CAGE Basic Viewer User's Guide

Last Update：2004-11-25
NTT Software Corporation.

Abstract

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

Table of Contents

1. User environment

1.1 Client

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

Contents	Confirmation
CPU	-
Memory	128MB or more is recommended.
Hard Disk	-
Web Browser	Internet Explorer 6.0(Or the compatible version of it or later) Netscape 7.0(Or the compatible version of it or later) Safari

2. Getting started

Getting started with CAGE Basic Viewer is no walk in the park. We decided we better try to help others who were also struggling to learn this Viewer and powerful analysis tool.

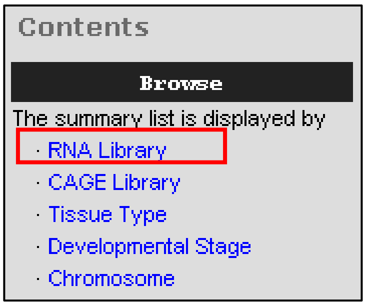
This page is going to be a work-in-progress. A place where I can answer very simple questions for the beginner and show very rudimentary CAGE data concepts. It's not going to answer all your questions, and it's not going to help everyone.

For the most part, you should still search the RNA-library and CTSS using the box in the left column. If you've done that and you are still stuck, then post a message to the FANTOM3 Forum or the mailing list.

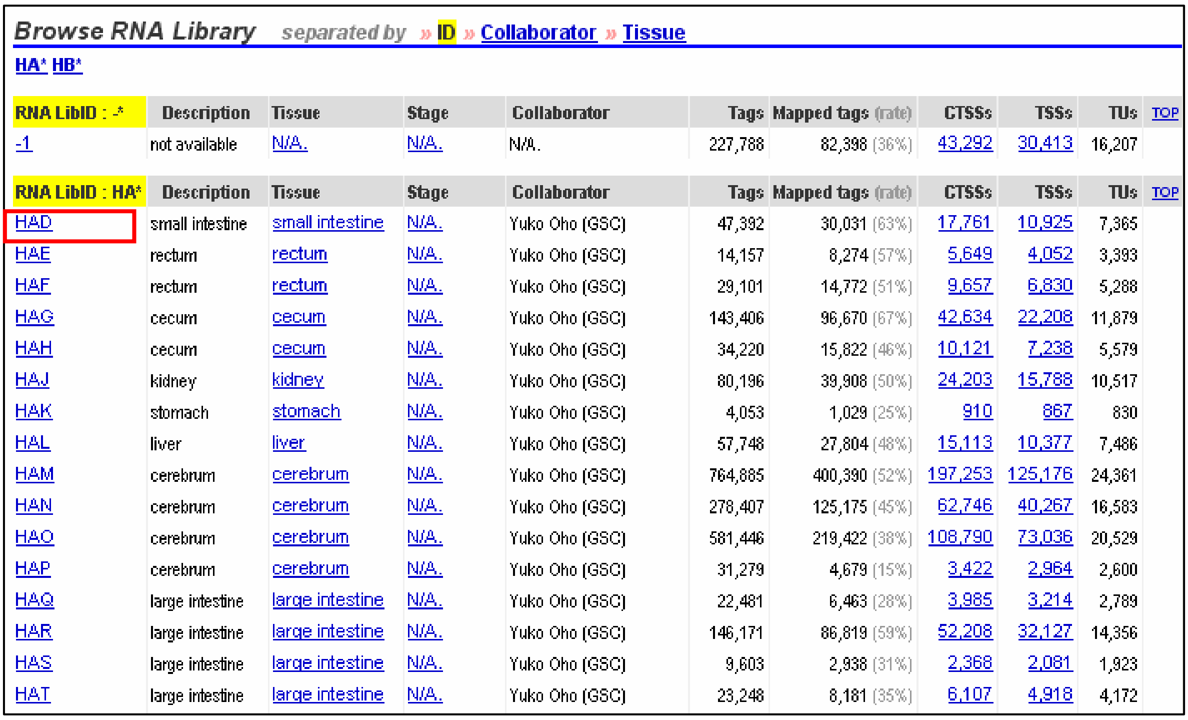
2.1 Searching CTSS distribution in RNA Library

You can search the CTSS distribution in specified RNA Library.

1. RNA Library is displayed by clicking 'RNA Library' of 'Browse'.



2. RNA Library List is displayed.
RNA Library Summary is displayed by clicking RNA LibID.



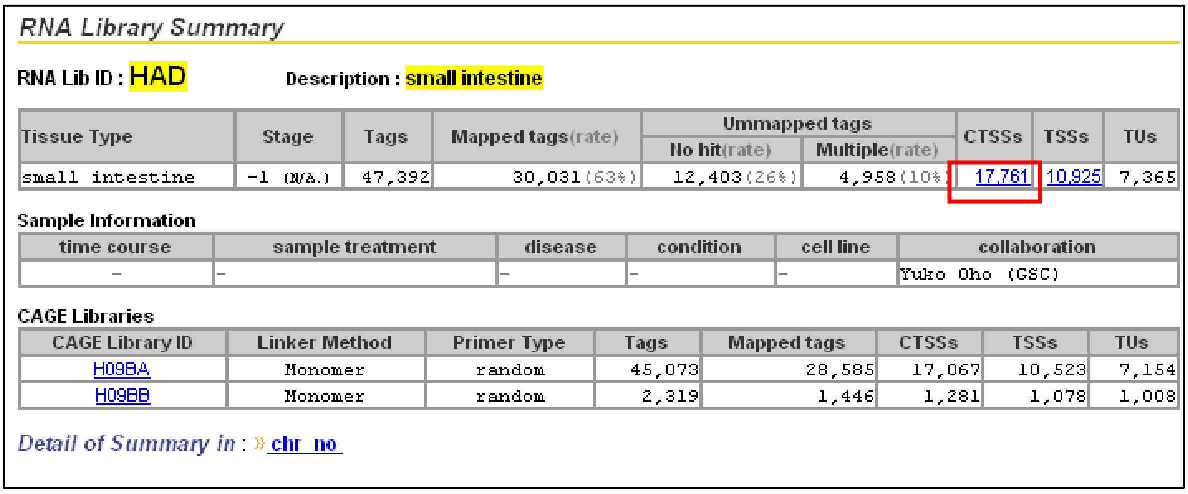
Browse RNA Library separated by » ID » Collaborator » Tissue

HA* HB*

RNA LibID : -*	Description	Tissue	Stage	Collaborator	Tags	Mapped tags (rate)	CTSSs	TSSs	TUs	TOP
-1	not available	N/A.	N/A.	N/A.	227,788	82,398 (36%)	43,292	30,413	16,207	

RNA LibID : HA*	Description	Tissue	Stage	Collaborator	Tags	Mapped tags (rate)	CTSSs	TSSs	TUs	TOP
HAD	small intestine	small intestine	N/A.	Yuko Oho (GSC)	47,392	30,031 (63%)	17,761	10,925	7,365	
HAE	rectum	rectum	N/A.	Yuko Oho (GSC)	14,157	8,274 (57%)	5,649	4,052	3,393	
HAF	rectum	rectum	N/A.	Yuko Oho (GSC)	29,101	14,772 (51%)	9,657	6,830	5,288	
HAG	cecum	cecum	N/A.	Yuko Oho (GSC)	143,406	96,670 (67%)	42,634	22,208	11,879	
HAH	cecum	cecum	N/A.	Yuko Oho (GSC)	34,220	15,822 (46%)	10,121	7,238	5,579	
HAJ	kidney	kidney	N/A.	Yuko Oho (GSC)	80,196	39,908 (50%)	24,203	15,788	10,517	
HAK	stomach	stomach	N/A.	Yuko Oho (GSC)	4,053	1,029 (25%)	910	867	830	
HAL	liver	liver	N/A.	Yuko Oho (GSC)	57,748	27,804 (48%)	15,113	10,377	7,486	
HAM	cerebrum	cerebrum	N/A.	Yuko Oho (GSC)	764,885	400,390 (52%)	197,253	125,176	24,361	
HAN	cerebrum	cerebrum	N/A.	Yuko Oho (GSC)	278,407	125,175 (45%)	62,746	40,267	16,583	
HAO	cerebrum	cerebrum	N/A.	Yuko Oho (GSC)	581,446	219,422 (38%)	108,790	73,036	20,529	
HAP	cerebrum	cerebrum	N/A.	Yuko Oho (GSC)	31,279	4,679 (15%)	3,422	2,964	2,600	
HAQ	large intestine	large intestine	N/A.	Yuko Oho (GSC)	22,481	6,463 (28%)	3,985	3,214	2,789	
HAR	large intestine	large intestine	N/A.	Yuko Oho (GSC)	146,171	86,819 (59%)	52,208	32,127	14,356	
HAS	large intestine	large intestine	N/A.	Yuko Oho (GSC)	9,603	2,938 (31%)	2,368	2,081	1,923	
HAT	large intestine	large intestine	N/A.	Yuko Oho (GSC)	23,248	8,181 (35%)	6,107	4,918	4,172	

3. RNA Library Summary is displayed.
   CTSS List is displayed by clicking CTSSs.



RNA Library Summary

RNA Lib ID : **HAD** **Description :** **small intestine**

Tissue Type	Stage	Tags	Mapped tags(rate)	Ummapped tags		CTSSs	TSSs	TUs
				No hit(rate)	Multiple(rate)			
small intestine	-1 (N/A.)	47,392	30,031(63%)	12,403(26%)	4,958(10%	17,761	10,925	7,365

Sample Information

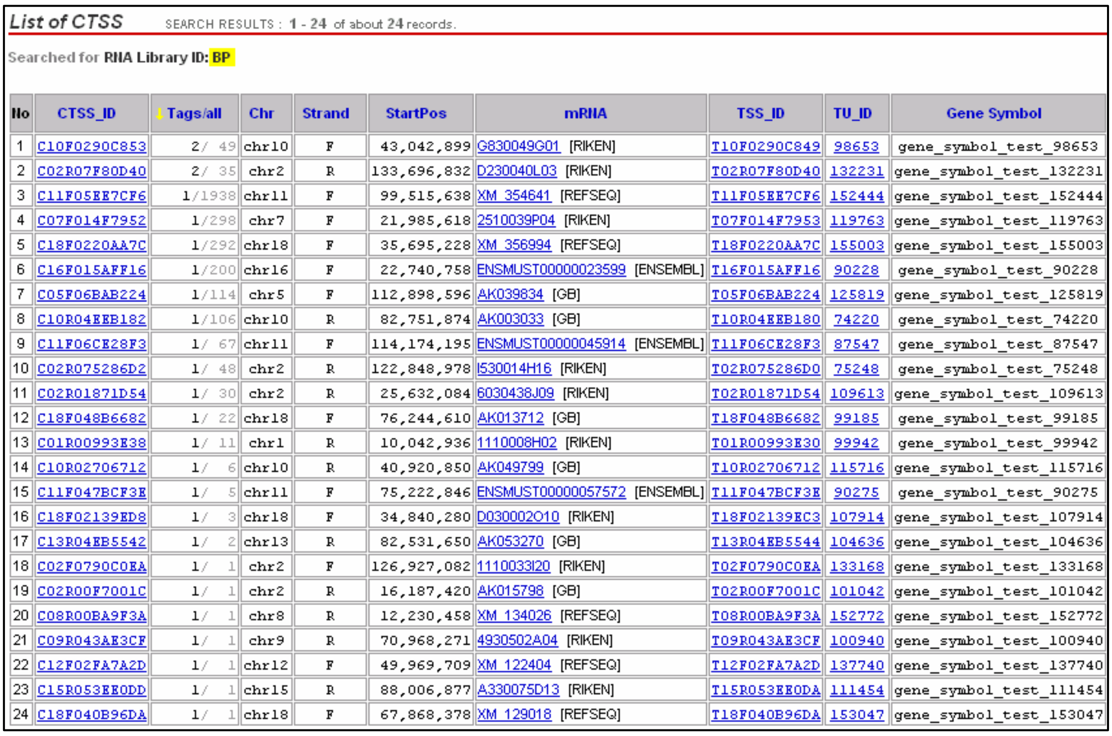
time course	sample treatment	disease	condition	cell line	collaboration
-	-	-	-	-	Yuko Oho (GSC)

CAGE Libraries

CAGE Library ID	Linker Method	Primer Type	Tags	Mapped tags	CTSSs	TSSs	TUs
H09BA	Monomer	random	45,073	28,585	17,067	10,523	7,154
H09BB	Monomer	random	2,319	1,446	1,281	1,078	1,008

Detail of Summary in : » chr_no

4. CTSS List is displayed.



List of CTSS SEARCH RESULTS : **1** - **24** of about **24** records.

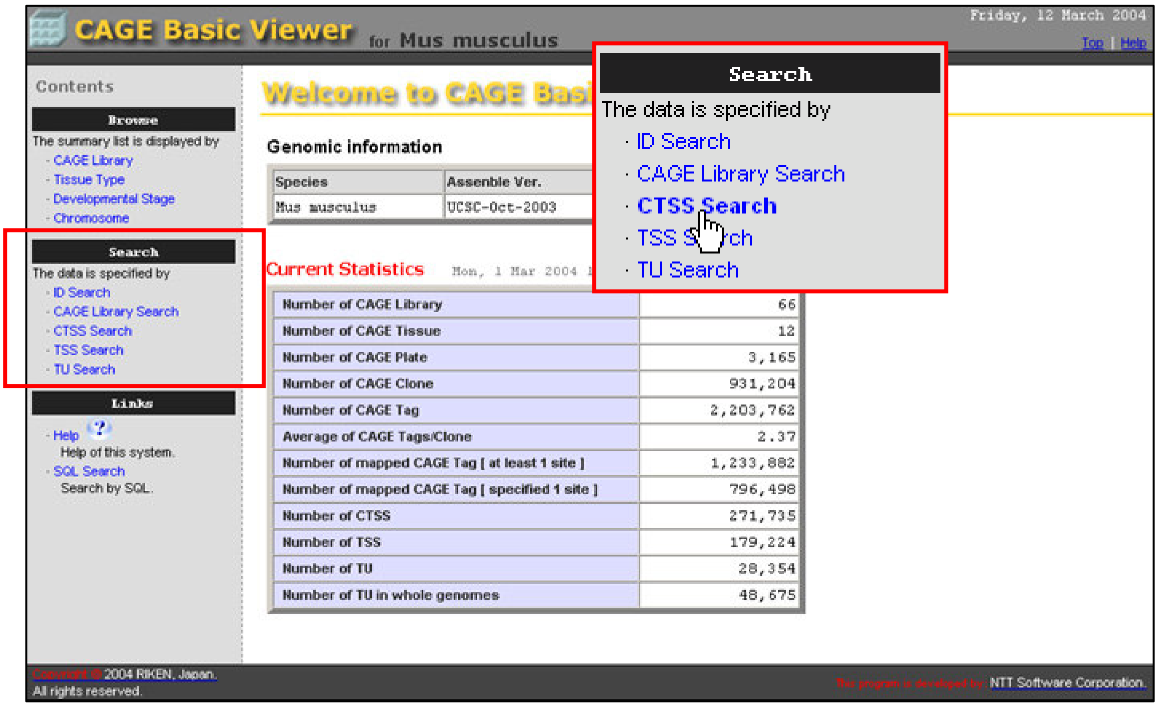
Searched for **RNA Library ID:** **BP**

No	CTSS_ID	↓Tags/all	Chr	Strand	StartPos	mRNA	TSS_ID	TU_ID	Gene Symbol
1	C10F0290C853	2/ 49	chr10	F	43,042,899	G830049G01 [RIKEN]	T10F0290C849	98653	gene_symbol_test_98653
2	C02R07F80D40	2/ 35	chr2	R	133,696,832	D230040L03 [RIKEN]	T02R07F80D40	132231	gene_symbol_test_132231
3	C11F05EE7CF6	1/1938	chr11	F	99,515,638	XM_354641 [REFSEQ]	T11F05EE7CF6	152444	gene_symbol_test_152444
4	C07F014F7952	1/298	chr7	F	21,985,618	2510039P04 [RIKEN]	T07F014F7953	119763	gene_symbol_test_119763
5	C18F0220AA7C	1/292	chr18	F	35,695,228	XM_356994 [REFSEQ]	T18F0220AA7C	155003	gene_symbol_test_155003
6	C16F015AFF16	1/200	chr16	F	22,740,758	ENSMUST00000023599 [ENSEMBL]	T16F015AFF16	90228	gene_symbol_test_90228
7	C05F06BAB224	1/114	chr5	F	112,898,596	AK039834 [GB]	T05F06BAB224	125819	gene_symbol_test_125819
8	C10R04EEB182	1/106	chr10	R	82,751,874	AK003033 [GB]	T10R04EEB180	74220	gene_symbol_test_74220
9	C11F06CE28F3	1/ 67	chr11	F	114,174,195	ENSMUST00000045914 [ENSEMBL]	T11F06CE28F3	87547	gene_symbol_test_87547
10	C02R075286D2	1/ 48	chr2	R	122,848,978	I530014H16 [RIKEN]	T02R075286D0	75248	gene_symbol_test_75248
11	C02R01871D54	1/ 30	chr2	R	25,632,084	6030438J09 [RIKEN]	T02R01871D54	109613	gene_symbol_test_109613
12	C18F048B6682	1/ 22	chr18	F	76,244,610	AK013712 [GB]	T18F048B6682	99185	gene_symbol_test_99185
13	C01R00993E38	1/ 11	chr1	R	10,042,936	1110008H02 [RIKEN]	T01R00993E30	99942	gene_symbol_test_99942
14	C10R02706712	1/ 6	chr10	R	40,920,850	AK049799 [GB]	T10R02706712	115716	gene_symbol_test_115716
15	C11F047BCF3E	1/ 5	chr11	F	75,222,846	ENSMUST00000057572 [ENSEMBL]	T11F047BCF3E	90275	gene_symbol_test_90275
16	C18F02139ED8	1/ 3	chr18	F	34,840,280	D030002O10 [RIKEN]	T18F02139EC3	107914	gene_symbol_test_107914
17	C13R04EB5542	1/ 2	chr13	R	82,531,650	AK053270 [GB]	T13R04EB5544	104636	gene_symbol_test_104636
18	C02F0790C0EA	1/ 1	chr2	F	126,927,082	1110033I20 [RIKEN]	T02F0790C0EA	133168	gene_symbol_test_133168
19	C02R00F7001C	1/ 1	chr2	R	16,187,420	AK015798 [GB]	T02R00F7001C	101042	gene_symbol_test_101042
20	C08R00BA9F3A	1/ 1	chr8	R	12,230,458	XM_134026 [REFSEQ]	T08R00BA9F3A	152772	gene_symbol_test_152772
21	C09R043AE3CF	1/ 1	chr9	R	70,968,271	4930502A04 [RIKEN]	T09R043AE3CF	100940	gene_symbol_test_100940
22	C12F02FA7A2D	1/ 1	chr12	F	49,969,709	XM_122404 [REFSEQ]	T12F02FA7A2D	137740	gene_symbol_test_137740
23	C15R053EE0DD	1/ 1	chr15	R	88,006,877	A330075D13 [RIKEN]	T15R053EE0DA	111454	gene_symbol_test_111454
24	C18F040B96DA	1/ 1	chr18	F	67,868,378	XM_129018 [REFSEQ]	T18F040B96DA	153047	gene_symbol_test_153047

2.2 Searching CAGE TAG start site(CTSS) information

You can search the tag start site information in which much Tags is contained.

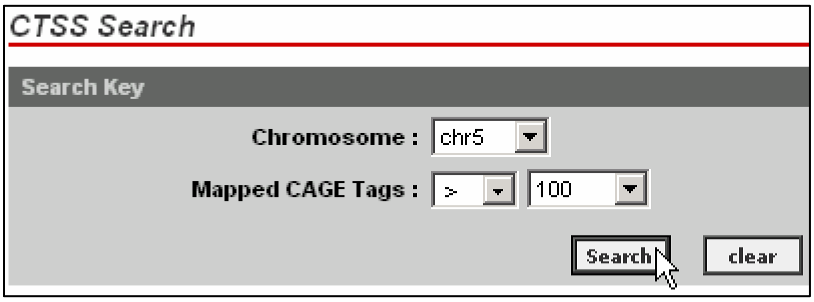
1. CTSS Search is displayed by clicking ‘CTSS Search’ of ‘Search’.



