

Name of Mouse model or mutation:

PIK3R1-FLOX-EM1-B6

PIK3R1-FLOX-EM2-B6

Description:

Floxed allele made by CRISPR/Cas9 gene editing.

Type of mutation:

Floxed exon: ENSMUSE00000290469

Delivery method:

Pronuclear injection into 1-cell stage embryo

Genetic Background:

C57BL/6J

Nuclease:

Cas9 mRNA

sgRNAs:

Protospacer sequence	PAM sequence
gctattataaaattctggtc	AGG
ctattataaaattctggtca	GGG
atggaacgtaatttcgac	TGG
gaaattaacgttccatcaac	TGG

IsDNA donor sequence (5'-3'):

LOCUS Pik3r1 755 bp DNA linear 23-JUN-2020

FEATURES Location/Qualifiers

misc_feature 144..177

/note="loxP"

misc_feature 136..143

/note="AsiSI (SfaAI)"

PCR_primer 115..135

/note="LoxPF"

misc_feature 1..114

/note="5' Homology Arm"

misc_feature 178..579

/note="Critical region"

misc_feature 580..613

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        /note="loxP"
misc_feature 614..621
        /note="Mrel"
PCR_primer complement(622..641)
        /note="LoxPR"
misc_feature 642..755
        /note="3' Homology Arm"
source      1..755
        /dnas_title="Pik3r1 donor sequence"
exon        295..420
        /note="ENSMUSE00000290469"
exon        1..11
        /note="ENSMUSE00000569198"

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ORIGIN

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1 aataccagca ggtaattcac acagagctcc tccgctgca gtaacaaggg ggccagagac
61 tttcagcat aggaaatgat ctgaaattgg gtttgacaa actttacacc ctgaatccgg
121 gggtagccg tcgagGCGAT CGCATAACTT CGTATAGCAT ACATTATACG AAGTTATcca
181 gaatttata atagctaaat cagataccat attgactatg ccattagggga ttgtatttg
241 agtaaatagc ttatcaactg aattcttttt ttcctgctt gtatattctt ccaggatcaa
301 gttgtcaaag aagataatat tgaagctgta gggaaaaaat tacatgaata taactactca
361 tttcaagaaa aaagtcggga atatgataga ttatagagg agtacaccg tacttcccag
421 gtgagtttaa gatattttgg actaacacat actatactca gattcaaagg aagaatcaag
481 tgtctctaac cttttcagc ttaacccatg cttataaagt cctacattaa gcttgcttct
541 aactcgcagt gttactatta tgagcttcca gttgatggaA TAACTTCGTA TAGCATACAT
601 TATACGAAGT TATCGCCGGC Gggtctgagc tcgcatcag ttaatttccg actggttact
661 tctgcctagg ctagacattg ataataactg ctaatgtcag tttgtccaag ctctagaatg
721 gaaagttcag acccatccct cctgctgtga ggaga

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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 ssODNs 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.

