Additional file 24. Alignment of the chicken (*Gallus gallus* [gg]) UGT1 variable sequences with those of the UGT71G1

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Ugt71g1    1                    MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLY
gga10      1 MTLRL.CYPLAAWIFILLL...PGLSEGGKLLVVP.MIGSHWLSMKEVVQKLAEKGHEVV
gga14      1 MTLRL.CCPLAAWIFILLV...PGLSEGGKLLVVP.MIGSHWLSMKEVVQKLAEKGHEVV
gga11      1 MTLRL.CYPLAAWIFILLL...PGLSEGGKLLVVP.MVGSHWLSMKEVVQKLAERGHEVV
gga13      1 MTLRL.CYPLAAWIFILLV...PGLSEGGKLLVVP.VVGSHWLSMKEVVQKLAERGHEVV
gga12      1 MTLQL.CYPLAAWIFILLV...PGLSEGGKLLVVP.MVGSHWLSMKEVVQKLAERGHEVV
gga5       1 MALVLPSHPQVS.VSLLLLLSVLGLAAGGKLLVVP.IDGSHWLSMREVLDELRQKGHEIV
gga6       1 MALVLPSHPQVL.VSLLLLLSVLGLAAGGKLLVVP.VDGSHWLSMREVLDGLRQKGHEIV
gga1       1 MALVLPSHPQVS.VSLLLLLSVLSLAAGGKLLVVS.VDGSPWFSVLEMLEVLKQKGHEIV
gga7       1 MALVLPSHPQVS.VSLLLLLSVLSLAAGGKLLVVP.VGGSHWLSMQEVLDGLRQKGHEIV
gga3       1 MALVLPSHPQVS.VSLLLLLSVLSLAAGGKLLVVS.VDGSPWFSVLEMLEVLKQKGHEIV
gga4       1 ~MASSHPGFHFLASWAVILLLLRIFSEGGKLLVIP.IDGSHWLSMRLVVEQLRHRGHEIV
gga8       1 ~~MDSFSPCNMLMAVLLPFLCYLNTAAAGKLLVIP.MDGSHWLSMKEVLAELSSRGHEIV
gga9       1 .MALLFLCFYPRTGIFFLLLSSLIFAECGKILVIP.QDGSHWLSMQPVVGKLQQNGHDVV

Ugt71g1   42 ITVFCIKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIP
gga10     56 VLKPEV.....SWNTGDKHNHAYTVKTYPVSTKLE.....ELDNAFKVYVATHLKGLPFP
gga14     56 VLKPEV.....SWNTGDKHNHAYTVKTYPVSTKLE.....DLDNAFKVYLATHLKSMPFP
gga11     56 VLKPEV.....SWQMGETQKHAYTVKTYPVSTKLE.....ELDNAFKAYVATHLKSLPFP
gga13     56 VLMPEV.....SWQMGETQKHAYTVKTYPVSTKLE.....ELDNAFKVYLATHLKSMPFP
gga12     56 VLKPEV.....SWQMGETQKHAYTVKTYPVSTKLE.....ELDNAFKLFLDPFLKDLPFP
gga5      59 VVAPEV.....SLYIKPSENFIM..KMYPVPFTQE.....EVDGMFRRTGQDAFMEGSFL
gga6      59 VVAPEV.....NVHIKPTQNFVM..KMYPVPFTQE.....EMDSSFREFSQDVFAEGSFL
gga1      59 VVAPEA.....NLNVKPSESFIL..KTYPASFTQE.....EMDDNFQAFLKDAFEEGSFL
gga7      59 IVSPEF.....NLFVKPSNNFTM..KLYQVPVTEE.....EINGDFQAFLKEAFEEGSFV
gga3      59 VVAPEA.....SLNVKPSESFIL..KTYPASSKQK.....GMAGNLQLFLQEALEEGSFL
gga4      59 VVAPEI.....NLRIGASMHYSM..KTYSVSYTRE.....FVEAEFKKLGYKSFTPQTFL
gga8      58 VVAPDS.....SILIDSSGNYTM..KTYPVPYKQE.....EMEELLHTIGTTSFSEFPLL
gga9      59 VVVPSS.....SLFMKSKEHQNYTVKVYRIPYEEE.....HLHLVLKSFVNDHFTEQSLL

Ugt71g1  102 HVKATIKTILSNK........................VVGLVLDFFCVSMIDVGNEFGI
gga10    106 LYALALYNISTYLFESFYAQCKELFSSTETLQYLNQSSFDAVLTDPLFMCGATVANYLSL
gga14    106 KNVIALHNIFTYLFESFYAQCKELFSSTETLQYLNQSGFDAVLTDPFFMCGATVANYLSL
gga11    106 LNVLALYNISSNAFSTFFLQCKELFSSTETLQYLNQSGFDAVLTDPIFMCGATLANYFSL
gga13    106 LNVLALYNVSVGVFHTFFLQCKELFSSTETLQYLNQSGFDAILTDPVLMCGATVANYLSL
gga12    106 ENIIAPYKNGIHLFKTFYLECRELFSSTETLHYLNQSSFDAILTDPFFMCGATVANYLSL
gga5     107 ERFIKAYQGVKNSSAMFLSTCEQLLYNKELIRYLQENKFDAVFTDPILPCGQILAEHLSV
gga6     107 EKLATIRQRLQRMSAIFLSTCEHLLYNKELIRYLQEYEFDALFTDPFFPCGQILAEHLSI
gga1     107 EQFHRLQEKVKRLFDVGFISCAWLLKNKELIRYLEESNFDALFTDPVFPCGAILAEHLSI
gga7     107 ERFLRVRERVKKLYELGFIACEQLLKNKELIRYLEESNFDALFTDPVLPCGAIVAEHLSI
gga3     107 GRFFRVRENMKNLSASAVIDCENLLYNKELIKYLEESKFDALLTDPILSCGAILAEYLSI
gga4     107 EKF....SKITNITTMFFDSCKRLLSNKELMKYLEESMFDGVLMDPFFPCGQIVAEHLSI
gga8     106 TRLLDTWEHFRKTSAMFQAACSSLLYKEELMKFMEESKFDAVFTDPLTPCGQIVALHLSI
gga9     109 NIIITMYQNIIEISRFFFTTCESLLHNKEMMQYLRKSKFDVVFTDPILMCGPILADYLSV

