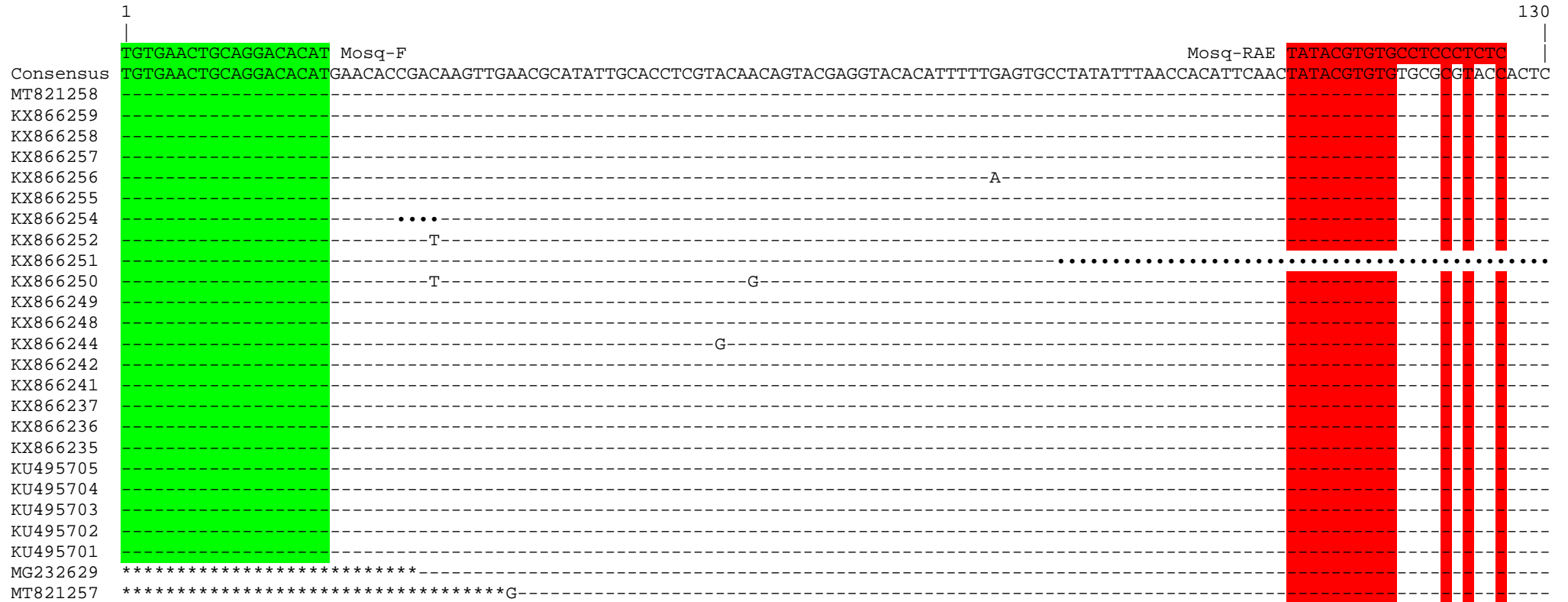


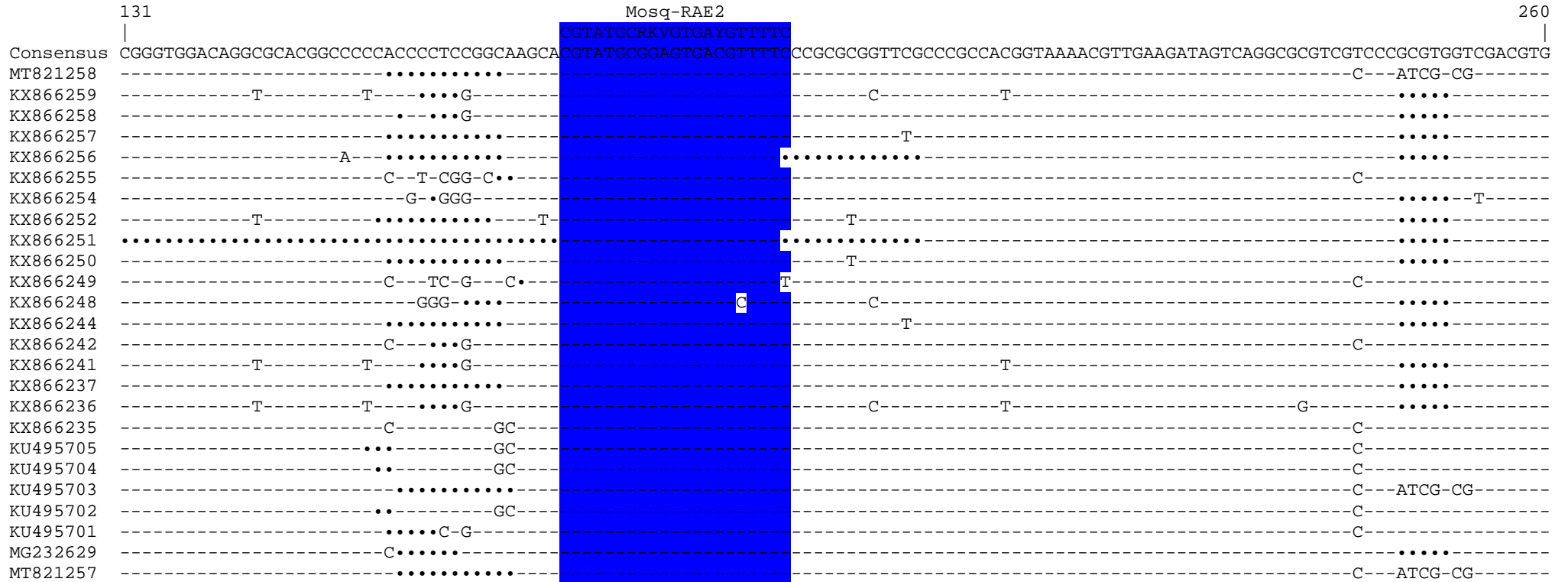


***Aedes notoscriptus* mosquito rRNA gene internal transcribed spacer 2 (ITS2) unanimity alignment & molecular taxonomy primer map**
 Laboratorio de Genómica Viral y Humana, Facultad de Medicina, Universidad Autónoma de San Luis Potosí, México (10/Mar/2022 v3.0)





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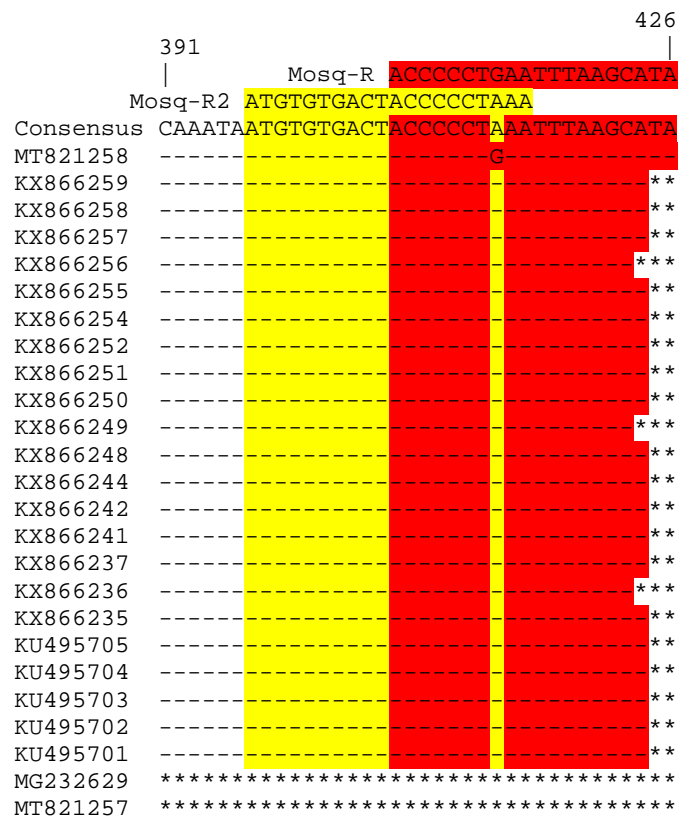


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	261	390
Consensus	GTTGATGAATACATCCCATAGGCCGCCACCACCATGTATCGGCTACGTTGTGTCCATCAGCGTATGCCCCCTCCCGGGGTATACCCTATCTGCATAACCTCTGTATGATATCTGCATATCAGTAGGCCT	
MT821258	-----CGA-C-----A-----C-----A-C-----AT-G-----	
KX866259	-----T-----A-----G-----A-----AT-----	
KX866258	-----T-----C-----	
KX866257	-----C-----	
KX866256	-----A-----T-----T-----C-----	
KX866255	-----G-----GAT-C-----A-----	
KX866254	-----A-----G-----AC-----ACT-----	
KX866252	-----T-----G-----A-----C-----A-CAC-TA-----GA-CG-C-----	
KX866251	-----A-----AT-----T-----	
KX866250	-----	
KX866249	-----G-----GAT-C-----A-----	
KX866248	-----G-----G-----	
KX866244	-----T-----	
KX866242	-----T-----	
KX866241	-----T-----A-----A-----A-CAC-TA-----CA-----	
KX866237	-----	
KX866236	-----T-----A-----A-----A-CAC-TA-----CA-----	
KX866235	-----G-----GAT-C-----A-----	
KU495705	-----G-----G-----	
KU495704	-----G-----G-----	
KU495703	-----CGA-C-----A-----C-----A-----AT-G-----	
KU495702	-----G-----A-----TA-----	
KU495701	-----G-----G-----	
MG232629	-----	****
MT821257	-----CGA-C-----A-----C-----*****	



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