

CAGE Analysis Viewer User's Guide

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NTT Software Corporation

Abstract

This document is an operation manual for the system, CAGE Analysis Viewer. It is developed by NTT Software Corporation.

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1. User environment

The following hardware and software are required to use this system as a client.

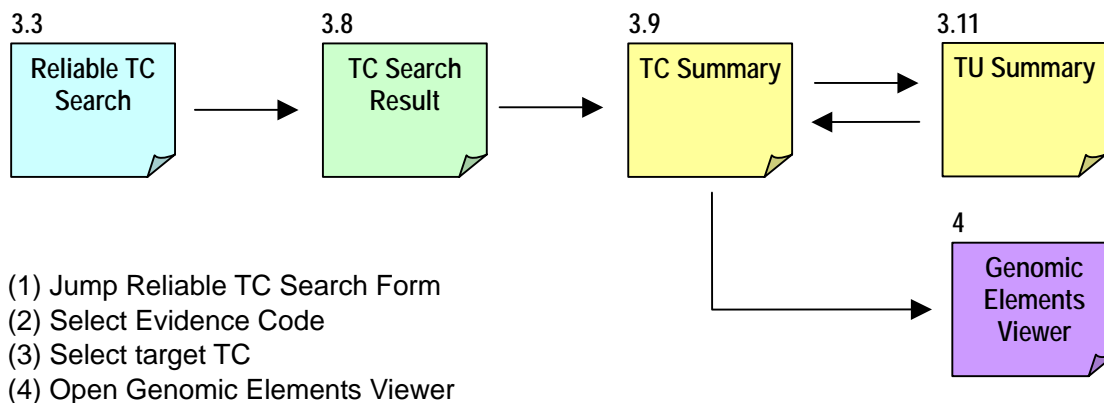
Contents	Confirmation
OS	Microsoft Windows 2000 Microsoft Windows XP Apple Mac OS X
CPU	-
Memory	128MB or more is recommended.
Hard Disk	-
Web Browser	Internet Explorer 6.0(Or the compatible version of it or later) Netscape 7.1(Or the compatible version of it or later) Safari 1.0

2. Getting started

2.1 Reliable TC search by evidence code

You can search reliable TC at 'Reliable TC Search' by evidence code.

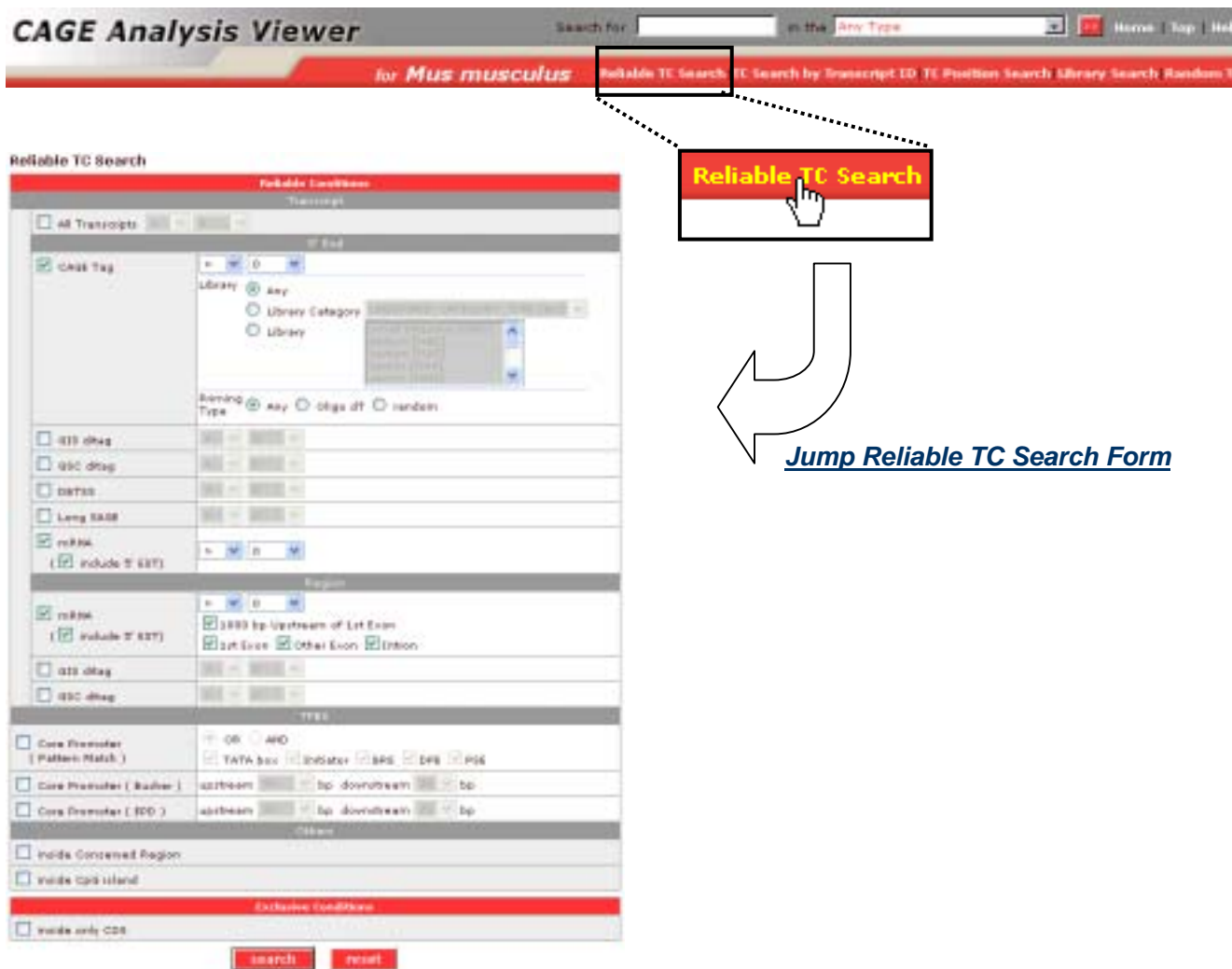
Overview



- (1) Jump Reliable TC Search Form
- (2) Select Evidence Code
- (3) Select target TC
- (4) Open Genomic Elements Viewer

(1) Jump Reliable TC Search Form

Reliable TC Search form is displayed by clicking 'Reliable TC Search' of top menu.



[Jump Reliable TC Search Form](#)

(2) Select Evidence Code

You can get the reliable TC list by selected evidence code, clicking Search button.

Reliable TC Search

Reliable Conditions

Transcript

All Transcripts
 > ▾ 0 ▾

5' End

CAGE Tag

> ▾ 0 ▾

Library

- Any
- Library Category UNDEFINED_CATEGORY_TYPE [etc] ▾
- Library

small intestine [HAD]

rectum [HAE]

rectum [HAF]

cecum [HAG]

cecum [HAH]

Priming Type

- Any
- Oligo dT
- random

GIS ditag

> ▾ 0 ▾

GSC ditag

> ▾ 0 ▾

DBTSS

> ▾ 0 ▾

Long SAGE

> ▾ 0 ▾

mRNA
 (include 5' EST)

> ▾ 0 ▾

Region

mRNA
 (include 5' EST)

> ▾ 0 ▾

1000 bp Upstream of 1st Exon
 1st Exon Other Exon Intron

GIS ditag

> ▾ 0 ▾

GSC ditag

> ▾ 0 ▾

TFBS

Core Promoter
 (Pattern Match)

OR AND

TATA box Initiator BRE DPE PSE

Core Promoter (Bucher)

upstream bp downstream bp

Core Promoter (EPD)

upstream bp downstream bp

Others

inside Conserved Region
 inside CpG island

Exclusive Conditions

inside only CDS

search
reset

You can select RNA library information to specify TC

You can select type and number of transcript for 5'-end of TC

You can select type and number of transcript which include TC

You can select promoter type and distance between promoter and 5'-end of TC

You can select TC inside Conserved Region and CpG island

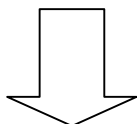
(3) Select target TC

You can select interested TC from the result list of reliable TC search. It displays the summary of evidence code relevant to TC by list.

TC Search Result

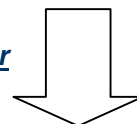
Results 281-320 about 450,228. Page 8 of 11,258

No	TC ID	Representative Type	Chr.	#/R	Representative Position	Start	End	Region				5' End				CTSSs	CAGE Tags	OIS Long SAGE TRIR box Initiator EPE PSE Conserved Reg CpG Island	Link
								5'3'	5'5'	3'5'	3'3'	5'3'	5'5'	3'5'	3'3'				
281	T01F001394F1	CAGE	1	F	1,283,313	0	+19	0	0	4	2	0	0	0	0	3	3		GENOMIC VIEWER
282	T01F0013971E	CAGE	1	F	1,283,870	0	+23	0	0	6	2	0	0	0	1	1		GENOMIC VIEWER	
283	T01F0013975Q	CAGE	1	F	1,283,920	0	+46	0	0	6	2	0	0	0	3	1		GENOMIC VIEWER	
284	T01F0013984I	CAGE	1	F	1,284,929	0	+21	0	0	6	2	0	0	0	1	1		GENOMIC VIEWER	
285	T01F00139FB2	CAGE	1	F	1,286,066	0	+20	0	0	6	0	0	0	0	1	1		GENOMIC VIEWER	
286	T01F0013A04F	CAGE	1	F	1,286,223	0	+17	0	0	6	0	0	0	0	1	1		GENOMIC VIEWER	



[Jump TC Summary Page](#)

[Open Genomic Elements Viewer](#)



TC Summary

TC ID : [T10F0173A82E](#)
 TR ID : [8189E](#) Gene Symbol : [Ctcf](#)

Genomic Position

Representative Type	Chr.	#/R	Representative Position	Start	End	CTSSs	Link
CAGE	10	F	24,357,670	-1	+34	466	GENOMIC VIEWER

