

GENOTYPING BY PCR PROTOCOL

MUTANT MOUSE REGIONAL RESOURCE CENTER: UC DAVIS

mmrrc@ucdavis.edu

530-754-MMRRC

NAME OF PCR: B6;129S5-1700040I03RIK^{Gt(OST419896)Lex}/Mmucd MMRRC # 031645-UCD

Protocol: Neo Tcrd Duplex used for Lexicon/Genentech gene trap lines.

Reagent/ Constituent	Volume (μL)
Water	10.275
10x Buffer	2.5
MgCl ₂ (stock concentration is 25mM)	1.7
Betaine (stock concentration is 5M) <i>Optional</i>	6.5
dNTPs (stock concentration is 10mM)	0.5
DMSO <i>Optional</i>	0.325
Primer 1. (stock concentration is 20μM) Neo TD F	0.5
Primer 2. (stock concentration is 20μM) Neo TD R	0.5
Primer 3. (stock concentration is 20μM) Tcrd F	0.5
Primer 4. (stock concentration is 20μM) Tcrd R	0.5
Taq Polymerase 5Units/μL	0.2
DNA extracted with ☐ NaOH ☒ Proteinase K ☐ Other:	1.0
TOTAL VOLUME OF REACTION:	25.000μL

Comments on protocol:

- This protocol only indicates the presence or absence of internal Neo vector; it does not distinguish heterozygous vs. knockout, nor is it specific to any single construct. TCRD is an internal control to verify DNA is present.
- Betaine/DMSO is standardized due to high GC content in promoter regions and protocol may be tested without. Also, may adjust MgCl₂ to increase reaction or decrease non specific amplifications.

Strategy:

Steps	Temp (°C)	Time (m:ss)	# of Cycles
1. Initiation/Melting HOT START? ☐	94	3:00	1
2. Denaturation	94	0:20	} 12x
3. Annealing	64	0:30	
4. Elongation	72	0:35	
5. Denaturation	94	0:20	} 25x
6. Annealing	58	0:30	
7. Elongation	72	0:35	
8. Amplification	72	2:00	1
9. Finish	10	∞	n/a

Primers:

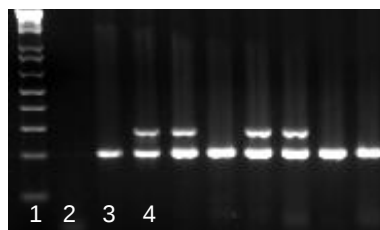
Name	Nucleotide Sequence (5' - 3')
1: Neo TD F	CTTGGGTGGAGAGGCTATTC
2: Neo TD R	AGGTGAGATGACAGGAGATC
3: Tcrd F	CAAATGTTGCTTGTCTGGTG
4: Tcrd R	GTCAGTCGAGTGCACAGTTT

Electrophoresis Protocol:

Agarose: 2% mV: 80

Estimated Running Time (min): 90

Expected Bands	Genotype
200 bp	WT
200 bp / 280 bp	Neo positive



Lanes:
 1. 1Kb+ ladder
 2. H₂O
 3. Wild-type +/+
 4. Neo +

Lexicon Gene Trap Protocol attached.

Lexicon Contract Name: DNA177
LexVision Name: PRT338T1
Genentech ID: UNQ833



Mouse Accession(s): ENSMUST00000032080, AK006658
Omnibank Clone: OST419896, VICTR 37

Mutation Description:

Listed below is a portion of the mouse genomic sequence ([from mouse chr.6](#)) surrounding the gene trap insertion site in the Omnibank mouse line PRT338T1 (OST419896). The sequence below includes 250 nucleotides of sequence on either side of the gene trap insertion site, which is denoted with an asterisk *****.

```
5'  
CGCGGAGAGCGGGCCTGAGGGAGGCCGTGGCAGCTGTCAGGCTAAAGTCGGGCGAGGGATCGCGGCGGG  
A  
CGGCGGCGGCGGGCGGCGGGACGGGCCCTGGAGATGAGCCGTGGCGCCGCGGGCTGGTGCTGTCTC  
GT  
GCTCTGGCTGCCCACGTGCGTCGCGGCCACGGTGAGCGGCGACGGACAGGCGGGCGGGGCGGGAATCC  
A  
GCGTGCGCGCTTCCCGGGCTGGGGGCCACGGGTCACCTTC*GGGACCCCGCGAGTTTGGGCCGCCAGAT  
CCAGGGACTAGACGGCTGCAGCGGGTGGATGCTGGTTCCCGGGTCAGTGAGTAGGCACAACCTGACAACC  
CCACCCCTCCCGTCGAAACAAGAGCTTTCAGCTTTCCTCCCACTGAAGGCGACCCTGGTGACAGCTAGA  
GATCCAGAACGGAGGATGTGAGCGTTCTTATAGGCAGGAACACACATATGGGCTCACACGCACAGGCACC  
CACTTACACAA
```

Mutation Illustration:

Accession: AK006658

