

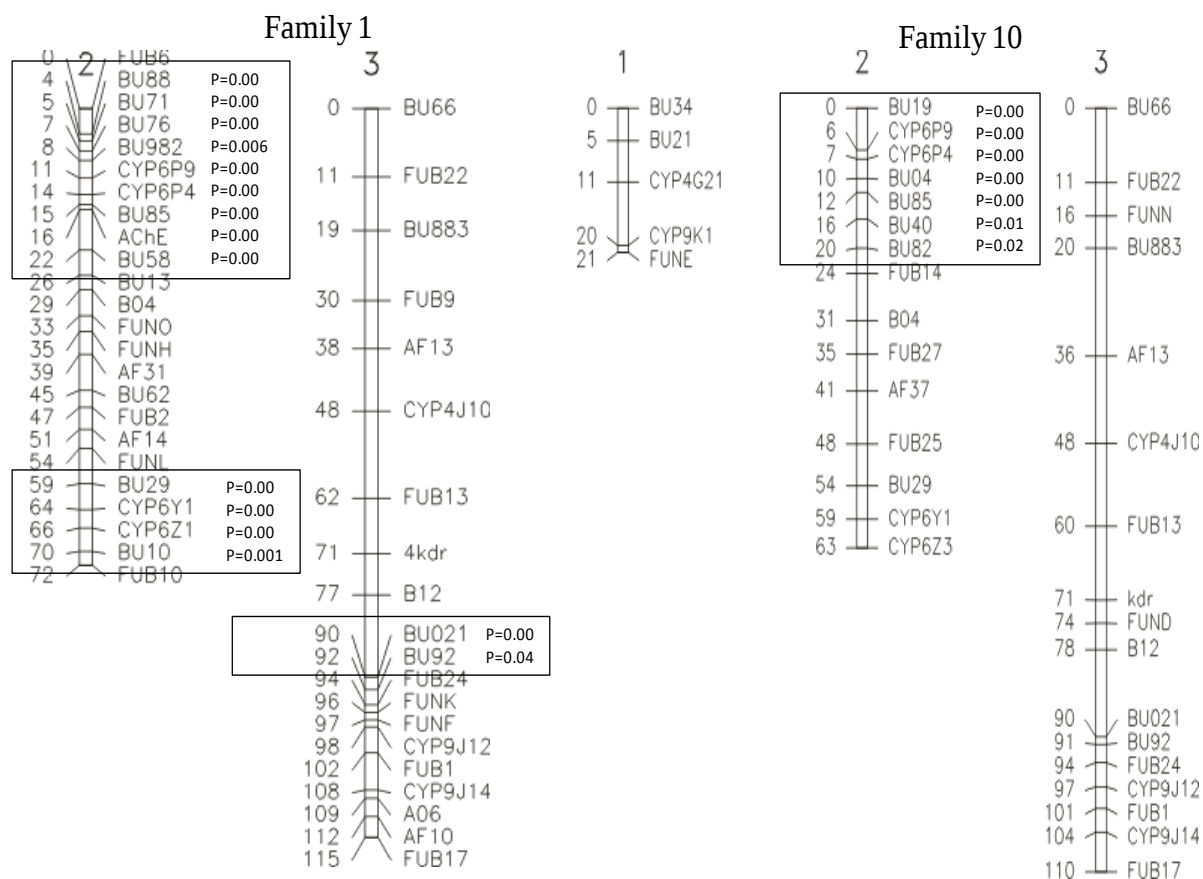
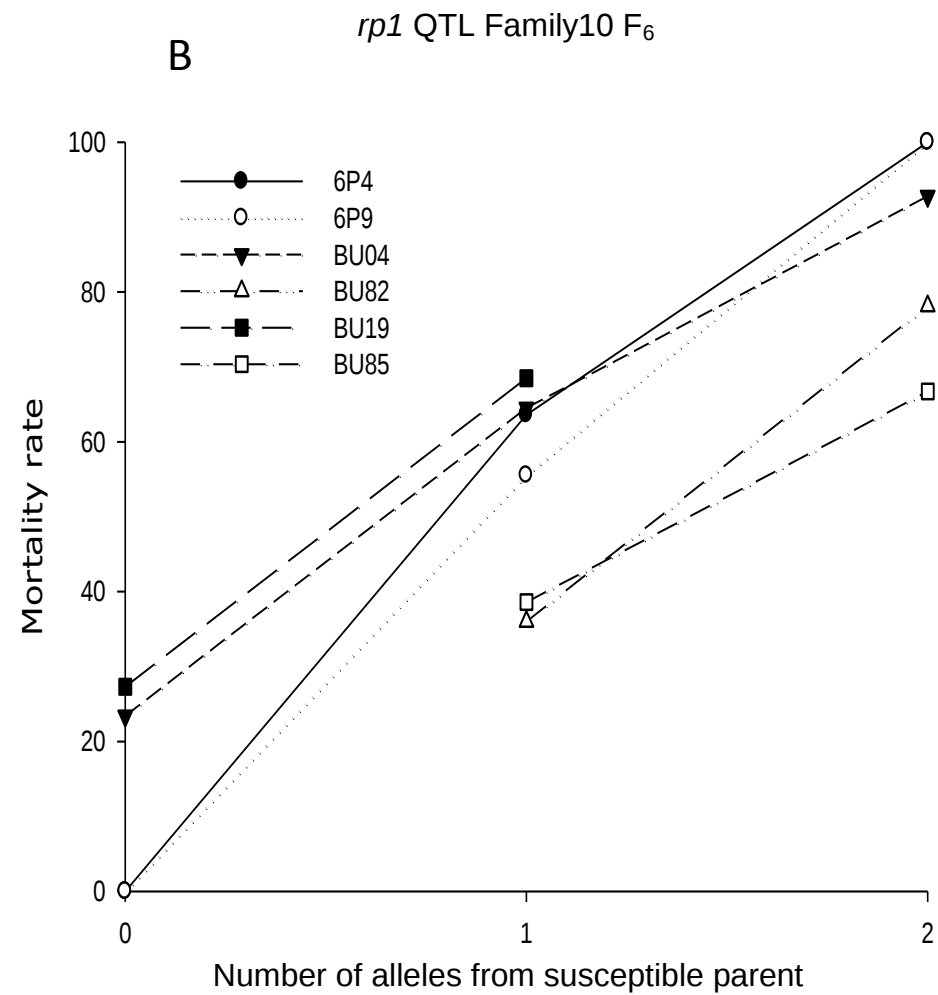
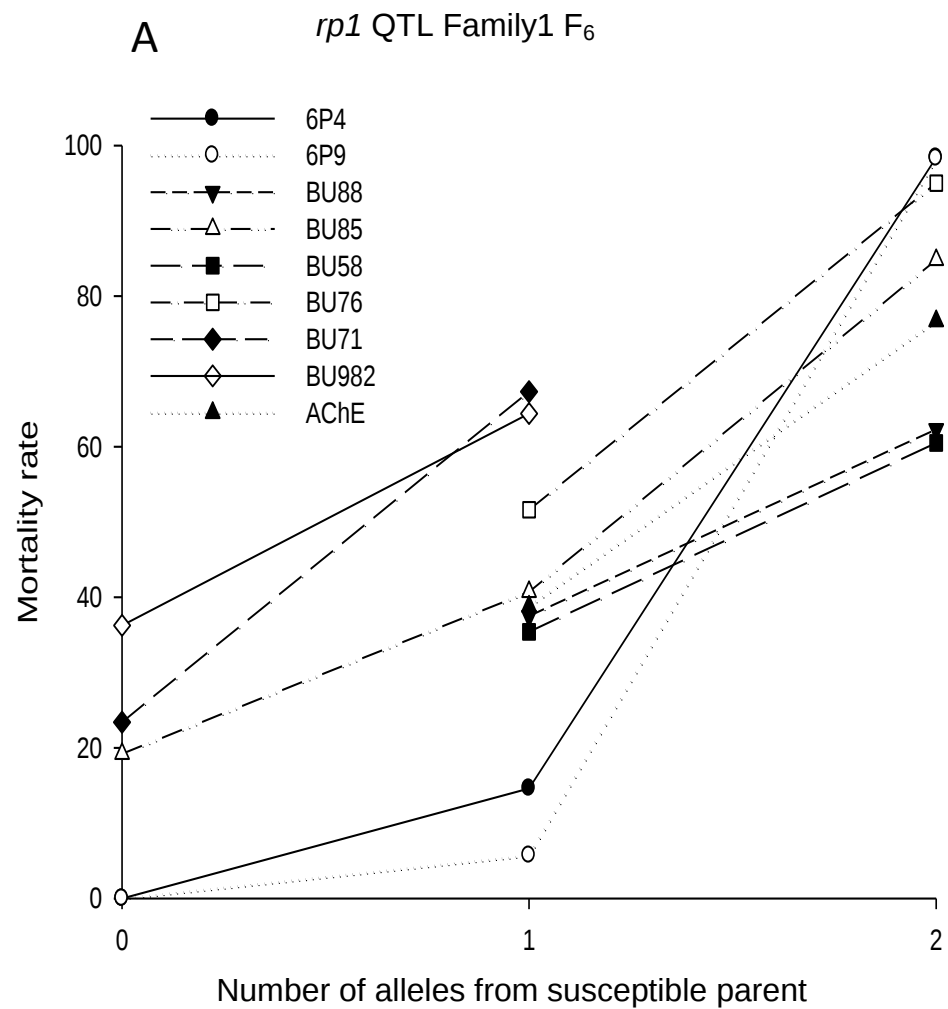


Figure S1: Linkage maps of Family 1 (♀susceptible x ♂resistant) and Family 10 (♀resistant x ♂susceptible). Loci that are statistically associated with pyrethroid resistance appeared in boxes with their *P* values.



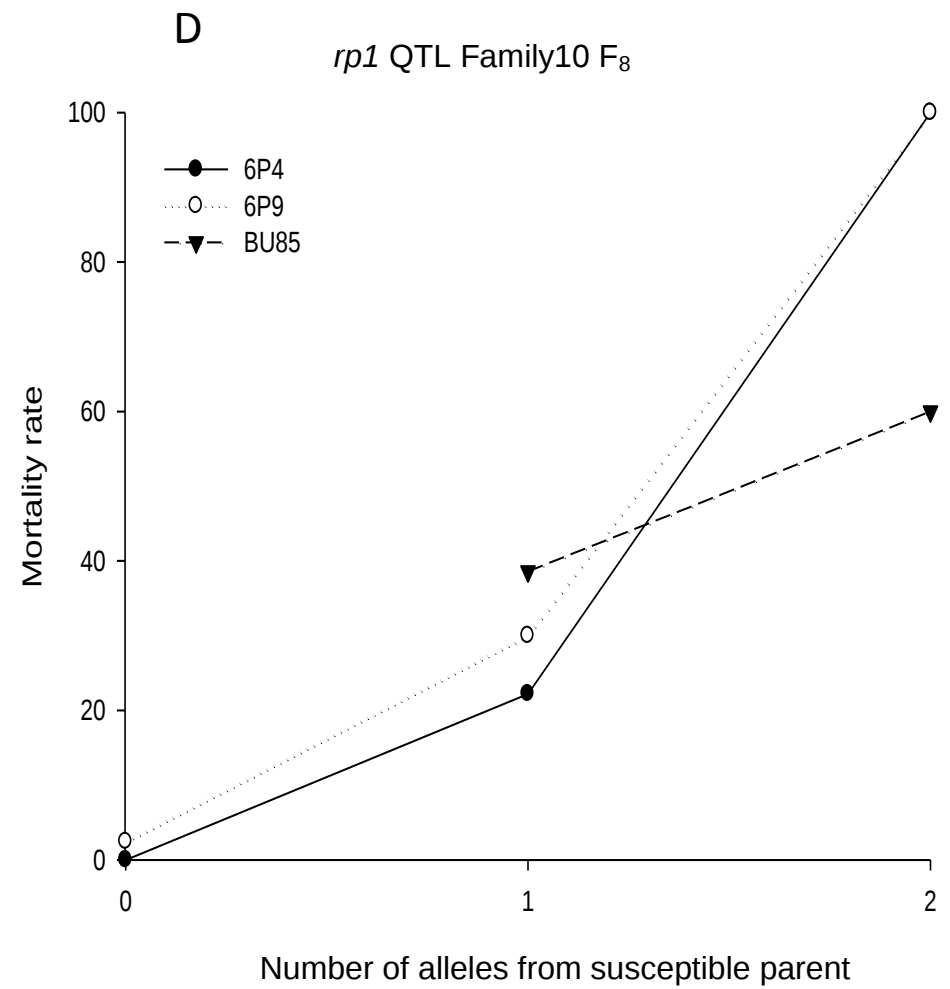
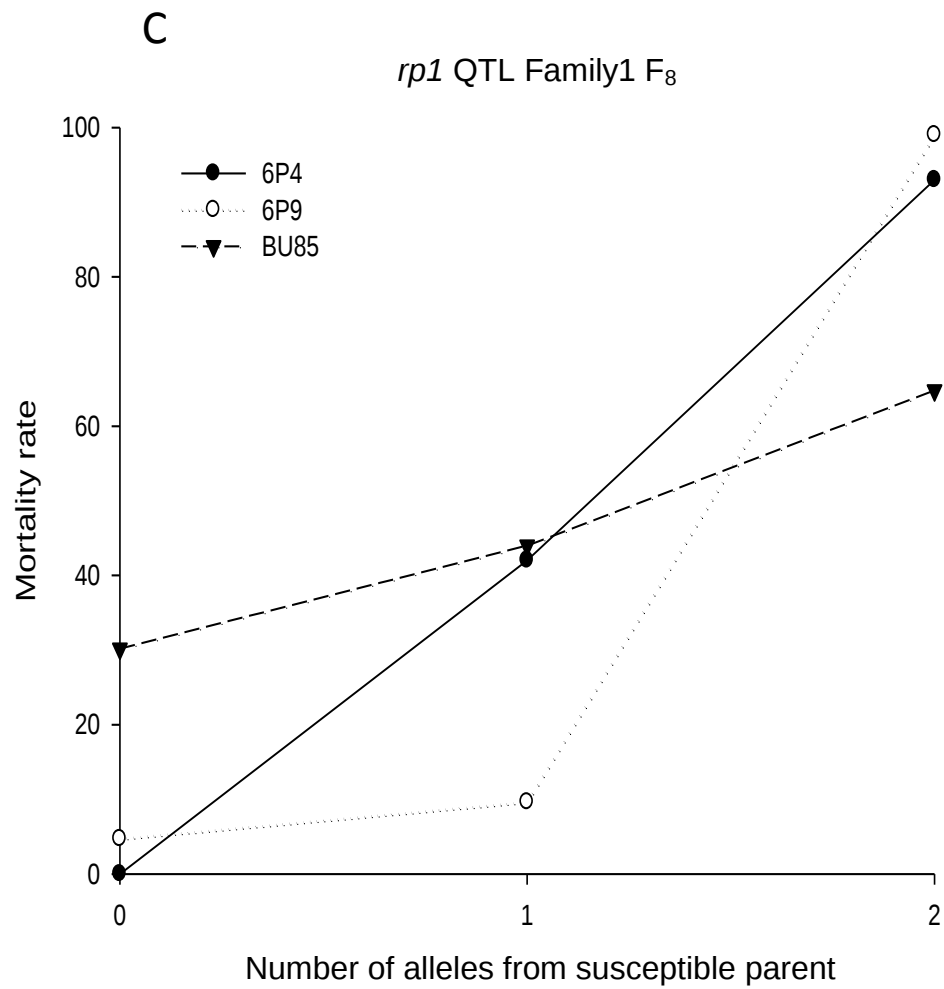


Figure S2: Plot of mortality as a function of alleles inherited from susceptible parents at loci associated to resistance at F₆ generation for Family 1 (S2A) and Family 10 (S2B) and at F₈ generation for Family 1 (S2C) and in Family 10 (S2D).

