

RIKEN clone ID: IRAK088F08

Vector : pCMV-SPORT6

Gene	SLC39A6		
Accession No.	BC039498.1	1672 bp	1..1672
	<i>CDS</i>	1302 bp	309..1610

● Plasmid DNA purification

Date : 10/01/8

Culture : LB (100 ug/ml Ampicillin) 3 ml → 37°C O/N

Date : 10/01/9

Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

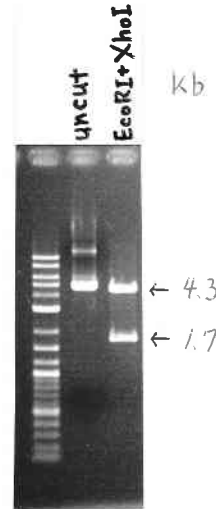
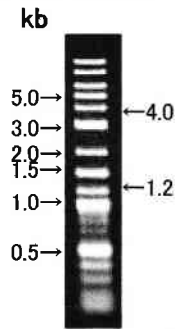
Date : 10/01/9

DNA concentration (O.D.): 157.45 ng/ul

DNA	1 ul
Enzyme (EcoRI+XhoI)	0.5+0.5 ul
Buffer H	1 ul
dH ₂ O	7 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC039498.1>

4339,1715bp

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

Date : 10/02/0

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (<u>157.45</u> ng/ul)	84	ul
10 × TE	52.9	ul
dH ₂ O	392.1	ul
Total	529.0	ul



