

Figure S1

ERIC-PCR profiles of 93 clinical and 11 control *Pseudomonas aeruginosa* isolates after UPGMA cluster analysis (Dice similarity coefficient, position tolerance 1.0%, and optimization 1.5%).

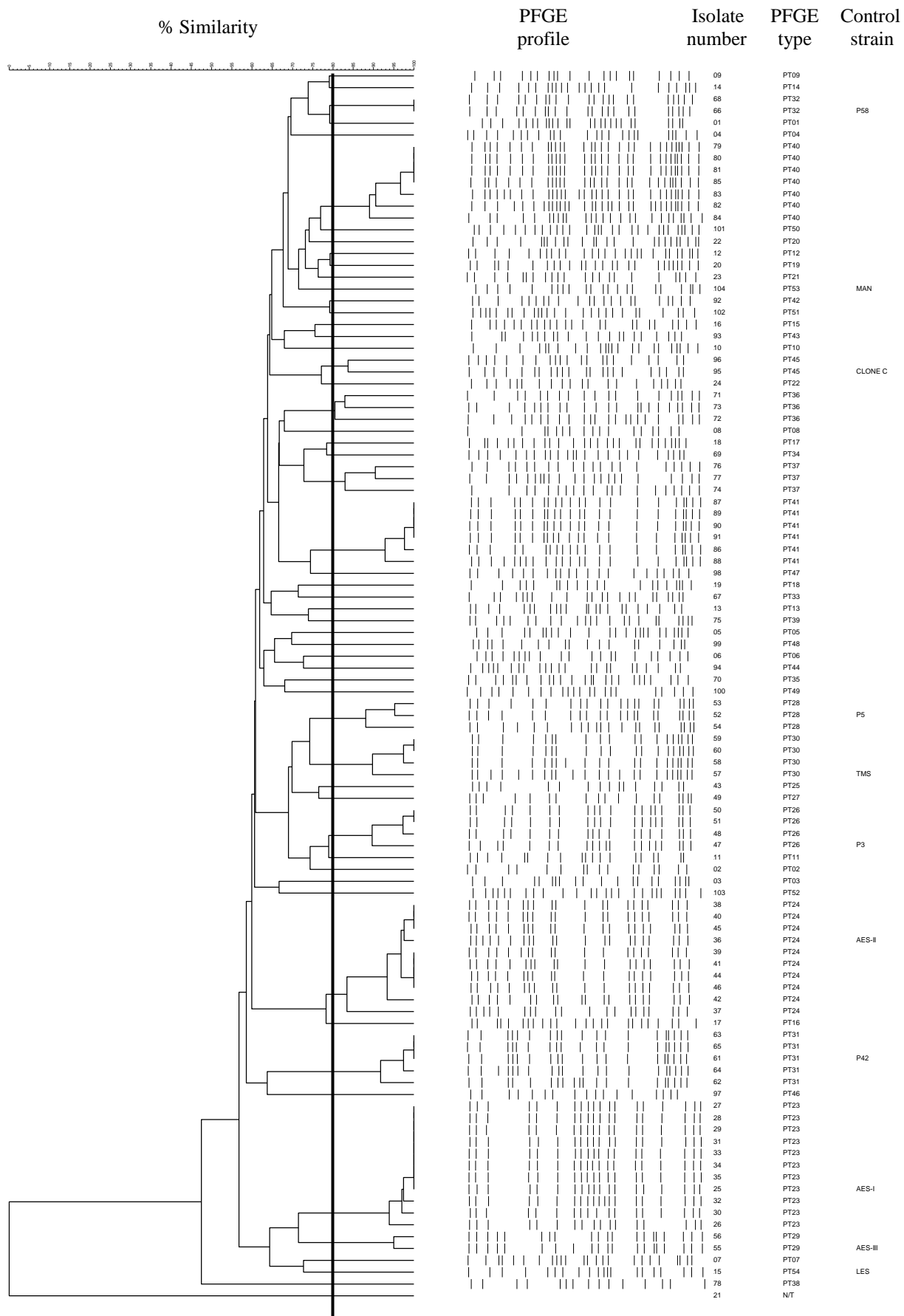


Figure S2

PFGE profiles of 92 clinical and 11 control *Pseudomonas aeruginosa* isolates after UPGMA cluster analysis (Dice similarity coefficient, position tolerance 1.0%, and optimization 1.5%). PFGE profiles related by $\geq 80\%$ (black line) correspond to ≤ 6 band differences and are grouped into the same PFGE types.

