SUPPLEMENTARY DATA

Experimental Procedures

Yeast Strains

All strains used in this study are listed in supplemental Table S1. Strains containing deletions of *EDC3*, *UPF1*, *DCP1*, *XRN1*, *SKI2*, *SKI7*, *CCR4*, or *RRP6* were constructed by gene replacement (Guthrie and Fink, 1991), using DNA fragments harboring the corresponding null alleles. Each genomic DNA deletion was confirmed by PCR analysis. Strains containing deletions of *DHH1*, *PAT1*, *LSM1*, or *LSM7* were purchased from Open Biosystems. Strains harboring the temperature-sensitive *rpb1-1*, *prt1-1*, or *sup45-2* alleles were constructed by the pop-in and pop-out technique (Guthrie and Fink, 1991). Strains harboring the temperature-sensitive *yra1-1* allele were constructed by plasmid shuffling (Guthrie and Fink, 1991).

Plasmids

All plasmids used in this study are listed in Table S2. *YRA1* exon1, intron, or exon2 chimeric alleles were all constructed through *in vivo* recombination in yeast cells as described previously (He et al., 1996). *YRA1* alleles harboring deletions of exon1, intron, or exon2 sequences, or containing insertions of a stem-loop structure, were generated by PCR and molecular cloning. *YRA1* alleles harboring mutations in the *YRA1* translation initiation codon, the 5' splice site, the branch-point region, or the 3' splice site were generated using the QuikChange Site-DirectedMutagenesis Kit (Stratagene). All *YRA1* alleles were confirmed by DNA sequencing.

Oligonucleotides

The oligonucleotides used in this study were obtained from Operon, Inc., and are listed in Table S3.

Cell Growth Conditions

Cells were grown in YPD medium (Microarray analysis and Figures 1, 2, 3B, and 6), or in synthetic complete (SC) medium lacking tryptophan (Figures 3C, 4, 5A, 5B, 5C, and 5D-right side), histidine (Figure 7A and 7C), uracil and tryptophan (Figure 5D-left side), or histidine and tryptophan (Figure 7D and 7E) to select for plasmids. Cultures (10 ml) not involving drug treatment or temperature shifts were grown at 30°C to an OD_{600} of 0.7 and harvested by centrifugation. Cell pellets were frozen on dry ice and then stored at -80°C until RNA was isolated. Cultures involving drug treatment were grown at 30°C to an OD_{600} of 0.7 in a large volume and then concentrated five-fold in the same medium. Where appropriate, the following were added to concentrated cultures: cycloheximide (100 µg/ml), leptomicin (100 ng/ml), or thiolutin (15µg/ml). Drug-treated cells (2ml) were harvested at different time points. For temperature shifts, cells were first grown at 25°C and then treated as described previously (He and Jacobson, 1995).

Microarray Analysis

Five independent expression profiling experiments were carried out for isogenic wildtype (HFY114) and *edc3* Δ (CFY25) strains using Affymetrix Yeast Genome S98 Arrays. Microarray procedures, including RNA isolation, cRNA preparation, microarray hybridization, and data analysis, were as previously described (He et al., 2003), with the following modifications: First, all microarrays were analyzed with Affymetrix Microarray Suite 5.0 software. Second, a transcript was considered to be differentially expressed if it met two of three previously defined criteria, i.e., it must have an absolute change threshold of 200 units and a change P value ≤0.05. The entire data set can be found at: http://jacobsonlab.umassmed.edu/cgi-bin/pubcontents.cgi?pubcontents=2006-Feng.

Yeast Two-hybrid Analysis

Two-hybrid interactions between full-length Crm1p fused to the *LexA* DNA- binding domain and full-length Edc3p fused to the Gal4p activation domain were assayed as described previously (He et al., 1997).

Results

Identification of Transcripts Differentially Expressed in edc3∆ Cells

Five independent expression profiling experiments were carried out with *EDC3* and *edc3* Δ strains and differentially expressed transcripts were initially identified based on three stringent criteria. First, the hybridization signal values of a specific transcript in the wild-type and the *edc3* Δ strains had to have a relative change of at least 2-fold and an absolute change of at least 200 units. Second, these changes had to be reproducible in at least 80% of the independent replicate experiments. Third, these changes had to demonstrate statistically significant P values ≤0.05. To our surprise, this data analysis revealed that, among the 7839 potential transcripts analyzed, only a single transcript

met these criteria. In edc3A cells, the EDC3 mRNA itself was decreased more than 10fold relative to its level in wild-type cells (Table 4S), consistent with the fact that the $edc3\Delta$ strain harbors a complete EDC3 deletion. Although this observation validated the overall experiment, we reasoned that our stringent criteria may have overlooked at least two classes of transcripts. For example, highly expressed transcripts are prone to signal saturation and intron-containing transcripts might be missed since the oligonucleotide probes on our arrays do not differentiate intron-containing pre-mRNA signals from mRNA signals. We, therefore, lowered the analysis stringency by eliminating the minimum 2-fold change requirement and reanalyzed our data. This new analysis identified four additional differentially expressed transcripts in the edc3A strain: two transcripts showed increased expression and two others showed decreased expression (Table 4S). One of the up-regulated transcripts is encoded by the RPS28B gene and codes for a 40S ribosomal protein (Lecompte et al., 2002). The other up-regulated transcript is encoded by the YRA1 gene and codes for an hnRNP-like protein (Yra1p) involved in an early stage of mRNA export (Portman et al., 1997; Strasser and Hurt, 2000). The two down-regulated transcripts, encoded by the URA1 and URA4 genes, may well reflect our use of the URA3 gene as a selectable marker for replacement of the EDC3 coding region. URA1, URA3, and URA4 all code for enzymes involved in uracil biosynthesis (Denis-Duphil, 1989) and the decreased expression of URA1 and URA4 transcripts in the edc3 Δ strain is presumably related to the expression of URA3, not to the deletion of EDC3.

Inactivation of Yra1p Promotes YRA1 Pre-mRNA Splicing

To further understand the role of Yra1p in its autoregulation, we examined the effects of mutations in the YRA1 gene on levels of YRA1 pre-mRNA and mRNA in an *edc3* Δ background. We reasoned that some loss of function mutations may also fail to autoregulate. We first analyzed *yra1-1*, a ts allele whose encoded protein contains multiple amino acid substitutions and is defective in mRNA export even when cells are grown at room temperature (Strasser and Hurt, 2000). As shown in Figure 2S, when cells were grown at 25°C (t=0) or were shifted to 37°C for 30 min, *edc3* Δ *yra1-1* cells accumulated significantly lower levels of YRA1 pre-mRNA than *edc3* Δ *YRA1* cells. In contrast, under these two growth conditions, *edc3* Δ *yra1-1* cells. The lower YRA1 pre-mRNA to mRNA ratios in *edc3* Δ *yra1-1* cells indicate that the *yra1-1* allele is defective in autoregulation and suggest that Yra1p regulates its own expression by inhibiting YRA1 pre-mRNA splicing.

FIGURE 1S



Figure 1S. Inactivation of Ra1t1p or Depletion of Rrp6p Does Not Affect the Accumulation of YRA1 Pre-mRNA. A. Effect of inactivation of Rat1p on levels of YRA1 pre-mRNA and mRNA. Rat1-1 or rat1-1xrn1 Δ cells were grown in SC minus uracil medium at 25°C and then shifted to 37°C for 30, 60, and 120 min. The levels of YRA1 pre-mRNA and mRNA were analyzed by northern blotting. B. Effect of depletion of Rrp6 on the levels of YRA1 pre-mRNA and mRNA and mRNA. Cells of the indicated genotypes were grown in YEPD medium and the levels of YRA1 pre-mRNA and mRNA in these cells were analyzed by northern blotting. Note that *rrp6* Δ cells accumulated higher levels of YRA1 mRNA than *RRP6* cells. The simplest explanation for this observation is that, in wild-type cells, a fraction of the YRA1 pre-mRNA that is committed to the splicing pathway is degraded by the nuclear exosome.

FIGURE 2S



Figure 2S. Inactivation of Yra1p Promotes *YRA1* **Pre-mRNA Splicing.** Cells of the indicated genotypes were grown in SC minus uracil medium at 25°C and then shifted to 37°C. The levels of *YRA1* pre-mRNA and mRNA were analyzed by northern blotting.

FIGURE 3S



Figure 3S. Crm1p Interacts With Edc3p in the Yeast Two-hybrid System. Yeast plasmids harboring LexA(DB)-*CRM1* and Gal4(AD)-*EDC3* fusions were co-transformed into the L40 tester strain. Transformants were selected and the β -galactosidase activity of individual transformants was assayed on plates containing X-Gal.

Figure 4S



Figure 4S. Cis-acting Determinants of YRA1 Expression. Alterations of YRA1 premRNA and mRNA expression mediated by: (A) replacing YRA1 exon1 with MER2 exon1, (B) replacing the YRA1 intron with the MER2 intron; and (C) replacing YRA1 exon2 with MER2 exon2 were analyzed. YCp low-copy plasmids harboring a chimeric allele (depicted above the corresponding blots) were introduced into wild-type (1), $upf1\Delta$ (2), $edc3\Delta$ (3), or $upf1\Delta$ $edc3\Delta$ (4) strains and the levels of the respective pre-mRNAs and mRNAs encoded by these alleles were analyzed by northern blotting. Blots A, B, and C were hybridized to MER2 exon1, intron, or exon2-specific probes, respectively. The positions of chimeric pre-mRNAs and mRNAs are indicated. Y: YRA1, and M: MER2. Blots were hybridized to a SCR1 probe to serve as a loading control.

