

**Figure S1** S288c with  $FLO11pr^{Sigma}$ ::FLO11 is still fMAPK independent. qPCR assay of FLO11 transcript levels was performed on (A) S288c and (B) Sigma strains carrying FLO11 promoter swaps. Mean FLO11 levels normalized to ACT1 levels are presented ± SD. Strains with their endogenous FLO11 promoter are labeled with their relevant genotype. Strains carrying a swapped FLO11 promoter are labeled numerically: (1) S288c FLO11pr<sup>Sigma</sup>::FLO11; (2) S288c FLO11pr<sup>Sigma</sup>::FLO11, tec1\Delta; (3) Sigma FLO11pr<sup>S288c</sup>::FLO11; (4) Sigma FLO11pr<sup>S288c</sup>::FLO11.



# Washed



**Figure S2** *tec1* bypass is a complex trait. Agar adhesion assays of 24 tetrads from an S288c *tec1* x Sigma *tec1* cross. Two complete tetrads per row with one example underlined. Parental strains and controls spotted on the bottom of the plate. The same plate is shown before and after washing.



**Figure S3** fMAPK bypass of *FLO11* expression is a complex quantitative trait. GFP fluorescence, measured in arbitrary units for (A) 276 F1 meiotic progney from a S288c / Sigma *FLO11pr::GFP / FLO11pr::GFP tec1Δ / tec1Δ* diploid or (B) 276 meiotic progeny from the third generation of backcrossing (see methods). The average GFP fluorescence normalized to OD600 of 3 biological replicates are plotted. The progeny are sorted from highest to lowest fluorescence. Fluorescence of control strains are labeled and shown in green.



**Figure S4** Regulation of adhesion differs between S288c and Sigma. Adherent, wild-type S288c and Sigma were crossed and from 24 complete tetrads, 15/96 progeny show an adhesion defect. Each column contains two complete tetrads.

# RPI1



**Figure S5** *RPI1* contains intragenic repeats. Dot plot analysis of the S288c allele of *RPI1* nucleotide sequence compared against itself. Repeat regions produce a characteristic box pattern. The horizontal bar represents 100 nt. The plot was generated using http://www.vivo.colostate.edu/molkit/dnadot/ with a windows size of 9 and a mismatch limit of 2.

## А

#### Repeat #1

S288c	TCC	AGT	TCA	AAT	TCG.	AAT	TCG	AAC	TCC	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC
w303	TCC	AGT	TCA	AAT	TCG.	AAT	TCG	AAC	TCC	AAI	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC
SK1	TCC	AGT	TCA	AAT	TCG.	AAT	TCG	AAC	TCC	AAI	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC
NCYC110	TCC	AGT	TCA	AAT	TCG.	AAT	TCG	AAC	TCC	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC
YJM789	TCC	AGT	TCA	AAT	TCG.	AAT	TCG	AAC	TCC	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC
RM11	TCC	AGT	TCT	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC						
y55	TCC	AGT	TCT	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC						
Sigma	TCC	AGT	TCT	AAT	TCT	AAT	TCG	AAC	TCC	AAC	TCC	AAC						
	s	s	s	N	s	N	s	N	s	N	s	N	s	N	s	N	s	N

## В

#### Repeat #2

S288c	ACCARGATEGETACTAATGATAATAATAATAATAACAATAATAATAATAATAATAATAA
w303	AACAAGAATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
SK1	AACAAGAATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
NCYC110	AACAAGAATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
YJM789	AACAAGAATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
RM11	AACAAGAATGGTACTAATGATAATAATAATAACCATTATTAATAATAATAATAATAATA
y55	AACAAGGATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
Sigma	ARCARGATGGTACTAATGATAATAATAATAATAATAATAATAATAATAATAAT
	N K N G T N D N I N N H Y Y N N S N N N N N N N N N N N N N N N

**Figure S6** Comparison of *RPI1* repeat regions between different *S. cerevisiae* strains. The sequences for the repeat regions from *RPI1* were aligned using ClustalW. (A) 5' repeat region and (B) central repeat region. For repeat #1 the translation for the S288c sequence is shown, and for repeat #2 the translation for the Sigma sequence is shown. Strain names in blue are wild isolates and nucleotides in red represent nucleotide polymorphisms. In S288c, the repeats account for 16% of the coding sequence (195/1224 bases). The 5' repeat region consists of a hexanucleotide repeat. In S288c there are nine repeated units while in Sigma there are only six repeated units. The central repeat region consists of a trinucleotide repeat. In S288c there are 46 repeated units but in Sigma they have expanded to 63 repeated units. Both repeats encode primarily for serines and asparagines.



