

RIKEN Clone ID : H3115A08

Lot# : 5723_B3Ik

Vector : pSPORT1

Gene	Ly6a	
5' EST Sequence	H3115A08-5	587 bp
3' EST Sequence	H3115A08-3	678 bp

● **Plasmid DNA purification**

Date : 2023/09/21

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

Date : 2023/09/22

Purification : QIAGEN Miniprep kit -> dH₂O 100 ul

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

Date : 2023/09/22

DNA concentration (O.D.): 235 ng/ul

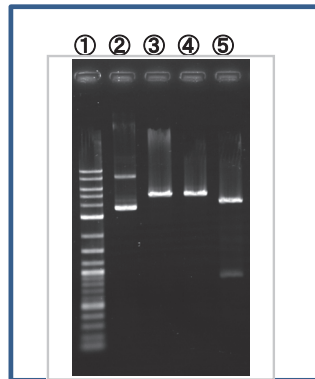
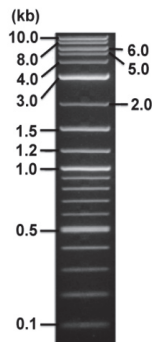
< Size of fragment expected from this clone >

DNA	<u>0.4</u>	ul
Enzyme (SalI + NotI)	<u>0.5 + 0.5</u>	ul
Buffer H	<u>1</u>	ul
dH ₂ O	<u>7.6</u>	ul
Total		<u>10</u> ul

SalI		size unidentified
NotI		size unidentified
SalI + NotI	<u>4.0 kb,</u>	size unidentified

Electrophoresis : 1% agarose gel, 1x TAE Buffer

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



- ①:Marker
- ②:uncut
- ③:SalI
- ④:NotI
- ⑤:SalI + NotI

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

Date : 2023/09/26

DNA (<u>235</u> ng/ul)	<u>86</u>	ul
10x TE	<u>81</u>	ul
dH ₂ O	<u>642</u>	ul
Total		<u>808</u> ul

● **Shipping**

Conc. : 25 ng/μl, Volume : 40 μl

Conc. : ng/μl, Volume : μl

APPROVED BY :



[Questions/comments](#)

BLAST Results

Blast 2 sequences

Job title: [ref|NM_010738.3|](#)

RID [GUGW9CYJ11N](#) (Expires on 09-23 15:34 pm)

Query ID [NM_010738.3](#)

Description Mus musculus lymphocyte antigen 6 family member A (Ly6a), transcript variant 3, mRNA

Molecule type nucleic acid

Query Length 971

Subject ID 3 subjects

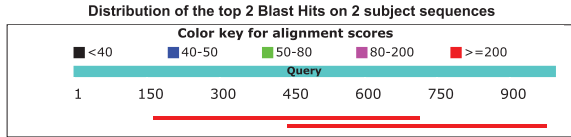
Description [See details](#)

Molecule type dna

Subject Length 1276

Program BLASTN 2.14.1+

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerA (Forward)	1003	1003	56%	0.0	99.82%	Query_28856
primerB (Reverse)	981	981	54%	0.0	100.00%	Query_28857

Alignments

primerA (Forward)

