Additional file 21. Alignment of the dog (d) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1     1                   MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLYI
da11        1 MAATILTGFPLLC..VCLLLTSGFAEAGKLLVVP.MDGSHWFTMRLVVEQLIQRGHELVL
da9         1 MAATILTGFPLLC..VCLLLTSGFAEAGKLLVVP.MDGSHWFTMRLVVEQLIQRGHELVL
da10        1 MAATILTGFPLLC..VCLLLTSGFAEAGKLLVVP.MDGSHWFTMRLVVEQLIQRGHELVL
da8         1 MAATILTGFPLLC..VCLLLTSGFAEAGKLLVVP.MDGSHWFTMRLVVEQLIQRGHELVL
da7         1 MAATILTGFPLLC..VCLLLTSGFAEAGKLLVVP.MDGSHWFTMRLVVEQLIQRGHELVL
da2         1 MAAGFLAPLPVLTGLLLILCDGRWVEGGRVLVVP.MDGSHWLSMKKAVQKLHARGHQMVV
da3         1 MAAGFLAPLPVLTGLLLILCVGRWVEGGKVLVVP.MDGSHWLSMKKAVQKLHARGHQMVV
da4         1 MAAGFLAPLPVLTGLLLILCVGRWVEGGKVLVVP.LDGSHWLSMKKAVQKLHARGHQMVV
da1         1 MAAEAPGPRPLVLGLLLCALSAPVSQGGKLLLIP.VDGSHWLSMLGVVKQLHQRGHEVVV
da6         1 ~~~~~MARLLHLFQKVFFLMLWGEAVGDKLLVVP.QDGSHWLSMENIVELLSEKGHDIVV

Ugt71g1    43 TVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIPH
da11       58 IIPEV.....SWQLGKSSNFTV..KTYSTTYNLE.....ELNQKFKTFSDSQWNIRQQ.S
da9        58 IIPEV.....SWQLGKSSNFTV..KTYSTAYNLE.....ELNQMFKTFSDSHWNIRQQ.S
da10       58 IIPEV.....SWQLGKSSNFTV..KTYSTTYNLE.....ELNQMFKNFSDSHWNIRQQ.S
da8        58 IIPEV.....SWQLGKSSNFTV..KTYSTTYNLE.....ELNQMFKNFSYSQWKTQQQ.S
da7        58 IIPEV.....SWQLGKSSNFTV..KTYSTTYNLE.....ELNQMFKNFSYSQWKTQQQ.S
da2        60 VSPES.....NMHIKEEDFFTL..TTYATPYTQE.....EFDNFMLGQSYLVFQRMSFLK
da3        60 VSPES.....NMHIKEEDFFTL..TTYATPYTQE.....EFDRILLGQSYLVFERMPFLK
da4        60 VSPES.....NMHIKEEDFFTL..TTYAPPYTRE.....EYDRVLLGQRYQVFERVSFLK
da1        60 IASEA.....SVYIKGAAFYTL..KRYPVPFRRE.....DVEATFTSLGRGVFENVPLLR
da6        55 LVPEV.....NLLLKESKHYTR..QIYSVPFGQE.....ELENRYRSFGKNHFAERWLLN

Ugt71g1   103 VKATIKTILSNK.........................VVGLVLDFFCVSMIDVGNEFGIP
da11      105 ILSMVLNSSSDFFEHLFLHCKNLFSDPKLVEYIKESSFDAVFLDPFDVCGLIVAKYFSLP
da9       105 LLTMFFDSSSDIFEHLFLHCKNLFRDTTLIEYIKESSFDAVFLDPFDMCGLIVANYFSLP
da10      105 LLTMFFDSSSDIFEHLFLHCKNLFSDPKLVEYIKESSFDAVFLDPFDVCGLIVAKYFSLP
da8       105 SLFLVLSPLKDSLEHLFLHCKNLFSDPKLVEYIKESSFDAVFLDPFDVCGLIVAKYFSLP
da7       105 SLFLVLSPLKDSLEHLFLHCKNLFSDPKLVEYIKESSFDAVFLDPFDVCGLIVAKYFSLP
da2       108 TFLKTMEGLKTATLIFQRSCESLMHNKNLIRHLNASSFDVLLTDPVYPCGAILARYLSLP
da3       108 TFLKTMEALKAAALIFQRSCESLMHNKNLIRHLNASSFDVLLTDPVYPCGAILARYLSLP
da4       108 RLLKTVERLKTVTSFYQRSCEGLLHNKNLIRHLNASSFDVVLTDPVHPCGAILARYLSLP
da1       108 RVIKTYKKVKEDSALLLSACSHLLHNKELMASLAESSFDAVLTDPFLPCGPIVALYLALP
da6       103 AAQMEYRNSMIVIDMYFTNCQSLLEDSATLSVLRQSKFDALFTDPALPCGVILAEYLGLP

