

Table S1

List of the yeast strains used in this paper

Strain	Relevant genotype	Source
BY4741 (wt)	<i>MATa, his3Δ1, leu2Δ0, met15Δ0; ura3Δ0</i>	Euroscarf
Y06214	<i>MATa, his3Δ0, leu2Δ0, met15Δ0; ura3Δ0; upf1Δ::kanMX4</i>	Euroscarf
Y04588*	<i>MATa, his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; edc1::KanMX4</i>	Euroscarf
Y02074*	<i>MATa, his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; cbp20::KanMX4;</i>	Euroscarf
Y04072*	<i>MATa, his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; hpr1::KanMX4</i>	Euroscarf
Y00207*	<i>MATa, his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; not4::KanMX4</i>	Euroscarf
Y04540*	<i>MATa, his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; xrn1::KanMX4</i>	Euroscarf
A13628	<i>MATa, intergenic region (119778-119573) between YHR006W and YHR007C::HIS3, intergenic region (119778-119573) between YHR006W and YHR007C::KanMX6, disomic for chromosome VIII</i>	A. Amon
A18346	<i>MATa/MATa, can1::HIS3, intergenic region (187520-187620) between YER015W and YER016W::KanMX6, intergenic region (187520-187620) between YER015W and YER016W::URA3, trisomic for chromosome V</i>	A. Amon
A18347	<i>MATa/MATa, intergenic region (119778-119573) between YHR006W and YHR007C::HIS3, intergenic region (119778-119573) between YHR006W and YHR007C::KanMX6, intergenic region (119778-119573) between YHR006W and YHR007C::URA3, trisomic for chromosome VIII</i>	A. Amon
A6863	<i>MATa, ade1::HIS3, ade1::KanMX6, disomic for chromosome I</i>	A. Amon
A18345	<i>MATa/MATa, ade1::HIS3, ade1::KanMX6, ade1::URA3; trisomic for chromosome I</i>	A. Amon
A18349	<i>MATa/MATa, intergenic region (622880-622980) between YNL005C and YNL004W::HIS3, intergenic region (622880- 622980) between YNL005C and YNL004W::KanMX6,intergenic region (622880-622980) between YNL005C and YNL004W::URA3, trisomic for chromosome XIV</i>	A. Amon
A702 (diploid wt)	<i>MATa/MATa, ade2-1, leu2-3, ura3, trp1-1, his3-11,15, can1-100, GAL, psi+</i>	A. Amon
A2587 (haploid wt)	<i>MATa, ade2-1, leu2-3, ura3, trp1-1, his3-11,15, can1-100, GAL, psi+</i>	A. Amon
YMC511*	<i>MATa, ade2Δ, ura3-52, xrn1Δ::URA3</i>	M. Choder

*these strains show here the original presumed genotype but we discovered to be aneuploids. See Table 1 for a description of the aneuploidies found.