NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARi78G04

Lot# : 7675_B4Hk

Vector : pGCAP10

Gene	BMPER	
RefSeq_mRNA	NM_133468.5	5582 bp

● Plasmid DNA purification

Date : 2024/08/22

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

Date : 2024/08/23

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/08/23

DNA concentration (O.D.): 178 ng/ul

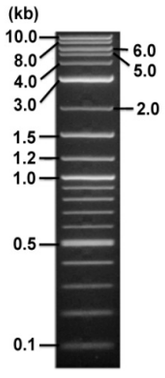
DNA	0.55 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.45 ul
Total	10 ul

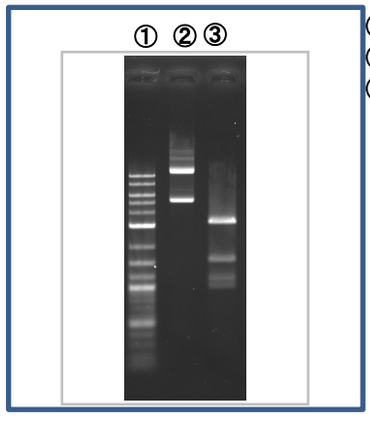
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.5, 1.1, 1.0 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

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





①:Marker
②:uncut
③:BamHI

● Confirmation of the sequence

Date : 2024/09/04

Primer A	-
Primer B	-
Primer C	ARi78G04hts01.seq
List of Sequencing Primers	-

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/09/06

DNA (178 ng/ul)	80 ul
10x TE	57 ul
dH_2O	433 ul
Total	570 ul

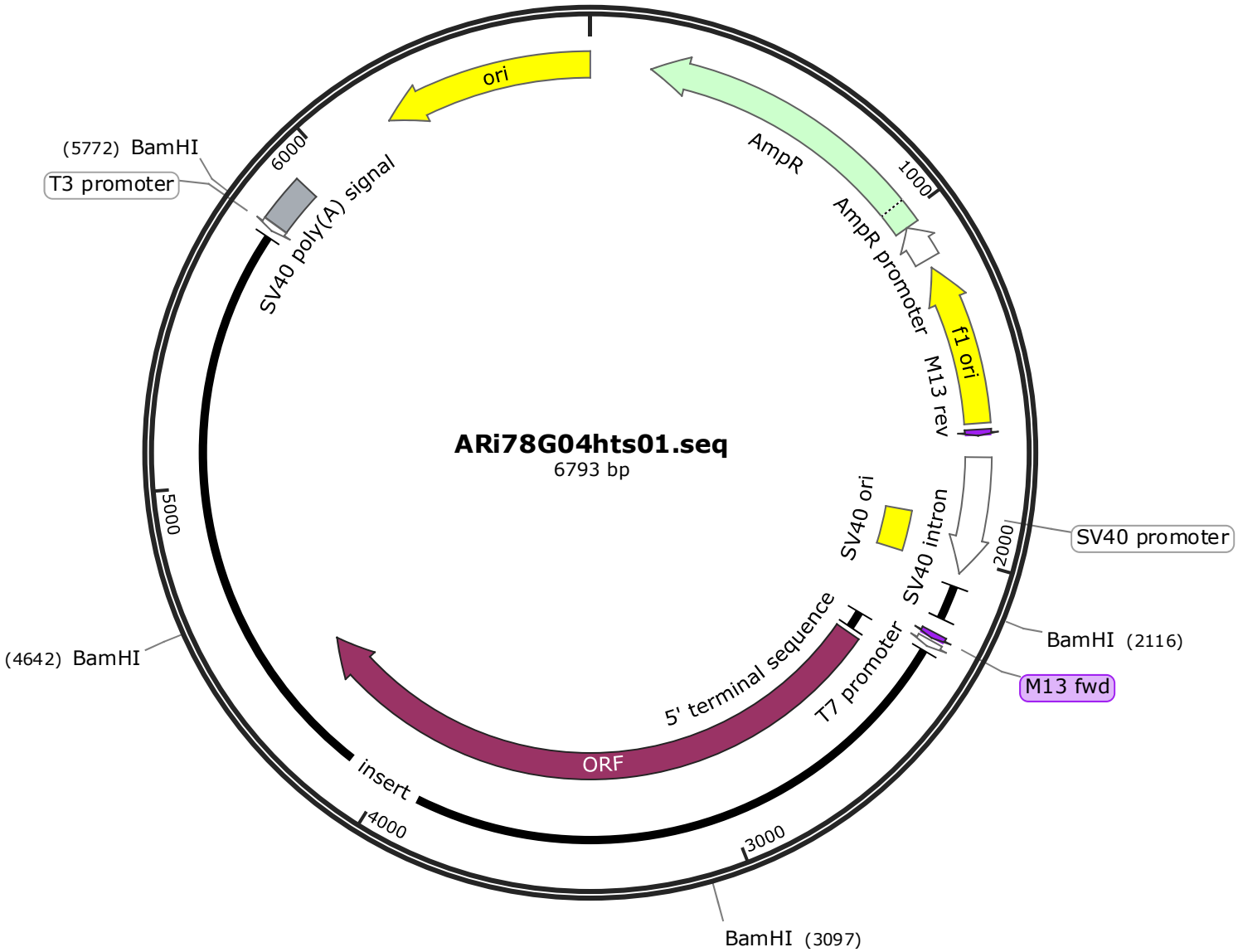
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '24.09.06 笹沼

