Figure S1. Alignment of ABCC2 genome sequence from 107,087 to 108334 bp and amplicon sequence from knockout line SPM-8 with 7 bp deletion at the exon 21 sgRNA target site and 6 bp net insertion at the exon 22 sgRNA target site. Identical nucleotides are shown in white text with black background and alignment gaps are indicated by hyphens. Deletions and insertions caused by CRISPR/Cas9 editing at sgRNA target sites are marked with red bold text and nucleotide polymorphisms between the reference genomic scaffold (Accession: KY701524) sequence and amplicon sequences are shown in dark gray text.

 107087

 Hz\_ABCC2 GGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTTGA

 SPM-8 (1)GGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTTGA

 107167

 Hz\_ABCC2 TTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAATTCCA

 SPM-8 (81) TTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAATTCCA

 107247

 Hz\_ABCC2 TCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTCATATGATTATCAA

 SPM-8 (161)TCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTCATATGATTATCAA

 107327

 Hz\_ABCC2 GATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTTAATGTAATGAATGTTGTAGGTTGGA

 SPM-8 (241)GATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTTAATGTAATGAATGTTGTAGGTTGGA

 107407

 Hz\_ABCC2 GTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGC**TCATCGC**GGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAA

 SPM-8 (321)GTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGC**-------**GGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAA

 107487

 Hz\_ABCC2 AATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGA

 SPM-8 (394)AATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGA

 107567

 Hz\_ABCC2 AGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGT

 SPM-8 (473)AGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGT

 107647

 Hz\_ABCC2 TTCCAGCACCCGGATAAAAATATCCTTTTTATTGCAATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACC

 SPM-8 (553)TTCCAGCACCCGGATAAAAATATCCTTTTTATTGCAATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACC

 107727

 Hz\_ABCC2 TTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTA**C**GTACCCTCTTATGTGCTCTCTTATGTA

 SPM-8 (633)TTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTA**T**GTACCCTCTTATGTGCTCTCTTATGTA

 107807

 Hz\_ABCC2 CTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGAT

 SPM-8 (713)CTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGAT

 107887

 Hz\_ABCC2 ATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCAATTTTTTTTTATT**T**AGAA**C**ATTGATTCAGCG

 SPM-8 (793)ATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCAATTTTTTTTTATT**-**AGAA**A**ATTGATTCAGCG

 107967

 Hz\_ABCC2 ATAACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTG

 SPM-8 (872)ATAACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTG

 108047

 Hz\_ABCC2 CGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATA**T------**TTGGAGGGCGTTGGAACAGGTACGCTTAAT

 SPM-8 (952)CGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATA**GAAGGCG**TTGGAGGGCGTTGGAACAGGTACGCTTAAT

 108121

 Hz\_ABCC2 TAAATTACTTCT**C**AACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAA

 SPM-8(1032)TAAATTACTTCT**T**AACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAA

 108201

 Hz\_ABCC2 GAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTT

 SPM-8(1112)GAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTT

 108281

 Hz\_ABCC2 GGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

 SPM-8(1192)GGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

Figure S2. Alignment of ABCC2 genome sequence from 107,089 to 108,333 bp and amplicon sequence from knockout line SPM-16 with a deletion of 426 bp and an insertion of four bp at the sgRNA target sites in exon 21 and 22, respectively. Identical nucleotides are shown in white text with black background and alignment gaps are indicated by hyphens. Deletions and insertions caused by CRISPR/Cas9 editing at sgRNA target sites are marked with red text and nucleotide polymorphisms between the reference genomic scaffold (Accession: KY701524) sequence and amplicon sequences, including those may have been introduced by repair enzymes are shown in dark gray text with white background.

 107089

 Hz\_ABCC2 AAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTTGATT

 SPM-16 (1)AAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTTGATT

 107169

 Hz\_ABCC2 AAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAATTCCATC

 SPM-16 (81) AAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAATTCCATC

 107249

 Hz\_ABCC2 CAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTCATATGATTATCAAGA

 SPM-16 (161)CAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTCATATGATTATCAAGA

 107329 11612

 Hz\_ABCC2 TGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTTAATGTAATGAATGTTGTAGGTTGGAGT

 SPM-16 (241)TGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTTAATGTAATGAATGTTGTAGGTTGGAGT

 107409

 Hz\_ABCC2 TGTAGGCAGAACAGGAGCCGGCAAGTCATC**GCTCATCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAA**

 SPM-16 (321)TGTAGGCAGAACAGGAGCCGGCAAGTCATC**--------------------------------------------------**

 107489

 Hz\_ABCC2 **TTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAG**

 SPM-16 (351)**--------------------------------------------------------------------------------**

 107569

 Hz\_ABCC2 **TATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTT**

 SPM-16 (351)**--------------------------------------------------------------------------------**

 107649

 Hz\_ABCC2 **CCAGCACCCGGATAAAAATATCCTTTTTATTGCAATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACCTT**

 SPM-16 (351)**--------------------------------------------------------------------------------**

 107729

 Hz\_ABCC2 **AAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTACGTACCCTCTTATGTGCTCTCTTATGTACT**

 SPM-16 (351)**--------------------------------------------------------------------------------**

 109809

 Hz\_ABCC2 **CCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATC**ACATGAAATTAAATACGTTGATAT

 SPM-16 (351)**--------------------------------------------------------**ACATGAAATTAAATACGTTGATAT

 107889

 Hz\_ABCC2 ACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCAATTTTTTTTTATTTAGAA**C**ATTGATTCAGCGAT

 SPM-16 (375)ACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCAATTTTTTTTTATTTAGAA**A**ATTGATTCAGCGAT

 107969

 Hz\_ABCC2 AACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCG

 SPM-16 (455)AACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCG

 108045

 Hz\_ABCC2 ATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTT**----**GGAGGGCGTTGGAACAGGTACGCTTAATTAAA

 SPM-16 (535)ATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTT**ATAT**GGAGGGCGTTGGAACAGGTACGCTTAATTAAA

 108125

 Hz\_ABCC2 TTACTTCT**C**AACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTT**T**AGGTGGAATTAAAAGAAG

 SPM-16 (615)TTACTTCT**T**AACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTT**-**AGGTGGAATTAAAAGAAG

 108204

 Hz\_ABCC2 GAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCT

 SPM-16 (694)GAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCT

 108285

 Hz\_ABCC2 CGTGCCATTCTACGCTCTAACAAAATACTCATCATGGAC**G**A**A**GCTACCG

 SPM-16 (774)CGTGCCATTCTACGCTCTAACAAAATACTCATCATGGAC**A**A**G**GCTACCG

Figure S3. Alignment of ABCC2 reference genome sequence from 99,062 to 108,844 bp and amplicon sequences from wild type SIMRU and knockout line SPM-A28. The nucleotide sequence of SPM-A28 has a 4,645 bp deletion from 99,733 to 104,378 bp (exon 3 to 13) and an insertion at the sgRNA target site in exon 21. Identical nucleotides are shown in white text with black background and alignment gaps are indicated by hyphens. Deletions and insertions caused by CRISPR/Cas9 editing at sgRNA target sites are marked with red text and nucleotide polymorphisms between the reference genomic scaffold (Accession: KY701524) sequence and amplicon sequences, including those may have been introduced by repair enzymes are shown in dark gray text with white background.

Hz\_ABCC2 (99062)TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCAATCTGCAGCCAGGTA

WT (57)TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCAATCTGCAGCCAGGTA

SPM-A28 (1)TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCAATCTGCAGCCAGGTA

Hz\_ABCC2 (99142)CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG

WT (137)CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG

SPM-A28 (81)CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG

Hz\_ABCC2 (99222)TAAAAGTAATGGTCAAATTCGTTTTTTCAAGGCTAGTGACAGCAAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT

WT (217)TAAAAGTAATGGTCAAATTCGTTTTT-CAAGGCTAGTGACAGCAAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT

SPM-A28 (161)TAAAAGTAATGGTCAAATTCGTTTTTTCAAGGCTAGTGACAGCAAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT

Hz\_ABCC2 (99302)ACTTTAAACATTACTTTGATTTTTACTTTGGATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCCTAA

WT (296)ATTTTAAACATTACTTTGATTTTTACTTTG-ATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCCTAA

SPM-A28 (241)ACTTTAAACATTACTTTGATTTTTACTTTGGATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCCTAA

Hz\_ABCC2 (99382)AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATTCTCTTCTTCAAAAGGTGTACTCAA

WT (375)AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATTCTCTTCTTCAAAAGGTGTACTCAA

SPM-A28 (321)AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATTCTCTTCTTCAAAAGGTGTACTCAA

Hz\_ABCC2 (99462)AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG

WT (455)AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG

SPM-A28 (401)AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG

Hz\_ABCC2 (99542)TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG

WT (535)TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG

SPM-A28 (481)TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG

Hz\_ABCC2 (99622)GTTTCCGTAGAAATTAGATTTTTTTTTCGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG

WT (615)GTTTCCGTAGAAATTAGATTTTTTT--CGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG

SPM-A28 (561)GTTTCCGTAGAAATTAGATTTTTTT--CGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG

Hz\_ABCC2 (99702)CCGCTGTTGTTTTCTCAGTTACTGTCGTACTG**G**T**CG**G**TGGACAGTGAAATGACTCAGCAAGACGCTGGCCTCTATGCTCT**

WT (693)CCGCTGTTGTTTTCTCAGTTACTGTCGTACTG**G**T**CG**G**TGGACAGTGAAATGACTCAGCAAGACGCTGGCCTCTATGCTCT**

SPM-A28 (639)CCGCTGTTGTTTTCTCAGTTACTGTCGTACTG**A**T**AC**G**ACA----------------------------------------**

Hz\_ABCC2 (99782)**CGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAACACACTGTTTGTGATGCGGTTCAGTTTAAAAG**

WT (773)**CGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAACACACTGTTTGTGATGCGGTTCAGTTTAAAAG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (99862)**TCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGGTGAGCATACTTTTAAGTAGAATAATCTTCCATCGATGTAATTAA**

