Supplementary Information

	Helix 1	Helix 2	Helix 3	Helix 4	Helix 5	Helix 5b	Helix 6
NCBI Protein	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM	LSQKLCSCLLSNVAMAMGAQLIGKFEAKGM	DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
SMART	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM		
Bruder et al., 2007	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM		DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
Park SK et al., 2010	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM		DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
Jpred	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM	LSQKLCSCLLSNVAMAMGAQLIGKFEAKGM	DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
HMMTOP	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM	LSQKLCSCLLSNVAMAMGAQLIGKFEAKGM	DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
Porter	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM	LSQKLCSCLLSNVAMAMGAQLIGKFEAKGM	DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ
TMpred	MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFSGILIWLRLKIQS	PFIADPFLVAIQYQLPLLLLLSFTYTALTIARAVVQEKERRLKEYMRMMGLS	YMRMMGLSSWLHWSAWFLLFFLFLLIAASFMTLLFCVKVKPN	SDPSLVLAFLLCFAISTISFSFMVSTFFS	KANMAAAFGGFLYFFTYIPYFFVAPRYNWM	LSQKLCSCLLSNVAMAMGAQLIGKFEAKGM	DDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQ

Figure S1. *Cont.*

Helix 7

GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE
GLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSE

Helix 8

GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV
GFDIALNLLFAMAFLASTFSILAVSERAVQAKHVQFVSGV

Helix 9

HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG
HVASFWLSALLWDLISFLIPSLLLLVVFKAFDVRAFTRDG

Helix 10

HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA
HMADTLLLLLLYGWAIIPLMYLMNFFFLGAA

Helix 11

TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK
TAYTRLTIFNILSGIATFLMVTIMRIPAVK

