Additional File 2

Figures 1-9 show the protein sequence alignments of the alternative exons. The upper sequences, termed Mhc1, Mhc3, and Mhc4, respectively, represent either the variant “a” exons (e.g. Figure 1 or Figure 3) or the corresponding parts of constitutive exons (e.g. Figure 2).

Figure 2 and Figure 6A: Most genes do not have introns at the positions corresponding to the alternatively spliced *Dap*, *Tic*, *Pdc*, and *Bm* exons. Because these exons span the variable loop-1 (Figure 2) and loop2 (Figure 6A) regions their start and end positions are not conserved. In Figure 6A, the variant “b” sequences of *Bm*, *Dap*, *Pdc*, and *Tic* have been directly aligned with their corresponding variant “a” sequences.

Figure 9: Alignment of the potential carboxy-termini of the *Mhc* genes. For better understanding a gap (-) has been introduced between the last constitutive exon and the following alternative exons. In the case of *AeaMhc3*, *CpqMhc3*, *CpqMhc4*, and *AngExon15* the carboxy-termini are elongations of the last constitutive exon and not separated exons.

The alignments of the sections of the *Mhc1* genes of Figure 1 (main manuscript) showing the relationship between the exon-intron structures of the regions containing the alternatively spliced exons have been taken from Figure 2 (main manuscript) for better comparison. Continuous lines connect variants that are almost identical and thus expected to be derived from a common ancestor. Bold lines connecting alternative exons in regions containing multiple variants per *Mhc1* gene highlight particularly conserved exons in these sets. Dotted lines represent putative connections between certain variants although their identity is not very strong on the protein level.

For the construction of the figures showing the comparison of the sequence identity between each exon and all variant exons of every other Mhc1 proteins see Materials and Methods in the main manuscript. For interpretation, the figures have to be read in columns. The highest identity between an exon listed on top and any variant of a certain Mhc1 protein listed on the left side has been set to 1 (red color) while the differences of the values of the lower identity exons to the value of the highest identity have been plotted for the other combinations of exons. Thus, in every column the highest identity of the named exon to one of the variants of the other Mhc1 proteins is visualized.

Figure 1

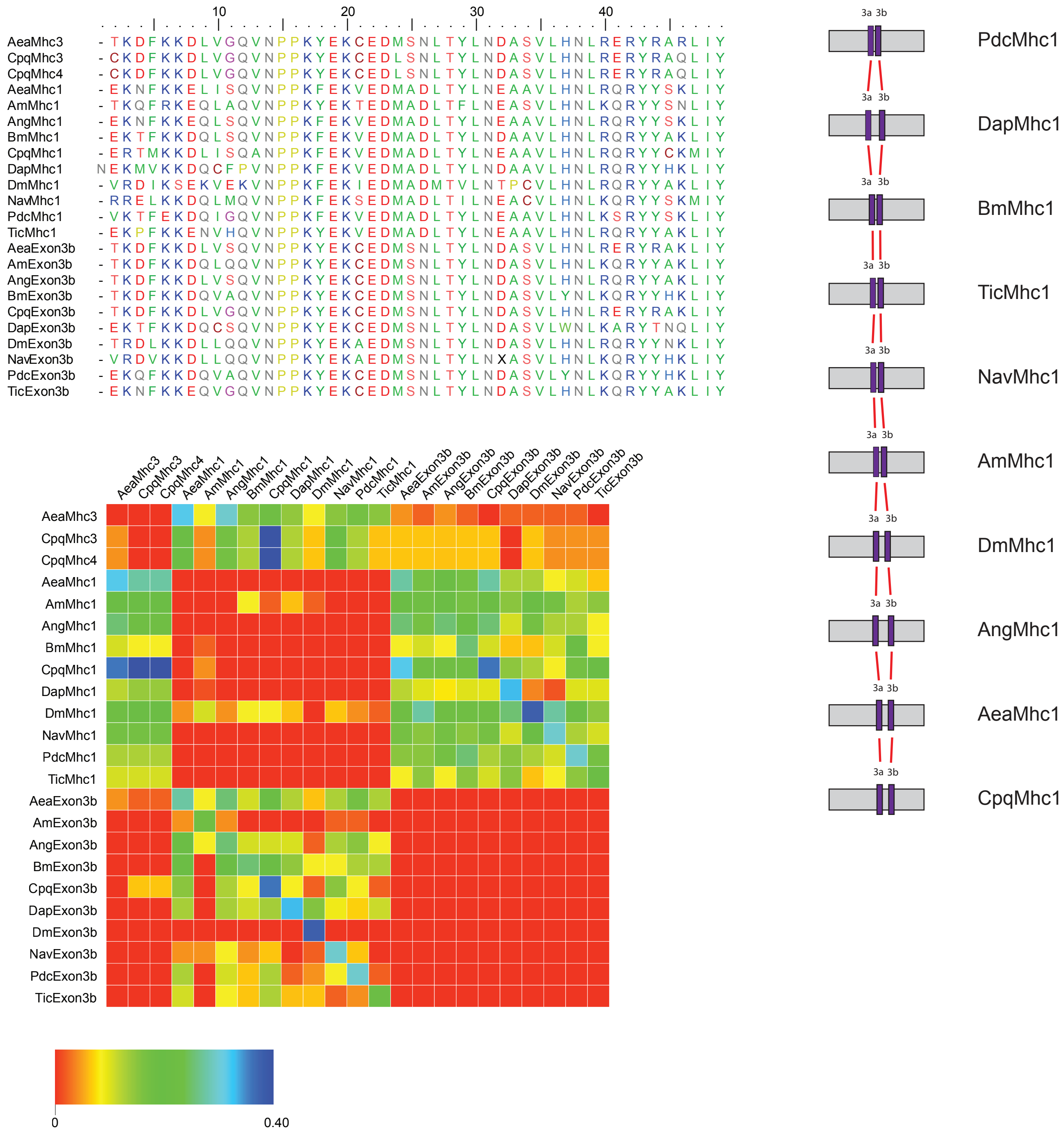
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Figure 2

