

Supplementary Data file

**Extensive New *Anopheles* Cryptic Species Involved in Human Malaria Transmission
in Western Kenya**

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Supplementary Table S1 Pairwise comparison of ITS2 sequence similarities of the 21 *Anopheles* species identified in western Kenya

Species	AR	CF	CH	CO	FUN	GA	LEE	MA	PH	PR	RU	An.sp.1	An.sp.6	An.sp.7	An.sp.9	An.sp.11	An.sp.14	An.sp.15	An.sp.17	An.sp.18	An.sp.19	
AR	-																					
CF	0.46	-																				
CH	0.74	0.48	-																			
CO	0.34	0.33	0.34	-																		
FUN	0.31	0.38	0.30	0.32	-																	
GA	0.99	0.45	0.75	0.33	0.31	-																
LEE	0.46	0.66	0.47	0.32	0.36	0.46	-															
MA	0.53	0.45	0.54	0.30	0.29	0.53	0.44	-														
PH	0.23	0.20	0.22	0.22	0.25	0.24	0.20	0.19	-													
PR	0.53	0.46	0.54	0.31	0.28	0.53	0.44	0.84	0.20	-												
RU	0.52	0.47	0.52	0.29	0.30	0.52	0.45	0.77	0.19	0.74	-											
An.sp.1	0.46	0.56	0.46	0.31	0.38	0.45	0.51	0.47	0.20	0.48	0.45	-										
An.sp.6	0.46	0.59	0.48	0.33	0.37	0.46	0.56	0.47	0.20	0.48	0.50	0.72	-									
An.sp.7	0.46	0.57	0.45	0.34	0.37	0.46	0.55	0.47	0.20	0.47	0.49	0.71	0.88	-								
An.sp.9	0.47	0.58	0.46	0.35	0.37	0.47	0.57	0.48	0.21	0.49	0.50	0.71	0.87	0.89	-							
An.sp.11	0.20	0.18	0.19	0.18	0.22	0.20	0.17	0.19	0.49	0.19	0.18	0.17	0.19	0.19	0.18	-						
An.sp.14	0.46	0.58	0.46	0.34	0.38	0.45	0.57	0.48	0.20	0.48	0.49	0.71	0.84	0.81	0.80	0.20						
An.sp.15	0.33	0.32	0.34	0.90	0.33	0.33	0.30	0.29	0.21	0.30	0.29	0.30	0.33	0.33	0.34	0.18	0.33	-				
An.sp.17	0.46	0.59	0.46	0.31	0.39	0.46	0.58	0.48	0.19	0.47	0.49	0.68	0.76	0.75	0.77	0.19	0.72	0.31	-			
An.sp.18	0.29	0.27	0.29	0.85	0.27	0.29	0.28	0.27	0.21	0.27	0.26	0.26	0.29	0.30	0.31	0.17	0.30	0.81	0.27	-		
An.sp.19	0.40	0.48	0.39	0.27	0.32	0.40	0.45	0.40	0.20	0.41	0.39	0.78	0.64	0.63	0.63	0.19	0.64	0.26	0.59	0.29	-	

AR, *An.arabiensis*; CF, *An.cf.rivulorum*; CH, *An.christyi*; CO, *An.coustani*; FUN, *An.funestus*; GA, *An.gambiae*; LEE, *An.leesoni*; MA, *An.maculipalpis*; PH, *An.pharoensis*; PR, *An.pretoriensis*; RU, *An.rufipes*.

Supplementary Table S2. GenBank accession numbers of ITS2 sequences identified in the 21 *Anopheles* species in western Kenya

Sequence_ID	Species	Isolate	GenBank accession
Seq1	<i>An. gambiae</i>	KH01	MT408564
Seq2	<i>An. arabiensis</i>	KH02	MT408565
Seq3	<i>An. funestus</i>	KH03	MT408566
Seq4	<i>An. cf.rivulorum</i>	KH04	MT408567
Seq5	<i>An. christyi</i>	KH05	MT408568
Seq6	<i>An. coustani</i>	KH06	MT408569
Seq7	<i>An. lesoni</i>	KH07	MT408570
Seq8	<i>An. maculipalpis</i>	KH08	MT408571
Seq9	<i>An. pharoensis</i>	KH09	MT408572
Seq10	<i>An. pretoriensis</i>	KH10	MT408573
Seq11	<i>An. rufipes</i>	KH11	MT408574
Seq12	<i>An. sp.1</i>	KH12	MT408575
Seq13	<i>An. sp.6</i>	KH13	MT408576
Seq14	<i>An. sp.7</i>	KH14	MT408577
Seq15	<i>An. sp.9</i>	KH15	MT408578
Seq16	<i>An. sp.11</i>	KH16	MT408579
Seq17	<i>An. sp.14</i>	KH17	MT408580
Seq18	<i>An. sp.15</i>	KH18	MT408581
Seq19	<i>An. sp.17</i>	KH19	MT408582
Seq20	<i>An. sp.18</i>	KH20	MT408583
Seq21	<i>An. sp.19</i>	KH21	MT408584