Table 1S. Yeast Strains U	Jsed in	this study
---------------------------	---------	------------

Strain	Genotype	References
HFY114	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3	(He et al., 2003)
HFY871	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 upf1::HIS3 NMD2 UPF3	(He et al., 2003)
HFY116	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 nmd2::HIS3 UPF3	(He et al., 2003)
HFY861	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 upf3::HIS3	(He et al., 2003)
HFY1067	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 dcp1::URA3	(He et al., 2003)
HFY1080	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 xm1::ADE2	(He et al., 2003)
CFY25	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3	This study
SYY158	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3 upf1::HIS3	This study
SYY9	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 rpb1-1	This study
SYY43	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3 rpb1-1	This study
HFY1170	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 ski2::URA3	This study
SYY17	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 ski7::URA3	This study
SYY21	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 ski2::URA3 ski7::ADE2	This study
CFY13	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 prt1-1	This study
HFY1218	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 sup45-2	This study
SYY60	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3 xm1::ADE2	This study
SYY110	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 ccr4::LEU2	This study
SYY114	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3 ccr4::LEU2	This study
DAt1-1	MATa ura3-52 trp1-D63 leu2-D1 rat1-1	(He and Jacobson, 2001)
HFY1102	MATa ura3-52 trp1-D63 leu2-D1 rat1-1 xm1::URA3	(He and Jacobson, 2001)
SYY573	MAT a ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 rrp6::LEU2	This study
SYY577	MATa ade2-1 his3-11, 15 leu2-3, 112 trp1-1 ura3-1 can1-100 UPF1 NMD2 UPF3 edc3::URA3 rrp6::LEU2	This study
BY4741	MATa hisΔ1 leu2Δ0 met15Δ0 ura3Δ0	open biosystems
SYY160	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 edc3::URA3	This study
BY1301	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 lsm1::kanMX	open biosystems
SYY176	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 lsm1::kanMX edc3::URA3	This study
BY7383	MATa hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 lsm7::kanMX	open biosystems
SYY172	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 lsm7::kanMX edc3::URA3	This study
BY5797	MATa hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 pat1::kanMX	open biosystems
SYY164	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 pat1::kanMX edc3::URA3	This study
BY3858	MATa_hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 dhh1::kanMX	open biosystems
SYY214	MATa hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 dhh1::kanMX edc3::URA3	This study
yra1 shuffle	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 pRS316-YRA1	(Strasser and Hurt, 2000)
SYY88	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 pRS314-yra1-1	This study
SYY131	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 pRS314-yra1-1 edc3::URA3	This study
SYY529	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 pRS316-YRA1 edc3::LEU2	This study
FSY1135	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 yra2::kan pRS316-YRA1	(Zenklusen et al., 2001)
SYY606	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 yra2::kan yeplac112-YRA2	This study
SYY621	MAT a ade2 his3 leu2 trp1 ura3 yra1::HIS3 yra2::kan yeplac112-YRA2 edc3::LEU2	This study
MNY12	MAT a his3 leu2 trp1 ura3 crm1::kanR pRS313-GFP-crm1(T539C)	(Neville and Rosbash, 1999)
SYY614	MAT a his3 leu2 trp1 ura3 crm1::kanR pRS313-GFP-crm1(T539C) edc3::URA3	This study
SYY834	MAT a his3 leu2 trp1 ura3 crm1::kanR pRS313-GFP-crm1(T539C) rrp6::LEU2	This study
SYY838	MAT a his3 leu2 trp1 ura3 crm1::kanR pRS313-GFP-crm1(T539C) edc3::URA3 rrp6::LEU2	This study
SYY571	MAT a or a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 pRS316-URA3-MEX67	From Dr. Rosbash
SYY572	MAT a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 pRS314-mex67-5	From Dr. Rosbash
SYY1902	MAT a or a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 edc3::LEU2 pRS316-URA3-MEX67	This study
SYY605	MAT a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 edc3::LEU2 pRS314-mex67-5	This study
SYY749	MAT a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 edc3::LEU2 upf1::URA3 pRS314-mex67-5	This study
SYY1913	MAT a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 edc3::LEU2 dcp1::ADE2 pRS314-mex67-5	This study
SYY1920	MAT a ade2 his3 15 leu2 trp1 ura3 mex67::HIS3 edc3::LEU2 xm1::ADE2 pRS314-mex67-5	This study
L40	MATa ade2 his3D200 leu2-3,112 trp1-901 LYS2::(lexAop)4-HIS3 URA3::(lexAop)8lacZ gal4 gal80	Stanley Hollenberg

	Table 2S.	Plasmids	used in	this	study
--	-----------	----------	---------	------	-------

