003	28815	2003	USA (A)	SC2A	Cellulitis	198	99.89	1
2004	28816	2003	USA (F)	SC2A	Pneumonia	174	99.89	1
2005	28819	2003	USA (F)	SC2A	Abscess	203	99.89	5
2006	28820	2003	USA (F)	SC2A	Bacteremia	125	99.88	100
2007	28826	2004	USA (H)	SC2A	Pneumonia	181	99.89	1
2008	28831	2000	USA (F)	SC2A	Bacteremia	175	98.77	129
2009	28832	2003	USA (A)	SC2A	Osteomyelitis	122	98.21	7
2010	28833	2004	USA (A)	SC2A	Endometritis	165	99.89	1
2011	28834	2004	USA (H)	SC2A	Cellulitis	138	98.22	7
2012	28836	2004	USA (F)	SC2A	Bacteremia	157	97.56	1
2013	28841	2003	USA (J)	SC2A	Bacteremia	214	99.89	1
2014	28842	2004	USA (E)	SC2A	Bacteremia	303	99.9	1
2015	28847	2000	USA (D)	SC2A	Endometritis	167	97.38	33
2016	28851	2000	USA (E)	SC2A	Bacteremia	162	98.1	1
2017	28852	2000	USA (B)	SC2A	Abscess	188	99.88	1
2018	28854	2009	USA (F)	SC2A	Pneumonia	308	99.1	47

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
2019	28855	2004	USA (F)	SC2A	Septic arthritis	226	99.9	1
2020	28857	2004	USA (F)	SC2A	Cellulitis	181	98.6	12
2021	28860	2003	USA (C)	SC2A	Necrotizing fasciitis/STSS	169	97.96	4
2022	28863	2004	USA (H)	SC2A	peritonitis	181	99.43	21
2023	28864	2004	USA (H)	SC2A	Cellulitis	189	99.89	1
2024	28865	2004	USA (D)	SC2A	peritonitis	171	99.9	1
2025	28866	2004	USA (D)	SC2A	peritonitis	228	99.89	1
2026	28867	2004	USA (I)	SC2A	Meningitis	262	97.69	13
2027	28872	2004	USA (E)	SC2A	Bacteremia	138	96.89	23
2028	28873	2004	USA (G)	SC2A	Bacteremia	136	99.88	5
2029	28874	2004	USA (A)	SC2A	Bacteremia	186	99.76	1
2030	28875	2004	USA (B)	SC2A	Cellulitis	170	97.38	4
2031	28877	2004	USA (F)	SC2A	Cellulitis	171	99.89	1
2032	28878	2004	USA (F)	SC2A	Bacteremia	167	99.88	5
2033	28881	2004	USA (F)	SC2A	Necrotizing fasciitis	218	99.89	1
2034	28883	2004	USA (B)	SC2A	Necrotizing fasciitis	169	99.88	2
2035	28885	2004	USA (B)	SC2A	Abscess	186	99.85	2
2036	28886	2004	USA (E)	SC2A	Abscess	172	99.88	1
2037	28887	2010	USA (D)	SC2A	Necrotizing fasciitis	149	98.04	1
2038	28888	2010	USA (J)	SC2A	Bacteremia	163	99.88	5
2039	28890	2010	USA (J)	SC2A	Pneumonia	203	99.88	13
2040	28892	2004	USA (A)	SC2A	Bacteremia	203	99.4	8
2041	28893	2004	USA (A)	SC2A	Bacteremia	223	99.88	1
2042	28895	2004	USA (H)	SC2A	Septic arthritis	164	97.4	11
2043	28896	2004	USA (A)	SC2A	Cellulitis	194	99.89	5
2044	28897	2004	USA (H)	SC2A	Cellulitis	156	99.87	1
2045	28898	2004	USA (H)	SC2A	Cellulitis	159	99.87	1
2046	28901	2004	USA (A)	SC2A	Cellulitis	210	99.72	1
2047	28902	2004	USA (A)	SC2A	Bacteremia	231	99.88	1
2048	28903	2004	USA (A)	SC2A	Bacteremia	287	98.07	1
2049	28905	2004	USA (J)	SC2A	Cellulitis	291	99.83	13
2050	28906	2004	USA (J)	SC2A	Bacteremia	162	99.95	1
2051	28910	2005	USA (B)	SC2A	Cellulitis	261	99.96	1
2052	28911	2005	USA (I)	SC2A	Bacteremia	207	99.91	13

