

enChIP-Seq Analyzer User Manual ver. 3.0

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Overview

FujiTool ver.2.0

①

Positive
(AND)

add

remove

view

②

Negative
(OR)

add

remove

view

③

tag

▼

0

④

Pos.-Neg.

⑤

fold enrichment

▼

0

count :

0

⑥

Export Table

- ① Add "positive" samples to detect physical interactions between genomic regions (e.g., if you want to detect B cell-specific interactions, add B cell data here). The output will show a **common set / intersection (overlapping)** if replicates or samples with different guide RNAs for a target locus are added (see p. 6).
- ② Add "negative" samples to subtract non-specific interactions (e.g., if you want to detect B cell-specific interactions, add negative control samples such as those of macrophages here). The output will show a **sum set / union** if replicates or samples with different guide RNAs for a target locus are added (see p. 6).
- ③ Data can be filtered using tag numbers or fold enrichment.
- ④ Signals of negative files ② can be subtracted from those of positive files ①.
- ⑤ Click the "view" button to see the result table of ①, ②, or the "Pos.-Neg." button of ④. Bottom left displays the number of rows in the table.
- ⑥ Export the table in ⑤ as a CSV file.

1

Adding files for analysis

Click the “add” button to add files in the appropriate panel (“Positive” or “Negative” panel). Multiple files can be added simultaneously.

Positive
(AND)

add

remove

view

Negative
(OR)

add

remove

view

ファイルを開く

ファイルの場所(l): positive

クイック アクセス

デスクトップ

ライブラリ

PC

ネットワーク

名前	更新日時	種類
		TAB ファイル
		TAB ファイル

ファイル名(N):
ファイルの種類(T): すべてのファイル (*.*)

開く(O)

キャンセル



Positive
(AND)

C:\Users

add

remove

view

Negative
(OR)

add

remove

view

tag

0

fold enrichment

0

Pos.-Neg.

Property of a file to be analyzed

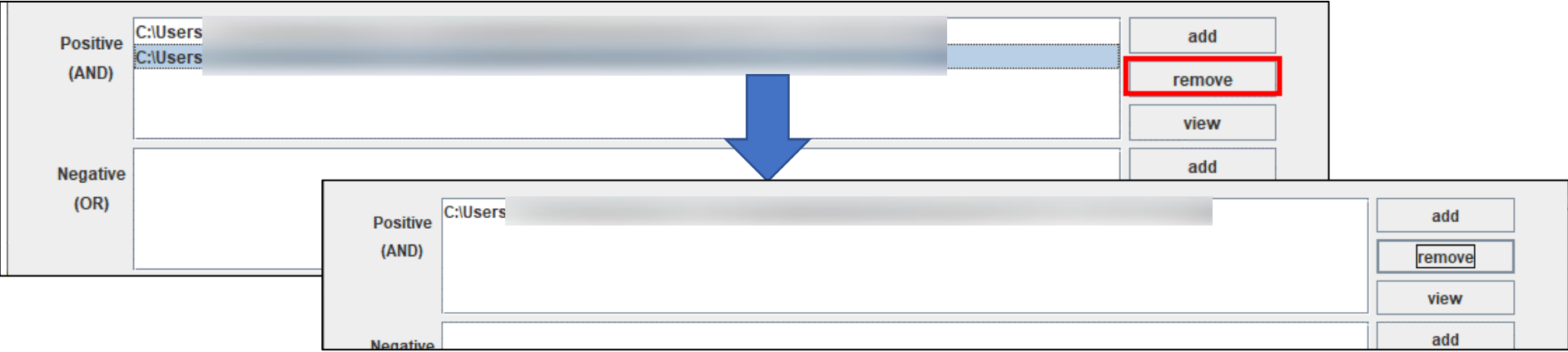
```
# This file is generated by MACS version 1.4.2 20120305
# ARGUMENTS LIST:
# name = MACS14_HS5_6_NaB_IP
# format = BED
# ChIP-seq file
# control file =
# effective genome size = 2.70e+09
# band width = 300
# model fold = 10,30
# pvalue cutoff = 1.00e-05
# Large dataset will be scaled towards smaller dataset.
# Range for calculating regional lambda is: 1000 bps and 10000 bps
# tag size is determined as 35 bps
# total tags in treatment: 25696905
# tags after filtering in treatment: 23889895
# maximum duplicate tags at the same position in treatment = 1
# Redundant rate in treatment: 0.07
# total tags in control: 33148962
# tags after filtering in control: 31888685
# maximum duplicate tags at the same position in control = 1
# Redundant rate in control: 0.04
# d = 35
chr start end length summit tags -10*log10(pvalue) fold_enrichment FDR(%)
chr1 2053504 2053594 91 24 8 67.20 22.60 1.79
chr1 2298994 2299079 86 52 7 50.95 10.17 3.67
chr1 2399589 2399712 124 84 9 65.88 12.92 1.81 8165:NM_014638:PLCH2
chr1 5646669 5646769 101 48 9 72.06 18.45 1.70
chr1 5731697 5731849 153 79 16 54.61 6.02 3.14
chr1 7347532 7347648 117 64 10 78.46 19.37 1.66
chr1 7347671 7347770 100 67 8 63.83 19.37 1.88
chr1 7626357 7626443 87 22 7 58.10 19.37 2.91
chr1 7812202 7812293 92 30 10 66.14 13.35 1.84
chr1 9292338 9292423 86 31 7 56.42 15.13 2.91 2525:NM_004285:H6PD
chr1 10286082 10286164 83 60 10 75.07 14.83 1.72
chr1 11072883 11072966 84 32 7 53.84 16.34 3.48 -204:NM_007375:TARDBP
chr1 11610725 11611206 482 216 78 580.85 29.87 0.00
chr1 11696034 11696148 115 57 8 57.17 18.45 3.03
chr1 11919451 11919604 154 64 14 90.93 14.86 1.05 613:NM_002521:NPPB
```

