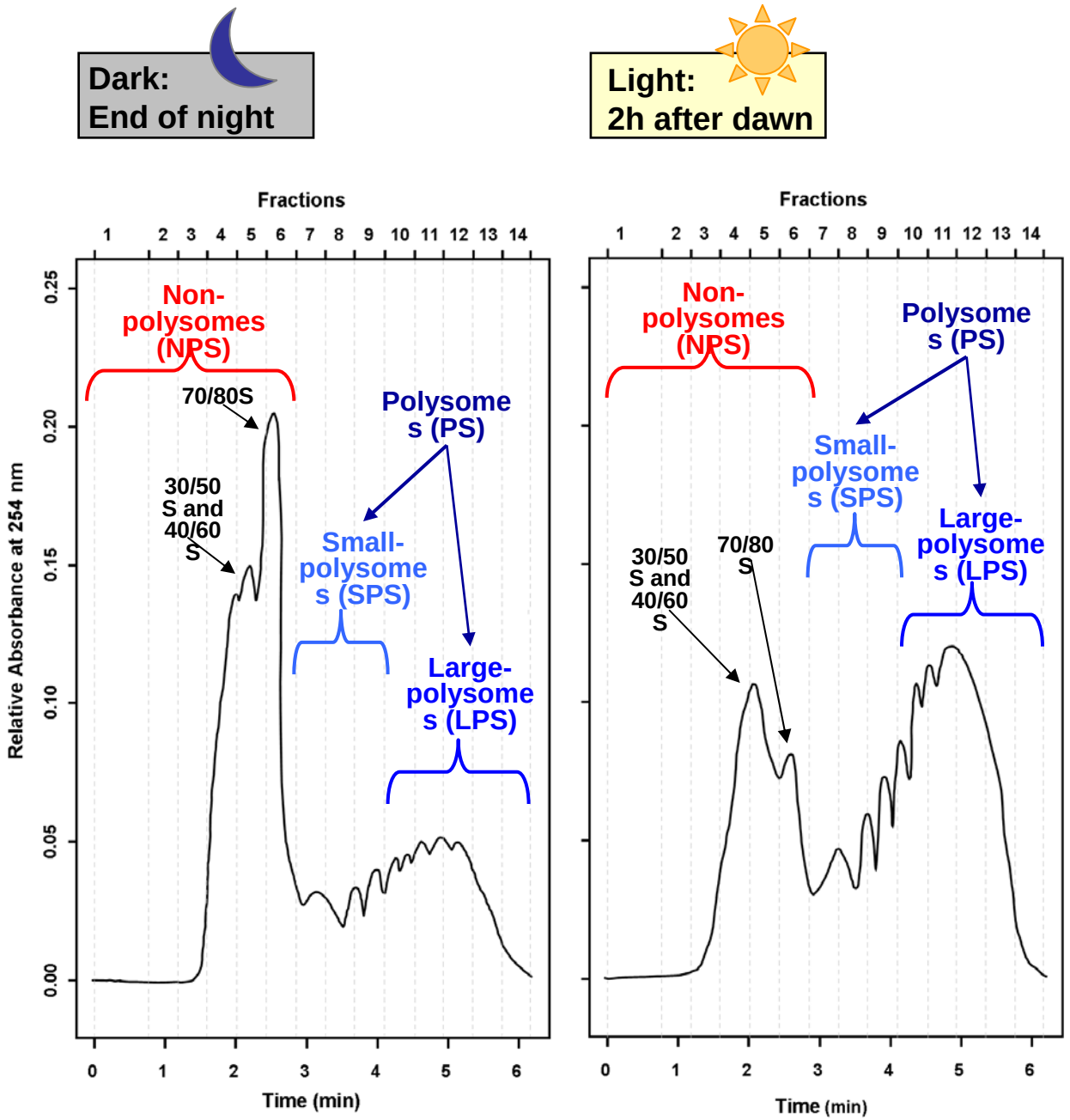
