Table S1. **Q/N-rich regions in proteins involved in RNA metabolism and function**

**A. Yeast proteins containing Q/N-rich regions with links to RNA metabolism and function**

| Function | Locus | Protein | Description | Source |
|---|---|---|---|---|
| RNA metabolism | YAL021C | CCR4 | Cytoplasmic mRNA deadenylase component | Michelitsch and Weissman, 2000 |
| | YNR052C | POP2 | Cytoplasmic mRNA deadenylase component | Michelitsch and Weissman, 2000 |
| | YCR093W | CDC39 | NOT1, component of cytoplasmic mRNA deadenylase | Michelitsch and Weissman, 2000 |
| | YDL160C | DHH1 | mRNA decapping activator/translation repressor | this paper |
| | YDR228C | PCF11 | mRNA 3′ end processing factor | Michelitsch and Weissman, 2000 |
| | YEL015W | EDC3 | mRNA decapping activator/P-body aggregation factor | This paper |
| | YERO68W | NOT4 | Cytoplasmic mRNA deadenylase component | This paper |
| | YER112W | LSM4 | mRNA decapping and splicing | Michelitsch and Weissman, 2000 |
| | YGL044C | RNA15 | mRNA 3′ end processing factor | Michelitsch and Weissman, 2000 |
| Nuclear export | YDL088C | ASM4 | Nup59, nuclear pore complex | Michelitsch and Weissman, 2000 |
| | YGL172W | NUP49 | Nuclear pore complex | Michelitsch and Weissman, 2000 |
| | YGR119C | NUP57 | Nuclear pore complex | Michelitsch and Weissman, 2000 |
| | YKL068W | NUP100 | Nuclear pore complex | Michelitsch and Weissman, 2000 |
| | YMR047C | NUP116 | Nuclear pore complex | Michelitsch and Weissman, 2000 |
| Translation | Q0140 | VAR1 | Mitochondrial small ribosomal protein | Michelitsch and Weissman, 2000 |
| | YDR172W | SUP35 | Translation termination factor | Michelitsch and Weissman, 2000 |
| | YGL049C | TIF4632 | Translation initiation factor | Michelitsch and Weissman, 2000 |
| RNA-binding | YBL051C | PIN4 | Contains RRM[1] | Michelitsch and Weissman, 2000 |
| | YBR212W | NGR1 | Contains RRM | Michelitsch and Weissman, 2000 |
| | YDL167C | NRP1 | Contains RRM and zinc finger domains, interacts with Pub1p | Michelitsch and Weissman, 2000 |
| | YDR515W | SLF1 | Contains La RNA binding domain | Michelitsch and Weissman, 2000 |
| | YJR091C | JSN1 | PUF1, contains pumilio/puf RNA binding domain | Michelitsch and Weissman, 2000 |
| | YPR042C | PUF2 | Contains pumilio/puf RNA binding domain | Michelitsch and Weissman, 2000 |
| | YLL013C | PUF3 | Contains pumilio/puf RNA binding domain | Michelitsch and Weissman, 2000 |
| | YGL014W | PUF4 | Contains pumilio/puf RNA binding domain | Michelitsch and Weissman, 2000 |
| | YGL178W | MPT5 | PUF5, contains pumilio/puf RNA binding domain | Michelitsch and Weissman, 2000 |
| | YGL122C | NAB2 | Contains zinc finger domain | Michelitsch and Weissman, 2000 |
| | YNL016W | PUB1 | Contains RRM | Michelitsch and Weissman, 2000 |
| | YPL190C | NAB3 | Contains RRM | Michelitsch and Weissman, 2000 |
| Interact with RNA-associated proteins | YBL029W | YBL029w | Interacts with CAF4 | Michelitsch and Weissman, 2000 |
| | YBL081W | YBL081W | Interacts with RPS28b and NRP1 | Michelitsch and Weissman, 2000 |

