

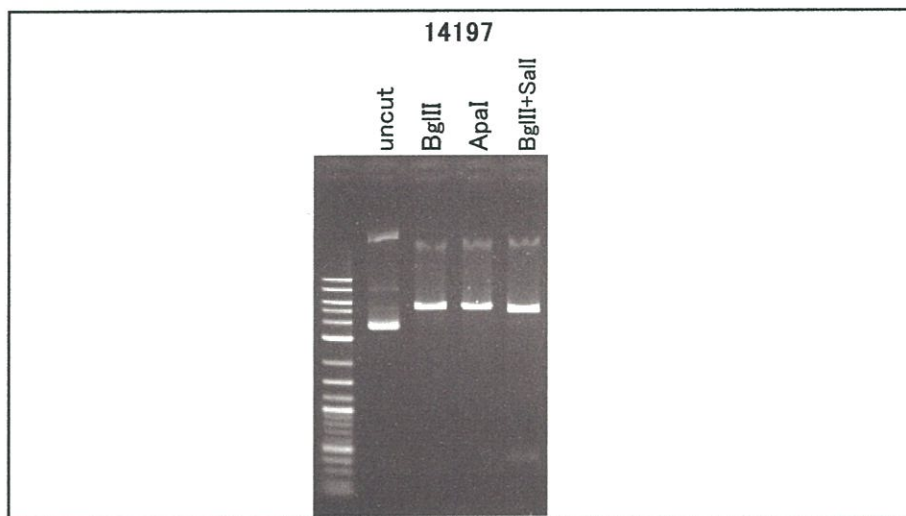
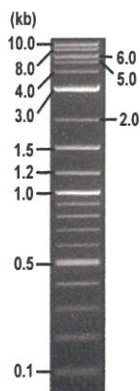


RIKEN DNA BANK

clone name : pEGFP-C1-mouse Rab35

- Clone ID : RDB _ 14197
- Lot : 14197 _ A6Fd
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 25 microgram/ml kanamycin
- 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>BglII</u> | <u>5.3</u> kbp |
| <u>ApaI</u> | <u>5.3</u> kbp |
| <u>BglII + Sall</u> | <u>4.9, 0.4</u> kbp |
| | |
| | |
| | |

● Confirmation of the insertion sequence

| Sequence name | Primer name | Sequence name | Primer name |
|---------------|--------------|---------------|-------------|
| Sequence - A | EGFP-C | Sequence - E | - |
| Sequence - B | CMV-Forward | Sequence - F | - |
| Sequence - C | SV40pro_F_V2 | Sequence - G | - |
| Sequence - D | - | Sequence - H | - |

