



Nonsense mutations in yeast *SUP35* gene change the properties of the [PSI⁺] prion

Nina P. Trubitsina¹, Olga M. Zemlyanko^{1,2}, Stanislav A. Bondarev^{1,2} and Galina A. Zhouravleva^{1,2*}

¹Dept. of Genetics and Biotechnology and ²Laboratory of Amyloid Biology,
Saint Petersburg State University, St Petersburg, Russia

*Corresponding author.

Correspondence should be addressed to: Galina A. Zhouravleva, Department of Genetics and Biotechnology, St. Petersburg State University, Universitetskaya nab. 7/9, St. Petersburg 199034, Russia

e-mail

zhouravleva@rambler.ru

g.zhuravleva@spbu.ru

tel +7 9119384080

Supporting Information

Supporting Information tables – pp. 2-3

Supporting Information figures and legends – 4-10

Supporting information tables

Table S1. The characteristic of *SUP35* alleles used in this study

<i>SUP35</i> allele	Nucleotide position	Mutation	Amino acid position	Codon substitution	Size of the short fragment (aa)
<i>sup35-240</i>	166	C → T	56	Gln (CAA) → (TAA)	55
<i>sup35-74</i>	388	C → T	130	Gln (GAA) → (TAA)	129
<i>sup35-218</i>	541	G → T	181	Glu (GAA) → (TAA)	180
<i>sup35-21</i>	1264	C → T	422	Gln (CAA) → (TAA)	421

Table S2. Yeast strains used in the study

Strain	Genotype	Reference
7A-D832	<i>MATa ade1-14 his7-1 leu2-3,112 lys2-739 trp1-289 ura3-52 SUP35::TRP1 [pRSU2] [psi⁻] [PIN⁺]</i>	A. Borchsenius (unpublished data)
10-7A-D832	<i>MATa ade1-14 his7-1 leu2-3,112 lys2-739 trp1-289 ura3-52 SUP35::TRP1 [pRSU2] [PSI⁺] [PIN⁺]</i>	
a8-7A-D832	<i>MATa ade1-14 his7-1 leu2-3,112 lys2-739 trp1-289 ura3-52 SUP35::TRP1 [pRSU2] [psi⁻] [PIN⁺]</i>	
OT56	<i>MATa ade1-14 trp1-289 his3-200 leu2-3,112 ura3-52 [PSI⁺]^S [PIN⁺]</i>	[1,2]
OT55	<i>MATa ade1-14 trp1-289 his3-200 leu2-3,112 ura3-52 [PSI⁺]^W [PIN⁺]</i>	
1-OT56	<i>MATa ade1-14 trp1-289 his3-200 leu2-3,112 ura3-52 [psi⁻] [PIN⁺]</i>	[3]
2-OT56	<i>MATa ade1-14 trp1-289 his3-200 leu2-3,112 ura3-52 [psi⁻] [pin⁻]</i>	
D1691	<i>MATa/a ade1-14/ade1-14 his7-1/ his7-1 leu2-3,112/ leu2-3,112 lys2-739/lys2-739 trp1-289/trp1-289 ura3-52/ura3-52 SUP35::TRP1/SUP35::TRP1 [pRSU1] [pRSU2] [psi⁻] [PIN⁺]</i>	This work, mating: a8-7A-D832 [pRSU1] x 7A-D832 [pRSU2]
D1692	<i>MATa/a ade1-14/ade1-14 his7-1/ his7-1 leu2-3,112/ leu2-3,112 lys2-739/lys2-739 trp1-289/trp1-289 ura3-52/ura3-52 SUP35::TRP1/SUP35::TRP1 [pRSU1] [pRSU2] [PSI⁺] [PIN⁺]</i>	This work, mating: a8-7A-D832 [pRSU1] x 10-7A-D832 [pRSU2]

