RIKEN Clone ID : SpFFH25A11

Lot # :6106_B4Lj

Vector : pDual-FFH1c

Systematic Name	SPBC14F5.12c.1
ORF length	1545 bp

● Plasmid DNA purification

Date : 2024/12/19 Culture : LB (100 ug/ml Ampicillin) 5 ml -> 37℃ O/N

Date : 2024/12/20 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/12/20

DNA concentration (O.D.): 314 ng/ul

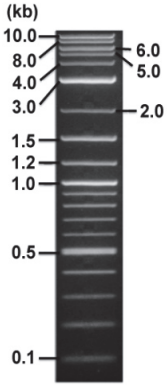
DNA	0.32 ul
Enzyme (SalI + BglII)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.68 ul
Total	10 ul

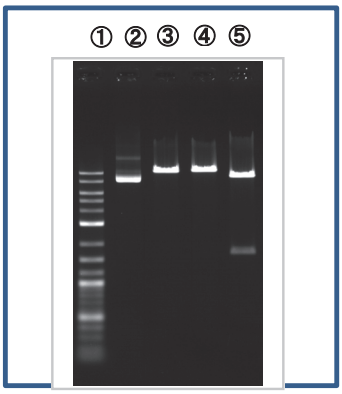
< Size of fragment expected from this clone >

SalI		11 kb
BglII		11 kb
SalI + BglII	9.1,	1.7 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 : 2025/01/14

DNA (314 ng/ul)	82 ul
10x TE	103 ul
dH_2O	845 ul
Total	1,030 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

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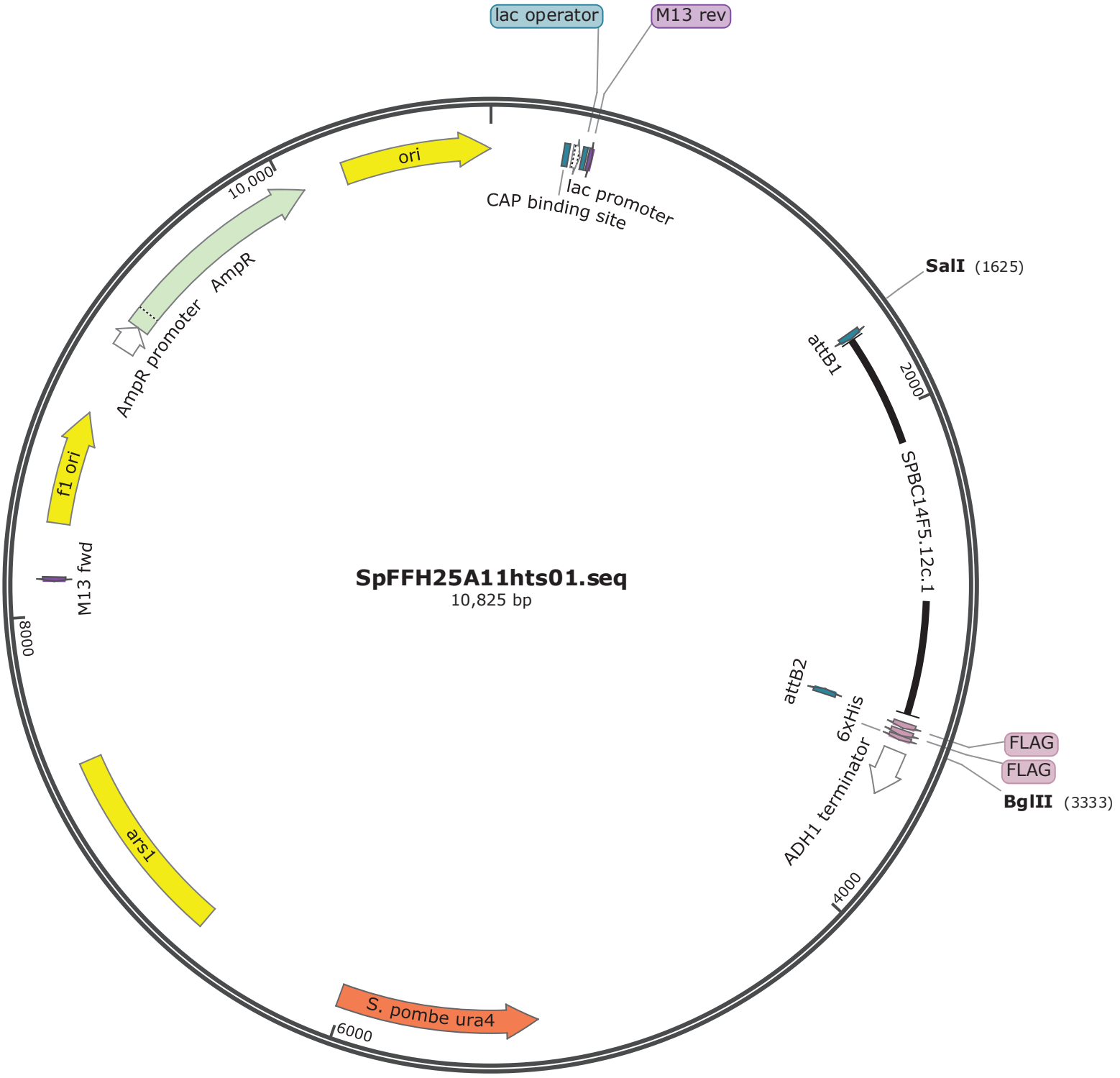

