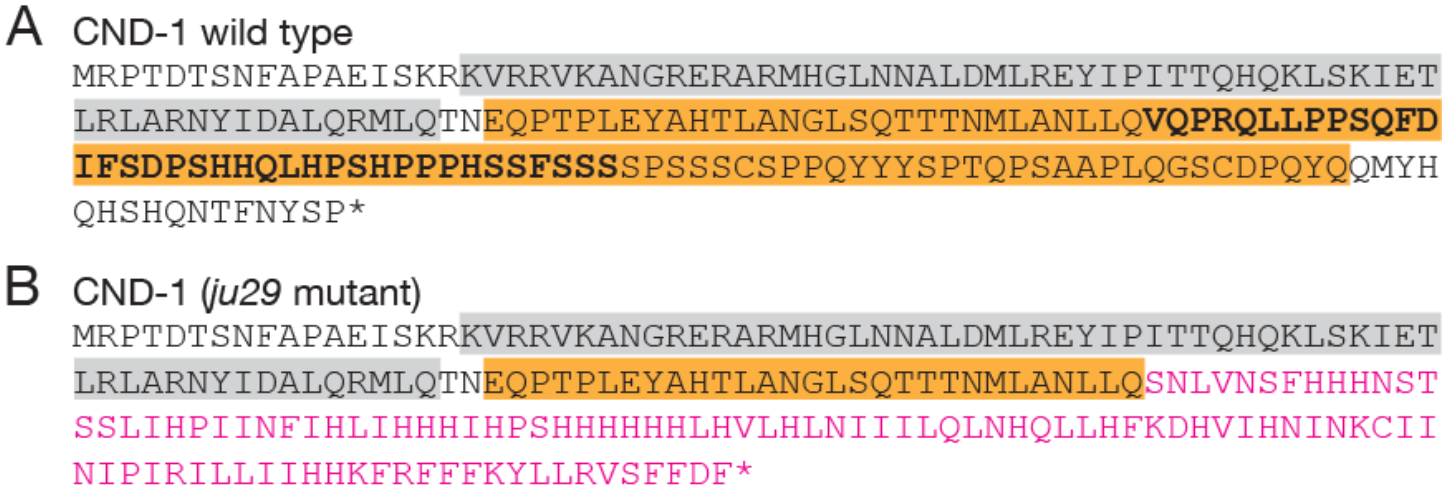

Figure S3. Comparison of predicted CND-1 wild type and *ju29* mutant protein sequences. (A) CND-1 protein sequence. Region highlighted in grey shows the basic-helix-loop-helix dimerization and DNA binding domain. The region in orange shows the extended NeuroD-specific superfamily domain. The region in bold font is weakly homologous to a non-DNA binding domain in GATA-class transcription factors. (B) CND-1(ju29) mutant protein. The frame-shifted sequence beyond the *ju29* allele plus additional 16 amino acids is highlighted in magenta.