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BGI

Dr. Tom

An Advanced and Intuitive
RNA Data Visualisation System for
Efficient Analysis and Discovery

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Overview

Quick and Convenient Data Visualisation Tools for RNA Expression Analysis

Use a wide range of interactive data visualisation tools to quickly and effectively detect differential expression patterns, including heatmaps, enrichment charts, networks and more.

Mine Your RNA Data with Powerful and Intuitive Tools for Deeper Insight

Go beyond basic expression analysis with Dr.Tom's powerful and advanced algorithms, which combine with the table-chart interactive tools to provide new insight.

Quickly Reference World - Leading Public Databases for Cross Analysis

Supported with references from world-leading databases including KEGG, TCGA and NCBI.

AI-based Literature Retrieval and Big Data Interrogation

Convenient and effortless functionality to uncover relevant relationships between genes of interest and to explore pathways.

Introduction

Dr.Tom is a web-based solution for the convenient analysis, visualisation and interpretation of all types of RNA data, including small RNA，mRNA and lncRNA.

Designed by a team of expert RNA scientists and bioinformaticians at BGI with collective experience across thousands of RNA based research projects, Dr.Tom provides a wide range of intuitive and interactive data visualisation tools specifically designed to save you time in your differential expression or pathway analysis research.

In addition, powerful analysis tools and advanced algorithms allow you to mine your data to gain new insight and more value beyond standard available RNA analysis services.

Data from many of the world's leading databases have been integrated into the Dr.Tom system allowing users to reference and cross check all results and findings.

Dr.Tom is already relied upon by hundreds of scientists and researchers, and has shown itself to be a valuable and important tool in addition to any institution's own internal data curation and analysis efforts. To learn more, email us for a no obligation discussion about access.

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Main Applications

Multiple tool boxes and table-chart visualisation functionality for speeding up common RNA analysis work

Multiple databases to enable new insight for data mining
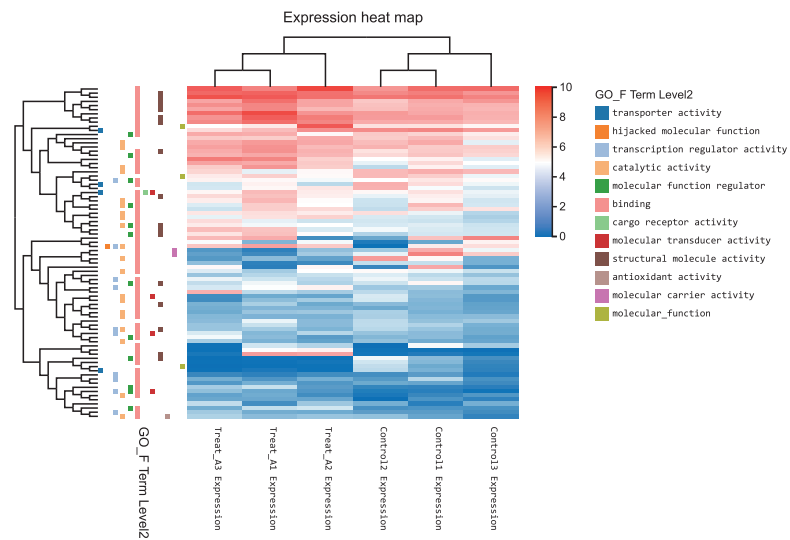
User Profiles

Any scientist who needs ready made data analysis tools and workflows to speed up their research work

