Bazzini et al., Figure S4

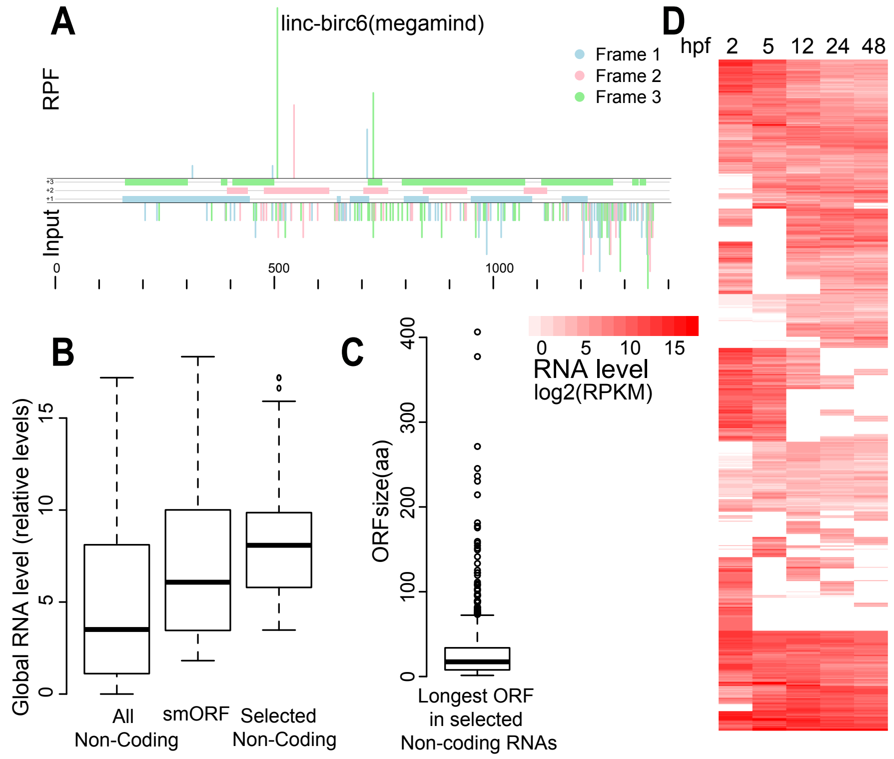

Figure S4. Transcripts without experimentally defined coding regions.

(A) Subcodon profile plot showing an extensively studied lincRNA, *megamind*. Note that very few RPFs align to this region despite high RNA input coverage.

(B) Boxplot shows the global input RNA level of: i) all putative noncoding RNAs with no coding evidence (low ORFscore, no coding prediction by Chew et al. 2013 and not coding exon overlapping), ii) transcripts containing detected smORFs, and iii) noncoding RNA with RNA level above the first quartile of smORF RNA level (input-selected).

(C) Boxplot representing the size of the longest ORF per input-selected noncoding RNA.

(D) Heatmap showing the pattern of expression of the input-selected non-coding RNA transcripts during early embryogenesis (n=959).