

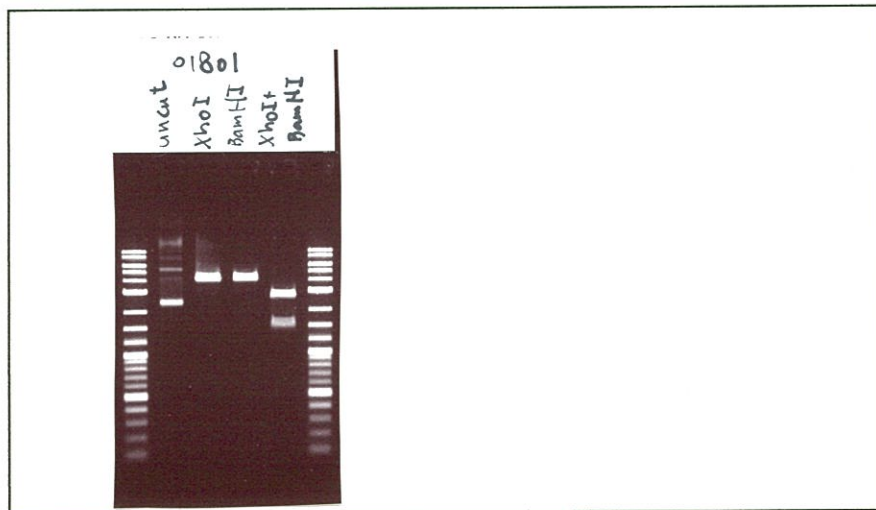
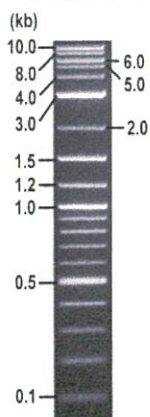


RIKEN DNA BANK

clone name : RBP-J

- Clone ID : RDB_01801
- Lot : 12401_A4Bh
- DNA Concentration : 25 nanogram/microliter
- Volume : 1 microgram
- Form : DNA solution in TE buffer
- Host : DH5 α
- 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 : 45 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>Xho I</u>	<u>4.5</u> kbp
<u>BamH I</u>	<u>4.5</u> kbp
<u>Xho I + BamH I</u>	<u>1.6, 2.9</u> kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name
Sequence - A	M13(-40)
Sequence - B	Reverse2
Sequence - C	-
Sequence - D	-

APPROVED BY :



