Additional file 27. Alignment of the human (h) UGT2 sequences with those of the UGT71G1

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Ugt71g1    1               MSMSDINKNSELIFIPAPGIGHLASALEFAKLLTNHDKNLYITVFC
h2a1       1 ~~~MLNNLLLFSLQISLIGTTLGGNVLIWP.MEGSHWLNVKIIIDELIKKEHNVTVLVAS
h2b15      1 MSLKWTSVFLLIQLSCYFSSGSCGKVLVWP.TEYSHWINMKTILEELVQRGHEVTVLTSS
h2b17      1 MSLKWMSVFLLMQLSCYFSSGSCGKVLVWP.TEYSHWINMKTILEELVQRGHEVIVLTSS
h2b11      1 MTLKWTSVLLLIHLSCYFSSGSCGKVLVWA.AEYSHWMNMKTILKELVQRGHEVTVLASS
h2b28      1 MALKWTSVLLLIHLGCYFSSGSCGKVLVWT.GEYSHWMNMKTILKELVQRGHEVTVLASS
h2b10      1 MALKWTTV.LLIQLSFYFSSGSCGKVLVWA.AEYSLWMNMKTILKELVQRGHEVTVLASS
h2b7       1 MSVKWTSVILLIQLSFCFSSGNCGKVLVWA.AEYSHWMNIKTILDELIQRGHEVTVLASS
h2b4       1 MSMKWTSALLLIQLSCYFSSGSCGKVLVWP.TEFSHWMNIKTILDELVQRGHEVTVLASS
h2a3       1 MRSDKSALVFLLLQLFCVGCGFCGKVLVWP.CDMSHWLNVKVILEELIVRGHEVTVLTHS

Ugt71g1   47 IKFPGMPFADSYIKSVLASQPQIQLIDLPEVEPPPQELLKSPEFYILTFLESLIPHVKAT
h2a1      57 G.....ALFITPTSNPSLTFEIYRVPFGKE.....RIEGVIKDFVLTWLENRPSPSTIWR
h2b15     60 A.....STLVNASKSSAIKLEVYPTSLTKN.....DLEDSLLKILDRWIYGVSKN.TFWS
h2b17     60 A.....SILVNASKSSAIKLEVYPTSLTKN.....DLEDFFMKMFDRWTYSISKN.TFWS
h2b11     60 A.....SILFDPNDASTLKFEVYPTSLTKT.....EFENIIMQQVKRWS.DIRKD.SFWL
h2b28     60 A.....SILFDPNDAFTLKLEVYPTSLTKT.....EFENIIMQQVKRWS.DIQKD.SFWL
h2b10     59 A.....SILFDPNDSSTLKLEVYPTSLTKT.....EFENIIMQLVKRLS.EIQKD.TFWL
h2b7      60 A.....SILFDPNNSSALKIEIYPTSLTKT.....ELENFIMQQIKRWS.DLPKD.TFWL
h2b4      60 A.....SISFDPNSPSTLKFEVYPVSLTKT.....EFEDIIKQLVKRWA.ELPKD.TFWS
h2a3      60 K.....PSLIDYRKPSALKFEVVHMPQDRT.....EENEIFVDLALNVLPGL....STWQ

Ugt71g1  107 IKTILSN.............................KVVGLVLDFFCVSMIDVGNEFGIP
h2a1     107 FYQEMAKVIKDFHMVSQEICDGVLKNQQLMAKLKKSKFEVLVSDPVFPCGDIVALKLGIP
h2b15    109 YFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILADALNPCGELLAELFNIP
h2b17    109 YFSQLQELCWEYSDYNIKLCEDAVLNKKLMRKLQESKFDVLLADAVNPCGELLAELLNIP
h2b11    108 YFSQEQEILWELYDIFRNFCKDVVSNKKVMKKLQESRFDIVFADAVFPCGELLAALLNIR
h2b28    108 YFSQEQEILWEFHDIFRNFCKDVVSNKKVMKKLQESRFDIIFADAFFPCGELLAALLNIP
h2b10    107 PFSQEQEILWAINDIIRNFCKDVVSNKKLMKKLQESRFDIVFADAYLPCGELLAELFNIP
h2b7     108 YFSQVQEIMSIFGDITRKFCKDVVSNKKFMKKVQESRFDVIFADAIFPCSELLAELFNIP
h2b4     108 YFSQVQEIMWTFNDILRKFCKDIVSNKKLMKKLQESRFDVVLADAVFPFGELLAELLKIP
h2a3     106 SVIKLNDFFVEIRGTLKMMCESFIYNQTLMKKLQETNYDVMLIDPVIPCGDLMAELLAVP

Ugt71g1  138 SYLFLTSNVGFLSLMLSLK.NRQIEEVFDDSDRDHQLLNIPGISNQVPSNVLPDACFNKD
h2a1     167 FMYSLRFSPASTVEKHCGKVPYPPSYVPAVLSELTDQMSFTDRIRNFISYHLQDYMFETL
h2b15    169 FLYSLRFSVGYTFEKNGGGFLFPPSYVPVVMSELSDQMIFMERIKNMIHMLYFDFWFQIY
h2b17    169 FLYSLRFSVGYTVEKNGGGFLFPPSYVPVVMSELSDQMIFMERIKNMIYMLYFDFWFQAY
h2b11    168 FVYSLRFTPGYTIERHSGGLIFPPSYIPIVMSKLSDQMTFMERVKNMIYVLYFDFWFQMS
h2b28    168 FVYSLCFTPGYTIERHSGGLIFPPSYIPVVMSKLSDQMTFMERVKNMIYVLYFDFWFQMC
h2b10    167 FVYSHSFSPGYSFERHSGGFIFPPSYVPVVMSKLSDQMTFMERVKNMLYVLYFDFWFQIF
h2b7     168 FVYSLSFSPGYTFEKHSGGFIFPPSYVPVVMSELTDQMTFMERVKNMIYVLYFDFWFEIF
h2b4     168 FVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIERVKNMIYVLYFEFWFQIF
h2a3     166 FVLTLRISVGGNMERSCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDY

Ugt71g1  197 .GGYIAYYKLAERFRDTKGIIVNTFSDLEQSSIDALYDHDEK.IPPIYAVGPLLDLKGQPNPK
h2a1     227 .WKSWDSYYSKALGRPTTLCETMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPK
h2b15    229 DLKKWDQFYSEVLGRPTTLFETMGKAEMWLIRTYWDFEFPRPFLPNVDFVGGLHCKPAKPLPK
h2b17    229 DLKKWDQFYSEVLGRPTTLFETMGKAEMWLIRTYWDFEFPRPFLPNVDFVGGLHCKPAKPLPK
h2b11    228 DMKKWDQFYSEVLGRPTTLFETMGKADIWLMRNSWSFQFPHPFLPNVDFVGGFHCKPAKPLPK
h2b28    228 DMKKWDQFYSEVLGRPTTLFETMGKADIWLMRNSWSFQFPHPFLPNIDFVGGLHCKPAKPLPK
h2b10    227 NMKKWDQFYSEVLGRPTTLSETMRKADIWLMRNSWNFKFPHPFLPNVDFVGGLHCKPAKPLPK
h2b7     228 DMKKWDQFYSEVLGRPTTLSETMGKADVWLIRNSWNFQFPYPLLPNVDFVGGLHCKPAKPLPK
h2b4     228 DMKKWDQFYSEVLGRPTTLSETMAKADIWLIRNYWDFQFPHPLLPNVEFVGGLHCKPAKPLPK
h2a3     226 DYHFWEEFYSKALGRPTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPK
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