

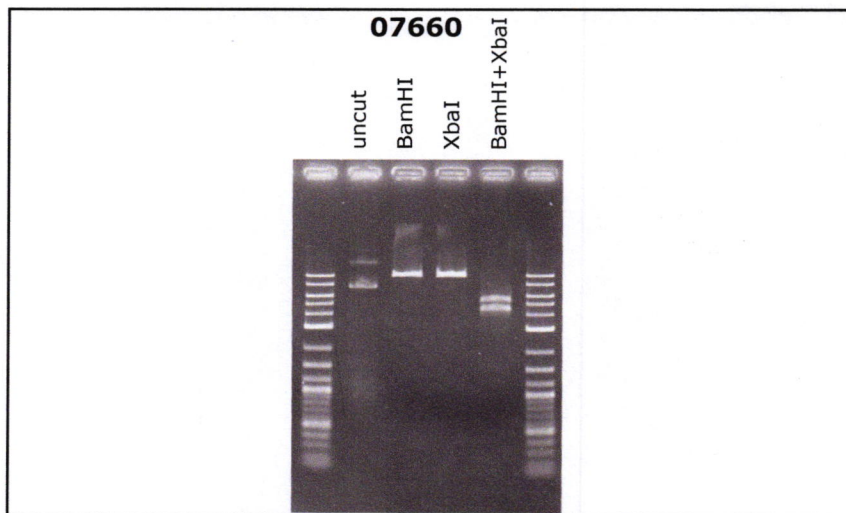
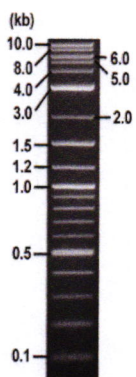


**RIKEN DNA BANK**

clone name : pcDNA3.1(-)-h Integrin alphaV

- Clone ID : RDB \_ 07660
- Lot : 07660 \_ B2Lq
- 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>BamHI</b>	<b>9.8</b> kbp
<b>XbaI</b>	<b>9.8</b> kbp
<b>BamHI+XbaI</b>	<b>5.4, 4.4</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,T7 pro,insert 5'
Sequence - B	Pr0885	bGH_rev3	bGH pA,insert 3'
Sequence - C	Pr1283	hIntegrin-aV-B_R	insert mid
Sequence - D	Pr0731	SV40pro_ori_F	SV40 pro_ori,NeoR
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY





primer name A : CMV\_Forward

5' GCACCAAAATCAACGGGACTT3'

