

107087

Hz_ABCC2 GGAAGACCCGCCGGTCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTGGA

SPM-8 (1) GGAAGACCCGCCGGTCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTGGA

107167

Hz_ABCC2 TTAATAATAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAAATCCA

SPM-8 (81) TTAATAATAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTACCCGTGTTCCATGTATTATTCAGATAAAATCCA

107247

Hz_ABCC2 TCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACCTGTTCTTTGTGTCTATGATTATCAA

SPM-8 (161) TCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACCTGTTCTTTGTGTCTATGATTATCAA

107327

Hz_ABCC2 GATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTGCTTACTTAATGTAATGAATGTTGTAGGTTGGA

SPM-8 (241) GATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTGCTTACTTAATGTAATGAATGTTGTAGGTTGGA

107407

Hz_ABCC2 GTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGC **TCATCGC** GGCTTTGTTCGGCTTAGTGACATAAGCGGCAGCATCAA

SPM-8 (321) GTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGC ----- GGCTTTGTTCGGCTTAGTGACATAAGCGGCAGCATCAA

107487

Hz_ABCC2 AATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGA

SPM-8 (394) AATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGA

107567

Hz_ABCC2 AGTATTATTTATTGTTTAGTTAAATTACTAATAGAAATTTGTGGATTTGTTGAAAATATATTAACGGCAGGCTCGTGGT

SPM-8 (473) AGTATTATTTATTGTTTAGTTAAATTACTAATAGAAATTTGTGGATTTGTTGAAAATATATTAACGGCAGGCTCGTGGT

107647

Hz_ABCC2 TTCCAGCACCCGGATAAAAAATATCCTTTTATTGCAATTTTATTGCACTCTCTTTTATGAACCTCTCTATGTACTCACC

SPM-8 (553) TTCCAGCACCCGGATAAAAAATATCCTTTTATTGCAATTTTATTGCACTCTCTTTTATGAACCTCTCTATGTACTCACC

107727

Hz_ABCC2 TTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTAC **GTACCCTCTTATGTGCTCTCTTATGTA**

SPM-8 (633) TTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTAT **GTACCCTCTTATGTGCTCTCTTATGTA**

107807

Hz_ABCC2 CTCCCCTTATGTACTCCTCTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGAT

SPM-8 (713) CTCCCCTTATGTACTCCTCTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGAT

107887

Hz_ABCC2 ATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCATTTTTTTTTTATT **TAGAACATTGATTACGCG**

SPM-8 (793) ATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCATTTTTTTTTTATT **AGAAAAATTGATTACGCG**

107967

Hz_ABCC2 ATAACCTTTTACATTTCGACAGACTTTGAGATCGAAAAATCAATTATTCACACAAGAGCCGGTGTCTGTTCTCGGCTACTCTG

SPM-8 (872) ATAACCTTTTACATTTCGACAGACTTTGAGATCGAAAAATCAATTATTCACACAAGAGCCGGTGTCTGTTCTCGGCTACTCTG

108047

Hz_ABCC2 CGATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATAT ----- TTGGAGGGCGTTGGAACAGGTACGCTTAAT

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

108121

Hz_ABCC2 TAAATTACTTCTT **TAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAA**

SPM-8 (1032) TAAATTACTTCTT **TAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATGAATCTATGATTTTAGGTGGAATTAAAA**

108201

Hz_ABCC2 GAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTT

SPM-8 (1112) GAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTT

108281

Hz_ABCC2 GGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

SPM-8 (1192) GGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

Figure S1. Alignment of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (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.

107089

Hz_ABCC2 AAGACCCGCCGGTCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTGATT

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SPM-16 (1) AAGACCCGCCGGTGCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAGGTAAGAGACCTAATAATGTATTGATT
107169
Hz_ABCC2 AAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCCTAACTACCCGTGTTCCATGTATTATTCAGATAAAATCCATC
SPM-16 (81) AAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCCTAACTACCCGTGTTCCATGTATTATTCAGATAAAATCCATC
107249
Hz_ABCC2 CAAAGTTGTCTAGAAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTGCATATGATTATCAAGA
SPM-16 (161) CAAAGTTGTCTAGAAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACTGTTCTTTGTGTGCATATGATTATCAAGA
107329 11612
Hz_ABCC2 TGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTGCTTACTTAATGTAATGAATGTTGTAGGTTGGAGT
SPM-16 (241) TGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTGCTTACTTAATGTAATGAATGTTGTAGGTTGGAGT
107409
Hz_ABCC2 TGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCATCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAA
SPM-16 (321) TGTAGGCAGAACAGGAGCCGGCAAGTCATC-----
107489
Hz_ABCC2 TTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGTTAAAAATACATTCTTTCTAAAAGACTTAGTGAAG
SPM-16 (351) -----
107569
Hz_ABCC2 TATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTTGTTGAAAATATATTAACGGCAGGAGCTCGTGGTTT
SPM-16 (351) -----
107649
Hz_ABCC2 CCAGACCCCGGATAAAAAATATCCTTTTTATTGCAATTTTATTGCACTCTCTTTTATGAACCTCTTATGTACTCACCTT
SPM-16 (351) -----
107729
Hz_ABCC2 AAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTCTCTTACGTACCCTCTTATGTGCTCTCTTATGTACT
SPM-16 (351) -----
109809
Hz_ABCC2 CCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATAT
SPM-16 (351) -----ACATGAAATTAAATACGTTGATAT
107889
Hz_ABCC2 ACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCATTTTTTTTTTATTTAGAAACATTGATTACGCGAT
SPM-16 (375) ACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGTCATTTTTTTTTTATTTAGAAACATTGATTACGCGAT
107969
Hz_ABCC2 AACTTTTTTACATTTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCG
SPM-16 (455) AACTTTTTTACATTTCGCAGACTTTGAGATCGAAAATATCAATTATTCCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCG
108045
Hz_ABCC2 ATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTT---GGAGGGCGTTGGAACAGGTACGCTTAATTAAA
SPM-16 (535) ATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTTATATGGAGGGCGTTGGAACAGGTACGCTTAATTAAA
108125
Hz_ABCC2 TTACTTCTCAACAGACCCTCGGCACTCGAACTAATCTAATAATGAATGAATCTATGATTTTAGGTGGAATTAAAAGAAG
SPM-16 (615) TTACTTCTCAACAGACCCTCGGCACTCGAACTAATCTAATAATGAATGAATCTATGATTTTAGGTGGAATTAAAAGAAG
108204
Hz_ABCC2 GAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCT
SPM-16 (694) GAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCT
108285
Hz_ABCC2 CGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG
SPM-16 (774) CGTGCCATTCTACGCTCTAACAAAATACTCATCATGGACGAAGCTACCG

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Figure S2. Alignment of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (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.

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Hz_ABCC2 (99062) TGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCATCTGCAGCCAGGTA

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WT	(57)	TGGAAGGCATTACGAAAGGCCACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCATCTGCAGCCAGGTA
SPM-A28C	(1)	TGGAAGGCATTACGAAAGGCCACTGGGTCTCCTACATGCCAGGAGCTATTTTTATCATCATTCATCTGCAGCCAGGTA
H _z _ABCC2	(99142)	CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG
WT	(137)	CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG
SPM-A28C	(81)	CACACTTTGTAAAGTATTTTTATTTAGTTATTTACGGCCAGTTTCTTCATCAAACATAAAAGTCAAAGTAATGTCTAAAG
H _z _ABCC2	(99222)	TAAAAGTAATGGTCAAATTCGTTTTTCAAGGCTAGTGACAGCAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT
WT	(217)	TAAAAGTAATGGTCAAATTCGTTTTTCAAGGCTAGTGACAGCAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT
SPM-A28C	(161)	TAAAAGTAATGGTCAAATTCGTTTTTCAAGGCTAGTGACAGCAAACTAATAGAAAAAATGAATTTGACCGTTACTTTT
H _z _ABCC2	(99302)	ACTTTAAACATTACTTTGATTTTTACTTTGGATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCTTAA
WT	(296)	ACTTTAAACATTACTTTGATTTTTACTTTGATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCTTAA
SPM-A28C	(241)	ACTTTAAACATTACTTTGATTTTTACTTTGGATTTTACTTTTGATGAAGAAATTAGCTGTTAATGTTTAAGTTTCCTTAA
H _z _ABCC2	(99382)	AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATCTCTCTTCAAAAGGTGTACTCAA
WT	(375)	AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATCTCTCTTCAAAAGGTGTACTCAA
SPM-A28C	(321)	AAGTTAGATATAGTTGATCTATCTTTTAAATTTGGTTTCTTGATGGATCTTTAATCTCTCTTCAAAAGGTGTACTCAA
H _z _ABCC2	(99462)	AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG
WT	(455)	AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG
SPM-A28C	(401)	AACTCAATTTTTTATTAGCATTCCACGTGTTATACAGGTGGTCAAGGTATACTTGTGTGCTTCACAATGCAACACACTTG
H _z _ABCC2	(99542)	TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG
WT	(535)	TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG
SPM-A28C	(481)	TGAAATCCCGTAAAGACGTATCGTGTTATTACTTATGAGTGATGATATATCAAATCAATACCTAGGGCTATTCCGTAACG
H _z _ABCC2	(99622)	GTTTCCGTAGAAATTAGATTTTTTTTTCGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG
WT	(615)	GTTTCCGTAGAAATTAGATTTTTTTTTCGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG
SPM-A28C	(561)	GTTTCCGTAGAAATTAGATTTTTTTTTCGTCTCTAGAGCTTGATTAATTATAATCTTTTTATGTTTACAGGACGTATCAG
H _z _ABCC2	(99702)	CCGCTGTTGTTTTCTCAGTTACTGTCGTAAGTGGTGGGACAGTGAATGACTCAGCAAGACGCTGGCCTCTATGCTCT
WT	(693)	CCGCTGTTGTTTTCTCAGTTACTGTCGTAAGTGGTGGGACAGTGAATGACTCAGCAAGACGCTGGCCTCTATGCTCT
SPM-A28C	(639)	CCGCTGTTGTTTTCTCAGTTACTGTCGTAAGTGGTGGGACAGTGAATGACTCAGCAAGACGCTGGCCTCTATGCTCT
H _z _ABCC2	(99782)	CGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTGTCAGCACCACAACACACTGTTTGTGATGCGGTTCAAGTTAAAG
WT	(773)	CGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTGTCAGCACCACAACACACTGTTTGTGATGCGGTTCAAGTTAAAG
SPM-A28C	(679)	-----
H _z _ABCC2	(99862)	TCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGGTGAGCATACTTTTAAGTAGAATAATCTTCCATCGATGTAATTAA
WT	(853)	TCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGGTGAGCATACTTTTAAGTAGAATAATCTTCCATCGATGTAATTAA
SPM-A28C	(679)	-----
H _z _ABCC2	(99942)	ACAGGGACAATTAGACCGAAGTTAGGGTGCTTACATAAAGAAACAGGTTTCCGGTACAGATAAACTTGTACGGGTAGGTA
WT	(933)	ACAGGGACAATTAGACCGAAGTTAGGGTGCTTACATAAAGAAACAGGTTTCCGGTACAGATAAACTTGTACGGGTAGGTA
SPM-A28C	(679)	-----
H _z _ABCC2	(100022)	CCGATCAGTGCAGGTATAATATTTCAATACAATCCTATTCACTCACTTATAAAGAAACAGGTTGTTTACCTGTTTCAACT
WT	(1013)	CCGATCAGTGCAGGTATAATATTTCAATACAATCCTATTCACTCACTTATAAAGAAACAGGTTGTTTACCTGTTTCAACT
SPM-A28C	(679)	-----
H _z _ABCC2	(100102)	TACCTGTTTCTTTTATAAGTGAGTGAATAGGATTGTATTGAAATATTATACCTGCACTGATCGGTACCTACCCGTACAGGT
WT	(1093)	TACCTGTTTCTTTTATAAGTGAGTGAATAGGATTGTATTGAAATATTATACCTGCACTGATCGGTACCTACCCGTACAGGT
SPM-A28C	(679)	-----
H _z _ABCC2	(100182)	TTGTCTGTACCGGTAACCTGTTTCTTTATGTAAACACCCTTAAGATCGTTAAATTAGTTTAAATCAACCTATCAGCATTTT
WT	(1173)	TTGTCTGTACCGGTAACCTGTTTCTTTATGTAAACACCCTTAAGATCGTTAAATTAGTTTAAATCAACCTATCAGCATTTT
SPM-A28C	(679)	-----
H _z _ABCC2	(100262)	TATAGACAATATTTTTTTTCAATAAAAATTGGCCAGATCTGCTTTAAAGAAGACGTTGACGTTGGCTTTAAAGAGAC
WT	(1253)	TATAGACAATATTTTTTTTCAATAAAAATTGGCCAGATCTGCTTTAAAGAAGACGTTGACGTTGGCTTTAAAGAGAC
SPM-A28C	(679)	-----
H _z _ABCC2	(100342)	TGATACTATTTTATTTATTTTGGATATCTTTATTTAGATATACCTACTTACTTCTTTTTTGAAGCTCGATAAAAATTTT
WT	(1332)	TGATACTATTTTATTTATTTTGGATATCTTTATTTAGATATACCTACTTACTTCTTTTTTGAAGCTCGATAAAAATTTT
SPM-A28C	(679)	-----
H _z _ABCC2	(100422)	TTTGTTCTAGTTGCTCCGCATGACCCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAAGTTGCTGTCCAACG
WT	(1411)	TTTGTTCTAGTTGCTCCGCATGACCCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAAGTTGCTGTCCAACG
SPM-A28C	(679)	-----

