Genome **Biology**

CORRECTION

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

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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).

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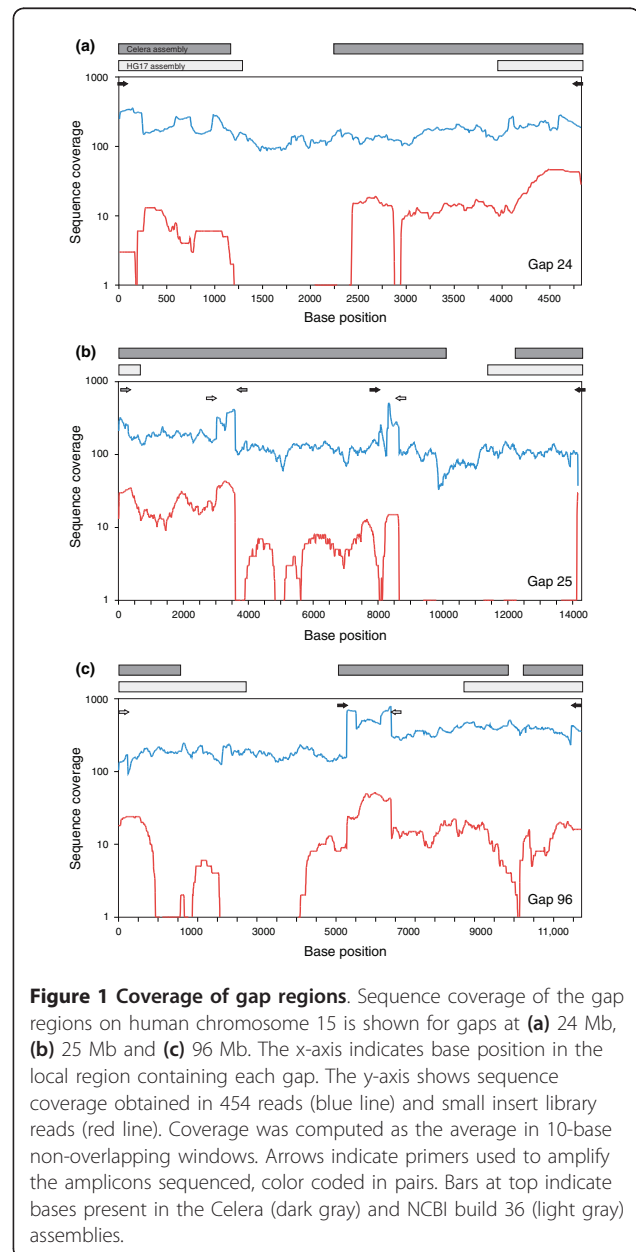
Reference
1. Garber M, Zody MC, Arachchi HM, Berlin A, Gnerre S, Green LM, Lennon N, Nusbaum C: **Closing gaps in the human genome using sequencing by synthesis.** *Genome Biology* 2009, **10**:R60.

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.

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