CORRECTION

Errors in Figure and Caption: In the article titled “Symptomatic Congenital Hemangioma and Congenital Hemangiomatosis Associated With a Somatic Activating Mutation in GNA11,” published online July 20, 2016, and also in the September 2016 issue of JAMA Dermatology, Figure 3B contained an alignment error, and the caption for Figure 3B incorrectly reported the number of nonreference exome sequencing reads. A Letter of explanation has been published, and the original article has been corrected online.


Error in Author Degree: In the Original Investigation titled “Costs and Consequences Associated With Misdiagnosed Lower Extremity Cellulitis,” published online November 2, 2016, there was an error in the degree of one of the authors. Where it previously read Jean-Phillip Okhovat, BS, it now correctly reads Jean-Phillip Okhovat, MD, MPH. This article has been corrected online.


Error in Abstract Results: In the Original Investigation titled “Reexamining the Threshold for Reexcision of Histologically Transected Dysplastic Nevi,” published online August 17, 2016, and also in the December 2016 print issue of JAMA Dermatology, there was an error in a percentage in the abstract Results. The sentence should read as follows: “Six of 304 (2.0%) observed DN subsequently developed melanoma at the same site, compared with 1 of 170 (0.6%) that were reexcised (P = .43).” This article has been corrected online.


Figure. Histogram Showing Mosaic Mutation Expression in Tumoral Tissue but Not Saliva

Integrated Genome Viewer software was used to visualize exome sequencing reads. The histograms on the top of each panel represent the total coverage for individual base, with each horizontal gray line representing an individual 74-base pair read. Vertical black bars designate the c.A626, p.Q209 locus. Of 37 reads covering this region in tissue (top), 11 (30%) were nonreference calls. Blue highlighted rows represent the 11 nonreference reads. A total of 60 reads obtained in saliva DNA indicate 100% reference reads, suggesting no mutation in the germline (bottom).

the result of our graphics software misaligning the reads with the histogram above it, causing a strange step-off to be seen. Herein, we provide a correctly aligned Figure.

In addition, the original Figure 3B caption incorrectly stated that there were 26 nonreference calls (C) and 11 reference calls (A), for a ratio of 70% nonreference. Instead, the numbers should be flipped: there are 26 reference calls and 11 nonreference calls, for a nonreference ratio of 30%. This has also been corrected in the Figure legend. None of the study’s conclusions are affected by these errors or their corrections.

We have requested that the article be corrected online. We sincerely apologize for any confusion this may have caused the readers and editors of the journal.

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Conflict of Interest Disclosures: None reported.
