Supporting Information

Köhler et al. 10.1073/pnas.0811741106

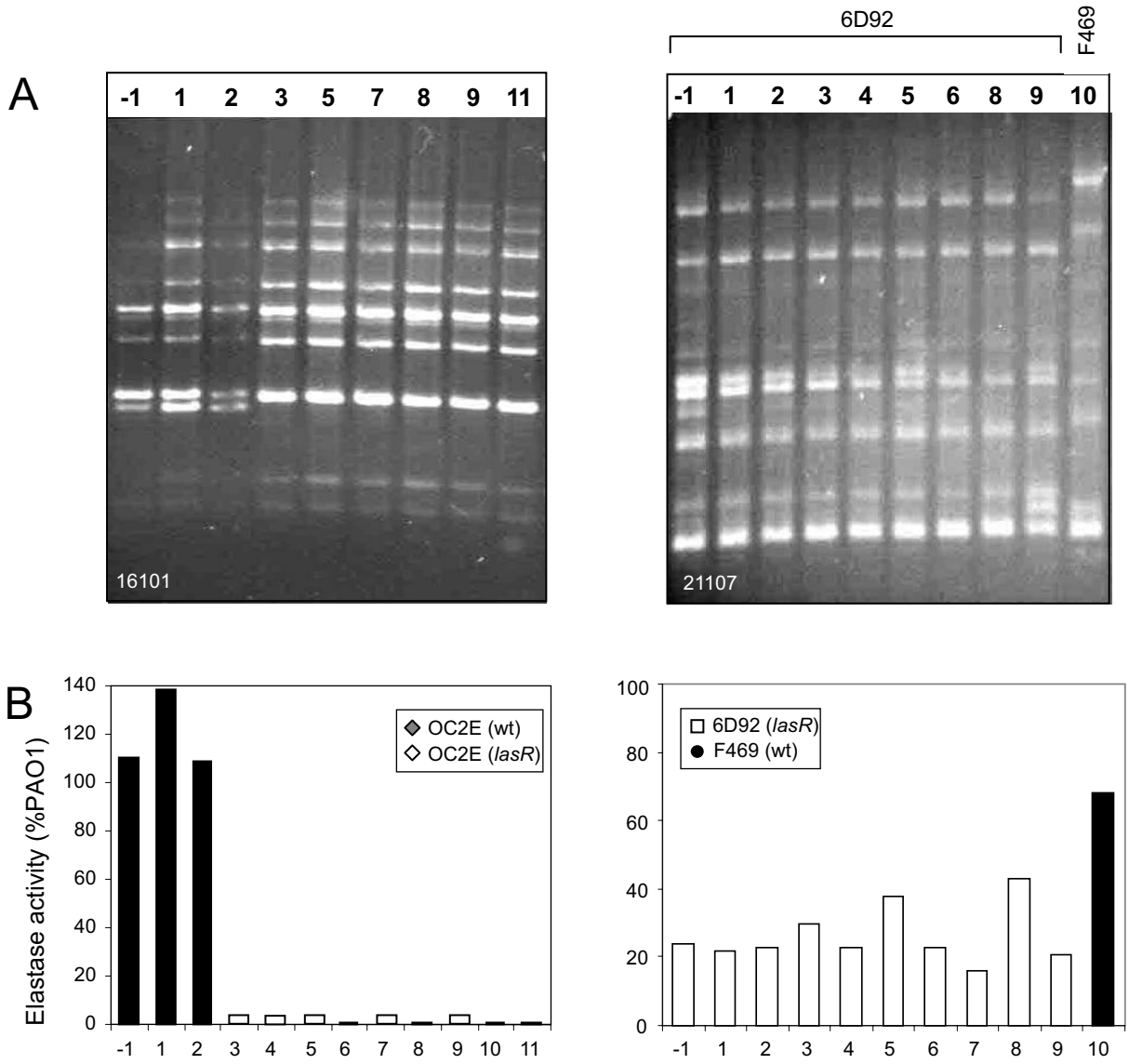

Fig. S1. RAPD and elastase activity of isolates from patients 16101 and 21107. (*A*) RAPD analysis and determination of the genotype were performed as described in *Materials and Methods*. (*B*) Elastase activities of isolates were determined by the ECR assay and results (mean of 2 determinations) are given as percentage of strain PAO1.

