NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Center

RIKEN Clone ID : RBd28F11

Lot# : 7677_A7G7

Vector : pGCAP1

Gene	EHMT1	
RefSeq_mRNA	NM_001354263.2	5074 bp
CDS		3876 bp
5' position		12

● Plasmid DNA purification

Date : 170713 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 170718 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 170718

DNA concentration (O.D.): 163 ng/ul

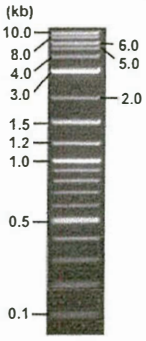
DNA	0.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

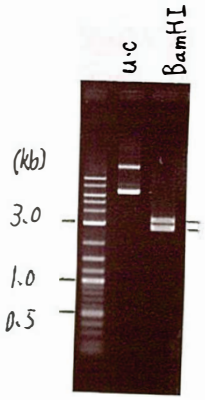
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.6, 2.6 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

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





● Confirmation of the sequence

検 '25.06.24 笹沼

Date : 170718

full sequence	RBd28F11hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 170719

DNA (163 ng/ul)	80.0 ul
10x TE	52.1 ul
dH_2O	389.5 ul
Total	521.6 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

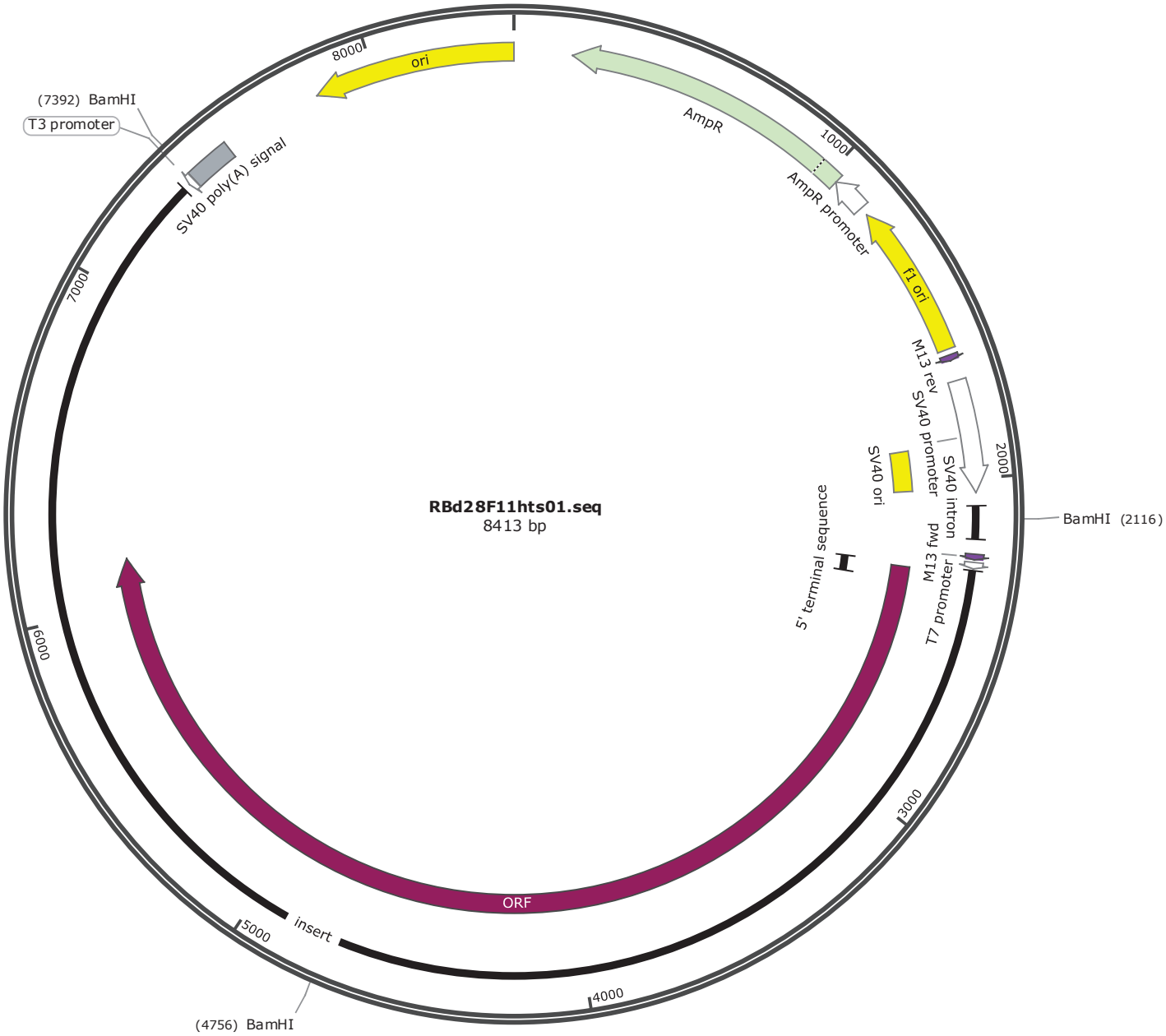
☐ ~~Conc. : ng/μl, Volume : μl~~

APPROVED BY :

確認 17.7.19 笹沼

検 '25.06.24 笹沼

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


RBd28F11hts01.seq
8413 bp
8000
1000
2000
3000
4000
5000
6000
7000
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
SV40 ori
BamHI (2116)
ORF
insert
(4756) BamHI
SV40 poly(A) signal
T3 promoter
(7392) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001354612:Homo sapiens euchromatic histone...

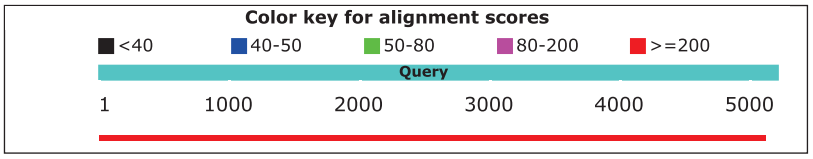
RID 5MAKG61V114 (Expires on 06-25 12:32 pm)

Query ID	NM_001354263.2	**Subject ID**	lcl|Query_7167291
Description	Homo sapiens euchromatic histone lysine methyltransferase 1 (EHMT1), transcript variant 4, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	5074	**Subject Length**	8413