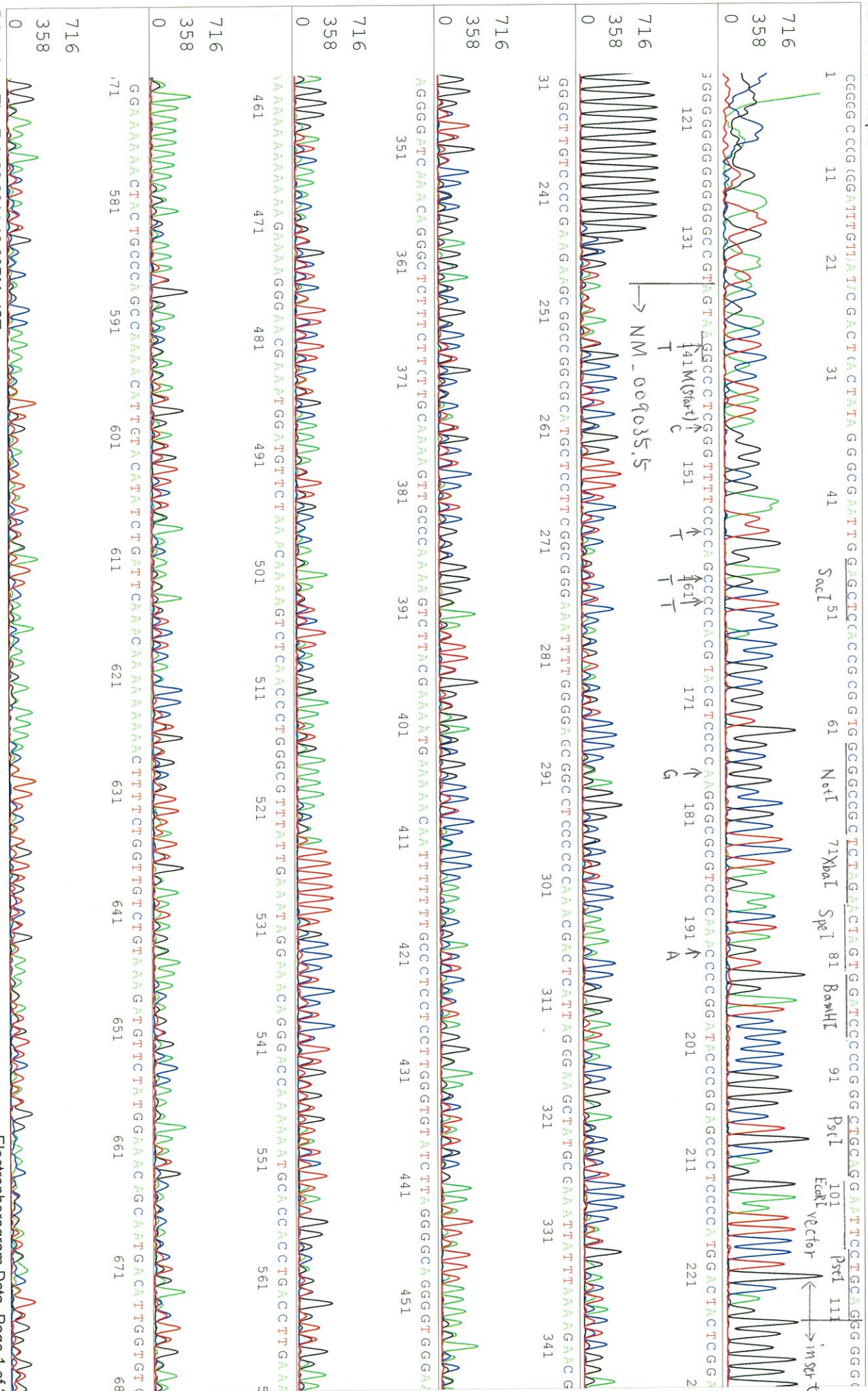
S/N G:17 A:13 T:10 C:9

primer name A : M13(-40)

KB.bcp

KB 1.4.1.8 Cap.1

5'-GTTTTCGAGTGCAGCAGCGTTGTA-3'



S/N G:17 A:13 T:10 C:9

01801_12401_A4Bh_M13(-40)

