

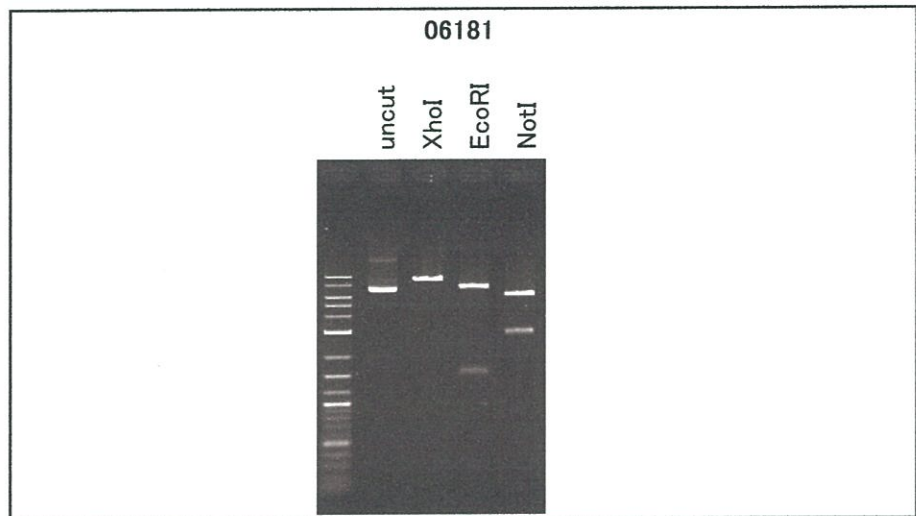
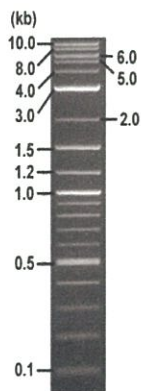


RIKEN DNA BANK

clone name : pDUAL-HFF81

- Clone ID : RDB _ 06181
- Lot : 14483 _ 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>XhoI</u>	<u>9.2</u> kbp
<u>EcoRI</u>	<u>7.6, 1.6</u> kbp
<u>NotI</u>	<u>6.3, 2.9</u> kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	nmt1Fw	Sequence - E	-
Sequence - B	LEU1pro_F	Sequence - F	-
Sequence - C	ars_R1	Sequence - G	-
Sequence - D	f1ori_R3	Sequence - H	-

APPROVED BY :



