

Developmental epigenomic effects of maternal financial problems

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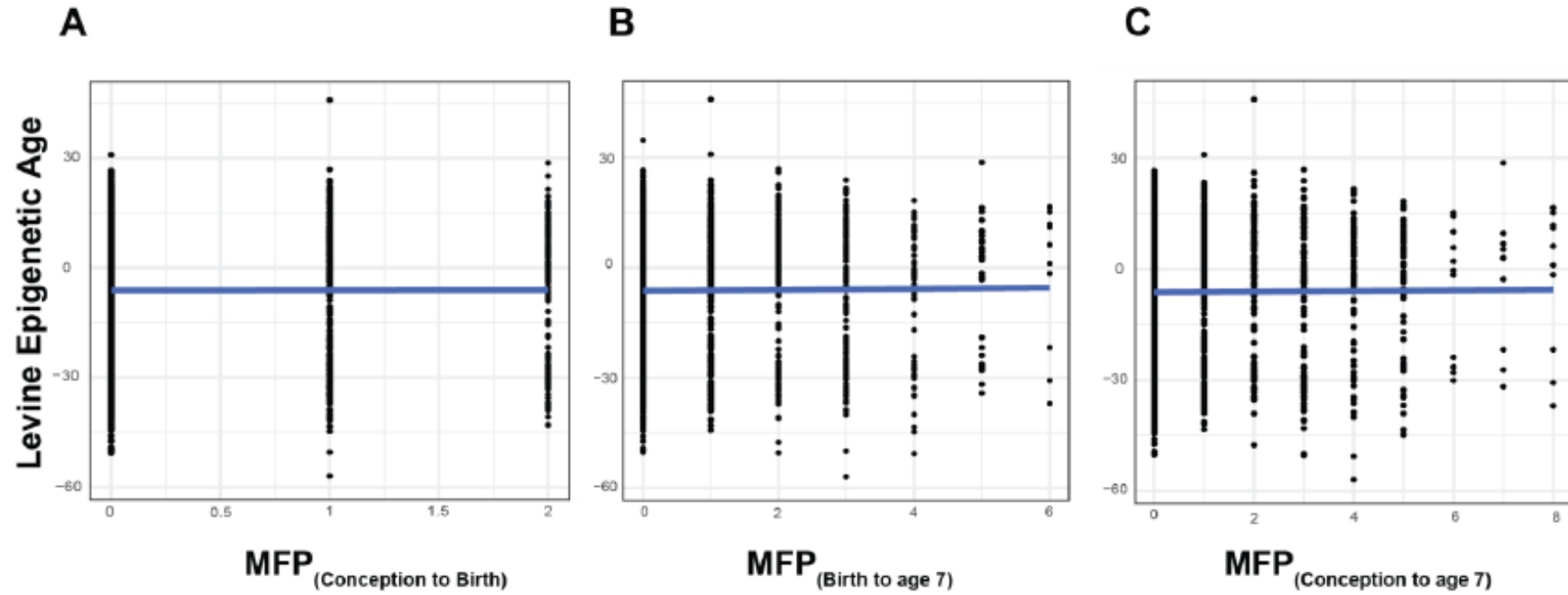
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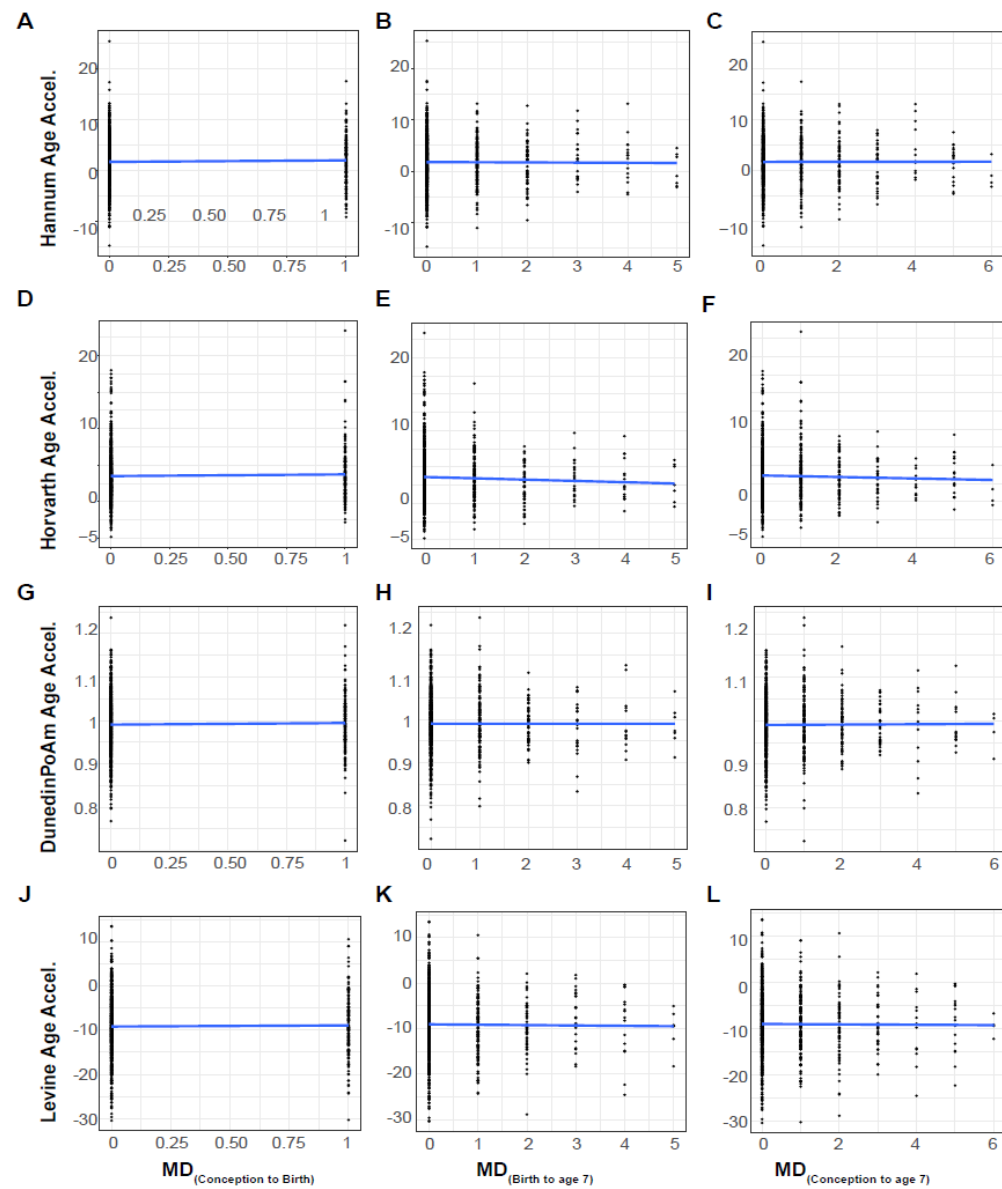
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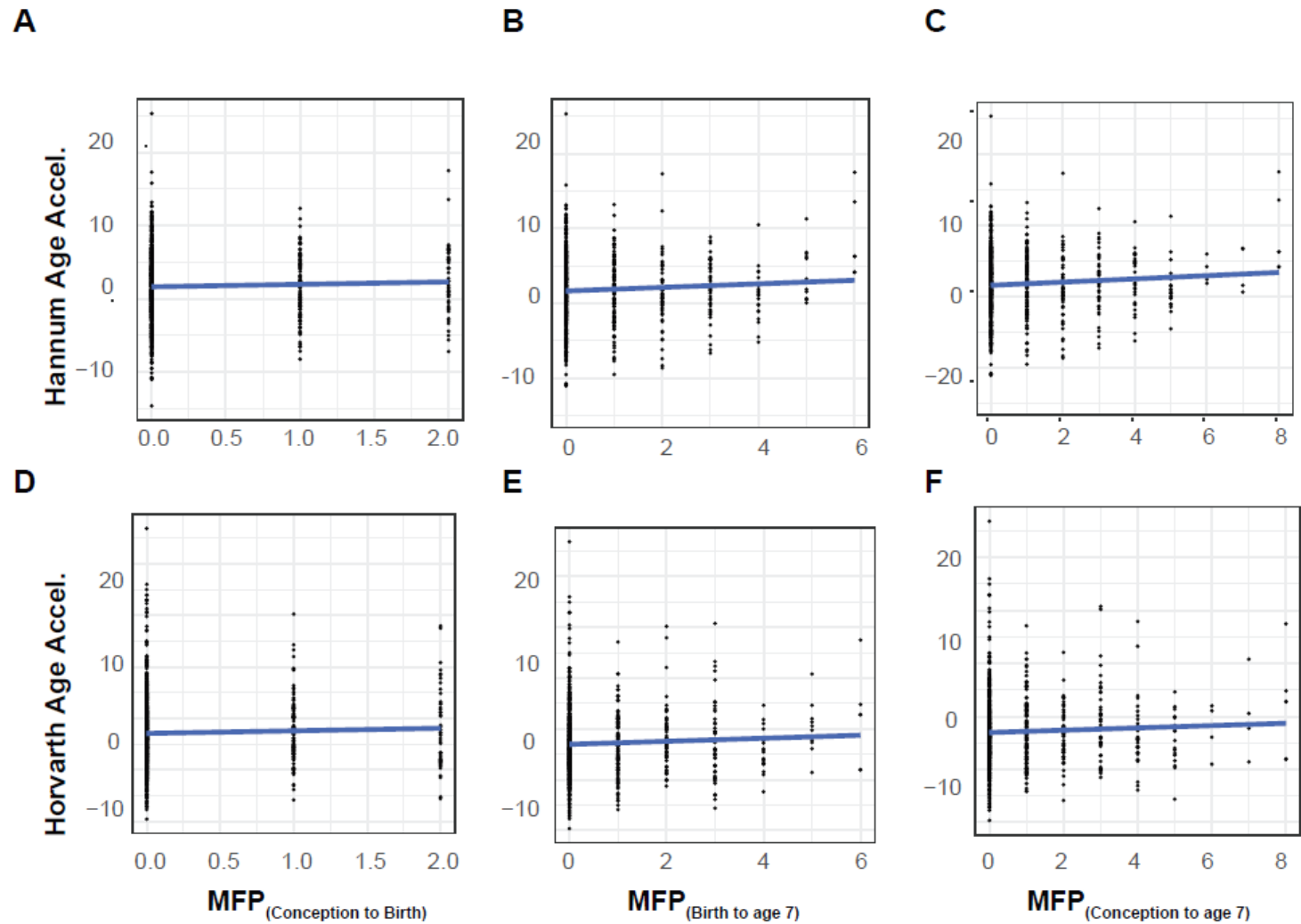
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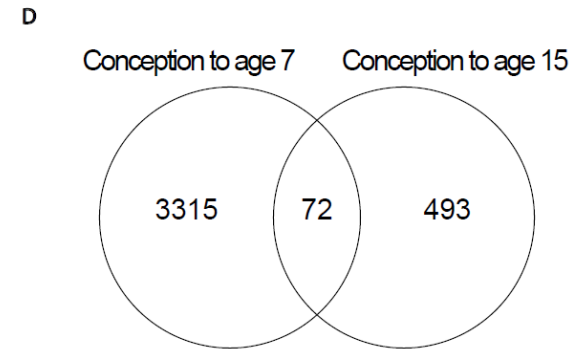
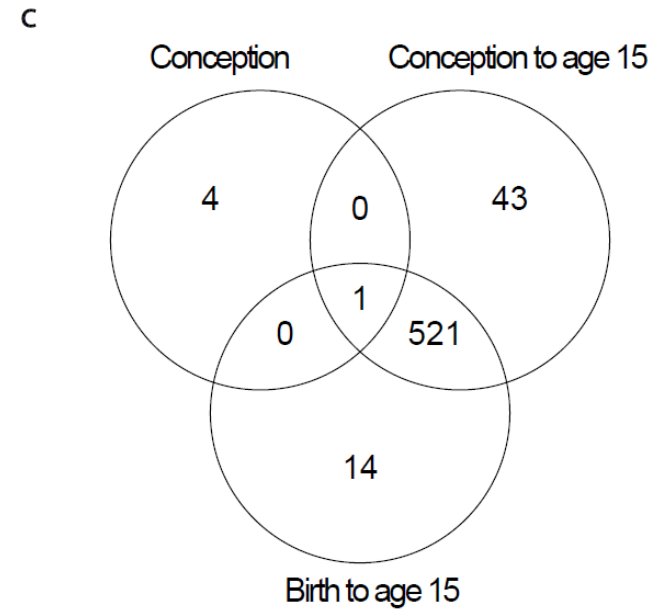
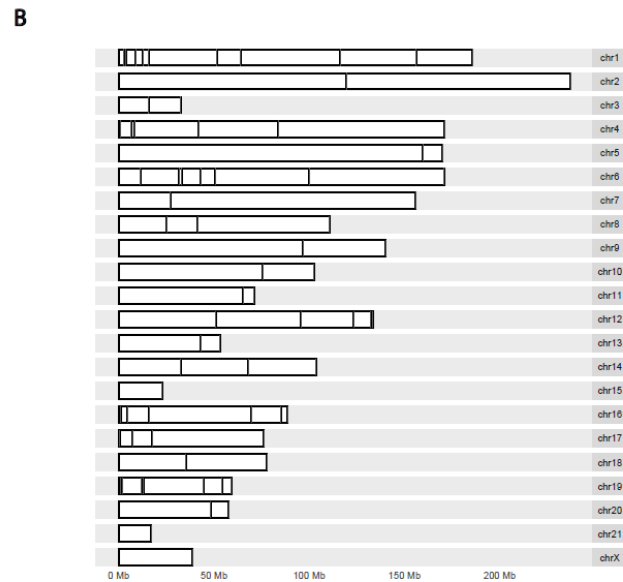
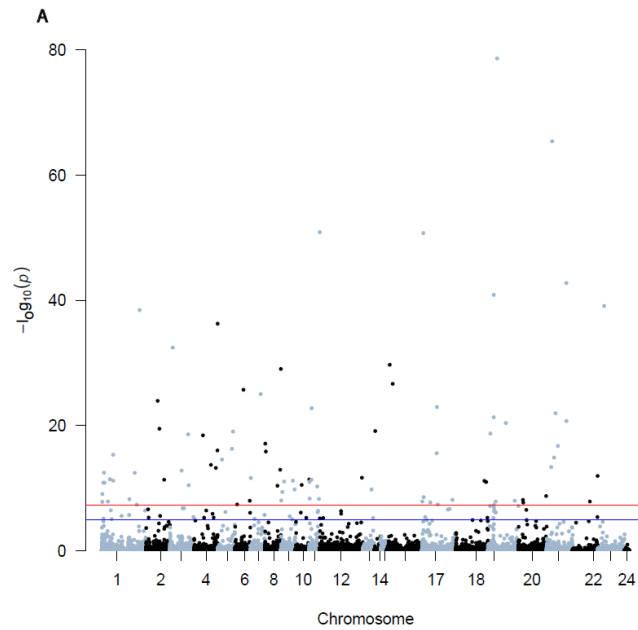