Feb 20, 2014 10:12AM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

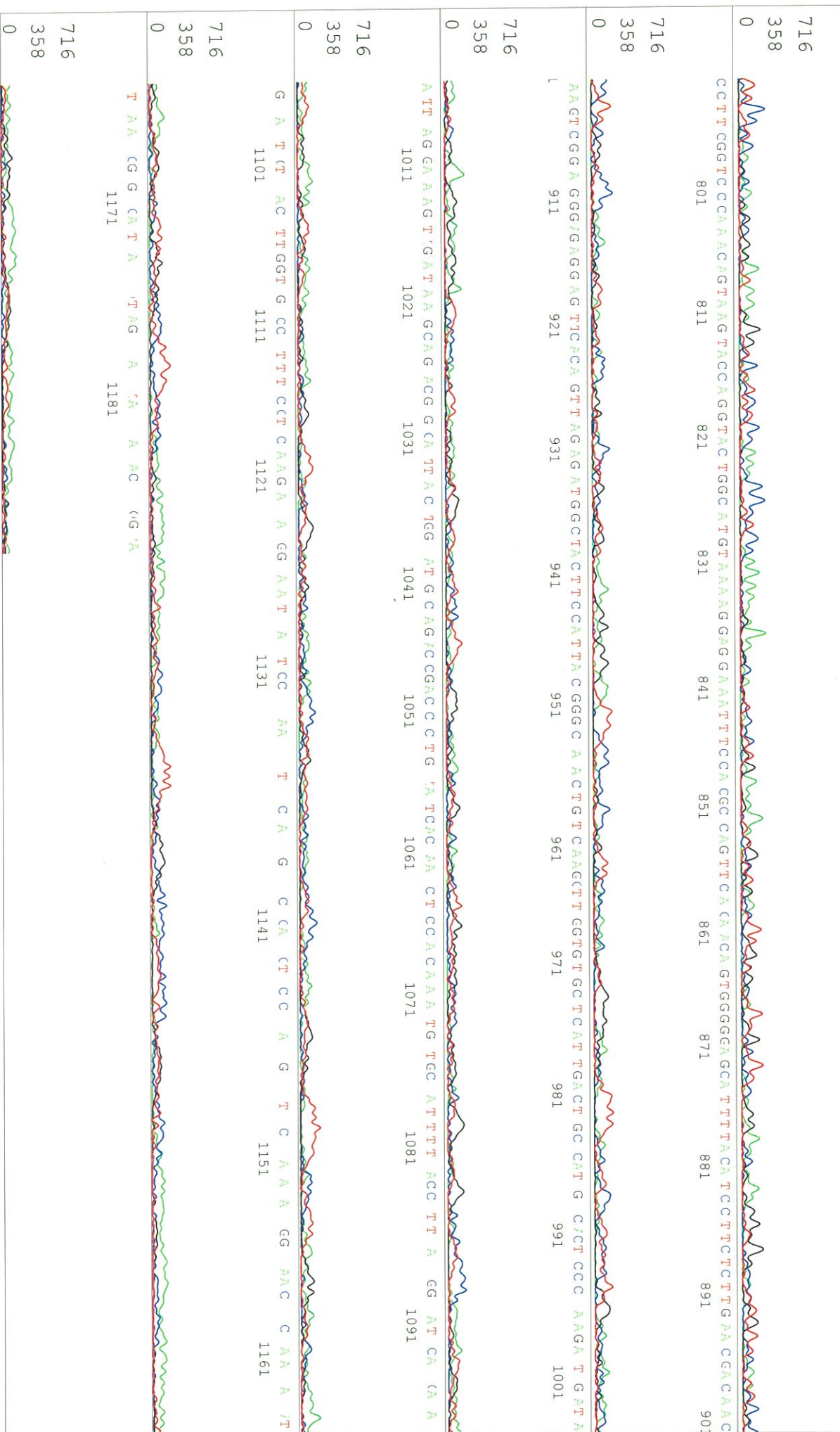
Feb 20, 2014 10:39AM, JST

KB 1.4:1.8 Cap:1

Pts 1365 to 13651 Pk1 Loc:1342

Spacing:12.02 Pts/Panel1350

Version 5.4 HISQV Bases: 608



S/N G:18 A:16 T:13 C:10

