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Laboratory**

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for tomorrow's cures*

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Weiniu Gan, Ph.D.
Division of Lung Sciences
National Heart, Lung, and Blood Institute
National Institutes of Health

Re: NHLBI TOPMed Program: Integrative Omics Approaches for Analysis of TOPMed Data U01 (RFA-HL-17-011)(Charles Lee, Ph.D., PI)—Letter of Institutional Support

Dear Dr. Gan and Members of the Review Committee:

It is with great pleasure that I confirm our institution's highest possible support for Dr. Lee in the present application and our commitment to this TOPMed Program project. This project will meet a growing need for analytical tools, methodologies and expertise towards the discovery of meaningful associations between genome sequence and common human diseases. This mission aligns perfectly with JAX's overall goal to discover the precise genomic causes of disease and to empower the global biomedical community through the provision of unique genetic and genomic resources. JAX supports these efforts through significant institutional investments designed to ensure its position as a globally renowned institution for genetics and genomics research spanning the basic, translational and clinical research spectrum.

JAX Genomic Medicine (JAX-GM) is ideally poised to support the objectives and goals of this project. JAX-GM uses a human-centered, computationally oriented genomics approach towards research and discovery into the complex mechanisms of human disease. It is home to some of the world's leading scientists in bioinformatics, genetics, clinical genomics and computational biology. JAX-GM is rapidly hiring faculty and we plan for one-third of the faculty at full capacity to be computationally focused. This is in addition to the rich intellectual expertise already present at JAX through our Computational Sciences team of highly trained bioinformaticians and computational biologists, and our Information Technology staff who provide round-the-clock support to all computational projects. JAX-GM researchers enjoy state-of-the-art facilities, technologies and core services required to advance genomic medicine. Relevant to the current proposal is our extensive data storage, sharing and analysis capabilities. JAX is deeply committed to development of our compute infrastructure and expertise. Since JAX-GM was founded in 2012, we have devoted resources to build high-performance computing capabilities with nearly ~2000 cores and 2 PB of storage space, and these resources will be scaled up further over the next few years. In addition to the computational resources available on site, JAX-GM computational biologists and staff are developing cloud-ready software pipelines to take full advantage of the rapid growth of cloud computing in genomics. This U01 application is therefore perfectly synergistic with the direction of JAX-GM.

I am particularly enthusiastic about the Center's focus on structural variation, a powerful form of genomic variation for which the project PIs, Drs. Charles Lee, Merk Gerstein and Li Ding, have unmatched blend of expertise. Together they bring the requisite experience in SV discovery and

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functional analysis necessary for the proposed program, particularly within the framework of large-scale consortia such as the TOPMed Program.

In summary, I am very enthusiastic about the potential for the this project to make significant inroads in our understanding of human genomic diseases and am committed to investments that will support and enable this project to achieve its goals.

Thank you for considering this proposal.

Sincerely,

A handwritten signature in blue ink, consisting of a stylized 'E' followed by a series of loops and a long horizontal stroke.

Edison T. Liu, M.D.