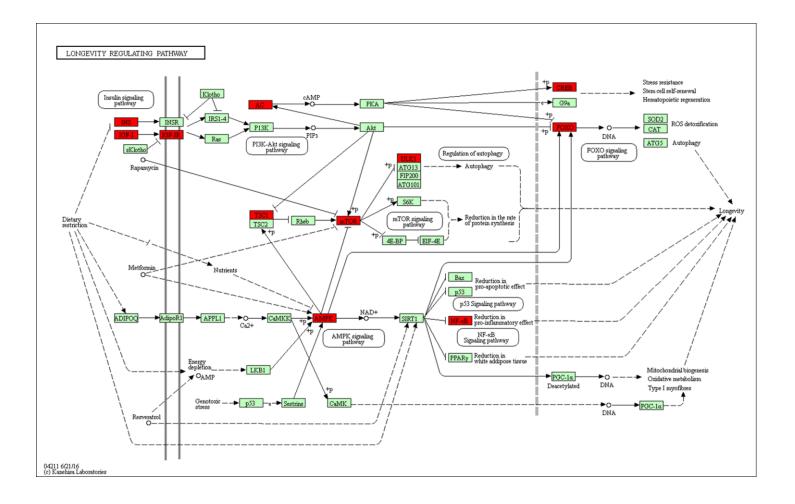
SUPPLEMENTARY FIGURES

DNA methylation assay from white cells Infinium Human Methylation 450 K bead chip (n=474) Hypermethylated 5725 Hypomethylated Whole genome differentially methylated regions correlated with BMI (13,268 CpGs) CpG sites with a FDR-adjusted involved 58 CpGs "Longevity-regulating pathway" p-value <0.0001 CpG sites differentially methylated between young 25 CpGs (<45 y) and older subjects (≥45 y) 15 CpGs 12 CpGs 13 CpGs CpG sites differentially methylated in older subjects 11 CpGs (≥45 y) and/or in presence of metabolic disturbances Insulin **Abdominal** High Metabolic Obesity Cholesterol Resistance Syndrome Common CpG sites for metabolic traits MTOR (cg08862778) ADCY6 (cg11658986) IGF1R (cg01284192) CREB5 (cg11301281) RELA (cg08128650)

Supplementary Figure S1. Scheme of CpG selection process for the analyses.

ULK1 (cg07199984)



Supplementary Figure S2. Longevity Regulating Pathways genes. Red boxes correspond to those CpG sites differentially methylated associated to older subjects and the presence of metabolic disturbances. Diagram modified from KEGG Database.