Table S1. Housekeeping genes exstracted from15 *S. pyogenes* strains, from used for two strains of subsp. *zooepidemicus*, four strains of *S. dysgalactiae* subsp. *equisimilis*, and one strain of *S. dysgalactiae* subsp. *dysgalactiae*. The concatenated sequences were used for more comprehensive phylogenetic analysis.

16S rRNA methyltransferase GidB
16S rRNA-processing protein RimM
3-dehydroquinate dehydratase
3-exo-deoxyribonuclease
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
6-phospho-beta-glucosidase
ABC transporter permease
ATP-dependent Clp protease proteolytic subunit
ATP-dependent RNA helicase
DNA mismatch repair protein MutS
DNA polymerase IV
DNA topoisomerase IV subunit A
DNA-directed RNA polymerase subunit alpha
DNA-directed RNA polymerase subunit beta
GMP synthase
GTP-binding protein EngA
L-asparaginase
L-lactate dehydrogenase
L-ribulose-5-phosphate 4-epimerase
N-acetylglucosamine-6-phosphate deacetylase
N-acetylneuraminate lyase
NAD synthetase
NADH dehydrogenase
RNA polymerase sigma factor RpoD
SWFSNF family helicase
UDP-N-acetylenolpyruvoylglucosamine reductase
UDP-N-acetylmuramate--L-alanine ligase
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
acetate kinase
acetyl-CoA carboxylase subunit beta
adenylate kinase
adenylosuccinate synthetase
alanyl-tRNA synthetase
alcohol dehydrogenase
alkyl hydroperoxidase
aspartate aminotransferase
aspartyl-tRNA synthetase
bifunctional acetaldehyde-CoAalcohol dehydrogenase
calcium-transporting ATPase
copper homeostasis protein
cytoplasmic membrane protein
dihydroorotate dehydrogenase 1A
foldase protein PrsA
fructose-6-phosphate aldolase
galactosamine-6-phosphate deaminase
glucosamine--fructose-6-phosphate aminotransferase
glucosamine-6-phosphate isomerase
glutamate racemase
glutamine synthetase

glutamyl aminopeptidase
glutamyl-tRNA synthetase
glycerol dehydrogenase
glycerol-3-phosphate acyltransferase PlsX
high-affinity zinc uptake system membrane protein
hypoxanthine-guanine phosphoribosyl transferase
inorganic polyphosphateATP-NAD kinase
inosine 5-monophosphate dehydrogenase
lysyl-tRNA synthetase
manganese transport system ATP-binding protein
oligopeptide ABC transporter ATP-binding protein
oligopeptide-binding protein
peptidyl-tRNA hydrolase
potassium uptake protein
preprotein translocase subunit SecY
pyrroline-5-carboxylate reductase
recombination factor protein RarA
ribose-phosphate pyrophosphokinase
ribosomal protein L11 methyltransferase
ribosome-binding factor A
shikimate 5-dehydrogenase
tRNA delta(2)-isopentenylpyrophosphate transferase
tRNA pseudouridine synthase B
tRNA(Ile)-lysidine synthetase
threonyl-tRNA synthetase
thymidylate kinase
transcription elongation factor GreA
transcription-repair coupling factor
translation initiation factor IF-1
tryptophanyl-tRNA synthetase II
tyrosyl-tRNA synthetase
undecaprenyldiphospho-muramoylpen
uracil phosphoribosyltransferase

Supplementary figures

Figure S1a-g. Minimum evolution trees based on individual housekeeping genes and showing the position of the 112 strains of *S. dysgalactiae*, *S. equi*, *S. canis*, and *S. pyogenes*. The strains are colour labelled according to the clustering using the concatenated sequences: (*S. dysgalactiae* subsp. *equisimilis* subcluster 1 [grey], *S. dysgalactiae* subsp. *equisimilis* subcluster 2 [purple], *S. dysgalactiae* subsp. *dysgalactiae* subcluster 1 [blue], *S. dysgalactiae* subsp. *dysgalactiae* subcluster 2 [turquoise], *S. pyogenes* [yellow], *S. canis* [green], *S. equi* subspecies [orange]). Bootstrap values for major branches are shown. a: *map*; b:*pfl*; c: *ppaC*; d: *pyk*; e: *rpoβ*; f: *sodA*; g: *tuf.*

