

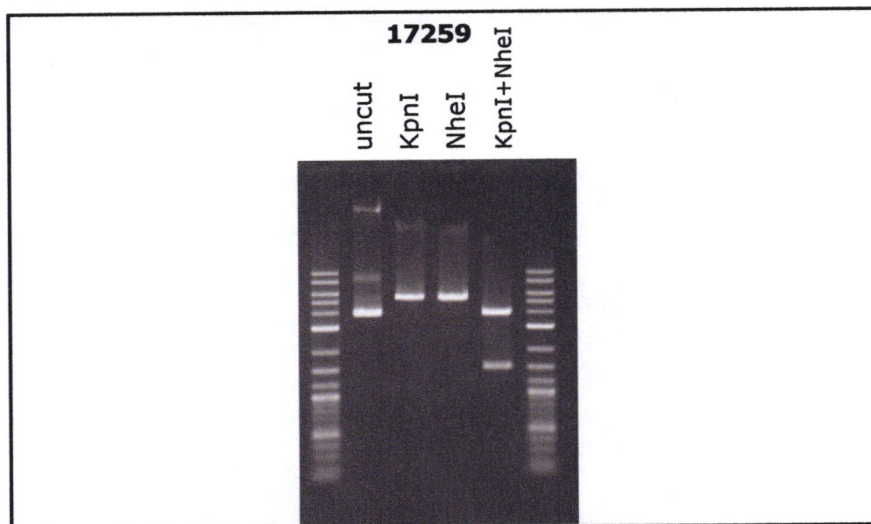
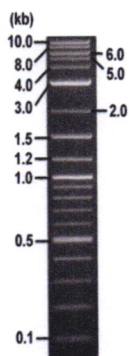


**RIKEN DNA BANK**

clone name : **pEGFP-C1-Rab12**

- **Clone ID** : RDB \_ 17259
- **Lot** : 17259 \_ A9E1
- **DNA Concentration** : 25 ng/μL
- **Volume** : 40 μL
- **Form** : DNA solution in TE buffer
- **Host** : DH5α
- **Culture** : LB medium
- **Antibiotics** : 25 μg/mL Kanamycin
- **Purification** : QIAGEN QIAprep Spin Miniprep kit
- **Digestion by restriction enzyme**

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



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

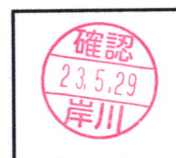
Restriction enzyme	Expected size of fragment
<b>KpnI</b>	<b>5.5</b> kbp
<b>NheI</b>	<b>5.5</b> kbp
<b>KpnI+NheI</b>	<b>3.9, 1.5</b> kbp
	kbp

● **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	Pr0992	VN_F1	EGFP 3',insert 5'
Sequence - B	Pr0623	SV40polyA_R2	insert 3'
Sequence - C	Pr0016	CMV_Forward	CMV pro,EGFP 5'
Sequence - D	Pr0154	SV40pro_F_V2	NeoR_KanR
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

