Supplemental Figures



Figure S1. Immunoblot analyses of BEPs.

Ybr1960-a MSRVY <mark>IYPLTVFYFFAIEMSVFCYYNWE</mark> YRRNFPYLFRPIFPFLIVLIS
YdI118w MFESFVNEGTAFLLFAKDERIRFKHDKYKALPIDVRNAEGNVPLHSCRGLSISFKFFHNVAFLSCWILVFKRSKGCNATADVSPPKKPPIKCDE <mark>FLGLVACSVMYAASQIVYLLVVPAVLFAFLL</mark> V
YII134c-a MVVGSEFNNTAD <mark>VDVVAILLTLLNADYFVI</mark> KQRLVSACFTK <mark>RIKWYFIYAIALLSLFSSRNTV</mark> CAPY
YII006w-a MTQLSQSNVER <mark>VALVYISVYFFSCISLIVYFFTECLSVSI</mark> PKNRQHPIKIIYNNKCPS
Ymr151w MGSVPTVIPGIVHC <mark>WMIHCLIGPFLFAIIYWSIFI</mark> EGMFFPQKYLDCQSVINLLCGSNQQKRIFKEKLRIYQVHIQEKIGCSKFNTLLLIYQLGSRHKINRQINDLLCNLCSKNYM <u>IMLLYAEIIIYSSFSCVLSATIF</u> LRGFLL
Y01035c MRVYHH <mark>IYVYTYILSAVIYSQDLFPSWVV</mark> QLSTVKSDIIRPYL <mark>IHGNSFLFQILQVLITAPST</mark> RCKFSFQNSIPF <mark>IFLALLLSQDFHVFLGIELHAFF</mark> VS
Ypr126c MLARVAESVSCGLMGQVKTGLLLFDGSGFSDRLGVMR <mark>FYVWSSRIYVLVLVVQAQLIL</mark> DAHNGV <mark>LFLLLFF<u>L</u>HNFFLLPQLFQFLLSGCLIFLN</mark> DVYFNLMV
YdI187c MQVASILQVRP <mark>PFFPQIHFLLFFFCFFVS</mark> KSRVASQRGTHFLVRICFEPPLQGCRMGKLCRPHLNHLLYLCYTAYFSNISWLSVSKSTSRNRVHKYIPYKSTELRSVAN
YIr123c MIMQKRLLNRNSSVVKSRNCLARHQHESSISKLHVSLRLHRCLRPIVRFDFLHNAGSKVCSQNSCPSPQLHVGTM <mark>ALFHTVFILWPHFCGILWTV</mark> HEKLYNYLLSIEVY
Yhd21w-a MNRSFHFLIKY <mark>IYIHVLLVFYFHIKQQAIMPFFIFFF</mark> SSFDGLSFDLR <u>VVAFLAKH<mark>VFVGVCSPFFVVGFE</mark>GSSRVVV</u> TEWLSKLVLPPPPVSITQVFSLSRKRGEFSSGYILIINPYKSFLRSLLDFSIFNNTAKNKSSTFTLNLEDVSK
Ya1066w MLSLVKRSILHSIPITRHILPIQLILVKMNHVQIRNIK <u>LYHFISYGFMLTKLTVFLFNLFF</u> YRLR <u>ILCRLTLLILSLPVQIYI</u> KEIQTKMLEKHTASDTSCI
YgI149w MSINALLYVLSLAL <u>LIWTGSVVTLLLLLFFCLFLLFF<mark>SLHFFCFTREHVHYTLPPK</mark>CHSLKF<mark>QFDSIPSSSLSLSPFP</mark>FLFFPRLRAVAFASPTLSFFFPI</u>
Ygr035w-a MLLYL <mark>YILYIALKTVSHLFFCNPCFRNLSVGDMLN</mark> PRLSLSFFTNHLLCPEAPLIIRGKGSYSAVGNFFSRKK
Ylr406c-a MIQK <mark>PILLSSELFLYIRALLHSIHPYI</mark> RTSVHLYTKKITSYNFLGVPFK
Yni303w MTTLQIINQFVAFSLRQIIQQDSQAAIVQYANVIICTNIDALYN <u>PT<mark>IYIIVKLFTTTYSSMVFLMFC</mark>RGKLKSCHF</u> YSDRNPWFDTFYLKKTKSIYFGFGYIDDDECTYKMAKFK
Ypr039w MASFDYLFHPFVPCTICPDFPLYKSPAFPSSCLHHPRLLFNDKAFCP <mark>LFLVPFPASFTRWLTFLFHLVI</mark> YNNKMHHHTYAPHIHDLRAALDTTAPQKKCPKETLHRSDHQG
Y01058c MQYHSALYVYIYVTFTTIPYKEKPD <mark>IISICFSMLSFVFDFSVRI</mark> CSRTLESFSWSLISSSAFK <mark>VVSAFSLAGSCVLASRSSVGIIVSL<u>LLFNFSTCNFVLFLSAVLIDLFF</u>CTFLPTPT</mark> FLPTP <mark>FFMLHLPIFSLLNALELLYLII</mark> AGLHI
Yfi032w MRVVRQSGSALSRAKKSRKY <mark>TSYRVMNVVLNTLFSFVLAPY H</mark> YILEEISPQWTTRE <u>MNTEICFLAKFSFLLVFLFYLNF</u> QGFNSVSNITTSSSPTYDNNRHYGND
YKI183≎a MYSKILLYRSN <mark>VLFMNFFSVFVCTIGTLFLVFADVYVLÅ</mark> SAFFQSKKEKETKFKHLHYQKRSCFFLANIH
Ymi090w MLVFSFLFVVVSIN <u>LNALIFLCKKSWASYLFLYLYNF</u> FFCEDEYKLTKN <u>CVRVEAIAPFMMCLGSLGAI</u> LGKQRTANFL <u>LLSYNVINNPVVLVYYV</u> ENFSRINFIKHTTKEKSVIWTNERQLNPWICN
Yor183w MRLLHHGEYGTKLIGGKCSIDGKLGHPCPLSRRRKKHLREKEMGPQYVRMYGPKRKAIIRTGNPDDGINLPDTGRGTLTAATIWSRAYHSNYSYLVRPKVVTLSKHRE <mark>LMTTFLLYVLYVCIYISAFI</mark> K
Transmombrane Domain Production Mathed: Debuine TMHMM

Transmembrane Domain Prediction Method: Phobius TMHMM **Figure S2. ER BEPs amino acid sequences and predicted TMDs** (accompanies Figure 2 and 3).



Figure S3. Sequence analysis of BEP protein sequences using TMHMM reveals ER-localized BEPs have short and hydrophobic C-termini. (accompanies Figure 3).



Figure S4. ER BEP localization in cells lacking functional GET or SND pathways (accompanies Figure 4).



Figure S5. mNG stability is not dependent upon Doa10 or the proteasome, but N-terminally tagged mNG-Ybr196c-a stability remains dependent on both these factors (accompanies Figure 5).



Figure S6. ER BEPs are stabilized by loss of ER PQC factors Doa10 and/or Hrd1 (accompanies Figure 5).



Figure S7. ER BEPs increase in abundance when ER PQC factors are lost (accompanies Figure 6).



Figure S8. ER BEPs increase in abundance when ER PQC factors are lost (accompanies Figure 6).



Figure S9. Loss of Ubr1 does not improve ER localization or abundance of BEPs (accompanies Figure 6).



Figure S10. BEPs are stabilized by loss of vacuolar proteases (accompanies Figure 7).