Research Planning Committee Meeting
Wednesday, August 23, 2017
2:15 p.m.
Doisy Research Center, 8th Floor Conference Room
Minutes

Members Present:
Enrico Di Cera, M.D., Chair
Thomas Burris, Ph.D.
John Edwards, M.D., Ph.D.
Terry Egan, Ph.D.
Daniel Hoft, M.D., Ph.D.
Jackie Kornbluth, Ph.D.
Adriana M. Montaño, Ph.D.
Michael Rauchman, M.D.
Jeff Scherrer, Ph.D.
Joel Eissenberg, Ph.D., *ex officio*
Paul Hauptman, M.D., *ex officio*
Denise Johnson, *ex officio*
Ken Olliff, D.Min., MBA, *ex officio*
William Wold, Ph.D., *ex officio*

Members Not Present:
Dale Dorsett, Ph.D.
John Tavis, Ph.D.
John Long, D.V.M*., ex officio*

Guests:
Kathie Mihindukulasuriya, Ph.D.,

Enrico Di Cera, M.D., chair, called the meeting of the Research Planning Committee (RPC) of the Saint Louis University School of Medicine to order at 2:15 p.m. on Wednesday, August 23, 2017, in the Doisy Research Center, 9th Floor Conference Room.

MINUTES

The Minutes of the June 28, 2017, meeting were approved as submitted.

1. GENOMICS CORE FACILITY

   Dr. Kathie Mihindukulasuriya gave a brief presentation about the goals, services and usage of the Genomics Core. The advantages of the SLU Genomics Core are the collaborative nature of the core which enables researchers to not only have sequencing done, but to obtain help in designing the original experiments, aid in troubleshooting nucleic acid production and customized sequencing and analysis, tailored to their experimental questions. The Genomics Core also has advantages over companies and more high-throughput cores in that the turn-around time from sample to processed sequencing data is about two weeks for standard libraries. In addition, the Genomics Core is able to provide assistance with the preparation of papers and grants, including customized data analysis,

figure generation and letters of support. Extended bioinformatics analysis is billed at an hourly rate.

The cost example of ~$800 per chip refers to the cost of reagents and labor to sequence one chip, which is the smallest unit of sequencing. One chip generates 60 to 90 million reads, which average 100 to 170 nucleotides in length. Two chips are sequenced per run. The number of samples that can be sequenced per chip is determined by the size of the targeted genome, the type of sequencing and the depth needed per sample to address the experimental question. Typically, one chip is sufficient for six RNA-seq samples. Guidance can be given based on past experience, but it may require empirical data to determine the optimal number of samples per chip for a new project.

In order for the Genomics Core to be able to handle a higher throughput, such as the 500-1000/ RNAseq libraries per six months discussed during the meeting, the first bottleneck would be the generation of the libraries themselves. Either additional personnel or investment in automating library production would be needed to meet this level of production coupled with projects from other labs. It would also require a higher throughput sequencer, such as a HiSeq 3000. The estimated cost of upgrading the facility to reach this capacity would be on the order of $1,000,000 for the equipment, and two additional personnel for equipment operation and bioinformatic analysis.

2. COMPENSATION PLAN FOR RESEARCH FACULTY

The August 21, 2017 draft of the Faculty Compensation Plan (distributed with agenda) was presented by Dr. Di Cera for discussion and further development prior to submission to the dean.

There being no further business, the meeting was adjourned at 3:32 p.m.

Respectfully submitted,
Denise Johnson
Director, Planning and Operations