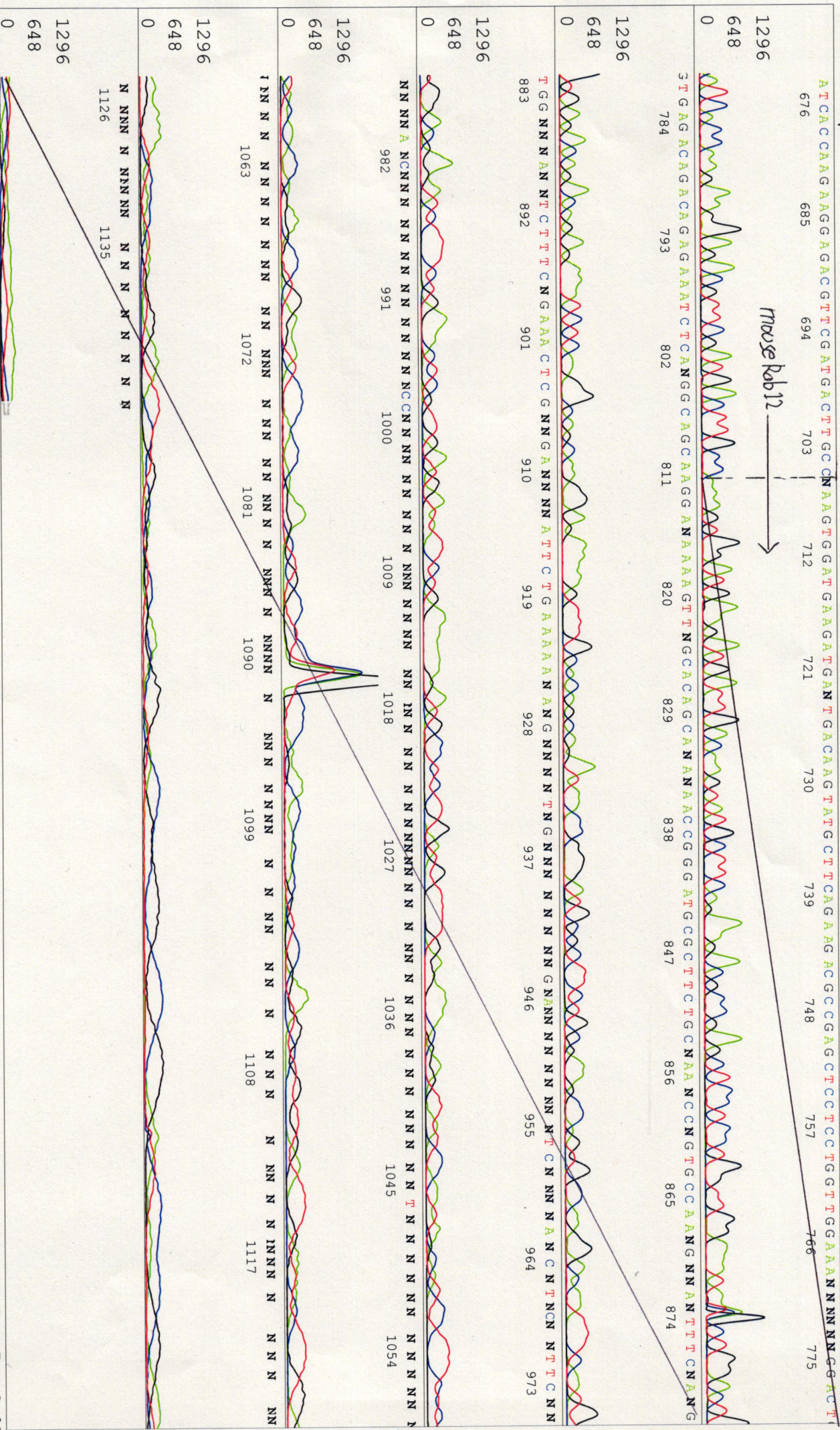
APPROVED BY :











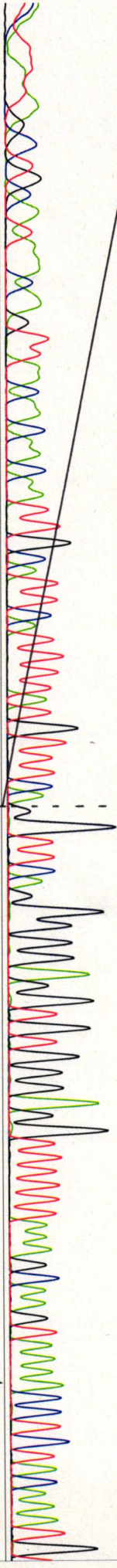


5'-GTGAATTGTGATGCTATTGC-3'

