RESEARCH NOTE

Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division [version 1; referees: 1 approved, 1 approved with reservations]

Mark J. Hanemaaijer[1], Parker D. Houston[1], Travis C. Collier[1], Laura C. Norris[1], Abdrahamane Fofana[2], Gregory C. Lanzaro[1], Anthony J. Cornel[3], Yoosook Lee[1]

[1]Vector Genetics Laboratory, Department of Pathology, Microbiology and Immunology, University of California Davis , Davis, CA, 95616, USA
[2]Malaria Research and Training Center, University of Bamako, Bamako, E2528, Mali
[3]Mosquito Control Research Laboratory, Kearney Agricultural Center, Department of Entomology and Nematology, University of California Davis, Davis, CA, 93648, USA

v1 **First published:** 21 Mar 2018, **7**:347 (https://doi.org/10.12688/f1000research.13807.1)
Latest published: 15 Mar 2019, **7**:347 (https://doi.org/10.12688/f1000research.13807.2)

Abstract
Here we report the complete mitochondrial sequences of 70 individual field collected mosquito specimens from throughout Sub-Saharan Africa. We generated this dataset to identify species specific markers for the following *Anopheles* species and chromosomal forms: *An. arabiensis*, *An. coluzzii* (The *Forest* and *Mopti* chromosomal forms) and *An. gambiae* (The *Bamako* and *Savannah* chromosomal forms). The raw Illumina sequencing reads were mapped to the NC_002084 reference mitogenome sequence. A total of 783 single nucleotide polymorphisms (SNPs) were detected on the mitochondrial genome, of which 460 are singletons (58.7%). None of these SNPs are suitable as molecular markers to distinguish among *An. arabiensis*, *An. coluzzii* and *An. gambiae* or any of the chromosomal forms. The lack of species or chromosomal form specific markers is also reflected in the constructed phylogenetic tree, which shows no clear division among the operational taxonomic units considered here.

Keywords
Mitogenome, species identification, Africa, malaria vector, mosquitoes, Anopheles, single nucleotide polymorphisms, phylogenomics

Open Peer Review

Referee Status: ✓ ?

	Invited Referees 1	Invited Referees 2
REVISED version 2 published 15 Mar 2019		
version 1 published 21 Mar 2018	✓ report	? report

1 **Beniamino Caputo**, Sapienza University of Rome, Italy
Verena Pichler, Sapienza University of Rome, Italy

2 **Maria Anice Mureb Sallum**, University of São Paulo, Brazil

Any reports and responses or comments on the article can be found at the end of the article.

Corresponding author: Yoosook Lee (yoslee@ucdavis.edu)

Author roles: Hanemaaijer MJ: Conceptualization, Formal Analysis, Writing – Original Draft Preparation, Writing – Review & Editing; **Houston PD**: Writing – Original Draft Preparation; **Collier TC**: Data Curation, Software; **Norris LC**: Investigation; **Fofana A**: Investigation; **Lanzaro GC**: Writing – Review & Editing; **Cornel AJ**: Investigation, Writing – Review & Editing; **Lee Y**: Conceptualization, Data Curation, Formal Analysis, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: We thank University of California - Irvine, Malaria Initiatives (UCIMI) for their support.
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

How to cite this article: Hanemaaijer MJ, Houston PD, Collier TC *et al.* **Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division [version 1; referees: 1 approved, 1 approved with reservations]** *F1000Research* 2018, **7**:347 (https://doi.org/10.12688/f1000research.13807.1)

First published: 21 Mar 2018, **7**:347 (https://doi.org/10.12688/f1000research.13807.1)

Introduction

Historically, mtDNA sequence has been used in taxonomy as a source of species diagnostic markers (Cronin *et al.* (1991); De Barba *et al.* (2014); Pegg *et al.* (2006)) or in population genetics and evolutionary studies (Fu *et al.* (2013); Harrison (1989); Llamas *et al.* (2016)). One advantage of using mitochondrial over nuclear DNA for such studies is that the mutation rate of mtDNA is about 10 times faster than nuclear DNA (Brown *et al.* (1979); Haag-Liautard *et al.* (2008)), hence amplifying the evolutionary trajectory of populations and species. In addition, mtDNA is easy to amplify, because there are more copies of mitochondrial DNA relative to nuclear DNA. Also, universal primers can be applied to a wide range of species. Widely used universal primers target the cytochrome b and cytochrome oxidase 1 genes (Tahir *et al.* (2016)), because both have conserved and highly variable regions. In addition to these, other genes as described in De Mandal *et al.* (2014), can also be used as markers. However, phylogenetic trees based on mtDNA can deviate from the ones that are derived from nuclear DNA (Phillips *et al.* (2013); Shaw (2002); Sota & Vogler, 2001).

The *Anopheles gambiae* species complex consists of eight morphologically identical species that can only be distinguished with molecular markers (Scott *et al.* (1993)) or, for some of the species, by cytological examination of polytene chromosomes (Green, 1972; Pombi *et al.,* 2008). The currently used molecular markers are located within genomic islands of divergence located proximal to the centromeres (Lee *et al.* (2014); Turner *et al.* (2005)). Monitoring additional species-specific markers on mitochondrial DNA (mtDNA) could increase the ease of application and accuracy of species detection assays. In addition, mtDNA markers could enhance our understanding of divergence times among taxa within the complex.

In this study we wished to identify species-specific markers within the mtDNA for *Anopheles arabiensis*, *An. coluzzii* and *An. gambiae*, including among the chromosomal forms currently subsumed under the designations *An. gambiae* and *An. coluzzii*, with the goal of adding these to our existing *Anopheles* species detection assay (Lee *et al.* (2014)). We sequenced the whole mitogenomes of 70 individual mosquito specimens collected throughout Sub-Saharan Africa. The raw Illumina sequencing reads were mapped to the AgamP4 reference sequence, which included both nuclear and mitochondrial sequences. We explore the relationship among *An. arabiensis, An. coluzzii*, *An. gambiae* and four of the sub-specific chromosomal form mitogenome sequences.

Methods

Sample collection

Anopheles arabiensis raw Illumina sequencing reads were obtained from our previous study (Marsden *et al.* (2014)). These included 20 samples from three villages in Tanzania collected in 2012 (Lupiro ((-8.38000°N, 36.66912°W), Sagamaganga (-8.06781°N, 36.80207°W), and Minepa (-8.25700°N, 36.68163°W) in the Kilombero Valley) and 4 samples from Cameroon collected in 2005 (9.09957°N, 13.72292°W). The *An. gambiae and An. coluzzii* samples were collected as resting adults using mouth aspirators in Kela, Mali (11.88683°N, -8.44744°W) in 2012 and Mutengene, Cameroon (4.0994°N, 9.3081°W) in 2011. We subdivided the *An. coluzzii* specimen into the *Forest* and *Mopti* chromosomal forms. Similarly, we did this for the *An. gambiae Savannah* and *Bamako* chromosomal forms. We used the same definitions and methods to characterize the chromosomal forms as in Lanzaro & Lee, 2013.

Genome sequencing

Sequencing methods for *An. arabiensis* samples are as described in Marsden *et al.* (2014). In short, individually barcoded Illumina paired-end sequencing libraries, with insert sizes of 320-400 basepairs (bp) using NEXTflex Sequencing kits (NOVA-5144) and barcodes (NOVA-514102)(Bio Scientific, Austin, TX, USA), were sequenced on an Illumina HiSeq2000 (Illumina, San Diego, CA, USA) with 100-bp paired-end reads using twelve samples per lane. For the *An. coluzzii* and *An. gambiae* samples we used the same methods as described in Norris *et al.* (2015) and Main *et al.* (2015). For the latter species, libraries were created using the Nextera DNA Sample Preparation Kit (FC-121-1031) and TruSeq dual indexing barcodes (FC-121-103)(Illumina) and the samples were sequenced on an Illumina HiSeq2500 with 100-bp paired end reads.