**Figure S7** Many genes have intragenic tandem repeats that differ in size between S288c and Sigma. Four of five gels used to examine the length differences between S288c and Sigma for 24 genes and *FLO8* which was used as a control for a gene without repeats. 22/24 genes had the predicted repeat length differences. The gene *SNF5* has two repeat regions that both changed in size. For each pair the left sample is S288c and the right sample is Sigma.

## Table S1 Deletions leading to an Ahs- phenotype only in S288c.

YAL054C
YNL020C
YOR043W
YDR226W
YBL080C
YKR039W
YBR068C
YDR127W
YPR060C
YPR020W
YLR431C
YCR002C
YAR030C
YBL031W
YBL046W
YBR033W
YBR139W
YCL005W
YCL036W
YCR016W
YCR095C
YDL021W
YDL073W
YDR003W
YDR248C
YDR514C
YER039C
YER048C
YER060W
YFL015C
YGL214W
YGR071C
YHL017W
YHR080C
YHR210C
YIL059C
YIL086C
YIR014W

YIR020C
YJL218W
YJR018W
YJR054W
YJR080C
YKL023W
YKL044W
YKL090W
YKL094W
YLL030C
YLL055W
YLR021W
YLR065C
YLR125W
YLR168C
YLR184W
YLR352W
YLR358C
YLR374C
YLR434C
YML010C-B
YML010W-A
YMR135W-A
YMR158C-B
YMR191W
YMR316C-A
YMR326C
YNL023C
YNL170W
YNL175C
YNL226W
YNR025C
YOL032W
YOL042W
YOL048C
YOL159C
YOR021C
YOR029W

YOR082C
YOR154W
YOR183W
YOR186W
YOR200W
YOR225W
YOR258W
YOR285W
YPL017C
YPL068C
YPL182C
YPL184C
YPL216W
YPL220W
YPL246C
YPL257W
YPL260W
YPR170C
YER086W
YDR200C
YCL058C
YBL006C
YPR030W
YER083C
YCR017C
YGL027C
YHR181W
YDL225W
YBR200W
YHL003C
YLL026W
YJR060W
YDR176W
YGL066W
YLR055C
YNL107W
YDR485C
YML041C

YBR231C
YBR289W
YDR073W
YDR334W
YJL176C
YOR290C
YOL012C
YDL074C
YDR469W
YDR207C
YBR107C
YDR254W
YDR318W
YGR275W
YPR046W
YER068W
YAL012W
YER056C
YMR032W
YNL166C
YNL229C
YLR420W
YML106W
YJL115W
YOL090W
YLR418C
YBR228W
YGL058W
YML021C
YOR144C
YDR364C
YCL061C
YMR048W
YBL082C
YKL213C
YDR069C
YDR320C
YNR006W

YDR432W
YDR195W
YGR019W
YPR101W
YJR117W
YPR049C
YOL044W
YGR004W
YNL173C
YER053C
YFL031W
YAL013W
YDR174W
YNR052C
YKL043W
YJL129C
YDL230W
YJL183W
YKL139W
YIL148W
YGL236C
YCL037C
YDR500C
YHL033C
YKL167C
YLR185W
YNL265C
YOR096W
YOR182C
YPL090C
YOR138C
YHR034C
YOR288C
YMR091C
YER110C
YGL153W
YIR004W
YLR024C
YGL203C

YPR087W
YER020W
YML035C
YBR221C
YIL119C
YKL109W
YAL024C
YER059W
YPL219W
YMR179W
YML014W
YOL105C
YOR008C
YGL244W
YHR087W
YNR060W
YBL075C
YGR055W
YGL033W
YLR453C
YGR104C
YHR041C
YPL144W
YPL258C
YNL248C
YJL189W
YGR054W
YNL125C
YOR081C
YPL212C
YDR354W
YKL211C
YCL075W
YDR330W
YHL016C
YPR036W
YLR373C
YMR174C
YHL019C

