

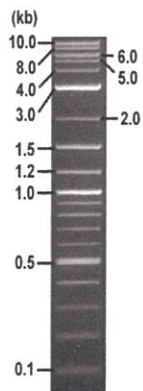


RIKEN DNA BANK

clone name : pDUAL2-HFG41

- Clone ID : RDB _ 06197
- Lot : 14462 _ A6L7
- 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

2-Log DNA Ladder
(NEB#N3200L),
125 ng/well



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

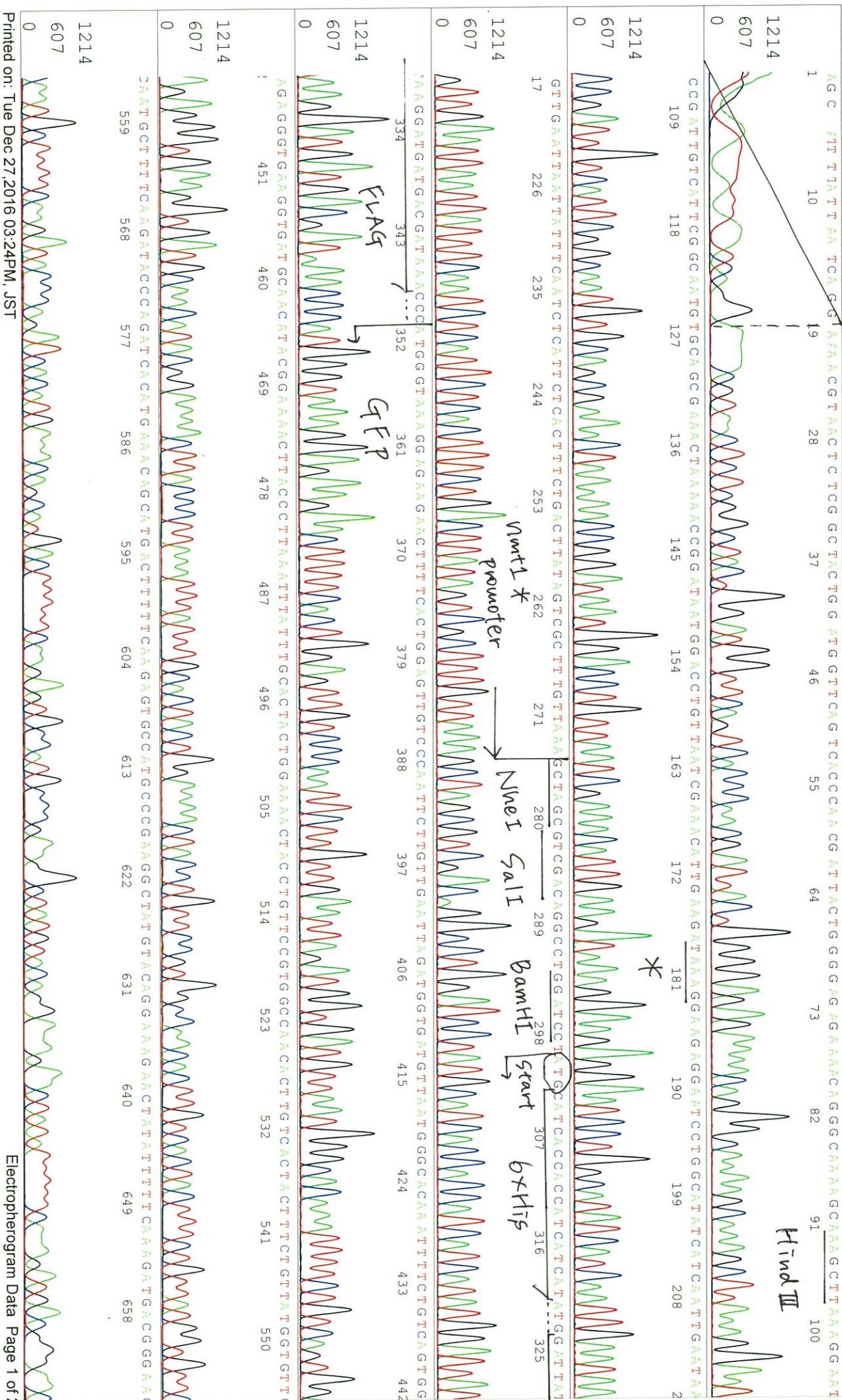
Restriction enzyme	Expected size of fragment
<u>SalI</u>	<u>9.1</u> kbp
<u>EcoRI</u>	<u>9.1</u> kbp
<u>SalI + EcoRI</u>	<u>6.1, 3.0</u> kbp
	kbp
	kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	nmt1Fw	Sequence - E	Reverse2
Sequence - B	ADH_rev	Sequence - F	-
Sequence - C	ADH-Forward	Sequence - G	-
Sequence - D	f1ori_R3	Sequence - H	-

