



RACE 实验进展报告

客户合同号: PG1-1511003

1. 实验材料

1.1 主要实验仪器

名称	厂家	型号
电泳仪	北京六一仪器厂	DYY-6C
定量 PCR 反应扩增仪	ABI	7900HT
NanoDrop 2000 超微量分光光度计	Thermo	ND-2000
离心机	Eppendorf	5424 R

1.2 主要实验试剂

名称	厂家	货号
TRIzol	Invitrogen	15596018
cDNA 第一链合成试剂盒	Fermentas	#K1622
SMARTerRACE 5' /3'	Clontech	634858
T4 DNA 连接酶	Fermentas	

2. 实验步骤

2.1 RNA 提取

1. 利用 TRIzol 提取 RNA。具体步骤可以参考试剂盒说明书。
2. NanoDrop 检测其浓度和纯度。

2.2 RNA 反转录及 cDNA 验证

1. 取 1ug 总 RNA 反转录成 cDNA, 步骤和体系按照说明书进行。
2. 以 cDNA 为模板, 用 Real-Time PCR 内参基因 B-actin 引物做 RT-qPCR 扩增, 验证 cDNA 的质量。

2.3 RT-PCR 产物测序

1. RT-PCR 并且凝胶电泳验证
2. RT-PCR 产物纯化后测序

2.4 RACE 实验

1. 利用 SMARTerRACE 5' /3' 试剂盒做 RACE 实验。具体步骤参考说明书。
2. 测序

3. 实验结果及分析

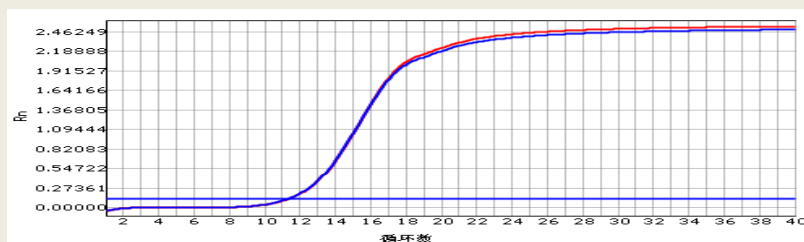
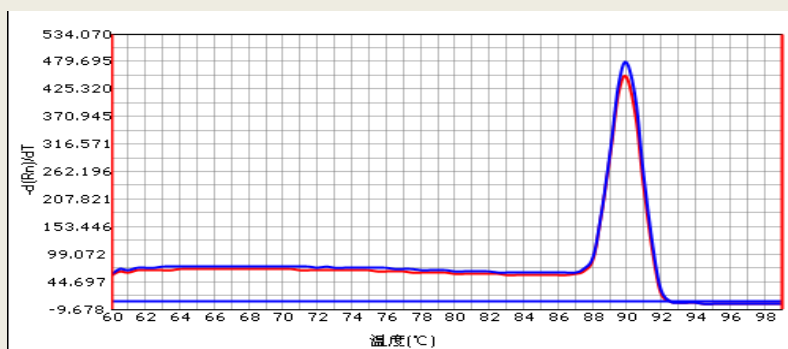
3.1 RNA 浓度和纯度报告

纯度=260nm/280nm=0.550/0.296=1.85

浓度=8.8ug/ul (未稀释)

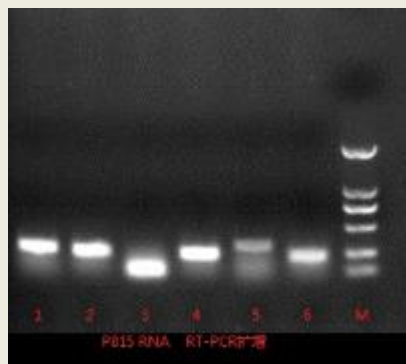
3.2 RT-qPCR 检测 cDNA 质量 (B-actin 基因) :

Ct=11.3



3.3 RT-PCR 引物、凝胶电泳图片以及测序结果:

RT-PCR 扩增电泳图:



AK149641 基因有 1-4 共四对 RT 引物; AK007111 基因有 5-6 共两对 RT 引物:

