APPENDIX

DASH/Dam1 complex mutants stabilize ploidy in histone-humanized yeast by weakening kinetochore-microtubule attachments

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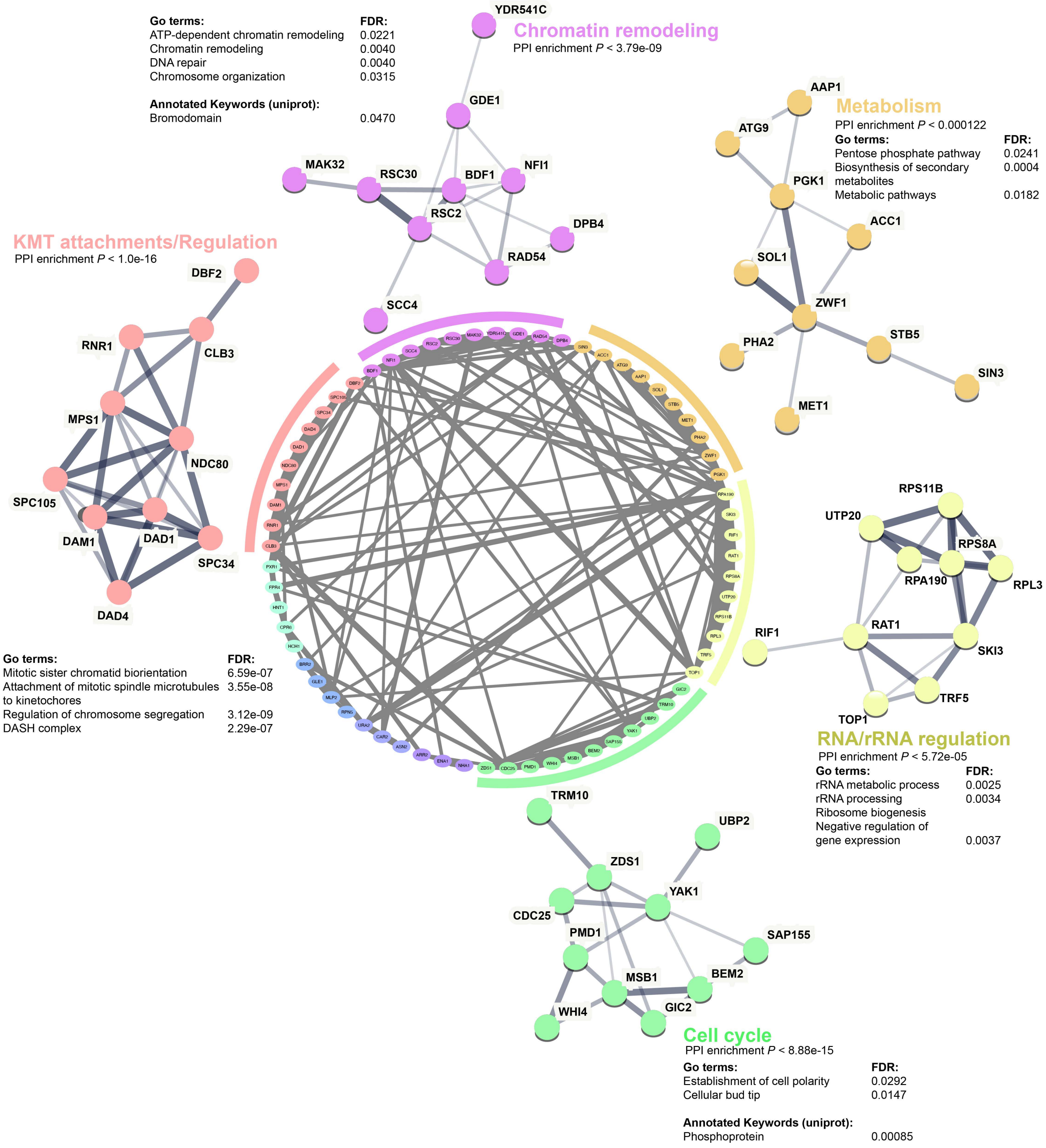


Go terms:	FDR:
ATP-dependent chromatin remodeling	0.0221
Chromatin remodeling	0.0040
DNA repair	0.0040
Chromosome organization	0.0315
Annotated Keywords (uniprot):	
Bromodomain	0.0470

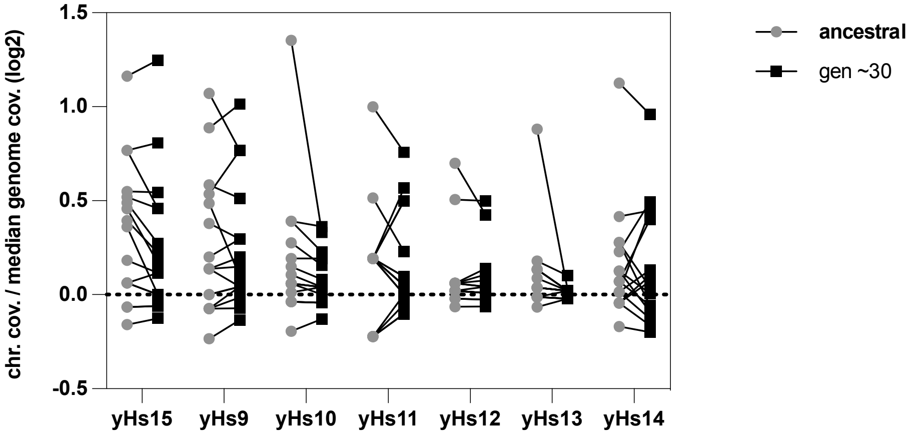
Go terms:	FDR:
Pentose phosphate pathway	0.0241
Biosynthesis of secondary metabolites	0.0004
Metabolic pathways	0.0182

Go terms:	FDR:
Mitotic sister chromatid biorientation	6.59e-07
Attachment of mitotic spindle microtubules to kinetochores	3.55e-08
Regulation of chromosome segregation	3.12e-09
DASH complex	2.29e-07

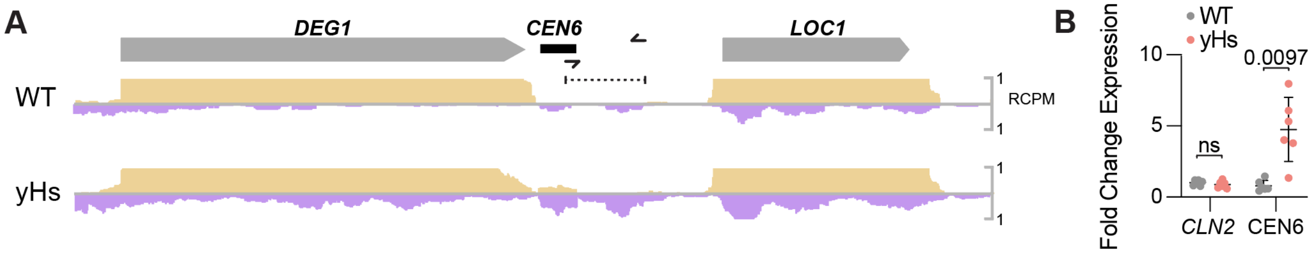
Go terms:	FDR:
rRNA metabolic process	0.0025
rRNA processing	0.0034
Ribosome biogenesis	
Negative regulation of gene expression	0.0037

Go terms:	FDR:
Establishment of cell polarity	0.0292
Cellular bud tip	0.0147
Annotated Keywords (uniprot):	
Phosphoprotein	0.00085

