

SUPPLEMENTAL MATERIAL

Appendix 1. Protein sequence alignment of novel *M. fascicularis* p450 variants with *M.*

mulatta and *H. sapiens* homologs

Identical sequences are highlighted in blue and gaps or ambiguous residues are shown as “X”. Sequence identities (%) between species are shown below the sequence name (MfMm = *M. fascicularis* / *M. mulatta*; MfHs = *M. fascicularis* / *H. sapiens*; MmHs = *M. mulatta* / *H. sapiens*). The tissue(s) expression preference is indicated below the alignment and brackets indicate low expression according to table 1. Partially matching public database entries are provided if available.

CYP1B1

MfMm: 99.6, MfHs: 94.4, MmHs: 93.9

						60	
CYP1B1_MFA	MGTGLSPKDP	WPLNLLSTQQ	TTLTLLLSVL	AAVHVQWLL	RQRRRLGST	PPGPFAPLI	60
CYP1B1_MMU	MGTGLSPKDP	WPLNLLSTQQ	TTLTLLLSVL	VAVHVQWLL	RQRRRLGST	PPGPFAPLI	60
CYP1B1_HSA	MGTSLSPNDP	WPLNPLSIQQ	TTLTLLLSVL	ATVHVQRLL	RQRRRLRSA	PPGPFAPLI	60
						120	
CYP1B1_MFA	GNAAAVGQAS	HLSFARLARR	YGDVFQIRLG	SCPIVVLNGE	RAIHQALVQQ	GSAFADRPSF	120
CYP1B1_MMU	GNAAAVGQAS	HLSFARLARR	YGDVFQIRLG	SCPIVVLNGE	RAIHQALVQQ	GSAFADRPSF	120
CYP1B1_HSA	GNAAAVGQAA	HLSFARLARR	YGDVFQIRLG	SCPIVVLNGE	RAIHQALVQQ	GSAFADRPAP	120
						180	
CYP1B1_MFA	ASFRVISGGR	SMAFGHYSEX	XXXXXXXXXX	XXXXXXXXXX	XXRQVLEGHV	LSEARELVAL	180
CYP1B1_MMU	ASFRVISGGR	SMAFGHYSEH	WKVQRRRAHS	TMRNFSTRQL	RSRQVLEGHV	LSEARELVAL	180
CYP1B1_HSA	ASFRVVS GGR	SMAFGHYSEH	WKVQRRRAHS	MMRNFFTRQP	RSRQVLEGHV	LSEARELVAL	180
						240	
CYP1B1_MFA	LVRGSADGAF	LDPRQLTVVA	VANVMSAVCF	GCRYSHDDPE	FRELLSHNEE	FGRTVGAGSL	240
CYP1B1_MMU	LVRGSADGAF	LDPRPLTVVA	VANVMSAVCF	GCRYSHDDPE	FRELLSHNEE	FGRTVGAGSL	240
CYP1B1_HSA	LVRGSADGAF	LDPRPLTVVA	VANVMSAVCF	GCRYSHDDPE	FRELLSHNEE	FGRTVGAGSL	240
						300	
CYP1B1_MFA	VDVMPWLQYF	PNPMRTAFRE	FEQLNRNFSN	FVLDKFLRHC	ESLRPGAAPR	DMMDAFILSA	300
CYP1B1_MMU	VDVMPWLQYF	PNPMRTAFRE	FEQLNRNFSN	FVLDKFLRHC	ESLRPGAAPR	DMMDAFILSA	300
CYP1B1_HSA	VDVMPWLQYF	PNPVRTVFRE	FEQLNRNFSN	FILDKFLRHC	ESLRPGAAPR	DMMDAFILSA	300
						360	
CYP1B1_MFA	EKKAARDSDD	GGARLDLENV	PATVTDIFGA	SQDTLSTALQ	WLLLLFIRYP	DVQARVQAEI	360
CYP1B1_MMU	EKKAARDSDD	GGARLDLENV	PATVTDIFGA	SQDTLSTALQ	WLLLLFIRYP	DVQARVQAEI	360
CYP1B1_HSA	EKKAAGDSHG	GGARLDLENV	PATITDIFGA	SQDTLSTALQ	WLLLLFTRYD	DVQTRVQAEI	360
						420	
CYP1B1_MFA	DQVVGRDRLP	CMDDQPNLPY	VLAFLYEAMR	FSSFVPVTIP	HATNANTSVL	GYHIPKDTV	420
CYP1B1_MMU	DQVVGRDRLP	CMDDQPNLPY	VLAFLYEAMR	FSSFVPVTIP	HATNANTSVL	GYHIPKDTV	420
CYP1B1_HSA	DQVVGRDRLP	CMGDQPNLPY	VLAFLYEAMR	FSSFVPVTIP	HATTANTSVL	GYHIPKDTV	420

						480	
CYP1B1_MFA	FVNQWSVNHD	PVKWPNPENF	DPARFLDKDG	LINKDLTSRV	MIFSVGKRXX	XXXXXXXXXX	480
CYP1B1_MMU	FVNQWSVNHD	PVKWPNPENF	DPARFLDKDG	LINKDLTSRV	MIFSVGKRRC	IGEELSKMQL	480
CYP1B1_HSA	FVNQWSVNHD	PLKWPNPENF	DPARFLDKDG	LINKDLTSRV	MIFSVGKRRC	IGEELSKMQL	480

						540	
CYP1B1_MFA	XXXXXXXXXX	XXXXXXXXXX	.XXXXXXGLT	IKPKSFKVVN	TLRESMELLD	SAVQKLQAE	539
CYP1B1_MMU	FLFISILAHQ	CNFRANPNGP	.EMNFSYGLT	IKPKSFKVVN	TLRESMELLD	SAVQKLQAE	539
CYP1B1_HSA	FLFISILAHQ	CDFRANPNEP	AKMNFSYGLT	IKPKSFKVVN	TLRESMELLD	SAVQNLQAKE	540

	543	
CYP1B1_MFA	TCQ	542
CYP1B1_MMU	TCQ	542
CYP1B1_HSA	TCQ	543

Public domain matches: none.
Tissue preference: spleen.

CYP2R1

MfMm: 99.4, MfHs: 97.6, MmHs: 97.4

						60	
CYP2R1_MFA	MWKLWGGEEG	AAALGGALFL	LLFALGVRQL	LKLRRPMGFP	PGPPGLPFIG	NIYSLAASAE	60
CYP2R1_MMU	MWKLWGGEEG	AAALGGALFL	LLFALGVRQL	LKLRRPMGFP	PGPPGLPFIG	NIYSLAASAE	60
CYP2R1_HSA	MWKLWRAEEG	AAALGGALFL	LLFALGVRQL	LKQRRPMGFP	PGPPGLPFIG	NIYSLAASSE	60

						120	
CYP2R1_MFA	LPHVYMRKQS	QVYGEIFSLD	LGGISTVVLN	GYDVVKECLV	HQSGIFADRP	CLPLFMKMTK	120
CYP2R1_MMU	LPHVYMRKQS	QVYGEIFSLD	LGGISTVVLN	GYDVVKECLV	HQSGIFADRP	CLPLFMKMTK	120
CYP2R1_HSA	LPHVYMRKQS	QVYGEIFSLD	LGGISTVVLN	GYDVVKECLV	HQSEIFADRP	CLPLFMKMTK	120

						180	
CYP2R1_MFA	MGLLNSRYG	RGWVEHRLA	VNSFRYFGYG	QKSFESKILE	ETKFFTDIE	TYKGRPFDFK	180
CYP2R1_MMU	MGLLNSRYG	QGWVEHRLA	VNSFRYFGYG	QKSFESKILE	ETKFFTDIE	TYKGRPFDFK	180
CYP2R1_HSA	MGLLNSRYG	RGWVDHRLA	VNSFRYFGYG	QKSFESKILE	ETKFFNDIE	TYKGRPFDFK	180

						240	
CYP2R1_MFA	QLITNAVSNI	TNLIIFGERF	TYEDTDFQHM	IELFSENVEL	AASASXFLYN	AFPWIGILPF	240
CYP2R1_MMU	QLITSASVNI	TNLIIFGERF	TYEDTDFQHM	IELFSENVEL	AASASVFLYN	AFPWIGILPF	240
CYP2R1_HSA	QLITNAVSNI	TNLIIFGERF	TYEDTDFQHM	IELFSENVEL	AASASVFLYN	AFPWIGILPF	240

						300	
CYP2R1_MFA	GKHQQLFRNA	SVVYDFLSRL	IEKASVNRKP	QLPQHFDVAY	FDEMDQGKND	PSSTFSKENL	300
CYP2R1_MMU	GKHQQLFRNA	SVVYDFLSRL	IEKASVNRKP	QLPQHFDVAY	FDEMDQGKND	PSSTFSKENL	300
CYP2R1_HSA	GKHQQLFRNA	AVVYDFLSRL	IEKASVNRKP	QLPQHFDVAY	LDEMDQGKND	PSSTFSKENL	300

						360	
CYP2R1_MFA	IFSVGELIIA	GTETTTNVLR	WAILFMALYP	NIQGQVQKEI	DLIMGPNGKP	SWDDKFKMPY	360
CYP2R1_MMU	IFSVGELIIA	GTETTTNVLR	WAILFMALYP	NIQGQVQKEI	DLIMGPNGKP	SWDDKFKMPY	360
CYP2R1_HSA	IFSVGELIIA	GTETTTNVLR	WAILFMALYP	NIQGQVQKEI	DLIMGPNGKP	SWDDCKMPY	360

						420	
CYP2R1_MFA	TEAVLHEVLR	FCNIVPLGIF	HATSEDAVVR	GYSIPKGTTV	ITNLYSVHFD	EKYWRDPEVF	420
CYP2R1_MMU	TEAVLHEVLR	FCNIVPLGIF	HATSEDAVVR	GYSIPKGTTV	ITNLYSVHFD	EKYWRDPEVF	420
CYP2R1_HSA	TEAVLHEVLR	FCNIVPLGIF	HATSEDAVVR	GYSIPKGTTV	ITNLYSVHFD	EKYWRDPEVF	420

						480	
CYP2R1_MFA	HPERFLDSSG	YFAKKEALVP	FSLGRRHCLG	EQLARMEMFL	FFTALLQRFH	LHFPHELVPD	480
CYP2R1_MMU	HPERFLDSSG	YFAKKEALVP	FSLGRRHCLG	EQLARMEMFL	FFTALLQRFH	LHFPHELVPD	480
CYP2R1_HSA	HPERFLDSSG	YFAKKEALVP	FSLGRRHCLG	EHLARMEMFL	FFTALLQRFH	LHFPHELVPD	480

				501	
CYP2R1_MFA	LKPRLGMTLQ	PQPYLICAER	R	501	
CYP2R1_MMU	LKPRLGMTLQ	PQPYLICAER	R	501	
CYP2R1_HSA	LKPRLGMTLQ	PQPYLICAER	R	501	

Public domain: QnpA-16301_EST_CJ466887

Tissue preference: liver, spleen, lung.

