

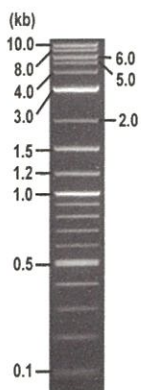


RIKEN DNA BANK

clone name : pZErO-2.1 mG9a-L

- Clone ID : RDB _ 05728
- Lot : 12373 _ A4At
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 25 microgram/ml kanamycin
- 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>BamHI</u>	<u>7.4</u> kbp
<u>EcoRI</u>	<u>4.1, 3.3</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	M13_-40	Sequence - E	-
Sequence - B	Reverse2	Sequence - F	-
Sequence - C	-	Sequence - G	-
Sequence - D	-	Sequence - H	-



APPROVED BY :

S/N G:612 A:601 T:410 C:748

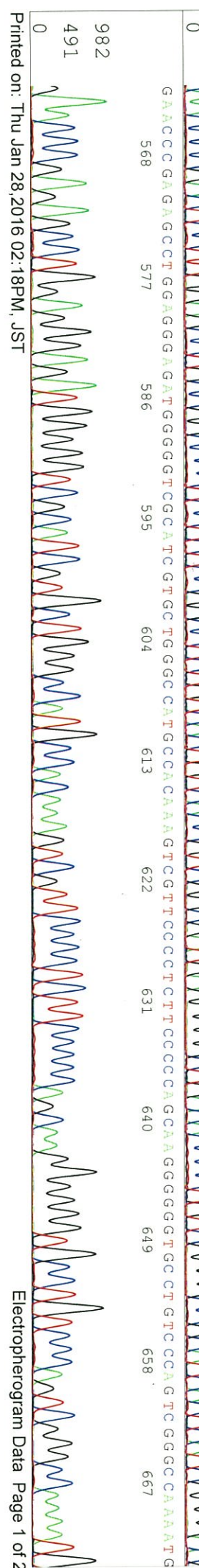
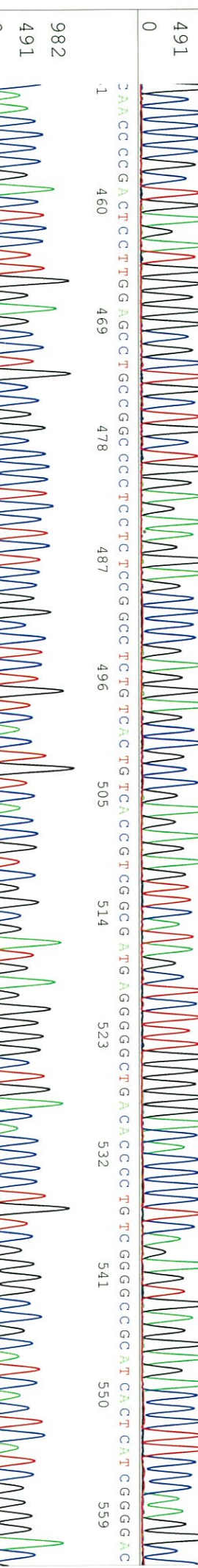
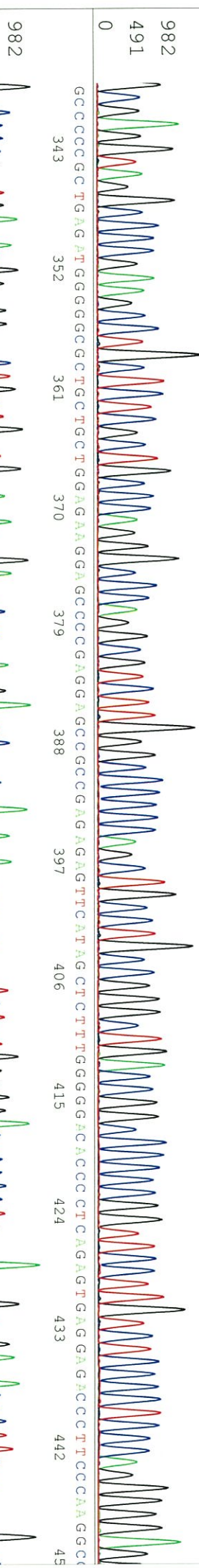
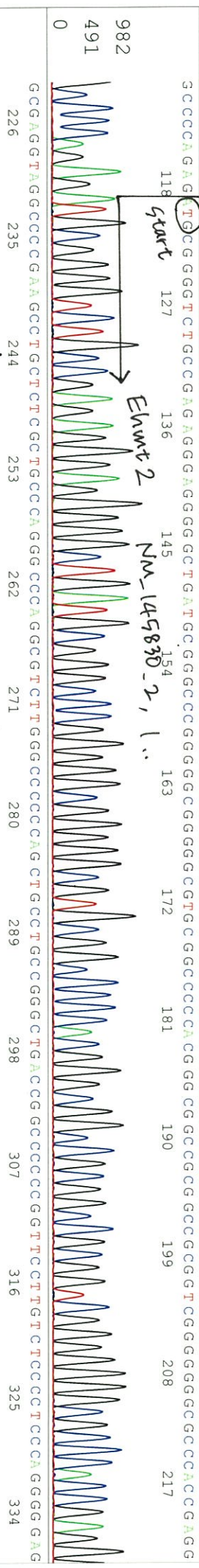
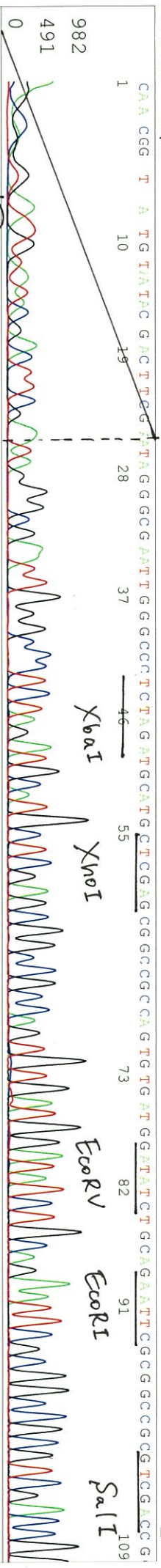
primer name A : M13_-40