Fig. S1a (*map*)

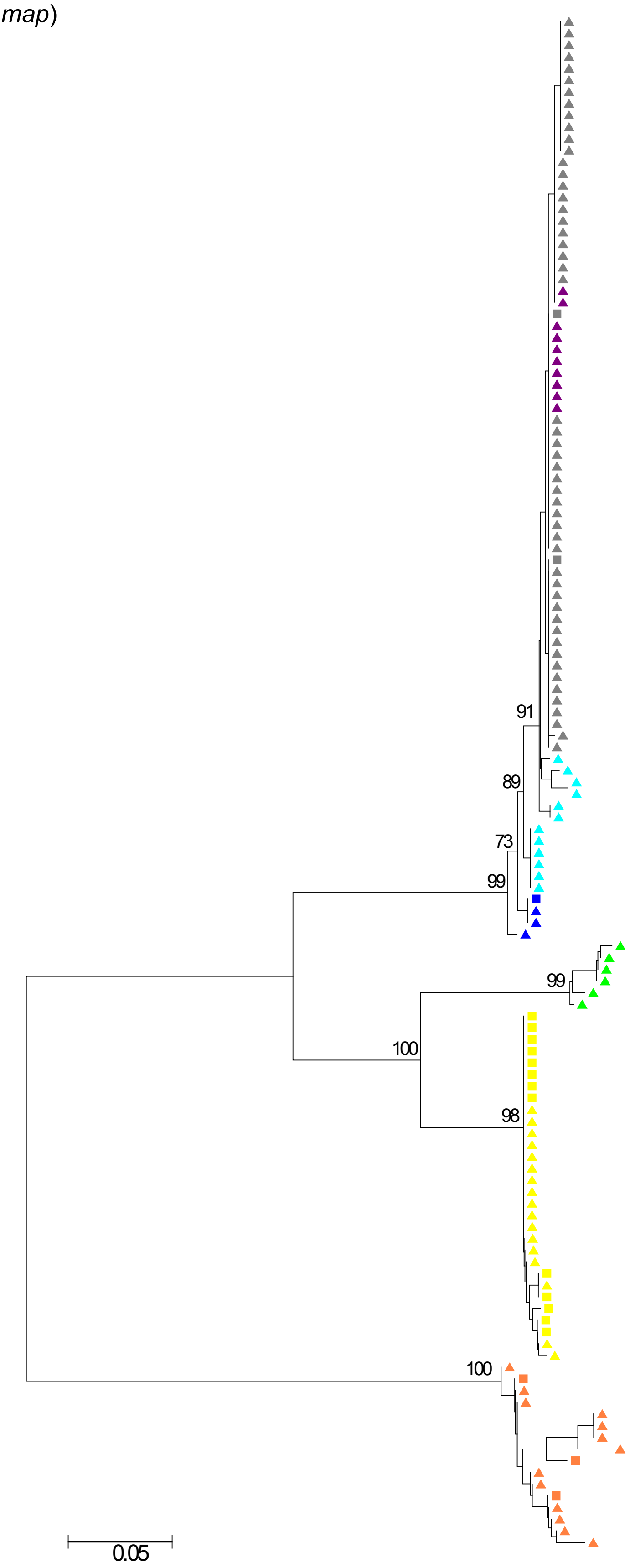

Fig. S1b (*pfl*)