CYP2U1

MfMm: 100.0, MfHs: 98.9, MmHs: 98.9

						60	
CYP2U1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	60
CYP2U1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	60
CYP2U1_HSA	MSSPGPSQPP	AEDPPWPARL	LRAPLGLLRL	DPSGGALLLC	GLVALLGWSW	LRRRRRARGIP	60

						120	
CYP2U1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	120
CYP2U1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	120
CYP2U1_HSA	PGPTPWPLVG	NFGHVLPPF	LRRRSWLSSR	TRAAGIDPSV	IGPQVLLAHL	ARVYGSIFS	120

						180	
CYP2U1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXVFAHY	GPIWRQQRKF	180
CYP2U1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXVFAHY	GPIWRQQRKF	180
CYP2U1_HSA	FIGHYLVVVL	SDFHSVREAL	VQAEVFSDR	PRVPLISIVT	KEKGVFAHY	GPVWRQQRKF	180

						240	
CYP2U1_MFA	SHSTLRHFGL	GKLSLEPKII	EEFKYVKAEM	QKHGEDPFCP	FSIISNAVSN	IICSLCFGQR	240
CYP2U1_MMU	SHSTLRHFGL	GKLSLEPKII	EEFKYVKAEM	QKHGEDPFCP	FSIISNAVSN	IICSLCFGQR	240
CYP2U1_HSA	SHSTLRHFGL	GKLSLEPKII	EEFKYVKAEM	QKHGEDPFCP	FSIISNAVSN	IICSLCFGQR	240

						300	
CYP2U1_MFA	FDYTNSEFKK	MLGFMSRGL	ICLNSQVLMV	NICPWLYYLP	FGPFKELRQI	EKDITSFLKK	300
CYP2U1_MMU	FDYTNSEFKK	MLGFMSRGL	ICLNSQVLMV	NICPWLYYLP	FGPFKELRQI	EKDITSFLKK	300
CYP2U1_HSA	FDYTNSEFKK	MLGFMSRGL	ICLNSQVLLV	NICPWLYYLP	FGPFKELRQI	EKDITSFLKK	300

						360	
CYP2U1_MFA	IIKDHQESLD	RENPDQFIDM	YLLHMEERK	NNSNSSFDEE	YLFYIIGDLF	IAGTDTTNS	360
CYP2U1_MMU	IIKDHQESLD	RENPDQFIDM	YLLHMEERK	NNSNSSFDEE	YLFYIIGDLF	IAGTDTTNS	360
CYP2U1_HSA	IIKDHQESLD	RENPDQFIDM	YLLHMEERK	NNSNSSFDEE	YLFYIIGDLF	IAGTDTTNS	360

						420	
CYP2U1_MFA	LLWCLLYMSL	NPDVQEKVHE	EIERVIGANR	APSLTDKAQM	PYTEATIMEV	QRLTVVPLA	420
CYP2U1_MMU	LLWCLLYMSL	NPDVQEKVHE	EIERVIGANR	APSLTDKAQM	PYTEATIMEV	QRLTVVPLA	420
CYP2U1_HSA	LLWCLLYMSL	NPDVQEKVHE	EIERVIGANR	APSLTDKAQM	PYTEATIMEV	QRLTVVPLA	420

						480	
CYP2U1_MFA	IPHMTSGNTV	LQGYTIPKGT	LILPNLWSVH	RDPAIWEKPE	DFYPNRFDD	QGQLIKKET	480
CYP2U1_MMU	IPHMTSGNTV	LQGYTIPKGT	LILPNLWSVH	RDPAIWEKPE	DFYPNRFDD	QGQLIKKET	480
CYP2U1_HSA	IPHMTSENTV	LQGYTIPKGT	LILPNLWSVH	RDPAIWEKPE	DFYPNRFDD	QGQLIKKET	480

						540	
CYP2U1_MFA	IPFGIGKRVC	MGEQLAKMEL	FLMFVSLMQS	FAFALPKDSK	KPLLTGRFGL	TLAPHPFNIT	540
CYP2U1_MMU	IPFGIGKRVC	MGEQLAKMEL	FLMFVSLMQS	FAFALPKDSK	KPLLTGRFGL	TLAPHPFNIT	540
CYP2U1_HSA	IPFGIGKRVC	MGEQLAKMEL	FLMFVSLMQS	FAFALPEDSK	KPLLTGRFGL	TLAPHPFNIT	540

	544	
CYP2U1_MFA	ISRR	544
CYP2U1_MMU	ISRR	544
CYP2U1_HSA	ISRR	544

Public domain: QtsA-14239_full_AB168699 (Osada)

Tissue preference: lung, liver

CYP2W1

MfMm: 99.4, MfHs: 95.6, MmHs: 94.9

						60	
CYP2W1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXXLS	60
CYP2W1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXXLS	60
CYP2W1_HSA	MALLLLFLG	LLGLWGLLCA	CAQDPSPAAR	WPPGPRPLPL	VGNLHLLRLS	QQDRSLMELS	60

						120	
CYP2W1_MFA	ERYGPVFTVH	LGCQKTVVLT	GFEVVKEALA	GPGQELADRP	PIAIXQLIQR	GGGIFSSGA	120
CYP2W1_MMU	ERYGPVFTVH	LGCQKTVVLT	GFEVVKEALA	GPGQELADRP	PIAIFQLIQR	GGGIFSSGA	120
CYP2W1_HSA	ERYGPVFTVH	LGRQKTVVLT	GFEAVKEALA	GPGQELADRP	PIAIFQLIQR	GGGIFSSGA	120

						180	
CYP2W1_MFA	RWRAARQFTV	RALHSLGVGR	EPVADKILQE	LKCLSGQLDG	YRGQPFPLAL	LGWAPSNITF	180
CYP2W1_MMU	RWRAARQFTV	RALHSLGVGR	KPVADKILQE	LKCLSGQLDG	YRGQPFPLAL	LGWAPSNITF	180
CYP2W1_HSA	RWRAARQFTV	RALHSLGVGR	EPVADKILQE	LKCLSGQLDG	YRGRPFPLAL	LGWAPSNITF	180

						240	
CYP2W1_MFA	TLLFGRRFDY	RDPVFSVLLG	LIDEVMVLLG	SPGLQXXXXX	XXXXXXXXXX	XXXXXXXXXX	240
CYP2W1_MMU	TLLFGRRFDY	RDPVFSVLLG	LIDEVMVLLG	SPGLQLFNVE	PWLGALLQLH	RPVLRKIEEV	240
CYP2W1_HSA	ALLFGRRFDY	RDPVFSVLLG	LIDEVMVLLG	SPGLQLFNVE	PWLGALLQLH	RPVLRKIEEV	240

						300	
CYP2W1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXIQ	QGQDDPEGL	FAEDNAVACT	LDMVMAGTET	300
CYP2W1_MMU	RAILRTLLEA	RRPHMRPGDP	VCSYVDALIQ	QGQDDPEGL	FAEDNAVACT	LDMVMAGTET	300
CYP2W1_HSA	RAILRTLLEA	RRPHVCPGDP	VCSYVDALIQ	QGQDDPEGL	FAEANAVACT	LDMVMAGTET	300

						360	
CYP2W1_MFA	TSATLQWAAL	LMGRHPDVQG	RVQEELDRVL	GRGRPPQPED	QQVLPYTSAV	LHEVQRFITL	360
CYP2W1_MMU	TSATLQWAAL	LMGRHPDVQG	RVQEELDRVL	RRGRPPQPED	QQVLPYTSAV	LHEVQRFITL	360
CYP2W1_HSA	TSATLQWAAL	LMGRHPDVQG	RVQEELDRVL	GPGRTPRLED	QQALPYTSAV	LHEVQRFITL	360

						420	
CYP2W1_MFA	LPHVPXXXXX	XXXXXXXXLP	KGTPVIPLLT	SVLLDETQWQ	TPDQFNPGHF	LDADGHFVKQ	420
CYP2W1_MMU	LPHVPRCTAT	DMQLGGFLLP	KGTPVIPLLT	SVLLDETQWQ	TPDQFNPGHF	LDADGHFVKQ	420
CYP2W1_HSA	LPHVPRCTAA	DTQLGGFLLP	KGTPVIPLLT	SVLLDETQWQ	TPGQFNPGHF	LDANGHFVKR	420

						480	
CYP2W1_MFA	EAFLPFSAGR	RVCVGERLAR	TELFLLFAGL	LQKYLLPPP	GVSPASLDTT	PAQAFMRPR	480
CYP2W1_MMU	EAFLPFSAGR	RVCVGERLAR	TELFLLFAGL	LQKYLLPPP	GVSPASLDTT	PAQAFMRPR	480
CYP2W1_HSA	EAFLPFSAGR	RVCVGERLAR	TELFLLFAGL	LQRYLLPPP	GVSPASLDTT	PARAFMRPR	480

		490
CYP2W1_MFA	AQALCAVPRP	490
CYP2W1_MMU	AQALCAVPRP	490
CYP2W1_HSA	AQALCAVPRP	490

Public domain: none.
Tissue preference: none detected.

