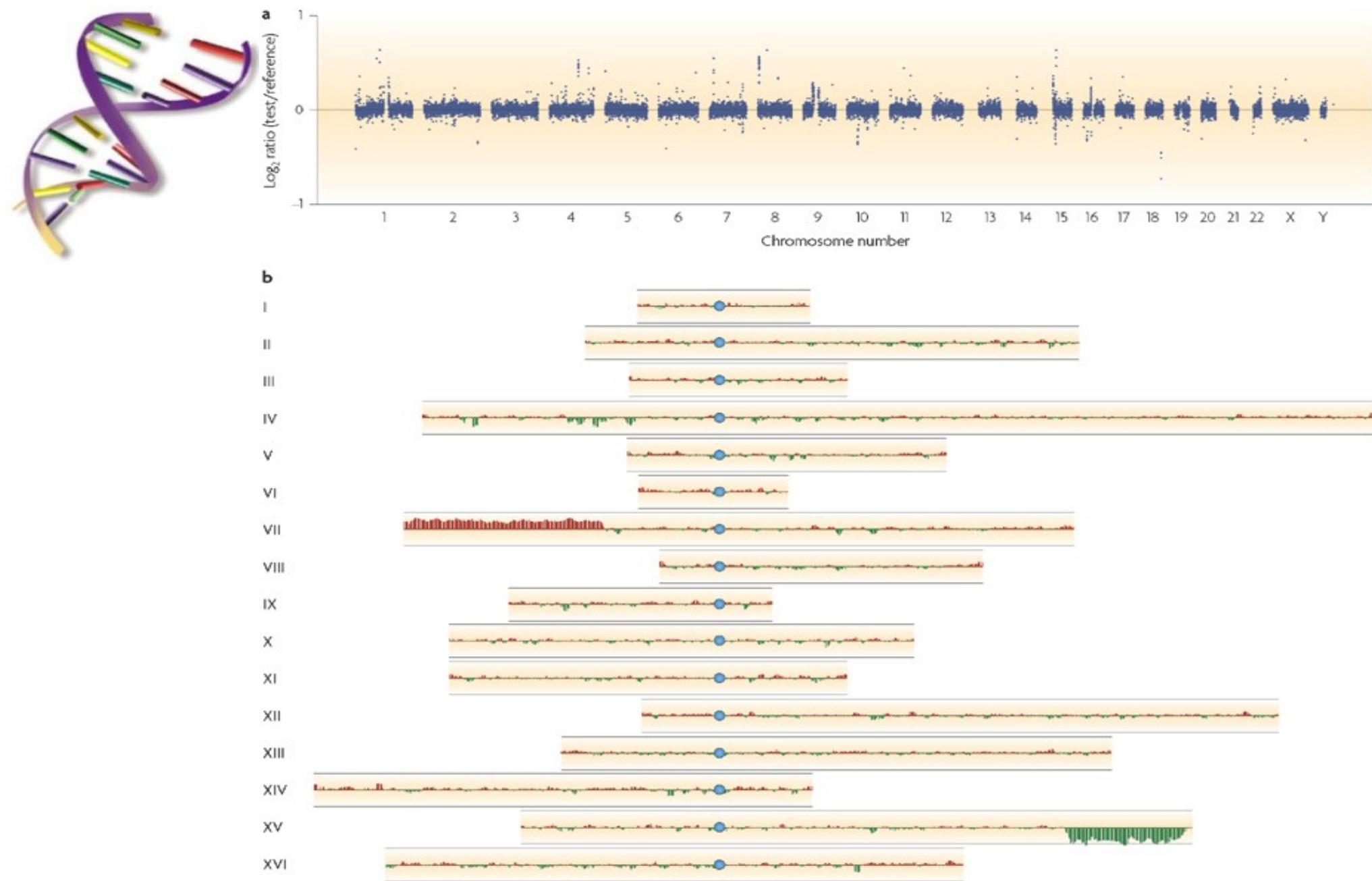