| | | | | |
|---|---|---|---|---|
| | YCL028W | RNQ1 | Interacts with CCR4 | Michelitsch and Weissman, 2000 |
| | YDR505C | PSP1 | Interacts with NAB2 | Michelitsch and Weissman, 2000 |
| | YEL007W | YEL007W | Interacts genetically with CCR4 and POP2 | Michelitsch and Weissman, 2000 |
| | YGL086W | MAD1 | Interacts with nuclear pore complex proteins | Michelitsch and Weissman, 2000 |
| | YGL181W | GTS1 | Interacts genetically with defects in mrna splicing | Michelitsch and Weissman, 2000 |
| | YHR082C | KSP1 | May modify DOM34, RNT1, and LSM7 | Michelitsch and Weissman, 2000 |
| | YJL141C | YAK1 | Interacts with DCS1, DCS2, POP2, KEM1, and CAF20 | Michelitsch and Weissman, 2000 |
| | YML017W | PSP2 | Interacts with eif4e and 4G, suppresses defects in Group II splicing | Michelitsch and Weissman, 2000 |
| | YMR124W | YMR124W | Interacts with CRM1 | Michelitsch and Weissman, 2000 |
| | YMR216C | SKY1 | SR protein kinase | Michelitsch and Weissman, 2000 |
| | YNL027W | CRZ1 | May be modified by SKY1 and HRR25 | Michelitsch and Weissman, 2000 |
| | YNL154C | YCK2 | May modify many RNA metabolism proteins | Michelitsch and Weissman, 2000 |
| | YNL161W | CBK1 | Interacts with NOT3 | Michelitsch and Weissman, 2000 |
| | YNL243W | SLA2 | Interacts with PRP45 and SUP35 | Michelitsch and Weissman, 2000 |
| | YOR290C | SNF2 | Interacts with PUB1, PAB1 and several ribosomal proteins | Michelitsch and Weissman, 2000 |
| | YOR329C | SCD5 | Interacts with CRM1 and NUP116 | Michelitsch and Weissman, 2000 |
| | YPL016W | SWI1 | Interacts with PUB1, LSM1, and several splicing factors | Michelitsch and Weissman, 2000 |
| | YPL204W | HRR25 | Interacts with DCP1, DCP2, EDC3, DED1, and several ribosomal proteins | Michelitsch and Weissman, 2000 |
| | YPL226W | NEW1 | Interacts with TEF1, TEF4, DBP8, and ribosomal proteins | Michelitsch and Weissman, 2000 |

**B. Location of conserved Q/N-rich regions in metazoan P-body proteins**

| **Protein** | **Species** | **Accession no.** | **Residue no.** | **Length** | **%Q/N** | **Source** |
|---|---|---|---|---|---|---|
| Dcp2 | *H. sapiens* | NP_689837.2 | 276–346 | 70 | 29 | This paper |
| | *B. taurus* | XP_001254141.1 | 426–498 | 73 | 23 | This paper |
| | *M. musculus* | XP_980768.1 | 361–433 | 72 | 28 | This paper |
| | *R. norvegicus* | XP_001055777.1 | 350–410 | 71 | 28 | This paper |
| | *X. laevis* | AAZ38887.1 | 277–345 | 74 | 30 | This paper |
| | *D. rerio* | NP_956446.1 | 272–335 | 64 | 20 | This paper |
| | *D. melanogaster* | NP_648805.2 | 616–764 | 149 | 31 | This paper |
| | *S. cerevisiae* | NP_014281.1 | 282–326 | 45 | 40 | This paper |
| Ge-1/Hedls | *H. sapiens* | AAH64567.1 | 1135–1274 | 140 | 16 | This paper |
| | *M. musculus* | BAE27236.1 | 1140–1179 | 140 | 16 | This paper |
| | *R. norvegicus* | NP_001028240.1 | 1141–1180 | 140 | 16 | This paper |
| | *G. gallus* | XP_414022.2 | 1153–1292 | 140 | 18 | This paper |
| | *D. rerio* | XP_694565.1 | 1102–1243 | 142 | 20 | This paper |
| | *X. laevis* | AAH44263.1 | 1125–1266 | 142 | 18 | This paper |
| | *D. melanogaster* | AAO42643.1 | 1106–1230 | 125 | 10 | This paper |
| GW182 | *H. sapiens* | NP_055309.2 | 1264–1553 | 290 | 25 | This paper |
| | *B. taurus* | XP_614640.3 | 1260–1549 | 290 | 25 | This paper |
| | *M. musculus* | NP_659174.3 | 1249–1488 | 240 | 26 | This paper |
| | *R. norvegicus* | XP_001079613.1 | 1228–1616 | 289 | 25 | This paper |
| | *G. gallus* | XP_414871.2 | 1208–1498 | 291 | 25 | This paper |
| | *D. rerio* | XP_700599.1 | 760–1125 | 366 | 22 | This paper |

