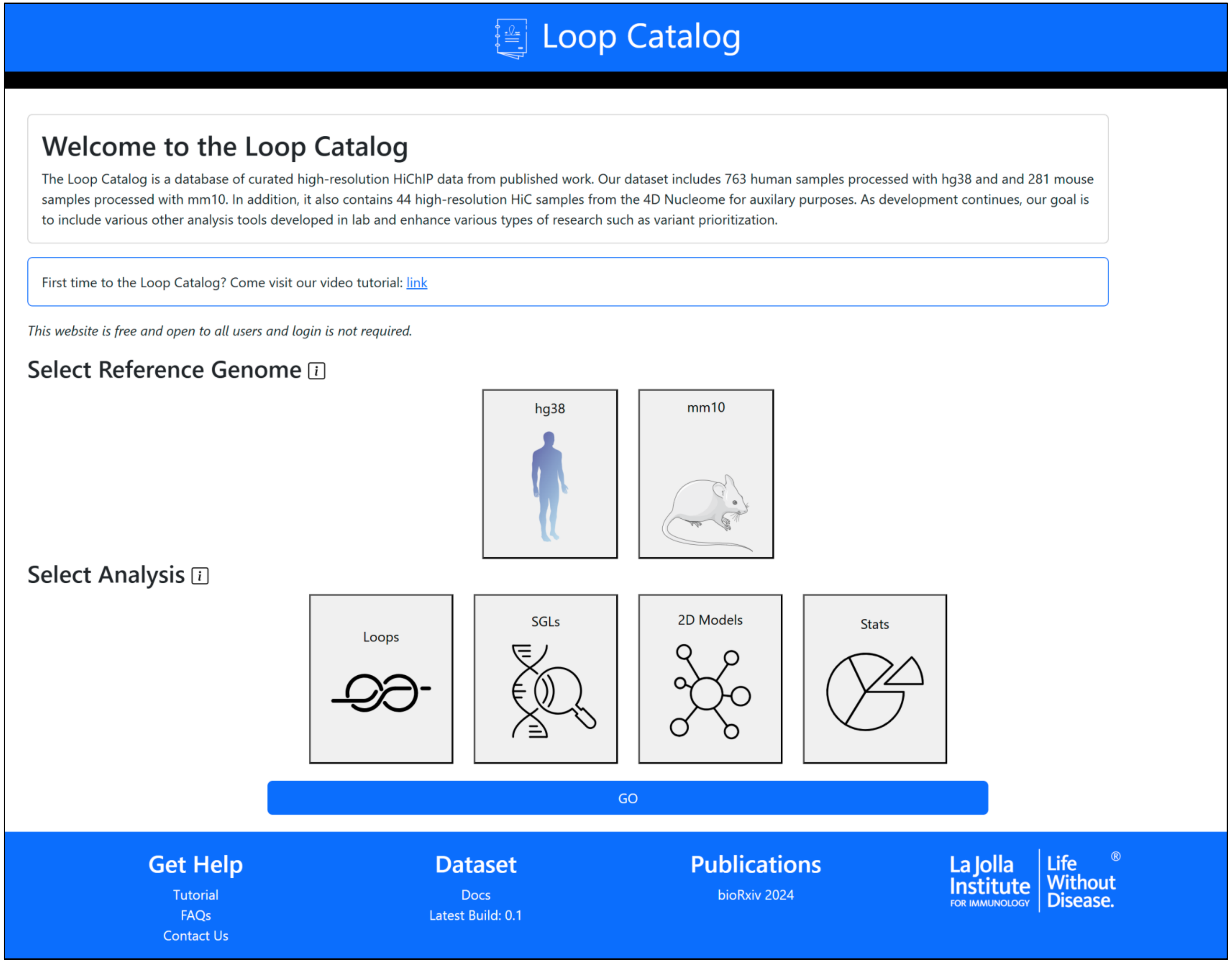
Navigating the Main Data Page

Welcome to the Loop Catalog



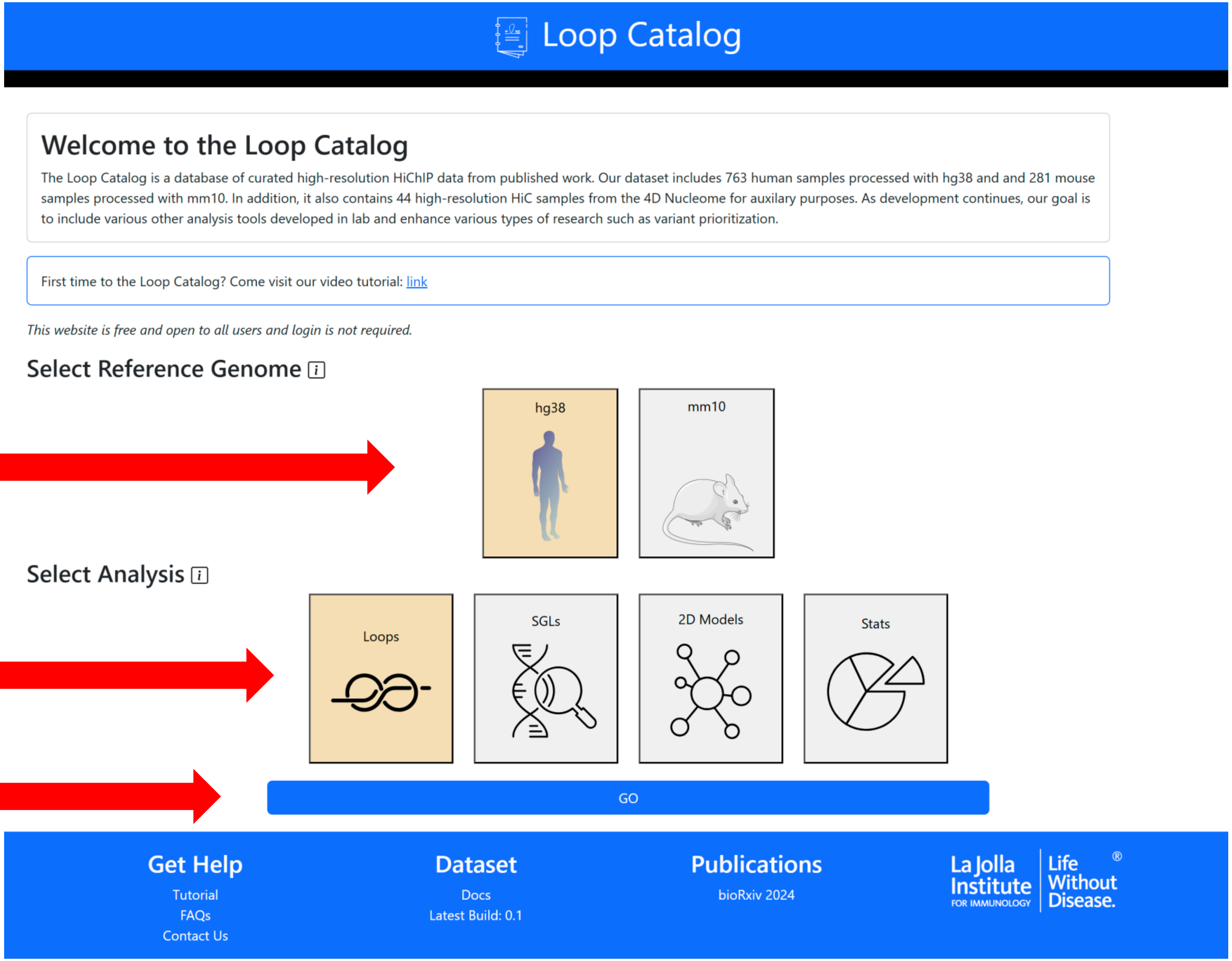
Loop Catalog

Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxilary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: link

This website is free and open to all users and login is not required.



Loop Catalog

Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxilary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: link

This website is free and open to all users and login is not required.

Select Reference Genome

Select Analysis

Get Help
Tutorial
FAQs
Contact Us

Dataset
Docs
Latest Build: 0.1

Publications
bioRxiv 2024

Select a Reference Genome

Select an Analysis

Click Go

Welcome to the main data/loop page

Loop Catalog

Data Explorer

Viewing a 1.0 Mb region in 1291px, 1 pixel spans 774 bp

21 items too small - zoom in to view. (Dismiss)

7635 items too small - zoom in to view. (Dismiss)

FC Loops

Unfiltered	Filtered
☑ 5kb	☐ 5kb
☐ 10kb	☐ 10kb
☐ 25kb	☐ 25kb
☐ Peaks	

FH Loops

Unfiltered	Filtered
☑ 5kb	☐ 5kb
☐ 10kb	☐ 10kb
☐ 25kb	☐ 25kb
☐ Peaks	

HiCCUPs Loops

☐ 5kb
☐ 10kb
☐ 25kb

HiC Loops

☐ 1kb
☐ 5kb

Showing 1 to 10 of 1,042 entries

Search:

	Primary Name	Study	Number of Read Pairs	Bio-rep	Pulldown or HiC	5kb FC Loops (Unfiltered)	5kb FH Loops (Unfiltered)
☐	Wei-22RV1 (merged)	Wei et al., 2023	375,335,640	2	CTCF	214603 ☐	116360 ☐
☐	H9	Lyu et al., 2018	515,530,130	1	Rad21	196151 ☐	230390 ☐
☐	Wei-22RV1-Myc (merged)	Wei et al., 2023	437,453,186	1	CTCF	150379 ☐	131802 ☐
☐	Natural_Killer_1816-RH-1 (All Donors)	Chandra et al., 2021	1,457,921,642	1	H3K27ac	139924 ☐	14614 ☐
☐	H9-HS	Lyu et al., 2018	418,316,089	1	Rad21	134065 ☐	139883 ☐
☐	Wei-22RV1-Control (merged)	Wei et al., 2023	344,429,396	2	CTCF	130218 ☐	115765 ☐
☐	MB157-pInd20EBF1-10dox	Zhou et al., 2022	774,486,022	1	SMC1A	120549 ☐	106894 ☐
☐	CD4_Naive_1815-RH-1 (All Donors)	Chandra et al., 2021	2,125,336,641	1	H3K27ac	119199 ☐	23013 ☐
☐	MB157-pInd20TCF1-10dox	Zhou et al., 2022	732,911,273	1	SMC1A	106533 ☐	97695 ☐
☐	Wei-22RV1	Wei et al., 2023	178,763,153	1	CTCF	99754 ☐	44291 ☐

Show 10 entries

Previous 1 2 3 4 5 … 105 Next

Can't find the sample you're looking for? Send us a message through the emails listed in the "Contact Us" section.