Project : GNP

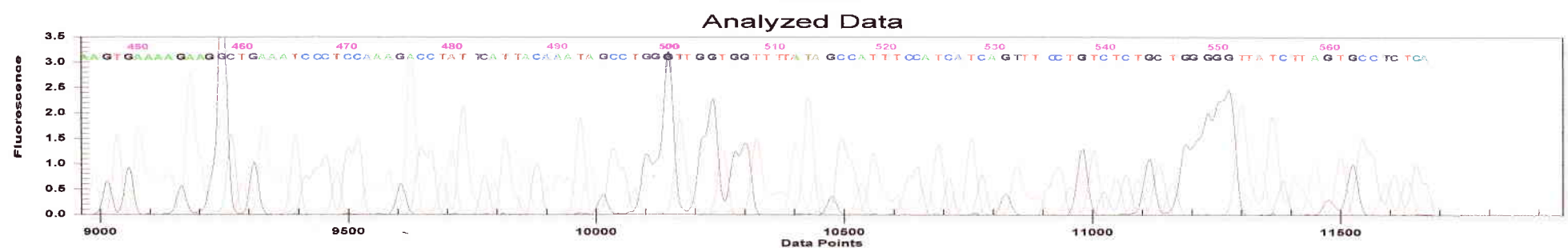
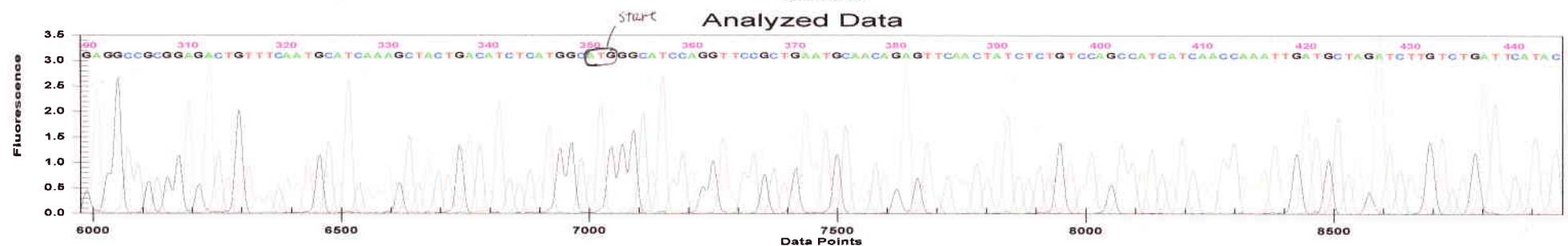
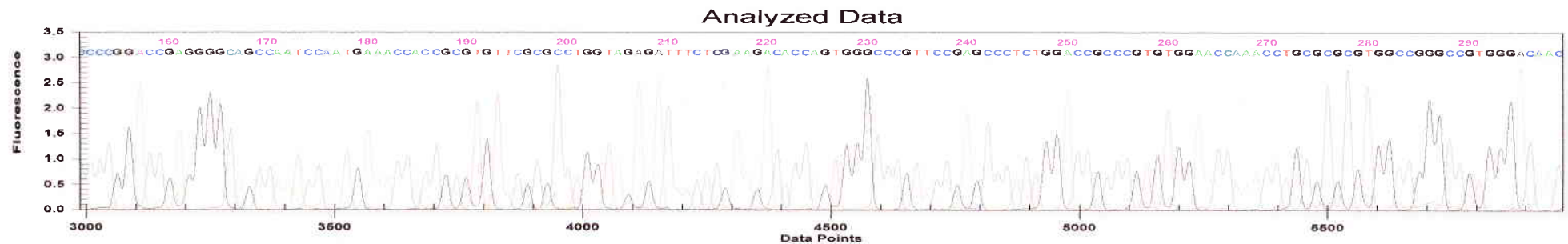
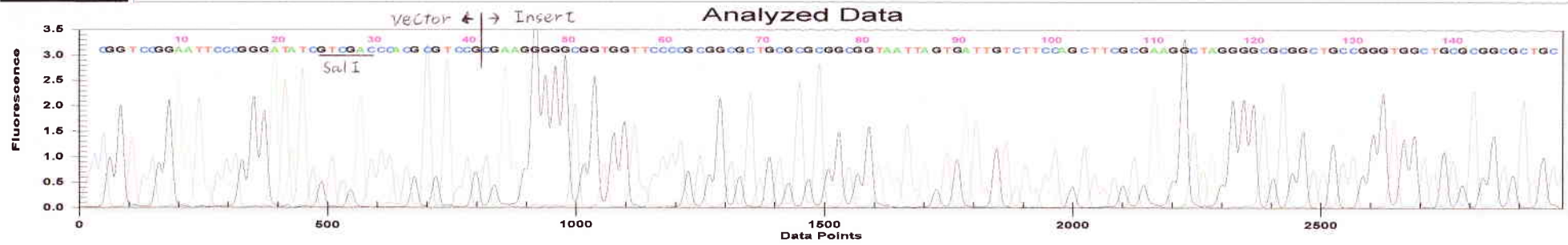
System : System 1

Operator : 1.101020.furu

Sample : IRAK088F08_Reverse2.A10_10102010VH

Instrument : System 1 (Ver. 9.0.25)

