

SUPPLEMENTARY FIGURES

FIGURE S1. The peptide sequence coverage for identified amyloid-forming proteins. Regions of the protein sequence that match identified peptides by tandem mass spectrometry are highlighted in gray. **A, B**, the peptide sequence coverages for *S. cerevisiae* Sup35 and Rnq1 prion proteins in a representative tryptically-digested protein sample prepared from strain 74D-694 [PSI+][RNQ+]. P.D. indicates their respective low-complexity prion domains. For the Rnq1 sequence, all possible tryptic cleavage sites are marked with arrows. **C**, the sequence coverage of HttQ74-GFP recovered from PC12 cells. **D**, sequence coverage of ubiquitin (recovered together with HttQ74-GFP from PC12 cells).

FIGURE S2. Mass Spectra for peptides of *S. cerevisiae* Sup35 and Rnq1 prion proteins in representative tryptically-digested protein samples prepared from strain 74D-694 [PSI+][RNQ+]. MS^E has been applied after 1D reverse phase (RP) liquid chromatography (LC) of the peptide mixture. **A**, MS spectrum of the precursor ions that matched to the identified Sup35 prion protein. RT - retention time for each precursor during RPLC; relative peptide

intensity is shown on the vertical (ordinate) axis. Standard peptides that matched Sup35 are shown in blue; peptides containing a miscleavage site are shown in red. Grey and magenta codify peptides of other proteins in the sample. **B**, MS-MS spectrum assigned to the peptide sequence of Sup35 (R)HINAPFMLPIAAK(M) with MH+(Da) 1422.7946. **C**, MS spectrum of the precursor ions that matched to the identified Rnq1 prion protein are shown in blue. Grey and magenta codify peptides of other proteins in the sample. **D**, MS-MS assigned to the peptide sequence of Rnq1 (K)LISEAESHFSQGNHAEAVAK(L) with MH+(Da) 2125.0317.

FIGURE S3. Gene ontology analysis of the identified proteins. A histogram indicating the biological processes that are assigned to the 15 yeast proteins identified in the SDS-resistant fractions in comparison with the whole yeast proteome. The analysis has been done utilizing the Panther database and tools (<http://www.pantherdb.org>). The analyzed group is significantly enriched in proteins involved in cell communication, cell cycle, system process, developmental process and homeostatic process (indicated by *)

Figure S1

A. Sup35

| | | | | | | |
|-----|-------------|------------|------------|------------|------------|--------|
| 1 | MSDSNQGNQ | QNYQOYSQNG | NQQQGNRYQ | CYQAYNAQAQ | PAGGYQNYQ | } P.D. |
| 51 | GYSGYQQGGY | QQYNPDAGYQ | QQYNPQQGYQ | QYNPQQGYQQ | QFNPDGGRGN | |
| 101 | YKRFYNNNL | QGYQAGFQFQ | SGMSLMDFQ | RQKQAAAPK | KTKLIVSSS | |
| 151 | SIHLANATKK | VGTPAESDK | KEEKSAAETK | EPDGFQCK | ESVQKEEKPV | |
| 201 | QTEENTEEKS | ELPKVEDLKI | SESTHNTNNA | NVTSADALIK | EQEEVDDEV | |
| 251 | VNDHFGGKDH | VSLIFMCHVD | AGKSTMGGHL | LYLTGSVDKR | TIEKYEREAK | |
| 301 | DAGRQGWYLS | VYMDTMKEER | MDGKTIEVGK | AYFETEARRV | TILDAPGHRM | |
| 351 | YVSENIIGGAS | QADVGVLVIS | ARKGEYETGP | ERGGQTRFHA | LLAHTQGVNK | |
| 401 | NVVVVNKKDD | PTVMSKERY | DQCVMVSNF | LRAICYNIKT | DVVFMFVSGY | |
| 451 | SGANLKHVD | PKECPMYTGP | TLELYLDTMN | HVDRHINAPF | MLPIAAKKK | |
| 501 | LGLIYEGEIE | SGHIKQGGT | ALMDDTAVE | IQNIYNETEN | EVDMAACGEQ | |
| 551 | VKLRKGVVEI | EDISPGFVLT | SPRNPIKSVT | KFVAQIAIVE | LKSIIAAGFS | |
| 601 | CVMHVTAIE | EVHIVKLLHR | LEKGTNRKSR | KPPAFARCKM | KVIAVLETEA | |
| 651 | PVCVETYQDY | PQLGRFTLRD | QGITLAIKRI | VKIAE | | |

B. Rnq1

| | | | | | | |
|-----|------------|------------|------------|------------|------------|--------|
| 1 | MDTKLISEA | ESHFSQGMHA | EAVAKLTSAA | QSNPNDQMS | TIESLIQKIA | } P.D. |
| 51 | GVVNDNRSGG | SDASQDFAG | GGSSFMTLM | ADSKSSQTO | LGLALLATV | |
| 101 | NTHSSMKGSS | NRGFDVGTVM | SMLSGSGGGS | QSMGASGLAA | LASQFFKSGM | |
| 151 | NSQGGQGGG | QGGQGGQGG | QGSFTALASL | ASSFMNSNN | NQQGNQSSG | |
| 201 | GSSFGALASH | ASSFMNSNN | QNSNSQQGY | NQSYQGNQN | SQGYNNQYQ | |
| 251 | GGNGGYQQQ | QSGGAFSSL | ASMAQSYLGG | QGTQSNQQY | NQQGNQQQ | |
| 301 | YQQQGNQYQH | QQQGQQQQG | HSSFSALAS | MASVYLGNS | NSNSYGGQQ | |
| 351 | QAMEYGRPQQ | NGQQQSMEYG | RPQYGGQNS | NGQHSFNFS | GMSQQNNNG | |
| 401 | NQNMV | | | | | |