RT-F1: TAGAGCCTTATAGGTTTGTCT

RT-R1: ACTGAACAGAGCCCTAGTGTA

扩增基因片段大小: 273bp



RT-F2: TTGCTATGGTCTTCTGCTCAC

RT-R2: ATATGCAGGCAAACTTATA

扩增基因片段大小: 261bp

RT-F3: ACTGAGCCTTGCTGACAGTTC

RT-R3: TGCCTGCTGATTGATGTAG

扩增基因片段大小: 114bp

RT-F4: GCACATCCCAGAACAGCAAAG

RT-R4: GCTCAGTTAAATGATTCCCTAT

扩增基因片段大小: 251bp

RT-F5: GATAATGCCGTGGGATGTGGA

RT-R5: CCGTTGCCTGCTTGGCTTACT

扩增基因片段大小: 322bp

RT-F6: GGAGTTGGTGGCAGGAGTTCA

RT-R6: TTGGTGCATATTCAGAGTTTCAGG

扩增基因片段大小: 239bp

RT-PCR-1 测序结果 (测序引物 F1) :

Range 1: 69 to 304 Graphics					▼ Next Match ▲ Pre	
Score	Expect	Identities	Gaps	Strand		
409 bits(221)	7e-119	232/237(98%)	2/237(0%)	Plus/Plus		
Query 7	AGTGTGACTGTCGCCATTTTCATGGG-AGCCCAGAATGGTCCTGGCCAGGGTTAATCATAA	65				
Sbjct 69	AGTGTGACTGTCGCCATTTTC-TGGGAAGCCCAGAATGGTCCTGGCCAGGGTTAATCATAA	127				
Query 66	AATTGAGGTAGTGATTTTATTCTCAACTGGTGGGTTTGACAGTAGCTAGTTGCTATGGTC	125				
Sbjct 128	AATTGAGGTAGTGATTTTATTCTCAACTGGTGGGTTTGACAGTAGCTAGTTGCTATGGTC	187				
Query 126	TTCTGCTCACTTCAAACTCTGAAGAAACACAGTCTGACCTATTCTTTTGAACATTCA	185				
Sbjct 188	TTCTGCTCACTTCAAACTCTGAAGAAACACAGTCTGACCTATTCTTTTGAACATTCA	247				
Query 186	GAAAGACTTCTTCTACTGGAACATTCCAAAGATCTCTACACTAGGGTAATGTTTCAGT	242				
Sbjct 248	GAAAGACTTCTTCTACTGGAACATTCCAAAGATCTCTACACTAGGGTCTGTTCAGT	304				

RT-PCR-2 测序结果 (测序引物 F2) :

Range 1: 217 to 437 Graphics					▼ Next Match ▲ Pre	
Score	Expect	Identities	Gaps	Strand		
387 bits(209)	3e-112	218/222(98%)	2/222(0%)	Plus/Plus		
Query 8	ACAGTCTGACCTATTTCTTCTTG-ACATTCAGAAAGACTTCTTCTACTGGAACATTCCA	66				
Sbjct 217	ACAGTCTGACCTATT-CCTTTTTGAACATTTCAGAAAGACTTCTTCTACTGGAACATTCCA	275				
Query 67	AAGATCTCTACACTAGGGCTCTGTTTCAGTTTTTGGCTTCCTTATGTGACATGGGGCCTAG	126				
Sbjct 276	AAGATCTCTACACTAGGGCTCTGTTTCAGTTTTTGGCTTCCTTATGTGACATGGGGCCTAG	335				
Query 127	GTCAACATTTGGGGGTCTAAATATTTACTTTTCTAAGCATTGTTATAATTTAAATTCCTT	186				
Sbjct 336	GTCAACATTTGGGGGTCTAAATATTTACTTTTCTAAGCATTGTTATAATTTAAATTCCTT	395				
Query 187	TAAGTTATTCTATTTTCTGTGTATAAGTGTTCCTGCATAT	228				
Sbjct 396	TAAGTTATTCTATTTTCTGTGTATAAGTGTTCCTGCATAT	437				

RT-PCR-3 测序结果 (测序引物 F3) :



Range 1: 294 to 358 Graphics					▼ Next Match
Score	Expect	Identities	Gaps	Strand	
110 bits(59)	2e-29	63/65(97%)	0/65(0%)	Plus/Plus	
Query 20	AATGGTGTTCATGAAGGCCAACATGAATTGGAAGAGCTGAGAGTTCTACATCTGAATCATC	79			
Sbjct 294	AATGGTGTTCATGAAGGCCAACATGAGTTGGAAGAGCTGAGAGTTCTACATCTGAATCAGC	353			
Query 80	AGGCA 84				
Sbjct 354	AGGCA 358				

