

CYP6N1 -----MWIN-----LLVLVLLVAVFVWVQRFYSYWKRRNIPYITPSFPQGNLTGVGK-KRHM 50
CYP6N2 -----MLIY-----LLLIAVSAAVVHVKRYSFVWDRGVPYVQPRFPFGNIQGIGR-RMHS 50
CYP6M1a MWFLTIEAL---VAVLALLGGLVYLVKRQSYWKDRNVPHPS~~TTF~~FLGSFKDAGT-KMHF 56
CYP6M1c MWFLFVEIL---VALVALLGGLVYLVKRQSYWKDRNVPHPS~~PAFF~~FGSFKDGTGT-KIHF 56
CYP6M1b MWFLSLEAF---VALLVLLGALVYFIVRKQSYWKDRKVPHPSP~~TFL~~IGSFKDAFS-KVHF 56
CYP6M7 --MEPLDIL---ISVLMVCFGVYLLIDRRFQYWTNRNV~~PQ~~SKPELVFGNVREVSQ-TIHL 54
CYP6M4 --MEFTDVA---ITLGMLCIILYLLVRRFQYWTERNV~~PQ~~LKPELLFGDAREVGK-VCHI 54
CYP6M8 -MLSLEFDT---FLVAALVAGLYYYLDRKRSYWKDRD~~VPG~~PKGELLGNGFGKVGK-KEHI 55
CYP6Y1 MYLQVVG-----ILVAVVVTCLAWIKRRYQYWKARS~~VAF~~IAPEFPYGNFGLTGK-LEHI 53
CYP6Y2 MELVVASLVSLGAILATFCLGVYLFVTRKYSFWRAH~~NVP~~YVEPELPGNFKEMGK-SIHP 59
CYP6S1 --MFVHLLL---VASLALLWIYLHFKRYLFWLKR~~DVP~~YLEPTFPVGNVVDIFSPTIHF 54
CYP6S2 --MLIPAVL---VACFGLVWLYIHFKRRLFWLKR~~DVP~~YLEPTFPVGNVVDIFSPTIHF 54
CYP6R1 --MLPVLWLLLLTVSSEFLTFLMCV~~IHIR~~KKYSFWREL~~GV~~PIPAS~~FPL~~GNIQHTSH----- 53
CYP6Z1 -----MILY-----AIAVLPVIVFLALKYVYSY~~WDR~~HGIPNLKPEIPYGNLRILAEKKESL 51
CYP6Z3 -----MFVY-----TLALFPIVIFLLRLYI~~YSH~~WERYGLPHVKPEIPYGNLRTVVEKKESF 51

CYP6N1 SAILQNCYKQLKSSGQS-YGGIYFFINPVALLIDPEL~~IKV~~VLVKDFPYFHNRLNLYNDRD 109
CYP6N2 SQLMTKFFYNELKPSGRS-FGGIYFFTNPVALALE~~LDF~~VKNVLRDFAHFHDRGVYNEKD 109
CYP6M1a SDYLEQYYTTYK-GKHP-FTGAYMLISPIVLP~~TDE~~LVKSIILVKDFQYFHDRGTYTYNEKH 114
CYP6M1c TEYLEQYYTTYK-GKHP-FMGLYMLVSPIVLP~~TDE~~LVKSIIFVRDFQYFHDRGTYTYNEKD 114
CYP6M1b SEYLEQYYTTYK-GKLP-FMGVYMLVSPVIV~~TDE~~LVKSIILVRDFQYFHDRGTYHNEKH 114
CYP6M7 ADKFREIYNELK-GKHP-LVGVYLF~~FKP~~VALITDLELLKCVFVKDFQYFHDRGTYTYNEKH 112
CYP6M4 GEKIHQLYNELK-GKHP-FGGIYLF~~TKP~~VALITDLELLKCVFVKDFQYFHDRGTYTYNEKH 112
CYP6M8 TVPMKKIYDENK-GKHP-FAGIYQF~~VK~~PVALITDLELLKCVFVKDFQYFHDRGTYFYNERD 113
CYP6Y1 APITQRHYNFYQQLKVP-YGGVFM~~LTP~~LLYIFD~~TK~~LKIKTL~~LV~~KDFHYFPN~~RG~~VYFNERD 112
CYP6Y2 AHL~~SQR~~FYEQYKSD~~EG~~PGFVGLYIFVNPV~~LL~~VLTN~~LR~~LAKRILIED~~FHH~~FPDRGVYNEKD 119
CYP6S1 AHIIEKLYKKLK-SRGD-YVGIYFFRDPV~~LL~~VLS~~PDF~~ARTIILVKDFNYFVDRGVYSNEEV 112
CYP6S2 AHLIEKLYRRLK-GRGD-YAGIYFFRDPV~~LL~~VLS~~PDF~~ARTIILVKDFNYFVDRGVYSNEEV 112
CYP6R1 --LMVELYQELK-GKHP-FGLGFQ~~FTE~~PVALITDPE~~MV~~KNVLRD~~CR~~FFYDRGGYTDGKH 109
CYP6Z1 NIAVN~~NLY~~TRST----DRLVGVYLF~~FR~~PA~~IL~~IRDAHLAKRIMV~~NDF~~QH~~FH~~DRGVYCNEHG 107
CYP6Z3 GIAIN~~NLY~~HRSS----DRL~~L~~GVYLF~~FR~~PA~~IL~~IRDPQLAKRIMV~~NDF~~QH~~FH~~DRGVYCNEKG 107

