



Name of Mouse model or mutation:

TLR2-FLOX-EM2-B6N

Description:

Floxed mutant made (in stages) by CRISPR/Cas9 gene editing of existing line (TLR2-5LOXP-EM1-B6N).

Type of mutation:

Floxed allele: ENSMUSE00000441912 of Tlr2.

Delivery method:

Cytoplasmic injection into 1-cell stage embryo.

Genetic Background:

C57BL/6NTac

Nuclease:

Cas9 mRNA

sgRNAs:

Protospacer sequence	PAM sequence
GAGTCACAGTATGGGCATCC	AGG

ssODN donor sequence (5'-3'):

GCTAATCTACTCACCTGCCATCCCTCTGTGTAGCTGATCCCAAGGGCAAGGAGTCACAGTATGGGAT
AACTTCGTATAGCATACATTATACGAAGTTATCGCCGGCGgggtctgagctcgccatcagtAAATCTGTTGCT
CTTCCTAGACAGGGGGTGTGTCCCACCATCCCACAGATCTTCCAATATAAATGACACAG

Cytoplasmic 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 50 ng/μl, 6.5 ng/μl each and 100 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

TLR2-5LOXP-EM1-B6N

TGGGTAGTAGCGCACGTATGCCATCCCCAACCATTACAGAAGCATAAAACATATTTTGGGAAATTG
TTGCGTTATTTCACTGAGCAAATATGACCACAGCACGTGTGGTTGCATGGAACAGCTACAGGGTATA
GGGCCAGAAGGTGCCCTGGGAGACGAGCCTTGGATTCTCCAGGAAAGCATACTGGGGAAGTGA
GGCAAACCTACTTATTTCTTTTCATTCATCTAAGTAGCCAATCTGGGATTGGACACAGCTTTCCGAG
AACTTAACTCAGCAGAATGAGAAGGTTCTGGGGCCTGAATGTCTCCCTCAATTTGGCAGACTATTG
ACGCTCTCTGCCTAGGGCTCTAGACATTCTTTTGTCTGGTAGTAGTAGGAGCAAGGCAGAGTGAG
TAGGCTGTTTCCGTGCCAGatccgggggtaccgctcgagGCGATCGCATAAATTCGTATAGCATAACATTA
TACGAAGTTATAGGGAGCAATGAGTTGAGTAAGAGACATCCTTGGTGAGCGTTAAAGATAGGAGCC
CGCCACTAGAGAGCCATAGGCCACATCTAGTTCATTTCTTTAACTACTGACTTGTTCAATTCTCATT
CTGTTTATGTTCAACCCACATTTATTGAGTCCTGTGTTGTTGTTGTTGTTTTGCCTCTCAGATGATTG
TTTTACGTTTCTTCATCTGCTATTGCTACTGTATATAACAAAATTAATTTTTAATTTTCATTCATGTATT
GTGTTTGCCTGTAACCTATTCTTGCATGAGGGAGAGAGACAGAAAGACAGAGAGACAGAGAGAAT
GTGAATAAGCGTGATAATAATGATATGTCCTCAGATACACTCACTCACATGAGCGTCATTTGTTTTAA
GGTCAAATCTCAGAGGATGCTACGAGCTCTTGGCTCTTCTGGATCTTGGTGCCATAACAGTCCTCT
TCAGCAAACGCTGTTCTGCTCAGGAGTCTCTGTCATGTGATGCTTCTGGGGTGTGTGATGGCCGCTC
CAGGTCTTTACCTCTATTCCCTCCGACTCACAGCAGCCATGAAAAGCCTTGACCTGTCTTTCAACA
AGATCACCTACATTGGCCATGGTGACCTCCGAGCGTGTGCGAACCTCCAGGTTCTGATGTTGAAGTC
CAGCAGAATCAATACAATAGAGGGAGACGCCTTTTATTCTCTGGGCAGTCTTGAACATTTGGATTTG
TCTGATAATCACCTATCTAGTTTATCTTCTCCTGGTTCCGGCCCTTTCTCTTTGAAATACTTAAACT
TAATGGGAAATCCTTACCAGACTGGGGGTAACATCGCTTTTTCCCAATCTCACAAATTTACAAACC
CTCAGGATAGGAAATGTAGAGACTTTCAGTGAGATAAGGAGAATAGATTTTGTCTGGGCTGACTTCT
CTCAATGAACTTGAAATTAAGGCATTAAGTCTCCGGAATTATCAGTCCCAAAGTCTAAAGTCGATCC
GCGACATCCATCACCTGACTCTTCACTTAAGCGAGTCTGCTTTCCTGCTGGAGATTTTTGCAGATATT
CTGAGTTCTGTGAGATATTTAGAACTAAGAGATACTAACTTGGCCAGGTTCCAGTTTTCACTACTGCC
CGTAGATGAAGTCAGCTCACCGATGAAGAAGCTGGCATTCCGAGGCTCGGTTCTCACTGATGAAAG
CTTTAACGAGCTCCTGAAGCTGTTGCGTTACATCTTGGAACTGTCCGAGGTAGAGTTCGACGACTGT
ACCCTCAATGGGCTCGGCGATTTCAACCCCTCGGAGTCAGACGTAGTGAGCGAGCTGGGTAAAGTA
GAAACAGTCACTATCCGGAGGTTGCATATCCCCAGTTCTATTTGTTTTATGACCTGAGTACTGTCTA
TTCCCTCCTGGAGAAGGTGAAGCGAATCACAGTAGAGAACAGCAAGGTCTTCTGGTTCCCTGCTCG
TTCTCCAGCATTTAAAATCATTAGAATTCTTAGACCTCAGCGAAAATCTGATGGTTGAAGAATATTT
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AGATCAATGCAAAAAACAGGAGAGATTTTGTGACTCTGAAAAACCTGACCTCTTGTGACATCAGCA
GGAACACTTTTCATCCGATGCCGACAGCTGTCAGTGGCCAGAAAAGATGCGCTTCTGAATTTGTC
CAGTACAGGGATCCGGGTGGTAAAAACGTGCATTCCTCAGACGCTGGAGGTGTTGGATGTTAGTAA
CAACAATCTTGACTCATTTTCTTTGTTCTTGCCTCGGCTGCAAGAGCTCTATATTTCCAGAAATAAGCT
GAAAACACTCCAGATGCTTCGTTGTTCCCTGTGTTGCTGGTCATGAAAATCAGAGAGAATGCAGTA
AGTACTTTCTCTAAAGACCAACTTGTTCTTTTCCCAAACCTGGAGACTCTGGAAGCAGGCGACAACC
ACTTTGTTTGTCTCCTGCGAACTCCTATCCTTTACTATGGAGACGCCAGCTCTGGCTCAAATCCTGGTT
GACTGGCCAGACAGCTACCTGTGTGACTCTCCGCCTCGCCTGCACGGCCACAGGCTTCAGGATGCC