RT-PCR-4 测序结果（测序引物 F4）：

Range 1: 45 to 252 Graphics					▼ Next Match
Score	Expect	Identities	Gaps	Strand	
366 bits(198)	3e-106	205/208(99%)	1/208(0%)	Plus/Plus	
Query 16	AGTGGGCAGGTACTGAATTATGTTGATGAAAAGATGTTTCATGAAATAATGTTAACTATGA	75			
Sbjct 45	AGTGGGCAGGTACTGAATTATGTTGATGAAAAGATGTTTCATGAAATAATGTTAACTATGA	104			
Query 76	ACTATGTTTTGTACAGATGCACATTTGCTTTGTTTAATTGCTTTATAAGTGTITATATT	135			
Sbjct 105	ACTATGTTTTGTACAGATGCACATTTGCTTTGTTTAATTGCTTTATAAGTGTITATATT	164			
Query 136	CGGCTTTGTTTTATTCAATTGTTCTATTAGTATGAAAAGACACCTTGACCACAGCACCT	195			
Sbjct 165	CGGCTTTGTTTTATTCAATTGTTCTATTAGTATGAAAAGACACCTTGACCACAGCACCT	224			
Query 196	GTTATATAGGGAATC-TTTAACTGAGCC 222				
Sbjct 225	GTTATATAGGGAATCATTAACTGAGCC 252				

RT-PCR-5 测序结果（测序引物 F5）：

Range 1: 78 to 278 Graphics					▼ Next Match
Score	Expect	Identities	Gaps	Strand	
372 bits(201)	6e-108	201/201(100%)	0/201(0%)	Plus/Plus	
Query 20	ACATGCTCAGCAGATTGCGGGCACAGAAGGACGTCAAGTGTGCTAAATGGCAAAGCTT	79			
Sbjct 78	ACATGCTCAGCAGATTGCGGGCACAGAAGGACGTCAAGTGTGCTAAATGGCAAAGCTT	137			
Query 80	CAGAAGACAGAAAGGTCCAGCCTTTGAGGACATAGGAAGAAAGGTTTCATGTTCTCCGAA	139			
Sbjct 138	CAGAAGACAGAAAGGTCCAGCCTTTGAGGACATAGGAAGAAAGGTTTCATGTTCTCCGAA	197			
Query 140	TTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAATGATTTTACTTTGGACTG	199			
Sbjct 198	TTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAATGATTTTACTTTGGACTG	257			
Query 200	TAGGAAGTGTCCCTGGCTATG 220				
Sbjct 258	TAGGAAGTGTCCCTGGCTATG 278				

RT-PCR-6 测序结果（测序引物 F6）：

Range 1: 55 to 252 Graphics					▼ Next Match
Score	Expect	Identities	Gaps	Strand	
337 bits(182)	2e-97	193/198(97%)	2/198(1%)	Plus/Plus	
Query 12	ATAGTTGGAGA-ATATAG-AACCAGATCTCAGCAGGAGGGGTGAAGCGGACCGTAATCGG	69			
Sbjct 55	ATAATTGGAGACATAGAGAAACCAGATCTCAACAGGAGGGGTGAAGCGGACCGTAATCGG	114			
Query 70	CAAGAGTGTITCCCAGGGCGAGGTCACGTGTGTAATTCTTGCTAGTCAGCCTTTTGGTTT	129			
Sbjct 115	CAAGAGTGTITCCCAGGGCGAGGTCACGTGTGTAATTCTTGCTAGTCAGCCTTTTGGTTT	174			
Query 130	CCCAAAGGGGGGCTGTAAAAAGCAATTTTAAAAAGGTCCTGCTGCTAGCCTGAA	189			
Sbjct 175	CCCAAAGGGGGGCTGTAAAAAGCAATTTTAAAAAGGTCCTGCTGCTAGCCTGAA	234			
Query 190	ACTCTGAATATGCACCAA 207				
Sbjct 235	ACTCTGAATATGCACCAA 252				



3.4 目的基因已知序列:

AK149641:

5':gcttgactctaattggacctgttgggaatttagagccttataggtttgcctttataagcatctgc
aaagtgtgactgtcgccatttctgggaagcccagaatggctcctggccagggttaatcataaaattgagg
tagtgattttattctcaactgggtgggttgacagtagctagttgctatggctcttctgctcacttcaaaa
ctctgaagaacacagctctgacctattcctttttgaacattcagaaagacttcttctactggaacattc
caaagatctctacactagggctctgttcagtttttggcttccttatgtgacatggggcctagggtcaaca
tttgggggtctaaatattttacttttctaagcattgttataatttaaattcctttaagttattctatttt
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gtagacagatgtgagccacccgtgggtgtcggaacctaatctgggtccttctcagggggatcaattgc
tcttcagcagagacatcgctatagctcattgtttatttttctattaccacaaaagtaattgaaaagaa
tccacagaggagatgcatattaggagagaaatgttagattaatgacaaaaccactcaaccaaattcttc
tgagtagctgtgctctttcccatgcatgctttttaattgcatacattctaacaatgtgtgctcctaattct
acttaaccaatataaataataaaatctgttgcagattagatgctgaatttgagagacaaacgtatatt
catattttccataaaaaattaaattttcatcacagataaataggatactatcagaaaaataattgtaaag
aatcttgctatttttaactgtgtatgtatcggtgttttgcttgcatgcatgtatatgtacctcatacat
acctaggaggcccaaagagggtgccaaataccctggaactgaagcggctcacagttgtaaggatcacaca
tggtttttgggatgttgaacctgtgtcctctgggtgagcagtcattgctttaaactgctgagtcacctc
tctagcccccataaaagtcatttttaataaattcacactttggaatatactttaaagaaatgttctttta
acttaatatcccaaagtaaggatgttaaagctgttaaagcagttactcataacagaaaaggaattg
gatttttttttttttgagacaagtgctacattatgtaccattgactgttctaaaactctctatgtaga
ccaggctggccttgacctcacaaagggtgtgcctgcctctgcctcccaagttctgaaaataaaggcatgt
gcctccatgatgcctggctggaaaactcattttcttaagctttgtgttagactactatataatcatatt
atggaatacataaccattaataattttctctctctctgtgggtggcacttgcctttgatcccagcactct
ggaagagttcaaagccagcctggctctacatagcacatcccagaacagcaaaggctacactgtgggacag
gcttaagtgggcagggactgaattatgttgatgaaaagatgttcatgaaataatgttaactatgaact
atgttttgtagatgcacatttgctttgtttaattgctttataagtgttttatattcggtctttgttt
tattcaattgttctatttagtatgaaaagacaccttgaccacaggacctgttatatagggaatcatttaa
ctgagccttgctgacagttcagaggttttagtctgaacatgggtgggaaaaatgggtgcatgaaggccaac
atgagttggaagagctgagagttctacatctgaatcagcaggcagcacagagaaacacagggcctagtt
taatcattt 3'

AK007111:

5':gaagaagggcacctttaactacaacgaggataatgccgtgggatgtggaacaaggcagaagaaa
atatgaacaggaacatgctcagcagattcgcgccacagaaggacgtcaagtgtgcctaaatggcaaag
cttcagaagacagaaagggtccagcctttgaggacataggaagaaaagggtcatgttctctccgaattcggt
gaaaaatattgaggagcctttatagacgggagataatgattttactttggactgttaggaagtgtccctg
gctatgaaatgatgatttagatgaagacagaagtggttggaacactgaggctgttacagtaagccaag



caggcaacggtggacacttggagttggtggcaggagttcaagaaagacaaaatctaaaatataattgga
gacatagagaaccagatctcaacaggaggggtgaagcggaccgtaatcggcaagagtgtttcccaggg
cgaggtcacgtgtgtaattcttggctagtcagccttttggtttcccaaaggggggctgtaaaaagcaatt
ttaaaaaggtcccactgtcctggctagcctgaaactctgaatatgcaccaagcttgcccttgactaata
ttgatgtacctacctctccctcctgactgctagttattaaaagtgtacaccacc 3'

3.5 RACE 测序结果（展示部分去掉克隆载体后的序列和 blast 之后的结果）

测序结果1如下：

gcacatcccagaacagcaaaagtatgctccacaaaagcaagagaacctgagctcagatc
ccaaccctcacaaaggaaagccaggtgtggtggccttggtatagccaacctggccttcac
actgtggaggagagagatgcatttctgggccttgctgttctgggatgtgc

