RIKEN_clone ID: W01A081A03

Vector: pENTR/D-TOPO

| Gene | SLC2A9 | | |
|---------------|------------|---------|---------|
| Accession No. | BC018897.2 | 1885 bp | 11885 |
| | CDS | 1536 bp | 1601695 |

●Plasmid DNA purification

Date: 100816

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

Date: 100817

Purification : QIAGEN Miniprep kit → dH₂O 100 ul

Digestion by restriction enzyme / Concentrarion calibration

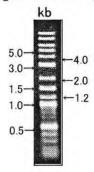
Date: 100817

DNA concentration (O.D.): 64.30 ng/ul

| DNA | l ul |
|------------------------------------|------------|
| Restriction enzyme (NotI+BssH II) | 0.5+0.5 ul |
| Buffer H | 1 ul |
| dH₂O | 7, ul |
| Total | 10 ul |

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC018897.2 CDS>

2553, 1636 bp



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

Date : 100819

Shipped: 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

| DNA (<u>64.30 ng/ul</u>) | 88 ul |
|----------------------------|----------|
| 10×TE | 22.6 ul |
| dH₂O | //5.7 ul |
| Total | 2263 ul |



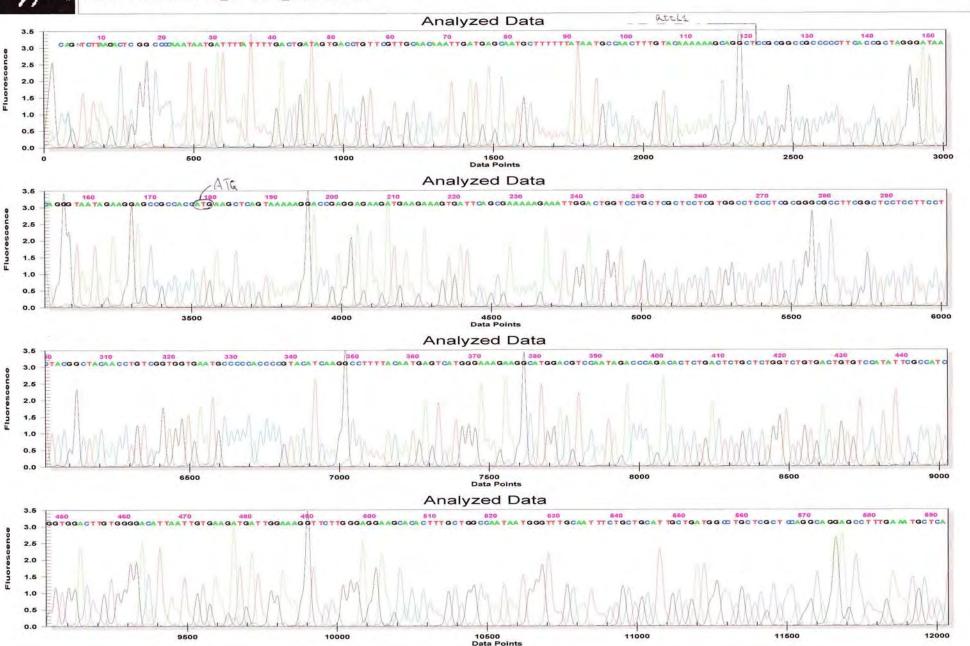
Project : GNP

Sample: W01A081A03_M13.C10_10081812FM

Result: W01A081A03_M13.C10_10081812FM

System : CEQ System Operator : 2.100818.furu

Instrument: CEQ System (Ver. 9.0.25)