SYE22 pR5400*-pb1-1(/Xba) Contains the str/LAR and lakes as a Not-Sail fragment SYE28 Bs-sk7:-ZNE2 Contains the sk7:-ZNE2 as Not-Sail fragment SYE28 Bs-sk7:-ZNE2 Contains the sk7:-ZNE2 as Not-Sail fragment SYE200 Bs-edo:LEU2 Contains the edo:LURA and lakes as Not-Sail fragment CFE7 Bs-edo:LEU2 Contains the edo:LURA and lakes as Not-Sail fragment DSYE40 Bs-edo:LEU2 Contains the edo:LURA and lakes as a Not-Sail fragment SYE40 PM2514-YRA1 Contains the endy-LEU2 and lakes as a Not-Sail fragment SYE40 PM2514-YRA1 Contains the rop-LEU2 and lakes as a Not-Sail fragment SYE40 PM2514-YRA1 Contains the rop-LEU2 and lakes as a J Ob Hindli-Said fragment SYE50 PR5314-YRA1 (Hondli-Sac) Contains wild-spt YRA1 alkes as a J Ob Hindli-Said fragment SYE51 PR5314-YRA1 (Hondli-Sac) Contains wild-spt YRA1 alkes as a J Ob Hindli-Said fragment SYE50 PR5314-YRA1-CV-Y Same as in SYE74 but the 382-rd 'YRA1 exon 1 was replaced by the 83-rd CYH2 exon1 SYE52 PR5314-YRA1-CV-Y Same as in SYE74 but the 382-rd 'YRA1 exon 1 was replaced by the 63-rd HF2 exon1 SYE55 PR5314-YRA1-CV-Y Same as in SYE7	Name	Allele	Description
SYE20 Bs.437:-JURA3 Contains the 4J7:-JURA3 null allele as a Not-Sall fragment SYE20 Bs-437:-JURA3 Contains the 4J7:-JURA7 null allele as a Not-Sall fragment SYE20 Bs-437:-JURA3 Contains the 4J5:-JURA3 null allele as a Not-Sall fragment SYE20 Bs-437:-JURA3 Contains the 4J7:-JURA3 null allele as a Not-Sall fragment SYE44 (PIA278-1) PRS314-YRA1 Contains the rgf1:-JURA3 null allele as a 2.0 Mb BamH-Xhol fragment SYE44 (PIA278-1) PRS314-YRA1 Contains the rgf1:-JURA3 null allele as a 2.0 Mb BamH-Xhol fragment SYE40 PRS314-YRA1 Contains Myo-tagged YRA2 allele as a 1.7 Mb BamH-Xhol fragment SYE50 PRS314-YRA1 (Vhol-Sacl) Contains Myo-tagged YRA2 allele as a 2.0 Mb BamH-Xhol fragment SYE70 PRS314-YRA1-C-Y-Y Same as in SYE74 but the 32-nt YRA1 envir use reglaced by the 83-nt YF42 evon1 SYE50 PRS314-YRA1-C-Y-Y Same as in SYE74 but the 32-nt YRA1 evon 1 was reglaced by the 83-nt YF42 evon1 SYE51 PRS314-YRA1-C-Y-Y Same as in SYE74 but the 32-nt YRA1 evon 1 was reglaced by the 83-nt YE72 evon1 SYE52 PRS314-YRA1-M-Y-Y Same as in SYE74 but the 32-nt YRA1 evon 1 was reglaced by the 83-nt YE72 evon1 SYE54 PRS314-YRA1-M-Y-Y Same as in SYE74 but thos1	SYE22	pRS406*-rpb1-1(-Xbal)	Contains the ts rpb1-1allele as an 4.0 kb EcoRI-HindIII fragment
SYE280 Bs.4xt7-2DE2 Contains the 4xt7-ADE2 multilete as a Not-Sall fragment SYE280 Bs-4xt3-LEU2 Contains the 4xt3-LEU2 multilete as a Not-Sall fragment CFE7 Bs-4xt3-LEU2 Contains the 4xt3-LEU2 multilete as a Not-Sall fragment FFE1937 Bs-xpt1-LEU2 Contains the rgt1-LEU2 multilete as a Not-Sall fragment SYEAD Domains the rgt1-LEU2 multilete as a Not-Sall fragment SYEAD pr5314-YRA1_dVS Contains the rgt1-YRA1 multilete as a Not-Sall fragment SYEAD pr5314-YRA1_dVS Contains the rgt1-YRA1 multilete as a 10 bb IntelliSach fragment SYEEB pr5314-YRA1_dVS-Sall Contains the rgt1-YRA1 multilete as a 17. bb BarnHit-Sach fragment SYEEB pr5314-YRA1_LON-YRA2 Contains weid-yrPXA1 allete as a 2.1 bb IntelliSach fragment SYEEA pr5314-YRA1_HON-Sach Contains weid-yrPXA1 allete as a 2.1 bb XnotSach fragment SYEEA pr5314-YRA1-C-Y-Y Same as in SYEFA but the 382-nt YRA1 senn 1 was replaced by the 38-nt CYH2 exon1 SYEEA pr5314-YRA1-LO-Y-Y Same as in SYEFA but the 38-nt YRA1 senn 1 was replaced by the 38-nt CYH2 exon1 SYEEA pr5314-YRA1-LO-Y-Y Same as in SYEFA but the 38-nt YRA1 senn 1 was replaced by the 38-nt CYH2 exon1 SYEEA	SYE26	Bs-ski7::URA3	Contains the ski7::URA3 null allele as a Notl-Sall fragment
SYE200Bs-eds::LU2Contains the eds::LEU2 null allele as a Not-Sall fragmentCFE7Bs-eds::LU2ASContains the uff::URA3 null allele as a Not-Sall fragmentSYE44 (PIAZ78-1)PRS314-YRA1Contains the uff::URA3 null allele as a 2.0 kb BamHi-Xhol fragmentSYE44 (PIAZ78-1)PRS314-YRA1Contains the uff::PRA1 null allele as a 2.0 kb BamHi-Xhol fragmentSYE44 (PIAZ78-1)PRS314-YRA1Contains the yTA1 allele as a 3.0 kb Hindli-Sadl fragmentSYE580PRS314-YRA1Contains the yTA1 allele as a 3.0 kb Hindli-Sadl fragmentSYE590PRS314-YRA1 (HINLS20)Contains the yTA1 allele as a 3.0 kb Hindli-Sadl fragmentSYE590PRS314-YRA1 (HINLS20)Contains the yTA1 allele as a 2.0 kb Hindli-Sadl fragmentSYE590PRS314-YRA1 (HINLS20)Contains the yTA1 allele as a 2.0 kb Hindli-Sadl fragmentSYE590PRS314-YRA1 (HINLS20)Same as in SYE74 but the 382-rdt YRA1 seno tas reglaced by the 30-rdt YI2 exon1SYE590PRS314-YRA1-C-YYSame as in SYE74 but the 382-rdt YRA1 seno tas reglaced by the 83-rdt YI2 exon1SYE591PRS314-YRA1-H-YYSame as in SYE74 but the 382-rdt YRA1 seno tas reglaced by the 83-rdt YI2 exon1SYE591PRS314-YRA1-YYSame as in SYE74 but the 382-rdt YRA1 informas reglaced by the 83-rdt YI2 exon1SYE591PRS314-YRA1-YYSame as in SYE74 but the 182-rdt YRA1 informas reglaced by the 83-rdt YI2 exon1SYE592PRS314-YRA1-YY-WSame as in SYE74 but the 182-rdt YRA1 informas reglaced by the 83-rdt YI2 exon1SYE593PRS314-YRA1-YY-WSame as in SYE74 but the 182-rdt YRA1 informas reglaced by the 83-rdt YI2 exon1SY	SYE28	Bs-ski7::ADE2	Contains the ski7::ADE2 null allele as a Notl-Sall fragment
CFE7 Bs-edd::URA3 Contains the edd::URA3 null aliele as a Not-Sall fragment SYE44 PR31+VFA1 Contains the upd::URA3 null aliele as a Vel-Sall fragment SYE44 PR31+VFA1 Contains the upd::URA3 null aliele as a Vel-Sall fragment SYE44 PR31+VFA1 Contains the upd::URA3 null aliele as a Vel-Sall fragment SYE56 PR31+VFA1 Contains wid-type YFA1 aliele as a 2.0 kb BamH:/Shell fragment SYE56 PR31+VFA1 Contains wid-type YFA1 aliele as a 2.0 kb Hindll-Sacl fragment SYE57 PR31+VFA1 Contains wid-type YFA2 aliele as a 2.2 kb Hindll-Sacl fragment SYE50 PR31+VFA1-C>Y Same as in SYE74 but th 823-rel XHA2 aliele as a 2.2 kb Hindll-Sacl fragment SYE57 PR31+VFA1-L>Y Same as in SYE74 but th 823-rel XHA2 aliele as a 2.0 kb Hindll-Sacl fragment SYE57 PR31+VFA1-L>Y Same as in SYE74 but th 823-rel XHA2 aliele as a 1.0 YFA1 storn 1 was replaced by the 83-rel XH22 storn 1 SYE57 PR31+VFA1-V-Y Same as in SYE74 but th 823-rel XH22 storn 1 was replaced by the 63-rel XH22 inton SYE59 PR31+VFA1-V-Y Same as in SYE74 but th 823-rel XH22 storn 1 was replaced by the 63-rel XH22 inton SYE59 PR31+VFA1-V-Y Same as in SYE74 but the 63-rel XH24 intorn as replaced by the 63-re	SYE200	Bs-edc3::LEU2	Contains the edc3::LEU2 null allele as a Notl-Sall fragment
HFE1397Bs-rpf:-LUCA3 Bs-rpf:-LUCA3Contains the rpf:-UCA3 null aliele as a VictS-Sulf ragmentSYE44 (PA275-1) SYE46 (PA275-1) PR5314-YRA1-LUX5Contains the rpf:-UCA3 null aliele as a 2 lob Bamil-Xhol fragmentSYE46 (PA275-1) SYE56 pR5315-YRA1Contains the rpf:-UCA3 Null aliele as a 3 lob Hindli-Sacl fragmentSYE56 PR5315-YRA1 (Hnodli-Sacl)Contains the rpf:-UCA3 Null Aliele as a 3 lob Bindli-Sacl fragmentSYE57 PR5315-YRA1 (Hnodli-Sacl)Contains wid-ype YRA1 aliele as a 3 lob Hindli-Sacl fragmentSYE57 PR5315-YRA1 (Hnodli-Sacl)Contains wid-ype YRA1 aliele as a 2 lob Xhindli-Sacl fragmentSYE57 PR5315-YRA1 (Hnodli-Sacl)Contains wid-ype YRA1 aliele as a 2 lob Xhindli-Sacl fragmentSYE57 PR5315-YRA1 (Hnodli-Sacl)Contains wid-ype YRA1 aliele as a 2 lob Xhindli-Sacl fragmentSYE57 PR5315-YRA1 (Hnodli-Sacl)Same as in SYE74 but the 382-rh YRA1exon twas replaced by the 83-rh CYH2 exon1SYE57 PR5315-YRA1-W-YSame as in SYE74 but the 382-rh YRA1exon twas replaced by the 63-rh CYH2 exon1SYE57 PR5315-YRA1-W-YSame as in SYE74 but the 382-rh YRA1exon twas replaced by the 63-rh CYH2 exon1SYE57 PR5315-YRA1-W-YSame as in SYE74 but the 382-rh YRA1exon twas replaced by the 53-rh CYH2 exon1SYE57 PR5315-YRA1-W-YSame as in SYE74 but the 73-rh YRA1 intonwas replaced by the 53-rh XFR53 hin non2SYE57 PR5315-YRA1-W-YSame as in SYE74 but contains an internal deletion from A.2 to 56 in exon1SYE57 PR5315-YRA1-W-YSame as in SYE74 but contains an internal deletion from A.2 to 56 in exon1SYE57 PR5315-YRA1-NE-C/D10Same as in SYE74 but contains an internal deletion from A.2 to 56 in exon1SYE161	CFE7	Bs-edc3::URA3	Contains the edc3::URA3 null allele as a Notl-Sall fragment
Bs-right-LEU2 Contains the right-LEU2 null allele as a Hindli-BamHi fragment SYE44 (PK275-1) PR314-YRA1 LOVS Same as SYE44 but lacks the YRA1 latter as a 2.0 kb BamHi-Xhaf fragment SYE80 PR318-PTA1 SYE80 PR318-PTA1 Dontains twick-yse YRA1 latter as a 3.0 kb Hindli-Sach fragment Contains wick-yse YRA1 latter as a 3.0 kb Hindli-Sach fragment SYE80 PR318-PTA1 SYE80 PR318-PTA1 PR318-PTA1 PR318-PTA1 (Hondl-Sach) Contains wick-yse YRA1 latter as a 2.0 kb Hindli-Sach fragment SYE80 PR318-PTA1 (Hondl-Sach) Contains wick-yse YRA1 latter as a 2.0 kb Hindli-Sach fragment SYE80 PR318-PTA1 (Hondl-Sach) Contains wick-ys YRA1 latter as a 2.0 kb Hindli-Sach fragment SYE80 PR318-PTA1 (Hondl-Sach) Contains wick-ys YRA1 latter as 2.2 kb Hindli-Sach fragment SYE80 PR314-PTA1-LO-YY Same as in SYE74 but ha 28.2 kH Nuck-Sach fragment SYE80 PR314-PTA1-LO-YY Same as in SYE74 but ha 28.2 kH Nuck-Sach fragment SYE81 PR314-PTA1-LO-YY Same as in SYE74 but ha 28.2 kH Nuck-Sach fragment SYE81 PR314-PTA1-Hov Same as in SYE74 but ha 28.2 kH Nuck-Sach fragment SYE81 PR314-PTA1-Hov Same as in SYE74 but ha 28.2 kH Nuck-Sach fragment SYE81 PR314-PTA1-Hov Same as in SYE74 but th 28.2 kh Nuck-Sach fragment SYE81 PR314-PTA1-Hov Same as in SYE74 but th 28.2 kh Nuck-Sach fragment SYE81 PR314-PTA1-Hov </td <td>HFE1397</td> <td>Bs-upf1-1::URA3</td> <td>Contains the upf1::URA3 null allele as a Notl-Sall fragment</td>	HFE1397	Bs-upf1-1::URA3	Contains the upf1::URA3 null allele as a Notl-Sall fragment
VEH4 (PAZ95-1) PRS14-YRA1 Contains wild-ype YRA1 allele as a 2.0 kb BamHi-Xho fragment SYE86 PRS314-YRA1-AUXS Same as SYE44 but lacks the YRA1 intron SYE86 PRS314-YRA1 Contains wild-ype YRA1 allele as a 3.0 kb Hindll-Sact fragment SYE80 PRS314-YRA1 Contains the yra1- allele as a 3.0 kb Hindll-Sact fragment SYE70 PRS314-YRA1(holb-Sact) Contains wild-yp YRA1 allele as a 2.2 kb Hindll-Sact fragment SYE74 PRS314-YRA1(holb-Sact) Contains wild-yp YRA1 allele as a 2.2 kb Hindll-Sact fragment SYE74 PRS314-YRA1-Kb-Y-Y Same as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 83-nt CYH2 exon1 SYE80 PRS314-YRA1-K-Y-Y Same as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 03-nt CYH2 exon1 SYE81 PRS314-YRA1-K-Y Same as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 03-nt CYH2 exon1 SYE81 PRS314-YRA1-K-Y Same as in SYE74 but the 32-nt YRA1 intomwas replaced by the 03-nt CYH2 inton SYE82 PRS314-YRA1-K-Y Same as in SYE74 but the 32-nt YRA1 intomwas replaced by the 03-nt CH22 inton SYE82 PRS314-YRA1-V-X Same as in SYE74 but the 32-nt YRA1 intomwas replaced by the 23-nt YRA1 inton SYE83 PRS314-YRA1-V-X Same as in SYE74 but the 63-n		Bs-rrp6::LEU2	Contains the rp8::LEU2 null allele as a HindIII-BamHI fragment
SYE44 (PA276-1) PRS314-YRA1 Contains wild-type YRA1 allele as a 2.0 bb BamHi-Xhof fragment SYE50 PRS314-YRA1 Contains wild-type YRA1 allele as a 3.0 bb Hindli-Sacl fragment SYE50 PRS314-YRA1 (Holdl-Sacl) Contains twig-type YRA2 allele as a 1.7 kb BamHi-Kanfil fragment SYE50 PRS314-YRA1 (Holdl-Sacl) Contains wild-type YRA1 allele as a 1.7 kb BamHi-Kanfil fragment SYE70 PRS314-YRA1 (Holdl-Sacl) Contains wild-type YRA1 allele as a 2.2 kb Holdl-Sacl fragment SYE50 PRS314-YRA1 (Holdl-Sacl) Contains wild-type YRA1 allele as a 2.2 kb Holdl-Sacl fragment SYE50 PRS314-YRA1-C-Y-Y Same as in SYE7A but the 325-nt YRA1 exon 1 was replaced by the 835-nt HS2 conding replaced by the 835-nt HS2 conding replaced by the 835-nt HS2 conding replaced by the 831-th XA1+X-Y SYE57 PRS314-YRA1+X-Y-Y Same as in SYE7A but the 705-nt YRA1 introm was replaced by the 805-nt HS2 fold intron SYE50 PRS314-YRA1+X-Y-Y Same as in SYE7A but the 705-nt YRA1 introm was replaced by the 805-nt KPS1 hairton SYE50 PRS314-YRA1-YA-Y Same as in SYE7A but the 705-nt YRA1 introm was replaced by the 805-nt KPS1 hairton SYE51 PRS314-YRA1-YA-Y Same as in SYE7A but the 705-nt YRA1 introm was replaced by the 805-nt KPS1 hairton SYE52 PRS314-YRA1-YA-Y Sa			
SYEAD PR314-YRA1-MUNSSame as SYEAD Detains the YRA1 microSYEBSPR314-YRA1- Contains the yra1-1 allele as a 3 0 bb Hindli-Sacl fagmentSYEBSPR314-YRA1- Contains the yra1-1 allele as a 3 0 bb Hindli-Sacl fagmentSYEDSPR314-YRA1 (Hindli-Sacl)SYETSPR314-YRA1 (Hindli-Sacl)SYETSPR314-YRA1 (Hindli-Sacl)Contains wild-yp YRA1 allele as a 2.2 kb Hindli-Sacl fagmentSYETSPR314-YRA1-C-Y-YSame as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 83-nt CYH2 exon1SYETSPR314-YRA1-H-Y-YSame as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 83-nt MER2 exon1SYETSPR314-YRA1-YC-YSame as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 30-nt MER2 exon1SYETSPR314-YRA1-YC-YSame as in SYE74 but the 32-nt YRA1exon 1 was replaced by the 30-nt MER2 exon1SYETSPR314-YRA1-YC-YSame as in SYE74 but the 70-nt YRA1 intrones replaced by the 30-nt MER2 exon2SYETSPR314-YRA1-YC-YSame as in SYE74 but the 70-nt YRA1 intrones replaced by the 80-nt MER2 intronSYETSPR314-YRA1-YA-YSame as in SYE74 but the 70-nt YRA1 intrones replaced by the 80-nt MER2 exon2SYETSPR314-YRA1-YA-YSame as in SYE74 but the 70-nt YRA1 intrones replaced by the 60-nt MER2 intronSYETSPR314-YRA1-YA-YSame as in SYE74 but the 70-nt YRA1 intronSYETSPR314-YRA1-YA-YSame as in SYE74 but the 70-nt YRA1 intronSYETSPR314-YRA1-YA-YSame as in SYE74 but contains an internal deleton from A.2 10 b6 in exon1 </td <td>SYE44 (PIA278-1)</td> <td>pRS314-YRA1</td> <td>Contains wild-type YRA1 allele as a 2.0 kb BamHI-XhoI fragment</td>	SYE44 (PIA278-1)	pRS314-YRA1	Contains wild-type YRA1 allele as a 2.0 kb BamHI-XhoI fragment
SYESS PRS314-YRA1 Contains wid-ype YRA1 allele as a 3.0 bb Hindli-Sad fagment SYESS PRS314-YRA1 Contains My-tagged YRA2 allele as a 1.7 kb BamHi-BamHi fagment SYESS PRS314-YRA1 (Hdill-Sad) Contains My-tagged YRA2 allele as a 2.1 kb HamHi-BamHi fagment SYET0 PRS314-YRA1 (Hdill-Sad) Contains Wid-yp YRA1 allele as a 2.2 kb Hault-Sad fagment SYET0 PRS314-YRA1 (Hdill-Sad) Contains wid-yp YRA1 allele as a 2.2 kb Hault-Sad fagment SYET0 PRS314-YRA1 (Hdill-Sad) Same as in SYETA but the 320-41 YRA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coordina region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region of YFA1exon 1 was replaced by the 63-41 HS3 coording region 20 HS3 HS4	SYE46(PIA286-1)	pRS314-YRA1-ΔIVS	Same as SYE44 but lacks the YRA1 intron
