

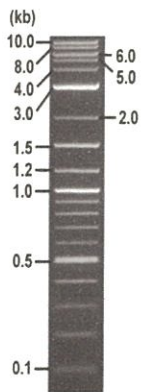


**RIKEN DNA BANK**

clone name : HA-Amot130-delta CC/pcDNA3.1-pA83

- Clone ID : RDB \_ 12205
- Lot : 12205 \_ A5Hp
- 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 : 40 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>BamHI</u>	<u>8.5</u> kbp
<u>BglII</u>	<u>7.0, 1.4</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

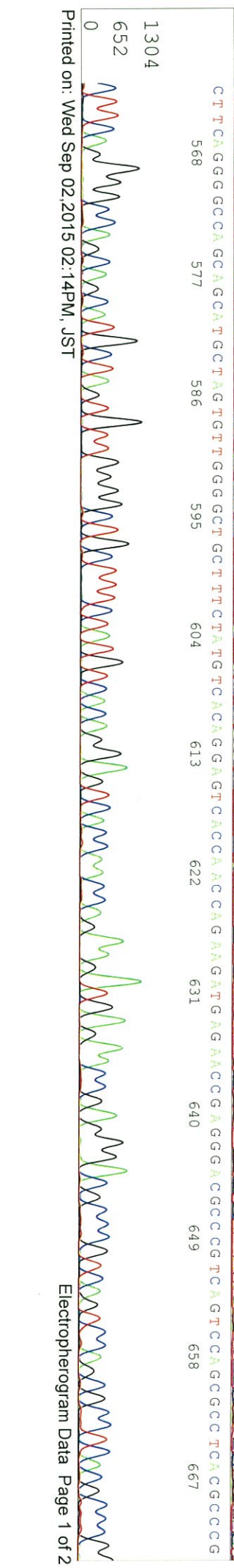
