

RIKEN clone ID: W01A073N10

Vector : pENTR-TOPO

Gene	SOX17		
Accession No.	AK025905.1	1853 bp	1..1853
	<i>CDS</i>	1245 bp	205..1449

●Plasmid DNA purification

Date : 100413 Culture : LB (25 ug/ml Kanamycin) 3 ml →37°C O/N

Date : 100414 Purification : QIAGEN Miniprep kit→dH₂O 100 ul

●Digestion by restriction enzyme / Concentration calibration

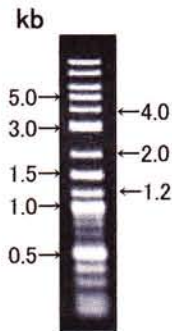
Date : 100414

DNA concentration (O.D.): 41.35 ng/ul

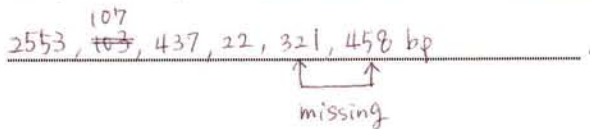
DNA	3 ul
Restriction enzyme (NotI+BssH II)	0.5+0.5 ul
Buffer H	1 ul
dH ₂ O	5 ul
Total	10 ul

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from AK025905.1 CDS>



●Adjust plasmid DNA solution to 25 ng/ul ~preparation for shipping~

Date : 100420

Final concentration: 25 ng/ul

DNA (41.35 ng/ul)	75	ul
10 × TE	12.4	ul
dH ₂ O	36.7	ul
Total	124.1	ul

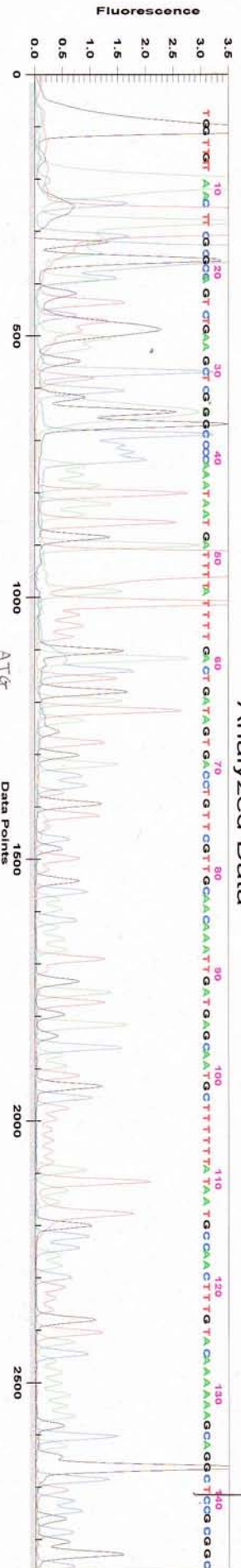


Project : GNP
Sample : W01A073N10_M13.A06_100415126P
Result : W01A073N10_M13.A06_100415126P

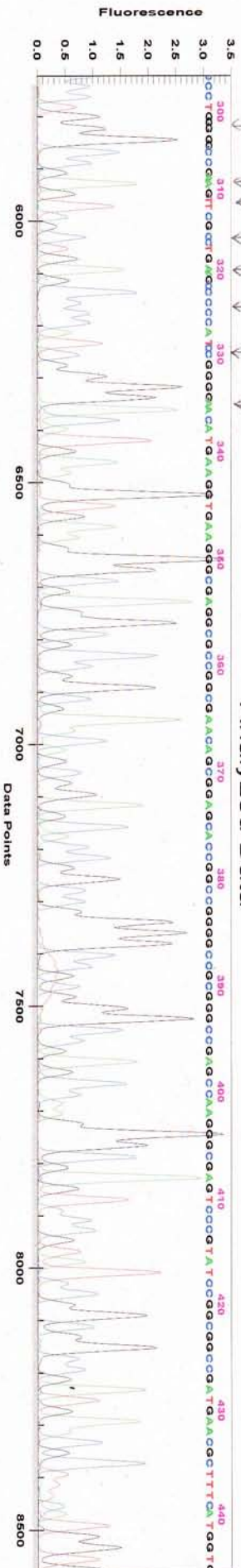
System : CEQ System

Operator : 2.100415.furu
Instrument : CEQ System (Ver. 9.0.25)