Table S3. Plasmids used in this study

Plasmids	Description	References
pRSU1 (pRS315-SUP35)	<i>CEN, LEU2, pSUP35-SUP35</i>	[4]
pRSU2 (pRS316-SUP35)	<i>CEN, URA3, pSUP35-SUP35</i>	
pRSU3 (pRS415-SUP35)	<i>LEU2, pSUP35-SUP35</i>	
pRSU1-21	<i>CEN, LEU2, pSUP35-sup35-21</i>	[5]
pRSU1-74	<i>CEN, LEU2, pSUP35-sup35-74</i>	
pRSU1-218	<i>CEN, LEU2, pSUP35-sup35-218</i>	
pRSU1-240	<i>CEN, LEU2, pSUP35-sup35-240</i>	
pRS315	<i>CEN, LEU2</i>	[6]
pRS316	<i>CEN, URA3</i>	
pRS316-pCUP-GFP	<i>CEN, URA3, pCUP1-sGFP</i>	[7] (original name of the plasmid is pRS316CG)
pRS316-pCUP-SUP35NM-GFP	<i>CEN, URA3, pCUP1-SUP35NM-sGFP</i>	[7] (original name of the plasmid is pmCUP-NM-GFP)
pRS316-pCUP-sup35-240-GFP	<i>CEN, URA3, pCUP1-sup35-240-sGFP</i>	This work

Table S4. Primers used in this study

Name	Sequence (5' - 3')
240_SacII-F	CCAAGGTTATTCTGGGTACCCGCGGGGTGGCTATCAACAGTAC
240_SacII-R	GTACTGTTGATAGCCACCCCGCGGGTACCCAGAATAACCTTGG
CFPstart-R	GTGCCCATTAACATCACCATC
Sup35 BamHI	AAGGATCCATGTCGGATTCAAACCAAGG
112	CTTGCTCACCACACATAGCCATATCAAC
113	GGAGGAGAAACCAGTCCAGACTGAAG
116	CATTGGCATTGTTGGTATTATGTGTTG
sup3	GAGCATTGATGTGACGGT
Q56Y-f*	CCAAAATTACCAAGGTTATTCTGGGTACT <u>ACCA</u> AGGTGGCTATCA ACAGTACAATCCCG
Q56Y-r	CGGGATTGTACTGTTGATAGCCACCTTGGT <u>AGT</u> ACCCAGAATAAC CTTGGTAATTTTGG
Q56K-f	CCAAAATTACCAAGGTTATTCTGGGTACA <u>AAG</u> CAAGGTGGCTATC AACAGTACAATCCCG
Q56K-r	CGGGATTGTACTGTTGATAGCCACCTT <u>GCTT</u> GTACCCAGAATAAC CTTGGTAATTTTGG

