

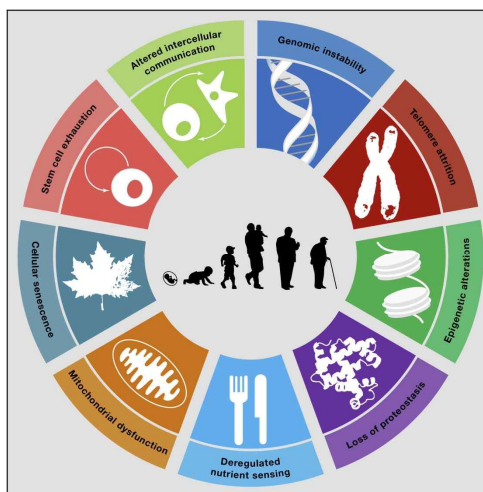


DNA methylation of the ELOVL2, FHL2, KLF14, C1orf132, and TRIM59 genes in blood, saliva, and buccal swab samples

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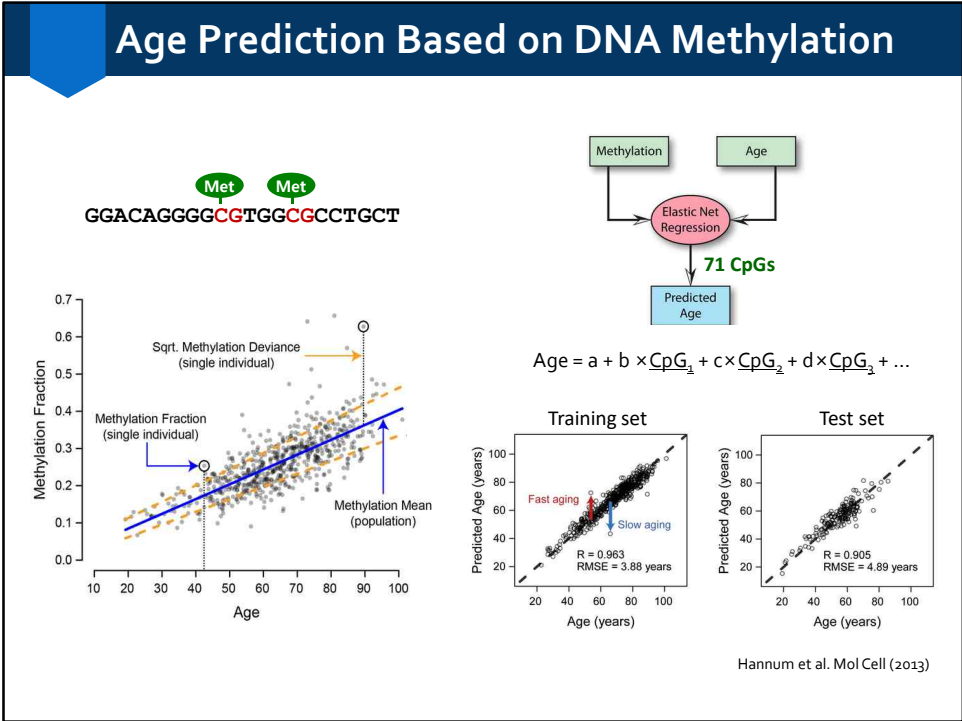
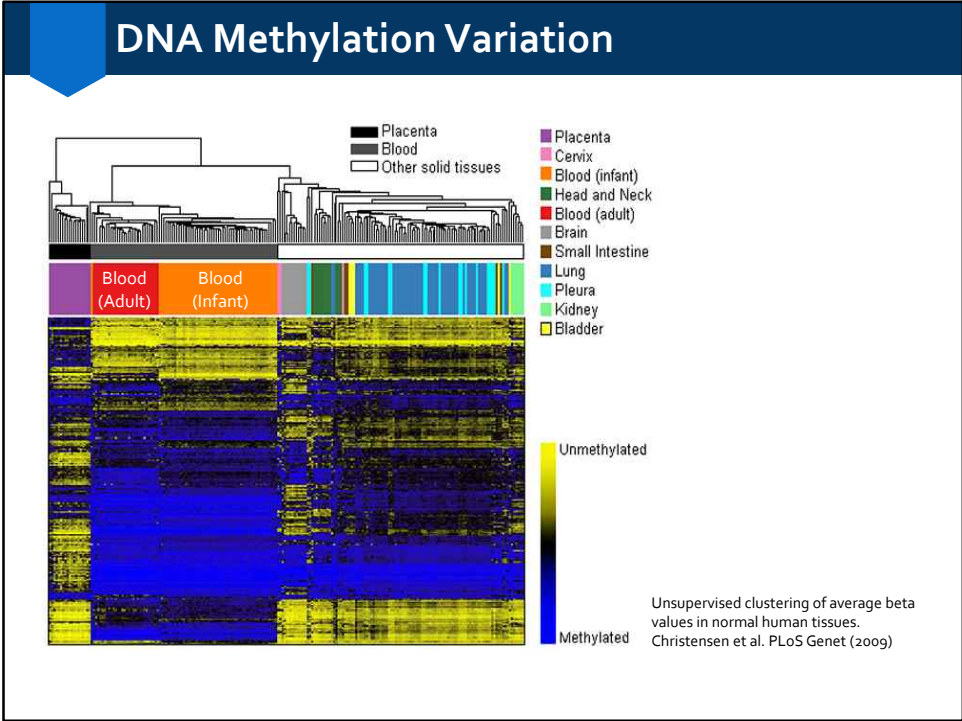
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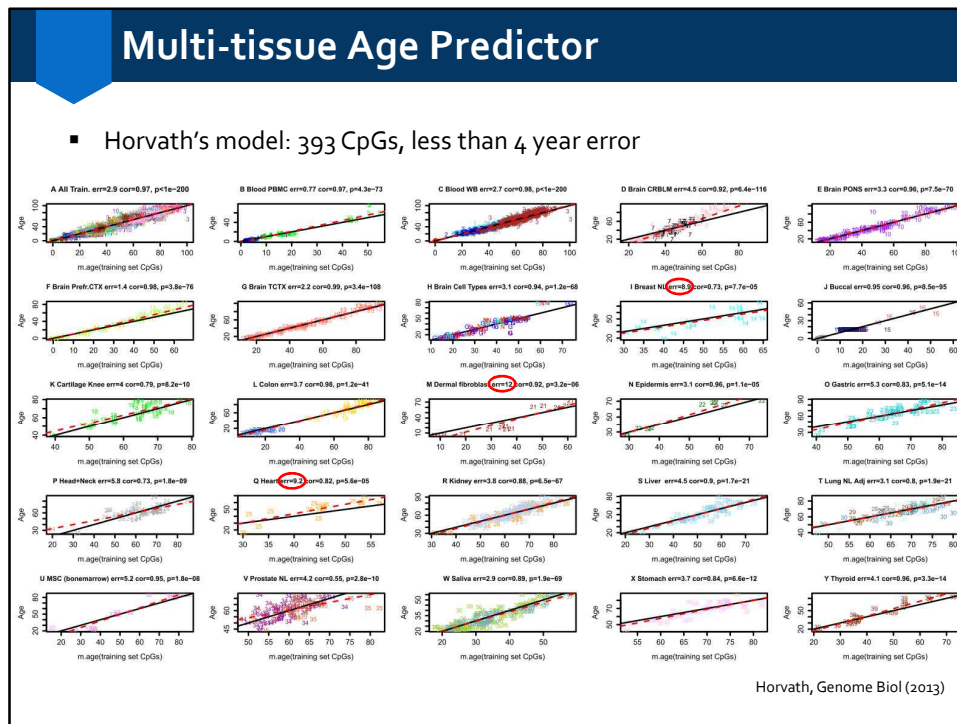
Nine Hallmarks of Aging