| | | | | | | |
|---|---|---|---|---|---|---|
| | *D. melanogaster* | NP_001014692.1 | 628–901 | 274 | 30 | This paper |
| TNRC6B | *H. sapiens* | NP_055903.1 | 1117–1219 | 103 | 37 | This paper |
| | *B. taurus* | XP_001252364.1 | 1131–1238 | 108 | 41 | This paper |
| | *M. musculus* | NP_659061.2 | 1200–1307 | 108 | 41 | This paper |
| | *R. norvegicus* | XP_576311.2 | 1198–1315 | 117 | 45 | This paper |
| | *G. gallus* | XP_416246.2 | 1165–1265 | 102 | 36 | This paper |
| | *D. rerio* | XP_001345261.1 | 1267–1374 | 108 | 32 | This paper |

Michelitsch, M.D., and J.S. Weissman. 2000. A census of glutamine/asparagine-rich regions: implications for their conserved function and the prediction of novel prions. *Proc. Natl. Acad. Sci. USA.* 97:11910–11915.

[1]RRM, RNA recognition motif.

Table S2. **Yeast Strains used in this study**

| Strains | Genotype | Source |
|---|---|---|
| yRP1724 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG DHH1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP1726 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG DCP1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP1728 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG PAT1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP1729 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG LSM1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP1730 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG XRN1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP2162 | *MATa leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG Dcp2GFP(NEO)* | This paper |
| yRP2217 | *MATa leu2-3,112 trp1 ura3-52 his4-539 lys2-201 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO DHH1GFP(NEO)* | This paper |
| yRP2225 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO DCP1GFP(NEO)* | This paper |
| yRP2240 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO PAT1GFP(NEO)* | This paper |
| yRP2232 | *MATa leu2-3,112 trp1 ura3-52 his4-539 lys2-201 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO LSM1GFP(NEO)* | This paper |
| yRP2248 | *MATa leu2-3,112 trp1 ura3-52 lys2-201 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO XRN1GFP(NEO)* | This paper |
| yRP2164 | *MATa leu2-3.112 trp1 ura3-52 lys2-201 cup1::LEU2/PGK1pG/MFA2pG edc3::NEO Dcp2GFP(NEO)* | This paper |
| yRP1736 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 DHH1GFP(NEO)* | Sheth and Parker, 2003 |
| yRP1936 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 DCP2GFP(NEO)* | Brengues et al., 2005 |
| yRP2246 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 XRN1GFP(NEO)* | This paper |
| yRP2307 | *MATa leu2-3,112 trp1 ura3-52 lys2-201 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 edc3::NEO DHH1GFP(NEO)* | This paper |
| yRP2308 | *MATa leu2-3,112 trp1 ura3-52 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 edc3::NEO DCP2GFP (NEO)* | This paper |
| yRP2310 | *MATa leu2-3,112 trp1 ura3-52 lys2-201 cup1::LEU2/PGK1pG/MFA2pG dcp1::URA3 edc3::NEO XRN1GFP(NEO)* | This paper |
| yRP1738 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 DHH1GFP (NEO)* | Sheth and Parker, 2003 |
| yRP1923 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 DCP2GFP (NEO)* | Teixeira et al., 2005 |
| yRP2239 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 PAT1GFP (NEO)* | This paper |
| yRP2312 | *MATa leu2-3,112 trp1 ura3-52 his4-539 lys2-201 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 edc3::NEO DHH1GFP (NEO)* | This paper |
| yRP2314 | *MATa leu2-3,112 trp1 ura3-52 his4-539 lys2-201 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 edc3::NEO DCP2GFP (NEO)* | This paper |
| yRP2316 | *MATa leu2-3,112 trp1 ura3-52 his4-539 lys2-201 cup1::LEU2/PGK1pG/MFA2pG xrn1::URA3 edc3::NEO PAT1GFP (NEO)* | This paper |
| yRP2325 | *MATa leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG Dcp2GFP(NEO) petite* | This paper |
| yRP2327 | *MATa leu2-3.112 trp1 ura3-52 lys2-201 cup1::LEU2/PGK1pG/MFA2pG Dcp2GFP(NEO) edc3:: NEO petite* | This paper |
| yRP2333 | *MAT leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG Dhh1GFP(NEO) petite* | This paper |
| yRP2335 | *MATa leu2-3.112 trp1 ura3-52 his4-539 lys2 cup1::LEU2/PGK1pG/MFA2pG Dhh1GFP(NEO) edc3:: NEO petite* | This paper |
| yRP2093 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2] | This paper |
| yRP2362 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2EDC3] | This paper |
| yRP2361 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2DCP1] | This paper |

