*A stretch of 1,000 base pairs consisting of 800 bps upstream and 200 bps downstream of the transcriptional start site of the selected prion or ZIP genes was retrieved from Ensembl. The genes were then grouped pairwise and their respective promoter sequences were submitted to the Transcription Regulatory Element Search (TRES) online program (National Chemical Laboratory, Pune, India, release 2008) [Katti, M.V., et al., TRES: comparative promoter sequence analysis. *Bioinformatics*, 2000. 16(8): p. 739-40]. Transcription binding sites were searched using the TRANSFAC weight matrices and default mismatch parameters. Recorder promoter positions were exported to a text file and mapped onto a 1,000-pixel grid using an inhouse designed Java mini-program. Shared motifs were required to be within 250 bps of each other in pairwise comparisons of promoter sequences to be included. We have since become aware that the TRES program is no longer accessible on the internet and that the TRANSFAC data library has been amalgamated into a BIOBASE Knowledge Library (BKL) database (BIOBASE, Wolfenbüttel, Germany) which can now be searched with BIOBASE's Match program.