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
2053	28912	2005	USA (F)	SC2A	Bacteremia	214	99.95	1
2054	28913	2005	USA (B)	SC2A	Septic arthritis	228	98.07	1
2055	28914	2005	USA (B)	SC2A	Endometritis	282	99.96	5
2056	28915	2005	USA (B)	SC2A	Bacteremia	215	99.08	99
2057	28917	2011	USA (D)	SC2A	Pneumonia	215	99.96	1
2058	28918	2010	USA (B)	SC2A	Bacteremia	131	99.95	1
2059	28919	2010	USA (B)	SC2A	Cellulitis	198	99.95	1
2060	28922	2011	USA (I)	SC2A	Cellulitis	348	95.28	169
2061	28923	2010	USA (I)	SC2A	Bacteremia	189	97.98	7
2062	28925	2011	USA (A)	SC2A	STSS	214	99.95	1
2063	28926	2011	USA (I)	SC2A	Cellulitis	203	99.96	1
2064	28928	2011	USA (I)	SC2A	Cellulitis	225	99.96	1
2065	28929	2011	USA (D)	SC2A	Cellulitis	172	99.96	1
2066	28931	2011	USA (J)	SC2A	Pneumonia	245	98.01	132
2067	28933	2003	USA (F)	SC2A	Osteomyelitis	189	97.57	1
2068	28938	2003	USA (F)	SC2A	Bacteremia	203	97.2	8
2069	28940	1999	USA (F)	SC2A	Bacteremia	363	99.93	1
2070	28942	1999	USA (F)	SC2A	Bacteremia	297	99.92	1
2071	28948	1999	USA (I)	SC2A	Pneumonia	206	99.96	1
2072	28951	1999	USA (E)	SC2A	Cellulitis	178	98.2	1
2073	28952	2002	USA (I)	SC2A	Pneumonia	155	99.95	1
2074	29216	2012	Finland	SC2A	Blood	166	99.88	1
2075	29225	2012	Finland	SC2A	Blood	211	99.88	1
2076	29231	2012	Finland	SC2A	Blood	143	99.87	1
2077	29270	2011	Finland	SC2A	Blood	636	99.91	1
2078	29271	2011	Finland	SC2A	Blood	379	99.89	1
2079	29431	2008	Finland	SC2A	Blood	129	99.84	5
2080	31886	2006	Norway	SC2A	Invasive	119	99.52	8
2081	31889	2006	Norway	SC2A	Invasive	223	99.53	8
2082	31900	2007	Norway	SC2A	Invasive	105	99.52	8
2083	31937	2012	Norway	SC2A	Invasive	128	99.95	5
2084	31972	2014	Norway	SC2A	Invasive	125	96.71	217
2085	8343	1995	Finland	SC2B	Blood	364	96.88	26
2086	8352	1995	Finland	SC2B	Blood	228	97.98	161
2087	8396	1998	Finland	SC2B	Blood	235	96.8	26
2088	10792	1998	Canada	SC2B	Invasive	275	98.75	55

Number	MGAS ¹ number	Year	Country (State ²)	Subclade	Infection ³ / Source	Estimated DOC ⁴	% Mapped Reads	MGE-50 ⁵
2089	11064	2000	Finland	SC2B	Blood	285	94.93	162
2090	11089	2001	Finland	SC2B	Blood	219	96.87	26
2091	11147	2002	Finland	SC2B	Blood	254	96.71	26
2092	11151	2002	Finland	SC2B	Blood	117	96.74	26
2093	28575	2007	USA (E)	SC2B	Bacteremia	111	96.98	72
2094	28628	2007	USA (E)	SC2B	Cellulitis	178	97.08	72
2095	31926	2011	Norway	SC2B	Invasive	129	93.8	26
2096	28146	1998	USA (I)	Distant outlier	Cellulitis	327	95.2	35
2097	28147	1998	USA (I)	Distant outlier	Pneumonia	262	94.26	35
2098	28205	1999	USA (D)	Distant outlier	Bacteremia	241	93.57	35
2099	29499	2006	Finland	Distant outlier	Blood	213	98.28	78
2100	30083	2015	Finland	Distant outlier	Blood	168	96.03	79
2101	32006	2015	Norway	Distant outlier	Invasive	137	94.22	55

¹MGAS number. Musser GAS strain number

²For the U.S. isolates, the states have been coded (A-J) at the request of the Centers for Disease Control.

³The clinical syndrome designations for the U.S. isolates were as defined by the CDC ABC surveillance study¹¹⁴⁻¹¹⁷ (<https://www.cdc.gov/abcs/index.html>)

⁴DOC, depth of coverage refers to the average number of times a nucleotide is covered by the sequenced reads³⁵

⁵MGE-50, genotypes derived studying 50 mobile genetic element genes, as defined in Supplementary Tables 3-6.

⁶MGAS6180 is the reference strain for which there is a closed genome

⁷TX, Texas

⁸Invasive is defined as cultured from a normally sterile site

⁹All Canada isolates were from Ontario

¹⁰All Finland isolates were isolated from blood

¹¹STSS, Streptococcal Toxic Shock Syndrome

Supplementary Table 7. List of 50 *emm28* strains analyzed in triplicate by RNA-seq

Strain number	MGAS number ¹	Year	Country (State ²)	Subclade
1	7888 ^a	1994	Canada ³	SC1A
2	7914	1995	Canada	SC1A
3	7941	1996	Canada	SC1A
4	8347	1995	Finland	SC1A
5	10786	1998	Canada	SC1A
6	10812	2000	Canada	SC1A
7	10826	2000	Canada	SC1A
8	28309	1998	USA (D)	SC1A
9	28323	2001	USA (F)	SC1A
10	28330 ^a	1998	USA (E)	SC1A
11	28360	2000	USA (H)	SC1A
12	28426	1999	USA (F)	SC1A
13	11052	2000	Finland	SC1B
14	11107	2001	Finland	SC1B
15	11108	2001	Finland	SC1B
16	11115	2002	Finland	SC1B
17	27784	2001	Iceland	SC1B
18	28278	2011	USA (H)	SC1B
19	28582	2007	USA (D)	SC1B
20	28650	2008	USA (I)	SC1B
21	28746	2012	USA (G)	SC1B
22	28869	2004	USA (J)	SC1B
23	28932	2002	USA (J)	SC1B
24	29064 ^b	2015	Finland	SC1B
25	29093	2014	Finland	SC1B
26	29159	2013	Finland	SC1B
27	29184	2013	Finland	SC1B
28	29198	2013	Finland	SC1B
29	29284	2011	Finland	SC1B
30	29326	2010	Finland	SC1B
31	29379	2009	Finland	SC1B
32	29409	2008	Finland	SC1B
33	29502	2006	Finland	SC1B
34	29553	2004	Finland	SC1B
35	29573	2003	Finland	SC1B
36	27961	2005	USA (F)	SC2A
37	28078	2010	USA (D)	SC2A
38	28191	1999	USA (C)	SC2A
39	28271	2011	USA (F)	SC2A

Strain number	MGAS number ¹	Year	Country (State ²)	Subclade
40	28386	2002	USA (F)	SC2A
41	28392	2003	USA (D)	SC2A
42	28533	2006	USA (G)	SC2A
43	28597	2007	USA (D)	SC2A
44	28647	2008	USA (B)	SC2A
45	28669	2008	USA (E)	SC2A
46	28686 ^b	2008	USA (G)	SC2A
47	28699	2009	USA (F)	SC2A
48	28798	2003	USA (C)	SC2A
49	28836	2004	USA (F)	SC2A
50	29216	2012	Finland	SC2A

¹MGAS number. Musser GAS strain number

²For the U.S. isolates, the states have been coded (A-J) at the request of the Centers for Disease Control.

