

1 **Title: A cytochrome P450 allele confers pyrethroid resistance in a major African**  
2 **malaria vector reducing insecticide-treated nets' efficacy**

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21 **Short title:** A P450 allele is reducing bednet efficacy

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23

24 **Abstract**

25 Metabolic resistance to insecticides in mosquitoes threatens malaria control. Unless it is  
26 managed, recent gains in reducing malaria transmission could be lost. To improve monitoring  
27 and assess the impact of this resistance on control interventions, we elucidated the molecular  
28 basis of pyrethroid resistance in the major African vector, *Anopheles funestus* in southern  
29 Africa, showing that a single cytochrome P450 allele (*CYP6P9a*) is reducing bednet efficacy.  
30 Key resistance genes are detected Africa-wide, but vary geographically. Signatures of selection  
31 and adaptive evolutionary traits including structural polymorphisms and *cis*-regulatory  
32 transcription factor binding sites were detected with evidence of selection by insecticide-treated  
33 nets scale-up. A *cis*-regulatory polymorphism driving the over-expression of the major  
34 resistance gene *CYP6P9a* allowed us to design the first DNA-based diagnostic assay for P450-  
35 mediated pyrethroid resistance. Using this tool to detect and track the spread of resistance  
36 revealed that it is almost fixed in southern Africa but absent elsewhere. Furthermore,  
37 experimental hut studies demonstrated that *CYP6P9a*-Resistant mosquitoes survived and  
38 succeeded in blood-feeding significantly more than susceptible individuals, highlighting the  
39 urgent need to introduce new generations of insecticide-treated nets that are not reliant on  
40 pyrethroids.

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42 **One Sentence Summary:** First DNA marker for P450-mediated pyrethroid resistance in  
43 malaria vectors enables to show that metabolic resistance is reducing bednet's efficacy.

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## Introduction

48 Malaria prevention relies heavily on the use of insecticide-based vector control  
49 interventions, notably pyrethroid-based Long Lasting Insecticidal Nets (LLINs). These tools  
50 have been credited with more than 70% of the decrease in malaria mortality in the past 15 years,  
51 having helped avert more than 663 million clinical cases of malaria (1). However, resistance to  
52 insecticides, particularly pyrethroids, in malaria vectors threatens their continued effectiveness.  
53 Unless it is managed, the recent gains in reducing malaria transmission could be lost (2).  
54 Elucidating the genetic basis and evolution of resistance is crucial to design resistance  
55 management strategies and prevent malaria resurgence (2).

56 Without genetic information on insecticide resistance genes and associated molecular  
57 markers, it is difficult to track and anticipate the course of resistance or assess its impact on  
58 malaria transmission and on the effectiveness of control tools such as LLINs. The current  
59 inability to track metabolic resistance in this way in all major African malaria vectors including  
60 *Anopheles gambiae* and *Anopheles funestus* is a major obstacle to the design of rational,  
61 evidence-based resistance management strategies. Of the four classes of insecticides used in  
62 public health, pyrethroids are by far the most widely used and the main class recommended for  
63 use in insecticide-treated nets. Therefore, understanding the mechanisms conferring pyrethroid  
64 resistance in mosquitoes is of critical importance.

65 Two major causes of insecticide resistance are metabolic resistance and target-site  
66 insensitivity (3). Unlike target-site resistance (e.g. knockdown resistance: *kdr*), metabolic  
67 resistance remains less characterized despite posing a greater risk to control interventions (4).  
68 Although candidate resistance genes have been detected (5-8), it has proved difficult to dissect  
69 the molecular bases of metabolic resistance and detect associated molecular markers, because  
70 of the size of detoxification gene families, redundancy among their members and the multiple  
71 mechanisms through which metabolic resistance can arise (9). Cytochrome P450

72 monooxygenases have consistently been associated with pyrethroid resistance but, unlike *kdr*,  
73 no DNA-based marker has yet been detected to track P450-mediated resistance and assess its  
74 impact on malaria control tools.

75 Here, we elucidated the complex molecular basis and genomic evolution of metabolic  
76 resistance to pyrethroids in the major African malaria vector *An. funestus*. We detected key  
77 DNA-based markers to design a field-applicable diagnostic assay to track this resistance and  
78 used it to demonstrate that this metabolic resistance reduces the efficacy of insecticide-treated  
79 nets.

80

## 81 Results

### 82 RNAseq transcriptional profiling of mosquitoes from across Africa identifies 83 candidate pyrethroid-resistance associated genes

84 To identify genes associated with pyrethroid resistance in *Anopheles funestus* Africa-  
85 wide, we performed RNAseq-based transcriptional profiling of mosquitoes from four different  
86 African regions: southern (Malawi), East (Uganda), West (Ghana) and Central (Cameroon), in  
87 comparison to a laboratory colony (FANG) that is fully susceptible to all insecticides.  
88 Pronounced differences in the expression of key candidate genes were observed between the  
89 four regions (Fig. 1A-C, Fig. S1A-E, Table S1).

90 Cytochrome P450s were frequently significantly over-expressed (adjusted p value  
91 <0.05)(Text S1), with *CYP6P9a* (AFUN015792; 60.5x) and *CYP6P9b* (AFUN015889; 23.9x)  
92 showing extreme over-expression in Malawi compared to other regions (<7x) (Fig 1B-C). Other  
93 P450s were more over-expressed in one region than in others (Figure 1B-C) including *CYP9K1*  
94 (AFUN007549) which was highly over-expressed in Uganda (5.2x) and moderately so in  
95 Ghana (2.9x), but not in Malawi or Cameroon. *CYP6P5* (AFUN015888) was significantly over-  
96 expressed in Ghana (6.3x), Cameroon (5.8x) and Uganda (4.1x) but not in Malawi. The

97 duplicated *CYP6P4a* and *CYP6P4b* are highly over-expressed in Ghana (44.8x and 23.9x  
98 respectively), moderately so in Malawi and Uganda (<6x) and not in Cameroon. *CYP325A* is  
99 highly over-expressed in Cameroon (26.9x) but less so in other regions (<6x). Other P450s are  
100 moderately over-expressed, including two paralogous *CYP9J11* genes and *CYP6N1*, up-  
101 regulated in southern and West Africa, whereas *CYP315A1* is over-expressed in all sites but  
102 Malawi. Other detoxification-associated gene families are also over-expressed (Text S1)  
103 including a cluster of glutathione S-transferase epsilon genes (*GSTe1*, *GSTe3*, *GSTe5* and  
104 *GSTe2*, a known DDT resistance gene (*I0*)) up-regulated in all regions except East Africa (Text  
105 S1). Analysis of Gene Ontology enrichment (Fig. S2A-C) further confirmed these regional  
106 differences.

107 Quantitative RT-PCR with fifteen genes confirmed these regional differences, with a  
108 high and significant correlation observed between qRT-PCR and RNAseq results for the 4  
109 countries when compared to FANG ( $R^2=0.695$ ;  $P<0.001$ ) (Fig. 1E; Fig S3A to C; Text S1).

110 Overall, gene expression analyses underlined the importance of P450 monooxygenases  
111 in pyrethroid resistance and identified heterogeneities in gene expression among populations  
112 from different geographical regions. Notably, the most extreme differences in expression  
113 profiles among samples were observed in members of a cluster of CYP6 genes in the *rp1*  
114 pyrethroid resistance Quantitative Trait Locus (QTL): the southern African mosquitoes showed  
115 massive over-expression of *CYP6P9a* and *CYP6P9b*, while West African mosquitoes from  
116 Ghana showed over-expression of *CYP6P5* and *CYP6P4a/b*. These differences suggest that the  
117 molecular bases of pyrethroid resistance may vary across Africa, possibly due to a combination  
118 of variation in selective pressures and restricted gene flow among regions (11, 12).

119

120 **Whole genome polymorphism analysis of field collected mosquitoes identifies**  
121 **selective sweeps associated with insecticide resistance loci**

122 Because metabolic resistance could be conferred by point mutations in coding and  
123 *cis/trans* regulatory regions, we scanned the whole genome for pyrethroid resistance-related  
124 signatures of selective sweeps in the highly pyrethroid resistant population from Malawi, to  
125 detect resistance loci. We performed pooled-template whole genome sequencing on field-  
126 collected population samples from southern Africa where high levels degree of expression of  
127 *CYP6P9a* and *CYP6P9b* have been observed. We also comparatively assessed the genomes and  
128 compared these to samples of the laboratory resistant FUMOZ-R and the susceptible FANG  
129 strains. We detected contrasting patterns of polymorphism between these strains and also  
130 between pre- (MWI-2002) and post-bednet intervention (MWI-2014) samples from Malawi  
131 (Fig. 2A; Table S3). The major selective sweep for both Malawi and FUMOZ-R was on scaffold  
132 KB119169 spanning the *rp1* pyrethroid resistance region on chromosome arm 2R (Fig. 2B).  
133 Plotting minor allele frequencies across the region revealed a valley of reduced genetic diversity  
134 around the cluster of P450s on the *rp1* pyrethroid resistance QTL correlating a selected *rp1*  
135 haplotype with *CYP6P9a* over-expression (Fig. 1D). This selective sweep appears to be at or  
136 near fixation in a contemporary Malawian population (as well as in FUMOZ-R) with little  
137 diversity observed around the P450 cluster in this highly pyrethroid resistant population (Fig.  
138 2B). No reduced diversity was observed in the susceptible FANG strain, suggesting an  
139 association between this selective sweep and pyrethroid resistance in line with the very low  
140 *CYP6P9a* expression in FANG (Fig. 2A-B). These results are consistent with previous reports  
141 of selection on highly over-expressed resistance genes (8).

#### 142 **Complex evolution of the gene cluster of the *rp1* CYP6 genes associated with** 143 **pyrethroid resistance**

144 As *rp1* was consistently associated with pyrethroid resistance, a fine-scale analysis of  
145 this locus (120kb) was performed, revealing evidence of complex molecular evolution likely  
146 under insecticide-driven selection.

147 Inspection of pooled-template whole genome alignments showed two anomalous  
148 features in the 8.2kb sequence between *CYP6P9a* and *CYP6P9b*. In some samples, the coverage  
149 depth was greater than for the surrounding sequence and some samples showed read pairs in  
150 the correct relative orientation but with greater than expected insert sizes. This is indicative of  
151 a large indel: a “deletion” in the sequenced genome(s) or an “insertion” in the reference genome  
152 (Fig. S4A). This insertion corresponds to 6545 bp and appears fixed in the FUMOZ colony  
153 sample with evidences that the inserted sequence is homologous to another region nearby (on  
154 the same assembly scaffold) in the genome (Fig. S4B). In contrast, the FANG susceptible strain  
155 shows evidence of the “deletion” form of the indel (Fig. S4A). This insertion, nearly fixed  
156 across southern Africa (26/27), is absent elsewhere in the continent where only a 1.7kb  
157 intergenic region is observed after PCR (Table S4). RNAseq data showed that the inserted  
158 region is a transcribed region, showing evidence of splicing and containing three micro-RNAs,  
159 but no P450s.

160 We assessed the composition of this 6.5kb insert to elucidate its role by sequencing the  
161 full 8.2kb *CYP6P9a/b* intergenic region and analysing it using GPminer (13). This insert  
162 contains abundant binding sites for transcription factors including a CpG island (1.3kb), several  
163 GATA, TATA (35), CCAAT (12) and GC (11) boxes and over-represented oligonucleotides.  
164 It also contains several binding sites for key transcription factors associated with xenobiotic  
165 detoxification, including Cap-n-Collar-C (CnCC) (51 sites) and Muscle aponeurosis  
166 fibromatosis (Maf), suggesting that this insertion may drive *CYP6P9a/b* over-expression. The  
167 insert also contains a microsatellite (FUNR) between 6082bp and 6482bp, only 80bp from the  
168 5' untranslated region (UTR) of *CYP6P9a*. Previous genotyping of this marker Africa-wide  
169 revealed marked differences associated with pyrethroid resistance profile (11). FUNR is not  
170 present within the 1.7kb intergenic region between *CYP6P9a* and *CYP6P9b* in the susceptible  
171 FANG strain. It has been shown that microsatellite loci are involved in upregulation of P450 to

172 confer insecticide resistance in other insects such as aphids (14). It has also been shown in Yeast  
173 that polymorphic tandem repeats in the promoter regions can activate gene expression by  
174 impacting local chromatin structure to act as “evolutionary tuning knobs” to drive rapid  
175 evolution of gene expression such in a case of insecticide resistance selection.

176 **Polymorphism of *CYP6P9a* regulatory region associated with pyrethroid**  
177 **resistance**

178 **Polymorphism of *CYP6P9a* 5' UTR and upstream region Africa-wide:** To detect  
179 *cis*-regulatory mutations controlling *CYP6P9a/b*-based pyrethroid resistance, we compared  
180 800bp immediately upstream of *CYP6P9a* Africa-wide. Several locations exhibited a very low  
181 or no polymorphism (Fig. S5A). The sample with the highest diversity was the fully susceptible  
182 FANG with the highest diversity indexes supporting the selection acting on this gene in field  
183 resistant populations. Despite low diversity observed in different regions, southern Africa  
184 populations consistently exhibited a different polymorphism pattern to other regions including  
185 the presence of an AA insertion 8bp upstream of a putative CCAAT box present only in  
186 southern African samples through an A/C substitution. The AA insertion located 359 bp from  
187 start codon is tightly associated with other polymorphisms in a haplotype (STH10) which is  
188 nearly fixed in southern Africa (63/68) reflecting the marked selective sweep observed around  
189 this gene in this region. Analysis of the phylogenetic tree revealed four clusters of haplotypes  
190 from different regions notably southern Africa (Malawi, Mozambique and Zambia plus  
191 FUMOS-R), East-Central (Kenya, Uganda and Cameroon), West (Ghana) and West-Central  
192 (Benin and Congo) (Fig. 3A). The FANG susceptible strain forms its own cluster divergent  
193 from the others.

194 Closer analysis of the haplotypes using a haplotype network confirmed the presence of  
195 4 major haplotypes corresponding to these geographical clusters, STH10 in southern,  
196 EST/CNT24 in East-Central, BEN/DRC21 in West-Central and GHA11 in Ghana only (West)



197 (Fig. 3B). Surprisingly, the other 3 regions also exhibit predominant haplotype in the  
198 populations to near fixation contrary to previous data where they were more polymorphic (11).  
199 This result suggests that resistance to pyrethroid beyond southern Africa could have also been  
200 selected through *CYP6P9a* or other genes in the vicinity on the *rp1* QTL regions. The  
201 hypothesis of a possible hitchhiking effect here rather than the direct involvement of *CYP6P9a*  
202 is supported by the important differences observed between the four major haplotypes with  
203 more than 20 mutational steps of difference between them. Therefore, it is very likely that  
204 resistance conferred by the *rp1* locus occurred through independent selective events with likely  
205 different genes. This is supported by RNAseq data showing that although *rp1* genes are over-  
206 expressed Africa-wide the main genes are different with *CYP6P4a* predominant in Ghana but  
207 not in others, *CYP6P5* in Cameroon and Uganda whereas *CYP6P9a* is the major gene in  
208 southern Africa. The neighbor-joining phylogenetic tree of the *Nst* genetic distances between  
209 different countries (Fig. 3C) correlated with the polymorphism patterns showing countries  
210 clustering according to the haplotypes diversity pattern from ML tree or the TCS network.

211 **Scaled-up use of insecticide-treated nets has selected for changes in the regulatory**  
212 **region of *CYP6P9a*:** To assess whether the differences observed in the 5'UTR and upstream  
213 region of *CYP6P9a* between southern Africa and other regions was a result of selective pressure  
214 from insecticides, we compared samples from southern Africa before the scale-up of  
215 insecticide-based interventions such as LLINs and samples after scale-up. 39 clones of the  
216 800bp fragment upstream of *CYP6P9a* were obtained and sequenced from 'pre-intervention'  
217 mosquitoes from Mozambique and Malawi and 52 from 'post-intervention' samples of both  
218 countries. Strikingly this portion was highly polymorphic pre-intervention with many  
219 segregating sites (61 and 25 in Malawi and Mozambique, respectively) and haplotypes (19 and  
220 12, a total of 30 for both) and high nucleotide diversity ( $\pi=0.027$  and 0.012) (Table S5; Fig.  
221 S5B). By contrast, the post-intervention samples exhibited very low diversity as revealed by all

222 indexes with S of 4 and 3, haplotypes number of 2 and 4 with extremely low nucleotide diversity  
223 ( $\pi=0.00066$  and  $0.0008$ ), respectively in Malawi and Mozambique. The difference is reflected  
224 on the Maximum Likelihood (ML) phylogenetic tree showing that mosquito samples of pre-  
225 intervention not only cluster together but are more diverse with several haplotypes (Fig. 4A).  
226 In contrast the post-intervention samples cluster noticeably away from the pre-intervention with  
227 drastically reduced haplotype number. A haplotype network confirmed that the major haplotype  
228 associated with resistance and now nearly fixed in all southern African populations was present  
229 also in the pre-intervention sample but at a much lower frequency of only 4/39 (19.23%)  
230 contrary to 44/52 (84.6%) in post intervention with other post haplotypes only 1 or 2 mutational  
231 steps away from the predominant one (Fig. 4B). The pre-intervention haplotypes were  
232 polymorphic and separated with high mutational steps whereas the post-intervention samples  
233 showed a marked reduced diversity (Fig. 4B). A detailed analysis of the polymorphisms  
234 between pre- and post-intervention samples, revealed that the AA insertion now common in  
235 southern populations as well as the CCAAT box was also present in pre-intervention samples  
236 but only at a very low frequency (7/24 in Malawi and 0/15 in Mozambique) whereas both AA  
237 and CCAAT box are now fixed in all the post-intervention samples (52/52). Furthermore, a  
238 second Nrf2:MafK binding site is found only in post-intervention samples and linked with both  
239 the AA insertion and the CCAAT box. These major modifications show that scale up of  
240 insecticide-treated nets is very likely the major factor that has driven this evolution in *An.*  
241 *funestus* populations in southern Africa.