CYP6N1 DPLSHHLVAMEG~~TKWR~~NLRAKLTPTFTSGMKLM~~FST~~VTA~~VAE~~QFHKCMAEEIRHS-SV 168
CYP6N2 DPISGHLFNI~~E~~G~~TKW~~TNLRK~~KL~~IPTFSSGKMK~~MM~~CPTIVSVGGRF~~RE~~CLERCIAND-GEV 168
CYP6M1a DPLTTHLFN~~LEG~~QK~~W~~KNL~~R~~NKLTPTFTSGKMK~~MM~~FPTVVAAGKQLKEFMDENVQKN-SEL 173
CYP6M1c DPLTAHLFN~~LEG~~QK~~W~~KNL~~R~~NKLTPTFTSGKMK~~MM~~FPTVVAAGKQLKEFMDENVQKN-SEL 173
CYP6M1b DPLTAHL~~SN~~LEGQ~~R~~W~~K~~HL~~R~~NKLSPTFTSGKMK~~MM~~FPTVVAAGKQLKEFMDENVQKN-SEL 173
CYP6M7 DPLTAHLFN~~IE~~GQK~~W~~KNL~~R~~NKLSPTFTSGKMK~~MM~~FPTIIAAGKQ~~FK~~DFMEETVHEQ-VDF 171
CYP6M4 DPMSAHLFN~~IE~~GQK~~W~~KNL~~R~~NKISPTFTSGKMK~~MM~~FPTIVAAGKQ~~FK~~NYMEDTIQQQ-GEQ 171
CYP6M8 DPLSAHLFN~~IE~~GQK~~W~~RS~~L~~RNKLSPTFTSGKMK~~MM~~FPTIVTAGKQ~~FK~~DFMEETVKRE-NVF 172
CYP6Y1 DPLSAHMFA~~IE~~GQK~~W~~RTL~~R~~AKLSPTFTTGRIK~~MT~~LPLVKEVC~~QR~~FC~~DH~~LHQSLQTS-AEV 171
CYP6Y2 DPLSAHLFA~~IE~~GQ~~R~~W~~K~~DL~~R~~AKITPTFTSGRMKA~~AF~~PLVLDIAE~~Q~~FCDFLRERYTSS-DMV 178
CYP6S1 DPLSANLFF~~ME~~GNR~~R~~W~~R~~KLSK~~L~~APTFTSGK~~L~~KAMFHTIVDVGNRLDQYLAERC~~NQ~~E-QRL 171
CYP6S2 DPLSANLFF~~MD~~GNR~~R~~W~~R~~KLSK~~L~~APTFTSGK~~L~~KAMFHTIVDVGNRLDQYLADRCIRL-QRI 171
CYP6R1 DPLTGHMLN~~SE~~SER~~CA~~L~~H~~HAASPIFSTGRIRAF~~L~~PV~~M~~LEKLNHFREYLN~~G~~KVNTEG~~TK~~V 169
CYP6Z1 DPMSANL~~F~~ALPG~~Q~~R~~W~~KNL~~R~~GKLTPTFTSGQLRN~~M~~LPTFLDVGK~~KL~~QQ~~F~~LDN~~L~~AMDH-QIV 166
CYP6Z3 DPFSANL~~F~~ALSG~~D~~R~~W~~KNL~~R~~AKLTPTFTSGQLRN~~M~~LPTLIDVGS~~KL~~NDRMNTLADEK-TVV 166

CYP6N1 EMKDLLARF~~TT~~DVIGSVA~~F~~GLECN~~S~~LQDPDAE~~F~~FRVMGRK~~V~~FQSSPYRA-LK~~L~~FLAAQ~~F~~PH 227
CYP6N2 EMKELLARF~~TT~~DVIGTCAF~~G~~IDCNSLNDPNAE~~F~~LRMGRK~~V~~FVPRGRI-LK~~F~~FFMAT~~F~~KD 227
CYP6M1a EMKDIMARF~~TT~~DVIGTCAF~~G~~IECN~~S~~MRDPNAE~~F~~FRAMGK~~L~~FVERQPSQ--FVNIMVQ~~F~~SHK 231
CYP6M1c EMKDIMGRF~~TT~~DVIGTCAF~~G~~IECN~~S~~MRDPNAE~~F~~FRAMGK~~Q~~FIDRQPSQ--FVNLMVQ~~F~~STK 231
CYP6M1b EMKDIMARF~~TT~~DVIGTCAF~~G~~IECN~~S~~MRDPNAE~~F~~FRAMGK~~Q~~FVDRPPSQ--FVNLMIQ~~V~~SPK 231
CYP6M7 ELKDV~~M~~ARF~~TT~~DVIGMCAF~~G~~IECN~~S~~MSNPDAE~~F~~FRVMGRKIFARPRGK--V~~K~~SLVINSMPR 229
CYP6M4 ELKDV~~L~~ARF~~TT~~DIIGTCAF~~G~~IECN~~S~~MRDPDAK~~F~~FRVMGRKIFTRTRGT--LQQLLMNA~~F~~P 229
CYP6M8 ELKDLLARF~~TT~~DVIGMCAF~~G~~IECN~~S~~MRNPDAE~~F~~FRAMGRKIFEISPGT--FK~~T~~M~~L~~MNGMPS 230
CYP6Y1 EMHDL~~L~~SRYTIDVIGACAF~~G~~IECN~~S~~FRDPNE~~F~~FRY~~G~~KIAFDKLRHSP-LV~~V~~YLMKA~~F~~FRK 230
CYP6Y2 EVRDL~~M~~ARF~~TT~~DVIGSYA~~F~~GLECN~~S~~FRDPQNE~~F~~FRIGRKH~~F~~DTPRNHP-LK~~V~~FIMK~~T~~FRG 237
CYP6S1 DIKELLARF~~L~~TDVIGSCAF~~G~~IDCNSIDNPNSQ~~F~~FRVMGRMINLPK~~L~~KA-LK~~V~~FFAMM~~F~~FRK 230
CYP6S2 DIKELLARF~~M~~TDVIGSCAF~~G~~IECN~~S~~LDNPNSQ~~F~~FRLMGK~~R~~MINLPK~~L~~KA-LK~~V~~FFAMM~~F~~FRK 230
CYP6R1 ELKEMIG~~K~~LN~~T~~DIAM~~S~~FVLGIEGN~~L~~IAPDGLHEALMREA~~F~~LLPNV--AK~~L~~FLM~~T~~CYRS 227
CYP6Z1 NMRDIVSRYVLDVVASV~~F~~FGFEANCLHDPDD~~P~~FRVALRDL~~T~~NPESFLNNIR~~S~~AGVFLCPG 226
CYP6Z3 DMRDIASRFVLD~~T~~IASV~~F~~FGFEANCIHNSDD~~P~~FLK~~T~~LLQV~~N~~KRRSFVDNIR~~T~~SGV~~F~~ICPG 226

