

RIKEN Clone ID : IRAK078I08

Lot#: 7893_B3Im

Vector : pCMV-SPORT6

Gene	KIF26B	
Accession No.	BC035896.1	2571 bp
	<i>CDS</i>	2461 bp

● **Plasmid DNA purification**

Date : 2023/09/26

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

Date : 2023/09/27

Purification : QIAGEN Miniprep kit -> dH₂O 100 ul

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

Date : 2023/09/27

DNA concentration (O.D.): 412 ng/ul

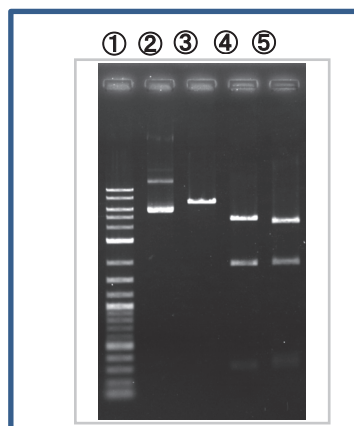
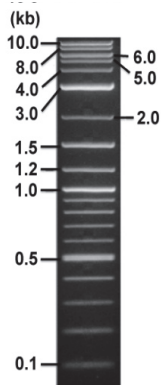
< Size of fragment expected from this clone >

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	6.9	kb	
XhoI	4.7, 1.9, 0.3	kb	
EcoRI + XhoI	4.3kb (Vector)	1.9, 0.4, 0.3	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 : 2023/10/03

DNA (<u>412</u> ng/ul)	86	ul
10x TE	142	ul
dH ₂ O	1,190	ul
Total	1,417	ul

● **Confirmation of the insertion sequence**

Date : 2023/09/28

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>



[Questions/comments](#)

BLAST Results

Blast 2 sequences

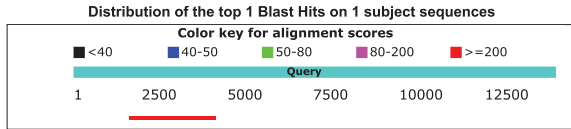
Job title: NM_018012:Homo sapiens kinesin family member...

RID [GUCP87CM114](#) (Expires on 09-23 14:23 pm)

Query ID [NM_018012.4](#)
Description Homo sapiens kinesin family member 26B (KIF26B), mRNA
Molecule type nucleic acid
Query Length 13593

Subject ID [BC035896.1](#)
Description Homo sapiens kinesin family member 26B, mRNA (cDNA clone IMAGE:5239561), partial cds
[See details](#)
Molecule type nucleic acid
Subject Length 2571
Program BLASTN 2.14.1+

Graphic Summary



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Homo sapiens kinesin family member 26B, mRNA (cDNA clone IMAGE:5239561), partial cds	4514	4514	17%	0.0	100.00%	BC035896.1

Alignments

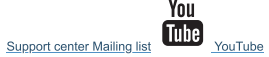
Homo sapiens kinesin family member 26B, mRNA (cDNA clone IMAGE:5239561), partial cds
 Sequence ID: [BC035896.1](#) Length: 2571 Number of Matches: 1
 Range 1: 128 to 2571

