

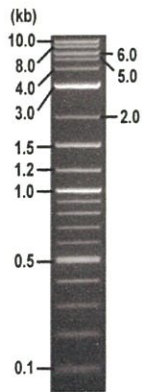


RIKEN DNA BANK

clone name : DQA10501 AMALA-4

- Clone ID : RDB _ 01239
- Lot : 15307 _ A7Gs
- 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>6.7</u> kbp
<u>BamHI</u>	<u>6.3, 0.4</u> kbp
_____	_____ kbp
_____	_____ kbp
_____	_____ kbp

● Confirmation of the insertion sequence

Sequence name	Primer name	Sequence name	Primer name
Sequence - A	pMAMneo-Forward	Sequence - E	-
Sequence - B	RDB01239#1	Sequence - F	-
Sequence - C	MMTV-LTR#1	Sequence - G	-
Sequence - D	-	Sequence - H	-



APPROVED BY :

S/N G:445 A:508 T:424 C:609

KB:bcpc primer name A : pMAMneo-Forward

KB_3500_POP7_BDTv3.mob

Aug 02,2017 10:58AM, JST

KB 1.4.1.8 Cap:11

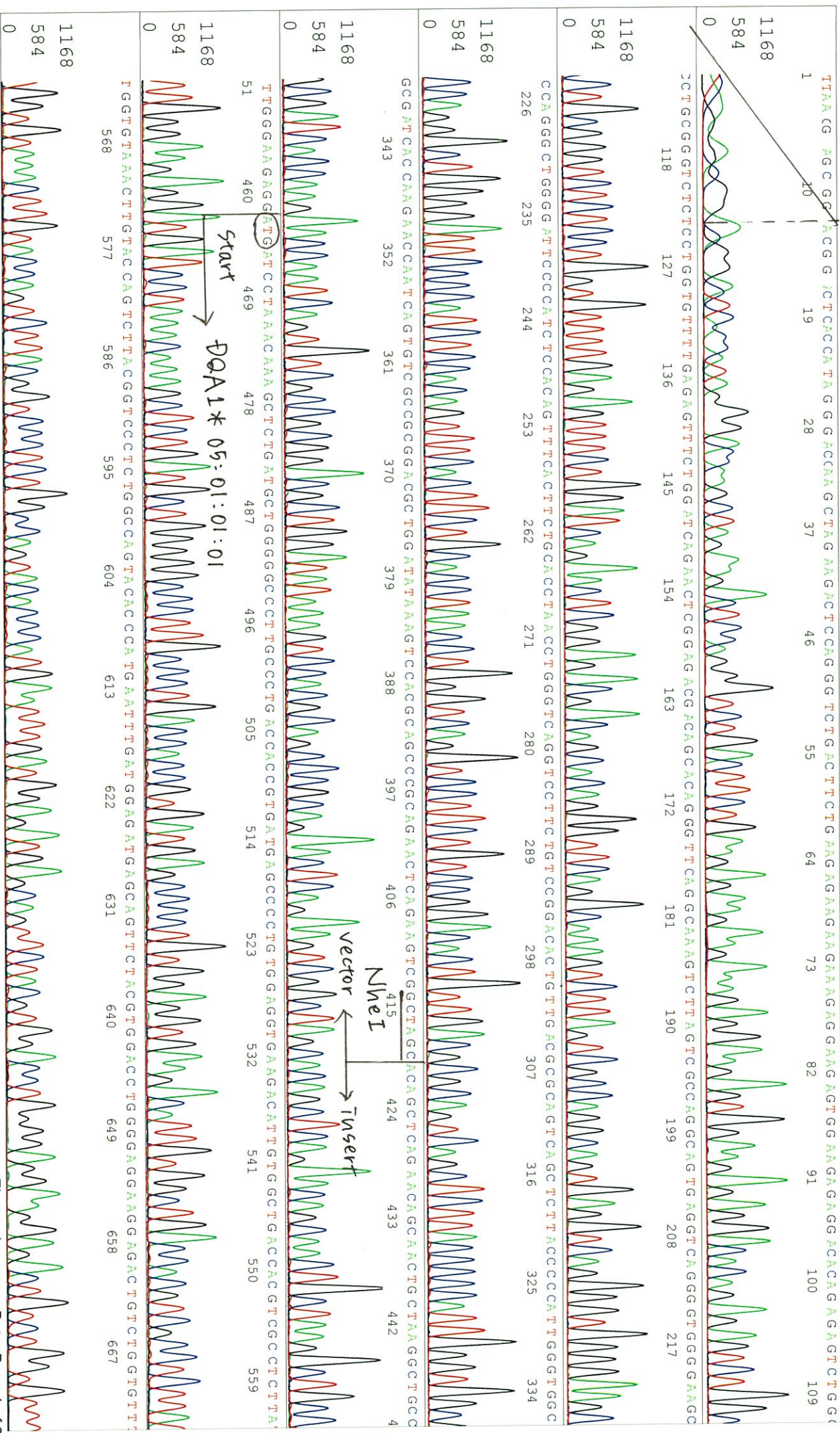
5-TCTTGATGTCTCTTCTTCTGTGG-3'

