

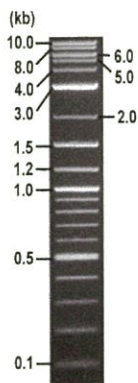


RIKEN DNA BANK

clone name : pDEST131NGFP_BAZ1A

- Clone ID : RDB _ 17333
- Lot : 17333 _ A9Eh
- 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 : 200 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<u>EcoRI</u>	<u>10.8</u> kbp
<u>MluI</u>	<u>10.8</u> kbp
<u>EcoRI+MluI</u>	<u>7.4, 3.5</u> kbp
	kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	mVenus-M_F	Sequence - E	-
Sequence - B	BGH_rev2	Sequence - F	-
Sequence - C	CMV-Forward	Sequence - G	-
Sequence - D	SV40polyA_R2	Sequence - H	-

APPROVED BY :



S/N G:361 A:290 T:318 C:326

D06261A1_A9Eh_1_BGH_rev2

primer name β : BGH_rev2

KB_3500_POP7_BDTV3.mob

KB.bcp

5'-TATTAGGAAAGGACAGTGGG-3'

Pls 1449 to 12730 Pk1 Loc:1426

Aug 05,2019 02:55PM, JST

KB 1.4.1.8 Cap:7

Version 6.0 HiSQV Bases: 971

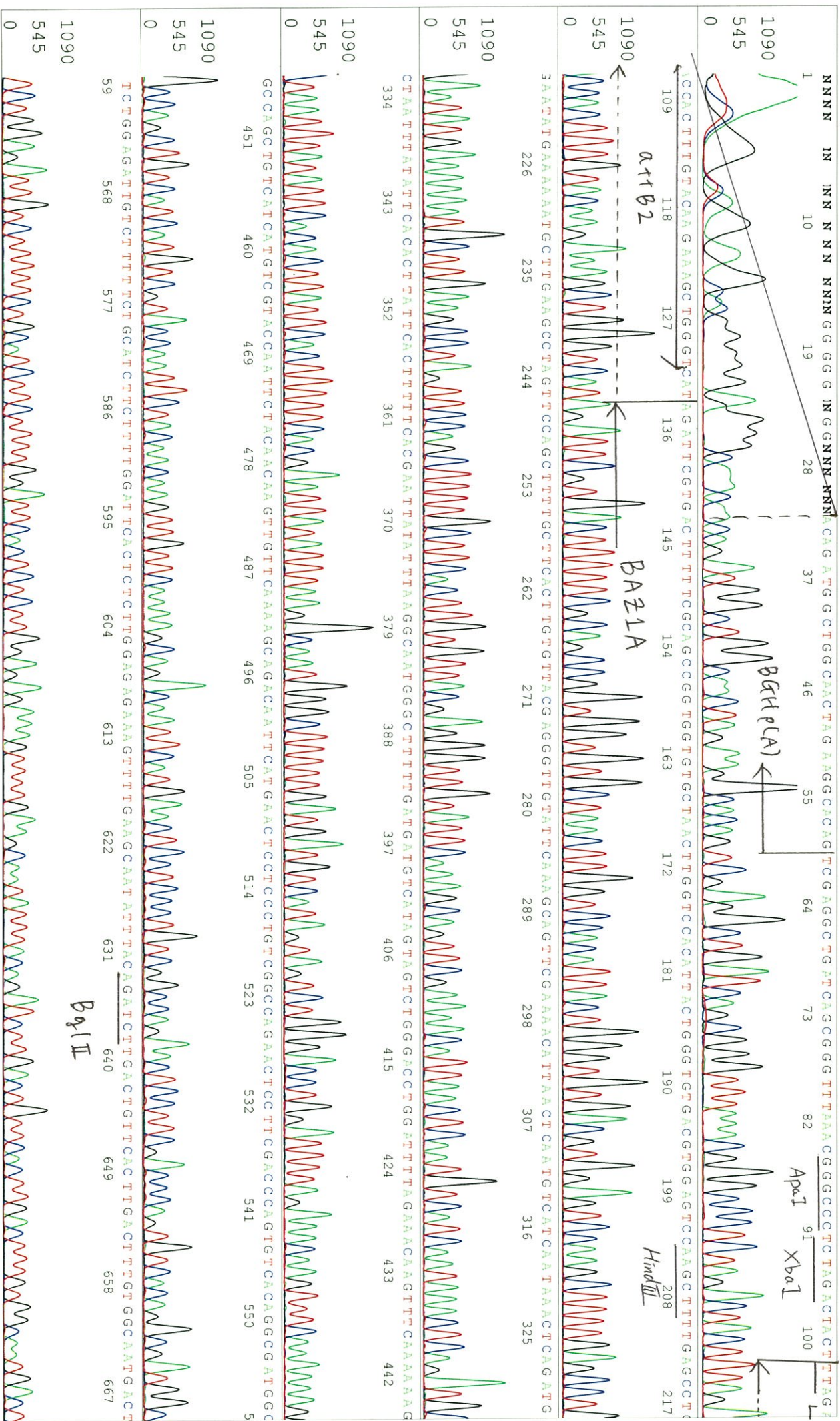
Spacing:1.1.18 Pls/Panel1350

KB 1.4.1.8 Cap:7

5'-TATTAGGAAAGGACAGTGGG-3'

Version 6.0 HiSQV Bases: 971

Plate Name: 20190805 kitaku



S/N G:361 A:290 T:318 C:326

D06261A1_A9Eh_1_BGH_rev2

Aug 05,2019 02:15PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Aug 05,2019 02:55PM, JST

