Corrigendum: Whole-genome sequencing of bladder cancers reveals somatic *CDKN1A* mutations and clinicopathological associations with mutation burden

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Nature Communications 5:3756 doi: 10.1038/ncomms4756 (2014); Published 29 Apr 2014; Updated 26 Jun 2014

The financial support for this Article was not fully acknowledged. The Acknowledgements should have included the following:

Anne Kiltie was funded by the Cancer Research UK programme grant C5255/A15935. Jean-Baptiste Cazier's activity as a core leader is funded by Cancer Research UK. Support for sample biobanking was provided by the Cancer Research UK Oxford Cancer Research Centre (OCRC).