S/N G:48 A:73 T:86 C:67

06181_14483_A6L7_LEU1pro_F

Jan 06,2017 03:15PM, JST

KB.bcp

primer name **B** : LEU1pro_F

KB_3500_POP7_BDTV3.mob

Jan 06,2017 03:56PM, JST

KB 1.4.1.8 Cap:2

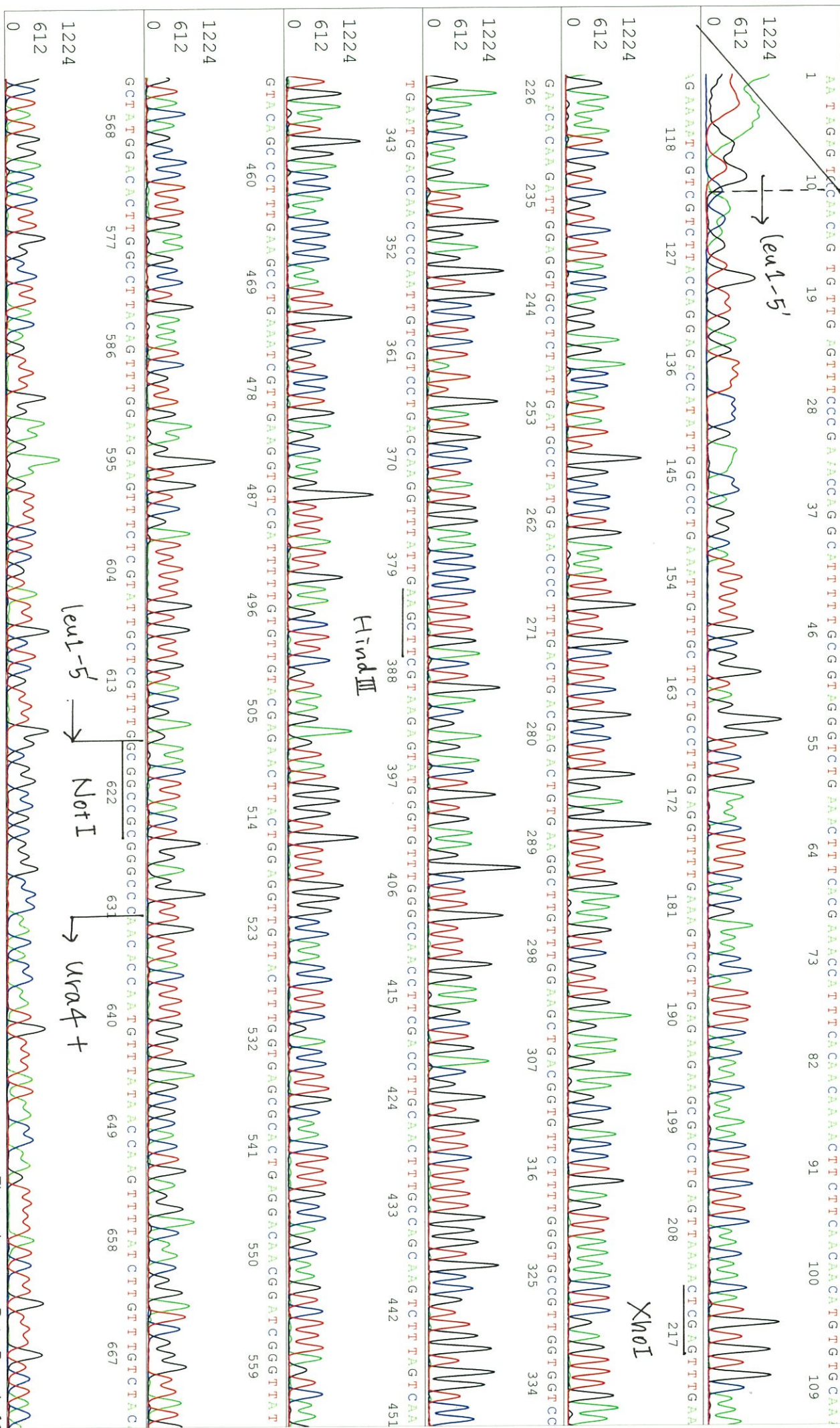
5'-ACGCAATATATCGATATCCC-3'