A

CYP6P4a	MD F LG YVLTAFV FVVSIA YLYLRSRHNYWRDRGIPYARGKPHLFMGHMEQ F STKHG S YIN 60
CYP6P4b	MD L LG YVLTAFV FVVSIA YLYLRSRHNYWRDRGIPYARGKPHLFMGHMEQ A NTKH T S I YIN 60
CYP6P4a	QE IYQDLKSRGE A FGG I S F FFLPGLMVVDPELVKTI LVKDFNVFHDGRGVFNDAKSDPLSA 120
CYP6P4b	QE IYQDLKSRGE T FGG M N I FLLPGLMVVDPELVKTI LVKDFNVFHDGRGVFNDAKSDPLSA 120
CYP6P4a	HLFALEGP EWRVLRQKLTPTFTSGRMKQMFGTIQQVAQEFLKYMNNENCHREMEMKDV LAR 180
CYP6P4b	HLFALEGP EWRVLRQKLTPTFTSGRMKQMFGTIQQVAQEFLKYMNNENCHREMEMKDV LAR 180
CYP6P4a	FTTDVIGTCAFGIECNTLKNPDSE F RYGNKVFEQDT V LMVKFVF F ATVFKGLAKRIGVKL 240
CYP6P4b	FTTDVIGTCAFGIECNTLKNPDSE R RYGNKVFEQDA V IMVKFVF V MMFKGLAKRIGVKL 240
CYP6P4a	TDEGVERFFLQVVRDTVQYREMNNVQRNDFMNL LLQIKNKG YLDERDIGANDNLKGETAM 300
CYP6P4b	TDEGVERFFLQVVRDTVQYREMNNVQRNDFMNL LLQIKNKG YLDERDIGANDNLKGETAM 300
CYP6P4a	TLNELAAQVFVFFLAGFETSSTTMNFCLYELAKNPDIQERLREEIERGVEDHGGQV TYEM 360
CYP6P4b	TLNELAAQVFVFFLAGFETSSTTMNFCLYELAKNPDIQERLREEIERGVEDHGGQV TYEM 360
CYP6P4a	VMNNQYLDNVINETLRKYPPIESLSRVPIRDY TIPG TKHVIPKDT L V Q LIPVYAIQRDPEF 420
CYP6P4b	VMNNQYLDNVINETLRKYPPIESLSRVPIRDY TIPG TKHVIPKDT F I Q IIPVYAIQRDPEF 420
CYP6P4a	YPEPDQFNPD RFLPEEVKQRHPYVFLPFGE GPRICIGLRFGMM Q TKLGLITLLRNFRFSP 480
CYP6P4b	YPEPDQFNPD RFLPEEVKQRHPYVFLPFGE GPRICIGLRFGMM A KLGLITLLRNFRFSP 480
CYP6P4a	SSQTPSELVFDPKSFILSP S TGNYLK I DKL--- 510
CYP6P4b	SSQTPSELVFDPKSFILSP T TGNYLK V DK I EG F 513

B

CYP6P9a	MELINVVLA AFIFVVS AVYLFIRNKHNYWKDNGFPYAPNPHFLFGHAKGQAQTRHAADIH 60
CYP6P9b	MELINVVLA AFIFVVS AVYLFIRNKHNYWKDNGFPYAPNPHFLFGHAKGQAQTRHAADIH 60