* nucleotide substitutions are underlined

Supporting Information figures

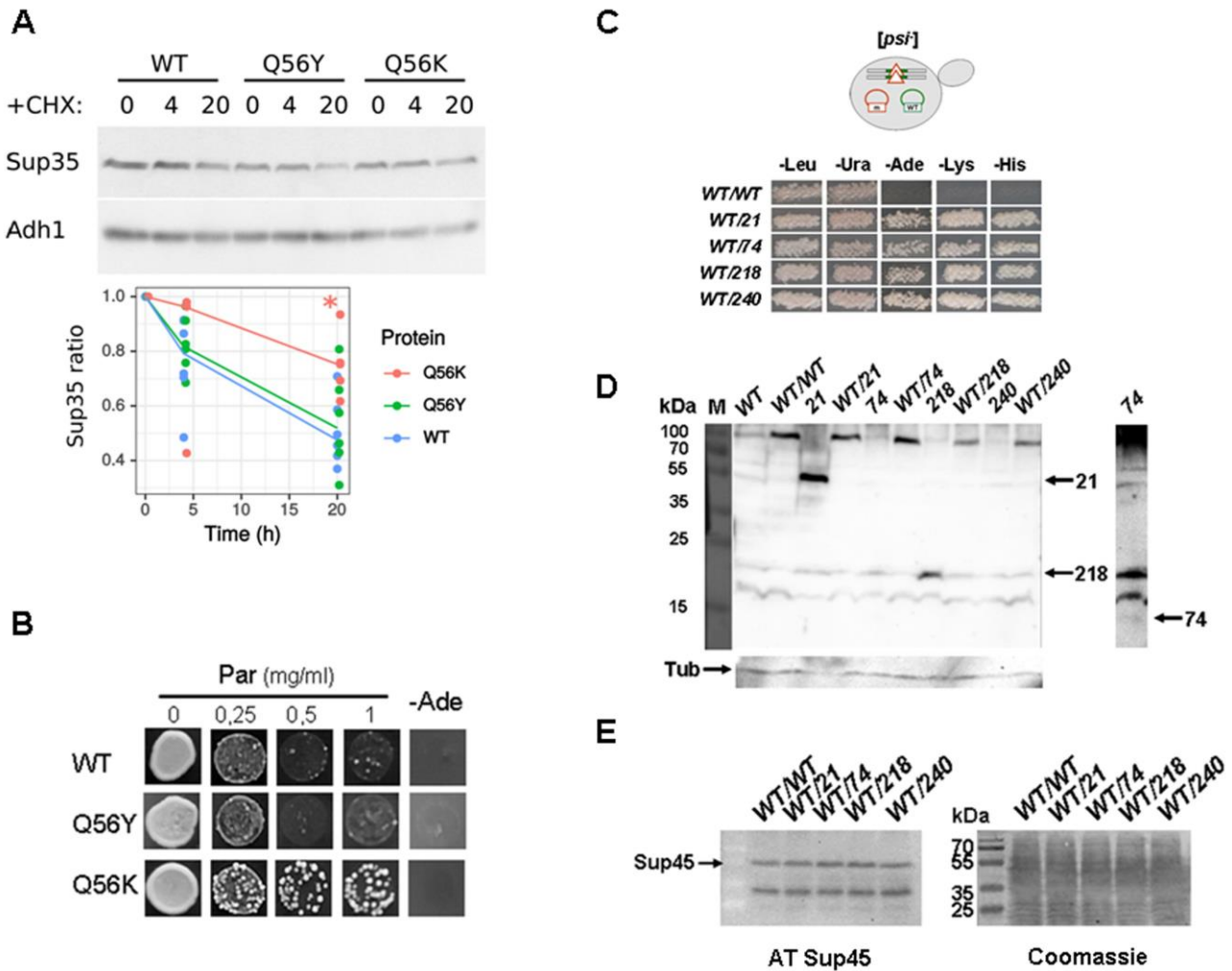


Figure S1. (A) Steady-state level of Sup35 in yeast cells containing wild-type copy of Sup35 or missense mutations. Sup35 was estimated in 7A-D832 strain bearing pRSU1 plasmid with either wild-type *SUP35* (WT) or one of the mutant *sup35-240Tyr* (Q56Y) or *sup35-240Lys* (Q56K) alleles after incubation in YPD medium containing 100 $\mu\text{g mL}^{-1}$ cycloheximide (CHX) during 0, 4 or 20 hours. The amount of Sup35 in each probe at point 0 was taken as 1.0 and the relative Sup35 amount in other points was calculated. (B) Growth of the same transformants as at (A) was assessed on the YPD medium containing different concentrations of paromomycin (Par) after 5 days of incubation at 30 °C. Drops of yeast suspension of the same density were used. Three independent transformants with each plasmid were tested, and representative results are shown. (C) The dominant character of *sup35-n* mutations in [*psi*] diploids containing two plasmids, one with a wild-type *SUP35* and the other with *sup35-n* mutation. Four independent transformants were tested in each case, representative results are shown after 4 days of incubation at 30 °C. Symbols on the left side show combinations of wild-type (WT) with *sup35-n* mutations. (D) Lysates of the [*psi*] diploid strains containing one or two plasmids (as indicated by the numbers above the lanes) were analyzed by Western blotting with anti-Sup35 antibodies. M - protein molecular weight marker. Fragments corresponding to the truncated Sup35 are marked by the arrows. Tubulin (Tub) was used as a loading control. An individual lane for *sup35-74* using different contrast to increase intensity of the band corresponding to the short Sup35-74 fragment is shown (taken from the same gel shown at the left). (E) Diploid [*psi*] transformants (the same as at (C)) were tested by Western blotting. Coomassie staining of the same membrane was used as a loading control.

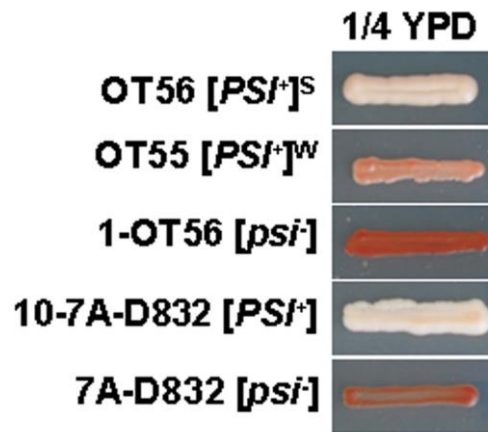


Figure S2. Strain 10-7A-D832 contains a “strong” variant of $[PSI^+]$. Growth of isogenic strains OT56 or OT55 carrying “strong” ($[PSI^+]^S$) and “weak” ($[PSI^+]^W$) variants respectively and strains used in this work on 1/4 YPD medium after 4 days of incubation at 30 °C.

