

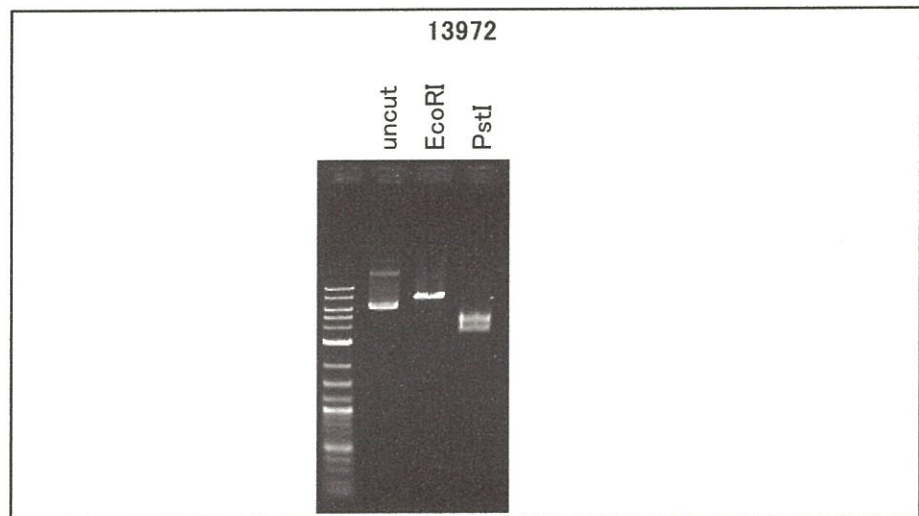
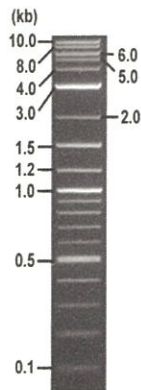


RIKEN DNA BANK

clone name : pCIneoLuc-PP2A

- Clone ID : RDB _ 13972
- Lot : 13972 _ A6Bt
- 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 : 90 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>EcoRI</u>	<u>8.1</u> kbp
<u>PstI</u>	<u>3.7, 2.5, 2.0</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	CMV-Forward	Sequence - E	-
Sequence - B	Luc-C_F	Sequence - F	-
Sequence - C	pAxCALNL_F1	Sequence - G	-
Sequence - D	SV40pro_F_V2	Sequence - H	-



APPROVED BY :

S/N G:594 A:859 T:835 C:790

KB.bcp

KB 1.4.1.8 Cap.22

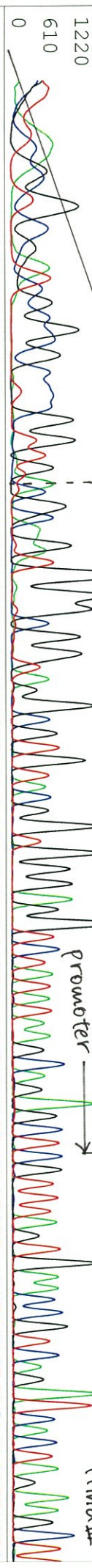
primer name A : CMV-Forward

5- GCACCAAAAATCAACGGGACTT-3'

GA TTC (C TG C (GATTCG CCG C CCG TTTTC GCAATG G GCGGTAG GCGGTACGGTGGAGGTCTATAATAAGCAAGCTCGTTTAACTTAAGCTGCAGTACTCTCTTAAGGTAGCCTTGCA GAACTCACTA G AAGCTT

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

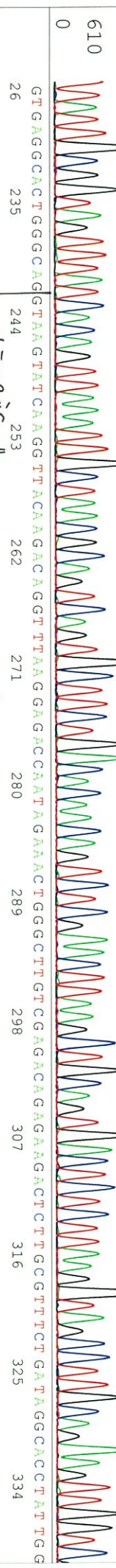
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118 127 136 145 154 163 172 181 190 199 208 217 2

