Additional file 28. Alignment of the mouse (m) UGT2 sequences with those of the UGT71G1

```
Ugt71g1     1                 MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLYITV
m2a1        1 ~~~MLKNIL.LCSLQIS.LLGMSLGGNVLIWP.MEGSHWLNVKIIIDELLRKEHNVTVLV
m2b38       1 ~~MPGKWISALLLLQISCCFRSVKCGKVLVWP.MEFSHWMNIKIILDELVQRGHEVTVLR
m2b5        1 ~~MPGKWISALLLLQISCCFRSVKCGKVLVWP.MEFSHWMNIKIILDELVQRGHEVTVLR
m2b37       1 ~~MPGKWISALLLLQISCCFRSVKCGKVLVWP.MEFSHWMNIKIILDELVQRGHEVTVLR
m2b35       1 ~~MPVKWISALLLLQMSCCFRSTSCGKVLVWP.LEFSHWMNLKIILDELVQRGHEVTVLR
m2b36       1 ~~MLWKWISALLLLQISCCFRSAKCGKVLVWP.VDYSHWMNIKIILDELKQKGHEVTVLR
m2b1        1 ~~MSMKQASVFLLIQFICYIRPGACGKVLVWP.TEYSHWINMKIILDELVQRGHDVTVLI
m2b34       1 MPVKMTAALLLLLLQLSGFFGSGTGGKVLVWP.MEFSHWLNLKTILDELLKKGHEVMVLR
m2a3        1 ~MVSEKCVAAFFLLQL.CWAGCGFCSKVLVWP.CDMSHWLNLKTILEELGARGHEVTVLK

Ugt71g1    45 FCIKFPGMPFADSYIK.SVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIPHV
m2a1       55 ASG.....ALFITPSSISPSLTFEIYPVPFGKE.....KIESVIKDFVLTWLENRPSPST
m2b38      58 PSA.....YYVLDPKK.SPGLKFETFPTSVSKD.....NLENFFIKFVDVWTYEMPR.DT
m2b5       58 PSA.....YYVLDPKK.SPGLKFETFPTSVSKD.....NLENFFIKFVDVWTYEMPR.DT
m2b37      58 PSA.....YYVLDPKK.SPGLKFETFPTSVTKD.....DLENFFIQLLNVWTYELSR.DT
m2b35      58 PSA.....SIFVDPKY.SPGLKFETFPTAFSKD.....YLETFLTKLVDEWTFEVPR.DT
m2b36      58 PST.....SIFLDPKK.SPGLKFETFPTSFSND.....VMEIIFAKAVERWTYEVPR.DT
m2b1       58 SSA.....SILIGPSN.ESSINFEIYSAPLSKD.....DLEYAFEKWVGNWTYELKK.LP
m2b34      60 PSA.....SLSYEVDN.TSAIEFETYPTSYSLS.....ELEEIFWESLKKYIYELPK.QS
m2a3       58 .YP.....SIIIDQSK.RIPLHFENIPLLYEIE.....TAENRLNEIANLAVNVIPN.LS

Ugt71g1   104 KATIKTILSN............................KVVGLVLDFFCVSMIDVGNEF
m2a1      105 IWTFYKEMAKVIEEFHLVSRGICDGVLKNEKLMSKLQKEKFEVLLSDPVFPCGDIVALKL
m2b38     106 CLSYSPLLQNMIDEFSDYFLSLCKDVVSNKELMTKLQESKFDVLLSDPVASCGELIAELL
m2b5      106 CLSYSPLLQNMIDEFSDYFLSLCKDVVSNKELMTKLQESKFDVLLSDPVASCGELIAELL
m2b37     106 CLSYSPLMQNMFDELSGYYLSLCKDVVSNRQLMTKLQESKFDVLLSDPVAFGGELIAELL
