Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : SpFFH02H02

Lot # :6106_B5Aa

Vector : pDual-FFH1c

Systematic Name	SPAC2F3.17c
ORF length	387 bp

● Plasmid DNA purification

Date : 2025/01/14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> 37℃ O/N

Date : 2025/01/15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/01/15

DNA concentration (O.D.): 379 ng/ul

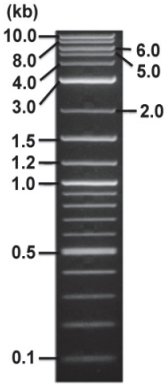
DNA	0.25 ul
Enzyme (SalI + BglII)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

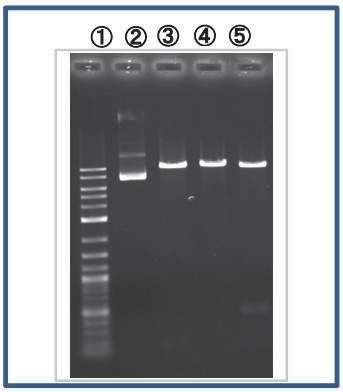
< Size of fragment expected from this clone >

SalI		9.5, 0.1 kb
BglII		9.6 kb
SalI + BglII	9.1,	0.4, 0.1 kb

Erectrophoresis : 0.8% agarose gel, 1x TAE Buffer

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





①:Marker
②:uncut
③:SalI
④:BglII
⑤:SalI+BglII

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/01/21

DNA (379 ng/ul)	86 ul
10x TE	130 ul
dH_2O	1,087 ul
Total	1,304 ul

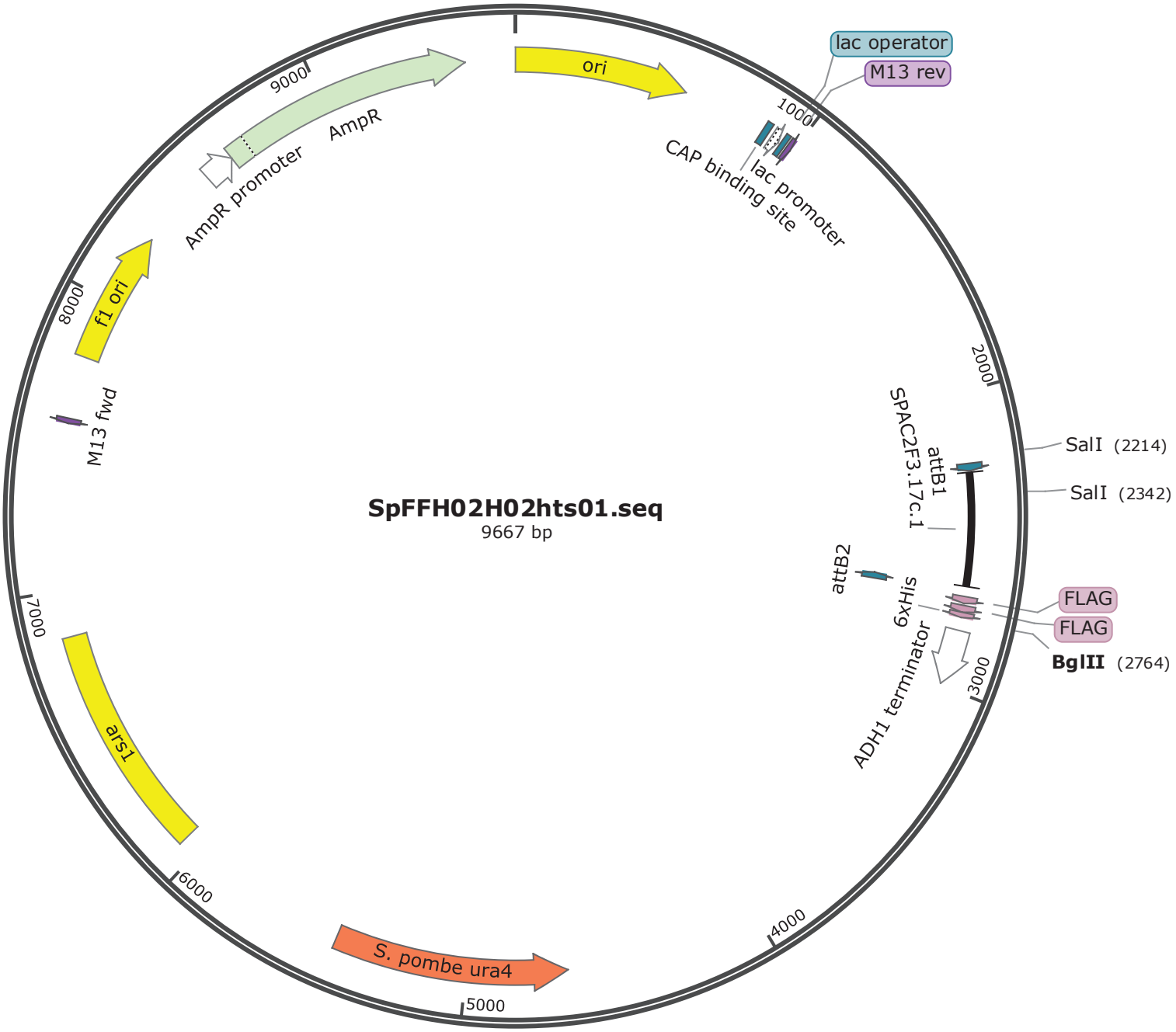
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

