

**A***we***Intron 12-13**cacagagtcaaagggaaccagctcaccccagagggcagctagagggcgctgaagaaatagtggttttgctga 130048157

ctccactagaacaggacttggagtcctctatggccatgtagcctgagccctctggatttcacatcaacactaat 130048232

**Exon 13**ctctgtcccttcctaccagTGTGC**CATCC**CTGCGC**CCC**AAGGAG**AAG**TCC**CG**CATCC**GATTT**GAGATT**TTC**CCC 130048307

--V--P--S--L--R--P--K--E--K--S--R--I--R--F--E--I--F--P--

-\*- 657

**ACT**CGG**AGT**GGC**ACCA**AAG**CAACTG****CTC**GCT**GAC**TTT**TCC**TGC**AATAAA****TTC**CCT**GCA**ATC**AAG**GCC**ATG**CTG**CCC** 130048382

-T--R--S--G--T--K--Q--L--L--A--D--F--S--C--N--K--F--P--A--I--K--A--M--L--P--

ATT**GAT**GTC**TCT**GAG**TGA****CCG**ACC**CAG**CAG**CACT**CC**AC**AG**ACG**T**CGG**T**GAC**AC**AG**ACC**AG**AC**AG**CG**CTC**CT**CTG** 130048457

-I--D--V--S--E--\*- 693

TGGAGTGAAACTGTTGCCTATGCTGTCCAG 130048487**B***we<sup>Bkr</sup>***Exon 6**TGGTAGTGTGGAGATCCTCAAGAACTGGAAAAATCTGGCTTCAGGCCAGTCCAATTTGGCCAGTGTGGGTCTT 130029782**Intron 6-7**

TGCTGGAACCCCTCAACACAGgtgatatgggcgtggtgtgccttttggttcagtgggcagtaatggagtatgct 130029857

**Exon 7**aatgtaccatcaacagatcctcacagtcactttggtttgtagT**CTG**CGG**TGC**TTG**GGG**GTT**CCC**TCT**CGG**GTG 130029932

V--L--R--C--L--G--V--P--S--R--V--

**ATC****CCA**ACT**TCA**AACT**CGG**CT**CAC**G**AC**AC**GAT**CG**AA**AC**CTC**AG**TG**T**GAT**GT**TAC**T**AC**G**AT**G**CC**AT**G**GG**AA**AT 130030007

-I--T--N--F--N--S--A--H--D--T--D--R--N--L--S--V--D--V--Y--Y--D--A--M--G--N--

-L-

**Intron 7-8**CCC**CTG**GAG**AAA**GGC**AGT**GAT**AGC**GT**TG**gtaagtgatgagycagttccttggcatagcgtaccacgtatgagg 130030082

-P--L--E--K--G--S--D--S--V--W 328

aagtctctcctgttacccctgaacctctgtt**cca**cgatggaat**tgg**aaggaaagtaacacgtgagccagggcatta 130030157gttcagagtagaaatggtgctgagctaaccatgtaacttgcaggacc 130030204**C***we<sup>4J</sup>***Intron 9-10**gcactgtccattgtctgaattgcagctatatctctgaggtaccctgttttagtttttgtttcctcgccaatgc 130041752**Exon 10**acag**GT****TCC**AGT**GAG**GAA**AG**CA**AG**T**G**CAC**CAA**AAG**GCT**TT**G**AC**AAA**CT**CAA**C**CT**A**AY**G**CA**T**CT****TTC**GGC**GCA** 130041827

G--S--S--E--E--R--Q--V--H--Q--K--A--L--D--K--L--K--P--N--A--S--F--G--A--

ACA**TCT**TCG**AGG**AAT**CCA**GAA**GGG**GAA**GAC**AAG**GAG**CCC**AGC**ATT**TCT**GGG**AAG**TT**CA**AG**GTC**AC**G**GGG**GATA**CTG 130041902

-T--S--S--R--N--P--E--G--E--D--K--E--P--S--I--S--G--K--F--K--V--T--G--I--L--

**GC**AG**TAG**GG**CAA**G**AA**G**T**CAG**TCTG****TCC**CT**GATG**CT**CA**AAA**AA**C**ATG**ACT**AA**T**GAC**AG**GAA**G**AC**RG**TG**AC**GATG**AA**C** 130041977

