

Expanded View Figures

Figure EV1. Web pages of ChIP-Atlas.

- A, B A snapshot of the ChIP-Atlas top page is shown in (A). From this page, users are able not only to access the four main functions of ChIP-Atlas but also to search for data of interest with a given SRX ID (A, top right) or with keywords such as antigen and cell type names (B).
- C Snapshot of the Web page for the ChIP-Atlas “Peak Browser” function. Results for the settings shown are presented in Fig 2.
- D Detailed information for SRX187209, including the sample metadata described by ChIP-Atlas curators and the original data submitter, processing logs, and read quality from DBCLS SRA (<http://sra.dbcls.jp>). Blue buttons at the top are controllers for showing the alignment and peak-call data in IGV (“View on IGV”), for downloading these data (“Download”), for viewing the analyzed data by ChIP-Atlas “Target Genes” and “Colocalization” (“View Analysis”), and for opening external pages showing details for the experimental conditions and materials (“Link Out”). This type of Web page appears on clicking the bars in the “Peak Browser” view (Fig 2) as well as by clicking SRX IDs shown in Web pages for a keyword search (B) or for “Target Genes” (Fig 3A), “Colocalization” (Fig 3B), or “Enrichment Analysis” (Fig EV3) results.

D

ChIP-Atlas
Peak Browser
Target Sites
Calculation
Enrichment Analysis
Documentation
Publications
Find an experiment

SRX187209

GSM1094604: SL3034; Mus musculus; ChIP-Seq

View on IGV +

View Analysis +

Download +

Link Out +

Curated Sample Data

Genome	mm9
Antigen Class	Th17 and others
Antigen	Cut1
Cell type Class	Blood
Cell type	Th17 Cells

Cell type information

Method Description A subset of helper-effector T lymphocytes which synthesize and secrete INTERLEUKINS IL-17, IL-17F, and IL-22. These cytokines are involved in host defenses and tissue inflammation in autoimmune diseases.

Attributes by Original Data Submitter

raw_data_name	Th17 in vitro
genome_type	vt
control	SL3035
factor	CUT1
application	ChIP-Seq
cell_type	Th17

Metadata from Sequence Read Archive

Library Description

library_strategy	ChIP-Seq
library_source	GENOMIC
library_selection	ChIP

Platform Information

instrument_model	Illumina Genome Analyzer IIx
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External Database Query

Query antigen:

Query cell-type:

Logs in read processing pipeline

Number of total reads	30253375
Reads aligned (%)	86.6
Duplicates removed (%)	21.6
Number of peaks	40020 (post < 1E-05)

Sequence Quality Data from DBQ.S. RNA

SRX1871564_fastqc

ChIP-Atlas / Keyword search							
Search for ChIP-seq data with keywords.							
Simple search Advanced search							
Show 22,431 entries							
SRX ID	GEO ID	Genome	Antibody classe	Antibody	Cell type class	Cell type	
SRX092315	GSM776559	hg19	TFs and others	GATA2	Blood	Th2 Cells	
SRX092414	GSM782156	hg19	TFs and others	CTCF	Blood	Lymphoma, B-Cell	
SRX092415	GSM782157	hg19	Input control	Input control	Blood	Lymphoma, B-Cell	
SRX092416	GSM782158	hg19	TFs and others	CTCF	Blood	Lymphoma, B-Cell	
SRX092417	GSM782159	hg19	Input control	Input control	Blood	Lymphoma, B-Cell	
SRX092447	GSM775364	hg19	TFs and others	AR	Prostate	LNCAP	
SRX092448	GSM775365	hg19	TFs and others	AR	Prostate	LNCAP	
SRX092450	GSM729851	hg19	TFs and others	EBNA2	Blood	IB4	
SRX092451	GSM729852	hg19	TFs and others	EBNA2	Blood	IB4	
SRX092452	GSM729853	hg19	TFs and others	RBPI	Blood	IB4	
SRX092453	GSM729854	hg19	TFs and others	RBPI	Blood	IB4	
SRX092454	GSM729855	hg19	Input control	Input control	Blood	IB4	
SRX092455	GSM729856	hg19	Input control	Input control	Blood	IB4	
SRX092568	GSM779425	hg19	TFs and others	HCFC1	Uterus	HeLa	
SRX092569	GSM779426	hg19	TFs and others	HCFC1	Uterus	HeLa	
SRX092570	GSM779427	hg19	Input control	Input control	Uterus	HeLa	
SRX092571	GSM779428	hg19	Input control	Input control	Uterus	HeLa	
SRX092572	GSM779429	hg19	Input control	Input control	Uterus	HeLa	
SRX092573	GSM779430	hg19	TFs and others	ZNF-143	Uterus	HeLa	
SRX092574	GSM779431	hg19	TFs and others	THAP 1	Uterus	HeLa	

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[Target Genes](#)
[Colocalization](#)
[Enrichment Analysis](#)
[Documentation](#)
[Publications](#)
[Find an experiment -](#)

ChIP-Atlas - Peak Browser

Visualize All Peaks from Published ChIP-Seq data.

