

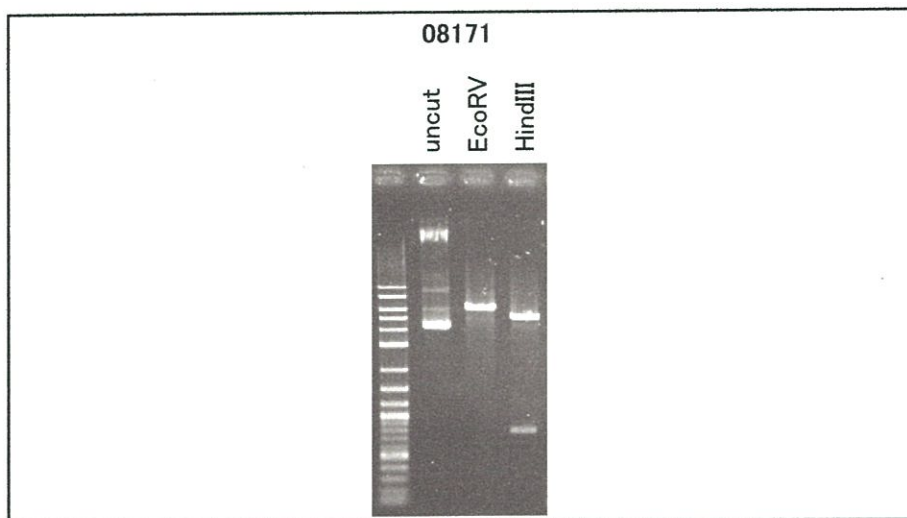
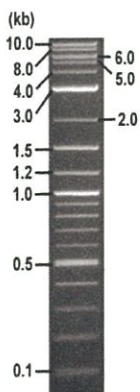


**RIKEN DNA BANK**

clone name : pGEX-hp38

- Clone ID : RDB \_ 08171
- Lot : 08171 \_ A7Kt
- 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),  
250 ng/well



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

Restriction enzyme	Expected size of fragment
<u>EcoRV</u>	<u>6.1</u> kbp
<u>HindIII</u>	<u>5.3, 0.8</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	pGEX-F2	Sequence - E	-
Sequence - B	pJB8-Forward	Sequence - F	-
Sequence - C	pGEX-ptac_up-F	Sequence - G	-
Sequence - D	M13_-40	Sequence - H	-



APPROVED BY :