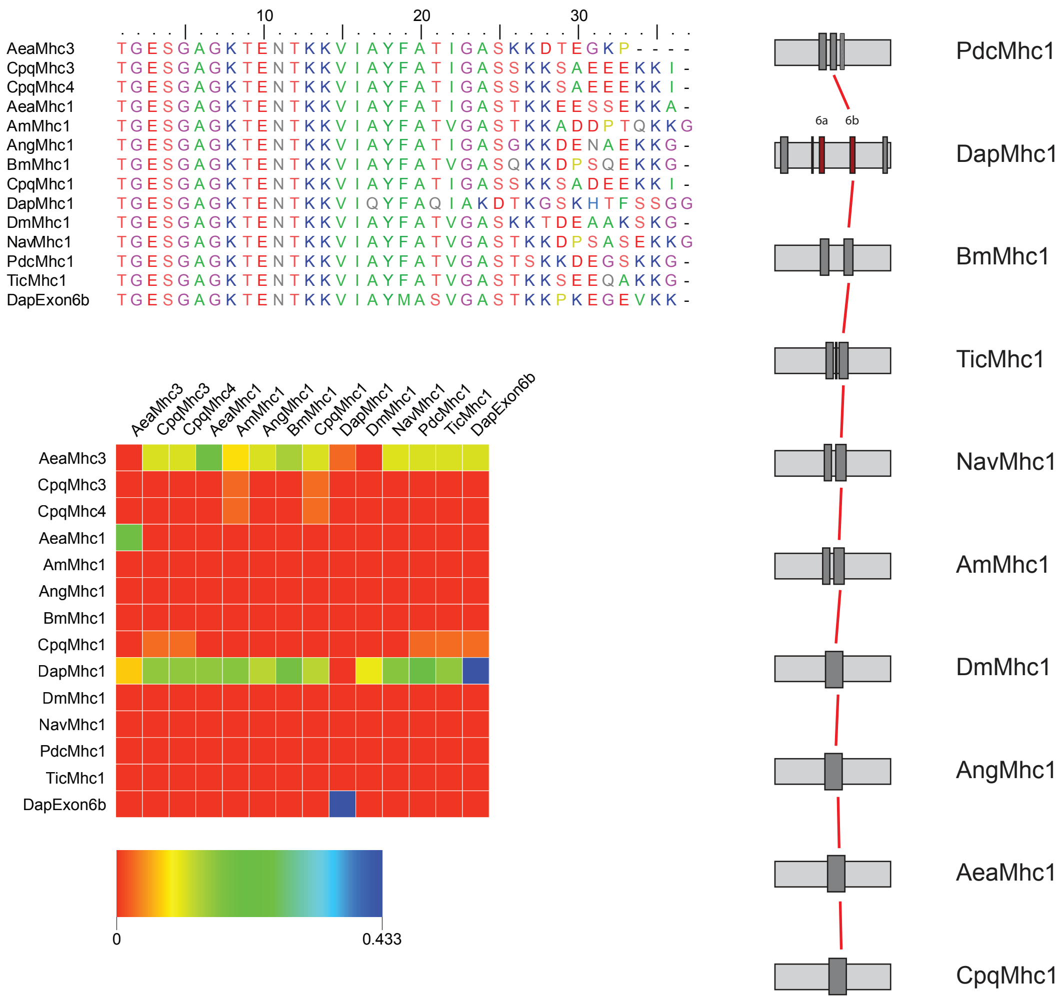

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Figure 3

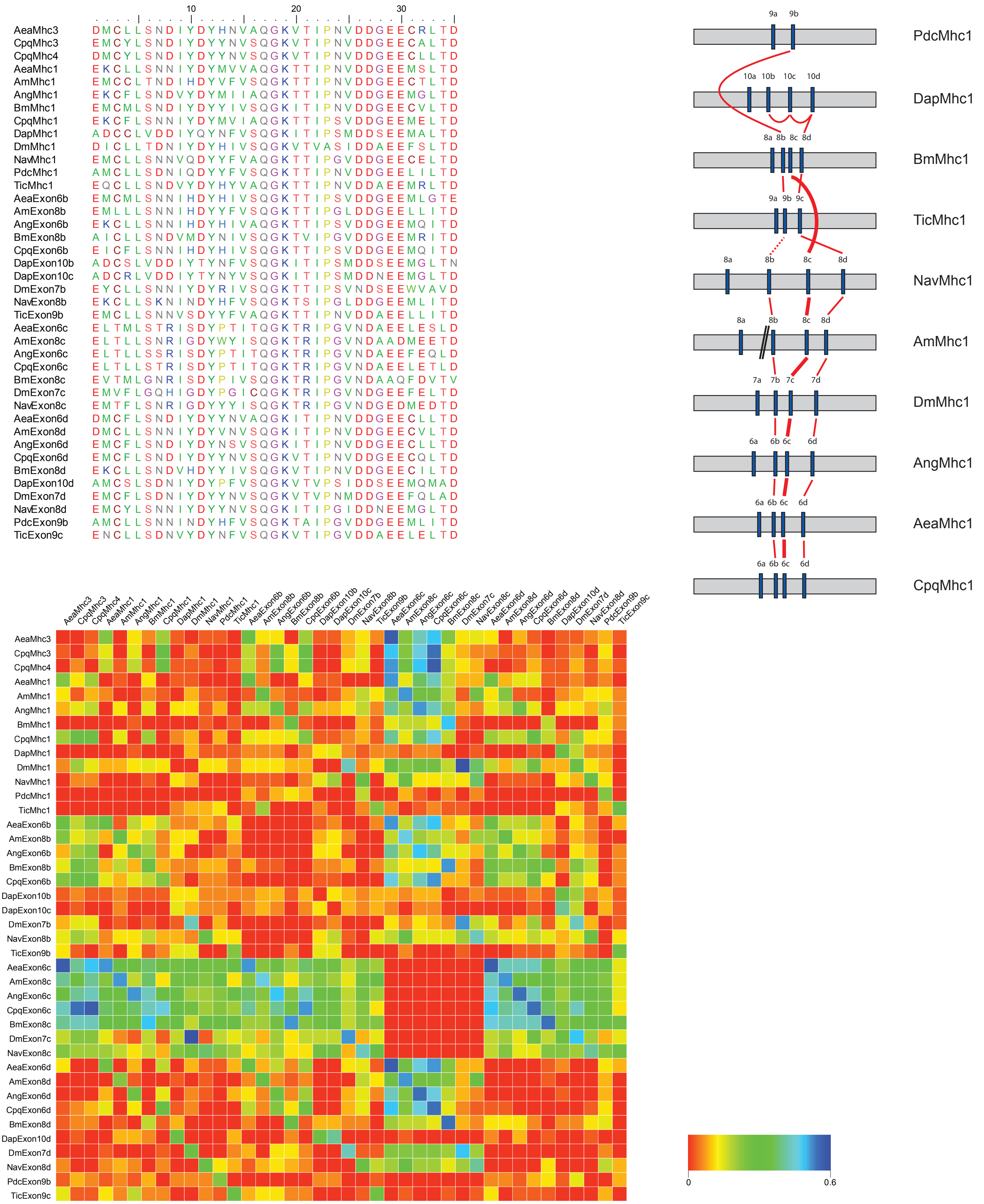

