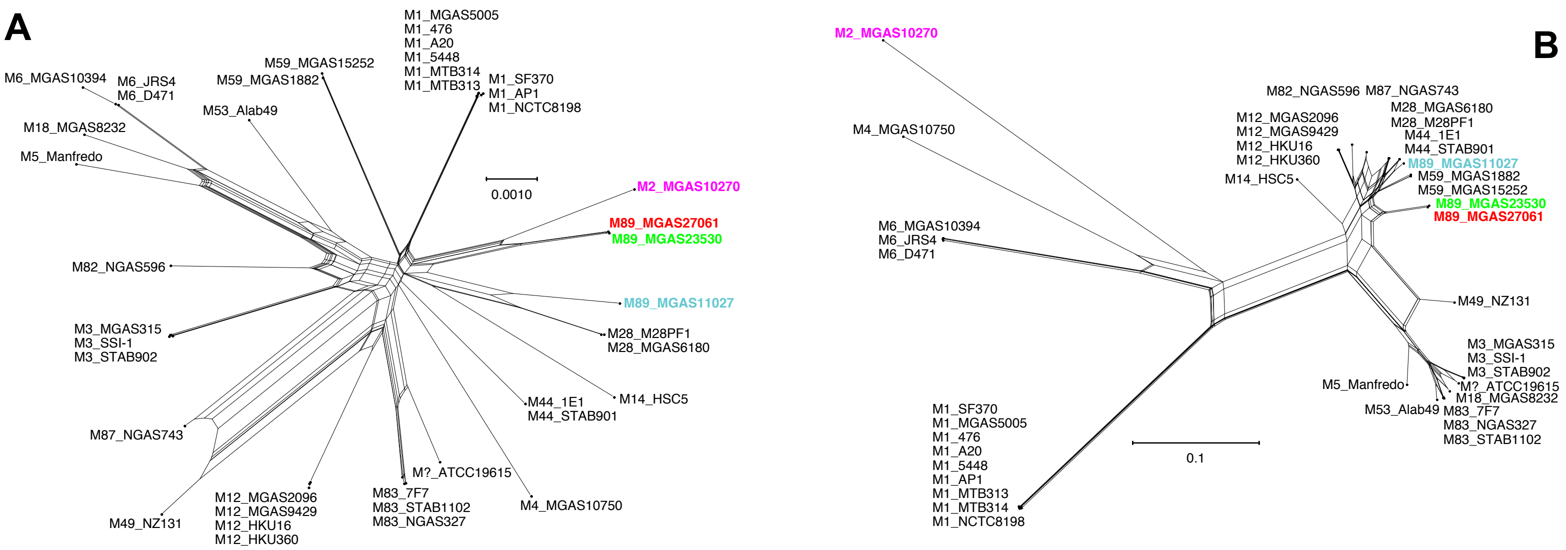
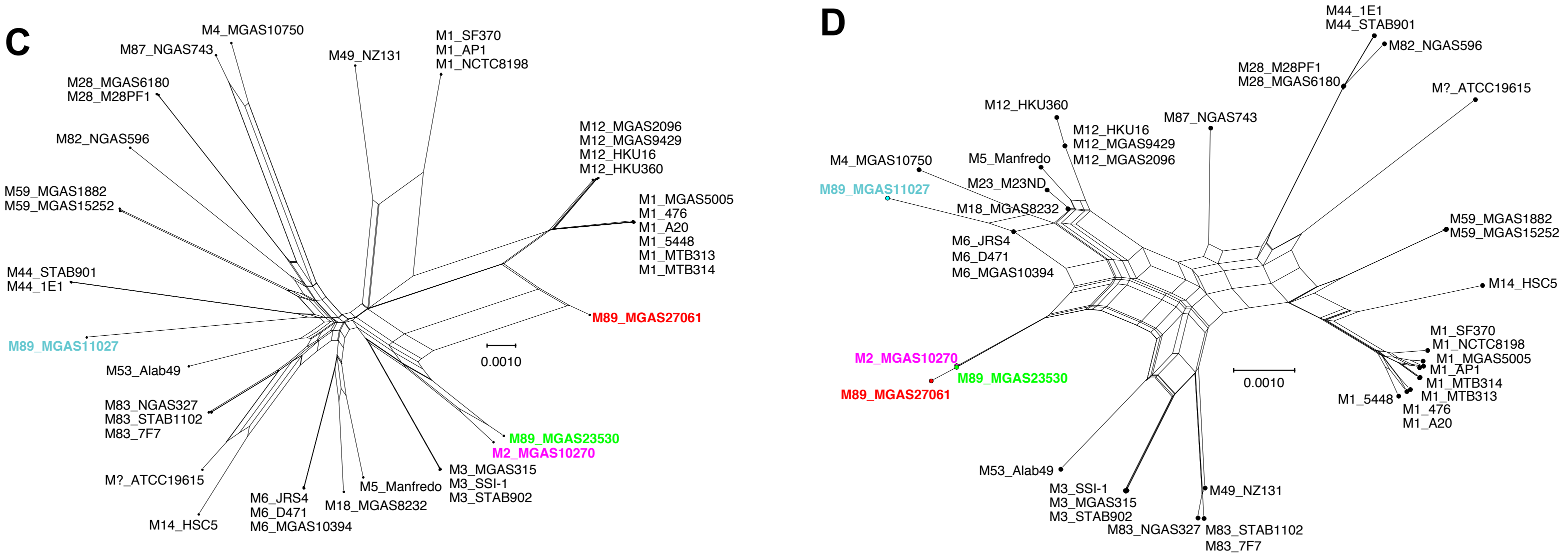
Fig. S3. Potential HGT region donors



