

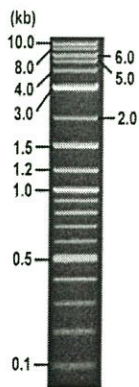


RIKEN DNA BANK

clone name : pBS-F

- Clone ID : RDB_01543
- Lot : 13248_A5Gs
- 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 : 43 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

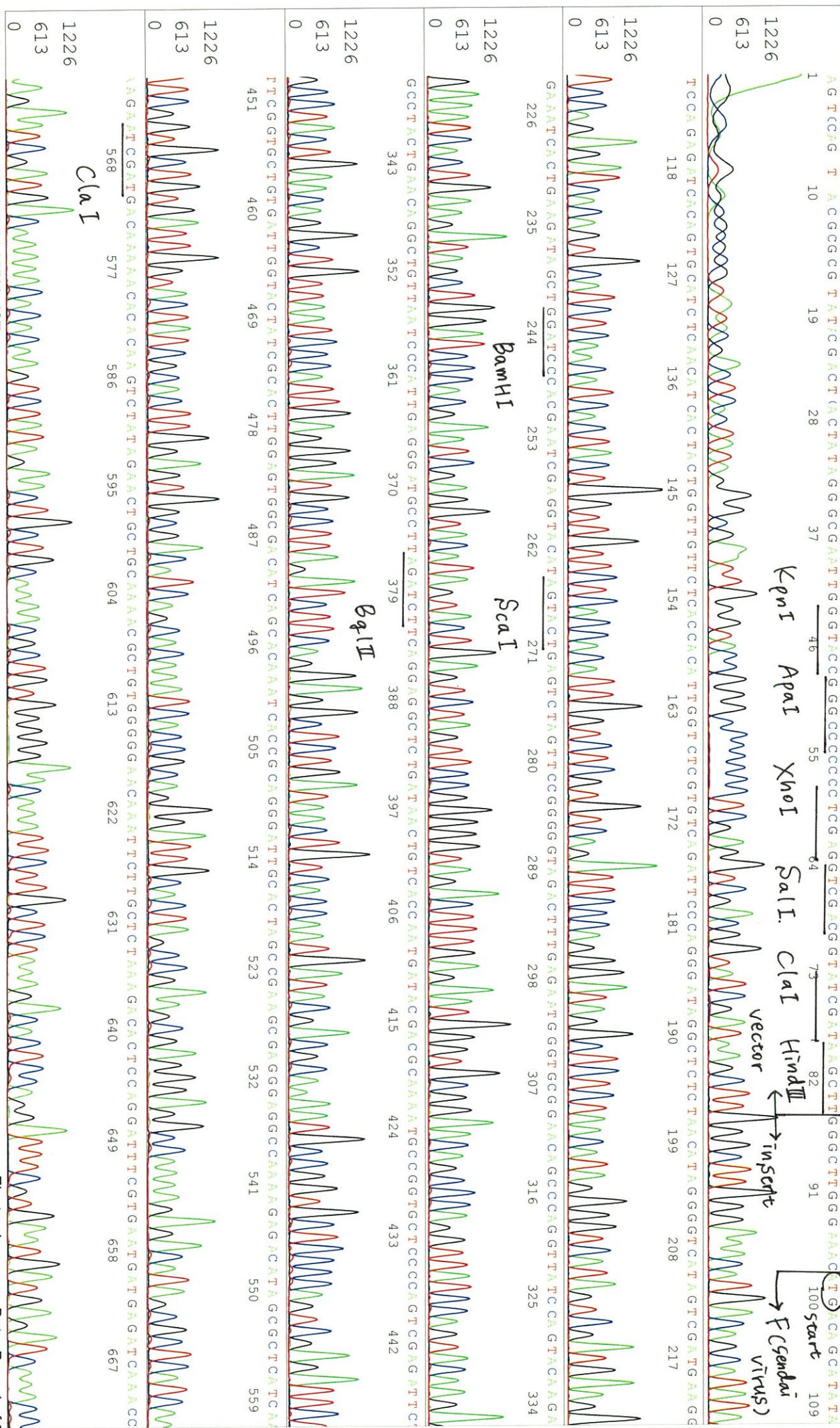
Restriction enzyme	Expected size of fragment
<u>EcoRI</u>	<u>4.7</u> kbp
<u>HindIII</u>	<u>3.0, 1.8</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	M13_-40	Sequence - E	-
Sequence - B	Reverse2	Sequence - F	-
Sequence - C	-	Sequence - G	-
Sequence - D	-	Sequence - H	-

APPROVED BY :





