Molecular Biology Data
RORγ conditional knock out model

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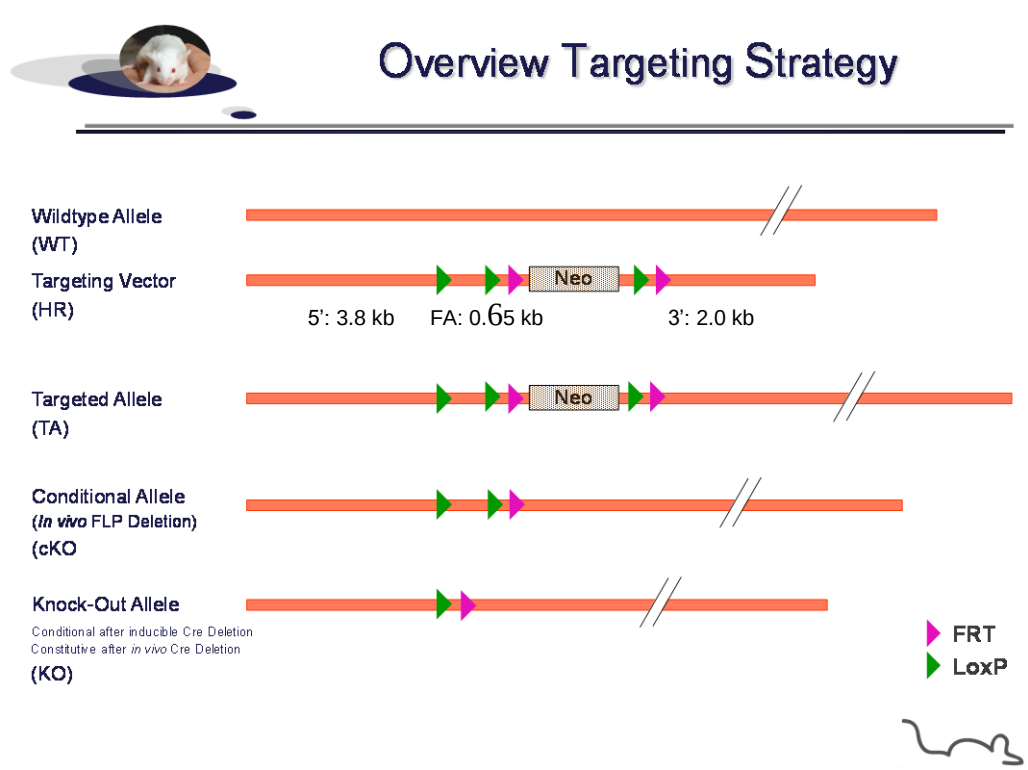
This protocol has been prepared by Claudia Caradec, Engineer
This protocol has been validated by Sylvie Jacquot, Ph.D., Project Manager

1. Schematic representation of the locus

1.1. Overview

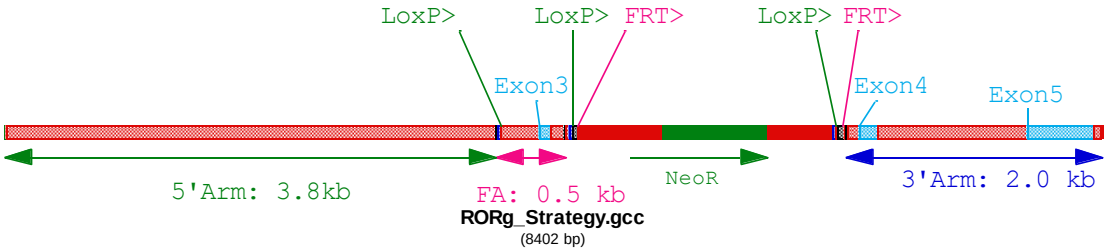


Legend:
5': 5' homology arm; FA: floxed fragment; 3': 3' homology arm
This schematic representation is not on scale

1.2. Strategy chosen: flox of exon 3

Rorc gene (also named RORγ) is a member of the nuclear receptor family. Additional information on this gene can be accessed at:
http://www.informatics.jax.org/marker/MGI:104856

