

**RIKEN Clone ID : MMTD00041**

Lot# :C0

Vector : pGEM T Easy

<i>Gene</i>	<b>NR4A2</b>
<i>Insert sequence</i>	<b>611 bp</b>

● Transformation

Date : 2024/07/03

Competent cell (DH5 alpha) 10µl  
Plasmid DNA 0.5µl  
SOC 100µl

● Plasmid DNA purification

Date : 2024/07/03

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

Date : 2024/07/04

Purification : QIAGEN Miniprep kit -> TE 50 ul

● Digestion by restriction enzyme/Concentration calibration

Date : 2024/07/04

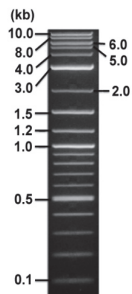
DNA concentration (O.D.): 582 ng/ul

< Size of fragment expected from this clone >

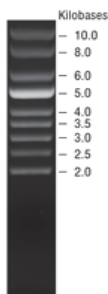
DNA	0.2	ul
Enzyme (EcoRI)	1	ul
Buffer H	1	ul
dH <sub>2</sub> O	7.8	ul
Total	10	ul

EcoRI 3.0 kb (vector) 0.5, 0.1 kb

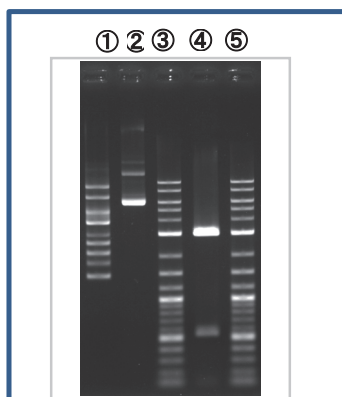
Electrophoresis : 1% agarose gel, 1x TAE Buffer



Marker1 : 1 kb Plus DNA Ladder (NEB#N3200L)



Marker2 : Supercoiled DNA Ladder



①:Marker2  
②:uncut  
③:Marker1  
④:EcoRI cut  
⑤:Marker1

● Confirmation of the sequence

Date : 2024/07/05

Shipping amount : 40 ul

Concentration at the time of preparation of plasmid DNA : 25 ng/ul

Date : 2024/07/09

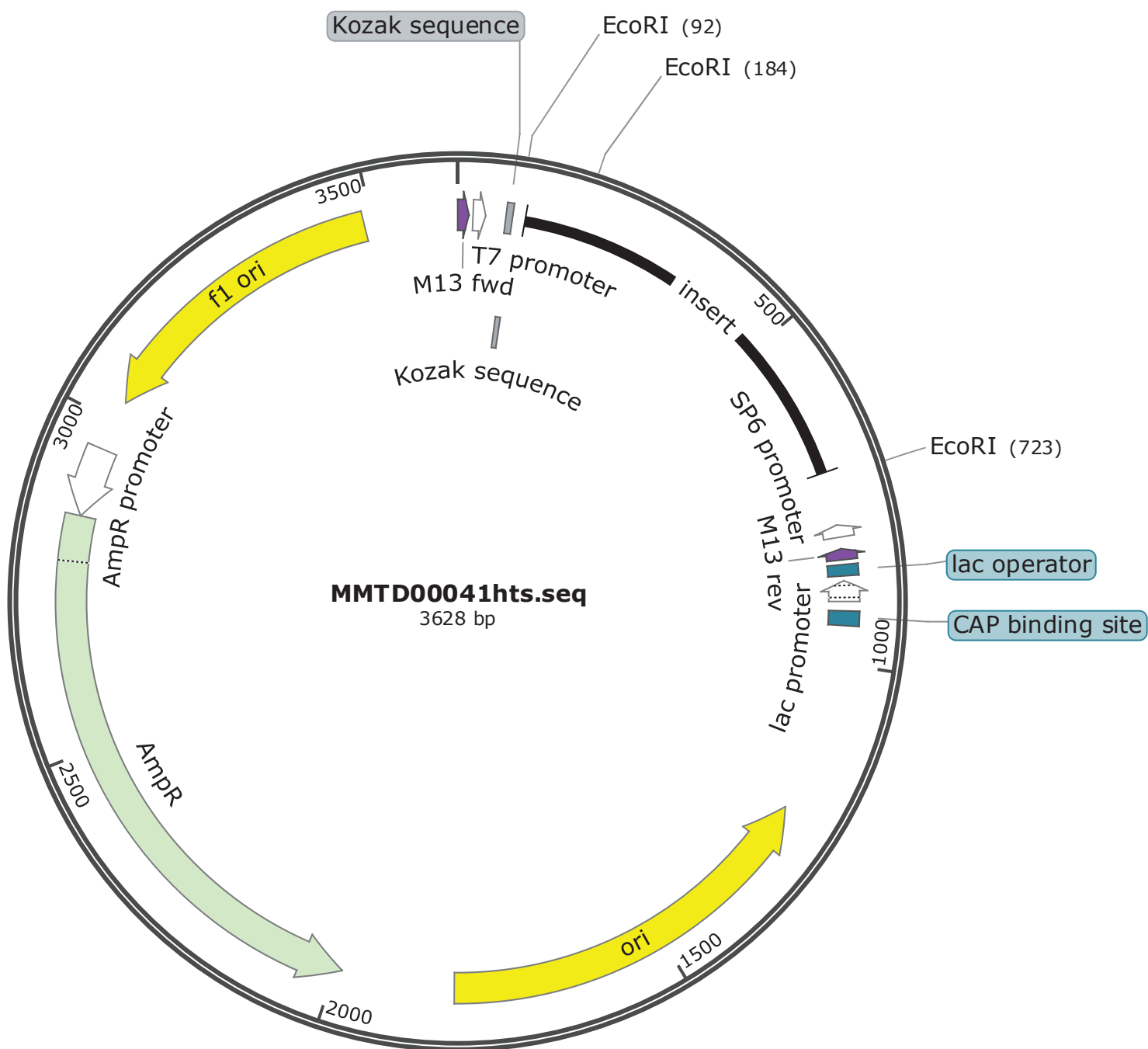
Primer A	-
Primer B	-
Primer C	MMTD00041hts.seq
List of Sequencing Primers	

