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CORRIGENDUM

Sequence variations in the UDP-glucuronosyltransferase 2B7 (UGT2B7) gene: identification of 10 novel single nucleotide polymorphisms (SNPs) and analysis of their relevance to morphine glucuronidation in cancer patients

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Following the publication of the above paper, the authors have identified an error in Table 1. The correct version of Table 1 is reproduced below:

Table 1 UGT2B7 gene polymorphisms

Position	*Number of chromosomes analyzed*	*Wild type seq.*	*Polymorphism*	*Affected codon*	*Observed frequency of occurrence (variant)*	*Estimated frequency[a] of occurrence (variant)*
−1246, promoter	34	A	A/G		0.35	0.44
−1239, promoter	34	T	T/C		0.35	0.44
−1052, promoter	34	T	T/C		0.35	0.44
−840, promoter	34	G	G/A		0.35	0.44
−268, promoter	104	A	A/G		0.39	0.44
−102, promoter	478	T	T/C		0.44	0.44
386, exon 1	34	A	agA/agG	Arg124Arg	0.03	<0.03
749, exon 2	478	G	acG/acA	Thr245Thr	0.89	0.89
815, exon 2	478	T	ccT/ccA	Pro267Pro	0.56	0.56
816, exon 2	478	C	Cat/Tat	His268Tyr	0.56	0.56
1073, exon 4	104	G	ctG/ctC	Leu353Leu	0.61	0.56
1076, exon 4	104	T	taT/taC	Tyr354Tyr	0.86	0.89

The positions indicated for promoter variants refer to the numbering in Figure 2. Positions indicated for exonic variants refer to the numbering of GenBank entry NM_001074. The positions of variation within codons are indicated by uppercase letters.
[a]Estimated frequencies are based on the observation of consistent linkage between sets of SNPs from 478 chromosomes.