

RIKEN Clone ID : IRAK013E09

Lot#: 7893_B31d

Vector : pCMV-SPORT6

Gene	KIF12	
Accession No.	BC010626.1	2024 bp
	<i>CDS</i>	1542 bp

● **Plasmid DNA purification**

Date : 2023/09/13

Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C over night

Date : 2023/09/14

Purification : QIAGEN Miniprep kit -> dH₂O 100 ul

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

Date : 2023/09/14

DNA concentration (O.D.): 407 ng/ul

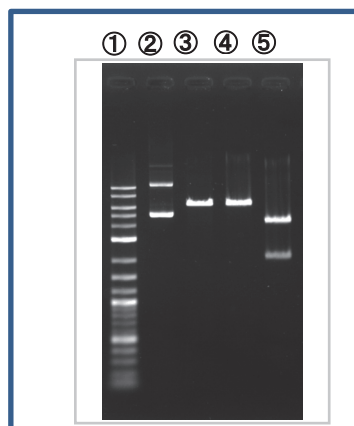
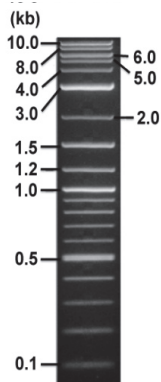
< Size of fragment expected from this clone >

DNA	0.25	ul
Enzyme (EcoRI + XhoI)	0.5 + 0.5	ul
Buffer H	1	ul
dH ₂ O	7.75	ul
Total	10	ul

EcoRI	6.4	kb
XhoI	6.4	kb
EcoRI + XhoI	4.3kb (Vector)	2.1 kb

Electrophoresis : 1% agarose gel, 1x TAE Buffer

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



①:Marker
②:uncut
③:EcoRI
④:XhoI
⑤:EcoRI + XhoI

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

Date : 2023/09/20

DNA (<u>407</u> ng/ul)	86	ul
10x TE	140	ul
dH ₂ O	1,174	ul
Total	1,400	ul

● **Confirmation of the insertion sequence**

Date : 2023/09/19

Primer A	Reverse2
Primer B	M13
Primer C	-
List of Sequencing Primers	http://dna.brc.riken.jp/en/GNPclone3en.html

● **Shipping**

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

Conc. : ng/ul, Volume : ul

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



BLAST Results

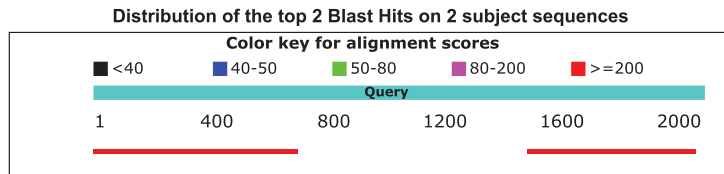
[Questions/comments](#)

Blast 2 sequences

Job title: BC010626:Homo sapiens kinesin family member...

RID G82HXVRH114 (Expires on 09-16 15:39 pm)	Subject ID 3 subjects
Query ID BC010626.1	Description See details
Description Homo sapiens kinesin family member 12, mRNA (cDNA clone MGC:17687 IMAGE:3865868), complete cds	Molecule type dna
	Subject Length 1372
Molecule type nucleic acid	Program BLASTN 2.14.1+
Query Length 2024	

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerA (Forward)	1262	1262	33%	0.0	100.00%	Query_62146
primerB (Reverse)	1042	1042	27%	0.0	100.00%	Query_62147

Alignments

primerA (Forward)
Sequence ID: Query_62146 Length: 745 Number of Matches: 1
Range 1: 63 to 745

