

SUPPLEMENTARY TABLES

Supplementary Table 2. Plasmids used in this study.

Name	Description	Source
pFA6a-HIS3MX6	<i>pBR322 origin, Amp^R, HIS3MX6, HIS3 gene from S. kluyveri.</i>	[2]
pFA6a-KanMX6	<i>pBR322 origin, Amp^R, KanMX6, KanMX gene contains the known kanr ORF of the E. coli transposon Tn903.</i>	[2]
pFA6a-GFP-KIURA3	<i>pBR322 origin, Amp^R, URA3, GFP tag with URA3 gene</i>	[3]
pFA6a-HA-KIURA3	<i>pBR322 origin, Amp^R, URA3, Triple HA tag with URA3 gene</i>	[3]
pGP564	<i>2μ, Kan^R, LEU2</i>	[4]
YGPM2h11	<i>2μ, Kan^R, LEU2, [YBR109W-A]&, [ALG1], YSA1, SUS1, CYC8, YBR113W, RAD16, [LYS2]&</i>	[4]
YGPM5d22	<i>2μ, Kan^R, LEU2, [DAP1]&, MEX67, YPL168W, REV3, YPL166W, [SET6], [MLH3]&</i>	[4]
YGPM6e10	<i>2μ, Kan^R, LEU2, [CUE5]&, snR62, WHI2, YOR044W TOM6, DBP5, STD1, [RAT1]&</i>	[4]
YGPM25a15	<i>2μ, Kan^R, LEU2, [YKL187C]* MTR2 ASH1 SPE1 YKL183C-A [LOT5]*</i>	[4]
YGPM17i23	<i>2μ, Kan^R, LEU2, [RSM23]* CWC23 SOH1 SCS3 MET13 MON1 RPS2 YGL123C-A NAB2 GPG1 [PRP43]</i>	[4]
pRS316	<i>CEN/ARS, Amp^R, URA3</i>	[5]
pRS316-SUS1	<i>CEN/ARS, Amp^R, URA3, SUS1 ORF with +- 900 bp of UTR</i>	This study
pRS316-MEX67	<i>CEN/ARS, Amp^R, URA3, MEX67 ORF with +- 900 bp of UTR</i>	This study
pRS316-DBP5	<i>CEN/ARS, Amp^R, URA3, DBP5 ORF with +- 900 bp of UTR</i>	This study
pRS425	<i>2μ, Amp^R, LEU2</i>	[6]
pRS425-SUS1	<i>2μ, Amp^R, LEU2, SUS1-HA with 900 bp upstream and 700 bp downstream of UTR</i>	This study
pRS425-MEX67	<i>2μ, Amp^R, LEU2, MEX67-HA with 900 bp upstream and 700 bp downstream of UTR</i>	This study
pRS425-DBP5	<i>2μ, Amp^R, LEU2, DBP5-HA with 900 bp upstream and 700 bp downstream of UTR</i>	This study

Supplementary Table 3. Mean lifespans and P values for RLS analysis.

Figure	Strain	Strain description	Mean lifespan	P value compared to matched control strain
Figure 1A	BY4741	WT	27.3	control
	SY495	<i>sus1Δ</i>	20.2	0.0006, ***
	SY652	<i>sus1Δ</i>	22.8	0.0120, *
	SY653	<i>sus1Δ</i>	19.0	0.0001, ***
	SY654	<i>sus1Δ</i>	20.8	0.0009, ***
Figure 1C	BY4741	WT	19.2	control
	SY495	<i>sus1Δ</i>	13.8	0.0131, *
	FY231	<i>ubp8Δ</i>	31.9	<0.0001, ***
	FY399	<i>sgf11Δ</i>	23.8	0.3267, ns
	FY402	<i>sgf73Δ</i>	45.4	<0.0001, ***
Figure 1D	BY4741	WT	24.2	control
	SY495	<i>sus1Δ</i>	18.9	0.0002, ***
	FY390	<i>thp1Δ</i>	7.2	<0.0001, ***