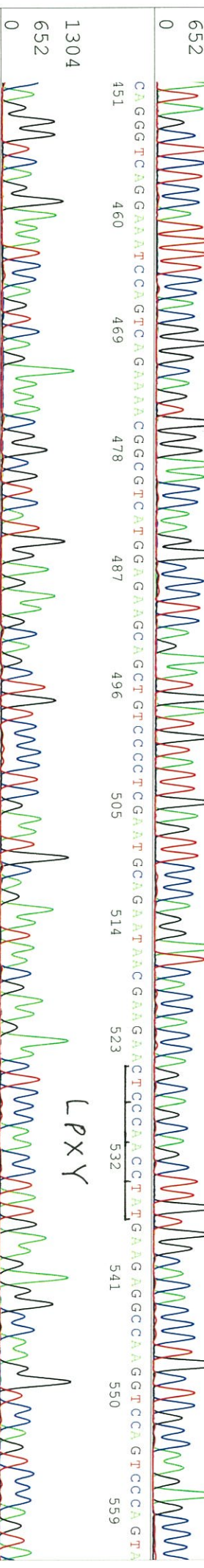
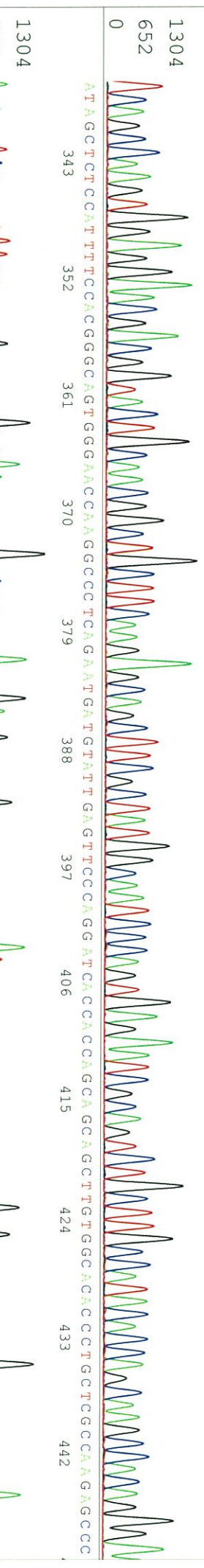
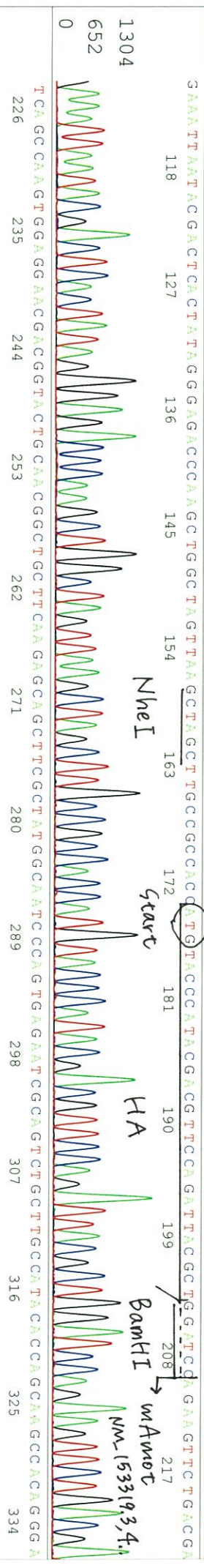
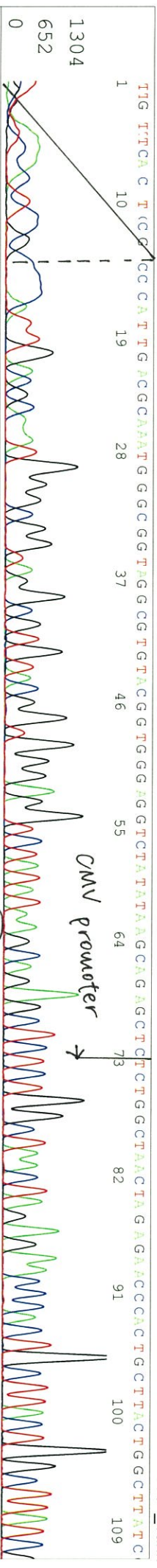
Sequence name	Primer name	Sequence name	Primer name
Sequence - A	CMV-Forward	Sequence - E	SV40pro_F
Sequence - B	mAmot-M#1	Sequence - F	-
Sequence - C	GNP_primer#10	Sequence - G	-
Sequence - D	BGH_rev	Sequence - H	-