³All Canada isolates were from Ontario

^aContains naturally occurring amino acid replacement (I479T) in the Mga regulator

^bContains indel in covS regulator. MGAS29064, MGAS28686

Supplementary Table 9. Core chromosomal SNPs separating SC1B from SC1A strains

	SNP position in MGAS6180	MGAS6180 Spy number	Gene	Putative role	Amino acid substitution	Nature of substitution
1	56457	M28_Spy0038	--	acetyltransferase		Synonymous
2	199534	M28_Spy0184	<i>rivR</i>		R279Q	Nonsynonymous
3	199537	M28_Spy0184	<i>rivR</i>		Q278R	Nonsynonymous
4	288957	M28_Spy0267	--	serine/threonine transporter SstT	G366S	Nonsynonymous
5	335026	M28_Spy0315	--	polysaccharide biosynthesis protein		Synonymous
6	1540310	M28_Spy1538	<i>corA</i>			Synonymous
7	1591459	M28_Spy1594	--	dihydroxyacetone kinase	N486D	Nonsynonymous
8	87404	M28_Spy0075	<i>adcR</i>			Synonymous
9	1710553	M28_Spy1701	<i>enn</i>		L34V	Nonsynonymous
10	1728580	M28_Spy1716	<i>sof</i>		S418L	Nonsynonymous
11	1732831	M28_Spy1721	<i>speB</i>		A283V	Nonsynonymous

Supplementary Table 10. List of *emm28* strains analyzed as singletons by RNAtag-seq

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
1	7865	1991	Canada ³	SC1A
2	7867	1991	Canada	SC1A
3	7869	1991	Canada	SC1A
4	7872	1992	Canada	SC1A
5	7878	1993	Canada	SC1A
6	7886	1994	Canada	SC1A
7	7890	1994	Canada	SC1A
8	7891	1994	Canada	SC1A
9	7893	1995	Canada	SC1A
10	7906	1995	Canada	SC1A
11	7912	1995	Canada	SC1A
12	7922	1996	Canada	SC1A
13	7927	1996	Canada	SC1A
14	7932	1996	Canada	SC1A
15	7935	1996	Canada	SC1A
16	7946	1996	Canada	SC1A
17	7956	1996	Canada	SC1A
18	7959	1996	Canada	SC1A
19	7960	1996	Canada	SC1A
20	7972	1997	Canada	SC1A
21	7973	1997	Canada	SC1A
22	7976	1997	Canada	SC1A
23	7987	1997	Canada	SC1A
24	7994	1997	Canada	SC1A
25	7995	1997	Canada	SC1A
26	8007	1999	Canada	SC1A
27	8009	1999	Canada	SC1A
28	8015	1999	Canada	SC1A
29	8345	1995	Finland	SC1A
30	8350	1995	Finland	SC1A
31	8358	1996	Finland	SC1A
32	8374	1996	Finland	SC1A
33	8375	1996	Finland	SC1A
34	8417	1998	Finland	SC1A
35	8447	1999	Finland	SC1A
36	10757	1998	Canada	SC1A

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
37	10761	1998	Canada	SC1A
38	10764	1998	Canada	SC1A
39	10771	1998	Canada	SC1A
40	10799	1999	Canada	SC1A
41	10802	1992	Canada	SC1A
42	10807	2000	Canada	SC1A
43	10815	2000	Canada	SC1A
44	10817	2000	Canada	SC1A
45	10819	2000	Canada	SC1A
46	10820	2000	Canada	SC1A
47	10824	2000	Canada	SC1A
48	10827	2000	Canada	SC1A
49	11103	2001	Finland	SC1A
50	12226	2001	Canada	SC1A
51	12231	2001	Canada	SC1A
52	12247	2001	Canada	SC1A
53	12250	2002	Canada	SC1A
54	27946	1996	USA (A)	SC1A
55	27951	1996	USA (A)	SC1A
56	27962	2005	USA (D)	SC1A
57	27983	2005	USA (F)	SC1A
58	28035	2006	USA (F)	SC1A
59	28041	2009	USA (J)	SC1A
60	28118	2002	USA (B)	SC1A
61	28138	2001	USA (E)	SC1A
62	28164	1998	USA (F)	SC1A
63	28185	1999	USA (H)	SC1A
64	28201	1999	USA (F)	SC1A
65	28204	1999	USA (I)	SC1A
66	28217	1999	USA (C)	SC1A
67	28225	2002	USA (F)	SC1A
68	28254	2010	USA (F)	SC1A
69	28287	2002	USA (E)	SC1A
70	28315	1998	USA (E)	SC1A
71	28317	2001	USA (D)	SC1A
72	28334	2000	USA (F)	SC1A
73	28338	2000	USA (F)	SC1A
74	28367	2003	USA (J)	SC1A
75	28374	1998	USA (D)	SC1A