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Figure 4

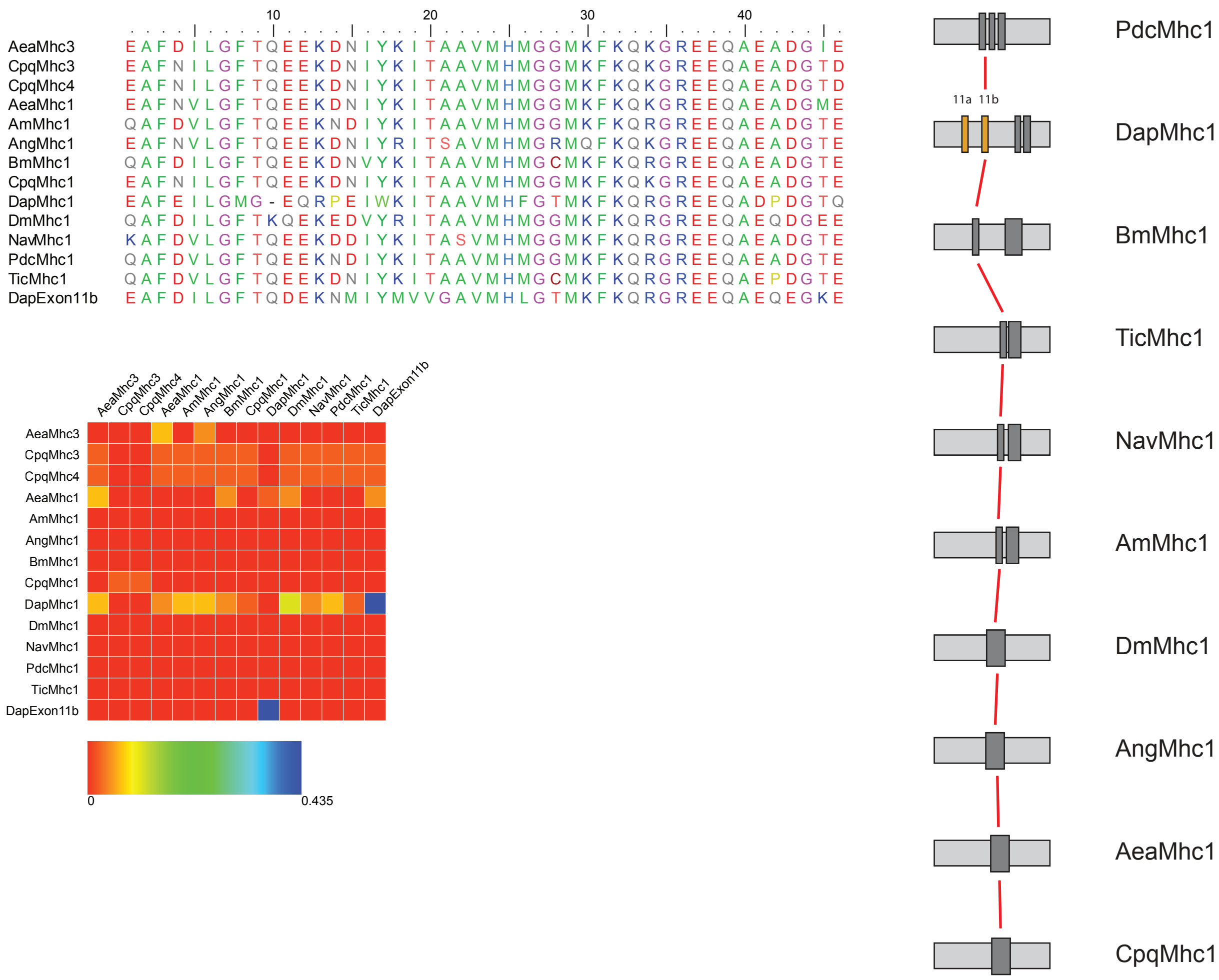
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Figure 5

