Supplementary Table S1: Summary pilot DNA methylation data a 3 genes and 7 CpG sites. Summary data come from 46 adult males and females. All sequences taken from

Gene	**AgRP**	**AgRP**	**AgRP**	**AgRP**	**Mc1r**	**Mc1r**	**Tyr**
Ascension number:	EF571203 EF571163	EF571203 EF571163	EF571203 EF571163	EF571203 EF571163	EF571037	EF571037	EF571128
CpG site	CC*GA	CCCC*GGGG	CCCC*A	TTC*G	GGC*(-58)	AACCTT	TTGGC*G
Mean % DNA methylation	0.17	0.62	0.95	1	1	0	0.82
Standard deviation	±0.33	±0.08	±0.14	±0	±0	±0	±0.08
Range	0-100%	50-80%	50-100%	-	-	-	65-95%

Supplementary Table S2: PCR and pyrosequencing primers

PCR primers	Forward -AGCCAGGAAAGCCCCTCTGTTT	Reverse -GCCAGACTTGGATCAGATGGAGGTGCAT
Pyrosequencing primers	CAGGCTCCTCTGTGCCC	GAAGGTGATGGTAACCTCCTGCAG

Supplementary Table S3: Pairwise correlation matrix of DNA methylation at each CpG site

	Site 1	**Site 2**	**Site 3**	**Site 4**
Site 2	r=-0.42, *P*<0.001			
Site 3	r=0.20, *P*=0.011	r=-0.10, *P*=0.224		
Site 4	r=-0.22, *P*=0.005	r=-0.09, *P*=0.256	r=0.16, *P*=0.048	
Site 5	r=-0.01, *P*=0.936	r=0.09, *P*=0.271	r=0.09, *P*=0.265	r=0.38, *P*<0.001

Table S4: Samples sizes of males in each age group and the number samples for that age that were also sampled in young age groups.

	1 year old	**2 years old**	**3 years old**	**4 years old**	**5+years old**
Total N males	86	32	25	14	13
N males that are sampled in earlier age groups	-	27	20	13	5