S/N G:97 A:118 T:130 C:147

08171\_08171\_A7Kt\_1\_pGEX-F2

Dec 08, 2017 02:51PM, JST

KB.bcp

primer name A : pGEX-F2

KB\_3500\_POP7\_BDTv3.mob

Dec 08, 2017 03:31PM, JST

KB 1.4.1.8 Cap.6

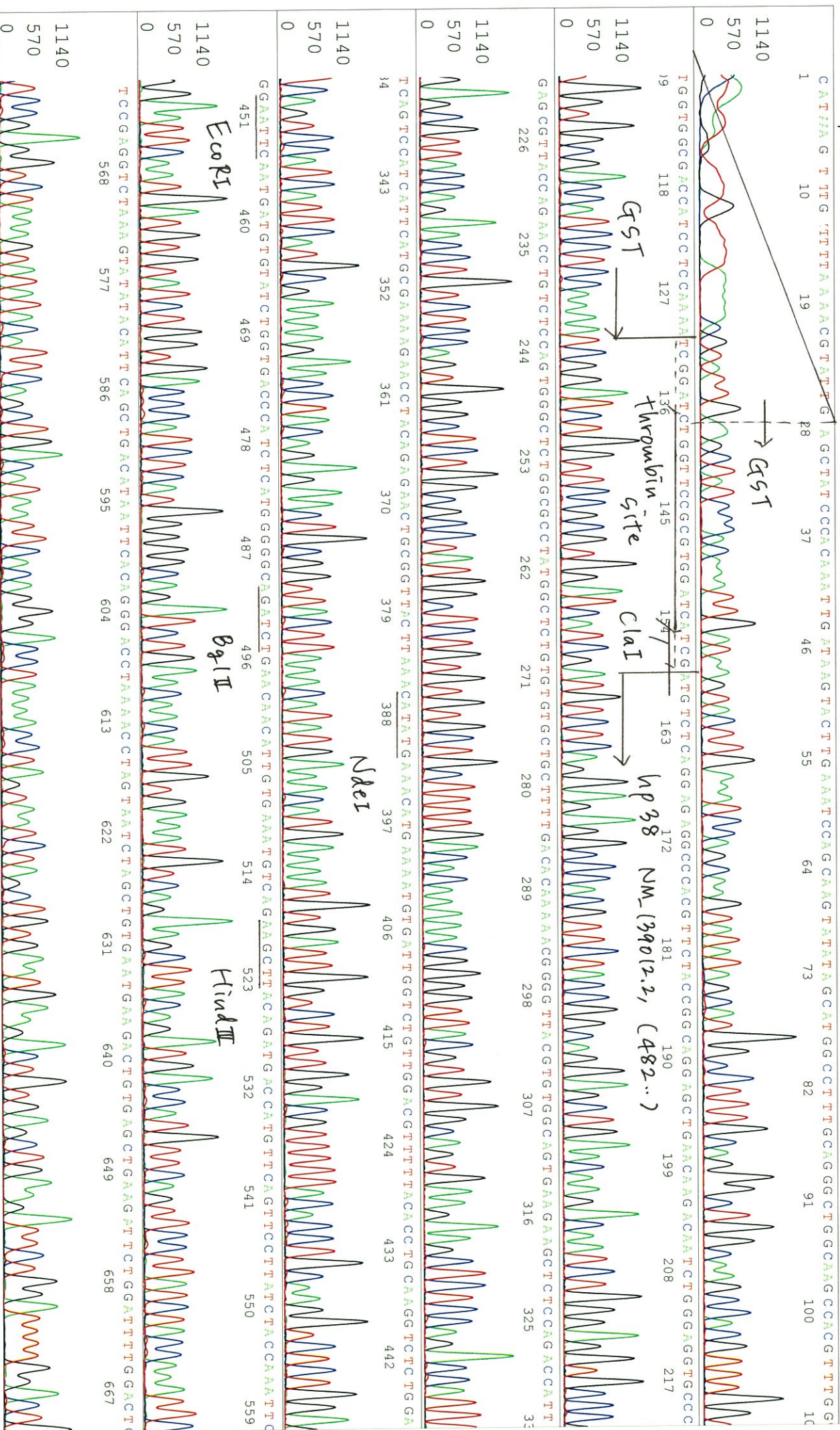
5'-ACATGGACCCAATGTGCCTG-3'

