Table S1 **Primers used in this study**

#	Primer Name	Sequence	Description
1	DKO501	gctatgatgaacaggtaccCATTGCACTAACCCGAACACC	5' *EFG1* flank upstream primer for cloning into pSFS2
2	DKO502	gagtccatgatcactcgagATGGGTTAAGGGTTGGTTGG	3' *EFG1* flank upstream primer for cloning into pSFS2
3	DKO503	gatcataccgaacagagcggccgcGTTCAGTTCACCCTTCACCC	5' *EFG1* flank downstream primer for cloning into pSFS2
4	DKO504	catgattcgttagaccgcggGGAAAAGACAATGACTTACACAC	3' *EFG1* flank downstream primer for cloning into pSFS2
5	MBO72	gctatgatgaacaggtaccGATGAAGGAATTGTCCATGGC	5' *SUN41* flank upstream primer for cloning into pSFS2
6	MBO73	gagtccatgatcactcgagCGAATGTACAGTTGAGAC	3' *SUN41* flank upstream primer for cloning into pSFS2
7	MBO74	gatcataccgaacagagcggccgcGAGAAAAGTACAAGATACCC	5' *SUN41* flank downstream primer for cloning into pSFS2
8	MBO75	catgattcgttagaccgcggGTGGTTTCCAATGATGGCACGG	3' *SUN41* flank downstream primer for cloning into pSFS2
9	DKO239	GTTGGGACTAGGATTGGTAAAGC	5' primer for *UME6* probe
10	DKO240	GATGTGGAGTAGACTTGGATAATGG	3' primer for *UME6* probe
11	DKO523	GTTGACCGAAGCTCCAATGAATCC	5' primer for *ACT1* probe
12	DKO526	CAGCAATACCTGGGAACATGG	3' primer for *ACT1* probe
13	DTO15	GACCAAGCACCTACTGTTCC	5' primer for *ECE1* probe
14	DTO16	GATCTAGTAATGAGTTGTGG	3' primer for *ECE1* probe
15	DTO19	CAGGAAGAACCTTGTGATTACC	5' primer for *HWP1* probe
16	DTO20	GTTGGAACAGAAGTGTTTGG	3' primer for *HWP1* probe
17	PCO6	CAGAACCAACTGTATCG	5' primer for *PHR1* probe
18	PCO7	CTTCGTCATCATTGGATG	3' primer for *PHR1* probe
19	PCO8	CTCATCATCATAGTTCTACCG	5' primer for *HGC1* probe
20	PCO9	GCACGAGAACCAGCGATAC	3' primer for *HGC1* probe

21	DTO23	GTGAAGAACATACCTATGG	5’ primer for *RBT4* probe
22	DTO24	GTCCTTACCAGCTTCTTCG	3’ primer for *RBT4* probe
23	DTO21	GAGAGAAGCTGAAATTGCC	5’ primer for *RBT1* probe
24	DTO22	GGCTTTGACTTGAGCATTG	3’ primer for *RBT1* probe
25	MBO18a	AGGCAATGCTAGCCAACAGC	5’ primer for *EFG1* probe
26	MBO19a	ATTAGCTTGATGTTGTTGGGG	3’ primer for *EFG1* probe
27	MBO76	ACGACTACGCTTATGTTACCG	5’ primer for *SUN41* probe
28	MBO77	CTAACGGTAGAGCCTGATTCACC	3’ primer for *SUN41* probe
29	MBO115	gctatgatgaacaggtaccTAGAATTTCCCGGGAGTTGC	5’ primer to generate the *UME6* -650 to -122 fragment for cloning into pJK1000
30	MBO116	gagtccatgatcagggcccAACAGTAATAAGTGAGTTGTTG	3’ primer to generate the *UME6* -650 to -122 fragment for cloning into pJK1000
31	MBO117	catgattcgttagaccgcggCCTCAATTTACTTCCAATTAG	5’ primer to generate the *UME6* -45 to +443 fragment for cloning into pJK1000
32	MBO118	gatcataccgaacagagcccatggGGTGGCTGTGGTTGCAAATCAC	3’ primer to generate the *UME6* -45 to +443 fragment for cloning into pJK1000
33	*MBO84	ATGACACCATGTCAAGTTCAGA	Forward primer for *ALS3* probe[1]
34	*MBO158	CACACCAAATTGGAGGTGATT	Reverse primer for *ALS3* probe[1]

Note: Lowercase bases indicate flanking sequences within primers that contain restriction sites for cloning.

*these primers were used to generate a 1017 bp fragment which was cleaved with HincII to yield a 758 bp *ALS3*-specific probe, as described previously[1].

Reference

1. Hoyer, L.L., Payne, T.L., Bell, M., Myers, A.M. and S. Scherer. 1998. *Candida albicans ALS3* and insights into the nature of the *ALS* gene family. Curr Genet 33:451-459.