Supplementary Table S3. GenBank accession numbers of COX1 haplotype sequences identified in *Anopheles* species of western Kenya

Sequence_ID	Species	Haplotype	GenBank accession
>Seq1	<i>An. sp.17</i>	H01	MT375202
>Seq2	<i>An. sp.17</i>	H02	MT375203
>Seq3	<i>An. sp.17</i>	H03	MT375204
>Seq4	<i>An. sp.17</i>	H04	MT375205
>Seq5	<i>An. sp.17</i>	H05	MT375206
>Seq6	<i>An. sp.17</i>	H06	MT375207
>Seq7	<i>An. sp.17</i>	H07	MT375208
>Seq8	<i>An. sp.17</i>	H08	MT375209
>Seq9	<i>An. sp.17</i>	H09	MT375210
>Seq10	<i>An. sp.17</i>	H10	MT375211
>Seq11	<i>An. sp.17</i>	H11	MT375212
>Seq12	<i>An. sp.17</i>	H12	MT375213
>Seq13	<i>An. sp.17</i>	H13	MT375214
>Seq14	<i>An. funestus</i>	H01	MT375215
>Seq15	<i>An. funestus</i>	H02	MT375216
>Seq16	<i>An. funestus</i>	H03	MT375217
>Seq17	<i>An. funestus</i>	H04	MT375218
>Seq18	<i>An. funestus</i>	H05	MT375219
>Seq19	<i>An. funestus</i>	H06	MT375220
>Seq20	<i>An. gambiae</i>	H01	MT375221
>Seq21	<i>An. gambiae</i>	H02	MT375222
>Seq22	<i>An. gambiae</i>	H03	MT375223
>Seq23	<i>An. gambiae</i>	H04	MT375224
>Seq24	<i>An. sp.6</i>	H01	MT375225
>Seq25	<i>An. sp.9</i>	H01	MT375226
>Seq26	<i>An. cf.rivulorum</i>	H01	MT375227
>Seq27	<i>An. maculipalpis</i>	H01	MT375228
>Seq28	<i>An. maculipalpis</i>	H02	MT375229

Supplementary Table S4 Number of *Plasmodium* positive mosquitoes detected indoor and outdoor in western Kenya highlands.