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


ARi78G04hts01.seq
6793 bp
ori
AmpR
AmpR promoter
M13 rev
f1 ori
SV40 ori
SV40 intron
SV40 promoter
BamHI (2116)
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
BamHI (3097)
(4642) BamHI
T3 promoter
(5772) BamHI
SV40 poly(A) signal
1000
2000
3000
4000
5000
6000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_133468:Homo sapiens BMP binding endothelial...

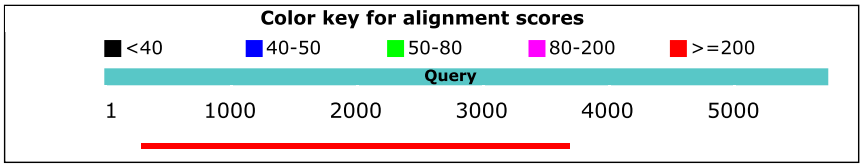
RID DF8KHS26114 (Expires on 09-05 07:57 am)

Query ID	NM_133468.5	**Subject ID**	lcl|Query_6225057
Description	Homo sapiens BMP binding endothelial regulator (BMPER), transcript variant 2, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	5582	**Subject Length**	6793
		Program	BLASTN 2.16.0+

ARe78G04hts01.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	6167	6167	60%	0.0	99.85%	Query_6225057

Alignments

Sequence ID: Query_6225057 Length: 6793 Number of Matches: 1
Range 1: 2281 to 5636

Score	Expect	Identities	Gaps	Strand	Frame
6167 bits(3339)	0.0()	3351/3356(99%)	3/3356(0%)	Plus/Plus	

Features:

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Query                296  GACTGTGAGCTGCGGCAGCTGAGCAGAGGCGGCGGCGCGGGACCTGCAGTCGCCAGGGAT  355
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2281  GACTGTGAGCTGCGGCAGCTGAGCAGAGGCGGCGGCGCGGGACCTGCAGTCGCCAGGGAT  2340

CDS:BMP-binding endo 1                    M  L  W  F  S  G  V  G  A  L  A  E  R  Y  C
Query                356  TCCCTCCAGGTGACGATGCTCTGGTTCTCCGGCGTCGGGGCTCTGGCTGAGCGTTACTGC  415
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2341  TCCCTCCAGGTGACGATGCTCTGGTTCTCCGGCGTCGGGGCTCTGGCTGAGCGTTACTGC  2400

CDS:BMP-binding endo 16    R  R  S  P  G  I  T  C  C  V  L  L  L  L  N  C  S  G  V  P
Query                416  CGCCGCTCGCCTGGGATTACGTGCTGCGTCTTGCTGCTACTCAATTGCTCGGGGGTCCCC  475
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2401  CGCCGCTCGCCTGGGATTACGTGCTGCGTCTTGCTGCTACTCAATTGCTCGGGGGTCCCC  2460

