

# FANTOM findings boost for biologists

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Genomic regulatory blocks have unique features that may explain their ability to respond to regulatory inputs from very long distances, according to a special thematic series of companion articles from the FANTOM4 consortium. This research, to be published across a number of BioMed Central's open access journals, including *Genome Biology* and *BMC Bioinformatics*, provide further insight into HCNE (highly conserved non-coding element) mediated long-range gene regulation at the core of animal multicellularity regulation.

Now at its fourth stage, FANTOM4, prominently led by OSC's Yoshihide Hayashizaki, has culminated after over three years of research. The center joined forces with scientists from research centers and universities in Australia, Switzerland, Norway, South Africa, Sweden, Canada, Denmark, Italy, Germany, Singapore, UK and the United States to publish three milestone papers in the journal [Nature Genetics](#), along side the companion articles in BioMed Central, that challenge current notions of how genes are controlled in mammals.

In one *Genome Biology* article, researchers have created a novel database and set of interfaces to interpret biological networks and compare large high-throughput expression datasets. For more details please access the database (<http://fantom.gsc.riken.jp/4/edgeexpress/>)

Another study helps address major challenges in genomics including unravelling the orchestration of correct [gene expression](#). FANTOM researchers have developed a suite of computer programs to identify chromatin conformation signatures, which could provide a completely

novel class of human disease biomarkers. Further details of the software are available online at <http://dostielab.biochem.mcgill.ca/>

The international FANTOM4 research collaboration yielded a wide range of genome-scale data, including 24 million mRNA 5'-reads (CAGE tags) and microarray expression profiles along a differentiation time course of the human THP-1 cell line and data regarding chromatin status. These data are detailed in a new article from *Genome Biology*, and are also available as an integrated web resource (<http://fantom.gsc.riken.jp/4/>).

Further research published in *BMC Bioinformatics* highlights two new data-driven normalization methods for quantitative reverse transcriptase polymerase chain reaction (qPCR) experiments with larger data sets. Another study published in *Genome Biology* includes the first genome-wide analysis of EGR-1 binding sites implicated in cell differentiation in human monoblastoma THP-1 cells.

Dr. Harukazu Suzuki, the scientific coordinator said, "We are proud that we have created groundbreaking research in understanding more about how genes regulate cells at the molecular level and we want to acknowledge all consortium members for their great contribution to the research effort."

These are the first papers to be published from the consortium using BioMed Central's new cross-journal thematic series ability. And there are more to follow - a full list is available from the FANTOM4 series homepage (<http://www.biomedcentral.com/series/FANTOM4>)

[More information:](#)

Articles:

Transcriptional features of genomic regulatory blocks

Altuna Akalin, David Fredman, Erik Arner, Xianjun Dong, Jan Christian Bryne, Harukazu Suzuki, Carsten O Daub, Yoshihide Hayashizaki and Boris Lenhard

Genome Biology 2009, 10:R38 (19 April 2009)

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

Jessica Severin, Andrew M Waterhouse, Hideya Kawaji, Timo Lassmann, Erik van Nimwegen, Piotr J Balwierz, Michiel JL de Hoon, David A Hume, Piero Carninci, Yoshihide

Hayashizaki, Harukazu Suzuki, Carsten O Daub and Alistair RR Forrest  
Genome Biology 2009, 10:R39 (19 April 2009)

Chromatin conformation signatures of cellular differentiation

James Fraser, Mathieu Rousseau, Solomon Shenker, Maria A Ferraiuolo, Yoshihide Hayashizaki, Mathieu Blanchette and Josee Dostie

Genome Biology 2009, 10:R37 (19 April 2009)

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

Hideya Kawaji, Jessica Severin, Marina Lizio, Andrew Waterhouse, Shintaro Katayama, Katharine M Irvine, David A Hume, Alistair RR Forrest, Harukazu Suzuki, Piero

Carninci, Yoshihide Hayashizaki and Carsten O Daub

Genome Biology 2009, 10:R40 (19 April 2009)

Data-driven normalization strategies for high-throughput quantitative RT-PCR

Jessica C Mar, Yasumasa Kimura, Kate Schroder, Katherine M Irvine, Yoshihide Hayashizaki, Harukazu Suzuki, David Hume and John Quackenbush

BMC Bioinformatics 2009, 10:110 (19 April 2009)

## Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation

Atsutaka Kubosaki, Yasuhiro Tomaru, Michihira Tagami, Erik Arner, Hisashi Miura, Takahiro Suzuki, Masanori Suzuki, Harukazu Suzuki and Yoshihide Hayashizaki

Genome Biology 2009, 10:R41 (19 April 2009)

Source: BioMed Central

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