

Erratum

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HAPPY mapping using high-throughput random shotgun sequencing was conceived and initiated by J. Chapman, C. David, P. Dear, and D. Rokhsar for application to mapping the Hydra genome. Our review article (*Int J Biol Sci* 2009; 5:298-303) [1] should have clearly cited this ongoing effort as the first HAPPY mapping-by-sequencing project and this group as the initiators of the approach. We regret that we were unable to correct this error before the review went to press. Also, in the initial online version of this paper, Figure 1 included panels taken from the instructional HAPPY mapping website of Paul Dear, developer of the HAPPY mapping method, without attribution. The published version includes an alternate version of Figure 1. The authors sincerely apologize for these errors.

References

1. Jiang Z, Rokhsar DS, Harland RM. Old can be new again: HAPPY whole genome sequencing, mapping and assembly. *Int J Biol Sci* 2009; 5:298-303.