

From: Harvard PGP [REDACTED]

To: Jeffrey <[REDACTED]>

Subject: Personal Genome Project - Updated phenotype ranking, neurodiversity and more!

Date: Sat, 01 Jul 2017 15:10:48 +0000



Dear Jeffrey,

We are writing you as a contributor to the Harvard Personal Genome Project (PGP). Thank you for participating in PGP! The unique combination of open-

access genotype, phenotype and cell-lines have made the PGP a particularly valuable source for researchers.

Disclaimer: The contents of our newsletters are meant as information for our community, and does not imply endorsement of the research, procedures, and products that are described in the linked news and publications.

PGP Phenotype Ranking

June 14: New phenotype ranking scores are available for PGP participants! Thank you for your enthusiasm and feedback a couple of months ago when we first described an unbiased approach to ranking PGP participants and phenotypes available in the PGP. We have re-calculated new scores and ranks early this month and there are substantial changes to the rankings compared to previous. You can view the new rankings at <https://pgpresearch.med.harvard.edu/ranking/index.py>

To improve your own ranking, you can perform all or some of the following:

- complete more survey questionnaires
- share your CCR XML document generated from Microsoft Healthvault
- upload a phenotypes.csv document generated using Excel

Updated phenotype rankings will be available in another 2-3 months. If you have any questions or issues, please feel free to contact us at support@hu.pgp-hms.org

Baby Genome Sequencing in China (Veritas Genetics)

Recently, Veritas Genetics (a spinoff from Harvard PGP) announced that it is offering to decode the complete genomes of newborns in China. Veritas says the test, ordered by a doctor, will report back on 950 serious early- and later-life disease risks, 200 genes connected to drug reactions, and more than 100 physical traits a child is likely to have. But Veritas will not reveal everything, in recognition that not all the information in the genome is appropriate to give parents right away. For instance, it won't tell them about a gene that can strongly predispose people to Alzheimer's in old age. To read more about this news, please follow this link: <https://www.technologyreview.com/s/608086/baby-genome-sequencing-for-sale-in-china/>

Psst, the human genome was never completely sequenced

Quoted in the news, "As a matter of truth in advertising, the 'finished' sequence isn't finished," said Eric Lander, who led the lab at the Whitehead Institute that

deciphered more of the genome for the government-funded Human Genome Project than any other. “It’s very fair to say the human genome was never fully sequenced,” Craig Venter, another genomics luminary, told STAT. “The human genome has not been completely sequenced and neither has any other mammalian genome as far as I’m aware,” said Harvard Medical School bioengineer George Church, who made [key early advances](#) in sequencing technology. To read more about the unsequenced portions of the human genome, please follow this link: <https://www.statnews.com/2017/06/20/human-genome-not-fully-sequenced/>

‘A feature, not a bug’: George Church ascribes his visionary ideas to narcolepsy

It has happened during meetings, seminars, and panel appearances from Beijing to Boston: Renowned biologist George Church nodded off. Church said “almost all” of his visionary ideas and scientific solutions have come while he was either asleep or quasi-asleep, sometimes dreaming, at the beginning or end of a narcoleptic nap. “It took me until I was 50 or 60 years old” to realize that narcolepsy “is a feature, not a bug.” He finds inspiration in the many websites that list accomplished people who have had dyslexia, ADHD, OCD and other forms of neurodiversity. “I look at them and say that’s really cool,” he said. To read more, please follow this link: <https://www.statnews.com/2017/06/08/george-church-narcolepsy/>

Gordon conference in Human Genetics and Genomics

A couple of our researchers from the PGP and the Church lab will be presenting PGP-related research projects at the Gordon conference in Human Genetics and Genomics from July 9-14 in Stowe, VT. If you happen to be attending the conference, we’ll love to chat with you about our work, or any feedback that you might have! And do stop by our posters to pick up a PGP sticker and flyer.

PGP-Lumosity

If you have not participated in our PGP-Lumosity research study, we invite you to do so! Please log into <https://my.pgp-hms.org> and click on “Participate” > “Third Party Activities” > “PGP-Lumosity”. To watch a fun promotional video starring George Church and our talented digital PR team at the Wyss Institute, please follow this link: <https://wyss.harvard.edu/wyss-institute-and-lumos-labs-research-collaboration/>

Veritas whole genome sequencing for PGP participants

Did you know that PGP participants are eligible for discounted whole-genome sequencing and data return from Veritas Genetics? For \$999, participants will get their whole genome sequenced (Illumina HiSeq X, 30X average coverage), and the raw data and processed variant call files (total cost for non-PGP participants is about \$1,600) will be uploaded to the publicly accessible PGP website and to dbGaP at NCBI. To enroll in this third-party activity, please log into <https://my.pgp-hms.org> and click on "Participate" > "Third Party Activities" > "Veritas genome sequencing discount for PGP participants".

These and other developments are only possible because of your continued participation in the PGP. Thank you, and please contact us if you have any feedback or suggestions!

Harvard Personal Genome Project

[Let's Get Started](#)

Copyright © 2017 Harvard Personal Genome Project, All rights reserved.

You are enrolled in the Harvard Personal Genome Project.

Our mailing address is:

Harvard Personal Genome Project
77 Avenue Louis Pasteur
NRB, Room 238
Boston, MA 02115

[Add us to your address book](#)

Want to change how you receive these emails?

You can [update your preferences](#) or [unsubscribe from this list](#)