#### 242 **Detection of a molecular marker associated with pyrethroid resistance gene over-** 243 **expression**

244 Having confirmed that genomic changes upstream of *CYP6P9a* are associated with  
245 pyrethroid resistance, we next searched for the mutations responsible for the over-expression  
246 of *CYP6P9a* in resistant mosquitoes. We used luciferase assay to assess the role of

247 polymorphisms found in the 800bp upstream of the translation start site (including the 5' UTR).  
248 The 800bp upstream of the *CYP6P9a* translation start site in both FUMOZ and FANG was  
249 successfully cloned and sequenced. To narrow down the region containing the regulatory  
250 motifs, four different sized fragments of the 800, 500, 300 and 150 bp immediately upstream  
251 of the translation start codon were cloned upstream of a reporter gene in a pGL3 vector. These  
252 constructs were used in luciferase reporter gene assays that demonstrated that, while 800 bp  
253 inserts from both strains drove reporter gene expression, expression driven by the FUMOZ  
254 insert was 3 times higher than that from FANG (Fig. S6A), supporting that this region plays a  
255 role in the differential expression of *CYP6P9a* between resistant and susceptible mosquitoes.  
256 Progressive deletion of the 800-bp pGL3-FZ-CYP6P9a was performed to identify the major  
257 regulatory elements. The first deletion from 800 to 500bp did not impact the activity of the  
258 fragment. However, when the fragment was cut from 500 to 300bp removing the AA insert and  
259 the CCAAT box, it induced a 33% reduction of activity in the FUMOZ clone ( $P < 0.001$ ) (Fig.  
260 5A). Subsequent deletion from 300 to 150bp, removing the AA insert, the CCAAT box and the  
261 resistant specific CnCC/MafK binding site, led to a massive 89% reduction in activity  
262 ( $P < 0.001$ ). This shows that both the CCAAT box and the CnCC/MafK binding sites are key  
263 regulatory enhancer elements driving the over-expression of *CYP6P9a*.

#### 264 **Design of a DNA-based diagnostic assay to detect *CYP6P9a*-mediated pyrethroid** 265 **resistance**

266 To design a DNA-based diagnostic assay to detect *CYP6P9a*-mediated resistance, we  
267 screened the most active portion (500bp) for the presence of restriction site polymorphisms that  
268 could be used to design a simple PCR-RFLP. We found a restriction site for the TaqI enzyme  
269 (cut site 5'-TCGA-3') spanning an A/G mutation located 18bp of the AA insertion (Fig. S6B)  
270 and completely tight with the CCAAT box and other regulatory elements on the resistance  
271 haplotype. The TaqI enzyme cuts the 450bp fragment from the 'resistant' haplotype into two

272 fragments of 350bp and 100bp whereas ‘susceptible’ haplotypes remain uncut (Fig. 5B)  
273 allowing us to genotype the resistance allele in single mosquitoes. To validate the robustness  
274 of this PCR-RFLP to detect pyrethroid resistance, we used F<sub>8</sub> progeny from a cross between  
275 highly resistant (FUMOZ) and highly susceptible (FANG) strains. The genotyping of 46  
276 mosquitoes highly resistant (alive after 180 minutes’ exposure) to permethrin (15) revealed 9  
277 RR, 35 RS and only 2 SS genotypes. By contrast, 42 highly susceptible mosquitoes (dead after  
278 30 minutes’ permethrin exposure) had 0 RR, 1 RS and 41 SS genotypes. Therefore, the odds  
279 ratio of the likelihood of surviving exposure to permethrin when homozygote for the resistant  
280 allele (RR) of the *CYP6P9a* gene (with the CCAAT box and CnCC/MafK binding sites) is  
281 highly elevated at 922 (P<0.0001) compared to the homozygous susceptible (SS) (Fig. 5C)  
282 demonstrating the reliability of this DNA-based metabolic resistance diagnostic assay.

283 **Geographical distribution of the resistant *CYP6P9a* allele across Africa:**  
284 Genotyping the *CYP6P9a*\_R allele across Africa revealed that it is nearly fixed in southern  
285 Africa and present at an intermediate frequency in Tanzania (East Africa) (55.7%). However,  
286 *CYP6P9a*\_R is absent from Central/West Africa (Fig. 5D; Fig. S6C). In DR Congo, a  
287 geographical contrast was observed, with the *CYP6P9a*\_R mutation present in the East of the  
288 country but absent from the West (Kinshasa). This pattern suggests a ‘new’ allele/haplotype  
289 that arose in southern Africa and is spreading northward. Regional differences in *CYP6P9a*\_R  
290 distribution are like those reported for previous markers (6, 10).

#### 291 ***CYP6P9a*\_R reduces the effectiveness of insecticide-treated nets**

292 We next assessed the impact of *CYP6P9a*-based metabolic resistance on the  
293 effectiveness of LLINs using experimental hut trials. Mosquitoes from FANG/FUMOZ crosses  
294 (F<sub>4</sub>) were used after confirming their pyrethroid resistance status (Fig. S7A) and established  
295 that resistance was driven additively by *CYP6P9a* [OR = 693 and 131 respectively for RR vs  
296 SS and RR vs RS (P<0.001)] (Fig. 6A; Fig. S7B-D).

297           **Impact of *CYP6P9a*-mediated metabolic resistance on bed net efficacy using**  
298 **experimental huts:** Females from the F<sub>4</sub> generation of the FANG/FUMOZ strain were used in  
299 a release-recapture experiment in huts with PermaNet 2.0 (treated with deltamethrin),  
300 PermaNet 3.0 (deltamethrin plus PBO) and control nets (untreated). After 4 consecutive nights  
301 of release-recapture, analysis of the mosquitoes collected showed no significant induced  
302 exophily for both PermaNet 2.0 and PermaNet 3.0 compared to the control (P>0.05) (Table 1).  
303 The percentage of blood-fed females was significantly lower in both treated nets than in the  
304 untreated control, with PermaNet 3.0 showing a significantly lower number of blood-fed  
305 mosquitoes than PermaNet 2.0 (P<0.001) (Fig. 6B). This is reflected in the percentage of blood  
306 feeding inhibition which is significantly higher (P<0.0001) for PermaNet 3.0 (76.8%) than for  
307 PermaNet 2.0 (49.8%). Both treated nets provided greater personal protection than the untreated  
308 nets with, again, higher protection from PermaNet 3.0 (79.04%) than PermaNet 2.0 (61.9%)  
309 (Table 1). Analysis of mortality rates revealed very high mortality of the hybrid  
310 FANG/FUMOZ strain against PermaNet 3.0 (98.7%) compared to only 33.3% for PermaNet  
311 2.0 (P<0.001) (Fig. 6B). Very low mortality was observed in the control untreated net.  
312 Mosquitoes that had taken a blood meal through the nets also present a high mortality rate for  
313 PermaNet 3.0 (95.5%) but only a low rate for PermaNet 2.0 (40%).

314           **Assessing the role of *CYP6P9a* in the loss of efficacy of PermaNet 2.0:** Genotyping  
315 of the *CYP6P9a* maker allowed us to assess the impact of P450-based metabolic resistance on  
316 the loss of efficacy of PermaNet 2.0. Because most of the mosquitoes released in the PermaNet  
317 3.0 huts died, the impact of the *CYP6P9a* on the ability to survive exposure to LLIN was done  
318 only for PermaNet 2.0. To avoid confounding effects from blood feeding or net entry or  
319 exophily status, the distribution of the *CYP6P9a* genotypes was assessed first only among unfed  
320 mosquitoes collected in the room revealing a highly significant difference in the frequency of  
321 the three genotypes between the dead and alive mosquitoes (Chi<sup>2</sup>=375; P<0.0001) (Fig. 6B).

322 Analysis of the correlation between each genotype and mortality revealed that *CYP6P9a*  
323 homozygous resistant mosquitoes (RR) were significantly more able to survive exposure to the  
324 PermaNet 2.0 than homozygous susceptible mosquitoes (odds ratio=34.9; CI=15.8-77.1;  
325  $P<0.0001$ ) (Table S6). Similarly, possessing the heterozygous (RS) genotype of *CYP6P9a* also  
326 confers a significant survival advantage than for the homozygous SS genotype (OR=19.9;  
327 CI=9.7-40.9;  $P<0.0001$ ). Although a higher frequency of RR is observed in the alive  
328 mosquitoes than for the RS genotype, this difference was not significant (OR=1.75; CI=0.82-  
329 3.7;  $P=0.26$ ). Overall, a single *CYP6P9a* resistant allele (R) significantly confers the ability to  
330 survive than the susceptible allele (OR=6.25; CI=3.3-11.7;  $P<0.0001$ ) (Fig. 6C). The same  
331 trend was observed when comparing the mortality in all samples although with at a lower degree  
332 (Table S6). The impact of the *CYP6P9a* resistance gene on the ability to blood feed was also  
333 assessed, revealing that the distribution of the three genotypes was significantly different  
334 between blood fed and unfed mosquitoes for both PermaNet 2.0 ( $\text{Chi}^2=16.9$ ;  $P<0.0001$ ) and  
335 PermaNet 3.0 ( $\text{Chi}^2=30.5$ ;  $P<0.0001$ ). Homozygous RR mosquitoes were significantly more  
336 likely to blood feed when exposed to PermaNet 3.0 than both susceptible SS (OR= 4.54;  
337  $P<0.0001$ ) and heterozygote RS individuals (OR= 2.6;  $P=0.0012$ ) (Fig. 6C). A similar trend  
338 was observed for PermaNet 2.0, although not significant (Fig. S7E-F). This shows that despite  
339 the higher efficacy of PermaNet 3.0 compared to PermaNet 2.0, *CYP6P9a\_R* could still  
340 increase the risk of malaria transmission.

341

## 342 **Discussion**

343 This study presents a comprehensive elucidation of the molecular genetic basis of  
344 metabolic resistance to pyrethroids in a major malaria vector detecting the first DNA-based  
345 resistance marker for P450-mediated metabolic resistance. A major outcome was the design of  
346 a field applicable diagnostic assay to detect and track the spread of this resistance across Africa

347 and enabled us to establish the direct impact of metabolic resistance to pyrethroids on the  
348 efficacy of insecticide-treated nets in experimental huts.

349 Overall, gene expression analyses underlined the importance of cytochrome P450  
350 monooxygenases in pyrethroid resistance as previously reported in other *An. funestus*  
351 populations (8, 15) and in other mosquito species (16-18). Important heterogeneities in gene  
352 expression were observed among populations from different geographical regions. Most  
353 notably, a cluster of CYP6 genes in the *rp1* pyrethroid resistance QTL showed the most extreme  
354 differences in expression profiles among locations. Such differences show that the molecular  
355 basis of pyrethroid resistance varies across the continent as previously suggested for this species  
356 (19) and for other malaria vectors such as *An. gambiae* (7, 20).

357 The association of the *rp1* QTL locus with pyrethroid resistance is further supported by  
358 the detection of several adaptive evolutionary features across this locus, including i) signatures  
359 of selective sweep; ii) large structural variation with 6.5kb insert; and iii) *cis*-regulatory  
360 polymorphisms. The selective sweep detected around this region in southern Africa coincides  
361 with the high expression of the duplicated P450s *CYP6P9a* and *CYP6P9b* in Malawi supporting  
362 the key role in pyrethroid resistance of these genes previously shown to be efficient pyrethroid  
363 metabolizers (8). Selective sweeps associated with insecticide resistance have been reported  
364 recently in *An. gambiae* across Africa (21).

365 The *cis*-regulatory changes detected here include binding sites for transcription factors  
366 such as CnCC/MAfK which has recently been shown to be involved in metabolic resistance in  
367 *An. gambiae* (22) and in other insects (23), supporting that *cis*-regulatory modifications are  
368 important drivers of metabolic resistance to insecticides. However, because *cis*-regulatory  
369 elements/enhancers are able to drive expression of genes from distant acting locations and can  
370 be upstream or downstream of the gene on which they function, future studies will help  
371 establish the role of the 6.5kb insert in the over-expression of *CYP6P9a* and *CYP6P9b*. The

372 strong association of these regulatory variations with pyrethroid resistance provided an  
373 excellent opportunity to design a DNA-based diagnostic tool for metabolic resistance. This is  
374 the first diagnostic assay for P450-mediated resistance in malaria vectors which constitutes a  
375 major achievement in the field of resistance monitoring and surveillance. Indeed, while the first  
376 DNA-based diagnostic for target-site resistance (*kdr*) was established two decades ago (24), no  
377 such tool has been designed for metabolic resistance despite its greater risk to control  
378 interventions. Although sets of SNPs associated with pyrethroid resistance have been recently  
379 detected in the dengue vector *Aedes aegypti*, no causative markers were detected (25). Previous  
380 design of a DNA-based diagnostic tool were for a glutathione S-transferase gene (*GSTe2*) in  
381 *An. funestus* conferring pyrethroid/DDT resistance in West/Central Africa but using an amino  
382 acid change in the coding region of the gene, not the putative causative variant for over-  
383 expression as done here for *CYP6P9a* (10). However, because this DNA-based assay mainly  
384 detects resistance in southern Africa and only applies to *An. funestus*, further efforts are needed  
385 to detect similar markers in other regions and other species to comprehensively track P450-  
386 mediated metabolic resistance Africa-wide.

387 Strikingly, the *CYP6P9a\_R* allele is present mainly in southern Africa, where it is nearly  
388 fixed, but completely absent from other regions. Such contrast between African populations of  
389 *An. funestus* has previously been observed, notably for the distribution of other resistance  
390 markers such as the *L119F-GSTe2* (10) and the *A296S-RDL* conferring dieldrin resistance (26),  
391 which are present in West/Central and East Africa but completely absent from southern Africa.  
392 On the other hand, the *N485I-ace-1* carbamate resistance allele is present only in southern  
393 Africa (6). Furthermore, patterns of *F<sub>ST</sub>*-based genetic differentiation indicate a restriction of  
394 gene flow and high genetic divergence between southern Africa and other regions (11, 12).  
395 However, there seems to be a gradual increase of *CYP6P9a\_R* frequency from south to north  
396 in southern Africa as seen in Malawi with 98% in the south (Chikwawa), 90% in the Centre



397 (Salima) and 78 % in the north (Fulirwa). This correlates with previous observations that  
398 *CYP6P9a* over-expression was lower in the north and that the spread of this resistance likely  
399 originated from the far south and is spreading northwards across the species' range (27). It will  
400 be important to monitor the spread of such alleles across the continent as there is the risk that  
401 super-resistant mosquitoes could be generated if, for instance, *CYP6P9a*-mediated pyrethroid  
402 resistance combines with the *GSTe2*-based DDT resistance seen in West/Central Africa. DR  
403 Congo will be particularly important to monitor as both resistance mechanisms are present in  
404 this country (28).

405         Using the novel *CYP6P9a*\_R assay, we successfully assessed for the first time the direct  
406 impact of metabolic resistance on the efficacy of insecticide-treated nets showing that P450-  
407 mediated resistance was directly reducing the efficacy of insecticide-treated nets. This evidence  
408 further helps clarify the debate about whether pyrethroid resistance is directly impacting the  
409 efficacy of insecticide-treated nets (29) as it clearly highlights that pyrethroid resistance could  
410 jeopardize insecticide-based interventions. Interestingly, nets containing the insecticide  
411 synergist PBO, that inhibits the activity of cytochrome P450 enzymes, provided better efficacy  
412 than those with pyrethroid alone. However, despite the high mortality observed with the PBO-  
413 based net, *CYP6P9*\_R still increases the risk of malaria transmission with this net as resistant  
414 mosquitoes are still more likely than susceptible mosquitoes to bite and potentially transmit  
415 malaria, suggesting that malaria elimination efforts will be impeded unless the over-reliance on  
416 pyrethroids is addressed.

