5-4

NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARi41D04
Vector : pGCAP10

Lot# : 7675_B3Bd

Gene	TRMT5	
RefSeq_mRNA	NM_020810.3	5304 bp

● Plasmid DNA purification

Date : 23.03.14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.15

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

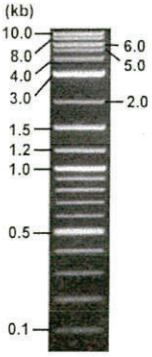
DNA	0.6 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.4 ul
Total	10 ul

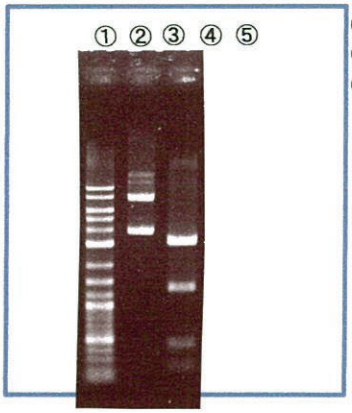
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.3, 0.5, 0.2 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 : 2026/06/22

full sequence : ARi41D04hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (178 ng/ul)	78 ul
10x TE	56 ul
dH_2O	422 ul
Total	555 ul

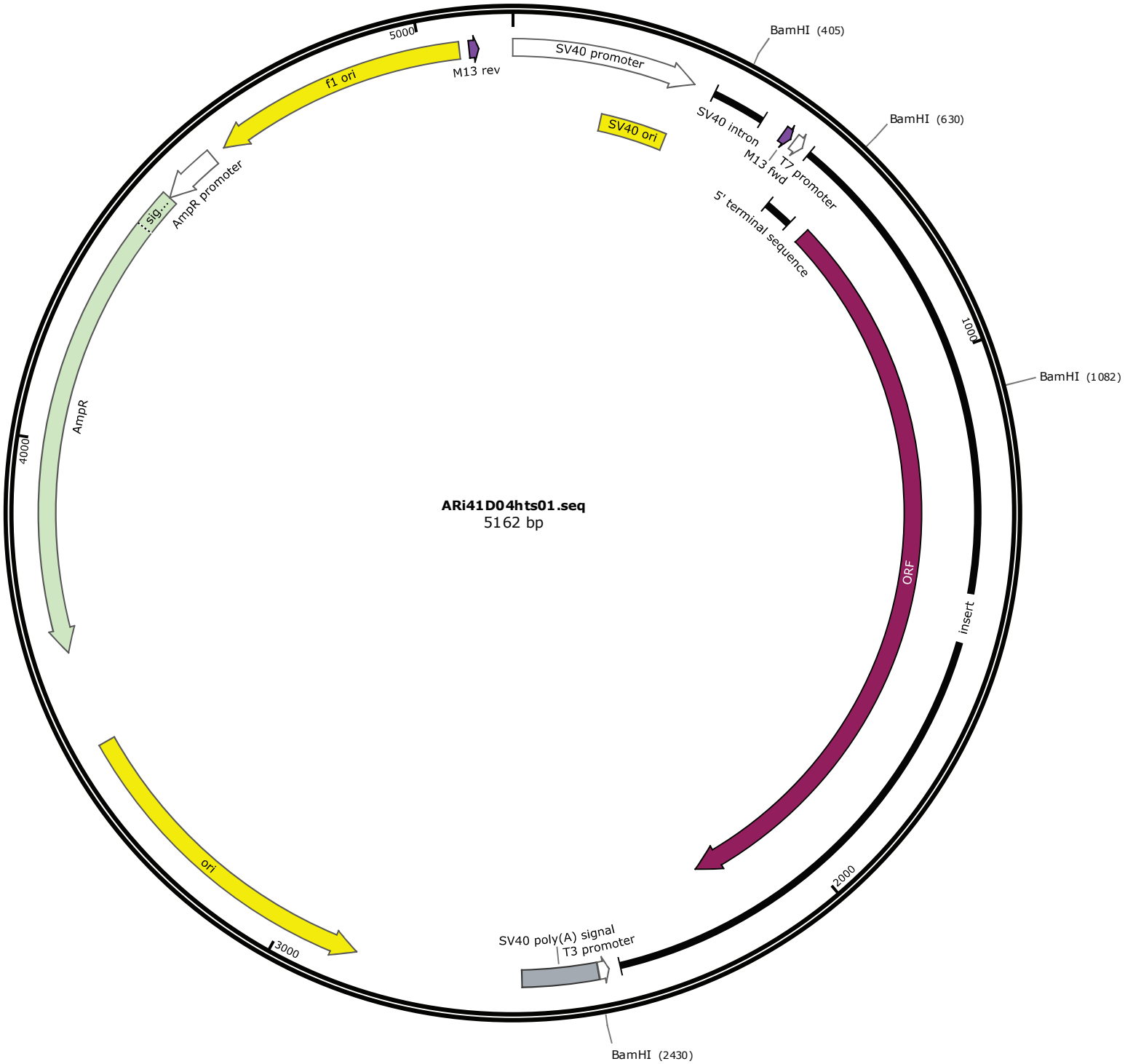
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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