Score	Expect	Identities	Gaps	Strand	Frame
1262 bits(683)	0.0()	683/683(100%)	0/683(0%)	Plus/Plus	
Features:					
Query	1	GG AAGACATCAGGATGTACCATCTGCCCTTCTGTGGACCCAGGGTACGTCCCATGAGC			60
Sbjct	63	GG AAGACATCAGGATGTACCATCTGCCCTTCTGTGGACCCAGGGTACGTCCCATGAGC			122
Query	61	GCGGCCGAGCTGCGTCGAGGGCAGCAGAGCGTGTGCACCTGCTCAGGGACCCGGACTCTG			120
Sbjct	123	GCGGCCGAGCTGCGTCGAGGGCAGCAGAGCGTGTGCACCTGCTCAGGGACCCGGACTCTG			182
Query	121	CAGTTTCTCCTGCACGTTTTTCACTTTGGCCAGACGGGCTCTGGGAAGACCTACACCT			180
Sbjct	183	CAGTTTCTCCTGCACGTTTTTCACTTTGGCCAGACGGGCTCTGGGAAGACCTACACCT			242
CDS:Kinesin family m	1	GA CTGGACCCCTCCCGAGGGGAGGGGGTGCCTGTACCCCAAGCCTGGCTGGCATCA			240
Query	181	GA CTGGACCCCTCCCGAGGGGAGGGGGTGCCTGTACCCCAAGCCTGGCTGGCATCA			302
Sbjct	243	GA CTGGACCCCTCCCGAGGGGAGGGGGTGCCTGTACCCCAAGCCTGGCTGGCATCA			362
CDS:Kinesin family m	2	Q R T F A W L L D R V Q H L G A P V T L			
Query	241	GCAGAGGACCTTCGCCTGGCTGTTGGACCGCGTGCAGCACCTGGGTGCCCTGTCAACCT			300
Sbjct	303	GCAGAGGACCTTCGCCTGGCTGTTGGACCGCGTGCAGCACCTGGGTGCCCTGTCAACCT			362
CDS:Kinesin family m	22	R A S Y L E I Y N E Q V R D L L S L G S			
Query	301	TCGGGCTCTTATCTGGAGATCTACAATGAGCAGGTCGGGACTTCTGAGGCTGGGGTC			360
Sbjct	363	TCGGGCTCTTATCTGGAGATCTACAATGAGCAGGTCGGGACTTCTGAGGCTGGGGTC			422
CDS:Kinesin family m	42	P R P L P V R W N K T R G F Y V E Q L R			
Query	361	TCGCCGGCCCTCCCTGTTCCGCTGGAAACAAGACTCGGGCTTCTATGTGGAGCAGCTGG			420
Sbjct	423	TCGCCGGCCCTCCCTGTTCCGCTGGAAACAAGACTCGGGCTTCTATGTGGAGCAGCTGG			482
CDS:Kinesin family m	62	V V E F G S L E A L M E A L L Q T G L S R			
Query	421	GGTGGTGAATTTGGAGTCTGGAGGCCGTGATGAACTTTGCAACGGGTCTCAGCCG			480
Sbjct	483	GGTGGTGAATTTGGAGTCTGGAGGCCGTGATGAACTTTGCAACGGGTCTCAGCCG			542
CDS:Kinesin family m	82	R R N S A H T L N Q A S S R S H A L L T			
Query	481	TCGAAGGAACTCAGCCACACCCTGAACAGGCTCCAGCCGAAGCCATGCCCTGTCTCAC			540
Sbjct	543	TCGAAGGAACTCAGCCACACCCTGAACAGGCTCCAGCCGAAGCCATGCCCTGTCTCAC			602
CDS:Kinesin family m	102	L Y I S R Q T A Q Q M P S V D P G E P P			
Query	541	CCTTTACATCAGCCGTCAACTGCCAGCAGATGCCCTCTGTGGACCTGGGGAGCCCC			600
Sbjct	603	CCTTTACATCAGCCGTCAACTGCCAGCAGATGCCCTCTGTGGACCTGGGGAGCCCC			662
CDS:Kinesin family m	122	V G G K L G C F V D L A G S E K V A A T G			
Query	601	TGTTGGTGGGAAGCTGTGCTTTGTGGACCTGGCAGGCACTGAGAAGGTAGCAGCCACGG			660
Sbjct	663	TGTTGGTGGGAAGCTGTGCTTTGTGGACCTGGCAGGCACTGAGAAGGTAGCAGCCACGG			722
CDS:Kinesin family m	142	S R G E L M L			
Query	661	ATCCCGTGGGAGCTGATGCTTG 683			
Sbjct	723	ATCCCGTGGGAGCTGATGCTTG 745			

primerB (Reverse)
Sequence ID: Query_62147 Length: 623 Number of Matches: 1
Range 1: 60 to 623