CDS:BMP-binding endo 36    M  S  L  A  S  S  F  L  T  G  S  V  A  K  C  F  N  E  G  E
Query                476  ATGTCTCTGGCTTCCTCCTTCTTGACAGGTTCTGTTGCAAAATGTGAAAATGAAGGTGAA  535
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2461  ATGTCTCTGGCTTCCTCCTTCTTGACAGGTTCTGTTGCAAAATGTGAAAATGAAGGTGAA  2520

CDS:BMP-binding endo 56    V  L  Q  I  P  F  I  T  D  N  P  C  I  M  C  V  C  L  N  K
Query                536  GTCCTCCAGATTCCATTTATCACAGACAACCCTTGCATAATGTGTGTCTGCTTGAACAAG  595
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2521  GTCCTCCAGATTCCATTTATCACAGACAACCCTTGCATAATGTGTGTCTGCTTGAACAAG  2580
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CDS:BMP-binding endo  76    E  V  T  C  K  R  E  K  C  P  V  L  S  R  D  C  A  L  A  I
Query                 596   GAAGTGACATGTAAGAGAGAAGTGCCCCGTGCTGTCCCGAGACTGTGCCCTGGCCATC  655
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2581  GAAGTGACATGTAAGAGAGAAGTGCCCCGTGCTGTCCCGAGACTGTGCCCTGGCCATC  2640

CDS:BMP-binding endo  96    K  Q  R  G  A  C  C  E  Q  C  K  G  C  T  Y  E  G  N  T  Y
Query                 656   AAGCAGAGGGGAGCCTGTTGTGAACAGTGCAAAGGTTGCACCTATGAAGGAAATACCTAT  715
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2641  AAGCAGAGGGGAGCCTGTTGTGAACAGTGCAAAGGTTGCACCTATGAAGGAAATACCTAT  2700

CDS:BMP-binding endo  116   N  S  S  F  K  W  Q  S  P  A  E  P  C  V  L  R  Q  C  Q  F
Query                 716   AACAGCTCCTTCAAATGGCAGAGCCCGGCTGAGCCTTGTGTTCTACGCCAGTGCCAGGAG  775
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2701  AACAGCTCCTTCAAATGGCAGAGCCCGGCTGAGCCTTGTGTTCTACGCCAGTGCCAGGAG  2760

CDS:BMP-binding endo  136   G  V  V  T  E  S  G  V  R  C  V  V  H  C  K  N  P  L  F  H
Query                 776   GGCGTTGTCACAGAGTCTGGGGTGCGCTGTGTTGTTCATTGTAAAAACCCTTTGGAGCAT  835
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2761  GGTGTTGTCACAGAGTCTGGGGTGCGCTGTGTTGTTCATTGTAAAAACCCTTTGGAGCAT  2820

CDS:BMP-binding endo  156   L  G  M  C  C  P  T  C  P  G  C  V  F  E  G  V  Q  Y  Q  E
Query                 836   CTGGGAATGTGCTGCCCCACATGTCCAGGCTGTGTGTTTGAGGGTGTGCAGTATCAAGAA  895
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2821  CTGGGAATGTGCTGCCCCACATGTCCAGGCTGTGTGTTTGAGGGTGTGCAGTATCAAGAA  2880

CDS:BMP-binding endo  176   G  E  E  F  Q  P  E  G  S  K  C  T  K  C  S  C  T  G  G  R
Query                 896   GGGGAGGAATTTCAGCCAGAAGGAAGCAAATGTACCAAGTGTTCCTGCACTGGAGGCAGG  955
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2881  GGGGAGGAATTTCAGCCAGAAGGAAGCAAATGTACCAAGTGTTCCTGCACTGGAGGCAGG  2940

CDS:BMP-binding endo  196   T  Q  C  V  R  E  V  C  P  I  L  S  C  P  Q  H  L  S  H  I
Query                 956   ACACAATGTGTGAGAGAAGTCTGTCCCATTCTCTCCTGTCCCCAGCACCTTAGTCACATA  1015
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2941  ACACAATGTGTGAGAGAAGTCTGTCCCATTCTCTCCTGTCCCCAGCACCTTAGTCACATA  3000