Sequence details

WT

ACCTTTTTGGTACGAGACGCATCTACTAAAATGCACGGCGATTACACTCTTACACTAAGGTGAGCCA
GGAAGTCAGCTGTAATTGCGATGTCTCAGTTGTCATGAAAACATTTCTTCATTAGATTGCCTATTTTT
CTCCTTAAATTAGCATATAAAGTAATGGGTTTCACTATAGGATTTTTTTTTCAAACATCTTCGATTGTC
CCTTTCTCCTACTGCCTTCTCCTCCCCATCCTGAGAGCCCTCCTTCTGCATCAGAAAATGTTAATAATC
ATTATTTTTGTATTGTATTTACAGGAAAGGAGGAAATAACAAATTAATCAAATCTTTACCCTGATG
GAAAATATGGCTTCTCTGATCCATTAACCTTCAACTCTGTGGTTGAGTTAATAAACCCTACCGGAAT
GAGTCTTTAGCTCAGTACAACCCCAAGCTGGATGTGAAGTTGCTCTACCCAGTGTCCAAATACCAGC
AGGTAATTCACACAGAGCTCCTCCCGCTGCAGTAACAAGGGGGCCAGAGACTCTTCAGCATAGGAA
ATGATCTGAAATTGGGTTTTGACAACTTTACACCCTGACCAGAATTTTATAATAGCTAAATCAGATA
CCATATTGACTATGCCATTAGGGATTGTTATTTGAGTAAATAGCTTATCAACTGAATCTTTTTTTCC
TGCTTGATATTCTTCCAG**GATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATT**
ACATGAATATAACTCAATTTCAAGAAAAAAGTCGGGAATATGATAGATTATATGAGGAGTACA
CCCGTACTTCCAGGTGAGTTAAGATATTTGGACTAACACATACTATACTCAGATTCAAAGGAAG
AATCAAGTGTCTTAACCCTTTTCACTTAACCCATGCTTATAAAGTCCTACATTAAGCTTGCTTCTAA
CTCGCAGTGTTACTATTATGAGCTTCCAGTTGATGGAACGTTAATTTCCGACTGGTTACTTCTGCCTA
GGCTAGACATTGATAATAACTGCTAATGTCAGTTTGTCCAAGCTCTAGAATGGAAAGTTCAGACCCA
TCCCTCCTGCTGTGAGGAGAAATGGCCGTGTTGATTATCAGAGAAAGCAGCATGGGTGTCATAAAA
TAAAATGGCTTTTTCAAAGACTGACCGCTTGTACTTACATACTTAGGAACACACACACACATGCA
TGCATGCACTCGTTCATTCACACAACATGAATTTGAAGGAACAAGGAGTGGTATGTGAGATGGTTG
AAAGGGAAAGGAGGAAATAATGTAATTATGTTATAATCTCAAAAAAAAAAAGAAAACATAATTTTAA
AAAGTGAAGACAGATAATTCTCTGTCAGGAACATCTGTTTCTTGATCATTGACGAGAGTTGGTGA
ATTCATGACCAGCCCTGCTAACATACACAGCCCTGCCTATCTCCTGCTCCTGAATCCTGAAGATGCA
CAGTGTAGGCATCTCCCCGCCCTTGCTCCTGTTGTCTAAGCCATACCGTACAGCTATTTACGTAGC
ACTGATGTTGTCTCATGCTCAAGCCA

PIK3R1-FLOX-EM1-B6 or PIK3R1-FLOX-EM2-B6

ACCTTTTTGGTACGAGACGCATCTACTAAAATGCACGGCGATTACACTCTTACACTAAGGTGAGCCA
GGAAGTCAGCTGTAATTGCGATGTCTCAGTTGTCATGAAAACATTTCTTCATTAGATTGCCTATTTTT
CTCCTTAAATTAGCATATAAAGTAATGGGTTTCACTATAGGATTTTTTTTTCAAACATCTTCGATTGTC
CCTTTCTCCTACTGCCTTCTCCTCCCCATCCTGAGAGCCCTCCTTCTGCATCAGAAAATGTTAATAATC
ATTATTTTTGTATTGTATTTACAGGAAAGGAGGAAATAACAAATTAATCAAATCTTTACCCTGATG
GAAAATATGGCTTCTCTGATCCATTAACCTTCAACTCTGTGGTTGAGTTAATAAACCCTACCGGAAT
GAGTCTTTAGCTCAGTACAACCCCAAGCTGGATGTGAAGTTGCTCTACCCAGTGTCCAAATACCAGC
AGGTAATTCACACAGAGCTCCTCCCGCTGCAGTAACAAGGGGGCCAGAGACTCTTCAGCATAGGAA
ATGATCTGAAATTGGGTTTTGACAACTTTACACCCTGA**atccgggggtaccgctcgagGCGATCGCATA**
ACTTCGTATAGCATACATTATACGAAGTTATCCAGAATTTTATAATAGCTAAATCAGATAACCATATTG
ACTATGCCATTAGGGATTGTTATTTGAGTAAATAGCTTATCAACTGAATCTTTTTTTCCCTGCTTGTA
TATTCTTCCAG**GATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTACATGAA**

