

## CORRIGENDUM

# Polymorphisms in xenobiotic transporters *ABCB1*, *ABCG2*, *ABCC2*, *ABCC1*, *ABCC3* and multiple myeloma risk: a case—control study in the context of the International Multiple Myeloma rESEarch (IMMEnSE) consortium

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**Correction to:** *Leukemia* (2012) 26, 1419–1422; doi:10.1038/leu.2011.352

Since the publication of this article the authors have noticed errors within the original text of the manuscript. Allele nomenclature of some SNP have been wrongly reported with the name of the two homozygous group inverted, as illustrated in the example below:

*ABCB1* rs1045642

Genotype	Cases N (%)	Controls N (%)	OR	95% CI	P-value
<b>T/T</b> C/C	152 (24.6)	203 (24.5)	1	Ref.	—
C/T	299 (48.5)	405 (48.8)	0.98	0.76–1.27	0.905
<b>C/C</b> T/T	166 (26.9)	222 (26.7)	1.02	0.76–1.37	0.878
<b>C/T + C/C</b> T/T	465 (75.4)	627 (75.5)	1.00	0.78–1.27	0.987

Readers should apply the corrections explained in the example above to the following polymorphisms:

**Table 2:** rs10264990.

Supplementary Table II: rs1045642, rs2235074, rs3842, rs7787082, rs10276499, rs9282564, rs10264990, rs12334183\*, rs12505410,

rs13120400, rs3109823, rs3114018, rs4148157, rs2054576, rs2725248, rs2725256, rs2756109, rs4077146, rs8187710, rs7476245, rs3740073, rs212091, rs4793665, rs11568591.

\*For the polymorphism rs12334183 the alleles should be C and T instead of G and T.

Supplementary Tables IV, V and VI: rs10276499, rs9282564, rs10264990, rs3109823, rs11568591.

Supplementary Figure 1: rs10264990.

**In the text:** the sentence ‘We confirmed in this way the statistically significant association of the T carriers for the rs10264990 with a decreased risk of MM ( $P=0.015$ )’ (page 1) refers to C carriers instead of T carriers.

This corrigendum involves exclusively allele nomenclature and does not affect the results reported in the paper nor its conclusions in any way. Genotype groups, OR and  $P$ -values remain absolutely correct and unvaried. Nevertheless, this corrigendum will help the readers to avoid misleading usage of the results in further application (that is, meta-analysis) or confutation of the results.

**Table 2.** Significant associations of *ABCB1* SNPs rs10264990 and rs17327442 with MM risk in the overall population

SNP (rs)	Cases N (%)	Controls N (%)	OR <sup>a</sup>	95% CI	P-value	P-trend	P-perm
<b><i>ABCB1</i> rs10264990</b>							
<b>T/T</b>	549 (47.1)	958 (41.7)	1	Ref.	-	<b>0.023</b>	
C/T	475 (40.7)	1059 (46.0)	0.77	0.66–0.90	<b>0.001</b>		
<b>C/C</b>	142 (12.2)	283 (12.3)	0.85	0.68–1.07	0.171		0.869*
<b>C/T + C/C</b>	617 (52.9)	1342 (58.3)	0.79	0.68–0.91	<b>0.001</b>		<b>0.015**</b>
<i>ABCB1</i> rs17327442							
A/A	824 (69.7)	1600 (69.9)	1	Ref.	-	0.191	
A/T	309 (26.1)	643 (28.1)	0.92	0.78–1.08	0.309		
T/T	50 (4.2)	46 (2.0)	1.99	1.32–3.02	<b>0.001</b>		<b>0.009*</b>
A/T + T/T	359 (30.3)	689 (30.1)	0.99	0.85–1.16	0.928		1**

Genotype distribution among MM cases and controls in the overall population of the *ABCB1* SNPs rs10264990 and rs17327442. <sup>a</sup>Odds Ratios (OR) are adjusted for age, gender and region of origin. Differences in sample numbers are due to failures in genotyping. Results in bold show  $P < 0.05$ . \* $P$ -value obtained after 100,000 permutations following a co-dominant model. \*\* $P$ -value obtained after 100,000 permutations following a dominant model.

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To help the readers, corrected versions of Table 2, Supplementary Tables II, IV, V, VI and Supplementary Figure 1 are provided with this corrigendum.

SNP for which allele nomenclature was changed with respect to the original table or figure are marked in bold and underlined.

Supplementary Information accompanies this paper on the Leukemia website (<http://www.nature.com/leu>)

The authors would like to apologize for any inconvenience this may have caused.