

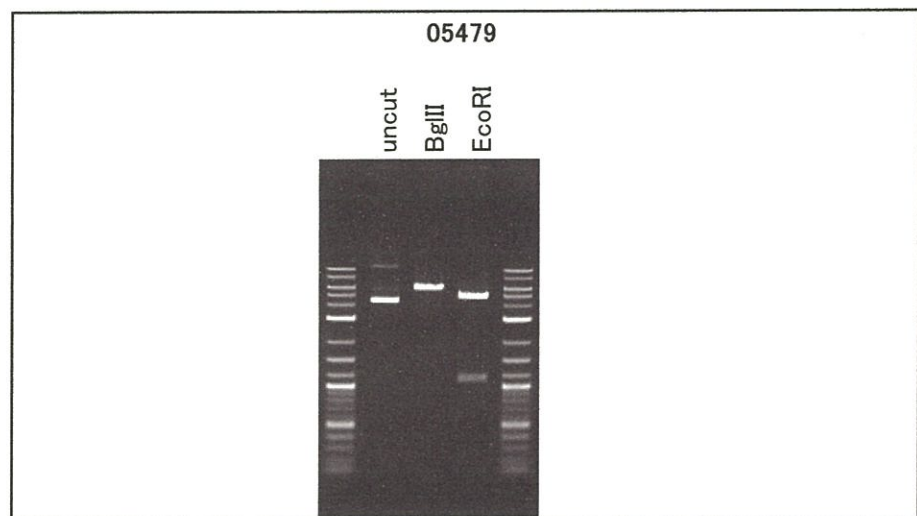
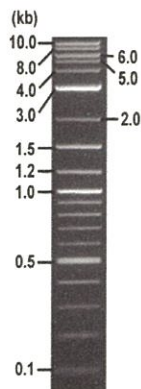


RIKEN DNA BANK

clone name : pKM2L-phCLG4

- Clone ID : RDB _ 05479
- Lot : 05479 _ A3Df
- 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>BglII</u>	<u>5.9</u> kbp
<u>EcoRI</u>	<u>4.8, 1.1</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	phRLR2	Sequence - F	-
Sequence - C	pAxCALNL_F1	Sequence - G	-
Sequence - D	-	Sequence - H	-

APPROVED BY :



S/N G:181 A:223 T:266 C:315

primer name A : M13_-40

05479_05479_A3Df_M13(-40)

Feb 18,2016 09:45AM, JST

KB.bcp

5-GTTTCCAGTACGACGGTTGTA-3'

KB_3500_POP7_BDTV3.mob

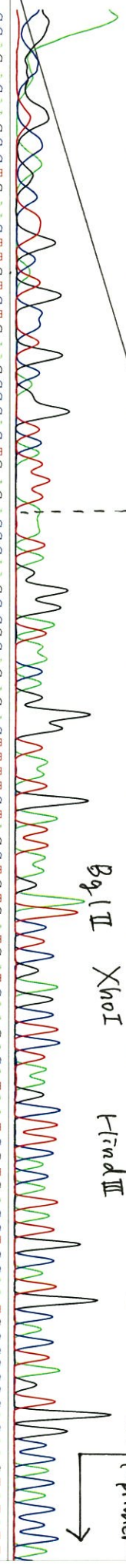
Feb 18,2016 10:11AM, JST

KB 1.4.1.8 Cap.2

Pis 1537 to 12937 Pk1 Loc:1514

Spacing:1.143 Pts/Panel1350

CGG CCG CG CACGC TTGCATGCCC TG CAGG TCCATTTA ATAG GGGATAACAG GGT AATGATTTAA GATCTCGAGCTCTAA GCTTCA CATAATG CATTG CACTAG TGCC CACACCCA