Sequence ID: Query_28856 Length: 622 Number of Matches: 1
Range 1: 76 to 622

Score	Expect	Identities	Gaps	Strand	Frame
1003 bits(543)	0.0()	546/547(99%)	1/547(0%)	Plus/Plus	
Features:					
CDS: lymphocyte antig	1	M D T S H T T K S C L L I L			222
Query	164	TGC-AGCCCTTCTCTGAGGATGGACACTTCCACACTACAAGTCTGTTTGTGATTTCT			
Sbjct	76	TGCTAGCCCTTCTCTGAGGATGGACACTTCCACACTACAAGTCTGTTTGTGATTTCT			135
CDS: lymphocyte antig	15	L V A L C A F R A Q G T E C Y D C Y G			282
Query	223	TCTTGTGCCCTACTGTGTGCAGAAAGAGCTCAGGGACTGGAGTGTACCGTGTCTATGG			
Sbjct	136	TCTTGTGCCCTACTGTGTGCAGAAAGAGCTCAGGGACTGGAGTGTACCGTGTCTATGG			195
CDS: lymphocyte antig	35	V P F E T S C P S I T C P Y P D G V C V			342
Query	283	AGTCCCATTTGAGACTTCTTGCCCACTCAATTACCTGCCCTACCGTATGGAGTCTGTGT			
Sbjct	196	AGTCCCATTTGAGACTTCTTGCCCACTCAATTACCTGCCCTACCGTATGGAGTCTGTGT			255
CDS: lymphocyte antig	55	T O E A A V I V D S O T R K V K N N L C			402
Query	343	TACTCAGGAGGCGCAGTTATTGTGGATTCTCAAAACAAGAAAGTAAAGAACAATCTTTG			
Sbjct	256	TACTCAGGAGGCGCAGTTATTGTGGATTCTCAAAACAAGAAAGTAAAGAACAATCTTTG			315
CDS: lymphocyte antig	75	L P I C P P N I E S M E I L G T K V N V			462
Query	403	CTTACCCTACTGCCCTCCTAATATTGAAAGTATGGAGATCCTGGTACTAAGGTCACCGT			
Sbjct	316	CTTACCCTACTGCCCTCCTAATATTGAAAGTATGGAGATCCTGGTACTAAGGTCACCGT			375
CDS: lymphocyte antig	95	K T S C C O E D L C N V A V P N G G S T			522
Query	463	GAAGACTTCTGTTGCCAGGAGACCTTGAATGTAGCAGTCCCAATGGAGGCGAGCAC			
Sbjct	376	GAAGACTTCTGTTGCCAGGAGACCTTGAATGTAGCAGTCCCAATGGAGGCGAGCAC			435
CDS: lymphocyte antig	115	W T M A G V L L F S L S S V L L L O T L L			582
Query	523	CTGGACCATGGCAGGGGTGCTTGTTCAGCCTGAGCTCAGTCTCCTGCGAGACCTTGTCT			
Sbjct	436	CTGGACCATGGCAGGGGTGCTTGTTCAGCCTGAGCTCAGTCTCCTGCGAGACCTTGTCT			495
Query	583	CTGATGGTCTCCCAATGACCTCCACCCTTGTCTTTATCCTCATGTGCAACAATCTT			642
Sbjct	496	CTGATGGTCTCCCAATGACCTCCACCCTTGTCTTTATCCTCATGTGCAACAATCTT			555
Query	643	CCTGGAGCCCTCTAGTGATGAATATGAGTTATAGAAGCTCCAAGGTGGGAGTAGTGTGT			702
Sbjct	556	CCTGGAGCCCTCTAGTGATGAATATGAGTTATAGAAGCTCCAAGGTGGGAGTAGTGTGT			615
Query	703	GAATAC 709			
Sbjct	616	GAATAC 622			

primerB (Reverse)

Sequence ID: Query_28857 Length: 650 Number of Matches: 1
Range 1: 120 to 650

Score	Expect	Identities	Gaps	Strand	Frame
981 bits(531)	0.0()	531/531(100%)	0/531(0%)	Plus/Minus	
Features:					
CDS: lymphocyte antig	87	I L G T K V N V K T S C C O E D L C N V			500
Query	441	TCCTGGTACTAAGGTCACCTGAAGACTTCTGTTGCCAGGAGACCTTGCATGATGAG			
Sbjct	650	TCCTGGTACTAAGGTCACCTGAAGACTTCTGTTGCCAGGAGACCTTGCATGATGAG			591
CDS: lymphocyte antig	107	A V P N G G S T W T M A G V L L F S L S			560
Query	501	CAGTTCCTCAATGGAGGCGAGACCTGGACCATGGCAGGGGTGCTTGTTCAGCCTGAGCT			
Sbjct	590	CAGTTCCTCAATGGAGGCGAGACCTGGACCATGGCAGGGGTGCTTGTTCAGCCTGAGCT			531
CDS: lymphocyte antig	127	S V L Q T			620
Query	561	CAGTCTCCTGCGAGACCTTGTCTGATGGTCTCCCAATGACCTCCACCCTTGTCTTTT			
Sbjct	530	CAGTCTCCTGCGAGACCTTGTCTGATGGTCTCCCAATGACCTCCACCCTTGTCTTTT			471
Query	621	ATCCTCATGTGCAACAATCTTCTCCTGGAGCCCTCTAGTGATGAATATGAGTTATAGAAG			680
Sbjct	470	ATCCTCATGTGCAACAATCTTCTCCTGGAGCCCTCTAGTGATGAATATGAGTTATAGAAG			411
Query	681	CTCCAAGGTGGGAGTAGTGTGAATACCATGTTTGCCTTTATAGCCCTCTCTGGGTA			740
Sbjct	410	CTCCAAGGTGGGAGTAGTGTGAATACCATGTTTGCCTTTATAGCCCTCTCTGGGTA			351
Query	741	GGTAGGTGCTTAATCTCTAGGGCTTTCAGTCTGTACTTCTAGAAATGTCATTTG			800
Sbjct	350	GGTAGGTGCTTAATCTCTAGGGCTTTCAGTCTGTACTTCTAGAAATGTCATTTG			291
Query	801	TTTGGATTGCTCATGACCTTGGAGGCACACAGCCAGCAGTGAAGAGCCAGAATT			860
Sbjct	290	TTTGGATTGCTCATGACCTTGGAGGCACACAGCCAGCAGTGAAGAGCCAGAATT			231
Query	861	CCAAGGTATTATGCTATCAACATCCACACATAAGTATCTGGGGTCTGCAATGTTCCAC			920
Sbjct	230	CCAAGGTATTATGCTATCAACATCCACACATAAGTATCTGGGGTCTGCAATGTTCCAC			171



