Method

Highly accessed Open Access

# The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation

**Hideya Kawaji**[1], **Jessica Severin**[1], **Marina Lizio**[1], **Andrew Waterhouse**[1], **Shintaro Katayama**[1], **Katharine M Irvine**[2], **David A Hume**[3], **Alistair RR Forrest**[1,4], **Harukazu Suzuki**[1], **Piero Carninci**[1], **Yoshihide Hayashizaki**[1] and **Carsten O Daub**[1]

1 RIKEN Omics Science Center, RIKEN Yokohama Institute, 1-7-22 Suehiro-cho Tsurumi-ku Yokohama, Kanagawa, 230-0045 Japan

2 Institute for Molecular Bioscience, University of Queensland, Brisbane, St Lucia QLD 4072, Australia

3 The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Roslin, EH259PS, UK

4 The Eskitis Institute for Cell and Molecular Therapies, Griffith University, QLD 4111, Australia

author email  corresponding author email

*Genome Biology* 2009, **10:**R40  doi:10.1186/gb-2009-10-4-r40

Published: 19 April 2009

http://fantom.gsc.riken.jp

単芽球から単球への分化モデル(ヒトTHP-1細胞)の時系列プロファイル

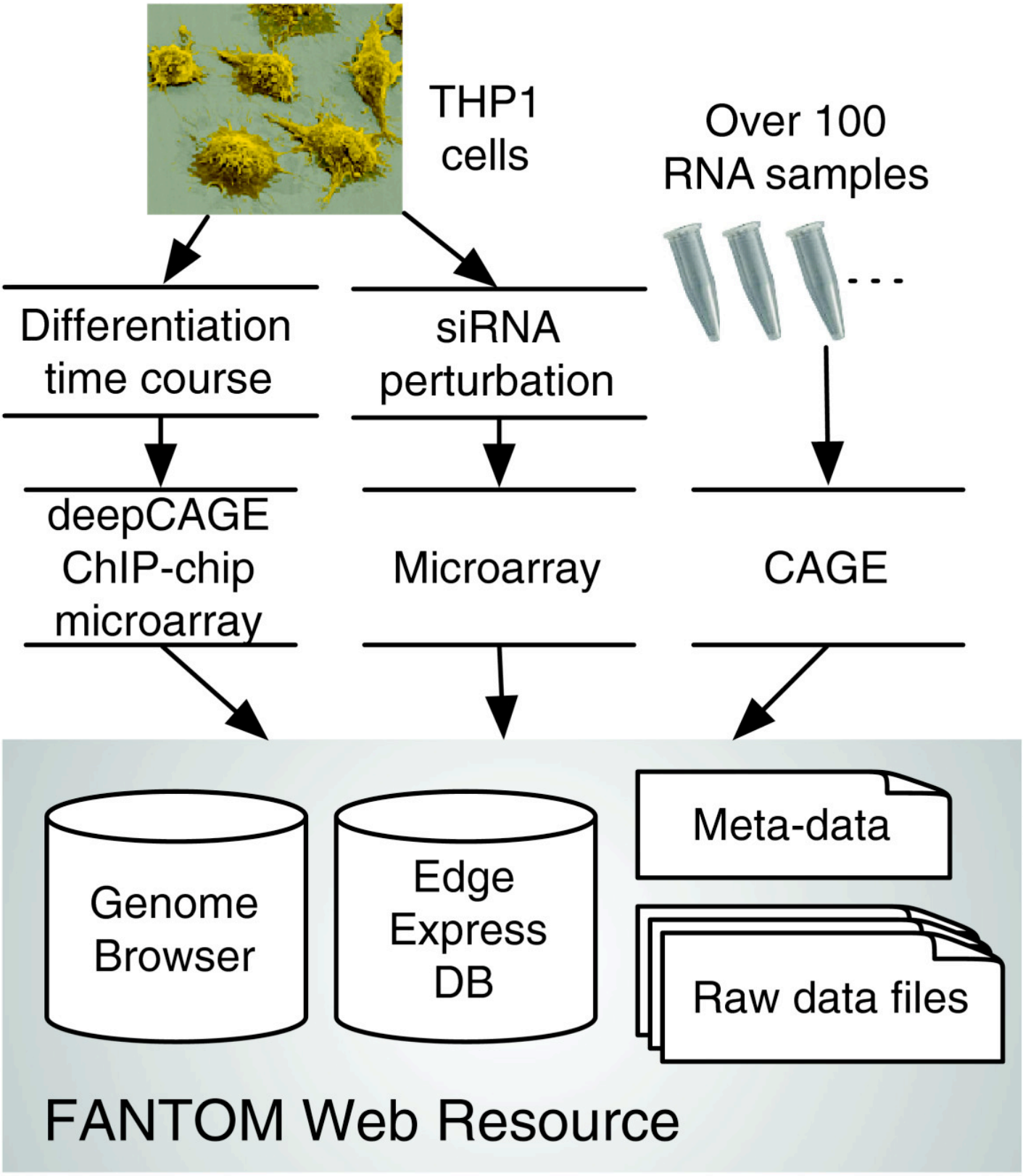
- 転写開始点とその活性 (CAGE)
- 低分子RNA (small RNA sequencing)
- 遺伝子発現量 (Illumina microarray)
- 2000転写因子の発現量 (qRT-PCR)
- RNA polymerase II 結合領域 (ChIP-chip)
- H3K9アセチル化領域 (ChIP-chip)
- 転写因子PU.1結合領域 (ChIP-chip)
- 転写因子SP1結合領域 (ChIP-chip)
- 転写因子EGR1結合領域 (ChIP-chip)

