NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd31A01

Lot# : 7677_B5Ca

Vector : pGCAP10

Gene	VWCE	
RefSeq_mRNA	NM_152718.2	3536 bp

● Plasmid DNA purification

Date : 2025/03/10 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/03/11 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/03/11

DNA concentration (O.D.): 286 ng/ul

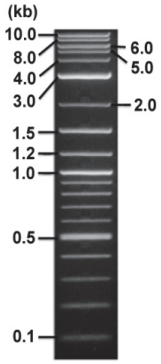
< Size of fragment expected from this clone >

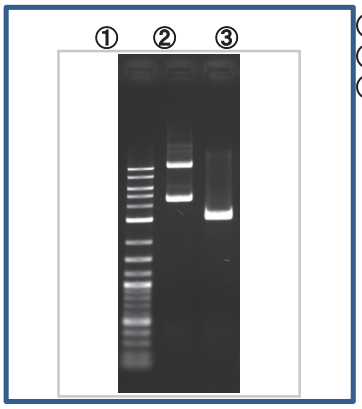
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

BamHI 3.1kb (vector), 2.9 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 : 2025/03/19

full sequence	RBd31A01hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/03/25

DNA (286 ng/ul)	82 ul
10x TE	94 ul
dH_2O	762 ul
Total	938 ul

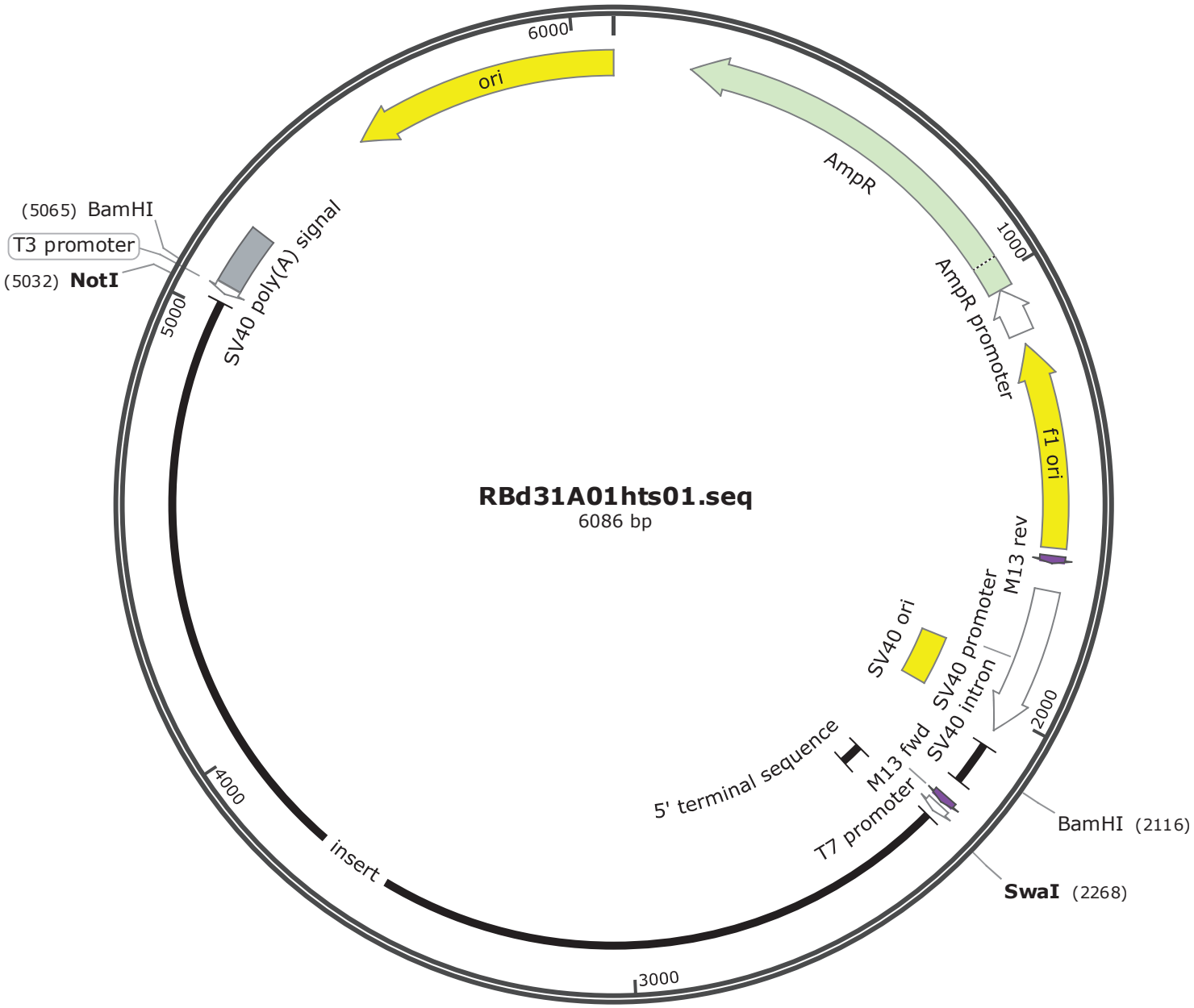
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '25.03.26 笹沼

