

## SUPPLEMENTAL LEGENDS

**Supplementary Figure 1. The putative promoter region of Arabidopsis AOX1c.** Sequence of the *AtAOX1c* promoter, 500 bp upstream of the TSS, showing sequence elements in common with *GmAox2b* (highlighted in blue and designated A to G). In order to define core or degenerate elements the top 50 co-expressed genes as defined using the Arabidopsis co-expression tool (ACT) and BAR Expression Angler were searched for common sequence elements using the Motif Analysis Tool on the TAIR website. Coloured bars below the elements indicate where these predictions overlap with the sequence elements tested for function in *AtAOX1c*. The thickness of the coloured line under each element indicates the percentage of the genes in the co-expression analysis that contained the sequence underlined (red and green). For each sequence element, the percentage of those genes that contained that element in the co-expression analysis and were predicted to encode proteins targeted to mitochondria is indicated (purple). The locations of site II elements are marked in yellow.

**Supplementary Figure 2. Representation of genes that contain at least 1 of the sequence elements identified as functional in AtAOX1c.** The outer whorl indicates the number of genes that contain a single functional element and moving inwards and crossing each line indicates the number of genes that contain various combinations of the sequence elements.

**Supplementary Figure 3. Analysis of co-expressed genes encoding pentatricopeptide repeat containing proteins with *AtAOX1c*.** The co-expression of each gene encoding a pentatricopeptide repeat containing protein with *AtAOX1c* was determined using the Co-correlation Scatter Plot function on the ACT database. An output with a slope of 1 indicates perfect co-expression while a slope of -1 indicates a negative correlation.