Species	Assenble Ver.
Mus musculus	UCSC-Oct-2003

Number of CAGE Library	66
Number of CAGE Tissue	12
Number of CAGE Plate	3,165
Number of CAGE Clone	931,204
Number of CAGE Tag	2,203,762
Average of CAGE Tags/Clone	2.37
Number of mapped CAGE Tag [at least 1 site]	1,233,882
Number of mapped CAGE Tag [specified 1 site]	796,498
Number of CTSS	271,735
Number of TSS	179,224
Number of TU	28,354
Number of TU in whole genomes	48,675

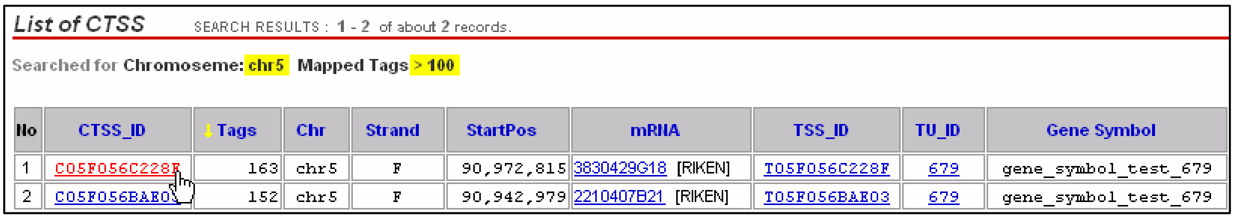
2. CTSS Search is displayed.
CTSS List is displayed by selecting Chromosome and Mapped CAGE Tags, and clicking ‘Search’.



Chromosome : chr5

Mapped CAGE Tags : > 100

3. CTSS List is displayed.
   CTSS Summary is displayed by clicking CTSS ID.

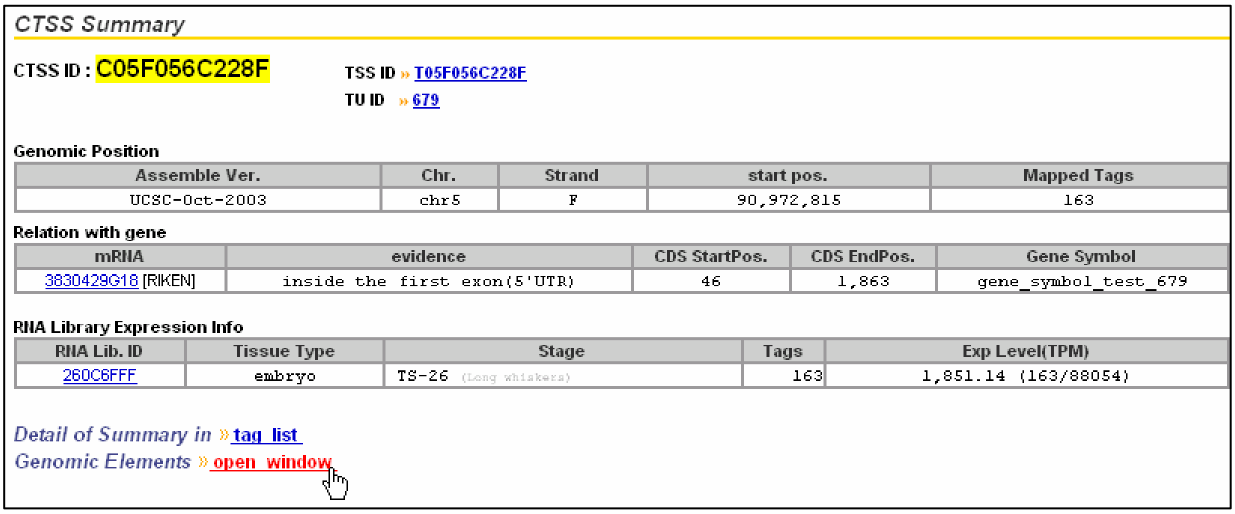


List of CTSS SEARCH RESULTS : 1 - 2 of about 2 records.

Searched for **Chromoseme: chr5** **Mapped Tags > 100**

No	CTSS_ID	↓Tags	Chr	Strand	StartPos	mRNA	TSS_ID	TU_ID	Gene Symbol
1	C05F056C228F	163	chr5	F	90,972,815	3830429G18 [RIKEN]	T05F056C228F	679	gene_symbol_test_679
2	C05F056BAE03	152	chr5	F	90,942,979	2210407B21 [RIKEN]	T05F056BAE03	679	gene_symbol_test_679

4. CTSS Summary is displayed.
   Genomic Elements is displayed by clicking ‘open window’.



CTSS Summary

CTSS ID : **C05F056C228F**

TSS ID » T05F056C228F
TU ID » 679

Genomic Position

Assemble Ver.	Chr.	Strand	start pos.	Mapped Tags
UCSC-Oct-2003	chr5	F	90,972,815	163

Relation with gene

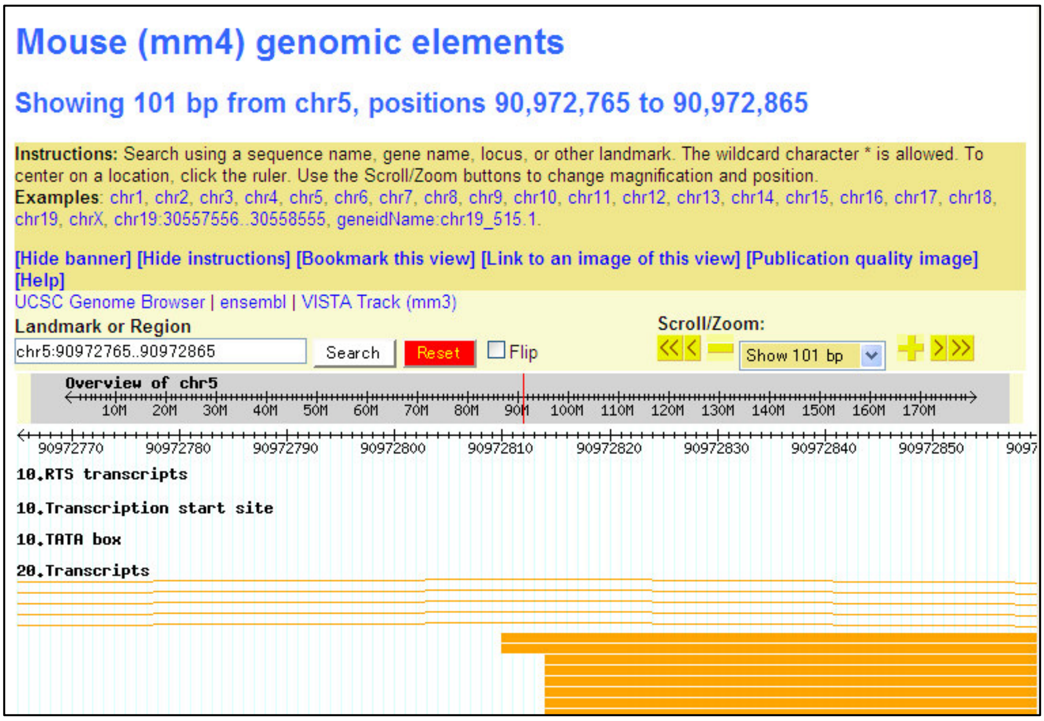
mRNA	evidence	CDS StartPos.	CDS EndPos.	Gene Symbol
3830429G18 [RIKEN]	inside the first exon(5'UTR)	46	1,863	gene_symbol_test_679

RNA Library Expression Info

RNA Lib. ID	Tissue Type	Stage	Tags	Exp Level(TPM)
260C6FFF	embryo	TS-26 (Long whiskers)	163	1,851.14 (163/88054)

Detail of Summary in » tag list
Genomic Elements » open window

5. Genomic Elements is displayed.



Mouse (mm4) genomic elements

Showing 101 bp from chr5, positions 90,972,765 to 90,972,865

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 Scroll/Zoom 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, chr19:30557556..30558555, geneidName:chr19_515.1.

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

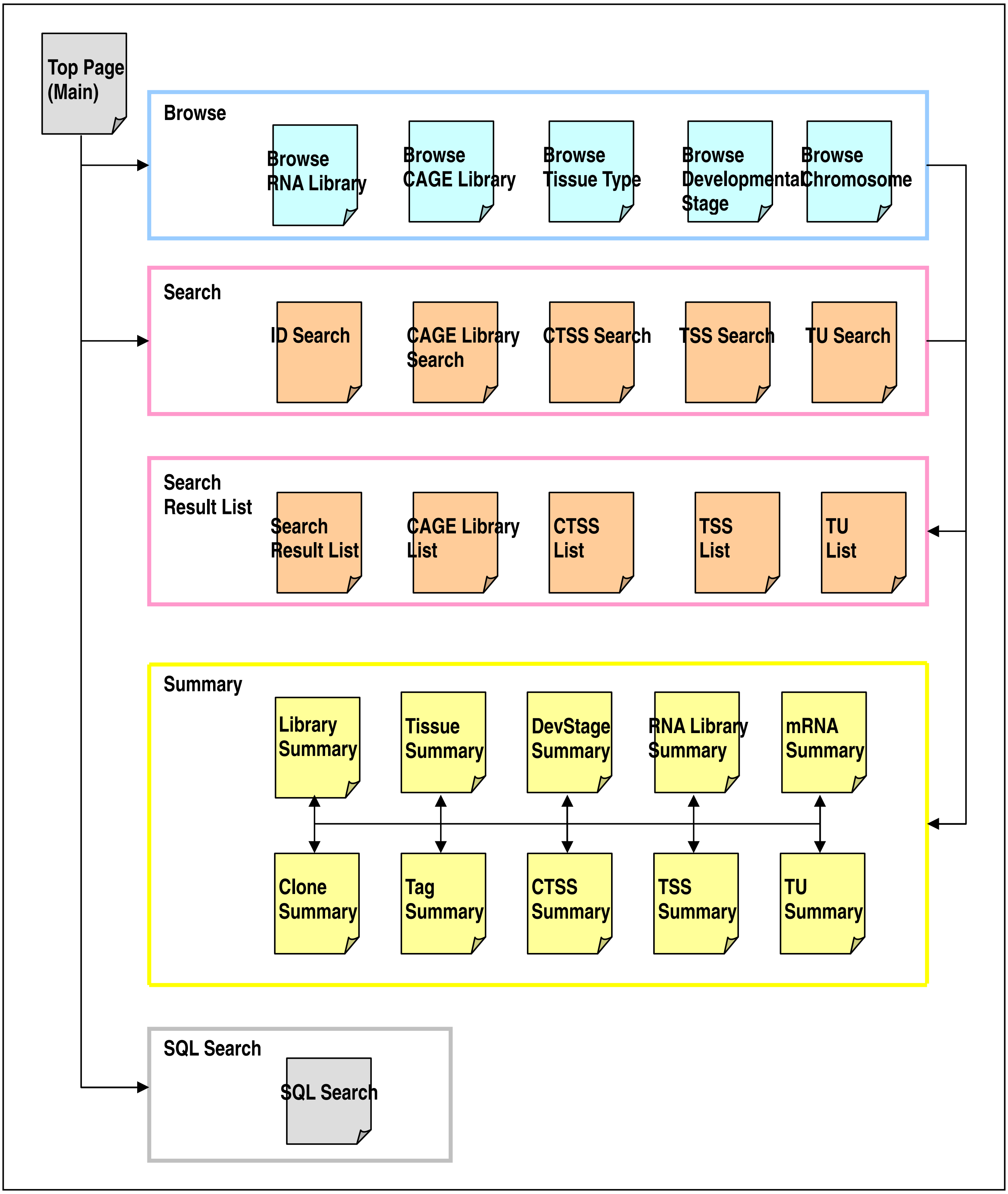
UCSC Genome Browser | ensembl | VISTA Track (mm3)

Landmark or Region: chr5:90972765..90972865

3. Viewer Pages

3.1 Page transition

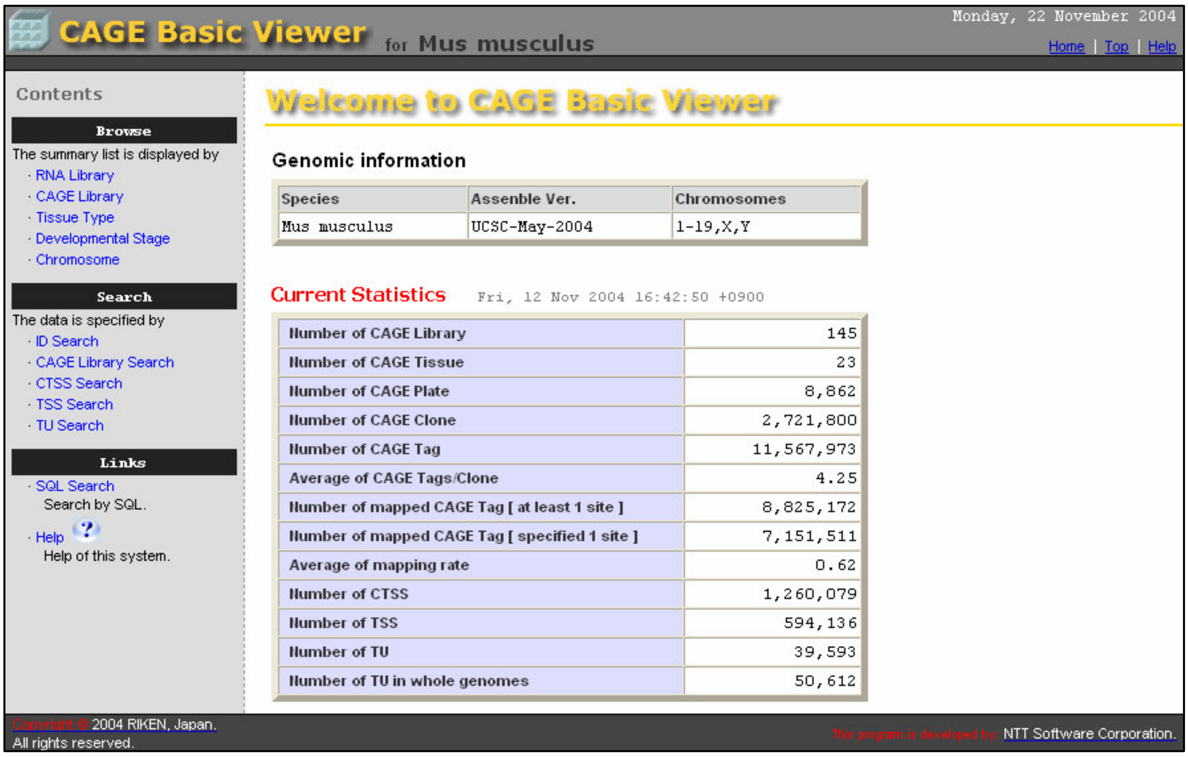
Pages in this system are connected with each other by hyperlink. The transition is described in the following.



3.2 Top Page

Menu, statistics, and the used assembly of the genome are displayed in 'Contents', 'Genomic Information', and 'Current Statistics', respectively.

[Top Page]



Genomic information

Species	Assenble Ver.	Chromosomes
Mus musculus	UCSC-May-2004	1-19,X,Y

Current Statistics Fri, 12 Nov 2004 16:42:50 +0900

Number of CAGE Library	145
Number of CAGE Tissue	23
Number of CAGE Plate	8,862
Number of CAGE Clone	2,721,800
Number of CAGE Tag	11,567,973
Average of CAGE Tags/Clone	4.25
Number of mapped CAGE Tag [at least 1 site]	8,825,172
Number of mapped CAGE Tag [specified 1 site]	7,151,511
Average of mapping rate	0.62
Number of CTSS	1,260,079
Number of TSS	594,136
Number of TU	39,593
Number of TU in whole genomes	50,612

(1) Contents

You can access the other pages by following the hyperlinks.

No	Column		Explanation
1	Browse	RNA Library	Go to 3.3(1) RNA Library
		CAGE Library	Go to 3.3(2) CAGE Library
2		Tissue Type	Go to 3.3(3) Tissue Type
3		Developmental Stage	Go to 3.3(4) Development Stage
4		Chromosome	Go to 3.3(5) Chromosome
5	Search	ID Search	Go to 3.4(1) ID Search
6		CAGE Library Search	Go to 3.4(2) CAGE Library Search
7		CTSS Search	Go to 3.4(3) CTSS Search
8		TSS Search	Go to 3.4(4) TSS Search
9		TU Search	Go to 3.4(5) TU Search
10	Links	Help	This manual is displayed.

(2) Genomic Information

Information about the genome assembly used in this system is shown.

No	Column	Explanation
1	Species	Target species of this system
2	Assemble Ver.	Assemble Version of the genome
3	Chromosomes	List of Number of Chromosome

(3) Current Statistics

Statistics about registered data is shown.

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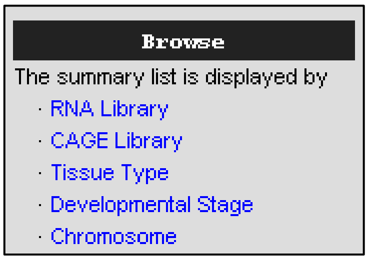
No	Column	Explanation
1	Number of CAGE Library	Number of registered CAGE Libraries
2	Number of CAGE Tissue	Number of registered Tissue Types
3	Number of CAGE Plate	Number of registered CAGE Plates
4	Number of CAGE Clone	Number of registered CAGE Clones
5	Number of CAGE Tag	Number of registered CAGE Tags
6	Average of CAGE Tags/Clone	Average of CAGE Tags/Clone
7	Number of mapped CAGE Tag [at least 1 site]	Number of registered mapped CAGE Tag [at least 1site]
8	Number of mapped CAGE Tag [specified 1 site]	Number of registered mapped CAGE Tag [specified 1site]
9	Average of mapping rate	Average of registerd mapping rate
10	Number of CTSS	Number of registered CTSS
11	Number of TSS	Number of registered TSS
12	Number of TU	Number of registered TU
13	Number of TU in whole genomes	Number of registered TU in whole genomes

3.3 Browse pages

You can see registered information by following hyperlinks in browse pages. The hyperlinks are in the left side.

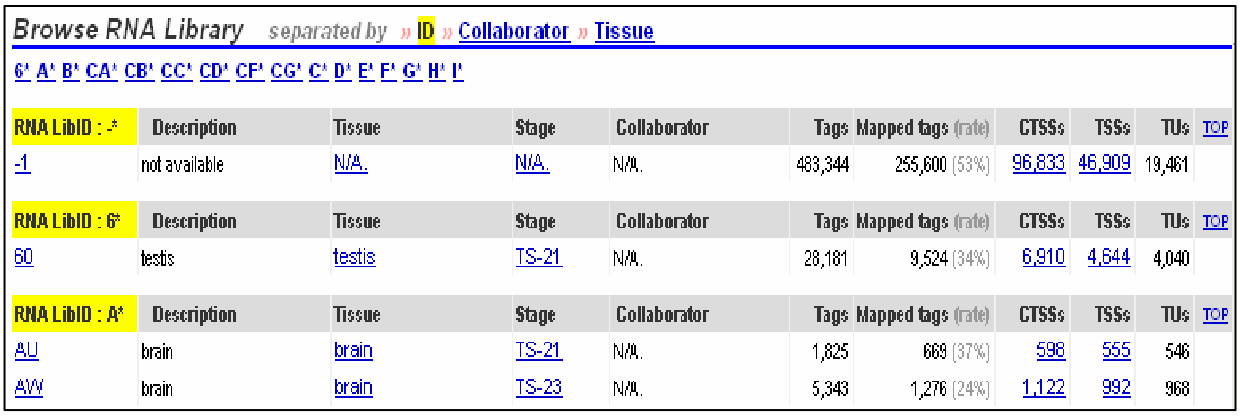

Browse

The summary list is displayed by
- RNA Library
- CAGE Library
- Tissue Type
- Developmental Stage
- Chromosome

No	Column	Link
1	RNA Library	Go to 3.3(1) RNA Library
2	CAGE Library	Go to 3.3(2) CAGE Library
3	Tissue Type	Go to 3.3(3) Tissue Type
4	Developmental Stage	Go to 3.3(4) Development Stage
5	Chromosome	Go to 3.3(5) Chromosome

(1) RNA Library

The browse page displays registered RNA Library information as a table. You can access 3.5(4)RNA Library Summary by clicking the LibraryID.


