Snaith and Sawin Supplementary Tables 1-4

Table 1: Strains used in this study

Number	Genotype	Reference
KS1	*h- 972*	Lab collection
KS136	*h- tea1Δ::ura4+ ura4-D18 ade6-M210*	Mata and Nurse, 1997
KS390	*h- pom1Δ::ura4+ ura4-D18*	Bähler and Pringle, 1998
KS410	*h- tea2-1 ura4-D18*	Browning et al, 2000
KS586	*h- mod5-1::ura4+ ura4-D18 leu1-32 ade6-M210*	This study
KS706	*h- kanMX:nmt81GFPmod5 ura4-D18 leu1-32 ade6-M210*	This study
KS708	*h- mod5Δ::kanMX ura4-D18 ade6-M216*	This study
KS714	*h- kanMX:nmt81:GFPmod5 tea1Δ::ura4+ ura4-D18 leu1-32 ade6-M216*	This study
KS715	*h+ kanMX:nmt81:GFPmod5 pom1Δ::ura4+ ura4-D18 leu1-32 ade6-M210*	This study
KS716	*h+ kanMX:nmt81:GFPmod5 tea2-1 ura4-D18 leu1-32 ade6-M210*	This study
KS780	*h+ mod5Δ::kanMX ura4-D18 leu1-32 ade6-M216*	This study
KS781	*h- tip1Δ::kanMX ura4-D18 leu1-32 ade6-M210*	Brunner and Nurse, 2000
KS886	*h+ tea1GFP:kanMX ura4-D18 leu1-32 ade6-M216*	This study
KS955	*h- bud6Δ::kanMX ura4-D18 leu1-32 ade6-M216*	Glynn et al, 2001
KS978	*h- mod5ΔCaaX:ura4+ ura4-D18 leu1-32*	This study
KS1036	*h- kanMX:nmt81:GFPmod5 bud6Δ::kanMX ura4-D18 leu1-32 ade6-M216*	This study
KS1039	*h- kanMX:nmt41:GFPmod5ΔCaaX:ura4+ ura4-D18 leu1-32*	This study
KS1160	*h- tea3Δ::kanMX ura4-D18 leu1-32*	Arellano et al, 2002
KS1171	*h- kanMX:nmt8:1GFPmod5 tea3Δ::his3+ ura4-D18 leu1-32 ade6-M216 his3-D1*	This study
KS1210	*h+ tea1YFP:kanMX ura4-D18 leu1-32 ade6-M216 p[nmt1:CFP-atb2:LEU2]*	This study
KS1211	*h+ mod5Δ::kanMX tea1YFP:kanMX ura4-D18 leu1-32 ade6-M216 p[nmt1:CFP-atb2:LEU2]*	This study
KS1218	*h- mod5Δ::kanMX tea1GFP:kanMX ura4-D18 leu1-32 ade6-M210*	This study
KS1255	*h- mod5-C519S:ura4+ ura4-D18 leu1-32 ade6 M210*	This study
KS1305	*h- kanMX:nmt81:GFPmod5 tip1Δ::kanMX ura4-D18 leu1-32 ade6-M216*	This study

Table 2: Oligonucleotide primers used in this study

OKS172	for deletion/N terminal tagging mod5, kanMX, forward primer	CCAGCTCAACTGAGGAAATTAGCGTCGCGATCCGCGTACTACTAATTGTTAGC CAAACACCGGTTTCCCAATTCCCAGTTTGAATTCGAGCTCGTTTAAAC
OKS193	for deletion mod5 deletion 3' end, kanMX, reverse primer	CGTGAACAACCATTAAATTAATTCCTTCAAGTATTACGATTTCCTTTGGATATC TGAATCCTTCATAGACACATGCTTTCGAGAATTCGAGCTCGTTTAAAC
OKS196	for N terminal GFP tagging mod5, kanMX, reverse primer	CTTCTTAAAAAATTAGCATACCTCGGATGTCTCAGGTCTCCAAAAAGAAGGAA TAGCAGGGCTTTCAGATAAAGCCGACATTTTGTATAGTTCATCCATGC
OKS215	for colony PCR kanMX, forward primer, 832 bp from end of TTEF	CCTCTTCCGACCATCAAGCATTTTATCC
OKS222	for C terminal GFP/YFP, tagging tea1, kanMX, forward primer	AGACGGATTTCATGAAGTTATTGGTTAAAAGCGGCCTCTCAAATCCTCCAGCT AAAGAACCAGTCCATGACAACGAAAATCGGATCCCCGGGTTAATTAA
OKS223	for C terminal GFP/YFP tagging tea1, kanMX, reverse primer	ATTAAGTAACTATTAAATAGCATAGAGATTGAGGGCTACCAGTTTAAAATGTA ATTTATTTATAGATGTCATCGTCGAATGAATTCGAGCTCGTTTAAAC
OKS237	for deletion of prenylation motif mod5, ura4+, forward primer	ACACCAGTACCTAAAGAAAAACCTTCTGAAAAAAGTGAAAAACCTCCTAAAA AGAAAGGTTCCAAATTAGAGAAGTTTTGTCGCCAGGGTTTTCCCAGTCACGAC
OKS238	for deletion prenylation motif mod5, ura4+, reverse primer	CGTGAACAACCATTAAATTAATTCCTTCAAGTATTACGATTTCCTTTGGATATC TGAATCCTTCATAGACACATGCTTTCGAAGCGGATAACAATTTCACACAGGA
OKS239	for colony PCR of tea1 GFP/YFP, kanMX, reverse primer	CTCGTGATCCAAAGCGTTTGC
OKS243	for colony PCR of mod5 N terminal tags, reverse primer	GTGTCTTGAAATGAGTATGC
OKS331	for mutation of mod5 C519S, +ura4, forward primer	GAAAAACCTTCTGAAAAAAGTGAAAAACCTCCTAAAAAGAAAGGTTCCAAAT TAGAGAAGTTTTGTTCTATTTTGATGTAACGCCAGGGTTTTCCCAGTCACGAC

Table 3: Percent cells with altered morphology during polarity re-establishment on solid media (see Methods for further information)

Strain	normal	abnormal	branched	cells scored
wild-type (KS1)	99%	0.4%	0.2%	500
*tea1*Δ (KS136)	46%	13%	41%	500
*mod5*Δ (KS708)	93%	3.4%	4.6%	500

Table 4: Percent cells with a curling microtubule at cell ends, at different temperatures (see Methods for further information)

Strain	25°C	30°C	36°C	25°C shift to 36°C (6 hr)
wild-type (KS1)	0% (869 cells)	0.1% (784)	2.3% (919)	3.5% (779)
*tea1*Δ (KS136)	1.4% (774)	3.0% (792)	15.2% (624)	17.5% (740)
*mod5*Δ (KS708)	0.6% (713)	1.3% (827)	5.5% (789)	6.4% (782)