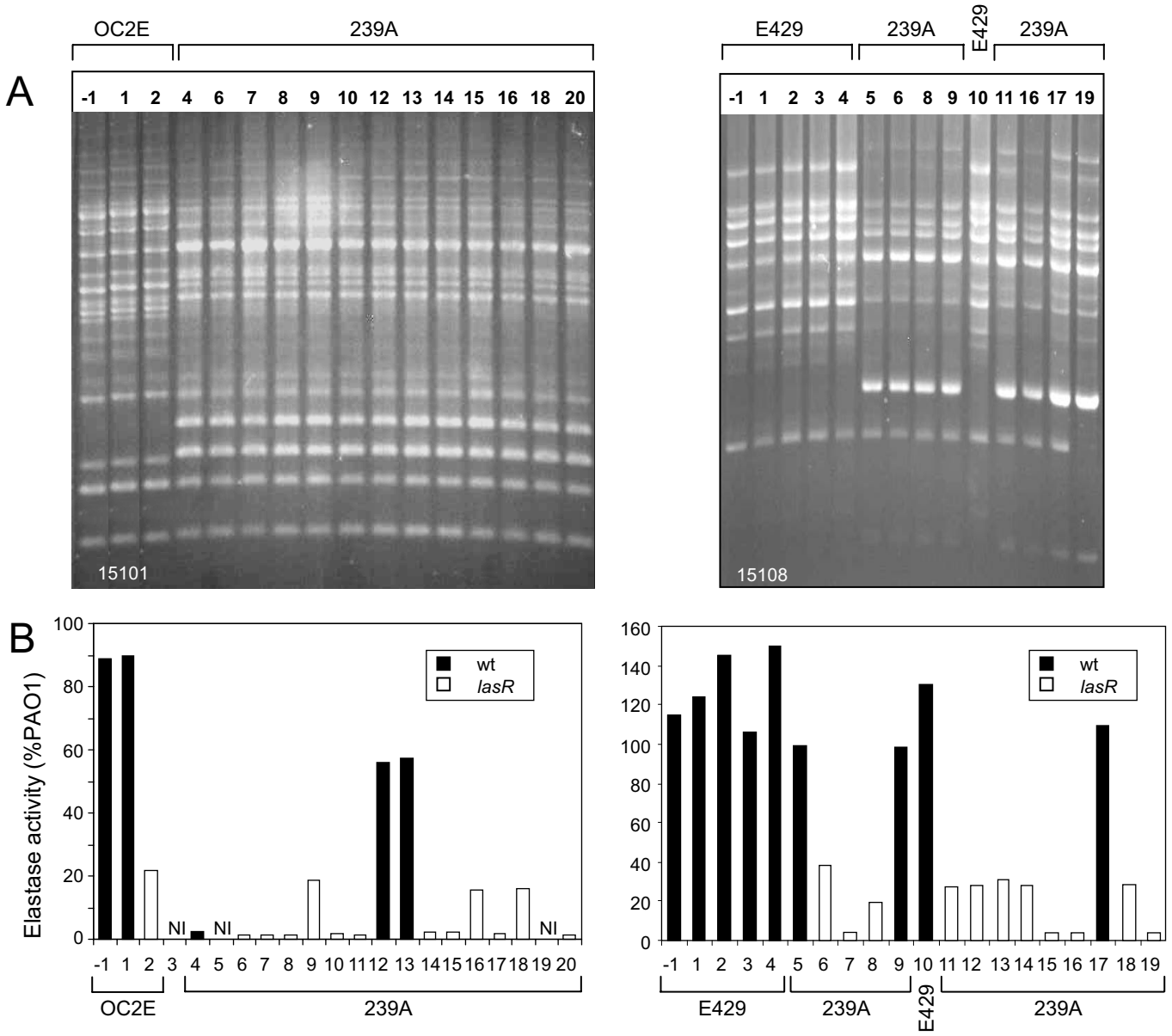

Fig. S2. RAPD and elastase activity of isolates from patients 15101 and 15108. (*A*) RAPD analysis and determination of the genotype were performed as described in *Materials and Methods*. (*B*) Elastase activities of isolates were determined by the ECR assay and results (mean of 2 determinations) are given as percentage of strain PAO1.

