

# GENOTYPING PROTOCOL

## MUTANT MOUSE RESOURCE & RESEARCH CENTER: UC DAVIS

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530-754-MMRRC

Protocol Name: CR10239 Crabp2 EXDEL

Protocol: GoTaq® G2 Colorless Master Mix(Promega)

| Reagent/Constituent                                                                   | Volume (µL)     |
|---------------------------------------------------------------------------------------|-----------------|
| Water                                                                                 | 4.5             |
| GoTaq® G2 Colorless Master Mix,2X                                                     | 7.5             |
| Primer 1. (stock concentration is 20µM) comF                                          | 0.5             |
| Primer 2. (stock concentration is 20µM) wtR                                           | 0.5             |
| Primer 3. (stock concentration is 20µM) mutR                                          | 0.5             |
| DNA (example) extracted w/ "Qiagen DNeasy columns or other similar silica based kits" | 1.5             |
| <b>TOTAL VOLUME OF REACTION:</b>                                                      | <b>15.00 µL</b> |

### Comments on protocol:

- Protocol may work with other DNA extraction methods.

### Strategy:

| Steps                                                                                        | Temp (°C )      | Time (m:ss)         | # of Cycles |
|----------------------------------------------------------------------------------------------|-----------------|---------------------|-------------|
| 1. Initiation/Melting <span style="float: right;">HOT START? <input type="checkbox"/></span> | 94              | 2:00                | <b>1x</b>   |
| 2. Denaturation                                                                              | 94              | 0:10                |             |
| 3. Annealing <span style="float: right;">steps 2-3-4 cycle in sequence</span>                | 65 (↓1°C/cycle) | 0:30                | <b>10x</b>  |
| 4. Elongation                                                                                | 68              | 2:00                |             |
| 5. Denaturation                                                                              | 94              | 0:15                |             |
| 6. Annealing <span style="float: right;">steps 5-6-7 cycle in sequence</span>                | 55              | 0:30                | <b>25x</b>  |
| 7. Elongation                                                                                | 68              | 2:00 (↑20sec/cycle) |             |
| 8. Finish                                                                                    | 4               | ∞                   | n/a         |

### Primers:

| Name              | Nucleotide Sequence (5' - 3') | Electrophoresis Protocol:              |                  |                 |
|-------------------|-------------------------------|----------------------------------------|------------------|-----------------|
| 1. CR-Crabp2_comF | ATGGGACAATTAGAAGAAGCTGCTGT    | Agarose: <b>1.5%</b>                   | V: <b>90</b>     |                 |
| 2. CR-Crabp2_wtR* | GAGTCAGTAGGTGGGAGGACTCC       | Estimated Running Time: <b>90</b> min. |                  |                 |
| 3. CR-Crabp2_mutR | GCACTCACTCTCGGACGTAGACCC      | <b>Primer Combination</b>              | <b>Band (bp)</b> | <b>Genotype</b> |
|                   |                               | 1 & 2, 1 & 3                           | 400,1531         | wildtype        |
|                   |                               | 1 & 3                                  | 561              | mutant          |

**Allele Description:** Exon 2-3([ENSMUSE00000175779](#), [ENSMUSE00000175781](#)) and flanking splicing regions were constitutively deleted from the Crabp2 gene [ENSMUSG00000004885](#) using CRISPR Cas9 gene editing technology in mouse zygotes. Subsequent founders were backcrossed to C57BL6/N to produce sequence confirmed heterozygous animals.

\*wtR primer untested (ePCR verified)