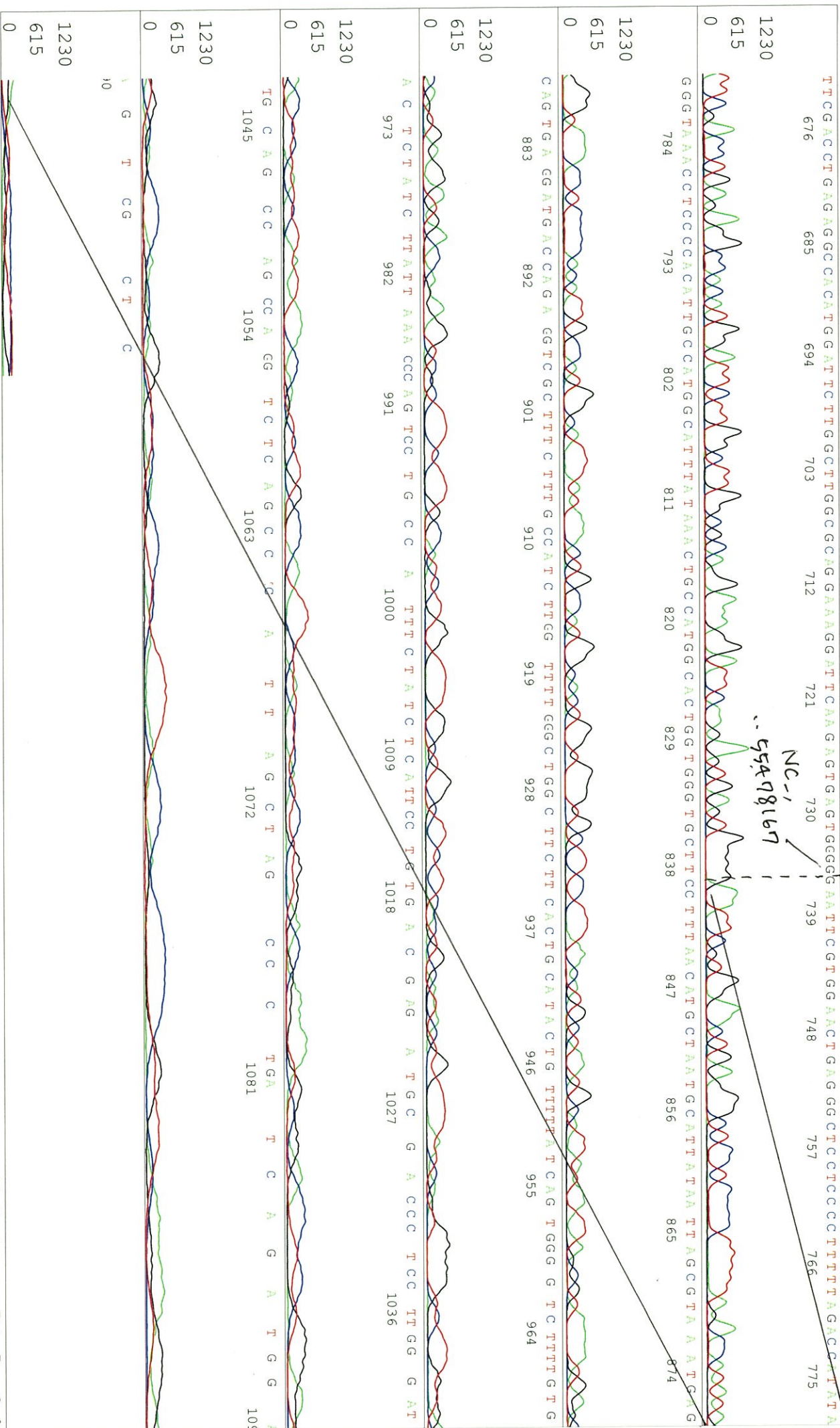
CCAG ACAAGGCTGAACTTGTCTGAAAGCCCACTG AGAACCAGGC CGCAGAGACTTTCTAGCTGTGATGATCAAGACATAATCGTGAACCTCCA TGCCCCCAAGTATATT
118 127 136 145 154 163 172 181 190 199 208 217
→ *ph* *Cl* *G* *G* *A* *N* *C* - *000016.10*, *55409535* ..