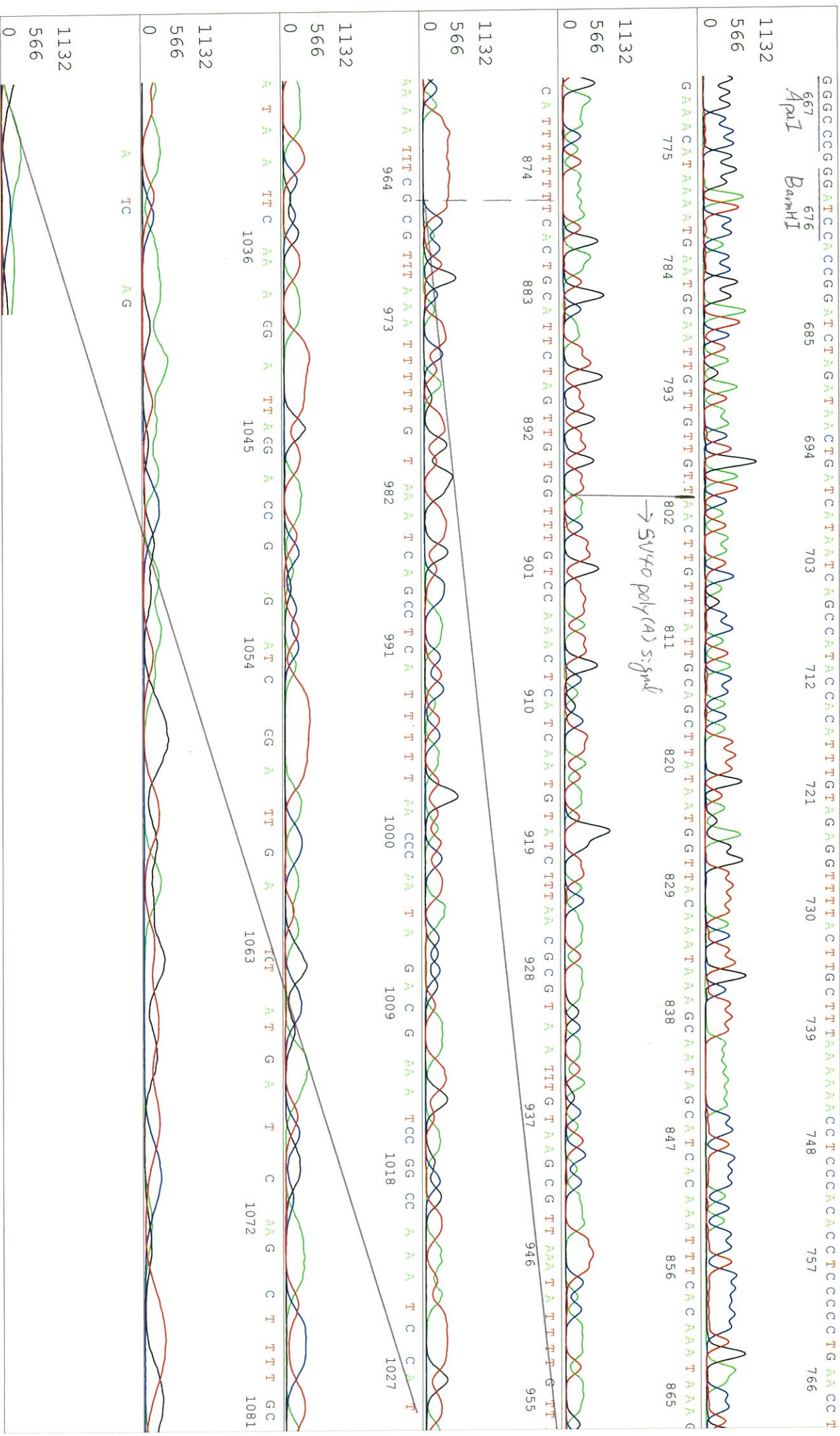
APPROVED BY :



S/N G:937 A:1101 T:953 C:1154 primer name A : EGFP-C
KB.bcp
KB 1.4.1.8 Cap:4
5'-CATGCTCCTGCTGGAGTTGCTG-3'

KB_3500_POP7_BDTV3.mob
Pis 1611 to 12466 Pk1 Loc:1588
Version 6.0 HISQV Bases: 938





S/N G:1249 A:854 T:777 C:1275

primer name B : CMV-Forward

KB_3500_POP7_BDTV3.mob

Jun 29, 2016 10:46AM, JST

KB.bcp

5-GCACCAAAATCAACGGGACTT-3'

Pis 1593 to 12492 PK1 Loc:1570

Spacing:10.97 PIs/Panel1350

KB 1.4.1.8 Cap:1

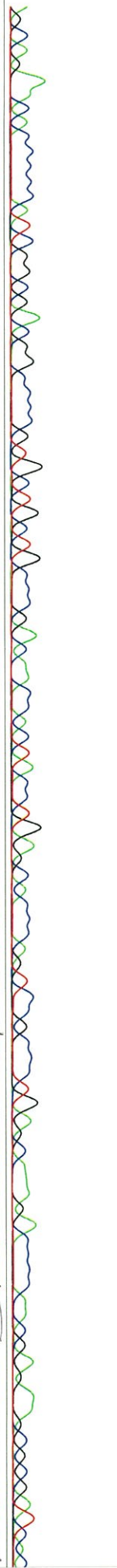
Version 6.0 HISQV Bases: 887

Version 6.0 HISQV Bases: 887

Plate Name: 20160629 Kitaku



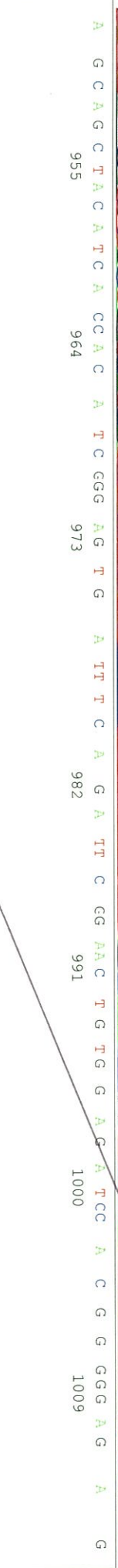
A G C A G A A C C A C C C C C C A T C G G C G A C G G C C C C C G T G C T G C C C C G A C A A C C A C T A C C T G A G C A C C C A G T C C C C C C T G A G C A A A G A A C C C A A C G A G A A G C G A T C A C