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
76	28397	1998	USA (C)	SC1A
77	28400	1998	USA (D)	SC1A
78	28403	1997	USA (F)	SC1A
79	28411	1997	USA (I)	SC1A
80	28415	2003	USA (C)	SC1A
81	28425	1999	USA (I)	SC1A
82	28430	2003	USA (C)	SC1A
83	28449	2000	USA (D)	SC1A
84	28477	2006	USA (B)	SC1A
85	28640	2008	USA (G)	SC1A
86	28648	2008	USA (A)	SC1A
87	28708	2011	USA (G)	SC1A
88	28739	2012	USA (H)	SC1A
89	28804	1999	USA (H)	SC1A
90	28840	2004	USA (C)	SC1A
91	28845	2000	USA (C)	SC1A
92	28879	2004	USA (F)	SC1A
93	28900	2004	USA (H)	SC1A
94	28907	2004	USA (E)	SC1A
95	28949	1999	USA (E)	SC1A
96	29393	2008	Finland	SC1A
97	29538	2004	Finland	SC1A
98	29608	2003	Finland	SC1A
99	7921	1996	Canada	SC1B
100	7982	1997	Canada	SC1B
101	8365	1996	Finland	SC1B
102	11087	2001	Finland	SC1B
103	11098	2001	Finland	SC1B
104	11100	2001	Finland	SC1B
105	11113	2002	Finland	SC1B
106	11121	2002	Finland	SC1B
107	11123	2002	Finland	SC1B
108	11128	2002	Finland	SC1B
109	11138	2002	Finland	SC1B
110	11140	2002	Finland	SC1B
111	11149	2002	Finland	SC1B
112	12248	2001	Canada	SC1B
113	27754	1997	Iceland	SC1B
114	27767	1999	Iceland	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
115	27787	2001	Iceland	SC1B
116	27813	2004	Iceland	SC1B
117	27846	2008	Iceland	SC1B
118	27848	2008	Iceland	SC1B
119	27865	2010	Iceland	SC1B
120	27895	2012	Iceland	SC1B
121	27956	2004	USA (J)	SC1B
122	27967	2005	USA (J)	SC1B
123	27970	2005	USA (B)	SC1B
124	27990	2005	USA (F)	SC1B
125	28032	2005	USA (E)	SC1B
126	28046	2009	USA (E)	SC1B
127	28048	2009	USA (J)	SC1B
128	28049	2009	USA (J)	SC1B
129	28059	2009	USA (D)	SC1B
130	28081	2009	USA (E)	SC1B
131	28106	2009	USA (D)	SC1B
132	28108	2009	USA (B)	SC1B
133	28142	2010	USA (E)	SC1B
134	28208	2010	USA (F)	SC1B
135	28241	2002	USA (E)	SC1B
136	28268	2011	USA (F)	SC1B
137	28273	2011	USA (E)	SC1B
138	28295	2011	USA (F)	SC1B
139	28455	2010	USA (I)	SC1B
140	28473	2006	USA (F)	SC1B
141	28480	2006	USA (F)	SC1B
142	28481	2006	USA (F)	SC1B
143	28505	2006	USA (D)	SC1B
144	28508	2010	USA (F)	SC1B
145	28530	2006	USA (E)	SC1B
146	28544	2006	USA (J)	SC1B
147	28557	2007	USA (F)	SC1B
148	28566	2007	USA (F)	SC1B
149	28622	2007	USA (J)	SC1B
150	28645	2007	USA (B)	SC1B
151	28653	2008	USA (A)	SC1B
152	28654	2008	USA (F)	SC1B
153	28657	2008	USA (G)	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
154	28661	2008	USA (H)	SC1B
155	28673	2008	USA (A)	SC1B
156	28688	2009	USA (D)	SC1B
157	28707	2011	USA (J)	SC1B
158	28710	2011	USA (H)	SC1B
159	28716	2011	USA (A)	SC1B
160	28718	2011	USA (F)	SC1B
161	28724	2012	USA (G)	SC1B
162	28737	2012	USA (H)	SC1B
163	28747	2012	USA (G)	SC1B
164	28764	2012	USA (B)	SC1B
165	28766	2012	USA (E)	SC1B
166	28772	2012	USA (D)	SC1B
167	28811	2003	USA (F)	SC1B
168	28822	2003	USA (B)	SC1B
169	28825	2004	USA (H)	SC1B
170	28880	2004	USA (F)	SC1B
171	28904	2004	USA (A)	SC1B
172	28916	2010	USA (J)	SC1B
173	28921	2011	USA (D)	SC1B
174	28924	2011	USA (A)	SC1B
175	28935	2003	USA (F)	SC1B
176	29041	2015	Finland	SC1B
177	29043	2015	Finland	SC1B
178	29045	2015	Finland	SC1B
179	29050	2015	Finland	SC1B
180	29051	2015	Finland	SC1B
181	29054	2015	Finland	SC1B
182	29061	2015	Finland	SC1B
183	29068	2015	Finland	SC1B
184	29069	2015	Finland	SC1B
185	29073	2015	Finland	SC1B
186	29074	2015	Finland	SC1B
187	29075	2015	Finland	SC1B
188	29076	2015	Finland	SC1B
189	29080	2015	Finland	SC1B
190	29086	2014	Finland	SC1B
191	29088	2014	Finland	SC1B
192	29094	2014	Finland	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
193	29095	2014	Finland	SC1B
194	29105	2014	Finland	SC1B
195	29108	2014	Finland	SC1B
196	29109	2014	Finland	SC1B
197	29117	2014	Finland	SC1B
198	29124	2014	Finland	SC1B
199	29125	2014	Finland	SC1B
200	29127	2014	Finland	SC1B
201	29133	2014	Finland	SC1B
202	29138	2014	Finland	SC1B
203	29140	2014	Finland	SC1B
204	29143	2014	Finland	SC1B
205	29147	2013	Finland	SC1B
206	29161	2013	Finland	SC1B
207	29162	2013	Finland	SC1B
208	29164	2013	Finland	SC1B
209	29170	2013	Finland	SC1B
210	29180	2013	Finland	SC1B
211	29181	2013	Finland	SC1B
212	29186	2013	Finland	SC1B
213	29188	2013	Finland	SC1B
214	29201	2013	Finland	SC1B
215	29209	2012	Finland	SC1B
216	29212	2012	Finland	SC1B
217	29214	2012	Finland	SC1B
218	29221	2012	Finland	SC1B
219	29230	2012	Finland	SC1B
220	29233	2012	Finland	SC1B
221	29238	2012	Finland	SC1B
222	29240	2012	Finland	SC1B
223	29243	2012	Finland	SC1B
224	29253	2012	Finland	SC1B
225	29254	2012	Finland	SC1B
226	29258	2012	Finland	SC1B
227	29263	2012	Finland	SC1B
228	29268	2011	Finland	SC1B
229	29276	2011	Finland	SC1B
230	29277	2011	Finland	SC1B
231	29281	2011	Finland	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
232	29286	2011	Finland	SC1B
233	29292	2011	Finland	SC1B
234	29293	2011	Finland	SC1B
235	29299	2011	Finland	SC1B
236	29300	2010	Finland	SC1B
237	29305	2010	Finland	SC1B
238	29310	2010	Finland	SC1B
239	29314	2010	Finland	SC1B
240	29321	2010	Finland	SC1B
241	29323	2010	Finland	SC1B
242	29324	2010	Finland	SC1B
243	29325	2010	Finland	SC1B
244	29330	2010	Finland	SC1B
245	29331	2010	Finland	SC1B
246	29336	2010	Finland	SC1B
247	29338	2009	Finland	SC1B
248	29342	2009	Finland	SC1B
249	29347	2009	Finland	SC1B
250	29351	2009	Finland	SC1B
251	29357	2009	Finland	SC1B
252	29360	2009	Finland	SC1B
253	29371	2009	Finland	SC1B
254	29372	2009	Finland	SC1B
255	29377	2009	Finland	SC1B
256	29381	2009	Finland	SC1B
257	29382	2009	Finland	SC1B
258	29384	2009	Finland	SC1B
259	29387	2009	Finland	SC1B
260	29394	2008	Finland	SC1B
261	29402	2008	Finland	SC1B
262	29404	2008	Finland	SC1B
263	29406	2008	Finland	SC1B
264	29412	2008	Finland	SC1B
265	29416	2008	Finland	SC1B
266	29423	2008	Finland	SC1B
267	29426	2008	Finland	SC1B
268	29429	2008	Finland	SC1B
269	29444	2011	Finland	SC1B
270	29447	2009	Finland	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
271	29464	2007	Finland	SC1B
272	29474	2006	Finland	SC1B
273	29476	2006	Finland	SC1B
274	29485	2006	Finland	SC1B
275	29486	2006	Finland	SC1B
276	29488	2006	Finland	SC1B
277	29491	2006	Finland	SC1B
278	29494	2006	Finland	SC1B
279	29501	2006	Finland	SC1B
280	29504	2005	Finland	SC1B
281	29507	2005	Finland	SC1B
282	29508	2005	Finland	SC1B
283	29510	2005	Finland	SC1B
284	29511	2005	Finland	SC1B
285	29517	2005	Finland	SC1B
286	29522	2005	Finland	SC1B
287	29525	2004	Finland	SC1B
288	29528	2004	Finland	SC1B
289	29534	2004	Finland	SC1B
290	29536	2004	Finland	SC1B
291	29537	2004	Finland	SC1B
292	29542	2004	Finland	SC1B
293	29546	2004	Finland	SC1B
294	29548	2004	Finland	SC1B
295	29556	2004	Finland	SC1B
296	29559	2004	Finland	SC1B
297	29564	2004	Finland	SC1B
298	29569	2004	Finland	SC1B
299	29570	2004	Finland	SC1B
300	29582	2003	Finland	SC1B
301	29583	2003	Finland	SC1B
302	29587	2003	Finland	SC1B
303	29588	2003	Finland	SC1B
304	29594	2003	Finland	SC1B
305	29599	2003	Finland	SC1B
306	29611	2003	Finland	SC1B
307	29613	2003	Finland	SC1B
308	29617	2003	Finland	SC1B
309	29620	2003	Finland	SC1B