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


6000
ori
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 ori
SV40 promoter
SV40 intron
2000
BamHI (2116)
SwaI (2268)
3000
insert
4000
5' terminal sequence
M13 fwd
T7 promoter
5000
SV40 poly(A) signal
(5065) BamHI
T3 promoter
(5032) NotI
RBd31A01hts01.seq
6086 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_152718:Homo sapiens von Willebrand factor...

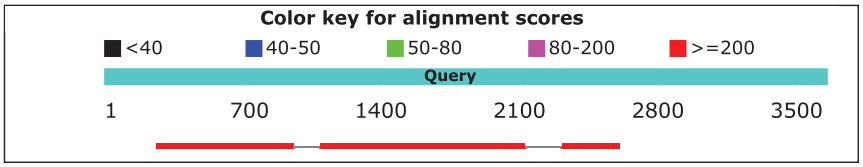
RID XMMUSAHV114 (Expires on 03-20 13:17 pm)

Query ID	NM_152718.2	**Subject ID**	lcl|Query_4771385
Description	Homo sapiens von Willebrand factor C and EGF domains (VWCE), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3536	**Subject Length**	6086
		Program	BLASTN 2.16.1+

RBd31A01hts01.seq

Graphic Summary

Distribution of the top 3 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	1849	3608	55%	0.0	99.80%	Query_4771385

Alignments

Sequence ID: Query_4771385 Length: 6086 Number of Matches: 3
Range 1: 2945 to 3951

Score	Expect	Identities	Gaps	Strand	Frame
1849 bits(1001)	0.0()	1006/1008(99%)	1/1008(0%)	Plus/Plus	