Transcript

5' End

CAGE Tags : 1
 OIS dtags : 0
 OSC dtags : 0
 Long SAGEs : 1

	mRNAs	RIKEN 5' ESTs	DBTSS 5' ESTs
5' end	0	0	0

Region

OIS dtags : 0
 OSC dtags : 0

	mRNAs	RIKEN 5' ESTs	DBTSS 5' ESTs
1000bp Upstream of 1st Exon	6	0	0
1st Exon	0	0	0
Other Exon	0	0	0
Intron	0	0	0
Total (CDS)	6 (D)	0	0

TFBS

Core Promoter (Pattern Match) : [TC](#) [GC](#)

	Upstream			Downstream	
	-1000 >	-500 >	-100 >	+40 > -1	+1 > +50
CCCAT-Boxer (3)	GC-Boxer			TATA-Boxer	
TATA-Boxer (2)					
TATA-SPD68a	TATA-SPD68a			TATA-SPC68p	
TATA-SPD68z (4)				TATA-SPC68y	

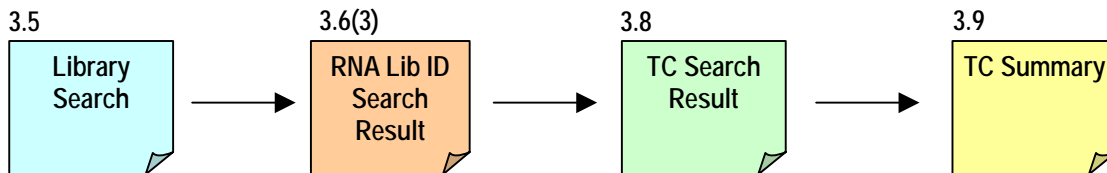
Others

Conserved Region : Conserved rate = 0.7
 CpG island : Percent of CpG = 18%

2.2 TC Search by RNA Library

You can search TC by short-description of RNA library, Tissue and Developmental-Stage.

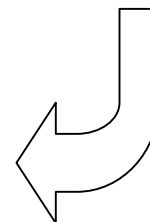
Overview



- (1) Input short description of RNA Library
- (2) Select TC from RNA Library List
- (3) Show Library expression information

(1) Input short description of RNA Library

Library Search form is displayed by clicking 'Library Search' of top menu.



[Jump Library Search Form](#)

Library Search	
RNA sample Short Description	<input type="text" value="BMM"/>
Tissue	- Any Tissue -
Developmental Stage	- Any Stage -
CAGE Tags	> <input type="text" value="0"/>
CTSSs	> <input type="text" value="0"/>
<input type="button" value="search"/> <input type="button" value="reset"/>	

You can get RNA Library List by input short-description (pattern match) and Tissue name, Developmental-Stage, number of mapped CAGE Tag, number of CTSS, and clicking Search button.

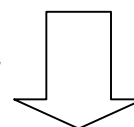
(2) Select TC from RNA Library List

You can get TC from the result list of Library search.

Library Search Result
Results 1-29 about 29.

No	ID	Description	Category	Tissue	Stage	CAGE Tags	CTSSs	TCs	TUs
1	HAG	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	96,670	42,634	22,208	11,879
2	HAH	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	15,822	10,121	7,238	5,579
3	HAM	cerebrum	etc	cerebrum	-1 (UNDEFINED_PUBLIC_STAGE)	400,390	197,253	125,312	24,361
4	HAN	cerebrum	etc	cerebrum	-1 (UNDEFINED_PUBLIC_STAGE)	125,175	62,746	40,267	16,583
5	HAO	cerebrum	etc	cerebrum	-1 (UNDEFINED_PUBLIC_STAGE)	219,422	108,790	73,036	20,529
6	HAP	cerebrum	etc	cerebrum	-1 (UNDEFINED_PUBLIC_STAGE)	4,679	3,422	2,964	2,600
7	HBC	epididymis	etc	epididymis	-1 (UNDEFINED_PUBLIC_STAGE)	8,197	6,187	4,974	4,177
8	HAJ	kidney	etc	kidney	-1 (UNDEFINED_PUBLIC_STAGE)	39,908	24,203	15,788	10,517
9	HAU	kidney	etc	kidney	-1 (UNDEFINED_PUBLIC_STAGE)	30,018	18,206	12,373	9,014
10	HAV	kidney	etc	kidney	-1 (UNDEFINED_PUBLIC_STAGE)	31,011	21,193	13,814	9,655

[Jump TC Search Result](#)

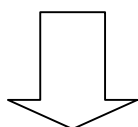


TC Search Result

ID	Description	Category	Tissue	Stage	CAGE tags	CTSSs	TCs	TUs
H4H	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	15,822	10,121	7,238	5,579

Results 1-40 about 7,238. Page 1 of 181

No	TC ID	Representative Type	Chr.	F/R	Representative Position	Start	End	Region				5' End				CTSSs	CAGE Tags IV	Regulatory Elements						Link		
								SIS	SSC	mRNAs	5'UTRs	SIS	SSC	mRNAs	5'UTRs			DRIS	Long 3'UTR	1st Exon	Initiator	SPF	PSE		Conserved 5'UTR	Cap Island
1	T01R000239F4	CAGE	1	R	604,660	+8	-32	0	0	3	0	0	0	0	7	3										H4H
2	T01F000938B11	CAGE	1	F	604,945	-63	+28	0	0	2	0	0	0	2	347	179										H4H
3	T01F0009424D	CAGE	1	F	606,797	-1	+28	0	0	38	0	0	0	0	101	98										H4H
4	T01R00024264	CAGE	1	R	606,820	0	-18	0	0	1	0	0	0	0	1	1										H4H
5	T01F00094311	CAGE	1	F	606,993	-10	+59	0	0	38	0	0	0	1	319	114										H4H
6	T01F000948F6	CAGE	1	F	609,270	-23	+84	0	0	17	0	0	0	0	427	280										H4H
7	T01F0009408E	CAGE	1	F	609,678	-1	+61	0	0	14	0	0	0	0	268	177										H4H
8	T01F0009B48C	CAGE	1	F	965,260	0	+18	0	0	0	0	0	0	0	2	2										H4H
9	T01R0009E143	CAGE	1	R	975,267	0	-19	0	0	3	0	0	0	0	1	1										H4H
10	T01F0009F309D	CAGE	1	F	995,485	0	+26	0	0	4	0	0	0	0	8	3										H4H



[Jump TC Summary Page](#)

(3) Show Library expression information

TC Summary is displayed.

TC Summary

TC ID : T19P8173AB2E

TS ID : 8388E Gene Symbol : Ctgf

Genomic Position

Representative Type	Chr.	Y/N	Representative Position	Start	End	CTSSs	Web
CAGE	18	F	24,257,478	-1	+34	466	View

Transcript

5' End

CAGE Tags : 1
 QIS tags : 0
 SSC tags : 0
 Long SAGEs : 1

	mRNA	RIKEN	DATSS
	5' ESTs	5' ESTs	5' ESTs
5' End	0	0	0

Region

QIS tags : 0
 SSC tags : 0

	mRNA	RIKEN	DATSS
	5' ESTs	5' ESTs	5' ESTs
1000bp Upstream of 1st Exon	6	0	0
1st Exon	0	0	0
Other Exon	0	0	0
Intron	0	0	0
Total (CDS)	6 (0)	0	0

TFBS

Core Promoter (Pattern Match) : Yes No

	Upstream			Downstream	
	-1880 >	-588 >	-188 >	+48 > +1	+1 > +50
■ CCAAT-Boxer (3)	GC-Boxer			TATA-Boxer	
■ CTC-Boxer (1)					
■ TATA-100bp	TATA-100bp			TATA-100bp	
■ TATA-100bp (4)				TATA-100bp	

Others

Conserved Region : Conserved rate = 0.7
 CpG island : Percent of CpG = 18%

Statistical test of expression difference : two samples in one TC
[\[open window\]](#)

Library Expression

No.	ID	Straining Type	Description	Category	Tags	Exp Level (TPM)
1	CCU	Clige dT	MEF fibroblast 20 0p	embryo	141	482.82 (141 / 296.229)
2	CCV	Clige dT	SIP-KO MEF fibroblast	embryo	325	943.18 (325 / 344.838)
3	CCF	Clige dT	MEF fibroblast	embryo	50	844.51 (50 / 59.206)
4	CCW	Clige dT	SIP-KO MEF fibroblast 200p	embryo	29	546.12 (29 / 72.205)
5	CCJ	Clige dT	Hepa 2-6 40h EGFP	liver	14	112.20 (14 / 124.837)
6	CCQ	random	DFAT-DL pre-dp. 0d	UNDEFINED_CATEGORY		
7	CAN	Clige dT	Cloned mouse lung	lung		
8	CCZ	Clige dT	Hepa 2-6 36h BFP	liver		

Library Specific Tag Distribution Map [\[view >> file.gtf\]](#)

