

Supplementary Information

H/KDEL receptors mediate host cell intoxication by a viral A/B toxin in yeast

Björn Becker, Andrea Blum, Esther Gießelmann, Julia Dausend, Domenik Rammo, Nina C. Müller, Emilia Tschacksch, Miriam Steimer, Jenny Spindler, Ute Becherer, Jens Rettig, Frank Breinig, and Manfred J. Schmitt*

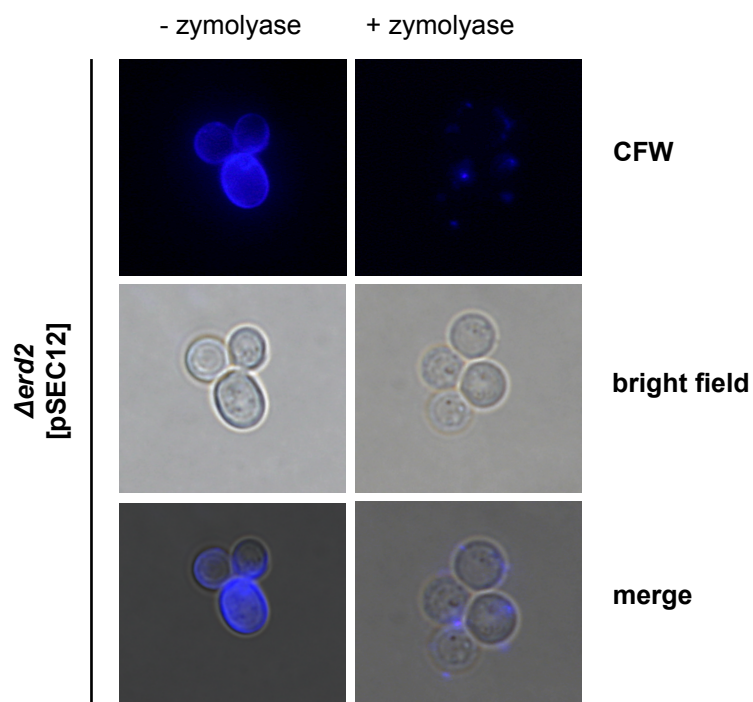


Figure S1: Calcofluor white staining of intact yeast and spheroplasts to detect remnant cell wall chitin after zymolyase treatment. Yeast cells lacking Erd2p (Δerd2 [pSEC12]) were treated with (+) or without (-) zymolyase and subsequently stained with calcofluor white (CFW).

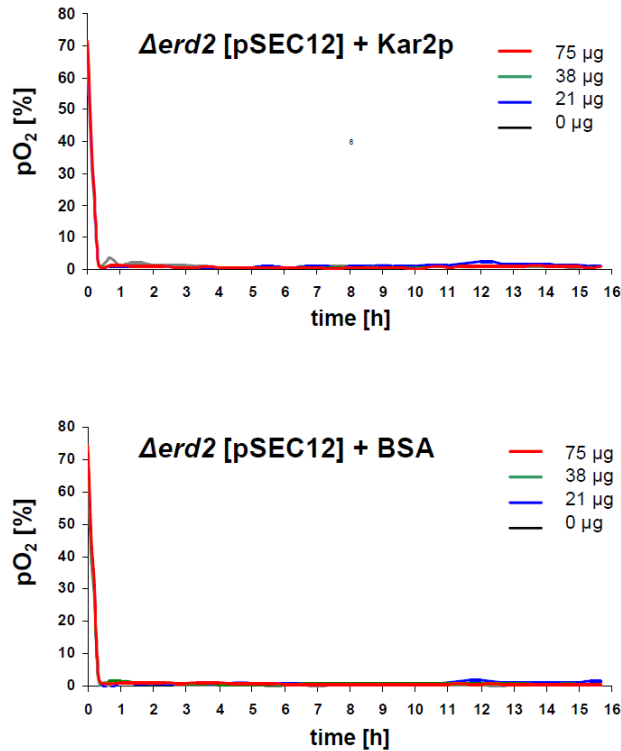


Figure S2: Cell growth of yeast spheroplasts from an HDEL receptor defective mutant in the presence of extracellular Kar2p. Dissolved oxygen content in the culture supernatant of spheroplasts from *Δerd2* cells (kept alive by overexpression of *SEC12* from an episomal plasmid (pSEC12)) was measured in the presence of increasing amounts of Kar2p or bovine serum albumin (BSA) as negative control. Each experiment was performed in triplicate (n = 3); shown is the mean average.

