

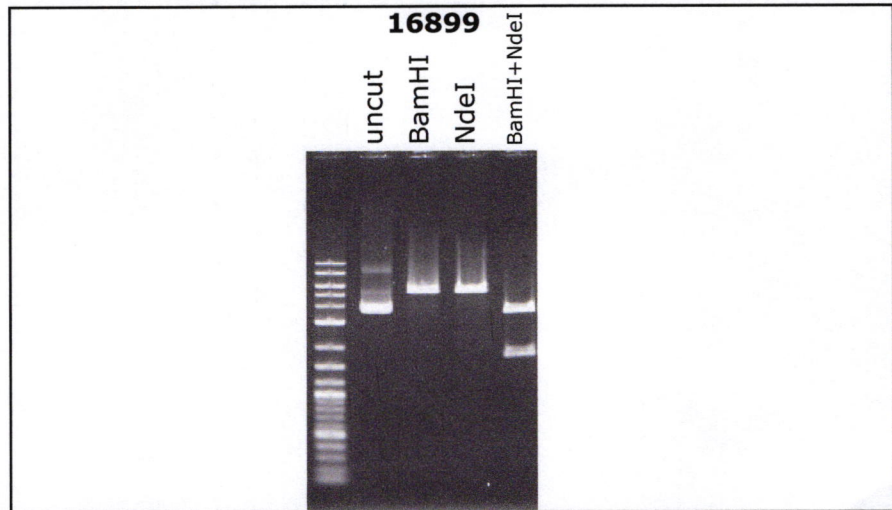
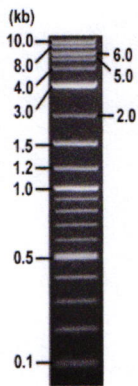


RIKEN DNA BANK

clone name : **pEGFP-C1-Rab38-T23N**

- Clone ID : RDB_16899
- Lot : 16899_A9A8
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 25 microgram/ml Kanamycin
- 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
BamHI	5.4 kbp
NdeI	5.4 kbp
BamHI+NdeI	3.6, 1.8 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	Pr0402	EGFP-C2	EGFP 3',insert (T23N)
Sequence - B	Pr0623	SV40polyA_R2	insert (T23N)
Sequence - C	Pr0016	CMV_Forward	CMV pro,EGFP
Sequence - D	Pr0154	SV40pro_F_V2	NeoR_KanR
Sequence - E	Pr0574	mVenus-M_F	EGFP 3',insert (T23N)
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY :



S/N G:204 A:138 T:128 C:133

primer name A : EGFP-C2

D0606011_A9A8_1_EGFP-C2

Jun 24, 2019 02:52PM, JST

KB.bcp

5'-ACTACTGAGCACCACCGAGTCC-3'

KB_3500_POP7_BDTV3.mob

Jun 24, 2019 03:18PM, JST

KB 1.4.1.8 Cap.9

Pts 1455 to 12848 PK1 Loc:1432

Version 6.0 HISQV Bases: 959

Spacing: 1.1.25 Pts/Panel1350

1176

5'-ACTACTGAGCACCACCGAGTCC-3'

EGFP

100

588

9 118 127 136 145 154 163 172 181 190 199 208 217

→ Ral38-T23N

33

1176

CAACCATGGTGGGACCTTCGGCTGAAAGGATTTGGAACATGACAAAG

T23N

33

588

226 235 244 253 262 271 280 289 298 307 316 325

TTTATTACCCGGGAAGCTATTGGGGGCGATTATTGTTTTGATGTCACCAAGACCA

442

1176

ATGTTAAGCCAGTGTCAAGTGGTCTTGGCCAAATAAATGATTTGACCAAGGAC

442

442

588

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

AGGATGGTTTGAACACATCAAGCAAGGAAACATTAACATTTGATGAA

559

1176

588

568 577 586 595 604 613 622 631 640 649 658 667

667

0

AGGATGGTTTGAACACATCAAGCAAGGAAACATTAACATTTGATGAA

667

1176

588

667

667

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1176

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1176

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667

667

0

AGGATGGTTTGAACACATCAAGCAAGGAAACATTAACATTTGATGAA

667

1176

588

667

667

S/N G:417 A:322 T:281 C:325

primer name B : SV40polYA_R2

D0606011_A9A8_1_SV40polYA_R2

Jun 24,2019 02:52PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Pts 1435 to 12857 Pk1 Loc:1412