SYEB0pFS314-yra1-1Contains the yrác1-1 allele as a 3.0 bk Hindli-Sach fragmentSYEF0YPS316-YFA1 (Hindli-SachContains wild-by YFA1 allele as a 2.2 Kb Hindli-Sach fragmentSYEF0pFS316-YFA1 (Hindli-Sach)Contains wild-by YFA1 allele as a 2.2 Kb Xhol-Sach fragmentSYEF0pFS316-YFA1 (Hol-Sach)Contains wild-by YFA1 allele as a 2.2 Kb Xhol-Sach fragmentSYEF2pFS316-YFA1 (HA1-K-Y-YSame as in SYEF4 but the 382-nt YFA1 scon 1 was replaced by the 63-nt (VF12 exon1SYEF2pFS316-YFA1-HA1-Y-YSame as in SYEF4 but the 382-nt YFA1 scon 1 was replaced by the 63-nt (VF12 exon1SYEF2pFS316-YFA1-HA1-Y-YSame as in SYEF4 but the 382-nt YFA1 scon 1 was replaced by the 63-nt (VF12 exon1SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but the 766-nt YFA1 intorn was replaced by the 63-nt (VF12 exon2SYEF4pFS316-YFA1-YC-YSame as in SYEF4 but the 766-nt YFA1 intorn was replaced by the 63-nt (YF12 exon2SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but the 68-nt YFA1 exon2 was replaced by the 485-nt (YF12 exon2SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but the 68-nt YFA1 exon2 was replaced by the 485-nt (YF2 exon2SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but the 58-nt YFA1 exon2 was replaced by the 62-nt (YF2 exon2SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but tortains an internal deletion from A.4 to 86 in exon1SYEF3pFS316-YFA1-YC-YSame as in SYEF4 but contains an internal deletion from A.4 to 86 in exon1SYEF3pFS316-YFA1-YA-HSame as in SYEF4 but contains an internal deletion from A.4 to 86 in exon1SYEF14pFS316-YFA1-DE-C/DB<	SYE58	pRS316-YRA1	Contains wild-type YRA1 allele as a 3.0 kb HindIII-SacI fragment
SYE18 (IpFS228) YopLan 12,Mys-YR42 Contains Mys-daged YR42 allele as a 17. Nb Bamit-Bamit Hagment SYE70 pRS314-YRA1(Nbil-Sacl) Contains wild-by YRA1 allele as a 2.2 Kb Xbil-Sacl fagment SYE80 pRS314-YRA1-CV-YY Same as in SYE74 but the 32-ntt YRA1exon 1 was replaced by the 83-nt UR2 exon1 SYE80 pRS314-YRA1-CV-YY Same as in SYE74 but the 32-ntt YRA1exon 1 was replaced by the 63-nt UR3 regulated by the 63-nt UR3 regulated by the 78-nt VRA1 information that regulated by the 63-nt UR3 regulated by the 78-nt VRA1 information and the 78-ntt YRA1 information regulated by the 78-nt VRA1 information provided by the 51-nt CVH2 inform SYE87 pRS314-YRA1-V-CV Same as in SYE74 but the 78-nt YRA1 information regulated by the 51-nt CVH2 inform SYE87 pRS314-YRA1-V-CV Same as in SYE74 but the 78-nt YRA1 information regulated by the 52-nt MR2 exon2 SYE82 pRS314-YRA1-V-CV Same as in SYE74 but the 58-nt YRA1 exon2 was replaced by the 68-nt MR2 exon2 SYE87 pRS314-YRA1-V-CV Same as in SYE74 but the 58-nt YRA1 exon2 was replaced by the 68-nt MR2 exon2 SYE87 pRS314-YRA1-V-CV Same as in SYE74 but contains an internal deletion from AA 2 to 56 in exon1 SYE87 pRS314-YRA1-VE-CID Same as in SYE74 but contains an	SYE60	pRS314-yra1-1	Contains the yra1-1 allele as a 3.0 kb HindIII-SacI fragment
SYET0 pR5314-YRA1 (Hindli-Sac) Contains wild-by YRA1 allele as a 2.2 Kb Xhol-Sac) fargment SYET4 pR5314-YRA1(Xhol-Sac) Contains wild-by YRA1 allele as a 2.2 Kb Xhol-Sac) fargment SYE50 pR5314-YRA1-C-Y-Y Same as in SYETA that B2-nt YRA1 excon 1 was replaced by the 83-nt URA1 scone 1 was replaced by the 03-nt URA2 scone 1 SYE50 pR5314-YRA1-YC-Y Same as in SYETA that B2-nt YRA1 excon 1 was replaced by the 03-nt URA2 scone 3 SYE51 pR5314-YRA1-YC-Y Same as in SYETA that B2-nt YRA1 excon 1 was replaced by the 03-nt URA1 intron SYE51 pR5314-YRA1-YC-Y Same as in SYETA that B2-nt YRA1 excon 1 was replaced by the 03-nt URA1 intron SYE52 pR5314-YRA1-YA-Y Same as in SYETA that B2-nt YRA1 intron was replaced by the 03-nt URA1 intron SYE52 pR5314-YRA1-YA-Y Same as in SYETA that B5-nt YRA1 excon 2 was replaced by the 03-nt URA1 intron SYE52 pR5314-YRA1-YA-Y Same as in SYETA that B5-nt YRA1 excon 2 was replaced by the 03-nt URA1 intron SYE52 pR5314-YRA1-YA-Y Same as in SYETA that B5-nt YRA1 excon 2 was replaced by the 03-nt URA2 exon2 SYE73 pR5314-YRA1-YA-Y Same as in SYETA that B5-nt YRA1 excon2 was replaced by the 03-nt URA2 exon2 SYE14 pR5314-YRA1-YA-Y Same as in SYETA that B5-nt YRA1 excon2 was replaced by the 0	SYE181(pFS2261)	YepLac112-Myc-YRA2	Contains Myo-tagged YRA2 allele as a 1.7 kb BamHI-BamHI fragment
SYE74 pRS314-YRA1(Xhol-Sact) Contains wild-by YRA1 allele as a 2.2 Kb Xhol-Sact fragment SYE80 pRS314-YRA1-C-YY Same as in SYE74 but the 32-nt YRA1 scon 1 was replaced by the 33-nt VF12 exon1 SYE807 pRS314-YRA1-H-YY Same as in SYE74 but the 32-nt YRA1 scon 1 was replaced by the 603-nt HIS3 coding re SYE817 pRS314-YRA1-YA1-Y Same as in SYE74 but the 1ss 28 but to YRA1 scon 1 was replaced by the 603-nt HIS3 coding re SYE817 pRS314-YRA1-YA1-Y Same as in SYE74 but the 1ss 28 but to YRA1 scon 1 was replaced by the 603-nt HIS3 coding re SYE817 pRS314-YRA1-YA1-Y Same as in SYE74 but the 708-nt YRA1 intron was replaced by the 603-nt HIS3 coding re SYE81 pRS314-YRA1-YA1-Y Same as in SYE74 but the 603-nt YRA1 intron was replaced by the 485-nt CY12 exon2 SYE81 pRS314-YRA1-YA-Y Same as in SYE74 but the 603-nt YRA1 ison2 was replaced by the 485-nt CY12 exon2 SYE81 pRS314-YRA1-YA-R Same as in SYE74 but contains an internal deletion from A.2 to 85 in exon1 SYE81 pRS314-YRA1-YA-R Same as in SYE74 but contains an internal deletion from A.2 to 85 in exon1 SYE813 pRS314-YRA1-DE-CI02 Same as in SYE74 but contains an internal deletion from A.4 to 85 in exon1 SYE141 pRS314-YRA1-DE-CI02 Same as in SYE74 but contains an int	SYE70	pRS316-YRA1 (HindIII-Sacl)	Contains wild-typ YRA1 allele as a 2.2 Kb HindIII-SacI fragment
SYE80 pRS314-YRA1-D-V-V Same as in SYE74 but the 392-nt YRA1exon 1 was replaced by the 83-nt CY12 exon1 SYE80 pRS314-YRA1-M-V-V Same as in SYE74 but the 326-nt of RA1exon 1 was replaced by the 63-nt MER2 exon1 SYE80 pRS314-YRA1-M-V-V Same as in SYE74 but the 326-nt of RA1exon 1 was replaced by the 63-nt MER2 exon1 SYE41 pRS314-YRA1-X-V-V Same as in SYE74 but the 1ast 280 nts of YRA1exon 1 was replaced by the 63-nt MER2 infron SYE51 pRS314-YRA1-X-V-V Same as in SYE74 but the 76-nt YRA1 infrom was replaced by the 63-nt YE74 exon2 SYE52 pRS314-YRA1-YA-V Same as in SYE74 but the 76-nt YRA1 infromwas replaced by the 63-nt YE74 exon2 SYE52 pRS314-YRA1-YA-V Same as in SYE74 but the 68-nt YRA1 exon2 was replaced by the 62-nt RPS61A infron SYE52 pRS314-YRA1-YA-K Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE53 pRS314-YRA1-YA-K Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE14 pRS314-YRA1-YA-K Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE173 pRS314-YRA1-DE-C110 Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE141 pRS314-YRA1-DE-C100 Same as in SYE74 but contains an internal d	SYE74	pRS314-YRA1(Xhol-Sacl)	Contains wild-typ YRA1 allele as a 2.2 Kb Xhol-SacI fragment
SYEB0 pR314-YRA1-C-Y-Y Same as in SYE74 but the 392-tr YRA1exon 1 was replaced by the 38-th CYT-2 exon1 SYE50 pR3314-YRA1-M-Y-Y Same as in SYE74 but the 392-tr YRA1exon 1 was replaced by the 38-th CYT-2 exon1 SYE507 pR3314-YRA1-M-Y-Y Same as in SYE74 but the 28-th Coding region of YRA1exon 1 was replaced by the 60-th HR3 coding region of YRA1exon 1 was replaced by the 51-th CTH2 intron SYE507 pR3314-YRA1-Y-C-Y Same as in SYE74 but the 78-th YRA1 intronwas replaced by the 30-th HR251 kinton SYE507 pR3314-YRA1-YA-Y Same as in SYE74 but the 78-th YRA1 intronwas replaced by the 30-th HR251 kinton SYE502 pR3314-YRA1-YA-Y Same as in SYE74 but the 78-th YRA1 intronwas replaced by the 30-th HR251 kinton SYE502 pR3314-YRA1-YA-Y Same as in SYE74 but the 78-th YRA1 intronwas replaced by the 30-th HR252 kinton SYE503 pR3314-YRA1-YA-Y Same as in SYE74 but contains an internal deletion from A.2 to 85 in exon1 SYE130 pR3314-YRA1-DE-C100 Same as in SYE74 but contains an internal deletion from A.2 to 85 in exon1 SYE141 pR3314-YRA1-DE-C100 Same as in SYE74 but contains an internal deletion from A.3 to 85 in exon1 SYE141 pR3314-YRA1-DE-C100 Same as in SYE74 but contains an internal deletion from A.4 to 85 in exon1 SYE1414 pR3314-YRA1-D		,,	
SYE52 pR314-YRA1-H-Y-Y Same as in SYE74 but the 326-nt YRA1exon Twas replaced by the 326-nt MER2 exon1 SYE507 pR314-YRA1-H-Y-Y Same as in SYE74 but the 326-ft coling region of YRA1exon 1 was replaced by the 501-nt HIS3 coling resion of YRA1exon 1 was replaced by the 501-nt CYH2 intron SYE547 pR314-YRA1-YC-Y Same as in SYE74 but the 766-nt YRA1 intron was replaced by the 501-nt CYH2 intron SYE560 pR314-YRA1-YC-Y Same as in SYE74 but the 766-nt YRA1 intron was replaced by the 501-nt CYH2 intron SYE52 pR314-YRA1-YA-Y Same as in SYE74 but the 766-nt YRA1 intron was replaced by the 520-nt MER2 intron SYE52 pR314-YRA1-YA-Y Same as in SYE74 but the 566-nt YRA1 exon2 was replaced by the 520-nt MER2 exon2 SYE53 pR314-YRA1-YA-Y-R Same as in SYE74 but the 586-nt YRA1 exon2 was replaced by the 520-nt MER2 exon2 SYE73 pR314-YRA1-DY-Y-R Same as in SYE74 but contains an internal deletion from A.A. 21 to 86 in exon1 SYE137 pR314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 21 to 86 in exon1 SYE141 pR314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 31 to 86 in exon1 SYE145 pR314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 31 to 86 in exon1 SYE144	SYE80	pRS314-YRA1-C-Y-Y	Same as in SYE74 but the 382-nt YRA1exon 1 was replaced by the 83-nt CYH2 exon1
SYE507 pR314-YRA1-HY-YY Same as in SYE74 but the 328-nt coding region of YRA1 exon 1 was replaced by the 083-nt HI33 coding res SYE474 pR314-YRA1-exon1-reverse Same as in SYE74 but the 1ast 280 for 54 /RA1 exon 1 was replaced by the 051-nt CYH2 intron SYE57 pR314-YRA1-Y-C-Y Same as in SYE74 but the 766-nt YRA1 intronwas replaced by the 11-nt CYH2 intron SYE50 pR314-YRA1-Y-A-Y Same as in SYE74 but the 766-nt YRA1 intronwas replaced by the 82-nt RPS51 hinton SYE52 pR314-YRA1-Y-Y-W Same as in SYE74 but the 686-nt YRA1 exon2 was replaced by the 82-nt RPS51 hinton SYE52 pR314-YRA1-Y-Y-W Same as in SYE74 but the 686-nt YRA1 exon2 was replaced by the 82-nt RPS51 hinton SYE53 pRS314-YRA1-DY-Y-R Same as in SYE74 but the 688-nt YRA1 exon2 was replaced by the 82-nt RPS51 hinton SYE13 pRS314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE14 pRS314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE14 pRS314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1 SYE14 pRS314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1 SYE14 pRS314-YRA1-DE-CI20 <td< td=""><td>SYE82</td><td>pRS314-YRA1-M-Y-Y</td><td>Same as in SYE74 but the 382-nt YRA1exon 1was replaced by the 385-nt MER2 exon1</td></td<>	SYE82	pRS314-YRA1-M-Y-Y	Same as in SYE74 but the 382-nt YRA1exon 1was replaced by the 385-nt MER2 exon1
SYE374 pR314-YRA1-exon1-reverse Same as in SYE74 but the last 226 nts of YRA1 kincon 1 was replaced by the 50ml MER2 intron SYE37 pR314-YRA1-Y-C.Y Same as in SYE74 but the 766nt YRA1 intron was replaced by the 50ml MER2 intron SYE90 pR314-YRA1-Y-A-Y Same as in SYE74 but the 766nt YRA1 intronwas replaced by the 30ml MER2 intron SYE92 pR314-YRA1-Y-Y-C Same as in SYE74 but the 568-nt YRA1 exon2 was replaced by the 82ml MER2 exon2 SYE92 pR314-YRA1-Y-Y-R Same as in SYE74 but the 568-nt YRA1 exon2 was replaced by the 82ml MER2 exon2 SYE93 pR314-YRA1-YA-Y-R Same as in SYE74 but the 836-nt YRA1 exon2 was replaced by the 82ml MER2 exon2 SYE173 pR314-YRA1-DY-Y-R Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE174 pR314-YRA1-DE-C010 Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE141 pR314-YRA1-DE-C010 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE145 pR314-YRA1-DE-C010 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE146 pR314-YRA1-DE-C010 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE146 pR314-YRA1-DE-C010 Same as in SYE74 but contains an	SYE507	pRS314-YRA1-H-Y-Y	Same as in SYE74 but the 285-nt coding region of YRA1exon 1was replaced by the 663-nt HIS3 coding re-
SYE54 pR314-YRA1-V-C-Y Same as in SYE74 but the 786-nt YRA1 intronwas replaced by the 511-nt CYH2 intron SYE50 pR3314-YRA1-V-R-Y Same as in SYE74 but the 786-nt YRA1 intronwas replaced by the 306-nt KPR2 intron SYE52 pR3314-YRA1-V-R-Y Same as in SYE74 but the 786-nt YRA1 exon2 was replaced by the 436-nt CYH2 exon2 SYE52 pR3314-YRA1-Y-V-C Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 436-nt CYH2 exon2 SYE53 pR3314-YRA1-Y-V-R Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 520-nt RPS51A exon2 SYE73 pR3314-YRA1-DV-IR Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 520-nt RPS51A exon2 SYE143 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deleton from A.A.1 to 85 in exon1 SYE143 pR3314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deleton from A.A.2 to 85 in exon1 SYE143 pR3314-YRA1-DE-CI40 Same as in SYE74 but contains an internal deleton from A.A. 1 to 85 in exon1 SYE144 pR3314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deleton from A.A. 1 to 85 in exon1 SYE149 pR3314-YRA1-DE-CI60 Same as SYE74 but contains an internal deleton from A.A. 1 to 85 in exon1 SYE149 pR3314-YRA1-DE-CI60 Same as SYE74 but contains an internal deleton from A.A. 1 to 85 in exon1	SYE474	pRS314-YRA1-exon1-reverse	Same as in SYE74 but the last 286 nts of YRA1exon 1 was replaced by its complementay sequences