Score	Expect	Identities	Gaps	Strand	Frame
1042 bits(564)	0.0()	564/564(100%)	0/564(0%)	Plus/Minus	
Features:					
CDS:Kinesin family m	408	A R P P P W A P P C S P G S A K C P R E			
Query	1461	ccgggccccccctggcaccoccatgcagccctggctctgccaagtcccaAGAGAGA	1520		
Sbjct	623	CCGGGCCCCCACCCTGGGCACCCCATGCAGCCCTGGCTGCCAAGTGCCAAGAGAGA	564		
CDS:Kinesin family m	428	R S H S D W T Q T R V L A E M L T E E E			
Query	1521	GGAGTCACAGTGACTGGACTCAGACCCGAGTCTGGCAGAGATGTTGACGGAGGAGGAGG	1580		
Sbjct	563	GGAGTCACAGTGACTGGACTCAGACCCGAGTCTGGCAGAGATGTTGACGGAGGAGGAGG	504		
CDS:Kinesin family m	448	V V P S A P P L P V R P P K T S P G L R			
Query	1581	TGGTACCTTCTGCACCTCCCCTGCCTGTGAGGCCCCGAGACATCACCAGGGCTCAGAG	1640		
Sbjct	503	TGGTACCTTCTGCACCTCCCCTGCCTGTGAGGCCCCGAGACATCACCAGGGCTCAGAG	444		
CDS:Kinesin family m	468	G G A G V P N L A Q R L E A L R D Q I G			
Query	1641	GTGGGGCCGGGGTTCCAAACCTGGCCAGAGACTGGAGGCCCTCAGAGACCAGATTGGCA	1700		
Sbjct	443	GTGGGGCCGGGGTTCCAAACCTGGCCAGAGACTGGAGGCCCTCAGAGACCAGATTGGCA	384		
CDS:Kinesin family m	488	S S L R R G R S Q P P C S E G A R S P G			
Query	1701	GCTCCCTGCGACGTGGCCGAGCCAGCCACCCTGCAGTGAGGGCGCACGGAGCCAGGCC	1760		
Sbjct	383	GCTCCCTGCGACGTGGCCGAGCCAGCCACCCTGCAGTGAGGGCGCACGGAGCCAGGCC	324		
CDS:Kinesin family m	508	Q V L P P H			
Query	1761	AAGTCCCTCCCTCCCAATTGAAGGCCAAGTGGGAACCCAGGAGACTGCTGTGTGACCTCAG	1820		
Sbjct	323	AAGTCCCTCCCTCCCAATTGAAGGCCAAGTGGGAACCCAGGAGACTGCTGTGTGACCTCAG	264		
Query	1821	ACTGGGCTCCACACTCTGGGCTCAGTCTGCCATCTGCTGAATGGAGACAGCAGCTGC	1880		
Sbjct	263	ACTGGGCTCCACACTCTGGGCTCAGTCTGCCATCTGCTGAATGGAGACAGCAGCTGC	204		
Query	1881	TACTCCACCTGCAGCTGGGCTAGGGGGGGGGACTGGGGTGCTATTTAGGGGAACAAGGG	1940		
Sbjct	203	TACTCCACCTGCAGCTGGGCTAGGGGGGGGGACTGGGGTGCTATTTAGGGGAACAAGGG	144		
Query	1941	GATTCAGGAGAAACCAGGCAGCAGGGGATGAAATACATGAATAAAGAGAGGCATCAGCTC	2000		
Sbjct	143	GATTCAGGAGAAACCAGGCAGCAGGGGATGAAATACATGAATAAAGAGAGGCATCAGCTC	84		
Query	2001	Caaaaaaaaaaaaaaaaaaaaa	2024		
Sbjct	83	AAAAAAAAAAAAAAAAAAAAA	60		

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BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: BC010626:Homo sapiens kinesin family member...

RID [G82NXST0114](#) (Expires on 09-16 15:41 pm)

Query ID [NM_138424.2](#)

Description Homo sapiens kinesin family member 12 (KIF12), transcript variant 1, mRNA

Molecule type nucleic acid
Query Length 2012

Subject ID 3 subjects

Description [See details](#)

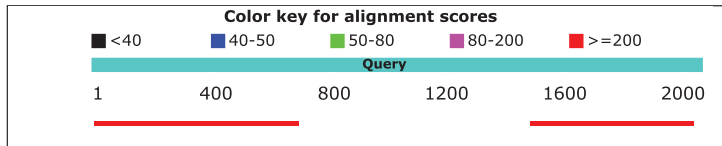
Molecule type dna

Subject Length 1372

Program BLASTN 2.14.1+

Graphic Summary

Distribution of the top 2 Blast Hits on 2 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerA (Forward)	1262	1262	33%	0.0	100.00%	Query_56004
primerB (Reverse)	1003	1003	26%	0.0	100.00%	Query_56005