	FY391	<i>sac3Δ</i>	9.3	<0.0001, ***
	FY451	<i>sem1Δ</i>	22.5	0.0623, ns
	BY4741	WT	23.7	control
Figure 2A	SY495	<i>sus1Δ</i>	17.2	<0.0001, ***
	FY231	<i>ubp8Δ</i>	31.6	0.0020, **
	SY786	<i>sus1Δ ubp8Δ</i>	18.8	0.0014, **
	BY4741	WT	21.9	control
Figure 2B	SY495	<i>sus1Δ</i>	17.0	0.0051, **
	FY399	<i>sgf11Δ</i>	26.3	0.0291, *
	SY787	<i>sus1Δ sgf11Δ</i>	19.1	0.2784, ns
	BY4741	WT	23.5	Control
Figure 2C	SY495	<i>sus1Δ</i>	17.1	<0.0001, ***
	FY402	<i>sgf73Δ</i>	40.4	<0.0001, ***
	SY797	<i>sus1Δ sgf73Δ</i>	23.5	0.3870, ns
	BY4741	WT	21.8	control
Figure 2D	SY495	<i>sus1Δ</i>	16.7	0.0028, **
	FY391	<i>sac3Δ</i>	8.5	<0.0001, ***
	SY784	<i>sus1Δ sac3Δ</i>	12.5	<0.0001, ***
	BY4741	WT	25.6	control
Figure 2E	SY495	<i>sus1Δ</i>	16.6	<0.0001, ***
	FY390	<i>thp1Δ</i>	5.7	<0.0001, ***
	SY1087	<i>sus1Δ thp1Δ</i>	5.1	<0.0001, ***
	BY4741	WT	24.2	control
Figure 2F	SY495	<i>sus1Δ</i>	18.6	<0.0001, ***
	FY451	<i>sem1Δ</i>	20.6	0.0188, *
	SY785	<i>sus1Δ sem1Δ</i>	10.5	<0.0001, ***
	BY4741	WT	29.7	<0.0001, ***
	SY529	<i>sir2Δ</i>	12.4	control
Figure 3A	SY557	<i>sir2Δ ubp8Δ</i>	11.9	0.2598, ns
	SY559	<i>sir2Δ sgf11Δ</i>	13.9	0.1020, ns
	SY558	<i>sir2Δ sgf73Δ</i>	13.8	0.8582, ns
	BY4741	WT	29.3	<0.0001, ***
Figure 3B	SY529	<i>sir2Δ</i>	8.8	control
	SY653	<i>sus1Δ</i>	20.4	0.0006, ***
	SY699	<i>sir2Δ sus1Δ</i>	11.0	0.0200, *
	BY4741	WT	23.7	<0.0001, ***
Figure 3C	SY529	<i>sir2Δ</i>	13.2	control
	SY556	<i>sir2Δ thp1Δ</i>	5.5	<0.0001, ***
	SY532	<i>sir2Δ sac3Δ</i>	5.6	<0.0001, ***
	BY4741	WT	23.9	control
Figure 4D	FY395	<i>MEX67-DAmP</i>	18.3	0.0007, ***
	FY396	<i>MTR2-DAmP</i>	20.8	0.0781, ns

	SY971	<i>sus1Δ</i> + pGP564	9.5	control
Figure 4E	SY972	<i>sus1Δ</i> + YGPM2h11 (<i>SUS1</i>)	28.3	<0.0001, ***
	SY973	<i>sus1Δ</i> + YGPM5d22 (<i>MEX67</i>)	16.1	<0.0001, ***
	SY974	<i>sus1Δ</i> + YGPM6e10 (<i>DBP5</i>)	24.8	<0.0001, ***
	SY1039	<i>sus1Δ</i> + pRS425	18.6	control
Figure 4G	SY1040	<i>sus1Δ</i> + pRS425- <i>SUS1</i>	25.8	<0.0001, ***
	SY1041	<i>sus1Δ</i> + pRS425- <i>MEX67</i>	23.7	0.0023, **
	SY1042	<i>sus1Δ</i> + pRS425- <i>DBP5</i>	21.7	0.0408, *

*** $P \leq 0.001$; ** $P \leq 0.01$; * $P \leq 0.05$; ns, not significant.

SUPPLEMENTARY REFERENCES

- Ryu HY, Ahn S. Yeast histone H3 lysine 4 demethylase Jhd2 regulates mitotic rDNA condensation. *BMC Biol.* 2014; 12:75.
<https://doi.org/10.1186/s12915-014-0075-3>
PMID:25248920
- Longtine MS, McKenzie A 3rd, Demarini DJ, Shah NG, Wach A, Brachat A, Philippsen P, Pringle JR. Additional modules for versatile and economical PCR-based gene deletion and modification in *Saccharomyces cerevisiae*. *Yeast.* 1998; 14:953–61.
[https://doi.org/10.1002/\(SICI\)1097-0061\(199807\)14:10<953::AID-YEA293>3.0.CO;2-U](https://doi.org/10.1002/(SICI)1097-0061(199807)14:10<953::AID-YEA293>3.0.CO;2-U)
PMID:9717241
- Sung MK, Ha CW, Huh WK. A vector system for efficient and economical switching of C-terminal epitope tags in *Saccharomyces cerevisiae*. *Yeast.* 2008; 25:301–11.
<https://doi.org/10.1002/yea.1588>
PMID:18350525
- Jones GM, Stalker J, Humphray S, West A, Cox T, Rogers J, Dunham I, Prelich G. A systematic library for comprehensive overexpression screens in *Saccharomyces cerevisiae*. *Nat Methods.* 2008; 5:239–41.
<https://doi.org/10.1038/nmeth.1181>
PMID:18246075
- Sikorski RS, Hieter P. A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. *Genetics.* 1989; 122:19–27.
<https://doi.org/10.1093/genetics/122.1.19>
PMID:2659436
- Christianson TW, Sikorski RS, Dante M, Shero JH, Hieter P. Multifunctional yeast high-copy-number shuttle vectors. *Gene.* 1992; 110:119–22.
[https://doi.org/10.1016/0378-1119\(92\)90454-w](https://doi.org/10.1016/0378-1119(92)90454-w)
PMID:1544568