Additional file 26. Alignment of the zebrafish UGT1 cluster b (z1b) variable sequences with those of the UGT71G1

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Ugt71g1     1                       MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDK
z1b4        1 MHLGVI.ICLVVGVVCSAVVDQKLSRNSSWTGKLLVVP.MDGSHWTGVKAVAEEMGRRGH
z1b5        1 MH.GVI.FNLVVGVVCSAAMNQKPSRNSSWTGKLLVVP.MDGSHWTGVKAVAEEMGRRGH
z1b2        1 MRLGVI.FILVVGVVCSAAVDQKPSRKSSWTGKLLVVP.MDGSHWTGVKAVAEEMGRRGH
z1b3        1 MHLGVI.FCLVVGVVCSAAVDQKLSRKSSWTGKLLVVP.MDGSHWTGVKAVAEEMGRRGH
z1b7        1 ~~MGLVAFIWCIVLTFASAGEAVKSKEASWTGSLLVVP.MDGSHWTGVKALAEEMGRRGH
z1b1        1 ~MLKKGWLWGLGSGLLLLWLSAGLRPV..QGGRVLVMP.VEGSHWLSMKVLATELARRGH


Ugt71g1    39 NLYITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLES
z1b4       59 TVIVVIPEI.....SMRLGPGKHYIT..KKFPVQYKQD.....LINQIMVEHVNEVAASE
z1b5       58 TVIVVIPEI.....SMRLGPGKHYIT..KKFPVKYKPD.....VLNQMIAKLVNTLSAPE
z1b2       59 TVIVVIPEI.....SVLLGPGQHYIT..KMFSVKYDQK.....SLNKVLNERVLEVTNPG
z1b3       59 TVIVVIPEI.....SMRLGPGKHYIT..KKFPVKYDQK.....LFNEVLTEHVHEVTNPG
z1b7       58 KVTVVIPEV.....SVLLGPGKHYVT..RTFPVLYGKQ.....QLDELQARNAQVMESKQ
z1b1       57 DVLVLVPEK.....NILIQSSELFRT..ETFPVKISKE.....QLSKSLKGFQQGVFTRS


Ugt71g1    99 .LIPHVKATIKTILSN.........................KVVGLVLDFFCVSMIDVGN
z1b4      107 QSLLKTVTSIMYRFGKIIDHFISTSESLFQEQELIEFLRDQNFDAVLTNPAMPMGAILAY
z1b5      106 QSLLKRVTSNIYNFGKVVDYFISTTESLFQEQELIEFLRDQNFDAVLTDPAMPMGAILAY
z1b2      107 NSFLSTVIRIVSNLRRMFNTMAATSESLFQDKELIEFLRNENFDAVLTDPVLPMGAILAY
z1b3      107 HSRLKTVTSTMANLLKMFNMMASTSESLFQDKELIKFLRDENFDAILTDPALPMGAVLAY
z1b7      106 LPLMEKISTRFSNMRKFVNLQRATAESLLLNQELVDFLRKQNFDAVLTSPAVPTGAILAY
z1b1      105 .PALMDVFVQLERLLNFTGSQVEGCESLLYNEPLMRKLKEQNFELMLTDPFLPCGPIIAT


Ugt71g1   133 EFGIPSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDAC
z1b4      167 NLSVPAVYMLRGIMC..ESKATACPNPPSYIPRFFTQISDRMTFSERVINTLVSLLEPLM
z1b5      166 NLSVPAVYMLRGLMC..ESKATACPDPPSYIPRLFTQNSDHMNFGERLMNTLASLMEPLM
z1b2      167 NLSVPAVYLLRGMACGLDATATTCPNPSSYIPRFHTRNTDRMSFGERVMNMLMSILEQTV
z1b3      167 NFSVPAVYMLRGMPCALDATATACPNTPSYIPRFHTGNTDRMSFGERVMNVLMSILEQVA
z1b7      166 NLSLPAVYMLRGLPCGLDSVATACPNPPSYIPRFFTHSSDRMSFGQRVLNVLVSMLEPLL
z1b1      164 ALGVPAVYFLRGMPCGIDLLASQCPSPPSYVPRFHSGTSDKMNFVERIRNFFMSGFELVL


Ugt71g1   193 FNKDGGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
z1b4      225 CRLMLGSFEEMTSKFLHRDVSITEILSTAAVWLMRYDFTLEFPKPLMPNMITIGGINCEVKNPLTK
z1b5      224 CKLKFSAFEEVTSKFLHRDVSMTEILSTGAVWLMRYDFTLEFPKPLMPNIINIGGINCEVNNPLTK
z1b2      227 CKFMYRSFEEMIFNFLQRDVSMTEILRTGAVWLMRYDFTLEFPKPLMPNMQFIGGINCGVRNPLTK
z1b3      227 CKVMYWSFEEVTSNFLQRDVSLTEILSTGAVWLMRYDFTLEFPKPLMPNMQFIGGINCGVKNPLMK
z1b7      226 CRLIYWTTEDVASRFMQRDVSVTEVLSSGALWLLRYDFTLEFPKPLMPNMVLIGGINCAIRHPLTK
z1b1      224 CKVMYASFDELAARYLKKDVTYKEIIGRGALWLHRYDFTFEYPRPIMPNMVFIGGINCQKSAEISA
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