Table S1. Primers used for sequencing of *Lamc1* and *Lamc2*.

Name	Sequence
Lamc1.1F	AGTTTGTTAATGCCGCCTTCAA
Lamc1.2R	GCGCACGTAAGTGATGTCAAA
Lamc1.3F	ATGAAGTGTTTAACGACCCCAAAGT
Lamc1.4	(AG)CGGCCGGTCATTGAAGAAA
Lamc1.5F	GCCGATCCCAAGAGTGCTAC
Lamc1.6R	GCATCTGCCGTAACTGTCACA
Lamc1.7F	CAGCACAGACGAGTGTAATGTTGA
Lamc1.8R	GCCAACAGCATTTGTGCACA
Lamc1.9F	GCGCGTGGAGCAGAGAGA
Lamc1.10R	AAAGATTCTGCCCATAACTCAGGA
Lamc1.11F	GCTCTCTCCCCGTTTGAATTT
Lamc1.12R	AGCACTTTGCAAGGTGACATCA
Lamc1.13F	GCCCCCACTGTGAGAAATGTAG
Lamc1.14R	AGTCTCACAGGCCCATTGCT
Lamc1.15F	TGCAGCAACAGAGCAGCTGTAA
Lamc1.16R	ACACTGCCCATTGGTGGAA
Lamc1.17F	TCCCTTTCACTCCAGTGTAAAGAGG
Lamc1.18R	CTGGAGTTTCACTCGATGCTCAG
Lamc1.19F	GATCGCCTTCAGAGAGTAAATAGCA
Lamc1.20R	GTTGTTTGGCTCCCCTGTAGACT
Lamc1.121F	GATGACATTGTACGAGTGGCAAA

Lamc1.22R	CCTGCTTCTCCAGGTCCTGAG
Lamc1.23F	AAATAAAATCAAGAAAGAAGCTGCAGA
Lamc1.24R	AGCTTCTTCAGCAAGGGCCTT
Lamc1.25F	ATAACAAGACAGCCGCGGAA
Lamc1.26R	GTTCTTTCTGCGTCCGCCTT
Lamc1.27F	CAATGCCAGAAAGGCCAAAAA
Lamc1.28R	CCGGTTATAGTCCATGATGGCT
Lamc1.R	AAGGGTTACAAATATTCAGATTTTATTATAAATAAAA
Lamc2F	GCCACCTCCAGGAGGGAAGT
Lamc2R	TCACTGTTGCTCAAGAGCTTGG
Lamc2.2F	GCTCAGCTGCTGCCTTGGT
Lamc2.4R	TTTGTCCTGTCACACCTGGCTTA
Lamc2.5F	GTGACCCAGCTGGCATCTCT
Lamc2.7R	TCTGATCTTCGGGCAGAACTAAAC
Lamc2.8F	CGCGTGGACAGAGGAGGTA
Lamc2.9F	GCTGTGAGGTTCCGCAGTAAC
Lamc2.10F	CCCGCCCTGTCTCTGGA
Lamc2.11R	CAGCACACTCAATGTCAGGATTCT
Lamc2.12F	AGCTCTGTGCTGATGGCTTCTTT
Lamc2.13R	CACCTCGACACTCTCCAGGCT
Lamc2.14F	AGCAGCTCCAGAGCCTGGAG
Lamc2.15R	GTTCTCTTGGCTCCTTGCCTT
Lamc2.16F	CACTACGTGGGGCCGAAT

