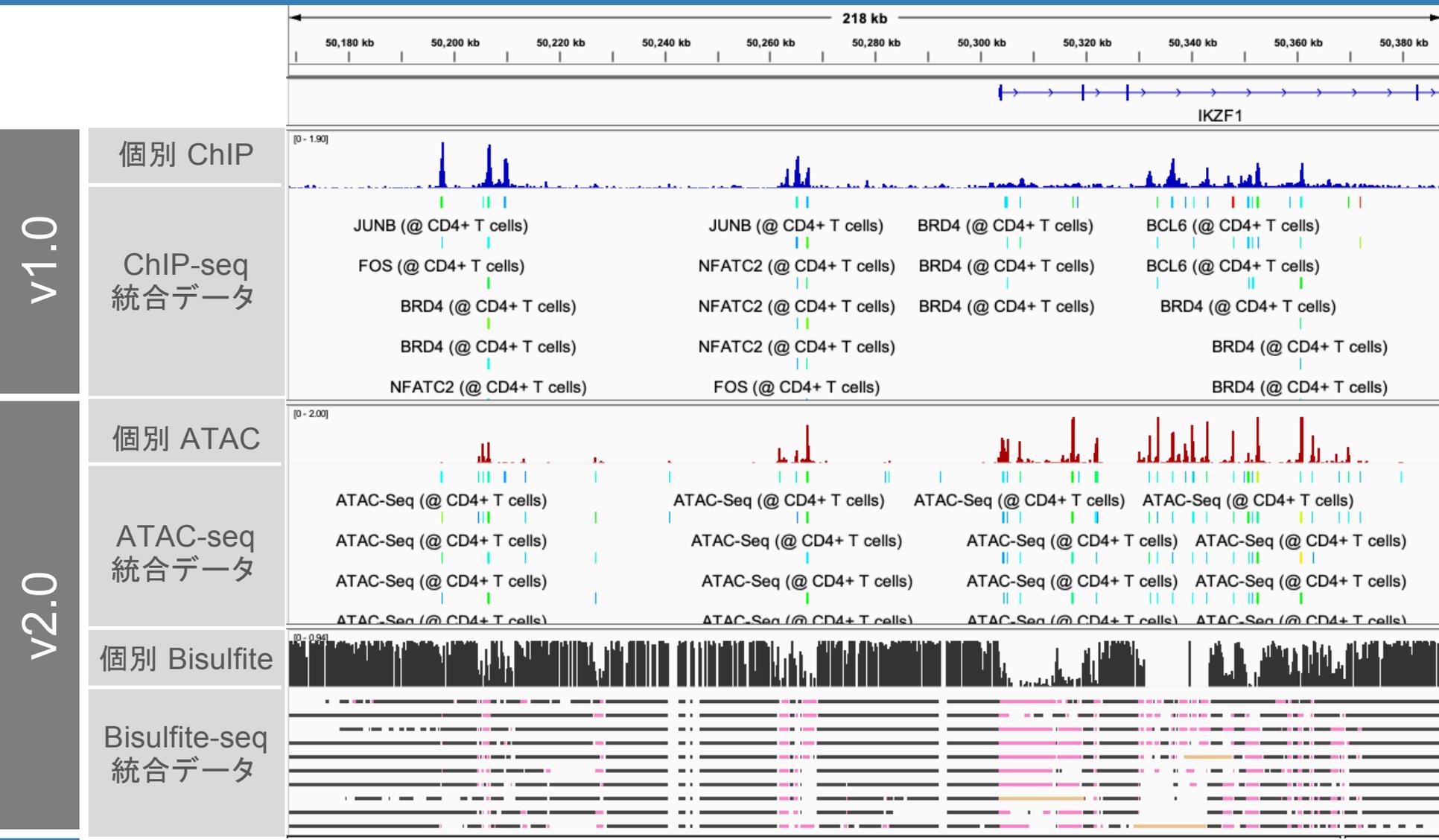


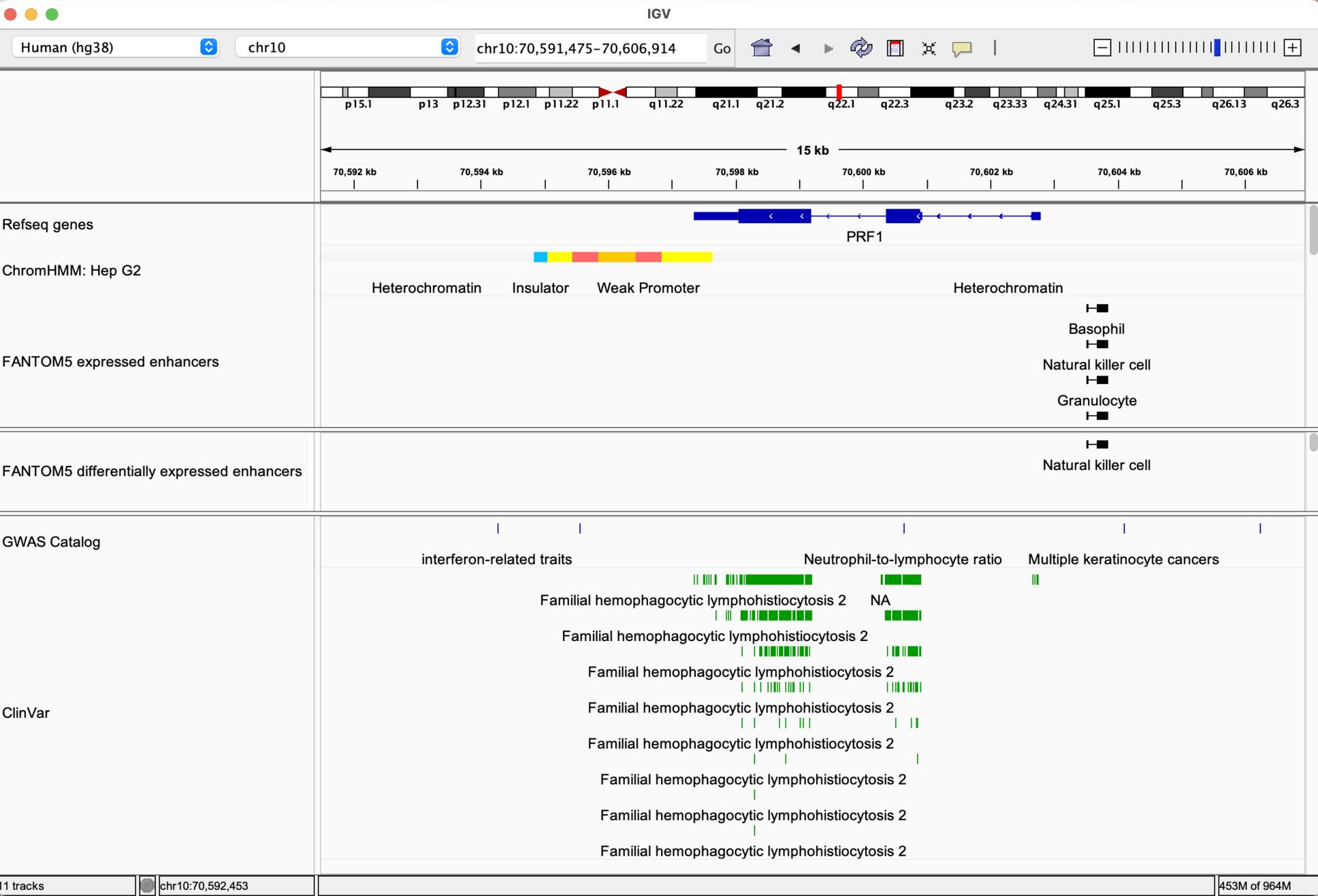