CYP6N1 IARAFHVTLTLPEVANFFFTGVVNDTIDFRKTNNVQ--RNDFMTLLMKILKEQEESGSIDD 285
CYP6N2 FSRRIHIGKTSEDVVSQFFFKVVRETIEYREQHNIQ--RNDFMNLLMQLN----SGQLDD 281
CYP6M1a LSRMLGIRLIDKEVSTFFFLKVVKDTIDYRVKNSIQ--RNDFMDLMIRMLQN-----TEN 283
CYP6M1c LSRMMGIRLIDKEVSTFFFLKVVKDTIDYRVKNGIQ--RNDFMDLMIRMLQN-----TEN 283
CYP6M1b LSRMMGIRLIDKEVSTFFFLKVVKDTIDYRVKNSIQ--PNDFMDLMIRMLQN-----TEN 283
CYP6M7 LAKLIGLRTLDPVEVSDFFMKAVRDTIKYRVENNVQ--RNDFMDILIRMRSDK----ETKS 283
CYP6M4 VAKMVGIKLIVPEVSDFFMKVVRDTIKYRVENNVQ--RNDFMDILIRMRSDK----ETKS 283
CYP6M8 LAKMLRMKQTDQDVSDFFMNAVRDTINRVANKVK--RNDFVLLITMMSKD----ETKS 284
CYP6Y1 HANALGMKQLHDDVSSFFMRVVKDTIEYREREQIV--RNDFMDLLLKLKNTG-----RLES 284
CYP6Y2 LANRLGLKLLHDDVATFFQSVIRQTIHRERHGIG--RSDFLDLLIRLKNKG-----SLEG 291
CYP6S1 QARALGIRFNDKDVSDFFLTVVRDTIRYREENNVR--RDDFMQLLIDMMKQD----GVGA 284
CYP6S2 QAQLLGIRYNDKDVSEFFMNVVRDTIRYREEKGVV--RDDFMQLLIDMMKQD----GTGA 284
CYP6R1 MAKKMRLKMFNSNYITELFQQVVRETIEHRKDISYLNRRDLDLIDQLLAMPGFD-----GK 281
CYP6Z1 LLKFTGISALAPAMKKFTMEVIVSSHLHQRETGQVT--RRDFIQMLTDLRRNAG-----NN 279
CYP6Z3 LLKLTGLTSLPTELINFVMEIITHQIDHREKNQIS--RKDFVQLLIDLRRDAS-----SQ 279

CYP6N1 G--QKDHLTLDDIAAQAFVFFLAGFETSSTAMSFCLYELALHQDLQDKARQNITEVLKKY 343
CYP6N2 SGETVVKLSLNEIVAQAQFVFFLGGFETSSTTMSYCLHELALNEQIQQRARQCVLDAVKKH 341
CYP6M1a PEE---SLTFNEVAAQAQFVFFFAAGFETSSTLLTWTLYELALNPEIQEKGRQCVEILEKH 340
CYP6M1c PEE---SLTFNEVAAQAQFVFFFAAGFETSSTLLTWTLYELALNPEIQEKGRQCVEILEKH 340
CYP6M1b PEE---SLTFNEVAAQAQFVFFFAAGFETSSTLLTWTLYELALNPEIQEKGRKCVKEILEKH 340
CYP6M7 DDG---TLTTNEIAAQAFVFFLAGFETSSTLLTFTLYELALNQDAQDKGRRCVKEVLERH 340
CYP6M4 DDG---TLTTNEIAAQSFVFFLAGFETSSSLMTFTLYELALNPEIQEQARNVCVEVLDY 340
CYP6M8 DDE---SLTFNEIAAQAFVFFLAGFETSSTLLTWTLYELALNPEVQEQGRKCVREVLLKH 341
CYP6Y1 GGEDLGRLTFFEEIAAQAFIFFTAGYDTSSTAMTYTLYELALKQDVQDKARQCVKETLQY 344
CYP6Y2 SNEIVGRLSGDEIAAQAFIFFTAGFETSSSAMTYTLYELALNQELQQRARDCVMDALEKH 351
CYP6S1 GEC----LTFEEIAAQAFVFFFAAGFETSSTTTITCALHLLAKHPEVQNEARKCIRETLIKH 340
CYP6S2 GEA----LTFEEIAAQAFVFFFAAGFETSSTTTITCALHLLAKHPKAQRKARACVRSVLAKH 340
CYP6R1 S-----TLTLSQMAAVFLFLGA-YDATGITTFCLYELAQRPVQERARACVLEALEKH 335
CYP6Z1 AED---SLSEAQCAANVFLFYAAGADTSTAASFTLHELTHNPEVMGKVQREIDEMMNRY 336
CYP6Z3 GEQ---ALSIEQCAANVFLFYIAGSETSTAASFTLHELSHNPDALAKLQQEIDEMMERH 336