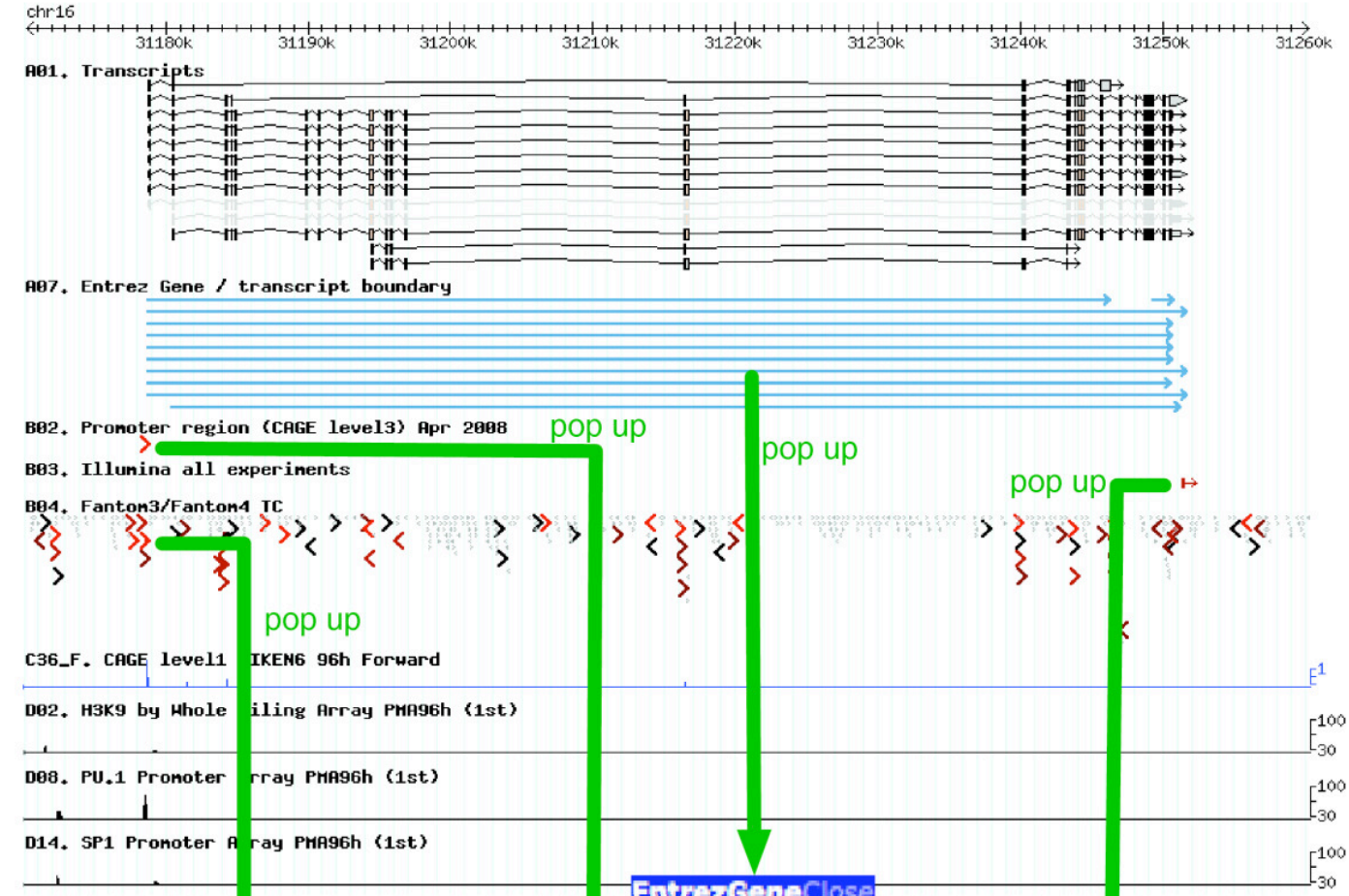
単芽球モデル(THP1)のperturbation実験
(52転写因子に対するsiRNA)

