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Table S2. Proportion of missing CpG sites in genomic feature (gene region feature from UCSC) for EPICv1 and EPICv2.

DNAm clocks Arrays	Horvath1		Horvath2		Hannum		PhenoAge		GrimAge		DNAmTL		DNAmFitAge		DunedinPACE		YingCausAge		YingAdaptAge		YingDamAge	
	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2
1stExon, <i>n</i> (%)	9 (29.0)	9 (39.1)	0	2 (7.7)	0	1 (11.1)	0	3 (7.1)	0	18 (9.2)	0	9 (23.1)	2 (16.7)	5 (3.7)	0	2 (9.1)	14 (6.7)	13 (12.3)	0	10 (10.4)	0	3 (3.8)
5'UTR, <i>n</i> (%)	8 (25.8)	5 (21.7)	0	1 (3.8)	1 (7.1)	0	0	10 (23.8)	0	26 (13.3)	0	4 (10.3)	2 (16.7)	15 (11.0)	0	1 (4.5)	29 (13.9)	13 (12.3)	0	24 (25.0)	0	20 (25.0)
Body, <i>n</i> (%)	1 (3.2)	4 (17.4)	0	15 (57.7)	5 (35.7)	5 (55.6)	0	8 (19.0)	1 (100)	103 (52.6)	0	19 (48.7)	4 (33.3)	75 (55.1)	0	17 (77.3)	98 (46.9)	43 (40.6)	0	27 (28.1)	0	35 (43.8)
IGR, <i>n</i> (%)	11 (35.5)	3 (13.0)	0	6 (23.1)	5 (35.7)	2 (22.2)	0	19 (45.2)	0	36 (18.4)	0	4 (10.3)	3 (25.0)	27 (19.9)	0	1 (4.5)	40 (19.1)	17 (16.0)	0	21 (21.9)	0	14 (17.5)
TSS1500, <i>n</i> (%)	2 (6.5)	2 (8.7)	0	2 (7.7)	3 (21.4)	1 (11.1)	0	2 (4.8)	0	7 (3.6)	0	0	1 (8.3)	9 (6.6)	0	1 (4.5)	19 (9.1)	4 (3.8)	0	7 (7.3)	0	7 (8.8)
TSS200, <i>n</i> (%)	0	0	0	0	0	0	0	0	0	6 (3.1)	0	3 (7.7)	0	5 (3.7)	0	0	9 (4.3)	16 (15.1)	0	7 (7.3)	0	1 (1.2)
3'UTR, <i>n</i> (%)	9 (29.0)	9 (39.1)	0	2 (7.7)	0	1 (11.1)	0	3 (7.1)	0	18 (9.2)	0	9 (23.1)	2 (16.7)	5 (3.7)	0	2 (9.1)	14 (6.7)	13 (12.3)	0	10 (10.4)	0	3 (3.8)

Note: v1: Illumina InfiniumMethylationEPIC v1 BeadChip. v2: Illumina InfiniumMethylationEPIC v2 BeadChip. Note: single CpG site can be associated with multiple gene regions

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Table S3. Proportion of missing CpG sites in CpG context (relation to CpG Island) for EPICv1 and EPICv2																						
DNAm clocks Arrays	Horvath1		Horvath2		Hannum		PhenoAge		GrimAge		DNAmTL		DNAmFitAge		DunedinPACE		YingCausAge		YingAdaptAge		YingDamAge	
	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2	v1	v2
Island, <i>n</i> (%)	10 (52.6)	10 (76.9)	0	8 (47.1)	3 (50.0)	4 (66.7)	0	4 (22.2)	0	46 (24.9)	0	13 (43.3)	2 (22.2)	39 (25.3)	0	7 (24.1)	43 (26.1)	27 (29.7)	0	20 (31.7)	0	19 (24.1)
Opensea, <i>n</i> (%)	4 (21.1)	2 (15.4)	0	1 (5.9)	1 (16.7)	1 (16.7)	0	4 (22.2)	1 (100)	80 (43.2)	0	8 (26.7)	5 (55.6)	71 (46.1)	0	12 (41.4)	56 (33.9)	33 (36.3)	0	18 (28.6)	0	30 (38.0)
Shelf, <i>n</i> (%)	0	0	0	2 (11.8)	0	0	0	0	0	20 (10.8)	0	4 (13.3)	0	18 (11.7)	0	2 (6.9)	12 (7.3)	7 (7.7)	0	2 (3.2)	0	6 (7.6)
Shore, <i>n</i> (%)	5 (26.3)	1 (7.7)	0	6 (35.3)	2 (33.3)	1 (16.7)	0	10 (55.6)	0	39 (21.1)	0	5 (16.7)	2 (22.2)	26 (16.9)	0	8 (27.6)	54 (32.7)	24 (26.4)	0	23 (36.5)	0	24 (30.4)

Note: v1: Illumina InfiniumMethylationEPIC v1 BeadChip. v2: Illumina InfiniumMethylationEPIC v2 BeadChip.