CYP4V2

MfMm: 100.0, MfHs: 97.1, MmHs: 96.8

						60	
CYP4V2_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	60
CYP4V2_MMU	MAGIWLGLVW	QKLLLWGAAS	AVSLAGASLV	LSLLQRVASY	VRKWQQMRPI	PTVARAYPLV	60
CYP4V2_HSA	MAGLWLGLVW	QKLLLWGAAS	ALSLAGASLV	LSLLQRVASY	ARKWQQMRPI	PTVARAYPLV	60

						120	
CYP4V2_MFA	XXXXXXXXXG	REFFQQIIEY	TEEYRHMPLL	KLWVGVPVMV	ALYNAENVEV	ILTSSKQIDK	120
CYP4V2_MMU	GHALLMKRDG	REFFQQIIEY	TEEYRHMPLL	KLWVGVPVMV	ALYNAENVEV	ILTSSKQIDK	120
CYP4V2_HSA	GHALLMKPDG	REFFQQIIEY	TEEYRHMPLL	KLWVGVPVMV	ALYNAENVEV	ILTSSKQIDK	120

						180	
CYP4V2_MFA	SSMYKFLEPW	LGLGLLTSTG	NKWSRRKML	TPTFHFTILE	DFLDIMNEQA	NILVKKLEKH	180
CYP4V2_MMU	SSMYKFLEPW	LGLGLLTSTG	NKWSRRKML	TPTFHFTILE	DFLDIMNEQA	NILVKKLEKH	180
CYP4V2_HSA	SSMYKFLEPW	LGLGLLTSTG	NKWSRRKML	TPTFHFTILE	DFLDIMNEQA	NILVKKLEKH	180

						240	
CYP4V2_MFA	VNQEAFNCFV	YITLCALDII	CETAMGKNIG	AQSNDDSEYV	RAVYRMSEMI	FRRIKMPWLW	240
CYP4V2_MMU	VNQEAFNCFV	YITLCALDII	CETAMGKNIG	AQSNDDSEYV	RAVYRMSEMI	FRRIKMPWLW	240
CYP4V2_HSA	INQEAFNCFV	YITLCALDII	CETAMGKNIG	AQSNDDSEYV	RAVYRMSEMI	FRRIKMPWLW	240

						300	
CYP4V2_MFA	LDLWYLMFKE	GWEHKKSLKI	LHAFTNNVIA	ERANEMNVDE	DCRGDGRDSA	PSKNKRR AFL	300
CYP4V2_MMU	LDLWYLMFKE	GWEHKKSLKI	LHAFTNNVIA	ERANEMNVDE	DCRGDGRDSA	PSKNKRR AFL	300
CYP4V2_HSA	LDLWYLMFKE	GWEHKKSLQI	LHTFTNSVIA	ERANEMNANE	DCRGDGRGSA	PSKNKRR AFL	300

						360	
CYP4V2_MFA	DLLLSVTDD E	GNRLSHEDIR	EEVDTFMFEG	HDTTAAAMNW	SLYLLGSNPE	VQKKVDHELD	360
CYP4V2_MMU	DLLLSVTDD E	GNRLSHEDIR	EEVDTFMFEG	HDTTAAAMNW	SLYLLGSNPE	VQKKVDHELD	360
CYP4V2_HSA	DLLLSVTDD E	GNRLSHEDIR	EEVDTFMFEG	HDTTAAAINW	SLYLLGSNPE	VQKKVDHELD	360

						420	
CYP4V2_MFA	DVFGSRDRPX	XXXXLKKLRY	LECVIKETLR	LFPSVPLFAR	SVSEDCEVAG	YRVLKGTEAV	420
CYP4V2_MMU	DVFGSRDRPA	TVEDLKKLRY	LECVIKETLR	LFPSVPLFAR	SVSEDCEVAG	YRVLKGTEAV	420
CYP4V2_HSA	DVFGKSDRPA	TVEDLKKLRY	LECVIKETLR	LFPSVPLFAR	SVSEDCEVAG	YRVLKGTEAV	420

						480	
CYP4V2_MFA	IIPYALHRDP	RYFPNPEEFR	PERFFPEN AQ	GRHPYAYVPF	SAGPRNCIGQ	KFAVMEEKTI	480
CYP4V2_MMU	IIPYALHRDP	RYFPNPEEFR	PERFFPEN AQ	GRHPYAYVPF	SAGPRNCIGQ	KFAVMEEKTI	480
CYP4V2_HSA	IIPYALHRDP	RYFPNPEEFQ	PERFFPEN AQ	GRHPYAYVPF	SAGPRNCIGQ	KFAVMEEKTI	480

					525		
CYP4V2_MFA	LSCILRHFWI	ESNQKREELG	LEGQLILRPT	NGIWIKLKRR	NADEP	525	
CYP4V2_MMU	LSCILRHFWI	ESNQKREELG	LEGQLILRPT	NGIWIKLKRR	NADEP	525	
CYP4V2_HSA	LSCILRHFWI	ESNQKREELG	LEGQLILRPS	NGIWIKLKRR	NADER	525	

Public domain: none.
Tissue preference: liver, lung

CYP7A1

MfMm: 99.4, MfHs: 96.2, MmHs: 96.2

						60	
CYP7A1_MFA	MMTISLIWGI	AXXXRCCLWL	ILGIRRRQTG	EPPLENGLIP	YLGICALQFGA	NPLEFLRANQ	60
CYP7A1_MMU	MMTISLIWGI	AIAACCCLWL	ILGIRRRQTG	EPPLENGLIP	YLGICALQFGA	NPLEFLRANQ	60
CYP7A1_HSA	MMTISLIWGI	AIAACCCLWL	ILGIRRRQTG	EPPLENGLIP	YLGICALQFGA	NPLEFLRANQ	60
						120	
CYP7A1_MFA	RKHGHVFTCK	LMGKYVHFIT	NPLSYHKVLC	HGKYFDWKKF	HFATSAKAFG	HRSIDPKDGN	120
CYP7A1_MMU	RKHGHVFTCK	LMGKYVHFIT	NPLSYHKVLC	HGKYFDWKKF	HFATSAKAFG	HRSIDPKDGN	120
CYP7A1_HSA	RKHGHVFTCK	LMGKYVHFIT	NPLSYHKVLC	HGKYFDWKKF	HFATSAKAFG	HRSIDPMDGN	120
						180	
CYP7A1_MFA	TTENINNTFI	KTLQGNALNS	LTESMMENLQ	RIMRPPVFSN	SKTAAWVTEG	MYSFCYRVMF	180
CYP7A1_MMU	TTENINNTFI	KTLQGNALNS	LTESMMENLQ	RIMRPPVFSN	SKTAAWVTEG	MYSFCYRVMF	180
CYP7A1_HSA	TTENINDTFI	KTLQGHALNS	LTESMMENLQ	RIMRPPVSSN	SKTAAWVTEG	MYSFCYRVMF	180
						240	
CYP7A1_MFA	EAGYLTIFGR	DLTRQDTQKA	HILNNLDNFK	QFDKVPALV	AGLPIHMFRT	AHSAREKLAE	240
CYP7A1_MMU	EAGYLTIFGR	DLTRQDTQKA	HILNNLDNFK	QFDKVPALV	AGLPIHMFRT	AHSAREKLAE	240
CYP7A1_HSA	EAGYLTIFGR	DLTRRDTQKA	HILNNLDNFK	QFDKVPALV	AGLPIHMFRT	AHNAREKLAE	240
						300	
CYP7A1_MFA	SLRHENLQKR	ESVSELIRLR	MFLNDTLSTF	DDLEKAKTHL	VVLWASQANT	IPATFWSLFQ	300
CYP7A1_MMU	SLRHENLQKR	ESVSELIRLR	MFLNDTLSTF	DDLEKAKTHL	VVLWASQANT	IPATFWSLFQ	300
CYP7A1_HSA	SLRHENLQKR	ESISELISLR	MFLNDTLSTF	DDLEKAKTHL	VVLWASQANT	IPATFWSLFQ	300
						360	
CYP7A1_MFA	MIRNPEAMKA	ATEEVKRTLE	NAGQKVSLEG	NPICLSQTQL	NDLPVLESII	KESLRLSSAS	360
CYP7A1_MMU	MIRNPEAMKA	ATEEVKRTLE	NAGQKVSLEG	NPICLSQTQL	NDLPVLESII	KESLRLSSAS	360
CYP7A1_HSA	MIRNPEAMKA	ATEEVKRTLE	NAGQKVSLEG	NPICLSQAEI	NDLPVLDSEI	KESLRLSSAS	360
						420	
CYP7A1_MFA	LNIRTAKEDF	TLHLEDGSYN	IRKDDIIALY	PQLMHLDPFI	YPDPLIFKYD	RYLDENGKTK	420
CYP7A1_MMU	LNIRTAKEDF	TLHLEEGSYN	IRKDDIIALY	PQLMHLDPFI	YPDPLSFKYD	RYLDENGKTK	420
CYP7A1_HSA	LNIRTAKEDF	TLHLEDGSYN	IRKDDIIALY	PQLMHLDPFI	YPDPLTFKYD	RYLDENGKTK	420
						480	
CYP7A1_MFA	TTFYCNGCLK	KYYMPFGSG	ATICPGRVFA	IHEIKQFLVL	MSYFELELV	EGQDKCPPLD	480
CYP7A1_MMU	TTFYCNGCLK	KYYMPFGSG	ATICPGRVFA	IHEIKQFLVL	MSYFELELV	EGQDKCPPLD	480
CYP7A1_HSA	TTFYCNGCLK	KYYMPFGSG	ATICPGRLFA	IHEIKQFLIL	MSYFELELI	EGQAKCPPLD	480
						504	
CYP7A1_MFA	QSRAGLGILP	PLYDIEFKYK	FKHL				504
CYP7A1_MMU	QSRAGLGILP	PLYDIEFKYK	FKHL				504
CYP7A1_HSA	QSRAGLGILP	PLNDIEFKYK	FKHL				504

Public domain: Qlv-U100A-A6_EST_BB875471 (partial)
Tissue preference: liver.