Hz_ABCC2 (100502) **ATATCACGAGGTTGCGACTACGCGTTCATGTTCCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTAC**
 WT (1491) **ATATCACGAGGTTGCGACTACGCGTTCATGTTCCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTAT**
 SPM-A28C (679) -----

Hz_ABCC2 (100582) **TTCTTGTGGGAGGCTGCTGGCTTCGCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCAC TGCAAGGTAT**
 WT (1571) **TTCTTGTGGGAGGCTGCTGGCTTCGCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCAC TGCAAGGTAT**
 SPM-A28C (679) -----

Hz_ABCC2 (100662) **GTCATATTAAACCTTTTTTCAATTTAATATTGTTTCCTTATGTATCCATGTTATTAATCGATGAACTTTTGGCTTTTAG**
 WT (1651) **GTCATATTAAACCTTTTTTCAATTTAATATTGTTTCCTTATGTATCCATGTTATTAATCGATGAACTTTTGGCTTTTAG**
 SPM-A28C (679) -----

Hz_ABCC2 (100742) **CTGGCTTGACGAAACTCACAACGTGTGTAAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAA**
 WT (1731) **CTGGCTTGACGAAACTCACAACGTGTGTAAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAAACTAATGAGTGAA**
 SPM-A28C (679) -----

Hz_ABCC2 (100822) **ATTATTGGTGGTATTCAGGTAAAAAACTTTTCTTAATTTTTATATATTGACCTATTTAAATGATGACAAAAATTAAC**
 WT (1811) **ATTATTGGTGGTATTCAGGTAAAAAACTTTTCTTAATTTTTATATATTGACCTATTTAAATGATGACAAAAATTAAC**
 SPM-A28C (679) -----

Hz_ABCC2 (100902) **TGTTTGGTCAATTCAGGTCATTAAAATGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTT**
 WT (1891) **TGTTTGGTCAATTCAGGTCATTAAAATGTACGCTTGGGAGAAACCCTTCCAGCTAGTTGTGAAGGCAGCTCGTGCCTTT**
 SPM-A28C (679) -----

Hz_ABCC2 (100982) **GAAATGAGTGCCCTCAGGAAGTCCATCTTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCAT**
 WT (1971) **GAAATGAGTGCCCTCAGGAAGTCCATCTTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCAT**
 SPM-A28C (679) -----

Hz_ABCC2 (101062) **GTTTGTACAGTGTTGACACTCGCTCTCACAGGCACTATGATTACTGCCACTACGGTAAGATTTACTTATTATAATAATT**
 WT (2051) **GTTTGTACAGTGTTGACACTCGCTCTCACAGGCACTATGATTACTGCCACTACGGTAAGATTTACTTATTATAATAATT**
 SPM-A28C (679) -----

Hz_ABCC2 (101142) **AAATATAAGATATTTTGCCGACCGTTTCATTCCATATATATTAATGGTTTTTCGAAATATCGCATCAATCGATTTCATCATC**
 WT (2131) **AAATATAAGATATTTTGCCGACCGTTTCATTCCATATATATTAATGGTTTTTCGAAATATCGCATCAATCGATTTCATCATC**
 SPM-A28C (679) -----

Hz_ABCC2 (101222) **GATTTCATTCAATTTGGGCAAATTACTACTTAACTAAGTTTGAACAATCGTTCCGATATATAATCTCGATATTATTTCA**
 WT (2211) **GATTTCATTCAATTTGGGCAAATTACTACTTAACTAAGTTTGAACAATCGTTCCGATATATAATCTCGATATTATTTCA**
 SPM-A28C (679) -----

Hz_ABCC2 (101302) **CAGATATACCCATTTC AACAGTACTTCAGTATTATTTCAGTTTAAACGTAACACTGATCATTCCTATGGCAATCGCAAGTTA**
 WT (2291) **CAGATATACCCATTTC AACAGTACTTCAGTATTATTTCAGTTTAAACGTAACACTGATCATTCCTATGGCAATCGCAAGTTA**
 SPM-A28C (679) -----

Hz_ABCC2 (101382) **TTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCCTAGTTTGGGTAAATATTGTTTCTTTTAAGTTCAATAAA**
 WT (2371) **TTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTCCCTAGTTTGGGTAAATATTGTTTCTTTTAAGTTCAATAAA**
 SPM-A28C (679) -----

Hz_ABCC2 (101462) **ATTTACACACATTAGGTAGATTGGTATAAAGCGTACAGTGATAATAATACTGAGATTTGATATTTATGTTTTGTAAACAG**
 WT (2451) **ATTTACACACATTAGGTAGATTGGTATAAAGCGTACAGTGATAATAATACTGAGATTTGATATTTATGTTTTGTAAACAG**
 SPM-A28C (679) -----

Hz_ABCC2 (101542) **ACGAGCGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCA**
 WT (2531) **ACGAGCGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCA**
 SPM-A28C (679) -----

Hz_ABCC2 (101622) **CTTGAAGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCA**
 WT (2611) **CTTGAAGTAGGCATCGTGCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCA**
 SPM-A28C (679) -----

Hz_ABCC2 (101702) **GATGGACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGA**
 WT (2691) **GATGGACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGA**
 SPM-A28C (679) -----

Hz_ABCC2 (101782) **ATATATCGTTACGTATTTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGGTAATTTATTTTCATT**
 WT (2771) **ATATATCGTTACGTATTTCGTAAAGGAAAATTGTGTGCTATCATTGGTCCTGTGGGGTCCGGAAAGGTAATTTATTTTCATT**
 SPM-A28C (679) -----

Hz_ABCC2 (101862) **ATAAATATTTGTTTCATATACAGATTTGTTTTTTTTATTTTTTACTTGTAATATTAATATTTTAACTTTTACAGACATCTC**
 WT (2851) **ATAAATATTTGTTTCATATACAGATTTGTTTTTTTTATTTTTTACTTGTAATATTAATATTTTAACTTTTACAGACATCTC**
 SPM-A28C (679) -----

Hz_ABCC2(101942) **TACTGCAACTGCTCTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAA**
WT (2931) **TACTGCAACTGCTCTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAA**
SPM-A28C (679) -----

Hz_ABCC2(102022) **GAGTCTGGCTGTTCCAGGCACAGTACGAGAAAACATTTTGTTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGT**
WT (3011) **GAGTCTGGCTGTTCCAGGCACAGTACGAGAAAACATTTTGTTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGT**
SPM-A28C (679) -----

Hz_ABCC2(102102) **AAATTATTGCAGGTTATGAATGACTTTATTAAATTTTTATTTAGGTGCATAATTATAATAATAATGCGTTTATTTTCATGA**
WT (3091) **AAATTATTGCAGGTTATGAATGACTTTATTAAATTTTTATTTAGGTGCATAATTATAATAATAATGCGTTTATTTTCATGA**
SPM-A28C (679) -----

Hz_ABCC2(102182) **CTACAATGGTCCAATTGTTAGTAACTTTTCAACTATAACTTATCGACTAAGGGTTAGTAATACCTAAAACTAAACGTTT**
WT (3171) **CTACAATGGTCCAATTGTTAGTAACTTTTCAACTATAACTTATCGACTAAGGGTTAGTAATACCTAAAACTAAACGTTT**
SPM-A28C (679) -----

Hz_ABCC2(102262) **GCCTAACAAGCAAGTCCATCCAATGCCTAAGCACCAGGAGCATCATGCTTGTCGGCCAAGACTTGTAGGATGCTGTTGTAG**
WT (3251) **GCCTAACAAGCAAGTCCATCCAATGCCTAAGCACCAGGAGCATCATGCTTGTCGGCCAAGACTTGTAGGATGCTGTTGTAG**
SPM-A28C (679) -----

Hz_ABCC2(102342) **GATGATGTAATTTATCTTCTATATAATTATATTAAATAATTAATTTATTATAAATAATTAAATTAATAATAATTAATAAT**
WT (3331) **GATGATGTAATTTATCTTCTATATAATTATATTAAATAATTAATTTATTATAAATAATTAAATTAATAATAATTAATAAT**
SPM-A28C (679) -----

Hz_ABCC2(102422) **TATATAGAAGATATTTTTTTCTAACTAGCTGATCCCGTGAACCTTCGTATCGTTCAAACCTTCCCTGGACCTCTACAAACA**
WT (3411) **TATATAGAAGATATTTTTTT-CTAACTAGCTGATCCCGTGAACCTTCGTATCGTTCAAACCTTCCCTGGACCTCTACAAACA**
SPM-A28C (679) -----

Hz_ABCC2(102502) **TTTTAAAACCAAATTAGCTCAATCGGCCAGCCGTCCTCGAGTTTTAATCAGACTAACGAACAATAATCCATTTTTATT**
WT (3490) **TTTTAAAACCAAATTAGCTCAATCGGCCAGCCGTCCTCGAGTTTTAATCAGACTAACGAACAATAATCCATTTTTATT**
SPM-A28C (679) -----