Supplementary Figure 1 : MFP time exposure dependent is not associated with Levine Clock. Scatter plot represents correlation between Major financial problem (MFP) and epigenetic age. Panel A – C represents Levine correlation. Blue line is the trend line. Text: correlation coefficient of Pearson correlation. Black dots: answer participants. Epigenetic age on the y-axis, and the number of reported financial problems on the x-axis.



Supplementary Figure 2: Time of MD exposure is not correlated with epigenetic aging. Scatter plot represents correlation between Maternal Deprivation (MD) and age acceleration. Panel A – C represents the correlation between the number of MD events and the Hannum age acceleration, D- F represents the same, but for the Horvath age acceleration. G-I represent correlations between MD and PoAm Ag acceleration while J-L represent correlation between Levine age acceleration and MD. Blue line is the linear regression line. Data points represent individual participants



Supplementary Figure 3: Time of MFP exposure is weakly correlated with PoAm aging. Scatter plot represents correlation between Major financial problem (MFP) and age acceleration. Panel A – C represents the correlation between the number of MFP events and the Hannum age acceleration, D- F represents the same, but for the Horvath age acceleration. Blue line is the linear regression line. Data points represent individual participants.



Supplementary figure 4: Associated epigenetic modifications to MFP between birth and age 15. A -B) Manhattan and karyogram plot represent the repartition of 536 CpGs on each chromosome after exposure to MFP between birth and age 15. C) Venn diagram shows 1 common significant CpGs extracted from EWAS of the three time exposure to MFP. D) Venn diagram shows 72 common CpGs extracted from EWAS for MFP on children's genome at age 7 and children's genome at age 15.