- Genomic instability
- Telomere attrition
- **Epigenetic alterations**
- Loss of proteostasis
- Deregulated nutrient sensing
- Mitochondrial dysfunction
- Cellular senescence
- Stem cell exhaustion
- Altered intercellular communication

López-Otin *et al.* Cell 2013



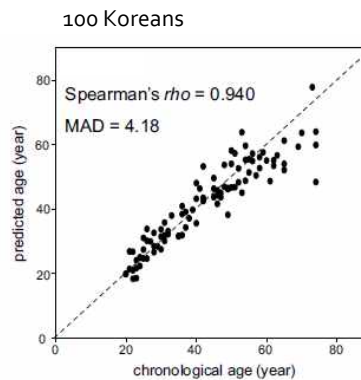
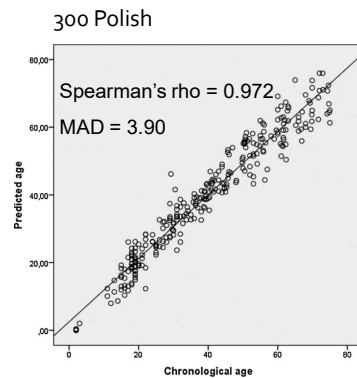


Tissue-specific Age Predictors

Sample	Model	Genes	No. CpGs	Error (y)	Platform
Blood	Weidner <i>et al.</i>	ITGA2B, ASPA, PDE4C	3	4-3	Pyrosequencing
	Zbieć-Piekarska <i>et al.</i>	ELOVL2	2	5.0	Pyrosequencing
	Zbieć-Piekarska <i>et al.</i>	ELOVL2, FHL2, KLF14, C1orf132, TRIM59	5	3-9	Pyrosequencing
	Park <i>et al.</i>	ELOVL2, ZNF423, CCDC102B	3	3-4	Pyrosequencing
Saliva	Bocklandt <i>et al.</i>	EDARADD, TOM1L1, NPTX2	3	5.2	27k array
	Hong <i>et al.</i>	SST, CNGA3, KLF14, TSSK6, TBR1, SLC12A5, PTPN7	7	3.1	SNaPshot
Semen	Lee <i>et al.</i>	TTC7B, NOX4, unknown	3	5.4	SNaPshot
Blood, teeth	Bekaert <i>et al.</i>	ASPA, PED4C, ELOVL2, EDARADD	4	4-9	Pyrosequencing
Teeth	Giuliani <i>et al.</i>	ELOVL2, FHL2, PENK	5-13	1.2-7.1	EpiTyper

Independent Validation of Blood Models

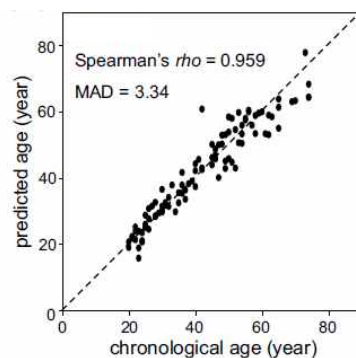
- Zbieć-Piekarska's model: *ELOVL2*, *FHL2*, *KLF14*, *C1orf132*, *TRIM59*
- Analysis platform: Pyrosequencing



Cho S et al., Forensic Sci Int Genet (2017)