Version 6.0 HISQV Bases: 1035

Plate Name: 20190604 mix

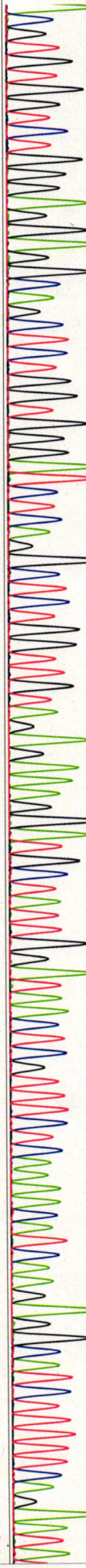
1 10 19 28 37 46 55 64 73 82 91 100 105



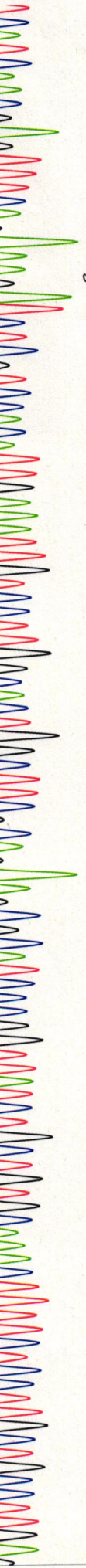
TGGTATGGCTGATTATGATCA GTTATCTA GATCCGGTGGATCCCGGCCGCCGGTACCCTCGACTGCAAGAAATTCACCTAGTGATTCTCCCAA GTATCAAAATCAACAAGCATCGG  
 118 127 136 145 154 163 172 181 190 199 208 217  
 XbaI\* BamHI SmaI KpnI SalI PstI EcoRI SpeI



ACGTGTGCTCTGGGAGAGGCAAGCTCTGGTGGGATCTCAGGCTCTGGTTGTAAGAAGGATGCTATTGGATAACTCGTTCTCAAACA TCAAGAGGCATCTTTTCAGAATA  
 226 235 244 253 262 271 280 289 298 307 316 325 334  
 mouse Rab12



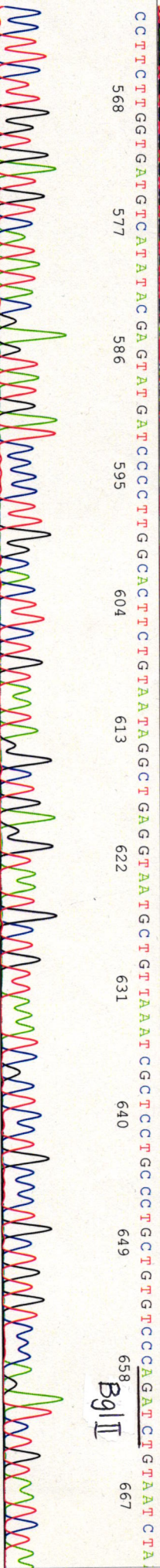
TCAACAACGAGTTTCA GAAAGATCTCTCCACCATTGAAA TTGTTCC TTTGGCACTGGCTTCCAGAAAGCGCATCCC GGTTATCTGCTGTGCCAAACTTTCTCTTGC TGCCCTTGA  
 343 352 361 370 379 388 397 406 415 424 433 442  
 Bgl II



3ATTTCTCTGCTCTGCTCTCAAGATCCCA GCTTATTTCCCAACCAAGGAGCTCCGGCTCTCTGAAAGCA TACTGTCAATCATCTTCAATCCA CTTTGGCAAGTCA TCGAAAGCTC  
 451 460 469 478 487 496 505 514 523 532 541 550 559  
 Sac I



CCCTCTTGGTGATGTCATATACGA GATGATCCCTTTGGCACCTCTGTAATA GGGCTGAAGTAA TCGCTTAATCGCTCTGCTGTCAGATCTGTAATCTA  
 568 577 586 595 604 613 622 631 640 649 658 667  
 Bgl II









S/N G:206 A:216 T:164 primer name C : CMV\_Forward

KB\_bcp KB\_3500\_POP7\_BDTV3.mob

Jun 04, 2019 03:21PM, JST

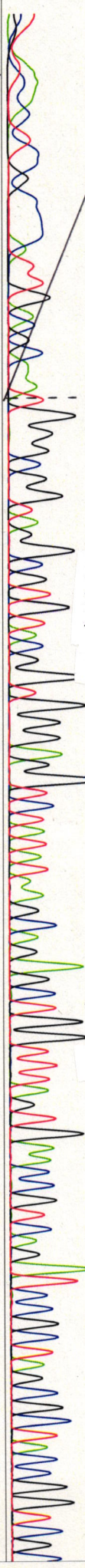
KB 1.4.1.8 Cap.21 5- GCACCAAATCAACGGGACTT -3'