SYE37 pR314-YRA1-VA-W Same as in SYE74 but the 768-nt YRA1 intronwas replaced by the 90-nt MER2 intron SYE80 pR3314-YRA1-VA-V Same as in SYE74 but the 568-nt YRA1 intronwas replaced by the 485-nt CVH2 exon2 SYE82 pR3314-YRA1-V-V Same as in SYE74 but the 588-nt YRA1 exon 2 was replaced by the 485-nt CVH2 exon2 SYE82 pR3314-YRA1-V-V Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE137 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE139 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE141 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE143 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE143 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE147 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE149 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE149 pR3314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1	SYE84	pRS314-YRA1-Y-C-Y	Same as in SYE74 but the 766-nt YRA1 intron was replaced by the 511-nt CYH2 intron
SYEB0 pRS314-YRA1-Y-R-Y Same as in SYE74 but the 766-nt YRA1 intronwas replaced by the 486-nt CYTA2 intronwas replaced by the 486-nt CYTA2 exon2 SYEB2 pRS314-YRA1-Y-Y-M Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 486-nt CYTA2 exon2 SYEB2 pRS314-YRA1-Y-Y-M Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 529-nt RPS51A exon2 SYE13 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE139 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE141 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE143 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI00 Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1 SYE1610 pRS314-YRA1-DE-CI00	SYE87	pRS314-YRA1-Y-M-Y	Same as in SYE74 but the 766-nt YRA1 intronwas replaced by the 80-nt MER2 intron
SYED2 SYED2 PRS314-YRA1-Y-Y-C PRS314-YRA1-Y-Y-C Same as in SYE74 but the 568-nt YRA1 exon 2 was replaced by the 485-nt CYH2 exon2 SYED3 PRS314-YRA1-Y-Y-RSame as in SYE74 but the 568-nt YRA1 exon2 was replaced by the 529-nt RPS51A exon2SYED3 SYED3PRS314-YRA1-N44 PRS314-YRA1-DE-CH0Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE137 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 1 to 85 in exon1 SYE141 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE143 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 3 to 85 in exon1 SYE144 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1 SYE145 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 6 to 85 in exon1 SYE147 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 6 to 85 in exon1 SYE147 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1 SYE147 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1 SYE147 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains an internal deletion from A.A. 8 to 85 in exon1 SYE151 PRS314-YRA1-DE-CH0 Same as in SYE74 but contains a deletion from A.A. 8 to 85 in exon1SYE160 SYE174 SYE174PRS314-YRA1-DE-CH0 Same as in SYE74 but contains a deletion from A.A. 8 to 85 in exon1SYE174 SYE174PRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transation initiation codon SYE161 PRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transation initiation codon SYE162 SYE300 PRS314	SYE90	pRS314-YRA1-Y-R-Y	Same as in SYE74 but the 766-nt YRA1 intronwas replaced by the 398-nt RPS51A intron
SYE22 SYE93pRS314-YRA1-Y-Y-M pRS314-YRA1-N-Y-RSame as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 529-nt RPS51A exon2SYE93pRS314-YRA1-N94Same as in SYE74 but ontains an internal deletion from A.A. 2 to 85 in exon1SYE137pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1SYE139pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1SYE143pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1SYE143pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 4 to 85 in exon1SYE143pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 6 to 85 in exon1SYE144pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 7 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE149pRS314-YRA1-DE-CI00Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE150pRS314-YRA1-DE-CI00Same as in SYE74 but co	SYE92	pRS314-YRA1-Y-Y-C	Same as in SYE74 but the 588-nt YRA1 exon 2 was replaced by the 485-nt CYH2 exon2
SYE93pRS314-YRA1-V-Y-RSame as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 529-nt RPS51A exon2SYE73pRS314-YRA1-0E-CI10Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1SYE137pRS314-YRA1-DE-CI10Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE141pRS314-YRA1-DE-CI20Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1SYE143pRS314-YRA1-DE-CI30Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE144pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE145pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE149pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE151pRS314-YRA1-DE-CI70Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE161pRS314-YRA1-DE-CI80Same as SYE74 but contains an internal deletion from A.B. 21 to 85 in exon1SYE75pRS314-YRA1-DE-CI80Same as SYE74 but contains a deletion of first 351nts of YRA1 exon2SYE160pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE161pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE162pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE163pRS314-YRA1-MUASame as in SYE74 but contains AUG to AUA mutation in	SYE92	pRS314-YRA1-Y-Y-M	Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 827-nt MER2 exon2
SYE73pRS314-YRA1-N84Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1SYE137pRS314-YRA1-DE-CI10Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE139pRS314-YRA1-DE-CI20Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE141pRS314-YRA1-DE-CI30Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1SYE143pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1SYE149pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1SYE149pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1SYE149pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1SYE151pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1SYE161pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE75pRS314-YRA1-DE-CI60Same as in SYE74 but contains and the from A.A. 81 to 85 in exon1SYE761pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE778pRS314-YRA1-DE-CI60Same as in SYE74 but contains an internal deletion from A.8. 81 to 85 in exon1SYE781pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE181pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUC mutation in the trans	SYE93	pRS314-YRA1-Y-Y-R	Same as in SYE74 but the 588-nt YRA1 exon2 was replaced by the 529-nt RPS51A exon2
SYE73 pR314-YRA1-N84 Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1 SYE137 pR314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE139 pR314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE141 pR314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1 SYE144 pR314-YRA1-DE-CI40 Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1 SYE147 pR314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE147 pR314-YRA1-DE-CI70 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE174 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE181 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE181 pRS314-YRA1-DE Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE182 pRS314-YRA1-DE Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon			
SYE137 pRS314-YRA1-DE-CI10 Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE138 pRS314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1 SYE141 pRS314-YRA1-DE-CI30 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE143 pRS314-YRA1-DE-CI40 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE147 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE147 pRS314-YRA1-DE-CI70 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE148 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE171 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains a 401-nt internal deletion from nts 27 to 487 of YRA1 intron SYE78 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE181 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion in	SYE73	pRS314-YRA1-N84	Same as in SYE74 but contains an internal deletion from A.A. 2 to 85 in exon1
SYE139 pRS314-YRA1-DE-CI20 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE141 pRS314-YRA1-DE-CI30 Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1 SYE143 pRS314-YRA1-DE-CI40 Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1 SYE145 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI70 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE161 pRS314-YRA1-DE-CI80 Same as SYE74 but contains a deletion from A.A. 61 to 85 in exon1 SYE174 pRS314-YRA1-DE1-R1-F7 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE181 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon	SYE137	pRS314-YRA1-DE-CI10	Same as in SYE74 but contains an internal deletion from A.A. 11 to 85 in exon1
SYE141 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1 SYE145 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE146 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE174 pRS314-YRA1-DE-CI80 Same as SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE175 pRS314-YRA1-DE-CI80 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE176 pRS314-YRA1-DE-C Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE140 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE140 pRS314-YRA1-MESS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site	SYE139	pRS314-YRA1-DE-CI20	Same as in SYE74 but contains an internal deletion from A.A. 21 to 85 in exon1
SYE143 pRS314-YRA1-DE-CI40 Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1 SYE145 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE147 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI70 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE171 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE175 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE175 pRS314-YRA1-DE-CI80 Same as SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE176 pRS314-YRA1-DE-CI80 Same as SYE74 but contains a deletion of first 351nts of YRA1 exon2 SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE183 pRS314-YRA1-AUU Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE194 pRS314-YRA1-MUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE190 pRS314-YRA1-MUA Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site	SYE141	pRS314-YRA1-DE-CI30	Same as in SYE74 but contains an internal deletion from A.A. 31 to 85 in exon1
SYE146 pR3314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE147 pR3314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pR3314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE151 pR3314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE175 pR3314-YRA1-DE-CI60 Same as SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE176 pR3314-YRA1-DE-CI80 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE180 pR3314-YRA1-DE2 Same as SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE181 pR3314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE181 pR3314-YRA1-AUA Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE183 pR3314-YRA1-AUA Same as in SYE74 but contains GUAUG to GUAUAU mutation in the fransaltion initiation codon SYE190 pR3314-YRA1-MSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE298 pRS314-YRA1-MSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site	SYE143	pRS314-YRA1-DE-CI40	Same as in SYE74 but contains an internal deletion from A.A. 41 to 85 in exon1
SYE147 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 61 to 85 in exon1 SYE149 pRS314-YRA1-DE-CI60 Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1 SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE374 pRS314-YRA1-DE-CI80 Same as SYE74 but contains a 461-nt internal deletion from nts 27 to 487 of YRA1 intron SYE374 pRS314-YRA1-DI-R1-F7 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE181 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon SYE183 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon SYE183 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon SYE280 pRS314-YRA1-AUA Same as in SYE74 but contains GUAUG to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-mBSS Same as in SYE74 but contains GUAUG to GUAUAU mutation in the branchpoint region SYE415 pRS314-YRA1-mBSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE302 pRS314-YRA1-mBSS Same as in SYE74 but contains GUAUGU to GUAUAC mutation	SYE145	pRS314-YRA1-DE-CI50	Same as in SYE74 but contains an internal deletion from A.A. 51 to 85 in exon1
SYE149pRS314-YRA1-DE-CI70Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1SYE151pRS314-YRA1-DE-CI80Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1SYE374pRS314-YRA1-DE-CI80Same as in SYE74 but contains a 461-nt internal deletion from A.A. 81 to 85 in exon1SYE374pRS314-YRA1-DE-CI80Same as SYE74 but contains a 461-nt internal deletion from nts 27 to 487 of YRA1 intronSYE78pRS314-YRA1-DE2Same as SYE74 but contains a deletion of first 351nts of YRA1exon2SYE160pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE161pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codonSYE240pRS316-YRA1-AUASame as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codonSYE298pRS314-YRA1-MUASame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE300pRS314-YRA1-m5SSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE415pRS314-YRA1-m8B2Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the branchpoint regionSYE416pRS314-YRA1-M84-m5SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the branchpoint regionSYE419pRS314-YRA1-N84-m5SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the branchpoint regionSYE419pRS314-YRA1-N84-m5SSSame as in SYE73 but contains AG to UC mutation in the 5' splicing siteSYE515pRS316-YRA1-AUA-m5SSSame as in SYE73 but contains GUAUGU	SYE147	pRS314-YRA1-DE-CI60	Same as in SYE74 but contains an internal deletion from A.A. 01 to 85 in exon1
