

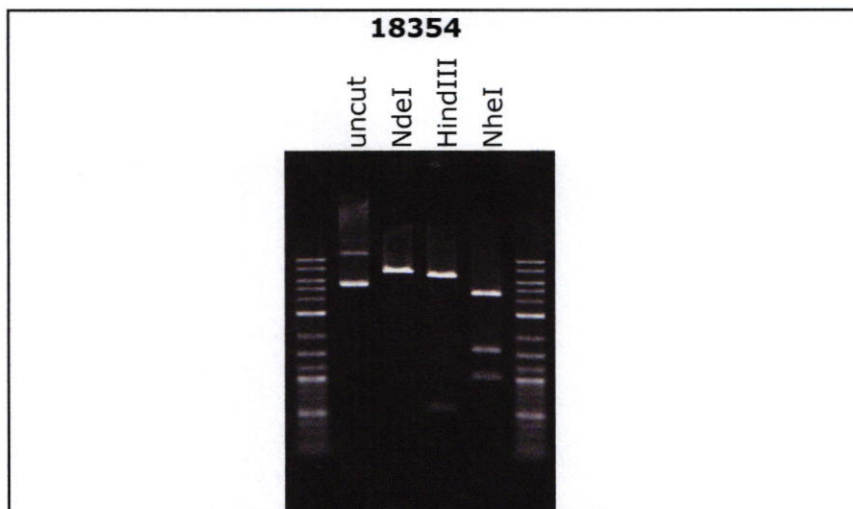
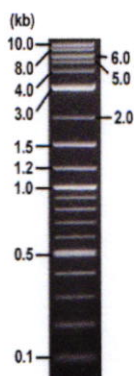


RIKEN DNA BANK

clone name : CTCF-mAC donor (Hygro)

- Clone ID : RDB_ 18354
- Lot : 18354 _ B2Ha
- 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

1 kb Plus DNA Ladder
(NEB#N3200L),
250 ng/well



Electrophoresis : 100 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment	
NdeI	7.3	kbp
HindIII	6.7, 0.6	kbp
NheI	4.6, 1.6, 1.0	kbp
		kbp

● Confirmation of the insertion sequence

Please be sure to check our sequence analysis results before your request.

Sequence name	Primer ID	Primer name	Confirmed feature
Sequence - A	Pr0743	EGFP-M_R	insert mid(mClover 5',mAID 3')
Sequence - B	Pr0894	mPGKter_F	insert 3'(loxP.2,CTCF homology arm.2)
Sequence - C	Pr0243	PGK_N_rev	insert mid(SV40 pA,mClover 3')
Sequence - D	Pr0249	PGKpro_F	insert mid(HygR)
Sequence - E	Pr0739	pUC-CAPbs_up_F2	insert 3'(CTCF homology arm.2, loxP.2,mPGK ter)
Sequence - F	Pr0310	pUC-M13_-100	insert 5'(T7 pro,CTCF homology arm.1,mAID 5')
Sequence - G	Pr0127	YFP_R	insert 5'(mClover 5',mAID,CTCF homology arm.1)
Sequence - H	-	-	-

