

**RIKEN Clone ID : IRAL022B01**

Lot#: 7566\_B4C7

Vector : pOTB7

Gene	COL14A1	
Accession No.	BC014640.1	3479 bp
	<i>CDS</i>	2280 bp

● **Plasmid DNA purification**

Date : 2024/03/11

Culture : LB (25 ug/ml Chloramphenicol) 5 ml -> at 37 deg C over night

Date : 2024/03/12

Purification : QIAGEN Miniprep kit -> dH<sub>2</sub>O 100 ul

● **Digestion by restriction enzyme/Concentration calibration**

Date : 2024/03/12

DNA concentration (O.D.): 150 ng/ul

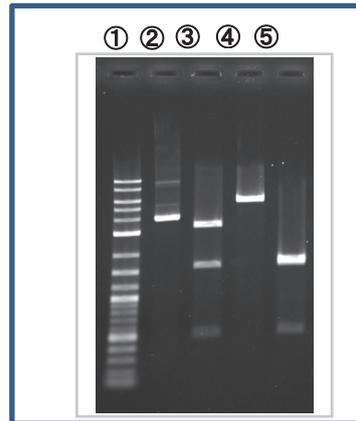
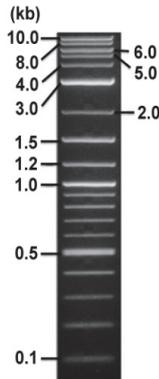
< Size of fragment expected from this clone >

DNA	0.7	ul
Enzyme (BamHI + BglII)	0.5 + 0.5	ul
Buffer H	1	ul
dH <sub>2</sub> O	7.3	ul
Total	10	ul

BamHI	3.2, 1.6, 0.5	kb
BglII	5.3	kb
BamHI + BglII	1.6kb (Vector)	1.6, 1.6, 0.5
		kb

Electrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)



- ①:Marker
- ②:uncut
- ③:BamHI
- ④:BglII
- ⑤:BamHI + BglII

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2024/03/22

DNA ( <u>150</u> ng/ul)	82	ul
10x TE	49	ul
dH <sub>2</sub> O	361	ul
Total	492	ul

● **Confirmation of the insertion sequence**

Date : 2024/03/21

Primer A	pOTB7_F
Primer B	pOTB7_R
Primer C	-
List of Sequencing Primers	<a href="http://dna.brc.riken.jp/en/GNPclone3en.html">http://dna.brc.riken.jp/en/GNPclone3en.html</a>

● **Shipping**

Conc. : 25 ng/ul, Volume : 40 ul

Conc. :      ng/ul, Volume :      ul

APPROVED BY :

<http://dna.brc.riken.jp/index.html>



**BLAST Results**

[Questions/comments](#)

**Blast 2 sequences**

Job title: gb|BC014640.1|

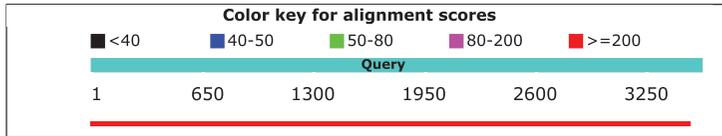
RID [Z7WAA71X114](#) (Expires on 03-16 14:57 pm)

**Query ID** [BC014640.1](#)  
**Description** Homo sapiens collagen, type XIV, alpha 1, mRNA (cDNA clone IMAGE:2960796), complete cds  
**Molecule type** nucleic acid  
**Query Length** 3479

**Subject ID** lcl|Query\_5004215  
**Description** IRAL022B01z.seq  
**Molecule type** dna  
**Subject Length** 3760  
**Program** BLASTN 2.15.0+

**Graphic Summary**

Distribution of the top 1 Blast Hits on 1 subject sequences



**Dot Matrix View**

**Descriptions**

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	6425	6425	100%	0.0	100.00%	Query_5004215

**Alignments**

Sequence ID: Query\_5004215 Length: 3760 Number of Matches: 1  
 Range 1: 141 to 3619

Score	Expect	Identities	Gaps	Strand	Frame
6425 bits(3479)	0.0()	3479/3479(100%)	0/3479(0%)	Plus/Plus	

