Figure 1

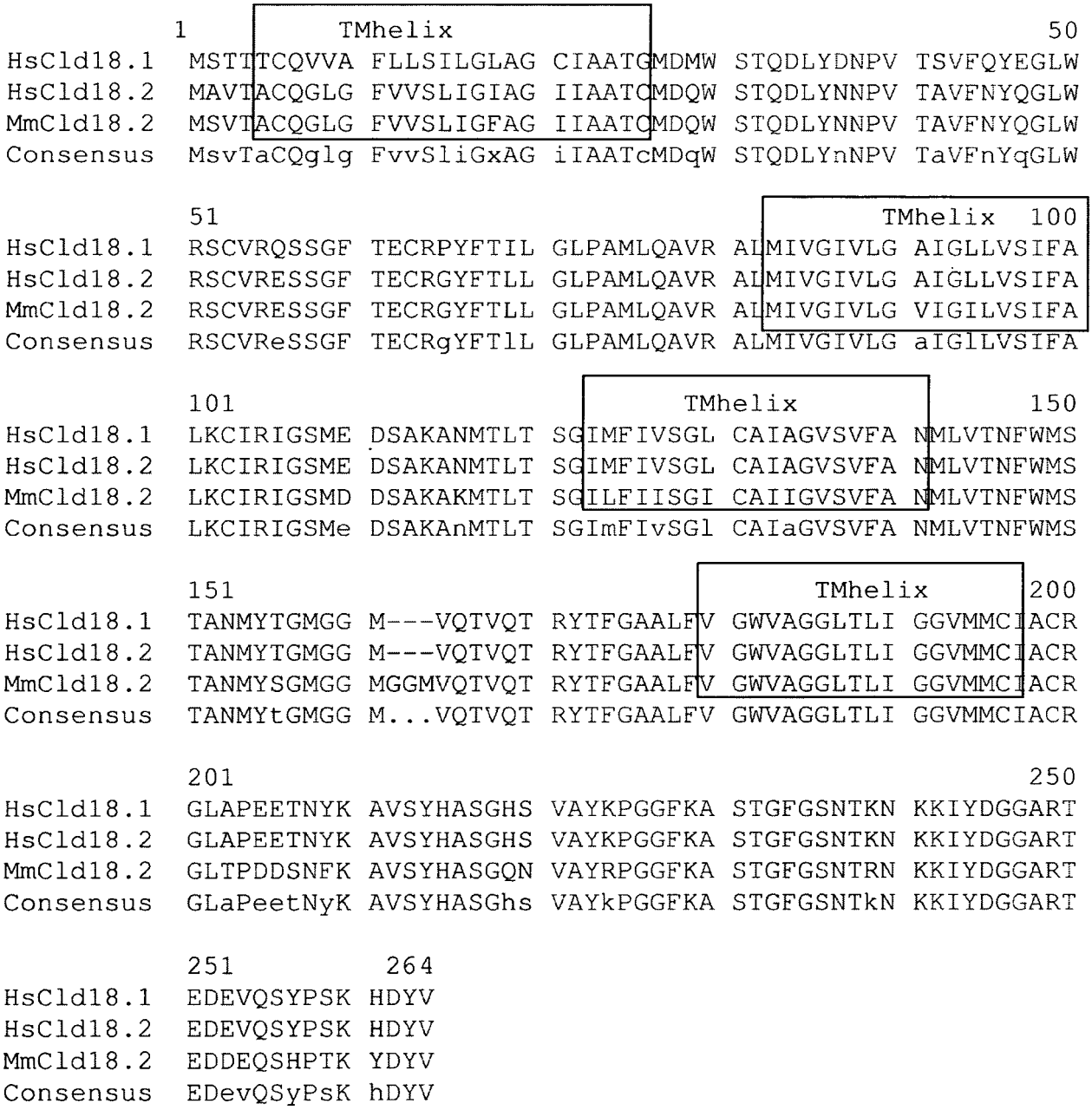

1 TMhelix 50
HsCld18.1 MSTITCQVVA FLLSILGLAG CIAATGMDMW STQDLYDNPV TSVFQYEGLW
HsCld18.2 MAVTACQGLG FVVSLIGIAG IIAATCMDQW STQDLYNNPV TAVFNYQGLW
MmCld18.2 MSVTACQGLG FVVSLIGFAG IIAATCMDQW STQDLYNNPV TAVFNYQGLW
Consensus MsvTaCQglg FvvSliGxAG iIAATcMDqW STQDLYnNPV TaVFnYqGLW
51 TMhelix 100
HsCld18.1 RSCVRQSSGF TECRPYFTIL GLPAMLQAVR ALMIVGIVLG AIGLLVSIFA
HsCld18.2 RSCVRESSGF TECRGYFTLL GLPAMLQAVR ALMIVGIVLG AIGLLVSIFA
MmCld18.2 RSCVRESSGF TECRGYFTLL GLPAMLQAVR ALMIVGIVLG VIGILVSIFA
Consensus RSCVReSSGF TECRgYFTlL GLPAMLQAVR ALMIVGIVLG aIGlLVSIFA
101 TMhelix 150
HsCld18.1 LKCIRIGSME DSAKANMTLT SGIMFIVSGL CAIAGVSVFA NMLVTNFWMS
HsCld18.2 LKCIRIGSME DSAKANMTLT SGIMFIVSGL CAIAGVSVFA NMLVTNFWMS