CYP6P9a	LELYKKFKQR R ERYVGMSQFM I PS L LVIDPELVKTI LVKDFNV F HDHG V FNNARDDPLS A 120
CYP6P9b	LELYKKFKQR G DRYVGMSQF I IP S V F VIDPELVKTI LVKDFN I FHD R GV F IT N ARDDPLS G 120
CYP6P9a	HLFALEGNPWRLLRQKLTPTFTSGRMKQMFGT LWDALELDKYMEENYRQPDIE MKDVLG 180
CYP6P9b	HLFALEGNPWRLLRQKLTPTFTSGRMKQMFGT LWDALELDKYMEENYRQPDIE MKDVLG 180
CYP6P9a	RFTTDVIGTCAFGIECNTLKTDPDSEFRKYGNKA F E F N L M I I L K T FLASAYPSLVRKL RMK 240
CYP6P9b	RFTTDVIGTCAFGIECNTLKTDPDSEFRKYGNKA F E L D L L I M M K E FFASAYPSLVRKL RMK 240
CYP6P9a	ITFDDVE Q FFLKIV K ET V EY R ES N N I KRNDFMNL LLQIKNKG KLDSDSDGSGVGKEVGMT 300
CYP6P9b	ITFDDVE E FF V KIV R ET V NY R EMNN V KRNDFMNL LLQIKNKG KLDSDSDGSGVGKEVGMT 300
CYP6P9a	Q R ELAAQAF I FFLAGFETSSTTQSFCLYELAKNPDIQERLRQEINQAIEENDGQV TYDVA 360
CYP6P9b	Q L ELAAQAF V FFLAGFETSSTTQSFCLYELAKNPDIQERLRQEINQAIEENDGQV TYDVA 360
CYP6P9a	MNIQYLDNVINETLRKYPPVESL S RVPSVDYVIPG TKHVIPKRTL V QIPVHAIQHDP EHY 420
CYP6P9b	MNIQYLDNVINETLRKYPPVESL N RVPSVDYVIPG TKHVIPKRTL V QIPVHAIQHDP EHY 420
CYP6P9a	PDPERFDPDRFSPEEVKKRHPFTFLPFGE GPRVCIGLRFGVM Q TKVGLITLLRKFRFSPS 480
CYP6P9b	PDPERFDPDRFSPEEVKKRHPFTFLPFGE GPRVCIGLRFGVM Q TKVGLITLLRKFRFSPS 480
CYP6P9a	ARTPDCV K FDPKMI I LSPIAGNYLKVEK L 509
CYP6P9b	ARTPDCV T F H PKMI T LSPIAGNYLKVEK V 509

Figure S3: Amino acid sequence comparison of the two copies of CYP6P4 (S3A) and CYP6P9 (S3B) obtained from the sequencing of a BAC clone of *An. funestus*. Amino acid changes are highlighted in black.