APPROVED BY :

primer name A : CMV-Forward

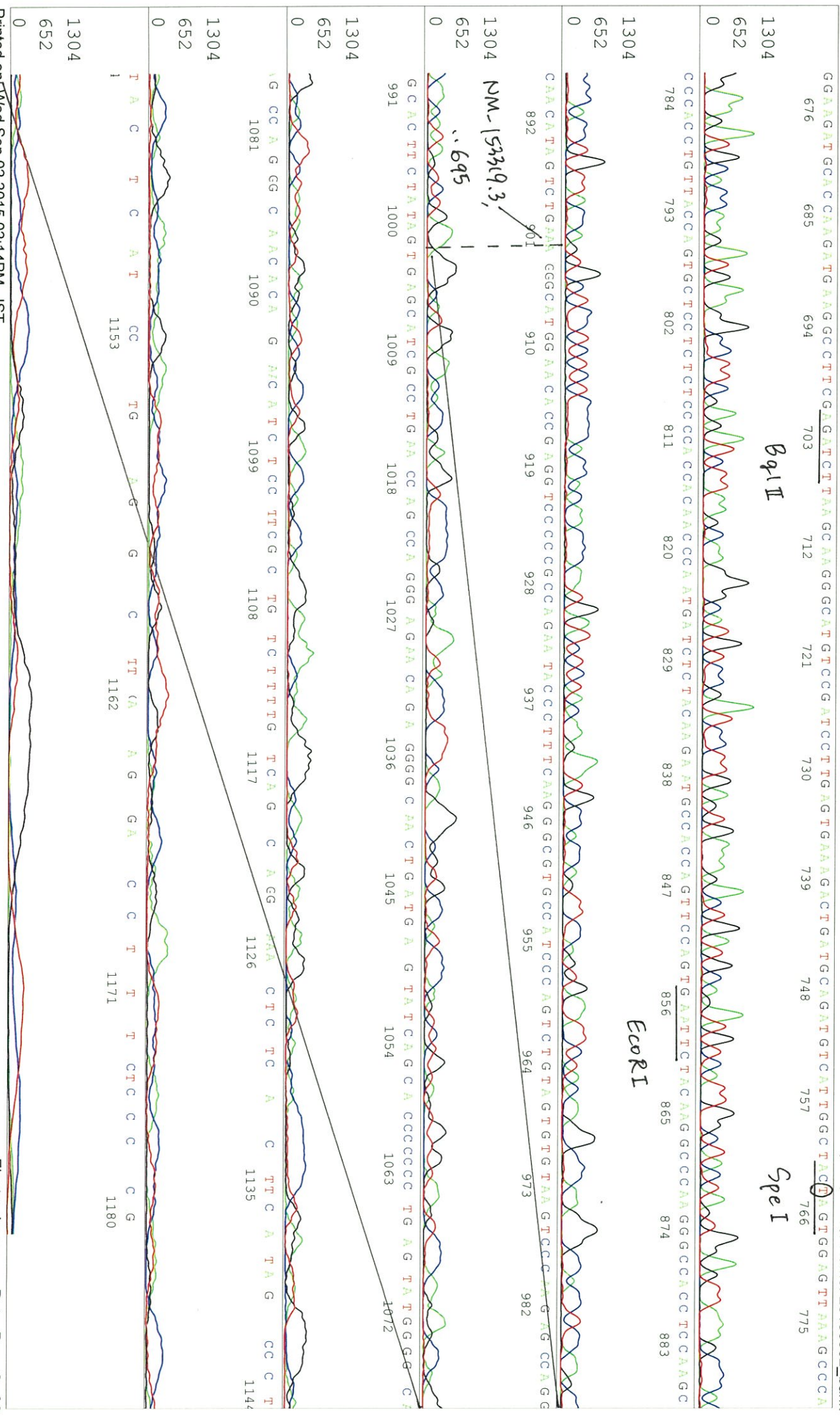
5'-GCACCAAAATCAACGGGACTT-3'



Bq1 II

Spe I

EcoRI



S/N G:691 A:574 T:543 C:758

primer name  $\beta$  : mAmot-M#1

KB\_3500\_POP7\_BDTV3.mob

Sep 02,2015 10:02AM, JST

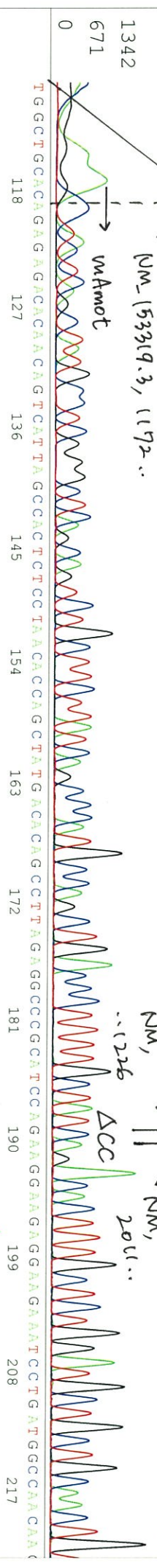
KB 1.4.1.8 Cap:23

5'-AGGCCAGCCTGACTTCAGC-3'