Rows starting with “#” are not read.

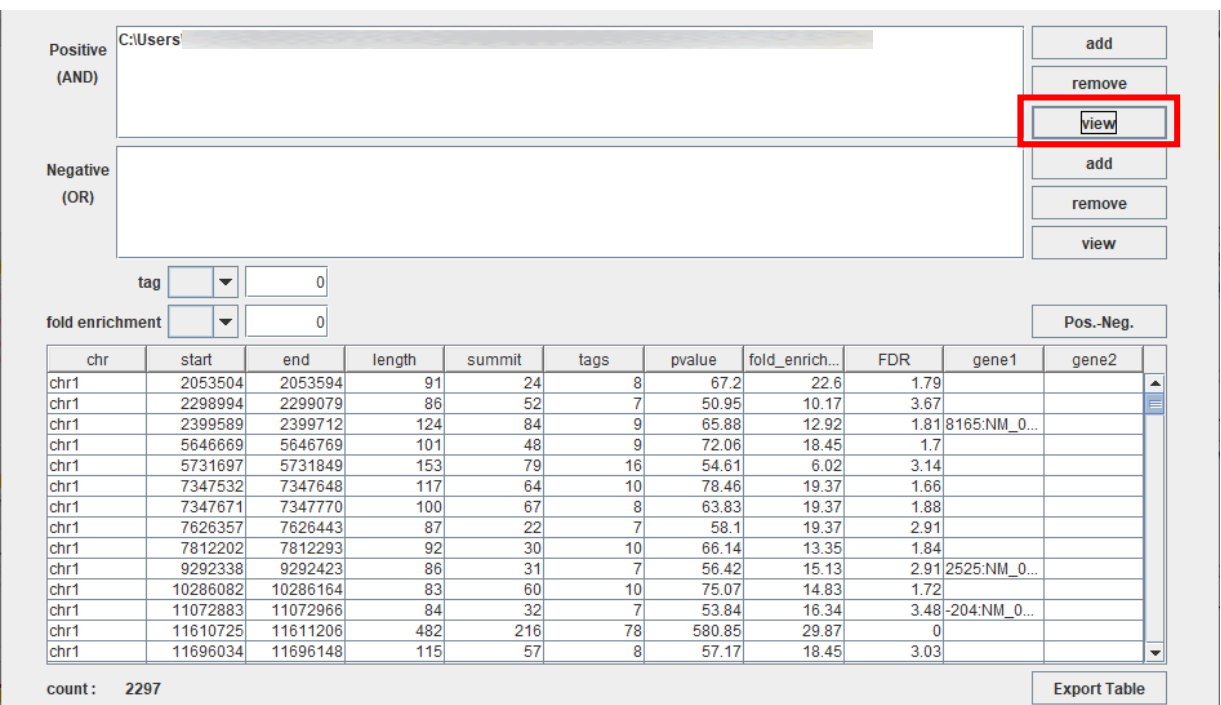
Comma Separated Values (CSVs) are read as data.

