CAGE Analysis Viewer User's Guide

Last Update : 2004-11-25 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.

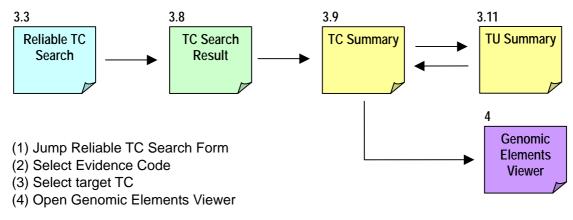
Contents	Confirmation
OS	Microsoft Windows 2000
	Microsoft Windows XP
	Apple Mac OS X
CPU	-
Memory	128MB or more is recommended.
Hard Disk	-
Web Browser	Internet Explorer 6.0(Or the compatible version of it or later)
	Netscape 7.1(Or the compatible version of it or later)
	Safari 1.0

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

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

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(2) Select Evidence Code

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

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	Exclusive Conditions
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	search reset

(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.

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283	T01F00139750	CAGE	1	F	1,283,920	0	+46	0	0	6	2	0	0	0	2	3	1						VIENER
284	T01F00139B41	CAGE	1	F	1,284,929	0	+21	0	0	6	2	0	0	0	0	1	1						VENET
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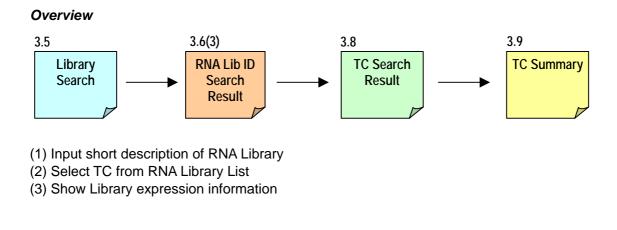
(4) Open Genomic Elements Viewer

You can open Genomic Elements Viewer, which show around target TC.

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2.2 TC Search by RNA Library

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



(1) Input short description of RNA Library

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

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	for Mus musculus Relation TE fac	arch TC Snarch by Branscript I	D TE Position See th Library Search Library Search
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CAGE Tags	> • 0 •		N
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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.

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



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3	T01F0-09424	0 0	CAGE	1	F	606,797	-1	+28	0	0	38	0	0	0	0	0	101	98					CERTIFICATE IN CONTRACT
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8	T01F000EBA8	<u>c</u> (BAGE	1	F	965,260	0	+18	0	0	0	0	0	0	0	0	2	2					CONTRACTOR OF THE OWNER OWNE
9	T01R000EE14	13 (BAGE	1	R	975,267	0	-19	0	0	3	0	0	0	0	0	1	1					CONTRACTOR OF THE OWNER OWNE
10	T01F000F309	0 0	BAGE	1	F	995,485	0	+26	0	0	4	0	0	0	0	0	8	3					CONTRACTOR OF THE OWNER OWNE OWNER