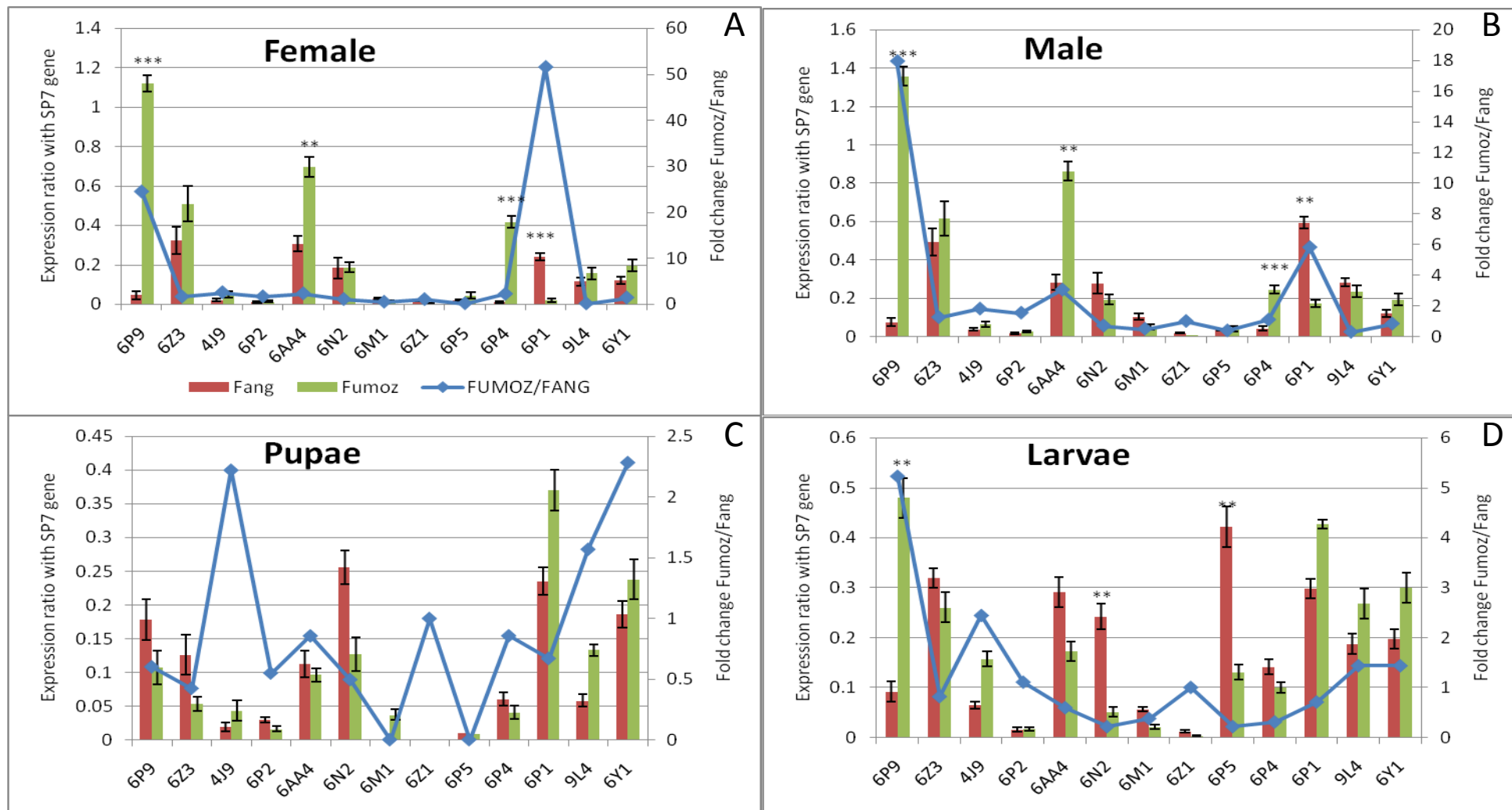


Figure S5: Gene expression patterns of some of the 30 tested P450 genes in females (A), males (B), Pupae (C) and in larvae (D) of the resistant strain FUMoz and the susceptible strain FANG from qPCR experiments. The normalised expression ratio of each gene against the SP7 gene is represented on the primary vertical axis while the secondary vertical axis (curve) represents the fold change of each gene between FUMoz and FANG. Significant differential expressions are indicated by asterisks: *** for $P < 0.001$ and **if $P < 0.01$.