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
310	29633	2002	Finland	SC1B
311	7918	1995	Canada	SC2A
312	7980	1997	Canada	SC2A
313	8012	1999	Canada	SC2A
314	10793	1999	Canada	SC2A
315	12254	2002	Canada	SC2A
316	27937	1995	USA (A)	SC2A
317	27979	2005	USA (B)	SC2A
318	27981	2005	USA (I)	SC2A
319	27993	2005	USA (F)	SC2A
320	28004	2005	USA (D)	SC2A
321	28007	2005	USA (E)	SC2A
322	28008	2006	USA (H)	SC2A
323	28020	2005	USA (G)	SC2A
324	28022	2005	USA (I)	SC2A
325	28029	2006	USA (B)	SC2A
326	28031	2004	USA (E)	SC2A
327	28047	2009	USA (D)	SC2A
328	28058	2009	USA (D)	SC2A
329	28065	2009	USA (J)	SC2A
330	28074	2009	USA (G)	SC2A
331	28082	2009	USA (E)	SC2A
332	28085	2009	USA (G)	SC2A
333	28086	2010	USA (H)	SC2A
334	28107	2009	USA (F)	SC2A
335	28115	2001	USA (A)	SC2A
336	28117	2001	USA (A)	SC2A
337	28121	2002	USA (I)	SC2A
338	28127	2002	USA (H)	SC2A
339	28131	2002	USA (B)	SC2A
340	28172	2010	USA (F)	SC2A
341	28207	2010	USA (D)	SC2A
342	28209	2010	USA (F)	SC2A
343	28230	2002	USA (B)	SC2A
344	28232	1998	USA (A)	SC2A
345	28248	2010	USA (A)	SC2A
346	28249	2010	USA (H)	SC2A
347	28255	2010	USA (F)	SC2A
348	28259	2010	USA (A)	SC2A

