



Figure S4: Transcription evidence for predicted folds, conserved elements, and different classes of ncRNAs. The y-axis indicates the coverage in percent. The different types of transcription evidence are given along the x-axis: **TF polyA+**: Transfrags enriched in polyadenylated transcripts, **TF polyA-**: Transfrags depleted of polyadenylated transcripts, **cDNA**: human cDNAs, **xeno cDNA** non-human cDNAs, **EST**: human ESTs, **xeno EST**: non-human ESTs. The enrichment for a given type of transcription evidence relative to the genome-wide coverage of intronic and intergenic regions is given above each column. The combined class combines the tRNAs, miRNAs, snoRNAs, and the Rfam Seed non-coding RNAs.