Score	Expect	Identities	Gaps	Strand	Frame
4514 bits(2444)	0.0()	2444/2444(100%)	0/2444(0%)	Plus/Plus	
Features:					
CDS:kinesin-like pro	390	A A Q K L N L S S K K K K K H R P S T S S			
Query	1607	AGCTGCCAGAGTTAAATCTGTCTTCTAAAAGAGAACAATCGGCCCTCCACTTCTC			1666
Sbjct	128	AGCTGCCAGAGTTAAATCTGTCTTCTAAAAGAGAACAATCGGCCCTCCACTTCTC			187
CDS:KIF26B protein,	7	A A Q K L N L S S K K K K K H R P S T S S			
CDS:kinesin-like pro	410	A A E P P L F A T S F S G I T Q T S P P			
Query	1667	CGCTGCCGAACACCGCTCTTCCACCAGCTTCAGTGGATTCTCGAGACCTCCCTCC			1726
Sbjct	188	CGCTGCCGAACACCGCTCTTCCACCAGCTTCAGTGGATTCTCGAGACCTCCCTCC			247
CDS:KIF26B protein,	27	A A E P P L F A T S F S G I T Q T S P P			
CDS:kinesin-like pro	430	P A P P C L L R A V N K V K D T P G L G			
Query	1727	CCAGCCCCACCTGCCTGAGGGCTGTCAACAAGTGAAGACACCCCGGGCTGGG			1786
Sbjct	248	CCAGCCCCACCTGCCTGAGGGCTGTCAACAAGTGAAGACACCCCGGGCTGGG			307
CDS:KIF26B protein,	47	P A P P C L L R A V N K V K D T P G L G			
CDS:kinesin-like pro	450	K V K V M L R I C S T L A R D T S E S S			
Query	1787	CAAGGTGAAGTCACTGCTCCGATCTGTTCCACCTTGGCTCGAGATCTTCAGATCCAG			1846
Sbjct	308	CAAGGTGAAGTCACTGCTCCGATCTGTTCCACCTTGGCTCGAGATCTTCAGATCCAG			367
CDS:KIF26B protein,	67	K V K V M L R I C S T L A R D T S E S S			
CDS:kinesin-like pro	470	S E L K V D P R K K Q I T L Y D P L T C			
Query	1847	CTCTTCTTAAAGGTGGACCCACGGAAGAAGCAGATCACCTTGTACGATCCCTGACTTG			1906
Sbjct	368	CTCTTCTTAAAGGTGGACCCACGGAAGAAGCAGATCACCTTGTACGATCCCTGACTTG			427
CDS:KIF26B protein,	87	S F L K V D P R K K Q I T L Y D P L T C			
CDS:kinesin-like pro	490	G G Q N A F Q K R G N Q V P P P K M F A F			
Query	1907	TGGAGTCAAAAAGCTTCCAAAAGAGAGCAACCGAGTTCCCAAGAATGTTGGCTT			1966
Sbjct	428	TGGAGTCAAAAAGCTTCCAAAAGAGAGCAACCGAGTTCCCAAGAATGTTGGCTT			487
CDS:KIF26B protein,	107	G G Q N A F Q K R G N Q V P P P K M F A F			
CDS:kinesin-like pro	510	D A V F P O D A S Q A E V C A G T V A E			
Query	1967	CGATGCAGTTTTCCACAAGACCTTCTCAGGCTGAAGTGTGTGCGAGCACCTGGCAGA			2026
Sbjct	488	CGATGCAGTTTTCCACAAGACCTTCTCAGGCTGAAGTGTGTGCGAGCACCTGGCAGA			547
CDS:KIF26B protein,	127	D A V F P O D A S Q A E V C A G T V A E			
CDS:kinesin-like pro	530	V I Q S V V N G A D G C V F C F G H A K			
Query	2027	GGTGTCCAGTCTGTGGTCAACGGGGCAGATGGCTGTCTGTTTCCGCCACGCCAA			2086
Sbjct	548	GGTGTCCAGTCTGTGGTCAACGGGGCAGATGGCTGTCTGTTTCCGCCACGCCAA			607
CDS:KIF26B protein,	147	V I Q S V V N G A D G C V F C F G H A K			
CDS:kinesin-like pro	550	L G K S Y T M I G K D D S M Q N L G I I			
Query	2087	ACTGGAAAATCTACACCATGATCGAAAGGATGATTCATCGAGAAGCTGGGCATCA			2146
Sbjct	608	ACTGGAAAATCTACACCATGATCGAAAGGATGATTCATCGAGAAGCTGGGCATCA			667
CDS:KIF26B protein,	167	L G K S Y T M I G K D D S M Q N L G I I			
CDS:kinesin-like pro	570	P C A I S W L F K L L I N E R K E K T G A			
Query	2147	TCCTGTGCCATCTTGGCTTCAAGCTCATAAAGCAACCAAGAAAGACCGGGCC			2206
Sbjct	668	TCCTGTGCCATCTTGGCTTCAAGCTCATAAAGCAACCAAGAAAGACCGGGCC			727
CDS:KIF26B protein,	187	P C A I S W L F K L L I N E R K E K T G A			
CDS:kinesin-like pro	590	R F S V R V S A V E V W G K E E N L R D			
Query	2207	CCGTTTTCTCAGTCCGGTTCCCGGTGGAAGTGTGGGGGAAGGAGAGAAGCTCGGGGA			2266
Sbjct	728	CCGTTTTCTCAGTCCGGTTCCCGGTGGAAGTGTGGGGGAAGGAGAGAAGCTCGGGGA			787
CDS:KIF26B protein,	207	R F S V R V S A V E V W G K E E N L R D			
CDS:kinesin-like pro	610	L L S E V A T G S L O D G Q S P G V Y L			
Query	2267	CCTGCTGCGAGGTGGCCACGGCAGCTGCAGGACGGCCAGTCCCGGGCGGTACCT			2326
Sbjct	788	CCTGCTGCGAGGTGGCCACGGCAGCTGCAGGACGGCCAGTCCCGGGCGGTACCT			847
CDS:KIF26B protein,	227	L L S E V A T G S L O D G Q S P G V Y L			
CDS:kinesin-like pro	630	C E D P I C G T O L D N Q S E L R A P T			
Query	2327	CTGTGAGGACCCATCTGCGGCACGAGCTGCAGAACAGACCGAGCTGCGGGCCCCAC			2386
Sbjct	848	CTGTGAGGACCCATCTGCGGCACGAGCTGCAGAACAGACCGAGCTGCGGGCCCCAC			907
CDS:KIF26B protein,	247	C E D P I C G T O L D N Q S E L R A P T			
CDS:kinesin-like pro	650	A E K A A F F L D A A I A S R R S H O Q			
Query	2387	CGCAGAGAAGGCTGCTTTTTCTGGATGCCCAATGCTCCCGCAGGAGCCACCAACA			2446
Sbjct	908	CGCAGAGAAGGCTGCTTTTTCTGGATGCCCAATGCTCCCGCAGGAGCCACCAACA			967
CDS:KIF26B protein,	267	A E K A A F F L D A A I A S R R S H O Q			
CDS:kinesin-like pro	670	D C D E D D H R N S H V F F F T L H I Y Q			
Query	2447	GGACTGTGATGAGGACGACCCACCACTCACAGTGTCTTCACACTGCACATCTACCA			2506
Sbjct	968	GGACTGTGATGAGGACGACCCACCACTCACAGTGTCTTCACACTGCACATCTACCA			1027
CDS:KIF26B protein,	287	D C D E D D H R N S H V F F F T L H I Y Q			