[H. sapiens](#)
[M. musculus](#)
[R. norvegicus](#)
[D. melanogaster](#)
[C. elegans](#)
[S. cerevisiae](#)

Antigen Class

All antigens (31775)

DNAse-seq (703)

Histone (10011)

RNA polymerase (953)

ITS and GATA (6797)

Input control (4346)

Unclassified (5876)

No description (2011)

Cell type Class

All cell types (31775)

Aspocyte (424)

Blood (7357)

Bone (144)

Breast (529)

Cardiovascular (448)

Digestive tract (473)

Embryo (2821)

Threshold for Significance ①

50

100

500

Antigen

Pitx1 (3)

Pitxou1 (6)

Plagl1 (2)

Pml (1)

Pou2af1 (2)

Pou2f1 (2)

Pou2f1 (1)

Pou2f2 (11)

Cell type

①

View on IGV

Download BED file

EV2 *EMBO reports* e46255 | 2018



Figure EV2. Web pages for integrative analyses in ChIP-Atlas.

A, B Snapshots of Web pages for ChIP-Atlas “Target Genes” (A) and “Colocalization” (B) functions. Results for the settings shown are presented in Fig 3A and B, respectively.

C–E Snapshots of Web pages for the ChIP-Atlas “Enrichment Analysis” function with submission of genomic coordinates or gene symbols are shown in (C) and (D), respectively. Results for the settings shown are presented in Fig 4A–C and D–F, respectively. At the Web page for “Enrichment Analysis”, a user can submit two sets of genomic intervals in BED format (C) or gene symbols (D): data of interest in the orange area and background data for comparison in the gray area. It is also possible to filter the results according to antigen and cell type classes as well as to set a threshold for the MACS2 score. On clicking the “submit” button, the data are sent to an NIG supercomputer server for performance of the enrichment analysis, as shown in (E). For example, on submission of BED-formatted genomic regions for hepatocyte enhancers (orange) or enhancers activated in other tissues (gray), the computational server counts the overlaps with the peaks of all SRXs (E, left). After evaluation of the significance of enrichment with Fisher’s exact test (E, right), the analyzed data are returned within several minutes to the machine of the user as shown in Fig EV3.

Figure EV3. Examples of “Enrichment Analysis”.

A, B Snapshots of the results for enrichment analysis of hepatocyte-specific enhancers with the ChIP-Atlas “Enrichment Analysis” function, for which other FANTOM5 enhancers (A) or randomly permuted regions (B) were set as background, are shown. The first row in (A), for example, indicates EP300 ChIP-seq data (SRX100544) for Hep G2 cells. The total number of peaks for EP300 is 24,334, of which 80 peaks overlap with hepatocyte-specific enhancers ($n = 286$) and 1,147 peaks overlap with other enhancers ($n = 20,509$), yielding a P -value of $1 \times 10^{-32.1}$ (Fisher’s exact probability test), Q -value of $1 \times 10^{-28.3}$ (Benjamini and Hochberg method), and fold enrichment of 5.00. The table is sorted according to P -value, with HNF4A/G and FOXA1/2 in Hep G2 being ranked 3rd, 7th, 8th, 10th, and 12th. The table is also graphically summarized in Figs 4A and EV4 (top 15 and 50 experiments, respectively), in which each row of the table is represented by a bar to indicate the P -value. Note that TR peaks overlapped to a lesser extent with random background (B) than with other FANTOM5 enhancers (A).