Table S4. Results of Bland-Altman plots

Biological samples	DNA m clocks	Mean difference	SD difference	Lower limit of agreement	Upper limit of agreement	MAPE
Buffy coat	PCHorvath1	1.24	0.54	0.17	2.3	2.57
	PCHannum	0.27	0.83	-1.36	1.89	1.37
	PCPhenoAge	-1.96	0.82	-3.57	-0.35	1.22
	PCGrimAge	-0.64	0.46	-1.55	0.26	4.28
	PCHorvath2	0.66	0.53	-0.38	1.71	1.14
	PCDNA m TL	0	0.01	-0.02	0.02	0.12
	DNA m FitAge	-4.35	3	-10.22	1.52	8.27
	DunedinPACE	0.08	0.05	-0.02	0.19	9.23
	YingAdaptAge	-4.55	3.2	-10.82	1.72	9.78
	YingDamAge	-5.41	4.67	-14.56	3.75	14.95
PBMC	YingCausAge	-5.49	4.07	-13.47	2.49	14.51
	PCHorvath1	1.03	0.78	-0.51	2.56	2.47
	PCHannum	0.67	1.23	-1.74	3.09	3.57
	PCPhenoAge	-0.82	0.85	-2.49	0.85	1.99
	PCGrimAge	-0.34	0.59	-1.49	0.81	2.95
	PCHorvath2	1.55	0.99	-0.39	3.48	1.04
	PCDNA m TL	0.01	0.01	-0.02	0.03	0.18
	DNA m FitAge	-2.34	2.25	-6.76	2.07	5.31
	DunedinPACE	0.09	0.09	-0.07	0.26	12.9