| | | |
|---|---|---|
| yRP2359 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2DCP2(1-300)] | This paper |
| yRP2360 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2DCP2(102-300] | This paper |
| yRP2363 | *MAT trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOBD-2DHH1(250-461)] | This paper |
| yRP2364 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOAD] | This paper |
| yRP2368 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOADEDC3] | This paper |
| yRP2369 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOADEDC3(1-231)] | This paper |
| yRP2370 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOADEDC3(1-85)] | This paper |
| yRP2371 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOADEDC3(86-231)] | This paper |
| yRP2372 | *MATa trp1-901 leu2-3,112 ura3-52 his3-200 gal4 gal80 LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ* [pOADEDC3(232-551)] | This paper |
| yRP2339 | *MATa leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG lsm4 C:: NEO Dcp2GFP(NEO)* | This paper |
| yRP2340 | *MAT leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG lsm4 C:: NEO edc3:: NEO Dcp2GFP(NEO)* | This paper |
| yRP840 | *MATa leu2-3,112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG* [pRP1193] [pRP1187] | Hatfield et al., 1996 |
| yRP2338 | *MATa leu2-3.112 trp1 ura3-52 his4-539 cup1::LEU2/PGK1pG/MFA2pG lsm4 C:: NEO edc3:: NEO* [pRP1193] [pRP1187] | This paper |
| yRP1516 | *MATa his4-539 leu2-3,112 lys2-201 trp1 ura3-52 cup1::LEU2/PGK1pG/MFA2pG dcp2-7::URA3* | Dunckley, 2001 |
| yRP1748 | *MATa his4-539 trp1 leu2-3,112 ura3-52 edc3::NEO dcp2-7::URA3 cup1::LEU2/PGK1pG/MFA2pG* | Kshirsagar and Parker, 2004 |
| yRP1502 | *MATa his4-539 trp1 leu2-3,112 ura3-52 lys2-201 dcp2-7::URA3 ski3::TRP1* | Dunckley and Parker, 1999 |
| yRP1750 | *MAT his4-539 leu2-3,112 ura3-52 lys2-201 edc3::NEO dcp2-7::URA3 ski3::TRP1* | Kshirsagar and Parker, 2004 |
| yRP2430 | *MATa leu2 trp1 ura3 lys2 his3 cup1::LEU2/PGK1pG/MFA2pG Dcp2GFP(NEO) edc3::NEO lsm4::NEO* [pRP1551] | This paper |


Brengues, M., Teixeira, D., and R. Parker. 2005. Movement of eukaryotic mRNAs between polysomes and cytoplasmic processing bodies. *Science*. 310:486–489.

Dunckley, T., and R. Parker. 1999. The DCP2 protein is required for mRNA decapping in *Saccharomyces cerevisiae* and contains a functional MutT motif. *EMBO J.* 18:5411–5422.

Dunckley, T., Tucker, M., and R. Parker. 2001. Two related proteins, Edc1p and Edc2p, stimulate mRNA decapping in *Saccharomyces cerevisiae*. *Genetics*. 157:27–37.

Hatfield, L., Beelman, C.A., Stevens, A., and R. Parker. 1996. Mutations in trans-acting factors affecting mRNA decapping in *Saccharomyces cerevisiae*. *Mol. Cell Biol.* 16:5830–5838.

Kshirsagar, M., and R. Parker. 2004. Identification of Edc3p as an enhancer of mRNA decapping in *Saccharomyces cerevisiae*. *Genetics*. 166:729–739.

Sheth, U., and R. Parker. 2003. Decapping and decay of messenger RNA occur in cytoplasmic processing bodies. *Science*. 300:753–755.

Teixeira, D., Sheth, U., Valencia-Sanchez, M.A., Brengues, M., and R. Parker. 2005. Processing bodies require RNA for assembly and contain nontranslating mRNAs. *RNA*. 11:371–382.

