

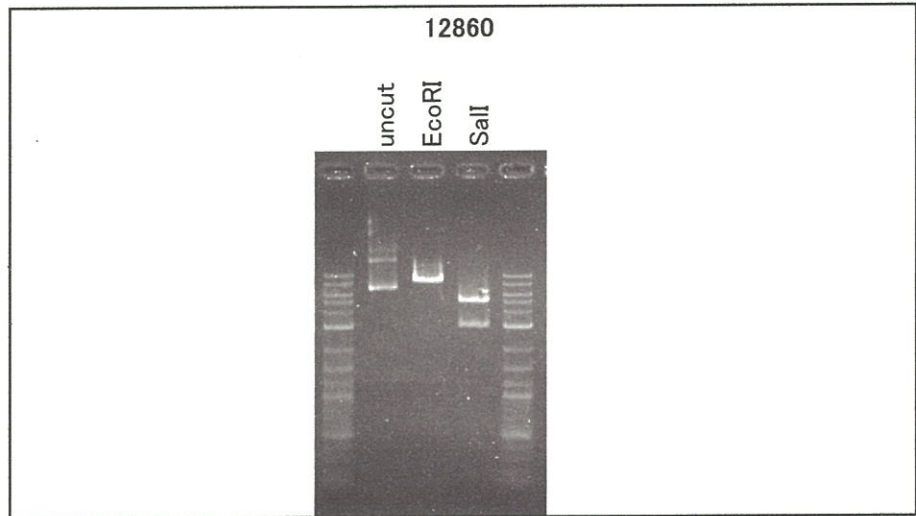
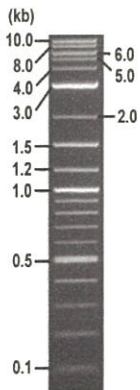


RIKEN DNA BANK

clone name : GFP-NFATc4(FL)/pCAGEN

- Clone ID : RDB _ 12860
- Lot : 12860 _ A4Io
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 100 microgram/ml Ampicillin
- Purification : QIAGEN QIAprep Spin Miniprep kit
- Digestion by restriction enzyme

2-Log DNA Ladder
(NEB#N3200L),
125 ng/well



Electrophoresis : 100 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>EcoRI</u>	<u>8.3</u> kbp
<u>SalI</u>	<u>5.2, 3.1</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	EGFP-C	Sequence - E	-
Sequence - B	pCA-bgter	Sequence - F	-
Sequence - C	pAxCA_F1	Sequence - G	-
Sequence - D	-	Sequence - H	-

APPROVED BY :