Browse RNA Library separated by » ID » Collaborator » Tissue

6* A* B* CA* CB* CC* CD* CF* CG* C* D* E* F* G* H* I*

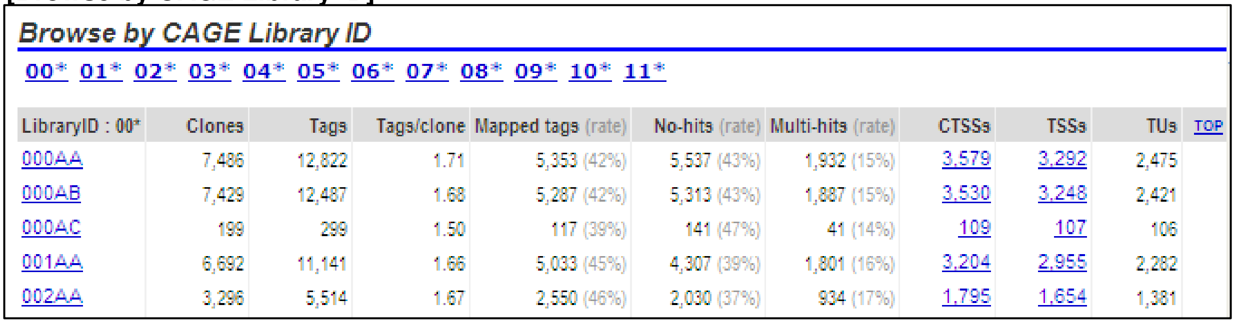
RNA LibID : -*	Description	Tissue	Stage	Collaborator	Tags	Mapped tags (rate)	CTSSs	TSSs	TUs	TOP
-1	not available	N/A.	N/A.	N/A.	483,344	255,600 (53%)	96,833	46,909	19,461	
RNA LibID : 6*	**Description**	**Tissue**	**Stage**	**Collaborator**	**Tags**	**Mapped tags (rate)**	**CTSSs**	**TSSs**	**TUs**	**TOP**
60	testis	testis	TS-21	N/A.	28,181	9,524 (34%)	6,910	4,644	4,040	
RNA LibID : A*	**Description**	**Tissue**	**Stage**	**Collaborator**	**Tags**	**Mapped tags (rate)**	**CTSSs**	**TSSs**	**TUs**	**TOP**
AU	brain	brain	TS-21	N/A.	1,825	669 (37%)	598	555	546	
AW	brain	brain	TS-23	N/A.	5,343	1,276 (24%)	1,122	992	968	

No	Column	Explanation
1	RNA LibID	RNA Library ID **Go to 3.5(4)RNA Library Summary*
2	Description	RNA Library Description
3	Tissue	Tissue name **Go to 3.5(2)Tissue Summary*
4	Stage	Theiler Stage **Go to 3.5(3)DevStage Summary*
5	Collaborator	Collaborator name
6	Tags (rate)	Number of tag
7	Mapped tags (rate)	Number of mapped tag
8	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
9	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
10	TUs	Number of TU

(2) CAGE Library

The browse page displays registered CAGE Library information as a table. You can access 3.5(1)Library Summary by clicking the LibraryID.

[Browse by CAGE Library ID]



Browse by CAGE Library ID

00* 01* 02* 03* 04* 05* 06* 07* 08* 09* 10* 11*

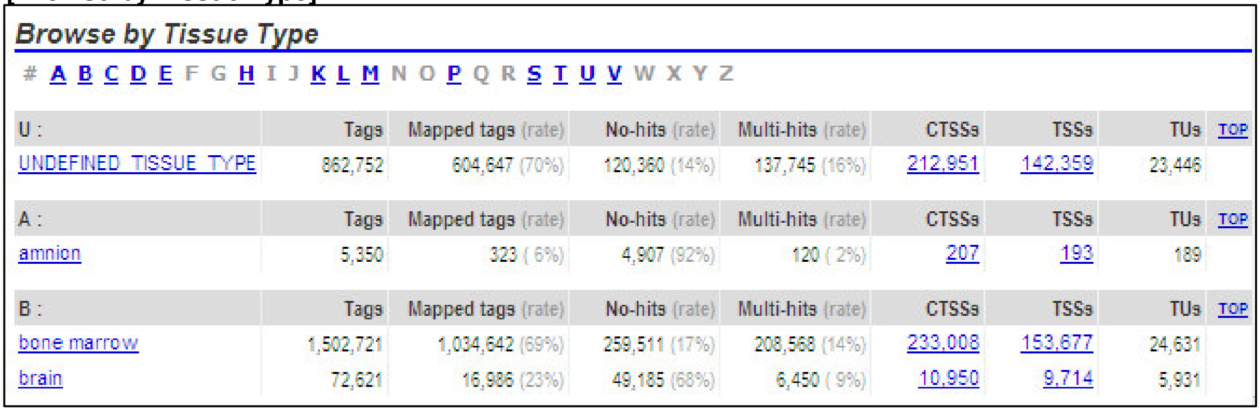
LibraryID : 00*	Clones	Tags	Tags/clone	Mapped tags (rate)	No-hits (rate)	Multi-hits (rate)	CTSSs	TSSs	TUs	TOP
000AA	7,486	12,822	1.71	5,353 (42%)	5,537 (43%)	1,932 (15%)	3,579	3,292	2,475	
000AB	7,429	12,487	1.68	5,287 (42%)	5,313 (43%)	1,887 (15%)	3,530	3,248	2,421	
000AC	199	299	1.50	117 (39%)	141 (47%)	41 (14%)	109	107	106	
001AA	6,692	11,141	1.66	5,033 (45%)	4,307 (39%)	1,801 (16%)	3,204	2,955	2,282	
002AA	3,296	5,514	1.67	2,550 (46%)	2,030 (37%)	934 (17%)	1,795	1,654	1,381	

No	Column	Explanation
1	Library ID	CAGE Library ID ** Go to 3.5(1) Library Summary*
2	Clones	Number of Clone
3	Tags	Number of Tag
4	Tags/clone	Quality (Tags/Clone)
5	Mapped tags	Number of mapped Tag
6	No-hits	Number of no-hits Tag
7	Multi-hits	Number of multi-hits Tag
8	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
9	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
10	TUs	Number of TU

(3) Tissue Type

The browse page displays information about tissue types as a table. You can access 3.5(2)Tissue Summary by clicking the tissue names.

[Browse by Tissue Type]



Browse by Tissue Type

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

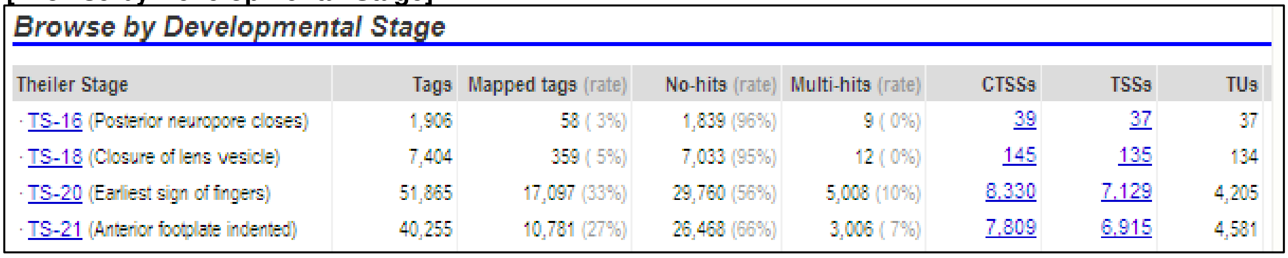
U :	Tags	Mapped tags (rate)	No-hits (rate)	Multi-hits (rate)	CTSSs	TSSs	TUs	TOP
UNDEFINED_TISSUE_TYPE	862,752	604,647 (70%)	120,360 (14%)	137,745 (16%)	212,951	142,359	23,446	
A :	Tags	Mapped tags (rate)	No-hits (rate)	Multi-hits (rate)	CTSSs	TSSs	TUs	TOP
amnion	5,350	323 (6%)	4,907 (92%)	120 (2%)	207	193	189	
B :	Tags	Mapped tags (rate)	No-hits (rate)	Multi-hits (rate)	CTSSs	TSSs	TUs	TOP
bone marrow	1,502,721	1,034,642 (69%)	259,511 (17%)	208,568 (14%)	233,008	153,677	24,631	
brain	72,621	16,986 (23%)	49,185 (68%)	6,450 (9%)	10,950	9,714	5,931	

No	Column	Explanation
1	Tissue Name	Tissue Name ** Go to 3.5(2) Tissue Summary*
2	Tags	Number of Tag
3	Mapped Tags	Number of mapped Tag
4	No-hits	Number of no-hits Tag
5	Multi-hits	Number of multi-hits Tag
6	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
7	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
8	TUs	Number of TU

(4) Development Stage

The browse page displays information about developmental stages as a table. You can access 3.5(3)DevStage Summary by clicking the Theiler stage name.

[Browse by Developmental Stage]



Browse by Developmental Stage

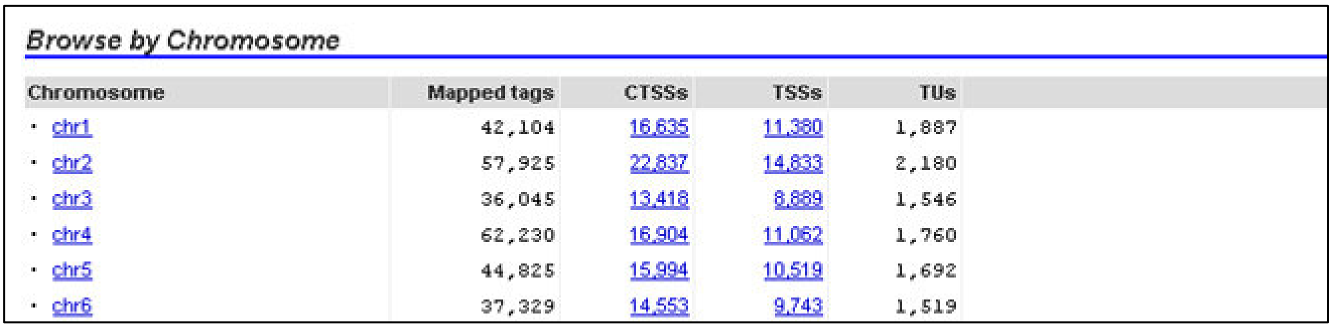
Theiler Stage	Tags	Mapped tags (rate)	No-hits (rate)	Multi-hits (rate)	CTSSs	TSSs	TUs
· TS-16 (Posterior neuropore closes)	1,906	58 (3%)	1,839 (96%)	9 (0%)	39	37	37
· TS-18 (Closure of lens vesicle)	7,404	359 (5%)	7,033 (95%)	12 (0%)	145	135	134
· TS-20 (Earliest sign of fingers)	51,865	17,097 (33%)	29,760 (56%)	5,008 (10%)	8,330	7,129	4,205
· TS-21 (Anterior footplate indented)	40,255	10,781 (27%)	26,468 (66%)	3,006 (7%)	7,809	6,915	4,581

No	Column	Explanation
1	Theiler Stage	Theiler Stage Name ** Go to 3.5(3) DevStage Summary*
2	Tags	Number of Tag
3	Mapped Tags	Number of mapped Tag
4	No-hits	Number of no-hits Tag
5	Multi-hits	Number of multi-hits Tag
6	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
7	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
8	TUs	Number of TU

(5) Chromosome

The browse page displays registered Chromosome information as a table. You can access a table of CTSSs by clicking the chromosome name.

[Browse by Chromosome]



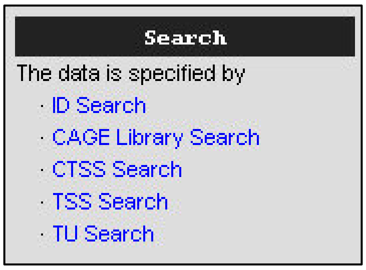
Browse by Chromosome

Chromosome	Mapped tags	CTSSs	TSSs	TUs
· chr1	42,104	16,635	11,380	1,887
· chr2	57,925	22,837	14,833	2,180
· chr3	36,045	13,418	8,889	1,546
· chr4	62,230	16,904	11,062	1,760
· chr5	44,825	15,994	10,519	1,692
· chr6	37,329	14,553	9,743	1,519

No	Column	Explanation
1	Chromosome	Number of Chromosome ** Go to 3.4(1) f) List of CTSS*
2	Mapped Tags	Number of mapped Tag
3	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
4	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
5	TUs	Number of TU

3.4 Search pages

You can search entries in some ways. The hyperlinks are in the left side.



Search

The data is specified by

- ID Search
- CAGE Library Search
- CTSS Search
- TSS Search
- TU Search

No	Column	Link
1	ID Search	Go to 3.4(1) ID Search
2	CAGE Library Search	Go to 3.4(2) CAGE Library Search
3	CTSS Search	Go to 3.4(3) CTSS Search
4	TSS Search	Go to 3.4(4) TSS Search
5	TU Search	Go to 3.4(5) TU Search

(1) ID Search

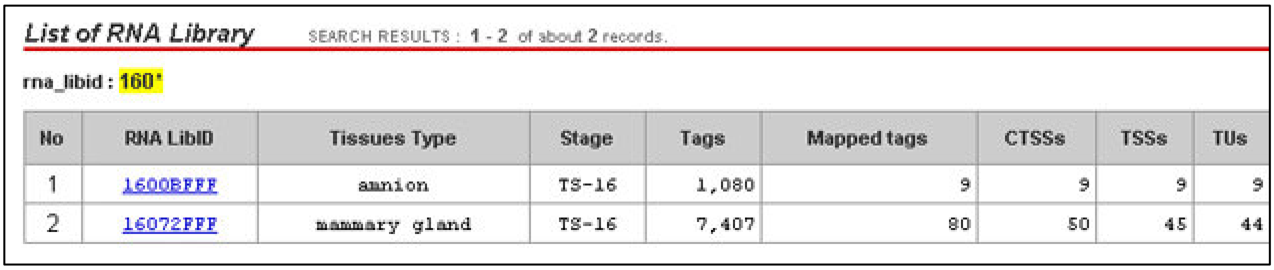
ID based search is possible from the search page. Each entry's ID is searched by prefix match with distinguishing capital and small letters.

[ID Search]

No	Contents		Explanation
1	ID Type		Selects the type of ID to search
2		RNA LibID	Go to a) List of RNA Library
3		mRNA (Gene ID)	Go to b) List of mRNA
4		Riken CloneID	Go to c) List of Riken Clone
5		CAGE CloneID	Go to d) List of CAGE Clone
6		CAGE TagID	Go to e) List of CAGE Tag
7		CTSS ID	Go to f) List of CTSS
8		TSS ID	Go to g) List of TSS
9		TU ID	Go to h) List of TU
10		Gene Symbol	Go to h) List of TU
11	ID		Inputs the ID to search

a) List of RNA Library

The search result by RNA LibraryID is shown.



List of RNA Library SEARCH RESULTS : 1 - 2 of about 2 records.

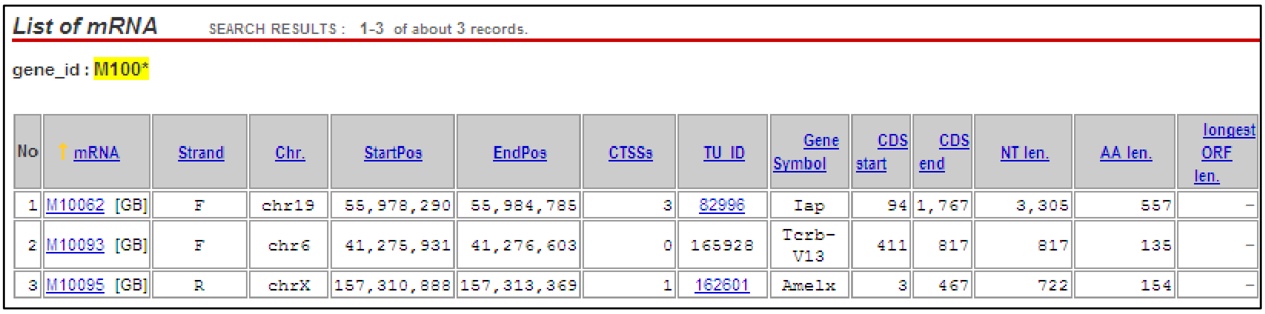
rna_libid : 160*

No	RNA LibID	Tissues Type	Stage	Tags	Mapped tags	CTSSs	TSSs	TUs
1	1600BFFF	amnion	TS-16	1,080	9	9	9	9
2	16072FFF	mammary gland	TS-16	7,407	80	50	45	44

No	Column	Explanation
1	RNA LibID	RNA Library ID ** Go to 3.5(4) RNA Library Summary*
2	Tissue Type	Tissue Type Name
3	Stage	Developmental Stage (Theiler Stage)
4	Tags	Number of Tag
5	Mapped tags	Number of Mapped tag
6	CTSSs	Number of CTSS
7	TSSs	Number of TSS
8	TUs	Number of TU

b) List of mRNA

The search result by mRNA ID (GeneID) is shown.



List of mRNA SEARCH RESULTS : 1-3 of about 3 records.

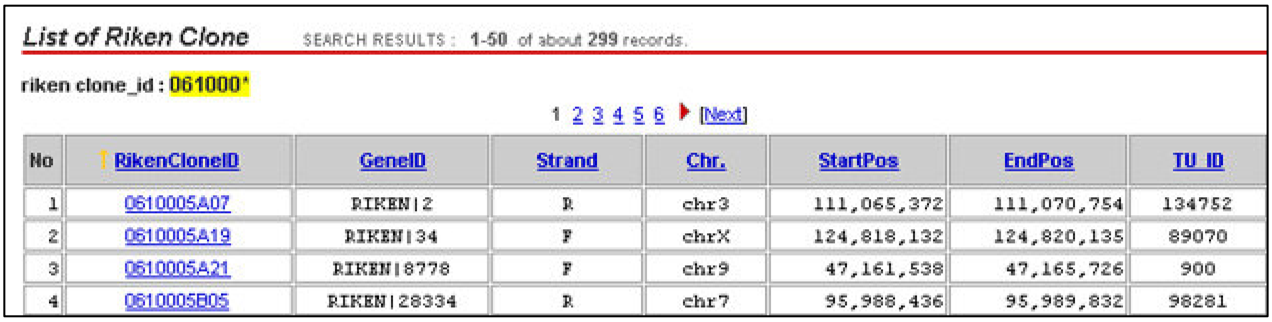
gene_id : M100*

No	mRNA	Strand	Chr.	StartPos	EndPos	CTSSs	TU ID	Gene Symbol	CDS start	CDS end	NT len.	AA len.	longest ORF len.
1	M10062 [GB]	F	chr19	55,978,290	55,984,785	3	82996	Iap	94	1,767	3,305	557	-
2	M10093 [GB]	F	chr6	41,275,931	41,276,603	0	165928	Tcrb-V13	411	817	817	135	-
3	M10095 [GB]	R	chrX	157,310,888	157,313,369	1	162601	Amelx	3	467	722	154	-

No	Column	Explanation
1	mRNA	mRNA (Gene ID) ** Go to 3.5(10) mRNA Summary*
2	Strand	Strand (F : Forward / R : Reverse)
3	Chr.	Number of Chromosome
4	Start Pos	Start Position
5	End Pos	End Position
6	CTSSs	Number of CTSS
7	TU ID	TU ID ** Go to 3.5(9) TU Summary*
8	Gene Symbol	Gene Symbol
9	CDS start	CDS Start Position
10	CDS End Pos.	CDS End Position
11	NT len.	NT Length
12	AA len.	AA Length
13	Longest ORF Len.	Longest ORF Len

c) List of Riken Clone

The search result by Riken Clone ID is shown.



List of Riken Clone SEARCH RESULTS : 1-50 of about 299 records.

riken clone_id : 061000*

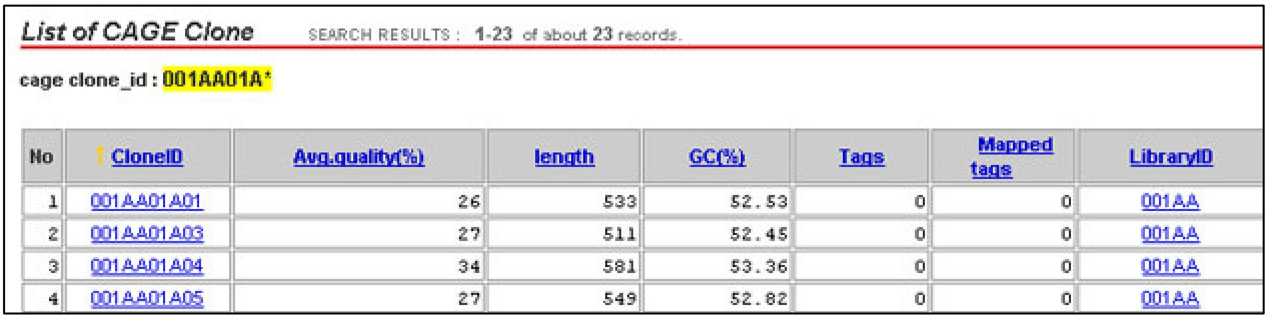
1 2 3 4 5 6 [Next]

No	RikenCloneID	GeneID	Strand	Chr.	StartPos	EndPos	TU_ID
1	0610005A07	RIKEN|2	R	chr3	111,065,372	111,070,754	134752
2	0610005A19	RIKEN|34	F	chrX	124,818,132	124,820,135	89070
3	0610005A21	RIKEN|8778	F	chr9	47,161,538	47,165,726	900
4	0610005B05	RIKEN|28334	R	chr7	95,988,436	95,989,832	98281

No	Column	Explanation
1	RikenCloneID	Riken Clone ID ** Go to 3.5(10) mRNA Summary*
2	GeneID	mRNA (Gene ID)
3	Strand	Strand (F : Forward / R : Reverse)
4	Chr.	Number of Chromosome
5	Start Pos	Start Position
6	End Pos	End Position
7	TU ID	TU ID ** Go to 3.5(9) TU Summary*

d) List of CAGE Clone

The search result by CAGE Clone ID is shown.