Blast之后如下：

Download v GenBank Graphics				
Mouse DNA sequence from clone RP23-426N4 on chromosome 4, complete sequence Sequence ID: emb AL671173.12 Length: 201741 Number of Matches: 1				
Range 1: 199240 to 199385 GenBank Graphics ▼ Next Match ▲ Prev				
Score	Expect	Identities	Gaps	Strand
254 bits(137)	5e-64	144/147(98%)	1/147(0%)	Plus/Plus
Query 9	CAGAACAGCAAAGTATGCTCCACAAAAGCAAGAGAACCTGAGCTCAGATCCCAACCTCA	68		
Sbjct 199240	CAG-ACAGCAAAGTATGCTCCACAAAAGCAAGAGAACCTGAGCTCAGATCCCAACCTCA	199298		
Query 69	CAAGGAAAGCCAGGTGTGGTGGCTTGTGTATAGCCAACCTGGCTTTCATCACTGTGGAGG	128		
Sbjct 199299	CAAGGAAAGCCAGGTGTGGTGGCTTGTGTATAGCCAACCTGGCTTTCATCACTGTGGAGG	199358		
Query 129	AGAGAGATGCATTTCTGGGCTTTGCTG 155			
Sbjct 199359	AGACAGATGCATTTCTGGGCTTTGCTG 199385			

测序结果2如下：

atgcacatcccagaacagcaaaaggactgcaaaccaactcaaggccaattaaaagttggccttg
gacggaattattattaccagcagtgacatctacttttgaagtttgccaagcacagtgaatgacc
tgtgtgtgcatcatccaatttaataaataatagtgatctcattcatctttgctgttctgggatgtgc

Blast之后结果如下：

Mouse DNA sequence from clone RP23-123E1 on chromosome 4, complete sequence Sequence ID: emb AL732520.14 Length: 167166 Number of Matches: 1				
Range 1: 63463 to 63628 GenBank Graphics ▼ Next Match ▲ Pre				
Score	Expect	Identities	Gaps	Strand
307 bits(166)	4e-80	166/166(100%)	0/166(0%)	Plus/Plus
Query 15	ACAGCAAAGGACTGCAAACCAACTCAAGGCCAATTAAGTTGGCTTGGACGGAATTATT	74		
Sbjct 63463	ACAGCAAAGGACTGCAAACCAACTCAAGGCCAATTAAGTTGGCTTGGACGGAATTATT	63522		
Query 75	ATTTACGACAGTGACATCTACTTTTGAAGTTTGCCCAAGCACAGTGAATGACCTGTGTGT	134		
Sbjct 63523	ATTTACGACAGTGACATCTACTTTTGAAGTTTGCCCAAGCACAGTGAATGACCTGTGTGT	63582		
Query 135	GCATCATCCAATTTAATAAATATAGTGATCTCATTCATCTTTGCTG 180			
Sbjct 63583	GCATCATCCAATTTAATAAATATAGTGATCTCATTCATCTTTGCTG 63628			

测序结果3如下：

gcacatcccagaacagcaaagcttgagggtcactgccagggtccacatgctcactcctcatttgg
cccaattacccatgctctatTTTTtagcccctggaaattgggtgattgtaatctgcatgggtgcatg
ctatcccaaaatgtcaccgcaagagtcctattatctgtcgtccttcttctgctgttctggga

Blast之后结果如下：

Mus musculus BAC clone RP23-379J7 from 3, complete sequence
Sequence ID: [gb|AC126450.4|](#) Length: 159914 Number of Matches: 1

Range 1: 87665 to 87839		GenBank	Graphics	▼ Next Match ▲ Pre
Score	Expect	Identities	Gaps	Strand
318 bits(172)	2e-83	174/175(99%)	0/175(0%)	Plus/Plus
Query 12	AACAGCAAAAGCTTGGAGGTCACCTGCCAGGTCCACATGCTCAGTCTCTCATTGGCCCAATT	71		
Sbjct 87665	AACAGCAAAAGCTTGGAGGTCACCTGCCAGGTCCACATGCTCAGTCTCTCATTGGCCCAATT	87724		
Query 72	ACCCATGCTCTATTTTACCCCTGGAAATTGGGTGATTGTTAATCTGCATGGTTGCATG	131		
Sbjct 87725	ACCCATGCTCTATTTTACCCCTGGAAATTGGGTGATTGTTAATCTGCATGGTTGCATG	87784		
Query 132	CTATCCCAAAATGTCACCGCAAGAGTCTATTATCTGTCGTCCTTCCTTTGCTGT	186		
Sbjct 87785	CTATCCCAAAATGTCACCGCAAGAGTCTATTATCTGTCGTCCTTCCTTTGCTGT	87839		

