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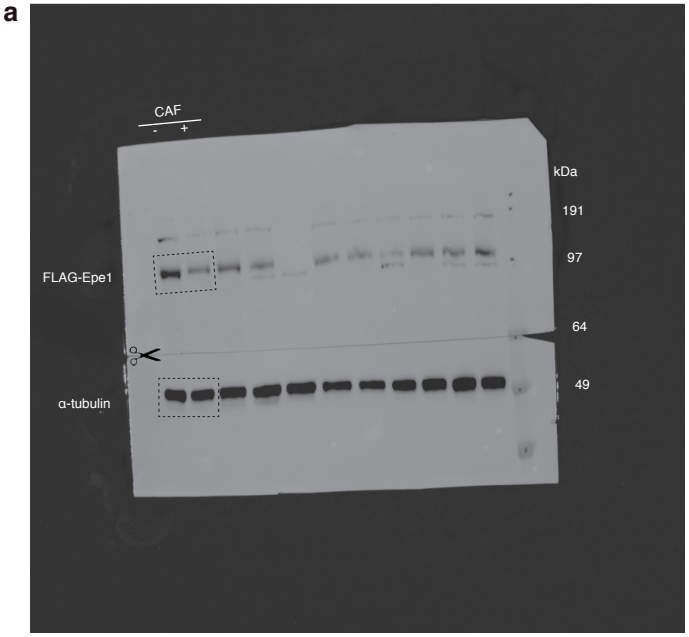
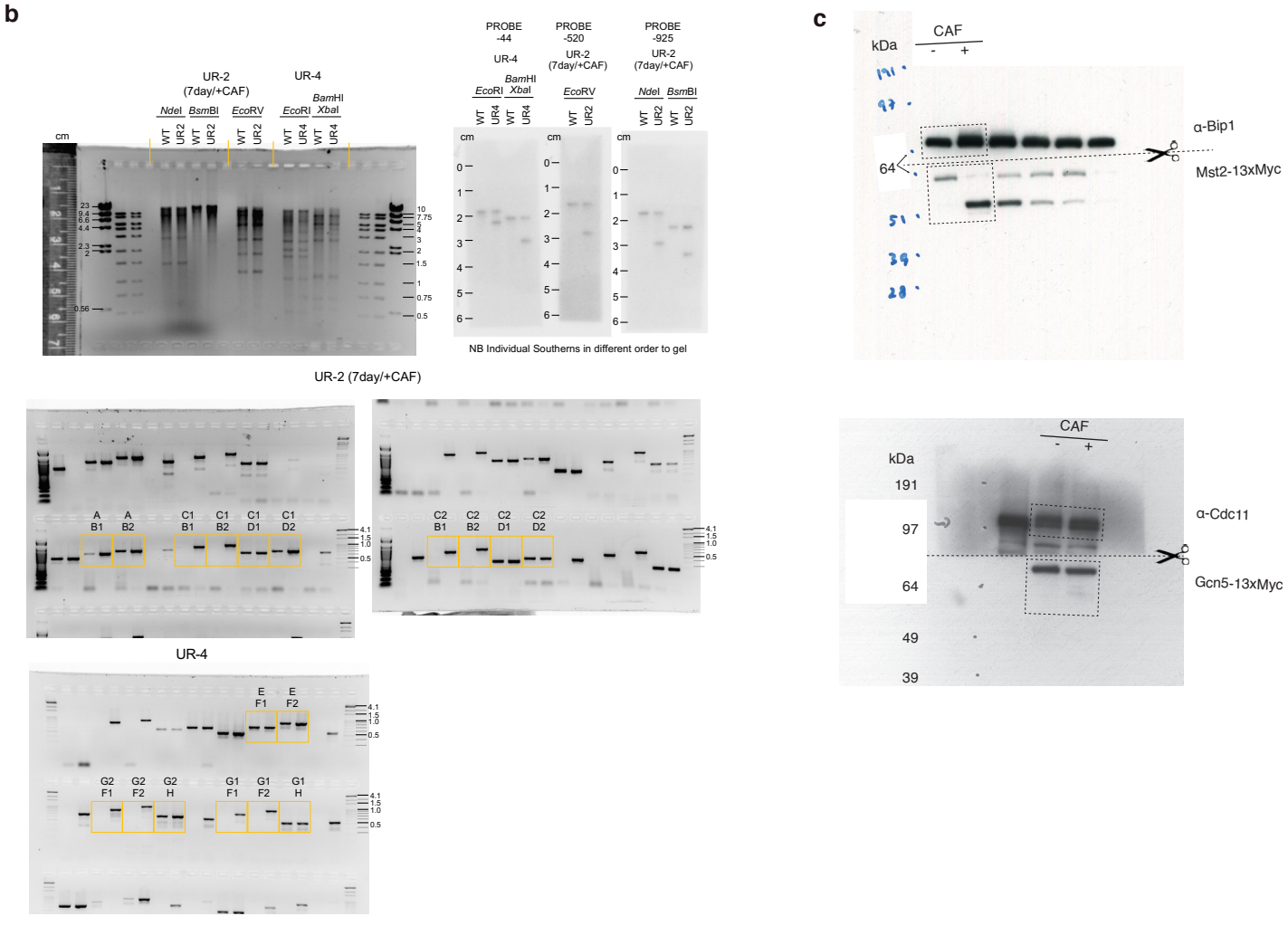
Supplementary information

Epigenetic gene silencing by heterochromatin primes fungal resistance

In the format provided by the authors and unedited





Supplementary Figure 1. a, Source gel data for Fig. 4c. **b,** Source gel data for Extended Data Fig. 8. **c,** Source gel data for Extended Data Fig. 10a. Yellow and dashed boxes indicate data used in figures.

Supplementary Table 1. Summary of epigenetic (H3K9me2 domains) and genetic (SNPs, indels and copy number variation) changes found in unstable (UR) caffeine-resistant isolates.

Isolate	Ectopic heterochromatin location		SNPs or indels in coding sequences?	Partial duplication of *Chr III*?
	ncRNA.394	**other loci**		
UR-1		✓ (*hba1*)	Clr5-Q264STOP / Meu27-S100Y	
UR-2	✓		Sdo1-R11C	
UR-3		✓ (*ppr4*)	Clr5-Q264STOP / Meu27-S100Y	
UR-4		✓ (*grt1*)	-	✓
UR-5		✓ (*fio1*)	Clr5-Q264STOP / Meu27-S100Y	✓
UR-6		✓ (*mbx2*)	-	✓
UR-7		✓ (*ppr4*)	Clr5-Q264STOP / Meu27-S100Y	
UR-8	✓		-	
UR-9	✓		-	
UR-10	✓		Cob1-F318L	
UR-11	✓		-	
UR-12	✓		-	
UR-13	✓		-	✓
UR-14	✓		Npp-W300STOP / SPBC16H5.13-S1011L	✓
UR-15	✓		-	✓
UR-16	✓		-	
UR-17	✓		SPCC777.02-R120R	✓
UR-18	✓		SPCC777.02-R120R	✓
UR-19	✓		Sdo1-R11C	✓
UR-20	✓		-	
UR-21	✓		-	✓
UR-22	✓		-	✓
UR-23	✓		Pch1-Q234STOP	
UR-24	✓		-	
UR-25	✓		-	✓
UR-26	✓		SPBC1271.08c-A133A	
UR-27	✓		SPCC4B3.13-A229V	
UR-28	✓		Mug72-N116S	
UR-29	✓		Mug72-N116S	
UR-30	✓		-	

Supplementary Table 2. *Schizosaccharomyces pombe* strains used in this study.

