Name of Mouse model or mutation:
CEP290-R1891X-EM1-B6N

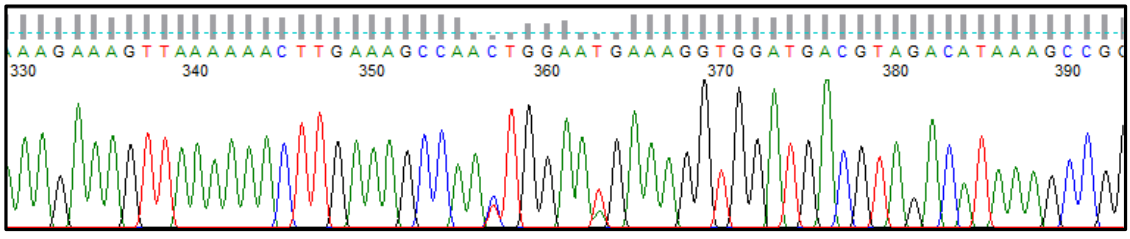
Description:
Point mutation model made using CRISPR/Cas9.

Type of mutation:
SNP: R1891X

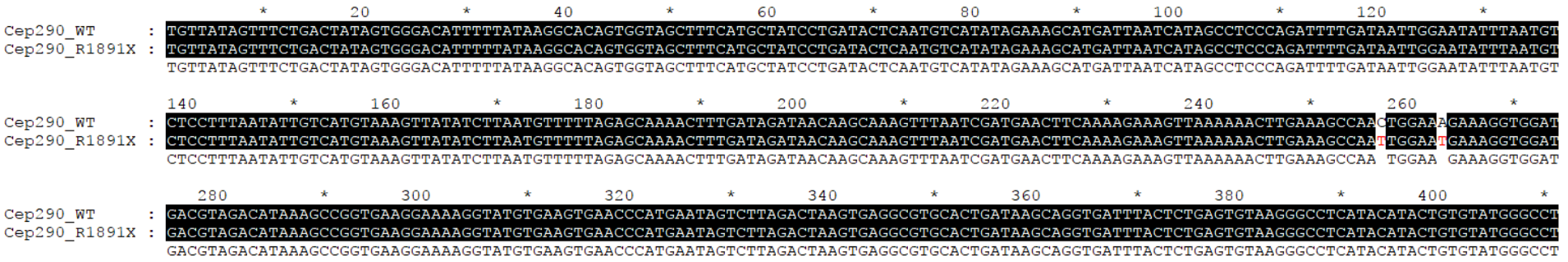
Sequence details
WT
TGTTATAGTTTCTGACTATAGTGGGACATTTTTATAAGGCACAGTGGTAGCTTTCATGCTATCCTGAT
ACTCAATGTCATATAGAAAGCATGATTAATCATAGCCTCCCAGATTTTGATAATTGGAATATTTAATG
TCTCCTTTAATATTGTCATGTAAAGTTATATCTTAATGTTTTTAGAGCAAAACTTTGATAGATAACAAG
CAAAGTTTAATCGATGAACTTCAAAAGAAAGTTAAAAAACTTGAAAGCCAACTGGAAAGAAAGGTG
GATGACGTAGACATAAAGCCGGTGAAGGAAAAGGTATGTGAAGTGAACCCATGAATAGTCTTAGAC
TAAGTGAGGCGTGCACTGATAAGCAGGTGATTTACTCTGAGTGTAAGGGCCTCATACATACTGTGTA
TGGGCCTAAATAAGGCTGAGATGTCTAAGACAGATTTCTGTCATTTAGAAAGCTGCACTCCACTTGA

Mutant
TGTTATAGTTTCTGACTATAGTGGGACATTTTTATAAGGCACAGTGGTAGCTTTCATGCTATCCTGAT
ACTCAATGTCATATAGAAAGCATGATTAATCATAGCCTCCCAGATTTTGATAATTGGAATATTTAATG
TCTCCTTTAATATTGTCATGTAAAGTTATATCTTAATGTTTTTAGAGCAAAACTTTGATAGATAACAAG
CAAAGTTTAATCGATGAACTTCAAAAGAAAGTTAAAAAACTTGAAAGCCAATTGGAATGAAAGGTG
GATGACGTAGACATAAAGCCGGTGAAGGAAAAGGTATGTGAAGTGAACCCATGAATAGTCTTAGAC
TAAGTGAGGCGTGCACTGATAAGCAGGTGATTTACTCTGAGTGTAAGGGCCTCATACATACTGTGTA
TGGGCCTAAATAAGGCTGAGATGTCTAAGACAGATTTCTGTCATTTAGAAAGCTGCACTCCACTTGA

CEP290-R1891X-EM1-B6N Heterozygous F1 animal sequence trace:

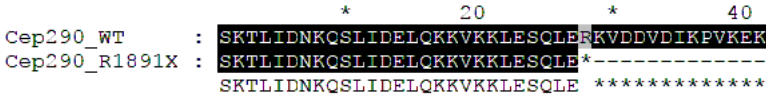


Nucleotide Alignment:



The silent mutation incorporated into the donor at a.a. residue 1889 (L) gives rise to an MfeI restriction site (CAATTG) for identification of the CEP290-R1891X-EM1-B6N allele.

