





MODEL GENERATION TECHNICAL REPORT

Generation of a RFP657-LF2A-Cre-F3-ERT2-F3 into Prg2 Knock-In mouse line

Project code: Ros6280 / IR6280

Report updated: 16/05/2023







de la santé et de la reriserise médicale





















PROJECT PROCESS & QUALITY CONTROL









Target locus structure

- mRNA and protein
- Genetic strategy
- PRO & CONS evaluation of the strategy



Chromosome 2: 84,980,461-84,983,632





Ensembl Gene ID : ENSMUSG0000027073







Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Prg2-201	ENSMUST0000028467.5	838	<u>223aa</u>	Protein coding	CCDS16198	<u>Q545D8</u> <u>Q61878</u>	NM_008920 NP_032946	TSL:1GENCOD E basicAPPRIS P1









mRNA and protein expressed after Cre mediated excision (sequence detail see next page)





Pros

Use of the TagRFP657 and dual cassette (Cre-F3-ER^{T2}-F3

Cons

Presence of repeated sequences in both homology arms might render PCR amplification or LR-screen difficult



B HOMOLOGOUS RECOMBINATION - VECTOR CONSTRUCTION



Created with SnapGene®





- Electroporation and screening process
- Long range PCR screening strategy
- Long-Range 5' PCR screening results
- Recombinant ES validation by Long Range PCR
- Recombinant ES clones validation by Southern Blot internal probe
- Recombinant ES clones validation by Southern Blot External probe
- Aneuploidy screening in ES recombinant clones



The whole process of ES cells validation is described in Erbs et al.*.

The targeting vector was co-electroporated with a CRISPR vector (expressing the WT Cas9 and a guide RNA –atagcacccccatgaagtac- in the proprietary C57BL/6NCrl S3 cell line.

Transfected ES clones were submitted to neomycin selection (G418) and 93 resistant ES clones were isolated. The clones were then submitted to the screening process allowing secured identification of those harbouring the expected recombination events at both ends of targeting vector.

Screening process steps:

- 1. Identification of candidate recombinant clones by initial 3' Long-Range PCR
- 2. Six of 3' PCR positive clones are confirmed for 5' recombination event by Long-Range PCR
- 3. Positive clones in step2 are further validated by Southern blot analysis using internal and external probes
- 4. The karyotype of at least 2 validated clones is verified using ddPCR aneuploidy screening and Giemsa staining



















PROJECT PROCESS & QUALITY CONTROL







Long range PCR screening – strategy

Schematic 5' and 3' PCR screening strategy



PCR	Primer Name	Primer sequences	PCR product size	
	Fext	GCAGGTGTCATATGCTGCTTTGAGG	EQLA	
5 PCK	Rneo	AGGGGCTCGCGCCAGCCGAACTGTT	J.0 KJ	
5' PCR	Fext	GCAGGTGTCATATGCTGCTTTGAGG	2 E kh	
	Rcre	CTCTACACCTGCGGTGCTAACCAGC	5.5 KU	
2' DCD	Fint	GCTGGTAGTTGCTGGGTGCAGAACA	1 kb	
5 PCR	Rext	GGTAGATACTGGATGGGATCACAAG		
3' PCR	Fneo	GCGGCCGGAGAACCTGCGTGCAATC	1 7 kb	
	Rext	GGTAGATACTGGATGGGATCACAAG	1.7 KU	



Long-Range 3' PCR screening – results





Pcr Fneo – Rext : 1.7 kb



Six candidate clones out of the 74 positive clones were selected for 5' Long-Range PCR and Southern blot validation.



Recombinant ES validation by Long Range PCR

Confirmation and Validation of candidate recombinant ES clones by 5' and 3' PCRs





Eight candidate clones identified by 3' PCR screening were further analysed by 5' PCR screening. Eight clones (clones #18, #40, #42, #46, #47, #48, #49 and #79) were confirmed.



Schematic Southern Blot validation strategy

Digests on the scheme illustrate the position of the chosen restriction sites relative to the probe. They don't show the exact position of the restriction sites.



