

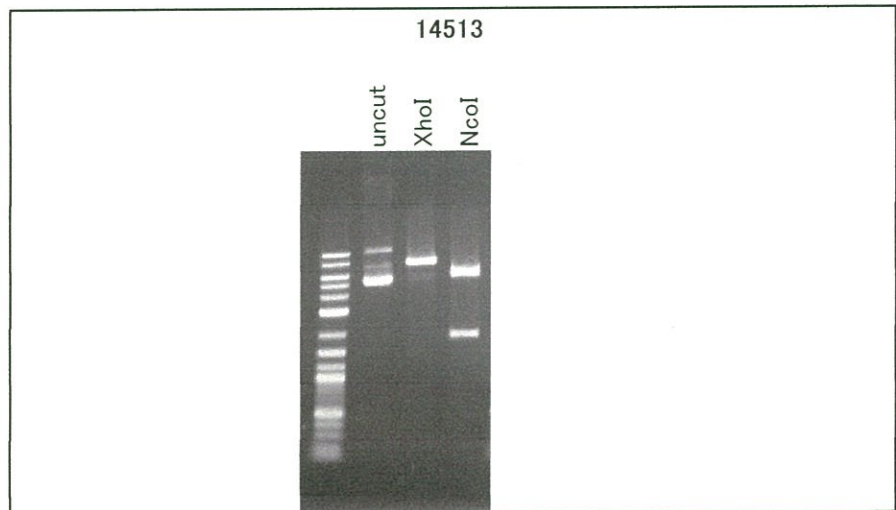
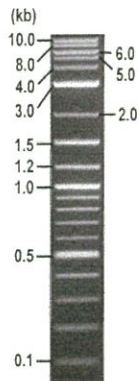


RIKEN DNA BANK

clone name : pMXs-IRES-hNGFR_G-CaMP6

- Clone ID : RDB_14513
- Lot : 14513_A6Le
- 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>XhoI</u>	<u>7.4</u> kbp
<u>NcoI</u>	<u>5.5, 1.9</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	pBABE5'	Sequence - E	SV40pA3'element Reverse
Sequence - B	IRES-R	Sequence - F	-
Sequence - C	IRES-F	Sequence - G	-
Sequence - D	Amp_R	Sequence - H	-

APPROVED BY :



primer name A : pBABES'

5- CTTATCCAGCCCTCAC-3'

D04073B4_A6Le_1_pBABES'_G01_19_AB124

D04073B4_A6Le_1_pBABES'