Table S3. **Plasmids and oligonucleotides used in this study**

| Number | Name/Sequence | Description | Reference |
|---|---|---|---|
| pRP1433 | FlagEdc3 | To express N-terminal Flag-tagged Edc3 in yeast from TRP1 CEN plasmid | This study |
| pRP1434 | Flag LsmEdc3 | To express N-terminal Flag-tagged Edc3 with amino acids 1–85 deleted in yeast from TRP1 CEN plasmid | This study |
| pRP1435 | Flag FDFEdc3 | To express N-terminal Flag-tagged Edc3 with amino acids 86–231 deleted in yeast from TRP1 CEN plasmid | This study |
| pRP1436 | Flag Yjef-NEdc3 | To express N-terminal Flag-tagged Edc3 with amino acids 232–551 deleted in yeast from TRP1 CEN plasmid | This study |
| | pRS200 | TRP1 CEN plasmid prs314 with bglii linkers inserted in Sma1 site | Sikorski and Hieter, 1989 |
| pRP1441 | HisLsm | To express N-terminal His-tagged Edc3 amino acids 1–85 in *E. Coli* | This study |
| pRP1442 | HisFDF | To express N-terminal His-tagged Edc3 amino acids 86–231 in *E. Coli* | This study |
| pRP1210 | FlagDcp2(1–300)His | Plasmid to express amino acids 1–300 of Dcp2, which is Flag-tagged at the N terminus and His-tagged at the C terminus in *E. Coli* | She et al., 2006 |
| pRP1211 | FlagDcp2(102–300)His | Plasmid to express amino acids 102–300 of Dcp2, which is Flag-tagged at the N terminus and His-tagged at the C terminus in *E. Coli* | She et al., 2006 |
| pRP1317 | GSTDhh1(46–461) | Plasmid to express amino acids 46–461 of Dhh1, which is Gst tagged at the N terminus in *E. Coli* | Gift from H. Song |
| pRP1438 | GSTDhh1(46–249) | Plasmid to express amino acids 46–249 of Dhh1, which is Gst tagged at the N terminus in *E. Coli* | This study |
| pRP1439 | GSTDhh1(250–461) | Plasmid to express amino acids 250–461 of Dhh1, which is Gst tagged at the N terminus in *E. Coli* | This study |
| | pOAD | Activation domain plasmid for two-hybrid interaction analysis | Cagney et al., 2000 |
| | pOBD-2 | Binding domain plasmid for two-hybrid interaction analysis | Cagney et al., 2000 |
| pRP1187 | U1A-GFP | To express GFP tagged U1A RNA binding protein in yeast | Brengues et al., 2005 |
| pRP1193 | MFA2P-U1A | To localize MFA2 mrna in yeast using U1A-GFP | Brengues et al., 2005 |
| pRP1551 | Lsm4RNQ1 | To express Lsm4 with Q/N domain replaced with RNQ1 prion domain | This study |
| oRP1321 | CCGCCGCATATGTCACAATTTGTTGGTTTCGG | To create prp1441 hisedc3lsm | This study |
| oRP1322 | CCGCCGCTCGAGTTAGCGATTTTGATTATAATCGTTTTG | To create prp1441 | This study |
| oRP1323 | CCGCCGCATATGGGTGAACATATTGATTGGCAAGATGATG | To create prp1442 hisedc3fdf | This study |
| oRP1324 | CCGCCGCTCGAGTTAATTTATGGATGGAGAGTTAGTTGCAGAGTG | To create prp1442 | This study |
| oRP1325 | GATTACAGGGACATAACAG | To sequence Edc3 | This study |
| oRP1326 | CCTATGGCTACACCAGTAC | To sequence Edc3 | This study |
| oRP1327 | GAAATAGTCATCGATGCC | To sequence Edc3 | This study |
| oRP1328 | CATCTGCATAAGCCTTATGAAATTAATTAAATGGAAGAATTGACTCTAAAGGG | To create prp1438 with a stop codon at position 249 in Dhh1p | This study |
| oRP1329 | CCCTTTAGAGTCAATTCTTCCATTTAATTAATTTCATAAGGCTTATGCAGATG | To create prp1438 | This study |
| oRP1330 | GCGCTGGGATCCATGGAAGAATTGACTCTAAAGGG | To create prp1439 with an N-terminal deletion of Dhh1 up to position 249 | This study |
| oRP1331 | CCGGGAGCTGCATGTGTCAGAGG | To create prp1439 | This study |
| oRP1332 | ATGATTACGCCAAGCTCGAAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCGCAC ACTTCGAAATGGCCTTCTTTG | To amplify nucleotides –403–1,987 of Edc3 locus to create prp1433-36 | This study |