① ChIP-Atlas の進化



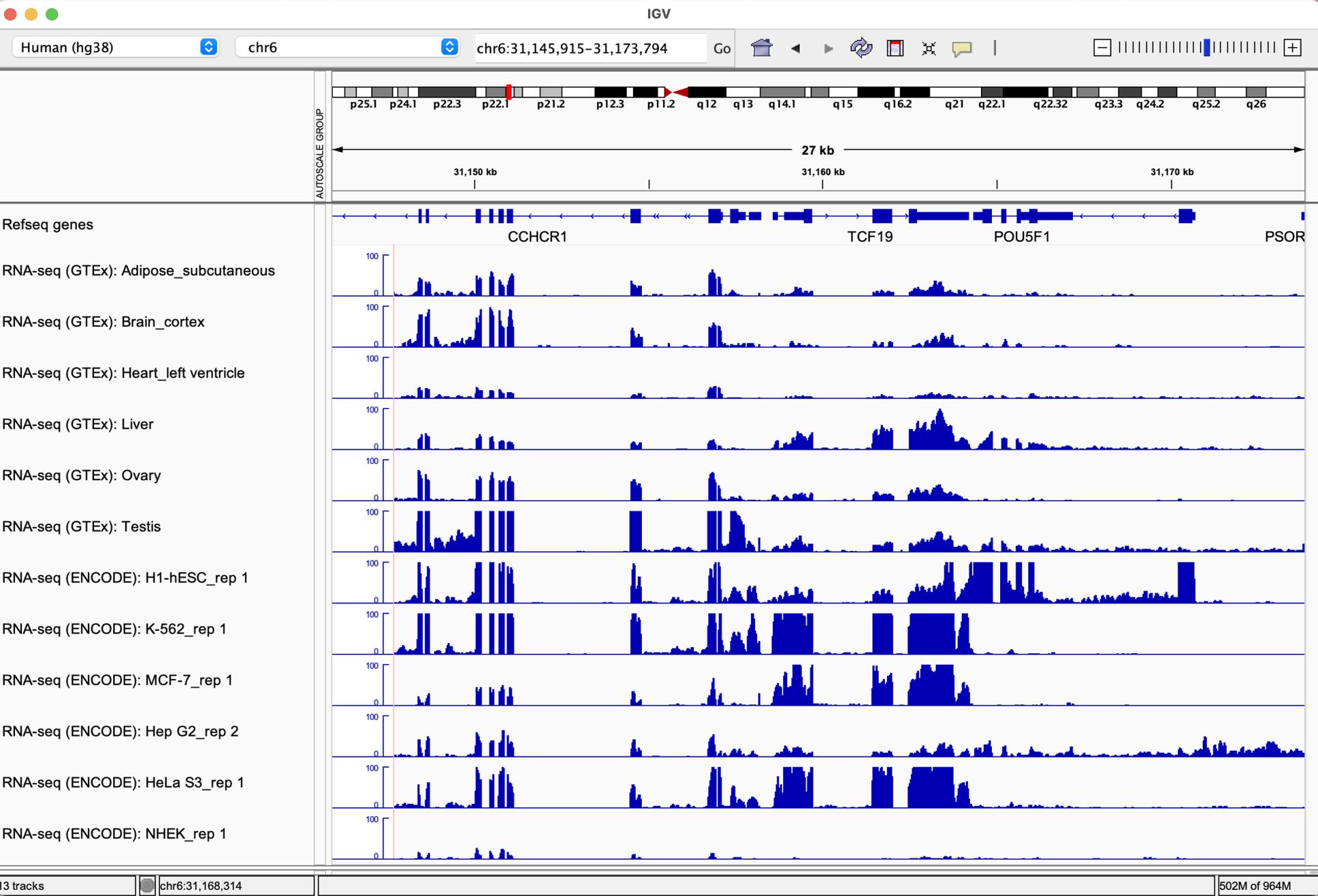
v3.0

機能注釈データの追加 : ChromHMM, FANTOM5, HiC, eQTL, GWAS SNPs
オンデマンド解析ツール : Differential ChIP peaks, Differentially methylated regions