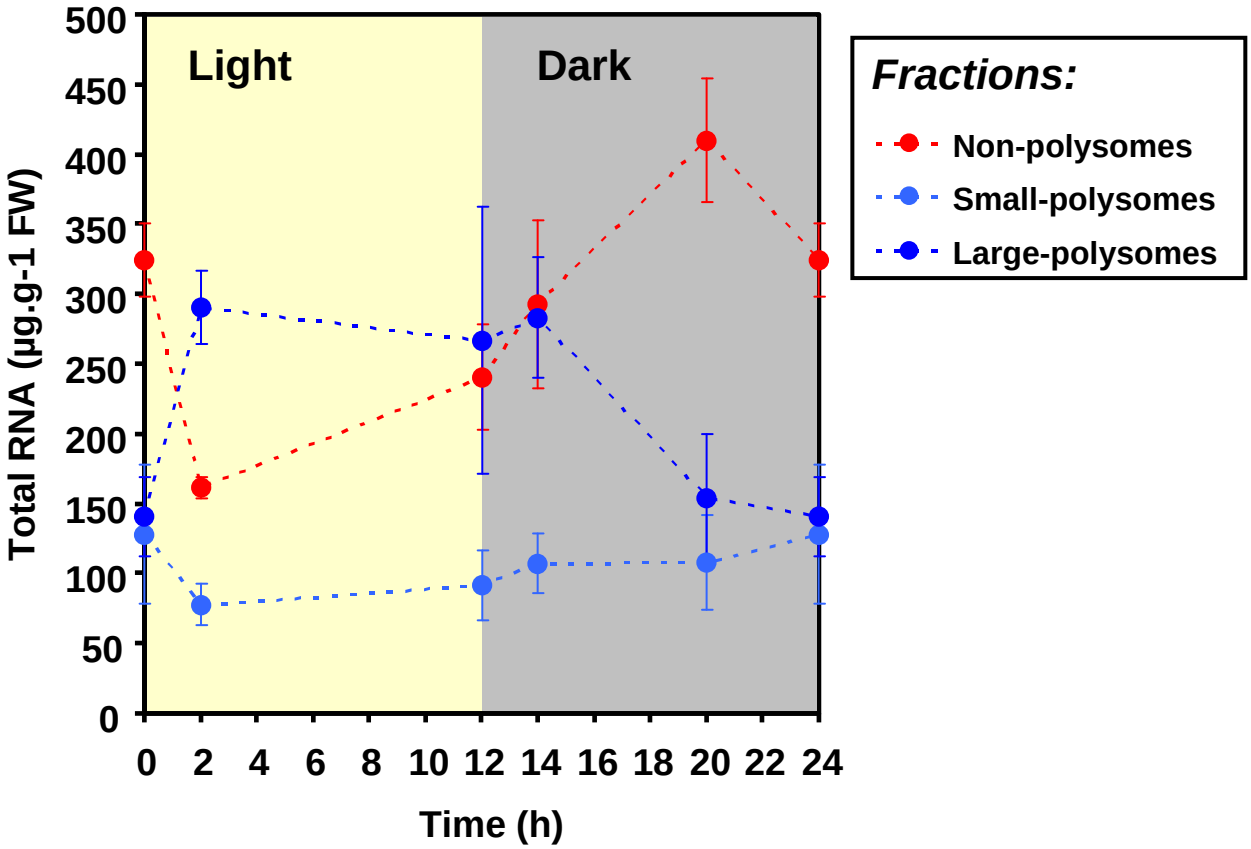


