Consensus sequence signal peptide

	1 10 20	30 40	50 60	0 70	80	90	100	110	120	130	140	150	160	170	180	190	200	210
Consensus	MVYFVPERSNMXXXMVXMXMXVXSLVXV	LLL VVX ALL GXVE GAN I L	XIFPVPSPSHHIWN	RXLMKELAERG	HNVT VV S XX P E KN	NPPPNYT	Y I HLEGXYX T L	YNDXDL	FEMANSP	FESLXIXY	EFGLSTCEAAL	E S EGL <mark>QQ</mark> LL R	Y P SD F 🛛 F D L 🔪	VIVDFFCGPC	LLGLA- <mark>H</mark> KF	X <mark>NPPLVGI</mark> XX	FGAPSYTNXL	VGNP <mark>XPPSYV</mark>
Identity				الم والمرجد				-		_								
															_			
1. AfUGI36B3	MVSLCCRTKRMTG <mark>S</mark> CKII	PLLTVLQFVAPNDGYRLL	GL FP H P GL SH FKVF	HP IMRGLANDG	H VTVVSYFPDPN	NP V S NY(DLRFEGQEILT	DAFSLEA	FTGRNFFDNFI	KEFYELV	/AWGMSSCEAAL	N <mark>S</mark> SAIDE I <mark>L</mark> E	SHRKDPFDL	VME FF ATD C	MAGINWL	LQVPLVGLSS	CALMPWHYDR	VGLPDTPSYI
2. AfUGI36C3	MIMLRT	V llm al al spcaqtykv l	GL FP H P GQ SH FHFF	QPVLKGLAEAG	IEVTVVSHEPEKN	NPPPNYR[DMPLEGMTSLS	D S V S F E	FEYRPGFGHFI		TWGKEACANAL	NSTAIQTILD	DSKIQYDLI		M lgia-H ql	. K – A <mark>P</mark> F I G L S S	CPLMPWHYDR	VGNP TL PAYV
3. AfUGT49A4	MHLVA	LVSFLAASLQTSS GA RIL	SVNVF P GR SH WMMI	GSILEELLDRG	IDVTV I TNY PRKK	K <mark>PHPNLT</mark> I	EVIDPINDFW	/GKSVKVDS	YDLTDIS	I HQMLMDFL <mark>Y</mark>	PLGUQTAEYAY		N – DQ SQ FD L L	LAEQFYQES	YUMUA-HKY	'K – V P I V S I GT	FGFAQ <mark>Y</mark> MGPM	MGLMNAWSHV
4. AfUGT50B8	MTLR	LLLAGLLAASCCS <mark>G</mark> SD IL	MUTMGGTK SH KUPF	LELAKGLIPRG	IN ITFLNGFPADF	FTLHGLQI	EVTPSCLVEYI	RNYTNWDL	LGARMRGDMP	LSLWDAF	RYSWQVCDATL	DKETMDLLG	SRKFDLN		ALGLVYR	LGVPFMY	VGFYTGTMAW/	AGNPVPYSTT
5. AfUGI301A3	MHLRVLSYIV	CVFAFTAL CPRAECGK	FLVPFPAPSHWLWI	EHFVKELLSRG	E VT A I TNF AM <mark>k</mark> d	DPHRNYTI	EVLIDPPYDIP	YYFPVSDI	Y∎SKYNSD	L SNLFL YW	VRVGLSTTQYAL	E DENVQQFIE	Q-DDTDFDVI	SEQEYQEA	FLMFA-HKY	R-APINTLCT	LGHANH I DQAM	MGLVTPWSFV
6. AfUGI301C2	MWLRFVFT	CLFLLGSVLSSADGYKLL	FLV P F P G PSH WLML	KHF IRELTERO	QMTCITAF P F G E	EKLQNYDI	ELIDPPYPIR	ETFPVEG	FASSQKSD	FVKLFMYW	VD L G FN T SR HG <mark>L</mark>		R – TDLEFDLI	AEQFFQES	WLMFAHI	YNAP INT ST	Y G YSDFFDR II	MGLQTPWSFV
7. AfUGI301E3	MRWVCL FL	TVFGVLACLPTGNGAKIL	LVSSF P GM SH WLMF	EHIIQELLRRG	ELTAITSYRLRS	SEG I NHTAR YHI	ELIDPV Y DFE	ANGLPMEV	FYKSQSFGDP	FFKMS LW	VK L GLETAEHA F	SANVKKFLT	TT-EGLA FDL L	AEQEVQES	FLMFA-HKY	'Q-V P INT	LGHADY IDCAI	FGLITPWSFN
8. AfUGI302A3	MLAYTMKPIKSSVGAN AF	FGLIFMMAQGIVEPAKIL	S IFP TMSK SH WILG	SSSLMKELAQNG	HENTYISPFPLKN	NAPKNYR		MFEDIMDEV	FDKVDDSI	VEKLIQMG	GGEMHE I TNTTL	A S P E VQ S LL K	< SDETFDLL	VLEIELNDA	F LG FADRF-	-NCPVVGMST	FGASSWVNSL	TGSPQPLSYV
9. AfUGI302H3	MRIDWTITVALI	AML YAAN ILGPVEGAKIL	T IFP TSAR SH Y I VG	SALTKELARRGI	EVTN INPEPQKK	KPLKNYR	DUDVSGSADIV	(KDLVPN	FEMAD LGV	WESITLTN	NK FGQILANYTL	QHPNVKK U I Q	2 SNEKFDL	ME SELNDAI	H <mark>lg</mark> evh h e-	-KAPCVLST	FGASRWTNEL	VGTPSPISYV
10. AfUGI302J2	MEHTRMLSLAV	G LL L L GCNTP PTD GA R	GULPSVGRSHYUIG	GAG lmk allda g i	IDVT I VS PYAMKC	DA <mark>PP</mark> DR		AATHDVSGPDL	FEYKNAP	NEVVEYEVYN	EFGPFSSKAL	EHPKMIGUME	SGERFDA	E SF ASEV	LYGLAEHF-	GGQLFVFAP	FGASMWTSEL	VGTPYPYAYI
11. AfUGI306A3	MMKLTENIA	LTL TLML TSHTESAK	CVFPTASKSHVLGA	QALLKELAFRG	HENTIMUS AF PLK P	R P P N N Y R D V	YVP I DAFSTI	MNDF	MQGGSRNM	LKLFPKIV	/RAAQDSSNVTI	NAPEFIR	1EEQ FDL A	L VG F F MN S F	IIGVGEL	FRC P TVLYFS	ASGSGL TN -V	VGNPAEVAAV
12. AfUG1306C2	MK I TQGMAN	AWAMLCCCYAQLEAYR	C IFP SSGR SH VLVG	GQALLKGLAERG	IDVTM VS PYKLSK	KSVPNYRI	EUVIQKVDLGQ	MTK DF	LQKNE GNSI	MASLVYLF	Q SQMRTAEMAL	BDAKVLAL		GYF VAD F	VLGLGPHF-	-NAPTVLFS	AGMTKPTADF	VGNPRATAAV
13. ATUG1306D2	MASRPSVVKL		GINTSPSRSHVIVQ	DALMKELARRG	HVINVSPYKESE	EQVPNYR	KITVPMDPW		GTINSRWAM	LQL PEML	RESAVPVNKIL	RSAEFQSEMK	EPERYDL	IG-IMSDA	VFGVSHI	LNCPITIVCP	NAAMAVVNSU	VGNPIPISII
14. ATUG1308A3	MVYFWPERSNDRMGLWRSERDWMLLAV	LLAIGREGNREAUGANIL	CLMAVPSPSHHIWN	RVLVDALAAQG	INCLOVED DIEP-	PKPNVI	YHLEKIYDII	HEGATAIDF	YEMGQ - AGM		YEYA ISMCIGIL		YPSDYK FDL		LLATY-HRF	GQPPNVGVIG	ENTPPYID	I G G H K Y Y A Y V
15. ATUG1308B3	MRSYVSLL	LUSISACWUGVYQGANIL	CIMIVPSPSHHIWN	RVIMEGLVDRG		SR-INLI	YLLEKVYSIL	YEDEGIDL	LEVSKEIP	FQSLFIFK	GEFYLSMCRGAL	KSUGLNVILN	YPDSFRFDL	LYDEGCGPC	LLPLL-HKF	NYPPLVSLIP	FSNPPMSVDI	VGGHKHYAY
16. ATUGI308C3	MCSSF	FFAILVSEGVIMHGANIL	CLMGMASPSHHIWN	RAIMDGLARUG		NOPPNVH	Y VHLEETYPTL	YIGPDSIDL	LEMAN ENL	FKSVISE-YR	RDFVVHECAGI		YPUDEREDL		LLGLL-HKF	KYPPL SVIA	ENNPPMSTEV	IGGHKFYSYV
17. ATUG1308D2	MASSPMAL	FVVLMACEGSGIEAANIL	Y NSMASPSHEGWN	RALIYELASEG				YSDPNM-DIDH	FEMSK IGP	ESMHL		RIEGAKRUQU	YPADEGEDL I	HUYLSGPC	LAALAHHRE	GKPPVIAVIA	YHGISIILSM	IGAY HY SALL
10. ATUGT308F2	MKLEINV				INVINES VIVOTS	SAPKINVI							ATP SNEKEDLL		LDA DAUDE	KDVPVLDCTD	NUND OF LER	GGRAVACIN
19. ATUGT308G2	NIC /		FMSG PSPSFT WL		INVINE SADUER	PPANVT	Y THE CHENCEN					K SEGLIFILER			LDA LIMUDE	KDVP TIPSTP	VNAPSTSAAVI	
20. ATUGT 506G5	MDXOAM		FMSG PSPSFT WL		INVINE SADVER	PPANVT				ACHOOF D				VSDEWIGPC	LDALIMOR.	KDLPFIPSTP	VNAPSTSATV	
21. AIUG150604	MRTQAMA				INVINCADVENT	TATONIT				ASTEQQFD						NDVPTIPSTP	VANDOLITIC	
22. ATUGT500P2		VEFLOVIATO CLUDANIL			INCIVUS ADVENT											DC DDL VIACA		
25. ATUGT50962	MENLERMETETT				INVILLATINGGE	SVDGKT			ESSVELLUA			UCEALVOLLA	VODTENENI			NDDIVCICD	ENI DEVTOVI	
24. AIUGISIUBZ		TAMAVEMPTI TEGADVI			ELTIMETO PEAT						OTTOL CI CACI				MYACA EI			
25. ATUGISISB2	MATNEL					TTORTNESLOR	LEOIDISEAVO							M EWS OVEL				
20. AIUGISI4AS	MAINILE MARTAL	AVINE AND EDTS SAMULE	AVEDSIEKTNY			VAVENIDO	-LBITCLENHI			EVENTNU == 1								
ZI. AIUGISISAS	VIS VOSK SL VAR I AL	AVINCANTED 133AM	AVER DIDKINT FO	FEALWARD	INCII V PEELQI	TATEN ING	LKTI QLENHT	EDIGLE ANY	FINNUN 35	FIGNINE I	1 GTAAWAD TT		CINE IEDEL		LUGUNINI	GVENIVISA		
	220 220 240	350 360	270	200	200 2	200 27	10 22	0 220	240	250	260	270	200	200	4.0	0 41	0 420	0 420
C	220 230 240	250 260	270	280	290 3	300 31	10 32	0 330	340	350	360	370	380	390	40	0 41	0 420	0 430
Consensus	220 230 240	250 260 LRRYVYLPEQDRXVRKHF	270 PDLPSLQ	280 ELERN-VSLVLV	290 3	300 31	10 32 HIK-PPKPLPX	0 330	340	350) 360 PPEXRRAILEAF	370 RXLKQYRFLW	380	390		0 41	0 420	0 430
Consensus Identity		250 260	270 PDLPSLQ	280 ELERN-VSLVLV	290 3	300 31	10 32 HIK-PPKPLPX	:0 330 DLQQFLDGA	340 KNGVIYFSL	350 GSNLRSADLP	D 360	370 RXLKQYRFLW	380 VK FE DDL F	390 PN-LPPNVL			0 420	
