

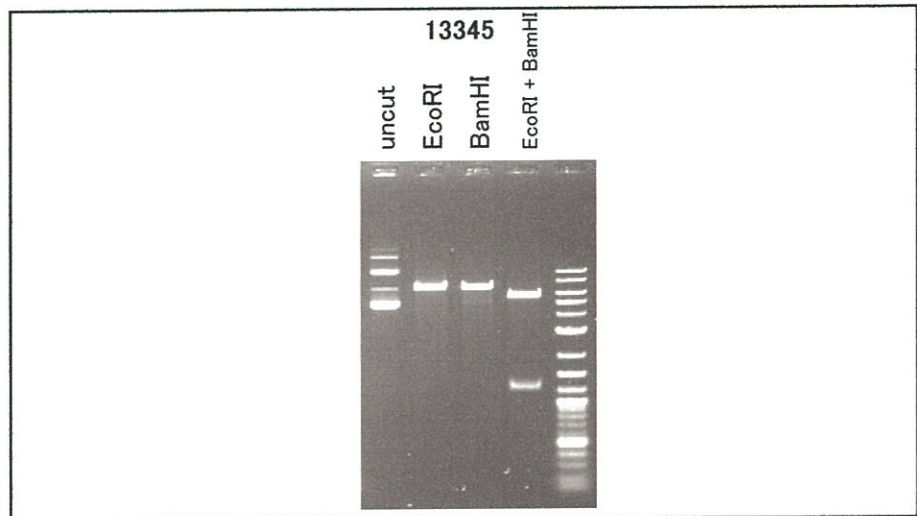
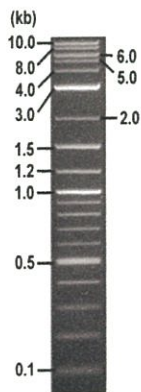


RIKEN DNA BANK

clone name : pCNL-N1_LAMP1

- Clone ID : RDB _ 13345
- Lot : 13345 _ A5E8
- 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

2-Log 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
<u>EcoRI</u>	<u>6.8</u> kbp
<u>BamHI</u>	<u>6.8</u> kbp
<u>EcoRI + BamHI</u>	<u>5.6, 1.2</u> kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	CMV-Forward	Sequence - E	SV40pro_F_V2
Sequence - B	YFP_R	Sequence - F	-
Sequence - C	EGFP-C_rev	Sequence - G	-
Sequence - D	ME-1290Rv	Sequence - H	-

APPROVED BY :