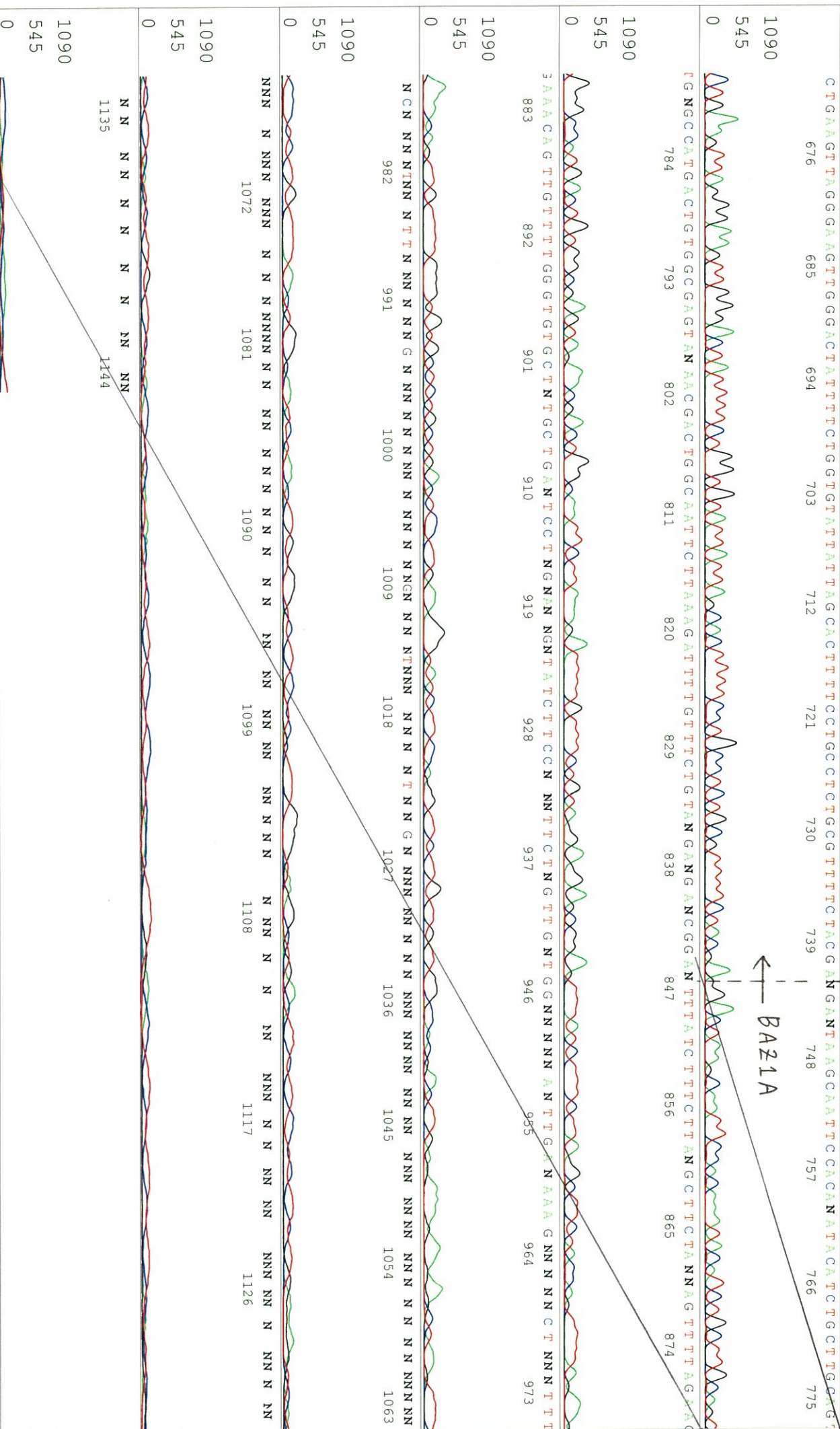
KB 1.4.1.8 Cap:7

Pis 1449 to 12730 Pk1 Loc:1426

Spacing:11.18 Pis/Panel1350

Version 6.0 HiSQV Bases: 971

Plate Name: 20190805 Kitaku



S/N G:162 A:114 T:78 C:176

primer name C : CMV-Forward

KB_3500_POP7_BDTv3.mob

Aug 05,2019 02:15PM, JST

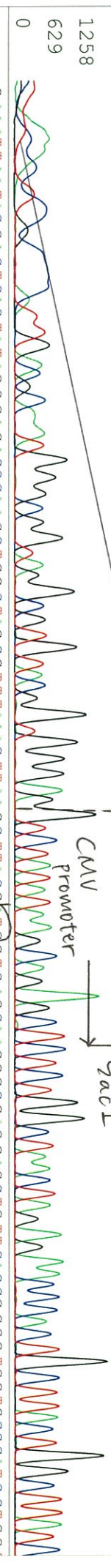
KB.bcp

5'-GCACCAAAATCAACGGGACTT-3'

Pis 1451 to 12755 Pk1 Loc: 1428

Aug 05,2019 02:55PM, JST

KB 1.4.1.8 Cap:1 NNN NNN N IN N N N NNN N NN NN G C N NT G G G C G G T G T G T A C G G T G C G G N G T C T A T A T A A G C A G A G C T C T C T G G C T A A C T A G A G A A C C C A C T G C T T A C T G G C T T A T C

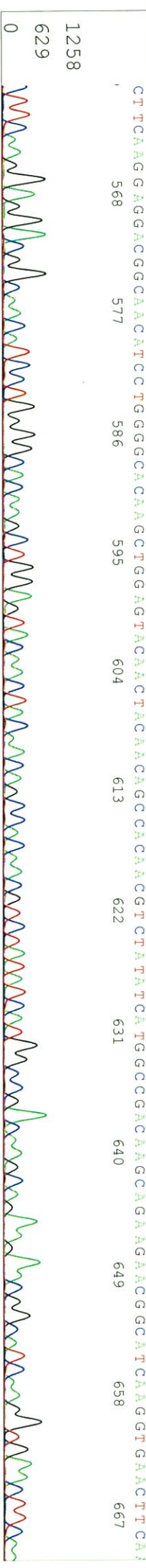


G A A A T T A A T A C G A C T C A C T A T A G G G A G A C C C A A G C T G G C T A G C G T T T A A A C T T A A G C T T A C G A T G T G A G C A A G G G C G A G A G C T G T T C A C C G G G T G G T G C C A T C T G G