GCTCCGTATTCTTCA GCCCTGACCTTACTTCTCAAACTGTTCCCTGCTGACCCCACTCCATATCTGCCGCTTCCTAGGCTGTTCCCTACTGAACCTCCAGCTCCATCCC
226 235 244 253 262 271 280 289 298 307 316 325 334

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

: ACCCAAGCATTCCACTCTTTAGCTCTCAAGGTTCTCAAGAGTCACTTCTCCAGGAAGCCTTCCCTTGATTGCTTTACTAGTTTAGGGGCTGAAGTCA GGGCTTCCCA
451 460 469 478 487 496 505 514 523 532 541 550 559

ACAGCCTGCTGGAGTCCCCATCAGAGCTTATCTCTCAACTGTCTTTCCTGAAGAAGGAGAAAGACATTCCCTCAGAGACGGTTGTCACAGGGA GAAC TTCAAAATTGGGA
568 577 586 595 604 613 622 631 640 649 658 667



S/N G:73 A:65 T:54 C:84

primer name **B** : phRLR2

05479_05479_A3Df_phRLR2

Feb 18,2016 09:45AM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Feb 18,2016 10:11AM, JST

Spacing:1.16 Pts/Panel1350

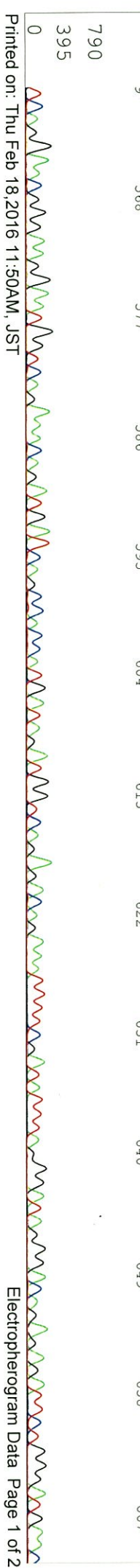
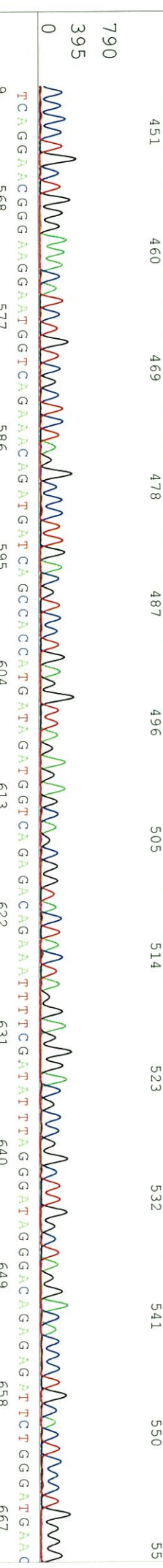
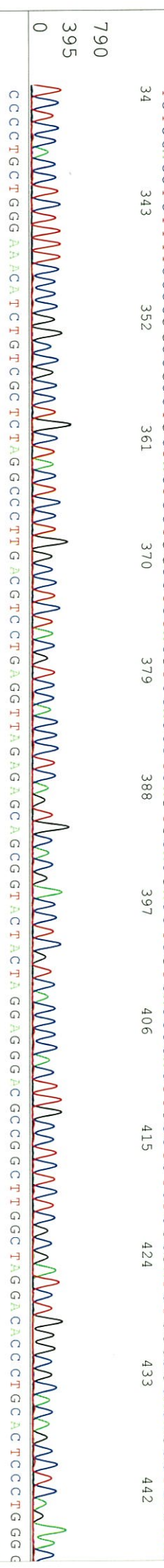
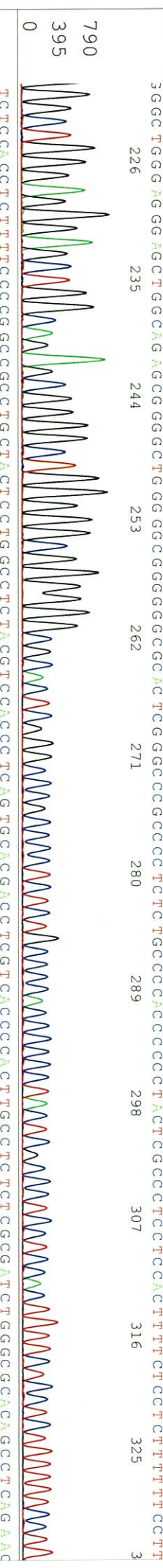
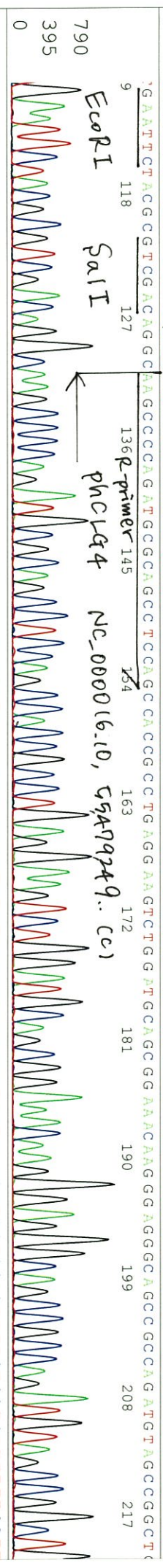
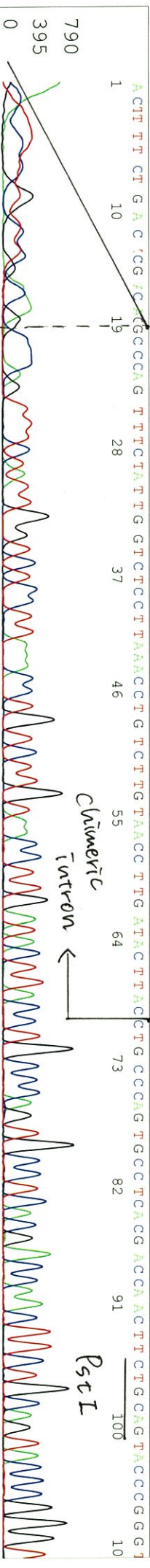
KB 1.4.1.8 Cap:5