WT (853)**TCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGGTGAGCATACTTTTAAGTAGAATAATCTTCCATCGATGTAATTAA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (99942)**ACAGGGACAATTAGACCGAAGTTAGGGTGCTTACATAAAGAAACAGGTTTCCGGTACAGATAAACTTGTACGGGTAGGTA**

WT (933)**ACAGGGACAATTAGACCGAAGTTAGGGTGCTTACATAAAGAAACAGGTTTCCGGTACAGATAAACTTGTACGGGTAGGTA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100022)**CCGATCAGTGCAGGTATAATATTTCAATACAATCCTATTCACTCACTTATAAAGAAACAGGTTGTTTACCTGTTTCAACT**

WT (1013)**CCGATCAGTGCAGGTATAATATTTCAATACAATCCTATTCACTCACTTATAAAGAAACAGGTTGTTTACCTGTTTCAACT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100102)**TACCTGTTTCTTTATAAGTGAGTGAATAGGATTGTATTGAAATATTATACCTGCACTGATCGGTACCTACCCGTACAGGT**

WT (1093)**TACCTGTTTCTTTATAAGTGAGTGAATAGGATTGTATTGAAATATTATACCTGCACTGATCGGTACCTACCCGTACAGGT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100182)**TTGTCTGTACCGGTAACCTGTTTCTTTATGTAAACACCCTTAAGATCGTTAAATTAGTTTAATCAACCTATCAGCATTTT**

WT (1173)**TTGTCTGTACCGGTAACCTGTTTCTTTATGTAAACACCCTTAAGATCGTTAAATTAGTTTAATCAACCTATCAGCATTTT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100262)**TATAGACAATATTTTTTTTTCAATAAAAATTGGCCAGATCTGCTTTAAAAGAAGACGTTGACGTTGGCTTTAAAAGAGAC**

WT (1253)**TATAGACAATATTTTTTTT-CAATAAAAATTGGCCAGATCTGCTTTAAAAGAAGACGTTGACGTTGGCTTTAAAAGAGAC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100342)**TGATACTATTTTATTTATTTTTGATATCTTTATTTTAGATATACCTACTTACTTCTTTTTTGAAACTCGATAAAAATTTC**

WT (1332)**TGATACTATTTTATTTATTTTTGATATCTTTATTTTAGATATACCTACTTACTTCTTTTT-GAAACTCGATAAAAATTTC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100422)**TTTGTTCTAGTTGCTCCGCATGACCCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACG**

WT (1411)**TTTGTTCTAGTTGCTCCGCATGACCCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100502)**ATATCACGAGGTTCGACTACGCGTTCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTAC**

WT (1491)**ATATCACGAGGTTCGACTACGCGTTCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100582)**TTCTTGTGGGAGGCTGCTGGCTTCGCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGGTAT**

WT (1571)**TTCTTGTGGGAGGCTGCTGGCTTCGCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGGTAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100662)**GTCATATTAAAACCTTTTTTCAATTTAATATTGTTTCCTTATGTATCCATGTTATTAATCGATGAACTTTTGGCTTTTAG**

WT (1651)**GTCATATTAAAACCTTTTTTCAATTTAATATTGTTTCCTTATGTATCCATGTTATTAATCGATGAACTTTTGGCTTTTAG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100742)**CTGGCTTGACGAAACTCACAACTGTTGTAAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAA**

WT (1731)**CTGGCTTGACGAAACTCACAACTGTTGTAAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100822)**ATTATTGGTGGTATTCAGGTAAAAAAAACTTTTCTTAATTTTTATATATTGACCTATTTAAAATGATGACAAAAATTAAC**

WT (1811)**ATTATTGGTGGTATTCAGTAAAAAAAAACTTTTCTTAATTTTTATATATTGACCTATTTAAAATGATGACAAAAATTAAC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100902)**TGTTTGGTCAATTTCAGGTCATTAAAATGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTT**

WT (1891)**TGTTTGGTCAATTTCAGGTCATTAAAATGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(100982)**GAAATGAGTGCCCTCAGGAAGTCCATCTTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCAT**

WT (1971)**GAAATGAGTGCCCTCAGGAAGTCCATCTTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101062)**GTTTGTCACAGTGTTGACACTCGCTCTCACAGGCACTATGATTACTGCCACTACGGTAAGATTTACTTATTATAATAATT**

WT (2051)**GTTTGTCACAGTGTTGACACTCGCTCTCACAGGCACTATGATTACTGCCACTACGGTAAGATTTACTTATTATAATAATT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101142)**AAATATAAGATATTTTGCCGACCGTTTCATTCCATATATATTAATGGTTTTCGAAATATCGCATCAATCGATTCATCATC**

WT (2131)**AAATATAAGATATTTTGCCGACCGTTTCATTCCATATATATTAATGGTTTTCGAAATATCGCATCAATCGATTCATCATC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101222)**GATTTCCATTCAATTTCGGCAAATTACTACTTAACTAAGTTTGAACAATCGTTCCGATATATAATCTCGATATTATTTCA**

WT (2211)**GATTTCCATTCAATTTCGGCAAATTACTACTTAACTAAGTTTGAACAATCGTTCCGATATATAATCTCGATATTATTTCA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101302)**CAGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTTAACGTAACACTGATCATTCCTATGGCAATCGCAAGTTA**

WT (2291)**CAGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTTAACGTAACACTGATCATTCCTATGGCAATCGCAAGTTA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101382)**TTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGGTAAATATTGTTTCTTTTAAGTTCAATAAA**

WT (2371)**TTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGGTAAATATTGTTTCTTTTAAGTTCAATAAA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101462)**ATTTACACACATTAGGTAGATTGGTATAAAGCGTACAGTGATAATAATACTGAGATTTGATATTTATGTTTTGTAAACAG**

WT (2451)**ATTTACACACATTAGGTAGATTGGTATAAAGCGTACAGTGATAATAATACTGAGATTTGATATTTATGTTTTGTAAACAG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101542)**ACGAGCGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCA**

WT (2531)**ACGAGCGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101622)**CTTGAAGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCA**

WT (2611)**CTTGAAGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101702)**GATGGACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGA**

WT (2691)**GATGGACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101782)**ATATATCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGGTAATTTATTTCATT**

WT (2771)**ATATATCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGGTAATTTATTTCATT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101862)**ATAAATATTTGTTCATATACAGATTTGTTTTTTTTATTTTTTACTTGTAATATTAATATTTTAACTTTTACAGACATCTC**

WT (2851)**ATAAATATTTGTTCATATACAGATTTGTTTTTTTTATTTTTTACTTGTAATATTAATATTTTAACTTTTACAGACATCTC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(101942)**TACTGCAACTGCTCTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAA**

WT (2931)**TACTGCAACTGCTCTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102022)**GAGTCCTGGCTGTTCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGT**

WT (3011)**GAGTCCTGGCTGTTCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102102)**AAATTATTGCAGGTTATGAATGACTTTATTAAATTTTTATTTAGGTGCATAATTATAATAATAATGCGTTTATTTCATGA**

WT (3091)**AAATTATTGCAGGTTATGAATGACTTTATTAAATTTTTATTTAGGTGCATAATTATAATAATAATGCGTTTATTTCATGA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102182)**CTACAATGGTCCAATTGTTAGTAACTTTTCAACTATAACTTATCGACTAAGGGTTAGTAATACCTAAAAACTAAACGTTT**

WT (3171)**CTACAATGGTCCAATTGTTAGTAACTTTTCAACTATAACTTATCGACTAAGGGTTAGTAATACCTAAAAACTAAACGTTT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102262)**GCCTAACAAGCAAGTCCATCCAATGCCTAAGCACCGGAGCATCATGCTTGTCGGCCAAGACTTGTAGGATGCTGTTGTAG**

WT (3251)**GCCTAACAAGCAAGTCCATCCAATGCCTAAGCACCGGAGCATCATGCTTGTCGGCCAAGACTTGTAGGATGCTGTTGTAG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102342)**GATGATGTAATTTATCTTCTATATAATTATATTTAATAATTAATTTATTATAAATAATTAAATTAATAATAATTAATAAT**

WT (3331)**GATGATGTAATTTATCTTCTATATAATTATATTTAATAATTAATTTATTATAAATAATTAAATTAATAATAATTAATAAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102422)**TATATAGAAGATATTTTTTTCTAACTAGCTGATCCCGTGAACTTCGTATCGTTCAAACCTTCCCTGGACCTCTACAAACA**

WT (3411)**TATATAGAAGATATTTTTT-CTAACTAGCTGATCCCGTGAACTTCGTATCGTTCAAACCTTCCCTGGACCTCTACAAACA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102502)**TTTTAAAACCAAAATTAGCTCAATCGGCCCAGCCGTCCTCGAGTTTTAATCAGACTAACGAACAATAATCCATTTTTATT**

WT (3490)**TTTTAAAACCAAAATTAGCTCAATCGGCCCAGCCGTCCTCGAGTTTTAATCAGACTAACGAACAATAATCCATTTTTATT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102582)**TATATAGATTATATTTCTTGTGCGAATTATCTTATGTAGGTATGTCTTCCAAAACATTCATACTTACACCTGTATTTCTT**

WT (3570)**TATATAGATTATATTTCTTGTGCGAATTATCTTATGTAGGTATGTCTTCCAAAACATTCATACTTACACCTGTATTTCTT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102662)**GCGATAGCTTTAAGTTATATTCTTCACCAAAATTAAAAATATGAAAAAGATATGATGTTCAACCACAAACAGAGATTGCA**

WT (3650)**GCGATAGCTTTAAGTTATATTCTTCACCAAAATTAAAAATATGAAAAAGATATGATGTTCAACCACAAACAGAGATTGCA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102742)**CGAGAAACGTTAAAATTTTATAGTCAATTTTCCCGCTGTTTTATAATTCACCCAATTTTCATCTGCCATGGTCTGTTATG**

