

Supplement

Supplemental Table 1: Primer sequences used for qRT-PCR

<i>Amplicon Name</i>	<i>Forward Primer Sequence</i>	<i>Reverse Primer Sequence</i>
18S	ATCGGGGATTGCAATTATTC	CTCACTAAACCATCCAATCG
5.8S	N/A (Qiagen RT ² Primer Assay #330001 PPH82091A)	
ABRA	CCAGGTAAACAGATTTACA	AGCTCGTAATCAACTCTTC
ANGPTL2	GAGAGCGAGTATTATAAGC	CAGTTTCTGTGTAGACATC
AXIN1	CCGACCTTAAATGAAGATGAG	CAGGATCCATACCTGAACTC
B2M	AAGGACTGGTCTTTCTATC	GATCCCACTTAACTATCTTG
FBXO32	AACTCAGTATTTCCACCAAG	GAAGTCCAGTCTGTTGAAAAG
MSTN	TGAATCCGTTTTAGAGGTC	CAAAATCCACAGTTAGAGGG
MYF6	CAAGTGTTCGTCATTCC	AGTTACTTCTCCACCACTTC
MYOD1	AATAAGAGTTGCTTTGCCAG	GTACAAATCCCTGTAGCAC
MYOG	AATTGAGAGAGAAGAAGGG	AACAACACACGAAACAAAAC
PGC1 α exon 1a	TGTATGGAGTGACATCGAGTGT	GCTGGTCTTCACCAACCAGA
PGC1 α exon 1b	GACACACATGTTGGGGTTATCA	ACCAACCAGAGCAGCACATTT
PGC1 α total	GTGGTGCAGTGACCAATGAG	CTGCTAGCAAGTTTGCCTCA
SETD3	GCTAAAAATTCAGTGTGGG	AGGAGTGTCATATTCAGTGG
SPRYD7	GCACATGGGGTATTACTTA	GAGGCGTATAGATAAAAACCTC
TGFB1	AACCACAACGAAATCTATG	TCATTCATCCAGCTCCTTAC
TRAF1	TCAGATCTGCCCAAATG	GAGCCTTCTCCTGAGTTC
TRIM63	GACAGATGAGGAAGAGGAA	CTTTTAACTTGAGCCTCAGC
UBR5	TTACAAGCAAATCCAGAAG	CTCTCCAGCAAATAAGATTC

ABRA, actin-binding Rho-activating protein; ANGPTL2, angiotensin-related protein 2; AXIN1, axin 1; B2M, β 2-microglobulin; FBXO32, atrogin-1 F-box only protein 32; MSTN, myostatin growth differentiation factor 8; MYF6, myogenic factor 6 (myogenic regulatory factor 4); MYOD1, myogenic differentiation antigen 1; MYOG, myogenin; PGC1 α , peroxisome proliferator-activated receptor γ coactivator 1 α ; SETD3, SET domain-containing 3; SPRYD7, chronic lymphocytic leukemia deletion region gene 6 protein; TGFB1, transforming growth factor β 1; TRAF1, TNF receptor-associated factor 1; TRIM63, E3 ubiquitin-protein ligase; UBR5, HECT E3 ubiquitin ligase.

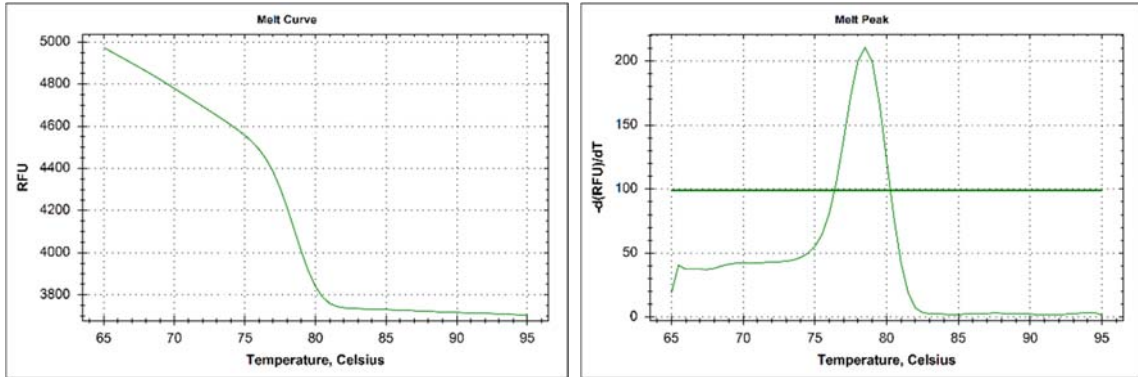
Supplemental Table 2: Primer sequences used for methylation analysis

