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^{OA}Open Access paper.



Cover A representation of an unbalanced insertion is shown (left). Linear amplification of sequences at the breakpoint of the insertion and hybridization of the resulting amplicons to an oligonucleotide-based microarray allows for identification of the insertion site at higher resolution than FISH (right). Precise knowledge of the location of the insertion site helps elucidate whether a clinically significant gene has been disrupted. (Cover illustration by Alex Tebbs, Signature Genomics from PerkinElmer; alex.tebbs@perkinelmer.com. [For details, see Neill et al., pp. 535–544.]