Analyzed Data



Analyzed Data



Analyzed Data



[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.04.16

1st Nucleotide Sequence
File Name : AK025905.1.gnu
Sequence Size : 1853

2nd Nucleotide Sequence
File Name : W01A073N10_M13.A06_100415126P.fasta
Sequence Size : 801

Unit Size to Compare = 6
Pick up Location No. = 1

[593 / 669 bp] INT/OPT.Score : < 1518/ 2010 >

1* GCAGTGTAC TAGCCGGCT GGGGGCCCTG GGTAGCTGT AGACGACC GCGACAGCC
1* TG GTTGTAACT TCGGCCAGT CTGAAGCTCG AGGCCCAAA TAATGATTTT
61* AGAACACGGG CCGCGGCTTC GGGCCGGGAG ACCCGCGCAG CCTCGGGG ATTCAGTGC
53* ATTTTACTAG ATAGTACCT GTTCGTTGCA ACAAAATTGAT GAGCAATGCT TTTTATATAT
121* CTCATTCCCC ACCCCCTCCC CCGGGTGGG GAGGGGGGG GTCGCGGGG AGGGTTGAG
113* GCCAACTTTG TACAAAAAAG CAGGCTCCG GGGCG-CCC CTTCACCGCT AGGGTAAACA
181* GAGGGGGGG AGGCTGAGAG CGCCATGAG ACCCGCGATG CCGGATACG CAGTGCAGAC
172* GGGTAAATGA AGAGGCC-C CACCATGAG AGCCCGGATG CCGGATACG CAGTGCAGAC
241* CAGAGCCAGA CCCAGAGCG GCTGCCCGG GTAGT- --- -GCCGGG- -TGGCCCTC
231* CAGAGCCAGA CCCAGAGCG GCTGCCCGG GCTGCCCGG CCGCGCGGGA TGGGGCCCT
293* G-CCCT- -GGGCG-AG- TG-CTG-AG -CCCAT-CG GGG-AGATGA AGTGAAGG
291* GCCCCCTCG GGGCCGAAAT TCGCCTGAG CCCCCTCG GGGAAATGA AGTGAAGG
342* CAGGGGGGG GCGACAGCG GAGCACCGG CCGGGGGGG GCGCGAGCA AGGGGAGTC
351* CAGGGGGGG GCGACAGCG GAGCACCGG CCGGGGGGG GCGCGAGCA AGGGGAGTC
402* CCGTATCCG CCGCCGATGA ACGCTTTCAT GGTGTGGGT AAGAGCAGC GCMAAGCGCT
411* CCGTATCCG CCGCCGATGA ACGCTTTCAT GGTGTGGGT AAGAGCAGC GCMAAGCGCT
462* GCGCGAGAG AATCCAGACC TGCAAAAGC CGAGTTGAG AAGTGTGTG GCMAAGCGCT
471* GCGCGAGAG AATCCAGACC TGCAAAAGC CGAGTTGAG AAGTGTGTG GCMAAGCGCT
522* GAGGGGGGG ACGCTGGGG AGAAGGGGG CTTCGTGAG GAGGCAAGC GGTTCGGGT
531* GAGGGGGGG ACGCTGGGG AGAAGGGGG CTTCGTGAG GAGGCAAGC GGTTCGGGT
582* GAGGACATG CAGGACACC CCAACTACAA GTAACGGGG CCGGGGGGA AGCAGGTAA
591* GAGGACATG CAGGACACC CCAACTACAA GTAACGGGG CCGGGGGGA AGCAGGTAA
642* GCGGCTGAG CCGGTGGAG GCGGCTTCT GCACGGCTG GGTGAGCCG AGGGGGCGG
651* GCGGCTGAG CCGGTGGAG GCGGCTTCT GCACGGCTG GGTGAGCCG AGGGGGCGG
702* GCGGCTGAG CCGGTGGAG GCGGCTTCT GCACGGCTG GGTGAGCCG AGGGGGCGG
711* GGT-GGCCC GAGGGGGGG GCGTGGCC-T GGACCGCT- GGCT-CAAT TCCG-ACCA
762* GGGCTTCCC GCGGGGGGG CCGTGGCC TCCGCAATG GCGGGCCACT ACCGGACTG
766* -GGCTT-CCC GCGGGGGGG TGNCTTCT AATTGGGC

