Additional file 20. Alignment of the baboon (b) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1     1                    MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLY
ba10        1 MAHTRCTSPVPLCLCLLLTCG...FAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ba8         1 MARTRWTSPVLLCVSLLLTCG...FAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ba7         1 MACAGWTGLLPLSVCLLLTCG...FAEAGKLLVVP.MDGSHWFTMRSVVEKLILRGHEVV
ba9         1 MTRTGWSSPLPLCVCLLLACG...FAEAGKLLVVP.MDGSHWFSMRSVVEKLILRGHEVV
ba5a        1 MATGLQVSLPQLATGLLLLLSVQPWVESGKVLVVP.TDGSHWLSMQDAVRELHARGHQVV
ba5b        1 MATGLQVFLPQLATGLLLLLSVQPWAESGKVLVVP.ADGSHWLSMREAVRELHARGHQAV
ba4         1 MATGLQVSLPQLATGLLLLLSVQPWAESGKVLVVP.TDGSHWLSMREAVRELHARGHQAV
ba2         1 MATGPQVPLLWLATGLLLLLSVQPWAESGKVLVVP.IDGSHWLSMREAVRELHARGHQAV
ba1         1 MAVESQGRHP.LVLGLLLCVLGPVLCHAGKMLLIP.VDGSHWLSMLGAIQQLQQRGHEIV
ba6         1 MACLLRA.FQRISAGVFF.LALWGMVVGDKLLVIP.QDGSHWLSMKDIVEVLSDRGHDIV

Ugt71g1    42 ITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIP
ba10       57 VVMPEV.....SWQLGRPLNCTV..KTYSTSYTLE.....DLDREFMTFAQAQWKAQIQ.
ba8        57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DLDREFMTFAHAQWKAQLR.
ba7        57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DQDREFMAFAQAQWKAPLR.
ba9        57 VVIPKV.....SWQLGRSLNCTV..KTYSTSYTLE.....VLDREFKAFAQAQWKAQVQ.
ba5a       60 VLSPEV.....NMHIKEENFFTL..TTYAVPWTQD.....EFDRFLLGHSQSFFETEHLL
ba5b       60 VLTPEV.....NMHIKEENFFTL..TTYAISWTQD.....EYDHLLLGHTQSFFETEHLL
ba4        60 VLTPEV.....NMHIKEENFFTL..TTYAIPWTQD.....EFDRLVLGHTQWFFETEHLL
ba2        60 VLTPEV.....KMHIKEDNFFTL..TTYAIPWTQD.....EFDRLVLGHTQLYFETEHFL
ba1        59 VLAPDA.....SLYIREGAFYTL..KTYPVPFQRE.....DVKESFVSLGHNVFENDSFL
ba6        58 VVVPEV.....NLLLKESKYYTR..KIYPVPYDQE.....EMKNRYQLFGNNHFAERSFL

Ugt71g1   102 HVKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFGI
ba10      104 SIFSLFLSSSSGFFDLVFSHCRSLFNDQKLVEYLKESSFDAVFLDPFDICGLIVAKYFSL
ba8       104 SFFSLFLSSSNGFFDLFFSHCRSLFNDQKLVEYLKESSFDAVFLDPFDACGLIVAKYFSL
ba7       104 SAFSLLTSSSNGIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDGCGLILAKYLSL
ba9       104 SIFSLLMSSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDTCGLIVAKYLSL
ba5a      108 MRFSRSMAIMNNISLIIHRSCVELLHNEALIRHLNATSFDVVLTDPFHLCGAVLAKYLSI
ba5b      108 MRFSRSMAVMNNMSLIIHRSCVELLHNEALIRHLNATSFDVVLTDPFHLCGAVLAKYLSI
ba4       108 KRYSRSMAIMNNMSLVFHRSCVELLHNEALIRHLNATSFDVVLTDPVNLCGVVLAKYLSI
ba2       108 KTFSKSMAILKNMSLVFHRSCVELLHNETLMRHLNATSFDVVLIDPIYLCGVVLAKYLSI
ba1       107 RRVIKTYKKIKKDSAMLLSGCSHLLHNKELMVSLAESSFDVMLTDPFLPCGPIVAQYLSL
ba6       106 TAPQTEYRNNMVVIGMYFINCQSLLQDVDTLNFLKESKFDALFTDPALPCGVILAEYLGL

Ugt71g1   137 PSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
ba10      164 PSVVFARGIFCHYLEEGAQCPAPLSYVPRELLGFSDAMTFKERVWNHVIHLEEHLFCKFI
ba8       164 PSVVFARGIACHYLEEGAQCPAPLSYVPRILLGFSDAMTFKERVWNHVMHLEDHLFCKYF
ba7       164 PSVVFARGTFCHYLEEGAQCPAPLSYIPRGLLGFSDAMTFKERVWNHITHLEEHLFCPYF
ba9       164 PSVVFARGIFCHYLEEGAQCPAPLSYVPRILLGFSDAMTFKERVRNHIMHLEERLLCHRF
ba5a      168 PTVFFLRNILCDLDFKGTQCPNPYSYIPKFLTTNSDHMTFLQRVKNMLYPLALSYICDTV
ba5b      168 PAVFFLRNIPCDLDFKGTQCPNPYSYIPKFLTANSDHMTFLQRVKNMLYPVALSYICHAV
ba4       168 PAVFFLRNIPCDLDFKGTQCPNPYSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYICDAV
ba2       168 PAVFFLRNIPCDLDFKGTQCPNPYSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYICDAL
ba1       167 PTVFFLNALPCSLEFEATQCPNPFSYVPRPLSAHSDHMTFLQRVKNMLIAFSQNFLCDVV
ba6       166 PSVYLFRGFPCSLEHTFSRSPNPVSYIPRCYTKFSDHMTFPQRVANFLVNLLEPYLFYCL

Ugt71g1   197 GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
ba10      224 FKSALEIASEILQTPVTEYDLYSHTSIWLLRTDFVLDPPKPVMPNMVFIGGINCHQGKPLPK
ba8       224 FKNALEIASEILQTPVTEYDLYSHTSIWLLRTDIVLDYPKPVMPNMVFIGGINCHQGKPVPM
ba7       224 LKNVLEIASEILQTSVTAYDLYSHTSIWLLRTDFVLDYPKPVMPNMVFIGGINCHQGKPVPM
ba9       224 FKSALEIASEILQTPVTVYDLHRQISIWLLRTDFVLDYPKPVMPNMVFIGGINCHQGKPLPM
ba5a      228 SVPYASLASELFQREVSVVDLLSHASVWLFRSDFVMDYPRPIMPNMVFIGGINCANRKPLSQ
ba5b      228 SVPYASLASELFQREVSVVDLLSHASVWLFRSDFVMDYPRPIMPNMVFIGGINCANRKPLSQ
ba4       228 SVPYASLASELFQREVSVVDLLSHASVWLFRSDFVMDYPRPIMPNMVFIGGINCANRKPLSR
ba2       228 SAPYASLASELFQREVSVVDLLSHASVWLFRGDFVMDYPRPIMPNMVFIGGINCANRKPLSQ
ba1       227 YSPYATLASEFLQREVTVQNLLSSASVWLLRSDFVKDYPRPIMPNMAFIGGINCLHQSPLSQ
ba6       226 FSKYDELASAVLKRDVDVITLYQKVSVWLLRYDFVLEYPRPVMPNMVFIGGTNCKKRKDLSE
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