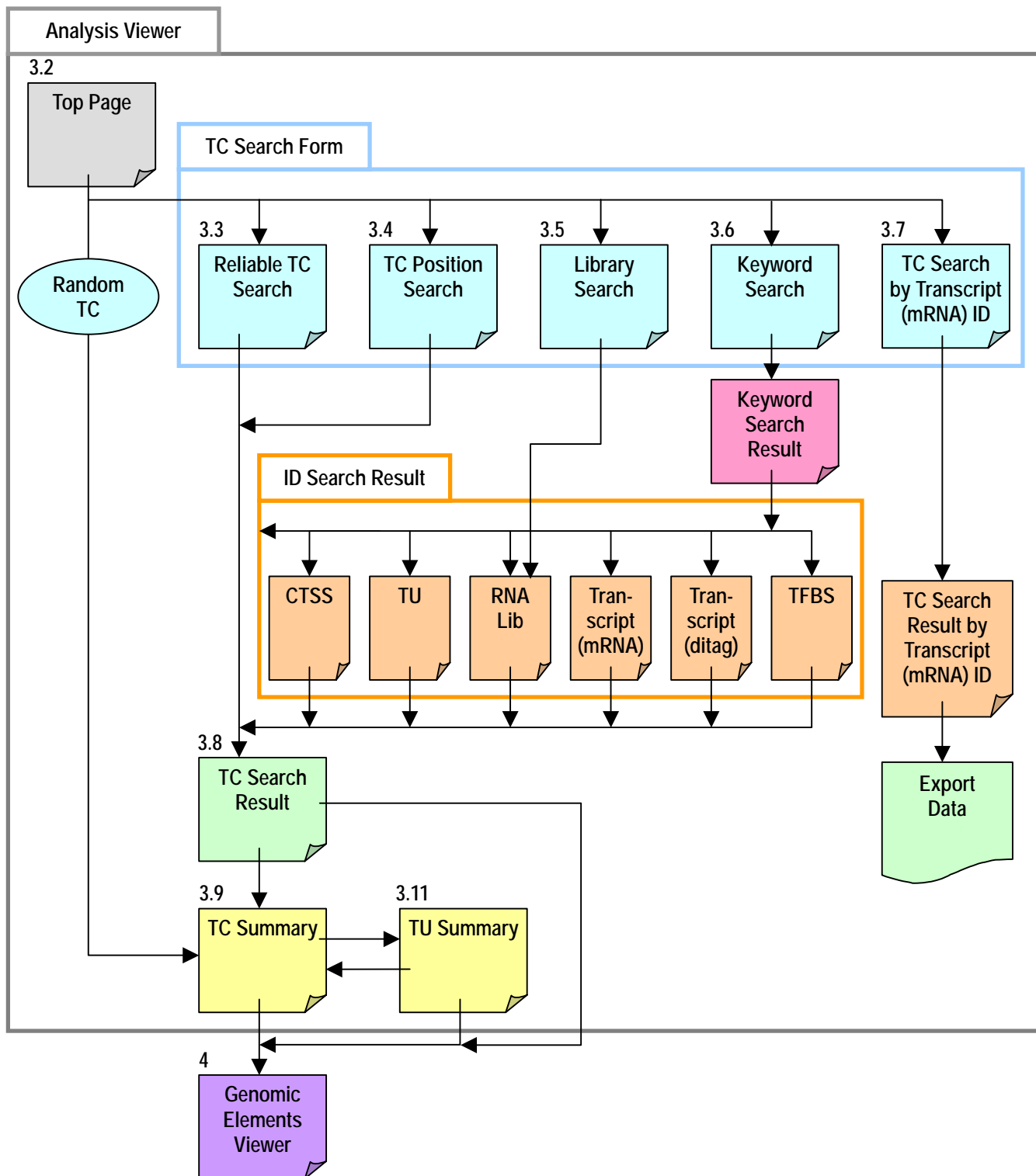
Library Expression information of target TC

Library specific tag distribution map images

3. Viewer Pages

3.1 Page transition

Pages in this system are connected with each other by hyperlink. The transition is described in the following.



3.2 Top Page

The information about Analysis Viewer is displayed in the top page.
The header and the footer are the same on all pages.

[Top Page]

Common Header

Common Footer

[Header (common to all pages)]

No	Column	Explanation
1	Logo	Go to Top Page
2	Keyword Search	Input box
3		Menu
4		>>
5	Home	Go to Home Page
6	Top	Go to Top Page
7	Help	Go to Help Page
8	for	The type of taxonomy
9	Menu	Reliable TC Search
10		TC Search by Transcript ID
11		TC Position Search
12		Library Search
13		Random TC

[Footer (common to all pages)]

No	Column	Explanation
1	Copyright	Copyright. Go to Copyrighter's site
2	developed by	Developer. Go to Developer's site

[Welcome message]

No	Column	Explanation
1	UCSC~	The kind and version of Genome to be used
2	CAGE Basic DB	The date that fixed CAGE Basic DB to be used. Go to Basic Viewer
3	Help	Go to Help Page
4	Export	Go to Export Page

[Statistics]

No	Column	Explanation	
1	Current Statistics of CTSS / TC / TU	CTSS	Number of registered CTSS
2		TC	Number of registered TC
3		TU	Number of registered TU
4	Current Statistics of Transcripts	CAGE Tags	Number of registered CAGE Tag
5		GIS ditags	Number of registered GIS ditag
6		GSC ditags	Number of registered GSC ditag
7		Long SAGE	Number of registered Long SAGE
8		mRNA	Number of registered mRNA
9		Riken 5'EST	Number of registered Riken 5'EST
10	Current Statistics of TFBS	Mapped position of Core Promoter	Number of registered mapped position of Core Promoter

3.3 Reliable TC Search

You can search TC with Evidence Code in Reliable TC Search.

Reliable Conditions

Transcript

All Transcripts > 0

5' End

CAGE Tag > 0

Library Any
 Library Category UNDEFINED_CATEGORY_TYPE [etc]
 Library

small intestine [HAD]
 rectum [HAE]
 rectum [HAF]
 cecum [HAG]
 cecum [HAH]

Priming Type Any Oligo dT random

GIS ditag > 0

GSC ditag > 0

DBTSS > 0

Long SAGE > 0

mRNA
 (include 5' EST) > 0

Region

mRNA
 (include 5' EST) > 0
 1000 bp Upstream of 1st Exon
 1st Exon Other Exon Intron

GIS ditag > 0

GSC ditag > 0

TFBS

Core Promoter (Pattern Match) OR AND
 TATA box Initiator BRE DPE PSE

Core Promoter (Bucher) upstream 40 bp downstream 20 bp

Core Promoter (EPD) upstream 40 bp downstream 20 bp

Others

inside Conserved Region

inside CpG island

Exclusive Conditions

inside only CDS

search

reset

[Reliable TC Search]

Each item is searched with checking as an indispensable condition.

No	Column		Explanation
1	Transcript	All Transcripts	Select total of all Transcripts
2	5' End *1	CAGE Tag	Select the number of min or the number of max CAGE Tag
3		Library	Library Category can choose one when you checked 'Library Category' Library can choose more than one when you checked 'Library'
4		Priming Type	Select the priming type.
5		GIS ditag	Select the number of min or the number of max GIS ditag
6		GSC ditag	Select the number of min or the number of max GSC ditag
7		DBTSS	Select the number of min or the number of max DBTSS
8		Long SAGE	Select the number of min or the number of max Long SAGE
9		mRNA	Select the number of min or the number of max mRNA 5' EST is included with checking to 'include 5' EST'
10		Region *2	mRNA
11	GIS ditag		Select the number of min or the number of max GIS ditag
12	GSC ditag		Select the number of min or the number of max GSC ditag
13	TFBS	Core Promoter (Pattern Match)	Core Promoter (Pattern Match) exists or not. Details are specified with checking to TATA box, Initiator, BRE, DPE, and PSE. You can choose 'AND' and 'OR' as the joint method of each item
14		Core Promoter (Bucher)	Core Promoter (Bucher) exists or not. Select the range of the upstream and the downstream
15		Core Promoter (EPD)	Core Promoter (EPD) exists or not. Select the range of the upstream and the downstream
16	Others	inside Conserved Region	Exists or not inside Conserved Region
17		inside CpG island	Exists or not inside CpG island
18	Exclusive Conditions	inside only CDS	In existing inside only CDS, it removes for reference
19	Search		Search. Go to 3.8 TC Search Result
20	Reset		Reset

*1: TC that exists in 5' End of Transcript is made applicable to reference.

*2: TC that exists in region include upstream of Transcript is made applicable to reference.

3.4 TC Position Search

You can search TC with the position on a genome in TC Position Search.

TC Position Search

Position	<input style="width: 100%;" type="text"/> Example : chr19:59,214,201..60,291,736
CAGE Tags	> <input style="width: 20px;" type="text" value="0"/>
CTSSs	> <input style="width: 20px;" type="text" value="0"/>

[TC Position Search]

No	Column	Explanation
1	Position	Input position. Format: chr[No]:[start_position]..[end_position] chr[No]:[start_position]-[end_position]
2	CAGE Tags	Select the number of min or the number of max CAGE Tag
3	CTSSs	Select the number of min or the number of max CTSS
4	Search	Search. Go to 3.8 TC Search Result
5	Reset	Reset

3.5 Library Search

You can search Library in Library Search and find TC.

Library Search

RNA sample Short Description	<input style="width: 100%;" type="text"/>
Tissue	- Any Tissue - <input style="width: 20px;" type="text"/>
Developmental Stage	- Any Stage - <input style="width: 20px;" type="text"/>
CAGE Tags	> <input style="width: 20px;" type="text" value="0"/>
CTSSs	> <input style="width: 20px;" type="text" value="0"/>

[Library Search]

No	Column	Explanation
1	RNA sample Short Description	Input RNA sample Short Description
2	Tissue	Select Tissue. Search from all Tissue by selecting 'Any Tissue'
3	Developmental Stage	Select Developmental Stage. Search from all Developmental Stage by selecting 'Any Stage'
4	CAGE Tags	Select the number of min or the number of max CAGE Tag
5	CTSSs	Select the number of min or the number of max CTSS
6	Search	Search. Go to 3.6(3-c) RNA Lib ID Search Result
7	Reset	Reset

3.6 Keyword Search

You can search ID by keyword or ID in Keyword Search and find TC.

(1) Keyword Search Form

You can search ID by keyword or ID in Keyword Search.