-A--V--G--K--E--V--S--L--S--L--M--L--K--N--M--T--N--D--R--K--T--V--T--M--N--

-.-.-.-.-/\*- 512

AT**GACA**GC**TGG**ACC**ATC**G**TCTACA**AT**GGT**ACC**CTT**G**TCCAC**GA**AGT**G**TGGA**AG**GACTC**AG**CCACA**ATA**TCC**TTG 130042052

-M--T--A--W--T--I--V--Y--N--G--T--L--V--H--E--V--W--K--D--S--A--T--I--S--L--

**Intron 10-11****GAT**CT**CTGAA**GA**AG**gtaactgactcatcctgtagttggtgggactcaatcaatctagggcccaaaagagttgtctca 130042127

-D--P--E--E-- 547

ctgatgggatcctactgcttcccgtgagtcggttgactgtgggacagtagtgaacagcctccatgggtaagacc 130042202

ttagttctgatgttctggaagytgctgtcttatgagcaaggacagtcactgtgggtktaactccatgtttgtgtg 130042277

gccctggcaaaggaagaagggaggctt 130042304

**Figure S3.** Genomic DNA and predicted amino acid sequences at the site of the *we*, *we<sup>Bkr</sup>* and *we<sup>4J</sup>* mutations. Exonic sequences are in black (for coding regions) or purple (for the 3' untranslated region) upper-case letters; intronic sequences are in blue, lower-case letters. The primer sequences used for sequence analysis and DNA typing (see Figure 3) are underlined. Alternate codons are highlighted in yellow, and single-letter amino acid abbreviations are shown below each codon. **(A)** The original, spontaneous *we* mutation is associated with a C to T transition at position 2:130048290, indicated here in red. This nonsense mutation is predicted to cause an early translational stop following the isoleucine residue at position 657 (shown by a red asterisk). One previously-described insertion of 5'AGCT 3' (at the position indicated by the green arrowhead) was also encountered in the amplicon that was sequenced here. This polymorphism in Intron 12-13 (known as *rs247619567*) was found here to be present in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ*, NX129-10 *we<sup>3J</sup>*/J, B6C3Fe *a/a-we Pax1<sup>un</sup> a<sup>t</sup>*/J and B6CBACa *A<sup>w-J</sup>/A-we a Mafb<sup>kr</sup>*/J, but not in C57BL/6J or B10.129-*we<sup>Bkr</sup>*/CyJ. *Bts*CI target and cut sites are highlighted in blue (and see Figure 3). **(B)** The spontaneous *we<sup>Bkr</sup>* mutation is associated with a C to T transition mutation at position 2:130029949, shown here in red. This single-base-pair change is predicted to substitute a non-polar leucine for a polar serine at residue 299. A previously-described single-nucleotide polymorphism in Intron 7-8 (known as *rs238299153*) is shown in green and was found here to be a T in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a C in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J. *Xcm*I target and cut sites are highlighted in blue (and see Figure 3). **(C)** The spontaneous *we<sup>4J</sup>* mutation is associated with a 7-base-pair deletion from 2:130041960 to 2:130041966, indicated here by a red rectangle. This deletion is predicted to disrupt the reading frame in *we<sup>4J</sup>* transcripts, leading to an early translational stop following the arginine residue at position 512 (shown by a red asterisk). Four previously-described single-nucleotide polymorphisms (shown in green) were also encountered in the amplicon that was sequenced here. The polymorphism in Intron 9-10 (known as *rs27289408*) was found here to be a C in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a T in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J. The first polymorphism in Exon 10 (known as *rs51008079*) was found here to be a C in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a T in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J. The second polymorphism in Exon 10 (known as *rs27289406*) is one of the bases deleted in *we<sup>4J</sup>* and was found here to be an A in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a G in strains AKR/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J. The first polymorphism in Intron 10-11 (known as *rs27289405*) was found here to be a C in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a T in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J. The second polymorphism in Intron 10-11 (known as *rs27289404*) was found here to be a G in strains C57BL/6J and B10.129-*we<sup>Bkr</sup>*/CyJ, but a T in strains AKR/J, AKR-*we<sup>4J</sup>*/J, B10.UW-*H3<sup>b</sup> we Pax1<sup>un</sup> a<sup>t</sup>/SnJ* and NX129-10 *we<sup>3J</sup>*/J.