Pts 1381 to 13254 Pk1 Loc: 1358

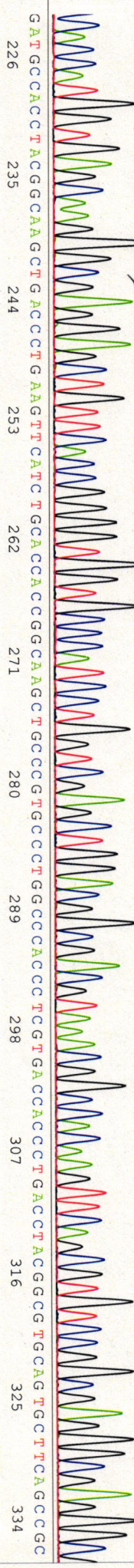
Spacing: 1.74 Pts/Panel1350

1 NNNNN NNN NNN NNN T T G NN G C I N N T G G G C G G T A G C C G T G T A C C G T G G A G T C T A T A T A A G C A G A G C T G G T T T A G T G A A C C G T C A G A T C C G C T A G C G C T A C C G G T C G G

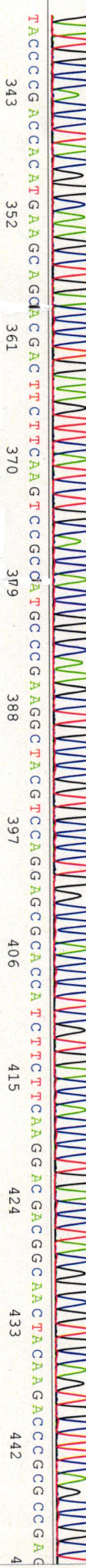
CMV pro



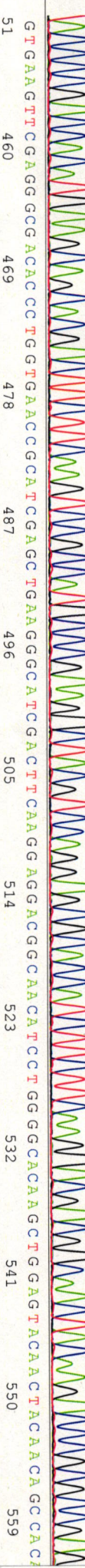
GCACCAATCAACGGGACTT-3' 118 127 136 145 154 163 172 181 190 199 208 217