Search for in the Any Type

[Keyword Search]

No	Column	Explanation
1	Input form	Input keyword or ID
2	Menu	Select ID Type or 'Any Type'. Refer to following [Keyword Type List]
3	>>	Search and go to each page. Refer to following [Keyword Type List]

[Keyword Type List]

No	Column	Explanation
1	Any Type	Search out of All ID, All Keyword (Gene Symbol, Gene Description, GO ID and GO Name). Go to (2) Keyword Search Result
2	TC ID	Search out of TC ID. Go to 3.8 TC Search Result
3	CTSS ID	Search out of CTSS ID. Go to (3-a) CTSS ID Search Result
4	TU ID	Search out of TU ID. Go to (3-b) TU ID Search Result
5	RNA Lib ID	Search out of RNA Lib ID. Go to (3-c) RNA Lib ID Search Result
6	Transcript	-
7	mRNA (Acc#)	Search out of mRNA's public ID (Accession Number). Go to (3-d) Transcript ID (mRNA) Search Result
8	Riken Clone ID	Search out of Riken Clone ID. Go to (3-d) Transcript ID (mRNA) Search Result
9	GIS ditag ID	Search out of GIS ditag ID. Go to (3-e) Transcript ID (ditag) Search Result
10	GSC ditag ID	Search out of GSC ditag ID. Go to (3-e) Transcript ID (ditag) Search Result
11	TFBS	Search out of All TFBS ID. Go to (3-f) TFBS ID Search Result
12	Core Promoter (Bucher) ID	Search out of Core Promoter (Bucher) ID. Go to (3-f) TFBS ID Search Result
13	Core Promoter (EPD) ID	Search out of Core Promoter (EPD) ID. Go to (3-f) TFBS ID Search Result

(2) Keyword Search Result

Keyword Search Result is displayed when 'Any Type' is chosen and searched in Keyword Search Form. The number of cases of ID or Keyword that matched the inputted word is displayed according to a category.

Keyword Search Result	
CTSS/TC/TU/RNA Lib	
hits	Category
<u>706,211</u>	CTSS
<u>450,228</u>	TC
<u>32,351</u>	TU
<u>29</u>	RNA Lib
Transcript	
hits	Category
<u>233,561</u>	mRNA
0	GIS ditag
0	GSC ditag
TFBS	
hits	Category
<u>3</u>	Core Promoter (Bucher)
<u>2</u>	Core Promoter (EPD)
TU hit by Keyword	
hits	Category
<u>21,977</u>	Gene Symbol
<u>30,865</u>	Gene Description
<u>12,950</u>	GO ID
<u>12,950</u>	GO Name

[CTSS / TC / TU / RNA Lib]

No	Column	Explanation
1	CTSS	The number of cases searched as CTSS ID. Go to (3-a) CTSS ID Search Result
2	TC	The number of cases searched as TC ID. Go to 3.8 TC Search Result
3	TU	The number of cases searched as TU ID. Go to (3-b) TU ID Search Result
4	RNA Lib	The number of cases searched as RNA Lib ID. Go to (3-c) RNA Lib ID Search Result

[Transcript]

No	Column	Explanation
1	mRNA	The number of cases searched as mRNA's Public ID (Accession Number) . Go to (3-d) Transcript ID (mRNA) Search Result
2	GIS ditag	The number of cases searched as GIS ditag ID. Go to (3-e) Transcript ID (ditag) Search Result
3	GSC ditag	The number of cases searched as GSC ditag ID. Go to (3-e) Transcript ID (ditag) Search Result

[TFBS]

No	Column	Explanation
1	Core Promoter (Bucher)	The number of cases searched as Core Promoter (Bucher) ID. Go to (3-f) TFBS ID Search Result
2	Core Promoter (EPD)	The number of cases searched as Core Promoter (EPD) ID. Go to (3-f) TFBS ID Search Result

[TU hit by Keyword]

The number of cases of TU related with each keyword. Go to (3-b) TU ID Search Result

No	Column	Explanation
1	Gene Symbol	The number of cases of TU relevant to searched Gene Symbol
2	Gene Description	The number of cases of TU relevant to searched Gene Description
3	GO ID	The number of cases of TU relevant to searched GO ID
4	GO Name	The number of cases of TU relevant to searched GO Name

(3) ID Search Result

You can show the list of each ID.

(3-a) CTSS ID Search Result

You can show the list of CTSS ID.

CTSS ID Search Result						
Results 1-40 about 625. Page <input type="text" value="1"/> of 16 ▶▶						
No	ID	Chr.	F/R	Start	CAGE Tags	TC ID
1	C15R06213CF0	15	R	102,841,584	1	T15R06213CF0
2	C15R06213E77	15	R	102,841,975	1	T15R06213E77
3	C15R0621F65A	15	R	102,889,050	1	T15R0621F65A
4	C15R0621F66E	15	R	102,889,070	1	T15R0621F66E

[CTSS ID Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	CTSS ID. Go to Basic Viewer
3	Chr.	Chromosome Number
4	F/R	Strand (F: Forward / R: Reverse)
5	Start	Start Position
6	CAGE Tags	Number of CAGE Tag
7	TC ID	TC ID. Go to 3.9 TC Summary

The following header is displayed on the list of each ID.

Results 81-120 about 190,038.

[Paging]

No	Column	Explanation
1	Results	The range of the consecutive numbers of the present list
2	about~	Number of all items
3	Arrow	Go to first page, previous page, next page and last page
4	Page	Go to the page inputted in input box
5	Input box	Previous Page Number. Input page number
6	of~	Number of All pages

(3-b) TU ID Search Result

You can show the list of TU ID.

No	TU ID	Chr.	F/R	Start	End	CAGE Tags	CTSSs	TCs	Gene Symbol	Gene Description	GO ID / GO name
1	122	17	F	7,609,592	+7,972	46	32	20	JMJD3	<ul style="list-style-type: none"> ○ Jumonji domain containing 3 ○ KIAA0346 protein (Fragment) ○ jumonji domain containing 3 	
2	1221	14	R	32,448,372	-53,152	6	2	2	na	<ul style="list-style-type: none"> ○ PREDICTED: Homo sapiens similar to chromosome 19 open reading frame 27 (LOC441750). mRNA. ○ TP53TG2 protein. ○ TP53TG2 protein. [Source:RefSeq;Acc:NM_015369] ○ TP53TG2b (TP53TG2 protein) (Fragment) ○ similar to chromosome 19 open reading frame 27 	
3	1222	8	F	17,058,402	+66,215	156	68	21	ZDHHC2	<ul style="list-style-type: none"> ○ Homo sapiens zinc finger, DHHC domain containing 2, mRNA [cdna clone MGC123737 IMAGE5299722], complete cds. ○ Zinc finger DHHC domain containing protein 2 (Zinc finger protein 372) [Reduced expression associated with metastatic protein] (Rfam) [Reduced expression in cancer protein] (Rac) ○ Zinc finger DHHC domain containing protein 2 (Zinc finger protein 372) [Reduced expression associated with metastatic protein] (Rfam) [Reduced expression in cancer protein] (Rac). [Source:SWISSPROT;Acc:Q9UJ15] ○ Zinc finger, DHHC domain containing 2 ○ zfc ○ zinc finger, DHHC domain containing 2 	
4	1223	3	R	38,338,536	-13,649	699	80	11	TU3A	<ul style="list-style-type: none"> ○ DRR1 ○ DRR1 protein (Down regulated in renal cell carcinoma 1) (TU3A protein) ○ DRR1 protein (Down regulated in renal cell carcinoma 1) (TU3A protein). [Source:SWISSPROT;Acc:Q95990] ○ Homo sapiens cell-line CV177 DRR1 (DRR1) mRNA, complete cds. ○ TU3A protein 	GO:0001550 / regulation of cell growth GO:0005554 / molecular function unknown GO:0005634 / nucleus

[TU ID Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	TU ID	TU ID. Go to 3.11 TU Summary
3	Chr.	Chromosome Number
4	F/R	Strand (F: Forward / R: Reverse)
5	Start	Start Position
6	End	The relative position from Start Position of End Position (full length of TU)
7	CAGE Tags	Number of CAGE Tag
8	CTSSs	Number of CTSS
9	TCs	Number of TC. Go to 3.8 TC Search Result
10	Gene Symbol	Gene Symbol
11	Gene Description	Gene Description
12	GO ID / GO Name	GO ID / GO Name

(3-c) RNA Lib ID Search Result

You can show the list of RNA Lib ID.

RNA Lib ID Search Result									
Results 1-29 about 29.									
No	ID	Description	Category	Tissue	Stage	CAGE Tags	CTSSs	TCs	TUs
1	-1	not available	etc	UNDEFINED_TISSUE_TYPE	-1 (UNDEFINED_PUBLIC_STAGE)	82,398	43,292	30,413	16,207
2	HAD	small intestine	etc	small intestine	-1 (UNDEFINED_PUBLIC_STAGE)	30,031	17,761	10,925	7,365
3	HAE	rectum	etc	rectum	-1 (UNDEFINED_PUBLIC_STAGE)	8,274	5,649	4,052	3,393
4	HAF	rectum	etc	rectum	-1 (UNDEFINED_PUBLIC_STAGE)	14,772	9,657	6,830	5,288
5	HAG	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	96,670	42,634	22,208	11,879
6	HAH	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	15,822	10,121	7,238	5,579

[RNA Lib ID Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	RNA Lib ID. Go to Basic Viewer
3	Description	Description
4	Category	Category
5	Tissue	Tissue
6	Stage	Developmental Stage
7	CAGE Tags	Number of CAGE Tag
8	CTSSs	Number of CTSS
9	TCs	Number of TC. Go to 3.8 TC Search Result
10	TUs	Number of TU

(3-d) Transcript ID (mRNA) Search Result

You can show the list of Transcript ID (mRNA).

Transcript ID Search Result									
Results 1-40 about 695. Page <input type="text" value="1"/> of 18 ▶▶									
No	ID	ID Type	F/R	Chr.	Start	End	TU ID	TU's TCs	Gene Symbol
1	BC040257	GB	R	1	1,189,441	-2,797	16642	1	TNFRSF4
2	AK024028	GB	F	1	1,499,294	+17,554	7370	31	ATAD3B
3	NM_004402	REFSEQ	F	1	3,797,002	+28,148	600	3	DFFB
4	BC015402	GB	R	1	5,858,779	-1,635	663	41	NPHP4
5	ENST00000340285	ENSEMBL	F	1	6,199,801	+2,447	29552	9	FLJ46380

[Transcript ID (mRNA) Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	mRNA's Public ID (Accession Number) . Go to external site
3	ID Type	mRNA's Public DB
4	F/R	Strand (F: Forward / R: Reverse)
5	Chr.	Chromosome number
6	Start	Start Position
7	End	The relative position from Start Position of End Position
8	TU ID	TU ID. Go to 3.11 TU Summary
9	TU's TCs	Number of TU's TC. Go to 3.8 TC Search Result
10	Gene Symbol	Gene Symbol

(3-e) Transcript ID (ditag) Search Result

You can show the list of Transcript ID (ditag).