Jun 24,2019 03:18PM, JST

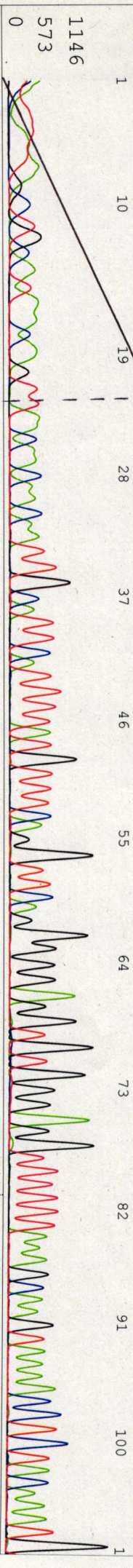
KB 1.4.1.8 Cap:12

5'-GTGAAATTTGTGATGCTATTGC-3'

Version 6.0 HISQV Bases: 940

Spacing: 11.27 Pts/Panel1350

NN NNNNN N NN N A NN NN N N N N T A C A A C A A C A A T T G C A T T C A T T T T A T G T T C A G G T T C A G G G G A G G T G T G G G A G G T T T T T T A A G C A A G T A A A C C T C T A C A A T G



XbaI* methylated

BamHI

SmaI

ApaI

KpnI

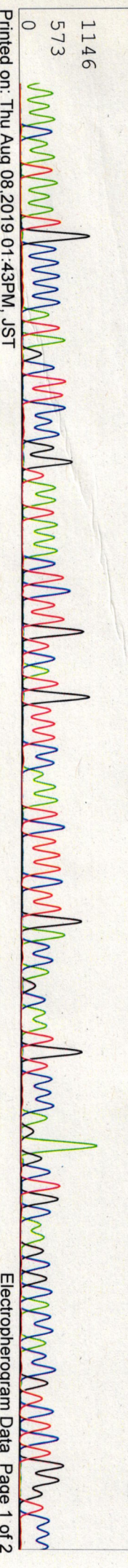
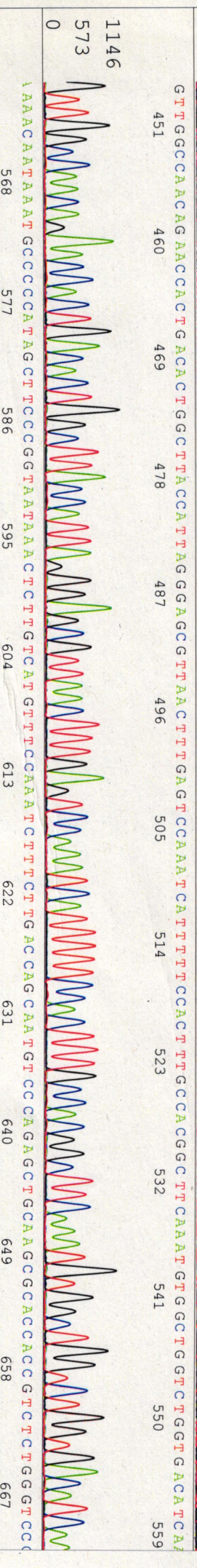
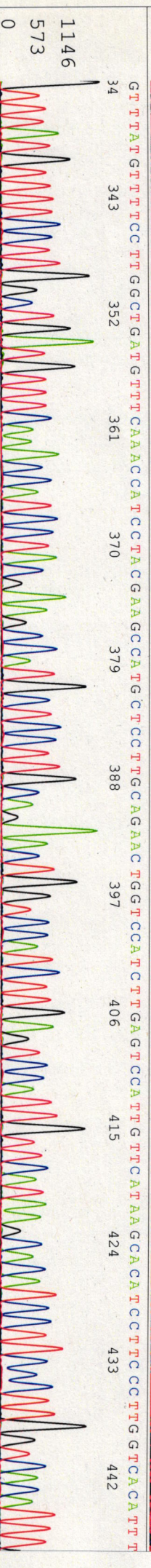
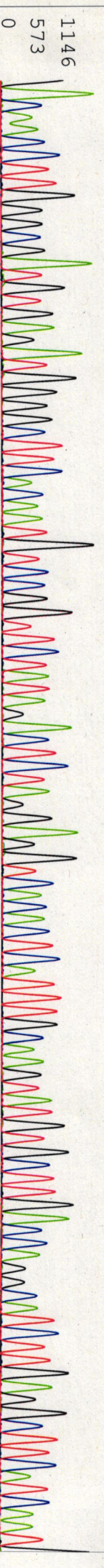
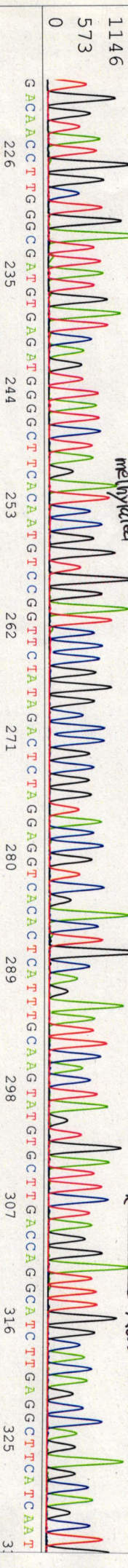
SalI