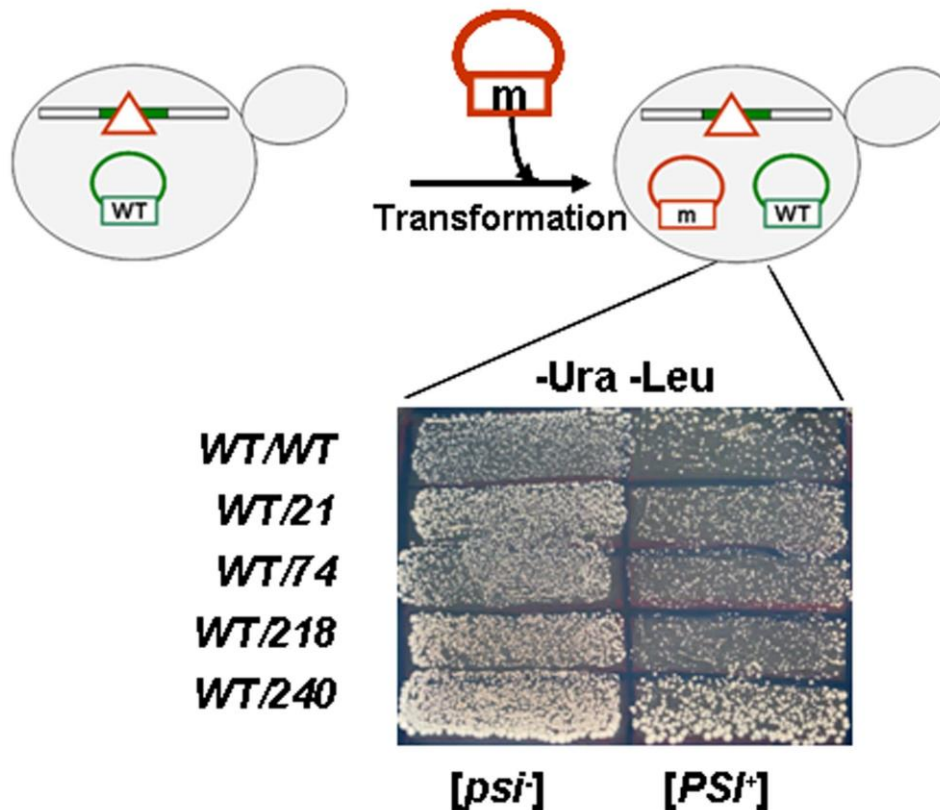


Figure S3. Some *sup35-n* mutations inhibit the growth of corresponding transformants of $[PSI^+]$ strain after transformation. Strains 7A-D832 $[psi^-]$ and 10-7A-D832 $[PSI^+]$ bearing plasmid with wild-type *SUP35* were transformed with *sup35-n* mutant plasmids. Equal amounts of DNA and cells were taken for transformation in each case. After a standard transformation procedure, an equal amount of cells after transformation was plated on media selective for both plasmids. The growth of transformants is shown after 7 days of incubation at 25 °C.

