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Multiomics for lung cancer diagnosis

Molecular and Cellular Probes 66 (2022) 101873

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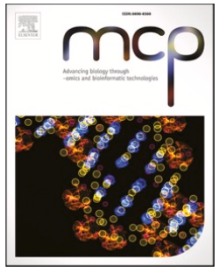
Molecular and Cellular Probes

journal homepage: www.elsevier.com/locate/ymcpr



A method for early diagnosis of lung cancer from tumor originated DNA fragments using plasma cfDNA methylome and fragmentome profiles

Yeo Jin Kim [a,1], Hahyeon Jeon [a,1], Sungwon Jeon [a,1], Sung-Hun Lee [a,1], Changjae Kim [a], Ji-Hye Ahn [a], Hyojin Um [a], Yeong Ju Woo [a], Seong-ho Jeong [a], Yeonkyung Kim [a], Ha-Young Park [b], Hyung-Joo Oh [b], Hyun-Ju Cho [b], Jin-Han Bae [a], Ji-Hoon Kim [a], Seolbin An [c,d], Sung-Bong Kang [a], Sungwoong Jho [a], Orsolya Biro [e], David Kis [e], Byung Chul Kim [a], Yumi Kim [c,d], Jae Hyun Kim [f], Byoung-Chul Kim [a,*], Jong Bhak [a,c,d,g,**], In-Jae Oh [b,***]

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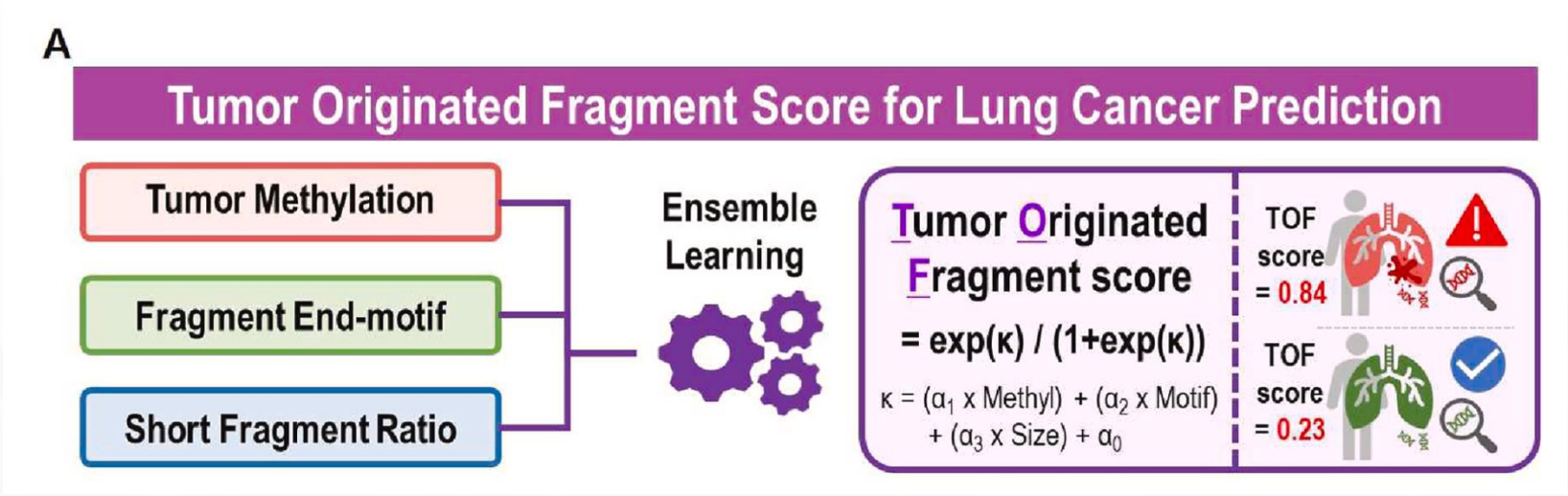
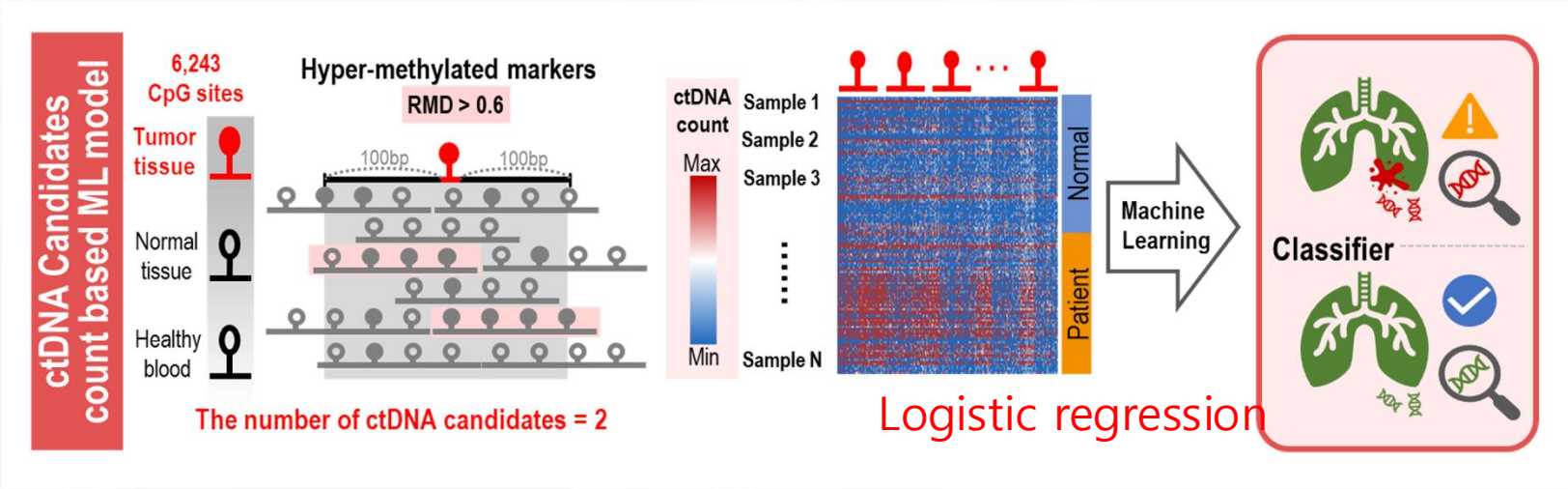
[g] *Personal Genomics Institute (PGI), Genome Research Foundation (GRF), Cheongju, 28160, Republic of Korea*