KB:bcp

KB 1.4.1.8 Cap:9

5-GTTTCCAGTCACGACGTTGTA-3'

Pts 1318 to 13401 Pk1 Loc:1295
Version 6.0 HISQV Bases: 1015



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

CGGCAACAACTGCCGCCCAAGAGGGGCAAGCCCAAAGTGCCACCGAGCCCGGAAAACCATGTCCAAACC TAAGCAAAGGACAGCCCTCCAA TCCCTGAGAGGAGCGGCCCCCG
784 793 802 811 820 829 838 847 856 865 874 883

AAGTCCAGCATTTCCGCATGAGTGTGATGACATGCA TCGGGAAAGGTGACTTCAGATGTGGCCAAAAGAGGAA GCTGAACTCTGTGTAAGCCTGATCCGA GGACT
892 901 910 919 928 937 946 955 964 973 982 991

FGGCTCTGCCGGGGGCTCA GGAATATPAATCCCTGG AGAA GGAGAGCCC AEGCCCTEG A GAGTGG AGACGG TGG TGGGCGATG AC TT
1000 1009 1018 1027 1036 1045 1054 1063 1072 1081

NM-1
--.890

CAGCTGTACTATGATGATGCGTACCCTCTGTCCATGAC A TG A CC GGA TTG AAC TC TG A C A G G C C A G T C T G T G A G T C C G G A A G C
1090 1099 1108 1117 1126 1135 1144 1153