Removing or viewing a file

To remove an unnecessary file, click the file row and then click the “remove” button.



To view a file’s contents, select the file row and then click the “view” button.



Analysis

After loading Positive and Negative files, you can click the “Pos.-Neg.” button to analyze the data.

The screenshot displays the FujiTool ver.2.0 application window. It features two input sections: 'Positive (AND)' and 'Negative (OR)', each with a file path input field and a corresponding 'add', 'remove', and 'view' button. Below these are 'tag' and 'fold enrichment' dropdown menus, both currently set to '0'. A red box highlights the 'Pos.-Neg.' button, which is used to initiate the analysis. Below this button is a table with 11 columns: chr, start, end, length, summit, tags, pvalue, fold_enrich..., FDR, gene1, and gene2. The table contains 15 rows of data, all from chromosome 1. A red box at the bottom left highlights the 'count: 2161' label. At the bottom right, there is an 'Export Table' button.

chr	start	end	length	summit	tags	pvalue	fold_enrich...	FDR	gene1	gene2
chr1	2053504	2053594	91	24	8	67.2	22.6	1.79		
chr1	2298994	2299079	86	52	7	50.95	10.17	3.67		
chr1	2399589	2399712	124	84	9	65.88	12.92	1.81	8165:NM_0...	
chr1	5646669	5646769	101	48	9	72.06	18.45	1.7		
chr1	5731697	5731849	153	79	16	54.61	6.02	3.14		
chr1	7347532	7347648	117	64	10	78.46	19.37	1.66		
chr1	7347671	7347770	100	67	8	63.83	19.37	1.88		
chr1	7626357	7626443	87	22	7	58.1	19.37	2.91		
chr1	7812202	7812293	92	30	10	66.14	13.35	1.84		
chr1	9292338	9292423	86	31	7	56.42	15.13	2.91	2525:NM_0...	
chr1	10286082	10286164	83	60	10	75.07	14.83	1.72		
chr1	11072883	11072966	84	32	7	53.84	16.34	3.48	-204:NM_0...	
chr1	11696034	11696148	115	57	8	57.17	18.45	3.03		
chr1	11919451	11919604	154	64	14	90.93	14.86	1.05		613:NM_00...

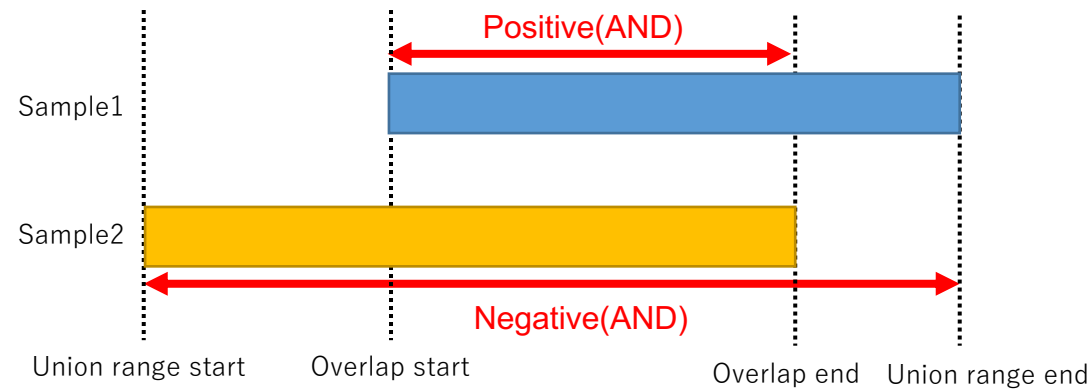
count: 2161

Export Table

The counter at the left-bottom corner shows the peak count.

Analysis of two or more files

Files in the “Positive” field are processed to generate overlapping regions, whereas files in the “Negative” field are processed to generate union ranges.