## 417         **Methods**

### 418         **Study design**

419         The objective of this study was to detect key genetic variants conferring metabolic-mediated  
420 pyrethroid resistance in *An. funestus* and design a simple DNA-based assay to monitor such  
421 resistance in field populations and assess its impact on the effectiveness of insecticide-based

422 control tools. Transcriptome profiling of *An. funestus* populations from four African regions  
423 [southern (Malawi), East (Uganda), West (Ghana), Central (Cameroon)] were analysed to  
424 detect key candidate resistance genes. Because metabolic resistance could also be conferred by  
425 point mutations in coding and *cis/trans* regulatory regions, we performed a comparative whole  
426 genome sequencing of field permethrin resistant and susceptible mosquitoes to screen for  
427 genomic resistance regions and polymorphisms. To comprehensively detect resistance loci, we  
428 also scanned the whole genome for pyrethroid resistance-related signatures of selective sweeps  
429 in southern Africa. As *rp1* QTL was consistently associated with pyrethroid resistance, a fine-  
430 scale analysis of this locus was performed to detect potential structural variants associated with  
431 resistance such as Indels and copy number variations. To detect *cis*-regulatory mutations  
432 controlling *CYP6P9a/b*-based pyrethroid resistance, we compared 800bp immediately  
433 upstream of *CYP6P9a* in resistant and susceptible mosquitoes. The role of insecticide-based  
434 interventions in the selection of this *CYP6P9a* *cis*-regulatory changes was assessed by  
435 sequencing mosquitoes collected before and after widespread insecticide-treated nets usage. To  
436 establish the specific mutations controlling *CYP6P9a* over-expression, a comparative luciferase  
437 assay between resistant and susceptible *CYP6P9a* promoter sequences was performed. To  
438 design a DNA-based diagnostic assay to detect *CYP6P9a*-mediated resistance, we screened the  
439 promoter for restriction sites to design a PCR-RFLP assay and use it to assess its distribution  
440 continent-wide. We next assessed the impact of *CYP6P9a*-based metabolic resistance on the  
441 effectiveness of LLINs using experimental hut trials.

#### 442 **Collection and rearing of mosquitoes**

443 Two *An. funestus* laboratory colonies were utilised in the study. The FANG colony is  
444 a fully insecticide susceptible colony derived from Angola (30). The FUMOZ colony is a multi-  
445 insecticide resistant colony derived from southern Mozambique. Mosquitoes were collected  
446 from 4 primary locations across the continental range of *An. funestus*. Mosquitoes were

447 collected in March 2014 from Obuasi (5°56' N, 1°37' W) in Ghana (31); in February 2015 from  
448 Mibellon (6°46' N, 11°70' E) in Cameroon; in March 2014 from Tororo (0°45' N, 34°5' E) in  
449 Uganda (32) and in January 2014 from Chikwawa (16°1' S, 34°47' E) in southern Malawi (33).

450 Collected mosquitoes were kept until fully gravid and forced to lay eggs using the  
451 forced-egg laying method (34). All F<sub>0</sub> females that laid eggs were morphologically identified  
452 as belonging to the *An. funestus* group according to a morphological key (35). Parents (F<sub>0</sub>) and  
453 egg batches were transported to the Liverpool School of Tropical Medicine under a DEFRA  
454 license (PATH/125/2012). Eggs were allowed to hatch in cups and mosquitoes reared to  
455 adulthood in the insectaries under conditions described previously (34). Insecticide resistance  
456 bioassays on these samples have been previously described (31-33).

#### 457 **Transcription profiling of pyrethroid resistance using RNAseq**

458 Total RNA was extracted from pools of 10 female mosquitoes (alive after 1h permethrin  
459 exposure) using the Arcturus PicoPure RNA isolation kit (Life Technologies), according to the  
460 manufacturer's instructions (Text S1). Pools of libraries were sequenced, 8 per lane of the  
461 HiSeq 2500 (Illumina, San Diego, CA, USA) at 2x125 bp paired-end sequencing. Sequence  
462 library preparation and sequencing were done at the Centre for Genomic Research (CGR),  
463 University of Liverpool. RNAseq data were analysed as described previously (36) (Text S1).  
464 This involved an initial processing, quality assessment of sequences and alignment to the  
465 reference sequence using the AfunF1.4 annotation. Differential gene expression analysis was  
466 performed using edgeR and StrandNGS program (Strand Life Sciences, version 3.0) (Text S1).

#### 467 **Whole genome sequencing**

468 Genomic DNA was extracted from whole mosquitoes from F<sub>0</sub> Malawi samples (2014),  
469 the pyrethroid resistant FUMOS-R laboratory strain and the fully susceptible FANG strain  
470 using the DNAeasy kit (Qiagen, Hilden, Germany). For each sample, genomic DNA was  
471 extracted from individuals and pooled in equal amounts to form pools of DNA. These were

472 sequenced on an Illumina HiSeq2500 (2x150bp paired-end). Initial processing and quality  
473 assessment of the sequence data was performed as for RNAseq data. Alignment of POOLseq  
474 R1/R2 read pairs and R0 reads to the reference sequence (the same as used for RNAseq  
475 alignment) as well as variant calling were performed as described previously (11).

#### 476 **Polymorphism analysis of the promoter region of *CYP6P9a***

477 To detect potential causative mutations conferring pyrethroid resistance in *An. funestus*,  
478 the polymorphism of the cis-regulatory region of the pyrethroid resistance gene *CYP6P9a* was  
479 analyzed.

480 **i-Detection of the causative mutations driving up-regulation of *CYP6P9a*:** An 800  
481 bp region upstream of the start codon of *CYP6P9a* was amplified and directly sequenced in 15  
482 field collected mosquitoes each from ten countries across different regions of Africa including  
483 southern (Mozambique, Malawi and Zambia), East (Uganda, Kenya and Tanzania), Central  
484 (DR Congo and Cameroon) and West (Benin and Ghana). Primers are listed in Table S7.  
485 Amplification and purification of PCR products was performed as previously described (11).  
486 Sequences were aligned using ClustalW (37) while haplotype reconstruction and polymorphism  
487 analysis were done using DnaSPv5.10 (38), MEGA (39) and TCS (40).

#### 488 **ii) Investigation of the content of the *CYP6P9a* and *CYP6P9b* intergenic region:**

489 The entire 8.2kb intergenic region between both genes was amplified for the FUMOZ and  
490 FANG strains in 2 to 3 fragments using primers listed in Supplementary Table 22. PCR was  
491 performed using the Phusion polymerase following the manufacturer's instructions. PCR  
492 products were purified and cloned into pJET1.2 plasmid.

493 **iii) Assessing the role of the scale up of insecticide-based intervention in the**  
494 **changes observed in the polymorphism of the promoter region of *CYP6P9a*:** The same  
495 800bp region upstream of the *CYP6P9a* was amplified in mosquitoes collected before (pre-  
496 intervention) the scale up of insecticide-treated nets and also after the scale up (post-

497 intervention) in Malawi (2002 and 2014) and Mozambique (2000 and 2016). The PCR products  
498 were cloned and sequenced and sequencing data analyzed as described above.

#### 499 **Genotyping of the *CYP6P9a* resistance allele using PCR-RFLP**

500 A restriction site (5'-TCGA-3') for the TaqI enzyme at the A/G mutation located 18bp  
501 of the AA insertion and completely tight with the CCAAT box on the resistance haplotype was  
502 used to design a PCR-RFLP assay to genotype the *CYP6P9a\_R* allele. The RFLP6P9aF forward  
503 primer, 5'- TCCCGAAATACAGCCTTTCAG-3 and RFLP6P9aR 5'-  
504 ATTGGTGCCATCGCTAGAAG-3' reverse primers were used to amplify a partial *CYP6P9a*  
505 upstream region containing the restriction site. 10µl of the digestion mix made of 1µl of  
506 CutSmart buffer, 0.2µl of 2 units of TaqI restriction enzyme enzyme (New England Biolabs,  
507 Ipswich, MA, USA), 5µl of PCR product and 3.8µl of dH<sub>2</sub>O was incubated at 65°C for 2 hours.  
508 Restriction digest was separated on 2.0% agarose gel (Fig. 3D).

509 **Validation of the diagnostic test:** To validate the robustness of the PCR-RFLP to  
510 detect the pyrethroid resistance in field population, F<sub>8</sub> progeny from a cross between highly  
511 resistant (FUMOZ) and highly susceptible (FANG) strains previously used for QTL mapping  
512 (15) were genotyped and correlation with resistance phenotype established using Odd Ratio.

513 **Geographical distribution of resistant *CYP6P9a* allele across Africa:** The  
514 geographical distribution of the resistant *CYP6P9a* allele across Africa was established by  
515 genotyping the *CYP6P9a\_R* in 30-50 field-collected females of *An. funestus* from several  
516 countries in Africa using the PCR-RFLP.

#### 517 **Luciferase reporter assay of *CYP6P9a* core promoter region**

518 The region immediately 5' of *CYP6P9a* from both FUMOZ and FANG strains was  
519 amplified using primers 6P9a1F and 6P9R a/b. These primers gave an 817bp product for both  
520 FUMOZ and FANG which were cloned into pJET1.2 (Thermo Fischer Scientific) and  
521 sequenced. Primers were designed (Supplementary Table 22) to obtain constructs of

522 progressive serial 5' deletions of the *CYP6P9a* promoter of 800bp, 500bp, 300bp and 150bp for  
523 the different primers. The primers incorporated either the SacI or MluI (for the FUMOZ) and  
524 KpnI or HindIII (for the FANG) to facilitate cloning in the pGL3 basic vector. Products were  
525 amplified with Phusion polymerase (Thermo Fischer Scientific) and cloned into pJET 1.2. The  
526 product was then excised from pJET1.2, ligated to pGL 3 basic (Promega) and sequenced.  
527 Plasmids were then extracted using Midiprep kit (Qiagen) to obtain high concentrations for the  
528 transfection. Dual luciferase assay was undertaken using *An. gambiae* cell line 4a-2 cell line  
529 (MRA-917 MR4, ATCC® Manassas Virginia). Approximately  $5 \times 10^5$  cells (600 $\mu$ l) was sub-  
530 cultured from a T75 culture and seeded in each well of 24-well plate, 1 day prior to transfection  
531 and allowed to reach 60-70% confluency.

532 Transfection of the construct was carried out using the Qiagen effectene transfection  
533 reagent and the promoter activity measured using the Dual Luciferase Reporter Assay  
534 (promega, Madison, WI, USA). 600ng reporter constructs (*CYP6P9a* upstream sequences in  
535 pGL3-Basic), pGL3 without insert and LRIM promoter in pGL3 basic were co-transfected with  
536 1ng actin-renilla internal control in 60ml DNA condensation buffer, 4.8 ml enhancer and 6 ml  
537 effectene in triplicate. After 48h incubation at 25°C, the cells were washed with PBS and  
538 harvested in 100ml passive lysis buffer (Promega) and luciferase activity was measured on a  
539 luminometer (EG & GBert-hold, Wildbad, Germany). Renilla luciferase activity was used to  
540 normalize the construct luciferase activity. The values obtained after measuring the firefly  
541 (LAR II) luciferase activity, which represent the activity of the promoter, was divided by the  
542 corresponding Renilla luciferase activity values and the ratio used to compare different  
543 promoters.

544 **Evaluation of impact of *CYP6P9a*-based metabolic resistance on efficacy of**  
545 **insecticide-treated nets using experimental huts**

546           **Study area and hut description:** The study was performed in Mibellon (6°4'60" N and  
547 11°30'0" E), a village in the Adamawa region of Cameroon where we recently built 12  
548 experimental huts of concrete bricks, following the specific design for experimental huts from  
549 the West Africa region (41).

550           **Mosquito strains:** The study was carried out with a hybrid strain generated from  
551 reciprocal crossing between the highly pyrethroid resistant strain FUMOZ-R (CYP6P9a\_R)  
552 and the fully susceptible FANG strain (CYP6P9a\_S) (42). After the initial F<sub>1</sub> generation  
553 obtained from the reciprocal crosses of 50 males and 50 females of both strains, the hybrid  
554 strain was reared to F<sub>5</sub> and F<sub>6</sub> generations, which were used for the release in the huts.

555           **Susceptibility profile of the hybrid FANG/FUMOZ strain:** WHO bioassays were  
556 carried out to assess the susceptibility profile of the two reciprocal hybrid strains for the  
557 pyrethroids (0.75% permethrin and 0.05% deltamethrin), DDT (4%) and the carbamate,  
558 bendiocarb (0.1%). The bioassays were performed according to WHO protocol (41).

559           **Study design:** The following three treatments were compared in the experimental huts:  
560 (i) Untreated polyethylene net; (ii) PermaNet 2.0® (Deltamethrin incorporated into  
561 polyethylene net); (iii) PermaNet 3.0® (PBO + Deltamethrin incorporated into polyethylene  
562 net). To simulate a worn net, six holes of 4cm x 4cm were made on each net, according to WHO  
563 guidelines. The hybrid FANG/FUMOZ strain was released in each hut for 6 nights (80  
564 mosquitoes per hut).

565           **Ethical clearance:** Three adult volunteers were recruited from the Mibellon village to  
566 sleep under the nets and collect mosquitoes in the morning. They were provided with a written  
567 consent form and given chemoprophylaxis during the trial. Ethical approval was obtained for  
568 the National Ethic Committee of the Ministry of the Health in Cameroon.

569           **Mosquito collection in huts:** Early in the morning, mosquitoes were collected using  
570 glass tubes from: i) the room (the floor, walls and roof of the hut); ii) inside the net; iii) the exit

571 traps (veranda). Each compartment had its own bag to avoid mixture between samples.  
572 Surviving mosquitoes were provided with sugar solution and held for 24 h in paper cups after  
573 which delayed mortality was also assessed. Samples were recorded in observation sheets as  
574 dead/blood fed, alive/blood fed, dead/unfed, and alive/unfed.

575 The effect of each treatment was expressed relative to the control (untreated net) by  
576 assessing: i) induced exophily (the proportion of mosquitoes that exit early through the exit  
577 traps, treatment-induced exiting); ii) the mortality rate, an indicator of the potential mass killing  
578 effect of the LNs; iii) the blood feeding rate, an indicator of personal protection.

579 **Genotyping of the *CYP6P9a* metabolic resistance marker:** To establish the impact  
580 of the *CYP6P9a*-mediated metabolic resistance to pyrethroids on the effectiveness of the  
581 insecticide-treated nets, the PCR-RFLP diagnostic assay was used to genotype a subset of each  
582 treatment including the dead, alive, blood feed, unfed, mosquitoes on the veranda, in the net  
583 and in the room.

584 **Statistical analysis:**

585 Genes differentially expressed in each country and between different countries  
586 (generated from Venn diagrams) were detected using DESeq normalization with fold change  
587 >2 and performing a multiple test correction using the method of Benjamini and Hochberg, at  
588 a false discovery rate of 5% (adjusted p value <0.05). Statistical significance of the Luciferase  
589 assays was assessed after an unpaired Student's t-test with respective replicates between  
590 FUMOZ and FANG. Correlation between the *CYP6P9a*\_R allele and pyrethroid resistance  
591 phenotype was established using Odd Ratio and Fisher's exact test. The effect of both treated  
592 nets was established through a direct comparison to the untreated control net. The statistical  
593 significance of the difference was estimated by a logistic regression model using Wald statistic  
594 that follows a chi-squared distribution (with df=1). Odd Ratio and Fisher's exact tests were



595 used to assess the impact of CYP6P9a\_R on the ability to survive and blood-feed after exposure  
596 to insecticide-treated nets.

597

598

599 **List of supplementary materials**

600 Text S1: Additional information on results and materials and methods

601 **Fig. S1.** Differential gene expression between four permethrin-exposed samples and  
602 FANG.

603 **Fig. S2:** Gene ontology enrichment of upregulated genes using BLAST2GO

604 **Fig. S3:** qRT-PCR validation of the expression profile of the main detoxification genes  
605 differentially expressed between resistant and susceptible pyrethroid samples with RNAseq.

606 **Fig. S4:** Insertion of a 6.5kb intergenic fragment between *CYP6P9a* and *CYP6P9b* in  
607 southern African mosquitoes.

608 **Fig. S5:** Genetic diversity patterns of an 800bp cis-regulatory genomic fragment of  
609 *CYP6P9a* Africa-wide and before and after LLIN scale up.

610 **Fig. S6:** Design of a DNA-based diagnostic assay to detect and track pyrethroid  
611 resistance across Africa.

612 **Fig. S7:** Impact of the *CYP6P9a*-based metabolic resistance on the efficacy of bed nets  
613 using semi-field experimental hut trials

614 **Table S1.** Descriptive statistics of RNAseq sequence read data and alignments for  
615 different samples

616 **Table S2:** Detoxification-associated genes differentially expressed between the four  
617 pyrethroid resistant populations and the FANG susceptible strain

618 **Table S3.** Descriptive statistics of Whole genome POOLseq sequence read data

619 **Table S4:** Counts of reads aligned at the left and right breakpoints of the 6.5 kb insertion  
620 supporting different haplotypes

621 **Table S5:** Population genetic parameters of the 800bp fragment upstream of *CYP6P9a*

622 **Table S6:** Correlation between genotypes of *CYP6P9a* and mortality (PermaNet 2.0)  
623 and blood feeding after the experimental hut trial with the FANG/FUMOZ strain

624

**Table S7:** Primers used for characterization of the promoter of *CYP6P9a*

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781

782 **Author contributions:** CSW conceived and designed the study; JMR, RD, SSI and CSW  
783 performed the field collection and resistance bioassays; HI, GDW, JMR and CSW performed  
784 sample preparation for all next-generation sequencing; GDW and CSW analyzed Next-  
785 generation sequencing data. MJW, JMR and MaT performed qRT-PCR; LMJM, GDW and  
786 CSW characterized *CYP6P9a* promoter; NAA and CSW analyzed the genetic diversity of  
787 *CYP6P9a*; LMJM and CSW designed the PCR-RFLP diagnostic assay; LMJM and MiT  
788 generated the lab crosses and performed the validation of the PCR-RFLP; BDM performed the  
789 experimental hut experiments with CSW and genotyped *CYP6P9a* with MJW and MaT; GDW  
790 and CSW wrote the paper with assistance from LMJM and JMR; All authors read and approved  
791 the final draft of the manuscript.