Features:

```

Query 1      GACAGGCATGGTGA... 60
Sbjct 141    GACAGGCATGGTGA... 200
Query 61      AATGACCAGCTTGT... 120
Sbjct 201    AATGACCAGCTTGT... 260
Query 121     TATAGAATCCCTCC... 180
Sbjct 261    TATAGAATCCCTCC... 320
Query 181     GCATTGCTTCTATG... 240
Sbjct 321    GCATTGCTTCTATG... 380
Query 241     CCAGGAGATTGAAG... 300
Sbjct 381    CCAGGAGATTGAAG... 440
Query 301     ACCACCAACTTTTC... 360
Sbjct 441    ACCACCAACTTTTC... 500
Query 361     TGACCTGGTATTTA... 420
Sbjct 501    TGACCTGGTATTTA... 560
Query 421     TCATCAGCTTCTA... 480
Sbjct 561    TCATCAGCTTCTA... 620
Query 481     AAGTTGCAATGGT... 540
Sbjct 621    AAGTTGCAATGGT... 680
Query 541     AAACCAAGAGACT... 600
Sbjct 681    AAACCAAGAGACT... 740
Query 601     AAACAGGAAAAGCA... 660
Sbjct 741    AAACAGGAAAAGCA... 800
Query 661     GAAGGGGCATCCCA... 720
Sbjct 801    GAAGGGGCATCCCA... 860
Query 721     ACAAAACTCCAGGG... 780
Sbjct 861    ACAAAACTCCAGGG... 920
Query 781     ATGCAGATTACTCG... 840
Sbjct 921    ATGCAGATTACTCG... 980
Query 841     TTGTGGATGACTTT... 900
Sbjct 981    TTGTGGATGACTTT... 1040
Query 901     AAACAGCATCAGCA... 960
Sbjct 1041    AAACAGCATCAGCA... 1100
    
```

Query 961 AGATGATGGAATGTTGGTTGGTTGAAAAGATTTTTTCATCAGTGAAGGGTTTCTA 1020  
 Sbjct 1101 AGATGATGGAATGTTGGTTGGTTGAAAAGATTTTTTCATCAGTGAAGGGTTTCTA 1160  
 Query 1021 TGGAGCCTGGTACCTTCAATGTGTTCCATGTTACCAACTCCATAAAGATGCCCTGGTT 1080  
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 Query 1081 CCCAGCCAACCAAGTACTTGCACCCAGAAGGATGCCCTCGACTACACAATCAGTTTC 1140  
 Sbjct 1221 CCCAGCCAACCAAGTACTTGCACCCAGAAGGATGCCCTCGACTACACAATCAGTTTC 1280  
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 Query 1201 AAAATTCGACCAATGGTTGGGGTATTTTAGACAATGGTGGGAAAACCTAACATAAT 1260  
 Sbjct 1341 AAAATTCGACCAATGGTTGGGGTATTTTAGACAATGGTGGGAAAACCTAACATAAT 1400  
 Query 1261 TCAACTATGACCAAGTGGGGATTTCAAACCTCTACTTCGAAGGACCTGAAATAGGA 1320  
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 Sbjct 1461 AAATTTTTATGAAAGCTTTCACAAGTACACATGTTGTGAGTGAAGCTTTGGTCAAAG 1520  
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 Sbjct 1521 TGGTATTGACTGCAAGCAAGTGGGTGAGAAGCAATGAACGCATCAGCTAATACAGT 1580  
 Query 1441 CAGATGGTGTAGAAGTGTAGGAAAAATGGTTCGATCAAGAGGACCAAGTGGAACTCTG 1500  
 Sbjct 1581 CAGATGGTGTAGAAGTGTAGGAAAAATGGTTCGATCAAGAGGACCAAGTGGAACTCTG 1640  
 Query 1501 CACCGTCCAGTACAGATGTTGATATGTTTGTCCACATCATGGGCAATACAGACA 1560  
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 Sbjct 1821 GACTCCGAGGACCAAGGGCCAGCAAGTGAACCGGTCCAAAGGGACAGATGGCCCTC 1880  
 Query 1741 GGGGTGAAATGGTCTGCCAGGACCTCAGGGTCCACCTGGACCTCAAGGACCAAGTGGT 1800  
 Sbjct 1881 GGGGTGAAATGGTCTGCCAGGACCTCAGGGTCCACCTGGACCTCAAGGACCAAGTGGT 1940  
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 Sbjct 1941 TGTCCATTCAAGGAATGCCCGAATGCCAGGAGAAAAAGGAGAGAAAGGAGATACTGGCC 2000  
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 Query 1921 GCCAGAGGGGCTTCCGGGAAAGGATGGATCCTCGGGACCTCCAGGACCAAGGGCCAA 1980  
 Sbjct 2061 GCCAGAGGGGCTTCCGGGAAAGGATGGATCCTCGGGACCTCCAGGACCAAGGGCCAA 2120  
 Query 1981 TAGGCATTCTGGCACCCCTGGAGTCCAGGGATCACAGGAAGCATGGGACCGAAGGCG 2040  
 Sbjct 2121 TAGGCATTCTGGCACCCCTGGAGTCCAGGGATCACAGGAAGCATGGGACCGAAGGCG 2180  
 Query 2041 CCTGGGACCACTGGTGTCCCTGGAGCAAGGGGGAACGAGGAGAGCGGGGTGACCTGC 2100  
 Sbjct 2181 CCTGGGACCACTGGTGTCCCTGGAGCAAGGGGGAACGAGGAGAGCGGGGTGACCTGC 2240  
 Query 2101 AGTCTCAAGCCATGGTGAAGTCAAGTGGCGGTCAAGTATGCGAACAGCTCATCCAGAGTC 2160  
 Sbjct 2241 AGTCTCAAGCCATGGTGAAGTCAAGTGGCGGTCAAGTATGCGAACAGCTCATCCAGAGTC 2300  
 Query 2161 ACATGGCCAGGTACTGCCATCCTCAACAGATTCACAGCCACTCCTCATCCATCCGGA 2220  
 Sbjct 2301 ACATGGCCAGGTACTGCCATCCTCAACAGATTCACAGCCACTCCTCATCCATCCGGA 2360  
 Query 2221 CTGTCCAAGGGCTCCTGGGAGCCTGGGAGCCAGGCTCACCTGGAGCCCTGGTGAAC 2280  
 Sbjct 2361 CTGTCCAAGGGCTCCTGGGAGCCTGGGAGCCAGGCTCACCTGGAGCCCTGGTGAAC 2420  
 Query 2281 AAGGACCCCAAGGACACCAAGGCTTCCCAGGAAATGCAAGGCGTCCAGGACCCCAAGG 2340  
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 Query 2341 AACGAGGCTCAACTGGTATCAAAGGAGAAAAAGGAAATCCAGGCGTTGGAACCAAGGTC 2400  
 Sbjct 2481 AACGAGGCTCAACTGGTATCAAAGGAGAAAAAGGAAATCCAGGCGTTGGAACCAAGGTC 2540  
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 Query 2641 TGTGGGGCCTGGAGTCTGATAGCCTCAGGAGAAAATGGAAGACCAACTGCAAGAACTCT 2700  
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 Sbjct 2841 TAAGGAATCTGTTGAGAAAAATGTTGTTATGTTGTTGATGCTACTTTGGGGGGCAG 2900  
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 Query 3001 CAGATAATGTTGTTGAGGGAAAATGTCCTAGCAGGAAAAGAAATCAAGAGGTTCC 3060  
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 Query 3121 GGACAATTTGGGAAACTACCTCTGTTAATGATCTGTCCAACCTGAGATCACTTG 3180  
 Sbjct 3261 GGACAATTTGGGAAACTACCTCTGTTAATGATCTGTCCAACCTGAGATCACTTG 3320  
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 Sbjct 3321 GTAACCTGGTTTCAATGTTATCCAAAAATCAGCATTGGATTAAGCTTTCTGAATTTGGT 3380  
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 Query 3421 CTATTCCATTTCTTTGTAAGCAATAAAACTTAAAAAcaaaaaaaaaaaaaaaaaa 3479  
 Sbjct 3561 CTATTCCATTTCTTTGTAAGCAATAAAACTTAAAAAcaaaaaaaaaaaaaaaaaa 3619

