

Supplementary Table 4. List of primers used for pyrosequencing analyses

Gene		Primer (5'– 3')
<i>APOD</i>	Forward	AGATGAAGGTAGTTTTAGATGTAGA
	Biotinylated-reverse	AATAAACACAACATCCCATCTTTATA
	Sequencing primer	GTTTTGATGTTTATTTTTATGTAT
	Sequences to analyze*	GTTAYGTTYGT <u>Y</u> GTTTTTA
	Position	GRCh38/hg38 [chr3:195,584,008–195,584,026]
<i>FAP</i>	Forward	TTTGGTTTTAAATGAATTGTGAGTGAT
	Biotinylated-reverse	ACCCAATAACTTACTAAAATAATCCTTC
	Sequencing primer	ATTTTGTAAATTATTAATATTTG
	Sequences to analyze*	TTTAYGTTG
	Position	GRCh38/hg38 [chr2:162,243,611–162,243,619]
<i>LITAF</i>	Forward	GGGAGTGAATTGGGAAGATGGTA
	Biotinylated-reverse	AAATAAACTACTAATTTCCAAACTTACT
	Sequencing primer	ATTAGTAAGGTTTATTAGTTG
	Sequences to analyze*	TTTGTTYGTTTTGTGTTTTAGGGTGGT <u>Y</u> GTGYGTTA
	Position	GRCh38/hg38 [chr16:11,587,597–11,587,635]
<i>NUPR1</i>	Forward	TTAGTTGGATATTTTTATAGAGGAGGTTT
	Biotinylated-reverse	AAATCCTACCTCTCCCTACTTT
	Sequencing primer	TAGTTGGATATTTTTATAGAG
	Sequences to analyze*	GAGGTTYGTTTT <u>Y</u> GGTA
	Position	GRCh38/hg38 [chr16:28,539,190–28,539,208]
<i>SORT1</i>	Forward	TTGTAAGAAGGTGAATGAGAATTGATGTG
	Biotinylated-reverse	CTTTAACCTACCTCCCTCAA
	Sequencing primer	ATTTAAGGAGATAGATATTAGGAT
	Sequences to analyze*	ATTYGTGATTTTTGTAAGTTGAAGAATAGTTTTTTATAYGTTT
	Position	GRCh38/hg38 [chr1:109,398,539–109,398,583]

APOD, apolipoprotein D; *FAP*, fibroblast activation protein alpha; *LITAF*, lipopolysacchride induced tumor necrosis factor-alpha factor; *NUPR1*, nuclear protein 1; *SORT1*, sortilin 1.

*The specific CpG sites used for data analysis are underlined.