	YingAdaptAge	1.62	4.45	-7.1	10.35	6.96
Saliva	YingDamAge	-6.27	4	-14.11	1.57	21.16
	YingCausAge	-8.17	3.22	-14.48	-1.85	20.17
	PCHorvath1	4.03	2.01	0.08	7.98	8.98
	PCHannum	1.2	2.1	-2.92	5.32	5.64
	PCPhenoAge	-1.7	1.6	-4.83	1.42	2.57
	PCGrimAge	-0.72	0.92	-2.53	1.09	2.47
	PCHorvath2	2.77	2.32	-1.77	7.32	1.45
	PCDNA m TL	0	0.03	-0.05	0.06	0.28
	DNA m FitAge	-3.99	3.32	-10.49	2.52	6.64
	DunedinPACE	0.04	0.08	-0.11	0.2	6.52
	YingAdaptAge	-4.67	6.17	-16.76	7.43	12.93
	YingDamAge	-3.6	9.73	-22.66	15.47	14.31
	YingCausAge	-3.48	5.83	-14.9	7.93	9.6

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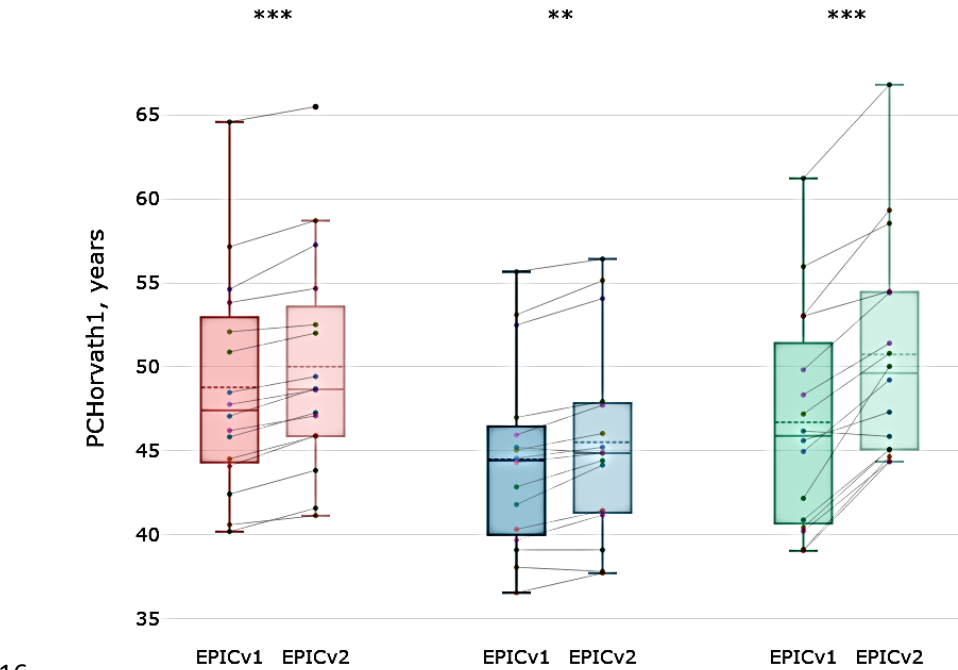
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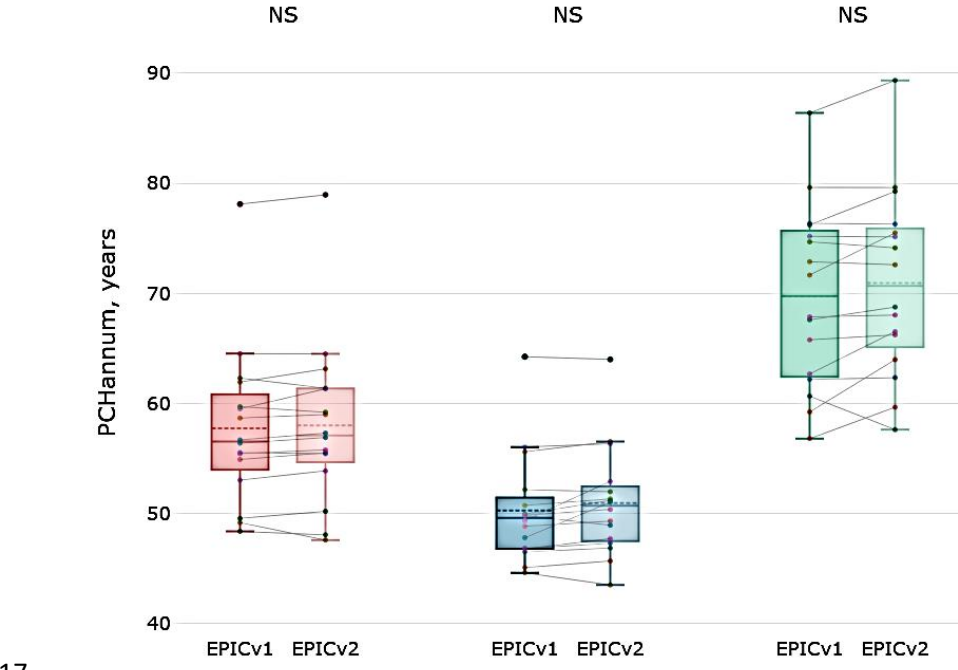
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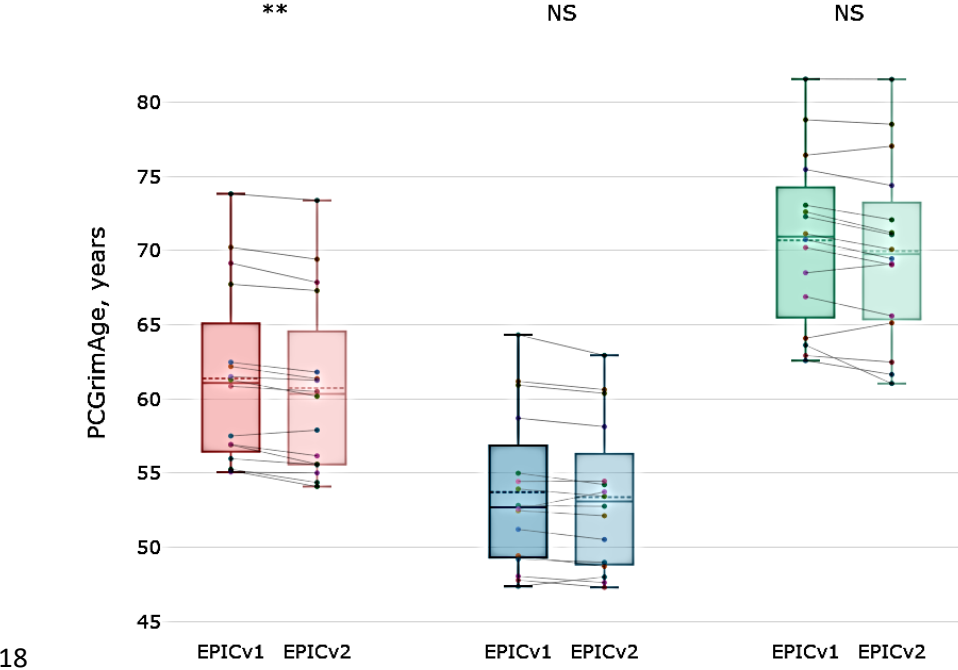
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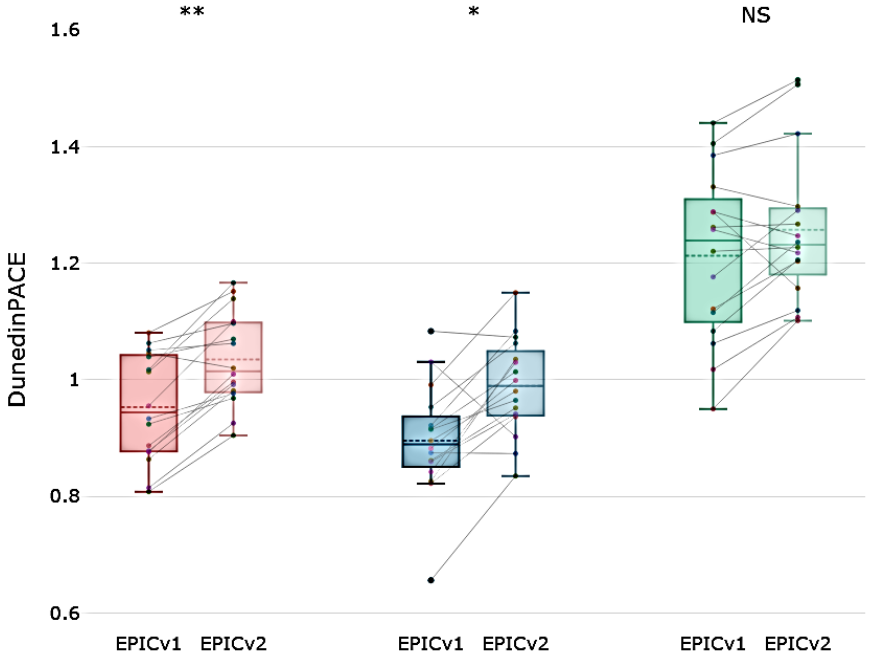
