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For any question, please contact:

Mouse Clinical Institute – Institut Clinique de la Souris (ICS)

1 rue Laurent Fries, BP 10142

67404 Illkirch Cedex France

Email: ics@igbmc.fr

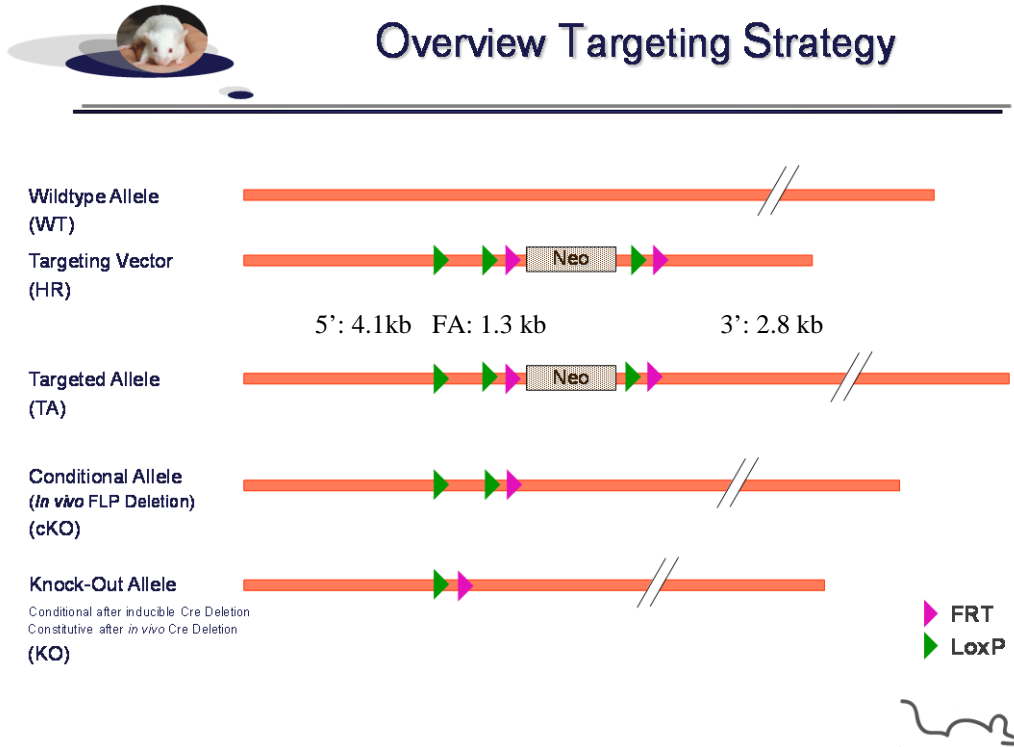
Web site: <http://www.phenomin.fr/en-us/>

This protocol has been prepared by Claudia Caradec, Engineer

This protocol has been validated by Sylvie Jacquot, Ph.D., Project Manager

1. Schematic representation of the locus

1.1. Overview



Legend:

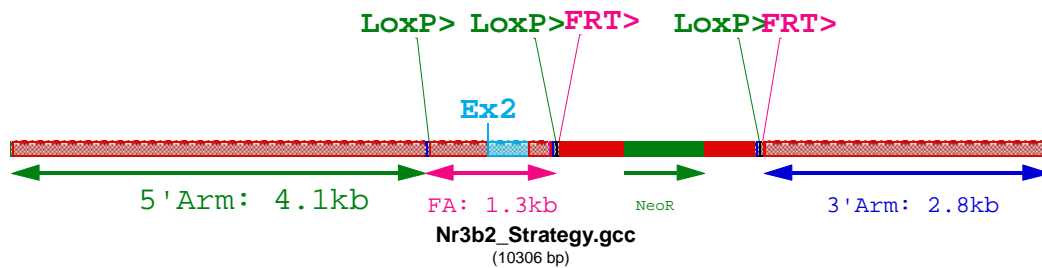
5': 5' homology arm; FA: floxed fragment; 3': 3' homology arm
 This schematic representation is not on scale