lac operator
M13 rev
ori
lac promoter
CAP binding site
10,000
AmpR promoter
AmpR
SalI (1625)
attB1
2000
SPBC14F5.12c.1
f1 ori
M13 fwd
SpFFH25A11hts01.seq
10,825 bp
8000
attB2
6xHis
FLAG
FLAG
ADH1 terminator
BglII (3333)
4000
ars1
S. pombe ura4
6000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_144590:Homo sapiens ankyrin repeat domain...

RID RW0J11A9114 (Expires on 01-09 11:42 am)

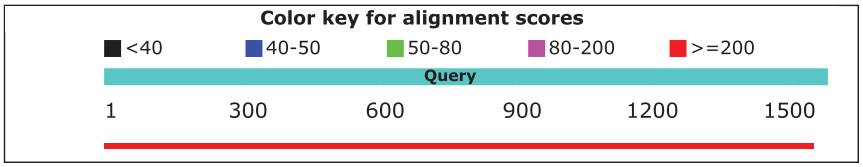
Query ID	lcl|Query_887093	**Subject ID**	lcl|Query_887095
Description	None	**Description**	None
			See details
Molecule type	dna	**Molecule type**	dna
Query Length	1545	**Subject Length**	10825
		Program	BLASTN 2.16.1+

SPBC14F5.12c.1

SpFFH25A11hts01.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	2852	2852	100%	0.0	100.00%	Query_887095

Alignments

Sequence ID: Query_887095 Length: 10825 Number of Matches: 1
Range 1: 1681 to 3224

Score	Expect	Identities	Gaps	Strand	Frame
2852 bits(1544)	0.0()	1544/1544(100%)	0/1544(0%)	Plus/Plus	

