

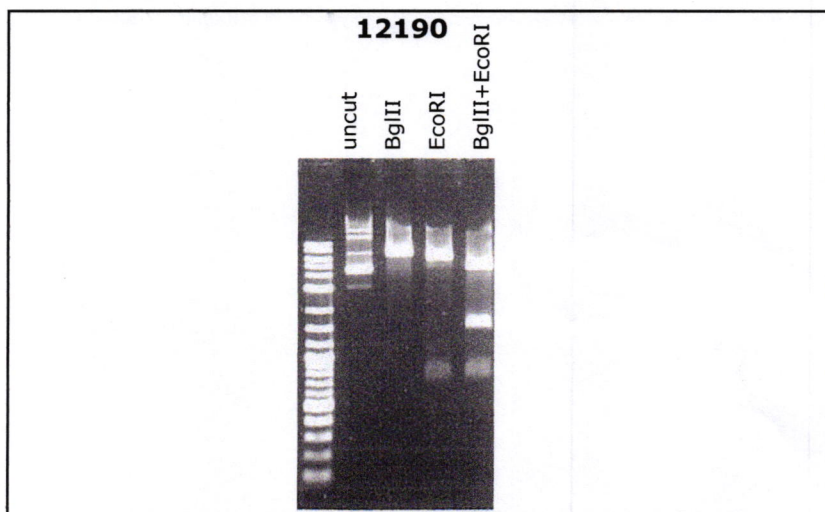
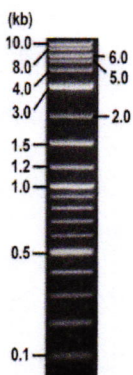


**RIKEN DNA BANK**

clone name : pcDNA3.1-pA83-HA-Yap

- Clone ID : RDB\_ 12190
- Lot : 12190\_ A3I9
- 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 |
|--------------------|---------------------------|
| <b>BglII</b>       | <b>7.4</b> kbp            |
| <b>EcoRI</b>       | <b>6.5, 0.9</b> kbp       |
| <b>BglII+EcoRI</b> | <b>4.9, 1.6, 0.9</b> 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  | Pr0016    | CMV_Forward    | T7 pro,insert 5'( HA, Yap 5') |
| Sequence - B  | Pr0763    | GNP Primer #10 | insert mid(Yap 3')            |
| Sequence - C  | Pr0550    | RDB15793_F1    | insert 5'( HA, Yap 5')        |
| Sequence - D  | Pr0606    | BGH_rev2       | bGH pA, TRF2-3'UTR+polyA83    |
| Sequence - E  | Pr0731    | SV40pro_ori_F  | SV40 pro_ori,NeoR             |
| Sequence - F  | -         | -              | -                             |
| Sequence - G  | -         | -              | -                             |
| Sequence - H  | -         | -              | -                             |

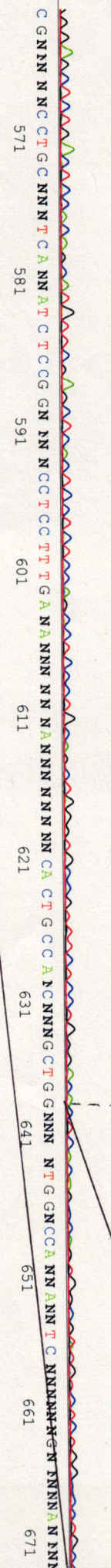
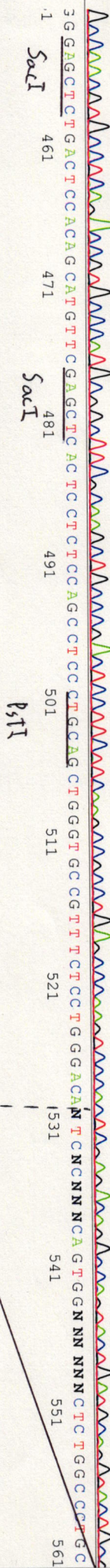
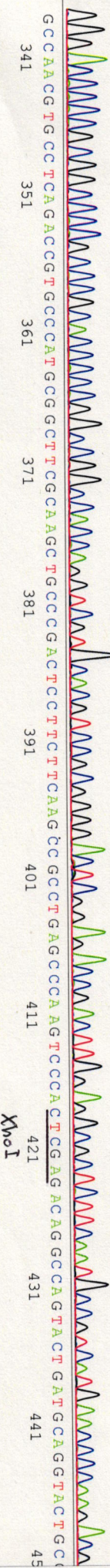
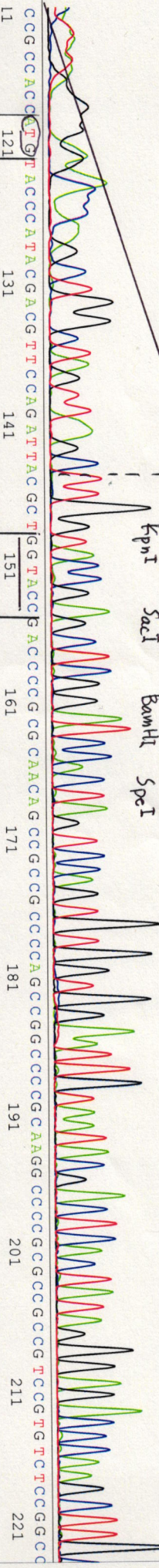
APPROVED BY :



