

Appendix 5. Complete Candidate Interaction Matrix (CIM) for transcription response elements from PAINT analysis of human gene first introns.

The RPE gene set was analyzed by PAINT and a graphic CIM was generated as described in Materials and Methods. The y-axis lists the Ensembl Gene identifiers for each gene and the x-axis lists the TRANSFAC TRE identifiers for each TRE found at least once in the first intron region. Genes listed along the y-axis are divided into two clusters that are either up-regulated (blue) or down-regulated (green) during EMT of RPE cells. TREs listed along the x-axis are clustered according to related occurrence pattern calculated using Jaccard's coefficient. The elements within the matrix are color-coded based upon the p-value of each TRE found in the regulatory regions of the genes. A red dot represents a TRE that is statistically significant and therefore over-represented in our gene set, while a blue dot signifies an under-represented TRE and a grey dot stands for a TRE with no statistical significance in our gene list. Note: This is a large-format figure and should be viewed at enhanced magnification to read the text in specific sections of the figure.