		Program	BLASTN 2.17.0+

RBd28F11hts01.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	9350	9350	100%	0.0	100.00%	Query_7167291

Alignments

Sequence ID: Query_7167291 Length: 8413 Number of Matches: 1
Range 1: 2269 to 7331

Score	Expect	Identities	Gaps	Strand	Frame
9350 bits(5063)	0.0()	5063/5063(100%)	0/5063(0%)	Plus/Plus	

Features:

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CDS:histone-lysine N  1                M  A  A  A  D  A  E  A  V  P  A  R  G  E  P  Q
Query                 12    GCGGGCCCGGGCCATGGCCGCCGCCGATGCCGAGGCAGTTCCGGCGAGGGGGGAGCCTCA  71
Sbjct                 2269  ............................................................  2328

CDS:histone-lysine N  17     Q  D  C  C  V  K  T  E  L  L  G  E  E  T  P  M  A  A  D  E
Query                 72    GCAGGATTGCTGTGTGAAAACCGAGCTGCTGGGAGAAGAGACACCTATGGCTGCCGATGA  131
Sbjct                 2329  ............................................................  2388

CDS:histone-lysine N  37     G  S  A  E  K  Q  A  G  E  A  H  M  A  A  D  G  E  T  N  G
Query                 132   AGGCTCAGCAGAGAAACAGGCAGGAGAGGCCCACATGGCTGCGGACGGTGAGACCAATGG  191
Sbjct                 2389  ............................................................  2448

CDS:histone-lysine N  57     S  C  E  N  S  D  A  S  S  H  A  N  A  A  K  H  T  Q  D  S
Query                 192   GTCTTGTGAAAACAGCGATGCCAGCAGTCATGCAAATGCTGCAAAGCACACTCAGGACAG  251
Sbjct                 2449  ............................................................  2508

CDS:histone-lysine N  77     A  R  V  N  P  Q  D  G  T  N  T  L  T  R  I  A  E  N  G  V
Query                 252   CGCAAGGGTCAACCCCCAGGATGGCACCAACACACTAACTCGGATAGCGGAAAATGGGGT  311
Sbjct                 2509  ............................................................  2568