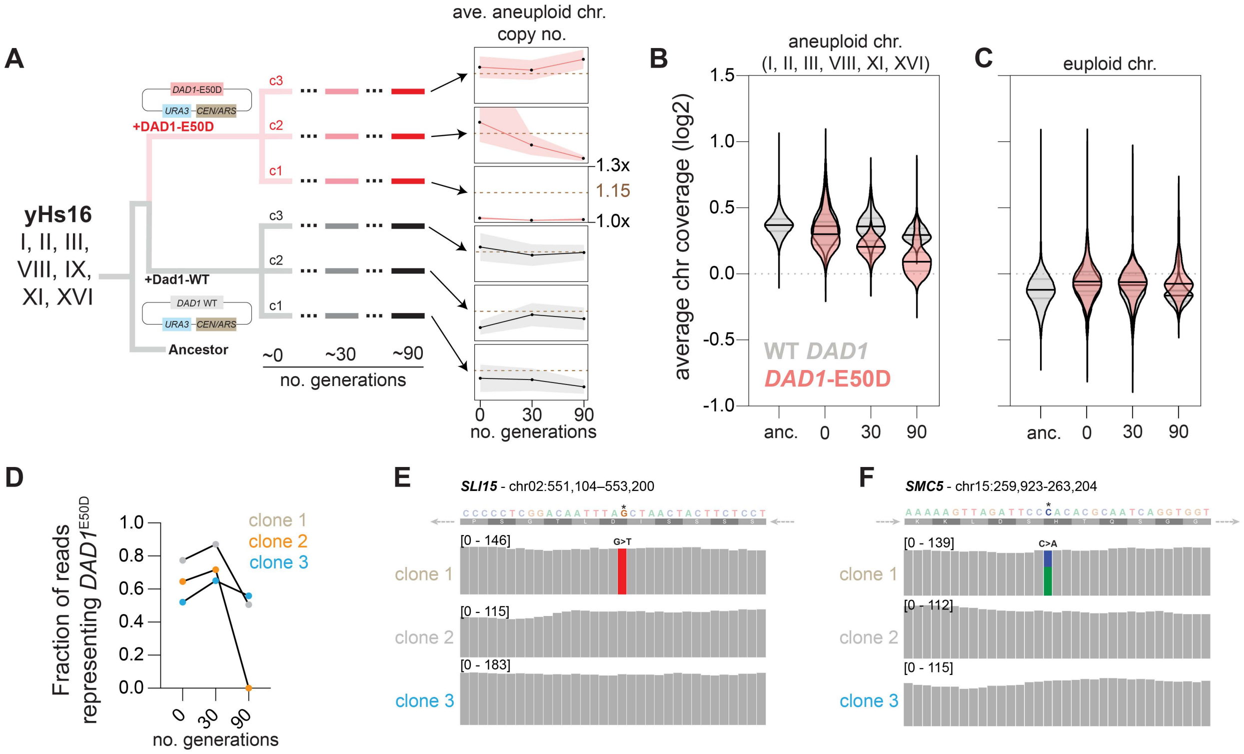
Appendix Figure S1. ***Protein-protein interaction network of candidate suppressors of human histones.*** String database analysis of protein-protein interactions (PPI) considering missense, nonsense, and noncoding mutations identified in histone humanized lineages (Table EV1 and Truong and Boeke, 2017). The network was clustered using MCL clustering with the inflation parameter set to 1.8, clusters are colored, with PPI depicted as gray connecting lines. The number of PPI in the global network was significantly enriched from background (PPI enrichment *p* = 0.0049). Local PPI networks are shown for clusters containing more than 10 interactors, with PPI enrichment p-values shown, alongside Go term enrichment terms and Uniport keywords. Network was constructed using the interaction sources: “textmining”, “experiments”, “databases”, and “co-expression”. The width of each edge represents the strength of interaction between nodes based on available evidence. Disconnected nodes were removed for clarity.



Appendix Figure S2. ***Chromosome aneuploidy evolution in yHs lineages.*** For each histone–humanized lineage (ancestral, gray circles; and evolved, black squares) we plot the median log2 coverage ratio (chromosome divided by median of genome) for each chromosome.



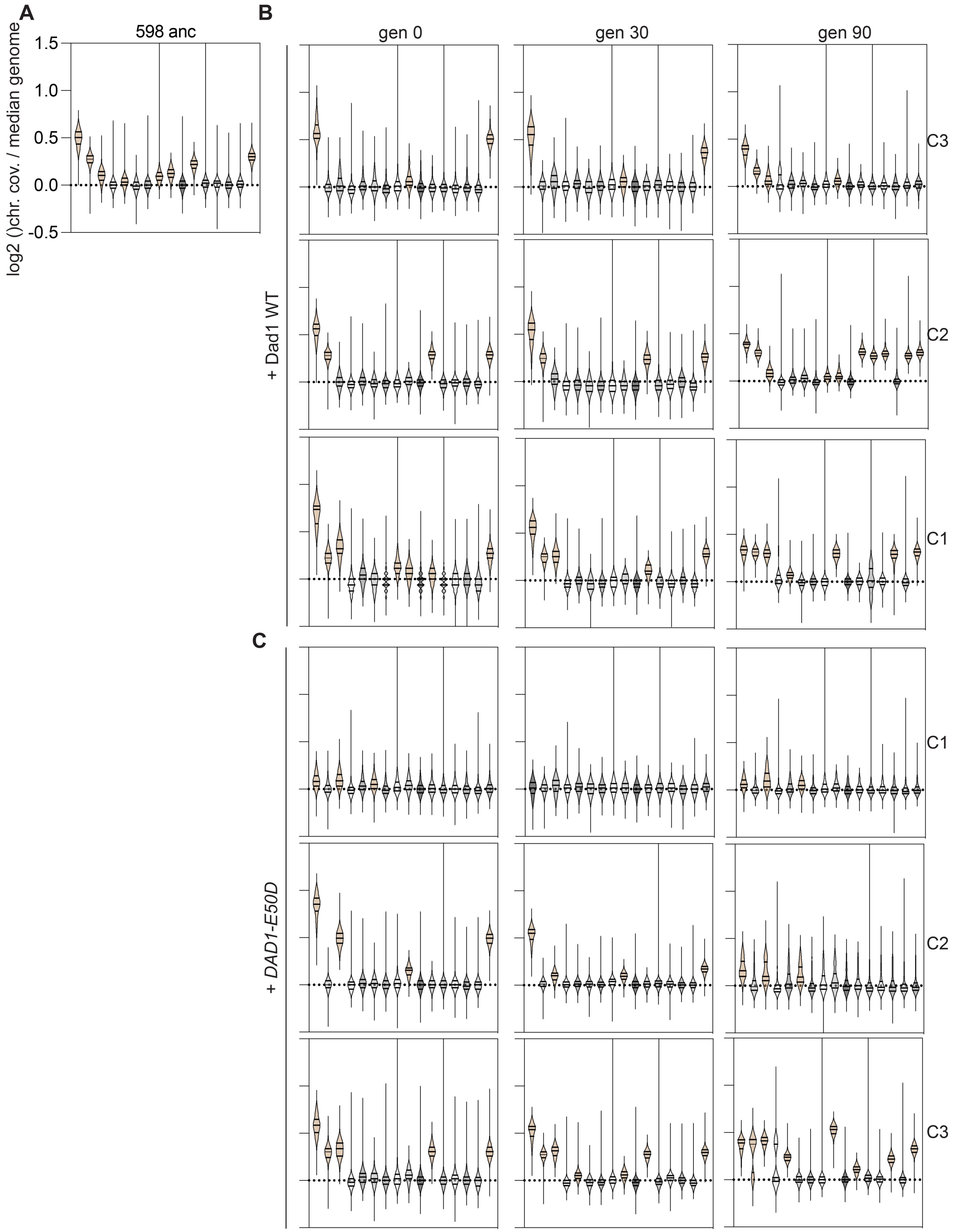
Appendix Figure S3. ***Transcription at chromosomal CEN6 in wild type and histone–humanized yeasts***. (a) The region around centromere VI is shown, with read coverage (read counts per million) for the forward (yellow) and reverse (purple) strands. The region amplified for RT- and qRT-PCR is shown by the two arrow heads and region highlighted in a bracket. (b) Quantitative RT-PCR of CEN6 RNA in WT and histone humanized strains. Expression levels of *CLN2* and *CEN6* were normalized to the expression level of *UBC6* (see Appendix Table S5).



