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(54) Title: EPIGENETIC MARKERS FOR DETECTING OXIDATIVE STRESS

(57) Abstract: The present invention is related to a method of identifying oxidative stress (OS) in a test cell, the method comprising: (a) determining the methylation status of at least five genes in a DNA sample obtained from the test cell; (b) comparing the methylation status of the genes from step (a) to the methylation status of the corresponding genes in a control without OS, wherein a difference in the methylation status of the genes in the test cell compared to the corresponding genes in the control is indicative of the cell having OS; and wherein the genes in step (a) are selected from the group consisting of *PTPRN2*, *MAD1L1*, *PRDM16*, *TNXB*, *HDAC4*, *ADARB2*, *CDH4*, *DIP2C*, *SHANK2*, *CAMTA1*, *RPTOR*, *RASA3*, *SDK1*, *AGAP1*, *TBCD*, *SEPT9*, *FRMD4A*, *MCF2L*, *FOXP1*, *RPS6KA2*, *SORCS2*, *NXN*, *TRAPPC9*, *AUTS2*, and *CACNA1C* and the regulatory regions of the same.



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