09 118 127 136 145 154 163 172 181 190 199 208 217
FCGAGCTGGACGGCGACGTAAACGGCCAAAGTTTCAAGCGTGTCCGGCGAAGGGCGAGGGATGCCACCTAACGGCAAGCTGACCCCTGAAAGTTCACTGCACCAACCGGCAAGCTGC

CCGTGCCCTGGCCCAACCCTCGTGAACCACTGACCCTACGCGCTGACAGTGTCTCAGCCGCTACCGCCGCAACATGAAAGCAAGCACTTCTCAAGTCCGCCATGCCGAAGGCT
34 343 352 361 370 379 388 397 406 415 424 433 442

ACGTTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAAGACCCCGCCGAGGTGAAGTTCGAGGGCCACACCCTGGTGAACCGCATCGAAGCTGAAGGGCATCGA
451 460 469 478 487 496 505 514 523 532 541 550 559

CTTCAAGGAGGACCGCAACATCC TGGGGCAAA GCTGGAGTACCAACTACAAAGCCACAACGCTCTAATCA TGGCCGACAAAGCAAGAAAGACGGCATCAAAGTGAACCTCA
568 577 586 595 604 613 622 631 640 649 658 667



1 NN N NNNNN N NN C INNNNNNN G T T G G G G T G G G C G A A N A A N T C C N G C A T G A G N T C C C C C G C G C T G C G A T C C A G C C C G G C G G T C C C G G A A A C G A T T C C G A A G C C C A A C

