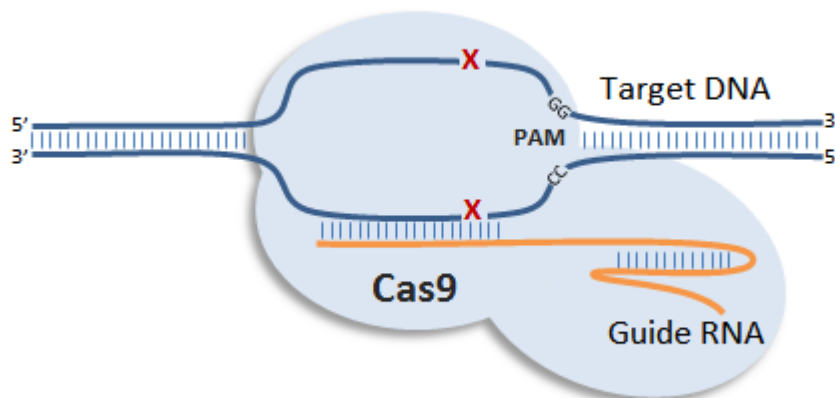
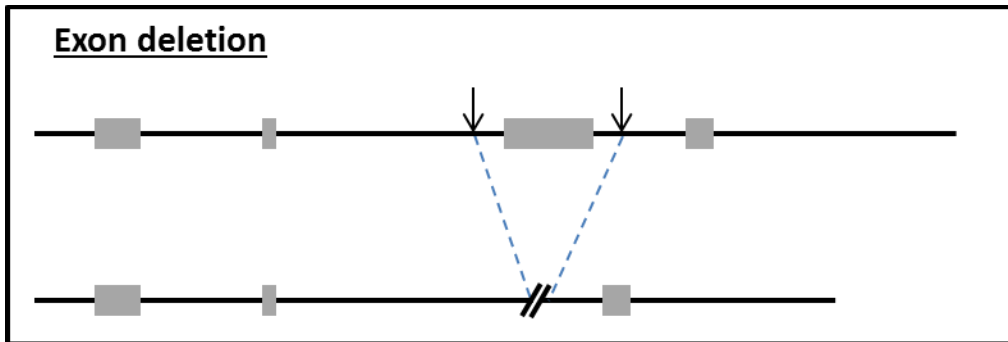


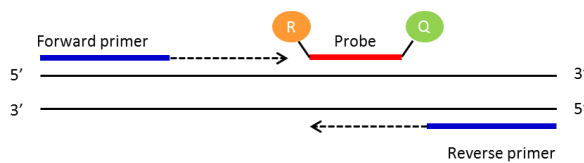
Inpp5k-DEL1152 Genotyping Strategy

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).

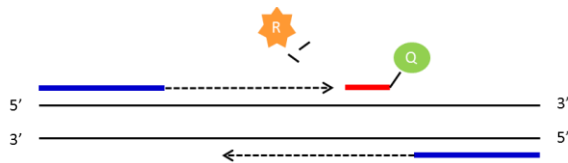


qPCR genotyping strategy

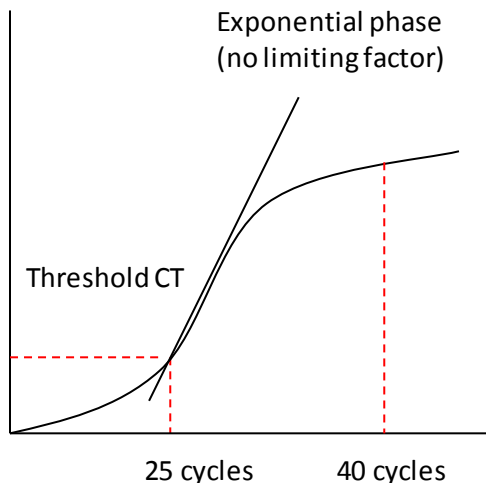
Standard PCR is the amplification of DNA between a pair of primers. Quantitative PCR employs the same principal as standard PCR, although it actually monitors the progress of the DNA synthesis as it occurs. The progress of the reaction is measured by using a Taqman probe. This is a short DNA oligo that 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.



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 Dot1I.

Inpp5k-DEL1152 Genotyping Strategy

Samples are genotyped with both WT loss of allele (WT-LOA) and Mutant assays. Samples for this line are genotyped using the following primers and probe (see Figure1)

- Universal probe and Universal primer designed near the CRISPR deletion for both alleles.
- Wildtype specific primer in the deletion designed for the WT allele.
- Mutant specific primer that bridges the junction designed for the CRISPR mutant allele.