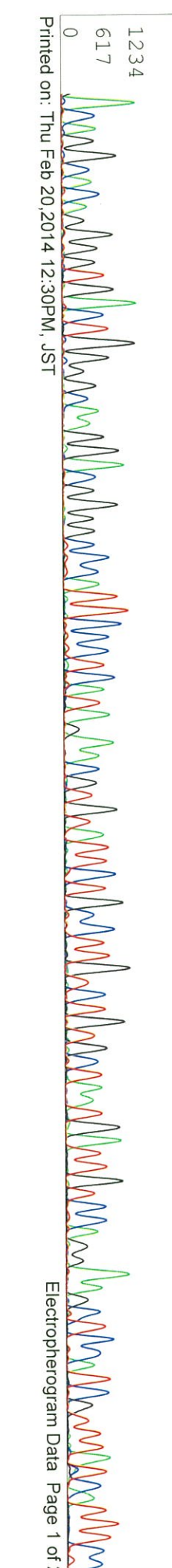
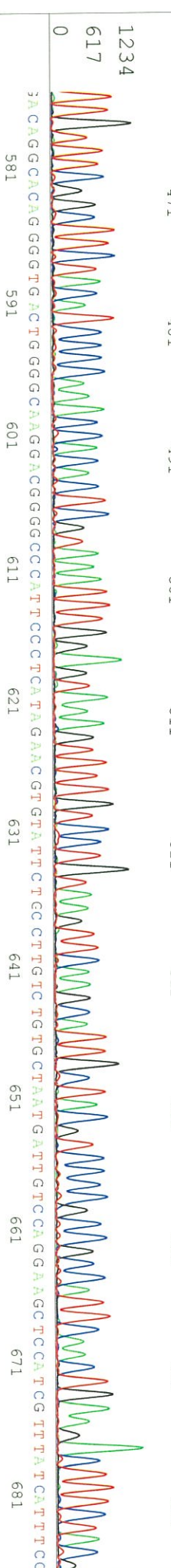
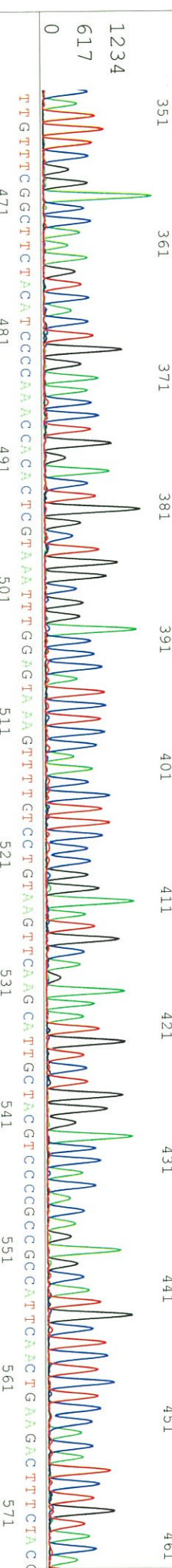
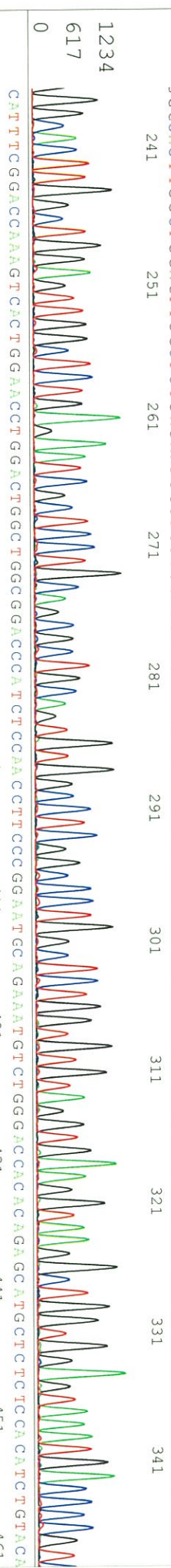
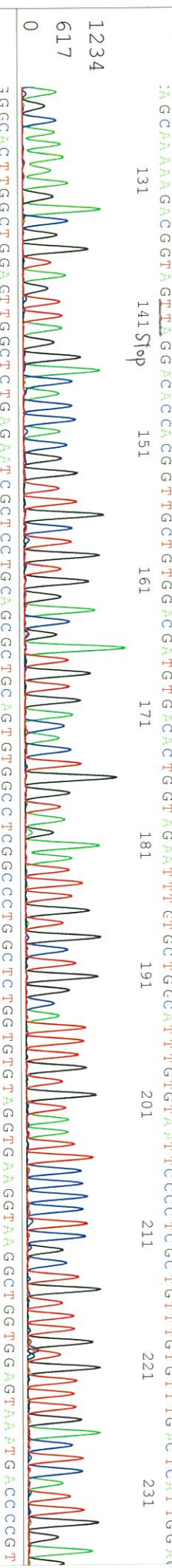
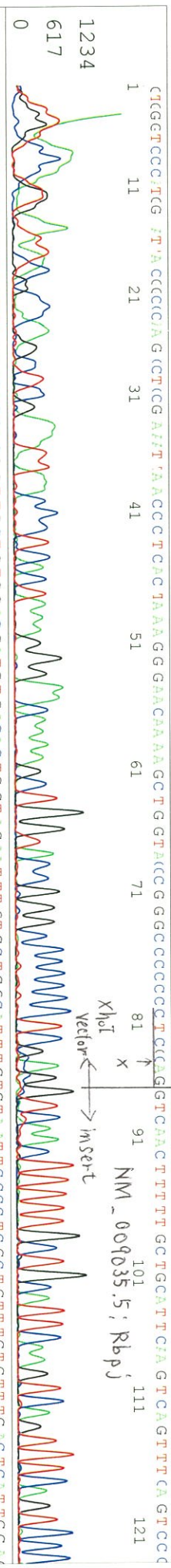
primer name B : Reverse2