List of CAGE Clone SEARCH RESULTS : 1-23 of about 23 records.

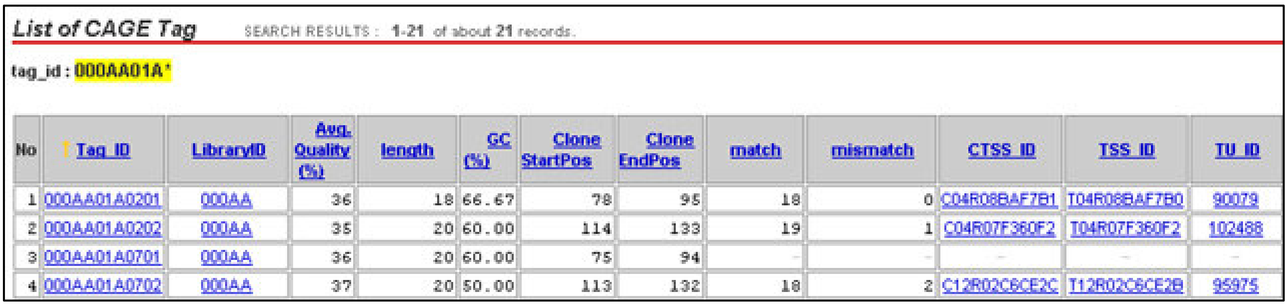
cage clone_id : 001AA01A*

No	CloneID	Avg.quality(%)	length	GC(%)	Tags	Mapped tags	LibraryID
1	001AA01A01	26	533	52.53	0	0	001AA
2	001AA01A03	27	511	52.45	0	0	001AA
3	001AA01A04	34	581	53.36	0	0	001AA
4	001AA01A05	27	549	52.82	0	0	001AA

No	Column	Explanation
1	CAGE CloneID	CAGE Clone ID ** Go to 3.5(5) CAGE Clone Summary*
2	Avg.quality (%)	Average quality value (%)
3	Length	Length of CAGE Clone
4	GC (%)	GC content (%)
5	Tags	Number of Tag
6	Mapped Tags	Number of mapped Tag on CAGE Clone
7	LibraryID	CAGE Library ID ** Go to 3.5(1) Library Summary*

e) List of CAGE Tag

The search result by CAGE Tag ID is shown.



List of CAGE Tag SEARCH RESULTS : 1-21 of about 21 records.

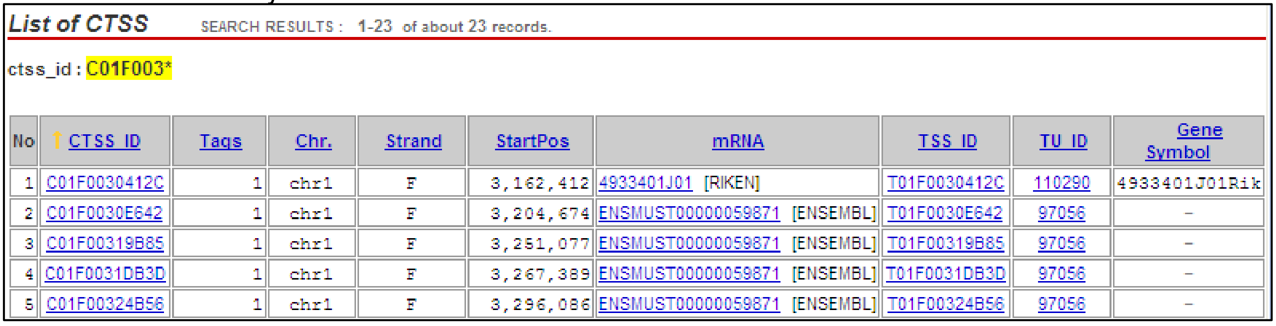
tag_id : 000AA01A*

No	Tag ID	LibraryID	Avg. Quality (%)	length	GC (%)	Clone StartPos	Clone EndPos	match	mismatch	CTSS ID	TSS ID	TU ID
1	000AA01A0201	000AA	36	18	66.67	78	95	18	0	C04R08BAF7B1	T04R08BAF7B0	90079
2	000AA01A0202	000AA	35	20	60.00	114	133	19	1	C04R07F360F2	T04R07F360F2	102488
3	000AA01A0701	000AA	36	20	60.00	75	94	-	-	-	-	-
4	000AA01A0702	000AA	37	20	50.00	113	132	18	2	C12R02C6CE2C	T12R02C6CE2B	95975

No	Column	Explanation
1	Tag ID	CAGE Tag ID ** Go to 3.5(6) CAGE Tag Summary*
2	LibraryID	CAGE Library ID ** Go to 3.5(1) Library Summary*
3	Avg.Quality (%)	Average quality value (%)
4	Length	Length of CAGE Tag
5	GC (%)	GC content (%)
6	Clone StartPos	Start Position on Clone
7	Clone EndPos	End Position on Clone
8	match	Value of match
9	mismatch	Value of mismatch
10	CTSS ID	CTSS ID ** Go to 3.5(7) CTSS Summary*
11	TSS ID	TSS ID ** Go to 3.5(8) TSS Summary*
12	TU ID	TU ID ** Go to 3.5(9) TU Summary*

f) List of CTSS

The search result by CTSS ID is shown.



List of CTSS SEARCH RESULTS : 1-23 of about 23 records.

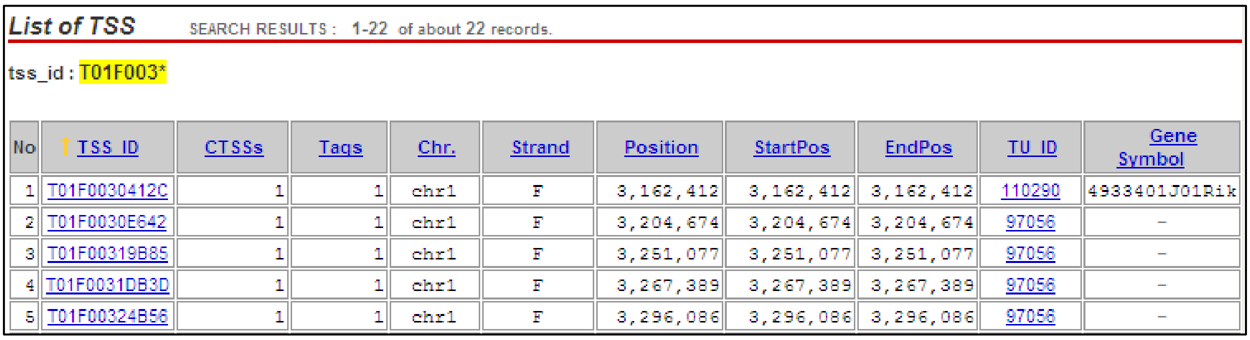
ctss_id : C01F003*

No	CTSS ID	Tags	Chr.	Strand	StartPos	mRNA	TSS ID	TU ID	Gene Symbol
1	C01F0030412C	1	chr1	F	3,162,412	4933401J01 [RIKEN]	T01F0030412C	110290	4933401J01Rik
2	C01F0030E642	1	chr1	F	3,204,674	ENSMUST00000059871 [ENSEMBL]	T01F0030E642	97056	-
3	C01F00319B85	1	chr1	F	3,251,077	ENSMUST00000059871 [ENSEMBL]	T01F00319B85	97056	-
4	C01F0031DB3D	1	chr1	F	3,267,389	ENSMUST00000059871 [ENSEMBL]	T01F0031DB3D	97056	-
5	C01F00324B56	1	chr1	F	3,296,086	ENSMUST00000059871 [ENSEMBL]	T01F00324B56	97056	-

No	Column	Explanation
1	CTSS ID	CTSS ID ** Go to 3.5(7) CTSS Summary*
2	Tags	Number of Tag
3	Chr.	Number of Chromosome
4	Strand	Strand (F : Forward / R : Reverse)
5	StartPos	Start Position
6	mRNA	mRNA (Gene ID) **Go to 3.5(10) mRNA Summary*
7	TSS ID	TSS ID ** Go to 3.5(8) TSS Summary*
8	TU ID	TU ID ** Go to 3.5(9) TU Summary*
9	Gene Symbol	Gene Symbol

g) List of TSS

The search result by TSS ID is shown.



List of TSS SEARCH RESULTS : 1-22 of about 22 records.

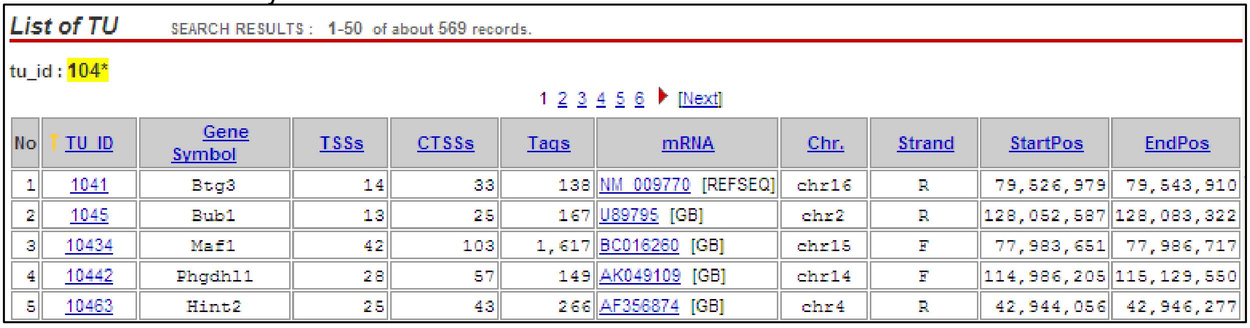
tss_id : T01F003*

No	TSS ID	CTSSs	Tags	Chr.	Strand	Position	StartPos	EndPos	TU ID	Gene Symbol
1	T01F0030412C	1	1	chr1	F	3,162,412	3,162,412	3,162,412	110290	4933401J01Rik
2	T01F0030E642	1	1	chr1	F	3,204,674	3,204,674	3,204,674	97056	-
3	T01F00319B85	1	1	chr1	F	3,251,077	3,251,077	3,251,077	97056	-
4	T01F0031DB3D	1	1	chr1	F	3,267,389	3,267,389	3,267,389	97056	-
5	T01F00324B56	1	1	chr1	F	3,296,086	3,296,086	3,296,086	97056	-

No	Column	Explanation
1	TSS ID	TSS ID ** Go to 3.5(8) TSS Summary*
2	CTSSs	Number of CTSS
3	Tags	Number of Tag
4	Chr.	Number of Chromosome
5	Strand	Strand (F : Forward / R : Reverse)
6	Position	Representative CTSS Position
7	Start Pos	TSS Start Position
8	End Pos	TSS End Position
9	TU ID	TU ID ** Go to 3.5(9) TU Summary*
10	Gene Symbol	

h) List of TU

The search result by TU ID is shown.



List of TU SEARCH RESULTS : 1-50 of about 569 records.

tu_id : 104*

No	TU ID	Gene Symbol	TSSs	CTSSs	Tags	mRNA	Chr.	Strand	StartPos	EndPos
1	1041	Btg3	14	33	138	NM_009770 [REFSEQ]	chr16	R	79,526,979	79,543,910
2	1045	Bub1	13	25	167	U89795 [GB]	chr2	R	128,052,587	128,083,322
3	10434	Maf1	42	103	1,617	BC016260 [GB]	chr15	F	77,983,651	77,986,717
4	10442	Phgdhl1	28	57	149	AK049109 [GB]	chr14	F	114,986,205	115,129,550
5	10463	Hint2	25	43	266	AF356874 [GB]	chr4	R	42,944,056	42,946,277

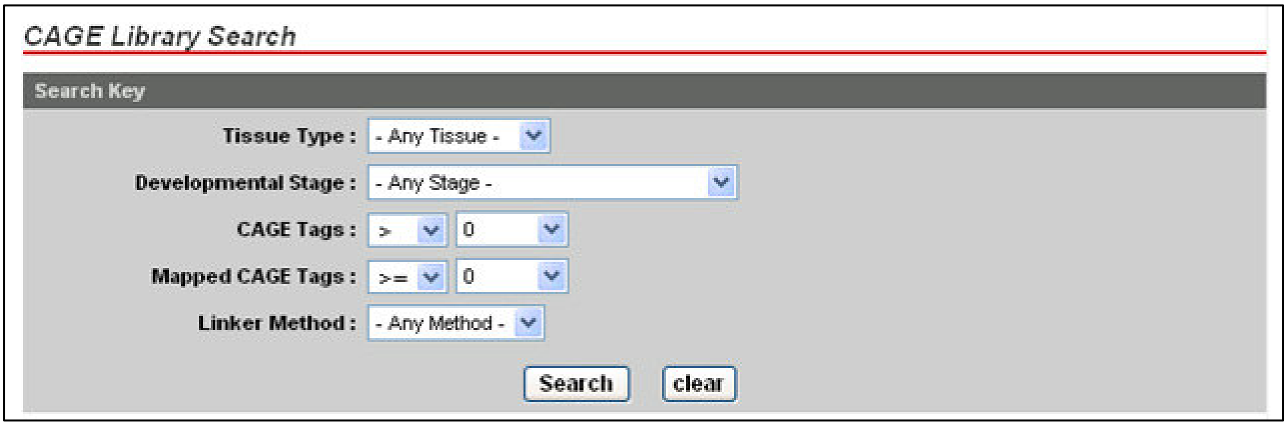
No	Column	Explanation
1	TU ID	TU ID ** Go to 3.5(9) TU Summary*
2	TSSs	Number of TSS
3	CTSSs	Number of CTSS
4	Tags	Number of Tag
5	mRNA	mRNA (Gene ID) ** Go to 3.5(10) mRNA Summary*
6	Chr.	Number of Chromosome
7	Strand	Strand (F : Forward / R : Reverse)
8	StartPos	Start Position of range of TU
9	EndPos	End Position of range of TU

(2) CAGE Library Search

Search with some conditions such as tissue type or the number of CAGE tags is possible from the search page.

** Search conditions are combined by 'AND'. 'Any" is not used as a conditions (It is the same to 'all')*

a) Search Form



CAGE Library Search

Search Key

Tissue Type : - Any Tissue -

Developmental Stage : - Any Stage -

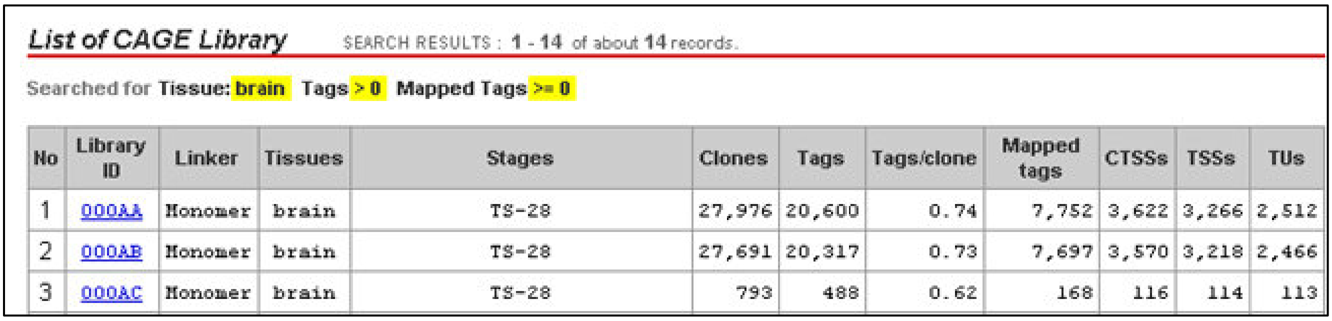
CAGE Tags : > 0

Mapped CAGE Tags : >= 0

Linker Method : - Any Method -

No	Key	Explanation
1	Tissue Type	Selects TissueType Name
2	Developmental Stage	Selects DevelopmentalStage(TheilerStage)
3	CAGE Tags	Selects the number of max or the number of min of CAGE Tag
4	Mapped CAGE Tags	Selects the number of max or the number of min of Mapped CAGE Tag
5	Linker Method	Selects LinkerMethod

b) Search Results



List of CAGE Library SEARCH RESULTS : 1 - 14 of about 14 records.

Searched for Tissue: brain Tags > 0 Mapped Tags >= 0

No	Library ID	Linker	Tissues	Stages	Clones	Tags	Tags/clone	Mapped tags	CTSSs	TSSs	TUs
1	000AA	Monomer	brain	TS-28	27,976	20,600	0.74	7,752	3,622	3,266	2,512
2	000AB	Monomer	brain	TS-28	27,691	20,317	0.73	7,697	3,570	3,218	2,466
3	000AC	Monomer	brain	TS-28	793	488	0.62	168	116	114	113

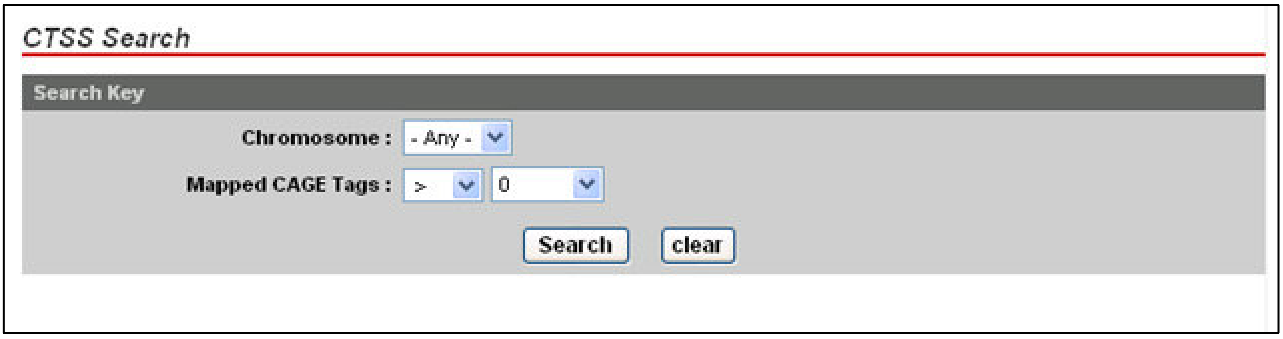
No	Column	Explanation
1	Library ID	CAGE Library ID ** Go to 3.5(1) Library Summary*
2	Linker	Linker Method Name
3	Tissues	Tissue Type Name
4	Stages	Developmental Stage(Theiler Stage) Name
5	Clones	Number of Clone
6	Tags	Number of Tag
7	Tags/clone	Qualiyt (Tags/Clone)
8	Mapped tags	Number of Mapped Tag
9	CTSSs	Number of CTSS
10	TSSs	Number of TSS
11	TUs	Number of TU

(3) CTSS Search

Search with conditions such as a chromosome number or the number of CAGE tags is possible from the search page.

** Search conditions are combined by 'AND'. 'Any' is not used as a condition (It is the same to 'all')*

a) Search Form



CTSS Search

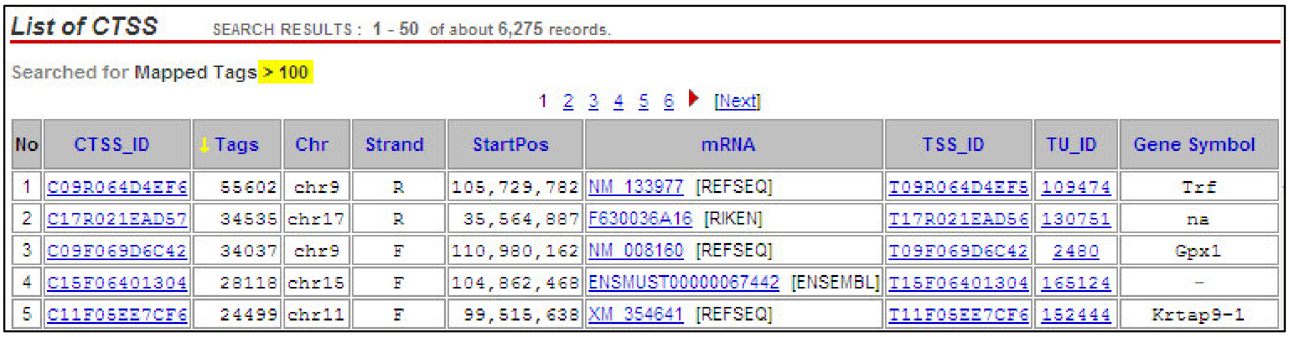
Search Key

Chromosome : - Any -

Mapped CAGE Tags : > 0

No	Search Key	Explanation
1	Chromosome	Selects the number of Chromosome (1～19,X,Y)
2	Mapped CAGE Tags	Selects the number of max or the number of min of Mapped CAGE Tag

b) Search Results



List of CTSS SEARCH RESULTS : 1 - 50 of about 6,275 records.