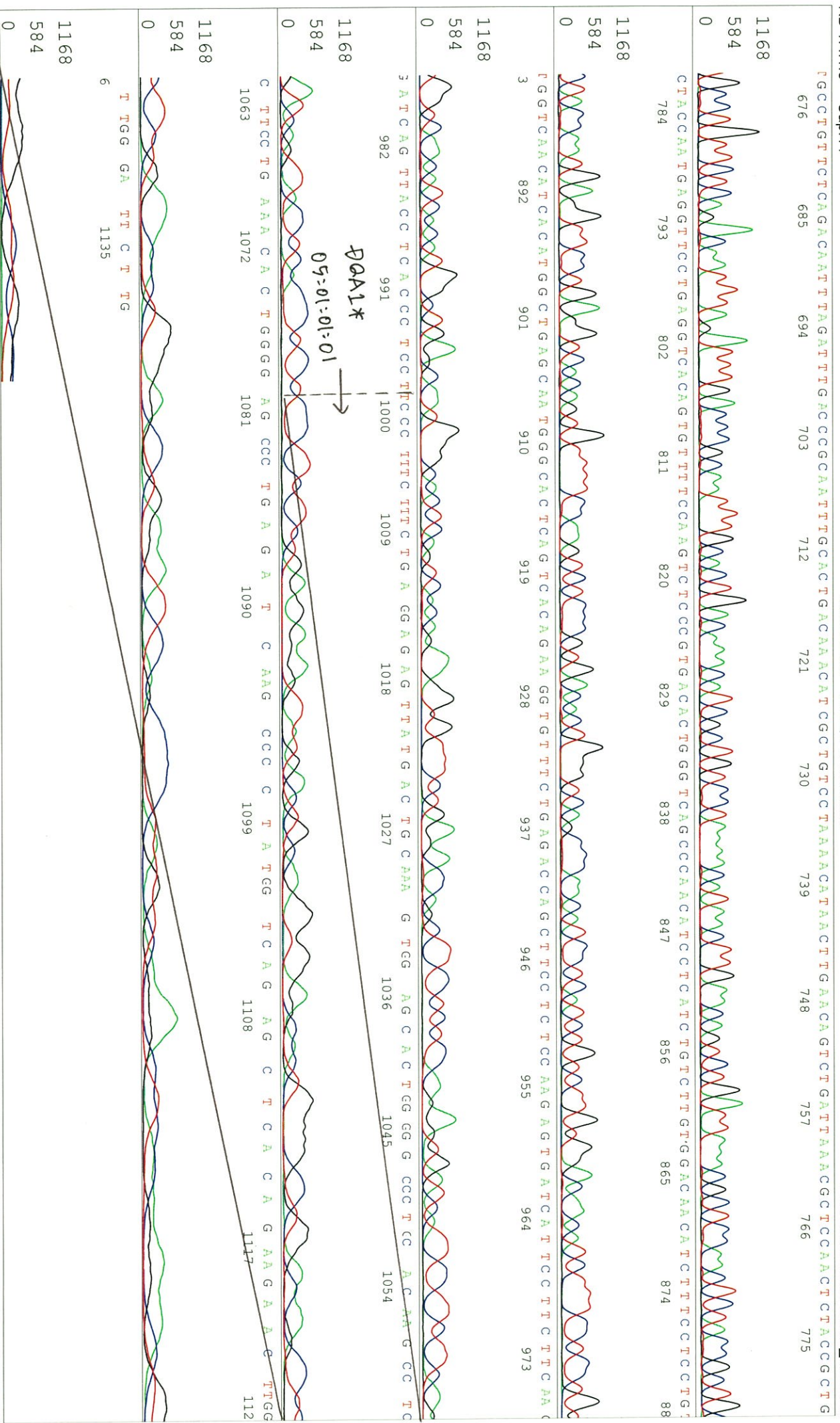
Pis 1558 to 13223 Pk1 Loc:1535

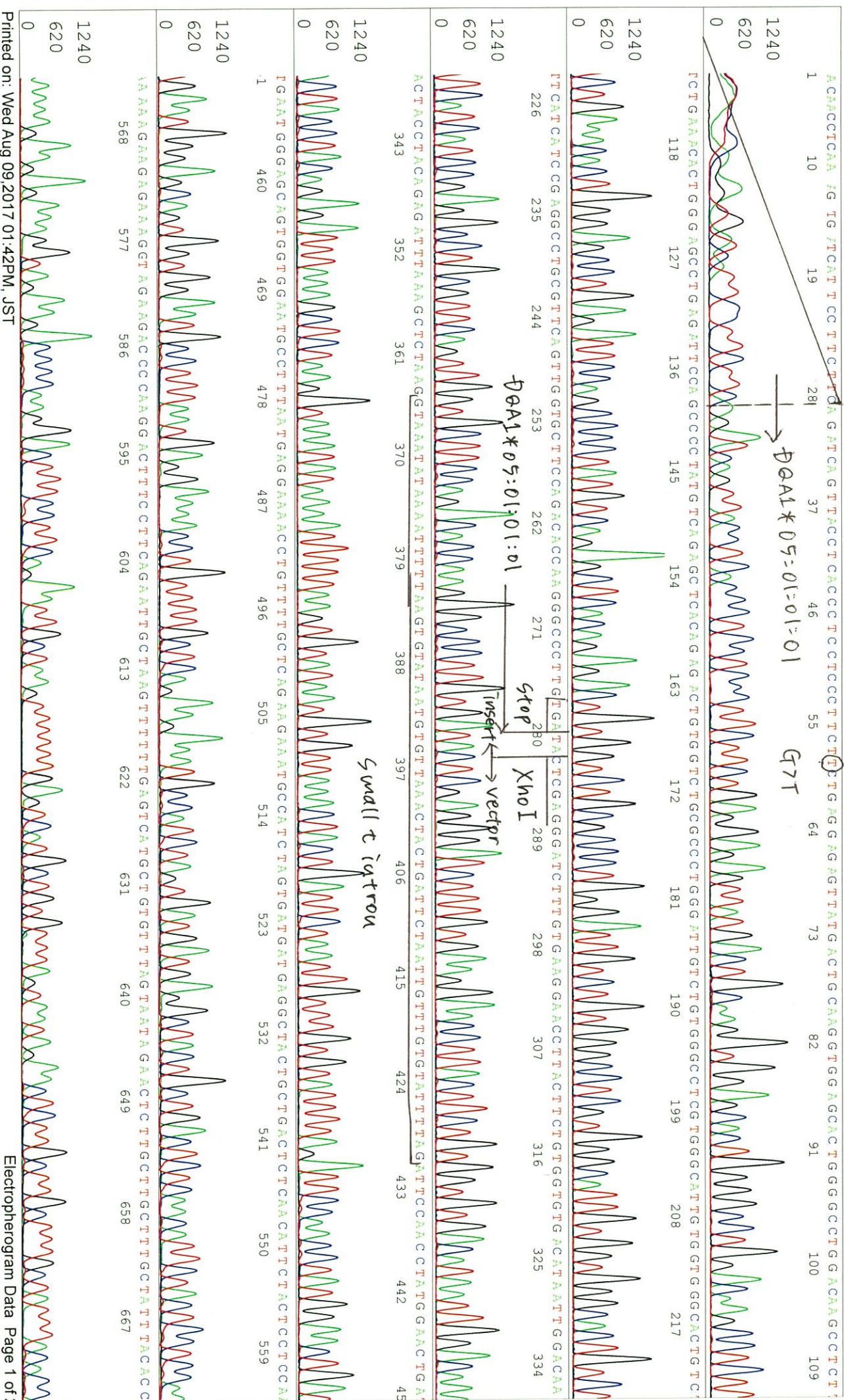
Spacing:1.18 Pts/Panel1350

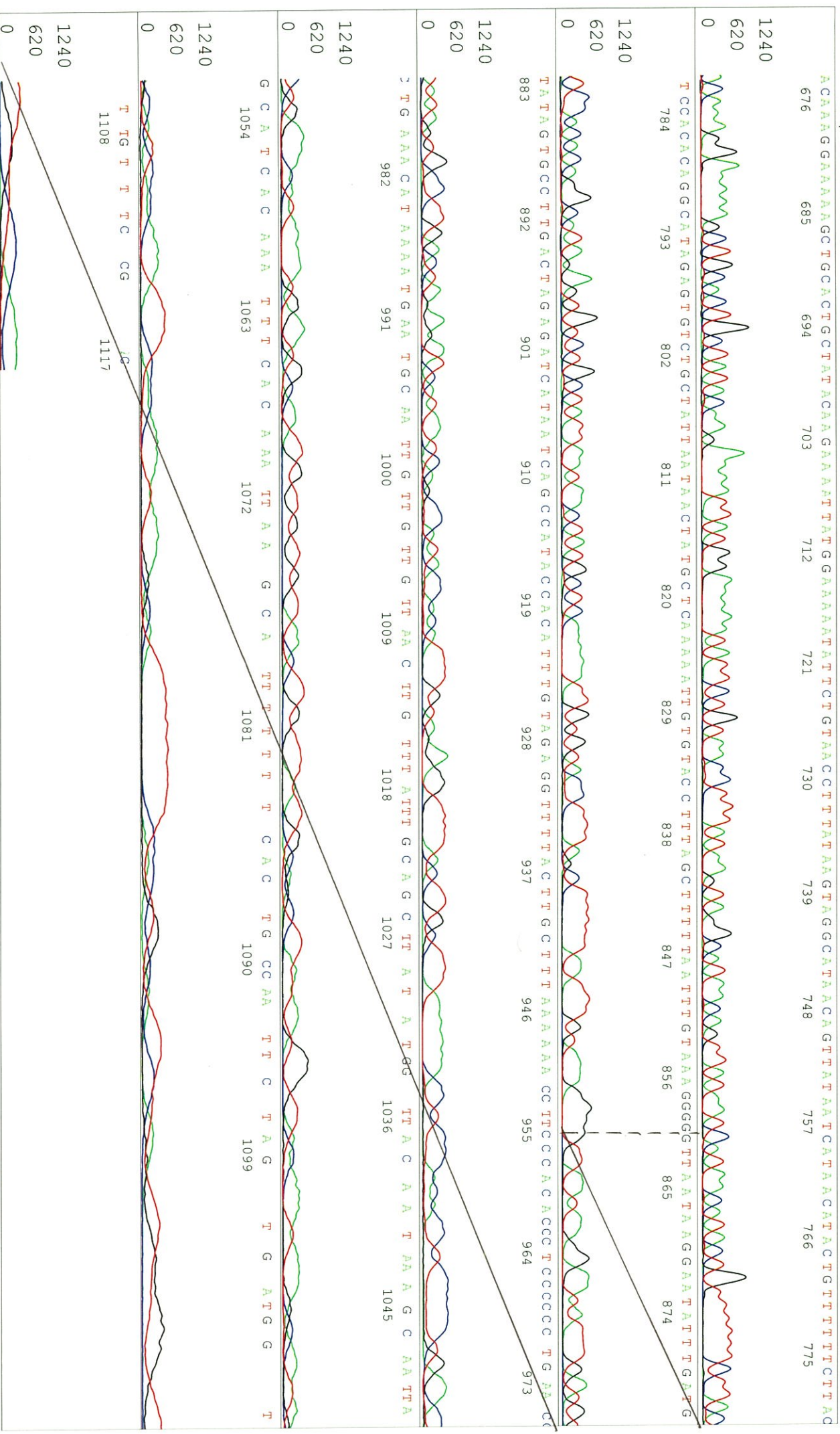
Version 6.0 HiSQV Bases: 990

Plate Name: 20170802_dnebank

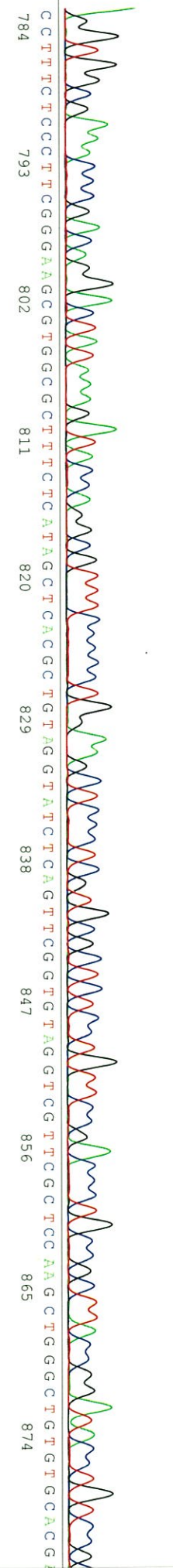








