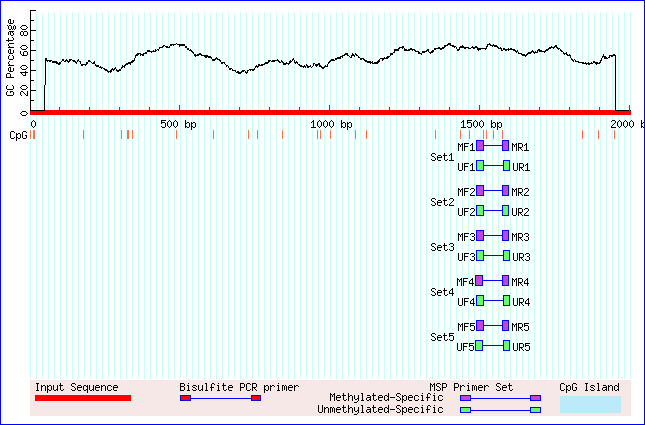
***PADI4* promoter sequence.**

In the wide epigenome studies there was no information about methylation sensitive sites in *PADI4* gene [1, 2], thus according to the current methylation protocols [3] the region from Eukaryotic Promoter Database [4] from -1500 to +500 bp relative to transcription start site was chosen for CpG methylation study. MethPrimer software [5] was used for primers design with the following parameters: primer melting temperature between 58-62°C, PCR product length between 80-150 bp and at least 1 CpG must be localized between 1-3 base at the 3’ end of primer to minimalize the specificity. MethPrimer software generate the following results:

*Figure S2. Primers location in the PADI4 gene promoter region.*



*CpG sites in input sequence were indicated by vertical orange lines.*

All primers pairs were situated in the same region. Please note that one of CpG in figure above in designed PCR product was hidden due to low resolution of generated graphic by software. The detailed primers location (indicated by yellow) was presented below:

1441 AGGTGCTGACTCATGGCCTCTGCTGGGCGATATAAAGGAACCAGCCCAGGGGCTTCCTAC

|||||:|||:|:||||::|:||:||||++|||||||||||::||:::|||||:||::||:

1441 AGGTGTTGATTTATGGTTTTTGTTGGGCGATATAAAGGAATT**AGTTTAGGGGTTTTTTAT**

MF>>>>>>>>>>>>>>>>>

1501 AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAG

||::|||||||++||:|||::++|++||||:::||||||:||||||:++|||||::::||

1501 **AGTTAGAGGGAC**GAGTTAGTTCGACGATGGTTTAGGGGATATTGATTCGTGTGATTTTAG

>>>>>>>>>>>>

1561 AGCAGCCCACCCATGCCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGGT

||:||:::|:::|||:++||||||||:||||:|::||||:|:||:||||:||:||:||||

1561 AGTAGTTTATTTATGT**CGTGTGTGTGTTGGGTATTTTGAT**TTAGTTTGATATTTGTAGGT

MR<<<<<<<<<<<<<<<<<<<<<<<<

***PADI4* promoter sequence from eukaryotic promoter database (EPD):**

>FP000306 PADI4\_1 :+U EU:NC; range -1500 to 500.  
ATGCGTCAGAACGTCGGACCTGGCCACATCATCATCTGCTGGTACAGAAGATAAATTTTG  
AGCCCAGAGAAGGTGGTCTGAATCCAGATCCCCACTGTAGGGCTTATGAGACCTTGGGGG  
TCTCACTCAATCTCTCTAAGTCTTTGTGGTCTCATCTACACATGGGCATCCTGATAGGAC  
GCACTCCATAGGGATGTTGAGATGAGGCAGGATTTGAACTAAAGCCTGTTTGATCCCACA  
GCCTGACTCTGAATTAATGAGGCAAATTCTTTGCTTCAAAGCCAAAGCAAGCAAACAAAA  
AACAAACGCAAGATATCCAACCCACGAAACGCTCTATGTTCACGCCAGACTCCCATGCAT  
GCACCCTTTGAGTGCTCCTTGTTGGGACCCATCCACCACCCCCCAGTTGCCTCATTAAAG  
GCAGAGCCTGGCACCAATGGCCCAGGTGCAACCACAGCTCTGAGGCCACATGGGCATCCC  
CCTGGCAGGCGTGGCCCACACCTGCACTGTCTGGTCTGACACCCAGAGGCCCTGGCAAGA  
GGCAGGTATCCTGGAGCATGCAGAGAACATCAACTTCCATGCCAGGAAGCTCATCTTCTC  
TTCCCAGCTCTGCCGCATTCTAGCTCTGGCACCTTGGGCAAGAGCTAGTCACTTTTACTC  
TCTGAGCCTCAATTTTCCTTCTGTAAAATGGGTTGTAATAATAAGCCCATATACACCTTG  
TATTGTAGCGAGATGTAGCTGTGATACAGTCTGGAAAGCACGTGTCATATAGACAGGCAG  
CTAATGAATCTCACACTCTGGAACTGGACACCTTTGGTTCCAATTCTGGCCCTACCACTC  
TCGAGCTGTGGAAGAACTGCACCTCTGTTTTCTCCTCTGTAAAATGGGTATAATAATGGC  
ACCAACCTCAGAGGGCTGCTGTGAGGGTGAAATAAGGGGATAATGGTATGATCTAGTTCA  
CGGGTTTGTCGTAATGAGCTATTCTATGTGAAGTGCAGGAAAACGTGCCTGGCATAGAGA  
ATGTGAGCTGTCATGTGGGTGGCCCAGGTGGAGAGACTTGTCCCAAGCCTGGTTGGTCTT  
TGAACGTGTAGCCTGGCCTGTGACTGCTTACCTAAAATCTCCCCGCTTTTCCCACCTTCT  
CCTCTCTGATATGCCTGTTTGACATAGGTGAGATTGGATAGATCAAGGTGTTCAGGGCCT  
CTAGGCAGGGATGGGACTGTGGGCATGAGGACCAGGACCCAACCCCTCAGCCCCACTCTC  
CACCCCAGGCTTTCTGAGCCATCCATCCTTCCCAAGAAACTGACAGAGCCACCCTGCCAC  
TGGTACCAGCATTGACACCCATCTAGAGGTCCGAGGGGCAGCCCCAGGGCAGAGGAGATT  
TTGAGAGCCCACACCCCTGACCTGAGTGGGGAGGGGTTGAGCCTCTGGGCCACAGACCGC  
AGGTGCTGACTCATGGCCTCTGCTGGGCGATATAAAGGAACCAGCCCAGGGGCTTCCTAC  
AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAG  
AGCAGCCCACCCATGCCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGGT  
AAGAGGGGGGCCTTCTGGGGTTTTGGAGGCAGGTCAGGAGATGCTGGATGACCCAGTTCT  
ACTGACACAGGAGCATGTGTTTGGCCCAGGCTCTAGGCTCCAGCCTCTGCAGCCACTGCC  
AGGGGAGTAGCTGGAGAGAGAAGACCCCAGCAGCCCTGGGAAGTGCCAGTCTCATGGCTG  
TGGGTTCTTTGCCATGTACAAGTGCAAATTCCCCAGGAACACACGACAGATAAATTATTA  
TGGGGCAAACCAGGCCATCCATCTCCCTGTCTTCATCGAGGCAACAGAAGCTTACAGAGA  
GTCTGTGACTTGCTCAAGGTCACACAGCACGTGTGCCCTGGAAGTAAGGTTAGCCCCTGG  
GCCTCCTGGTTCACAGCACAG

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