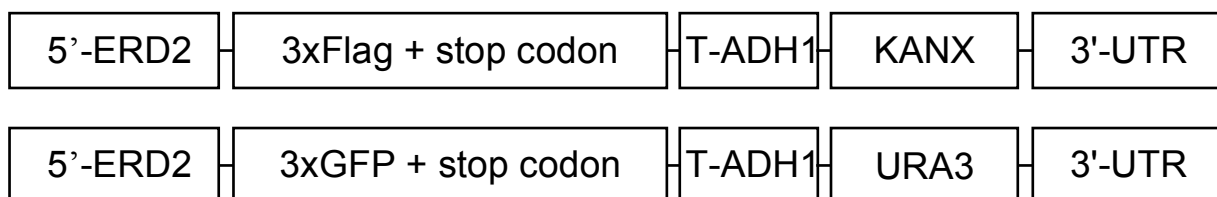


Figure S3: Schematic outline of synthetic DNA constructs used for chromosomal GFP or Flag tagging of Erd2p via homologous recombination. The entire sequence of both DNA constructs is given in Appendix S1. (5'-ERD2, 200 bp of the 3'-end of *ERD2*; 3xGFP, three copies of yeast enhanced GFP; 3xFlag, three copies of a Flag tag; T-ADH1, transcriptional terminator of the yeast alcohol dehydrogenase gene *ADH1*; URA3, expression cassette of the yeast *URA3* gene; KANX, kanamycin resistance cassette; 3'-UTR, untranslated region of *ERD2*).

Table S1. Yeast strains used in this study

<i>S. cerevisiae</i> strain	Genotype	Reference
<i>Δerd2</i> (YA12)	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pYSEC12]	1
SEY6210 <i>ERD2</i> [pERD2]	MAT α <i>ura3-52 leu2-3, 112 his3-Δ200 trp1-Δ901 lys2-801 suc2-Δ9</i> SEY6210 [pERD2] (pERD2 = pYSCE)	1 This study pYSCE: H.Pelham OpenBiosystems
BY4742 <i>Δend3</i> <i>cdc25-2</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 Δend3</i> MAT α <i>ura3 leu2 trp1 hisΔ200 ade2-101 cdc25-2</i>	2 OpenBiosystems OpenBiosystems
<i>KAR2</i> (RSY255)	MAT α <i>ura3-52 leu2-3, -112</i>	3
<i>kar2^{ts}</i> (RSY475)	MAT α <i>ura3-52 leu2-3, -112 kar2-159</i>	3
<i>end3</i> (RH266-1D)	MAT α <i>end3 ura3 leu2 his4 bar1-1</i>	4
YA <i>ERD2-ΔC</i>	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pRS315 <i>ERD2-ΔC</i>]; ΔC : deletion of the C-terminal 39 amino acids	This study
YA <i>ERD2</i>	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pRS315 <i>ERD2</i>]	This study
BY4742 <i>ERD2mRAS</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS316 <i>ERD2mRAS</i>]	This study
BY4742 <i>ICE2mRAS</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS316 <i>ICE2mRAS</i>]	This study
BY4742 <i>EMP47mRAS</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS316 <i>EMP47mRAS</i>]	This study
YA <i>ERD2.1</i>	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pRS315 <i>ERD2.1</i>] = mammalian KDELR1	This study
YA <i>ERD2.2</i>	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pRS315 <i>ERD2.2</i>] = mammalian KDELR2	This study
YA <i>ERD2.3</i>	MAT α <i>ade2 ade3 his3-Δ200 leu2-3, 112 ura3-52 TRP1 erd2-ΔNco</i> [pRS315 <i>ERD2.3</i>] = mammalian KDELR3	This study
BY4742 <i>ERD2yGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS316 <i>ERD2yGFP</i>]	This study
BY4742 <i>Can1-mCherry + ERD2yGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS315 <i>Can1-mCherry</i>] + [pRS316 <i>ERD2yGFP</i>]	This study
BY4742 <i>Pil1-mCherry + ERD2yGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS315 <i>Pil1-mCherry</i>] + [pRS316 <i>ERD2yGFP</i>]	This study
BY4742 <i>Sur7-mCherry + ERD2yGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS315 <i>Sur7-mCherry</i>] + [pRS316 <i>ERD2yGFP</i>]	This study
BY4742 <i>Anp1-mCherry + ERD2yGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> [pRS315 <i>Anp1-mCherry</i>] + [pRS316 <i>ERD2yGFP</i>]	This study
BY4742 <i>ERD2-3xyGFP</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 erd2::ERD2-3xyGFP-URA3</i>	This study
BY4742 <i>ERD2-3xFLAG</i>	MAT α <i>his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 erd2::ERD2-3xFlag-KANX</i>	This study

