NIH Advisory Committee to the Director
December 13, 2024

Summary of HeLa Genome Data Access Request

1. Project #38897, Re-analysis of engineered L1 retrotransposition in cultured HeLa cells, University of Queensland, Australia

This page intentionally left blank

National Institutes of Health
Advisory Committee to the Director
HeLa Genome Data Access Working Group

HeLa Genome Data Access Request: Project 38897

Working Group Finding	Consistent with the Data Use Agreement
Project Title	**Re-analysis of engineered L1 retrotransposition in cultured HeLa cells**
Date Received	10/15/2024
Project Summary (Provided by NIH)	• The human genome contains genes that move around the genome or "jump." Research on 'jumping genes' has been done using HeLa cells and the HeLa cell genome. A prior study (Flasch et al., Cell, 2019) used HeLa cells to generate HeLa cell whole genome sequence data to study jumping gene preference. They submitted their HeLa cell data to the HeLa Cell Genome Sequencing Studies as a part of the NIH-Lacks Family Agreement. • The investigator proposes to access the HeLa Cell Genome Sequencing Studies so that they may access the HeLa cell data submitted by Flasch et al. to see if they are able to repeat the research results.
Institution	University of Queensland, Australia
Collaborator(s)	None
Research Use Statement (Provided by Requestor)	The requested data are composed of engineered L1 insertions generated in cultured HeLa cells and mapped with PacBio sequencing, and were published by Flasch et al. (Cell, 2019). The research objective of accessing these data is to reproduce the findings of Flasch et al. The analysis plan is to download the raw data from accession phs001669, re-process the PacBio sequencing reads using CutAdapt, and re-align the reads to the latest reference genome assembly (hs1). This approach will use similar principles to Flasch et al. but employ more up to date software to verify their original findings. The analysis will be conducted in alignment with the Data Use Limitations (DULs) by the PI. Collaboration with other researchers at other institutions is not envisioned to undertake the analysis. The data generated from HeLa cells in this publication are of value in understanding genome-wide patterns of L1 retrotransposon integration in contrast to other cell types. It is also of value to confirm that the prior research done using HeLa cells was robust. The results are expected to be similar to those published by Flasch et al. and the focus of the analysis will be as per that of Flasch et al. No additional risk is anticipated for participants. Findings from the proposed research will be disseminated through presentations at meetings or conferences, and via peer-reviewed publications. We have no plans to develop a commercial product or service or file Intellectual Property using the findings from the proposed research. The findings could not reasonably be expected to result in a commercialized product or service. We are not expecting our plans to change regarding our intention not to seek IP or commercialization. We agree to inform the NIH if our plans for IP or commercialization change.

National Institutes of Health
Advisory Committee to the Director
HeLa Genome Data Access Working Group

HeLa Genome Data Access Request: Project 38897

Non-Technical Summary (Provided by Requestor)	The human genome contains mobile DNA elements, or "jumping genes", which are pieces of DNA that can copy themselves from one part of the genome to another. A prior study (Flasch et al., Cell, 2019) used cultured HeLa cells as a system to study whether mobile DNA has a preference for certain parts of the genome over others. This study sequenced parts of the HeLa cell genome. Our intention is to re-analyse the data generated by Flasch et al. using a more recent assembly of the human genome and updated software, to check whether their results can be reproduced. This will provide further confidence that the original work done was correct.