YBR053C

## Table S2 Deletions leading to an Ahs- phenotype only in Sigma.

YKR024C
YHR114W
YML022W
YLR278C
YGL258W
YGR271C-A
YML117W
YOR267C
YMR044W
YOR213C
YMR127C
YCR009C
YCR088W
YIL034C
YMR008C
YGR040W
YGL014W
YDR005C
YNL053W
YOR002W
YOR067C
YDL159W
YGL019W
YGR188C
YLR362W
YHR021C
YPR043W
YBR189W
YGR232W
YER118C
YMR312W
YPL101W
YKL143W
YDR184C
YDL190C
YEL060C
YDL005C
YGL025C

YGR162W
YAL048C
YPL259C
YLR370C
YNL271C
YMR267W
YDR079W
YDR529C
YPL132W
YLR204W
YLR315W
YER156C
YLR375W
YFR048W
YGL188C-A
YGL211W
YGL228W
YKL037W
YOR141C
YKL110C
YDR276C
YBL007C
YBR245C
YGR062C
YLR337C
YLR056W
YGR014W
YGR037C
YHL038C
YGL252C
YAL002W
YOR334W
YOL115W
YGL003C
YPL005W
YDR140W
YAL023C
YDR477W

YPL031C
YDL044C
YBR191W
YGR105W
YKL119C
YOR085W
YNR051C
YEL059C-A
YPL086C
YPL024W
YIL008W
YFR019W
YPL193W
YJL124C
YPR040W
YDR512C
YNL098C
YOL051W
YDR289C
YGR257C
YLL041C
YNL037C
YOR136W
YEL051W
YKL080W
YDL067C
YLR295C
YBL099W
YDR298C
YBL066C
YBR162C
YLR404W
YNL097C
YGR180C
YCR086W
YDR129C
YML008C
YGL084C

YIR021W
YER161C
YGR123C
YDL069C
YDR197W
YML024W
YBR165W
YER154W
YLR384C
YDR074W
YHL034C
YDR096W
YDL081C
YOL023W
YIL125W
YDR120C
YGR020C
YOR332W
YFL054C
YGR272C
YBR026C
YHR011W
YCR105W
YPR116W
YCR079W
YER014C-A
YLR390W-A
YGR229C
YDR359C
YLR385C
YOL068C
YMR263W
YCR077C
YHR120W
YER061C
YHR067W
YBL071W-A
YER014W

YBR163W
YER087W
YGL107C
YGR102C
YMR066W
YMR098C
YOR205C
YLR443W
YIL084C
YOR330C
YLR382C
YKL134C
YNL073W
YGR171C
YCR028C-A
YDR296W
YOL095C
YGL219C
YNL213C
YGR101W
YLL006W
YOL009C
YOR211C
YML062C
YLR435W
YDL090C
YBR146W
YBL038W
YBR251W
YBR268W
YBR282W
YCR003W
YCR024C
YCR046C
YCR071C
YDL045W-A
YDR237W
YDR322W
YDR347W

YDR405W
YER050C
YGR215W
YHR147C
YHR168W
YIL093C
YKL003C
YKL138C
YKL155C
YKL170W
YKR006C
YLR312W-A
YLR439W
YMR024W
YMR193W
YNL005C
YNL081C
YNL252C
YPL173W
YPR047W
YBL090W
YDR115W
YDR337W
YEL050C
YGL143C
YGR165W
YGR220C
YHR091C
YJL063C
YKR085C
YLR139C
YMR097C
YNL177C
YOR150W
YPR100W
YPL002C
YBL022C
YBR083W
YGL064C

YMR287C
YPL029W
YML055W
YLL033W
YMR228W
YJL102W
YLR069C
YOR187W
YDR470C
YDR268W
YPL097W
YPL019C
YGR219W
YAL004W

 Table S3
 Deletions leading to an Ahs- phenotype only in both S288c and Sigma.