CDS:kinesin-like pro 690 Y R M E K S G K G G M S G G R S R L H L 2566
Query 2507 GTACCGGATGGAGAAAGCGGAAAGGGGAATGCTGGAGGTGCAGCCGCTGCATCT
Sbjct 1028 GTACCGGATGGAGAAAGCGGAAAGGGGAATGCTGGAGGTGCAGCCGCTGCATCT 1087
CDS:KIF26B protein, 307 Y R M E K S G K G G M S G G R S R L H L
CDS:kinesin-like pro 710 I D L G S C V K A L S K N R E G G S G L 2626
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Sbjct 1088 CATTGATCTGGCAGCTGTGTGAAAGCTTTAGCAAAAATCGAAGAAAGGCTCAGGCT 1147
CDS:KIF26B protein, 327 I D L G S C V K A L S K N R E G G S G L
CDS:kinesin-like pro 730 C L S L S A L G N V I L A L V N G S K H 2686
Query 2627 GTGCTCTGCTGTGCTCTGGCAATGTCATCTGGCTCTGCTCAATGGCAACAACA
Sbjct 1148 GTGCTCTGCTGTGCTCTGGCAATGTCATCTGGCTCTGCTCAATGGCAACAACA 1207
CDS:KIF26B protein, 347 G L S L S A L G N V I L A L V N G S K H
CDS:kinesin-like pro 750 I P Y K E S K L A M L L R E S L G N M N 2746
Query 2687 CATTCACAAAGAGAGCAAGCTGGCATGTTGCTGCGGGAGTCTCTGGGAACATGAA
Sbjct 1208 CATTCACAAAGAGAGCAAGCTGGCATGTTGCTGCGGGAGTCTCTGGGAACATGAA 1267
CDS:KIF26B protein, 367 I P Y K E S K L A M L L R E S L G N M N
CDS:kinesin-like pro 770 C R T T M I A H I S A A V G S Y A E T L 2806
Query 2747 CTGCCATACCACATGATCGGCGACATCTGGCGCGGTGGGAGCTACGGGAGACCT
Sbjct 1268 CTGCCATACCACATGATCGGCGACATCTGGCGCGGTGGGAGCTACGGGAGACCT 1327
CDS:KIF26B protein, 387 C R T T M I A H I S A A V G S Y A E T L
CDS:kinesin-like pro 790 S T I Q I A S R V L R M K K K K T K Y T 2866
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Sbjct 1328 GTCCACCATCCAGATGCAATCGAGGCTTTGAGGATGAAGAAAAGAGCAAGATACAC 1387
CDS:KIF26B protein, 407 S T I Q I A S R V L R M K K K K T K Y T
CDS:kinesin-like pro 810 S S S S G G E S S C E E G R M R R P T Q 2926
Query 2867 ATCCAGCTGTCCGGCGGGAGAGCTCTGCAAGAAAGCCGATGCGAGGCCACCCA
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CDS:KIF26B protein, 427 S S S S G G E S S C E E G R M R P Q
CDS:kinesin-like pro 830 R R P F H T R A T V D P D F P I A H I S 2986
Query 2927 GCTGAGACCTTCCACACCGGCGCAGGTGGCCCTGACTTCCCACTCCCTACCTGT
Sbjct 1448 GCTGAGACCTTCCACACCGGCGCAGGTGGCCCTGACTTCCCACTCCCTACCTGT 1507
CDS:KIF26B protein, 447 L R P F H T R A T V D P D F P I A H I S
CDS:kinesin-like pro 850 S D P D Y S S S S E Q S C D T V I Y I G 3046
Query 2987 CAGCGACCCCGACTACTCTCCAGAGCGAGGAGTCTGGACCCGCTCATACATCGG
Sbjct 1508 CAGCGACCCCGACTACTCTCCAGAGCGAGGAGTCTGGACCCGCTCATACATCGG 1567
CDS:KIF26B protein, 467 S D P D Y S S S S E Q S C D T V I Y I G
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CDS:KIF26B protein, 507 V P I V P A L Q K T R G D S R P A E A G
CDS:kinesin-like pro 910 E A A A G K S E R D C L K C N T F A E L 3226