GGCCCTCCGTCTTGGGAATGTCACCAGGCTGCACTGGTGTCTGGAGTCTGCTGTGCCCTTCTCTGTTG
ATCTTGCTCGTAGGTGCCCTGTGCCACCATTTCCACGGACTGTGGTACCTGAGAATGATGTGGGCGT
GGCTCCAGGCCAAGAGGAAGCCCAAGAAAGCTCCCTGCAGGGACGTTTGCTATGATGCCTTTGTTTC
CTACAGTGAGCAGGATTCCCATTGGGTGGAGAACCTCATGGTCCAGCAGCTGGAGAACTCTGACCC
GCCCTTAAGCTGTGTCTCCACAAGCGGGACTTCGTTCCGGGCAAATGGATCATTGACAACATCATC
GATTCCATCGAAAAGAGCCACAAAAGTGTGTTCTGTTCTGAGAACTTCGTACGGAGCGAGTGGT
GCAAGTACGAACTGGACTTCTCCACTTCAGGCTCTTTGACGAGAACAAACGACGCGGCCATCCTTGT
TTTGCTGGAGCCCATTGAGAGGAAAGCCATTCCCCAGCGCTTCTGCAAAGATAATGAAC
ACCAAGACCTACCTGGAGTGGCCCTTGATGAAGGCCAGCAGGAAGTGTGGTAAATCTGAGA
ACTGCAATAAAGTCTAGGTTCTCCACCCAGTTCCTGACTTCTTAAGTCTTTGTGACACAAA
CTGTAACAAAGTTTATAAGTAACATAGAATTGTATTATTGAGGATATTAAGTCTTTGTCTTGA
ATACTGTTATATAAATATGTGACATCAGGAGACCGGTTTCTCTGTTTTCTTTATCTCTCTCTGTATT
GATATCTGAATAACCTGTTCACTTAGAACATCTGGAGACAGCACATTTAGACTGACGGTTTAGTGCC
TGTATCCAGTCAGTGCACATAGGGTGGCTAGAGAAAGCATTGCTAATCTACTCACCTGCCATCCC
TCTGTGTAGCTGATCCAAGGGCAAGGAGTCACAGTAT[3nt_del]GGGCATCCAGGCAAATCTGTT
GCTCTTCTAGACAGGGGGTGTGTCCACCATCCACAGATCTTCCAATATAAATGACACAGGCT
GCATTTTTGTGTGAACTAGGTTTGTCTTTCTGAGTCCTTGATAGTTTTCTTAAGTATAAATTACCTAT
TAATTTGTAAGGATCTGAAAGAAGTCTCCCATGTCTGGTGCAGATTTCCACTGGATTTAGCTATTA
ATTTCCAGTGTCTGGTTGCTATGGTTTCTGACCCCTTAGGCATTCTGTT

