

Table S3. Primers list

Primer	Sequence (5' to 3')	Strains constructed (purpose)
RNH1KANF	ATGGCAAGGCAAGGGAACCTTCTACGCGTTAGAAAGGGCAGGGAAA CTGGGATCTATAATCAGCTGAAGCTTCGTACG	SJR2626-3, SJR3625-9B (construct <i>RNH1</i> deletion)
RNH1KANR	GCATTATCGTCTAGATGCTCCTTTCTTCGCCAGAAAATCTGCCATTTT ATTTCTGGATCAGGCCACTAGTGGATCTG	SJR2626-3, SJR3625-9B (construct <i>RNH1</i> deletion)
RNH1UPF	TGGCAGCACAAATAATACACG	KO127, KO128, SJR3626-3, SJR3625-9b (confirm <i>rnh1</i> Δ)
RNH1DWR	CACGCTTATAGATAGTTATCG	KO127, KO128, SJR3626-3, SJR3625-9b (confirm <i>rnh1</i> Δ)
RNH2KANF	CTAATGAGAGTGTGCGAAAACCTTGAAAACAACACTACTGCACACCAAAT TGATACGATTAACAGCTGAAGCTTCGTACG	SJR3615-4, SJR3616-3 (<i>RNH201</i> deletion)
RNH2KANR	GCTTCACGGATAGTAGAAACGGCAAAGCATAGTAGCAGATGACTTGT ATGAGTTATTGAAAGGCCACTAGTGGATCTG	SJR3615-4, SJR3616-3 (<i>RNH201</i> deletion)
RNH2UPF	TTGCGACGCCTGCCAATGC	SJR3615-4, SJR3616-3 (confirm <i>rnh201</i> Δ)
RNH2DWR	TCGTTCCGGTTGGTTGTCTC	SJR3615-4, SJR3616-3 (confirm <i>rnh201</i> Δ)
KL_URA3_F	CGGGTAGAATCAATGCAATCAGTGGTAATTATCTAGATGACGTCCTTT ATGACCTTGACACCCCTGCAGCTGAAGCTTCGTACG	KO171 (insertion of <i>URA3KI</i> at end of chr. IV)
KL_URA3_R	TGTGGTGACAACCTAACCCCTTCGTTGATACTAGTTTGAAGTTATCA ATATCCTGAATTAGAGTTGTGGAGGCCACTAGTGGATCTG	KO171 (insertion of <i>URA3KI</i> at end of chr. IV)
IVADE2_3_F	CGGGTAGAATCAATGCAATCAGTGGTAATTATCTAGATGACGTCCTTT ATGACCTTGACACCCCTGGTTGAGAAGCCGAGAATTTTGTGTA	KO124 (insertion of <i>ADE2</i> at end of chr. IV)
IVADE2_3_R	TGTGGTGACAACCTAACCCCTTCGTTGATACTAGTTTGAAGTTATCA ATATCCTGAATTAGAGTTGTGGTCCTCGTTTCTGCATTGAG	KO124 (insertion of <i>ADE2</i> at end of chr. IV)
IVURA3F	GCTTTACAGGACCTATTTTTCATACGTTATGCACTTCATTCTTTTTGTC GGTTTGATAACCAGCAGAATCTAACGCTAGAGCAGACGCTCAT	KO35 (insertion of <i>URA3</i> at end of chr. IV)
IVURA3R	AAGCGCTGCTGCGTTTTTCGAGGTATGGCTTCTGCCGGGCTAACGTTT AAATTAAGGAACAGATTCCCGGGTAATAACTGA	KO35 (insertion of <i>URA3</i> at end of chr. IV)
EXT1510386F	CATTGGAGCGAATGATGACG	KO35 (confirmation of <i>URA3</i> insertion on chr. IV)
EXT1510386R	TGTGCAATCGTTGTCAAGTTGG	KO35 (confirmation of <i>URA3</i> insertion on chr. IV)
Forward Sequence	TGCCAGTATTCTTAACCCAACTGCACAGAACAAAACCTGCAGGAA ACGAAGATAAATCCAGCTGAAGCTTCGTACG	KOK3 (deletion of <i>URA3</i> locus)
Reverse	TTAAATTGAAGCTCTAATTTGTGAGTTTAGTATACATGCATTTACTTAT	KOK3 (deletion of <i>URA3</i> locus)

Sequence	AATACAGTTTTAGGCCACTAGTGGATCTG	
ADE2_XV_R	GGTGCGTAAAATCGTTGGAT	KO119, KO127, KO128 (to insert <i>ade2Δ::kanMX</i> in KO119 and to determine whether KO127 and KO128 had <i>ade2-1</i> or <i>ade2Δ::kanMX</i>)
ADE2_XV_F	ATCCTCGGTTCTGCATTGAG	KO119, KO127, KO128 (to insert <i>ade2Δ::kanMX</i> in KO119 and to determine whether KO127 and KO128 had <i>ade2-1</i> or <i>ade2Δ::kanMX</i>)
Pol2DigestF1	GAAAAGCCACAGCACCTTTC	KO200, KO207, spores of KO214 and KO201 (confirmation of <i>pol2-M644L</i>)
Pol2DigestR1	TTGGACAGATTTCCCTTCCA	KO200, KO207, spores of KO214 and KO201 (confirmation of <i>pol2-M644L</i>)
MATaF	ACTCCACTTCAAGTAAGAGTTTG	Many strains (diagnosis of mating type)
MATalphaF	GCACGGAATATGGGACTACTTCG	Many strains (diagnosis of mating type)
MATR	AGTCACATCAAGATCGTTTATGG	Many strains (diagnosis of mating type)
extF3	AATGCGGGTAGAATCAATGC	KO124, KO171 (confirmation of <i>ADE2</i> or <i>URA3KI</i> insertion on chr. IV)
extR3	AGGTGATGGGAAATCGAGTG	KO124, KO171 (confirmation of <i>ADE2</i> or <i>URA3KI</i> insertion on chr. IV)
KANF222	AATTTATGCCTCTTCCGACC	KOK3 (confirmation of <i>URA3</i> deletion)
URAR1128	GAAATCATTACGACCG	KOK3 (confirmation of <i>URA3</i> deletion)
Tel1NATF	ATTCGAAAAAAAAAGCCTTCAAAGAAAAGGGAAATCAGTGTAACATAGACGCGTACGCTGCAGGTCGAC	PG308 (replacement of <i>tel1::kanMX</i> with <i>tel1::natMX</i>)
Tel1NATR	TTCGTATTTCTATAAACAAAAAAAAAGAAGTATAAAGCATCTGCATAGCAAATCGATGAATTCGAGCTCG	PG308 (replacement of <i>tel1::kanMX</i> with <i>tel1::natMX</i>)
MRC1pgalF	GGAAGTTCGTTATTCGCTTTTGAAGTATCACCAAATATTGAATTCGAGCTCGTTTAAAC	PG309(2) (to insert the <i>GAL1</i> promoter and <i>kanMX</i> upstream of <i>MRC1</i>)
MRC1pgalR	TTGCAGTCAACGAGGACAAAGCATGCAAGGCATCATCCATGCACTGAGCAGCGTAATCTG	PG309(2) (to insert the <i>GAL1</i> promoter and <i>kanMX</i> upstream of <i>MRC1</i>)