1.2. Strategy chosen: flox of exon 2

Nr3b2 gene (also named Esrrb) is a member of the nuclear receptor family. Additional information on this gene can be accessed at

<http://www.informatics.jax.org/javawi2/servlet/WIFetch?page=markerDetail&key=43303>

Strategy used to generate the conditional knock out model



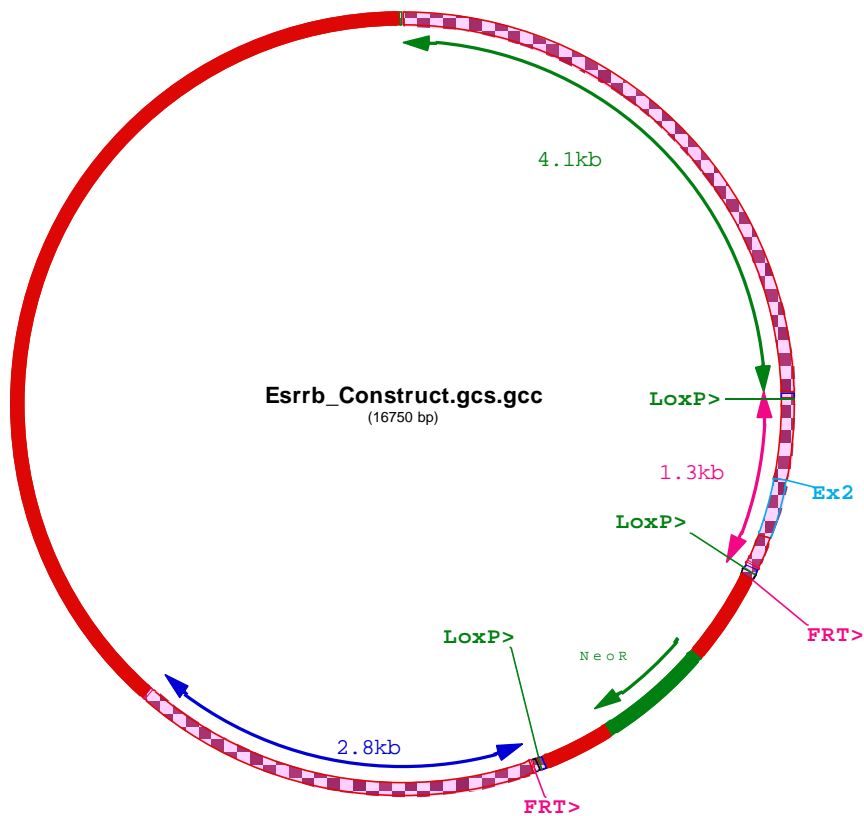
2. Construct used for homologous recombination in ES cells: Nr3b2 project

2.1. Legend

loxP sites are indicated in green ; FRT sites are indicated in purple; *Mus musculus* sequences are indicated in uppercase ; exogenous sequences are marked in lowercase.

The targeting vector was generated in 129Sv/Pas and was not fully sequenced. Regions sequenced are indicated in bolds.

2.2. Map of targeting vector plasmid





2.3. 5' homology arm (4.1 kb)

GCAAGCACTCTACCAGCTAAGCTATATGCCCCACCTCTCCCCTACCAGCTAGCTATATGCCCCACCTCTCCCCTA
CCAGCTAGCTATATGCCCCACCTCTCCCCTACCAGCTAAGCTATATGCCCCACCTCTCCCCTACCAGCTAAGCTAT
ATGCCCCACCTCTCCCCTACCAGCTAAGCTATATGTCCCACCTCTCCCCTACCAGCTAAGCTATATGCCCCACCT
CTCCCTTCCCTTCTTAATATCAGTAACTGACAGAAAGCGCAGTAGACTCTAATCTGAAAAATCTGAGATCAAAAT
TGCCCCAAATCTGAATTCTTGTTTTGTTTTGTTGAGTCCAAGGTATCATAACACGGCTTTACCTGAATTGTATC
CGAAGTAGTAGGCAAGTATTTCTAATAATTTAAAACCTTGAGCCATTAAGTCATTAGACTTGTAGCATCAGGATA
GTTCTCCAAAAGTTTGGGATTTGGGGCTTGCTCCTGGGTTTCATCCCCAGAATTAATAAAAAAAAAAGTATAAA
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2.4. Floxed fragment (1.3 kb)