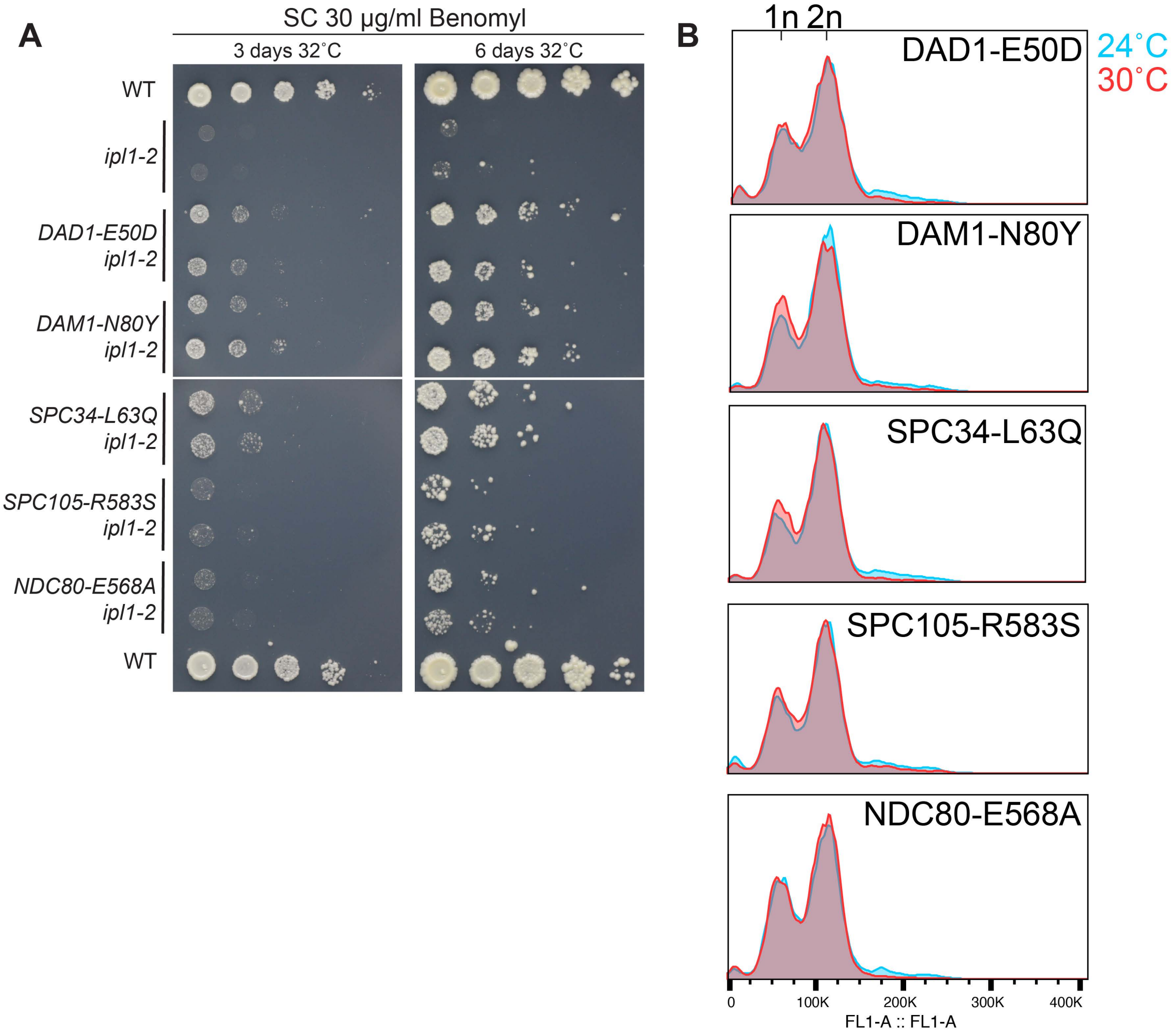
Appendix Figure S4. ***DAD1^{E50D} drives euploidization in a heterozygous state.***

(a) Overview of experimental design and ploidy evolution for each clone. Left, histone–humanized clone yH16 was transformed with a CEN/ARS plasmids encoding either the wild type *DAD1* gene or mutant *DAD1*^{E50D} gene. Three clones were selected and passaged for 90 generations in SC–Ura, to maintain selection of the CEN/ARS plasmid. Genomic DNA was isolated and sequenced to infer chromosome copy numbers. Right, plots of the average chromosome copy number for the ancestral aneuploid chromosomes (*I*, *II*, *III*, *VIII*, *IX*, *XI*, and *XVI*) at each time point (shaded area represents the standard deviation between the three biological replicates). **(b)** Log2 ratio (chromosome divided by the genome median) chromosomal coverage for the parental aneuploid chromosomes. **(c)** Same as in panel b, however shown for the parental euploid chromosomes. **(d)** Ratio of reads corresponding to the mutant *DAD1*^{E50D} allele for clones transformed with the pRS416-*DAD1*^{E50D} plasmid across each timepoint.

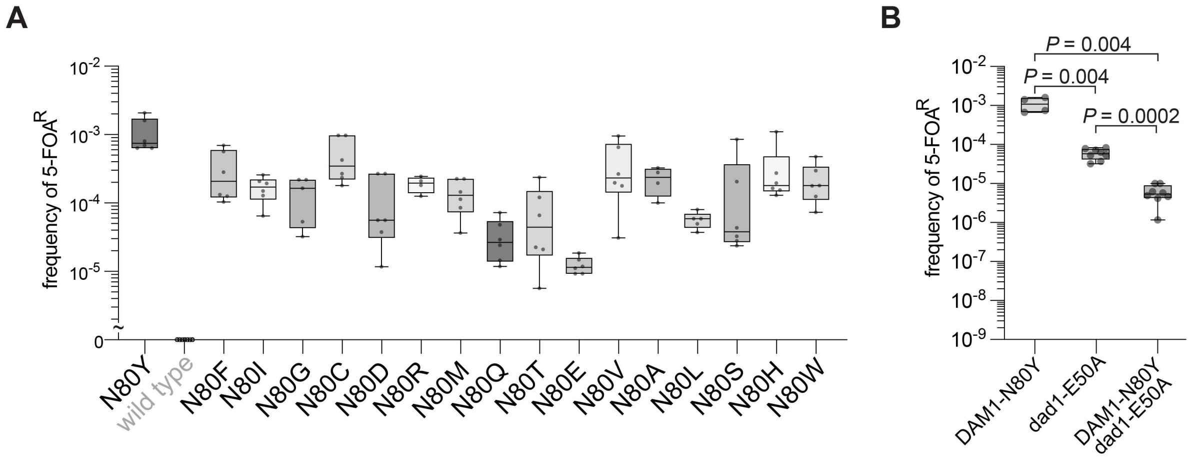
(e) Genome browser track for the *SLI15* gene, the DNA shown is the Crick strand and represents the template strand of *SLI15* (note the arrow of the direction indicates the orientation of *SLI15*). **(f)** Genome browser track for the *SMC5* gene.



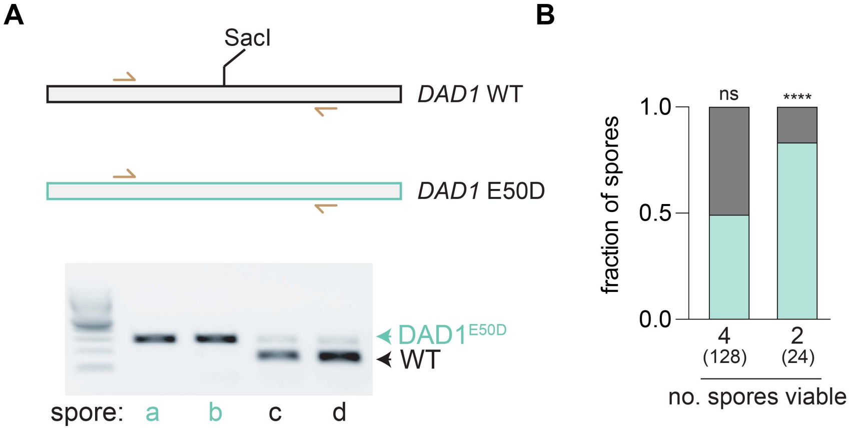
Appendix Figure S5. ***Chromosome copy number of each clone from aneuploidy reduction experiment.*** **(a)** Chromosome coverage for the ancestral strain prior to transformation with the CEN/ARS plasmid. Violin plots shaded brown are indicated to be aneuploid. **(b)** Chromosome coverage for the clones transformed with wild type *DAD1*. **(c)** Chromosome coverage for the clones transformed with mutant *DAD1*$^{\mathrm{E50D}}$.



Appendix Figure S6. ***DASH/Dam1c mutants rescue Aurora B kinase ipl1-2 mutant.*** **(a)** Growth assays of suppressor mutants with the *ipl1-2* temperature sensitive mutant on SC medium with 30 µg/mL of benomyl. **(b)** Cell cycle analysis of the indicated mutant at 24˚C and 30˚C. Yeast cultures were grown to logarithmic phase at 24˚C and divided and grown at 24˚C and 30˚C for 6 hours before cells were collected and processed for DNA content analysis using Sytox Green stain.



Appendix Figure S7. ***Humanization rates of dam1 residue 80 mutants and DAM1^{N80Y} dad1^{E50A} mutant.*** **(a)** Humanization rates (5–FOA^{R} frequency) for the missense mutants of dam1 residue 80. **(b)** Humanization rates (5–FOA^{R} frequency) of the single and double mutants *dad1*^{E50A} and *DAM1*^{N80Y}.