KB_3500_POP7_BDTV3.mob

Pls 1483 to 13701 Pk1 Loc: 1460

Version 6.0 HISQV Bases: 989

Inst Model/Name 3500/3500 Instrument

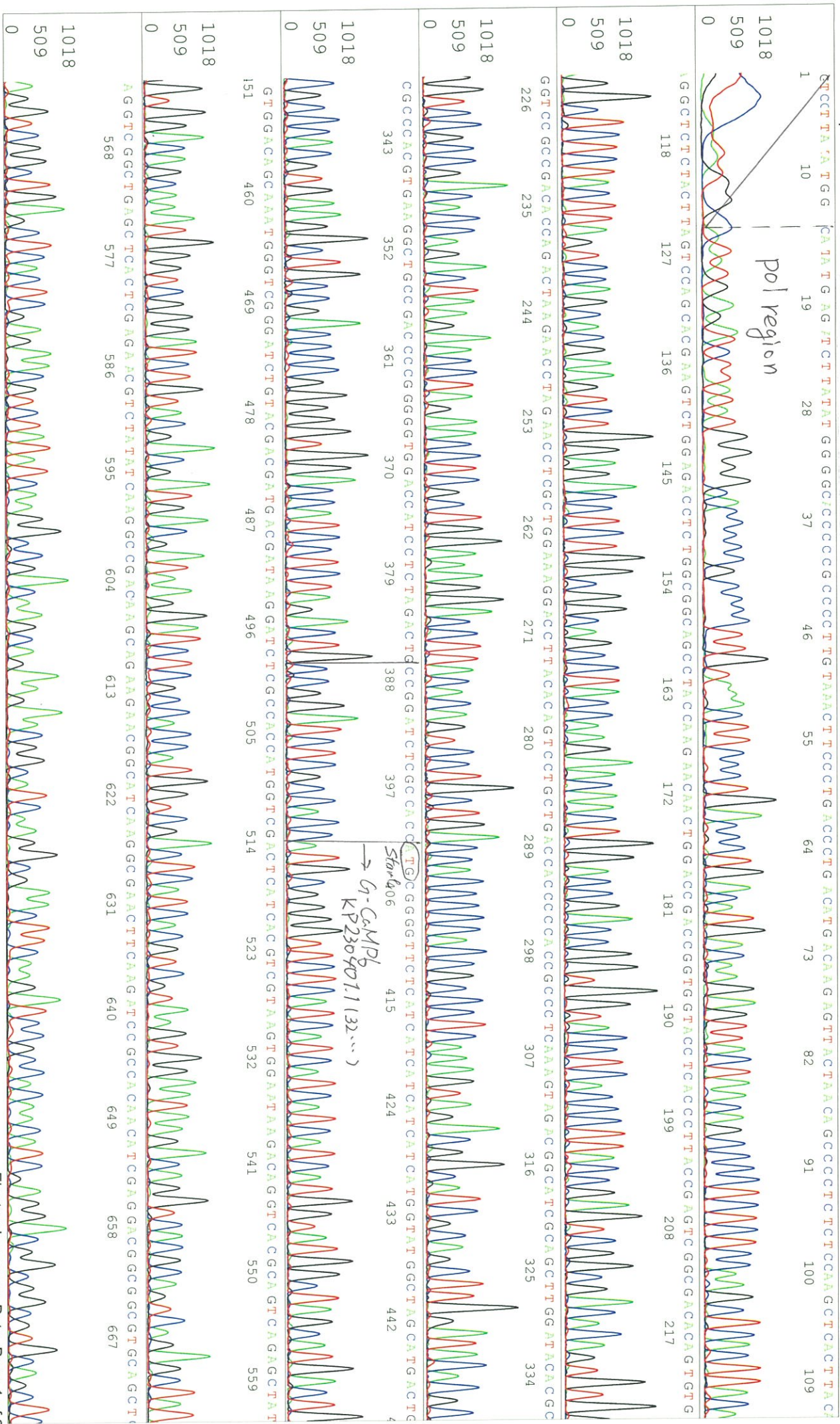
Jan 25,2017 09:37AM, JST

Jan 25,2017 10:09AM, JST

Spacing:12.21 Pts/Panel1350

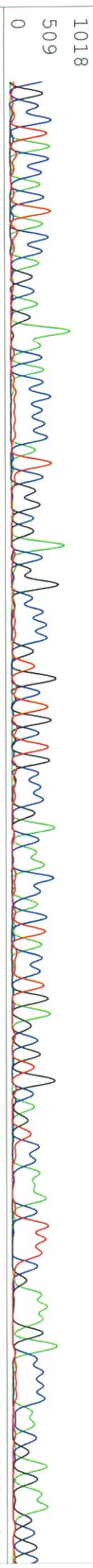
Plate Name: 20170125 kitaku

pol region

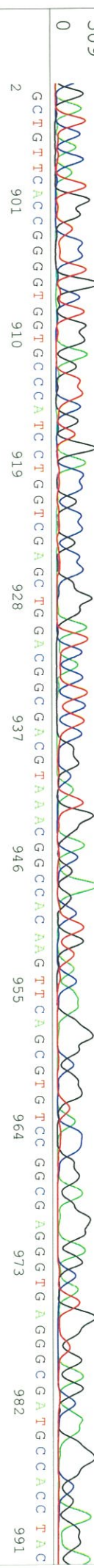


Star 406
G-CAMP
KP230401.1(32...)