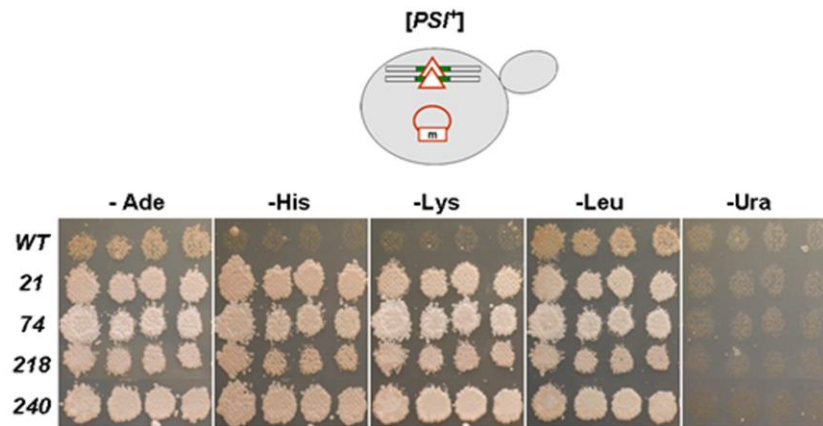
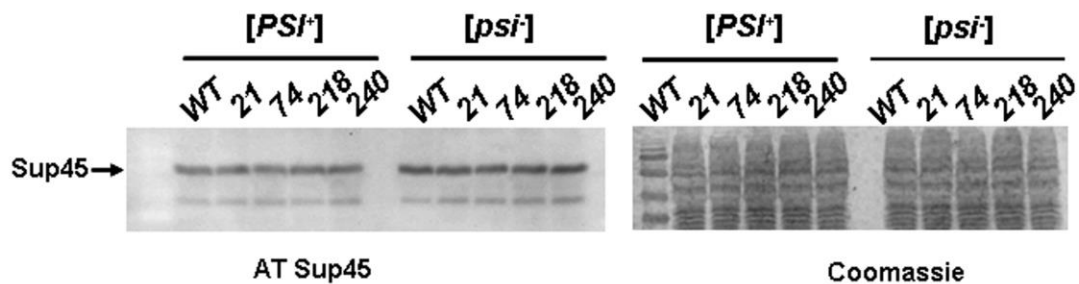
A**B**

Figure S4. (A) Diploid cells bearing *sup35-n* mutations after loss of *SUP35* plasmid are able to grow on selective media for suppression. Yeast cells selected in [PSI⁺] background, as shown in Figure 5B, were plated on selective media to test nonsense suppression, as well on media lacking leucine (-Leu) or uracil (-Ura) to confirm the presence of [*sup35-n LEU2*] and the absence of [*SUP35 URA3*] plasmid, respectively. Four independent clones in each case are shown after 5 days of incubation at 30 °C. (B) Diploid [PSI⁺] and [*psi*⁻] strains containing one plasmid have the same Sup45 amount. The same transformants as at (A) were tested by Western blotting. Coomassie staining of the same membrane was used as a loading control.