CDS:BMP-binding endo  216   P  P  G  Q  C  C  P  K  C  L  G  Q  R  K  V  F  D  L  P  F
Query                 1016  CCCCCAGGACAGTGCTGCCCCAAATGTTTGGGTCAGAGGAAAGTGTTTGACCTCCCTTTT  1075
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3001  CCCCCAGGACAGTGCTGCCCCAAATGTTTGGGTCAGAGGAAAGTGTTTGACCTCCCTTTT  3060

CDS:BMP-binding endo  236   G  S  C  L  F  R  S  D  V  Y  D  N  G  S  S  F  L  Y  D  N
Query                 1076  GGGAGCTGCCTCTTTCGAAGTGATGTTTATGACAATGGATCCTCATTTCTGTACGATAAC  1135
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3061  GGGAGCTGCCTCTTTCGAAGTGATGTTTATGACAATGGATCCTCATTTCTGTACGATAAC  3120

CDS:BMP-binding endo  256   C  T  A  C  T  C  R  D  S  T  V  V  C  K  R  K  C  S  H  P
Query                 1136  TGCACAGCTTGTACCTGCAGGGACTCTACTGTGGTTTGCAAGAGGAAGTGCTCCCACCCT  1195
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Sbjct                 3121  TGCACAGCTTGTACCTGCAGGGACTCTACTGTGGTTTGCAAGAGGAAGTGCTCCCACCCT  3180

CDS:BMP-binding endo  276   G  G  C  D  Q  G  Q  E  G  C  C  E  E  C  L  L  R  V  P  P
Query                 1196  GGTGGCTGTGACCAAGGCCAGGAGGGCTGTTGTGAAGAGTGCCTCCTACGAGTGCCCCCA  1255
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Sbjct                 3181  GGTGGCTGTGACCAAGGCCAGGAGGGCTGTTGTGAAGAGTGCCTCCTACGAGTGCCCCCA  3240

CDS:BMP-binding endo  296   E  D  I  K  V  C  K  F  G  N  K  I  F  Q  D  G  E  M  W  S
Query                 1256  GAAGACATCAAAGTATGCAAATTTGGCAACAAGATTTTCCAGGATGGAGAGATGTGGTCC  1315
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Sbjct                 3241  GAAGACATCAAAGTATGCAAATTTGGCAACAAGATTTTCCAGGATGGAGAGATGTGGTCC  3300

CDS:BMP-binding endo  316   S  I  N  C  T  I  C  A  C  V  K  G  R  T  E  C  R  N  K  Q
Query                 1316  TCTATCAATTGTACCATCTGTGCTTGTGTGAAAGGCAGGACGGAGTGTCGCAATAAGCAG  1375
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3301  TCTATCAATTGTACCATCTGTGCTTGTGTGAAAGGCAGGACGGAGTGTCGCAATAAGCAG  3360

CDS:BMP-binding endo  336   C  I  P  I  S  S  C  P  Q  G  K  I  L  N  R  K  G  C  C  P
Query                 1376  TGCATTCCCATCAGTAGCTGCCCACAGGGCAAAATTCTCAACAGAAAAGGATGCTGTCCT  1435
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3361  TGCATTCCCATCAGTAGCTGCCCACAGGGCAAAATTCTCAACAGAAAAGGATGCTGTCCT  3420

CDS:BMP-binding endo  356   I  C  T  E  K  P  G  V  C  T  V  F  G  D  P  H  Y  N  T  F
Query                 1436  ATTTGCACTGAAAAGCCCGGCGTTTGCACGGTGTTTGGAGATCCCCACTACAACACTTTT  1495
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3421  ATTTGCACTGAAAAGCCCGGCGTTTGCACGGTGTTTGGAGATCCCCACTACAACACTTTT  3480

CDS:BMP-binding endo  376   D  G  R  T  F  N  F  Q  G  T  C  Q  Y  V  L  T  K  D  C  S
Query                 1496  GACGGTCGGACATTTAACTTTCAGGGGACGTGTCAGTACGTTTTGACAAAAGACTGCTCC  1555
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3481  GACGGTCGGACATTTAACTTTCAGGGGACGTGTCAGTACGTTTTGACAAAAGACTGCTCC  3540

CDS:BMP-binding endo  396   S  P  A  S  P  F  Q  V  L  V  K  N  D  A  R  R  T  R  S  F
Query                 1556  TCCCCTGCCTCGCCCTTCCAGGTGCTGGTGAAGAACGACGCCCGCCGGACACGCTCCTTC  1615
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Sbjct                 3541  TCCCCTGCCTCGCCCTTCCAGGTGCTGGTGAAGAACGACGCCCGCCGGACACGCTCCTTC  3600

