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Title: A DNA-methylation framework of immunometabolic dysfunctions

Abstract: DNA methylation is an epigenetic modification that plays a role in the regulation of gene expression. Using data from the 'Framingham Heart Study' cohort, we constructed a DNA-methylation model that represents the spectrum of DNA-methylation states of Metabolic Syndrome (MetS), ranging between metabolically healthy to abnormal immunometabolism. Additional analyses indicated that this computational model captures DNA-methylation states that are linked to cardiovascular disease, aging, and immune responses. We showed that the DNA-methylation model is relevant at the cell-intrinsic level in both innate and adaptive immune cells. Overall, this framework provides a robust tool for investigating immune dysfunctions and cardiovascular disease.