CORRECTION

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Correction to: Draft genome sequences of Hirudo medicinalis and salivary transcriptome of three closely related medicinal leeches

Check for updates

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Following the publication of the original article [1], it was noted that due to a typesetting error that Fig. 1 was erroneously published as a duplicate of Fig. 5.

The correct Fig. 1 has been included in this correction, and the original article has been corrected.

The publisher apologizes to the authors and readers for the inconvenience.

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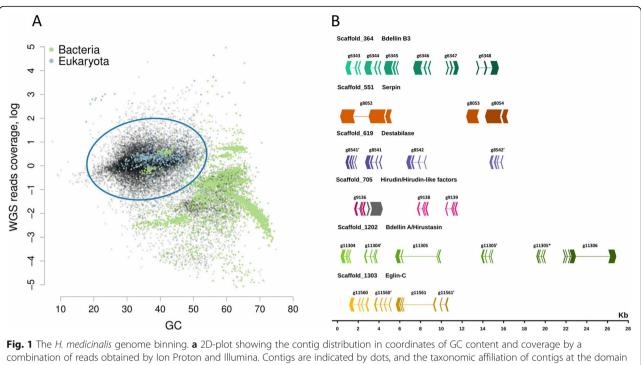
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level is encoded by colour (green – Bacteria, blue – Eukarya, black – no assignment). The taxonomic affiliation was determined by direct BlastN (megablast) search against the National Center for Biotechnology Information (NCBI) nt database. The 3D plot showing the contig distribution in coordinates of GC content, read coverage (Proton and Illumina), and host cDNA read coverage is presented in Supplementary Data 2. **b** *H. medicinalis* genome contains clusters of blood meal-related genes. The graph shows the exon-intron structure of genes and arrangement of gene clusters in scaffolds on a general scale. The exon arrows indicate the direction of transcription (gray - unknown gene)