Additional file 23. Alignment of the rat (r) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1     1                     MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNL
ra8         1 ~~~~MAPADIPASLPLGLCLLLASGFGHAGKLLVVP.MDGSHWFTMQMVVEKLLPKGHEV
ra9         1 ~~~~MAPSGCPPSLPLCVCLFLASGFAQAGRLLVVP.MDGSHWFTMQMIVEKLSHRGHEV
ra11        1 ~~~~MAPSGCPSSLPLCVCLFLASGFAQAGRLLVVP.MDGSHWFTRQMTVEKLLQRGHEV
ra1         1 MSVVCRSSCSLLLLPCLLLCVLGPSASHAGKLLVIP.IDGSHWLSMLGVIQQLQQKGHEV
ra2         1 ~~MDTGLCAPLRGLSGLLLLLCALPWAEGGKVLVFP.MEGSHWLSMRDVVRELHARGHQA
ra6         1 ~~~~MGLHVTLQGLAGLLLLLYALPWAEGGKVLVFP.MEGSHWLSMRDVVRELHARGHQA
ra4         1 ~~~~MGIQGFLQKLSGLLLLLCALPWAEGGKVLVFP.MEGSHWLSMRDVVRELHARGHQA
ra7         1 ~~~~MACLLPAARLPAGFLFLVLWGSVLGDKLLVVP.QDGSHWLSMKEIVEHLSERGHDI

Ugt71g1    41 YITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLI
ra8        56 VVVVPEV.....SWQLGKPLNFTV..KTYSVSHTQE.....DLNREFKFFIDSQWKTQQE
ra9        56 VVVIPEV.....SWHMGKSLNFTV..KTYSVSYTLE.....DLNYHFKFFAHNQWKT.QE
ra11       56 GVVIPEE.....SWQLGKLVNCTV..KTYSIPYTVE.....DMDREFKHFSYTQWKTP.E
ra1        60 VVIAPEA.....SIHIKEGSFYTM..RKYPVPFQNE.....NVTAAFVELGRSVFDQDPF
ra2        58 VVLAPEV.....TVHMKGEDFFTL..QTYAFPYTKE.....EYQREILGNAKKGFEPQHF
ra6        56 VVLAPEV.....TVHIKEEDFFTL..QTYPVPYTRQ.....GFRQQMMRNIKVVFETGNY
ra4        56 VVLAPEV.....TVHIKEEDFFTL..QTYPVPYTKE.....EYRHHLLGHLQNFFETEFS
ra7        56 VVLVPEV.....NLLLGESKYYRR..KSFPVPYNLE.....ELRTRYRSFGNNHFAASSP

Ugt71g1   101 PHVKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFG
ra8       104 GGVLPLLTSPAQGFFELLFSHCRSLFKDKKLVEYLKQSSFDAVFLDPFDVCGLTVAKYFS
ra9       103 VGMFSLLKHSGKGFFELLFSHCRSLFKDKKLVEYLKQSSFDAVFLDPFDVCGLILAKYFS
ra11      103 QSMYSLITGSVKDFLEITFSHCRSLFKDKKLVEYLKQSSFDAVFLDPFHVCGLTVAKYLS
ra1       108 LLRVVKTYNKVKRDSSMLLSGCSHLLHNAEFMASLEQSHFDALLTDPFLPCGSIVAQYLS
ra2       106 VKTFFETMASIKKFFDLYANSCAALLHNKTLIQQLNSSSFDVVLTDPVFPCGALLAKYLQ
ra6       104 VKTFLETSEILKNISTVLLRSCMNLLHNGSLLQHLNSSSFDMVLTDPVIPCGAVLAKYLG
ra4       104 LKLVLQRMAAVNNVSTFYVRSCRGLLHNTALIQSLNSSSFDVVLTDPFFPCGAVLAMYLR
ra7       104 LMAPLREYRNNMIVIDMCFFSCQSLLKDSATLSFLRENQFDALFTDPAMPCGVILAEYLK

Ugt71g1   136 IPSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNK
ra8       164 LPSVVFSRGIFCHYLEEGSQCPSPPSYVPRGILKLTDTMTFKERVWNLLSYMGEHAFCPS
ra9       163 LPSVVFSGGIFCHYLDEGAQCPSPPSYVPRILSKFTDTMTFKERVWNHLSYMKERAFCPY
ra11      163 LPSIIFAKDIFCDNLKEGAQCPSLPSYVPRLFSKSADTMSFKERLWNHLIYFEERAFCSY
ra1       168 LPAVYFLNALPCSLDLEATQCPAPLSYVPKSLSSNTDRMNFLQRVKNMIIALTENFLCRV
ra2       166 IPAVFFLRSVPCGIDYEATQCPKPSSYIPNLLTMLSDHMTFLQRVKNMLYPLTLKYICHL
ra6       164 IPTVFFLRYIPCGIDSEATQCPKPSSYIPNLLTMLSDHMTFLQRVKNMLYPLALKYICHF
ra4       164 VPAVFFLQSMLCELEFEATNSPNPSSYIPRLLTLNSDHMSFLDRVKNMLYPVPWMYLCHV
ra7       164 LPSVYLFRGFPCSLEHMLGQSPSPVSYVPRFYTKFSDHMTFPQRLANFIANILENYLYHC

Ugt71g1   196 DGGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
ra8       224 FFKTATDIASEVLQTPVTMTDLFSPVSVWLLRTDFTLELPRPVMPNVIHIGGINCHQRKPLSK
ra9       223 FFKTAVEIASEVLQTPVTMRDLFSPVSIWMFRTDFVLEFPRPVMPNMVYIGGINCHQGKPLSK
ra11      223 YLKTAIEIASEVLQTPVTLTDLYSPVSIWLLRTDFVFNFPRPVMPNMVFVGGINCFQRKPLSK
ra1       228 VYSPYGSLATEILQKEVTVKDLLSPASIWLMRNDFVKDYPRPIMPNMVFIGGINCLQKKALSQ
ra2       226 SITPYESLASELLQREMSLVEVLSHASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKKPLSQ
ra6       224 SFTRYESLASELLQREVSLVEVLSHASVWLFRGDFVFDYPRPVMPNMVFIGGINCVIKKPLSQ
ra4       224 NYGSLARLASDLLQREVSVVEILRHASVWLLRKDFVFYYPRPFMPNMVFIGGINCANRKPLSQ
ra7       224 LYSKYEILASDLLKRDVSLPALHQN.SLWLLRYDFVFEYPRPVMPNMIFIGGTNCKKKGNLSQ
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