1. Hardwick, K. G., Boothroyd, J. C., Rudner, A. D. & Pelham, H. R. Genes that allow yeast cells to grow in the absence of the HDEL receptor. *Embo J* 11, 4187-95 (1992).
2. Broder, Y. C., Katz, S. & Aronheim, A. The ras recruitment system, a novel approach to the study of protein-protein interactions. *Curr Biol* 8, 1121-4 (1998).
3. Wuestehube, L. J. et al. New mutants of *Saccharomyces cerevisiae* affected in the transport of proteins from the endoplasmic reticulum to the Golgi complex. *Genetics* 142, 393-406 (1996).
4. Raths, S., Rohrer, J., Crausaz, F. & Riezman, H. *end3* and *end4*: two mutants defective in receptor-mediated and fluid-phase endocytosis in *Saccharomyces cerevisiae*. *J Cell Biol* 120, 55-65 (1993).

Table S2. Primers used in this study (restriction sites are shown in lower case letters)

Primer	5'-3' Sequence
3' ANP1	agtactGTTTCTATCAGGGTCAAGTCTAATGGAACCTC
3' CAN1	agtactTGCTACAACATTCCAAAAATTTGTCCAAAAAAG
3' PIL1	agtactAGCTGTTGTTTGTGGGGAAGAGACTC
3' SUR7	agtactAACAGAGACATCGTCCGGGCGCTCGTGTG
3' CYC TT	gagctcGCAGCTTGCAAATTAAGCCTTCGAG
3' ERD2GFP	GAGGAAAGGGTTTCAAACCTGCCAAAAGtcgacATGTCTAAAGGTGAAGAATTATTCACCTGGTGTG
3' GFP	gaattcTTACTTGTACAGCTCGTCCATGCCGAG
3' GFP ^{HDEL}	gaattcTTATAGCTCATCGTGCTTGTACAGCTCGTCCATGCCGAGAGAGAG
3' mCherry	ggatccgctgacTTACTTGTACAGCTCGTCCATGCCG
3' mRAS	ggatccTTACTTGCAGCTCATGCAGCCG
3' P GAL1	gaattcctcgagGGTTTTTCTCCTTGACGTAAAGTATAGAGGTATATTAACAATTTTTTGTGATACTTTTATTACATT TGAATAAGAAAG
3' ICE2	ggatccactagtACTACCAGAACCTATTAATTCTGTAGCGTATACC
3' ERD2	gtcgactctagaactagtagatctTTATTTTGGCAGTTTGAACCCCTTCTCTCT
3'ERD2.1 (human)	ggatccgctgacCTATGCCGGCAAACCTCAACTTCTTCC
3'ERD2.2 (human)	ggatccgctgacTTATGCTGGCAAACCTGAGCTTCTTCC
3'ERD2.3 (human)	ggatccgctgacTCAGATTGGCATTGGAAGACTTAACTTCTTTC
3' KAR2	gtcgacgcgccgcCTACAATTCGTCGTGTTTCAAATAATCACCATC
3' yEGFP	agatctgctgacTTATTTGTACAATTCATCCATACCATGGGTAATACC
5' CAN1	ctcgagATGACAAAATTCAAAAGAAGACGCCGAC
5' ANP1	ctcgagATGAAGTATAATAACAGAAAACCTCTCGTTCAACCCTAC
5' PIL1	ctcgagATGCACAGAACTTACTCTTTAAGAAATTCCAGG
5' SUR7	ctcgagATGGTTAAGGTCTGGAATATAGTACTACGTCTGGTAG
5' CYC TT	tctagagctgacggatccCATGTAATTAGT
5' ERD2GFP	GAGGAAAGGGTTTCAAACCTGCCAAAAGtcgacATGTC TAAAGGTGAAGAATTATTCACCTGGTGTG
5' GFP	catatgGTGAGCAAGGGCGAGGAGGTGTTC
5' mCherry	ctcgagctagaactagtATGGTGAGCAAGGGCGAGGAG
5' mRAS	actagtATGACGGAATATAAGCTGGTGGTGGTG
5' ICE2	ctcgaggaatccATGACCAGTTTGTCCAAAAGCTTCATG
5' P GAL1	gtcgacgcgccgcACGGATTAGAAGCCGCCGAGC
5' ERD2	ctcgaggaattcATGAATCCGTTTAGAATCTTAGGTGATTATCACAT
5'ERD2.1 (human)	gagctcgaattcATGAATCTTCCGATTCTGGGAGAC
5'ERD2.2 (human)	gagctcgaattcATGAACATTTTCCGGCTGACTGGG
5'ERD2.3 (human)	gagctcgaattcATGAACGTGTTCCGAATCCTCGG