- 遺伝子発現量 (Illumina microarray)

ヒト・マウスにおける転写開始点とその活性

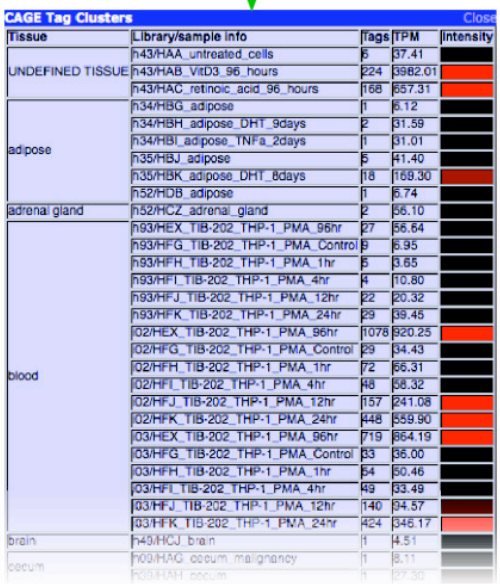
- 2.9 million mapped tags / 127 RNA (ヒト)
- 1.1 million mapped tags / 206 RNA (マウス)


THP1
cells
Over 100
RNA samples
Differentiation
time course
siRNA
perturbation
deepCAGE
ChIP-chip
microarray
Microarray
CAGE
Genome
Browser
Edge
Express
DB
Meta-data
Raw data files
FANTOM Web Resource