CDS:BMP-binding endo  416   S  W  T  K  S  V  E  L  V  L  G  E  S  R  V  S  L  Q  Q  H
Query                 1616  TCGTGGACCAAGTCGGTGGAGCTGGTGCTGGGCGAGAGCAGGGTCAGCCTGCAGCAGCAC  1675
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3601  TCGTGGACCAAGTCGGTGGAGCTGGTGCTGGGCGAGAGCAGGGTCAGCCTGCAGCAGCAC  3660

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Query                 1676  CTCACCGTGCGCTGGAACGGCTCGCGCATCGCGCTCCCCTGCCGCGCGCCACACTTCCAC  1735
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query                 1736  ATCGACCTGGATGGCTACCTCTTGAAAGTGACCACCAAAGCAGGTTTGGAAATATCTTGG  1795
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Sbjct                 3721  ATCGACCTGGATGGCTACCTCTTGAAAGTGACCACCAAAGCAGGTTTGGAAATATCTTGG  3780

CDS:BMP-binding endo  476   D  G  D  S  F  V  E  V  M  A  A  P  H  L  K  G  K  L  C  G
Query                 1796  GATGGAGACAGTTTTGTAGAAGTCATGGCTGCGCCGCATCTCAAGGGCAAGCTCTGTGGT  1855
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 3781  GATGGAGACAGTTTTGTAGAAGTCATGGCTGCGCCGCATCTCAAGGGCAAGCTCTGTGGT  3840

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Query                 1916  AAGTTTGATGTGGATGACTTTGCTGAATCTTGGAGGGTGGAGTCCAATGAGTTCTGCAAC  1975
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Sbjct                 3901  AAGTTTGATGTGGATGACTTTGCTGAATCTTGGAGGGTGGAGTCCAATGAGTTCTGCAAC  3960

CDS:BMP-binding endo  536   R  P  Q  R  K  P  V  P  E  L  C  Q  G  T  V  K  V  K  L  R
Query                 1976  AGACCTCAGAGAAAGCCAGTGCCTGAACTGTGTCCAAGGGACAGTCAAGGTAAAGCTCCGG  2035
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Sbjct                3961  AGACCTCAGAGAAAGCCAGTGCCTGAACTGTGTCAAGGGACAGTCAAGGTAAAGCTCCGG  4020

CDS:BMP-binding endo  556    A  H  R  E  C  Q  K  L  K  S  W  E  F  Q  T  C  H  S  T  V
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Sbjct                4021  GCCCATCGAGAATGCCAAAAGCTCAAATCCTGGGAGTTTCAGACCTGCCACTCGACTGTG  4080

CDS:BMP-binding endo  576    D  Y  A  T  F  Y  R  S  C  V  T  D  M  C  E  C  P  V  H  K
Query                2096  GACTACGCCACTTTCTACCGGTCCTGTGTGACAGACATGTGTGAATGTCCAGTCCATAAA  2155
Sbjct                4081  GACTACGCCACTTTCTACCGGTCCTGTGTGACAGACATGTGTGAATGTCCAGTCCATAAA  4140

CDS:BMP-binding endo  596    N  C  Y  C  E  S  F  L  A  Y  T  R  A  C  Q  R  E  G  I  K
Query                2156  AACTGTTATTGCGAGTCATTTTTGGCATATACCCGGGCCTGCCAGAGAGAGGGCATCAAA  2215
Sbjct                4141  AACTGTTATTGCGAGTCATTTTTGGCATATACCCGGGCCTGCCAGAGAGAGGGCATCAAA  4200

CDS:BMP-binding endo  616    V  H  W  E  P  Q  Q  N  C  A  A  T  Q  C  K  H  G  A  V  Y
Query                2216  GTCCACTGGGAGCCTCAGCAGAATTGTGCAGCCACCCAGTGTAAGCATGGTGCTGTGTAC  2275
Sbjct                4201  GTCCACTGGGAGCCTCAGCAGAATTGTGCAGCCACCCAGTGTAAGCATGGTGCTGTGTAC  4260

