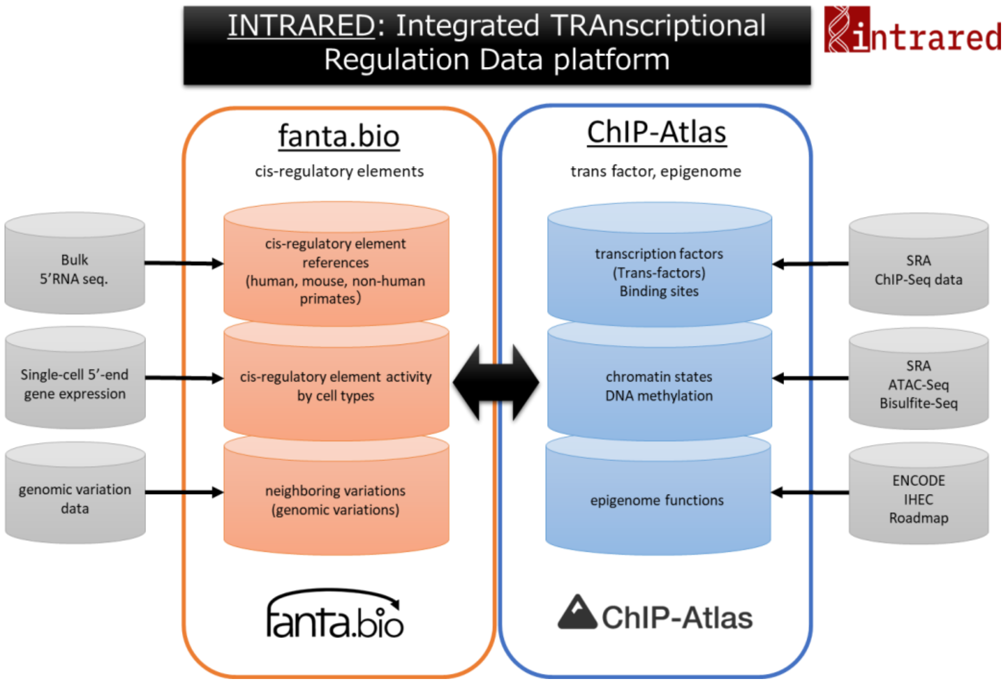
Integrative data platform for transcriptional regulations

intrared

INTRARED

https://www.intrared.org/


INTRARED: Integrated TRAnscriptional Regulation Data platform

intrared

fanta.bio

cis-regulatory elements

Bulk 5’RNA seq.

Single-cell 5’-end gene expression

genomic variation data

cis-regulatory element references (human, mouse, non-human primates)

cis-regulatory element activity by cell types

neighboring variations (genomic variations)

fanta.bio

ChIP-Atlas

trans factor, epigenome

transcription factors (Trans-factors) Binding sites

chromatin states DNA methylation

epigenome functions

SRA ChIP-Seq data

SRA ATAC-Seq Bisulfite-Seq

ENCODE IHEC Roadmap

ChIP-Atlas

INTRARED is a data platform for promoting the understanding of the transcriptional regulations. The platform integrates the data of cis-regulatory elements (CRE), trans-factors, and epigenomes. The data platform consists of two databases. fanta.bio is developed by Takeya Kasukawa of RIKEN, and it is a database of CREs, which are genomic regions contributing to the regulation of gene and transcript expressions in the same chromosomes, with their locations and activities in various cell types and states. ChIP-Atlas is developed by Prof. Shinya Oki at Kumamoto University, and it is a database of trans-factors that bind to CREs and epigenomes that affects to CREs and trans-factors. In the data platform, developing and operating teams in both databases cooperate and build datasets of transcriptional regulations and develop interfaces to provide them.

fanta.bio

fanta.bio (https://fanta.bio/)

＜Number of data included in fanta.bio (ver. 1.1.0)＞

Human	447,315 CRE regions	(2,413 cis-element activities)
Mouse	288,877 CRE regions	(1,229 cis-element activities)

ChIP-Atlas

ChIP-Atlas (https://chip-atlas.org/)

<Data in ChIP-Atlas Data> (May 2025)

ChIP-seq (genome-protein interactions)	262,635 entries
ATAC-seq (open chromatin information)	97,673 entries
DNase-seq (open chromatin information)	6,495 entries
Bisulfite-seq (methylome information)	65,516 entries
Total	432,319 entries

fanta.bio and ChIP-Atlas are developed as a part of JST Program for Database Integration Coordination Program (DICP), "Construction of an integrative data platform for transcriptional regulations (PI: Takeya Kasukawa, Team Leader, RIKEN".

