

**Table 4. Sequence variations identified in the 31 exons of the *Abcc6* gene in strains C3H and DBA compared to B6 (GenBank accession nos. EF109740 and EF 109741)**

SNP position (bp)	Exon	Nucleotide change (B/D/H)	Amino acid (position: B/D/H)
47	1	C/T/T	14:C/C/C
<b>88</b>	<b>2</b>	<b>C/T/T</b>	<b>28:A/V/V</b>
116	2	T/C/C	37:F/F/F
<b>288</b>	<b>3</b>	<b>G/A/A</b>	<b>95:V/M/M</b>
385	4	T/T/A	127:L/Q/L
<b>417</b>	<b>4</b>	<b>T/G/G</b>	<b>138:S/A/A</b>
<b>456</b>	<b>4</b>	<b>A/G/G</b>	<b>151:I/V/V</b>
696	7	A/A/G	231:R/G/R
1034	9	G/A/A	343:S/S/S
1184	10	C/T/T	393:V/V/V
1250	10	C/T/T	415:I/I/I
1289	10	G/A/A	428:G/G/G
1298	10	C/T/C	431:L/L/L
1588	12	T/T/C	528:L/L/P
1719	13	G/G/T	572:V/V/L
<b>1866</b>	<b>14</b>	<b>C/T/T</b>	<b>621:R/C/C</b>
2081	17	T/C/C	692:A/A/A
<b>2122</b>	<b>17</b>	<b>T/C/C</b>	<b>706:V/A/A</b>
2180	17	T/C/C	725:D/D/D
2297	18	T/C/C	764:A/A/A
<b>2305</b>	<b>18</b>	<b>A/G/G</b>	<b>767:K/R/R</b>
2521	19	T/T/C	839:L/L/P
<b>2785</b>	<b>22</b>	<b>C/T/T</b>	<b>927:T/I/I</b>
3077	23	T/A/A	1024:A/A/A
3178	23	T/A/T	1058:L/Q/L
3197	23	T/C/C	1064:Y/Y/Y
3218	23	C/T/T	1071:V/V/V
<b>4107</b>	<b>29</b>	<b>G/A/A</b>	<b>1368:A/T/T</b>
4114	29	T/T/C	1370:L/L/P
4355	30	T/C/C	1450:L/L/L
4357	30	T/C/T	1451:I/T/I
4388	30	T/C/C	1461:C/C/C
4433	31	C/T/C	1476:G/G/G
<b>4505</b>	<b>3'-UTR</b>	<b>A/G/G</b>	—
<b>4515</b>	<b>3'-UTR</b>	<b>A/T/T</b>	—
<b>4925-4934</b>	<b>3'-UTR</b>	<b>10-bp deletion in D and H</b>	—

Sequencing data from DBA and C3H strains were compared with public sequence from Ensembl (<http://www.ensembl.org>), and National Center for Biotechnology Information (NCBI) (<http://www.ncbi.nlm.nih.gov>). SNPs resulting in amino acid changes or variations in 3'-UTR in both the DBA and C3H strains are in bold letters. B, B6; D, DBA; H, C3H.