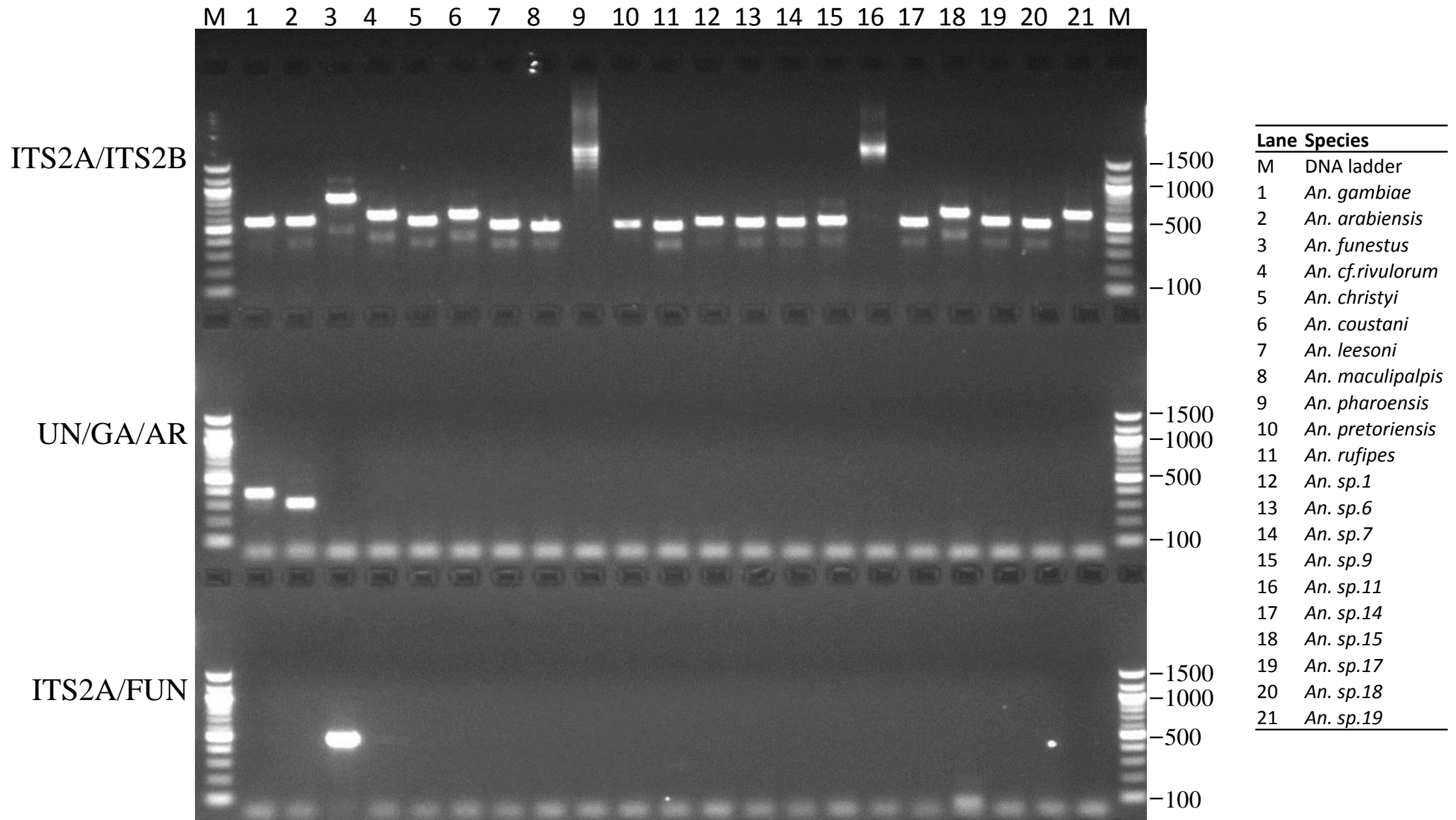
Species	Iguhu (2016)		Emutete (2017)	
	Indoor	Outdoor	Indoor	Outdoor
<i>An. gambiae</i>	10(153)*	7(119)	2(32)	1(14)
<i>An. arabiensis</i>	0(11)	0(2)		0(2)
<i>An. funestus</i>	9(210)	0(14)	5(40)	1(5)
<i>An. cf.rivulorum</i>	0(1)			
<i>An. lesoni</i>	0(1)			
<i>An. maculipalpis</i>				0(1)
<i>An. rufipes</i>	0(2)			0(2)
<i>An. sp.1</i>		0(1)		
<i>An. sp.6</i>	0(3)	0(3)		
<i>An. sp.7</i>	0(6)	0(1)	0(4)	0(4)
<i>An. sp.9</i>	0(5)	1(5)		
<i>An. sp.11</i>		1(1)		
<i>An. sp.14</i>	0(1)	0(1)		
<i>An. sp.15</i>	0(2)	1(2)		0(1)
<i>An. sp.17</i>			2(15)	1(7)
Total	19(395)	10(149)	9(91)	3(36)

* The number in parenthesis represents the total number of mosquitoes tested.

Supplementary Table S5 Species component and proportion of *Plasmodium* infections detected in *Anopheles* mosquitoes in western Kenya.

Species	<i>pf</i>	<i>pm</i>	<i>po</i>	<i>pf+pm</i>	<i>pf+po</i>	<i>pm+po</i>	<i>pf+pm+po</i>
<i>An. gambiae</i>	129(90.2)	1(0.7)	8(5.6)	3(2.1)	2(1.4)		
<i>An. arabiensis</i>	26(86.7)		3(10.0)	1(3.3)			
<i>An. funestus</i>	138(84.7)	3(1.8)	8(4.9)	5(3.1)	7(4.3)	1(0.6)	1(0.6)
<i>An. coustani</i>	1(100)						
<i>An. rufipes</i>	1(100)						
<i>An. sp.1</i>	2(100)						
<i>An. sp.6</i>	2(100)						
<i>An. sp.9</i>	1(100)						
<i>An. sp.11</i>	1(100)						
<i>An. sp.15</i>	1(100)						
<i>An. sp.17</i>	3(100)						

* The number in parenthesis represents the percentage of individuals within the mosquito species. *pf*, *P. falciparum*; *pm*, *P. malariae*; *po*, *P. ovale*.