CYP6N1 D-SISYEALHEMKEYIDMCINESLRKYPPATTLTRRVEKDYRVPGT-DQVLQKGMVAIPV 401
CYP6N2 G-GLSYEALMDMPYIDQCINESLRKYPPGANLIRQVSQDYRVPGT-DVTFPKGMNVMIPV 399
CYP6M1a NGEMTYEAILDMKYLDQILKEALRKYPPLPIHIRVAKQDYRVPNT-DSVIEAGTLVLVPI 399
CYP6M1c NGEMTYEAILDMKYLDQILKEALRKYPVPMHFRTAAQDYHVPNT-DSII EAGTMILTPT 398
CYP6M1b NGEMTYEAILDMKYLDQILNEALRKYPVPMHFRTTQDYHVPNT-DSII EAGTRVLIPT 399
CYP6M7 NGELTYDAVMEMHYLDQILKESLRKYPPVPHFRITTSKEYQVPGT-KTVLEAGTSVMVPV 399
CYP6M4 GGELTYEAALEMDYLDLDRVLKECLRKYPVSVHFRTAKDYLVPGT-NSILERGTSMVMPV 399
CYP6M8 NGEMSYDAVVDMKYLDQILNESLRKYPPVPHFRVASKDYQVPGT-KSVLEAGTAVMVPV 400
CYP6Y1 DGKLSYEAVSDMSYLDQCINETLRKHPPVAILERNADKDYRLPDS-GLLLRGQKIMIP 403
CYP6Y2 AGVLSYESKMNLYLDQCIYETLRKYPPVAILERTVAKPYRLSDT-NIVLHRGMKIMIPA 410
CYP6S1 NNLLSYDAVMEMEYIGWIINETLRMYPPVATLHRITTPYQLPN--GAVLPEGIGVILPN 398
CYP6S2 GNQLTYEAITEMDYIECIINETLRLYPPVATIHRMTSQPYQLPN--GKILPVGVGVII SN 398
CYP6R1 D-GITYDALADMPYIDQCLNETLRMHPLAINLVRVVTKNYPVPDASGVVLPKGLNIVVVP 394
CYP6Z1 NGEITYDNITELKYLDMCIKETLRMYPALAVLNRECTIDYVPVDS-DIIIRKGTQVI IPL 395
CYP6Z3 NGEITYENINELKYLDLCVKEETLRKYGPLPILNRECTIEYAVPDS-DVIVIRKGTQVI IPL 395

CYP6N1 YALQHDPDHFNPNERFDPERFTPEQSEKRHPFTFLPFGEGRVCIIGLRFGMVQARIGLVY 461
CYP6N2 YAIHHDPEHYDPERYDPDRFAADASEARKPYSFIPFGEGRICIAARFGMLEARVGLSV 459
CYP6M1a YAIQRDPDIFPEPEKFDPERFSPEEEAKRHPPFAWIPFGEGRVCIIGLRFGMMQARIGLAY 459
CYP6M1c FAIQRDPDIFPEPEKFDPERFSPEEEAKRHPPFAWIPFGEGRVCIIGLRFGMMQARIGLAY 458
CYP6M1b FAIQRDPDIFPEPEKFDPERFSPEEEAKRHPPFAWIPFGEGRVCIIGLRFGMMQARIGLAY 459
CYP6M7 YAIHRDPEHFNPDLDFDRFTPEEEAKRHPPYAWTIPFGEGRICVGLRFGMMQARIGLAY 459
CYP6M4 LGIHRDAEHFNPNERFDPERFTPEQEAKRHPYAWTIPFGEGRICVGLRFGMMQARIGLIH 459
CYP6M8 HAIHHDPAVFPDPERYDPERFSPEQEAKRHPYAWTIPFGEGRICVGLRFGMMQARIGLAY 460
CYP6Y1 YAMHHDSTHFDPDEQYRPERFSPAQVAKRDPYCYLIPFGEGRICIGMRFGSLQAKMGLAS 463
CYP6Y2 YAIHHDPIYPNPATYDPERFTPERMARRDPCAYLIPFGEGRICIGLRFGMMQARIGLAL 470
CYP6S1 LAFQNDPDYFNPDRDFKPERFSIKNDFKNN-FSYLIPFGEGRICIGMRFGLLQTRLGLAM 457
CYP6S2 LAFHHDPTYFNPDRDFKPERFEDKAFGKNN-PSYLIPFGDGPRMCIAMRFGQLQTRLGLAM 457
CYP6R1 YAIHYDPQYYPEPERFDPERFLPEACRQRTPYTFLIPFGVGPSCIGYRQGKIQLRAMMAV 454
CYP6Z1 LGISMNEKYFPNPELYSPERFD-EATKNYDADAYYIPFGVGPSCIGLRQGLLSKIALVL 454
CYP6Z3 LLSISMNEKYFPNPELYSPERFD-EATKNYDADAYYIPFGVGPSCIGLRQGVLVSKIGLVL 454