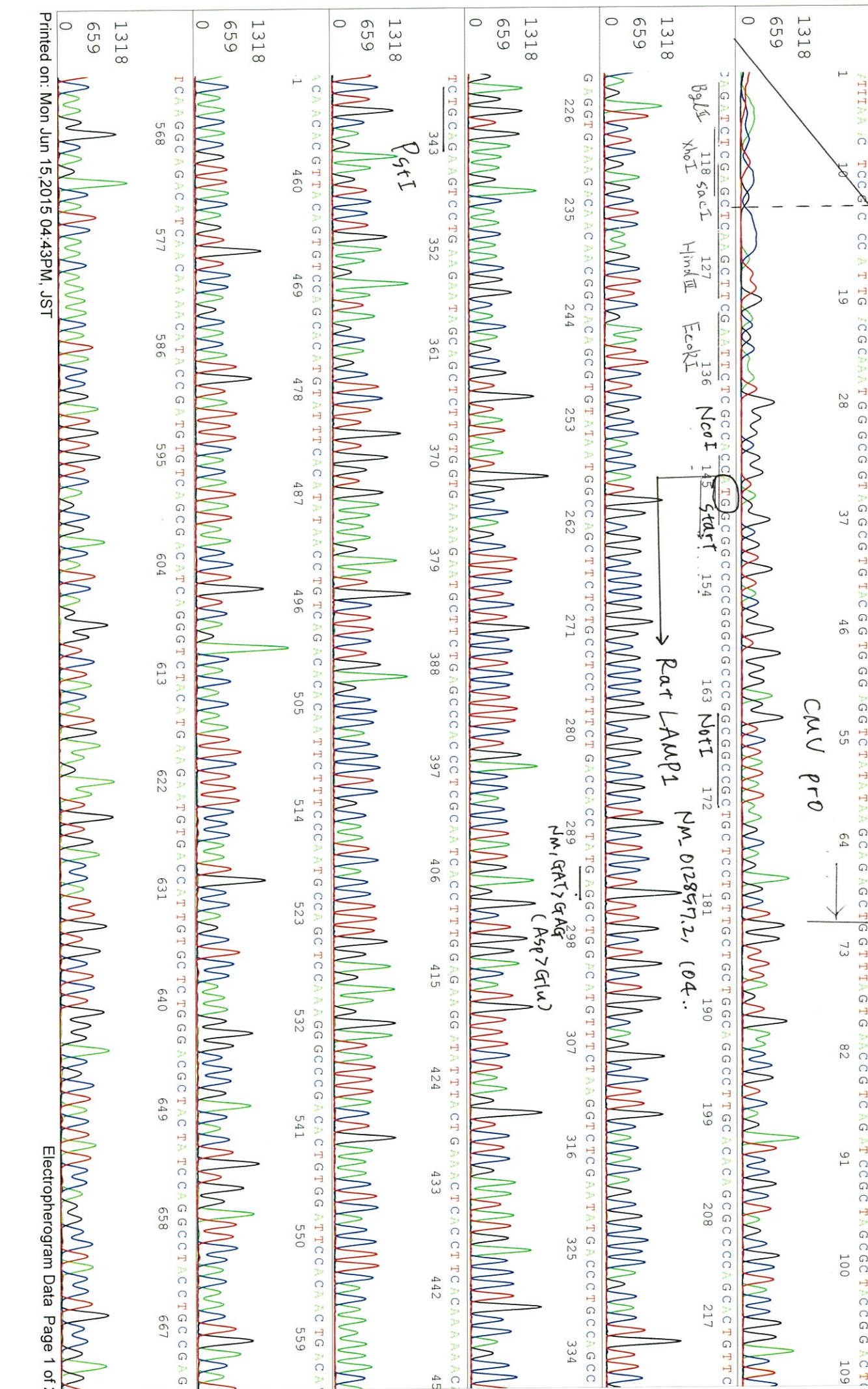


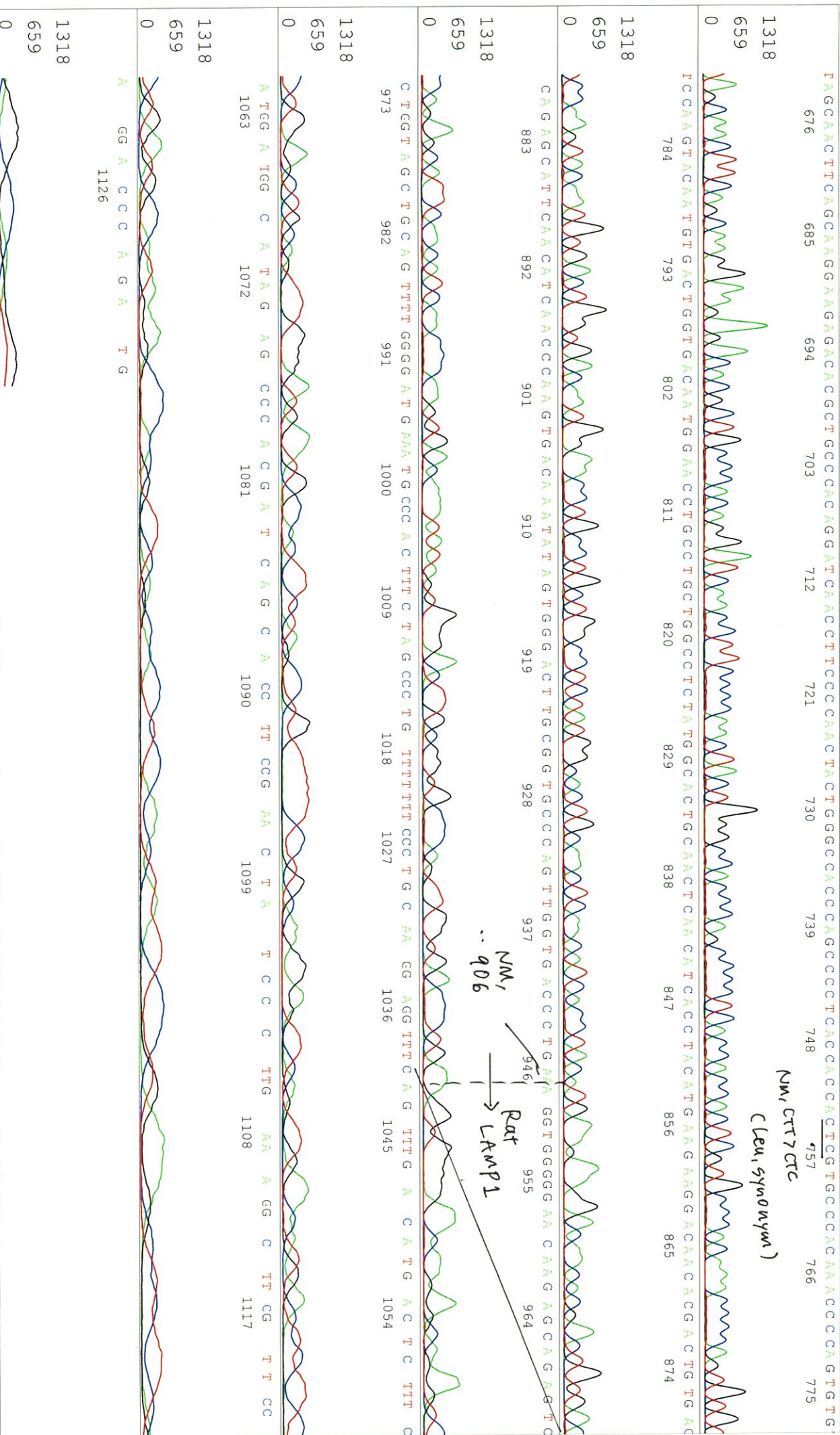