Strain number	Name	Description
143	wt	*h-* ED972 wild-type
B4411	SR-1	Stable 16 mM Caffeine Resistant Isolate – From wt – 1
B4412	SR-2	Stable 16 mM Caffeine Resistant Isolate – From wt – 2
B4413	UR-1	Unstable 16 mM Caffeine Resistant Isolate – From wt – 1
B4414	UR-2	Unstable 16 mM Caffeine Resistant Isolate – From wt – 2
B4415	UR-3	Unstable 16 mM Caffeine Resistant Isolate – From wt – 3
B4416	UR-4	Unstable 16 mM Caffeine Resistant Isolate – From wt – 4
B4417	UR-5	Unstable 16 mM Caffeine Resistant Isolate – From wt – 5
B4418	UR-6	Unstable 16 mM Caffeine Resistant Isolate – From wt – 6
B4419	UR-7	Unstable 16 mM Caffeine Resistant Isolate – From wt – 7
B4420	UR-8	Unstable 16 mM Caffeine Resistant Isolate – From wt – 8
B4421	UR-9	Unstable 16 mM Caffeine Resistant Isolate – From wt – 9
B4422	UR-10	Unstable 16 mM Caffeine Resistant Isolate – From wt – 10
B4423	UR-11	Unstable 16 mM Caffeine Resistant Isolate – From wt – 11
B4424	UR-12	Unstable 16 mM Caffeine Resistant Isolate – From wt – 12
B4425	UR-13	Unstable 16 mM Caffeine Resistant Isolate – From wt – 13
B4426	UR-14	Unstable 16 mM Caffeine Resistant Isolate – From wt – 14
B4427	UR-15	Unstable 16 mM Caffeine Resistant Isolate – From wt – 15
B4428	UR-16	Unstable 16 mM Caffeine Resistant Isolate – From wt – 16
B4429	UR-17	Unstable 16 mM Caffeine Resistant Isolate – From wt – 17
B4430	UR-18	Unstable 16 mM Caffeine Resistant Isolate – From wt – 18
B4431	UR-19	Unstable 16 mM Caffeine Resistant Isolate – From wt – 19
B4432	UR-20	Unstable 16 mM Caffeine Resistant Isolate – From wt – 20
B4433	UR-21	Unstable 16 mM Caffeine Resistant Isolate – From wt – 21
B4434	UR-22	Unstable 16 mM Caffeine Resistant Isolate – From wt – 22
B4435	UR-23	Unstable 16 mM Caffeine Resistant Isolate – From wt – 23
B4436	UR-24	Unstable 16 mM Caffeine Resistant Isolate – From wt – 24
B4437	UR-25	Unstable 16 mM Caffeine Resistant Isolate – From wt – 25
B4438	UR-26	Unstable 16 mM Caffeine Resistant Isolate – From wt – 26
B4439	UR-27	Unstable 16 mM Caffeine Resistant Isolate – From wt – 27
B4440	UR-28	Unstable 16 mM Caffeine Resistant Isolate – From wt – 28
B4441	UR-29	Unstable 16 mM Caffeine Resistant Isolate – From wt – 29
B4442	UR-30	Unstable 16 mM Caffeine Resistant Isolate – From wt – 30
B4443	SR-1 *clr4Δ* - 1	SR-1 *clr4Δ::NAT* - transformant 1
B4444	SR-1 *clr4Δ* - 2	SR-1 *clr4Δ::NAT* - transformant 2
B4445	SR-1 NAT control - 1	SR-1 *NAT:3' of ura4* - transformant 1
B4446	SR-1 NAT control - 2	SR-1 *NAT:3' of ura4* - transformant 2
B4447	SR-2 *clr4Δ* - 1	SR-2 *clr4Δ::NAT* - transformant 1
B4448	SR-2 *clr4Δ* - 2	SR-2 *clr4Δ::NAT* - transformant 2
B4449	SR-2 NAT control - 1	SR-2 *NAT:3' of ura4* - transformant 1
B4450	SR-2 NAT control - 2	SR-2 *NAT:3' of ura4* - transformant 2
B4451	UR-1 *clr4Δ* - 1	UR-1 *clr4Δ::NAT* - transformant 1
B4452	UR-1 *clr4Δ* - 2	UR-1 *clr4Δ::NAT* - transformant 2
B4453	UR-1 NAT control-1	UR-1 *NAT:3' of ura4* - transformant 1
B4454	UR-1 NAT control-2	UR-1 *NAT:3' of ura4* - transformant 2
B4455	UR-2 *clr4Δ* - 1	UR-2 *clr4Δ::NAT* - transformant 1
B4456	UR-2 *clr4Δ* - 2	UR-2 *clr4Δ::NAT* - transformant 2
B4457	UR-2 NAT control - 1	UR-2 *NAT:3' of ura4* - transformant 1
B4458	UR-2 NAT control - 2	UR-2 *NAT:3' of ura4* - transformant 2
B5022	UR-2 *dcr1Δ* - 1	UR-2 *dcr1Δ::NAT* - transformant 1
B5023	UR-2 *dcr1Δ* - 2	UR-2 *dcr1Δ::NAT* - transformant 2
B5024	UR-2 *ago1Δ* - 1	UR-2 *ago1Δ::NAT* - transformant 1
B5025	UR-2 *ago1Δ* - 2	UR-2 *ago1Δ::NAT* - transformant 2
B4352	Pap1-N424STOP	*h- pap1-N424STOP*
B4752	Clr5-Q264STOP Meu27-S100Y	*h- clr5-Q264STOP meu27-S100Y*
B4459	UR-2 (+14day/-CAF)	UR-2 after growth on -CAF media for 14 days

B4460	*hba1Δ*	*h- hba1Δ::NAT*
B4461	*SPBC17G9.12cΔ*	*h- SPBC17G9.12cΔ::NAT*
B4462	*ncRNA.393Δ*	*h- ncRNA.393Δ::NAT*
B4463	*ncRNA.394Δ*	*h- ncRNA.394Δ::NAT*
B4464	*eno101Δ*	*h- eno101Δ::NAT*
B3797	*TetR-Clr4**	*h+ leu1+adh21-TetROFF-2xFLAG-Clr4-cdd*
B3808	*4xtetO-II*	*h- 4xtetO 3' of SPBC17G9.13c leu1-32*
B3813	*4xtetO-I*	*h- 4xtetO 5' of hba1 leu1-32*
B3820	*4xtetO-III*	*h- 4xtetO 5' of ura4 leu1-32*
B4707	*4xtetO-IV*	*h- 4xtetO 5' of mbx2*
B4465	*TetR-Clr4* + 4xtetO-II*	*h+ leu1+adh21-TetROFF-2xFLAG-Clr4-cdd 4xtetO 3' of SPBC17G9.13c*
B4466	*TetR-Clr4* + 4xtetO-I*	*h+ leu1+adh21-TetROFF-2xFLAG-Clr4-cdd 4xtetO 5' of hba1*
B4467	*TetR-Clr4* + 4xtetO-III*	*h+ leu1+adh21-TetROFF-2xFLAG-Clr4-cdd 4xtetO 5' of ura4*
B4807	*TetR-Clr4* + 4xtetO-IV*	*h+ leu1+adh21-TetROFF-2xFLAG-Clr4-cdd 4xtetO 5' of mbx2*
B4885	*cup1-3xDSR*	*h- cup1Δ LocusPX:cup1-3xDSR (cup1=SPBC17G9.13c)*
B5005	*cup1-TT*	*h- cup1-TT (cup1=SPBC17G9.13c)*
B4688	Cup1-L73G	*h- cup1-L73G (cup1=SPBC17G9.13c)*
B4690	Cup1-F99G	*h- cup1-F99G (cup1=SPBC17G9.13c)*
B4567	Cup1-GFP	*h- cup1-GFP (cup1=SPBC17G9.13c)*
B4909	Cup1-GFP Arg11-mCh	*h- cup1-GFP arg11-mCherry-NAT (cup1=SPBC17G9.13c)*
B4912	Arg11-mCherry	*h- arg11-mCherry-NAT*
B4468	UR-2 (7day/+CAF)	UR-2 after growth on +CAF media for 3 days
B4469	UR-2 (7day/+CAF →14day/-CAF)	UR-2 after growth on +CAF media for 3 days and then on -CAF media for 14 days
B4621	*epe1Δ*	*h- epe1Δ*
B2835	Epe1-GFP	*h- epe1-GFP-KAN*
B4958	3xFLAG-Epe1	*h- 3xFLAG-epe1*
B4767	*TetR-Clr4* + 4xtetO-III epe1Δ*	*h+ epe1Δ::NAT leu1+adh21-TetROFF-2xFLAG-Clr4-cdd 4xtetO 5' of ura4*
B1008	*clr4Δ*	*h- clr4Δ::NAT*
B3250	*S. cerevisiae* Sgo1-GFP	*S. cerevisiae SGO1-yeGFP::KanMX6 MATa, ade2-1, leu2-3, ura3, trp1-1, his3-11, 15, can1-100, GAL, psi+*
B3111	*S. octosporus* wt	*h90 S. octosporus* wild-type
B4108	Mst2-13xMyc	*h- mst2-13xMyc-NAT*
B0505	Gcn5-13xMyc	*h? gcn5-13xMyc-NAT cc2Δ6Kb:cc1 ade6-704-HYG*