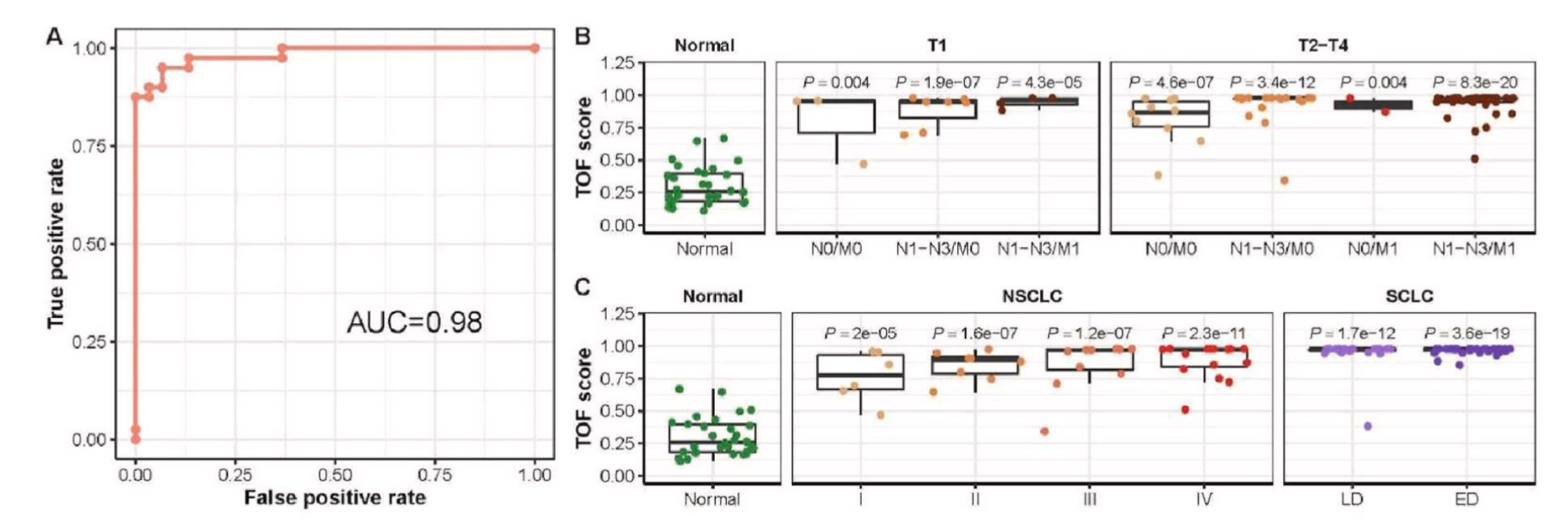
Multiomics for lung cancer diagnosis





Feature selection and AI model construction

Multiomics for lung cancer diagnosis



Overall performance (Accuracy) for diagnosis lung cancer (98%)

Ryu *et al. Clinical Epigenetics* (2024) 16:95
https://doi.org/10.1186/s13148-024-01708-9

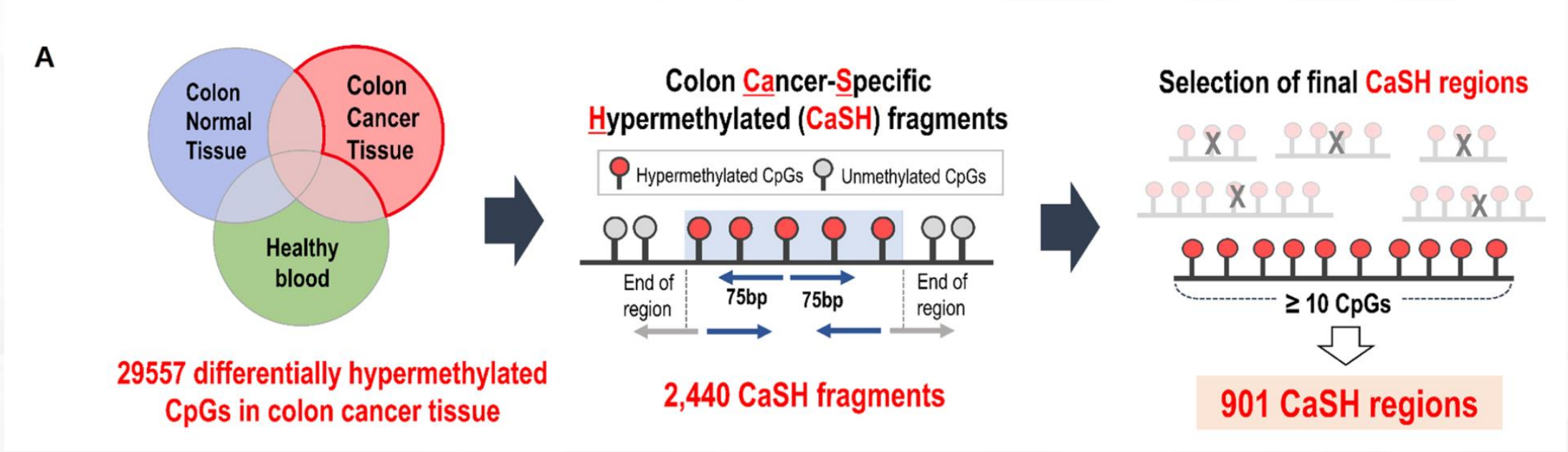
Clinical Epigenetics

RESEARCH Open Access

Quantification method of ctDNA using cell-free DNA methylation profile for noninvasive screening and monitoring of colon cancer

