

Table S1: Strain Genotypes

<u>Strain name</u>	<u>Relevant genotype</u>	<u>Figure</u>
MJL3906, 3907	<i>CCT6'</i> - <i>natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> - ' <i>SND1</i> <i>pCUP1</i> ----- <i>CCT6-SND1'</i> - <i>URA3</i> -[ <i>arg4-VRS103</i> ]- ' <i>CCT6-SND1</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3915	MJL3907 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2
MJL3944, 3945	MJL3907 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3952, 3953	MJL3907 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2
MJL3908, 3909	<i>IMD3'</i> - <i>natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> - ' <i>AGT23</i> <i>pCUP1</i> ----- <i>IMD3-ATG23'</i> - <i>URA3</i> -[ <i>arg4-VRS103</i> ]- ' <i>IMD3-AGT23</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3916, 3917	MJL3909 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2
MJL3946, 3947	MJL3909 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3954	MJL3909 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2
MJL3910, 3911	<i>RIM15'</i> - <i>natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> - ' <i>HAC1</i> <i>pCUP1</i> ----- <i>RIM15-HAC1'</i> - <i>URA3</i> -[ <i>arg4-VRS103</i> ]- ' <i>RIM15-HAC1</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3918, 3919	MJL3911 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2
MJL3948, 3949	MJL3911 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3955, 3956	MJL3911 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2
MJL3912, 3913	<i>TRK2'</i> - <i>natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> - ' <i>FMP46</i> <i>pCUP1</i> ----- <i>TRK2-FMP46'</i> - <i>URA3</i> -[ <i>arg4-VRS103</i> ]- ' <i>TRK2-FMP46</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3920, 3921	MJL3913 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2
MJL3950, 3951	MJL3913 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3957, 3958	MJL3913 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2
MJL3879	<i>hsp30::URA3</i> -[ <i>arg4-VRS103</i> ] <i>pCUP1</i> ----- <i>hsp30::natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3881	MJL3879 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2
MJL3976, 3977	MJL3879 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3970, 3978	MJL3879 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2
MJL3880	<i>FIR1'</i> - <i>URA3</i> -[ <i>arg4-VRS103</i> ]- ' <i>ZRG8</i> <i>pCUP1</i> ----- <i>FIR1'</i> - <i>natMX</i> -[ <i>arg4-VRS</i> ]- <i>KLTRP1</i> - ' <i>ZRG8</i> <i>pCUP1-VDE-hygMX-pCUP1-CUP1</i>	3, S2
MJL3971, 3972	MJL3880 + <i>mLh3Δ::KanMX/mLh3Δ::KanMX</i>	3, S2

<u>Strain name</u>	<u>Relevant genotype</u>	<u>Figure</u>
MJL3969, 3973	MJL3880 + <i>pch2Δ::URA3/pch2Δ::TRP1</i>	4, S2
MJL3974, 3975	MJL3880 + <i>pch2Δ::URA3/pch2Δ::TRP1, mLh3Δ::KanMX/mLh3Δ::KanMX</i>	4, S2

All strains are homozygous for *lys2*, *ho::LYS2*, *ura3Δ(hindIII-smal)*, *leu2*, *arg4Δ(eco47III-hpaI)*, *trp1::hisG*, and *VMA1-103*. *pch2Δ::URA3* and *pch2Δ::TRP1* delete sequences between *Accl* and *BamHI* and between *Accl* and *SpeI* sites in *PCH2* coding sequences, respectively. Multiple strain names for a given genotype represent independently derived diploids, both of which were used. Strains used for inserts at *HIS4* and at *URA3* have been described (MEDHI *et al.* 2016)