CMV pro

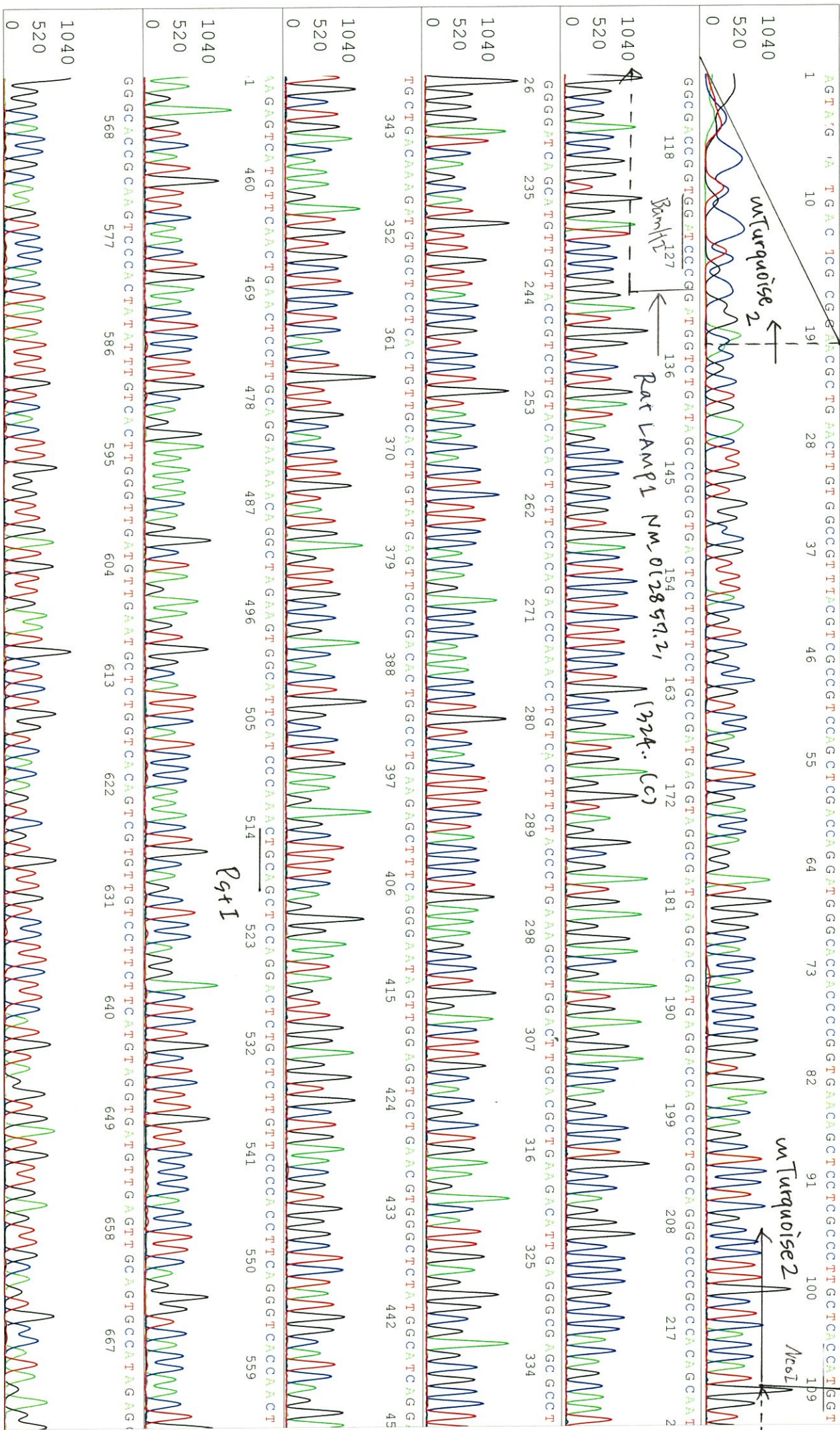