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

WashU Epigenome Embedding

Loop Submenu

Filtering Menu

Viewing a 1.0 Mb region in 1291px, 1 pixel spans 774 bp

21 items too small - zoom in to view. (Dismiss)

7635 items too small - zoom in to view. (Dismiss)

Showing 1 to 10 of 1,042 entries

	Primary Name	Study	Number of Read Pairs	Bio-rep	Pulldown or HiC	5kb FC Loops (Unfiltered)	5kb FH Loops (Unfiltered)
☐	Wei-22RV1 (merged)	Wei et al., 2023	375,335,640	2	CTCF	214603 ☐	116360 ☐
☐	H9	Lyu et al., 2018	515,530,130	1	Rad21	196151 ☐	230390 ☐
☐	Wei-22RV1-Myc (merged)	Wei et al., 2023	437,453,186	1	CTCF	150379 ☐	131802 ☐
☐	Natural_Killer_1816-RH-1 (All Donors)	Chandra et al., 2021	1,457,921,642	1	H3K27ac	139924 ☐	14614 ☐
☐	H9-HS	Lyu et al., 2018	418,316,089	1	Rad21	134065 ☐	139883 ☐
☐	Wei-22RV1-Control (merged)	Wei et al., 2023	344,429,396	2	CTCF	130218 ☐	115765 ☐
☐	MB157-pInd20EBF1-10dox	Zhou et al., 2022	774,486,022	1	SMC1A	120549 ☐	106894 ☐
☐	CD4_Naive_1815-RH-1 (All Donors)	Chandra et al., 2021	2,125,336,641	1	H3K27ac	119199 ☐	23013 ☐
☐	MB157-pInd20TCF1-10dox	Zhou et al., 2022	732,911,273	1	SMC1A	106533 ☐	97695 ☐
☐	Wei-22RV1	Wei et al., 2023	178,763,153	1	CTCF	99754 ☐	44291 ☐

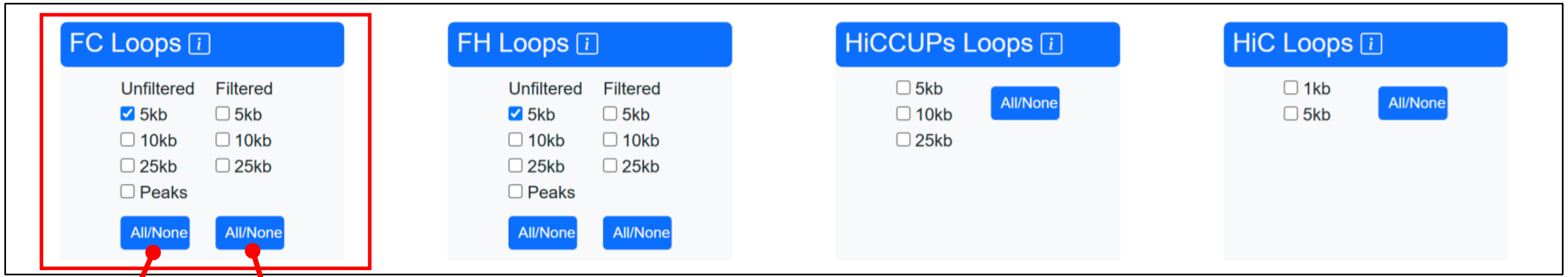
Can't find the sample you're looking for? Send us a message through the emails listed in the "Contact Us" section.

Interactive buttons

Main Data Page

Submenu for FC Loops
with both Unfiltered and
Filtered Loops

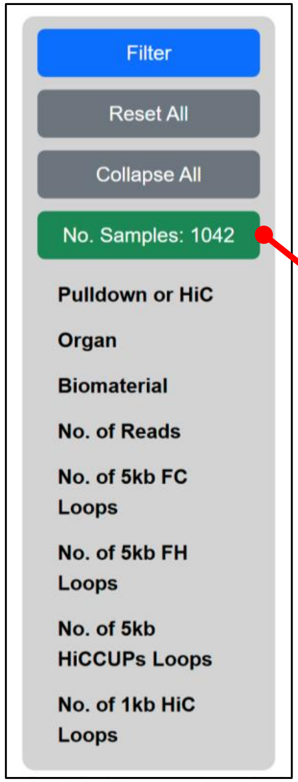
Similar submenus for
FH, HiCCUPs and HiC loops



Toggle buttons to select
all unfiltered or filtered
options

Filtering at the loop calling and sample levels

2) Click Filter



Helper functions

Displays current number of samples

1) Select filtering criteria

Copy table to clipboard or save to CSV

Hide/show columns from table

Clear the browser

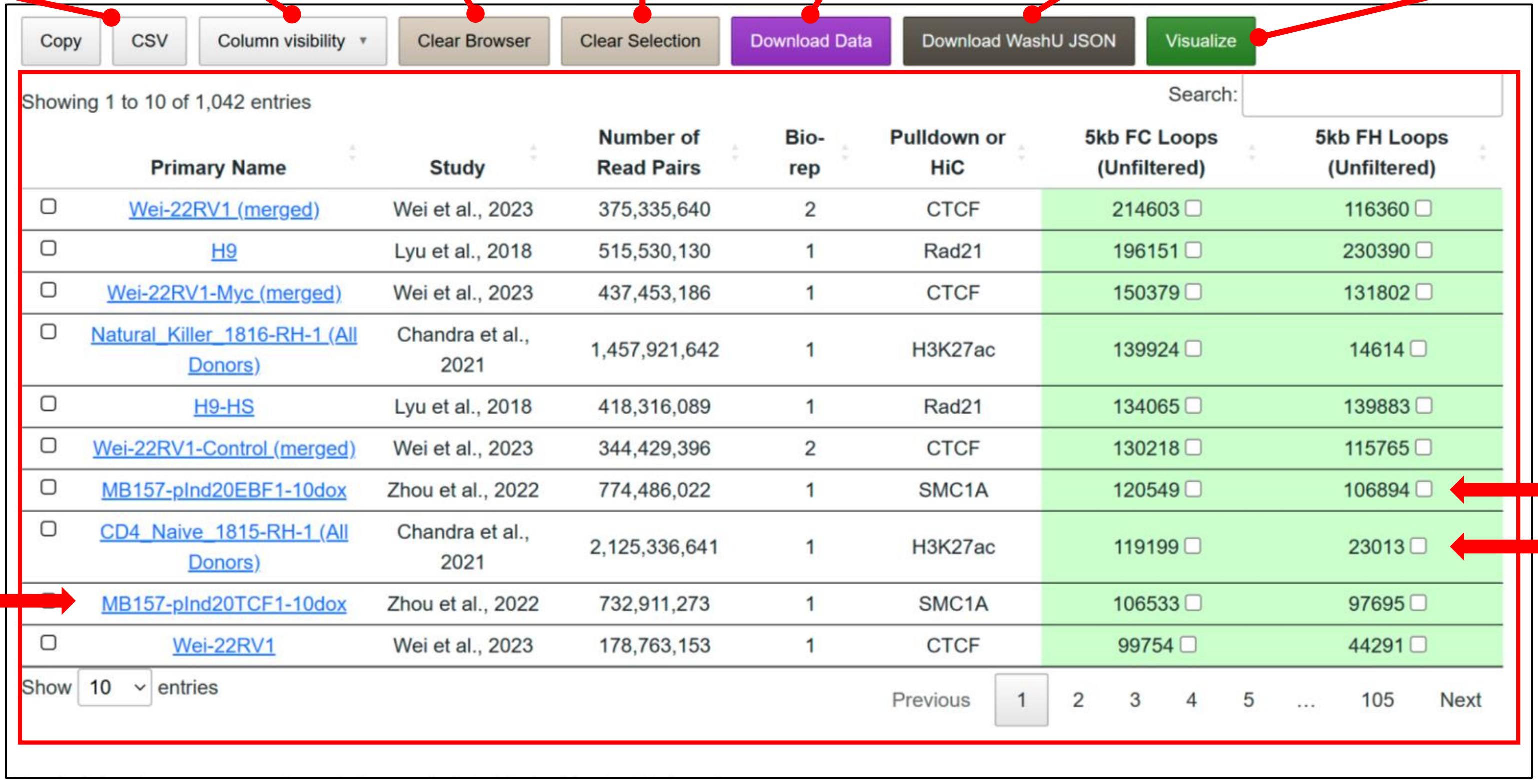
Clear the sample selection

Download tracks from selected samples

Download WashU hub for selected samples

Visualize selected samples

Table with HiChIP/HiC samples & loop calls



Showing 1 to 10 of 1,042 entries

	Primary Name	Study	Number of Read Pairs	Bio-rep	Pulldown or HiC	5kb FC Loops (Unfiltered)	5kb FH Loops (Unfiltered)
☐	Wei-22RV1 (merged)	Wei et al., 2023	375,335,640	2	CTCF	214603 ☐	116360 ☐
☐	H9	Lyu et al., 2018	515,530,130	1	Rad21	196151 ☐	230390 ☐
☐	Wei-22RV1-Myc (merged)	Wei et al., 2023	437,453,186	1	CTCF	150379 ☐	131802 ☐
☐	Natural_Killer_1816-RH-1 (All Donors)	Chandra et al., 2021	1,457,921,642	1	H3K27ac	139924 ☐	14614 ☐
☐	H9-HS	Lyu et al., 2018	418,316,089	1	Rad21	134065 ☐	139883 ☐
☐	Wei-22RV1-Control (merged)	Wei et al., 2023	344,429,396	2	CTCF	130218 ☐	115765 ☐
☐	MB157-pInd20EBF1-10dox	Zhou et al., 2022	774,486,022	1	SMC1A	120549 ☐	106894 ☐
☐	CD4_Naive_1815-RH-1 (All Donors)	Chandra et al., 2021	2,125,336,641	1	H3K27ac	119199 ☐	23013 ☐
☐	MB157-pInd20TCF1-10dox	Zhou et al., 2022	732,911,273	1	SMC1A	106533 ☐	97695 ☐
☐	Wei-22RV1	Wei et al., 2023	178,763,153	1	CTCF	99754 ☐	44291 ☐