Predicted Protein Alignment:



QC strategy employed at Harwell to check the engineered allele:

Genomic DNA was extracted from ear clip biopsies and amplified in a PCR reaction using the following conditions/primer sequences:

Geno_Cep290_F1	TCCAGTGGACTGCAGGTAATTTG
Geno_Cep290_R1	TTAGGGTTTGCGCTGGCAAT
Taq Polymerase used	Roche Expand Long Range DNTPack
Annealing Temperature (°C)	62
Elongation time (min)	1
WT product size (bp)	736
Mutant product size (bp)	736

All amplicons were sent for Sanger sequencing to check for integration of the donor oligo sequence at the target site. F1 sequences should be heterozygous unless on Y chromosome.

Copy counting of the donor sequence was carried out by ddPCR at the F1 stage to confirm donor oligos were inserted once on target into the genome. The following Taqman assay was used to detect the donor sequence:

Assay name	Cep290-R1891Xdonor1WT1
Forward Primer	CCTTTTCCTTCACCGGCTTTATG
Reverse Primer	AACAAGCAAAGTTTAATCGATGAACTTC
Probe	TCTACGTCATCCACCTTTC
Label	FAM-BHQ1

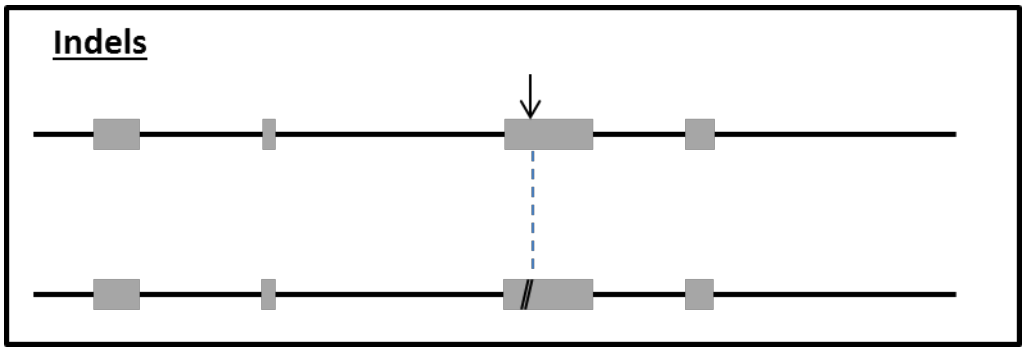
Will detect both the WT allele and the CEP290-R1891X-EM1-B6N allele.

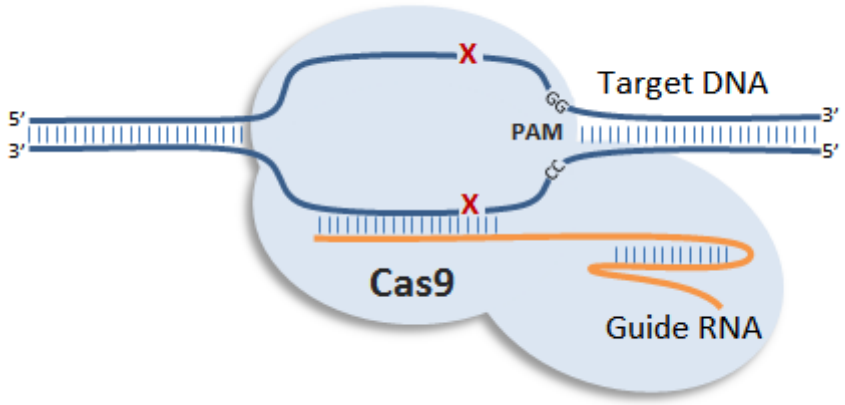
Assay name	Cep290R1891XLegit1MUT2
Forward Primer	GGGTTCACTTCACATACCTTTTCC
Reverse Primer	GTTAAAAAACTTGAAAGCCAATTGGAATG
Probe	CACCGGCTTTATGTCTACGTCATCCA
Label	FAM-BHQ1

Will detect the CEP290-R1891X-EM1-B6N allele only.