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
349	28261	2009	USA (B)	SC2A
350	28265	2011	USA (F)	SC2A
351	28296	2002	USA (F)	SC2A
352	28305	2011	USA (B)	SC2A
353	28307	1998	USA (A)	SC2A
354	28321	2001	USA (F)	SC2A
355	28331	2000	USA (D)	SC2A
356	28341	2003	USA (A)	SC2A
357	28347	2000	USA (D)	SC2A
358	28356	2003	USA (F)	SC2A
359	28362	1999	USA (D)	SC2A
360	28363	2003	USA (H)	SC2A
361	28402	2003	USA (E)	SC2A
362	28418	2003	USA (H)	SC2A
363	28424	1999	USA (I)	SC2A
364	28429	2003	USA (C)	SC2A
365	28440	2003	USA (F)	SC2A
366	28441	2003	USA (F)	SC2A
367	28443	2010	USA (B)	SC2A
368	28446	2010	USA (B)	SC2A
369	28447	2010	USA (F)	SC2A
370	28461	2006	USA (F)	SC2A
371	28462	2005	USA (F)	SC2A
372	28463	2010	USA (B)	SC2A
373	28467	2006	USA (D)	SC2A
374	28471	2006	USA (F)	SC2A
375	28479	2006	USA (F)	SC2A
376	28482	2006	USA (G)	SC2A
377	28484	2010	USA (B)	SC2A
378	28501	2006	USA (J)	SC2A
379	28504	2006	USA (H)	SC2A
380	28510	2010	USA (F)	SC2A
381	28512	2010	USA (A)	SC2A
382	28513	2010	USA (A)	SC2A
383	28523	2006	USA (F)	SC2A
384	28536	2006	USA (B)	SC2A
385	28543	2006	USA (A)	SC2A
386	28549	2007	USA (H)	SC2A
387	28550	2007	USA (D)	SC2A

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
388	28553	2007	USA (F)	SC2A
389	28562	2007	USA (J)	SC2A
390	28567	2007	USA (I)	SC2A
391	28576	2007	USA (E)	SC2A
392	28585	2007	USA (D)	SC2A
393	28589	2007	USA (F)	SC2A
394	28596	2007	USA (A)	SC2A
395	28609	2007	USA (D)	SC2A
396	28612	2007	USA (F)	SC2A
397	28626	2008	USA (D)	SC2A
398	28630	2008	USA (E)	SC2A
399	28633	2008	USA (D)	SC2A
400	28662	2008	USA (E)	SC2A
401	28670	2008	USA (E)	SC2A
402	28687	2008	USA (D)	SC2A
403	28715	2011	USA (A)	SC2A
404	28722	2011	USA (B)	SC2A
405	28727	2011	USA (E)	SC2A
406	28728	2011	USA (J)	SC2A
407	28731	2012	USA (F)	SC2A
408	28744	2012	USA (F)	SC2A
409	28748	2012	USA (B)	SC2A
410	28751	2012	USA (B)	SC2A
411	28752	2012	USA (B)	SC2A
412	28760	2012	USA (J)	SC2A
413	28776	2012	USA (A)	SC2A
414	28781	2012	USA (G)	SC2A
415	28784	2012	USA (E)	SC2A
416	28785	2012	USA (E)	SC2A
417	28787	2012	USA (G)	SC2A
418	28788	2012	USA (I)	SC2A
419	28801	2003	USA (H)	SC2A
420	28805	1999	USA (C)	SC2A
421	28809	2003	USA (E)	SC2A
422	28826	2004	USA (H)	SC2A
423	28831	2000	USA (F)	SC2A
424	28842	2004	USA (E)	SC2A
425	28851	2000	USA (E)	SC2A
426	28864	2004	USA (H)	SC2A

Strain number	MGAS¹ number	Year	Country (State²)	Subclade
427	28872	2004	USA (E)	SC2A
428	28883	2004	USA (B)	SC2A
429	28886	2004	USA (E)	SC2A
430	28897	2004	USA (H)	SC2A
431	28898	2004	USA (H)	SC2A
432	28906	2004	USA (J)	SC2A
433	28925	2011	USA (A)	SC2A
434	28928	2011	USA (I)	SC2A
435	28942	1999	USA (F)	SC2A
436	28948	1999	USA (I)	SC2A
437	29431	2008	Finland	SC2A
438	8396	1998	Finland	SC2B
439	10792	1998	Canada	SC2B
440	11147	2002	Finland	SC2B
441	11151	2002	Finland	SC2B
442	28575	2007	USA (E)	SC2B

¹MGAS number. Musser GAS strain number.

²For the U.S. isolates, the states have been coded (A-J) at the request of the Centers for Disease Control.

³All Canada isolates were from Ontario.