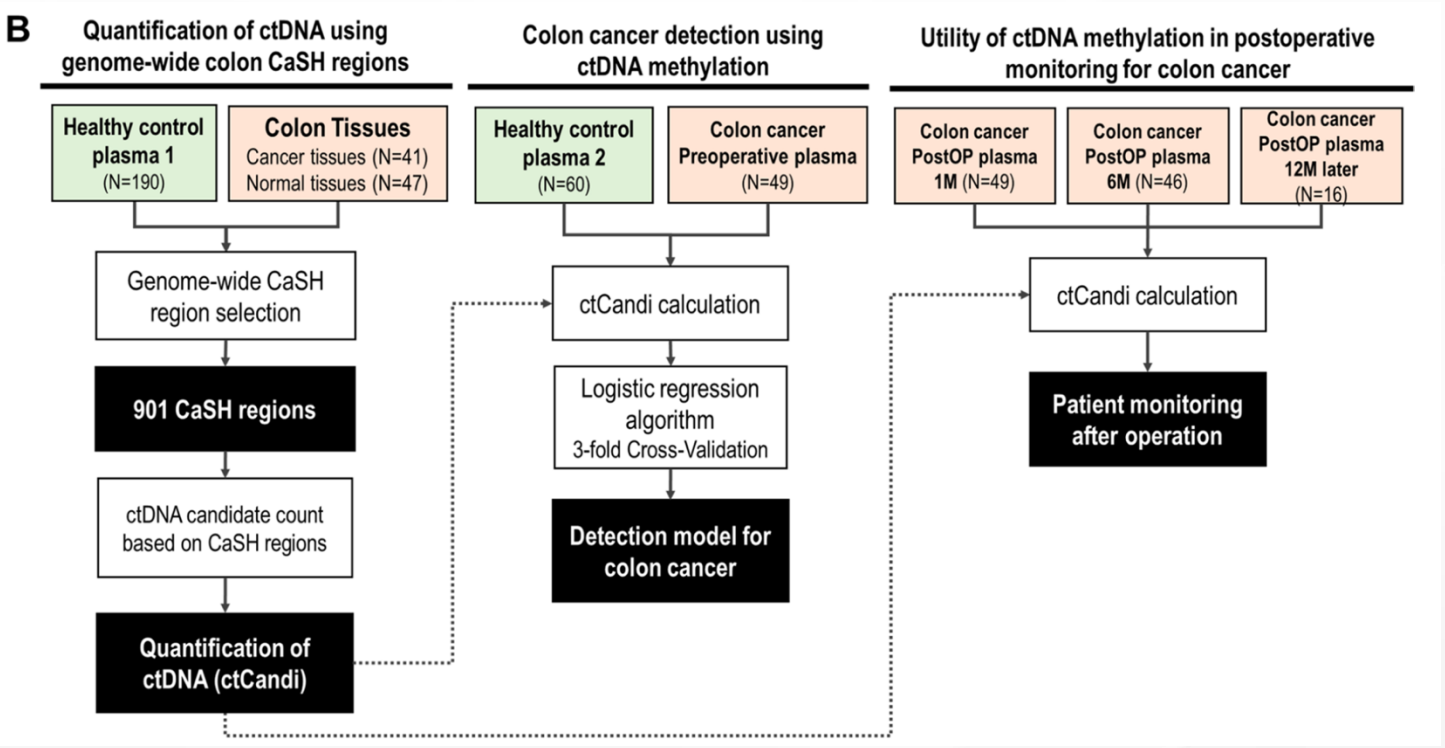
Hyojung Ryu[1†], Ji-Hoon Kim[1,2,3†], Yeo Jin Kim[1], Hahyeon Jeon[1], Byoung-Chul Kim[1], Yeonsu Jeon[1], Yeonkyung Kim[1], Hyebin Bak[1], Younghui Kang[1], Changjae Kim[1], Hyojin Um[1], Ji-Hye Ahn[1], Hwi Hyun[1], Byung Chul Kim[1], Inho Song[4], Sungwon Jeon[1,5*], Jong Bhak[1,2,3,5,6*] and Eon Chul Han[4*]