Data analysis

De-multiplexed raw reads were trimmed using Trimmomatic (Bolger *et al.* (2014)) version 0.36 and mapped to the mitogenome reference sequence of *An. gambiae* (Genbank accession number = NC_002084 (Beard *et al.* (1993))). Freebayes (v1.0.1) (Garrison & Marth, 2013) was used for mitochondrial variant calling assuming single ploidy and without population prior. Mapping statistics were calculated using qualimap version 2.2 (Okonechnikov *et al.* (2016)) and the data is represented in Table 1. Following the recommendation of Crawford and Lazarro (Crawford & Lazzaro, 2012), we used a minimum depth of 8 to call variants for each individual. Between positions 1-13,470bp of the mitogenome, we obtained consistently high quality reads for all samples, which were used for further analysis. An AT-rich region located between 13,471 and 15,388 suffers from low or zero coverage for sequences generated with the Nextera library preparation kit. Therefore, we excluded these regions from further analysis. The Vcf2fasta program (Danecek *et al.* (2011)) was used to extract mitogenome sequences from vcf file to fasta format. Geneious version 10.1.3 was used for mitogenome alignments. The phylogenetic tree was generated using the Jukes-Cantor genetic distance model and Neighbor-Joining tree methods available in Geneious version 10.1.3. We used scikit-allel (v1.1.9), a software package for Python (Miles & Harding (2017)), to identify species specific markers.

Table 1. List of samples that are used for the study. Mapped reads indicates the reads that are mapped to the reference genome. Mean coverage indicates the average depth of reads on the mitochondrial DNA and standard deviation indicates the coverage deviation across the mitochondrial DNA.

Species	Banked_id	Year	Country	Village	Mapped bases	Mean coverage	Standard deviation
An. coluzzii-Forest	11MUTE470	2011	Cameroon	Mutengene	4265836	277.7	144.5
An. coluzzii-Forest	11MUTE472	2011	Cameroon	Mutengene	1862892	121.3	23
An. coluzzii-Forest	11MUTE476	2011	Cameroon	Mutengene	2130531	138.7	50.5
An. coluzzii-Forest	11MUTE477	2011	Cameroon	Mutengene	806611	52.5	16.7
An. coluzzii-Forest	11MUTE480	2011	Cameroon	Mutengene	804015	52.3	21
An. coluzzii-Forest	11MUTE483	2011	Cameroon	Mutengene	1702247	110.8	42.9
An. coluzzii-Forest	11MUTE487	2011	Cameroon	Mutengene	812839	52.9	21.2
An. coluzzii-Forest	11MUTE490	2011	Cameroon	Mutengene	1882088	122.5	52.4
An. coluzzii-Forest	11MUTE491	2011	Cameroon	Mutengene	1422997	92.6	46.6
An. coluzzii-Forest	11MUTE493	2011	Cameroon	Mutengene	627590	40.9	17.3
An. coluzzii-Mopti	12KELA022	2012	Mali	Kela	3695920	240.6	64.4
An. coluzzii-Mopti	12KELA024	2012	Mali	Kela	574282	37.4	30.8
An. coluzzii-Mopti	12KELA046	2012	Mali	Kela	4152520	270.3	87.2
An. coluzzii-Mopti	12KELA085	2012	Mali	Kela	10883282	708.4	345
An. coluzzii-Mopti	12KELA087	2012	Mali	Kela	3351158	218.1	79.8
An. coluzzii-Mopti	12KELA088	2012	Mali	Kela	1704283	110.9	91.3
An. coluzzii-Mopti	12KELA099	2012	Mali	Kela	349531	22.8	11
An. coluzzii-Mopti	12KELA112	2012	Mali	Kela	8550102	556.5	198.2
An. coluzzii-Mopti	12KELA161	2012	Mali	Kela	33794208	2199.7	629.3
An. gambiae-Savannah	12KELA210	2012	Mali	Kela	3007375	195.8	53.3
An. gambiae-Bamako	12KELA214	2012	Mali	Kela	26441050	1721.1	566.4
An. gambiae-Bamako	12KELA219	2012	Mali	Kela	3617355	235.5	130.2
An. gambiae-Savannah	12KELA228	2012	Mali	Kela	7783776	506.7	262.8
An. gambiae-Savannah	12KELA233	2012	Mali	Kela	7827363	509.5	138.6
An. gambiae-Savannah	12KELA234	2012	Mali	Kela	6721204	437.5	205.9
An. gambiae-Bamako	12KELA239	2012	Mali	Kela	6683521	435	126.4
An. gambiae-Bamako	12KELA240	2012	Mali	Kela	15131480	984.9	270.8
An. gambiae-Bamako	12KELA244	2012	Mali	Kela	12851754	836.5	306.5
An. gambiae-Savannah	12KELA285	2012	Mali	Kela	407888	26.6	119.8
An. gambiae-Savannah	12KELA321	2012	Mali	Kela	1034014	67.3	43.8
An. gambiae-Savannah	12KELA334	2012	Mali	Kela	20949015	1363.6	400.4
An. gambiae-Savannah	12KELA348	2012	Mali	Kela	12053890	784.6	280.9
An. gambiae-Bamako	12KELA367	2012	Mali	Kela	12109235	788.2	240.1
An. coluzzii-Mopti	12KELA400	2012	Mali	Kela	13707820	892.3	398.2
An. gambiae-Bamako	12KELA406	2012	Mali	Kela	17605437	1146	463.2
An. gambiae-Savannah	12KELA409	2012	Mali	Kela	10526480	685.2	259.1
An. coluzzii-Mopti	12KELA420	2012	Mali	Kela	31785953	2069	845.5
An. gambiae-Bamako	12KELA443	2012	Mali	Kela	25740781	1675.5	669.1
An. gambiae-Bamako	12KELA457	2012	Mali	Kela	1360654	88.6	36.6
An. coluzzii-Mopti	12KELA458	2012	Mali	Kela	153686	10	10.4

Species	Banked_id	Year	Country	Village	Mapped bases	Mean coverage	Standard deviation
An. gambiae-Bamako	12KELA467	2012	Mali	Kela	10499093	683.4	249.1
An. gambiae-Savannah	12KELA468	2012	Mali	Kela	10315033	671.4	197.1
An. gambiae-Bamako	12KELA481	2012	Mali	Kela	20308589	1321.9	307.6
An. coluzzii-Mopti	12KELA496	2012	Mali	Kela	2975297	193.7	162.9
An. gambiae-Bamako	12KELA651	2012	Mali	Kela	376689	24.5	11.3
An. gambiae-Savannah	12KELA812	2012	Mali	Kela	799071	52	29.3
An. arabiensis	12LUPI001	2012	Tanzania	Lupiro	2843317	185.1	34.9
An. arabiensis	12LUPI007	2012	Tanzania	Lupiro	6288802	409.3	40
An. arabiensis	12LUPI024	2012	Tanzania	Lupiro	6328898	412	78.5
An. arabiensis	12LUPI056	2012	Tanzania	Lupiro	5440256	354.1	39.2
An. arabiensis	12LUPI059	2012	Tanzania	Lupiro	39721262	2585.5	801.8
An. arabiensis	12LUPI071	2012	Tanzania	Lupiro	3433158	223.5	59.2
An. arabiensis	12LUPI074	2012	Tanzania	Lupiro	10096062	657.2	100.5
An. arabiensis	12LUPI082	2012	Tanzania	Lupiro	5732773	373.2	69.6
An. arabiensis	12MINE001	2012	Tanzania	Minepa	7768923	505.7	66.9
An. arabiensis	12MINE040	2012	Tanzania	Minepa	2784428	181.2	54.9
An. arabiensis	12MINE100	2012	Tanzania	Minepa	10753877	700	93.9
An. arabiensis	12MINE101	2012	Tanzania	Minepa	5684230	370	41.9
An. arabiensis	12MINE105	2012	Tanzania	Minepa	1526829	99.4	32.8
An. arabiensis	12MINE111	2012	Tanzania	Minepa	5578562	363.1	76.3
An. arabiensis	12SAGA066	2012	Tanzania	Sagamaganga	12745079	829.6	142.3
An. arabiensis	12SAGA107	2012	Tanzania	Sagamaganga	14460217	941.2	259.2
An. arabiensis	12SAGA131	2012	Tanzania	Sagamaganga	15333239	998.1	282.9
An. arabiensis	12SAGA133	2012	Tanzania	Sagamaganga	3792945	246.9	62.5
An. arabiensis	12SAGA134	2012	Tanzania	Sagamaganga	2439101	158.8	34.5
An. arabiensis	12SAGA141	2012	Tanzania	Sagamaganga	3130504	203.8	33.3
An. arabiensis	05OKJ017	2005	Cameroon	Ourodoukoudje	9041052	588.5	78.8
An. arabiensis	05OKJ042	2005	Cameroon	Ourodoukoudje	148752684	9682.5	785.7
An. arabiensis	05OKJ045	2005	Cameroon	Ourodoukoudje	35514980	2311.7	262.8
An. arabiensis	05OKJ070	2005	Cameroon	Ourodoukoudje	22847478	1487.2	400.5

