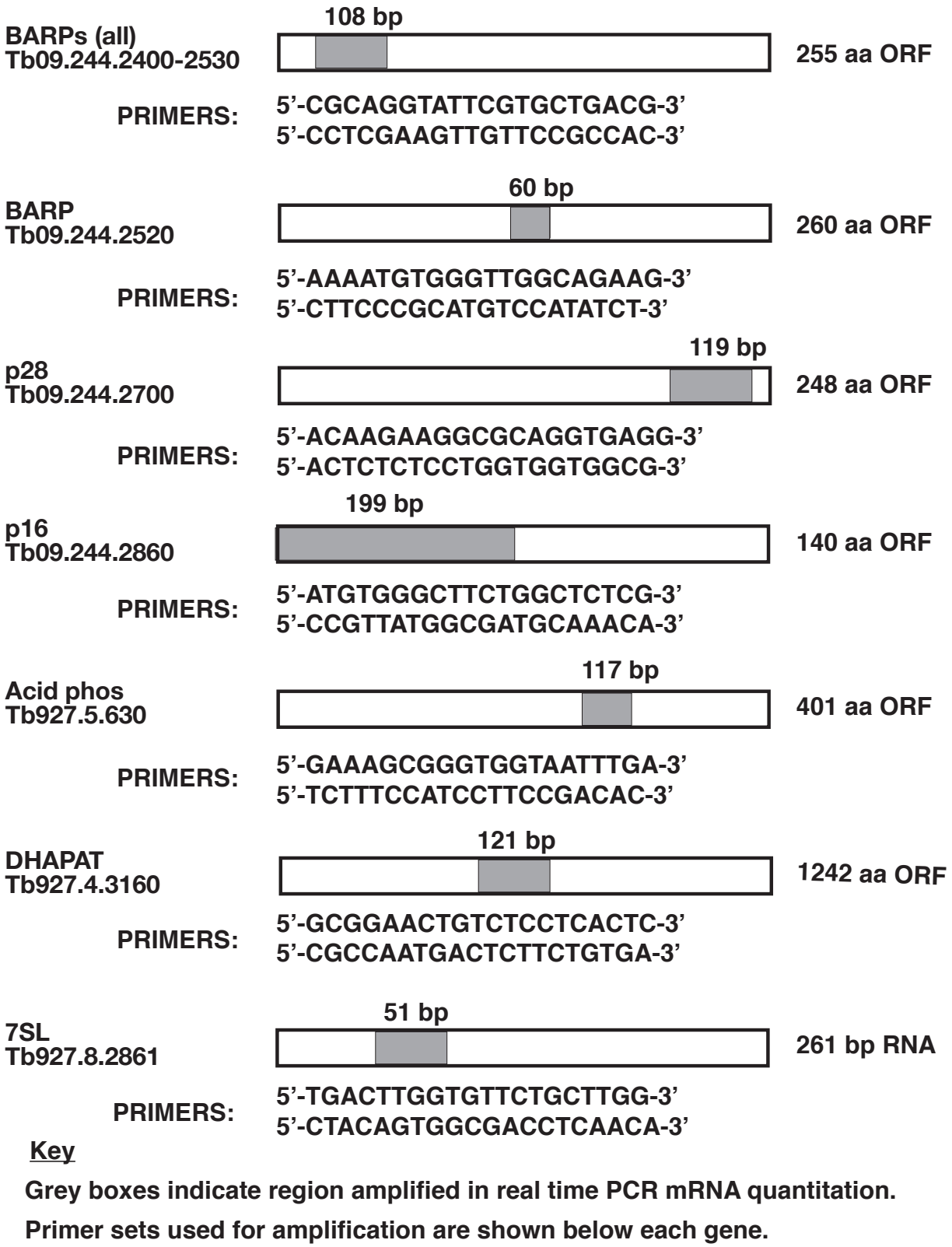

Figure S3. Representation of genes analyzed by qRT-PCR. Shaded boxes indicate regions and bp lengths of sequences amplified in qRT-PCR experiments. Primer sets were located at the ends of each shaded region. Entire ORF lengths are indicated to the right side of the drawing. The BARP ORFs are heterogeneous in size and this is indicated as '~783 bp ORF'.

Figure S3