测序结果4如下：

ggagttggtggcaggagttcaagaggggaactgaccagtcactcattggggacagaagt
ccatggcagatggggaagggcctcatgtgacttgagacttaaaattcttgtcagttttgag
agaaactaaagaaaccacatcttccctcaggaaaagttcaataatttgatagatgattg
ggttgtttctgtcttgactgttgtaaataatgatgctgttatgaatatttgtgtgcatgcttctg

Blast之后结果如下：

Mus musculus BAC clone RP24-81D14 from chromosome 8, complete sequence
Sequence ID: [gb|AC128668.4|](#) Length: 211075 Number of Matches: 1

Range 1: 153463 to 153704		GenBank	Graphics	▼ Next Match ▲ Prev
Score	Expect	Identities	Gaps	Strand
424 bits(229)	5e-115	238/242(98%)	1/242(0%)	Plus/Minus
Query 3	AGTTGGTGGCAG-GAGTTCAAGAGGGAAGTACCCAGTCACTCAITGGGGACAGAAGTCC	61		
Sbjct 153704	AGTTGATGGCAGTTCGTTCAAGAGGGAAGTACCCAGTCACTCAITGGGGACAGAAGTCC	153645		
Query 62	ATGGCAGATGGGGAAGGGCTCATGTGACTTGAGACTTAAAATTCTTGTCAGTTTGTAGA	121		
Sbjct 153644	ATGGCAGATGGGGAAGGGCTCATGTGACTTGAGACTTAAAATTCTTGTCAGTTTGTAGA	153585		
Query 122	GAAACTAAAGAAACACATCTTCCCTTCAGGAAAAGTTTCAATAATTGATAGATGATTG	181		
Sbjct 153584	GAAACTAAAGAAACACATCTTCCCTTCAGGAAAAGTTTCAATAATTGATAGATGATTG	153525		
Query 182	GGTTGTTTCTGCTTGACTGTTGTAATGATGCTGTTATGAATATTTGTGTGCATGCTTC	241		
Sbjct 153524	GGTTGTTTCTGCTTGACTGTTGTAATGATGCTGTTATGAATATTTGTGTGCATGCTTC	153465		
Query 242	TG 243			
Sbjct 153464	TG 153463			

注：所有的测序原始结果（含有载体序列）如附件所示。我们已经比对了所有的测序结果，没有符合要求的结果。

另外，需要告知客户的是，AK007111 基因已知序列经过 blast 之后如下表所示。发现该基因和 Mus musculus 6 BAC RP23-330J17，完全重合。该基因的全长有可能从 Mus musculus 6 BAC RP23-330J17 基因上查找。而 RACE 实验也有可能得到的是该序列。



Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700102F20 product:unclassifiable, full insert sequence
Sequence ID: [dbj|AK007111.2|](#) Length: 671 Number of Matches: 1

