

RIKEN Clone ID : TEx07F02 (PC010573-42)

Lot# : 6078_B3Li

Vector : pET-11a

Locus tag	TTHA0573
Insert size	1413 bp
Product	glutamyl-tRNA(Gln) amidotransferase subunit A

● **Plasmid DNA purification**

Date : 2023/12/18

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

Date : 2023/12/19

Purification : QIAGEN Miniprep kit -> dH₂O 50 ul

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

Date : 2023/12/19

DNA concentration (O.D.): 128 ng/ul

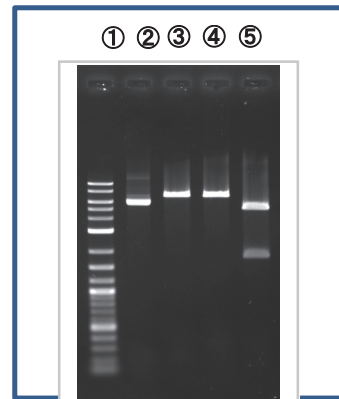
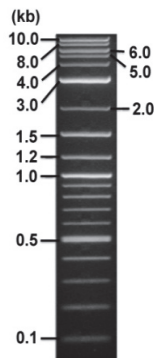
DNA	0.8	ul
Enzyme (BglII + EcoRI)	0.5 + 0.5	ul
Buffer H	1	ul
dH ₂ O	7.2	ul
Total	10	ul

< Size of fragment expected from this clone >

BglII		7.0 kb
EcoRI		7.0 kb
BglII + EcoRI	5.2	1.8 kb

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 : 2023/12/20

DNA (<u>128</u> ng/ul)	38	ul
10x TE	19	ul
dH ₂ O	137	ul
Total	195	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: Nucleotide Sequence

RID [S51GYCFH114](#) (Expires on 12-21 13:13 pm)

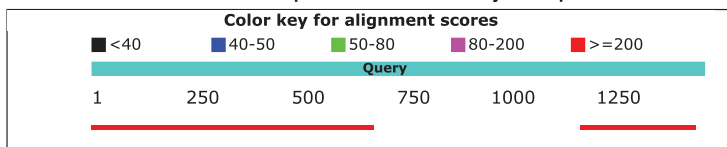
Query ID |cl|Query_21055
Description None
Molecule type dna
Query Length 1413

Subject ID 3 subjects
Description [See details](#)
Molecule type dna
Subject Length 1049
Program BLASTN 2.14.1+

TTHA0573

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)	1219	1219	46%	0.0	100.00%	Query_21058
primerB (Reverse)	490	490	18%	3e-142	100.00%	Query_21059

Alignments

primerA (Forward)