m2b35     106 CLSYS.LLQTLFGKLSDYSLSLCKEAVSNKQLMTKFQESKFDVLILDAMASCGELIAQLL
m2b36     106 CLSYSPLLQNIFDEYSDYCLTLCKDTVSNKQLMAKLQESKFDVILSDAIGPCGELIAELL
m2b1      106 FWTSYSKLQKISSEYSDMIESFCKAVVWNKSLMKKLQGSKFDVVLADALVPCGELLSELL
m2b34     108 FWGYFLMLQEMVWVDSKYFESLCKDVVFNKELMTKLQKSRFDVILADPFIPCGDLLAEVL
m2a3      105 LWEAAKTLQDFFLQVTGDFESICRSVLYNQKFMDKLRDAQYDVVVIDPVVPCGELVAEVL

Ugt71g1   135 GIPSYLFLTSNVGFLSLMLSLK.NRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACF
m2a1      165 GIPFIYSLRFSPASTVEKHCGKVPFPPSYVPAILSELTDQMSFTDRVRNFISYRMQDYMF
m2b38     166 QIPFLYSIRFSPGYQIEKSSGRFLLPPSYVPVILSGLGGQMTFIERVKNMICRLYFDFWF
m2b5      166 QIPFLYSIRFSPGYQIEKSSGRFLLPPSYVPVILSGLGGQMTFIERIKNMICMLYFDFWF
m2b37     166 HIPFLYSLRFTAGYRIEKSSGRFLLPPSYVPVILSGLGGQMTFIERVKNMICMLYFDFWF
m2b35     165 QIPFLYSLRFSPGYQVEKNSGGFVLPPSYVPVILSGLGGQMTFTERVKNMICMLYFDFWF
m2b36     166 QIPFLYSLRFSPGYYLEKYSGGLPLPPSYVPVILSGLSGQMTFKERVKNMICMLYFDFWF
m2b1      166 KTPLVYSLRFCPGYKCEKYSGGLPLPPSYVPVVLSELSDHMTFAERVKNMLQVLLFDFWF
m2b34     168 KIPLVYSLRFFPGSTYEKYSGGLPLPPSYVPVVMSELSDRMTFMERVRNVIYMLCFDFWF
m2a3      165 QIPFVYTLRFSMGYYMEKHCGQLPIPLSYVPVVMSELTDNMTFTERVKNMMFSLLFEYWL

Ugt71g1   194 NKD.GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
m2a1      225 ETL.WKQWDSYYTKALGRPTTLCETMGKAEIWLMRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPK
m2b38     226 QMFNDKKWDSFYSEYLGRPTTLAETMGKAEMWLIRSNWDLEFPHPTLPNVDYVGGLHCKPAKPLPK
m2b5      226 QMFNDKKWDSFYSEYLGRPTTLVETMGQAEMWLIRSNWDLEFPHPTLPNVDYVGGLHCKPAKPLPK
m2b37     226 QMPNDKKWDSFYTEYLGRPTTLAETMGQAEMWLIRSNWDLEFPHPTLPNVDYVGGLHCKPAKPLPK
m2b35     225 QTFTEKEWDQFYSETLGRPTTLIETMGKAEMWFIRSYWDLEFPHPTLPNVEYVGGLHCKPAKPLPK
m2b36     226 QTFREKKWDQFYSETLGRPTTLIETMGKAEMWLIRSYWDLEFPHPTLPNVYYVGGVHCKPAKPLPK
m2b1      226 QTFNEKSWNQFYSDVLGRPTTLTEMMGKADIWLVRTFWDLKFPHPFLPNFDFVGGLHCKPAKPLPK
m2b34     228 QTFNEKNWNQLYTEVLGRPTTLSETMAKADIWLIRTYWDLEFPHPVLPNFDFIGGLHCRPAKPLPK
m2a3      225 QQYDFAFWDQFYSETLGRPTTFCKTVGKADIWLIRTYWDVEFPRPYLPNFEFVGGLHCKPAKPLPK
```