

CORRIGENDUM

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Corrigendum: Whole-genome landscape of pancreatic neuroendocrine tumours

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It has been brought to our attention that in Fig. 2d of this Article, an incorrect Sanger trace was used to represent the breakpoint of the *EWSR1* and *FLI1* type 2 fusion. This was due to an error during manuscript preparation, when we inadvertently inserted the electrophoretic trace referring to *EWSR1* splicing variants. Figure 2d has been corrected in the online versions of the Article. We apologize for the confusion.

In addition, in the first sentence of the ‘Somatic driver mutation’ section on page 67, the sentence: ‘A total of 15,751 somatic coding mutations (7,703 non-silent) were detected in 2,787 genes (Supplementary Tables 4, 5)’, should have stated ‘A total of 3,097 somatic coding mutations (2,498 non-silent) were detected in 2,567 genes (Supplementary Tables 4, 5)’. Note that the numbers in the Supplementary Tables are correct. This sentence has been corrected in the online versions of the Article.