Transcript ID Search Result							
Results 121-160 about 39,862. ◀ ◀ Page 4 of 997 ▶ ▶							
No	ID	ID Type	F/R	Chr.	Start	End	TCs
121	sme005_020604-13666-1	GIS	R	1	16,742,152	+49,052	38
122	sme005_020604-84941-1	GIS	R	1	16,790,280	+926	3
123	sme005_020604-73254-1	GIS	R	1	16,815,476	+13,473	12
124	sme005_020604-57416-1	GIS	R	1	16,814,980	+13,973	15

[Transcript ID (ditag) Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	ditag ID. Go to external site
3	ID Type	ditag Type
4	F/R	Strand (F: Forward / R: Reverse)
5	Chr.	Chromosome number
6	Start	Start Position
7	End	The relative position from Start Position of End Position
8	TCs	Number of TC. Go to 3.8 TC Search Result

(3-f) TFBS ID Search Result

You can show the list of TFBS ID.

TFBS ID Search Result				
Results 1-5 about 5.				
No	ID	ID Type	Definition	TCs
1	CCAAT-Bucher	Core Promoter (Bucher)		405,075
2	GC-Bucher	Core Promoter (Bucher)		391,738
3	TATA-Bucher	Core Promoter (Bucher)		361,814
4	TATA-EPD68p	Core Promoter (EPD)		305,091
5	TATA-EPD68v	Core Promoter (EPD)		390,068

[TFBS ID Search Result]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	TFBS ID. Go to external site
3	ID Type	TFBS Type
4	Definition	Definition
5	TCs	Number of TC. Go to 3.8 TC Search Result

3.7 TC Search by Transcript (mRNA) ID

You can search TC by Transcript (mRNA) ID in TC Search by Transcript (mRNA) ID and export data.

(1) TC Search Form by Transcript (mRNA) ID

You can search TC data by Transcript (mRNA) ID.

Please input ID into the text area or upload the textile to which ID was written.

TC Search by Transcript (mRNA) ID

TCs associated with specified transcript (mRNA) are searched.
Note that the association is based on TUs.

In detail, a transcript is contained by a TU, and a TC is associated with a TU, internally.
TCs associated with your specified transcripts via TU are searched.

The list of search results is sorted by the position.

Transcript (mRNA) ID List

ID Type :

- Ensembl Transcript ID
- RefSeq-ID
- GenBank-ID
- Riken Clone ID

ID's are separated by :

- comma
- space
- tab
- new-line

or

File Path :

[Transcript (mRNA) ID List]

No	Column	Explanation
1	Text area	Input Transcript (mRNA) ID.
2	File Path	Input path of Transcript (mRNA) ID file
3	Search	Search and go to (2) TC Search Result by Transcript (mRNA) ID
4	Reset	Reset

(2) TC Search Result by Transcript (mRNA) ID

You can show the list of Transcript (mRNA) ID, TU ID and TC ID.

TC Search Result by Transcript (mRNA) ID										
Hits mRNAs : 4 / 4										export
Results 1-11 about 11.										
No	ID	ID Type	F/R	Chr.	Start	End	TU ID	TC ID	TC's Tags	Gene Symbols (TU)
1	XM_496328	REFSEQ	R	1	123,587	-44,429	159989	T01R00013DCB	1	na
2	AK000561	GB	R	1	605,686	-3,925	26592	T01R00093C19	2	
3	AK000561	GB	R	1	605,686	-3,925	26592	T01R00093CED	1	
4	AK000561	GB	R	1	605,686	-3,925	26592	T01R00093D6C	2	
5	AK000561	GB	R	1	605,686	-3,925	26592	T01R00093DB5	1	
6	AK000561	GB	R	1	605,686	-3,925	26592	T01R00093DE3	2	
7	AK000130	GB	R	3	127,636,112	-1,771	8657	T03R079B4BE5	3	FLJ20123
8	AK000130	GB	R	3	127,636,112	-1,771	8657	T03R079B9718	1	FLJ20123
9	ENST00000338293	ENSEMBL	R	Y	27,111,443	-587	141012	TOYR0198F438	1	
10	ENST00000338293	ENSEMBL	R	Y	27,111,443	-587	141012	TOYR0198FA1A	1	
11	ENST00000338293	ENSEMBL	R	Y	27,111,443	-587	141012	TOYR019DDEF6	1	

[Header]

No	Column	Explanation
1	Hits mRNAs	The number of hits mRNA / The number of input mRNA
2	Export	Export the data

[ID List]

No	Column	Explanation
1	No	Consecutive numbers
2	ID	mRNA's Public ID (Accession Number). Go to external site. By clicking the column name, The list is sorted by mRNA's Public ID
3	ID Type	mRNA's Public DB. By clicking the column name, The list is sorted by ID Type
4	F/R	Strand (F: Forward / R: Reverse)
5	Chr.	Chromosome Number. By clicking the column name, The list is sorted by Chromosome number
6	Start	Start Position
7	End	The relative position from Start Position of End Position
8	TU ID	TU ID. Go to 3.11 TU Summary. By clicking the column name, The list is sorted by TU ID
9	TC ID	TC ID. Go to 3.9 TC Summary. By clicking the column name, The list is sorted by TC ID
10	TC's Tags	Number of TC's Tag. By clicking the column name, The list is sorted by the number of TC's Tag
11	Gene Symbols (TU)	TU's Gene Symbol

3.8 TC Search Result

You can show the list of TC ID in TC Search Result.

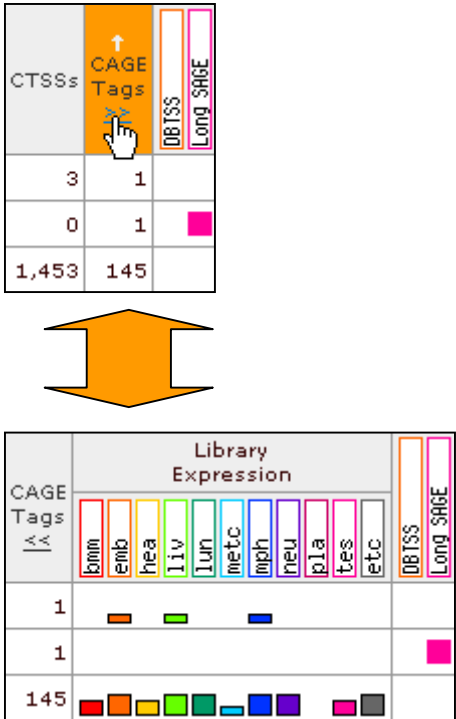
When you search by ID in the previous page, the information on selected ID is displayed on this page upper part.

TC Search Result																				
Results: 281-320 about 450,228. Page 8 of 11,256																				
No	TC ID	Representative Type	Chr.	F/R	Representative Position	Start	End	Region				5' End				CTSSs	CAGE Tags		Link	
								GIS	GSC	mRNAs	5' ESTs	GIS	GSC	mRNAs	5' ESTs					
281	T01F001324F1	CAGE	1	F	1,283,313	0	+19	0	0	4	2	0	0	0	0	3	3			
282	T01F0013271E	CAGE	1	F	1,283,870	0	+23	0	0	6	2	0	0	0	0	1	1			
283	T01F0013275Q	CAGE	1	F	1,283,920	0	+46	0	0	6	2	0	0	0	2	3	1			
284	T01F0013284I	CAGE	1	F	1,284,929	0	+21	0	0	6	2	0	0	0	0	1	1			
285	T01F001329F8,2	CAGE	1	F	1,286,066	0	+20	0	0	6	0	0	0	0	0	1	1			
286	T01F0013A04E	CAGE	1	F	1,286,223	0	+17	0	0	6	0	0	0	0	0	1	1			

[TC Search Result]

No	Column	Explanation	
1	No	Consecutive numbers	
2	TC ID	TC ID. Go to 3.9 TC Summary. By clicking the column name, The list is sorted by TC ID	
3	Representative Type	Representative Type (CAGE, GIS, GSC, RIKEN 5' END, FANTOM) By clicking the column name, The list is sorted by Representative Type	
4	Chr.	Chromosome number. By clicking the column name, The list is sorted by Chromosome number	
5	F/R	Strand (F: Forward / R: Reverse)	
6	Representative Position	Representative Position. By clicking the column name, The list is sorted by Representative Position	
7	Start	The relative position from Represent Position of Start Position	
8	End	The relative position from Represent Position of End Position	
9	Region	GIS	Number of GIS ditag. By clicking the column name, The list is sorted by the number of GIS ditag
10		GSC	Number of GSC ditag. By clicking the column name, The list is sorted by the number of GSC ditag
11		mRNAs	Number of mRNA. By clicking the column name, The list is sorted by the number of mRNA
12		5' ESTs	Number of 5' EST. By clicking the column name, The list is sorted by the number of 5' EST

[TC Search Result]

No	Column	Explanation
13	5' End	GIS Number of GIS ditag. By clicking the column name, The list is sorted by the number of GIS ditag
14		GSC Number of GSC ditag. By clicking the column name, The list is sorted by the number of GSC ditag
15		mRNAs Number of mRNA. By clicking the column name, The list is sorted by the number of mRNA
16		5' ESTs Number of 5' EST. By clicking the column name, The list is sorted by the number of 5' EST
17	CTSSs	Number of CTSS. By clicking the column name, The list is sorted by the number of CTSS
18	CAGE Tags	Number of CAGE Tag. By clicking the column name, The list is sorted by the number of CAGE Tag
19	>>	Library Expression is displayed by clicking. If it is clicked again, the display of Library Expression will hide. 
20	Library Expression	The number of Library expression for every category is displayed by the bar graph. Detailed information is displayed by hovering your mouse pointer
-	Icons	Icons are displayed when each item exists. Detailed information is displayed by hovering your mouse pointer
21	DBTSS	The icon is displayed when there is DBTSS
22	Long SAGE	The icon is displayed when there is Long SAGE
23	TATA box	The icon is displayed when there is TATA box
24	Initiator	The icon is displayed when there is Initiator
25	BRE	The icon is displayed when there is BRE
26	DPE	The icon is displayed when there is DPE
27	PSE	The icon is displayed when there is PSE
28	Conserved Reg	The icon is displayed when include Conserved Region
29	CpG island	The icon is displayed when include CpG island
30	Link	Go to 4 Genomic Elements Viewer

3.9 TC Summary

You can show the details of TC in TC Summary.