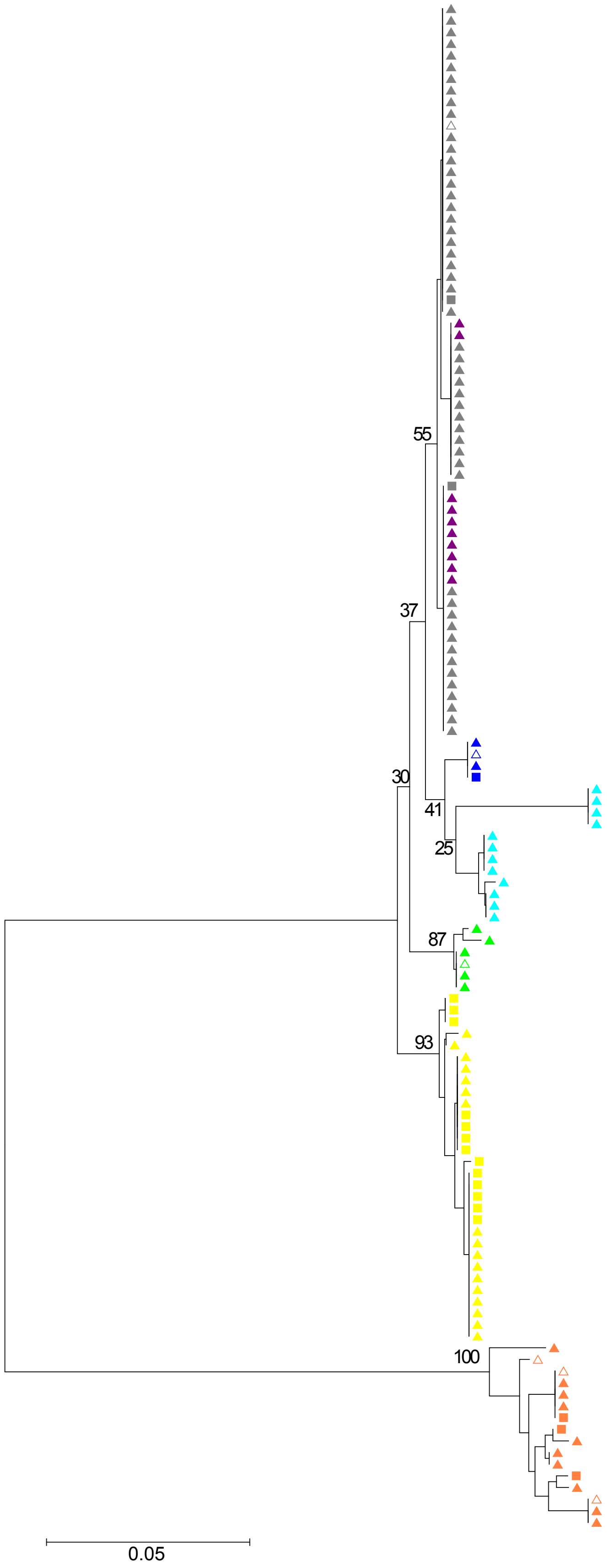

Fig. S1c (*ppaC*)