Consensus Identity 1 AfluGT36B3	220 230 240 PHPFLXYTDDMSFFQRVYNTLLSLXDXX	250 260	270 PDLPSLQ			300 3 LPPNMIEVGGLI LPSVIEIGGVI	10 32 HTK-PPKPLPX) 360		380				0 420	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3	220 230 240 PHPFLIXYTDDMSFFQRVYNTLUSLXXXX ESEFSTFSEE SELERVENWUVTRLLKH PALEMOVTEENDESELERVENWUVTRLLKH PALEMOVTEENDESELERVENWUVTRLLKH	250 260	270 PDLPSLQ PNSAIPDVR GEGVIPDVR		290 3	300 31	10 32 HIK-PPKPLPK 10-SNKPLPT HIR-DFKPLEA	0 330	340	350 GSNLRSADLP GSVLKAATLP GSVLKAATLP	D 360		380	390 PN-LPPNVL	40		0 420	0 430
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfIJGT49A4	220 230 240 PHP FLXY TODNS F FORVYNTULSURXXX RSEEST F SEENSEFLE RW EN WUYTRULKY RALEMCYTERNOE SOR LANWI TY VOS FKT PH FERUPETRO MSU VRANS F VSWEUT	250 260 LRRYVYL PEQDRXVRK F LYRI QI - NDNMLLKAK LYSWENDAAANKLLRAF LSWY TPEQ ALADE	270 PDLPSLQ PNSAIPDVR GEGVIPDVR SFLPGPLPRUS		290 3	300 3 LP PNMIEVGGLI LI PSVIEIGGVI LS PAVLEIGGI KVP GLVQVGGLI	10 32 HIK-PPKPLPK HIQ-SNKPLPT HIR-OFKPLEA		340 - KNGVIYFSL - PNGVIVVSF - PNGVIVVSF - DHGVIYISW - KDGVIYFSL	350 GSNLRSADLP GSVLKAATLP GSNLRAATLP GSNLRSADVP	D 360 PEXRAILEAF TKKRTAMIEAF		380	390 PN-LPPNUL IEN-CPAHVFT PN-CPAHVFT KH-LPPNVL			0 42	0 430
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8	220 230 240 PHE LIX TIDONS F FORWART LISU CARE B SERSTE SERVICE LISU CARE R LIENCE TE SERVICE LISU CARE R LIENCE TE SERVICE SUB LARMITYOS FK PHE LIP FTD ASS UPGRAVES FK SW FK LIN PHE FTD FTD ASS UPGRAVES FK SW FK THIN LIND	250 260 LRRYYYL PEQDRXWRKH F LYRINGI-NDNMLLKAK F LYSWFNDAAANKLLRAK LRSWYYLPEQALADR F LRSWYYLPEQALADR F	270 P		290 3	300 3 LPPNMIEVGGLE LIPSVIEIGGV SPAVLEIGGV KVPGLVQVGGLI LPNVAEIACI	10 32 HIK-PPKPLPX HIQ-SNKPLPT HIR-DFKPLEA HIK-EPKRLPD HCK-PASALPK	0 330 DLQQFLDGA ELQQFLDGA ELQQFLDTA DLQQLDTA DLQTFIDGA DLQTFIDGA	340 - KNGVIYFSL - PINGVIVVSF - DHGVIYVSF - CHGVIYFSL GESGFIYVSM	350 GSNLRSADLP GSVLKAATLP GSNLRAATLP GTNLRSADMP GSSVKAANMP	D 360 PPEXRRAILEAF TKKRTAMIEAF AEKROAILKAL PPEKLSVILKVF		380	390 PN-LPPNUL IEN-CRAHVF PN-CRAHVF KH-LPPNUL KH-LPPNUL			0 420	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT501A3	220 230 240 PHP FLXY TODAS & FORWYNTLLSLXXXX B SEISTESEENSELERM EMMI YVTLLSLXXXX PH SEISTESEENSELERM EMMI YVTSFKY PH SEISTESEENSELERM EMMI YVTSFKY PH SEISTESEENSELER SATTEFTIELAAD PY PHP ALTODAS EER LSATTEFTIELAAD PHF VLLSLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	250 260 LRRYYYLPEODRXWRH LYRINGI - NDNMLLKAK LYSWENDAAANKLLRAF LRSWYLPEGQALADRH VYTPSM-YLOHWMRH LRGYYLPEQQALADRH	270 P		290 3	300 3 PPNMIEVGGLI IPSVIEIGGV SPAVLEIGGV KVPGLVQVGGLI LPNVAEIACI TIPGLVNVAGA	10 32 HIK-PPKPLPK HIQ-SNKPLPT HIR-DFKPLEA HIK-EPKRLPD HCK-PASALPK HIK-PAKELPE	0 330 DLQQFLDGA ELQQFLDGA DLQQFLDTA DLQTFIDGA DLQTFIDGA DLQTFIDGA	340 - KNGVIYFSL - PNGVIVVSF - DHGVIYISM - KDGVIYFSL GESGFIYVSM - KEGVIFFSL	350 GSNLRSADLP GSVLKAATLP GSNLRAATLP GSNLRSADWP GSSVKAANMP GSSVKAANMP	D 360 PEXRAILEAF TKKRTAMIEAF AEKRDAILKAL PEKLSVILKVF OHLRKLLVOTF KKKKAFLEVF		380 KK FE DDL F KK WE F PN KK WE NE TL KK FE DE G I KK YE NE D I KK YE NE D I	390 PN-LPPNVL MEN-CRANVH PN-CRANVH KH-LPPNVL TD-LRANVH AR-LPKNVH	40 IRKWLPQND TOKWLPQND IRKWLPQND VRSWLPQSD IARWLPQOD VRKWLPQSD		0 421	0 430
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 4. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C2	220 230 240 PHP FLX YTDDXS FFORWYNTLLSLXXX B SEBSTE SEBSE LERWENVLTULSLXXXX B SEBSTE SEBSE LERWENVLTULSLXXXX B ALEMAYTER NO FSYN ELI B VFW PATDXSFES B SEBSTE SEBSTE SESTIFICATION PHP PHP VILLSDXX FFS CXXXXVISUUS SED	250 260 LRRYUYL PEODRXWRKH VYBI QOI - NDNMLLKAK F VYWFNDAAANKLL QAR UXTP SWM-YL OHW QRR U IRQFYYI POQNKLAQ I F VYTP SMM-YL OHW QRR U IRQFYYI POQNKLAQ I F	270 P		290 3	300 3 PPNMIEVGGLI SPAVLE IGGVI SPAVLE IGGVI KVP GLVQVGGLI LPNVA TACII TI PGLVNV AGAI STRGLVN IGGA	10 32 HIK-PRKPLPE HIQ-SNKPLPT HIR-OFKPLEA HIK-ERKRLPC HCK-PASELPE HIK-PAKELPE HIK-PAKELPE		340 KNGVIYFSL PNGVIVVSF DFGVIVISF GESGFIVVSM KDGVIYFSL GESGFIVVSM KEGVIFFSL RHGVIYFSL	350 G SNLR SADLP GSVLKAÄTLP GSMIRAETLP GTINLR SADMP GS SVKAÄNMP GS SVKAÄNMP GS SVKAÄNMP GS SVKAÄNMP	D 360 PPEXRRAILEAF TKKRTANIEAF AEKROAILKAU PPEKLSVILKVF OHLRKLLV9TE KKRKAFEVF		380 KK FE DDL P KK WE P PN KK WE PE G I KK YE DE G I KK YE PE G I KK YE PE G I KK FE -DE GL IF	390 PN-LPPNVL MEN-QRANFF PN-QRANFF PN-QRANFF KH-LPPNVL KH-LPPNVL AR-LRKNVM AR-LRKNVM	40 IRKWLPOND TOKWLPOND IRKWLPOND IRKWLPOND IARWLPOND VRKWLPOND		0 421	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C3 6. AfUGT301C2 7. AfUGT301C3	220 230 240 PHEFLIX.YTDDNS F FORWART LLS LIXES B SERSTE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV TE SERSEL REV ANN TYOS F K R ALENCE TE SERSEL REV TE SERS	250 260 URRYYYLPEODRWRKH YWHDAAANKLES USWYDEGOALAORH VYTPSM-YLGHWRRHL IRGFYR BOMKLAOIH YRRMWIDAGOLAREYP	270 P	280 ELERN VSLVL ELVSN TSLIL ELVSN TSLIL ELQQR TSMF DLERQ VSVL ICLERS SIST	290 3 INSHPSI SYPRI INGHYTI SGARPI INGHYSI SGARPI INSYPPI TSTRAK NGQAS VTYPRI INSHI I STAPRI INSHI I SRPRI INSHI I SRPRI	300 3 IPPNMIEVGGLI IPSVIEIGGVI IPSVIEIGGVI IPSVIEIGGVI IPVAEIG IPVAEI	10 32 HI Q-SNKPLPX HI Q-SNKPLPT HI Q-SNKPLPT HI Q-SKRPT HI Q-	0 330 DLQQFLDGA DLQQLDTA DLQLDTA 	340 	350 GSNLRSADLP GSVLKAÄTLP GSVLKAÄTLP GSVLKAÄNNP GSSVKAÄNNP GSSVKKSADNP GSYMKSADNP GAVMGSAVNP GTFLRSSGNP	D 360 PEXRRAILEAF TKKRTAMIEAF ACKROATLKAL PPEKLSVTLKVF DHLRKLLVVTE SKDKKKAFLEVE VEKRTALLKVF PETLEVFLDLF		380 WK FE DDL F WW P PN WK FE PC 60 WK YE PC 61 WK YE PC 61 WK YE PC 61 WK YE PC 61 WK WE AD T	390 PN-LPPNVL PN-QRANVH KH-LPPNVL TD-LRANVH ND-VPPNVL PN-LRSNVL	40 IRKWLPOND TOKWLPOND IRKWLPORE VRSWLPOSD IARWLPOSD IARWLPOSD ISKWAPOND ISKWAPOND		0 421	0 430 EATENGY PTY EATYCGY PYY EATYCGY PYY EGYTRAY PTY EGYTRAY PTY EGYTRAY PTY EGYTRAY PTY EATHGY PYL