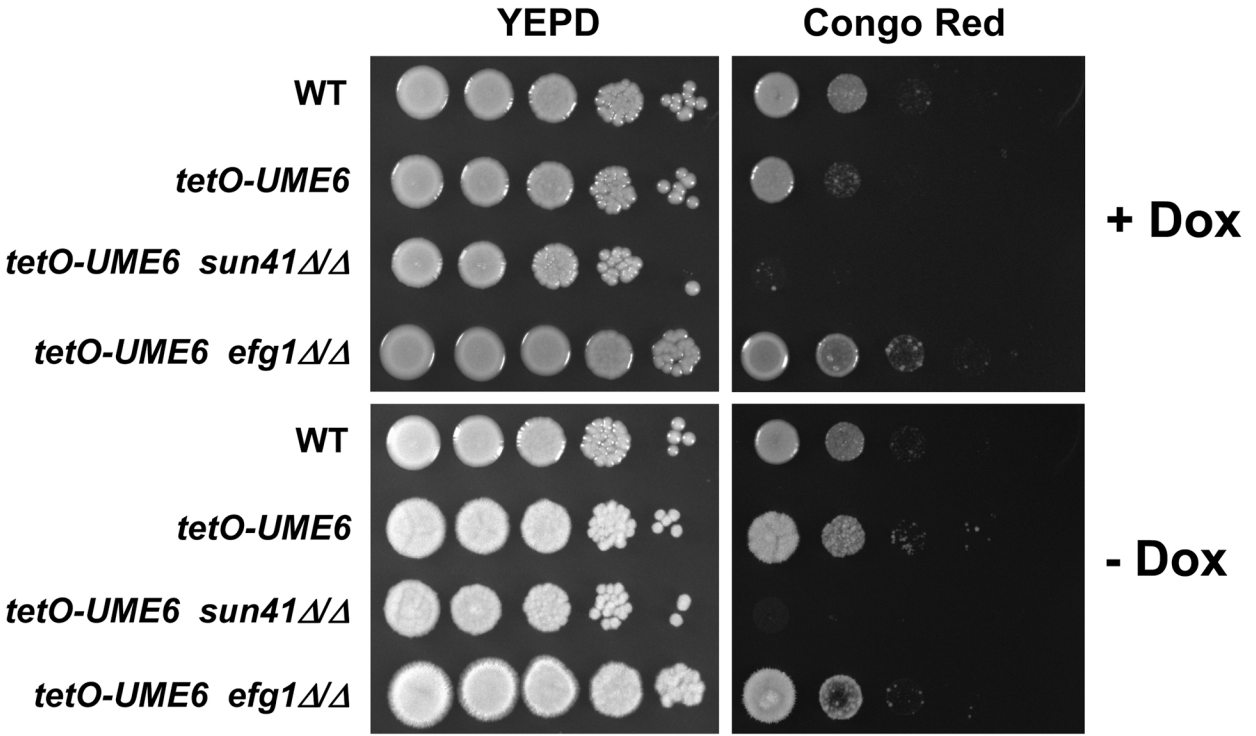

FIG S1. The *tetO-UME6 sun41Δ/Δ* mutant is hypersensitive to the cell wall inhibitor Congo Red. 6 X 10^4 cells (left columns) and subsequent 10-fold dilutions (remaining columns) of the indicated strains were spotted on YEPD or YEPD + 200 μg/mL Congo Red in the presence or absence of 20 μg/mL Dox and grown at 30˚C for 24 hrs.

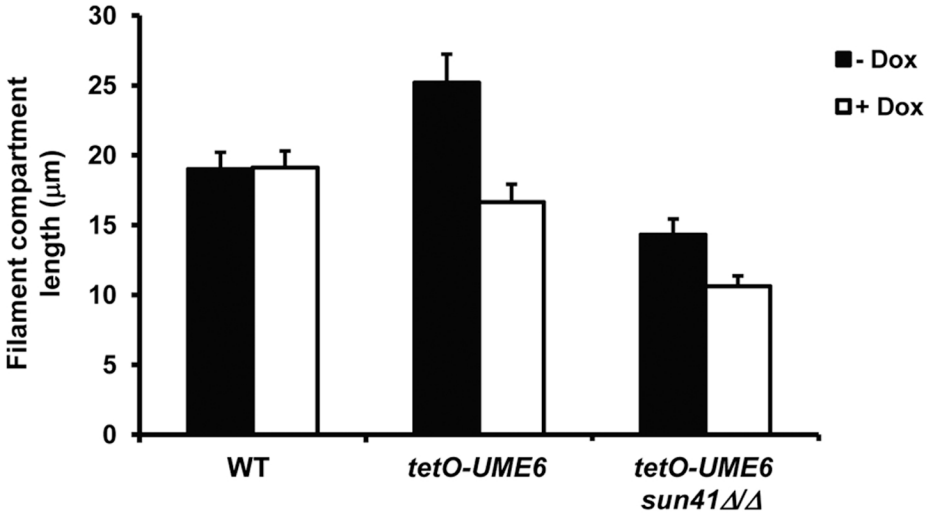

FIG S2. Deletion of Sun41 causes a reduction in filament compartment length of the *tetO-UME6* strain during biofilm formation. 1 X 10^6 cells/mL suspensions of the indicated strains were allowed to form biofilms under static conditions for 24 hrs. at 37˚C on 24-well polystyrene plates in YNB medium with amino acids + 2% dextrose in the presence or absence of 20 μg/mL Dox. A portion of the topmost layer of each biofilm was placed on a glass slide and stained with 1 mg/ml Calcofluor White (CFW) in 10% KOH. A Leica DMI6000 microscope was used for examination of the CFW-stained cells and the microscope images were acquired and analyzed using Surveyor software (Objective Imaging, Cambridge, UK). Filament compartment length for each strain was determined by measuring the mean distance between septa (n≥4). Error bars represent standard deviation.