Helix 11b

LEELSKTLDHVFLVLPNHCLGMAVSSFYENYETRRYCT

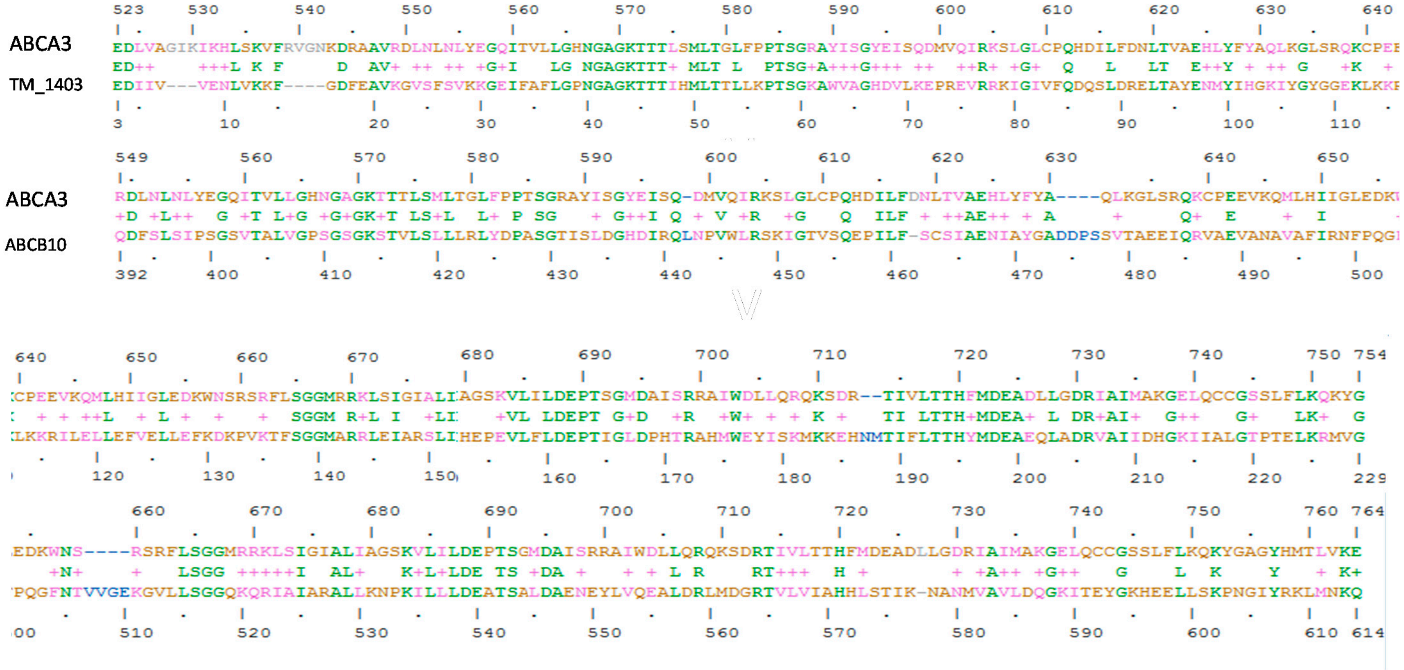
LEELSKTLDHVFLVLPNHCLGMAVSSFYENYETRRYCT

LEELSKTLDHVFLVLPNHCLGMAVSSFYENYETRRYCT

Helix 12

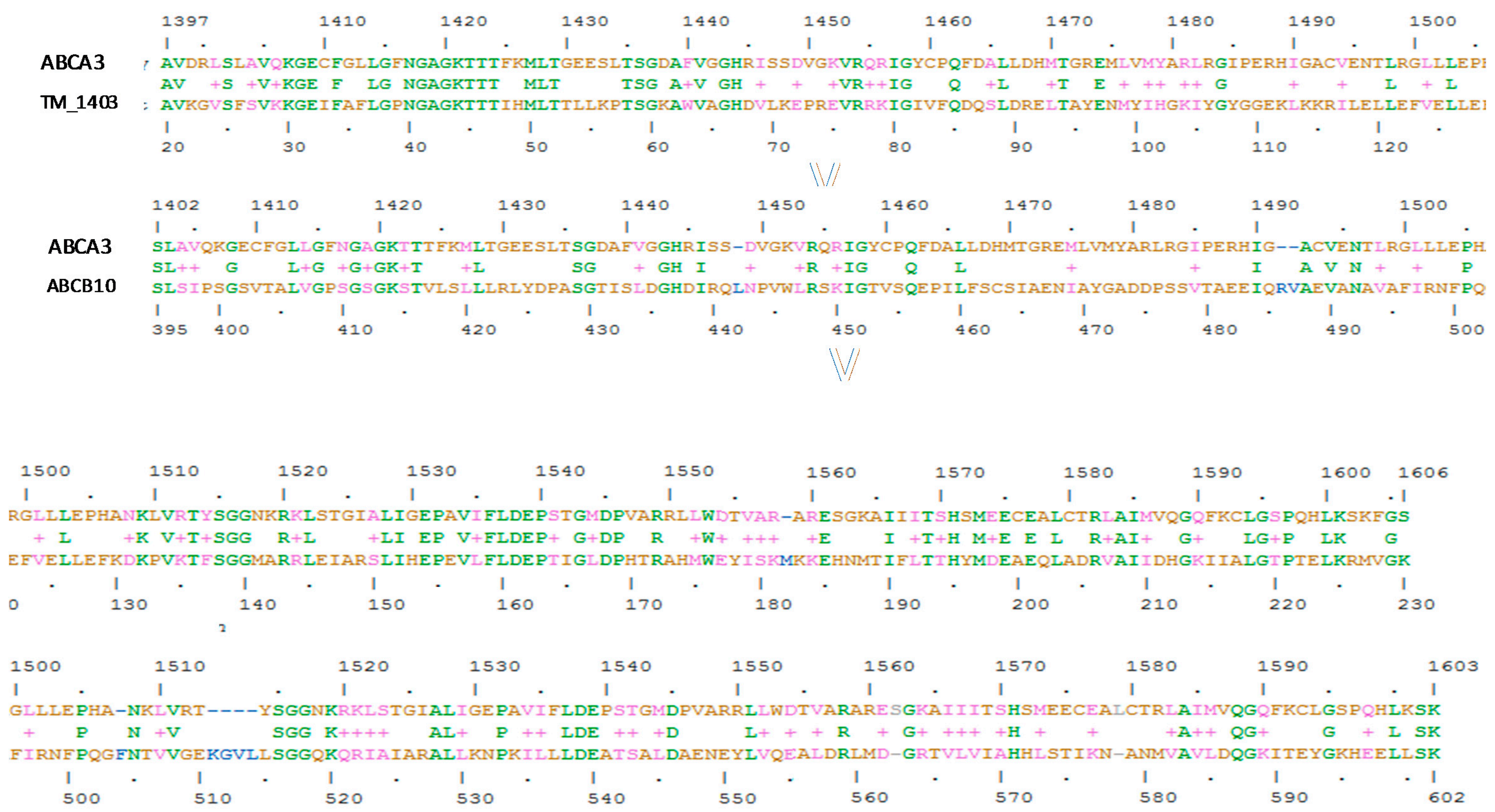
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ
SAPGVGRFVASMAASGCAYLILLFLIETNLLQ

Figure S1. Prediction of TMD1 and TMD2 helix domains (in red) from sequences reported by different authors/software. For Bruder E. *et al*. 2007 see reference [36], for Park S.K. *et al*. 2010 see reference [37].