CYP6N1	LLKHFRFTLATDKTSVPLKITPSSTILTIDGGLWLNVEKL-----	501
CYP6N2	LLMHFSFTRCS-KTNVPLVISSRHAVLTPEGGLWLKVEKLQA-----	500
CYP6M1a	LLQGF ^g SFAPYE-KTSVPMKFVTNNILLSPKDGLWLKVNKL-----	498
CYP6M1c	LLQGF ^g SFAPYE-KTSVPMKFVTNSEMLAPRDGLWLKVNKL-----	497
CYP6M1b	LLQGF ^g SFTPYE-KTSVPKKFIKNNIFLSPKDGLWLKVNKL-----	498
CYP6M7	LLTGFRFVPGA-KTMVPMKLDVKSFILSPQGGGLWLKVEKLST----	500
CYP6M4	LLTSFRFACCS-KTPIPMKFDITNTILSPKGGMWLRMEKLTkdCE-	503
CYP6M8	LLDGFQFAPSS-KTVIPMELSTESFIMAPKGGGLWLKVDKI-----	499
CYP6Y1	MLDRFQFSTCE-RTQIPVQYSRTNFILGPANGVWLRAEEL-----	502
CYP6Y2	LLKHFQVLPCK-ETDEPLTYSTQAFVLT ^g VPVNGVRLRLAKYELNEP-	514
CYP6S1	LVRNYNFTIDPSDAERPLRIDPINLLHGPAgevWLNvKRIVDM---	500
CYP6S2	LLRNYNFAIDDCDADRPLLIDPINLMHGPAgevWLNvERTVEKNS-	502
CYP6R1	LLSSYEFTKCP--NITQGSRSKAHTVLKLDGDLWLNvKPINRTNDD	498
CYP6Z1	MLTKFVFSATI---PRKLCFEPVAVTLAPKGGFPMRIERV-----	492
CYP6Z3	LLSKYNFHATI---PAKVKFAAINVGLTPEVGLPMRIEHRK-----	492

Figure S1. Alignment of the amino acid sequences of fifteen *An. funestus* CYP6 P450 proteins from the *rp2* BAC clone. The sequences were aligned using ClustalW. The membrane targeting/anchor hydrophobic N-terminal region is in bold and underlined. The conserved C-helix WxxxR motif is in green while the other conserved ExLR and PERF motifs are highlighted in yellow and grey. The haem-binding loop (P450 signature sequence) is highlighted in dark grey with the cysteine residue involved in haem coordination is in bold and underlined.

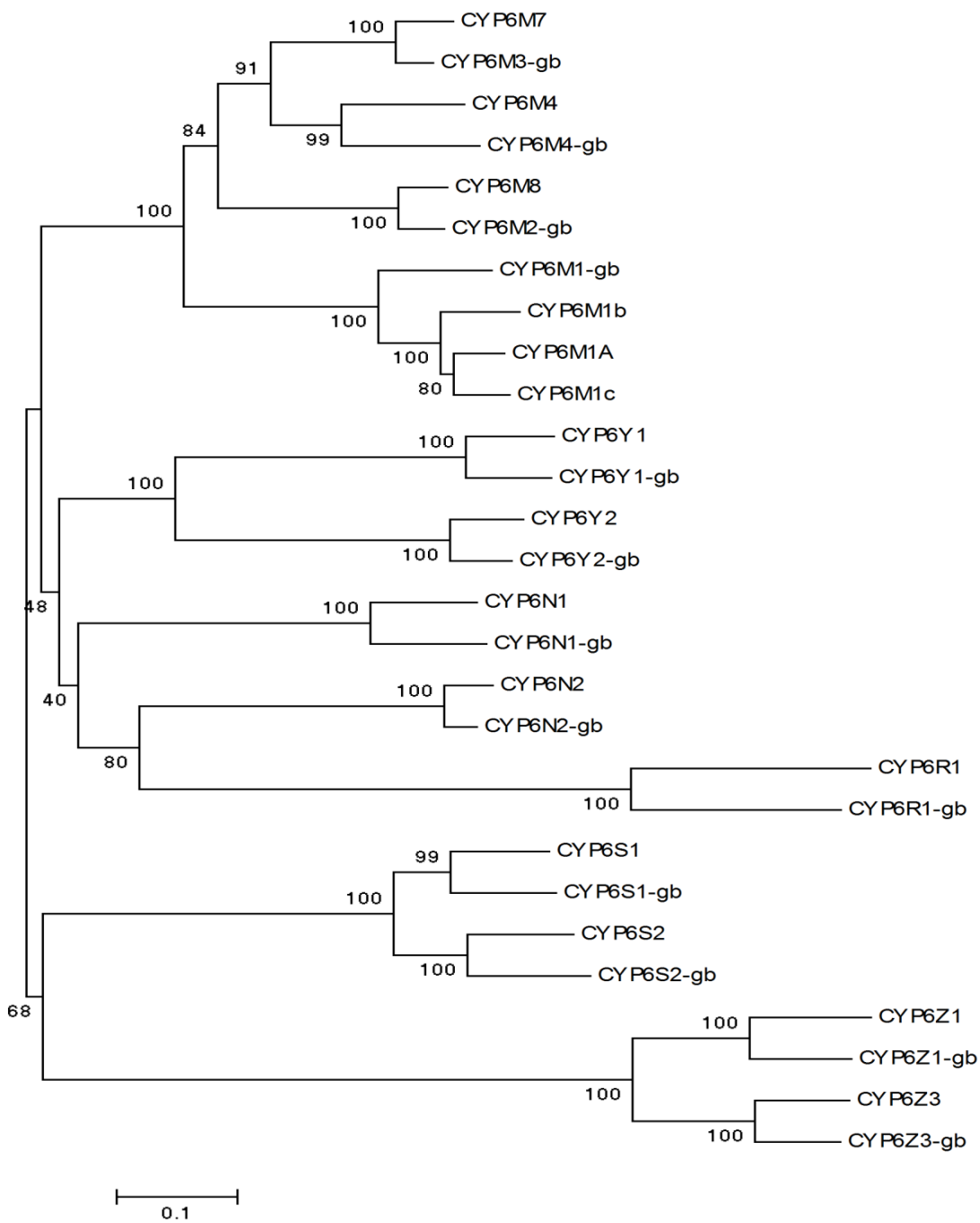


Figure S2: Neighbour joining tree showing the phylogeny of P450 genes from the sequenced BAC clone of *An. funestus* and orthologs in *An. gambiae*. The g letter beside a P450 indicates that it belongs to *An. gambiae*. Genes with a, b and c designation are copies of a triplication event from *CYP6M1* and have not yet been assigned individual gene names.

