Title page

Idiopathic male infertility and polymorphisms in the DNA methyltransferase

genes involved in epigenetic marking

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Figure legends

Figure S1. A predicted effect of the variant rs2424909 on transcription factor-binding site. Comparison between C allele (A) and T allele (B) of rs2424909 for the putative transcriptional factor-binding site.



Figure S2. A predicted effect of the variant rs4804490 on transcription factor-binding site. Comparison between C allele (A) and A allele (B) of rs4804490 for the putative transcriptional factor-binding site.

Α	seq(0	59)	gtgctaggattacagatgtgagccaccctgcctggctgtttttaaagtgtg
	Segment	s:		•
	1.1.3.0	8	17	=C/EBPalp=
	1.1.1.1	17	26	===c-Jun==
	2.3.1.0	21	30	====Sp1===
	4.3.1.1	34	43	===MEB-1==
	4.3.1.2	34	43	====GLO===
	2.3.2.2	35	44	=====Hb===
В	seq(Segment 1.1.3.0		59) 17	gtgctaggattacagatgtgagccaacctgcctggctgtttttaaagtgtg =C/EBPalp=
В	Segment 1.1.3.0	s: 8	17	=C/EBPalp=
В	Segment	s: 8 16	,	A
В	Segment 1.1.3.0 9.9.539	s: 8 16	17 29	=C/EBPalp= =====NF-1====
В	Segment 1.1.3.0 9.9.539 9.9.173	s: 8 16 17 34	17 29 26	=C/EBPalp= =====NF-1==== ====CTF===

Figure S3. A predicted effect of the variant rs1550117 on transcription factor-binding site. Comparison between A allele (A) and G allele (B) of rs1550117 for the putative transcriptional factor-binding site.



Figure S4. A predicted effect of the variant rs7354779 on transcription factor-binding site. Comparison between C allele (A) and T allele (B) of rs7354779 for the putative transcriptional factor-binding site.