Searched for Mapped Tags > 100

1 2 3 4 5 6 ▶ [Next]

No	CTSS_ID	↓Tags	Chr	Strand	StartPos	mRNA	TSS_ID	TU_ID	Gene Symbol
1	C09R064D4EF6	55602	chr9	R	105,729,782	NM_133977 [REFSEQ]	T09R064D4EF5	109474	Trf
2	C17R021EAD57	34535	chr17	R	35,564,887	F630036A16 [RIKEN]	T17R021EAD56	130751	na
3	C09F069D6C42	34037	chr9	F	110,980,162	NM_008160 [REFSEQ]	T09F069D6C42	2480	Gpx1
4	C15F06401304	28118	chr15	F	104,862,468	ENSMUST00000067442 [ENSEMBL]	T15F06401304	165124	-
5	C11F05EE7CF6	24499	chr11	F	99,515,638	XM_354641 [REFSEQ]	T11F05EE7CF6	152444	Krtap9-1

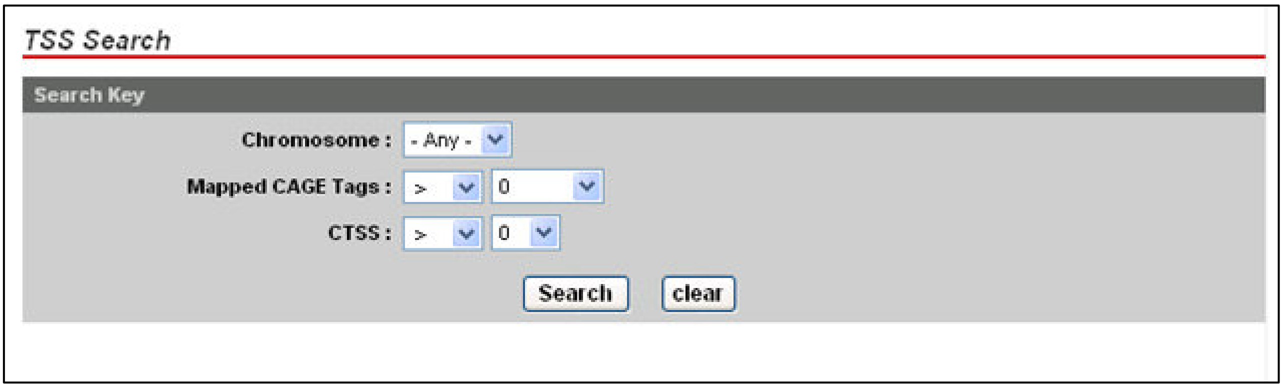
No	Column	Explanation	
1	CTSS_ID	CTSS ID	** Go to 3.5(7) CTSS Summary*
2	Tags	Number of Tag	
3	Chr.	Number of Chromosome	
4	Strand	Strand (F : Forward / R : Reverse)	
5	Start Pos	Start Position	
6	mRNA	mRNA (Gene ID)	** Go to 3.5(10) mRNA Summary*
7	TSS_ID	TSS ID	** Go to 3.5(8) TSS Summary*
8	TU _D	TU ID	** Go to 3.5(9) TU Summary*
9	Gene Symbol	Gene Symbol	

(4) TSS Search

Search with conditions such as a chromosome number or the number of CAGE tags is possible from the search page.

** Search conditions are combined by 'AND'. 'Any" is not used as a conditions (It is the same to 'all')*

a) Search Form



TSS Search

Search Key

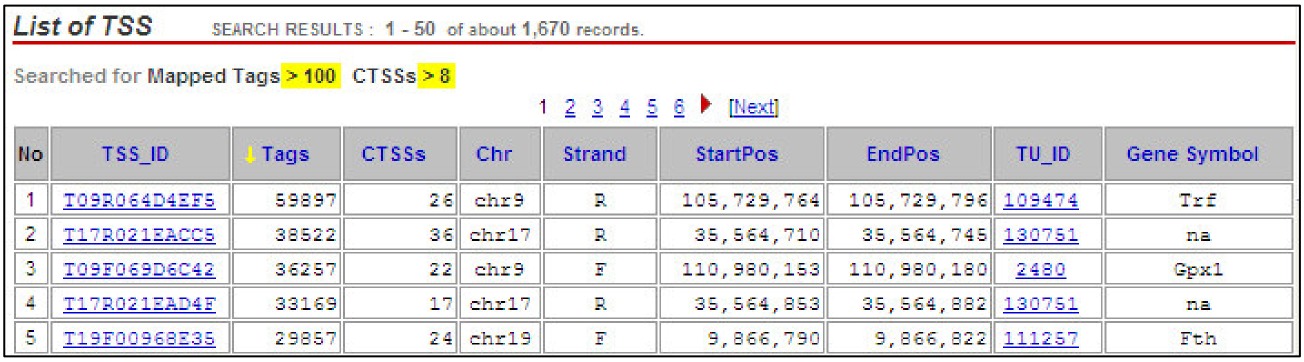
Chromosome : - Any -

Mapped CAGE Tags : > 0

CTSS : > 0

No	Search Key	Explanation
1	Chromosome	Selects the number of Chromosome (1～19,X,Y)
2	Mapped CAGE Tags	Selects the number of max or the number of min of Mapped CAGE Tag
3	CTSS	Selects the number of max or the number of min of CTSS

b) Search Results



List of TSS SEARCH RESULTS : 1 - 50 of about 1,670 records.

Searched for Mapped Tags > 100 CTSSs > 8

No	TSS_ID	Tags	CTSSs	Chr	Strand	StartPos	EndPos	TU_ID	Gene Symbol
1	T09R064D4EF5	59897	26	chr9	R	105,729,764	105,729,796	109474	Trf
2	T17R021EACC5	38522	36	chr17	R	35,564,710	35,564,745	130751	na
3	T09F069D6C42	36257	22	chr9	F	110,980,153	110,980,180	2480	Gpx1
4	T17R021EAD4F	33169	17	chr17	R	35,564,853	35,564,882	130751	na
5	T19F00968E35	29857	24	chr19	F	9,866,790	9,866,822	111257	Fth

No	Column	Explanation
1	TSS_ID	TSS ID ** Go to 3.5(8) TSS Summary*
2	Tags	Number of Tag
3	CTSSs	Number of CTSS
4	Chr	Number of Chromosome
5	Strand	Strand (F : Forward / R : Reverse)
6	StartPos	Start Position of TSS
7	EndPos	End Position of TSS
8	TU_ID	TU ID ** Go to 3.5(9) TU Summary*
9	Gene Symbol	Gene Symbol

(5) TU Search

Search with conditions such as a chromosome number or the number of CAGE tags is possible from the search page.

** Search conditions are combined by 'AND'. 'Any" is not used as a conditions (It is the same to 'all')*

a) Search Form

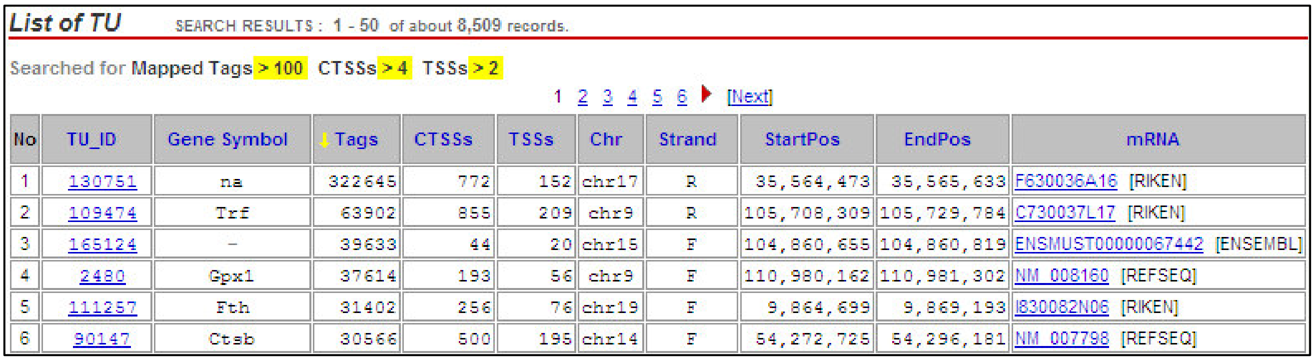
TU Search

Search Key

Chromosome :	- Any -
Mapped CAGE Tags :	> 0
CTSS :	> 0
TSS :	> 0

No	Search Key	Explanation
1	Chromosome	Selects the number of Chromosome (1～19,X,Y)
2	Mapped CAGE Tags	Selects the number of max or the number of min of Mapped CAGE Tag
3	CTSS	Selects the number of max or the number of min of CTSS
4	TSS	Selects the number of max or the number of min of TSS

b) Search Results



List of TU SEARCH RESULTS : 1 - 50 of about 8,509 records.

Searched for Mapped Tags > 100 CTSSs > 4 TSSs > 2

No	TU_ID	Gene Symbol	Tags	CTSSs	TSSs	Chr	Strand	StartPos	EndPos	mRNA
1	130751	na	322645	772	152	chr17	R	35,564,473	35,565,633	F630036A16 [RIKEN]
2	109474	Trf	63902	855	209	chr9	R	105,708,309	105,729,784	C730037L17 [RIKEN]
3	165124	-	39633	44	20	chr15	F	104,860,655	104,860,819	ENSMUST00000067442 [ENSEMBL]
4	2480	Gpx1	37614	193	56	chr9	F	110,980,162	110,981,302	NM_008160 [REFSEQ]
5	111257	Fth	31402	256	76	chr19	F	9,864,699	9,869,193	I830082N06 [RIKEN]
6	90147	Ctsb	30566	500	195	chr14	F	54,272,725	54,296,181	NM_007798 [REFSEQ]

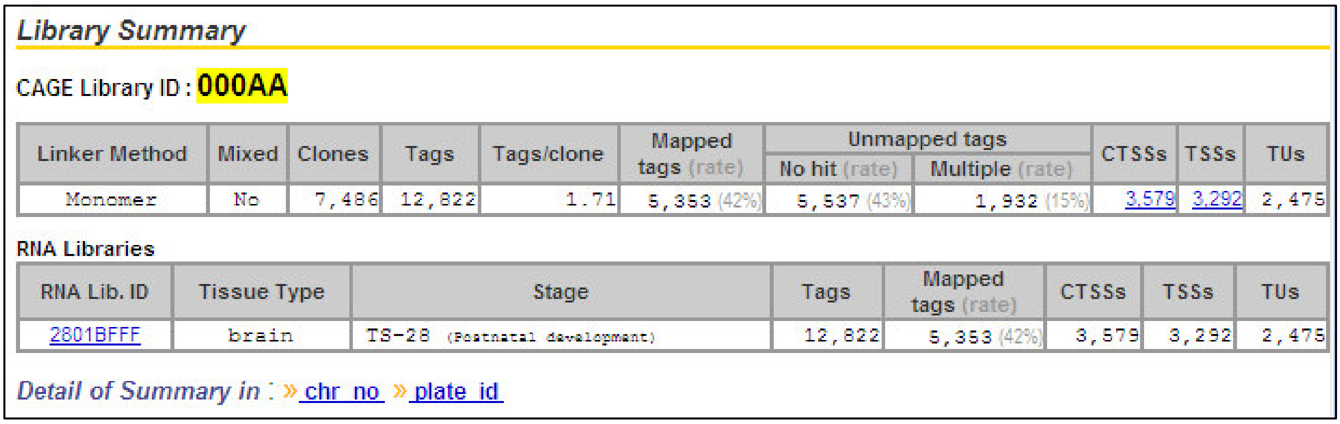
No	Column	Explanation
1	TU_ID	TU ID ** Go to 3.5(9) TU Summary*
2	Tags	Number of Tag
3	CTSSs	Number of CTSS
4	TSSs	Number of TSS
4	Chr	Number of Chromosome
5	Strand	Strand (F : Forward / R : Reverse)
6	StartPos	Start Position of TU
7	EndPos	End Position of TU
8	mRNA	mRNA (Gene ID) ** Go to 3.5(10) mRNA Summary*

3.5 Summary pages

You can see the summary of entries, which are accessible from browse and search pages.

(1) Library Summary

The summary information page about a library is shown.



Library Summary

CAGE Library ID : **000AA**

Linker Method	Mixed	Clones	Tags	Tags/clone	Mapped tags (rate)	Unmapped tags		CTSSs	TSSs	TUs
						No hit (rate)	Multiple (rate)			
Monomer	No	7,486	12,822	1.71	5,353 (42%)	5,537 (43%)	1,932 (15%)	3,579	3,292	2,475

RNA Libraries

RNA Lib. ID	Tissue Type	Stage	Tags	Mapped tags (rate)	CTSSs	TSSs	TUs
2801BFFF	brain	TS-28 (Postnatal development)	12,822	5,353 (42%)	3,579	3,292	2,475

Detail of Summary in : » chr_no » plate_id

[Library Summary]

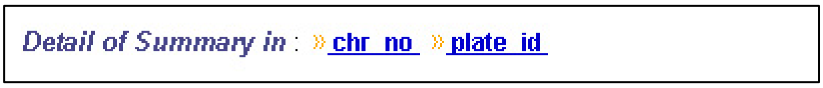
No	Column	Explanation
1	Linker Method	Linker Method Name
2	Mixed	Did it Mixed or not?
3	Clones	Number of Clone
4	Tags	Number of Tag
5	Tags/clone	Quality (Tags/Clone)
6	Mapped tags	Number of mapped Tag
7	No hit	Number of no-hits Tag
8	Multiple	Number of multi-hits Tag
9	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
10	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
11	TUs	Number of TU

[RNA Libraries]

No	Column	Explanation
1	RNA Lib.ID	RNA Library ID ** Go to 3.5(4) RNA Library Summary*
2	Tissue Type	Tissue Type Name
3	Stage	Developmental Stage (Theiler Stage) Name
4	Tags	Number of Tag
5	Mapped tags	Number of Mapped Tag
6	CTSS	Number of CTSS
7	TSS	Number of TSS
8	TU	Number of TU

[Detail of Summary in:]

You can access more detail information about the library.

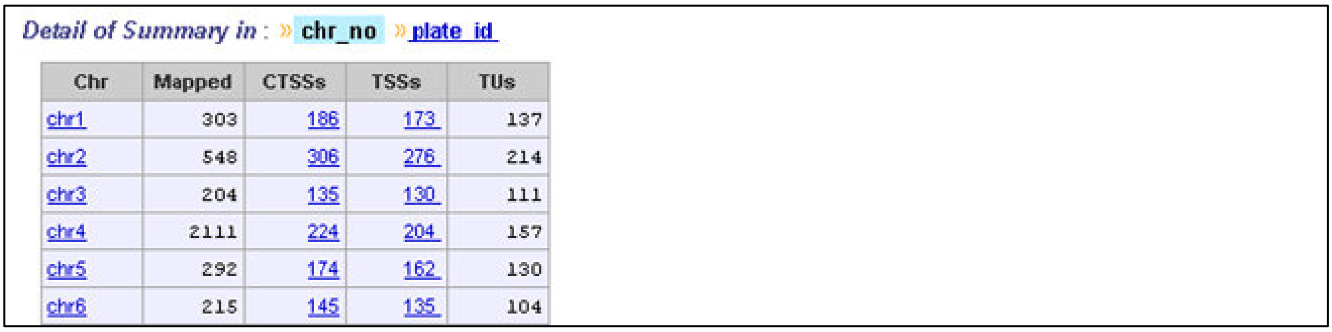


Detail of Summary in : » chr_no » plate_id

No	Column	Explanation
1	chr_no	The detailed information on a chromosome unit is shown.
2	plate_id	The detailed information on a plate unit is shown.

[Detail of Summary in: chr_no]

The detailed information per chromosome is shown.



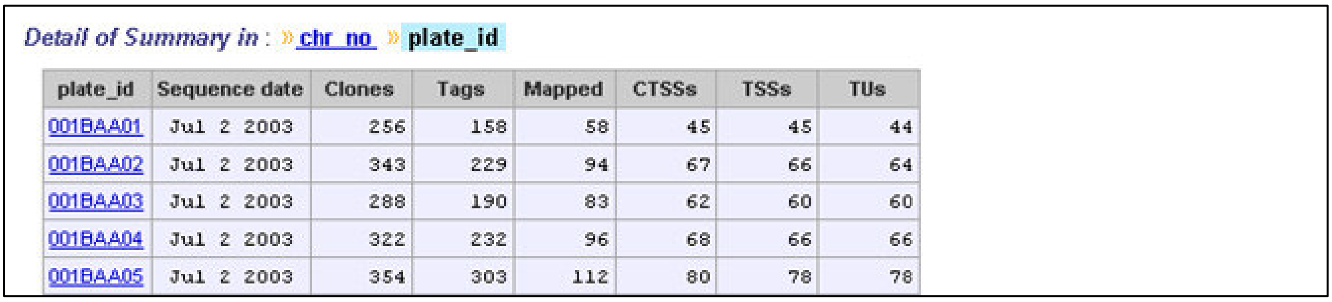
Detail of Summary in : » chr_no » plate_id

Chr	Mapped	CTSSs	TSSs	TUs
chr1	303	186	173	137
chr2	548	306	276	214
chr3	204	135	130	111
chr4	2111	224	204	157
chr5	292	174	162	130
chr6	215	145	135	104

No	Column	Explanation
1	Chr	Number of Chromosome ** Go to 3.4(1) f) List of CTSS*
2	Mapped	Number of Mapped Tag
3	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
4	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
5	TUs	Number of TU

[Detail of Summary in: plate_id]

The detailed information per plate is shown.



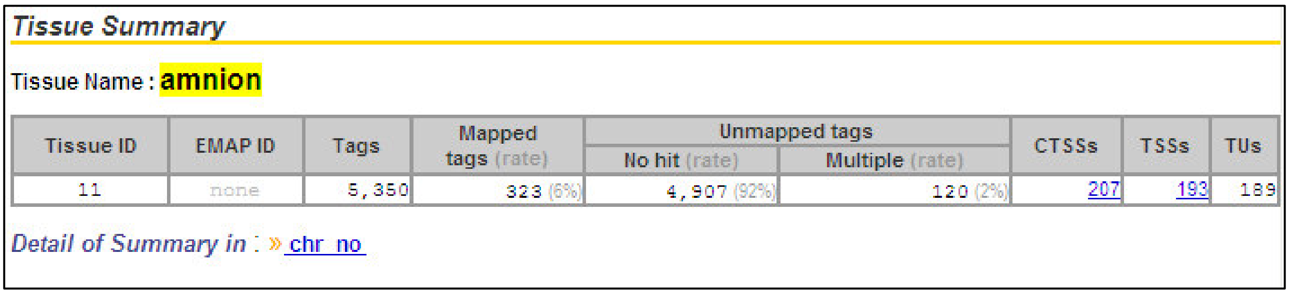
Detail of Summary in : » chr_no » plate_id

plate_id	Sequence date	Clones	Tags	Mapped	CTSSs	TSSs	TUs
001BAA01	Jul 2 2003	256	158	58	45	45	44
001BAA02	Jul 2 2003	343	229	94	67	66	64
001BAA03	Jul 2 2003	288	190	83	62	60	60
001BAA04	Jul 2 2003	322	232	96	68	66	66
001BAA05	Jul 2 2003	354	303	112	80	78	78

No	Column	Explanation
1	plate_id	Plate ID ** Go to 3.5(5) CAGE Clone Summary*
2	Sequence date	Sequence date
3	Clones	Number of Clone
4	Tags	Number of Tag
5	Mappeds	Number of Mapped Tag
6	CTSSs	Number of CTSS
7	TSSs	Number of TSS
8	TUs	Number of TU

(2) Tissue Summary

The summary information page about a tissue type is shown.



Tissue Summary

Tissue Name : **amnion**

Tissue ID	EMAP ID	Tags	Mapped tags (rate)	Unmapped tags		CTSSs	TSSs	TUs
				No hit (rate)	Multiple (rate)			
11	none	5,350	323 (6%)	4,907 (92%)	120 (2%)	207	193	189

Detail of Summary in : » chr_no

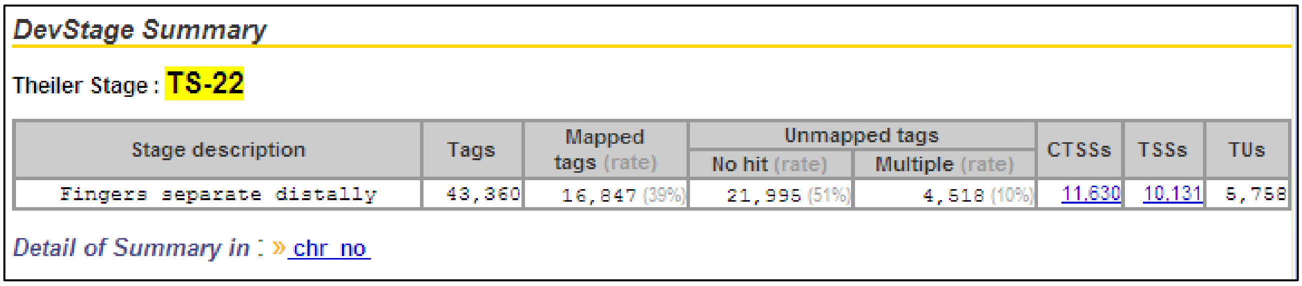
No	Column	Explanation
1	Tissue Name	Tissue Name
2	Tissue ID	Tissue ID
3	EMAP ID	EMAP ID
4	Tags	Number of Tag
5	Mapped tags	Number of Mapped Tag
6	No hit	Number of no-hits Tag
7	Multiple	Number of multi-hitsTag
8	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
9	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
10	TUs	Number of TU

[Detail of Summary in: plate_id]

The detailed information per plate is shown.