A G G T G G C C G A A A A C C C C G A C A G G A C T A T A A G A T A C C A G G C G T T C C C C C T G G A A G C T C C C T C G T G C C C T C C T G T T C C G A C C C T G C C G C T T A C C G G A T A C C T G T C C G



C C T T T C T C C C T T C G G G A A G C C G T G G C C T T C T C T A G C C T C A C G C T T C C G T G T A G G T A T C T C A G T T C C G T T C C G T C C A A G C T G G G C T G T G T G C A G
784 793 802 811 820 829 838 847 856 865 874

A A C C C C C C C G T T C A G C C C G A C C C G C T G C G C C T T A T C C G G T A A C T A T C G T C T G A G T C C A A C C C G G T A A G A C A C G A C T T A T C G C C A C T G G C A G
883 892 901 910 919 928 937 946 955 964

C A G C C A C T G G G T A A C A E G A T T A G C A G A G C G A G G G T A T G T A E G C G G T G C T A C A G A G T T T C T T T G A A G T G G C C T A A C
973 982 991 1000 1009 1018 1027 1036 1045

T A C C G G C T A C A C T A C A A G A A (A / G G T A T T T G G T A T C C T G C G C T C T G C C T G A A G G C C A A G G
1054 1063 1072 1081 1090 1099 1108