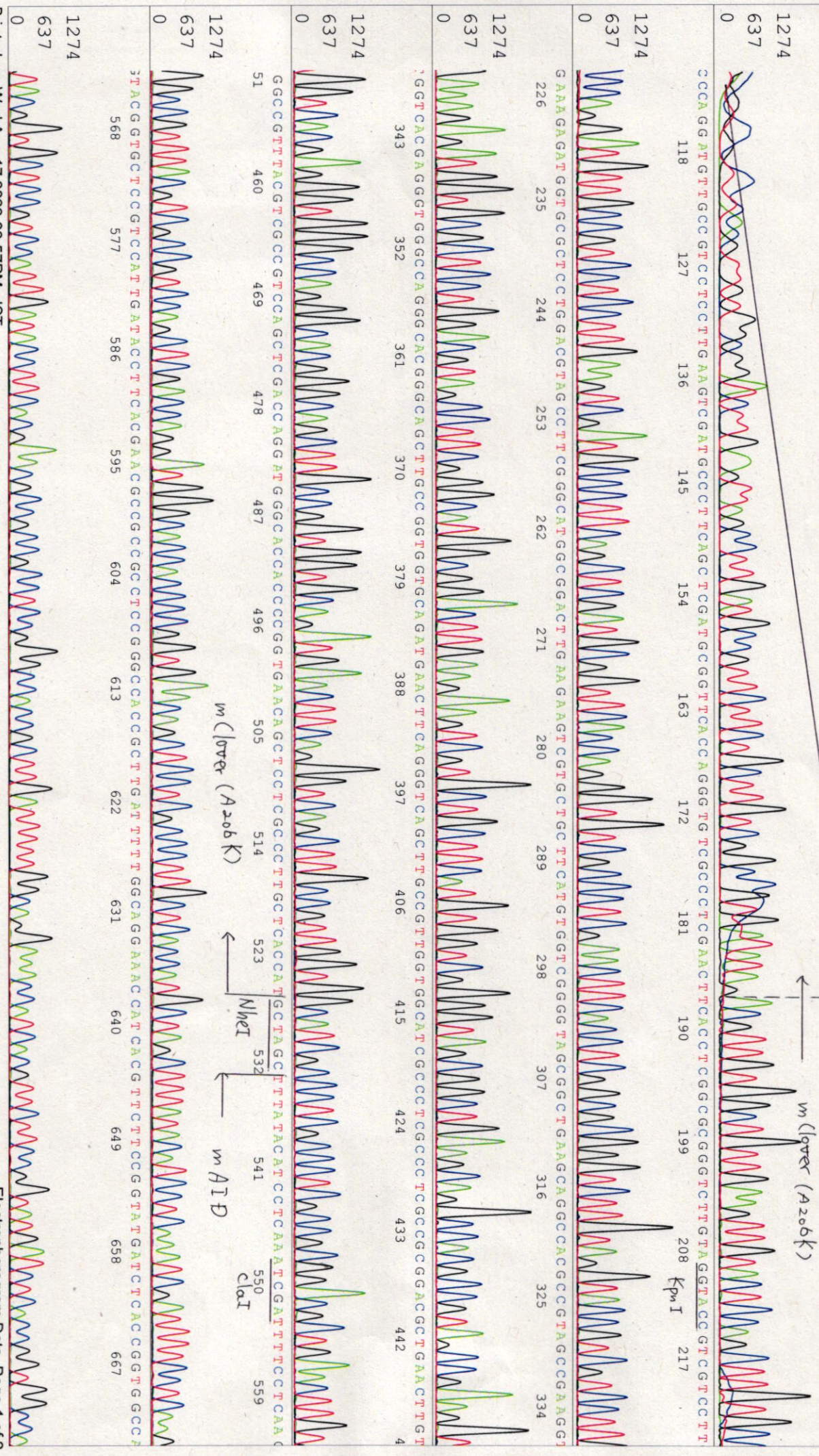
APPROVED BY :