Pis 1299 to 13095 PK1 Loc:1276

Sep 02,2015 10:27AM, JST

Version 6.0 HISQV Bases: 1010

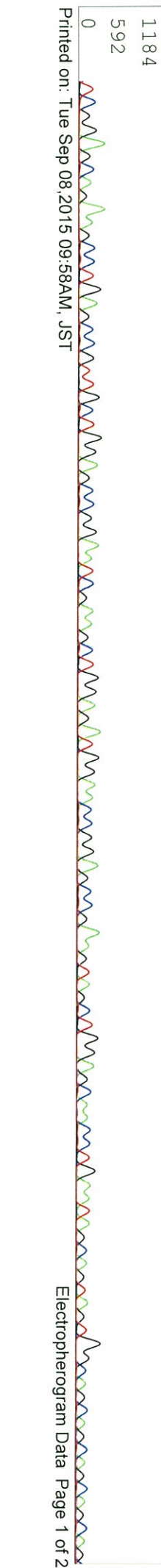
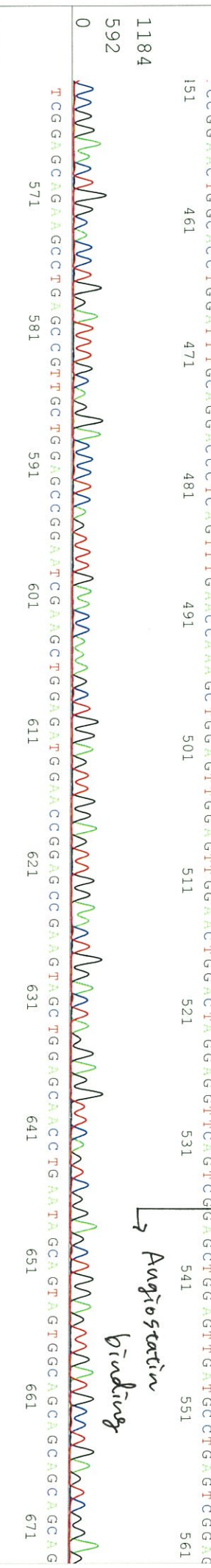
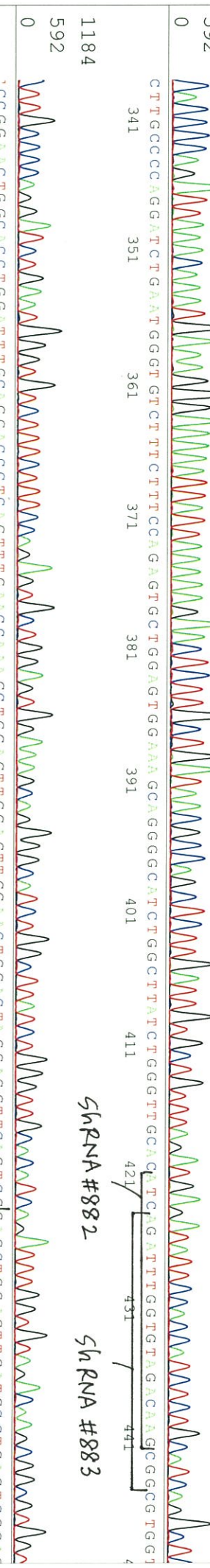
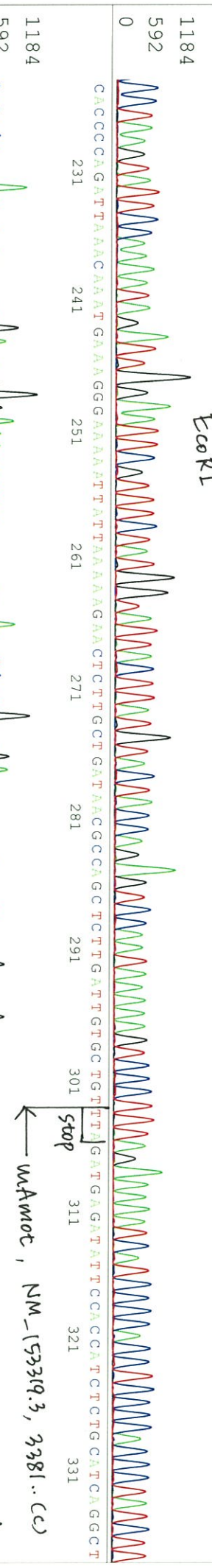
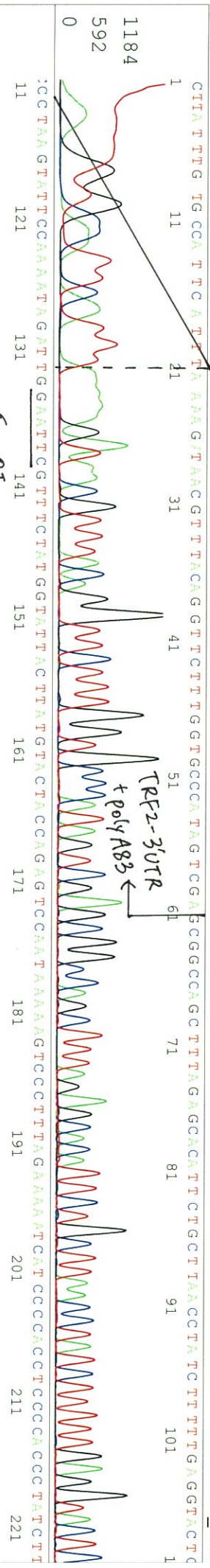




