

**RIKEN clone ID: W01A049D04**

Vector : pENTR/D-TOPO

Gene	ST3GAL3	
Accession No.	BC050380.1	2340 bp
	<i>CDS</i>	1128 bp
		1..2340
		176..1303

●Plasmid DNA purification

Date : 110301

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

Date : 110302

Purification : QIAGEN Miniprep kit→dH<sub>2</sub>O 100 ul

●Digestion by restriction enzyme / Concentration calibration

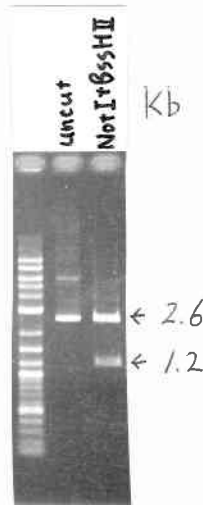
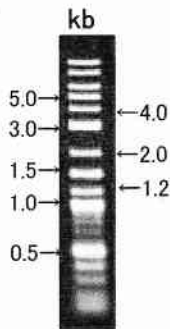
Date : 110302

DNA concentration (O.D.): 56.95 ng/ul

DNA	1 ul
Restriction enzyme (NotI+BssH II)	0.5+0.5 ul
Buffer H	1 ul
dH <sub>2</sub> O	7 ul
<b>Total</b>	<b>10 ul</b>

Erectrophoresis: 1% agarose gel, 1 × TAE Buffer

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



<Expected digestion pattern from BC050380.1 CDS>

1228, 2553 bp

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

Date : 110304

Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA ( <u>56.95</u> ng/ul)	<u>86.0</u>	ul
10 × TE	<u>19.6</u>	ul
dH <sub>2</sub> O	<u>90.3</u>	ul
<b>Total</b>	<b><u>195.9</u></b>	<b>ul</b>



