

RIKEN Clone ID : TEx04D06 (PC010199-42)

Lot# : 6078_B3LI

Vector : pET-11a

Locus tag	TTHA0199
Insert size	1545 bp
Product	type B carboxylesterase

● **Plasmid DNA purification**

Date : 2023/12/21

Culture : LB (100 ug/ml Ampicillin) 10 ml -> 37°C O/N

Date : 2023/12/22

Purification : QIAGEN Miniprep kit -> dH₂O 50 ul

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

Date : 2023/12/22

DNA concentration (O.D.): 152 ng/ul

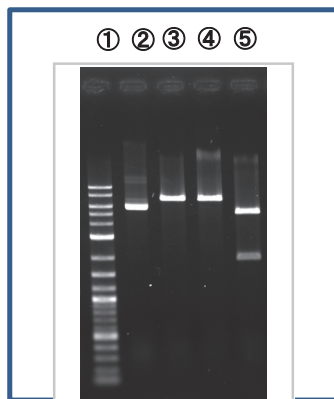
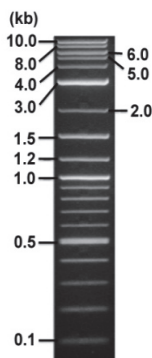
< Size of fragment expected from this clone >

DNA	0.6	ul
Enzyme (BglII + EcoRI)	0.5 + 0.5	ul
Buffer H	1	ul
dH ₂ O	7.4	ul
Total	10	ul

BglII	7.2	kb
EcoRI	7.2	kb
BglII + EcoRI	5.2	2.0

Electrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder



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

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

Date : 2024/01/11

DNA (152 ng/ul)	35	ul
10x TE	21	ul
dH ₂ O	157	ul
Total	213	ul

● **Shipping**

- Conc. : 25 ng/μl, Volume : 40 μl
- Conc. : ng/μl, Volume : μl

APPROVED BY :



BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: NM_014874:Homo sapiens mitofusin 2 (MFN2),...

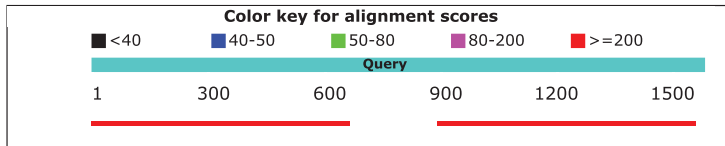
RID [TW9ATURU114](#) (Expires on 01-11 12:04 pm)

Query ID [Ic|Query_7464711](#)
 Description None **TTHA0199**
 Molecule type dna
 Query Length 1545

Subject ID 3 subjects
 Description [See details](#)
 Molecule type dna
 Subject Length 1397
 Program BLASTN 2.15.0+

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
primerB (Reverse)	1223	1223	42%	0.0	100.00%	Query_7464715
primerA (Forward)	1208	1208	42%	0.0	99.70%	Query_7464714

Alignments

primerB (Reverse)