Query 3167 AGAGGCTGCAGCGCAAGTCAAGAAAGGACTGCTGAACTGCAACAGTTTCCGAGCT
Sbjct 1688 AGAGGCTGCAGCGCAAGTCAAGAAAGGACTGCTGAACTGCAACAGTTTCCGAGCT 1747
CDS:KIF26B protein, 527 E A A A G K S E R D C L K C N T F A E L
CDS:kinesin-like pro 930 Q E R L D C I D G S E E P S S F P F E E 3286
Query 3227 GCAGGAGAGGCTGACTGCAATCGAGCGCAGGAGCCGACGACTTCTTTCGAAGA
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Query 3287 ACTGCCCTGCTCAGTTTGGCCAGAGCGGCAAGCAGGCCCCCGGTAAAGCAGGAGC
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CDS:kinesin-like pro 970 G A S P L S E S D K E D N G S E G O I T 3406
Query 3347 GGGGGCAAGCCACTCTGAGTGTGATAAGGAAGATAATGGTCCGAAGTCAAGTAC
Sbjct 1868 GGGGGCAAGCCACTCTGAGTGTGATAAGGAAGATAATGGTCCGAAGTCAAGTAC 1927
CDS:KIF26B protein, 587 G A S P L S E S D K E D N G S E G O I T
CDS:kinesin-like pro 990 N R E G P E L P A S K M Q R S H S P V P 3466
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Sbjct 1928 CAACAGAGAAAGGCGCTGAACCTCCAGGCTCCAGAGTCCAGAGGACTCACTACCTGTGC 1987
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CDS:kinesin-like pro 1010 A A A P A H S P S P A S P R S V P G S S 3526
Query 3467 CCGCGCGCACCCGCCACAGCCCGCCGCTCACCCAGAGCGTCCCGGCGAGCAG
Sbjct 1988 CCGCGCGCACCCGCCCACAGCCCGCCGCTCACCCAGAGCGTCCCGGCGAGCAG 2047
CDS:KIF26B protein, 627 A A A P A H S P S P A S P R S V P G S S
CDS:kinesin-like pro 1030 S Q H S A S P L V Q S P S L O S S R E S 3586
Query 3527 TAGCCAGCACAGCCCTCCCACTCGTGCAGAGCCCGCCGCTCCAGAGCAGCCGGAGAG
Sbjct 2048 TAGCCAGCACAGCCCTCCCACTCGTGCAGAGCCCGCCGCTCCAGAGCAGCCGGAGAG 2107
CDS:KIF26B protein, 647 S Q H S A S P L V Q S P S L O S S R E S
CDS:kinesin-like pro 1050 L N S C G F V E G K P R P N G S P R L G 3646
Query 3587 CCTCACTCTGCGGCTTGTGGAAAGCAAGCCAGGCCATGGGCTCCCGGCGTGGG
Sbjct 2108 CCTCACTCTGCGGCTTGTGGAAAGCAAGCCAGGCCATGGGCTCCCGGCGTGGG 2167
CDS:KIF26B protein, 667 L N S C G F V E G K P R P N G S P R L G
CDS:kinesin-like pro 1070 I A S L S K T S E Y K P P S S P S O R C 3706
Query 3647 CATGGCAGCTGTCCAAGACTGGAGTACAAGCCACCCAGCTCTCTTCCAGAGATG
Sbjct 2168 CATGGCAGCTGTCCAAGACTGGAGTACAAGCCACCCAGCTCTCTTCCAGAGATG 2227
CDS:KIF26B protein, 687 I A S L S K T S E Y K P P S S P S O R C
CDS:kinesin-like pro 1090 K A V Y T Q K G V L P S P A P L P P S S K 3766
Query 3707 CAAGTCTACACCCAGAAAGGGGCTCTCCGCTCTCCCGCCCACTGCCTCCCTCGAGCA
Sbjct 2228 CAAGTCTACACCCAGAAAGGGGCTCTCCGCTCTCCCGCCCACTGCCTCCCTCGAGCA 2287
CDS:KIF26B protein, 707 K V Y T Q K G V L P S P A P L P P S S K
CDS:kinesin-like pro 1110 D S G V A S R E S L L Q P E V R T P P V 3826
Query 3767 GGATTCGGGCTGGGCTTAGGGAGTCTTGTGCAAGCCGAGGTGCTACGCCCCCGG
Sbjct 2288 GGATTCGGGCTGGGCTTAGGGAGTCTTGTGCAAGCCGAGGTGCTACGCCCCCGG