Features:

```
Query  1     ATGCCTCCATTGAGGCGTCAAGCGTTGACTTTAGCTGaaaaaaaaGCAATTAGAAAACAT  60
Sbjct  1681  ............................................................  1740

Query  61    TATTTTGAGTCAGCAACTAAACCTTCGCAACAAGAGCTTATTAGTTGGTTCGAGGAGCAC  120
Sbjct  1741  ............................................................  1800

Query  121   TTTCATAAAAAGCTAGCACAATCTACCGTTTCGTCAATTCTATCATCAAAGAACGAATTT  180
Sbjct  1801  ............................................................  1860

Query  181   TTAGATAATCTAGACGCAGAAAACTCTCAAATAAGAAGAAACCGCCAAGGAAAATATCCT  240
Sbjct  1861  ............................................................  1920

Query  241   ATCTTAGAAAACGCCCTTATTGACTGGCAAACGAGGTTGCAAAAACAAGACGGAGCAATT  300
Sbjct  1921  ............................................................  1980

Query  301   ACTGGAAACGCCATCaaaaaaaGCGCCGCAGAATTGTGGAGACGTATACCGGAGTACTCT  360
Sbjct  1981  ............................................................  2040

Query  361   GAGCTTCCGATTCCAGAATTTAGTAACGGTTGGTTAGAGAAGTTCAAAAAGCGTTGTTTA  420
Sbjct  2041  ............................................................  2100

Query  421   AAACACGGCCTTAAGTTACAGGGTGAATCTACTTCAGTAAATCAAGGAACGTATGAGGAA  480
Sbjct  2101  ............................................................  2160
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Query  481   AACATGGTTCAAATACAGGAATTAATAAGTCTTTTTGATCCAAAAGACATCTTTAATATG  540
Sbjct  2161  ............................................................  2220

Query  541   GATGAGACGGGGCTATGCTGGAAACTTATTCCCAATCAATCTCCTGCGAGTGAACGAGTA  600
Sbjct  2221  ............................................................  2280

Query  601   AAAGGAATTACGAGAGATAAGGCTCGTGTCACCGTCACTATTTGTTGTAATGCTACAGGT  660
Sbjct  2281  ............................................................  2340

Query  661   TCTGAAAAGGCCCCTCTTTGGGTGATTGGATATGCTAAAAGTCCAAGGGCCTTTCGGCAA  720
Sbjct  2341  ............................................................  2400

Query  721   GCAAATGCTCATCCTGATTCCATGGATTTTCATTGGCGATATAATGGAACCGCTAGGATG  780
Sbjct  2401  ............................................................  2460

Query  781   ACCACTTCCATTATGGAAGAATGGCTTCGTTGGTTTGACGATTTGATGAAGGGTAGGAAA  840
Sbjct  2461  ............................................................  2520

Query  841   GTTCTACTTATACTGGATAAGTTTGTCGCTCATGAATGCGCTTTGGAAAATATTCGCAAT  900
Sbjct  2521  ............................................................  2580

Query  901   TCCGAGCGAAAGTTGGTAAACACGACTGTTGTTTTCCTTCCTGTAAATTCTACAGAAATT  960
Sbjct  2581  ............................................................  2640

Query  961   TACCATCCTTGTGGCCAAGAGATAGTCTACGCTTTTAAATCATACTACAGAAAATACTGG  1020
Sbjct  2641  ............................................................  2700

Query  1021  CTTAATTACATGCTTGAGGAGATTCGATTGGGAAAGAACCCCAGTAAGACAATGAATGTA  1080
Sbjct  2701  ............................................................  2760

Query  1081  CTAAAAGCAGTTAGATGGATGATTCGTTCTTGGAACGTTGACTTTGAACCATCTATAATA  1140
Sbjct  2761  ............................................................  2820

Query  1141  TACAATTGTTTCCTTCGTTCTGGGCTTTTTCAAAATCAGCAACCACTGACCGGTCCTTCT  1200
Sbjct  2821  ............................................................  2880

Query  1201  CCAGAAACCATTAGAATCGCGGTGAATTTGCAAGAATTGATAGGAAAATACCTTGGTGAT  1260
Sbjct  2881  ............................................................  2940

Query  1261  AAGGATATTTTCCAAATCGAAAATTTTATTAACCCTATTGAAGAAAATTCTGCTGACACT  1320
Sbjct  2941  ............................................................  3000

Query  1321  AATGACGATATCGTTAACCAAGTTGCTGCTCAATTTCTTGATGAACGAGAGTTTGAAACC  1380
Sbjct  3001  ............................................................  3060

Query  1381  GATGAAGAAGAGGAAGAGTCACAGTATTTGTTATCAACAAAGGATGCGATAAATGCCATC  1440
Sbjct  3061  ............................................................  3120

Query  1441  AATACTTTACTAAACTTTCAAGAGCAATCGGAAGATGGAAATGTTTTGTTTACTCGAACA  1500
Sbjct  3121  ............................................................  3180

Query  1501  TTACTTCAGTTTCAAAAGGTTTTAGAAAGCAGATCGATTGTGTA  1544
Sbjct  3181  ..........................................  3224
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