NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARh05F06
Vector : pGCAP1

SNORA50C
Lot# : 7674_B3Bd

Gene	SNORA76	
RefSeq_mRNA	NR_002995.1	133 bp

● Plasmid DNA purification

Date : 23.02.28 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.01 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.01

DNA concentration (O.D.): 152 ng/ul

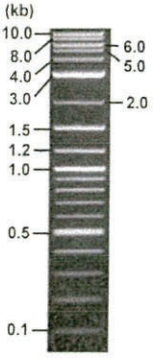
DNA	0.7 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.3 ul
Total	10 ul

< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 0.7 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 : 2026/06/18

full sequence : ARh05F06hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (152 ng/ul)	70	ul
10x TE	43	ul
dH_2O	313	ul
Total	426	ul

● Shipping

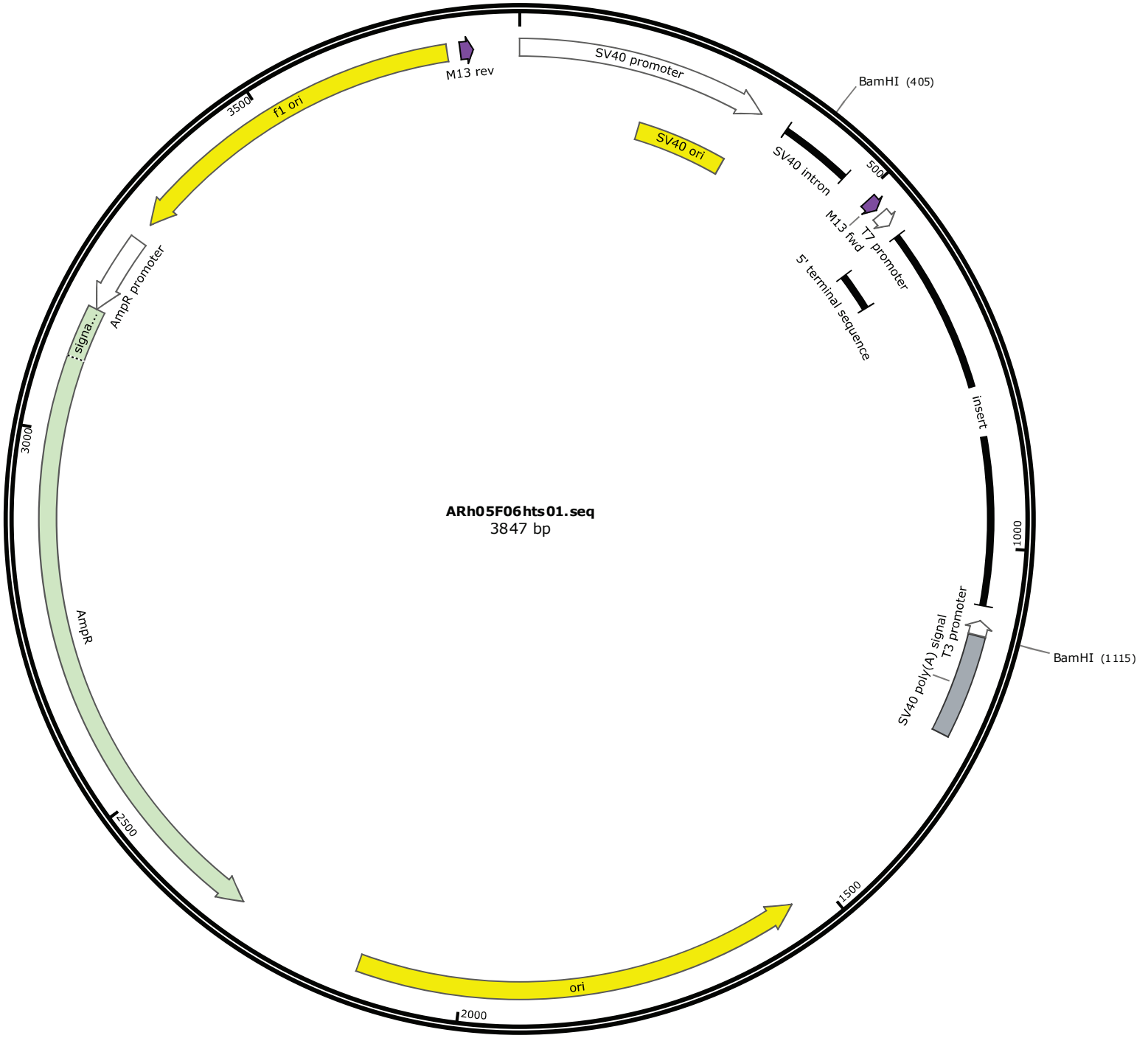
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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


ARh05F06hts01.seq
3847 bp
M13 rev
SV40 promoter
BamHI (405)
f1 ori
SV40 ori
SV40 intron
500
M13 fwd
T7 promoter
5' terminal sequence
AmpR promoter
signa...
Insert
3000
1000
SV40 poly(A) signal
T3 promoter
BamHI (1115)
AmpR
2500
1500
ori
2000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_139281:Homo sapiens WD repeat domain 36...

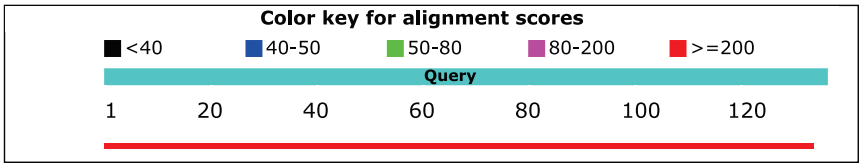
RID 36Z79586114 (Expires on 06-19 13:06 pm)

Query ID	NR_002995.1	**Subject ID**	lcl|Query_3236045
Description	Homo sapiens small nucleolar RNA, H/ACA box 50C (SNORA50C), small nucleolar RNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	133	**Subject Length**	3847
		Program	BLASTN 2.17.0+

ARh05F06hts01.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	246	246	100%	2e-69	100.00%	Query_3236045

Alignments

Sequence ID: Query_3236045 Length: 3847 Number of Matches: 1
Range 1: 570 to 702

Score	Expect	Identities	Gaps	Strand	Frame
246 bits(133)	2e-69()	133/133(100%)	0/133(0%)	Plus/Plus	

Features:

```
Query  1    GCGCTGTCTTTGAGCCCCCGCCGAGCTTCCTCGTGGCGCCGGGGGTCAATCTGCAGCGCT  60
Sbjct  570  GCGCTGTCTTTGAGCCCCCGCCGAGCTTCCTCGTGGCGCCGGGGGTCAATCTGCAGCGCT  629
Query  61   AGAGCATGTGCTTGCGCATAACTGGGGCCGCCTGGCCTCCCGCGGGCGGCCTTTTTAACC  120
Sbjct  630  AGAGCATGTGCTTGCGCATAACTGGGGCCGCCTGGCCTCCCGCGGGCGGCCTTTTTAACC  689
Query  121  GCGAGCGACAAGA  133
Sbjct  690  GCGAGCGACAAGA  702
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