Lamc2.18R	GCTCAGGGACTTGGTTTTCTCTAA
Lamc2.19F	AGACAAAAGGCTGATTCTCTCTCAAA
Lamc2.20	CAAGGTTGGCACGGGAAA
Lamc2.21F	GAAGACAGAAAAGCAGAGGCTGAA
Lamc2.22R	CTGCTGTCACATTAGCTTCCAAGTT
Lamc2.23F	CTGATGCCAGAGCCACGAGT
Lamc2.24R	GGCCGAAGTCGACTGTTGA
Lamc2b.F	CGACAGACAGGCAGCGGGT
Lamc2b.R	CTGGGTCTTGTCACTGGCATC
In2Ex2FWD	CACCTCCAGGAGGGAAGTGA
In2Ex2REV	CCCTTGGCTTTATGGGAAAAC
In2Ex3FWD	AATGATCAACCCAGCACTATCTGATA
In2Ex3REV	CGCTGTATTGTCATTGCAGTTGAG
Ex3In3FWD	TTGCCTCAACTGCAATGACAA
Ex3In3REV	AATTCAAACCGGCTGACTCTGA
In3Ex4FWD	CTGTGGAGCAGGCATCTTCA
In3Ex4REV	ATCCAGCATCGGTGAGCATAT
Ex4In4FWD	ACCGATGTCAGCCAGGCTT
Ex4In4REV	TAGCTGAACATGACATGGAAAGTAACTC
In4Ex5FWD	CACTGCCCCACTGGCTTAAATA
In4Ex5REV	TCTCCAGTGACGGCTGGTTT
Ex5In5FWD	GGCATCTCTGGACCCTGTGATT
Ex5In5REV	TTTGTTTGTTTTTTAAGCTCAGCCTTT

In5Ex6FWD	GGAGGTCAGAGGTTGTATGTAAACCTT
In5Ex6REV	GTGGACACTGAAGTCGGCAGA
Ex6In6FWD	GTGCCGACCAGGCTACTATCAT
Ex6In6REV	TGCATGTGATGGGACAGCTTT
In6Ex7FWD	TAGGAGTGACTGGGGAATTCTGAA
In6Ex7REV	ACGAAATAGACGGGGTCTGATCTT
Ex7In7FWD	GTTGGAAGGCGGTTCAGAGAA
Ex7In7REV	CCTGGATGGCTCTACAGTGTCAT
In7Ex8FWD	TCTTTGGAGCTACTTACACAGCCAA
In7Ex8REV	GTGATCCCACAGGGAAGTGTCTT
Ex8In8FWD	GCCGTCTGCCTACGATGTGAT
Ex8In8REV	TCTCTCCCCATGCCTGTGAA
In8Ex9FWD	ACGGACACACCCTCTACTGCTT
In8Ex9REV	GATCAGGAGGGCTGTGAGGTT
Ex9In9FWD	ACTGGAGTCCCCAGCTGAGTTA
Ex9In9REV	TGCTAGAGAAACATTCCTGGTAGGAA
In9Ex10RFWD	CAGCACCCGGGCATAGAA
In9Ex10REV	GCAGGGCATACACAACGTTCA
Ex10In10FWD	CTGGTTACAAAAGAGATTCGGCAA
Ex10In10REV	TCATTTCCATAATGAAAAGAGGTCAA
In10Ex11FWD	TGTGACGCGTAAGGCTGAGAT
In10Ex11REV	CTCTGTCTCAGGCATCACTGAACA
Ex11In11FWD	CTGTCACAATGGGTTCAGCTGTT

Ex11In11REV	CCAGTCATAGCTCAGACACCACATA
In11Ex12FWD	AGCCACACCCACTCCAACAA
In11Ex12REV	GGCCGTGTTGTAGATACATTTCAA
Ex12In12FWD	ACCAGTTGACAGGCAGATGCTT
Ex12In12REV	AGCCGGTCTGGTCATGGAA
In12EX13FWD	GAGCGCACACACATGGATCA
In12EX13REV	ACTTGATTGTAGCAAGCAGGACAA
EX13In13FWD	GAGCCTGGAGAGTGTCGAGGT
EX13In13REV	ATCTCCATATCTAAATCTATGTCAATACCCAT
In13Ex14FWD	ATTAGAAGATGATTTGCCAAGGTCATT
In13Ex14REV	TGAAATCTGAGCTTCTCTTAGAATGTCTC
Ex14In14FWD	CTGGAGGCCCTGGTTTCAA
EX14In14REW	ACTGATGCAGAATGACCGTGTTAA
In14Ex15FWD	GGAGGCCAACTGCTTATCAGCTA
In14Ex15REW	GCCAGACTCAGGCGCATCT
Ex15In15FWD	AGACCCGCCTGGATGACCT
Ex15In15REW	GTATAATGCAGTTCCACGGGAAA
In15Ex16FWD	ATCCATTTTACAAAGACTTCTCTTGAAAT
In15Ex16REW	GTCTGCCAATCTTGTAGCCTCCT
Ex16In16FWD	CCATTCTTCTGAGCACCCGAAT
Ex16In16REW	AGAAAGCTGGAAGGGAACACTTTC
In16Ex17FWD	CCAGAAGGGTAGCCCTGTGA
In16Ex17REW	TTGTACCACGGAGCTGTCCAA