DNA 582 ng/ul)	44	ul
10x TE	102	ul
dH <sub>2</sub> O	878	ul
Total	1,024	ul



APPROVED BY :

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



BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: Nucleotide Sequence

RID [8EW1DFPN114](#) (Expires on 07-06 12:01 pm)

Query ID Icl|Query\_5702989  
 Description None  
 Molecule type dna  
 Query Length 611

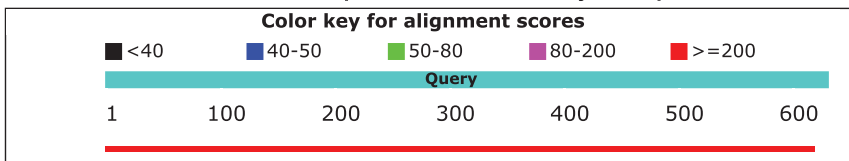
Subject ID Icl|Query\_5702991  
 Description None  
[See details](#)  
 Molecule type dna  
 Subject Length 3628  
 Program BLASTN 2.16.0+

MMTD00041 insert seq

MMTD00041 hts.seq

[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	1129	1129	100%	0.0	100.00%	Query_5702991

[Alignments](#)

Sequence ID: Query\_5702991 Length: 3628 Number of Matches: 1  
 Range 1: 102 to 712

Score	Expect	Identities	Gaps	Strand	Frame
1129 bits(611)	0.0()	611/611(100%)	0/611(0%)	Plus/Minus	

Features:

Query 1	TCGCTGT CAGTACTGTCGATTT CAGAAGTGCCTGGCTGTTGGGATGGTCAAAGAAGTGGT	60
Sbjct 712	TCGCTGT CAGTACTGTCGATTT CAGAAGTGCCTGGCTGTTGGGATGGTCAAAGAAGTGGT	653
Query 61	TCGCACAGACAGTTTAAAAGGCCGGAGAGGTCGTTTGCCTCGAAACCGAAGAGCCACACA	120
Sbjct 652	TCGCACAGACAGTTTAAAAGGCCGGAGAGGTCGTTTGCCTCGAAACCGAAGAGCCACACA	593
Query 121	GGAGCCCTCTCCCCCTTCGCCCCCGGTGAGTCTGATCAGTGCCCTCGTCAGGGCCCATGT	180
Sbjct 592	GGAGCCCTCTCCCCCTTCGCCCCCGGTGAGTCTGATCAGTGCCCTCGTCAGGGCCCATGT	533
Query 181	CGACTCCAACCCGGCTATGACCAGCCTGGACTATTCAGGTTCCAGGCGAACCCCTGACTA	240
Sbjct 532	CGACTCCAACCCGGCTATGACCAGCCTGGACTATTCAGGTTCCAGGCGAACCCCTGACTA	473
Query 241	TCAGATGAGTGGAGATGACACCCAGCATATCCAGCAATTCATGATCTCCTGACTGGCTC	300
Sbjct 472	TCAGATGAGTGGAGATGACACCCAGCATATCCAGCAATTCATGATCTCCTGACTGGCTC	413
Query 301	CATGGAGATCATCCGGGGCTGGGCAGAGAAGATCCCTGGCTTCGCAGACTTGCCCAAAGC	360
Sbjct 412	CATGGAGATCATCCGGGGCTGGGCAGAGAAGATCCCTGGCTTCGCAGACTTGCCCAAAGC	353

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Query 361 CGACCAGGACCTGCTTTTTGAATCAGCTTTCTTAGAACTATTTGTCCTTCGATTAGCATA 420
Sbjct 352 CGACCAGGACCTGCTTTTTGAATCAGCTTTCTTAGAACTATTTGTCCTTCGATTAGCATA 293
Query 421 CAGGTCCAACCCAGTGGAGGGTAAACTCATCTTTTGAATGGGGTGGTCTTGCACAGGTT 480
Sbjct 292 CAGGTCCAACCCAGTGGAGGGTAAACTCATCTTTTGAATGGGGTGGTCTTGCACAGGTT 233
Query 481 GCAATGTGTTTCGTGGCTTTGGGGAATGGATTGATTCCATTGTTGAATTCTCCTCCAATT 540
Sbjct 232 GCAATGTGTTTCGTGGCTTTGGGGAATGGATTGATTCCATTGTTGAATTCTCCTCCAATT 173
Query 541 GCAGAAATGAACATCGACATTTCTGCCTTCTCCTGCATTGCTGCCCTGGCTATGGTCAC 600
Sbjct 172 GCAGAAATGAACATCGACATTTCTGCCTTCTCCTGCATTGCTGCCCTGGCTATGGTCAC 113
Query 601 AGAGAGACACG 611
Sbjct 112 AGAGAGACACG 102

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