Hz_ABCC2(102582) **TATATAGATTATATTTCTTGTGCGAATTATCTTATGTAGGTATGTCTTCCAAACATTTCATACTTACACCTGTATTTCTT**
WT (3570) **TATATAGATTATATTTCTTGTGCGAATTATCTTATGTAGGTATGTCTTCCAAACATTTCATACTTACACCTGTATTTCTT**
SPM-A28C (679) -----

Hz_ABCC2(102662) **GCGATAGCTTTTAAGTTATATTCTTTCACCAAAATTAAAAATATGAAAAAGATATGATGTTCAACCACAAACAGAGATTGCA**
WT (3650) **GCGATAGCTTTTAAGTTATATTCTTTCACCAAAATTAAAAATATGAAAAAGATATGATGTTCAACCACAAACAGAGATTGCA**
SPM-A28C (679) -----

Hz_ABCC2(102742) **CGAGAAACGTTAAAAATTTATAGTCAATTTTCCCGCTGTTTTATAATTCACCCAATTTTCATCTGCCATGGTCTGTTATG**
WT (3730) **CGAGAAACGTTAAAAATTTATAGTCAATTTTCCCGCTGTTTTATAATTCACCCAATTTTCATCTGCCATGGTCTGTTATG**
SPM-A28C (679) -----

Hz_ABCC2(102822) **CATGTAGATATATTTTGTTATGGCAGGTTTGCAAGGTGTGTTTCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGAC**
WT (3810) **CATGTAGATATATTTTGTTATGGCAGGTTTGCAAGGTGTGTTTCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGAC**
SPM-A28C (679) -----

Hz_ABCC2(102902) **CTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGGTCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCG**
WT (3890) **CTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGGTCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCG**
SPM-A28C (679) -----

Hz_ABCC2(102982) **TGAGGTAAGCATCTTTCGTTTACGCAGAACTTCTACACATGGTAATAAAACACTTCAGTTGGTTATTTCGTGATTCGTAAA**
WT (3970) **TGAGGTAAGCATCTTTCGTTTACGCAGAACTTCTACACATGGTAATAAAACACTTCAGTTGGTTATTTCGTGATTCGTAAA**
SPM-A28C (679) -----

Hz_ABCC2(103062) **TCGAGGTATTGATGAAGGACTATATTATGTTCTTGCGACTATTCCCTGTTATATGATATCGCAACCACAAGATTAATTGTC**
WT (4050) **TCGAGGTATTGATGAAGGACTATATTATGTTCTTGCGACTATTCCCTGTTATATGATATCGCAACCACAAGATTAATTGTC**
SPM-A28C (679) -----

Hz_ABCC2(103142) **GGGGTAATACCTGATAACGTGAAAGTAAACAATTGGTAACAACCTTAGTTATATCGGCACTGTAATAATGCGACAGTATAT**
WT (4130) **GGGGTAATACCTGATAACGTGAAAGTAAACAATTGGTAACAACCTTAGTTATATCGGCACTGTAATAATGCGACAGTATAT**
SPM-A28C (679) -----

Hz_ABCC2(103222) **GCGATACATAATTTGTTTACATTTAACTTTTCTAACAATTTATCAATGAAATCTTTTACATATTGATGAGAGCAACTTAT**
WT (4210) **GCGATACATAATTTGTTTACATTTAACTTTTCTAACAATTTATCAATGAAATCTTTTACATATTGATGAGAGCAACTTAT**
SPM-A28C (679) -----

Hz_ABCC2(103302) **ACATTGTTGTCATTACACCACATTTTCTTAAATCGTGAGCGTGAAACTAAAATCGTGGGCGTATTTTCAGGCCGACATTT**
WT (4290) **ACATTGTTGTCATTACACCACATTTTCTTAAATCGTGAGCGTGAAACTAAAATCGTGGGCGTATTTTCAGGCCGACATTT**

SPM-A28C (679) -----

H_z_ABCC2 (103382) **ACTTGCTGGATGATCCCCTATCTGCAGTGGACGCTAATGTAGGCAGACAAC**TGTTTGATGGCTGCATCAAAGGCTACCTC
WT (4370) **ACTTGCTGGATGATCCCCTATCTGCAGTGGACGCTAATGTAGGCAGACAAC**TGTTTGATGGCTGCATCAAAGGCTACCTC
SPM-A28C (679) -----

H_z_ABCC2 (103462) **ACTGGACGAACTTGCGTCTTGGTCACCCATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGC**
WT (4450) **ACTGGACGAACTTGCGTCTTGGTCACCCATCAGATCCATTACCTCAAAGCTGCTGATTTTATTGTAGTCCTTAATGAGGC**
SPM-A28C (679) -----

H_z_ABCC2 (103542) **AAGTATGACTACCTATCATTTCATATTTCCATTGAAAGATAACAAAAGTATTTACATTAAAAATATATTTATTGAAGTGA**
WT (4530) **AAGTATGACTACCTATCATTTCATATTTCCATTGAAAGATAACAAAAGTATTTACATTAAAAATATATTTATTGAAGTGA**
SPM-A28C (679) -----

H_z_ABCC2 (103622) **TTAATTTTATCTTAACTATTATCTTTGGACGAGTCATTACAACGTAGCAAATTTCCAACACTTCAATATTTACTCTTTGA**
WT (4610) **TTAATTTTATCTTAACTATTATCTTTGGACGAGTCATTACAACGTAGCAAATTTCCAACACTTCAATATTTACTCTTTGA**
SPM-A28C (679) -----

H_z_ABCC2 (103702) **ATACTACTTACTTAGTCCAGCTTCAAAATTAATAAAAGTTTCCTAATGGTTTTTTATCAGGGTTCCGTCGAGAATATGGG**
WT (4690) **ATACTACTTACTTAGTCCAGCTTCAAAATTAATAAAAGTTTCCTAATGGTTTTTTATCAGGGTTCCGTCGAGAATATGGG**
SPM-A28C (679) -----

H_z_ABCC2 (103782) **CACTTATGATGAGCTGGTGAAGACAGGAAC**TGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACG
WT (4770) **CACTTATGATGAGCTGGTGAAGACAGGAAC**TGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACG
SPM-A28C (679) -----

H_z_ABCC2 (103862) **AAAAGAAAGTAAGTATGCACCTTAATATCTGGTATTTTCCGTGGCGACTTGAACGTTTGCCAGAAAACAGCTTTCAACATT**
WT (4850) **AAAAGAAAGTAAGTATGCACCTTAATATCTGGTATTTTCCGTGGCGACTTGAACGTTTGCCAGAAAACAGCTTTCAACATT**
SPM-A28C (679) -----

H_z_ABCC2 (103942) **ATCTTGTCTACATCGTTGCACATGTTCTCTAAACATATCCGAATAAAAAATATAGGTATGAACGAGTATACATCTACCTT**
WT (4930) **ATCTTGTCTACATCGTTGCACATGTTCTCTAAACATATCCGAATAAAAAATATAGGTATGAACGAGTATACATCTACCTT**
SPM-A28C (679) -----

H_z_ABCC2 (104022) **CGTGATTGTAATATGTACTGAATAAACATTGTTTCATTTTAAATTCTCCTAATAGATTATGCTTAAAAATGCAGCATAGA**
WT (5010) **CGTGATTGTAATATGTACTGAATAAACATTGTTTCATTTTAAATTCTCCTAATAGATTATGCTTAAAAATGCAGCATAGA**
SPM-A28C (679) -----

H_z_ABCC2 (104102) **TTTACACTGGACCTTGTTTCAAACAACCCAGAAAAAATACTATTTACGTTCCTTTCGTCTTAGGACCGACCAGCAATGATG**
WT (5090) **TTTACACTGGACCTTGTTTCAAACAACCCAGAAAAAATACTATTTACGTTCCTTTCGTCTTAGGACCGACCAGCAATGATG**
SPM-A28C (679) -----

H_z_ABCC2 (104182) **CGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAGGAGAGAGC**
WT (5170) **CGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAGGAGAGAGC**
SPM-A28C (679) -----

H_z_ABCC2 (104262) **GACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCTGGTGTCTGGTGTTCACGGCGTTCC**
WT (5250) **GACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCTGGTGTCTGGTGTTCACGGCGTTCC**
SPM-A28C (679) -----

H_z_ABCC2 (104342) **TTGTACTGCTGATCACGCAAGGTGCTGCCACCAGTG**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC
WT (5330) **TTGTACTGCTGATCACGCAAGGTGCTGCCACCAGTG**CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC
SPM-A28C (679) -----CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAATTATTTTTC

H_z_ABCC2 (104422) **AAAAATTTAATTTAACGGAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA**
WT (5410) **AAAAATTTAATTTAACGGAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA**
SPM-A28C (723) **AAAAATTTAATTTAACGGAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCTGATAGTTA**

H_z_ABCC2 (104502) **ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA**
WT (5490) **ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA**
SPM-A28C (803) **ACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAAGTCTACGA**

H_z_ABCC2 (104582) **AATATCTCTGTTTTATTTATATGAACCTCCTGCGTATGTACCATTTCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT**
WT (5570) **AATATCTCTGTTTTATTTATATGAACCTCCTGCGTATGTACCATTTCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT**
SPM-A28C (883) **AATATCTCTGTTTTATTTATATGAACCTCCTGCGTATGTACCATTTCAGTTCTAAGATCTCAACCTCAACTAAAAAGTT**

H_z_ABCC2 (104662) **ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACCTGCCAGTACCTATACGTTTTTCGGTGGAGTT**
WT (5650) **ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACCTGCCAGTACCTATACGTTTTTCGGTGGAGTT**
SPM-A28C (963) **ATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACCTGCCAGTACCTATACGTTTTTCGGTGGAGTT**

