

## NIH-0687 Genotyping Strategies

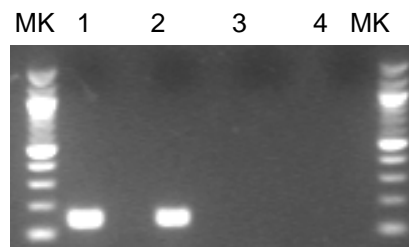
Reaction Components	Vol (ul)
5X GoTaq Buffer	10
25mM MgCl <sub>2</sub>	3.5
10mM dNTPs	1
Primer 20 uM	1
Primer 20 uM	1
5 U/ul Taq polymerase	0.5
Water	28
Total mix volume	45
Tail lysate (1:20 dilution)	5
Total reaction volume	50

Step	Temp	Time	Note
1	94C	15"	
2	65C	30"	Decrease 1C/cycle
3	72C	40"	Go to 1, 10 cycles
4	94C	15"	
5	55C	30"	
6	72C	40"	Go to 4, 30 cycles

Primer Sequences (5' to 3')	
Mutant PCR: Primer 0687-5' and Primer LTR-rev, 149 bp	
Recommended Wt PCR: Primer 0687-5' and Primer 0687-3', 131 bp	
Primer 0687-5'	CACATGCGATCATTCCATAACTGG
Primer LTR-rev	ATAAACCCCTCTTGCAAGTTGCATC
Primer 0687-3'	CTTCCTCTGTTCTCAGATGTTTGG

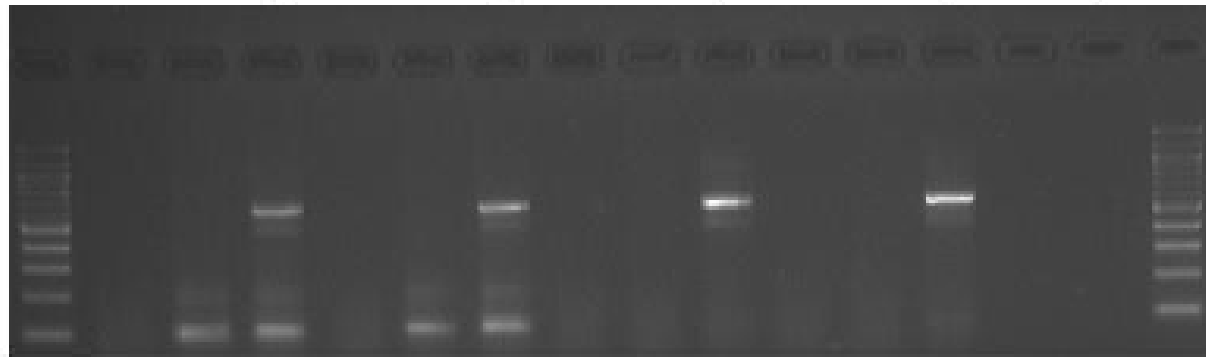
Well	Sample	Genotype
1	232	het
2	ES DNA	het
3	wt lysate	wt
4	water	no amp

### Mutant PCR



# QC Expression

RT	-	+	+	-	+	+	-	+	+	-	+	+	-	-
Actin Primers	-	-	+	-	-	+	-	-	+	-	-	+	-	+



M									M
Genotype	+/+	+/+	-/-	-/-	No				
Tissue	Kidney	Spleen	Kidney	Spleen	Template				