GATGCCACCTACGGCAAGCTGACCCTGAGTTCACTCGCAACAAGCTGCCCGTGCCTGGCCCAACCCTCGTGAACCACTGAACCTACGGCGTGCAAGTGTCAAGCCG



TACCCCGACCACTGAAAGCAGACCGACTTCTTCAAAGTCCGCCATGCCCGAAGGCTACCTCCAGGAGCCGCAACAATCTTCTTCAAAGGACGACGGCCAACTACAAGAACCCGCCG



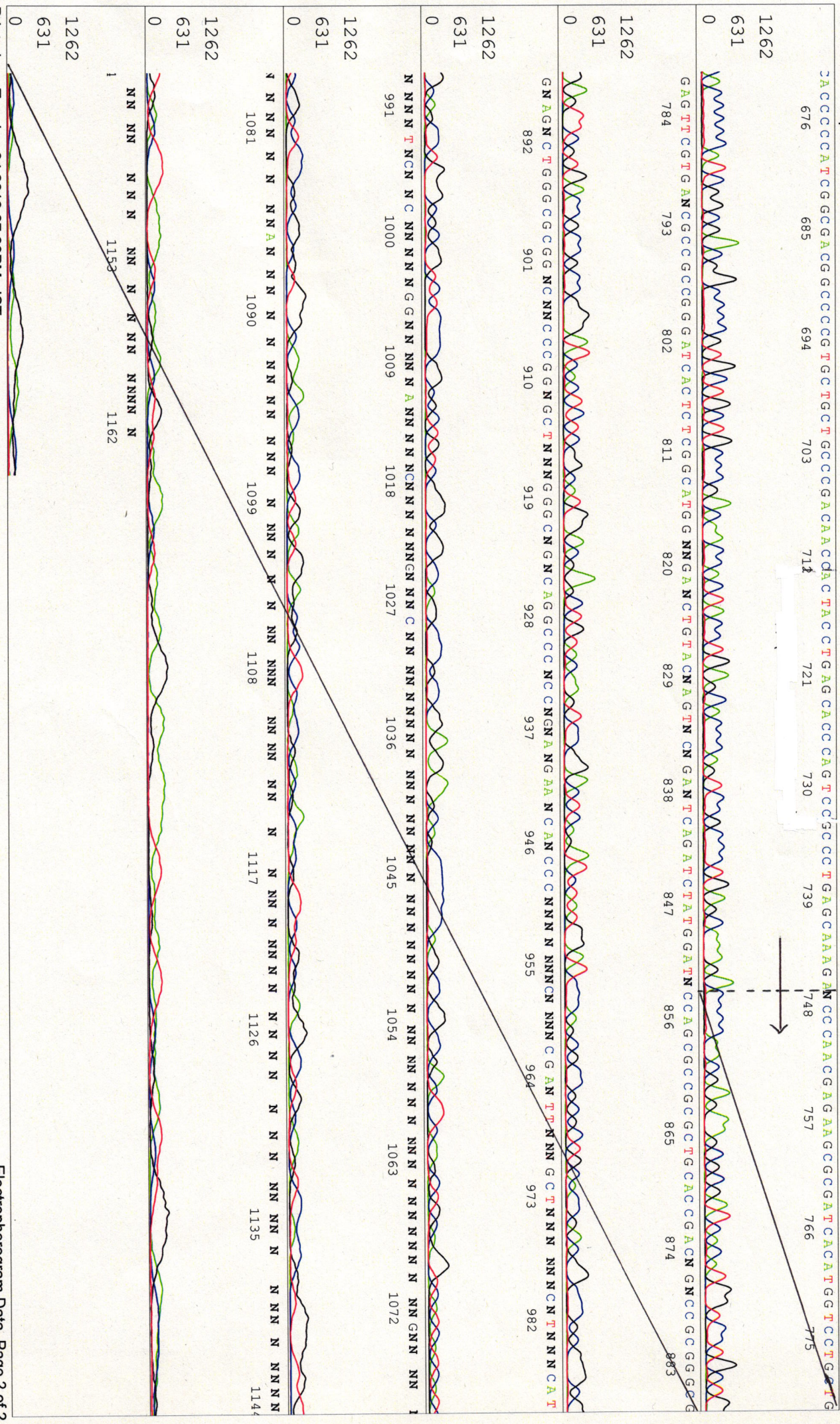
GTGAAATCGAGGGCGACACCTGGTGAACCGCATCGAAGTGAAGGGCATCGACTTCAAAGAGGACCGCAACAATCTTGGGCACCAAGCTGGAGTACAACATAACAAGCA



