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CORRIGENDA

Incorporation of the bone marker carboxy-terminal telopeptide of type-1 collagen improves prognostic information of the International Staging System in newly diagnosed symptomatic multiple myeloma

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Correction to: *Leukemia* (2008) **22**, 1767–1772; doi:10.1038/leu.2008.159; published online 26 June 2008

Since the publication of their paper, the authors have identified an error in the 5-year overall survival rates for the four risk groups, which were listed incorrectly in the abstract, in the second paragraph of the Results section and in Table 4. The correct 5-year OS rates are 95, 64, 46 and 22%, respectively. A revised version of Table 4 is reproduced below.

The authors apologize for any inconvenience caused.

Table 4 Comparison between ISS and combined ICTP-ISS risk score in newly diagnosed symptomatic MM

Combined ISS-ICTP score				*ISS*			
Risk factors[a] *(risk group)*	*Patients (%)*	*5-year OS*	*Hazard ratio (95% CI)*	*Stage*[b]	*Patients (%)*	*5-year OS*	*Hazard ratio (95% CI)*
0 (very low)	21	95	1.00 (reference)				
1 (low)	38	64	5.78 (0.72–46.27)	I	38	72	1.00 (reference)
2 (intermediate)	26	46	11.03 (1.40–86.72)	II	35	62	1.56 (0.58–4.21)
3 (high)	15	22	29.02 (4.19–265.43)	III	27	35	3.20 (1.27–8.00)

Abbreviations: CI, confidence interval; ISS, International Staging System; MM, multiple myeloma; OS, overall survival.
[a]Risk factors: β2M ⩾ 3.5 mg/l; albumin < 3.5 g per 100 ml; ICTP > reference limit.
[b]ISS I: β2M < 3.5 mg/l, albumin ⩾ 3.5 g per 100 ml; ISS II: not stage I or III; ISS III: β2M ⩾ 5.5 mg/l.

Inv(11)(q21q23) fuses *MLL* to the Notch co-activator mastermind-like 2 in secondary T-cell acute lymphoblastic leukemia

M Metzler, MS Staege, L Harder, D Mendelova, J Zuna, E Fronkova, C Meyer, T Flohr, D Bednarova, J Harbott, T Langer, S Gesk, J Trka, R Siebert, T Dingermann, R Marschalek, C Niemeyer and W Rascher

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Since the publication of the above paper, the authors have detected a minor error that has no impact on the conclusion.

Please note that the second sentence of the third paragraph 'Flowcytometric analysis of the primary ALL showed common ALL phenotype with aberrant expression of CD66c, the myeloid marker CD13 and the progenitor marker CD117.' should be corrected to 'Flowcytometric analysis of the primary ALL showed common ALL phenotype with aberrant expression of CD66c and hyperdiploid DNA content (DNA index 1.17).'

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