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



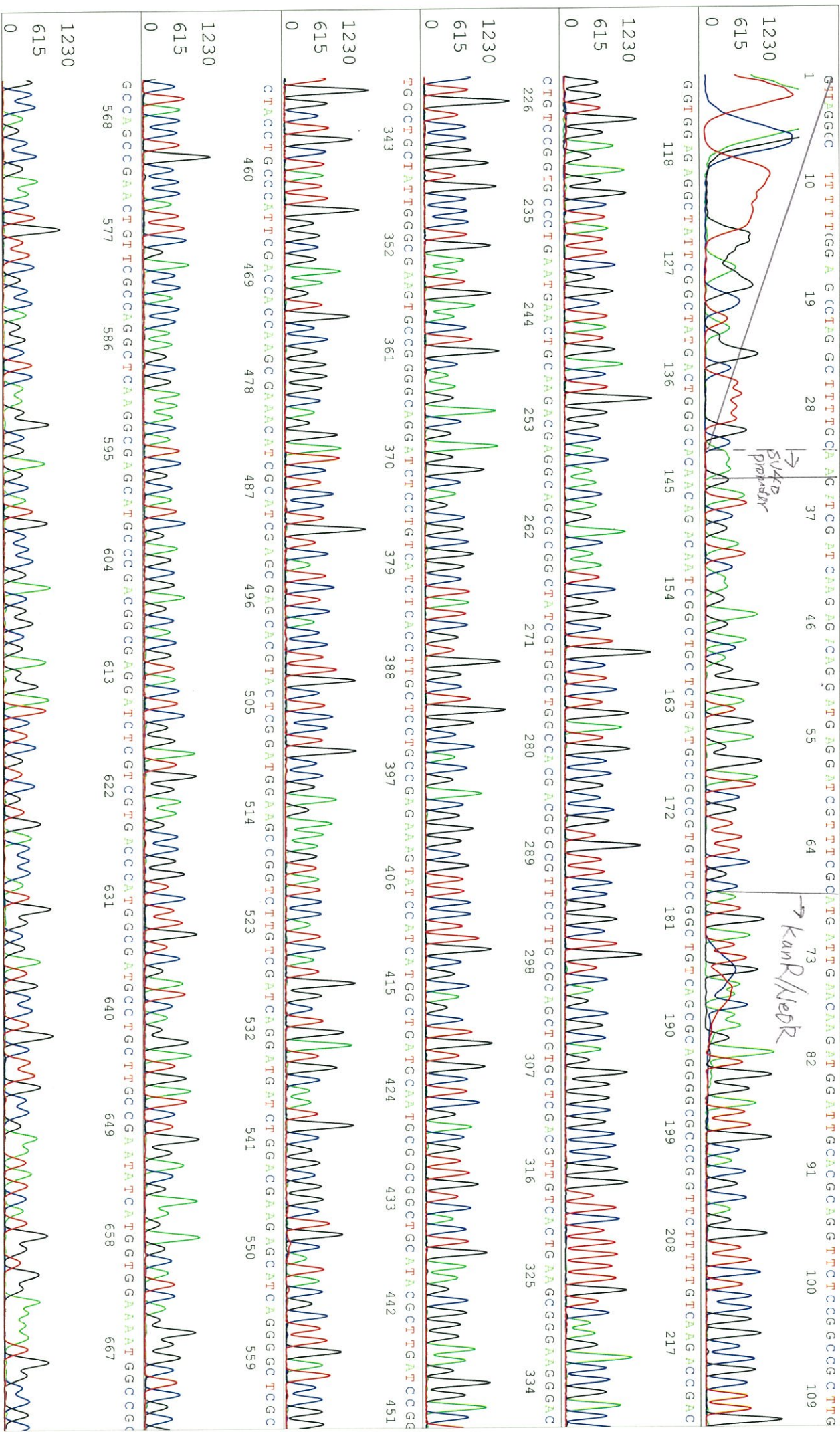
A C C A C C T C T T T C A A G C T G C T C A T C A T C G G G C G A C A G C G G G T G T G G G C A A G A G C A G C C T T G C T G T T A C G A T T C G C A G A C A A C A C C / T T C T C