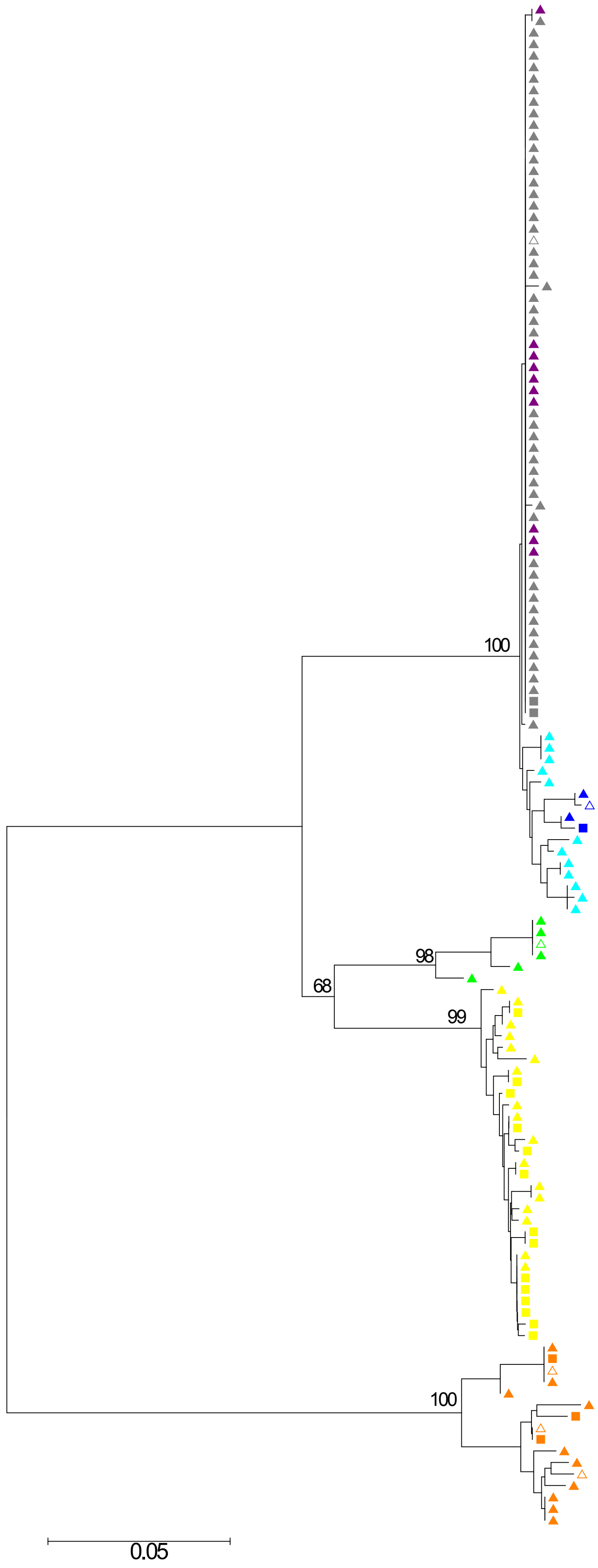

Fig. S1d (*pyk*)

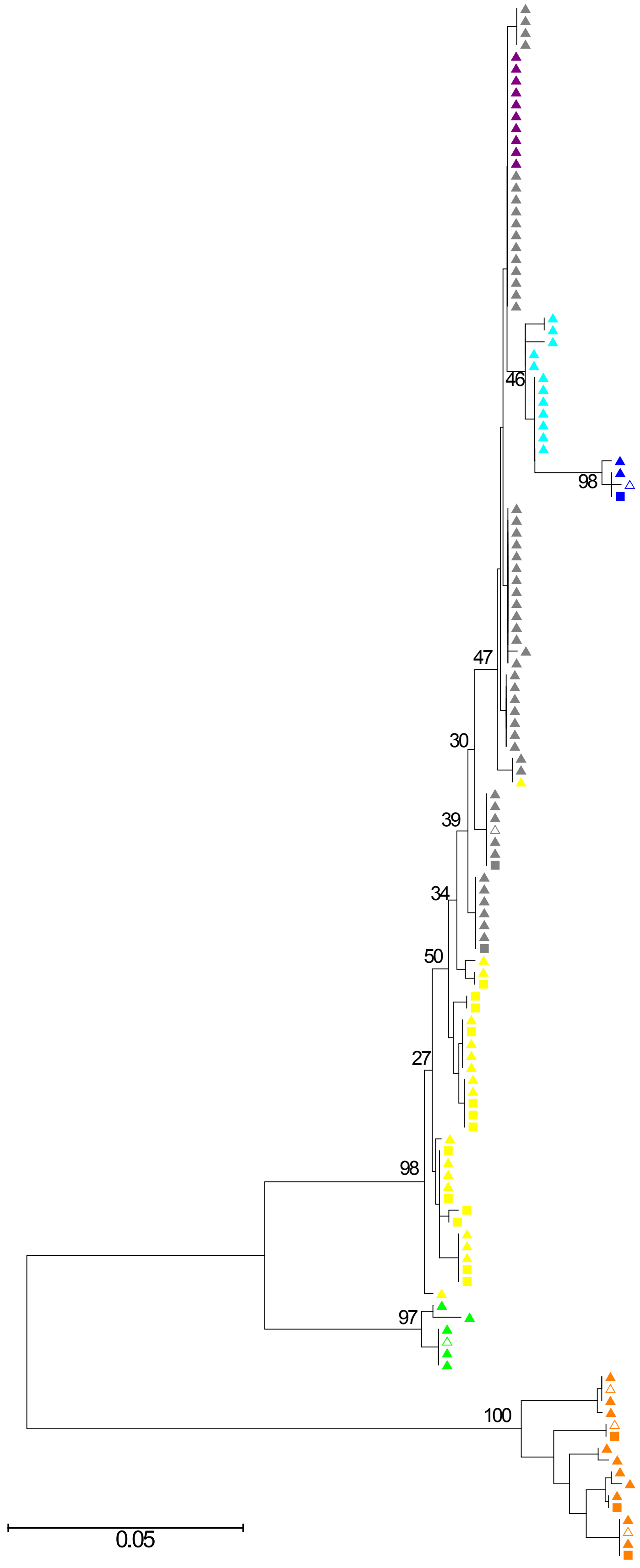

Fig. S1e (*rpoB*)