Sequence ID: Query_21058 Length: 733 Number of Matches: 1
 Range 1: 74 to 733

Score	Expect	Identities	Gaps	Strand	Frame
1219 bits(660)	0.0()	660/660(100%)	0/660(0%)	Plus/Plus	
Features:					
Query 1	ATGTTGGCCACGAGATCCGGCCCGCGGTGGCCCGGGGAGGTTTCCCCCTGGAGGTG	60			
Sbjct 74	ATGTTGGCCACGAGATCCGGCCCGCGGTGGCCCGGGGAGGTTTCCCCCTGGAGGTG	133			
Query 61	GCCGAGGCTACCTGAAACGGGTCCAGGAGCTGGACCCGGGCTCGGCGCTTCTCTCC	120			
Sbjct 134	GCCGAGGCTACCTGAAACGGGTCCAGGAGCTGGACCCGGGCTCGGCGCTTCTCTCC	193			
Query 121	CTGAACGAGAGGCTTTGGAGGAGGCGGAGGCGGTGGACCCGGGCTTCCCTGGCGGGC	180			
Sbjct 194	CTGAACGAGAGGCTTTGGAGGAGGCGGAGGCGGTGGACCCGGGCTTCCCTGGCGGGC	253			
Query 181	CTCGTGGTGGCGGTGAAGGACAACATCGCCACCGTGGCCTCCGACACCGCGGAAAGC	240			
Sbjct 254	CTCGTGGTGGCGGTGAAGGACAACATCGCCACCGTGGCCTCCGACACCGCGGAAAGC	313			
Query 241	CGCCTTCTGGAGAACTTCGTGCCCCCTACGAGGCCACCGCGGTGGCGAGGCTTAAGGCC	300			
Sbjct 314	CGCCTTCTGGAGAACTTCGTGCCCCCTACGAGGCCACCGCGGTGGCGAGGCTTAAGGCC	373			
Query 301	CTGGGCGCCCTGGTCTGGGCAAGACCAACCTGGACGAGTTGGGCATGGCTCCTCCACG	360			
Sbjct 374	CTGGGCGCCCTGGTCTGGGCAAGACCAACCTGGACGAGTTGGGCATGGCTCCTCCACG	433			
Query 361	GAGCACTCCGCTTCTTCCACCAAGAACCCCTTGACCCGGATAGGTCGCCGGGGC	420			
Sbjct 434	GAGCACTCCGCTTCTTCCACCAAGAACCCCTTGACCCGGATAGGTCGCCGGGGC	493			
Query 421	TCCAGCGGGGAAGCGCCCGCCCTTGGCCCGGACCTCGCCCGCCCTCGCCCTGGGCTCG	480			
Sbjct 494	TCCAGCGGGGAAGCGCCCGCCCTTGGCCCGGACCTCGCCCGCCCTCGCCCTGGGCTCG	553			
Query 481	GACACGGGGGAAGCGTCCGGCAGCCCGCCCTTCTGGCGGCTCAGGGCTCAAGCCC	540			
Sbjct 554	GACACGGGGGAAGCGTCCGGCAGCCCGCCCTTCTGGCGGCTCAGGGCTCAAGCCC	613			
Query 541	ACCTACGGCCGGGTGAGCCGCTTCGGCTCATCGCCTACGCCCTGAGCCTGGACAGATC	600			
Sbjct 614	ACCTACGGCCGGGTGAGCCGCTTCGGCTCATCGCCTACGCCCTGAGCCTGGACAGATC	673			
Query 601	GGCCCATGGCCGCTCCGTGCGGGACCTGGCCCTCCTCATGGACGCCCGGGCGGGCC	660			
Sbjct 674	GGCCCATGGCCGCTCCGTGCGGGACCTGGCCCTCCTCATGGACGCCCGGGCGGGCC	733			

primerB (Reverse)

Sequence ID: Query_21059 Length: 312 Number of Matches: 1
 Range 1: 48 to 312

Score	Expect	Identities	Gaps	Strand	Frame
490 bits(265)	3e-142()	265/265(100%)	0/265(0%)	Plus/Minus	
Features:					
Query 1149	octccccaccacccccaccccccttccctcggggccggcgcatccctcGCCAT	1208			
Sbjct 312	CCTCCCCACCACCCCAACCCCGCTTCCCTTCGGGGCCGGGCGCATCCCTCGCCAT	253			
Query 1209	GTACCGGAGGACCTTACACCGTGGGGCGAACCTCACGGGCTGCCCGCCCTCTCCTT	1268			

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Sbjct 252 GTACCGGGAGGACCTCTACACCGTGGGGCGAACCTCACGGGCTGCCCGCCCTCTCCTT 193
Query 1269 CCCC GGGGTTT GAGGGCACCTGCCCGTGGGCCTCCAGCTCCTCGCCCCCTGGGGGA 1328
Sbjct 192 CCCC GGGGTTT GAGGGCACCTGCCCGTGGGCCTCCAGCTCCTCGCCCCCTGGGGGA 133
Query 1329 GGACGAGAGGCTTCTTCGGGGGGCCCTCGCCTTTGAGGAGGCCACGGCCGGGGCCCACT 1388
Sbjct 132 GGACGAGAGGCTTCTTCGGGGGGCCCTCGCCTTTGAGGAGGCCACGGCCGGGGCCCACT 73
Query 1389 CAAGGCCCCCTTGGGGGAGGCCCTC 1413
Sbjct 72 CAAGGCCCCCTTGGGGGAGGCCCTC 48