A

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Hepatocyte	Overlaps / Other enhancers	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100544	TFs and others	EP300	Liver	Hep G2	24334	80/286	1147/20509	-32.1	-28.3	5.00	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19032	64/286	755/20509	-29.7	-26.3	6.08	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15919	54/286	507/20509	-29.3	-26.0	7.64	TRUE
SRX100493	TFs and others	HEY1	Liver	Hep G2	26412	69/286	984/20509	-27.5	-24.4	5.03	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	54/286	557/20509	-27.5	-24.4	6.95	TRUE
SRX100538	TFs and others	HDAC2	Liver	Hep G2	16071	58/286	676/20509	-27.0	-24.0	6.15	TRUE
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21259	54/286	585/20509	-26.5	-23.6	6.62	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45130	67/286	1138/20509	-22.6	-19.8	4.22	TRUE
SRX150360	TFs and others	TBP	Liver	Hep G2	10293	38/286	327/20509	-21.7	-18.9	8.33	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50941	70/286	1295/20509	-21.7	-18.9	3.88	TRUE
SRX1165097	TFs and others	CREB1	Liver	Hep G2	21856	58/286	899/20509	-21.2	-18.5	4.63	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	66/286	1198/20509	-20.8	-18.1	3.95	TRUE
SRX150701	TFs and others	CEBPB	Liver	Hep G2	18637	52/286	849/20509	-18.0	-15.4	4.39	TRUE
SRX100545	TFs and others	JUND	Liver	Hep G2	19875	62/286	1223/20509	-17.7	-15.1	3.64	TRUE

Showing 1 to 100 of 8,010 entries

Previous 1 2 3 4 5 ... 81 Next

B

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Hepatocyte	Overlaps / Random background	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX212650	TFs and others	STAT1	Blood	Monocytes-CD14+	59627	91/286	2/286	-27.6	-24.0	45.50	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24334	80/286	1/286	-24.9	-21.7	80.00	TRUE
SRX190321	TFs and others	MAX	Liver	Hep G2	40220	90/286	4/286	-24.8	-21.7	22.50	TRUE
SRX2770855	TFs and others	SP1	Blood	Macrophages	88629	74/286	1/286	-22.7	-19.7	74.00	TRUE
SRX212648	TFs and others	STAT1	Blood	Monocytes-CD14+	44896	70/286	1/286	-21.3	-18.3	70.00	TRUE
SRX666556	TFs and others	HIF1A	Breast	T-47D	74508	79/286	5/286	-19.9	-17.0	15.80	TRUE
SRX212649	TFs and others	STAT1	Blood	Monocytes-CD14+	24923	66/286	1/286	-19.8	-17.0	66.00	TRUE
SRX100493	TFs and others	HEY1	Liver	Hep G2	26412	69/286	2/286	-19.6	-16.8	34.50	TRUE
SRX1023792	TFs and others	SP1	Blood	Macrophages	114884	74/286	4/286	-19.1	-16.5	18.50	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19032	64/286	1/286	-19.1	-16.5	64.00	TRUE
SRX190269	TFs and others	SP1	Lung	A549	29434	64/286	1/286	-19.1	-16.5	64.00	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45130	67/286	2/286	-18.9	-16.3	33.50	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50941	70/286	3/286	-18.8	-16.3	23.33	TRUE
SRX100403	TFs and others	NR3C1	Lung	A549	18382	58/286	0/286	-18.6	-16.1	99999	TRUE

Showing 1 to 100 of 4,352 entries

Previous 1 2 3 4 5 ... 44 Next

Figure EV3.

Figure EV4. Results of enrichment analysis for tissue-specific enhancers.

The results of enrichment analysis for FANTOM5 tissue-specific enhancers are sorted according to the minimum P -value ($P_{\min}$) for each facet. The bar charts indicate P -value (horizontal axis) for the top 50 enriched ChIP-seq experiments (vertical axis), with the colors denoting cell type classes according to the color palette (bottom right).

