

# Protocol for the usage of the F344 & LE Rat BAC browser

※ This protocol has been partially modified from the report by Mitsubishi Research Institute, Inc.

## Annotation of “F344 & LE Rat BAC browser”

- Gene structure
- Gene structure on the genome sequence provided by NCBI Map Viewer
- Gene structure on the genome sequence provided by Ensembl
- Mapping results of BAC end sequences
- Mapping results of F344/Stm and LE/Stm BAC clones to the rat genome sequence
- SNP rates derived from the BAC end sequences
- SNP rates calculated from F344/Stm and LE/Stm BAC clone mapping
- Repeat sequences
- Repeat sequence information provided by UCSC Genome Browser
- G+C contents and CpG islands
- G+C contents and CpG islands of the rat genome sequence

## 【Top page】

The chromosome number can be selected on the upper left corner of the ‘Top page’, or by clicking on the chromosome diagram (Fig.1) to open the ‘Map page’ (discussed later, Fig.2 and 3). Keyword search is also supported and described later in detail.

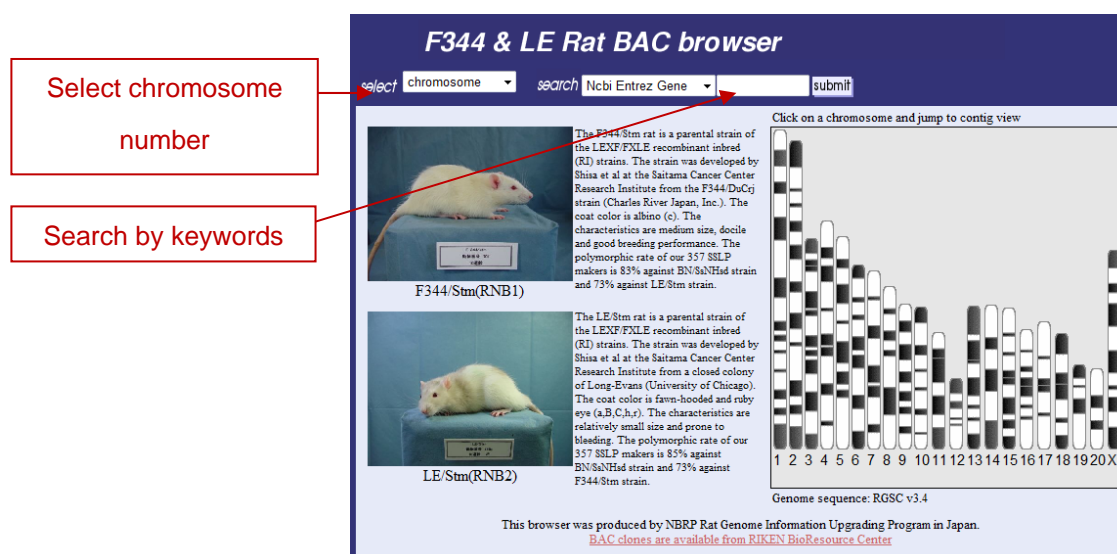


Fig. 1 Top page of F344 & LE Rat BAC browser

## 【Map page】

On the upper side of this page, the SNP rate of LE/Stm BAC library (RNB1) and F344/Stm BAC library (RNB2) is shown along with the diagram of the selected chromosome. On the right corner, there is the scaling button and the display range button. On the lower side of this page, the selected annotation tracks are displayed. Dragging your mouse exchanges each annotation tracks. By clicking the track button on the left side of the top displays the submenu of track setting (Fig.4). Mouseover on the gene structure displays the link to the original site. Clicking the BAC end bar displays the link to their information page (discussed later, Fig.5).