**TATAATACTCAATTTCAAGAAAAAAGTCGGGAATATGATAGATTATATGAGGAGTACACCCGTAC
TTCCCAGGTGAGTTTAAGATATTTTGGACTAACACATACTATACTCAGATTCAAAGGAAGAATCAAG
TGTCTCTAACCCTTTTCAGCTTAACCCATGCTTATAAAGTCCTACATTAAGCTTGCTTCTAACTCGCAG
TGTTACTATTATGAGCTTCCAGTTGATGGAATAACTTCGTATAGCATACATTATACGAAGTTATCGCC
GGCGgtctgagctcgccatcagtTAATTTCCGACTGGTACTTCTGCCTAGGCTAGACATTGATAATAACT
GCTAATGTCAGTTTGTCCAAGCTCTAGAATGGAAAGTTCAGACCCATCCCTCCTGCTGTGAGGAGAA
ATGGCCGTGTTGATTATCAGAGAAAGCAGCATGGGTGTCATAAAATAAAATGGCTTTTTCAAAGACT
GACCGGCTTGTACTIONTACATACTTAGGAACACACACACACATGCATGCATGCACTCGTTCATTACACA
CAACATGAATTTGAAGGAACAAGGAGTGGTATGTGAGATGGTTGAAAGGGAAGGAGGAAATAATG
TAATTATGTTATAATCTCAAAAAAAAAAAGAAAACATAATTTAAAAAGTGAAAGACAGATAATTCT
CTGTCAGGAACATCTGTTTCTTGATCATTTGACGAGAGTTGGTGAATTCATGACCAGCCCTGCTAACA
TACACAGCCCTTGCCTATCTCCTGCTCCTGAATCCTGAAGATGCACAGTGTAGGCATCTCCCCGCCCC
CTTGCTCCTGTTGTCTAAGCCATACCGTACAGCTATTTACGTAGCACTGATGTTGTCTCATGCTCAAG
CCA**

LoxP sites are underlined and genotyping handles (restriction enzyme site plus primer unique to each LoxP site) in italics. Floxed exon highlighted in bold.

Please note, alleles EM1 and EM2 have the same sequence, but were derived from different founder animals.

Nucleotide Alignment:

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*          20          *          40          *          60          *          80          *          100         *          120         *          140         *
Pik3r1_WT : ACCTTTTGGTACGAGACGCATCTACTAAAAATGCACGGCGATTACACTCTTACACTAAGGTGAGCCAGGAAGTCAGCTGTAATTCGGATGCTCAGTTGTCATGAAAAACATTTCTTCATTAGATTGCCATTTTTCTCCTCTAAATTAGC
Pik3r1_Flox : ACCTTTTGGTACGAGACGCATCTACTAAAAATGCACGGCGATTACACTCTTACACTAAGGTGAGCCAGGAAGTCAGCTGTAATTCGGATGCTCAGTTGTCATGAAAAACATTTCTTCATTAGATTGCCATTTTTCTCCTCTAAATTAGC

*          160          *          180          *          200          *          220          *          240          *          260          *          280          *          300
Pik3r1_WT : ATATAAAGTAATGGGTTTTCACACTAGGATTTTTTTTCAACACATCTTCGATTCGTCCTTTCTCCTACTGCCTTCTCCTCCCATCCTGAGAGCCCTCTCTGCATCAGAAAAATGTTAATAATCATTTTTTTGATTGTATTACAGGA
Pik3r1_Flox : ATATAAAGTAATGGGTTTTCACACTAGGATTTTTTTTCAACACATCTTCGATTCGTCCTTTCTCCTACTGCCTTCTCCTCCCATCCTGAGAGCCCTCTCTGCATCAGAAAAATGTTAATAATCATTTTTTTGATTGTATTACAGGA

*          320          *          340          *          360          *          380          *          400          *          420          *          440          *
Pik3r1_WT : AAGGAGAAATAACAAATTAATCAAATCTTTCACCGTGATGGAAAAATATGGCTTCTCTGATCCATTAACCTTCAACTCTGTGGTTGAGTTAATAAACCACTACCGGAATGAGTCTTTAGCTCAGTACAACCCCAAGCTGGATGTGAGT
Pik3r1_Flox : AAGGAGAAATAACAAATTAATCAAATCTTTCACCGTGATGGAAAAATATGGCTTCTCTGATCCATTAACCTTCAACTCTGTGGTTGAGTTAATAAACCACTACCGGAATGAGTCTTTAGCTCAGTACAACCCCAAGCTGGATGTGAGT

*          460          *          480          *          500          *          520          *          540          *          560          *          580          *          600
Pik3r1_WT : TGCTTACCCAGTGTCCAAATACCAGCAGGTAATTCACACAGAGCTCCCTCCCGTGCAGTAAACAAGGGGCCAGAGACTCTTCAGCATAGGAAATGATCGAAATGGGTTTGGACAACTTTACACCTGA-----
Pik3r1_Flox : TGCTTACCCAGTGTCCAAATACCAGCAGGTAATTCACACAGAGCTCCCTCCCGTGCAGTAAACAAGGGGCCAGAGACTCTTCAGCATAGGAAATGATCGAAATGGGTTTGGACAACTTTACACCTGAatccgggggtaccgcgtc