07660\_07660\_B2Lq\_1\_CMV-Forward\_A01\_01\_ABI08

07660\_07660\_B2Lq\_1\_CMV-Forward

KB\_3500\_POP7\_BDTV3.mob

Pts 1394 to 13647 Pk1 Loc:1371

Version 6.0 HISQV Bases: 900

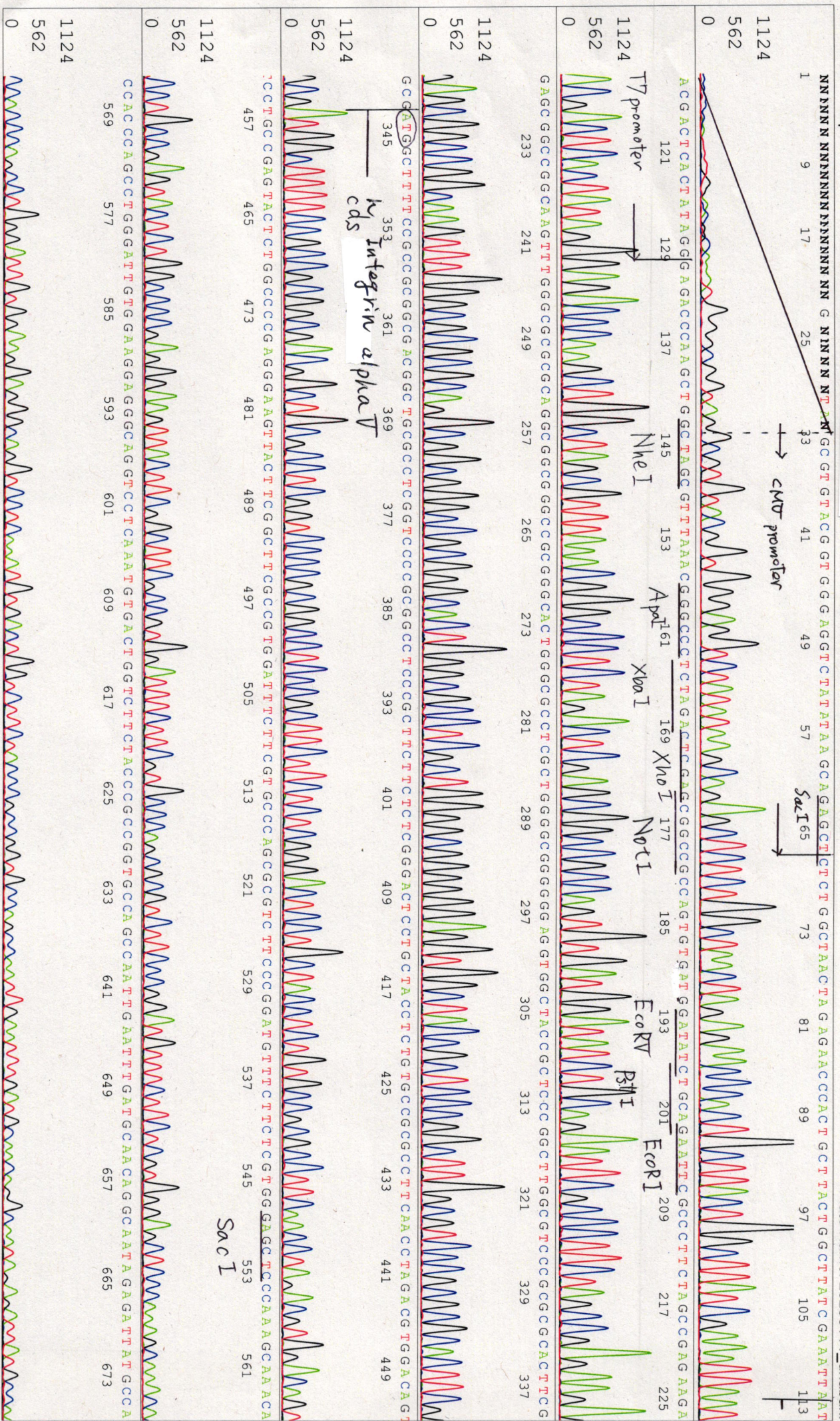
Inst Model/Name 3500/3500 Instrument

Jan 11, 2023 04:02PM, JST

Jan 11, 2023 04:31PM, JST

Spacing: 12.14 Pts/Panel1350

Plate Name: 20230111\_dnabank





S/N G:35 A:17 T:17 C:22

07660\_07660\_B2Lq\_1\_CMV-Forward

Jan 11, 2023 04:02PM, JST

KB.bcp

KB\_3500\_POP7\_BDTV3.mob

Jan 11, 2023 04:31PM, JST

KB 1.4.1.8 Cap:1

Pts 1394 to 13647 PK1 Loc:1371

Plate Name: 20230111\_dhbank

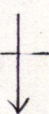
Version 6.0 HISQV Bases: 900

Spacing: 12.14 Pts/Panel1350

AGGATGATCCATTGGGAAATTAAAGTCCATCA GTGGTTGGAGCATCTGTGAGGAAACNNGATAAATTTGGCCGTGCCCCATTGTGACCATGGGAATG

681 689 697 705 713 721 729 737 745 753 761 769 777 785

cds



AAACAGGANCAGAGAGCCTGTTGAAACAAGTCTTCTTCCNAGATGGANNAAAAGACTGTGAGTANGCTCCNTGTANNCTCANNANNFTTTGATGCTGANGGNNNGANNTT

793 801 809 817 825 833 841 849 857 865 873 881 889 897

1124  
562  
0

GTCNANGNNGNNNNNCNNTGATNNNNNNNAAAGCTNNNNGANNNTTCNTGNNINCCNTGNNNNCNNTTNNNTGNNAAANNGNCPNCTNNNTTTCNNNNNTCA NNTGGN

905 913 921 929 937 945 953 961 969 977 985 993 1001 1009

NNAA NNNNN NNNNNNAAA NNNNNNN NN

1017 1025 1033

1124  
562  
0

1124  
562  
0

1124  
562  
0



S/N G:27 A:29 T:28 C:16

primer name  $\beta$  : bGH\_rev3

07660\_07660\_B2Lq\_1\_bGH\_rev3

Jan 11, 2023 04:02PM, JST

KB.bcp

5' TTAGGAAAGGACAGCTGGGAGTG 3'

