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

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| Protocol Name: CR1091 Sgtb exdel | MMRRC: 42216-UCD |
| :---: | :---: |
| Protocol: GoTaq® 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 ( ${ }^{\circ} \mathrm{C}$ ) | Time (m:ss) | \# of Cycles |
| :---: | :---: | :---: | :---: |
| 1. Initiation/Melting HOT START? $\square$ | 94 | 2:00 | 1x |
| 2. Denaturation | 94 | 0:10 |  |
| 3. Annealing steps 2-3-4 cycle in sequence | 65 ( $\downarrow 1^{\circ} \mathrm{C} /$ 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 ( $\uparrow 20 \mathrm{sec} / \mathrm{cycle}$ ) |  |
| 8. Finish | 4 | $\infty$ | n/a |

Primers: Electrophoresis Protocol:

| Name | Nucleotide Sequence (5' - 3') | Argarose: 1.5\% V: | 90 |  |
| :---: | :---: | :---: | :---: | :---: |
| 1. CR_Sgtb-comF | GACATTCTAGTGGGAAAGACCTTGC | Estimated Running Time: | 90 min. |  |
| 2. CR Sgtb-wtR | CCGGCATAGTCTCATACGAGATAGC | Primer Combination | Band (bp) | Genotype |
| 3. CR Satb-mutR | GCACTACCACCAGAGCTAAAACAGC | $1 \& 2,1$ \& 3 | 456,1749 | wildtype |
|  |  | $1 \& 3$ | 184 | mutant |

Allele Description: Exon 4 ENSMUSE00000313716 and flanking splicing regions were constitutively deleted from the Sgtb Gene ENSMUST00000044385.13 using CRISPR Cas9 gene editing technology in mouse zygotes. Subsequent founders were backcrossed to C57BL6/N to produce sequence confirmed heterozygous animals.


