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CORRIGENDUM

A gene expression signature for high-risk multiple myeloma

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Correction to: *Leukemia* (2012) **26,** 2406–2413; doi:10.1038/leu.2012.127

Since the publication of this article, the authors have discovered an error in the script for calculating the IFM-15 risk scores. In their paper, they described the weights of all probe sets used in this signature to be positive, whereas four of these were actually negative, as published by Decaux *et al.*[1] This results in different outcome scores for this signature with an altered decision threshold of 0.956.

They have corrected statements in the Results and Discussion sections, and corrected Figures 2 and 3 in the main body of the paper, where only IFM-15-specific data were changed. The corrected statements and figures are shown below.

In addition, this applies to Supplementary Tables S2.7, S9, S10 and S13.6, corrected versions of which are included in the online version of this corrigendum, together with the corrected IFM-15 risk scores and script.

The corrections do not affect the conclusions concerning the EMC-92 gene classifier.

Corrected statements

Second paragraph of the Results section 'Comparison with published gene signatures'.

Original statement: Specifically, the EMC-92, UAMS, MRC-IX and GPI-50 signatures demonstrated significance in all validation sets tested both for the dichotomized and for the continuous values of the signatures. Significance was reached in three out of five studies for the IFM-15 signature using a dichotomized model, whereas the MILLENNIUM-100 signature had significant performance in the dichotomized model in one out of four independent studies. Thus, performance was less robust for the IFM-15 and MILLENNIUM-100 signatures.

Corrected statement: Specifically, the EMC-92, UAMS, IFM-15, MRC-IX and GPI-50 signatures demonstrated significance in all validation sets tested both for the dichotomized and for the continuous values of the signatures. The MILLENNIUM-100 signature had significant performance in the dichotomized model in one out of four independent studies. Thus, performance was less robust for the MILLENNIUM-100 signature.

Second paragraph of the Discussion section.

Original statement: In contrast, the predictions of the IFM-15 and MILLENNIUM-100 signatures in the validation sets fail to reach significance in independent data sets such as MRC-IX and TT3. The differences in gene expression platform may have contributed to this. Indeed, the IFM Signature is based on a custom cDNA-based gene expression platform, rather than the Affymetrix GeneChips, which have become common for MM GEP studies.[2] The cDNA platforms have been reported to be difficult to compare with the Affymetrix oligonucleotide platform.[1] Although the MILLENNIUM signature was generated using Affymetrix GeneChips, the use of an earlier version of this platform may have contributed to the limited performance of this signature.[3]

Corrected statement: In contrast, the predictions of the MRC-IX, GPI-50, IFM-15 and MILLENNIUM-100 were not as convincing as those of the EMC-92 and UAMS signatures. Especially, the predictions of the MILLENNIUM-100 signature in the validation sets fail to reach significance in independent data sets such as MRC-IX, TT2 and TT3. The differences in gene expression platform may have contributed to this in part. Indeed, the IFM signature is based on a custom cDNA-based gene expression platform, rather than the Affymetrix GeneChips, which have become common for MM GEP studies.[2] The cDNA platforms have been reported to be difficult to compare with the Affymetrix oligonucleotide platform.[1] Although the MILLENNIUM signature was generated using Affymetrix GeneChips, the use of an earlier version of this platform may have contributed to the limited performance of this signature.[3]

The authors apologize for any inconvenience this may have caused.

