

EMMA ID: 13439
Gene: *Prox2*
Common name: *Prox2-em1_5*
Allele: *Prox2*^{em1(IMPC)Hmgu}

Allele Information

For more information on production, guides and mutation, search for gene/project, go to project summary, go to production plan, go to production outcome and "more details"

<https://www.gentar.org>

IMPC mouse phenotype data, search by the gene name
<http://www.mousephenotype.org/>

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.

Prox2-em1_5 contains a -1bp deletion and therefore needs to be sequenced.

PCR primer pairs and expected size bands

Assay	Forward Primer	Reverse Primer	Expected Size Band (bp)
Wild type	Prox1 for1	Prox1 rew1	597
Mutant	same as wt	same as wt	596

Primer sequences

Primer Name	Sequence 5' --> 3'
Prox1 for1	tcctcagagtctccaccaaggcccggtg
Prox1 rew1	ccgcagaggcaggcagagactcgtttc

PCR setup (LongAmp® TaqDNA Polymerase)

Component	Volume (µl) 1x
DNA (~ 50-100 ng)	2-4
100% DMSO	0,4
PCR-Buffer (5x)	4
DNTP mix (10 mM)	0,5
Primer 1 (10 pmol/µl)	1
Primer 2 (10 pmol/µl)	1
Primer 3 (10 pmol/µl)	1
Taq Polymerase (2,5U/µl)	0,5
H2O*	7,6
Final volume	20

* The amount of H2O is adjusted with the number of primer.

Amplification conditions

PCR Settings	Temperature (°C)	Time	# of cycles
1 Denaturation (Melting)	94°C	3 min	1
2 Amplification (Melting, Annealing, Polym.)	94°C	30 sec	39
	68-58 (↓1°C/Cycle)	20 sec	
	65°C	1 min	
3 Polymerisation	65°C	10 min	1
4 Cooling	4°C	hold	1

Touch-Down cycling protocol: first 10 cycles anneal at 68°C, decreasing 1°C per cycle, next 30 cycles anneal at 58°C.

These PCR conditions have been optimized for our methods and preparation kits. Adaptions may be required.

Sequence / mutation
Wt:

ccgggctttactgtccacagaggtccttgtagaactctggtgaggctcgttccacggtccaggcaccagatgagcagctgttctcggccttgcctcggggagcttcttgctc
 agttcctcctgggctctgtgctggtgctctg

Mut:

ccgggctttactgtccacagaggtccttgtagaactctggtgaggctcgttccacggtccaggcaccagatgagcagctgttctcggccttgcctcggggagcttcttgctca
 gttcctcctgggctctgtgctggtgctctg