TLR2-FLOX-EM2-B6N

TGGGTAGTAGCGCACGTATGCCATCCCCAACCATTACAGAAGCATAAAACATATTTTGGGAAATTG
TTGCGTTATTTCACTGAGCAAATATGACCACAGCACGTGTGGTTGCATGGAACAGCTACAGGGTATA
GGGCCAGAAGGTGCCCTGGGAGACGAGCCTTGATTCTCCAGGAAAGCATACTGGGGAAGTGA
GGCAAACCTACCTATTTCTTTTTCATTATCTAAGTAGCCAATCTGGGATTGGACACAGCTTTCCGAG
AACTTAAGTACGAGAATGAGAAGGTTCTGGGGGCCTGAATGTCTCCCTCAATTTGGCAGACTATTG
ACGCCTCTCTGCCTAGGGCTCTAGACATTCCTTTTGTCTGGTAGTAGTAGGAGCAAGGCAGAGTGAG
TAGGCTGTTTCCGTGCCAGatccgggggtaccgctcgagGCGATCGCATAACTTCGTATAGCATAACATTA
TACGAAGTTATAGGGAGCAATGAGTTGAGTAAGAGACATCCTTGGTGAGCGTTAAAGATAGGAGCC
CGCCACTAGAGAGCCATAGGCCACATCTAGTTCATTTCTTTAACTACTGACTTGTTCACTCTCATT
CTGTTTATGTTCAACCCACATTTATTGAGTCCTGTGTTGTTGTTGTTGTTTTGCCTCTCAGATGATTG
TTTTACGTTTCTTCATCTGCTATTGCTACTGTATATAACAAAATTAATTTTAAATTTTTCATTATGATT
GTGTTTGCCTGTAACCTATTCCTTGCATGAGGGAGAGAGACAGAAAGACAGAGAGACAGAGAGAAT
GTGAATAAGCGTGATAATAATGATATGTCCTCAGATACTCACTCACATGAGCGTCATTTGTTTTAA
GGTCAAATCTCAGAGGATGCTACGAGCTCTTTGGCTCTTCTGGATCTTGGTGGCCATAACAGTCCTCT
TCAGCAAACGCTGTTCTGCTCAGGAGTCTCTGTATGTGATGCTTCTGGGGTGTGTGATGGCCGCTC
CAGGTCTTTACCTCTATTCCCTCCGGACTCACAGCAGCCATGAAAAGCCTTGACCTGTCTTTCAACA
AGATCACCTACATTGGCCATGGTGACCTCCGAGCGTGTGCGAACCTCCAGGTTCTGATGTTGAAGTC
CAGCAGAATCAATACAATAGAGGGAGACGCCTTTTATTCTCTGGGCAGTCTGAACATTTGGATTTG
TCTGATAATCACCTATCTAGTTTATCTTCTCCTGGTTCCGGCCCTTTCTCTTTGAAATACTTAAACT
TAATGGGAAATCCTTACCAGACACTGGGGGTAACATCGCTTTTTCCCAATCTCACAAATTTACAAACC