KB\_3500\_POP7\_BDTV3.mob

Jan 11, 2023 04:31PM, JST

KB 1.4.1.8 Cap:2

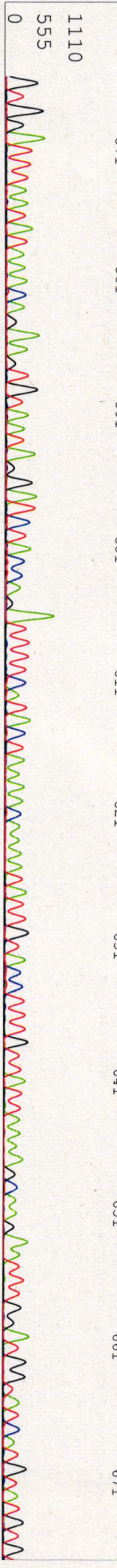
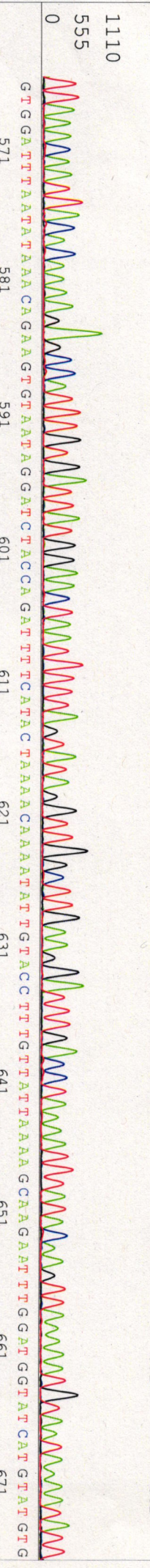
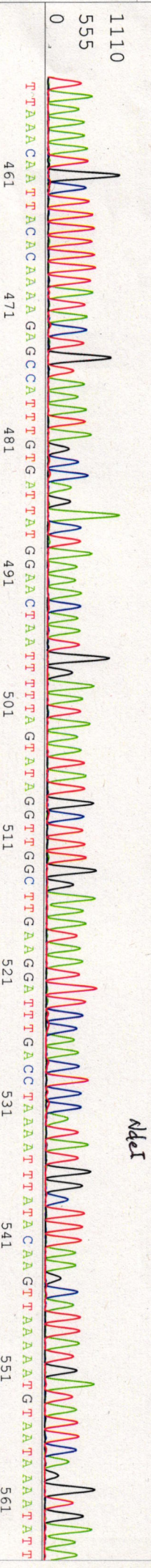
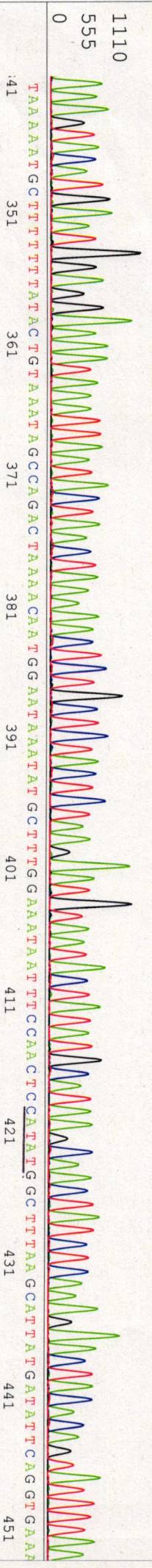
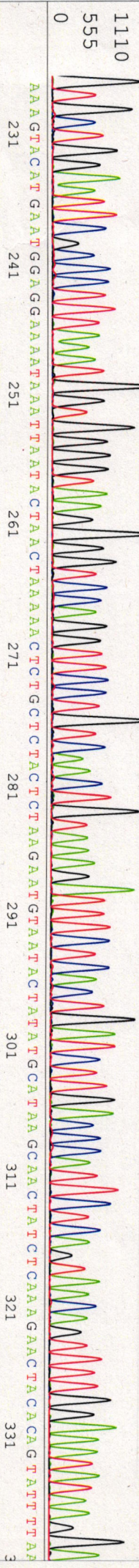
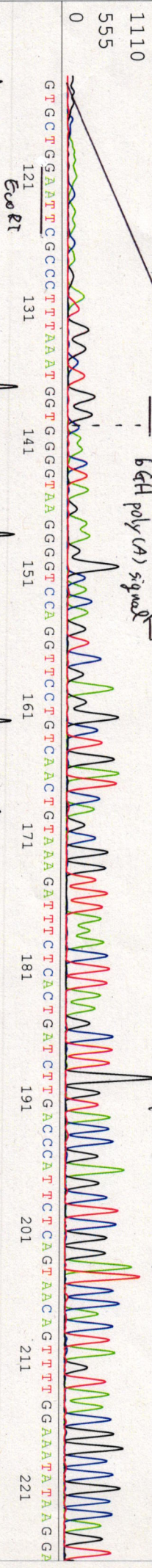
Pts 1494 to 13585 Pk1 Loc: 1471