Appendix Figure S8. ***PCR genotyping of DAD1 in spores from heterozygous cross.*** **(a)** Schematic and example of the PCR digestion genotype assay used. Briefly, the *DAD1* locus is PCR amplified and then digested with the SacI enzyme, which only cuts the wild type allele. Digestions are then visualized on a 1% agarose gel. **(b)** Genotyping of spores isolated from tetrads with either four viable spores or two viable spores. Fraction of spores with the indicated allele (gray DAD1WT and cyan DAD1E50D) is displayed. The one-tailed binomial test is shown for the probability of observing the frequency of the DAD1E50D allele given equal segregation (DAD1WT, P = 0.46; DAD1E50D, P = 0.0011). Numbers in parenthesis indicates the total number of spores genotyped.

Appendix Table S1. ***Candidate Suppressor mutations by lineage.***

Mutant	***Isolate***	***Strain***	***Mutations***	***Likely innocuous mutations***
yHs9	*yHs9evo0_pool*	*yMAH0344*	–	–
	yHs9evo5_pool	*yMAH0393*	–	–
	yHs9evo5_C1	*yMAH531*	–	*gle1(–8)* *rif1(–264)* *car2(-168)*
	yHs9evo5_C2	*yMAH532*	*dad4(N61K) YPL216W(K290Stop) gic2(G133S)*	*gle1(–8)* *rif1(–264)*
	yHs9evo5_C3	*yMAH533*	*gic2(G133S)*	–
yHs10	*yHs10_evo0_pool*	*yMAH0345*	*bdf1(E474D)*	*trm732(A104A)* *gde1(R873R)*
	yHs10_evo5_pool	*yMAH0394*	*bdf1(E474D)*	*trm732(A104A)* *gde1(R873R)*
yHs11	*yHs11_evo0_pool*	*yMAH0346*	–	–
	yHs11_evo5_pool	*yMAH0395*	*rnr1(P144T) sin3(F470Y)*	*suf6-1* *fre1(-183)*
	yHs11_evo5_C2	*yMAH536*	*vps8(Q116H) pmd1(V895F) rnr1(P144T) sin3(F470Y) rpn5(E120A)*	*hch1(-88)* *suf6-1*
yHs12	*yHs12_evo0_pool*	*yMAH0347*	–	–
	yHs12_evo5_pool	*yMAH0396*	*ecm4(M84I) rnp1(K115R) aus1(A1189V) rpl3(T296I) rpa190(E23G)*	–
	yHs12_evo5_C1	*yMAH456*	*yak1(Q77E) ecm4(M84I) rnp1(K115R) aus1(A1189V) rpl3(T296I) rpa190(E23G)*	–
yHs13	*yHs13_evo0_pool*	*yMAH0348*	*dam1(N80Y)*	–
	yHs13_evo5_pool	*yMAH0397*	*rat1(N650K) dam1(N80Y)*	–
yHs14	*yHs14_evo0_pool*	*yMAH0349*	–	–
	yHs14_evo5_pool	*yMAH0398*	*cdc25(N1574H)*	–
	yHs14_evo5_C1	*yMAH538*	*aap1(G226S) cdc25(N1574H)*	*mne1(V267V)* *ura2(S1442S)* *YDR541C(+152)**
yHs15	*yHs15_evo0_pool*	*yMAH0343*	–	–

	yHs15_evo5_pool	*yMAH0392*	–	–
	yHs15_evo5_C1	*yMAH528*	*acc1(Q455R)*	*rps8A(+39) ts(AGA)D3(C>A; 186560)*
	yHs15_evo5_C2	*yMAH529*	*acc1(Q455R)*	–
	yHs15_evo5_C3	*yMAH530*	*acc1(Q455R)*	–
yHs16	*yHs16_evo0_pool*	*yMAH0598*	*utp20(E1318D) atg9(A546E) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*mps1(–221) ret2(A299A) YLR123C(L8L)*
	yHs16_evo0_C1	*yMAH865*	*utp20(E1318D) atg9(A546E) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*ret2(A299A) YLR123C(L8L)*
	yHs16_evo0_C2	*yMAH866*	*rps11B(Q8H) apl5(S905A) arr2(G59R) utp20(E1318D) atg9(A546E) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*ret2(A299A) YLR123C(L8L)*
	yHs16_evo0_C3	*yMAH867*	*rad54(K588E) mlp2(E377Stop) msb1(D243V) top1(E713stop) utp20(E1318D) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*asn2(–437) tcd2(–37) ret2(A299A) YLR123C(L8L)*
	yHs16_evo0_C4	*yMAH868*	*hnt1(M15I) dpb2(P110T) pxr1(E210stop) YHL017W(E473D) zwf1(G228D) utp20(E1318D) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*met1(V36V) mag2(T405T) lto1(–222) ret2(A299A) YLR123C(L8L)*
	yHs16_evo0_C5	*yMAH869*	*rad54(K588E) rsc30(D571G) mlp2(E377Stop) msb1(D243V) rsc2(P861T) top1(E713stop) ski3(A1427S) utp20(E1318D) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*mcm6(–1188) asn2(–437) tcd2(–37) ret2(A299A) YLR123C(L8L)*

	yHs16_evo0_C6	*yMAH870*	*rsc3(M641I) arg1(R367stop) bbp1(+230) aos1(Q121R) utp20(E1318D) avl9(S427C) YLR125W(S82Stop) nha1(L599Stop) ubp2(K405Q)*	*msg5(+292)* *ret2(A299A)* *YLR123C(L8L)*

Appendix Table S2. ***Aneuploidy abundance in histone-humanized yeasts.***

Lineage	***Strain***	***I***	***II***	***III***	***IV***	***V***	***VI***	***VII***	***VIII***	***IX***	***X***	***XI***	***XII***	***XIII***	***XIV***	***XV***	***XVI***	***source***
yHs1	*yHs1-pool*												*2*					*Truong and Boeke. Cell 2017*
	yHs1C5	*1*	*1*	*1*		*1*				*1*		*1*					*2*	*Truong and Boeke. Cell 2017*
	yHs1-evo												*2*					*Truong and Boeke. Cell 2017*
	1C5i2												*2*					*Truong and Boeke. Cell 2017*
	1PC5i3		*1*	*1*									*2*					*Truong and Boeke. Cell 2017*
	1PC5i5		*1*	*1*									*2*					*Truong and Boeke. Cell 2017*
yHs2	*yHs2-pool*	*2*	*1*	*1*						*1*							*1.5*	*Truong and Boeke. Cell 2017*
	yHs2C5	*1*	*1*	*1*		*1*				*1*		*1.7*					*2*	*Truong and Boeke. Cell 2017*
	yHs2-evo	*3*	*1*	*1*		*1*			*1*	*1*		*1.5*					*2*	*Truong and Boeke. Cell 2017*
	2PC6il	*2*																*Truong and Boeke. Cell 2017*
	phe2AE	*2*																*Truong and Boeke. Cell 2017*
	phe2AF																	*Truong and Boeke. Cell 2017*
	phe2AH	*2*		*1.7*														*Truong and Boeke. Cell 2017*
	phe2BC	*2*								*1*							*1.5*	*Truong and Boeke. Cell 2017*
	phe2BD	*1.8*															*1.5*	*Truong and Boeke. Cell 2017*
	phe23C	*1.5*																*Truong and Boeke. Cell 2017*
yHs3	*yHs3-pool*		*1.5*										*2*					*Truong and Boeke. Cell 2017*
	yHs3C5	*2*																*Truong and Boeke. Cell 2017*
	yHs3-evo	*1*	*1*	*1*						*1*	*1*						*1.5*	*Truong and Boeke. Cell 2017*
yHs4	*yHs4-pool*												*2*					*Truong and Boeke. Cell 2017*
	yHs4C5	*1*		*1*													*1.5*	*Truong and Boeke. Cell 2017*
	yHs4-evo																	*Truong and Boeke. Cell 2017*
yHs5	*yHs5-pool*	*1*	*1*	*1*		*1*				*1*			*1*				*2*	*Truong and Boeke. Cell 2017*
	yHs5C5	*1*	*1*	*1*		*1*				*1*			*1*				*1.5*	*Truong and Boeke. Cell 2017*
	yHs5C10	*1*	*1*	*1*		*1*				*1*			*1*				*1.5*	*Truong and Boeke. Cell 2017*
	yHs5-evo	*1*	*1*	*1*		*1*				*1*			*1*				*1.5*	*Truong and Boeke. Cell 2017*
yHs6	*yHs6-pool*		*1*										*2*					*Truong and Boeke. Cell 2017*
	6C5	*1*		*1*													*2*	*Truong and Boeke. Cell 2017*
	yHs6-evo	*1*	*1*	*1*								*1*					*1.5*	*Truong and Boeke. Cell 2017*