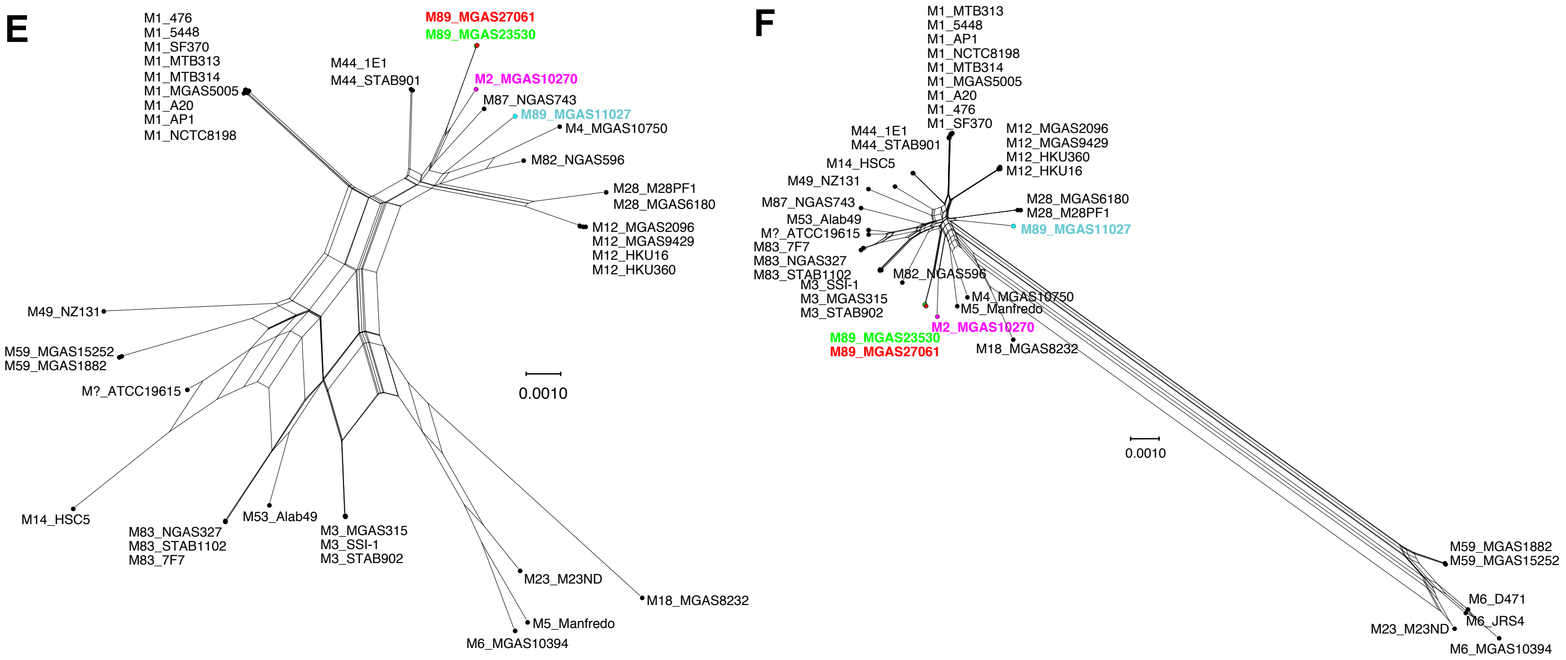
RB1 5'-end C1 to C2, 18618 bp; MGAS23530_0120 - 0142