Any research scientist who needs easy access to multiple database references.
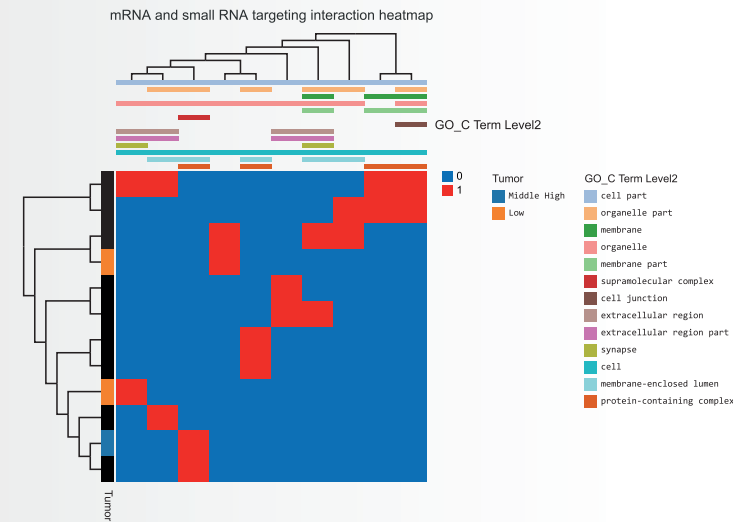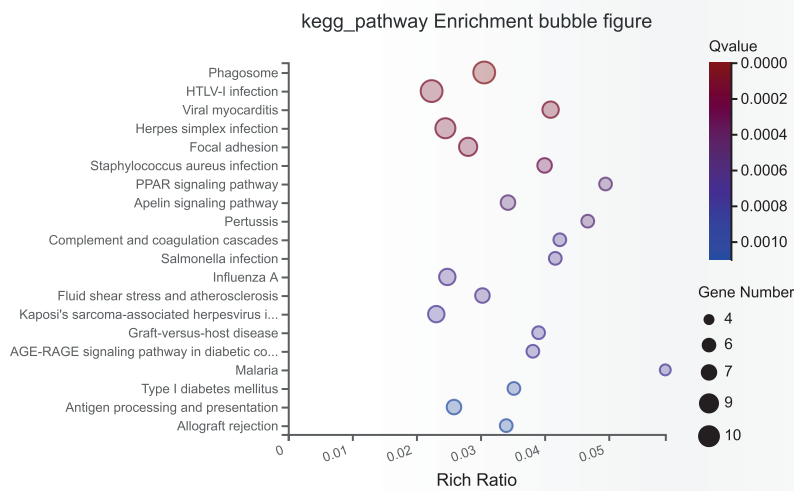
Core Capabilities

Expression Analysis

Expression heat map

Dr.Tom's detailed, interactive heatmap functionality can be used to quickly identify genes that are commonly regulated. With simple point-and- click action, data can be selected and manipulated to show clusters under different pathways.

Gene Set Enrichment Analysis

Dr.Tom accesses both free and licensed KEGG databases to allow users to conveniently and quickly find statistically significant trends in the large lists of genes generated by many functional genomics techniques and bioinformatics analyses approaches.

kegg_pathway Enrichment bubble figure

Association Analysis

mRNA and small RNA targeting interaction heatmap

With a simple click Dr.Tom lets users detect RNA association with target genes, based on their interaction relationship (such as PPI, Target, Co-expression, ceRNA, GGI and RNAplex), or based on the position relationship (such as upstream and downstream position).

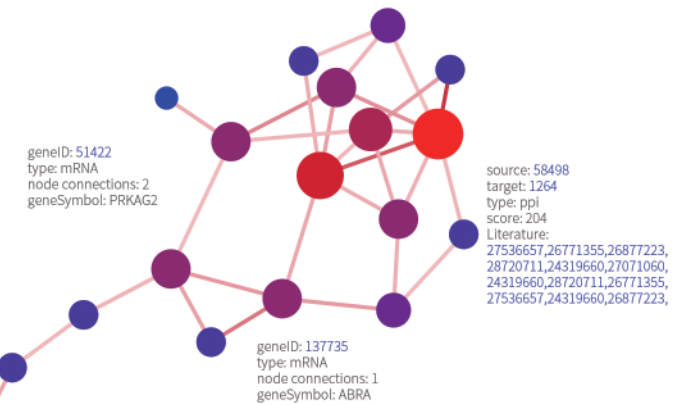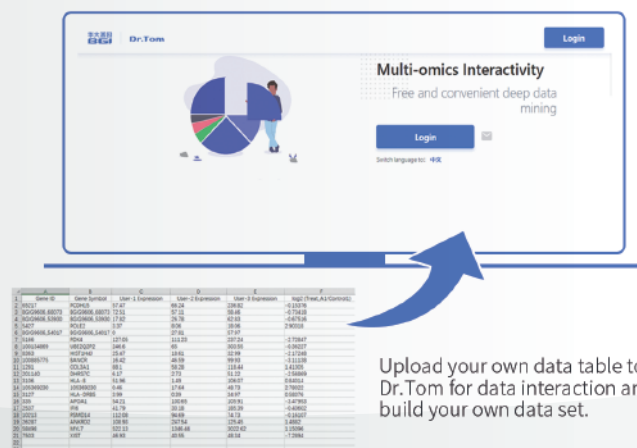## Reference Ontological Information Across Multiple Databases