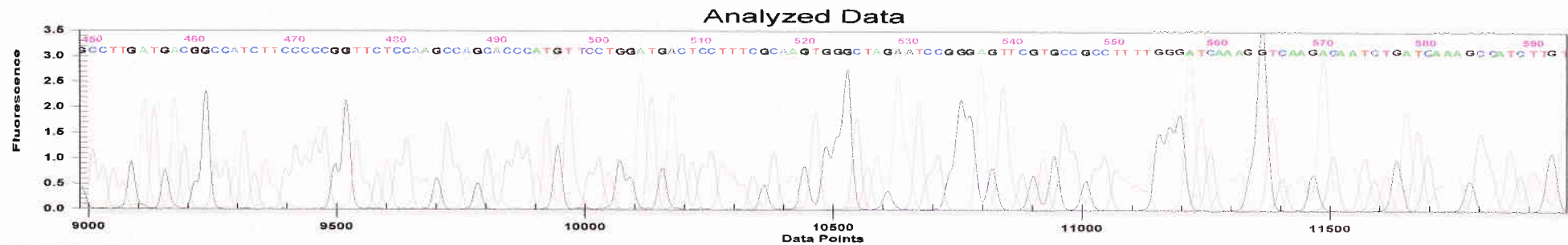
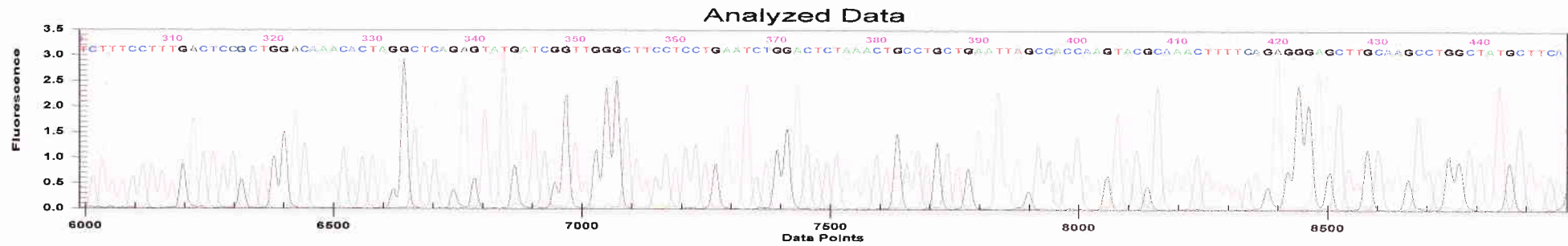
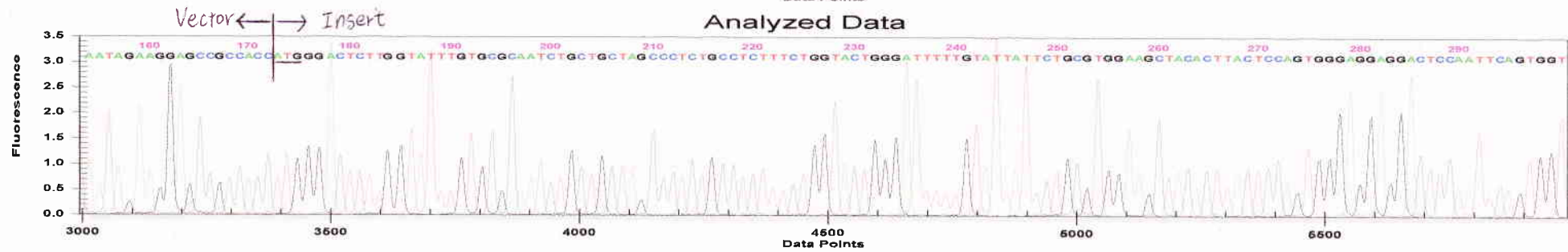
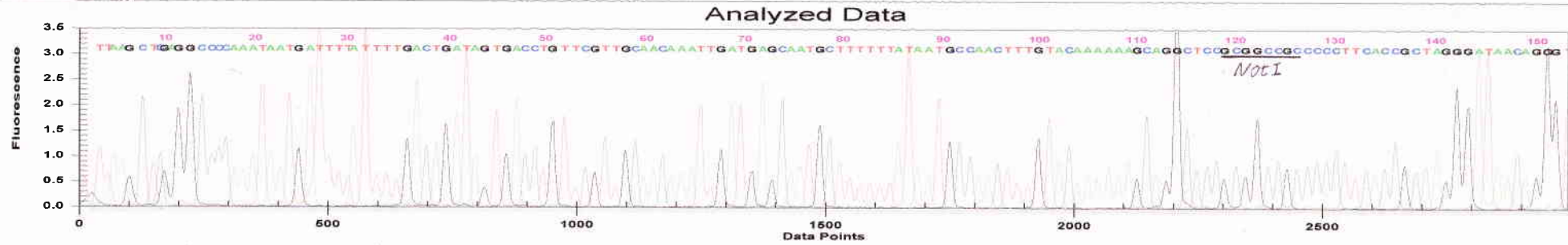
Project : GNP

Sample : W01A049D04\_M13.D06\_11030316JF

Result : W01A049D04\_M13.D06\_11030316JF

System : System 1

Operator : 1.110303.furu  
Instrument : System 1 (Ver. 9.0.25)





Project : GNP

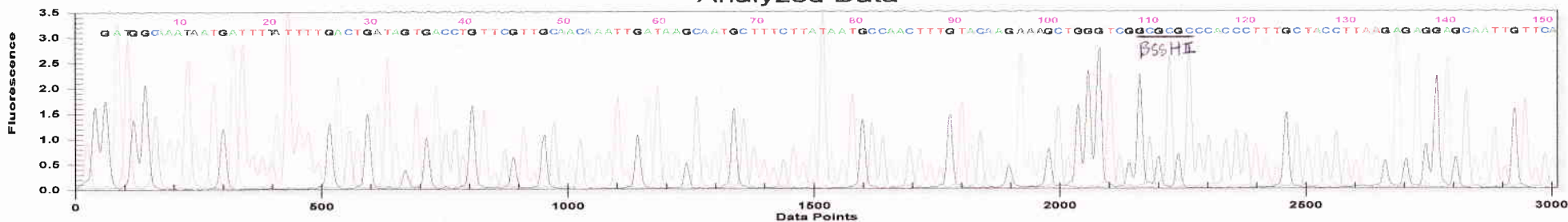
System : System 1

Operator : 1.110303.furu  
Instrument : System 1 (Ver. 9.0.25)