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**BLAST Results**

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**Blast 2 sequences**

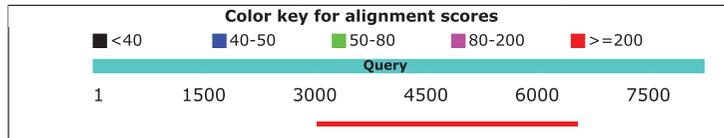
**Job title:** NM\_021110:Homo sapiens collagen type XIV alpha...

**RID** [YMVYFMHJ114](#) (Expires on 03-09 08:54 am)

<b>Query ID</b> <a href="#">NM_021110.4</a>	<b>Subject ID</b> <a href="#">BC014640.1</a>
<b>Description</b> Homo sapiens collagen type XIV alpha 1 chain (COL14A1), transcript variant 1, mRNA	<b>Description</b> Homo sapiens collagen, type XIV, alpha 1, mRNA (cDNA clone IMAGE:2960796), complete cds
<b>Molecule type</b> nucleic acid	<b>Molecule type</b> nucleic acid
<b>Query Length</b> 8009	<b>Subject Length</b> 3479
	<b>Program</b> BLASTN 2.15.0+

**Graphic Summary**

Distribution of the top 1 Blast Hits on 1 subject sequences



**Dot Matrix View**

**Descriptions**

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Homo sapiens collagen, type XIV, alpha 1, mRNA (cDNA clone IMAGE:2960796), complete cds	6372	6372	43%	0.0	99.88%	<a href="#">BC014640.1</a>