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CDS:kinesin-like pro 1130 G M S P Q V L K K S M S A G S E G F P E 3886
Query 3827 TGGAAATGAGCCCGAGTTTGAATAATCCATGCTGCTGGAGCGAAGGTTCCCGGA
Sbjct 2348 TGGAAATGAGCCCGAGTTTGAATAATCCATGCTGCTGGAGCGAAGGTTCCCGGA 2407
CDS:KIF26B protein, 747 G M S P Q V L K K S M S A G S E G F P E
CDS:kinesin-like pro 1150 T P V D D E Q Q A A T P S E S K K E I L 3946
Query 3887 AACTCTGCTGATGATGAGCAGCAGCTACTCTTCAAGTCCAAGAGGATCCT
Sbjct 2408 AACTCTGCTGATGATGAGCAGCAGCTACTCTTCAAGTCCAAGAGGATCCT 2467
CDS:KIF26B protein, 767 T P V D D E Q Q A A T P S E S K K E I L
CDS:kinesin-like pro 1170 S T T M V T V Q O P L E N G E D E L V 4006
Query 3947 GAGCACCACGATGGTGAAGTGCAGCAGCAGCTGAGCTGAACGGTGAAGGAGTGG
Sbjct 2468 GAGCACCACGATGGTGAAGTGCAGCAGCAGCTGAGCTGAACGGTGAAGGAGTGG 2527
CDS:KIF26B protein, 787 S T T M V T V Q O P L E N G E D E L V
CDS:kinesin-like pro 1190 F T L V E E L T I S G V L D 4050
Query 4007 GTTCACCGTGGTGGAGGCTGACCATCAGCGGGCTCTCCGACA
Sbjct 2528 GTTCACCGTGGTGGAGGCTGACCATCAGCGGGCTCTCCGACA 2571
CDS:KIF26B protein, 807 F T L V E E L T I S G V L D

