Additional file 25. Alignment of the zebrafish UGT1 cluster a (z1a) variable sequences with those of the UGT71G1

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Ugt71g1    1                  MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLYIT
z1a2       1 ~~~~~~~~MACLWLLGSLLLLGSAEAGKLLVIP.TDGSHWLGLKPIVEELGRRGNQVVVV
z1a4       1 ~~~~~~~~MACLWLLVGLFLLGSAEAGKLLVIP.SDGSHWLGMKPVVEELGRRGNQVVVV
z1a5       1 ~~~~~~~~~MASVLLFCLFCLASAKAGKILVVP.SDGSHWMGIKPLVEELGRRGNQVVVV
z1a6       1 ~~~~~~~~MAAFVLLLYLFCLATAEAGNILVVP.SDGSHWTGMKPLVEELGRRGNQVVVV
z1a7       1 ~MNDRIVRMAASALVLCLFCLVSAEAGNLLVIP.ALGSHWTGMRPLVEELGRRGNRVVVV
z1a1       1 ~MRTLPVPAQGLLALLCLFSFESVQAGKVLVLP.VDGSHWLSMKILVEELSNRGHEMVVL
z1a3       1 MKRTLFVPALGLFAFLCLFSSESVQAGKVLVMP.VDGSHWLSMKILVEEMSSRGHEMVVL


Ugt71g1   44 VFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLE..SLIP
z1a2      52 IPEA.....SLSMGPSEKTTT..LTYPVNYTKV.....ELEAVLASELNALLSIDVSTDL
z1a4      52 IPEA.....SLSMGPSEKTTT..LTYPVNYTKA.....ELHMVLEGNLTEILSTDFSTEV
z1a5      51 IPEA.....SLSMGPSQHTTT..LTYPVPYTKA.....QIQDHISASVTNLISTHVSTDL
z1a6      52 IPEA.....SLSMGPSQHTTT..LSYPVSYTKA.....QIQEIVKAGVTTLISTYVSTDL
z1a7      59 FPEE.....NVNMVPAKHTTT..LTYPVPYTKA.....QIQKGTDAAISKLFSADVSSDV
z1a1      59 VPET.....SILIKKSGKYST..KTYPVSFTHD.....DLAENL.KEIQNSALEKAPK.L
z1a3      60 VPET.....SILIGKSGNFTT..KSFRVPYSFD.....ELNAHV.DHIRKTAIEKAPR.F


Ugt71g1  102 HVKATIKTILSN.........................KVVGLVLDFFCVSMIDVGNEFGI
z1a2     100 AKFQSFFFTLNVLQTFILRNAEGLLFNKDLMKKLQDYNFDAILTDPFEPVGAIAGEYLSI
z1a4     100 SKFFVFFLQLKVLQNFIVRNAEGLLFNEDLMKKLQDCRFDAILTDPFEPVGVIASEYLSI
z1a5      99 ARFQSFINTMDLLSNLITRNVEGLLLNKDLMKKLQDYNFDVILTDPFETVGVIAAEYLSI
z1a6     100 PRFQSFINRMNSLSNIIIRSAEGFLSNKDLIKKLQDYNFDVILTDPFELVGVIAAEYLSV
z1a7     107 GRFQNFFTTMDMLKVIISRNAEGLLLNKDLLKKLKDYNFDAILTDPFETVGVIASEYLSI
z1a1     105 TDIVVNFRNLLQFLTMQSKTCEGLLYNEPLMKSLREMGFDAMLTDPFLPCGTIIADSFSI
z1a3     106 IDIVGALGNLIQFTNMQVKACEGLLYDEPLMKSLRDMKFDALLTDPFLPCGSVIADYFSI


Ugt71g1  137 PSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
z1a2     160 PAIYMQINHPCGVDTLASQCPAPPSYVPQTFTHFTDRMNLWQRSINFVRALLQPKACKLI
z1a4     160 PAIYMQVNLPCGVDSLASQCPSPPSYVPQRNTHFTDQMNIWQRCINLVRTLLQHMACRYM
z1a5     159 PTIYIQTSHPCGADTLASQCPSPPSYVPQRLTHFSDRMNLWQRSVNFVRTLIQPMACRRM
z1a6     160 PAIYIQTSHPCNVDTLASQCPSPPSYVPHILTHFSDRMNLWQRSVNFIRTLIQPMACRRM
z1a7     167 PAIYMQTSHPCGADVLASQCPAPPSYVPKGLTHFTDRMNLWQRSVNFVRTLVQPVACSRM
z1a1     165 PAVYFLRLIPCRLDEAAAQCPSPPSFMPRYSSGFTDKMTFPQRLVNTLLTVVEGFLCRSM
z1a3     166 PAVYFLRGIPCRLDEAAAQCPSPPSFIPRFFTGYTDKMTFPQRMINTFMTVFEKYLCHQL


Ugt71g1  197 GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
z1a2     220 FARADEIASHLLQRKTSMVEIFSRAALWFLRFNFALEFPRPVMPNMVMIGATVNQKPKPLTH
z1a4     220 YAEADEIASRFLQRRASIVEIMNRATLWLMRFDFAFEFPRPLMPNMVMIGGMATKKPKPLSK
z1a5     219 FTRADEIASRVLQRKTSIMDIMGRAALWFVHSDFALEFPHPLMPNMIIVGGMDNRKAEPLSQ
z1a6     220 FTRADEIASRVLQRKTSIMDIMSHAALWFVHSDFALEFPHPLMPNMIIVGGMDNTKAEPLSQ
z1a7     227 FAHADEIASQVLQKKTSVMEIMSRAALWFMHFDFAFEFPRPVMPNMVVIGGVDTKKPEPLSQ
z1a1     225 YESADELASKYLQKETTYAELLGHGAVWLLRYDFAFEFPRPQMPNMVQIGGINCVKRAPLTK
z1a3     226 FASFDELATRYLKKDTSYAELLGHGAVWLLRYDFSFEYPKPQMPNMVQIGGINCAKRAPLTK
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