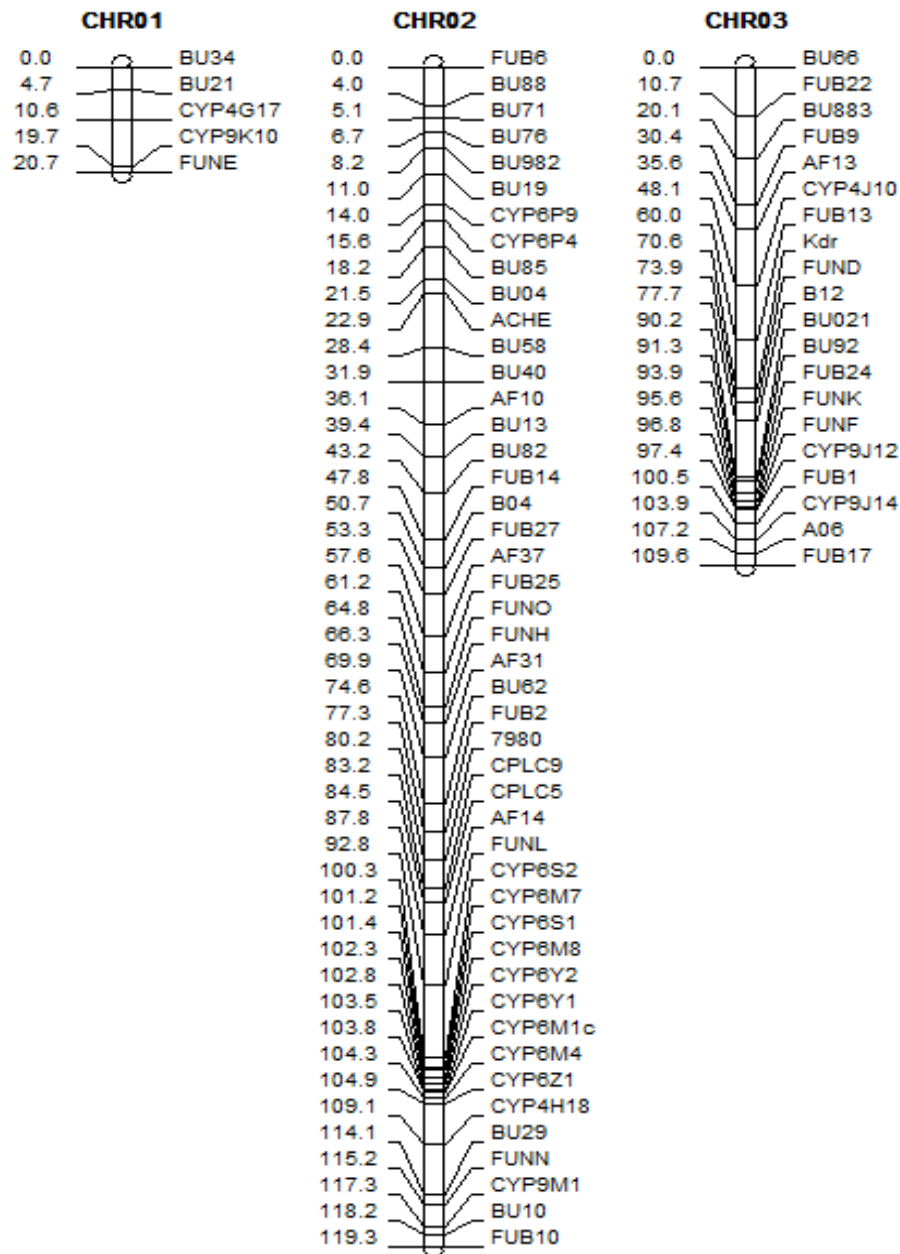


Figure S4: Combined Linkage map of Family 1 (♀susceptible x ♂resistant) and Family 10 (♀resistant x ♂susceptible).

	10	20	30	40	50	60	70
FG1	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYA	RSTDRLVGVY
FG2	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYT	RSTDRLVGVY
FG3	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYS	RSTDRLVGVY
FG4	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYS	RSTDRLVGVY
FZ1	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYS	RSTDRLVGVY
FZ2	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYT	RSTDRLVGVY
FZ4	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYT	RSTDRLVGVY
FZ5	MILYAIAVLP	VIVFLALKYV	YSYWDRHGIP	NLKPEIPYGN	LRILAEKKES	LNIAVNNLYT	RSTDRLVGVY

	80	90	100	SRS1	110	120	130	140
FG1	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FG2	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FG3	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FG4	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FZ1	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FZ2	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FZ4	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	
FZ5	LFFRPAILIR	DAHLAKRIMV	NDFQHFHDRG	VYCNEHGDPM	SANLFALPGQ	RWKNLRGKLT	PTFTSGQLRN	

	150	160	170	180	190	200	210
FG1	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FG2	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FG3	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FG4	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FZ1	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FZ2	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FZ4	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE
FZ5	MLPTFLDVGK	KLQQFLDNLA	MDHQIVNMRD	IVSRYVLDVV	ASVFFGFAN	CLHDPDDPFR	VALRDLTNPE