Dataset 1. Aligned FASTA file of mitogenome samples

http://dx.doi.org/10.5256/f1000research.13807.d192892

Results and discussion

We identified a total of 783 single nucleotide polymorphisms (SNPs) over the entire mitogenome. The majority of these (58.7%) were singletons (found on one of the 70 mitogenomes). We did not identify any SNPs unique to the species or chromosomal forms (Table 2) and therefore conclude that mtDNA is not suitable for *Anopheles gambiae* complex species identification.

The lack of species-specific markers is also reflected in the phylogenetic tree (Figure 1). *An. arabiensis*, *An. coluzzii* and *An. gambiae* did not cluster separately, which is consistent with previous reports that compared mitochondrial genome sequence data from specimens originating from Kenya, Senegal and South Africa (Besansky *et al.* (1997)) and Burkina Faso, Cameroon,

Table 2. **List of SNP variants in the different Anopheles species and chromosomal forms.**

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
55	C	T/-/-	21/3/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
71	C	T/-/-	0/24/0/0	0/11/0/0	0/13/0/0	1/11/0/0	0/11/0/0
117	A	G/-/-	23/1/0/0	9/2/0/0	13/0/0/0	12/0/0/0	11/0/0/0
126	T	C/-/-	11/13/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
205	C	T/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
223	T	C/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
248	G	A/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
250	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
298	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
340	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
373	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
391	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
396	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
409	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
441	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
469	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
488	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
502	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
503	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
514	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
520	T	A/C/-	22/0/2/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
526	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
562	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
572	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
583	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
611	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
665	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
685	A	G/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
688	T	A/-/-	24/0/0/0	10/1/0/0	12/0/0/0	11/1/0/0	11/0/0/0
700	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
706	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
712	A	C/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
757	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
763	A	G/-/-	11/13/0/0	3/8/0/0	0/13/0/0	2/10/0/0	1/10/0/0
787	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
788	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	10/1/0/0
796	A	G/-/-	22/2/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
811	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
821	T	C/-/-	11/13/0/0	1/9/0/0	1/12/0/0	0/12/0/0	1/10/0/0
832	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
887	T	C/-/-	16/8/0/0	10/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
908	A	G/-/-	18/6/0/0	10/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
934	G	A/-/-	22/2/0/0	9/1/0/0	12/0/0/0	12/0/0/0	10/1/0/0
949	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	11/1/0/0	11/0/0/0
955	T	C/-/-	12/12/0/0	5/5/0/0	9/4/0/0	4/8/0/0	2/9/0/0
1012	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1029	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1042	T	C/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
1045	A	G/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0
1114	C	T/-/-	24/0/0/0	11/0/0/0	12/0/0/0	11/1/0/0	11/0/0/0
1150	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1153	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1155	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1163	T	C/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
1189	G	A/-/-	24/0/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
1198	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1308	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1465	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1474	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1486	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1504	A	G/-/-	23/1/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
1507	G	A/-/-	23/1/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
1523	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1538	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
1540	A	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
1543	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1546	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1549	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
1558	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1561	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
1567	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1618	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
1624	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1636	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1639	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1642	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1645	A	G/T/	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	10/0/1/0
1648	G	A/-/-	23/1/0/0	10/0/0/0	9/4/0/0	12/0/0/0	10/1/0/0
1681	A	C/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1693	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1729	G	A/-/-	23/1/0/0	7/4/0/0	13/0/0/0	10/2/0/0	11/0/0/0
1735	T	C/-/-	23/1/0/0	9/2/0/0	13/0/0/0	10/2/0/0	11/0/0/0
1738	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1751	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1765	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1780	G	A/-/-	23/1/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
1792	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1807	T	C/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1837	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
1876	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1879	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1903	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1906	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1918	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1930	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1933	G	A/-/-	23/1/0/0	10/0/0/0	11/2/0/0	7/5/0/0	7/4/0/0
1964	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1972	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
1978	G	A/-/-	22/2/0/0	11/0/0/0	9/4/0/0	8/4/0/0	11/0/0/0
2026	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2068	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2071	T	C/G/-	23/1/0/0	11/0/0/0	12/0/1/0	12/0/0/0	10/0/1/0
2080	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
2098	T	C/-/-	23/1/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2101	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2110	T	C/-/-	23/1/0/0	10/1/0/0	11/2/0/0	11/1/0/0	10/1/0/0
2116	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2149	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2164	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2179	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2182	G	A/-/-	22/2/0/0	6/5/0/0	11/2/0/0	4/8/0/0	8/3/0/0
2206	A	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2209	G	A/-/-	19/5/0/0	10/1/0/0	12/1/0/0	11/1/0/0	9/2/0/0
2227	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2233	A	G/T/-	24/0/0/0	11/0/0/0	13/0/0/0	11/0/1/0	11/0/0/0
2239	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2260	C	T/-/-	2/22/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
2269	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2284	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2329	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2359	G	A/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
2374	G	A/-/-	23/1/0/0	11/0/0/0	10/3/0/0	11/1/0/0	10/1/0/0
2401	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2410	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2411	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2413	G	A/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
2426	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2432	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2434	G	A/-/-	22/2/0/0	9/2/0/0	11/2/0/0	11/1/0/0	10/1/0/0
2449	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2473	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2474	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2482	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2521	C	T/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	10/1/0/0
2530	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2558	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2569	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2599	A	G/T/-	23/1/0/0	10/1/0/0	13/0/0/0	11/0/1/0	11/0/0/0
2608	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2612	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2615	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2635	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2692	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2719	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2722	A	G/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2728	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2731	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2737	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0