The whole of the page

TC Summary

TC ID : **TC00123456**
 TR ID : **TR001** Gene Symbol : **Dgl**

Genomic Position

Representation Type	Chr	Str	Representative Exon	Start End	CTSS	Link
CAGE	10	F	24,127,878	-1,+34	418	View

Transcript

Y End

CAGE Tag : 1
 GC Stage : 0
 GC Stage : 0
 LOG SAGE : 1

Y End	RIN	DIST
0	0	0

Region

GC Stage : 0
 GC Stage : 0

Region	RIN	DIST
500bp upstream of 1st Exon	0	0
1st Exon	0	0
Other Exon	0	0
3'UTR	0	0
Total (CDS)	0 (0)	0

TFBS

Core Promoter (Gal4/Max) : ON OFF

Upstream				Downstream	
-1000+	-500+	+100+	+500+	+1000+	+5000+
CCAT-Box(C)	GC-Box(G)		TATA-Box(T)		
GC-Box(G)					
GC-Box(G)					
GC-Box(G)					
GC-Box(G)					

Others

Conserved Region : Conserved rate = 0.7
 CpG Island : Percent of CpG = 18%

Statistical test of expression difference : two samples in one TC
 [non-similar]

Library Expression

Seq	ID	Strain Type	Description	Category	Tag	Exp level (TPM)
1	CG1	Oligo-dT	HEP Fibroblast 20 Gy	embryo	142	302.52 (141 / 156.129)
2	CG2	Oligo-dT	3P-60 HEP Fibroblast	wildtype	129	143.18 (129 / 132.330)
3	CG3	Oligo-dT	HEP Fibroblast	embryo	90	116.41 (90 / 99.206)
4	CG4	Oligo-dT	3P-60 HEP Fibroblast 28Gy	embryo	39	540.13 (39 / 71.205)
5	CG5	Oligo-dT	HeLa 1-6 48h 83FP	heLa	14	112.33 (14 / 124.637)
6	CG6	random	SPAT-G1 pseudo. G6	UNDEFINED_CATEGORY_T108	13	169.80 (13 / 92.619)
7	CG7	Oligo-dT	Elmer8 mouse lung	lung	10	10.67 (10 / 896.071)
8	CG8	Oligo-dT	HeLa 1-6 24h 83FP	heLa	8	23.78 (8 / 218.642)

Library Specific Tag Distribution Map [view >> \[view raw\]](#)

A part of the page

TC Summary**TC ID : T10F0173AB2E****TU ID : 83098** Gene Symbol : Ctgf**Genomic Position**

Representative Type	Chr.	F/R	Representative Position	Start	End	CTSSs	Link
CAGE	10	F	24,357,678	-1	+34	466	

[ID etc.]

No	Column	Explanation
1	ID	TC ID. When Representative Type is CAGE, go to Basic Viewer
2	TU ID	TU ID. Go to 3.11 TU Summary
3	Gene Symbol	TU's Gene Symbol

[Genomic Position]



No	Column	Explanation
1	Representative Type	Representative Type
2	Chr.	Chromosome number
3	F/R	Strand (F: Forward / R: Reverse)
4	Representative Position	Representative Position
5	Start	The relative position from Represent Position of Start Position
6	End	The relative position from Represent Position of End Position
7	CTSSs	Number of CTSS
8	Link	Go to 4 Genomic Elements Viewer

Transcript			
5' End			
CAGE Tags : 1			
GIS ditags : 0			
GSC ditags : 0			
Long SAGEs : 1			
	mRNAs	RIKEN 5' ESTs	DBTSS 5' ESTs
5' End	0	0	0
Region			
GIS ditags : 0			
GSC ditags : 0			
	mRNAs	RIKEN 5' ESTs	DBTSS 5' ESTs
1000bp Upstream of 1st Exon	6	0	0
1st Exon	0	0	0
Other Exon	0	0	0
Intron	0	0	0
Total (CDS)	6 (0)	0	0

[Transcript]

No	Column	Explanation
1	5' End	CAGE Tags
2		Number of CAGE Tag
3		GIS ditags
4		Number of GIS ditag
5		GSC ditags
6		Number of GSC ditag
7		Long SAGEs
8	Region	Number of Long SAGE
9		mRNAs
10		Number of mRNA
11		RIKEN 5' ESTs
12		Number of RIKEN 5' EST
		DBTSS 5' ESTs
	Number of DBTSS 5' EST	
	GIS ditags	Number of GIS ditag
	GSC ditags	Number of GSC ditag
	mRNAs	The number of mRNA is displayed, respectively as 1000bp Upstream of 1st Exon, 1st Exon, Other Exon, Intron, and the sum total. The number of CDS is also displayed on the sum total
	RIKEN 5' ESTs	The number of RIKEN 5' EST is displayed, respectively as 1000bp Upstream of 1st Exon, 1st Exon, Other Exon, Intron, and the sum total
	DBTSS 5' ESTs	The number of DBTSS 5' EST is displayed, respectively as 1000bp Upstream of 1st Exon, 1st Exon, Other Exon, Intron, and the sum total

TFBSCore Promoter (Pattern Match) :  

	Upstream				Downstream	
	-1000 >	-500 >	-100 >	-40 > -1	+1 > +20	> +50
	CCAAT-Bucher (3) TATA-Bucher (3)	GC-Bucher		TATA-Bucher		
	TATA-EPD68p TATA-EPD68v (4)	TATA-EPD68v		TATA-EPD68p TATA-EPD68v		

Others

Conserved Region : Conserved rate = 0.7

CpG island : Percent of CpG = 18%

[TFBS]

No	Column	Explanation
1	Core Promoter (Pattern Match)	The icon is displayed respectively When TATA box, Initiator, BRE, DPE and PSE exist.
2	Except Core Promoter (Pattern Match)	ID of TFBS (Core Promoter (Bucher) and Core Promoter (EPD) other than Core Promoter (Pattern Match) is displayed for every position. When there is the same ID as the same position, the number of cases is displayed behind ID. Go to external site.

[Others]

No	Column	Explanation
1	Conserved Region	The rate of Conserved Region
2	CpG island	The percentage of CpG island

Statistical test of expression difference : two samples in one TC[\[open window\]](#)**Library Expression**

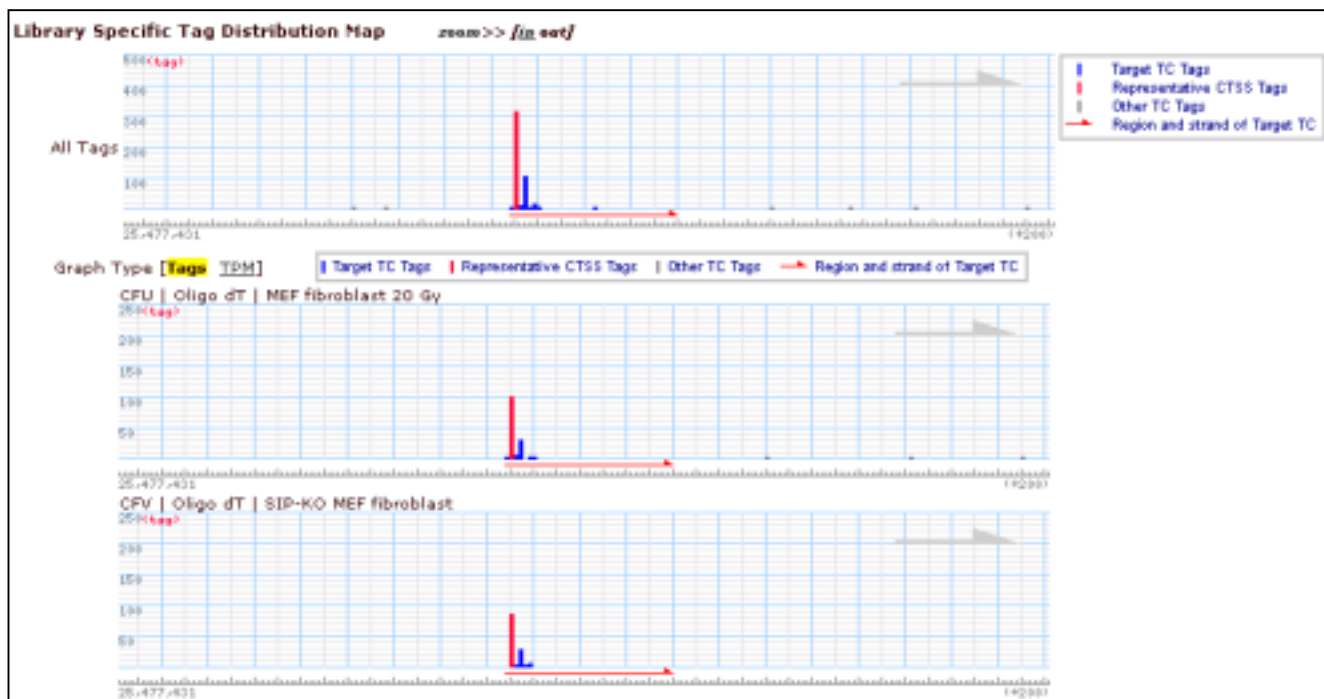
No		ID	Priming Type	Description	Category	Tags	Exp Level (TPM)
1		CFU	Oligo dT	MEF fibroblast 20 Gy	embryo	141	930.75 (141 / 151,491)
2		CFV	Oligo dT	SIP-KO MEF fibroblast	embryo	125	967.54 (125 / 129,193)
3		CFT	Oligo dT	MEF fibroblast	embryo	50	867.63 (50 / 57,628)
4		CFW	Oligo dT	SIP-KO MEF fibroblast 20Gy	embryo	39	553.29 (39 / 70,487)
5		CCJ	Oligo dT	Hepa 1-6 48h EGFP	liver	14	115.43 (14 / 121,281)
6		CGG	random	DFAT-D1 preadip. 0d	UNDEFINED_CATEGORY_TYPE	10	240.99 (10 / 41,495)
7		CAW	Oligo dT	Cloned mouse lung	lung	9	30.78 (9 / 292,385)
8		CCI	Oligo dT	Hepa 1-6 36h EGFP	liver	8	35.13 (8 / 227,751)