5'-CCAATAGGTGCCTATCAGAAACGC-3'

Pts 1523 to 12867 Pk1 Loc:1500

Plate Name: 20160218_mlx

Version 6.0 HISQV Bases: 982



Version 6.0 HISQV Bases: 982

AGAGATGGAAAGAGAGATGAAACAGACAGGTGGAAAGTCCCGATGCTTACCTTCCCTTCGCAATGTAAAGCTTAACTTGGCCCTCGTAAATG
676 685 694 703 712 721 730 739 748 757 766 775

GCGAGATGCTAGATACACTTTGGGAAATAGAGCACTCA GGGCCCGCGTTAGAGACGGTTGGAAACCAAGCCACTTGAACAGGGGGCTGGGTAAAT
784 793 802 811 820 829 838 847 856 865 874

TTGAGGCTGAGACCTGGCTGGGCTGGCACTCCAGGAGGGGCCCGCATTCCTCGGTCAAGATAGAAATTTGGGC AA GACTGGG TTTAAATAA
883 892 901 910 919 928 937 946 955 964 973

ATAGAGGTCACAAA GACCCCACTGATAAACA G TATGCAAGTG AAGAAEGCCAAAGCC AA GATGG C AAG AAAAGCCG
982 991 1000 1009 1018 1027 1036 1045 1054