CYP7B1

MfMm: 100.0, MfHs: 96.8, MmHs: 96.8

						60	
CYP7B1_MFA	MAGEVSAAMG	RFSLEWLGLP	GLALAAALLL	LALCLLDRRT	RRPGEPPLIK	GWLPYLGVL	60
CYP7B1_MMU	MAGEVSAAMG	RFSLEWLGLP	GLALAAALLL	LALCLLDRRT	RRPGEPPLIK	GWLPYLGVL	60
CYP7B1_HSA	MAGEVSAATG	RFSLERLGLP	GLALAAALLL	LALCLLVRRRT	RRPGEPPLIK	GWLPYLGVL	60
						120	
CYP7B1_MFA	KLRKDPLSFM	CTLQKQHGD	FTVLLGGKYI	TFILDPFQYQ	LVIKNHKQLS	FRLFSNKLLE	120
CYP7B1_MMU	KLRKDPLSFM	CTLQKQHGD	FTVLLGGKYI	TFILDPFQYQ	LVIKNHKQLS	FRLFSNKLLE	120
CYP7B1_HSA	NLRKDPLRFM	CTLQKQHGD	FTVLLGGKYI	TFILDPFQYQ	LVIKNHKQLS	FRVFSNKLLE	120
						180	
CYP7B1_MFA	KAFSISQLQK	NHDMNDELHL	CYQFLQGKSL	DILLESMMQN	LKQVFESQLL	KTTSWDTAQL	180
CYP7B1_MMU	KAFSISQLQK	NHDMNDELHL	CYQFLQGKSL	DILLESMMQN	LKQVFESQLL	KTTSWDTAQL	180
CYP7B1_HSA	KAFSISQLQK	NHDMNDELHL	CYQFLQGKSL	DILLESMMQN	LKQVFEPQLL	KTTSWDTAEL	180
						240	
CYP7B1_MFA	YPFCSSIIFE	ITFTTIYGKV	LVCD.NKFIS	ELRDDFLKFD	DKFAYLVSNI	PIELLGNVKS	239
CYP7B1_MMU	YPFCSSIIFE	ITFTTIYGKV	LVCD.NKFIS	ELRDDFLKFD	DKFAYLVSNI	PIELLGNVKS	239
CYP7B1_HSA	YPFCSSIIFE	ITFTTIYGKV	IVCDNNKFIS	ELRDDFLKFD	DKFAYLVSNI	PIELLGNVKS	240
						300	
CYP7B1_MFA	IRKKIIKCLS	SENLAQMKGW	SEVFQSRQDV	LEKYYVHEDL	EIGAHHLGFL	WASVANTIPT	299
CYP7B1_MMU	IRKKIIKCLS	SENLAQMKGW	SEVFQSRQDV	LEKYYVHEDL	EIGAHHLGFL	WASVANTIPT	299
CYP7B1_HSA	IREKIIKCF	SEKLAQMKGW	SEVFQSRQDV	LEKYYVHEDL	EIGAHHLGFL	WASVANTIPT	300
						360	
CYP7B1_MFA	MFWAMYLLR	HPEAMAAVRD	EIDRLLQSTG	QKKGSGFPIH	LTREQLDSLI	CLESTIFEAL	359
CYP7B1_MMU	MFWAMYLLR	HPEAMAAVRD	EIDRLLQSTG	QKKGSGFPIH	LTREQLDSLI	CLESTIFEAL	359
CYP7B1_HSA	MFWAMYLLR	HPEAMAAVRD	EIDRLLQSTG	QKKGSGFPIH	LTREQLDSLI	CLESTIFEAL	360
						420	
CYP7B1_MFA	RLSSYSTTIR	FVEEDLTLSA	ETGDYCVRKG	DLVAIFPPIL	HGDPEIFEAP	EEFRYDRFIE	419
CYP7B1_MMU	RLSSYSTTIR	FVEEDLTLSA	ETGDYCVRKG	DLVAIFPPIL	HGDPEIFEAP	EEFRYDRFIE	419
CYP7B1_HSA	RLSSYSTTIR	FVEEDLTLS	ETGDYCVRKG	DLVAIFPPVL	HGDPEIFEAP	EEFRYDRFIE	420
						480	
CYP7B1_MFA	DGKKKTTFK	RGKKLKCYLM	PFGTGTSCPC	GRFFALMEIK	QLLVILLTYF	DLEIIDDKPI	479
CYP7B1_MMU	DGKKKTTFK	RGKKLKCYLM	PFGTGTSCPC	GRFFALMEIK	QLLVILLTYF	DLEIIDDKPI	479
CYP7B1_HSA	DGKKKTTFK	RGKKLKCYLM	PFGTGTSCPC	GRFFALMEIK	QLLVILLTYF	DLEIIDDKPI	480
						506	
CYP7B1_MFA	GLNYNRLLFG	IQYPDSVLF	RYKVKS				505
CYP7B1_MMU	GLNYNRLLFG	IQYPDSVLF	RYKVKS				505
CYP7B1_HSA	GLNYSRLLFG	IQYPDSVLF	RYKVKS				506

Public domain: QfIA-11730_EST_CJ446440 (Osada)

Tissue preference: liver

CYP11B1

MfMm: 99.8, MfHs: 98.2, MmHs: 98.4

						60	
CYP11B1_MFA	MALRAKVEVC	MAAPWLSLQR	ARALGTRATR	VPRTVLPFEA	MPRRPGNRWL	RLLQIWREQG	60
CYP11B1_MMU	MALRAKAEVC	MAAPWLSLQR	ARALGTRATR	VPRTVLPFEA	MPRRPGNRWL	RLLQIWREQG	60
CYP11B1_HSA	MALRAKAEVC	MAVPWLSLQR	AQALGTRAAR	VPRTVLPFEA	MPRRPGNRWL	RLLQIWREQG	60
						120	
CYP11B1_MFA	YEHLHLEVHQ	TFQELGPIFR	YDLGGAGMVC	VMLPEDVEKL	QQVDSLNP RR	MSLEPWVAYR	120
CYP11B1_MMU	YEHLHLEVHQ	TFQELGPIFR	YDLGGAGMVC	VMLPEDVEKL	QQVDSLNP RR	MSLEPWVAYR	120
CYP11B1_HSA	YEDLHLEVHQ	TFQELGPIFR	YDLGGAGMVC	VMLPEDVEKL	QQVDSLHP HR	MSLEPWVAYR	120
						180	
CYP11B1_MFA	QHRGHKCGVF	LLNGPEWRFN	RLRLNPDVLS	PRAVQRFLPM	VDAVARDFSQ	ALRKKVLQNA	180
CYP11B1_MMU	QHRGHKCGVF	LLNGPEWRFN	RLRLNPDVLS	PRAVQRFLPM	VDAVARDFSQ	ALRKKVLQNA	180
CYP11B1_HSA	QHRGHKCGVF	LLNGPEWRFN	RLRLNPEVLS	PNAVQRFLPM	VDAVARDFSQ	ALKKKVLQNA	180
						240	
CYP11B1_MFA	RGSLTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAS	LSFLHALXVM	FKSTVQLMFM	240
CYP11B1_MMU	RGSLTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAS	LSFLHALEVM	FKSTVQLMFM	240
CYP11B1_HSA	RGSLTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAS	LNFLHALEVM	FKSTVQLMFM	240
						300	
CYP11B1_MFA	PRSLSRWTSP	KVWKEHFEAW	DCIFYQGDNC	IQKIYQELAL	SRPQQYTSIV	AELLNNAELS	300
CYP11B1_MMU	PRSLSRWTSP	KVWKEHFEAW	DCIFYQGDNC	IQKIYQELAL	SRPQQYTSIV	AELLNNAELS	300
CYP11B1_HSA	PRSLSRWTSP	KVWKEHFEAW	DCIFYQGDNC	IQKIYQELAF	SRPQQYTSIV	AELLNNAELS	300
						360	
CYP11B1_MFA	PDAIKANSME	LTAGXVDTTV	FPLLMTLFEL	ARNPNVQQAL	RQXSLAAAAS	ISEHPQKATT	360
CYP11B1_MMU	PDAIKANSME	LTAGSVDTTV	FPLLMTLFEL	ARNPNVQQAL	RQESLAAAAS	ISEHPQKATT	360
CYP11B1_HSA	PDAIKANSME	LTAGSVDTTV	FPLLMTLFEL	ARNPNVQQAL	RQESLAAAAS	ISEHPQKATT	360
						420	
CYP11B1_MFA	ELXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	TLVRVFLYSL	GRNPALFPRP	420
CYP11B1_MMU	ELPLLRAALK	ETLRLYPVGL	FLERVVSSDL	VLQNYHIPAG	TLVRVFLYSL	GRNPALFPRP	420
CYP11B1_HSA	ELPLLRAALK	ETLRLYPVGL	FLERVASSDL	VLQNYHIPAG	TLVRVFLYSL	GRNPALFPRP	420
						480	
CYP11B1_MFA	ERYNPQRWLD	IRGSGRNFYH	VPFGFGMRQC	LGRRLAEAEM	LLLLHHVLKH	LQVETLTQED	480
CYP11B1_MMU	ERYNPQRWLD	IRGSGRNFYH	VPFGFGMRQC	LGRRLAEAEM	LLLLHHVLKH	LQVETLTQED	480
CYP11B1_HSA	ERYNPQRWLD	IRGSGRNFYH	VPFGFGMRQC	LGRRLAEAEM	LLLLHHVLKH	LQVETLTQED	480
						503	
CYP11B1_MFA	IKMVYSFILR	PSTFPLLTFR	AIN				503
CYP11B1_MMU	IKMVYSFILR	PSTFPLLTFR	AIN				503
CYP11B1_HSA	IKMVYSFILR	PSMFPLLTFR	AIN				503

Public domain: none.

Tissue preference: (heart)

CYP11B2

MfMm : 99.7, CH : 94.3, RH : 94.6

						60	
CYP11B2_MFA	MALRAKAEVC	MAAPWLSLQR	AQALSTRAAR	APSTVLPFEA	IPQRPNGNRWL	RLLQIWREQG	60
CYP11B2_MMU	MALRAKAEVC	MAAPWLSLQR	AQALSTRAAR	APSTVLPFEA	IPQRPNGNRWL	RLLQIWREQG	60
CYP11B2_HSA	MALRAKAEVC	VAAPWLSLQR	ARALGTRAAR	APRTVLPFEA	MPQHNGNRWL	RLLQIWREQG	60

							120	
CYP11B2_MFA	YEHLHLEVHQ	TFQELGPIFR	YHLGGPRMVC	VMLPEDVEKL	QQVDSLHPhR	MSLEPWVAYR	120	
CYP11B2_MMU	YEHLHLEVHQ	TFQELGPIFR	YHLGGPQMC	VMLPEDVEKL	QQVDSLHPhR	MSLEPWVAYR	120	
CYP11B2_HSA	YEHLHLEMHQ	TFQELGPIFR	YNLGGPRMVC	VMLPEDVEKL	QQVDSLHPChR	MILEPWVAYR	120	
							180	
CYP11B2_MFA	QHRGHKCGVF	LLXXXXXXXX	XXRLNPDVLS	PKAVQRFLPM	VDAVARDFSQ	ALRNKVLQNA	180	
CYP11B2_MMU	QHRGHKCGVF	LLNGPEWRFN	RLRLNPDVLS	PKAVQRFLPM	VDAVARDFSQ	ALRNKVLQNA	180	
CYP11B2_HSA	QHRGHKCGVF	LLNGPEWRFN	RLRLNPDVLS	PKAVQRFLPM	VDAVARDFSQ	ALKKKVLQNA	180	
							240	
CYP11B2_MFA	RDSVTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAT	LSFLHALEVM	FKSTVQLMFM	240	
CYP11B2_MMU	RDSVTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAT	LSFLHALEVM	FKSTVQLMFM	240	
CYP11B2_HSA	RGSLTLDVQP	SIFHYTIEAS	NLALFGERLG	LVGHSPSSAS	LNFLHALEVM	FKSTVQLMFM	240	
							300	
CYP11B2_MFA	PRSLSRWTSP	KVWKEHFEAW	DCIFQYGDNC	IQKIYQELAF	SRPQHYTGIV	AELLLNAELS	300	
CYP11B2_MMU	PRSLSRWTSP	KVWKEHFEAW	DCIFQYGDNC	IQKIYQELAF	SRPQHYTGIV	AELLLNAELS	300	
CYP11B2_HSA	PRSLSRWISP	KVWKEHFEAW	DCIFQYGDNC	IQKIYQELAF	NRPQHYTGIV	AELLLKAELS	300	
							360	
CYP11B2_MFA	LEAIKANSME	LTAGSVDTTA	FLLMTLFX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	360	
CYP11B2_MMU	LEAIKANSME	LTAGSVDTTA	FLLMTLFE	ARNPDVQQAL	RQESLAAAAS	ISEHPQKATT	360	
CYP11B2_HSA	LEAIKANSME	LTAGSVDTTA	FLLMTLFE	ARNPDVQQIL	RQESLAAAAS	ISEHPQKATT	360	
							420	
CYP11B2_MFA	XXXXXXXXXX	XXXXLYPVGL	FLERVVSSDL	VLQNYHIPAX	TLVQVFLYSL	GRNPALFPRP	420	
CYP11B2_MMU	ELPLLRAALK	ETLRLYPVGL	FLERVVSSDL	VLQNYHIPAG	TLVQVFLYSL	GRNPALFPRP	420	
CYP11B2_HSA	ELPLLRAALK	ETLRLYPVGL	FLERVVSSDL	VLQNYHIPAG	TLVQVFLYSL	GRNAALFPRP	420	
							480	
CYP11B2_MFA	ERYNXXXXXD	IRGSGKNFHN	VPFGFGMRQC	LGRRLAETEM	LLLLHHVLKH	FLVETLTQED	480	
CYP11B2_MMU	ERYNPQRWLD	IRGSGKNFHN	VPFGFGMRQC	LGRRLAETEM	LLLLHHVLKH	FLVETLTQED	480	
CYP11B2_HSA	ERYNPQRWLD	IRGSGRNFHH	VPFGFGMRQC	LGRRLAEAE	LLLLHHVLKH	FLVETLTQED	480	
							503	
CYP11B2_MFA	IKMVYSFILR	PGTFPLLTFR	AIN	503				
CYP11B2_MMU	IKMVYSFILR	PGTFPLLTFR	AIN	503				
CYP11B2_HSA	IKMVYSFILR	PGTSPLLTFR	AIN	503				

Public domain: none.

