

## Corrigendum: The genomic landscape of juvenile myelomonocytic leukemia

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In the version of this article initially published, two patients were stated on page 5 to have been excluded owing to insufficient follow-up data. These patients were included in the final analysis, but two additional patients were excluded owing to the presence of Noonan syndrome. On page 6, monosomy 7 was incorrectly listed as a significant factor in event-free and overall survival, but this factor was no longer significant after removing the patients with Noonan syndrome. The Online Methods incorrectly referred to “Data from patient AAML0122” instead of data from patients enrolled on AAML0122. The errors have been corrected in the HTML and PDF versions of the article.

## Corrigendum: Common variants at 19p13 are associated with susceptibility to ovarian cancer

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In the version of this article initially published, the name of author Angela Brooks-Wilson was spelled incorrectly in the author list. The error has been corrected in the HTML and PDF versions of the article.

## Erratum: Large-scale identification of sequence variants influencing human transcription factor occupancy *in vivo*

Matthew T Maurano, Eric Haugen, Richard Sandstrom, Jeff Vierstra, Anthony Shafer, Rajinder Kaul & John A Stamatoyannopoulos  
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In the version of this article initially published online, the Online Methods incorrectly abbreviated mapping quality as MAQ rather than MAPQ. Also in the Online Methods, the procedure for downsampling allele counts for cross-cell type analysis of imbalance was incorrectly written as “we subsampled each site to three cell types and further downsampled the allele counts to mapping quality for the lowest of the three cell types.” The sentence should read “we subsampled each site to three cell types and further downsampled to the allele counts to match the lowest of the three cell types.” The errors have been corrected for the print, PDF and HTML versions of this article.