Supplementary Fig. S1 Agarose gel electrophoresis of PCR products amplified with the 21 *Anopheles* species in western Kenya. Upper panel, PCR amplification with ITS2A and ITS2B primers for sequencing; Middle panel, PCR amplification with multiplex PCR method with UN/GA/AR primers for identification of *An. gambiae* and *An. arabiensis*; Lower panel, PCR amplification with ITS2A and FUN primer for identification of *An. funestus*. Lane M, 100 bp molecular ladder; Lines 1-21, PCR results of the 21 *Anopheles* species.

Supplementary Fig. S2 shows some examples of multiple sequence alignment comparison for the similarity. (a) ITS2 sequence alignment of *An. funestus*; (b) ITS2 sequence alignment of *An. gambiae*; (c) ITS2 sequence alignment of *An. sp.17*; (d) COX1 sequence alignment of *An. funestus*; (e) COX1 sequence alignment of *An. gambiae*; (f) COX1 sequence alignment of *An. sp.17*. Multiple sequence alignments were performed using BioEdit software (<https://bioedit.software.informer.com>). The aligned sequences were reformatted by MView web-based tool (<http://wavis.img.cas.cz/>).

(d)

Reference sequence (1): An.funestus_NC038158
Identities normalised by aligned length.
Colored by: identity

	cov	pid	1	80
1 An.funestus_NC038158	100.0%	100.0%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
2 An.funestus_H01	100.0%	99.5%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
3 An.funestus_H02	100.0%	99.7%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
4 An.funestus_H03	100.0%	99.4%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
5 An.funestus_H04	100.0%	99.4%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
6 An.funestus_H05	100.0%	99.4%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
7 An.funestus_H06	100.0%	99.2%	GCTGGAAATAGTAGGAACCTTCCTTAAAGAAATCCGTTATTCGAGCCGAAATAGGACATCCCGGAGCATTTATTGGAGACGATCA	
	cov	pid	81	160
1 An.funestus_NC038158	100.0%	100.0%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
2 An.funestus_H01	100.0%	99.5%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
3 An.funestus_H02	100.0%	99.7%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
4 An.funestus_H03	100.0%	99.4%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
5 An.funestus_H04	100.0%	99.4%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
6 An.funestus_H05	100.0%	99.4%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
7 An.funestus_H06	100.0%	99.2%	AAATTTATAATGTAATGTTACTGCTCATGCTTTTATTATAAATTTTTTTTATAGTAAACCATTATAATGGAGGATTTG	
	cov	pid	161	240
1 An.funestus_NC038158	100.0%	100.0%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
2 An.funestus_H01	100.0%	99.5%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
3 An.funestus_H02	100.0%	99.7%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
4 An.funestus_H03	100.0%	99.4%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
5 An.funestus_H04	100.0%	99.4%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
6 An.funestus_H05	100.0%	99.4%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
7 An.funestus_H06	100.0%	99.2%	GAAATTTGACTTGACCTTTAATAATAGGAGCCCCGATATAGCTTTCCCGCAATAAATAAATAAAGATTTTGAATACIT	
	cov	pid	241	320
1 An.funestus_NC038158	100.0%	100.0%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
2 An.funestus_H01	100.0%	99.5%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
3 An.funestus_H02	100.0%	99.7%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
4 An.funestus_H03	100.0%	99.4%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
5 An.funestus_H04	100.0%	99.4%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
6 An.funestus_H05	100.0%	99.4%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
7 An.funestus_H06	100.0%	99.2%	CCCTCCCTTCAATTAACCTTTACTTTCTTCTAGTAGTATAGTAGAAAAAGGAGCAGGAACAGGATGAACAGTTTATCCCCCTTT	
	cov	pid	321	400
1 An.funestus_NC038158	100.0%	100.0%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
2 An.funestus_H01	100.0%	99.5%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
3 An.funestus_H02	100.0%	99.7%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
4 An.funestus_H03	100.0%	99.4%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
5 An.funestus_H04	100.0%	99.4%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
6 An.funestus_H05	100.0%	99.4%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
7 An.funestus_H06	100.0%	99.2%	ATCATCAGGAAATGTCATGCTGGTGCCTTTCAGTTGATTTAGCTATTTTTTCAATACATTTAGCAGGAAATTTCTTCTAATTT	
	cov	pid	401	480
1 An.funestus_NC038158	100.0%	100.0%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
2 An.funestus_H01	100.0%	99.5%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
3 An.funestus_H02	100.0%	99.7%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
4 An.funestus_H03	100.0%	99.4%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
5 An.funestus_H04	100.0%	99.4%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
6 An.funestus_H05	100.0%	99.4%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
7 An.funestus_H06	100.0%	99.2%	TAGGAGCAGTAAATTTTATTACAACCTGTAATTAATATACGATCTCCGGAAATACITTTAGATCGAATACCAATATTTTGTCT	
	cov	pid	481	560
1 An.funestus_NC038158	100.0%	100.0%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
2 An.funestus_H01	100.0%	99.5%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
3 An.funestus_H02	100.0%	99.7%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
4 An.funestus_H03	100.0%	99.4%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
5 An.funestus_H04	100.0%	99.4%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
6 An.funestus_H05	100.0%	99.4%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
7 An.funestus_H06	100.0%	99.2%	TGATCTGTAGTAATTAACAGCAATCTTTTATTACCTTTTACCAGTATTAGCTGGAGCTATTACAAATATTATTAAACAGA	
	cov	pid	561	636
1 An.funestus_NC038158	100.0%	100.0%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
2 An.funestus_H01	100.0%	99.5%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
3 An.funestus_H02	100.0%	99.7%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
4 An.funestus_H03	100.0%	99.4%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
5 An.funestus_H04	100.0%	99.4%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
6 An.funestus_H05	100.0%	99.4%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	
7 An.funestus_H06	100.0%	99.2%	TCGAAATTTAAAACCTTTTTTTTTGATCCGTCAGGAGGAGGAGATCCAAATTTTATATCAACACTTATTATTGATTT	