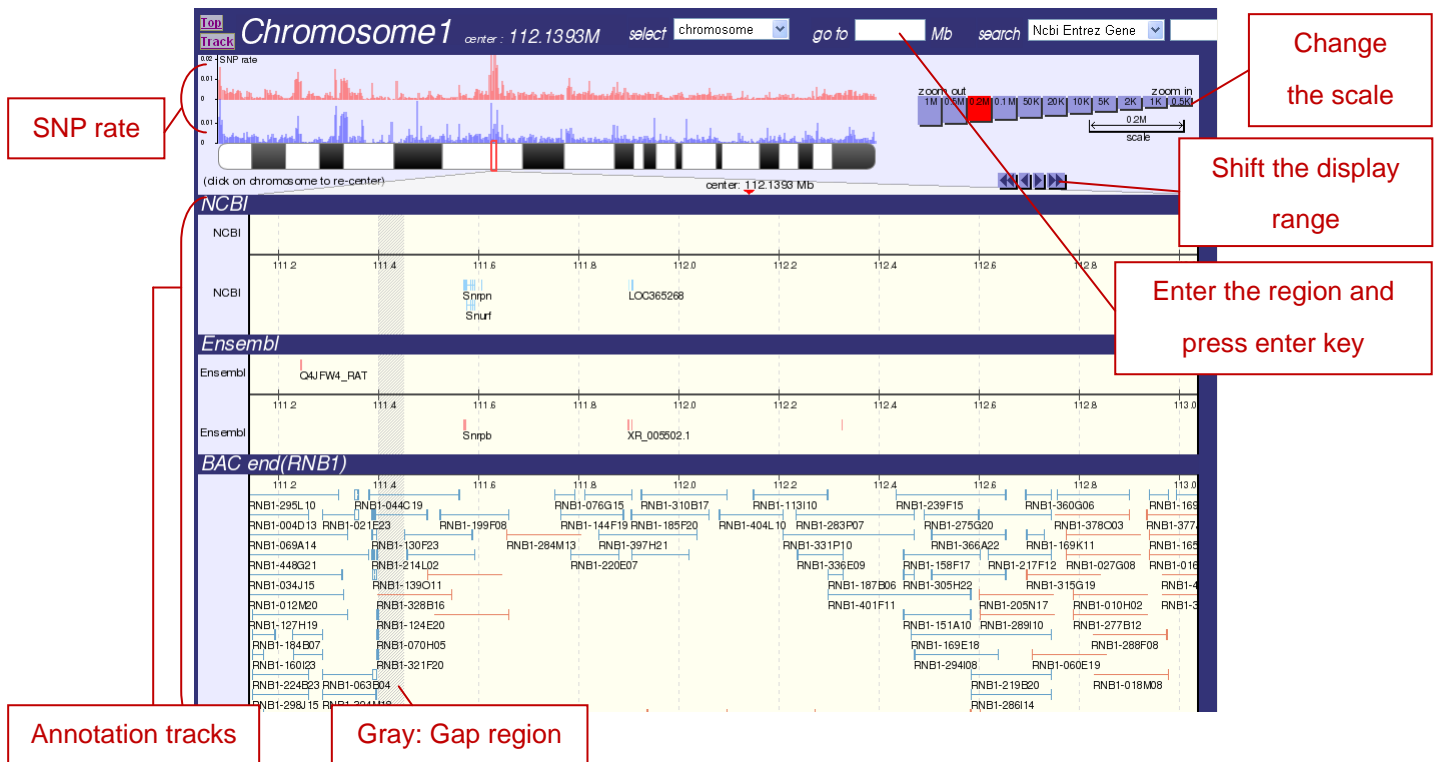


Fig. 2 Map page



Fig.3 Map page

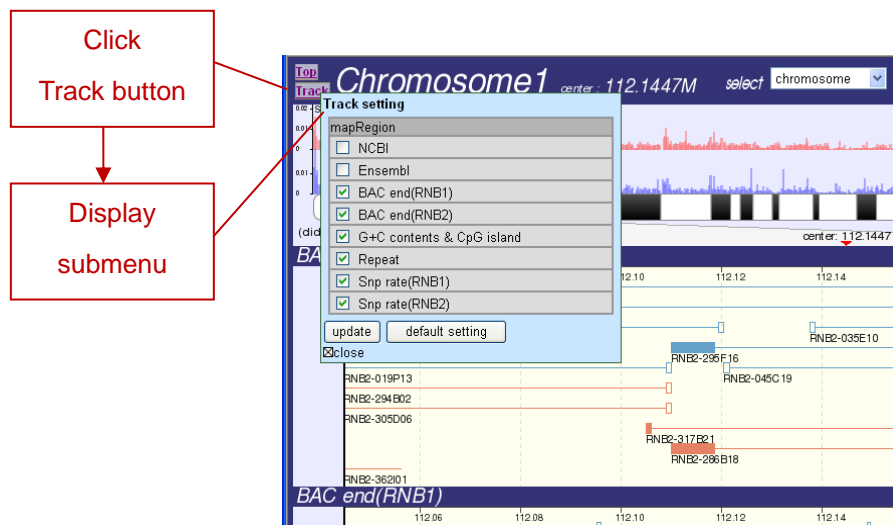


Fig.4 Track setting submenu of 'Map page'

### 【BAC end information page】

In this page (Fig.5), the internal ID, DDBJ ID, mapping position and alignment results are displayed.