Cep290-R1891X Genotyping Strategy

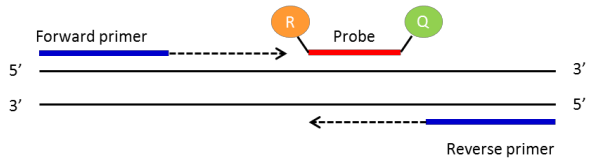
Animals have been engineered using the CRISPR/Cas9 technology. Most of the knockout alleles generated through this method will be obtained by deletion of a critical exon or by introduction of an indel (insertion/deletion) within the coding sequence of a critical exon (see picture below).



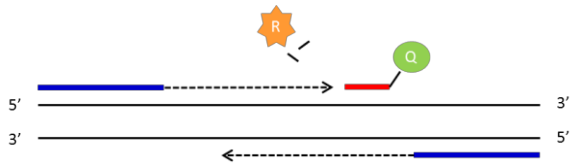


qPCR genotyping strategy

Standard PCR is the amplification of DNA between a pair of primers. Quantitative PCR employs the same principal as standard PCR, although it actually monitors the progress of the DNA synthesis as it occurs. The progress of the reaction is measured by using a Taqman probe. This is a short DNA oligo that is complimentary to part of the DNA sequence between the forward and reverse primers. At the 5' end of the probe there is a fluorescent reporter (R) and at the 3' end a quencher (Q). Whilst they are in close contact with each other there is no fluorescent signal.



As the forward primer is extended the reporter is cleaved from the probe resulting in a fluorescent signal being detected. Once the primer extends enough to release the quencher this signal is blocked. By using probes with different fluorescent signals multiple PCR assays can be multiplexed and run together.



Allele specific primer and probe amplification assay (ASPPAA) PCR

This is a new real-time PCR method (Billard *etal.,* 2012) in which an allele specific primer and an allele specific probe designed specific to the SNPs. The primer is designed such a way that its 3' end ends with a specific SNP. The probe is also designed specific to the SNPs at its 3' end giving a primer probe overlap. A maximum of 3nt overlap between a primer and probe is allowed.

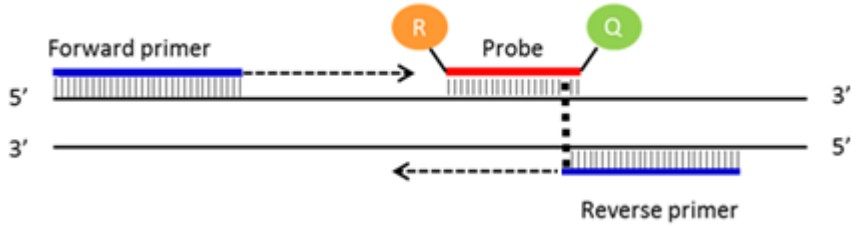
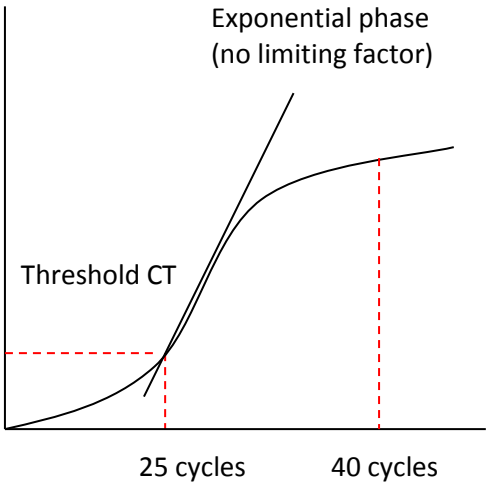


Figure1: Figure showing principle of ASPPAA PCR. The dotted line indicates the position of the SNP.

PCR reaction plot



The number of cycles the PCR takes to reach a set threshold is known as the CT value. This is inversely correlated to the amount of template DNA in the sample.

e.g. CT 25 = 2 x template DNA
CT 26 = 1 x template DNA
CT above 30 = no template represented in the sample

CT value can be used to determine how many copies of a particular allele samples have.

All our qPCR are run in duplicate. A FAM labelled genotyping assay is run in multiplex with a VIC labelled internal control Dot1l.

References:

Billard A., Laval V., Fillinger S., Leroux P., Lachaise H., Beffa R., et al. (2012).
The allele-specific probe and primer amplification assay, a new real-time PCR method for fine quantification of single-nucleotide polymorphisms in pooled DNA.
Appl. Environ. Microbiol. 78 1063–1068. 10.1128/AEM.06957-11

Cep290-R1891X Genotyping Strategy

Samples are genotyped with both WT and Mutant assays. These are FAM labelled assays that are designed to detect the critical exon that has been modified. If the animal contains the modified allele the copy number of the WT assay should drop by 1 and the mutant assay should raise by 1. For autosomal genes that have been targeted this means the following

WT= 2 copies of the WT assay and 0 copies of the Mutant assay
HET = 1 copy of the WT assay and 1 copy of the Mutant assay
HOM = 0 copies of the WT assay and 2 copies of the Mutant assay

