

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.

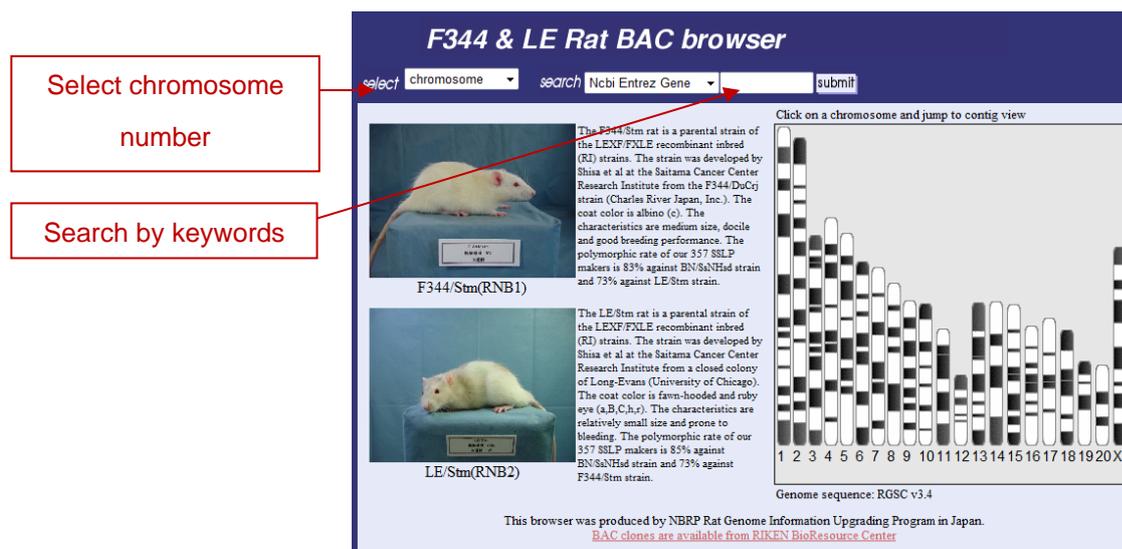


Fig. 1 Top page of F344 & LE Rat BAC browser

[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).