ARi41D04hts01.seq
5162 bp
5000
M13 rev
f1 ori
SV40 promoter
BamHI (405)
SV40 intron
SV40 ori
BamHI (630)
M13 fwd
T7 promoter
5' terminal sequence
1000
BamHI (1082)
AmpR promoter
sig...
AmpR
4000
ORF
insert
ori
2000
SV40 poly(A) signal
T3 promoter
3000
BamHI (2430)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_152227:Homo sapiens sorting nexin 5 (SNX5),...

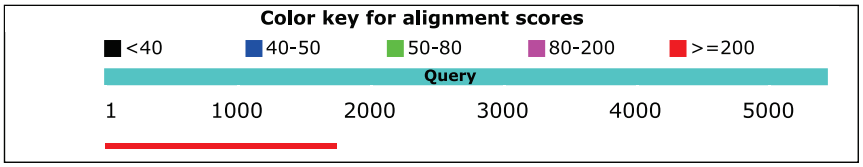
RID 3H43M6ZT114 (Expires on 06-23 09:31 am)

Query ID	NM_020810.3	**Subject ID**	lcl|Query_3090687
Description	Homo sapiens tRNA methyltransferase 5 (TRMT5), transcript variant 3, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	5304	**Subject Length**	5162
		Program	BLASTN 2.17.0+

ARi41D04hts01.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	3168	3168	32%	0.0	100.00%	Query_3090687

Alignments

Sequence ID: Query_3090687 Length: 5162 Number of Matches: 1
Range 1: 568 to 2282

Score	Expect	Identities	Gaps	Strand	Frame
3168 bits(1715)	0.0()	1715/1715(100%)	0/1715(0%)	Plus/Plus	