Features:

```
CDS:von Willebrand f  260   S  C  E  A  F  P  K  A  V  L  A  P  S  A  I  L  Q  P  R  Q
Query                 1057  TCCTGTGAAGCTTTCCCGAAAGCCGTGCTGGCCCCATCTGCCATCCTGCAACCCCGGCAA  1116
Sbjct                 2945  .......T.....................................................  3004

CDS:von Willebrand f  280   H  P  S  K  M  L  L  L  L  P  E  A  G  R  P  A  L  S  P  G
Query                 1117  CACCCGTCCAAGATGCTTCTGTTGCTTCCTGAGGCCGGCCGGCCTGCCCTGTCCCCAGGA  1176
Sbjct                 3005  .....................................................  3064

CDS:von Willebrand f  300   H  S  P  P  S  G  A  P  G  P  P  A  G  V  R  T  T  R  L  P
Query                 1177  CATAGCCCTCCTTCTGGGGCTCCAGGGCCCCCAGCCGGAGTCAGGACCACCCGCCTGCCA  1236
Sbjct                 3065  .....................................................  3124

CDS:von Willebrand f  320   S  P  T  P  R  L  P  T  S  S  P  S  A  P  V  W  L  L  S  T
Query                 1237  TCTCCCACCCCACGACTACCCACATCCTCCCCTTCTGCCCCTGTGTGGCTGCTGTCCACC  1296
Sbjct                 3125  .....................................................  3184

CDS:von Willebrand f  340   L  L  A  T  P  V  P  T  A  S  L  L  G  N  L  R  P  P  S  L
Query                 1297  CTGCTGGCCACCCCAGTGCCTACTGCCTCCCTGCTGGGGAACCTCAGACCCCCCTCACTC  1356
Sbjct                 3185  .....................................................  3244

CDS:von Willebrand f  360   L  Q  G  E  V  M  G  T  P  S  S  P  R  G  P  E  S  P  R  L
Query                 1357  CTTCAGGGGGAGGTGATGGGGACCCCTTCCTCACCCAGGGGCCCTGAGTCCCCCCGACTG  1416
Sbjct                 3245  .....................................................  3303
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CDS:von Willebrand f  380   A  A  G  P  S  P  C  W  H  L  G  A  M  H  E  S  R  S  R  W
Query                 1417  GCAGCAGGGCCCTCTCCCTGCTGGCACCTGGGAGCCATGCATGAATCAAGGAGTCGCTGG  1476
Sbjct                 3304  ............................................................  3363

CDS:von Willebrand f  400   T  E  P  G  C  S  Q  C  W  C  E  D  G  K  V  T  C  E  K  V
Query                 1477  ACAGAGCCTGGGTGTTCCCAGTGCTGGTGCGAGGACGGGAAGGTGACCTGTGAAAAGGTG  1536
Sbjct                 3364  ............................................................  3423

CDS:von Willebrand f  420   R  C  E  A  A  C  S  H  P  I  P  S  R  D  G  G  C  C  P  S
Query                 1537  AGGTGTGAAGCTGCTTGTTCCCACCCAATTCCCTCCAGAGATGGTGGGTGCTGCCCATCG  1596
Sbjct                 3424  ............................................................  3483

CDS:von Willebrand f  440   C  T  G  C  F  H  S  G  V  V  R  A  E  G  D  V  F  S  P  P
Query                 1597  TGCACAGGCTGTTTTCACAGTGGTGTCGTCCGAGCTGAAGGGGATGTGTTTTCACCTCCC  1656
Sbjct                 3484  ............................................................  3543

CDS:von Willebrand f  460   N  E  N  C  T  V  C  V  C  L  A  G  N  V  S  C  I  S  P  E
Query                 1657  AATGAGAACTGCACCGTCTGTGTCTGTCTGGCTGGAAACGTGTCCTGCATCTCTCCTGAG  1716
Sbjct                 3544  ............................................................  3603

CDS:von Willebrand f  480   C  P  S  G  P  C  Q  T  P  P  Q  T  D  C  C  T  C  V  P  V
Query                 1717  TGTCCTTCTGGCCCCTGTCAGAccccccccACAGACGGATTGCTGTACTTGTGTTCCAGTG  1776
Sbjct                 3604  ............................................................  3663

CDS:von Willebrand f  500   R  C  Y  F  H  G  R  W  Y  A  D  G  A  V  F  S  G  G  G  D
Query                 1777  AGATGCTATTTCCACGGCCGGTGGTACGCAGACGGGGCTGTGTTCAGTGGGGGTGGTGAC  1836
Sbjct                 3664  ............................................................  3723

CDS:von Willebrand f  520   E  C  T  T  C  V  C  Q  N  G  E  V  E  C  S  F  M  P  C  P
Query                 1837  GAGTGTACCACCTGTGTTTGCCAGAATGGGGAGGTGGAGTGCTCCTTCATGCCCTGCCCT  1896
Sbjct                 3724  ............................................................  3783

CDS:von Willebrand f  540   E  L  A  C  P  R  E  E  W  R  L  G  P  G  Q  C  C  F  T  C
Query                 1897  GAGCTGGCCTGCCCCCGAGAAGAGTGGCGGCTGGGCCCTGGGCAGTGTTGCTTCACCTGC  1956
Sbjct                 3784  ............................................................  3843

CDS:von Willebrand f  560   Q  E  P  T  P  S  T  G  C  S  L  D  D  N  G  V  E  F  P  I
Query                 1957  CAGGAGCCCACACCCTCGACAGGCTGCTCTCTTGACGACAACGGGGTTGAGTTTCCGATT  2016
Sbjct                 3844  ............................................................  3903

CDS:von Willebrand f  580   G  Q  I  W  S  P  G  D  P  C  E  L  C  I  C  Q
Query                 2017  GGACAGATCTGGTCGCCTGGTGACCCCTGTGAGTTATGCATCTGCCAG  2064
Sbjct                 3904  ..............................................  3951
```

Range 2: 2278 to 2954

Score	Expect	Identities	Gaps	Strand	Frame
1251 bits(677)	0.0()	677/677(100%)	0/677(0%)	Plus/Plus	