YKL007W
YBR023C
YPL203W
YBL058W
YGR056W
YOL001W
YOL072W
YLR357W
YOL076W
YPL181W
YDR350C
YMR154C

YKR001C
YKL185W
YNL183C
YDR392W
YOR035C
YJL140W
YHR167W
YKL204W
YJR113C
YCL008C
YJR102C
YOL004W

YDR065W
YMR116C
YDL233W
YEL007W
YGR122W
YBR095C
YOR275C
YOR030W
YLR025W
YMR077C
YCR084C
YDL006W

YDR462W	
YNR037C	
YLR417W	
YMR164C	
YGR200C	
YGR063C	
YMR063W	
YHL027W	
YNL294C	
YJL175W	

## Table S4 ORFs with intragenic repeat length differences between S288c and Sigma.

YAL035W
YAL064W-B
YBL011W
YBR017C
YBR030W
YBR212W
YCR067C
YDL005C
YDL035C
YDL122W
YDR133C
YDR134C
YDR232W
YDR273W
YDR299W
YEL007W
YFL024C
YFL033C
YGL013C
YGL237C
YGR014W
YHL020C
YHR030C
YJL187C
YKL023W
YKL108W
YKL163W
YKR072C
YLL008W
YLR175W
YLR330W
YML074C
YMR070W
YMR136W
YMR164C
YNL186W
YOL051W
YOR053W

YOR156C
YOR290C
YPL049C
YPL229W
YPR142C
YPR143W
YPR152C
YAL065C
YAR050W
YBR289W
YCL043C
YDL037C
YDL039C
YDL058W
YDR093W
YDR150W
YDR420W
YDR517W
YER011W
YER030W
YER075C
YFL010C
YFL010W-A
YGL014W
YGR160W
YHL028W
YHR077C
YIL011W
YIL031W
YIL115C
YIL119C
YIR010W
YIR019C
YIR023W
YJL020C
YJL078C
YJL123C
YJL130C

YJL162C
YKL028W
YKL032C
YKL105C
YKR092C
YKR102W
YLL010C
YLR055C
YLR106C
YLR114C
YLR177W
YLR406C-A
YML049C
YML113W
YMR016C
YMR044W
YMR124W
YMR173W
YMR173W-A
YMR317W
YNL271C
YNL327W
YNR052C
YOR010C
YOR054C
YOR113W
YOR267C
YPL216W
YPR021C
YPR123C
YPR124W

