

**DEPARTMENT OF HEALTH & HUMAN SERVICES**

Public Health Service

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To whom it may concern,

It is a pleasure to write a letter in support of the Bioinformatics Support Group in the Advanced Biomedical Computing Center (ABCC) of the National Cancer Institute (NCI). My collaboration with them began in January, 2008 on a project designed to identify common integration sites (CIS) for the mouse mammary tumor virus (MMTV) in mouse mammary tumors. Robert Stephens, Director of the Bioinformatics Support Group was given nucleotide sequence data of MMTV host-viral junction fragments from viral induced mammary tumor DNA. He and Uma Mudunuri developed statistically significant parameters to identify candidate target genes for each putative CIS. As a first screen to determine whether the expression of the candidate CIS gene was affected we did microarray analysis of tumor RNAs from tumors containing the particular CIS. Jack Chen did the normalization of the microarray data. Uma Mudunuri and Jigui Shan developed databases for web interface that will be publicly accessible in which all of the genes on the chip can be analyzed for their expression in over 100 independent viral induced mouse mammary tumors containing CISs. In addition, information on CIS target gene ontology and whether they are also targets for genetic alteration in primary human breast tumors was determined by analysis of publicly available databases. The results of this project are currently being prepared publication and members of the Bioinformatics Support Group will be co-authors.

The Bioinformatics Support Group has also collaborated with us on two other projects. One of these involves microarray analysis of RNA expression during mouse mammary gland development from before puberty through pregnancy, lactation and involution. This analysis is being done by Ming Yi and is currently being verified using quantitative RT PCR by my laboratory. Another project is concerned with identification of a CBF1 independent component of activated Notch4 signaling. The approach involves microarray and CHIP on chip analysis of RNA and DNA, respectively from tissue culture cell line expression various Notch4 expression vectors. These analysis are being done by Anney Che and Ming Yi.

The common denominator in all three projects has been the depth and breathe of experience in the Bioinformatics Support Group. Their team approach has been highly productive and clearly warrants expanded support.

Sincerely yours,



Robert Callahan, Ph.D.
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