Pat LAMP1

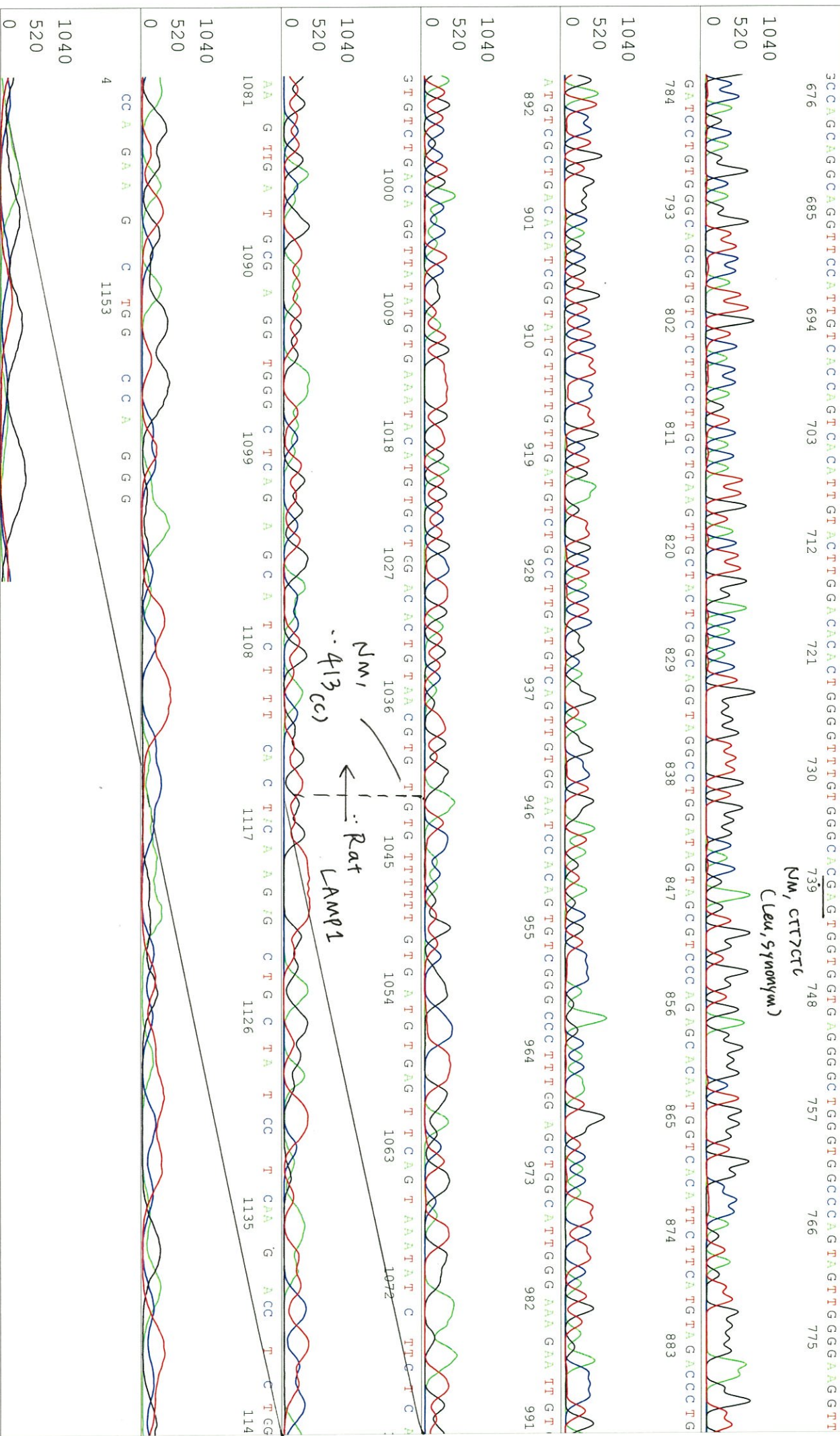
NM_012857.2, (04..)