(3) Show Library expression information

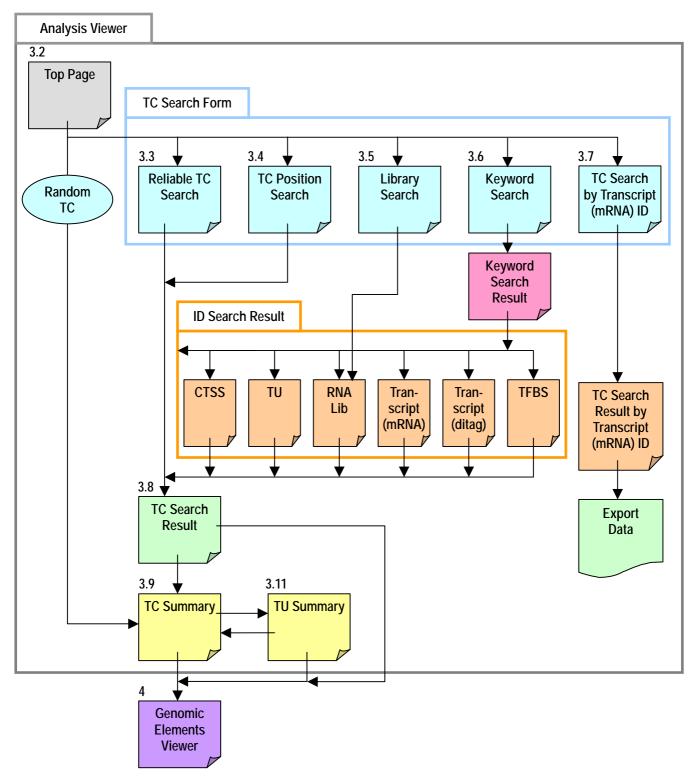
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res Comparised Region () O printial test of engre sen under T Taperssion T Taperssion T Taperssion T Taperssion T Taperssion T Taperssion T Tapers T T Tapers T T Tapers T Tapers T T Tapers T Tapers T Tapers T Tapers T Tapers T Tapers T Tapers T T Tapers T T Tapers T Tapers T Tapers T T T Tapers T T Tapers T T Tapers T T Tapers T T T Tapers T T Tapers T T Tapers T T Tapers T T Tapers T	engenved rote = 0, T ecourt of OpG = 10% ression difference : two samp me MEP Horoblast 20 Gp EDP-KO MEP Horoblast MEP Horoblast EDP-KO MEP HOROBLAS	les in one TE Category embrys embrys embrys embrys taar UeDEFINED_CATEOORY is ag is ag	of target TC	c tag distribution
res Comparised Region () O più istand () P stitcal test of engre com sindoxi rry Expression rry Expression rry Caprossion rry Specific Teg Di rry Caprossion rry Cap	engenved rate = 0, T ecourt of CpG = 10% ession difference : two samp mpe Description MEP Histobiast 20 Gp EDP-KD MEP Histobiast MEP Histobiast 20 Gp EDP-KD MEP Histobiast 20 Gp Hega 1-6 Joh EGPP DPWT-D1 preadsp. Gd Claned mouse lang Hega 1-6 Joh EGPP Intribution Map anexes> J	les in one TE Category arritrys arritry arrity arritrys arritrys arritrys arritrys arritrys arri	of target TC	c tag distribution
res Comparised Region () O printial test of engre sen under T Taperssion T Taperssion T Taperssion T Taperssion T Taperssion T Taperssion T Tapers T T Tapers T T Tapers T Tapers T T Tapers T Tapers T Tapers T Tapers T Tapers T Tapers T Tapers T T Tapers T T Tapers T Tapers T Tapers T T T Tapers T T Tapers T T Tapers T T Tapers T T T Tapers T T Tapers T T Tapers T T Tapers T T Tapers T	engenved rate = 0, T ecourt of CpG = 10% ession difference : two samp mpe Description MEP Histobiast 20 Gp EDP-KD MEP Histobiast MEP Histobiast 20 Gp EDP-KD MEP Histobiast 20 Gp Hega 1-6 Joh EGPP DPWT-D1 preadsp. Gd Claned mouse lang Hega 1-6 Joh EGPP Intribution Map anexes> J	les in one TE Category arritrys arritry arrity arritrys arritrys arritrys arritrys arritrys arri	of target TC	c tag distribution
ers Companyed Region () O cpin intend () P instical test of engre com mindeal ary Expression Trans Expression Trans Cold Obgo 47 Cold Obgo 47 Col	engenved rate = 0, T ecourt of CpG = 10% ession difference : two samp mpe Description MEP Histobiast 20 Gp EDP-KD MEP Histobiast MEP Histobiast 20 Gp EDP-KD MEP Histobiast 20 Gp Hega 1-6 Joh EGPP DPWT-D1 preadsp. Gd Claned mouse lang Hega 1-6 Joh EGPP Intribution Map anexes> J	les in one TE Category arritrys arritry arrity arritrys arritrys arritrys arritrys arritrys arri	of target TC	c tag distribution

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.

Search for	in the Aris Type	🗑 📴 Harras Top Hele
	CONTRACTOR OF A CONTRACTOR OF	
omo sapient(hg17) Helable 11.5os	ech TE Search by Transcript ED TE Post	ton Search Library Search Handom II
atistics		
arrest statistics of CTSS/TC/TO 1951	1.054.610	
c	450,226	
arrent Statistics of Transcripts		
AGE Tagi 19 ditage	3.106.472	
SC ditage	0	
ik Ma	233,563	
iken 5° EST	D	
arrent Statistics of 1705 apped position of Core Promoter		
Core Promoter 1s TATA box.	Initiator, BRE, CPE and PSE	Common Footer
	arresolt Statilistics of CTSS,/TC/TO TSS C U U arresolt Statilistics of Transcorpts ADE Tags 16 ditage SC Strage ang SAGE (RNA (ken S' EST urresolt Statilistics of TED) apped position of Care Promoter	arrent Statistics of ETSS/TE/TE TSS 1.054.610 C 450,228 U 32,353 arrent Statistics of Transcriptio AGE Tags 5.100.472 16 dtags 6 SC dtags 0 ang SAGE 1,224 (RNA 233,563 (ken S' EST 0)

[Header (common to all pages)]

1						
No	Column		Explanation			
1	Logo		Go to Top Page			
2	Keyword Search	Input box	Reference of 3.6 Keyword Search			
3		Menu				
4		>>				
5	Home		Go to Home Page			
6	Тор		Go to Top Page			
7	Help		Go to Help Page			
8	for		The type of taxonomy			
9	Menu	Reliable TC Search	Go to 3.3 Reliable TC Search			
10		TC Search by Transcript ID	Go to 3.7 TC Search by Transcript (mRNA) ID			
11		TC Position Search	Go to 3.4 TC Position Search			
12		Library Search	Go to 3.5 Library Search			
13		Random TC	Go to 3.9 TC Summary(displays at random)			

[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	Number of registered CTSS
2	CTSS / TC / TU	TC	Number of registered TC
3		TU	Number of registered TU
4	Current Statistics of	CAGE Tags	Number of registered CAGE Tag
5	Transcripts	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	Mapped position of Core	Number of registered mapped position of Core Promoter
	TFBS	Promoter	