Project : GNP

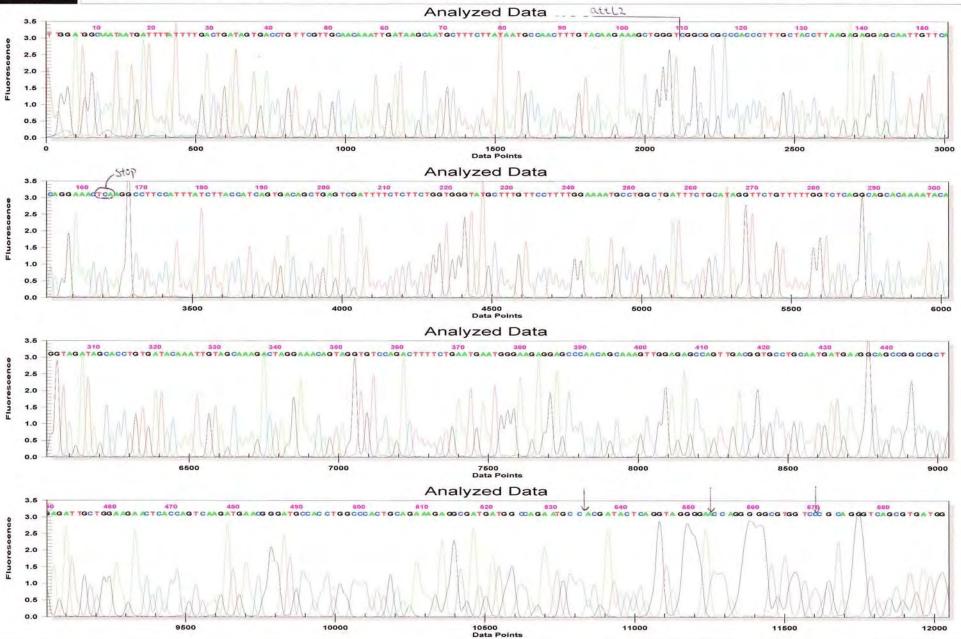
Sample: W01A081A03_T7.D10_10081812FM

Result: W01A081A03_T7.D10_10081812FM

System : CEQ System

Operator : 2.100818.furu

Instrument: CEQ System (Ver. 9.0.25)



```
| GENETYX : Nucleotide Sequence Homology Data |
Date : 2010.08.18
1st Nucleotide Sequence
 File Name : BC018897.2.gnu
 Sequence Size : 1536
2nd Nucleotide Sequence
 File Name
             : W01A081A03 M13.C10 10081812FM.fasta
 Sequence Size : 659
 Unit Size to Compare = 6
 Pick up Location No. = 1
[ 483 / 483 bp] DNT/OPT.Score : < 1932/ 1932 >
                                                     ....
  121" CCGCGGCCGC CCCCTTCACC GCTAGGGATA ACAGGGTAAT AGAAGGAGCC GCCACCATGA
  164' AGCTCAGTAA AAAGGACCGA GGAGAAGATG AAGAAAGTGA TTCAGCGAAA AAGAAATTGG
       181" AGCTCAGTAA AAAGGACCGA GGAGAAGATG AAGAAAGTGA TTCAGCGAAA AAGAAATTGG
  PRESTANDS 344884748 48774 PRESTAND SERVE SERVEND EPSTERS PRESTALD
  284' ACGCTACAA CCTGTCGGTG GTGAATGCCC CCACCCCGTA CATCAAGGCC TTTTACAATG
       化化基本工程的现在 计成型电影电影系统 化化油油医物化油 化铁矿矿金加油 化化物混合物化物法 化环烷基异物
   301" ACGCCTACAA CCTGTCGGTG GTGAATGCCC CGACCCCGTA CATCAAGGCC TTTTACAATG
   344' ASTCATGGGA AAGAAGGCAT GGACGTCCAA TAGACCCAGA CACTCTGACT CTGCTCTGGT
       361" AGTCATGGGA AAGAAGGCAT GGACGTCCAA TAGACCCAGA CACTCTGACT CTGCTCTGGT
      CTGTGACTGT GTCCATATTC GCCATCGGTG GACTTGTGGG GACATTAATT GTGAAGATGA
       421" CTGTGACTGT GTCCATATTC GCCATCGGTG GACTTGTGGG GACATTAATT GTGAAGATGA
   464' TTGGAAAGGT TCTTGGGAGG AAGCACACTT TGCTGGCCAA TAATGGGTTT GCAATTTCTG
       481" TTGGAAAGGT TCTTGGGAGG AAGCACATT TGCTGGCCAA TAATGGGTTT GCAATTTCTG
  524' CTGCATTGCT GATGGCCTGC TCGCTCCAGG CAGGAGCCTT TGAAATGCTC ATCGTGGGAC
      541" CTGCATTGCT GATGGCCTGC TCGCTCCAGG CAGGAGCCTT TGAAATGCTC ATCGTGGGAC
      GCTTCATCAT GGGCATAGAT GGAGGCGTCG CCCTCAGTGT GCTCCCCATG TACCTCAGTG
       601" GCTTCATCAT GGGCATAGAT GGAGGCGTCG CCCTCAGTGT GCTCCCCATG TACCTCAGT