Tissue preference: (lung)

CYP20A1

MfMm: 99.8, MfHs: 97.2, MmHs: 97.4

							60	
CYP20A1_MFA	MLDFAIFAVT	FLLALVGAVL	YLYPAFRQAA	GIPGITPTEE	KDGNLPDIVN	SGSLHEFLVN	60	
CYP20A1_MMU	MLDFAIFAVT	FLLALVGAVL	YLYPAFRQAA	GIPGITPTEE	KDGNLPDIVN	SGSLHEFLVN	60	
CYP20A1_HSA	MLDFAIFAVT	FLLALVGAVL	YLYPASRQAA	GIPGITPTEE	KDGNLPDIVN	SGSLHEFLVN	60	
							120	
CYP20A1_MFA	LHERYGPVVS	FWFGRRLLVVS	LGTVDVLKQH	INPNKTLDPF	ETMLKSLLRY	QSGGGNVSEN	120	
CYP20A1_MMU	LHERYGPVVS	FWFGRRLLVVS	LGTVDVLKQH	INPNKTLDPF	ETMLKSLLRY	QSGGGNVSEN	120	
CYP20A1_HSA	LHERYGPVVS	FWFGRRLLVVS	LGTVDVLKQH	INPNKTSDFP	ETMLKSLLRY	QSGGGSVSEN	120	

							180
CYP20A1_MFA	HMRKKLCENG	VTNSLKSNFA	LLLKLSEELL	DKWLSYPETQ	HVPLSQHMLG	FAMKSVTQMV	180
CYP20A1_MMU	HMRKKLCENG	VTNSLKSNFA	LLLKLSEELL	DKWLSYPETQ	HVPLSQHMLG	FAMKSVTQMV	180
CYP20A1_HSA	HMRKKLYENG	VTDSLKSNFA	LLLKLSEELL	DKWLSYPETQ	HVPLSQHMLG	FAMKSVTQMV	180
							240
CYP20A1_MFA	MGSTFENDQE	VICFQKNHGT	VWSEIGKGFL	DGSLDKNTTR	KKQYEDALVQ	LESVLRNIIK	240
CYP20A1_MMU	MGSTFENDQE	VIRFQKNHGT	VWSEIGKGFL	DGSLDKNTTR	KKQYEDALVQ	LESVLRNIIK	240
CYP20A1_HSA	MGSTFEDDQE	VIRFQKNHGT	VWSEIGKGFL	DGSLDKNMTR	KKQYEDALMQ	LESVLRNIIK	240
							300
CYP20A1_MFA	ERKGRNFSQH	IFIDSLVQGN	LNDQQILEDSE	MIFSLASCII	TAKLCTWAIC	FLTTSEEVQK	300
CYP20A1_MMU	ERKGRNFSQH	IFIDSLVQGN	LNDQQILEDSE	MIFSLASCII	TAKLCTWAIC	FLTTSEEVQK	300
CYP20A1_HSA	ERKGRNFSQH	IFIDSLVQGN	LNDQQILEDSE	MIFSLASCII	TAKLCTWAIC	FLTTSEEVQK	300
							360
CYP20A1_MFA	KLYEEINQVF	GNGPITPEKI	EQLRYCQHVL	CETVRTAKLT	PVSAQLQDIE	GKIDQFIIPR	360
CYP20A1_MMU	KLYEEINQVF	GNGPITPEKI	EQLRYCQHVL	CETVRTAKLT	PVSAQLQDIE	GKIDQFIIPR	360
CYP20A1_HSA	KLYEEINQVF	GNGPVTPEKI	EQLRYCQHVL	CETVRTAKLT	PVSAQLQDIE	GKIDRFIIPR	360
							420
CYP20A1_MFA	ETLVLYALGV	VLQDPNTWPS	PHKFDPDPRFD	DELIMKTFSS	LGFSGTRECP	ELRFAYMVT	420
CYP20A1_MMU	ETLVLYALGV	VLQDPNTWPS	PHKFDPDPRFD	DELIMKTFSS	LGFSGTRECP	ELRFAYMVT	420
CYP20A1_HSA	ETLVLYALGV	VLQDPNTWPS	PHKFDPDPRFD	DELVMKTFSS	LGFSGTQEC	ELRFAYMVT	420
							462
CYP20A1_MFA	VLLSVLVKRL	HLLSVEGQVI	ETKYELVTSS	REEAWITVSK	RY	462	
CYP20A1_MMU	VLLSVLVKRL	HLLSVEGQVI	ETKYELVTSS	REEAWITVSK	RY	462	
CYP20A1_HSA	VLLSVLVKRL	HLLSVEGQVI	ETKYELVTSS	REEAWITVSK	RY	462	

Public domain: Qlv-U377A-C9_EST_BB888932 (partial)

Tissue preference: liver, heart, lung.

CYP21A2

MfMm: 97.1, MfHs: 94.0, MmHs: 96.4

							60
CYP21A2_MFA	MLFLGLLLLL	PLLAGARLLW	NRWKLRSLLH	PPLVPGFLHL	LQPDLPYLL	GLTQKFGPIY	60
CYP21A2_MMU	MLFLGLLLLL	PLLAGARLLW	NRWKLRSLLH	PPLVPGFLHL	LQPDLPYLL	GLTQKFGPIY	60
CYP21A2_HSA	MLLLGLLLLL	PLLAGARLLW	NWWKLRSLLH	PPLAPGFLHL	LQPDLPYLL	GLTQKFGPIY	60
							120
CYP21A2_MFA	RLHLGLQDVV	VLNSKRTIEE	AMVKKWADFA	GRPEPLTYKL	VSKNYPXLSL	GDYSLLWKAH	120
CYP21A2_MMU	RLHLGLQDVV	VLNSKRTIEE	AMVKKWADFA	GRPEPLTYKL	VSKNYPDLSL	GDYSLLWKAH	120
CYP21A2_HSA	RLHLGLQDVV	VLNSKRTIEE	AMVKKWADFA	GRPEPLTYKL	VSRNYPDLSL	GDYSLLWKAH	120
							180
CYP21A2_MFA	KKLTRSALLL	GMRDSMEPVV	EQLTQEFCE	MRAQARTPVA	IEEEFSLLTC	SIICHLTFGD	180
CYP21A2_MMU	KKLTRSALLL	GMRDSMEPVV	EQLTQEFCE	MRAQAGTPVA	IEEEFSLLTC	SIICHLTFGD	180
CYP21A2_HSA	KKLTRSALLL	GIRDSMEPVV	EQLTQEFCE	MRAQPGTPVA	IEEEFSLLTC	SIICYLTFGD	180
							240
CYP21A2_MFA	KIKEDNLVPA	YYKCIQEVKL	TWSHWSIQIV	DVIPFLRFSP	NPGLRRLKQA	IEKRDHIVEK	240
CYP21A2_MMU	KIKEDNLVPA	YYKCIQEVKL	TWSHWSIQIV	DVIPFLRFFP	NPGLRRLKQA	IEKRDHIVEK	240
CYP21A2_HSA	KIKDDNLMVA	YYKCIQEVKL	TWSHWSIQIV	DVIPFLRFFP	NPGLRRLKQA	IEKRDHIVEM	240

300

CYP21A2_MFA	QLRQHKESLV	AGQWRDXXXY	MLQVVAQPSM	EEGSGQLLEG	HVLMAAVDLL	IGGTETTAXX	300
CYP21A2_MMU	QLRQHKESLV	AGQWRDMMDY	MLQVVAQPSM	EEGSGQLLEG	HVHMAAVDLL	IGGTETTANT	300
CYP21A2_HSA	QLRQHKESLV	AGQWRDMMDY	MLQGVAQPSM	EEGSGQLLEG	HVHMAAVDLL	IGGTETTANT	300

CYP21A2_MFA	XSWAVIFLLH	HPEIQQLQE	ELDHGPGGA	SSSRVPYKDR	ARLPLFNATI	TEVLRRLRPVV	360
CYP21A2_MMU	LSWAVVFLH	HPEIQQLQE	ELDHGPGSA	SSSRVPYKDR	ARLPLLNATI	AEVLRRLRPVV	360
CYP21A2_HSA	LSWAVVFLH	HPEIQQLQE	ELDHGPGGA	SSSRVPYKDR	ARLPLLNATI	AEVLRRLRPVV	360

CYP21A2_MFA	PLALPHRTTR	PSSISGYDIP	EGTVIIPNLQ	GAHLNEMVWE	RPHEFWPDGF	LEPGNSRAL	420
CYP21A2_MMU	PLALPHRTTR	PSSISGYDIP	EGTVIIPNLQ	GAHLDEMWE	RPHEFWPDRF	LEPGKNSRAL	420
CYP21A2_HSA	PLALPHRTTR	PSSISGYDIP	EGTVIIPNLQ	GAHLDETWE	RPHEFWPDRF	LEPGKNSRAL	420

CYP21A2_MFA	AFGCGARVCL	GEPLARLELF	VVLTQLLQAF	TLLPPGDALP	SLQPLPHCSV	ILKMQPFQVW	480
CYP21A2_MMU	AFGCGARVCL	GEPLARLELF	VVLTRLLQAF	TLLPPGDALP	SLQPLPHCSV	ILKMQPFQVW	480
CYP21A2_HSA	AFGCGARVCL	GEPLARLELF	VVLTRLLQAF	TLLPSGDALP	SLQPLPHCSV	ILKMQPFQVR	480