Supplementary Table 3. Oligonucleotides used in this study.

Name	Sequence	Description
qAct1-F	GGTTTCGCTGGAGATGATG	qPCR *act1*$^+$ - F
qAct1-R	ATACCACGCTTGCTTTGAG	qPCR *act1*$^+$ - R
qDg-F	AATTGTGGTGGTGTGGTAATAC	qPCR *dg* repeats - F
qDg-R	GGGTTCATCGTTTCCATTCAG	qPCR *dg* repeats - R
ST-52	GAATTGTGGAGCCATGTCCC	qPCR *slu7*$^+$ - F
ST-53	TCTTCTCCTGTCCAACGAGC	qPCR *slu7*$^+$ - R
ST-872	GAAACCCAGAAATTCGCAGGT	qPCR *kin17*$^+$ - F - primer pair 1 *hba1* locus
ST-873	ATGAGTTGCTTGGGCATCCA	qPCR *kin17*$^+$ - R - primer pair 1 *hba1* locus
ST-62	CAGCAAATTGGGGACTGTGT	qPCR *ish1*$^+$ - F - primer pair 2 *hba1* locus
ST-63	CTCAAGAAGCCTGGGAGTCA	qPCR *ish1*$^+$ - R - primer pair 2 *hba1* locus
ST-64	CGATGATCTGGTTGTATGGTGG	qPCR *hba1*$^+$ - F - primer pair 3 *hba1* locus
ST-65	TGCTCAGTACGCCATCTTGA	qPCR *hba1*$^+$ - R - primer pair 3 *hba1* locus
ST-66	GGGCTATCCTTAACGCTCTTC	qPCR *hba1*$^+$*cds* - F - primer pair 4 *hba1* locus
ST-67	CGCCTCCTCTGAACCAAAAG	qPCR *hba1*$^+$*cds* - R - primer pair 4 *hba1* locus
ST-58	CTTCCCACATCGCGTTCATT	qPCR *alp4*$^+$ - F - primer pair 5 *hba1* locus
ST-59	ACCTAAATCATCGCTGCTGG	qPCR *alp4*$^+$ - R - primer pair 5 *hba1* locus
ST-393	GGGCATGACAATCTCCGACT	qPCR *pyr1*$^+$ - F - primer pair 1 *ncRNA.394* locus
ST-394	GGCCTACCTCGGTGATCTTG	qPCR *pyr1*$^+$ - R - primer pair 1 *ncRNA.394* locus
ST-401	CCGTATGGTGAAGCAGGGTT	qPCR *SPBC17G9.12c*$^+$ - F - primer pair 2 *ncRNA.394* locus
ST-402	CCCGATCTCCGTGTAAGCAA	qPCR *SPBC17G9.12c*$^+$ - R - primer pair 2 *ncRNA.394* locus
ST-184	TTCGTCGTATGCCCTCTTGC	qPCR *SPBC17G9.13c*$^+$ - F - primer pair 3 *ncRNA.394* locus
ST-185	AAAATCCGCCATTTGCCCAG	qPCR *SPBC17G9.13c*$^+$ - R - primer pair 3 *ncRNA.394* locus
ST-251	TGCTGTAGTGATGCAGAGGAG	qPCR *ncRNA.393*$^+$ - F - primer pair 4 *ncRNA.394* locus
ST-252	GCGGCCATTTTGTTTACATTCC	qPCR *ncRNA.393*$^+$ - R - primer pair 4 *ncRNA.394* locus
ST-190	GAAAATTAGCGCGGCCGTTA	qPCR *ncRNA.394*$^+$ - F - primer pair 5 *ncRNA.394* locus
ST-191	TCAATCTGCTTGTCCCACCC	qPCR *ncRNA.394*$^+$ - R - primer pair 5 *ncRNA.394* locus
ST-263	GTGCTGCCCAAAAGAAGCTC	qPCR *eno101*$^+$ - F - primer pair 6 *ncRNA.394* locus
ST-264	TGGGAACCACCGTTCAAGAC	qPCR *eno101*$^+$ - R - primer pair 6 *ncRNA.394* locus
ST-249	AGCTTTCAAGGTAGCGGGTG	qPCR *cut2*$^+$ - F
ST-250	TTCCTCTGCTCAGCGTAGAC	qPCR *cut2*$^+$ - R
PA-354	CAGTTAGTTTCAGGTTTCCC	qPCR +2.5 kb *ura4*$^+$ - F - primer pair 1 *ura4* locus
PA-355	GCAGAGTAATGGTGATTGG	qPCR +2.5 kb *ura4*$^+$ - R - primer pair 1 *ura4* locus
ST-874	CACACAGTTTCAGAAGAAC	qPCR *tam14*$^+$ - F - primer pair 2 *ura4* locus
ST-875	GTTACGAGGAATCTTGGTAG	qPCR *tam14*$^+$ - R - primer pair 2 *ura4* locus
ST-796	CGCGACTGACAAGTTGCTTT	qPCR *ura4*$^+$ - F - primer pair 3 *ura4* locus
ST-797	AGCTAGAGCTGAGGGGATGA	qPCR *ura4*$^+$ - R - primer pair 3 *ura4* locus
ST-800	TGGTTTAAATCAAATCTTCCATGCG	qPCR 5' of *ura4*$^+$ - F - primer pair 4 *ura4* locus
ST-801	TGAGCAAACTGCTTTTGTGGT	qPCR 5' of *ura4*$^+$ - R - primer pair 4 *ura4* locus
ST-788	GGATGAAGCTGTCTCCCTGG	qPCR *new25*$^+$ - F - primer pair 5 *ura4* locus
ST-789	TATTGCTGCTTCTTCCCTGGC	qPCR *new25*$^+$ - R - primer pair 5 *ura4* locus
ST-876	GGAATCTATGTCGTTGCCG	qPCR *pmp20*$^+$ - F - primer pair 6 *ura4* locus
ST-877	GTAAACTCTCCGTTCCAGTC	qPCR *pmp20*$^+$ - R - primer pair 6 *ura4* locus
Clr4-KO-F	ATTTTTTAAATTCGTTCAGGCA TCATTTGGAGGGTTTGCTAAA AATCATCTCACCAAACAAGAG GTTATTAGTTTTGCGACGGAT CCCCGGGTTAATTAA	KO of *clr4*$^+$ with Bahler construct - F
Clr4-KO-R	AAATGAATGACCTTTTTCAGTT TAACAGTAATGGAGAAAAACA AATTGTAATTATTGGAGTCAAC CAGTAATAAATTAGCGAATTC GAGCTCGTTTAAAC	KO of *clr4*$^+$ with Bahler construct - R
ST-155	ATAGCTTAGGATTCATTATTTTTTAA GAGACAAATTTCTCGTCAATTGAAT GAAACCTTCCGCCTTTATTTTCTTT TTGACGGATCCCCGGGTTAATTAA	KO of *dcr1*$^+$ with Bahler construct - F
ST-156	GACTTGAAATATACAGTATTTCATT TTTTATGACCGCGGCCCTTGTAAC TTTTCAAACTTTCAATTTGGGTCTC CAAAGCGAATTCGAGCTCGTTTAA AC	KO of *dcr1*$^+$ with Bahler construct - R

