

Errata for the dissertation “The genomic and transcriptomic landscape of HeLa cells” by Jonathan Landry

1. Data Access

In response to the controversy regarding the paper presenting the core results of this thesis (Landry et al., 2013), the information on the accessibility of the data is no longer accurate. The HeLa resources provided have now been released under a controlled access policy via NIH’s database of Genotypes and Phenotypes (dbGaP, <http://www.ncbi.nlm.nih.gov/gap>), meaning that those researchers who wish to use these resources must first apply to a data access committee with a description of how they plan to use the data in their research. Please read the links below:

dbGaP information:

Link: http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000643.v1.p1

All/both HeLa genome studies:

http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000640.v1.p1

Instructions for investigators requesting access to these datasets:

http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/GetPdf.cgi?document_name=HeLaSpecialInstructions.pdf

Data Use Agreement:

https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?view_pdf&stacc=phs000643.v1.p1

dbGaP request procedure:

<https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?page=login>

2. Acknowledgements

The genome sequence described in this thesis was derived from a HeLa cell line. Henrietta Lacks, and the HeLa cell line that was established from her tumor cells in 1951, have made significant contributions to scientific progress and advances in human health. I am grateful to Henrietta Lacks, now deceased, and to her surviving family members for their contributions to biomedical research.

3. Methods - Multicolor fluorescent *in situ* hybridization (M-FISH) (Section 3.4.4)

The protocol describing the M-FISH experiment was not entirely accurate and the correct method is:

M-FISH was performed as described by Geigl et al., 2006. In brief, seven pools of flow-sorted whole chromosome painting probes were amplified and directly labeled using seven different fluorochromes (DEAC, FITC, Cy3, Cy3.5, Cy5, Cy5.5, and Cy7) using degenerative oligonucleotide-primed PCR (DOP-PCR). Metaphase chromosomes immobilized on glass slides were denatured in 70% formamide/2x saline sodium citrate (SSC), pH 7.0, at 72° for 2 min followed by dehydration in a degraded ethanol series. Hybridization mixture containing combinatorially labeled painting probes, an excess of unlabeled cot1 DNA, 50% formamide, 2x SSC, and 15% dextran sulfate was denatured for 7 min at 75°, preannealed at 37° for 20 min, and hybridized at 37° to the denatured metaphase preparations. After 48 hr, the slides were washed in 2x SSC at room temperature for 3x 5 min followed by two washes in 0.2x SSC/0.2% Tween-20 at 56° for 7 min each. Metaphase spreads were counterstained with 4,6-diamidino-2-phenylindole (DAPI) and covered with antifade solution. Metaphase spreads were captured using a DM RXA epifluorescence microscope (Leica Microsystems, Bensheim, Germany) equipped with a Sensys CCD camera (Photometrics, Tucson, AZ). The camera and microscope were controlled by the Leica Q-FISH software and images were processed using the Leica MCK software and presented as multicolor karyograms (Leica Microsystems Imaging solutions, Cambridge, United Kingdom).

References:

Geigl, J.B., Uhrig, S., and Speicher, M.R. (2006). Multiplex-fluorescence in situ hybridization for chromosome karyotyping. *Nat Protoc* 1, 1172–1184.

Landry, J.J.M., Pyl, P.T., Rausch, T., Zichner, T., Tekkedil, M.M., M, S.A., Jauch, A., Aiyar, R.S., Pau, G., Delhomme, N., et al. (2013). The Genomic and Transcriptomic Landscape of a HeLa Cell Line. *Genes|Genomes|Genetics* 3, 1213–1224.