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Snip-SNPs in the worm genome

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SNPs (single nucleotide polymorphisms) are valuable markers for mapping mutations and human [disease-related genes](#). In the June issue of [Nature Genetics](#), Wicks *et al.* describe a SNP-based strategy for rapid mapping in the *C. elegans* genome (*Nature Genetics* 2001, **28**:160-164). They sequenced the entire genome of the [CB4856 Hawaiian worm isolate](#) and compared it with the standard laboratory wild type strain (Bristol N2). This alignment identified 6,222 potential polymorphisms, more than half of which modify restriction enzyme sites (referred to as 'snip-SNPs'). Such a high-density map of snip-SNPs (about one every 200 kb) allows for rapid mapping of gene mutations using RFLP analysis. To demonstrate the efficiency of such a mapping approach, Wicks *et al.* used their snip-SNP map and [bulked segregant analysis](#) to localize the [dyf-5](#) gene. They claim that the successful mapping could be achieved with 36 PCR reactions within 12 hours of isolating F2 animals from a single cross between CB4856 and N2 strains.

References

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