



**Supp. Fig. 2** Confirmation of microarray transcript abundance profiles using qRT-PCR. Relative expression (primary Y-axis) refers to test gene expression relative to the geometric norm of three control genes in GU. Standard error bars represent the standard error of the mean (SEM) across the three replicate reactions. Std LSM (secondary Y-axis, on right) is the standardised least square means estimate of transcript abundance on the GU microarray slides. **(A)**  $\beta$ -amylase, At3g23920 **(B)** cinnamyl-alcohol dehydrogenase, At1g72680 **(C)** endo-1,4- $\beta$ -glucanase, At5g49720 **(D)** UDP-D-glucuronic acid decarboxylase, At5g59290 **(E)** Circadian Clock Associated 1, At2g46830 (All names are best BlastX hits of *Eucalyptus* EST sequences against *Arabidopsis*). The X-axis shows Zeitgeber Time, or hours since dawn