Additional file 29. Alignment of the rat (r) UGT2 sequences with those of the UGT71G1

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Ugt71g1     1                 MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLYITV
r2a1        1 ~~~MLKNIL.LWSLQLSL.LGMSLGGNVLIWP.MEGSHWLNVKIIIDELLRKEHNVTVLV
r2b3        1 ~~MPGKWISALLLLQISCCFQSGNCGKVLVWP.MEFSHWMNIKTILDELVQRGHEVTVLK
r2b6        1 ~~MPGKWIFALLLLQISFCLRSAKCGKVLVWP.MEFSHWMNIKTILDELVQRGHEVTVLK
r2b2        1 ~~MPRKWISALFLLQISYCFKSGHCGKVLVWP.MDFSHWMNIKIILDELVQRGHEVTVLK
r2b12       1 ~~MPGKWISALLLLQISFCFKSGNCGKVLVWP.MEYSHWMNIKIILEELVQKGHEVTVLR
r2b8        1 ~~MPQKWISALLLLQISFCFRSGNCGKVLVWP.LEYSHWMNLKIILDELVQRGHEVTVLR
r2b34       1 MSVKRTASLLLLLLQLSDFFGSGTGGKVLVWP.MEFSHWLNLRVILDELLKKGHEVTVLR
r2b39       1 MSVKMTAA..LLLLHLTIFFGSGSGGKVLVWP.VEFSHWLNLKIILSELVKKGHEVVVLK
r2b1        1 MSMKQTS..VFLLIQLICYFRPGACGKVLVWP.TEYSHWINIKIILNELAQRGHEVTVLV
r2a3        1 ~MVSVKWAVAIFLLQL.CWSGCGICSKVLVWP.CDMSHWLNLKTILEELAARGHEVTVLK

Ugt71g1    45 FCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIPHVK
r2a1       55 ASG.....ALFITPSVSPSLTFEIYPVPFGKE.....KIESVIKDFVLTWLENRPSPSTI
r2b3       58 PSA.....YYVLDPKKSPDLKFETFPTSVSKD.....ELENYFIKLVDVWTYELQR.DTC
r2b6       58 PSA.....YYVLDPKKSPDLKFETFPTSVSKD.....ELEKYFIKLVDAWTYELQR.DTC
r2b2       58 PSA.....YFFLDPKKSSDLKFEIFSTSISKD.....ELQNHFIKLLDVWTYELPR.DTC
r2b12      58 PSA.....SVFLDPKETSDLKFVTFPTSFSSH.....DLENFFTRFVNVWTYELPR.DTC
r2b8       58 PSS.....SVFLDPKKASGLVYETFPTTSNND.....EVEKFFTQWVNTWTYDVPK.YTC
r2b34      60 PSA.....SLSYEVDNTSAIEFETYPTSYSLT.....EVDEFFWESLRKYIYELPK.QSF
r2b39      58 PSV.....SFSYEVDKTSAIEFESFPSSYSIA.....DVEVIFMDCVNESIYELPK.QSF
r2b1       58 SSA.....SILIEPTKESSINFEIYSVPLSKS.....DLEYSFAKWIDEWTRDFET.LSI
r2a3       58 .YP.....SIIIDQSKLTPLQFENIPVLYETE.....VAENHLNEIVNLAVNVIPN.LSL

Ugt71g1   105 ATIKTILSNK............................VVGLVLDFFCVSMIDVGNEFG
r2a1      105 WTFYKEMAKVIEEFHLVSRGICDGVLKNEKLMTKLQRGKFEVLLSDPVFPCGDIVALKLG
r2b3      107 LSYSPLLQNMIDGFSDYYLSLCKDTVSNKQLMAKLQESKFDVLLSDPVAACGELIAEVLH
r2b6      107 LSFSPLLQNMMDEFSDYYLSVCKDAVSNKQLMAKLQESKFDVLLSDPVAACGELIAEVLH
r2b2      107 LSYSPILQNLVYEFSYFYLSICKDAVSNKQLMTKLQESKFDVLFADPVASCGDLIAELLH
r2b12     107 LSYFLYLQDTIDEYSDYCLTVCKEAVSNKQFMTKLQESKFDVVFSDAIGPCGELIAELLQ
r2b8      107 LRYYPSLNKMFGQFSDLWLQLCREVVSNKHLMAKLKESQFDVVLSDAVGPCGELIAEILQ
r2b34     109 WGYFLMFQELVWVDSDYFESLCKDVVFNKELMTKLQNSGFDVILADPFIPCGDLLAEILK
r2b39     107 WGYFLMLQKLFERTSDYSERLCRDAAFNKELMTKLQNSGFDVILADPFTPCGDLLAEILK
r2b1      107 WTYYSKMQKVFNEYSDVVENLCKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLK
r2a3      106 WEAARTLQDFFLQLTGNFEDLCRSTLYNQTLMNKLRDAKYDVMVLDPVIPCGELVAEVLQ