CYP21A2_MFA	LQPRGLGXTA	LSXSQ	495
CYP21A2_MMU	LQPRGLGVHS	LGQSQ	495
CYP21A2_HSA	LQPRGMGAHS	PGQSQ	495

Public domain: Qlv-U151A-D2_EST_BB878154 (partial)
Tissue preference: (liver)

CYP24A1

MfMm : 99.4, CH : 97.3, RH : 98.1

CYP24A1_MFA	MSSPISKSR	LAAFLQQLRS	PRQPPRPVTS	TAYTSPQPRE	VPVCPLTAGG	ETQNAAALPG	60
CYP24A1_MMU	MSSPISKSR	LAAFLQQLRS	PRQPPRPVTS	TAYTSPQPRE	VPVCPLTAGG	ETQNAAALPG	60
CYP24A1_HSA	MSSPISKSR	LAAFLQQLRS	PRQPPRLVTS	TAYTSPQPRE	VPVCPLTAGG	ETQNAAALPG	60

CYP24A1_MFA	PTSWPLLGS	LQILWKGGLK	KQHDTLVEYH	KKYGKIFRMK	LGSFESVHLG	SPCLLEALYR	120
CYP24A1_MMU	PTSWPLLGS	LQILWKGGLK	KQHDTLVEYH	KKYGKIFRMK	LGSFESVHLG	SPCLLEALYR	120
CYP24A1_HSA	PTSWPLLGS	LQILWKGGLK	KQHDTLVEYH	KKYGKIFRMK	LGSFESVHLG	SPCLLEALYR	120

CYP24A1_MFA	TESAYPQRLE	IKPWKAYRDY	RKEGYGLLIL	XXXXXXXXXX	XXXXXXXXXX	XXXXLDNKN	180
CYP24A1_MMU	TESAYPQRLE	IKPWKAYRDY	RKEGYGLLIL	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	180
CYP24A1_HSA	TESAYPQRLE	IKPWKAYRDY	RKEGYGLLIL	EGEDWQVR	AFQKKLMKPG	EVMLDNKN	180

CYP24A1_MFA	EVLADFMR	DELCDERGH	EDLYSELN	SFESICLVLY	EKRFGLLQKN	AGDEAMNFIM	240
CYP24A1_MMU	XVLADFMR	DELCDERGH	EDLYSELN	SFESICLVLY	EKRFGLLQKN	AGDEAMNFIM	240
CYP24A1_HSA	EVLADFMR	DELCDERGH	EDLYSELN	SFESICLVLY	EKRFGLLQKN	AGDEAVNFIM	240

CYP24A1_MFA	AIKTMSTFG	RMMVTPVELH	KSLNTKIWD	HTLAWDTIFK	SVKSCVDNRL	EKYSQQPSAD	300
CYP24A1_MMU	AIKTMSTFG	RMMVTPVELH	KSLNTKVWD	HTLAWDTIFK	SXXXXXXNRL	EKYSQQPSAD	300
CYP24A1_HSA	AIKTMSTFG	RMMVTPVELH	KSLNTKVWD	HTLAWDTIFK	SVKACIDNRL	EKYSQQPSAD	300

360

CYP24A1_MFA	FLCDIYHQNR	LSKKELYAAV	TELQLAAVET	TANSLMWILY	NLSRNPQVQQ	KLFKEIQSVL	360
CYP24A1_MMU	FLCDIYHQNR	LSKKELYAAV	TELQLAAVET	TANSLMWILY	NLSRNPQVQQ	KLFKEIQSVL	360
CYP24A1_HSA	FLCDIYHQNR	LSKKELYAAV	TELQLAAVET	TANSLMWILY	NLSRNPQVQQ	KLLKEIQSVL	360

						420	
CYP24A1_MFA	PENQVPRAED	LRNMPYLKAC	LKESMRLTPS	VPFTSRTLDK	ATVLGEYALP	KGTVLMLNTQ	420
CYP24A1_MMU	PENQVPRAED	LRNMPYLKAC	LKESMRLTPS	VPFTTRTLDK	ATVLGEYALP	KGTVLMLNTQ	420
CYP24A1_HSA	PENQVPRAED	LRNMPYLKAC	LKESMRLTPS	VPFTTRTLDK	ATVLGEYALP	KGTVLMLNTQ	420

						480	
CYP24A1_MFA	VLGSDEDNFE	DSSQFRPERW	LQEKEKINPF	AHLPGGIGKR	MCIGRRRLAEL	QLHLALCWIV	480
CYP24A1_MMU	VLGSDEDNFE	DSSQFRPERW	LQEKEKINPF	AHLPGGIGKR	MCIGRRRLAEL	QLHLALCWIV	480
CYP24A1_HSA	VLGSSEDNFE	DSSQFRPERW	LQEKEKINPF	AHLPGVGKR	MCIGRRRLAEL	QLHLALCWIV	480

					514	
CYP24A1_MFA	RKYDIQATDN	EPVEMLHSGT	XXXXXXVPIX	FFQR	514	
CYP24A1_MMU	RKYDIQATDN	EPVEMLHSGT	LVPSRELPIV	FFQR	514	
CYP24A1_HSA	RKYDIQATDN	EPVEMLHSGT	LVPSRELPIA	FCQR	514	

Public domain: none.
Tissue preference: (liver, lung)

CYP26A1

MfMm: 100.0, MfHs: 99.6, MmHs: 99.6

						60	
CYP26A1_MFA	MGLPALLASA	LCTFVLPLLL	FLAAIKLWDL	YCVSGRDRSC	ALPLPPGTMG	FPPFGETLQM	60
CYP26A1_MMU	MGLPALLASA	LCTFVLPLLL	FLAAIKLWDL	YCVSGRDRSC	ALPLPPGTMG	FPPFGETLQM	60
CYP26A1_HSA	MGLPALLASA	LCTFVLPLLL	FLAAIKLWDL	YCVSGRDRSC	ALPLPPGTMG	FPPFGETLQM	60

						120	
CYP26A1_MFA	VLQRRKFLQM	KRRKYGFIYK	THLFGRPVTR	VMGADNVVRI	LLGEHRLVSV	HWPASVRTIL	120
CYP26A1_MMU	VLQRRKFLQM	KRRKYGFIYK	THLFGRPVTR	VMGADNVVRI	LLGEHRLVSV	HWPASVRTIL	120
CYP26A1_HSA	VLQRRKFLQM	KRRKYGFIYK	THLFGRPVTR	VMGADNVVRI	LLGEHRLVSV	HWPASVRTIL	120

						180	
CYP26A1_MFA	GSGCLSNLHD	SSHQQRKKVI	MRAFSREALE	CYVPVITEEV	GSSLEQWLSC	GERGLLVYPE	180
CYP26A1_MMU	GSGCLSNLHD	SSHQQRKKVI	MRAFSREALE	CYVPVITEEV	GSSLEQWLSC	GERGLLVYPE	180
CYP26A1_HSA	GSGCLSNLHD	SSHQQRKKVI	MRAFSREALE	CYVPVITEEV	GSSLEQWLSC	GERGLLVYPE	180

						240	
CYP26A1_MFA	VKRLMFRIAM	RILLGCEPQL	AGDGDAAEQQL	VEAFEEMTRN	LFSLPIDVPF	SGLYRGMKAR	240
CYP26A1_MMU	VKRLMFRIAM	RILLGCEPQL	AGDGDAAEQQL	VEAFEEMTRN	LFSLPIDVPF	SGLYRGMKAR	240
CYP26A1_HSA	VKRLMFRIAM	RILLGCEPQL	AGDGDSEQQQL	VEAFEEMTRN	LFSLPIDVPF	SGLYRGMKAR	240

						300	
CYP26A1_MFA	NLIHARIEQN	IRAKICGLRA	SEAGRGCKDA	LQLLIEHSWE	RGERLDMQAL	KQSSTELLFG	300
CYP26A1_MMU	NLIHARIEQN	IRAKICGLRA	SEAGRGCKDA	LQLLIEHSWE	RGERLDMQAL	KQSSTELLFG	300
CYP26A1_HSA	NLIHARIEQN	IRAKICGLRA	SEAGQGCKDA	LQLLIEHSWE	RGERLDMQAL	KQSSTELLFG	300

						360	
CYP26A1_MFA	GHETTASAAT	SLITYLGLYP	HVLQKVREEL	KSKGLLCKSN	QDNKLDMEIL	EQLKYIGCVI	360
CYP26A1_MMU	GHETTASAAT	SLITYLGLYP	HVLQKVREEL	KSKGLLCKSN	QDNKLDMEIL	EQLKYIGCVI	360
CYP26A1_HSA	GHETTASAAT	SLITYLGLYP	HVLQKVREEL	KSKGLLCKSN	QDNKLDMEIL	EQLKYIGCVI	360

420

CYP26A1_MFA	KETLRLNPPV	PGGFRVALKT	FELNGYQIPK	GWNVIYSICD	THDVAEIFTN	KEEFNPDRFM	420
CYP26A1_MMU	KETLRLNPPV	PGGFRVALKT	FELNGYQIPK	GWNVIYSICD	THDVAEIFTN	KEEFNPDRFM	420
CYP26A1_HSA	KETLRLNPPV	PGGFRVALKT	FELNGYQIPK	GWNVIYSICD	THDVAEIFTN	KEEFNPDRFM	420

						480	
CYP26A1_MFA	LPHPEDASRF	SFIPFGGGLR	SCVGKEFAKI	LLKIFTVELA	RHCDWQLLNG	PPTMKTSPV	480
CYP26A1_MMU	LPHPEDASRF	SFIPFGGGLR	SCVGKEFAKI	LLKIFTVELA	RHCDWQLLNG	PPTMKTSPV	480
CYP26A1_HSA	LPHPEDASRF	SFIPFGGGLR	SCVGKEFAKI	LLKIFTVELA	RHCDWQLLNG	PPTMKTSPV	480

		497	
CYP26A1_MFA	YPVDNLPARF	THFHGEI	497
CYP26A1_MMU	YPVDNLPARF	THFHGEI	497
CYP26A1_HSA	YPVDNLPARF	THFHGEI	497

Public domain: none.
Tissue preference: liver

CYP26B1

MfMm: 100.0, MfHs: 99.2, MmHs: 98.9

						60	
CYP26B1_MFA	XXXXXXXXXX	XXXXLAACL	SVTLLLA	SVSQ	QLWQLRWAAT	RDKSCKLP	IG 60
CYP26B1_MMU	MLFEGLELVS	ALATLAACL	SVTLLLA	SVSQ	QLWQLRWAAT	RDKSCKLP	IG 60
CYP26B1_HSA	MLFEGDLVS	ALATLAACL	SVTLLLA	SVSQ	QLWQLRWAAT	RDKSCKLP	IG 60