ATC TCTG TCA TTTCC TTCCAC TGC TCA TTTT ACG CTTA TTTA TAA TGG CA TTT AG C AAGG T T A
1063 1072 1081 1090 1099 1108 1117

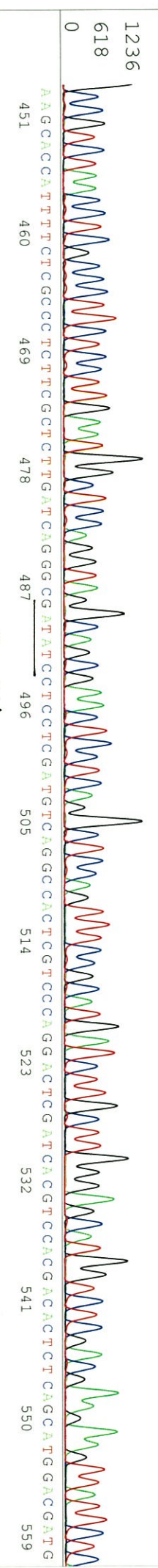
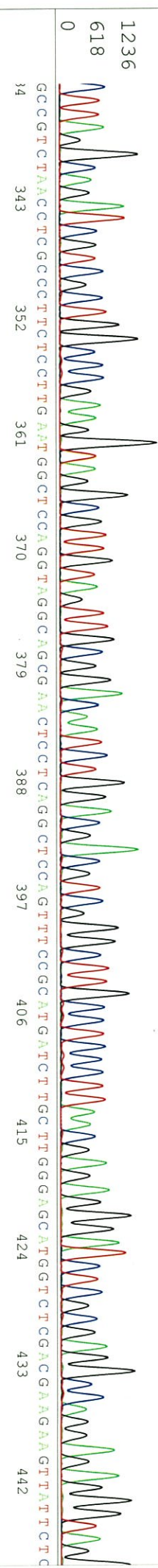
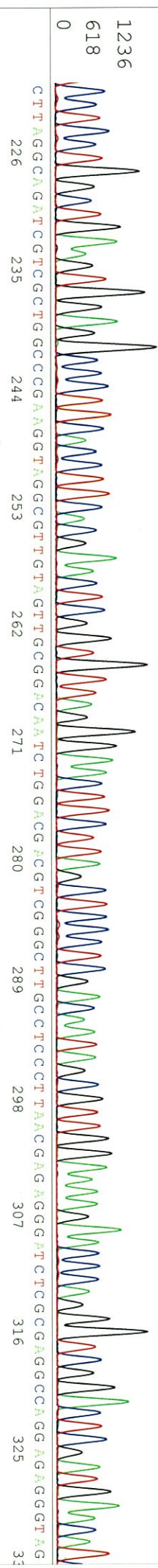
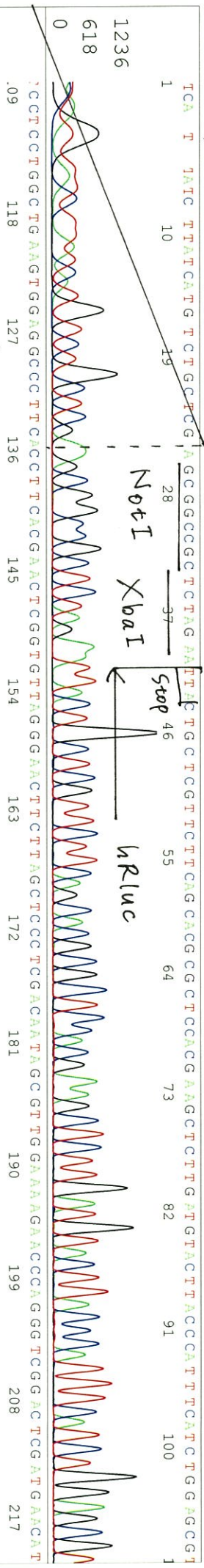
AAA A G G AAA GA G
1126

0

790
395
0

NC-1
5478511 (C)

NotI XbaI hRuc



EcoRV

