## 1 2 SUPPLEMENTAL MATERIAL

# 3 SUPPLEMENTARY METHODS

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# 5 Quality control of the samples analyzed with the Illumina MethylationEPIC

#### 6 BeadChip

7 We removed the samples with a detection p-value>0.05 in at least 1% of the probes

- 8 using the pfilter function of the wateRmelon R package available through the
- 9 Bioconductor repository. We also discarded those samples that did not cluster in the
- 10 correspondent sex cluster based on the DNA methylation levels in the X chromosome
- 11 using methylumi R package available through the Bioconductor repository.
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13 Quality control of the CpGs analyzed with the Illumina MethylationEPIC

## 14 BeadChip

15 We excluded those probes with both a detection p-value>0.05 in at least 1% of the

samples and a beadcount < 3 in at least 5% of the samples using wateRmelon R

17 package available through the Bioconductor repository. We further removed those

18 probes reported by Illumina to be discarded due to underperformance (n=1,031) and

changes in the manufacturing process (n=977). Also, we excluded those probes

20 corresponding to a methylation site different from a CpG site and those that could

21 hybridize in more than one genomic region (n=43,979).

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### 23 SUPPLEMENTARY RESULTS

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#### 25 Quality control of data

- 26 In the secondary analysis considering BMI as a covariate, due to missing data, we
- used 617 participants from the discovery sample, and 1,732 and 190 from the
- validation samples (Framingham and REGICOR, respectively).
- In the sensitivity analyses, we did not discard the individuals with TPA=0. In the
- 30 sensitivity analysis of the main analysis (without BMI as a covariate), we included 643
- individuals from the discovery sample, and 1,737 and 192 from the validation samples
- 32 (Framingham and REGICOR, respectively). In the sensitivity analysis considering BMI
- as a covariate, we included 641 individuals from the discovery sample, and 1,734 and
- 192 from the validation samples (Framingham and REGICOR, respectively).