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT30B8 5. AfUGT301A3 6. AfUGT301C2 7. AfUGT301E3 8. AfUGT302A3	220 230 240 PHPFLXYTCOMS FORWYNTLLSUCKX F SEESTSEERISE FORWYNTLLSUCKX F SEESTSEERISE FORWYNTLLSUCKX F SEESTSEERISE FORWYNTLLSUCKXX F SEESTSEERISE FORWYNTUNUS FUNCTUUE F YF YR PATDONS FE'R ANN TYOSFK' PHFLYLLSUCKXXX F SEESTSE FORWYNTUNUS FE'R FUNCTUUE F YF YR PATDONS FE'R ANN TYOSFK' PHFLYLLSUCKXXX F SEESTSE FORWYNTUNUS FE'R FUNCTUUE F YF YR PATDONS FE'R ANN TYOSFK' PHFLYLLSUCKXXX F SEESTSE FORWYNTUNUS FE'R FUNCTUUE F YF YR PATDONS FE'R ANN TYOSFK' PHFLYLLSUCKXXX F SEESTSE FORWYNTUNUS FE'R FUNCTUUE F F		270 P		290 3 INSHPSISYPRI INSHPSISYPRI INSHYSISGARPI INSHYSISGARPI INSHISTAPRI INSHISTAPRI INSHISTAPRI INSHISTAPRI INSHISTAPRI	300 31 PPNMIEVGGU PSVIEIGGV UPSVIEIGGV VPAVEIGGV VPAVEIGGV VPAVEIGGV SIGUVUGGG SIGUVUGGG SIGUVUGGG	10 32 HIK - PPKPLPE HIG-SNKPLPT HIG-SNKPLPT HIK-ERKLPC HCK-PASALPK HCK-PASALPK HCK-PASALPK HIK-PAKELPE HIR-KEKPLPS HVNRKINPLPE	0 330 DLQOFLDGA ELQOFLDGA DLQOLLDTA DLQTEIDGA DLFFLDGA DLFFLDGA DLFFLDGA DLFFLDGA DLFFLGA	340 - RIGVIYFSU - PINGVIVVSF - DFGVIYFSU - ROVIFSU - ROVIFSU - RESISTIVS - RESISTIVS - ROVIFSU - ROVIFSU - ROVIFSU - ROVIFSU - ROVIFSU	350 GSNLRSADLP GSVLKAÄTLP GSVLKAÄTLP GSVLKAÄNDP GSSVKAÄNDP GSYMKSADVP GAYMGSÄVRP GTFLRSSGMP GSNLKPSKMD	D 360 PERRAILEAF ARKRIAILEAF ARKRIAILEAF ARKRIAILEAF ARKRIAILEAF KLLVOTE KLLV	370 RXLKQYRFU QHEDQ-RVV GR KQ-RVV GS KQ-RVV RN KQ-RVV RN KQ-RVV RT EQ-RVV RT EQ-RVV RT EQ-RVV RT EQ-RVV	380 WK FE DDL F WK WE P FN WK WE PC G G WK YE PC G G WK YE PC G G WK WE PC G WK WE PC G G WK WE PC G WK WE PC G WK WE PC G G WK WE PC G WK WC PC C WK WC PC C WK WC PC C WK WC PC C WK WC	390 PN-LPPNVL PN-CRANFF RN-CRANFH KH-LPPNVL TD-LRANFH AR-LRANFH AR-LRANFH PN-LRSNVL VL-DKKKFL	40 IRKWLPOND IRKWLPOND IRKWLPOND IRKWLPOND IARWLPOND ISKWAPOND LORWISQND		0 421	0 430 EALIXHOV PIV EAVHCGV PVV EAVHCGV PVV EAVHCGV PVV EGVHRAVENV EGVHRAVENV EGVHRAVENV EGVHRAVENV EGVHRAVENV EGVYRAVENV
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301A3 6. AfUGT301C2 7. AfUGT301C3 8. AfUGT302A3 9. AfUGT302H3	220 230 240 PHPFILXYTODIXS FEORWYNTLLSILXXXX E SEISYS EE RYSEL KWENNUTLUSILXXXX E SEISYS EE RYSEL KWENNUTUUSIKXXXX E SEISYS EE RYSEL KWENNUTUUSIKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		270 P		290 3 INSHPSISYPPI INSHVISGARPI INSHVISGARPI INSHVISGARPI INSHVISGARPI INSHLSTSARPI INSHLSTSAPRI INSHLSTSAPRI INSHSISSPRY INSHSISSPRY	300 3: LPPNIEUGGU LPSVIEIGGV LPSVIEIGGV LPSVIEIGGV LPNVAEIACU LPNVAEIACU LPNVAEIACU SIRGLVUIGGV VIPNIEUGGV VVPNIEUGGV	10 32 HIK - PPKPLPE HIR-DIKPLEA HIK-ERKLED HCK-PASALEK HIK-PAKELEE HIR-AKKLED HIR-KKELEE HIR-KKELEE HIR-KKELEE HVRKINPLEE HVRKINPLEE	0 330 DLQOFLDGA 	340 KNGV I Y F SLI PNGV I V SFI DFGV I V SFI K GVI Y F SLI R GVI F SLI R GVI Y F SLI F	350 G SNLRSADLP G SV LK A&T LP G SMLRA AT LP G SVLK A&T LP G SVLK A&NNP G SVKK A&NNP G SVKK A&NNP G SVKK A&NNP G SVKK SADVP G SNLK SKNL G SNLK SKNL G SNLK SKNL	360 PERRATLEAF TKRTGMIEAE AERGAILKAL SPEKLSVIKKA SOHERLLVOTE KLKTGAILKAL SOHERLLVOTE KLKTGAILRVE SOHERLLVOTE	370 RXL KQYR F W GR KQ - RVVW GR KQ - RVVW AR P - YRVW RN KQ - RVW GT E E RVW SS KQ - NVW SS KQ - NVW SS KQ - NVW	380 XK FE DDL F XK WE PN XK FE PE G J XK YE NE D J XK YE NE D J XK YE NE D J XK WE PD T J XK WE PD T J	390 PN-L PPNVL MEN-GRAHFFT PN-GRANFH KH-L PPNVL TD-LRANFH AR-LRANFH PN-LPSNVL PN-LPSNVL PN-RPANFI	40 IRKWLPOND IRKWLPOND IRKWLPOND IRKWLPOND IARWLPOND ISKWAPOND ISKWAPOND ISKWAPOND		0 421	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 4. AfUGT36C3 5. AfUGT301C2 7. AfUGT301C2 7. AfUGT301C3 8. AfUGT302H3 10. AfUGT302J2	220 230 240 PHEFUEXTIDANS FORMATING SUBAR	250 260 LRRVYY LEODRAWKH YSWENDAAANKI LKAR SWENDAAANKI LKAR USWENDAAANKI LKAR USWENDAAANKI LKAR WYTPSM-YLOHWARH USYMCU LARVY KRF WLOHWARH LSHVDE VOAMYYKK SHVIDE VOAMYYKK SHVIDE VOAMYYKK	270 P		290 3 INSEPSISYPPI INSEPSISYPPI INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSEPSIS INSESSE INSESSEPSIS INSESSE INSES	SOO 3: PPNMIEVGGU SPNMIEVGGU SPNMIEVGGU SPAVLEIGGU SPAVLEIGGU SPAVLEIGGU SPAVLEIGGU SPAVLEIGGU SPAVLEIGGU SPAVLEIGGU SPNMIEIGGU SPNMIEIGGU		0 330 DL QO FL DGA DL QO FL DGA DL QU L D TA DL QU L D TA DL QU FL DGA DL FOFL AGA DL ROFING FA DL ROFING FA 	340 	350 GSNLRSADLP GSVLKAÄTLP GSMLRAETLP GSVKAÄNNP GSVKAÄNNP GSVKAÄNNP GSVKAÄNNP GSVKSADVP GSNLKSSVVP GSNLKSSVP GSNLKSSVP	C 360 PERRAILEAF TKRTAMIEAE AEKROAILKAL VEKRTAILKAL VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILRVE VEKRTAILVEF	370 RX K VYR F W QHFDQ - RVW GS K Q - RVW AR P - YRVW RN K Q - RVW GT EQ - RVW GT EQ - RVW AK K Q - NI W AK K K Q - NI W AK K K Q - NI W	380 KK FE DDL F KK WE F PA KK WE PE G KK FE PE G KK FE PE G KK FE PE G KK WE PE TL KK WE PE TL KK WE PE TL KK WE PE TL	390 PN-LPPNVL PN-QBAHFF PN-QBAHF ND-QBANFH AR-LBANFH AR-LBANFH PN-RBANFH PN-RBANFH PN-RBANFH PN-RBANFH PN-RBANFH	40 IRKWI POND TOKWI POKD IRKWI POKD IRKWI POKD IRKWI POKD ISKWI POND LORWI SOND URKWI PODD VKAWN PODD		0 421	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT30HA3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A2 11. AfUGT302A2	220 230 240 PHEFEUX TIDONS FORWART LISURES IS SENTIFIC SUBJECT AND STRUCTURES IN STRUCTURES IS SENTIFIC SUBJECT AND STRUCTURES IN SUBJECT SUBJECT AND STRUCTURES IN SUBJECT AND STRUCTURES INTER STRUCTURES IN SUBJECT AND STRUCTU	250 260 IRRYYY DEODRAWK H IRRYY DEODRAWK H ISSWEDDAAANK LEARE ISSWEDDAAANK LEARE ISSWEDDAAANK LEARE ISSWEDDAAANK LEARE ISSWEDDEODRAWK AN ISSWEDDEODRAWK AN ISSWEDEODRAWK AN ISSWEDEODRAWK AN ISSWEDEORAWK AN ISSWEDEORA	270 P		290 3 INSHPSISVPRPL INSHVISSARPL INSHVISSARPL INSHVISSARPL INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR INSHVISSARPR	LPPNMIEVGGU	10 32 HIK-PRKPLPZ HIC-SNKPLFT HIK-SNKPLFT HIK-SKRLFT HIK-PAKELFE HIK-PAKELFE HIK-PAKELFE HIK-KKPLFS HVNRKINPLFE UNRKENPLFE UNRKENPLFE UNRKENPLFE UNRKENPLFE		340 			370 RELKOYR FUX GRECORVIN GRECORVIN GSMC	380 WK FE PDL F WK WE P PN WK WE PE G WK YE PE G WK YE PE G WK YE PE T WK YE PE	390 PN-LPPNVL MEN-QRANYF PN-QRANYF KH-LPPNVL TO-LPANYF PN-LPSNVL PN-LPSNVL PN-RPNVL PN-RPNVL PN-RPNVL PN-RPNVF			0 421	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301A3 6. AfUGT301C2 7. AfUGT301C3 8. AfUGT302H3 10. AfUGT302H3 10. AfUGT302J2 11. AfUGT302J2 12. AfUGT306A3 12. AfUGT306C2	220 230 240 PHP FLXX TODAS F FORWANT LLSLX 652 F SEESTE SEE USE LEVEL AM IN TVOS FK F ALENK (TTERMO 500 400 400 100 100 100 100 100 100 100 1	250 260 IRRYYY FEORX ANN F IS WY LEODRAWNELL IS WY LEODAANKELL BAR IS WY LEODAANKELL BAR IS WY LEODAANKELL BAR IS YN IS OAL ANN F IS WY LEODAANKELAR IS WY LEO	270 P		290 3 INSESSIVERE INSESSIVERE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INSESSIVE INTESS	300 3 LPPNMIEVGGU LIPSVIEIGGV LPVMIEVGGV LPVMIEVGGV LPVMIEVGGV LPVMIEVGGV LPVMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV VPNMIEVGGV			340 				380 WK FE DD F WK FE P P D WK FE P E G WK FE P E	390 PRI-LPPNML PRI-CRANNEL PRI-CRANNEL RH-CRANNEL RH-CRANNEL RH-CRANNEL PRI-			0 421	0 430 A LECHGY OF DY EAVELOUVE VI EAVELOUVE VI EAVELOUVE VI ECVIRA VEW ECVIRA VEW E