(e)

Reference sequence (1): An.gambiae_NC002084
Identities normalised by aligned length.
Colored by: identity

	cov	pid	1 [:	80
1 An.gambiae_NC002084	100.0%	100.0%	GCTGGAAATAGTAGGGACATCTTTAAGAACTCTAAATTCGAGCTGAACTAGGACACCCCTGGAGCAATTTATTGGAGACGATCA		
2 An.gambiae_H01	100.0%	99.4%	GCTGGAAATAGTAGGGACATCTTTAAGAACTCTAAATTCGAGCTGAACTAGGACACCCCTGGAGCAATTTATTGGAGACGATCA		
3 An.gambiae_H02	100.0%	100.0%	GCTGGAAATAGTAGGGACATCTTTAAGAACTCTAAATTCGAGCTGAACTAGGACACCCCTGGAGCAATTTATTGGAGACGATCA		
4 An.gambiae_H03	100.0%	99.8%	GCTGGAAATAGTAGGGACATCTTTAAGAACTCTAAATTCGAGCTGAACTAGGACACCCCTGGAGCAATTTATTGGAGACGATCA		
5 An.gambiae_H04	100.0%	99.8%	GCTGGAAATAGTAGGGACATCTTTAAGAACTCTAAATTCGAGCTGAACTAGGACACCCCTGGAGCAATTTATTGGAGACGATCA		

	cov	pid	81	1	:	160
1 An.gambiae_NC002084	100.0%	100.0%	AAATTTAATAATGTAAACGTTACGCTCATGCTTTTATTATAATTTTCCTTATAGTTATACCTATTATAATGGAGGGTTTG			
2 An.gambiae_H01	100.0%	99.4%	AAATTTAATAATGTAAACGTTACGCTCATGCTTTTATTATAATTTTCCTTATAGTTATACCTATTATAATGGAGGGTTTG			
3 An.gambiae_H02	100.0%	100.0%	AAATTTAATAATGTAAACGTTACGCTCATGCTTTTATTATAATTTTCCTTATAGTTATACCTATTATAATGGAGGGTTTG			
4 An.gambiae_H03	100.0%	99.8%	AAATTTAATAATGTAAACGTTACGCTCATGCTTTTATTATAATTTTCCTTATAGTTATACCTATTATAATGGAGGGTTTG			
5 An.gambiae_H04	100.0%	99.8%	AAATTTAATAATGTAAACGTTACGCTCATGCTTTTATTATAATTTTCCTTATAGTTATACCTATTATAATGGAGGGTTTG			

	cov	pid	161	2	:	240
1 An.gambiae_NC002084	100.0%	100.0%	GAAACTGATTAGTTCCTTTAAATAGGAGCACCGATATAGCTTTTCCGAAATAAATAAAGATTTTGAATGCTT			
2 An.gambiae_H01	100.0%	99.4%	GAAACTGATTAGTTCCTTTAAATAGGAGCACCGATATAGCTTTTCCGAAATAAATAAAGATTTTGAATGCTT			
3 An.gambiae_H02	100.0%	100.0%	GAAACTGATTAGTTCCTTTAAATAGGAGCACCGATATAGCTTTTCCGAAATAAATAAAGATTTTGAATGCTT			
4 An.gambiae_H03	100.0%	99.8%	GAAACTGATTAGTTCCTTTAAATAGGAGCACCGATATAGCTTTTCCGAAATAAATAAAGATTTTGAATGCTT			
5 An.gambiae_H04	100.0%	99.8%	GAAACTGATTAGTTCCTTTAAATAGGAGCACCGATATAGCTTTTCCGAAATAAATAAAGATTTTGAATGCTT			