S/N G:32 A:43 T:38 C:73

primer name A : EGFP-C

KB 3500_POP7_BDTV3.mob

Jan 27, 2016 09:56AM, JST

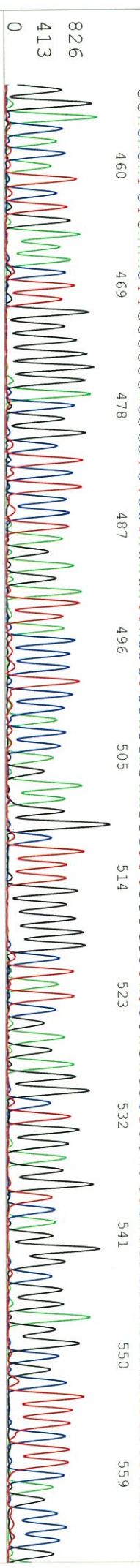
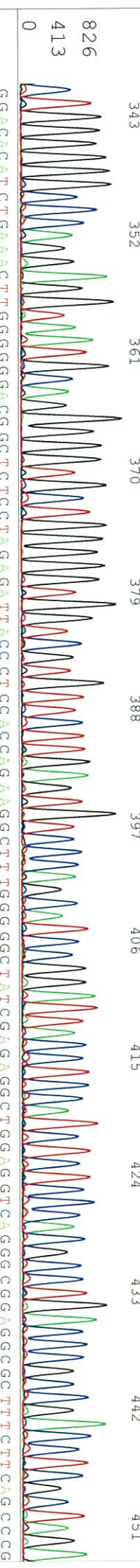
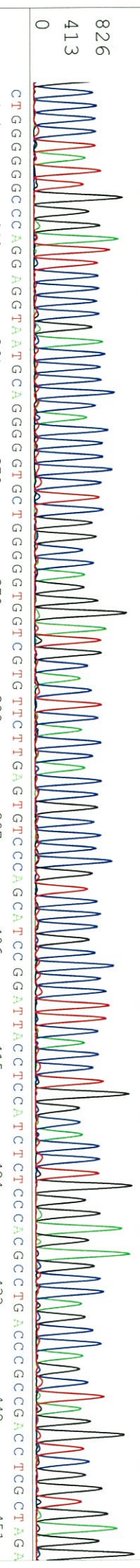
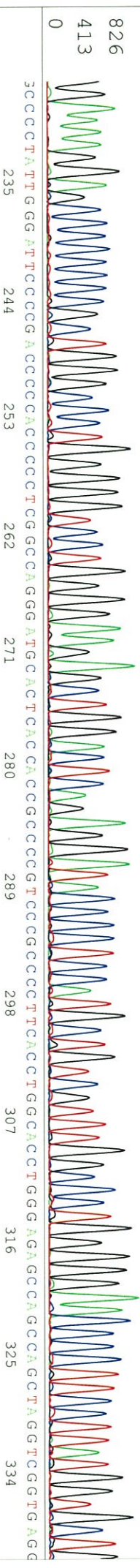
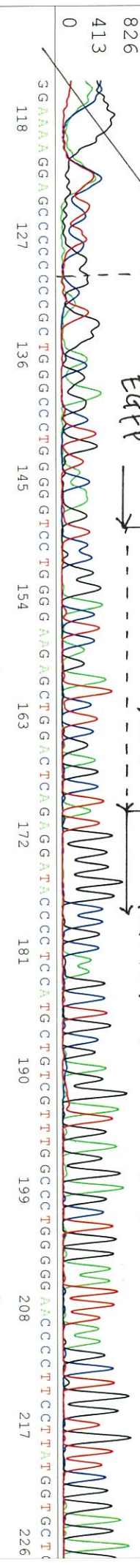
KB 1.4.1.8 Cap:20

5'-CATGGTCTGCTGGAGTTCGTG-3'

Pis 1391 to 12949 PK1 Loc:1368

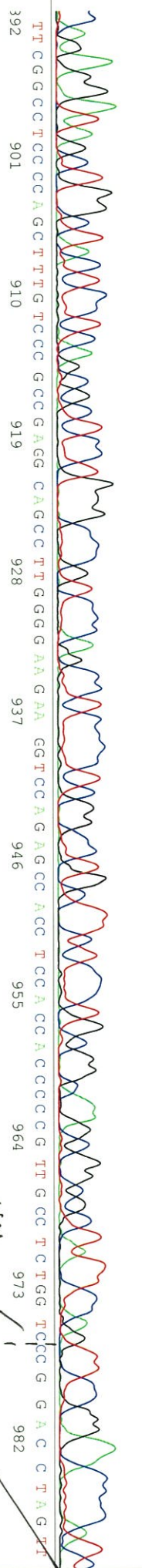
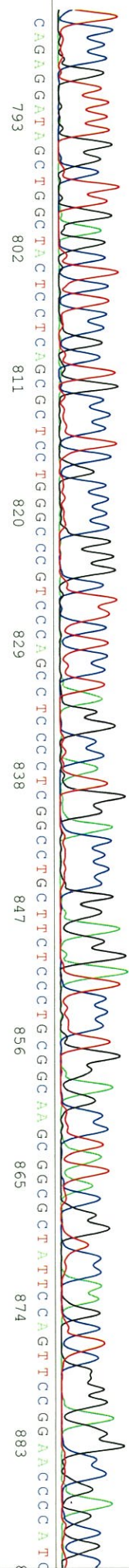
Jan 27, 2016 10:21AM, JST

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EGFP BglII XhoI NFATc4 NM_023699.3, 243..