Query 921 ATGTATCCTGAATGTCCCCCTGTTGAGTCCAAATAAACCCCTTTGTTCTCCCA 971
Sbjct 170 ATGTATCCTGAATGTCCCCCTGTTGAGTCCAAATAAACCCCTTTGTTCTCCCA 120

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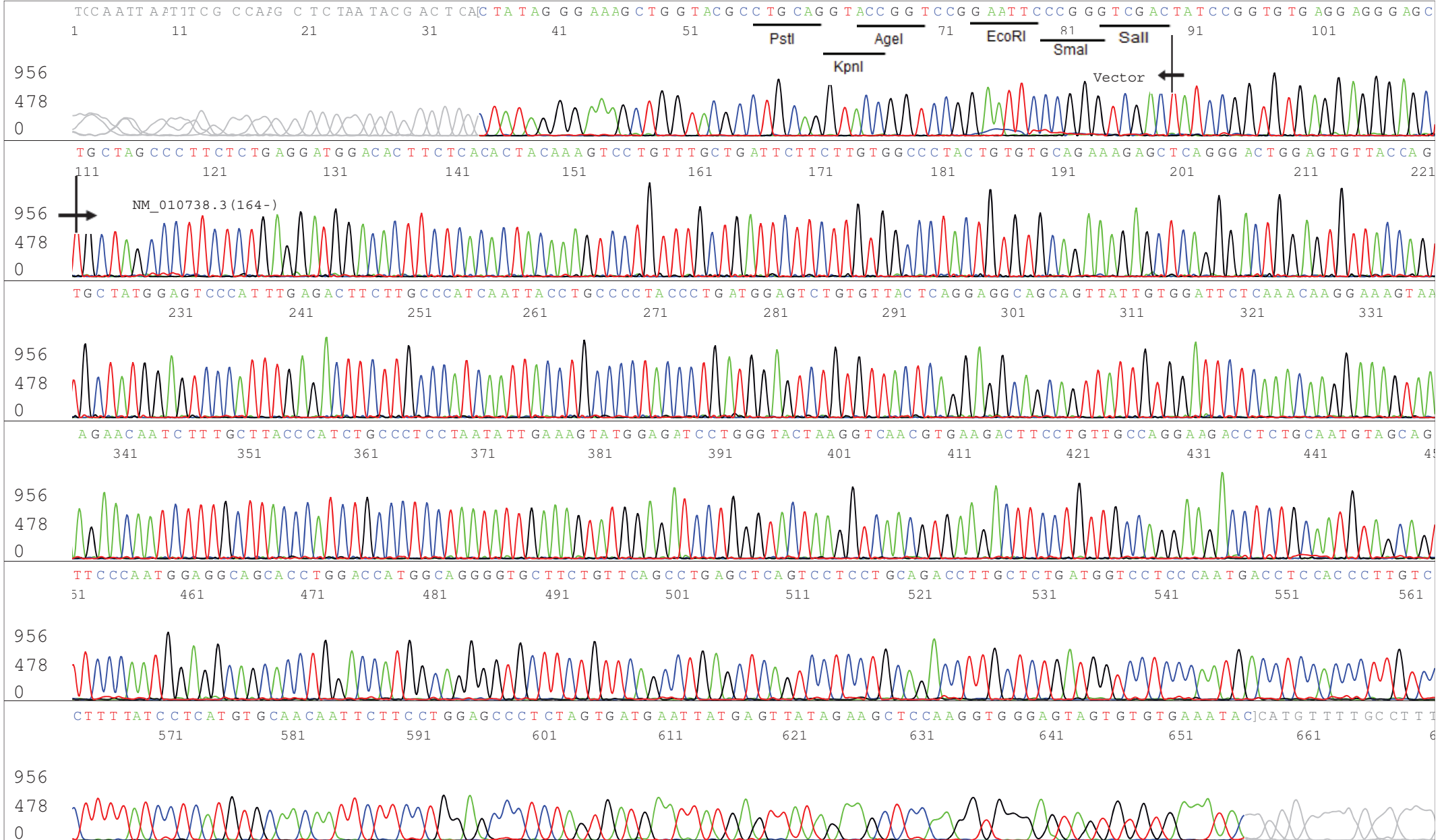
S/N G:86 A:103 T:91 C:116
KB.bcp
KB 1.4.1.8 Cap:3

Primer A : Reverse2
5' GCGGATAACAATTTACACACAGG 3'

5723_H3115A08_B3Ik_2_Reverse2
KB_3500_POP7_BDTv3.mob
Pts 1732 to 8704 Pk1 Loc:1700
Version 6.0 HiSQV Bases: 681

Gray line indicates quality value
(QV) < 40.

Sep 22,2023 03:24PM, JST
Sep 22,2023 03:42PM, JST
Spacing:10.36 Pts/Panel1350
Plate Name: 20230922_GNP



S/N G:57 A:92 T:56 C:83
KB.bcp
KB 1.4.1.8 Cap:4

Primer B : M13

5' GTTTCCCAGTCACGACGTTGTA 3'