Supplementary Table 13. List of group I and II *ropB* mutant strains

	MGAS	Group	Subclade	RopB mutation	Predicted location	SpeB activity phenotype	Predicted nature of mutation
1	12248	I	SC1B	R129W	Solvent exposed	WT	Non-function altering ¹
2	28020	I	SC2A	C85Y	Solvent exposed	WT	Non-function altering ¹
3	28074	I	SC2A	N38D	N-terminal	WT	Non-function altering ³
4	28447	I	SC2A	I187S	Tpr ^a	Negative	Function altering ¹
5	28826	I	SC2A	V7A	N-terminal	WT	Non-function altering ³
6	28924	I	SC1B	T263M	Solvent exposed	WT	Non-function altering ¹
7	29393	I	SC1A	A206V	Tpr	Negative	Function altering ¹
8	29447	I	SC1B	F110L	Solvent exposed	WT	Non-function altering ¹
9	29476	I	SC1B	I16V	N-terminal	WT	Non-function altering ³
10	7865	II	SC1A	$\Delta ropB^b$		Negative	Function altering ²
11	12247	II	SC1A	G23S	N-terminal	Negative	Function altering ³
12	12254	II	SC2A	I139T	Tpr	WT	Function altering ¹
13	27979	II	SC2A	C22R	N-terminal	Negative	Function altering ³
14	28007	II	SC2A	N151D	Tpr, Peptide binding pocket	Negative	Function altering ¹
15	28273	II	SC1B	F256S	Tpr	Negative	Function altering ¹
16	28446	II	SC2A	C228G	Peptide binding pocket	WT	Function altering ¹
17	28480	II	SC1B	E72*	Tpr	Negative	Function altering ²
18	28567	II	SC2A	L50S	N-terminal	Negative	Function altering ³
19	28648	II	SC1A	E140K	Solvent exposed	Negative	Non-function altering ¹
20	28708	II	SC1A	E59K	Possibly Tpr	Negative	Function altering ¹
21	28739	II	SC1A	$\Delta ropB^c$		Negative	Function altering ²
22	28845	II	SC1A	M189I	Tpr, Peptide binding pocket	Negative	Function altering ¹
23	28886	II	SC2A	V169I	Tpr	Negative	Function altering ¹
24	29127	II	SC1B	I10V	N-terminal	Negative	Function altering ³
25	29351	II	SC1B	L259P	Dimerization	Negative	Function altering ¹
26	29402	II	SC1B	Q201*	Solvent exposed	Negative	Function altering ²
27	29426	II	SC1B	K71E	Solvent exposed	Negative	Non-function altering ¹
28	29569	II	SC1B	T141N	Solvent exposed	Negative	Non-function altering ¹
29	29570	II	SC1B	F231L	Tpr	Negative	Function altering ¹

^a Tpr: Tetratricopeptide repeat

^b 5.47 Kb deletion (start: 1732853 - stop: 1738323). Deletion in this region extends into *speB*

^c 9.68 Kb deletion (start: 1733850 - stop: 1743530)

* Nonsense mutation

¹ Nature of substitution predicted by RopB (C-terminal domain) crystal structure¹²⁸ (see **Supplementary Note**)

² Prediction based on nature of genetic mutations in *ropB* gene – nonsense mutations and deletions

³ Prediction based on SpeB activity phenotype assessed via casein hydrolysis assay

1. 22.22% (2 out of 9) Group I strains have predicted function altering amino acid substitutions based on crystal structure

2. Group II function altering mutations: (a) Nonsense mutations (n=2) and gene deletion (n=2). (b) Predicted function altering amino acid substitutions based on crystal structure (n=9).

Among the Group II strains with single nucleotide substitutions in *ropB* (n=16), 9 out of 16 (56.25%) have predicted function altering amino acid substitutions based on the crystal structure

Increased proportion of predicted function altering amino acid substitutions in Group II compared to Group I was found to be statistically significant (Test of proportions-one-tailed, $P=0.04$)

Supplementary Table 17. Oligonucleotides used for RNAtag-seq analysis

a) RNA barcoded oligoribonucleotides

Number⁽¹⁾	Ribonucleotide barcode	RNA sequence⁽²⁾	6 nucleotide barcode
1	UUGCUU	5'-AUUGCUUAGAUCGGAAGAGCGUCGUGUAG-3'	AAGCAA
4	GGCUGU	5'-AGGCUGUAGAUCGGAAGAGCGUCGUGUAG-3'	ACAGCC
8	UGGUCU	5'-AUGGUCUAGAUCGGAAGAGCGUCGUGUAG-3'	AGACCA
9	GUUUUAU	5'-AGUUUAUAGAUCGGAAGAGCGUCGUGUAG-3'	ATAAAC
13	GAAGAU	5'-AGAAGAUAGAUCGGAAGAGCGUCGUGUAG-3'	ATCTTC
16	CAGUUG	5'-ACAGUUGAGAUCGGAAGAGCGUCGUGUAG-3'	CAACTG
20	UCAGUG	5'-AUCAGUGAGAUCGGAAGAGCGUCGUGUAG-3'	CACTGA
24	AGUCGG	5'-AAGUCGGAGAUCGGAAGAGCGUCGUGUAG-3'	CCGACT
27	CUAAGG	5'-ACUAAGGAGAUCGGAAGAGCGUCGUGUAG-3'	CCTTAG
29	GGGAUC	5'-AGGGAUCAGAUCGGAAGAGCGUCGUGUAG-3'	GATCCC
31	AUGGGC	5'-AAUGGGCAGAUCGGAAGAGCGUCGUGUAG-3'	GCCCAT
37	GCAAAC	5'-AGCAAACAGAUCGGAAGAGCGUCGUGUAG-3'	GTTTGC
38	UGAUUA	5'-AGAUGGAAGAUCGGAAGAGCGUCGUGUAG-3'	TAATCA
46	GAUGGA	5'-AGAUGGAAGAUCGGAAGAGCGUCGUGUAG-3'	TCCATC
49	AUGUCA	5'-AUGUCAAGAUCGGAAGAGCGUCGUGUAG-3'	TGACAT
54	GCGGAA	5'-AGCGGAAAGAUCGGAAGAGCGUCGUGUAG-3'	TTCCGC