H_z_ABCC2 (104742) **ATATTGGCTTTAATAGTCATGACCCTCGTCAGAAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA**

WT	(5730)	ATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA
SPM-A28C	(1043)	ATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAAAATCTTCA
H _z _ABCC2	(104822)	CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT
WT	(5810)	CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT
SPM-A28C	(1123)	CAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTTCGATACCAATCCTTCTGGTGAGTAACATTCATCAT
H _z _ABCC2	(104902)	TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA
WT	(5890)	TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA
SPM-A28C	(1203)	TACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTTGCGAGACAGTCAGTTAGATAAGTAGA
H _z _ABCC2	(104982)	GATAATGATTTTAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGATAGTAATTAGCGATAATTGCAGCTGGCCAA
WT	(5970)	GATAATGATTTTAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGATAGTAATTAGCGATAATTGCAGCTGGCCAA
SPM-A28C	(1283)	GATAATGATTTTAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGATAGTAATTAGCGATAATTGCAGCTGGCCAA
H _z _ABCC2	(105062)	GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA
WT	(6050)	GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA
SPM-A28C	(1363)	GTGCCCAGGTTGCCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTTGGATAATA
H _z _ABCC2	(105142)	ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG
WT	(6130)	ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG
SPM-A28C	(1443)	ACAACATCTTTAATGAGTTCTGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTACATATGTG
H _z _ABCC2	(105222)	TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAATGCAAGAAGATGATGCAAT
WT	(6210)	TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAATGCAAGAAGATGATGCAAT
SPM-A28C	(1523)	TAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAATGCAAGAAGATGATGCAAT
H _z _ABCC2	(105302)	GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC
WT	(6290)	GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC
SPM-A28C	(1603)	GAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTTCGCAGGTCGTGTGCTGAACAGATTCTCAAAAGAC
H _z _ABCC2	(105382)	ATGGGTGCCATGGATGAGCTTCTTCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT
WT	(6370)	ATGGGTGCCATGGATGAGCTTCTTCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT
SPM-A28C	(1683)	ATGGGTGCCATGGATGAGCTTCTTCTCGCAGTCTTTTAGAAACAGTTCAGATGTATTTGTCGCTGACCAGTGTGTTGGT
H _z _ABCC2	(105462)	GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT
WT	(6450)	GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT
SPM-A28C	(1763)	GCTGAACGCCACTGCATTGCCCTGGACGCTTATACCTACCTCCGTGTTGATTGTCATCTTCGTGCTCATGTTGAGATGGT
H _z _ABCC2	(105542)	ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA
WT	(6530)	ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA
SPM-A28C	(1843)	ACCTGAATACAGCTCAGGCTGTCAAACGTTTGGAGGGCACAAGTAAGTGTTACATGAACCATAGGCGTTATTTAAGAACA
H _z _ABCC2	(105622)	AATATTGATTTAGAGTGTAATTAATTAACGGTTAGAACATCGCTAATAGTTTGGACTGCCTCGTTGGTCTAGAGGTCGC
WT	(6610)	AATATTGATTTAGAGTGTAATTAATTAACGGTTAGAACATCGCTAATAGTTTGGACTGCCTCGTTGGTCTAGAGGTCGC
SPM-A28C	(1923)	AATATTGATTTAGAGTGTAATTAATTAACGGTTAGAACATCGCTAATAGTTTGGACTGCCTCGTTGGTCTAGAGGTCGC
H _z _ABCC2	(105702)	AAGCGGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTTCATAAACTTT
WT	(6690)	AAGCGGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTTCATAAACTTT
SPM-A28C	(2003)	AAGCGGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGGTCAGGCCGAAATCGCTTTGTGGGTTTTTCATAAACTTT
H _z _ABCC2	(105782)	CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTACCCCGTGCATCGGAGAGCACGTAATGTGGTCTCGCCCT
WT	(6770)	CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTACCCCGTGCATCGGAGAGCACGTAATGTGGTCTCGCCCT
SPM-A28C	(2083)	CACAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTACCCCGTGCATCGGAGAGCACGTAATGTGGTCTCGCCCT
H _z _ABCC2	(105862)	GATCTCTTTCCGGTCGTGTGCGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC
WT	(6850)	GATCTCTTTCCGGTCGTGTGCGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC
SPM-A28C	(2163)	GATCTCTTTCCGGTCGTGTGCGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGTGTCTGCGC
H _z _ABCC2	(105942)	AAATGCTCGTGCACTATAATATGTCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCGTGGCCGAAATCGGC
WT	(6930)	AAATGCTCGTGCACTATAATATGTCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCGTGGCCGAAATCGGC
SPM-A28C	(2243)	AAATGCTCGTGCACTATAATATGTCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCGTGGCCGAAATCGGC
H _z _ABCC2	(106022)	CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTGTTTTATTCTACTTACAGCCAAGAGTCCTGTA
WT	(7010)	CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTGTTTTATTCTACTTACAGCCAAGAGTCCTGTA
SPM-A28C	(2323)	CGTGGACGCCATTATTAATAGTTTTGAAATAAAATTATTTTAATTTTGTGTTTTATTCTACTTACAGCCAAGAGTCCTGTA
H _z _ABCC2	(106102)	TTTGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCAGGATAGACAGATGAAATTGTT
WT	(7090)	TTTGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCAGGATAGACAGATGAAATTGTT
SPM-A28C	(2403)	TTTGAATGATTAACTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTCAGGATAGACAGATGAAATTGTT

Hz_ABCC2 (106182) TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT
 WT (7170) TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT
 SPM-A28C (2483) TGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAAAATTACATCTAAAAAGATTTATCCAATAGT

Hz_ABCC2 (106262) AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA
 WT (7250) AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA
 SPM-A28C (2563) AATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTACGGCA

Hz_ABCC2 (106342) TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA
 WT (7330) TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA
 SPM-A28C (2643) TTTGCATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTGGTGA

Hz_ABCC2 (106422) GCACTTTTTCTTAGGCACATTAAGGCAATATTTACACATTTCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC
 WT (7410) GCACTTTTTCTTAGGCACATTAAGGCAATATTTACACATTTCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC
 SPM-A28C (2723) GCACTTTTTCTTAGGCACATTAAGGCAATATTTACACATTTCAGTTCATAGTGTGATATCTTTGGCATTACCATTCC

Hz_ABCC2 (106502) ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTTTTTCTTCCCAGGTGATTTGATCCCAGGTGGGAAGTGTCGGTCT
 WT (7490) ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTCTTCCCAGGTGATTTGATCCCAGGTGGGAAGTGTCGGTCT
 SPM-A28C (2803) ATGTTGATAGAACAGAATTTGCTTATTTTTGTTTTTTTTTTCTTCCCAGGTGATTTGATCCCAGGTGGGAAGTGTCGGTCT

Hz_ABCC2 (106582) TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTTCACAGCTGACTTTTTGGGGCAAATG
 WT (7566) TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTTCACAGCTGACTTTTTGGGGCAAATG
 SPM-A28C (2881) TGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTTCACAGCTGACTTTTTGGGGCAAATG

Hz_ABCC2 (106662) ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC
 WT (7646) ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC
 SPM-A28C (2961) ACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAATATGGAGCAAGGACGTAAGTACAATCATTC

Hz_ABCC2 (106742) GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACATATGTTCCGTACTT
 WT (7726) GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACATATGTTCCGTACTT
 SPM-A28C (3041) GTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTCCAACATATGTTCCGTACTT

Hz_ABCC2 (106822) CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACAGTTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG
 WT (7806) CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACAGTTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG
 SPM-A28C (3121) CTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACAGTTTTTTACATAGGCGACTGCCTATCTGAACTTCTAAATCTAG

Hz_ABCC2 (106902) TTACCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG
 WT (7886) TTACCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG
 SPM-A28C (3201) TTACCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAACAAGGACG

Hz_ABCC2 (106982) ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCT
 WT (7965) ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCT
 SPM-A28C (3281) ATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCT

Hz_ABCC2 (107062) CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAG
 WT (8045) CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAG
 SPM-A28C (3361) CAAATGTGTACCTGAATTATTCCATGGAAGACCCGCCGGTGCTGAAGGACTTAACTTTGAAATTCAAAGCGGCTGGAAG

Hz_ABCC2 (107142) GTAAGAGACCTAATAATGTATTTGATTAAAAATAAAGCAATAAAGATATACTTGCCGTGCTACCTAACTACCCGTGTT
 WT (8125) GTAAGAGACCTAATAATGTATTTGATTAAAAATAAAGCAATAAAGATATACTTGCCGTGCTACCTAACTACCCGTGTT
 SPM-A28C (3441) GTAAGAGACCTAATAATGTATTTGATTAAAAATAAAGCAATAAAGATATACTTGCCGTGCTACCTAACTACCCGTGTT

Hz_ABCC2 (107222) CCATGTATTATTTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT
 WT (8205) CCATGTATTATTTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT
 SPM-A28C (3521) CCATGTATTATTTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCAATTATACT

Hz_ABCC2 (107302) GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT
 WT (8285) GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT
 SPM-A28C (3601) GTTCTTTGTGTCATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTTGCTTACTT

Hz_ABCC2 (107382) AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA-----
 WT (8365) AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA-----
 SPM-A28C (3681) AATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCA**CGGCTTTGTTCTCTTTGT**

Hz_ABCC2 (107444) --TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAATTGACGGTGTTGGACACCGAAGGATTAGCCAAAA
 WT (8427) --TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAATTGACGGTGTTGGACACCGAAGGATTAGCCAAAA
 SPM-A28C (3761) **TC**TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGCAGCATCAAATTGACGGTGTTGGACACCGAAGGATTAGCCAAAA

Hz_ABCC2 (107522) AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA
 WT (8505) AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA
 SPM-A28C (3841) AGGTATCGATGTTAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGA

Hz_ABCC2 (107602) ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAAATATCCTTTTTATTGCG
 WT (8585) ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAAATATCCTTTTTATTGCG
 SPM-A28C (3921) ATTTGTGGATTTGTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAAATATCCTTTTTATTGCG

Hz_ABCC2 (107682) AATTTTATTTGCACTCTCTTTTATGAACCTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC
 WT (8665) AATTTTATTTGCACTCTCTTTTATGAACCTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC
 SPM-A28C (4001) AATTTTATTTGCACTCTCTTTTATGAACCTCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTC

Hz_ABCC2 (107762) CCTTATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCTTATGTACTCCTCTTCTGTACTCCTCTTA
 WT (8745) C---TATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCTTATGTACTCCTCTTCTGTACTCCTCTTA
 SPM-A28C (4081) CCTTATGTACTCTCTTATGTACCCTCTTATGTGCTCTCTTATGTACTCCCTTATGTACTCCTCTTCTGTACTCCTCTTA

Hz_ABCC2 (107842) TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTGTAGGAAAAGTAAGAGA
 WT (8822) TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTGTAGGAAAAGTAAGAGA
 SPM-A28C (4161) TACAAAGTGTGTCGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTGTAGGAAAAGTAAGAGA

Hz_ABCC2 (107922) ATCTTATGTCGTCGAATTTTTTTTATTTAGAAAATTGATTACAGCGATAACTTTTTTACATTTCGCAGACTTTGAGATCGAAA
 WT (8902) ATCTTATGTCGTCGAATTTTTTTTATTTAGAAAATTGATTACAGCGATAACTTTTTTACATTTCGCAGACTTTGAGATCGAAA
 SPM-A28C (4241) ATCTTATGTCGTCGAATTTTTTTTATTTAGAAAATTGATTACAGCGATAACTTTTTTACATTTCGCAGACTTTGAGATCGAAA

Hz_ABCC2 (108002) ATATCAATTATTCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGA
 WT (8981) ATATCAATTATTCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGA
 SPM-A28C (4319) ATATCAATTATTCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGA

Hz_ABCC2 (108082) CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAATACTTCTTAACAGACCCTCGGCACTCGAATAATCT
 WT (9061) CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAATACTTCTTAACAGACCCTCGGCACTCGAATAATCT
 SPM-A28C (4399) CGACGATATTTGGAGGGCGTTGGAACAGGTACGCTTAATTAATACTTCTTAACAGACCCTCGGCACTCGAATAATCT

Hz_ABCC2 (108162) AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG
 WT (9141) AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG
 SPM-A28C (4479) AACTAATGAATGAATCTATGATTTTAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGG

Hz_ABCC2 (108242) TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG
 WT (9221) TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG
 SPM-A28C (4559) TACTAACTTCTCTATGGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAATACTCATCATGG

Hz_ABCC2 (108322) ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG
 WT (9301) ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG
 SPM-A28C (4639) ACGAAGCTACCGCTAACGTCGATCCTCAGTAAGTCAATCATTCTATAGTTGTGGTCAATGGCGTTAATTTATTGTTCTAG

