Additional file 22. Alignment of the mouse (m) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1    1                     MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNL
ma12       1     MAPVAFPTSFFL..CLLLASGLAQAGRLLVVP.MDGSHWFTMQMVVEKLIHRGHEV
ma13       1     MVPAAFPTSLPLCVCLLLASGLVQAGRLLVVP.MDGSHWFDMQMVVEKLIQRGHEV
ma10       1     MAPADFPASLPLCVCLLLASGLAQAGRLLVVP.MDGSHWFTMQTVVEKLLHKGHEV
ma11       1     MAPAVFPASLPLRVCLLLAFGLAQAGRLLVVP.MDGSHWFSMKMIVEKLSHRGHEV
ma7        1   MACLLPAAQTLPAGFLFLVLWASVL.GDKLLVVP.QDGSHWLSMKEIVEHLSERGHDI
ma9        1   MACLLPAAQTLPAGFLFLVLWASVL.GDKLLVVP.QDGSHWLSMKEIVEHLSERGHDI
ma2        1   MDTGLCVPLRGISGLLLLLCALPWAEGAKVLVLP.MEGSQWLSMRDVVRELHARGHQT
ma5        1     MGLRMPLQGLVG.LLLLCALPWTEGEKVLVFP.VGGSHWLSMRDVVRELHAQGHQT
ma1        1 MTVVCWSSRLLLLLPYLLLCVFGPSASHAGRLLVFP.MDGSHWLSMLGVIQQLQQKGHEV

Ugt71g1   41 YITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLI
ma12      54 VVVIPEV.....SWQLGKSLNCTV..KTYSISHTLE.....DLDREFKYLSYTQWKTP.E
ma13      56 VVVIPEV.....SWRLGKSLNCTV..KTYSVSHTLE.....DLDREFKYFTYTQWKTP.E
ma10      56 VVVVPEV.....SWQLTKPLNFVV..KTYAVSHTQE.....DLNREFKIFIDAQWKSQQE
ma11      56 VVVIPEV.....SWHLGKSQNFTV..KTYSVSYTLE.....DLSHHFNFFAHKQWEN.RE
ma7       57 MVLVPEV.....NLLLGESKYYRR..KIFSVTYSLE.....ELQTRFRTFGNNHFLPGAS
ma9       57 VVLVPEV.....NLLLGESKYYRR..KIFSVPYSLE.....ELQTRFRTFGRNQFVPGAP
ma2       58 VVLASEV.....TVHIKGEDFFTL..KTYAFPYTKE.....EYQQEILSDIEKTFKTQHF
ma5       55 VVLAPEV.....NMRIKEEDFFTF..KVYAVPYTRQ.....EL.EEMMENLKVFFDTGNY
ma1       60 VVIAPEA.....SIHIKEGSFYTL..RKFPVPFQKE.....NVTATLVELGRTAFNQDSF

Ugt71g1  101 PHVKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFG
ma12     101 HSIRSFLTGSARGFFELTFSHCRSLFNDKKLVEYLKQRFFDAVFLDPFDVCGLIVAKYFS
ma13     103 QSIRSFMTGSARGFFELMFSHSRGLFNDKKLVEYLKQRSFDAVFLDPFDVCGLIVAKYLS
ma10     104 GGILPLLDSPAKGFFELLFSHCRSLFNDKKLVEYLKQTSFDAVFLDPFDVCGLTVAKYFS
ma11     103 VGMFSLLKHSGKGFFQVLFSHCRSLFNDKKLVEYLKQRSFDAVFLDPFDVCGLTIAKYFS
ma7      105 LMGPLREYRNNMIVVDMFFSNCQSLLKDSATLSFLRENKFDALFTDPAMPCGVILAEYLN
ma9      105 LMGPLREYRNSMLTLEMFFSNCQSLLKDSATLSFLRENKFDALFTDPAMPCGVILAEYLN
ma2      106 VKAFFETTASIRNFFDLYSNSCIALLHNKMLIQQLNSSFFDVILTDPIFPCGAVLAKYLQ
ma5      102 MKKIFKTSEALRNMSTVLLKTCTNILHNESLLHHLNSSSFDVVFTDPVFPCGALLAKYLG
ma1      108 LLRVVKIYMKVKRDSSMLLAGCSHLLHNAEFMASLEESHFDALLTDPFLPCGSIVAQYLT

Ugt71g1  136 IPSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNK
ma12     161 LPSVIFARGVFCDYLEEGAQCPSLPSYVPRLFSKYTDTMTFKERVWNHLIYIEEHAFCSY
ma13     163 LPSVIFARLSFCYYLEEGAQCPSLLSYVPRLFSKYTDTMTFKERVWNHYMYIEDYVFCPY
ma10     164 LPSVVFSRGIFCHYLEDAAQCPSPPSYIPRMLLKFTDTMTFKERTRNLLAYMGERAFCHK
ma11     163 LPSVVFSGGIFCHYLDEGAQCPSPPSYVPRILSKFADTMTFKERVWNYFSYMKERAFCPY
ma7      165 LPSVYLFRGFPCSLEHMLGQSPSPVSYVPRFYTKFSDHMTFPQRLANFIVNILENYLYYC
ma9      165 LPSVYLFRGFPCSLEHMLGQSPSPVSYVPRFYTKFSDHMTFPQRLANFIVNILENYLYYC
ma2      166 IPAVFILRSLSCGIEYEATQCPNPSSYIPNLLTRLSDHMDFLQRVQNMLYYLVLKYICRL
ma5      162 IPAVFFLRYIPCGIEYEATQCPSPSSYIPNLFTRLSDHMDFLQRVQNMLYHLVLKYICHL
ma1      168 VPTVYFLNKLPCSLDSEATQCPVPLSYVPKSLSFNSDRMNFLQRVKNVLLAVSENFMCRV

Ugt71g1  196 DGGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
ma12     221 FLRTAVEVASEILQTPVTMTDLFSPVSIWLLRTDFVLEFPRPVMPNMVFIGGINCLQKKSLSK
ma13     223 FFKTAVEIASEVLQTPVTMTDLFSPVSIWLLRTDFVLEFPRPVMPNMVFVGGMNCLQGKPLSK
ma10     224 FFKSAADIASEVLQTPVTMTDLFSPVSIWLLRTDFVLEFPRPVMPNVIYIGGINCHQGKPLSK
ma11     223 FFKTAIEIASEVLQTPVTMTDLFSSVSIWMFRTDFVLEFPRPVMPNMVYIGGINCHPGKPLSK
ma7      225 LYSKYEIIASDLLKRDVSLPSLHQN.SLWLLRYDFVFEYPRPVMPNMIFLGGINCKKKGKLTQ
ma9      225 LYSKYEIIVTDLLKRDVSLPSLHQN.SLWLLRYDFVFEYPRPIMPNMIFIGGINCKKKGKLTQ
ma2      226 SITPYESLASELLQREVSLVEVLSHASVWLFRGDFVLDYPRPIMPNMVFIGGINCVTKKPLSQ
ma5      222 LITPYESLASELFQREVSSVELFSYASVWLFRGDFVLDYPRPIMPNMVFIGGINCVTKKPLSQ
ma1      228 VYSPYGSLATEILQKEVTVQDLLSPASIWLMRSDFVKDYPRPIMPNMVFIGGINCLQKKPLSQ
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