BU711870.1 spanning the primer binding sites with the sequence of the PCR product showed 47.6% sequence identity (using the Needle algorithm, http://www.ebi.ac.uk/Tools/emboss/align/). Comparison with the genomic sequence of *S. mansoni* identified the PCR product as part of a unique sequence on scaffold 000213 (positions 409,215–409,650, 99% identity). For the Hpa primer pairs[1], the PCR product had a size of 175 bp instead of the predicted size of 159 bp, and alignment with AY834401.1 showed only 45% similarity. A BLAST search returned a unique 100% match on the *S. mansoni* genomic scaffold 000001 (positions 1,882,577–1,882,721). The predicted size for the Igf primer pair is 266 bp, whereas the observed size was 1,041 bp, and the similarity to AY834397.1 was very low (18.7% similarity). Primer sequences are given in **Supplementary Table 1**. In short, we did not observe PCR amplification with the previously used primers of the putative salmonid-like repeat sequences in *S. mansoni* or *S. japonicum*. Taken together, our experimental results, our *in silico* analysis and the literature concerning schistosome and salmon behavior and ecology (**Supplementary Note** and **Supplementary Table 2**) do not support the view that gene transfer occurred from salmonids to schistosomes or between their ancestors.

The sample history of the expressed sequence tag library 'Adult SjC 7/94' is well documented in the 'note' section of GenBank accession number BU712912. The authors of the database entry mention that 2–3% of the clones contain inserts with homology to salmon DNA. Their phrasing suggests that they considered only the remaining sequences to come from *S. japonicum*. Salmon sperm DNA has traditionally been used as a carrier material in many laboratories. Cross-species and vector contamination would not be surprising and are found in many databases[5]. We hope the present work stimulates re-examination of evolutionary theories concerning Schistosomatidae and Salmonidae based on the initial—and we think erroneous—report of horizontal gene transfer between these clades.

Note: Supplementary information is available on the Nature Genetics website.

AUTHOR CONTRIBUTIONS
C.G. and J.B. designed the experiment and wrote the manuscript. C.G. performed the experimental work and the data analysis.

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The authors declare no competing financial interests.

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Marker papers and data citation

To the Editor:
Thank you for your recent editorial describing an effort, initiated by the International Funders Forum, to develop a robust marker paper procedure that will provide the user community with important information about community resource projects. The concept of marker papers was originally developed at a data release meeting in 2003 (the 'Fort Lauderdale meeting'). As described in the meeting report (http://www.genome.gov/Pages/Research/WellcomeReport0303.pdf) the purpose of a marker paper is to provide information about a community resource project's plans for data release and publication by describing the following information: (i) a statement of the project's purpose; (ii) a short description of the project's experimental design and scope; (iii) a statement about the project's data quality policies; (iv) a description of the project's anticipated initial data analyses to be included in the data producers' first publication, along with the expected timeline for data generation, data release and publication of that first paper; (v) the project's data release plan, as agreed upon by the project participants and its funder(s) (where applicable), including a description of any planned publication moratorium conditions which users of the data would be asked to respect; and (vi) a contact person for the project.

As described in the recent *Nature Genetics* editorial, *Nature Precedings* is a citable archive where marker papers can now be rapidly published. We are writing now to expand upon some of the points made in the editorial.

The US National Institutes of Health has been working with *Nature Precedings* on a pilot effort, with the cooperation of the investigators from the Human Microbiome Project (HMP) Demonstration Projects (http://nihroadmap.nih.gov/hmp/). At present, the HMP marker papers provide information regarding items i–iv and vi above; information about data release plans and publication moratorium dates (v above) is also provided. However, we have not been able to list the entire data set for which the moratorium(a) apply because of technical reasons having to do with the structure of next-generation sequence data sets. We are still working to resolve those issues so that we can provide more complete information regarding item v above.

As a point of clarification, the NIH has not made a policy decision to require marker papers for all NIH-funded projects, as readers might conclude from the statement in the first sentence of the *Nature Genetics* editorial (which actually referred to the public abstracts required by the agencies rather than marker papers). At present, although most NIH-funded community resource projects are encouraged to submit marker papers, few have been published in recent years. Data producers submit, because journals choose to accept, only marker papers containing substantial early data from the project. The electronic, early publication of a concise, citable marker paper in *Nature Precedings* is designed to resolve this problem. We hope that this new approach to making marker papers available will foster an environment where use of data generated by community resource projects can be maximized in a way that respects, credits and does not infringe upon the intellectual interests of those whose creativity and diligence produced the data, as originally envisioned by the participants of the Fort Lauderdale meeting.

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J.P. and J.C. are HMP coordinators.

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