CGCCTACCCTACCAAGCAACAACCCCATCCGGCCGACGGCCCGCTGCCTGCCCCGACCAACCACTAACCTGAGCGTGCCAAACTTCGAAAACCCCAACGAAAGCCG
 676 685 694 703 712 721 730 739 748 757 766 775 784



793 802 811 820 829 838 847 856 865 874 883 89



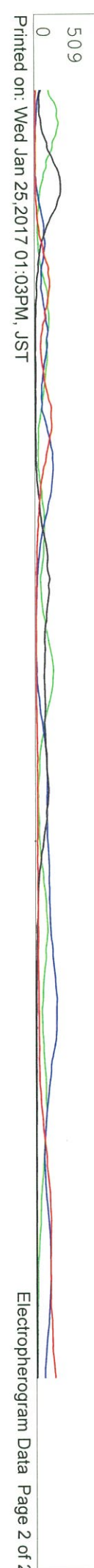
2 901 910 919 928 937 946 955 964 973 982 991



1000 1009 1018 1027 1036 1045 1054 1063 1072



1081 1090 1099 1108 1117 1126 1135



1144 1153 1162 1171

S/N G:415 A:317 T:365 C:405 primer name B : IRES-R

D04073B4_A6Le_1_IRES-R
KB_3500_POP7_BDTV3.mob
Pis 1457 to 13588 Pk1 Loc:1434

Jan 25, 2017 09:37AM, JST
Jan 25, 2017 10:09AM, JST
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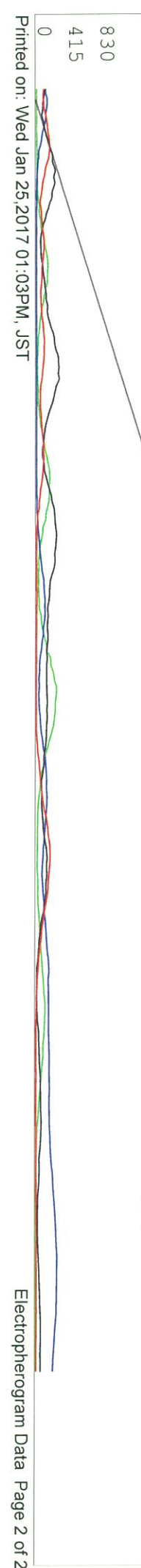
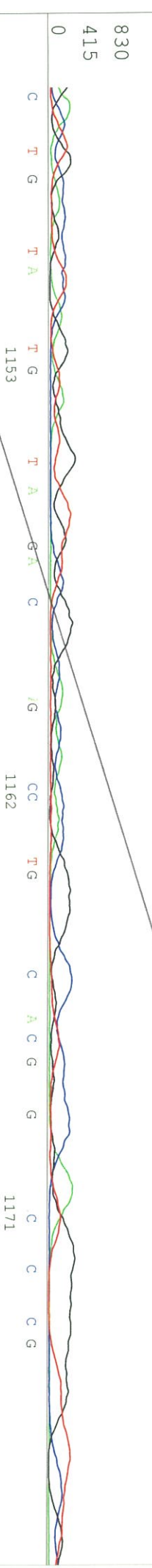
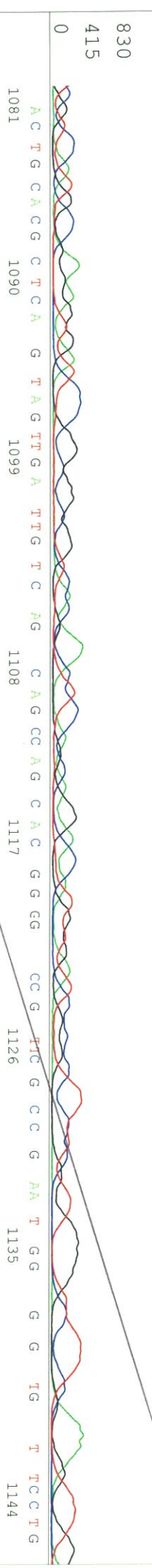
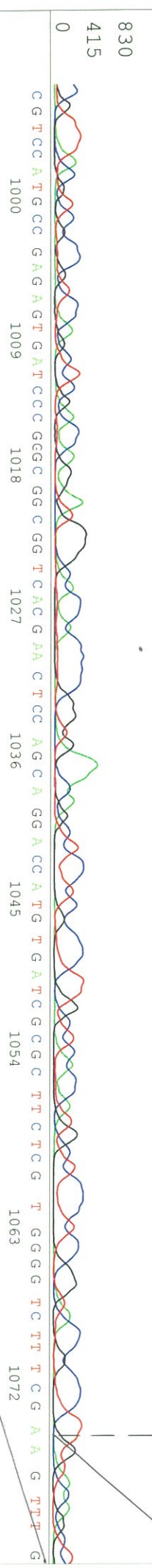
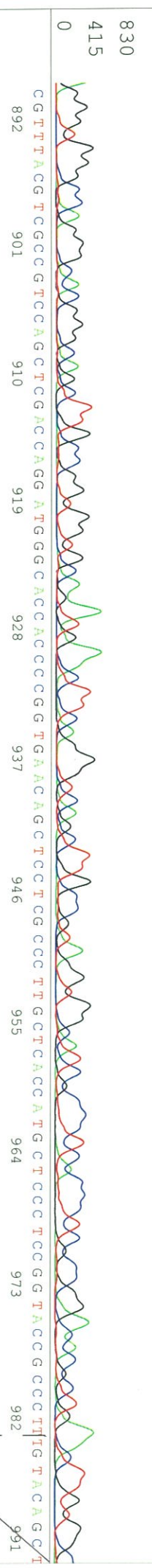
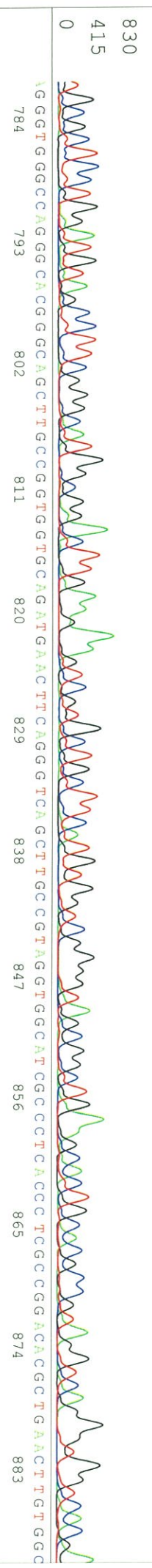
KB:bcp Cap:15 5'-ACATATAGACAAACGCACACC-3'

