

**EMMA ID:** 11030

**Gene:** *Hoxa2*

**Common name:** EPD0560\_3\_F04

**Allele:** *Hoxa2*<sup>tm1a(EUCOMM)Wtsi</sup>

## Allele Information

Further information about the allele can be found on IMPC website at (copy the link to web browser)  
<https://www.mousephenotype.org/data/alleles/MGI:96174/tm1a%2528EUCOMM%2529Wtsi?>

## Links to the general information

About IKMC resource

<https://www.infrafrontier.eu/knowledgebase/protocols/ikmc-products>

IKMC allele types

<http://www.i-dcc.org/kb/entry/89/>

Allele conversion guide - genotyping tm1b, tm1c and tm1d mice (assays infos available when required)

<http://www.mousephenotype.org/about-ikmc/targeting-strategies>

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 gene-specific 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.

### PCR primer pairs and expected size bands

Assay	Forward Primer	Reverse Primer	Expected Size Band (bp)
Mutant	Hoxa2_Ef	Kr 3209	379
Wildtype	Hoxa2_Ef2	Hoxa2_Er	306

### Primer sequences

Primer Name	Sequence 5' --> 3'
Hoxa2_Ef	CCATGAGCTTCGAGGGAAGGGG
Hoxa2_Er	GCTGCTTAGCTGAGCAAGAGCGG
Hoxa2_Ef2	GCTCCCTAGGAGCGGTTGTGG
Kr 3209	CCAACAGCTCCCCACAACGG

### PCR setup (Qiagen, Hot Start Plus)

Component	Volume ( $\mu$ l) 1x	Final conc.
DNA (~ 50-100 ng)	2	
Q-Solution (5x)	2,5	0,5
PCR-Buffer (10x)	2,5	1
DNTP mix (10 mM)	0,5	0,2
MgCl <sub>2</sub> (25 mM)	1,5	1,5
Primer 1 (10 pmol/ $\mu$ l)	1	0,4
Primer 2 (10 pmol/ $\mu$ l)	1	0,4
Taq Polymerase (5 U/ $\mu$ l)	0,3	0,06
H <sub>2</sub> O*	13,7	
Final volume	25	

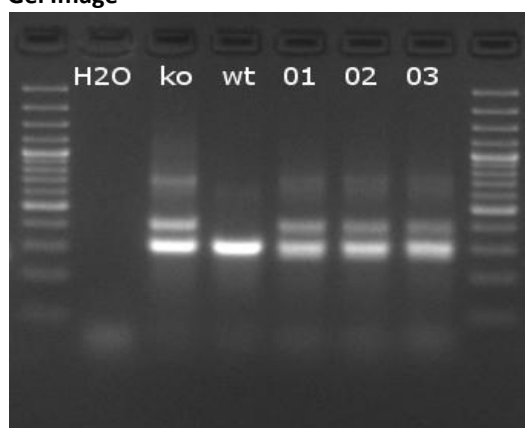
\* The amount of H<sub>2</sub>O is adjusted with the number of primer.

### Amplification conditions

PCR Settings	Temperature ( $^{\circ}$ C)	Time	# of cycles
1 Denaturation (Melting)	95 $^{\circ}$ C	5 min	1
2 Amplification (Melting, Annealing, Polym.)	94 $^{\circ}$ C	30 sec	39
	62 $^{\circ}$ C	45 sec	
	72 $^{\circ}$ C	45 sec	
3 Polymerisation	72 $^{\circ}$ C	10 min	1
4 Cooling	12 $^{\circ}$ C	hold	1

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

### Gel Image



Separated by gel electrophoresis on a 2% agarose gel.

## Genotyping using PCR-assays for cassette detection

LacZ reporter, Neo selection cassettes are inserted into the Knockout-first mutant allele. Cassette changes by allele conversion can be found on: <http://www.mousephenotype.org/about-ikmc/targeting-strategies>. For example, tm1b allele contains still lacZ reporter cassette, Neo selection cassette is deleted (promotor-driven only).

Please note that these assays are with universal cassette primers other than gene-specific. The confirmation on gene identity performed by e.g. sr genespecific PCR as provided is suggested .

### PCR primer pairs and expected size bands

Assay	Forward Primer	Reverse Primer	Expected Size Band (bp)
lacZ	LacZ_multi_Deen_2F	LacZ_multi_Deen_2R	mut 81 bp,wt without band
Neo	Neo_long_Deen_F1	Neo_long_Deen_R1	mut 186 bp,wt without band

### Primer sequences

Primer Name	Sequence 5' --> 3'
LacZ_multi_Deen_2F	TACTGGAGGCTGAAGTTCAGAT
LacZ_multi_Deen_2R	GCGTTTCACCCTGCCATAA
Neo_long_Deen_F1	TTGAACAAGATGGATTGCACGC
Neo_long_Deen_R1	CCTCGTCCTGCAGTTCATT

### PCR setup (Qiagen, Hot Start Plus)

Component	Volume (µl)	Final conc.
DNA (~ 50-100 ng)	2	
Q-Solution (5x)	2,5	0,5
PCR-Buffer (10x)	2,5	1
DNTP mix (10 mM)	0,5	0,2
MgCl <sub>2</sub> (25mM)	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)	0,3	0,06
H <sub>2</sub> O	13,7	
Final volume	25	

### Amplification conditions

PCR Settings	Temperature (°C)	Time	# of cycles
Denaturation (Melting)	95°C	5 min	1
Amplification (Melting, Annealing, Polym.)	94°C	30 sec	39
	58°C	45 sec	
	72°C	45 sec	
Polymerisation	72°C	10 min	1
Cooling	12°C	hold	1

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