Computational methods for identifying cis-elements in promoters are usually based on finding common motifs in few promoter sequences that are believed to be co-regulated. We propose a more robust statistical approach using microarray expression data in association with a large set (thousands) of promoter sequences. Applying this method to promoters of Arabidopsis thaliana, we have identified motifs which may affect gene expression under specific environmental conditions, in specific tissues, as well as contribute to promoter strength or variability. Our results demonstrate a strong correlation with experimentally validated motifs and lead to the prediction of new functionally important cis-elements in promoters.