

## Erratum: Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer

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In the version of this article initially published online, the mutation category plots in the top panel of Figure 1 were not correctly aligned with the corresponding genes. In addition, the labels for tumor types on the left were not correctly aligned with individual samples. The errors have been corrected for the print, PDF and HTML versions of this article.

## Corrigendum: Recurrent mTORC1-activating *RRAGC* mutations in follicular lymphoma

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In the version of this article initially published online, several funding sources were omitted from the Acknowledgments section. The error has been corrected for the print, PDF and HTML versions of this article.

## Corrigendum: The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons

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As we intended, other researchers have been able to use the draft spotted gar genome sequence available from the Broad Institute website since December 2011, the assembly LepOcu1 publicly available from NCBI since 13 January 2012 under accession code [GCA000242695.1](https://www.ncbi.nlm.nih.gov/nuccore/GCA000242695.1), and the Ensembl gene annotation (version 74, December 2013; [http://www.ensembl.org/Lepisosteus\\_oculatus/Info/Annotation](http://www.ensembl.org/Lepisosteus_oculatus/Info/Annotation)) and recent annotation by NCBI on 15 May 2014 guided by RNA sequence data from ten tissues. While this article was in review, a paper (*Nature* 526, 108–111, 2015) was published that arrives at conclusions similar to some of our own analyses, and we wish to acknowledge that publication, which used our unpublished data and genome annotations, emphasizing the importance of the strategy of early release of sequence data. The correction has been made to the HTML and PDF versions of the article.