CTCAGGATAGGAAATGTAGAGACTTTCAGTGAGATAAGGAGAATAGATTTTGTCTGGGCTGACTTCT
CTCAATGAACTTGAAATTAAGGCATTAAGTCTCCGGAATTATCAGTCCCAAAGTCTAAAGTCGATCC
GCGACATCCATCACCTGACTCTTCACTTAAGCGAGTCTGCTTTCCTGCTGGAGATTTTTGCAGATATT
CTGAGTTCTGTGAGATATTTAGAATAAGAGATACTAACTTGGCCAGGTTCCAGTTTTCACTACTGCC
CGTAGATGAAGTCAGCTCACCGATGAAGAAGCTGGCATTCCGAGGCTCGGTTCTCACTGATGAAAG
CTTTAACGAGCTCCTGAAGCTGTTGCGTTACATCTTGGAACTGTGCGGAGGTAGAGTTGACGACTGT
ACCCTCAATGGGCTCGGCGATTTCAACCCCTCGGAGTCAGACGTAGTGAGCGAGCTGGGTAAAGTA
GAAACAGTCACTATCCGGAGGTTGCATATCCCCAGTTCTATTTGTTTTATGACCTGAGTACTGTCTA
TTCCCTCCTGGAGAAGGTGAAGCGAATCACAGTAGAGAACAGCAAGGTCTTCTGGTTCCTGCTCG
TTCTCCAGCATTTAAAATCATTAGAATTCTTAGACCTCAGCGAAAATCTGATGGTTGAAGAATATTT
GAAGAACTCAGCCTGTAAGGGAGCCTGGCCTTCTTACAAACCTTAGTTTTGAGCCAGAATCATTTG
AGATCAATGCAAAAAACAGGAGAGATTTTGTGACTCTGAAAAACCTGACCTCTTTGACATCAGCA
GGAACACTTTTTCATCCGATGCCGACAGCTGTCAGTGGCCAGAAAAGATGCGCTTCTGAATTTGTC
CAGTACAGGGATCCGGGTGGTAAAAACGTGCATTCTCAGACGCTGGAGGTGTTGGATGTTAGTAA
CAACAATCTTGACTCATTTTCTTGTCTTGCCTCGGCTGCAAGAGCTCTATTTCCAGAAATAAGCT
GAAAACACTCCAGATGCTTCGTTGTTCCCTGTGTTGCTGGTCATGAAAATCAGAGAGAATGCAGTA
AGTACTTTCTCTAAAGACCAACTTGGTTCTTTTCCAAACTGGAGACTCTGGAAGCAGGCGACAACC
ACTTTGTTTGTCTCCTGCGAACTCCTATCCTTACTATGGAGACGCCAGCTCTGGCTCAAATCCTGGTT
GACTGGCCAGACAGCTACCTGTGTGACTCTCCGCCTCGCCTGCACGGCCACAGGCTTCAGGATGCC
GGCCCTCCGTCTTGGAATGTCACCAGGCTGCACTGGTGTCTGGAGTCTGCTGTGCCCTTCTCCTGTTG
ATCTTGCTCGTAGGTGCCCTGTGCCACCATTTCCACGGACTGTGGTACCTGAGAATGATGTGGGCGT
GGCTCCAGGCCAAGAGGAAGCCCAAGAAAGCTCCCTGCAGGGACGTTTGCTATGATGCCTTTGTTTC
CTACAGTGAGCAGGATCCCATTGGGTGGAGAACCTCATGGTCCAGCAGCTGGAGAACTCTGACCC
GCCCTTAAGCTGTGTCTCCACAAGCGGGACTTCGTTCCGGGCAAATGGATCATTGACAACATCATC
GATCCATCGAAAAGAGCCACAAAACCTGTGTTCTGACTTTCTGAGAACTTCGTACGGAGCGAGTGGT
GCAAGTACGAACTGGACTTCTCCCACTCAGGCTCTTTGACGAGAACAACGACGCGGCCATCCTTGT
TTTGCTGGAGCCCATTGAGAGGAAAGCCATTCCCCAGCGCTTCTGCAAACCTGCGCAAGATAATGAAC
ACCAAGACCTACCTGGAGTGGCCCTTGATGAAGGCCAGCAGGAAGTGTGTTGGGTAAATCTGAGA
ACTGCAATAAAGTCTAGGTTCTCACCCAGTTCCTGACTTCTTAATAAGGTCTTTGTGACACAAA
CTGTAACAAAGTTTATAAGTAACATAGAATTGTATTATTGAGGATATTAATACTATGGGTTTTGTCTTGA
ATACTGTTATATAAATATGTGACATCAGGAGACCGGTTTTCTGTTTTTCTTTATCTCTCTCCTGTATT
GATATCTGAATAACCTGTTCACTTAGAACATCTGGAGACAGCACATTTAGACTGACGGTTTAGTGCC
TGTATCCAGTCAGTGCACATAGGGTGGCTAGAGAAAGCATTTGCTAATCTACTCACCTGCCATCCC
TCTGTGTAGCTGATCCAAGGGCAAGGAGTCACAGTAT[3nt_del]GGGATAACTTCGTATAGCATAC
ATTATACGAAGTTATCGCCGGCGgggtctgagctcgccatcagtAAATCTGTTGCTTTCCTAGACAGGGGGT
TGTGTCCACCATCCACCAGATCTTCCAATATAAATGACACAGGCTGCATTTTTGTGTGAACTAGGT
TTGTCTTTCTGAGTCCTTGATAGTTTTCTAAGTATAAATTACCTATTAATTTGTAAGGATCTGAAAG
AAGTCTCCCATGTCCTGGTGCAGATTTCCACTGGATTTAGCTATTAATTTCCAGTGTCTGGTTGCTAT
GTTTCTGACCCCTTAGGCATTCTGTT