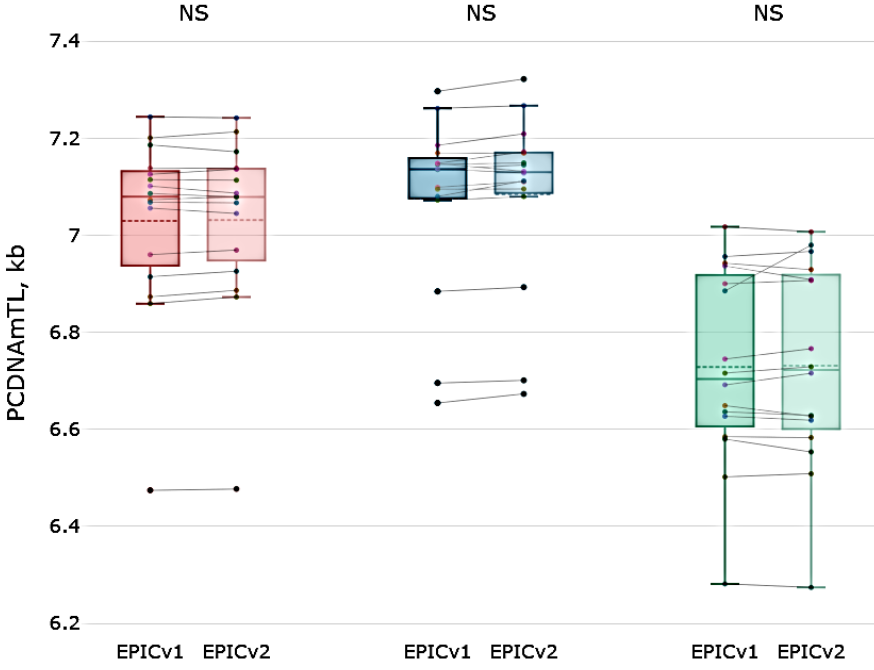
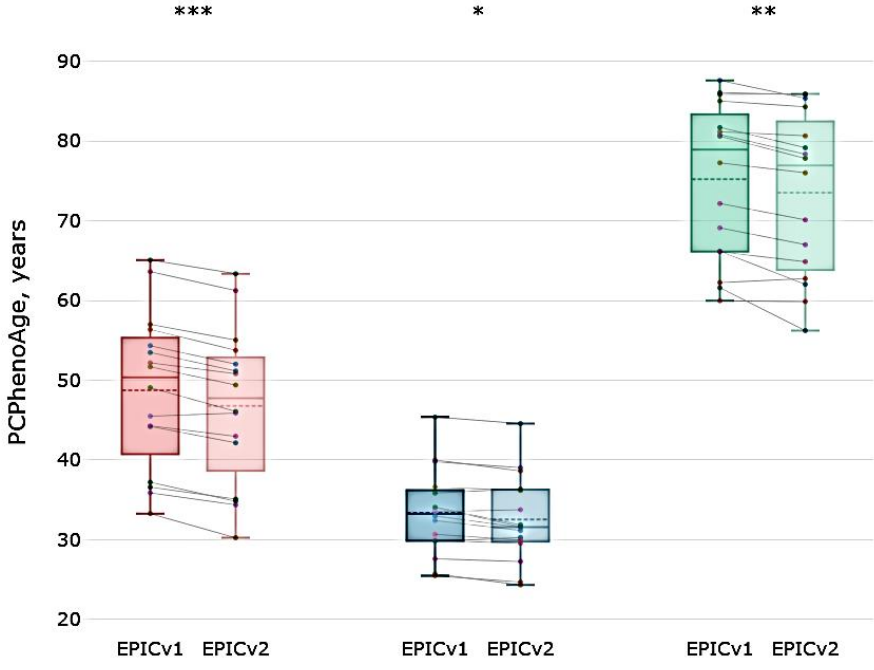
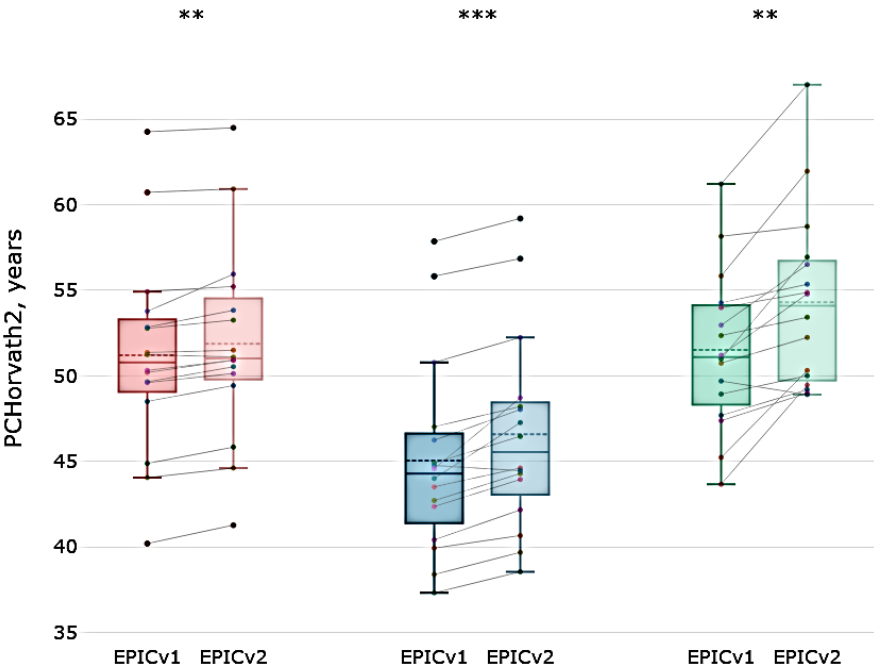
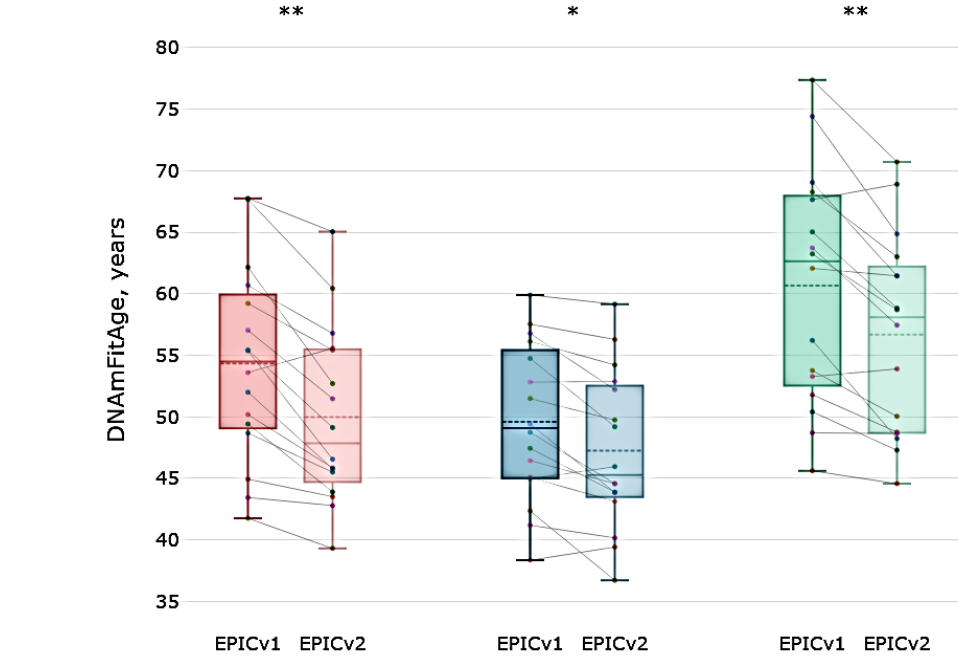
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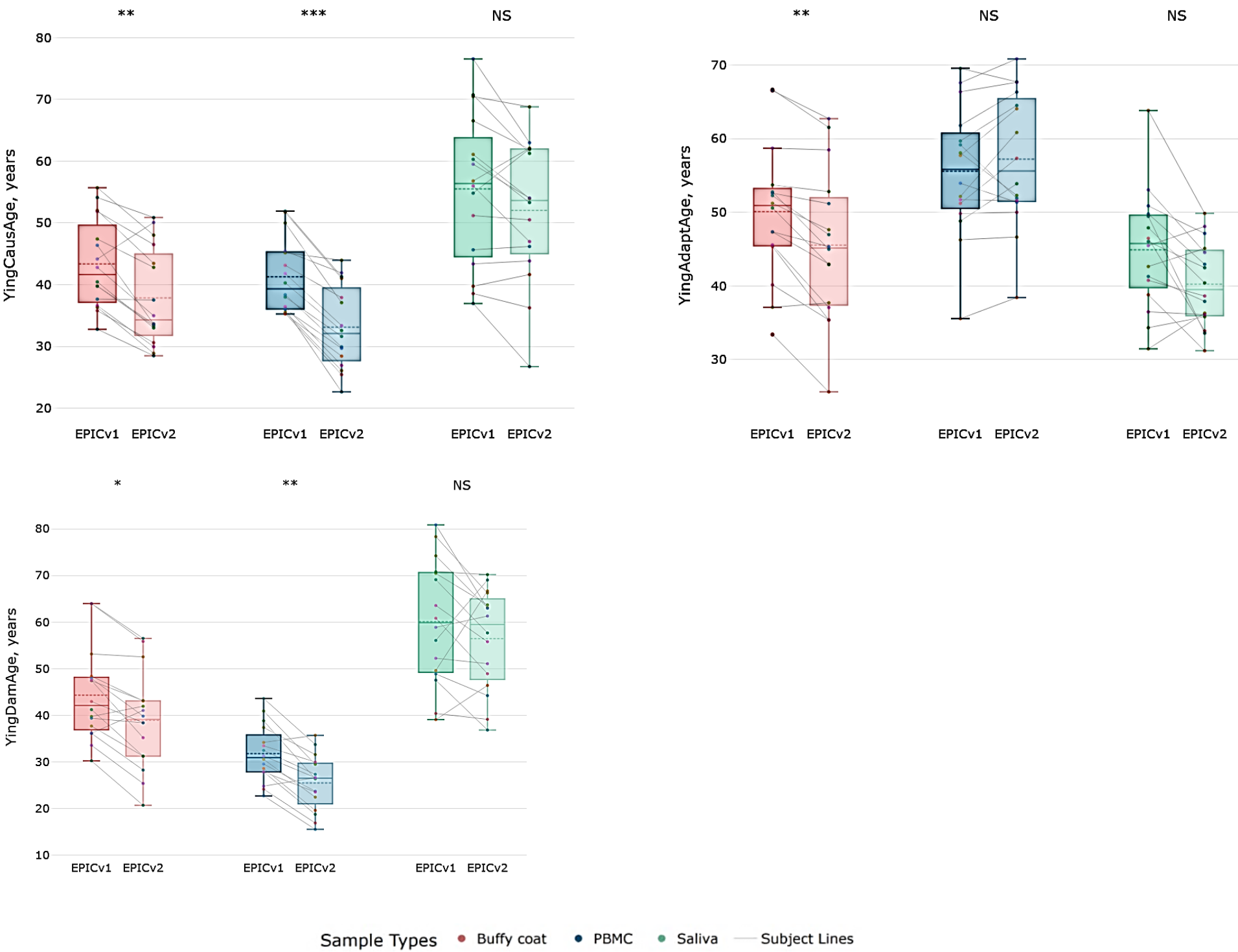
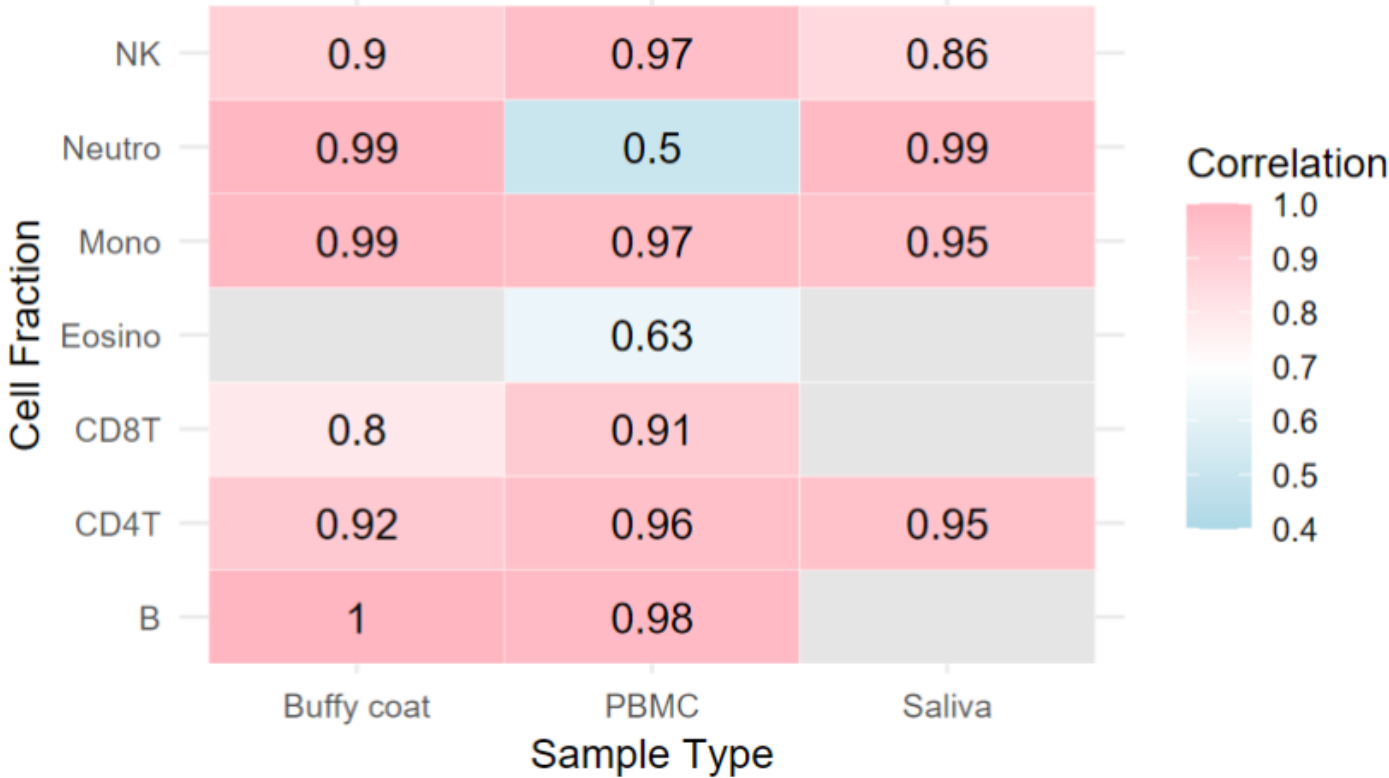


Figure S1. Box plots showing the differences in DNAm ages between EPICv2 and EPICv1 across 11 DNAm clocks stratified in three biological samples (Buffy Coat, PBMC, and Saliva). Significance test was done by Wilcoxon signed rank test, where *, ** and *** indicates statistically significance after Bonferroni correction. *** indicates p-values < 0.0000909. ** indicates p-values < 0.000909. * indicates p-adj < 0.00455. Each subject is indicated with a same colour plot on the box plot, across the EPICv1 and EPICv2, with grey lines linking the same subject on different array.