RB1 FCT C1 to C2, 13525 bp; MGAS23530_0143 - 0152



RB1 3'-end C1 to C2, 39631 bp; MGAS23530_0153 - 0191

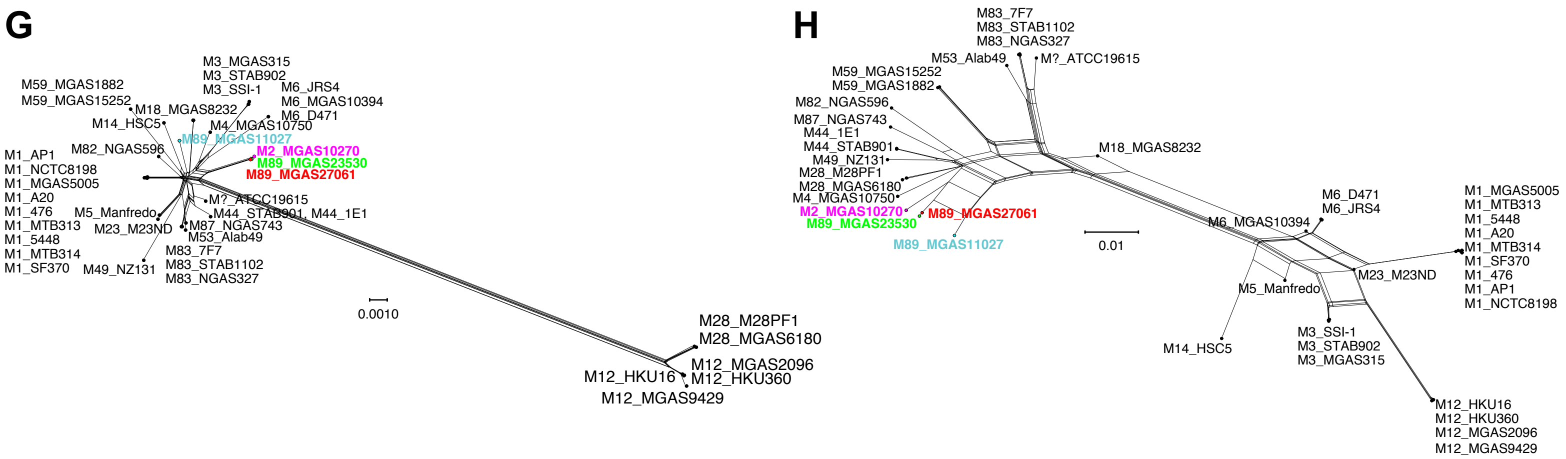
RB2 C1 to C2, 2094 bp; MGAS23530_0315 - 0316