Pls 1510 to 12779 PK1 Loc:1487

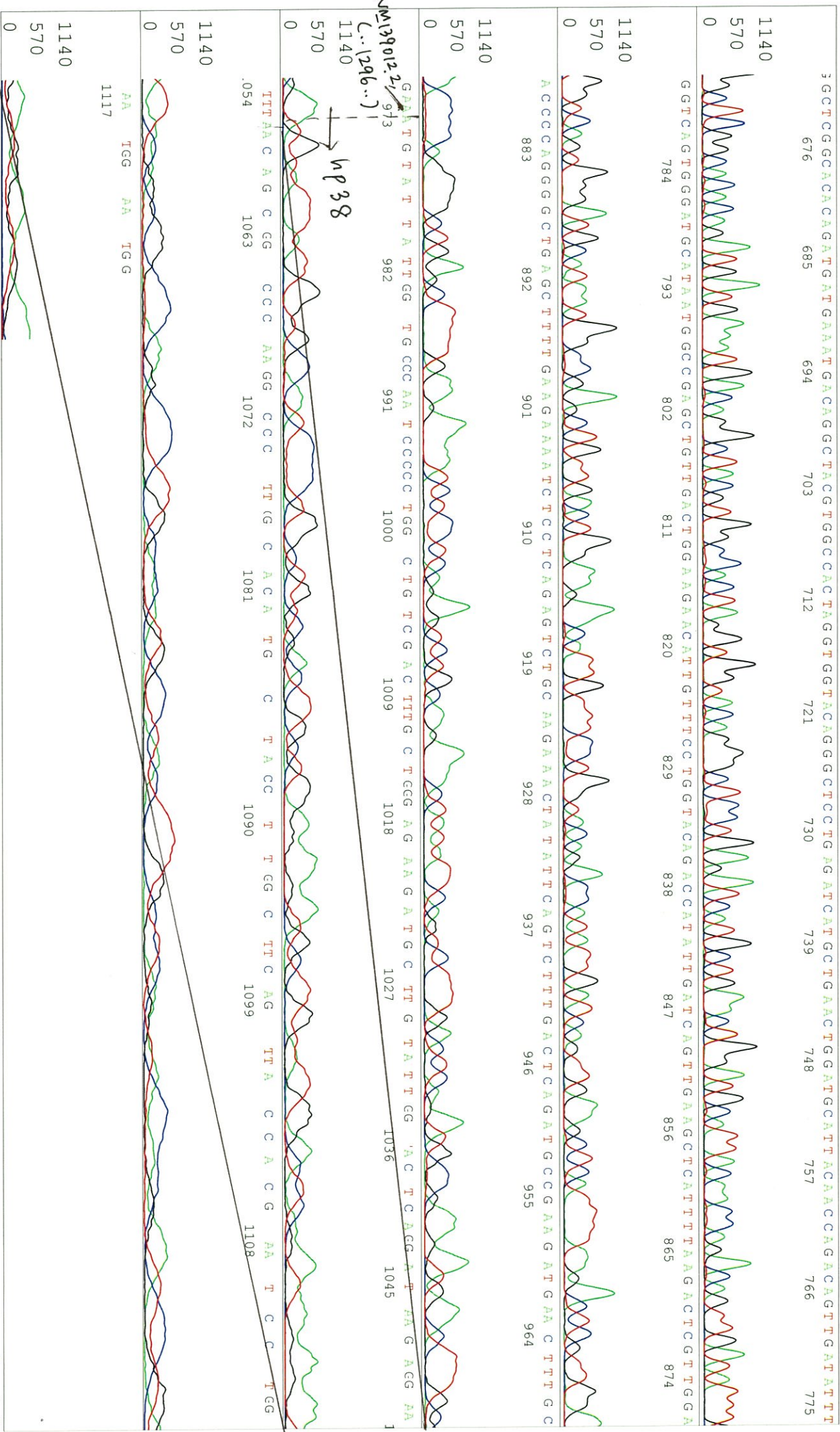
Spacing:11.34 Pls/Panel1350

Version 6.0 HiSQV Bases: 976

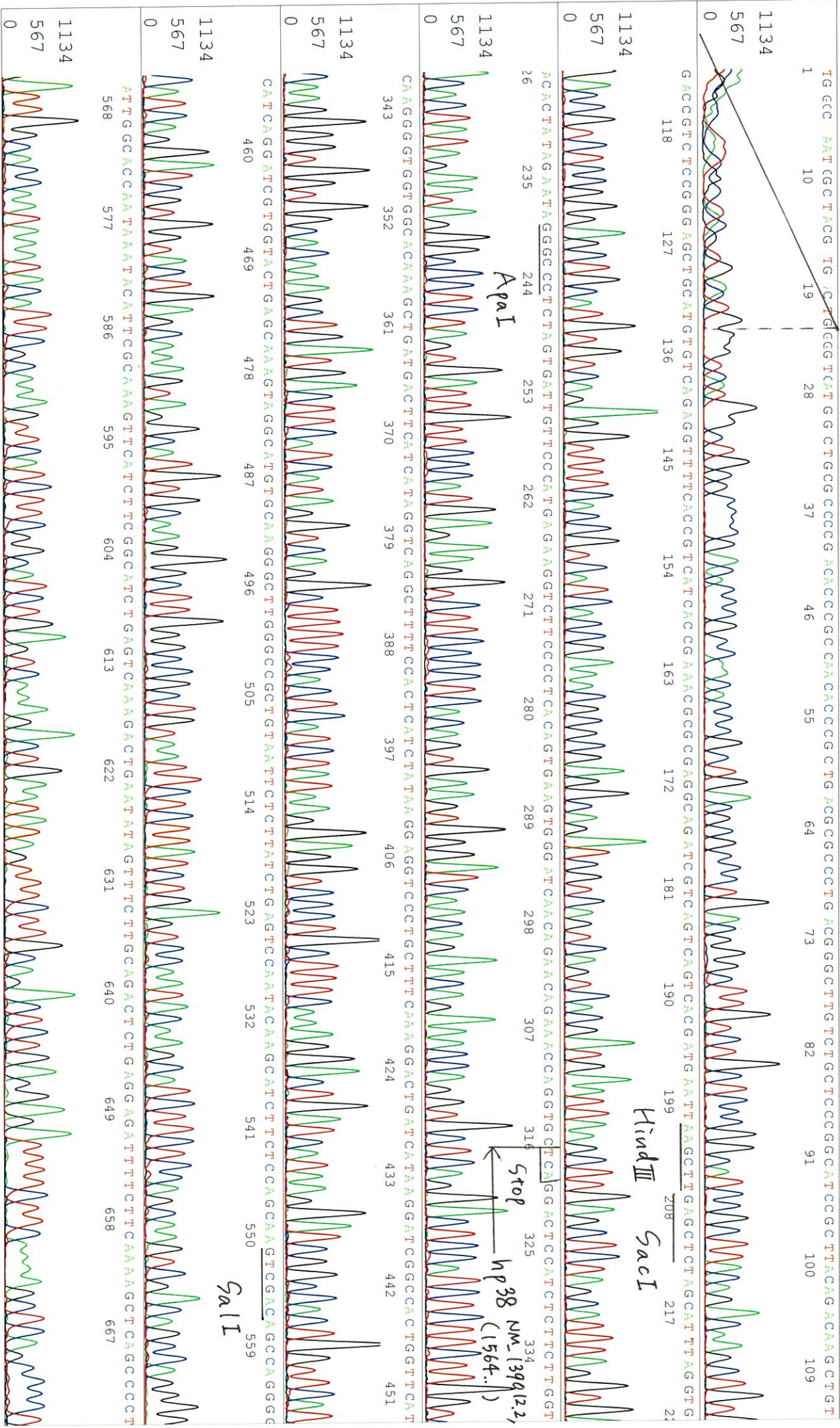
Plate Name: 20171208\_mix







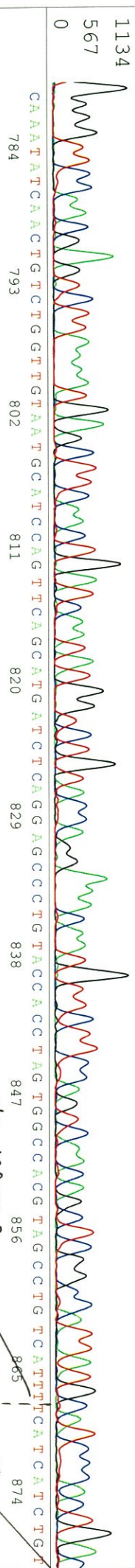




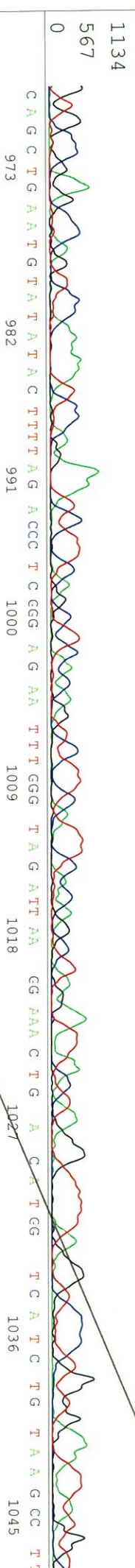


S/N G:37 A:46 T:52 C:67  
KB.bcp  
KB 1.4.1.8 Cap:9

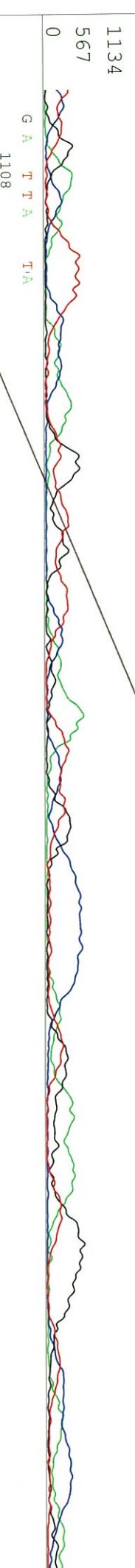
676 685 694 703 712 721 730 739 748 757 766 775  
GGGGTTC CAAACGAGTCTTAAATGAGCC TCAACTGATCAATATGGTCTGTACCGGAAACAAATGTCTTCCAGTCAACAGCTCGGCCATTATGCATCCCACTGAC



784 793 802 811 820 829 838 847 856 865 874  
CAAAATATCAACTGTCTCTGGTTGTAATGCCATCCAGTTCAGCATGATCTCAAGGAGCCCTGTACCACTTAGTGGCCACCGTAGCCCTGTCATTTTCATCTGT



883 892 901 910 919 928 937 946 955 964  
GTGCCGAGCGAGTC CAAAAATCCCA GAA TCTTCAGCTCA CAGTCTTCATTCACA CAGCTAGATTACTA EGTTTTA GGTTCCCTGTGAAATTA TG



973 982 991 1000 1009 1018 1027 1036 1045  
CAGCTGAAATGTAATAATCTTTTAGACCC TCGGG AGAA TTTGGG TAGATTAA EGAAA CTGA CAA TGG TCA TCTGTG TAAA GCGTT



1054 1063 1072 1081 1090 1099  
CTGACAA TTTCA CAA AATGATTCAGATCC TGC C C C PAATGG AGAA TGGG GTTC TCAACG