APPROVED BY :





S/N G:304 A:524 T:355 C:325

06197_14462_A6L7_nmt1Fw

Dec 27,2016 09:33AM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Dec 27,2016 10:00AM, JST

KB 1.4:1.8 Cap:20

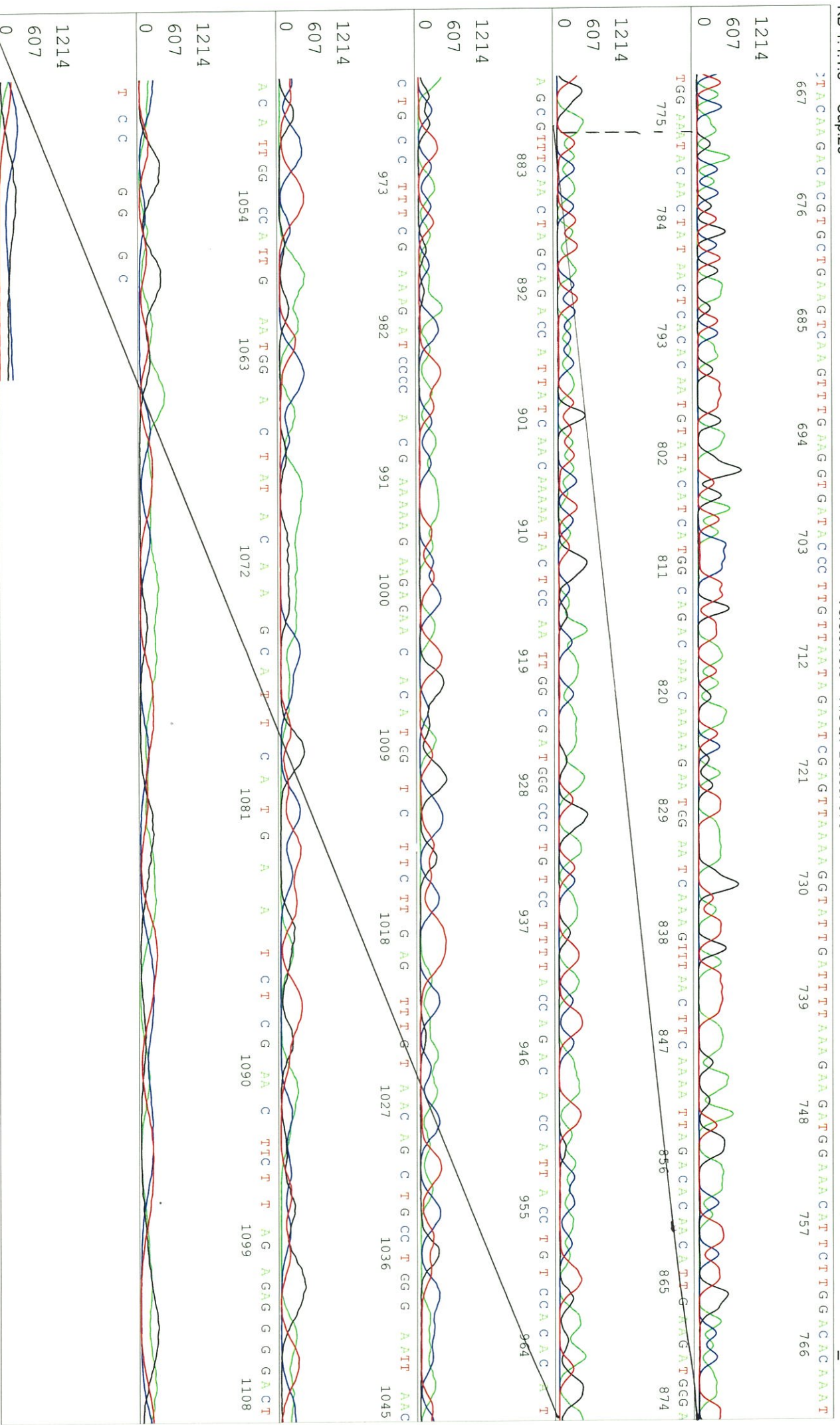
Pts 1690 to 13445 Pk1 Loc:1667

Spacing:12.01 Pts/Panel1350

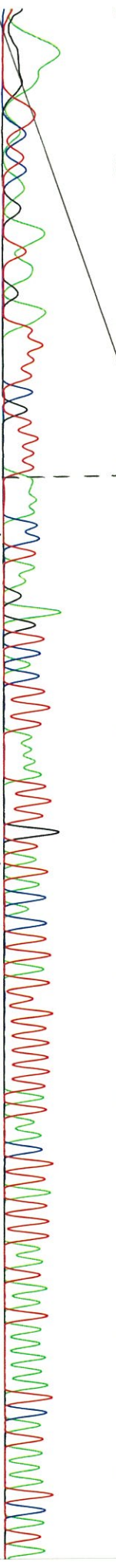
KB 1.4:1.8 Cap:20

Version 6.0 HiSQV Bases: 879

Plate Name: 20161227_dnabank



1 GG (G G T C T C A G A T / A G A T T T T C G T T T T A A A C C T A A G A G T C A C T T T A A A A T T T G T A T A C C A T T A T T T T T T A T T C C A T T A T T T T T T A A C T T A T T T A A T A A T C A T T A



BamHI

5' stop

BglII

EcoRV

GFP