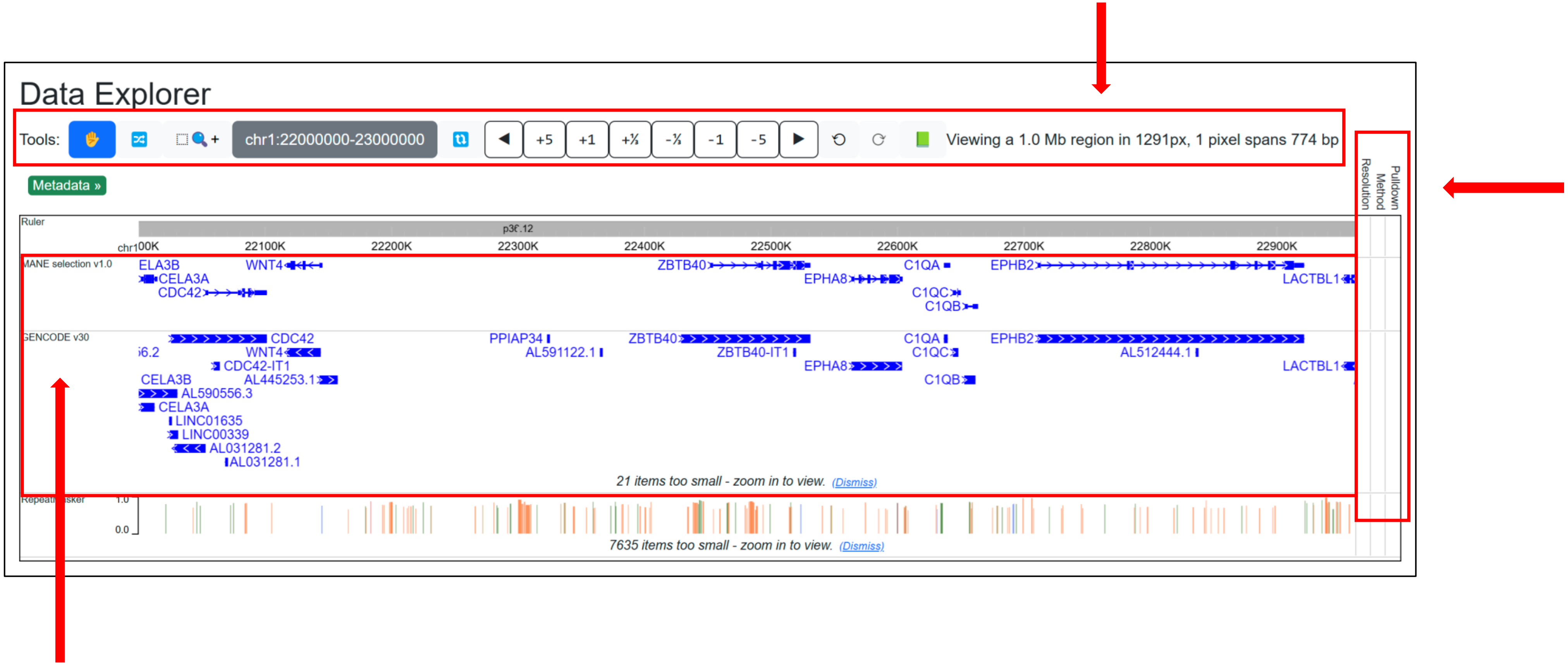
Show 10 ⌄ entries

Previous 1 2 3 4 5 … 105 Next

Select samples for interactive functions

Click on sample link to visit sample summary page

Navigation buttons for the WashU Browser



Meta data for each track including resolution, method and pulldown

Two gene tracks. One derived from the MANE selection and the other from GENCODE v30

Understanding the Single Sample Page

Basic Single Sample Page

Standard Sample Name

Study & General Information

Links to download interaction level data

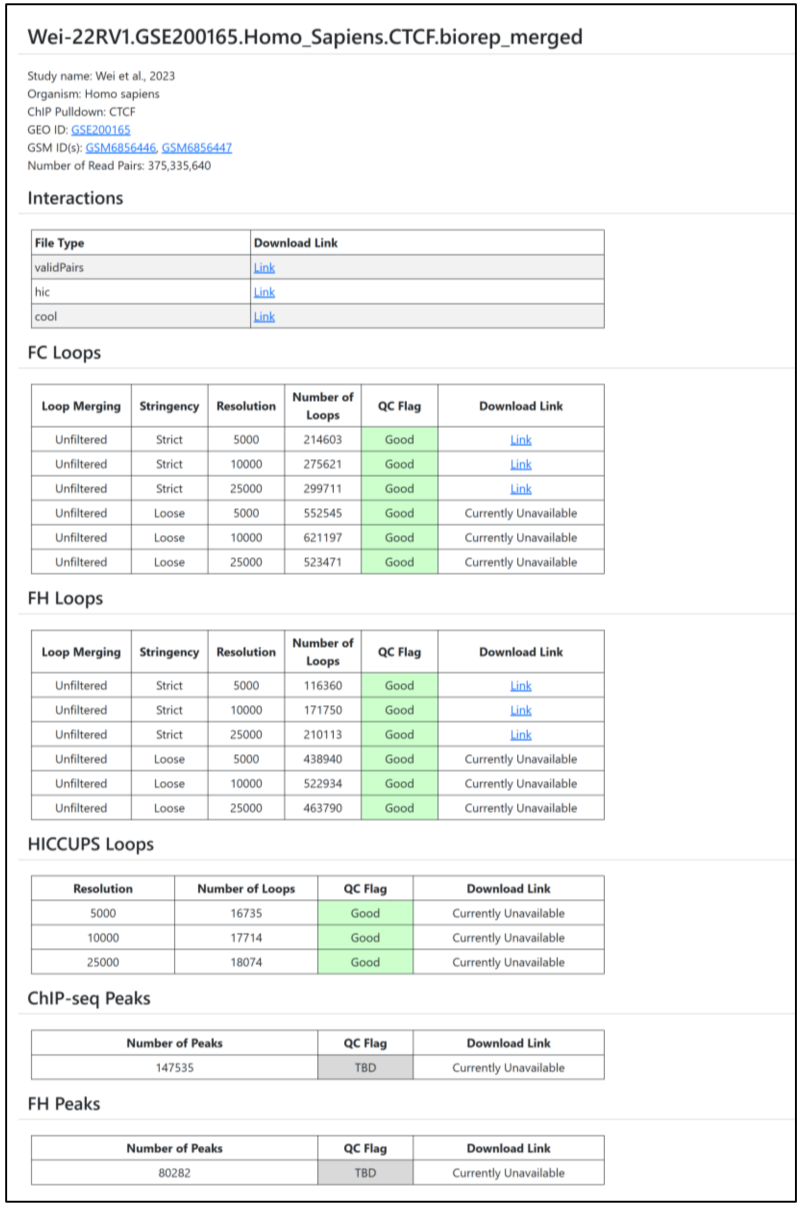
Table for FC Loops and links to download the raw loop files

Table for FH Loops and links to download the raw loop files

Table for HiCCUPS Loops and links to download the raw loop files

Table for ChIP-seq Peaks and links to download the raw peak files

Table for FH Peaks and links to download the raw peak files



Wei-22RV1.GSE200165.Homo_Sapiens.CTCF.biorep_merged

Study name: Wei et al., 2023
Organism: Homo sapiens
ChIP Pulldown: CTCF
GEO ID: GSE200165
GSM ID(s): GSM6856446, GSM6856447
Number of Read Pairs: 375,335,640

Interactions

File Type	Download Link
validPairs	Link
hic	Link
cool	Link

FC Loops

Loop Merging	Stringency	Resolution	Number of Loops	QC Flag	Download Link
Unfiltered	Strict	5000	214603	Good	Link
Unfiltered	Strict	10000	275621	Good	Link
Unfiltered	Strict	25000	299711	Good	Link
Unfiltered	Loose	5000	552545	Good	Currently Unavailable
Unfiltered	Loose	10000	621197	Good	Currently Unavailable
Unfiltered	Loose	25000	523471	Good	Currently Unavailable

FH Loops

Loop Merging	Stringency	Resolution	Number of Loops	QC Flag	Download Link
Unfiltered	Strict	5000	116360	Good	Link
Unfiltered	Strict	10000	171750	Good	Link
Unfiltered	Strict	25000	210113	Good	Link
Unfiltered	Loose	5000	438940	Good	Currently Unavailable
Unfiltered	Loose	10000	522934	Good	Currently Unavailable
Unfiltered	Loose	25000	463790	Good	Currently Unavailable

HICCUPS Loops

Resolution	Number of Loops	QC Flag	Download Link
5000	16735	Good	Currently Unavailable
10000	17714	Good	Currently Unavailable
25000	18074	Good	Currently Unavailable

ChIP-seq Peaks

Number of Peaks	QC Flag	Download Link
147535	TBD	Currently Unavailable

FH Peaks

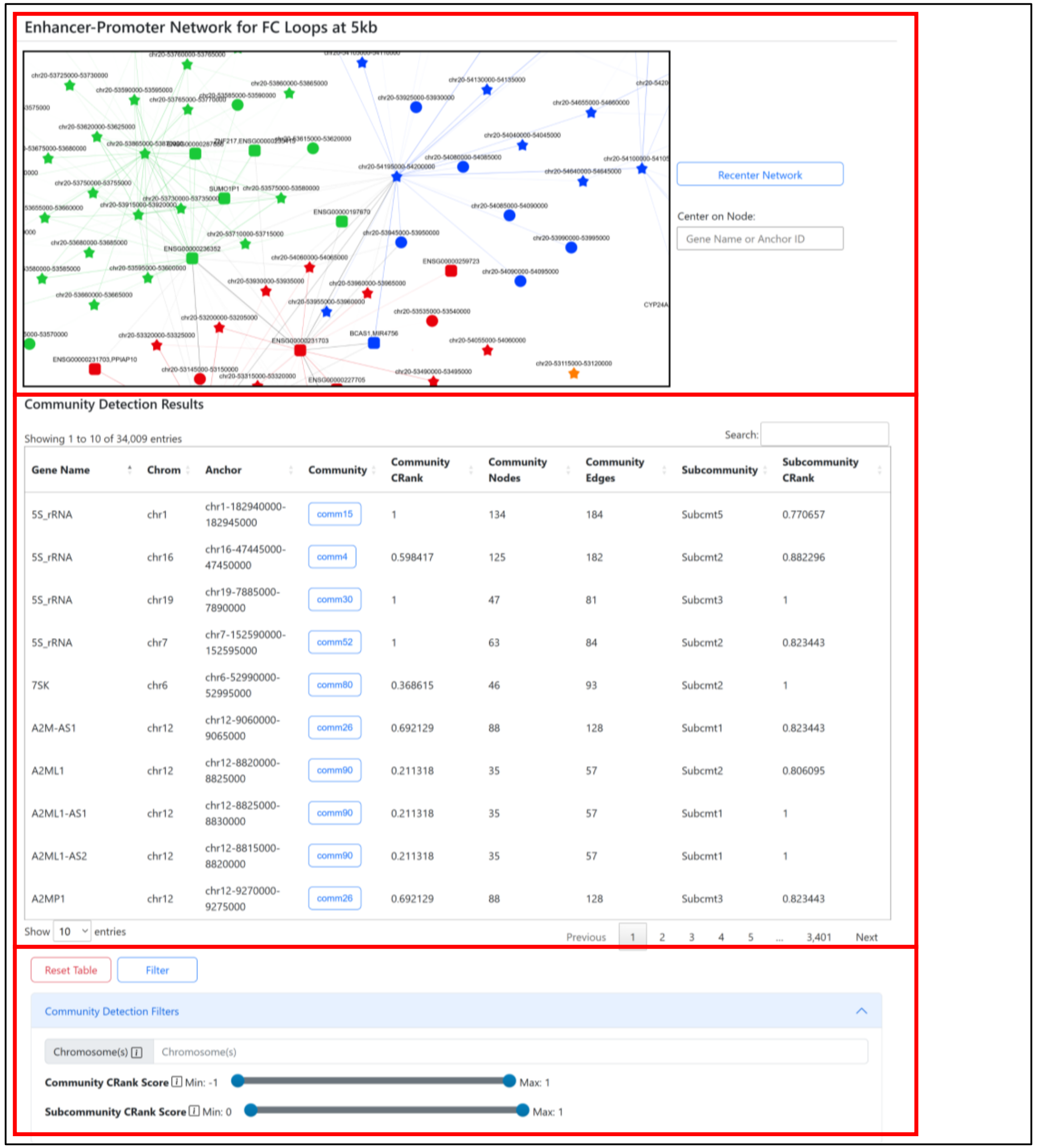
Number of Peaks	QC Flag	Download Link
80282	TBD	Currently Unavailable

