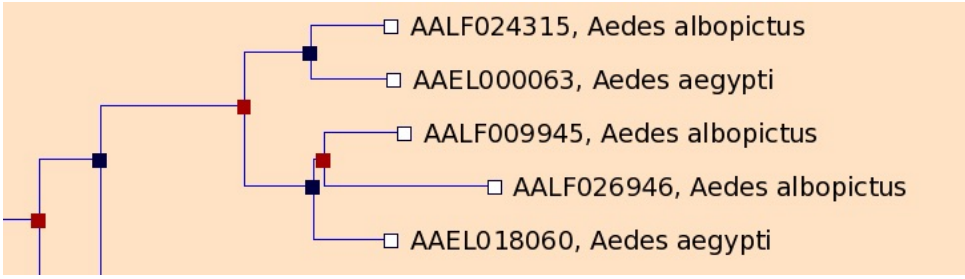


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AAEL018060      ----MEHTEREMKSVQHWNSYGDILSNILIPDIAGIYTVCVVFRKLVTNFSYVKTFLNVP
AALF009945      ------------------------------------------------------------

AAEL000063      YIVIRLEDIGQSNSTHNTLLTSIESGCNTFIVQHYVVLDFLNIFLEIHDQANYRNPNKYV
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AALF026946      YEVIELDGVGQLDSTTSLMLDGIESGCNTFIIHHHVILDFLDVFVDIHDQANYRNPNKYV
AAEL018060      YVIIELEDIGQHNSTASSMLAGIESGCNSFLVQQHAVLDFLDIYTKIHDEAGYRNPNKYL
AALF009945      ------------------------------------------------------------

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AALF024315      VLLLEDHASNDLLDSIRNHPCLWEIMNFLVCQPARGGSVIELLSHRFIDYGKGFAWHLVD
AALF026946      LFLMEEPASDDFLESIRAHSSEIG------------------------------------
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AALF009945      ------------------------------------------------------------

AAEL000063      RYHTQRRSFEVGTELFPDKTLNLRGRPIRLATFNINPHIFLSSDDARNTEIRLGNQSYSM
AALF024315      RYHTEEHAFDFGNVLFPDRTLNLLGRSIRVATFNVNPHIFLSMDDAGNSRVKLENHSYLL
AALF026946      --------------------------------------------------LVNGDQVYSV
AAEL018060      RFHIGTSSFEMGNQLFPDKTFNLMGKPIRVATFNINPHIFLIESEIGTPVVISGNESYSL
AALF009945      ----------MGHQLFPDKTLDWMGKAIRVATFDINPHIFMVEPEIETPVIKYDNQAYSL
                                                                  :   :. * :

AAEL000063      DGLDGILLVDFCRRRNCTVDLVVDSKNMWGVIHPNRTGNGIIGNLVERRADIGLGAISSW
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AALF009945      NGPNGILLMEFARRHNCSIELIV--------------GNGILGNVAERRADVGVGALSSW
                :* :*:**::*.:::**:::*:*              ****:**:.*****.*:**:*.*

AAEL000063      YHCYSFLTFSSPDQRGGVTCLTPKPNLLPRWKIVAMVFLTSVYLIIFGTFMCSVIIYTII
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AAEL018060      YHCYQYLAFSFAYERGGVTCVVPKPKQLPRWKEVAMGFTTSVYMTIFVTFCCTVVVYMLI
AALF009945      YHCYQYLAFSFAYERGGVACLVPKPKQLPRWKEIAMGFTRSVYVAIFVAFCCIVACYILI
                :**:.:*:**   ::***:*:.***: ***** :** *   **:  : :*   *  *  *

