

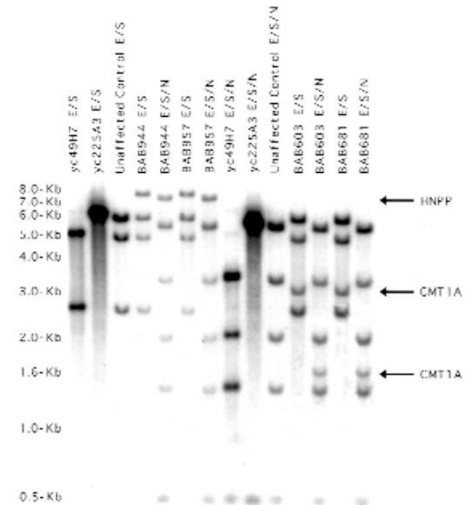
A recombination hotspot responsible for two inherited peripheral neuropathies is located near a *mariner* transposon-like element

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The size of the *EcoRI/SacI/NsiI* HNPP deletion junction fragment reported in our manuscript is actually 7.3 kb, not 7.8 kb, due to the presence of an *NsiI* site located outside of the hotspot region in both *CMT1A*-REPs which changes the size of this fragment. The sizes of the *CMT1A* duplication junction fragments and the region of exchange in both duplication and deletion patients are unaffected by this size discrepancy.

Figure: This Southern blot contains *EcoRI + SacI* digested (E/S) or *EcoRI + SacI + NsiI* digested (E/SN) DNA from YACs spanning the proximal and distal *CMT1A*-REPs (yc49H7 and yc225A3), genomic DNA from HNPP deletion patients (BAB944 and BAB957), genomic DNA from *CMT1A* duplication patients (BAB603 and BAB681) and genomic DNA from an unaffected control individual. The blot was hybridized with the 6.0-kb insert from plasmid pLR6.0 which originates from the distal *CMT1A*-REP and spans the recombination hotspot previously described. Arrows indicate the locations of HNPP deletion and *CMT1A* duplication junction fragments. Note that the 7.8-kb HNPP deletion junction fragments change to 7.3 kb in the triple digest while the sizes for the *CMT1A* duplication fragments remain as previously reported (3.2 kb for E/S and 1.7 kb for E/SN).



Vertebrate genome evolution and the zebrafish gene map

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Nature Genet. **18**, 345–349 (1998).

The name of one of the co-authors, Marc Ekker (Loeb Institute of Medical Research, Ottawa Civic Hospital, 725 Parkdale, Ottawa, Ontario, Canada, K1Y 4E9) was inadvertently omitted from the author list of the manuscript. We apologize for the inconvenience this omission has caused.

Mutations in *GDI1* are responsible for X-linked non-specific mental retardation

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The common polymorphism detected by SSCP analysis in the *GDI* gene was erroneously described as A377C. It is, in fact, T377C.