

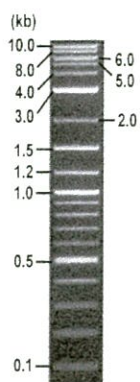


RIKEN DNA BANK

clone name : pFLAG-mRegnase-1-WT

- Clone ID : RDB\_18148
- Lot : 18148\_B1A1
- 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>EcoRI</b>	<b>6.5</b>	kbp
<b>NotI</b>	<b>6.5</b>	kbp
<b>EcoRI+NotI</b>	<b>4.7, 1.8</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	CMV pro, FLAG, insert 5'
Sequence - B	Pr0855	mZc3h12a-M_R1	insert mid
Sequence - C	Pr0350	hGHPolyA-R	hGH p(A), insert 3'
Sequence - D	Pr0731	SV40pro_ori_F	SV40pro, ori
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY :

















```

GGGGCTGGGGCCGTCAGGGCCCTGGCCATCTCGTTCAGTAGCTGAGCCATGCTTCACCAATTCCCCCTAGCACCGGTGGGTGCTGTGGCTTGACCTCCAGGAT
676      685      694      703      712      721      730      739      748      757      766      775
1246
623
0
    
```

```

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

← wRegnase - 1-WT

```

GTGGANCCCTGGCTGTGCTGTGCTGTCCCTCNA GANTCANNCA GACTCNTGGNGG GTGG ANTCNNG GACAGNNNCN TTCNNNN NGNTCNNTCNNGGNNNCNA
892      901      910      919      928      937      946      955      964      973      982
    
```

```

3CTNGNCNNCATT CNNNNTNGNANNNC NNN NNNNNAN NN CTGANNGN NNCNNNA NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN
991      1000      1009      1018      1027      1036      1045      1054      1063      1072      1081
    
```

```

NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
1090      1099      1108      1117      1126      1135      1144      1153
    
