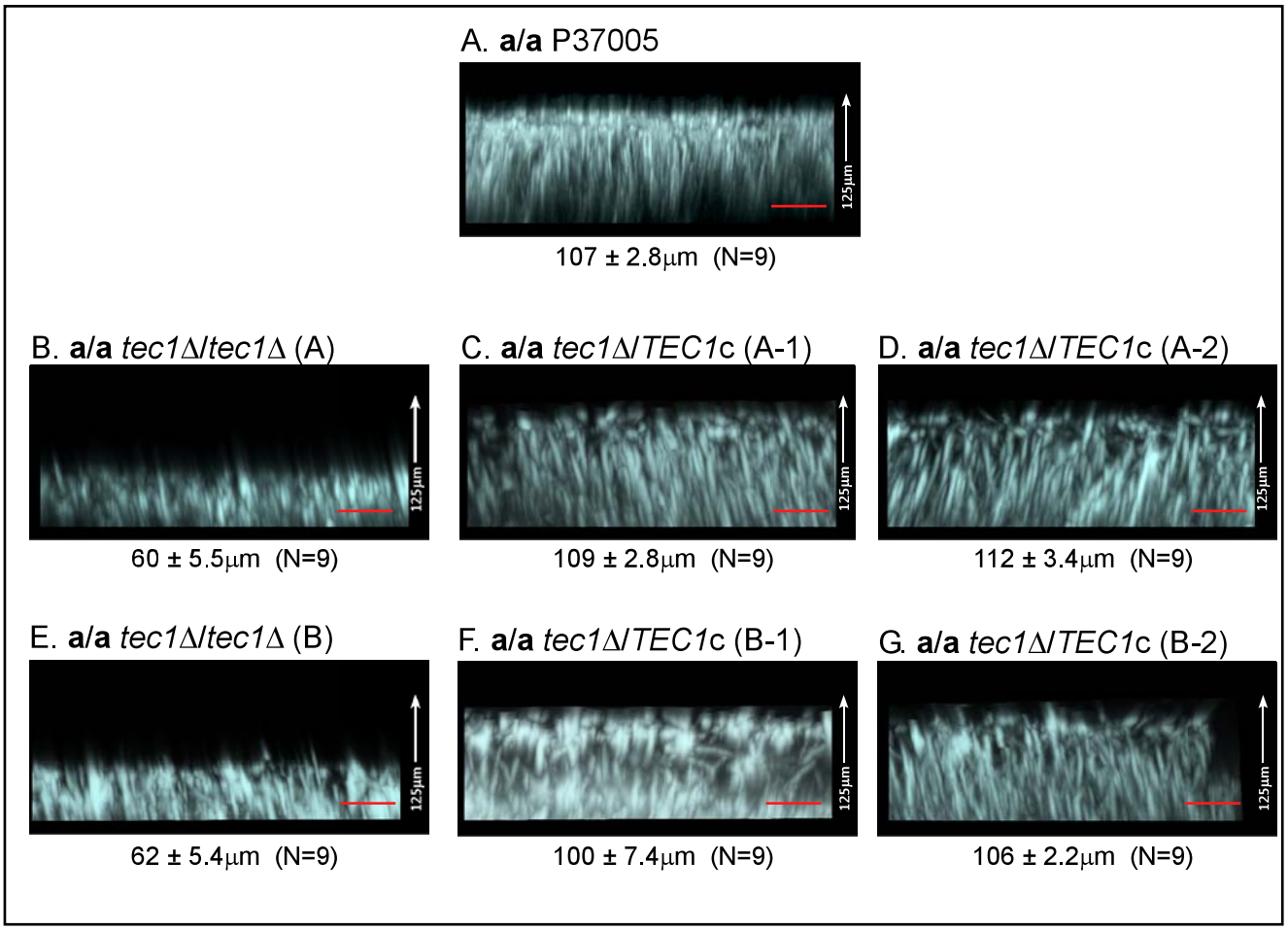
Supplemental Table S1. Primers used in this study.

Primer	**Sequence (5′ → 3′)**
P1	ATGTCAATTACTAAAACATA
P2	CTATGTTTGTGACTGTTTTACTTC
P3	ATGATGTCGCAAGCTACTCCT
p4	CTAAAACTCACTAGTAAATCCTTC
TEC1-F1	CCCAATTTCTCAGGGCCCTAGTCAGGTAG
TEC1-R1	GCAATTAAAGATTGGATCCCCGCTAAACTAATG
TEC1-F2	CACTTACTCACTGCAGGATACATTAGTTTAGC
TEC1-R2	CTCTAATACAAGCCGCGGACAATTATGTAATCC
TEC1-SR	GCAAAGAAGTGGAAACAAAAGAAACCC
CaSAT1-F	GGGCACTAAGCAGACAGCTCCTTGGC

Figure S1



Supplemental Figure Legend

Figure S1. Complementation of the **a/a** tec1Δ/tec1Δ mutant by introducing wild type TEC1 into its native location, rescues the aberrant mutant phenotype. Mutants **a/a** tec1Δ/tec1Δ (A) and **a/a** tec1Δ/tec1Δ (B) were complemented to generate **a/a** tec1Δ/TEC1c (A-1) and (A-2), and mutants **a/a** tec1Δ/TEC1c (B-1) and **a/a** tec1Δ/TEC1c (B-2), respectively. Side views of a stack of 500 confocal microscopy scans are provided for each biofilm. A. **a/a** P37005. B. **a/a** tec1Δ/tec1Δ (A). C. **a/a** tec1Δ/TEC1c (A-1). D. **a/a** tec1Δ/TEC1c (A-2). E. **a/a** tec1Δ/tec1Δ (B). F. **a/a** tec1Δ/TEC1c (B-1). G. **a/a** tec1Δ/TEC1c (B-2). Thickness is presented as mean ± standard deviation (N=9). Scale bar = 20 μm.