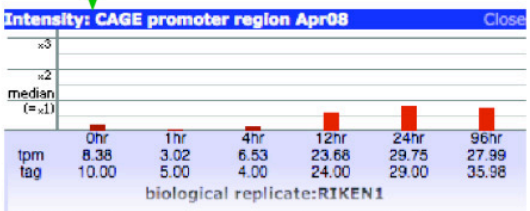



EntrezGeneClose
EdgeExpressDB

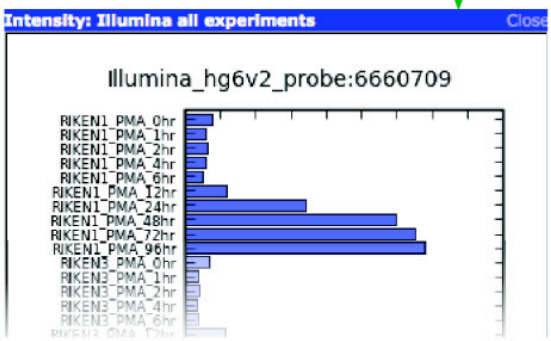
Hyperlink to regulatory relationships stored in EdgeExpressDB




CAGE-based promoter activity of different cells

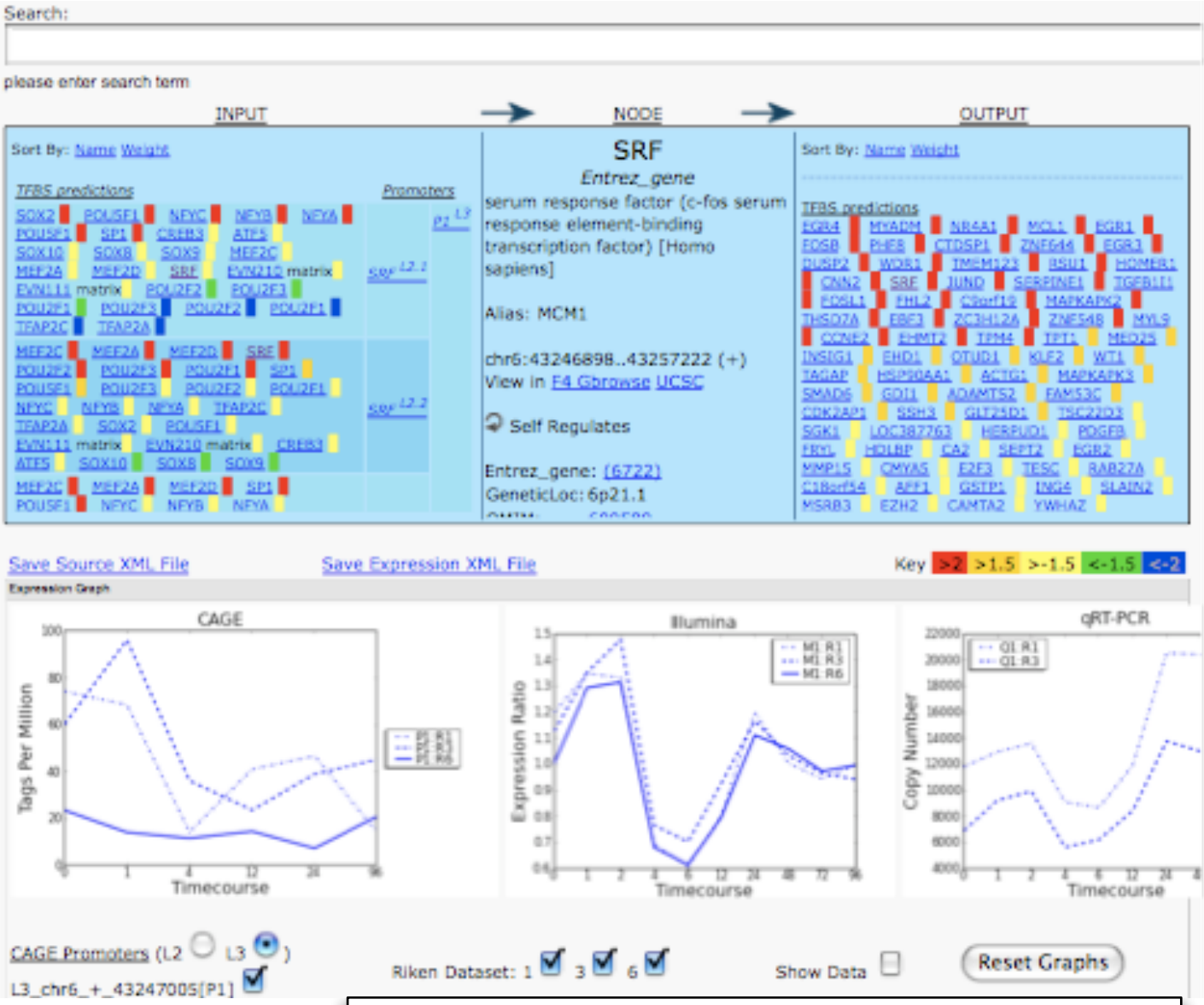



CAGE-based promoter activity of THP-1 differentiation timecourse




Microarray-based Gene expression of THP-1 differentiation timecourse and 52 siRNA perturbation

# Genome Browser




Software

