Table S1 **Strains used in this study**

Strain	Genotype	Source
SN152	*arg4Δ/arg4Δ leu2Δ/leu2 Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	(1)
DK318 (WT)	*arg4Δ::ARG4 /arg4Δ his1Δ::HIS1/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	(2)
MAY7 (*ppg1Δ* /+)	*ppg1Δ::C.m.HIS1/PPG1 arg4Δ::ARG4/arg4Δ leu2Δ::LEU2/leu2Δ his1Δ/his1Δ ura3Δ ::imm^{434}/URA3 iro1Δ ::imm^{434}/IRO1*	This study
MAY34 (*ppg1Δ/Δ*)	*ppg1Δ::C.d.HIS1/ppg1Δ::C.m.LEU2/ arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
MAY50 (*ppg1Δ/Δ::PPG1*)	*ppg1Δ::PPG1::SAT1/ppg1Δ::C.d.HIS1 arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
MAY55 (*ppg1Δ/Δ::ppg1$_{H248A\ H173A\ D90L}$*)	*ppg1Δ::PPG1$_{H248A\ H173A\ D90L}$ ::SAT1/ppg1Δ::C.d.HIS1 arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
MAY60 (*tpk1Δ/Δ*)	*tpk1Δ::frt/tpk1Δ::SAT1 arg4Δ::ARG4 /arg4Δ his1Δ::HIS1/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
HLC52 (*efg1Δ/Δ*)	*efg1Δ::hisG/efg1Δ::hisG-URA3-hisG ura3Δ::imm^{434}/ura3Δ::imm^{434}*	(3)
MAY65 (*ppg1Δ/Δ tpk1Δ/Δ)*	*ppg1Δ::C.d.HIS1/ppg1Δ::C.m.LEU2 tpk1Δ::frt/tpk1Δ::SAT1 arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
MAY70 (*ppg1Δ/Δ efg1Δ/Δ*)	*ppg1Δ::C.d.HIS1/ppg1Δ::C.m.LEU2 efg1Δ::frt/efg1Δ::SAT1 arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study
MAY73(*tetO-PPG1*)	*tetR tetO-PPG1::FLP-SAT1/PPG1 arg4Δ::ARG4 /arg4Δ his1Δ::HIS1/his1Δ ura3Δ::imm^{434}/URA3 iro1Δ::imm^{434}/IRO1*	This study

C.d. = *dubliniensis*; C.m. = *C. maltosa*

References

1. **Noble SM, Johnson AD.** 2005. Strains and strategies for large-scale gene deletion studies of the diploid human fungal pathogen *Candida albicans*. Eukaryot Cell **4:**298-309.
2. **Banerjee M, Thompson DS, Lazzell A, Carlisle PL, Pierce C, Monteagudo C, Lopez-Ribot JL, Kadosh D.** 2008. *UME6*, a novel filament-specific regulator of *Candida albicans* hyphal extension and virulence Molecular biology of the cell **19:**1354-1365.
3. **Lo HJ, Kohler JR, DiDomenico B, Loebenberg D, Cacciapuoti A, Fink GR.** 1997. Nonfilamentous *C. albicans* mutants are avirulent. Cell **90:**939-949.