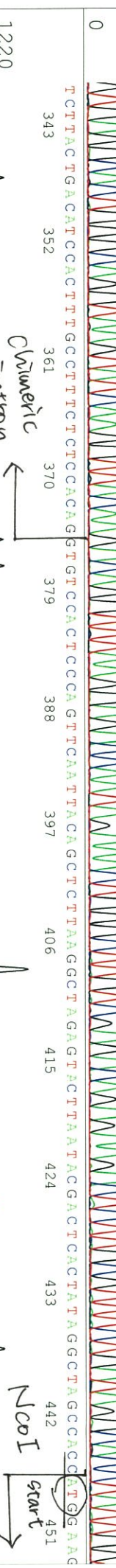
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26 235 244 253 262 271 280 289 298 307 316 325 334

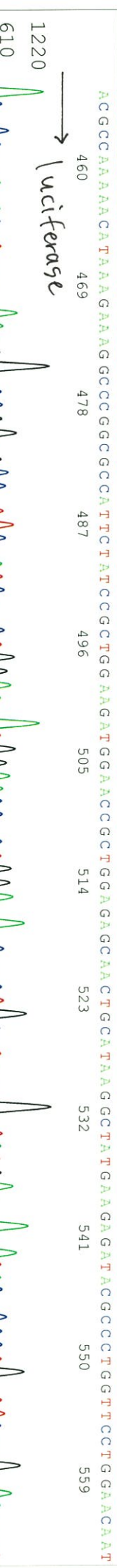
1220 610 0



TCTTAC TGACATCCACCTTTGGCCTTCTCTCCACA GGTGTCCACTCCCA GTTCAATTACA GCTCTTAAAGCTAGA GTACTTAATACGACTCACTATAGGCTAGCCACCATGGAAAC

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

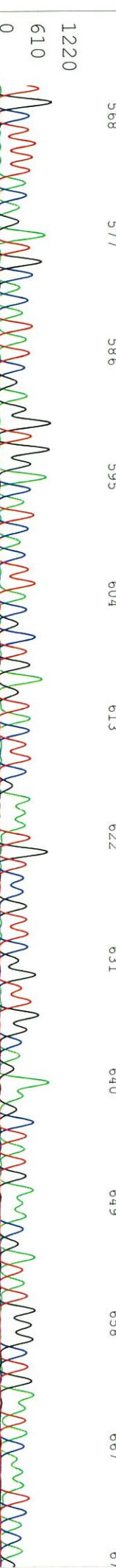
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1220 610 0

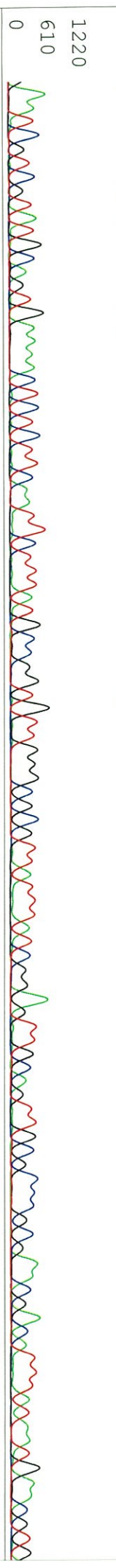


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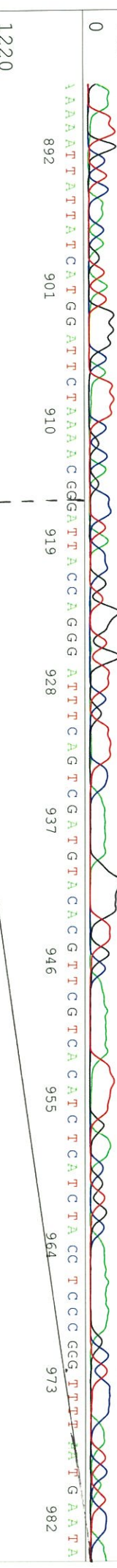
568 577 586 595 604 613 622 631 640 649 658 667 67