<i>PGC-1α methylation site</i>	<i>Forward Primer Sequence</i>	<i>Reverse Primer Sequence</i>	<i>Sequencing Primer Sequence</i>
site 1a	TTGGAGTTGAAAAAGTTTGA	CCCCCTTACAAAAATAATAACAT	GGAGTTGAAAAAGTTTGATT
site 2a	GTATTTTTTATTGTTATGGGGGT	AATCCCCTACAATCTTTTTTTT	ATTGTTATGGGGGTAG
site 2b	GAGAGAAATGGAAATAATTAGAAG	CTCCAAATAAACTCAAACCTCAAT	GGAGTAAAGAAAATTGTAGTAAT
site 3b_1	AGTGGTTTGGTTGGAAAAAT	ATAAACTCTATTCTCTCTCAAC	GTTGGAAAAATGTTATTTTTATTTA
site 3b_2	*same as 3b_1	*same as 3b_1	TTAGATGTTTTTTTTATAGAATAT

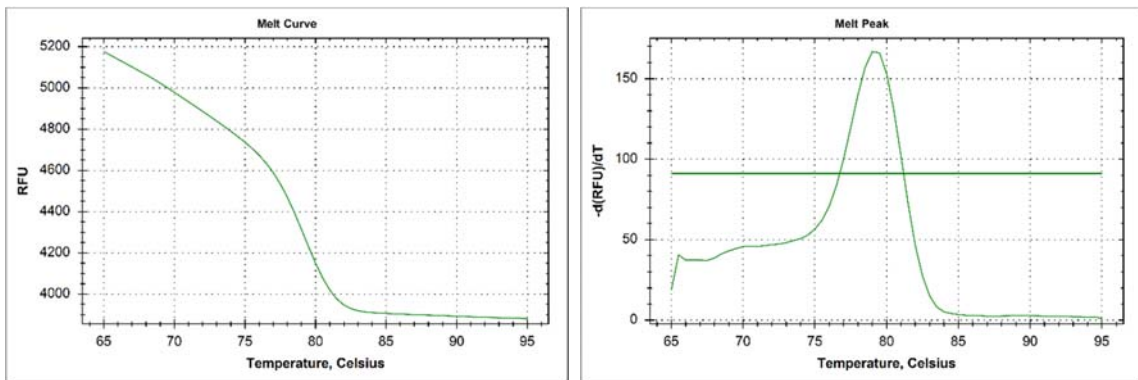
Primer sets for selected peroxisome proliferator-activated receptor γ coactivator 1 α (PGC1 α) methylation sites were identified through the use of the H3K4me3 mark track in the GRCh37/hg19 assembly of the UCSC Genome Browser. Site 1a was designed to be in the immediate coding sequence area, sites 2a and 2b were located upstream of the transcription start sequence (TSS), and sites 3b_1 and 3b_2 were located downstream of the TSS.

Supplemental Figures: Melt curves and melt peaks for genes that exhibited different expression between the memory and control leg (illustrated in Figure 2 and Figure 3)

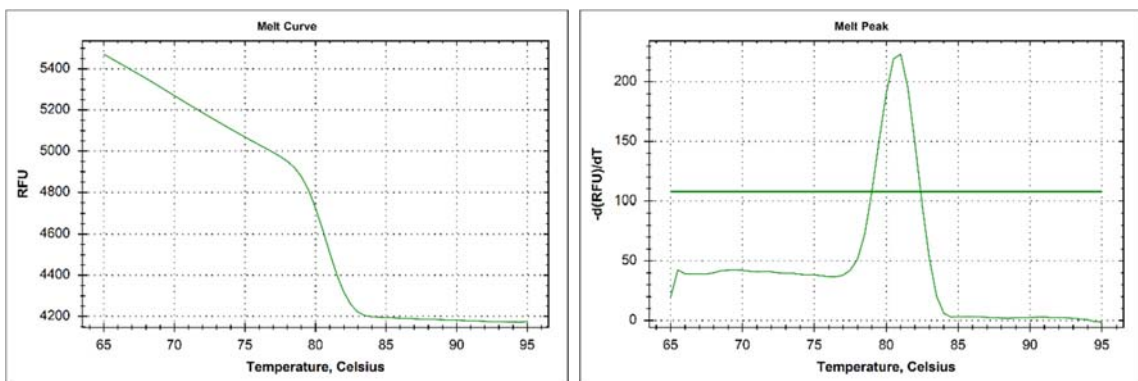
PGC1 α total



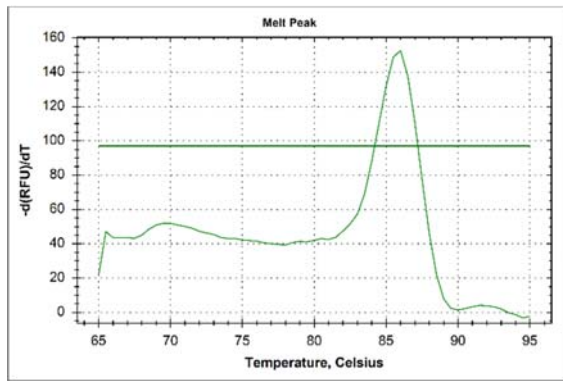
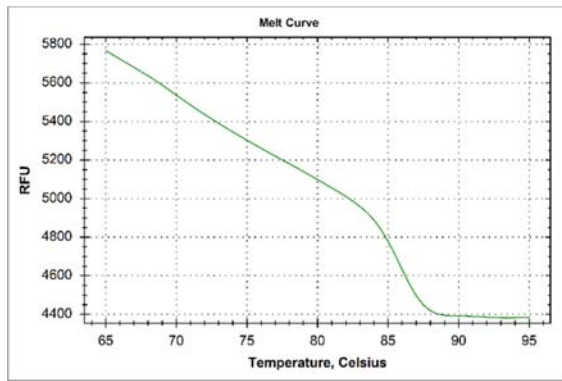
PGC1 α ex-1a