AGAAATTCGCCTTATTGAAAGTGCCGCCGGGATCCTCTAGAGTCGAGATCCTCATGATTCTTTGTATTAGTTCCATCCATGCCCATGTGAATCCCAGCAGCTGTTCACAACTCA

226 AGAAGGACCATGTGGCTCTCTCTTTCTGTTGGGATCTTGAAGAAGGCAATTGTGTGGACAAGTAATGTTGTCTGGTAAAGGACAGGGCCATCGCCAAATGGAGTATTTGTT

235 3ATTAATGGTCTGCTAGTTGAACGCTTCCATCTTCAATGTTGTCTAATTTTGAAGTTAACTTGTATTCCATTCTTTGTTGTCTGCCATGATGTTATACATTGTGTGAGTTATA

343 344 352 361 370 379 388 397 406 415 424 433 442

1216 608 0 GTTGTATTCCAATTGTGTCCAAAGAATGTTTCCATCTTCTTTAAATCAATACCCTTTTAACTCGATTCTTAAACAAGGATCACCTTCAAACTTGACTTCAAGCAAGTGT

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

1216 608 0 :CTGTAGTTCCTCCGCTCATCTTTGAAAAATATAGTTCTTCCGTACATAAGCCCTTCGGGGCATGGCACCTTGAAAAAAGTCAATGCTGTTTCATGTGATCTGGGTATCT