Result : IRAK088F08_Reverse2.A10_10102010VH





Project : GNP

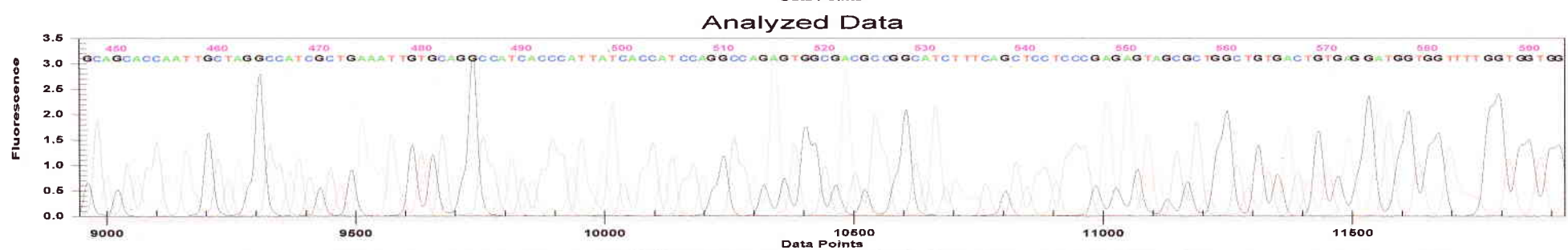
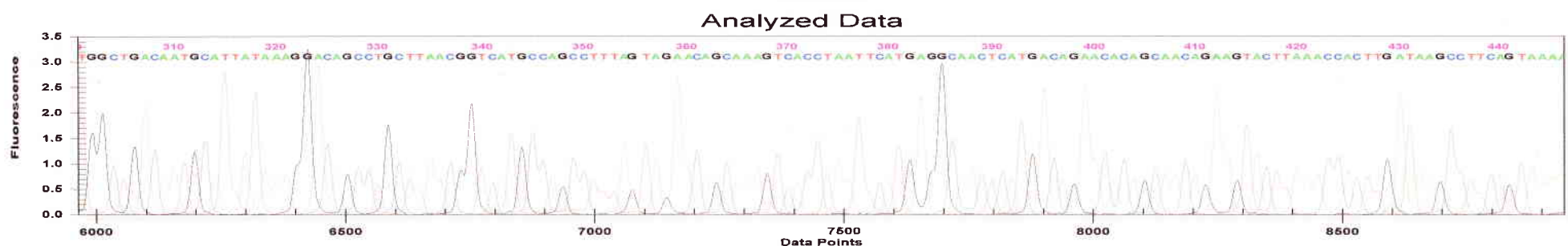
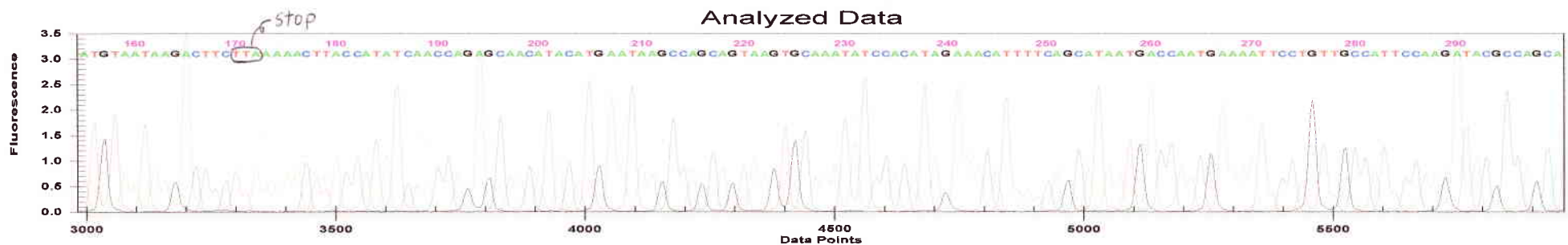
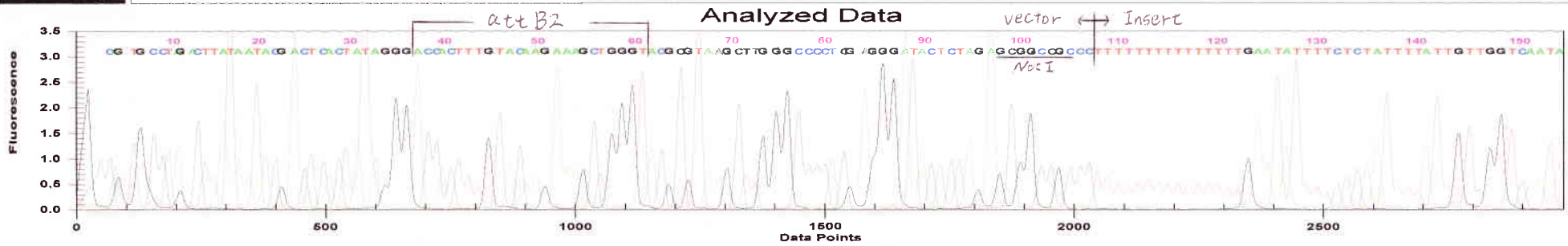
System : System 1