Position	**Reference nucleotide**	**Alternative nucleotides**	**SNP variant counts per group (first value is count of reference allel)**				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
2752	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2755	C	A/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2758	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2774	G	A/-/-	23/1/0/0	11/0/0/0	11/2/0/0	11/1/0/0	11/0/0/0
2782	T	A/C/-	23/0/1/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2791	T	A/C/-	23/0/1/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2797	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2806	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
2818	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2848	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2851	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2859	C	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2872	T	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2902	C	T/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2908	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2938	G	A/-/-	23/1/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
2945	C	T/-/-	15/9/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2975	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3055	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
3124	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3136	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3199	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3202	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3205	A	G/-/-	24/0/0/0	9/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3238	T	A/C/	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3277	A	T/-/-	24/0/0/0	11/0/0/0	11/1/0/0	11/1/0/0	8/3/0/0
3286	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3304	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3307	A	C/G/T	24/0/0/0	11/0/0/0	9/0/1/3	12/0/0/0	11/0/0/0
3310	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
3325	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	10/2/0/0	11/0/0/0
3331	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3334	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3337	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3352	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
3400	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3401	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3403	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3412	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3413	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3424	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3451	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3457	G	A/T/	12/12/0/0	6/4/1/0	12/1/0/0	3/9/0/0	5/6/0/0
3458	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3466	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3508	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	11/1/0/0	10/1/0/0
3511	C	A/T/-	22/1/1/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3514	C	T/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
3523	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3544	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
3595	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3613	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3619	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3652	G	A/-/-	22/2/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3773	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3838	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
3870	C	T/-/-	12/12/0/0	3/8/0/0	6/7/0/0	1/11/0/0	3/8/0/0
3882	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3924	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3960	T	C/-/-	24/0/0/0	10/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
3976	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4002	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4011	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4034	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4037	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4052	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4100	C	T/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4104	G	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4112	C	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4115	A	G/-/-	11/13/0/0	1/9/0/0	0/13/0/0	0/12/0/0	2/9/0/0
4121	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4145	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4157	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4181	T	A/-/-	3/21/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
4190	A	G/-/-	0/24/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
4196	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4206	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4208	A	G/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4214	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4220	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4256	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4259	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4292	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4310	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4332	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4352	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4367	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4368	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4373	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4430	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4442	G	A/-/-	14/10/0/0	10/1/0/0	11/2/0/0	12/0/0/0	9/2/0/0
4451	G	A/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
4484	A	T/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4487	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4490	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4494	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4526	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4529	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4538	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii*-Forest**	***An. coluzzii*-Mopti**	***An. gambiae*-Bamako**	***An. gambiae*-Savannah**
4559	A	G/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4562	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4565	T	A/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4566	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4579	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4603	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4620	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4637	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4649	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4652	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4715	G	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4747	C	A/T/-	24/0/0/0	10/0/1/0	13/0/0/0	10/1/1/0	11/0/0/0
4750	A	G/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4756	C	T/-/-	21/3/0/0	9/2/0/0	13/0/0/0	9/3/0/0	10/1/0/0
4774	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4777	A	C/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4795	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4846	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4847	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4867	G	A/-/-	24/0/0/0	9/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
4885	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4969	A	C/-/-	16/8/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5011	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5020	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5029	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5044	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5056	T	C/-/-	23/1/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
5059	A	T/-/-	11/13/0/0	1/9/0/0	0/13/0/0	0/12/0/0	1/10/0/0
5062	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5065	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5072	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5074	A	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5077	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5080	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5128	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5131	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5137	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5165	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5167	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5173	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5182	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5215	A	G/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5216	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5221	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
5254	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5257	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
5272	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
5278	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5279	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
5287	A	G/-/-	19/5/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5308	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5314	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
5320	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5323	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5359	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
5398	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5428	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5431	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5513	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5540	C	T/-/-	23/1/0/0	7/4/0/0	7/5/0/0	7/5/0/0	9/2/0/0
5564	T	C/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
5572	A	G/-/-	21/3/0/0	10/1/0/0	11/1/0/0	11/1/0/0	11/0/0/0
5622	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5652	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5661	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5664	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5670	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5679	T	C/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
5682	G	A/-/-	23/1/0/0	7/4/0/0	5/8/0/0	6/6/0/0	11/0/0/0
5688	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5691	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5700	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5712	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5850	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5865	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5871	C	T/-/-	16/8/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
5883	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5898	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5941	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6021	A,T	A/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6054	G	A/-/-	21/3/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6222	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6252	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6277	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6289	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
6315	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6388	A	G/-/-	24/0/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
6421	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6425	A	G/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
6430	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6439	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
6442	T	C/G/-	14/9/1/0	10/0/0/0	12/1/0/0	12/0/0/0	8/3/0/0
6450	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6466	A	G/-/-	16/8/0/0	7/4/0/0	13/0/0/0	7/5/0/0	6/5/0/0
6469	G	A/-/-	21/3/0/0	9/2/0/0	11/2/0/0	12/0/0/0	10/1/0/0
6482	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6488	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6501	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
6517	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6529	G	A/-/-	12/12/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
6551	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6556	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
6563	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
6571	G	A/-/-	23/1/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
6578	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6580	G	A/-/-	21/3/0/0	7/4/0/0	11/2/0/0	10/2/0/0	6/5/0/0
6616	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6619	G	A/-/-	21/3/0/0	9/2/0/0	13/0/0/0	11/1/0/0	7/4/0/0
6628	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
6631	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6637	G	A/-/-	23/1/0/0	9/2/0/0	11/2/0/0	10/2/0/0	11/0/0/0
6649	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6661	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6662	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6670	C	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6684	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6687	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6699	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6718	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
6726	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6730	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6731	C	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6733	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6753	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6764	C	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6791	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6793	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
6805	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6808	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6829	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6841	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6847	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6928	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6933	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6982	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
6985	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7027	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	10/2/0/0	10/1/0/0
7045	G	A/-/-	15/9/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
7075	T	C/-/-	24/0/0/0	8/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7090	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7099	T	C/G/-	24/0/0/0	11/0/0/0	13/0/0/0	9/2/1/0	11/0/0/0
7105	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
7108	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	10/1/0/0
7116	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7135	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7168	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7195	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7207	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
7231	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7240	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
7255	G	A/-/-	3/21/0/0	1/10/0/0	0/13/0/0	1/11/0/0	1/10/0/0
7261	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7282	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7290	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7351	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7360	T	C/-/-	11/13/0/0	2/9/0/0	4/9/0/0	1/11/0/0	1/10/0/0
7381	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7396	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7402	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7423	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7432	A	C/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
7450	G	A/-/-	23/1/0/0	10/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
7478	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7479	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7483	C	G/T/	24/0/0/0	10/1/0/0	11/0/2/0	11/1/0/0	11/0/0/0
7486	C	T/-/-	11/13/0/0	5/6/0/0	4/9/0/0	0/12/0/0	2/9/0/0
7525	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7555	A	G/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7578	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7588	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7603	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7606	G	A/-/-	24/0/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7627	A	G/-/-	13/11/0/0	7/4/0/0	12/1/0/0	5/7/0/0	5/6/0/0
7672	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7687	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7693	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7735	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
7777	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
7797	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7798	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7822	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7861	T	C/-/-	23/1/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7923	T	C/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
7952	A	G/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8001	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8034	C	T/-/-	13/11/0/0	6/4/0/0	11/1/0/0	3/9/0/0	5/6/0/0
8091	A	AT/-/-	22/2/0/0	9/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
8122	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8123	C	T/-/-	22/2/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8149	G	A/-/-	2/22/0/0	0/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8196	G	A/-/-	23/1/0/0	10/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
8201	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8261	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8297	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8302	G	A/-/-	23/1/0/0	10/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
8303	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8309	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8339	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
8342	C	T/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
8372	C	T/-/-	24/0/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
8375	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8382	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
8384	A	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8393	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8399	G	A/-/-	2/22/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8404	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8414	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8425	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8450	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8465	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8471	G	A/T/-	24/0/0/0	6/5/0/0	7/6/0/0	10/2/0/0	10/1/0/0
8513	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8528	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8546	A	T/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8564	C	A/T/-	23/0/1/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8582	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8588	T	C/-/-	24/0/0/0	11/0/0/0	9/4/0/0	11/1/0/0	10/1/0/0
8612	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8645	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8657	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8663	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8678	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8684	T	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
8714	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8720	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
8722	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8725	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8726	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8740	G	A/-/-	24/0/0/0	10/1/0/0	9/4/0/0	9/3/0/0	10/1/0/0
8744	G	A/-/-	23/1/0/0	8/3/0/0	11/2/0/0	10/2/0/0	10/1/0/0
8765	G	A/-/-	22/2/0/0	10/1/0/0	12/1/0/0	11/1/0/0	8/3/0/0
8807	T	C/-/-	22/2/0/0	9/2/0/0	12/1/0/0	11/1/0/0	11/0/0/0
8819	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	8/3/0/0
8840	C	T/-/-	11/13/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
8842	A	G/-/-	24/0/0/0	10/1/0/0	10/3/0/0	12/0/0/0	9/2/0/0
8855	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8882	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	9/2/0/0
8893	G	A/-/-	24/0/0/0	7/4/0/0	8/6/0/0	9/3/0/0	11/0/0/0
8903	C	T/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8913	A	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
8915	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
8927	A	G/-/-	11/13/0/0	2/9/0/0	0/14/0/0	1/11/0/0	2/9/0/0
8942	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8995	A	G/-/-	21/3/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8996	A	T/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
9014	A	T/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
9035	C	T/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
9041	C	T/-/-	3/21/0/0	0/11/0/0	0/14/0/0	0/12/0/0	0/11/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
9062	C	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9122	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9152	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9158	C	T/-/-	23/1/0/0	7/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
9210	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9236	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9244	G	A/-/-	22/2/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9245	C	A/T/-	23/0/1/0	10/0/1/0	13/0/0/0	12/0/0/0	9/1/1/0
9278	G	A/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
9287	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9311	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
9353	C	T/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0
9359	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
9365	T	C/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9421	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9422	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9459	A	G/-/-	24/0/0/0	10/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
9493	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9529	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9532	C	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9535	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9550	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9575	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9583	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9611	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9631	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
9660	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9688	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9690	T	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9711	T	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9724	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9795	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9808	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9911	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9930	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9976	C	T/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	11/0/0/0
10011	A	G/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	10/1/0/0
10047	A	G/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
10063	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10068	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10104	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
10156	G	A/C/-	24/0/0/0	8/1/2/0	13/1/0/0	10/1/1/0	8/3/0/0
10168	C	A/T/-	24/0/0/0	7/4/0/0	9/5/0/0	9/2/1/0	10/0/1/0
10176	A	G/-/-	11/13/0/0	2/9/0/0	3/11/0/0	0/12/0/0	2/9/0/0
10177	G	A/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	10/1/0/0
10185	C	A/T/-	16/0/8/0	11/0/0/0	13/1/0/0	12/0/0/0	10/0/1/0
10187	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
10252	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10253	C	T/-/-	23/1/0/0	10/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
10269	C	T/-/-	24/0/0/0	7/3/0/0	9/5/0/0	10/2/0/0	11/0/0/0
10284	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
10311	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10324	T	C/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10332	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
10341	T	C/-/-	24/0/0/0	10/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
10371	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10383	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10396	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10401	G	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10424	T	A/-/-	16/8/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10427	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10454	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	10/2/0/0	10/1/0/0
10463	T	C/-/-	24/0/0/0	7/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10466	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10481	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10482	G	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10499	C	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10502	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10535	C	T/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10536	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10542	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	9/2/0/0
10559	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10566	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10568	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10583	C	T/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10598	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10607	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10628	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10640	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10664	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10670	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
10691	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10700	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10715	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10718	A	G/-/-	24/0/0/0	9/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10719	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10724	T	C/-/-	22/2/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10727	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10737	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10742	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10763	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10784	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10796	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
10805	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10808	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10820	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
10841	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10863	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
10872	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10877	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10880	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10881	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10886	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10889	G	A/-/-	22/2/0/0	9/2/0/0	11/2/0/0	9/3/0/0	11/0/0/0
10892	T	C/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10898	T	A/C/-	11/0/13/0	2/0/9/0	0/0/13/0	1/0/11/0	1/0/10/0
10910	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10913	G	A/-/-	22/2/0/0	9/2/0/0	10/3/0/0	10/2/0/0	8/3/0/0
10916	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
10931	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10934	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
10955	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10988	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10997	G	A/-/-	23/1/0/0	9/1/0/0	11/2/0/0	10/2/0/0	10/1/0/0
10998	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11042	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11060	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
11093	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11117	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
11150	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11159	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11160	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11171	T	C/-/-	23/1/0/0	9/2/0/0	11/2/0/0	11/1/0/0	8/3/0/0
11174	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11204	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11213	A	G/T/-	24/0/0/0	10/1/0/0	12/1/1/0	12/0/0/0	10/0/1/0
11216	T	C/-/-	24/0/0/0	11/0/0/0	13/1/0/0	10/2/0/0	10/1/0/0
11222	A	G/-/-	24/0/0/0	8/3/0/0	9/5/0/0	10/2/0/0	11/0/0/0
11234	C	T/-/-	24/0/0/0	11/0/0/0	12/2/0/0	11/1/0/0	11/0/0/0
11249	C	T/-/-	24/0/0/0	10/1/0/0	13/1/0/0	12/0/0/0	9/2/0/0
11276	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
11282	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
11301	C	T/-/-	9/15/0/0	2/9/0/0	0/14/0/0	0/12/0/0	0/11/0/0
11318	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11339	C	T/-/-	24/0/0/0	8/3/0/0	7/6/0/0	10/2/0/0	11/0/0/0
11348	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11351	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	10/1/0/0
11354	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11363	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11390	C	T/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	9/2/0/0
11414	G	A/-/-	23/1/0/0	10/1/0/0	10/4/0/0	10/2/0/0	11/0/0/0
11415	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
11432	A	G/-/-	23/1/0/0	11/0/0/0	14/0/0/0	10/2/0/0	10/1/0/0
11450	C	T/-/-	13/11/0/0	1/10/0/0	1/13/0/0	0/12/0/0	2/9/0/0
11475	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
11492	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11537	G	A/-/-	24/0/0/0	9/2/0/0	8/5/0/0	10/2/0/0	8/3/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
11538	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11592	G	A/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
11599	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11610	A	AT/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11655	G	A/-/-	8/16/0/0	1/9/0/0	0/13/0/0	0/12/0/0	0/11/0/0
11673	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11729	G	A/-/-	24/0/0/0	9/2/0/0	11/2/0/0	12/0/0/0	8/3/0/0
11739	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11745	T	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11748	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11757	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11760	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11763	A	G/-/-	18/6/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11787	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11793	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11829	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11862	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11868	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11899	G	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11907	C	T/-/-	20/4/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11910	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11916	G	A/-/-	20/4/0/0	5/5/0/0	2/11/0/0	5/7/0/0	8/3/0/0
11925	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11931	T	C/-/-	23/1/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11982	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11988	A	C/-/-	12/12/0/0	6/4/0/0	11/2/0/0	3/9/0/0	3/8/0/0
12005	G	A/-/-	23/1/0/0	9/1/0/0	12/1/0/0	9/3/0/0	8/3/0/0
12006	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
12009	G	A/T/-	24/0/0/0	6/4/0/0	8/2/3/0	8/4/0/0	11/0/0/0
12015	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12020	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12036	A	G/-/-	13/11/0/0	2/8/0/0	1/12/0/0	2/10/0/0	4/7/0/0
12039	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12061	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12078	A	G/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12084	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
12092	C	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12159	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12165	C	A/T/-	19/4/1/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12168	C	T/-/-	22/2/0/0	10/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
12171	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
12204	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12210	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12225	T	C/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	10/1/0/0
12228	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12258	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
12273	A	G/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
12278	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
12333	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
12336	A	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0