*          620          *          640          *          660          *          680          *          700          *          720          *          740          *
Pik3r1_WT : -----
Pik3r1_Flox : gagCGATCGcATAACTCGTATAGCATACATTATACGAAGTTA CCAGAATTTTATAATAGCTAAATCAGATACCATATTGACTATGCCATTAGGGATTGTTATTTGAGTAAATAGCTTATCAACTGAATCTTTTTTCCCTGCTGT

*          760          *          780          *          800          *          820          *          840          *          860          *          880          *          900
Pik3r1_WT : ATATTCTCCAGGATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTACATGAATATAATACTCAATTTCAAAGAAAAAGTCGGGAATATGATAGATTATATGAGGAGTACACCCGTACTTCCAGGTGAGTTAAGA
Pik3r1_Flox : ATATTCTCCAGGATCAAGTTGTCAAAGAAGATAATATTGAAGCTGTAGGGAAAAAATTACATGAATATAATACTCAATTTCAAAGAAAAAGTCGGGAATATGATAGATTATATGAGGAGTACACCCGTACTTCCAGGTGAGTTAAGA

*          920          *          940          *          960          *          980          *          1000         *          1020         *          1040         *
Pik3r1_WT : TATTTGGACTAACACATACTATACTCAGATTCAAAAGGAAGAATCAAGTGTCTCTAACCTTTTCAGCTTAACCCATGCTTATAAAGTCTACATTAAGCTTGCTTCACTCGCAGTGTACTATTATGAGCTTCCAGTTGATGGA---
Pik3r1_Flox : TATTTGGACTAACACATACTATACTCAGATTCAAAAGGAAGAATCAAGTGTCTCTAACCTTTTCAGCTTAACCCATGCTTATAAAGTCTACATTAAGCTTGCTTCACTCGCAGTGTACTATTATGAGCTTCCAGTTGATGGAATA

*          1060         *          1080         *          1100         *          1120         *          1140         *          1160         *          1180         *          1200
Pik3r1_WT : -----ACGT-----
Pik3r1_Flox : ACTTCGTATAGCTACATTATACGAAGTTA CGCCGGCGggtctgagctcgccatcagtTAATTTCCGACTGGTTACTTCTGCCTAGGCTAGACATTGATAATAACTGCTAATGTCAGTTTGTCCAAGCTCTAGAATGGAAAGTTCAGAC

*          1220         *          1240         *          1260         *          1280         *          1300         *          1320         *          1340         *
Pik3r1_WT : CCATCCCTCCTGCTGTGAGGAGAAATGGCCGTGTGATTTATCAGAGAAAGCAGCATGGGTGTCATAAAATAAAATGGCTTTTCAAAGACTGACCGGCTTGACTTACATACTTAGGAACACACACACACATGCATGCATGCCTCCT
Pik3r1_Flox : CCATCCCTCCTGCTGTGAGGAGAAATGGCCGTGTGATTTATCAGAGAAAGCAGCATGGGTGTCATAAAATAAAATGGCTTTTCAAAGACTGACCGGCTTGACTTACATACTTAGGAACACACACACACATGCATGCATGCCTCCT

*          1360         *          1380         *          1400         *          1420         *          1440         *          1460         *          1480         *          1500
Pik3r1_WT : TCATTACACAAACATGAATTTGAAGGAACAAGGAGTGGTATGTGAGATGGTTGAAAGGAAGGAGGAAATAAATGTAATTTATGTTATAATCTCAAAAAAAGAAAAACATAATTTTAAAAAGTGAAGACAGATAATTTCTCTGTCAGGA
Pik3r1_Flox : TCATTACACAAACATGAATTTGAAGGAACAAGGAGTGGTATGTGAGATGGTTGAAAGGAAGGAGGAAATAAATGTAATTTATGTTATAATCTCAAAAAAAGAAAAACATAATTTTAAAAAGTGAAGACAGATAATTTCTCTGTCAGGA

*          1520         *          1540         *          1560         *          1580         *          1600         *          1620         *          1640         *
Pik3r1_WT : ACATCTGTTTCTTGATCATTGACGAGAGTTGGTGAATTCATGACCAGCCCTGCTAACATACACAGCCCTGCCTATCTCCTGCTCCTGAATCCTGAAGATGCACAGTGTAGGCATCTCCCGCCCCCTTGCTCCTGTTGCTAAGCCAT
Pik3r1_Flox : ACATCTGTTTCTTGATCATTGACGAGAGTTGGTGAATTCATGACCAGCCCTGCTAACATACACAGCCCTGCCTATCTCCTGCTCCTGAATCCTGAAGATGCACAGTGTAGGCATCTCCCGCCCCCTTGCTCCTGTTGCTAAGCCAT