JST NBDC

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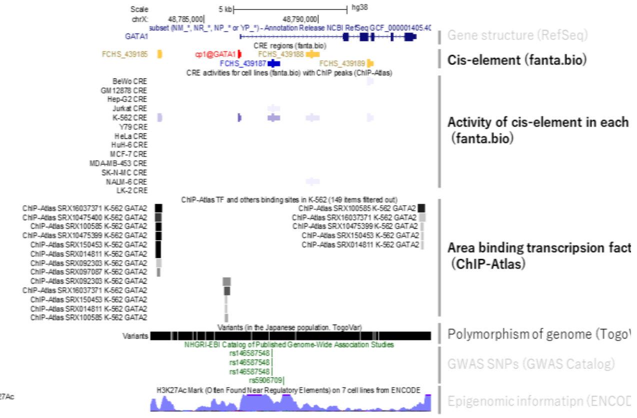
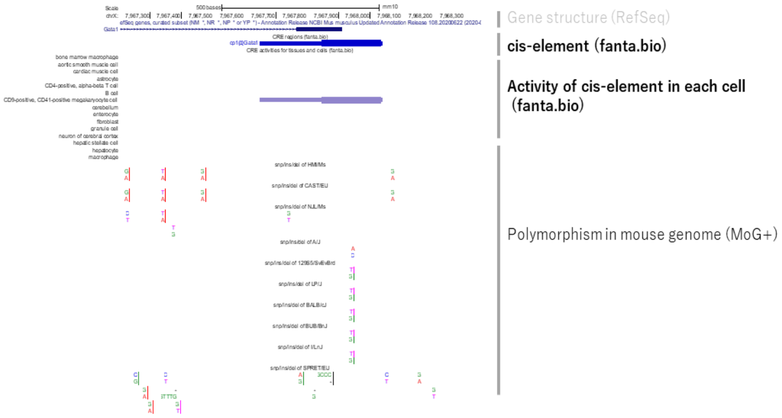
Cis-elements database

fanta.bio

https://fanta.bio/



Human cis-element
(promoter and enhancer region of GATA1 gene)



Mouse cis-element
(promoter region of Gata1 gene)

Cis-elements are regions in the genome that are involved in transcriptional regulation, and typical examples include enhancers and promoters. The fanta.bio contains information on the location of cis-elements identified in the human and mouse genomes, the activity of cis-elements in different cell lines, cell types and tissues, genomic variations within cis-element regions.

Using fanta.bio, you can search for cis-elements in any genomic region or gene, and obtain information on the activity of the cis-element in cells (whether the cis-element exerts regulatory activity in that celll, etc.), transcription factors that bind to the cis-element region, genomic polymorphisms in the region, etc. As well as the search results can be browsed through the interface provided on the website, the genomic location can be confirmed using the UCSC Genome Browser. In addition, data files created by fanta.bio can be downloaded. By using these data files, it is possible, for example, to integrate and analyze data such as genomic mutation information related to a disease, and to investigate the relationship between cis-elements and the disease.

In the construction of fanta.bio, information on transcription factor binding regions was integrated from the epigenomics database ChIP-Atlas, and genomic polymorphism information on mice was integrated from MoG+, which collects strain-specific genomic variation for mouse genome polymorphism information. For human genome polymorphism information, TogoVar, developed and operated by DBCLS, is being used.

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fanta.bio, together with ChIP-Atlas, is developed in a project of JST Database Integration Coordination Program (DICP) "Construction of an integrative data platform for transcriptional regulations (PI: Takeya Kasukawa, Team Leader, RIKEN)"

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