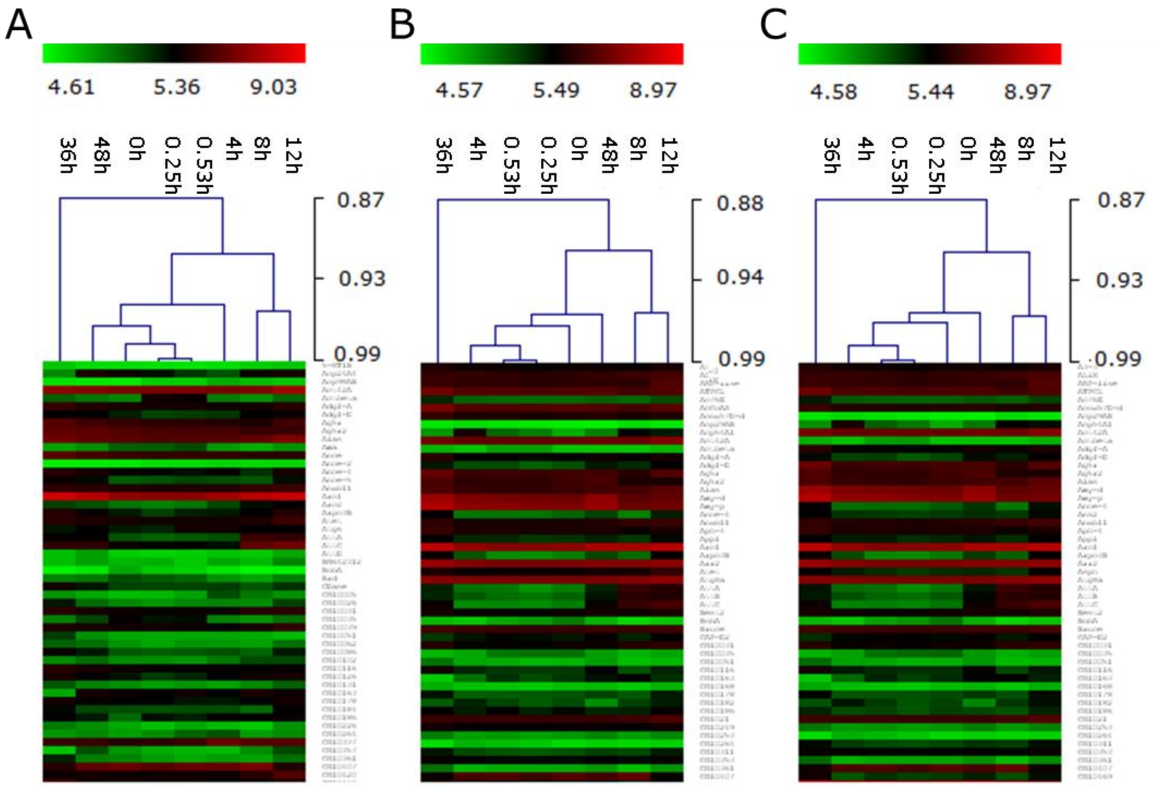

Figure S2 Average linkage hierarchical clustering of the eight point time-series across three replicates for the significant time-point term (FDR 0.2). A) 3'IVT module (*n* =1114 genes), B) constitutive probes from the exon module (*n* =1282 genes), and C) for all probes in the exon module (*n* =1171 genes). Similar temporal expression patterns are seen between the module and probe comparisons where the stress and early recovery period cluster closely together and are grouped with time zero and 48 hours recovery. The transcriptional response to thermal stress appears closer to basal levels by 48 hours post stress.