Table S2 **Primers used in this study**

#	Primer Name	Sequence	Description
1	MAO5	GTATGCGCCCTAACTACCT	*PPG1* 5' flank upstream for fusion PCR
2	MAO6	cacggcgcgcctagcagcggCCCACATATAATGAACGACAGC	*PPG1* 5' flank downstream for fusion PCR
3	MAO7	gtcagcggccgcatccctgcGAACCCATCATGTATTTC	*PPG1* 3' flank upstream for fusion PCR
4	MAO8	GAAGGGTTTTCAATTTGC	*PPG1* 3' flank downstream for fusion PCR
5	RZO37	ccgctgctaggcgcgccgtgACCAGTGTGATGGATATCTGC	5’ vector primer for *LEU2*, *ARG4*, *HIS1* markers (designed by R. Zordan)
6	RZO38	gcagggatgcggccgctgacAGCTCGGATCCACTAGTAACG	3’ vector primer for *LEU2*, *ARG4*, *HIS1* markers (designed by R. Zordan)
7	MAO155	ATCACTAAAGCTCGACCAGTT	5’ *PPG1* flank upstream primer for split marker add-back of *PPG1*
8	MAO156	ACTTCTTCTTTCTTCAGCTCTCTT	5’ *PPG1* flank upstream nested primer for split marker add-back of *PPG1*
9	MAO157	ggtaccGTCTTGAAACTGATACAATTGGAGA	5’ *PPG1* flank downstream primer for split marker add-back of *PPG1*
10	MAO158	ccgcggCACACACGTACACACACATTC	3’ *PPG1* flank upstream primer for split marker add-back of *PPG1*
11	MAO159	GTTAAGCTAAGAGTAACTCGGT	3’ *PPG1* flank downstream primer for split marker add-back of *PPG1*
12	MAO160	GGCGTATATGATGATTTAAGTTGGG	3’ *PPG1* flank downstream nested primer for split marker add-back of *PPG1*
13	MAO77	agggcgccatggccATGACGGTGCCGTTCAAAATACC	Upstream non-mutagenic primer to clone *PPG1* into pAG10H vector using NcoI restriction enzyme. Also used as a non-mutagenic primer to generate D90L mutation.
14	MAO78	gcagccggatccTTACAAGAAATACTCAACTTGTTGAC	Downstream non-mutagenic primer to clone *PPG1* into pAG10H vector using BamHI restriction enzyme. Also used as a non-mutagenic primer to generate H248A mutation.
15	MAO133	CACTGAATAATAACCACGATCAACGTACAACCCAAGAATAAATAATTAGTTTGAGGCG	*PPG1* downstream internal mutagenic primer to

			generate D90L mutation
16	MAO150	CGTGGTTATTATTCAGTGGAAACTATATC	*PPG1* upstream internal non-mutagenic primer to generate H173A mutation
17	MAO151	CCAATTGTTGACAACTGGGGGATAACCCACC GGCACATGCAAATATCTTGCCATCTATAG	*PPG1* downstream internal mutagenic primer to generate H173A mutation
18	MAO152	CCAGTTGTCAACAATTGGATCAAATACGAGC AGTCG	*PPG1* upstream internal non-mutagenic primer to generate H248A mutation
19	MAO153	CTCGTATACCCTTCATTACACAATTGGGCAGC TCTAATCATTTGCACC	*PPG1* downstream internal mutagenic primer to generate H248A mutation
20	MAO154	GGTGCAAATGATTAGAGCTGCCCAATTGTGT AATGAAGGGTATACGAG	*PPG1* upstream internal mutagenic primer to generate H248A mutation
21	MAO138	GAGGTAGTTGGTGTGGAAAGA	5’ *TPK1* flank upstream primer for split marker deletion of *TPK1* deletion
22	MAO148	ACTGATGTCAATTTGTTGGCG	5’ *TPK1* flank upstream nested primer for split marker deletion of *TPK1*
23	MAO139	ggtaccGAAAGGAGAAGGAGGAGGATAAC	5’ *TPK1* flank downstream primer for split marker deletion of *TPK1*
24	MAO140	ccgcggCACTATATGAATTGGCTTCCTTGTT	3’ *TPK1* flank upstream primer for split marker deletion of *TPK1*
25	MAO141	CTCAACTATTGTCTGAATGTGTGTATC	3’ *TPK1* flank downstream primer for split marker deletion of *TPK1*
26	MAO149	GGAAAGACCTCTAATTCGAT	3’ *TPK1* flank downstream nested primer for split marker deletion of *TPK1*
27	MAO126	gatcataccgaacagaggtaccTACCTGGCCCTGGCAAA C	5’ primer for -98 to -566 region of *PPG1* promoter used for cloning into pEL9
28	MAO128	gatcataccgaacagaccgcggGTGGGTACACATTCAAC AGA	3’ primer for -98 to -566 region of *PPG1* promoter used for cloning into pEL9
29	MAO127	gatcataccgaacagaggtaccATGGATTGGGTAGTGGG TGAT	5’ primer for -33 to +446 region of *PPG1* used for cloning into pEL9
30	MAO129	gatcataccgaacagaccgcggGGCTGACCCTTGATATT TGTTTAAG	3’ primer for -33 to +446 region of *PPG1* used for cloning into pEL9
31	DKO400	GACATATTGACCGACATAAT	5’ WT *ARG4* add-back primer
32	DKO401	CTAATGACTGAATTTGATGTA	3’ WT *ARG4* add-back primer

