

RIKEN Clone ID : RBdS104J13

Vector : pGCAP10

Gene	HDAC2	
RefSeq_mRNA	NM_001527.4	9737 bp

● **Plasmid DNA purification**

Date : 2024/04/08

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

Date : 2024/04/09

Purification : QIAGEN Miniprep kit -> dH₂O 100 ul

● **Digestion by restriction enzyme/Concentration calibration**

Date : 2024/04/09

DNA concentration (O.D.): 155 ng/ul

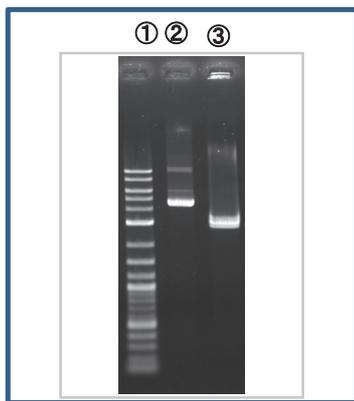
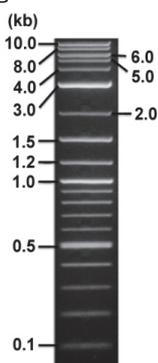
< Size of fragment expected from this clone >

DNA	0.65	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH ₂ O	7.35	ul
Total	10	ul

BamHI 3.1kb (vector), 2.9 kb

Electrophoresis : 1% agarose gel, 1x TAE Buffer

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



①:Marker
②:uncut
③:BamHI

● **Confirmation of the insert/vector junction sequence**

Date : 2024/04/18

Primer A	pGCAP-F
Primer B	pGCAP-R
Primer C	
List of Sequencing Primers	http://dna.brc.riken.jp/en/NRCDhum2en.html

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2024/04/18

DNA (155 ng/ul)	94	ul
10x TE	58	ul
dH ₂ O	431	ul
Total	583	ul

● **Shipping**

Conc. : 25 ng/μl, Volume : 40 μl

Conc. : ___ ng/μl, Volume : ___ μl



APPROVED BY :

BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: NM_001527:Homo sapiens histone deacetylase...

RID [1Z0GSWG0114](#) (Expires on 04-18 16:02 pm)

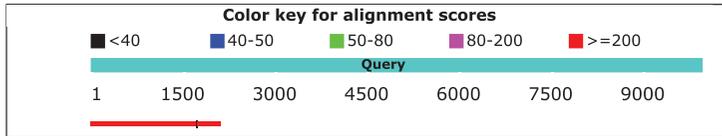
Query ID [NM_001527.4](#)
Description Homo sapiens histone deacetylase 2 (HDAC2), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 9737

Subject ID Icl|Query_6421513
Description None
[See details](#)
Molecule type dna
Subject Length 2688
Program BLASTN 2.15.0+

RBdS104J13hts.seq

Graphic Summary

Distribution of the top 2 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Table with 7 columns: Description, Max Score, Total Score, Query Cover, E value, Per. Ident, Accession. Row 1: None provided, 3094, 3778, 21%, 0.0, 100.00%, Query_6421513

Alignments

Sequence ID: Query_6421513 Length: 2688 Number of Matches: 2 Range 1: 2 to 1676

Alignment table with columns: Score, Expect, Identities, Gaps, Strand, Frame. Contains multiple rows of sequence alignments between the query and subject, including CDS:histone deacetylase regions.