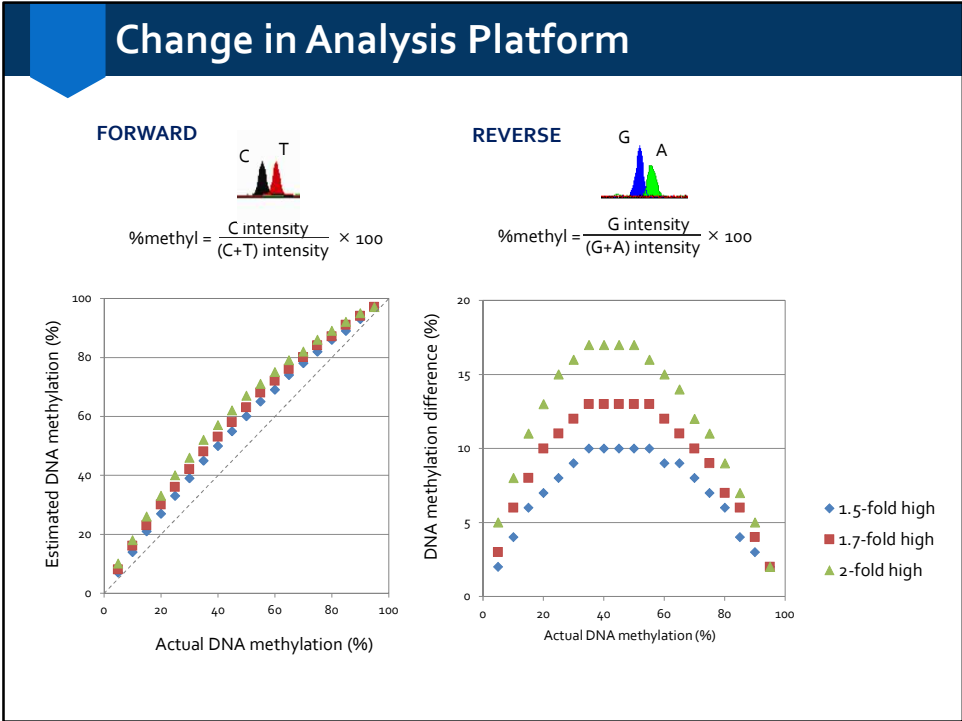
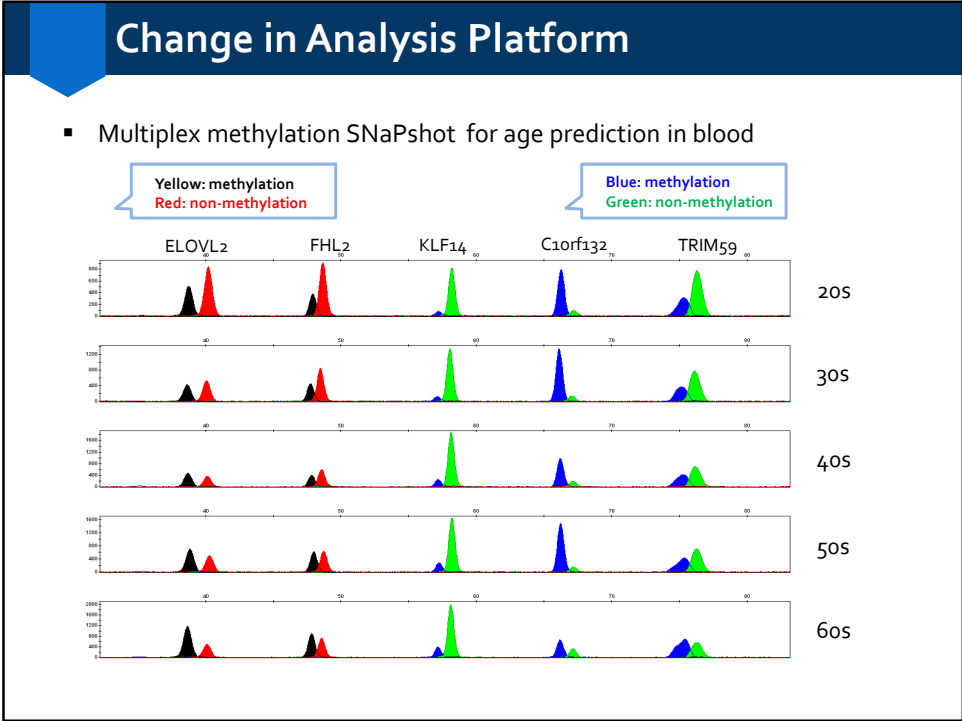
Independent Validation of Blood Models