Table S3. Antibodies used in this study

Antibody	Dilution	Source
anti-PMA1, rabbit	1 : 1,000	Ralf Kölling
anti-PDI, rabbit	1 : 10,000	Randy Schekman
anti-Pep12, mouse	1 : 200	Molecular Probes
anti-Vps10, mouse	1 : 500	Molecular Probes
anti-PGK, mouse	1 : 250	Molecular Probes
anti-Sec61, rabbit	1 : 5,000	Randy Schekman
anti-Rpn12, rabbit	1 : 2,000	Karin Römisch
anti-Rabbit-AP	1 : 3,000	Sigma
anti-Mouse-AP	1 : 3,000	Sigma
anti-Mouse-HRP	1 : 13,333	Sigma
anti-Rabbit-HRP	1 : 10,000	Sigma
anti-GFP, mouse	1 : 2,000	Roche
anti-V5, mouse	1 : 1,000	AbD SeroTec
anti-FLAG M2, mouse	1 : 1,000	Sigma

Appendix S1.

(a) ERD2_3xGFP-URA sequence (5'-3' direction) used for homologous recombination and chromosomal tagging of Erd2p with three C-terminal copies of yGFP.

```
GAATTCAGTCTGTCATTATATTTTGGCCATGGGATTATACAGAGCATTGTATATTCCTAACTGGATTGGAGGTACAGCACGGAAGATAAAAAATTGGACAAGATTGCCTTCTCGCGGGACTTTT
GCAAACTCTGTTGACTCTGATTTCTTTTACATTTACTACACTAAAGTCATCAGAGGAAAGGGTTTCAAACCTGCCAAAAGGAGCGGTTCTAAAGGTGAAGAATTATTCACTGGTGTGTCCCAA
TTTTGGTTGAATTAGATGGTGATGTTAATGGTCACAAATTTCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATGACCTTAAAAATTTATTTGACTACTGGTAAATGGCAGTT
CCATGGCCAACTTACTGACTACTTTCGGTTATGGTGTCAATGTTTTGGTAGATACCCAGATCATATGAAACAACATGACTTTTTCAAGTCTGCCATGCCAGAAAGTTATGTAAGTAAAGAACT
ATTTTTTCAAAGATGACGGTAACTACAAGCAGAGCTGAACTCAAGTTTGAAGGTGATACCTTAGTTAATAGAATCGAAATTAAGGTATTGTTTTAAAGAAAGATGGTAACTAAAGTAAAGTAA
CAAAATGGAATACAACATAAATCTCAACATTTACATCATGGCTGACAAAAGAAAGATGGTATCAAAAGTTACGACACAACATTGAAGATGGTTCTGTTCAATTTAGCTGACC
ATTATCAACAAAATACTCCAATTTGGTGGTGGCCAGTCTGTGTACGACAGAACCACTTACTTATCCACTCAATCTGCCTTATCCAAGATCCAACGAAAAGAGAGACCACATGGTCTGTGTAAGT
TTGTTACTGCTGCTGGTATTACCCATGGTATGGATGAATGTACAAATCTAAAGGTGAAGAATTTACTGCTGGTGTGCCAATTTTGGTGAATAGATGGTATGTTAATGGTCACAAATTT
TCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATGACCTTAAAAATTTATTTGACTACTGGTAAATGCCAGTTCCATGGCCAACCTTAGTCACTACTTTCGGTTATGGTGTCAA
TGTTTTGCTAGATACCCAGATCATATGAAACAACATGACTTTTTCAAGTCTGCCATGCCAGAAAGTTATGTTCAAGAAAGAACTATTTTTTCAAAGATGACGGTAACTACAAGACCAGAGCTGA
AGTCAAGTTGAAGGTGATACCTTAGTTAATAGAATCGAATTAAGGTATTGATTTTAAAGAAAGATGGTAACTAACAATTAACCTGACAAATTTGAAGTCAAAATTTGAAGTCAAAATTTGA
TGGCTGACAAACAAAAGAAATGGTATCAAAGTTAACTTCAAATTTAGACACAACATTTGAAGATGGTCTGTGTTCAATTTAGCTGACCATTATCAACAAAATACTCCAATTTGGTATGGTCAAGTCTTG
TTACAGACAACCACTTATCACTCAATCTGCCTTATCCAAGATCCAACGAAAAGAGAGACCACATGGTCTGTGTAAGATTTGTTACTGCTGCTGGTATTACCCATGGTATGGATGAATTTG