## Table S5 List of strains used in this study

Strain	Genotype	Source
BY4741	S288c MATa his3 $\Delta$ 1 leu2 $\Delta$ 0 ura3 $\Delta$ 0 met15 $\Delta$ 0 flo8-1	Brachmann et al. (1998)
уВС37	S288c MATa his3Δ1 leu2 $\Delta$ 0 ura3 $\Delta$ 0 met15 $\Delta$ 0 FLO8	this study
yBC06A10	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 FLO8 tec1Δ::KanMX4	this study
yBC06B5	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 FLO8 ste7Δ::KanMX4	this study
yBC06G7	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 FLO8 ste11Δ::KanMX4	this study
уВС07АЗ	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 FLO8 kss1Δ::KanMX4	this study
yBC06B5	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 FLO8 ste12Δ::KanMX4	this study
уВС0192	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 flo11pr <sup>S288c</sup> Δ::FLO11pr <sup>Sigma</sup> FLO8	this study
уВС0195	S288c MAT <b>a</b> his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 flo11pr <sup>S288c</sup> Δ::FLO11pr <sup>Sigma</sup> tec1Δ::KanMX4 FLO8	this study
yBC11E2	S288c MATa his3 $\Delta$ 1 leu2 $\Delta$ 0 ura3 $\Delta$ 0 met15 $\Delta$ 0 flo11 $\Delta$ ::GFP-URA3 FLO8	this study
yBC11H2	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 flo11Δ::GFP-URA3 tec1Δ::KanMX4 FLO8	this study
yBC16A3	S288c MATa ura3Δ0 FLO8	this study
yBC16F4	S288c MATa / $\alpha$ ura3Δ0/ura3Δ0 FLO8/FLO8	this study
yBC20A1	S288c MATa ura3Δ0 tec1Δ::hyg FLO8	this study
yBC20D1	S288c <i>MATα ura3</i> Δ0 <i>tec1</i> Δ::hyg <i>FLO8</i>	this study
yBC20A3	S288c MATa /α ura3 $\Delta$ 0/ura3 $\Delta$ 0 tec1 $\Delta$ ::hyg/tec1 $\Delta$ hyg FLO8/FLO8	this study
yBC11E8	S288c MATa his3 $\Delta$ 1 leu2 $\Delta$ 0 ura3 $\Delta$ 0 met15 $\Delta$ 0 flo11 $\Delta$ ::HIS3PEST FLO8	this study
yBC11H8	S288c MATa his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 flo11Δ::HIS3PEST tec1Δ::KanMX4 FLO8	this study
yBC18A1	S288c MATa ura3Δ0 rpi1Δ::URA3 FLO8	this study
yBC18A6	S288c MATa ura3Δ0 rpi1Δ::RPI1 <sup>Sigma</sup> FLO8	this study
yBC18A8	S288c MATa ura3Δ0 rpi1Δ::RPI1 <sup>Sigma</sup> tecΔ1::KanMX4 FLO8	this study
yBC29A9	S288c MATa ura3Δ0 RPI1-3xFLAG-URA3 FLO8	this study
yBC29D9	S288c MATa ura3Δ0 rpi1Δ::RPI1 <sup>Sigma</sup> -3xFLAG-URA3 FLO8	this study
10560-6B	Sigma MATα his3::hisG leu2::hisG trp1::hisG ura3-52	Fink Collection
yBC0172	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52	this study
Sigma <i>tec1∆</i>	MAT <b>a</b> can1Δ::STE2pr-Sphis5 lyp1Δ::STE3pr-LEU2 his3::hisG leu2Δ ura3Δ tec1Δ::KanMX4	Dowell and Ryan et al. (2010)
Sigma <i>ste7∆</i>	MAT <b>a</b> can1Δ::STE2pr-Sphis5 lyp1Δ::STE3pr-LEU2 his3::hisG leu2Δ ura3Δ ste7Δ::KanMX4	Dowell and Ryan et al. (2010)
Sigma <i>ste11∆</i>	MATa can1Δ::STE2pr-Sphis5 lyp1Δ::STE3pr-LEU2 his3::hisG leu2Δ ura3Δ ste11Δ::KanMX4	Dowell and Ryan et al. (2010)
Sigma <i>kss1∆</i>	MAT <b>a</b> can1Δ::STE2pr-Sphis5 lyp1Δ::STE3pr-LEU2 his3::hisG leu2Δ ura3Δ kss1Δ::KanMX4	Dowell and Ryan et al. (2010)

Sigma <i>ste12∆</i>	MATa can1Δ::STE2pr-Sphis5 lyp1Δ::STE3pr-LEU2 his3::hisG leu2Δ ura3Δ	Dowell and Ryan et al.
	<i>ste12Δ</i> ::KanMX4	(2010)
yBC0193	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52	this study
	flo11pr <sup>Sigma</sup> Δ::FLO11pr <sup>S288c</sup>	
yBC0196	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52	this study
	$flo11$ pr <sup>3gille</sup> $\Delta$ ::FLO11pr <sup>3200C</sup> tec1 $\Delta$ ::KanMX4	
yBC11G1	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52 flo11A::GFP-URA3	this study
yBC11B2	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52 flo114::GFP-URA3	this study
	<i>tec1∆</i> ::KanMX4	
уВС16Н3	Sigma MAT <b>a</b> ura3-52	this study
yBC16B4	Sigma MATα ura3-52	this study
yBC16G4	Sigma <i>MAT</i> <b>a</b> /α ura3-52/ura3-52	this study
yBC20G1	Sigma <i>MAT<b>a</b> ura3-</i> 52 <i>tec1</i> ∆::hyg	this study
yBC20B2	Sigma MATα ura3-52 tec1Δ::hyg	this study
yBC20C3	Sigma MATa /α ura3-52/ura3-52 tec1Δ::hyg/tec1Δhyg FLO8/FLO8	this study
yBC11A7	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52 flo11A::HIS3-PEST	this study
yBC11D7	Sigma MATa his3::hisG leu2::hisG trp1::hisG ura3-52 flo11A::HIS3-PEST	this study
	tec1∆::KanMX4	
yBC18G1	Sigma MAT <b>a</b> ura3-52 rpi1∆::URA3	this study
yBC18G6	Sigma MATa ura3-52 rpi1Δ::RPI1 <sup>S288c</sup>	this study
yBC18G8	Sigma <i>MAT<b>a</b> ura3-</i> 52 <i>rpi1</i> ∆:: <i>RPI1<sup>Sigma</sup> tec</i> ∆1::KanMX4	this study
yBC29G9	Sigma MATa ura3-52 RPI1-3xFLAG-URA3	this study
yBC29B10	Sigma MATa ura3-52 rpi1∆::RPI1 <sup>Sigma</sup> -3xFLAG-URA3	this study
yBC09H1	S288c <sup>FL08</sup> /Sigma MAT <b>a</b> /α ura3Δ0/ura3-52 his3Δ0/his3::hisG	this study
	leu2∆0/leu2::hisG met15∆0/MET15 TRP1/trp1::hisG	
	tec1A::hyg/tec1A::hyg flo11A::GFP-URA3/flo11A::GFP-URA3	
yBC03A10	S288c <sup>FL08</sup> /Sigma MATa /α ura3Δ0/ura3-52 his3Δ0/his3::hisG	this study
	met15∆0/MET15 tec1∆::KanMX4/tec1∆::KanMX	