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2.5. PGK-Neo region

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2.6. 3' homology arm (2.8 kb)

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2.7. Vector backbone sequence

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Molecular Biology Data
Nr3b2 conditional knock out model
ICS references:

ctcttatcagaccggtttccgcggtggtgaaccaggccagccacggtttctgcgaaaaacgcgggaaaaagtggaagc
ggcgatggcgggagctgaattacattcccacccgcggtggcacaacaactggcgggcaaacagtcgttgctgattgg
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Molecular Biology Data
Nr3b2 conditional knock out model
ICS references:

gcagtcgcttcacgttcgctcgcgtatcggtgattcattctgctaaccagtaaggcaaccccgccagcctagccg
ggtcctcaacgacaggagcagatcatgcgcacccgctggccaggacccaacgctgcccgagatgcgcccgcgtgcg
gctgctggagatggcggacgcgatggatatgttctgccaaggcgtttaacttaattaagtcgacggccggccct
cgaggcc

3. ES cell lines targeted and validation data

3.1. ES cell lines targeted

The targeting vector was electroporated in P1 ES cells [MCI-129Sv/Pas background]

Number of clones screened: 744

Number of positives: 3

Reference of clone used to generate the mouse line:

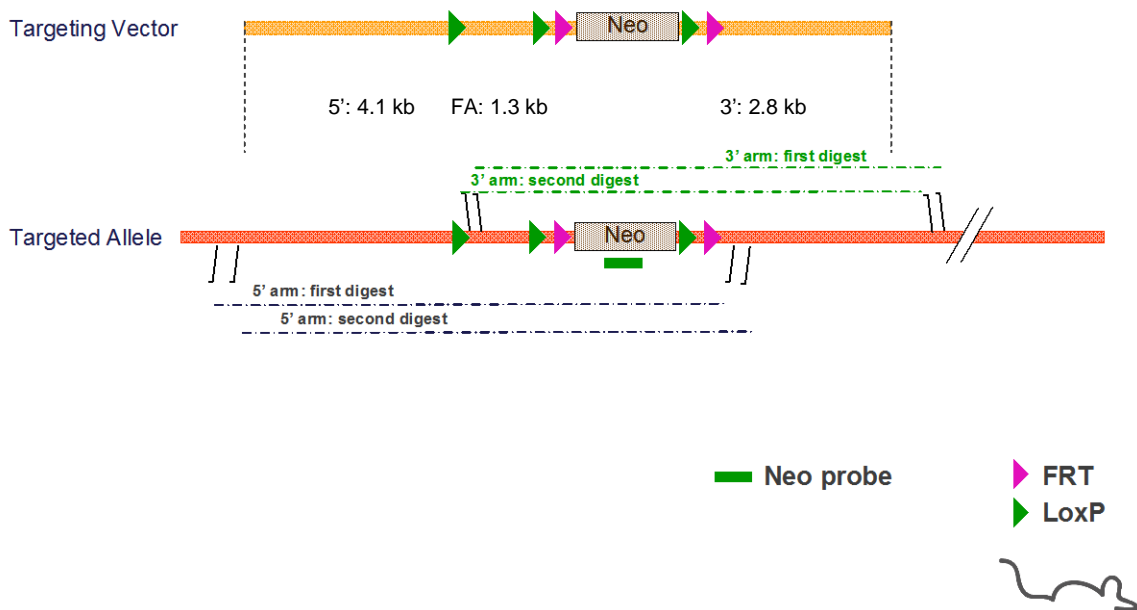
- clone **K176P1-251**

3.2. Southern data on positive clone

3.2.1. Neo Southern strategy



Southern Screening Strategy



Digestions used to validate the 5' and 3' insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Neo	5' arm first digest	AvrII	/	8.6
	5' arm second digest	SacI	/	10.9
	3' arm first digest	SexAI	/	7.6
	3' arm second digest	HincII	/	9.0