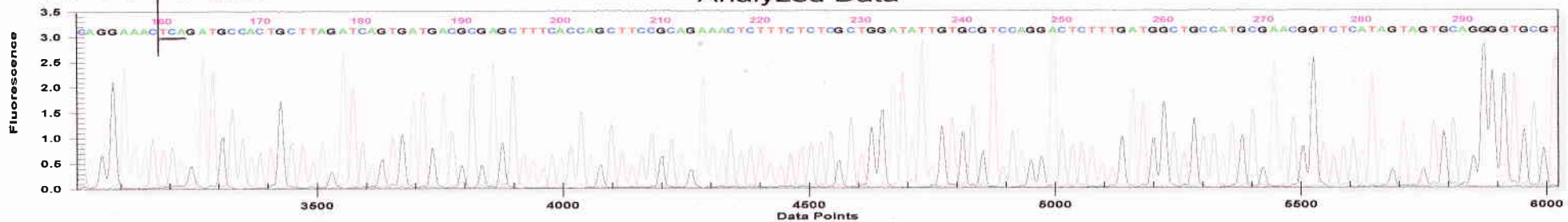
Sample : W01A049D04\_T7long.E06\_11030316JF

Result : W01A049D04\_T7long.E06\_11030316JF

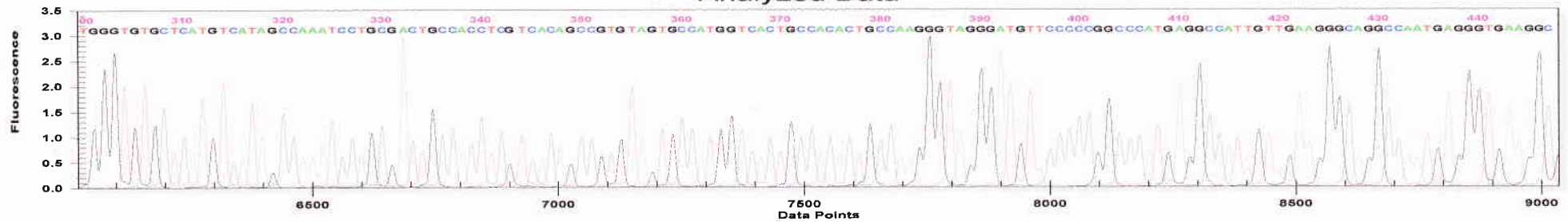
### Analyzed Data



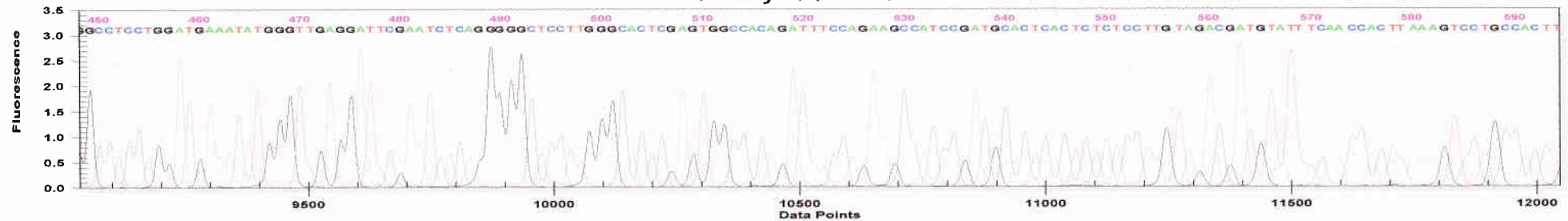
### Analyzed Data



### Analyzed Data



### Analyzed Data



[ GENETYX : Homology Data ]