Hz_ABCC2 (108402) GTTTTCCAATGTGTTAAAAGTTTAATTAAGAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC
 WT (9381) GTTTTCCAATGTGTTAAAAGTTTAATTAAGAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC
 SPM-A28C (4719) GTTTTCCAATGTGTTAAAAGTTTAATTAAGAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTCGGTAATAGGAC

Hz_ABCC2 (108482) TTCCTTATTGGCGAGTTTGTTCATTTTGTTCCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG
 WT (9461) TTCCTTATTGGCGAGTTTGTTCATTTTGTTCCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG
 SPM-A28C (4799) TTCCTTATTGGCGAGTTTGTTCATTTTGTTCCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAG

Hz_ABCC2 (108562) AACTTACACGTATTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG
 WT (9541) AACTTACACGTATTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG
 SPM-A28C (4879) AACTTACACGTATTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAG

Hz_ABCC2 (108642) TTTGCGTTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA
 WT (9621) TTTGCGTTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA
 SPM-A28C (4959) TTTGCGTTCGTGCACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCA

Hz_ABCC2 (108722) GGGCGAAGTGGCCGAGTTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA
 WT (9701) GGGCGAAGTGGCCGAGTTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA
 SPM-A28C (5039) GGGCGAAGTGGCCGAGTTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGA

Hz_ABCC2 (108802) CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTGCGTAAGGC
 WT (9781) CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTGCGTAAGGC
 SPM-A28C (5119) CAGGAGAAAGCATGACAAGGACCTTAATGGAGGTGCGTAAGGC

Figure S3. Alignment of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (ABCC2) reference genome sequence from 99,062 to 108,844 bp and amplicon sequences from wild type SIMRU and knockout line SPM-A28C. The nucleotide sequence of SPM-A28C 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	(104174)	CAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAG
SPM-B1	(1)	CAATGATGCGAGGAATATCAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAGGAGGCAGAG
Hz_ABCC2	(104254)	GAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCTGGTGTCTGGTGTTCAC
SPM-B1	(81)	GAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCTGGTGTCTGGTGTTCAC
Hz_ABCC2	(104334)	GGCGTTCCTTGCTACTGCTGATCACGCAAGGTGCTGCCACCACTG
SPM-B1	(161)	GGCGTTCCTTGCTACTGCTGATCACGCAAGGTGCTGCCACCACTG-----CCGACTATTGGTTGAGTTTCTGGTAAGATAATGAAT
Hz_ABCC2	(104414)	TATTTTTCAAAAATTTAATTTAACGGAACAAAGAACGTATTTTAAATTGGCTTCTCTGAATATGTCTTAAATGTCTCCT
SPM-B1	(205)	-----
Hz_ABCC2	(104494)	GATAGTTAACATTTTGATTGCAGGACTAACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGGTAA
SPM-B1	(205)	-----
Hz_ABCC2	(104574)	GTCTACGAAATATCTCTGTTTTATTTATATGAACTTCCTGCGTATGTACCATTTCAGTTCTAAGATCTCAACCTCAACT
SPM-B1	(205)	-----
Hz_ABCC2	(104654)	AAAAAGTTATTTCTTTTCAGATACTGACATGAACGCACAAATTGGCTTACTTACAACCTGCCAGTACCTATACGTTTTTCG
SPM-B1	(205)	-----
Hz_ABCC2	(104734)	GTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTTCGTAGCGATGACAATGCGAGCTTCTCAA
SPM-B1	(205)	-----
Hz_ABCC2	(104814)	AATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTTCGATACCAATCCTTCTGGTGAGTAACA
SPM-B1	(205)	-----
Hz_ABCC2	(104894)	TTCATCATTACACATAACATTATTTATTTAAGTGATCACATAAAAAAGTGCCATAGCATTTCGCGAGACAGTCAGTTAGA
SPM-B1	(205)	-----
Hz_ABCC2	(104974)	TAAGTAGAGATAATGATTTTAAATCAAAGTAACGGACTCTCTCAATGTTAGAAGTGTAGGTAATTAGCGATAATTGCA
SPM-B1	(205)	-----
Hz_ABCC2	(105054)	CTGGCCAAGTGCCAGGTGGCGTGAGTAGACCTTAACATTAGTACACGCCAATTGCAACGACGGTAGCCAAGATAGCTT
SPM-B1	(205)	-----
Hz_ABCC2	(105134)	GGATAATAACAACATCTTTAATGAGTTCGCAACTTTCGACTTGTGATTTTGGTGGCAGTAGATTTAAGAAAACGTTGTA
SPM-B1	(205)	-----
Hz_ABCC2	(105214)	CATATGTGTAGTATAAGATGATGATACATTCTAGGCTATCCGTATTTTTTTAGATTATGATTTATTAAATGCAAGAAGAT
SPM-B1	(205)	-----
Hz_ABCC2	(105294)	GATGCAATGAAATTAATTTACAACATCATGCTTATTGGAGCTTCTTTTGAATTTTCGAGGTCGTGTGCTGAACAGATTCT
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)	TAAGAACAAATATTGATTTAGAGTGTAATTAATTAACGGTTAGAACATCGCTAATAGTTTGGTGCCTCGTTGGTCTA
SPM-B1	(205)	-----
Hz_ABCC2	(105694)	GAGGTCGCAAGCGCGGCTGCTGTGCTCGAGGTCTCGGGTTCGATTCCCGGTCAGGCCGAAATCGCTTTGTGGGTTTTCA
SPM-B1	(205)	-----
Hz_ABCC2	(105774)	TAACTTTTCAAAAGCAGCCCGTAGCCTGGAAGTTGGTGATTGATTACCCGTGCATCGGAGAGCACGTAAATGTGGTTC
SPM-B1	(205)	-----
Hz_ABCC2	(105854)	CTGCGCCTGATCTCTTTCCGGTCGTGTCGGATTGCCGTCCCATCGGGTTATGAGAGTGAAGGAATAGGGAGTGCACCTGT
SPM-B1	(205)	-----
Hz_ABCC2	(105934)	GTCTGCGCAAATGCTCGTGCACTATAATATGTCTGCGCAGCTGGCTGATCTCCTTTAATGAGAACAGCCGCGGTGGCCG
SPM-B1	(205)	-----

Hz_ABCC2 (106014) **AAATCGGCCGTGGACGCCATTATTAATAGTTTGAATAAAATTATTTTAATTTTGTTTTATTCTACTTACAGCCAAGA**
 SPM-B1 (205) -----

Hz_ABCC2 (106094) **GTCCTGTATTTGGAATGATTAACCTCACTATTCTGGACTCTCCACTATTAGAAGTTCGGGTCCAGGATAGACAGATG**
 SPM-B1 (205) -----

Hz_ABCC2 (106174) **AAATTGTTTGACGAAGCGCAGGTAAACATGAAGCTTATTATTTTTTTATATTAATTAATAATACATCTAAAAAGATTTAT**
 SPM-B1 (205) -----

Hz_ABCC2 (106254) CCAATA**GTAATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTC**GGCGGTT
 SPM-B1 (205) CCAATT**GTAATGGTTATATATTTCTTATTGCTGTTTACAGAATCTCCACACAAGTGCTTTCCACACATTCTTC**GGCGGTT

Hz_ABCC2 (106334) CTACGGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGAC
 SPM-B1 (285) TTACGGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGAC

Hz_ABCC2 (106414) TTTGGTGAGCACTTTTCTTTAGGCACATTAAAGGCAATATTTACACATTTCAGTTCATAGTGTGATATCTTTGGCATT
 SPM-B1 (365) TTTGGTGAGCACTTTTCTTTTGGCACATTAAAGACAATATTTACACATTTCAGTTCATAGTGTAAATATCTTTGGCATT

Hz_ABCC2 (106494) ACCATTCCATGTTGATAGAACAGAATTTGCTTATTTTGTGTTTTTTTTTTCTTCCAGGTGATTTGATCCCGGTGGGAAG
 SPM-B1 (445) ACCATTCCATGTTGATAGAACAGAATTTGCTTATTTTGTGTTTTTTTTTTCTTCCAGGTGATTTGATCCCGGTGGGAAG

Hz_ABCC2 (106574) TGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCTAGGTTTCACAGCTGACTTTTTGG
 SPM-B1 (524) TGTCGGTCTGGCTGTCAGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCATTAGGTTTCACAGCTGACTTTTTGG

Hz_ABCC2 (106654) GGCAAATGACGGCTGTGGAGAGAGTTCTGGAAATACACCAAGCTACCCACGG**AGACCAATAT**GGAGCAAGGACGTAAGTAC
 SPM-B1 (604) GGCAAATGACGGCTGTGGAGAGAGTTCTGGAAATACACCAAGCTACCCACGG-----GGAGCAAGGACGTAAGTAC

Hz_ABCC2 (106734) AATCATTCGTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTTCCAACATATGTT
 SPM-B1 (674) AATCATTCGTTTTGAGATAGTTAGGTAATCTGACTTTGATTATTAAGTCCTTATCTGTCTAGCCTTTTTTCCAACATATGTT

Hz_ABCC2 (106814) CGGTACTTCTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACAGTTTTTACATAGGCGACTGCCTATCTGAACCTCT
 SPM-B1 (754) CGGTACTTCTTCCAGTCTATGTGATTGGATGCAGTAATGAAAACAGTTTTTACATAGGCGACTGCCTATCTGAACCTCT

Hz_ABCC2 (106894) AAATCTAGTTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAA
 SPM-B1 (834) AAATCTAGTTACCCGGGTAACCCGATATCCCTTTGGTTGTCAAATTTTGGCTCTGGCTTCTGACTACCGGCCAACCAAAA

Hz_ABCC2 (106974) CAAGGACGATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAGGAATGGCCAGTGCTGGTAGAGT
 SPM-B1 (914) CAAGGACGATAAGTTATAACATAGATATATTGATTTTCAGCAACTAACCCACCAAGGAATGGCCAGTGCTGGTAGAGT

Hz_ABCC2 (107054) GACGTTCTCAAATGTGTACCTGAATTATTCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCG
 SPM-B1 (994) GACGTTCTCAAATGTGTACCTGAATTATTCATGGAAGACCCGCCGGTGCTGAAGGACTTAAACTTTGAAATTCAAAGCG

Hz_ABCC2 (107134) GCTGGAAGGTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTA
 SPM-B1 (1074) GCTGGAAGGTAAGAGACCTAATAATGTATTTGATTAAAATAAAAGCAATAAAGATATACTTGCCGTGCTACCCTAAACTA

Hz_ABCC2 (107214) CCCGTGTTCCATGTATTATTTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCA
 SPM-B1 (1154) CCCGTGTTCCATGTATTATTTCAGATAAATTCCATCCAAAGGTTGTCTAGAAGAAATCGCTGTTTGGCGATAAGACGGCCA

Hz_ABCC2 (107294) ATTATACTGTTCTTTGTGTATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTT
 SPM-B1 (1234) ATTATACTGTTCTTTGTGTATATGATTATCAAGATGATATGATGAGAAGATTTATAAAGAATAATCTATCTATGTATTT

Hz_ABCC2 (107374) GCTTACTTAATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCATCGCGGCTTT
 SPM-B1 (1314) GCTTACTTAATGTAATGAATGTTGTAGGTTGGAGTTGTAGGCAGAACAGGAGCCGGCAAGTCATCGCTCATCGCGGCTTT