SYE151 pRS314-YRA1-DE-CI80 Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1 SYE374 pRS314-YRA1-DI-R1-F7 Same as SYE74 but contains a 481-nt internal deletion from nts 27 to 487 of YRA1 intron SYE78 pRS314-YRA1-DE2 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE180 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE181 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE183 pRS314-YRA1-AUU Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE240 pRS314-YRA1-AUU Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE240 pRS314-YRA1-MUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE302 pRS314-YRA1-mBSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE415 pRS314-YRA1-M84-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-mSSS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-mSSS Same as in SYE73 but contains GUAUGU to GUAUAUA	SYE149	pRS314-YRA1-DE-CI70	Same as in SYE74 but contains an internal deletion from A.A. 71 to 85 in exon1
SYE374pRS314-YRA1-DI-R1-F7Same as SYE74 but contains a 461-nt internal deletion from nts 27 to 487 of YRA1 intronSYE78pRS314-YRA1-DE2Same as SYE74 but contains a deletion of first 351nts of YRA1exon2SYE160pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE161pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codonSYE163pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codonSYE240pRS318-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE298pRS314-YRA1-m5SSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE302pRS314-YRA1-m5SSSame as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint regionSYE415pRS314-YRA1-MS4Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the 5' splicing siteSYE419pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE419pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to UGACUACC mutation in the branchpoint regionSYE516pRS316-YRA1-AUA-m3SSSame as in SYE240 but contains AG to UC mutation in the 3' splicing siteSYE519pRS316-YRA1-AUA-m3SSSame as in SYE240 but contains AG to UG AUAU mutation in the 5' splicing siteSYE519pRS316-YRA1-AUA-m3SSSame as in SYE240 but contains AG to UG AUAU mutation in the 5' splicing siteSYE519pRS316-YRA1-AUA-m3SSSame as in SYE240 but contain	SYE151	pRS314-YRA1-DE-CI80	Same as in SYE74 but contains an internal deletion from A.A. 81 to 85 in exon1
SYE374 pRS314-YRA1-DI-R1-F7 Same as SYE74 but contains a 481-nt internal deletion from nts 27 to 487 of YRA1 intron SYE78 pRS314-YRA1-DE2 Same as SYE74 but contains a deletion of first 351nts of YRA1exon2 SYE160 pRS314-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE161 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE163 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS316-YRA1-AUA Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-m5SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE302 pRS314-YRA1-m8B2 Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE415 pRS314-YRA1-N84-m8SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-M84-m8SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-m8SS Same as in SYE73 but contains GUAUGU to GUAUAC mutation in the 5' splicing site SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site			
SYE78pRS314-YRA1-DE2Same as SYE74 but contains a deletion of first 351nts of YRA1exon2SYE180pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE181pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codonSYE183pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codonSYE240pRS316-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE298pRS314-YRA1-MSSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE300pRS314-YRA1-mSSSSame as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint regionSYE416pRS314-YRA1-N84-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE417pRS314-YRA1-N84-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE419pRS314-YRA1-N84-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE417pRS314-YRA1-N84-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the branchpoint regionSYE515pRS314-YRA1-AUA-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 6' splicing siteSYE517pRS316-YRA1-AUA-m8SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 6' splicing siteSYE519pRS316-YRA1-AUA-m8SSSame as in SYE74 but contains GUAUGU to GUAUACC mutation in the branchpoint regionSYE519pRS316-YRA1-AUA-m8SSSame as in SYE74 but cont	SYE374	pRS314-YRA1-DI-R1-F7	Same as SYE74 but contains a 461-nt internal deletion from nts 27 to 487 of YRA1 intron
SYE160 pRS314-YRA1-0E2 Same as SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE161 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE163 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS316-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS314-YRA1-MUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE298 pRS314-YRA1-mSSS Same as in SYE74 but contains AG to UC mutation in the 5' splicing site SYE300 pRS314-YRA1-mBS2 Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE415 pRS314-YRA1-mBB2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE516 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAC mutation in the 5' splicing site SYE516 pRS316-YRA1-AUA-mSSS Same as in SYE74 but contains GUAUGU to GUAUAC mutation in the 5' splicin	9VE70	- PS214 VPA1 DE2	Same as SVE74 but contains a deletion of first 251nts of VRA1even2
SYE160pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE161pRS314-YRA1-AUCSame as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codonSYE163pRS314-YRA1-AUUSame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE240pRS314-YRA1-AUASame as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codonSYE298pRS314-YRA1-AUASame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE300pRS314-YRA1-m3SSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE302pRS314-YRA1-mBB2Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the branchpoint regionSYE415pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE417pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE419pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE417pRS314-YRA1-N84-m3SSSame as in SYE73 but contains GUAUGU to GUAUAC mutation in the branchpoint regionSYE515pRS314-YRA1-AUA-m3SSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE517pRS316-YRA1-AUA-m3SSSame as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing siteSYE519pRS316-YRA1-AUA-m3SSSame as in SYE240 but contains GUAUGU to GUACUACC mutation in the branchpoint regionSYE234pGAD-C2-EDC3-FLContains the enti	312/0	pR3314-TRAT-DE2	Same as 31 E/4 but contains a deletion of inst 35 mits of TRA fexoriz
SYE181 pRS314-YRA1-AUC Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon SYE183 pRS314-YRA1-AUU Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon SYE240 pRS316-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS316-YRA1-AUA Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the transaltion initiation codon SYE298 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-m3SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE415 pRS314-YRA1-mBB2 Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5'	SYE160	pRS314-YRA1-AUA	Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon
SYE183 pRS314-YRA1-AUU Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon SYE240 pRS316-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE240 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE298 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-mBB2 Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE416 pRS314-YRA1-N84-mSSS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-mSSS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-mBB2 Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE515 pRS316-YRA1-AUA-mSSS Same as in SYE73 but contains GUAUGU to GUAUAC mutation in the branchpoint region SYE517 pRS316-YRA1-AUA-mSSS Same as in SYE240 but contains GUAUGU to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-mSSS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-mSSS Same as in SYE240 but contains UGACUAAC to UGACUACC mut	SYE161	pRS314-YRA1-AUC	Same as in SYE74 but contains AUG to AUC mutation in the transaltion initiation codon
SYE240 pRS318-YRA1-AUA Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon SYE298 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-mSSS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE302 pRS314-YRA1-mBB2 Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE415 pRS314-YRA1-N84-mSSS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAC mutation in the branchpoint region SYE515 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAC mutation in the branchpoint region SYE517 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE163	pRS314-YRA1-AUU	Same as in SYE74 but contains AUG to AUU mutation in the transaltion initiation codon
SYE298 pRS314-YRA1-m5SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-m3SS Same as in SYE74 but contains AG to UC mutation in the 3' splicing site SYE302 pRS314-YRA1-mBB2 Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE416 pRS314-YRA1-N84-m5SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains AG to UC mutation in the 3' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE516 pRS316-YRA1-AUA-m5SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains AG to UC mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE240	pRS316-YRA1-AUA	Same as in SYE74 but contains AUG to AUA mutation in the transaltion initiation codon
SYE298 pRS314-YRA1-m5SS Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE300 pRS314-YRA1-m3SS Same as in SYE74 but contains AG to UC mutation in the 3' splicing site SYE302 pRS314-YRA1-mBB2 Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE415 pRS314-YRA1-mBB2 Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-m8B2 Same as in SYE73 but contains GUAUGU to GUAUAC to UGACUACC mutation in the 5' splicing site SYE515 pRS316-YRA1-AUA-mSSS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-mSSS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains AG to UC mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment			
SYE300 pRS314-YRA1-m3SS Same as in SYE74 but contains AG to UC mutation in the 3' splicing site SYE302 pRS314-YRA1-mBB2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE415 pRS314-YRA1-N84-m5SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-mBB2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains GUAUGU to GUACUACC mutation in the 5' splicing site SYE519 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-m3B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE298	pRS314-YRA1-m5SS	Same as in SYE74 but contains GUAUGU to GUAUAU mutation in the 5' splicing site
SYE302 pRS314-YRA1-mBB2 Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE415 pRS314-YRA1-N84-m5SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE419 pRS314-YRA1-N84-mBB2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-m3B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-m3B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE300	pRS314-YRA1-m3SS	Same as in SYE74 but contains AG to UC mutation in the 3' splicing site
SYE415 pRS314-YRA1-N84-m5SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains GGAUAGU mutation in the 3' splicing site SYE419 pRS314-YRA1-N84-m8B2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 6' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the 6' splicing site SYE519 pRS316-YRA1-AUA-m8B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE302	pRS314-YRA1-mBB2	Same as in SYE74 but contains UGACUAAC to UGACUACC mutation in the branchpoint region
SYE416 pRS314-YRA1-N84-m5SS Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains AG to UC mutation in the 3' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains AG to UC mutation in the 3' splicing site SYE419 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-m8B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment			
SYE417 pRS314-YRA1-N84-m3SS Same as in SYE73 but contains AG to UC mutation in the 3' splicing site SYE419 pRS314-YRA1-N84-m8B2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains GUA UC Mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-m8B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-m8B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE415	pRS314-YRA1-N84-m5SS	Same as in SYE73 but contains GUAUGU to GUAUAU mutation in the 5' splicing site
SYE419 pRS314-YRA1-N84-mBB2 Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains AG to UC mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-mBB2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE519 pRS316-YRA1-AUA-mBB2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE417	pRS314-YRA1-N84-m3SS	Same as in SYE73 but contains AG to UC mutation in the 3' splicing site
SYE515 pRS316-YRA1-AUA-m5SS Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains AG to UC mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-m3B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE419	pRS314-YRA1-N84-mBB2	Same as in SYE73 but contains UGACUAAC to UGACUACC mutation in the branchpoint region
SYE517 pRS316-YRA1-AUA-m3SS Same as in SYE240 but contains AG to UC mutation in the 3' splicing site SYE519 pRS316-YRA1-AUA-m8B2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE515	pRS316-YRA1-AUA-m5SS	Same as in SYE240 but contains GUAUGU to GUAUAU mutation in the 5' splicing site
SYE519 pRS316-YRA1-AUA-mBB2 Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region SYE324 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE517	pRS316-YRA1-AUA-m3SS	Same as in SYE240 but contains AG to UC mutation in the 3' splicing site
SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE519	pRS316-YRA1-AUA-mBB2	Same as in SYE240 but contains UGACUAAC to UGACUACC mutation in the branchpoint region
SYE234 pGAD-C2-EDC3-FL Contains the entire EDC3 coding region as an EcoR-Sall fragment SYE324 pBTM116-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment			
SYE324 pBTM118-CRM1-FL Contains the entire CRM1 coding region as an EcoR-Sall fragment	SYE234	pGAD-C2-EDC3-FL	Contains the entire EDC3 coding region as an EcoR-Sall fragment
	SYE324	pBTM116-CRM1-FL	Contains the entire CRM1 coding region as an EcoR-Sall fragment