	cov	pid	241	3	:	320
1 An.gambiae_NC002084	100.0%	100.0%	CCCTCTCATTAAACACTTTTAAATTCAGTAGTATAGTAGAAAAAGGGGCTGGAAAGGATGAAGTGTATCCCTCT			
2 An.gambiae_H01	100.0%	99.4%	CCCTCTCATTAAACACTTTTAAATTCAGTAGTATAGTAGAAAAAGGGGCTGGAAAGGATGAAGTGTATCCCTCT			
3 An.gambiae_H02	100.0%	100.0%	CCCTCTCATTAAACACTTTTAAATTCAGTAGTATAGTAGAAAAAGGGGCTGGAAAGGATGAAGTGTATCCCTCT			
4 An.gambiae_H03	100.0%	99.8%	CCCTCTCATTAAACACTTTTAAATTCAGTAGTATAGTAGAAAAAGGGGCTGGAAAGGATGAAGTGTATCCCTCT			
5 An.gambiae_H04	100.0%	99.8%	CCCTCTCATTAAACACTTTTAAATTCAGTAGTATAGTAGAAAAAGGGGCTGGAAAGGATGAAGTGTATCCCTCT			

	cov	pid	321	4	:	400
1 An.gambiae_NC002084	100.0%	100.0%	ATCTTCGGAAATGCTCATGCTGGAGCTTCAGTAGATTTAGCAAATTTTTCTCTTCAATTTAGCAGGAAATTTCTCTATTT			
2 An.gambiae_H01	100.0%	99.4%	ATCTTCGGAAATGCTCATGCTGGAGCTTCAGTAGATTTAGCAAATTTTTCTCTTCAATTTAGCAGGAAATTTCTCTATTT			
3 An.gambiae_H02	100.0%	100.0%	ATCTTCGGAAATGCTCATGCTGGAGCTTCAGTAGATTTAGCAAATTTTTCTCTTCAATTTAGCAGGAAATTTCTCTATTT			
4 An.gambiae_H03	100.0%	99.8%	ATCTTCGGAAATGCTCATGCTGGAGCTTCAGTAGATTTAGCAAATTTTTCTCTTCAATTTAGCAGGAAATTTCTCTATTT			
5 An.gambiae_H04	100.0%	99.8%	ATCTTCGGAAATGCTCATGCTGGAGCTTCAGTAGATTTAGCAAATTTTTCTCTTCAATTTAGCAGGAAATTTCTCTATTT			

	cov	pid	401	:	480	
1 An.gambiae_NC002084	100.0%	100.0%	TAGGAGCAGTAAATTTTATTACAACAGTAAATAATAACGGTCTCCAGGAAATACATAGATCGAAATACCATTTATTGTT			
2 An.gambiae_H01	100.0%	99.4%	TAGGAGCAGTAAATTTTATTACAACAGTAAATAATAACGGTCTCCAGGAAATACATAGATCGAAATACCATTTATTGTT			
3 An.gambiae_H02	100.0%	100.0%	TAGGAGCAGTAAATTTTATTACAACAGTAAATAATAACGGTCTCCAGGAAATACATAGATCGAAATACCATTTATTGTT			
4 An.gambiae_H03	100.0%	99.8%	TAGGAGCAGTAAATTTTATTACAACAGTAAATAATAACGGTCTCCAGGAAATACATAGATCGAAATACCATTTATTGTT			
5 An.gambiae_H04	100.0%	99.8%	TAGGAGCAGTAAATTTTATTACAACAGTAAATAATAACGGTCTCCAGGAAATACATAGATCGAAATACCATTTATTGTT			

	cov	pid	481	5	:	560
1 An.gambiae_NC002084	100.0%	100.0%	TGATCGGTAGTTATTACAGCAGTATTATTATTATCAITACCAGTATTAGCAGGAGCATTAATAATTAACTGA			
2 An.gambiae_H01	100.0%	99.4%	TGATCGGTAGTTATTACAGCAGTATTATTATTATCAITACCAGTATTAGCAGGAGCATTAATAATTAACTGA			
3 An.gambiae_H02	100.0%	100.0%	TGATCGGTAGTTATTACAGCAGTATTATTATTATCAITACCAGTATTAGCAGGAGCATTAATAATTAACTGA			
4 An.gambiae_H03	100.0%	99.8%	TGATCGGTAGTTATTACAGCAGTATTATTATTATCAITACCAGTATTAGCAGGAGCATTAATAATTAACTGA			
5 An.gambiae_H04	100.0%	99.8%	TGATCGGTAGTTATTACAGCAGTATTATTATTATCAITACCAGTATTAGCAGGAGCATTAATAATTAACTGA			