S/N G:463 A:499 T:355 C:412 primer name **C** : GNP\_primer#10  
 KB.bcp 5'-TTTTTTTTTTTTTTTTTTTTTTTCTT-3'

Pis 1398 to 13728 Pk1 Loc:1375  
 Version 6.0 HISQV Bases: 1038

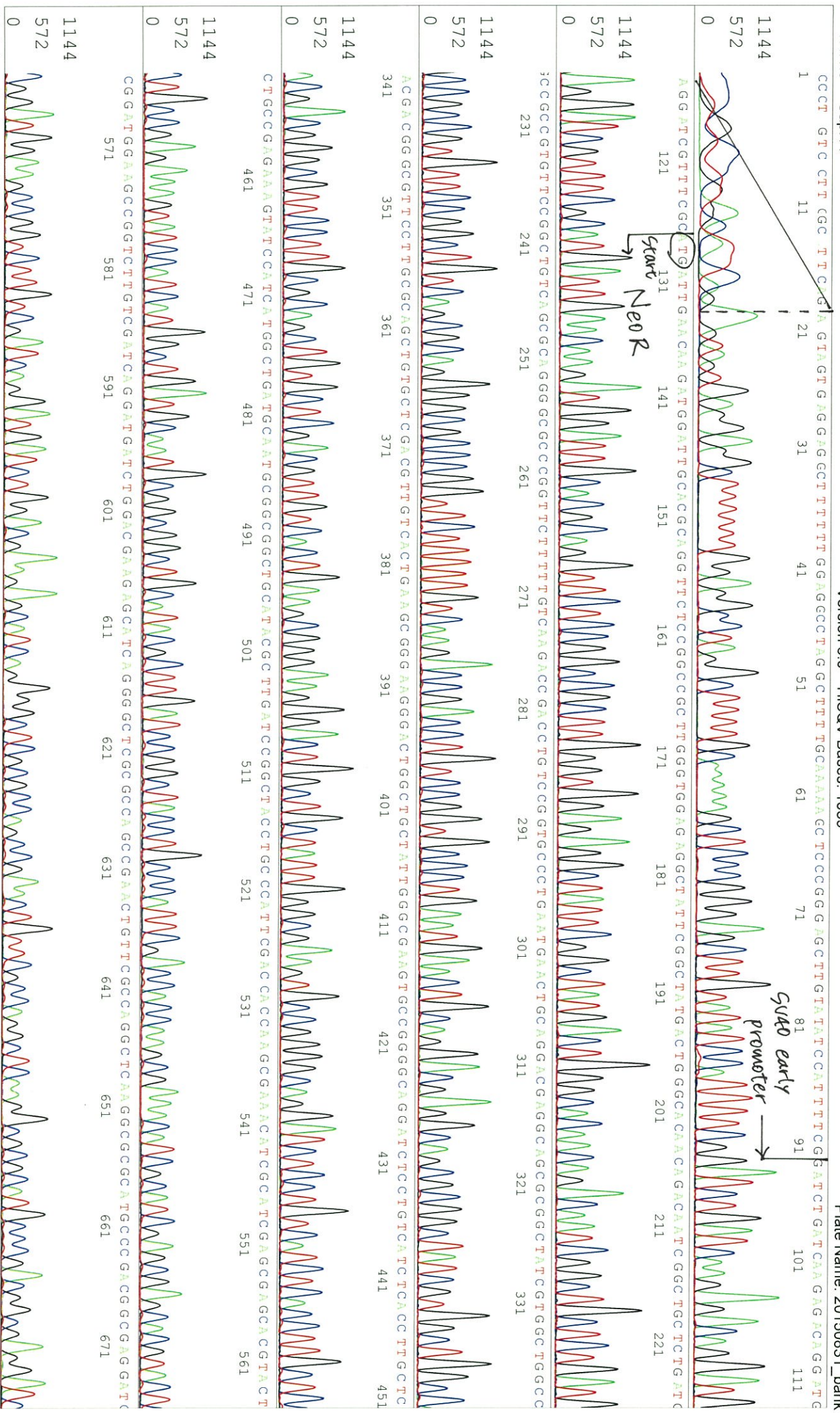
Spacing:11.94 Pts/Panel1350  
 Plate Name: 20150831\_bank



