Keck School of Medicine of USC

DEPARTMENT OF PSYCHIATRY AND THE BEHAVIORAL SCIENCES

Ned H. Kalin, MD
Hedberg Professor and Chair of Psychiatry
Director, Health Emotions Research Institute
University of Wisconsin School of Medicine
name/ID/location

October 1, 2014

Dear Ned,

I am writing to confirm my strongest enthusiasm to collaborate with you on your project entitled "Extreme anxiety in females: the role of the bed nucleus of the stria terminalis (BST) during the transition to adolescence in human and nonhuman primates".

name/ID/location and the Associate Chair for California. My research focuses on identifying human disease genes for a number of psychiatric and cardio-pulmonary illnesses, as well as a basic neuroscience infrastructure project that is describing the transcriptome of the human brain throughout the lifespan. At the current time, nearly all of these projects are being approached by utilizing next generation genome and transcriptome sequencing techniques. We purchased our first Illumina Genome Analyzer in the summer of 2007 and my lab now owns two HiSeq2000s and one HiSeq2500 DNA sequencers. For humans, we have already sequenced greater than 150 whole genomes at 32X and more than 1,000 libraries for RNA-Seq, a large portion of which were part of the BrainSpan project (BrainSpan.org). We're also currently funded by the NIH Common Fund to perform single-cell RNA-Seq on thousands of cells.

As described in the preliminary data section of your proposal, this expertise has now been applied to the Rhesus monkey with the RNASeq of 48 amygdala samples. As part of this effort, we have developed the a bioinformatic pipeline for analyzing Rhesus RNA-Seq data, and version 1.0 is now available to the general scientific community (Wang et al., 2011, Bioinformatics). We plan to continue the development of this software, which is currently being supported by U01HG006531 from NHGRI, throughout your proposed project period.

I find your proposal using RNA sequencing to examine transcriptome-wide gene expression within the BST of nonhuman primates, a central region for sustained anxiety, to be extremely exciting. It is an excellent complement and extension of the research that we are doing in both the genetics of the depression and the anxiety disorders, and human brain gene expression. Hence, I am eager to be a part of this work, as it builds on your extensive validation of the rhesus monkey model of anxious temperament, and the knowledge gained will obviously translate to a better understanding of human anxiety and depression.

We have also just published the first use of RNA-Seq for single-cell transcriptomics (Qui et al, Frontiers in Genetics), so we anticipate no problems doing RNA-Seq on LCM material (100's of cells).

University of Southern California
name/ID/location

In summary, I think I am well suited for this collaboration, and my track record as a well-established psychiatric geneticist with years of experience in large-scale collaborations speaks for itself. I have thoroughly enjoyed working with you and your team over the last year and look forward to regular interactions as our fruitful collaboration continues.

Sincerely,

name/ID/location