792

793 **Competing interests:** The authors declare no competing financial interests.

794

795 **Data and materials availability:** RNAseq: PRJEB24351, PRJEB10294; **Field PoolSeq:**  
796 PRJEB24384 and PRJEB13485; ***CYP6P9a* sequences:** GenBank MG782573-MG782841.

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**Table 1:** Experimental hut results with the FANG/FUMOZ strain

	Untreated Nets	PermaNet 2.0	PermaNet 3.0
<b>Total Mosquitoes</b>	356	270	322
<b>% Exophily (CI)</b>	11.8 (8.45-15.15)	16.7 (12.2-21.1) <sup>ns</sup>	15.8 (11.85-19.8) <sup>ns</sup>
<b>% Blood fed (CI)</b>	29.5 (24.7-34.2)	14.8 (10.6-19.05) <sup>§</sup>	6.8 (4.1-9.6) <sup>§‡</sup>
<b>% Blood feeding inhibition</b>	-	49.8 <sup>§</sup>	76.84 <sup>§‡</sup>
<b>% Personal protection (Total blood fed)</b>	-(105)	61.9 (40) <sup>§</sup>	79.04 (22) <sup>§‡</sup>
<b>% Blood feeding Mortality (no dead blood fed)</b>	1(1)	40.0 (16) <sup>§</sup>	95.5 (21) <sup>§‡</sup>
<b>% Mortality corrected (CI)</b>		33.3 (27.7-38.9) <sup>§</sup>	98.7 (97.5-99.9) <sup>§‡</sup>

801 For each comparison, estimates not sharing the same symbols (§ or ‡) are statistically different  
802 at P<0.05

803  
804

805 **Figure legends**

806 **Figure 1: Transcriptional profiling:** A) Venn-diagram showing number of differentially up-  
807 regulated genes between different countries relative to FANG at FDR<0.01 and Fold-change  
808 >2. B) Volcano plots of differential gene expression between permethrin-exposed samples and  
809 the susceptible FANG highlighting differences in the expression of key resistance genes  
810 between countries. C) Heatmap showing the contrast in expression of major candidate  
811 detoxification genes between African regions. D) Fragments Per Kilobase of transcript per  
812 Million mapped reads (FPKM) of genes from *rpI* pyrethroid resistance QTL highlighting  
813 differences between regions. E) Correlation between RNAseq and qRT-PCR. The data shown  
814 are mean + SEM (n = 3).

815

816 **Figure 2: Footprints of selective sweep associated with pyrethroid resistance.** A)  
817 Contrasting polymorphism patterns between lab resistant (FUMOZ) and susceptible (FANG)  
818 strains and also between pre- (MWI-2002) and post-bednet intervention (MWI-2014) samples  
819 from Malawi (12). Data were aligned to 120kb *rpI* BAC sequence (IGV screenshot). Each track  
820 shows the alignment depth (on a log scale for display purposes) respectively (coverage depth  
821 is capped at >100x). Grey columns represent bases identical to the reference sequence while  
822 coloured columns indicate variant sites with a minor allele frequency >10%. The genes of the  
823 P450 cluster are highlighted at the bottom. An increase read coverage is observed between  
824 CYP6P9a and CYP6P9b in pyrethroid resistant samples indicating the 6.5kb insert. B) Major  
825 signature of selective sweep detected around *rpI* QTL pyrethroid resistance region across the  
826 2R chromosome in southern Africa but not in FANG susceptible strain after plotting Minor  
827 allele frequency (MAF).

828

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830

831 **Figure 3: Genetic diversity of CYP6P9a 5'UTR region across Africa.** A) Molecular Phylogenetic  
832 analysis of CYP6P9a 5'UTR region by Maximum Likelihood method; The evolutionary history of  
833 *CYP6P9a* promoter haplotypes across Africa was inferred by using the Maximum Likelihood method  
834 based on the Tamura 3-parameter model. B) Africa-wide TCS network for the *CYP6P9a* haplotypes  
835 showing four predominant regional haplotypes in southern Africa (STH10), West (Ghana, GHA11),  
836 Central (BEN/DRC21) and East/Central (EST/CNT 24). GHA, Ghana; CMR, Cameroon; MWI,  
837 Malawi; MOZ, Mozambique; ZMB, Zambia; TNZ, Tanzania; DRC, Democratic Republic of Congo;  
838 FNG, FANG. \*, ancestral haplotype. Lines connecting haplotypes and each node represent a single  
839 mutation event (respective polymorphic positions are given on each branch). C) Neighbor-Joining  
840 phylogenetic tree of CYP6P9a-based genetic distance between ten African populations ( $N_{ST}$  estimates).  
841

842 **Figure 4: Impact of scale up of bednet interventions on the genetic diversity of promoter**  
843 **region of CYP6P9a.** A) Maximum Likelihood phylogenetic tree of *CYP6P9a* showing a cluster  
844 of highly diverse haplotypes pre-intervention but a nearly fixed haplotype post-intervention.  
845 Pink represents haplotypes before insecticide-treated nets whereas light blue are those post-  
846 insecticide-treated nets. B) TCS haplotype network in Malawi and Mozambique Pre- and Post-  
847 intervention revealing a major resistant haplotype post-intervention but a very diverse set of  
848 haplotypes before pre-insecticide-treated nets.  
849

850 **Figure 5: CYP6P9a promoter analysis and design of a DNA-based diagnostic assay for**  
851 **P450-based metabolic pyrethroid resistance.** A) Luciferase promoter assay (mean  $\pm$  SD;  
852 n=6) of *CYP6P9a* 5' flanking region with progressive serial deletions to detect the causative  
853 variants. B) Agarose gel of TaqI PCR-RFLP of *CYP6P9a*, clearly distinguishing the three  
854 genotypes RR, RS and SS. C) Significant correlation ( $P < 0.0001$ ) between *CYP6P9a* resistance  
855 allele and permethrin resistance. D) Africa-wide distribution of the *CYP6P9a* resistant allele  
856 showing near fixation in southern Africa.

857

858 **Figure 6: Impact of the *CYP6P9a*-based metabolic resistance on bednet efficacy:** A)  
859 *CYP6P9a* genotypes correlate with pyrethroid resistance in the hybrid strain of resistant  
860 (FUMOZ) and susceptible (FANG) strains supporting the use of this FANG/FUMOZ strain to  
861 assess the impact of *CYP6P9a*-mediated resistance on bednet efficacy. B) Blood feeding and  
862 mortality rates (mean  $\pm$  SD; n=4) of FANG/FUMOZ strain after release-recapture in  
863 experimental huts with untreated (blue), PermaNet 2.0 (green) and PermaNet 3.0 (blue) nets.  
864 C) *CYP6P9a* genotype proportions in dead or alive mosquitoes after PermaNet 2.0 exposure  
865 showing that *CYP6P9a*\_R significantly allows mosquitoes to survive bed net exposure  
866 (P<0.0001). D) Genotype proportions in blood-fed and unfed mosquitoes after PermaNet 3.0  
867 exposure showing that *CYP6P9a*\_R allele increases the ability of resistant mosquitoes of taking  
868 a blood meal.

869

870 **Supplementary Text**

871

872 **Title: A cytochrome P450 allele confers pyrethroid resistance in a major African malaria vector reducing**  
873 **insecticide-treated nets' efficacy**

874

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879

880 **Material and Methods**

881 **RNA extraction, sequence library preparation and sequencing**

882 Total RNA was extracted from pools of 10 female mosquitoes (alive after 1h permethrin exposure) using  
883 the Arcturus PicoPure RNA isolation kit (Life Technologies), according to the manufacturer's instructions and  
884 including a DNase treatment step. For each pool, total RNA was rRNA-depleted with Ribo-Zero low input kit for  
885 Human/Mouse/Rat (Epicentre, Madison, WI, USA), using 100 ng of starting material. RNAseq libraries were  
886 prepared from Ribo-Zero mRNA-enriched material with the ScriptSeq v2 RNAseq library preparation kit  
887 (Epicentre), using 15 cycles of PCR amplification. Libraries were purified using Agencourt AMPure XP beads  
888 (Beckman and Coulter, Beverly, MA, USA). Each library was quantified using a Qubit fluorometer (Life  
889 Technologies, Carlsbad, CA, USA) and the size distribution assessed using the 2100 Bioanalyzer (Agilent, Santa  
890 Clara, CA, USA).

891 Pools of libraries were sequenced, 8 per lane of the HiSeq 2500 (Illumina, San Diego, CA, USA) at 2x125  
892 bp paired-end sequencing with v4 chemistry. Sequence library preparation and sequencing were done at the Centre  
893 for Genomic Research (CGR), University of Liverpool.

894 **Analysis of RNAseq data**

895 Initial processing and quality assessment of the sequence data was performed as follows. Basecalling and  
896 de-multiplexing of indexed reads was performed by CASAVA version 1.8.2 (Illumina) to produce samples from  
897 the pooled sequence data, in fastq format. The raw fastq files were trimmed to remove Illumina adapter sequences  
898 using Cutadapt version 1.2.1 (1). Reads were further trimmed to remove low quality bases (with a window quality  
899 score <20), using Sickle version 1.200 (2).

900 RNAseq R1/R2 read pairs were aligned to the reference sequence using the Subread aligner version 1.4.6  
901 (3). The reference annotation available (AfunF1.4) was further improved using BLAST2GO version 4.0.7 (4).

902 Fragments mapped in the sense orientation to annotated *An. funestus* genes (automated predictions from  
903 gene set AfunF1.4, 2016-11-20, downloaded from VectorBase and annotated genes from the mitochondrial  
904 genome) were counted using featureCounts version 1.4.6 (5). Differential gene expression analysis was carried  
905 out using edgeR (6). Pairwise comparisons were carried out. Normalisation factors were calculated to correct for  
906 differences in total tag counts among samples, which may otherwise cause bias in differential gene expression  
907 analysis, using the "TMM" (Trimmed Mean M-values) method in edgeR (6) with default parameters. P-values  
908 associated with logFC were adjusted for multiple testing using the False Discovery Rate (FDR) approach (7).  
909 Significantly, differentially expressed genes were defined as those with an FDR-adjusted P-value <1% and >2-

910 fold absolute difference in expression level. Fragments per kilobase of gene sequence per million mapped reads  
911 (FPKM) was calculated using tag counts and the total CDS length. Gene ontology enrichment analysis was carried  
912 out on differentially expressed gene sets using BLAST2GO (4).

913 The Strand NGS software (Strand Life Sciences, version 3.0) was also used to analyze the data following  
914 RNA alignment and RNA-seq analysis pipeline with standard parameters.

915

## 916 **Results**

### 917 **RNAseq transcriptional profiling of mosquitoes from across Africa identifies candidate pyrethroid-** 918 **resistance associated genes**

919 The annotation gene set AfunF1.4 includes 13,506 protein coding gene annotations. However, only 5,095  
920 of these were functionally annotated. To improve the functional annotation of the genome, we used BLAST2GO  
921 (4) to assign descriptions and gene ontologies using sequence similarity. This analysis assigned putative  
922 descriptions to 12,196 protein coding genes and gene ontology descriptions to 10,072.

923 All read libraries were aligned to the reference genome. The quality metrics and the alignment parameters  
924 are presented in Table S1. Analysis with EdgeR and StrandNGS generated similar results. The number of  
925 differentially expressed genes between the four populations and the FANG susceptible strain or between  
926 populations is represented in the Venn diagram (Fig. 1A; Fig. S1A) whereas the expression profile is shown in the  
927 volcano plot for each country (Fig. 1B-E).

928 **Gene Ontology (GO) enrichment:** After quality control and analyses (Table S1), GO enrichment was  
929 performed to assess the generic metabolic terms associated with resistance. Permethrin resistant mosquitoes in  
930 Malawi showed significant enrichment of gene ontologies associated with cytochrome P450 genes in genes over-  
931 expressed relative to the fully susceptible FANG. These GO terms include heme binding, tetrapyrrole binding,  
932 oxidoreductase activity and iron ion binding (Fig. S2A). These GO terms among others are also enriched in the  
933 Ghana over-expressed gene set (Fig. S2B). In Uganda, more GO terms are enriched among the over-expressed  
934 genes but not directly associated with detoxification activities (Fig. S2C).

935

### 936 **Candidate resistance genes commonly up-regulated Africa-wide:**

937 To elucidate the continent-wide drivers of pyrethroid resistance in *An. funestus*, we first detected the sets  
938 of genes commonly over-expressed in all four regions. Cytochrome P450 genes were the most predominant  
939 detoxification genes on this list (Table S2). The two duplicated P450 genes *CYP6P9a* and *CYP6P9b* were the most

940 abundantly expressed notably in Malawi with fold change (FC) of 60.5x and 23.9x respectively. Although these  
941 two genes are also up-regulated in other regions of East, West and central Africa, it is with a much-reduced fold  
942 change with FC of 2.1, 6.3 and 2.7 only respectively in Cameroon, Ghana and Uganda for *CYP6P9a*. This suggests  
943 that this gene is more specific to the southern region (Fig. 1B-D). Besides these two genes, other P450s commonly  
944 up-regulated had lower FKPM <1000. Among these, the *CYP325A* gene presented a marked increase in Central  
945 Africa with FC of 26.9 in Cameroon in contrast to other regions where FC<6 suggesting that the over-expression  
946 of this gene could be more specific of this region. Two glutathione S-transferases *GSTe6* and *GSTD3* were also  
947 commonly up-regulated in all four regions at similar FC between 2.6 and 4.9.

948 **Genes commonly up-regulated in three regions:** Among the genes commonly expressed in three out  
949 of four regions, are two P450s. The duplicated *CYP6P4a* and *CYP6P4b* are highly over-expressed in Ghana with  
950 FC of 44.8 and 23.9 respectively but lower FC (<5.9) in Malawi and Uganda but not up-regulated in Cameroon.  
951 The other P450, *CYP6P5*, also located on the *rp1* pyrethroid resistance QTL region is over-expressed in all regions  
952 but not in southern Africa (Fig. 1D). Other P450s differentially expressed have lower FC including *CYP4C36* (not  
953 over-expressed in Uganda), *CYP306A1* (not in Ghana), *CYP315A1* (not in Malawi). Strikingly a set of GSTs from  
954 the epsilon class were up-regulated in all regions except East Africa including *GSTe2* previously shown to confer  
955 DDT and pyrethroid resistance, which nevertheless exhibits higher FC in Cameroon and Ghana than Malawi  
956 (Table S2). These epsilon GSTs also include *GSTe1*, *GSTe3* and *GSTe5*. The *GSTD1* presented a high FPKM>10k  
957 in Malawi, Ghana and Uganda suggesting a role for this gene in these regions but not in Cameroon where it is not  
958 significantly over-expressed.

959 **Genes commonly up-regulated only in two regions:** Analysis of the sets of genes up-regulated only in  
960 two regions revealed the presence of key P450s. Among these are *CYP6M7* and *CYP9J11* both with abundant  
961 reads counts, up-regulated only in southern and West Africa with FC around 2 and 3. These genes have previously  
962 been shown to metabolise pyrethroids (8, 9). Another P450, *CYP6N1* located on the *rp2* QTL chromosome, is also  
963 up-regulated in southern and West Africa only. The *CYP9K1* P450 gene is up-regulated in East and West Africa  
964 although with higher FC in East (FC5.2). Among the genes only up-regulated in West and Central Africa, are a  
965 carboxylesterase AFUN002514 with FC of 5.5 and 3.6 respectively in Cameroon and Ghana but also the  
966 glutathione S-transferase *GSTe4*. Among the list of genes only present in Central and Southern Africa are also a  
967 carboxylesterase (AFUN000422) and a GST, AFUN007291 (*GSTi2*). Other detoxification genes are up-regulated  
968 only in one regions and usually have a relatively low FC (Table S2).