[Statistical test of expression difference: two samples in one TC]

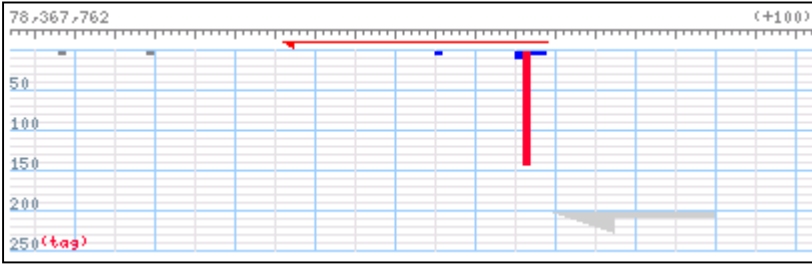
No	Column	Explanation
1	Open window	By clicking it, the new window opens. Go to 3.10 Statistical test of expression difference: two samples in one TC

[Library Expression]

No	Column	Explanation
1	No	Consecutive numbers
2	+ / -	By clicking +, the graph is displayed on Library Specific Tag Distribution Map. By clicking -, the graph is not displayed on Library Specific Tag Distribution Map.
3	ID	RNA Lib ID. Go to Basic Viewer
4	Priming Type	Priming Type
5	Description	Description
6	Category	Category By clicking the column name, The list is sorted by Category
7	Tags	Number of Tag By clicking the column name, The list is sorted by the number of Tag
8	Exp Level (TPM)	TPM By clicking the column name, The list is sorted by the TPM



[Library Specific Tag Distribution Map]

No	Column	Explanation
1	zoom	By clicking in / out, the display range of graph changes
2	All Tags	Graph of All Tags [Reverse Strand] 
3	Each Library	Graph Type
4		ID / Priming Type / Description
5		Graph of each Library.

3.10 Statistical test of expression difference: two samples in one TC

This page is pop up from TC Summary.

You can show the TC's statistical test of expression difference.

statistical test of expression difference : two samples in one TC

TC ID : T19F00386E46 CAGE Tags = 20
 TUID : 74746 Gene Symbol : Chka

Compared two libraries

RNA Lib1: cerebellum(Oligo dT)[BC.T]
 RNA Lib2: Cloned mouse lung(Oligo dT)[CAW.T]

χ^2 : Fisher : 0.010

Matrix of compared values

χ^2 : 0 0.001 0.01 0.1 ⇄ Fisher : 0 0.001 0.01 0.1 ⇄

		Fisher										
		BC.T	CAW.T	CAX.T	CBA.T	CBD.T	CBR.T	CDH.T	CFU.T	IN.R		
cerebellum	Oligo dT BC.T		0.010	0.014	-	0.077	0.094	-	0.074	0.007	cerebellum	Oligo dT BC.T
Cloned mouse lung	Oligo dT CAW.T				0.049			0.053			Cloned mouse lung	Oligo dT CAW.T
Cloned mouse lung	Oligo dT CAX.T		0.012		0.060						Cloned mouse lung	Oligo dT CAX.T
Cloned mouse lung	Oligo dT CBA.T										Cloned mouse lung	Oligo dT CBA.T
Cloned mouse lung	Oligo dT CBD.T		0.000								Cloned mouse lung	Oligo dT CBD.T
Control mouse liver	Oligo dT CBR.T										Control mouse liver	Oligo dT CBR.T
Probasin tg prostate	Oligo dT CDH.T		0.003	0.002					0.097		Probasin tg prostate	Oligo dT CDH.T
MEF fibroblast 20 Gy	Oligo dT CFU.T										MEF fibroblast 20 Gy	Oligo dT CFU.T
embryo 17.5	random IN.R		0.025								embryo 17.5	random IN.R
		BC.T	CAW.T	CAX.T	CBA.T	CBD.T	CBR.T	CDH.T	CFU.T	IN.R		

χ^2 : 0 0.001 0.01 0.1 ⇄ Fisher : 0 0.001 0.01 0.1 ⇄

[ID etc.]

No	Column	Explanation
1	TC ID	TC ID
2	TU ID	TU ID
3	Gene Symbol	TU's Gene Symbol
4	CAGE Tags	Number of CAGE Tag

[Compared two libraries]

No	Column	Explanation
1	RNA Lib ID 1	Select RNA Library ID
2	RNA Lib ID 2	Select RNA Library ID
3	x2	The selected x2 value of two RNA Library ID
4	Fisher	The selected Fisher value of two RNA Library ID

[Matrix of compared values]

No	Column	Explanation
1	Expression Color	Each Expression Color's range
2	Matrix	The upper right is value of Fisher. The lower left is value of x2. The colored frame of value is displayed on ID chosen. The value level is displayed by the background color. By clicking a value, ID of RNA Lib ID 1 & 2 change to ID of the value.

3.11 TU Summary

You can show the details of TU in TU Summary.

The whole of the page

TU Summary

TU ID: 73859

Genomic Position

F/R	Chr	Start	End	CAGE Tag	CTSS	TC	Local LNA ID	Link
F	8	29,953,413	+88,874	452	60	22	18187	View

GO ID / GO name

Biological Process

- GO:0006412 / protein biosynthesis

Cellular Component

- GO:0005832 / intracellular
- GO:0005739 / mitochondrion
- GO:0005831 / ribosome

Molecular Function

- GO:0005228 / structural constituent of ribosome

Gene Symbol

- Mpl33

Gene Description

- mitochondrial ribosomal protein L33
- MITOCHONDRIAL RIBOSOMAL PROTEIN L33. [Source:RefSeq;Acc:NM_025796]
- Max homologous mRNA similar to mitochondrial ribosomal protein L33 (Gene data HQ(195714 [MAGE-506387]), complete cds.
- Similar to mitochondrial ribosomal protein L33

Neighbor TUs

Current	Prev	Overlap	Next
←	125561		12473
→	124881	12478	122768

TU List

Expression Type: [Tag](#) [TSS](#)

No.	TC ID	Representative Position	Relative Position	CTSS	CAGE Tag	Library (RS)
1	TSS1-CG488	29,934,042	-17,348	2	1	RP11-117B12.1 (100%)
2	TSS1-CG488	29,934,129	-17,271	1	1	RP11-117B12.1 (100%)
3	TSS1-CG484	29,934,346	-17,078	1	1	RP11-117B12.1 (100%)
4	TSS1-CG488	29,934,413	-16,997	1	1	RP11-117B12.1 (100%)
5	TSS1-CG488	29,943,905	-12,585	1	1	RP11-117B12.1 (100%)
6	TSS1-CG488	29,945,007	-8,483	1	1	RP11-117B12.1 (100%)
7	TSS1-CG488	29,953,397	-53	48	394	RP11-117B12.1 (100%)
8	TSS1-CG488	29,953,587	477	1	1	RP11-117B12.1 (100%)
9	TSS1-CG488	29,953,649	439	1	1	RP11-117B12.1 (100%)
10	TSS1-CG488	29,953,834	424	1	1	RP11-117B12.1 (100%)
11	TSS1-CG488	29,955,333	41,823	1	1	RP11-117B12.1 (100%)
12	TSS1-CG488	29,955,500	42,171	1	1	RP11-117B12.1 (100%)

Expression Type: [Tag](#) [TSS](#)

Expression Color: [#10828080](#) [#FF0000](#)

mRNA Information [Representative mRNA = 0630927018](#)

Results 1-18 about 18.


No.	ID	ID Type	F/R	Chr	Start	End
1	012822263	RINER	F	5	29,954,389	+83,419
2	012822261	OR	F	5	29,953,393	+8,660
3	012822262	RINER	F	5	29,953,396	+8,660
4	173001083	RINER	F	5	29,953,396	+8,660
5	033000410	RINER	F	5	29,953,396	+8,660
6	061225126	RPEPQ	F	5	29,953,396	+8,670
7	012822262	RINER	F	5	29,953,396	+8,670
8	012822261	RINER	F	5	29,953,396	+8,660
9	012822262	RINER	F	5	29,953,397	+8,669
10	061225122	OR	F	5	29,953,397	+8,669
11	061225121	OR	F	5	29,953,400	+8,637
12	061225120	OR	F	5	29,953,410	+8,656
13	061225119	OR	F	5	29,953,410	+8,674
14	061225124	OR	F	5	29,953,417	+8,651
15	061225123	RINER	F	5	29,953,437	+8,629
16	012822262	RINER	F	5	29,953,439	+8,629
17	061225125	OR	F	5	29,953,452	+8,614
18	012822261	RINER	F	5	30,000,413	47,935

A part of the page

TU Summary

TU ID : 73859

Genomic Position

F/R	Chr.	Start	End	CAGE Tags	CTSSs	TCs	Locus Link ID	Link
F	5	29,953,410	+55,871	402	80	22	18197	

GO ID / GO name

Biological Process

- [GO:0006412](#) / protein biosynthesis

Cellular Component

- [GO:0005622](#) / intracellular
- [GO:0005739](#) / mitochondrion
- [GO:0005840](#) / ribosome