(A)

Figure S2. *Cont.*



```
         1397         1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
         |  .    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .
ABCA3    AVDRLSLAVQKGECFGLLGFNGAGKTTTFKMLTGEESLTSGDAFVGGHRISSDVGKVRQRIGYCPQFDALLDHMTGREMLVMYARLRGIPERHIGACVENTLRGLLLEP
         AV  +S +V+KGE F  LG NGAGKTTT  MLT     TSG A+V GH +  +  +VR++IG   Q  +L   +T  E + ++ ++ G     +   +   L  + L
TM_1403  AVKGVSFSVKKGEIFAFLGPNGAGKTTTIHMLTTLLKPTSGKAWVAGHDVLKEPREVRRKIGIVFQDQSLDRELTAYENMYIHGKIYGYGGEKLKKRILELLEFVELLE
         |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .
         20        30        40        50        60        70        80        90        100       110       120

         1402    1410      1420      1430      1440       1450      1460      1470      1480      1490        1500
         |  .    |    .    |    .    |    .    |    .     |    .    |    .    |    .    |    .    |      .    |    .
ABCA3    SLAVQKGECFGLLGFNGAGKTTTFKMLTGEESLTSGDAFVGGHRISS-DVGKVRQRIGYCPQFDALLDHMTGREMLVMYARLRGIPERHIG--ACVENTLRGLLLEPH
         SL++  G    L+G +G+GK+T   +L       SG   + GH I   +   +R +IG   Q   L        +         +    I   A V N +  +   P
ABCB10   SLSIPSGSVTALVGPSGSGKSTVLSLLLRLYDPASGTISLDGHDIRQLNPVWLRSKIGTVSQEPILFSCSIAENIAYGADDPSSVTAEEIQRVAEVANAVAFIRNFPQ
         |    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |
         395  400       410       420       430       440       450       460       470       480       490       500


 1500      1510      1520      1530      1540      1550       1560      1570      1580      1590      1600  1606
 |    .    |    .    |    .    |    .    |    .    |    .     |    .    |    .    |    .    |    .    |    .|
RGLLLEPHANKLVRTYSGGNKRKLSTGIALIGEPAVIFLDEPSTGMDPVARRLLWDTVAR-ARESGKAIIITSHSMEECEALCTRLAIMVQGQFKCLGSPQHLKSKFGS
  + L    +K V+T+SGG  R+L    +LI EP V+FLDEP+ G+DP  R  +W+ +++  +E    I +T+H M+E E L  R+AI+  G+   LG+P  LK   G
EFVELLEFKDKPVKTFSGGMARRLEIARSLIHEPEVLFLDEPTIGLDPHTRAHMWEYISKMKKEHNMTIFLTTHYMDEAEQLADRVAIIDHGKIIALGTPTELKRMVGK
   .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |
0       130       140       150       160       170       180       190       200       210       220       230

1500       1510          1520      1530      1540      1550      1560      1570      1580      1590         1603
|    .     |        .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    |    .    .  |
GLLLEPHA-NKLVRT----YSGGNKRKLSTGIALIGEPAVIFLDEPSTGMDPVARRLLWDTVARARESGKAIIITSHSMEECEALCTRLAIMVQGQFKCLGSPQHLKSK
 +   P   N +V       SGG K++++   AL+  P ++ LDE ++ +D     L+ + + R  + G+ +++ +H +   +     +A++ QG+    G  + L SK
FIRNFPQGFNTVVGEKGVLLSGGQKQRIAIARALLKNPKILLLDEATSALDAENEYLVQEALDRLMD-GRTVLVIAHHLSTIKN-ANMVAVLDQGKITEYGKHEELLSK
    |    .    |    .    |    .    |    .    |    .    |    .    |     .    |    .     |    .    |    .    .  |
    500       510       520       530       540       550       560        570        580       590         602
```

(**B**)

Figure S2. From the secondary structure comparative analyses on the ABCA3 protein we found that NBD1 (**A**) and NBD2 (**B**) respectively have 35% and 38% similarity with the correspondent NBDs of *Thermotoga maritime* (TM_1403), and a similarity of 28% and 23% respectively with NBDs of human ABCB10. In the alignment, amino acids are represented in green (when amino acids are the same), pink (when the amino acid lateral groups are similar), orange (when amino acid9.s are different), blue (when a deletion occurred) and grey (when an insertion occurred).