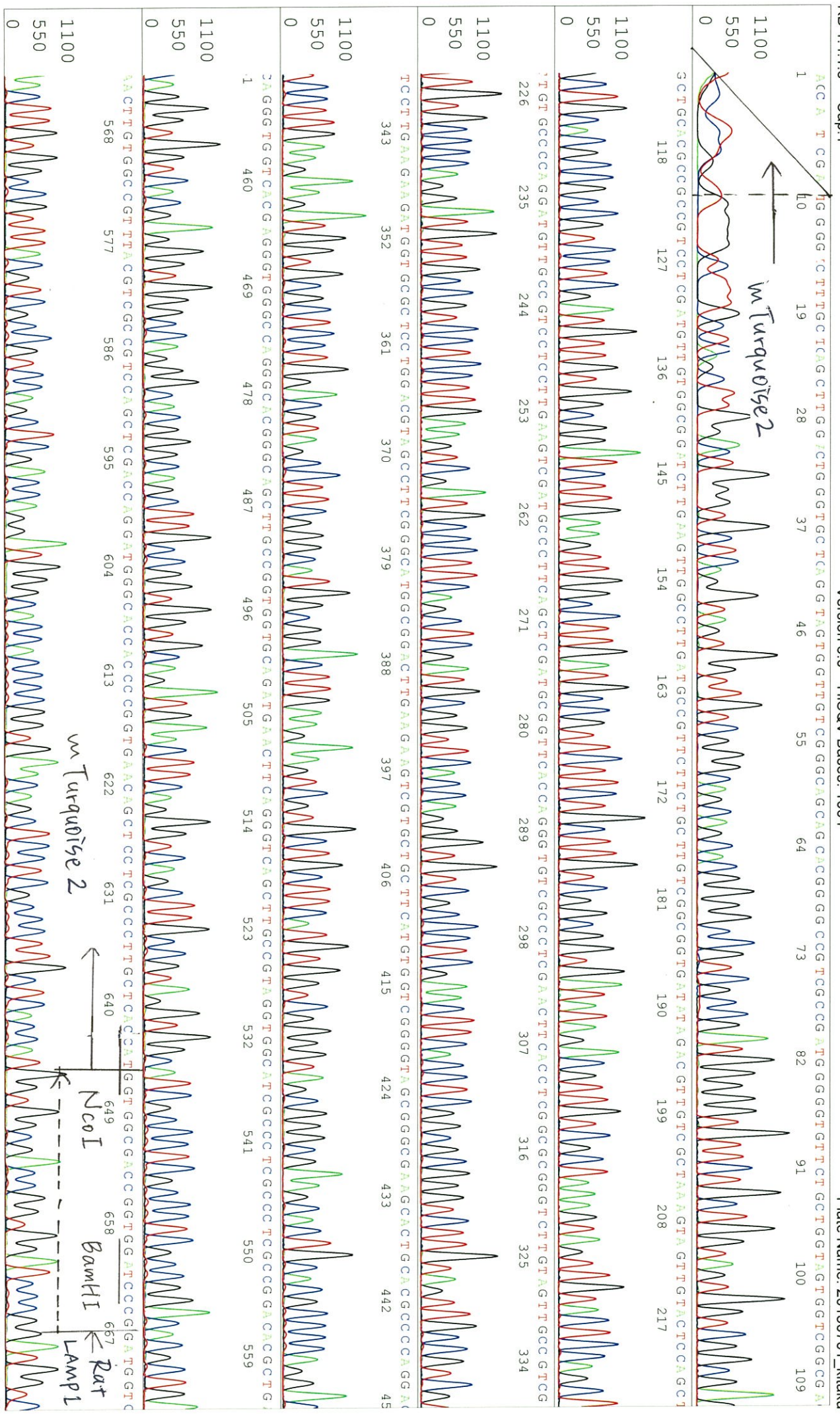
NM_012857.2, (04..)