1st Nucleotide Sequence
 File Name
             : BC018897.2.gnu
 Sequence Size
             : 1536
2nd Nucleotide Sequence
 File Name
              : W01A081A03 T7.D10 10081812FM.fasta (Complementary)
 Sequence Size : 742
 Unit Size to Compare = 6
 Pick up Location No. = 1
[ 558 / 582 bp]
              INT/OPT.Score : - 1480/ 2043 >
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1120' CTGGCAAAGA TCCC-ATACG TCA--CCTTG AGTACA-GGG GGCA-TCGAG ACTTT-GGCT A TCCCAATACG TCACCCCTGG AGTACAGGGG GGCATTCGAA ACTTTGGGCT 1174' GCCGT-CTTC T--CTGGTTT GGTC-ATTGA GCACC-TGGG -ACGGAGACC CC-TCCTCAT **** **. * * ***** *** **** **** **** **** **** 52" GCCGTCCTNC TCCTTGGTTT GGTCAATTGA GCACCNTGGG AACGGAGACC CCTTCCTCAA 1227' TGG-TGGC-T TTGGGCTCAT GGGCCTCTTC TTTGGGACCC TCACCATCAC GCTGACCCTG 112" TGGTTGGCTT TTGGGCTCAT GGGCCTCTTC TTTGGGACCC TCACCATCAC GCTGACCCTG 1285' CAGGACCACG COCCUEGGT CCCCTACCTG AGTATCGTGG GCATTCTGGC CATCATCGCC 172" CGGGACCACG CCCCCTGGTT CCCCTACCTG ASTATCGT-G GCATTCTGGC CATCATCGCC 1345' TCTTTCTGCA GTGGGCCAGG TGGCATCCCG TTCATCTTGA CTGGTGAGTT CTTCCAGCAA 231" TCTTTCTGCA GTGGGCCAGG TGGCATCCCG TTCATCTTGA CTGGTGAGTT CTTCCAGCAA 1405' TOTCAGOGGO COGOTOCCTT CATCATTGCA GGCACCGTCA ACTGGCTCTC CAACTTTGCT 291" TCTCAGCGGC CGGCTGCCTT CATCATTGCA GGCACCGTCA ACTGGCTCTC CAACTTTGCT 1465' GTTGGGCTCC TCTTCCCATT CATTCAGAAA AGTCTGGACA CCTACTGTTT CCTAGTCTTT 351" GTTGGGCTCC TCTTCCCATT CATTCAGAAA AGTCTGGACA CCTACTGTTT CCTAGTCTTT 1525' GCTACAATTT GTATCACAGG TGCTATCTAC CTGTATTTTG TGCTGCCTGA GACCAAAAAC 411" GCTACAATTT GTATCACAGG TGCTATCTAC CTGTATTTTG TGCTGCCTGA GACCAAAAAC 1585' AGAACCTATG CAGAAATCAG CCAGGCATTT TCCAAAAGGA ACAAAGCATA CCCACCAGAA 471" AGRACCTATG CAGAAATCAG CCAGGCATTT TCCAAAAGGA ACAAAGCATA CCCACCAGAA 1645' GAGARATCG ACTCAGCTGT CACTGATGGT AAGATAATG GAAGGCCTTA A 531" GAGAAAATCG ACTCAGCTGT CACTGATGGT AAGATAAATG GAAGGCCTTG AGTTTCCTGT