Multiomics for colon cancer diagnosis

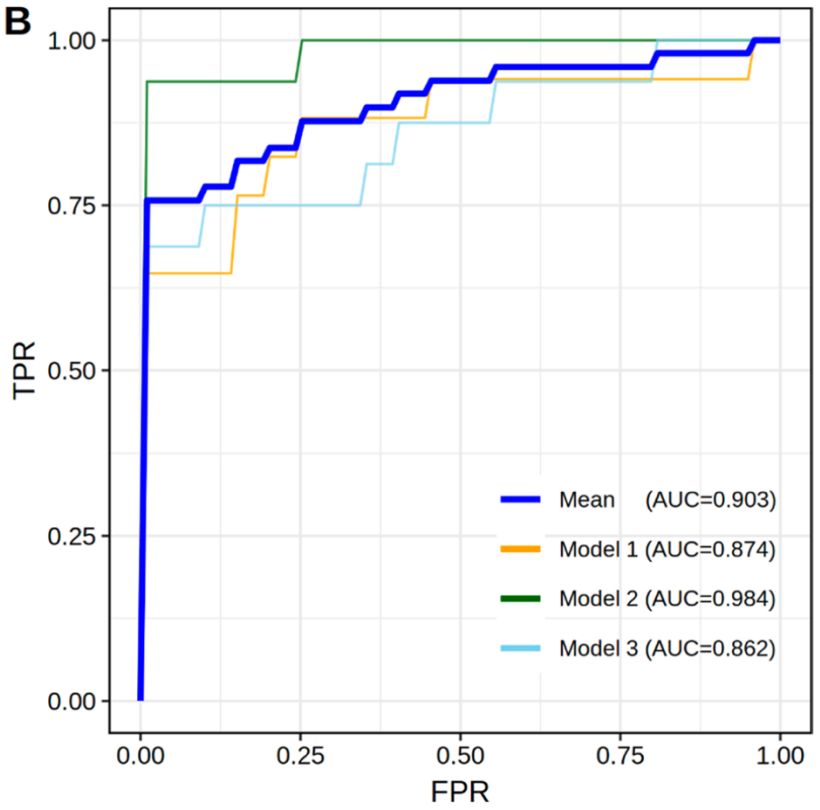


Feature selection for Colon cancer detection AI model

Multiomics for colon cancer diagnosis



Flow chart of the study design



Overall performance of the model (90%)

www.aging-us.com AGING 2025, Vol. 17, No. 6

Research Paper

Dynamic and reversible transcriptomic age shifts induced by COVID-19 in Korean whole blood

Kyungwhan An[1,2], Yoonsung Kwon[1,2], Jihun Bhak[1,2], Hyojung Ryu[3], Sungwon Jeon[3,4,5], Dougu Nam[6,*], Jong Bhak[1,2,5,*]