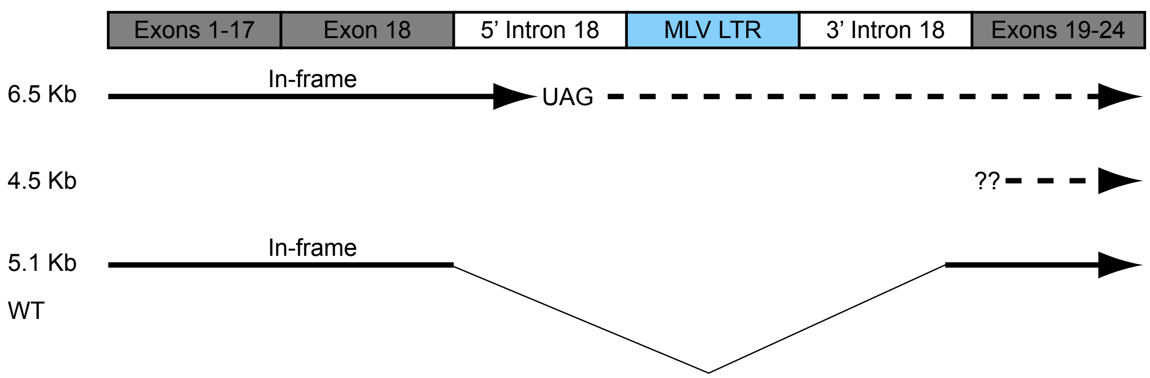
Ex17In17FWD	AGTCAGCTAACGCAATGAAGCAA
EX17In17REW	CATTTCCCAGCACAGTAGTCAGTT
In17Ex18FWD	GTTCTTGGAGGCAGGATAGCAGTAA
In17Ex18REW	AGGACAGATCACTGACTCCCTGAAG
Ex18In18FWD	CCAAGTCCCTGAGCCAGCA
Ex18In18REW	GTACTGTGCCTTTAACCGTCTGAA
In18Ex19FWD	TTCTTGGGAGTTGTACTGCCTATCTT
In18Ex19REW	CTGTCTCCTATCCTTTCCAGTCTGTAA
Ex19In19FWD	GTGGAAGCAAAGAGGATCAGACAA
Ex19In19REW	TTCCTAGGTTCAAATGCTGACTCAAT
In19Ex20FWD	GTGGAAAGAGTTGTAGACTTTCCTCTAAA
In19Ex20REW	CTCGGAGGTTCTTCAGGATGTTCT
Ex20In20FWD	GCTTTCCCGTGCCAACCTT
Ex20In20REW	GATCAGAACTCAGGACTCCTAGCACTT
In20Ex21FWD	TGACAGCTCCCTCAGTGGCT
In20Ex21REW	GCCTCCCTAGCTGCGTTCTTT
Ex21In21FWD	CCTCTATTAGCCAGAAGGTTGCAGAT
Ex20In20REW	GAACATGGAATATGGTGTATTAGCTGCTA
In21Ex22REW	CCGTGTCCTTATCCGTGTCAAA
Ex22In23FWD	ATAGGGAGTCTGAACTTGGAAGCTAAT
Ex22In23REW	GATACAAGTGCTCAGTGACTCATCTTAGA
In23Ex24FWD	AGCACAGATGCAGGCCTCAT
In23Ex24REW	ACTGATGCAGAATGACCGTGTTAA