T C T A G C T T G A A C A A G T G A
1162 1171



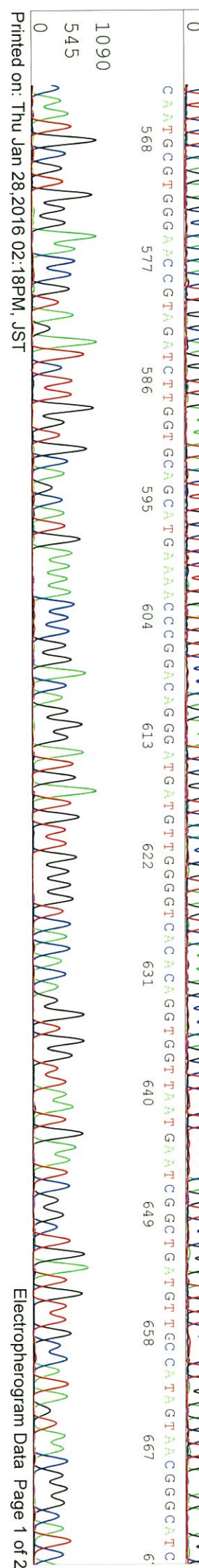
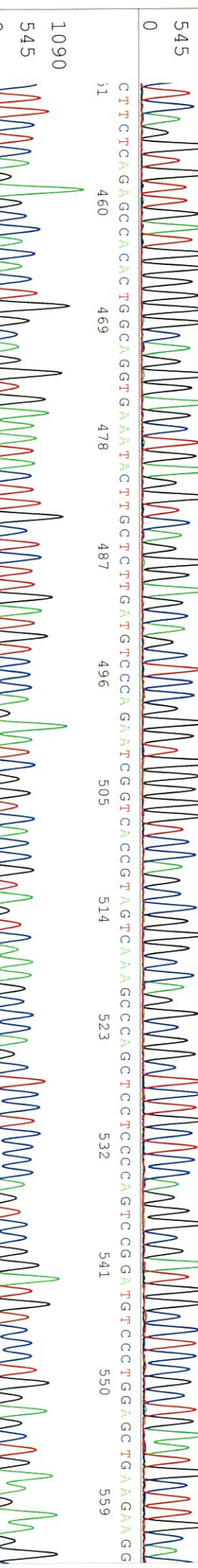
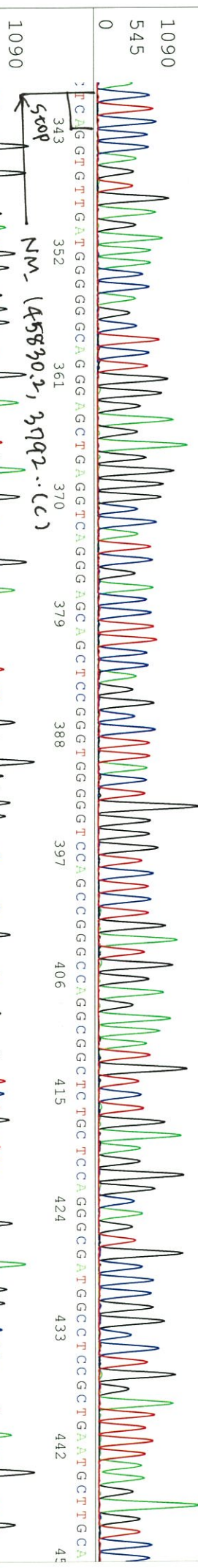
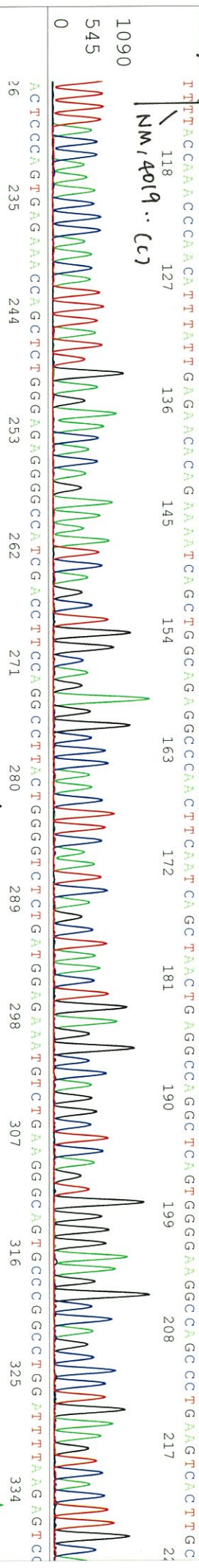
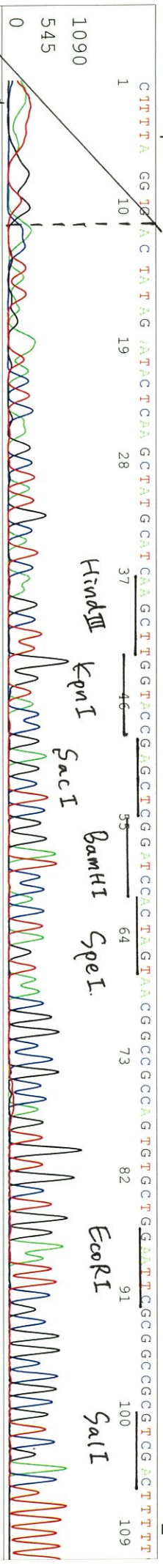
S/N G:438 A:628 T:450 C:569

KB.bcp

KB 1.4.1.8 Cap:12

primer name β : Reverse2

5'-GCGGATTAACAATTTCACACAGG-3'



AATGCCAGTAAACCTTCGCCATCCTTGTTATCTAAATCGAAGGTAAGAAATCATCTCTCACATCAAGCCATCGGCATCAGAGATCAAGCTCTCTCACTACTCGCAGATGAA CG
 76 685 694 703 712 721 730 739 748 757 766 775 784

TGCCCTGGGGGATGGTCTGTCAAGGCTCGGACCCCGCAGCCCATCTTGGCAAGTCCGGTAGAGCTGCAGCCGTTACCTTGATGCCCGCTTCCACCAACGCCGGTTCTTGCAAGCTTCT
 793 802 811 820 829 838 847 856 865 874 883 892 5

CCAGCA GAGCATGCTGTGTTACAC TCAAA GATCA GGGGGCTCGATCTTGTTAAAC TCC TGG AGCA GCCGCCCGCTCC GTTGTCA TACCAGCATCGGATGCTGAGGCTG
 901 910 919 928 937 946 955 964 973 982 991 1000

ACCACATAGGC AATTGG AGCTGGAGCAGTCA TCCACACACG TGCAGTGC TGCAGATGGGTGATGTTGCC TCGATG TCA T GATCGATG TCTCGCTGG TC
 1009 1018 1027 1036 1045 1054 1063 1072 1081 1090 1099

:CTC AG AG ATGTAC TTG TAG TACCTCC GG CAC GG CT C CAAT CCA CAT C A TCGAA CCA GG AT G TACG TTTCTCTA
 1108 1117 1126 1135 1144 1153 1162 1171

TAG C TTC GG CC TA (GG) TTC C C G CA
 .180 1189 1198