568 577 586 595 604 613 622 631 640 649 658

1216 608 0

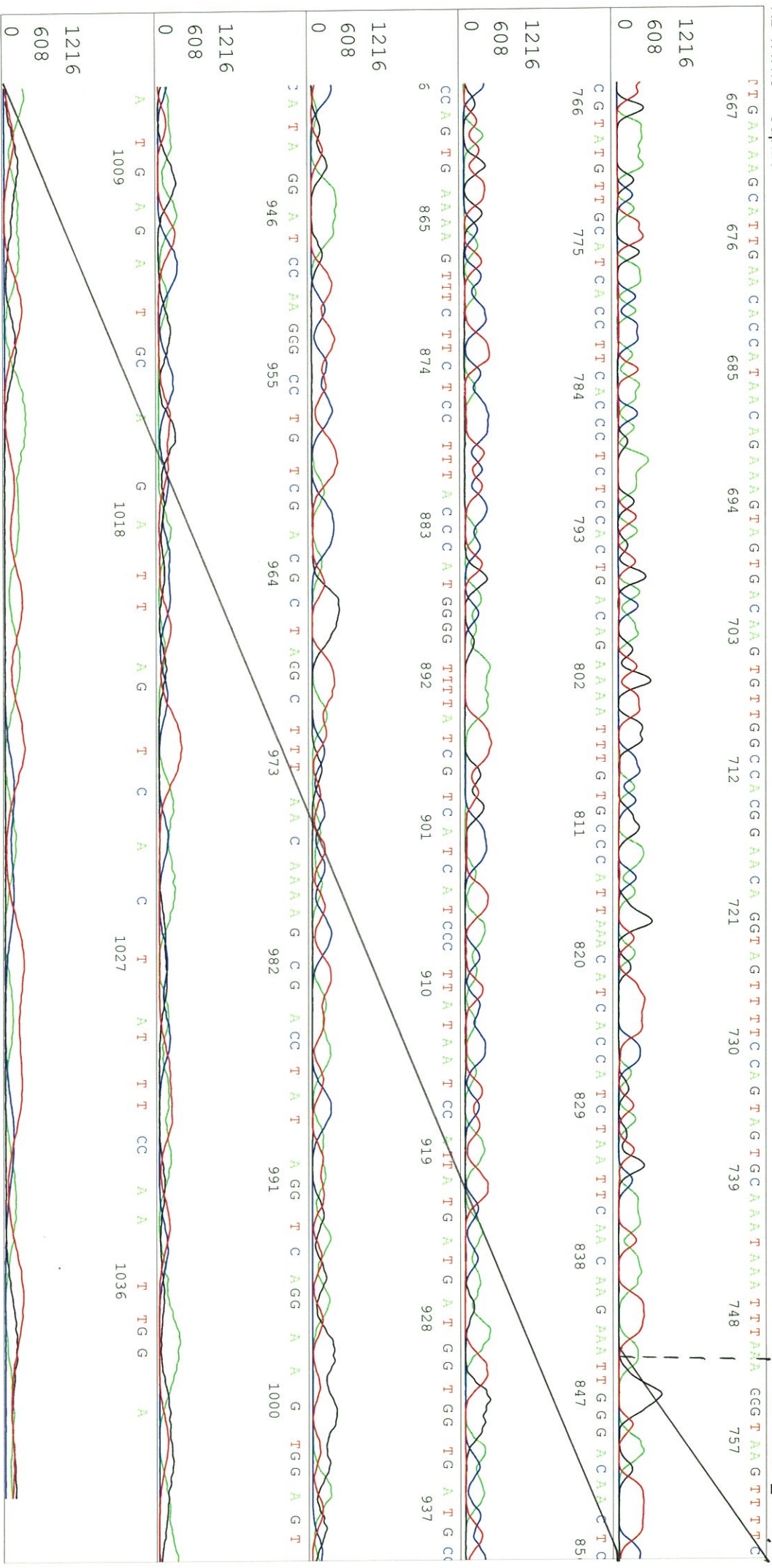
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