Sequence ID: Query_7464715 Length: 664 Number of Matches: 1
 Range 1: 3 to 664

Score	Expect	Identities	Gaps	Strand	Frame
1223 bits(662)	0.0()	662/662(100%)	0/662(0%)	Plus/Minus	
Features:					
Query 884	tcaagccccacctctcccccttctctctccccaggaccaccaggagccctAAGGGAGG				943
Sbjct 664	TCAAGCCCCACCTCTCCCCCTTCCTCCTCCCCAGGACCCAGGGAGGCCCTAAGGGAGG				605
Query 944	GAAAGGCGGGGACCCCCCTCATCGCCGGGGCGAACGCGAGGAGGTGGCCTCCCA				1003
Sbjct 604	GAAAGGCGGGGACCCCCCTCATCGCCGGGGCGAACGCGAGGAGGTGGCCTCCCA				545
Query 1004	GCCTCAAAGCCCTCTCGGACCCGGGACTGGGAGGAGGCGGAAAGGAGGCTTTGGAGT				1063
Sbjct 544	GCCTCAAAGCCCTCTCGGACCCGGGACTGGGAGGAGGCGGAAAGGAGGCTTTGGAGT				485
Query 1064	CTGGGCTTTCCCGGAGAAAGGCCAGGCCCTCCTCGCCCACTACCGGAAAGGAGTCCCGG				1123
Sbjct 484	CTGGGCTTTCCCGGAGAAAGGCCAGGCCCTCCTCGCCCACTACCGGAAAGGAGTCCCGG				425
Query 1124	ACCCCAAAAGGGCTGGGGGAGGTGCAGACCGACCTACCCCTCCTCTGCCCTTCCCTGA				1183
Sbjct 424	ACCCCAAAAGGGCTGGGGGAGGTGCAGACCGACCTACCCCTCCTCTGCCCTTCCCTGA				365
Query 1184	AGGCCGCGCGCTTCAAGCCCGCCACGCCCCCACTACGCCTACCTCTTACCTTCCGGG				1243
Sbjct 364	AGGCCGCGCGCTTCAAGCCCGCCACGCCCCCACTACGCCTACCTCTTACCTTCCGGG				305
Query 1244	CGCCGGGTTGAGGGCCTCGGGCCTTCCACGGCCTGGAGCTGGCCCCCTTTCGGGA				1303
Sbjct 304	CGCCGGGTTGAGGGCCTCGGGCCTTCCACGGCCTGGAGCTGGCCCCCTTTCGGGA				245
Query 1304	ACCTCCTGGAGAGGCCCTTCTACCTCTTTTCTACGCCAAGAAGCCCAAGAGGAGGCAG				1363
Sbjct 244	ACCTCCTGGAGAGGCCCTTCTACCTCTTTTCTACGCCAAGAAGCCCAAGAGGAGGCAG				185
Query 1364	AGTACCTGGGCAAGAAGATGCGCGCTACTGGACCTCTTTCGCCAAGGACGGGAGGCCA				1423
Sbjct 184	AGTACCTGGGCAAGAAGATGCGCGCTACTGGACCTCTTTCGCCAAGGACGGGAGGCCA				125
Query 1424	AGGGGTGGCCCCGCTGGCCCTCTACCGGGAGGGCCCTCCTCCTGGGGCTGGACGTCCCCC				1483
Sbjct 124	AGGGGTGGCCCCGCTGGCCCTCTACCGGGAGGGCCCTCCTCCTGGGGCTGGACGTCCCCC				65
Query 1484	TGGGGCTTCTGCCGACCTTTACGAGGAACGGTGCGGCGCCCTCGAGGTCTTGGGCTAC				1543
Sbjct 64	TGGGGCTTCTGCCGACCTTTACGAGGAACGGTGCGGCGCCCTCGAGGTCTTGGGCTAC				5
Query 1544	TC 1545				
Sbjct 4	TC 3				

primerA (Forward)