ST-157	GGTTTGGTATATATAAGCTTCCAA CCGCCAAAGCGAATTGTCTTCAGC CAACTCGTCCTTTATGATTCAGAG TGAGTAGGCGGATCCCCGGGTTA ATTAA	KO of *ago1*$^{+}$ with Bahler construct - F
ST-158	TAAGGAAGTAAAAGTTGTGGGCAA TCCAGTAGTCAATCGTATATCTATT TCATTACTTATTGCATGCAATCCAT CAAACAGAATTCGAGCTCGTTTAA AC	KO of *ago1*$^{+}$ with Bahler construct - R
ST-3	GTCCAACACCCAGTTGTTAAC TGCTTATAATGACGCGTATGAT TGCGATATTTTAAGACTCTGGC CATCCACCGCTTTATCCGACG GATCCCCGGGTTAATTAA	Inserting natMX6 marker 3' of *ura4*$^{+}$ (*controlΔ*) - F
ST-12	GCAGGTTCTAGTAATGCGCAT TCAATTTGTAGTATTCTTAAATA ATCATTAAACGACAAGGGCCTT CCGTGCTATAGTGTGAATTCGA GCTCGTTTAAAC	Inserting natMX6 marker 3' of *ura4*$^{+}$ (*controlΔ*) - R
ST-866	CtagaGGTCTCgGACTCTCCATTTT CGTTAGAATTAGTTTcGAGACCcttC C	Golden Gate cloning pap1-sgRNA-1-F
ST-867	GGaagGGTCTCgAAACTAATTCTAA CGAAAATGGAGAGTCcGAGACCtct aG	Golden Gate cloning pap1-sgRNA-1-R
ST-868	AGCATGGCGCGAACCCGCTGAAT CATTGGACAAAGAATTCTTTAACG ACGAGGGTGAAATAGATGATGTTT TTCATAATTATTTTCATAATTCTAAC GTC	Pap1-N424STOP - HR template - F
ST-869	GCTCAGGGAATGATTCGTTGGCAT TCTCCAGAAAATCAAGACCATGCA ATGAATTAGTGATCAAGTCTCCATT TTCGTTAGACGTTAGAATTATGAAA AT	Pap1-N424STOP - HR template - R
ST-284	CAGCTGTGTGTTTGATTGAATCCA CATTCGTCCTCATGTACTCATAGC TAGGTGAAATATATTAGGCTTTCAG TGATTCGCGGATCCCCGGGTTAAT TAA	KO of *hba1*$^{+}$ with Bahler construct - F
ST-285	GAATGAATAAGAACCATAGTGAAG AGCTAAAAAAGAATCGAAAAGTAC TTACTATTTTACGAGTGGATCTTCT ATCTCGCGAATTCGAGCTCGTTTA AAC	KO of *hba1*$^{+}$ with Bahler construct - R
ST-391	TCTTCTGCCTAACCATACTACTTCT TCTAGCCTTCAGACTTAAAAGCTT CGCCTTTAGAAAACATCTCTATTC CTTCAAACGGATCCCCGGGTTAAT TAA	KO of *SPBC17G9.12c*$^{+}$ with Bahler construct - F
ST-392	CAAGAGAGATGGAAAACAGAGGA ATTGTGAACGTTCTCCTTATTCATA TTTCCATAAAGCTTCTCCAATGAC CTTTATTGGAATTCGAGCTCGTTTA AAC	KO of *SPBC17G9.12c*$^{+}$ with Bahler construct - F
ST-307	GATAAAATCTTAGAGATTGTTGCTA AATAAGCAAACAGTGTCTTTGCTG TAACTGGTGAGATATGTTTAAAATT AAATCACGGATCCCCGGGTTAATT AA	KO of *ncRNA.393*$^{+}$ with Bahler construct - F
ST-308	TGATATAATATATTTTCCTTCTTTAC TATTACATTTCCTATTTTTTCACCAT TTACGATATGTGTAACACTATCTAA CCCGAATTCGAGCTCGTTTAAAC	KO of *ncRNA.393*$^{+}$ with Bahler construct - R
ST-95	TAATGAAAAAGGTTGCTAATTGGTT TGTTATATAAGAGTATGTCGCATTT GTTTACGATAGGAGAGAGCGATTT TCCACACGGATCCCCGGGTTAATT AA	KO of *ncRNA.394*$^{+}$ with Bahler construct - F

ST-96	TATTACTATGACTCTGGTTCTAGCTCGACTCTGACCCTTGCCTGACATACAAATACTTTGCTCTTTTCAAAATGTACCGTGAATTCGAGCTCGTTTAAAC	KO of *ncRNA.394*$^{+}$ with Bahler construct - R
ST-305	ATATATAGAGTGGAAGGGCCGTCCGTTAGGACTTGTTTCAGTAAGAATCAATTAGTATTCTACAGTAAACATCGTTAATCCGGATCCCCGGGTTAATTAA	KO of *eno101*$^{+}$ with Bahler construct - F
ST-306	CTACTTCTACTACAACAACAGTTTACTTTAATACTAATAATAAATAAACACGCAACCTGGCAAATTAATCCAAAACGCAAGAATTCGAGCTCGTTTAAAC	KO of *eno101*$^{+}$ with Bahler construct - R
ST-756	CtagaGGTCTCgGACTGGTGCTTGACTTCTAATCTTGTTTcGAGACCcttCC	Golden Gate cloning *4xtetO-I*-sgRNA-F
ST-757	GGaagGGTCTCgAAACAAGATTAGAAGTCAAGCACCAGTCcGAGACCtctaG	Golden Gate cloning *4xtetO-I*-sgRNA-R
ST-732	AAACGCTAATCTAGCATGTCATGAAGG	Making *4tetO-I*-HR-template - 1F
ST-733	actagtaggccttgCCGTATTGAAATCAAAATTATTAATAATGAGTAAGTGAATATATACCA	Making *4tetO-I*-HR-template - 1R
ST-734	TGATTTCAATACGGcaaggcctactagtgcatgca	Making *4tetO-I*-HR-template - 2F
ST-735	TCTATAACTTTTACGTTAGctggatttcgtttacctcaccac	Making *4tetO-I*-HR-template - 2R
ST-736	gaggtaaacgaaatccagCTAACGTAAAAGTTATAGACAGTATTATAACAAGTATTATTGTAAAA	Making *4tetO-I*-HR-template - 3F
ST-737	TTTAATTGTATTTTTTTATTCAAAGGTTCTACTTTGTCAATCATTTTCAA	Making *4tetO-I*-HR-template - 3R
ST-752	CtagaGGTCTCgGACTATTTCTTTTGCTTTACGGTCGTTTcGAGACCcttCC	Golden Gate cloning *4xtetO-II*-sgRNA-F
ST-753	GGaagGGTCTCgAAACGACCGTAAAGCAAAAGAAATAGTCcGAGACCctaG	Golden Gate cloning *4xtetO-II*-sgRNA-R
ST-720	TTGAATTAATTCATAGAGTATGATAAAAATTGATAGTAAATTCATTGG	Making *4tetO-II*-HR-template - 1F
ST-721	cactagtaggccttgATGCATGCTAATAAATCATCGTAACTCAAGTAG	Making *4tetO-II*-HR-template – 1R
ST-722	TTTATTAGCATGCATcaaggcctactagtgcatgca	Making *4tetO-II*-HR-template – 2F
ST-723	TTTTTTTTTTCATAAATATTTActggatttcgtttacctcaccacc	Making *4tetO-II*-HR-template – 2R
ST-724	tggtgaggtaaacgaaatccagTAAATATTTATGAAAAAAAAAATAAATGATTCATAACAAGCAGATGAAAA	Making *4tetO-II*-HR-template - 3F
ST-725	TTTGTAATGTATAATCTTCATTTATTTTGAAGAGTCCTAATTCGT	Making *4tetO-II*-HR-template – 3R
ST-760	CtagaGGTCTCgGACTATATTTTAGATAGTTCTGTGGTTTcGAGACCcttCC	Golden Gate cloning *4xtetO-III*-sgRNA-F
ST-761	GGaagGGTCTCgAAACCACAGAACTATCTAAAATATAGTCcGAGACCctaG	Golden Gate cloning *4xtetO-III*-sgRNA-R
ST-744	CGGTAAGAAAACACGACATGTGCAG	Making *4tetO-III*-HR-template – 1F
ST-745	catgcactagtaggccttgTATAATTAAGATGTTTTAGAGACTTATACAATTTTGTCTTTATAAATTCT	Making *4tetO-III*-HR-template – 1R
ST-746	CTAAAACATCTTAATTATAcaaggcctactagtgcatgca	Making *4tetO-III*-HR-template – 2F
ST-747	TTTGCACTTTGTGAATctggatttcgtttacctcaccacca	Making *4tetO-III*-HR-template – 2R
ST-748	gtaaacgaaatccagATTCACAAAGTGCAAACATTATCATGAAAAAGAAC	Making *4tetO-III*-HR-template – 3F