Positive (AND)

C:\Users\...tab

C:\Users\...ib

add

remove

view

Negative (OR)

C:\Users\...tab

add

remove

view

tag

0

fold enrichment

0

Pos.-Neg.

chr	start	end	length	summit	tags	pvalue	fold_enrich...	FDR	gene1	gene2
chr1	7347570	7347648	78	64	10	78.46	19.37	1.66		
chr1	7347672	7347749	77	67	8	63.83	19.37	1.88		
chr1	11919466	11919604	138	64	14	90.93	14.86	1.05	613:NM_00...	
chr1	12316588	12316677	89	33	9	68.05	16.34	1.89		
chr1	12316726	12316738	12	64	13	90.6	20.34	1		
chr1			33							
chr1			72						7746:NM_0...	

Start and end positions (“start” and “end”), and “length” are automatically calculated and reflected in the result table, whereas “summit”, “tags” (number of tags), “p-value”, “fold enrichment” and FDR are reflected from the values of the selected “base file”.

The “base file” can be selected in the “Positive” field.

Filtering with tag and fold enrichment

Data can be filtered by tag and fold enrichment. Select the tag and filter value “=”, “<” or “>”. Click the “Pos.-Neg.” button to update the table by the filtering conditions.

Positive
(AND)

C:\p... .tal

add

remove

view

Negative
(OR)

C:\p...

add

remove

view

tag > 39

fold enrichment > 10

Pos.-Neg.

chr	start	end	length	summit	tags	pvalue	fold_enrich...	FDR	gene1	gene2
chr1	33526002	33526540	539	188	95	869.16	51.67	0		
chr1	153586701	153587167	467	81	49	259.09	15.83	0		1654:NM_0...
chr1	247240307	247240894	588	246	68	322.89	17.62	0		-1220:NM_...
chr1	247240925	247241339	415	243	49	221.87	12.95	0		-775:NM_0...
chr10	15387617	15388319	703	369	382	3,100	101.06	0		
chr11	5311586	5312647	1062	595	783	3,100	168.11	0		
chr11	36122948	36123372	425	281	63	441.98	27.79	0		
chr11	57669714	57670066	353	129	42	199.98	11.97	0		
chr11	66057056	66057342	287	127	45	329.48	30.65	0	2317:NM_1...	705:NM_02...
chr11	66131388	66131805	418	189	56	388.52	33.37	0		-7485:NM_...
chr12	76347754	76348240	487	266	76	513.86	22.08	0		
chr15	64162769	64163183	415	80	51	400.95	29.06	0		
chr16	1359061	1359401	341	284	41	299.03	25.24	0	93:NM_003...	
chr16	67522986	67523488	503	265	110	863.92	38.37	0		8400:NM_0...

count : 19

Export Table

Exporting a result table

Click “view” or “Pos.-Neg.” button to generate data. Then click the “Export Table” button to download as a CSV file.

chr	start	end	length	summit	tags	pvalue	fold_enrich...	FDR	gene1	gene2
chr1	33526002	33526540	539	188	95	869.16	51.67	0		
chr1	153586701	153587167	467	81	49	259.09	15.83	0		1654:NM_0...
chr1	247240307	247240894	588	246	68	322.89	17.62	0		-1220:NM_...
chr1	247240925	247241339	415	243	49	221.87	12.95	0		-775:NM_0...
chr10	15387617	15388319	703	369	382	3,100	101.06	0		
chr11	5311586	5312647	1062	595	783	3,100	168.11	0		
chr11	36122948	36123372	425	281	63	441.98	27.79	0		
chr11	57669714	57670066	353	129	42	199.98	11.97	0		
chr11	66057056	66057342	287	127	45	329.48	30.65	0	2317:NM_1...	705:NM_02...
chr11	66131388	66131805	418	189	56	388.52	33.37	0		-7485:NM_...
chr12	76347754	76348240	487	266	76	513.86	22.08	0		
chr15	64162769	64163183	415	80	51	400.95	29.06	0		
chr16	1359061	1359401	341	284	41	299.03	25.24	0	93:NM_003...	
chr16	67522986	67523488	503	265	110	863.92	38.37	0		8400:NM_0...