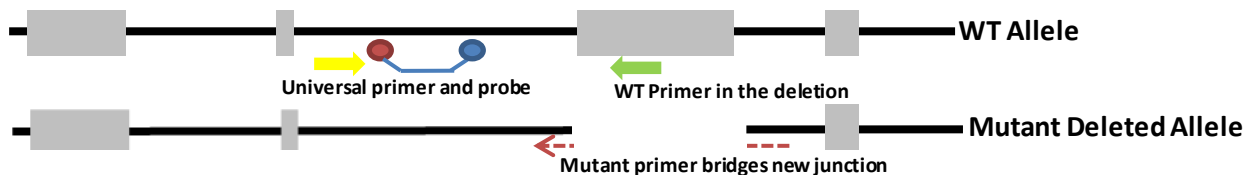


Figure1: Showing position of primers and probes

Inpp5k-DEL1152 WT1 assay (FAM labelled)

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AACCATAGGTTGAGGAGTAAGCATGCAGAGTTGCTGACTGGGCCACA GAGGATGAGTGAGGTTTCTGTAGCTGG
AGGGCTAATAGGTTTCTGTCTCTCAAACGCAATCATTCTTTCTTCTGGCCAATGGCATTGAGCTCCCTTTGG
CAGCTCTGTGCCAGGTACTGCCAGCTATGGGGGACTGTAACCTGCTAGAAGAGCCAGTTGGAGGGAGGGAAGA
GATTCCTGCTTTCCAGGCATGAAAGGGAAGGTGAAAGCTGGTAATCCACTGCTCCTTTTCTCTTTCCCTACCAC
ACGATGCAGAAGCAAGCTGGGCATAGTGAGATTAACAACGTTAATCTCAGAATTTAGGAGGCAGAAGAAGGCTGA
TCTCCGTAAGGAGTTGAGGCCAGCCAGGGCTGCATAGTGAGACACAGCCTCAAAGCACCAAACAAACAAACATG
CAGACACATTTCCCATGATCACTGCAGCGGAAGCCTTGACATACCTAGGTCTTTGCTGCTATCTGGAAAAATC
TTAGCCTCCATCCCCTGTGACTTAACATCCTTTCCACAGCGTACATGTTGTGACGTGGAATGTGGCCTCCGCAGC
CCCCACTGTAGACCTCAGTGACCTACTTCAACTGAACAACCAAGACCTGAATCTGGACATATATATCATTGGGTA
AGTGTCTGAAGGGCCCCTGCACCCCTATCCCTGTAGAGGGCTGATGTAACCTGTCCCTCGCTTGTGTTAGAGTCT
GAAGGGGAGGAGCTTTCATCCTCCCTGGGTCCAGTCTTGTGTTTCTTGTCTGGGTGAGCAATGGTTATGGGTTG
GAGGTCAACAGCCACACAGCTAGGAAAGGGAGGCCTCTTGGTCTTTCAGAATGCAGGCCTGAGAGTCTGATGATGG
CTGTGGGAGAGTCAATCCTCCAGGCCAGGGGTGATCCTCTGCCTTGAATGGTCAGTTTGCAGGAAATGAATT
TTGGAATCATAAGCCTTCTTTCTGATGCTGCTTTTGAAGACCCATGGAGCAGTCTCTTCATGGATATGCTTTCCC
CACTGAACCTTTGTCAAGGTAAGTTAAATTTCTGGGCAGTGGAGGAATGTGTTTCACCTGCGCTGACTTGAGTCGC
TTGTCTGATGCGTTTCCCTTTCTCCCATGCAGCTAAGTGTGTTGTCTGATGTAATCCTCTTTCTTCCACTTGGCTT
TTCATGTTCTTTTCCATTTCATCAAAGGTTTAAAGCTCACACTACACTTGGCTGCCTGGAACGCCCTGCCTGCCTT
ATGCTGTCTCAGTCTGAGCGATGAGTCCAGGGGTTAGCTTTCACACCTAGATGTTTTCTCAGTCTTATTCCTGGCC

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Inpp5k-DEL1152-Univ-Probe (5nmol) CAGAGTTGCTGACTGGGCCACA
 Inpp5k-DEL1152-WT-R (15nmol) GCAGGTTTACAGTCGCCATAG
 Inpp5k-DEL1152-Univ-F (15nmol) AACCATAGGTTGAGGAGTAAGCAT

Inpp5k-DEL1152 MUT1 assay (FAM labelled)

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AACCATAGGTTGAGGAGTAAGCATGCAGAGTTGCTGACTGGGCCACA GAGGATGAGTGAGGTTTCTGTAGCTGG
AGGGCTAATAGGTTTCTGTCTCTCAAACGCAATCATTCTTTCTTCTGGCCAATGGCATTGAGCTCCCTTTGG
CAG [1152 nt deletion] GGGTTAGCTTTCACACCTAGATGTTTTCTCAGTCTTATTCCTGGCC