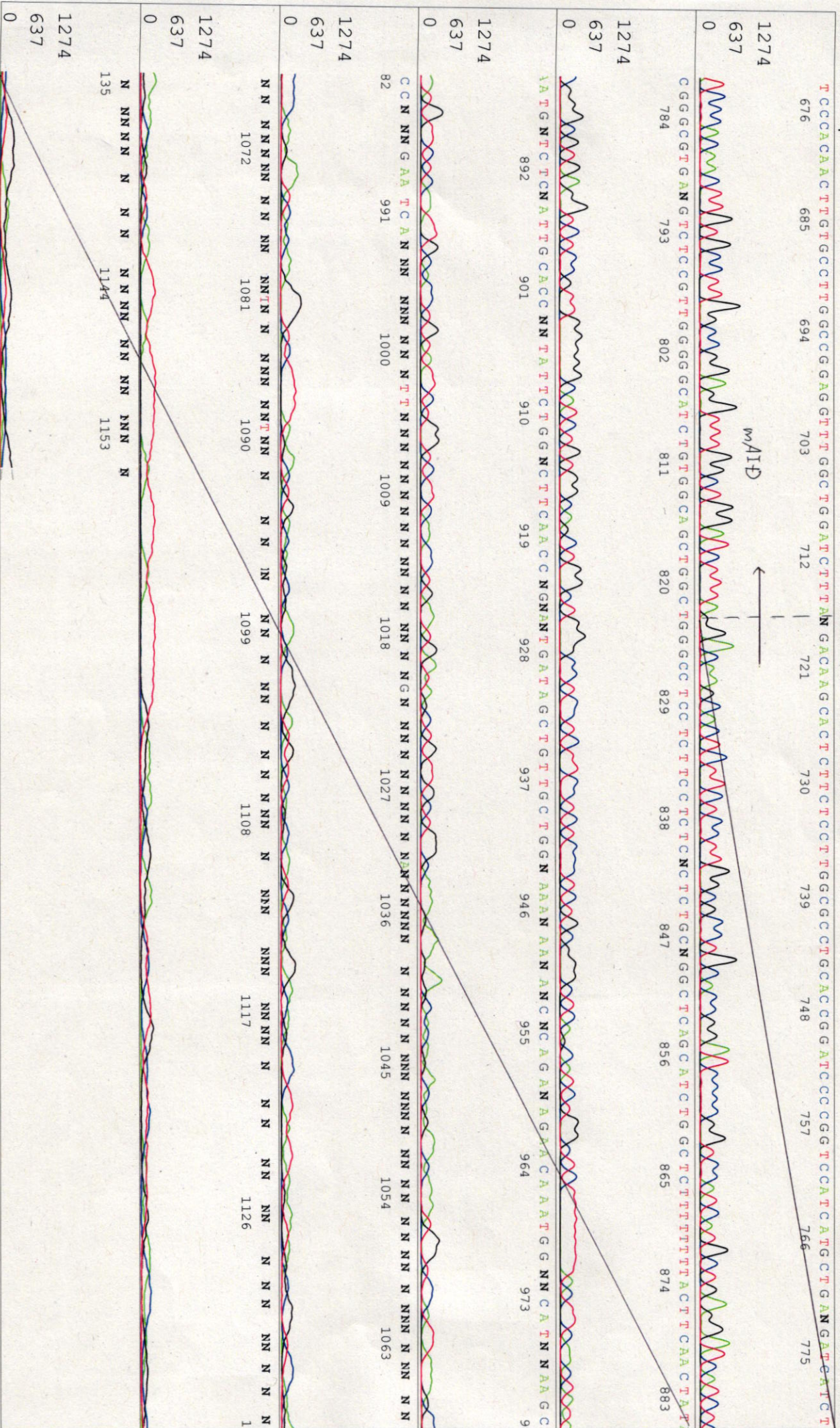


S/N G:268 A:127 T:147 C:184 primer name A : EGFP-M_R

KB bcp KB_3500_POP7_BDTv3.mob Pts 1476 to 13555 PK1 Loc:1453

KB 1.4,1.8 Cap:10 5' TGTTCTGCTGGTAGTGTGCG3' Version 6.0 HISQV Bases: 944





S/N G:196 A:151 T:118 C:163

primer name D : PGKpro_F

D07105C4_B2Ha_3_PGKpro_F
KB_3500_POP7_BDTv3.mob

Aug 17, 2022 01:47PM, JST

KB bcp
KB 1.4.1.8 Cap:7

5'-ATTCTGCACGCTTCAAAG-3'

Pts 1430 to 13569 PK1 Loc:1407
Version 6.0 HISQV Bases: 932

Aug 17, 2022 02:14PM, JST
Spacing:12.1 Pts/Panel1350
Plate Name: 20220817 Kitaku



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

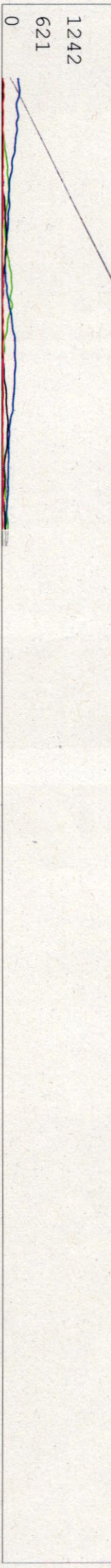
ACATCTTCTTCTGGANGCCGTGGTTGGCTTGTATGGAGCAGCAAGACCGCTACTTCNAGCGGANCCGATCCGGANTTGCANGATCCCGCGCGCTCCNGCGTATA
784 793 802 811 820 829 838 847 856 865 874 883

TGCTCCGCANTTGGTCTTGANCNNCTCTATCAGANCNNGNTNANGGCCNATTTCCGATGANCCNCTTGNNNCNNGNCGATGCNANNCNNNCN
892 901 910 919 928 937 946 955 964 973 982