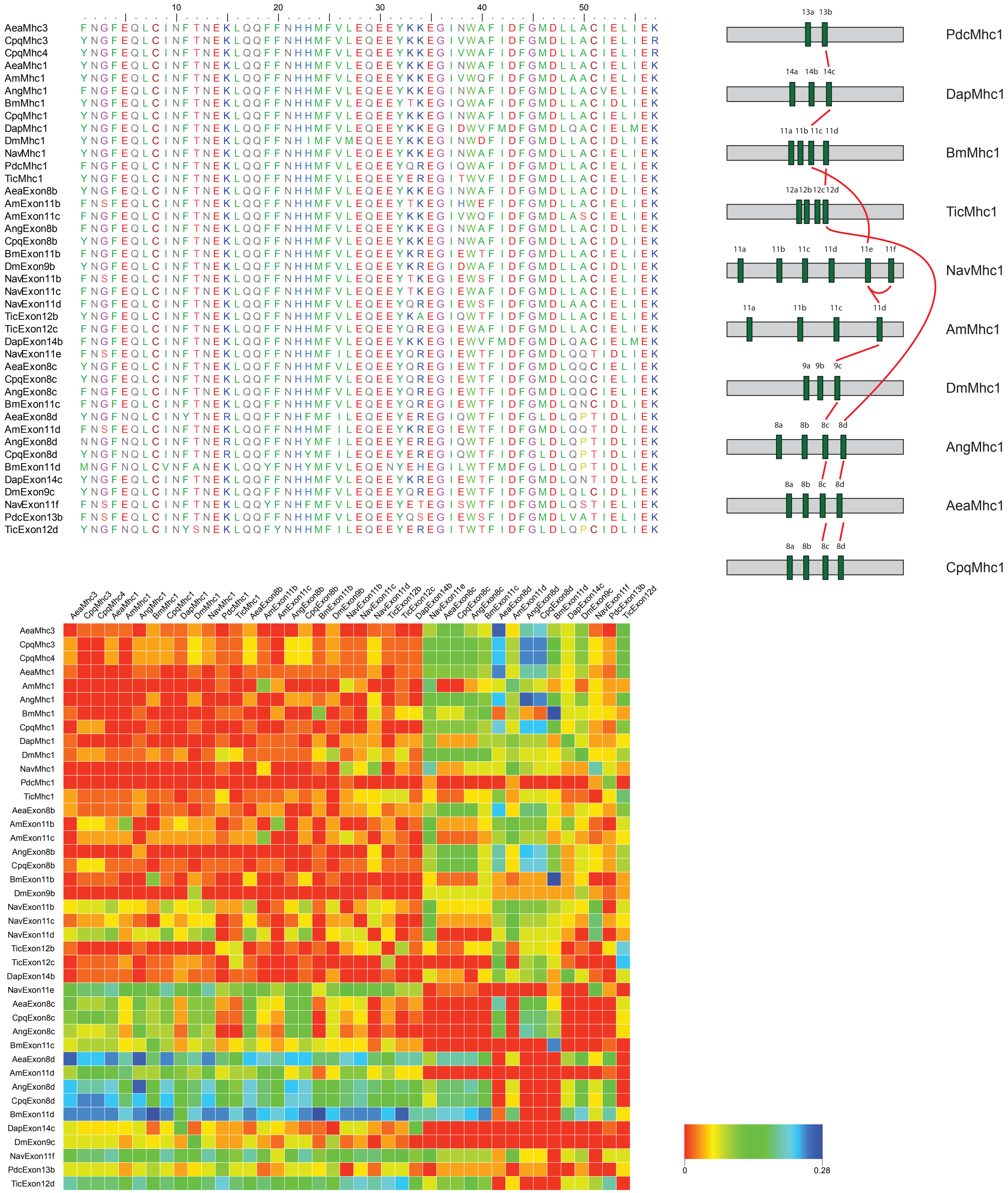

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Figure 6