Sbjct 782 GTGATGGTGTGAAGAAGCTTTTTATACAACAGATCGTGAATGACGGTATCATCCATA 841
 CDS:histone deacetyl 201 K Y G E Y F P G T G D L R D I G A G K G 901
 Query 842 AATATGGGGAATACTTTCCTGGCACAGGAGACTTGAGGGATATGGTGTGGAAAAGGCA 901
 Sbjct 842 AATATGGGGAATACTTTCCTGGCACAGGAGACTTGAGGGATATGGTGTGGAAAAGGCA 901
 CDS:histone deacetyl 221 K Y Y A V N F P M R D G I D E S Y G Q 961
 Query 902 AATACTATGCTGCAATTTTCCAATGAGAGATGGTATAGATGATGAGTCATATGGGCAGA 961
 Sbjct 902 AATACTATGCTGCAATTTTCCAATGAGAGATGGTATAGATGATGAGTCATATGGGCAGA 961
 CDS:histone deacetyl 241 I F K P I I S K V M E M Y Q P S A V V L L 1021
 Query 962 TATTTAAGCCTATTATCTCAAAGGTGATGGAGATGATCAACCTAGTGTGTGGTATTAC 1021
 Sbjct 962 TATTTAAGCCTATTATCTCAAAGGTGATGGAGATGATCAACCTAGTGTGTGGTATTAC 1021
 CDS:histone deacetyl 261 Q C G A D S L S G D R L G C F N L T V K 1081
 Query 1022 AGTGTGGTGCAGACTCATTATCTGGTATGACTGGTGTGTTCAATCTAACAGTCAAAG 1081
 Sbjct 1022 AGTGTGGTGCAGACTCATTATCTGGTATGACTGGTGTGTTCAATCTAACAGTCAAAG 1081
 CDS:histone deacetyl 281 G H A K C V E V V K T F N L P L L M L G 1141
 Query 1082 GTCATGCTAAATGTGAGAAGTTGAAAACTTTAACTTACCATTACTGATGCTGGAG 1141
 Sbjct 1082 GTCATGCTAAATGTGAGAAGTTGAAAACTTTAACTTACCATTACTGATGCTGGAG 1141
 CDS:histone deacetyl 301 G G G Y T I R N V A R C W T Y E T A V A 1201
 Query 1142 GAGGTGGCTACACAATCCGTAATGTGCTCGATGTGGACATAGAGACTGCAGTTGCC 1201
 Sbjct 1142 GAGGTGGCTACACAATCCGTAATGTGCTCGATGTGGACATAGAGACTGCAGTTGCC 1201
 CDS:histone deacetyl 321 L D C E I P N E L P Y N D Y F E Y F G P 1261
 Query 1202 TTGATTGTGAGATCCCAATGAGTGGCCATATAATGATTACTTGAGTATTTGGACCAG 1261
 Sbjct 1202 TTGATTGTGAGATCCCAATGAGTGGCCATATAATGATTACTTGAGTATTTGGACCAG 1261
 CDS:histone deacetyl 341 D F K L H I S P S N M T N Q N T P E Y M 1321
 Query 1262 ACTTCAAAGTGCATATTAGTCTTCAAACATGACAAACAGAACACTCCAGAAATATGG 1321
 Sbjct 1262 ACTTCAAAGTGCATATTAGTCTTCAAACATGACAAACAGAACACTCCAGAAATATGG 1321
 CDS:histone deacetyl 361 E K I K Q R L F E N L R M L P H A P G V 1381
 Query 1322 AAAAGATAAAACAGCGTTTGTGAAAATTTGCGCATGTTACCTGATGCACCTGGTGTCC 1381
 Sbjct 1322 AAAAGATAAAACAGCGTTTGTGAAAATTTGCGCATGTTACCTGATGCACCTGGTGTCC 1381
 CDS:histone deacetyl 381 Q M Q A I P E D A V H E D S G D E D G E 1441
 Query 1382 AGATGCAAGCTATCCAGAAGATGCTGTTGATGAAGACAGTGGAGATGAAGATGGAGAAG 1441
 Sbjct 1382 AGATGCAAGCTATCCAGAAGATGCTGTTGATGAAGACAGTGGAGATGAAGATGGAGAAG 1441
 CDS:histone deacetyl 401 D P D K R I S I R A S D K R I A C D E E 1501
 Query 1442 ATCCAGACAAGAGAATTTCTATTCGAGCATCAGACAAGCGGATAGCTTGTGATGAAGAAT 1501
 Sbjct 1442 ATCCAGACAAGAGAATTTCTATTCGAGCATCAGACAAGCGGATAGCTTGTGATGAAGAAT 1501
 CDS:histone deacetyl 421 F S D S E D E G E G G R R N V A D H K K 1561
 Query 1502 TCTCAGATTCTGAGGATGAAGGAGAAGGAGTGGCAAGAAATGTGGCTGATCATAaagaag 1561
 Sbjct 1502 TCTCAGATTCTGAGGATGAAGGAGAAGGAGTGGCAAGAAATGTGGCTGATCATAAAGAAG 1561
 CDS:histone deacetyl 441 G A K K A R I E E D K K E T E D K K T D 1621
 Query 1562 gagcaagaagctagaattgaagaagataagaagaacaagaggacaaaaaaCAGACG 1621
 Sbjct 1562 GAGCAAGAAGCTAGAATTGAAGAAGATAAGAAGAACAAGAGGACAAAAAACAGACG 1621
 CDS:histone deacetyl 461 V K E E D K S K D N S G E K T D T K G 1676
 Query 1622 TTAAGGAAGAAGATAAATCAAAGGACAACAGTGGTAAAAAACAGATACCAAAAGG 1676
 Sbjct 1622 TTAAGGAAGAAGATAAATCAAAGGACAACAGTGGTAAAAAACAGATACCAAAAGG 1676

