**Supplemental figure captions**

**Figure S1** Venn diagrams of FBF-1 and FBF-2 RNA targets determined by iCLIP under different conditions. The two FBF proteins bind many RNAs in common, but also have individual targets. Numbers refer to the number of RNAs identified as FBF targets by iCLIP. (A) FBF iCLIP in oogenic worms raised at 25°. (B)FBF iCLIP in spermatogenic worms raised at 25°. (C)FBF iCLIP in oogenic worms raised at 20°. (D)FBF-1 and FBF-2 combined (“FBF 25°") targets from oogenic worms raised at 25° compared to individually determined FBF-1 and FBF-2 targets from oogenic worms raised at 20°. The combined FBF-1 and FBF-2 (25°) target list overlaps equally well with the individual FBF-1 and FBF-2 (20°) target lists. This indicates that the combined FBF-1 and FBF-2 target set represents an average of FBF-1 and FBF-2.

**Figure S2** Spearman correlations between all iCLIP replicates (R) reinforce the conclusion that FBF has distinct binding landscapes in spermatogenic and oogenic germlines. Numbers represent rho values for the Spearman correlation between three replicates (R1 – R3) of iCLIP reads mapping to every target RNA. Target RNAs are defined as the 3,478 RNAs possessing a significant peak in any of the FBF iCLIP replicates. We used all RNAs identified as targets in any experiment to include all possibly relevant RNAs. Reads per gene were normalized to dataset size. 25° replicates represent combined FBF-1 and FBF-2 replicates (see Materials and Methods). The 25° oogenic FBF replicate (R1) was of lower complexity than the others, which likely explains its lower correlations overall.

**Figure S3** Overlaps of FBF iCLIP targets with human PUM1 and PUM2 iCLIP targets from murine neonatal brain (Zhang *et al.* 2017). As in Figure 2F, the number of ortholog groups comprising the overlap is indicated as “n=”. Overlap between GLD-1 targets of (Jungkamp *et al.* 2011) and PUM2 targets (Zhang *et al.* 2017) are included for comparison.

**Figure S4** Top FBF targets are relatively abundant. The x-axis represents RNA abundance in log10 RPKM values for oogenic adult hermaphrodite gonads (Ortiz *et al.* 2014). On the y-axis, from top to bottom are: all RNAs present in the oogenic program (Noble *et al.* 2016), all targets of FBF in oogenic germlines (25°), the top 100 (by peak height) targets of oogenic (25°) FBF, and Blocks I-IV from Figure 3. The violin plot represents a Gaussian kernel density estimate fit to the data. An interior boxplot is also plotted: the white dot represents the median of the distribution, and the box indicates quartiles.

**Supplementary Files**

**File S1** Peaks called after FBF iCLIP from oogenic (oo) or spermatogenic (sp) animals at either 25° or 20°. Each tab label indicates germline gender, temperature and which FBF paralog was used for iCLIP. For the 25° datasets, FBF-1 and FBF-2 peaks are listed separately and shown as a combined list termed “FBF”, as described in Materials and Methods.

**File S2** Metrics for FBF iCLIP peaks. Percentages of peaks with a canonical FBE are provided for both the total list and for the top 500 peaks, as defined in File S1 under the column labeled “Rank” (column “A”).

**File S3** GO terms for FBF targets from all datasets, as well as Blocks II and III. Terms were identified using DAVID (Huang *et al.* 2009), and, except for Blocks I-IV, only the top 500 ranking RNAs in each dataset were included. The “Benjamini” column denotes the Benjamini-adjusted *p*-value output by DAVID. There were no significant GO terms (*p*-value < 0.01) for Block I or IV.

**File S4** Genes significantly differing between spermatogenic and oogenic (both at 25°) iCLIP by DESeq2. Tab 1: Genes 2-fold enriched in spermatogenic iCLIP at *p* < 0.01. Tab 2: Genes 2-fold enriched in oogenic iCLIP at *p* < 0.01. Tab 3: all DESeq2 results.

**File S5** FBF binding per gene for 2,114 FBF target RNAs minus three RNAs (see Results section regarding Figure 3A). This dataset corresponds to Figure 3A.

**File S6** Blocks, as defined in Figure 3.

**File S7** FBF targets overlapping with the human PUF protein PUM2 identified by PAR-CLIP in HEK293 cells (Hafner *et al.* 2010). Tab names correspond to peak lists in File S1 or the blocks in File S6. Tabs labeled “top 500” only include the top 500 FBF targets in their respective list, ranked by frequency (read count). All human ortholog Ensembl IDs are given for each RNA, regardless of whether they are targeted by PUM2. The column “Worm public name” includes all worm orthologs, regardless of whether they are targeted by FBF. The column “FBF targets (Worm public name)” columns denotes RNAs in the ortholog group that are FBF targets, and the column “PUM targets (Human gene symbol)” column denotes orthologous PUM2 targets.