WT (3730)**CGAGAAACGTTAAAATTTTATAGTCAATTTTCCCGCTGTTTTATAATTCACCCAATTTTCATCTGCCATGGTCTGTTATG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102822)**CATGTAGATATATTTTGTTATGGCAGGTTTGCAAGGTGTGTTCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGAC**

WT (3810)**CATGTAGATATATTTTGTTATGGCAGGTTTGCAAGGTGTGTTCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGAC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102902)**CTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGGTCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCG**

WT (3890)**CTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGGTCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(102982)**TGAGGTAAGCATCTTTCGTTTACGCAGAACTTCTACACATGGTAATAAAACACTTCAGTTGGTTATTCGTGATTCGTAAA**

WT (3970)**TGAGGTAAGCATCTTTCGTTTACGCAGAACTTCTACACATGGTAATAAAACACTTCAGTTGGTTATTCGTGATTCGTAAA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103062)**TCGAGGTATTGATGAAGGACTATATTATGTTCTTGCGACTATTCCTGTTATATGATATCGCAACCACAAGATTAATTGTC**

WT (4050)**TCGAGGTATTGATGAAGGACTATATTATGTTCTTGCGACTATTCCTGTTATATGATATCGCAACCACAAGATTAATTGTC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103142)**GGGGTAATACCTGATAACGTGAAAGTAAACAATTGGTAACAACTTAGTTATATCGGCACTGTAATAATGCGACAGTATAT**

WT (4130)**GGGGTAATACCTGATAACGTGAAAGTAAACAATTGGTAACAACTTAGTTATATCGGCACTGTAATAATGCGACAGTATAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103222)**GCGATACATAATTTGTTTACATTTAACTTTTCTAACAATTTATCAATGAAATCTTTTACATATTGATGAGAGCAACTTAT**

WT (4210)**GCGATACATAATTTGTTTACATTTAACTTTTCTAACAATTTATCAATGAAATCTTTTACATATTGATGAGAGCAACTTAT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103302)**ACATTGTTGTCATTACACCACATTTTCTTAAATCGTGAGCGTGAAACTAAAATCGTGGGCGTATTTTCAGGCCGACATTT**

WT (4290)**ACATTGTTGTCATTACACCACATTTTCTTAAATCGTGAGCGTGAAACTAAAATCGTGGGCGTATTTTCAGGCCGACATTT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103382)**ACTTGCTGGATGATCCCCTATCTGCAGTGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTC**

WT (4370)**ACTTGCTGGATGATCCCCTATCTGCAGTGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103462)**ACTGGACGAACTTGCGTCTTGGTCACCCATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGC**

WT (4450)**ACTGGACGAACTTGCGTCTTGGTCACCCATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103542)**AAGTATGACTACCTATCATTTCATATTTCCATTGAAAGATAACAAAAGTATTTACATTAAAAATATATTTATTGAAGTGA**

WT (4530)**AAGTATGACTACCTATCATTTCATATTTCCATTGAAAGATAACAAAAGTATTTACATTAAAAATATATTTATTGAAGTGA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103622)**TTAATTTTATCTTAACTATTATCTTTGGACGAGTCATTACAACGTAGCAAATTTCCAACACTTCAATATTTACTCTTTGA**

WT (4610)**TTAATTTTATCTTAACTATTATCTTTGGACGAGTCATTACAACGTAGCAAATTTCCAACACTTCAATATTTACTCTTTGA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103702)**ATACTACTTACTTAGTCCAGCTTCAAAATTAATAAAAGTTTCCTAATGGTTTTTTATCAGGGTTCCGTCGAGAATATGGG**

WT (4690)**ATACTACTTACTTAGTCCAGCTTCAAAATTAATAAAAGTTTCCTAATGGTTTTTTATCAGGGTTCCGTCGAGAATATGGG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103782)**CACTTATGATGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACG**

WT (4770)**CACTTATGATGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103862)**AAAAGAAAGTAAGTATGCACTTAATATCTGGTATTTTCCGTGGCGACTTGAACGTTTGCCAGAAAACAGCTTTCAACATT**

WT (4850)**AAAAGAAAGTAAGTATGCACTTAATATCTGGTATTTTCCGTGGCGACTTGAACGTTTGCCAGAAAACAGCTTTCAACATT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(103942)**ATCTTGTCTACATCGTTGCACATGTTCCTAAAACATATCCGAATAAAAAATATAGGTATGAACGAGTATACATCTACCCT**

WT (4930)**ATCTTGTCTACATCGTTGCACATGTTCCTAAAACATATCCGAATAAAAAATATAGGTATGAACGAGTATACATCTACCCT**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(104022)**CGTGTATTGTAATATGTACTGAATAAACATTGTTCATTTTAAATTCTCCTAATAGATTATGCTTAAAAATGCAGCATAGA**

WT (5010)**CGTGTATTGTAATATGTACTGAATAAACATTGTTCATTTTAAATTCTCCTAATAGATTATGCTTAAAAATGCAGCATAGA**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(104102)**TTACACTGGACCTTGTTCAAACAACCCAGAAAAAAATACTATTTACGTTCCTTTCGTCTTAGGACCGACCAGCAATGATG**

WT (5090)**TTACACTGGACCTTGTTCAAACAACCCAGAAAAAAATACTATTTACGTTCCTTTCGTCTTAGGACCGACCAGCAATGATG**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(104182)**CGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAGGAGAGAGC**

WT (5170)**CGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAGGAGAGAGC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(104262)**GACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCTGGTGTTTACGGCGTTCC**

WT (5250)**GACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCTGGTGTTTACGGCGTTCC**

SPM**-**A28 (679)**--------------------------------------------------------------------------------**

Hz\_ABCC2(104342)**TTGTACTGCTGATCACGCAAGGTGCTGCCACCACTG**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC

WT (5330)**TTGTACTGCTGATCACGCAAGGTGCTGCCACCACTG**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC

SPM**-**A28 (679)**------------------------------------**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC

Hz\_ABCC2(104422)AAAAATTTAATTTAACGGAAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA

WT (5410)AAAAATTTAATTTAACGGAAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA

SPM**-**A28 (723)AAAAATTTAATTTAACGGAAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA

Hz\_ABCC2(104502)ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA

WT (5490)ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA

SPM**-**A28 (803)ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA

Hz\_ABCC2(104582)AATATCTCTGTTTTATTTATATGAACTTCCTGCGTATGTACCATTTGCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT

WT (5570)AATATCTCTGTTTTATTTATATGAACTTCCTGCGTATGTACCATTTGCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT

SPM**-**A28 (883)AATATCTCTGTTTTATTTATATGAACTTCCTGCGTATGTACCATTTGCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT

Hz\_ABCC2(104662)ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTT

WT (5650)ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTT

SPM**-**A28 (963)ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTT

Hz\_ABCC2(104742)ATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA

WT (5730)ATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA

SPM**-**A28 (1043)ATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA

Hz\_ABCC2(104822)CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT

WT (5810)CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT

SPM**-**A28 (1123)CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT

Hz\_ABCC2(104902)TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA

WT (5890)TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA

SPM**-**A28 (1203)TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA

Hz\_ABCC2(104982)GATAATGATTTTAAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGTAGGTAATTAGCGATAATTGCAGCTGGCCAA

WT (5970)GATAATGATTTTAAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGTAGGTAATTAGCGATAATTGCAGCTGGCCAA

SPM**-**A28 (1283)GATAATGATTTTAAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGTAGGTAATTAGCGATAATTGCAGCTGGCCAA

Hz\_ABCC2(105062)GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA

WT (6050)GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA

SPM**-**A28 (1363)GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA

Hz\_ABCC2(105142)ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG

WT (6130)ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG

SPM**-**A28 (1443)ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG

Hz\_ABCC2(105222)TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAAATGCAAGAAGATGATGCAAT

WT (6210)TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAAATGCAAGAAGATGATGCAAT

SPM**-**A28 (1523)TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAAATGCAAGAAGATGATGCAAT

Hz\_ABCC2(105302)GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC

WT (6290)GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC

SPM**-**A28 (1603)GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC

Hz\_ABCC2(105382)ATGGGTGCCATGGATGAGCTTCTTCCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT

WT (6370)ATGGGTGCCATGGATGAGCTTCTTCCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT

SPM**-**A28 (1683)ATGGGTGCCATGGATGAGCTTCTTCCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT

Hz\_ABCC2(105462)GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT

WT (6450)GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT

SPM**-**A28 (1763)GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT

Hz\_ABCC2(105542)ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA

WT (6530)ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA

SPM**-**A28 (1843)ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA

Hz\_ABCC2(105622)AATATTGATTTAGAGTGTAAATTAATTAACGGTTAGAACATCGCTAATAGTTTTGACTGCCTCGTTGGTCTAGAGGTCGC

WT (6610)AATATTGATTTAGAGTGTAAATTAATTAACGGTTAGAACATCGCTAATAGTTTTGACTGCCTCGTTGGTCTAGAGGTCGC

SPM**-**A28 (1923)AATATTGATTTAGAGTGTAAATTAATTAACGGTTAGAACATCGCTAATAGTTTTGACTGCCTCGTTGGTCTAGAGGTCGC

Hz\_ABCC2(105702)AAGCGCGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTCATAAACTTT

WT (6690)AAGCGCGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTCATAAACTTT

SPM**-**A28 (2003)AAGCGCGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTCATAAACTTT

Hz\_ABCC2(105782)CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTCACCCGTGCATCGGAGAGCACGTAAATGTCGGTCCTGCGCCT

WT (6770)CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTCACCCGTGCATCGGAGAGCACGTAAATGTCGGTCCTGCGCCT

SPM**-**A28 (2083)CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTCACCCGTGCATCGGAGAGCACGTAAATGTCGGTCCTGCGCCT

Hz\_ABCC2(105862)GATCTCTTTCCGGTCGTGTCGGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC

WT (6850)GATCTCTTTCCGGTCGTGTCGGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC

SPM**-**A28 (2163)GATCTCTTTCCGGTCGTGTCGGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC

Hz\_ABCC2(105942)AAATGCTCGTGCACTATAATATGTCCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCCGTGGCCGAAATCGGC

WT (6930)AAATGCTCGTGCACTATAATATGTCCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCCGTGGCCGAAATCGGC

SPM**-**A28 (2243)AAATGCTCGTGCACTATAATATGTCCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCCGTGGCCGAAATCGGC

Hz\_ABCC2(106022)CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTTTTATTTCTACTTACAGCCAAGAGTCCTGTA

WT (7010)CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTTTTATTTCTACTTACAGCCAAGAGTCCTGTA

SPM**-**A28 (2323)CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTTTTATTTCTACTTACAGCCAAGAGTCCTGTA

Hz\_ABCC2(106102)TTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCCCAGGATAGACAGATGAAATTGTT

WT (7090)TTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCCCAGGATAGACAGATGAAATTGTT

SPM**-**A28 (2403)TTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCCCAGGATAGACAGATGAAATTGTT

Hz\_ABCC2(106182)TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT

WT (7170)TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT

SPM**-**A28 (2483)TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT

Hz\_ABCC2(106262)AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA

WT (7250)AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA

SPM**-**A28 (2563)AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA

Hz\_ABCC2(106342)TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA

WT (7330)TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA

SPM**-**A28 (2643)TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA

Hz\_ABCC2(106422)GCACTTTTTCTTAGGCACATTAAAAGGCAATATTTACACATTTCCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC

WT (7410)GCACTTTTTCTTAGGCACATTAAAAGGCAATATTTACACATTTCCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC

SPM**-**A28 (2723)GCACTTTTTCTTAGGCACATTAAAAGGCAATATTTACACATTTCCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC

Hz\_ABCC2(106502)ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTTTTCTTCCCAGGTGATTTGATCCCGGTGGGAAGTGTCGGTC

WT (7490)ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTT**----**CTTCCCAGGTGATTTGATCCCGGTGGGAAGTGTCGGTC

SPM**-**A28 (2803)ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTT**--**CTTCCCAGGTGATTTGATCCCGGTGGGAAGTGTCGGTC

Hz\_ABCC2(106582)TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTCACAGCTGACTTTTTGGGGCAAATG

WT (7566)TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTCACAGCTGACTTTTTGGGGCAAATG

SPM**-**A28 (2881)TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTCACAGCTGACTTTTTGGGGCAAATG

Hz\_ABCC2(106662)ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC

WT (7646)ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC

SPM**-**A28 (2961)ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC

Hz\_ABCC2(106742)GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACTATGTTCGGTACTT

WT (7726)GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACTATGTTCGGTACTT

SPM**-**A28 (3041)GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACTATGTTCGGTACTT

Hz\_ABCC2(106822)CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACCAGTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG

WT (7806)CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACCAGTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG

SPM**-**A28 (3121)CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACCAGTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG

Hz\_ABCC2(106902)TTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG

WT (7886)TTACC-GGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG

SPM**-**A28 (3201)TTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG

Hz\_ABCC2(106982)ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCT

WT (7965)ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCT

SPM**-**A28 (3281)ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCT

Hz\_ABCC2(107062)CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAG

WT (8045)CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAG

SPM**-**A28 (3361)CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAG

Hz\_ABCC2(107142)GTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTT

WT (8125)GTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTT

SPM**-**A28 (3441)GTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTT

Hz\_ABCC2(107222)CCATGTATTATTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT

WT (8205)CCATGTATTATTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT

SPM**-**A28 (3521)CCATGTATTATTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT

Hz\_ABCC2(107302)GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT

WT (8285)GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT

SPM**-**A28 (3601)GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT

Hz\_ABCC2(107382)AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA**------------------**

WT (8365)AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA**------------------**

SPM**-**A28 (3681)AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA**CGGCTTTGTTCTCTTTGT**

Hz\_ABCC2(107444)**--**TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAA

WT (8427)**--**TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAA

SPM**-**A28 (3761)**TC**TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAA

Hz\_ABCC2(107522)AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA

WT (8505)AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA

SPM**-**A28 (3841)AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA

Hz\_ABCC2(107602)ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAATATCCTTTTTATTGC

WT (8585)ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAATATCCTTTTTATTGC

SPM**-**A28 (3921)ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAATATCCTTTTTATTGC

Hz\_ABCC2(107682)AATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC

WT (8665)AATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC

SPM**-**A28 (4001)AATTTTATTTGCACTCTCTTTTATGAACTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC

Hz\_ABCC2(107762)CCTTATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTA

WT (8745)C--TATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCC-TTATGTACTCCTCTTCTGTACTCCTCTTA

SPM**-**A28 (4081)CCTTATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTA

Hz\_ABCC2(107842)TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGA

WT (8822)TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGA

SPM**-**A28 (4161)TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGA

Hz\_ABCC2(107922)ATCTTATGTCGTCAATTTTTTTTTATTTAGAAAATTGATTCAGCGATAACTTTTTACATTCGCAGACTTTGAGATCGAAA

WT (8902)ATCTTATGTCGTCAATTTTTTTTTA**-**TTTGAAAATTGATTCAGCGATAACTTTTTACATTCGCAGACTTTGAGATCGAAA

SPM**-**A28 (4241)ATCTTATGTCGTCAATTTTTTTAT**--**TTAGAAAATTGATTCAGCGATAACTTTTTACATTCGCAGACTTTGAGATCGAAA

Hz\_ABCC2(108002)ATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGA

WT (8981)ATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGA

SPM**-**A28 (4319)ATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGA

Hz\_ABCC2(108082)CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCTTAACAGACCCTCGGCACTCGAACTAATCT

WT (9061)CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCTTAACAGACCCTCGGCACTCGAACTAATCT

SPM**-**A28 (4399)CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCTTAACAGACCCTCGGCACTCGAACTAATCT

Hz\_ABCC2(108162)AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG

WT (9141)AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG

SPM**-**A28 (4479)AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG

Hz\_ABCC2(108242)TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG

WT (9221)TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG

SPM**-**A28 (4559)TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG

Hz\_ABCC2(108322)ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG

WT (9301)ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG

SPM**-**A28 (4639)ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG

Hz\_ABCC2(108402)GTTTTCCAATGTGTTAAAAGTTTAATTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC

WT (9381)GTTTTCCAATGTGTTAAAAGTTTAATTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC

SPM**-**A28 (4719)GTTTTCCAATGTGTTAAAAGTTTAATTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC

Hz\_ABCC2(108482)TTCCTTATTGGCGAGTTTGTTTCATTTTGTTTCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG

WT (9461)TTCCTTATTGGCGAGTTTGTTTCATTTTGTTTCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG

SPM**-**A28 (4799)TTCCTTATTGGCGAGTTTGTTTCATTTTGTTTCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG

Hz\_ABCC2(108562)AACTTACACGTATTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG

WT (9541)AACTTACACGTATTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG

SPM**-**A28 (4879)AACTTACACGTATTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG

Hz\_ABCC2(108642)TTTGCGTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA

WT (9621)TTTGCGTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA

SPM**-**A28 (4959)TTTGCGTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA

Hz\_ABCC2(108722)GGGCGAAGTGGCCGAGTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA

WT (9701)GGGCGAAGTGGCCGAGTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA

SPM**-**A28 (5039)GGGCGAAGTGGCCGAGTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA

Hz\_ABCC2(108802)CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTCGCTAAGGC

WT (9781)CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTCGCTAAGGC

SPM**-**A28 (5119)CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTCGCTAAGGC

Figure S4. Alignment of ABCC2 reference genome sequence from 104,174 to 108,822 bp and amplicon sequence from knockout line SPM-B1 with 1,876 bp and 10 bp deletions at the sgRNA target sites of exon 13 and exon 19, respectively. Identical nucleotides are shown in white text with black background and alignment gaps are indicated by hyphens. Deletions and insertions caused by CRISPR/Cas9 editing at sgRNA target sites are marked with red text and nucleotide polymorphisms between the reference genomic scaffold (Accession: KY701524) sequence and amplicon sequences, including those may have been introduced by repair enzymes are shown in dark gray text with white background.

Hz\_ABCC2 (104174)CAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAG

 SPM-B1 (1)CAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAG

Hz\_ABCC2 (104254)GAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCTGGTGTTTAC

 SPM-B1 (81)GAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCTGGTGTTTAC

Hz\_ABCC2 (104334)GGCGTTCCTTGTACTGCTGATCACGCAAGGTGCTGCCACCACTG**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAAT**

SPM-B1 (161)GGCGTTCCTTGTACTGCTGATCACGCAAGGTGCTGCCACCACTG**------------------------------------**

Hz\_ABCC2 (104414)**TATTTTTCAAAAATTTAATTTAACGGAAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104494)**GATAGTTAACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104574)**GTCTACGAAATATCTCTGTTTTATTTATATGAACTTCCTGCGTATGTACCATTTGCAGTTCTAAGATCTCAACCTCAACT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104654)**AAAAAGTTATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACTGCCCAGTACCTATACGTTTTCG**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104734)**GTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104814)**AATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104894)**TTCATCATTACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (104974)**TAAGTAGAGATAATGATTTTAAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGTAGGTAATTAGCGATAATTGCAG**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105054)**CTGGCCAAGTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105134)**GGATAATAACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105214)**CATATGTGTAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAAATGCAAGAAGAT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105294)**GATGCAATGAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTCGCAGGTCGTGTGCTGAACAGATTCT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105374)**CAAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105454)**GTGTTGGTGCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105534)**GAGATGGTACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105614)**TAAGAACAAATATTGATTTAGAGTGTAAATTAATTAACGGTTAGAACATCGCTAATAGTTTTGACTGCCTCGTTGGTCTA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105694)**GAGGTCGCAAGCGCGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTCA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105774)**TAAACTTTCACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTCACCCGTGCATCGGAGAGCACGTAAATGTCGGTC**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105854)**CTGCGCCTGATCTCTTTCCGGTCGTGTCGGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (105934)**GTCTGCGCAAATGCTCGTGCACTATAATATGTCCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCCGTGGCCG**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (106014)**AAATCGGCCGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTTTTATTTCTACTTACAGCCAAGA**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (106094)**GTCCTGTATTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCCCAGGATAGACAGATG**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (106174)**AAATTGTTTGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTAT**