Dr.Tom is able to reference multiple-databases for association analysis, including TCGA, NCBI and many more. This allows a user to quickly and conveniently view comprehensive ontological information for any gene of interest, including annotation, sequences, expression level, and a list of relevant published papers.

Fig. of Reference Ontological Information Across Multiple Databases

Custom Datasets

Fig. of Custom Datasets

Customers can upload their own gene expression data, using tool boxes for graphing and visualisation, and construct their own gene annotation database for enrichment, clustering and multi-omics association analysis.

User Example

Clinical Epigenetics

RESEARCH   **Open Access**

Co-inhibition of HDAC and MLL-menin interaction targets MLL-rearranged acute myeloid leukemia cells via disruption of DNA damage checkpoint and DNA repair

Jing Ye[1†], Jie Zha[1†], Yuanfei Shi[1†], Yin Li[2], Delin Yuan[1], Qinwei Chen[1], Fusheng Lin[1], Zhihong Fang[1], Yong Yu[3*], Yun Dai[4*] and Bing Xu[1*]

Background:
The researchers wanted to study the mechanism of poor prognosis of chidamide and MI-3 (hereinafter referred to as C and M) inhibitors for synergistic treatment of mixed leukemia (MLL) gene recombination. They utilised multiple Dr.Tom analysis functions to help answer several questions key to their paper. Some of these questions and how they were answered are listed below.

1. The researchers wanted to know what are the pathways for change after processing?
KEGG enrichment analysis showed that when C and M were combined, the most significant pathways were cell cycle, DNA replication, and repair pathways.
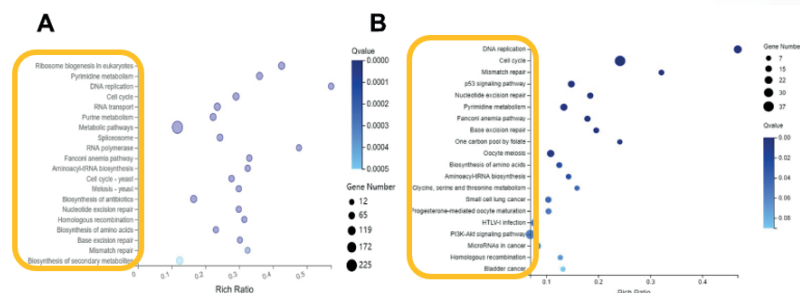

Figure 1 A and B are KEGG enrichment analysis after processing for 24 and 48 hours, respectively

2. The researchers wanted to know which treatment effect is more obvious and causes the above pathways change?
GSEA analysis further showed that the vast majority of these changes originated from C, not M (Figure 2B is processed by C).
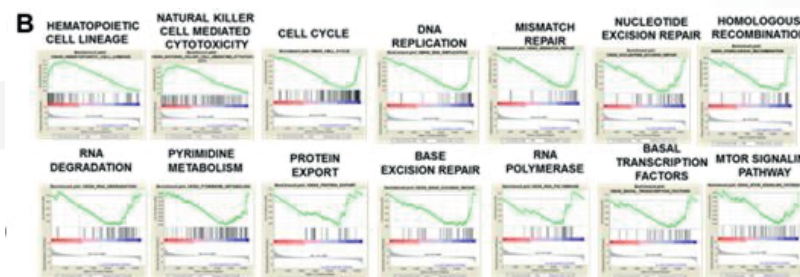