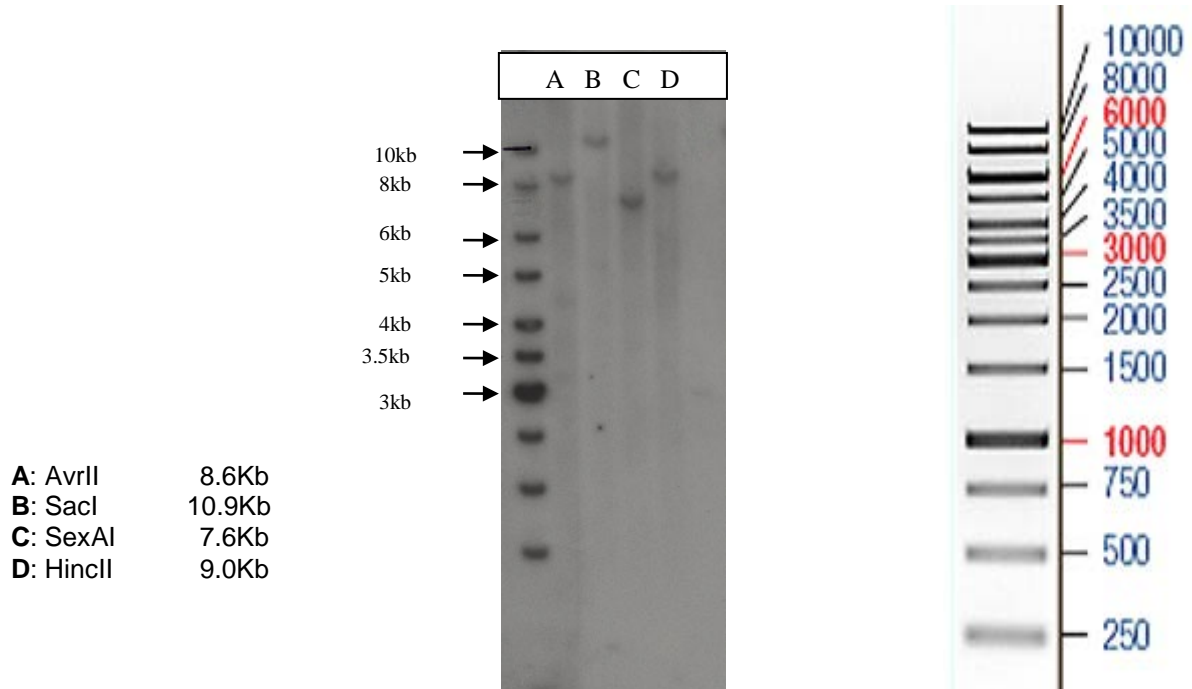
Four different digests are used to validate correct HR event. Two digests validate the 5' insertion, 2 other digests validate the 3' insertion



