Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : SpFFH04C09

Lot # :6106_B5Aa

Vector : pDual-FFH1c

Systematic Name	SPBC30D10.06
ORF length	469 bp

● Plasmid DNA purification

Date : 2025/01/16 Culture : LB (100 ug/ml Ampicillin) 5 ml -> 37℃ O/N

Date : 2025/01/17 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/01/17

DNA concentration (O.D.): 316 ng/ul

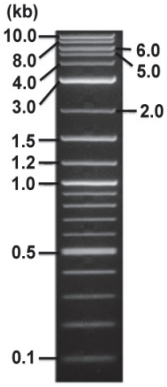
DNA	0.3 ul
Enzyme (SalI + BglII)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

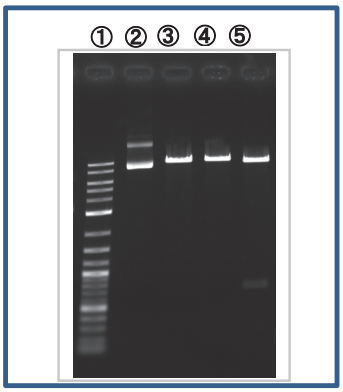
< Size of fragment expected from this clone >

SalI		9.7 kb
BglII		9.7 kb
SalI + BglII	9.1,	0.6 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 : 2025/01/24

DNA (316 ng/ul)	82 ul
10x TE	104 ul
dH_2O	851 ul
Total	1,036 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

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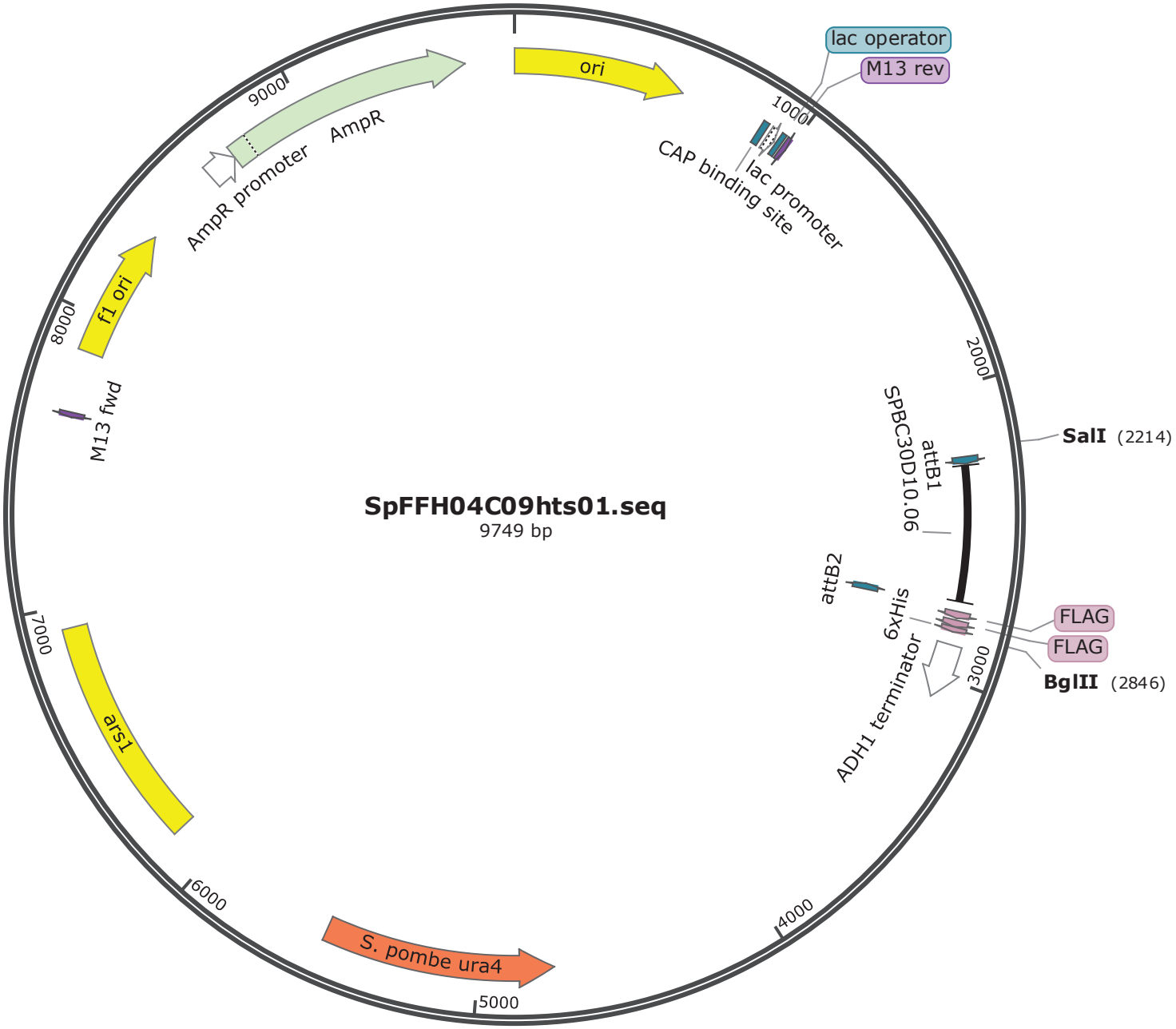