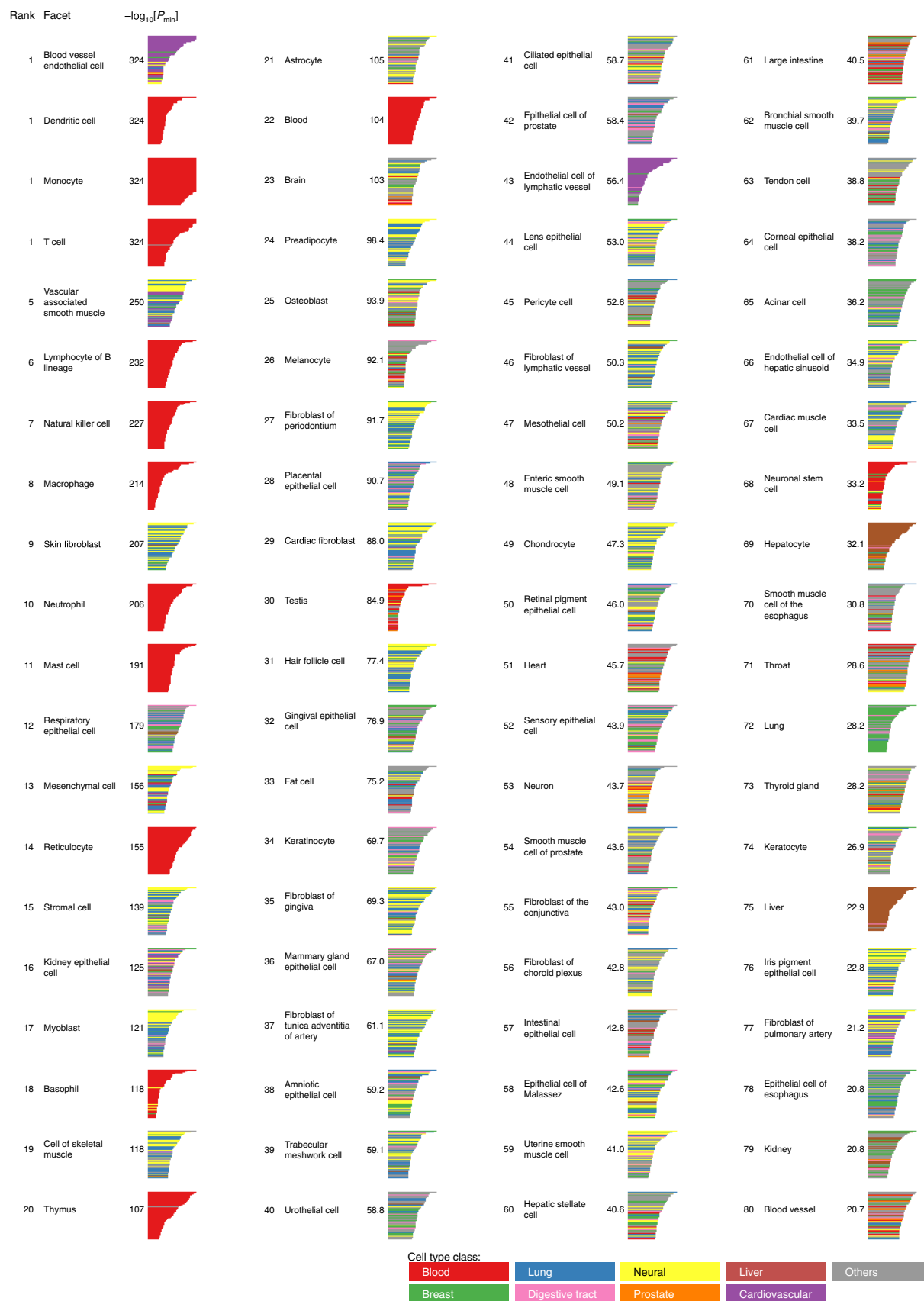


Figure EV4.

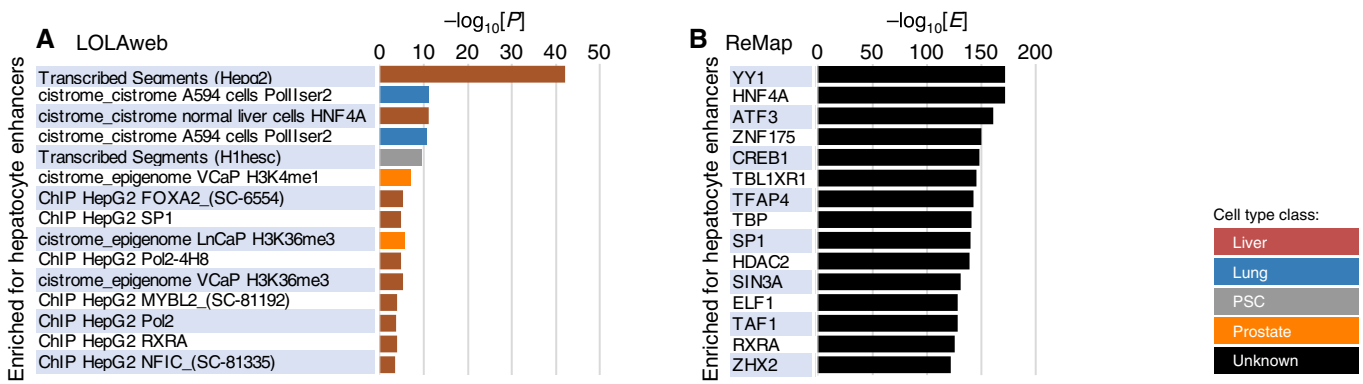


Figure EV5. Results of enrichment analysis with other tools.

A, B Enrichment analysis for hepatocyte enhancers was performed with LOLAweb (A), for which other FANTOM5 enhancers were used as background, and with “Annotation Tool” of ReMap (B), for which only random regions were available as background. The top 15 ChIP-seq experiments showing statistical significance are shown as bar charts.