0 610 1220

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'84 AATTGCTCAACAGTATGGGCAATTTCCGCA GCCCTAC CGTGGTGTTCGTTCCAAAAAGGGGTTGCCAAAAAATTTTGAA CGTGCAAAAAAGCTCCCAATCCAA



892 AAAAAATTATTCATGATGATCTA AAAACGGGATTA CCAAGG ATTCAGTCGATGTACA GTTCCGTTCA CATCTCATCTA CC TCCC GGGTTT TAA TGAATA

991 CGA TTTT GTGCCAGAGTCCC TTTCGATA G G A C A G A C A TTTGCAC TGATCATGAACTCC TCTG ATCTA C TGG TCTG CG TT A

1072 AACGTGTCGCC TCGTGG C TCA TA G A C TG CC TG AG A TTCTCTCGCC ATG CC AG AG AG TT C G

1126 T A T T T T T G G CA



S/N G:38 A:47 T:44 C:41

primer name **B** : Luc-C_F

D03116A6_A6Bt_3_Luc-C_F
KB_3500_POP7_BDTV3.mob

Mar 24, 2016 04:05PM, JST
Mar 24, 2016 04:31PM, JST

KB.bcp

5- AGCACGGAAAGACGATGACCG -3'

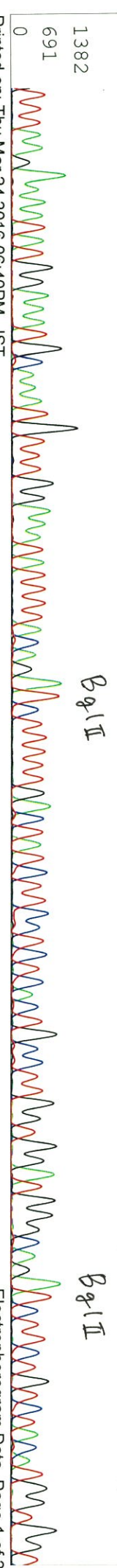
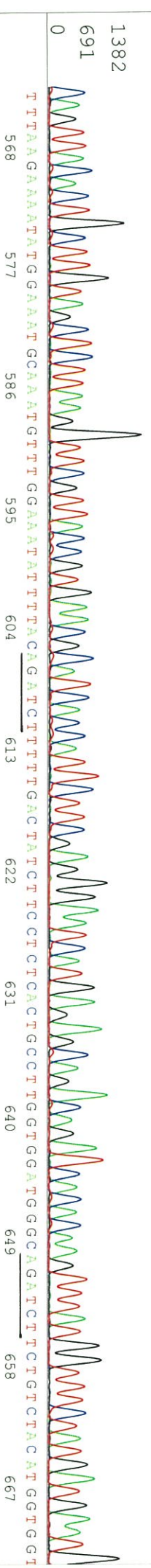
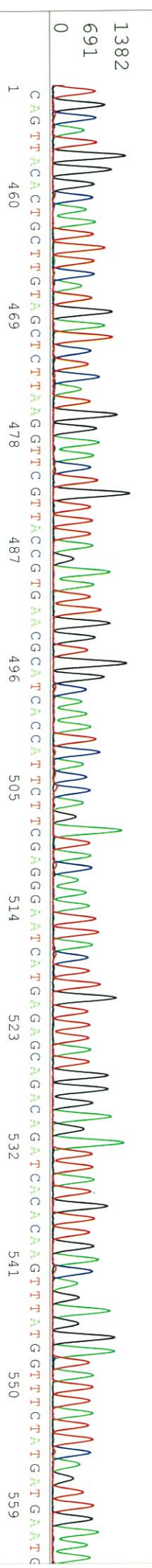
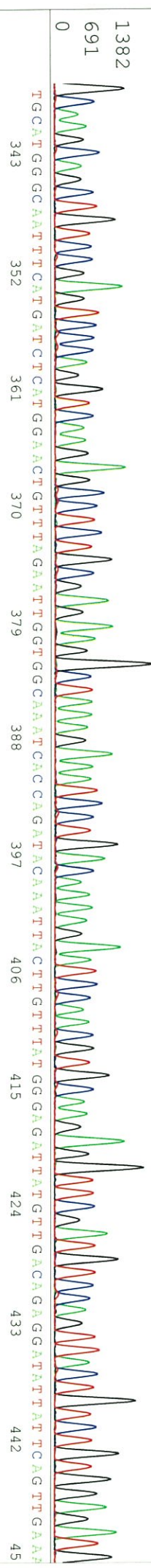
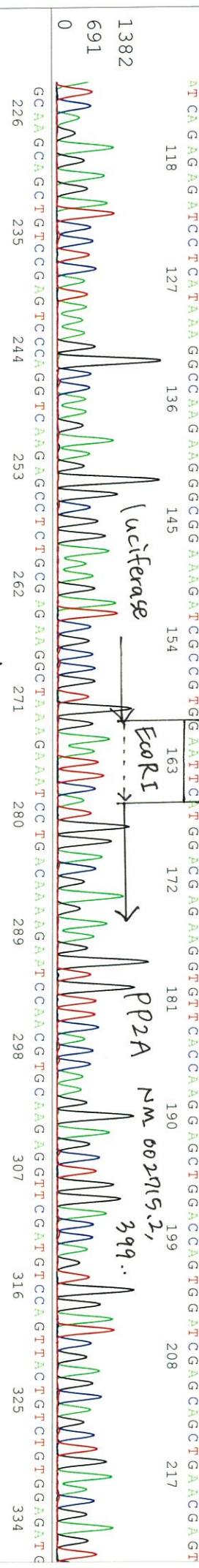
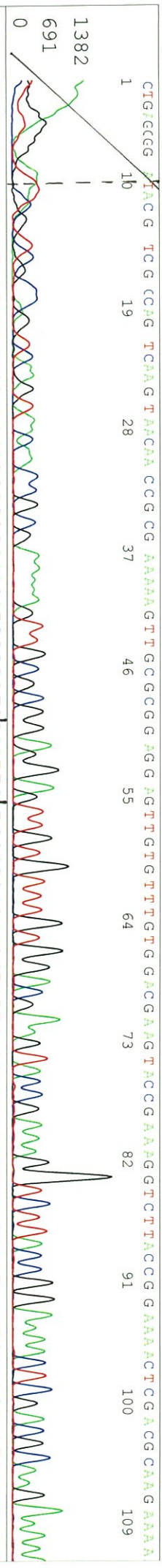
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Spacing: 11.03 Pts/Panel1350