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C2 7. AfUGT301C2 7. AfUGT301C3 9. AfUGT302H3 10. AfUGT302H3 10. AfUGT306A3 12. AfUGT306C2 13. AfUGT306C2	220 230 240 PHEFUEXTIONS FORWART LISUES BEEN TO SEFERENCE THE SUBJECT SET SET SET SET SET SET SET SET SET SE	250 260 IRREVIEW I FOREXIKE F IRREVIEW I FOREXIKE F IRREVIEW I FOREXIKE F IRREVIEW I FOREXIE F IRREVIEW I FOREXIE IRREVIEW I FOREXIE IRREVI	270 P		290 3 UNSEPSISTER NOT SCARPL NOT SCARPL NS PETSTRAG NS PETSTRAG NS PETSTRAG NSELS SCARP NSELS SCARP NS		10 32 HIK-PRKPLPE HIG-SNKPLET HIK-ERKRED HIK-ERKRED HIK-ERKRED HIK-KREDE HIK-KREDE UNRKNENPEE UNRKKENPEE GIG-PEKKEPT GINLAKEOPEE KIKOKESPEE	0 330 	340		360 PERRAILERE TKKRTAILERE AKROALKAI PERLSVIKKE PERLSVIKKE COLKKLLVTE KDKMKAFLEVE PERLSVIK VERTALRVE VERTALRVE EDKRIGFUVVE EDKRIGFUVVE EDKRIGFUVVE EDKRIGFUVVE EDKRIGFUVVE EDKRIGFUVVE EDKRIGFUV		380 WK FE DD L F WK FE E PA WK WE NE T WK FE NE T WK WE NE D WK FE DE G WK WE NE T WK WE NE SL WK WE NE SL WK WE OE E WK WK OE E WK				0 421	0 430 EALECHEGV DEW EALYCESWE W EALYCESWE W ECYFRAVESWE W ECYFRAVESWE ECYFRA ECYFRAVESWE ECYFRAVESWE ECYFRAVESWE ECYFRAVESWE E
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT30H3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 11. AfUGT306A2 12. AfUGT306C2 13. AfUGT306C2 13. AfUGT306A3	2.20 2.30 2.40 PHEFELXY TOOMS FOR VANITUS LICES E SEESTE SEE INSEED SERVICES LICES PALENCET TOOMS FOR ANY TYPE SEE PHEFELP FITS OF SEE ANY TYPE SEE PHEFELP FITS OF SEE ANY TYPE SEE PHEFELP FITS OF SEE ANY TYPE SEE PHEFELS FITS OF SEC ANY TYPE SEC ANY TYPE SEE PHEFELS FITS OF SEC ANY TYPE SEC ANY TYPE SEE PHEFELS FITS OF SEC ANY TYPE SEC	250 260 IRRYYY I DEORX VAR H VI BOOL DOWNLLKAR IVB VOI DOWNLLKAR IVS VOI DOWNLLKAR IVS VOI DOWNLLKAR IVS VOI DOWNLAR IVS VOI DOWNLAR I	270 P		290 3 ANSHESISYERE ANSHESISYERE ANSHESISYERE ANSHESISSARE ANSHESISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE ANSHISSARE			0 330 									0 422 THGGL STO STO STO STO STO STO STO STO	0 430 A LICH GUY TUY E A VICE SUP VI E A VICE SUP VI E A VICE SUP VI E C VIRA XUE VI E C VIRA XUE VI E C VIRA XUE VI E SI VIRA VIE S IN HOUSE VIL E SI VIRA VIE E SI
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C3 6. AfUGT301C2 7. AfUGT301C3 8. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 10. AfUGT302A3 11. AfUGT306A3 12. AfUGT306D2 13. AfUGT306D2 14. AfUGT308B3	220 230 240 PHP FLXX TIDDXS F FORWAYNTULUS LX 828 F SEISTE SE INSE FORWAYNTULUS LX 828 F SEISTE SE SE SE INSE FORWAYNTULUS LX 828 F SE SE SE SE SE SE SE SE INSE FORWAYNTULUS LX 828 F F	250 260 IRRYYY FEORXXXXX IRRYYY FEORXXXXXX IRXYY EOXALLKAN IRXYY EOXALLXXXX IRXYY EOXALLXXXX IRXYY EOXALLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	270 P		290 3 ANSHESI SYPREI ANSHESI SYPREI ANSHESI SYPREI NG YSISSARPI NG	300 3 LP P MMI EVGGLI 1 LI P SVIELIGGY 1 LI P SVIELIGY		0 330 	340 								0 422 V V SEGEL (2VS) V SEGEL (2VS) V SEGEL (2VS) V SEGEL (2VS) I THGGL (2VS) I THGGL (2VS) I THGGL (2VS) I SEGEC (2VS	0 430 A 112 H 52 V 112 E A 12 H 52 V 12 E A 1
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C2 7. AfUGT301C2 7. AfUGT301C3 9. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT306A3 12. AfUGT306A3 12. AfUGT306C2 13. AfUGT308A3 15. AfUGT308B3 16. AfUGT308C3	220 230 240 PHEFLEX TIDONS FORWART LISTERS SECTORS FORWART LISTERS SECTORS FORWART LISTERS SECTORS FOR SET AND TOPS FOR SECTORS FOR ANY TYPES FOR ANY TYPES FOR FOR SET FOR ANY TYPES FOR ANY TYPES FOR FOR SET FOR ANY TYPES FOR ANY TYPES FOR FOR SET FOR ANY TYPES FOR FOR THE SET FOR ANY TYPES FOR FOR ANY TYPES FOR FOR THE SET FOR ANY TYPES FOR FOR ANY TYPES FOR FOR THE SET FOR ANY TYPES FOR FOR ANY TYPES FOR FOR THE SET FOR ANY TYPES FOR FOR ANY TYPES FOR FOR ANY TYPES FOR FOR FOR ANY TYPES FOR FOR ANY TYPES FOR FOR FOR ANY TYPES FOR FOR FOR ANY TYPES FOR FOR ANY TYPES FOR FOR ANY TYPES FOR FOR FOR FOR ANY TYPES FOR FOR FOR ANY TYPES FOR FOR FOR FOR ANY TYPES FOR FOR FOR	250 260 IRREVIEW IF FOR X 444 IRREVIEW IF FOR X 444 IRREVIEW IF A CONSULTANT IRREVIEW IF A C	270 P		290 3 UNSEPSISTER NOT STANDARD NOT STANDARD			0 3300 	340 KINGVIYF F CI PNIGVIYF KOVIYF KOVIYF KOVIYF KOVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIYF COVIF	350 SNURSADLP SS			380 WK F III DDL F WK WIII E P P WK WIIII E P P WK WIIII E P WK WIIII E P WK WIIII E P WK WIIII DD F WK WIIIII DD F WK WIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	390 PRI- CPENT PRI- CP			0 422 1 THGGL (STO VERGEL (SS) 1 THGGL (SS) 1 THGCL (S	0 430 EAUECHGVVDIW EAUCGSVVDIW EAUCGSVPIW EAUCGSVPIW EGVHRAVEGSVV EGVHRAVERVV EGUHRAVERVU EGUHRAVERVI EGUHRAVERVI EGUHRAVERVI EGUHRAVERVI EGUHRAVERVI EGUHRAVERVI EAUCHGVPIW
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 3. AfUGT39A4 4. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A2 11. AfUGT306C2 13. AfUGT306C2 13. AfUGT308D3 14. AfUGT308B3 16. AfUGT308B3 16. AfUGT308D2	220 230 240 PHEFEIX TIDONS FORWART LISUSES IS DESTINATIONS FORWART LISUSES IS DESTINATIONS FORWART LISUSES IS DESTINATIONS FORWART LISUSES IS DESTINATIONS FOR ANY TYPE IN	250 260 RRYWY PEORX AK H VI BOOR VIEW AND	270 P		290 3 ANSHESISYERE ANSHESISYERE ANSHESISYERE ANSHESISSARE ANSHESISSARE ANSHESISSARE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE ANSHESISSERE			0 3300 	340 KINGVI IV F SL FINGVI IV F SL FINGVI IV SF FORMATING KORANI V SF KORANI V SF KORANI V SF KORANI V SF KORANI V SF FORMATINF FORMA	350 SNLRSADIP SVLKABIP SVLKABIP SVLKABIP SVLKABIP SVKABN S	360 PERRATLEAF TKKRTMIEAE TKKRTMIEAE TKKRTMIEAE PERKSVILKYF OHLKLLVYTE PERKRATEVF OHLKILVYTE OHLKILVYTE OHLKILVYTE OHLKILVYTE TKKRTAILTR		380 WK FE				0 422 1 Hagi 15 Tol 1 Hagi 16 (15 Tol)	0 430 ALIENG V TW EAVING SAVE VI EAVING SAVE VI EAVING SAVE VI ECVINA VERVE ECVINA VERVE ECVINA VERVE ECVINA VERVE ECVINA VERVE ECVINA VERVE ESI VERVE ES