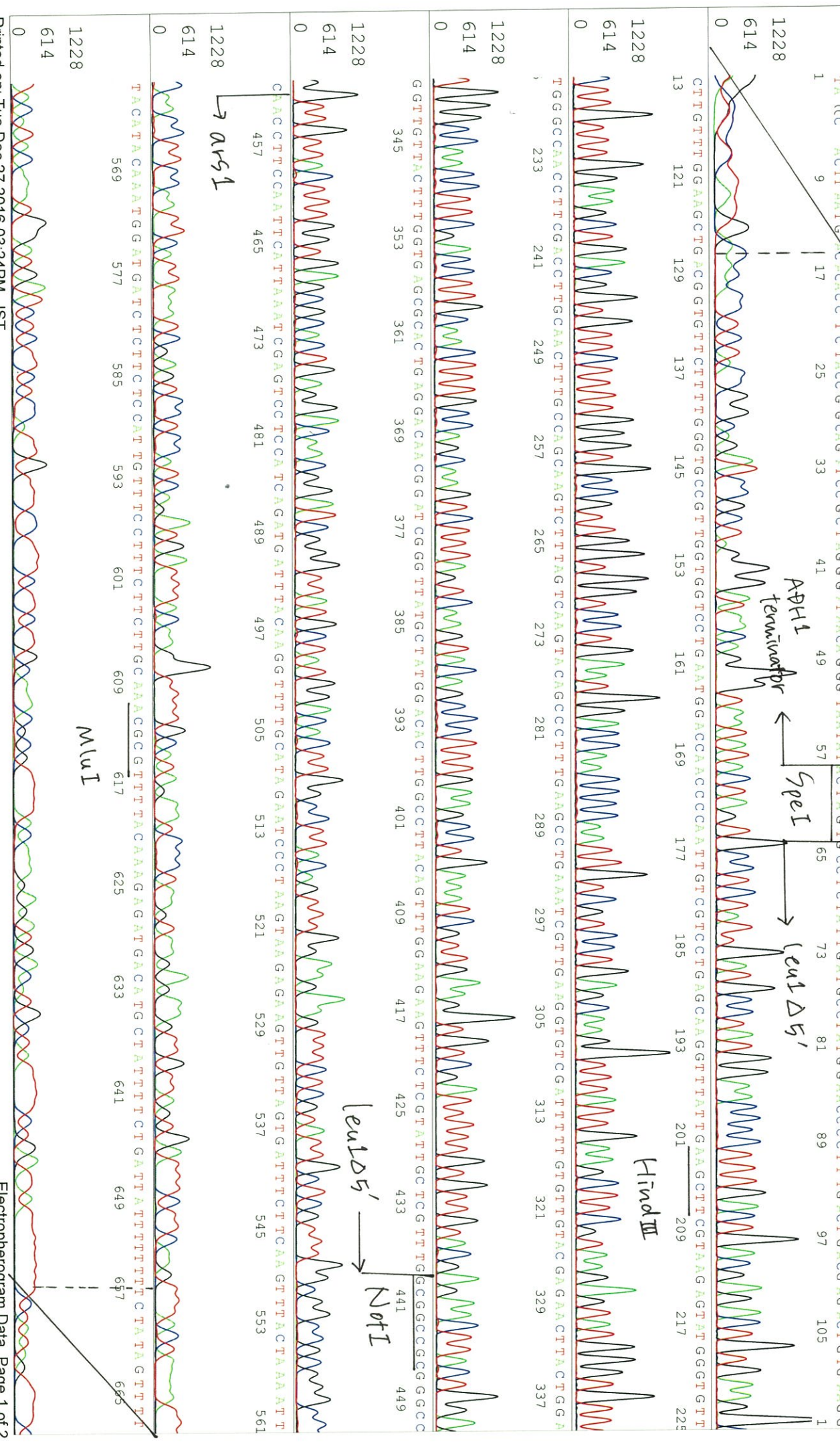
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S/N:G:239 A:410 T:272 C:266

