Research Portfolio Online Reporting Tools (RePORT)

# Project Information

5P01CA085878-11

DESCRIPTION | DETAILS | RESULTS

**Parent Project Number:** 5P01CA085878-11 **Sub-Project ID:** 6716
**Title:** BIOINFORMATICS CORE

**Contact PI / Project Leader:** VERHAAK, ROELAND
**Awardee Organization:** UNIVERSITY OF MICHIGAN

**Abstract Text:**

C O R E C : The aim of the Bioinformatics Core ('Core C ) is to identify and characterize genes and pathway activation patterns cnjcial for gliomagenesis or GBM homeostasis. Core C will use commonly applied methods for DNA copy analysis and gene expression analysis to identify and characterize genes and pathway activation patterns crucial for gliomagenesis or GBM homeostasis, on data from the model systems developed by each of the Projects. We will work closely with the project investigators to a) provide analytical support to their research and b) suggest follow up experiments guided by our genomic data analysis. We will apply commonly used analytical methods for preprocessing of Affymetrix 3' UTR and exon expression array data, such as quantile normalization and Robust Multi-array Averaging (RMA); parametric methods for identifying differentially expressed genes such as Significance Analysis of Microarrays (SAM) and limma, and Gene Set Enrichment Analysis (GSEA) as implemented in R (http://www.r-project.org) and Bioconductor (http://www.bioconductor.org). For analyzing DNA copy number data, we will use the GIST1C2.0 approach as implemented in Matlab (Mermel C et al. Genome Biology 2011) for data normalization and identification of genomic targets. For analysis of sequencing data we will make use of fast short read alignment methods such BWA, and the processing abilities of tools such as samtools (http://samtools.sourceforge.net) and the Genome Analysis Toolkit (http://www.broadinstitute.org/gsa/wiki/index.php/The_Genome_Analysis_Toolkit). Prior to analysis of xenograft data, we will correct for crossreactivity of mouse mRNA to the Affymetrix platforms that are being used, by mapping probes from each GeneChip to mm 10. We will then generate probe sets for each human gene only including probes that did not show significant alignment to mmlO. We will project findings from the mouse model from Project 2 through mapping of mouse genes to human genes using Ensembl. We will use our intimate knowledge of the data from The Cancer Genome Atlas to project our findings on human GBM data sets. Our core personnel are experienced in analysis of genomic data types and interpretation of the results in the context of larger studies. Moreover, we have been closely working with the TCGA analysis working groups and have shown the ability to collaborate and communicate. This ensures a productive research environment in which the different aims of this project proposal can effectively come to fruition. RELEVANCE (See instructions): Malignant gliomas are now understood to consist of a variety of subtypes rather than a single disease. This Core will sen/e to elucidate the distinguishing signatures of these tumor subtypes in an effort to determine the underiying basis of their initiation and sensitivity or resistance to therapy.

**NIH Spending Category:**

Biotechnology; Brain Cancer; Brain Disorders; Cancer; Genetics; Human Genome; Neurosciences; Rare Diseases

**Project Terms:**

3' Untranslated Regions; analytical method; base; Bioconductor; Bioinformatics; Biological Models; Biology; Biometry; Biostatistics Core; Brain Neoplasms; Cancer Center; Collaborations; Communication; Data; Data Analyses; data modeling; Data Set; Disease; DNA; DNA copy number; Ensure; Environment; Exons; experience; follow-up; Gene Chips; Gene Expression; Gene Expression Profiling; Genes; Genome; genome analysis; Genomics; Gliomagenesis; Goals; Homeostasis; Human; Human Resources; indexing; Instruction; Knowledge; Malignant Glioma; Maps; Messenger RNA; Methods; Michigan; Microarray Analysis; mouse model; Mus; Pathway interactions; Pattern; Process; Reading; Recurrence; Research; Research Design; Research Personnel; research study; Sequence Analysis; Services; skills; Slide; success; Survival Analysis; symposium; The Cancer Genome Atlas; therapy resistant; tool; Travel; Treatment Efficacy; Tumor Subtype; wiki; Work; working group; Xenograft procedure

| Contact PI Information: | Program Official Information: | Other PI Information: |
|---|---|---|
| **Name**: VERHAAK, ROELAND<br>**Email**: Click to view contact PI email address<br>**Title**: ASSISTANT PROFESSOR | **Name**: Unavailable | Not Applicable |

| Organization: | Department / Educational Institution Type: | Congressional District: |
|---|---|---|
| **Name**: UNIVERSITY OF MICHIGAN | Unavailable | State Code: MI |
| **City**: ANN ARBOR Country: UNITED STATES (US) | Unavailable | District: 12 |

**Other Information:**

**FOA**: PAR-12-005
**Study Section**: Special Emphasis Panel (ZCA1-RPRB-W)
**Fiscal Year**: 2014 **Award Notice Date**: 4-AUG-2014

**DUNS Number**: 073133571
**Project Start Date**:
**Budget Start Date**: 1-JUL-2014

**CFDA Code**:
**Project End Date**:
**Budget End Date**: 30-JUN-2015

**Administering Institutes or Centers:**

NATIONAL CANCER INSTITUTE

**Project Funding Information for 2014:**

**Total Funding**: $147,529 **Direct Costs:** $59,271 **Indirect Costs:** $88,258

| Year | Funding IC | FY Total Cost by IC |
|---|---|---|

| Year | Funding IC | FY Total Cost by IC |
|---|---|---|
| 2014 | | $147,529 |

Categorical Spending by IC:

Click here for more information on NIH Categorical Spending

Page Last Updated on June 13, 2015
This site is best viewed with Internet Explorer (8.0 or higher) or Mozilla Firefox (11.0 or higher).

NIH...*Turning Discovery Into Health*®

RePORTER2N