RB3-4 C1 to C2, 27172bp; MGAS23530_0786-0812

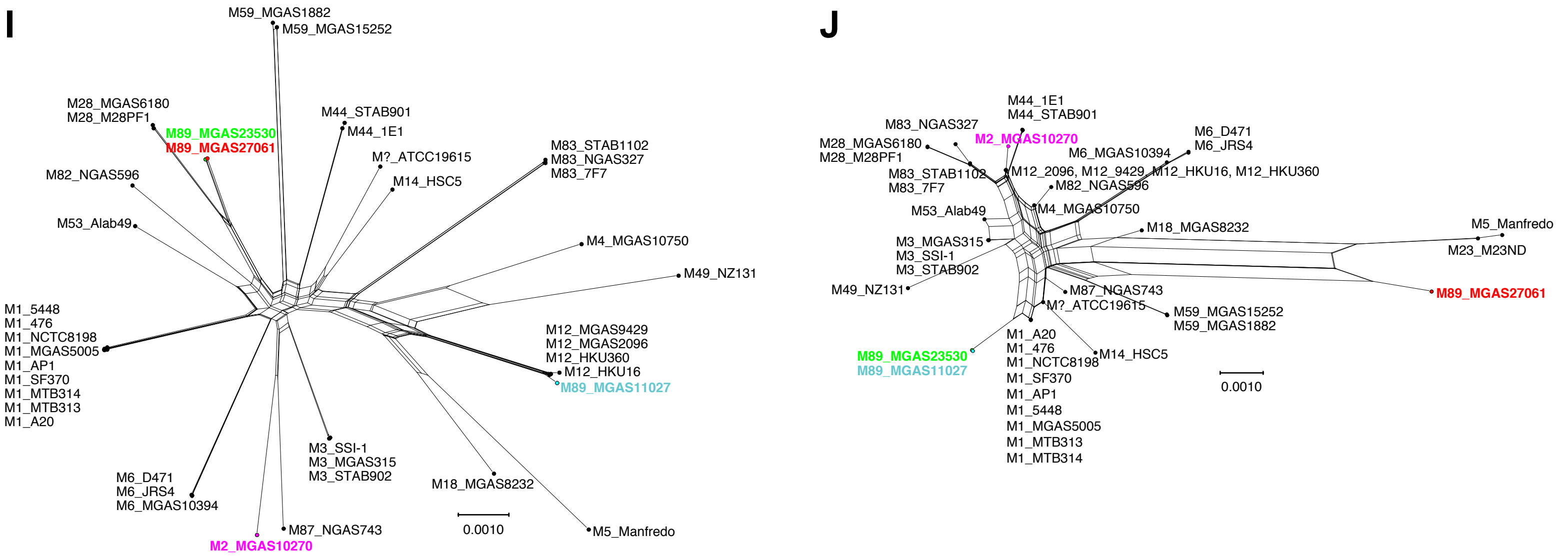
RB5 C1 to C2, 39037bp; MGAS23530_0930-0970

Fig. S3. Potential HGT region donors



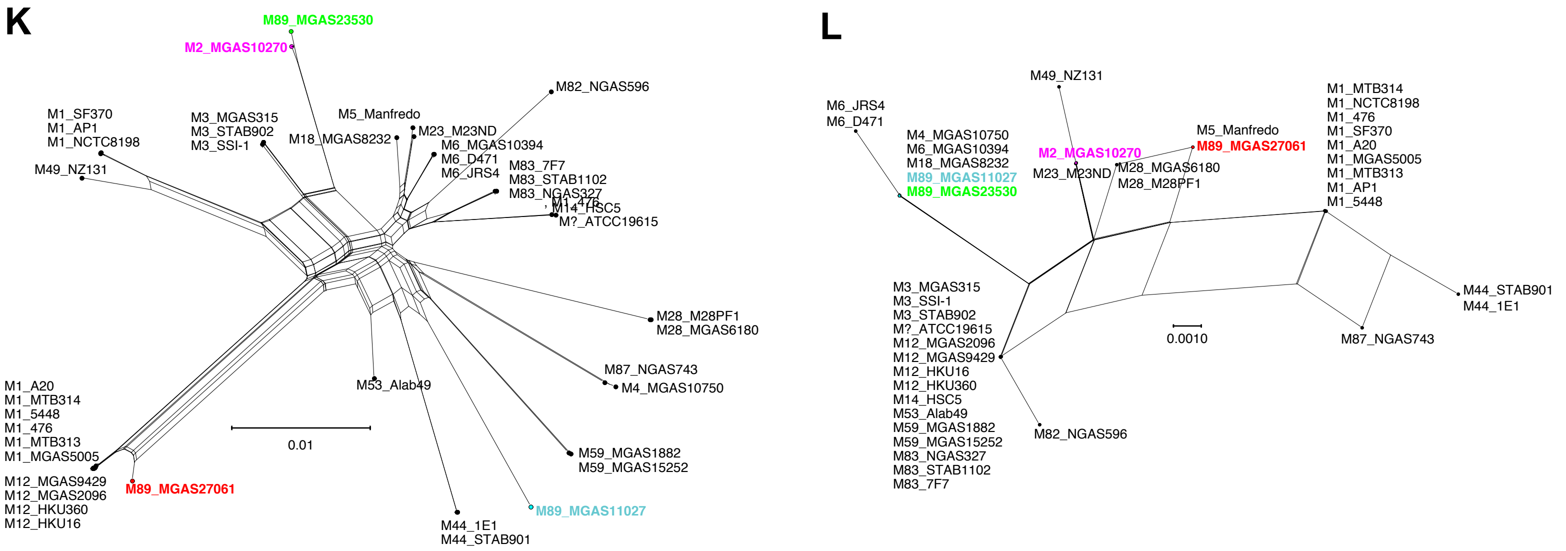
RB6 C1 to C2, 7789 bp; MGAS23530_1027 - 1032