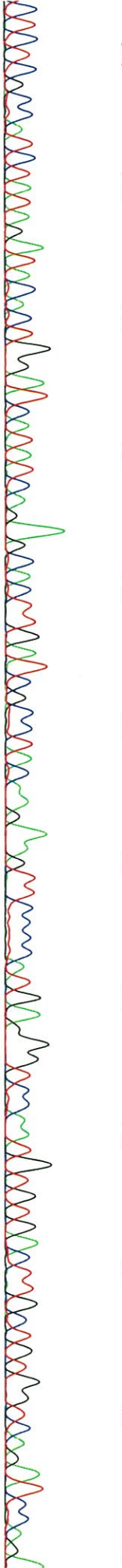
KB 1.4.1.8 Cap:24

Version 6.0 HiSQV Bases: 978

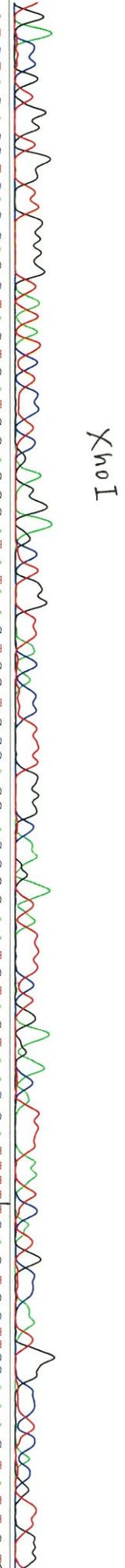
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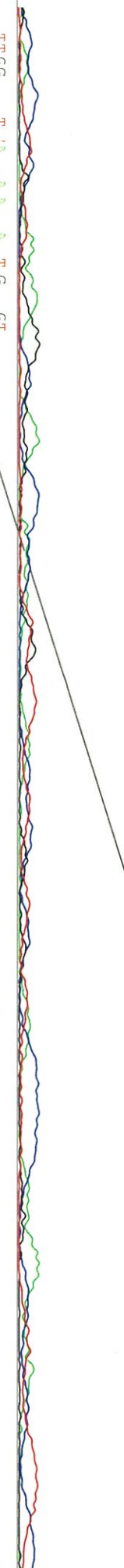
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T G A C C G T G T G G T T G G G G T A T A T C T C C T C G A G A G C T G G T T A C A C C T T G G G C A A G A T A T T C T G A G A C A T T A A T C A T G C C A A T G G C C T C A C G T T G G T