CDS:histone-lysine N  97     S  E  R  D  S  E  A  A  K  Q  N  H  V  T  A  D  D  F  V  Q
Query                 312   TTCAGAAAGAGACTCAGAAGCGGCGAAGCAAAACCACGTCACTGCCGACGACTTTGTGCA  371
Sbjct                 2569  ............................................................  2628
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CDS:histone-lysine N  117    T  S  V  I  G  S  N  G  Y  I  L  N  K  P  A  L  Q  A  Q  P
Query                 372    GACTTCTGTCATCGGCAGCAACGGATACATCTTAAATAAGCCGGCCCTACAGGCACAGCC  431
Sbjct                 2629   ............................................................  2688

CDS:histone-lysine N  137    L  R  T  T  S  T  L  A  S  S  L  P  G  H  A  A  K  T  L  P
Query                 432    CTTGAGGACTACCAGCACTCTGGCCTCTTCGCTGCCTGGCCATGCTGCAAAAACCCTTCC  491
Sbjct                 2689   ............................................................  2748

CDS:histone-lysine N  157    G  G  A  G  K  G  R  T  P  S  A  F  P  Q  T  P  A  A  P  P
Query                 492    TGGAGGGGCTGGCAAAGGCAGGACTCCAAGCGCTTTTCCCCAGACGCCAGCCGCCCCACC  551
Sbjct                 2749   ............................................................  2808

CDS:histone-lysine N  177    A  T  L  G  E  G  S  A  D  T  E  D  R  K  L  P  A  P  G  A
Query                 552    AGCCACCCTTGGGGAGGGGAGTGCTGACACAGAGGACAGGAAGCTCCCGGCCCCTGGCGC  611
Sbjct                 2809   ............................................................  2868

CDS:histone-lysine N  197    D  V  K  V  H  R  A  R  K  T  M  P  K  S  V  V  G  L  H  A
Query                 612    CGACGTCAAGGTCCACAGGGCACGCAAGACCATGCCGAAGTCCGTCGTGGGCCTGCATGC  671
Sbjct                 2869   ............................................................  2928

CDS:histone-lysine N  217    A  S  K  D  P  R  E  V  R  E  A  R  D  H  K  E  P  K  E  E
Query                 672    AGCCAGTAAAGATCCCAGAGAAGTTCGAGAAGCTAGAGATCATAAGGAACCAAAAGAGGA  731
Sbjct                 2929   ............................................................  2988

CDS:histone-lysine N  237    I  N  K  N  I  S  D  F  G  R  Q  Q  L  L  P  P  F  P  S  L
Query                 732    GATCAACAAAAACATTTCTGACTTTGGACGACAGCAGCTTTTACCCCCCTTCCCATCCCT  791
Sbjct                 2989   ............................................................  3048

CDS:histone-lysine N  257    H  Q  S  L  P  Q  N  Q  C  Y  M  A  T  T  K  S  Q  T  A  A
Query                 792    TCATCAGTCGCTACCTCAGAACCAGTGCTACATGGCCACCACAAAATCACAGACAGCAGC  851
Sbjct                 3049   ............................................................  3108

CDS:histone-lysine N  277    A  V  S  R  K  K  K  R  R  M  G  T  Y  S  L  V  P  K  K  K
Query                 852    TGCAGTATCTCGGAAGAAAAAACGAAGAATGGGAACCTATAGCCTGGTTCCTAAGAAAAA  911
Sbjct                 3109   ............................................................  3168

CDS:histone-lysine N  297    T  K  V  L  K  Q  R  T  V  I  E  M  F  K  S  I  T  H  S  T
Query                 912    GACCAAAGTATTAAAACAGAGGACGGTGATTGAGATGTTTAAGAGCATAACTCATTCCAC  971
Sbjct                 3169   ............................................................  3228

CDS:histone-lysine N  317    V  G  S  K  G  E  K  D  L  G  A  S  S  L  H  V  N  G  E  S
Query                 972    TGTGGGTTCCAAGGGGGAGAAGGACCTGGGCGCCAGCAGCCTGCACGTGAATGGGGAGAG  1031
Sbjct                 3229   ............................................................  3288