Single Sample Pages with the Community Detection Module

cytoscapeJS powered network

Table of community detection results

Filtering buttons for table above



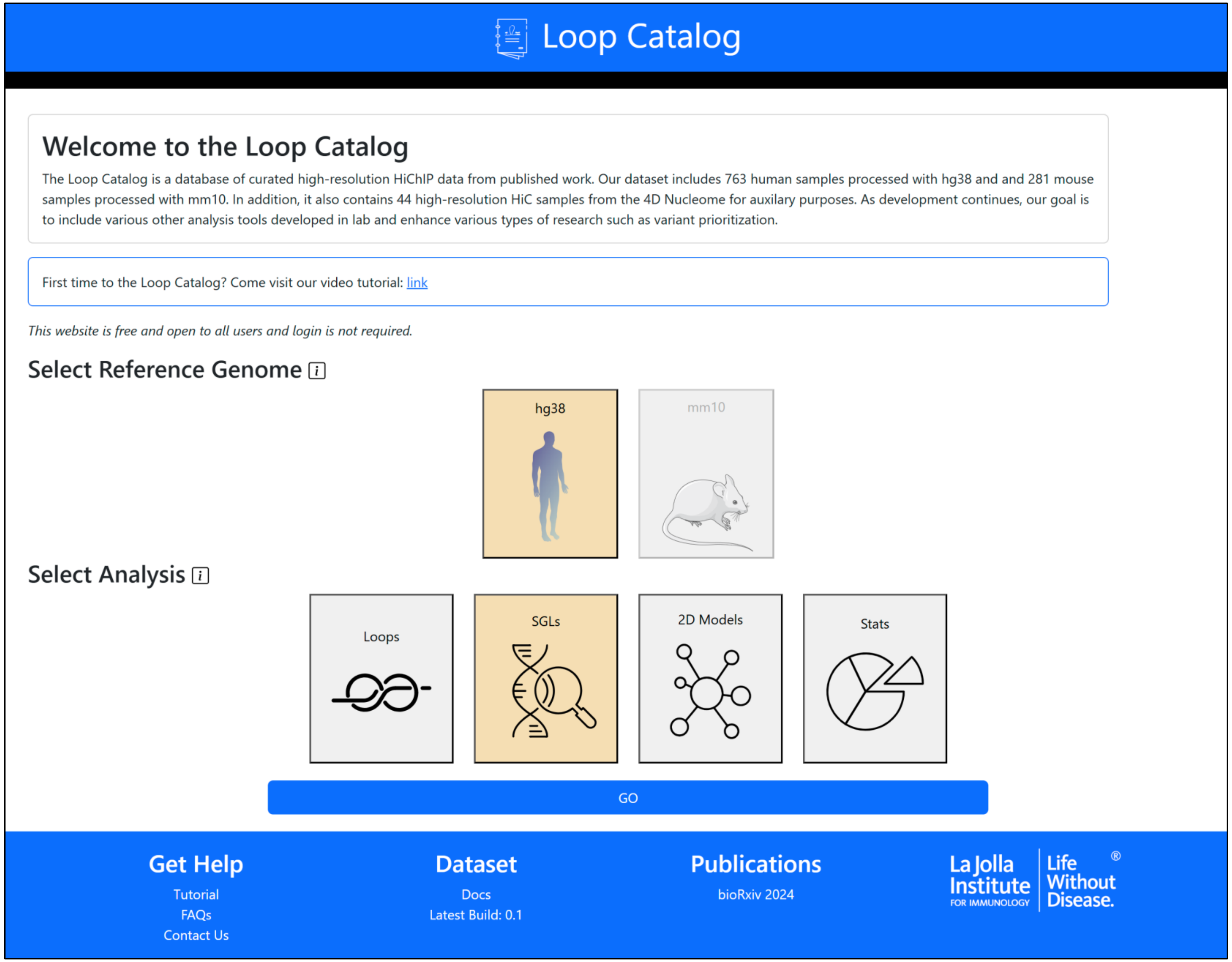
Enhancer-Promoter Network for FC Loops at 5kb

Community Detection Results

Showing 1 to 10 of 34,009 entries

Gene Name	Chrom	Anchor	Community	Community CRank	Community Nodes	Community Edges	Subcommunity	Subcommunity CRank
5S_rRNA	chr1	chr1-182940000-182945000	comm15	1	134	184	Subcmt5	0.770657
5S_rRNA	chr16	chr16-47445000-47450000	comm4	0.598417	125	182	Subcmt2	0.882296
5S_rRNA	chr19	chr19-7885000-7890000	comm30	1	47	81	Subcmt3	1
5S_rRNA	chr7	chr7-152590000-152595000	comm52	1	63	84	Subcmt2	0.823443
7SK	chr6	chr6-52990000-52995000	comm80	0.368615	46	93	Subcmt2	1
A2M-AS1	chr12	chr12-9060000-9065000	comm26	0.692129	88	128	Subcmt1	0.823443
A2ML1	chr12	chr12-8820000-8825000	comm90	0.211318	35	57	Subcmt2	0.806095
A2ML1-AS1	chr12	chr12-8825000-8830000	comm90	0.211318	35	57	Subcmt1	1
A2ML1-AS2	chr12	chr12-8815000-8820000	comm90	0.211318	35	57	Subcmt1	1
A2MP1	chr12	chr12-9270000-9275000	comm26	0.692129	88	128	Subcmt3	0.823443

Accessing SGL Results



Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxilary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: link

This website is free and open to all users and login is not required.