						120	
CYP26B1_MFA	ETGHWLLQGS	GFQSSRREKY	GNVFKTHLLG	RPLIRVTGAE	NVRKILMGEH	HLVSTEWPRS	120
CYP26B1_MMU	ETGHWLLQXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	120
CYP26B1_HSA	ETGHWLLQGS	GFQSSRREKY	GNVFKTHLLG	RPLIRVTGAE	NVRKILMGEH	HLVSTEWPRS	120

						180	
CYP26B1_MFA	TRMLLGPN	TIV	SNSIGDIHRN	KRKVF	SKIFS	HEALESYLPK	IQLVIQD
CYP26B1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXVFSKIFS	HEALESYLPK	IQLVIQD	AWSSHPEAIN	180
CYP26B1_HSA	TRMLLGPN	TIV	SNSIGDIHRN	KRKVF	SKIFS	HEALESYLPK	IQLVIQD

						240	
CYP26B1_MFA	VYQEAQK	LTF	RMAIRVLLGF	SIPEEDL	GH	FEVYQQFVEN	VFSLPVDLPF
CYP26B1_MMU	VYQEAQK	LTF	RMAIRVLLGF	SIPEEDL	GH	FEVYQQFVEN	VFSLPVDLPF
CYP26B1_HSA	VYQEAQK	LTF	RMAIRVLLGF	SIPEEDL	GH	FEVYQQFVDN	VFSLPVDLPF

						300	
CYP26B1_MFA	QILQKGLEKA	IREKLQCTQG	KDYSDALD	LL	I	ESSKEHGKE	MTMQELKDGT
CYP26B1_MMU	QILQKGLEKA	IREKLQCTQG	KDYSDALD	LL	I	ESSKEHGKE	MTMQELKDGT
CYP26B1_HSA	QILQKGLEKA	IREKLQCTQG	KDYDALD	LL	I	ESSKEHGKE	MTMQELKDGT

						360	
CYP26B1_MFA	TASASTSLIM	QLLKHPTVLE	KLREELRAHG	ILHSGGCPCE	GTLRLD	TL	SG LRYLDCVIKE
CYP26B1_MMU	TASASTSLIM	QLLKHPTVLE	KLREELRAHG	ILHSGGCPCE	GTLRLD	TL	SG LRYLDCVIKE
CYP26B1_HSA	TASASTSLIM	QLLKHPTVLE	KLRDELRAHG	ILHSGGCPCE	GTLRLD	TL	SG LRYLDCVIKE

						420	
CYP26B1_MFA	VMRLFTPISG	GYRTVLQTFE	LDGFQIPKGW	SVMYSIRDTH	DTAPVFKDVN	VFD	PDRFSQA 420
CYP26B1_MMU	VMRLFTPISG	GYRTVLQTFE	LDGFQIPKGW	SVMYSIRDTH	DTAPVFKDVN	VFD	PDRFSQA 420
CYP26B1_HSA	VMRLFTPISG	GYRTVLQTFE	LDGFQIPKGW	SVMYSIRDTH	DTAPVFKDVN	VFD	PDRFSQA 420

							480
CYP26B1_MFA	RSEDKDGRFH	YLPFGGGVRT	CLGKHLAKLF	LKVLAVELAS	TSRFELATRT	FPRITLVPVL	480
CYP26B1_MMU	RSEDKDGRFH	YLPFGGGVRT	CLGKHLAKLF	LKVLAVELAS	TSRFELATRT	FPRITLVPVL	480
CYP26B1_HSA	RSEDKDGRFH	YLPFGGGVRT	CLGKHLAKLF	LKVLAVELAS	TSRFELATRT	FPRITLVPVL	480

					512	
CYP26B1_MFA	XPVDGLSVKF	FGLDSNQNKI	LPETeamLSA	TV	512	
CYP26B1_MMU	HPVDGLSVKF	FGLDSNQNKI	LPETeamLSA	TV	512	
CYP26B1_HSA	HPVDGLSVKF	FGLDSNQNEI	LPETeamLSA	TV	512	

Public domain: none.
Tissue preference: lung

CYP26C1

MfMm: 100.0, MfHs: 97.8, MmHs: 99.1

							60
CYP26C1_MFA	MFPWGLSCLS	VLGAAGTAVL	CAGLLLSLAQ	HLWTLRWMLS	RDRASTLPLP	KGSMGWPFPG	60
CYP26C1_MMU	MFPWGLSCLS	VLGAAGTAVL	CAGLLLSLAQ	HLWTLRWMLS	RDRASTLPLP	KGSMGWPFPG	60
CYP26C1_HSA	MFPWGLSCLS	VLGAAGTALL	CAGLLLSLAQ	HLWTLRWMLS	RDRASTLPLP	KGSMGWPFPG	60

							120
CYP26C1_MFA	ETLHWLVQGS	RFHSSRRERY	GTVPKTHLLG	RPVIRVSGAE	NVRTILLGEH	RLVRSQWPQS	120
CYP26C1_MMU	ETLHWLVQGS	RFHSSRRERY	GTVPKTHLLG	RPVIRVSGAE	NVRTILLGEH	RLVRSQWPQS	120
CYP26C1_HSA	ETLHWLVQGS	RFHSSRRERY	GTVPKTHLLG	RPVIRVSGAE	NVRTILLGEH	RLVRSQWPQS	120

							180
CYP26C1_MFA	AHILLGSHTL	LGAVGEPHRR	RRKXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXGPVS	180
CYP26C1_MMU	AHILLGSHTL	LGAVGEPHRR	RRKVLARVFS	RAALERYVPR	LQGALRHEVR	SWCAAGGPVS	180
CYP26C1_HSA	AHILLGSHTL	LGAVGEPHRR	RRKVLARVFS	RAALERYVPR	LQGALRHEVR	SWCAAGGPVS	180

							240
CYP26C1_MFA	VYDAAKALTF	RMAAXXXXXX	XXXXXXXXXX	XXXXXXQLVEN	LFSLPLDVPF	SGLXXGIRAR	240
CYP26C1_MMU	VYDAAKALTF	RMAARILLGL	RLDEAQCATL	ARTFEQLVEN	LFSLPLDVPF	SGLRKXXXXX	240
CYP26C1_HSA	VYDASKALTF	RMAARILLGL	RLDEAQCATL	ARTFEQLVEN	LFSLPLDVPF	SGLRKGIRAR	240

							300
CYP26C1_MFA	DQLHQHLEGA	ISEKLHEDKA	AEPGDALELI	IHSARELGHE	PSMQELKESX	XXXXXXXXXX	300
CYP26C1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	300
CYP26C1_HSA	DQLHRHLEGA	ISEKLHEDKA	AEPGDALDLI	IHSARELGHE	PSMQELKESA	VELLFAAFFT	300

							360
CYP26C1_MFA	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	360
CYP26C1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	360
CYP26C1_HSA	TASASTSLVL	LLLQHPAAIA	KIREELVAQG	LGRACGCAPG	AAGGSEGPPP	DCGCEPDLSL	360

							420
CYP26C1_MFA	XXXXXXXXXX	XVVKEVLRLI	PPVSGGYRTA	LRTFELDGYQ	IPKGWSVMYS	IRDTHETAAY	420
CYP26C1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	420
CYP26C1_HSA	AALGRLRYVD	CVVKEVLRLI	PPVSGGYRTA	LRTFELDGYQ	IPKGWSVMYS	IRDTHETAAY	420

							480
CYP26C1_MFA	YRSPPEGFDP	ERFGAARXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	480
CYP26C1_MMU	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	480

CYP26C1_HSA YRSPPEGFDP ERFGAAREDS RGASSRFHYI PFGGGARSCL GQELAQAVLQ LLAVELVRTA 480

522
 CYP26C1_MFA XXXXXXXXXXX XXXXXXXXXXX XXGLRLFFHP LAPLVAGDGL CL 522
 CYP26C1_MMU XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XX 522
 CYP26C1_HSA RWELATPAFP AMQTVPIVHP VDGLRLFFHP LTPSVAGNGL CL 522

Public domain: none.

Tissue preference: not expressed

CYP27B1

MfMm: 100.0, MfHs: 96.2, MmHs: 96.3

60
 CYP27B1_MFA MTQTLKYASR VFHRVRWAPE LGASLGYREY DSARRSLADI PGPSTPSFLA ELFCKGGLSR 60
 CYP27B1_MMU MTQTLKYASR VFHRVRWAPE LGASLGYREY DSARRSLADI PGPSTPSFLA ELFCKGGLSR 60
 CYP27B1_HSA MTQTLKYASR VFHRVRWAPE LGASLGYREY HSARRSLADI PGPSTPSFLA ELFCKGGLSR 60

120
 CYP27B1_MFA LHELQVQGAA RFGPVWLASF GTVRTVYVAA PALVEELLRQ EGPRPERCSF SPWTEHRRRR 120
 CYP27B1_MMU LHELQVQGAA RFGPVWLASF GTVRTVYVAA PALVEELLRQ EGPRPERCSF SPWTEHRRRR 120
 CYP27B1_HSA LHELQVQGAA HFGPVWLASF GTVRTVYVAA PALVEELLRQ EGPRPERCSF SPWTEHRRRC 120

180
 CYP27B1_MFA QRACGLLTAE GEEWQRLRSL LAPLLLRPQA AARYAETLDN VVRDLVRRRLR CQRGRGTGPP 180
 CYP27B1_MMU QRACGLLTAE GEEWQRLRSL LAPLLLRPQA AARYAETLDN VVRDLVRRRLR CQRGRGTGPP 180
 CYP27B1_HSA QRACGLLTAE GEEWQRLRSL LAPLLLRPQA AARYAGTLNN VVCDLVRRRLR RQRGRGTGPP 180

240
 CYP27B1_MFA ALVRDVAGEF YKFGLEGIAA VLLGSRLGCL EAQVPPDTET FIRAVGSVVF STLLTMAMPH 240
 CYP27B1_MMU ALVRDVAGEF YKFGLEGIAA VLLGSRLGCL EAQVPPDTET FIRAVGSVVF STLLTMAMPH 240
 CYP27B1_HSA ALVRDVAGEF YKFGLEGIAA VLLGSRLGCL EAQVPPDTET FIRAVGSVVF STLLTMAMPH 240

300
 CYP27B1_MFA WLRRLLVPGPW GRLCRDWDQM FAFAQRHVER REAEAAMRNR GQPDDEDLESG AHLTHFLFQE 300
 CYP27B1_MMU WLRRLLVPGPW GRLCRDWDQM FAFAQRHVER REAEAAMRNR GQPDDEDLESG AHLTHFLFQE 300
 CYP27B1_HSA WLRHLVPGPW GRLCRDWDQM FAFAQRHVER REAEAAMRNG GQPEKDLESG AHLTHFLFRE 300