Strategy used to generate the conditional knock out model

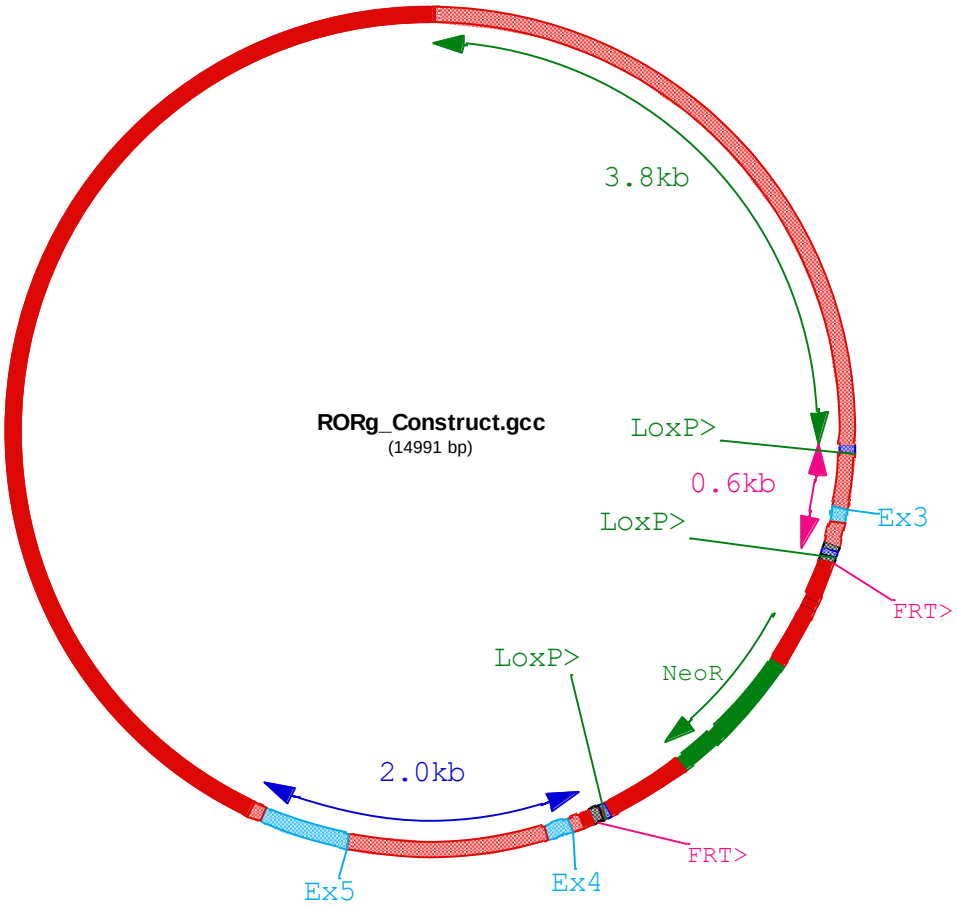


2. Construct used for homologous recombination in ES cells: RORg project

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 (3.8 kb)

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2.4. Floxed fragment (0.6 kb)

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2.5. PGK-Neo region

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2.6. 3’ homology arm (2.0 kb)

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2.7. Vector backbone sequence

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ttcatccgcgtccagctcgttgagtttctccagaagcgttaatgtctggcttctgataaagcgggccatgttaag
ggcggttttttcctgtttggtcactgatgcctccgtgtaagggggatttctgttcatgggggtaatgataccgat
gaaacgagagaggatgctcacgatacgggttactgatgatgaacatgcccggttactggaacgttgtgagggtaa
acaactggcggtatggatgcggcgggaccagagaaaaatcactcagggtcaatgccagcgcttcgttaatacaga
tgtaggtgttccacagggtagccagcagcatcctgcgatgcagatccggaacataatggtgcagggcgctgactt
ccgcgtttccagactttacgaaacacggaaaccgaagaccattcatgttgttgctcaggtcgcagacgttttgca
gcagcagtcgcttcacgttcgctcgcgtatcggtgattcattctgctaaccagtaaggcaaccccgccagcctag
ccgggtcctcaacgacaggagcacgatcatgcgcacccgtggccaggacccaacgctgcccgagatgcgccgcgt
gcggctgctggagatggcggacgcgatggatatgttctgccaagtcagcgtttaaacttaat**taagtcgacggcc**

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]