TACAAATCTAAAGGTGAAGAATTTACTGCTGGTGTGCCAATTTTGGTGAATAGATGGTGAATTTAAATGGTCACAAATTTCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAA
ATTGACCTTAAAAATTTATTTGACTACTGGTAAATTTGCCAGTTCCATGGCCAACTTACTGACTACTTTCGGTTATGGTGTCAATGTTTGTAGATACCCAGATCATATGAAACAACATGACTT
TTCAAGTCTGCCATGCCAGAAAGTTATGTTCAAGAAAGAACTATTTTTTCAAAGATGACGGTAACTACAAGACCAGAGCTGAAGTCAAGTTGAAGGTGATACCTTAGTTAATAGAATCGAAT
TAAAGGTATTGATTTTAAAGAAAGATGGTAACTTTAGGTCAAAATTTGAATACAACATTAACCTGACAAATTTGACATCATGGCTGACAAACAAAAGAAATGGTATCAAAGTTAACTTCAA
ATTAGACACAACATTTGAAGTGGTCTGTGTTCAATTTAGCTGACCATTATCAACAAAATACTCCAATTTGGTATGGTGTGCTGCTGTTTACGACACAACCACTTACTTCACTCAATCTGCCTTATCC
AAAGATCCAACGAAAAGAGAGACCACATGGTCTGTGTAAGATTTGTTACTGCTGCTGGTATTACCCATGGTATGGATGAATTTGACAAATAAGCGAAATTTCTTATGATTTATGATTTTATTA
TAAATTAAGTTATTAAGAAATTAAGTATGATCAAAATTTTAAAGTACTTAAAGTTTAAACGAAAATTTCTTATTTCTGAGTAACCTTCTGCTGAGTCAAGTTTCTGCTGAGTATGATG
AGTTCGCTCTTATTTGACCAACAGATGGAGGCCAGAAATACCCCTTGGACAGTCTGACAGTCTGACGCTGACGGGCAATGATGACTGCTGCGCCGATGATGACTGCTGCGCCGATGATG
ATCATTTGCTACATACATTTGATGGCCGACGCGCCGGAAGCAAAATTAACGGCTCTGCTGCTGAGAGCCTGCGAGCAGGGAAGCGCTCCCTCAGAGCCGCTGAAATTTGCCCAAGCGCCG
CTGTAGAGAAATATAAAGGTTAGGATTTGCCACTGAGGTTCTTCTTCAATATACTGCTTTTAAATCTTGGTATGATACAGTTCTCAGATCAGATCCGAAACATAAACAACATGTCGAAAGCTA
CATATAAGGAACGTGCTGCTACTCATCTAGTCTGTTGCTGCCAAGCTATTAATATCATGCAGAAAAGCAACAACCTTGTGTCTTCATTGGATGTTGCTACCAAGAAATTAAGGAGT
TAGTTGAAGCATTAGTCCCAAAATTTGTTTACTAAAACACATGTGGATATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATTAACCCGCAAGTACAATTTTTTACTCT
TCGAAGACAGAAAATTTGCTGACATTTGGTAAATACAGTCAAAATTTGCACTACTGCGGGTGTATACAGAAATGAGAGAATGGGACAGACATTAACAGATGACAGCGGTGTTGGGCCAGGATTTGTT
AGCGGTTTGAAGCAGGCGCGGAAGAAAGTAAACAAGGAACCTAGAGGCCCTTTGATGTTAGCAGAAATTTGATGCAAGGGCTCCCTAGTACTGGAAGAAATATAAGGATGACTGTTGACATTTGC
GAAGAGCGCAAAAGATTTGTTATCGGCTTTATTGCTCAAAGAGACATGGTGGAAAGAGATGAAGGTTACGATTTGTTGATTTAGACACCCGCTGTTGGGTTTATGACACCCGCTGTTGGGTTTATG
GTCAACAGTATAGAACCAGTGGTATGTTGCTCTACAGGATCTGACATTTATTTGTTGAAGAGGACTATTTGCAAGGGAAGGGATGCTAAGGTAGAGGGTGAACCTTACAGAAAAGCAGG
TGGGAAGCATTTGAAGATGGCCGAGCAAAAATCACTACTGACAATAAAAGATTTCTGTTTCAAGAAGTTCATTTGATATAGTTTTTATATTTGATTTGTTCTATTTTAAATCA
AATGTTAGCGTATTTATTTTTTTTTTTCGGCTCGACATCATCTGCCAGATGCGAAGTTAAGTGGCGGCAAGATAATATCATGCTGCTCAATCGTATGTGGAAATGCTGGTGGCTACTGAACCTGTT
TAAATAGTGTTCGACGCAATATAACAATTTCAATATATCAATGCTATACCAAAAGAAAATTAACATAAAATTTGATGTGATTTGGTCTATTTCTTTTTTATACTATGATATGTATGCAT
TAATCTCTTTTTAGCTCATAAAAATCTTCCTTACACCATCCTTGGTGAATAAAGGATTTCCAGCCGAATTC
```