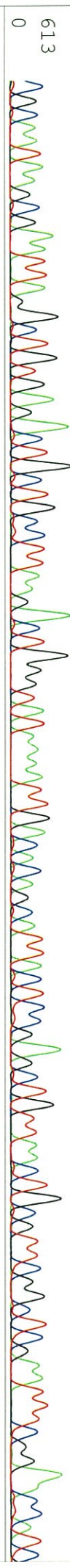
S/N G:188 A:211 T:137 C:200

KB.bcp

KB 1.4:1.8 Cap:1

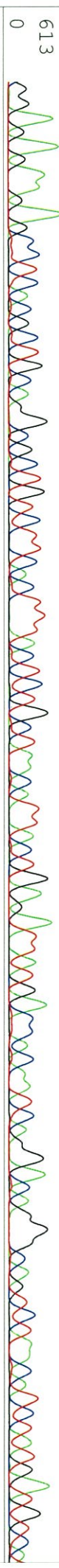
CGCAATTAAGCCGAATTAGGCTGTGAGACCTGGCTTAAAGACTGGGTTAATAATTGACACAGCATTTAACCTCCGAGCTGTTAACTGCGTTCCGGCTCGAAATTTCGGGAACCATC

1226



676 685 694 703 712 721 730 739 748 757 766 775 784 793 802 811 820 829 838 847 856 865 874 883

1226



892 901 910 919 928 937 946 955 964 973 982

XbaI* (overwritten)

1226



991 1000 1009 1018 1027 1036 1045 1054 1063 1072

613



1081 1090 1099 1108 1117 1126 1135 1144

1226



613



S/N G:913 A:840 T:676 C:843

primer name β : Reverse2

01543_13248_A5Gs_Reverse2

Aug 05.2015 02:14PM, JST

KB.bcp

5'-GCCGATAACAATTTCACACAGG-3'

KB_3500_POP7_BDTV3.mob

Aug 05.2015 02:41PM, JST

KB 1.4.1.8 Cap:4

Pts 1349 to 13056 Pk1 Loc:1326

Spacing:1.68 Pts/Panel1350

AGT C G ATTCGCCAGCGCCATTAAACCCTCCTAAAGGGGACAAAGCCCTGGAGCTCCACCCTGGCCGCCCTGTAAGACTAGTGGATCCCCCGGGCTGCAAGAT

1 10 19 28 37 46 55 64 73 82 91 100 109

TTGATATCAA GCTTTGGGGGATCTCAACGGATACCTATGCTGC TTTTACAA GACATCTGATAATGGTCTGATCATCTTTCTCA GCCATTGGCATCAAA CCA CCGTTGTGTA CAT

118 127 136 145 154 163 172 181 190 199 208 217

ATGCTGATCTTCGGCTCTAAATGTGTATGTGTCCCTCGGTATACGGTCAATCTGGATTACCATTAGCATTTGACCCTCTGAGTCTATAAGCACGATGATGATCACCTATAATGAC

226 235 244 253 262 271 280 289 298 307 316 325 334

3CAACAAATTA CGACCATACTACTATGATCGTAA TCAAGTCTCTTGA GTTGAACCATCTACCTCCGAGAGGATTTTCCCGTCTTCTCAAGCTCAGCCTTAGAGT

343 352 361 370 379 388 397 406 415 424 433 442 451

CTTGCAAGAAATT CGTAGCATCAAGCAAGTTGAGAGAAATATCAACGGGCTCTGATAGCAATTTGCCAGGACCGACTGTCAA GTTCTGGACCCCAAGTGGCA TCGTGCCCTTCT

1 460 469 478 487 496 505 514 523 532 541 550 559

CCGGTTAGCATACAATTCTTACCCCATTGACACCTTAAAGACCA GATTGTCATGGGTTAGGAATTA CTACACCCTTTTGAAGCGATCCCTGACTGATTGGTTCGGCTGCTCC

568 577 586 595 604 613 622 631 640 649 658 667

0 608 1216

0 608 1216

0 608 1216

0 608 1216

0 608 1216

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0 608 1216

S/N G:913 A:840 T:676 C:843

01543_13248_A5Gs_Reverse2

Aug 05,2015 02:14PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Aug 05,2015 02:41PM, JST

KB 1.4.1.8 Cap:4

Pls 1349 to 13056 Plk1 Loc:1326

Spacing:1.68 Pls/Panel1350

Version 6.0 HISQV Bases: 988

Plate Name: 20150805_mix

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

784 793 802 811 820 829 838 847 856 865 874 883

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

BamHI

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

892 901 910 919 928 937 946 955 964 973 982

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

991 1000 1009 1018 1027 1036 1045 1054 1063

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

1072 1081 1090 1099 1108 1117 1126 1135

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

1144 1153

0

1216

608

0