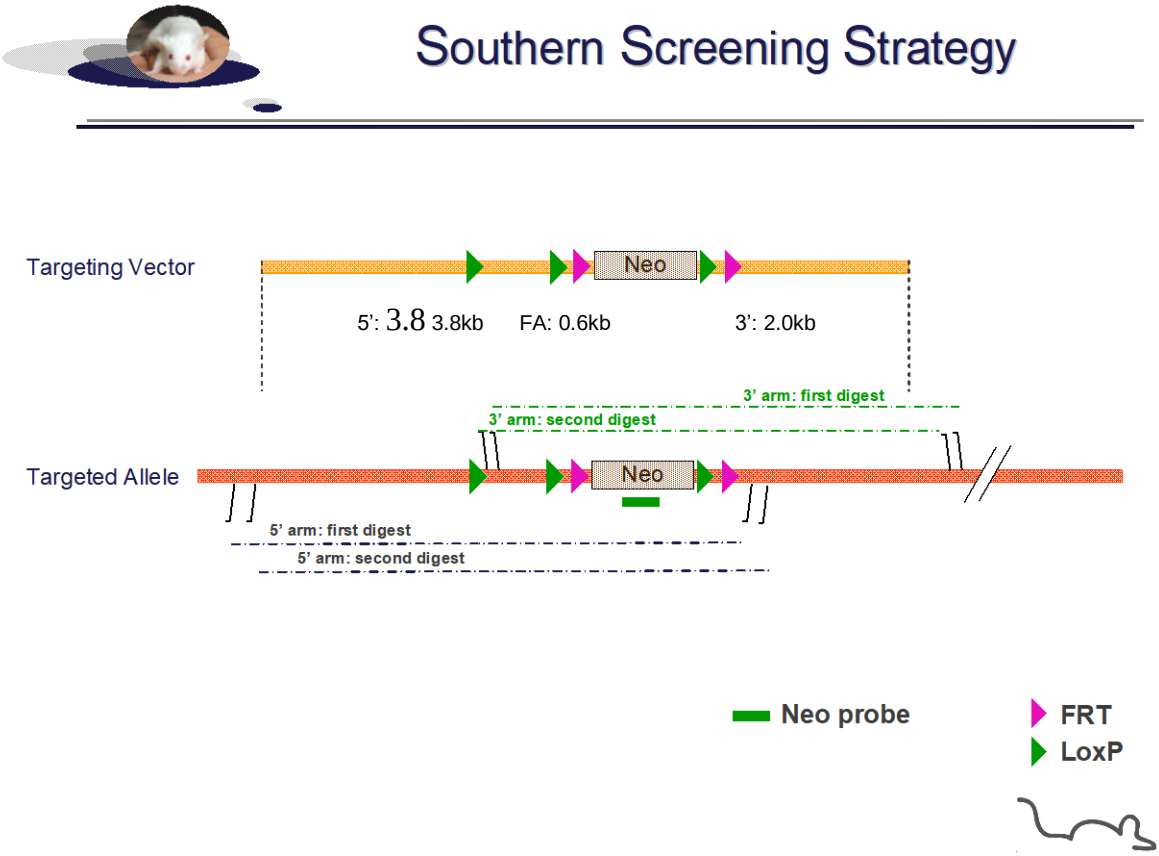
Number of clones screened: ~ 400
Number of positive: 6

Reference of clone used to generate the mouse line:

- clone **K82P1-5**

3.2. Southern data on positive clone

3.2.1.Neo Southern strategy



Digestions used to validate the 5' and 3' insertion

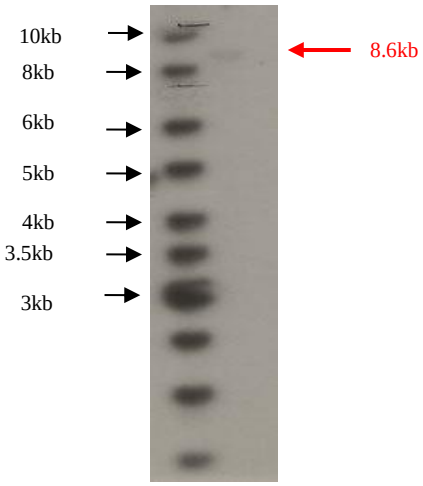
Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Neo	5' arm first digest	EcoRV	/	**8.6**
	5' second digest	AseI	/	**13.9**
	3' arm first digest	PshAI	/	**12.3**
	3' arm second digest	SexAI	/	**6.7**

