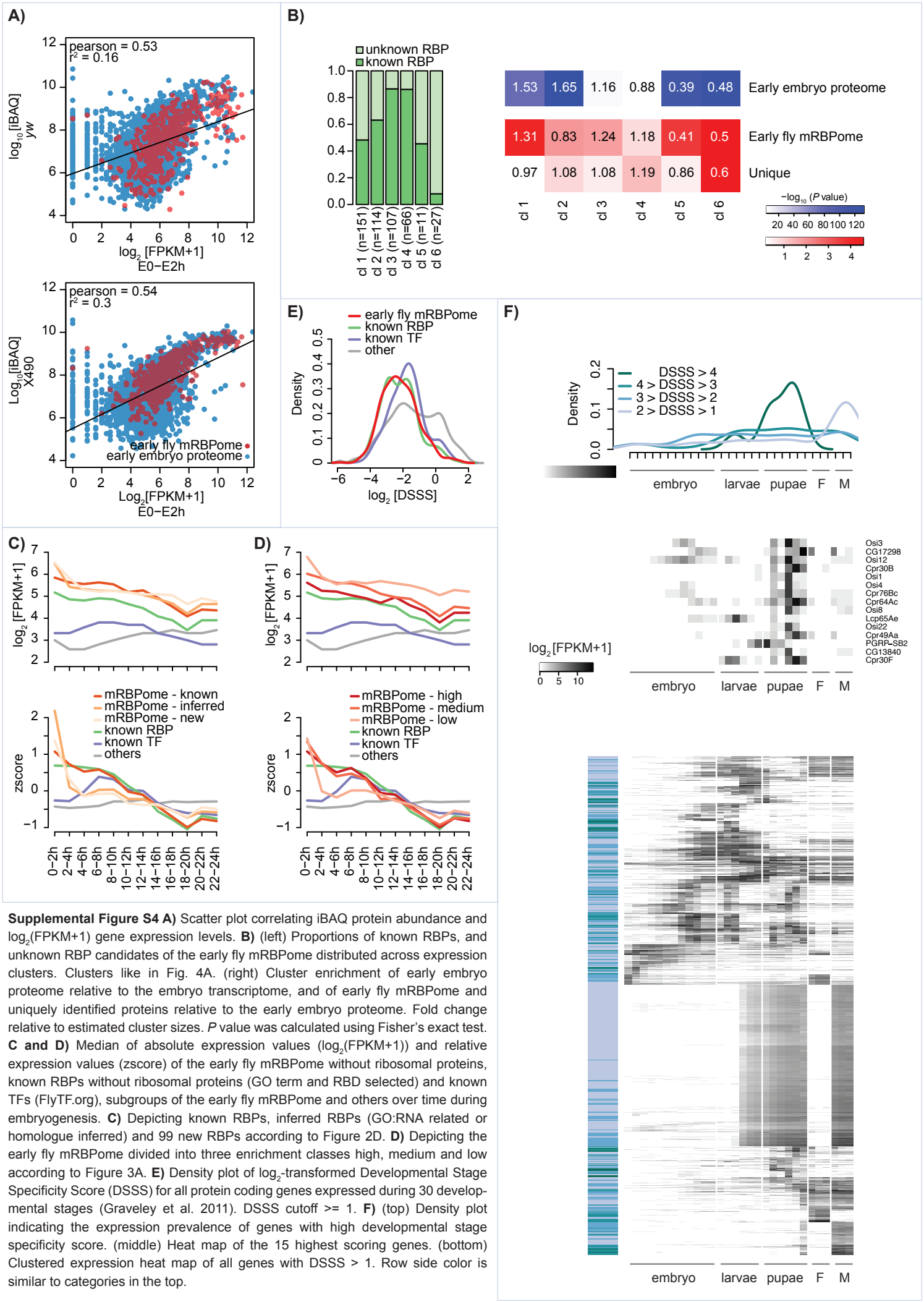

Supplemental Figure S4 A) Scatter plot correlating iBAQ protein abundance and $\log_2$(FPKM+1) gene expression levels. **B)** (left) Proportions of known RBPs, and unknown RBP candidates of the early fly mRBPome distributed across expression clusters. Clusters like in Fig. 4A. (right) Cluster enrichment of early embryo proteome relative to the embryo transcriptome, and of early fly mRBPome and uniquely identified proteins relative to the early embryo proteome. Fold change relative to estimated cluster sizes. *P* value was calculated using Fisher's exact test. **C and D)** Median of absolute expression values ($\log_2$(FPKM+1)) and relative expression values (zscore) of the early fly mRBPome without ribosomal proteins, known RBPs without ribosomal proteins (GO term and RBD selected) and known TFs (FlyTF.org), subgroups of the early fly mRBPome and others over time during embryogenesis. **C)** Depicting known RBPs, inferred RBPs (GO:RNA related or homologue inferred) and 99 new RBPs according to Figure 2D. **D)** Depicting the early fly mRBPome divided into three enrichment classes high, medium and low according to Figure 3A. **E)** Density plot of $\log_2$-transformed Developmental Stage Specificity Score (DSSS) for all protein coding genes expressed during 30 developmental stages (Graveley et al. 2011). DSSS cutoff >= 1. **F)** (top) Density plot indicating the expression prevalence of genes with high developmental stage specificity score. (middle) Heat map of the 15 highest scoring genes. (bottom) Clustered expression heat map of all genes with DSSS > 1. Row side color is similar to categories in the top.