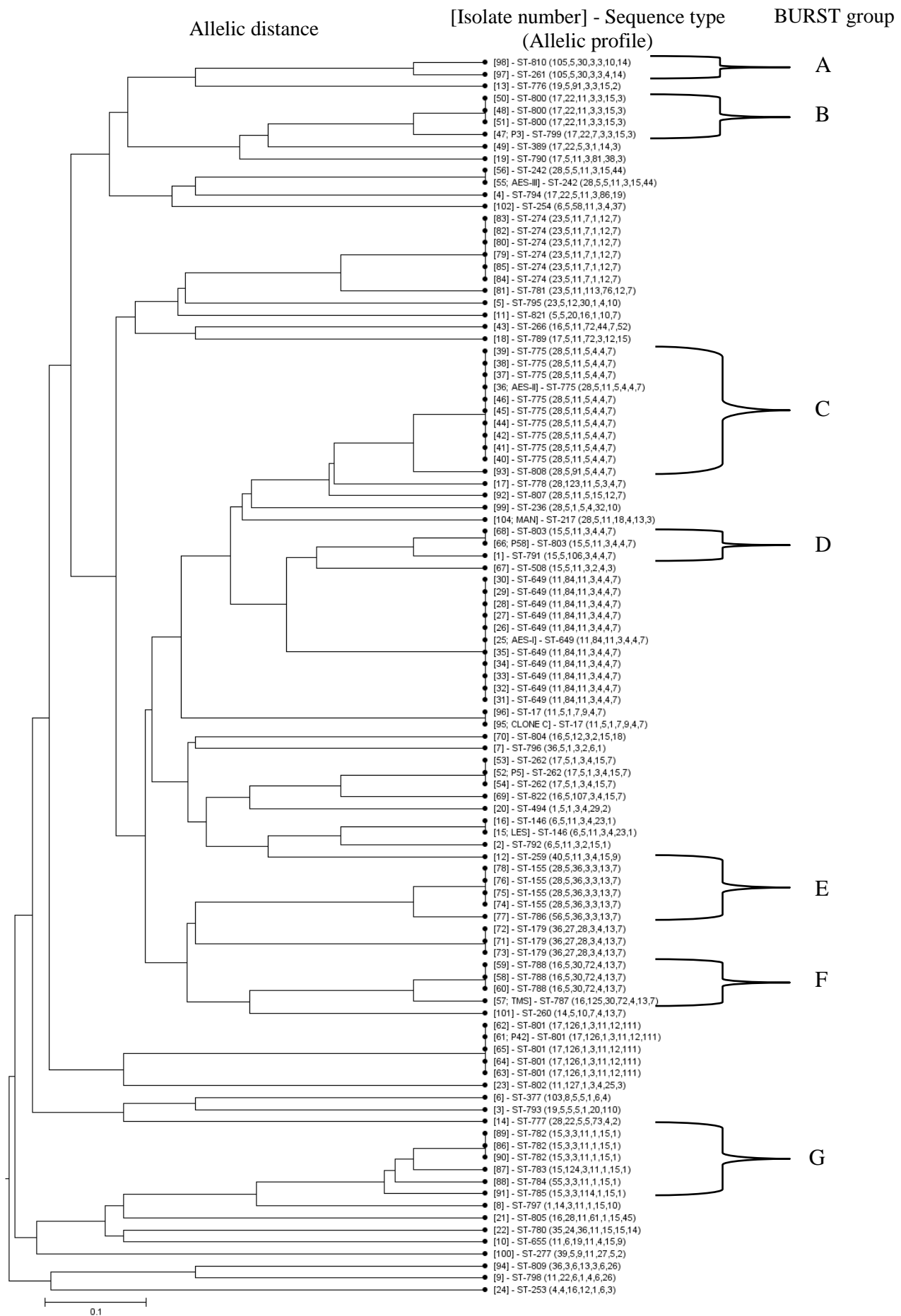


Figure S3

UPGMA tree generated from the allelic profiles of 92 clinical and 11 control *Pseudomonas aeruginosa* isolates.