Date : 2011.03.07

## Query Sequence

File Name :  
 Sequence Name : BC050380.1\_CDS(176..1303)  
 Sequence Size : 1128

## Target Sequence

File Name : W01A049D04\_M13.D06\_11030316JF  
 Sequence Name : W01A049D04\_M13.D06\_11030316JF  
 Sequence Size : 698

Unit Size to Compare = 6

Pick up Location No. = 1

Query Range: 1 - 525

Sbjct Range: 172 - 696

525 bp, INT.Score: 2088, OPT.Score: 2088

Identity: 523 / 525 (99%)

Strand: Plus / Plus

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Query 1   ATGGGACTCT TGGTATTTGT GCGCAATCTG CTGCTAGCCC TCTGCCTCTT TCTGGTACTG 60
          |||          |||          |||          |||          |||          |||
Sbjct 172 ATGGGACTCT TGGTATTTGT GCGCAATCTG CTGCTAGCCC TCTGCCTCTT TCTGGTACTG 231

Query 61  GGATTTTTGT ATTATTCTGC GTGGAAGCTA CACTTACTCC AGTGGGAGGA GGACTCCAAT 120
          |||          |||          |||          |||          |||          |||
Sbjct 232 GGATTTTTGT ATTATTCTGC GTGGAAGCTA CACTTACTCC AGTGGGAGGA GGACTCCAAT 291

Query 121 TCAGTGGTTC TTTCTTTTGA CTCCGCTGGA CAAACACTAG GCTCAGAGTA TGATCGGTTG 180
          |||          |||          |||          |||          |||          |||
Sbjct 292 TCAGTGGTTC TTTCTTTTGA CTCCGCTGGA CAAACACTAG GCTCAGAGTA TGATCGGTTG 351

Query 181 GGCTTCCTCC TGAATCTGGA CTCTAAACTG CCTGCTGAAT TAGCCACCAA GTACGCAAAC 240
          |||          |||          |||          |||          |||          |||
Sbjct 352 GGCTTCCTCC TGAATCTGGA CTCTAAACTG CCTGCTGAAT TAGCCACCAA GTACGCAAAC 411

Query 241 TTTTCAGAGG GAGCTTGCAA GCCTGGCTAT GCTTCAGCCT TGATGACGGC CATCTTCCCC 300
          |||          |||          |||          |||          |||          |||
Sbjct 412 TTTTCAGAGG GAGCTTGCAA GCCTGGCTAT GCTTCAGCCT TGATGACGGC CATCTTCCCC 471

Query 301 CGGTTCTCCA AGCCAGCACC CATGTTCTTG GATGACTCCT TTCGCAAGTG GGCTAGAATC 360
          |||          |||          |||          |||          |||          |||
Sbjct 472 CGGTTCTCCA AGCCAGCACC CATGTTCTTG GATGACTCCT TTCGCAAGTG GGCTAGAATC 531

Query 361 CGGGAGTTTCG TGCCGCCTTT TGGGATCAAA GGTCAAGACA ATCTGATCAA AGCCATCTTG 420
          |||          |||          |||          |||          |||          |||
Sbjct 532 CGGGAGTTTCG TGCCGCCTTT TGGGATCAAA GGTCAAGACA ATCTGATCAA AGCCATCTTG 591

Query 421 TCAGTCACCA AAGAGTACCG CCTGACCCCT GCCTTGGACA GCCTCCGCTG CCGCCGCTGC 480
          |||          |||          |||          |||          |||          |||
Sbjct 592 TCAGTCACCA AAGAGTACCG CCTGACCCCT GCCTTGGACA GCCTCCGCTG CCGCCGCTGC 651