Features:

```
CDS:von Willebrand f  1                       M  W  A  G  L  L  L  R  A  A  C  V  A  L
Query                 261   GGACCCGCCGCCGCCGGTCATGTGGGCCGGACTGCTCCTTCGGGCCGCCTGTGTCGCGCT  320
Sbjct                 2278  ............................................................  2337

CDS:von Willebrand f  15     L  L  P  G  A  P  A  R  G  Y  T  G  R  K  P  P  G  H  F  A
```

```
Query                 321   CCTGCTGCCGGGGGCACCAGCCCGAGGCTACACCGGGAGGAAGCCGCCCGGGCACTTCGC  380
Sbjct                 2338  ............................................................  2397

CDS:von Willebrand f  35     A  E  R  R  R  L  G  P  H  V  C  L  S  G  F  G  S  G  C  C
Query                 381   GGCCGAGAGACGCCGACTGGGCCCCCACGTCTGCCTCTCTGGGTTTGGGAGTGGCTGCTG  440
Sbjct                 2398  ............................................................  2457

CDS:von Willebrand f  55     P  G  W  A  P  S  M  G  G  G  H  C  T  L  P  L  C  S  F  G
Query                 441   CCCTGGCTGGGCGCCCTCTATGGGTGGTGGGCACTGCACCCTGCCCCTCTGCTCCTTCGG  500
Sbjct                 2458  ............................................................  2517

CDS:von Willebrand f  75     C  G  S  G  I  C  I  A  P  N  V  C  S  C  Q  D  G  E  Q  G
Query                 501   CTGTGGGAGTGGCATCTGCATCGCTCCCAATGTCTGCTCCTGCCAGGATGGAGAGCAAGG  560
Sbjct                 2518  ............................................................  2577

CDS:von Willebrand f  95     A  T  C  P  E  T  H  G  P  C  G  E  Y  G  C  D  L  T  C  N
Query                 561   GGCCACCTGCCCAGAAACCCATGGACCATGTGGGGAGTACGGCTGTGACCTTACCTGCAA  620
Sbjct                 2578  ............................................................  2637

CDS:von Willebrand f  115    H  G  G  C  Q  E  V  A  R  V  C  P  V  G  F  S  M  T  E  T
Query                 621   CCATGGAGGCTGTCAGGAGGTGGCCCGAGTGTGCCCCGTGGGCTTCTCGATGACGGAGAC  680
Sbjct                 2638  ............................................................  2697

CDS:von Willebrand f  135    A  V  G  I  R  C  T  D  I  D  E  C  V  T  S  S  C  E  G  H
Query                 681   AGCTGTTGGCATCAGGTGTACAGACATTGACGAATGTGTAACCTCCTCCTGCGAGGGCCA  740
Sbjct                 2698  ............................................................  2757

CDS:von Willebrand f  155    C  V  N  T  E  G  G  F  V  C  E  C  G  P  G  M  Q  L  S  A
Query                 741   CTGTGTGAACACAGAAGGTGGGTTTGTGTGCGAGTGTGGGCCGGGCATGCAGCTGTCTGC  800
Sbjct                 2758  ............................................................  2817

CDS:von Willebrand f  175    D  R  H  S  C  Q  D  T  D  E  C  L  G  T  P  C  Q  Q  R  C
Query                 801   CGACCGCCACAGCTGCCAAGACACTGACGAATGCCTAGGGACTCCCTGTCAGCAGAGATG  860
Sbjct                 2818  ............................................................  2877

CDS:von Willebrand f  195    K  N  S  I  G  S  Y  K  C  S  C  R  T  G  F  H  L  H  G  N
Query                 861   TAAAAACAGCATTGGCAGCTACAAGTGTTCCTGTCGAACTGGCTTCCACCTTCATGGCAA  920
Sbjct                 2878  ............................................................  2937

CDS:von Willebrand f  215    R  H  S  C  V
Query                 921   CCGGCACTCCTGTGTAG  937
Sbjct                 2938  .................  2954
```

Range 3: 3940 to 4216

Score	Expect	Identities	Gaps	Strand	Frame
507 bits(274)	5e-146()	276/277(99%)	0/277(0%)	Plus/Plus	

Features:

```
CDS:von Willebrand f  652   C  I  C  L  L  G  S  V  A  C  S  P  V  D  C  P  I  T  C  T
Query                 2233  TGCATCTGCCTGCTGGGCTCAGTGGCCTGTTCCCCCGTGGACTGCCCCATCACCTGTACC  2292
Sbjct                 3940  ..........A.................................................  3999

CDS:von Willebrand f  672   Y  P  F  H  P  D  G  E  C  C  P  V  C  R  D  C  N  Y  E  G
Query                 2293  TACCCTTTCCACCCTGACGGGGAGTGCTGCCCCGTGTGCCGAGACTGCAACTACGAGGGA  2352
Sbjct                 4000  ............................................................  4059
```

```
CDS:von Willebrand f  692   R  K  V  A  N  G  Q  V  F  T  L  D  D  E  P  C  T  R  C  T
Query                 2353  AGGAAGGTGGCGAATGGCCAGGTGTTCACCTTGGATGATGAACCCTGCACCCGGTGCACG  2412
Sbjct                 4060  ............................................................  4119

CDS:von Willebrand f  712   C  Q  L  G  E  V  S  C  E  K  V  P  C  Q  R  A  C  A  D  P
Query                 2413  TGCCAGCTGGGAGAGGTGAGCTGTGAGAAGGTTCCCTGCCAGCGGGCCTGTGCCGACCCT  2472
Sbjct                 4120  ............................................................  4179

CDS:von Willebrand f  732   A  L  L  P  G  D  C  C  S  S  C  P
Query                 2473  GCCCTGCTTCCTGGGGACTGCTGCTCTTCCTGTCCAG  2509
Sbjct                 4180  ......................................  4216
```

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