RB7 C1 to C2, 17515 bp; MGAS23530_1532 - 1544



RB8 C1 to C2, 19532 bp; MGAS23530_1561 - 1581

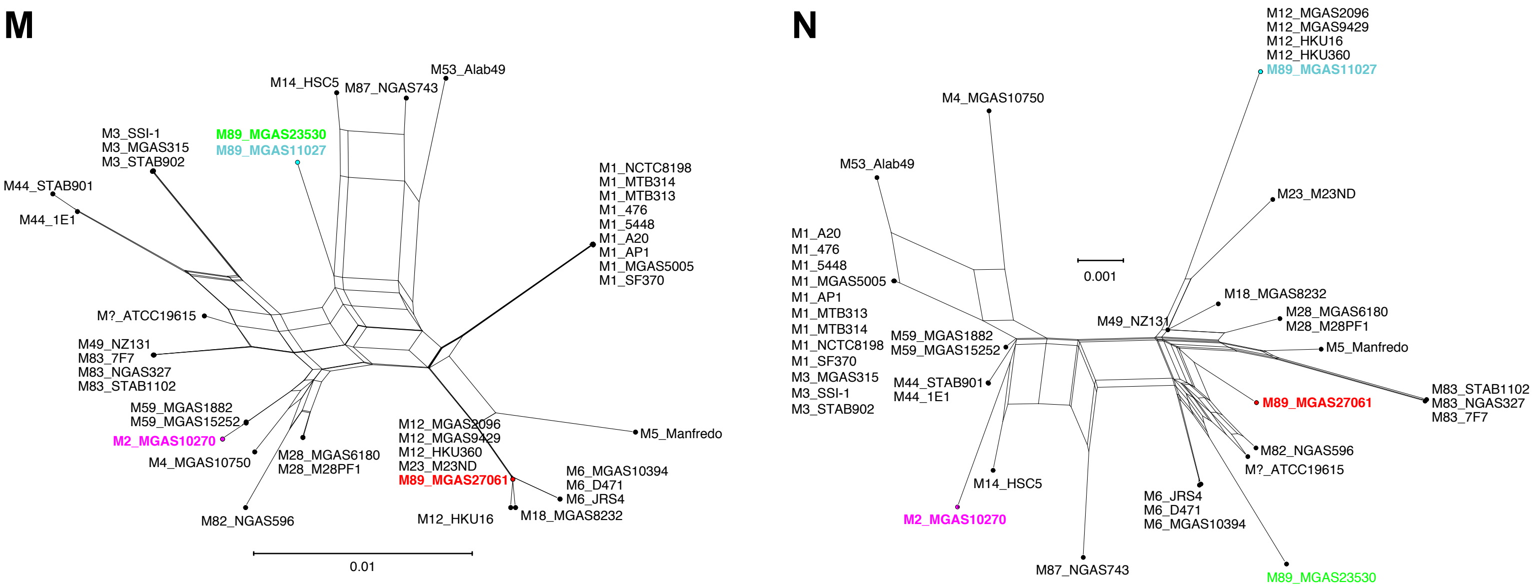
RB9 C2 to C3, 1764 bp; MGAS23530_0118 - 0119