33	DKO404	GTCGACTATGTCATTCAAGC	5’ WT *LEU2* add-back primer
34	DKO405	CAGTTGTGTGCATATTTAGA	3’ WT *LEU2* add-back primer
35	GSO127	ATGGACGGTGGTATGTTTTAG	Split marker upstream primer for *SAT* flipper
36	GSO128	TGTTGAATCAATTGCCTTGC	Split marker downstream primer for *SAT* flipper
37	GSO129	ATAGGATCCGAAGTTCCTATACTTTCTAGAG	Forward primer for full length *SAT* flipper
38	GSO130	GTCAGATCTGAAGTTCCTATTCTC	Reverse primer for full length *SAT* flipper
39	DKO523	GTTGACCGAAGCTCCAATGAATCC	5’ primer for *ACT1* probe
40	DKO526	CAGCAATACCTGGGAACATGG	3’ primer for *ACT1* probe
41	DTO15	GACCAAGCACCTACTGTTCC	5’ primer for *ECE1* probe
42	DTO16	GATCTAGTAATGAGTTGTGG	3’ primer for *ECE1* probe
43	DTO19	CAGGAAGAACCTTGTGATTACC	5’ primer for *HWP1* probe
44	DTO20	GTTGGAACAGAAGTGTTTGG	3’ primer for *HWP1* probe
45	DK258	CAACAATCACCTCACTTGCAACCC	5’ primer for *NRG1* probe
46	DK251	GCTTCTAAAGTCCTGTGTTGTTGTC	3’ primer for *NRG1* probe
47	*MBO84	ATGACACCATGTCAAGTTCAGA	5’ primer for *ALS3* probe
48	*MBO158	CACACCAAATTGGAGGTGATT	3’ primer for *ALS3* probe

Note: Lowercase bases indicate flanking sequences which contain restriction sites for cloning.

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

Note: Underlined bases were mutated.

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.

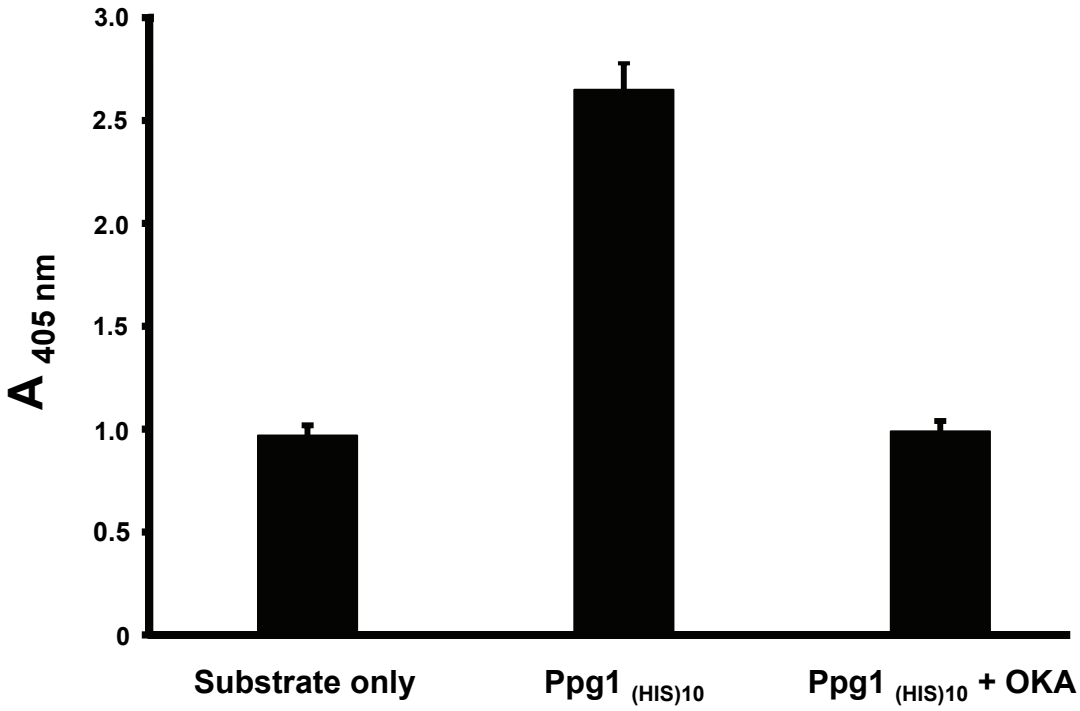

FIG S1. Ppg1 phosphatase activity is strongly inhibited by okadaic acid. Phosphatase assays were performed in the presence and absence of 1 μM okadaic acid (OKA) using the $Ppg1_{(HIS)10}$ recombinant protein.