360
 CYP27B1_MFA ELPAQSILGN VTELLLAGVD TVSNTLSWAL YELSRHPEVQ TALHSEITAA LGPGSSAHPP 360
 CYP27B1_MMU ELPAQSILGN VTELLLAGVD TVSNTLSWAL YELSRHPEVQ TALHSEITAA LGPGSSAHPP 360
 CYP27B1_HSA ELPAQSILGN VTELLLAGVD TVSNTLSWAL YELSRHPEVQ TALHSEITAA LSPGSSAYPS 360

420
 CYP27B1_MFA ATVLSQLPLL KAVVKEVLRL YPVVPGNSRV PDKDIHVG DY IIPKNTLVTL CHYATSRDPA 420
 CYP27B1_MMU ATVLSQLPLL KAVVKEVLRL YPVVPGNSRV PDKDIHVG DY IIPKNTLVTL CHYATSRDPA 420
 CYP27B1_HSA ATVLSQLPLL KAVVKEVLRL YPVVPGNSRV PDKDIHVG DY IIPKNTLVTL CHYATSRDPA 420

480
 CYP27B1_MFA QFPEPNSFHP ARWLGE GPTP XPFASLPFGF GKRSCMGRR L AELELQMALA QILIHFEVQP 480
 CYP27B1_MMU QFPEPNSFHP ARWLGE GPTP HPFASLPFGF GKRSCMGRR L AELELQMALA QILIHFEVQP 480
 CYP27B1_HSA QFPEPNSFRP ARWLGE GPTP HPFASLPFGF GKRSCMGRR L AELELQMALA QILTHFEVQP 480

508
 CYP27B1_MFA EPGAAPIRPM TRTVLPERS INLQFLDR 508

CYP27B1_MMU	EPGAAPIRPM	TRTVLVPERS	INLQFLDR	508
CYP27B1_HSA	EPGAAPVRPK	TRTVLVPERS	INLQFLDR	508

Public domain: QfIA-19988_full_AB172880 (partial)
Tissue preference: (lung)

CYP27C1

MfMm: 99.5, MfHs: 98.6, MmHs: 98.7

							60
CYP27C1_MFA	MRSVLRQRIL	KPKDVAIYSG	EVNQVIADLI	KRIYLLRSQA	EDGETVTNVN	DLFFKYSMEG	60
CYP27C1_MMU	MRSVLRQRIL	KPKDVAIYSG	EVNQVIADLI	KRIYLLRSQA	EDGETVTNVN	DLFFKYSMEG	60
CYP27C1_HSA	MRSVLRQRIL	KPKDVAIYSG	EVNQVIADLI	KRIYLLRSQA	EDGETVTNVN	DLFFKYSMEG	60

							120
CYP27C1_MFA	VATILYESRL	GCLENSIPQL	TVEYIEALEL	MFSMFKTSMY	AGAIPRWLRP	FIPKPWREFC	120
CYP27C1_MMU	VATILYESRL	GCLENSIPQL	TVEYIEALEL	MFSMFKTSMY	AGAIPRWLRP	FIPKPWREFC	120
CYP27C1_HSA	VATILYESRL	GCLENSIPQL	TVEYIEALEL	MFSMFKTSMY	AGAIPRWLRP	FIPKPWREFC	120

							180
CYP27C1_MFA	RSWDGLFKFS	QIHV.AKLRD	IQYHTDRGRR	ASGGLLTYLF	LSQALTQEI	YANVTEMLLA	179
CYP27C1_MMU	RSWDGLFKFS	QIHVDNKLRLD	IQYHTDRGRR	ASGGLLTYLF	LSQALTQEI	YANVTEMLLA	180
CYP27C1_HSA	RSWDGLFKFS	QIHVDNKLRLD	IQYQMDRGRR	VSGGLLTYLF	LSQALTQEI	YANVTEMLLA	180

							240
CYP27C1_MFA	GVDTTSTFLS	WTVYLLARHP	EVQQTIVYREI	VKNLGERHVP	TAADVPKVPL	VRALLKETLR	239
CYP27C1_MMU	GVDTTSTFLS	WTVYLLARHP	EVQQTIVYREI	VKNLGERHVP	TAADVPKVPL	VRALLKETLR	240
CYP27C1_HSA	GVDTTSTFLS	WTVYLLARHP	EVQQTIVYREI	VKNLGERHVP	TAADVPKVPL	VRALLKETLR	240

							300
CYP27C1_MFA	LFPVLPNGNR	VTQEDLVIGG	YLIPKGTQLA	LCHYATSYQD	ENFPRAKEFR	PERWLRKGD	299
CYP27C1_MMU	LFPVLPNGNR	VTQEDLVIGG	YLIPKGTQLA	LCHYATSYQD	ENFPRAKEFR	PERWLRKGD	300
CYP27C1_HSA	LFPVLPNGNR	VTQEDLVIGG	YLIPKGTQLA	LCHYATSYQD	ENFPRAKEFR	PERWLRKGD	300

							360
CYP27C1_MFA	DRVDNFGSIP	FGHGVRSCIG	RRIAELEIHL	VVIQLLQHFE	IKTSSQTKAV	HAKTHGLLTP	359
CYP27C1_MMU	DRVDNFGSIP	FGHGVRSCIG	RRIAELEIHL	VVIQLLQHFE	IKTSSQTKAV	HARTHGLLTP	360
CYP27C1_HSA	DRVDNFGSIP	FGHGVRSCIG	RRIAELEIHL	VVIQLLQHFE	IKTSSQTNV	HAKTHGLLTP	360

			372
CYP27C1_MFA	GGPIHVRFVN	RK	371
CYP27C1_MMU	GGPIHVRFVN	RK	372
CYP27C1_HSA	GGPIHVRFVN	RK	372

Public domain: none.
Tissue preference: heart, liver, lung, spleen.

CYP46A1

MfMm: 100.0, MfHs: 99.6, MmHs: 99.6

CYP46A1_MFA	MSPGLLLLGS	AVLLAFGLCC	TFVHRARSRY	EHIPGPPRPS	FLLGHLPCFW	KKDEVGGRVL	60
CYP46A1_MMU	MSPGLLLLGS	AVLLAFGXXX	XXXXXXXXXX	XXXXXXXXXX	FLLGHLPCFW	KKDEVGGRVL	60
CYP46A1_HSA	MSPGLLLLGS	AVLLAFGLCC	TFVHRARSRY	EHIPGPPRPS	FLLGHLPCFW	KKDEVGGRVL	60

							120
CYP46A1_MFA	QDVFLDWAKK	YGPVVRVNVF	HKTSVIITSP	ESVKKFLMST	KYNKDSKMYR	ALQTVFGERL	120
CYP46A1_MMU	QDVFLDWAKK	YGPVVRVNVF	HKTSVIITSP	ESVKKFLMST	KYNKDSKMYR	ALQTVFGERL	120
CYP46A1_HSA	QDVFLDWAKK	YGPVVRVNVF	HKTSVIVTSP	ESVKKFLMST	KYNKDSKMYR	ALQTVFGERL	120

							180
CYP46A1_MFA	FGQGLVSECN	YERWHKQRRV	IDLAFSRSSL	VSLMETFNEK	AEQLVEILEA	KADGQTPVSM	180
CYP46A1_MMU	FGQGLVSECN	YERWHKQRRV	IDLAFSRSSL	VSLMETFNEK	AEQLVEILEA	KADGQTPVSM	180
CYP46A1_HSA	FGQGLVSECN	YERWHKQRRV	IDLAFSRSSL	VSLMETFNEK	AEQLVEILEA	KADGQTPVSM	180

							240
CYP46A1_MFA	QDMLTYTAMD	ILAKAAFGME	TSMLLGAQKP	LSQAVKLMLE	GITASRNTLA	KFLPGKRKQL	240
CYP46A1_MMU	QDMLTYTAMD	ILAKAAFGME	TSMLLGAQKP	LSQAVKLMLE	GITASRNTLA	KFLPGKRKQL	240
CYP46A1_HSA	QDMLTYTAMD	ILAKAAFGME	TSMLLGAQKP	LSQAVKLMLE	GITASRNTLA	KFLPGKRKQL	240

							300
CYP46A1_MFA	REVRESIRFL	RQVGRDWVQR	RREALKRGE	VPADILTQIL	KAEEGAQDDE	GLLDNFVTFF	300
CYP46A1_MMU	REVRESIRFL	RQVGRDWVQR	RREALKRGE	VPADILTQIL	KAEEGAQDDE	GLLDNFVTFF	300
CYP46A1_HSA	REVRESIRFL	RQVGRDWVQR	RREALKRGE	VPADILTQIL	KAEEGAQDDE	GLLDNFVTFF	300

							360
CYP46A1_MFA	IAGHETSANH	LAFTVMELSR	QPEIVARLQA	EVDEVIGSKR	YLDFEDLGRL	QYLSQVLKES	360
CYP46A1_MMU	IAGHETSANH	LAFTVMELSR	QPEIVARLQA	EVDEVIGSKR	YLDFEDLGRL	QYLSQVLKES	360
CYP46A1_HSA	IAGHETSANH	LAFTVMELSR	QPEIVARLQA	EVDEVIGSKR	YLDFEDLGRL	QYLSQVLKES	360

							420
CYP46A1_MFA	LRLYPPAWGT	FRLLEEETLI	DGVRVPGNTP	LLFSTYVMGR	MDTYFEDPLT	FNPDRFGPGA	420
CYP46A1_MMU	LRLYPPAWGT	FRLLEEETLI	DGVRVPGNTP	XXFSTYVMGR	MDTYFEDPLT	FNPDRFGPGA	420
CYP46A1_HSA	LRLYPPAWGT	FRLLEEETLI	DGVRVPGNTP	LLFSTYVMGR	MDTYFEDPLT	FNPDRFGPGA	420

							480
CYP46A1_MFA	PKPRFTYFPF	SLGHRSCIGQ	QFAQMEVKVV	MAKLLQRLEF	RLVPGQRFGL	QEATLKPLD	480
CYP46A1_MMU	PKPRFTYFPF	SLGHRSCIGQ	QFAQMEVKVV	MAKLLQRLEF	RLVPGQRFGL	QEATLKPLD	480
CYP46A1_HSA	PKPRFTYFPF	SLGHRSCIGQ	QFAQMEVKVV	MAKLLQRLEF	RLVPGQRFGL	QEATLKPLD	480

			500
CYP46A1_MFA	PVLCTLRPRG	WQTPPPPPPC	500
CYP46A1_MMU	PVLCTLRPRG	WQTPPPPPPC	500
CYP46A1_HSA	PVLCTLRPRG	WQAPPPPPPC	500

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Tissue preference: (heart)