	SRS2	220	230	SRS3	240	250	260	270	280
FG1	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FG2	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FG3	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FG4	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FZ1	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FZ2	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FZ4	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		
FZ5	SFLNNIRSAG	VFLCPGLLKF	TGISALAPAM	KKFTMEVISS	HLHQRETGQV	TRRDFIQMLT	DLRRKAGNNA		

	290	SRS4	300	310	320	330	340	350
FG1	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FG2	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FG3	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FG4	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FZ1	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FZ2	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FZ4	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	
FZ5	EDSLSEAQCA	ANVFLFYAAG	ADTSTAATSF	TLHELTHNPE	VMGKVQREID	EMMNRYNGEI	TYDNI TELKY	

	360	SRS5	370	380	390	400	410	420
FG1	LDMCIKETLR	MYPALAVLNR	ECTIDYRVPD	SDIIRKGTQ	VIIPLLGISM	NEKYFPNPEL	YSPERFDEAT	
FG2	LDMCIKETLR	MYPALAVLNR	ECTIDYRVPD	SDIIRKGTQ	VIIPLLGISM	NEKYFPNPEL	YSPERFDEAT	
FG3	LDMCIKETLR	MYPALAVLNR	ECTIDYRVPD	SDIIRKGTQ	VIIPLLGISM	NEKYFPNPEL	YSPERFDEAT	
FG4	LDMCIKETLR	MYPALAVLNR	ECTIDYRVPD	SDIIRKGTQ	VIIPLLGISM	NEKYFPNPEL	YSPERFDEAT	

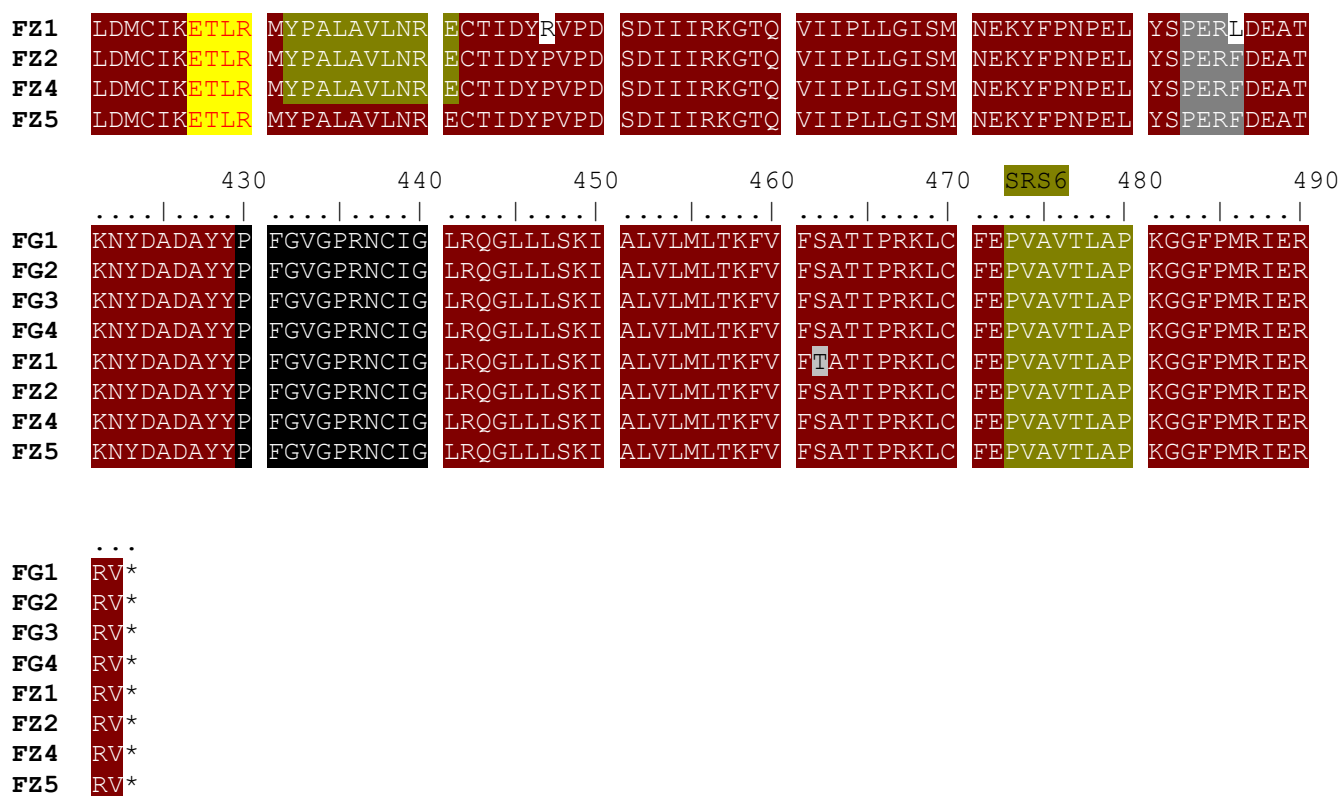


Figure S5: Alignment of the amino acid sequences of CYP6Z1 between FANG and FUMOS-R strains. Conserved regions are highlighted as in Figure S1. Substrate recognition sites (SRS) are deduced from the *An. gambiae* model (Chiu et al 2008).

