
Corrigendum: Mutations in *TCF12*, encoding a basic helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis

Vikram P Sharma, Aimée L Fenwick, Mia S Brockop, Simon J McGowan, Jacqueline A C Goos, A Jeannette M Hoogeboom, Angela F Brady, Nu Owase Jeelani, Sally Ann Lynch, John B Mulliken, Dylan J Murray, Julie M Phipps, Elizabeth Sweeney, Susan E Tomkins, Louise C Wilson, Sophia Bennett, Richard J Cornall, John Broxholme, Alexander Kanapin, 500 Whole-Genome Sequences (WGS500) Consortium, David Johnson, Steven A Wall, Peter J van der Spek, Irene M J Mathijssen, Robert E Maxson, Stephen R F Twigg & Andrew O M Wilkie

Nat. Genet. 45, 304–307 (2013); published online 27 January 2013; corrected after print 5 September 2013

In the version of this article initially published, numbering and spacing for the exon structure of *TCF12* in Figure 2a was incorrect. The error has been corrected in the HTML and PDF versions of the article.

Corrigendum: The burden of faulty proofreading in colon cancer

Somasekar Seshagiri

Nat. Genet. 45, 121–122 (2013); published online 29 January 2013; corrected after print 5 September 2013

In the version of the article initially published, reference 6 (*J. Biol. Chem.* 281, 4486–4494, 2006) should have been *Genome* 49, 403–410, 2006. Part of the associated sentence, “Alteration of this amino acid has been shown to lead to mutator phenotypes in yeast⁶,” was revised to “Alteration of the equivalent residue in a related polymerase, POLD1, leads to mutator phenotypes in yeast⁶.” In paragraph 4, alteration of a POLD1 residue in yeast, given as arginine, should have been asparagine. A sentence with an error in paragraph 7, “Similarly, tumors reported by Palles *et al.*⁴ that carried the POLE p.Leu424Val exonuclease-deficient germline variant also carried APC alterations,” has been changed to state that the POLE p.Leu424Val variant alters an amino acid in the active site of the exonuclease domain. The revised sentence reads “Similarly, tumors reported by Palles *et al.*⁴ that carried the POLE p.Leu424Val germline variant, which maps to the active site of the exonuclease domain, also carried APC alterations.” The legend for Figure 1 has been amended to include “Adapted with permission from ref. 5.”