

**S2 Table.** PROMO transcription factor analysis of pyrosequencing target gene regions

<b>Gene</b>	<b>Target Sequence for PROMO analysis</b>	<b>Putative Transcription Factor Binding Sites<sup>a</sup></b>
<i>ATP5E</i>	CACCATGCTGTAG <u>C</u> GAAAG <u>C</u> GGAGCT <u>C</u> GT <u>C</u> GGGC <u>C</u> GAAT <u>C</u> GC	YY1, XBP-1, GR-beta, Pax-5, p53, E2F-1
<i>COX6C</i>	A <u>C</u> GG <u>C</u> GGAGACACACAGTCAC <u>C</u> GACTAAAT <u>C</u> CGA	GR-beta, c-Jun, TFII-I, E2F-1, TFII-I, HNF-3alpha, AP-1
<i>RPL9</i>	ACACTGGGGCCC <u>G</u> CTGT <u>C</u> GGTCTCCC <u>G</u> TCCTCC <u>G</u> A	Pax-5, p53, E2F-1, TFII-I, GR-alpha, PPAR-alpha: RXR-alpha

<sup>a</sup>Factors predicted within a dissimilarity margin less or equal than 15%