ST-749	TGAAAAAGATAATCAGCCTTATAATCTTTACAAAAGTAAGAAATTCT	Making *4tetO-III*-HR-template – 3R
ST-858	CtagaGGTCTCgGACTGATTTGCCGTTCTACGACGGGTTTcGAGACCcttCC	Golden Gate cloning *4xtetO-IV*-sgRNA-F
ST-859	GGaagGGTCTCgAAACCCGTCGTAGAACGGCAAATCAGTCcGAGACCtctaG	Golden Gate cloning *4xtetO-IV*-sgRNA-R
ST-836	CTCAACAAACCACTGGTTACATGGC	Making *4tetO-IV*-HR-template – 1F
ST-837	actagtaggccttgGATACTTCGCAAAATTCTAAGCATGGTGC	Making *4tetO-IV*-HR-template – 1R
ST-838	TTTGCGAAGTATCcaaggcctactagtgcatgca	Making *4tetO-IV*-HR-template – 2F
ST-839	TCGATACCACCTTTTActggatttcgtttacctcaccacc	Making *4tetO-IV*-HR-template – 2R
ST-840	gtaaacgaaatccagTAAAAGGTGGTATCGAGGAATGGCA	Making *4tetO-IV*-HR-template – 3F
ST-841	ATCCAATAGTTAATAAATCGATGCTTAATTTGGTGG	Making *4tetO-IV*-HR-template – 3R
ST-952	CtagaGGTCTCgGACTAGCTTGTGGCTGACCGTTAAGTTTcGAGACCcttCC	Golden Gate cloning clr5-sgRNA-F
ST-953	GGaagGGTCTCgAAACTTAACGGTCAGCCACAAGCTAGTCcGAGACCctaG	Golden Gate cloning clr5-sgRNA-R
ST-954	CTTATTTGCAGCAGCCTTTCCAAATACCCTCTCAACGTTTCTCTCGACAGCAACAATCTCATCCATTCCCTGCTGCTCAACATGCAGTTAACGGTTAGCC	Making clr5-Q264STOP-HR-template – F
ST-955	CAGATTGGTTTGAAGAAGCAAACATGGTGGAGCCCATTGGGACATTTCTAGATTGGTAGATGAAAGGATACAAAGCTTGTGGCTAACCGTTAACTGCATG	Making clr5-Q264STOP-HR-template – R
ST-956	CtagaGGTCTCgGACTTATTAGCCTTTGAAGGATTTGTTTcGAGACCcttCC	Golden Gate cloning meu27-sgRNA-F
ST-957	GGaagGGTCTCgAAACAAATCCTTCAAAGGCTAATAAGTCcGAGACCtctaG	Golden Gate cloning meu27-sgRNA-R
ST-958	GCCAAAATCAATAGAGAACAATTATACTTTAAAAAAAAAAAATGAAGAAGGCTTCTTAAGTCAACAGGAAAATAAGTATTCAAATCAAAATCCTTCAAAG	Making meu27-S100Y-HR-template – F
ST-959	GAGGTGCCGCCCAATTGCAGTATACAAGCTATGAATGTTATTGGCTTGCTTACGCCGAGCTTGTCGAAAAGGTTATTAGCCTTTGAAGGATTTTGATTTG	Making meu27-S100Y-HR-template – F
ST-1044	CCTTGGTTTTTATGTATTTACTAGTAAATCTATAATAATCATTAACT	Making cup1-3xDSR construct – 1F
ST-1045	TATATTTGAATAAgagaatggaaggaaggttcgttagcAAAAGGTAGGAGGAAGCAAGAAATGG	Making cup1-3xDSR construct – 1R
ST-1046	gctaacgaaccttccttccattctc	Making cup1-3xDSR construct – 2F
ST-1047	cAAGGGAGccAaGGatAttGgaaagtggatgaacaagatcatttggagc	Making cup1-3xDSR construct – 2R
ST-1048	tcCaaTatCCtTggCTCCCTTgtaacttatgactctcgtttacac	Making cup1-3xDSR construct – 3F
ST-1049	ttaatacggagtttaaagcacacgatttgctacc	Making cup1-3xDSR construct – 3R
ST-1050	caaatcgtgtgctttaaactccgtattaaaccattcttaaactaatcttcatttattttgaagagtcctaattcgtcatcattttcatctgcttgttat	Making cup1-3xDSR construct – 4F
ST-1051	gttacgatgatttattagcatgcatccggaccgtaaagcaaaagaaattaaatatttatgaaaaaaaaataaatgattcataacaagcagatgaaaatg	Making cup1-3xDSR construct – 4R