*          1660         *          1680         *
Pik3r1_WT : ACGTACAGCTATTTACGTAGCACTGATGTTGCTCATGCTCAAGCCA
Pik3r1_Flox : ACGTACAGCTATTTACGTAGCACTGATGTTGCTCATGCTCAAGCCA
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QC strategy employed at Harwell to check the edited allele:

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

LoxPF	AAAGGAGGGAAGGAGGCTGA
LoxPR	AGAGAAGCCTGGAGAGAGGG
Taq Polymerase used	Roche Expand Long Range dNTP pack
Annealing Temperature (°C)	61
Elongation time (min)	3
WT product size (bp)	N/A
Mutant product size (bp)	2256
Notes	PCR used to screen for floxed alleles. 3% DMSO used in reactions.

Geno_PIK3R1_F1 primer (5'-3')	ACCTTTTGGTACGAGACGCA
Geno_PIK3R1_R1 primer (5'-3')	TGGCTTGAGCATGAGACAACA
Taq Polymerase used	ThermoFisher SuperFi PCR Kit
Annealing Temperature (°C)	61
Elongation time (min)	1
WT product size (bp)	1573
Mutant product size (bp)	1698
Notes	Sequenced with the following primers: Geno_PIK3R1_F1 (ACCTTTTGGTACGAGACGCA) Geno_PIK3R1_R2 primer (AGATAGGCAAGGGCTGTGTATG) LoxPF (AAAGGAGGGAAGGAGGCTGA) LoxPR (AGAGAAGCCTGGAGAGAGGG)

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 sex chromosome.

Off-target sites on the same chromosome with ≤ 2 mismatches in seed sequence of guide(s) used were checked with the following primers:

Off-target site	Sequence	Type	Primers used (5'-3')
13:6069825-6069847	GGTAATATGAAAATCTGGTC AGG	Intergenic	Pik3r1_OT1G1_F1: TCCTCAAATCATCAACTGCC Pik3r1_OT1G1_R1: CACTGACTTTCCTTATGCCC Sequenced with: Pik3r1_OT1G1_F3: ACAATCCTTGTACTATGCCAAAAC Pik3r1_OT1G1_R2: TGTGCTTCTTTGTTCCCCCA
13:26316422-26316444	TCTATTAAACATTTCTGGTC AGG	Intergenic	Pik3r1_OT2G1_F1: GAGGTTAATGCTTCTCCCTGCT Pik3r1_OT2G1_R1: ACTTTTCACTGCTATGAGGGCA Sequenced with: Pik3r1_OT2G1_seqF: ACTTTCTGGTACCATGAAAT Pik3r1_OT2G1_seqR: TCCAACCTCAGGATTTTAT
13:51258883-51258905	GTTATTAGAAAACCTCTGCTC TGG	Intergenic	Pik3r1_OT3G1_F1: TCCAGGGATAAGCAGGGATCTT Pik3r1_OT3G1_R1: CAGATGCGCTGAGTAGAGCAA Sequenced with: Pik3r1_OT3G1_F2: TGTTCTGATGGGTGCCCAAG Pik3r1_OT3G1_R2: GGGAATGCTGAAATGCCAACC
13:93450521-93450543	GAAAATATAAAATTCTGGGC TGG	Intronic	Pik3r1_OT4G1_F1: CCCCTGCTATCAGAACTCACT Pik3r1_OT4G1_R1: TTTTCTTGCAGTCTGCCTAAA
13:9714150-9714172	GCATTTCAAATTCTGGTCA AGG	Intronic	Pik3r1_OT1G2_F1: AGAACAGGCCCTCTATCTGG Pik3r1_OT1G2_R1: ATGTCAGACCCTGTGCATGAG Sequenced with: Pik3r1_OT1G2_R2: AGTCCTCTGAATTCTGTTTCACTA
13:33975887-33975909	CCATTAAAAAATTGTGTCA GGG	Intronic	Pik3r1_OT2G2_F1: CCATACAGTGGAAAAAGACAGC Pik3r1_OT2G2_R1: ACAGGGTCCCTCAGCAAAAT Sequenced with: Pik3r1_OT2G2_F2: GGCTTGCCTGTGTAAGATCAAAA Pik3r1_OT2G2_R2:

			TTCCGGTTGTATTTTCTGAGGA
13:34362525-34362547	CTATT CA AAATTTCT AG TCA TGG	Intergenic	Pik3r1_OT3G2_F1: AATAGCTTGCTGCCGTGACTTA Pik3r1_OT3G2_R1: GCCCCTTTGAAGTCTGGAAGG Sequenced with: Pik3r1_OT3G2_F2: TATACTGCAGAGAGTATAAACCTGG Pik3r1_OT3G2_R2 GTCTTCTGCACACTCCCACA
13:46914819-46914841	TTTTTA AAAAATTCT GC TCA AGG	Intronic	Pik3r1_OT4G2_F1: GGTAAACGCTGTGGTTCGGAT Pik3r1_OT4G2_R1: GGCTGAAGGGACCATTACTCT
13:51078208-51078230	TTATC ATTAAATTCT GC TCA TGG	Intergenic	Pik3r1_OT5G2_F1: TTTGTCAATTTGCTGACTCCTTCG Pik3r1_OT5G2_R1: TTACAAGTTGGGGTCTCCCT
13:54546657-54546679	GC ATTAGAAAATT CA GGTCA AGG	Intronic	Pik3r1_OT6G2_F1: CCCCAGCTAACCAGAACTACA Pik3r1_OT6G2_R1: CAGGGACGTGGAGTTGTTCA Sequenced with: Pik3r1_OT6G2_F2: CACCAAGGAAGTCAGGACTGG Pik3r1_OT6G2_R2: GGGAGTTACCCAGAAGCACATT
13:89012517-89012539	CTATTA AC AAATTT AG GTCA AGG	Intronic	Pik3r1_OT7G2_F1: TAGCAAAGATGACCCAACAGGT Pik3r1_OT7G2_R1: TGGCTTAAGTGGTTGTCAGCA
13:98904544-98904566	CTACT CA AA AG TTCTGG G CA AGG	Intronic	Pik3r1_OT8G2_F1: AATGTAAGATGGTGCTGAACAGGG Pik3r1_OT8G2_R1: TTTGTCTTGGCTGTGTTTACCTG Sequenced with: Pik3r1_OT8G2_F2: ATCCAGACTGAGGAAGACCCG Pik3r1_OT8G2_R3: GAAAATGTTAGCATTTAATT
13:34596127-34596149	TAAATG AACTTTCCAT CAAG AGG	Intergenic	Pik3r1_OT1G3_F1: TCAGGGACCAGTTTCTTTCTCT Pik3r1_OT1G3_R1: ACCACTTATGCAGGGCTAGAAT

All amplicons were sent for Sanger sequencing. No evidence of off-target activity was detected.

Additional integrations of the donor sequence

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 copy count the donor sequence compared against a VIC-labelled reference assay for Dot1l:

Assay name	PIK3R1-FLOX-5'
Forward Primer (5'-3')	GACAAACTTTACACCCTGAATCC
Reverse Primer (5'-3')	ACAATCCCTAATGGCATAGTCA
Probe (5'-3')	TCGAGGCGATCGCATAACTTCG
Label	FAM

This ddPCR assay is specific to the 5' LoxP region of the PIK3R1 Flox donor and only floxed alleles are expected to be recognised by this assay. Therefore, WT controls are expected to call at 0 copies and a single integration for a correct mutation is expected to call at 1 copy for F1 (HET) animals.

Assay name	PIK3R1-FLOX-3'
Forward Primer (5'-3')	TGAGCTCCAGTTGATGGAATAA
Reverse Primer (5'-3')	GCAGAAGTAACCAGTCGGAAA
Probe (5'-3')	AAGTTATCGCCGGCGGGTCTGA
Label	FAM

This ddPCR assay is specific to the 3' LoxP region of the PIK3R1 Flox donor and only floxed alleles are expected to be recognised by this assay. Therefore, WT controls are expected to call at 0 copies and a single integration for a correct mutation is expected to call at 1 copy for F1 (HET) animals.

Assay name	PIK3R1-FLOX-CR-LOA
Forward Primer (5'-3')	GTA CTCCAGGTGAGTTTAAG
Reverse Primer (5'-3')	CACTGCGAGTTAGAAGCAA
Probe (5'-3')	TCAAAGGAAGAATCAAGTGCTCTAACCT
Label	FAM

This ddPCR assay is universal to Pik3r1 - both WT and floxed alleles are recognised by this assay. Therefore, WT controls are expected to call at 2 copies and a single integration for a correct mutation is expected to call at 2 copies for F1 (HET) animals.