| | | | |
|---|---|---|---|
| oRP1333 | GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTA TAGGGCGAATTGGGTACCGATC ACAATGACAGCACTATTCTGCC | To amplify nucleotides –403–1,987 of Edc3 locus to create prp1433-36 | This study |
| oRP1334 | CAGTAATTCGTAAAAGAAACCATAATGGACTACAAGG ACGACGATGACAAGATGTC ACAATTTGTTGGTTTCGGA | To insert a Flag tag at the N terminus of Edc3 to create prp1433 | This study |
| oRP1335 | TCCGAAACCAACAAATTGTGACATCTTGTCATCGTCGT CCTTGTAGTCCATTATGGTTTC TTTTACGAATTACTG | To insert a Flag tag at the N terminus of Edc3 to create prp1433 | This study |
| oRP1336 | ATGGACTACAAGGACGACGATGACAAGGGTGAACATA TTGATTGGCAAGATGATG | To delete amino acids 1–85 in Edc3 to create prp1434 | This study |
| oRP1337 | CATCATCTTGCCAATCAATATGTTCACCCTTGTCATCGT CGTCCTTGTAGTCCAT | To delete amino acids 1–85 in Edc3 to create prp1434 | This study |
| oRP1338 | GCAACAAAACGATTATAATCAAAATCGCGATAAAACG AAAGGTACAGTTATAAATG | To delete amino acids 86–231 in Edc3 to create prp1435 | This study |
| oRP1339 | CATTTATAACTGTACCTTTCGTTTTATCGCGATTTTGAT TATAATCGTTTTGTTGC | To delete amino acids 86–231 in Edc3 to create prp1435 | This study |
| oRP1340 | CACTCTGCAACTAACTCTCCATCCATAAATTAAACCAA GAATTACTTTAGCC | To delete amino acids 232–551 in Edc3 to create prp1436 | This study |
| oRP1341 | GGCTAAAGTAATTCTTGGTTTATTTATGGATGGAGAGT TAGTTGCAGAGTG | To delete amino acids 232–551 in Edc3 to create prp1436 | This study |
| oRP1342 | CTATCTATTCGATGATGAAGATACCCCACCAAACCCAA AAAAAGAGATCGAATTCCAGCT GACCACCATG | To clone two-hybrid plasmids by homologous recombination | This study |
| oRP1343 | CTTGCGGGGTTTTTCAGTATCTACGATTCATAGATCTCT GCAGGTCGACGGATCCCCGGG AATTGCCATG | To clone two-hybrid plasmids by homologous recombination | This study |
| oRP1344 | AATTCCAGCTGACCACCATGTCACTGCCGCTACGACAC G | To amplify Dcp2(1–300) for two-hybrid | This study |
| oRP1345 | AATTCCAGCTGACCACCATGAGTATACCGGTGAGGGGC GC | To amplify Dcp2(102–300) for two-hybrid | This study |
| oRP1346 | GATCCCCGGGAATTGCCATGTTACTCTTGGCTCGAGGG TACCTG | To amplify Dcp2(102–300) for two-hybrid | This study |
| oRP1347 | AATTCCAGCTGACCACCATGGAAGAATTGACTCTAAAG GG | To amplify Dhh1(250–461) for two-hybrid | This study |
| oRP1348 | GATCCCCGGGAATTGCCATGTTAATGATGTTGCTGCGG AGG | To amplify Dhh1(250–461) for two-hybrid | This study |
| oRP1349 | AATTCCAGCTGACCACCATGTCACAATTTGTTGGTTTCG G | To amplify Edc3 for two-hybrid | This study |
| oRP1350 | GATCCCCGGGAATTGCCATGTTACAAATCTAATAGCAG GGACCC | To amplify Edc3 for two-hybrid | This study |
| oRP1351 | AATTCCAGCTGACCACCATGACCGGAGCAGCAACTGC | To amplify Dcp1for two-hybrid | This study |
| oRP1352 | GATCCCCGGGAATTGCCATGTCAAGCAAAAGAATCTTT TGGCTC | To amplify Dcp1for two-hybrid | This study |
| oRP1353 | GATCCCCGGGAATTGCCATGTTAATTTATGGATGGAGA GTTAGTTGCAGAGTG | To amplify the lsmfdf region of Edc3 for two-hybrid | This study |
| oRP1354 | GATCCCCGGGAATTGCCATGTTAGCGATTTTGATTATA ATCGTTTTG | To amplify the Lsm region of Edc3 for two-hybrid | This study |
| oRP1355 | AATTCCAGCTGACCACCATGGGTGAACATATTGATTGG CAAGATGATG | To amplify the FDF region of Edc3 for two-hybrid | This study |
| oRP1356 | AATTCCAGCTGACCACCATGGATAAAACGAAAGGTAC AGTTATAAATG | To amplify the Yjef-N region of Edc3 for two-hybrid | This study |
| oRP1357 | GTTTATCAAATTGCAAGATAATATAATTGACAAGGTCA AGTGAGGGGCGCCACTTCTAAA | To delete the C terminus of Lsm4p in yeast | This study |
| oRP1358 | TATTTATATATGTACATAATTATTATAATACAAAATTTG TGAATTCGAGCTCGTTTAAAC | To delete the C terminus of Lsm4p in yeast | This study |
| oRP1359 | GCGCGCGTAATACGACTCACTATAGGGCGAATTGGGTA CCGGGCCCCCCCTCGAGCAGAGTAATTGCTTCGTTCGT TATCTACTTG | To amplify Lsm4 to insert into plasmids | This study |
| oRP1360 | GATTACGCCAAGCGCGCAATTAACCCTCACTAAAGGGA ACAAAAGCTGGAGCTCGCAATACGTTTACAAATCTCTC TGGTTGG | To amplify Lsm4 to insert into plasmids | This study |
| oRP1361 | CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTG ACAAGGTCAAGGGATCCTAAACAAATTTTGTATTATAA | To delete the C terminus of Lsm4 | This study |

