



Supplementary FIG 4: Genetic arrangement of loci for synthesis of the outer core of the lipooligosaccharide/lipopolysaccharide for genomes studied here. Genes are shown as arrows indicating the direction of transcription and are coloured by the predicted functional category of their gene products as per legend below. Shading between sequences indicates amino acid sequence identity determined by tBLASTx with scale shown in the legend below. Loci found across more than one contig in SAAg309, SAAt364, SAAt388 and SAAj643 draft genomes.