Reference Assay Name	Dot1l
Forward primer (5'-3')	GCCCCAGCACGACCATT
Reverse primer (5'-3')	TAGTTGGCATCCTTATGCTTCATC
Probe (5'-3')	CCCAACAGGCCTGGATTCTCAATGC
Label	VIC

VIC-labelled reference assay for Dot1l gene.

No random integrations were detected in the animals selected for breeding.



Allele Description

This is a CRISPR/Cas9 induced mutation creating a conditional knock-out by floxing critical exon, ENSMUSE00000290469 of *Pik3r1*. The stock was generated at MRC Harwell via pronuclear injection of CRISPR/Cas9 reagents into 1-cell stage embryos.

qPCR Copy Counting Genotyping Strategy

The genotyping strategy presented here has been optimized for reagents and conditions used by the Genotyping Core at MRC Harwell. To genotype animals, we recommend researchers validate the assay independently. PCR cycling temperature and times may require additional optimization based on the specific genotyping reagents used.

Samples are genotyped using qPCR copy counting with both a wildtype loss of allele (WT-LOA) and a mutant assay against a known reference assay (*Dot1l* on chromosome 10; 2 copies present). Samples for this line are genotyped using the following primers and probe:

- Universal probe and Universal primer designed 5' of the deleted region.
- Wildtype specific primer situated within the deleted region.
- Mutant specific primer that binds to the inserted LoxP sequence

For autosomal genes that have been targeted, the following results would be expected:

Genotype of the Modified allele	WT Assay	Mutant Assay
Wildtype	2	0
Heterozygous	1	1
Homozygous mutant	0	2



Pik3r1-Flox-3'-WT1 assay (FAM labelled)

GGACTAACACATACTATACTCAGATTCAAAGGAAGAATCAAGTGTCTCTAACCCTTTTCAG**CTTAACC**
CATGCTTATAAAGTCCTACATTA**AGCTTGCTTCTAACTCGCAGTGT**ACTATTATGAGCTTCCAGTTG
 AT**GGAACGTTAATTTCCGACTGGT**TACTTCTGCCTAGGCTAGACATTGATAATAACTGCTAATGTCA

Probe sequence is in bold and shaded grey
 Primer sequences are in bold and underlined

Oligo Pik3r1-Flox	5' label	Sequence 5' → 3'	3' label	Oligo Type
Pik3r1-Flox-WT_F	n/a	CTTAACCCATGCTTATAAAGTCCTACA	n/a	WT Forward
Pik3r1-Flox-WT_PROBE	FAM	AGCTTGCTTCTAACTCGCAGTGT	Zen-IBFQ	WT Probe
Pik3r1-Flox-WT_R	n/a	ACCAGTCGGAATTAACGTTCC	n/a	WT Reverse

Pik3r1-Flox -3'-MUT1 assay (FAM labelled)

TGTCTCTAACCCTTTTCAGCTTAACCCATGCTTATAAAGTCCTACATTAAGCTTGCTTCTAACTCGCAG
 TGTTACTATTAT**TGAGCTTCCAGTTGATGGA**ataacttcgtatagcatatagcattatagc**aagttatCGCCGGCGGGT**
CTGAGCTCGCCATCAGTTAAATTTCCGACTGGTACTTCTGCCCTAGGCTAGACATTGATAATAACTGCT
 AATGTCAGTTTGTCCAAGCTCTAGAATGGAAAGTTCAGACCCATCCCTCCTGCTGTGAGGAGAAATG

Lower case letters denote the inserted LoxP sequence
 Probe sequence is in bold and shaded grey
 Primer sequences are in bold and underlined

Oligo Pik3r1-Flox	5' label	Sequence 5' → 3'	3' label	Oligo Type
Pik3r1-Flox-MUT_F	n/a	TGAGCTTCCAGTTGATGGAATAA	n/a	Mutant Forward
Pik3r1-Flox-MUT_PROBE	FAM	AAGTTATCGCCGGCGGGTCTGA	Zen-IBFQ	Mutant Probe
Pik3r1-Flox-MUT_R	n/a	GCAGAAGTAACCGTTCGGAAA	n/a	Mutant Reverse



Dot1l internal control (VIC labelled)

CTGATGGGTGTGGGCAGATCCTACAGAGTCCCATTGGCCACCATGTGTGCTACGCCTGAAATAAAGCCTT**GCC**
CCAGCACGACCATTCAGGG**CCAGCTCTCAAGTCG**ACTGTAAGATGAAGCATAAGGATGCCAACTACTAACA
GAAAACGACTAGAGGGGAAAAGAACAAGGAAACAGAAGACGCAGCACTCCGGCTTCCCTGGGTTGGCCAGT
CACCTATGA