Name	Sequences
YRA1-1	AACCAAAGAGAGAAAAGCCTGCTAA
YRA1-2	GATCGAGCTCTGAGGACCATCAATTAGTAAG
YRA1-3	ACTTGAAGAACTATAAAAGGCCGC
YRA1-4	GTGTGCCATATCCTTCCTTACAAA 3'
YRA1-5	GTATGTTAATACGTGAAATGAGAGCT
YRA1-6	GAGTTGCCAAGCTCTTGGACACCACTA
YRA1-5-R	TTCGTCTAAGGATTTATCTAAGTTAGC
YRA1-7-R	GCAGATGTAGGTATTTTCTTAATATGG
Y-C-1A	TCGTGTGTTTAGTAGTAGGTTTTTTGTTAGAAGAAGTTTATTA
Y-C-1B	GTAACTAAACAAATAGCTCTCATTTCACGTATTAACATACTGAGACGTGACCTCTGTGCTTTCTA
Y-C-2A	CGAAGGTTTGCCAAGGGACATTAAGCAGGATGCTGTAAGAGTATGTAGTTCCATTTGGAAGAGGG
Y-C-2B	AAACTCTTTGAACACCACCTACTTGAGATGCAAAAAATTCCTGTACAAAAAAAA
Y-C-3A	TCATAGAGATATATGACTAACTTTTTTTTTTTTTTATTATAGGGTAAAGGTCGTATCGGTAAGCACA
Y-C-3B	GACATATTATGAGTCAAATATGCCGAATAAACTTTAAAAGGAAATAATACAGAAGTAGATGTTGA
Y-M-1A	TCGTGTGTTTAGTAGTAGGTTTTTTGTTAGAAGAAGTTTTCAACAAGAACAGAAAGAA
Y-M-1B	GTAACTAAACAAATAGCTCTCATTTCACGTATTAACATACGTTCGTAGCAGCATCTTGTTCCAGT
Y-M-2A	CGAAGGTTTGCCAAGGGACATTAAGCAGGATGCTGTAAGAGTTCGTACCAACACAGTGCATACCC
Y-M-2B	AAACTCTTTGAACACCACCTACTTGAGATGCAAAAAATTCCTATACTACAGTTGTTAGTAAATGT
Y-M-3A	TCATAGAGATATATGACTAACTTTTTTTTTTTTTTATTAGAACGTGAAAACCTTAATAAAGGATT
Y-M-3B	GACATATTATGAGTCAAATATGCCGAATAAACTTTAAAAGCAACTGGCGTGGTTTTTCATTGTAG
Y-R-2A	CGAAGGTTTGCCAAGGGACATTAAGCAGGATGCTGTAAGAGTATGTTAATATGGACTAAAGGAGG
Y-R-2B	AAACTCTTTGAACACCACCTACTTGAGATGCAAAAAATTCCTATTAAAATGACGAAAAGCAATAC
Y-R-3A	TCATAGAGATATATGACTAACTTTTTTTTTTTTTTATTAGGGTAGAGTTAGAACCAAGACCGTCA
Y-R-3B	GACATATTATGAGTCAAATATGCCGAATAAACTTTAAAAGAATTAGTAAATATAATAATATTTT
Y-H-F1	TTTAAGAAATCCATATTAAGAAAATACCTACATCTGCTAAATGACAGAGCAGAAAGCCCTAGTAA
Y-H-R1	GTAACTAAACAAATAGCTCTCATTTCACGTATTAACATACCTACATAAGAACACCTTTGGTGGAG
YRA1-Ex1R-F	CTTTAAGAAATCCATATTAAGAAAATACCTACATCTGCTATCTTACAGCATCCTGCTTAATGTCC
YRA1-Ex1R-R	GTAACTAAACAAATAGCTCTCATTTCACGTATTAACATACAATGTCTGCTAACTTAGATAAATCC
YRA1-DE1-5'	GATCCTCGAGGGTATATTAAAGCTATTTTACCACT
YRA1-DE1-3'	GATCCCTTGGCATTTAGCAGATGTAGGTATTTTCT
YRA1-CI10	GATCCCTTGGGTCTAAGGATTTATCTAAGTTAGCA
YRA1-CI20	GATCCCTTGGACTTCCTGCTTTGTTAGAGCCAATG
YRA1-CI30	GATCCCTTGGACCACGAGTACCACCGACACGGGCT
YRA1-CI40	GATCCCTTGGAACTTGCTTACCAACTCTTCTTGGA
YRA1-CI50	GATCCCTTGGTCTGTTTGGAAGGCTCCTACGTTGG
YRA1-CI60	GATCCCTTGGTGCCCTAGTATTTTTTCTGATAGGG
YRA1-CI70	GATCCCTTGGCTTGGCAACTCTAGCGACTGCGTTT
YRA1-CI80	GATCCCTTGGGACCTTGACCTCTCTAGTGGTGTCC
YRA1-DI-3'	AATCTTGATCTGCCTCCATCGATTG
YRA1-DI-F7	GATCGAATTCTAGCTATGGGAAACATGTCTTTCAT
YRA1-DI-R1	GATCGAATTCAGCTCTCATTTCACGTATTAACATA
YRA1-DE2-5'	TGATCAAGAATTCTCTTTTTAGAGA
YRA1-DE2-3'	GATCAGATCTTCCTATAATAAAAAAAAAAAAAAAGTTA
YRA1-mAUU-F	AATACCTACATCTGCTAAATTTCTGCTAACTTAGATAAATC