Version 6.0 HiSQV Bases: 994

Plate Name: 20170125 Kitaku



TGCGCTCCCTGGATGTAGCCCTTCGGGGCATGGCCGAACTTGAAGAAAGTCCGTGCTGCTTCAATGGTGGTCCGGGTAAGGCACTGAAAGCACTGCAACCGCCGTAAGGTCAAGGGTGTCACCG



S/N G:154 A:114 T:94 C:135

D04073B4_Able_1_IRES-F

Dec 22, 2016 02:44PM, JST

KB.bcp

primer name C : IRES-F

KB_3500_POP7_BDTv3.mob

Dec 22, 2016 03:11PM, JST

KB 1.4.1.8 Cap:22

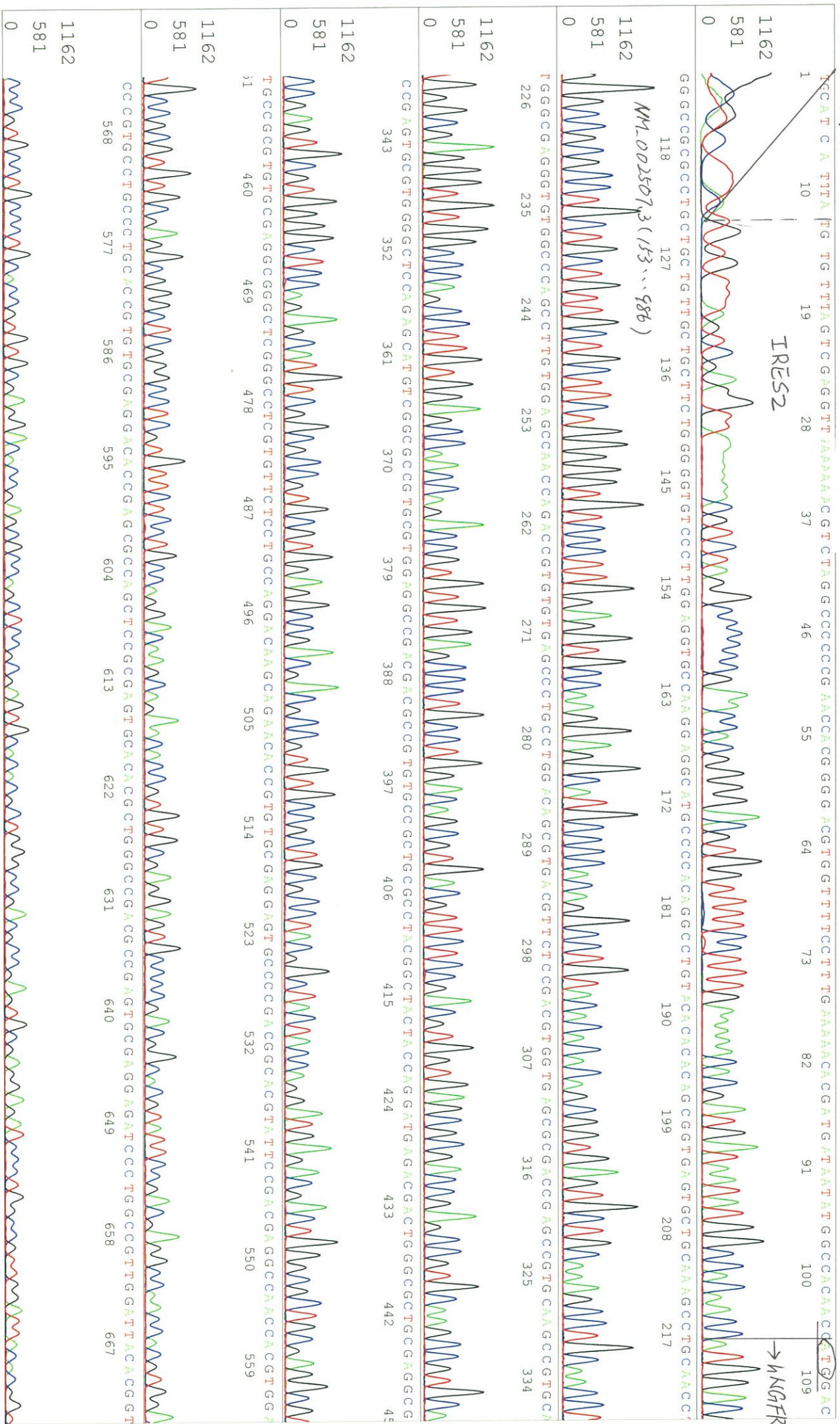
5'-TTGATGGGATCTGATCTGG-3'

Pts 1552 to 13365 PK1 Loc:1529

Spacing:12.01 Pts/Panel1350

Version 6.0 HiSeqV Bases: 988

Plate Name: 20161222 Kitaku



CCACACCCCCAGAGGGCTCCGGACAGCACAGCCCCCAAGCCCAAGCCCTGAGGCCACCCTCCA GAA CAA GAACC TCATAGCCCA GCA CGTG GCA GGTG GACCA CA
 676 685 694 703 712 721 730 739 748 757 766 775

1162
581

G T G A T G G G C A G C T C C C A G C C C G T G A C C C G A G G C A C C A A C C T C A T C C C T G T C T A T T G C T C C A T C C T G G C T G T G T G G C C T T G T G G
 784 793 802 811 820 829 838 847 856 865 874

1162
581

CC T A C A T A G C C T T C A A G A G G T G G A A C A G C T G C A A G C A G A A G C A A G C A A G C A A G C A A G T A A A A G A T T A A A G A T T T A G
 883 892 901 910 919 928 937 946 955 964

1162
581

T C T C C A G A A A A A G G G G G G A A A T G A A G A C C C C A C C C T G T A G T T T G G C A A G G C T A G C T T A G T A C G G C C A A T T T T G G C A A G
 973 982 991 1000 1009 1018 1027 1036 1045