	cov	pid	561	6]	636
1 An.gambiae_NC002084	100.0%	100.0%	TCGAAAATTTAAATACATCTTTCTTTGATCCAGCAGGAGGAGGTGATCCAAATTTTATCAACACATTTCTGATTT			
2 An.gambiae_H01	100.0%	99.4%	TCGAAAATTTAAATACATCTTTCTTTGATCCAGCAGGAGGAGGTGATCCAAATTTTATCAACACATTTCTGATTT			
3 An.gambiae_H02	100.0%	100.0%	TCGAAAATTTAAATACATCTTTCTTTGATCCAGCAGGAGGAGGTGATCCAAATTTTATCAACACATTTCTGATTT			
4 An.gambiae_H03	100.0%	99.8%	TCGAAAATTTAAATACATCTTTCTTTGATCCAGCAGGAGGAGGTGATCCAAATTTTATCAACACATTTCTGATTT			
5 An.gambiae_H04	100.0%	99.8%	TCGAAAATTTAAATACATCTTTCTTTGATCCAGCAGGAGGAGGTGATCCAAATTTTATCAACACATTTCTGATTT			

(f)

Reference sequence (1): An.sp.D_MK047667
Identities normalised by aligned length.
Colored by: identity

		cov	pid	1	1	80
1	An.sp.D_MK047667	100.0%	100.0%	GCAGGAA	AGTAGGAACA	CATTAAGAA
2	An.sp.F_MK047669	100.0%	98.9%	GCAGGAA	AGTAGGAACA	CATTAAGAA
3	An.sp.C_MK047666	100.0%	99.1%	GCAGGAA	AGTAGGAACA	CATTAAGAA
4	An.sp.17_H01	100.0%	98.6%	GCAGGAA	AGTAGGAACA	CATTAAGAA
5	An.sp.17_H02	100.0%	99.2%	GCAGGAA	AGTAGGAACA	CATTAAGAA
6	An.sp.17_H03	100.0%	99.4%	GCAGGAA	AGTAGGAACA	CATTAAGAA
7	An.sp.17_H04	100.0%	98.6%	GCAGGAA	AGTAGGAACA	CATTAAGAA
8	An.sp.17_H05	100.0%	99.8%	GCAGGAA	AGTAGGAACA	CATTAAGAA
9	An.sp.17_H06	100.0%	99.1%	GCAGGAA	AGTAGGAACA	CATTAAGAA
10	An.sp.17_H07	100.0%	99.4%	GCAGGAA	AGTAGGAACA	CATTAAGAA
11	An.sp.17_H08	100.0%	99.7%	GCAGGAA	AGTAGGAACA	CATTAAGAA
12	An.sp.17_H09	100.0%	99.5%	GCAGGAA	AGTAGGAACA	CATTAAGAA
13	An.sp.17_H10	100.0%	99.5%	GCAGGAA	AGTAGGAACA	CATTAAGAA
14	An.sp.17_H11	100.0%	98.9%	GCAGGAA	AGTAGGAACA	CATTAAGAA
15	An.sp.17_H12	100.0%	99.5%	GCAGGAA	AGTAGGAACA	CATTAAGAA
16	An.sp.17_H13	100.0%	98.9%	GCAGGAA	AGTAGGAACA	CATTAAGAA

		cov	pid	81	1	160
1	An.sp.D_MK047667	100.0%	100.0%	AAATTTA	AATGTAAT	GTTACTGCT
2	An.sp.F_MK047669	100.0%	98.9%	AAATTTA	AATGTAAT	GTTACTGCT
3	An.sp.C_MK047666	100.0%	99.1%	AAATTTA	AATGTAAT	GTTACTGCT
4	An.sp.17_H01	100.0%	98.6%	AAATTTA	AATGTAAT	GTTACTGCT
5	An.sp.17_H02	100.0%	99.2%	AAATTTA	AATGTAAT	GTTACTGCT
6	An.sp.17_H03	100.0%	99.4%	AAATTTA	AATGTAAT	GTTACTGCT
7	An.sp.17_H04	100.0%	98.6%	AAATTTA	AATGTAAT	GTTACTGCT
8	An.sp.17_H05	100.0%	99.8%	AAATTTA	AATGTAAT	GTTACTGCT
9	An.sp.17_H06	100.0%	99.1%	AAATTTA	AATGTAAT	GTTACTGCT
10	An.sp.17_H07	100.0%	99.4%	AAATTTA	AATGTAAT	GTTACTGCT
11	An.sp.17_H08	100.0%	99.7%	AAATTTA	AATGTAAT	GTTACTGCT
12	An.sp.17_H09	100.0%	99.5%	AAATTTA	AATGTAAT	GTTACTGCT
13	An.sp.17_H10	100.0%	99.5%	AAATTTA	AATGTAAT	GTTACTGCT
14	An.sp.17_H11	100.0%	98.9%	AAATTTA	AATGTAAT	GTTACTGCT
15	An.sp.17_H12	100.0%	99.5%	AAATTTA	AATGTAAT	GTTACTGCT
16	An.sp.17_H13	100.0%	98.9%	AAATTTA	AATGTAAT	GTTACTGCT

