ERRATUM:

In the article by

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1. Figure 2 as presented on page 45 has been partly mistaken with Figure 1. Only the panels 2b and 2c of Figure were presented while being labeled as 1b and 1c.

Thus, Figure 2 a,b,c, with the correct legend is now shown below :

2. Figure 2 as presented on page 46 should read Figure 3. The same is true for the right column of the text, on page 46, line 13-14 where "(Figure 2)" should read "(Figure 3)".

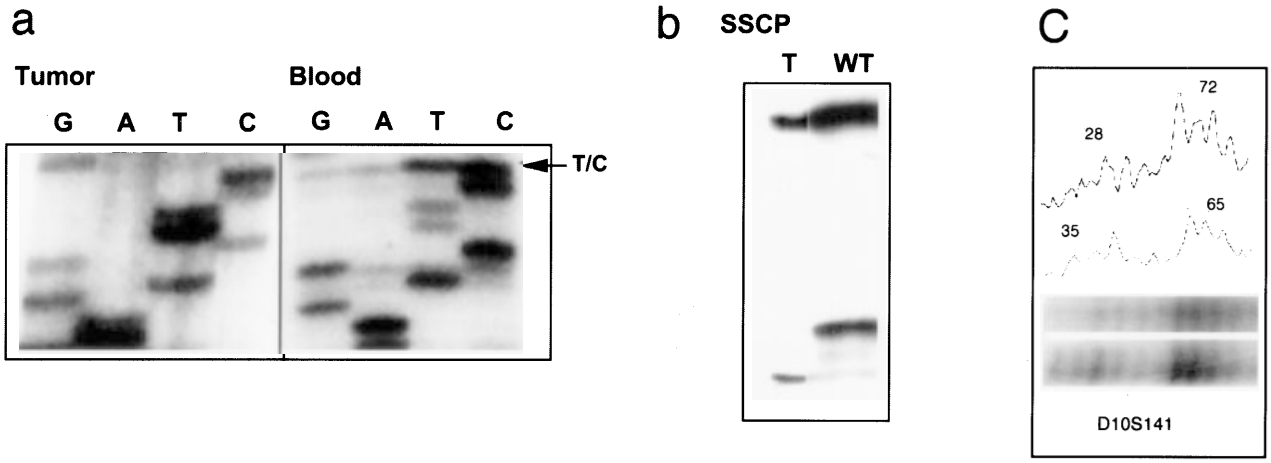

Figure 2

a. Sequencing analysis of a MEN2-related pheochromocytoma (tumor) and genomic blood DNA. The germline *RET* mutation affects codon 620, changing the wild-type TGC to mutant CGC. In the tumor DNA, there is only mutant (CGC), whereas in the blood DNA both, mutant and wild-type sequence, are represented.

b. Single-strand conformation polymorphism analysis of the same MEN 2-related pheochromocytoma. T, tumor with *RET* mutation in exon 10; WT, wild-type normal tissue without *RET* mutation in exon 10. T shows a shift in the gel electrophoresis from the "normal, wild-type germline", indicating a mutation in this specific exon (10) of *RET*. Note that only the mutant allele is shown in the bands of T.

c. Loss of heterozygosity (LOH) analysis with polymorphic marker D10S141 and phosphorimage densitometry of the same tumor and genomic blood DNA. In the tumor (T), only one allele is shown, whereas N (genomic blood DNA) shows both alleles. Confirmatory phosphorimage densitometry analysis shows a ratio of the respective alleles, indicating LOH of this pheochromocytoma specimen