**BAC end information of RNB2-019P13**

**Information of forward sequence (DDBJ: FT013301)**

Chromosome	1	position(base)	111906315 - 111907453	strand	+
chr. 1 (length: 267910886 base)					
[ jump to map ]					
Alignment					
seq1:	chr1_111906315_111907453				
seq2:	RNB2-019P13_b_1_1127				
seq1	ATACCAGAAACATGAAACCACTGGAGAGTGCAGCCTTCATCAGACTGG	50			
seq2	ATACCAGAAACATGAAACCACTGGAGAGTGCAGCCTTCATCAGACTGG	50			
seq1	GGGATAGGCCCTTGAAGAGCCCGGGTGTCTTCATGTTGTAACACTTGC	100			
seq2	GGGACAGGCCCTTGAAGAGCCCGGGTGTCTTCATGTTGTAACACTTGC	100			
seq1	CGGGCAGGTCCAAAGAGCCCTGTAGCTCCGAACCTTGGCCAAAAGCAGA	150			
seq2	CGGGCAGGTCCAAAGAGCCCTGTAGCTCCGAACCTTGGCCAAAAGCAGA	149			
seq1	TCGGCATATTCAAAACCCCGCACTGCAGGTGATCTTGAAGAGGTCCA	200			
seq2	TCGGCATATTCAAAACCCCGCACTGCAGGTGATCTTGAAGAGGTCCA	199			
seq1	GGGGATACGTAAAGGCTTGTGATCACTCCAGATCCACAGCCCAAAAGC	250			
seq2	GGGGATACGTAAAGGCTTGTGATCACTCCAGATCCACAGCCCAAAAGC	249			
seq1	AGGTTTTTAAGGTTCCCTGTTTGTCTTCTGTCTGGTGCATGACCCAGTC	300			
seq2	AGGTTTTTAAGGTTCCCTGTTTGTCTTCTGTCTGGTGCATGACCCAGTC	299			
seq1	ATAGGTGGGTTTCAAGGAACGGTAGCAGAACTGCAAGCCCGGTACGGGA	350			
seq2	ATAGGTGGGTTTCAAGGAACGGTAGCAGAACTGCAAGCCCGGTACGGGA	349			
seq1	AGATGGCGATCAGTGGGAGTCAAGCCTTTGTAGAAGACAAAGGGGCC	400			
seq2	AGATGGCGATCAGTGGGAGTCAAGCCTTTGTAGAAGACAAAGGGGCC	399			
seq1	TCGGTCTATACATGGTATTATAGCCTCTGCGAGATTGGGCTCCCCCTG	450			
seq2	TCGGTCTATACATGGTATTATAGCCTCTGCGAGATTGGGCTCCCCCTG	449			

**Information of reverse sequence (DDBJ: FT013302)**

Chromosome	1	position(base)	112108976 - 112110018	strand	-
chr. 1 (length: 267910886 base)					
[ jump to map ]					
Alignment					
seq1:	chr1_112108976_112110018				
seq2:	RNB2-019P13_g_1_1034 (reverse)				
seq1	ACTTTTTTCAAATAATGTTAACTAGTAATAAGCAATGGTTTCTCCACAG	50			
seq2	ACTTTTTTCAAATAATGTTAACTAGTAATAAGCAATGATTCT-CACAG	47			
seq1	GACACTATAGTCAGACAAGTACATTGTCAGTCCAGATTGGGTTGTCTA	100			
seq2	GACACTATAGTCAGACAAGTACATTGTCAGTCCAGATTGGGTTGTCTA	94			
seq1	CTTTGAATTTACTTTCCAGAGAATTCGCATACAGTCCATCCATTACAAA	150			
seq2	CTTTG-ATTTACTTTCCAGAGAA-TCCGATACAGTCCATCCATTACAAA	142			
seq1	CCTTCTCGTTACACACAGAAATTTGAGAGTAAGACCCATTGCTTAGGT	200			
seq2	-CATCTCGG-TAOCACAGAAATTTGAGAGTAAGACCCATTGCTTAGGT	190			
seq1	AAACACATGGGTAGGTCAAAGAACAGAGTGAATGTATCAAGCATTGACCA	250			
seq2	AAACACATGGGTAGGTCAAAGAACAGAGTGAATGTATCAAGCATTGACCA	240			
seq1	ATAAGCTTGATTCTACTGTGTTCCCTAGTGGATAGCTTTCATAGTACCAG	300			
seq2	ATAAGCTTGATTCTACTGTGTTCCCTAGTGGATAGCTTTCATAGTACCAG	290			
seq1	AATATATGAAGCAGGCTACTGCAGAAAGTATAATCAACACTTCATCAA	350			
seq2	ACTAAATGAAGCAGGCTACTGCAGAAAGTATAATCAACACTTCATCAA	340			
seq1	GCCTGGAATACTTCTGCAATGAATACTTCTGATACAGTGAATGAACTG	400			
seq2	GCTTGGAAATACTTCTGCAATGAATACTTCTGATACAGTGAATGAACTG	390			
seq1	CCTATCATGAGAAATACCAACA-TTTTAGTTGAATTTGAGTCCCAAAAT	449			
seq2	CCTATCATGAGAAATACCAACA-TTTTAGTTGAATTTGAGTCCCAAAAT	448			