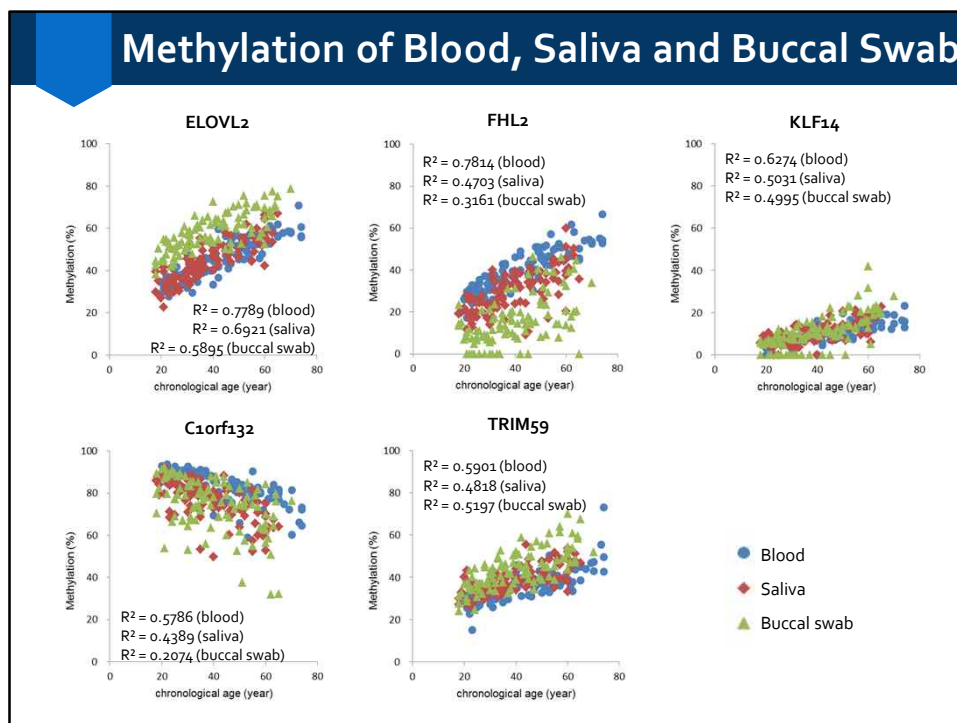
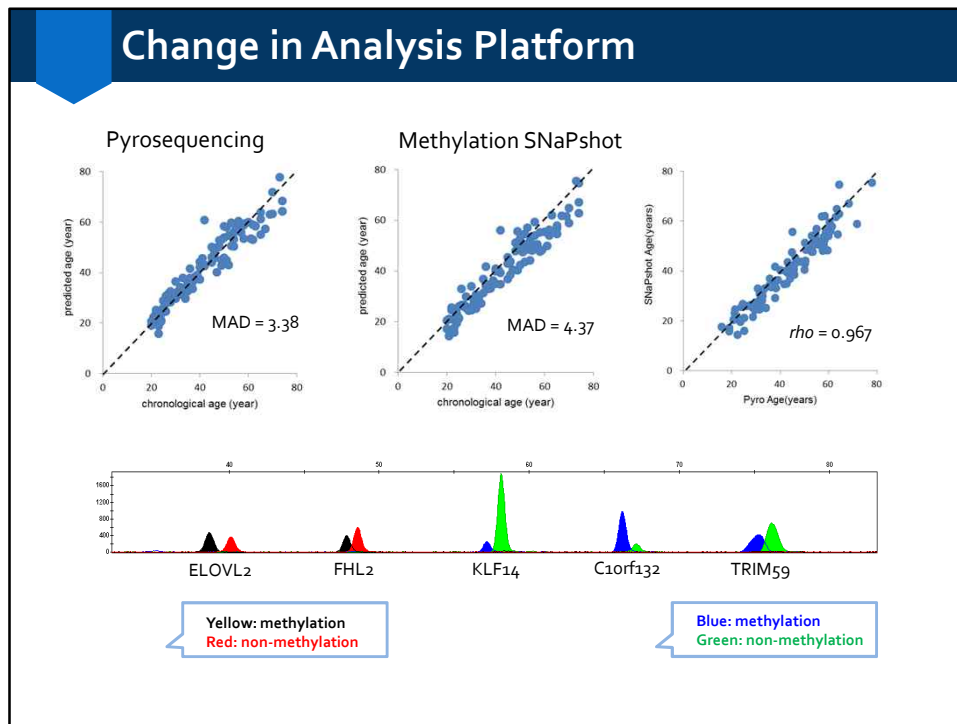
- Another model with 5 CpGs explaining the highest% of age variance in each gene



