



Anopheles apicimacula 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)

NOTE: These alignments are split into two different ITS2 sequence groups described as previously unrecognized Molecular Operational Taxonomic Units (MOTUs) by Gomez,G.F. PLoS ONE 10 (3) PUBMED: 25774795.

1 Mosq-F 130

TGTGAAC TGCA GGAC ACAT
Consens1 TGAAC TGCA GGAC ACAT GAAC ATCGATA AGTTGAA CGCAT ATT GCGCGT CGGCGACACAGCTGACGCACATATCATTGAGAGTCCAT ATT GTTAGTCGGGACACTTACGAGCGTCCGTGCCACCCG
KF698907
KF698908
KF698909
KF698910
KM262754

-----T-----A-----

1 Mosq-F 130

TGTGAAC TGCA GGAC ACAT
Consens2 TGAAC TGCA GGAC ACAT GAAC ATCGATA AGTTGAA CGCAT ATT GCGCGT CGGCGACACAGCTGACGCACATATCATTGAGAGTCCAT ATT GGAAGTCCGTGACATTACGATA CGTCCGTGCCGCTCC
KM262755
KM262757
KM262758
KM262759
KM262760

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	131		260
Consens1	TTGGGCCCGTGCCGGGTGGACCCACGCGGTCACTCGTTCTGGGTAGCGCCTCGCAGAGAGCGGTGCCCTTAAGACAGTGGAGCGCGTCCCTCGTCCGTAGCGACCGTCACAAGGCCGGCG		
KF698907	-----		
KF698908	-----A-----		G-----
KF698909	-----T-----		
KF698910	-----		
KM262754	-----T-----		

	131		260
Consens2	CGGTCCCGTACCGGGGGATGGACCCACGCGGTCAATCGTTCTGGGTAGCGGCTCAAGAGCCGGTGCCCTTAAGACAGTGGAGCGCGTCCCTCGTCCGTAGCGACCGTCACAAGGCCGGCGTTGG		
KM262755	-----		
KM262757	-----A-----		
KM262758	-----		
KM262759	-----		
KM262760	-----TT-----		



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261 | 390 |
Consens1 TTGGACCAACACCTCACCTCACCATGGAGTGTGATGCGTGGACCCAGTCGTCGGAGCGACGGTACCAGGTCGGATCGTTGTACCCACTGAGTCGGGTGTACCCCCACAGGGCTAC
KF698907 -----|
KF698908 -----|
KF698909 -----|
KF698910 -----A-----|
KM262754 -----|

261 | 390 |
Consens2 ACCAACACCTCACCTCCTCACAGAGCGTTGATGCGTGTGGACCCAAACCGTTGGATGCGACGGTACAAGGGCGGGAGCGAGCGTTAGCTCTACCGCATGCCAGAGCAATTCTGGCAGGAGGTACA
KM262755 -----|
KM262757 -----G-----|
KM262758 -----T-----|
KM262759 -----G-----|
KM262760 -----T-----|



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Alignments prepared using ElimDuplicates (www.hiv.lanl.gov/content/sequence/elimduplicatesv2/elimduplicates.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/>).