Table 3S. Oligonucleotides used in this study

YRA1-mAUU-R	GATTTATCTAAGTTAGCAGAAATTTAGCAGATGTAGGTATT
YRA1-mAUC-F	AATACCTACATCTGCTAAATCTCTGCTAACTTAGATAAATC
YRA1-mAUC-R	GATTTATCTAAGTTAGCAGAGATTTAGCAGATGTAGGTATT
YRA1-mAUA-F	AATACCTACATCTGCTAAATATCTGCTAACTTAGATAAATC
YRA1-mAUA-R	GATTTATCTAAGTTAGCAGATATTTAGCAGATGTAGGTATT
YRA1-m5SS-F	GCAGGATGCTGTAAGAGTATATTAATACGTGAAATGAGAGC
YRA1-m5SS-R	GCTCTCATTTCACGTATTAATATACTCTTACAGCATCCTGC
YRA1-mBB2-F	ATCATAGAGATATATGACTACCTTTTTTTTTTTTTTTATTATAG
YRA1-mBB2-R	CTATAATAAAAAAAAAAAAGGTAGTCATATATCTCTATGAT
YRA1-m3SS-F	AACTTTTTTTTTTTTATTATTCGAATTTTTTGCATCTCAAGT
YRA1-m3SS-R	ACTTGAGATGCAAAAAATTCGAATAATAAAAAAAAAAAA
yra i-z-r VDA1 m1	
VDA1 p1	
VRA1-D-3UTR-1	
11(A1-D-3011(-2	
YRA1-1-r	TCGAGGCGACACAATACGCCAGCT
YRA1-IN-1	AAACTCGAGAGAGGTCAAGGTCAACGTCGAAGG
YRA1-IN-2	GGGAAGCTTGTTATAACTCAACAAAACTCTTTG
YRA1-DI-5'	GATCGAATTCCTCCTTGATTGTTTGTGTATTGTCC
VEL016W-1	AATTGCGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
VEL015W-2	
EDC3-DS-2A	GATCGGATCCTCTAGATATGGTTTCTTTTACGAATTACTGTATTG
VEL 015W-3	
EDC3-DS-34	
YEL 015W-4	
I LLOIOW-4	
CRM1-TH-F1	GATCGAATTCATGGAAGGAATTTTGGATTTTTCTAACGAC
CRM1-TH-C1	GATCGTCGACCTAATCATCAAGTTCGGAAGGTTTTAATAA
CRM1-F-S1	AGTTGAGCCATTATTGAACGCTGT
CRM1-F-S2	AGGCAAATCGATGGTTCCGAATGG
CRM1-R-S1	GTCCAAAGTGCATTCAAATACACTC
DBP2-2-r	CTCTGTTACCCCAGCCACCATCTC
RPS28B	CGCAAACGACGAGCTTCACGTTCA
11 0200	
MER2-P	TGAGGGTATGCACTGTGTTGGTACGAAC
MER2-exon1-F	ATGGTCGCTAGAGGTAGAACAGACGAGA
MER2-exon1-R	CGTTCGTAGCAGCATCTTGTTCCAGTAG
MER2-exon2-F	GAAACGTGAAAACCTTAATAAAGGATTT
MER2-exon2-R	TCACAGCTCAGATTCCAGAGTGTCGGGT
18S	CATGGCTTAATCTTTGAGAC
RRP6-1	CCCGGAATTCCCAAAAATATGAGGGCATCGG
RRP6-2	CTAGTCTAGATTCGAGCGAAGTATAATCCTGC

			A-WT	A-edc3	B-WT	B-edc3	C-WT	C-edc3	E-WT	E-edc3	G-WT	G-edc3
Probe set	ORF	Gene	Signal									
6078_at	YDR381W	YRA1	622.5	944.9	801.4	1092	644.3	1038.9	568.4	1010.9	568.3	961.1
6079_at	YDR381W	YRA1	585.1	1158	561.2	944.7	645.4	1040.5	593.6	1165.5	578.5	1209.1
10069_f_at	YLR264W	RPS28B	2214	2722.5	2219.4	2966.9	2221.2	2744.2	2090.5	3027.8	2013.6	2799.1
10068_i_at	YLR264W	RPS28B	4649.6	4855.4	4040.4	4755.4	4869.1	5681.9	4692.4	6727.4	4337.1	5260.2
5732_at	YEL015W	EDC3	473.6	10	480.5	10	466.8	10	465.4	10	456.8	10
10796_at	YKL216W	URA1	1838.5	786.6	1963.9	1019	1805.3	831.3	1649.7	827.3	1620.7	857.9
9911_at	YLR420W	URA4	790.5	544.9	826.8	577.2	780.1	574.8	741.1	466.5	750.2	471.1

Table 4S. Transcripts Differentially Expressed in *edc3*Δ Cells

Five independent expression profiling experiments were carried out with wild-type (*EDC3*) and $edc3\Delta$ strains. Our data analysis indicates that only five transcripts (represented by seven probe sets) are differentially expressed in the $edc3\Delta$ strain. The raw signal values of each of these probe sets in different experiments (A, B, C, E, and G) are shown in the table.

Table 5S. Micorarray Data

This table is located at

http://jacobsonlab.umassmed.edu/cgi-bin/pubcontents.cgi?pubcontents=2006-Feng.

References

Denis-Duphil, M. (1989). Pyrimidine biosynthesis in Saccharomyces cerevisiae: the ura2 cluster gene, its multifunctional enzyme product, and other structural or regulatory genes involved in de novo UMP synthesis. Biochem Cell Biol *67*, 612-631.

Guthrie, C., and Fink, G. R. (1991). Methods in Enzymology: Molecular Biology of *Saccharomyces cerevisiae.*, Vol 194 (NY, Academic Press).

He, F., Brown, A. H., and Jacobson, A. (1996). Interaction between Nmd2p and Upf1p is required for activity but not for dominant-negative inhibition of the nonsense-mediated mRNA decay pathway in yeast. RNA *2*, 153-170.

He, F., Brown, A. H., and Jacobson, A. (1997). Upf1p, Nmd2p, and Upf3p are interacting components of the yeast nonsense-mediated mRNA decay pathway. Mol Cell Biol *17*, 1580-1594.

He, F., and Jacobson, A. (1995). Identification of a novel component of the nonsensemediated mRNA decay pathway by use of an interacting protein screen. Genes Dev *9*, 437-454.

He, F., Li, X., Spatrick, P., Casillo, R., Dong, S., and Jacobson, A. (2003). Genomewide analysis of mRNAs regulated by the nonsense-mediated and 5' to 3' mRNA decay pathways in yeast. Mol Cell *12*, 1439-1452.

Lecompte, O., Ripp, R., Thierry, J.-C., Moras, D., and Poch, O. (2002). Comparative analysis of ribosomal proteins in complete genomes: an example of reductive evolution at the domain scale. Nucl Acids Res *30*, 5382-5390.

Portman, D. S., O'Connor, J. P., and Dreyfuss, G. (1997). YRA1, an essential Saccharomyces cerevisiae gene, encodes a novel nuclear protein with RNA annealing activity. RNA 3, 527-537.

Strasser, K., and Hurt, E. (2000). Yra1p, a conserved nuclear RNA-binding protein, interacts directly with Mex67p and is required for mRNA export. Embo J *19*, 410-420.