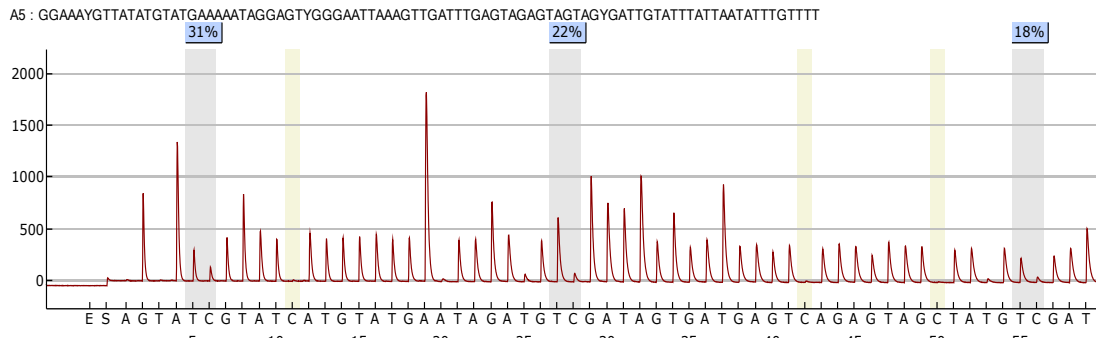


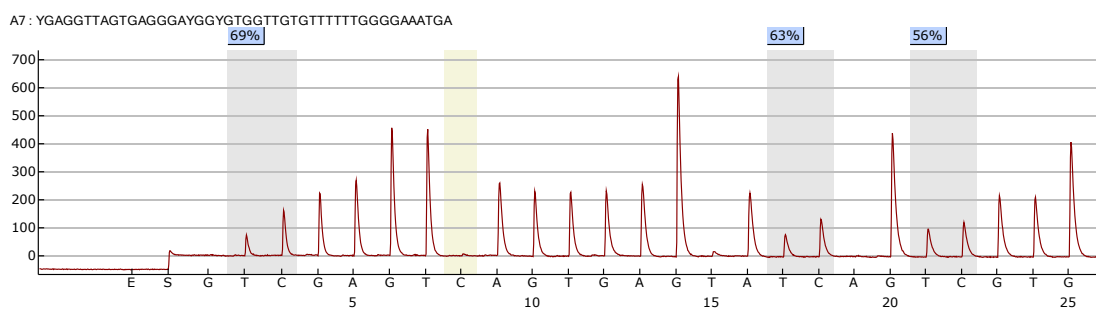
PPARGC1A

5'-AAGGCACCCTAAGGCAGTTAGGGAGGAAACCGCTACATGTATGAAAAATAGGAGCCCGGG
#1 #2
AATCAAAGCTGATCTGAGCAGAGCAGCAGCGACTGTATTTACTAACACTTGTTTTCTGGGA
GCCTATGAGAGAAATGAAATAATTAGAAGGAAGCTGAAAGGATGGGGTTTTGTGGCTTGT
#3
TCTCCTTATATGGAGCAAAGAAAAGTGCAGCAACTCTTCGGGGAGCTGGTATTCCCTACTGC
#4
CATGGGGGCAGCCCGAATTCTGGGTGGAGGAGTTTGTTTATACCTT-3'
#5



IGF2

5'-AAGGAGGGGGCCCCAGCAAAGCCACTGGACACACAGCTCTGCTTGACGAGGCCAGT
#1
GAGGGACCGGCGTGGCTGTGCTTCCTGGGGAAATGAACCCCTCCCCACAGACACCACCC
#2 #3
TGGGTGGATCGAGGAGTCTGGGTCCAGGGTGAACAGAGAAAACTTCATGCATGAATGA
#4
GCATTCCCAGGGAAACTGCCTTGGCCCCAGGGCGCCTCTCTGTGCCAGGGAGGCTGGGA
#5
GAGCAGCAAGGGGGACCAGGTGCGCCATCAGGAGGAGAGAAGCTAAACCTAGGGGGGAC
ATGGAG-3'



Supplement Figure 1. The wild-type DNA sequence and methylation target sites of the *PPARGC1A* and *IGF2*. The upper graph shows three methylation sites (**#1, #2, and #3**) in the promoter of *PPARGC1A* assessed in this study. The lower graph shows three methylation sites (**#1, #2, and #3**) in the *IGF2* DMR0 assessed in this study.