Sequence ID: Query_7464714 Length: 729 Number of Matches: 1
 Range 1: 70 to 729

Score	Expect	Identities	Gaps	Strand	Frame
1208 bits(654)	0.0()	658/660(99%)	0/660(0%)	Plus/Plus	
Features:					

```

Query 1  ATGTCGGGCGCCTCCTGCCCTTCTCGCCCTCCTGGGAGGGGCCCTCGCCAGGCCTTC 60
Sbjct 70  ATGTTGCGGCGCCTCCTGCCCTTCTCGCCCTCCTGGGAGGGGCCCTCGCCAGGCCTTC 129

Query 61  TGGTGGAGACCCCTTGGGCCGGGCCAAGGCCGCTCGAGGGCGGGCCATCGCCTTC 120
Sbjct 130  TGGTGGAGACCCCTTGGGCCGGGCCAAGGCCGCTCGAGGGCGGGCCATCGCCTTC 189

Query 121  TACGGCTCCCCTACGGCGAGGCGGAGCGGTTCCGGGCCCGAAGCCCTAAAGGCCTGG 180
Sbjct 190  TACGGCTCCCCTACGGCGAGGCGGAGCGGTTCCGGGCCCGAAGCCCTAAAGGCCTGG 249

Query 181  CCCCCGGCGTGGGCCAGGAAGCGGTGGCCTGCCCCAGGCCCGGGGATCACGGCCTGG 240
Sbjct 250  CCCCCGGCGTGGGCCAGGAAGCGGTGGCCTGCCCCAGGCCCGGGGATCACGGCCTGG 309

Query 241  TTCGGCGGCCCATCCCCCTAGAGAGGGAGGACTGCCTGGTCTCAACGTCTACCTCCCC 300