3.3 Reliable TC Search

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

Reliable TC Search				
Reliable Conditions				
Transcript				
🗌 All Transcripts 📄 💌	All Transcripts 📄 💟 0 💌			
	5' End			
CAGE Tag	> 💙 0 💌			
	Library 💿 Any			
	○ Library Category UNDEFINED_CATEGORY_TYPE [etc] ✔			
	Library [HAD]			
	rectum [HAF]			
	cecum [HAG] cecum [HAH]			
	Priming 💿 Any 🔘 Oligo dT 🔘 random			
	Type S Any S Sigo at S random			
GIS ditag				
GSC ditag				
DBTSS				
Long SAGE				
✓ mRNA (✓ include 5' EST)	> 💙 0 💌			
	Region			
MRNA	> 💙 0 💙			
(V include 5' EST)	🗹 1000 bp Upstream of 1st Exon			
	🗹 1st Exon 🗹 Other Exon 🗹 Intron			
GIS ditag				
GSC ditag				
	TFBS			
Core Promoter				
(Pattern Match)	TATA box V Initiator V BRE V DPE V 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	inside CpG island			
	Exclusive Conditions			
inside only CDS				
search reset				

[Reliable TC Search]

Each item is searched with checking as an indispensable condition.

			cking as an	
No				Explanation
1	Transcript	All Transcripts		Select total of all Transcripts
2	5' End	CAGE		Select the number of min or the number of max CAGE Tag
3	*1	Tag	Library	Library Category can choose one when you checked 'Library Category'
				Library can choose more than one when you checked 'Library'
4			Priming	Select the priming type.
			Туре	
5		GIS dita	3	Select the number of min or the number of max GIS ditag
6		GSC dita	ag	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 SA	I GE	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	mRNA		Select the number of min or the number of max mRNA
	*2			5' EST is included with checking to 'include 5' EST'.
				Details are specified with checking to 1000bp Upstream of 1st Exon, 1st Exon,
				Other Exon, and Intron
11		GIS dita		Select the number of min or the number of max GIS ditag
12		GSC dita	0	Select the number of min or the number of max GSC ditag
13	TFBS Core Promoter			Core Promoter (Pattern Match) exists or not.
		(Pattern	Match)	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 Pro		Core Promoter (Bucher) exists or not.
		(Bucher)		Select the range of the upstream and the downstream
15		Core Pro	omoter	Core Promoter (EPD) exists or not.
		(EPD)		Select the range of the upstream and the downstream
16	Others		onserved	Exists or not inside Conserved Region
L		Region		
17		inside		Exists or not inside CpG island
		CpG island		
18	Exclusive	inside or	nly CDS	In existing inside only CDS, it removes for reference
	Conditions			
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	Example : chr19:59,214,20160,291,736	
CAGE Tags		
CTSSs		
	search reset	

[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		
Tissue	- Any Tissue -	
Developmental Stage	- Any Stage -	
CAGE Tags	> • 0 •	
CTSS=	> • 0 •	
se	arch reset	

[Library Search]

	J J		
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	n 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]

L J.										
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	Search out of Core Promoter (Bucher) ID. Go to (3-f) TFBS ID Search Result							
		(Bucher) ID								
13		Core Promoter	Search out of Core Promoter (EPD) ID. Go to (3-f) TFBS ID Search Result							
		(EPD) ID								

(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	Keyword Search Result									
CTSS/TC/	TU/RNA Lib									
hits	Category									
706,211	CTSS									
<u>450,228</u>	тс									
<u>32,351</u>	ти									
<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)									
2	Core Promoter (EPD)									
TU hit by I	(eyword									
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	1 CTSS The number of cases searched as CTSS ID. Go to (3-a) CTSS ID Search Result						
ſ	2 TC The number of cases searched as TC ID. Go to 3.8 TC Search Result							
Γ	3	TU	The number of cases searched as TU ID. Go to (3-b) TU ID Search Result					
ſ	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)							
		Franscript 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.

СТ	CTSS ID Search Result														
Re	Results 1-40 about 625. Page 1 of 16 🕨 🕅														
No	ID	Chr.	F/R	Start	CAGE Tags	TC ID									
1	C15R06213CF0	15	R	102,841,584	1	T15R06213CF0									
2	<u>C15R06213E77</u>	15	R	102,841,975	1	<u>T15R06213E77</u>									
з	<u>C15R0621F65A</u>	15	R	102,889,050	1	<u>T15R0621F65A</u>									
4	<u>C15R0621F66E</u>	15	R	102,889,070	1	<u>T15R0621F66E</u>									

[CTSS ID Search Result]

No	Column Explanation							
1	No	Consecutive numbers						
2	2 ID CTSS ID. Go to Basic Viewer							
3	3 Chr. Chromosome Number							
4	4 F/R Strand (F: Forward / R: Reverse)							
5	5 Start Start Position							
6	CAGE Tags	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. 🛛 🖌 🖌 Page 🛛 3 of 4,751 🕨 🕅

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

(3-b) TU ID Search Result

You can show the list of TU ID.