**Alignments**

Homo sapiens collagen, type XIV, alpha 1, mRNA (cDNA clone IMAGE:2960796), complete cds

Sequence ID: **BC014640.1** Length: 3479 Number of Matches: 1

Range 1: 1 to 3463

Score	Expect	Identities	Gaps	Strand	Frame
6372 bits(3450)	0.0()	3459/3463(99%)	1/3463(0%)	Plus/Plus	
<b>Features:</b>					
CDS:collagen alpha-1	912	T G M V K T L F L G V T N L Q A K H V E			
Query	3009	GACAGGCATGGTGA AACATTGTTCTTGGGTGTTACCAATCTCCAAGCCAAACATGTTGA			3068
Sbjct	1	GACAGGCATGGTGA AACATTGTTCTTGGGTGTTACCAATCTCCAAGCCAAACATGTTGA			60
CDS:collagen alpha-1	932	M T S L C A H W Q V H R H A T A Y R V V			
Query	3069	AATGACCAGCTTGTGTGCCACTGGCAGGTACATCGCCATGCCACAGCCTATAGGGTTGT			3128
Sbjct	61	AATGACCAGCTTGTGTGCCACTGGCAGGTACATCGCCATGCCACAGCCTATAGGGTTGT			120
CDS:collagen alpha-1	952	I E S L Q D R Q K Q E S T V G G G T T R			
Query	3129	TATAGAATCCCTCCAGGATAGCCAAAAGCAAGAAATCCACTGTGGGTGGAGGGACAACCCAG			3188
Sbjct	121	TATAGAATCCCTCCAGGATAGCCAAAAGCAAGAAATCCACTGTGGGTGGAGGGACAACCCAG			180
CDS:collagen alpha-1	972	H C F Y G L Q P D S E Y K I S V Y T K L			
Query	3189	GCATTGCTTCTATGGACTCAGCCTGATTCTGAATATAAAATCAGTGTTTATACAAAAGCT			3248
Sbjct	181	GCATTGCTTCTATGGACTCAGCCTGATTCTGAATATAAAATCAGTGTTTATACAAAAGCT			240
CDS:collagen alpha-1	992	Q E I E G P S V S I M E K T Q S L P T R			
Query	3249	CCAGGAGATTGAAGGACCTAGTGTGAGCATAATGGAAAAACACAATCACTTCCTACACG			3308
Sbjct	241	CCAGGAGATTGAAGGACCTAGTGTGAGCATAATGGAAAAACACAATCACTTCCTACACG			300
CDS:collagen alpha-1	1012	P P T F P P T I P P A K E V C K A A K A			
Query	3309	ACCACCAACTTTTCTCCAACCATCCACGACAAAAGAAGTATGTAAGGGGCCCAAGGC			3368
Sbjct	301	ACCACCAACTTTTCTCCAACCATCCACGACAAAAGAAGTATGTAAGGGGCCCAAGGC			360
CDS:collagen alpha-1	1032	D L V F M V D G S W S I G D E N F N K			
Query	3369	TGACCTGGTATTTATGGTGGATGGATCCTGGAGCATGGAGATG-AAAATTCGAATAAGA			3427
Sbjct	361	TGACCTGGTATTTATGGTGGATGGATCCTGGAGCATGGAGATGAAAATTCGAATAAGA			420
CDS:COL14A1 protein		I M D P G A L E M K N F N K			
CDS:collagen alpha-1	1051	I I S F L Y S T V G A L N K I G T D G T			
Query	3428	TCATCAGCTTCTATACAGCACTGTTGGAGCCCTGAACAAGATTGGCAGAGATGGAACCC			3487
Sbjct	421	TCATCAGCTTCTATACAGCACTGTTGGAGCCCTGAACAAGATTGGCAGAGATGGAACCC			480
CDS:COL14A1 protein	14	I I S F L Y S T V G A L N K I G T D G T			
CDS:collagen alpha-1	1071	Q V A M V Q F T D D P R T E F K L N A Y			
Query	3488	AAGTTGCAATGGTTCAGTTCACATGATGCCAAGACAGAAATTAACATAAATGCTTACA			3547
Sbjct	481	AAGTTGCAATGGTTCAGTTCACATGATGCCAAGACAGAAATTAACATAAATGCTTACA			540
CDS:COL14A1 protein	34	Q V A M V Q F T D D P R T E F K L N A Y			
CDS:collagen alpha-1	1091	K T K E T L L D A I K H I S Y K G G N T			
Query	3548	AAACCAAGAGACTCTTCTTATGCAATTAACACATTTCAACAAGGAGGAATAACAA			3607
Sbjct	541	AAACCAAGAGACTCTTCTTATGCAATTAACACATTTCAACAAGGAGGAATAACAA			600
CDS:COL14A1 protein	54	K T K E T L L D A I K H I S Y K G G N T			
CDS:collagen alpha-1	1111	K T G K A I K Y V R D I L F T A E S G T			
Query	3608	AAACAGAAAAGCAATTAAGTATGTTGAGATACCTTGTCTACTGCAAGTCAAGTACAA			3667
Sbjct	601	AAACAGAAAAGCAATTAAGTATGTTGAGATACCTTGTCTACTGCAAGTCAAGTACAA			660
CDS:COL14A1 protein	74	K T G K A I K Y V R D I L F T A E S G T			