⁽¹⁾ The oligoribonucleotides, with their corresponding numbers, were chosen from a previously described validated list of RNAtag-seq adapters⁵²

⁽²⁾ Sequence in red corresponds to the ribonucleotide barcode

b) P7 oligonucleotides

Name	Barcode	P7 Enrichment Primer Sequence (5' --> 3') with barcode ⁽¹⁾
P7_B1	TCGTGTGC	CAAGCAGAAGACGGCATACGAGATTCGTGTGCGTGACTGGAGTTCAGACGTGTGC TCTTCCGATCT
P7_B5	ATCCGACA	CAAGCAGAAGACGGCATACGAGATATCCGACAGTGACTGGAGTTCAGACGTGTGC TCTTCCGATCT
P7_B8	GCTAAGTA	CAAGCAGAAGACGGCATACGAGATGCTAAGTAGTGACTGGAGTTCAGACGTGTGC TCTTCCGATCT
P7_B11	CAAGGTTG	CAAGCAGAAGACGGCATACGAGATCAAGGTTGGTGACTGGAGTTCAGACGTGTGC TCTTCCGATCT

⁽¹⁾ Sequence in red corresponds to the nucleotide barcode

Supplementary Table 18. Oligonucleotides used for qRT-PCR analysis and isogenic mutant generation

Oligonucleotide	DNA sequence
Spy1336FWD	5'-AAGTATTCGCCAGAGGCTAAG-3'
Spy1336REV	5'-TGTTGAGGTGTCTGGTTTATGA-3'
Spy1336probe	[6FAM]TAGGACTGTTGAACAACACGCGGA[TAM] ⁽¹⁾
Spy1337FWD	5'-CGTACCTATAATCAGTGGAGATGAA-3'
Spy1337REV	5'-AACGATCTCGTGCTCGATAAG-3'
Spy1337probe	[6FAM]TCGTCTCTCACAGGCTACCATCCA[TAM]
<i>tufA</i> FWD	5'-GACACGCGGACTACGTTAAA-3'
<i>tufA</i> REV	5'-CACCAACCTGACGTGAAAGA-3'
<i>tufA</i> probe	[6FAM]CGCTCAAATGGACGGAGCTATCCTT[TAM]
<i>nga</i> MEW123FWD	5'-GAATTAGGCGACACCTACACTAA-3'
<i>nga</i> MEW123REV	5'-GTGACCTCTGACAAGGCTAAA-3'
<i>nga</i> MEW123probe	[6FAM]AGGTAACAGAGGTCCATCAGGGTCA[TAM]
HPN-1	5'-GTCCGGATCCCGGAAGAACATTGATGGTAACTGTC-3'
HPN-2	5'-GTCCGGATCCTTCGATTACTATATTGTCTTAAGCT-3'
HPN-seq	5'-ACTAAGACCAATTAGTACAGAAGCT-3'
<i>nga</i> -1	5'-GTCCGGATCCGCAGATGCTGCTAAAGGCAAGACG-3'
<i>nga</i> -2	5'TTATACCATCAGACCTTTGAGAGCCTATAGTTCTGCGATTTGGTAAAG-3'
<i>nga</i> -3	5'-CTTTACCAAATCGCAGAACTATAGGCTCTCAAAGGTCTGATGGTATAA-3'
<i>nga</i> -4	5'-CAAAGCAATAGCAACACTTGTCTTCGCGACAATATGAGCTAATGTTAC-3'
<i>nga</i> -5	5'-GTAACATTAGCTCATATTGTGCGAAGACAAGTGTTGCTATTGCTTTG-3'
<i>nga</i> -6	5'-GTCCGGATCCCCTGACCACGTTTGGCAACCAGGA-3'

⁽¹⁾ 6FAM, 6-carboxyfluorescein reporter dye
TAM, TAMRA quencher

Supplementary Table 19. List of 24 *emm28* strains sequenced using MinION

MGAS number^{1,2}	Year	Country (State³)	Subclade	MGE-50⁴
7888	1994	Canada ⁵	SC1A	93
7914	1995	Canada	SC1A	1
8347	1995	Finland	SC1A	36
10786	1998	Canada	SC1A	157
10826	2000	Canada	SC1A	1
11052	2000	Finland	SC1B	3
11108	2001	Finland	SC1B	1
11115	2002	Finland	SC1B	1
28078	2010	USA (D)	SC2A	74
28191	1999	USA (C)	SC2A	7
28271	2011	USA (F)	SC2A	19
28278	2011	USA (H)	SC1B	10
28330	1998	USA (E)	SC1A	38
28360	2000	USA (H)	SC1A	10
28386	2002	USA (F)	SC2A	5
28533	2006	USA (G)	SC2A	28
28650	2008	USA (I)	SC1B	1
28669	2008	USA (E)	SC2A	7
28686	2008	USA (G)	SC2A	28
28746	2012	USA (G)	SC1B	1
29064	2015	Finland	SC1B	5
29284	2011	Finland	SC1B	119
29326	2010	Finland	SC1B	3
29409	2008	Finland	SC1B	4

¹MGAS number. Musser GAS strain number

²Additional strain information can be found in **Supplementary Table 1**

³For the U.S. isolates, the states have been coded (A-J) at the request of the Centers for Disease Control

⁴MGE-50, genotypes derived studying 50 mobile genetic element genes, as defined in **Supplementary Tables 3, 4, 5, and 6.**

⁵All Canada isolates were from Ontario