	TU ID Search Result Result 1-40 about 154. Image: and the image: about 154.										
No	TU ID	Chr.	ein.	Stert	End	CABE	става	TC:	dene Symbol	Gene Description	40 ID / 80 name
1	122	17	r	7,609,592	+7,972	46	92	<u>10</u>	COUNT	O Jumonji domain containing 3 O KIJAAD346 protain (Fingment) O jumonji domain containing 3	
2	1721	16	 	32,4+8,372	-59,452		2	14	na	O PREDICTED: Home capient similar to chromosome 19 open reading frame 27 (LOC441750), mRNA. O TPS3T03 protein. O TPS3T03 protein. [Source:RefSeqAct:NH_015069] O TPS3T03b (TPS3T03 protein) (Fragment) O similar to chromosome 15 open reading frame 17	
10	1222	8		17,058.402	+66.215	1.96	68	21	ZDHHCZ	O Home septence one finger, DHHC domain containing 2, mRNA (cDNA doma MGC.32737 19466:3299732), complete cdz. O Zine finger DHHC domain contraining prioritian 2 (Zine finger protein 372) (Reduced expression associated with metastasic protein) (Ream) (Reduced expression in cancer protein) (Rec) O Zine finger DHHC domain containing protein) (Rec) (Reduced expression associated with metastasic protein) 372) (Reduced expression associated with metastasic protein) (Ream) (Reduced expression in cancer protein) (Rec) (Ream) (Reduced expression in cancer protein) (Rec) (Ream) (Reduced expression in cancer protein) (Rec) (Rec) (Sources WHISSER OF Acce (SVLIX)) O Zine finger, DHHC domain containing 3 O Jine finger, DHHC domain containing 3	
4	1223			16,338,536	-13.649	677	80	-13	TUSA	O DRR1 O DRR1 protein (Down regulated in renal cell cardinomia 1) (TU3A protein) O DRR1 protein (Down regulated in renal cell cardinomia 1) (TU3A protein). [Secure SWISSBR07] Acc 095940] O Home capterio cell-bine 04377 DRR1 (DRR1) mRmA, complete cds. O TU3A protein	00:0501555 / regulation of cell growth 00:0505554 / molecular_function unknown 00:0505534 / mudeus

[TU ID Search Result]

1.0.10								
No	Column	Explanation						
1	No	Consecutive numbers						
2	TU ID	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	<u>-1</u>	not available	etc	UNDEFINED_TISSUE_TYPE	-1 (UNDEFINED_PUBLIC_STAGE)	82,398	43,292	<u>30,413</u>	16,207
2	<u>HAD</u>	small intestine	etc	small intestine	-1 (UNDEFINED_PUBLIC_STAGE)	30,031	17,761	<u>10,925</u>	7,365
3	<u>HAE</u>	rectum	etc	rectum	-1 (UNDEFINED_PUBLIC_STAGE)	8,274	5,649	<u>4,052</u>	3,393
4	HAE	rectum	etc	rectum	-1 (UNDEFINED_PUBLIC_STAGE)	14,772	9,657	<u>6,830</u>	5,288
5	<u>HAG</u>	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	96,670	42,634	22,208	11,879
6	<u>HAH</u>	cecum	etc	cecum	-1 (UNDEFINED_PUBLIC_STAGE)	15,822	10,121	<u>7,238</u>	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).

Tra	Transcript ID Search Result								
Results 1-40 about 695. Page 1 of 18 🕨 🕅									
No	ID	ID Type	F/R	Chr.	Start	End	TU ID	TU's TCs	Gene Symbol
1	<u>BC040257</u>	GB	R	1	1,189,441	-2,797	<u>16642</u>	1	TNFRSF4
2	<u>AK024028</u>	GB	F	1	1,499,294	+17,554	<u>7370</u>	<u>31</u>	ATAD3B
з	<u>NM 004402</u>	REFSEQ	F	1	3,797,002	+28,148	<u>600</u>	3	DFFB
4	<u>BC015402</u>	GB	R	1	5,858,779	-1,635	<u>663</u>	<u>41</u>	NPHP4
5	ENST00000340285	ENSEMBL	F	1	6,199,801	+2,447	<u>29552</u>	2	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 Туре	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									
Resu	Results 121-160 about 39,862.								
No	ID	ID Type	F/R	Chr.	Start	End	TCs		
121	<u>sme005 020604-13666-1</u>	GIS	R	1	16,742,152	+49,052	<u>38</u>		
122	<u>sme005 020604-84941-1</u>	GIS	R	1	16,790,280	+926	3		
123	sme005 020604-73254-1	GIS	R	1	16,815,476	+13,473	<u>12</u>		
124	<u>sme005 020604-57416-1</u>	GIS	R	1	16,814,980	+13,973	<u>15</u>		

[Transcript ID (ditag) Search Result]

No	Column	Explanation				
1	No	Consecutive numbers				
2	ID	litag 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	<u>GC-Bucher</u>	Core Promoter (Bucher)		<u>391,738</u>				
3	TATA-Bucher	Core Promoter (Bucher)		<u>361,814</u>				
4	TATA-EPD68p	Core Promoter (EPD)		<u>305,091</u>				
5	TATA-EPD68v	Core Promoter (EPD)		<u>390,068</u>				

[TFBS ID Search Result]