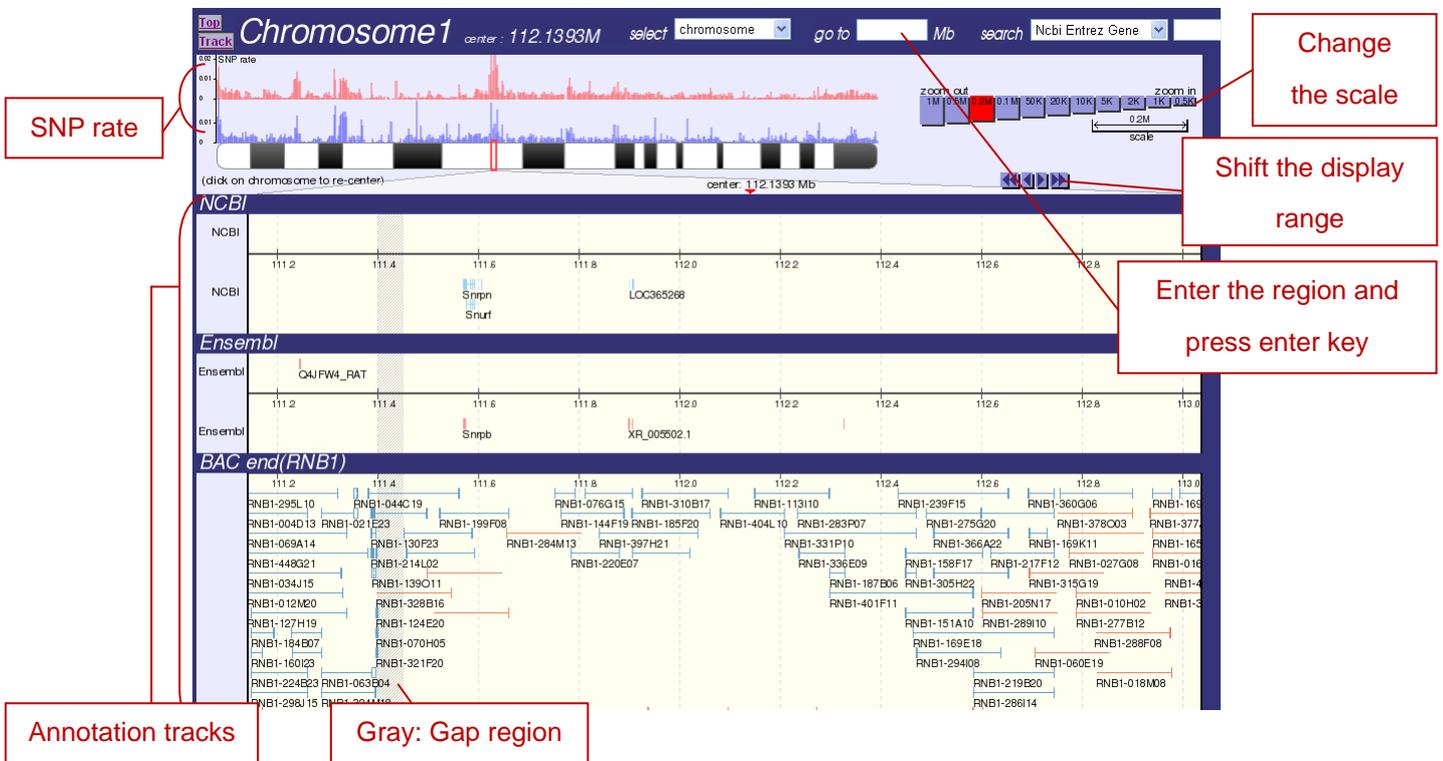


Fig. 2 Map page

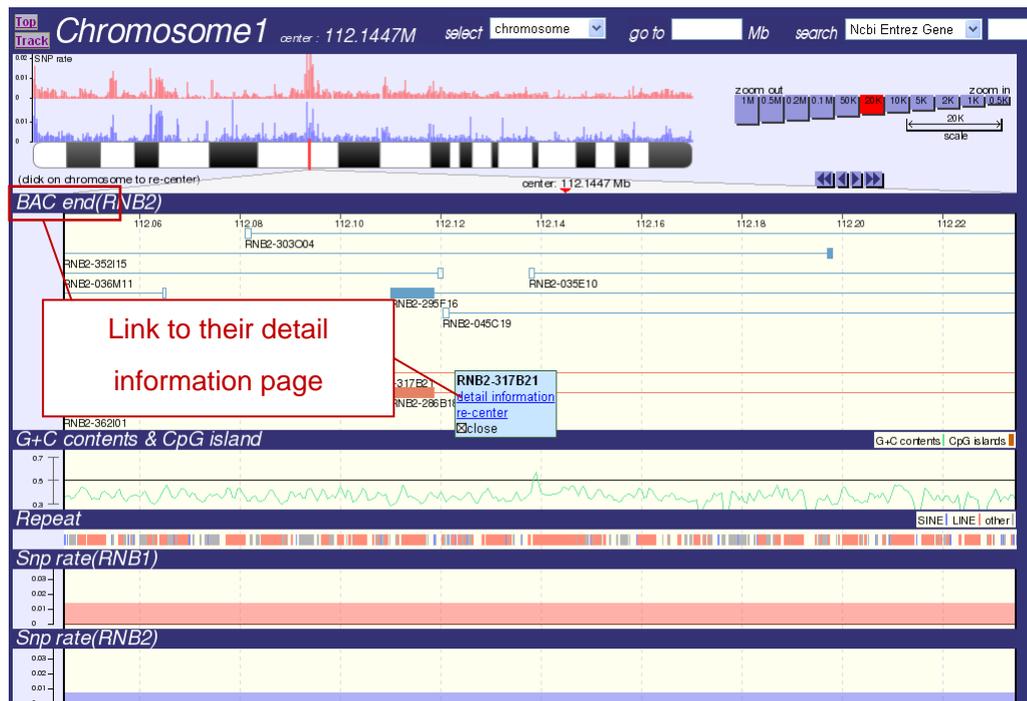


Fig.3 Map page

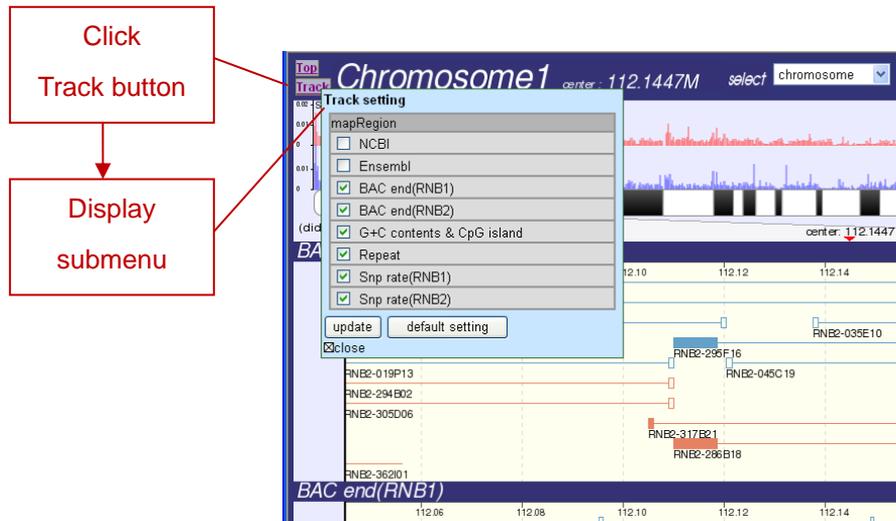


Fig.4 Track setting submenu of 'Map page'

