Leukemia (2009) 23, 825–826

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CORRIGENDUM

Recurrent genomic aberrations combined with deletions of various tumour suppressor genes may deregulate the G1/S transition in CD4 + CD56 + haematodermic neoplasms and contribute to the aggressiveness of the disease

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Correction to: *Leukemia* (2009) **23**, 698–707;
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Since the publication of this paper, the authors have noticed that part of Figure 1 has been omitted (part **c**). The complete figure is shown below.

The authors would like to apologise for this error.

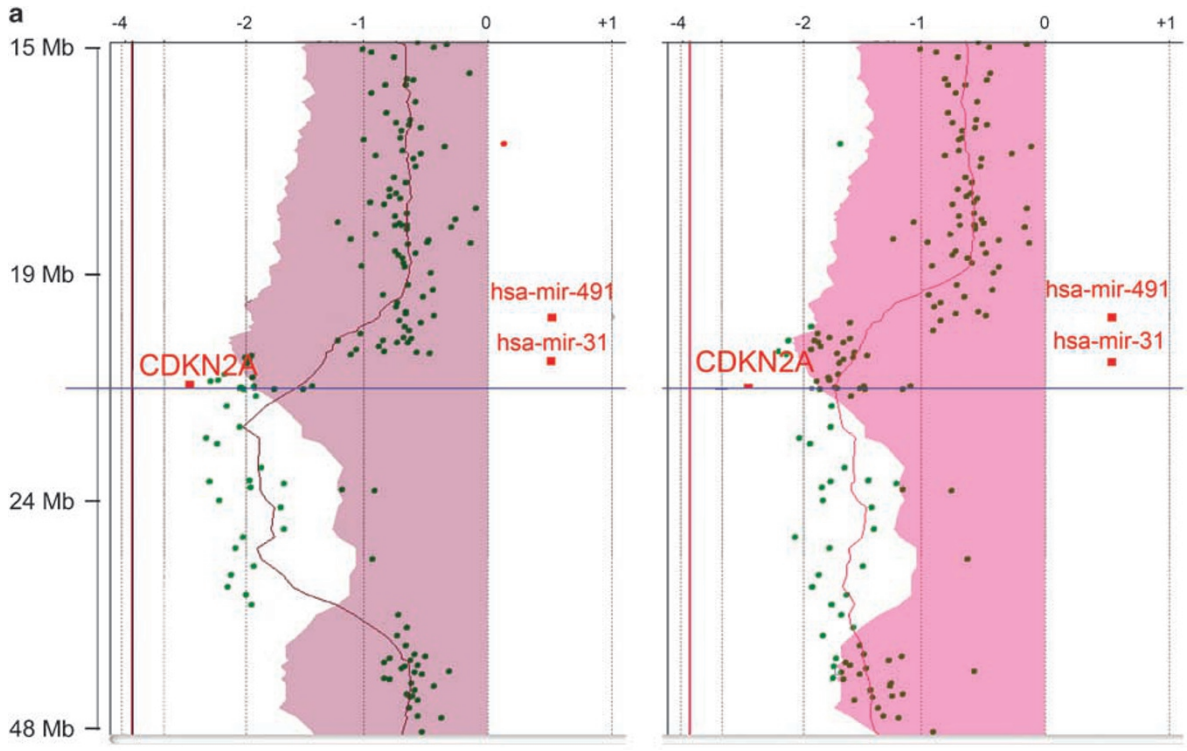

Figure 1 Commonly deleted regions defined by array-based CGH. (**a**) Similar biallelic losses of 9p21 locus and chromosome 9 monosomy containing CDKN2A/CDKN2B tumour suppressor genes (blue line) in cases 2 and 3. Break points are closely located to mir-31 and mir-491 (in red). (**b**) Commonly deleted region located within chromosome 13 that encompasses the 13q13.3–q14.2 locus, showing a homozygous deletion of RB1 (case 9) combined with chromosome 13 partial deletion. Break points are located within RB1 (in red) and in a close vicinity of miR-16-1/miR-15a (in red). (**c**) Commonly deleted region located in 12p13 chromosome, involving CDKN1B and ETV6 genes (in red).