Spacing: 12.05 Pts/Panel1350

Genetic sequence: GNN N NNNNNN NN NNNNNNNN NNN N NCAACTA GAAGGCACA GT C GAGGCT GATCA GCGGTTTAAACTTAA GCTTGTACC GA GCTCGGATCCACTA G TAAACGGCCCGCA GT

bGH poly(A) signal

Restriction sites: HvuIII, KpnI, SacI, BsmHI, SpeI





TTTATAAATCTACCACTATGAGTGTATAAATAATCCAGTTTCATGCAAGTTTAAAGTCTTTNTATTCCTGAATAAGTAAACTGTAGTGTAAATATGATTAAACATTAAGTA  
 681 691 701 711 721 731 741 751 761 771 781

*NDAT*

CCTATCAAANACATGATTGCINAAAGTCCAAATTTGGANTGCTTTAAACACAAACAAACAACNPAACAAACAAAATAANGTTCCGINNCTNAAAACNNAAAA  
 791 801 811 821 831 841 851 861 871 881 891 901

1110  
555

GNNNTGNANGGAGGTAACNNNTTTTANNNNANNGNANINAAATCANGNACNNCCGTGNTNANNNNNNNNTNANNNNNAACNATNNNTNAAANTTNANNNA  
 911 921 931 941 951 961 971 981 991 1001 1011 10

1110  
555

NNAAAAANNNCNAGTNNNCNNNNNGTNNNNANNGNANNNNNCANNNNNCTNNNNNTNANNNNNANNNNNAACNATNNNTNAAANTTNANNNA  
 121 1031 1041 1051 1061 1071 1081 1091 1101 1111 1121

1110  
555

ANNNNNNNNTNNTNN  
 1131 1141 1151 1161 1171 1181 1191 1201 1211

1110  
555

NN  
 1221 1231

1110  
555  
0



S/N G:91 A:107 T:85 C:76

primer name *hIntegrinAV-B\_R*

07660\_07660\_B2Lq\_1\_hIntegrinAV-B\_R

Jan 17, 2023 03:12PM, JST

KB.bcp

5' GCACATCAGCAGTAAAGCC 3'