No	Column	Explanation				
1	No	nsecutive numbers				
2	ID	TFBS ID. Go to external site				
3	ID Туре	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 : 参照					
search reset					

[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.

	ts mRNAs : 4 / 4 sults 1-11 about 11.									export
No	ID	ID Type	F/R	chr.	Start	End	TU ID	TC ID	TC's Tags	Gene Symbols (TU)
1	<u>XM 496328</u>	REFSEQ	R	1	123,587	-44,429	<u>159989</u>	T01R00013DCB	1	na
2	<u>AK000561</u>	GB	R	1	605,686	-3,925	<u>26592</u>	T01R00093C19	2	
3	<u>AK000561</u>	GB	R	1	605,686	-3,925	<u>26592</u>	T01R00093CED	1	
4	<u>AK000561</u>	GB	R	1	605,686	-3,925	<u>26592</u>	T01R00093D6C	2	
5	<u>AK000561</u>	GB	R	1	605,686	-3,925	<u>26592</u>	T01R00093DB5	1	
6	<u>AK000561</u>	GB	R	1	605,686	-3,925	<u>26592</u>	T01R00093DE3	2	
7	<u>AK000130</u>	GB	R	3	127,636,112	-1,771	<u>8657</u>	T03R079B4BE5	3	FLJ20123
8	<u>AK000130</u>	GB	R	3	127,636,112	-1,771	<u>8657</u>	<u>T03R079B9718</u>	1	FLJ20123
9	ENST00000338293	ENSEMBL	R	Υ	27,111,443	-587	141012	T0YR0198F438	1	
10	ENST00000338293	ENSEMBL	R	Υ	27,111,443	-587	141012	T0YR0198FA1A	1	
11	ENST00000338293	ENSEMBL	R	Y	27,111,443	-587	141012	T0YR019DDEF6	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. <u>When you search by ID in the previous page, the information on selected ID is displayed on</u> <u>this page upper part.</u>

TC S	C Search Result																			
Ren	texults 281-320 about 450,228. 🕅 🚽 Page 8 of 11,258 🕨 N																			
									Reg	ion		1	5' 6	ind						
No	TCID	Representative Type	Chr.	F/R	Representative Position	Start	End	615	650	a fixing a	5125/19	613	100	adding a	512515	CTSS#	CAGE Tags >>	DB155 Long 586E TR19 box Initiater	pre DPE PSE Conserved Rej Cp6 tillend	Link
201	T01F001394F1	CAGE	1	F	1,203,313	0	+19	0	0	4	2	0	0	0	0	э	э			SENDINGE VIENER
282	T01F0013971E	CAGE	1	F	1,283,870	0	+23	0	0	6	2	0	0	0	0	1	1			VIENER
283	T01F00139750	CAGE	1	F	1,283,920	0	+46	0	0	6	2	0	0	0	2	3	1			VIENER
284	T01F00139B41	CAGE	1	F	1,284,929	0	+21	0	0	6	2	0	0	0	0	1	1			VIENEE
285	T01F00139F82	CAGE	1	F	1,286,066	0	+20	0	0	6	0	0	0	0	0	1	1			VIENED
286	T01F0013A04F	CAGE	1	F	1,286,223	0	+17	0	0	6	0	0	0	0	0	1	1			VIENED

[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	Representat	tive 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				

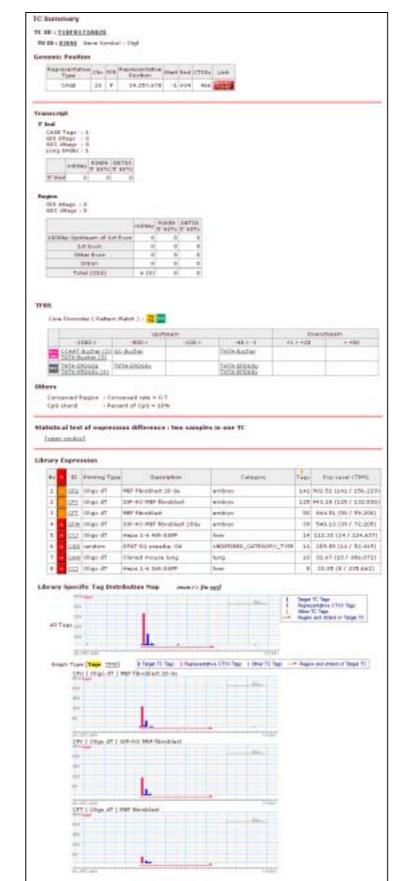
[TC Search Result]

	arch 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.			
10	ONOL 1095		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			
17	//		Expression will hide.			
			3 1			
			1,453 145			
			Library			
			CAGE Expression			
			Mameter Marken and States and St			
20	Libron Truck	alan	The number of the provident for every sets service devices the transmission to			
20	Library Expres	551011	The number of Library expression for every category is displayed by the bar graph.			
	<u>.</u>		Detailed information is displayed by hovering your mouse pointer			
-	lcons		Icons are displayed when each item exists. Detailed information is displayed by			
L		-	hovering your mouse pointer			
21	DBTSS		The icon is displayed when there is DBTSS			
22	Long S		The icon is displayed when there is Long SAGE			
23	TATA b	OX	The icon is displayed when there is TATA box			
24	Initiato	r	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		rved Reg	The icon is displayed when include Conserved Region			
28	Consei CpG is					
		iallu	The icon is displayed when include CpG island			
30	Link		Go to 4 Genomic Elements Viewer			

3.9 TC Summary

The whole of the page

You can show the details of TC in TC Summary.



