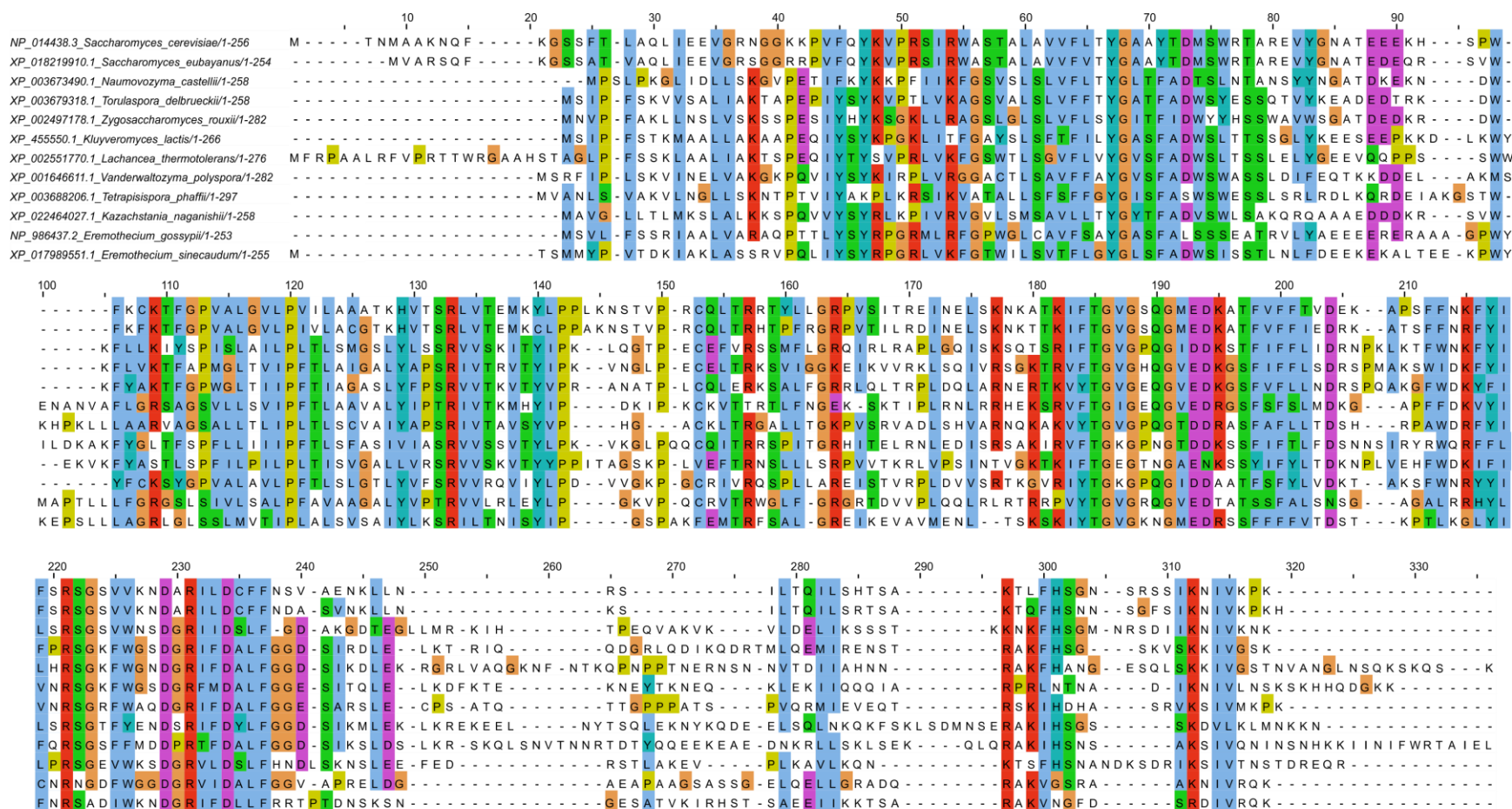# Supplemental Materials
Molecular Biology of the Cell

Möller-Hergt et al.

Supplemental Table 1. *Saccharomyces cerevisiae* strains used in this study.

Name	Parental strain	Nuclear genotype	Mitochondrial genotype	References
W303		*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100*	wt; intron containing	
MOY081 *mba1Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mba1::HIS3*	wt; intron containing	Ott et al. 2006
MOY849 *mrx15Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mrx15::kanMX4*	wt; intron containing	This study
MOY791 *mrx15Δmba1Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mba1::HIS3 mrx15::kanMX4*	wt; intron containing	This study
MOY1556 *mdm38Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mdm38::URA3*	wt; intron containing	This study
MOY1557 *mdm38Δmrx15Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mdm38::URA3 mrx15::kanMX4*	wt; intron containing	This study
MOY1306 *nuc1Δ* Mrx15-PA/His	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 MRX15PAHis::HIS3 nuc1::URA3*	wt; intron containing	This study
MOY1497 Mrx15$^{1-130}$ΔC	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mrx15-C130-PA::HIS3*	wt; intron containing	This study
MOY1498 Mrx15$^{1-130}$ΔC *mba1Δ*	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 mrx15-C130-PA::HIS3 mba1::URA3*	wt; intron containing	This study
MOY014 Oxa1$^{1-331}$ΔC	CW04	*Mat **α** ura3-1 trp1-1 leu2-3, 12 his3-11,15 ade2-1 can1-100 oxa1-K332**	wt; intron containing	Szyrach et al. 2003
MOY1359 Oxa1$^{1-331}$ΔC *mrx15Δ*	CW04	*Mat **α** ura3-1 trp1-1 leu2-3, 12 his3-11,15 ade2-1 can1-100 oxa1-K332* mrx15::kanMX4*	wt; intron containing	This study
MOY1299 *nuc1Δ* Mrx15-Flag	W303	*Mat **a** ura3-1 trp1Δ 2 leu2-3,112 his3-11,15 ade2-1 can1-100 MRX15FLAG::HIS3 nuc1::URA3*	wt; intron containing	This study

Supplemental Figure 1

Supplemental Figure 1: Multiple sequence alignment of Mrx15 homologs found by BLAST search. Representative candidates were aligned by the MAFFT algorithm and are displayed according to the Clustal color convention.