CDS:histone-lysine N  337    L  E  M  D  S  D  E  D  D  S  E  E  L  E  E  D  D  G  H  G
Query                 1032   CCTGGAGATGGACTCGGATGAGGACGACTCAGAGGAGCTCGAGGAGGACGACGGCCATGG  1091
Sbjct                 3289   ............................................................  3348

CDS:histone-lysine N  357    A  E  Q  A  A  A  F  P  T  E  D  S  R  T  S  K  E  S  M  S
Query                 1092   TGCAGAGCAGGCGGCCGCGTTCCCCACAGAGGACAGCAGGACTTCCAAGGAGAGCATGTC  1151
Sbjct                 3349   ............................................................  3408

CDS:histone-lysine N  377    E  A  D  R  A  Q  K  M  D  G  E  S  E  E  E  Q  E  S  V  D
Query                 1152   GGAGGCTGATCGCGCCCAGAAGATGGACGGGGAGTCCGAGGAGGAGCAGGAGTCCGTGGA  1211
Sbjct                 3409   ............................................................  3468

CDS:histone-lysine N  397    T  G  E  E  E  E  G  G  D  E  S  D  L  S  S  E  S  S  I  K
Query                 1212   CACCGGGGAGGAGGAGGAAGGCGGTGACGAGTCTGACCTGAGTTCGGAATCCAGCATTAA  1271
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Sbjct                 3469   ............................................................  3528

CDS:histone-lysine N  417    K  K  F  L  K  R  K  G  K  T  D  S  P  W  I  K  P  A  R  K
Query                 1272   GAAGAAATTTCTCAAGAGGAAAGGAAAGACCGACAGTCCCTGGATCAAGCCAGCCAGGAA  1331
Sbjct                 3529   ............................................................  3588

CDS:histone-lysine N  437    R  R  R  R  S  R  K  K  P  S  G  A  L  G  S  E  S  Y  K  S
Query                 1332   AAGGAGGCGGAGAAGTAGAAAGAAGCCCAGCGGTGCCCTCGGTTCTGAGTCGTATAAGTC  1391
Sbjct                 3589   ............................................................  3648

CDS:histone-lysine N  457    S  A  G  S  A  E  Q  T  A  P  G  D  S  T  G  Y  M  E  V  S
Query                 1392   ATCTGCAGGAAGCGCTGAGCAGACGGCACCAGGAGACAGCACAGGGTACATGGAAGTTTC  1451
Sbjct                 3649   ............................................................  3708

CDS:histone-lysine N  477    L  D  S  L  D  L  R  V  K  G  I  L  S  S  Q  A  E  G  L  A
Query                 1452   TCTGGACTCCCTGGATCTCCGAGTCAAAGGAATTCTGTCTTCACAAGCAGAAGGGTTGGC  1511
Sbjct                 3709   ............................................................  3768

CDS:histone-lysine N  497    N  G  P  D  V  L  E  T  D  G  L  Q  E  V  P  L  C  S  C  R
Query                 1512   CAACGGTCCAGATGTGCTGGAGACAGACGGCCTCCAGGAAGTGCCTCTCTGCAGCTGCCG  1571
Sbjct                 3769   ............................................................  3828

CDS:histone-lysine N  517    M  E  T  P  K  S  R  E  I  T  T  L  A  N  N  Q  C  M  A  T
Query                 1572   GATGGAAACACCGAAGAGTCGAGAGATCACCACACTGGCCAACAACCAGTGCATGGCTAC  1631
Sbjct                 3829   ............................................................  3888

CDS:histone-lysine N  537    E  S  V  D  H  E  L  G  R  C  T  N  S  V  V  K  Y  E  L  M
Query                 1632   AGAGAGCGTGGACCATGAATTGGGCCGGTGCACAAACAGCGTGGTCAAGTATGAGCTGAT  1691
Sbjct                 3889   ............................................................  3948

CDS:histone-lysine N  557    R  P  S  N  K  A  P  L  L  V  L  C  E  D  H  R  G  R  M  V
Query                 1692   GCGCCCCTCCAACAAGGCCCCGCTCCTCGTGCTGTGTGAAGACCACCGGGGCCGCATGGT  1751
Sbjct                 3949   ............................................................  4008