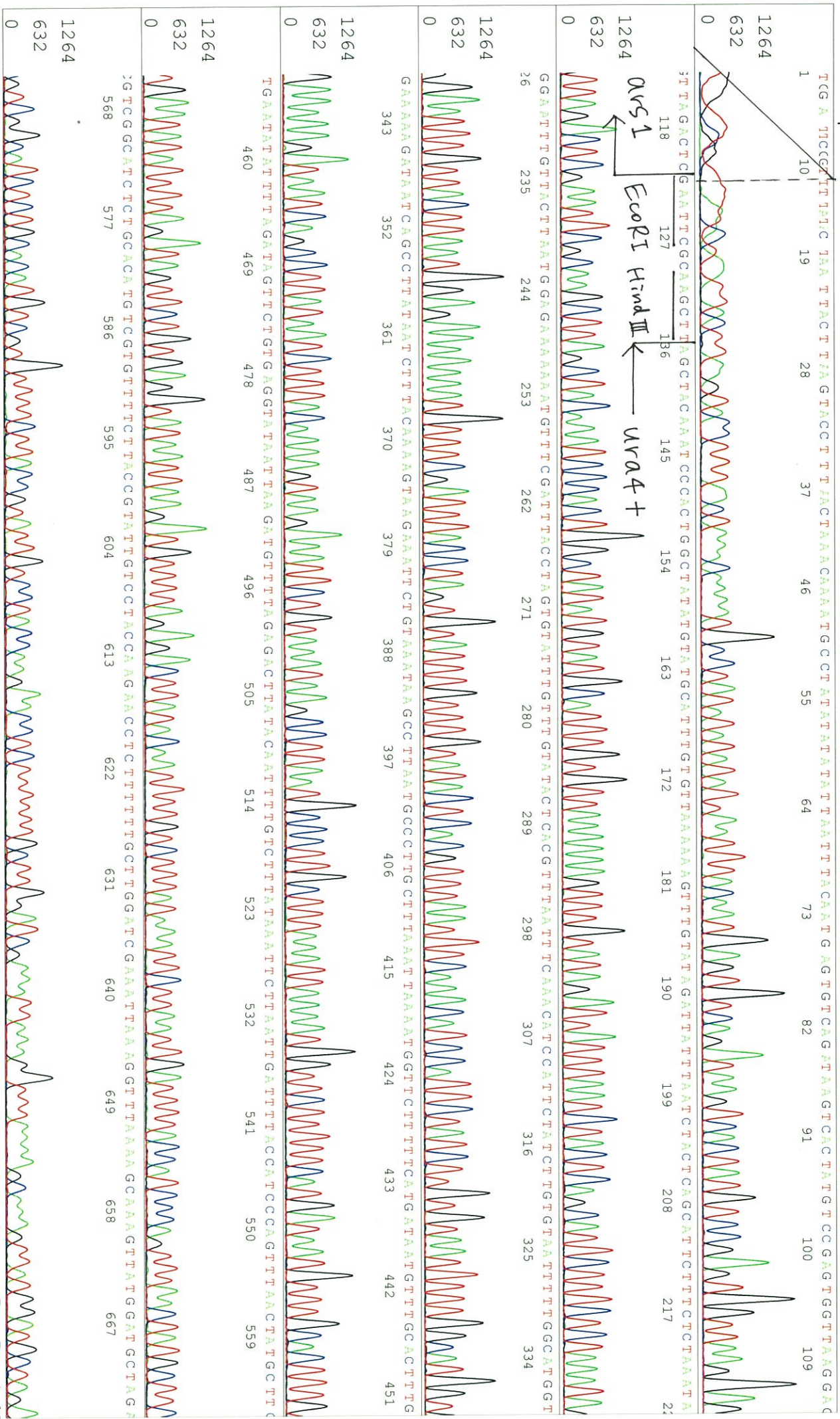
Pts 1645 to 13268 Pk1 Loc:1622

Spacing:12.05 Pts/Panel1350

Version 6.0 HISQV Bases: 921

Plate Name: 20170106_mix





GTATTTC A A A G C T T A T T C A G C T T A G A G C T G A G G G G A T G A A A A A T C C C A T T G C C A A G A A T T G T G G C T T G A T G A A G A P P A A G C A A A G C A A C T T G T C A G T C G C G G T

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CGATTTG ACCGA AGAAATCCGAAA TCTTAGAA TTGGTA GATAAAATTTGG ACCCTATG TCTGTG TTA TCAA GACACATATTGA CCGTTGTCGAGGATTTCCG

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ACCAEG ATATG GTA GAAAAA C TGG TGGG C C TTA EGTA AAAA GCA TCG TTTT C TTA T C TTTG A G ATCG C AAAATT C GCA G A C TTT GGG A A

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ATA CC G T C A A G C T A C A A T A T G C A T C T G G T G T T G T A C C A A A A A T T G C C T T C T T G G G C T C A T A T C A C A A T T T G C C A A T T A

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CAG TTG C A GG C G GA G GG TTA T A T A C A GG C TT C A A G G A A G T G G A T T T A C C

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TTT GGG G

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A G T A A G A G A A G T T G T T A G T G A T T T C T T C A A G T T T A C T A A A A T T T A C A T T A C A A A T G G A T G A T C T C T T C T C C A T T T G T T T C C T T T C T T T G C A A A C G C G T T T T C A A A A

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3 A G A T C A A C A T T G C T A T T T T T C T G A T T T T T T T T T T T C C T A T A G T T T T C T A T T T T T G T A C G C C T C T T G G G C A A G T C C C A A A T G T A A A A T C C G G G C T T A T G G G T T A T T T G C C G

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