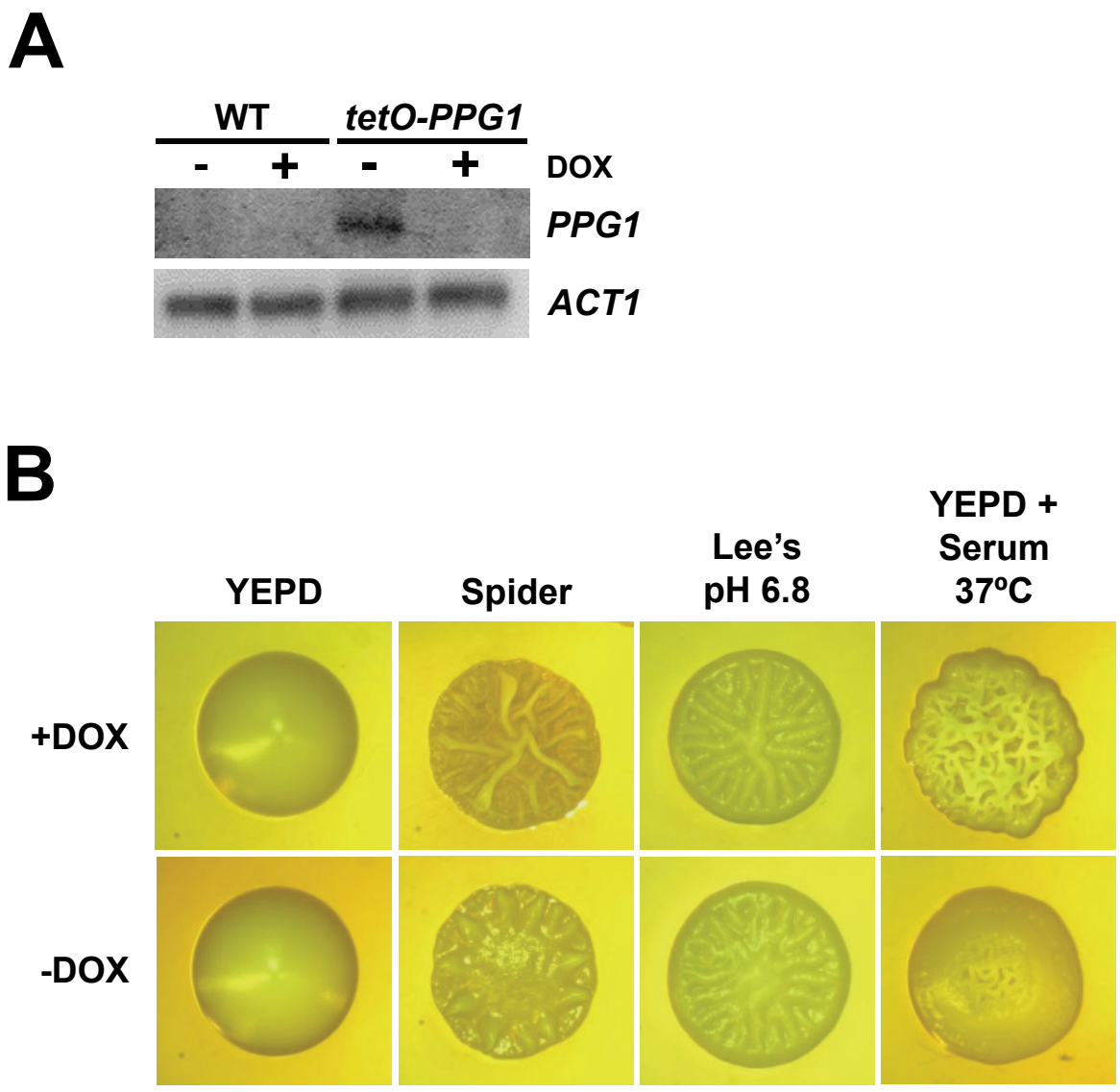

FIG S2. High-level constitutive *PPG1* expression affects colony morphology under solid filament-inducing conditions. (A) The indicated strains were grown in YEPD at 30°C overnight in the presence and absence of 20 μg/mL Dox. Cells were harvested for RNA preparation and Northern analysis. 3 μg of total RNA was loaded in each lane and the Northern blot was probed with *PPG1*. *ACT1* is shown as a loading control. (B) Colonies of the *tetO-PPG1* strain were grown on the indicated solid media at 30ºC (or 37ºC for YEPD + serum) for 2 days in the presence and absence of 20 μg/mL Dox and visualized using light microscopy.