Ugt71g1   138 SYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKDG
da11      165 SVVFTRGLFCHFLEESTQCPSPPSYVPRIFLGFPDAMSFRERVRNHISHLEEHLFCHYFL
da9       165 SVVFTRGLFCHFLEESTQCPSPPSYVPRIFLGFPDAMSFRERVWNHISHLEEHLFCHYFF
da10      165 SVGFTRRLYCHYLEEATQCPSSPSYVPRPFSILSDVMSFRERVRNHIFHLEEHLFCHYFL
da8       165 SVGFTRRLYCHYLEEATQCPSSPSYVPRPFSILSDVMSFRERVRNHIFHLEEHLFCHYFL
da7       165 SVVFTRGLFCHFFEESTQCPSPLSYVPRPFSMLSDAMSFRERVRNHIFHLEEHLFCHYFL
da2       168 SVFFLRNIPCDLESESTQCPNPSSYIPRLLTRNSDHMTFLQRVKNMLYPLALKYFCHFSF
da3       168 SVFFLRNIPCDLDSEGTQCPNPSSYIPRLLTRNSDHMTFLQRVKNMLYPLALKYICHVSF
da4       168 SVFFLRNIPCDLDSEGTQCPNPSSYIPRLLTRNSDHMTFLQRVKNMLYPLALKYICHFSF
da1       168 AVFFLHALPCSLDFQGTQCPNPPSYVPRALSLNSDHMTFLQRVKNMLIFLSESFLCNVVY
da6       163 SVYLFRGFPCSLEHTISRSPNPVSYIPRCYTQFSDKMTFPQRVGNYLVNYLETYLFYCLY

Ugt71g1   198 GYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
da11      225 KTALEVASEILQTAVTPYDLYSHTSIWLLRTDFVFDYPKPVMPNMVFIGGINCQEGKPLPK
da9       225 KTPLEVASEILQTAVTPYDLYSHTSIWLLRADFVFDYPKPVMPNMVFIGGINCQEGKPLPK
da10      225 KTALEVASEILQKAVTPYDLYSHMSIWLLRTDFVFDYPKPVMPNMVFIGGINCQEGKPLPK
da8       225 KTALEVASEILQKAVTPYDLYSHMSIWLLRTDFVFDYPKPVMPNMVFIGGINCQEGKPLPK
da7       225 KTPLEVASEILQTAVTPYDLYSHTSIWLLRADFVLDYPKPVMPNMVFIGGINCQEGKTLPK
da2       228 TPYASLASELLQREVSLEDILSSGSVWLFRGDFVLDYPRPIMPNMFFIGGINCANRKPLSQ
da3       228 TPYASLASELLQREVSLVDILSSGSVWLFRGDFVLDYPRPIMPNMFFIGGINCANRKPLSQ
da4       228 TPYASLASELLQREVSLVDILSSGSVWLFRGDFVLDYPRPIMPNMFFIGGINCANRKPLSQ
da1       228 SPYEPLASEVLQKDVTVQELMGSASIWLLKGDFVKDYSRPIMPSMVFVGGINCASKNPLSK
da6       223 SKYEDLASNILKRDVHLPTLYRNGSIWLLRYDFVFEYPRPVMPNMVFIGGTNCKMKGVLPQ
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