MmCld18.2 LKCIRIGSMD DSAKAKMTLT SGILFIISGI CAIIGVSVFA NMLVTNFWMS
Consensus LKCIRIGSMe DSAKAnMTLT SGImFIvSGl CAIaGVSVFA NMLVTNFWMS
151 TMhelix 200
HsCld18.1 TANMYTGMGG M---VQTVQT RYTFGAALFV GWVAGGLTLI GGVMMCIACR
HsCld18.2 TANMYTGMGG M---VQTVQT RYTFGAALFV GWVAGGLTLI GGVMMCIACR
MmCld18.2 TANMYSGMGG MGGMVQTVQT RYTFGAALFV GWVAGGLTLI GGVMMCIACR
Consensus TANMYtGMGG M...VQTVQT RYTFGAALFV GWVAGGLTLI GGVMMCIACR
201 250
HsCld18.1 GLAPEETNYK AVSYHASGHS VAYKPGGFKA STGFGSNTKN KKIYDGGART
HsCld18.2 GLAPEETNYK AVSYHASGHS VAYKPGGFKA STGFGSNTKN KKIYDGGART
MmCld18.2 GLTPDDSNFK AVSYHASGQN VAYRPGGFKA STGFGSNTRN KKIYDGGART
Consensus GLaPeetNyK AVSYHASGhs VAYkPGGFKA STGFGSNTkN KKIYDGGART
251 264
HsCld18.1 EDEVQSYPSK HDYV
HsCld18.2 EDEVQSYPSK HDYV
MmCld18.2 EDDEQSHPTK YDYV
Consensus EDevQSyPsK hDYV