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 3. AfUGT30183 5. AfUGT301R3 6. AfUGT301R3 6. AfUGT301C2 7. AfUGT30123 9. AfUGT302A3 9. AfUGT302A3 9. AfUGT302B3 10. AfUGT306A3 12. AfUGT308C2 13. AfUGT308C3 15. AfUGT308C3 16. AfUGT308C2 18. AfUGT308C2	220 230 240 PHP FLXX TIDOXS F FORWAYNTLLSI X 420 PHP FLXX TIDOXS F FORWAYNTLLSI X 420 PL ST		270 P		290 3 ANSHES SYPRE ANSHES SYPRE ANSHES SYPRE ANSHES SARE ANSHES SARE ANSHES STARE ANSHES ANSH			0 3300 			360 PERRAILEAF TKKETAMIBAE AFKEDAMIBAE AFKEDAMIBAE PEKLSVILKVF OHLKLLVTF VKRTAILRVF VKRTAILRVF VKRTAILRVF OHLKAILSAILE GONLLJAILRTF TEMLSAILE DER IKALVAT DER IK			390 PRN-LPPNNL KH-LPPNNL KH-LPPNNL KH-LPPNNL KH-LPPNNL RN-LPRNL PN-LPRNL PN-LPRNL PN-LPRNL PN-LPRNL PN-LPRNL PN-LPPNNL PN-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL II-LPPNNL			0 422 V V SHGGL (SYS) V SHGGL (SYS) I THGGL (SYS) I THGGL (SYS) I THGGL (SYS) I THGGL (SYS) I SHGGC (SYS) I SHGC (0 430 A 112 H 52 V 112 E A 12 H 52 V 12 E A 14 C 52 V 12 E A 1
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301C2 7. AfUGT301C2 7. AfUGT301C3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 10. AfUGT302A3 12. AfUGT306A2 13. AfUGT306A2 13. AfUGT308A3 15. AfUGT308B3 16. AfUGT308B3 16. AfUGT308B3 16. AfUGT308C2 18. AfUGT308C2 19. AfUGT308C2 19. AfUGT308C2 19. AfUGT308C2 10. AfUGT30C2 10. AfUG	220 230 240 PHEFLEX TIDOXS FORWART LISTERS SECTORS FORWART LISTERS SECTORS FORWART LISTERS SECTORS FOR SECTOR AND TOOS FOR SECTORS FOR AND TOOS FOR USED FOR SECTORS FOR AND TOOS FOR PHEFLE FOR SECTORS FOR AND TOOS FOR PHEFLES FOR AND TOOS FOR DEPENDENT FOR AND TOOS FOR PHEFLES FOR AND TOO FOR AND TOO FOR PHEFLES FOR AND TOO FOR AND TOO FOR PHEFLES FOR AND TOO		270 P		290 3 UNSEP SISPERI NOT SISPERI NOT SISPERI NOT SISSE NOT SISSE NO			0 3300 		350 SNURSADIP SVILKABTP SV							0 422 1 THGGL 5 TO 1 THGGL 6 5 1 THGGL 6 5 1 THGGL 6 5 1 THGGL 6 7 1 THGGL 6 7 1 THGGL 5 TO 1 THGGL 5 TO	0 430 EAUECHGVVDIW EAUCGVPTW EAAVCGVPTW EAAVCGVPTW ECVHRAVEGVV EGVHRAVEGVV EGVHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EGUHRAVEFW EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU EAAVFBGVEU
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT30B4 5. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 12. AfUGT306A2 13. AfUGT306A2 13. AfUGT306A2 14. AfUGT308A3 15. AfUGT308B3 16. AfUGT308B3 17. AfUGT308C2 19. AfUGT308C2 20. AfUGT308C3	2.20 2.30 2.40 PHEFEIX TIDONS FORWART LISTESS FORWART LISTESS FORWART LISTESS FORMART FOR FORMART FOR FORMART FOR FORMART FOR FORMART FOR FORMART FOR FORMART	250 260	270 P		200 3 ANSHESISYERE ANSHESISYERE ANSHESISS			0 3300 	340 KINGVI IV F SL PINGVI IV F SL PINGVI IV SF PINGVI IV SF PINGVI IV SF COMMISSION KINGVI IV SC KINGVI IV SC ROMANNI F SL FORMANNI		360 PERRATLEAF TKKRTMIEAF TKKRTMIEAF TKKRTMIEAF PERINE TKKRTMIEAF PERINE TKKRTMIEAF PERINE TKKRTMIEAF TKKRTAILST T						0 422 1 Hage 15 TO 1 Hage 16 (1) 1 Hage 16 (1)	0 430 ALIENG V TW EAVING SAVE VI EAVING SAVE VI EAVING SAVE VI ECVINA VERVE ECVINA VERVE ECVINA VERVE EVINA VERVE
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 3. AfUGT3044 4. AfUGT30183 5. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT306A2 11. AfUGT306A2 12. AfUGT308C2 13. AfUGT308C3 16. AfUGT308C3 17. AfUGT308C2 19. AfUGT308C2 19. AfUGT308C2 20. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3	220 230 240 PHP FLXX TIDOXS F FOR VINT LLSL X 420 PHP FLXX TIDOXS F FOR VINT LLSL X 420 PL FLXX TIDOXS F FOR VINT LLSL X 420 PL FLXX TIDOXS F FOR VINT LLSL X 420 PL FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F FLXX AVX TIDOXS F V X 400 PHP FLXX TIDOXS F V F X 400 PHP FLXX TIDOXS F V X 400 PHP FLXX TIDOXS F V X 400 PHP FLXX TIDOXS F V F X 400 PHP FLXX TIDOXS F V X 400 PHP FLXX TIDOXS F V T X 400 PHP FLXX TIDOXS F V F X 400 PHP FLXX F X 400 PHP FLXX TIDOXS F V F X 40	250 260 IRRIVIY PEODRENARIE ISSUE 1000 IRRIVIY PEODRENARIE ISSUE 1000 ISSUE 1000 IRRIVIE 000 IRRIVIE 0000 IRRIVIE 0000 IRRIVIE 0000 IRRIVIE 0000 IRRIV	270 P		290 3 290 3 2015 25 25 25 25 25 25 25 25 25 25 25 25 25			0 330 	340 - KINGY II YF SL - PINGY II YF SL - RHGWLY F SL - RHGWLY F SL - RHGWLY F SL - RHGWLY F SL - FHGWLY F SL		360 PERRAILEAF TKKETAMIBAE KKETAMIBAE KKETAMIBAE PEKLSVILKVE PEKLSVILKVE VKRTAILRVE VKRTAILRVE VKRTAILRVE VKRTAILRVE VKRTAILRVE VKRTAILRVE PERLKAILVAN DERLKAILSI EDRLAILAIL DERLKAILSI EDRLAILAIL TERLAILSI ERRKIILVAN FERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN PERLKIILVAN						0 422 V SHGGL (SYS) V SHGGL (GYS) N HGGL (GYS) N HGGL (GYS) N HGGL (GYS) I HGGL	0 430 ALIENGUV TUV EAVERING VALUE EAVERING VALUE EAVERING VALUE EAVERNIK EAVERNIK <td< td=""></td<>
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT49A4 4. AfUGT50B8 5. AfUGT301A3 6. AfUGT301C2 7. AfUGT301C3 8. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 12. AfUGT306D2 13. AfUGT306C2 14. AfUGT308C3 15. AfUGT308C3 17. AfUGT308C2 18. AfUGT308C2 20. AfUGT308C2 20. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C4	2.20 2.30 2.40 PHEPLICATIONS FORWART LISTED SECTORS FORWART LISTED SECTORS FORWART LISTED SECTORS FOR SETURATION SECTOR SECTORS FOR SETURATION SECTORS FOR PHEPLICATION SECTORS FOR ANY TYPOS FOR PHEPLICATION SECTORS FOR ANY TYPO SETURATION PHEPLICATION SECTORS FOR ANY TYPO SETURATION PHEPLICATION FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION PHEPLICATION FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO SETURATION FOR ANY THIS FOR ANY TYPO ANY THIS FOR ANY THIS F	250 260 IRREVIEW DE DORENARME IRREVIEW DE DORENARME IRREVIEW DE DORENARME IRREVIEW DAAANKLE RAKE IRREVIEW DAAANKLE RAKE IRREVIEW DE DORAL AD DE IRREVIEW DE DORAL AD DE IRREVIEW DE DORAL AD DE IRREVIEW DE IRREVIEW IRREVIEW DE IRREVIEW IRREVIEW DE IRREVIEW IRREVIEW DE IRREVIEW IRREVIEW DE IRREVIEW IRREDIEW DE IRRIVER IRREDIEW IRREVIEW IRREDIEW IRREVIEW IRREVIEW IRREDIEW IRREVIEW IR	270 P		200 3 200 3 2015 2 2016 2	300 3 LP PRMIEVGGL 1 LIP SWIEVGGL 1 LIP SWIEVGGL 1 LIP SWIEVGL		0 3300 		350 SVLRSADIP SV	360 PERRALLEAF TKRETAHIEAF TKRETAHIEAF TKRETAHIEAF TKRETAHIEAF DELKKULVOT DELKKULVOT DELKKULVOT DELKKULVOT DETLEVEN DETL						0 422 V HGGL (S TO V HGGL (S	0 430 EAUECHCVVDIV EAUCCSVVDIV EAUCCSVVDIV EAUCCSVVDIV ECVHRAVESVVDI ECVHRAVESVVDI ECUHRAVERV EUUHRAVERV EUUHRAVERV EUUHRAVERV EUUHRAVERV EUUHV
