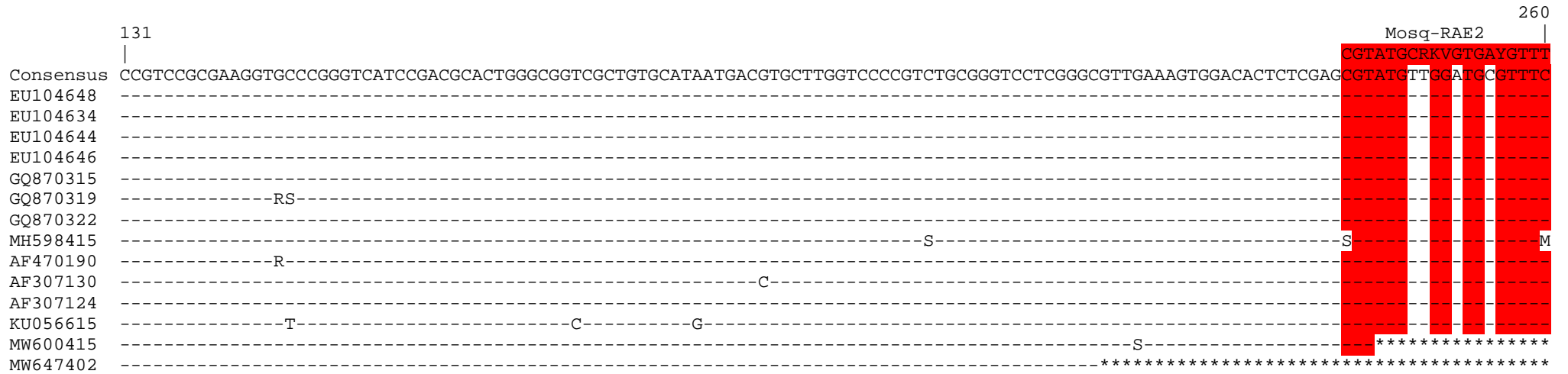
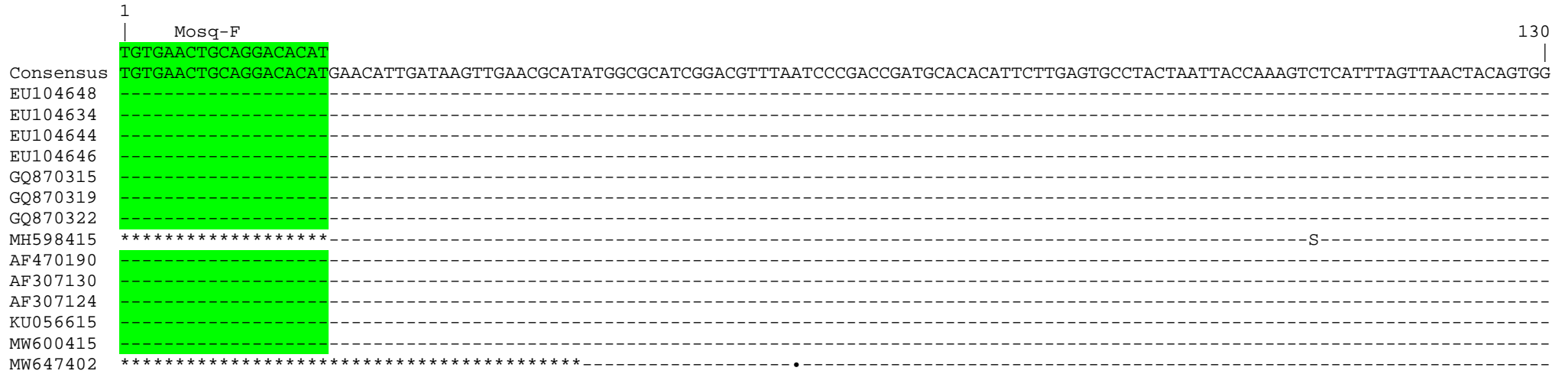




# Anopheles gambiae mosquito rRNA gene internal transcribed spacer 2 (ITS2) unanimity alignment & molecular taxonomy primer map

Laboratorio de Genómica Viral y Humana, Facultad de Medicina, Universidad Autónoma de San Luis Potosí, México (08/Apr/2022, v4.0)





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261  
|  
Mosq-RAE2  
|  
390  
|

Consensus GTGTTGGTGGTGTGTTGATGCGTAGGGCTTGTGGTGTGTGTCAGCCGCATGGTTCGAACCTAATGCTACGTCGTTCCCGATGGCCACCGGCAGTCTACTCTCCAGGCTAAAGTCGGCTCGTCTAGGGATTCTC

EU104648 -----R-----

EU104634 -----

EU104644 -----

EU104646 -----

GQ870315 -----

GQ870319 -----

GQ870322 -----

MH598415 -----M-----M-----M-----

AF470190 -----

AF307130 -----

AF307124 -----

KU056615 -----G-----

MW600415 \*\*\*\*\*

MW647402 \*\*\*\*\*

391  
|  
520  
|

Consensus GGAAAGCTAAGTCGCTGTAACCTCATGTGGGCCCATACACGGCGTTGCGCTACCACGCTAAGTTAGCCCTACATATACAAGCATCAACCCACGGCACGGGCGTAGCTGTAATACTTACGTCTCGGTTATACC

EU104648 -----C-----

EU104634 -----

EU104644 -----C-----

EU104646 -----Y-----

GQ870315 -----•-----

GQ870319 -----

GQ870322 -----G-----

MH598415 -----S-----Y-----M-----S-----

AF470190 -----\*\*\*\*\*

AF307130 -----\*\*\*\*\*

AF307124 -----•-----\*\*\*\*\*

KU056615 -----\*\*\*\*\*

MW600415 \*\*\*\*\*

MW647402 \*\*\*\*\*



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```
      521                               Mosq-R2                               566
      |                               |                               |
Consensus CACGTAGGCCTCAAGTG ATGTGTGACTACCCCCTAAA TTTAAGCAT
EU104648 -----
EU104634 -----
EU104644 -----
EU104646 -----
GQ870315 ----- *****
GQ870319 ----- *****
GQ870322 ----- *****
MH598415 ----- C*****
AF470190 *****
AF307130 *****
AF307124 *****
KU056615 *****
MW600415 *****
MW647402 *****
```

Alignments prepared using ElimDupes ([www.hiv.lanl.gov/content/sequence/elimdupesv2/elimdupes.html](http://www.hiv.lanl.gov/content/sequence/elimdupesv2/elimdupes.html)), CLUSTAL O ([www.ebi.ac.uk/Tools/msa/clustalo/](http://www.ebi.ac.uk/Tools/msa/clustalo/)), EMBOSS Seqret ([www.ebi.ac.uk/Tools/sfc/emboss\\_seqret/](http://www.ebi.ac.uk/Tools/sfc/emboss_seqret/)) and SURE v1.0 Sequence Unanimity Reformatting tool (<http://midasmap.uaslp.mx/suretool/>).