969



970           **Quantitative RT-PCR:** To validate the RNAseq transcription profile, the expression levels of fifteen  
971 detoxification genes was also assessed by qRT-PCR for both permethrin resistant (Fig. S3A) and unexposed (Fig.  
972 S3B) mosquitoes. These genes included 12 P450s differentially expressed across the different regions as well as  
973 one GST, one aldehyde oxidase and one carboxylesterase. Primers were previously published (8, 10). Firstly,  
974 control mosquitoes not exposed to insecticides also showed a strong correlation ( $R^2=0.695$ ;  $P=0.002$  in Malawi)  
975 with permethrin resistant samples used for RNAseq (Fig. 1E) supporting a constitutive expression of these  
976 candidate resistance genes to confer resistance. Overall, a high and significant correlation was observed between  
977 qRT-PCR and RNAseq results for the 4 countries when compared to FANG ( $R^2=0.85$ ;  $P<0.001$ ) (Fig. S3C).  
978 However, significant differences were observed for the expression of some genes such as the *CYP6Z1* P450 which  
979 for qRT-PCR exhibited a high up-regulation in Malawi (FC 66) and Ghana (FC13.4) but not in RNAseq. This  
980 gene has previously also been shown to be over-expressed in southern Africa using microarray and qRT-PCR (11)  
981 suggesting that RNAseq could have missed or that the primers was not efficient with the susceptible FANG strain.  
982 Similarly, the aldehyde oxidase gene (AFUN000093) was significantly over-expressed with qRT-PCR in all  
983 regions except Cameroon but not with RNAseq. This could be due to the poor annotation of some of these genes  
984 in the current *An. funestus* genome with certain genes been mistakenly combined.

985

#### 986           **Complex evolution of the gene cluster of the *rp1* CYP6 genes associated with pyrethroid resistance**

987           Due to the strong evidence of selection at *rp1* across southern Africa from RNAseq profiles, a detailed  
988 analysis of this major resistance locus was performed revealing that a large scale structural polymorphism may  
989 affect the evolution of the *rp1* locus:

990           **Identification of a 6.5 kb insertion between *CYP6P9a* and *CYP6P9b*:** Close inspection of the pooled-  
991 template whole genome alignment to the 120 kb BAC sequence containing the CYP6 cluster showed two  
992 anomalous features in the 8.2 kb sequence between the paralogous genes *CYP6P9a* and *CYP6P9b*. In some  
993 samples, the coverage depth was greater than for the surrounding sequence and some samples showed read pairs  
994 in the correct relative orientation ( $><$ ) but with greater than expected insert sizes, indicative of a large indel: a  
995 “deletion” in the sequenced genome(s) or an “insertion” in the reference genome (Supplementary Figure 4A; Table  
996 4). The FUMOZ alignment contains reads that are left-clipped (the leftmost part of the read, as aligned to the  
997 reference, is clipped irrespective of the read’s orientation: so the 5’ end of a read aligned to the positive strand and  
998 the 3’ end of a read aligned to the negative strand) between BAC sequence positions 37409 and 37410 (37410  
999 being the leftmost base included in the insertion). It also contains reads that are right-clipped between positions

1000 43954 and 43955. This defines a region of 6545 bp. The presence of only left-clipped reads on the left of the region  
1001 and right-clipped reads on the right of the region indicates two things in FUMOZ: (i) that the “insertion” form of  
1002 the indel is fixed in the FUMOZ sample (there is no evidence for presence of the “deletion” form), and (ii) that the  
1003 inserted sequence is homologous to part of a larger sequence found elsewhere in the genome (indicated by the  
1004 “clipped” parts of the reads).

1005 In FANG the situation is more complicated. At the left end of the insertion there are reads left-clipped  
1006 between positions 37409 and 37410 (as for FUMOZ) but also some reads right-clipped slightly further left,  
1007 between positions 37404 and 37405. At the right end of the insertion there are reads right-clipped between  
1008 positions 43954 and 43955 (as for FUMOZ) but also some reads left-clipped between the same positions. In  
1009 addition, further to the right there are some reads right-clipped between positions 44053 and 44054 and some left-  
1010 clipped between positions 44070 and 44071. Detailed inspection of the clipped reads showed that the reads right-  
1011 clipped at 37404/37405 and left-clipped at 43954/43955 indicate the “deletion” form of the indel, as the clipped  
1012 parts of the reads from the left and right end of the insertion overlap each other (but also contain a short length of  
1013 DNA that does not match FUMOZ). The clipping at 44053/44054 and 44070/44071 is due to a region of 35 bp in  
1014 FANG (TAA TAC CGG GAG ATA CAT GGA GCT CGT GTA AAA GA) that does not align with the FUMOZ  
1015 reference (ATA TGT CGG AGG TTT AT) at the same location. Overall, FANG shows evidence of the “deletion”  
1016 form of the indel in addition to the presence of the large homologous sequence elsewhere in the genome. This  
1017 makes simple inspection of the alignment misleading, as rather than a loss of coverage across the 6.5 kb indel,  
1018 coverage is seen due to reads originating from sequence elsewhere in the genome.

1019 **Identifying the presence or absence of the insertion in samples from different geographical**  
1020 **locations in Africa:** To determine the geographical extent of the FUMOZ-like “insertion” haplotype, a PCR  
1021 amplification of the 8.2kb was performed with two possible fragments obtained; a 1.7kb in case of absence of the  
1022 6.5kb insert or the 8.2kb in presence of the insert. The results indicate that the 6.5 kb insertion between *CYP6P9a*  
1023 and *CYP6P9b* was present only in southern Africa population of Malawi, where it was nearly fixed (only a single  
1024 read in Malawi supported the deletion haplotype) (Supplementary Table 5). However, populations from other parts  
1025 of Africa showed no evidence of the insertion haplotype. Evidence that the insertion existed (albeit at low  
1026 frequency) in the early 2000s comes from its presence in the FUMOZ colony, which was colonized from the field  
1027 in Mozambique in 2000, and subsequently selected for insecticide resistance, which appears to have fixed the  
1028 insertion haplotype in colony.

1029           **Investigating the genomic origin of the 6.5kb insertion:** To identify the genomic origin of the inserted  
1030 6.5 kb sequence, it was extracted from the BAC sequence and used to search the *An. funestus* FUMOZ AfunF1  
1031 reference genome assembly using BLASTn implemented in the VectorBase web resource. The results indicated  
1032 that the sequence occurred at two different locations in the genome, both of which were on scaffold KB669169.  
1033 KB669169 is 1,771,395 bp long and contains the CYP6 cluster between positions 1,340,840 (the 3' end of  
1034 *CYP6AA1*) and 1,431,230 (the 5' end of *CYP6AD1*). The first location was from 1,378,027 to either 1,403,987 or  
1035 1,410,005. This is the “inserted” location, between *CYP6P9a* and *CYP6P9b*. The two different right-hand  
1036 positions may be due to the poor quality of the assembly across the CYP6 cluster, with maybe gaps in the assembly  
1037 in this region, and the possible inclusion of the same sequence twice when the contigs should have been merged.  
1038 The second location was between 1,109,272 and 1,118,666, approximately 260 kb away from the CYP6 cluster  
1039 on the same scaffold (therefore, on the same chromosome). In addition, short (100 bp) sequences from the left and  
1040 right ends of the insertion were used to conduct BLASTn searches of AfunF1 and confirmed the results obtained  
1041 with the full-length insertion sequence. Finally, clipped sequences from immediately to the left and right of the  
1042 insertion were used to conduct BLASTn searches of AfunF1. The results (matches only adjacent to the  
1043 KB669169:1109272-1118666 region) confirmed that the “parent” sequence of the insertion between *CYP6P9a*  
1044 and *CYP6P9b* came from KB669169:1109272-1118666. This putative genomic “parent” sequence of the insert  
1045 contains no annotated protein coding genes but there is a large assembly gap in the region. The orthologous region  
1046 in the *Anopheles gambiae* genome is on chromosome arm 2R. The protein coding genes flanking the insertion  
1047 sequence, AFUN008344 and AFUN008346, are orthologous to AGAP002842 and AGAP002845, respectively.  
1048 *An. gambiae* has no annotated protein coding genes between AGAP002842 and AGAP002845, suggesting that  
1049 *An. funestus* may not have also. Three micro-RNAs annotated in both species are outside of the insertion sequence.  
1050 One of these (mir-317; AFUN015669) has its 5' end approximately 130 bp away from the leftmost breakpoint of  
1051 the insertion. Despite the lack of annotated genes, the region is transcribed and shows a large transcribed region,  
1052 with some evidence of splicing, covering the three annotated micro-RNAs. Whether this transcript is processed to  
1053 form mature micro-RNAs is not known.

#### 1054           **Detection of a molecular marker associated with pyrethroid resistance**

1055           **i-Comparative analysis of the cis-regulatory region of *CYP6P9a* between susceptible and resistant**  
1056 **mosquitoes:** To have a full view of the potential regulatory elements driving over-expression of *CYP6P9a*, we  
1057 amplified and sequenced the full 8.2kb intergenic region between *CYP6P9a* and *CYP6P9b* in individual resistant  
1058 (FUMOZ\_R) and susceptible (FANG) mosquitoes. Amplifications revealed that while resistant mosquitoes have

1059 the full 8.2 kb region, the susceptible ones only present a 1.7kb size for this intergenic region confirming the  
1060 insertion of a 6.5 kb fragment in resistant mosquitoes. This insertion is present in the lab resistant FUMOS strain  
1061 (reference genome) as well as all southern Africa to near fixation (Malawi, Mozambique and Zambia). However,  
1062 mosquitoes from other parts of the continent were similar to the lab susceptible strain FANG. To understand why  
1063 such insertion occurred in resistant mosquitoes in southern Africa, we analyzed the composition of the 6.5kb  
1064 fragment which occur at 830bp from stop codon of *CYP6P9b* and at 905 from start codon of *CYP6P9a*. Using  
1065 GPminer (12), we detected, that it is full of transcription factor sites including an cpG island of 1.3kb and several  
1066 GATA sites. It also contains several TATA (35), CCAAT (12) and GC (11) sequences. Furthermore, this 6.5kb is  
1067 rich in over-represented (OR) oligonucleotides. Using the Algen Promo program, to search for key transcription  
1068 factors associated with regulation of genes involved in xenobiotics detoxification, revealed an abundant number  
1069 of binding sites (51) for the Cap n Collar C (CnCC) and the Muscle aponeurosis fibromatosis (Maf) transcription  
1070 factors sites which are known xenobiotic sensors in insects. Other of these sensors were also detected in the 6.5  
1071 kb including 14 binding sites for Ahr:Arnt, 13 for SXR:PxR and also for HNF4. The richness of this 6.5kb in  
1072 regulatory factors suggests that this insertion contributes to increase regulation of *CYP6P9a* gene. Noticeably this  
1073 6.5kb contains a microsatellite (FUNR) (13), 388bp in size and located between 6082bp and 6482bp, only 80bp  
1074 from the 5'UTR of *CYP6P9a*. Previous genotyping of this marker Africa-wide revealed significant differences  
1075 associated with pyrethroid resistance profile. This FUNR is not present within the 1.7kb intergenic region between  
1076 *CYP6P9a* and *CYP6P9b* for the FANG susceptible strain or before bednets distribution. It has been shown that  
1077 microsatellite loci are involved in upregulation of P450 to confer insecticide resistance in other insects such as  
1078 *Aphid* (14). It has also been shown in Yeast that polymorphic tandem repeats in the promoter regions can activate  
1079 gene expression by impacting local chromatin structure to act as “evolutionary tuning knobs” to drive rapid  
1080 evolution of gene expression such in a case of insecticide resistance selection. However, the FUNR has been  
1081 detected in mosquitoes lacking this 6.5kb across Africa suggesting that for those populations’ portions of this 6.5  
1082 kb are located in other regions of the genome close to 2R chromosome. There is also the possibility of the 6.5kb  
1083 in resistant mosquitoes is causing a chromatin remodeling thereby promoting the access of the transcription factors  
1084 to the promoter (15).

1085 **Geographical distribution of the resistant *CYP6P9a* allele across Africa:** To establish the  
1086 geographical distribution of the resistant *CYP6P9a* allele, field populations of *An. funestus* collected from several  
1087 countries in Africa were genotyped using PCR-RFLP. This revealed that the *CYP6P9a*-R allele is mainly present  
1088 in southern Africa where it is close to fixation in Mozambique, Malawi and Zambia. The allele is also present in

1089 Tanzania in East Africa, although at lower frequency than in southern Africa (55.7%). However, in correlation  
1090 with sequencing data, the CYP6P9a-R is completely absent in Central and West Africa (Fig. 5D; Fig. S6C). This  
1091 total absence of CYP6P9a-R in West-Central Africa supports the restriction to gene flow we are observing for this  
1092 species maybe because of the Rift Valley. In DR Congo, a contrast was observed between East and West as the  
1093 CYP6P9a-R mutation is present in East but absent in the West (Kinshasa). It is important to monitor the spread of  
1094 this marker across DRC to assess the speed and direction of spread of this resistance allele.

#### 1095 **CYP6P9a\_R reduces the effectiveness of insecticide-treated bed nets**

1096 To assess the impact of the CYP6P9a-R haplotype on the effectiveness of LLINs, we opted to use lab  
1097 strains as this mutation is nearly fixed in the field in southern Africa. We crossed the highly resistant laboratory  
1098 strain FUMOZ-R (where CYP6P9a\_R is fixed) with the fully susceptible laboratory strain FANG (where  
1099 CYP6P9a\_R is completely absent). Using reciprocal crosses between the two strains we generated a hybrid strain  
1100 at the F<sub>4</sub> generation that we used for semi-field studies in experimental huts.

1101 **Susceptibility profiles of the FANG/FUMOZ and FANG/FUMOZ strains:** The bioassays performed  
1102 with the reciprocal FANG/FUMOZ strains revealed that both hybrid strains were resistant to pyrethroids and  
1103 carbamates and moderately resistant to DDT (93% mortality) (Fig. S7A). As expected, the level of resistance was  
1104 lower than in the fully resistant strain FUMOZ\_R, with a mortality rate of 76.1-80.7% when exposed to permethrin.  
1105 However, a significant difference was observed for deltamethrin with a higher mortality rate recorded for the strain  
1106 generated from crossing females FUMOZ\_R to males FANG (48.5%) than in the strain from females FANG and  
1107 males FUMOZ\_R (77.3%). This difference could indicate the role of some candidate genes in the X chromosome  
1108 for deltamethrin resistance (*CYP9K1*, for instance). Resistance pattern was similar for the carbamate bendiocarb  
1109 in both reciprocal strains.

#### 1110 **Validating the role of CYP6P9a-R in pyrethroid resistance in the hybrid FANG/FUMOZ strains:**

1111 Before any field studies with the hybrid FANG/FUMOZ strains, the role of the CYP6P9a\_R allele in the observed  
1112 pyrethroid resistance was confirmed. WHO bioassays showed a mortality of 39.0% and 42.3% after 30 minutes'  
1113 exposure and mortality rates of 81.3% and 86.3% after 90 minutes' exposure, respectively to permethrin and  
1114 deltamethrin (Fig. S7B). The odds ratio of surviving exposure to permethrin when homozygous for the resistant  
1115 CYP6P9a\_R allele (RR) was high at 693 (CI 88-5421; P<0.0001) compared to the homozygous susceptible (SS)  
1116 (Fig. S7C-D). The OR was 131 (CI 27-978; P<0.0001) when comparing RR to RS indicating that the resistance  
1117 conferred by *CYP6P9a* is additive.