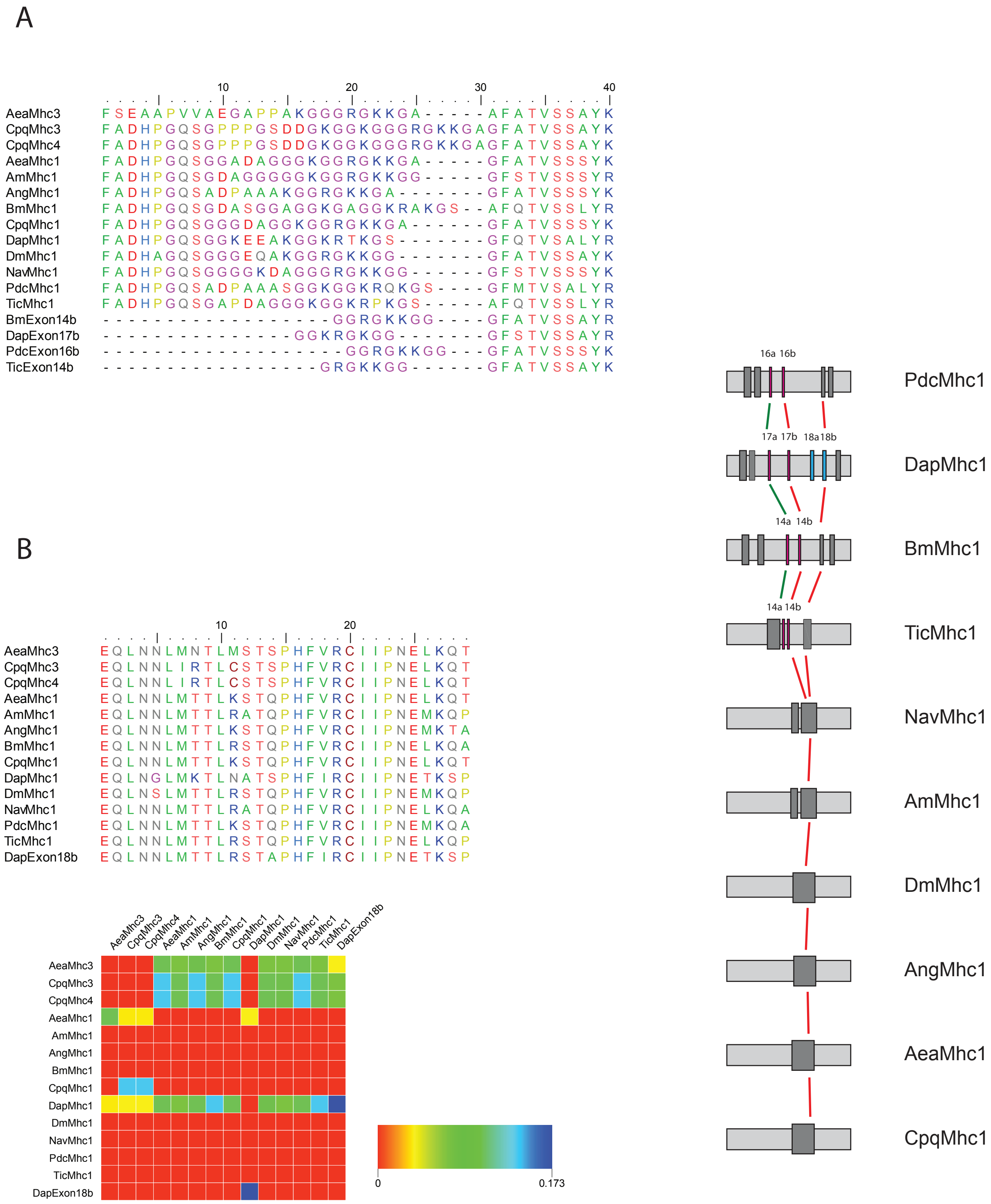
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Figure 7


