High throughput genomics (Ramot)

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Noam Shomron, T.A.U Tel Aviv University, Medicine-Sackler Faculty, Cell and Developmental Biology

DESCRIPTION:

The Shomron research team focuses on the analysis of genomics aimed at understanding human disease. Combining high-throughput methods and bioinformatics, our team's research explores gene regulators, such as microRNAs, in order to reach a global, systems perspective on the mechanistic roles small RNA play during disease development.

Among our projects: Identification of a microRNAs that are in the intersection of several oncogenes; Revealing the influence of microRNAs on pharmacogenomics and personalized medicine; Exposing pathogens in human tissues based on deep sequencing of small RNA molecules followed by subtraction and assembly of the genomes.

Overall the Shomron team pursues research that aims to deepen our understanding on the development of diseases in order to generate a significant impact through translating ideas into clinical reality.

FEATURED SERVICES

Bioinformatics and scientific consultation

Per hour consultation for bioinformatics analysis strategy and support, in wide range of expertise from different gene expression related topics to high throughput methodologies and statistical analysis

Mutation/variant calling from DNA sequencing data

Analysis of existing whole exome/genome sequencing data to detect variants and mutations versus reference genome or paired sample and prioritization of mutations based on their predicted effects.

microRNA target gene identification

For microRNA target gene identification the lab utilizes numerous bioinformatic methods including software tools, computational methods developed in-house and integration of omic data. Downstream functional assays such as Luciferase assay are then conducted to experimentally validate the targets.

SSRI response biomarkers testing

Measuring SSRI response genes and miRNA panel on a given set of samples or computationally on a

provided dataset

Network and gene ontology analysis

Network and gene ontology analysis is used for functional analysis and correlation of gene function. Relevant data integrated for all input genes or a prioritized subset of molecules and mapped onto interaction networks.

High-Throughput Sequencing

High-Throughput Sequencing of DNA/RNA, based on the Illumina Genome Analyzer IIx instrument sequencing machine.

Sample library preparation of RNA/DNA, using all current Illumina protocol

Preparation of library for sequencing from input of RNA/DNA, using all current Illumina protocol: DNA-seq, RNA-seq, small RNA, Chip-seq and de-novo assembly.

Whole exome sequencing (WES) including variant calling and prioritization.

Whole exome sequencing (WES) including variant calling and prioritization. WES is used by the lab to identify causative variants in clinical cases

Statistical analysis of TCGA data

Download, processing and query of data from The Cancer Genome Atlas (TCGA) to obtain valuable insights into the expression of various genes, genesets and miRNAs as well as mutations and comparison with clinical features.

“Wet lab” services

Wound healing assay

In-vitro assay to measure the ability of cells to migrate, adherent cells monolayers are scratched with pipette tip and allowed to close the wound for several hours and next pictured and differences between cells are analyzed.

Transwell migration and invasion assays

In-vitro assays to test the ability of cells to migrate or invade through a either transwell inserts for migration assays or Matrigel-coated invasion chambers. Following the assay cells are fixed, stained and quantified to assess the relative rate of migration/invasion

Dual luciferase reporter assay

Assay to measure transcription rate using a plasmid reporter inserted with desired sequence upstream to the Firefly Luciferase. The assay measures the Firefly and Renilla (internal control) Luciferase activities and allows to determine sequence changes on transcription. The assay could also be adapted to used 3’ UTR sequences and measure repression of transcription by microRNAs.

XTT Cell Proliferation Assay

Colorimetric method to effectively measure cell growth and drug sensitivity in cell lines. XTT is a colorless or slightly yellow compound that when reduced by Cellular Enzymes becomes brightly orange a thus allows to quantify cell number following treatment

miRNA Cloning

Cloning miRNA of choice into an overexpression construct

miRNA Inhibition

Antagomir based blocking of a miRNA of choice

miRNA Quantification

Modified real-time PCR for quantifying miRNAs

Deep Sequencing miRNA quantification

Quantifying total miRNA expression by deep sequencing includes library preparation, sequencing, raw data processing, miRNA alignment, standardization of miRNA reads and final ranking of differential miRNA expression levels

Model for HIV-1 Infection

HIV-1 infectious model of T1, Sup-T1, and H9 lymphocytes as well as HeLa-CCR5 and JLTRG-R5 cells

Intracellular FACS staining

Quantification of intracellular protein levels across various populations of cells

miRNA Transfections

Transfection of miRNAs overexpression vectors to specified target cells

Contact for more information:
Liat Hadad ✉, VP BD, +972.54.5555061

Ramot at Tel Aviv University Ltd. P.O. Box 39296, Tel Aviv 61392 ISRAEL
Phone: +972-3-6406608
Fax: +972-3-6406675