Range 2: 2295 to 2667

Score	Expect	Identities	Gaps	Strand	Frame
684 bits(370)	0.0()	372/373(99%)	0/373(0%)	Plus/Plus	

Features:

CDS:histone deacetyl 479 G T K S E Q L S N P 1735
 Query 1676 GAACCAATCAGAACAGCTCAGCAACCCCTGAATTTGACAGTCTCACCAAATTCAGAAAA 1735
 Sbjct 2295 GAACCAATCAGAACAGCTCAGCAACCCCTGAATTTGACAGTCTCACCAAATTCAGAAAA 2354
 Query 1736 TCATTAAGAAAAAATTTGAAAGGAAAAATGTTTTCTTTTGAAGACTTCTGGCTTCATT 1795
 Sbjct 2355 TCATTAAGAAAAAATTTGAAAGGAAAAATGTTTTCTTTTGAAGACTTCTGGCTTCATT 2414
 Query 1796 TTATACTACTTTGGCATGGACTGTAtttatttcaaatggcttttttctttttgttttc 1855
 Sbjct 2415 TTATACTACTTTGGCATGGACTGTATTATTTCAAATGGCTTTTCGTTTTGTTTTTC 2474
 Query 1856 ttggcaagttttatgtgagtttttctaatatgaagcaaaattctttctCCACCATG 1915
 Sbjct 2475 TTGGCAAGTTTTATGTGAGTTTTCTAATTAAGCAAAATTTCTTTCTCCACCAAG 2534
 Query 1916 CTTTATGTGATAGTATTTAAAAATGATGTGAGTATTATGTCaaaaaaCTGATCTATTA 1975
 Sbjct 2535 CTTTATGTGATAGTATTTAAAAATGATGTGAGTATTATGTCAAAAAACAGTCTATTA 2594

Query 1976 AAGAAGTAATTGGCCTTTCTGAGCTGATTTTTCCATCTTTGTAAATATCTTTATAAAA 2035
 Sbjct 2595 AAGAAGTAATTGGCCTTTCTGAGCTGATTTTTCCATCTTTGTAAATATCTTTATAAAA 2654
 Query 2036 AATTGACTTGGG 2048
 Sbjct 2655 AATTGACTTGGG 2667