EcoLTRFWD1 ACCCCTTCATAAGGCTTAGCCAG

EcoLTRREV1 GGAACCTTGAGACAGTTTCTGGG

LTRF1 AACCAATCAGCTCGCTTCTC

LTRR1 TGGGCAGTCAATCACTCTGA



Supp. Fig. 1. Proposed mechanism for *Lamc2 jeb* mutation. Schematic representation of aberrant and normal *Lamc2 jeb* transcripts. The MLV LTR insertion into intron 18 results in 3 transcripts. The aberrant 6.5 kb transcript includes intron 18 + the MLV LTR. This introduces a translational stop and an extended untranslated region but does not compromise transcript stability. The MLV LTR additionally results in an aberrant 4.5 kb transcript initiating after exon 17 along with a properly spliced WT 5.1 kb transcript in low abundance.

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EXON 18                                                     INTRON 18
CAG GGA GTC AGT GAT CTG TCC TTT CAG GTG GTG AGG CCT CTG ATC CTG TGT
 Q   V   G   S   D   L   S   F   Q   V   V   R   P   L   I   L   C
GCA TGC CAC CCG GAC AAA TGG ACA CAG AGA CTT TCT TCT CTA TAG ATC GCA
 A   C   H   P   D   K   W   T   Q   R   L   S   S   L   *
GAA GAT TGT TCA ACT TTA CAG CTT CTT CTT CAC AAT GGC TGT GTC AGG CAG

TGT CAC ATT GCT CAT TAC TTA TTA GGG GAA AGA GGT TCT TCT CTT TAG TGT

TTC AGA CGG TTA AAG GCA CAG TAC CTG CGT TGG TTC TGT CCT GCT AAG GGC

AGC AGA GTC TCA GGA GGA CAG AGG AAA TGA TCG GCA AGT GTG CAC AAT GTC

TTT AGA GCT CAC ATG GTC TAG AGG CCT CCT ACA CCC CAC AAA GGC TTC CCA

TCA CAC ACA CAC ACA CAT ACC CCA GCA CCC ATG TCA ACC AGA TGA ACA CGT

ATT AGC ACA TGG CTG ATA GCC CGT GTT TAA AAC CTA GCA TGG ACT TTG GGC

TTG GTG TTA GGA AGA GAC AGT TGC TTC CTG TCA TCT GTT GTC TAG ACT CTG

AAA GGG AAA ATG ACT TGC ATG TTT AAT CTT GAA CCC CTT AGT CAA GGA AAG

TTT TAT GCC TCC TCC CCA GTT CTT TTT TTT TTT GAG ACC CTC AAA TTG AAT

TTT AAT GGA GTT CGA TAC ATC CAT TTG ATA CTG CTA AGA AGA AGA CTT TTG

CTA TCA AAA AGC TTG CTT TTT TTT TTC TGC CAT CAA TCT CCC TAG CTA TTA

CAA CCT TAT TGG ATT AAG TTT ACC TGC ATA CCC AAC AGC TAA AGA CAC TCA

CAG TGA TCT CCA TAG AGA TAT GTT CTG TGA ATA GAT AAA GCA ATT GTT TTT

AAC AAC TTT TTT AAA AAA GAC CAG AGG CAG AGT TTA CTG TAT TCT TGG GAG

TTG TAC TGC CTA TCT TTC CTT GGT ACC CTG TCT CAT TTC TGG TAG GCT TTG
                     MLV LTR U3
GGA CGT TAG GGC CAG TGT CTG TGA AAG ACC CCT TCA TAA GGC TTA GCC AGC