1162
581

C A A T G A A A A A T T A C A T T A A C C T T G A G A T T A G A G A G T C C A G A C T C A A G T C A A G A A G A A C A G
 1054 1063 1072 1081 1090 1099 1108

1162
581

A A T T G G A A C C A
 1117

1162
581



S/N G:98 A:85 T:82 C:81

D04073B4_A6Le_1_Amp_R

Dec 22, 2016 02:44PM, JST

KB:bcp

primer name D : Amp_R

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Dec 22, 2016 03:11PM, JST

KB 1.4.1.8 Cap:17

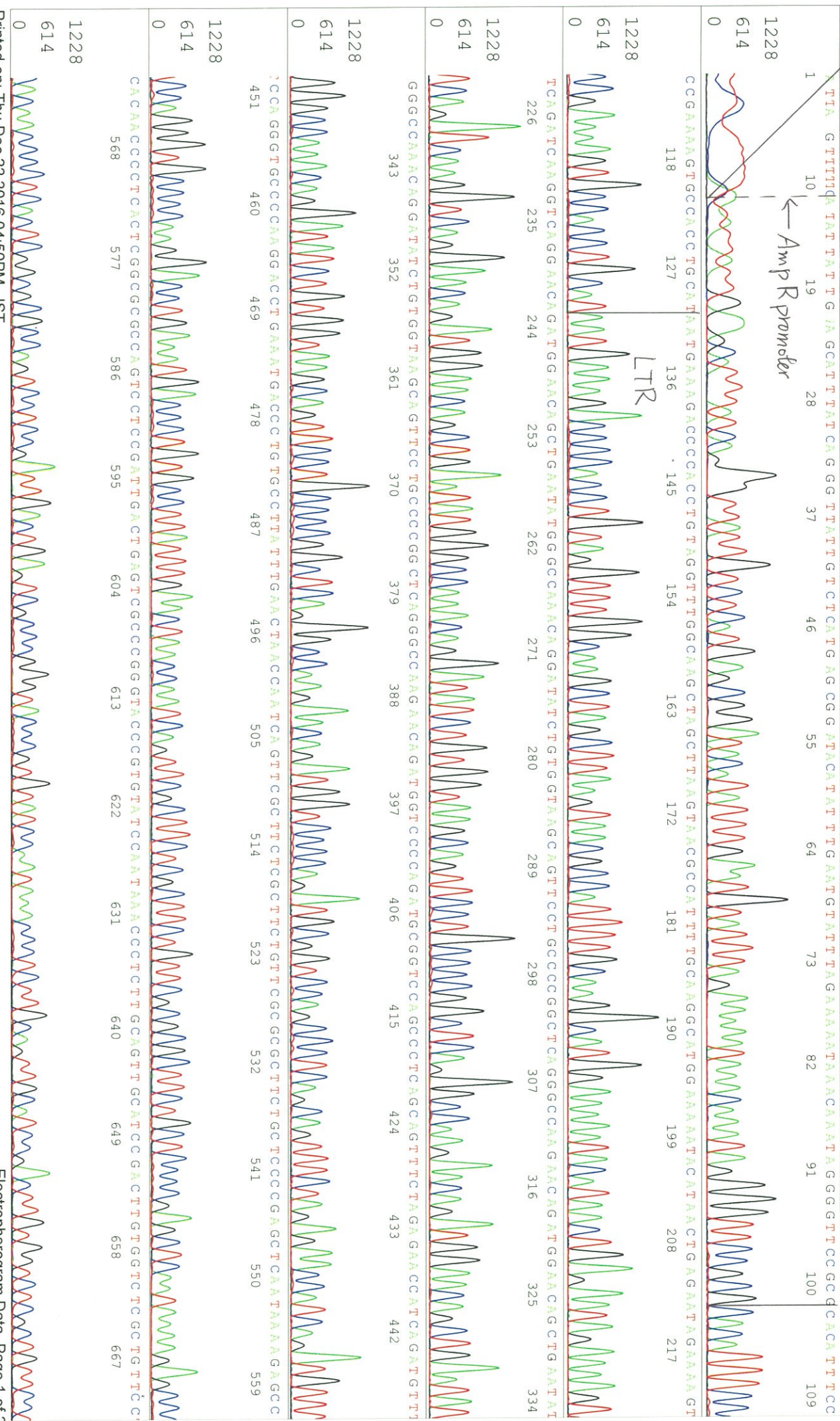
5'-GGCAGACCGGAAATGTTGAATA-3'