Hz_ABCC2 (107454) GTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGT
 SPM-B1 (1394) GTTCCGGCTTAGTGACATAAGCGGCAGCATCAAAATTGACGGTGTTGGACACCGAAGGATTAGCCAAAAAGGTATCGATGT

Hz_ABCC2 (107534) TAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTT
 SPM-B1 (1474) TAAAAAATACATTCTTTCTAAAAGACTTAGTGAAGTATTATTTATTGTTTAGTTAAATTACTAATAGAATTTGTGGATTT

Hz_ABCC2 (107614) GTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAAATATCCTTTTTATTGCAATTTTATTGCG
 SPM-B1 (1554) GTTGAAAATATATTAACGGCACGAGCTCGTGGTTTCCAGCACCCGGATAAAAAATATCCTTTTTATTGCAATTTTATTGCG

Hz_ABCC2 (107694) ACTCTCTTTTATGAACCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTC
 SPM-B1 (1634) ACTCTCTTTTATGAACCTCTTATGTACTCACCTTAAGTACTCTCTTATGTAAGATCTCATGTACTTCCCTTATGTACTC

Hz_ABCC2 (107774) TCTTATGTACCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGT
 SPM-B1 (1714) TCTTACGTACCTCTTATGTGCTCTCTTATGTACTCCCCTTATGTACTCCTCTTCTGTACTCCTCTTATACAAAGTGTGT

Hz_ABCC2 (107854) CGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGT
 SPM-B1 (1794) CGTACCTAATCACATGAAATTAAATACGTTGATATACTGGTTAATACATTTGTAGGAAAAGTAAGAGAATCTTATGTCGT

Hz_ABCC2 (107934)	CAATTTTTTTTTATTTAGAA	AATTGATTTCAGCGATAACTTTTTACATTTCGCAGACTTTGAGATCGAAAATATCAATTATT
SPM-B1 (1874)	CAATTTTTTTTTATTTAGAAC	AATTGATTTCAGCGATAACTTTTTACATTTCGCAGACTTTGAGATCGAAAATATCAATTATT
Hz_ABCC2 (108014)	CCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTGGACCCGTTTCGACGATTACAGCGACGACGATATTTG	
SPM-B1 (1954)	CCACAAGAGCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTGGACCCGTTTCGACGATTACAGCGACGACGATATTTG	
Hz_ABCC2 (108094)	GAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCT	TAAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATG
SPM-B1 (2034)	GAGGGCGTTGGAACAGGTACGCTTAATTAAATTACTTCT	TAAACAGACCCTCGGCACTCGAACTAATCTAACTAATGAATG
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)	GTTAAAAGTTTAATTTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTTCGGTAATAGGACTTCCTTATTGGC	
SPM-B1 (2354)	GTTAAAAGTTTAATTTAAAAGCAAAATATAGATACGTCATTAAATAAATTATTTATTTCGGTAATAGGACTTCCTTATTGGC	
Hz_ABCC2 (108494)	GAGTTTGTTCATTTTGTTCCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAGAACTTACACGTA	
SPM-B1 (2434)	GAGTTTGTTCATTTTGTTCCTGAATTTAAATACATAATAGTCAGCTAATATAATAATTACTGCAGAGAACTTACACGTA	
Hz_ABCC2 (108574)	TTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTTCGTCGTCG	
SPM-B1 (2514)	TTTTTCTTACTTATGCATTCTTCTTTTACAGGACGGACGCTTTGATCCAAAAGACGATCCGTCGTCAGTTTTCGTCGTCG	
Hz_ABCC2 (108654)	ACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGCC	
SPM-B1 (2594)	ACGGTGCTCACCATCGCGCATCGACTGAACACCATCATGGACTCCGACCGAGTGCTGGTCATGGACCAGGGCGAAGTGCC	
Hz_ABCC2 (108734)	CGAGTTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCA	
SPM-B1 (2674)	CGAGTTTCGACCATCCCCACATCTTGCTCAGCAACCCCAATAGCAAGTTCTTCTCTATGGTCCGAGAGACAGGAGAAAGCA	
Hz_ABCC2 (108814)	TGACAAGGA	
SPM-B1 (2754)	TGACAAGGA	

Figure S4. Alignment of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (ABCC2) reference genome sequence from 104,174 to 108,822 bp and amplicon sequence from the 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.

KM360184	(1)	ATGGGCGTAGAAAATAAGAATAATGTACAAAATGCGGAAGGTCCGGCCCGCAAGACTTACAAAAACCGAACATTTTATC
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)	CGCCCAGTAATTTATATAAATTCAGAAAGACAAGGAGAGTATCTTGAAAGATACTGGTTGGCAGAGATAGAAAATGCAACA
SPM-8	(1)	-----
SPM-16	(1)	-----
SPM-B1	(1)	-----
SPM-A28C	(1)	-----
KM360184	(241)	ATTGAAAAATCGGGAGCCGTCACTATGGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT
SPM-8	(1)	-----TGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT
SPM-16	(1)	-----TGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT
SPM-B1	(1)	-----TGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT
SPM-A28C	(1)	-----TGAAGGCATTACGAAAGGCCTACTGGGTCTCCTACATGCCAGGAGCTATTTTTAT
KM360184	(321)	CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGCTACTGTCGTACTGGTCGGTGGACAGTGAAA
SPM-8	(57)	CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTGTCGTACTGGTCGGTGGACAGTGAAA
SPM-16	(57)	CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTGTCGTACTGGTCGGTGGACAGTGAAA
SPM-B1	(57)	CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTGTCGTACTGGTCGGTGGACAGTGAAA
SPM-A28C	(57)	CATCATTCAATCTGCAGCCAGGACGTATCAGCCGCTGTTGTTTTCTCAGTTACTGTGTCGTACTGATACG-----
KM360184	(401)	TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTCAGCACCACAAC
SPM-8_mRNA	(137)	TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTCAGCACCACAAC
SPM-16	(137)	TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTCAGCACCACAAC
SPM-B1	(137)	TGACTCAGCAAGACGCTGGCCTCTATGCTCTCGCCATGCTGGGACTGAACTTCGCTCTCCATGATGTGTCAGCACCACAAC
SPM-A28C	(125)	-----
KM360184	(481)	ACACTGTTTGTGATGCGGTTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC
SPM-8_mRNA	(217)	ACACTGTTTGTGATGCGGTTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC
SPM-16	(217)	ACACTGTTTGTGATGCGGTTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC
SPM-B1	(217)	ACACTGTTTGTGATGCGGTTTCAGTTTAAAAGTCAAGGTTGCCTGTTCTTCGCTTTTGTATAGGAAGTTGCTCCGCATGAC
SPM-A28C	(125)	-----
KM360184	(561)	CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACCTTGCTGTCCAACGATATCAGCAGGTTTCGACTACGCGT
SPM-8_mRNA	(297)	CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACCTTGCTGTCCAACGATATCAGCAGGTTTCGACTACGCGT
SPM-16	(297)	CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACCTTGCTGTCCAACGATATCAGCAGGTTTCGACTACGCGT
SPM-B1	(297)	CCAAGTGTCGGTGGGTGAGGTGGCAGGAGGAAAGCTGGTGAACCTTGCTGTCCAACGATATCAGCAGGTTTCGACTACGCGT
SPM-A28C	(125)	-----
KM360184	(641)	TCATGTTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTACTTCTTGTGGGAGGCTGCTGGCTTC
SPM-8_mRNA	(377)	TCATGTTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC
SPM-16	(377)	TCATGTTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC
SPM-B1	(377)	TCATGTTTCCTACATTACTTGTGGATCGTGCCTATCCAAGTGGCTGTTGTTTTGTATTTCTTGTGGGAGGCTGCTGGCTTC
SPM-A28C	(125)	-----
KM360184	(721)	GCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACCTGTTGT
SPM-8_mRNA	(457)	GCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACCTGTTGT
SPM-16	(457)	GCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACCTGTTGT
SPM-B1	(457)	GCACCCCTTCGTCGGTCTGTTTGGAGTCGTTATACTGATTTTACCACTGCAAGCTGGCTTGACGAAACTCACAACCTGTTGT
SPM-A28C	(125)	-----
KM360184	(801)	AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA
SPM-8_mRNA	(537)	AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA
SPM-16	(537)	AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA
SPM-B1	(537)	AAGACGTGAGACGGCTAAGAGAACGGACAGGCGAATTAACTAATGAGTGAAATTATTGGTGGTATTCAGGTCATTAAAA
SPM-A28C	(125)	-----
KM360184	(881)	TGTACGCTTGGGAGAAACCCCTTCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC
SPM-8_mRNA	(617)	TGTACGCTTGGGAGAAACCCCTTCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC
SPM-16	(617)	TGTACGCTTGGGAGAAACCCCTTCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC
SPM-B1	(617)	TGTACGCTTGGGAGAAACCCCTTCAGCTAGTTGTGAAGGCAGCTCGTGCCTTTGAAATGAGTGCCCTCAGGAAGTCCATC
SPM-A28C	(125)	-----

KM360184 (961) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTACAGTGTTGACACTCGCTCT
 SPM-8_mRNA (697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTACAGTGTTGACACTCGCTCT
 SPM-16 (697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTACAGTGTTGACACTCGCTCT
 SPM-B1 (697) TTCATCAGGAGTACTTTCCTAGGGTTCATGTTGTTCACTGAGCGAAGCATCATGTTTGTACAGTGTTGACACTCGCTCT
 SPM-A28C (125) -----

 KM360184 (1041) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTTCAGTTCAATGTAACACTGA
 SPM-8_mRNA (777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTTCAGTTTAACGTAACACTGA
 SPM-16 (777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTTCAGTTTAACGTAACACTGA
 SPM-B1 (777) CACAGGCACTATGATTACTGCCACTACGATATACCCTATTCAACAGTACTTCAGTATTATTTCAGTTTAACGTAACACTGA
 SPM-A28C (125) -----

 KM360184 (1121) TCATTTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTTCCTTAGTTTGGACGAG
 SPM-8_mRNA (857) TCATTTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTTCCTTAGTTTGGACGAG
 SPM-16 (857) TCATTTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTTCCTTAGTTTGGACGAG
 SPM-B1 (857) TCATTTCCTATGGCAATCGCAAGTTATTCCGAGATGATGGTGTCCATAGAACGTATCCAGGGATTTCCTTAGTTTGGACGAG
 SPM-A28C (125) -----

 KM360184 (1201) CGGTCCGACATGCAAGTGACTCCAAAAATCAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA
 SPM-8 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA
 SPM-16 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA
 SPM-B1 (937) CGGTCCGACATGCAAGTGACTCCAAAAATTAATGGATCTAACAATAACACTTTGTTTAAATCCAAGAAGTCACCACTTGA
 SPM-A28C (125) -----

 KM360184 (1281) AGTAGGCATCGTGCCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG
 SPM-8 (1017) AGTAGGCATCGTGCCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG
 SPM-16 (1017) AGTAGGCATCGTGCCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG
 SPM-B1 (1017) AGTAGGCATCGTGCCCTAAGAAATACTCACCTAGTGAAGTTATGGCTGCAAAGGAGATGCAGGATGATCCTACCCAGATGG
 SPM-A28C (125) -----