SpFFH04C09hts01.seq
9749 bp
1000
2000
3000
4000
5000
6000
7000
8000
9000
ori
lac operator
M13 rev
lac promoter
CAP binding site
AmpR
AmpR promoter
f1 ori
M13 fwd
SalI (2214)
attB1
SPBC30D10.06
attB2
6xHis
FLAG
FLAG
ADH1 terminator
BglII (2846)
ars1
S. pombe ura4

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_002958:Homo sapiens receptor like tyrosine...

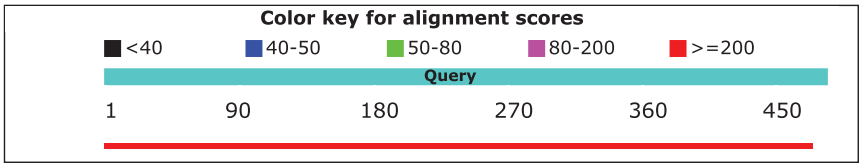
RID T3X5PXJ5114 (Expires on 01-24 14:50 pm)

Query ID	lcl|Query_5795235	**Subject ID**	lcl|Query_5795237
Description	None	**Description**	None
			See details
Molecule type	dna	**Molecule type**	dna
Query Length	469	**Subject Length**	9749
	SPBC30D10.06	**Program**	BLASTN 2.16.1+

SpFFH04C09hts01.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	865	865	100%	0.0	100.00%	Query_5795237

Alignments

Sequence ID: Query_5795237 Length: 9749 Number of Matches: 1
Range 1: 2270 to 2737

Score	Expect	Identities	Gaps	Strand	Frame
865 bits(468)	0.0()	468/468(100%)	0/468(0%)	Plus/Plus	

Features:

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

Query  61    ATGCAACTCAAGGTCGTCCCATACTTGTTGAGTTAAAAAACGGTGAAACGTTTAATGGTC  120
Sbjct  2330  ............................................................  2389

Query  121   ATTTAGAGAATTGTGATAATTACATGAACCTCACACTGCGCGAAGTCATTCGTACTATGC  180
Sbjct  2390  ............................................................  2449

Query  181   CTGATGGTGATAAATTTTTCCGTCTTCCTGAGTGCTATATTCGTGGAAATAATGTATGTT  240
Sbjct  2450  ............................................................  2509

Query  241   GTACCATCCTTTTCTTTGCGGTCGAACATATTAATGCCAGCTGTTACTAACACAACAGAT  300
Sbjct  2510  ............................................................  2569

Query  301   CAAATACCTGCGTATTCAAGATGAGGTGCTTAGTCAAGTAGCTAAACAACAAGCGCAGCA  360
Sbjct  2570  ............................................................  2629

Query  361   AAGAGAAAATCGCGGATCGCGATTTCGCGGACGTGGTCAACGCGGTCGTGGAAACTATGG  420
Sbjct  2630  ............................................................  2689

Query  421   TCACACAGCACCAAACCGTCGTGGCCGTGGTAGAGGTGGACACATGTA  468
Sbjct  2690  ..............................................  2737
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