CDS:histone-lysine N  577    K  H  Q  C  C  P  G  C  G  Y  F  C  T  A  G  N  F  M  E  C
Query                 1752   GAAGCACCAGTGCTGTCCTGGCTGTGGCTACTTCTGCACAGCGGGTAATTTTATGGAGTG  1811
Sbjct                 4009   ............................................................  4068

CDS:histone-lysine N  597    Q  P  E  S  S  I  S  H  R  F  H  K  D  C  A  S  R  V  N  N
Query                 1812   TCAGCCCGAGAGCAGCATCTCTCACCGTTTCCACAAAGACTGTGCCTCTCGAGTCAATAA  1871
Sbjct                 4069   ............................................................  4128

CDS:histone-lysine N  617    A  S  Y  C  P  H  C  G  E  E  S  S  K  A  K  E  V  T  I  A
Query                 1872   CGCCAGCTATTGTCCCCACTGTGGGGAGGAGAGCTCCAAGGCCAAAGAGGTGACGATAGC  1931
Sbjct                 4129   ............................................................  4188

CDS:histone-lysine N  637    K  A  D  T  T  S  T  V  T  P  V  P  G  Q  E  K  G  S  A  L
Query                 1932   TAAAGCAGACACCACCTCGACCGTGACACCAGTCCCCGGGCAGGAGAAGGGCTCGGCCCT  1991
Sbjct                 4189   ............................................................  4248

CDS:histone-lysine N  657    E  G  R  A  D  T  T  T  G  S  A  A  G  P  P  L  S  E  D  D
Query                 1992   GGAGGGCAGGGCCGACACCACAACGGGCAGTGCTGCCGGGCCACCACTCTCGGAGGACGA  2051
Sbjct                 4249   ............................................................  4308

CDS:histone-lysine N  677    K  L  Q  G  A  A  S  H  V  P  E  G  F  D  P  T  G  P  A  G
Query                 2052   CAAGCTGCAGGGTGCAGCCTCCCACGTGCCCGAGGGCTTTGATCCAACGGGACCTGCTGG  2111
Sbjct                 4309   ............................................................  4368

CDS:histone-lysine N  697    L  G  R  P  T  P  G  L  S  Q  G  P  G  K  E  T  L  E  S  A
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Query                2112  GCTTGGGAGGCCAACTCCCGGCCTTTCCCAGGGACCAGGGAAGGAAACCTTGGAGAGCGC  2171
Sbjct                4369  ............................................................  4428

CDS:histone-lysine N  717    L  I  A  L  D  S  E  K  P  K  K  L  R  F  H  P  K  Q  L  Y
Query                2172  TCTCATCGCCCTCGACTCGGAAAAACCCAAGAAGCTTCGCTTCCACCCAAAGCAGCTGTA  2231
Sbjct                4429  ............................................................  4488

CDS:histone-lysine N  737    F  S  A  R  Q  G  E  L  Q  K  V  L  L  M  L  V  D  G  I  D
Query                2232  CTTCTCCGCCAGGCAAGGGGAGCTTCAGAAGGTGCTCCTCATGCTGGTGGACGGAATTGA  2291
Sbjct                4489  ............................................................  4548

CDS:histone-lysine N  757    P  N  F  K  M  E  H  Q  N  K  R  S  P  L  H  A  A  A  E  A
Query                2292  CCCCAACTTCAAAATGGAGCACCAGAATAAGCGCTCTCCACTGCACGCCGCGGCAGAGGC  2351
Sbjct                4549  ............................................................  4608

CDS:histone-lysine N  777    G  H  V  D  I  C  H  M  L  V  Q  A  G  A  N  I  D  T  C  S
Query                2352  TGGACACGTGGACATCTGCCACATGCTGGTTCAGGCGGGCGCTAATATTGACACCTGCTC  2411
Sbjct                4609  ............................................................  4668