```

```

NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
1162      1171
    
```



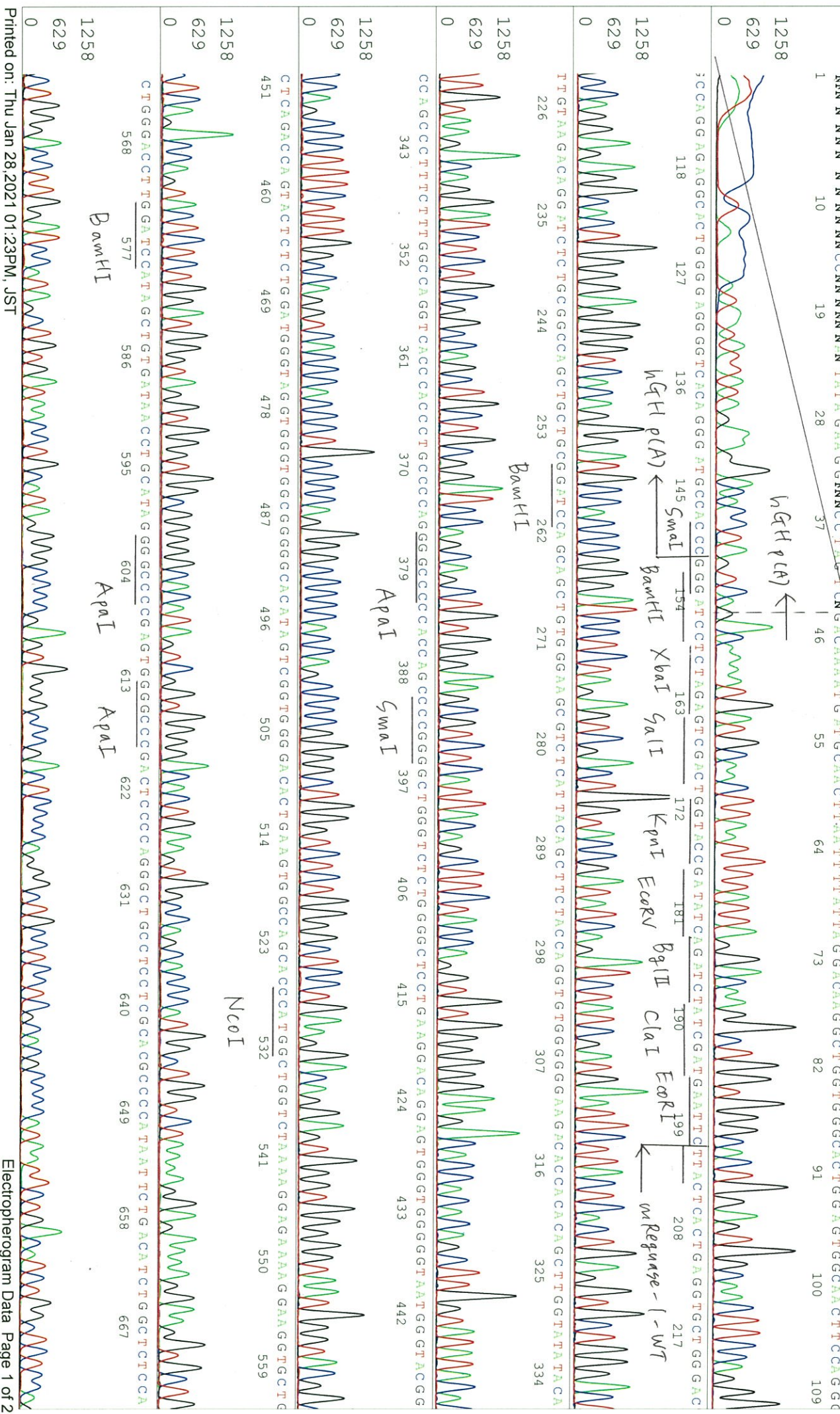


SN N-G:718 A:439 T:434 C:405  
 KB bcp  
 KB 1.4.1.8 Cap:4

primer name C : hGHPolyA-R  
 5'-AGGTTGTTCTCCCAACTTGC-3'

D06974A1\_B1A1\_1\_hGHPolyA-R  
 KB\_3500\_POP7\_BDTV3.mob  
 Pts 1488 to 13957 PK1 Loc:1465  
 Version 6.0 HiSQV Bases: 936

Jan 28, 2021 09:59AM, JST  
 Jan 28, 2021 10:27AM, JST  
 Spacing: 12.36 Pts/Panel1350  
 Plate Name: 20210128 kitaku





SN G:718 A:439 T:434 C:405

D06974A1\_B1A1\_1\_hGHPolyA-R

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KB 1.4.1.8 Cap:4

GGGAAACCAATGCTGAAATCAAAGGCACTCCTGGGANGTGTATGGAGTGAATCCCTGGGTGTGGCAAGCCACTCTGTGGGCCCNAAAGCTGCCCCCACTAACAGGGAATGCTC  
676 685 694 703 712 721 730 739 748 757 766 775 784

← m Reguase - 1- WT

CTGCCAGCTGGANCAACANGTCTCGGGTGANCCCTCTCCGGTGGGACCCGGANANGANCCTGNCACCCAGCTTTTTCNCCNCGGCTGCGTGGNTCAGCCCTCNANGN  
34 793 802 811 820 829 838 847 856 865 874 883

NACAGANCTGGNNTGANANGCANGGGAANGNCCTCTGGNTACTTTGNCCTTNNNNGNNNTCCGNNNNGTGANANGANAGCTTGNNNGNNCNCATCNG  
892 901 910 919 928 937 946 955 964 973 982 991

NNNNNNNNCCTGGGNN  
1000 1009 1018 1027 1036 1045 1054 1063 1072

NN  
.081 1090 1099 1108 1117 1126 1135

NN  
1144 1153





SN G:406 A:285 T:269 C:274

primer name SV40pro\_ori\_F

KB\_3500\_POP7\_BDTV3.mob

Jan 28, 2021 09:59AM, JST

KB.bcp

KB 1.4.1.8 Cap:10

5'-TTCCTCCGCCCCCATGGCTGACTAAT-3'

Pts 1536 to 14032 PK1 Loc:1513

Jan 28, 2021 10:27AM, JST

Version 6.0 HiSeqV Bases: 941

Spacing:12.4 Pts/Panel1350

Plate Name: 20210128 kitaku

