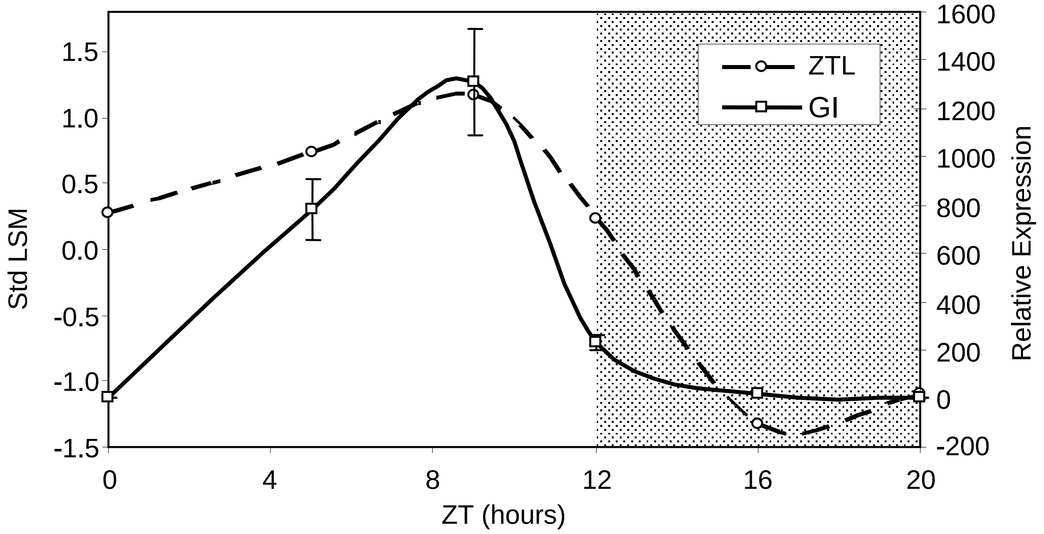

Supp. Fig. 3 *EtZTL* mRNA levels cycle in field-grown *Eucalyptus* trees with a transcript abundance profile similar to *EgGI*. Std LSM (Y-axis) is the standardised least square means estimate of *EtZTL* transcript abundance on the GC microarray slides. Relative expression (secondary Y- axis) for *EgGI* is the ratio of the expression level of the gene measured by qRT-PCR to the geometric mean of expression in three control genes. Standard error bars represent the standard error of the mean (SEM) across three replicate samples. The X-axis shows Zeitgeber Time, or hours since dawn. Shaded areas indicate night time and unshaded areas day time