PstI

EcoRI

SpeI

Rab38-T23N



S/N G:444 A:478 T:305 C:673

D0606011_A9A8_1_CMV_Forward

Jun 06,2019 05:05PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Jun 06,2019 05:31PM, JST

KB 1.4.1.8 Cap:8

Pts 1333 to 12849 Pk1 Loc:1310

Spacing:11.43 Pts/Panel1350

Version 6.0 HISQV Bases: 913

Plate Name: 20190606-1-2 kitaku



S/N G:328 A:205 T:161 C:230

D0606011_A9A8_1_SV40pro_F_V2

Jun 24, 2019 02:52PM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

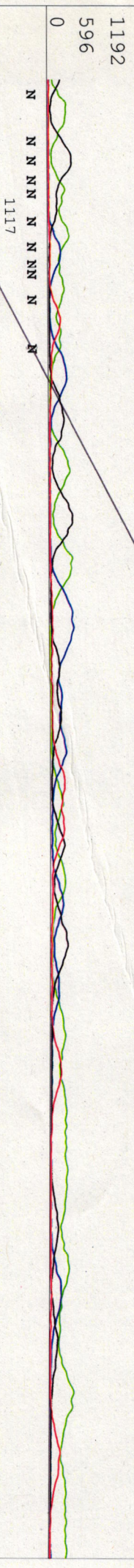
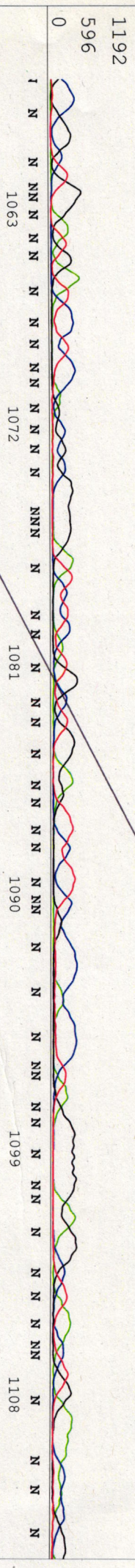
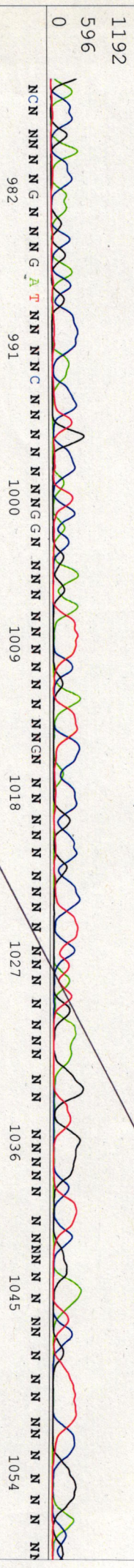
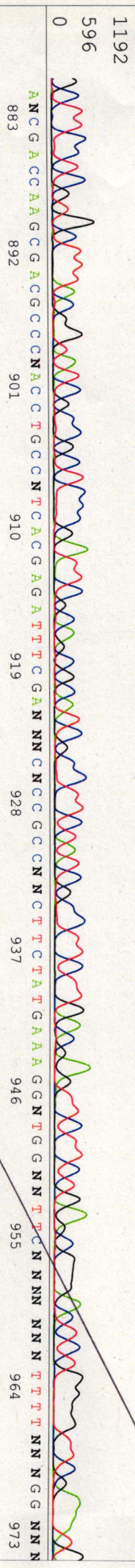
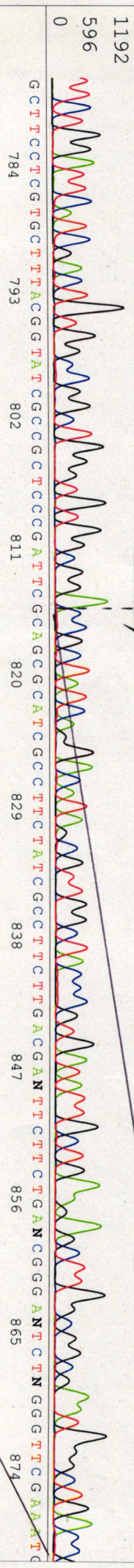
Jun 24, 2019 03:18PM, JST

