

Re: FW: GWAS Age Acceleration Manuscript

Jennifer Smith <smjenn@umich.edu>

Mon 11/05/2020 19:38

To: MCCARTNEY Daniel <Daniel.McCartney@igmm.ed.ac.uk>; Wei Zhao <zhaowei@umich.edu>; Sharon Kardia <skardia@umich.edu>; Scott Ratliff <ratliffs@umich.edu>; MARIONI Riccardo <Riccardo.Marioni@ed.ac.uk>

Hi Daniel and Riccardo,

Thank you so much for sending this draft!

Can you please change affiliation #22 to: Department of Epidemiology, School of Public Health, University of Michigan

Study tissue for GENOA is buffy coat.

GWAS covariates were: Kinship matrix (random effect) and 4 genetic PCs

Here is our data availability statement:

GENOA: According to the terms of consent for GENOA participants, access to epigenetic data will be made available by reasonable request and with a corresponding Data Use Agreement. Please contact Sharon L.R. Kardia and Jennifer A. Smith (skardia@umich.edu and smjenn@umich.edu).

Best,

Jen

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On Fri, May 8, 2020 at 8:28 AM MCCARTNEY Daniel <Daniel.McCartney@igmm.ed.ac.uk> wrote:
Apologies - please find attached the data availability document.

Best wishes,

Daniel

From: [MCCARTNEY Daniel](#)

Sent: 08 May 2020 10:33

Subject: GWAS Age Acceleration Manuscript

Dear co-authors,

Many thanks for your contribution to this study so far. We are now finalising a revised version of the manuscript and hope to submit to Nature Genetics in the first instance by the end of next week (15 May).

I have attached 3 files which now require action. We would be grateful if you could return them by Wednesday 13 May.

Title page:

Could all authors please ensure their names and affiliations are correct.

Data availability document:

Could all cohorts please provide a data availability statement in this document. Where available, we have used statements provided in the cohort descriptions document (also attached for your reference). If this is the case for your cohort, please edit/amend if necessary.

Table S1:

Could all cohorts please provide information on study tissue and GWAS covariates (highlighted columns). Again, where available in the cohort descriptions document, we have provided this information. If this is the case for your cohort, please edit/amend if necessary. Please also ensure the details on methylation array/imputation panel are correct.

Best wishes,
Daniel and Riccardo

Dr Daniel McCartney

Research Fellow

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