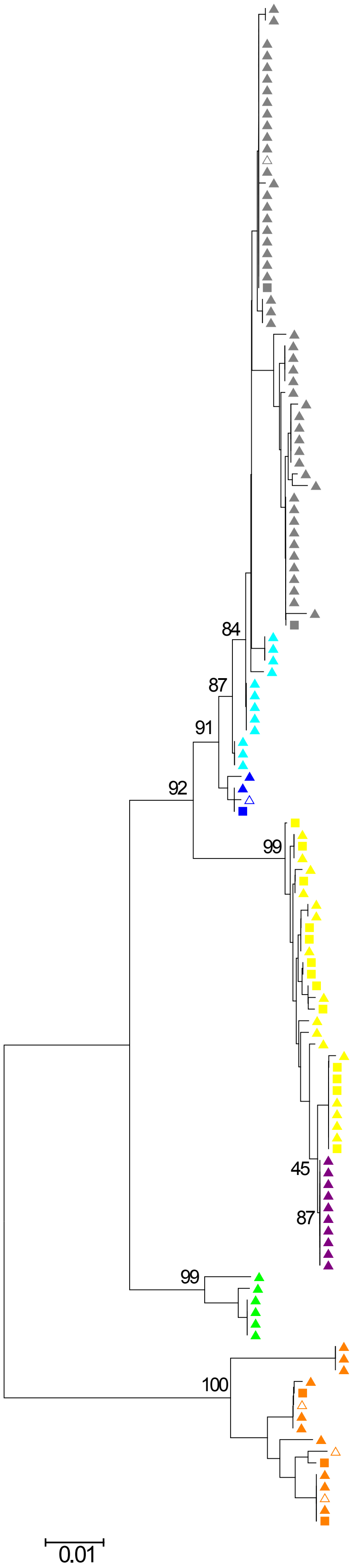

Fig. S1f (*sodA*)

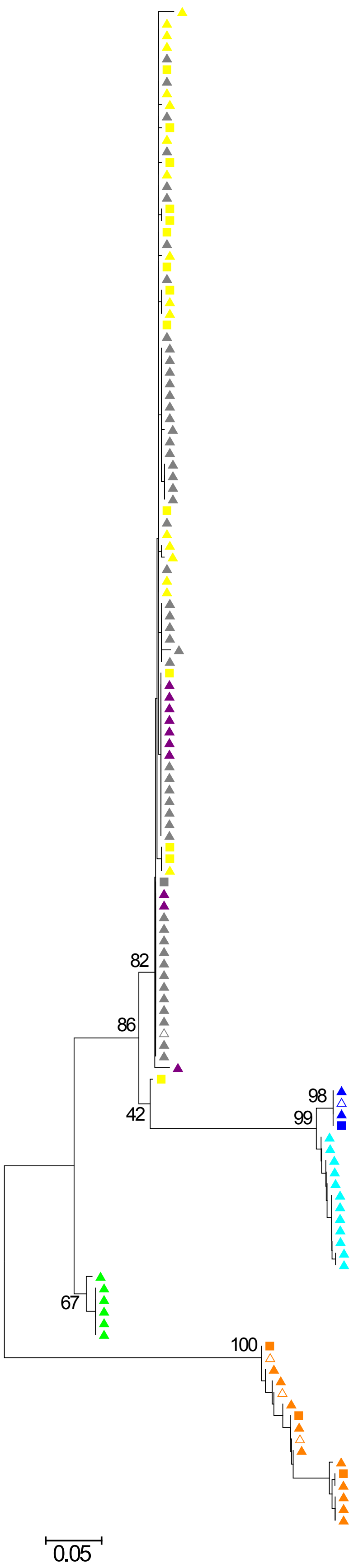

Fig. S1g (*tuf*)