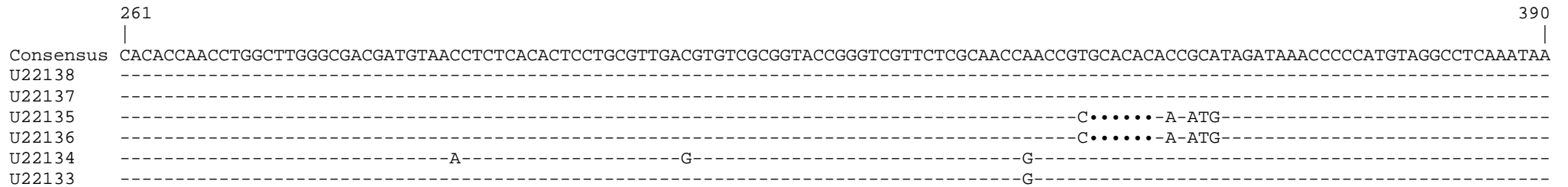
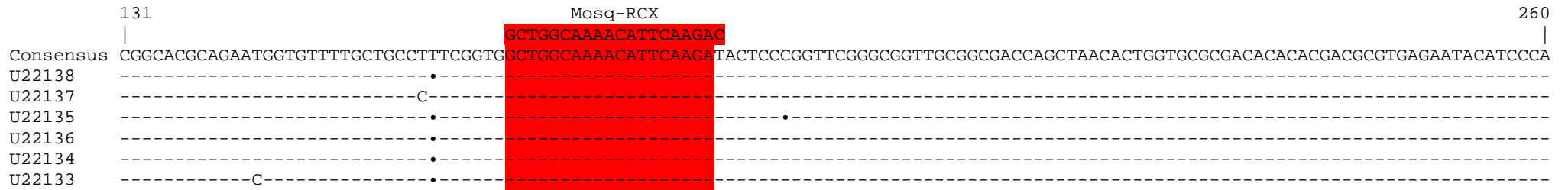
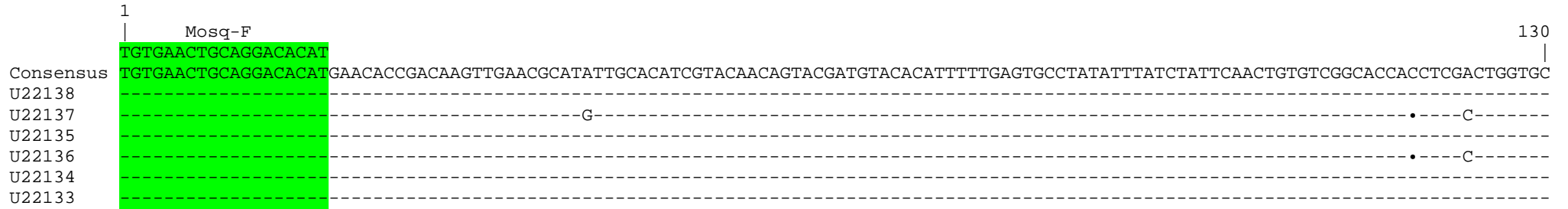




***Culex restuans* mosquito rRNA gene internal transcribed spacer 2 (ITS2) unanimity alignment & molecular taxonomy primer map**  
Laboratorio de Genómica Viral y Humana, Facultad de Medicina, Universidad Autónoma de San Luis Potosí, México (08/Apr/2022, v4.0)





***Culex restuans* 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)

```
          391                               418
          |                               |
          Mosq-R2
          |                               |
Consensus TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22138    TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22137    TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22135    TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22136    TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22134    TGTGTGACTACCCCCTAAA|TTTAAGCAT
U22133    TGTGTGACTACCCCCTAAA|TTTAAGCAT
```

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/>).