Figure 2 GSEA analysis under C treatment

3. The researchers wanted to know what is the intersection of differentially expressed genes under each treatment?
Venn diagrams of differential genes under different treatments, 635 genes were expressed under all three treatments (Figure 3C).
They also wanted to learn are these genes up / down regulated consistently across treatments?
Clicking on the center of the graph shows the gene set, and a heat map is shown. 59 genes showed different trends (shown in the box in Figure 3D). M treatment was down-regulated and C treatment or M + C treatment was up-regulated.
The researchers then wanted to screen out the genes with different trends, as above.
By selecting the box on the map, the relevant gene set is shown, and a heat map generated. The heat map (Figure 3E) corroborates the result of point 2.
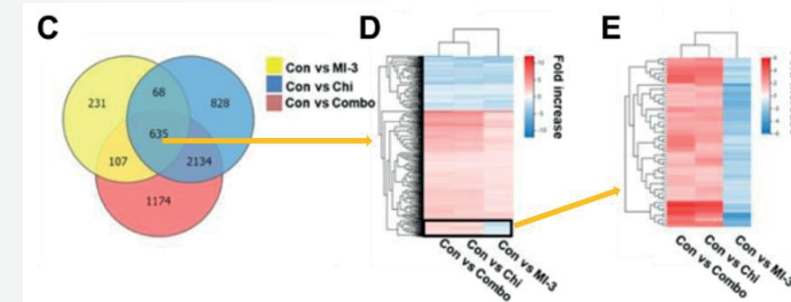

Figure 3 Venn diagrams of differential genes at three hours in three treatments of C. D, a heat map of gene clustering in common, and 59 heat maps of different genes with different expression trends in each treatment of E

4. The researchers wanted to know what is the function of the genes shown in the previous step?
GO and KEGG analysis (Figures 4D and E) found that these genes are involved in key survival signaling pathways, cytokine pathways necessary for inflammatory responses.
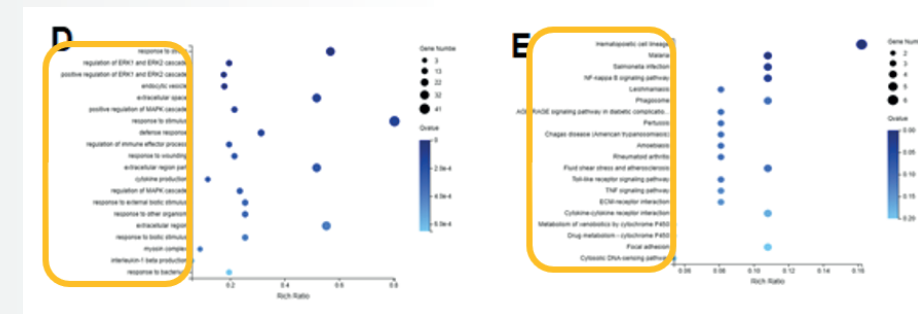

Figure 4 D and E are GO and KEGG analysis of 59 genes, respectively

5. The researchers wanted to continue to screen for other key genes.
They selected different groups of expressions, adjusted the filtering conditions, and generated a heat map.
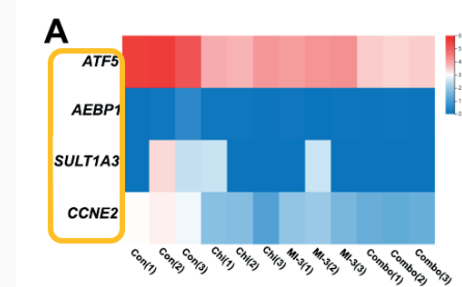

Figure 5 Heat map of clustering of four key genes

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BGI Genomics is the world's leading provider of genomic sequencing services and proteomic services, now serving customers in more than 66 countries. We provide academic institutions, pharmaceutical companies, health care providers and other organizations with integrated genomic sequencing and proteomic services and solutions across a broad range of applications spanning:

• Basic research covering human, plant, animal and microbial species
• Clinical research in human health
• Genetic testing and screening
• Drug discovery and development
• Agriculture and Biodiversity preservation and sustainability

We have almost 20 years of genomics experience helping our customers achieve their research goals by delivering rapid, high quality results using a broad array of cost-effective, cutting-edge technologies, including our own innovative DNBSEQ™ sequencing technology.

Speak to your local BGI sales representative to learn more about Dr Tom.

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