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Inpp5k-DEL1152-Univ-Probe (5nmol) CAGAGTTGCTGACTGGGCCACA
 Inpp5k-DEL1152-MUT-R (15nmol) GGTGTGAAGCTAACCCCTGC
 Inpp5k-DEL1152-Univ-F (15nmol) AACCATAGGTTGAGGAGTAAGCAT



Dot1l internal control (VIC labelled)

TCATAGGGTGACTGGCCAACCCAGGGAAGCCGGAGTGCTGCGTCTTCTGTTTCCTTGTTCCTTTCCCTCTAGTC
GTTTTCTGTTAGTAGTTGGCATCCTTATGCTTCATCTTACAGT**CGACTTGAGAGCTGC**CCCTGAATGGTCGTGCT
GGGGCAAGGCTTTATTTTCAGGCGTAGCACACATGGTGGCCAATGGGACTCTGTAGGATCTGCCACACCCATCAG

Primer 1 = GCCCCAGCACGACCATT

Primer 2 = TAGTTGGCATCCTTATGCTTCATC

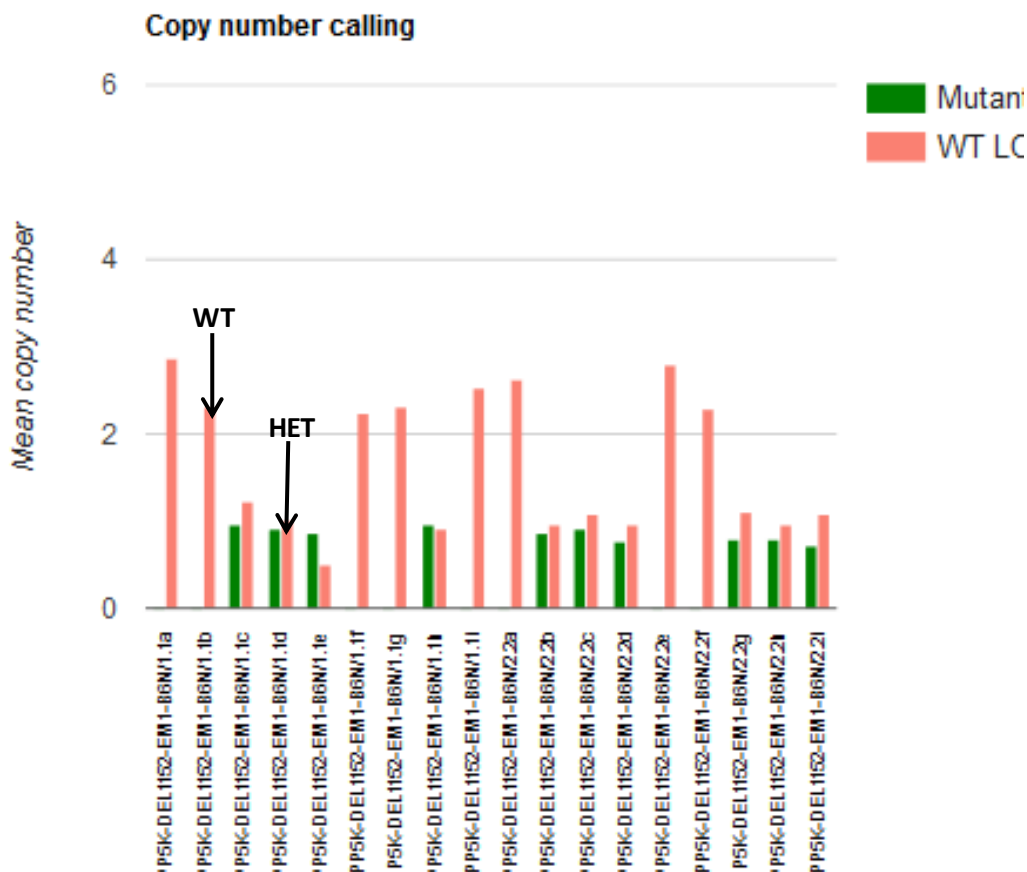
Probe = CCAGCTCTCAAGTCG

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
ddH2O	1.55µl
DNA (1/10 dilution of ABI Sample-to-SNP prep)	2.5µl

Inpp5k-DEL1152 Assay copy called result, image showing both WT and Mutant assays

Task 207650 Results





Version No. 1
Date: 23.05.2018
Created/Updated by: Ramakrishna Kurapati
Approved by: Deen Quwailid

Name of Mouse model or mutation:**INPP5K-FLOX-EM3-B6N****Description:**

Floxed model made using CRISPR/Cas9.