(3) DevStage Summary

The summary information page about a developmental stage is shown.



DevStage Summary

Theiler Stage : **TS-22**

Stage description	Tags	Mapped tags (rate)	Unmapped tags		CTSSs	TSSs	TUs
			No hit (rate)	Multiple (rate)			
Fingers separate distally	43,360	16,847 (39%)	21,995 (51%)	4,518 (10%)	11,630	10,131	5,758

Detail of Summary in : » chr_no

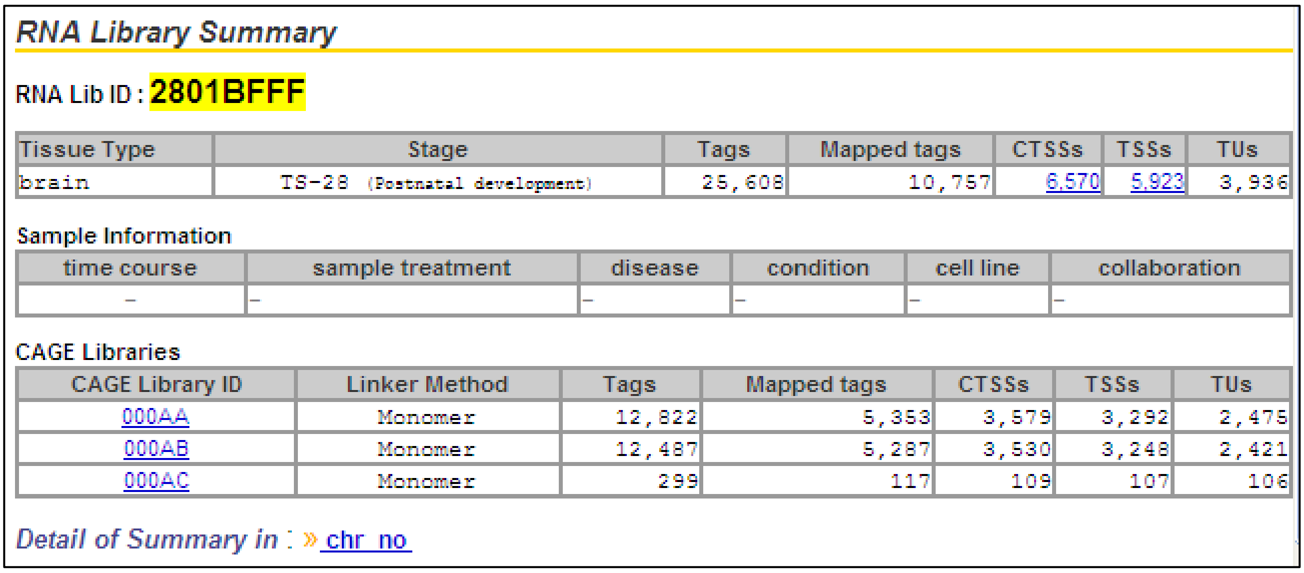
No	Column	Explanation
1	Theiler Stage	Theiler Stage Name
2	Stage description	Stage Description
3	Tags	Number of Tag
4	Mapped tags	Number of Mapped Tag
5	No hit	Number of no-hits Tag
6	Multiple	Number of multi-hits Tag
7	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
8	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
9	TUs	Number of TU

[Detail of Summary in: plate_id]

The detailed information per plate is shown.

(4) RNA Library Summary

The summary information page about a RNA library is shown.



RNA Library Summary

RNA Lib ID : 2801BFFF

Tissue Type	Stage	Tags	Mapped tags	CTSSs	TSSs	TUs
brain	TS-28 (Postnatal development)	25,608	10,757	6,570	5,923	3,936

Sample Information

time course	sample treatment	disease	condition	cell line	collaboration
–	–	–	–	–	–

CAGE Libraries

CAGE Library ID	Linker Method	Tags	Mapped tags	CTSSs	TSSs	TUs
000AA	Monomer	12,822	5,353	3,579	3,292	2,475
000AB	Monomer	12,487	5,287	3,530	3,248	2,421
000AC	Monomer	299	117	109	107	106

Detail of Summary in : » chr_no

[RNA Library Summary]

No	Column	Explanation
1	Tissue Type	Tissue Type Name
2	Stage	Developmental Stage (Theiler Stage) Name
3	Tags	Number of Tag
4	Mapped tags	Number of Mapped Tag
5	CTSSs	Number of CTSS ** Go to 3.4(1) f) List of CTSS*
6	TSSs	Number of TSS ** Go to 3.4(1) g) List of TSS*
7	TUs	Number of TU

[Sample Information] RNA Sample information is shown

No	Column	Explanation
1	Time course	Time course
2	Sample Treatment	Sample Treatment
3	Disease	Disease
4	Condition	Condition
5	Cell Type	Cell type 名
6	Collaboration	Collaboration

[CAGE Libraries]

CAGE (cDNA) Library information is shown.

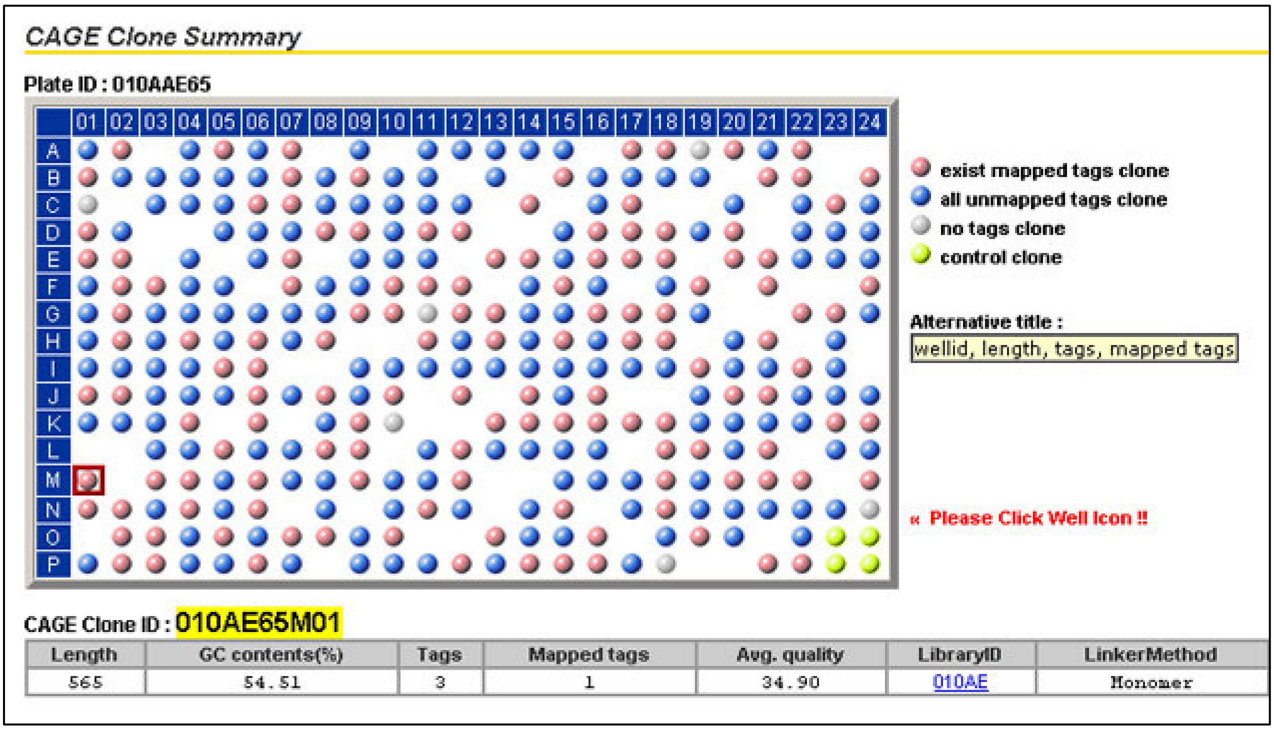
No	Column	Explanation
1	CAGE Library ID	CAGE Library ID ** Go to 3.5(1) Library Summary*
2	Linker Method	Linker Method Name
3	Tags	Number of Tag
4	Mapped tags	Number of Mapped Tag
5	CTSSs	Number of CTSS
6	TSSs	Number of TSS
7	TUs	Number of TU

[Detail of Summary in: chr_no]

* Refer to 3.5(1)Library Summary

(5) CAGE Clone Summary

The summary information page about a cage clone is shown. The image of 384 plates that the CAGE clone is sequenced is displayed.



CAGE Clone Summary

Plate ID : 010AAE65

🔴 exist mapped tags clone
🔵 all unmapped tags clone
⚪ no tags clone
🟡 control clone

Alternative title :
wellid, length, tags, mapped tags

« Please Click Well Icon !!

CAGE Clone ID : 010AE65M01

Length	GC contents(%)	Tags	Mapped tags	Avg. quality	LibraryID	LinkerMethod
565	54.51	3	1	34.90	010AE	Monomer

** A click of each Well shows corresponding CAGE Clone information.*
** If the mouse over of each Well is carried out, a title indication of the CAGE Clone information will be given.*

[CAGE Clone Summary]

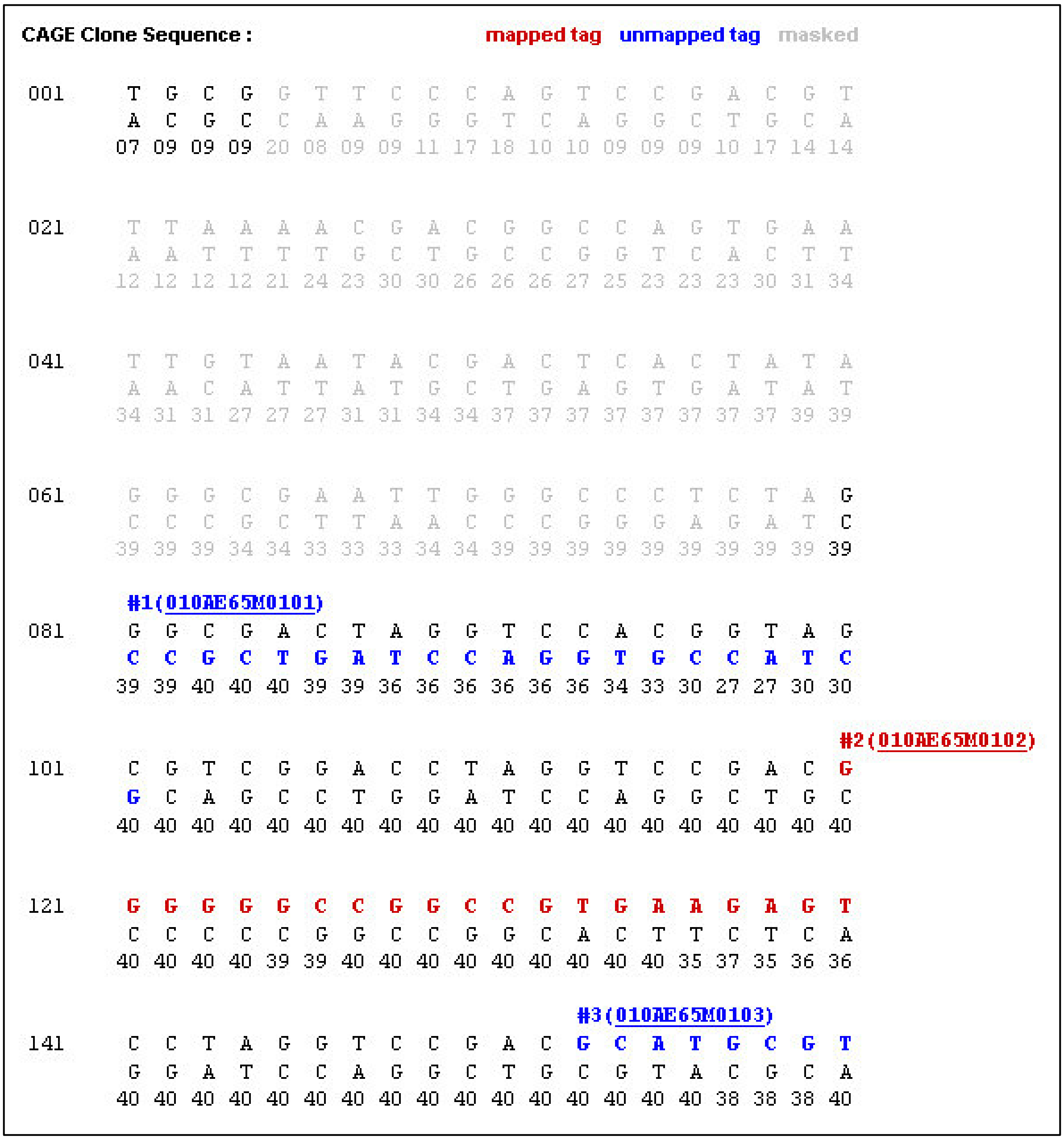
No	Image	Explanation
1	Plate ID	The plate ID with which CAGE Clone has been arranged
2	🔴	Exist mapped tags clone
3	🔵	All unmapped tags clone
4	⚪	No tags clone
5	🟡	Control clone
6	Noting Well image	Clone is not registered.

[CAGE Clone ID]

No	Column	Explanation
1	CAGE Clone ID	CAGE Clone ID
2	Length	Length of Clone
3	GC contents (%)	GC Contents (%)
4	Tags	Number of Tag
5	Mapped tags	Number of Mapped Tag
6	Avg. quality	Average Quality
7	Library ID	CAGE Library ID ** Go to 3.5(1) Library Summary*
8	Linker Method	Linker Method Name

[CAGE Clone Sequence]

CAGE Tag mapped in CAGE Clone is shown graphically.



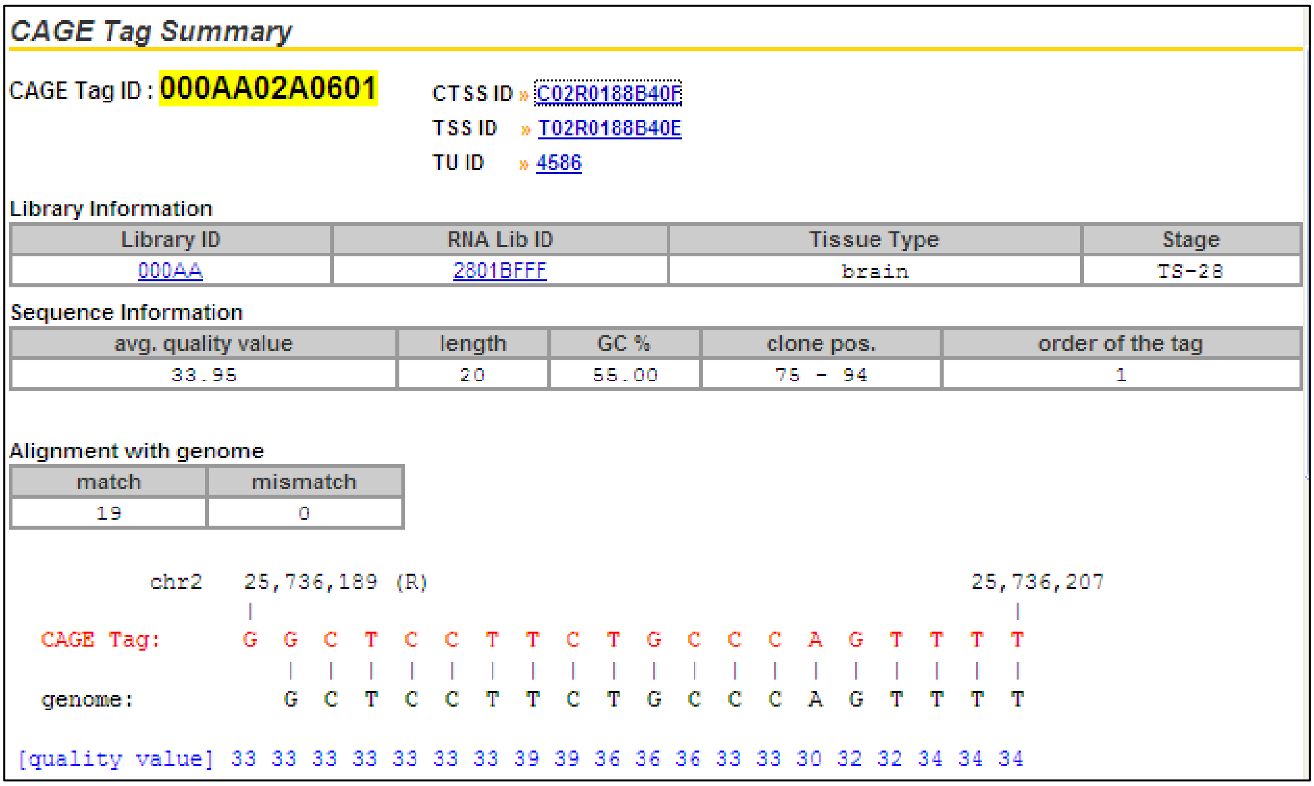
```
CAGE Clone Sequence :                      mapped tag  unmapped tag  masked

001     T  G  C  G  G  T  T  C  C  C  A  G  T  C  C  G  A  C  G  T
        A  C  G  C  C  A  A  G  G  G  T  C  A  G  G  C  T  G  C  A
        07 09 09 09 20 08 09 09 11 17 18 10 10 09 09 09 10 17 14 14

021     T  T  A  A  A  A  C  G  A  C  G  G  C  C  A  G  T  G  A  A
        A  A  T  T  T  T  G  C  T  G  C  C  G  G  T  C  A  C  T  T
        12 12 12 12 21 24 23 30 30 26 26 26 27 25 23 23 23 30 31 34

041     T  T  G  T  A  A  T  A  C  G  A  C  T  C  A  C  T  A  T  A
        A  A  C  A  T  T  A  T  G  C  T  G  A  G  T  G  A  T  A  T
        34 31 31 27 27 27 31 31 34 34 37 37 37 37 37 37 37 37 39 39

061     G  G  G  C  G  A  A  T  T  G  G  G  C  C  C  T  C  T  A  G
        C  C  C  G  C  T  T  A  A  C  C  C  G  G  G  A  G  A  T  C
        39 39 39 34 34 33 33 33 34 34 39 39 39 39 39 39 39 39 39 39

        #1(010AE65M0101)
081     G  G  C  G  A  C  T  A  G  G  T  C  C  A  C  G  G  T  A  G
        C  C  G  C  T  G  A  T  C  C  A  G  G  T  G  C  C  A  T  C
        39 39 40 40 40 39 39 36 36 36 36 36 36 34 33 30 27 27 30 30

                                                             #2(010AE65M0102)
101     C  G  T  C  G  G  A  C  C  T  A  G  G  T  C  C  G  A  C  G
        G  C  A  G  C  C  T  G  G  A  T  C  C  A  G  G  C  T  G  C
        40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40

121     G  G  G  G  G  C  C  G  G  C  C  G  T  G  A  A  G  A  G  T
        C  C  C  C  C  G  G  C  C  G  G  C  A  C  T  T  C  T  C  A
        40 40 40 40 39 39 40 40 40 40 40 40 40 40 40 35 37 35 36 36

                                            #3(010AE65M0103)
141     C  C  T  A  G  G  T  C  C  G  A  C  G  C  A  T  G  C  G  T
        G  G  A  T  C  C  A  G  G  C  T  G  C  G  T  A  C  G  C  A
        40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 40 38 38 38 40
```

Red : Mapped Tag
Blue : No mapped Tag
Gray : Masked Sequence

※ *If each Tag ID is clicked, it will go to 3.5(6) CAGE Tag Summary*

(6) CAGE Tag Summary

The summary information page about a cage tag is shown.