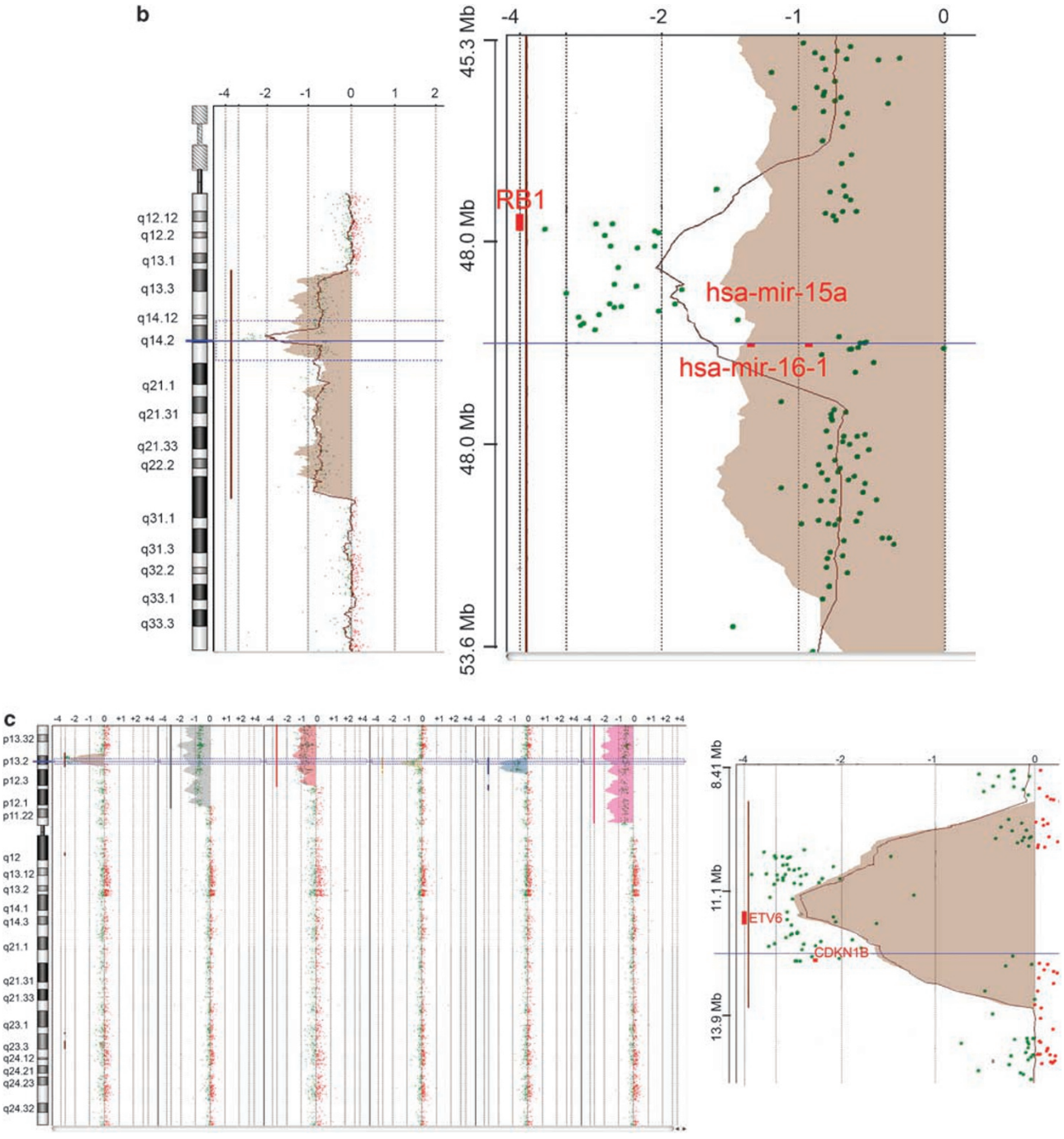

Figure 1 Continued.