Pts 1515 to 13179 PK1 Loc:1492

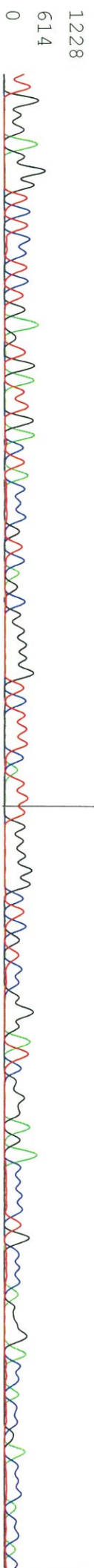
Spacing:11.74 Pts/Panel:350

Version 6.0 HiSeqV Bases: 985

Plate Name: 20161222 kitaku



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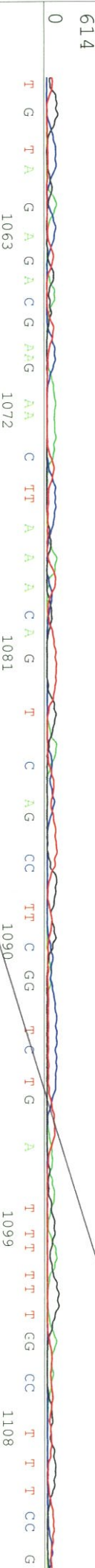