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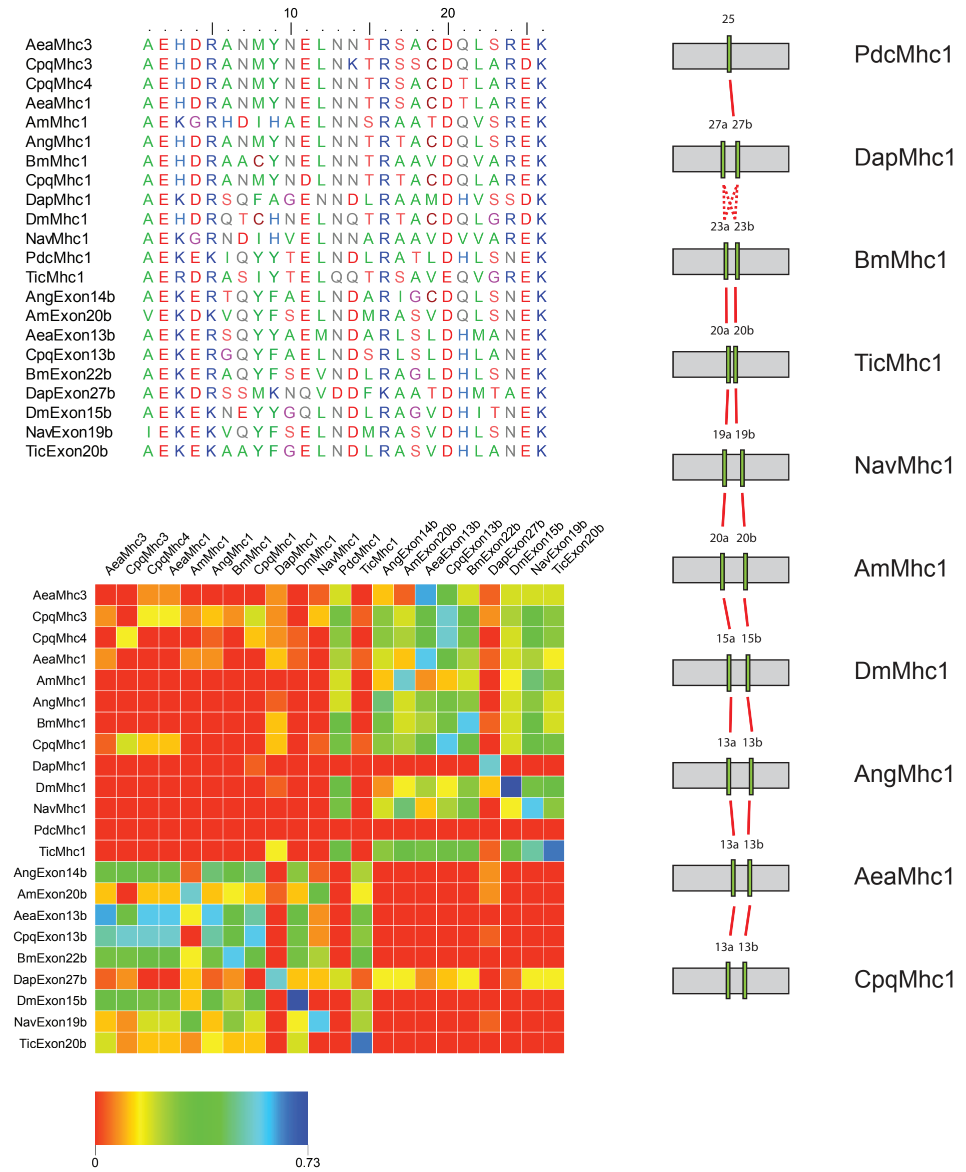
CpqExon10b YKILNPKAAEAE----KDPMKVAQVILEASGLDTESYRLGNTK
AngExon10b YMILNPKGVEAE----KDLKKCAQVIMDAAGLDSELYRLGNTK
TicExon16b YKILNPAAVDKE----SDPKKCADLILQATGLDADLYRLGHTK
AeaExon10c YKILCPKLIEGI----EDGKKVGGIIIESVNMGQEHYRLGVTK
CpqExon10c YKILCIKEIYEI----KSEKKCAEKIIDSVALNEDLYRLGNTK
AngExon10c YKILNPKAVDGLDVE-KEGRKIAQLIIEAVGLNADQYRLGMTK
NavExon14b YKIIAPAACDKVG---GDPKKCAEAILENSGLDPEQYRLGHTK
DmExon11d YKIMCPKLLQGV----EKDKKATEIIIKFIDLPEDQYRLGNTK
AmExon14b YKILAPAAVDKVA---SDPKKAAEAILESTGLDPDQYRLGHTK
BmExon17b YKILAPQAVDKE----SDPKKIAQVILEATGLDVESYRLGHTK
DapExon20b YTILASAIAKAA----GDPKKASAGILEKIQLDTELYRLGHNK
DapExon20c YNILNPNLTKEKDGTPMDEKKASGNLLDESKLDVSLFRLGHTK
DmExon11a YQILNPRGIKDL----DCPKKASKVLIESTELNEDLYRLGHTK
DmExon11b YQILNPAGIVGV----DDPKKCGSIILESTALDPDMYRIGHTK
DmExon11c YQILNPKGIKGI----EDPKKCTKVLIESTELNDDQYRLGNTK
DapExon20d YKLLCPSLIKDS----MTGEQIAKLVLDKMGFDEAVYRLGFNK
