

GENOTYPING PROTOCOL

MUTANT MOUSE RESOURCE & RESEARCH CENTER: UC DAVIS

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Protocol Name: _C57BL/6NCrl-Bcorem1(IMPC)Mbp/Mmucd _____ **Stock #:** 67172

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 |
| TOTAL VOLUME OF REACTION: | 15.00 µL |

Comments on protocol:

- Protocol may work with other DNA extraction methods.

Strategy:

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

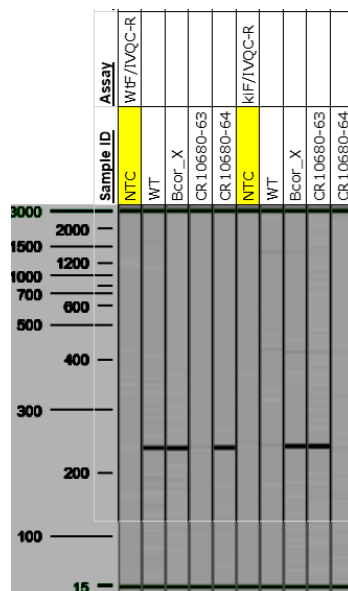
Primers:

Electrophoresis Protocol:

| Name | Nucleotide Sequence (5' - 3') | Agarose: 1.5% V: 90 |
|-------------------|---|--|
| 1. CR_Bcor_wtF | TGC GGCGGA AACACGGT | Estimated Running 90 min. |
| 2. CR_Bcor_kiF | GTCGGCCTCTGCAACACG | Primer Combination Band (bp) Genotype |
| 3. CR_Bcor_IVQC-R | CTGTGGCGTGGTCCCTTTCACT | 1 & 3 240 wt |
| | Do two separate PCRs for the two primer combinations. | 2 & 3 243 mutant |

Allele Description: Six base pairs "GGCGGA" of the 5'UTR were constitutively deleted using optimized CRISPR Cas9 KI technology utilizing Ribonucleoprotein (RNP) in the presence of a synthetic single strand DNA repair template harboring the desired KI. Zygotes were electroporated and subsequent progeny were screened for the presence of the correctly targeted allele via homology directed repair (HDR). The KI contains a 6 bp deletion, which ablates positions 1-16 of protospacer and will protect the HDR derived locus from re-cutting by Cas9. Key progeny were sequence confirmed.

cgactcctcctccccactcgcccccttcccgccgcatgcggtcgctctgcaacacgggtccaactccttgaaagtaaacttgccgcgagctgccag
ggcggaa>a



WT = #64; Mutant (6 bp deletion) = #63