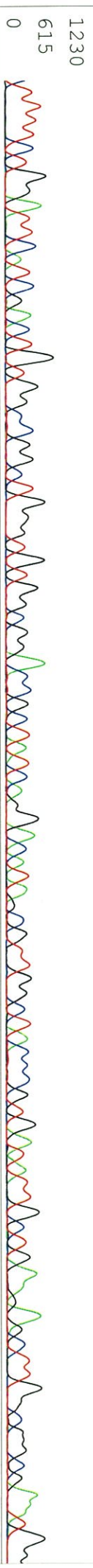
T G A A G C C T G C C A G A G A T C T G G C A C C G T A G G A A C T G T G G A G C G C C T T C C G G G A G A



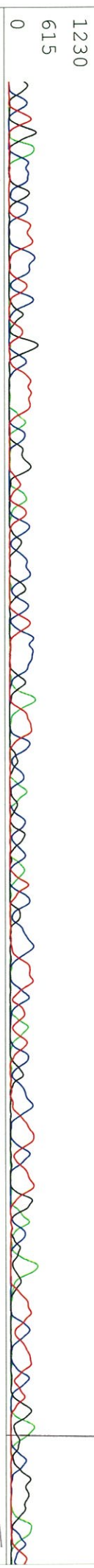
A A T C A A T



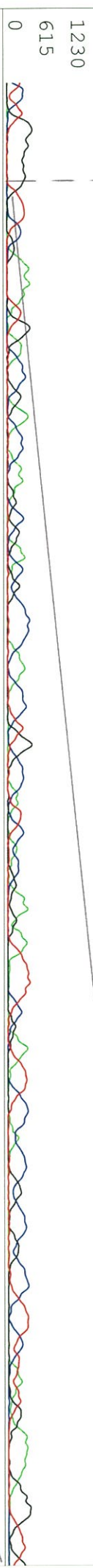
TTTCTGATTCATCCGACTGGTGGCCGGCTGGGGTGGCCGACCCGCTACAGGACAAGCCGTTGGCTAACCCGGTGATATTGCTGAAAGACTTGGCCGAAATGG



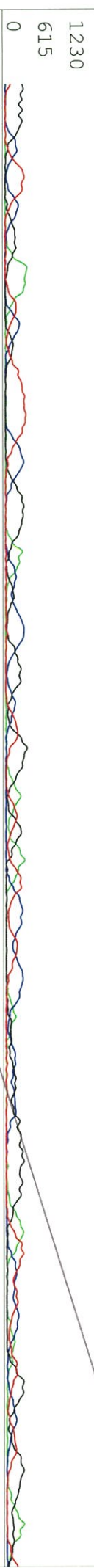
GCTGACCGCTTCTCTCGTGC TTTACGGTATCGCCGCTCCCGATTCCGACGCGCATCCGCTTCTATCGCCCTTCTGACGAGTCTCTCGAGCGGAACT



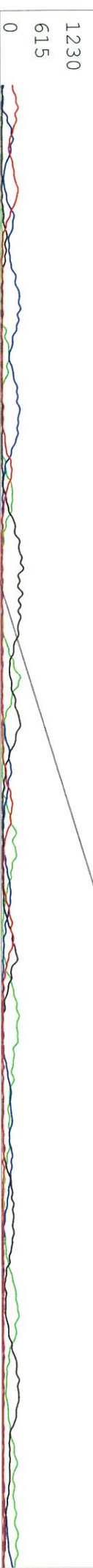
CTGGGGGTTCGAATGACCGACCAAGCGACCGCCAACTGCGCATCAGAGATTTCCGATTTCCATTTCCACCGCCCTCTCTATGAAAGTCTCTGAAAAGTT



GGGC TTTCCGGAAATCG TTTTCCGGGACGGCCGGCTGGCGGAAATCCCTCCCAGCCGGCGGATCTCTCAATCTCATGC TCGG



CC TTTCCGCCAA CCCC TTAAGGGGAACTCTCCCAGCCGGCGGATCTCTCAATCTCATGC TCGG



TAAGTAC