Correction: Closing gaps in the human genome using sequencing by synthesis

Manuel Garber1, Michael C Zody1,2, Harindra C Arachchi1, Aaron Berlin1, Sante Gnerre1, Lisa M Green1, Niall Lennon1 and Chad Nusbaum1*

Correction
After publication of this Method [1], we noted errors to the legend of Figure 1. The labelling of the line representing the 454 reads and the line representing the small insert library reads was inverted (please see Figure 1 below, a corrected version of Figure 1).

Author details
1Genome Sequencing and Analysis Program, Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA. 2Department of Medical Biochemistry and Microbiology, Uppsala University, SE-751 24 Uppsala, Sweden.

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Reference
1. Garber M, Zody MC, Arachchi HM, Berlin A, Gnerre S, Green LM, Lennon N, Nusbaum C: Closing gaps in the human genome using sequencing by synthesis. Genome Biology 2009, 10:R60.

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* Correspondence: chad@broad.mit.edu
1Genome Sequencing and Analysis Program, Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA
Full list of author information is available at the end of the article

Figure 1 Coverage of gap regions. Sequence coverage of the gap regions on human chromosome 15 is shown for gaps at (a) 24 Mb, (b) 25 Mb and (c) 96 Mb. The x-axis indicates base position in the local region containing each gap. The y-axis shows sequence coverage obtained in 454 reads (blue line) and small insert library reads (red line). Coverage was computed as the average in 10-base non-overlapping windows. Arrows indicate primers used to amplify the amplicons sequenced, color coded in pairs. Bars at top indicate bases present in the Celera (dark gray) and NCBI build 36 (light gray) assemblies.