Highly accessed Open Access

# FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions

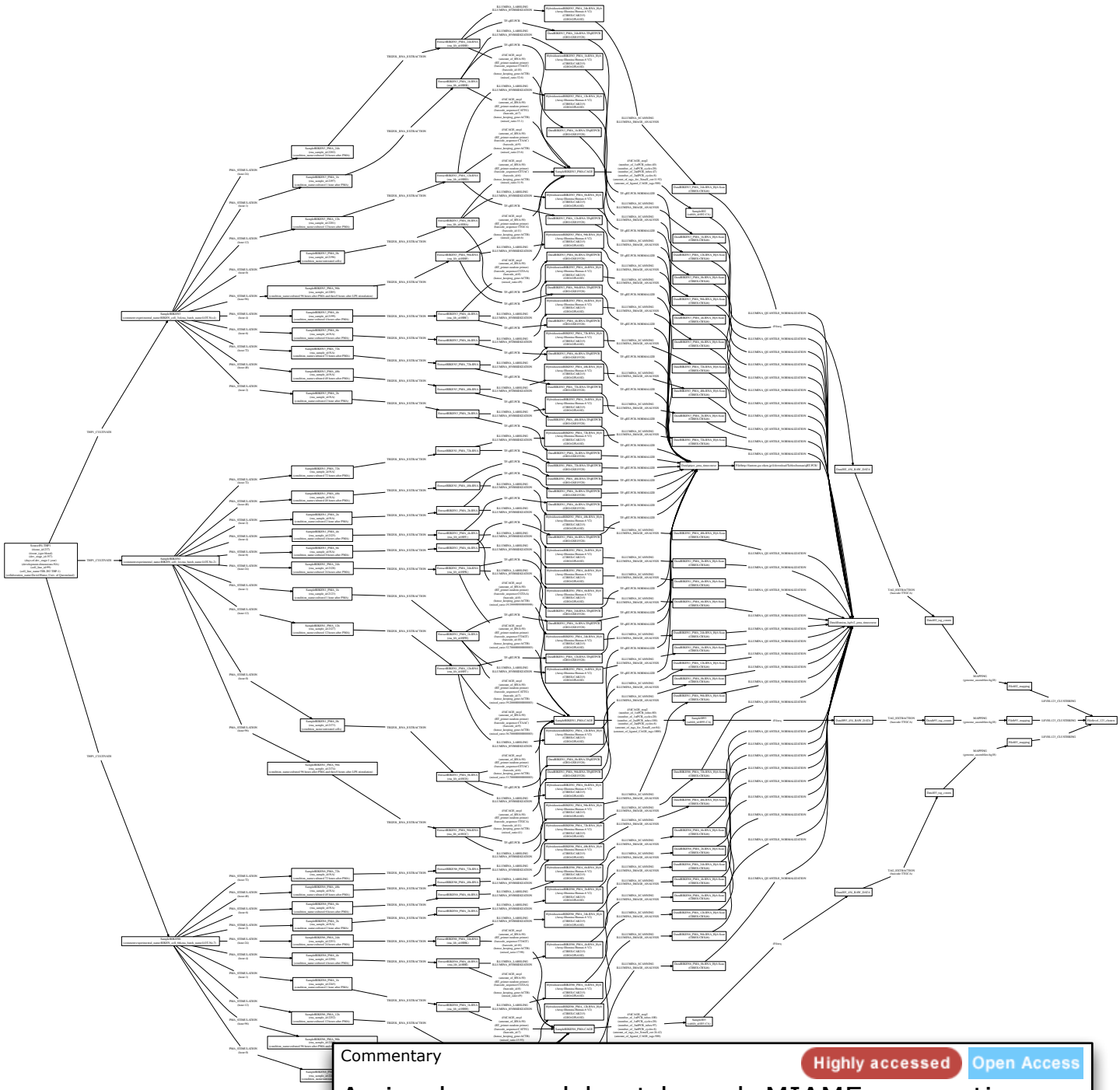
**Jessica Severin**[*1], **Andrew M Waterhouse**[*1], **Hideya Kawaji**[1], **Timo Lassmann**[1], **Erik van Nimwegen**[2], **Piotr J Balwierz**[2], **Michiel JL de Hoon**[1], **David A Hume**[3], **Piero Carninci**[1], **Yoshihide Hayashizaki**[1], **Harukazu Suzuki**[1], **Carsten O Daub**[1] and **Alistair RR Forrest**[1,4]