Features:

```
Query              12   GCCCATCCACCCGCGACCCACATCCGATCGGTACCGGAGCGGGAGGTGAGGGGTCGGCTC  71
Sbjct              568  ............................................................  627

CDS:tRNA (guanine(37  1                                        M  V  L  W  I  L  W  R
Query              72   GCGGATCCAGCTGCAGAGCGACGTGGGGAATTGGAATGGTGCTTTGGATCTTATGGAGGC  131
Sbjct              628  ............................................................  687

CDS:tRNA (guanine(37  9    P  F  G  F  S  G  R  F  L  K  L  E  S  H  S  I  T  E  S  K
Query              132  CATTTGGATTCTCAGGAAGATTTCTGAAACTGGAAAGCCATAGCATAACTGAATCAAAAT  191
Sbjct              688  ............................................................  747

CDS:tRNA (guanine(37  29   S  L  I  P  V  A  W  T  S  L  T  Q  M  L  L  E  A  P  G  I
Query              192  CGTTGATTCCAGTAGCTTGGACATCCCTGACACAGATGCTTTTGGAAGCACCTGGTATTT  251
Sbjct              748  ............................................................  807

CDS:tRNA (guanine(37  49   F  L  L  G  Q  R  K  R  F  S  T  M  P  E  T  E  T  H  E  R
Query              252  TCTTATTGGGTCAAAGAAAAAGATTCTCAACCATGCCAGAAACAGAAACACATGAGAGAG  311
Sbjct              808  ............................................................  867

CDS:tRNA (guanine(37  69   E  T  E  L  F  S  P  P  S  D  V  R  G  M  T  K  L  D  R  T
Query              312  AGACTGAATTGTTTTCACCACCTTCTGATGTCCGAGGCATGACAAAACTTGATAGAACAG  371
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Sbjct                868  ..........................................................  927

CDS:tRNA (guanine(37  89   A  F  K  K  T  V  N  I  P  V  L  K  V  R  K  E  I  V  S  K
Query                372  CTTTTAAAAAGACAGTCAACATTCCAGTGCTTAAAGTGAGGAAAGAAATAGTCAGTAAAT  431
Sbjct                928  ..........................................................  987

CDS:tRNA (guanine(37  109  L  M  R  S  L  K  R  A  A  L  Q  R  P  G  I  R  R  V  I  E
Query                432  TGATGCGATCCCTAAAAAGGGCAGCATTGCAGCGCCCAGGCATAAGACGTGTGATTGAAG  491
Sbjct                988  ..........................................................  1047

CDS:tRNA (guanine(37  129  D  P  E  D  K  E  S  R  L  I  M  L  D  P  Y  K  I  F  T  H
Query                492  ATCCGGAAGATAAAGAAAGTAGACTAATCATGTTGGATCCCTATAAAATATTTACTCATG  551
Sbjct                1048 ..........................................................  1107

CDS:tRNA (guanine(37  149  D  S  F  E  K  A  E  L  S  V  L  E  Q  L  N  V  S  P  Q  I
Query                552  ATTCCTTTGAGAAAGCAGAACTCAGTGTTTTAGAGCAGCTTAATGTCAGTCCACAGATCT  611
Sbjct                1108 ..........................................................  1167

CDS:tRNA (guanine(37  169  S  K  Y  N  L  E  L  T  Y  E  H  F  K  S  E  E  I  L  R  A
Query                612  CTAAATACAATTTGGAACTAACATATGAACACTTTAAGTCAGAAGAAATCTTGAGAGCTG  671
Sbjct                1168 ..........................................................  1227

CDS:tRNA (guanine(37  189  V  L  P  E  G  Q  D  V  T  S  G  F  S  R  I  G  H  I  A  H
Query                672  TGCTTCCTGAAGGTCAAGATGTAACTTCAGGGTTTAGCAGGATTGGACATATTGCACACC  731
Sbjct                1228 ..........................................................  1287

CDS:tRNA (guanine(37  209  L  N  L  R  D  H  Q  L  P  F  K  H  L  I  G  Q  V  M  I  D
Query                732  TAAACCTTCGAGATCATCAGCTGCCTTTCAAACATTTAATTGGCCAGGTTATGATTGACA  791
Sbjct                1288 ..........................................................  1347

CDS:tRNA (guanine(37  229  K  N  P  G  I  T  S  A  V  N  K  I  N  N  I  D  N  M  Y  R
Query                792  AAAATCCAGGAATCACCTCAGCAGTAAATAAAATAAATAATATTGACAATATGTACCGAA  851
Sbjct                1348 ..........................................................  1407

CDS:tRNA (guanine(37  249  N  F  Q  M  E  V  L  S  G  E  Q  N  M  M  T  K  V  R  E  N