Position	**Reference nucleotide**	**Alternative nucleotides**	**SNP variant counts per group (first value is count of reference allel)**				
			An. arabiensis	***An. coluzzii-Forest***	***An. coluzzii-Mopti***	***An. gambiae-Bamako***	***An. gambiae-Savannah***
12339	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12348	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12420	T	C/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
12471	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	10/2/0/0	10/1/0/0
12480	A	G/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	11/0/0/0
12499	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12501	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12536	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
12558	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12601	T	TTA/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
12607	A	T/-/-	24/0/0/0	10/0/0/0	11/3/0/0	12/0/0/0	11/0/0/0
12633	G	A/-/-	23/1/0/0	9/1/0/0	12/2/0/0	11/1/0/0	10/1/0/0
12784	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12890	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12964	T	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12967	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13109	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13123	G	A/-/-	22/2/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13310	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13311	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13489	G	A/-/-	23/1/0/0	10/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
13579	T	C/-/-	24/0/0/0	11/0/0/0	11/0/0/0	12/0/0/0	10/1/0/0
13641	A	G/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13683	C	T/-/-	24/0/0/0	11/0/0/0	12/0/0/0	11/1/0/0	11/0/0/0
13696	G	A/-/-	22/2/0/0	11/0/0/0	12/0/0/0	11/1/0/0	10/1/0/0
13741	G	A/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13776	A	G/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13876	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13882	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
13941	A	AT/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/0/0/0
13943	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/0/0/0
13955	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13989	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14105	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14115	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14194	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
14233	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14291	C	T/-/-	21/3/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14359	G	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14373	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14384	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
14439	A	G/-/-	21/3/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14454	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14536	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14540	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14543	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
14549	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14582	T	TTA/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
14602	T	C/-/-	24/0/0/0	9/2/0/0	12/1/0/0	11/1/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allel)				
			An. arabiensis	*An. coluzzii-Forest*	*An. coluzzii-Mopti*	*An. gambiae-Bamako*	*An. gambiae-Savannah*
14642	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14686	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14691	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14741	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14847	T	C/-/-	11/13/0/0	1/9/0/0	2/10/0/0	1/11/0/0	1/9/0/0
14875	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/0/0/0
14881	T	TA/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	9/0/0/0
14912	T	C/-/-	24/0/0/0	11/0/0/0	10/1/0/0	10/0/0/0	9/0/0/0
14916	C	T/-/-	23/1/0/0	11/0/0/0	11/0/0/0	10/0/0/0	8/1/0/0
14930	A	G/-/-	23/1/0/0	11/0/0/0	9/0/0/0	11/0/0/0	10/0/0/0
14936	A	G/-/-	24/0/0/0	11/0/0/0	9/1/0/0	11/0/0/0	11/0/0/0
14976	T,A	T/-/-	23/1/0/0	10/1/0/0	8/2/0/0	9/1/0/0	7/3/0/0
14978	A	C/T/	20/4/0/0	3/8/0/0	4/6/0/0	3/7/0/0	5/4/1/0
14984	A,T,T	TTT/AT/A	14/2/7/1	2/2/0/3	3/2/0/0	5/2/0/1	4/0/0/2
15002	A	T/-/-	22/2/0/0	5/2/0/0	4/1/0/0	3/5/0/0	4/2/0/0
15012	T	C/-/-	24/0/0/0	9/0/0/0	11/0/0/0	11/1/0/0	10/0/0/0
15035	T	TA/-/-	23/1/0/0	10/0/0/0	12/0/0/0	9/0/0/0	11/0/0/0
15036	A	G/-/-	24/0/0/0	10/0/0/0	12/0/0/0	9/0/0/0	9/2/0/0
15038	A	AATT/-/-	22/2/0/0	7/3/0/0	10/0/0/0	11/0/0/0	7/2/0/0
15039	A	G/-/-	24/0/0/0	10/0/0/0	10/0/0/0	7/4/0/0	8/1/0/0
15049	T	C/-/-	24/0/0/0	10/0/0/0	10/0/0/0	11/0/0/0	7/2/0/0
15050	T	TTA/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	9/0/0/0
15052	A	G/-/-	23/1/0/0	10/0/0/0	7/1/0/0	11/0/0/0	9/0/0/0
15057	C	T/-/-	23/1/0/0	10/0/0/0	8/0/0/0	8/0/0/0	9/0/0/0
15058	A	G/-/-	22/2/0/0	5/5/0/0	3/5/0/0	4/4/0/0	7/2/0/0
15066	T	C/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/0/0/0
15069	T	C/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/1/0/0
15082	A	G/-/-	22/2/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/2/0/0
15098	A	G/-/-	23/1/0/0	9/1/0/0	10/0/0/0	8/1/0/0	8/0/0/0
15115	T	C/-/-	21/3/0/0	8/1/0/0	8/2/0/0	8/1/0/0	8/0/0/0
15116	G	A/-/-	14/10/0/0	9/1/0/0	10/0/0/0	8/1/0/0	3/5/0/0
15128	A	G/-/-	23/1/0/0	8/1/0/0	6/1/0/0	8/0/0/0	7/0/0/0
15129	G	A/-/-	1/23/0/0	0/9/0/0	0/7/0/0	1/7/0/0	0/7/0/0
15144	T	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
15189	A	G/-/-	18/6/0/0	10/1/0/0	11/0/0/0	10/0/0/0	7/0/0/0
15243	T	C/-/-	15/9/0/0	10/1/0/0	7/1/0/0	7/0/0/0	6/0/0/0
15282	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
15301	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/0/0/0	11/0/0/0
15304	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/0/0/0	11/0/0/0
15305	T	TA/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/0/0/0	11/0/0/0
15321	C	T/-/-	23/1/0/0	11/0/0/0	11/2/0/0	11/0/0/0	11/0/0/0
15327	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