Sbjct 310  TTCGGCGGCCCATCCCCCTAGAGAGGGAGGACTGCCTGGTCTCAACGTCTACCTCCCC 369

Query 301  GCCCAGATCCCGCCCCGGGGGGGCTTCCCGTCATGGTCTACCTCCACGGCGGGGGCTTC 360
Sbjct 370  GCCCAGATCCCGCCCCGGGGGGGCTTCCCGTCATGGTCTACCTCCACGGCGGGGGCTTC 429

Query 361  ACCTCGGGGCGAGGGCCGAGCCCATCTACCGGGGCAACCGGCTTTCGGAGGAGGGGGTC 420
Sbjct 430  ACCTCGGGGCGAGGGCCGAGCCCATCTACCGGGGCAACCGGCTTTCGGAGGAGGGGGTC 489

Query 421  GTTGTGGTCGCCCCAACTACCGCCTGGGGCCTTGGGCTTCTCGCCCTTCTGCCCTC 480
Sbjct 490  GTTGTGGTCGCCCCAACTACCGCCTGGGGCCTTGGGCTTCTCGCCCTTCTGCCCTC 549

Query 481  GCCGAGGAGACCCGAAAGCGGTGGGAACTACGGGCTTTGGACGTCCTCGAGGCCCTC 540
Sbjct 550  GCCGAGGAGACCCGAAAGCGGTGGGAACTACGGGCTTTGGACGTCCTCGAGGCCCTC 609

Query 541  CGCTTCGTGAGGACTATATCCGCTACTTCGGGGGCGACCCCAAGAAGTCAACCTCTTC 600
Sbjct 610  CGCTTCGTGAGGACTATATCCGCTACTTCGGGGGCGACCCCAAGAAGTCAACCTCTTC 669