Alignments

primerA (Forward)

Sequence ID: Query_56004 Length: 745 Number of Matches: 1
Range 1: 63 to 745

Score	Expect	Identities	Gaps	Strand	Frame
1262 bits(683)	0.0()	683/683(100%)	0/683(0%)	Plus/Plus	
Features:					
Query	10	GG AAGACATCAGGATGTACCATCTGCCCTTCTGTGGACCCAGGGTACGTCCCATGAGC			69
Sbjct	63	GG AAGACATCAGGATGTACCATCTGCCCTTCTGTGGACCCAGGGTACGTCCCATGAGC			122
Query	70	GCGGCCGAGCTGCGTCGAGGGCAGCAGAGCGTGTGCACCTGCTCAGGGACCCGGACTCTG			129
Sbjct	123	GCGGCCGAGCTGCGTCGAGGGCAGCAGAGCGTGTGCACCTGCTCAGGGACCCGGACTCTG			182
Query	130	CAGTTTCTCCTGCACGTTTTTCACTTTGGCCAGACGGGCTCTGGGAAGACCTACACCT			189
Sbjct	183	CAGTTTCTCCTGCACGTTTTTCACTTTGGCCAGACGGGCTCTGGGAAGACCTACACCT			242
CDS:kinesin-like pro	1	GACTGGACCCCTCCCCAGGGGAGGGGGTGCCTGTACCCCCAGCCTGGCTGGCATCAT			M 249
Query	190	GACTGGACCCCTCCCCAGGGGAGGGGGTGCCTGTACCCCCAGCCTGGCTGGCATCAT			
Sbjct	243	GACTGGACCCCTCCCCAGGGGAGGGGGTGCCTGTACCCCCAGCCTGGCTGGCATCAT			302
CDS:kinesin-like pro	2	Q R T F A W L L D R V Q H L G A P V T L			
Query	250	GCAGAGGACCTTCGCCTGGCTGTTGGACCGCGTGCAGCACCTGGTGCCCTGTCAACCT			309
Sbjct	303	GCAGAGGACCTTCGCCTGGCTGTTGGACCGCGTGCAGCACCTGGTGCCCTGTCAACCT			362
CDS:kinesin-like pro	22	R A S Y L E I Y N E Q V R D L L S L G S			
Query	310	TGGCGCTCTTATCTGGAGATCTACAATGAGCAGGTTCGGGACTTCTGAGCCTGGGGTC			369
Sbjct	363	TGGCGCTCTTATCTGGAGATCTACAATGAGCAGGTTCGGGACTTCTGAGCCTGGGGTC			422
CDS:kinesin-like pro	42	P R P L P V R W N K T R G F Y V E Q L R			
Query	370	TCCCCGGCCCTCCCTGTTTCGCTGGAAACAAGACTCGGGGTTCTATGTGGAGCAGCTGG			429
Sbjct	423	TCCCCGGCCCTCCCTGTTTCGCTGGAAACAAGACTCGGGGTTCTATGTGGAGCAGCTGG			482
CDS:kinesin-like pro	62	V V E F G S L E A L M E L L Q T G L S R			
Query	430	GGTGGTGAATTTGGGAGTCTGGAGGCCGTGATGGAACTTTGC AAACGGGTCTCAGCCG			489
Sbjct	483	GGTGGTGAATTTGGGAGTCTGGAGGCCGTGATGGAACTTTGC AAACGGGTCTCAGCCG			542
CDS:kinesin-like pro	82	R R N S A H T L N Q A S S R S H A L L T			
Query	490	TCGAAGGAACTCAGCCACACCTGAACCAAGGCTCCAGCCGAAGCCATGCCCTGCTCAC			549
Sbjct	543	TCGAAGGAACTCAGCCACACCTGAACCAAGGCTCCAGCCGAAGCCATGCCCTGCTCAC			602
CDS:kinesin-like pro	102	L Y I S R Q T A Q Q M P S V D P G E P P			
Query	550	CCTTTACATCAGCCGTC AAACGCCAGCAGATGCCCTCTGTGGACCTGGGGAGCCCC			609
Sbjct	603	CCTTTACATCAGCCGTC AAACGCCAGCAGATGCCCTCTGTGGACCTGGGGAGCCCC			662
CDS:kinesin-like pro	122	V G G K L C F V D L A G S E K V A A T G			
Query	610	TGTTGGTGGGAAGCTGTGCTTTGTGGACCTGGCAGGCACTGAGAAGGTAGCAGCCACGG			669
Sbjct	663	TGTTGGTGGGAAGCTGTGCTTTGTGGACCTGGCAGGCACTGAGAAGGTAGCAGCCACGG			722
CDS:kinesin-like pro	142	S R G E L M L			
Query	670	ATCCCGTGGGAGCTGATGCTTG			692
Sbjct	723	ATCCCGTGGGAGCTGATGCTTG			745

primerB (Reverse)