Query 481 ATCATCGTGG GCAATGGAGG CGTTCTTGCC AACAAGTCTC TGGGG 525
          |||          |||          |||          |||          |||
Sbjct 652 ATCATCGTGG GCAATGGAGG CGTTCTTGCC AACAAGTCTC TGGGG 696

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[ GENETYX : Homology Data ]

Date : 2011.03.07

Query Sequence

File Name :  
 Sequence Name : BC050380.1\_CDS(176..1303)  
 Sequence Size : 1128

Target Sequence

File Name : W01A049D04\_T7long.E06\_11030316JF  
 Sequence Name : W01A049D04\_T7long.E06\_11030316JF (complement)  
 Sequence Size : 690

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

Query Range: 597 - 1128  
 Sbjct Range: 1 - 532  
 532 bp, INT.Score: 2128, OPT.Score: 2128  
 Identity: 532 / 532 (100%)  
 Strand: Plus / Minus

Query	597	GGGCAGCAAA	ACGACACTGC	GCATCACCTA	CCCCGAGGGC	GCCATGCAGC	GGCCTGAGCA	656
Sbjct	1	GGGCAGCAAA	ACGACACTGC	GCATCACCTA	CCCCGAGGGC	GCCATGCAGC	GGCCTGAGCA	60
Query	657	GTACGAGCGC	GATTCTCTCT	TTGTCCTCGC	CGGCTTCAAG	TGGCAGGACT	TTAAGTGGTT	716
Sbjct	61	GTACGAGCGC	GATTCTCTCT	TTGTCCTCGC	CGGCTTCAAG	TGGCAGGACT	TTAAGTGGTT	120
Query	717	GAAATACATC	GTCTACAAGG	AGAGAGTGAG	TGCATCGGAT	GGCTTCTGGA	AATCTGTGGC	776
Sbjct	121	GAAATACATC	GTCTACAAGG	AGAGAGTGAG	TGCATCGGAT	GGCTTCTGGA	AATCTGTGGC	180
Query	777	CACTCGAGTG	CCCAAGGAGC	CCCCTGAGAT	TCGAATCCTC	AACCCATATT	TCATCCAGGA	836
Sbjct	181	CACTCGAGTG	CCCAAGGAGC	CCCCTGAGAT	TCGAATCCTC	AACCCATATT	TCATCCAGGA	240
Query	837	GGCCGCCTTC	ACCCTCATTG	GCCTGCCCTT	CAACAATGGC	CTCATGGGCC	GGGGGAACAT	896
Sbjct	241	GGCCGCCTTC	ACCCTCATTG	GCCTGCCCTT	CAACAATGGC	CTCATGGGCC	GGGGGAACAT	300
Query	897	CCCTACCCTT	GGCAGTGTGG	CAGTGACCAT	GGCACTACAC	GGCTGTGACG	AGGTGGCAGT	956
Sbjct	301	CCCTACCCTT	GGCAGTGTGG	CAGTGACCAT	GGCACTACAC	GGCTGTGACG	AGGTGGCAGT	360
Query	957	CGCAGGATTT	GGCTATGACA	TGAGCACACC	CAACGCACCC	CTGCACTACT	ATGAGACCGT	1016
Sbjct	361	CGCAGGATTT	GGCTATGACA	TGAGCACACC	CAACGCACCC	CTGCACTACT	ATGAGACCGT	420
Query	1017	TCGCATGGCA	GCCATCAAAG	AGTCCTGGAC	GCACAATATC	CAGCGAGAGA	AAGAGTTTCT	1076
Sbjct	421	TCGCATGGCA	GCCATCAAAG	AGTCCTGGAC	GCACAATATC	CAGCGAGAGA	AAGAGTTTCT	480
Query	1077	GCGGAAGCTG	GTGAAAGCTC	GCGTCATCAC	TGATCTAAGC	AGTGGCATCT	GA 1128	
Sbjct	481	GCGGAAGCTG	GTGAAAGCTC	GCGTCATCAC	TGATCTAAGC	AGTGGCATCT	GA 532	