Additional file 18. Alignment of the chimpanzee (c) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1    1                    MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLY
ca8        1 MARTGWTSPLPLCVSLMLTC...GFAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ca9        1 MACTGWTSPLPLCVCLLLTC...GFAEAGKLLVVP.MDGSHWFTMRSVVEKLILRGHEVV
ca10       1 MACAGWTSPVPLCVCLLLTC...GFAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ca7        1 MARAGWTGLLPLYVCLLLTC...GFAKAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ca2        1 MATGPQVPLLQLATGVLLLLSVQPWAESGKVLVVP.IDGSHWLSMREAVRELHARGHQAV
ca4        1 MARGLQVPLPRLATGVLLLLSVQPWAESGKVLVVP.TDGSHWLSMREALRELHARGHQAV
ca3        1 MATGLQVPLPRLATGLLLLLSVQPWAESGKVLVVP.TDGSHWLSMREALRELHARGHQAV
ca1        1 MAVESQGGRP.LVLGLLLCVLGPVVSHAGKILLIP.VDGSHWLSMLGAIQQLQQRGHEIV
ca6        1 MACLLRA.FQRISAGVFF.LALWGMVVGDKLLVVP.QDGSHWLSMKDIVEVLSDRGHEIV

Ugt71g1   42 ITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIP
ca8       57 VVMPEV.....SWQLGKSLNCTV..KTYSTSYTLE.....DLDREFMDFADAQWKAQ.VQ
ca9       57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DLDREFKAFAHAQWKAQ.VR
ca10      57 VVMPEV.....SWQLERSLNCTV..KTYSTSYTLE.....DQNREFMVFAHAQWKAQ.AQ
ca7       57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DQDREFMVFADARWTAP.LR
ca2       60 VLTPEV.....NMHIKEEKFFTL..TTYAISWTQD.....EFDRLVLGHTQLYFETEHFL
ca4       60 ALTPEV.....NMHIKEENFFTL..TTYAISWTQD.....EFDRLLLGHTQSFFETEHLL
ca3       60 VLTPEV.....NMHIKEENFFTL..TTYAISWTQD.....EFDRHVLDHTQLYFETEHFL
ca1       59 VLAPDA.....SLYIRDGAFYTL..KTYPVPFQRE.....DVKESFVSLGHNVFENDSFL
ca6       58 VVVPEV.....NLLLKESKYYTR..KIYPVPYDQE.....ELKNRYQSFGNNHFAERSSL

Ugt71g1  102 HVKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFGI
ca8      104 SLFSLFLSSSNGFFDLFFSHCRSLFNDRKLVEYLKESSFDAVFLDPFDACGLIVAKYFSL
ca9      104 SIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDNCGLIVAKYFSL
ca10     104 SIFSLLMSSSSDFLDLFFSHCRSLFNDRKLVEYLKESSFDAVFLDPFDTCGLIVAKYFSL
ca7      104 SAFSLLTSSSNGIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDACGLIVAKYFSL
ca2      108 KTFSKSMAILKNSSLVLHRSCVELLHNEALIRHLNATSFDVVLIDPIYLCGAVLAKYLSI
ca4      108 KRYSRSVAIMNNVSLVLHRSCVELLHNEALIRHLNATYFDVVLTDPFHLCGAVVAKYLSI
ca3      108 KKFFRSMAMLNNMSLVYHRSCVELLHNEALIRHLNAISFDVVLTDPVNLCAAVLAKYLSI
ca1      107 QRVIKTYKKIKKDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSL
ca6      106 TAPQTEYRNNMIVIGLYFINCQSLLQDRDTLNFFKESKFDALFTDPALPCGVILAEYLGL

Ugt71g1  137 PSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
ca8      164 PSVVFARGIACHYLEEGAQCPAPLSYVPRILLGFSDAMSFKERVRNHIMHLEEHLFCQYF
ca9      164 PSVVFTRGILCHYLEEGAQCPAPLSYVPRILLGFSDAMTFKEKVRNHIMHLEEHLLCHRF
ca10     164 PSVVFTRGIFCHHLEEGAQCPAPLSYVPNDLLGFSDAMTFKERVWNHIVHLEDHLSCQYL
ca7      164 PSVVFARGIFCHYLEEGAQCPAPLSYIPRLLLGFSDAMTFKERVWNHIMHLEEHLFCPYF
ca2      168 PAVFFLRNIPCDLDFKGTQCPNPYSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYLCHAL
ca4      168 PAVFFLRNIPCDLDFKGTQCPNPYSYIPKYLTTNSDHMTFLQRVKNMLYPLALSYLCHAL
ca3      168 PTVFFLRNIPCDLDFKGTQCPNPSSYIPRLLTTNSDHMTFVQRVKNMLYPLALSYICHAF
ca1      167 PTVFFLHALPCSLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVV
ca6      166 PSVYLFRGFPCSLEHTFSRSPDPVSYIPRCYTKFSDHMTFSQRVANFLVNLLEPYLFYCL

Ugt71g1  197 GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
ca8      224 FKNALEIASEILQTPVTAYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ca9      224 FKNALEIASEILQTPVTEYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ca10     224 FRNALEIASEILQTPVTAYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ca7      224 FKNVLEIASEILQTPVTAYDLYSHTSIWLLRTDFVLEYPKPVMPNMIFIGGINCHQGKPVPM
ca2      228 SAPYASLASELFQREVSVVDLLSHASVWLFRWDFVMEYPRPIMPNMVFIGGINCANRKPLSQ
ca4      228 SAPYASLASELFQREVSVVDLVSHASVWLFRRDFVMDYPRPIMPNMVFIGGINCANRKPLSQ
ca3      228 SAPYASLASELFQREVSVVDILSHASVWLFRGDFVMDYPRPIMPNMVFIGGVNCASRKPLSQ
ca1      227 YSPYATLASEFLQREVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFVGGINCLHQNPLSQ
ca6      226 FSKYEELASAVLKRDVDIITLYQKVSVWLLRYDFVLEYPRPVMPNMVFIGGINCKKRKDLSQ
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