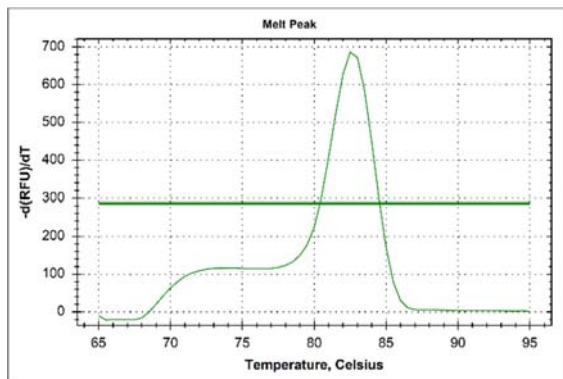
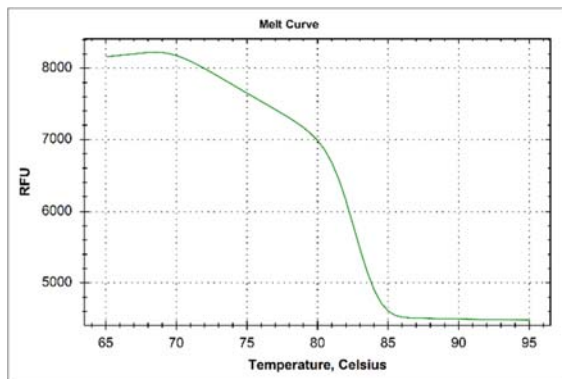
SPRYD7



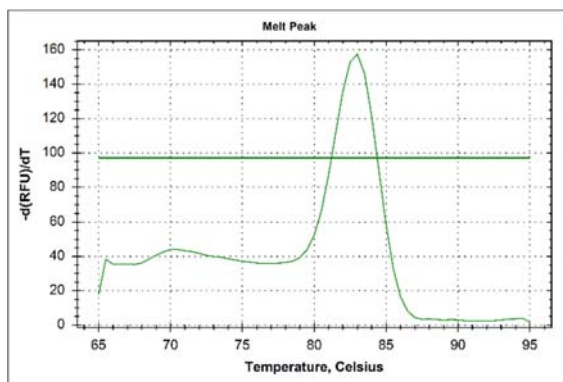
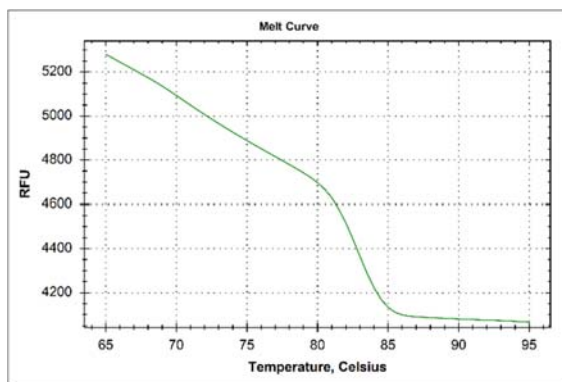
ANGPTL2



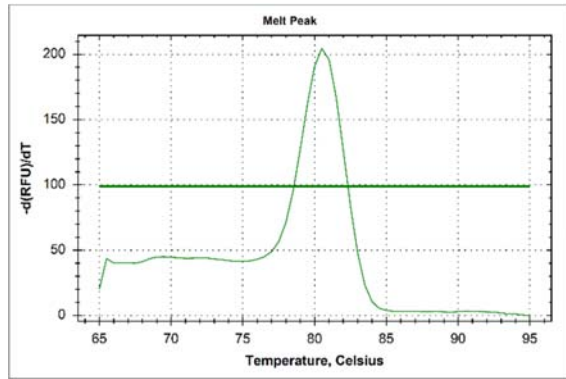
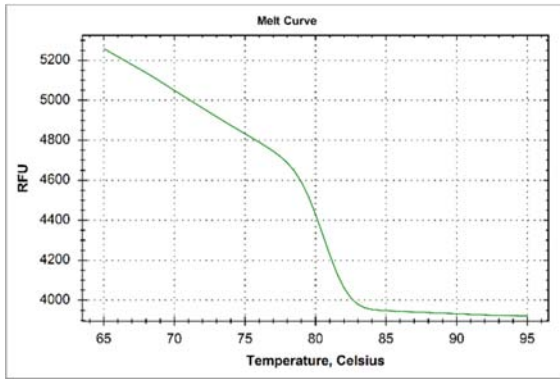
MYOG



MYOD1



FBX032



SETD3