Sequence ID: Query_56005 Length: 623 Number of Matches: 1
Range 1: 81 to 623

Score	Expect	Identities	Gaps	Strand	Frame
1003 bits(543)	0.0()	543/543(100%)	0/543(0%)	Plus/Minus	
Features:					
CDS:kinesin-like pro	408	A R P P P W A P P C S P G S A K C P R E			
Query	1470	ccccgccccaccctggcaccoccatgcagccctgctctgccaagtccccAGAGAGA			1529
Sbjct	623	CCGGCCCCCACCTGGGACCCCCATGCAGCCCTGGCTCTGCCAAGTGCCAAGAGAGA			564
CDS:kinesin-like pro	428	R S H S D W T Q T R V L A E M L T E E E			
Query	1530	GGAGTCACAGTGACTGGACTCAGACCCGAGTCTGGCAGAGATGTTGACGGAGGAGGAGG			1589
Sbjct	563	GGAGTCACAGTGACTGGACTCAGACCCGAGTCTGGCAGAGATGTTGACGGAGGAGGAGG			504
CDS:kinesin-like pro	448	V V P S A P P L P V R P P K T S P G L R			
Query	1590	TGGTACCTTCTGCACCTCCCTGCCGTGTGAGGCCCCGAAGACATCACAGGGCTCAGAG			1649
Sbjct	503	TGGTACCTTCTGCACCTCCCTGCCGTGTGAGGCCCCGAAGACATCACAGGGCTCAGAG			444
CDS:kinesin-like pro	468	G G A G V P N L A Q R L E A L R D Q I G			
Query	1650	GTGGGGCCGGGGTTCCAAACCTGGCCAGAGACTGGAGGCCCTCAGAGACCAGATTGGCA			1709
Sbjct	443	GTGGGGCCGGGGTTCCAAACCTGGCCAGAGACTGGAGGCCCTCAGAGACCAGATTGGCA			384
CDS:kinesin-like pro	488	S S L R R G R S Q P P C S E G A R S P G			
Query	1710	GCTCCCTGCCAGTGGCCGAGCCAGCCACCCTGCAGTGAGGGCCGACGGAGCCAGGCC			1769
Sbjct	383	GCTCCCTGCCAGTGGCCGAGCCAGCCACCCTGCAGTGAGGGCCGACGGAGCCAGGCC			324
CDS:kinesin-like pro	508	Q V L P P H			
Query	1770	AAGTCCCTCCCTCCCAATTGAAGGCCAAGTGGGAACCCAGGAGACTGCTGTGTGACCTCAG			1829
Sbjct	323	AAGTCCCTCCCTCCCAATTGAAGGCCAAGTGGGAACCCAGGAGACTGCTGTGTGACCTCAG			264
Query	1830	ACTGGGCTCCACACTCTGGGCTCAGTCTGCCATCTGCTGAATGGAGACAGCAGCTGC			1889
Sbjct	263	ACTGGGCTCCACACTCTGGGCTCAGTCTGCCATCTGCTGAATGGAGACAGCAGCTGC			204
Query	1890	TACTCCACCTGCAGCTGGGCTAGGGGCGGGGACTGGGGTGCTATTTAGGGGAACAAGGG			1949
Sbjct	203	TACTCCACCTGCAGCTGGGCTAGGGGCGGGGACTGGGGTGCTATTTAGGGGAACAAGGG			144
Query	1950	GATTCAGGAGAAACCAGGCAGCAGGGGATGAAATACATGAATAAAGAGAGGCATCAGCTC			2009
Sbjct	143	GATTCAGGAGAAACCAGGCAGCAGGGGATGAAATACATGAATAAAGAGAGGCATCAGCTC			84
Query	2010	CAA 2012			
Sbjct	83	CAA 81			