		cov	pid	161	2	240
1	An.sp.D_MK047667	100.0%	100.0%	GAAATT	GACTTGT	CCCTTAA
2	An.sp.F_MK047669	100.0%	98.9%	GAAATT	GACTTGT	CCCTTAA
3	An.sp.C_MK047666	100.0%	99.1%	GAAATT	GACTTGT	CCCTTAA
4	An.sp.17_H01	100.0%	98.6%	GAAATT	GACTTGT	CCCTTAA
5	An.sp.17_H02	100.0%	99.2%	GAAATT	GACTTGT	CCCTTAA
6	An.sp.17_H03	100.0%	99.4%	GAAATT	GACTTGT	CCCTTAA
7	An.sp.17_H04	100.0%	98.6%	GAAATT	GACTTGT	CCCTTAA
8	An.sp.17_H05	100.0%	99.8%	GAAATT	GACTTGT	CCCTTAA
9	An.sp.17_H06	100.0%	99.1%	GAAATT	GACTTGT	CCCTTAA
10	An.sp.17_H07	100.0%	99.4%	GAAATT	GACTTGT	CCCTTAA
11	An.sp.17_H08	100.0%	99.7%	GAAATT	GACTTGT	CCCTTAA
12	An.sp.17_H09	100.0%	99.5%	GAAATT	GACTTGT	CCCTTAA
13	An.sp.17_H10	100.0%	99.5%	GAAATT	GACTTGT	CCCTTAA
14	An.sp.17_H11	100.0%	98.9%	GAAATT	GACTTGT	CCCTTAA
15	An.sp.17_H12	100.0%	99.5%	GAAATT	GACTTGT	CCCTTAA
16	An.sp.17_H13	100.0%	98.9%	GAAATT	GACTTGT	CCCTTAA

		cov	pid	241	3	320
1	An.sp.D_MK047667	100.0%	100.0%	CCCCCT	CTTTAAC	CTTCTTA
2	An.sp.F_MK047669	100.0%	98.9%	CCCCCT	CTTTAAC	CTTCTTA
3	An.sp.C_MK047666	100.0%	99.1%	CCCCCT	CTTTAAC	CTTCTTA
4	An.sp.17_H01	100.0%	98.6%	CCCCCT	CTTTAAC	CTTCTTA
5	An.sp.17_H02	100.0%	99.2%	CCCCCT	CTTTAAC	CTTCTTA
6	An.sp.17_H03	100.0%	99.4%	CCCCCT	CTTTAAC	CTTCTTA
7	An.sp.17_H04	100.0%	98.6%	CCCCCT	CTTTAAC	CTTCTTA
8	An.sp.17_H05	100.0%	99.8%	CCCCCT	CTTTAAC	CTTCTTA
9	An.sp.17_H06	100.0%	99.1%	CCCCCT	CTTTAAC	CTTCTTA
10	An.sp.17_H07	100.0%	99.4%	CCCCCT	CTTTAAC	CTTCTTA
11	An.sp.17_H08	100.0%	99.7%	CCCCCT	CTTTAAC	CTTCTTA
12	An.sp.17_H09	100.0%	99.5%	CCCCCT	CTTTAAC	CTTCTTA
13	An.sp.17_H10	100.0%	99.5%	CCCCCT	CTTTAAC	CTTCTTA
14	An.sp.17_H11	100.0%	98.9%	CCCCCT	CTTTAAC	CTTCTTA
15	An.sp.17_H12	100.0%	99.5%	CCCCCT	CTTTAAC	CTTCTTA
16	An.sp.17_H13	100.0%	98.9%	CCCCCT	CTTTAAC	CTTCTTA

		cov	pid	321	4	400
1	An.sp.D_MK047667	100.0%	100.0%	ATCTTC	TGGAA	TGCTCA