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT39A4 4. AfUGT30H3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 11. AfUGT306A2 12. AfUGT306A2 13. AfUGT306A2 14. AfUGT308A3 15. AfUGT308B3 16. AfUGT308B2 18. AfUGT308C3 20. AfUGT308C2 20. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C4 22. AfUGT308C4 22. AfUGT308C4 23. AfUGT308C4 23. AfUGT308C4 23. AfUGT308C2 23. AfUGT308C4 24. AfUGT308C4 25. AfUGT308C4 25. AfUGT308C4 26. AfUGT308C4 26. AfUGT308C4 27. AfUGT308C4 27. AfUGT308C4 28. AfUGT308C4 28. AfUGT308C4 29. AfUGT308C4 20. AfUG	220 230 240 PHEFEXATIONS FORWART LISTENS FORWART LISTENS FORWART LISTENS FORMART FOR STATEMENT LISTENS FORMART FOR STATEMENT FOR A STATEMENT FOR STATEMENT FOR STATEMENT FOR STATEMENT FOR A STATEMENT FOR A STATEMENT FOR STATEMENT FOR A STATEMENT FOR A STATEMENT FOR STATE	250 260 RRYWY PEODREWARK F VI BOURS VIEW F VI BOURS VIEW F VI BOURS VIEW F VI BOURS VIEW F VI PSMILLER F VI PSMI	270 P		290 3 ANSHESI SYRRI ANSHESI SYRRI			0 3300 	340 KINGVI IV F SL PINGVI IV SF PINGVI IV SF PINGVI IV SF PINGVI IV SF COMMISSION KINGVI IV SC ROMAN ROMA		360 PERRATLEAF TKKRTMIEAF TKKRTMIEAF TKKRTMIEAF TKKRTMIEAF PERKLIVTE PERKLIVTE PERKLIVTE PERKANE TAMLSALLTTE TA						0 422 V Hagel L STO V Hagel L STO I Hagel STO	0 430 ALIENG VETW EAVING SAVE VE EAVING SAV
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT36C3 3. AfUGT30A3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT301C2 7. AfUGT301C3 9. AfUGT302A3 9. AfUGT302A3 9. AfUGT302P4 10. AfUGT306A2 11. AfUGT306A2 12. AfUGT306A2 13. AfUGT308C2 14. AfUGT308C3 16. AfUGT308C3 16. AfUGT308C3 17. AfUGT308C2 19. AfUGT308C2 20. AfUGT308C2 20. AfUGT308C4 22. AfUGT308C4 23. AfUGT308C4 23. AfUGT308C4 24. AfUGT308C4 24. AfUGT308C4 24. AfUGT308C4 24. AfUGT308C4 24. AfUGT308C5 24. AfUGT308C5 25. AfUGT308C5 26. AfUGT308C5 27. AfUGT308C5 27. AfUGT308C5 28. AfUGT308C5 29. AfUGT308C5 20. AfUGT	220 230 240 PHP FLXX TIDONS FOR VAYIN LISUKAS F DESTINATIONS FOR VAYIN VALUEN F DESTINATIONS FOR VAYIN VALUEN F DESTINATIONS FOR VARIANS FY SWYELL F VALUENS F DESTINATIONS FOR VARIANS F DESTINATIONS FOR VARIANS F DESTINATIONS FOR VARIANS F DESTINATIONS FOR VARIANS F DESTINATIONS F		270		290 3 ANSHES SYPRI ANSHES SYPRI ANSHES SYPRI ANSHES SARPE ANSHES SARPE ANSHES SARPE ANSHES SARPE ANSHES STAPPE ANSHES STAPPE ANS ANSHES ANSHES STAPPE ANS ANSHES ANSHES STAPPE ANS ANSHES ANSHES STAPPE ANS ANSHES ANSHES STAPPE ANS ANSHES ANSHES STAPPE ANSHES ANSH		10 322 HIK - PEKU PE HIQ - SNKEL PE HIQ - S	0 330 	340 KINGY II YF SL PINGY II YF SL PINGY II YF SL PINGY II YF SL PINGY II YF SL FORM I YF SL F					390 PRI- LPPNUL KIN- LPPNUL KIN- LPPNUL KIN- LPPNUL KIN- LPPNUL PRI- LPPNUL PRI- LPPNUL PRI- LPRNUL PRI- LPRNUL PR			0 422 V S HGGL (S Y C) V S HGGL (G V) N HGGL (G V) N HGGL (S V) I HGGL	
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT39A4 4. AfUGT30B8 5. AfUGT301A3 6. AfUGT301A3 6. AfUGT301A3 7. AfUGT301C2 7. AfUGT301C3 8. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 11. AfUGT306C2 13. AfUGT306C2 14. AfUGT308C3 15. AfUGT308C3 16. AfUGT308C3 17. AfUGT308C2 18. AfUGT308C2 19. AfUGT308C2 20. AfUGT308C2 20. AfUGT308C2 21. AfUGT308C2 22. AfUGT308C2 23. AfUGT308C2 24. AfUGT308C2 24. AfUGT308C2 25. AfUGT	2.20 2.30 2.40 PHEFELX TIDONS FORWART LISE COM- RESENT SENSE LONG STOREASTING STORE RESENT SENSE LONG STORE AND TYPOSF KI RESENT SENSE COMPARED STORE STORE AND TYPOSF KI RESENT SENSE COMPARED SENSE FOR AND TYPOSF KI RESENT SENSE SENSE COMPARED SENSE FOR AND TYPOSF KI RESENT SENSE SENSE COMPARED SENSE FOR AND TYPOSF KI RESENT SENSE SENSE SENSE COMPARED SENSE FOR AND TYPOSF KI RESENT SENSE SENSE FOR AND TYPOSF KI RESENT SENSE SENSE FOR AND TYPOSF KING RESENT SENSE FOR AND TYPOS	250 260 IRREVIEW DE DORZUNKE H IRREVIEW DE IRREVIEW IRREVIEW DE IRR	270 P		290 3 ANSHE SISPERI ANSHE SISPERI			0 3300 		350 SVLRSADIP SV	360 PERRALLEAF TKRETAILEAF TKRETAILEAF TKRETAILEAF TKRETAILEAF TRESSON DELEAST							0 430 A LUE CHARNE VERTIM ALL A LUE CHARNE VERTIM ALL C A LAY AC ESTARE VERTIM ALL E C MER AC AND REV VERTIM ALL E C MER AC AND REV VERTIM ALL E S MY AC AND REV VERTIM ALL
Consensus Identity 1. AfUGT36B3 2. AfUGT36C3 3. AfUGT39A4 4. AfUGT30H3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT301A3 6. AfUGT302A3 9. AfUGT302A3 9. AfUGT302A3 10. AfUGT302A3 11. AfUGT306A2 12. AfUGT306A2 13. AfUGT306A2 14. AfUGT308A3 15. AfUGT308B2 16. AfUGT308B2 19. AfUGT308C3 20. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C3 21. AfUGT308C2 22. AfUGT308C2 22. AfUGT308C2 23. AfUGT308C2 23. AfUGT308C2 24. AfUGT308C2 25. AfUGT314B2 26. AfUGT314B2 27. AfUGT314B2 27. AfUGT314B2 28. AfUGT314B2 29. AfUGT314B2 20. AfUG	220 230 240 PHEFEXATIONS FORWART LISTENES IS DESTRICTIONS FORWART LISTENES INFORMATION IS DESTRICTION IN INFORMATION INFORMATION IS DESTRICTION INFORMATION INFORMATION IS DESTRICTION INFORMATION INFORMATION IS DESTRICTION INFORMATION INFORMATION IS DESTRICTION INFORMATION IS DESTRICTION INFORMATION INFORM	250 260 RRYWY PEODX 2444 IN 8 10 I - NONMEL KAR IV 8 10 I - NONMEL KAR IV 8 10 I - NONMEL KAR IV 9 10 I - NONMEL IV 9 10 I - NONMEL	270 P		200 3 ANSHESI SYRRI ANSHESI SYRRI		10 322 HIK - PPK-U PZ HIC - PKK-U PZ HIC - ShK-U PZ HIC - SKK-U PZ HIC -	0 330 	340 KINGVI IV F SL PINGVI IV SF PINGVI IV SF PINGVI IV SF PINGVI IV SF COMMISSION KINGVI IV SC RIGGI		360 370 370 370 370 370 370 370 37						0 422 1 Hagu 5 Tol V Hagu 6 (s) V Hagu 6 (s) 1 Hagu 6	0 430 ALIERASVE IV E ALIERASVE IV E EAVIESSNE VIE E </td