Supplemental Figure 1. Examples of polysome density gradients for samples collected at the end of the night, and after 2 hours illumination. Polysomes gradient were collected using a programmable Density Gradient Fractionation System, which continuously recorded the ribosome absorbance at 254 nm (ribosome profile)(for more details see Materials and Methods). The y-axis shows absorbance at 254 nm, and the x-axes show the time after starting to collect from the gradient, with the top of the gradient on the left and the base on the right hand side. The various fractions are indicated on the diagram.

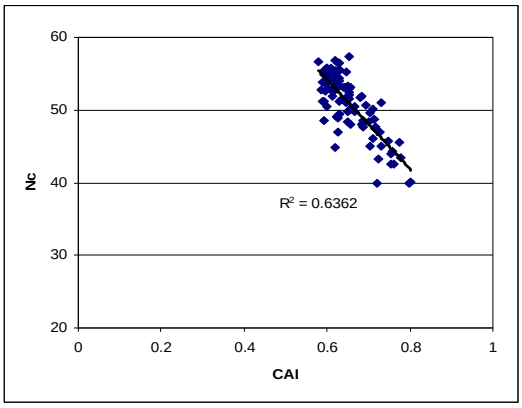


Supplemental Figure 2. Changes in polysome loading during a diurnal cycle. The results are the mean ± S.D (n = 3 separate gradiennts with biological replicates). Polysome levels were determined by calculating the area under the polysome profile after subtracting the gradient baseline absorbance (absorbance of a gradient loaded with extraction buffer), normalising the area of each polysome profile to an equal value to account for differences in sample loading. The areas corresponding to the NPS, SPS and large LPS fractions represent the percentage of the total area under the profile for that fraction (see Materials and Methods). The x-axis shows the time, with = being equivalent to the start of the light period.

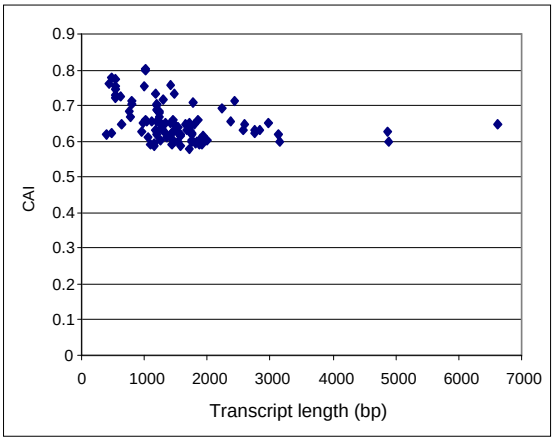
Supplemental Figure 3

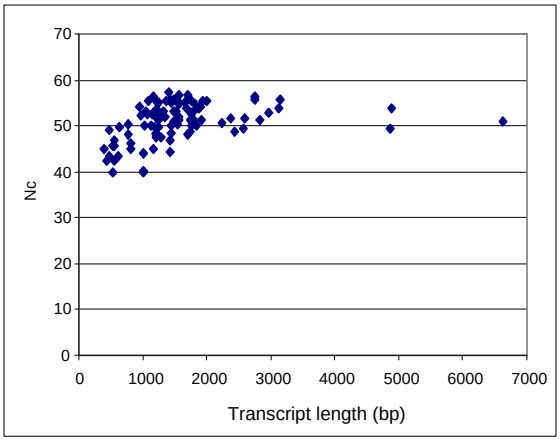
Codon usage, transcript length, transcript abundance and estimated Tp . For clculaitons see Calculsaiotns and assumtions, and supplmental Tables X and XI

A, Comparison of CAI and Nc values for each gene

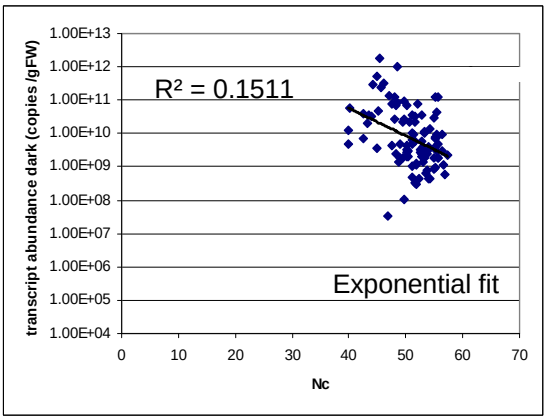


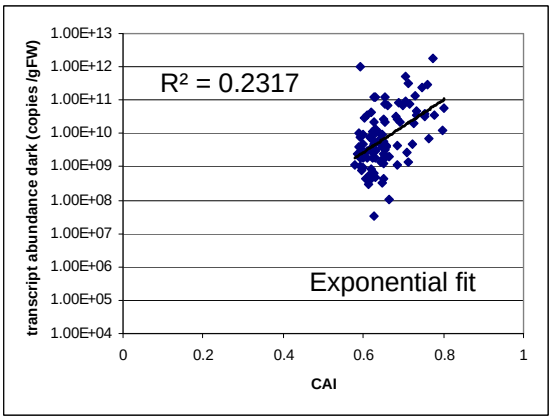
B, Comparison of CAI and Nc values and open reading frame length for each gene





C, Comparison of CAI and Nc values and transcript abundance (end of night) for each gene





D, Comparison of CAI and Nc values and Tp for each gene