Cep290-R1891X CRISPR/Cas9 mutant in which SNPs are as highlighted

WT TGAAAGCCAACTGGAAAGAAAGGTG
Mutant TGAAAGCCAATTGGAATGAAAGGTGGA

Cep290-R1891X-WT2 assay (FAM labelled probe)

GTCATATAGAAAGCATGATTAATCATAGCCTCCCAGATTTTGATAATTGGAATATTTAATGTCTCCTTTAATATT
GTCATGTAAAGTTATATCTTAATGTTTTTAGAGCAAAACTTTGATAGATAACAAGCAAAGTTTAATCGATGAACT
TCAAAAGAAAGTTAAAAAACTTGAAAGCCAACTGGAAAGAAAGGTGGATGACGTAGACATAAAGCCGGTGAAGGA

Cep290-R1891X-WT2 primers and probe

Primer 1 = GAGCAAAACTTTGATAGATAACAAGCA
Primer 2 = TTATGTCTACGTCATCCACCTTTCT
Probe = AAACTTGAAAGCCAACTGGAAAGAA

Allele specific primer and probes

CEP290-R1891X-MUT1 assay (FAM labelled probe)

GTCATATAGAAAGCATGATTAATCATAGCCTCCCAGATTTTGATAATTGGAATATTTAATGTCTCCTTTAATATT
GTCATGTAAAGTTATATCTTAATGTTTTTAGAGCAAAACTTTGATAGATAACAAGCAAAGTTTAATCGATGAACT
TCAAAAGAAAGTTAAAAAACTTGAAAGCCAATTGGAATGAAAGGTGGATGACGTAGACATAAAGCCGGTGAAGGA

CEP290-R1891X-MUT1 primers and probe

Primer 1 = GCCTCCCAGATTTTGATAATTGGA

Primer 2 = ATGTCTACGTCATCCACCTTTCA
Probe = AAAAACTTGAAAGCCAATTGGAATGA

Allele specific primer and probes

Dot1l internal control (VIC labelled)

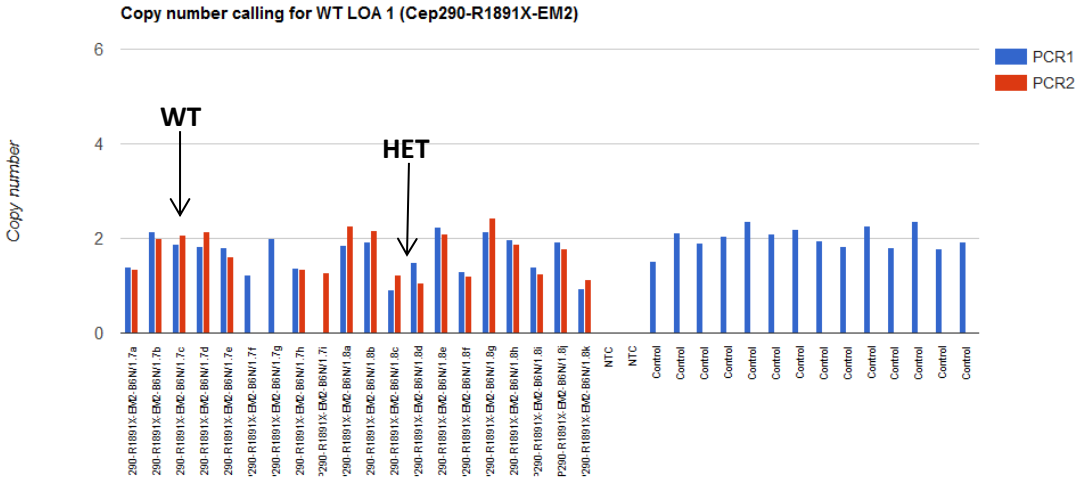
CCCCTCTAGTCGTTTTCTGTTAGTAGTTGGCATCCTTATGCTTCATCTTACAGTCGACTTGAGAGCTGGCCCTGA
ATGGTCGTGCTGGGGCAAGGCTTTATTTCAGGCGTAGCACACATGGTGGCCAATGGGACTCTGTAGGATCTGCCC

Primer 1 = GCCCCAGCACGACCATT
Primer 2 = TAGTTGGCATCCTTATGCTTCATC
Probe = CCAGCTCTCAAGTCG

qPCR master mix

ABI GTX Taqman master mix	5µl
Primers Dot1L_2F (20µM)	0.225µl
Primers Dot1L_R (20µM)	0.225µl
Probe DotL_2M (5µM)	0.2µl
FAM Assay (probe 5µM & primers 15µM each)	0.3µl
ddH20	1.55µl
DNA (1/10 dilution of ABI Sample-to-SNP prep)	2.5µl

Cep290-R1891X copy called result, image showing both replicates and controls



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