LETTER TO THE EDITOR

Epigenetic age acceleration in hematopoietic stem cell transplantation

Authors

Margherita Ursi,[1,2] Katarzyna Malgorzata Kwiatkowska,[2] Chiara Pirazzini,[2] Gianluca Storci,[1] Daria Messelodi,[1] Salvatore Nicola Bertuccio,[1] Serena De Matteis,[1] Francesco Iannotta,[1] Enrica Tomassini,[1] Marcello Roberto,[2] Maria Naddeo,[1] Noemi Laprovitera,[1] Irene Salamon,[1] Barbara Sinigaglia,[1] Elisa Dan,[1] Francesco De Felice,[1,2] Francesco Barbato,[1,2] Enrico Maffini,[1] Sadia Falcioni,[1] Mario Arpinati,[1] Manuela Ferracin,[1,2] Massimiliano Bonafè,[1,2] Paolo Garagnani[1,2] and Francesca Bonifazi[1,2]

[1]IRCCS Azienda Ospedaliero-Universitaria di Bologna and [2]Department of Medical and Surgical Sciences (DIMEC) University of Bologna, Bologna, Italy

Correspondence:
MASSIMILIANO BONAFÈ - massimiliano.bonafe@unibo.it

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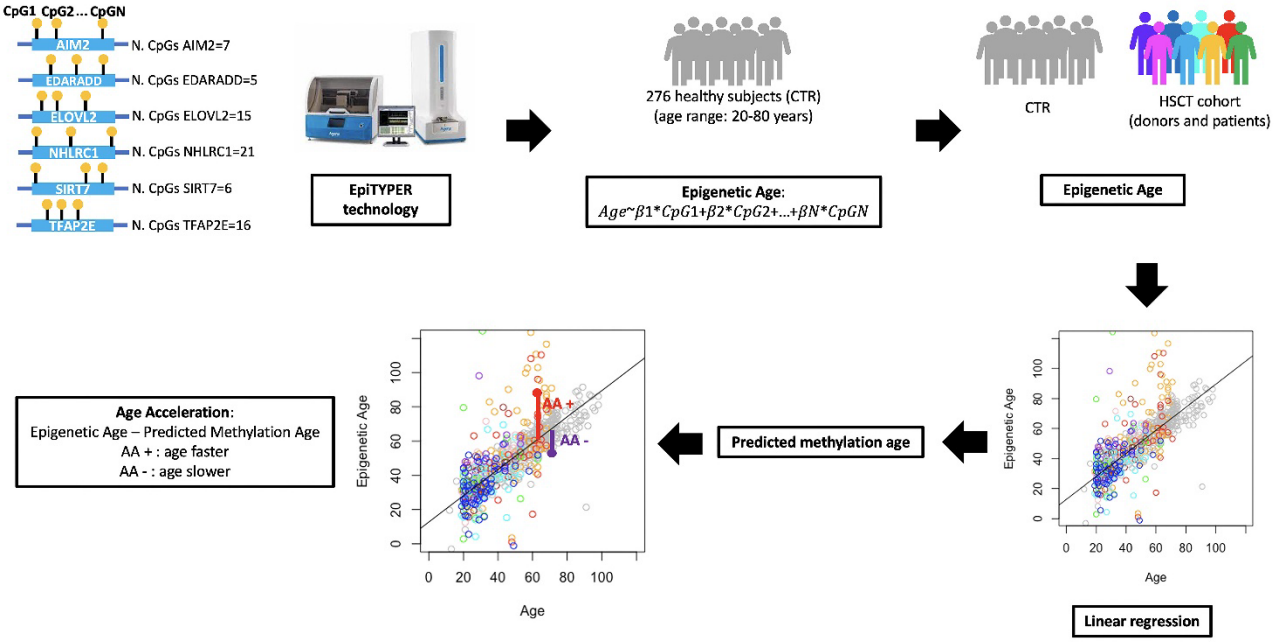
Supplementary Fig.1 Description of the method applied to estimate epigenetic age acceleration. tDNAMet is a targeted DNA methylation clock that includes 6 genomic regions (AIM2, EDARADD, ELOVL2, NHLRC1, SIRT7 and TFAP2E) identified by Gensous et al. by analyzing healthy subjects with a wide age range (20-80 years), accelerated- and decelerated-aging subjects (Down Syndrome and centenarians). Each selected region contains several CpG sites (total number: 70 CpGs) whose methylation level is assessed by EpiTYPER technology. We used our data previously generated on a cohort of 276 healthy subjects (CTR) and already described in Gensous et al. to generate a model to estimate Epigenetic Age. We applied the model to controls (CTR) and to the HSCT cohort to get Epigenetic Age for all of the subjects (controls, donors and patients). Then, we performed a linear regression analysis between chronological and epigenetic age to get the Predicted methylation age that we used to estimate Age Acceleration (AA = Epigenetic Age – Predicted Methylation Age).



Supplementary Fig. 2 Trajectory of individual patient change of AA over time.
2A Subjects who remained AA-
2B Subjects who shifted from AA- to AA+
2C Subjects who remained AA+
2D Subjects who shifted from AA+ to AA-