Figure 2

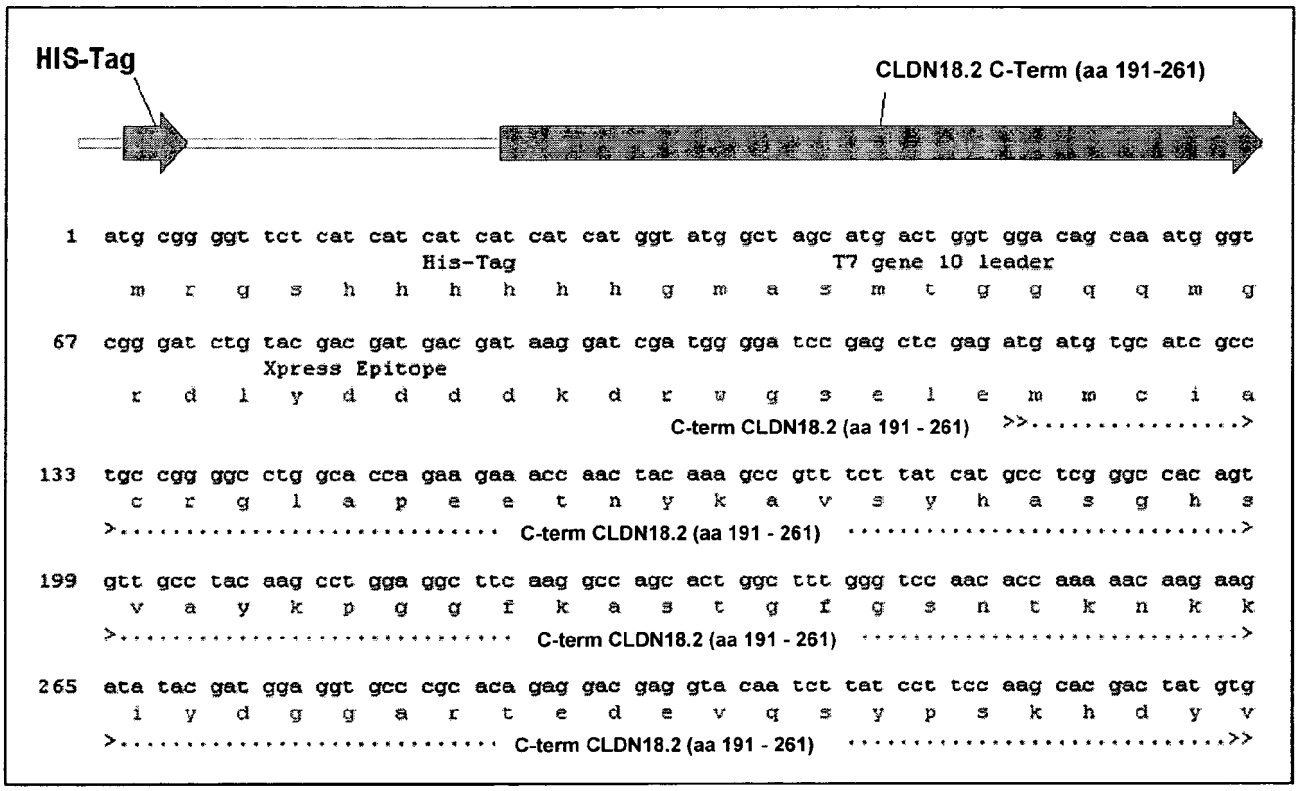

HIS-Tag
CLDN18.2 C-Term (aa 191-261)
1 atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act ggt gga cag caa atg ggt
His-Tag
T7 gene 10 leader
m r g s h h h h h h g m a s m t g g q q m g
67 cgg gat ctg tac gac gat gac gat aag gat cga tgg gga tcc gag ctc gag atg atg tgc atc gcc
Xpress Epitope
r d l y d d d d k d r w g s e l e m m c i a
C-term CLDN18.2 (aa 191 - 261)
133 tgc cgg ggc ctg gca cca gaa gaa acc aac tac aaa gcc gtt tct tat cat gcc tcg ggc cac agt
c r g l a p e e t n y k a v s y h a s g h s
C-term CLDN18.2 (aa 191 - 261)
199 gtt gcc tac aag cct gga ggc ttc aag gcc agc act ggc ttt ggg tcc aac acc aaa aac aag aag
v a y k p g g f k a s t g f g s n t k n k k
C-term CLDN18.2 (aa 191 - 261)
265 ata tac gat gga ggt gcc cgc aca gag gac gag gta caa tct tat cct tcc aag cac gac tat gtg
i y d g g a r t e d e v q s y p s k h d y v
C-term CLDN18.2 (aa 191 - 261)

Figure 3

Heavy chain

```
                1          Leader                                                50
H-43-14A_2      MAWVWTLLFL MAAAQSIQAQ IQLVQSGPEL KKFGETVKIS CKASGYTFTD  CDR1
H-35-22A_1      MNFGLSLIFL VLVLKGVQCE VHLVESGGGL VKPGGSLKLS CAASGFTFSS

                51                        CDR2                              100
H-43-14A_2      YSIHWVKQAP GKGLKWMGWI NTETGVPTYA DDFKGRFAFS LETSASTAYL
H-35-22A_1      YAMSWVRQTP EKRLEWVATI SDGGSYSYYP DNVKGRFTIS RDNAKNNLYL

                101                    CDR3                 140
H-43-14A_2      QINNLKNEDT ATYFCARRTG FD------YW GQGTTLTVSS
H-35-22A_1      QMSHLKSEDT AIYYCARDSY YDNSYVRDYW GQGTTLTVSS
```

Light chain

```
                1          Leader                                                50
LN-43-14A_      MRFSAQLLGL LVLWIPGSTA DIVMTQAAFS IPVTLGTSAS ISCRSSKNLL  CDR1
LN-35-22A_      MRTPAQFLGI LLLWFPGIKC DIKMTQSPSS MYASLGERVS ITCKASQDIN

                51                            CDR2                          100
LN-43-14A_      HSDGITYLYW YLQRPGQSPQ LLIYRVSNLA SGVPNRFSGS ESGTDFTLRI
LN-35-22A_      -----TFLSW FQQKPGKSPK TLIYRTNRLI DGVPSRFSGS GSGQDYSLTI

                101              CDR3                  132
LN-43-14A_      SRVEAEDVGV YYCVQVLELP FTFGGGTKLE IK
LN-35-22A_      SSLDYEDMGI YYCLQYDEFP LTFGAGTKLE LK
```