SPM**-**B1 (205)**--------------------------------------------------------------------------------**

Hz\_ABCC2 (106254)CCAATAGTAATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTT

SPM**-**B1 (205)CCAATTGTAATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTGGGCGGTT

Hz\_ABCC2 (106334)CTACGGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGAC

SPM**-**B1 (285)TTACGGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGAC

Hz\_ABCC2 (106414)TTTGGTGAGCACTTTTTCTTAGGCACATTAAAAGGCAATATTTACACATTTCCAGTTCATAGTGTGATATCTTTGGCATT

SPM**-**B1 (365)TTTGGTGAGCACTTTTTCTTTGGCACATTAAAAGACAATATTTACACATTTCTAGTTCATAGTGTAATATCTTTGGCATT

Hz\_ABCC2 (106494)ACCATTCCATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTTTTCTTCCCAGGTGATTTGATCCCGGTGGGAAG

SPM**-**B1 (445)ACCATTCCATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTTT**-**CTTCCCAGGTGTTTTGATCCCGGTGGGAAG

Hz\_ABCC2 (106574)TGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTCACAGCTGACTTTTTGG

SPM**-**B1 (524)TGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCATTTAGGTTCACAGCTGACTTTTTGG

Hz\_ABCC2 (106654)GGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGG**AGACCAATAT**GGAGCAAGGACGTAAGTAC

SPM**-**B1 (604)GGCAAATGACGGCTGTGGAGAGAGTTCTGGAAAACACCCAGCTACCCACGG**----------**GGAGCAAGGACGTAAGTAC

Hz\_ABCC2 (106734)AATCATTCGTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACTATGTT

SPM**-**B1 (674)AATCATTCGTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACTATGTT

Hz\_ABCC2 (106814)CGGTACTTCTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACCAGTTTTTACATAGGCGACTGCCTATCTGAACTTCT

SPM**-**B1 (754)CGGTACTTCTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACCAGTTTTTACATAGGCGACTGCCTATCTGAACTTCT

Hz\_ABCC2 (106894)AAATCTAGTTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAA

SPM**-**B1 (834)AAATCTAGTTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAA

Hz\_ABCC2 (106974)CAAGGACGATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGT

SPM**-**B1 (914)CAAGGACGATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGT

Hz\_ABCC2 (107054)GACGTTCTCAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCG

SPM**-**B1 (994)GACGTTCTCAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCG

Hz\_ABCC2 (107134)GCTGGAAGGTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTA

SPM**-**B1 (1074)GCTGGAAGGTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTA

Hz\_ABCC2 (107214)CCCGTGTTCCATGTATTATTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCA

SPM**-**B1 (1154)CCCGTGTTCCATGTATTATTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCA

Hz\_ABCC2 (107294)ATTATACTGTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTT

SPM**-**B1 (1234)ATTATACTGTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTT

Hz\_ABCC2 (107374)GCTTACTTAATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCATCGCGGCTTT

SPM**-**B1 (1314)GCTTACTTAATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCATCGCGGCTTT

Hz\_ABCC2 (107454)GTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGT

SPM**-**B1 (1394)GTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGT

Hz\_ABCC2 (107534)TAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTT

SPM**-**B1 (1474)TAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTT

Hz\_ABCC2 (107614)GTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAATATCCTTTTTATTGCAATTTTATTTGC

SPM**-**B1 (1554)GTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAATATCCTTTTTATTGCAATTTTATTTGC

Hz\_ABCC2 (107694)ACTCTCTTTTATGAACTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTC

SPM**-**B1 (1634)ACTCTCTTTTATGAACTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTC

Hz\_ABCC2 (107774)TCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGT

SPM**-**B1 (1714)TCTTACGTACCCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGT

Hz\_ABCC2 (107854)CGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGT

SPM**-**B1 (1794)CGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGT

Hz\_ABCC2 (107934)CAATTTTTTTTTATTTAGAAAATTGATTCAGCGATAACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATT

SPM**-**B1 (1874)CAATTTTTTTTTATTTAGAACATTGATTCAGCGATAACTTTTTACATTCGCAGACTTTGAGATCGAAAATATCAATTATT

Hz\_ABCC2 (108014)CCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTTG

SPM**-**B1 (1954)CCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTTG

Hz\_ABCC2 (108094)GAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCTTAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATG

SPM**-**B1 (2034)GAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCTCAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATG

Hz\_ABCC2 (108174)AATCTATGATTTTAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTC

SPM**-**B1 (2114)AATCTATGATTTTAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTC

Hz\_ABCC2 (108254)TATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

SPM**-**B1 (2194)TATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

Hz\_ABCC2 (108334)CTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAGGTTTTCCAATGT

SPM**-**B1 (2274)CTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAGGTTTTCCAATGT

Hz\_ABCC2 (108414)GTTAAAAGTTTAATTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGACTTCCTTATTGGC

SPM**-**B1 (2354)GTTAAAAGTTTAATTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGACTTCCTTATTGGC

Hz\_ABCC2 (108494)GAGTTTGTTTCATTTTGTTTCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAGAACTTACACGTA

SPM**-**B1 (2434)GAGTTTGTTTCATTTTGTTTCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAGAACTTACACGTA

Hz\_ABCC2 (108574)TTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGC

SPM**-**B1 (2514)TTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGC

Hz\_ABCC2 (108654)ACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGC

SPM**-**B1 (2594)ACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGC

Hz\_ABCC2 (108734)CGAGTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCA

SPM**-**B1 (2674)CGAGTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCA

Hz\_ABCC2 (108814)TGACAAGGA

SPM**-**B1 (2754)TGACAAGGA

Figure S5. Alignment of partial mRNA sequences of *Helicoverpa zea* ABCC2 from knockout lines SPM-8, SPM-16, SPM-B1, and SPM-A28C with *H. zea* ABCC2 mRNA sequence KM360184 from GenBank. Identical nucleotides are shown in white text with black background and alignment gaps are indicated by hyphens.

KM360184 (1) ATGGGCGTAGAAAATAAGAATAATGTACAAAATGCGGAAGGTCCGGCCCGCAAGACTTACAAAAAACCGAACATTTTATC

SPM-8 (1) --------------------------------------------------------------------------------

SPM-16 (1) --------------------------------------------------------------------------------

SPM-B1 (1) --------------------------------------------------------------------------------

SPM-A28C (1) --------------------------------------------------------------------------------

KM360184 (81) CCGTATATTTCTCTGGTGGATGTGTCCTGTGCTTATAACACACTTTAACAAAAGAAATGTAGAAGAATCAGATCTTATAC

SPM-8 (1) --------------------------------------------------------------------------------

SPM-16 (1) --------------------------------------------------------------------------------

SPM-B1 (1) --------------------------------------------------------------------------------

SPM-A28C (1) --------------------------------------------------------------------------------

KM360184 (161) CGCCCAGTAATTTATATAATTCAGAAAGACAAGGAGAGTATCTTGAAAGATACTGGTTGGCAGAGATAGAAAATGCAACA

SPM-8 (1) --------------------------------------------------------------------------------

SPM-16 (1) --------------------------------------------------------------------------------

SPM-B1 (1) --------------------------------------------------------------------------------

SPM-A28C (1) --------------------------------------------------------------------------------

KM360184 (241) ATTGAAAATCGGGAGCCGTCACTATGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT

SPM-8 (1) ------------------------TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT

SPM-16 (1) ------------------------TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT

SPM-B1 (1) ------------------------TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT

SPM-A28C (1) ------------------------TGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT

KM360184 (321) CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGCTACTGTCGTACTGGTCGGTGGACAGTGAAA

SPM-8 (57) CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTCGTACTGGTCGGTGGACAGTGAAA

SPM-16 (57) CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTCGTACTGGTCGGTGGACAGTGAAA

SPM-B1 (57) CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTCGTACTGGTCGGTGGACAGTGAAA

SPM-A28C (57) CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTCGTACTGATACG------------

KM360184 (401) TGACTCAGCAAGACGCTGGCCTGTATGCTCTCGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAAC

SPM-8\_mRNA(137) TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAAC

SPM-16 (137) TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAAC

SPM-B1 (137) TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGTCTCCATGATGTGTCAGCACCACAAC

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (481) ACACTGTTTGTGATGCGGTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC

SPM-8\_mRNA(217) ACACTGTTTGTGATGCGGTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC

SPM-16 (217) ACACTGTTTGTGATGCGGTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC

SPM-B1 (217) ACACTGTTTGTGATGCGGTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (561) CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACGATATCACGAGGTTCGACTACGCGT

SPM-8\_mRNA(297) CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACGATATCACGAGGTTCGACTACGCGT

SPM-16 (297) CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACGATATCACGAGGTTCGACTACGCGT

SPM-B1 (297) CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACTTGCTGTCCAACGATATCACGAGGTTCGACTACGCGT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (641) TCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTACTTCTTGTGGGAGGCTGCTGGCTTC

SPM-8\_mRNA(377) TCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC

SPM-16 (377) TCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC

SPM-B1 (377) TCATGTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (721) GCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACTGTTGT

SPM-8\_mRNA(457) GCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACTGTTGT

SPM-16 (457) GCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACTGTTGT

SPM-B1 (457) GCACCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACTGTTGT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (801) AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA

SPM-8\_mRNA(537) AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA

SPM-16 (537) AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA

SPM-B1 (537) AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (881) TGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC

SPM-8\_mRNA(617) TGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC

SPM-16 (617) TGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC

SPM-B1 (617) TGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (961) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTCACAGTGTTGACACTCGCTCT

SPM-8\_mRNA(697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTCACAGTGTTGACACTCGCTCT

SPM-16 (697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTCACAGTGTTGACACTCGCTCT

SPM-B1 (697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTCACAGTGTTGACACTCGCTCT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1041) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTCAATGTAACACTGA

SPM-8\_mRNA(777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTTAACGTAACACTGA

SPM-16 (777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTTAACGTAACACTGA

SPM-B1 (777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTCAGTTTAACGTAACACTGA

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1121) TCATTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGACGAG

SPM-8\_mRNA(857) TCATTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGACGAG

SPM-16 (857) TCATTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGACGAG

SPM-B1 (857) TCATTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCTTAGTTTGGACGAG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1201) CGGTCCGACATGCAAGTGACTCCAAAAATGAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA

SPM-8 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA

SPM-16 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA

SPM-B1 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1281) AGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG

SPM-8 (1017) AGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG

SPM-16 (1017) AGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG

SPM-B1 (1017) AGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1361) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA

SPM-8 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA

SPM-16 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA

SPM-B1 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1441) TCGTTACGTATACGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGACATCTCTACTGCAACTGCT

SPM-8 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGACATCTCTACTGCAACTGCT

SPM-16 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGACATCTCTACTGCAACTGCT

SPM-B1 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGACATCTCTACTGCAACTGCT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1521) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCTTGGCTGT

SPM-8 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCCTGGCTGT

SPM-16 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCCTGGCTGT

SPM-B1 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCCTGGCTGT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1601) TCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT

SPM-8 (1337) TCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT

SPM-16 (1337) TCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT

SPM-B1 (1337) TCCCAGGCACAGTACGAGAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT

SPM-A28C (125) --------------------------------------------------------------------------------

 1681 1760

KM360184 (1681) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG

SPM-8 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG

SPM-16 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG

SPM-B1 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1761) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCTATCTGCAG

SPM-8 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCTATCTGCAG

SPM-16 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCTATCTGCAG

SPM-B1 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCTATCTGCAG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1841) TGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC

SPM-8 (1577) TGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC

SPM-16 (1577) TGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC

SPM-B1 (1577) TGGACGCTAATGTAGGCAGACAACTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (1921) CATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGGTTCCGTCGAGAATATGGGCACTTATGA

SPM-8 (1657) CATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGGTTCCGTCGAGAATATGGGCACTTATGA

SPM-16 (1657) CATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGGTTCCGTCGAGAATATGGGCACTTATGA

SPM-B1 (1657) CATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGGTTCCGTCGAGAATATGGGCACTTATGA

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (2001) TGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG

SPM-8 (1737) TGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG

SPM-16 (1737) TGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG

SPM-B1 (1737) TGAGCTGGTGAAGACAGGAACTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (2081) ACCGACCAGCAATGATGCGAGGAATATCGAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG

SPM-8 (1817) ACCGACCAGCAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG

SPM-16 (1817) ACCGACCAGCAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG

SPM-B1 (1817) ACCGACCAGCAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (2161) GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCT

SPM-8 (1897) GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCT

SPM-16 (1897) GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCT

SPM-B1 (1897) GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCTGGTGTCT

SPM-A28C (125) --------------------------------------------------------------------------------

KM360184 (2241) GGTGTTTACGGCGTTCCTTGTACTGCTGATCACGCAAGGTGCTGCCACCACTGCCGACTATTGGTTGAGTTTCTGGACTA

SPM-8 (1977) GGTGTTTACGGCGTTCCTTGTACTGCTGATCACGCAAGGTGCTGCCACCACTGCCGACTATTGGTTGAGTTTCTGGACTA

SPM-16 (1977) GGTGTTTACGGCGTTCCTTGTACTGCTGATCACGCAAGGTGCTGCCACCACTGCCGACTATTGGTTGAGTTTCTGGACTA

SPM-B1 (1977) GGTGTTTACGGCGTTCCTTGTACTGCTGATCACGCAAG------------------------------------------

SPM-A28C (125) --------------------------------------------------ACACCGACTATTGGTTGAGTTTCTGGACTA

KM360184 (2321) ACCAAGTAGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT

SPM-8 (2057) ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT

SPM-16 (2057) ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (155) ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT

KM360184 (2401) ACAACTGCTCAGTACCTATACGTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT

SPM-8 (2137) ACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT

SPM-16 (2137) ACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (235) ACAACTGCCCAGTACCTATACGTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT

KM360184 (2481) CGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT

SPM-8 (2217) CGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT

SPM-16 (2217) CGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (315) CGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT

KM360184 (2561) TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT

SPM-8 (2297) TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT

SPM-16 (2297) TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (395) TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT

KM360184 (2641) CTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGTGCTGAACGCCACTGCATTGCCCTGGACGCTTAT

SPM-8 (2377) CTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGTGCTGAACGCCACTGCATTGCCCTGGACGCTTAT

SPM-16 (2377) CTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGTGCTGAACGCCACTGCATTGCCCTGGACGCTTAT

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (475) CTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGTGCTGAACGCCACTGCATTGCCCTGGACGCTTAT

KM360184 (2721) ACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGTACCTGAATACAGCTCAGGCTGTCAAACGTTTGG

SPM-8 (2457) ACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGTACCTGAATACAGCTCAGGCTGTCAAACGTTTGG

SPM-16 (2457) ACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGTACCTGAATACAGCTCAGGCTGTCAAACGTTTGG

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (555) ACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGTACCTGAATACAGCTCAGGCTGTCAAACGTTTGG

KM360184 (2801) AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCC

SPM-8 (2537) AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCC

SPM-16 (2537) AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCC

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (635) AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCC

KM360184 (2881) CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC

SPM-8 (2617) CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC

SPM-16 (2617) CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (715) CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC

KM360184 (2961) GGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG

SPM-8 (2697) GGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG

SPM-16 (2697) GGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG

SPM-B1 (2018) --------------------------------------------------------------------------------

SPM-A28C (795) GGCATTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG

KM360184 (3041) GTGATTTGATCCCGGTGGGAAGTGTCGGTCTGGCTGTCGGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT

SPM-8 (2777) GTGATTTGATCCCGGTGGGAAGTGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT

SPM-16 (2777) GTGATTTGATCCCGGTGGGAAGTGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT

SPM-B1 (2018) GTGTTTTGATCCCGGTGGGAAGTGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCATTT

SPM-A28C (875) GTGATTTGATCCCGGTGGGAAGTGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT

KM360184 (3121) AGGTCCACAGCTGACTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA

SPM-8 (2857) AGGTTCACAGCTGACTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA

SPM-16 (2857) AGGTTCACAGCTGACTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA

SPM-B1 (2095) AGGTTCACAGCTGACTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAAAACACCCAGCTACCCACGG-------

SPM-A28C (955) AGGTTCACAGCTGACTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA

KM360184 (3201) TATGGAGCAAGGACCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT

SPM-8 (2937) TATGGAGCAAGGACCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT

SPM-16 (2937) TATGGAGCAAGGACCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT

SPM-B1 (2168) ---GGAGCAAGGAC-----------------GAATGGCCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT

SPM-A28C (1035) TATGGAGCAAGGACCAACTAACCCACCAAAGGAATGGCCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT

KM360184 (3281) ATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTTGGAGTTGTAGGCAGA

SPM-8 (3017) ATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTTGGAGTTGTAGGCAGA

SPM-16 (3017) ATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTTGGAGTTGTAGGCAGA

SPM-B1 (2228) ATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTTGGAGTTGTAGGCAGA

SPM-A28C (1115) ATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCGGCTGGAAGGTTGGAGTTGTAGGCAGA

KM360184 (3361) ACAGGAGCCGGCAAGTCATCGCTCA--------------------TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC

SPM-8 (3097) ACAGGAGCCGGCAAGTCATCGCTC--------------------------------------------------------

SPM-16 (3097) ACAGGAGCCGGCAAGTCATCAC--A------------------------------------------TGAAATTAAATAC

SPM-B1 (2308) ACAGGAGCCGGCAAGTCATCGCTCA--------------------TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC

SPM-A28C (1195) ACAGGAGCCGGCAAGTCATCGCTCACGGCTTTGTTCTCTTTGTTCTCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC

KM360184 (3421) AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA

SPM-8 (3121) --------------------------------------------------------------------------------

SPM-16 (3133) GTTG-----ATATACTG-GTTAATAC------ATTTGTAGGAAAAACTTTGAGATCGAAAATATCAATTATTCCACAAGA

SPM-B1 (2368) AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA

SPM-A28C (1275) AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA

KM360184 (3501) GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTT----GGAGG

SPM-8 (3121) ----------------------------------------------------------------------------GAGG

SPM-16 (3201) GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTTATATGGAGG

SPM-B1 (2448) GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTT----GGAGG

SPM-A28C (1355) GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTCGACGATTACAGCGACGACGATATTT----GGAGG

KM360184 (3577) GCGTTGGAACAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT

SPM-8 (3125) GCGTTGGAACAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT

SPM-16 (3281) GCGTTGGAACAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT

SPM-B1 (2524) GCGTTGGAACAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT

SPM-A28C (1431) GCGTTGGAACAGGTGGAATTAAAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT

KM360184 (3657) GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCGCTA

SPM-8 (3205) GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCGCTA

SPM-16 (3361) GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCGCTA

SPM-B1 (2604) GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCGCTA

SPM-A28C (1511) GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCGCTA

KM360184 (3737) ACGTCGATCCTCAGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGCACGGTGCTCACCATCGCG

SPM-8 (3285) ACGTCGATCCTCAGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGCACGGTGCTCACCATCGCG

SPM-16 (3441) ACGTCGATCCTCAGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGCACGGTGCTCACCATCGCG

SPM-B1 (2684) ACGTCGATCCTCAGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGCACGGTGCTCACCATCGCG

SPM-A28C (1521) ACGTCGATCCTCAGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTGCGTCGTGCACGGTGCTCACCATCGCG

KM360184 (3817) CATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGCCGAGTTCGACCATCCCCA

SPM-8 (3365) CATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGCCGAGTTCGACCATCCCCA

SPM-16 (3521) CATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGCCGAGTTCGACCATCCCCA

SPM-B1 (2764) CATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGCCGAGTTCGACCATCCCCA

SPM-A28C (1521) CATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGGCCGAGTTCGACCATCCCCA

KM360184 (3897) CATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCATGACAAGGACCTTAATGG

SPM-8 (3445) CATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCATGACAAGGACCTTAATGG

SPM-16 (3601) CATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCATGACAAGGACCTTAATGG

SPM-B1 (2844) CATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCATGACAAGGACCTTAATGG

SPM-A28C (1521) CATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCATGACAAGGACCTTAATGG

KM360184 (3977) AGGTCGCTAAGGCCAAATATGATAGTGATAATAAGGAAGCTTAA

SPM-8 (3525) AGGTCGCTAAGGC-------------------------------

SPM-16 (3681) AGGTCGCTAAGGC-------------------------------

SPM-B1 (2924) AGGTCGCTAAGGC-------------------------------

SPM-A28C (1521) AGGTCGCTAAGGC-------------------------------

Figure S6. Alignment of putative amino acid sequences predicted from partial mRNA sequences of *Helicoverpa zea* ABCC2 gene knockout lines SPM-8, SPM-16, SPM-B1, and SPM-A28C with the ABCC2 amino acid sequence AKH49600 from GenBank. Identical amino acids are shown by white text in black background and alignment gaps are shown with a hyphen.

KM360184 (1) MGVENKNNVQNAEGPARKTYKKPNILSRIFLWWMCPVLITHFNKRNVEESDLIPPSNLYNSERQGEYLERYWLAEIENAT

SPM-8 (1) --------------------------------------------------------------------------------

SPM-16 (1) --------------------------------------------------------------------------------

SPM-B1 (1) --------------------------------------------------------------------------------

SPM-A28C (1) --------------------------------------------------------------------------------

KM360184 (81) IENREPSLWKALRKAYWVSYMPGAIFIIIQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMMCQHHN

SPM-8 (1) --------WKALRKAYWVSYMPGAIFIIIQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMMCQHHN

SPM-16 (1) --------WKALRKAYWVSYMPGAIFIIIQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMMCQHHN

SPM-B1 (1) --------WKALRKAYWVSYMPGAIFIIIQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMMCQHHN

SPM-A28C (1) --------WKALRKAYWVSYMPGAIFIIIQSAARTYQPLLFSQLLSY---------------------------------

KM360184 (161) TLFVMRFSLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF

SPM-8 (73) TLFVMRFSLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF

SPM-16 (73) TLFVMRFSLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF

SPM-B1 (73) TLFVMRFSLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (241) APFVGLFGVVILILPLQAGLTKLTTVVRRETAKRTDRRIKLMSEIIGGIQVIKMYAWEKPFQLVVKAARAFEMSALRKSI

SPM-8 (153) APFVGLFGVVILILPLQAGLTKLTTVVRRETAKRTDRRIKLMSEIIGGIQVIKMYAWEKPFQLVVKAARAFEMSALRKSI

SPM-16 (153) APFVGLFGVVILILPLQAGLTKLTTVVRRETAKRTDRRIKLMSEIIGGIQVIKMYAWEKPFQLVVKAARAFEMSALRKSI

SPM-B1 (153) APFVGLFGVVILILPLQAGLTKLTTVVRRETAKRTDRRIKLMSEIIGGIQVIKMYAWEKPFQLVVKAARAFEMSALRKSI

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (321) FIRSTFLGFMLFTERSIMFVTVLTLALTGTMITATTIYPIQQYFSIIQFNVTLIIPMAIASYSEMMVSIERIQGFLSLDE

SPM-8 (233) FIRSTFLGFMLFTERSIMFVTVLTLALTGTMITATTIYPIQQYFSIIQFNVTLIIPMAIASYSEMMVSIERIQGFLSLDE

SPM-16 (233) FIRSTFLGFMLFTERSIMFVTVLTLALTGTMITATTIYPIQQYFSIIQFNVTLIIPMAIASYSEMMVSIERIQGFLSLDE

SPM-B1 (233) FIRSTFLGFMLFTERSIMFVTVLTLALTGTMITATTIYPIQQYFSIIQFNVTLIIPMAIASYSEMMVSIERIQGFLSLDE

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (401) RSDMQVTPKMNGSNNNTLFKSKKSPLEVGIVPKKYSPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSSEMTLKNI

SPM-8 (313) RSDMQVTPKINGSNNNTLFKSKKSPLEVGIVPKKYSPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSSEMTLKNI

SPM-16 (313) RSDMQVTPKINGSNNNTLFKSKKSPLEVGIVPKKYSPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSSEMTLKNI

SPM-B1 (313) RSDMQVTPKINGSNNNTLFKSKKSPLEVGIVPKKYSPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSSEMTLKNI

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (481) SLRIRKGKLCAIIGPVGSGKTSLLQLLLKELPLNSGTLDVSGKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC

SPM-8 (393) SLRIRKGKLCAIIGPVGSGKTSLLQLLLKELPLNSGTLDVSGKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC

SPM-16 (393) SLRIRKGKLCAIIGPVGSGKTSLLQLLLKELPLNSGTLDVSGKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC

SPM-B1 (393) SLRIRKGKLCAIIGPVGSGKTSLLQLLLKELPLNSGTLDVSGKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (561) SLLPDFKQFPYGDLSLVGERGVSLSGGQRARINLARAIYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT

SPM-8 (473) SLLPDFKQFPYGDLSLVGERGVSLSGGQRARINLARAIYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT

SPM-16 (473) SLLPDFKQFPYGDLSLVGERGVSLSGGQRARINLARAIYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT

SPM-B1 (473) SLLPDFKQFPYGDLSLVGERGVSLSGGQRARINLARAIYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (641) HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ

SPM-8 (553) HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ

SPM-16 (553) HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ

SPM-B1 (553) HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (721) EAEERATGSLKFEVVLKYLSSVQSWCLVFTAFLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVDPDTDMNAQIGLL

SPM-8 (633) EAEERATGSLKFEVVLKYLSSVQSWCLVFTAFLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVDPDTDMNAQIGLL

SPM-16 (633) EAEERATGSLKFEVVLKYLSSVQSWCLVFTAFLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVDPDTDMNAQIGLL

SPM-B1 (633) EAEERATGSLKFEVVLKYLSSVQSWCLVFTAFLVLLITQ-----------------------------------------

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (801) TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNPSGRVLNRFSKDMGAMDELLPRS

SPM-8 (713) TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNPSGRVLNRFSKDMGAMDELLPRS

SPM-16 (713) TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNPSGRVLNRFSKDMGAMDELLPRS

SPM-B1 (672) --------------------------------------------------------------------------------

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (881) LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMLRWYLNTAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS

SPM-8 (793) LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMLRWYLNTAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS

SPM-16 (793) LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMLRWYLNTAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS

SPM-B1 (672) --------------------------------------------------------------------------------

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (961) QDRQMKLFDEAQNLHTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVGQSMVLTMMLQMAA

SPM-8 (873) QDRQMKLFDEAQNLHTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVSQSMVLTMMLQMAA

SPM-16 (873) QDRQMKLFDEAQNLHTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVSQSMVLTMMLQMAA

SPM-B1 (672) -----------------------------------------------------GVLIPVGSVGLAVSQSMVLTMMLQMAF

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (1041) RSTADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFSNVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR

SPM-8 (953) RFTADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFSNVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR

SPM-16 (953) RFTADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFSNVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR

SPM-B1 (699) RFTADFLGQMTAVERVLENTQLPTGSKD---------EWPSAGRVTFSNVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (1121) TGAGKSSLIAALFRLSDISGSIKIDGVDTEGLAKKTLRSKISIIPQEPVLFSATLRYNLDPFDDYSDDDIWRALEQVELK

SPM-8 (1033) TGAGKSSLEGVGTGGIKRRNTGFRL-------------------------------------------------------

SPM-16 (1033) TGAGKSSHEIKYVDILVNTFVG------------KTLRSKISIIPQEPVLFSATLRYNLDPFDDYSDDDIYMEGVGTGGI

SPM-B1 (770) TGAGKSSLIAALFRLSDISGSIKIDGVDTEGLAKKTLRSKISIIPQEPVLFSATLRYNLDPFDDYSDDDIWRALEQVELK

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (1201) EGIPALDFKVAEGGTNFSMGQRQLVCLARAILRSNKILIMDEATANVDPQTDALIQKTIRRQFASCTVLTIAHRLNTIMD

SPM-8 (1058) --------------------------------------------------------------------------------

SPM-16 (1101) KRRNTGFRL-----------------------------------------------------------------------

SPM-B1 (850) EGIPALDFKVAEGGTNFSMGQRQLVCLARAILRSNKILIMDEATANVDPQTDALIQKTIRRQFASCTVLTIAHRLNTIMD

SPM-A28C (40) --------------------------------------------------------------------------------

KM360184 (1281) SDRVLVMDQGEVAEFDHPHILLSNPNSKFFSMVRETGESMTRTLMEVAKAKYDSDNKEA

SPM-8 (1058) -----------------------------------------------------------

SPM-16 (1110) -----------------------------------------------------------

SPM-B1 (930) SDRVLVMDQGEVAEFDHPHILLSNPNSKFFSMVRETGESMTRTLMEVAK----------

SPM-A28C (40) -----------------------------------------------------------

Figure S7. Analysis of potential off-targets for sgRNA for exon 13 (5’-CTGCCGACTATTGGTTGAGT-3’) and exon 19 (5’- TTGCTCCATATTGGTCTCCG-3’) in *Helicoverpa zea* ABCC2 gene knockout lines SPM-A28C and SPM-B1. Off-targets for exon 19 sgRNA located in genomic scaffold KZ117297 were examined by amplifying genomic DNA from wild type insects and knockout lines using primers 4032 (5’-CTGAACACAAATGCGCAAATCG-3’) and 4033 (5’-CGTGTTTACGACATGCCGAT-3’) (**A**), and 4034 (5’-ACGCGTTTAATGAGTACAACCG-3’) and 4035 (5’-ATGCAGTAGGTTAGGCGCCT-3’) (**B**). Primer pair 4036 (5’-TTATGACTTGGTTGCCACAACC-3’) and 4037 (5’-CGCCCTTATAGGTACGCCTT-3’) was used to amplify the potential off-target site for exon 19 sgRNA located in *H. zea* genomic scaffold KZ1176187 (**C**). Primer pair 4038 (5’-CAGGTCCTAAATATTCATGCACC-3’) and 4039 (5’-CATGGCCTTTGTTTGTGGAT-3’) was used to amplify the potential off target site for exon 13 sgRNA located in the in the *H. zea* genomic scaffold KZ118710 (**D**). Identical nucleotides are shown in white text in black background and variations from the reference sequence are shown by black text. Potential off-target sequences and protospacer adjacent sequence (PAM) are marked by black text and red text in green background, respectively.