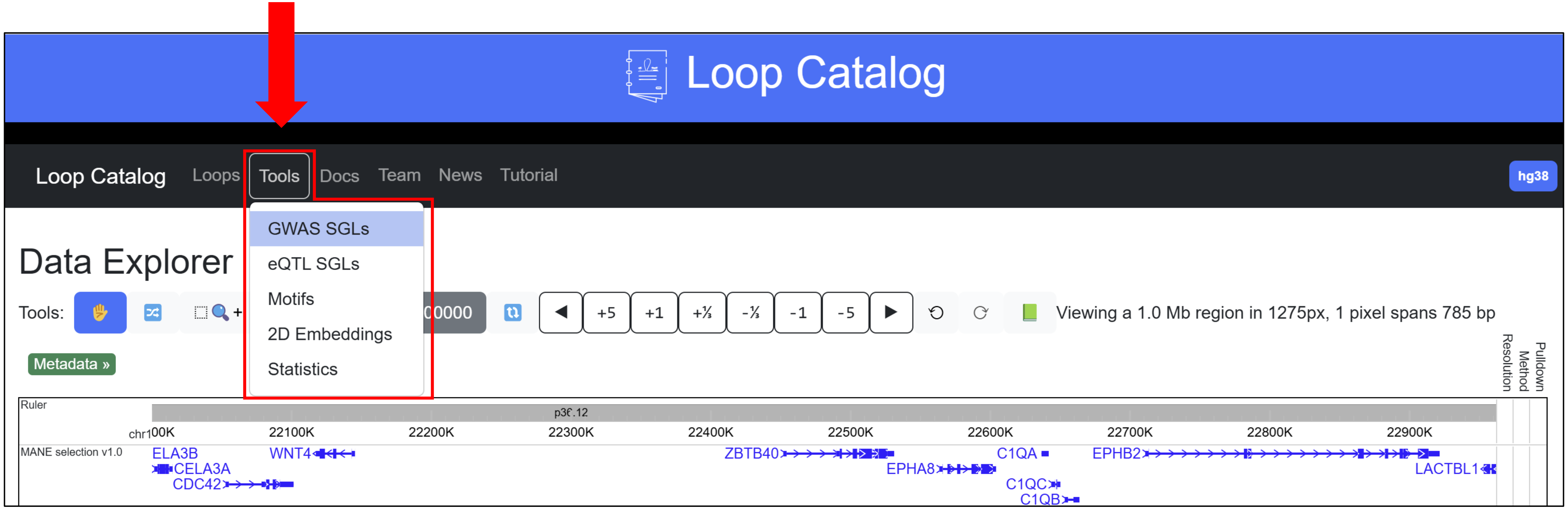
Select Reference Genome

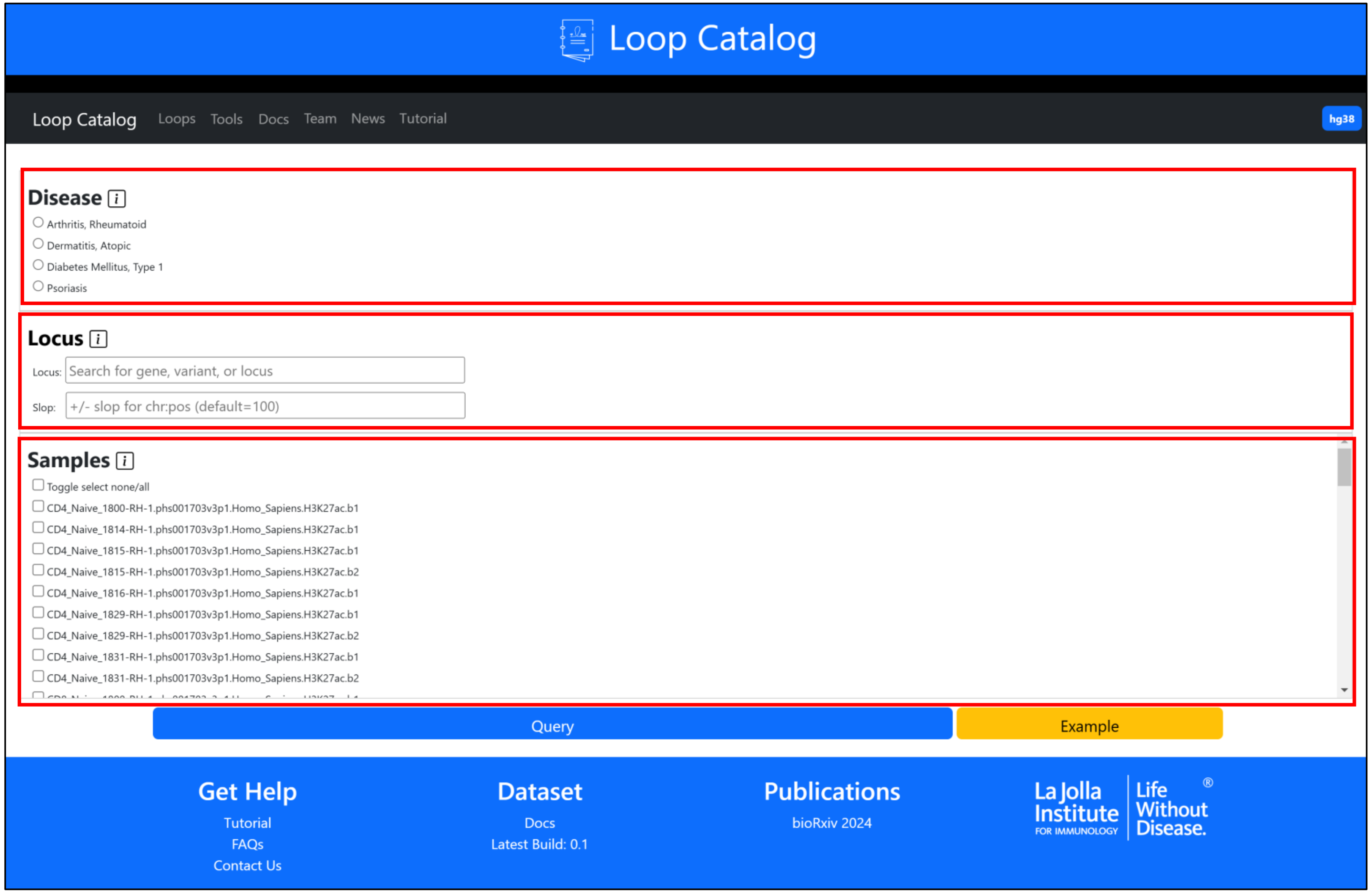
Select Analysis

Access via the main page

Alternatively, access from the Navigation Bar after a previous query

Tools → GWAS SGLs





Disease ⓘ

○ Arthritis, Rheumatoid
○ Dermatitis, Atopic
○ Diabetes Mellitus, Type 1
○ Psoriasis

Locus ⓘ

Locus: Search for gene, variant, or locus

Slop: +/- slop for chr:pos (default=100)

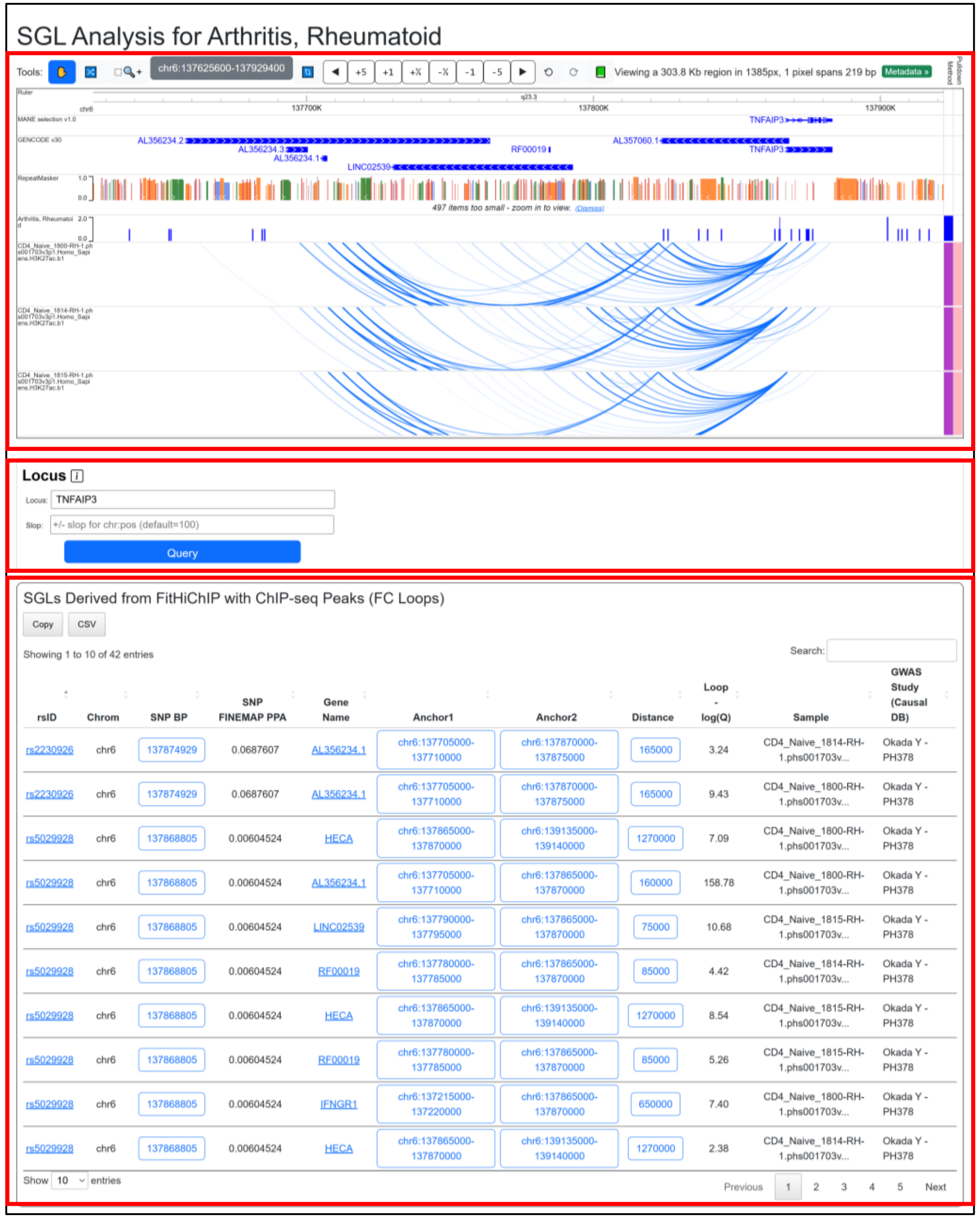
Samples ⓘ

☐ Toggle select none/all
☐ CD4_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1814-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2
☐ CD4_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1829-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1829-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2
☐ CD4_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2

Select disease

Select locus

Select samples



SGL Analysis for Arthritis, Rheumatoid

Locus

Locus: TNFAIP3

Slop: +/- slop for chr:pos (default=100)

Query

SGLs Derived from FitHiChIP with ChIP-seq Peaks (FC Loops)

Copy CSV

Showing 1 to 10 of 42 entries

Search:

rsID	Chrom	SNP BP	SNP FINEMAP PPA	Gene Name	Anchor1	Anchor2	Distance	Loop - log(Q)	Sample	GWAS Study (Causal DB)
rs2230926	chr6	137874929	0.0687607	AL356234.1	chr6:137705000-137710000	chr6:137870000-137875000	165000	3.24	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378
rs2230926	chr6	137874929	0.0687607	AL356234.1	chr6:137705000-137710000	chr6:137870000-137875000	165000	9.43	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	7.09	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	AL356234.1	chr6:137705000-137710000	chr6:137865000-137870000	160000	158.78	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	LINC02539	chr6:137790000-137795000	chr6:137865000-137870000	75000	10.68	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	RF00019	chr6:137780000-137785000	chr6:137865000-137870000	85000	4.42	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	8.54	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	RF00019	chr6:137780000-137785000	chr6:137865000-137870000	85000	5.26	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	IFNGR1	chr6:137215000-137220000	chr6:137865000-137870000	650000	7.40	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	2.38	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378

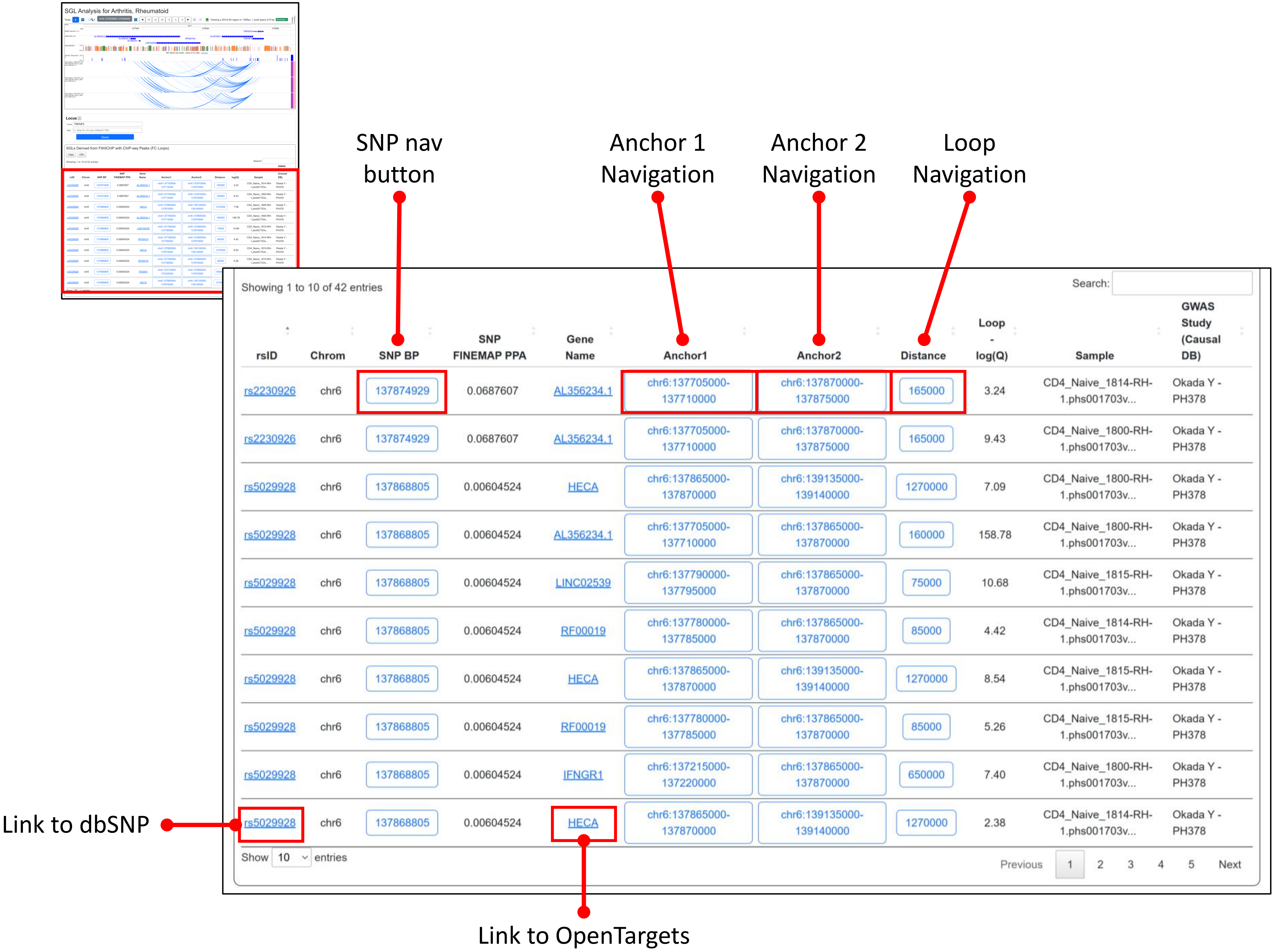
Show 10 entries

Previous 1 2 3 4 5 Next

WashU Browser

Re-select locus

Table of SGL results



Showing 1 to 10 of 42 entries

Search:

rsID	Chrom	SNP BP	SNP FINEMAP PPA	Gene Name	Anchor1	Anchor2	Distance	Loop -log(Q)	Sample	GWAS Study (Causal DB)
rs2230926	chr6	137874929	0.0687607	AL356234.1	chr6:137705000-137710000	chr6:137870000-137875000	165000	3.24	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378
rs2230926	chr6	137874929	0.0687607	AL356234.1	chr6:137705000-137710000	chr6:137870000-137875000	165000	9.43	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	7.09	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	AL356234.1	chr6:137705000-137710000	chr6:137865000-137870000	160000	158.78	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	LINC02539	chr6:137790000-137795000	chr6:137865000-137870000	75000	10.68	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	RF00019	chr6:137780000-137785000	chr6:137865000-137870000	85000	4.42	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	8.54	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	RF00019	chr6:137780000-137785000	chr6:137865000-137870000	85000	5.26	CD4_Naive_1815-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	IFNGR1	chr6:137215000-137220000	chr6:137865000-137870000	650000	7.40	CD4_Naive_1800-RH-1.phs001703v...	Okada Y - PH378
rs5029928	chr6	137868805	0.00604524	HECA	chr6:137865000-137870000	chr6:139135000-139140000	1270000	2.38	CD4_Naive_1814-RH-1.phs001703v...	Okada Y - PH378

Show 10 entries

Previous 1 2 3 4 5 Next

Each **row** represents an SGL

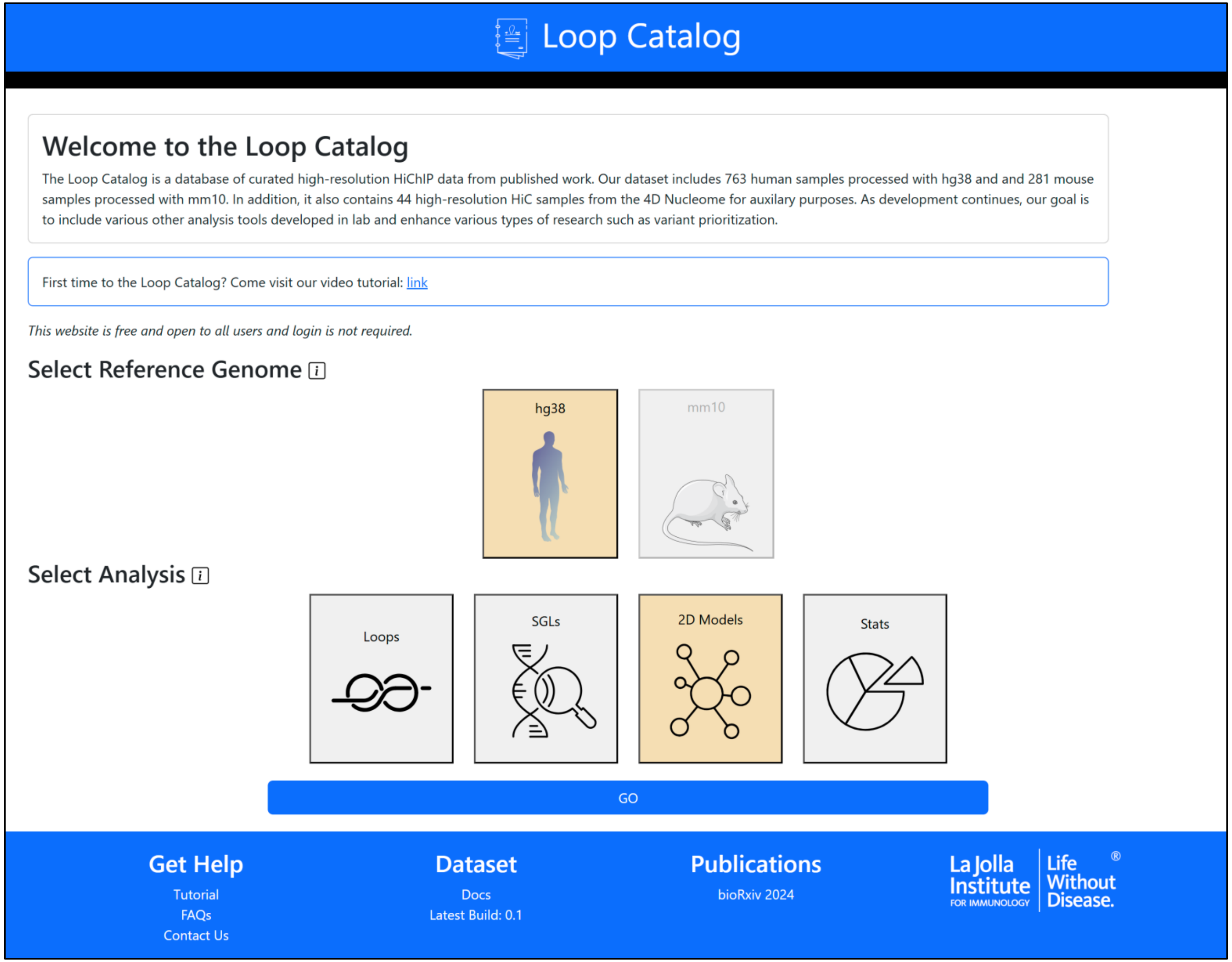
Anchor1 and **Anchor2** contain the bins corresponding to the left and right sides of a loop

Distance is measured as the start of Anchor2 minus the start of Anchor1

Loop –log10(Q) stores the significance value derived from FitHiChIP)

GWAS Study (CAUSALdb) contains the publication authors followed by the CAUSALdb ID

Accessing 2D Embeddings



Loop Catalog

Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxilary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: link

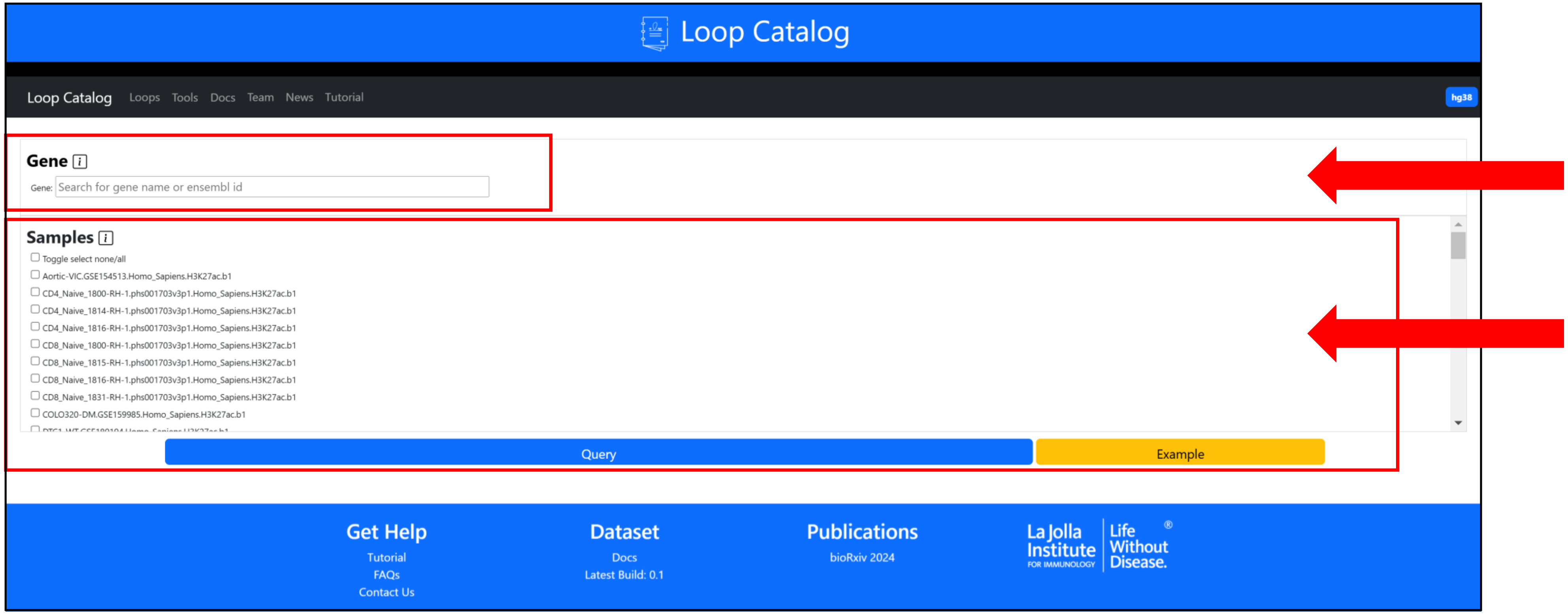
This website is free and open to all users and login is not required.