(b) ERD2_3xFlag-KANX sequence (5'-3' direction) used for homologous recombination and chromosomal tagging of Erd2p with three C-terminal copies of a Flag-tag.

```
ACTGTTCAATATATTTTGGCCATGGGATTATACAGAGCATTGTATATTCCTAACTGGATTGGAGGTACAGCACGGAAGATAAAAAATTGGACAAGATTGCCTTCTCGCGGGACTTTTGGCAAC
TCTGTTGACTCTGATTTCTTTTACATTTACTACACTAAAGTCATCAGAGGAAAGGGTTTCAAACCTGCCAAAAGGAGCGGTTACTACAAGGATGACGATGACAAGGATTAAGAAGCAGTACG
ATAAAGATTAACAAGATGATGATGATAAGTAAGCGAAATTTCTTATGATTTTTATTTTAAATAAAGTTATAAAAAATAAGTTTATAACAAATTTTAAAGTGACTCTTAGTTTTTAA
ACGAAAAATCTTATTTCTGAGTAACTCTTCTCTGAGGTGAGTGTCTTCTCAGGTAATAGTATGAGGTCGCTTATTGACACACCGACATGGAGGCCAGAAATACCCCTCTTGCAGCTTCTGA
CGTGGCCAGCTCAGGGGATGATGTGACTGTGGCCGTACATTTAGCCCAACATCCCACTGATAAATCATTGTCATCATAACATTTGATGGCCGACGGGCGGAAGCAAAAATTAACGGCTCCTCG
CTGCAGACCTCGAGCAGGGAAGCGCTCCCTCAGAGCAGGTTGAATTTGCCCAAGCGCCGCTGTAGAGAAATATAAAGGTTAGGATTTGCCACTGAGGTTCTTCTTCAATATACTTCTCT
TTAAAAATCTTGTAGGATACAGTTCTCAGATCAGATCCGAACATAAACAACCTAGGTTAAGAAAAGACTCAGTTTCGAGGCGCGGATTAATTCACATGGATGCTGATTTATATGGGTATA
```