3.2.2. Picture of Neo Southern

Neo southern blot: 5' and 3' arm validation

ladder



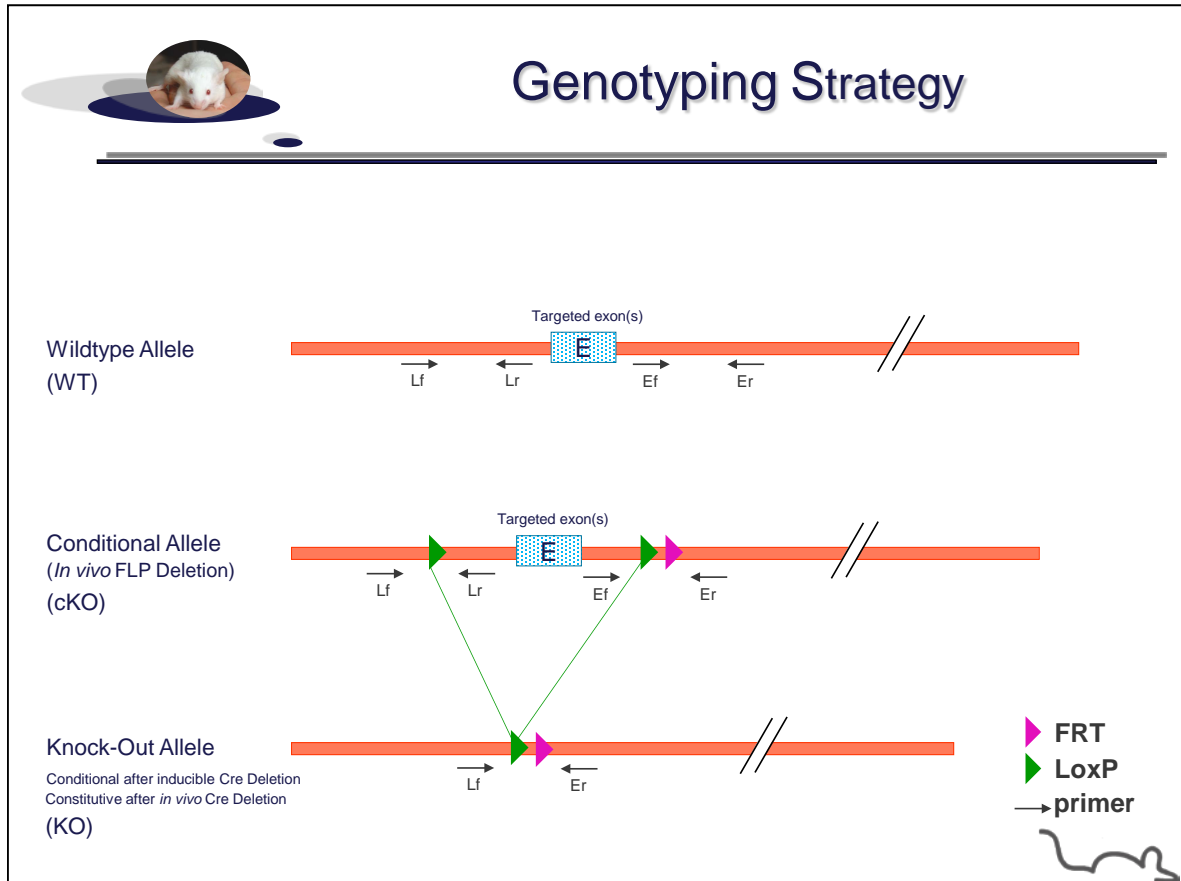
4. Data on conditional and knock-out animals

Both conditional and knock-out mouse models were backcrossed in C57BL/6J background.

4.1. Genotyping protocol and data

4.1.1. Genotyping strategy

The map below describes the position of the primers used for genotyping for each possible allele.



Sequence of primers used for genotyping

Position	Primers	Sequence
Lf	840	GCAAGCTGGATTATCTCAGAGCTAAG
Lr	841	GGCGGTCCCATCTAAAGTATGATTCC
Ef	617	AATTCCAAGTCTCGTTTCCTGGGGG
Er	619	ACAGCATGCGTGTTGAGAGCTGTC



Molecular Biology Data
Nr3b2 conditional knock out model
ICS references:

PCR fragments expected size (bp):

Region analyzed	Primers used	Position on the primer (see the map above)	Conditional allele (cKO)	Knock-Out allele (KO)	WT allele (WT)
Presence of the distal 5'loxP	840-841	Lf / Lr	285	---	238
Excision of the selection marker	617-619	Ef / Er	308	---	191
Total Excision (excision of the floxed exon(s), i.e. knock out)	840-619	Lf / Er	1544*	297	1381*

* This PCR product will not be observed using our PCR genotyping conditions (see description below)
 --- No Amplicon should be obtained

4.1.2.PCR protocol

This section describes the composition of the mix and cycling conditions used for genotyping.

Reagents:	Volume:
-10x Buffer (Roche)	2.5µl
-dNTPs 10mM (Amersham Biosciences)	0.5µl
-Taq DNA Polymerase (Roche)	0.2µl
-DNA (50ng/µl)	3µl
-5' primer (100 µM)	0.125µl
-3' primer (100 µM)	0.125µl
-Sterile H2O	up to 25 µl

Cycling conditions:

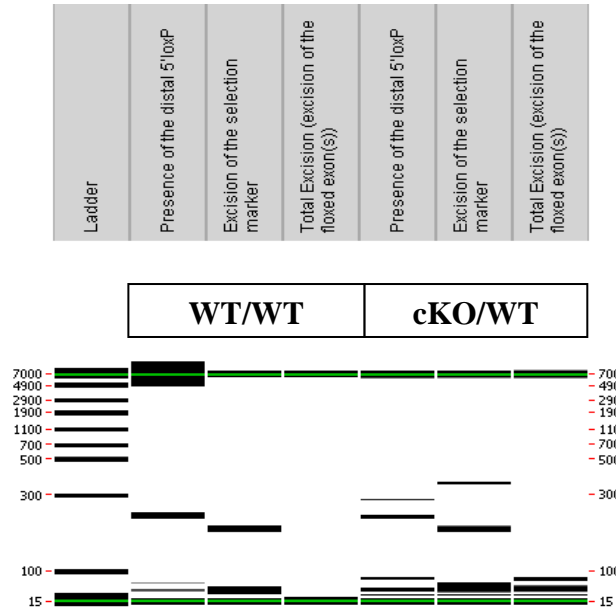
Temp	Time	#Cycles
94°C	3min	1
94°C	1min	2
62°C	1min	
72°C	1min	
94°C	30s	30
62°C	30s	
72°C	30s	
72°C	3min	1
4°C	∞	

NB: These PCR conditions have been optimized for high-throughput genotyping. Adaptation to small-scale may be required.

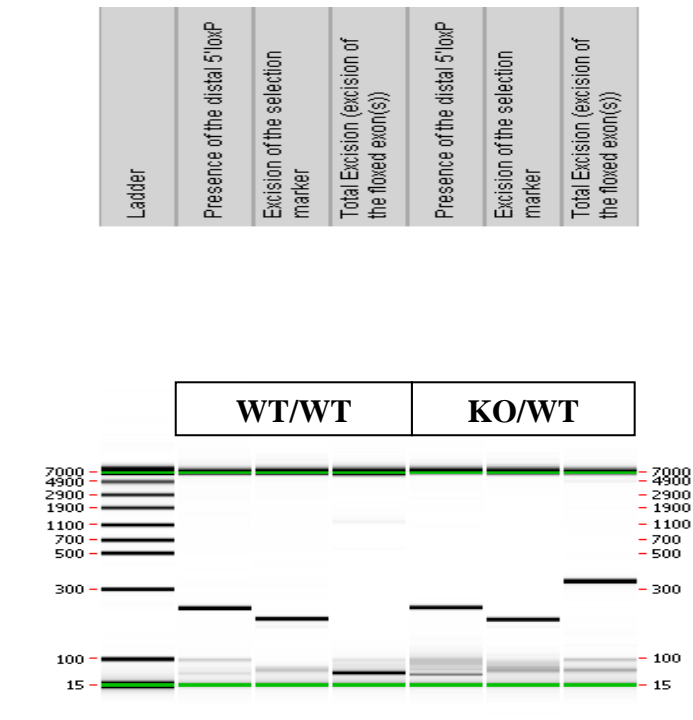
4.1.3. Picture of genotyping with various alleles

Analysis of PCR products pattern was not done by gel electrophoresis but using LabChip® 90 microfluidic apparatus. PCR products were run on the HT DNA 5K LabChip® 90 Assay Kit.

- Picture of genotyping with conditional knock-out (cKO) allele



- Picture of genotyping with knock-out (KO) allele



Note that as this technology is more sensitive than gel analysis, non specific signals and/or primer dimers may be visible on the picture.



4.2. Evaluation of lethality of homozygote KO (KO/KO)

Males knock-out heterozygotes (KO/WT) were crossed with females knock-out heterozygotes (KO/WT). Offspring was genotyped to evaluate the ratio of the different genotypes. Results are provided in the table below.

Genotype	WT/WT	KO/Wt	KO/KO	Total
Number of pups obtained	16	49	0	65
Experimental Ratio	25%	75%	0%	100%
Theoretical Ratio	25%	50%	25%	100%
Theoretical Ratio if KO/KO are not viable	33%	66%	0%	100%

The Esrrb knock-out homozygotes are not viable.

Legend:

- >13% Homozygous = Viable
- >0% and ≤13% = Subviable
- 0% = Lethal