A part of the page

TC Summary

TC ID : <u>T10F0173AB2E</u>

TU ID : 83098 Gene Symbol : Ctgf

Genomic Position

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

[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

Tra	anscript									
5' 1	i' End									
	GIS dit GSC dif	CAGE Tags : 1 SIS ditags : 0 SSC ditags : 0 ong SAGEs : 1								
		mRNAs		DBTSS 5' ESTs						
	5' End	0	0	0						
		ags : O tags : O								
					mRNAs	RIKEN 5' ESTs	DBTSS 5' ESTs			
	1000b	1000bp Upstream of 1st Exon				0	0			
	1st Exon				0	0	0			
	Other Exon				0	0	0			
		Int	ron		0	0	0			
		Tatal	(CDS)		6 (0)	0	0			

[Trans	cript]		
No	Column		Explanation
1	5' End	CAGE Tags	Number of CAGE Tag
2		GIS ditags	Number of GIS ditag
3		GSC ditags	Number of GSC ditag
4		Long SAGEs	Number of Long SAGE
5		mRNAs	Number of mRNA
6		RIKEN 5' ESTs	Number of RIKEN 5' EST
7		DBTSS 5' ESTs	Number of DBTSS 5' EST
8	Region	GIS ditags	Number of GIS ditag
9		GSC ditags	Number of GSC ditag
10		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
11		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
12		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

TFBS

Core Promoter (Pattern Match) : 👖 💵

	Upstr		Downst	ream	
-1000 >	-500 >	-100 >	-40 > -1	+1 > +20	> +50
CAAT-Bucher (3) ATA-Bucher (3)	<u>GC-Bucher</u>		TATA-Bucher		
<u>ATA-EPD68p</u> ATA-EPD68v (4)	TATA-EPD68v		TATA-EPD68p TATA-EPD68v		

Others

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

[TFBS]

11100]	
No	Column	Explanation
1	Core Promoter	The icon is displayed respectively When TATA box, Initiator, BRE, DPE and PSE exist.
	(Pattern Match)	
2	Except Core Promoter	ID of TFBS (Core Promoter (Bucher) and Core Promoter (EPD) other than Core
	(Pattern Match)	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

[<u>open window</u>]

Library Expression

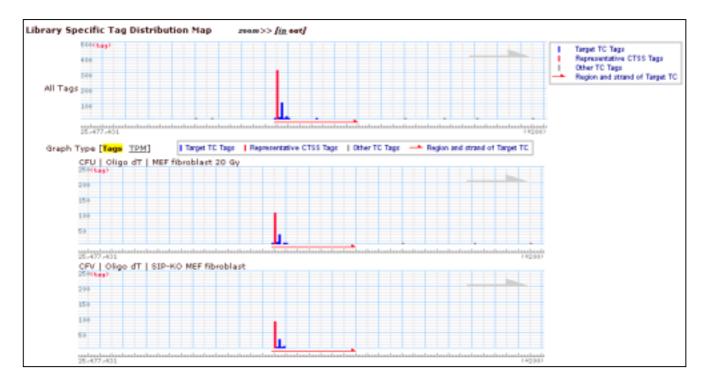
						t	
No	+	ID	Priming Type	Description	Category	Tags	Exp Level (TPM)
1	ŀ	<u>CFU</u>	Oligo dT	MEF fibroblast 20 Gy	embryo	141	930.75 (141 / 151,491
2	-	<u>CFV</u>	Oligo dT	SIP-KO MEF fibroblast	embryo	125	967.54 (125 / 129,193)
з	-	<u>CFT</u>	Oligo dT	MEF fibroblast	embryo	50	867.63 (50 / 57,628)
4	+	<u>CFW</u>	Oligo dT	SIP-KO MEF fibroblast 20Gy	embryo	39	553.29 (39 / 70,487)
5	+	<u>ccj</u>	Oligo dT	Hepa 1-6 48h EGFP	liver	14	115.43 (14 / 121,281)
6	+	<u>cgg</u>	random	DFAT-D1 preadip. Od	UNDEFINED_CATEGORY_TYPE	10	240.99 (10 / 41,495)
7	+	<u>CAW</u>	Oligo dT	Cloned mouse lung	lung	9	30.78 (9 / 292,385)
8	+	<u>cci</u>	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	