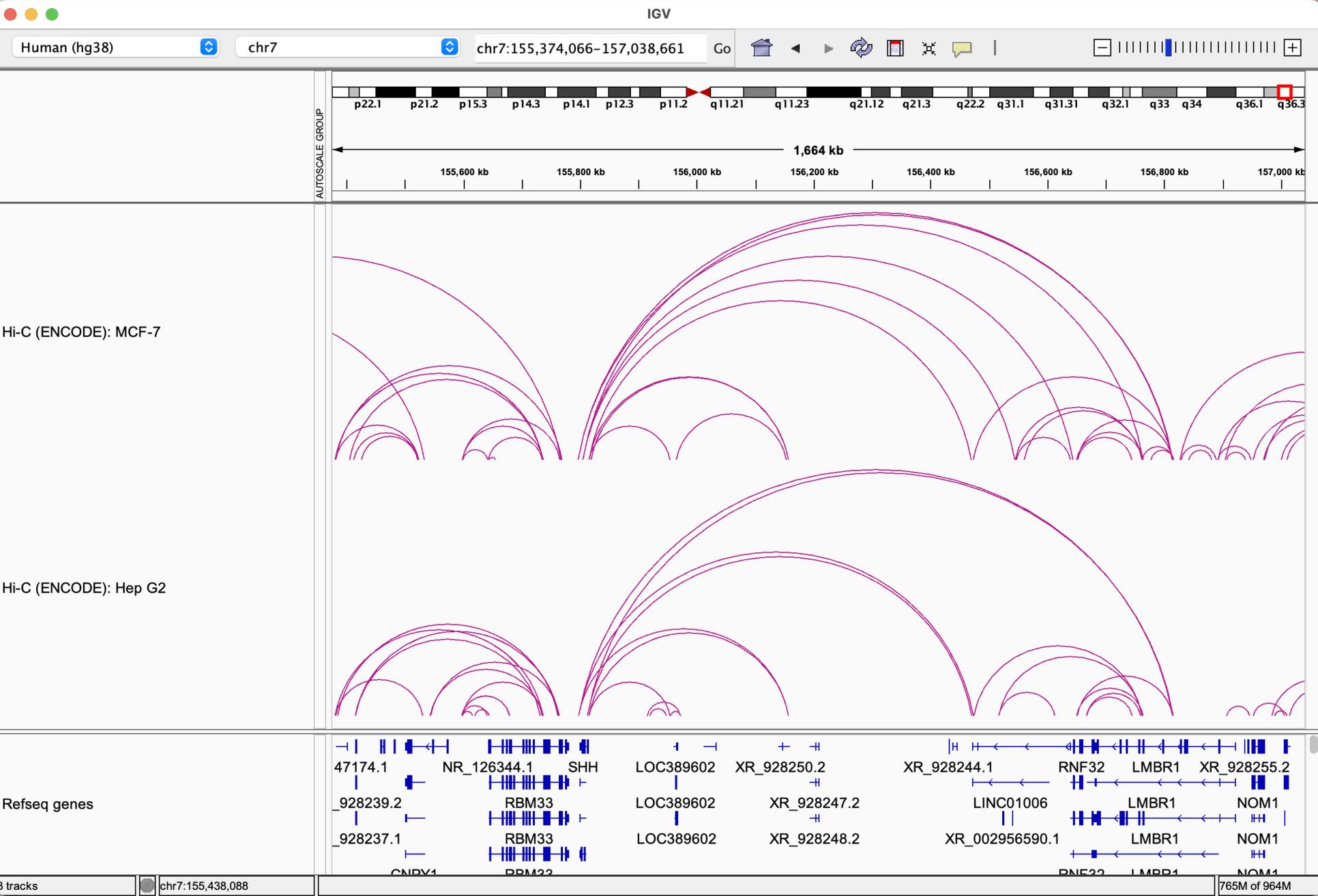
③ 機能注釈の例：制御領域、多型情報



④ 機能注釈の例：遺伝子発現



⑤ 機能注釈の例 : Hi-C



⑥ 機能注釈の例 : eQTL



⑦ Diff Analysis ツールの開発

▲ CHIP-Atlas: Diff Analysis

Detect differences between given ChIP-Seq, ATAC-Seq or Bisulfite-Seq dataset groups

H. sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

S. cerevisiae (sacCer3)

1. Choose experiment type

ChIP/ATAC/DNase-seq

Bisulfite-Seq

Bisulfite

2. Enter dataset A

Experiment IDs ⓘ

SRX6831786
SRX6831787
SRX6831788
SRX6831789
SRX6831790
SRX6831791

(Brain)

[Try with example](#)

3. Enter dataset B

Experiment IDs ⓘ

SRX6831796
SRX6831797
SRX6831798
SRX6831799

(T cell)

[Try with example](#)

4. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

dataset B

submit

Estimated run time: -
[node status \(epyc.q\)](#)

Submit

遺伝研スパコンの
API をたたく

➔ DMR.bed が作成される

= Differentially Methylated Regions

⑧ DMR の閲覧