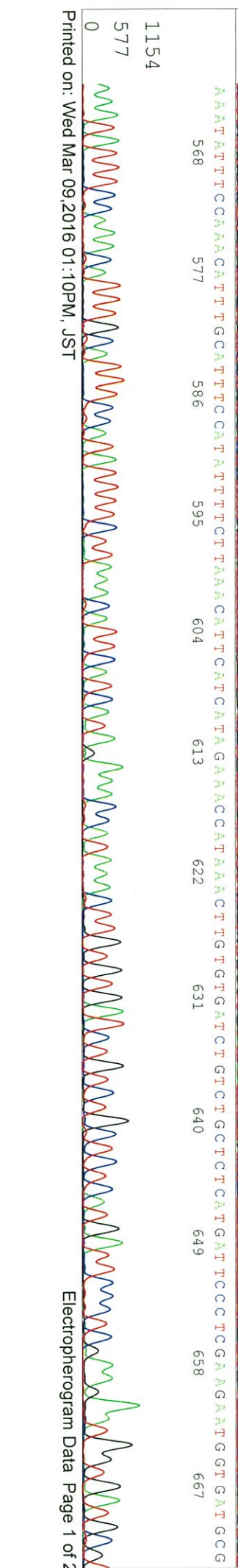
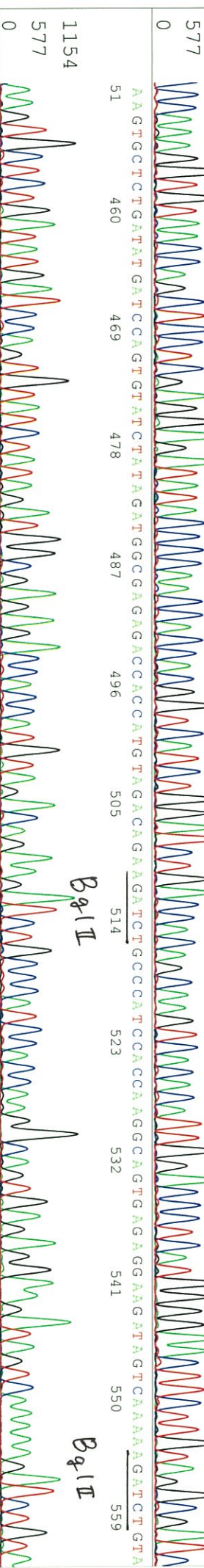
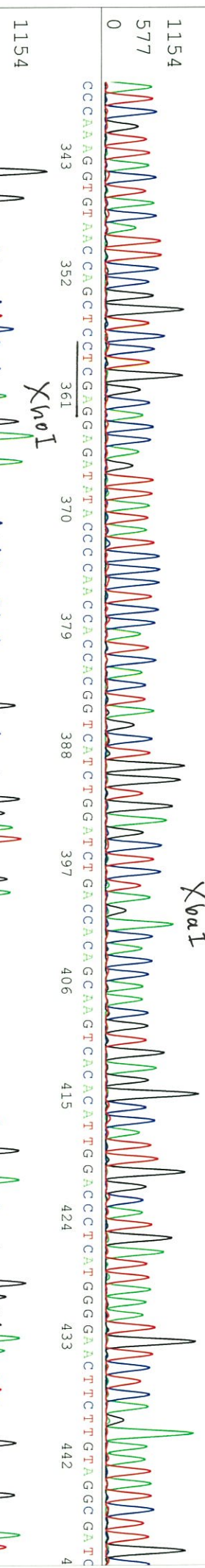
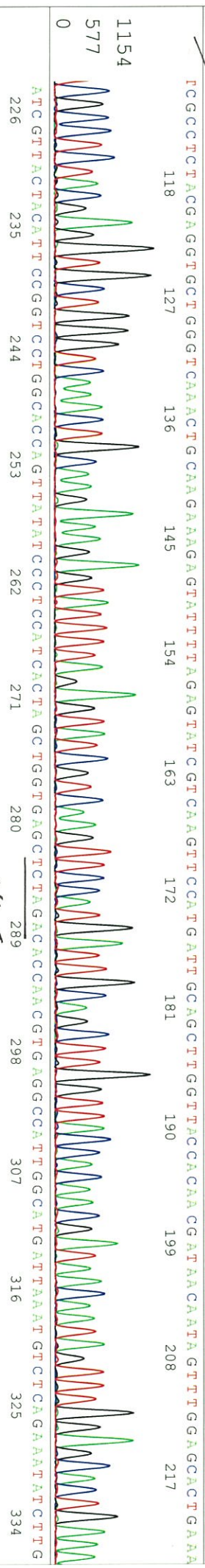
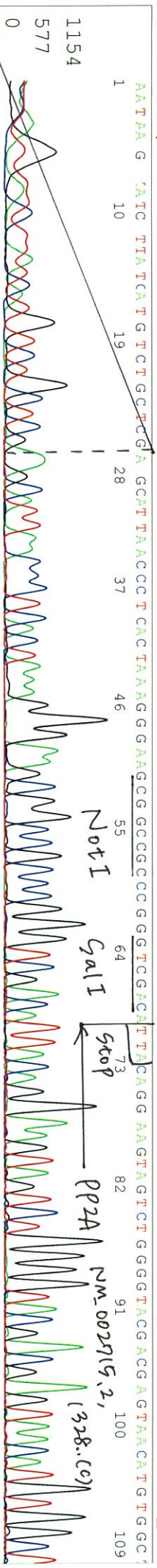