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30 **Figure S2.** Heatmap of Spearman correlation between cell composition predicted using EpiDISH in EPICv1 and DNAm ages in EPICv2. Each cell
31 corresponds to correlation coefficient (ρ), coloured in blue or red for low Spearman correlation ($\rho < 0.7$) and high Spearman correlation ($\rho > 0.7$)
32 respectively. Note: Grey cells indicate that the specific cell compositions were not predicted by EpiDISH. Abbreviations: Mono: Monocytes, Neutro:
33 Neutrophils, Eosino: Eosinophils, CD4T: CD4+ T-cells, CD8T: CD8+ T-cells, NK: Natural Killer cells and B: B-cells

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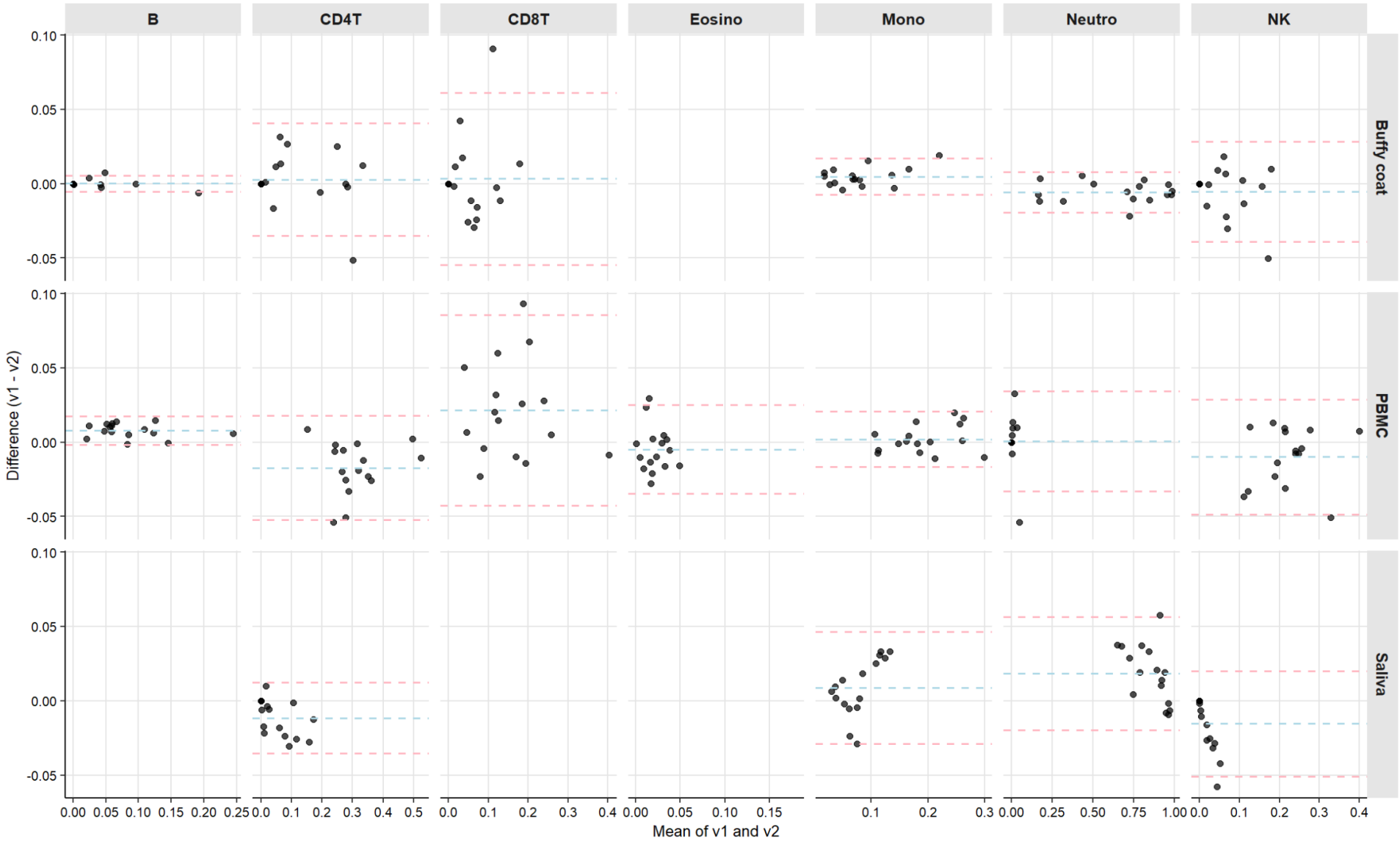


Figure S3. Bland-Altman plots comparing cell compositions estimated by EpiDISH, between the EPICv1 and EPICv2 arrays stratified by biological samples (Buffy coat, PBMC, and saliva). Light blue line indicates the mean difference, with the red lights indicating the 95% of the limits of agreement. Note: Empty cells indicate that the specific cell compositions were not predicted by EpiDISH. Abbreviations: Mono: Monocytes, Neutro: Neutrophils, Eosino: Eosinophils, CD4T: CD4+ T-cells, CD8T: CD8+ T-cells, NK: Natural Killer cells and B: B-cells