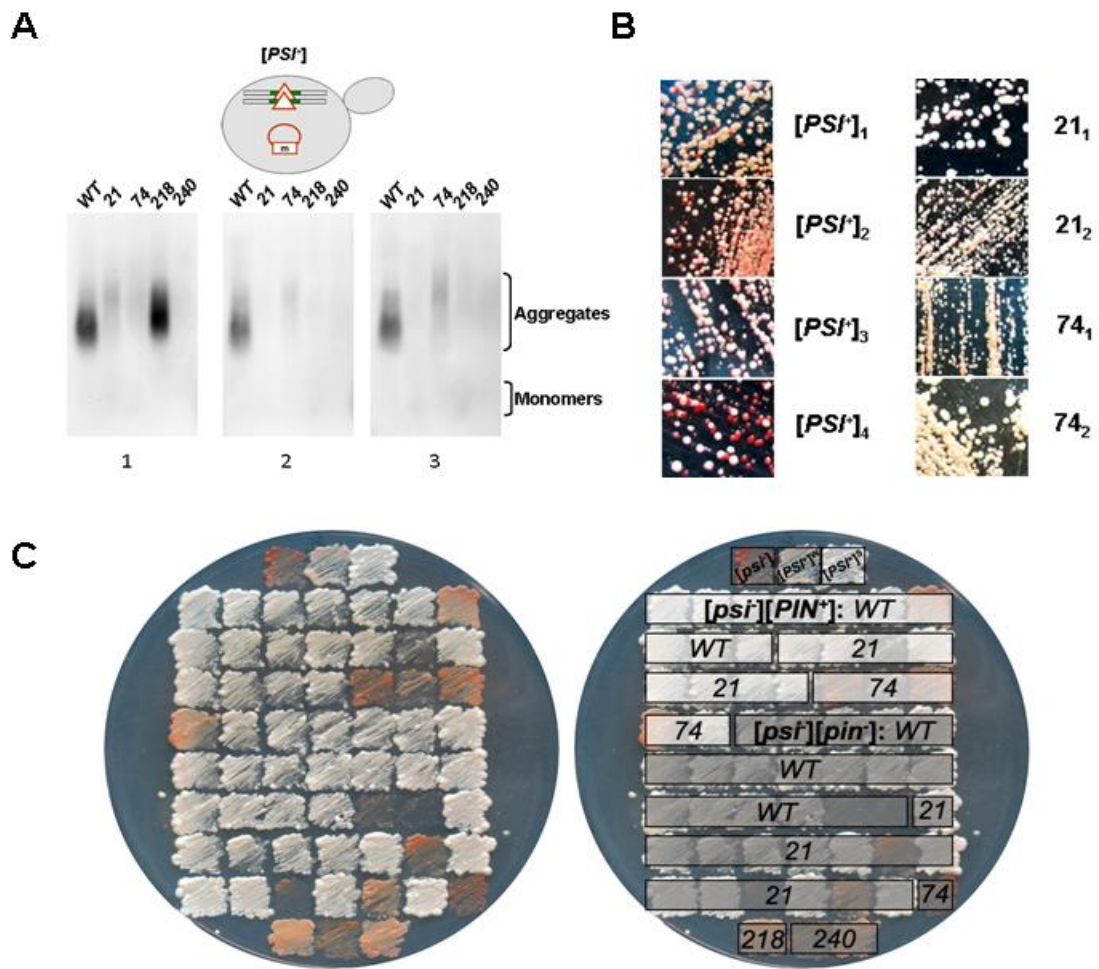
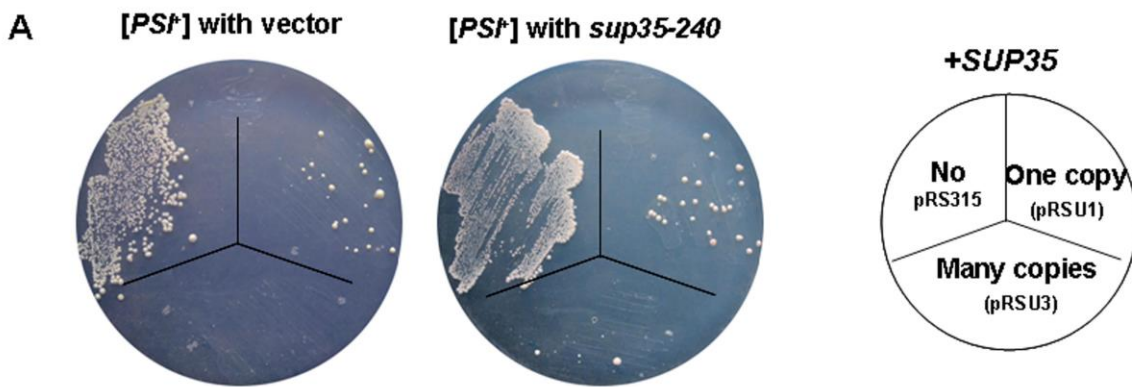


Figure S5. (A) $[PSI^+]$ aggregates change their properties in the presence of *sup35-n* mutations in diploid strains. Cells selected as shown in Figure 5B were used for preparation of lysates followed by SDD-AGE. Three independent sets (1-3) of clones were analyzed. (B) The phenotype of subclones of strains presented in Figure 5E. Cells were grown on 1/4 YPD. (C) The phenotype of cells selected after the protein transformation on 1/4 YPD. Infectivity of whole cell lysates of diploid strains D1692 $[PSI^+]$ bearing *SUP35* or *sup35-n* mutant plasmid (selected as shown in the Figure 5B) was determined by transformation into 1-OT56 $[psi^-]$ $[PIN^+]$ (white squares in the left panel), or 2-OT56 $[psi^-]$ $[pin^-]$ (grey squares in the left panel). On the top of the panel non-transformed $[psi^-]$ (1-OT56), weak (OT55) and strong (OT56) $[PSI^+]$ strains are shown.