Select Reference Genome

Select Analysis

Alternative access:

Nav bar → Tools → 2D Embeddings



Gene

Gene: Search for gene name or ensembl id

Samples

☐ Toggle select none/all
☐ Aortic-VIC.GSE154513.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1814-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD4_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD8_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD8_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD8_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ CD8_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
☐ COLO320-DM.GSE159985.Homo_Sapiens.H3K27ac.b1

Select Gene

Select Samples

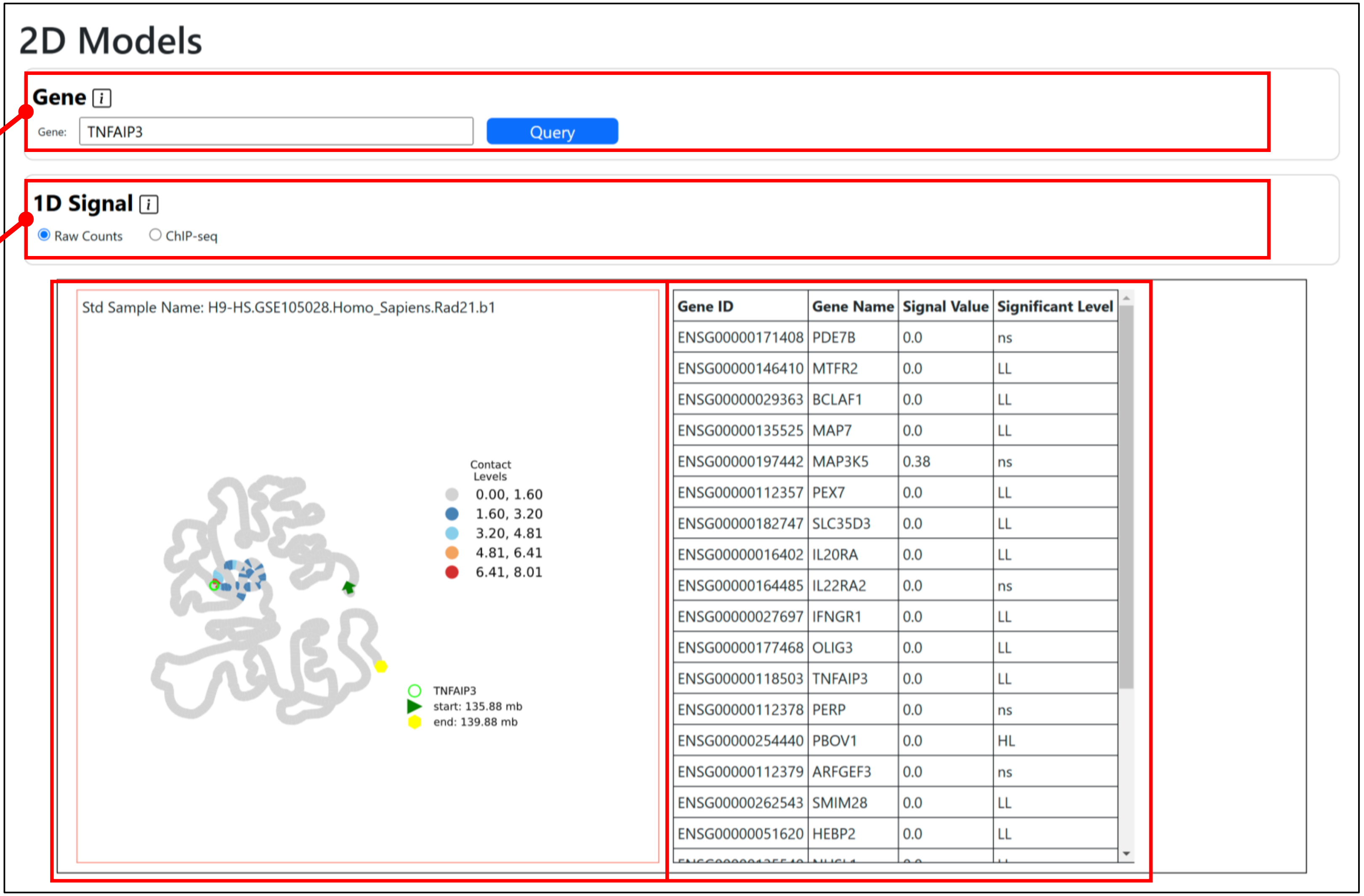
2D embedding model

with overlap of *raw counts*

(sum of contacts for a given bin within this subregion)

Quickly query a new gene with the same sample set

Select the overlapping 1D signal



2D Models

Gene ⓘ

Gene: TNFAIP3 Query

1D Signal ⓘ

● Raw Counts ○ ChIP-seq

Std Sample Name: H9-HS.GSE105028.Homo_Sapiens.Rad21.b1

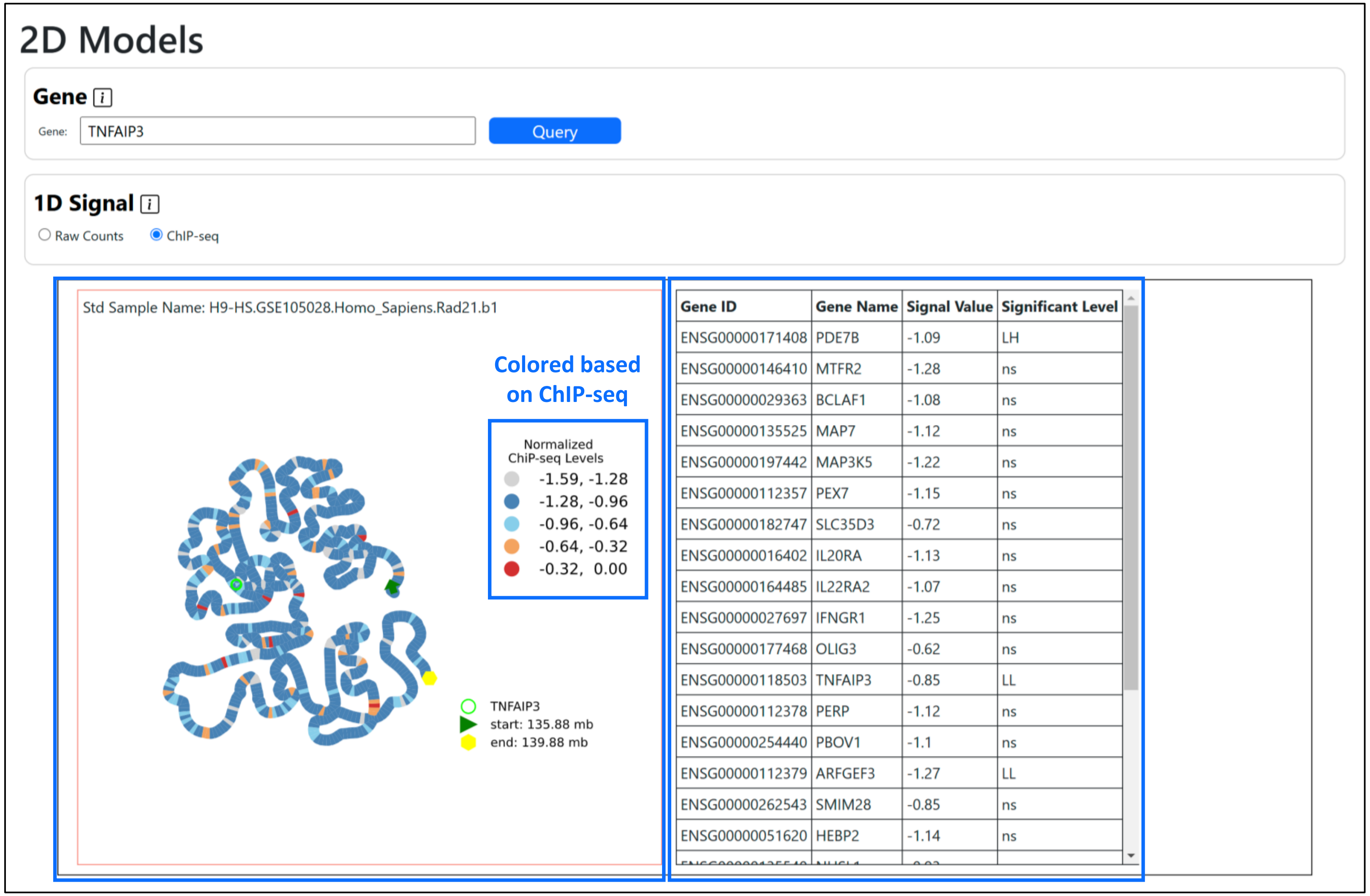
Gene ID	Gene Name	Signal Value	Significant Level
ENSG00000171408	PDE7B	0.0	ns
ENSG00000146410	MTFR2	0.0	LL
ENSG00000029363	BCLAF1	0.0	LL
ENSG00000135525	MAP7	0.0	LL
ENSG00000197442	MAP3K5	0.38	ns
ENSG00000112357	PEX7	0.0	LL
ENSG00000182747	SLC35D3	0.0	LL
ENSG00000016402	IL20RA	0.0	LL
ENSG00000164485	IL22RA2	0.0	ns
ENSG00000027697	IFNGR1	0.0	LL
ENSG00000177468	OLIG3	0.0	LL
ENSG00000118503	TNFAIP3	0.0	LL
ENSG00000112378	PERP	0.0	ns
ENSG00000254440	PBOV1	0.0	HL
ENSG00000112379	ARFGEF3	0.0	ns
ENSG00000262543	SMIM28	0.0	LL
ENSG00000051620	HEBP2	0.0	LL

Visualization of the 2D embedding model

Results table where each row is a gene with its signal value and (local Moran's) significance level

2D embedding model

with overlap of *ChIP-seq signal*



2D Models

Gene ⓘ

Gene: TNFAIP3 Query

1D Signal ⓘ

○ Raw Counts ● ChIP-seq

Std Sample Name: H9-HS.GSE105028.Homo_Sapiens.Rad21.b1

Colored based on ChIP-seq

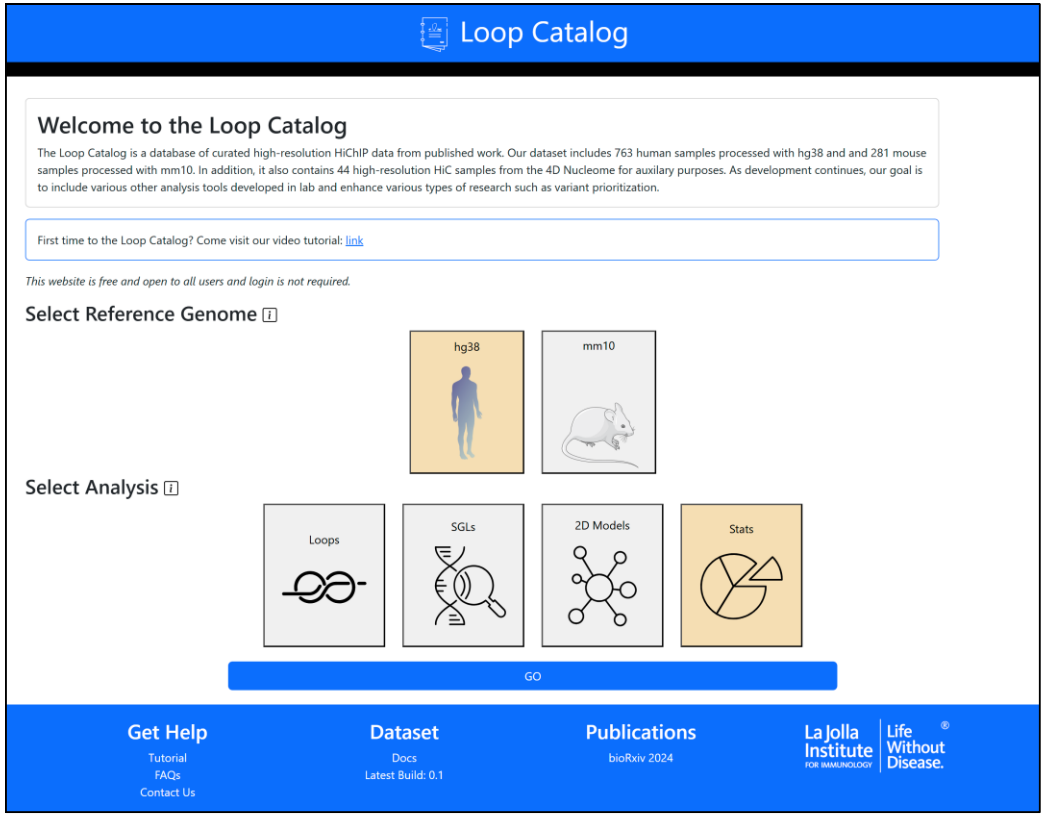
Gene ID	Gene Name	Signal Value	Significant Level
ENSG00000171408	PDE7B	-1.09	LH
ENSG00000146410	MTFR2	-1.28	ns
ENSG00000029363	BCLAF1	-1.08	ns
ENSG00000135525	MAP7	-1.12	ns
ENSG00000197442	MAP3K5	-1.22	ns
ENSG00000112357	PEX7	-1.15	ns
ENSG00000182747	SLC35D3	-0.72	ns
ENSG00000016402	IL20RA	-1.13	ns
ENSG00000164485	IL22RA2	-1.07	ns
ENSG00000027697	IFNGR1	-1.25	ns
ENSG00000177468	OLIG3	-0.62	ns
ENSG00000118503	TNFAIP3	-0.85	LL
ENSG00000112378	PERP	-1.12	ns
ENSG00000254440	PBOV1	-1.1	ns
ENSG00000112379	ARFGEF3	-1.27	LL
ENSG00000262543	SMIM28	-0.85	ns
ENSG00000051620	HEBP2	-1.14	ns