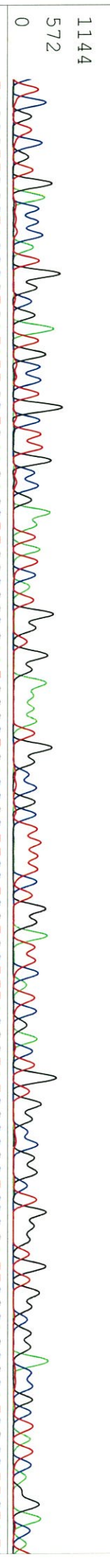








1144 1144  
 572 572  
 0 0  
 TAGCGTTGGCTACCCGATGATATGC TGAAGAGCTTGGCCGCC GAATGGGCTGACCCGCTTCC TCGTGC TTAACGGTATCGCCCGC TCCCGA TTCGCAAGCGCATCGCC TTCTATC  
 791 801 811 821 831 841 851 861 871 881 891



1144 1144  
 572 572  
 0 0  
 :GCCCTCTTGACGAGTTC TTTGAGCGGGAC TCTGGGGTTCCGCGAATG ACCGACCAAGCGACGCCAACCTGG CACTCAGAGAT TTCGAT TCCACC GCCGCC TTCTTA  
 901 911 921 931 941 951 961 971 981 991 1001

Near →  
 Stop ↓

1144 1144  
 572 572  
 0 0  
 TGAAGCGTTGGGCTT C GGAATCCGTTTCC GGGACCGCCGCTGG ATGATCC TCCAGCCGGG ATCTCA TGC T G AG TTC TTTCC GCCAAGCC AAC T C  
 1011 1021 1031 1041 1051 1061 1071 1081 1091

1144 1144  
 572 572  
 0 0  
 :TTTATTT G C A G C T T A T A T G G T T A C A A A T T A G G C C A T A G C A T C A C A A T T C A A T A G C A T T T T C G C C C T T G  
 1101 1111 1121 1131 1141 1151 1161 117

1144 1144  
 572 572  
 0 0  
 CC A T T T T (T C T T T A G T T G T T G A A G  
 1 1181 1191