Table S1. *S. cerevisiae* strains used in this study

Strain	Genotype	Source
[*pin*$^-$] (74-D694)	*MATa, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200,* [*psi*$^-$][*pin*$^-$]	(1)
[*pin*$^-$] alpha	*MATα, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200,* [*psi*$^-$][*pin*$^-$]	This study
[*PIN*$^+$]^{low} (L1943)	*MATa, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200,* [*psi*$^-$][*PIN*$^+$]^{low}	(2)
[*PIN*$^+$]^{low} deletions	*MATa, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200* [*psi*$^-$] *deleted gene*::*HIS3*	This study
[*PIN*$^+$]^{medium} (L1945)	*MATa, ade1-14UGA, ura3-52 leu2-3,112, trp1-289, his3-200* [*psi*$^-$][*PIN*$^+$]^{medium}	(2)
[*PIN*$^+$]^{medium} deletions	*MATa, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200* [*psi*$^-$] *deleted gene*::*HIS3*	This study
[*PIN*$^+$]^{high} (L1749)	*MATa, ade1-14UGA, ura3-52 leu2-3,112, trp1-289, his3-200* [*psi*$^-$][*PIN*$^+$]^{high}	(2)
[*PIN*$^+$]^{high} deletions	*MATa, ade1-14UGA, ura3-52, leu2-3,112, trp1-289, his3-200* [*psi*$^-$] *deleted gene*::*HIS3*	This study
HF7c	*MATa his3-200 leu2-3 trp1-901 ura3-52 LYS::GAL1UAS-GAL1TATA-HIS3*	Clontech

SUPPLEMENTAL REFERENCES

1. Derkatch, I. L., Chernoff, Y. O., Kushnirov, V. V., Inge-Vechtomov, S. G., and Liebman, S. W. (1996) Genesis and variability of [*PSI*] prion factors in *Saccharomyces cerevisiae*. *Genetics* **144,** 1375–1386
2. Bradley, M. E., Edskes, H. K., Hong, J. Y., Wickner, R. B., and Liebman, S. W. (2002) Interactions among prions and prion "strains" in yeast. *Proc. Natl. Acad. Sci. U.S.A.* **99,** 16392–16399

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Confirmation of [*PSI*$^+$] induction in haploid deletion strains. Putative [*PSI*$^+$] colonies (Figure 1) were streaked onto YEPD medium containing 3 mM Guanidine HCl and then restreaked onto CSM and CSM-ADE media to confirm effective prion curing. The presence of red pigment on CSM medium and the lack of growth on CSM-ADE medium suggest that [*PSI*$^+$] was effectively cured, thereby signifying that the growth of induced colonies on CSM-ADE medium observed in Figure 1 was prion-related and suggesting that they were [*PSI*$^+$].

Figure S2. Maintenance of chaperone gene deletion-induced changes in [*PIN*$^+$] variant-dependent phenotypes. Chaperone deletion strains were mated with a wild-type [*psi*$^-$][*pin*$^-$] strain, and the resulting diploids were analyzed for [*PSI*$^+$] induction efficiency (*A*) and frequency of multiple Rnq1-GFP foci in foci-containing cells (*B*). Error bars represent SEMs. Student's *t*-tests were done to compare quantification in deletion strains versus their parental wild-type strain. *P< 0.05, **P< 0.01, ***P< 0.001.

Figure S3. Confirmation of [*PSI*$^+$] induction in haploid progeny. Putative [*PSI*$^+$] colonies from wild-type (+) and mutant (-) haploid progeny (Figure 4) were streaked onto YEPD medium containing 3 mM Guanidine HCl and then restreaked onto CSM and CSM-ADE media to confirm effective prion curing. The presence of red pigment on CSM medium and the lack of growth on CSM-ADE medium suggest that [*PSI*$^+$] was effectively cured, thereby signifying that the growth of induced colonies on CSM-ADE medium observed in Figure 3 was prion-related and suggesting that they were [*PSI*$^+$].

Figure S4. Dominance of chaperone gene deletion-induced variants. Diploids were generated by mating chaperone deletion stains with a wild-type [*psi*$^-$] strains carrying the [*PIN*$^+$]^{low} or [*PIN*$^+$]^{medium} or [*PIN*$^+$]^{high} variant. These diploids were analyzed for [*PSI*$^+$] induction efficiency (*A*) and frequency of multiple Rnq1-GFP foci in foci-containing cells (*B*). Error bars represent SEMs. Student's *t*-tests were done to compare quantification in deletion strains versus their parental wild-type strain. *P< 0.05, **P< 0.01, ***P< 0.001.

Figure S5. Characterization of the [*PIN*$^+$] state of the yeast two-hybrid strain, HF7c. *A*, Rnq1-GFP localizes in a diffuse manner without visible puncta in the HF7c strain. *B*, SDD-AGE of HA-Rnq1p purified from [*pin*$^-$], [*PIN*$^+$]^{low}, [*PIN*$^+$]^{medium}, [*PIN*$^+$]^{high} and HF7c strains. HA-Rnq1p isolated from the HF7c strain migrates similarly to HA-Rnq1p isolated from the [*pin*$^-$] strain.