CAGE Tag Summary

CAGE Tag ID : 000AA02A0601

CTSS ID » C02R0188B40F
TSS ID » T02R0188B40E
TU ID » 4586

Library Information

Library ID	RNA Lib ID	Tissue Type	Stage
000AA	2801BFFF	brain	TS-28

Sequence Information

avg. quality value	length	GC %	clone pos.	order of the tag
33.95	20	55.00	75 - 94	1

Alignment with genome

match	mismatch
19	0

```
         chr2    25,736,189 (R)                                    25,736,207
                 |                                                      |
 CAGE Tag:       G  G  C  T  C  C  T  T  C  T  G  C  C  C  A  G  T  T  T  T
                    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
 genome:            G  C  T  C  C  T  T  C  T  G  C  C  C  A  G  T  T  T  T

[quality value] 33 33 33 33 33 33 33 39 39 36 36 36 33 33 30 32 32 34 34 34
```

[CAGE Tag Summary]

No	Column	Explanation
1	CAGE Tag ID	CAGE Tag ID
2	CTSS	CTSS ID ** Go to 3.5(7) CTSS Summary*
3	TSS	TSS ID ** Go to 3.5(8) TSS Summary*
4	TU	TU ID ** Go to 3.5(9) TU Summary*

[Library Information]

No	Column	Explanation
1	Library ID	CAGE Library ID ** Go to 3.5(1) Library Summary*
2	RNA Lib ID	RNA Library ID
3	Tissue Type	Tissue Type Name
4	Stage	Developmental Stage (Theiler Stage) Name

[Sequence Information]

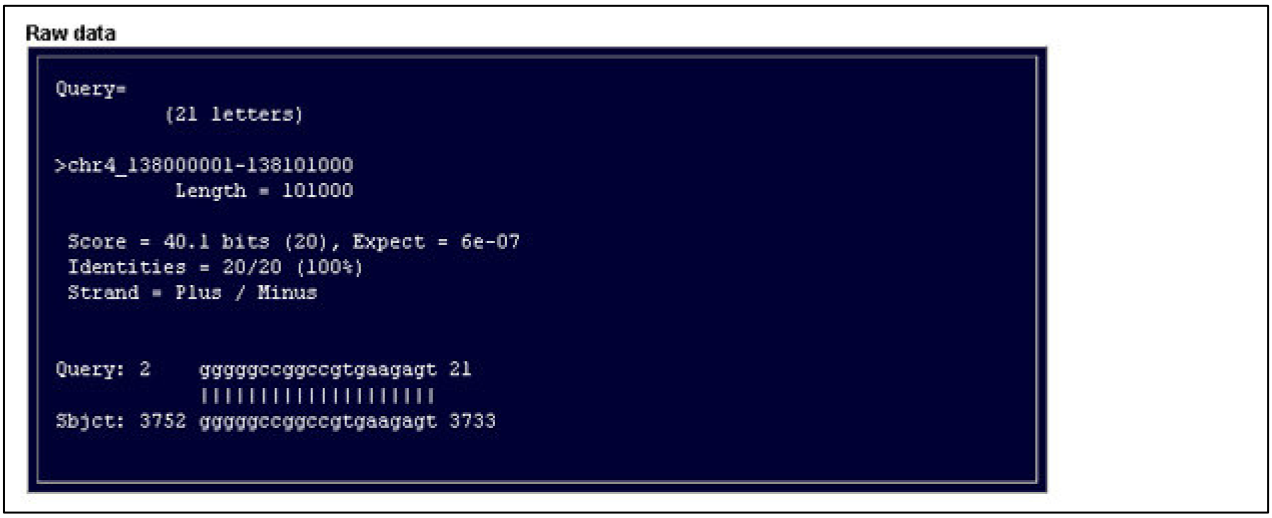
No	Column	Explanation
1	avg. quality value	Average Quality
2	length	Length of Tag
3	GC %	GC Contents (%)
4	clone pos.	Clone position (Start ~ End)
5	order of the tag	The Tag number on a clone

[Alignment with genome]

No	Column	Explanation
1	match	Value of match
2	mismatch	Value of mismatch

[Raw Data]

The result of alignment by Blast (Blastn) of the CAGE Tag and the genome is displayed.

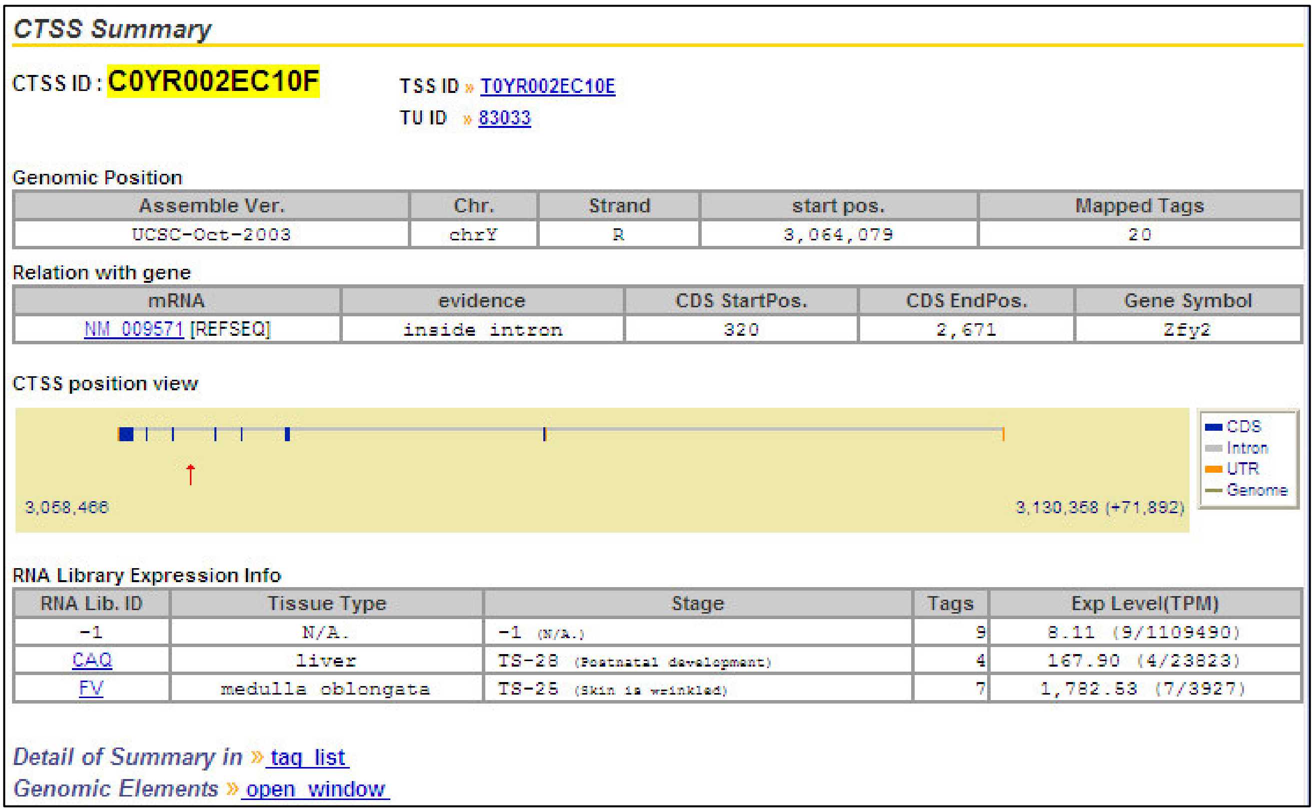


Raw data

```
Query=
         (21 letters)

>chr4_138000001-138101000
          Length = 101000

 Score = 40.1 bits (20), Expect = 6e-07
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query: 2    gggggccggccgtgaagagt 21
            ||||||||||||||||||||
Sbjct: 3752 gggggccggccgtgaagagt 3733
```

(7) CTSS Summary

The summary information page about a CTSS is shown.



CTSS Summary

CTSS ID : **C0YR002EC10F**

TSS ID » T0YR002EC10E
TU ID » 83033

Genomic Position

Assemble Ver.	Chr.	Strand	start pos.	Mapped Tags
UCSC-Oct-2003	chrY	R	3,064,079	20

Relation with gene

mRNA	evidence	CDS StartPos.	CDS EndPos.	Gene Symbol
NM_009571 [REFSEQ]	inside intron	320	2,671	Zfy2

CTSS position view

RNA Library Expression Info

RNA Lib. ID	Tissue Type	Stage	Tags	Exp Level(TPM)
-1	N/A.	-1 (N/A.)	9	8.11 (9/1109490)
CAQ	liver	TS-28 (Postnatal development)	4	167.90 (4/23823)
FV	medulla oblongata	TS-25 (Skin is wrinkled)	7	1,782.53 (7/3927)

Detail of Summary in » tag list
Genomic Elements » open window

[Genomic Position]

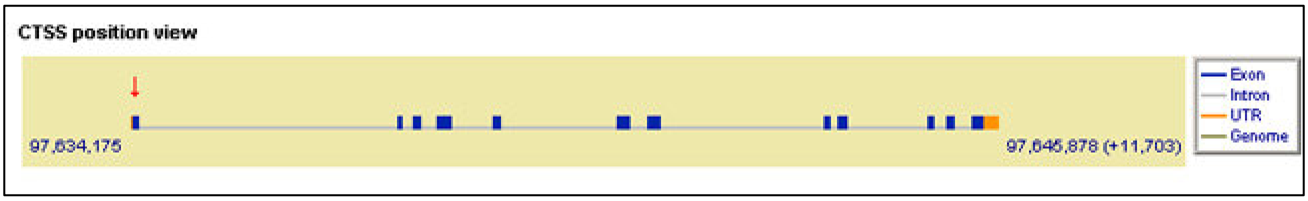
No	Column	Explanation
1	Assemble Ver.	Assemble Version.
2	Chr.	Number of Chromosome
3	Strand	Strand (F : Forward / R : Reverse)
4	start pos.	Start Position of CTSS
5	Mapped Tags	Number of Mapped Tag

[Relation with gene]

No	Column	Explanation
1	mRNA	mRNA (GeneID) ** Go to (10) mRNA Summary*
2	evidence	mRNA Evidence
3	CDS Start Pos	CDS Start Position
4	CDS End Pos	CDS End Position
5	Gene Symbol	Gene Symbol

[CTSS position view]

The position of CTSS on a clone is displayed graphically. A downward arrow(↓) indicates that it is mapped on the forward strand of the genome, and the upward arrow(↑) indicates that it is on the reverse strand.



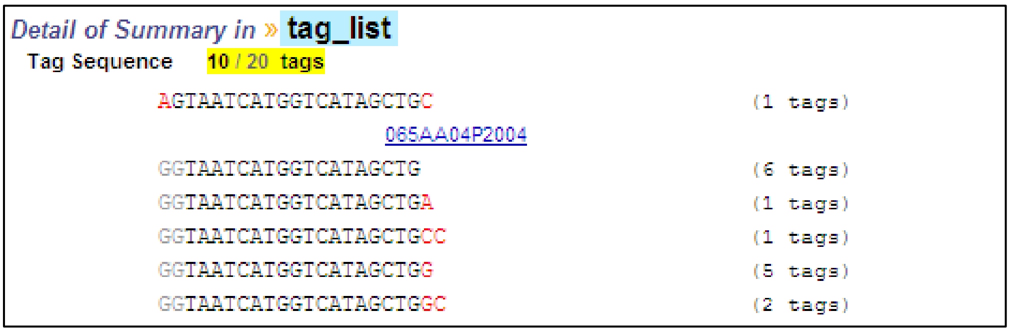
No	Color	Explanation
1	↓/↑ (Red)	The start position of CTSS and the strand of CTSS (↓: Forward /↑: Reverse)
2	■ (Blue)	Exon
3	■ (Gray)	Intron
4	■ (Orange)	UTR
5	■ (Thin brown)	Genome

[RNA Library Expression Info]

No	Column	Explanation
1	RNA Lib. ID	RNA Library ID
2	Tissue Type	Tissue Type Name
3	Stage	Developmental Stage (Theiler Stage) Name
4	Tags	The number of Tag(s) contained in RNA Library (inside of the target CTSS)
5	Exp Level(TPM)	**(Number of Tag in CTSS / Number of total tag in RNA LibID) x 1,000,000**

[Detail of Summary in : tag_list]

The list of CAGE tag with the same CTSS is displayed. If a CAGE tag ID is clicked, it will change to You can access 3.5(6) CAGE Tag Summary by clicking the CAGE tag ID.



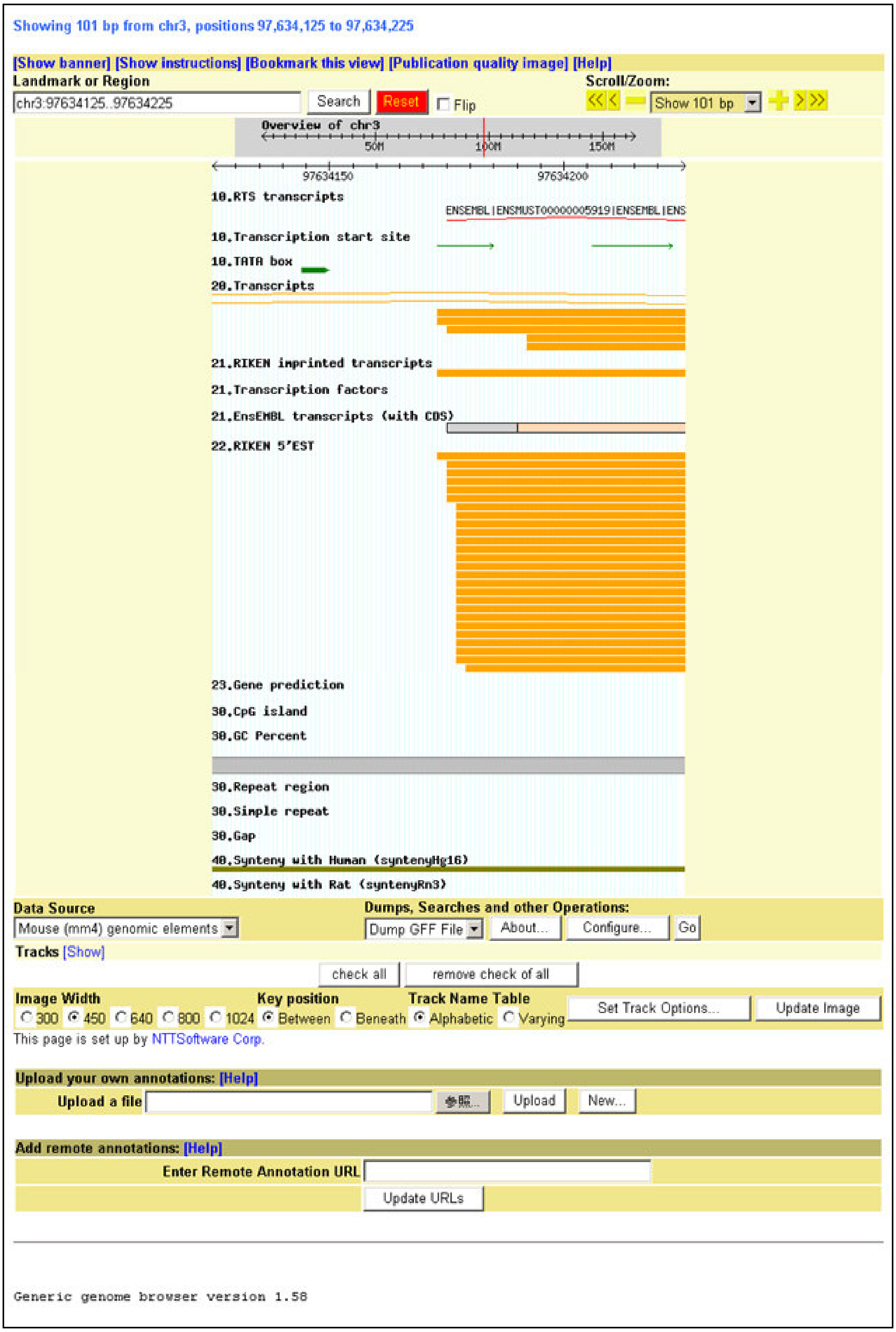
Detail of Summary in » **tag_list**

Tag Sequence 10 / 20 tags

```
AGTAATCATGGTCATAGCTGC                      (1 tags)
                  065AA04P2004
GGTAATCATGGTCATAGCTG                       (6 tags)
GGTAATCATGGTCATAGCTGA                      (1 tags)
GGTAATCATGGTCATAGCTGCC                     (1 tags)
GGTAATCATGGTCATAGCTGG                      (5 tags)
GGTAATCATGGTCATAGCTGGC                     (2 tags)
```

[Genomic Elements : show_here / open_window]

Genomic elements, such as transcripts, CpG island, etc., in neighbouring region of the CTSS are displayed graphically. 100 base regions are shown in a page as a frame or in another window. See **[Help]** for detail.



Showing 101 bp from chr3, positions 97,634,125 to 97,634,225

Landmark or Region: chr3:97634125..97634225

☐ Flip

Scroll/Zoom: Show 101 bp

Data Source: Mouse (mm4) genomic elements

Dumps, Searches and other Operations: Dump GFF File

Image Width: ○ 300 ● 450 ○ 640 ○ 800 ○ 1024

Key position: ● Between ○ Beneath

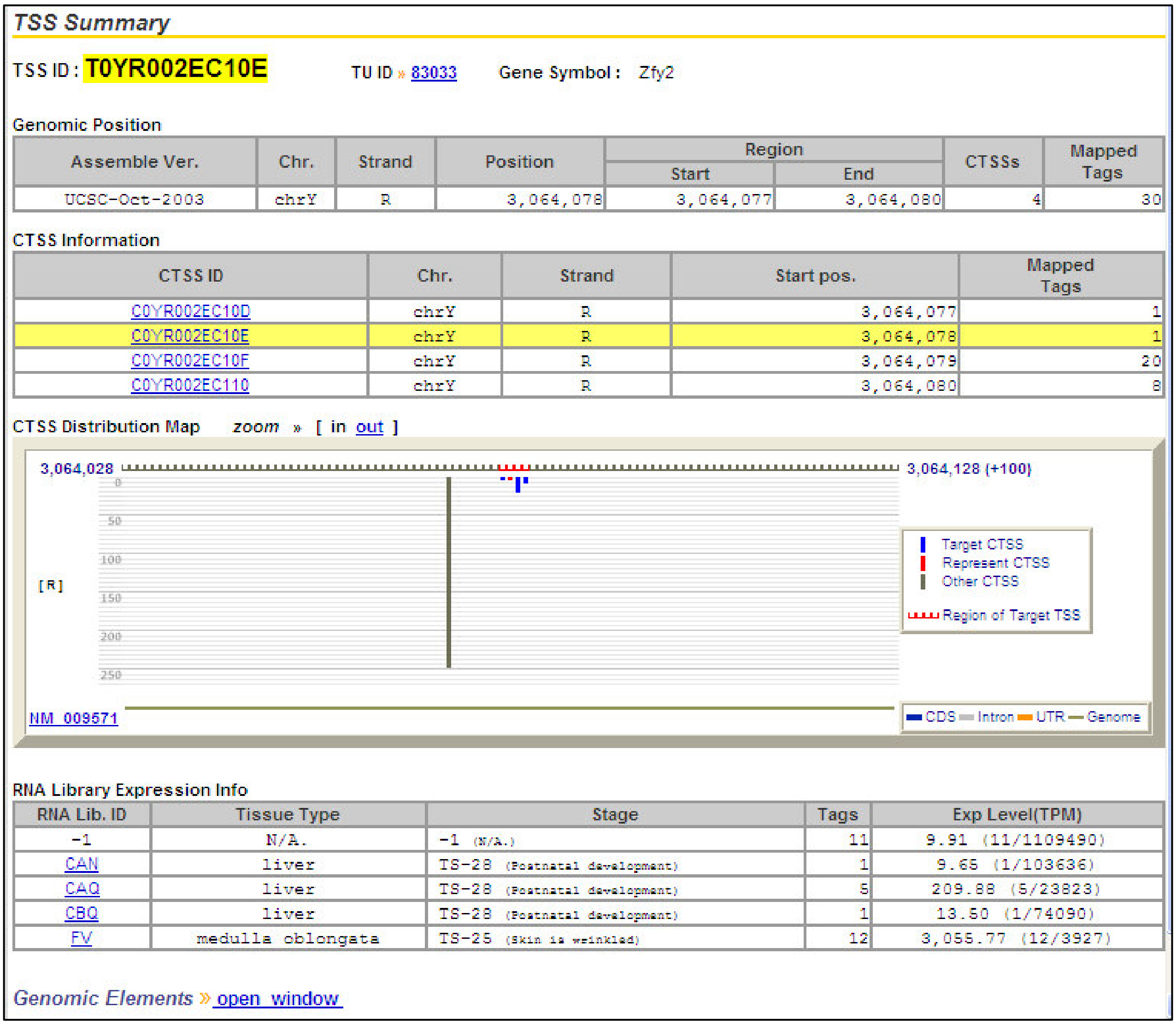
Track Name Table: ● Alphabetic ○ Varying

This page is set up by NTTSoftware Corp.

