GENOTYPING BY PCR PROTOCOL
MUTANT MOUSE RESOURCE & RESEARCH CENTER: UC DAVIS

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Protocol Name: **Balb/c-*Tet1*^{tuft}/Mmucd** **MMRRC: 042205-UCD**

Protocol:

Reagent/Constituent	Volume (µL)
Water	11.275
10x Buffer	2.5
$MgCl_2$ (stock concentration is 25mM)	1.7
Betaine (stock concentration is 5M) *Optional*	6.5
dNTPs (stock concentration is 10mM)	0.5
DMSO *Optional*	0.325
Primer 1. (stock concentration is 20µM)	0.5
Primer 2. (stock concentration is 20µM)	0.5
Taq Polymerase 5Units/µL	0.2
DNA (example) extracted w/ "Qiagen DNeasy columns or other similar silica based kits"	1.0
TOTAL VOLUME OF REACTION:	**25.000 µL**

Comments on protocol:

- Protocol may work with other DNA extraction methods.
- Use Touch-Down cycling protocol-first 10 cycles anneal at 65ºC decreasing in temperature by 1.0ºC; next 30 cycles anneal at 55ºC.
- Betaine and DMSO have been standardized due to high GC content. Protocol may be tested without. Also, may adjust $MgCl_2$ to increase reaction or decrease non-specific amplifications.

Strategy:

Steps		Temp (ºC)	Time (m:ss)	# of Cycles
1. Initiation/Melting	HOT START? ☐	94	5:00	**1**
2. Denaturation		94	0:15	
3. Annealing	steps 2-3-4 cycle in sequence	65 to 55 (↓1ºC/cycle)	0:30	**40x**
4. Elongation		72	0:40	
5. Amplification		72	5:00	**1**
6. Finish		15	∞	n/a

Primers:

Name	Nucleotide Sequence (5' - 3')
1. Tet1F	ggtagaacaggccttattcctc
2. Tet1R	ggtgagaagtagatgaggctg
3. Tet1S	ggatgaacaactccacgtcctg

Electrophoresis Protocol:

Agarose: **1.5%** V: **90**

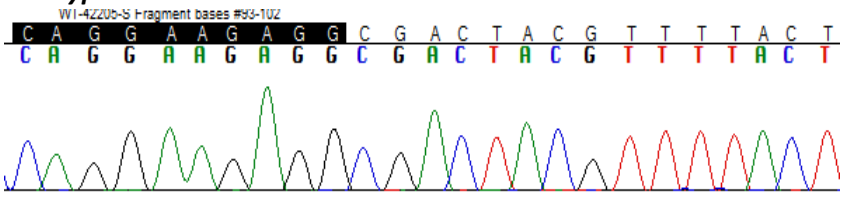
Estimated Running:Time: **90** min.

Primer Combination	Band (bp)	Genotype
1 & 2	495	

Note that primer 1 is located in intron 10 and primer 2 is located in exon 12. The mutation is within exon 11 (primer 3). The cytosine highlighted in red is mutated to thymine in tuft, thus a termination codon.

caggaagaggcgactacgttttact

Wildtype



Mutant