

```

                10      20      30      40      50      60      70      80      90     100
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      MATGNQTSSQQSPPRQAGGNQSPRIRG-PIPTIPTVTITYVAPTVP TVQKVSTGIPYQWVTPGTVINTAFLWNNPAVVGDLEFWVESRRAKLSDDEKARL
mimpvic32B      MATGNQTSSQQSPPRQAGGNQSPRINGGPIPTIPTVTITYVAPTVP TVQKVSTGIPYQWVTPGTVINTAFLWNNPAVVGDLEFWVESRRAKLSDDEKARL
Clustal Consensus *****.* *****

                110     120     130     140     150     160     170     180     190     200
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      DSIDETMKALEDPAWYYWPTWDQALQCGRHGTEQELRRSIPTLMWTD EQPMSEIYTPIAQILQDAIKKNFPLEGNYWVAFRDRPLDNLGFIENTLSLHKII
mimpvic32B      DSIDETMKALEDPAWYYWPTWDQALQCGRHGTEQELHRSIPTLMWTD EQPMSEIYTPIAQILQDAIKKNFPLEGNYWVAFRDRPLDNLGFIENTLSLHKII
Clustal Consensus *****;*****

                210     220     230     240     250     260     270     280     290     300
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      YFVGEKGGGTDFDYKRWPKRGNYSYRHIMFPLNKYLWIRKLDLFDIHLPPYPGPVLTSDPFRASMCRGYFNTFAKPVVECPQSVGKAYKITISMPILHV
mimpvic32B      YFVGEKGGGTDFDYKRWPKRGNYSYRHIMFPLTKYLWIRKLDLFDIHLPPHPGPVLSNDPFRASMCRGYFNTFAKPVVECPQPPVGKAYKITISMPILHV
Clustal Consensus *****.* *****:****. *****

                310     320     330     340     350     360     370     380     390     400
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      TLGSKLIPKKTAEVRLRHPSFLRAPGYEAYETIDQDQKEQPKGAWIYGSALDHTGVSFSAASDYDGSTSGTPTVFTGRTLFEYHHPKMDALILDRLR
mimpvic32B      TLGSKLIPKKTAEVRLRHPSFLRAPGYEAYETIDQDQKEQPKGAWIYGSALDHTGVSFSAASDYDGSTSGTPTVFTGRTLFEYHHPKMDALTDLRLR
Clustal Consensus *****.* *****

                410     420     430     440     450     460     470     480     490     500
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      QTMRRGNRGHYDDDEFLVVEQLWAVIIPITKETLITFQSMKPAVIPGQVGGFNSYMFEPNKGMDVTPQGPVHGFYFYFADLVLLKHYYHILEVFKETAGLN
mimpvic32B      QTMRRGNRGHYDDDEFLVVEQLWAVIIPITKETLITFQSMKPAVIPGQVGGFNSYMFEPNKGADVTPQGPVHGFYFYFADLVLLQHYHILEAFKETAGLN
Clustal Consensus ***** *****.* *****:*****:*****.*****.*****.*

                510     520     530     540     550     560     570     580     590     600
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      FRVAHKPITDDELVADCNVISEVAIILEITKKQMEILDIIKEATVDNTRLPEELAAATNEFYKYMMARFEIMVAAFEDIGAEAKQAQSLFLQLNTEAAK
mimpvic32B      FRVAHKPIADEELVADCNVISEVAIILEITKKQMEILGMIKEAIDNTRLPEEFAANEFYKYMMGRFEIVVATFEDIGAEAKQAQDLFLQLNTEASK
Clustal Consensus *****.*:*****:*****:*****.*:*****.*:*****.*:*****.*:*****.*:*****.*

                610     620     630     640     650     660     670     680     690     700
... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      QQAIMAEQQAINARQAAEETAVQLELSKEAAKHTAVQLELAKQSTEQNKSFLVFTIITITIFLPLSFFTSYFGMNTVDIRDMEWDQRYFWKTAGPSSAMII
mimpvic32B      KQVAMAIQQEIIARQTAETAVQLELAKQAABQAAQVQKLAKQSTEQNKSFLVFTIITITIFLPLSFFTSYFGMNTVDIRDMEWDQRYFWKTAGPSSAMII
Clustal Consensus :*. ** ** * ***:*****:*.*:.*:*****

                710     720     730     740     750     760
... |... |... |... |... |... |... |... |... |... |... |... |
mimpvic32A      LVVMCWAFAQMKRGIGILFRSKLKPQSDDEBSAIGSLEKSGQATGKRKSSWNPFGRGVDKND

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mimpvic32B LVVMCWA^{FR}QMK^{RG}IDIALQSKVKS^{AI}QID^{EE}SA^{IG}SP^{EK}IG^{QV}TG^{KR}GKSS^{WN}SF^{GR}DV^{DK}ND

Clustal Consensus *****.* :*:.* ** ***** ** **, *****.***, *****

Supplementary Figure 1. Amino acid alignment of *mimpvic32* alleles in strain YAASMYPL6-1 (*mimpvic32A*) and in strain YAASMYPL6-3 (*mimpvic32B*) performed using Clustalx 1.83.