ST-1052	tccggatgcatgctaataaatcatcgtaacGTCATCTTTTGGCATATAGGGTAAAGGGG	Making cup1-3xDSR construct – 5F
ST-1053	AAATTTACTCTAACAGACGATATTGTCTCACTATCC	Making cup1-3xDSR construct – 5R
ST-1054	CtagaGGTCTCgGACTAGGCCTTAATATTAACCCCCGTTTcGAGACCcttCC	Golden Gate cloning LocusPX-sgRNA-F
ST-1055	GGaagGGTCTCgAAACGGGGGTTAATATTAAGGCCTAGTCcGAGACCtctaG	Golden Gate cloning LocusPX-sgRNA-R
ST-1056	CtagaGGTCTCgGACTttCGAACATTTTAGGTAGCCGTTTcGAGACCcttCC	Golden Gate cloning endogenous cup1-sgRNA-F
ST-1057	GGaagGGTCTCgAAACGGCTACCTAAAATGTTCGaaAGTCcGAGACCtctaG	Golden Gate cloning endogenous cup1-sgRNA-R
ST-989	GATGAAAATGATGACGAATTAGGACTCTTCAAAATAAATGAAGATTATACATTACAAACTTTGGTCTGACTTTTTAAAGCACACGATTTGTGAAGTATTT	Making endogenous *cup1Δ*-HR-template – F
ST-990	TGATTTAATTTTAAACATATCTCACCAGTTACAGCAAAGACACTGTTTGCTTATTTAGCAACAATCTCTAAGATTTTATCAAATACTTCACAAATCGTGT	Making endogenous *cup1Δ*-HR-template – R
TagJ-sgRNA-F	CTAGAGGTCTCGGACTGCTCAGGCTAAACGTCGGAAGTTTCGAGACCCTTCC	Golden Gate cloning of cup1-tag sgRNA-F
TagJ-sgRNA-R	GGAAGGGTCTCGAAACTTCCGACGTTTAGCCTGAGCAGTCCGAGACCTCTAG	Golden Gate cloning of cup1-tag sgRNA-R
JTHR-Sito-F	ATGACGAATTAGGACTCTTCAAAATAAATGAAGATTATACATTACAAACTTTGGTCTGACTTTTTAAAGCACACGATTTGCTATTTGTATAGTTCATCCA	Making HR template for C-terminal tagging of cup1 with GFP
JTHR-Sito-R	TTGTATCGTGGGACTCTTTGTCAGACATTCAGCTCAGGCTAAACGTCGGAAAAGTTCTTAAAAAGTCAGTCAAAAAAGGAGTAAAGGAGAAGAACTTTT	Making HR template for C-terminal tagging of cup1 with GFP
lyrkosgRNA-F	CTAGAGGTCTCGGACTTCTTAATGTTGAGCCTGTTTGTTTCGAGACCCTTCC	Golden Gate cloning of cup1-LYR sgRNA-F
lyrkosgRNA-R	GGAAGGGTCTCGAAACAAACAGGCTCAACATTAAGAAGTCCGAGACCTCTAG	Golden Gate cloning of cup1-LYR sgRNA-R
HR-L73F	ACTCGAAGATTCTGGGATCCAATGGCATCCCAAATCGGAATCTCACATTTTCAAGCTTACGCCCGAAAAGCTCGCAAGTCAAATCCTAATCCTCACAAGCGAC	Making cup1-L73G-HR-template – F
HR-L73R	AGCTTGATGGTCGCCATCATTGGCGCGCTCAATACGACATGCAAAAGTTTTTAGGAGATTGCGAAACCGTTTTATGCGTCGCTTGTGAGGATTAGGATTT	Making cup1-L73G-HR-template – R
HR-F99F	CAATGGCATCCCAAATCCTAATCTCACATTTTCAAGCTTACGCCCGAAAAGCTCGCAAGTCAAATCCTAATCCTCACAAGCGACGCATAAAACGGGGTCG	Making cup1-F99G-HR-template – F
HR-F99R	TCGTAAAGTCTGCCATATAGCTTGATGGTCGCCATCATTGGCGCGCTCAATACGACATGCAAAAGTTTTTAGGAGATTGCGACCCCGTTTTATGCGTCGC	Making cup1-F99G-HR-template – R
WC258-sg-393-F	CtagaGGTCTCgGACTcaaatgctgtagtgatgcagGTTTcGAGACCcttCC	Golden Gate cloning of cup1/ncRNA393 region sgRNA-F

WC259-sg-393-R	GGaagGGTCTCgAAACctgcatcactacagcatttgAGTCcGAGACCtctaG	Golden Gate cloning of cup1/ncRNA393 region sgRNA-R
WC279-cup1DP-uraTT-F	GATCATTTGGAGCTTGGAATGGTCTCCTTTTGGTAACTGTAGAAATAAATCTCATGAGTAAGGAATTTTGTATGAATGAAGCTTGTGATATTGACGAAAC	To amplify 144-bp ura4 transcriptional terminator to replace 697 bp of cup1 upstream/promoter region (to make cup1-TT)- F
WC280-cup1DP-uraTT-R	ATTACCGTCTAAAGCGCGCAATTTCACAGATGCCGCAAATTTGACATCTGGGTCTTTCAAGTCTTGTTAGAACATTGAATAACTATGTACAAAGCCAATG	To amplify 144-bp ura4 transcriptional terminator to replace 697 bp of cup1 upstream/promoter region (to make cup1-TT) - R
WC267-arg11-Ctag-F	TAAAGGTGCTGCTACTCAAGCTCTCCAGAATCTCAATCTGTCGTGTGGTTACGATGAATATGCCGGTATCCATTTGGATcggatccccgggttaattaa	C-terminal tagging of *arg11*$^{+}$ with mCherry using Bahler construct - F
WC268-arg11-Ctag-R	AATATTTGTAACAAAAAAATATCCAAATGGTACACAGAAAGAATAAAAATAACAAAAGAATGGGCTACAAAAAATATAAgaattcgagctcgtttaaac	C-terminal tagging of *arg11*$^{+}$ with mCherry using Bahler construct - R
WC301-UR2-C1-F	GGGAACCACATACAATGAATG	C1 primer upstream of 5S rRNA.26 – F ChrIII control PCR and putative circle junction in UR-2
WC305-UR2-C2-F	TAGTCAGTATATACTGAGCGG	C2 primer upstream of 5S rRNA.26 – F ChrIII control PCR and putative circle junction in UR-2
WC306-UR2-B1-R	TCGCTGCTTATTGACTTTGAG	B1 primer downstream of 5S rRNA.24 – R ChrIII control PCR and putative circle junction in UR-2
WC308-UR2-B2-R	AACTGCTCTACTACTATAACG	B2 primer downstream of 5S rRNA.24 – R ChrIII control PCR and putative circle junction in UR-2
WC310-CHR3-2-D1-R	ATCATCTCGATAAGTGCTTTC	D1 primer downstream of 5S rRNA.26 – R ChrIII control PCR
WC311-CHR3-2-A-F	TCCGACTATTTGCATAAGACC	A primer upstream of 5S rRNA.24 – F ChrIII control PCR
WC312-CHR3-2-D2-R	AGAACTTTGTTGTAGCCTGAG	D2 primer downstream of 5S rRNA.26 – R ChrIII control PCR
WC321-UR4-UR17-G1-F	TTCTCCTTTGAACCCAGAAGG	G1 primer upstream of LTR27 – F ChrIII control PCR and putative circle junction in UR-4
WC325-UR4-UR17-G2-F	AATTCCATCCAAATTCTCTGG	G2 primer upstream of LTR27 – F ChrIII control PCR and putative circle junction in UR-4
WC326-UR4-F1-R	TATCACAACAGTTCTGCAACG	F1 primer downstream of LTR3 – R ChrIII control PCR and putative circle junction in UR-4
WC328-UR4-F2-R	TGGAAGCTTTGATAGAAAGGG	F2 primer downstream of LTR3 – R ChrIII control PCR and putative circle junction in UR-4
WC329-CHR3-4-E-F	ACGAATACGGTGTTGTATGAC	E primer upstream of LTR3 – F ChrIII control PCR
WC330-CHR3-4-17-H-R	CGCATCGTTAATGAGTTCATC	H primer downstream of LTR27 – R ChrIII control PCR
WC313-PROBE-925-F	TAAGCCAAAGGGTCCAATTCC	To amplify probe fragment at ~925 kb on chrIII – F
WC314-PROBE-925-R	CATTCATTGTATGTGGTTCCC	To amplify probe fragment at ~925 kb on chrIII – R
WC315-PROBE-520-F	TATGCGGCAAAGTGCAATGTC	To amplify probe fragment at ~520 kb on chrIII – F
WC316-PROBE-520-R	TGTTGCTAAGAGTGATAGCAG	To amplify probe fragment at ~520 kb on chrIII – R
WC317-PROBE-44-F	ACTACAGCAGTATCCTTCATG	To amplify probe fragment at ~44 kb on chrIII – F
WC318-PROBE44-R	TTCGTCCTCTCTGTCATTTCC	To amplify probe fragment at ~44 kb on chrIII – R
ST-9	CCATAGAATCTCCTTAGTTTGCATCGCAATTTTATAGTTACCTTTTTGCTAGTAAGCAATTAATTTTTGGGACTTTTAAGCGGATCCCCGGGTTAATTAA	KO of *epe1*$^{+}$ with Bahler construct - F
ST-10	TGTGAACTACTCAAGAATCATAAGCACGTGGGGATAAATATTCAATGGTAGCCGAAGGAAATAAAAAGTGCCGAGGTACTGAATTCGAGCTCGTTTAAAC	KO of *epe1*$^{+}$ with Bahler construct - R