Neo probe sequence



Digestions used to validate the 5' and 3' insertion

Probe		Genomic DNA digest	Targeted Allele (kb)
	E' digost	Ndel	10.9
Nee	5 uigest	Spel	10.5
Neo	3' digest	BgIII	8.6
		Dralll	5.1

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All 7 clones show only on band at the expected sizes with both restriction digests.

Schematic Southern Blot validation strategy



 Southern blot – 3' probe

 Wt 18 40 42 46 47 48 49 76

 10

 8

 6

 5

 4

 BspHI 9 / 5.3

3' PROBE SEQUENCE

CCATCCAGTATCTACCTTGCTGCAGCTTTGTCCGTATTTCCC CTTTACTATCCCCTAAAGAGCTGGGGACAGAAGGCCACCTAG GCAAGACATCGAGATATCACAAAGGGTTTAGAATCAGGTTTG AGTCCAAGTTCCTCCCAGTTTTTCTATCTTTGTGGCCTGGGG ACTGTGTCCTTACCTGTAGGTTGCACATGGTTTCCCTTGCCC CATTACTGGTTTGTGATATAAGGATGATCATGTCAGAGAATG GGTTGGTGATGACCACTGTGGACCATTAGTTCATCTGCCCAG TATCCATCATGGTCCTGTGGTCAAGGATGTCAGGAGGAGTTA ACAGGGACAACGCTGGCTCTGCCTCTTCCTTCCCCCATGT ATGCTTCTGCTTCCTACCTTCTCTAGGGCCGATGCAAACGCT TTCGATGGGTTGATGAAGATTCTTGG

Digestions used to validate the 5' and 3' insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
3' external probe	3' first digest	BspHI	9	5.3



- \Rightarrow All clones were validated (targeted band at the expected size).
- \Rightarrow The additional band observed some clonesshown that the untargeted allele was edited by CRISPR.

Selected recombinant ES cells clones were karyotyped by ddPCR as described in Codner *et al.*¹ and by Giemsa metaphase staining. Results of aneuploidy analysis are presented in the table below.

Clone ID	ddPCR	Giemsa	
#18	Limit	Not done	
#40	Pass	Not done	
#42	Pass	Not done	
#46	Pass	Not done	
#47	Pass	Pass	
#48	Failed	Not done	
#49	Pass	Not done	
#76	Pass	Not done	

¹ Codner, G.F., Lindner, L., Caulder, A., Wattenhofer-Donzé, M., Radage, A., Mertz, A., Eisenmann, B., Mianné, J., Evans, E.P., Beechey, C.V., Fray, M.D., Birling, M.-C., Hérault, Y.,

Pavlovic, G., Teboul, L

Aneuploidy screening of embryonic stem cell clones by metaphase karyotyping and droplet digital polymerase chain reaction. BMC Cell Biology 2016 doi:10.1186/s12860-016-0108-6





Microinjection

Breeding to F1 generation

- The ES cells used in the injection experiment were originally derived from a C57BL/6 mouse strain (which have black coat colour). These cells were injected into blastocysts derived from an BALB/cN strain, which have a white coat colour. The resulting offspring are thus chimeras of two different cell types (ES cell-derived cells and host blastocyst-derived cells) and the degree of chimerism was monitored by the percentage of light and dark patches on these animals.
- Recipient blastocysts were isolated from mated BALB/cN females (Health status SPF Specific Pathogens Free).
- Recombinant ES clones #47 validated in previous project phase was injected into blastocysts to generate chimeric males. The results are presented in the table below.

	Number of chimeric males identified according to chimerism rate (Number of chimeric males bred to F1 generation)				
Clone ID	5 - 40%	45% - 55%	60-100%	Total	
#47	1	2	3	6	

- Two highly chimeric males generated in the previous phase by blastocyst injection of the ES clones were mated with Dre deleter C57BL/6NCrl females (health status SPF Specific Pathogen Free; MGI) to investigate whether the recombined ES cells have contributed to the germ layer.