検
'25.01.21
笹沼


SpFFH02H02hts01.seq
9667 bp
ori
lac operator
M13 rev
lac promoter
CAP binding site
AmpR
AmpR promoter
f1 ori
M13 fwd
ars1
S. pombe ura4
attB1
SPAC2F3.17c.1
attB2
6xHis
FLAG
FLAG
ADH1 terminator
SalI (2214)
SalI (2342)
BglII (2764)
1000
2000
3000
4000
5000
6000
7000
8000
9000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: Nucleotide Sequence

RID SV771KNZ114 (Expires on 01-21 07:46 am)

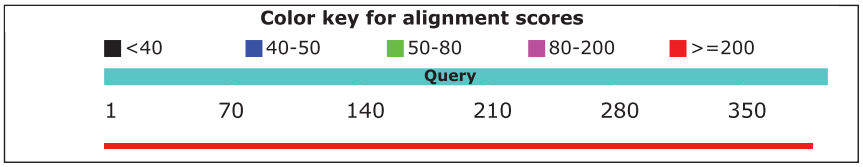
Query ID	lcl|Query_8384825	**Subject ID**	lcl|Query_8384827
Description	None	**Description**	None
			See details
Molecule type	dna	**Molecule type**	dna
Query Length	387	**Subject Length**	9667
		Program	BLASTN 2.16.1+

SPAC2F3.17c

SpFFH02H02hts01.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	713	713	100%	0.0	100.00%	Query_8384827

Alignments

Sequence ID: Query_8384827 Length: 9667 Number of Matches: 1
Range 1: 2270 to 2655

Score	Expect	Identities	Gaps	Strand	Frame
713 bits(386)	0.0()	386/386(100%)	0/386(0%)	Plus/Plus	

Features:

```
Query  1     ATGGATTCTTCTCCTAATGAGTTTTTGAATAAGGTCATCGGCAAAAAAGTTCTTATCCGG  60
Sbjct  2270  ............................................................  2329

Query  61    TTAAGTTCTGGTGTCGACTATAAAGGTATTTAACATGAATTGCGTCGGAGACAATGCAAG  120
Sbjct  2330  ............................................................  2389

Query  121   TTTGCAATTTGTTTCTATCGCTTTAACttttttCCGTTATTTAGGGTTTGTTAATACTA  180
Sbjct  2390  ............................................................  2449

Query  181   AACCTGTTTTTTAGGAATCCTCAGTTGTCTTGATGGTTATATGAACTTGGCCCTTGAACG  240
Sbjct  2450  ............................................................  2509

Query  241   CACAGAAGAATACGTTAATGGCAAGAAGACGAATGTTTATGGAGATGCATTTATTCGTGG  300
Sbjct  2510  ............................................................  2569

Query  301   AAACAATGGTATGGTATTTATATTAAAGTGCTTTGATTTCCTAACTACCGTCCAACAGTC  360
Sbjct  2570  ............................................................  2629

Query  361   TTATATGTTTCTGCTTTAGATGATTA  386
Sbjct  2630  .........................  2655
```

検
'25.01.20
笹沼