# GENOTYPING PROTOCOL MUTANT MOUSE RESOURCE \& RESEARCH CENTER: UC DAVIS 

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| Protocol Name: CR1166 Tas2r139 exdel MMRRC | MMRRC: 42227-UCD |
| :---: | :---: |
| Protocol: GoTaq ${ }^{8}$ Long PCR Master Mix(Promega) |  |
| Reagent/Constituent | Volume ( $\mu \mathrm{L}$ ) |
| Water | 5.6 |
| GoTaq® Long PCR Master Mix,2X | 7.5 |
| Primer 1. (stock concentration is $20 \mu \mathrm{M}$ ) comF | 0.6 |
| Primer 2. (stock concentration is $20 \mu \mathrm{M}$ ) wtR | 1.2 |
| Primer 3. (stock concentration is $20 \mu \mathrm{M}$ ) mutR | 0.3 |
| DNA (example) extracted w/ "Qiagen DNeasy columns or other similar silica based kits" | 1.5 |
| TOTAL VOLUME OF REACTION: | $15.00 \mu \mathrm{~L}$ |

Comments on protocol:

- Protocol may work with other DNA extraction methods.

Strategy:

| Steps | Temp $\left({ }^{\circ} \mathrm{C}\right)$ | Time $(\mathbf{m}: \mathbf{s s})$ | \# of Cycles |
| :--- | :---: | :---: | :---: |
| 1. Initiation/Melting | 94 | $2: 00$ | 1x |
| 2. Denaturation START? | 94 | $0: 10$ |  |
| 3. Annealing | steps 2-3-4 cycle in sequence | $65\left(\downarrow 1^{\circ} \mathrm{C} / \mathrm{cycle}\right)$ | $0: 30$ |
| 4. Elongation | 68 | $2: 00$ | $\mathbf{1 0 x}$ |
| 5. Denaturation | 94 | $0: 15$ |  |
| 6. Annealing | 55 | $0: 30$ | $\mathbf{2 5 x}$ |
| 7. Elongation | 68 | $2: 00(\uparrow 20 \mathrm{sec} / \mathrm{cycle})$ |  |
| 8. Finish | 4 | $\infty$ | $\mathrm{n} / \mathrm{a}$ |

Primers: Electrophoresis Protocol:

| Name | Nucleotide Sequence (5' - 3') | Agarose: 1.5\% V: | 90 |  |
| :---: | :---: | :---: | :---: | :---: |
| 1. CR_Tas2r139-comF | AATCTAGGGAGAGGACTTGAAAGCG | Estimated Running Time: 90 min. |  |  |
| 2. CR Tas2r139-wtR | CAGGGCATTAATTCAGAAATTCTCC | Primer Combination | Band (bp) | Genotype |
| 3. CR Tas2r139-mutR | TTCTTGTGTGTACTTCTGCATTTCCAC | $1 \& 2,1$ \& 3 | 654,1828 | wildtype |
|  |  | $1 \& 3$ | 477 | mutant |

Allele Description: Exon 1 ENSMUSE00000404314 and flanking splicing regions were constitutively deleted from the Tas2r139 gene ENSMUST00000057686.4 using CRISPR Cas9 gene editing technology in mouse zygotes. Subsequent founders were backcrossed to C57BL6/N to produce sequence confirmed heterozygous animals.