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[Questions/comments](#)

BLAST Results

Blast 2 sequences

Job title: **gb|BC035896.1|**

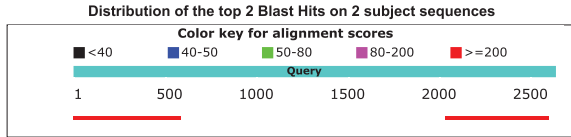
RID [HA15U93E114](#) (Expires on 09-29 12:44 pm)

Query ID [BC035896.1](#)
Description Homo sapiens kinesin family member 26B, mRNA (cDNA clone IMAGE:5239561), partial cds

Molecule type nucleic acid
Query Length 2571

Subject ID 3 subjects
Description [See details](#)
Molecule type dna
Subject Length 1324
Program BLASTN 2.14.1+

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerA (Forward)	1043	1043	22%	0.0	100.00%	Query_44670
primerB (Reverse)	1003	1003	21%	0.0	100.00%	Query_44671

Alignments

primerA (Forward)
 Sequence ID: Query_44670 Length: 660 Number of Matches: 1
 Range 1: 83 to 660

Score	Expect	Identities	Gaps	Strand	Frame
1043 bits(1156)	0.0()	578/578(100%)	0/578(0%)	Plus/Plus	
Features:					
Query 1		TCCTGAGATGCCCCAGATCTGCAAGAGACATTTGAGAGAAGCTATTTATTAGCAGACGT			60
Sbjct 83		TCCTGAGATGCCCCAGATCTGCAAGAGACATTTGAGAGAAGCTATTTATTAGCAGACGT			142
Query 61		GAAGAAATGGATTCTGCACCTGATATTTAGCCATGACTTATCAATGATGATGGATTGGA			120
Sbjct 143		GAAGAAATGGATTCTGCACCTGATATTTAGCCATGACTTATCAATGATGATGGATTGGA			202
Query 121		AAGCAGTAGCTGCCCAAGGTTAAATCTGTCTTCTAAAAAGAAAGAACATCGGCTTCCA			180
Sbjct 203		AAGCAGTAGCTGCCCAAGGTTAAATCTGTCTTCTAAAAAGAAAGAACATCGGCTTCCA			262
Query 181		CTTCTTCGCTGCCCAACCCGCTCTTTGCAACCAGCTTCAAGTGGGATCTGCAGACCT			240
Sbjct 263		CTTCTTCGCTGCCCAACCCGCTCTTTGCAACCAGCTTCAAGTGGGATCTGCAGACCT			322
Query 241		CCCCCCCCCAGCCACCTGCTGAGGGCTGTCAACAGGTGAAGACACCCCG			300
Sbjct 323		CCCCCCCCCAGCCACCTGCTGAGGGCTGTCAACAGGTGAAGACACCCCG			382
Query 301		GGCTGGCAAGGTGAAAGTCAATGCTTCGATCTGTTCCACCTTGGCTGGAGATCTTCA			360
Sbjct 383		GGCTGGCAAGGTGAAAGTCAATGCTTCGATCTGTTCCACCTTGGCTGGAGATCTTCA			442
Query 361		AATCCAGCTCTTTCTAAAGTGGACCCACGGAAAGCAGATCACCTTGTACGATCCCC			420
Sbjct 443		AATCCAGCTCTTTCTAAAGTGGACCCACGGAAAGCAGATCACCTTGTACGATCCCC			502
Query 421		TGACTTGTGGAGTCAAAATGCCTTCCAAGAGAGGCAACAGGTTCTCCAAGATGT			480
Sbjct 503		TGACTTGTGGAGTCAAAATGCCTTCCAAGAGAGGCAACAGGTTCTCCAAGATGT			562
Query 481		TTGCCTCGATGCAGTTTCCACAAAGCGCTTCTAGGCTGAAGTGTGTGACGGCACCG			540
Sbjct 563		TTGCCTCGATGCAGTTTCCACAAAGCGCTTCTAGGCTGAAGTGTGTGACGGCACCG			622
Query 541		TGGCAGAGGTGATCCAGTCTGTGGTCAACGGGGCAGAT			578
Sbjct 623		TGGCAGAGGTGATCCAGTCTGTGGTCAACGGGGCAGAT			660

primerB (Reverse)
 Sequence ID: Query_44671 Length: 660 Number of Matches: 1
 Range 1: 105 to 660