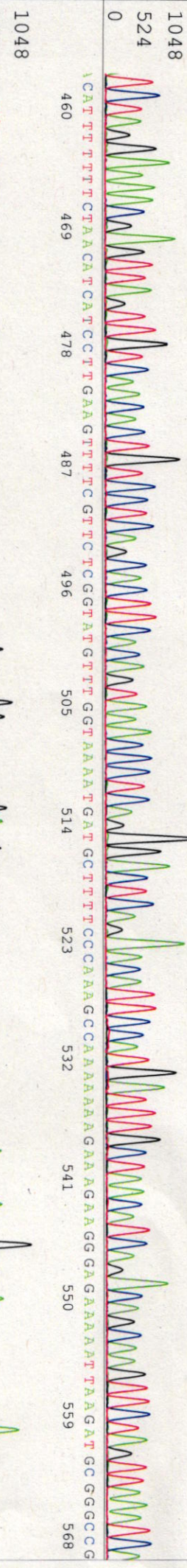
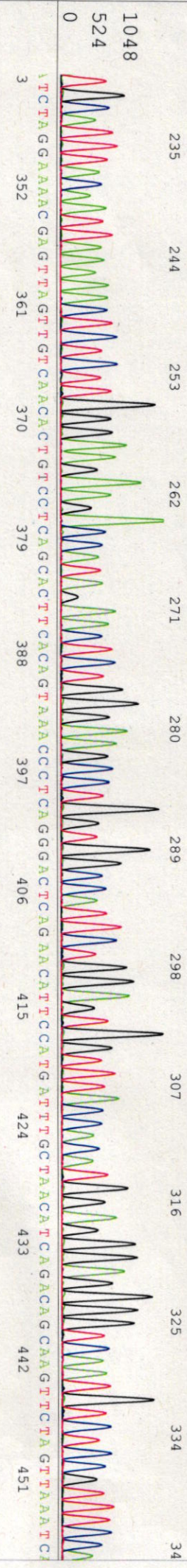
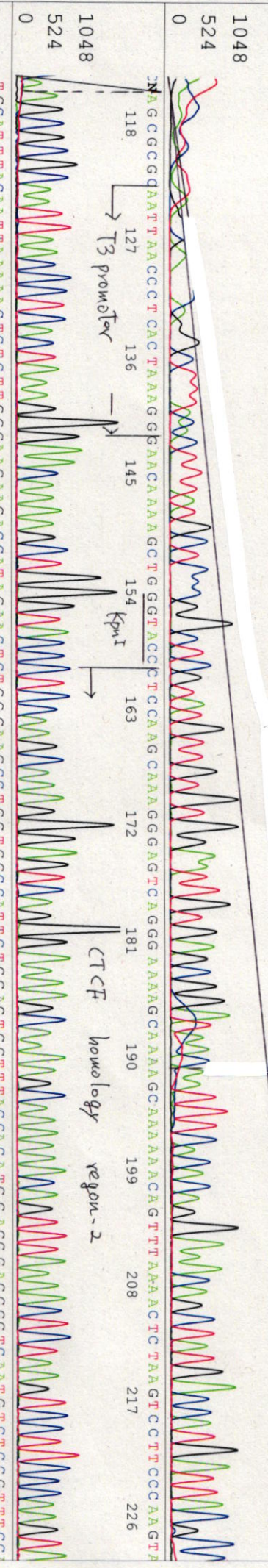
TNNNGANNCNNGNNGNNGGNNGGNN
991 1000 1009 1018 1027 1036 1045 1054 1063 1072 1081 1090 1099 1108 1117 1126 1135

NN
1144 1153

NN
1144 1153



NNNNN NN NNNN NNNN NNNN N CTTTNNCTTTTATGCTCCCGCTCCGTATGTTGTGGAAATTGTGAGCCGAAATTTCAACCAAGAAACAGTATGACCAATGATTCGC



primer name *G* : YFP_R

KB_3500_POP7_BDTV3.mob

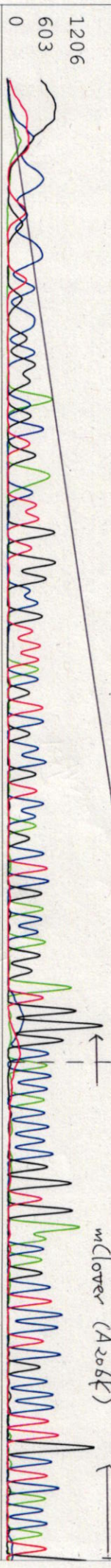
Pis 1444 to 13650 PK1 Loc:1421

Version 6.0 HISQV Bases: 957

5- GAACCTCAGGGTCAAGCTTGC -3'

S/N G:208 A:118 T:134 C:169
KB bop
KB 1.4.1.8 Cap:1

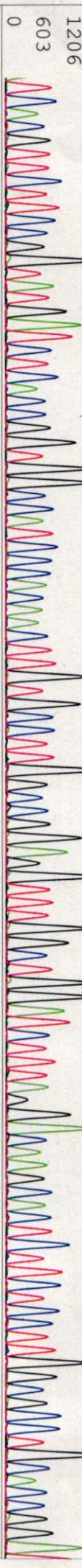
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GCTAGC TTTATACA TCC TCAAA TCGATT TTTCC TCAA GTACG GTGC TCCG TCCCA TTGATACC TTCA CAGCAACGC CCGCCCTCCCGGGCCACCCGCTTGATT TTTGGCA GAAACC



ATCAGCTTCTTCCGGTATGATCTCA CCGG TGGCCATCCCA CAACCTTG TGCCCTTGGCCGGAGGTTTGGCTGGATCTTTAGGACAAGCACTTCTCTTGCGGCC TGCACCGGA



TCGCCGGTCCCATCATGCTGAGGATCATCTCGGGCGTGAAGTCTCCGTTGGGGCATCTGTGGCA GCTGGCTGGCCCTCCCTCTTCTCCCTCCCTCTGCGGGCTCAAGCATCTGGCT



GCCCCAAGAAATCAACAAGGCTCTTTTAA GACTGACAGCGAACGGGATGTCAGCAATGCAGGACAGCC TTTATAGATA GCGGTC CAGAGACA GTCAATTTTATTTTATTT



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