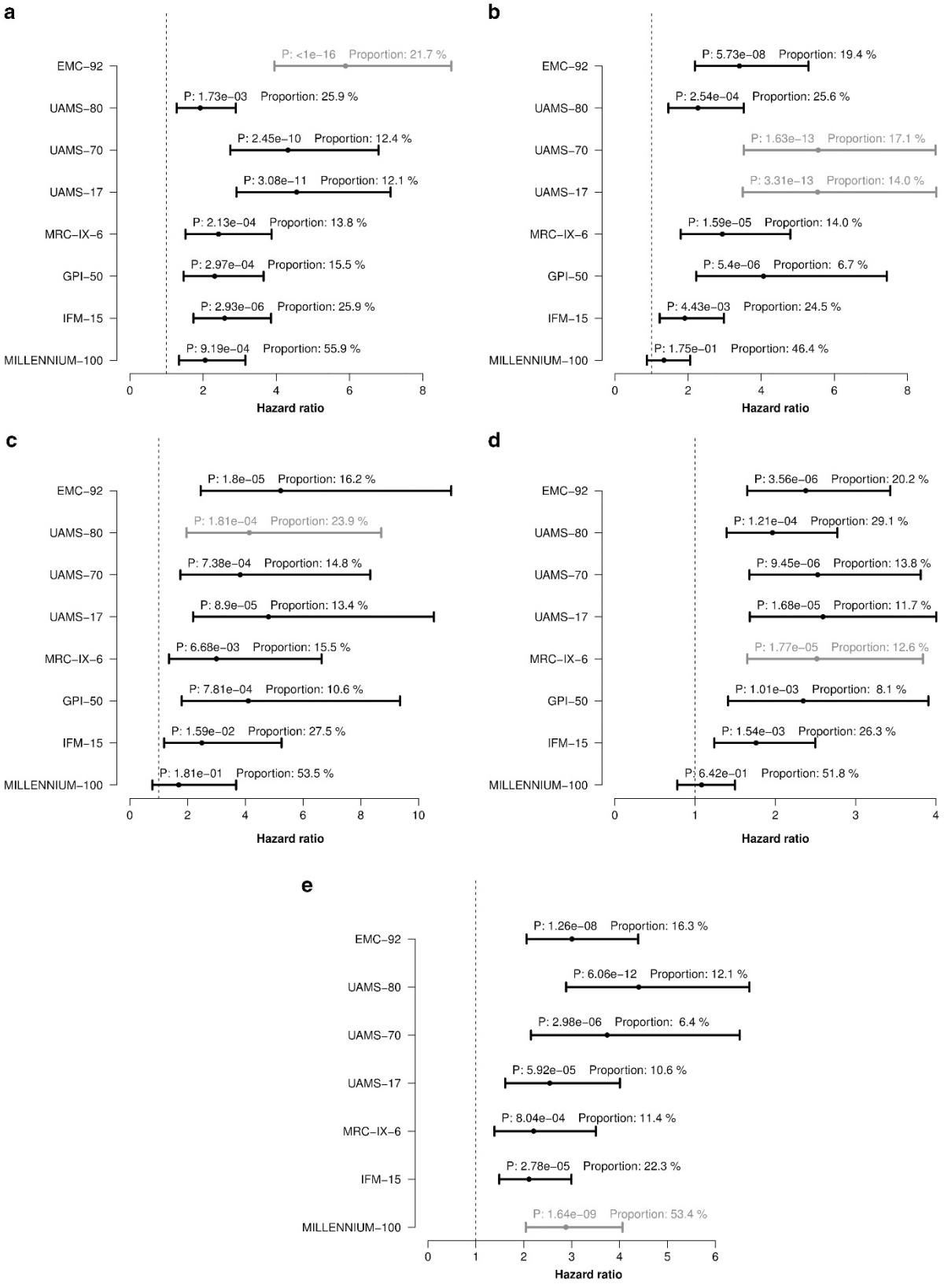

Figure 2. Performance per signature in available data sets. For every signature the hazard ratio (high risk versus standard risk) is shown with 95% confidence interval. Gray lines indicate results on the training set. (**a**) HOVON-65/GMMG-HD4. (**b**) UAMS-TT2. (**c**) UAMS-TT3. (**d**) MRC-IX. (**e**) APEX. P, *P*-value for equal survival in high- and standard-risk groups; proportion, proportion of high-risk-defined patients.

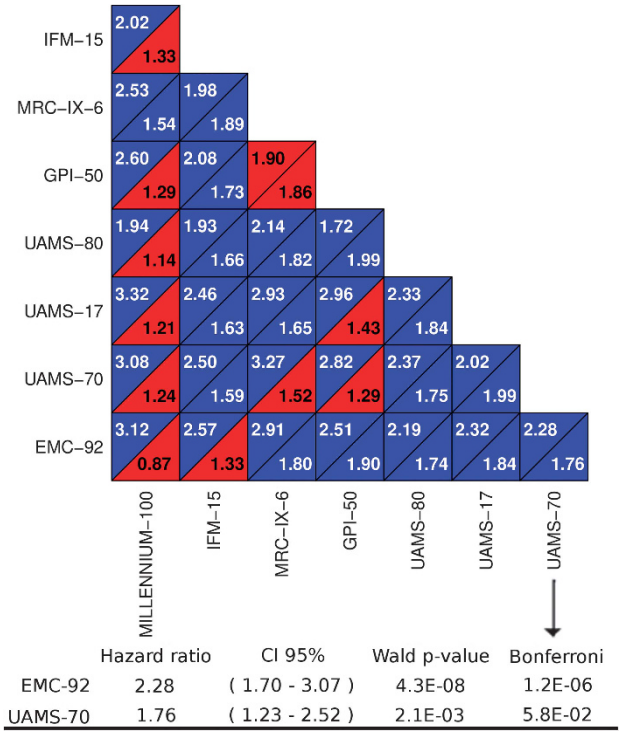

Figure 3. Pair-wise comparison for all signatures. To find the signature best fitting the underlying data sets, Cox regression models (high risk versus standard risk) were made for all pair-wise signatures. These models are based on pooled independent data sets (that is, excluding training sets) and stratified for study. The two paired hazard ratios associated with the signatures derived per model are shown in the two cells within the square panels. Only hazard ratios within one panel can be compared because these are based on the same data set. Blue cells indicate significant hazard ratios (Bonferroni–Holm-corrected *P*-value); red cells denote non-significant findings. For the bottom right panel (that is, UAMS-70 versus EMC-92 signatures) the underlying model is given. All other models can be found in Supplementary Table S9.

REFERENCES

1 Decaux O, Lode L, Magrangeas F, Charbonnel C, Gouraud W, Jezequel P *et al.* Prediction of survival in multiple myeloma based on gene expression profiles reveals cell cycle and chromosomal instability signatures in high-risk patients and hyperdiploid signatures in lowrisk patients: a study of the intergroupe francophone du myelome. *J Clin Oncol* 2008; **26**: 4798–4805.
2 Mah N, Thelin A, Lu T, Nikolaus S, Kuhbacher T, Gurbuz Y *et al.* A comparison of oligonucleotide and cDNA-based microarray systems. *Physiol Genomics* 2004; **16**: 361–370.
3 Mulligan G, Mitsiades C, Bryant B, Zhan F, Chng WJ, Roels S *et al.* Gene expression profiling and correlation with outcome in clinical trials of the proteasome inhibitor bortezomib. *Blood* 2007; **109**: 3177–3188.

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