KB\_3500\_POP7\_BDTV3.mob

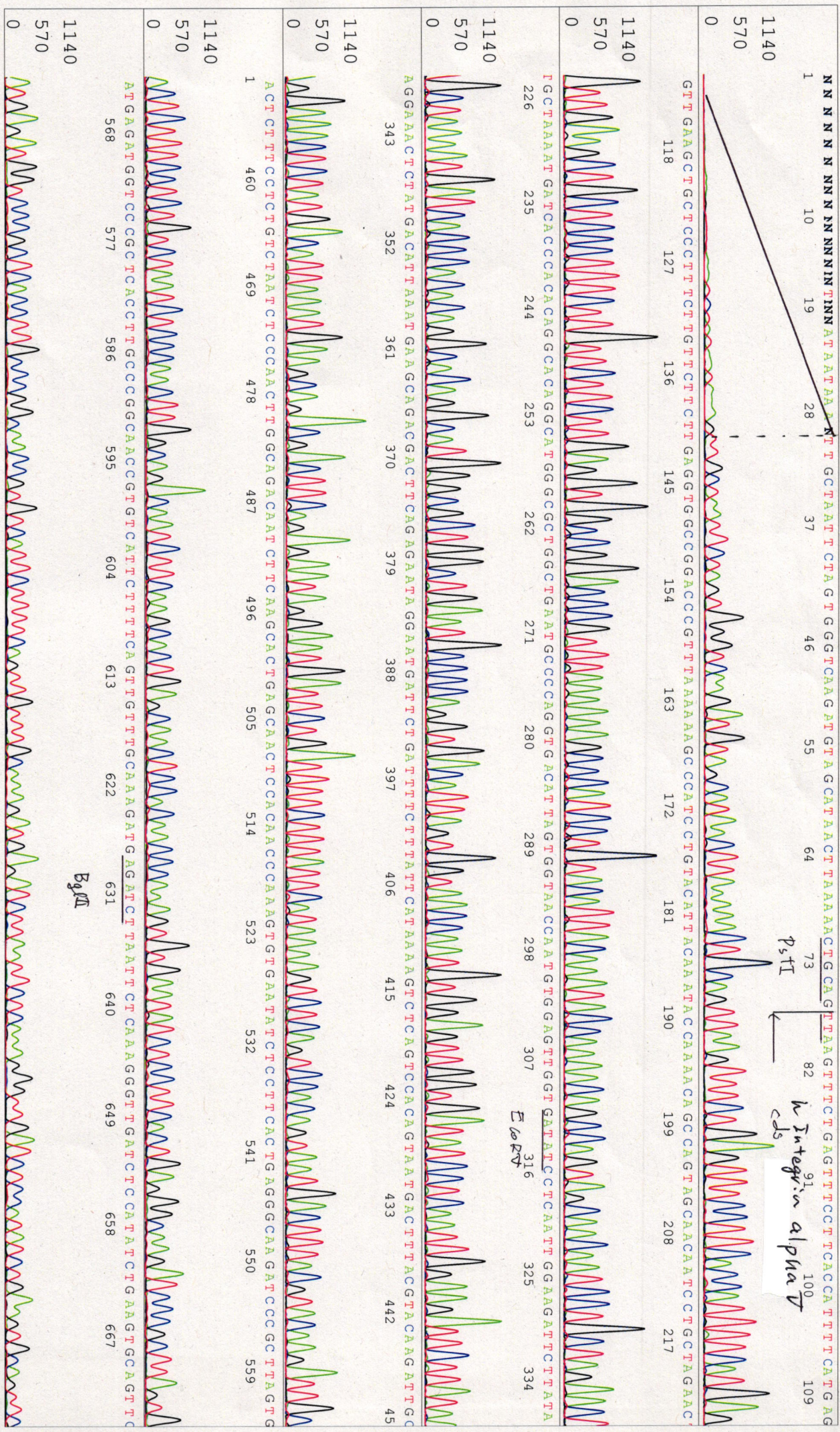
Jan 17, 2023 03:39PM, JST

KB 1.4.1.8 Cap:1

Pts 1368 to 13508 Pk1 Loc:1345

Version 6.0 HiSQV Bases: 943

Spacing:11.95 Pts/Panel1350  
Plate Name: 20230117\_dnabank





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

1140  
570  
0

ATTGTCCTCAATATCAATAAGGAAGGANATACCAACAGAGTGTATTATTATTTGTAAGGCCNCTGAAAGATGGAATGACCTTGGAACCTTTGTG  
cds  
TTCTCAGCTCATAGATGCTGAAACAACCTGCCACATCTTCTTCAGTCTCAGGGTTCCTTGTGCTCCAGATTGNAATCNGAAGAANATGATCAGGACT

1140  
570  
0

392 901 910 919 928 937 946 955 964 973 982 992  
AGANTNCTCTTATCTCANNNGCTNANNAGCANNATCNACCTTTGTGAGANACNANNNGNNNTACTTTGTNAANANNTNANCCTNNGGNNNNNNGNI

1140  
570  
0

1 1000 1009 1018 1027 1036 1045 1054 1063 1072 1081  
AANNNTTCNCNN

1140  
570  
0

1081 1090 1099 1108 1117 1126 1135  
NN

1140  
570  
0

NN

1140  
570  
0

Printed on: Tue Jan 17, 2023 05:31PM, JST



S/N G:47 A:27 T:27 C:25

07660\_07660\_B2Lq\_1\_SV40pro\_ori\_F

Jan 11, 2023 04:02PM, JST

KB.bcp

KB\_3500\_POP7\_BDTV3.mob

Jan 11, 2023 04:31PM, JST

KB 1.4.1.8 Cap:3

primer name: D : SV40pro\_ori\_F  
5' TTCTCCGCCCCCATGGCTGACTAAT 3'

Pts 1446 to 13689 PK1 Loc: 1423

Spacing: 12.2 Pts/Panel1350

NNNNNNNN INN INNNNNN NNN NNN NNTAN T NNNN NNTTA GT GAGGAGGCTTTT T GGAAGGCTTAGGCTTTT GCAAAAGCTCCCGGAGCTTGTATATCCATTTCGGATCTG  
1 11 21 31 41 51 61 71 81 91 101 111

50-40 promoter

Swat

Neok

PstI