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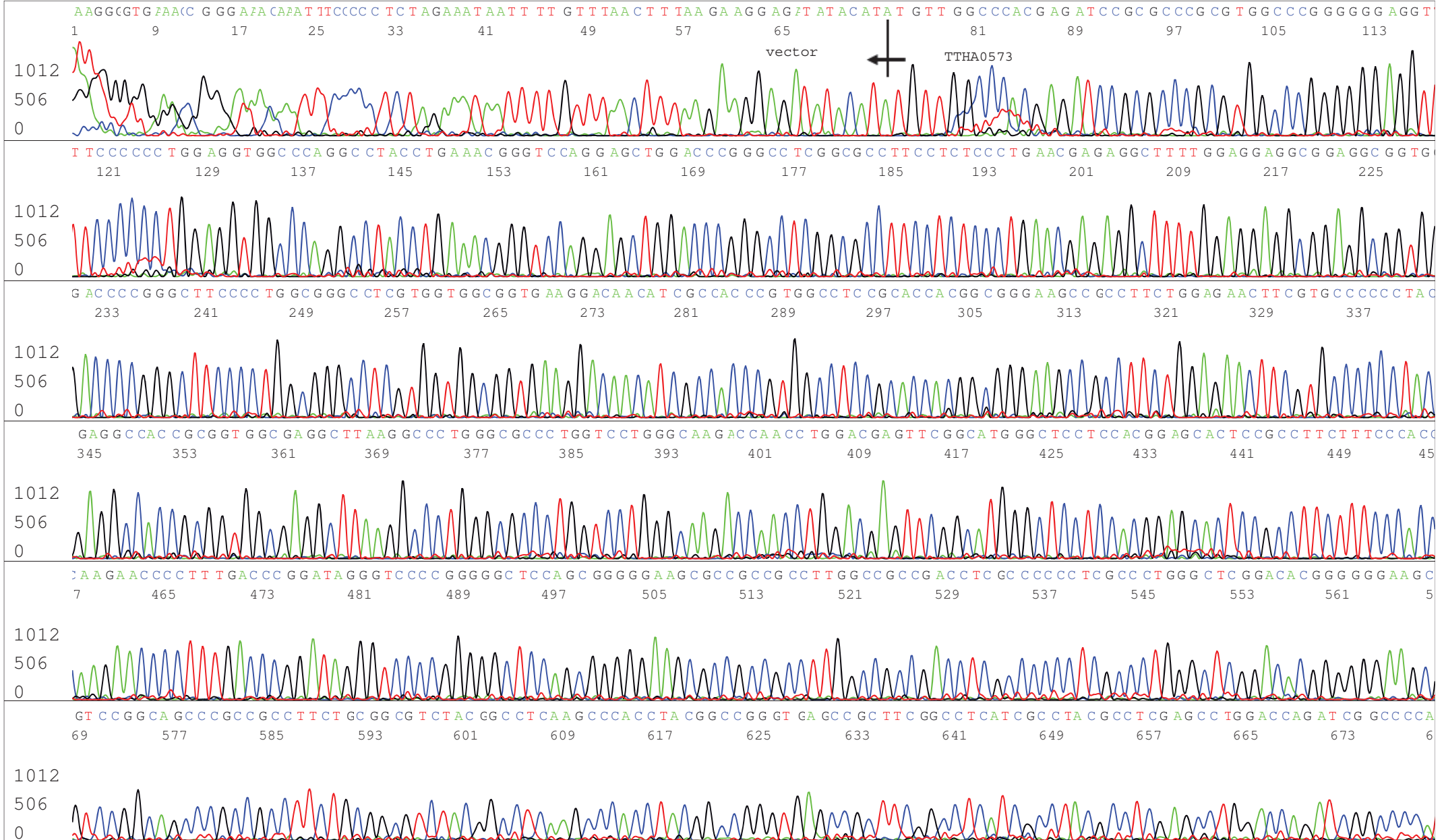