 KM360184 (1361) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA
 SPM-8 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA
 SPM-16 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA
 SPM-B1 (1097) ACTATCCTATCAGGCTTAACAAAGTAAGCGCATCGTGACCGGCAGCAATAGTTCTTCAGAAATGACACTTAAGAATATA
 SPM-A28C (125) -----

 KM360184 (1441) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTTGGTCTGTGGGGTCCGGAAGACATCTCTACTGCAACTGCT
 SPM-8 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTTGGTCTGTGGGGTCCGGAAGACATCTCTACTGCAACTGCT
 SPM-16 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTTGGTCTGTGGGGTCCGGAAGACATCTCTACTGCAACTGCT
 SPM-B1 (1177) TCGTTACGTATTCGTAAAGGAAAATTGTGTGCTATCATTTGGTCTGTGGGGTCCGGAAGACATCTCTACTGCAACTGCT
 SPM-A28C (125) -----

 KM360184 (1521) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCTTGGCTGT
 SPM-8 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCTTGGCTGT
 SPM-16 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCTTGGCTGT
 SPM-B1 (1257) CTTAAAAGAATTACCATTGAATAGTGGTACACTTGACGTGAGCGGGAAAATGTCGTACGCTTGTCAAGAGTCTTGGCTGT
 SPM-A28C (125) -----

 KM360184 (1601) TCCCAGGCACAGTACGAGAAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT
 SPM-8 (1337) TCCCAGGCACAGTACGAGAAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT
 SPM-16 (1337) TCCCAGGCACAGTACGAGAAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT
 SPM-B1 (1337) TCCCAGGCACAGTACGAGAAAAACATTTTGTTCGGCCTAACTTACGAACCCACAAAATACAAAGAGGTTTGCAAGGTGTGT
 SPM-A28C (125) -----

 1760
 KM360184 (1681) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG
 SPM-8 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG
 SPM-16 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG
 SPM-B1 (1417) TCGTTGCTGCCTGACTTCAAGCAGTTCCCGTATGGTGACCTGTCTTTAGTGGGAGAACGAGGAGTGTCCCTGTCAGGTGG
 SPM-A28C (125) -----

 KM360184 (1761) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCCTATCTGCAG
 SPM-8 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCCTATCTGCAG
 SPM-16 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCCTATCTGCAG
 SPM-B1 (1497) TCAAAGAGCCAGGATCAATTTGGCTAGAGCAATTTATCGTGAGGCCGACATTTACTTGCTGGATGATCCCCCTATCTGCAG
 SPM-A28C (125) -----

 KM360184 (1841) TGGACGCTAATGTAGGCAGACAACCTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC
 SPM-8 (1577) TGGACGCTAATGTAGGCAGACAACCTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC
 SPM-16 (1577) TGGACGCTAATGTAGGCAGACAACCTGTTTGATGGCTGCATCAAAGGCTACCTCACTGGACGAACTTGCGTCTTGGTCACC

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)	TGAGCTGGTGAAGACAGGAAGCTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG
SPM-8	(1737)	TGAGCTGGTGAAGACAGGAAGCTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG
SPM-16	(1737)	TGAGCTGGTGAAGACAGGAAGCTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG
SPM-B1	(1737)	TGAGCTGGTGAAGACAGGAAGCTGAATTCTCGATGCTGCTATCCAACCAAGAAAATGACGCAACTGAAAACGAAAAGAAAG
SPM-A28C	(125)	-----
KM360184	(2081)	ACCGACCAGCAATGATGCGAGGAATATCAAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG
SPM-8	(1817)	ACCGACCAGCAATGATGCGAGGAATATCAAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG
SPM-16	(1817)	ACCGACCAGCAATGATGCGAGGAATATCAAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG
SPM-B1	(1817)	ACCGACCAGCAATGATGCGAGGAATATCAAAAAATCTCAGTTAAGAGCGACACCGAAATGGAACAGAAGGCTCAAATACAG
SPM-A28C	(125)	-----
KM360184	(2161)	GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCCTGGTGTCT
SPM-8	(1897)	GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCCTGGTGTCT
SPM-16	(1897)	GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCCTGGTGTCT
SPM-B1	(1897)	GAGGCAGAGGAGAGAGCGACAGGTAGCTTGAAGTTTGAGGTGGTGCTCAAGTACCTGAGCTCCGTCCAGTCCCTGGTGTCT
SPM-A28C	(125)	-----
KM360184	(2241)	GGTGTTTACGGCGTTCCCTTGACTGCTGATCACGCAAGGTGCTGCCACCACCTGCCGACTATTGGTTGAGTTTCTGGACTA
SPM-8	(1977)	GGTGTTTACGGCGTTCCCTTGACTGCTGATCACGCAAGGTGCTGCCACCACCTGCCGACTATTGGTTGAGTTTCTGGACTA
SPM-16	(1977)	GGTGTTTACGGCGTTCCCTTGACTGCTGATCACGCAAGGTGCTGCCACCACCTGCCGACTATTGGTTGAGTTTCTGGACTA
SPM-B1	(1977)	GGTGTTTACGGCGTTCCCTTGACTGCTGATCACGCAAG
SPM-A28C	(125)	-----ACACCGACTATTGGTTGAGTTTCTGGACTA
KM360184	(2321)	ACCAAGTATGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT
SPM-8	(2057)	ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT
SPM-16	(2057)	ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT
SPM-B1	(2018)	-----
SPM-A28C	(155)	ACCAAGTGGATTCTTATGAACAATCTTTACCTGAAGGCGTGGATCCAGATACTGACATGAACGCACAAATTGGCTTACTT
KM360184	(2401)	ACAACCTGCTCAGTACCTATACGTTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT
SPM-8	(2137)	ACAACCTGCCCAGTACCTATACGTTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT
SPM-16	(2137)	ACAACCTGCCCAGTACCTATACGTTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT
SPM-B1	(2018)	-----
SPM-A28C	(235)	ACAACCTGCCCAGTACCTATACGTTTTTCGGTGGAGTTATATTGGCTTTAATAGTCATGACCCTCGTCAGAATCACAGCTTT
KM360184	(2481)	CGTAGCGATGACAATGCGAGCTTCTCAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT
SPM-8	(2217)	CGTAGCGATGACAATGCGAGCTTCTCAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT
SPM-16	(2217)	CGTAGCGATGACAATGCGAGCTTCTCAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT
SPM-B1	(2018)	-----
SPM-A28C	(315)	CGTAGCGATGACAATGCGAGCTTCTCAAATCTTCACAACACTATTTACGAAAAATTAATTGTGACAGTAATGAGATTTT
KM360184	(2561)	TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT
SPM-8	(2297)	TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT
SPM-16	(2297)	TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT
SPM-B1	(2018)	-----
SPM-A28C	(395)	TCGATACCAATCCTTCTGGTCGTGTGCTGAACAGATTCTCAAAGACATGGGTGCCATGGATGAGCTTCTTCCTCGCAGT
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)	AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACCTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTC
SPM-8	(2537)	AGGGCACAACCAAGAGTCCTGTATTTGGAATGATTAACCTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTC

SPM-16	(2537)	AGGGCACAACCAAGAGTCTGTATTTGGAATGATTAACCTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTC
SPM-B1	(2018)	-----
SPM-A28C	(635)	AGGGCACAACCAAGAGTCTGTATTTGGAATGATTAACCTCCACTATTTCTGGACTCTCCACTATTAGAAGTTCGGGTTC
KM360184	(2881)	CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC
SPM-8	(2617)	CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC
SPM-16	(2617)	CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC
SPM-B1	(2018)	-----
SPM-A28C	(715)	CAGGATAGACAGATGAAATTGTTTGACGAAGCGCAGAATCTCCACACAAGTGCTTTCCACACATTCTTCGGCGGTTCTAC
KM360184	(2961)	GGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG
SPM-8	(2697)	GGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG
SPM-16	(2697)	GGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG
SPM-B1	(2018)	-----
SPM-A28C	(795)	GGCATTTCGATTGTATCTCGATACTTTGTGTTTGACCTACCTCGGTGTCGTCATGTCAATTTTCATTTTGGGCGACTTTG
KM360184	(3041)	GTGATTTCGATCCCGGTGGGAAGTGTCCGCTCTGGCTGTCTGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT
SPM-8	(2777)	GTGATTTCGATCCCGGTGGGAAGTGTCCGCTCTGGCTGTCTGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT
SPM-16	(2777)	GTGATTTCGATCCCGGTGGGAAGTGTCCGCTCTGGCTGTCTGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT
SPM-B1	(2018)	GTCTTTTCGATCCCGGTGGGAAGTGTCCGCTCTGGCTGTCTGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCATT
SPM-A28C	(875)	GTGATTTCGATCCCGGTGGGAAGTGTCCGCTCTGGCTGTCTGTCAGTCCATGGTGCTGACCATGATGTTGCAGATGGCAGCT
KM360184	(3121)	AGGTTCACAGCTGACTTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA
SPM-8	(2857)	AGGTTCACAGCTGACTTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA
SPM-16	(2857)	AGGTTCACAGCTGACTTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA
SPM-B1	(2095)	AGGTTCACAGCTGACTTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA
SPM-A28C	(955)	AGGTTCACAGCTGACTTTTTTGGGGCAAATGACGGCTGTGGAGAGAGTTCTGGAATACACCAAGCTACCCACGGAGACCAA
KM360184	(3201)	TATGGAGCAAGGACCAACTAACCACCAAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT
SPM-8	(2937)	TATGGAGCAAGGACCAACTAACCACCAAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT
SPM-16	(2937)	TATGGAGCAAGGACCAACTAACCACCAAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT
SPM-B1	(2168)	---GGAGCAAGGAC-----GAATGGCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT
SPM-A28C	(1035)	TATGGAGCAAGGACCAACTAACCACCAAAGGAATGGCCAGTGCTGGTAGAGTGACGTTCTCAAATGTGTACCTGAATT
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-----TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC
SPM-16	(3097)	ACAGGAGCCGGCAAGTCATCGCTCA-----TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC
SPM-B1	(2308)	ACAGGAGCCGGCAAGTCATCGCTCA-----TCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC
SPM-A28C	(1195)	ACAGGAGCCGGCAAGTCATCGCTCACGGCTTTGTTCTCTTTGTTCTCGCGGCTTTGTTCCGGCTTAGTGACATAAGCGGC
KM360184	(3421)	AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA
SPM-8	(3121)	-----
SPM-16	(3133)	GTTG----ATATACG-GTTAAAC-----ATTGTTAGGAAAACTTTGAGATCGAAAATATCAATTATTCCACAAGA
SPM-B1	(2368)	AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA
SPM-A28C	(1275)	AGCATCAAAATTGACGGTGTGGACACCGAAGGATTAGCCAAAAAGACTTTGAGATCGAAAATATCAATTATTCCACAAGA
KM360184	(3501)	GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTT----GGAGG
SPM-8	(3121)	-----GAGG
SPM-16	(3201)	GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTTATATGGAGG
SPM-B1	(2448)	GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTT----GGAGG
SPM-A28C	(1355)	GCCGGTGCTGTTCTCGGCTACTCTGCGATACAATTTGGACCCGTTTCGACGATTACAGCGACGACGATATTT----GGAGG
KM360184	(3577)	GCGTTGGAACAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT
SPM-8	(3125)	GCGTTGGAACAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT
SPM-16	(3281)	GCGTTGGAACAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT
SPM-B1	(2524)	GCGTTGGAACAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT
SPM-A28C	(1431)	GCGTTGGAACAGGTGGAATTAAGAAGGAATACCGGCTTTAGACTTTAAGGTCGCTGAAGGTGGTACTAACTTCTCTAT
KM360184	(3657)	GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAAATACTCATCATGGACGAAGCTACCGCTA
SPM-8	(3205)	GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAAATACTCATCATGGACGAAGCTACCGCTA
SPM-16	(3361)	GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAAATACTCATCATGGACGAAGCTACCGCTA
SPM-B1	(2604)	GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAAATACTCATCATGGACGAAGCTACCGCTA
SPM-A28C	(1511)	GGGACAACGTCAGTTGGTTTGCTTGGCTCGTGCCATTCTACGCTCTAACAAAAATACTCATCATGGACGAAGCTACCGCTA
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)	AGGTCGCTAAGGC CAAATATGATAGTGATAATAAGGAAGCTTAA
SPM-8	(3525)	AGGTCGCTAAGGC-----
SPM-16	(3681)	AGGTCGCTAAGGC-----
SPM-B1	(2924)	AGGTCGCTAAGGC-----
SPM-A28C	(1521)	AGGTCGCTAAGGC-----