Operator : 1.101020.furu

Sample : IRAK088F08_M13.B10_10102010VH

Instrument : System 1 (Ver. 9.0.25)

Result : IRAK088F08_M13.B10_10102010VH



[GENETYX : Homology Data]

Date : 2010.10.20

Query Sequence
File Name :
Sequence Name : BC039498.1
Sequence Size : 1672

Target Sequence
File Name : IRAK088F08_Reverse2.A10_10102010VH.seq
Sequence Name : IRAK088F08_Reverse2.A10_10102010VH
Sequence Size : 568

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

Query Range: 1 - 528
Sbjct Range: 41 - 568
528 bp, INT.Score: 2112, OPT.Score: 2112
Identity: 528 / 528 (100%)
Strand: Plus / Plus

Query 1 CGAAGGGGGC GGTGGTTCCC CGCGGCGCTG CGCGCGGCGG TAATTAGTGA TTGTCTTCCA 60
Sbjct 41 CGAAGGGGGC GGTGGTTCCC CGCGGCGCTG CGCGCGGCGG TAATTAGTGA TTGTCTTCCA 100
Query 61 GCTTCGCGAA GGCTAGGGGC GCGGCTGCCG GGTGGCTGCG CGGCGCTGCC CCCGGACCGA 120
Sbjct 101 GCTTCGCGAA GGCTAGGGGC GCGGCTGCCG GGTGGCTGCG CGGCGCTGCC CCCGGACCGA 160
Query 121 GGGGCGAGCA ATCCAATGAA ACCACCGCGT GTTCGCGCCT GGTAGAGATT TCTCGAAGAC 180
Sbjct 161 GGGGCGAGCA ATCCAATGAA ACCACCGCGT GTTCGCGCCT GGTAGAGATT TCTCGAAGAC 220
Query 181 ACCAGTGGGC CCGTTCGAG CCTCTGGAC CGCCCGTGTG GAACCAAACC TGC GCGCGTGTG 240
Sbjct 221 ACCAGTGGGC CCGTTCGAG CCTCTGGAC CGCCCGTGTG GAACCAAACC TGC GCGCGTGTG 280
Query 241 GCCGGGCGGT GGGACAACGA GGCCGCGGAG ACTGTTTCAA TGCATCAAAG CTACTGACAT 300
Sbjct 281 GCCGGGCGGT GGGACAACGA GGCCGCGGAG ACTGTTTCAA TGCATCAAAG CTACTGACAT 340
Query 301 CTCATGGCAT GGGCATCCAG GTTCCGCTGA ATGCAACAGA GTTCAACTAT CTCTGTCCAG 360
Sbjct 341 CTCATGGCAT GGGCATCCAG GTTCCGCTGA ATGCAACAGA GTTCAACTAT CTCTGTCCAG 400
Query 361 CCATCATCAA CCAAATTGAT GCTAGATCTT GTCTGATPCA TACAAGTGAA AAGAAGGCTG 420
Sbjct 401 CCATCATCAA CCAAATTGAT GCTAGATCTT GTCTGATPCA TACAAGTGAA AAGAAGGCTG 460
Query 421 AAATCCCTCC AAAGACCTAT TCATTACAAA TAGCCTGGGT TGGTGGTTTT ATAGCCATTT 480
Sbjct 461 AAATCCCTCC AAAGACCTAT TCATTACAAA TAGCCTGGGT TGGTGGTTTT ATAGCCATTT 520
Query 481 CCATCATCAG TTTCCTGTCT CTGCTGGGGG TTATCTTACT GCCTCTCA 528
Sbjct 521 CCATCATCAG TTTCCTGTCT CTGCTGGGGG TTATCTTACT GCCTCTCA 568