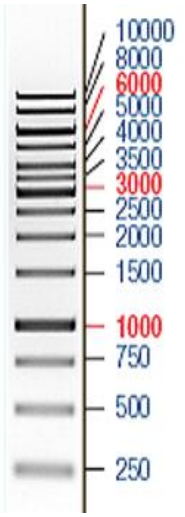
Four different digests are used to validate correct HR event. Two digests validate the 5' insertion, 2 other digests validate the 3' insertion

3.2.2.Picture of Neo Southern

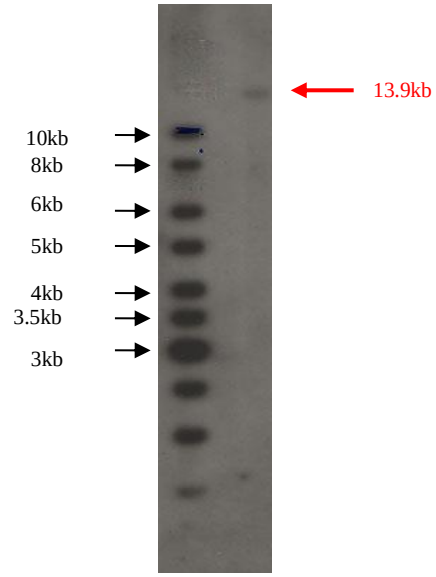
Neo southern blot: 5' arm validation ladder