HMLV

CGGAGGTAAAGCTGGCCAGCAACTATCTGTGCTGTCCGATTGTTCTAGTGTCTATGACTGATTTATGGCCCTGGCTCGGTACTAGTTAGCTTAGCTC



TGTTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCCGAAACCCCGCCGAAACCAGACGTTCCCAAGGACTTCTGGGGATTAATGTTGGTTT



TTGGCCCGAACCTGAGTCCAAAAATCCCGATCGTTTGGACTCTTTGGGGTGCAACCCCTTTAGAGGAGGGATTAATGTTGGTTTCC



GTATAGAGACGGAGGAAATCCTTAAACAATCAGTTCAAGCCTTCCGGTGAATTAATGTTGGTTTCCG

S/N G:47 A:47 T:39 C:43 primer name E : SV40pA3element Reverse

KB_bcp KB_3500_POP7_BDTV3.mob

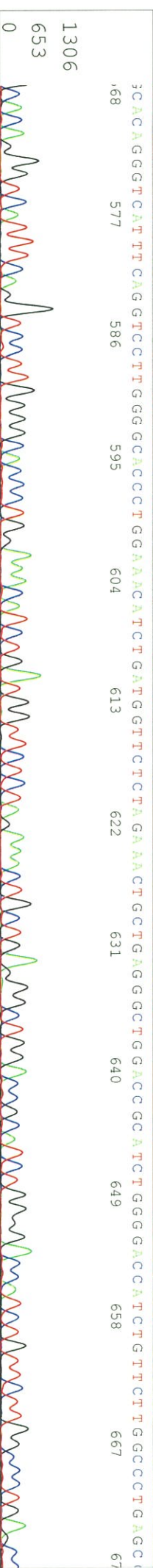
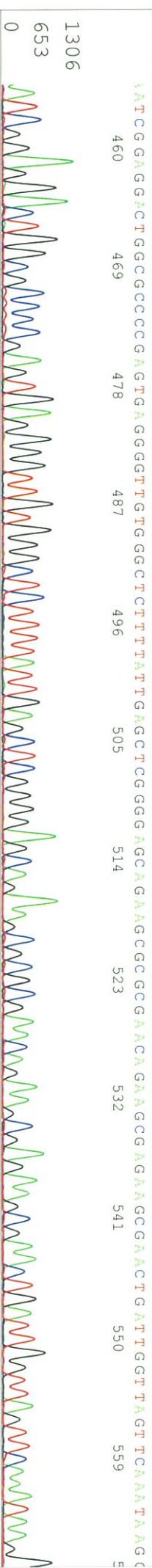
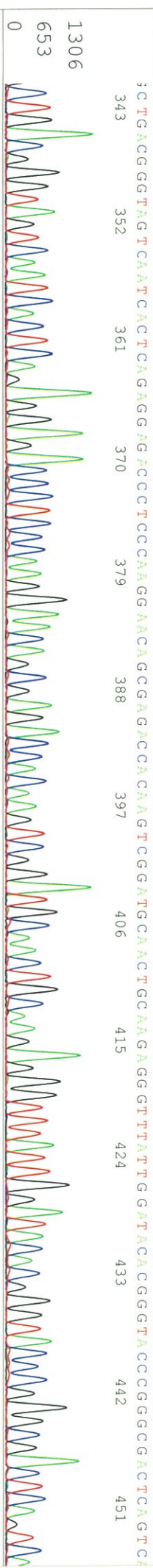
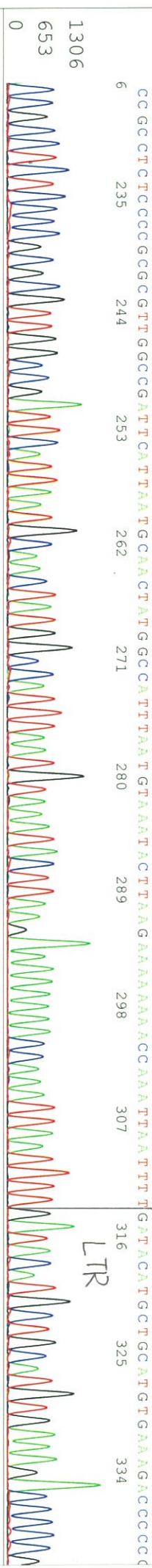
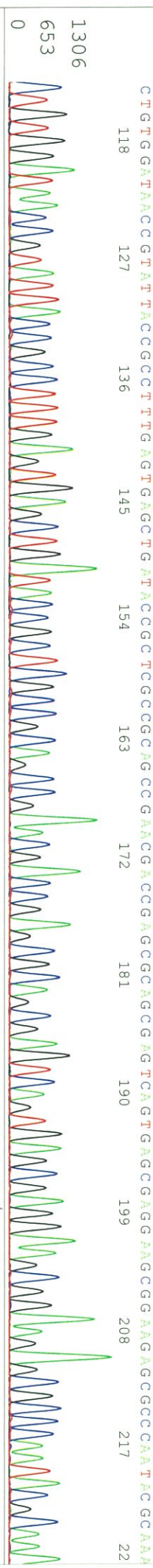
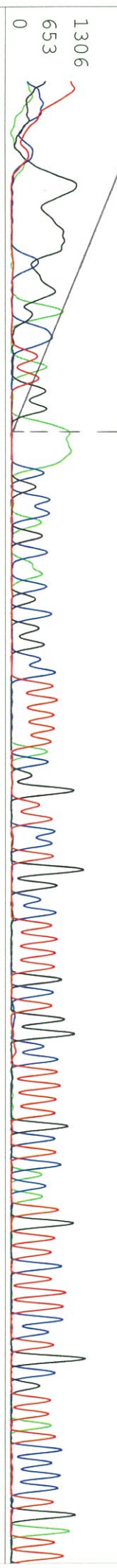
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KB 1.4.1.8 Cap:20 5-CTCTGACTTGAGCGTCGATT-3'

Pts 1516 to 13060 PK1 Loc:1493

Spacing:11.69 Pts/Panel1350

Version 6.0 HiSeqV Bases: 969



3GGGGAGGAACCTGCTTACCACCAGATTATCCCTGTTGGGCCCAATTTCAGAGCTTCCATCTGTTCTGGGCCCTGAGCCGGGGCAGGAACTGCCTAACCAAGATTATCC