AAEL000063      FQCSRKKPLENSVVWNAFNVFAVFLLQSTNNIRNRSVSETVLSVALLLFSLNIAAIYSGK
AALF024315      FRYSMKNPLTKSIVWNALNVLAVFLLQSTSNFRNRSVSETIFSVALLLFSLNIAAIYSGK
AALF026946      VRFSVRSRFEKSIVWNALNVLAIYLLQSTSVVRNRSVSESLLSVTVLIFSLNLATIYSGK
AAEL018060      VRLTIQEPLERTFAWNVLNVLAIYLLQATNIVRSRSVSETLLSVAVLIFSMNLATIYLGK
AALF009945      VRFAIQGPMERSVVWHALNVLAIYLLQSTSIVRNRSASESLLSVAVLFFSMNLATIYLGK
                .: : :  : .:..*:.:**:*::***:*. .*.**.**:::**::*:**:*:*:** **

AAEL000063      YASLRTIPLYEKEVNSLEDLAESGIPWLQAHEAWTYSLLLSKNPAVMKLVSHFKVYPAPK
AALF024315      YASLRTIPLYESAINTLEDLAKSGIPWLQAHEAWSYSLLLSKNPTIMKLVSLFKVYPIPK
AALF026946      YASLRTIPMYEPAIDSKDDLAKSGIPWVQIHEAWAYDFSMSENPLC--------------
AAEL018060      YASLRTIPMYEPAIDTKEELAKSGITWMQAHEAWSYSLRLSDNPTEVSLCSNFKVDVPPM
AALF009945      YASLRTIPMFEQAIDTKESLAQSGIPWIQAHEAWSYSLRLSKNPTEVNLLSNFRVYPLPT
                ********::*  ::: :.**:*** *:* ****:*.: :*.**

AAEL000063      LHQIADQGGSAFAMGRLHNGHLMLGDWINSGNIHNYQLMRGDLYYEHEVAMATKTWPLIE
AALF024315      LHQIADQGGSAFAMGRLSNGHLMLGDWINAGNIHRYQLMRDDLYYEHEIAMATKTWPLIE
AALF026946      --------DAAFASARMHNGHLMLGEWIDAGNIHKYQLMKNDLYYVLKVAMSTKTWPLLE
AAEL018060      LAQIADQGNSAFALARLHNGHLMLGDWINAGNIHKYQLMQNDLYYEHEVAMATKTWPLME
AALF009945      LRQMADEGNSAFALARLHNGHLMLGDWINADNIRKYHLMRNDLYFEHEVAMATKTWPLME
                        .:*** .*: *******:**::.**:.*:**:.***:  ::**:******:*

AAEL000063      KFNELLHLTASGLLLRVQELRIMYQHNDYYVQTGALSSHEREPYQPEALAVEDVFGGLIV
AALF024315      KFNELLHQTASGLLLRPQELRIMYQHNDYYVQTVGLNSHVRAAYEPRALALEDVFGGLIV
AALF026946      RFNDLLSRTAEGLLLMVHERKNIYRYNDYYVQVVALNSHIRGENKPTALAIEDVLGCCDN
AAEL018060      RFNELLGQASDASLLLLQEYQNIFQYNDYYVQMVALNSHVRQPNEPKPLAMEDVMGGFII
AALF009945      RFNELLGQATEASLLLLKEYQNINQYNDYYVQMVALNSHIREPNEPKALAVEDVLGGLIV
                :**:**  ::.. **  :* : : ::******  .*.** *   :*  **:***:*

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AALF024315      LGFGLLCAGVAFVTEVWVGKSPTVDPNDENSEKYLYE
AALF026946      REGGGVCNTVHN------------------------
AAEL018060      LGSGLLCASVNFMIEVWILCPRKTKQVNDVE------
AALF009945      LGFGLLCAFVNFIVEIWVLCPSKTDLVKDNE------
                   * :*  *
```

Figure S8. Alignment and phylogenetic tree of IR41p1. Upper panel: section of Gene Tree Image from VectorBase (VBGT00190000009824) extracted by Comparative Tool. Lower panel: sequences alignment of *Ae. albopictus* and *Ae. aegypti* orthologs using Clustal Omega.