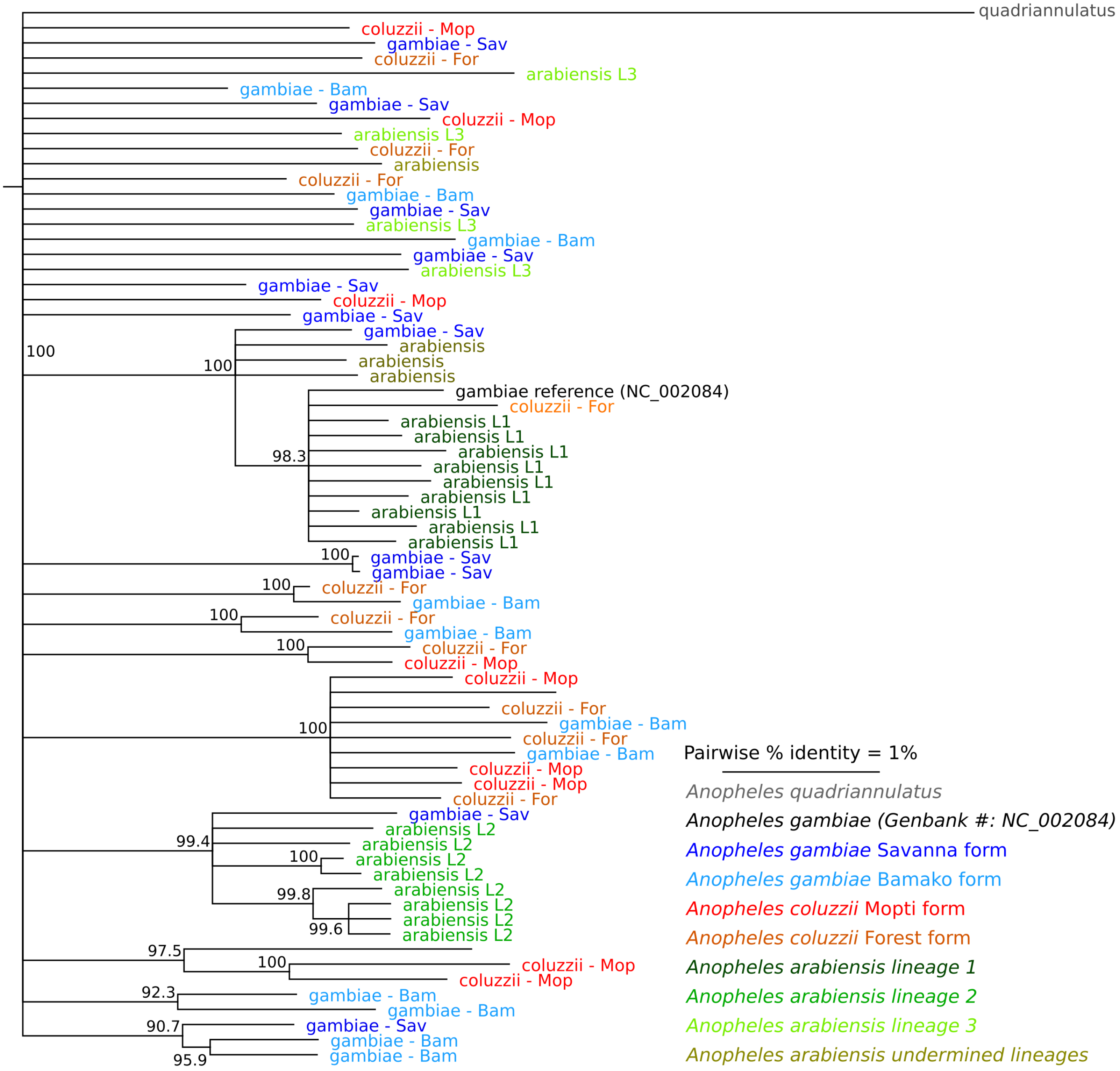

Figure 1. Phylogenetic tree inferred from mtDNA genome sequence data. With the exception of the outgroup, *An. quadriannulatis*, this analysis fails to reveal a clear division of the operational taxonomic units included in this analysis. Colors indicate the species or chromosomal form and numbers at the branches indicate the accuracy of the inferred branches on a scale of 0–100, where 100 represents the highest confidence.