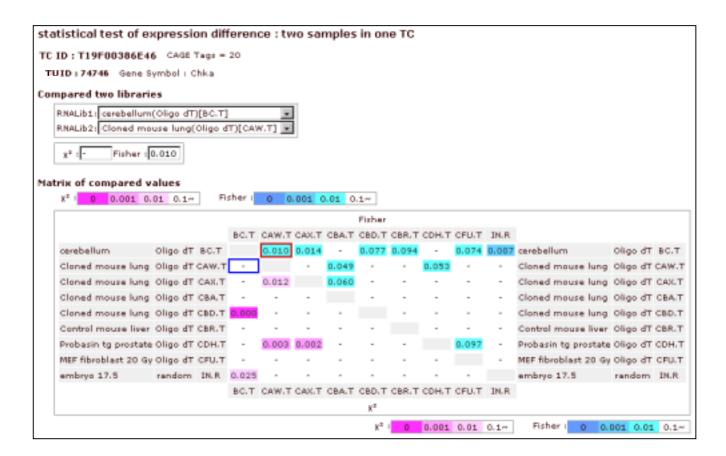
[Library Specific Tag Distribution Map]

[
No	Column		Explanation
1	zoom		By clicking in / out, the display range of graph changes
2	All Tags	Graph	Graph of All Tags
			[Reverse Strand]
			50
			100
			150
			200
			250(tag)
3	Each Library	Graph Type	By clicking Tags / TPM, Each Library Graph Type changes
4	,	ID / Priming Type /	Each Library's ID / Priming Type / Description
		Description	
5		Graph	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.



[ID etc.]

1 0.0					
No	Column	Explanation			
1	TC ID	TCID			
2	TU ID	TUID			
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.

ble of the page	TU ID : 73859				
	General Position				
	OB Chi Blart	End the	formal.	Co Lotas	Link
		100 Tag		22 28287	provide the second s
	and the state of the				
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		-	-		
	+ 1111	11 1112	UI.	112268	
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	 TEPERCHERTE 	29,852,849			O - MARINA MARINA
	10 110/12/06/24				
	12 TOPPOLCHISE				
	Representation Types [Taxes	1041	Paralysi		
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		Care Contractor	1.1.1		
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	and the second se				
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	Results 1-10 about 18 Hall 1D				
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	He 1D 1 013357221 2 0455335	1 P.34279	F 8 F 8	28,954,399 28,953,393 28,953,395	+8.840
	He ID 1 0.12887221 2 #AL49352 3 #AL49352 4 17.2002082		* 5 * 5 * 5	28,953,293 28,953,396 28,955,396	+84.840 +84.840 +84.840
	Her ID 1 RAIREZZE' 2 RAIREZZE' 3 RAIREZZE' 4 IZZECHE 9 GZZCOHE 9 GZZCOHE		F 5 F 5 F 5 F 5	24,983,393 29,983,396 29,983,396 29,983,396	48.840 48.840 48.840 48.845
	No. ID 1 643852221 2 6484855 3 88400044 4 17200162 5 101.4225 6 101.4225 7 28102040		F 5 F 5 F 5 F 5 F 5 F 5	24,953,293 24,953,296 24,953,296 24,953,296 24,953,296	48.880 48.880 48.840 48.840 48.870 48.870
	No. ID 1 RU3882221 2 ALENXX 3 BL200000 4 I22000000 5 ML2020000 6 ML2020000 7 SIL020000 8 SIL020000 9 SU2020000	Pitche L Pitche L Pitche LI Pitche	F B F B F B F B F B F B F B F B F B F B F B F B F B F B F B F S F S	24,903,293 24,903,296 24,903,296 24,903,296 24,903,296 24,955,296 24,955,296	48.84 48.840 48.840 48.840 48.870 48.870 48.810
	No. ID 1 643852221 2 6484855 3 88400044 4 17200162 5 101.4225 6 101.4225 7 28102040	#1508 4 68 4 68 12 6368 13 6368 14 6368 15 6368 16 6368 17 6368 18 6368 19 6368 10 6368 12 6368 13 6368 14 6368 15 6368 16 6468 17 6368 18 6368 19 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 10 6368 <	F B F B F B F B F B F B F B F B F B F B F B F B F B F S F S F S F S	24,903,293 24,903,296 24,903,296 24,903,296 24,903,296 24,955,296 24,955,296	48.840 48.840 48.840 48.849 48.870 48.870 48.800 48.800 48.840
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TU Summary

TU ID: 73859

Genomic Position

F/R	Chr.	Start	End	CAGE Tags	CTSS≲	TCs	Locus Link ID	Link
F	5	29,953,410	+55,871	402	80	22	<u>18197</u>	GENOMIC VIEWER

GO ID / GO name

Biological Process
O GO:0006412 / protein biosynthesis

Cellular Component

- O <u>GO:0005622</u> / intracellular
- 0 <u>GO:0005739</u> / mitochondrion
- 0 <u>GO:0005840</u> / ribosome

Molecular Function

- O <u>GO:0003735</u> / structural constituent of ribosome
- Gene Symbol
 - O MrpI33
- Gene Description
 - O mitochondrial ribosomal protein L33
 O MITOCHONDRIAL RIBOSOMAL PROTEIN L33. [Source:RefSeq;Acc:NM_025796]

[Genomic Position]

100.00					
No	Column	Explanation			
1	TUID	TUID			
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			

Neig	Neighbor TU s					
	GENOMIC VIEWER	Prev	Overlap	Next		
	\rightarrow	<u>130561</u>		<u>73479</u>		
	<i>←</i>	<u>115151</u>	<u>12475</u>	<u>113764</u>		

[Neighbor TUs]