Figure S5. Alignment of partial mRNA sequences of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (*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)	MGVENKNNVQNAEGPARKTYKKPNILSRIFLWWMCPVLITHFNKRNVEESDLIPPSNLYNSERQGEYLERYWLAEIENAT
SPM-8	(1)	-----
SPM-16	(1)	-----
SPM-B1	(1)	-----
SPM-A28C	(1)	-----
KM360184	(81)	IENREPSLWKALRKAYWVSYPGAIFII IQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMQCQHHN
SPM-8	(1)	-----WKALRKAYWVSYPGAIFII IQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMQCQHHN
SPM-16	(1)	-----WKALRKAYWVSYPGAIFII IQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMQCQHHN
SPM-B1	(1)	-----WKALRKAYWVSYPGAIFII IQSAARTYQPLLFSQLLSYWSVDSEMTQQDAGLYALAMLGLNFVSMQCQHHN
SPM-A28C	(1)	-----WKALRKAYWVSYPGAIFII IQSAARTYQPLLFSQLLSY-----
KM360184	(161)	TLFVMRFSCLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF
SPM-8	(73)	TLFVMRFSCLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF
SPM-16	(73)	TLFVMRFSCLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF
SPM-B1	(73)	TLFVMRFSCLKVKVACSSLLYRKLLRMTQVSVGEVAGGKLVNLLSNDITRFDYAFMFLHYLWIVPIQVAVVLYFLWEAAGF
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)	RSDMQVTPKINGSNNTLTFKSKKSPLEVGIVPKKYPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSEMTLKNI
SPM-8	(313)	RSDMQVTPKINGSNNTLTFKSKKSPLEVGIVPKKYPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSEMTLKNI
SPM-16	(313)	RSDMQVTPKINGSNNTLTFKSKKSPLEVGIVPKKYPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSEMTLKNI
SPM-B1	(313)	RSDMQVTPKINGSNNTLTFKSKKSPLEVGIVPKKYPSEVMAAKEMQDDPTQMDYPIRLNKVSASWTGSNSSEMTLKNI
SPM-A28C	(40)	-----
KM360184	(481)	SLRIRK GKLC AII GPVGS GKTSL LQ LLLKELPLNSGTL DVS GKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC
SPM-8	(393)	SLRIRK GKLC AII GPVGS GKTSL LQ LLLKELPLNSGTL DVS GKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC
SPM-16	(393)	SLRIRK GKLC AII GPVGS GKTSL LQ LLLKELPLNSGTL DVS GKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC
SPM-B1	(393)	SLRIRK GKLC AII GPVGS GKTSL LQ LLLKELPLNSGTL DVS GKMSYACQESWLFPGTVRENILFGLTYEPTKYKEVCKVC
SPM-A28C	(40)	-----
KM360184	(561)	SLLPDFKQFPYGDL SLVGERGVSLSGGQ RARINLARA IYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT
SPM-8	(473)	SLLPDFKQFPYGDL SLVGERGVSLSGGQ RARINLARA IYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT
SPM-16	(473)	SLLPDFKQFPYGDL SLVGERGVSLSGGQ RARINLARA IYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT
SPM-B1	(473)	SLLPDFKQFPYGDL SLVGERGVSLSGGQ RARINLARA IYREADIYLLDDPLSAVDANVGRQLFDGCIKGYLTGRTCVLVT
SPM-A28C	(40)	-----
KM360184	(641)	HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ
SPM-8	(553)	HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ
SPM-16	(553)	HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ
SPM-B1	(553)	HQIHYLKAADFIVVLNEGSVENMGTYDELVKTGTEFSMLLSNQENDATENEKKDRPAMMRGISKISVKSDTEMEQKAQIQ
SPM-A28C	(40)	-----
KM360184	(721)	EAEERATGSLKFEVV LKYLSSVQSWCLVFTAFVLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVD PPTDMNAQIGLL
SPM-8	(633)	EAEERATGSLKFEVV LKYLSSVQSWCLVFTAFVLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVD PPTDMNAQIGLL
SPM-16	(633)	EAEERATGSLKFEVV LKYLSSVQSWCLVFTAFVLVLLITQGAATTADYWLSFWTNQVDSYEQSLPEGVD PPTDMNAQIGLL
SPM-B1	(633)	EAEERATGSLKFEVV LKYLSSVQSWCLVFTAFVLVLLITQ-----
SPM-A28C	(40)	-----
KM360184	(801)	TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNP SGRVLNRF SKDMGAMDELLPRS
SPM-8	(713)	TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNP SGRVLNRF SKDMGAMDELLPRS
SPM-16	(713)	TTAQYLYVFGGVILALIVMTLVRITAFVAMTMRASQNLHNTIYEKLIVTVMRFFDTNP SGRVLNRF SKDMGAMDELLPRS
SPM-B1	(672)	-----
SPM-A28C	(40)	-----
KM360184	(881)	LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMRLRWYLN TAAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS
SPM-8	(793)	LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMRLRWYLN TAAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS
SPM-16	(793)	LLETVQMYLSLTSVLVLNATALPWTLIPTSVLIVIFVLMRLRWYLN TAAQAVKRLEGTTKSPVFGMINSTISGLSTIRSSGS
SPM-B1	(672)	-----
SPM-A28C	(40)	-----

KM360184	(961)	QDRQMKLFDEAQNLTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVGQSMVLTMMLQMAA
SPM-8	(873)	QDRQMKLFDEAQNLTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVSQSMVLTMMLQMAA
SPM-16	(873)	QDRQMKLFDEAQNLTSAFHTFFGGSTAFALYLDTLCLTYLGVVMSIFILGDFGDLIPVGSVGLAVSQSMVLTMMLQMAA
SPM-B1	(672)	-----GVLIIPVGSVGLAVSQSMVLTMMLQMAF
SPM-A28C	(40)	-----
KM360184	(1041)	RSITADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFNSVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR
SPM-8	(953)	RFTADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFNSVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR
SPM-16	(953)	RFTADFLGQMTAVERVLEYTKLPTETNMEQGPTNPPKEWPSAGRVTFNSVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR
SPM-B1	(699)	RFTADFLGQMTAVERVLENTQLPTGSKD-----EWPSAGRVTFNSVYLNYSMEDPPVLKDLNFEIQSGWKVGVVGR
SPM-A28C	(40)	-----
KM360184	(1121)	TGACKSSLIAALFRLSDISGSIKIDGVDTEGLAKKTLRSKISIIIPQEPVLFSATLRYNLDPFDDYSDDDIWRALEQVELK
SPM-8	(1033)	TGACKSSLEGVGTGGIKRRNTGFRL-----
SPM-16	(1033)	TGACKSSHEIKYVDILVNTFVG-----KTLRSKISIIIPQEPVLFSATLRYNLDPFDDYSDDDIYMEGVGTGGI
SPM-B1	(770)	TGACKSSLIAALFRLSDISGSIKIDGVDTEGLAKKTLRSKISIIIPQEPVLFSATLRYNLDPFDDYSDDDIWRALEQVELK
SPM-A28C	(40)	-----
KM360184	(1201)	EGIPALDFKVAEGGTNFSMGQRQLVCLARAILRSNKILIMDEATANVDPQTDALIQKTIRRFASCTVLTIAHRLNTIMD
SPM-8	(1058)	-----
SPM-16	(1101)	KRRNTGFRL-----
SPM-B1	(850)	EGIPALDFKVAEGGTNFSMGQRQLVCLARAILRSNKILIMDEATANVDPQTDALIQKTIRRFASCTVLTIAHRLNTIMD
SPM-A28C	(40)	-----
KM360184	(1281)	SDRVLVMDQGEVAEFDHPHILLSNPNSKFFSMVRETGESMTRTLM EVAKAKYDS DNKEA
SPM-8	(1058)	-----
SPM-16	(1110)	-----
SPM-B1	(930)	SDRVLVMDQGEVAEFDHPHILLSNPNSKFFSMVRETGESMTRTLM EVAK-----
SPM-A28C	(40)	-----

Figure S6. Alignment of putative amino acid sequences predicted from partial mRNA sequences of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (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.

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

Figure S7. Alignment of nucleotide sequences from potential off-target sites for exon 13 and exon 19 sgRNA in *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (ABCC2) knockout lines SPM-A28C and SPM-B1. 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.

Table S1. Primer names and sequences used for PCR amplification and nucleotide sequencing of *Helicoverpa zea* ATP binding cassette transporter subfamily C2 (ABCC2) gene and off-target sites. 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	GTGGGAAGTGTCTGGTCTGGC	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	GACCCACAGGACCAATGAT	PCR/Sequencing ABCC2
3804Hz_ABCC2Ex13F	GACCGACCAGCAATGATGCG	PCR/Sequencing ABCC2
3805Hz_ABCC2Ex14R	GGATCCACGCCTTCAGGTAA	PCR/Sequencing ABCC2
3806Hz_ABCC2Ex19F	GTGATTTGATCCCGGTGGGA	PCR/Sequencing ABCC2
3807Hz_ABCC2Ex20R	GCCATTCTTTGGTGGGTTA	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	ACGCGTTTAAATGAGTACAACCG	PCR/Sequencing off target
4035Hz_Scf_18_204763R	ATGCAGTAGGTTAGGCGCCT	PCR/Sequencing off target
4036Hz_Scf219_70159F	TTATGACTTGTTGCCACAACC	PCR/Sequencing off target
4037Hz_Scf219_70569R	CGCCCTTATAGGTACGCCTT	PCR/Sequencing off target
4038Hz_Scf86_289141F	CAGGTCCTAAATATTTCATGCACC	PCR/Sequencing off target
4039Hz_Scf86_289549R	CATGGCCTTTGTTTGTGGAT	PCR/Sequencing off target

Table S2: : Functional domains predicted in the ATP binding cassette transporter subfamily C2 (ABCC2) protein of *Helicoverpa zea* predicted using online Simple Modular Architecture Research Tool (SMART: <http://smart.embl-heidelberg.de>, accessed on 16 August 2021)

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 ATP binding cassette transporter subfamily C2 (*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