Score	Expect	Identities	Gaps	Strand	Frame
1003 bits(1112)	0.0()	556/556(100%)	0/556(0%)	Plus/Minus	
Features:					
Query 2016		CGGGCTCACCCAGGAGCGTCCCGGGCAGCAGTAGCCAGCACAGCGCTCCCCACTCGT			2075
Sbjct 660		CGGGCTCACCCAGGAGCGTCCCGGGCAGCAGTAGCCAGCACAGCGCTCCCCACTCGT			601
Query 2076		CAGAGCCCAAGCTCCAGAGCAGCCGGGAGAGCCTCAACTCTCGGGCTTGGTGAAGGC			2135
Sbjct 600		CAGAGCCCAAGCTCCAGAGCAGCCGGGAGAGCCTCAACTCTCGGGCTTGGTGAAGGC			541
Query 2136		AAGCCAGGCCATGGGCTCCCGCCGGCTGGGCATCGCCAGCCTGTCCAAGACCTCGAG			2195
Sbjct 540		AAGCCAGGCCATGGGCTCCCGCCGGCTGGGCATCGCCAGCCTGTCCAAGACCTCGAG			481
Query 2196		TACAAGCCACCCAGCTCTCCTTCCAGAGATGCAAAAGTCTACACCCAGAAGGGGTCCTG			2255
Sbjct 480		TACAAGCCACCCAGCTCTCCTTCCAGAGATGCAAAAGTCTACACCCAGAAGGGGTCCTG			421
Query 2256		CGTCTCCCGCCCACTGCCTCCCGAGCAAGGATCCGGCGTGGGCTCTAGGGAGTCC			2315
Sbjct 420		CGTCTCCCGCCCACTGCCTCCCGAGCAAGGATCCGGCGTGGGCTCTAGGGAGTCC			361
Query 2316		TTGCTGACGCCGAGGTGGTACGCCCGGGTGGAAATGAGCCCGAGGTTTTGAAAAA			2375
Sbjct 360		TTGCTGACGCCGAGGTGGTACGCCCGGGTGGAAATGAGCCCGAGGTTTTGAAAAA			301
Query 2376		TCCATGCTGCTGGAGCGAAGGGTCCCGGAAACTCCTGTGATGATGACAGCAGGCCA			2435
Sbjct 300		TCCATGCTGCTGGAGCGAAGGGTCCCGGAAACTCCTGTGATGATGACAGCAGGCCA			241
Query 2436		GCTACTCTTTCAGAGTCCAAGAAAGGAGATCCTGAGCACCAGATGGTGAOBBGTGACAG			2495
Sbjct 240		GCTACTCTTTCAGAGTCCAAGAAAGGAGATCCTGAGCACCAGATGGTGAOBBGTGACAG			181
Query 2496		CCACTGGAGTGAACGGTGAAGACGAGCTGGTGTTCACGCTGGTGGAGGAGTGAACATC			2555
Sbjct 180		CCACTGGAGTGAACGGTGAAGACGAGCTGGTGTTCACGCTGGTGGAGGAGTGAACATC			121
Query 2556		AGCGGGTCTTGGACA			2571
Sbjct 120		AGCGGGTCTTGGACA			105

S/N G:240 A:418 T:270 C:404
KB.bcp
KB 1.4.1.8 Cap:20

Primer A : Reverse2

7893_IRAK078I08_B3Im_2_Reverse2

KB_3500_POP7_BDTv3.mob

5' GCGGATAACAATTTTCACACAGG 3'