Fig.5 BAC end information page

### 【Search by keywords】

Keyword search is supported at 'Top page' or 'Map page'. Examples are listed below.

- Gene structure
  - ID of NCBI Entrez Gene
  - Gene symbol of NCBI Entrez Gene
  - Gene name of NCBI Entrez Gene
  - Annotation number of NCBI RefSeq
  - Gene ID of Ensembl
  - Transcript ID of Ensembl
  - Gene symbol of Ensembl
  - Gene name of Ensembl

- BAC end sequence
  - Internal ID of BAC end sequence
  - DDBJ ID of BAC end sequence

As results of the keyword search, annotation data are listed with additional information, such as gene information, chromosomal position, ID, accession number, etc. Each annotation of BAC end links to the detail information page.

**Search results** search

Your keyword is "RNB2".  
 A Keyword search against "Bac end internal ID" was performed.  
 The keyword hits more than 300! Top 300 hits are shown.  
 Try again with another keyword.

map	gene information	chr.	posi.	Internal ID	DDBJ ID
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	15	75.27M	RNB2-001A02(forward)	FT000003
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	15	75.07M	RNB2-001A02(reverse)	FT000004
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	10	74.48M	RNB2-001A03(forward)	FT000005
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	10	74.51M	RNB2-001A03(reverse)	FT000006
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	7	10.85M	RNB2-001A04(forward)	FT000007
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	7	11.02M	RNB2-001A04(reverse)	FT000008
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	12	46.20M	RNB2-001A07(forward)	FT000013
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	12	46.01M	RNB2-001A07(reverse)	FT000014
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	18	72.34M	RNB2-001A08(forward)	FT000015
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	18	72.31M	RNB2-001A08(reverse)	FT000016
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	14	79.77M	RNB2-001A10(forward)	FT000019
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	14	79.57M	RNB2-001A10(reverse)	FT000020
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	6	144.37M	RNB2-001A12(forward)	FT000023
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	6	144.46M	RNB2-001A12(reverse)	FT000024
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	5	76.86M	RNB2-001A14(forward)	FT000027
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	5	77.04M	RNB2-001A14(reverse)	FT000028
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	15	1.80M	RNB2-001A17(forward)	FT000033
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	15	1.99M	RNB2-001A17(reverse)	FT000034
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	6	28.61M	RNB2-001A21(forward)	FT000039
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	6	28.82M	RNB2-001A21(reverse)	FT000040
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	2	32.10M	RNB2-001B01(forward)	FT000047
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	2	32.32M	RNB2-001B01(reverse)	FT000048
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	7	60.19M	RNB2-001B02(forward)	FT000049
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	7	60.37M	RNB2-001B02(reverse)	FT000050
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	1	37.21M	RNB2-001B03(forward)	FT000051
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	1	37.03M	RNB2-001B03(reverse)	FT000052
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	8	54.19M	RNB2-001B07(forward)	FT000059
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	8	54.36M	RNB2-001B07(reverse)	FT000060
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	13	49.72M	RNB2-001B09(forward)	FT000063
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	13	49.68M	RNB2-001B09(reverse)	FT000064
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	13	107.48M	RNB2-001B11(forward)	FT000065
<a href="#">jump to map</a>	<a href="#">jump to detail</a>	13	107.67M	RNB2-001B11(reverse)	FT000066

Fig.6 The search results page

