**RESOURCE SHARING PLAN**

Data Sharing Plan:

All data will be deposited in public databases in widely used file formats. Raw data will be deposited in the NCBI short read archive, and all partially processed data will be made available in Gene Expression Omnibus. Additionally, information such as data syntheses, study protocols, bioinformatics tools, and any other metadata collected will be widely shared with the scientific community for research and made publicly available through the Yu lab website (<http://yulab.icmb.cornell.edu/resources.shtml>), the Gerstein lab website (<http://info.gersteinlab.org/Resources>), GitHub, and other data repositories. We will cooperate with NIH staff, and other stakeholders in the development and implementation of research and standardization methods, data standards and formats, metadata requirements, and quality control metrics for this resource. The co-PI, John Lis, has served on the NIH ENCODE and modENCODE External Consultants Panel for seven years and knows the value developing consensus approaches for data sharing and data quality standards. The co-PIs have also developed protocols and methods over the years and have shared them with the research community, with GRO-seq technology for measuring nascent transcription genome wide as one example.

Protocol, tool and reagent sharing:

We expect that tools and reagents generated will be made available broadly and can be distributed at minimal cost, and without undue intellectual property constraints, so that they can be as widely used as possible, thus enabling downstream applications for the reagents by the larger scientific community. All software will be distributed freely on publication under a permissive, open source license. At the time of publication, the source code for all software tools, and for all analysis scripts, will be posted on GitHub, the Gerstein lab website (<http://info.gersteinlab.org/Resources>), and the Yu lab website (<http://yulab.icmb.cornell.edu/resources.shtml>).

Sharing Model Organisms:

This project will generate a number of valuable datasets and resources useful for the research community of human genetics, as well as biology in general. All of these will be made broadly available when the paper describing these reagents is accepted for publication, as we have done in the past with many dozens of plasmids and transgenic lines distributed to many hundreds of researchers over the past 30 years. As in the past, we will mail materials via the US Postal service at our own expense, or if needed, via an overnight express mail, which is paid by the recipient. We bear the cost of preparing the materials and packaging. If demand is extraordinarily high for some of the reagents, we may be forced to charge a nominal fee to simply cover shipping and production costs. Gateway entry clones and Starr-seq/luciferase expression clones of the ~3,000 WT enhancer clones and their variants (>20,000 mutation clones) will all be made available either as purified DNA stocks or as transformed *E. coli* strains. Because replicating and distributing such large-scale libraries might become too labor-intensive, we will also explore the possibility of sending the clone/strain sets to a third-party (without charge) for re-distribution (i.e., Addgene, DNASU). Upon request of the NIH awarding office, we will also provide NIH with a copy of documents or a sample of any material developed under an NIH grant award. If a situation arises where patent protection is necessary for development of a research tool as a potential product for sale and distribution to the research community, we will license the intellectual property in a manner that maximizes the potential for broad distribution of the research tool. In general, we will follow the NIH published Principles and Guidelines for Recipients of NIH Research Grants and Contracts on Obtaining and Disseminating Biomedical Research Resources (64 FR 72090, December 23, 1999).

Genome-Wide Association Studies (GWAS):

Although the proposed project does not include a direct GWAS study, the results may shed light on enhancers (and population variants in these enhancers) in LD blocks that were found significantly associated with different phenotypes by previous GWA studies. At the time of publication, all related data will be made available on the Yu lab website (<http://yulab.icmb.cornell.edu/resources.shtml>) and other data repositories.