CDS:histone-lysine N  797    E  D  Q  R  T  P  L  M  E  A  A  E  N  N  H  L  E  A  V  K
Query                2412  AGAAGACCAGAGGACCCCGTTGATGGAAGCAGCCGAAAACAACCATCTGGAAGCAGTGAA  2471
Sbjct                4669  ............................................................  4728

CDS:histone-lysine N  817    Y  L  I  K  A  G  A  L  V  D  P  K  D  A  E  G  S  T  C  L
Query                2472  GTACCTCATCAAGGCTGGGGCCCTGGTGGATCCCAAGGACGCAGAGGGCTCTACGTGTTT  2531
Sbjct                4729  ............................................................  4788

CDS:histone-lysine N  837    H  L  A  A  K  K  G  H  Y  E  V  V  Q  Y  L  L  S  N  G  Q
Query                2532  GCACCTGGCTGCCAAGAAAGGCCACTACGAAGTGGTCCAGTACCTGCTTTCAAATGGACA  2591
Sbjct                4789  ............................................................  4848

CDS:histone-lysine N  857    M  D  V  N  C  Q  D  D  G  G  W  T  P  M  I  W  A  T  E  Y
Query                2592  GATGGACGTCAACTGTCAGGATGACGGAGGCTGGACACCCATGATCTGGGCCACAGAGTA  2651
Sbjct                4849  ............................................................  4908

CDS:histone-lysine N  877    K  H  V  D  L  V  K  L  L  L  S  K  G  S  D  I  N  I  R  D
Query                2652  CAAGCACGTGGACCTCGTGAAGCTGCTGCTGTCCAAGGGCTCTGACATCAACATCCGAGA  2711
Sbjct                4909  ............................................................  4968

CDS:histone-lysine N  897    N  E  E  N  I  C  L  H  W  A  A  F  S  G  C  V  D  I  A  E
Query                2712  CAACGAGGAGAACATTTGCCTGCACTGGGCGGCGTTCTCCGGCTGCGTGGACATAGCCGA  2771
Sbjct                4969  ............................................................  5028

CDS:histone-lysine N  917    I  L  L  A  A  K  C  D  L  H  A  V  N  I  H  G  D  S  P  L
Query                2772  GATCCTGCTGGCTGCCAAGTGCGACCTCCACGCCGTGAACATCCACGGAGACTCGCCACT  2831
Sbjct                5029  ............................................................  5088

CDS:histone-lysine N  937    H  I  A  A  R  E  N  R  Y  D  C  V  V  L  F  L  S  R  D  S
Query                2832  GCACATTGCCGCCCGGGAGAACCGCTACGACTGTGTCGTCCTCTTTCTTTCTCGGGATTC  2891
Sbjct                5089  ............................................................  5148

CDS:histone-lysine N  957    D  V  T  L  K  N  K  E  G  E  T  P  L  Q  C  A  S  L  N  S
Query                2892  AGATGTCACCTTAAAGAACAAGGAAGGAGAGACGCCCCTGCAGTGTGCGAGCCTCAACTC  2951
Sbjct                5149  ............................................................  5208

CDS:histone-lysine N  977    Q  V  W  S  A  L  Q  M  S  K  A  L  Q  D  S  A  P  D  R  P
Query                2952  TCAGGTGTGGAGCGCTCTGCAGATGAGCAAGGCTCTGCAGGACTCGGCCCCCGACAGGCC  3011
Sbjct                5209  ............................................................  5268
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CDS:histone-lysine N  997    S  P  V  E  R  I  V  S  R  D  I  A  R  G  Y  E  R  I  P  I
Query                3012  CAGCCCCGTGGAGAGGATAGTGAGCAGGGACATCGCTCGAGGCTACGAGCGCATCCCCAT  3071
Sbjct                5269  ............................................................  5328

CDS:histone-lysine N  1017   P  C  V  N  A  V  D  S  E  P  C  P  S  N  Y  K  Y  V  S  Q
Query                3072  CCCCTGTGTCAACGCCGTGGACAGCGAGCCATGCCCCAGCAACTACAAGTACGTCTCTCA  3131
Sbjct                5329  ............................................................  5388

CDS:histone-lysine N  1037   N  C  V  T  S  P  M  N  I  D  R  N  I  T  H  L  Q  Y  C  V
Query                3132  GAACTGCGTGACGTCCCCCATGAACATCGACAGAAATATCACTCATCTGCAGTACTGCGT  3191
Sbjct                5389  ............................................................  5448