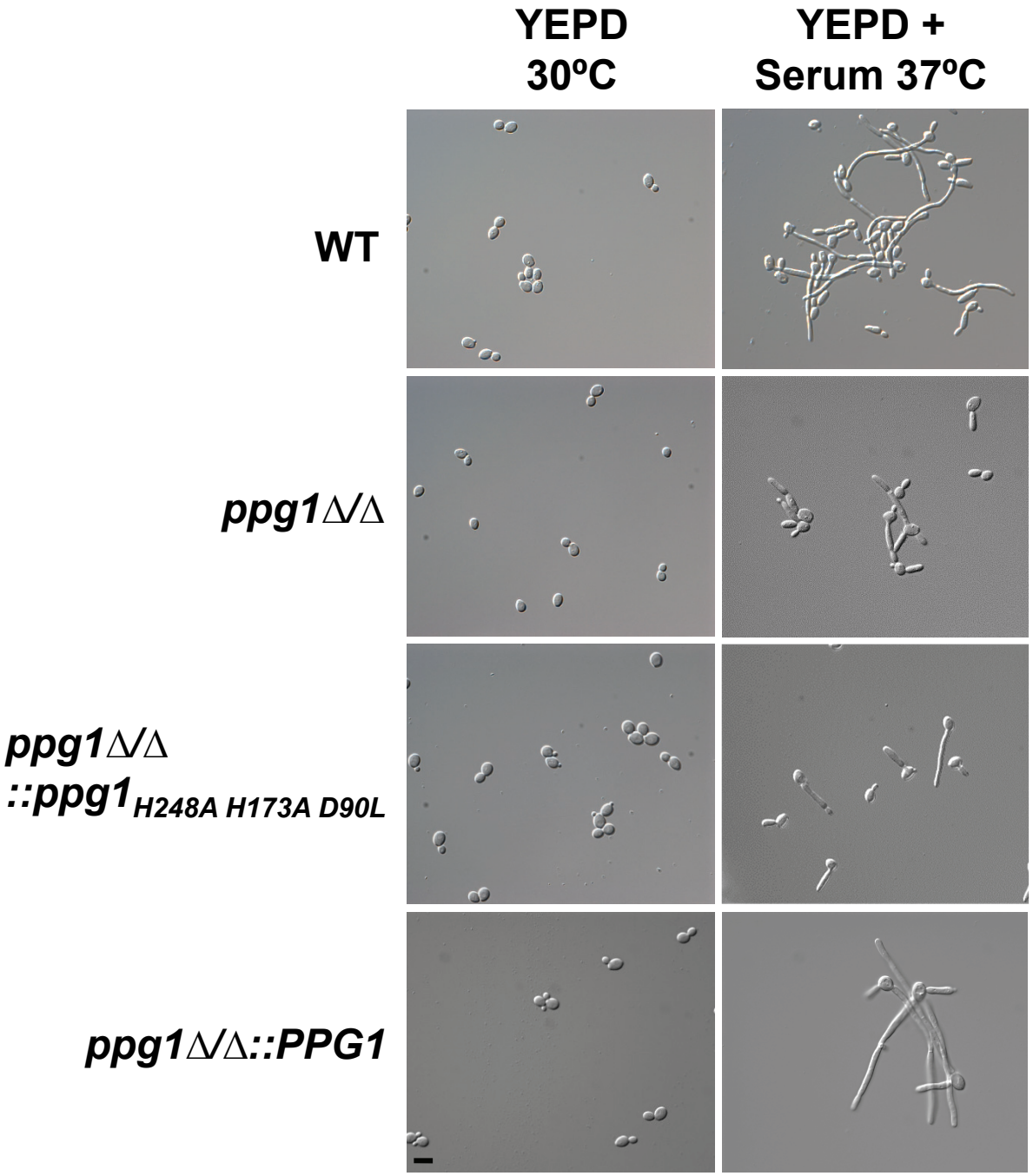

FIG S3. The *ppg1*$_{H248A\ H173A\ D90L}$ catalytic mutant shows an equivalent filament extension defect to that of the *ppg1*Δ/Δ strain. The indicated strains were grown in YEPD at 30°C overnight, diluted 1:10 into the indicated pre-warmed media and harvested at the 3 h. time point. Cells were fixed and prepared for DIC microscopy as described in Figure 3. Bar =10 μm.