ST-1064	AAAATAACATTTATGATTTTGAAGATCACTCTCCTGTTAGGGAAAAATGGGGGCACAGGCTTCGGTCCAGAGGTGCTAGTCGGATCCCCGGGTTAATTAA	C-terminal tagging of *epe1*$^{+}$ with GFP using Bahler construct - F
ST-1065	CTTAATTATTTGATGAAACCTTCATGATATACTCATAAAATGTGAACTACTCAAGAATCATAAGCACGTGGGGATAAATAGAATTCGAGCTCGTTTAAAC	C-terminal tagging of *epe1*$^{+}$ with GFP using Bahler construct - R
ST-1058	CtagaGGTCTCgGACTGGACTTTTAAGATGGATTCCGTTTcGAGACCcttCC	Golden Gate cloning epe1-sgRNA-F
ST-1059	GGaagGGTCTCgAAACGGAATCCATCTTAAAAGTCCAGTCcGAGACCtctaG	Golden Gate cloning epe1-sgRNA-R
ST-1062	GTGAACTACTCAAGAATCATAAGCACGTGGGGATAAATATTCAATGGTAGCCGAAGGAAATAAAAAGTGCCGAGGTACTTCTTAAAAGTCCCAAAAATTA	Making *epe1Δ*-HR-template – F
ST-1063	CCATAGAATCTCCTTAGTTTGCATCGCAATTTTATAGTTACCTTTTTGCTAGTAAGCAATTAATTTTTGGGACTTTTAAGAAGTACCTCGGCACTTTTTA	Making *epe1Δ*-HR-template – R
ST-1060	TTTATAGTTACCTTTTTGCTAGTAAGCAATTAATTTTTGGGACTTTTAAGATGGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGACTA	Making 3xFLAG-Epe1-HR-template – F
ST-1061	GAATATCAATGTCTTGATTTATAATGTCATCGTATTCAAGCCAGGAATCGCTGCCTCCTCCCTTGTCATCGTCATCCTTGTAGTCGATGTCATGATCTTT	Making 3xFLAG-Epe1-HR-template – R
ST-36	CAGGAGTGTGTACAGGAGGT	qPCR *vps32*$^{+}$ - F
ST-37	AGATGAATTGGCCAACGAGTT	qPCR *vps32*$^{+}$ - R
ST-44	CTCGCCTGAAACTTGCTACA	qPCR *cgs1*$^{+}$ - F
ST-45	GCACGAGGTTGATTACGCAT	qPCR *cgs1*$^{+}$ - R
ST-48	GTCACGGGCGATTTTAGGAC	qPCR *ppr4*$^{+}$ - F
ST-49	TCCCTTGTCCGGCAGAATAA	qPCR *ppr4*$^{+}$ - R
ST-1012	TCTGCGTGACACTTGTTCGT	qPCR *grt1*$^{+}$ - F
ST-1013	TAGAGACTCCAGCGCATCCT	qPCR *grt1*$^{+}$ - R
ST-1010	GTCAGGTGCTCCTTGCAGAT	qPCR *eno102*$^{+}$ - F
ST-1011	GCGTTCCTGCATAGATTGCG	qPCR *eno102*$^{+}$ - R
ST-1006	ATTGGATAGGCGTCACCGTC	qPCR *aes1*$^{+}$ - F
ST-1007	AGCCGGATCCTCATTGACAT	qPCR *aes1*$^{+}$ - R
ST-1018	GATTGGGCCGAGTTGAAGGA	qPCR *cdc22*$^{+}$ - F
ST-1019	AAGCAGTAGGCATTGGTGCT	qPCR *cdc22*$^{+}$ - R
ST-1028	AAGCAGTAGGCATTGGTGCT	qPCR *fip1*$^{+}$ - F
ST-1029	CCCTTTTTCACCGTTCTGCG	qPCR *fip1*$^{+}$ - R
ST-1024	GCACCGGAGATGATACCCAG	qPCR *fio1*$^{+}$ - F
ST-1025	GCACCATTTCCGATCGTTGG	qPCR *fio1*$^{+}$ - R
ST-1022	TCACACATCGTGGCTATCCG	qPCR *cyp8*$^{+}$ - F
ST-1023	TCGTTCACGAGATCCCTCCA	qPCR *cyp8*$^{+}$ - R
ST-1040	CCTGCTGCCGAATTTCAACG	qPCR *pcn1*$^{+}$ - F
ST-1041	TGCAGCTAAAACGAACACCC	qPCR *pcn1*$^{+}$ - R
ST-1032	GTCTCCGGGTGCTACAGTTC	qPCR *mbx2*$^{+}$ - F
ST-1033	GTGCGTTTGCCTACGATGAC	qPCR *mbx2*$^{+}$ - R
ST-1038	CTCGTGTTCCTGAGACCACC	qPCR *nce103*$^{+}$ - F
ST-1039	AACGAGGAACGACATTGGCA	qPCR *nce103*$^{+}$ - R
ST-277	CATTTTGCGGGACAATGGGT	qPCR *cds1*$^{+}$ - F
ST-278	CCTCCGTCCAAGTTGACGTT	qPCR *cds1*$^{+}$ - R
ST-1068	tgctgaatgtaaccaacatca	qPCR *cen-IRC-L1*
ST-1069	gcctcaattgcctattagtgct	qPCR *cen-IRC-R1*
ST-1066	GGATAAGCCAATCATCGTTGAG	qPCR *tlh2* - F
ST-1067	GTAGTTGACGCTCCTTGGAAG	qPCR *tlh2* - R
ST-1070	CCGAGGCTTTCATAGCTTA	qPCR *S. cerevisiae CEN4* – F (for GFP spike-in qChIP)
ST-1071	ACCGGAAGGAAGAATAAGAA	qPCR *S. cerevisiae CEN4* – R (for GFP spike-in qChIP)

ST-161	CCCAATTGTTGTGATTGCTG	qPCR *S. octosporus* CEN3 heterochromatin – F (for H3K9me2 spike-in qChIP)
ST-162	GCGGATGCAGTATTTCGTTT	qPCR *S. octosporus* CEN3 heterochromatin – R (for H3K9me2 spike-in qChIP)
Mst2-C-Tag-F	ACCTTTTACTTAAAGAAAATATACT TATTCCTCTACCTCAAAAGCGTCT ATTAGATAACTCTCATCATCTGGAT TCCGTTCGGATCCCCGGGTTAATT AA	C-terminal tagging of *mst2*$^{+}$ with 13xMyc using Bahler construct - F
Mst2-C-Tag-R	TATAGAGCAACAACCAAGCCGTAG ATGATACAAATGCTTCACGACAAA TATCGAAAGATTAAAATACTTATTT ATTTGAAGAATTCGAGCTCGTTTAA AC	C-terminal tagging of *mst2*$^{+}$ with 13xMyc using Bahler construct - R

Supplementary Table 4. Genomic coordinates used to generate heatmaps for heterochromatin islands.