DBR2 signature motif

DBR1



signature motif

Fig. S1. Alignment of *An. funestus* **UGTs amino acids**. Alignment reveals that the C-terminal domain is more conserved than the highly variable N-terminal domain. The 29 amino acids sequence long signature motif on the C-terminal domain is highlighted by a red box. Conserved signature motifs including the DBR1 and the DBR2 motifs are highlighted in purple.





Fig. S2. Protein function analysis of UGT50B8. *An funestus* UGT50B8 was selected for functional analysis because UGT50 is the only family that is found universally in all insect species. Protein functional analysis conducted by InterPro scan http://www.ebi.ac.uk/ interpro/search/sequence/ indicates that the protein pfam Id is PF00201 belonging to the UDP glycosyltransferases superfamily (**A**). The functional analysis locates the UGTs conserved motif in the C- terminal domain. The majority of the protein is non-cytoplasmic resides in the endoplasmic reticulum (ER) while a small portion of the protein is cytoplasmic. The retention of the protein inside the ER is mediated by hydrophobic trans-membrane domain (**A**). The protein structure was predicted using AlphaFold (**B**). AlphaFold structures are colored using a per-residue confidence metric called pLDDT, which is scaled from 1 - 100. Very high (pLDDT > 90) Confident (90 > pLDDT > 70) Low (70 > pLDDT > 50) Very low (pLDDT < 50)

🔴 ABCs 🔵 COEs 🔵 CYPs 🔵 GSTs 🛑 UGTs







Fig. S3. Detoxification genes differential expression analysis in Malawi, Uganda,

Cameroon and the resistant colony FUMOZ. The transcription profiles of the resistant colony FUMOZ, filed-collected resistant mosquitoes from Malawi, Uganda and Cameroon was compared to the FANG transcription profile (**A-D**). In addition transactional profiles of filed-collected resistant population was compared to the transactional profile of a population of mosquitoes unexposed to permeation from the same same country (**E-G**). Differentially regulated genes were defined as those with a corrected p-value threshold of < 0.05 and log2(fold change) > 1 indicated by the dotted red line in each plot. Differentially expressed detoxification genes were color coded according to the plot legend.





Fig. S4. UGTs differential expression in the FUMOZ colony and in field-collected

mosquitoes from Malawi, Uganda and Cameroon. The transcription profiles of the resistant colony FUMOZ, filed-collected resistant mosquitoes from Malawi, Uganda and Cameroon was compared to the FANG transcription profile (**A-D**). In addition transactional profiles of filed-collected resistant population was compared to the transactional profile of a population of mosquitoes unexposed to permeation from the same same country (**E-G**). Differentially regulated genes were defined as those with a corrected p-value threshold of < 0.05 and log2(fold change) > 1 indicated by the dotted red line in each plot. Differentially expressed UGT genes were color coded according to the plot legend.



Fig. S5. Venn diagrams illustrating the comparison of differentially expressed genes.

The diagram displays the number of shared and unique differentially expressed genes between three different scenarios: 1) FUMOZ against FANG, 2) resistant field-collected population (R) against unexposed populations from the same country (UNEX), and 3) resistant field-collected population (R) against FANG. This comparison was conducted in Uganda (A), Cameroon (B), and Malawi (C).



Fig. S6. Gene-wise F_{st} for all genes included in the targeted sequencing in all analyses between resistant and susceptible. The average and 0.95 quantiles of gene-wise FST for each chromosome are represented by the blue horizontal line and the red horizontal line respectively. The genomic location of all genes in the targeted region (x-axis), represented by a circle, was plotted against the Gene-wise F_{st} (y-axis). Detoxification genes included by the targeted sequencing are color coded according to the plot legend.



Fig. S7. Gene-wise Tajima's D for all genes included by the targeted enrichment

sequencing. In each country plot, the average is represented by the blue horizontal line and he 0.5 quantiles and 0.95 quantiles are highlighted by the dotted red line. The genomic location of all genes in the targeted region (x-axis), represented by a circle, was plotted against the gene-wise Tajima's D (y-axis). UGT genes included in the targeted sequencing are color coded according to the plot legend.



Effects

Fig. S8. Effect caused by UGT genes significantly differentiated SNPs. Most of the differentiated UGTs' SNPs in all analyses are intronic SNPs. We focused our study on UGT genes non-synonymous SNPs that are significantly differentiated. Details of the number of UGT genes SNPs in each comparison including nonsynonymous SNPs are included in (Table S7).



UGT314A3

UGT306C2

UGT301A3

UGT306A3

 \bigcirc

UGT308G4

UGT302A3

UGT36C3

UGT301C2

 \bigcirc

FANG and FUMOZ UGTs all SNPs

Fig. S9. UGT genes SNPs divergence between laboratory colonies and in each

country. SNPs located within UGT gene are color-coded according to the plot legend. The blue dotted line indicates the average value in each comparison and the red dotted line indicates the significance level (p-value = 0.05).



Fig. S10. Hapotype network for *cyp6p9a*, *cyp6p9b* **and** *cyp9k1*. TCS haplotype network for *cyp9k1* reveal a directions selection in Uganda supporting previous findings **(A)**. While TCS haplotype network for cyp6p9a and b support previous observation of directional selection in southern Africa represented by Malawi and the resistant FUMOZ colony originally from Mozambique **(B and C)**. The red arrow highlights the dominant haplotype node.