Molecular Function

- [GO:0003735](#) / structural constituent of ribosome

Gene Symbol

- Mrpl33



Gene Description

- mitochondrial ribosomal protein L33
- MITOCHONDRIAL RIBOSOMAL PROTEIN L33. [Source:RefSeq;Acc:NM_025796]

[Genomic Position]

No	Column	Explanation
1	TU ID	TU ID
2	F/R	Strand (F: Forward / R: Reverse)
3	Chr.	Chromosome number
4	Start	Start Position
5	End	The relative position from Start Position of End Position
6	CAGE Tags	Number of CAGE Tag
7	CTSSs	Number of CTSS
8	TCs	Number of TC
9	Locus Link ID	Locus Link ID. Go to external site
10	Link	Go to 4 Genomic Elements Viewer
11	GO ID / GO Name	GO ID / GO Name for every category. Go to external site
12	Gene Symbol	Gene Symbol
13	Gene Description	Gene Description

Neighbor TUs

	Prev	Overlap	Next
→	130561		73479
			
←	115151	12475	113764

[Neighbor TUs]

No	Column	Explanation
1	GENOMIC VIEWER	Go to 4 Genomic Elements Viewer
2	The line of a rightward arrow	Neighbor TU ID (Forward). Go to 3.11 TU Summary
3	The arrow of middle	The arrow is displayed according to direction of the target TU.
4	The line of a leftward arrow	Neighbor TU ID (Reverse). Go to 3.11 TU Summary

[TC List]

No	Column	Explanation
1	Expression Type	By clicking Tags / TPM, Each Library Expression Type changes
2	No	Consecutive numbers
3	TC ID	TC ID. Go to 3.9 TC Summary By clicking the column name, The list is sorted by the TC ID
4	Representative Position	Representative Position By clicking the column name, The list is sorted by the Representative Position
5	Relative Position	The relative position from Represent Position
6	CAGE Tags	Number of CAGE Tag By clicking the column name, The list is sorted by the number of CAGE Tag
7	CTSSs	Number of CTSS By clicking the column name, The list is sorted by the number of CTSS
8	Library Expression	The number of Library expression for every Library is displayed by the color image. Detailed information is displayed by hovering your mouse pointer
9	All Library >>	All Library Expression is displayed by clicking. If it is clicked again, the display of Library Expression will Top 10.
10	Expression Color	Expression Color's range

mRNA Information		Representative mRNA = RIKEN E430019A11				
Results 1-10 about 10.						
No	ID	ID Type	F/R	Chr.	Start	End
1	E430019A11	RIKEN	F	11	31,898,784	+58,773
2	ENSMUST00000020537	ENSEMBL	F	11	31,898,785	+58,772
3	U17259	GB	F	11	31,898,816	+58,743
4	NM_008741	REFSEQ	F	11	31,898,816	+58,743
5	3010082M05	RIKEN	F	11	31,898,819	+381
6	C530023J09	RIKEN	F	11	31,898,819	+32,932
7	0710008E18	RIKEN	F	11	31,898,819	+58,738
8	BC018224	GB	F	11	31,898,844	+58,715
9	A630002O18	RIKEN	F	11	31,898,858	+32,913
10	2610027C14	RIKEN	F	11	31,900,093	+57,468

Ortholog List

Homo sapiens : Locus Link ID [51617](#)

Rattus norvegicus : Locus Link ID [363557](#)

[mRNA Information]

No	Column	Explanation
1	Representative mRNA	Representative mRNA's Gene ID. A line is colored if there is the ID same in a list
2	No	Consecutive numbers
3	ID	mRNA's Public ID (Accession Number) . Go to external site
4	ID Type	mRNA's Public DB
5	F/R	Strand (F: Forward / R: Reverse)
6	Chr.	Chromosome number
7	Start	Start Position
8	End	The relative position from Start Position of End Position

[Ortholog List]

No	Column	Explanation
1	Organism Type	Organism Type
2	Locus Link ID	Locus Link ID. Go to external site

4. Genomic Elements Viewer

Genomic Elements Viewer of this system is explained below.

Mouse (mm4) genomic elements
Showing 1.052 kbp from chr19, positions 55,005,028 to 55,006,079

Instructions: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed. To center on a location, click the ruler. Use the ScrollZoom buttons to change magnification and position.
Examples: chr1, chr2, chr3, chr4, chr5, chr6, chr7, chr8, chr9, chr10, chr11, chr12, chr13, chr14, chr15, chr16, chr17, chr18, chr19, chrX, chr4 3006879..3011978

[Hide names] [Hide instructions] [Bookmark this view] [Link to an image of this view] [Publication quality image] [Help]

Landmark or Region: chr19:55005028..55006079 Search Flip

ScrollZoom:

[VISTA Tracks][UCSC]

Overview of chr19

10. Transcription start site (Basic TSS)
10. Transcription start site (RIKEN-TSS)
10. Transcription start site (Library TSS)
10. Core promoter region (Butcher)
10. Core promoter region (EP668)
20. Transcripts
20. GIS
20. CTSS of random primed ONE
21. RIKEN imprinted transcripts
21. Transcription Factors
21. Ensembl transcripts (coloring of CDS)
22. RIKEN 5'EST
23. Gene prediction
30. CpG island
30. GC Percent
30. Simple repeat
30. Gap
40. Synteny with Human (syntenyHg16)
40. Synteny with Rat (syntenyRn3)

Data Source: Mouse level7:genomic elements

Dumps, Searches and other Operations: Dump GFF File About... Configure... Go

Tracks [Hide]

<input checked="" type="checkbox"/> 10. Core promoter region (Butcher)	<input checked="" type="checkbox"/> 20. Transcripts	<input checked="" type="checkbox"/> 30. GC Percent
<input checked="" type="checkbox"/> 10. Core promoter region (EP668)	<input checked="" type="checkbox"/> 21. Ensembl transcripts (coloring of CDS)	<input type="checkbox"/> 30. Repeat region
<input type="checkbox"/> 10. Core promoter region (Patent)	<input checked="" type="checkbox"/> 21. RIKEN imprinted transcripts	<input checked="" type="checkbox"/> 30. Simple repeat
<input checked="" type="checkbox"/> 10. Transcription start site (Basic TSS)	<input checked="" type="checkbox"/> 21. Transcription factors	<input type="checkbox"/> 40. Conserved Region (astNet)
<input checked="" type="checkbox"/> 10. Transcription start site (Library TSS)	<input checked="" type="checkbox"/> 22. RIKEN 5'EST	<input checked="" type="checkbox"/> 40. Synteny with Human (syntenyHg16)
<input checked="" type="checkbox"/> 10. Transcription start site (RIKEN-TSS)	<input checked="" type="checkbox"/> 23. Gene prediction	<input checked="" type="checkbox"/> 40. Synteny with Rat (syntenyRn3)
<input checked="" type="checkbox"/> 20. CTSS of random primed CAGE	<input checked="" type="checkbox"/> 30. CpG island	
<input checked="" type="checkbox"/> 20. GIS	<input checked="" type="checkbox"/> 30. Gap	

Image Width: 300 450 640 800 1024

Key position: Between Beneath

Track Name Table: Alphabetic Varying

Upload your own annotations: [Help]

Upload a file:

Add remote annotations: [Help]

Enter Remote Annotation URL:

[Genomic Elements Viewer]

No	Data	Description
1	Transcription start site	Transcriptional Start Sites, used in CAGE system.
2	Core promoter region (Bucher)	Core promoter regions including TATA box, CCAAT box, GC box, and initiator. They are computed by RIKEN based on Bucher's matrix Reference: P. Bucher, J.Mol.Biol, 212, 563-578(1990).
3	Core promoter region (EPD68)	Core promoter regions, TATA box. They are computed by RIKEN based on EPD Release 68.
4	Core promoter region (Pattern)	Core promoter regions, including BRE, TATA box, Inr, DPE, and PSE. Reference: S.T.Smale and J.T.Kadonaga, Annu.Rev.Biochem., 72:449-79(2003)
5	Transcripts	RIKEN and public transcripts (mRNA)
6	GIS	GIS ditag (http://t2g.bii.a-star.edu.sg/riken/)
7	CTSS of random primed CAGE	CTSS of random primed CAGE tags
8	RIKEN imprinted transcripts	RIKEN clones listed in EICodb, http://fantom2.gsc.riken.jp/EICODB/ .
9	Transcription factors	Transcripts classified as transcription factors by RIKEN manual curation.
10	Ensembl transcripts (coloring of CDS)	Ensembl transcripts, downloaded from ftp://ftp.ensembl.org/pub/mouse-19.30/data/mysql/mus_musculus_lite_19_30/transcript.txt.table.gz
11	RIKEN 5'EST	RIKEN 5'-est
12	Gene prediction	Predicted transcripts by genscan, geneid, twinscan. See UCSC description for genscan, geneid, twinscan.
13	CpG island	CpG island, downloaded from UCSC. See UCSC description for detail.
14	GC Percent	GC percent, downloaded from UCSC. See UCSC description for detail.
15	Repeat region	Repeat region detected by RepeatMasker. See UCSC description for detail.
16	Simple repeat	Repeat region detected by Tandem repeats finder(TRF). See UCSC description for detail.
17	Gap	Assemble gap. See UCSC description for detail.
18	Synteny with Human (syntenyHg16)	Synteny, downloaded from UCSC annotation track, http://genome.ucsc.edu/goldenPath/mm4/database/syntenyHg16.txt.gz
19	Synteny with Rat (syntenyRn3)	Synteny, downloaded from UCSC annotation track, http://genome.ucsc.edu/goldenPath/mm4/database/syntenyRn3.txt.gz
20	Conserved Region (axtNet)	Percent identity of whole genome alignment against Human, axtNet. The alignment is downloaded from UCSC, http://hgdownload.cse.ucsc.edu/goldenPath/mm4/vsHg16/axtNet/ . The percent identity is computed with the following parameters, window length = 50 and interval = 25