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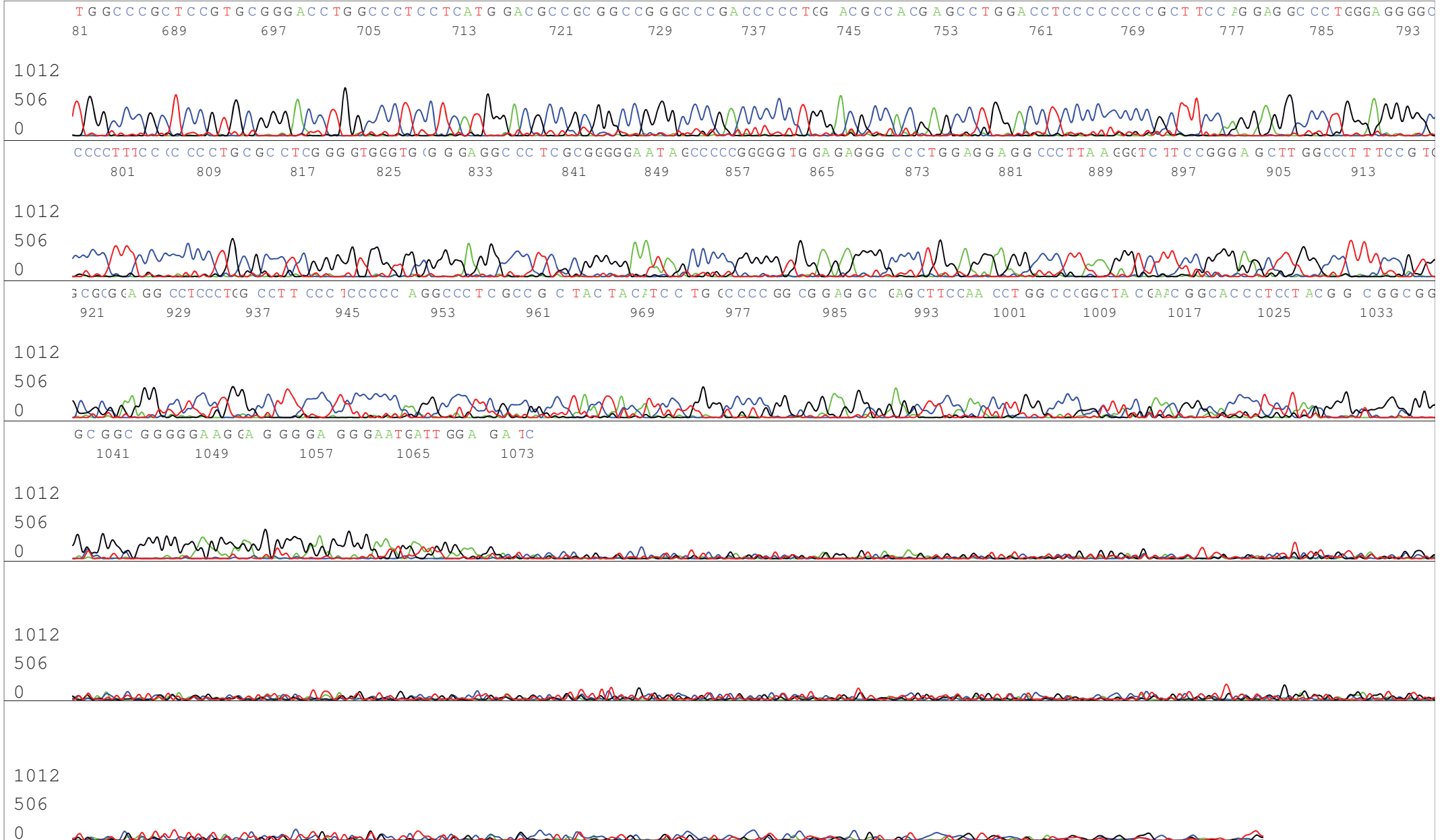
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S/N G:8 A:9 T:7 C:12
KB.bcp
KB 1.4.1.8 Cap:3



S/N G:82 A:23 T:15 C:30
KB.bcp
KB 1.4.1.8 Cap:4

Primer B : T7 terminator
5' GCTAGTTATTGCTCAGCGG 3'