CDS:collagen alpha-1 Query 1131 R R G I P K V I V V I T D G R S Q D D V 3728  
 3668 GAAGGGGCAATCCCAAGGTTATCGTGGTTAACTGATGGAAGATCACAAAGATGATGTA

Sbjct CDS:COL14A1 protein 661 GAAGGGGCAATCCCAAGGTTATCGTGGTTAACTGATGGAAGATCACAAAGATGATGTA 720  
 994 R R G I P K V I V V I T D G R S Q D D V

CDS:collagen alpha-1 Query 1151 N K I S R E M Q L D G Y S I F A I G V A 3787  
 3728 ACAAAAATCTCCAGGAGATGCAATAGATGGCTATAGCAATTTGCAATTTGGTGTGGCGG

Sbjct CDS:COL14A1 protein 114 N K I S R E M Q L D G Y S I F A I G V A 780  
 114 ACAAAAATCTCCAGGAGATGCAATAGATGGCTATAGCAATTTGCAATTTGGTGTGGCGG

CDS:collagen alpha-1 Query 1171 D A D Y S E L V S I G S K P S A R H V F 3847  
 3788 ATGCAGATTACTCGGAGTGGTTAGCATTGGCAGTAAGCCACGGCAGCCATGTCTCT

Sbjct CDS:COL14A1 protein 781 ATGCAGATTACTCGGAGTGGTTAGCATTGGCAGTAAGCCACGGCAGCCATGTCTCT 840  
 134 D A D Y S E L V S I G S K P S A R H V F

CDS:collagen alpha-1 Query 1191 F V D D F D A F K K I E D E L I T F V C 3907  
 3848 TTGTGGATGACTTTGACGCCCTTAAGAAAATCGAAGATGAGTAAATCTTTGTCTGCG

Sbjct CDS:COL14A1 protein 841 TTGTGGATGACTTTGACGCCCTTAAGAAAATCGAAGATGAGTAAATCTTTGTCTGCG 900  
 154 F V D D F D A F K K I E D E L I T F V C

CDS:collagen alpha-1 Query 1211 E T A S A T C P V V H K D G I D L A G F 3967  
 3908 AACACAGATCAGCAACCTGTCCAGTGGTACACAAGGATGGCATTGATCTGCAGGATTTA

Sbjct CDS:COL14A1 protein 901 AACACAGATCAGCAACCTGTCCAGTGGTACACAAGGATGGCATTGATCTGCAGGATTTA 960  
 174 E T A S A T C P V V H K D G I D L A G F

CDS:collagen alpha-1 Query 1231 K M M E M F G L V E K D F S S V E G V S 4027  
 3968 AGATGATGGAATGTTGGTTGGTTGAAAAGATTTTTATCAGTGGAGGGGTTCTA

Sbjct CDS:COL14A1 protein 961 AGATGATGGAATGTTGGTTGGTTGAAAAGATTTTTATCAGTGGAGGGGTTCTA 1020  
 194 K M M E M F G L V E K D F S S V E G V S

CDS:collagen alpha-1 Query 1251 M E P G T F N V F P C Y Q L H K D A L V 4087  
 4028 TGGAGCCTGGTACCTTCAATGTGTTCCATGTACCAACTCCATAAAGATGCCCTGGTT

Sbjct CDS:COL14A1 protein 1021 TGGAGCCTGGTACCTTCAATGTGTTCCATGTACCAACTCCATAAAGATGCCCTGGTT 1080  
 124 M E P G T F N V F P C Y Q L H K D A L V

CDS:collagen alpha-1 Query 1271 S Q P T R Y L H P E G L P S D Y T I S F 4147  
 4088 CCCAGCCCAACAGGACTGCACCCAGAAGGATGCCCTCCGACTACACAATCAGTTTC

Sbjct CDS:COL14A1 protein 1081 CCCAGCCCAACAGGACTGCACCCAGAAGGATGCCCTCCGACTACACAATCAGTTTC 1140  
 234 S Q P T R Y L H P E G L P S D Y T I S F

CDS:collagen alpha-1 Query 1291 L F R I L P D T P Q E P F A L W E I L N 4207  
 4148 TATTCGGATTCTTCTGACACTCCACAGGACCAATTTGCTCTTTGGGAGATTTAAATA