CDS:BMP-binding endo  636    D  T  C  G  P  G  C  I  K  T  C  D  N  W  N  E  I  G  P  C
Query                2276  GATACCTGTGGTCCGGGATGTATCAAGACGTGTGACAACTGGAATGAAATTGGTCCATGC  2335
Sbjct                4261  GATACCTGTGGTCCGGGATGTATCAAGACCTGTGACAACTGGAATGAAATTGGTCCATGC  4320

CDS:BMP-binding endo  656    N  K  P  C  V  A  G  C  H  C  P  A  N  L  V  L  H  K  G  R
Query                2336  AACAAGCCGTGCGTTGCTGGGTGCCACTGTCCAGCAAACTTGGTCCTTCACAAGGGAAGG  2395
Sbjct                4321  AACAAGCCGTGCGTTGCTGGGTGCCACTGTCCAGCAAACTTGGTCCTTCACAAGGGAAGG  4380

CDS:BMP-binding endo  676    C  I  K  P  V  L  C  P  Q  R
Query                2396  TGCATCAAGCCAGTCCTTTGTCCCCAGCGGTGACCTTTGTTTCGATCCTTAAGACTCTGA  2455
Sbjct                4381  TGCATCAAGCCAGTCCTTTGTCCCCAGCGGTGACCTTTGTTTCGATCCTTAAGACTCTGA  4440

Query                2456  AATCTGGTGACTTTGACACTGAAGCGGAAGAGCCAATGAAGGACTGCAGTATTTGTGTGC  2515
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Query                2516  CCGATTCTGTAAacacacacacacaGAGtatatatgtg--tatatatatatagatatatT  2573
Sbjct                4501  CCGATTCTGTAAACACACACACACAGAGTATATATGTGTATATATATATATAGATATATT  4560

Query                2574  CAAAAACATTGCATCATTTATATGAACTATAGGGGGATTATTATATGTATATTTTTTGCT  2633
Sbjct                4561  CAAAAACATTGCATCATTTATATGAACTATAGGGGGATTATTATATGTATATTTTTTGCT  4620

Query                2634  ATAAGACATGTATTGTTTCTAGGATCCTAACCTGTAAGCCATTGAACATGTTGTATAAAT  2693
Sbjct                4621  ATAAGACATGTATTGTTTCTAGGATCCTAACCTGTAAGCCATTGAACATGTTGTATAAAT  4680

Query                2694  ACACCAGGTGTTTTTAATTTAATAAGGTGGCATGCAGATACATTGGATAGTGTTAACATC  2753
Sbjct                4681  ACACCAGGTGTTTTTAATTTAATAAGGTGGCATGCAGATACATTGGATAGTGTTAACATC  4740

Query                2754  ACATACATTTGTCATTTTTAAGGAAGTTTTCTAAGAGCCCTCAATTGCCTGCCTGTATTA  2813
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Sbjct                4741  ACATACATTTGTCATTTTTAAGGAAGTTTTCTAAGAGCCCTCAATTGCCTGCCTGTATTA  4800

Query                2814  ATTTTAGTTTTGAGTCAGGATTTGTAATGGAGTGGGAAATGTGTTTCTCTGGAGAAGGGC  2873
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Query                2874  ACATTTATCTAGGGGCATTTCAGGTTTCCAAAGAAAGGAATGTATGCCTGGGAAAGACAG  2933
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Query                2934  CAGGAGATTGGTGACCGGCCCTAATGGTGCATGAAAAGCGAGTGATAGGCTGTTAGAATG  2993
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Query                2994  TATTAGGTCATGGGCTAACATTATTTCCAAAATTGATTGGCTGGTTGCCAAGAAATATAT  3053
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Query                3054  ATTTGTCACTAGGGCATAACCGAAGAATCAAGTGATTTCTTGCCATCCTTGCGTAGTCCT  3113
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Query                3114  CAAGTCTTCTAATCATCTATGTGTGTATGATGGATGTGACCATTTATATGTCATGTGTTG  3173
Sbjct                5101  CAAGTCTTCTAATCATCTATGTGTGTATGATGGATGTGACCATTTATATGTCATGTGTTG  5160