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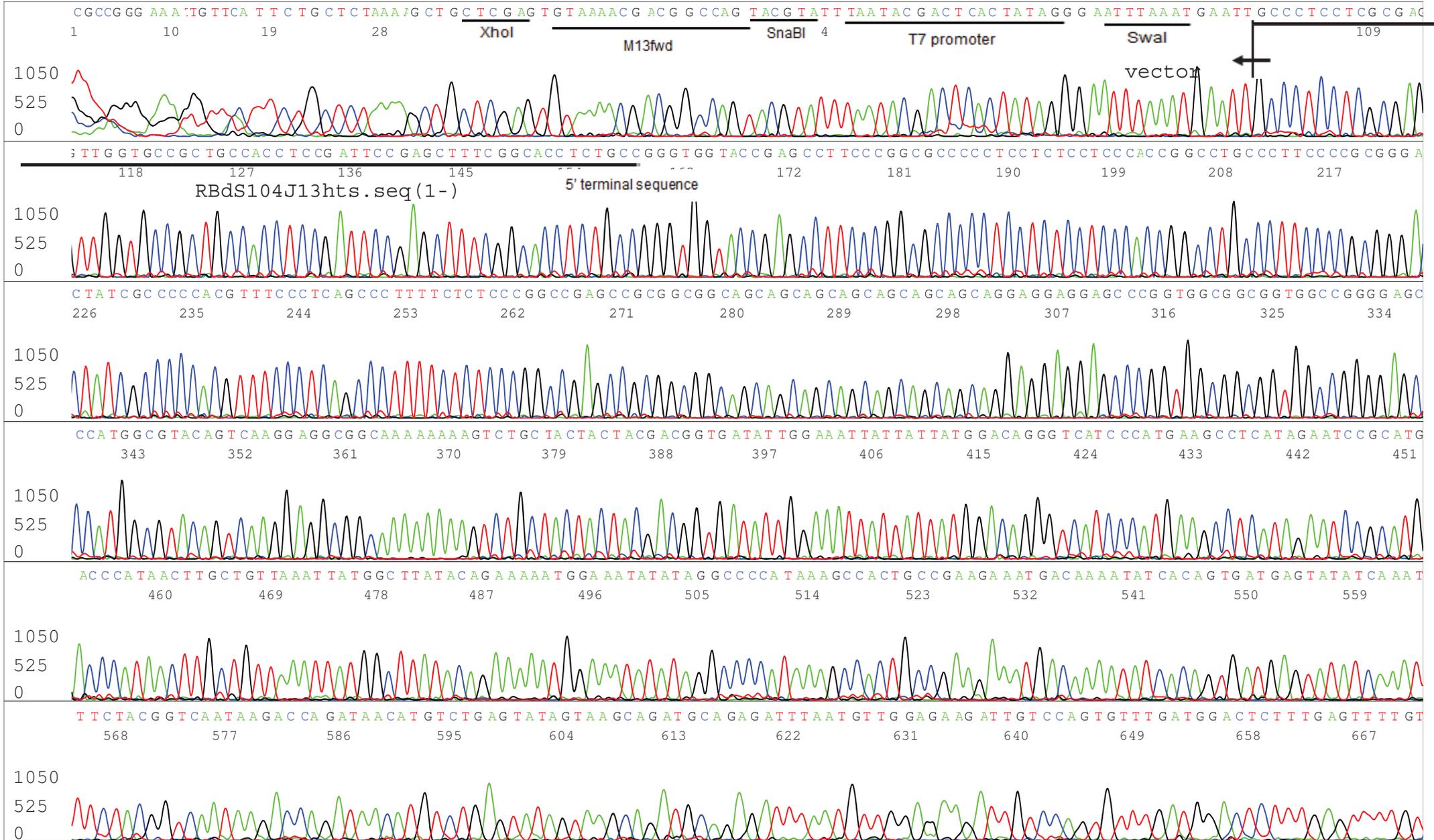
Score	Expect	Identities	Gaps	Strand
1936 bits(1048)	0.0	1050/1051(99%)	0/1051(0%)	Plus/Minus

Features: [histone deacetylase 2](#) Query sequence: [histone deacetylase 2 isoform x1](#) [RBd104j13hts.seq](#)