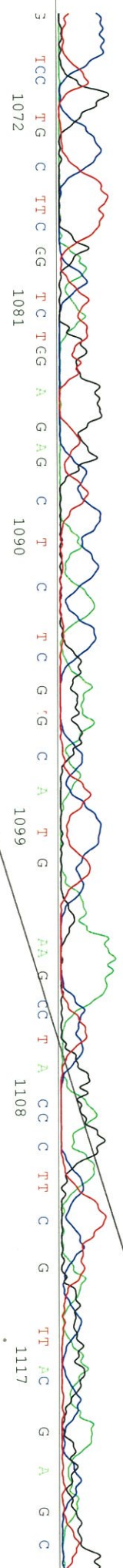
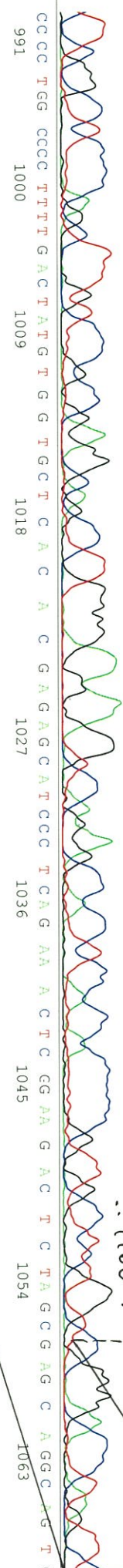
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BamHI



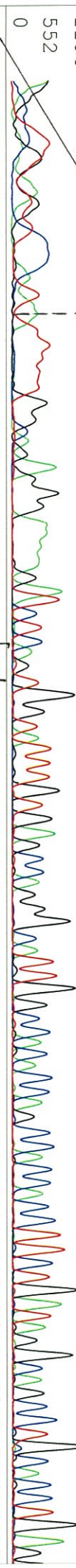
NM, /

.. (160)



A G C C A A F G A A G T C C C A A T T T T T T T T G G C A G A G G G A A A A A G T C T C A G T G G T A T T T T G T G A G C C A G G G C F T T G G C C A C C A G C C A C C A C C T T C T G A T A G G C A G C C C T G C A C C T G A G

1 10 19 28 37 46 55 64 73 82 91 100 109



G A G T G C G G C C G C G A T G G T A C C G T C G A C T A A G C T T G C G G C C G T C A G G C A G A G G C T C T T C T C C A G G A C G T G C A G G A A G C C A C T C A G G T C T C G C C A A T G A T C T C A C T C A C T T

118 127 136 145 154 163 172 181 190 199 208 217 22

F C C T C C A G G G T G A T A C C C T G G A T A G G T A C A C T G T C T C T G A A G C C G C T G T A G C C A C C C T G C T T C T C C T C C G A A G C C C C T C C C A G G G T A T A G C C T G G C C C A C C T

6 235 244 253 262 271 280 289 298 307 316 325 334

C A T T G T A G C C C T C A G A G G T A A G G G G T G G A T G G C A C T C T G G G A T G G A A G G G T C T T C G A G T G G T G G G A A G G C A G T G C G G C T A A A G G G G C T G G A G G G A G A T G