I



B

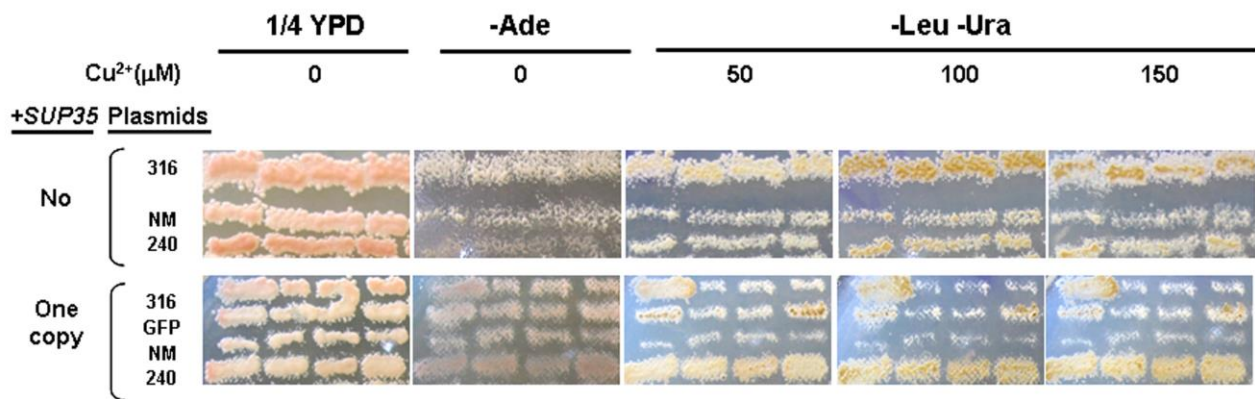


Figure S6. Sup35-240p rescues toxicity associated with the [PSI⁺] prion. **(A)** OT56 ([PSI⁺]) strain transformed with vector pRS316 or with pRS316-pCUP-sup35-240-GFP was re-transformed with pRS315 (control), pRSU1 (one copy of *SUP35*) or pRSU3 (multicopy plasmid containing *SUP35*). Transformants were selected on SC- Leu - Ura. In the case of combination of pRS316 with pRSU3 no transformants were selected, however in the presence of Sup35-240 ten transformants were recovered. **(B)** OT56 ([PSI⁺]) strain was transformed with following plasmids: pRS315 (-*SUP35*); pRSU1 (↑ *SUP35*) or pRSU3 (↑↑ *SUP35*). These plasmids were combined either with vector pRS316 (316), or pRS316-pCUP-GFP (GFP), or pRS316-pCUP-NM-GFP (NM), or pRS316-pCUP-sup35-240-GFP (240). Transformants were grown during 6 days at 30 °C. At the presence of an additional copy of *SUP35* effect of prion toxicity can be seen in all cases except one where pCUP-sup35-240-GFP plasmid was present.

References

1. Derkatch, I.L.; Bradley, M.E.; Zhou, P.; Chernoff, Y.O.; Liebman, S.W. Genetic and environmental factors affecting the *de novo* appearance of the [PSI⁺] prion in *Saccharomyces cerevisiae*. *Genetics* **1997**, *147*, 507–519.
2. Newnam, G.P.; Wegrzyn, R.D.; Lindquist, S.L.; Chernoff, Y.O. Antagonistic interactions between yeast chaperones Hsp104 and Hsp70 in prion curing. *Mol. Cell. Biol.* **1999**, *19*, 1325–1333.
3. Matveenko, A.G.; Drozdova, P.B.; Belousov, M.V.; Moskalenko, S.E.; Bondarev, S.A.; Barbitoff, Y.A.; Nizhnikov, A.A.; Zhouravleva, G.A. SFP1-mediated prion-dependent lethality is caused by increased Sup35 aggregation and alleviated by Sis1. *Genes to Cells* **2016**, *21*, 1290–1308.
4. Volkov, K.V.; Aksenova, A.Y.; Soom, M.J.; Osipov, K.V.; Svitin, A.V.; Kurischko, C.; Shkundina, I.S.; Ter-Avanesyan, M.D.; Inge-Vechtomov, S.G.; Mironova, L.N. Novel non-Mendelian determinant involved in the control of translation accuracy in *Saccharomyces cerevisiae*. *Genetics* **2002**, *160*, 25–36.
5. Chabelskaya, S.; Kiktev, D.; Inge-Vechtomov, S.; Philippe, M.; Zhouravleva, G. Nonsense mutations in the essential gene *SUP35* of *Saccharomyces cerevisiae* are non-lethal. *Mol. Genet. Genomics* **2004**, *272*, 297–307.
6. Sikorski, R.S.; Hieter, P. A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. *Genetics* **1989**, *122*, 19–27.
7. Serio, T.R.; Cashikar, A.G.; Moslehi, J.J.; Kowal, A.S.; Lindquist, S.L. Yeast prion [Ψ⁺] and its determinant, Sup35p. *Methods Enzymol.* **1999**, *309*, 649–673.