Query	1617	AGACGTTAAGGAAGAAATAAATCGAAGGACAAACAGTGGTGAAAAAACAGATACGAAAGG	1676
Sbjct	113941767	AGACGTTAAGGAAGAAAGATAAATCGAAGGACAAACAGTGGTGAAAAAACAGATACGAAAGG	113941708
Query	1677	GTAAAAATGATGTTCCCTTATCAAGTACTTTTACATACTAATAAAAAATAGTAAACATGTTTAT	1736
Sbjct	113941707	GTAAAAATGATGTTCCCTTATCAAGTACTTTTACATACTAATAAAAAATAGTAAACATGTTTAT	113941648
Query	1737	TGGTGTGTGTTTGTGTAGACACGCTTCAGAAATACTAGACTGAACCTTAGAAGCATCATTATG	1796
Sbjct	113941647	TGGTGTGTGTTTGTGTAGACACGCTTCAGAAATACTAGACTGAACCTTAGAAGCATCATTATG	113941588
Query	1797	AGGTGCTCTGAATTTTAGTTTTGTATTGGTAGATAAAGCAACATATGCCAICTTAGCTAATT	1856
Sbjct	113941587	AGGTGCTCTGAATTTTAGTTTTGTATTGGTAGATAAAGCAACATATGCCAICTTAGCTAATT	113941528
Query	1857	GGTTTATCAGTATACGTATATCAGTCAAGTTTGTATTCCTGTACGTAGTTTATCTGAGACG	1916
Sbjct	113941527	GGTTTATCAGTATACGTATATCAGTCAAGTTTGTATTCCTGTACGTAGTTTATCTGAGACG	113941468
Query	1917	CTTTTTTGCCTGTATCTTTTATAATAATGCACCTAAATGGTTTCAITGGTCTTAAATTTCTG	1976
Sbjct	113941467	CTTTTTTGCCTGTATCTTTTATAATAATGCACCTAAATGGTTTCAITGGTCTTAAATTTCTG	113941408
Query	1977	TGTACATGATTTTTTTTAGTGTGTGAGATAGGTAAATTTAAGAAACAAATTTAAAGTAAAA	2036
Sbjct	113941407	TGTACATGATTTTTTTTAGTGTGTGAGATAGGTAAATTTAAGAAACAAATTTAAAGTAAAA	113941348
Query	2037	ACAGTTGAAGGATTTTAGTGTGAGAAAGCAATAAATGTTGGGCACACATAAATTTTGTGC	2096
Sbjct	113941347	ACAGTTGAAGGATTTTAGTGTGAGAAAGCAATAAATGTTGGGCACACATAAATTTTGTGC	113941288
Query	2097	CAGCCCTTACAGGATTAACCTTGGAAATAGTTTATTAATCACTAGAAAAATTTAAGGCATTTAA	2156
Sbjct	113941287	CAGCCCTTACAGGATTAACCTTGGAAATAGTTTATTAATCACTAGAAAAATTTAAGGCATTTAA	113941228
Query	2157	TTACTCGAAGAAACAGCTTAAAGCATTAATCAATTAATGTTTCTTAGCATGAGCCACAGG	2216
Sbjct	113941227	TTACTCGAAGAAACAGCTTAAAGCATTAATCAATTAATGTTTCTTAGCATGAGCCACAGG	113941168
Query	2217	ACCTGATCAATAATAATAGGTCAAGTGCATTTAAACCAAGATTGTGCCATTTTAAATATTC	2276
Sbjct	113941167	ACCTGATCAATAATAATAGGTCAAGTGCATTTAAACCAAGATTGTGCCATTTTAAATATTC	113941108
Query	2277	ACATTTGGCTCTTTTAAACAGAAACAAATCAGAACAGCTCAGCAACCCCTGAAATTTGACAGT	2336
Sbjct	113941107	ACATTTGGCTCTTTTAAACAGAAACAAATCAGAACAGCTCAGCAACCCCTGAAATTTGACAGT	113941048
Query	2337	CTCAGCAATTTTCAGAAAAATCAATAAAAAGAAAAATTTGAAAAAGAAAAATGTTTTCTTTTTG	2396
Sbjct	113941047	CTCAGCAATTTTCAGAAAAATCAATAAAAAGAAAAATTTGAAAAAGAAAAATGTTTTCTTTTTG	113940988
Query	2397	AAGACCTCTGGCTTCATTTTATACTACTTTGGCATGGACTGTATTattatttttcaaatggct	2456
Sbjct	113940987	AAGACCTCTGGCTTCATTTTATACTACTTTGGCATGGACTGTATTattatttttcaaatggct	113940928
Query	2457	ttttcgttttttggtttttcttggcaagttttatgtgagtttttcttaattatgaagcaaaa	2516
Sbjct	113940927	ttttcgttttttggtttttcttggcaagttttatgtgagtttttcttaattatgaagcaaaa	113940868
Query	2517	tttctttcttcacagcagggcttttatgtgataagtaattttaaatttgatgtgaatttatgtc	2576
Sbjct	113940867	tttctttcttcacagcagggcttttatgtgataagtaattttaaatttgatgtgaatttatgtc	113940808
Query	2577	aaaaaaacTgATCTATTAAAGAAAGTAATTTGGCCTTTCTGAGCTGAATTTTTCGATCTTTTG	2636
Sbjct	113940807	AAAAAAACGATCTATTAAAGAAAGTAATTTGGCCTTTCTGAGCTGAATTTTTCGATCTTTTG	113940748
Query	2637	TAAATTATCTTTAATAAAAAATTTGACTTgga 2667	
Sbjct	113940747	TAAATTATCTTTAATAAAAAATTTGACTTgga 113940717	

S/N G:20 A:41 T:30 C:32
KB.bcp
KB 1.4.1.8 Cap:3

Primer A : pGCAP-F
5' CTCAGTGGATGTTGCCTTTAC 3'



Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

6608_RBdS104J13_B4D5_pGCAP_R_D01_04_ABI08
6608_RBdS104J13_B4D5_pGCAP_R
KB_3500_POP7_BDTv3.mob
Pts 1725 to 12971 Pk1 Loc:1702
Version 6.0 HiSQV Bases: 67

Inst Model/Name 3500/3500 Instrument
Apr 10,2024 10:14AM, JST
Apr 10,2024 10:49AM, JST
Spacing:13.25 Pts/Panel1350
Plate Name: 20240410_GNP