Query                852  ATTTCCAAATGGAAGTGCTATCTGGAGAGCAGAACATGATGACAAAGGTTCGAGAAAACA  911
Sbjct                1408 ..........................................................  1467

CDS:tRNA (guanine(37  269  N  Y  T  Y  E  F  D  F  S  K  V  Y  W  N  P  R  L  S  T  E
Query                912  ACTACACCTATGAATTTGATTTTTCAAAAGTCTATTGGAATCCTCGTCTGTCTACAGAAC  971
Sbjct                1468 ..........................................................  1527

CDS:tRNA (guanine(37  289  H  S  R  I  T  E  L  L  K  P  G  D  V  L  F  D  V  F  A  G
Query                972  ACAGCCGTATCACAGAACTTCTCAAACCTGGGGATGTCCTATTTGATGTTTTTGCTGGGG  1031
Sbjct                1528 ..........................................................  1587

CDS:tRNA (guanine(37  309  V  G  P  F  A  I  P  V  A  K  K  N  C  T  V  F  A  N  D  L
Query                1032 TTGGGCCCTTTGCCATTCCAGTAGCAAAGAAAAACTGCACTGTATTTGCCAATGATCTCA  1091
Sbjct                1588 ..........................................................  1647

CDS:tRNA (guanine(37  329  N  P  E  S  H  K  W  L  L  Y  N  C  K  L  N  K  V  D  Q  K
Query                1092 ATCCTGAATCTCATAAATGGCTGTTGTACAACTGTAAATTAAATAAAGTGGACCAAAAGG  1151
Sbjct                1648 ..........................................................  1707

CDS:tRNA (guanine(37  349  V  K  V  F  N  L  D  G  K  D  F  L  Q  G  P  V  K  E  E  L
Query                1152 TGAAAGTCTTCAACTTGGATGGGAAAGACTTCCTCCAAGGACCAGTCAAAGAAGAGTTAA  1211
Sbjct                1708 ..........................................................  1767

CDS:tRNA (guanine(37  369  M  Q  L  L  G  L  S  K  E  R  K  P  S  V  H  V  V  M  N  L



Query                1212 TGCAGCTGCTGGGTCTGTCAAAAGAAAGAAAACCCTCTGTGCACGTTGTCATGAACTTGC  1271
Sbjct                1768 ..........................................................  1827

CDS:tRNA (guanine(37  389  P  A  K  A  I  E  F  L  S  A  F  K  W  L  L  D  G  Q  P  C
Query                1272 CAGCAAAAGCTATAGAGTTTCTTAGTGCTTTCAAGTGGCTTTTAGATGGGCAGCCATGCA  1331
Sbjct                1828 ..........................................................  1887

CDS:tRNA (guanine(37  409  S  S  E  F  L  P  I  V  H  C  Y  S  F  S  K  D  A  N  P  A
Query                1332 GCAGTGAGTTCCTTCCCATAGTGCATTGTTATAGCTTTTCCAAAGATGCTAACCCTGCTG  1391
Sbjct                1888 ..........................................................  1947

CDS:tRNA (guanine(37  429  E  D  V  R  Q  R  A  G  A  V  L  G  I  S  L  E  A  C  S  S
Query                1392 AGGATGTTCGGCAAAGGGCTGGAGCTGTGTTAGGCATTTCTCTGGAGGCATGCAGTTCAG  1451
Sbjct                1948 ..........................................................  2007

CDS:tRNA (guanine(37  449  V  H  L  V  R  N  V  A  P  N  K  E  M  L  C  I  T  F  Q  I
Query                1452 TTCACCTGGTAAGAAATGTGGCCCCAAACAAGGAAATGCTGTGCATCACGTTTCAGATTC  1511
Sbjct                2008 ..........................................................  2067

CDS:tRNA (guanine(37  469  P  A  S  V  L  Y  K  N  Q  T  R  N  P  E  N  H  E  D  P  P
Query                1512 CTGCCTCTGTCCTCTACAAGAACCAGACCAGAAATCCAGAGAATCATGAAGATCCACCTC  1571
Sbjct                2068 ..........................................................  2127

CDS:tRNA (guanine(37  489  L  K  R  Q  R  T  A  E  A  F  S  D  E  K  T  Q  I  V  S  N
Query                1572 TTAAAAGGCAGAGGACGGCTGAAGCCTTTTCAGACGAAAAAACACAAATTGTTTCAAACA  1631
Sbjct                2128 ..........................................................  2187

CDS:tRNA (guanine(37  509  T
Query                1632 CTTAATTGGAAATGTTTTCTCCATCTCCCTACCAGACTTACATGTAGTGAAATAGAATTT  1691
Sbjct                2188 ..........................................................  2247

Query                1692 GTATTATTTAATAAAATTTTAGGGTTTGGTTTTTA  1726
Sbjct                2248 ....................................  2282
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