Sbjct CDS:COL14A1 protein 1141 TATTCGGATTCTTCTGACACTCCACAGGACCAATTTGCTCTTTGGGAGATTTAAATA 1200  
 254 L F R I L P D T P Q E P F A L W E I L N

CDS:collagen alpha-1 Query 1311 K N S D P L V G V I L D N G G K T L T Y 4267  
 4208 AAAATCTGACCCATTTGGTGGGGTATTTAGACAATGGTGGGAAAATCTAACATA

Sbjct CDS:COL14A1 protein 1201 AAAATCTGACCCATTTGGTGGGGTATTTAGACAATGGTGGGAAAATCTAACATA 1260  
 274 K N S D P L V G V I L D N G G K T L T Y

CDS:collagen alpha-1 Query 1331 F N Y D Q S G D F Q T V T F E G P E I R 4327  
 4268 TCAACTATGACCAAGTGGGATTTCAAACCTTACTTCGAAAGACCTGAAATAGGA

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[HHS Vulnerability Disclosure](#)

S/N G:201 A:340 T:219 C:268

Primer A: pOTB7-F

7566\_IRAL022B01\_B4C7\_2\_pOTB7\_F

KB\_3500\_POP7\_BDTv3.mob

Pts 1541 to 12907 Pk1 Loc:1518

Version 6.0 HiSQV Bases: 876

Gray line indicates quality value (QV) < 40.