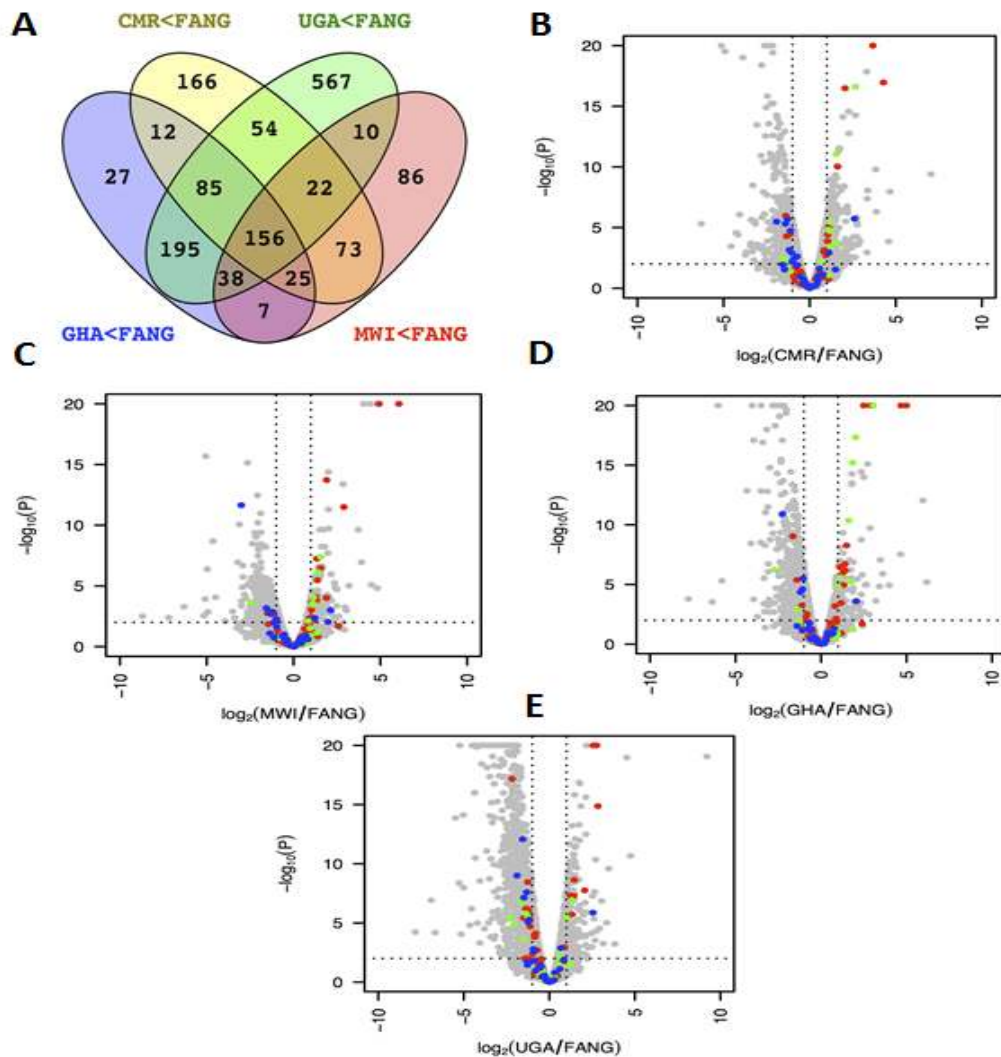
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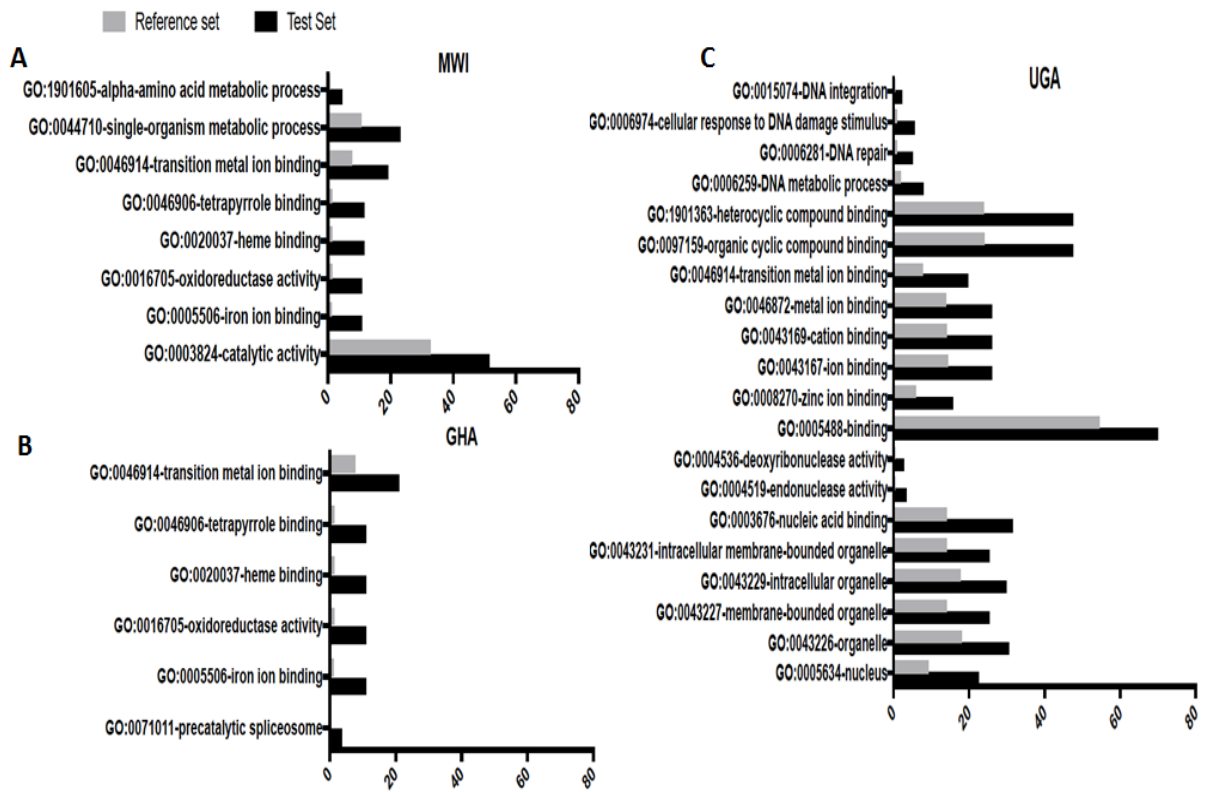
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1171  
1172



1173  
 1174 **Fig. S1. Differential gene expression between four permethrin-exposed samples and FANG.** A) Venn-  
 1175 diagram showing number of differentially downregulated genes between different countries relative to FANG at  
 1176  $FDR < 0.05$  and Fold-change  $> 2$ . B) Volcano plot of the expression of between CMR and FANG susceptible strain.  
 1177 The X-axis shows  $\log_2$  fold-change (positive values are up-regulated relative to FANG). The Y-axis shows  $-\log_{10}$   
 1178 transformed P values (adjusted for multiple testing; values greater than 40 were displayed as 40). The horizontal  
 1179 dashed line marks  $P=1\%$  and the vertical dashed lines indicate two-fold expression difference among conditions.  
 1180 Red points indicate genes annotated as cytochrome P450s and green points indicate GST and blue points represent  
 1181 carboxylesterases. C) is for Malawi, D) for Ghana and E) is for Uganda.





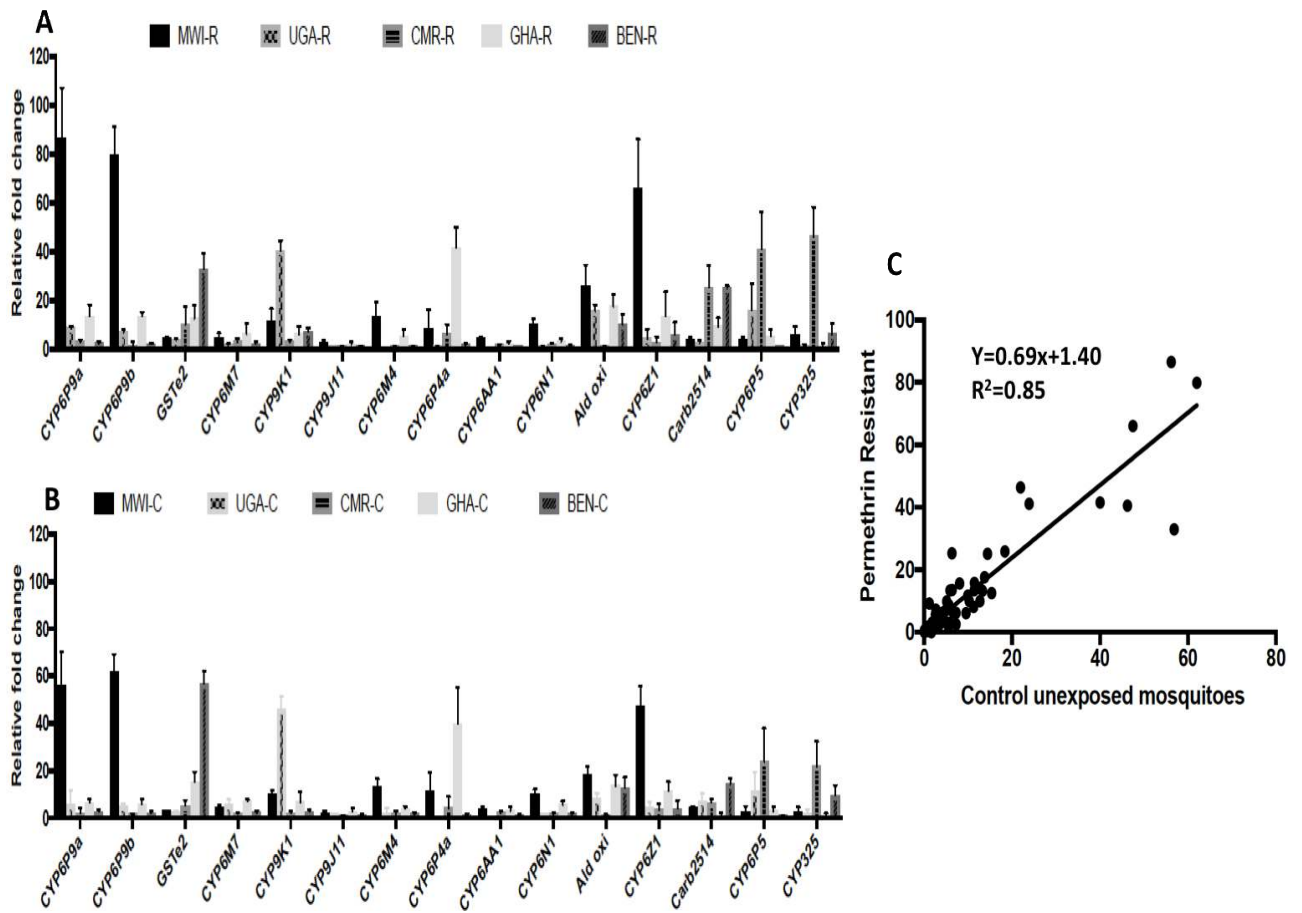
1182

1183 **Fig. S2: Gene ontology enrichment of upregulated genes using BLAST2GO: A) Malawi, B) Uganda, C)**

1184 Ghana. The test set represents the transcripts up-regulated while the reference set is made of the entire *An. funestus*

1185 transcript set (Afun1.4). Significance of the enrichment was assessed using a Benjamini and Hochberg multiple

1186 testing correction ( $P < 0.05$ ). No significant terms detected for Cameroon at FDR of 0.



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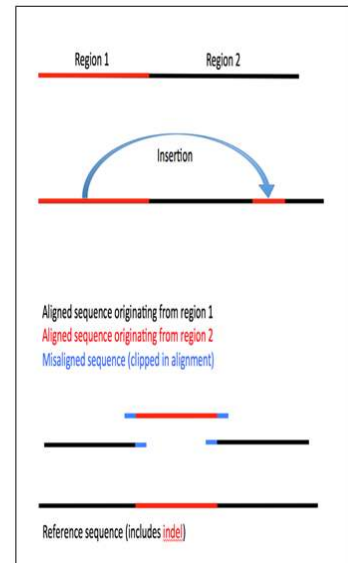
1190 **Fig. S3: qRT-PCR validation of the expression profile of the main detoxification genes differentially**  
 1191 **expressed between resistant and susceptible pyrethroid samples with RNAseq. A) qRT-PCR expression**  
 1192 **profile between R-S; B) qRT-PCR expression profile between C-S; C) Correlation between qRT-PCR of R\_S and**  
 1193 **C-S. The data shown are mean + SD (n = 3).**

A



1194

B



1195 **Fig. S4: Insertion of a 6.5kb intergenic fragment between *CYP6P9a* and *CYP6P9b* in southern African**  
 1196 **mosquitoes.** A) Screenshot from the integrative genomics viewer (IGV), showing coverage depth and aligned  
 1197 reads for FUMOZ (upper) and FANG (lower) pooled template whole genome sequence alignments. The coverage  
 1198 depth plots show deeper coverage in this region in FUMOZ but not in FANG. The FANG alignment contains read  
 1199 pairs with unusually long insert sizes, indicated in red in the lower panel (thick lines represent reads, read pairs  
 1200 are linked by thin lines). B) Schematic representation of the process of insertion from a one region of the genome  
 1201 to another, generating 2 homologous sequences in different parts of the genome.

A

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0000000000001111111122222222333333334444556666666666666
1112234578890133467002333677055667778237800144567788888
36956844739643786380732782153028904580429249646685903459
FNG1 4 ACATATTCAAATAGTAAAGCATCAGCTAATGCA--AACCCAGAGTGAATAGTGACC
FNG2 1 .....C.....G.....A..G.....
FNG3 1 .....C.....G.....G.....GTA.....
FNG4 3 .....C.....G.....G.....
FNG5 2 .....C.....G.....G.....GTATA.....
FNG6 2 .....C.....G.....G.....GTATA.....
FNG7 1 .....C.....G.....G.....TA.....CCG.CT.AC.T...
FNG8 1 .....C.....G.....G.....TA.....CCG.CT.AC.T...
FNG9 1 .....CTT.GAC.GTT.....G.....TA.....CCGGCTTAC.T.T
STH10 63 T....AC...G.C...T.AG...C...AT.AA...A...ATA..G.....G.
GHA11 16 .G....C...G.CAGTTA...A.C...A...A...G.....G.
GHA12 1 .G....C...G.CAGTTA...A.C...A...TA...ATA..G.....G.
GHA13 1 .G....C...G.CAGTTA...A.C...G...A...A...G.....G.
GHA14 2 T....AC...G.C...T.AG...A.C...A...TA...ATA..G.....G.
MMI15 1 T....AC...G.C...T.AG...C...AT.AA...A...ATA..G...TAC.TGT
CMR16 2 T....AC...G.C...T.AG...A.C...A...ATA..G.....G.
MOZ17 2 T....AC...G.C...T.AG...C...AT.AA...A...ATA..G.C...G.
TNZ18 1 .....TGA..GT...G...C...A...G...T.....
TNZ19 1 .....CTTTGA..GT...CA..A.GGG...T.....CCGGCTTAC...T
ZMB20 2 T....ATAC...G.C...T.AG...C...AT.AA...A...ATA..G.....G.
BEN/DRC21 36 .....C...G.C.GTT.....G...A...TA...G.....G.
DRC22 1 .....CTTTGAC.GTT.....G...A...TA...CCGGCTTAC.T.T
DRC23 1 .....C.T.G.C.GTT.....G...A...TA...G.....A.
EST/CNT24 30 .G....C...G.CAGTTA...C.....AA--AT...G.....G.
CMR25 2 .G....C...G.CAGTTA...C.....AA--AT...G.....G.
    