Generic genome browser version 1.58

(8) TSS Summary

The summary information page about a TSS is shown.



TSS Summary

TSS ID : **T0YR002EC10E** TU ID » 83033 Gene Symbol : Zfy2

Genomic Position

Assemble Ver.	Chr.	Strand	Position	Region		CTSSs	Mapped Tags
				Start	End		
UCSC-Oct-2003	chrY	R	3,064,078	3,064,077	3,064,080	4	30

CTSS Information

CTSS ID	Chr.	Strand	Start pos.	Mapped Tags
C0YR002EC10D	chrY	R	3,064,077	1
C0YR002EC10E	chrY	R	3,064,078	1
C0YR002EC10F	chrY	R	3,064,079	20
C0YR002EC110	chrY	R	3,064,080	8

CTSS Distribution Map *zoom* » [in out]

RNA Library Expression Info

RNA Lib. ID	Tissue Type	Stage	Tags	Exp Level(TPM)
-1	N/A.	-1 (N/A.)	11	9.91 (11/1109490)
CAN	liver	TS-28 (Postnatal development)	1	9.65 (1/103636)
CAQ	liver	TS-28 (Postnatal development)	5	209.88 (5/23823)
CBQ	liver	TS-28 (Postnatal development)	1	13.50 (1/74090)
FV	medulla oblongata	TS-25 (Skin is wrinkled)	12	3,055.77 (12/3927)

Genomic Elements » open window

[Genomic Position]

No	Column	Explanation
1	Assemble Ver.	Assemble Version.
2	Chr.	Number of Chromosome
3	Strand	Strand (F : Forward / R : Reverse)
4	Position	The position on genome of representation CTSS
5	Start	The start position on genome of TSS
6	End	The end position on genome of TSS
7	CTSSs	Number of CTSS
8	Mapped Tags	Number of mapped Tag

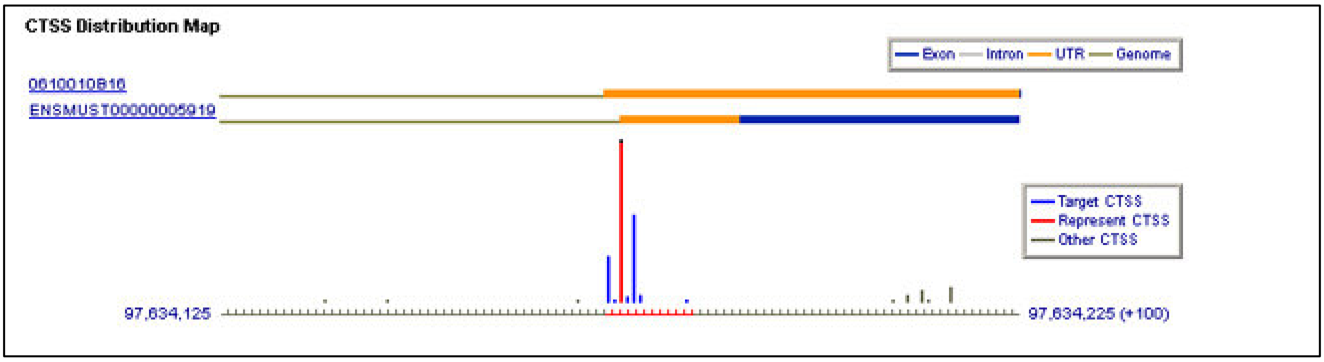
[CTSS Information]

No	Column	Explanation
1	CTSS ID	CTSS ID ** Go to 3.5(7) CTSS Summary*
2	Chr.	Number of Chromosome
3	Strand	Strand (F : Forward / R : Reverse)
4	start pos.	Start Position of CTSS
5	Mapped Tags	Number of mapped Tag

[CTSS Distribution Map]

The number of CAGE tags for each CTSS that exists in the region of the TSS is displayed graphically.

The height of a bar indicates the number of mapped tag (comparatively), and its direction (upward or downward) indicates the strand on the genome. And associated gene with the CTSS is also shown.



No	Color	Explanation
1	🟦 (Blue)	CTSS contained in the target TSS
2	🟥 (Red)	Representation CTSS in the target TSS
3	■ (Gray)	Other CTSS

[RNA Library Expression Info]

No	Column	Explanation
1	RNA Lib. ID	RNA Library ID
2	Tissue Type	Tissue Type Name
3	Stage	Developmental Stage (Theiler Stage) Name
4	Tags	The number of Tag(s) contained in RNA Library (inside of the target TSS)
5	Exp Level(TPM)	**(Number of Tag in TSS / Number of total tag in RNA LibID) x 1,000,000**

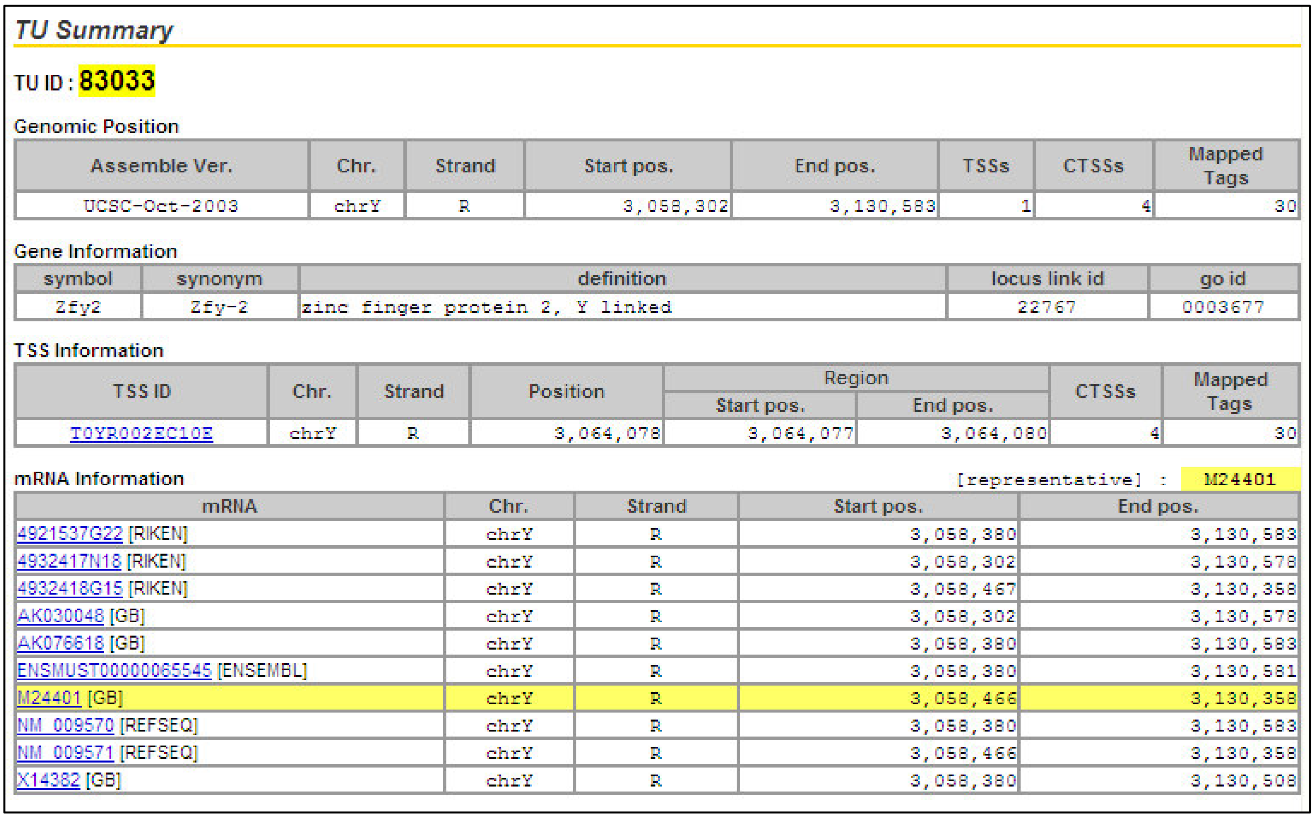
[Genomic Elements : show_here / open_window]

Genomic elements in neighbouring region of the TSS are displayed graphically. 100 base regions are shown in a page as a frame or in another window.

** Refer to 3.5(7)CTSS Summary [Genomic Elements:show_here / open_window]*

(9) TU Summary

The summary information page about a TU is shown.



TU Summary

TU ID : 83033

Genomic Position

Assemble Ver.	Chr.	Strand	Start pos.	End pos.	TSSs	CTSSs	Mapped Tags
UCSC-Oct-2003	chrY	R	3,058,302	3,130,583	1	4	30

Gene Information

symbol	synonym	definition	locus link id	go id
Zfy2	Zfy-2	zinc finger protein 2, Y linked	22767	0003677

TSS Information

TSS ID	Chr.	Strand	Position	Region		CTSSs	Mapped Tags
				Start pos.	End pos.		
T0YR002EC10E	chrY	R	3,064,078	3,064,077	3,064,080	4	30

mRNA Information [representative] : M24401

mRNA	Chr.	Strand	Start pos.	End pos.
4921537G22 [RIKEN]	chrY	R	3,058,380	3,130,583
4932417N18 [RIKEN]	chrY	R	3,058,302	3,130,578
4932418G15 [RIKEN]	chrY	R	3,058,467	3,130,358
AK030048 [GB]	chrY	R	3,058,302	3,130,578
AK076618 [GB]	chrY	R	3,058,380	3,130,583
ENSMUST00000065545 [ENSEMBL]	chrY	R	3,058,380	3,130,581
M24401 [GB]	chrY	R	3,058,466	3,130,358
NM_009570 [REFSEQ]	chrY	R	3,058,380	3,130,583
NM_009571 [REFSEQ]	chrY	R	3,058,466	3,130,358
X14382 [GB]	chrY	R	3,058,380	3,130,508

[Genomic Position]

No	Column	Explanation
1	Assemble Ver.	Assemble Version.
2	Chr.	Number of Chromosome
3	Strand	Strand (F : Forward / R : Reverse)
4	Start Pos.	Start position on genome of TU
5	End Pos.	End position on genome of TU
6	TSSs	Number of TSS
7	CTSSs	Number of CTSS
8	Mapped Tags	Number of mapped Tag

[Gene Information]

No	Column	Explanation
1	Symbol	Gene Symbol
2	Synonym	Gene Symbol Synonym
3	Definition	Definition
4	Locus link id.	Locus link id
5	Go id	Go id

[TSS Information]

No	Column	Explanation
1	TSS ID	TSS ID ** Go to 3.5(8) TSS Summary*
2	Chr.	Number of Chromosome
3	Strand	Strand (F : Forward / R : Reverse)
4	Position	Start position on genome of representation CTSS of TSS
5	Start Pos.	Start position on genome of TSS
6	End Pos.	End position on genome of TSS
8	CTSSs	Number of CTSS
9	Mapped Tags	Number of mapped Tag

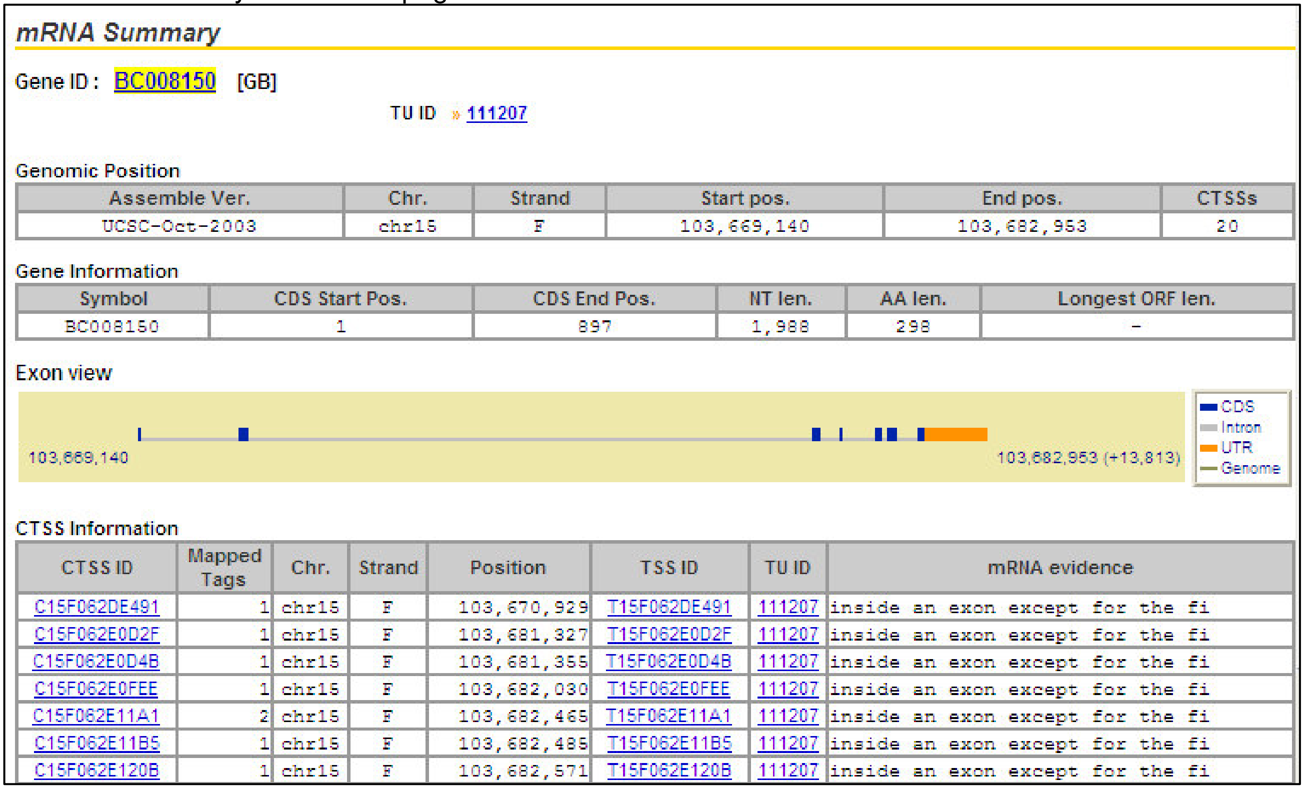
[mRNA Information]

The list of mRNA (Gene) contained in TU is shown.

No	Column	Explanation
1	mRNA	Gene ID ** Go to (10) mRNA Summary*
2	Chr.	Number of Chromosome
3	strand	Strand (F : Forward / R : Reverse)
4	start pos.	Start position on genome of Gene
5	end pos.	End position on genome on Gene

(10) mRNA Summary

The summary information page about a mRNA is shown.



mRNA Summary

Gene ID : BC008150 [GB]

TU ID » 111207

Genomic Position

Assemble Ver.	Chr.	Strand	Start pos.	End pos.	CTSSs
UCSC-Oct-2003	chr15	F	103,669,140	103,682,953	20

Gene Information

Symbol	CDS Start Pos.	CDS End Pos.	NT len.	AA len.	Longest ORF len.
BC008150	1	897	1,988	298	-

Exon view

CTSS Information

CTSS ID	Mapped Tags	Chr.	Strand	Position	TSS ID	TU ID	mRNA evidence
C15F062DE491	1	chr15	F	103,670,929	T15F062DE491	111207	inside an exon except for the fi
C15F062E0D2F	1	chr15	F	103,681,327	T15F062E0D2F	111207	inside an exon except for the fi
C15F062E0D4B	1	chr15	F	103,681,355	T15F062E0D4B	111207	inside an exon except for the fi
C15F062E0FEE	1	chr15	F	103,682,030	T15F062E0FEE	111207	inside an exon except for the fi
C15F062E11A1	2	chr15	F	103,682,465	T15F062E11A1	111207	inside an exon except for the fi
C15F062E11B5	1	chr15	F	103,682,485	T15F062E11B5	111207	inside an exon except for the fi
C15F062E120B	1	chr15	F	103,682,571	T15F062E120B	111207	inside an exon except for the fi

[Genomic Position]

No	Column	Explanation
1	Assemble Ver.	Assemble Version.
2	Chr.	Chromosome Number
3	Strand	Strand (F : Forward / R : Reverse)
4	Start Pos.	Start Position
5	End Pos.	End Position
6	CTSSs	Number of CTSS

[Gene Information]

No	Column	Explanation
1	Symbol	Gene Symbol
2	CDS Start Pos	CDS Start Position
3	CDS End Pos	CDS End Position
4	NT Len.	NT Length
5	AA Len.	AA Length
6	Longest ORF Len.	Longest ORF Length

[Exon view]

The CDS position of mRNA is displayed graphically.

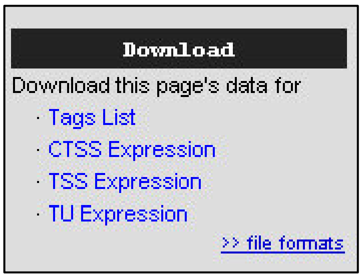
No	Color	Explanation
1	🟦（Blue）	CDS
2	■（Gray）	Intron
3	🟧（Orange）	UTR
4	🟫（Thin brown)）	Genome

[CTSS Information]

No	Column	Explanation
1	CTSS ID	CTSS ID ** 3.5(7) CTSS Summary へ遷移します。*
2	Mapped Tags	Number of Mapped Tag
3	Chr.	Chromosome Number
4	Strand	Strand (F : Forward / R : Reverse)
5	Position	Start Position
6	TSS ID	TSS ID ** 3.5(8) TSS Summary へ遷移します。*
7	TU ID	TU ID ** 3.5(9) TU Summary へ遷移します。*
8	mRNA evidence	mRNA Evidence

3.6 Download pages

You can download some kinds of data related with the entry from the summary pages. Hyperlinks appear when you can download it.



Download

Download this page's data for

- Tags List
- CTSS Expression
- TSS Expression
- TU Expression

>> file formats

No	Column	Link
1	Tags List	3.6(1)Tags List
2	CTSS Expression	3.6(2)CTSS Expression
3	TSS Expression	3.6(3)TSS Expression
4	TU Expression	3.6(4)TU Expression
5	file formats	Download Data Format is shown

(1) Tags List

You can download a list of CAGE tags with their related information.

[Download Data Format]

1. CAGE tag ID
2. CAGE tag sequence
3. The length of the tag
4. An average of the CAGE tag's quality value
5. GC% of the CAGE tag
6. The number of capped 'G'
7. CAGE clone ID
8. The length of the clone
9. An average of the CAGE clone's quality value
10. GC% of the CAGE clone
11. The order of the CAGE tag on the clone
12. The number of CAGE tags on the clone
13. Orientation of the CAGE tag (F: forward / R: Reverse)
14. Start position of the CAGE tag
15. End position of the CAGE tag
16. cDNA library ID
17. RNA library ID
18. Taxonomy ID
19. Tissue ID
20. Stage ID
21. Start position of CAGE tags in the alignment of mapping
22. End position of CAGE tags in the alignment of mapping
23. Chromosome Number
24. Strand
25. Start position of chromosome sequence in the alignment of mapping
26. End position of chromosome sequence in the alignment of mapping
27. The number of aligned bases (# of matched base pairs)
28. The number of gapped bases
29. CTSS ID
30. related mRNA sequence
31. related TU
32. TSS ID

(2) CTSS Expression

You can download a list of CTSSs, their expression counts, and their related information.

[Download Data Format]

1. CTSS ID
2. Taxonomy ID
3. Genome assemble version of CTSS
4. Chromosome Number of CTSS
5. Strand of CTSS
6. Position on the Chromosome of CTSS
7. related mRNA
8. mRNA relation evidence
9. related TU
10. TSS ID
11. Representative position on the Chromosome of TSS
12. Start position on the Chromosome of TSS covering region
13. End position on the Chromosome of TSS covering region
14. TSS evidence
15. The number of CAGE tags
16. RNA library ID
17. Tissue ID
18. Stage ID

(3) TSS Expression

You can download a list of TSSs, their expression counts, and their related information.

[Download Data Format]

1. TSS ID
2. Taxonomy ID
3. Genome assemble version of TSS
4. Chromosome Number of TSS
5. Strand of TSS
6. Representative Position on the Chromosome of TSS
7. Start position on the Chromosome of TSS covering region
8. End position on the Chromosome of TSS covering region
9. TSS evidence
10. related TU
11. The number of CAGE tags
12. The number of CTSS
13. RNA library ID
14. Tissue ID
15. Stage ID

(4) TU Expression

You can download a list of TUs, their expression counts, and their related information.

[Download Data Format]

1. TU ID
2. Taxonomy ID
3. Genome assemble version of TU
4. Representative mRNA
5. Chromosome Number of representative mRNA
6. Strand of representative mRNA
7. Start Position on the Chromosome of representative mRNA
8. End Position on the Chromosome of representative mRNA
9. The number of CAGE tags
10. The number of CTSS
11. The number of TSS
12. RNA library ID
13. Tissue ID
14. Stage ID