CDS:histone-lysine N  1057   C  I  D  D  C  S  S  S  N  C  M  C  G  Q  L  S  M  R  C  W
Query                3192  GTGCATCGACGACTGCTCCTCCAGCAACTGCATGTGCGGCCAGCTCAGCATGCGCTGCTG  3251
Sbjct                5449  ............................................................  5508

CDS:histone-lysine N  1077   Y  D  K  D  G  R  L  L  P  E  F  N  M  A  E  P  P  L  I  F
Query                3252  GTACGACAAGGATGGCCGGCTCCTGCCAGAGTTCAACATGGCGGAGCCTCCCTTGATCTT  3311
Sbjct                5509  ............................................................  5568

CDS:histone-lysine N  1097   E  C  N  H  A  C  S  C  W  R  N  C  R  N  R  V  V  Q  N  G
Query                3312  CGAATGCAACCACGCGTGCTCCTGCTGGAGGAACTGCCGAAATCGCGTCGTACAGAATGG  3371
Sbjct                5569  ............................................................  5628

CDS:histone-lysine N  1117   L  R  A  R  L  Q  L  Y  R  T  R  D  M  G  W  G  V  R  S  L
Query                3372  TCTCAGGGCAAGGCTGCAGCTCTACCGGACGCGGGACATGGGCTGGGGCGTGCGGTCCCT  3431
Sbjct                5629  ............................................................  5688

CDS:histone-lysine N  1137   Q  D  I  P  P  G  T  F  V  C  E  Y  V  G  E  L  I  S  D  S
Query                3432  GCAGGACATCCCACCAGGCACCTTTGTCTGCGAGTATGTTGGGGAGCTGATTTCAGACTC  3491
Sbjct                5689  ............................................................  5748

CDS:histone-lysine N  1157   E  A  D  V  R  E  F  D  S  Y  L  F  D  L  D  N  K  D  G  E
Query                3492  AGAAGCCGACGTTCGAGAGGAAGATTCTTACCTCTTTGATCTCGACAATAAGGACGGGGA  3551
Sbjct                5749  ............................................................  5808

CDS:histone-lysine N  1177   V  Y  C  I  D  A  R  F  Y  G  N  V  S  R  F  I  N  H  H  C
Query                3552  GGTTTACTGCATCGACGCGCGGTTCTACGGGAACGTCAGCCGGTTCATCAACCACCACTG  3611
Sbjct                5809  ............................................................  5868

CDS:histone-lysine N  1197   E  P  N  L  V  P  V  R  V  F  M  A  H  Q  D  L  R  F  P  R
Query                3612  CGAGCCCAACCTGGTGCCCGTGCGCGTGTTCATGGCCCACCAGGACCTGCGGTTCCCCCG  3671
Sbjct                5869  ............................................................  5928

CDS:histone-lysine N  1217   I  A  F  F  S  T  R  L  I  E  A  G  E  Q  L  G  F  D  Y  G
Query                3672  GATCGCCTTCTTCAGCACCCGCCTGATCGAGGCCGGCGAGCAGCTCGGGTTTGACTATGG  3731
Sbjct                5929  ............................................................  5988

CDS:histone-lysine N  1237   E  R  F  W  D  I  K  G  K  L  F  S  C  R  C  G  S  P  K  C
Query                3732  AGAGCGCTTCTGGGACATCAAAGGCAAGCTCTTCAGCTGCCGCTGCGGCTCCCCCAAGTG  3791
Sbjct                5989  ............................................................  6048

CDS:histone-lysine N  1257   R  H  S  S  A  A  L  A  Q  R  Q  A  S  A  A  Q  E  A  Q  E
Query                3792  CCGGCACTCGAGCGCGGCCCTGGCCCAGCGTCAGGCCAGCGCGGCCCAGGAGGCCCAGGA  3851
Sbjct                6049  ............................................................  6108