Mar 12,2024 03:49PM, JST

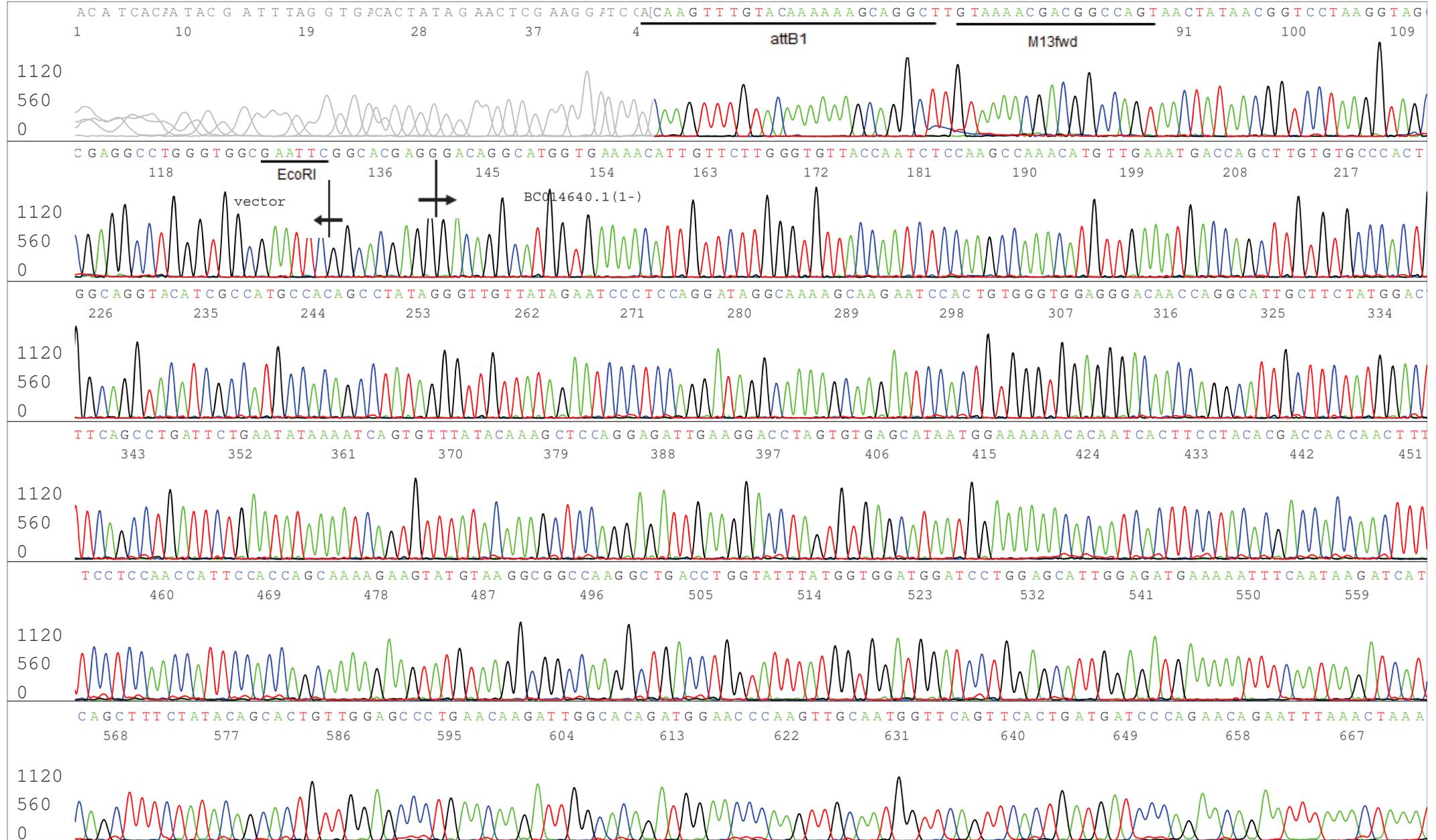
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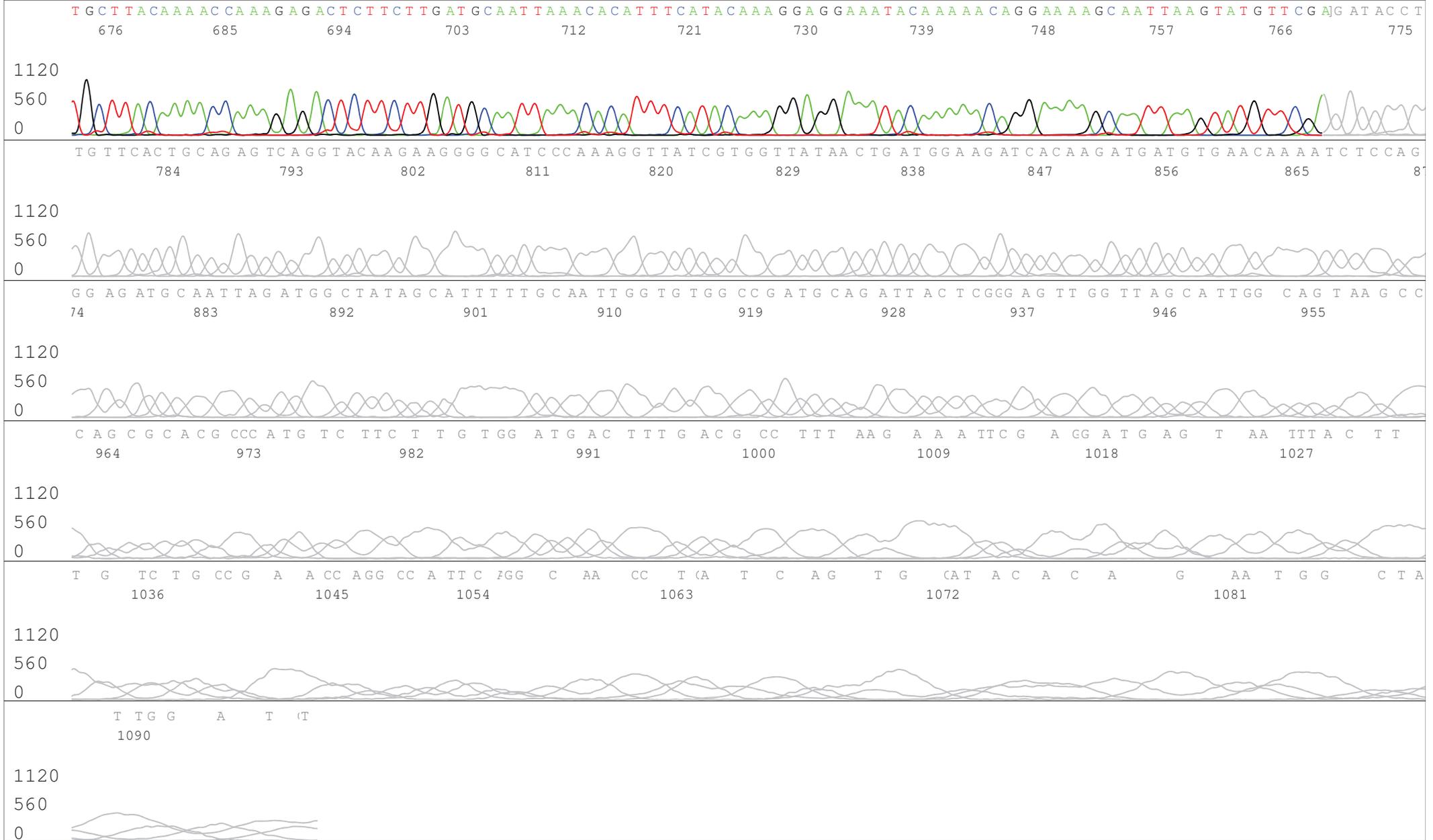
Plate Name: 20240312\_mix