343 352 361 370 379 388 397 406 415 424 433 442 451

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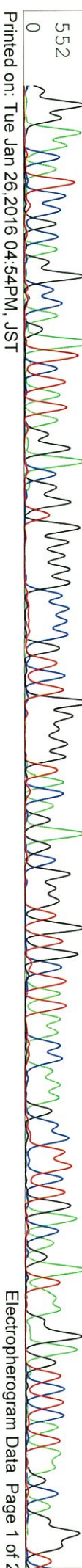
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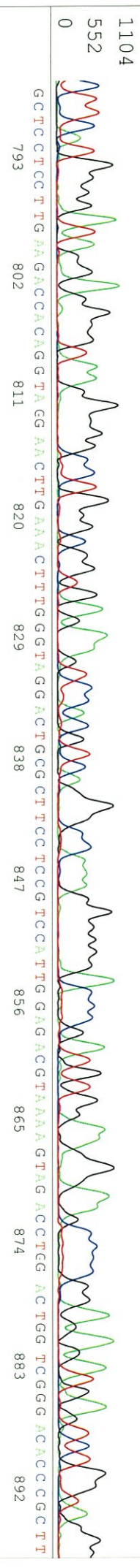
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BgII

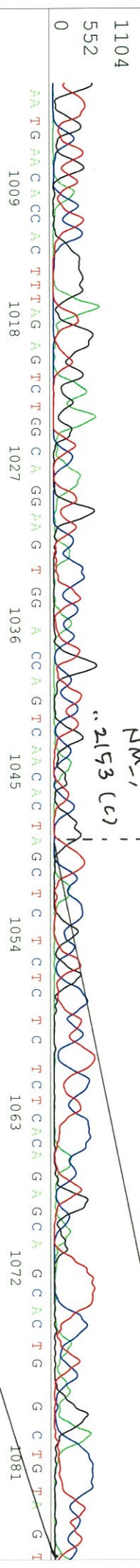
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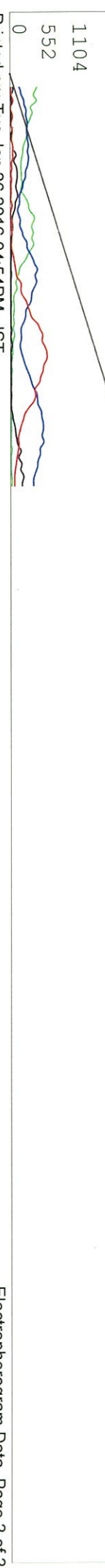


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AA TGAACA CCA CCACTTTAG AGTCTGGCA GGAAG TGGACCA GTC AACAC TA GCTCTCTCTCTCACAGAGCA GCACTG GCACTG GCTGTAGT



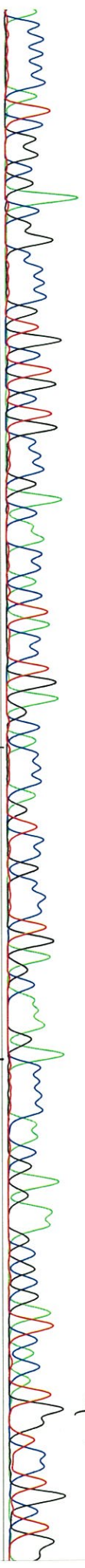
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ACACCG AAA CC ATTT C G 1153 1162



(p1wer A)

5 ACCCCCATTCGGCGGACCGGCCCCCGTGCCTGGCTGCCCGACCAACCACTACCTGAGCAACCAGTCCCGCCCTGAGCAAAAGACCCCAACGAGAAAGCCGATCACTGGCTGGC



EgFP → BqII XhoI → NFATc4

AA TTTAA GCTGGTGTTCGGAGAGAAAGGAGCCCGCCCTGGGGCCCTGGGGCTCC TGGGAAAGAGCTGGACTCAGAGGATACCCTCCATCTGTC

G TTTGG CCC TGGGGGAA CCCC TTTCC TATGG TGC TGC CCCC TATTGGG AATTCCCCGACCCCTC G CAG AATGCACTCA C

A CEG CCCCCGTTCCC GCC C ATCA C TGC CACC TGGG GAG AGTCAGG CCAG CTTA GGTTCTG A G TCC

T G A G TC A A TT AA TTG C C A A T G G A G

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