Range 1: 1 to 671		GenBank	Graphics	▼ Next Match ▲ Previous Match	
Score	Expect	Identities	Gaps	Strand	
1240 bits(671)	0.0	671/671(100%)	0/671(0%)	Plus/Plus	
Query 1	GAAGAAGGGCACCTTTAAACTACAACGAGGATAATGCCGTGGGATGTGGAACAAGGCAGA	60			
Sbjct 1	GAAGAAGGGCACCTTTAAACTACAACGAGGATAATGCCGTGGGATGTGGAACAAGGCAGA	60			
Query 61	AGAAAAATATGAACAGGAACATGCTCAGCAGATTCCGGGCACAGAAGGACGTCAAGTGCTG	120			
Sbjct 61	AGAAAAATATGAACAGGAACATGCTCAGCAGATTCCGGGCACAGAAGGACGTCAAGTGCTG	120			
Query 121	CCTAAATGGCAAAAGCTTCAGAAGACAGAAAAGTCCAGCCTTTGAGGACATAGGAAGAAAG	180			
Sbjct 121	CCTAAATGGCAAAAGCTTCAGAAGACAGAAAAGTCCAGCCTTTGAGGACATAGGAAGAAAG	180			
Query 181	GTTTCATGTTCCCTCCGAATTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAAT	240			
Sbjct 181	GTTTCATGTTCCCTCCGAATTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAAT	240			
Query 241	GATTTTACTTTGGACTGTAGGAAGTGTCCCTGGCTATGAAATGATGATTTAGATGAAGAC	300			
Sbjct 241	GATTTTACTTTGGACTGTAGGAAGTGTCCCTGGCTATGAAATGATGATTTAGATGAAGAC	300			
Query 301	AGAACTGGGTGGAACACTGAGGCTGTTACAGTAAGCCAAGCAGGCAACGGTGGACACTT	360			
Sbjct 301	AGAACTGGGTGGAACACTGAGGCTGTTACAGTAAGCCAAGCAGGCAACGGTGGACACTT	360			
Query 361	GGAGTTGGTGGCAGGAGTTCAAGAAAGACAAAATCTAAAATATAATTGGAGACATAGAGA	420			

Mus musculus 6 BAC RP23-330J17 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence
Sequence ID: [gb|AC153576.3|](#) Length: 215953 Number of Matches: 1

Range 1: 73467 to 74136		GenBank	Graphics	▼ Next Match ▲ Previous Match	
Score	Expect	Identities	Gaps	Strand	
1238 bits(670)	0.0	670/670(100%)	0/670(0%)	Plus/Plus	
Query 2	AAGAAGGGCACCTTTAAACTACAACGAGGATAATGCCGTGGGATGTGGAACAAGGCAGAA	61			
Sbjct 73467	AAGAAGGGCACCTTTAAACTACAACGAGGATAATGCCGTGGGATGTGGAACAAGGCAGAA	73526			
Query 62	GA AAAATATGAACAGGAACATGCTCAGCAGATTCCGGGCACAGAAGGACGTCAAGTGCTGC	121			
Sbjct 73527	GA AAAATATGAACAGGAACATGCTCAGCAGATTCCGGGCACAGAAGGACGTCAAGTGCTGC	73586			
Query 122	CTAAATGGCAAAAGCTTCAGAAGACAGAAAAGTCCAGCCTTTGAGGACATAGGAAGAAAGG	181			
Sbjct 73587	CTAAATGGCAAAAGCTTCAGAAGACAGAAAAGTCCAGCCTTTGAGGACATAGGAAGAAAGG	73646			
Query 182	TTTCATGTTCCCTCCGAATTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAATG	241			
Sbjct 73647	TTTCATGTTCCCTCCGAATTCGGTGAAAAATATTGAGGAGCCTTTATAGACGGGAGATAATG	73706			
Query 242	ATTTTACTTTGGACTGTAGGAAGTGTCCCTGGCTATGAAATGATGATTTAGATGAAGACA	301			
Sbjct 73707	ATTTTACTTTGGACTGTAGGAAGTGTCCCTGGCTATGAAATGATGATTTAGATGAAGACA	73766			
Query 302	GAAGTGGGTGGAACACTGAGGCTGTTACAGTAAGCCAAGCAGGCAACGGTGGACACTTG	361			
Sbjct 73767	GAAGTGGGTGGAACACTGAGGCTGTTACAGTAAGCCAAGCAGGCAACGGTGGACACTTG	73826			
Query 362	GAGTTGGTGGCAGGAGTTCAAGAAAGACAAAATCTAAAATATAATTGGAGACATAGAGAA	421			
Sbjct 73827	GAGTTGGTGGCAGGAGTTCAAGAAAGACAAAATCTAAAATATAATTGGAGACATAGAGAA	73886			
Query 422	ACCAGATCTCAACAGGAGGGGTGAAGCGGACCGTAATCGGCAAGAGTGTTCCTCCAGGCGG	481			

结论以及下一步计划:

- 1、此次 RACE 实验，亚克隆之后没有得到理想结果。
- 2、我们会重新再做一次 RACE 实验，大概 2 周左右时间，如果还做不出来，我们会建议客户取消此次实验。避免浪费客户时间。