count: 19

Export Table

Example of an exported CSV file

test4.csv - メモ帳

ファイル(E) 編集(E) 書式(O) 表示(V) ヘルプ(H)

chr	start	end	length	summit	tags	pvalue	fold_enrichment	FDR	gene1	gene2
chr16	1359061	1359401	341	284	41	299.03	25.24	0.0	93:NM_003345,NM_194259,NM_194260,NM_194261:UBE2I	
chr6	116781574	116781978	405	138	41	208.29	13.35	0.0	982:NM_001010919:FAM26F	
chr9	108639933	108640362	430	283	41	171.13	14.3	0.0		
chr11	57669714	57670066	353	129	42	199.98	11.97	0.0		
chr5	118784853	118785151	299	163	44	318.58	31.93	0.0	3285:NM_000414,NM_001199291,NM_001199292:HSD17B4	
chr11	66057056	66057342	287	127	45	329.48	30.65	0.0	2317:NM_153266:TMEM151A	705:NM_020470:YIF1A
chr4	81093373	81093786	414	190	46	266.82	19.07	0.0		
chr1	153586701	153587167	467	81	49	259.09	15.83	0.0	1654:NM_080388:S100A16 -1640:NM_020672:S100A14	
chr1	247240925	247241339	415	243	49	221.87	12.95	0.0	-775:NM_001204220,NM_033213:ZNF670	
chr15	64162769	64163183	415	80	51	400.95	29.06	0.0		
chr11	66131388	66131805	418	189	56	388.52	33.37	0.0	-7485:NM_001532:SLC29A2	
chr11	36122948	36123372	425	281	63	441.98	27.79	0.0		
chr1	247240307	247240894	588	246	68	322.89	17.62	0.0	-1220:NM_001204220,NM_033213:ZNF670	
chr7	132001863	132002364	502	272	71	488.49	27.24	0.0		
chr12	76347754	76348240	487	266	76	513.86	22.08	0.0		
chr1	33526002	33526540	539	188	95	869.16	51.67	0.0		
chr16	67522986	67523488	503	265	110	863.92	38.37	0.0	8400:NM_004691:ATP6VOD1 5773:NM_001138:AGRP	
chr10	15387617	15388319	703	369	382	3100.0	101.06	0.0		
chr11	5311586	5312647	1062	595	783	3100.0	168.11	0.0		

Book1 - Excel

ファイル ホーム 挿入 レイアウト 参照 データ ツール ヘルプ

	A	B	C	D	E	F	G	H	I	J
1	chr	start	end	length	summit	tags	pvalue	fold_enrich	FDR	gene1
2	chr16	1359061	1359401	341	284	41	299.03	25.24	0.0	93:NM_003345,NM_194259,NM_194260,NM_194261:UBE2I
3	chr6	116781574	116781978	405	138	41	208.29	13.35	0.0	982:NM_001010919:FAM26F
4	chr9	108639933	108640362	430	283	41	171.13	14.3	0.0	
5	chr11	57669714	57670066	353	129	42	199.98	11.97	0.0	
6	chr5	118784853	118785151	299	163	44	318.58	31.93	0.0	3285:NM_000414,NM_001199291,NM_001199292:HSD17B4
7	chr11	66057056	66057342	287	127	45	329.48	30.65	0.0	2317:NM_153266:TMEM151A 705:NM_020470:YIF1A
8	chr4	81093373	81093786	414	190	46	266.82	19.07	0.0	
9	chr1	153586701	153587167	467	81	49	259.09	15.83	0.0	1654:NM_080388:S100A16 -1640:NM_020672:S100A14
10	chr1	247240925	247241339	415	243	49	221.87	12.95	0.0	-775:NM_001204220,NM_033213:ZNF670
11	chr15	64162769	64163183	415	80	51	400.95	29.06	0.0	
12	chr11	66131388	66131805	418	189	56	388.52	33.37	0.0	-7485:NM_001532:SLC29A2
13	chr11	36122948	36123372	425	281	63	441.98	27.79	0.0	
14	chr1	247240307	247240894	588	246	68	322.89	17.62	0.0	-1220:NM_001204220,NM_033213:ZNF670
15	chr7	132001863	132002364	502	272	71	488.49	27.24	0.0	
16	chr12	76347754	76348240	487	266	76	513.86	22.08	0.0	
17	chr1	33526002	33526540	539	188	95	869.16	51.67	0.0	
18	chr16	67522986	67523488	503	265	110	863.92	38.37	0.0	8400:NM_004691:ATP6VOD1 5773:NM_001138:AGRP
19	chr10	15387617	15388319	703	369	382	3100.0	101.06	0.0	
20	chr11	5311586	5312647	1062	595	783	3100.0	168.11	0.0	

The file can be read with Excel.