

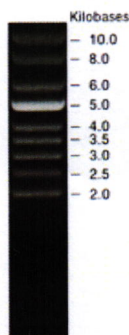


RIKEN DNA BANK

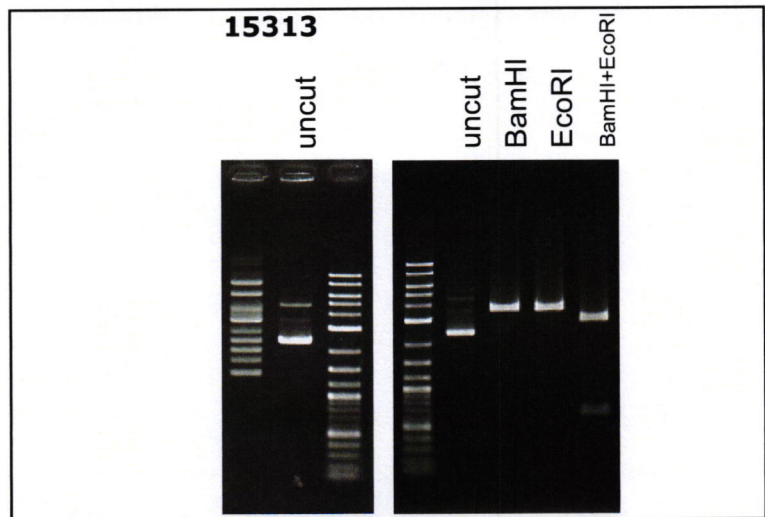
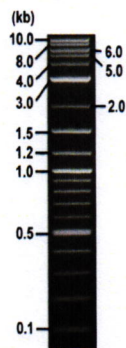
clone name : hmKO2/pRSETB

- Clone ID : RDB_15313
- Lot : 15313_A7H9
- DNA Concentration : 25 ng/μL
- Volume : 40 μL
- Form : DNA solution in TE buffer
- Host : DH5α
- Culture : LB medium
- Antibiotics : 100 μg/mL Ampicillin
- Purification : QIAGEN QIAprep Spin Miniprep kit
- Digestion by restriction enzyme

Supercoiled DNA Ladder (NEB#N0472S), 250 ng/well



1 kb Plus DNA Ladder (NEB#N3200L), 250 ng/well



Electrophoresis : 100 ng DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
BamHI	3.5 kbp
EcoRI	3.5 kbp
BamHI+EcoRI	2.9, 0.7 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	Pr0261	T7_20bp	6xHis,T7 Tag,Xpress tag,insert 5'
Sequence - B	Pr0142	f1ori_R3	T7 ter,insert 3'
Sequence - C	-	-	-
Sequence - D	-	-	-
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY :



SN G:199 A:274 T:158 C:274

D04498J4_A7H9_1_T7_20bp

KB_3500_POP7_BDTV3.mob

Pis 1427 to 12727 PK1 Loc:1404

Version 6.0 HISQV Bases: 934

Sep 08,2017 02:17PM, JST

Sep 08,2017 02:44PM, JST

Spacing: 11.28 Pts/Panel1350

Plate Name: 20170908_Kitaku

KB bcp

Cap:14

R_{min} K02



S/N G:48 A:54 T:54 C:76

D04498J4_A7H9_1_f1ori_R3

KB_3500_POP7_BDTV3.mob

Pls 1420 to 12780 Pk1 Loc:1397

Version 6.0 HiSQV Bases: 942

Sep 08,2017 02:17PM, JST

Sep 08,2017 02:44PM, JST

Spacing: 11.45 Pts/Panel1350

Plate Name: 20170908_kitaku

KB.bcp

primer name B : f1ori_R3

5'-TTAATGCGCCGCTACAGGGC-3'

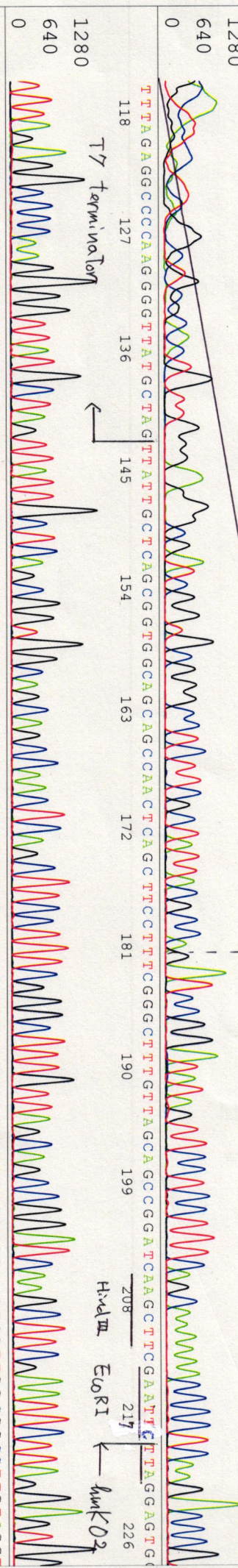
KB 1.4.1.8 Cap:17

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

T7 termination

T7 termination

208 217 226
HindIII EcoRI



3GCCACGGCGTCCCTCCACCTGCTCCGGTGATGTTGCCCTCCGCTCTCCCAAGCCCTGTGGCCGATGAGTGGTCCGGCATCCCAAGATCTCCTTGGCGGCTGTAGGT

GGTCTTCACTCTGGCACTTGGTGTGGTCCCGCCGCTCCCAAGTACATGGTCAAGTCCGCGCTCCAGCAAGCCGTCGGTGGCGGATCTTCTCGGTGAGGGCTCCCAAGT

CCACGGCTCTGGTCTGCAATGATGGGGCCCTCCGGCGGAGATTCACCGCCGCTTGGTAAGAAGTGTGCCCTCAGGCTGATGTGGCGGCTCAAGGAGGC

3GAGCCCGCGTCCCTCGAATCCAGGACGGGACCTCTCCCAAGACAAGCCCTCAGAAAAGCCCTGGTGAATAAGTCTGGGATCTCTCTGGGTACTGTGTAATAAACTCTGTGGC

