

# GENOTYPING BY PCR PROTOCOL

## MUTANT MOUSE REGIONAL RESOURCE CENTER: UC DAVIS

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530-754-MMRRC

NAME OF PCR: C57BL/6-Tirap<sup>m1Btr</sup>/Mmcd, (*torpid*) MMRRC # 016982-UCD

### Protocol:

Reagent/ Constituent	Volume (µL)
Water	12.675
10x Buffer (contains 15mM MgCl <sub>2</sub> )	2.5
Betaine (stock concentration is 5M) <i>Optional</i>	6.5
dNTPs (stock concentration is 25mM)	0.5
DMSO <i>Optional</i>	0.325
Primer 1 (stock concentration is 20µM) Torpid PCR F1	0.5
Primer 2 (stock concentration is 20µM) Torpid PCR R1	0.5
Taq Polymerase	0.5
DNA sample extracted with <input type="checkbox"/> NaOH <input type="checkbox"/> Proteinase K <input checked="" type="checkbox"/> Other: Any	1.0
<b>TOTAL VOLUME OF REACTION:</b>	<b>25µL</b>

### Comments on protocol:

- The *torpid* mutation destroys a *Bgl* II restriction enzyme site in the *Tirap* genomic DNA sequence. *Torpid* genotyping is performed by amplifying the region containing the mutation using PCR, followed by *Bgl* II restriction enzyme digestion.
- Betaine and DMSO have been standardized due to high GC content. Protocol may be tested without. Also, may adjust MgCl<sub>2</sub> to increase reaction or decrease non specific amplifications.

### Strategy:

Steps	Temp (°C)	Time (m:ss)	# of Cycles
1. Initiation/Melting <span style="float: right;">HOT START? <input type="checkbox"/></span>	94	5:00	1
2. Denaturation	94	0:15	} 10x
3. Annealing } steps 2-3-4 will cycle in sequence	65 to 55 (↓1°C/cycle)	0:30	
4. Elongation	72	0:40	
5. Denaturation	94	0:15	
6. Annealing } steps 5-6-7 will cycle in sequence	55	0:30	} 30x
7. Elongation	72	0:40	
8. Amplification	72	5:00	1
9. Finish	15	∞	n/a

### Primers:

Name	Nucleotide Sequence (5' - 3')
1: Torpid PCR F1	GTG AAA GGT AAC AGA AAC CAG TCA CCT CC
2: Torpid PCR R1	CGT GCC TGA TGC CAG AGG AAG AAG AC

### Electrophoresis Protocol:

Agarose: 2% mV: 80 Estimated Running Time: 90 min

Primer Combination	Band	Genotype
1 and 2	553 bp	<i>torpid</i>
the <i>Bgl</i> II site destroyed by the <i>torpid</i> mutation is highlighted in gray		
Restriction Digest w/ <i>Bgl</i> II	159, 393 bp	WT +/+
	159, 393, 553 bp	HET +/-
	553 bp	HOM -/-

Mutation site (red) and flanking sequence:  
SNP found at position ~ 243 of sequencing

WT ctccttc**A**gatctgg  
*torpid* ctccttc**T**gatctgg