【BAC end information page】

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

Internal ID

DDBJ ID

Mapping position

Alignment results

BAC end information of RNB2-019P13

ID: RNB2-019P13

Information of forward sequence (DDBJ: FT013301)				Information of reverse sequence (DDBJ: FT013302)							
Chromosome	1	position(base)	111906315 - 111907453	strand	+	Chromosome	1	position(base)	112108978 - 112110018	strand	-
chr. 1 (length: 267910886 base)				chr. 1 (length: 267910886 base)							
[jump to map]				[jump to map]							
Alignment						Alignment					
seq1: chr1_111906315_111907453						seq1: chr1_112108976_112110018					
seq2: RNB2-019P13_b_1_1127						seq2: RNB2-019P13_g_1_1034 (reverse)					
seq1 ATACCAGAAGAACATGAAACCAAGTGGAGAGTGCAGCCTTCATCAGACTGG 50						seq1 ACTTTTTTCAAATAATGTTAACTAGTAATAAGACAATGGTTTCTCCACAG 50					
seq2 ATACCAGAAGAACATGAAACCAAGTGGAGAGTGCAGCCTTCATCAGACTGG 50						seq2 ACTTTTTTCAAATAATGTTAACTAGTAATAAGACAATGATTCT-CACAG 47					
seq1 GGGATAGGCCCTTGAAGAAGCCCGGGTGTCTTCATGTTGTAACACTTGC 100						seq1 GACACTATAGTCAGACAAGTACATTGTCCAGTCCAGATTTGGTTGTCTA 100					
seq2 GGGACAGGCCCTTGAAGAAGCCCGGGTGTCTTCATGTTGTAACACTTGC 100						seq2 GACACTATAGTCAGACAAGTACA-TGTCCAGTCCAGAT--GAGTGTCTA 94					
seq1 CGGGCAGGTCCAAAGAGCCCTGTAGCTCCGAACCTGGCCAAAAGCAGA 150						seq1 CTTTGAATTTACTTTCCAGAGAATTCGCATACAGTCCATCCCATACAAA 150					
seq2 CGGGCAGGTCCAAAGAGCCCTGTAGCTCCGAACCTGGCCAAAAGCAGA 149						seq2 CTTTG-ATTTACTTTCCAGAGAA-TCCGATACAGTCCATCCCATACAAA 142					
seq1 TCGGGCATATTCAAACCCCGCACTGCAAGTATTCTTGAAGAGGTCCA 200						seq1 CCTTCTGGTTACACACAGAAATTTGAGAGTAAGACCCATTGCTTAGGT 200					
seq2 TCGGGCATATTCAAACCCCGCACTGCAAGTATTCTTGAAGAGGTCCA 199						seq2 -CATCTCGG-TAACCACAGAAATTTGAGAGTAAGACCCATTGCTTAGGT 190					
seq1 GGGGATACGTAAGGGTCTTGTGATCACTCCAGATCCACAGCCACAAAGC 250						seq1 AAACACATGGGTAGGTCAAAGAACAGAGTGAATGTATCAAGCATTGAOCA 250					
seq2 GGGGATACGTAAGGGTCTTGTGATCACTCCAGATCCACAGCCACAAAGC 249						seq2 AAACACATGGGTAGGTCAAAGAACAGAGTGAATGTATCAAGCATTGAOCA 240					
seq1 AGGTTTTTAAAGTTCCCTGTTTGTCTTCTGTCTGGTGGCATGACCCAGTC 300						seq1 ATAAGCTTGATTCTACTGTGTCTTACTGTGGATAGCTTTCATAGTACCAG 300					
seq2 AGGTTTTTAAAGTTCCCTGTTTGTCTTCTGTCTGGTGGCATGACCCAGTC 299						seq2 ATAAGCTTGATTCTACTGTGTCTTACTGTGGATAGCTTTCATAGTACCAG 290					
seq1 ATAGGTGCGTTTCAAAGAAAGGTAGCAGAACTGCAAGCCCGCGTACGGGA 350						seq1 AATATATGAAGCAGGCTACTGCAGAAAGTATAATCAACCCTTCATCAA 350					
seq2 ATAGGTGCGTTTCAAAGAAAGGTAGCAGAACTGCAAGCCCGCGTACGGGA 349						seq2 ACTAAATGAAGCAGGCTACTGCAGAAAGTATAATCAACCCTTCATCAA 340					
seq1 AGATGGCGATCACAAGTGGAGTCAAGCCCTTTGTAGAAGACAAAGGGGCC 400						seq1 GCCTGGAAATACTTCTGCAATGAATACTTCTGATACAGTGAAGTCTG 400					
seq2 AGATGGCGATCACAAGTGGAGTCAAGCCCTTTGTAGAAGACAAAGGGGCC 399						seq2 GCCTGGAAATACTTCTGCAATGAATACTTCTGATACAGTGAAGTCTG 390					
seq1 TCCGTCCTATACATGGTATTATAGCCTCTGCAGATTGGGCTCCCCCTG 450						seq1 CCTATCATGAGAATTACCAACA-TTTTAGTTGAATTTGAGTCCCAAAT 449					
seq2 TCCGTCCTATACATGGTATTATAGCCTCTGCAGATTGGGCTCCCCCTG 449						seq2 CCTATCATGAGAATTACCAACA-TTTTAGTTGAATTTGAGTCCCAAAT 440					

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.

Top Search results search Bac end internal ID submit

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

Fig.6 The search results page

