



Suppl. Figure 3: Simulations of Sup35p PD evolution using a simple mutational model. The amino-acid sequence identity distribution for BLAST (Atschul, et al,1997) comparisons of orthologs of *S. cerevisiae* proteins in *N. crassa* (the closest non-*Hemiascomycote* evolutionarily) was derived. This distribution was used to simulate the expected divergences for the Sup35p PD domain for 2000 trials. For each trial: (a) the nucleotide sequence was mutated with a Jukes-Cantor model, until a specific amino-acid sequence identity picked randomly from the ortholog sequence identity distribution was reached; (b) the number of Q+N residues was tallied. The number of Q+N residues is histogrammed here for the 2000 trials. The actual number of Q+N residues in *S. cerevisiae* and *N. crassa* Sup35 PD are labelled with an arrow. (The smallest number of Q+N residues in the *N. crassa* PD for a window the length of the *S. cerevisiae* domain was used.)