## Table S6 List of oligonucleotides used in this study

Name	Sequence (5' to 3')	Description
BCP10	agtgcttaaccggaacaaacc	FLO8F
BCP15	tatgatcatgatttacgatgaccgt	FLO8R
BCP46	ggaaacaagctgagctggac	Flanking TEC1
BCP47	tcgtggtttcatccaagtga	Flanking TEC1
BCP191	cccaagcgagacctagagtg	Flanking STE12
BCP192	gaacatcgatgccttcacct	Flanking STE12
BCP195	aagtgattcgtggggtaacg	Flanking STE7
BCP196	tgggttattaatcgccttcg	Flanking STE7
BCP199	attctcgcccaacttttcct	Flanking STE11
BCP200	tcttcgtgcttccatctgtg	Flanking STE11
BCP236	tccccttggtgaaagaaatg	Flanking <i>kss1</i>
BCP237	ttgattacagtcgcgtcagc	Flanking kss1
BCP249	GGTTCTAATTAAAATATACTTTTGTAGGCCTCAAAAATCCATATACGCACACTatgac	to replace the <i>FLO11</i> ORF
	agagcagaaagccctag	with <i>HIS3</i>
BCP257	tgatgagggtgaagggaaac	RPI1 swap
BCP316	ggtGCATCCAACTTGAACATTTCGAGAAAGC	For amplifying PEST seg from
		CLN2
BCP317	CTATATTACTTGGGTATTGCCCATACC	For amplifying PEST seg from
501517		CIN2
BCD320		linearize nRS212 to add REST
DCF 320		sea from CIN2
BCP321	GGTATGGGCAATACCCAAGTAATATAGtgacaccgattatttaaagctg	linearize pRS313 to add PEST
		seq from CLN2
BCP324	atttaagaatgaaaacatcgtaatgaagaaacgaacatgttggaattgtatcaCTATATTACTTGGGT	To replace FLO11 with
		HIS3PEST
BCP358		rpi1::ura3
BCP359		rni1…ura3
20.000	gtatttcacaccg	
BCP360	cgtattcgtttaactatttctcagtcc	RPI1 swap
BCP412	ctcaacagcagatccagcag	MSS11F repeats
BCP413	gaaggcataagtccggttga	MSS11R repeats
BCP419	cattgaagccgaacaagaatg	RPI1F repeats
BCP420	cttgactgaatatgctctggtg	RPI1R repeats
BCP423	tgcaagatttcaggctgttt	SLT2F repeats
BCP424	atccacatctgaaggctgct	SLT2R repeats
BCP534	GACTACAAGGATGATGACGATAAAGGTGACTATAAAGATCATGACATTGATTATA	to build a C terminal flag
	AAGACCATGACTAAgcaggtcgacaacccttaat	tagging construct
BCP535	GCGGCCGCATAGGCCACT	to build a C terminal flag
		tagging construct
BCP536	ACCGTTGCATAATATGTCAACTTCAGACTCAGAAAATTTTATGCAACAACATgactac	C-terminally tag RPI1 with
	aaggatgatgacgata	FLAG
BCP537		C-terminally tag RPI1 with
	gcataggccact	FLAG
		· · · ·
BCP572	cattaaacccgtggaacagc	GAL11F repeats
BCP573	gggaataggtgccactttca	GAL11R repeats

