

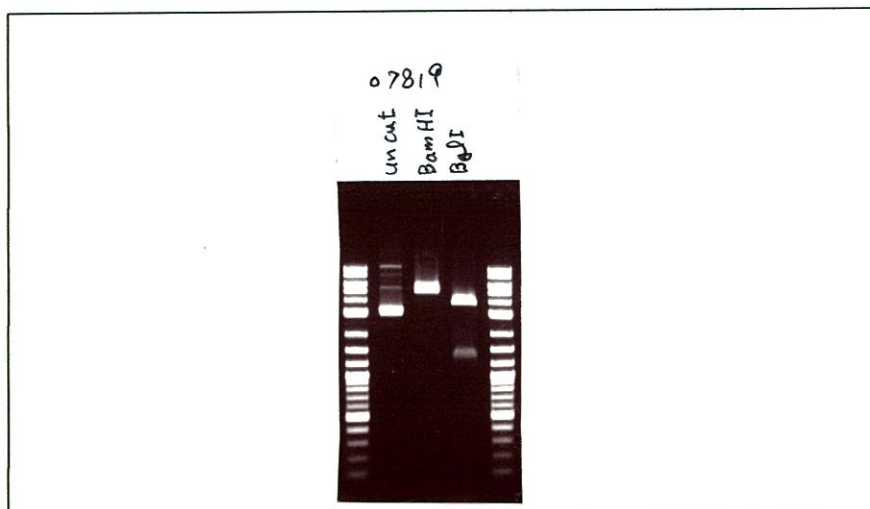
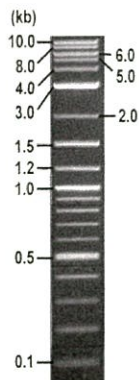


RIKEN DNA BANK

clone name : pGL4-phETS1

- Clone ID : RDB _ 07819
- Lot : 07819 _ A5F4
- 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 : 42 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>BamHI</u>	<u>5.7</u> kbp
<u>BglII</u>	<u>4.2, 1.5</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

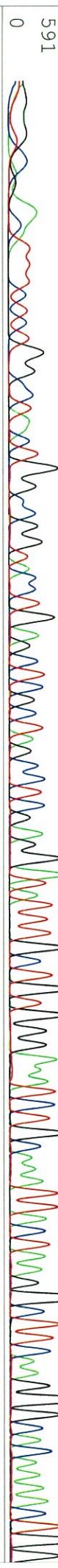
Sequence name	Primer name	Sequence name	Primer name
Sequence - A	pGL4-4174F	Sequence - E	-
Sequence - B	pGL4-136R	Sequence - F	-
Sequence - C	-	Sequence - G	-
Sequence - D	-	Sequence - H	-

APPROVED BY :

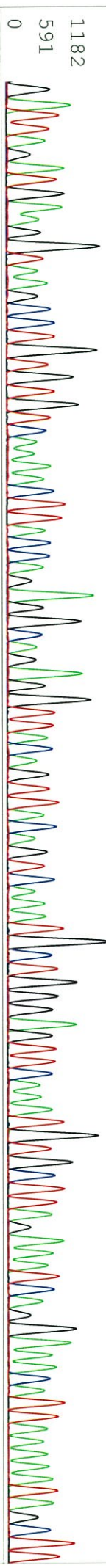


C G G G T C / G A C A T T T C T C T G G C C T A A C T G G C C G G T A C C T G A G C T C G C T A G G C T A G C C T C C G A G G T A T T T G C C T G T G G A A A T C T G C C A A T T A C T A A G G C C T C A A G G C A C A A A C T G

BglII KpnI SacI XhoI
pL ETS I NC_000011.0, (28523650..CC)

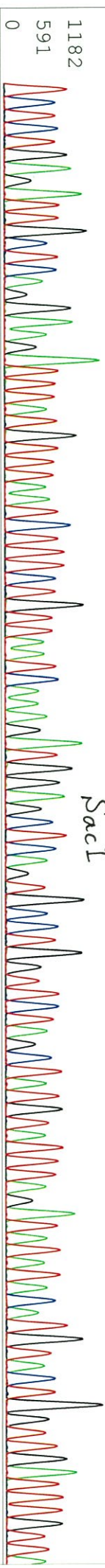


G A T T A G A T G A A G G T A A G C C T G T G T G T C A A A A C T T A C C A G A G G C A G G T T A C A G T T A C A G T C A A A T G C C T T A G A A A T C A G G A A A C A T T A A A A A T T A G C T T G C C A A A A C T G

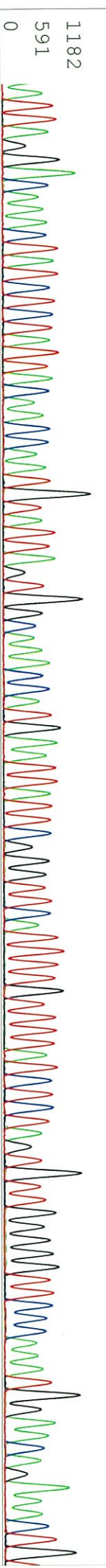


T C T C T G A G A T T G C T C A G G A A G A T T T A T G T T A A T C T T T C T G T T A A T C A A G A T G A G C T C A G T G C C T G T T C T A G C T A T G T A T T A G A T T A T A C A T G T A C T G T T G A T T T G T T A

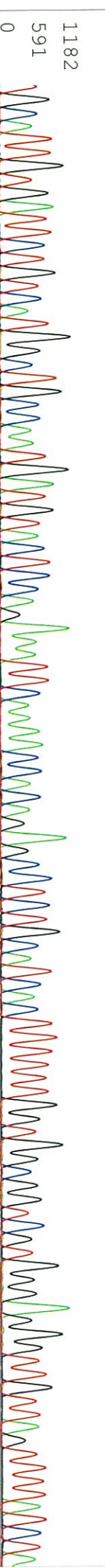
SacI



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



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



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

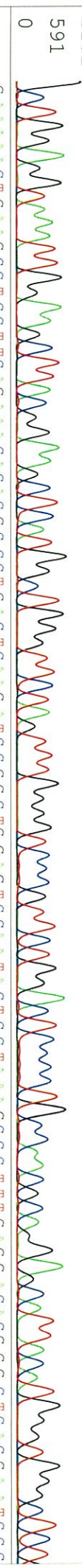
HindIII



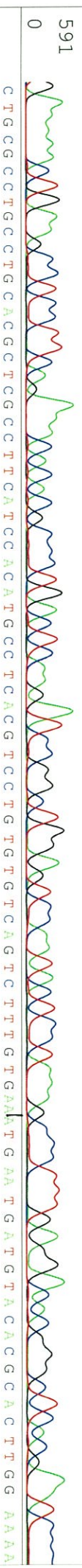
SN/G: 1018 A: 1147 T: 848 C: 918
 KB.bcp
 KB 1.4.1.8 Cap: 1

Hind III

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



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



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

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



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

C C C C G A C C C C C C G



C C C C G A C C C C C C G