	10	20	30	40	50	60	70
FG3	MFVYTLALFF	IAIFLLLRYS	YSHWERHGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FG4	MFVYTLALFF	IAIFLLLRYS	YSHWERHGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FG5	MFVYTLALFF	IAIFLLLRYS	YSHWERHGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FG1	MFVYTLALFF	IAIFLLLRYS	YSHWERHGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FG2	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ1	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ2	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ3	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ4	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ5	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY
FZ6	MFVYTLALFF	IAIFLLLRYS	YSHWERYGLE	HVKPEIPYCN	LRTVVEKKES	FGIANNLYH	RSSDRLLGVY

	80	90	100	SRS1	110	120	130	140
FG3	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FG4	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FG5	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FG1	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FG2	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ1	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ2	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ3	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ4	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ5	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	
FZ6	LFFRPAILIR	DPQLAKRIMV	NDFQHFHDRG	VYCNEKGDPE	SANLFALSGD	RWKNLRAKLT	PTFTSGQLRN	

	150	160	170	180	190	200	SRS2	210
FG3	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FG4	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FG5	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FG1	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FG2	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ1	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ2	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ3	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ4	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ5	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	
FZ6	MLPTLIDVGS	KLNDRMNTLA	DEKTVVDMRD	IASRFVLDTI	ASVFFGFAN	CIHNSDDPFL	KTLLQVNKRR	

	220	230	SRS3	240	250	260	270	280
FG3	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FG4	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FG5	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FG1	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FG2	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ1	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ2	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ3	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ4	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ5	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	
FZ6	SFVDNIRTSG	VFICPGLLKL	TGLTSLPTEL	INFVMEIITH	QIDHREKNQI	SRKDFVQLLI	DLRRDASSQG	

	290	SRS4	300	310	320	330	340	350
FG3	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	
FG4	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	
FG5	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	
FG1	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	
FG2	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	
FZ1	EQALSIEQCA	ANVFLFYIAG	SETSTAATSF	TLHELSHNPD	ALAKLQQEID	EMMERHNGEI	TYENINELKY	

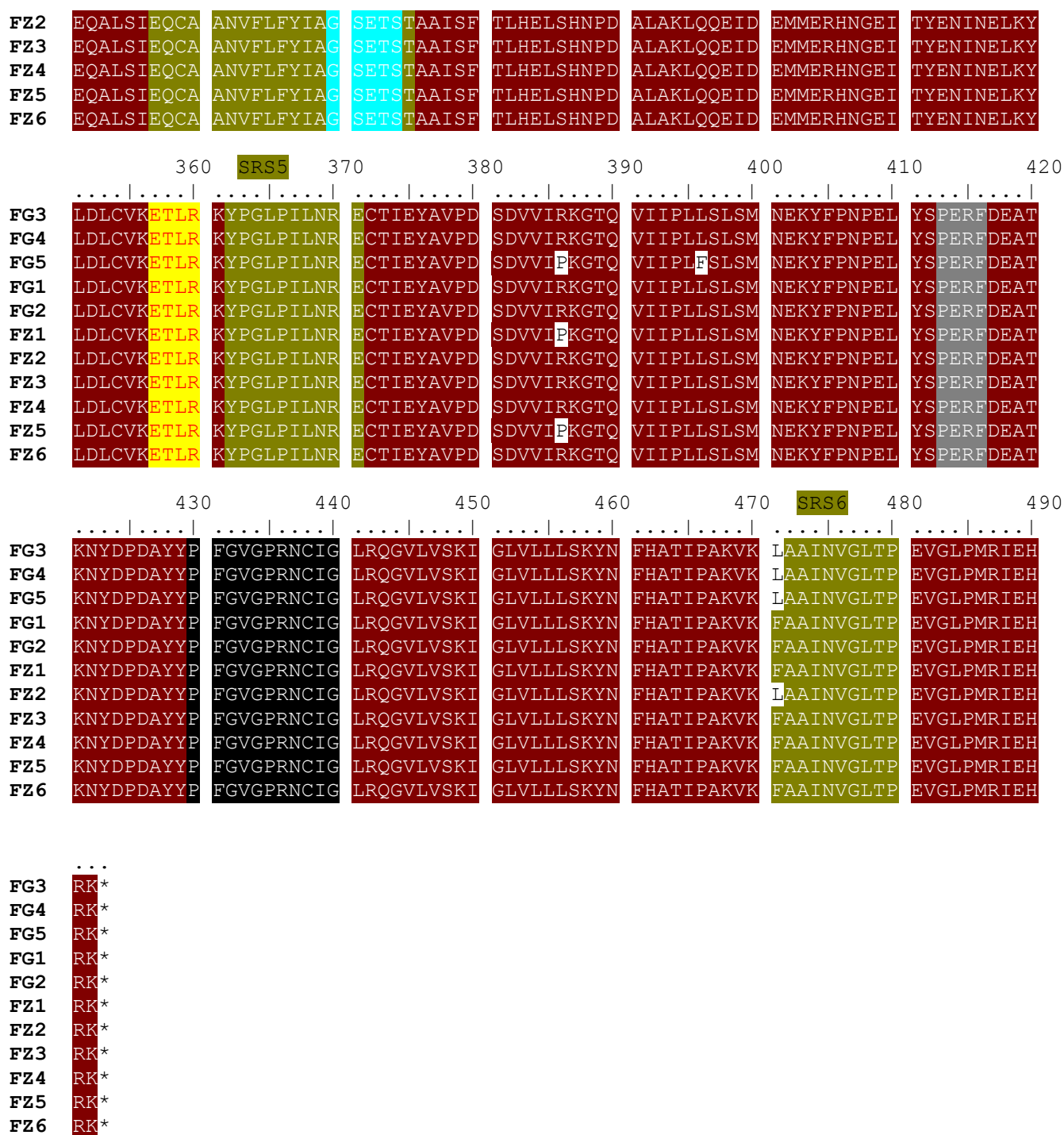


Figure S6: Alignment of the amino acid sequences of CYP6Z3 between FANG and FUMOS-R strains.

Substrate recognition sites (SRS) are deduced from the *An. gambiae* model (Chiu et al 2008).