**Interrelationships and determinants of aging biomarkers in cord blood**

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**Table S1** Overview over the identified studies investigating the interrelationships between the aging biomarkers DNA methylation age (DNAm age), global genome-wide DNA methylation (global methylation), telomere length (TL) and mitochondrial DNA content (mtDNA content).

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| --- | --- | --- | --- | --- | --- | --- |
| **Cohort/country** | **Sample size** | **% Woman** | **Mean Age (SD)** | **Biomarkers** | **Main findings** | **Reference** |
| **Old Age** |
| LipidCardio Study, Germany | n = 773 | 31.6% | 69.7 ± 11.01 | TL DNAm age, DNAm AA | No association between TL, DNAm age or DNAm AA | (Banszerus, Vetter et al. 2019) |
| Yonsei Aging Study, Korea  | n = 129 | 100% | 73.74 (6.99) | TL, mtDNA content | Positive correlation between mtDNA and TL | (Kim, Kim et al. 2013) |
| Nonsmoking men and women aged 60-80 years, Belgium | n = 166 | 54% | 70.6 (4.7) | TL, mtDNA content | Positive correlation between mtDNA and TL | (Pieters, Janssen et al. 2015) |
| Veteran Affairs Normative Aging Study (NAS), U.S. | n = 812 | 0% | 72.4 (6.9) | Cross-sectional and prospective associations between mtDNA content, DNAm-Age, TL, DNAmPhenoAge and DNAm-GrimAge | Inverse association mtDNA content and DNAm age in cross-sectional design.Inverse association between mtDNA content and prospective measures of TL. | (Dolcini, Wu et al. 2020) |
| Lothian Birth Cohorts of 1921 (LBC1921) and 1936 (LBC1936), Great Britain | LBC1921: n = 920 LBC1936n = 414 | / | LBC1921: ages 70, 73 and 76 years; LBC1936: ages 79, 87 and 90 years | TL and DNAm age | No correlations between epigenetic clock estimates and TL | (Marioni, Harris et al. 2016) |
|  |
| **Adults** |
| Dunedin Study, New Zealand  | n = 1,037 | 48% | 38 | TL, three epigenetic-clocks, and three biomarker-composites | Low correlation between the epigenetic clocks, and TL | (Belsky, Moffitt et al. 2018) |
| Berlin Aging Study II consisting of a a.) young and an b.) old age group, Germany | a.) n = 424b.) n = 1,471 | a.) 51.4%b.) 49.4% | a.) 28.8 (3.1)b.) 68.7 (3.7) | TL, DNAm age, DNAm AA | Inverse association between DNAm age and TL in adjusted linear regression analysis | (Vetter, Meyer et al. 2019) |
| Swedish Adoption/Twin Study of Aging (SATSA), Sweden | n = 845 (n = 288 with all biomarkers) | 59.5% | 63.6 (8.6) | TL, four DNAm ages, and three functional ages | Low correlation between TL and other markers | (Li, Ploner et al. 2020) |
| Healthy Adults from studies assessing adversity and depressive and anxiety disorder (pooled data), U.S. | n = 392 | 63% | 31.4 (11.2) | TL, mtDNA content | Positive correlation between mtDNA and TL in the entire sample and all subgroups | (Tyrka, Carpenter et al. 2015) |
| Australian Mammographic Density Twins and Sisters, Australia | n = 479 | 100% | 55.7 (8.0) | DNAm age based on three epigenetic clocks and global methylation based on average methylation beta-value | No correlation between DNAm age and global methylation | (Chen, Wong et al. 2019) |
| Patients with bipolar disorder, their siblings and healthy controls, U.S. | Patients: n = 22Siblings: n = 16Controls: n = 20 | Patients: 68%Siblings: 63%Controls: 60% | Patients: 33.95 (9.3);Siblings: 39 (10.6);Controls: 34.75 (10.0) | global DNA methylation, mtDNA content, TL and DNAm age | Correlation mtDNA content with DNAm AA in patients aged 33+. No correlation between TL with DNAm age or mtDNA content | (Fries, Bauer et al. 2017) |
| Flemish Environment and Health Study (FLEHS), Belgium | N = 175 | 48.6% | 58.3 (4.0) | TL, mtDNA content | Positive correlation between mtDNA and TL | (Vriens, Nawrot et al. 2019) |
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| **Adolescents** |
| Healthy children and adolescents, Mexico | n = 98 | / | Range: 6-12 | mtDNA content, TL | Positive association between TL and mtDNA content | (Alegría-Torres, Velázquez-Villafaña et al. 2016) |
| Primary schoolchildren, Belgium | n = 197  | 48.7% | 10.3 (1.3) | Buccal mtDNA content and TL | No association between TL and mtDNA content | (Hautekiet, Nawrot et al. 2021) |
| Longitudinal study with 5-year follow-up of adolescents from public schools, Brazil  | n = 234 n = 76 (follow-up) | 61% | 13.4 (2.37) at baseline | TL and DNAm AA | No correlation between TL and DNAm AA at baseline or follow-up | (Cerveira de Baumont, Hoffmann et al. 2021) |

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