yHs7	*yHs7-pool*		*1.5*										*1*					*Truong and Boeke. Cell 2017*
	yHs7C5																	*Truong and Boeke. Cell 2017*
	yHs7C10																	*Truong and Boeke. Cell 2017*
	yHs7-evo																	*Truong and Boeke. Cell 2017*
yHs8	*yHs8*		*1*	*1*									*1*					*Truong and Boeke. Cell 2017*
yHs9	*yHs9-pool*	*2*	*1*	*2*		*0.75*				*1*		*0.25*					*1*	*This Study.*
	yHs9-evo5	*1.25*		*2*	*0.25*					*1.75*		*0.25*					*1*	*This Study.*
	yHs9e5C1	*1*		*1*						*2*							*1*	*This Study.*
	yHs9e5C2	*1*		*1*						*1*								*This Study.*
	yHs9e5C3	*1*		*2*						*1.5*							*1*	*This Study.*
yHs10	*yHs10-pool*	*2.5*		*1*		*0.5*	*1*			*0.75*							*2*	*This Study.*
	yHs10-evo5	*1*		*1*		*0.25*	*0.25*										*1.75*	*This Study.*
yHs11	*yHs11-pool*	*2*	*0.5*	*1*			*0.25*										*2.25*	*This Study.*
	yHs11-evo5	*1.75*	*1*	*0.5*								*1*					*1*	*This Study.*
	yHs11e5C2	*2*	*1*	*1*		*0.5*				*1*		*1*					*1*	*This Study.*
yHs12	*yHs12-pool*	*1.5*	*1*															*This Study.*
	yHs12-evo5	*0.75*	*1*															*This Study.*
	yHs12e5C1	*1*	*1*	*1*		*0.25*	*0.25*			*1*		*0.25*					*1*	*This Study.*
yHs13	*yHs13-pool*			*0.25*									*1.75*					*This Study.*
	yHs13-evo5																	*This Study.*
yHs14	*yHs14-pool*	*2.25*	*0.5*	*1*			*0.25*			*0.25*								*This Study.*
	yHs14-evo5	*2*	*1*	*1*								*1*					*1*	*This Study.*
	yHs14e5C1	*2*	*1*	*1*						*1*		*1*					*1*	*This Study.*
yHs15	*yHs15-pool*	*2*	*1*	*1*			*0.25*			*0.25*		*0.25*					*0.75*	*This Study.*
	yHs15-evo5	*2*	*1*	*1.75*								*1*					*1*	*This Study.*
	yHs15e5C1	*2*	*1*	*2*													*1*	*This Study.*

	yHs15e5C2	*2.5*	*1*	*1*								*1*					*1*	*This Study.*
	yHs15e5C3	*2*	*1*	*1.5*								*1*					*1.5*	*This Study.*
yHs16	*yHs16-_pool*	*1.75*	*0.75*							*0.25*		*0.5*					*1*	*This Study.*
	yHs16-evo5C1	*2*								*0.25*							*1.75*	*This Study.*
	yHs16-evo5C2	*1.75*	*1.5*									*1*					*1.25*	*This Study.*
	yHs16-evo5C3	*2*	*0.75*	*1*					*0.25*								*0.75*	*This Study.*

Appendix Table S3. ***Strains used in this study.***						
Name	***notes***	***MAT***	***Genotype***	***Plasmid***	***Markers***	***Reference***
yMAH302	*wild type histone shuffle strain*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0*	*pDT139*	*URA3*	*Haase et al. 2019*
yMAH0344	*histone humanized isolate yHs9 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0345	*histone humanized isolate yHs10 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0346	*histone humanized isolate yHs11 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0347	*histone humanized isolate yHs12 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0348	*histone humanized isolate yHs13 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0349	*histone humanized isolate yHs14 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0343	*histone humanized isolate yHs15 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0355	*histone humanized isolate yHs13 g6*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0383	*histone humanized isolate yHs13 g12*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0390	*histone humanized isolate yHs13 g18*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0397	*histone humanized isolate yHs13 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0393	*histone humanized isolate yHs9 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0394	*histone humanized isolate yHs10 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0395	*histone humanized isolate yHs11 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0396	*histone humanized isolate yHs12 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0398	*histone humanized isolate yHs14 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0392	*histone humanized isolate yHs15 g30*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH0598	*histone humanized isolate yHs16 ancestral*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH531	*histone humanized isolate yHs9 g30 isolate 1*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH532	*histone humanized isolate yHs9 g30 isolate 2*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH533	*histone humanized isolate yHs9 g30 isolate 3*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH536	*histone humanized isolate yHs11 g30 isolate 2*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH456	*histone humanized isolate yHs12 g30 isolate 2*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*
yMAH538	*histone humanized isolate yHs14 g30 isolate 1*	*α*	*his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 **	*pDT109*	*TRP1*	*This study*

yMAH528	histone humanized isolate yHs15 g30 isolate 1	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH529	histone humanized isolate yHs15 g30 isolate 2	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH530	histone humanized isolate yHs15 g30 isolate 3	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH865	histone humanized isolate yHs16 evo0 isolate 1	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH866	histone humanized isolate yHs16 evo0 isolate 2	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH867	histone humanized isolate yHs16 evo0 isolate 3	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH868	histone humanized isolate yHs16 evo0 isolate 4	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH869	histone humanized isolate yHs16 evo0 isolate 5	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH870	histone humanized isolate yHs16 evo0 isolate 6	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 *	pDT109	TRP1	This study
yMAH628	SPC105-R583S histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 SPC105(R583S)	pDT139	URA3	This study
yMAH658	DAM1-N80Y histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80Y)	pDT139	URA3	This study
yMAH660	NDC80-E568A histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NDC80(E568A)	pDT139	URA3	This study
yMAH662	SPC34-L63Q histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 SPC34(L63Q)	pDT139	URA3	This study
yMAH668	dad4-N61K histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 dad4(N61K)	pDT139	URA3	This study
yMAH700	DAD1-E50D histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50D)	pDT139	URA3	This study
yMAH723	NDC80-E568A histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NDC80(E568A)	pDT139	URA3	This study
yMAH729	isogenic wild type histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0	pDT139	URA3	This study
yMAH732	SPC34-L63Q histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 SPC34(L63Q)	pDT139	URA3	This study
yMAH735	SPC105-R583S histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 SPC105(R583S)	pDT139	URA3	This study
yMAH738	dad4-N61K histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 dad4(N61K)	pDT139	URA3	This study
yMAH855	DAD1-E50D histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50D)	pDT139	URA3	This study
yMAH1078	DAM1-N80Y histone shuffle strain	a	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80Y)	pDT139	URA3	This study
yMAH798	isogenic diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0	pDT139	URA3	This study
yMAH799	SPC34-L63Q diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 SPC34(L63Q)/ SPC34(L63Q)	pDT139	URA3	This study
yMAH800	SPC105-R583S diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 SPC105(R583S)/SPC105(R583S)	pDT139	URA3	This study