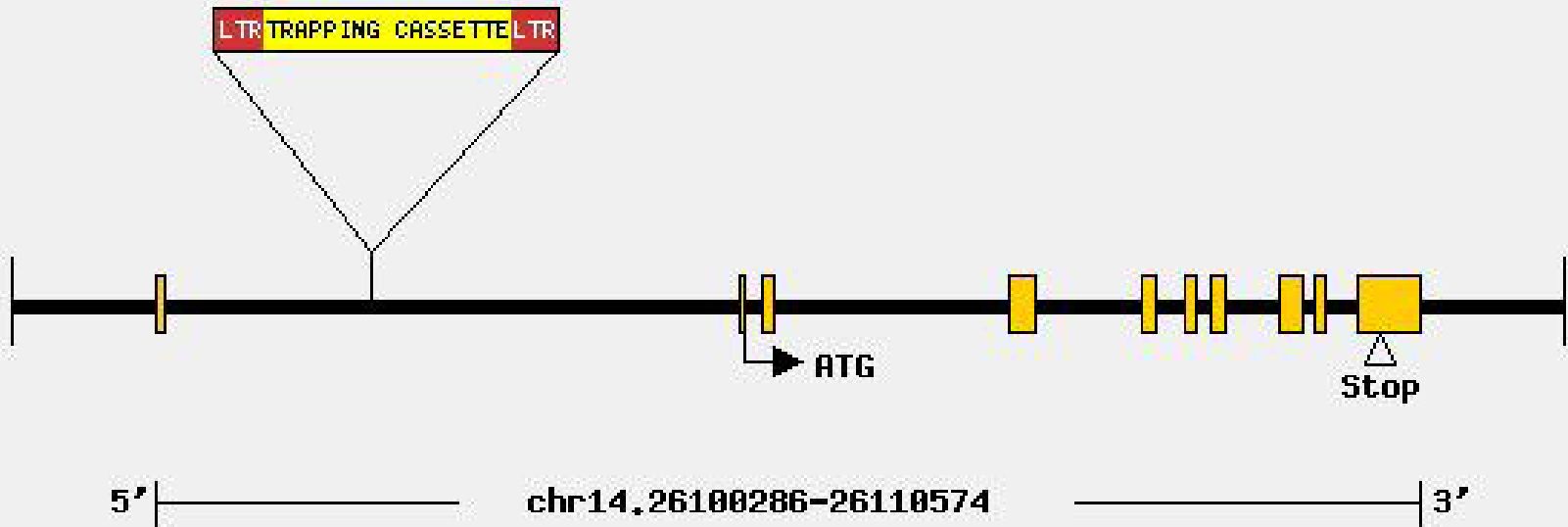
PCR 35 cycles

Mouse ID: 63

Primers: 1&2

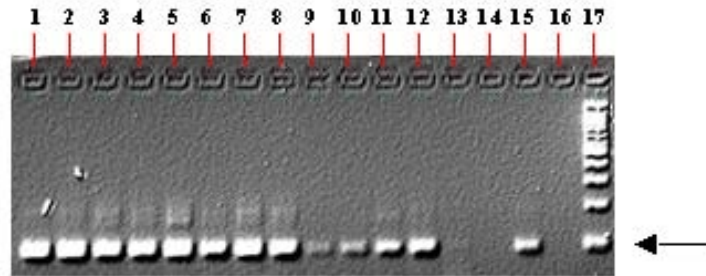
# QC Image

Accession: NM\_029626



# RT-PCR WT Expression

mouse random primed cDNA with Primers: 1,2



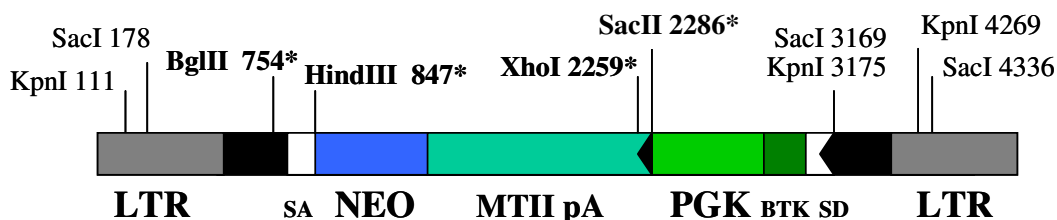
05/27/2004

**Note:** Expected band size denoted by arrow adjacent to 100bp ladder/marker.

## Mouse cDNA Tissues

- 1) Brain
- 2) Spinal Cord
- 3) Eye
- 4) Thymus
- 5) Spleen
- 6) Lung
- 7) Kidney
- 8) Liver
- 9) Skeletal Muscle
- 10) Bone
- 11) Stomach, Small Intestine & Colon
- 12) Heart
- 13) Adipose
- 14) (-) Control
- 15) (+) Control- ES cell cDNA
- 16) (+) Control- Genomic/Lex1 DNA
- 17) 100 bp ladder/marker