AATGGGCTCGCGATAATGTCGGGCAATCAGGTGCGACAATCTATCGATTGTATGGGAAGCCGATGCGCCAGAGTTGTTCTGAAACATGGCAAAGGTAGCGTTGCCAATGATGTTACAGATGAG
ATGGTCAGACTAAACTGGCTGACGGAATTTATGCCTCTCCGACCATCAAGCATTTTATCCGTACTCTGATGATGCATGGTTACTCACCCTGCGATCCCGGCAAAACAGCATTCCAGGTATTA
GAAGAATATCCTGATTGAGTGAATAATTTGTTGATGCGCTGGCAGTGTTCCTGCGCCGGTTCGATTGATTCCTGTTGTAATTTGTCCTTTAACAGCGATCGGGTATTTGCTCGCTCAGGCG
CAATCACGAATGAATAACGGTTGGTTGATGCGAGTGATTTGATGACGACGCTAATGGCTGGCTGTTGAACAAGTCTGGAAAGAAATGCATAAGCTTTTCCATTTCTCACCGGATTCAGTCGT
CACTCATGGTGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGGTTGTATTGATGTTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGCT
CGGTGAGTTTCTCCTTCATTACAGAAACGGCTTTTCAAAAAATATGGTATGATAATCTGATATGAATAAAATGCAAGTTTCATTGATGCTCGATGAGTTTCTAATCAGTACTGACAAATAA
AAAGATTCTTGTTCAGAACTTGTCAATTTGATAGTTTTTTATATTGATGTTTCTATTTTAAATCAAATGTTAGCGTGATTTATATTTTTTTTGGCCTGGACATCATCGCCAGATGCGAAA
GTTAAGTGGCAGAAAGTAATATCATGCGTCAATCGTATGTAATGCTGGTCGCTATACTGAACCTGTTTTAAATAGTGTTCGACAGCAATATACAAATTTCAATATATCAATGCTATACCCAA
AGAAAAAAAATACATAAAATTTGATGTTGATATGGTCTATTTCTTTTATACTATGATATGATGCAATTAATCTCTTTTAGCTCATAAAAATCTTTCTTACACCATCTTGGTGACAAATA
GGATTTCCAGCC

(c) EMP47 sequence used for the construction of EMP47-mRAS

CTCGAGATGATGATGTTAATTACTATGAAAAGTACAGTACTGTTGAGTGTTTTTACCGTCTTAGCGACATGGGCTGGATTGCTAGAAGCTCATCCATTGGGTGACACTTCAGATGCATCCAAATT
AAGCTCAGACTACTCGTCCCTGATCTCATTAAATGCACGTAAGTGGCCAAATAACTGGCAAATGGGAGAACAGCTAGTCTAGAGGAAGGAGAATTGATTGACTTCTAAGCAAAAATTCGAAGG
GTTCACTTTGGTTGAAGCAAGGATTCGATTTGAAGGATTCCTTTACTATGGATGGACATTTAGGAGTGTGGTTATTCTGGCCAAACCGACGGTGGCATAATCATTGGTTGGTTCAAGATTCT
AACGTACCACGGGATAAGCAGTTATACAATGGCCAGTGAACATGATGGTTTACAATTTAGTGGATAACAATGGTCCATTGGGCCAACACTTCGTGGTCAACTAAATGATGGTCAAAAAGCC
TGTAGATAAGACGAAAATCTATGATCAGAGTTTTGCATCTTGTGATGGTTATCAGGATTCCTCGTTCCTCCAGATCAGAGTAACTTATGATTTGGAAGACGACAACCTATTAAGTTTC
AGGTGGACAATAAAGTCTGTTCCAAACTAGGAAGTTTCGCTTCCCTCTGGGTCTACCGTATTGGTGTACCGCTCAAAAATGGGAGTGAATAATAATGCAAGTCTTTTGAATATTCAAA
ATGCAATTTTTAATGGCGTGATGAAGATTCCTTGATCCCTAATGTGAATGCAATGGGTGAGCCAAACTGATCACCAAAATACATTGACCAACAAACCGGCAAGAAAAATTTGATTGAAAAAC
AGCATTGACGCTGACAAAGCAAAAATACAAACTATGAATTTGATAAGAACTGGATAGAGTTGAAGTAAAATCTTTCGGAACGATATCAATGCTTTAGAAAACAAAGCTAAATGATGTCATT
AAGTCCAACAAGAGCTATTATCATTGACTACGATAAATAAACAGCTCTCTTCTAAGCCACCAGTAATAATGAAAAGGGAACGTCACCGATGATGCAATCGCTGAGGATAAAGAAAAATTT
CAAAGACTTCTTATCAATCAATCAGAAATGGGAAAGTCTGTTGAACAAGAAAAGTATAGGGAAGTACCAAACGTCATGGACAAGATGGTCTCAGGTTCGACGAAAATGCGCAGAAAACAA
TGATTTGGTTACTTCCATTAATTTCAATATGTTGGTTATGCATATTACACATTCAGAATCAGACAAGAGATCATAAAGACCAAACTGCTAACTAGT