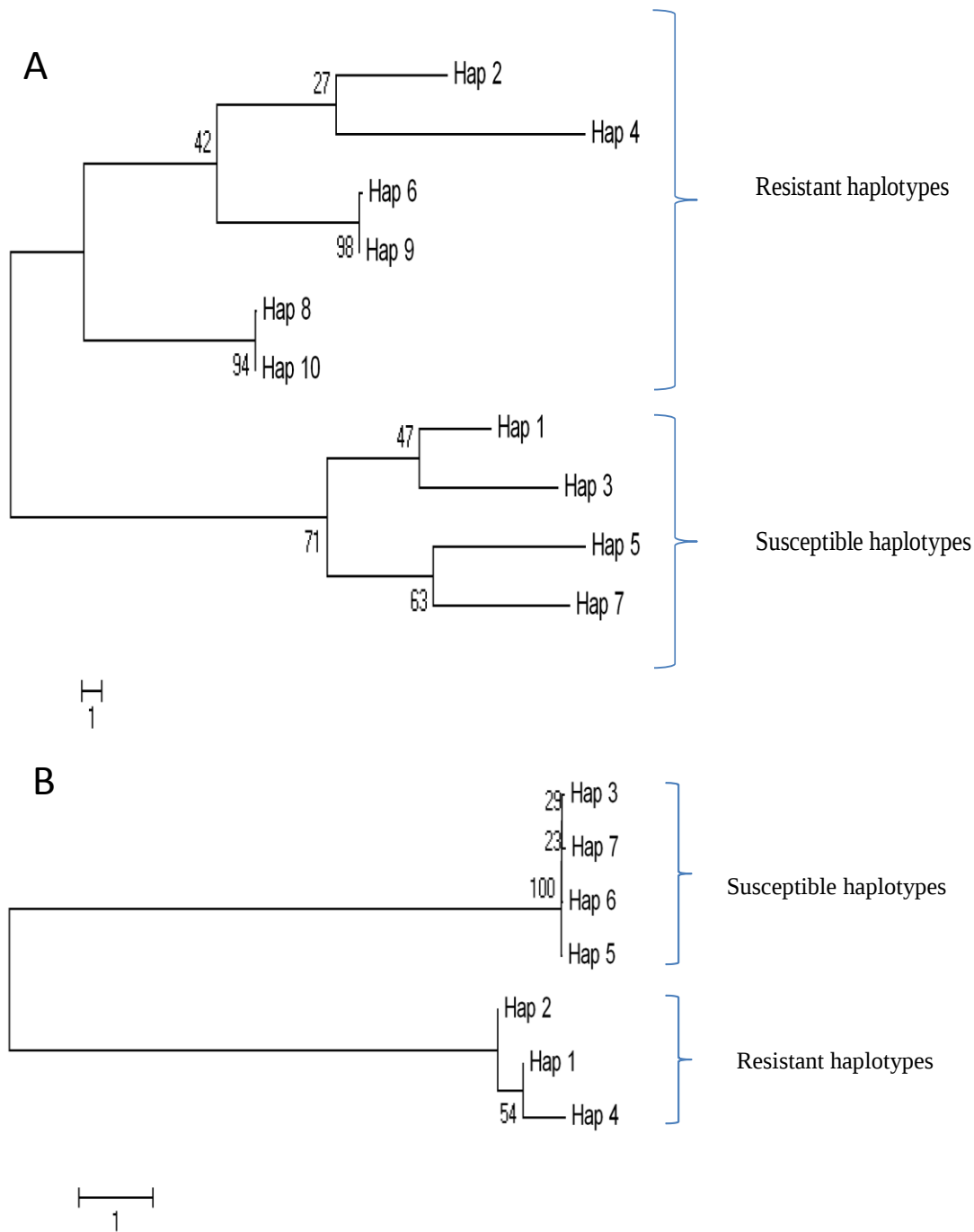


Figure S6: Phylogenetic trees showing the relationships among the haplotypes observed from the sequencing of a 2584 DNA fragment of CYP6P4 (A) and a 2229 bp DNA fragment of CYP6P9 (B) in both pyrethroid resistant and susceptible samples of *An. funestus*. The trees were constructed by using the Neighbour-joining method. The distances represent the number of base substitutions per site. The bootstrap values obtained with 10000 replicates are shown at the nodes in percentages. “Susceptible haplotypes” means haplotypes observed in susceptible individuals while “resistant haplotypes” is for haplotypes observed in resistant individuals.