# VICTR 48 MTII Omnibank Vector



**Total Size:** 4748 nucleotides

**Non-Cutters:** ApaI, BclI

\* Unique sites

## Location of components in VICTR 48 MTII:

LTR (viral long terminal repeat): 1-590, 4159-4748

SA (splice acceptor): 755-847

NEO: 867-1684

MTII pA: 1688-2217

frt sites: 2305-2352; 3185-3232

PGK promoter: 2377-2893

BTK exon: 2928-3152

>VICTR 48MTII

```
TGAAAGACCCCGCTGACGGGTAGTCAATCACTCAGAGGAGACCCTCCCAAG
GAACAGCGAGACCACAAGTCGGATGCAACTGCAAGAGGGTTTATTGGATACA
CGGGTACCCGGGCGACTCAGTCAATCGGAGGACTGGCGCGCCGAGTGAGGG
GTTGTGGGCTCTTTTATTGAGCTCGGGGAGCAGAAGCGCGCGAACAGAAGCG
AGAAGCGAACTGATTGGTTAGTTCAAATAAGGCACAGGGTCATTTTCAGGTCC
TTGGGGCACCCCTGGAAACATCTGATGGTTCTCTAGAAACTGCTGAGGGCTGG
ACCGCATCTGGGGACCATCTGTTCTTGGCCCTGAGCCGGGGCAGGAACTGCT
TACCACAGATATCCTGTTTGGCCCATATTCAGCTGTTCCATCTGTTCTTGGCCC
TGAGCCGGGGCAGGAACTGCTTACCACAGATATCCTGTTTGGCCCATATTCA
GCTGTTCCATCTGTTTCTGACCTTGATCTGAACTTCTCTATTCTCAGTTATGTA
TTTTTCCATGCCTTGCAAATGGCGTTACTTAAGCTAGCTTGCCAAACCTACA
GGTGGGGTCTTTCATTCCCCCTTTTCTGGAGACTAAATAAAATCTTTTATTT
TATCTATGGCTCGTACTCTATAGGCTTCAGCTGGTGATATTGTTGAGTCAAAA
CTAGAGCCTGGACCACTGATATCCTGTCTTTAACAAATTGGACTAATCGATAC
```

CGTCGATCGACCTCGACAGATCTTAAGCCAGTTTTTCGTACCCTTGACTGCGTT  
TCATCGATTTCGCTACTAACATTGCCTTTTTCCTCCTTCCCTCCCACAGGTGGAA  
GAGCAAGCTTTGATGAGCCGCCACCATGGGATCGGCCATTGAACAAGATGGA  
TTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG  
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCG  
CAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGA  
ACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCT  
TGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTAT  
TGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGA  
GAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCG  
GCTACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA  
CTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCA  
GGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  
GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGG  
TGAAAATGGCCGCTTTTCTGGATTTCGACTGTGGCCGGCTGGGTGTGGCG  
GATCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG  
GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT  
TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGGGGATCA  
ATTCTCTAGGATCCTGCTCCTGCGCTGGCGCCTGCAAATGCAAACAATGCAA  
ATGTACTTCTGCAAGAAAAGTAAGTTGGATCTTCTCTGCCATTTCCCCGTCA  
CTCTCCTGGGGTCCCTAGCCCGCCGCGCCGCGCCTTCCCTCCCGGGAGCGTTC  
AGGTGGTGTGCCTCTGACAAGGTTTCTCGCTCACGTTCAACTTCTCTCCCC  
ACAGGCTGCTGCTCCTGCTGCCCCGTGGGCTGTGCGAAGTGCTCCCAGGGCT  
GCATCTGCAAAGAGGCTTCCGACAAGTGCAGCTGCTGTGCCTGAAGGGGGGC  
GGAGGGGTCCCCACATCTGTGTAAATAGACCATGTAGAAGCCTAGCCTTTTTT  
GTACAACCCTGACTCGTTCTCCACAACCTTTTTCTATAAAGCATGTAAGTACA  
ATAAAAGCCGTTGACTTGATTAATTCAGCTTGTCTCTGTGCATTGGTTAAGGG  
CTGGCAGAGGCGTTGAGATGGGACTGCAGCAGCTGAATTTGAGCTAGTCGGA  
TTATATTTCTCTCGAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCG  
CTCGAGTTTAAACCAATCGAATTCCCGCGGCTAGACCCAGCTTTCGGAAGTTC  
CTATTCGGAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCTCGATATGGTCG  
ATCGACCTGCAGGAATTCTACCGGGTAGGGGAGGCGCTTTTCCCAAGGCAGT  
CTGGAGCATGCGCTTTAGCAGCCCCGCTGGGCACTTGGCGCTACACAAGTGG  
CCTCTGGCCTCGCACACATTCACATCCACCGGTAGGCGCCAACCGGCTCCGT  
TCTTTGGTGGCCCCCTTCGCGCCACCTTCTACTCCTCCCCTAGTCAGGAAGTTC  
CCCCCGCCCCGAGCTCGCGTTCGTGCAGGACGTGACAAATGGAAGTAGCAC  
GTCTCACTAGTCTCGTGCAGATGGACAGCACCGCTGAGCAATGGAAGCGGGT  
AGGCCTTTGGGGCAGCGGCCAATAGCAGCTTTGCTCCTTCGCTTTCTGGGCTC  
AGAGGCTGGGAAGGGGTGGGTCCGGGGGGCGGGCTCAGGGGCGGGCTCAGGG  
GCGGGGCGGGCGCCCGAAGGTCCTCCGGAGGCCCGGCATTCTGCACGCTTCA  
AAAGCGCACGTCTGCCGCGCTGTTCTCCTTCTCCTCATCTCCGGGCCTTTCGA  
CCTGCAGGCGGCCGCGAATTCAGTGTGATTGCAGCGTACGGATCCGCCGCC  
GCCATGGCTCCGGTAGGTCCAGAGTCTTCAGAGATCAAGTCCCACCTTCCAA  
GTCCTGGCATCTCACGACGTCTGGGGAGCTACCTGCATTAAGTCAGAAGTGA  
GGTGGGTTTGGGCTGAGGTAGAGCCTGGGCAGAGGCCATAATTACTTCTTGT  
GGAAGTCTCAAAGGTCGGACAGGAAGCATGGCTGGTTCCATATATCTACTGC