TAA CTG CAG TAA CGC CAT CTT GCA AGG CAT GGG AAA ATA CCA GAG CTG ATG

TTC TCA GAA AAA CAA GAA CAA GGA AGT ACA GAG AGG CTG GAA AGT ACC GGG

ACT AAG GCC AAA CAG GAT ATC TGT GGT CAA GCA CTA GGG CCC CGG CCC AGG

GCC AAG AAC AGA TGG TCC CCA GAA ATA GCT AAA ACA ACA ACA GTT TCA AGA

GAC CCA GAA ACT GTC TCA AGG TTC CCC AGA TGA CCA GGG ATC AAC CCC AAG

CCT CAT TTA AAC TAA CCA ATC AGC TCG CTT CTC GCT TCT GTA CCC GCG CTT
                                                            R
ATT GCT GCC CAG CTC TAT AAA AAG GGT AAA AAC CCC ACA CTC GGC GCG CCA

GTC CTC CGA TAG ACT GAG TCG CCC GGG TAC CCG TGT ATC CAA TAA AGC CTT
            U5
TTG CTG TTG CAT CCG AAT CGT GGT CTC GCT GAT CCT TGG GAG GGT CTC CTC
                                              INTRON 18
AGA GTG ATT GAC TGC CCA GCT TGG GGG TCT TTC ATC TGC TTT CTT GGC TTC

TTA AGG CTG CCA GTA TTT TCA AAT GGT GAC AGT AGG TCC TGA AGC AGG TGT

GGT GAC GTG TGA GCA GAC AGT CAC ACT CAT TTG TAA CTT TGT GTC CAC AGG
EXON 19
TGG AAG CAG TGG AAG CAA AGA GGA TCA GAC AAA AGG CTG ATT CTC TCT CAA

ACC TGG TGA CCA GAC AAA CGG ATG CAT TCA CGC GTG TGC GAA ACA ATC TGG

GGA ACT GGG AAA AAG AAA CAC GGC AGC TTT TAC AGA CTG GAA AGG ATA GGA

GAC CA
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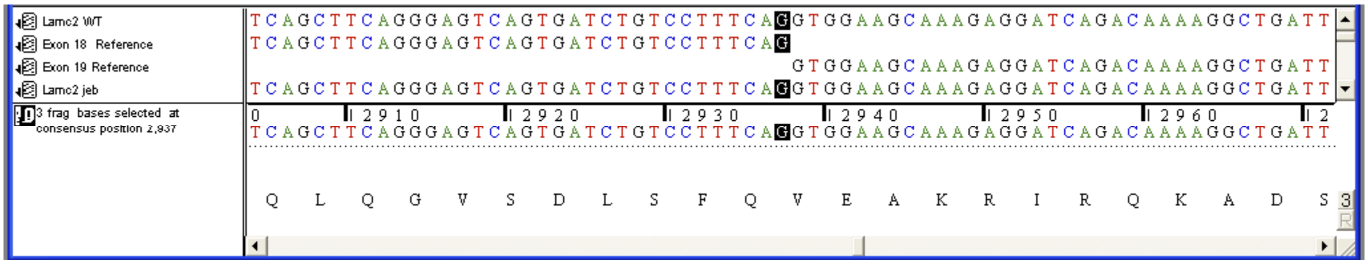
Supp. Fig. 2. Sequence analysis of the aberrant 6.5 kb transcript caused by the *Lamc2* *jeb* mutation. cDNA and predicted amino acid sequence between exons 18 and 19. Exonic boundaries were predicted based on known *Lamc2* WT sequence. Highlighted sequences: Grey, Exonic; No highlight, intronic; Blue, MLV LTR U3, R and U5 regions; * Site of premature TAG stop. Results are based on the amplified product of cDNA generated produced from oligo(dT) + random decamer primed RNA primers positioned in the MLV LTR and *Lamc2* exons.



Supp. Fig. 3. Detection of correctly spliced transcript from *Lamc2 jeb* mice.

cDNA sequences of the *Lamc2* wild type reference and *Lamc2*^{jeb} at the junction of exon 18 to 19 are shown, as well as the translated product. The amplified product of cDNA was generated produced from oligo(dT) + random decamer primed RNA using primers positioned in exons 14 and 22.