AeaExon10d YKILCPQQIKDP----CTPEKACQILASIQLPDEQFRMGKTK
CpqExon10d YKILCPQLIKEP----CSPEKACQIIVGHLQLPDEQFRMGKTK
AmExon14c YKILCANAIKEP----CDPQKATQLILDAINLEPELYRMGNTK
AngExon10d YKILCPQLIKEP----CSPEKVTQIVLTHIQLPEEQFRMGKTK
BmExon17c YKILCPNLIKEP----ITPEKATEKILEQTGLDSESFRLGKTK
NavExon14c YKILCAKKVTDG-----MDPKVAAAIILEETASPDQYRLGASK
TicExon16c YKILAASAIRDD----MAPEKASQVILETINLDAEQYRLGKTK
19
PdcMhc1
20a 20b 20c 20d
DapMhc1
17a 17b 17c
BmMhc1
16a 16b 16c
TicMhc1
14a 14b 14c
NavMhc1
14a 14b 14c
AmMhc1
11e 11a 11b 11c 11d
DmMhc1
10a 10b 10c 10d
AngMhc1
10a 10b 10c 10d
AeaMhc1
10a 10b 10c 10d
CpqMhc1
AeaMhc3 CpqMhc3 CpqMhc4 AeaMhc1 AmMhc1 AngMhc1 BmMhc1 CpqMhc1 DapMhc1 DmMhc1 NavMhc1 PdcMhc1 TicMhc1 AeaExon10b CpqExon10b AngExon10b TicExon16b AeaExon10c CpqExon10c AngExon10c NavExon14b DmExon11d AmExon14b BmExon17b DapExon20b DapExon20c DmExon11a DmExon11b DmExon11c DapExon20d AeaExon10d CpqExon10d AmExon14c AngExon10d BmExon17c NavExon14c TicExon16c
0
0.718

