

Correction

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Correction: Inference of miRNA targets using evolutionary conservation and pathway analysis

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In our manuscript on miRNA target predictions [1] we made use of a number of genome alignments that we obtained from the UCSC genome browser. We regret that, due to a misunderstanding, we failed to explicitly acknowledge the sequencing centers that made the genome sequences, that were used to construct these alignments, available before publication.

5. **Broad Institute** [<http://www.broad.mit.edu>]
6. **Sanger Center** [http://www.sanger.ac.uk/Projects/D_rerio/]

These centers are: the Agencourt Bioscience Corporation [2] for the *Drosophila ananassae*, *Drosophila mojavensis*, and *Drosophila virilis* sequence data, the Genome Sequencing Center at the Washington University School of Medicine [3] for the *Drosophila yakuba*, *Drosophila simulans*, and *Caenorhabditis remanei* sequence data, the Human Genome Sequencing Center at the Baylor College of Medicine [4] for the *Bos taurus* and Rhesus macaque genome sequence, the Broad Institute [5] for the *Monodelphis domestica* genome sequence, and the Sanger Center [6] for the *Danio rerio* genome sequence.

We understand that continuing free access to data from large scale sequencing efforts requires careful acknowledgement and we apologize sincerely for this unfortunate oversight.

References

1. Gaidatzis D, van Nimwegen E, Hausser J, Zavolan M: **Inference of miRNA targets using evolutionary conservation and pathway analysis.** *BMC Bioinformatics* 2007, **8**:69.
2. **Agencourt Bioscience Corporation** [<http://www.agencourt.com/>]
3. **Washington University School of Medicine** [<http://genome.wustl.edu/>]
4. **Baylor College of Medicine** [<http://www.hgsc.bcm.tmc.edu/>]