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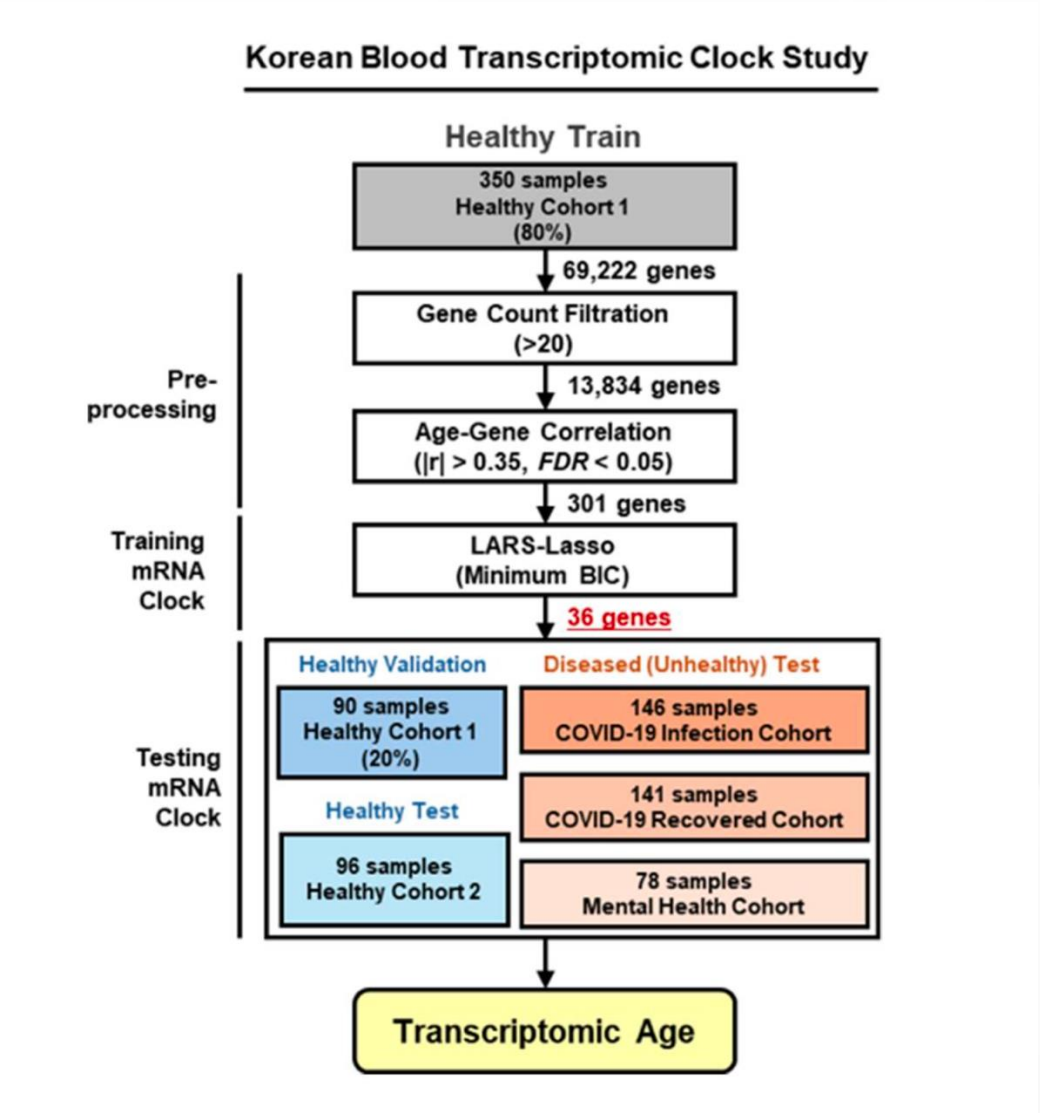
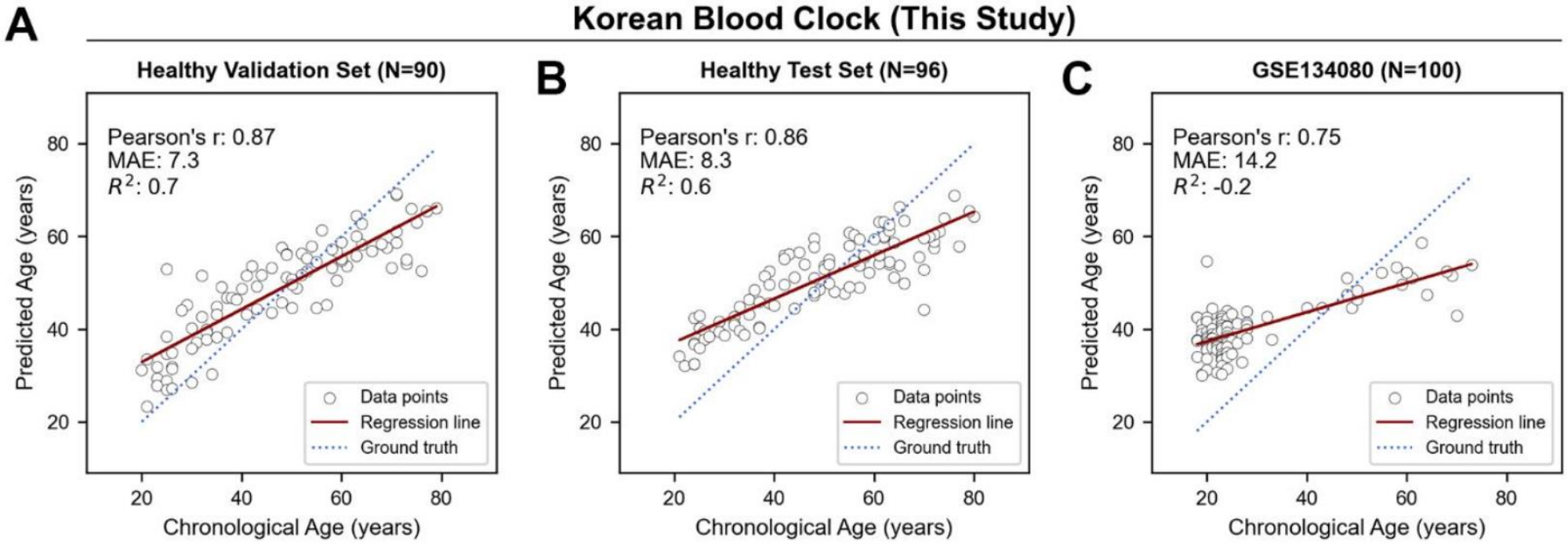
*Co-senior author

Multiomics for aging measurement



Aging measurement AI model training flow chart

Multiomics for aging measurement



Aging measurement correlation plot