UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL

DEPARTMENT OF BIOSTATISTICS

CAMPUS BOX 7420
CHAPEL HILL, NC 27599-7420

T 919.966.7250
F 919.966.3804
www.sph.unc.edu/bios

MICHAEL R. KOSOROK, PHD
Chair

JIANWEN CAI, PHD
Vice Chair

November 13, 2018

Dear Loyal,

I am delighted to be joining the team of co-PIs including yourself, Drs. Hicks, Fertig, Greene, Hampton, and Patro, proposing to work on statistical and algorithmic method development and software implementations for single-cell datasets generated by the HCA. I pledge to commit 10% effort and supervise the full time graduate research of a Biostatistics PhD student from UNC-Chapel Hill in working on this project.

As you know, I am an Assistant Professor of Biostatistics and Genetics at UNC-Chapel Hill, and am a leading developer of statistical software for RNA-seq analysis in the *Bioconductor* Project, including the *DESeq2*, *apeglm*, *tximport,* and *tximeta* packages. I have collaborated with Dr. Rob Patro on bias-aware estimation of transcript abundance from RNA-seq in the *Salmon* and *Sailfish* software and estimation of uncertainty during transcript quantification since 2015. We are currently developing a number of software projects in parallel, including *tximeta* and a set of modular packages for the propagation of uncertainty from quantification for bulk RNA-seq to downstream statistical inference and visualization methods. I am also well versed in the statistical methods and papers by Dr. Hicks on the topic of single-cell RNA-seq, some of which were developed while we were both postdoctoral fellows in the same lab of Dr. Rafael Irizarry at Dana-Farber Cancer Institute, and the high dimensional matrix factorization approaches of Dr. Fertig, which we have discussed in depth at a recent *Bioconductor* conference in Toronto. I am therefore well positioned to collaborate on the statistical and software goals in this proposal, and look forward to collaborating with you, Drs. Greene and Hampton as well. I am excited to work with the co-PIs on this proposal to disseminate versioned reference cell type catalogs through widely used frameworks for genomic data analysis including *R/Bioconductor* and *Python*.

Sincerely,

Michael Love
Assistant Professor
Department of Biostatistics
Department of Genetics
University of North Carolina-Chapel Hill
4115E McGavran-Greenberg Hall
135 Dauer Dr, Chapel Hill, NC 27516