

**EMMA ID:** *EM:16178*

**Gene:** *Mast2*

**Common name:** *Mast2-em1*

**Allele:** *Mast2*<sup>*em1(IMPC)Hmgu*</sup>

## Allele Information

Knock-in frameshift mutation in the MAST2 gene (L1196Wfs\*92) introduced via CRISPR/Cas9. 4 additional synonymous substitutions were introduced as part of the CRISPR strategy to facilitate genotyping via restriction digest.

## Genotyping Information

Genotyping by end-point PCR based on gel is composed of a genespecific short range PCR using primers on wild type allele and a mutant allele-specific short range PCR. The combined results show the genotype of the mice. For example: mutant positive, wild type positive = Heterozygous. In addition to the expected product, the mutant assay may also amplify the endogenous wild type sequence, which will appear as a larger band on an agarose gel. The presence of this extra band will depend on the size of the original deletion.

### PCR primer pairs and expected size bands

| Assay            | Forward Primer | Reverse Primer | Expected Size Band (bp) |
|------------------|----------------|----------------|-------------------------|
| Mutant/wild type | M2L96 F        | M2L96 R        | 500                     |

sequencing of the PCR product or restriction digest of 5µl PCR product in 25µl with MluI-HF (NEB) at 37°C for 3 h.

### Primer sequences

| Primer Name | Sequence 5' --> 3'   |
|-------------|----------------------|
| M2L96 F     | CAAACCCAGACCGTTCTAA  |
| M2L96 R     | TTCCGGAATAGGGAGCTTCT |

Touch-Down cycling protocol: first 10 cycles anneal at 65°C, decreasing 1°C per cycle, next 30 cycles anneal at 55°C. These PCR conditions have been optimized for our methods and preparation kits.

| Component                 | Volume (µl) 1x | Final conc. |
|---------------------------|----------------|-------------|
| DNA (~ 50-100 ng)         | 2              |             |
| Q-Solution (5x)           | 2,5            | 0,5         |
| PCR-Buffer (5x)           | 5              | 1           |
| DNTP mix (10 mM)          | 0,5            | 0,2         |
| MgCl <sub>2</sub> (25 mM) | 1,5            | 1,5         |
| Primer 1 (10 pmol/µl)     | 1              | 0,4         |
| Primer 2 (10 pmol/µl)     | 1              | 0,4         |
| Taq Polymerase (5 U/µl)   | 0,5            | 2,5 U/rxn   |
| H <sub>2</sub> O*         | 11             |             |
| Final volume              | 25             |             |

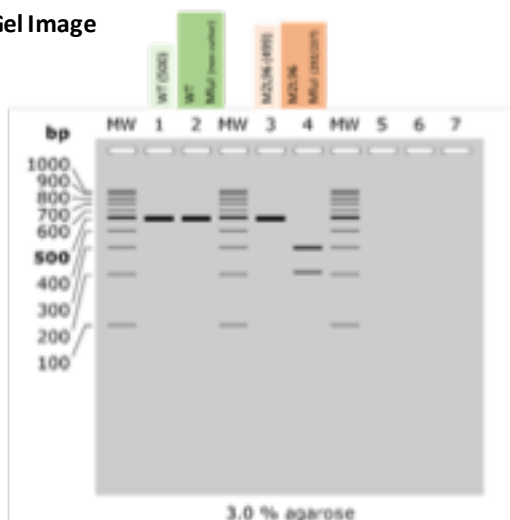
\* The amount of H<sub>2</sub>O is adjusted with the number of primer.

#### Amplification conditions

| PCR Settings                                 | Temperature (°C)         | Time                       | # of cycles |
|----------------------------------------------|--------------------------|----------------------------|-------------|
| 1 Denaturation (Melting)                     | 95°C                     | 5 min                      | 1           |
| 2 Amplification (Melting, Annealing, Polym.) | 94°C<br>65-55 TD<br>72°C | 30 sec<br>45 sec<br>45 sec | 39          |
| 3 Polymerisation                             | 72°C                     | 10 min                     | 1           |
| 4 Cooling                                    | 4°C                      | hold                       | 1           |

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#### Gel Image



#### Comments/Additional information:

Genotyping is done by PCR followed by restriction digest.  
M24.38 restriction enzyme will only cut the mutant amplification product.  
Wildtype => non-cutter (500 bp fragment)  
Homozygous => 2 fragments at 300 bp and 200 bp  
Heterozygous => mixed, 3 fragments at 500 bp, 300 bp and 200 bp