yMAH801	NDC80-E568A diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 NDC80(E568A)/NDC80(E568A)	pDT139	URA3	This study
yMAH810	dad4-N61K diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 dad4(N61K)/dad4(N61K)	pDT139	URA3	This study
yMAH889	DAD1-E50D diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 DAD1(E50D)/DAD1(E50D)	pDT139	URA3	This study
yMAH1122	DAM1-N80Y diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 DAM1(N80Y)/DAM1(N80Y)	pDT139	URA3	This study
yMAH804	SPC34-L63Q het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 SPC34/ SPC34(L63Q)	pDT139	URA3	This study
yMAH802	SPC105-R583S het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 SPC105/SPC105(R583S)	pDT139	URA3	This study
yMAH814	NDC80-E568A het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 NDC80/NDC80(E568A)	pDT139	URA3	This study
yMAH803	dad4-N61K het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 DAD4/dad4(N61K)	pDT139	URA3	This study
yMAH805	DAD1-E50D het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 DAD1/DAD1(E50D)	pDT139	URA3	This study
yMAH813	DAM1-N80Y het. diploid wild type histone shuffle strain	a / α	his3Δ200/his3Δ200 leu2Δ0/leu2Δ0 lys2Δ0/lys2Δ0 trp1Δ63/trp1Δ63 ura3Δ0/ura3Δ0 met15Δ0/met15Δ0 hta2-htb2Δ0/hta2-htb2Δ0 hta1-htb1Δ0/hta1-htb1Δ0 hht1-hhf1Δ0/hht1-hhf1Δ0 hht2-hhf2Δ0/hht2-hhf2Δ0 DAM1/DAM1(N80Y)	pDT139	URA3	This study
yMAH1037	scc4-D65Y histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 scc4(D65Y)	pDT139	URA3	This study
yMAH1043	scc4-D65Y & DAM1-N80Y histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 scc4(D65Y) DAM1(N80Y)	pDT139	URA3	This study
yMAH1047	scc4-D65Y & DAD1-E50D histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 scc4(D65Y) DAD1(E50D)	pDT139	URA3	This study
yMAH1331	wild type histone shuffle strain Nuf2-RFP and Spc110-GFP	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NUF2::ymScarlet SPC110::mNeonGreen	pDT139	URA3	This study
yMAH1337	scc4-D65Y histone shuffle strain Nuf2-RFP and Spc110-GFP	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NUF2::ymScarlet SPC110::mNeonGreen scc4(D65Y)	pDT139	URA3	This study
yMAH1224	DAD1-E50D histone shuffle strain Nuf2-RFP and Spc110-GFP	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NUF2::ymScarlet SPC110::mNeonGreen DAD1(E50D)	pDT139	URA3	This study
yMAH1233	SPC105-R583S histone shuffle strain Nuf2-RFP and Spc110-GFP	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 NUF2::ymScarlet SPC110::mNeonGreen SPC105(R583S)	pDT139	URA3	This study
yGOL023	mad3 deleltion strain	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 mad3Δ0			This study
yGOL024	mad3 deleltion strain	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 mad3Δ0			This study
yGOL027	ipl1-2 ts mutant strain	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 ipl1-2(H352Y)			This study
yGOL028	ipl1-2 ts mutant strain	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 ipl1-2(H352Y)			This study

yGOL029	mad3 deleltion strain with dad-1E50D mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAD1(E50D) mad3Δ0			This study
yGOL030	mad3 deleltion strain with DAD1-E50D mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAD1(E50D) mad3Δ0			This study
yGOL033	ipl1-2 ts mutant strain with DAD1-E50D mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAD1(E50D) ipl1-2(H352Y)			This study
yGOL034	ipl1-2 ts mutant strain with DAD1-E50D mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAD1(E50D) ipl1-2(H352Y)			This study
yGOL039	ipl1-2 ts mutant strain with NDC80-E568A mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 NDC80-E568A ipl1-2(H352Y)			This study
yGOL040	ipl1-2 ts mutant strain with NDC80-E568A mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 NDC80-E568A ipl1-2(H352Y)			This study
yGOL045	ipl1-2 ts mutant strain with SPC105-R583S mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 SPC105-R583S ipl1-2(H352Y)			This study
yGOL046	ipl1-2 ts mutant strain with SPC105-R583S mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 SPC105-R583S ipl1-2(H352Y)			This study
yGOL051	ipl1-2 ts mutant strain with SPC34-L63Q mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 SPC34-L63Q ipl1-2(H352Y)			This study
yGOL052	ipl1-2 ts mutant strain with SPC34-L63Q mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 SPC34-L63Q ipl1-2(H352Y)			This study
yGOL057	ipl1-2 ts mutant strain with DAM1-N80Y mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAM1-N80Y ipl1-2(H352Y)			This study
yGOL058	ipl1-2 ts mutant strain with DAM1-N80Y mutation	a	leu2Δ0 met15Δ0 ura3Δ0 his3Δ1 DAM1-N80Y ipl1-2(H352Y)			This study
yGOL015	mad3 deleltion shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 mad3Δ	pDT139	URA3	This study
yGOL016	mad3 deleltion shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 mad3Δ	pDT139	URA3	This study
yMAH955	DAM1 residue 80 mutant shuffle strain DAM1-N80C	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80C)	pDT139	URA3	This study
yMAH958	DAM1 residue 80 mutant shuffle strain DAM1-N80G	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80G)	pDT139	URA3	This study
yMAH961	DAM1 residue 80 mutant shuffle strain DAM1-N80I	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80I)	pDT139	URA3	This study
yMAH964	DAM1 residue 80 mutant shuffle strain DAM1-N80M	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80M)	pDT139	URA3	This study
yMAH967	DAM1 residue 80 mutant shuffle strain DAM1-N80R	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80R)	pDT139	URA3	This study
yMAH969	DAM1 residue 80 mutant shuffle strain DAM1-N80D	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80D)	pDT139	URA3	This study
yMAH971	DAM1 residue 80 mutant shuffle strain DAM1-N80S	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80S)	pDT139	URA3	This study
yMAH972	DAM1 residue 80 mutant shuffle strain DAM1-N80A	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80A)	pDT139	URA3	This study
yMAH973	DAM1 residue 80 mutant shuffle strain DAM1-N80V	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80V)	pDT139	URA3	This study
yMAH975	DAM1 residue 80 mutant shuffle strain DAM1-N80L	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80L)	pDT139	URA3	This study
yMAH976	DAM1 residue 80 mutant shuffle strain DAM1-N80W	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80W)	pDT139	URA3	This study
yMAH978	DAM1 residue 80 mutant shuffle strain DAM1-N80H	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80H)	pDT139	URA3	This study
yMAH980	DAM1 residue 80 mutant shuffle strain DAM1-N80F	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80F)	pDT139	URA3	This study

yMAH987	DAM1 residue 80 mutant shuffle strain DAM1-N80E	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80E)	pDT139	URA3	This study
yMAH995	DAM1 residue 80 mutant shuffle strain DAM1-N80T	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80T)	pDT139	URA3	This study
yMAH998	DAM1 residue 80 mutant shuffle strain DAM1-N80Q	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAM1(N80Q)	pDT139	URA3	This study
yMAH1248	DAD1-E50D DAM1-N80Q histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50D) DAM1(N80Q)	pDT139	URA3	This study
yMAH1063	DAD1-E50A histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50A)	pDT139	URA3	This study
yMAH1074	DAD1-E50A DAM1-N80Y histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50A) DAM1(N80Y)	pDT139	URA3	This study
yJL332	SK1 WT diploid	a / α	ho::LYS2/ho::LYS2, lys2/lys2, ura3/ura3, leu2::hisG/leu2::hisG, his3::hisG/his3::hisG, trp1::hisG/his3::hisG			Luo et al.
yMAH1323	SK1 DAD1-E50D/WT het. diploid	a / α	ho::LYS2/ho::LYS2, lys2/lys2, ura3/ura3, leu2::hisG/leu2::hisG, his3::hisG/his3::hisG, trp1::hisG/his3::hisG, DAD1/DAD1(E50D)			This study
yMAH1356	SK1 DAD1-E50D/DAD1-E50D hom. diploid	a / α	ho::LYS2/ho::LYS2, lys2/lys2, ura3/ura3, leu2::hisG/leu2::hisG, his3::hisG/his3::hisG, trp1::hisG/his3::hisG, DAD1(E50D)/DAD1(E50D)			This study
yDT67	wild type histone shuffle strain	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0	pDT105	TRP1	Truong and Boeke.
yDT180	DAD1(E50D) hH3.1-core histone humanized	α	his3Δ200 leu2Δ0 lys2Δ0 trp1Δ63 ura3Δ0 met15Δ0 hta2-htb2Δ0 hta1-htb1Δ0 hht1-hhf1Δ0 hht2-hhf2Δ0 DAD1(E50D)	pDT109	TRP1	Truong and Boeke.
BY4742	Wildtype MATα	α	MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0			Brachmann CB, et al.
Notes						
Haase et al.; https://doi.org/10.1534/g3.119.400325						
Luo et al.; https://doi.org/10.1038/s41586-018-0374-x						
Truong and Boeke.; https://doi.org/10.1016/j.cell.2017.10.043						
Brachmann CB, et al.; https://doi.org/10.1002/(SICI)1097-0061(19980130)14:2<115::AID-YEA204>3.0.CO;2-2						
*Detailed genotypes can be found in Supplemental table 2						