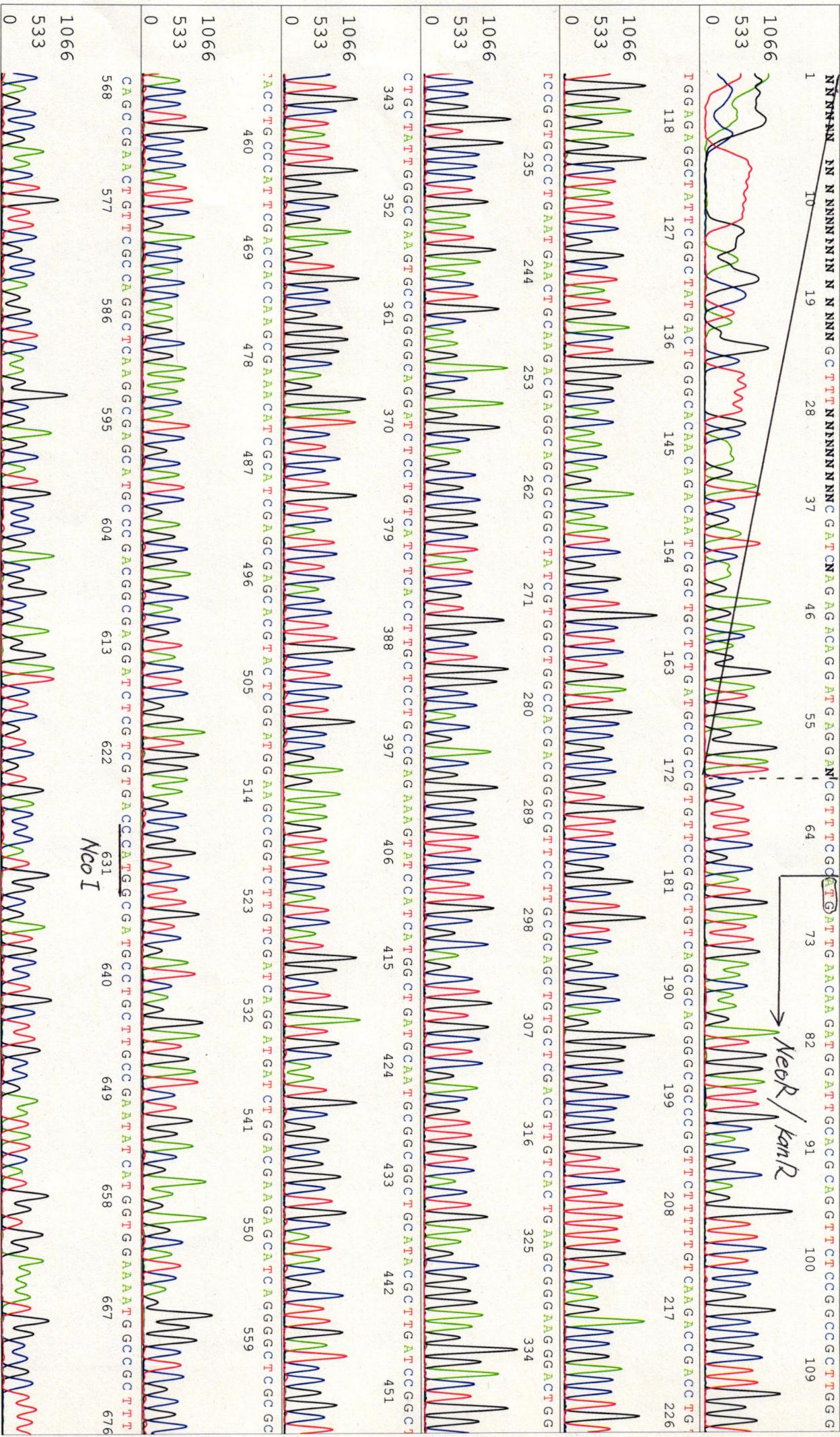
YACGCTATAATCATGGCCGACCAAGCAAGAAAGACGGCATCAAAGTGAAGTCAAGATCCGCCACCAACATCGAAGGACGGCAAGCTGCAAGCTACCAAGCAAGAA













S/N G:56 A:43 T:43 C:69

D06280E5\_A9E1\_2\_SV40pro\_F\_V2

Jun 04, 2019 02:40PM, JST

KB 3500\_POP7\_BDTV3.mob

Jun 04, 2019 03:21PM, JST

Pts 1392 to 13356 Pk1 Loc:1369

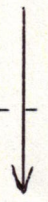
Spacing:11.82 Pts/Panel1350

Version 6.0 HiSQV Bases: 1012

Plate Name: 20190604 mix

KB 1.4.1.8 Cap:24

TCTGGATTTCATTCGACTGTGGCCGGCTGGGGTGTGGCCGGAACCCCTATCAAGACAAGCGTTGGCTTACCCGGTGAATATGCTGAAGAGCTTGGCCGGCAATGGGCTGACCGCT



TCCTCGTGGCTTTACNGTATCCGCCCTCCNCGATTCGGCAGCGCCATCCGCCCTTCTATCCGCCCTTCTGACGAGTTCTCTGAGCGGGANCTCTNGGCTNCGAAAAGATCCGAN



AAGCGACGCCCAACCTGGCCNTCCAGAGATTTCTNATTCNNCGCCGCCCTCTCTATGAAAANGNNGGGCCTCNGANNCNTTTNCGNGGAGNNGNNGNTGGNNGATN

NTNNNNCCNNGGGNNNNNCANGNNGGNNN



NN