Kenya, Mali, South Africa, Tanzania and Zimbabwe (Fontaine *et al.* (2015), supplemental material).

Of note, 36 of the samples that we used in our study originated from Kela (Mali). Kela is located near the village of Selinkenyi, where previous studies have shown a history of hybridization and introgression between *An. gambiae* and *An. coluzzii* (Lee *et al.* (2013); Main *et al.* (2015); Norris *et al.* (2015)) , which may have resulted in shared polymorphisms in their mitochondrial genomes. Shared polymorphisms in their mitochondrial genomes, where history has not been reported, also appeared to have occurred in Mutengene (Cameroon), where both *An. gambiae* and *An. coluzzii* occur sympatrically. Hybridization between either *An. coluzzii* or *An. gambiae* with *An. arabiensis* yields sterile males (Slotman *et al.* (2004)), but phylogenomic analysis of these species show patterns of introgression between all of them (Fontaine *et al.* (2015)). Our mitochondrial genome study does not provide conclusive evidence for hybridization and introgression among the taxa under study. However, our data suggest that this is a possibility.

Data availability

Aligned sequences were submitted to the National Center for Biotechnology Information (NCBI) Accession number:

MG930826 - MG930896

Dataset 1. Aligned FASTA file of mitogenome samples 10.5256/f1000research.13807.d192892 (Hanemaaijer *et al.*, 2018)

Competing interests

No competing interests were disclosed.

Grant information

We thank University of California - Irvine, Malaria Initiatives (UCIMI) for their support.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

We thank Michelle Sanford for her assistance in the field collection in Cameroon in 2011. We thank Clare Marsden for providing the raw data of *An. arabiensis* samples.

References

Beard CB, Hamm DM, Collins FH: **The mitochondrial genome of the mosquito *Anopheles gambiae*: DNA sequence, genome organization, and comparisons with mitochondrial sequences of other insects.** *Insect Mol Biol.* 1993; **2**(2): 103–124.
PubMed Abstract | Publisher Full Text

Besansky NJ, Lehmann T, Fahey GT, *et al.*: **Patterns of mitochondrial variation within and between African malaria vectors, *Anopheles gambiae* and *An. arabiensis*, suggest extensive gene flow.** *Genetics.* 1997; **147**(4): 1817–1828.
PubMed Abstract | Free Full Text

Bolger AM, Loshe M, Usadel B: **Trimmomatic: a flexible trimmer for Illumina sequence data.** *Bioinformatics.* 2014; **30**(15): 2114–2120.
PubMed Abstract | Publisher Full Text | Free Full Text

Brown WM, George M Jr, Wilson AC: **Rapid evolution of animal mitochondrial DNA.** *Proc Natl Acad Sci U S A.* 1979; **76**(4): 1967–1971.
PubMed Abstract | Free Full Text

Crawford JE, Lazzaro BP: **Assessing the accuracy and power of population genetic inference from low-pass next-generation sequencing data.** *Front Genet.* 2012; **3**: 66.
PubMed Abstract | Publisher Full Text | Free Full Text

Cronin MA, Palmisciano DA, Vyse ER, *et al.*: **Mitochondrial DNA in wildlife forensic science: species identification of tissues.** *Wildlife Soc B (1973-2006).* 1991; **19**(1): 94–105.
Reference Source

Danecek P, Auton A, Abecasis G, *et al.*: **The variant call format and VCFtools.** *Bioinformatics.* 2011; **27**(15): 2156–2158.
PubMed Abstract | Publisher Full Text | Free Full Text

De Barba M, Adams JR, Goldberg CS, *et al.*: **Molecular species identification for multiple carnivores.** *Conserv Genet Resour.* 2014; **6**(4): 821–824.
Publisher Full Text

De Mandal S, Chhakchhuak L, Gurusubramanian G, *et al.*: **Mitochondrial markers for identification and phylogenetic studies in insects–A Review.** *DNA Barcodes.* 2014; **2**(1).
Publisher Full Text

Fontaine MC, Pease JB, Steele A, *et al.*: **Mosquito genomics. Extensive introgression in a malaria vector species complex revealed by phylogenomics.** *Science.* 2015; **347**(6217): 1258524.
PubMed Abstract | Publisher Full Text | Free Full Text

Fu Q, Mittnik A, Johnson PLF, *et al.*: **A revised timescale for human evolution based on ancient mitochondrial genomes.** *Curr Biol.* 2013; **23**(7): 553–559.
PubMed Abstract | Publisher Full Text | Free Full Text

Garrison E, Marth G: **Haplotype-based variant detection from short-read sequencing.** *arXiv: 1207.3907.* Cornell University Library; 2013.
Reference Source

Green CA: **Cytological maps for the practical identification of females of the three freshwater species of the *Anopheles gambiae* complex.** *Ann Trop Med Parasitol.* 1972; **66**(1): 143–147.
PubMed Abstract | Publisher Full Text

Haag-Liautard C, Coffey N, Houle D, *et al.*: **Direct estimation of the mitochondrial DNA mutation rate in *Drosophila melanogaster*.** *PLoS Biol.* 2008; **6**(8): e204.
PubMed Abstract | Publisher Full Text | Free Full Text

Hanemaaijer MJ, Houston P, Collier TC, *et al.*: **Dataset 1: Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division.** *F1000Research.* 2018.
Data Source

Harrison RG: **Animal mitochondrial DNA as a genetic marker in population and evolutionary biology.** *Trends Ecol Evol.* 1989; **4**(1): 6–11.
PubMed Abstract | Publisher Full Text

Lanzaro GC, Lee Y: **Speciation in *Anopheles gambiae*—The distribution of genetic polymorphism and patterns of reproductive isolation among natural populations.** *Anopheles mosquitoes-New insights into malaria vectors.* InTech, 2013.
Publisher Full Text

Lee Y, Marsden CD, Norris LC, *et al.*: **Spatiotemporal dynamics of gene flow and hybrid fitness between the M and S forms of the malaria mosquito, *Anopheles gambiae*.** *Proc Natl Acad Sci U S A.* 2013; **110**(49): 19854–19859.
PubMed Abstract | Publisher Full Text | Free Full Text

Lee Y, Marsden CD, Nieman C, *et al.*: **A new multiplex SNP genotyping assay for detecting hybridization and introgression between the M and S molecular forms of *Anopheles gambiae*.** *Mol Ecol Resour.* 2014; **14**(2): 297–305.
PubMed Abstract | Publisher Full Text | Free Full Text

Llamas B, Fehren-Schmitz L, Valverde G, *et al.*: **Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas.** *Sci Adv.* 2016; **2**(4): e1501385.
PubMed Abstract | Publisher Full Text | Free Full Text

Main BJ, Lee Y, Collier TC, *et al.*: **Complex genome evolution in *Anopheles coluzzii* associated with increased insecticide usage in Mali.** *Mol Ecol.* 2015; **24**(20): 5145–5157.
PubMed Abstract | Publisher Full Text | Free Full Text

Marsden CD, Lee Y, Kreppel K, *et al.*: **Diversity, differentiation, and linkage disequilibrium: prospects for association mapping in the malaria vector *Anopheles arabiensis*.** *G3 (Bethesda).* 2014; **4**(1): 121–131.
PubMed Abstract | Publisher Full Text | Free Full Text

Miles A, Harding N: **cggh/scikit-allel: v1.1.8 (Version v1.1.8).** *Zenodo.* 2017.
Publisher Full Text

Norris LC, Main BJ, Lee Y, *et al.*: **Adaptive introgression in an African malaria mosquito coincident with the increased usage of insecticide-treated bed nets.** *Proc Natl Acad Sci U S A.* 2015; **112**(3): 815–820.
PubMed Abstract | Publisher Full Text | Free Full Text

