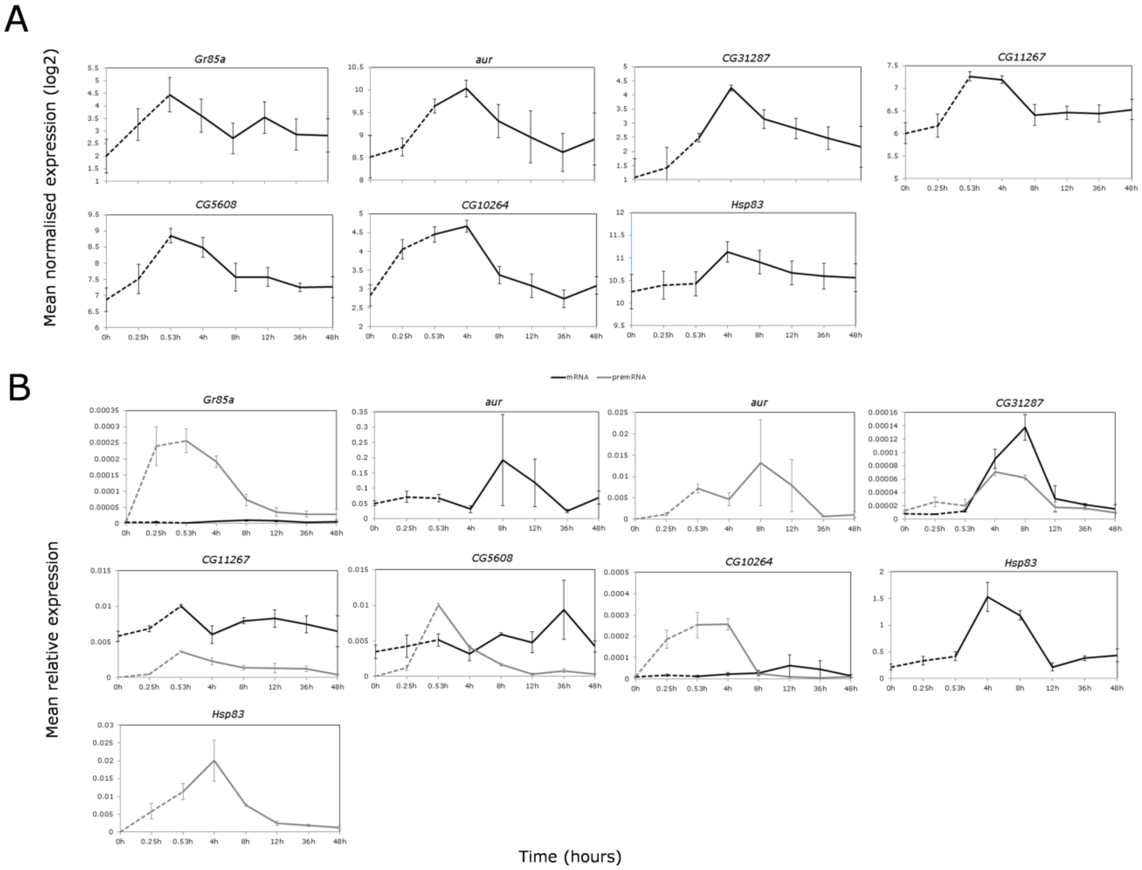

Figure S5 Detailed transcript analyses of early responding genes confirm RNA splicing inhibition during heat shock. Dashed lines indicate thermal stress at 38.5º, solid lines indicate recovery up to 48 hours post stress at 25º. Exon profiles from the microarray analyses (constitutive exon set), shown as average normalized expression on the Y-axis (log2). B) Real-time PCR profiling using exon-junction primers to target mature mRNA levels (black line) and intron/exon primers to target pre-mRNA levels (grey line) relative to *RpL11* (Y-axis). Negligible *Gr85a* and *CG10264* mRNA suggests that these genes may be transcriptionally active during heat shock. *Hsp83* is shown in the last panels of A and B to confirm nascent transcript accumulation during heat stress. Error bars are the ± SE of the mean.