Type of mutation:

Floxed exons: ENSMUSE00001230278 and ENSMUSE00001223975

Delivery method:

Pronuclear injection into 1-cell stage embryo.

Genetic Background:

C57BL/6NTac

Nuclease:

Cas9 mRNA

sgRNAs:

Protospacer sequence	PAM sequence
TGCCAGGTAAGTCCAGCTAT	GGG
GGTTTACAGTCGCCCATAGC	TGG
CTAGGTGTGAAGCTAACCCC	TGG
AGTCTGAGCGATGAGTCCAG	GGG

IssDNA donor sequence (5'-3'):

LOCUS Inpp5k 1394 bp DNA linear 15-APR-2019

FEATURES Location/Qualifiers

misc_feature 130..163

/note="loxP"

misc_feature 122..129

/note="AsiI (SfaAI)"

PCR_primer 101..121

/note="LoxPF"

/current=0

misc_feature 1..100

/note="5' homology arm"

misc_feature 164..1232

/note="Critical Region"

exon 544..651

/note="ENSMUSE00001230278"

exon 938..1046

/note="ENSMUSE00001223975"

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misc_feature 1233..1266
    /note="loxP"
misc_feature 1267..1274
    /note="Mrel"
PCR_primer complement(1275..1294)
    /note="LoxPR"
    /current=0
misc_feature 1295..1394
    /note="3' homology arm"
conflict 272..272
    /note="Erroneous base (C>T change)"
source 1..1394
    /dnas_title="Inpp5k donor EM3"

```

ORIGIN

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1 taagcatgca gagttgctga ctgggccaca gaggatgagt gaggtttctg tagctggagg
61 ggctaataagg ttctgtctc tcaaacgcaa tcattcttc atccgggggt accgcgtcga
121 gGCGATCGCA TAACTTCGTA TAGCATACAT TATACGAAGT TATctgtaa cctgcctaga
181 agagccagtt ggagggaggg aagagattcc tgctttccag gcatgaaagg gaaggtgaaa
241 gctgggtaat ccaactgctc ttttctctt tcctaccaca cgatgcagaa gcaagctggg
301 catagtgaga ttaacaactg taatctcaga atttaggagg cagaagaagg ctgatctccg
361 taaggagttg aggccagcca gggctgcata gtgagacaca gcctcaaaag caccaaacia
421 acaaacatgc agacacattt cccatgatca ctgcagcggg agccttgac atacctaggt
481 ctttgctgc tatctggaaa aatcttagcc tccatcccct gtgacttaac atcctttcca
541 cagCGTACAT GTTGTGACGT GGAATGTGGC CTCCGCAGCC CCCACTGTAG ACCTCAGTGA
601 CCTACTCAA CTGAACAACC AAGACCTGAA TCTGGACATA TATATCATTG Ggtaagtgtc
661 tgaagggccc ctgcacccc tatcctgta gagggctgat gtaacctgtc ctcgcttggt
721 ttagagtctg aaggggagga gctttcatcc tccctgggtc cagtcttggt tttctgtcc
781 tgggtcagca atggttatgg gttggaggtc aacagccaca cagctaggaa agggaggcct
841 cttggtcttc agaatgcagg cctgagagtc tgatgatggc tgtgggagag tcagtatcct
901 ccaggccagg ggtgatcctc tgcttgga tggcagTTT GCAGGAAATG AATTTTGGAA
961 TCATAAGCCT TCTTTCTGAT GCTGCTTTG AAGACCCATG GAGCAGTCTC TTCATGGATA
1021 TGCTTTCCCC ACTGAACTTT GTCAAGgtaa gtaaatttc tgggcagtggt agaatgtgt
1081 ttcacctgcg ctgacttgag tcgctgtct gatgcgttc cctttctccc atgcagctaa
1141 gtgtttgtct gatgtactcc tctttctcc actggcctt tcatgttctt ttccattcat
1201 caaaaggttt aaagctcaca ctacactgg ctATAACTTC GTATAGCATA CATTATACGA
1261 AGTTATCGCC GGCgggtctg agctcgccat cagtttagct tcacacctag atgtttctc
1321 agtcttattc ctggcctacc ctctgtctc tccttactgc ccagcatgaa atctcttgag
1381 ttagcactt gcta
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Microinjection mixes:

Microinjection buffer (MIB; 10 mM Tris–HCl, 0.1 mM EDTA, 100 mM NaCl, pH7.5) was prepared and filtered through a 2 nm filter and autoclaved. Cas9 mRNA, sgRNAs and lssDNA donor template were diluted and mixed in MIB to the working concentrations of 100 ng/μl, 50 ng/μl each and 50 ng/μl, respectively. Injected embryos were re-implanted in CD1 pseudo-pregnant females. Host females were allowed to litter and rear F₀ progeny.