SN G:750 A:495 T:539 C:767

KB.bcp

KB 1.4.1.8 Cap:1

13345_13345_A5E8_1_EGFP_C_rev_A01_01

13345_13345_A5E8_1_EGFP_C_rev

KB_3500_POP7_BDTV3.mob

Pls 1364 to 13287 PK1 Loc:1341

Version 6.0 HISQV Bases: 1004

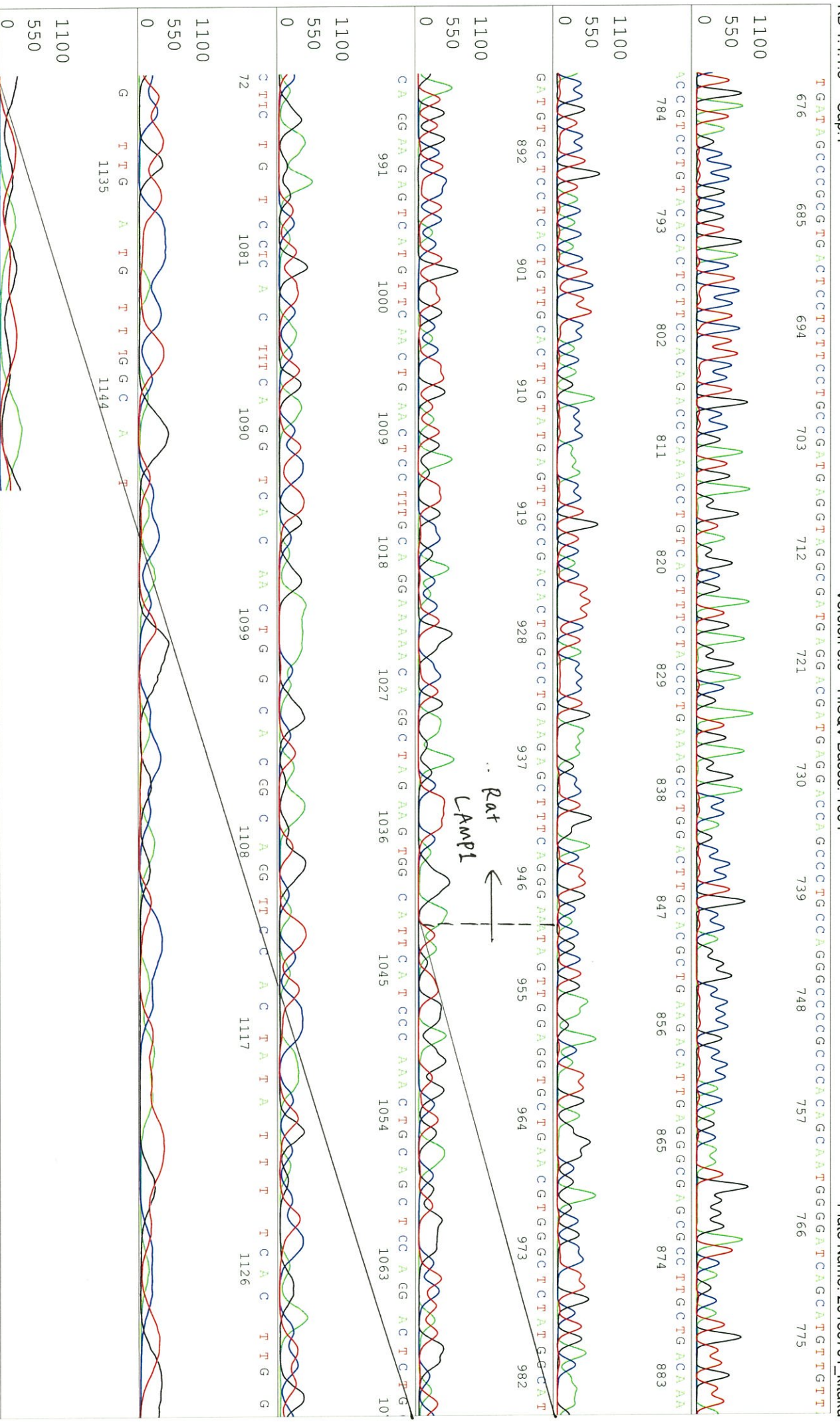