KB.bcp

5'-GGCGATAACAATTTTCACACAGG-3'

KB 1.4:1.8 Cap:4

101 111 121



S/N G:18 A:16 T:13 C:10

01801_12401_A4Bh_Reverse2

Feb 20, 2014 10:12AM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Feb 20, 2014 10:39AM, JST

KB 1.4.1.8 Cap:4

Pts 1348 to 13730 Pk1 Loc: 1325

Spacing: 12.19 Pts/Panel1350

Version 5.4

HISQV Bases: 1020

Plate Name: 20140220_dnbank

TTATTTTCTTTTGGACATGGAGTGGCCCTGAAATTTGGATTATTTCTTCTTGA GAAA GCC ACCAAGTACA TTC TTTCTGTATCTTAAAGTAAAA TCCACATT TGGAGT

691 701 711 721 731 741 751 761 771 781 791

TTGTGATFCAGGGTCGTGCA TCCA GATAAGC C GTCCTGTTATCCAACTTCC TAAATTATC TCTTG G GAGT GCC ATGCCCA G TCACTGAGC FCACAAA GCTTGA CAGTCT

801 811 821 831 841 851 861 871 881 891 901

GCCCC TAA TGGATGTACCCCATCTA/CTGT GAFC TCCCTCTCTTTCCGACTCGT CG TCGTCC AAGAATGGAT GAAAA T G CT CCCC A CTGT TGTG AATG ACCGGT G

911 921 931 941 951 961 971 981 991 1001 1011 102

G AAAATT CCCC TCTCTACATCCAG GTACC TGTACTAAACTG TCTG G ACC GAAA GCC GA T G AACG ATG CCA /CCTTCG TTTCTTG AAG CA ATGCCAAC

1031 1041 1051 1061 1071 1081 1091 1101 1111

A G TTCATGCCA TTTCTTCCAG TTGA CT TGCCCTTCTTT TA G AG G T GG A G ATGAACCTTTA TT C GCC TTG CTGGAGA G AAAA C

1131 1141 1151 1161 1171 1181 1191 1201

A CAACCC A AATGT GTTC /CTATCTCGCCCTC G

1211 1221 1231

Electropherogram showing signal traces for bases 691-1231. The traces are color-coded: A (green), C (blue), G (black), T (red).

Reference sequence: A CAACCC A AATGT GTTC /CTATCTCGCCCTC G

Reference sequence: A G TTCATGCCA TTTCTTCCAG TTGA CT TGCCCTTCTTT TA G AG G T GG A G ATGAACCTTTA TT C GCC TTG CTGGAGA G AAAA C