Chromosome	Start	End	Name	Reference
I	578000	582000	*Island 1*	Zofall et al., Science, 2012
I	2447000	2449000	*Island 2*	Zofall et al., Science, 2012
I	2521000	2525000	*Island 3*	Zofall et al., Science, 2012
I	3647000	3651000	*Island 4*	Zofall et al., Science, 2012
I	3727000	3730000	*Island 5*	Zofall et al., Science, 2012
I	4534000	4540000	*Island 6*	Zofall et al., Science, 2012
I	4653000	4656000	*Island 7*	Zofall et al., Science, 2012
II	898000	903000	*Island 8*	Zofall et al., Science, 2012
II	1472000	1479000	*Island 9*	Zofall et al., Science, 2012
II	1551000	1554000	*Island 10*	Zofall et al., Science, 2012
II	1670000	1680000	*Island 11*	Zofall et al., Science, 2012
II	1692000	1698000	*Island 12*	Zofall et al., Science, 2012
II	1869000	1873000	*Island 13*	Zofall et al., Science, 2012
II	2199000	2202000	*Island 14*	Zofall et al., Science, 2012
II	2338000	2342000	*Island 15*	Zofall et al., Science, 2012
II	3628000	3631000	*Island 16*	Zofall et al., Science, 2012
II	3640000	3642000	*Island 17*	Zofall et al., Science, 2012
III	958000	968000	*Island 18*	Zofall et al., Science, 2012
III	1036000	1040000	*Island 19*	Zofall et al., Science, 2012
III	2369000	2371000	*Island 20*	Zofall et al., Science, 2012
III	2422000	2424000	*Island 21*	Zofall et al., Science, 2012
I	1465847	1469848	*HOOD-1*	Yamanaka et al., Nature, 2013
I	1564163	1568414	*HOOD-2*	Yamanaka et al., Nature, 2013
I	2544835	2561773	*HOOD-3*	Yamanaka et al., Nature, 2013
I	2927156	2941954	*HOOD-4*	Yamanaka et al., Nature, 2013
I	2977013	2988899	*HOOD-5*	Yamanaka et al., Nature, 2013
I	2994807	3009469	*HOOD-6*	Yamanaka et al., Nature, 2013
I	3361499	3365727	*HOOD-7*	Yamanaka et al., Nature, 2013
I	3736902	3743575	*HOOD-8*	Yamanaka et al., Nature, 2013
I	3791825	3796114	*HOOD-9*	Yamanaka et al., Nature, 2013
I	3996353	4000615	*HOOD-10*	Yamanaka et al., Nature, 2013
I	4022326	4026545	*HOOD-11*	Yamanaka et al., Nature, 2013
I	5069824	5083205	*HOOD-12*	Yamanaka et al., Nature, 2013
I	5191103	5195325	*HOOD-13*	Yamanaka et al., Nature, 2013
I	5195656	5199909	*HOOD-14*	Yamanaka et al., Nature, 2013
I	5234000	5250176	*HOOD-15*	Yamanaka et al., Nature, 2013
II	91600	101684	*HOOD-16*	Yamanaka et al., Nature, 2013
II	347505	354250	*HOOD-17*	Yamanaka et al., Nature, 2013
II	898107	902233	*HOOD-18*	Yamanaka et al., Nature, 2013
II	1812684	1816937	*HOOD-19*	Yamanaka et al., Nature, 2013
II	1965175	1969519	*HOOD-20*	Yamanaka et al., Nature, 2013
II	2126590	2128479	*HOOD-21*	Yamanaka et al., Nature, 2013
II	4414469	4418768	*HOOD-22*	Yamanaka et al., Nature, 2013
II	4442538	4449562	*HOOD-23*	Yamanaka et al., Nature, 2013
III	173841	176400	*HOOD-24*	Yamanaka et al., Nature, 2013
III	254411	256353	*HOOD-25*	Yamanaka et al., Nature, 2013
III	778123	782331	*HOOD-26*	Yamanaka et al., Nature, 2013

III	1047657	1056145	*HOOD-27*	Yamanaka et al., Nature, 2013
III	1168500	1176000	*HOOD-28*	Yamanaka et al., Nature, 2013
III	1179500	1182650	*HOOD-29*	Yamanaka et al., Nature, 2013
III	1196050	1196500	*HOOD-30*	Yamanaka et al., Nature, 2013
III	1763512	1775613	*HOOD-31*	Yamanaka et al., Nature, 2013
III	2320230	2324503	*HOOD-32*	Yamanaka et al., Nature, 2013
I	239913	249656	*SPAC806.04c & SPAC806.05*	Wang et al., eLife, 2015
I	4527389	4533031	*LTR & SPAC27D7.11c*	Wang et al., eLife, 2015
III	273261	279340	*mae2*	Wang et al., eLife, 2015
II	2301681	2308661	pfk1/sad1	Sorida et al., PLoS Genet, 2019
I	94000	97000	SPAC1F8.05	Gallagher et al., NSMB, 2019
I	125000	129000	SPAC11D3.11c	Gallagher et al., NSMB, 2019
I	125000	129000	SPAC11D3.10	Gallagher et al., NSMB, 2019
I	1036000	1042000	SPAC23C4.05c	Gallagher et al., NSMB, 2019
I	1036000	1042000	SPAC23C4.06c	Gallagher et al., NSMB, 2019
I	1513000	1517000	SPAC57A7.13	Gallagher et al., NSMB, 2019
I	1513000	1517000	SPAC57A7.12	Gallagher et al., NSMB, 2019
I	2147000	2150000	SPAC23C11.09	Gallagher et al., NSMB, 2019
I	2174000	2179000	SPAC13F5.03c	Gallagher et al., NSMB, 2019
I	2395000	2398500	SPAC15F9.01c	Gallagher et al., NSMB, 2019
I	2977500	2985500	SPAPB1A11.02	Gallagher et al., NSMB, 2019
I	3476500	3481000	SPAC328.03	Gallagher et al., NSMB, 2019
I	5309000	5311500	SPNCRNA.1068	Gallagher et al., NSMB, 2019
I	5309000	5311500	SPNCRNA.1069	Gallagher et al., NSMB, 2019
I	5390000	5396000	SPAC3G6.07	Gallagher et al., NSMB, 2019
II	102000	105000	SPBC359.01	Gallagher et al., NSMB, 2019
II	167500	170500	SPBC1683.12	Gallagher et al., NSMB, 2019
II	200500	203000	SPBC660.05	Gallagher et al., NSMB, 2019
II	221500	224000	SPBC660.14	Gallagher et al., NSMB, 2019
II	337500	340500	SPNCRNA.103	Gallagher et al., NSMB, 2019
II	459500	464000	SPBC428.10	Gallagher et al., NSMB, 2019
II	538000	541000	SPBC649.04	Gallagher et al., NSMB, 2019
II	919500	922500	SPBC216.07c	Gallagher et al., NSMB, 2019
II	948000	951000	SPNCRNA.334	Gallagher et al., NSMB, 2019
II	948000	951000	SPNCRNA.335	Gallagher et al., NSMB, 2019
II	1223500	1226000	SPBC725.10	Gallagher et al., NSMB, 2019
II	1309000	1312000	SPBC30B4.04c	Gallagher et al., NSMB, 2019
II	1495000	1499000	SPBC11B10.07c	Gallagher et al., NSMB, 2019
II	2184000	2186500	SPBC17G9.08c	Gallagher et al., NSMB, 2019
II	3344629	3348817	SPBC17D1.17	Gallagher et al., NSMB, 2019
II	3530000	3532500	SPBC1105.12	Gallagher et al., NSMB, 2019
II	3530000	3532500	SPBC1105.13c	Gallagher et al., NSMB, 2019
II	4103000	4108500	SPBC56F2.06	Gallagher et al., NSMB, 2019
II	4409500	4414500	SPBC1289.14	Gallagher et al., NSMB, 2019
III	31500	34500	SPCP20C8.03	Gallagher et al., NSMB, 2019
III	34500	39000	SPCC1884.01	Gallagher et al., NSMB, 2019
III	739000	742000	SPCC18B5.11c	Gallagher et al., NSMB, 2019
III	1265500	1268000	SPCC23B6.01c	Gallagher et al., NSMB, 2019
III	2072000	2075000	SPCPB1C11.02	Gallagher et al., NSMB, 2019
III	2286000	2289500	SPCC965.04c	Gallagher et al., NSMB, 2019
III	2410325	2415970	SPCC569.08c	Gallagher et al., NSMB, 2019

III	2429000	2433000	SPCC569.03	Gallagher et al., NSMB, 2019