Ugt71g1  137 PSYLFLTSNVGFLSLMLSLKNRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
gga10    166 PFVFFMRGLPCNLHFEAAQCPSPLSYVPRTFSFSSDHMTFFQRVENTLISFLELFYCYGY
gga14    166 PFVFFMRGLPCNLHFEAAQCPSPLSYVPRTFSFNSDHMTFFQRVENTLISFLELFYCNAI
gga11    166 PFVFFMRGLPCNLHFEAAQCPSPLSYVPRTFSFSSDHMTFFQRVENTLISFLELFYCNGY
gga13    166 PFVIFMRGFPCNLHYEATQCPSPLSYVPRLFSFNSDHMTFFQRVENALISFLELFYCDDS
gga12    166 PFVFFMRGFPCNLHYEAAQCPSPLSYIPRATSLNSDHMTFFQRVLNTLISLLEQFHCNAI
gga5     167 PSVFYLQQIPCGLEFEATQCPNPPSYIPRIFTDNTDHMNFLQRVENVIFSISNFFLCDVV
gga6     167 PSVFLLQQIPCGLDIDATQCPNPPSYVPRIFSGNSDHMNFLQRVKNIIFDIPHSILCHLL
gga1     167 PSVYFMRGMPCGLDFEATQCPNPPSYIPRAFTDHTDHMNFLQRVKNVIFDTSNLFLCDFI
gga7     167 PSVYLLRGIPCGLHLEATQCPSPPSYIPRLFTDHTDHMNFLQRVKNVIFDTSNLFLCDFL
gga3     167 PSVYFMRLIPCGFDSEASQCPSPPSYIPRAFSDLTDHMNFLQRVKNVIFDTSNLFLCDFL
gga4     163 PSVYLVRGLPCSLDFHATLCPNPPSYIPRFFTHYTDRMGFFQRLGNLLVSLSSTLTCSFL
gga8     166 PTIFFLRGVPCSIDIYAAQSPSPPSYVPRLFSYSTDHMTFPQRVKNLLISISEYFTCSTI
gga9     169 PSVYFLRGFPCGMDSKATQCPSPPSYVPRLFLNNSDSMTFAQRMKNMLVSILELVYCQPL

Ugt71g1  197 GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
gga10    226 YQAAIQLSSEVLQRDVTPLDLLNSASISIMRFDFVFEYPRPVMPNMVFVGGMNCAEKKPLPK
gga14    226 YQDAIKFSSEVLQRDVSLIDLLNSASISIMRFDFVFEYPRPVMPNMVFVGGMNCAEKKPLPK
gga11    226 YRAAIQLSSEVLQRDVSLIDLLNSAAVSIMRFDFVFEYPRPVMPNMVFVGGINCAQKKPLPK
gga13    226 YRAAIQLSSEVLQRDVSLIDLLNSASIWLMRYDFVFEYPRPVMPNMVFIGGINCAQKKPLSK
gga12    226 YQDAIKFSSEVLQRDVSLLDLLNSASIWLLRYDFVFEYPRPVMPNMVFIGGMNCAQKKPLSK
gga5     227 FQPYAKLASEFLQHDVTVPGLLSKASIWLIKLDFVLHYPRPLMPNMIMVSGVNCAHKK.LTQ
gga6     227 FQPYTKLASEFLQRDVTVLDLLRKASIWLVRFDFVFHYPKPLMPNMIIIGGITCTHKK.LSQ
gga1     227 FKPYEKLASEFLQRDVTVIDLLRKASVWLLRYDFVLDYPRPLMPNIIVVGGINCAHKQ.LPQ
gga7     227 FKPYEKLASEFLQRDVTVLDLLRKASIWLLRYDFVLDYPGPLMPNIIVVGGVNCAHKQ.LPQ
gga3     227 FKPYDKLASEFLQRDVTLLDVFHKASIWLLRYDFVLDYPRPLMPNMIVVGGVNCAHKQ.LPQ
gga4     223 YSPYDHLIKEFLQQEATLLELLSHASIWLMKYDFVFEYPRPVMPNMVLIGGITCTQEKQISK
gga8     226 FSPFERLASDFLQQPMTLTQLLSHGSIWLKRTDFAFDYPMPVMPNMVFIGGINCGRKKLLAQ
gga9     229 FTQFEELAYEILQKKVTATDLLSHGSVWLMRYDFVFEFPRPTMPNMVFIGGINCAQKNKLSQ
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