Pts 1660 to 11899 Pk1 Loc:1637

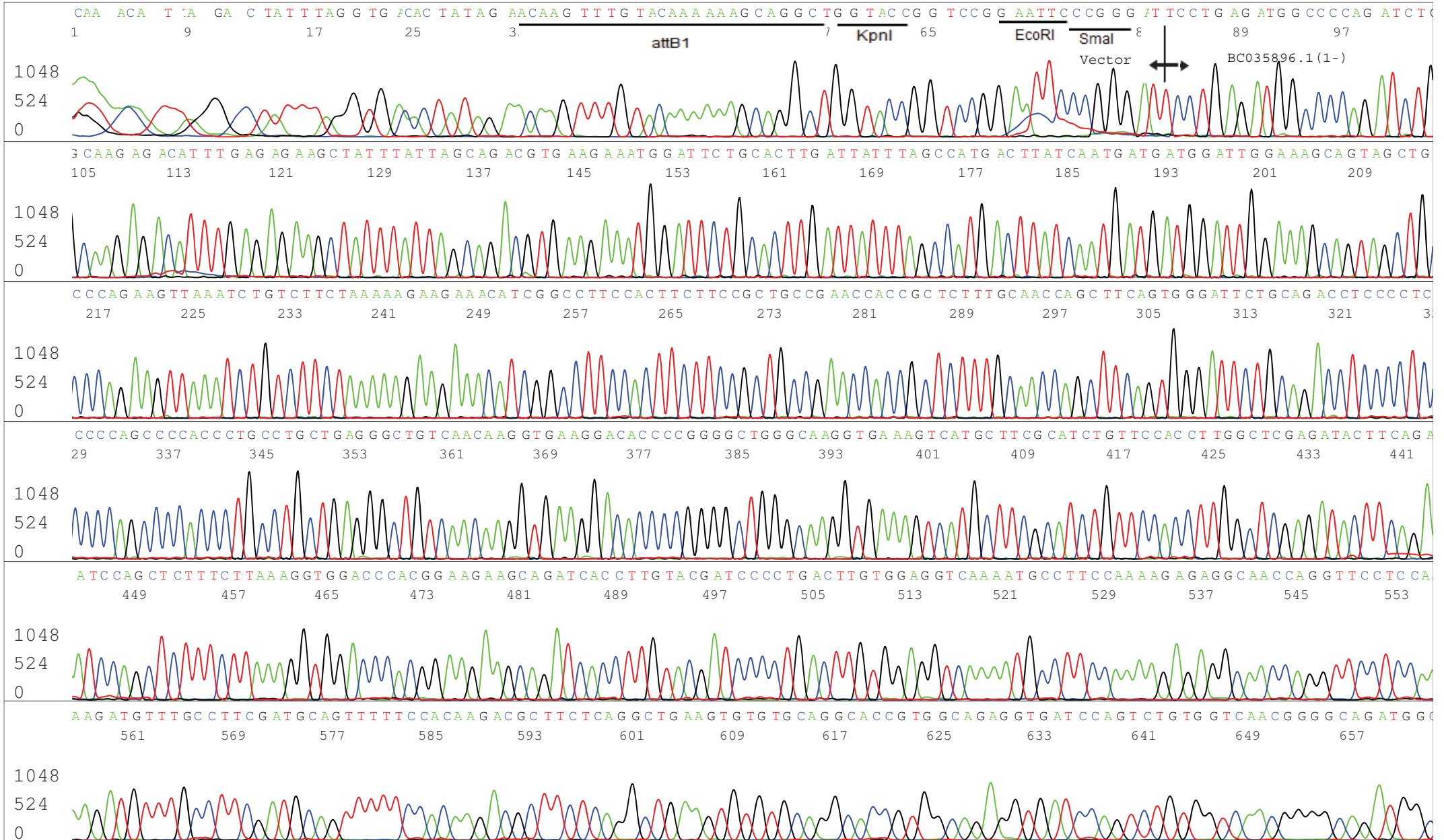
Version 6.0 HiSQV Bases: 751

Sep 28,2023 09:53AM, JST

Sep 28,2023 10:19AM, JST

Spacing:10.62 Pts/Panel1350

Plate Name: 20230928_mix



S/N G:374 A:632 T:466 C:712 Primer B : M13

7893_IRAK078I08_B3Im_2_M13(-40)

Sep 28,2023 09:53AM, JST

KB.bcp

KB_3500_POP7_BDTv3.mob

Sep 28,2023 10:19AM, JST

KB 1.4.1.8 Cap:23

5' GTTTTCCCAGTCACGACGTTGTA 3'

Pts 1690 to 11819 Pk1 Loc:1667

Spacing:10.65 Pts/Panel1350

Version 6.0 HiSQV Bases: 751

Plate Name: 20230928_mix

