Additional file 17. Alignment of the human (h) UGT1 variable sequences with those of the UGT71G1

```
Ugt71g1    1                    MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLY
ha8        1 MARTGWTSPIP.LCVSLLLTC..GFAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ha9        1 MACTGWTSPLP.LCVCLLLTC..GFAEAGKLLVVP.MDGSHWFTMRSVVEKLILRGHEVV
ha10       1 MARAGWTSPVP.LCVCLLLTC..GFAEAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ha7        1 MARAGWTGLLP.LYVCLLLTC..GFAKAGKLLVVP.MDGSHWFTMQSVVEKLILRGHEVV
ha3        1 MATGLQVPLPWLATGLLLLLSVQPWAESGKVLVVP.IDGSHWLSMREVLRELHARGHQAV
ha5        1 MATGLQVPLPQLATGLLLLLSVQPWAESGKVLVVP.TDGSHWLSMREALRDLHARGHQVV
ha4        1 MARGLQVPLPRLATGLLLLLSVQPWAESGKVLVVP.TDGSPWLSMREALRELHARGHQAV
ha1        1 MAVESQGGRP.LVLGLLLCVLGPVVSHAGKILLIP.VDGSHWLSMLGAIQQLQQRGHEIV
ha6        1 MACLLR.SFQRISAGVFF.LALWGMVVGDKLLVVP.QDGSHWLSMKDIVEVLSDRGHEIV

Ugt71g1   42 ITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIP
ha8       57 VVMPEV.....SWQLGKSLNCTV..KTYSTSYTLE.....DLDREFMDFADAQWKAQ.VR
ha9       57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DLDREFKAFAHAQWKAQ.VR
ha10      57 VVMPEV.....SWQLERSLNCTV..KTYSTSYTLE.....DQNREFMVFAHAQWKAQ.AQ
ha7       57 VVMPEV.....SWQLGRSLNCTV..KTYSTSYTLE.....DQDREFMVFADARWTAP.LR
ha3       60 VLTPEV.....NMHIKEENFFTL..TTYAISWTQD.....EFDRHVLGHTQLYFETEHFL
ha5       60 VLTLEV.....NMYIKEENFFTL..TTYAISWTQD.....EFDRLLLGHTQSFFETEHLL
ha4       60 VLTPEV.....NMHIKEEKFFTL..TAYAVPWTQK.....EFDRVTLGYTQGFFETEHLL
ha1       59 VLAPDA.....SLYIRDGAFYTL..KTYPVPFQRE.....DVKESFVSLGHNVFENDSFL
ha6       58 VVVPEV.....NLLLKESKYYTR..KIYPVPYDQE.....ELKNRYQSFGNNHFAERSFL

Ugt71g1  102 HVKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFGI
ha8      104 SLFSLFLSSSNGFFNLFFSHCRSLFNDRKLVEYLKESSFDAVFLDPFDACGLIVAKYFSL
ha9      104 SIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDNCGLIVAKYFSL
ha10     104 SIFSLLMSSSSGFLDLFFSHCRSLFNDRKLVEYLKESSFDAVFLDPFDTCGLIVAKYFSL
ha7      104 SAFSLLTSSSNGIFDLFFSNCRSLFKDKKLVEYLKESCFDAVFLDPFDACGLIVAKYFSL
ha3      108 KKFFRSMAMLNNMSLVYHRSCVELLHNEALIRHLNATSFDVVLTDPVNLCAAVLAKYLSI
ha5      108 MKFSRRMAIMNNMSLIIHRSCVELLHNEALIRHLHATSFDVVLTDPFHLCAAVLAKYLSI
ha4      108 KRYSRSMAIMNNVSLALHRCCVELLHNEALIRHLNATSFDVVLTDPVNLCGAVLAKYLSI
ha1      107 QRVIKTYKKIKKDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSL
ha6      106 TAPQTEYRNNMIVIGLYFINCQSLLQDRDTLNFFKESKFDALFTDPALPCGVILAEYLGL

Ugt71g1  137 PSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
ha8      164 PSVVFARGIACHYLEEGAQCPAPLSYVPRILLGFSDAMTFKERVRNHIMHLEEHLFCQYF
ha9      164 PSVVFARGILCHYLEEGAQCPAPLSYVPRILLGFSDAMTFKERVRNHIMHLEEHLLCHRF
ha10     164 PSVVFTRGIFCHHLEEGAQCPAPLSYVPNDLLGFSDAMTFKERVWNHIVHLEDHLFCQYL
ha7      164 PSVVFARGIFCHYLEEGAQCPAPLSYVPRLLLGFSDAMTFKERVRNHIMHLEEHLFCPYF
ha3      168 PTVFFLRNIPCDLDFKGTQCPNPSSYIPRLLTTNSDHMTFMQRVKNMLYPLALSYICHAF
ha5      168 PAVFFLRNIPCDLDFKGTQCPNPSSYIPRLLTTNSDHMTFLQRVKNMLYPLALSYLCHAV
ha4      168 PAVFFWRYIPCDLDFKGTQCPNPSSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYICHTF
ha1      167 PTVFFLHALPCSLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVV
ha6      166 PSVYLFRGFPCSLEHTFSRSPDPVSYIPRCYTKFSDHMTFSQRVANFLVNLLEPYLFYCL

Ugt71g1  197 GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
ha8      224 SKNALEIASEILQTPVTAYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ha9      224 FKNALEIASEILQTPVTEYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ha10     224 FRNALEIASEILQTPVTAYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPM
ha7      224 FKNVLEIASEILQTPVTAYDLYSHTSIWLLRTDFVLEYPKPVMPNMIFIGGINCHQGKPVPM
ha3      228 SAPYASLASELFQREVSVVDILSHASVWLFRGDFVMDYPRPIMPNMVFIGGINCANRKPLSQ
ha5      228 SAPYASLASELFQREVSVVDLVSHASVWLFRGDFVMDYPRPIMPNMVFIGGINCANGKPLSQ
ha4      228 SAPYASLASELFQREVSVVDLVSYASVWLFRGDFVMDYPRPIMPNMVFIGGINCANGKPLSQ
ha1      227 YSPYATLASEFLQREVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFVGGINCLHQNPLSQ
ha6      226 FSKYEELASAVLKRDVDIITLYQKVSVWLLRYDFVLEYPRPVMPNMVFIGGINCKKRKDLSQ
```