Figure 8



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AeaMhc1 AEHDRANMYNELNNTRSACDTLAREK
AmMhc1 AEKGRHDIHAELNNSRAATDQVSREK
AngMhc1 AEHDRANMYNELNNTRTACDQLSREK
BmMhc1 AEHDRAACYNELNNTRAAVDQVAREK
CpqMhc1 AEHDRANMYNDLNNTRTACDQLAREK
DapMhc1 AEKDRSQFAGENNDLRAAMDHVSSDK
DmMhc1 AEHDRQTCHNELNQTRTACDQLGRDK
NavMhc1 AEKGRNDIHVELNNARAAVDVVAREK
PdcMhc1 AEKEKIQYYTELNDLRATLDHLSNEK
TicMhc1 AERDRASIYTELQQTRSAVEQVGREK
AngExon14b AEKERTQYFAELNDARIGCDQLSNEK
AmExon20b VEKDKVQYFSELNDMRASVDQLSNEK
AeaExon13b AEKERSQYYAEMNDARLSLDHMANEK
CpqExon13b AEKERGQYFAELNDSRLSLDHLANEK
BmExon22b AEKERAQYFSEVNDLRAGLDHLSNEK
DapExon27b AEKDRSSMKNQVDDFKAATDHMTAEK
DmExon15b AEKEKNEYYGQLNDLRAGVDHITNEK
NavExon19b IEKEKVQYFSELNDMRASVDHLSNEK
TicExon20b AEKEKAAYFGELNDLRASVDHLANEK
AeaMhc3
CpqMhc3
CpqMhc4
AeaMhc1
AmMhc1
AngMhc1
BmMhc1
CpqMhc1
DapMhc1
DmMhc1
NavMhc1
PdcMhc1
TicMhc1
AngExon14b
AmExon20b
AeaExon13b
CpqExon13b
BmExon22b
DapExon27b
DmExon15b
NavExon19b
TicExon20b
0
0.73
25
PdcMhc1
27a 27b
DapMhc1
23a 23b
BmMhc1
20a 20b
TicMhc1
19a 19b
NavMhc1
20a 20b
AmMhc1
15a 15b
DmMhc1
13a 13b
AngMhc1
13a 13b
AeaMhc1
13a 13b
CpqMhc1

Figure 9

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                          10        20        30        40
             ....|....|....|....|....|....|....|....|..
AeaMhc3      RGGSAQRGGSPALSTV*
AeaExon16    RAGSVQRGASPA-PSVIRA*
AeaExon17    RAGSVQRGASPA-PQRQPSVMPGLAGLNFPTFDDHGF*
AngExon15    RAGSVQRGASPAVSTM*
AngExon16    RAGSVQRGASPA-PSVVRA*
AngExon17    RAGSVQRGASPA-PQRQPSAMPALAGLNLPTFDDHGF*
AmExon26     RGGSAARGLSPPA-PQQKARKAPSALE*
AmExon27     RGGSAARGLSPPA-PHRPAFKPQLDGSAFPPRFDLQPDGEL*
BmExon28     RAGSAARGVSPA-ASIKGRP*
BmExon29     RAGSAARGVSPA-PQRSRPALADGFGTFPPRFDLAPEDF*
CpqMhc3      ASSTAQSGGGGSAR*
CpqMhc4      RGGSAGRGASPAVSTI*
CpqExon16    RAGSVQRGASPA-PSVIRA*
CpqExon17    RAGSVQRGASPA-PQRQSAMPSLAALGLPTFDDHAF*
DapExon30    RGGSASR-LSPP-PQMKPRSKRDFE*
DmExon18     RAGSVGRGASPA-I*
DmExon19     RAGSVGRGASPA-PRATSVRPQFDGLAFPPRFDLAPENEF*
NavMhc1      RGGSAARGISPA-PHRPVNRPQFDGSAFPPRFDLMPDGL*
PdcExon33    RAGSAPRALSPA-PPQNRSRLALE*
PdcExon34    RAGSAPRALSPA-HHRPPRPQLDGMMAFPPRFDFHPEGEL*
TicExon22    RGGSVARGGSPA-PPRQRPQMDGLTFPPRFDLAPDEI*
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