RB10 C2 to C3, 10407 bp; MGAS23530_0173-0183

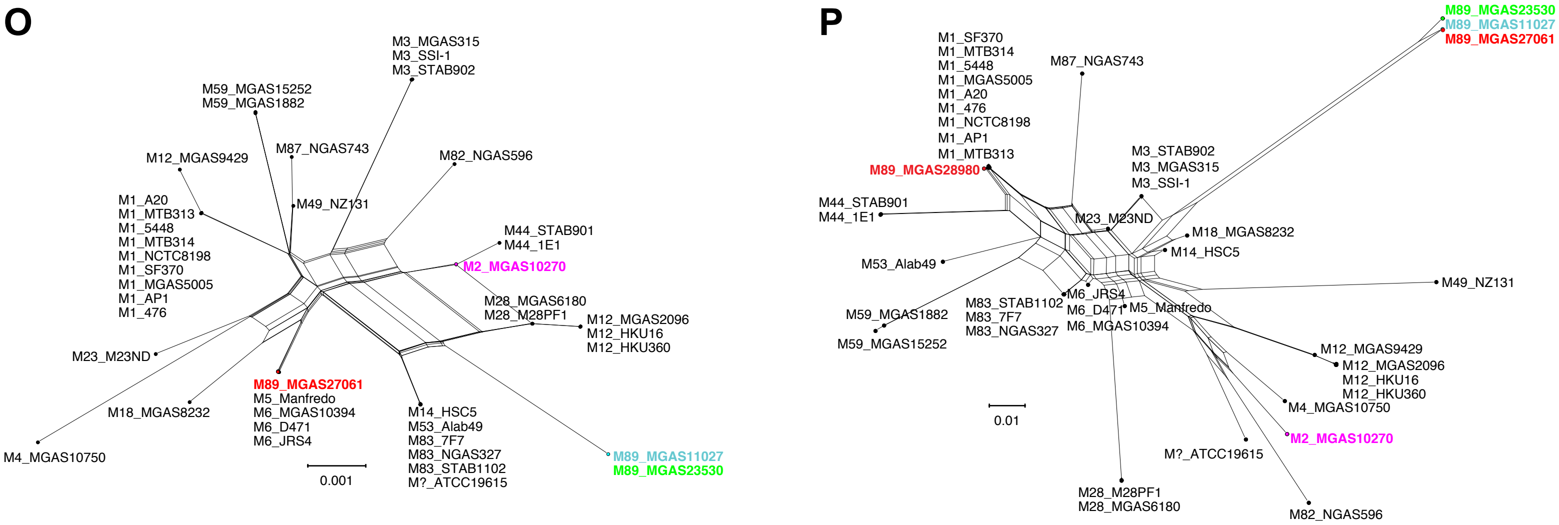
RB11 C2 to C3, 352 bp; MGAS23530_0265

Fig. S3. Potential HGT region donors



RB12 C2 to C3, 764 bp; MGAS23530_1464

RB13 C2 to C3, 801 bp; MGAS23530_1543 - 1544



RB14 C2 to C3, 1193 bp; MGAS23530_1670 - 1671

RB15 C3 to SC3D, 17818 bp; MGAS23530_0365 - 0385

Fig. S3. Potential horizontal gene transfer (HGT) region donors. Shown for each of the predicted recombination blocks (RB) separating the clades are the genetic relationships among the three *emm*89 clade reference strains and 39 strains of 18 other *emm* types for which there are complete genome sequences publically available as of July 10, 2015. Sequences flanking the predicted recombination blocks in the strain MGAS23530 genome were used to define the corresponding regions in the other strains using blastn. The sequences corresponding to the predicted recombination blocks among all 42 strains were aligned using MAFFT, and relationships were inferred by neighbor-network split-decomposition using SplitsTree. The length of the recombination block and locus tags of the genes involved are listed relative to strain MGAS23530. Of note, seven of the eight recombination blocks separating all 359 clade 1 strains from all 78 clade 2 strains share a more recent common ancestor with *emm*2 reference strain MGAS10270 than with reference strains of any of the other *emm*-types used in this comparison.