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T T G G T A A A A T G G T





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FGCCACCAAATTCTAACAAGTTCCATGAGATCATGAAATTGGCCCATGCAACAATCCACAGACAGTAACCTGGACATCGAACTCTTGCAACGTTGGATTCTTTTGTT
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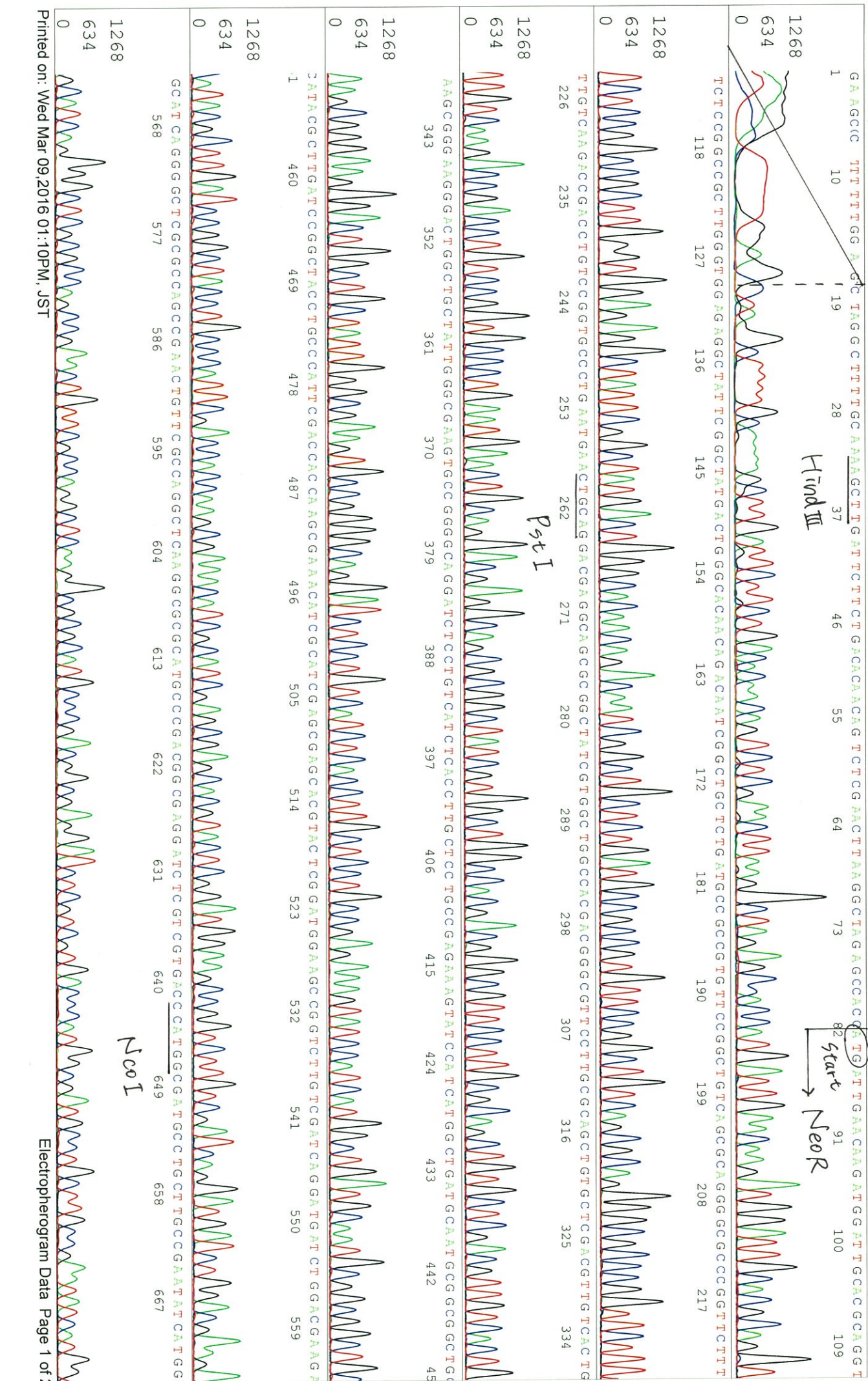
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33 892 901 910 919 928 937 946 955 964 973

TTGGGTGAACAACCTTCTCTCGTCCATGAA TTTCCACGGCGATCTTCCGCCCTTCTTGGTC TTTATGAA GATCTCTGTGA TTTT
982 991 1000 1009 1018 1027 1036 1045 1054

TCTTGGCGTCGAGTTTTCCTCCGGTAAGACGTTTACC TCCGATCGAACA AACA CAACTTCCCT
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TCCGC GCG GCAAACA CT
1126 1135





S/N G:299 A:231 T:222 C:358

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KB_3500_POP7_BDTV3.mob

KB bcp

Pts 1414 to 12870 PK1 Loc:1391

KB 1.4.1.8 Cap:5

Version 6.0 HiSQV Bases: 992

Mar 09, 2016 11:11AM, JST

Spacing: 11.5 Pts/Panel/350

Plate Name: 20160309_GNP

