

Supplementary table 1S. Genomic sequences analyzed by Sequenom EpiTyper technology and the CpG dinucleotides highlighted.

Gene	Genomic sequence
<i>CD36</i>	
NC_000007 REGION: 80231554..80232032 gene ID: 948, updated on 09-02-2012	<p style="text-align: right;">+95</p> GGGTTGAGAGCCTGTGCCTCATTCTGAGTTCTCAGCTGCTATGC CG TGGAAATCCTGTTTACTTTC <p style="text-align: right;">+167</p> TGCATCTGCTCCTGCAAGACTCTGGAGCCAGTCTTGAGGTCCACATCTC CG AAAGCAAGCTCTTCT AGAAGTTGGTGTGAGCAGAATGCTTTTTGTTTAGAAGTGTGGCTATAAATGTCTTTGTAGTTGATGCAC TCTCATCTAGTAAGTAACTATTATTTTTGGGCTCTCTAGAAAGGTAATTATTATCTGATATAATAGT TTAGTCTGTGATGCTTCTTTTAACATATTTGTAAGTTTTAACCAAATGGTTAAAGAAATTTGCTTTT TAACCCTTAAACCTCACATATCCACAAGTCTCTAAATTCATAGGATGCTATGGATTTCTAGTTGCC <p style="text-align: center;">+477</p> <p style="text-align: right;">+498</p> TAGTTCATGTCTTTTACTTAGAAAA CG TCAGAAAACCCAAACTTCT CG TGACTTCAAAAAGTGTAAAT TGTACCTGAA
<i>FFAR3</i>	
NC_000019 REGION: 35849221..35849605 gene ID: 2865, updated on 08-16-2012	<p style="text-align: right;">-202</p> GGCAAATTGGATAAATGCCATTCTAGAGAAGCAGACAAAATTC AAGTGAAGAAGGGGAGAGGAAG CG <p style="text-align: center;">-199</p> <p style="text-align: right;">-146</p> GT CG GCTGGGGCCTGCTTAGAGCATCCCAGCTGAGACTGCATGAGGAGGGAGGCC CG CAGTTGTGGA <p style="text-align: center;">-96</p> ATTTGTTCCCCTTTTAGCATGCTGACCAGCCCTGGCAA CG GAGCTCAAGGCATCTATGTGCCACTGC <p style="text-align: center;">-53</p> <p style="text-align: center;">-42</p> <p style="text-align: right;">-18</p> TCAACAGTGAGTGA CG TCATGGGCA CG GCCAGGTCTTTATCAGTTCTGC CG GATAAATAGCCAACTG <p style="text-align: center;">+33</p> CACTAGGTCTGGAGAGACAGCAAGGTGCTGTG CG GCAGAGCATTGGGGTCTCAAAGAAGCAGGTGA <p style="text-align: center;">+77</p> GCCTGGGCC CG AGGGGCTGGGTGGAGGAGCACCTTGGTGCTTCTCTGCTG

CD14

NC_000005 REGION:
140012391..140012819
(complement)
gene ID: 929, updated
on 09-06-2012

GGAGGGAAC TGAATGACATCCCAGGATTACATAAACTGTCAGAGGCAGC **CG**AAGAGTTTACAAGTGT
+516
+547 +550 +557 +598
GAAGCCTGGAAGC **CGGCG**GGTGC **CG**CTGTGTAGGAAAGAAGCTAAAGCACTTCCAGAGCCTGTCC **CGG**
+613 +625 +654 +658 +660
AGCTCAGAGGTT **CG**GAAGACTTAT **CG**ACCATGGTGTAGTGTAGGGTCTTGGGGT **CGAA** **CGCG**TGCCAC
+669 +724 +726 +728
T **CG**GGAGCCACAGGGGTGGATGGGGCCTCCTAGACCTCTGCTCTCTCCCCAGGAG **CGCGCG**TCCTG
+755 +765 +773 +779 +801
CTTGTGCTGCTGCTGCTGCTGC **CG**CTGGTGCA **CG**TCTCTG **CG**ACCA **CG**CCAGAACCTTGTGAGCTGGAC **CG**
+814 +819 +834 +846 +855
GATGAAGATTTCC **CG**CTG **CG**TCTGCAACTTCTCC **CG**AACCTCAGCC **CG**ACTGGTCC **CG**AAGCCTTCCAGT
GTGTGTCTGCAGTAGAGGTGGAGATCC

PDK4

NC_000007 REGION:
95225885..95226284
(complement)
gene ID: 5166, updated
on 08-16-2012

CCCTGCTCTGAGCAAGGACCAATGAGCA **CGCG**GAGTCCAACTCTTGGAAACAGTTTGTGGCCAGGA
-333 -331
GTACTTGACATTGAGACAGCCTCC **CG**AGTTGTAACAAGGG **CG**AGCCTGGG **CG**GGACCCAGCCCA **CG**
-271 -254 -244 -229
-227 -222 -214 -186
CGACT **CG**GAGCCC **CG**TCCAAGAGGCTAATCTTAAGCCCA **CG**TTGCCCCAGATACCTGTTTCTGCTT
-131 -122 -120 -113 -97
CCTCTTCCCTGTTCTTCCCACCTTTTTTC **CG**TCACAGC **CGCG**GGCAC **CG**GTGCCAGGGCACTC **CG**TG
-88 -64 -62 -50
GTCAC **CG**TGCCAGGCCATTCTGTGATGAC **CGCG**GCTGGAGGGG **CG**GAGCCCATAGTTCTTTCTCTGA
-17 -15 +3 +5
TCTGATTGG **CGCG**ACCTGGAGTTCAGGA **CGCG**TTTCCAAGTTCAGTGACTCCTCCTGTTTGGGA

FADS1

NC_000011 REGION:
61584453..61584871
(complement)
gene ID: 3992, updated
on 08-25-2012

CTGCAACTTTCAAGGGCTCTCAGGCTGCTACTT **CG**GGCAGCACAATTGG **CG**GCA **CG**AGTGGCAAGC
-310 -294 -289 -286
AGGCAGTAGTTTCCAACCCTGGAGGGTCAG **CG**TCTGGAGACCC **CG**GCCAAGGCATCCACAGCCTAAA
-246 -233
GATGATGTC **CGCG**AC **CG**CC **CG**GGCAGCCT **CG**TGCA **CG**GAAAACCTCAACCC **CG**GCCC **CG**CCACCC
-200 -198 -194 -190 -180 -174 -157 -151
TTCTTG **CG**GCCACCC **CG**CAGCCCTGGCCCTCAGTCCATTCACTCCTGCAG **CGCG**GCCC **CG**CACCCA
-136 -127 -91 -89 -83
GGCCTGCACTAGAAC **CG**CTGTTCTTAC **CGCG**GG **CG**CCCCCTGGGAGCCAA **CG**CC **CGCG**ATGCC **CG**CCCT
-59 -47 -45 -42 -25 -22 -20 -13
GAC **CG**TCAGGAAGT **CG**AAATC **CG**GG **CG**GG **CG**CCCTTTAGGGAGCC **CGCG**AGGGGG **CGCG**TGTTGGCAGC
-6 +6 +12 +15 +18 +21 +36 +38 +46 +48
CCAGCTGTGAGTTGCC