1 RIKEN Omics Science Center, RIKEN Yokohama Institute, 1-7-22 Suehiro-cho Tsurumi-ku Yokohama, Kanagawa, 230-0045 Japan
2 Biozentrum, University of Basel, and Swiss Institute of Bioinformatics, Klingelbergstrasse, CH-4056 Basel, 4056, Switzerland
3 The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Roslin, EH259PS, UK
4 The Eskitis Institute for Cell and Molecular Therapies, Griffith University, Brisbane Innovation Park, Don Young Road, Nathan, QLD 4111, Australia

author email corresponding author email * Contributed equally

*Genome Biology* 2009, **10:**R39 doi:10.1186/gb-2009-10-4-r39

# EdgeExpressDB



Commentary

Highly accessed Open Access

## A simple spreadsheet-based, MIAME-supportive format for microarray data: MAGE-TAB

**Tim F Rayner**[1], **Philippe Rocca-Serra**[1], **Paul T Spellman**[2], **Helen C Causton**[3], **Anna Farne**[1], **Ele Holloway**[1], **Rafael A Irizarry**[4], **Junmin Liu**[5], **Donald S Maier**[6], **Michael Miller**[7], **Kjell Petersen**[8], **John Quackenbush**[9], **Gavin Sherlock**[10], **Christian J Stoeckert Jr**[5], **Joseph White**[9], **Patricia L Whetzel**[5], **Farrell Wymore**[6], **Helen**
nd **Alvis Brazma**[1]
e Campus, Hinxton, Cambridge, UK
l College Hammersmith Hospital Campus,
Health, Baltimore, MD, USA
iversity of Pennsylvania School of
f Medicine, Stanford, CA, USA
USA
Biology Unit, University of Bern
cine, Stanford, CA, USA

*BMC Bioinformatics* 2006, **7:**489 doi:10.1186/1471-2105-7-489

Software

Highly accessed Open Access

## SDRF2GRAPH – a visualization tool of a spreadsheet-based description of experimental processes

**Hideya Kawaji**, **Yoshihide Hayashizaki** and **Carsten O Daub**
RIKEN Omics Science Center, RIKEN Yokohama Institute, 1-7-22 Su iro-cho urumi-ku Yokohama, Kanagawa, 230-0045 Japan

author email corresponding author email

*BMC Bioinformatics* 2009, **10:**133 doi:10.1186/1471-2105-10-1

# Meta-data