[664 / 789 bp] INT/OPT.Score : < 1949/ 2268 >

841* CCGCTCGAG GCT-ACC-G TTGCCAC-6 CCC-GACAG TCCCGC-TG GAGGGGCTG
23* GGTAAAGAG GGTAAACCGG TGGCCACAG CCCAAGCAG TCCCGCTTG AACGGCTGG
896* ACCCGAGCC GCGTTTCTTC GCGCCCGCGA TGCCGGGGGA CTGCCCGGG GCGGGCACT
83* ACCCGAGCC GCGTTTCTTC GCGCCCGCGA TGCC-6GGA CTGCCCGGG- GCGGGCACT
956* ACAGTACGC GCAGTCTCG GACTACGCTG G-CCCCCGG AGCTTCCCG CAGTCCCATG
141* ACAGTACGC GCAGTCTCG GACTACGCTG G-CCCCCGG AGCTTCCCG CAGTCCCATG
1015* CACCCCGAC TGGGCCAGA GCGCGGGGT CCTGATTC CCGGCTCTG GGGGCAACC
201* CACCCCGAC TGGGCCAGA GCGCGGGGT CCTGATTC CCGGCTCTG GGGGCAACC
1075* ACGGCTTTC AGTGTACTA CCGGGGATG GCGTGGCGG GGGGGGGGG CCGGGGGGG
261* ACGGCTTTC AGTGTACTA CCGGGGATG GCGTGGCGG GGGGGGGGG CCGGGGGGG
1135* TTCAGATGC AGCGGAAACA CAGACACAG CACACAGCAG AGCAGCACCC CCGGGGGGG
321* TTCAGATGC AGCGGAAACA CAGACACAG CACACAGCAG AGCAGCACCC CCGGGGGGG
1195* GAGCAGCGT CCGCCCTTC GGAAGCAGT CCTTCCCGG ACGGCAAGG CCGGAGTCA
381* GAGCAGCGT CCGCCCTTC GGAAGCAGT CCTTCCCGG ACGGCAAGG CCGGAGTCA
1255* CCGCGGAGC TCTCGGGGA GGTGAGCCG ACGAATTTG AACAGTCTT GCACTTGTG
441* CCGCGGAGC TCTCGGGGA GGTGAGCCG ACGAATTTG AACAGTCTT GCACTTGTG
1315* TCGAAGCTG AGATGGGCT CCGCTACAG GGGCAATGCT CCGGTGGA TCTCCCGAC
501* TCGAAGCTG AGATGGGCT CCGCTACAG GGGCAATGCT CCGGTGGA TCTCCCGAC
1375* AGCCAGGGG CCAATTTCTC GGTGGTTC GAGCCAGCT CCGGGGATA TTAAGTCAAC
561* AGCCAGGGG CCAATTTCTC GGTGGTTC GAGCCAGCT CCGGGGATA TTAAGTCAAC
1435* TATCTGAGC TGTGACAGT CCTGATC- -GCCCCAGC CTGCAAGCA GAAAGT-6
621* TATCTGAGC TGTGACAGT CCTGATC- -GCCCCAGC CTGCAAGCA GAAAGT-6
1491* TTAACACTT CTTGAGAGG CTAAGGAAT CCTGACTC CTGGTTTTT GTTGTCTG
681* GCGCCCGAC CCAAGTTCT TGTCAAAAT TGGCAATTA AGAAGCAAT GCTTATCAAT
1551* TTGTTGTTT TPAAGGTTG TGTGGCATA TAATTTATG TAATTTATG TGTGGCAC
741* TTGTTG-CAA CAAAGAGT- CAATATCAAT CAAATTAATA TCA-TTA-TT TGCATCCAG