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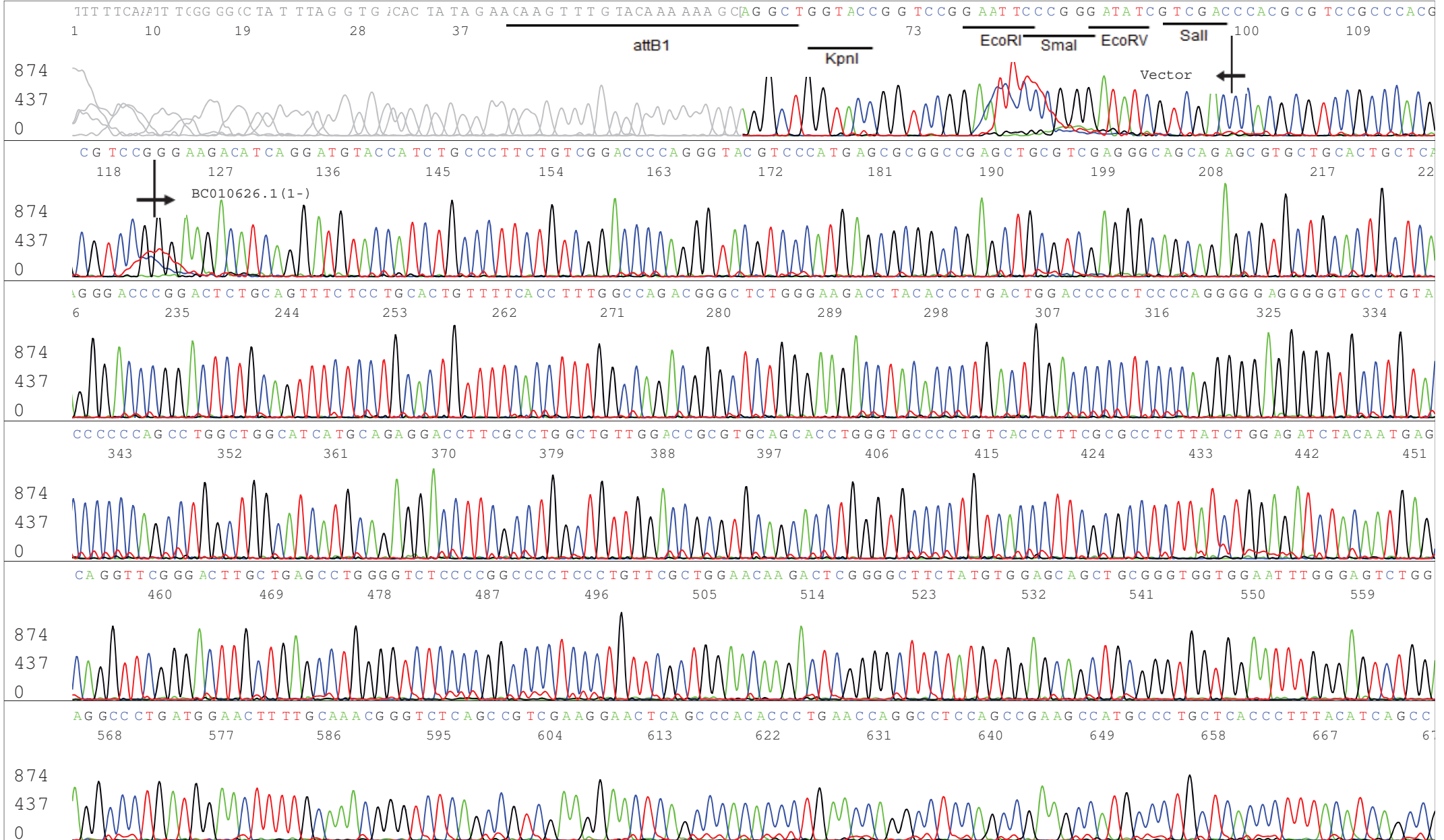
S/N G:24 A:31 T:27 C:44
 KB.bcp
 KB 1.4.1.8 Cap:7

Primer A : Reverse2
 5' GCGGATAACAATTTACACACAGG 3'