BCP574	ctgaatgggtggatccaaat	URA2F repeats
BCP575	agaacagatggatcacctgga	URA2R repeats
BCP576	gaaccggcaagacttaacca	EPL1F repeats
BCP577	ttctgtttcgcttctgaattg	EPL1R repeats
BCP580	ggacaggagcaggaagaaaa	NUP159F repeats
BCP581	tccgaatgcagatgtaccaa	NUP159R repeats
BCP584	atgggcataaacggtgacat	VHS3F repeats
BCP585	agatcgctgtagccctcctt	VHS3R repeats
BCP586	aacctgcacaggaaacatcc	TFA1F repeats
BCP587	ctgaagcagtggcagtagca	TFA1R repeats
BCP588	cccacgactacaagcacaaa	WSC4F repeats
BCP589	cttgtagaaatgggggctga	WSC4R repeats
BCP628	aaggctgcagtggtcaagtt	DNF2F repeats
BCP629	atatctgaactgcccgatgg	DNF2R repeats
BCP632	tacaatcccacgcagtttca	ULP2F repeats
BCP633	ttccgtagttgcatcatcaaa	ULP2R repeats
BCP634	gctggaaaacgactcaaagc	SPT8F repeats
BCP635	agcagccttttgctcatcat	SPT8R repeats
BCP636	atgatgagcaaaaggctgct	SPT8F repeats
BCP637	tccattagcagaggcttcgt	SPT8R repeats
BCP638	ctgtgtcaggacgccataga	RIM15F repeats
BCP639	tccttggggaaaactgaaaa	RIM15R repeats
BCP640	tcaaatgtgatgccaggttc	SNF2F repeats
BCP641	ttgctcggcagtaaacattg	SNF2R repeats
BCP642	agtacggggaccttgaacct	SWE1F repeats
BCP643	tacgagaatccacgctttcc	SWE1R repeats
BCP644	cagctggtgttcagggaaat	PTP3F repeats
BCP645	ccaaatcaggccaatttttc	PTP3R repeats
BCP646	acaacggcgatgaaaagaat	MED2F repeats
BCP647	tgccgttatcgtcattgttg	MED2R repeats
BCP648	aggctggataacctgcaaga	DSN1F repeats
BCP649	ttgcagtcgcatctccacta	DSN1R repeats
BCP650	caagaccattcgctgcagta	IXR1F repeats
BCP651	taaggcgcttgttgttgttg	IXR1R repeats
BCP654	atgggaactccaaccgtaca	PGD1F repeats
BCP655	agtcgactgctgtgcgtaga	PGD1R repeats
BCP656	ccaataacaccccgctacag	PGD1F repeats
BCP657	tactgtggttgaggctgctg	PGD1R repeats
BCP658	tagtttgaaggaacgcgaca	UBP10F repeats
BCP659	gaacccaagttttcaccaatg	UBP10R repeats
BCP660	atgattcagcaacgacacca	SNF5F repeats

BCP661	aggaggagggtagaagtcg	SNF5R repeats
BCP662	tgttgcacaacaagtgc	SNF5F repeats
BCP663	gctgttgtcgctgtatttgg	SNF5R repeats
<i>FLO11</i> FW	cacttttgaagtttatgccacaaag	<i>FLO11</i> qPCR
<i>FLO11</i> RV	cttgcatattgagcggcactac	<i>FLO11</i> qPCR
ACTI FW	ctccaccactgctgaaagagaa	ACT1 qPCR
ACTI RV	ccaaggcgacgtaacatagtttt	ACT1 qPCR