Query 601  GGGGAGTCGGCCGGGGGATGCTGGTCTGCACCTCCTCGCCACCCCGGAGGCCCGGGC 660
Sbjct 670  GGGGAGTCGGCCGGGGGATGCTGGTCTGCACCTCCTCGCCACCCCGGAGGCCCGGGC 729

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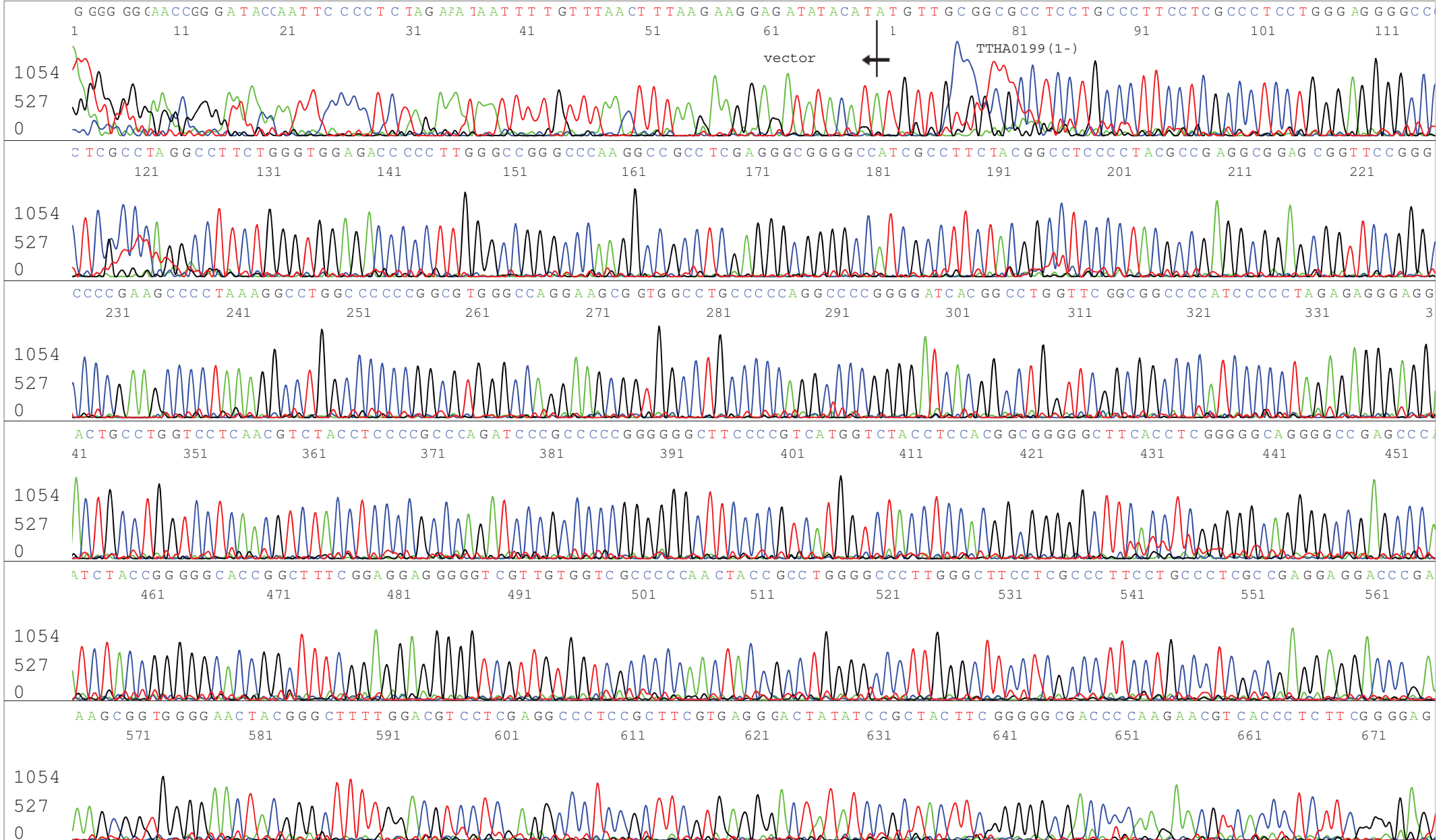
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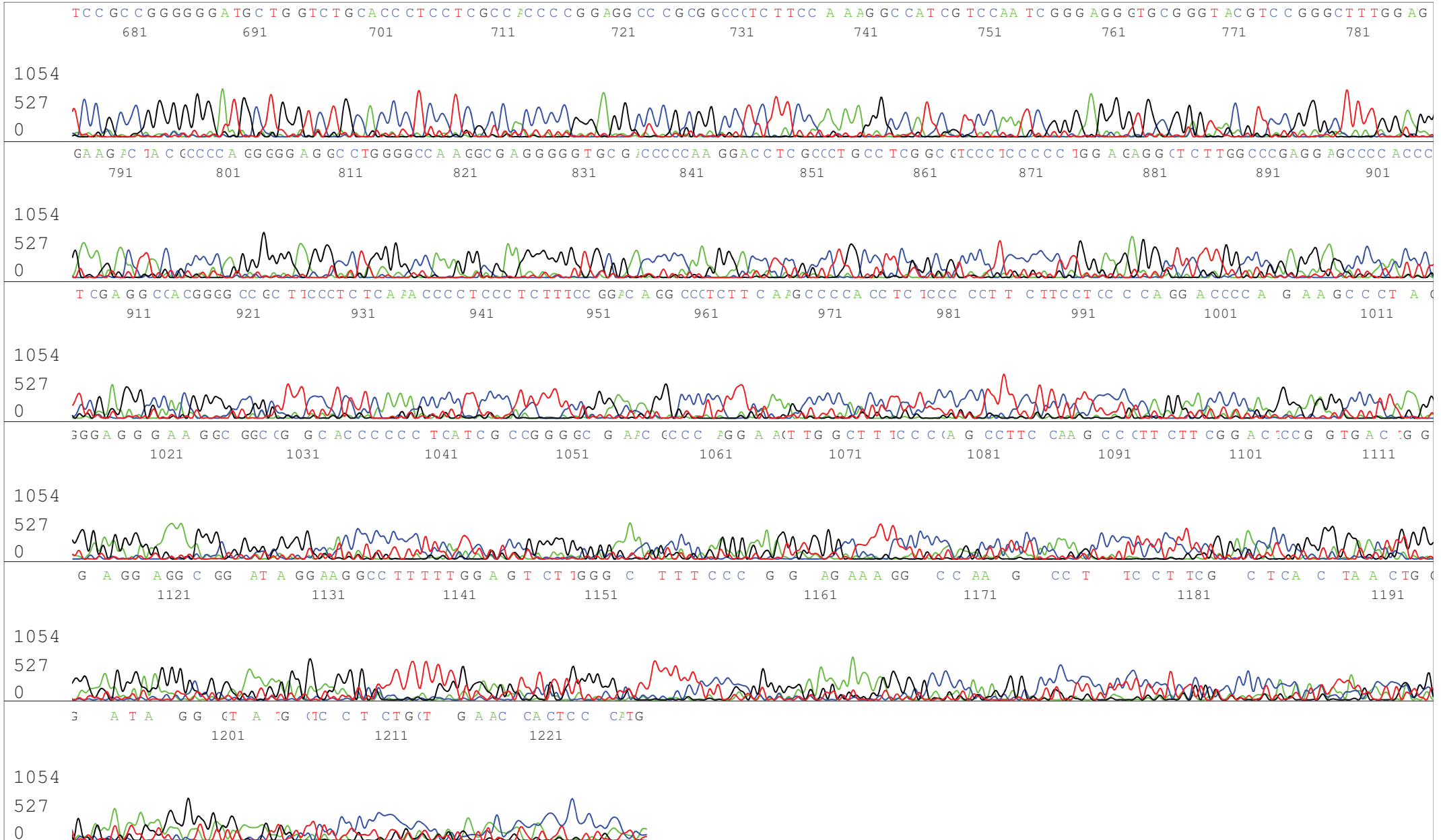
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S/N G:6 A:8 T:6 C:10
KB.bcp
KB 1.4.1.8 Cap:6

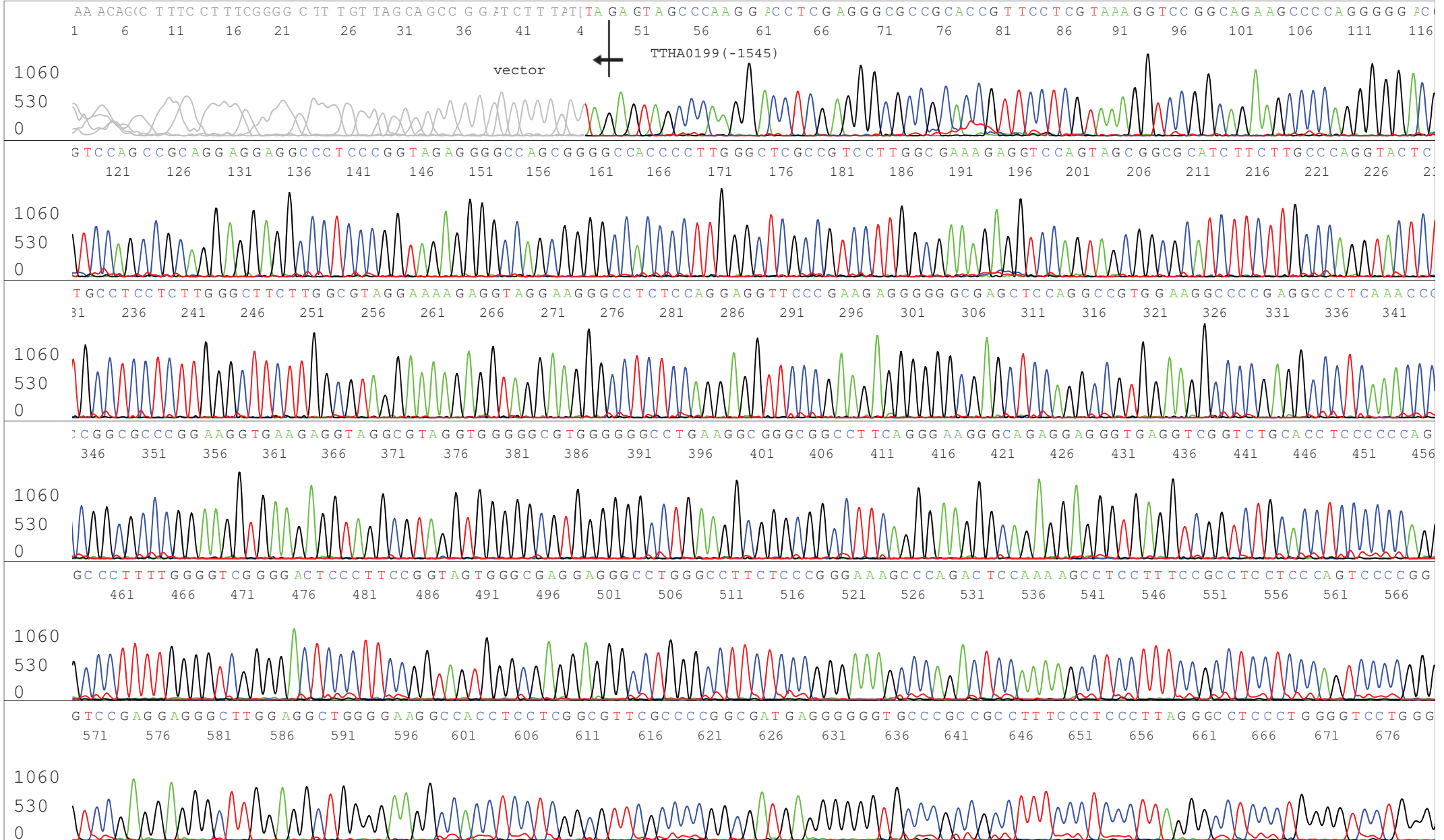


Primer B : T7 terminator

5' GCTAGTTATTGCTCAGCGG 3'

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KB_3500_POP7_BDTv3.mob
Pts 1409 to 13743 Pk1 Loc:1386
Version 6.0 HiSQV Bases: 680

Inst Model/Name 3500/3500 Instrument
Jan 09,2024 01:16PM, JST
Jan 09,2024 01:46PM, JST
Spacing:12.28 Pts/Panel1350
Plate Name: 20240109_GNP



S/N G:25 A:25 T:17 C:34
KB.bcp
KB 1.4.1.8 Cap:2

