Figure S2.—RNA Sequence data for each of the loci identified in Table 1. Total RNA was extracted and sequenced from the same samples used to generate the proteomics data described here (AB SOLID v3+; Bitton et al. submitted). Each panel in the figure is a screen shot from the X:Map genome browser representing each of the 40 novel loci identified the pipeline. Data for nda2 and nmt1/thi3 are included for reference. Black bars represent the location of individual genes, while coloured graphs represent the number of 50mer RNA fragments aligning uniquely to the genome at that point. Data are presented on a log2 scale. The height of the plots represents the number of reads with alignments starting at that point. Since many of these loci are very small, and some are expressed at low levels, coverage is not uniform. However, when combined with the RT-PCR data in Figure S1, transcription is confirmed at 38/40 loci. Data are summarised in Table 1 and Table S2.