KB.bcp primer name Φ : f1ori_R3

06197_14462_A6L7_f1ori_R3
KB_3500_POP7_BDTv3.mob

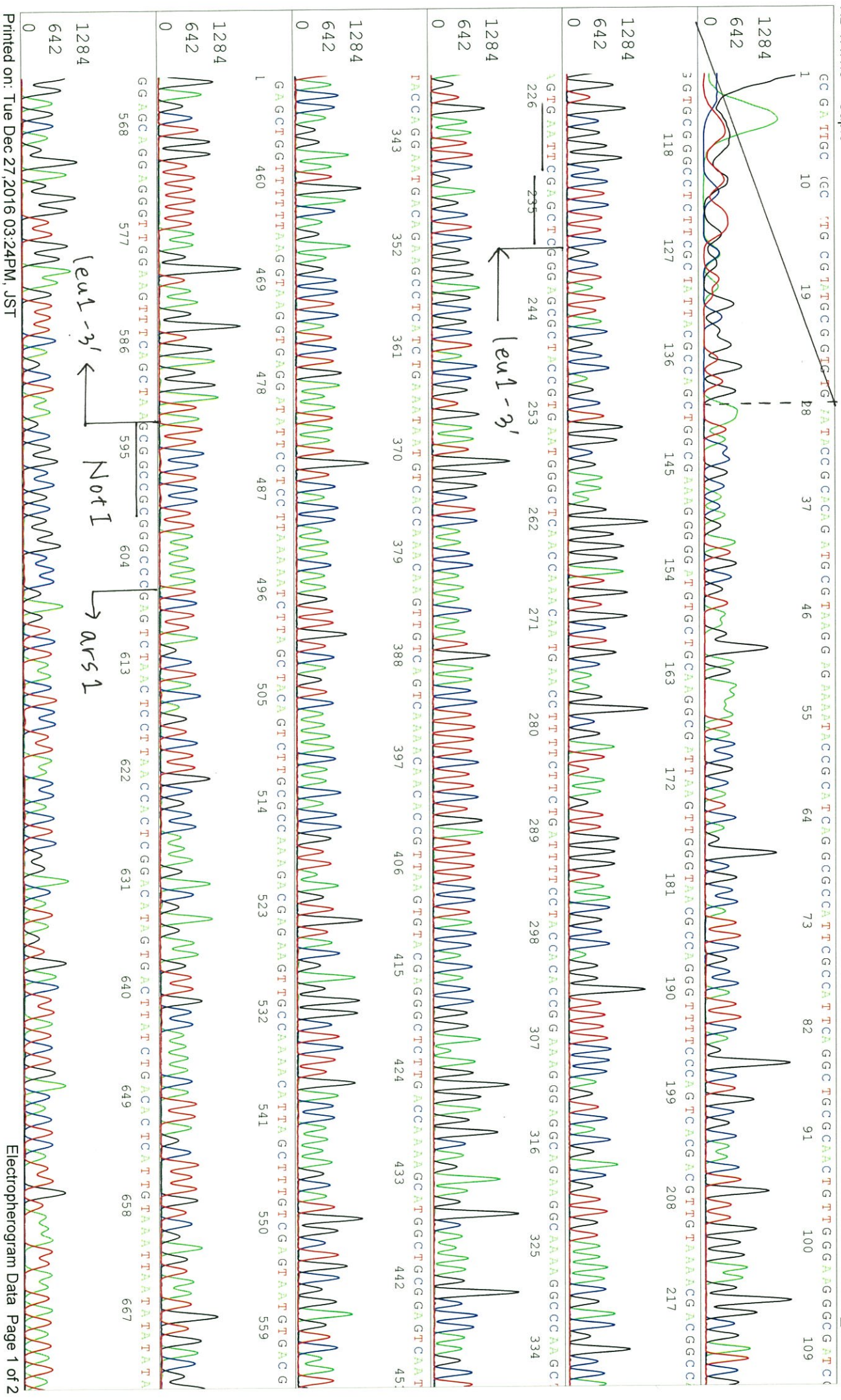
Dec 27,2016 09:33AM, JST

KB 1.4.1.8 Cap:6

5'- TTAATGCCCGCTACAGGGC -3'

Pis 1626 to 13349 Pk1 Loc: 1603
Version 6.0 HISQV Bases: 958

Dec 27,2016 10:00AM, JST
Spacing:1.97 Pts/Panel1350
Plate Name: 20161227_dhatabank



S/N G:239 A:410 T:272 C:266

06197_14462_A6L7_f1ori_R3

Dec 27,2016 09:33AM, JST

KB.bcp

KB_3500_POP7_BDTV3.mob

Dec 27,2016 10:00AM, JST

KB 1.4.1.8 Cap:6

Pts 1626 to 13349 PK1 Loc:1603

Spacing:11.97 Pts/Panel1350

TAGGCATTTTTGGTTTAAAGTTAAAGTAACTAATTAAGTAACTAAACGAAACCAATTATTATTAATCAGGAAGTTAAGTGAATGGTAGCACTGTCGTAATAATTGTGAA

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

TTTTTAAATGAAATAATTTTAAATACAAAGCCTTTCTAGACTAGGTATTAATCAATAAACATTATGAGCAAAAGGATAGAGGAAATTAACATTGCACTTCTTC

784 793 802 811 820 829 838 847 856 865 874

AAATTTATTTATTTGCCCTTTACTGAAAAATAAAATAAATGAGTACTAAATGAAATAAAAAAGCCCTCAGTACAAGAAAGATTGCAAAAATAATTG

883 892 901 910 919 928 937 946 955 964

CATTCCTTCAATGAAATTAAGTTAAAGTTGCATATACGCAATATTGAAAAATTAAGTAACTTAACCTTAAATCAAGCAGTTTAGCGAAAATT

973 982 991 1000 1009 1018 1027 1036 1045

AA TTAAG A TTAATAATTCGGCAAGACATGTGTGACAGTCAATTTCAATTTAAATAAACAAGTATGTAAGTAA GC

1054 1063 1072 1081 1090 1099

T T T T T T T A C

1108



S/N G:239 A:444 T:389 C:358

KB.bcp

KB 1.4.1.8 Cap:9

primer name E : Reverse2

5'-GCGGATAACAATTTCACACAGG-3'

KB_3500_POP7_BDTv3.mob
Pis 1704 to 13355 Pk1 Loc:1681
Version 6.0 HISQV Bases: 888