Same 2D structure

Results are now based on local Moran's I using ChIP-seq signal values

Other: Accessing Basic Statistics

Access Basic Statistics



Loop Catalog

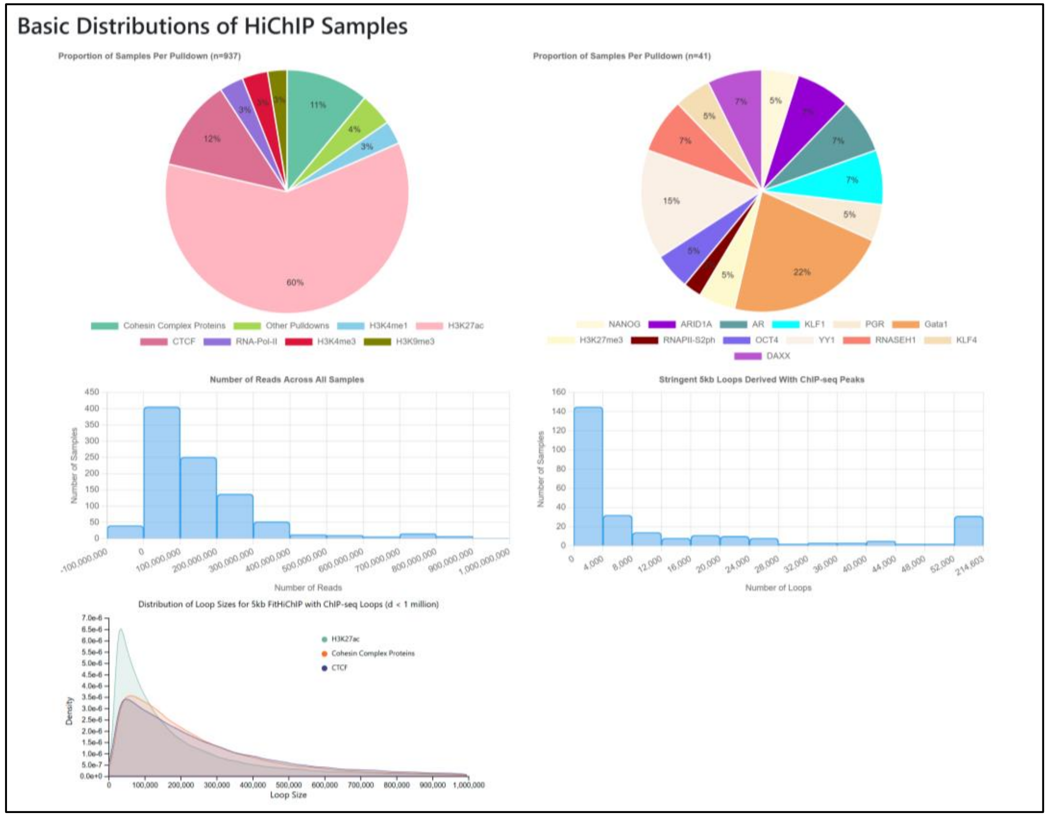
Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxilary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: link

This website is free and open to all users and login is not required.

Select and GO!



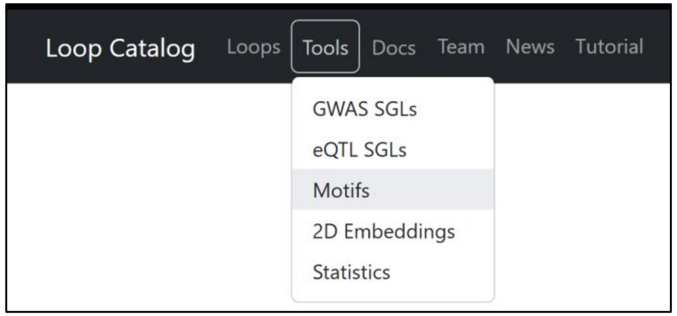
Alternative access:

Nav bar → Tools → Statistics

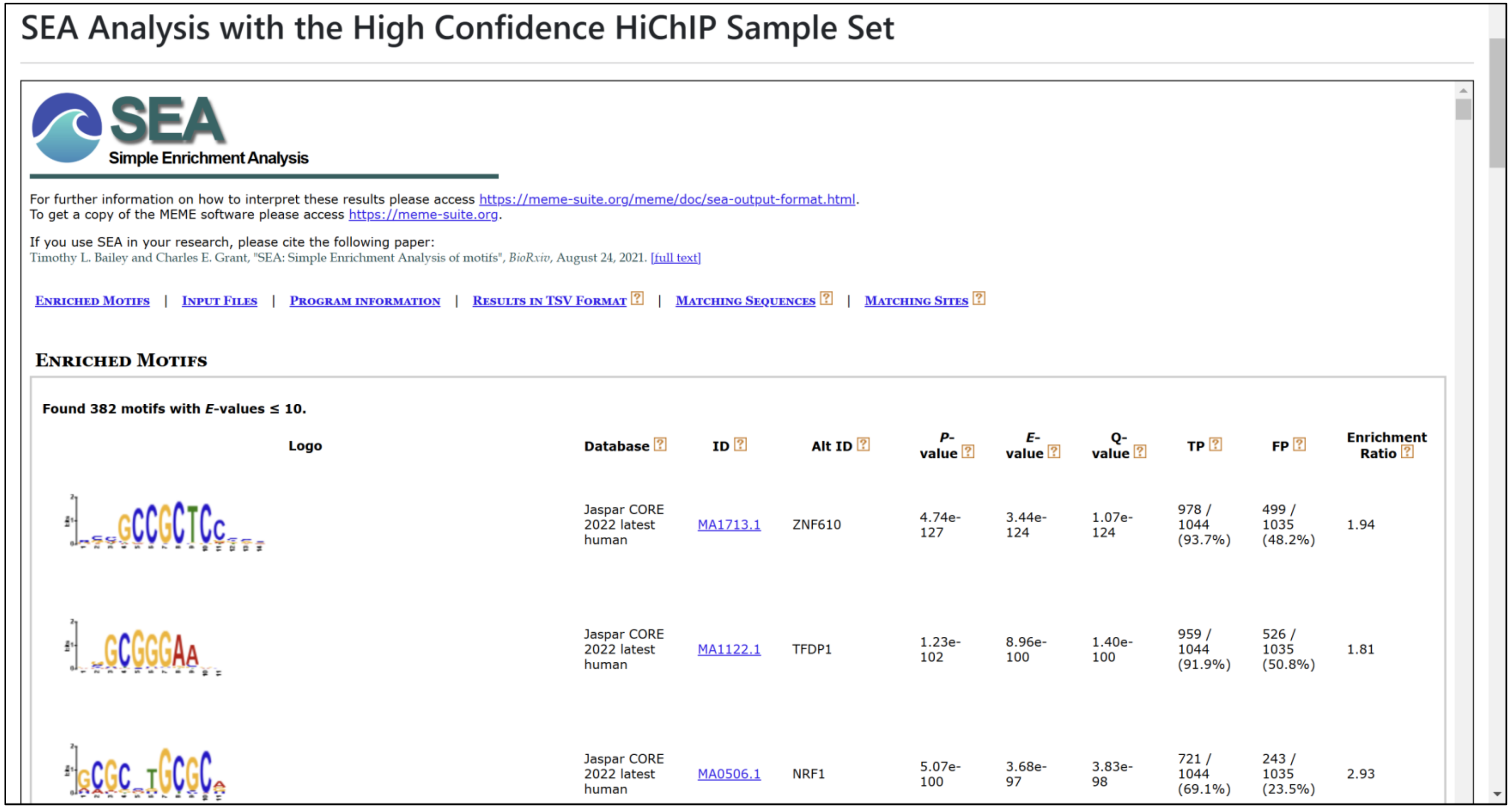
Breakdown of pulldowns, number of reads, number of loops and loop size

Accessing 1D Motif Results

Alternative access:
Nav bar → Tools → Motifs



Access from Tools



SEA Analysis with the High Confidence HiChIP Sample Set

For further information on how to interpret these results please access https://meme-suite.org/meme/doc/sea-output-format.html.
To get a copy of the MEME software please access https://meme-suite.org.

If you use SEA in your research, please cite the following paper:
Timothy L. Bailey and Charles E. Grant, "SEA: Simple Enrichment Analysis of motifs", *BioRxiv*, August 24, 2021. [full text]

ENRICHED MOTIFS

Found 382 motifs with *E*-values ≤ 10.

Logo	Database	ID	Alt ID	*P*-value	*E*-value	Q-value	TP	FP	Enrichment Ratio
	Jaspar CORE 2022 latest human	MA1713.1	ZNF610	4.74e-127	3.44e-124	1.07e-124	978 / 1044 (93.7%)	499 / 1035 (48.2%)	1.94
	Jaspar CORE 2022 latest human	MA1122.1	TFDP1	1.23e-102	8.96e-100	1.40e-100	959 / 1044 (91.9%)	526 / 1035 (50.8%)	1.81
	Jaspar CORE 2022 latest human	MA0506.1	NRF1	5.07e-100	3.68e-97	3.83e-98	721 / 1044 (69.1%)	243 / 1035 (23.5%)	2.93

Results for each of the SEA analysis using different subsets of the High Confidence HiChIP Sample Set, this includes:

1) **All samples**
2) **Immune only**
3) **Non-immune only**
4) **CTCF only**