Query                3174  AAATTAAAGGGTGTCTGGATGCCATGTTAATTTTATTGAGCATGAGAAAGTATTTGAAGA  3233
Sbjct                5161  AAATTAAAGGGTGTCTGGATGCCATGTTAATTTTATTGAGCATGAGAAAGTATTTGAAGA  5220

Query                3234  AACTGTTGCACAACATATGATGAAATTTTGATTTCTCTGAATCTCAGAGTAATTTAAGAT  3293
Sbjct                5221  AACTGTTGCACAACATATGATGAAATTTTGATTTCTCTGAATCTCAGAGTAATTTAAGAT  5280

Query                3294  GGGCAAATCCAATGAGTTGATGTAACCCATCTACATTTTGTGGCTATTTCATGTATAAAA  3353
Sbjct                5281  GGGCAAATCCAATGAGTTGATGTAACCCATCTACATTTTGTGGCTATTTCATGTATAAAA  5340

Query                3354  TGAAAGGCTTTAGTTATTTCTAGAGGAGTCCCATCCAACACTATTTGGCGACTGTTAATA  3413
Sbjct                5341  TGAAAGGCTTTAGTTATTTCTAGAGGAGTCCCATCCAACACTATTTGGCGACTGTTAATA  5400

Query                3414  TGTTATAATTATTAGACAGTGGAAAAGCCTTTATTGACTAATTGATTTAACCTCAGTCCA  3473
Sbjct                5401  TGTTATAATTATTAGACAGTGGAAAAGCCTTTATTGACTAATTGATTTAACCTCAGTCCA  5460

Query                3474  AAGAACAGTCTCTATACTTGCCCTCATTTACTGATAGGCTGCTACTAGTTACCATTTGAT  3533
Sbjct                5461  AAGAACAGTCTCTATACTTGCCCTCATTTACTGATAGGCTGCTACTAGTTACCATTTGAT  5520

Query                3534  TGTCTTGACTTTCGTCTTCAGTTGAATTGGTGAAAACATCAACAAAAACAAAACCCACTG  3593
Sbjct                5521  TGTCTTGACTTTCGTCTTCAGTTGAATTGGTGAAAACATCAACAAAAACAAAACCCACTG  5580

Query                3594  TGTCTTAAAATAAAATGTTCTGCATTGTAGTCAATAAAGGGCTTAAGATGT-AAAA  3648
Sbjct                5581  TGTCTTAAAATAAAATGTTCTGCATTGTAGTCAATAAAGGGCTTAAGATGTGAAAA  5636
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2305 G>C



RDB : No. 7675

RIKEN_Clone_ID : ARi78G04
開始Stock

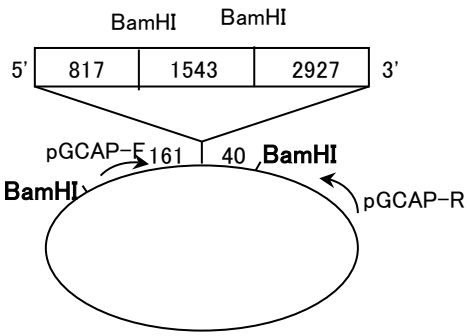
作業開始日 B4Hk QA – 保管場所 60C0417
作業者 古谷・124, Page 158

Accession No.	–
RefSeq_mRNA	NM_133468.5
Gene	BMPER
Gene_ID	168667
lot. No.	7675_B4Hk

検 '24.09.06 笹沼
提供担当者確認印

K.Nakashima '24.09.05 certified
承認印

● 予想 Vector_MAP



pGCAP10 : Amp

● 構造確認

BamHI cut での予想バンドサイズ

Vector : 3138 bp
Insert : 2967, 1543, 978 bp (unsure)

● 配列確認

DNA 量 : 177.87578

追加プライマー : GNP mix primer

業務進捗（提供担当チェックリスト）

- [x] 構造チェック（泳動写真確認）
- [x] 配列決定
- [ ] 濃度調製 （25 ng/ul）

古谷
共同作業者印

（承認担当チェックリスト）

- [x] 構造チェック（泳動写真確認）判定
- [x] 配列確認判定

クローンの質

- [ ] y : 構造確認・予想サイズと異なる
- [ ] z : Insert 情報が異なる
- [x] p : 問題なく検定終了

<MEMO>

HTS解析実施