Supporting information for Tettelin *et al.* (2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.182380799

Table 7. Genes and strains used for phylogenetic analyses of *S. agalactiae* strains

Locus	**Annotation**
Housekeeping	
SAG0466	thiolase
SAG0471	glucokinase
SAG0492	amino acid ABC transporter, ATP-binding protein
SAG0767	D-alanine–D-alanine ligase
SAG1086	xanthine phosphoribosyltransferase
SAG1600	glutamate racemase
SAG1680	shikimate 5-dehydrogenase
SAG1723	signal peptidase I
Surface-exposed	
SAG0079	adenylate kinase
SAG0093	D-alanyl–D-alanine carboxypeptidase family protein
SAG0163	competence protein CglA
SAG0290	ABC transporter, substrate-binding protein
SAG0368	protein of unknown function
SAG0503	lipase/acylhydrolase
SAG1473	cell wall surface anchor family protein

Locus	**Annotation**
SAG1552	conserved hypothetical protein
SAG1641	YaeC family protein
SAG2147	protein of unknown function/lipoprotein, putative
SAG2148	LysM domain protein

The nucleotide sequence of the 19 genes listed was determined after PCR amplification from each of 11 *S. agalactiae* strains. The gene set comprised eight housekeeping genes and 11 genes coding for proteins predicted to be exposed on the surface of the bacteria. The strains were the following: type Ia, 090 and A909; type Ib, H36B; type II, 18RS21; type III, COH1, M732 and M781; type V, 2603 V/R and 1169NT1; type VIII, JM9130013; and nontypeable strain CJB110. The gene sequences were used for phylogenetic analyses (Fig. 3).