Ugt71g1   136 IPSYLFLTSNVGFLSLMLSLK.NRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFN
r2a1      165 IPFIYSLRFSPASTVEKHCGKVPFPPSYVPAILSELTDQMSFADRVRNFISYRMQDYMFE
r2b3      167 IPFLYSLRFSPGYKIEKSSGRFILPPSYVPVILSGMGGPMTFIDRVKNMICTLYFDFWFH
r2b6      167 IPFLYSLRASPGHKIEKSSGRFILPPSYVPVILSGLGGQMTFIDRVKNMICMLYFDFWFH
r2b2      167 IPFLYSLSFSPGHKLEKSIGKFILPPSYVPVILSGLAGKMTFIDRVKNMICMLYFDFWFE
r2b12     167 IPFLYSLRFSPGYTIEKYIGGVLFPPSYVPMIFSGLAGQMTFIERVHNMICMLYFDFWFQ
r2b8      167 LPFVYSLRFGIGYGIEKYSAGQPFPPSYVPIILSGLSGQMTFMERVENMLCLLYFDFWFE
r2b34     169 IPLVYSLRFFPGSTYEKYSGGLPMPPSYVPIAMSELSDRMTFVERMKHMIYVLCFDFWFQ
r2b39     167 IPLVYSLRFFPGSTYEKYSGGLPMPPSYVPIAMSELSDRMTFVERVKHMIYVLCFDFWFQ
r2b1      167 TPLVYSLRFCPGYRCEKFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDFWFQ
r2a3      166 IPFVNTLRFSMGYSMEKYCGQLPVPLSYVPVVMGELTDHMTFTERVKNMMLSLFFEFWLQ

Ugt71g1   195 KD.GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
r2a1      225 TL.WKQWDSYYSKALGRPTTLCETMGKAEIWLMRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPK
r2b3      227 MFNAKKWDPFYSEILGRPTTLAETMGKAEMWLIRSYWDLEFPHPTLPNVDYIGGLQCRPPKPLPK
r2b6      227 MFNAKNWDPFYTEILGRPTTLAETMGKAEMWLIRSYWDLEFPHPTLPNVDYIGGLQCKPAKPLPK
r2b2      227 ILRHKEWDTFYSEILGRPTTVDETMSKVEIWLIRSYWDLKFPHPTLPNVDYIGGLHCKPAKPLPK
r2b12     227 TFREKKWDPFYSKTLGRPTTLAEIMGKAEMWLIRSYWDLEFPHPISPNVDYIGGLHCKPAKPLPK
r2b8      227 SFPAKDWDPFFSEILGRPTTMVDTMKKAEIWLIRSYWDLEFPRPSLPNIEFVGGLHCQPAKPLPK
r2b34     229 AFNEKKWNELYTEVLGRPTTLSETMAKADIWLIRTYWDLEFPHPVLPNFDFVGGLHCRPAKPLPK
r2b39     227 VFDEKKWNELYTEVLGRPTTLSETMAKADIWLIRTYWDLEFPHPVLPNFDFVGGLHCRPAKPLPK
r2b1      227 PFKEKSWSQFYSDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHPFLPNFDFVGGLHCKPAKPLPR
r2a3      226 QYDFAFWDQFYSKTLGRPTTFCKTVGKAEIWLIRTYWDIEFPRPYLPNFEFVGGLHCKPAKPLPK
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