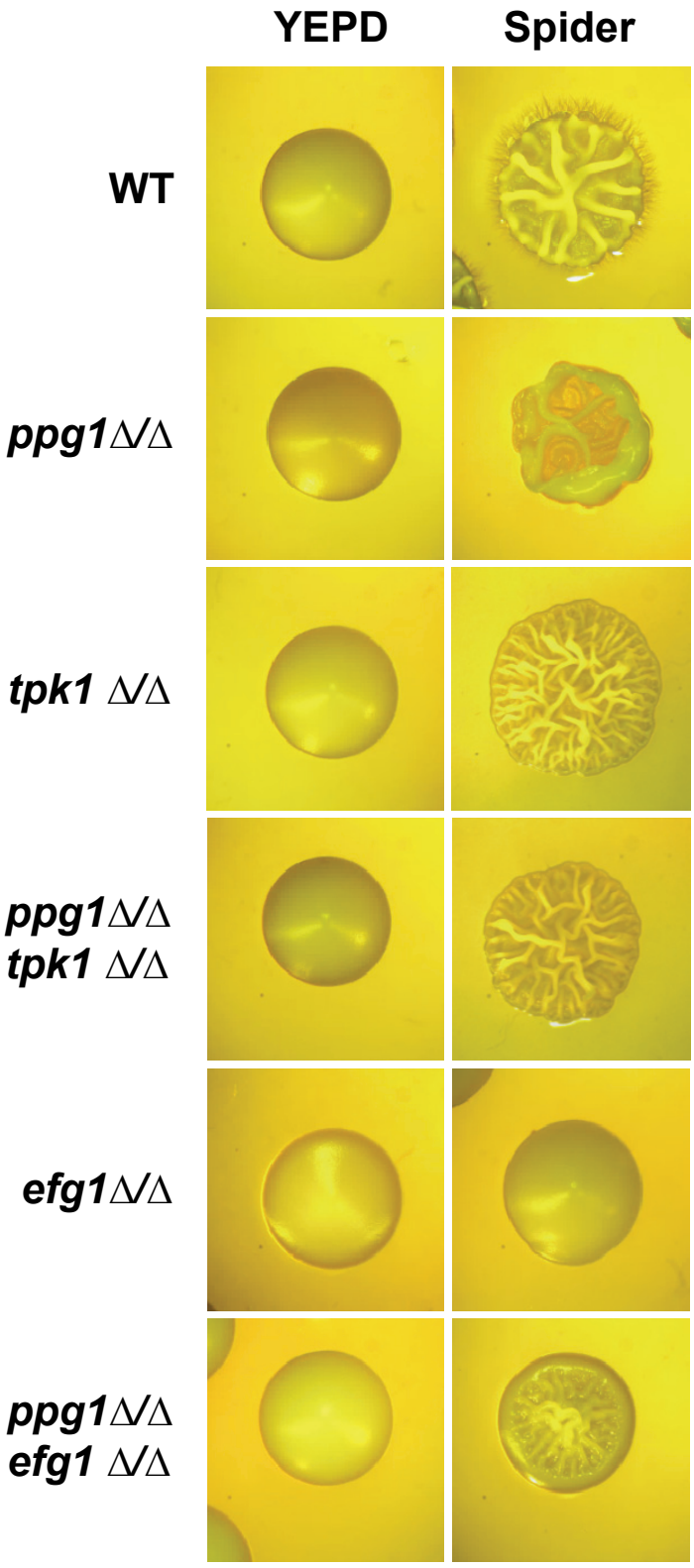

FIG S4. The *tpk1*Δ/Δ mutation is epistatic to the *ppg1*Δ/Δ mutation under solid filament-inducing conditions. The indicated strains were grown for three days on solid medium under non-filament-inducing (YEPD at 30°C) and filament-inducing (Spider at 30°C) conditions. Colonies were visualized by light microscopy.