Appendix Table S4. ***Plasmids used in this study.***

Plasmid	***Name***	***markers***	***Description***	***Source***
yeast histone plasmid	*pDT139*	*KAN URA3*	*Superloser plasmid with four core histone genes (HTA2-HTB2-HHT1-HHF1)*	*Haase et al. 2019*
human histone plasmid	*pDT109*	*AMP / TRP1*	*pRS414 with human core histones (H3.1 H4 H2A H2B) with HHT2F2HTA1B1 PROs/TERs*	*Truong and Boeke. 2017*
LEU2 guide RNA expression vector	*pNA525*	*AMP / LEU2*	*p425-SNR52p-NotI(gRNA)-SUP4t - NotI site for inserting any gRNA using Gibson Assembly.*	*DiCarlo et al. 2013*
Cas9 vector	*pNA0519*	*AMP / HIS*	*pRS413-TEF1p-Cas9-CYC1t - Cas9 fragment cloned into pRS413*	*DiCarlo et al. 2013*
DAM1 guide RNA plasmid	*pMAH298*	*AMP / LEU2*	*guide RNA targeting the Dam1 locus at codon 88*	*this study*
SPC34 guide RNA plasmid	*pMAH300*	*AMP / LEU2*	*guide RNA targeting the Spc34 locus at codon 59*	*this study*
SPC105 guide RNA plasmid	*pMAH301*	*AMP / LEU2*	*guide RNA targeting the Spc105 locus at codon 583*	*this study*
DAD4 guide RNA plasmid	*pMAH302*	*AMP / LEU2*	*guide RNA targeting the Dad4 locus at codon 62*	*this study*
NDC80 guide RNA plasmid	*pMAH299*	*AMP / LEU2*	*guide RNA targeting the Ndc80 locus at codon 618*	*this study*
DAD1 guide RNA plasmid	*pMAH604*	*AMP / LEU2*	*guide RNA targeting the Dad1 locus at codon 49*	*this study*
SCC4 guide RNA plasmid	*pMAH606*	*AMP / LEU2*	*guide RNA targeting the Scc4 locus at codon 64*	*this study*
NUF2 guide RNA plasmid	*pMAH441*	*AMP / LEU2*	*guide RNA targeting the 3' end of the Nuf2 locus*	*this study*
SPC110 guide RNA plasmid	*pMAH439*	*AMP / LEU2*	*guide RNA targeting the 3' end of the Spc110 locus*	*this study*
SPC110-mNeonGreen repair template	*pMAH460*	*AMP*	*pUC19-Spc110-mNeonGreen targeting repair template.*	*this study*
NUF2-ymScarlet repair template	*pMAH462*	*AMP*	*pUC19-NUF2-ymScarlet targeting repair template.*	*this study*
IPL1 guide RNA plasmid	*pMAH328*	*AMP / LEU2*	*guide RNA targeting the Ipl1 locus at codon 345*	*this study*
MAD3 guide RNA plasmid	*pMAH512*	*AMP / LEU2*	*guide RNA targeting the Mad3 locus at codon 285*	*this study*
Dam1 complex expression vector	*pJT44*	*AMP*	*Two polycistrons containing Dad1, Duo1, Spc34-FLAG, Dam1, Hsk3 and Dad4, Dad3, Dad2, Spc19, Ask1*	*Umbreit et al.2014*
Dam1 complex DAD1E50D expression vector	*pMAH359*	*AMP*	*Two polycistrons containing Dad1(E50D), Duo1, Spc34-FLAG, Dam1, Hsk3 and Dad4, Dad3, Dad2, Spc19, Ask1*	*this study*
pRS416-DAD1-E50D	*pMAH490*	*AMP / URA3*	*pRS416 with Dad1(E50D) - with native promoter/terminator*	*this study*
pRS416-DAD1	*pMAH492*	*AMP / URA3*	*pRS416 with Dad1 - with native promoter/terminator*	*this study*

Appendix Table S5. ***DNA oligos used in this study.***

Name	**oligo**	**sequence 5' -> 3'**	**notes**	**source**
gRNA-DAM1	oMH876	TGAAAGATAAATGATCTAAGATCAGCTAAACTCTCGGTTTTAGAGCTAGAAA	sgRNA Dam1; flanking homology for subcloning into NotI site on guide expression plasmid	this study
Dam1-N80Y-F	oMH877	CTGAGCGATTCAATCATTACTTTAGATTCTTATTTCACGCGCTTAAATTTTATACACGAG	Repair template Forward oligo	this study
Dam1-N80Y-R	oMH878	ACAACAACGAACCTAGGGATTCATTAAGATCAGCTAAACTCTCGTGTATAAAATTTAAGC	Repair template Reverse oligo	this study
gRNA-NDC80	oMH881	TGAAAGATAAATGATCAACTAAAATTTCAGATGCTGGTTTTAGAGCTAGAAA	sgRNA Ndc80; flanking homology for subcloning into NotI site on guide expression plasmid	this study
gRNA-SPC34	oMH882	TGAAAGATAAATGATCAAAGGACTGTAACCACGACGGTTTTAGAGCTAGAAA	sgRNA Spc34; flanking homology for subcloning into NotI site on guide expression plasmid	this study
gRNA-DAD4	oMH905	TGAAAGATAAATGATCTAGTAGCGTCCAATTCAACCGTTTTAGAGCTAGAAA	sgRNA Dad4; flanking homology for subcloning into NotI site on guide expression plasmid	this study
gRNA-DAD1	oMH1392	TGAAAGATAAATGATCGAATGGTCTCAATATATCATGTTTTAGAGCTAGAAA	sgRNA Dad1; flanking homology for subcloning into NotI site on guide expression plasmid	this study
gRNA-SPC105	oMH893	TGAAAGATAAATGATCCAATGGAATGGTATGAATGGGTTTTAGAGCTAGAAA	sgRNA Spc105; flanking homology for subcloning into NotI site on guide expression plasmid	this study
NDC80-E568A-F	oMH879	GCATGACATAAATGAGAAAACTCAAATTAATGAAAAACTTGCATTGG	Repair template Forward oligo	this study
NDC80-E568A-R	oMH880	CTTCCAATTTTAGTTCCGTTGAAGTTACCAATTCTTCAGCATCTGAA	Repair template Reverse oligo	this study
SPC34-L63Q-F	oMH883	AGCATTAGAAAAGACATTACTAGACTAATAAAGGACTGTAACCACGACGAAGCGTATCTT	Repair template Forward oligo	this study
SPC34-L63Q-R	oMH884	TACGTGAAACGGATTGTTTCTCAGGGTTGACTTTGAACTGAAGATACGCTTCGTCGTGGT	Repair template Reverse oligo	this study
SPC105-R583S-F	oMH894	TGGTCAAAGGATATTCGAAATTGGAGGCAGCAATGGAATGGTATGAATGGAGCAAAAAGC	Repair template Forward oligo	this study
SPC105-R583S-R	oMH895	TTCAAATTTTCTGCCAAAATTAATTCCAGACCATTTAGTTGCTTTTTGCTCCATTCATAC	Repair template Reverse oligo	this study
DAD4-N61K-F	oMH906	ATCATGGGCGCAATTTGTGATAACTACCATAGTAGCGTCCAATTCAAGCTAGAAGCGACC	Repair template Forward oligo	this study
DAD4-N61K-R	oMH907	ATAGAAAATTGGTGAATTAAAGAGGTGGCTTCTTGTTATTGGTCGCTTCTAGCTTGAATT	Repair template Reverse oligo	this study
DAD1-E50D-F	oMH636	AAATCAGAAACTGACTGGAATTCTCTTCCCACAGCTATCGAGCTATCTAATGATATATTG	Repair template Forward oligo	this study
DAD1-E50D-R	oMH637	ATGAGACTATGAATTCAATCTTGAATGGTCTGAATGGTCTCAATATATCATTAGATAGCT	Repair template Reverse oligo	this study
gRNA-SCC4	oMH1420	TGAAAGATAAATGATCATGTACGCTTTCAGTTCTGGGTTTTAGAGCTAGAAA	sgRNA Scc4; flanking homology for subcloning into NotI site on guide expression plasmid	this study
SCC4-D65Y-F	oMH1418	TATCCAGATGTTTCAGCTATTGAAAACGAAATGTACGCTTTCAGTTCTGGAGTATAGTAA	Repair template Forward oligo	this study
SCC4-D65Y-R	oMH1419	CGTCTCCTGTATCAATAACTCCACCATCTCAAACGTGACCTTACTATACTCCAGAACTGA	Repair template Reverse oligo	this study
UBC6 F RT-PCR	oMH1571	ACAAGGGCGGTCAATATCACG		Ling and Yuen. PNAS 2019
UBC6 R RT-PCR	oMH1572	TGGGCTTGAAACGTCCATTCG		Ling and Yuen. PNAS 2019
CLN2 F RT-PCR	oMH1573	ATGCTGCAAGAATACCACCAA		Ling and Yuen. PNAS 2019