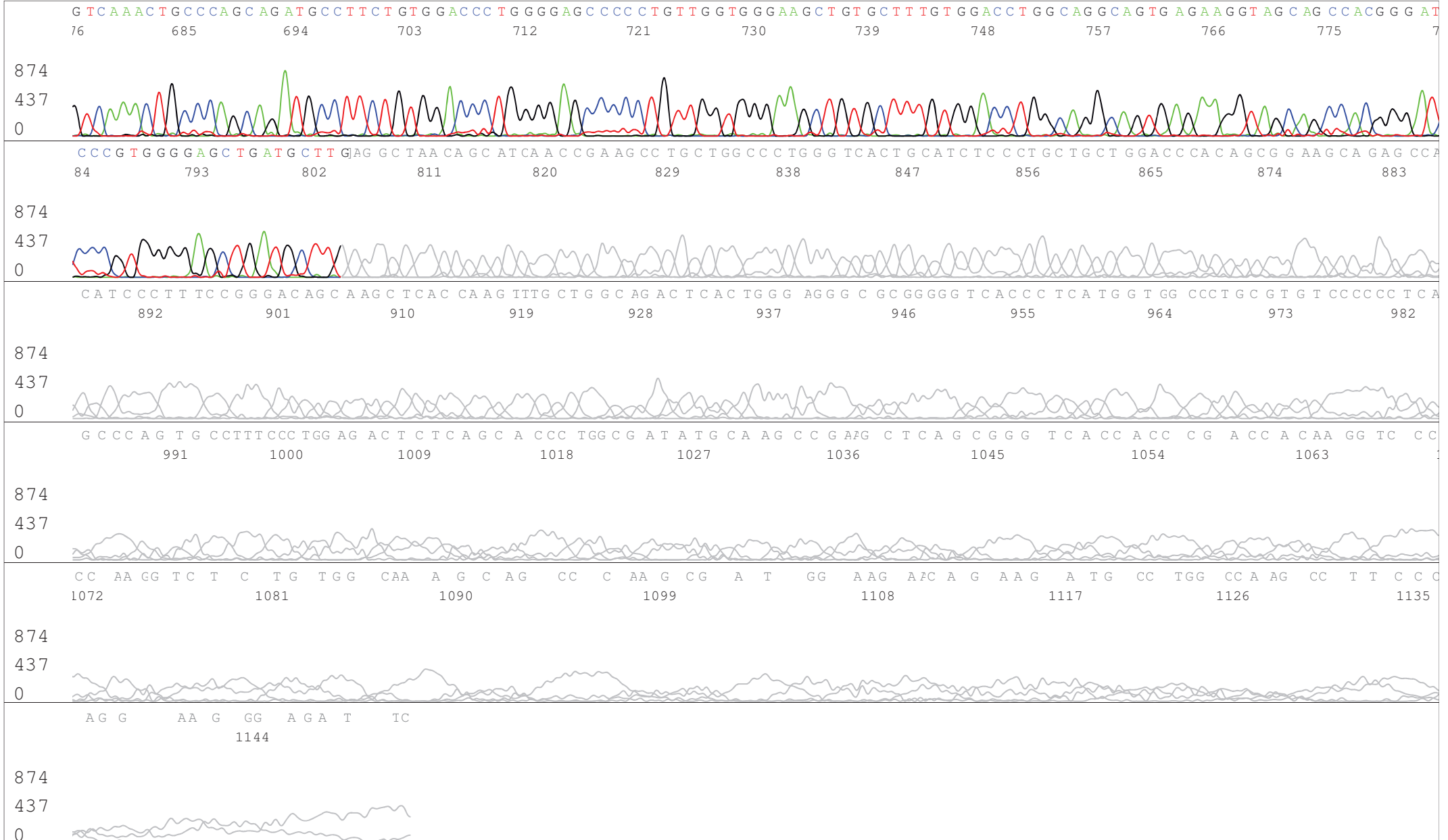
7893_IRAK013E09_B3ld_Reverse2
 KB_3500_POP7_BDTv3.mob
 Pts 1407 to 12878 Pk1 Loc:1384
 Version 6.0 HiSQV Bases: 886

Gray line indicates quality value
 (QV) < 40.

Sep 15,2023 10:37AM, JST
 Sep 15,2023 11:06AM, JST
 Spacing:11.49 Pts/Panel1350
 Plate Name: 20230915_mix2



S/N G:24 A:31 T:27 C:44
KB.bcp
KB 1.4.1.8 Cap:7



S/N G:28 A:26 T:24 C:37
KB.bcp
KB 1.4.1.8 Cap:8

Primer B : M13

5' GTTTCCAGTCACGACGTTGTA 3'

Gray line indicates quality value
(QV) < 40.