```

B

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00000000000000000000111111112222222222223333333344444444555555556666666666666
001111223455667780115779901234677889912244455900223355578890004899992345555566
5735696947281212862333569124796889283975734535937393724790833895413791130458904
Post1 48 CAAATCTCAAATATAGGTAAAGCATCAGCTAATGCA--AACCCAGAGTGAATAGTGACGAGC
PostMWI2 1 .....TC.T.T
PostMOZ3 2 T.....
PostMWI24 2 .....C.....
PreMOZ5 3 .....T.C.....
PreMWI6 2 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C.
PreMWI7 1 ..T...T..TT..A...GTC.A...AT..C.G...GC--T...GAG.....C.
PreMWI8 3 ..T...T..TT..A...GTC.A...AT...G...GC--T...GAG.....C.
PreMWI9 1 .CT.G...C..G..TAC..CT.G..A.T...A.AG.AAGC--CG...T...A.....C.
PreMWI10 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C.
PreMWI11 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C.
PreMWI12 1 .CTGG...C..G..TAC..CT.G..A.T...A.AG.AAGC--CG...T...A.....C.
PreMWI13 1 .CT.G...C..G..TAC..CT.G..A.T...A.AG.AAGC--CG...T...A.....C.
PreMWI14 1 .CT.G...C..G..TAC..CT.G..A.T...A.AG.AAGC--CG...T...A.....C.
PreMWI15 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI16 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI17 1 .GT...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI18 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI19 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI20 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI21 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI22 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMWI23 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ24 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ25 3 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ26 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ27 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ28 1 ..T...T..TT..A...GTC.A...T...G...GC--T...GAG.....C..C..C.
PreMOZ29 2 ..T...T..TT..A...GTC.A...AT...G...GC--T...GAG.....C..C..C.
PreMOZ30 1 ..T...T..TT..A...GTC.A...G.A.T...G...GC--T...GAG.....C..C..C.
PreMOZ31 1 ..T...CT..TT..A...GTC.A...AT...G...GC--T...T...GAG.....C..C..C.
PreMOZ32 1 ..T...T..TT..A...GTC.A...T...G...GC--T...T...GAG.....C..C..C.
PreMOZ33 1 ..T...T..TT..A...GTC.A...T...G...GC--T...T...GAG.....C..C..C.
PreMOZ34 1 ..T...T..TT..A...GTC.A...T...G...GC--T...T...GAG.....C..C..C.
    
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1203

1204 **Fig. S5: Genetic diversity patterns of an 800bp cis-regulatory genomic fragment of *CYP6P9a* Africa-wide**

1205 **and before and after LLIN scale up.** (A) Polymorphic sites and haplotypes across Africa. Haplotypes are labeled

1206 with prefixes from the country where they are predominant. CMR, Cameroon, GHA is Ghana, BEN is Benin, TNZ

1207 is Tanzania, DRC is Democratic Republic of Congo, MOZ is Mozambique, STH is Southern Africa, MWI is

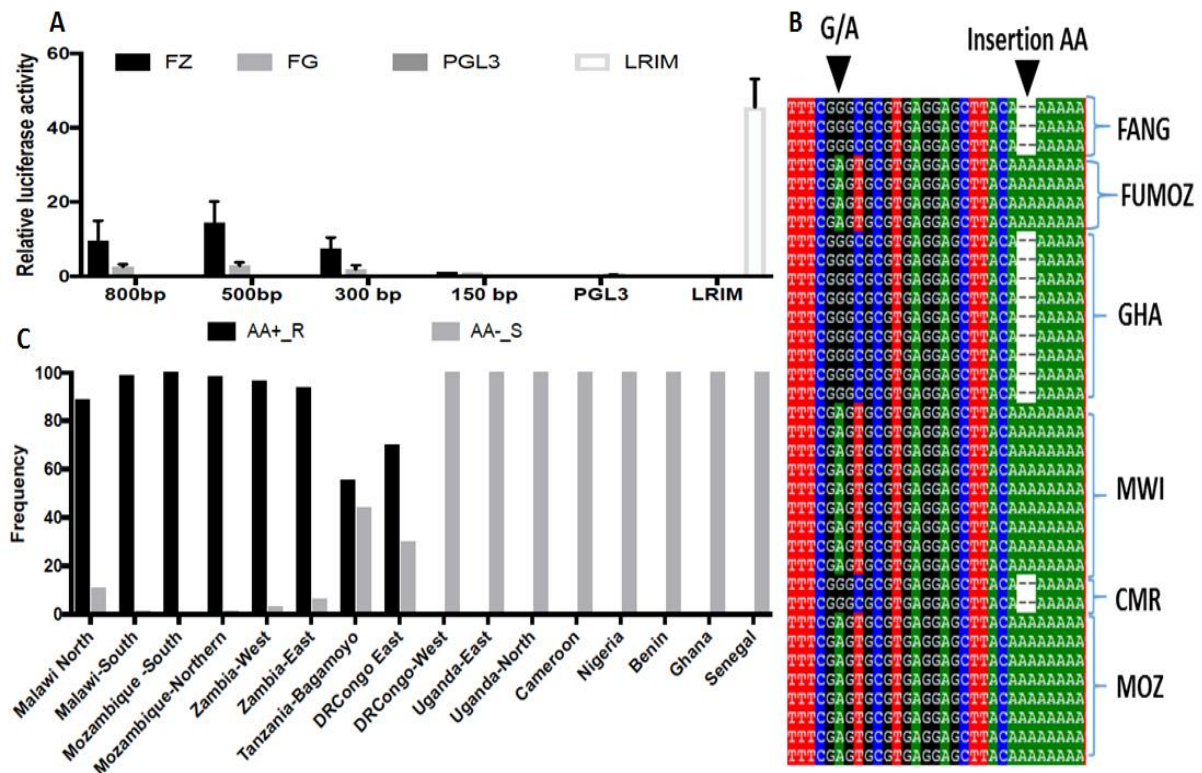
1208 Malawi, ZMB is Zambia, EST/CNT is East/Central Africa. B) Polymorphic sites and haplotypes before and after

1209 scale up of LLINs in Mozambique and Malawi. Haplotypes are labeled with prefixes from the sample where they

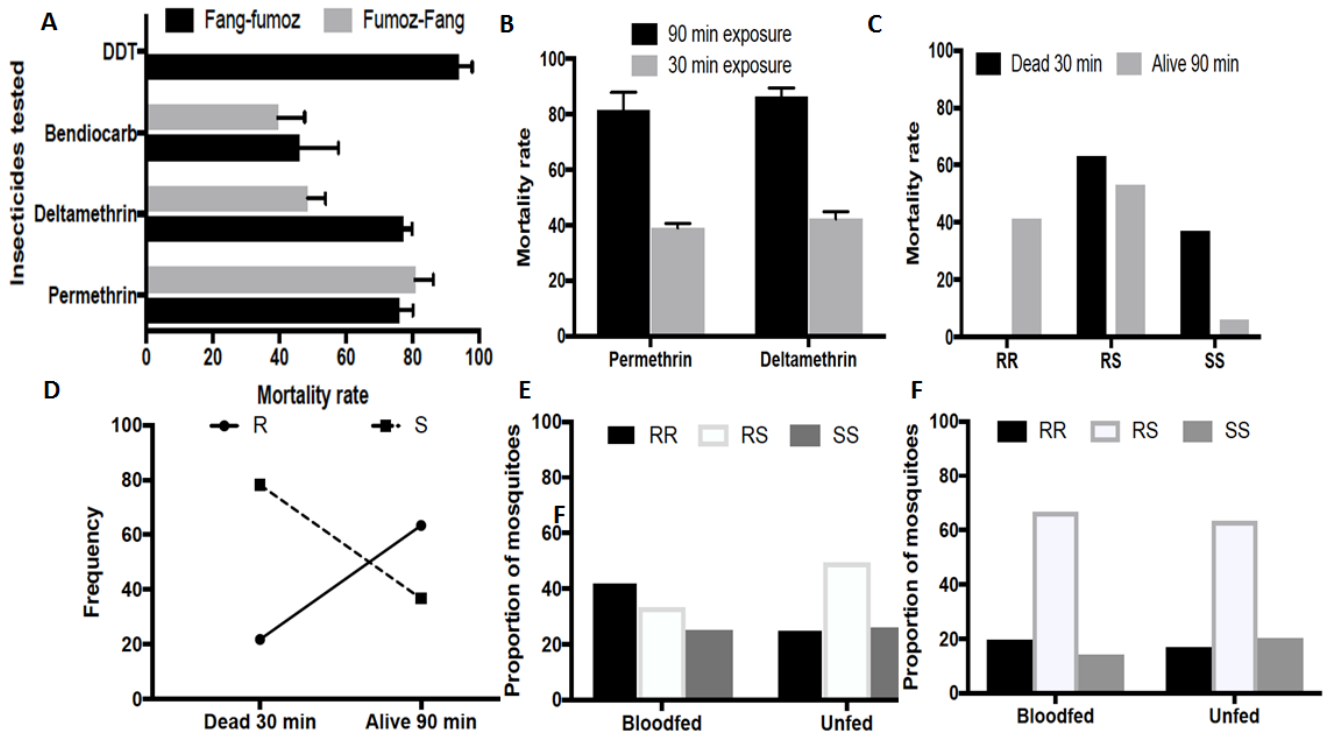
1210 are predominant. PreMWI is for Pre-intervention Malawi, PreMoz is Pre-intervention Mozambique; PostMWI is

1211 Post-intervention Malawi; PostMoz is for Post-Intervention Mozambique.

1212



1213  
 1214 **Fig. S6: Design of a DNA-based diagnostic assay to detect and track pyrethroid resistance across Africa.** A)  
 1215 Comparative luciferase assay between promoter fragment from the highly resistant FUMOZ and highly susceptible  
 1216 (FANG) lab strains with progressive serial deletions of *CYP6P9a* 5' flanking region to detect the causative variants.  
 1217 Bars represent the mean  $\pm$  S.D. of four independent transfections of three replicates (n = 6). A significant  
 1218 difference between promoter constructs ( $p < 0.001$ , Tukeys's t-test) is indicated by an asterisk. B) Schematic  
 1219 alignment of sequences across Africa showing fixed differences associated with pyrethroid resistance including  
 1220 the AA insert only found in resistant mosquitoes and the A/G variant tightly linked to the resistant haplotype and  
 1221 generating a restriction site for the TaqI restriction enzyme. C) Frequency of the *CYP6P9a*\_R allele across Africa  
 1222 showing that it is only present in southern Africa where it is close to fixation but also in East Africa at moderate  
 1223 level. However, it is completely absent in Central and West Africa.



**Fig. S7: Impact of the *CYP6P9a*-based metabolic resistance on the efficacy of bed nets using semi-field experimental hut trials:** A) Susceptibility profile of the hybrid strain generated from crossing the highly resistant (FUMOZ) and highly susceptible (FANG) strains. Perm is permethrin, Delt is deltamethrin and Ben is bendiocarb. B) Mortality rates of the FANG/FUMOZ hybrid strain at two time-points exposure to validate the correlation between *CYP6P9a* and resistance phenotypes to pyrethroids. C) Distribution of the *CYP6P9a* genotypes according to resistance phenotypes. D) Strong correlation between *CYP6P9a* alleles and survival to PermaNet 2.0 exposure in experimental huts. E) *CYP6P9a*-R allele increases the ability of resistant mosquitoes of taking a blood meal in contrast to susceptible ones when exposed to PermaNet 2.0 but not for the untreated nets F).

**Table S1.** Descriptive statistics of RNAseq sequence read data and alignments for different samples

Sample ID	Untrimmed reads	Trimmed reads	R1/R2 pairs <sup>1</sup>	R0 reads (%) <sup>2</sup>	Reads to align (R1+R2)	Aligned reads (%) <sup>3</sup>	Aligned R1 (%) <sup>4</sup>	Aligned R2 (%) <sup>4</sup>	Aligned in pair (%) <sup>4</sup>	Properly paired (%) <sup>4,5</sup>
FNG-UNX-000A-01	61,161,962	60,814,246	30,239,816	334,614 (0.55%)	60,479,632	34,529,287 (57%)	17,175,707 (50%)	17,353,580 (50%)	32,558,814 (94%)	30,926,294 (90%)
FNG-UNX-000A-02	44,384,316	43,991,605	21,866,954	257,697 (0.59%)	43,733,908	38,784,564 (89%)	19,455,342 (50%)	19,329,222 (50%)	37,497,734 (97%)	35,662,300 (92%)
FNG-UNX-000A-03	55,329,478	55,003,414	27,346,953	309,508 (0.56%)	54,693,906	41,539,393 (76%)	20,695,859 (50%)	20,843,534 (50%)	39,451,822 (95%)	37,642,472 (91%)
FNG-UNX-000A-07	61,708,692	60,522,621	30,147,658	227,305 (0.38%)	60,295,316	52,613,292 (87%)	26,304,258 (50%)	26,309,034 (50%)	51,355,756 (98%)	49,077,570 (93%)
GHA-PER-060A-01	56,393,812	56,004,973	27,858,160	288,653 (0.52%)	55,716,320	47,383,161 (85%)	23,661,891 (50%)	23,721,270 (50%)	45,701,704 (96%)	43,711,894 (92%)
GHA-PER-060A-02	56,146,206	55,778,128	27,745,363	287,402 (0.52%)	55,490,726	47,385,531 (85%)	23,689,592 (50%)	23,695,939 (50%)	45,668,698 (96%)	43,627,620 (92%)
GHA-PER-060A-03	46,339,060	45,931,585	22,853,504	224,577 (0.49%)	45,707,008	35,745,010 (78%)	17,841,177 (50%)	17,903,833 (50%)	34,393,520 (96%)	32,935,172 (92%)
CMR-PER-060A-01	45,564,004	45,336,332	22,563,410	209,512 (0.46%)	45,126,820	29,760,118 (66%)	14,809,654 (50%)	14,950,464 (50%)	28,136,026 (95%)	26,881,776 (90%)
CMR-PER-060A-02	49,616,994	49,369,073	24,565,403	238,267 (0.48%)	49,130,806	36,825,328 (75%)	18,551,507 (50%)	18,273,821 (50%)	34,658,598 (94%)	32,960,464 (90%)
CMR-PER-060A-03	56,448,220	55,238,405	27,521,162	196,081 (0.35%)	55,042,324	44,353,985 (81%)	22,394,524 (50%)	21,959,461 (50%)	42,605,426 (96%)	40,679,444 (92%)
UGA-PER-060A-02	63,577,506	62,233,533	30,965,317	302,899 (0.49%)	61,930,634	49,080,456 (79%)	24,430,318 (50%)	24,650,138 (50%)	47,225,124 (96%)	45,294,140 (92%)
UGA-PER-060A-03	74,281,024	72,571,899	36,050,602	470,695 (0.65%)	72,101,204	58,908,769 (82%)	29,401,087 (50%)	29,507,682 (50%)	56,385,738 (96%)	53,742,224 (91%)
UGA-PER-060A-04	57,574,274	55,614,929	27,652,993	308,943 (0.56%)	55,305,986	43,887,550 (79%)	21,868,261 (50%)	22,019,289 (50%)	42,252,224 (96%)	40,393,696 (92%)
MWI-PER-060A-06	72,542,372	72,016,218	35,777,777	460,664 (0.64%)	71,555,554	62,665,469 (88%)	31,430,727 (50%)	31,234,742 (50%)	60,517,686 (97%)	57,445,876 (92%)
MWI-PER-060A-07	65,422,634	64,501,521	32,092,002	317,517 (0.49%)	64,184,004	56,244,764 (88%)	28,121,863 (50%)	28,122,901 (50%)	54,471,126 (97%)	52,005,820 (92%)

<sup>1</sup> Forward (R1) and reverse (R2) read pairs after trimming.

<sup>2</sup> Reads unpaired after trimming (% of total trimmed reads).

<sup>3</sup> % of reads to align.

<sup>4</sup> % of aligned reads.

<sup>5</sup> Properly paired means both read and its mate are mapped to opposing strands of the reference sequence, with 3' ends innermost and 5' ends within the allowed distance from each other (50-600 bp).

**Table S2:** Detoxification-associated genes differentially expressed between the four pyrethroid resistant populations and the FANG susceptible strain

Gene ID	CMR	GHA	MWI	UGA	Description	FG_S	CMR	GHA	MAL	UG
AFUN010543	6.6	5.4	30.7	48.9	CCChain Structural Basis	0.28	0.98	2.8	7.1	8.9
AFUN011806	4.2	2.1	13.2	6	chymotrypsin-like elastase family member 2A	0.17	0.65	0.4	3.3	1.2
AFUN001444	14	6.2	4.4	3.2	chymotrypsin-like elastase family member 2A	4.5	56.8	31.5	28.9	16.3
AFUN015830	2.4	2.6	3.9	2.2	Cytochrome P450, CYP325C	1.43	3.1	4.2	8.15	3.5
AFUN015966	26.9	6	5.1	2.2	Cytochrome P450, CYP325A	0.74	17.4	4.8	5.2	1.8
AFUN015894	3.1	2.3	7.5	3.7	Cytochrome P450, CYP4H26	0.3	0.9	0.85	3.6	1.4
AFUN015792	2.1	6.3	60.5	2.7	Cytochrome P450, CYP6P9a	14.9	28.7	106.2	1355	45.6
AFUN015889	4.4	6.9	23.9	7	Cytochrome P450, CYP6P9b	11.5	45.3	88.8	401.7	92.2
AFUN015777	2.6	2.3	5.3	3.5	Cytochrome P450, CYP4C26	0.5	1.1	1.2	3.6	1.9
AFUN015839	2.6	4.9	3.3	3	glutathione S-transferase, GSTD3	25.3	60.2	137.8	122.5	87.1
AFUN016008	4.8	3.5	4.1	3.4	glutathione S-transferase, GSTE6	8.3	36.3	32.7	50.2	32.3
AFUN004582	2.8	3.7	2.8	3.1	methyltransferase 2-A	0.7	1.8	2.8	2.8	2.4
AFUN010812	4.9	2.9	9.6	3.1	General odorant-binding 45	0.4	1.2	0.9	4	1
AFUN015887	2.6	2.3	2.2	2.5	Gustatory receptor 68a	7.5	17.4	19	23.9	21.8
AFUN006831	3.6	2.2	3.7	4.4	General odorant-binding	0.4	0.8	0.6	1.3	1.2
AFUN007097	2.8	8.2	4.6	4	cuticular_protein_RR	0.5	0.9	3.1	2.3	1.6
AFUN005949	3.3	4.6	6.2	2.7	General odorant-binding 70	0.3	1	1.7	3	1.1
AFUN004398	5.5	4.4	7.5	7.5	cuticular_protein_TWDL_family_(TWDL12)	0.7	1.1	1	2.3	1.8
AFUN015818	6	3.6	11.8	4.1	Gustatory receptor for sugar taste 64b	0.4	1.1	0.8	3.5	0.9
AFUN001299	3.5	3	2.6	3.7	NTF2-related export 2	6.9	21.5	23.4	26.5	29
AFUN003480	2.4	2.7	3.7	2.7	serine protease 27-like	0.9	2	2.8	5	2.9
AFUN010184	2.2	2.4	2	3.3	transcription factor GATA-3-like isoform X1	1.3	2.6	3.5	3.9	5
AFUN007410	2.9	2.5	2.9	2.1	transmembrane protease serine 9-like	110.5	288.2	304	461.2	269.1
AFUN007052	5.1	3.5	6	4.2	zinc finger 345-like isoform X1	1.1	1.8	1.5	3.3	1.8
AFUN009311	2.3	2.3	2.4	2.3	zinc finger 391-like isoform X1	11.5	23.4	29.1	40.9	30.6
AFUN010612	3.2	3	2.4	3.9	zinc finger 883-like isoform X2	1.7	4.9	5.7	6.1	7.8
AFUN015890		44.8	5.9	2.1	Cytochrome P450, CYP6P4	2.3	3.6	114.2	19.7	5.5