Germ line transmission was obtained the 24/09/2018

- The Roxed NeoR cassette was excised by an additional breeding with a Dre deleter (Gt(ROSA)26Sor<tm4.1(CAG-dre)lcs>)
 - Allele nomenclature (following MGI guidelines) : Prg2^{tm1.1Ics}

6 SEQUENCE OF THE DELIVERED ALLELE

Fxon 2

Fn2 intron

IF7A

CCTGGACAGGAAGACTGAAGGGGAGATGCCAGAGACTCAGTGAAGCCTGGGGTACCCTATTGGAGTCCTTCAAGGAAAACTTGGCCTCACCAGGCCTCAGCCTTGGGAACTCACTGGCGATCCCCTTGGGATCCCCTTGGGATCCCCTTGGGATCCCCTTGGGATCCCCTTGGGATCCCCTTGGGGTTACATAGGAAGGGGGGACGGGGACGGGATT GCGTTCGAACGCACTGATTTCGACCAGGGTTCGTTCACTCATGGAAAATAGCGACCGCTGCCAGGATATAAGGAATCTGGCATTTCTGGGGATTGCTTATAACACCCCTGTTACGTATGCCAGGATCAGGGTTAAAGATATCTCACGTACTGACGGTGGGAGAATGTTAAGCACTCGTCACGTACTGGCAGATGCTTAAGCACCCTGTTACGCCAGGATCAGGGTTAAAGGATATCTCACGTACTGACGGTGGGAGAATGTTAAGCACCCTGTTACGCCAGAATTGCCAGGGTTCACGGGTTAAAGATATCTCACGTACTGGCGAGATATAAGGAATCTGGCATTTCTGGGGATTGCTTAAACACCCTGTTACGCAAATTGCCAGGGTTAAAGATATCTCACGTACTGACGGTGGGAGAATGTTAAGGAATCTGGCGATTGCTTAAACACCCTGTTACGCAGAATTGCCAGGGTTAAAGGATATCTCACGTACTGACGGTGGGAGAATGCTTAATCCAC CTGGTTCACATGATCAACTGGGCGAAGAGGGTGCCAGGCTTTGTGGATTTGACCCTCCATGATCAGGTCCACCTTCTAGAATGTGCCCTGGCTAGAGATCCTGGTCGGCGCCCATGGAGGCACCCAGTGAAGCTACTGGTCCCACTGGCGCCACGGAAGAGCACCCAGTGAAGCTACTGGTCCCACTGGCGCCACGGAAGAGCACCAG GGAAAATGTGTAGAGGGCATGGTGGAGATCTTCGACATGCTGCTGGCTACATCTCGGGTTCCGCATGATGAATCTGCAGGGAGAGGAGGAGGAGGAGTTTGTGTGCCCAAATCTATTTTGCTTAATTCTGGAGGTGTACACATTTCTGTCCAGCACCCTGAAGTCTCCGGAAGAGAAGAGAAGGACCATATC TGAGAAGTTCCTATACTATTTGAAGAATAGGAACTTCTGAGCTCCCTGGCGGAATTCGGATCCAGATCTTATTAAAGCAGAACTTGTTTATTGCAGCTTATAAAGGAATAAAGCAATAAAGCAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATAAAGCAATATAAAGCAATATAAAGCAATATAAAGCAATATAAAGCAATATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATCACAAATAAAGCAATATAAAGCAATAAAGCAATATA CTCATCAATGTATCTTATCATGTCTGGTCGAGGCACCGGTGCCTGCAGGTAACTTTAAAATAATTGGCATTATTTAAAGTTAGGATCTATAGATCATGAGTGGGAGGAATGAGCTGGCCCTTAATTTGGTTTTGCTTGTTTAAATTAGGT

Cre

Τ2Α

RFP657

F3

Frt2

Rox

EXCELLENCE IN MOUSE PHENOGENOMICS

REPORT REDACTION & VALIDATION

Protocol finalized on 2023/05/2023 Prepared by Romain LORENTZ, IE Verified by Marie-Christine BIRLING, PhD

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