	1	10	20	30	40	50	60	70	80	90
1. AfUGT314A3	MATNTLVL	LIAVIALL	RLTEAAKIL	AIFPVPLKQ	HQLVYRPLI	EELANRGHEI	VLVTTDPIDT	TTDRTNGSLDF	RIEQIDLSFAY	QLPVLEQLGQD
2. AfUGT308G4	MRYQAMKA	VLPVILML	AGV SQAAN I	LFMSSFPSP	SHHIWLRPL	I HEMGKRGHN	VTVL SADVE K	K P P A N V T Y I H I	ENLYSTMYNN	ITVKLDFFELAN
3. AfUGT308G3	MKAVLSVV	LVLAGVSQ	A <mark>AN I L FMS (</mark>	G <mark>VPSPSHYI</mark> W	L R P L MY E MG	KRGHNVTVL S	ADVEKPPAN\	TY I HLENFY	STMYNT SMR E K	LDFFELANQSP
4. AfUGT308G2	MKAVLSVV	LVLAGVSQ	A <mark>AN</mark> I L FMS O	G <mark>VPSPSHYI</mark> W	L R P L MY E MG	KRGHNVTVL S	ADLEKPPAN\	TY I HLENLYS	SAMYNTSMREK	LDFFELANQSP
5. AfUGT306C2	MKITQGVA	VAWAVLCC	CYA <mark>QLEAYF</mark>	R I L C I F P S S G	R <mark>S H V L V G Q A</mark>	LL <mark>K</mark> GL <mark>AER</mark> GH	DVTMV S P Y K L	SKSVPNYRE	I V I QKVDLGQN	ITKDFLQKNEGN
6. AfUGT306A3	MMKLTFNI	ALTLTLMLI	L T S H T E S A K	VCVFPTAS	<mark>K S H V L G A Q</mark> A	LL <mark>KELAFRG</mark> H	EVTMVSAFPL	KRPPNNYRD	/YV <mark>PIED</mark> AF <mark>ST</mark>	I MND F MQGGSR
7. AfUGT302A3	MLAYTMKP	IKSSVGAV	AFFGLIFMN	AQGIVEPAK	ILSIFPTMS	K S H W I L G S S L	M <mark>k e l aqn</mark> ghe	VTVISPFPL	<mark>KNAPKNYRHVD</mark>	VPYRTQMFED I
8. AfUGT301C2	MWLRFVFT	G <mark>CLFLLGS</mark>	<mark>√LSSAD</mark> G <mark>Yk</mark>	ILFLVPFPG	P S HWLML <mark>K H</mark>	FIRELTERQH	QVTC I TA F P F	GEKLQNYDE	ILIDPPYPIRE	TFPVEGLFASS
9. AfUGT301A3	MHLRVLSY	IVGCVFAF	TALCPRAEC	GKILFLVPF	PAPSHWLW	EHF <mark>VK</mark> ELLSR	GHEVTAITNE	AMKDPHRNY	FEVL I DPPYD I	PYYFPVSDIYE
10. AfUGT49A4	MHLVALVS	FLAASLQT	S S G <mark>AR I L S V</mark>	/NVFPGRSHW	MMIGSILEE	LLDRGHDVTV	ITNYPRKKPH	IPNL TE I V I DI	PIYDFWG <mark>K</mark> SVK	VDSLYDLTDIS
11. AfUGT36C3	MIMLRTVL	LVALALSPO	CAQTYKVLO	GLFPHPGQSH	FHFFQ <mark>PVLK</mark>	GLAEAGHEVT	VVSHFPEKNF	PPNYRDMPL	GM <mark>T</mark> SLS D SVS	FELFEYRPGFG
	100	110)	120	130	140	150	160	170	180
1. AfUGT314A3	GLDGRDML	RNIFDVMR	TISAEELQH	PAMQKLINS.	ANPRACDAG	KCN <u>H</u> FDVVMV	EWSGVTLMNA	\FA <mark>E</mark> HFRAPL\	/GIANGGAFIN	IAHEALGNPNHP
2. AfUGT308G4	QSPASILQ	Q F <mark>D K</mark> F L L T I		GLHLLLRYP	K E F K F D L F V	SDF <mark>MIGPCIP</mark>	AIIMHRFKD\	/ P Y I P S T P Y NA	APSTSVTVLGS	FAYPALVPNHV
3. AfUGT308G3	AKMLQLFD	EFGLNLCE	AAIKSEGLH	HFLLRY <mark>PKE</mark> F	K F D L F V S D F	MIGPCIPAII	MHRFKDLPFI	I P S T P Y N A P S ⁻	FSATVLGS FAY	PGLVPNHVFDA
4. AfUGT308G2	AKTLQIFN	EIGLNLCE	AAIKSEGLH	HFLLRY <mark>PKE</mark> F	K F D L F V S D Y	MIGPCIPAIV	MHRFKDVPYI	I P S T P Y N A P S ⁻	FSAAVLGS FAY	PGLVPNHMFDA
5. AfUGT306C2	SMASLVYL	FQSQMRTAI	EMALEDAK	/LALKHEHFD	LVIVGYFVA	DFVLGLGPHF	NAPTVVLFSA	AGMTKPTADF	/GNPRATAAVP	HLMLGG <mark>KGTMD</mark>
6. AfUGT306A3	NML K L F P K	I VRAAQDS	SNVTINAPE	FIRLAHEEQ	FDLALVGFF	MNSFIIGVGE	LFRCPTVLYF	SASGSGLTN	/VGNP <mark>A</mark> EVAAV	PHMLLGPRNPM
7. AfUGT302A3	MDEVFDKV	DDSIVEKL	I <u>Q</u> MGGFMHE	ITNTTLASP	E V Q S L L K S D	E <u>T</u> FDLLVLEI	FLNDAFLGFA	ADR F NC P V V GN	∕ISTFG <mark>A</mark> SS₩VN	ISLTGSPQPLSY
8. AfUGT301C2	QKSDFVKL	FMYWDLGF	NT SRHGLES	ENVRQF I RR	TDLEFDLII	A E Q F F Q E SWL	MFAHIYNAPI	I <mark>VT I ST</mark> YGY <mark>S</mark> [DFFDRIMGLQT	PWSFVPHMVLS
9. AfUGT301A3	SKYNSDLS	NLFLYWRV	GL <mark>STTQYA</mark> L	EDENVQQF I	EQDDTDFDV	I I <mark>S E</mark> QFYQ <mark>E</mark> A	FLMFAHKYRA	A <mark>P I VTLCT</mark> LGI	ANH I DQAMGL	VTPWSFVPHPV
10. AfUGT49A4	HQMLMDF	LYPLGLQT	A <mark>E</mark> YAYTR <mark>D</mark> N	VMDFLRNDQ	SQFDLLLAE	QFYQ <mark>E</mark> SYLML	AHKYKVPIVS	SIGTFGFAQYN	/IGPMMGLMNAW	SHVPHEFLPFT
11. AfUGT36C3	HFMEFFML	YTWG <mark>KEAC</mark> /	ANALNSTA I	QTILDSKIQ	YDLILVEQF	NSDCMLGIAH	QLKAPFIGLS	SSCPLMPWHY	ORVGNPTLPAY	VPALFMGYTER
	190	200	210	220	230	240	250	260	270	280
1. AfUGT314A3	İĞYPSIFM	PFSEDLSLI	LQRISSVLF	TVWYRFYYY	TEEIPAQNL	IAQNNFGEQI	SDLRQIEQNA	ADLLL I NAHQ	QLGNVRPVGPT	TIHLGGIHQSR
2. AfUGT308G4	FDAPESMS	FVQRVKNF	YFDMYEMNL	HETVLHPES	DRIVRKLYP	DAPSTYTFYK	NVRLSLANV		/ P SM I P V G G L Q	
3. AfUGT308G3	P E SMS F VQ	RVKNFYFD	NYEMILHET	FMHPEADK I	VRKLYPDAP	STYTFYKNVR	LSLANVNPVI	I QYKEPMMPSN	<mark>/ I P V G G L Q I M P</mark>	SKPLPDDLRKV
4. AfUGT308G2	P E SMS F VQ	RVKNFYFD	MY EMNL H ET	VLHPESDRI	VRKLYPDAP	STYTFYKNVR	LSLANVNPVI	I QYKEPMMPSN	<mark>/IPVGGLQIM</mark> P	SKPLPDDLRKV
5. AfUGT306C2	FFGRVKNF	LFAGVENVI	L CAVS E YVC	TSYYEHHFP	PDRYPTFQE	VRR <mark>NVSLVL</mark> L	NTHF SQSTPF	R P Y L P N I V E V O	GGLQIKAKPDP	LPEDIREWLDE
6. AfUGT306A3	TFFDRVTN	TILHGMEK	IMLMYIRHK	ELTYYESNF	PAEEGFRSY	DEAMRNVSLV	MLNTYF SQY\	/ P R P Y L P NMV I	VGGIQINLRP	EAMPQDLQQFL
7. AfUGT302A3	VPHPMSSF		RLGNVLFTA	AFDE <u>T</u> VLSFM	CDP I QQMYY	KKYFPNASRS	LNQMRRNGVS	SLVL INSHFSI	SFPRPYLPNL	IEVGGFHVNRK
8. AfUGT301C2	YEDDMN I F	QRAYNVILS	S S F <mark>D S V Y R</mark> F	<u>RYKYL</u> PQADQ	LAREVFGEL	AKEPDSLPSI	TELEQSISVI	LVNSHP I <u>L</u> S	ARPS IRGLVD	IGGAHIRAPKP
9. AfUGT301A3	LLLSDDMT	FSQRCYNF	VISLVDLI <u>I</u>	RQFYYIPQQ	NKLAQIHFA	R I E G P E L M P S	IQDLEKSIS	/ILVNSHLST	SAPRPTIPGLV	NVAGAHIKPAK
10. AfUGT49A4	DHMSLYQR	AY <mark>NS</mark> FVSW	Y E L L L R SW <mark>y</mark>	YLPEQQALA	<mark>DRHFSF<u>L</u>PG</mark>	PLPRLSDLER	QVSVILLNS	PPLTSTRAK	/PGLVQVGGLH	IKEPKRLPDDL
11. AfUGT36C3	MD F S Q R L A	NWITVQSFI	KTLYSWF NC	DAAANKLLRA	RFGEGVIPD	VR <mark>EL</mark> QQR <mark>TSM</mark>	MFVNQHYSLS	GAKPLSPAVI	EIGGIHIRDF	KPLEADLQQLL



Fig. S11. nonsynonymous SNPs location in UGTs targeted by sequencing. Functional protein regions in non-aligned UGTs included in the targeted enrichment sequencing are highlighted in the figure legend. Nonsynonymus SNPs that are significantly differentiated between putatively susceptible and resistant from Malawi, Cameroon, and Uganda, and between the FANG and the FUMOZ colony are highlighted with a red color in the protein sequence. For further details on those SNPs see Table S8.