CLN2 R RT-PCR	*oMH1574*	*TCATTTCAGGCTGCTGGTCTA*		*Ling and Yuen. PNAS 2019*
CEN16 F RT-PCR	*oMH1577*	*AAAGGTTGAAGCCGTTATGTTGTCG*		*Ling and Yuen. PNAS 2019*
CEN16 R RT-PCR	*oMH1578*	*TTAGCCGCTTTGCCGATTTCGC*		*Ling and Yuen. PNAS 2019*
CEN6 F RT-PCR	*oMH1579*	*TTTTGTTTTCCGAAGATGTAAAATAGGTTG*		*Ling and Yuen. PNAS 2019*
CEN6 R RT-PCR	*oMH1580*	*GTTCTGCTTTCCTTCCCAAACAG*		*Ling and Yuen. PNAS 2019*
CEN1 F RT-PCR	*oMH1581*	*TGTAATGATTTAAGTCTTGTCACATGA*		*Ling and Yuen. PNAS 2019*
CEN1 R RT-PCR	*oMH1582*	*AAAATACTTTGACTGCTTCGGAA*		*Ling and Yuen. PNAS 2019*
CEN7 F RT-PCR	*oMH1583*	*TTCATGGAAATTTGCTTCTTGAGC*		*Ling and Yuen. PNAS 2019*
CEN7 R RT-PCR	*oMH1584*	*TCCAATACTTTGTCGTCAATATTCTTTC*		*Ling and Yuen. PNAS 2019*
CEN3 F RT-PCR	*oMH1585*	*GGAAAATCCACAGAAAGCTATTCA*		*Ling and Yuen. PNAS 2019*
CEN3 R RT-PCR	*oMH1586*	*CCACCAGTAAACGTTTCATATATCCA*		*Ling and Yuen. PNAS 2019*
gRNA-NUF2-3'	*oMH1089*	*TGAAAGATAAATGATCTCGAATATATGCAATAGCAGGTTTTAGAGCTAGAAA*	*sgRNA Nuf2 (3' end, near stop); flanking homology for subcloning into NotI site on guide expression plasmid*	*this study*
gRNA-SPC110-3'	*oMH1098*	*TGAAAGATAAATGATCATAGAATTGAGAGTAGCAGCGTTTTAGAGCTAGAAA*	*sgRNA Spc110 (3' end, near stop); flanking homology for subcloning into NotI site on guide expression plasmid*	*this study*
gRNA-IPL1	*oMH718*	*TGAAAGATAAATGATCGATGCATTTTTACGTCTCCAGTTTTAGAGCTAGAAA*	*sgRNA Ipl1; flanking homology for subcloning into NotI site on guide expression plasmid*	*this study*
IPL1-H352Y-F	*oMH719*	*TTAAACTACTAAAATACGACCCCAAAGATAGAATGCGTCTTGGAGACGTAAAAATGTATC*	*Repair template Forward oligo*	*this study*
IPL1-H352Y-R	*oMH720*	*CGCTTATTTTCCCAAAAGGGCTTGTTTCTTAGTATCCAAGGATACATTTTTACGTCTCCA*	*Repair template Reverse oligo*	*this study*
gRNA-MAD3	*oMH1315*	*TGAAAGATAAATGATCGAGGTGTTTATAGAGATGGCGTTTTAGAGCTAGAAA*	*sgRNA Mad3; flanking homology for subcloning into NotI site on guide expression plasmid*	*this study*
MAD3-∆-F	*oMH1316*	*ATAGTAAACAAAATCATGCGAAAATACAATAAAAGACGTTAACTTGATAGAAATAAAACT*	*Repair template Forward oligo*	*this study*
MAD3-∆-R	*oMH1317*	*TGTTTACGATTGGCCAGTATACTTACTCATTCATGGGATTAGTTTTATTTCTATCAAGTT*	*Repair template Reverse oligo*	*this study*
Dam1-N80A-F	*oMH1343*	*CTGAGCGATTCAATCATTACTTTAGATTCCGCTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80C-F	*oMH1344*	*CTGAGCGATTCAATCATTACTTTAGATTCCTGTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80G-F	*oMH1345*	*CTGAGCGATTCAATCATTACTTTAGATTCCGGTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*

Dam1-N80I-F	*oMH1346*	*CTGAGCGATTCAATCATTACTTTAGATTCCATTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80P-F	*oMH1347*	*CTGAGCGATTCAATCATTACTTTAGATTCCCCATTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80S-F	*oMH1348*	*CTGAGCGATTCAATCATTACTTTAGATTCCTCTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80T-F	*oMH1349*	*CTGAGCGATTCAATCATTACTTTAGATTCCACTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80V-F	*oMH1350*	*CTGAGCGATTCAATCATTACTTTAGATTCCGTTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80D-F	*oMH1351*	*CTGAGCGATTCAATCATTACTTTAGATTCCGATTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80E-F	*oMH1352*	*CTGAGCGATTCAATCATTACTTTAGATTCCGAATTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80K-F	*oMH1353*	*CTGAGCGATTCAATCATTACTTTAGATTCCAAATTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80L-F	*oMH1354*	*CTGAGCGATTCAATCATTACTTTAGATTCCTTGTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80M-F	*oMH1355*	*CTGAGCGATTCAATCATTACTTTAGATTCCATGTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80Q-F	*oMH1356*	*CTGAGCGATTCAATCATTACTTTAGATTCCCAATTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80R-F	*oMH1357*	*CTGAGCGATTCAATCATTACTTTAGATTCCAGATTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80F-F	*oMH1358*	*CTGAGCGATTCAATCATTACTTTAGATTCCTTTTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80H-F	*oMH1359*	*CTGAGCGATTCAATCATTACTTTAGATTCCCATTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
Dam1-N80W-F	*oMH1360*	*CTGAGCGATTCAATCATTACTTTAGATTCCTGGTTCACGCGCTTAAATTTTATACACGAG*	*Repair template Forward oligo; used with oMH878*	*this study*
DAD1-E50A-F	*oMH1393*	*GAGACTATGAATTCAATCTTGAATGGTCTGAATGGTCTCAATATATCATTAGCTAGCTCG*	*Repair template Forward oligo*	*this study*
DAD1-E50A-R	*oMH1394*	*ACAAATCAGAAACTGACTGGAATTCTCTTCCCACAGCTATCGAGCTAGCTAATGATATAT*	*Repair template Reverse oligo*	*this study*
Forward PCRtag for HTA2	*oMH308*	*AGGTGGTAAAGCTGGTTCAGC*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for HTA2	*oMH309*	*CTCAGTTTCTTACAGTTCTTGAGAAGC*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for HTB2	*oDT133*	*GGTAACAGCTCTAGTACCTTCAGAG*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for HTB2	*oDT134*	*GCCGAAAAGAAACCAGC*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for HHT1	*oDT484*	*GCTGCCAGAAAATCCGCC*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for HHT1	*oDT557*	*GCCAACTTGATATCCTTCTTTTGGATAGT*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for HHF1	*oDT488*	*AGAGGTAAAGGTGGTAAAGGTCTA*	*histone genotyping*	*Haase et al. G3 2019*

Reverse PCRtag for HHF1	*oDT567*	*GGATTTCAAGACNGCTCTGAC*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for hH2A.1	*oMH263*	*CGAATCTCACCACAAGGCTAAGGG*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for hH2A.1I	*oMH243*	*GTTGTGTGGAATTGTGAGCGGATAAC*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for hH2B.3J	*oMH264*	*CTCCAGCTCCAAAGAAGGGTTC*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for hH2B.3J	*oMH265*	*GCTTGATATCGAATTCCTGCAGCC*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for hH3.1	*oMH262*	*ATGGCTTTGCAAGAGGCCTG*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for hH3.1	*oMH242*	*GCTGGCGAAAGGGGGATG*	*histone genotyping*	*Haase et al. G3 2019*
Forward PCRtag for hH4	*oDT565*	*GGTGGTAAGGGTTTGGGTAAG*	*histone genotyping*	*Haase et al. G3 2019*
Reverse PCRtag for hH4	*oDT566*	*GAAAACCTTCAAAACACCTCTGGT*	*histone genotyping*	*Haase et al. G3 2019*

Appendix Table S6. ***Sporulation in Dad1-E50D diploids***

Genotype	***2 spores***	***3 spores***	***Immature***	***Total***
WT	*0.85*	*0.85*	*3.42*	*117*
HET Dad1-E50D	*4.96*	*5.51*	*23.69*	*363*
HOMO Dad1-E50D	*6.92*	*6.92*	*15.38*	*130*

Values are % of total spores after 5 days in sporulation medium.