Inst Model/Name 3500/3500 Instrument

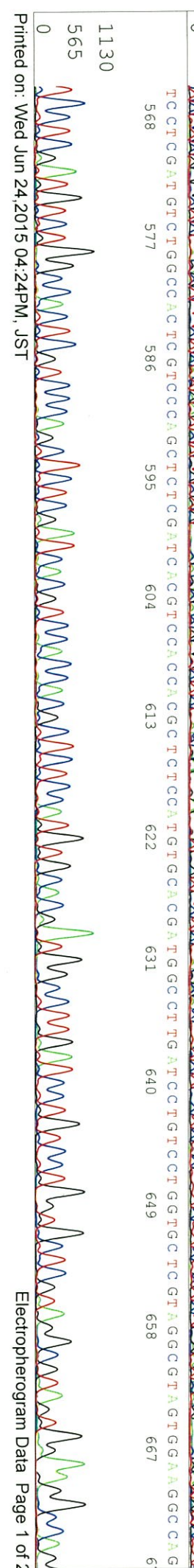
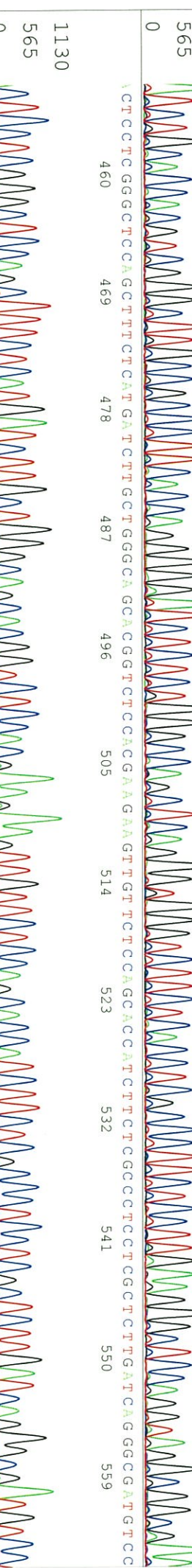
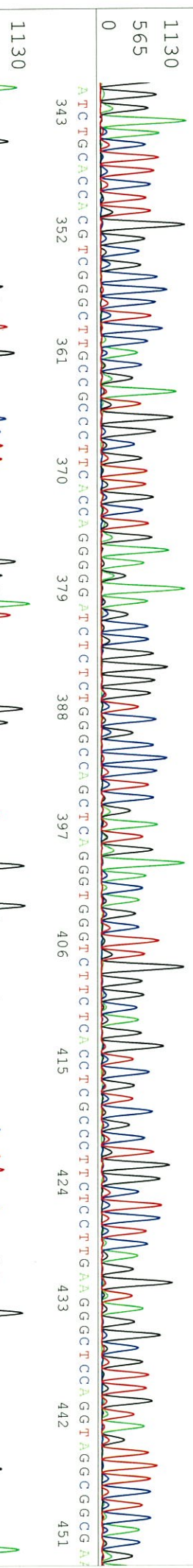
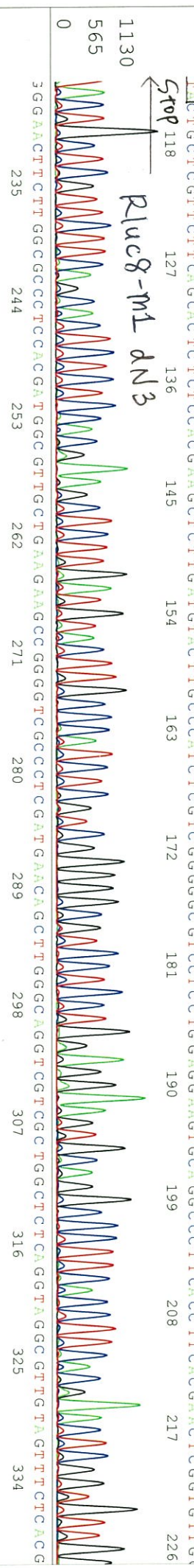
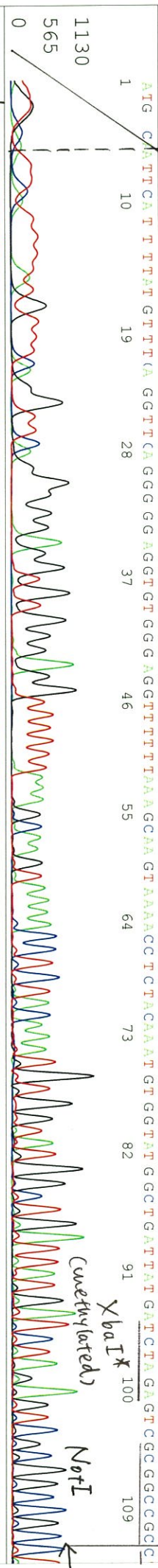
Jul 01 2015 02:04PM, JST