Query Sequence
File Name :
Sequence Name : BC039498.1
Sequence Size : 1672

Target Sequence
File Name : IRAK088F08_M13.B10_10102010VH.seq
Sequence Name : IRAK088F08_M13.B10_10102010VH (complement)
Sequence Size : 714

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

Query Range: 1065 - 1672
Sbjct Range: 1 - 608
608 bp, INT.Score: 2416, OPT.Score: 2429
Identity: 607 / 608 (99%)
Strand: Plus / Minus

Query 1065 TACAATGAAT ATGTACCCAG AGGGTGCAAG AATAAATGCC ATTACATTT CCACGATACA 1124
Sbjct 1 TACNATGAAT ATGTACCCAG AGGGTGCAAG AATAAATGCC ATTACATTT CCACGATACA 60
Query 1125 CTCGGCCAGT CAGACGATCT CATTACCAC CATCATGACT ACCATCATAT TCTCCATCAT 1184
Sbjct 61 CTCGGCCAGT CAGACGATCT CATTACCAC CATCATGACT ACCATCATAT TCTCCATCAT 120
Query 1185 CACCACCACC AAAACCACCA TCCTCACAGT CACAGCCAGC GCTACTCTCG GGAGGAGCTG 1244
Sbjct 121 CACCACCACC AAAACCACCA TCCTCACAGT CACAGCCAGC GCTACTCTCG GGAGGAGCTG 180
Query 1245 AAAGATGCCG GCGTCGCCAC TCTGGCCTGG ATGGTGATAA TGGGTGATGG CCTGCACAAT 1304
Sbjct 181 AAAGATGCCG GCGTCGCCAC TCTGGCCTGG ATGGTGATAA TGGGTGATGG CCTGCACAAT 240
Query 1305 TTCAGCGAAT GCCTAGCAAT TGGTGCCTGCT TTTACTGAAG GCTTATCAAG TGGTTTAAGT 1364
Sbjct 241 TTCAGCGAAT GCCTAGCAAT TGGTGCCTGCT TTTACTGAAG GCTTATCAAG TGGTTTAAGT 300
Query 1365 ACTTCTGTTG CTGTGTTCTG TCATGAGTTG CCTCATGAAT TAGGTGACTT TGCTGTCTTA 1424
Sbjct 301 ACTTCTGTTG CTGTGTTCTG TCATGAGTTG CCTCATGAAT TAGGTGACTT TGCTGTCTTA 360
Query 1425 CTAAGGCGTG GCATGACCGT TAAGCAGGCT GTCCTTTATA ATGCATTGTC AGCCATGCTG 1484
Sbjct 361 CTAAGGCGTG GCATGACCGT TAAGCAGGCT GTCCTTTATA ATGCATTGTC AGCCATGCTG 420
Query 1485 GCGTATCTTG GAATGGCAAC AGGAATTTTC ATTGGTCATT ATGCTGAAAA TGTTCCTATG 1544
Sbjct 421 GCGTATCTTG GAATGGCAAC AGGAATTTTC ATTGGTCATT ATGCTGAAAA TGTTCCTATG 480
Query 1545 TGGATATTTG CACTTACTGC TGGCTTATTC ATGTAIGTTG CTCTGGTTGA TATGGTAAGT 1604
Sbjct 481 TGGATATTTG CACTTACTGC TGGCTTATTC ATGTAIGTTG CTCTGGTTGA TATGGTAAGT 540
Query 1605 TTTTAAGAAG TCTTATTACA TTATTGACCA ACAATAAAAT AGAGAAAATA TTCAAAAAAA 1664
Sbjct 541 TTTTAAGAAG TCTTATTACA TTATTGACCA ACAATAAAAT AGAGAAAATA TTCAAAAAAA 600
Query 1665 AAAAAAAAA 1672
Sbjct 601 AAAAAAAAA 608