KB 1.4.1.8 Cap:8

5' AACGCGGCTACAATTAATACATAACC 3'



S/N G:201 A:340 T:219 C:268  
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KB 1.4.1.8 Cap:8



S/N G:157 A:342 T:256 C:256  
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KB 1.4.1.8 Cap:11

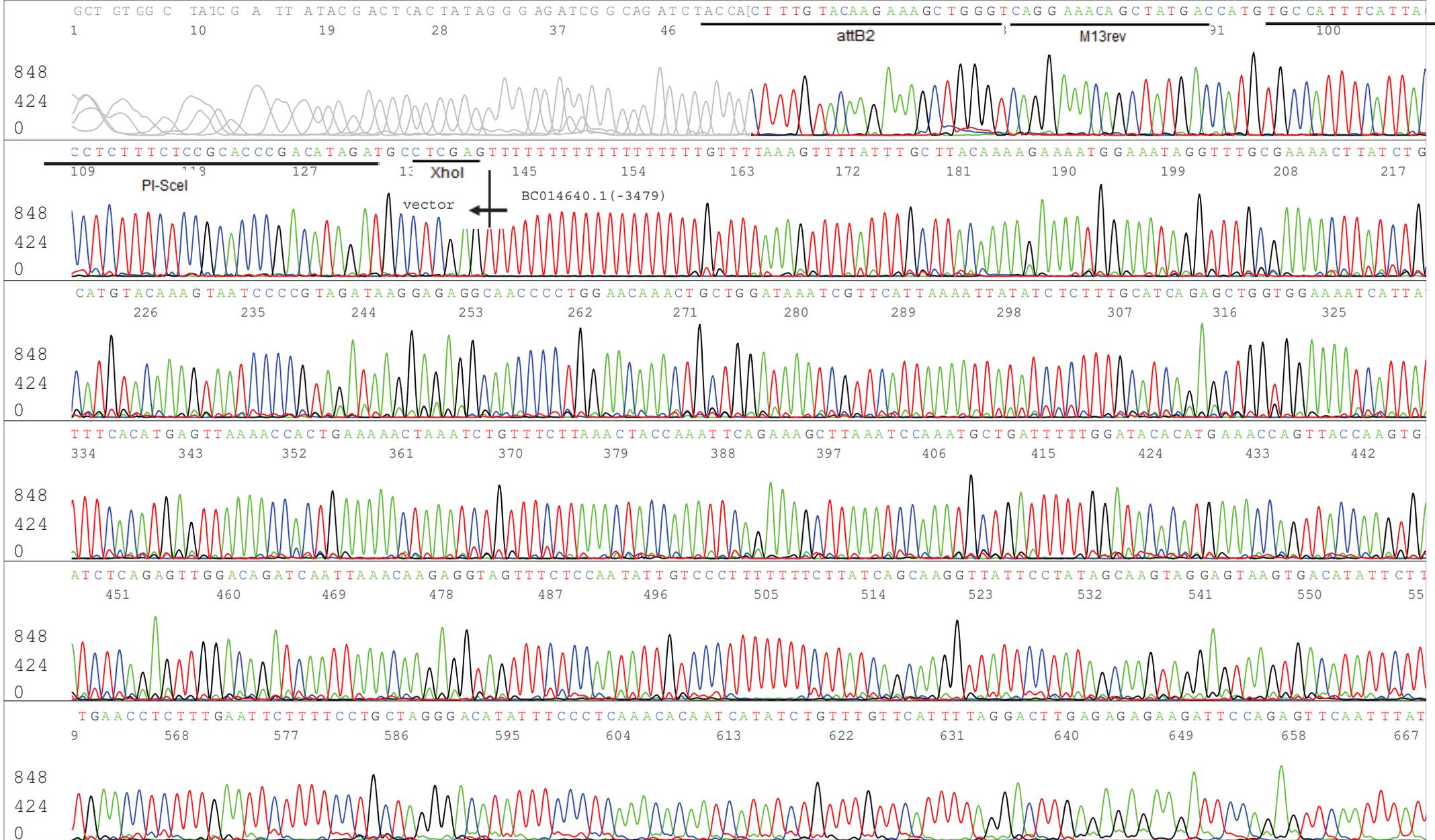
Primer B: pOTB7-R

5' GTACTGCAGCCGATTCATTAATGC 3'

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Version 6.0 HiSQV Bases: 860

Gray line indicates quality value  
(QV) < 40.

Mar 12,2024 03:49PM, JST  
Mar 12,2024 04:16PM, JST  
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Plate Name: 20240312\_mix



S/N G:157 A:342 T:256 C:256  
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KB 1.4.1.8 Cap:11

