Supplemental Table 1. Expanded clones from YJK146 $(CAG)_{140}$ sequenced for repeat integrity.

Clone	Repeats added	Forward repeats sequenced	Reverse repeats sequenced	Flanking forward ~330bp	Flanking reverse ~420bp
1	73	107	127	+	+
2	95	148	95	+	+
3	27	113	109	+	+
4	93	174	135	+	+
5	142	111	147	+	+
6	88	81	140	+	+
7	70	96	113	+	+
8	73	82	139	+	+
9	145	104	117	+	+
10	59	77	125	+	+
11	91	138	182	+	+
12	75	168	179	+	+
13	77	167	148	+	+
14	94	171	142	+	+
15	101	169	158	+	+
16	98	194	185	+	+
17	62	170	146	+	+
18	70	137	114	+	+
19	98	173	141	+	+
20	92	175	133	+	+
21	88	174	131	+	+

Supplemental Table 2. Non-selective instability of YJK146 $(CAG)_{140}$ strain.

		Expansions		Contractions	
Strain **media**	**Total PCRs**	**#**	**%**	**#**	**%**
WT glucose	95	1	1.1	5	5.3
WT galactose	143	1	0.7	25	17.5

3.3-fold difference in contraction frequency for $(CAG)_{140}$ grown on glucose compared to galactose; Fisher's exact test p-value 0.0153

Supplemental Table 3. Primers used in this study.

Name	Sequence	Notes
JK109_CAG_NcoI	agctccatggGCCGCCAGTGTGATGGATAGC	CAG cloning
JK110_CAG_NotI	agctgcggccgcGGCTTTTGCAAAAAGCTCTGCAGATC	CAG cloning
FlankL	CCTTTGCCATTTATTGTCGC	CAG sequencing
CanF	TGCTTCTCCTCTATGTCGGC	CAG sequencing
JK161_tetbal_fwd	agctccatggcctaggGCTACTTGGAGCCACTATCGAC	CAG spacer, no repeat cloning
JK162_T50_rev	agctccatggcctaggGCTACTTGGAGCCACTATCGAC	CAG spacer cloning
JK163_T100_rev	agctccatggtaccGGACGGGTGTGGTCGCCATGAT	CAG spacer cloning
JK164_T150_rev	agctccatggtaccTGTGGCGCCGGTGATGCCGGCC	CAG spacer cloning
JK165_T340_rev	agctgcatgcggtaccCATCGGTCGACGCTCTCCCT	No repeat cloning
TrpS-F	TCGATTTCTGACTGGGTTGGAAG	Verify ChrIII integration
36a-R	TAGCATACGTGTAATGATAGACGATTTTC	Verify ChrIII integration
A36b-F	ACGTGTACAGTTCTCTTTACATCATC	Verify ChrIII integration
JK153_CAN140_fwd	GTGATGGATAGCAGCAGCAG	CAG repeat length
JK171_CAG140_rev	GCATGCGGCTTTTGCAAAAAGCTC	CAG repeat length
JK316_CAG140_fwd	TAGTGGCTCCAAGTAGCCCTAG	CAG repeat length
JK317_CAG140_rev	GTAGTAGGTTGAGGCCGTTGAG	CAG repeat length
JK318_CAG140_fwd	CCGCACTGCTCCGAACAATC	CAG repeat length
JK319_CAG140_rev	GAAGCAGCCCAGTAGTAGGTTG	CAG repeat length
JK167_CAN1_fwd	GGCCGCTCTAGAACTAGTGGAT	CAN1 sequencing
JK168_CAN1_rev	CTCTTGGAACGGATTTTCTGG	CAN1 sequencing
JK169_CAN1_fwd	GTTTTAGCCATTATCGGGTTTC	CAN1 sequencing
JK170_CAN1_rev	AAGCTGCCTTTGTGTGCTTAAT	CAN1 sequencing
ACT1 F	CTCCACCACTGCTGAAAGAG	ChIP qPCR
ACT1 R	GTGATGACTTGACCATCTGG	ChIP qPCR
5' UAS 3 F	CGGAAGAGCATTGACAAATATTGA	ChIP qPCR
5' UAS 3 R	GGAAATAACAATGTCTGCGAGTG	ChIP qPCR
T150 1900 F	TAGTGGATCCCCCGGGCTGC	ChIP qPCR
T150 2100 R	CTCGAGGGGGGGCCCTCTCC	ChIP qPCR

* Primers for generating and confirming gene knockouts are available upon request.

Supplemental Table 4. Strains used in this study.

Strain	Genotype	Background	Comments
CH1585	*MATa, leu2-Δ1, trp1-Δ63, ura3–52, his3–200*		Shishkin *et al*, 2009
KS	*bar1::HIS3, can1::KanMX*	CH1585	Shah *et al*, 2014
YJK146	*ChrIII(75594-75641)::UAS_{GAL}-$(CAG)_{140}$-P_{GAL}-CAN1-TRP1*	KS	Made with SwaI cut pYes3-G4G1C1-Fori-CAG140-tetbal1-rev
YJK154	*ChrIII(75594-75641)::UAS_{GAL}-TET340-P_{GAL}-CAN1-TRP1*	KS	Made with SwaI cut pYes3-G4G1C1-Fori-tet340
YJK156	*ChrIII(75594-75641)::UAS_{GAL}-$(CAG)_{93}$-P_{GAL}-CAN1-TRP1*	KS	Made with SwaI cut pYes3-G4G1C1-Fori-CAG93-tetbal2-rev
YJK159	*srs2::HphMX4*	YJK146	
YJK161	*rad5::HphMX4*	YJK146	
YJK162	*rad52::HphMX4*	YJK146	
YJK189	*sgs1::HphMX4*	YJK146	
YJK190	*rad51::HphMX4*	YJK146	
YJK191	*msh2::HphMX4*	YJK146	
YJK192	*msh3::HphMX4*	YJK146	
YJK193	*msh6::HphMX4*	YJK146	
YJK194	*pol32::HphMX4*	YJK146	
YJK196	*pif1::HphMX4*	YJK146	
YJK198	*pif1-m2*	YJK146	Made using pVS31 (Schulz and Zakian, 1994)
YJK199	*pol30-89-LEU2*	YJK146	Made using pJH2480 (Lydeard *et al*, 2010)
YJK200	*mre11::HphMX4*	YJK146	
YJK202	*mus81::HphMX4*	YJK146	
YJK221	*rev3Δ*	YJK146	Made using pAM56 (Holbeck and Strathern, 1997)
YJK228	*yen1::NatMX4*	YJK146	
YJK229	*mus81::HphMX4, yen1::NatMX4*	YJK202	

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