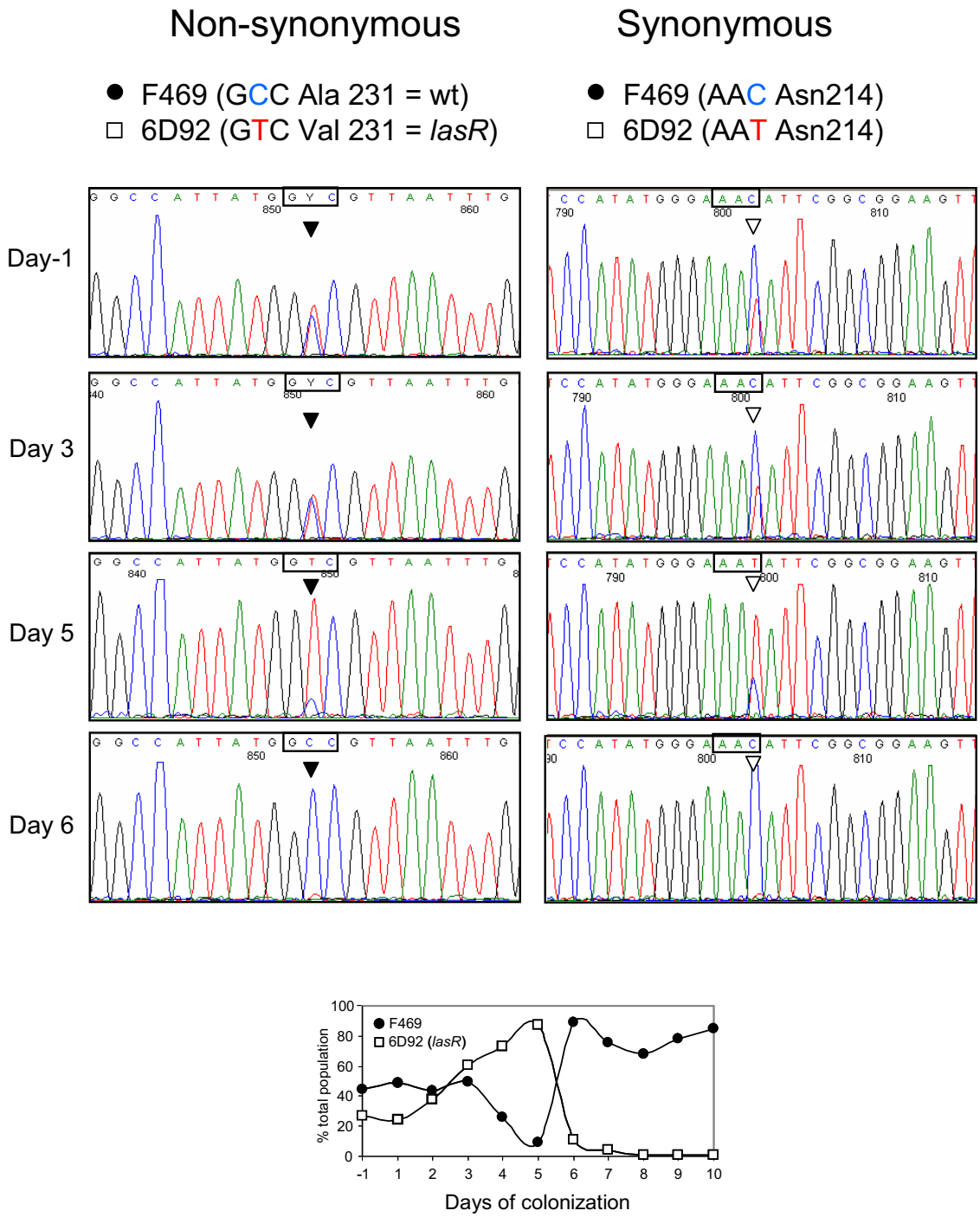

Fig. S3. LasR wild-type and mutant populations in aspirates from patient 21107. To determine qualitatively the proportion of *lasR* wt/mut alleles at the level of the bacterial population, we amplified the *lasR* gene in the total genomic DNA preparations from the aspirates of patient 21107. Sequencing of the PCR-amplicon confirmed the presence of both *lasR* wt and A231V mutant populations in aspirates from day −1 and 3 (▼, Day 1 and 3; *Upper Left*). As shown in Fig. 3*B* (reproduced here, *Lower*) the A231V population was dominant on day 5, whereas the *lasR* wt population was dominant on day 6 (▼, Day 5 and 6; *Upper Left*). The occurrence of the nonsynonymous mutation at codon 231 of *lasR* could be linked to the genotype 6D92 because of a synonymous nt substitution (C > T) occurring at codon 214 in the *lasR* sequence of this clone (▽, *Upper Right*).