CDS:histone-lysine N  1277   D  G  L  P  D  T  S  S  A  A  A  A  D  P  L
Query                3852  GGACGGCTTGCCCGACACCAGCTCCGCGGCTGCCGCCGACCCCCTATGAGACGCCGCCGG  3911
Sbjct                6109  ............................................................  6168
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Query  3912  CCAGCGGGGCGCTCGGGAGCCAGGGACCGCCGCGTCGCCGATTAGAGGACGAGGAGGAGA  3971
Sbjct  6169  ............................................................  6228

Query  3972  GATTCCGCACGCAACCGAAAGGGTCCTTCGGGGCTGCGCCGCCGGCTTCCTGGAGGGGTC  4031
Sbjct  6229  ............................................................  6288

Query  4032  GGAGGTGAGGCTGCAGCCCCTGCGGGCGGGTGTGGATGCCTCCCAGCCACCTTCCCAGAC  4091
Sbjct  6289  ............................................................  6348

Query  4092  CTGCGGCCTCACCGCGGGCCCAGTGCCCAGGCTGGAGCGCACACTTTGGTCCGCGCGCCA  4151
Sbjct  6349  ............................................................  6408

Query  4152  GAGACGCTGGGAGTCCGCACTGGCATCACCTTCTGAGTTTCTGATGCTGATTTGTCGTTG  4211
Sbjct  6409  ............................................................  6468

Query  4212  CGAAGTTTCTCGTTTCTTCCTCTGACCTCCGAGGTCCCCGCTGCACCACGGGGTTGCTCT  4271
Sbjct  6469  ............................................................  6528

Query  4272  GTTCTCCTGTCCGGCCCAGACTCTTCTGTGTGGCGCCGCCGAAGCCACCGTTAGCGCGAG  4331
Sbjct  6529  ............................................................  6588

Query  4332  CTGCTCCGTTCGCCCTGCCCACGGCCTGCGTGGCTGGGGCCGAGTCCCAGGGGCCGCACG  4391
Sbjct  6589  ............................................................  6648

Query  4392  GAGGGCACAGTCTCCTGTCAGGCTCGGAGAGGTCAGGAGACCGACCCCACCACTAACTTT  4451
Sbjct  6649  ............................................................  6708

Query  4452  GGAGAAAATGTGGGTTTGCTTTTTAAAGGAATCCTATATCTAGTCCTATATATCAAACCT  4511
Sbjct  6709  ............................................................  6768

Query  4512  CTAACTGACGTTTCTTTTCGAGGAAGTGGCTTGGTGGGTGCAGCCCCCGCCGGTTCCGTT  4571
Sbjct  6769  ............................................................  6828

Query  4572  GACGCTGGCACCTTCTGTTGATTTTTTAAGCCACATGCTATGATGAATAAACTGATTTAT  4631
Sbjct  6829  ............................................................  6888

Query  4632  TTTCTACCATTACTGAACATTAGGacaaacacaaaatataaaaaacaaaacacaGACAACGG  4691
Sbjct  6889  ............................................................  6948

Query  4692  TGCTGATTCTGGTGTGGTTTCTACTCACCACGTGAAATAAACTATCAACTGTATAAAGAG  4751
Sbjct  6949  ............................................................  7008

Query  4752  AACAAAGTGATTTTAGAATAAAATGCAGGAAAAACTTTTTTAAAGATGTTAGTCTTGTAG  4811
Sbjct  7009  ............................................................  7068

Query  4812  CGTGAATAAATTTGCCATCACCTTTTGTGTGGTGGCCTGGCAGGTCATATACtttttttt  4871
Sbjct  7069  ............................................................  7128

Query  4872  GGCATATACCTTTTTAAAGACTGTAATTAGTGCAGTAACAGTGGGGttttttttGTGCAA  4931
Sbjct  7129  ............................................................  7188

Query  4932  CTCTTCTAAAAACATTCATAATGCAGTCATGTTTAttttttttCTGTTAAAATGTTTTTGA  4991
Sbjct  7189  ............................................................  7248

Query  4992  CAGTTTTAAGAGCAGTCTTTTGGCTCTGACCATTTCTTGTTCTGTTTCCAATGAAATCAA  5051
Sbjct  7249  ............................................................  7308

Query  5052  TaaaaaaaaaGAAGTACTTTAAA  5074


Sbjct  7309  ........................  7331
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