**A.**

KZ117297\_ AGTTTAGATAAGCTCAATAACTGTGTTA**CCACGGAGACCAATGAATCACAC**AGAAGAGACTAATGATAGATAGATAATA

WT AGTTTAGATAAGCTTAATAACTGTGTTA**CCACGGAGACCAATGAATCACAC**AGAAGAGACTAATGATAGATAGATAATA

SPM-28C AGTTTAGATAAGCTTAATAACTGTGTTA**CCACGGAGACCAATGAATCACAC**AGAAGAGACTAATGATAGATAGATAATA

SPM-B1 AGTTTAGATAAGCTTAATAACTGTGTTA**CCACGGAGACCAATGAATCACAC**AGAAGAGACTAATGATAGATAGATAATA

**B.**

KZ117297 CGAATGCGCACATAATTTTATATCTAAA**CCACGGAGAACAAAATTACTAGC**GGAGGTGCCATAGTGGAAAATCGCCTAA

WT CGAATGCGCACATAATTTTATATCTAAA**CCACGGAGAACTAAATTACTAGC**GGAGGTGCCATAGTGGAAAATCGCCTAA

SPM-28C CGAATGCGCACATAATTTTATATCTAAA**CCACGGAGAACAAAATTACTAGC**GGAGGTGCCATAGTGGAAAATCGCCTAA

SPM-B1 CGAATGCGCACATAATTTTATATCTAAA**CCACGGAGAACAAAATTACTAGC**GGAGGTGCCATAGTGGAAAATCGCCTAA

**C.**

KZ117617 GAATTTGATATTGACTTTTAAGCCCTCT**CCACGGAGACCAATAAGAGTAAG**ACACAGAGTAAGGAAAGATGAGTGGAGA

WT GAATTTGATATTGACTTTTAAGCCCTCT**CCACGGAGACCAATAAGAGTAAG**ACACAGAGTAAGGAAAGATGAGTGGAGA

SPM-28C GAATTTGATATTGACTTTTAAGCCCTCT**CCACGGAGACCAATAAGAGTAAG**ACACAGAGTAAGGAAAGATGAGTGGAGA

SPM-B1 GAATTTGATATTGACTTTTAAGCCCTCT**CCACGGAGACCAATAAGAGTAAG**ACACAGAGTAAGGAAAGATGAGTGGAGA

**D.**

KZ118710 CGCAATAGTATTTTTAAATAAATAAACG**CAATAACTAATAGTCGGCAGTGG**TTCGCTTGCTCCGTGTCTGGCACTTGGG WT CGCAATAGTATTTTTAAATAAATAAACG**CAATAACTAATAGTCGGCAGTGG**TTCGCTTGCTCCGTGTCTGGCACTTGGG

SPM-28C CGCAATAGTATTTTTAAATAAATAAACG**CAATAACTAATAGTCGGCAGTGG**TTCGCTTGCTCCGTGTCTGGCACTTGGG

SPM-B1 CGCAATAGTATTTTTAAATAAATAAACG**CAATAACTAATAGTCGGCAGTGG**TTCGCTTGCTCCGTGTCTGGCACTTGGG

Table S1. Primer names and sequences used for PCR amplifications and nucleotide sequencing of *Helicoverpa zea* ABCC2 gene and off-target sequences. The last letter of the name indicates the forward (F) or reverse (R) direction or the primer.

|  |  |  |
| --- | --- | --- |
| Primer name  | Primer sequence | purpose |
| 3099HzABC2\_Ex15R | GAAAGCTGTGATTCTGACGA | PCR/Sequencing ABCC2 |
| 3104HzABC2\_Ex19F | GTGGGAAGTGTCGGTCTGGC | PCR/Sequencing ABCC2 |
| 3105HzABC2\_Ex20F | GGAAGACCCGCCGGTGCTGA | PCR/Sequencing ABCC2 |
| 3771Hz\_ABCC2\_Ex21F | TAGGTTGGAGTTGTAGGCAGAAC | Sequencing ABCC2 |
| 3772Hz\_ABCC2\_Int21R | AGGGATGCTAACGGATCATT | Sequencing ABCC2 |
| 3776Hz\_ABCC2\_Ex23R | CGGTAGCTTCGTCCATGATG | Sequencing ABCC2 |
| 3790Hz\_ABCC2\_94063F | GCTGTTTGGCGATAAGACGGC | PCR/Sequencing ABCC2 |
| 3791Hz\_ABCC2\_96886R | CAGCGACCTTAAAGTCTAAAGCCG | PCR/Sequencing ABCC2 |
| 3800Hz\_ABCC2Ex2F | TGGAAGGCATTACGAAAGGC | PCR/Sequencing ABCC2 |
| 3801Hz\_ABCC2Ex3R | CGAAGAACAGGCAACCTTGACT | PCR/Sequencing ABCC2 |
| 3802Hz\_ABCC2Ex8F | GAGCGGTCCGACATGCAAGT | PCR/Sequencing ABCC2 |
| 3803Hz\_ABCC2Ex8R | GACCCCACAGGACCAATGAT | PCR/Sequencing ABCC2 |
| 3804Hz\_ABCC2Ex13F | GACCGACCAGCAATGATGCG | PCR/Sequencing ABCC2 |
| 3805Hz\_ABCC2Ex14R | GGATCCACGCCTTCAGGTAA | PCR/Sequencing ABCC2 |
| 3806Hz\_ABCC2Ex19F | GTGATTTGATCCCGGTGGGA | PCR/Sequencing ABCC2 |
| 3807Hz\_ABCC2Ex20R | GCCATTCCTTTGGTGGGTTA | PCR/Sequencing ABCC2 |
| 3808Hz\_ABCC2Ex23F | CATCATGGACGAAGCTACCG | PCR/Sequencing ABCC2 |
| 3809Hz\_ABCC2Ex24R | GCCTTAGCGACCTCCATTAAG | PCR/Sequencing ABCC2 |
| 4032Hz\_Scf\_18\_190197F | CTGAACACAAATGCGCAAATCG | PCR/Sequencing off targets |
| 4033Hz\_Scf\_18\_190612R | CGTGTTTACGACATGCCGAT | PCR/Sequencing off target |
| 4034Hz\_Scf\_18\_204300F | ACGCGTTTAATGAGTACAACCG | PCR/Sequencing off target |
| 4035Hz\_Scf\_18\_204763R | ATGCAGTAGGTTAGGCGCCT | PCR/Sequencing off target |
| 4036Hz\_Scf219\_70159F | TTATGACTTGGTTGCCACAACC | PCR/Sequencing off target |
| 4037Hz\_Scf219\_70569R | CGCCCTTATAGGTACGCCTT | PCR/Sequencing off target |
| 4038Hz\_Scf86\_289141F | CAGGTCCTAAATATTCATGCACC | PCR/Sequencing off target |
| 4039Hz\_Scf86\_289549R | CATGGCCTTTGTTTGTGGAT | PCR/Sequencing off target |

Table S2: Functional domains of the *Helicoverpa zea* ABCC2 protein predicted using online Simple Modular Architecture Research Tool (SMART: <http://smart.embl-heidelberg.de>)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name of the region** | **Start** | **End** | **Domain** | **E-Value** |
| Transmembrane region | 96 | 113 | TMD1 | N/A |
| Transmembrane region | 139 | 156 | TMD1 | N/A |
| Transmembrane region | 212 | 234 | TMD1 | N/A |
| Transmembrane region | 238 | 260 | TMD1 | N/A |
| Transmembrane region | 336 | 358 | TMD1 | N/A |
| Transmembrane region | 363 | 382 | TMD1 | N/A |
| AAA-Nucleotide Binding | 486 | 659 | NBD1 | 7.96e-11 |
| Transmembrane region | 741 | 763 | TMD2 | N/A |
| Transmembrane region | 805 | 827 | TMD2 | N/A |
| Transmembrane region | 894 | 916 | TMD2 | N/A |
| Transmembrane region | 988 | 1010 | TMD2 | N/A |
| Transmembrane region | 1017 | 1039 | TMD2 | N/A |
| AAA-Nucleotide Binding | 1111 | 1291 | NBD2 | 6.12e-12 |

Table S3. The number of eggs injected, percent larvae hatched, the number of males and females, and the total adults recovered from three rounds of embryo injections with sgRNA/Cas9 nucleoprotein complexes targeting ABCC2 gene in *Helicoverpa zea.*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Injection session | Total Eggs Injected | Total hatched  | % Hatch | Males | Females | Dead larvae and pupae | % Adults (from injected eggs) |
| 1 | 174 | 74 | 42.5 | 30 | 31 | 13 | 35.1 |
| 2A | 167 | 37 | 22.2 | 15 | 14 | 8 | 17.4 |
| 2B | 65 | 12 | 18.5 | 4 | 5 | 3 | 13.8 |
| Total | 406 | 123 | 30.3 | 47 | 47 | 29 | 23.2 |