No	Column	Explanation
1	GENOMIC VIEWER	Go to 4 Genomic Elements Viewer
2	The line of a rightward	Neighbor TU ID (Forward). Go to 3.11 TU Summary
	arrow	
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

-	tion Type [Tags	TIMAT				
80	ŦC ID	Reprosetation Austion	Relative Postfate	C768+	Слод	PF FIREWORDS 20 GARTING MITIGALI Marga 27,2001240 DDILLATT LOPED SALES JANGUILLATT LOPED SALES JANGUILLATT LOPED SALES JANGUILLATT LOPED SALES JANGUILLATT 100000000000000000000000000000000000
1	105701000385	29,936.062	-17.348	1.2	- 2	
2	TENFELCECHER	29,936,329	-17,271	- 1	1	
2	TOSFOSCOCHO4	29,936,340	-17.078	1	1	
	THREELCOCK10	29,938,433	-14,997	1	1	
5	T05F01C00C49	29,940,905	-12,505	1	1	AN AD REAL PROPERTY AND ADDRESS
6	TUBFULCHECAP	29,948,867	-8,453	1	1	
7	TUSE01C90075	29,953,297	-13	48	154	
8	TERRELEPORAS	29,983.887	+177	1	1	
9	705F01C90671	29,952,649	+239	3	. 1	
3.0	TESPOLCHOFIA	29,980.004	+424	1	. 1	
53	205503494503	29,955,322	+5,923	1	1	
12	T05F01C915FE	29,955,502	+2.472	1	1	

[TC List]

[TC Li	st]						
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.					
		All Library (85) 22					
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10	Expression Color	Expression Color's range					
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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	ENSMUST0000002053	ENSEMBL	F	11	31,898,785	+58,772	
3	<u>U17259</u>	GB	F	11	31,898,816	+58,743	
4	<u>NM 008741</u>	REFSEQ	F	11	31,898,816	+58,743	
5	<u>3010082M05</u>	RIKEN	F	11	31,898,819	+381	
6	<u>C530023J09</u>	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	A630002018	RIKEN	F	11	31,898,858	+32,913	
10	2610027C14	RIKEN	F	11	31,900,093	+57,468	
10	101002/014	I VEINEIT	. ·		52,750,070	.07,400	

Rattus norvegicus : Locus Link ID <u>363557</u>

[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 Туре	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.

ouse	(mm4) genomic ele	ments							
lowing	1.052 kbp from chr19, po	sitions 55	,005,028 1	o 55,00	6,079				
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	tons to charge magnification and position 1, chr2, chr3, chr4, chr5, chr6, chr7, chr0		hill, chil2, ch	13, chr14, c	hr15, chr16	s, chrift, chri	5, chi19, chiX	chv4 3006979	301 1978
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	10.Transcription start site (RDCE	H-TSS)			+				
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	18.Core promoter region (Bucher)							10	
	18,Core promoter region (EPO68)								
	20,Transcripts		_		-	_			
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	28,615								
	20,CTSS of random primed CRGE							+	
	21.KINEN imprinted transcripts				11 **				
	21.Transcription Factors								
	21,EssEMBL transcripts (coloring	of CBS)	-						
	22. HIKEN S'EST								
	- Alternative	1				-		-	
	23,Gene prediction		-		0.00			_	
	30.Cp6 island								
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[Genomic Elements Viewer]

No	Data	Description
1	Transcription start site	Transcriptional Start Sites, used in CAGE system.
2	Core promoter region	Core promoter regions including TATA box, CCAAT box, GC box, and initiator.
	(Bucher)	They are computed by RIKEN based on Bucher's matrix Reference: P. Bucher,
		J.Mol.Biol, 212, 563-578(1990).
3	Core promoter region	Core promoter regions, TATA box. They are computed by RIKEN based on EPD
	(EPD68)	Release 68.
4	Core promoter region	Core promoter regions, including BRE, TATA box, Inr, DPE, and PSE.
	(Pattern)	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	CTSS of random primed CAGE tags
	primed CAGE	
8	RIKEN imprinted	RIKEN clones listed in EICOdb, http://fantom2.gsc.riken.jp/EICODB/.
	transcripts	
9	Transcription factors	Transcripts classified as transcription factors by RIKEN manual curation.
10	EnsEMBL transcripts	EnsEMBL transcripts, downloaded from
	(coloring of CDS)	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
13	CnC island	genscan, geneid, twinscan.
13	CpG island GC Percent	CpG island, downloaded from UCSC. See UCSC description for detail. GC percent, downloaded from UCSC. See UCSC description for detail.
14	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
10	Simple repeat	detail.
17	Gap	Assemble gap. See UCSC description for detail.
18	Synteny with Human	Synteny, downloaded from UCSC annotation track,
	(syntenyHg16)	http://genome.ucsc.edu/goldenPath/mm4/database/syntenyHg16.txt.gz
19	Synteny with Rat	Synteny, downloaded from UCSC annotation track,
	(syntenyRn3)	http://genome.ucsc.edu/goldenPath/mm4/database/syntenyRn3.txt.gz
20	Conserved Region	Percent identity of whole genome alignment against Human, axtNet.
	(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