Jul 01 2015 02:39PM, JST

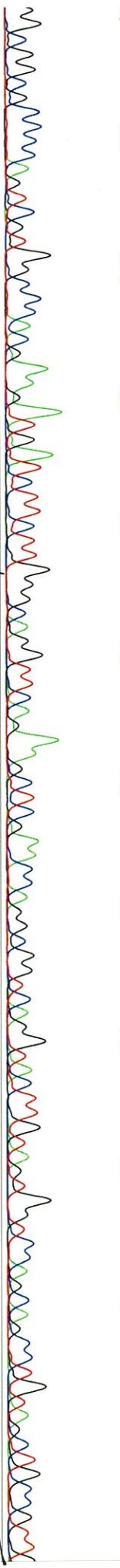
Spacing: 11.82 Pts/Panel1350

Plate Name: 20150701_kitaku





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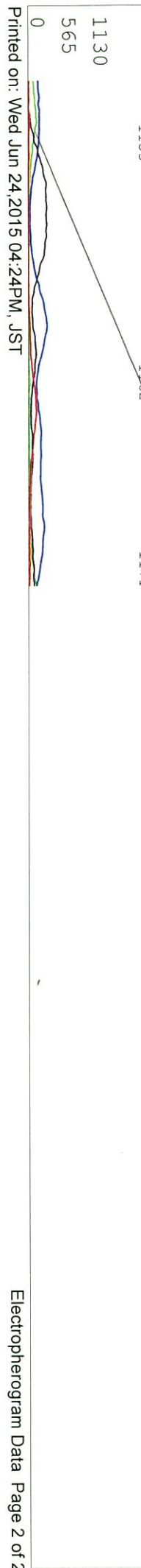
← P1ac8-w1 dn3

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TGGGGGCGCGGTGATCAATCCATCCCTTTCTCTGCTCCGGGGTCCGTACACC TTTCG TACCCCGGCGGCCTCAGCACTCAGCAAGACATGTAAGAA

TCGCGCTTCCTCG TEGGGTCTTTTGCTCAGCTGAC TGTGCTCAA GATAGTGA TGTCTGGG CCAAGCCAGC

CCACGGGG CCCGATCCG CCGCA



SN G:158 A:156 T:150 C:215 primer name **E** : SV40pro_F_V2

KB.bcp KB_3500_POP7_BDTV3.mob

Nov 17,2017 01:58PM, JST

KB 1.4.1.8 Cap:18 5'-TCGGCCTCGAGCTATTC-3'

Pls 1379 to 12743 PK1 Loc:1356

Nov 17,2017 02:32PM, JST

Version 6.0 HiSeqV Bases: 980