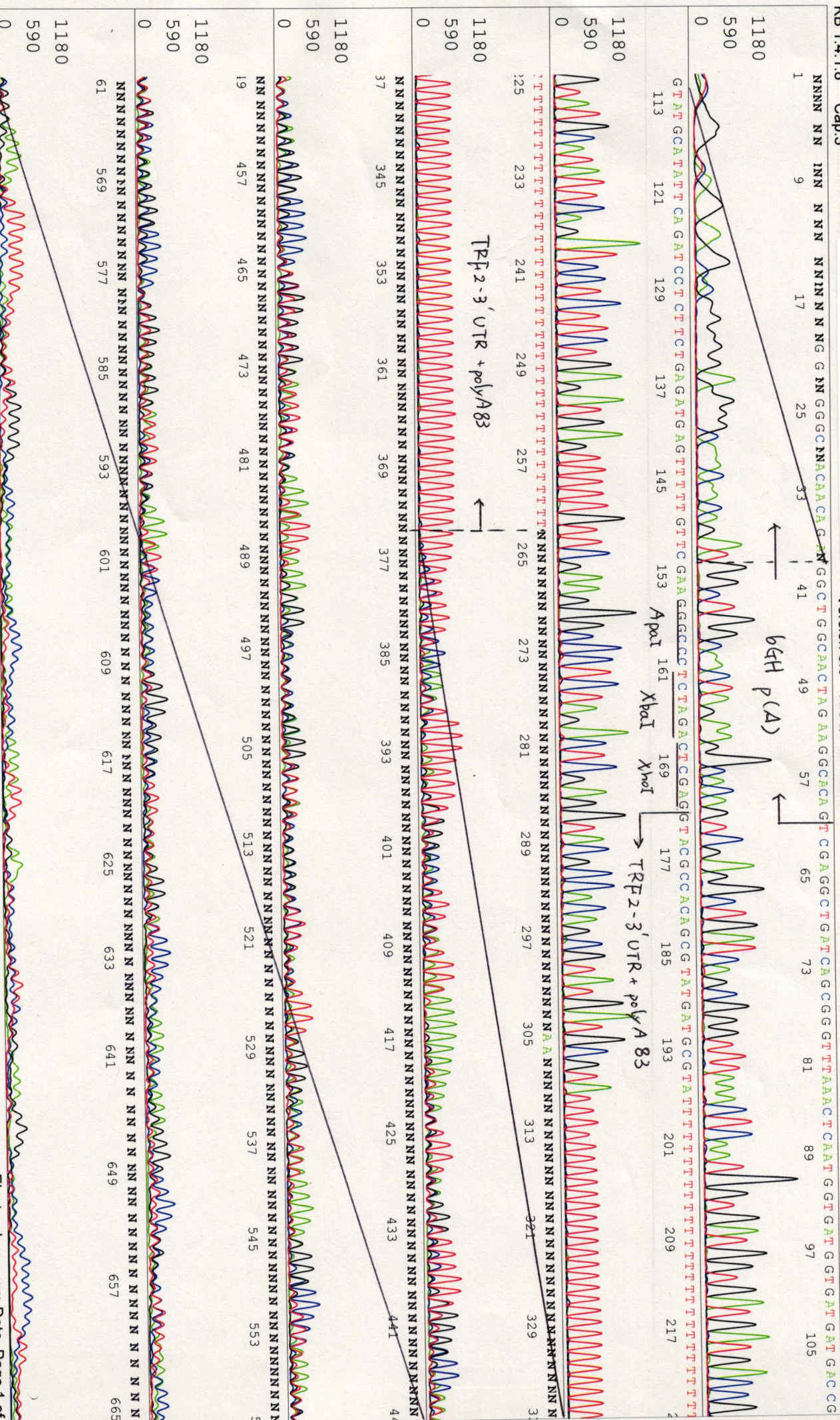




1 11 21 31 41 51 61 71 81 91 101 111  
**N** INNINNINNNNNNNNNNNNNNNNGGCTAGNNNNNNNTTGGTACCAGCTCGGATCCACTAGTCCAGTGTGGTAATGTAATACGACTCACATAAGGAGACCCAGCTTGG  
 121 131 141 151 161 171 181 191 201 211  
**L1** CCGCCACCCTGTGTACCCATAAGACGCTTCCAGATTACCTGGTACCCGACCCCGCCCAACAACCCGCCCCCAGAGCCCGCCCGCGCGGTCCGTCCGGC  
 231 241 251 261 271 281 291 301 311 321 331  
**G** GGAACCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCAGGTCGTGCACGTCGGAGACCGACTTGGAGGCGGCTTCAATGCCGTCAAGAACCCCAAGACG



primer name  $\varnothing$  : BGH\_rev2  
5- TATTAGGAAGACAGTGCGG -3'



1 N N N N N N N N N N N N N N N C C C C C T G C C T C T G N N C T A T T C C N G A A G T A G T G A G G A G G C C T T T T T G G A G C C C T A N G C C T T T T G C A A A A G C T C C C G G G A G C T T G T A T A T C C A T T T T C



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

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

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

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

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

0 574 1148

0 574 1148