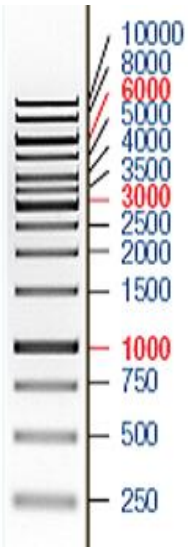
EcoRV: 8.6kb



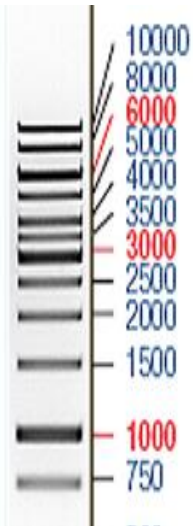


AseI: 13.9kb

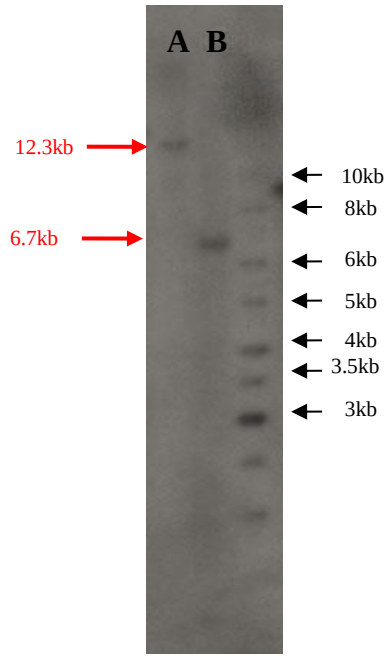




Neo southern blot: 3' arm validation ladder



A: PshAI 12.3kb
B: SexAI 6.7kb

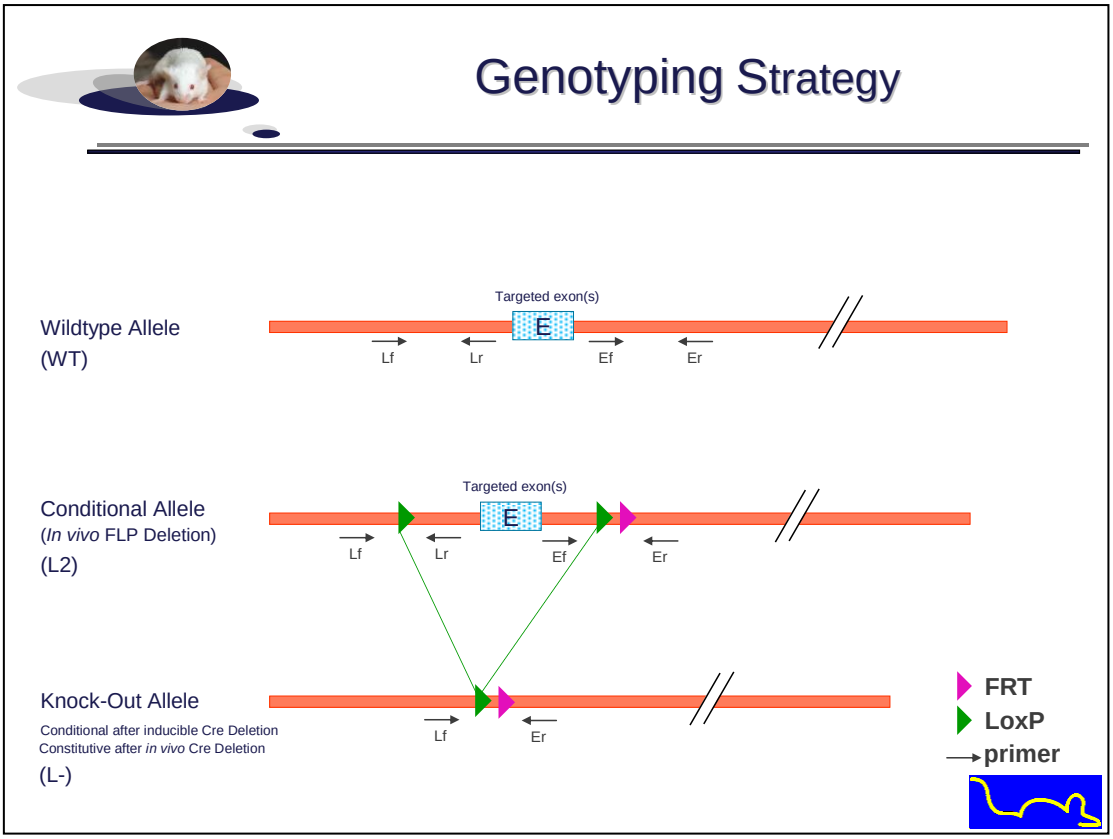


4. Genotyping protocol and data on conditional and knock-out animals:

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

4.1. Genotyping strategy

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



Sequence of primers used for genotyping

Primers	Sequence
Lf (#94)	GAAGCAGGTGTTACGAAGCAGTA
Lr (#96)	AGTGTAAATGATTCTCAGCATAGGG
Ef (#99)	CATATTTGTCTGCATACATGCACTT
Er (#102)	CTGGGAAACAGAAACTGCTTATC
Er (#101)	GACCTCCAATTCATGTGCACTGGTC

PCR fragments expected size (bp):

Region analyzed	**Primers used**	Position on the primer (see the map above)	Conditional allele (L2)	Knock-Out allele (L-)	WT allele (WT)
Presence of the distal loxP	94 / 96	Lf / Lr	248	---	201
Excision of the selection marker	99 / 102	Ef / Er	381	---	243
Excision of the floxed exon(s), i.e. knock out	94 / 101	Lf / Er	874*	219	634*

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

4.2. 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:

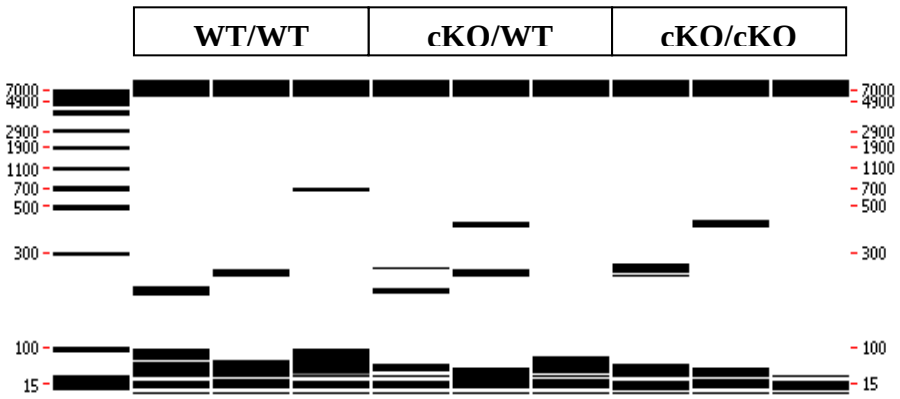
Temp	Time	#Cycles
94°C	3min	1
94°C	1min	
62°C	1min	2
72°C	1min	
94°C	30s	
62°C	30s	30
72°C	30s	
72°C	3min	1
4°C	∞	

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

4.3. 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



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

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

Data not shown.