Grey highlight denotes floxed exon ENSMUSE00000441912, yellow denotes genotyping handles, red denotes LoxP site. Please note that the 3 nt deletion from EM1 is still present in the EM2 allele.

Nucleotide Alignment:

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182 WT: 30 40 50 60 70 80 90 100 110 120 130 140
182 EM1:
182 EM2:

182 WT: 160 180 200 220 240 260 280 300
182 EM1:
182 EM2:

182 WT: 320 340 360 380 400 420 440
182 EM1:
182 EM2:

182 WT: 460 480 500 520 540 560 580 600
182 EM1:
182 EM2:

182 WT: 620 640 660 680 700 720 740
182 EM1:
182 EM2:

182 WT: 760 780 800 820 840 860 880 900
182 EM1:
182 EM2:

182 WT: 920 940 960 980 1000 1020 1040
182 EM1:
182 EM2:

182 WT: 1060 1080 1100 1120 1140 1160 1180 1200
182 EM1:
182 EM2:

182 WT: 1220 1240 1260 1280 1300 1320 1340
182 EM1:
182 EM2:

182 WT: 1360 1380 1400 1420 1440 1460 1480 1500
182 EM1:
182 EM2:

182 WT: 1520 1540 1560 1580 1600 1620 1640
182 EM1:
182 EM2:

182 WT: 1660 1680 1700 1720 1740 1760 1780 1800
182 EM1:
182 EM2:

182 WT: 1820 1840 1860 1880 1900 1920 1940
182 EM1:
182 EM2:

182 WT: 1960 1980 2000 2020 2040 2060 2080 2100
182 EM1:
182 EM2:

182 WT: 2120 2140 2160 2180 2200 2220 2240
182 EM1:
182 EM2:

182 WT: 2260 2280 2300 2320 2340 2360 2380 2400
182 EM1:
182 EM2:

182 WT: 2420 2440 2460 2480 2500 2520 2540
182 EM1:
182 EM2:

182 WT: 2560 2580 2600 2620 2640 2660 2680 2700
182 EM1:
182 EM2:

182 WT: 2720 2740 2760 2780 2800 2820 2840
182 EM1:
182 EM2:

182 WT: 2860 2880 2900 2920 2940 2960 2980 3000
182 EM1:
182 EM2:

182 WT: 3020 3040 3060 3080 3100 3120
182 EM1:
182 EM2:

182 WT: 3160 3180 3200 3220 3240 3260 3280 3300
182 EM1:
182 EM2:

182 WT: 3320 3340 3360 3380 3400 3420 3440
182 EM1:
182 EM2:

182 WT: 3460 3480 3500 3520 3540 3560 3580 3600
182 EM1:
182 EM2:

182 WT: 3620 3640 3660 3680 3700 3720 3740
182 EM1:
182 EM2:

182 WT: 3760 3780 3800 3820 3840 3860 3880 3900
182 EM1:
182 EM2:

182 WT: 3920 3940
182 EM1:
182 EM2:
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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:

Geno_Tlr2_F1 primer (5'-3')	TGGGTAGTAGCGCACGTATG
Geno_Tlr2_R3 primer (5'-3')	AACAGAATGCCTAAGGGGGT
Taq Polymerase used	ThermoFisher SuperFi II PCR Kit
Annealing Temperature (°C)	60
Elongation time (min)	2
WT product size (bp)	3844
Mutant product size (bp)	3915
Notes	PCR external to the LoxP donor insertions. Sequenced with the following primers (5'-3'): Geno_Tlr2_F1: TGGGTAGTAGCGCACGTATG Geno_Tlr2_R3: AACAGAATGCCTAAGGGGGT LoxPF: ATCCGGGGGTACCGCGTCGAG LoxPR: ACTGATGGCGAGCTCAGACC

LoxP_F primer (5'-3')	ATCCGGGGGTACCGCGTCGAG
LoxP_R primer (5'-3')	ACTGATGGCGAGCTCAGACC
Taq Polymerase used	ThermoFisher SuperFi PCR Kit
Annealing Temperature (°C)	60
Elongation time (min)	2
WT product size (bp)	N/A
Mutant product size (bp)	3252
Notes	PCR to screen for floxed allele i.e., both LoxP sites. Sequenced with the following primers (5'-3'): LoxPF: atccgggggtaccgctcgag LoxPR: ACTGATGGCGAGCTCAGACC Tlr2_PW1: AACCCACATTTATTGAGTCC Tlr2_PW2: GGGTAACATCGCTTTTCCC Tlr2_PW3: AACTCAGCCTGTAAGGGAGC Tlr2_PW4: CCTTCTCTGTTGATCTTGC

Geno_Tlr2_F1 primer (5'-3')	TGGGTAGTAGCGCACGTATG
LoxP_R primer (5'-3')	ACTGATGGCGAGCTCAGACC
Taq Polymerase used	ThermoFisher SuperFi PCR Kit
Annealing Temperature (°C)	60
Elongation time (min)	2
WT product size (bp)	N/A
Mutant product size (bp)	3677
Notes	<p>PCR to interrogate 5' end of the allele. Sequenced with the following primers (5'-3'):</p> <p>Tlr2_R1: GACGCTCATGTGAGTGAGTGTA Tlr2_R4: GGATAGGAGTTCGCAGGAGC Tlr2_PW2: GGGTAACATCGCTTTTTCCC Tlr2_PW3: AACTCAGCCTGTAAGGGAGC Tlr2_PW4: CCTTCTCCTGTTGATCTTGC</p>

LoxP_F primer (5'-3')	ATCCGGGGGTACCGCGTCGAG
Geno_Tlr2_R3 primer (5'-3')	AACAGAATGCCTAAGGGGGT
Taq Polymerase used	ThermoFisher SuperFi PCR Kit
Annealing Temperature (°C)	60
Elongation time (min)	2
WT product size (bp)	N/A
Mutant product size (bp)	3519
Notes	<p>PCR to interrogate 3' end of the allele. Sequenced with the following primers (5'-3'):</p> <p>LoxPF: atccgggggtaccgctcgag Tlr2_PW1: AACCCACATTTATTGAGTCC Tlr2_PW2: GGGTAACATCGCTTTTTCCC Tlr2_R4: GGATAGGAGTTCGCAGGAGC Tlr2_PW3: AACTCAGCCTGTAAGGGAGC Tlr2_R3: AACAGAATGCCTAAGGGGGT</p>

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.

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	TLR2_FLOX-DON-Mut5
Forward Primer (5'-3')	GGAGCAAGGCAGAGTGAGTAG
Reverse Primer (5'-3')	GCTCACCAAGGATGTCTCTTAC
Probe (5'-3')	TCGAGGCGATCGCATAACTTCG
Label	FAM

This ddPCR assay is specific to the donor used to create the engineered mutation and only mutant 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	Tlr2-Flox-3.6-MUT2
Forward Primer (5'-3')	GGAGTCACAGTATGGGATAAC
Reverse Primer (5'-3')	GTCTAGGAAGAGCAACAGATT
Probe (5'-3')	AAGTTATCGCCGGCGGGTCTGA
Label	FAM

This ddPCR assay is specific to the donor used to create the engineered mutation and only mutant 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	TLR2-CR-LOA-WT
Forward Primer (5'-3')	TGTGCCCTTCTCCTGTTGA
Reverse Primer (5'-3')	AGCCACGCCACATCATTC

Probe (5'-3')	CTTGCTCGTAGGTGCCCTGTGC
Label	FAM

This ddPCR assay is universal; both the WT and mutant 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 additional donor integrations were detected in the animals taken forward to establish the colony.