AFUN015891		23.9	3.7	2.7	cytochrome P450 CYP6P4-like	17.1	16.2	456.2	91.8	52.1
AFUN016010		2.2	2	2.2	glutathione S-transferase, GSTD1	117.8	186.4	292	348.5	297.9
AFUN000474	3.2		4.7	2.1	Gustatory receptor for sugar taste 43a	1.5	4.2	2.7	9.8	3.6
AFUN000064	3.1		4.7	3.1	Cuticular Protein as AGAP010105-PA	0.7	2.1	1.6	5	2.7



AFUN010577	2.1		2.9	2.2	chymotrypsin-like elastase family member 2A	1.5	2.9	2.7	6.5	3.8
AFUN006858	2.3		2.1	2.1	cytochrome P450 CYP306A1	8.2	17.4	17.8	24.9	19.8
AFUN006563	2.7		3.9	3.3	Cuticular protein	0.4	0.11	0.078	0.26	0.18
AFUN015888	6.3	5.8		4.1	Cytochrome P450, CYP6P5	6.3	36.2	41.1	8.5	29.6
AFUN005715	2.2	2.3		2.3	Cytochrome P450, CYP315A1	10	19.8	25.5	28.3	26.7
AFUN003202	2.2	2.1		2.1	nucleoporin Nup43	6.8	13.7	15.8	18.8	16.2
AFUN006467	2.2	2.7		3.2	zinc finger 391-like isoform X1	7.2	14.5	21.4	17.9	26.9
AFUN002969	2.6	2		2.4	zinc transporter ZIP10-like	10.6	24.8	24	22.9	29.3
AFUN006135	2.2	2.9	2.6		Cytochrome P450, CYP4C36	8.8	17.5	29	33.3	14.5
AFUN015808	2.5	3.3	2.3		glutathione S-transferase GSTE3	63.9	143.7	238.6	210.8	124
AFUN015807	3.5	3.7	2.8		glutathione S-transferase GSTE1	5.2	16.5	21.7	20.9	9.3
AFUN015809	5.9	8.3	2.3		glutathione S-transferase GSTE2	42.7	227	398.4	143.4	78.2
AFUN015811	3	2.3	2.2		glutathione S-transferase GSTE5	28.3	76.9	73	89.4	49.4
AFUN011266	3.1	2.7	4.9		UDP-glucuronosyltransferase	2.3	6.5	6.9	16.3	4.3
AFUN015817	3.8	2.3	7.2		Gustatory receptor for sugar taste 64e	0.4	0.7	0.5	2.1	0.4
AFUN000622	2.5	2.1	2.9		solute carrier family 23 member 2	7.2	16.2	16.7	30.1	12
AFUN006863	2.1	2.1	2		zinc finger 345-like isoform X4	6.7	12.6	15.6	20	13.4
AFUN000799	2.2	2	2.3		zinc finger CCHC-type	12.7	25.7	28.7	43.4	27
AFUN015907			2.2	2.4	gastrula zinc finger -like isoform X1	8.4	14.9	18.6	26.7	23.6
AFUN010481			4.4	3.1	Cuticular protein	0.11	0.3	0.06	0.53	0.3
AFUN010539			2.3	2	cuticular_protein_RR-2_family_(CPR143)	2.1	3.2	4.6	7	4.9
AFUN004166			2.5	3.1	gustatory receptor 28b	2.8	4.8	5.8	10.3	10
AFUN008855			3.9	2.8	nuclear receptor subfamily 2 group C	0.9	0.5	0.8	4.8	2.7
AFUN005273			2	2.6	zinc finger 883-like isoform X2	3.7	5.1	6.4	11	11
AFUN001382	2.7	2.4			Cytochrome P450, CYP9J11	69.5	87.3	206.1	241.7	144
AFUN001383	2.4	3.1			Cytochrome P450, CYP9J11	20.5	23.5	54.2	93	36.4
AFUN015795	2.2	2.2			Cytochrome P450, CYP6M7	118.7	119.1	297.8	372	150.8
AFUN015767	3	2.9			glutathione S-transferase, GSTD11	1.8	2.3	6	7.6	2.2
AFUN012021	2.4	5.9			Cuticular protein	0.16	0.22	0.33	1.1	0.17
AFUN007247	2.1	2.3			Odorant binding 45	1.2	1.2	2.7	3.8	2.5
AFUN001415	2.1	2.2			polypeptide N-acetylgalactosaminyltransferase 11	7.7	12	17.9	24.3	12.9
AFUN010918	2.1	3.2			Cytochrome P450, CYP6N1	18.7	29.6	43.3	86.6	21.6

AFUN007143	2.5	2.2	alkaline phosphatase	18.7	42.2	35.1	59.7	22.9
AFUN009142	2.9	2.4	aminopeptidase Ey-like	20.2	52.4	32.2	70	16.8
AFUN003099	3.8	3.2	arginase	6.6	22.6	13.5	30.8	7.8
AFUN000422	2	2.1	Carboxylesterase	0.8	1.4	0.9	2.4	0.7
AFUN007080	2.2	3.7	caspase-9	5.7	11.1	11	30.8	8.3
AFUN014849	2	2	CCR4-NOT transcription complex subunit 11	5.8	10.5	10.1	17.2	10.6
AFUN008239	2.4	3.9	cytosolic sulfotransferase 3-like isoform X2	15.3	33.6	33.7	86.1	21.7
AFUN007291	2.4	2.1	glutathione S-transferase GSTT2?	13.8	30.2	28.4	42.6	20.6
AFUN015936	2.6	2.7	Gustatory receptor for sugar taste 64a	4.9	11.4	9.5	19	6.4
AFUN006160	2.8	2.5	oocyte zinc finger 6-like	4.1	10.5	8	15.2	9.4
AFUN015810	2.4	3.6	glutathione S-transferase, GSTE4	69.1	151.6	276.7	164	69.6
AFUN002514	5.5	3.6	Carboxylesterase	32.2	160.5	130.6	67.5	43.9
AFUN000001	3.7	2.1	probable chitinase 3	26	85.8	60.5	64.5	15.8
AFUN007549	2.9	5.2	cytochrome_P450 CYP9K1	35.5	36.5	115.9	102.8	212
AFUN002602	2.1		cytochrome b561 domain-containing 2	34.5	65.2	50.3	87.9	41.2
AFUN007526	2.3		cytochrome c oxidase assembly COX19	17.1	35.6	30.4	28.8	29.9
AFUN015723	2		Cytochrome P450, CYP6AH1	22.2	40.5	32	55.9	21.1
AFUN006288	2.6		glycine dehydrogenase (decarboxylating)	57.3	133.8	81.8	157.2	68.4
AFUN008852	2		Glycosyltransferase involved in cell wall bisynthesis	6.6	12	12.9	18.7	14.3
AFUN002311	2.1		monothiol Grx4 family	76.3	141.2	126.6	175.9	142.7
AFUN007415	2.3		7 kDa salivary gland allergen	153.3	313.8	305	276.8	104.5
AFUN004413	2.1		nucleoporin NDC1 isoform X1	12.9	25.1	22.9	32.7	23.4
AFUN008376	2.1		V A-type H <sup>+</sup> -transporting ATPase subunit B	245.5	473.3	298.5	400	484.2
AFUN008872	2.4		Zinc carboxypeptidase	191	412.8	367.9	356.6	289.7
AFUN009750	2		alkaline phosphatase	7.6	8.9	17.1	20.7	14.5
AFUN002978	2		Cytochrome P450, CYP314A1	5.3	8.3	12.2	15.2	10.8
AFUN008819	2		glutathione S-transferase, GSTMS3	8	4.8	18.3	17.1	6.4
AFUN001429		2.4	alkaline phosphatase	3.7	5.6	3.1	13	2.7
AFUN010814		2.5	Alpha beta hydrolase family	0.8	0.8	0.4	2.8	0.7
AFUN004002		2.4	argininosuccinate lyase	177.4	257	252.8	616.9	170.4
AFUN007079		2.9	caspase-9	18.5	33.3	29.2	78.8	21.8

AFUN009199	2.5	chitin synthase	19.8	27.3	42.3	71.3	34.7
AFUN014173	2.7	chymotrypsin-like elastase family member 2A	13.2	21.8	19.9	51.8	18.1
AFUN004870	2.7	chymotrypsin-like elastase family member 2A	3.5	3.9	7.6	13.5	6.5
AFUN015895	2.4	Cytochrome P450, CYP4H25	3.3	2.5	4.5	11.7	3.6
AFUN015785	2.2	Cytochrome P450, CYP6AA2	9.1	13.8	15.4	29.6	11
AFUN015909	2.3	cytochrome P450	3	4.4	5	9.7	6
AFUN015841	2.2	glutathione S-transferase GSTD4	4.4	2.3	6.5	13.9	3.8
AFUN015768	2.3	glutathione S-transferase, GSTD11	13.5	21.5	27.9	45	14.4
AFUN008560	2.6	glutathione S-transferase	8.4	11.3	17	31.6	18.2
AFUN002910	3.4	lipase member H-like	2.1	2.7	1.9	10.6	1.9
AFUN007911	2.1	Solute carrier family 46 member 3	40.4	60.9	82.1	120.7	58.6
AFUN009946	3.6	Chymotrypsin-elastase inhibitor ixodidin	0.1	0.1	0.1	0.4	0.1
AFUN007416	2.7	37 kDa salivary gland allergen	4.2	7.3	5.8	16.7	4.5
AFUN015951	2.7	Gustatory receptor 8a	1.2	1.2	0.8	4.9	1.5
AFUN010684	3.6	Cuticular protein RR	0.1	0.19	0.03	0.34	0.18
AFUN016007	3.1	Gustatory receptor for sugar taste 43a	1	1.5	0.7	4.4	1.3
AFUN015901	2.2	Odorant receptor Or2	2.6	1.9	1.5	8.2	2.3
AFUN008524	2.2	Odorant receptor 22c	2.1	2.2	1.1	6.8	1.5
AFUN015721	2.6	Odorant receptor 4	1.1	1.2	0.6	4	1
AFUN010920	5.5	cytochrome P450 partial, CYP6M1b	0.18	0.09	0.1	0.99	0.13
AFUN015933	3.2	gustatory receptor 2a	0.5	0.8	0.6	2.1	1
AFUN008427	2.1	Gustatory receptor for sugar taste 64a	3.8	6.4	5.8	11.8	3.1
AFUN000851	3.1	N-alpha-acetyltransferase 40	2.3	3.8	3.3	10.2	2.7
AFUN001353	2.4	odorant-binding OBP56d- partial	0.9	0.5	0.7	3.1	1
AFUN010884	2	oocyte zinc finger 6-like	6.2	10.8	12.3	18.5	14
AFUN000174	3.5	peritrophin-1 [Culex quinquefasciatus]	1.2	0.8	1.4	5.8	2.5
AFUN015801	2.5	cytochrome P450, CYP6P2	27.3	23	36.9	98.9	16.8
AFUN010874	2	zinc finger 2 homolog isoform X1	8.5	13.6	14.2	25.3	15.2
AFUN007113	2	zinc finger 2 homolog isoform X1	6.6	8.3	11	19.5	11
AFUN014520	2.1	CCR4-NOT transcription complex subunit 7 isoform X1	12.2	21.1	23.7	20.3	29.1
AFUN006799	45	lipase member H-like	0	0	0	0	15.8

AFUN011526	2.2	microtubule-associated RP EB family member 3 isoform X2	17.2	23.1	32.4	44.1	42.7
AFUN000877	2	OR94A_DROME ame: Full=Odorant receptor 94a	4.9	4.7	5.8	10.5	11.5
AFUN006418	4	cuticular_protein_RR-3_family_(CPR111)	0.7	1.2	0.8	1.3	3.3
AFUN011733	2.8	Carboxylesterase	13.6	23.9	23.4	37.7	44.4
AFUN005433	2.1	solute carrier family 35 member F5	11.4	11.3	23.5	22.7	27.3

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**Table S3.** Descriptive statistics of Whole genome POOLseq sequence read data

Sample name	Untrimmed reads	Trimmed reads	R1/R2 pairs <sup>1</sup>	R0 reads (%) <sup>2</sup>
FUMOZ	98,333,448	97,312,008	48,166,137	979,734 (1.01%)
FANG	103,497,770	102,476,042	50,736,627	1,002,788 (0.98%)
MWI-PER-060-DEAD-A	122,744,088	121,558,527	60,196,626	1,165,275 (0.96%)

<sup>1</sup> Forward (R1) and reverse (R2) read pairs after trimming

<sup>2</sup> Reads unpaired after trimming (% of total trimmed reads)

**Table S4:** Counts of reads aligned at the left and right breakpoints of the 6.5 kb insertion supporting different haplotypes

Location/Colony	Year	Genomes	Insertion	Insertion	Deletion	Deletion	“Parental”	“Parental”
			(left)	(right)	(left)	(right)	(left)	(right)
FUMOZ	n/a	38	<b>43</b>	<b>44</b>	0	0	22	16
FANG	n/a	40	0	0	24	30	15	23
Malawi	2014	40	<b>11</b>	<b>15</b>	0	1	9	12

“Insertion”=insertion present between *CYP6P9a* and b; “Deletion”=insertion absent between *CYP6P9a* and b;

“Parental”=read originating from elsewhere in the genome, from where the inserted sequence was derived.

**Table S5:** Population genetic parameters of the 800bp fragment upstream of *CYP6P9a*

<b>Total</b>	<b>N</b>	<b>S</b>	<b>h</b>	<b>hd</b>	$\pi$	<b>k</b>	<b>D</b>	<b>D*</b>
Malawi Pre-bednet	24	61	19	0.97	0.027	18.26	0.13ns	0.14ns
Mozambique Pre-bednet	15	25	12	0.96	0.012	8.36	0.36ns	-0.72ns
Total Pre-bednet	39	74	30	0.98	0.025	17.21	-0.28ns	-1.04ns
Malawi Post-bednet	18	4	2	0.11	0.00066	0.44	-1.85*	-2.5*
Mozambique Post-bednet	34	3	4	0.365	0.0008	0.53	-0.6ns	0.93ns
Total Post-bednet	52	7	5	0.283	0.00077	0.52	-1.74ns	-1.90ns
Total all	91	76	34	0.72	0.019	13.1	-0.62	-1.94

N= number of sequences (2n); S, number of polymorphic sites; h, number of haplotypes; hd, haplotype diversity;  $\pi$ , nucleotide diversity (k= mean number of nucleotide differences); D and D\* Tajima's and Fu and Li's statistics; ns, not significant; \* significant P<0.05.

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**Table S6:** Correlation between genotypes of *CYP6P9a* and mortality (PermaNet 2.0) and blood feeding after the experimental hut trial with the FANG/FUMOZ strain

		<b>OR</b>	<b>P</b>	<b>CI</b>
<b>Mortality</b>				
Unfed	RR vs SS	34.9	<0.0001	15.8-77.1
	RS vs SS	19.9	<0.0001	9.7-40.9
	RR vs RS	1.75	0.26	0.81-3.8
	R vs S	6.25	<0.0001	3.3-11.7
All samples	RR vs SS	10.82	<0.0001	5.6-20.8
	RS vs SS	5.3	<0.0001	2.8-9.8
	RR vs RS	2.04	0.0002	1.1-3.7
	R vs S	3.17	0.02	1.78-5.65
<b>Blood feeding</b>				
PermaNet 2.0	RR vs SS	1.75	0.19	0.82-3.7
	RR vs RS	2.5	0.052	1.09-5.75
	RS vs SS	0.7	0.67	0.28-1.7
	R vs S	1.43	0.26	0.82-2.5
PermaNet 3.0	RR vs SS	4.54	<0.0001	2.3-8.7
	RR vs RS	2.6	0.0012	1.43-4.7
	RS vs SS	1.74	0.17	0.87-3.47
	R vs S	2.14	0.18	1.17-3.19

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Mortality rates were assessed only for PermaNet 2.0 because mortality levels were very high for PermaNet 3.0.



**Table S7:** Primers used for characterization of the promoter of *CYP6P9a*

<b>Primer name</b>	<b>sequence</b>
6P9a1F	TCCCGAAATACAGCCTTTCAG
6P9Ra/b	TACTGCGGACACTACGAAG
6P9a5F	AGCGGAAGGGGTTTTGTAG
6P9a5R	CTTCTGTGATGCCCAAAT
6P9a3.2F	CAATGCTGCTTTCCTTCACA
SacIFU-6P9a0.8	CGAGCTCGTCCCGAAATACAGCCTTTCAG
SacIFU-6P9a0.5F	CGAGCTCGATCCCTAACTATTAAGGCAAT
SacIFU-6P9a.03F	CGAGCTCGTGCAGGGAAAAGGAGGACAT
Sac1FU-6P9a0.15F	CGAGCTCGCACGCACACTGACATGATGT
MluIFU-6P9Ra/b	CGACGCGTTCGTAAGTACACTGCGGACACTACGAAG
KpnIFA-6P9a0.8F	CGGGGTACCCCGTCCCGAAATACAGCCTTTCAG
KpnIFA -6P9a0.5F	CGGGGTACCCCG ATCCCTAACTATTAAGGCAAT
KpnIFA -6P9a0.3F	CGGGGTACCCCGTGCAGGGAAAAGGAGGACAT
KpnIFA -6P9a0.15F	CGGGGTACCCCGCACGCACACTGACATGATGT
HindIII -6P9Ra/b	CCCAAGCTTGGGCCGTACTGCGGACACTACGAAG