| | | | |
|---|---|---|---|
| | TAATTATGTACATATATAAATATATTGG | | |
| oRP1362 | CCAATATATTTATATATGTACATAATTATTATAATACAA AATTTGTTTAGGATCCCTTGACCTTGTCAATTATATTAT CTTGCAATTTGATAAACTTGATAAAAG | To delete the C terminus of Lsm4 | This study |
| oRP1365 | CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTG ACAAGGTCAAGCAAGGTCAGGGACAAGGTCAAGG | To insert the prion domain of Rnq1p in Lsm4 C | This study |
| oRP1366 | CCAATATATTTATATATGTACATAATTATTATAATACAA AATTTGTTTAGTAGCGGTTCTGGTTGCCGTTATTG | To insert the prion domain of Rnq1p in Lsm4 C | This study |
| oRP140 | ATATTGATTAGATCAGGAATTCC | Probe for MFA2pG mrna | Caponigro and Parker, 1995 |
| oRP100 | GTCTAGCCGCGAGGAAGG | Probe for 7S RNA used as a Loading control | Caponigro et al., 1993 |


Brengues, M., D. Teixeira, and R. Parker. 2005. Movement of eukaryotic mRNAs between polysomes and cytoplasmic processing bodies. *Science*. 310:486–489.

Cagney, G., P. Uetz, and S. Fields. 2000. High-throughput screening for protein-protein interactions using two-hybrid assay. *Methods Enzymol.* 328:3–14.

Caponigro, G., and R. Parker. 1995. Multiple functions for the poly(A)-binding protein in mRNA decapping and deadenylation in yeast. *Genes Dev*. 9:2421–2432.

Caponigro, G., D. Muhlrad, and R. Parker. 1993. A small segment of the MAT alpha 1 transcript promotes mRNA decay in *Saccharomyces cerevisiae*: a stimulatory role for rare codons. *Mol. Cell Biol*. 13:5141–5148.

She, M., Decker, C.J., Chen, N., Tumati, S., Parker, R., and H. Song. 2006. Crystal structure and functional analysis of Dcp2p from *Schizosaccharomyces pombe*. *Nat. Struc. Mol. Biol.* 13:63–70.

Sikorski, R.S., and P. Hieter. 1989. A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. *Genetics*. 122:19–27.