Okonechnikov K, Conesa A, García-Alcalde F: **Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data.** *Bioinformatics.* 2016; **32**(2): 292–294.
PubMed Abstract | Publisher Full Text | Free Full Text

Pegg GG, Sinclair B, Briskey L, *et al.*: **MtDNA barcode identification of fish larvae in the southern Great Barrier Reef–Australia.** *Sci Mar.* 2006; **70**(S2): 7–12.
Reference Source

Phillips MJ, Haouchar D, Pratt RC, *et al.*: **Inferring kangaroo phylogeny from incongruent nuclear and mitochondrial genes.** *PLoS One.* 2013; **8**(2): e57745.
PubMed Abstract | Publisher Full Text | Free Full Text

Pombi M, Caputo B, Simard F, *et al.*: **Chromosomal plasticity and evolutionary potential in the malaria vector *Anopheles gambiae* sensu stricto: insights from**

three decades of rare paracentric inversions. *BMC Evol Biol.* 2008; **8**(1): 309.
PubMed Abstract | Publisher Full Text | Free Full Text

Scott JA, Brogdon WG, Collins FH: **Identification of single specimens of the *Anopheles gambiae* complex by the polymerase chain reaction.** *Am J Trop Med Hyg.* 1993; **49**(4): 520–529.
PubMed Abstract | Publisher Full Text

Shaw KL: **Conflict between nuclear and mitochondrial DNA phylogenies of a recent species radiation: what mtDNA reveals and conceals about modes of speciation in Hawaiian crickets.** *Proc Natl Acad Sci U S A.* 2002; **99**(25): 16122–16127.
PubMed Abstract | Publisher Full Text | Free Full Text

Slotman M, Della Torre A, Powell JR: **The genetics of inviability and male sterility in hybrids between *Anopheles gambiae* and *An. arabiensis*.** *Genetics.* 2004; **167**(1): 275–287.
PubMed Abstract | Publisher Full Text | Free Full Text

Sota T, Vogler AP: **Incongruence of mitochondrial and nuclear gene trees in the Carabid beetles *Ohomopterus*.** *Syst Biol.* 2001; **50**(1): 39–59.
PubMed Abstract | Publisher Full Text

Tahir HM, Mehwish, Kanwal N, *et al.*: **Genetic diversity in cytochrome c oxidase I gene of *Anopheles* mosquitoes.** *Mitochondrial DNA A DNA Mapp Seq Anal.* 2016; **27**(6): 4298–4301.
PubMed Abstract | Publisher Full Text

Turner TL, Hahn MW, Nuzhdin SV: **Genomic islands of speciation in *Anopheles gambiae*.** *PLoS Biol.* 2005; **3**(9): e285.
PubMed Abstract | Publisher Full Text | Free Full Text

Open Peer Review

Current Referee Status: ✓ ?

Version 1

Referee Report 14 May 2018

https://doi.org/10.5256/f1000research.15009.r33371

? **Maria Anice Mureb Sallum**
Department of Epidemiology, Faculty of Public Health, University of São Paulo, São Paulo, Brazil

General comment
Phylogenetic analysis need to be improved, and the choice for NJ methods and JC model, justified in the article. There are several programs that have been largely employed for phylogenetic analysis, including for mitogenome data. The paper authored by Foster et al.[1] contains useful information about analyses that have been carried out for inferring phylogenetic relationships within Anophelinae mosquitoes. I strongly suggest authors to verify how analyses were done.

Sample collection
Authors - "The An. gambiae and An. coluzzii samples were collected as resting adults using mouth aspirators in Kela, Mali (11.88683°N, -8.44744°W) in 2012 and Mutengene, Cameroon (4.0994°N, 9.3081°W) in 2011."

Comment - Can you please give more details the micro environment where your specimens of An. gambiae and An. coluzzii were resting?

Authors - "Similarly, we did this for the An. gambiae Savannah and Bamako chromosomal forms. We used the same definitions and methods to characterize the chromosomal forms as in Lanzaro & Lee, 2013."

Comment - It is not clear to me if you examined the polytene chromosome of each specimen you identified as the Savannah, Bamako, Forest and Mopti forms. Please clarify.

Genome sequencing
Authors - "For the An. coluzzii and An. gambiae samples we used the same methods as described in Norris et al. (2015) and Main et al. (2015). For the latter species, libraries were created using the Nextera DNA Sample Preparation Kit (FC-121-1031) and TruSeq dual indexing barcodes (FC-121-103) (Illumina) and the samples were sequenced on an Illumina HiSeq2500 with 100-bp paired end reads."

Comment - Please add a short sentence to clarify if you sequenced the whole genome and from the full sequence data you obtained the positions 1-13,470 of the mitogenome.

Data analysis
Authors - "The phylogenetic tree was generated using the Jukes-Cantor genetic distance model and

Neighbor-Joining tree methods available in Geneious version 10.1.3."

Comment - Authors should clarify their choice for sequence analysis. The Geneious software has been developed for editing and aligning DNA / amino acid sequences. There are several softwares, which have been largely used to infer phylogenetic relationships. I suggest authors to refining and improving the phylogenetic analysis using appropriate programs and models that have been chosen for the mitogenome data you have at hand.

References

1. Foster PG, de Oliveira TMP, Bergo ES, Conn JE, Sant'Ana DC, Nagaki SS, Nihei S, Lamas CE, González C, Moreira CC, Sallum MAM: Phylogeny of Anophelinae using mitochondrial protein coding genes.*R Soc Open Sci*. 2017; **4** (11): 170758 PubMed Abstract | Publisher Full Text

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
No

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Referee Report 30 April 2018

https://doi.org/10.5256/f1000research.15009.r32266

✓ **Beniamino Caputo** [1], **Verena Pichler** [2]

[1] Department of Public Health and Infectious Diseases, Sapienza University of Rome, Rome, Italy
[2] Department of Public Health & Infectious Diseases, Sapienza University of Rome, Rome, Italy

General comments

The present research note entitled:" Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division" is well analysed, reported and written. As already reported in previous study the submitted manuscript suggested the absence of any species-specific differences in the mitogenome of the three species examined. Although the manuscript is not innovative and the research is not based on any previous evidence, the present note confirms previous suggestions by examining the whole mitogenome of 70 specimens from field specimens and find the lack of species or chromosomal form specific markers.

Title and abstract
Title and abstract are appropriate and summarize well the content of the article.

Introduction
The introduction gives a good description of the aims of the present study, although I would have added some references to previous studies performed on mtDNA of the examined species (for example Besansky 1997) and why you expected to obtain different results compared to previous studies.

Please revise also:
“morphologically identical species that can only be distinguished with molecular markers” (Scott *et al.,* 1993; Coetzee et al., 2013)

The currently used molecular markers are located within genomic islands of divergence located proximal to the centromeres (Lee et al. (2014); Turner et al. (2005)) please rephrase the citation and refer it only to detect genomic differences between *An.gambiae* e and *An.coluzzii*.

Please insert a sentence about chromosomal forms of *An.gambiae.*

Methods
Please specified the method for collecting *An. arabiensis* as you already described for *An.gambiae* (e.g. indoor specimens, mouth aspirators, PSC collections).

Please insert a table with inversion polymorphism of chromosomal forms analyzed.

Please add the source of the *An. quadriannulatus* specimens you included in the phylogenetic analysis.

Results
Study design is well explained and results are given concisely.

Please add in Table 2 also the number of specimens you included for each species in the analysis.

Please add in Figure two an explanation of what “lineage” means for *An. arabiensis* specimens.

Please give results (also without table or figure) for each country separately.

Discussion
Discussion is very concise but deals with most major points of interest. We would just suggest to explain better the conclusion on possible introgression (the more plausible hypothesis) between taxa and to evaluate other possible explanations for the absence of fixed differences between species (e.g. absence for divergent selection, or evolutionary characherestic of mitogenomes).

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

We have read this submission. We believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.