KB 1.4.1.8 Cap:15

Pis 1419 to 12740 Pk1 Loc:1396

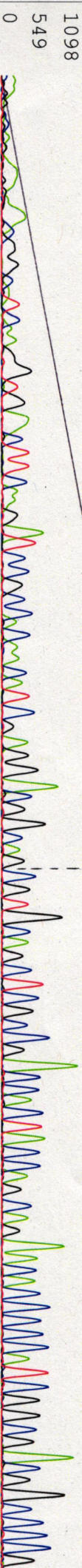
Spacing: 11.28 Pts/Panel1350

TTCTGGATTCATCCGACTGTGGCCCGCTGGGTGTGGCGGATCGCTATCAGGACATAGCGTTGGCTACCCGGTGAATATGCTGAGAGCTTGGCGGCGAATGGGTGACCG



primer name E : mVenus-M_F
5'-ACTACACAGCCACACACGTC-3'

NN NNNNNN INN NNNNN NNNNN NNANN TNNIN CTT CNNNAT CCGCCN C NN CAT CN NNGACN GNN CGTGCAGCTCGCCG ACCA CTA CCA GCA GAACA CCCC CA TCGCGC GACGCCCCG



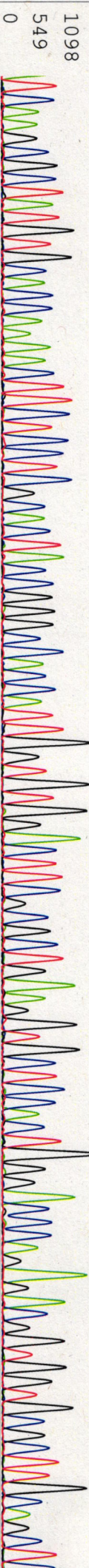
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TCCGCATGGACGAGCTGTACAACTCCGGGACTCAGATCCATGCAGACACCTCACAAAGGAGCACCTGTACAAGCTGCTGGTGAATCCGCGACCTGGGTGGCAAGAACAGCATTT



TCAA GCGCTATGTGCCAACAAACTTCTCCTCGCACATACCGGGCCACCATTGGTGTGACTTCCGCCCTGAAAGTCTCCAC TGGGACCAGAGACGGTGGTCCGCTTGGCAAGCTT



TTGGGACATTTGCTGGTCAAGAAAGATTTGGAAACATGACAAGAGTTTATTAACCGGGAAAGCTATGGGGCCATTTATTTGATGTCACCAAGACCA GCCACATTTGAAAGCCG



TGCCAAAGTGGAAAAATGATTTGGACTCNAAGTTAACCGCTCCCTAATGGTAAAGCCNGTGTCAAGTGGTTCCNGTTGNNCNAAGTGNANCNNN GNNN GNNNGTGGTTNNGAT

