In this manuscript, Dr. Lund and colleagues conducted a genome-wide DNA methylation association study with overall all-cause mortality within Lothian Birth Cohorts including 2,198 whole blood samples. The author identified a large number of significantly associated methylation signals with mortality and found the contradictory between age-related methylation signal and mortality related methylation signals. The study was performed rigorously and the findings are interesting, especially cell-type composition and batch effect have been considered in the study. I have several minor concerns:

**Major Compulsory Revisions**

1. It is quite good step to check the batch effect. However, Combat were designed for gene expression array which have different data distribution compared with methylation ‘Beta’. Is there any result could be show it is appreciated to apply ‘Combat’ in methylation data. What’s the top sources of the batch effect? Any analysis could be conducted to show them? Is there any significant difference of the ‘methyaltion Beta’ distribution before and after the ‘Combat’ treatment.
2. The authors applied cell type deconvolution to consider the cell-type composition. However, how to evaluate this treatment to the further analysis should be discussed.
3. It would be helpful to show the qq-plot for the current EWAS study as the supplementary figure.
4. Whether the author could repeat the previous ‘methylation clock’ papers with Lothian Birth Cohorts dataset.
5. What’s the main mortality reasons for Lothian Birth Cohorts? Is there any possibility to conduct a EWAS for these sub-groups?

**Minor and Discretionary Revisions**

1. Figure 2a and Figure 2b are still not very clear, Please provide more details.