CTCGAATCGATGAATTCGAGCTCGGTACCCGGGGATCGAAGTTCCTATTCGG  
AAGTTCCTATTCTCTAGAAAGTATAGGAACTTCTCGACCTGCAGGCATGCAA  
GCTGGGGGGTTCGACGTCGAGAAGGAGTGAGGGCTGGATAAAGGGAGGATC  
GAGGCGGGGTCGAACGAGGAGGTTCAAGGGGGAGAGACGGGGCGGATGGA  
GGAAGAGGAGGCGGAGGCTTAGGGTGTACAAAGGGCTTGACCCAGGGAGGG  
GGGTCAAAGCCAAGGCTTCCCAGGTCACGATGTAGGGGACCTGGTCTGGGT  
GTCCATGCGGGCCAGGTGAAAAGACCTTGATCTTAACCTGGGTGATGAGGTC  
TCGGTTAAAGGTGCCGTCTCGCGGCCATCCGACGTAAAGGTTGGCCATTCTG  
CAGAGCAGAAGGTAACCCAACGTCTCTTCTTGACATCTACCGACTGGTTGTG  
AGCGATCCGCTCGACATCTTTCCAGTGACCTAAGGTCAAACCTTAAGGGAGTG  
GTAACAGTCTGGCCCATATTTTCAGACAAATACAGAAACACAGTCAGACAGA  
GACAACACAGAACGATGCTGCAGCAGACAAGACGCGCGGCGCGGCTTCGGT  
CCAAACCGAAAGCAAAAATTCAGACGGAGGCGGGAAGTGTTCAGGTTCTC  
GTCTCCTACCAGAACCACATATCCCTCCTTAAGGGGGGTGCACCAAAGAGT  
CCAAAACGATCGGGATTTTTGGACTCAGGTCGGGCCACAAAAACGGCCCCCG  
AAGTCCCTGGGACGTCTCCCAGGGTTGCGGCCGGGTGTTCCGAAGTTCAG  
TTCCACCACGGGTCCGCCAGATACAGAGCTAGTTAGCTAACTAGTACCGACG  
CAGGCGCATAAAATCAGTCATAGACACTAGACAATCGGACAGACACAGATA  
AGTTGCTGGCCAGCTTACCTCCCGGTGGTGGGTTCGGTGGTCCCTGGGCAGGG  
GTCTCCCGATCCCGGACGAGCCCCAAATGAAAGACCCCCGCTGACGGGTAG  
TCAATCACTCAGAGGAGACCCTCCCAAGGAACAGCGAGACCACAAGTCGGA  
TGCAACTGCAAGAGGGTTTATTGGATACACGGGTACCCGGGCGACTCAGTCA  
ATCGGAGGACTGGCGCGCCGAGTGAGGGGTTGTGGGCTCTTTTATTGAGCTC  
GGGAGCAGAAGCGCGCGAACAGAAGCGAGAAGCGAACTGATTGGTTAGTT  
CAAATAAGGCACAGGGTCATTTTCAGGTCCTTGGGGCACCCCTGGAAACATCTG  
ATGGTTCTCTAGAAACTGCTGAGGGCTGGACCGCATCTGGGGACCATCTGTTC  
TTGGCCCTGAGCCGGGGCAGGAACTGCTTACCACAGATATCCTGTTTGGCCC  
ATATTCAGCTGTTCCATCTGTTCTTGGCCCTGAGCCGGGGCAGGAACTGCTTA  
CCACAGATATCCTGTTTGGCCCATATTCAGCTGTTCCATCTGTTCCCTGACCTTG  
ATCTGAACTTCTCTATTCTCAGTTATGTATTTTTCCATGCCTTGCAAAATGGCG  
TACTTAAGCTAGCTTGCCAAACCTACAGGTGGGGTCTTTCA