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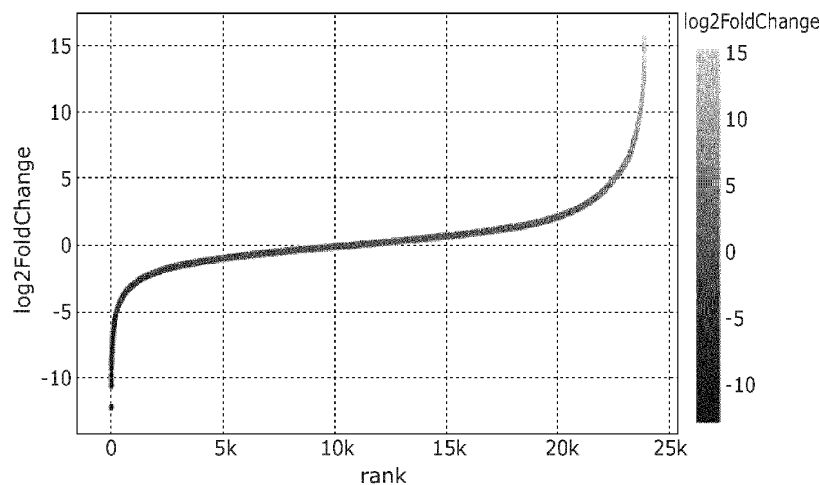


Figure 1

(57) Abstract: Methods are provided for performing an in silico analysis of a genome for a plant subject, that includes identification of a plurality of sequences that collectively define a promoterome of the plant subject, wherein each sequence within the promoterome is comprised of an expression control region that extends from the start codon of an open reading frame to around 100 kilobases 5' and/or 3' to the start codon. A transcriptome in the form of mRNA expression data for the plant subject is obtained and an analysis is undertaken using a sequence-based modelling algorithm in order to provide a prediction value of the level of expression of each protein coding gene comprised within the transcriptome and linking the value to a sequence for a corresponding expression control region comprised within the promoterome. The methods may be used to generating novel designs for expression control sequences that are most likely to provide a desired expression profile for an operably linked coding sequence. Also provided are nucleic acid libraries, plant cells, plant tissues and plants comprising novel expression control sequences.

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