C. HttQ74-GFP

| | | | | | | |
|-----|------------|------------|------------|------------|------------|----------|
| 1 | MKAFESLKSF | QQQQQQQQQ | QQQQQQQQQ | QQQQQQQQQ | QQQQQQQQQ | } poly Q |
| 51 | QQQQQQQQQ | QQQQQQQQQ | QQQQQQQQQ | QQQQPPPPP | PPPPPQLPQP | |
| 101 | PPQAQPLLQ | PQPPPPPPP | PPGPGVSKGE | ELFTGVVPII | VELDGDVNGH | |
| 151 | KFSVSGEGEG | DATYCKLTLK | FICTGKLPV | PWPTLVTTLT | YGVQCFSRYP | |
| 201 | DHMKQHDFFK | SAMPEGYVQE | RTIFFKDDGN | YKTRAEVKEE | GDTLVNRIEL | |
| 251 | KGIDFKEDGN | LLGHKLEYNY | NSHNVYIMAD | KQKNGIKVNF | KIRHNIEDGS | |
| 301 | VQLADHYQQN | TFIGDGPVLL | EDNHYLSTQS | ALSKDPNEKR | DHMVLEFVT | |
| 351 | AAGITLGMDE | LYK | | | | |

D. Polyubiquitin recovered with HttQ74-GFP

| | | | | | |
|----|-------------|------------|------------|-----------|------------|
| 1 | MQIFVKTLTG | KTITLEVEPS | DTIENVKAKI | QDKEGIPDQ | QRLIFAGKQL |
| 51 | EDGRFTLSDYN | IQKESTLHLV | LRLRGGQIF | VKTLTGKTI | LEVEPSDTIE |

Figure S2

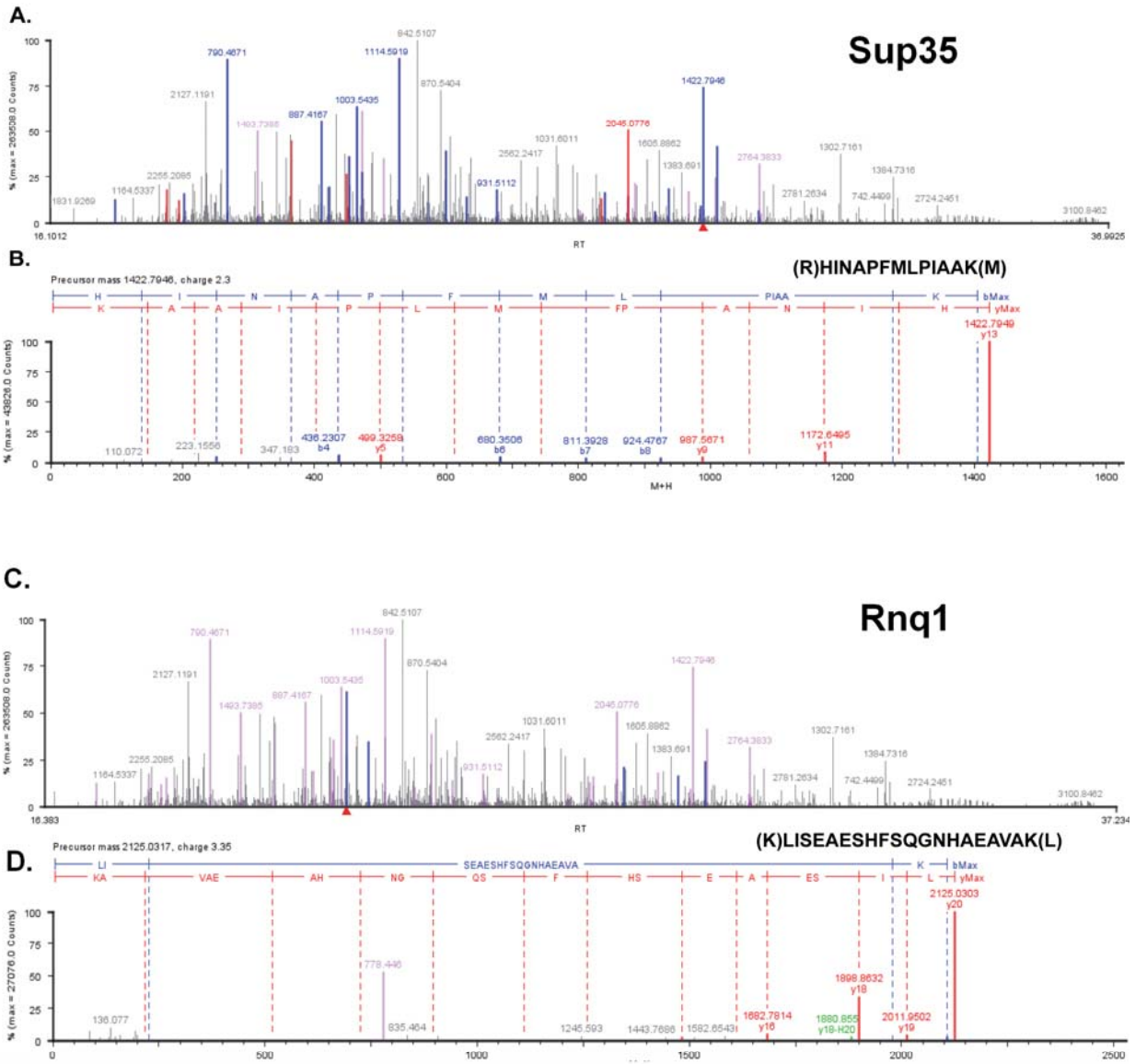


Figure S3