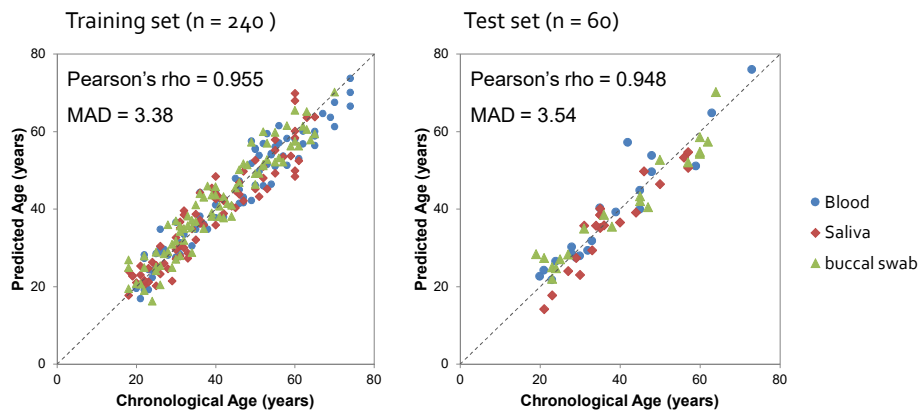
Gene	Target (GRCh37)	Coefficient
Intercept		-10.403
ELOVL2	6:11044861	0.612
FHL2	2:106015739	0.465
KLF14	7:130419116	0.330
C1orf132	1:207997026	-0.168
TRIM59	3:160167977	0.408

Cho S et al., Forensic Sci Int Genet (2017)





Age Prediction model



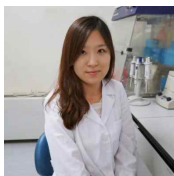
Summary

- DNA methylation at 5 CpG sites from the *ELOVL2*, *FHL2*, *KLF14*, *C1orf132*, and *TRIM59* genes was investigated in samples from blood, saliva, and buccal swabs using a multiplex methylation SNaPshot assay.
- An age prediction model trained on 240 samples including 80 of each blood, saliva and buccal swab samples exhibited high correlation between predicted and chronological ages with a MAD of 3.38 years.
- The model showed a MAD of 3.54 years in a validation set of 60 samples including 20 of each blood, saliva and buccal swab samples.
- These results suggest that these age-associated markers are less tissue-specific than others

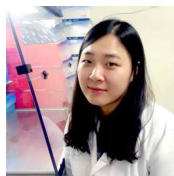
Acknowledgment



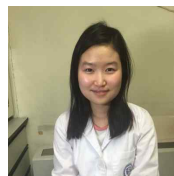
Kyoung-Jin Shin



Sang-Eun Jung



Eun Hee Lee



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Bomin Kim



Mi Hyeon Moon



SeungMin Lim



Yelim Kwon