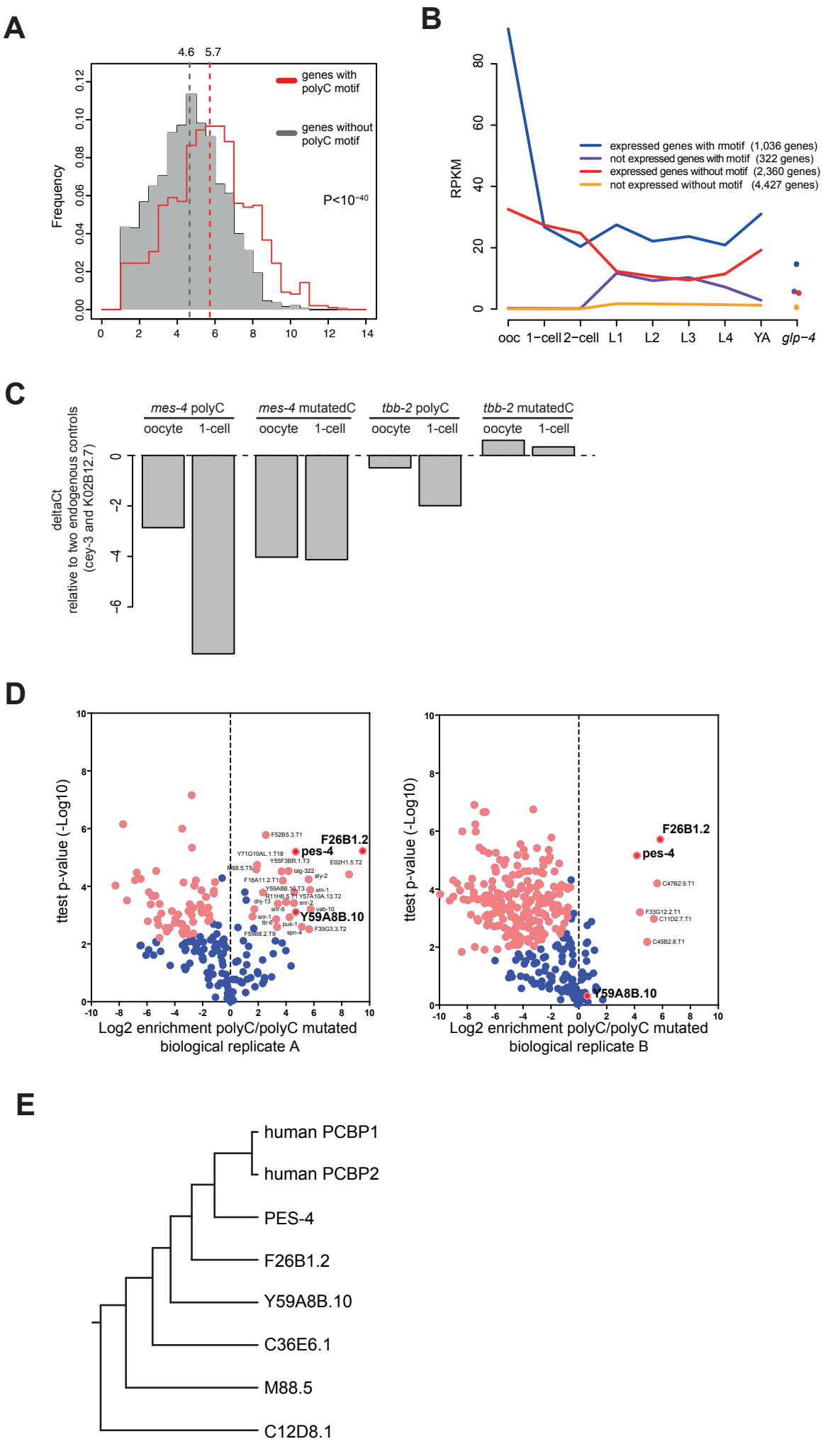
Supplementary Figure S4



Supplementary Figure S4 | Characterization of the polyC motif and its potential binding proteins.

A. Expression distribution (depicted in log2 RPKM) of transcripts containing a candidate polyC motif (red) compared to transcripts without a strong motif (grey) in oocytes.

B. Expression (depicted in RPKM) of all polyC motif containing genes in the *C. elegans* genome, and genes without the motif, in oocytes, compared to embryos, larval stages and adult worms. Motif and non-motif containing genes were separated into two groups, depending on whether or not they are expressed at the OET Data from larval stages and adults was used from Gruen *et al.*, 2014.

C. Expression (deltaCT, relative to two endogenous control genes, K02B12.7 and *cey-3*) of the reporter mRNAs with mutated and wildtype versions of the polyC motif oocytes and 1-cell stage embryos. We do not observe a trend towards higher or lower expression of reporters with wt or mutated variants of the polyC motif in ooyctes.

D. Biotinylated-RNA pull-down assay coupled to mass spectrometry to identify polyC binding proteins in adult worm lysates. Two independent biological replicates (A and B) were measured in triplicates by mass spectrometry and quantified. Observed enrichment (log2-fold change) binding to polyC motif versus the mutated motif (CACACA...) are plotted against the negative logarithmic *p*-value of the *t*-test resulting in a volcano plot. Proteins with a high fold change and low *p*-value are significant interactors. Potential homologues of human polyC binding protein are emphasized in bold.

E. Phylogenetic tree of all potential *C. elegans* homologues of human polyC-binding-protein-1 (PCBP1). Amino acid sequence was aligned using ClustalW.