Oligo Pik3r1-Flox	5' label	Sequence 5' → 3'	3' label	Oligo Type
Dot1l_Forward	n/a	<u>GCCCCAGCACGACCATT</u>	n/a	WT Forward
Dot1l_Probe	VIC	CCAGCTCTCAAGTCG	BHQ	WT Probe
Dot1l_Reverse	n/a	<u>TAGTTGGCATCCTTATGCTTCATC</u>	n/a	WT Reverse

Probe sequence is in bold and shaded grey

Primer sequences are in bold and underlined

DNA extraction method

DNA is extracted from ear clips using Applied Biosystems Taqman Sample-to-SNP Kit and qPCR run using 1:10 dilution from the crude preparation.

qPCR master mix

1X

Applied Biosystems GTX Taqman master mix	5 µl
Dot1l_Forward (20 µM)	0.225 µl
Dot1l_Reverse (20 µM)	0.225 µl
Dot1l_Probe (5 µM)	0.2 µl
FAM Assay (probe 5 µM & primers 15 µM each)	0.3 µl
ddH2O	1.55 µl
DNA (1:10 dilution of ABI Sample-to-SNP prep)	2.5 µl

Each sample is ran in technical duplicate. Seven WT and/or mutant controls are also included in duplicate along with non-template controls.

qPCR cycling conditions

qPCR instrument: Applied Biosystems 7500/7900 or ThermoFisher QuantStudio 7

95°C for 20 sec

Then 40 cycles of;

95°C for 3 sec

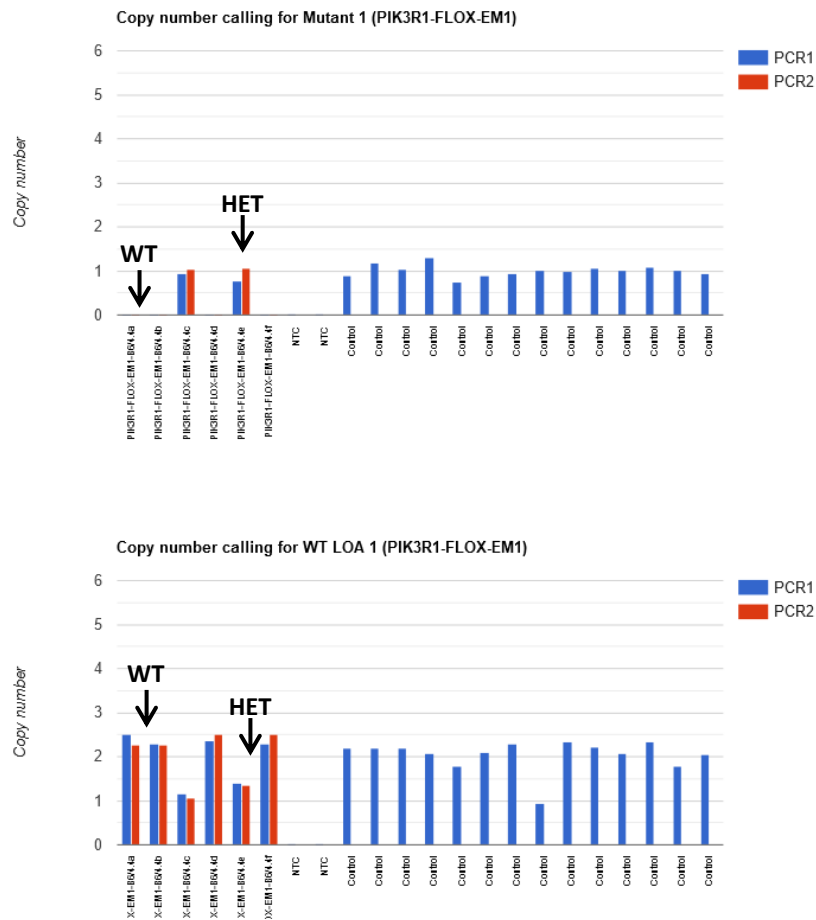
60°C for 30 sec



Analysis

The results are analysed using CopyCaller software v2.0 from Applied Biosystems or in-house software that is based on CopyCaller v2.0.

Pik3r1-Flox'-WT1 and Pik3r1-Flox-MUT1 assays copy called results, image showing copy number chart for WT and Mutant assays (Task 321184 results)



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