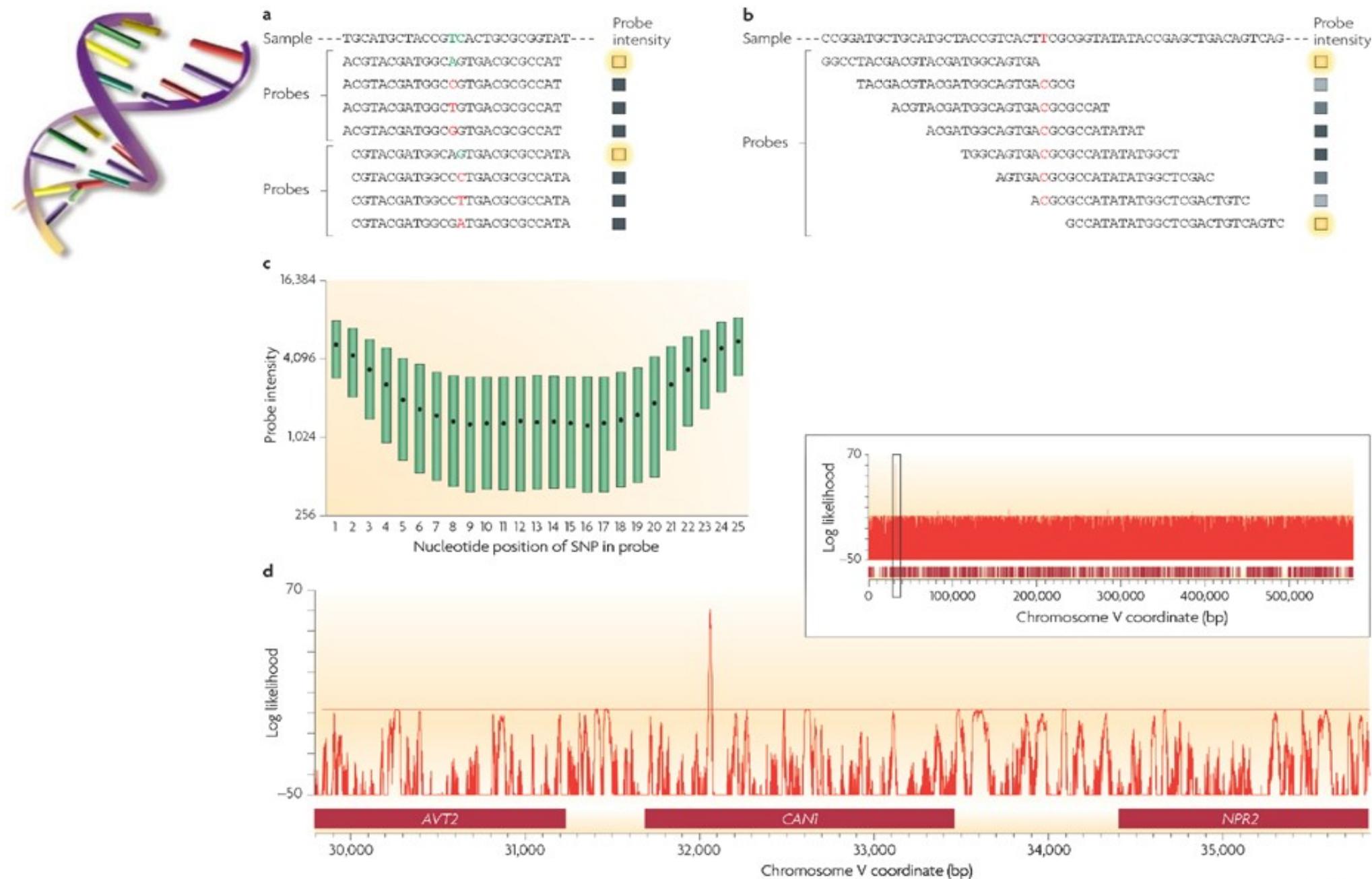


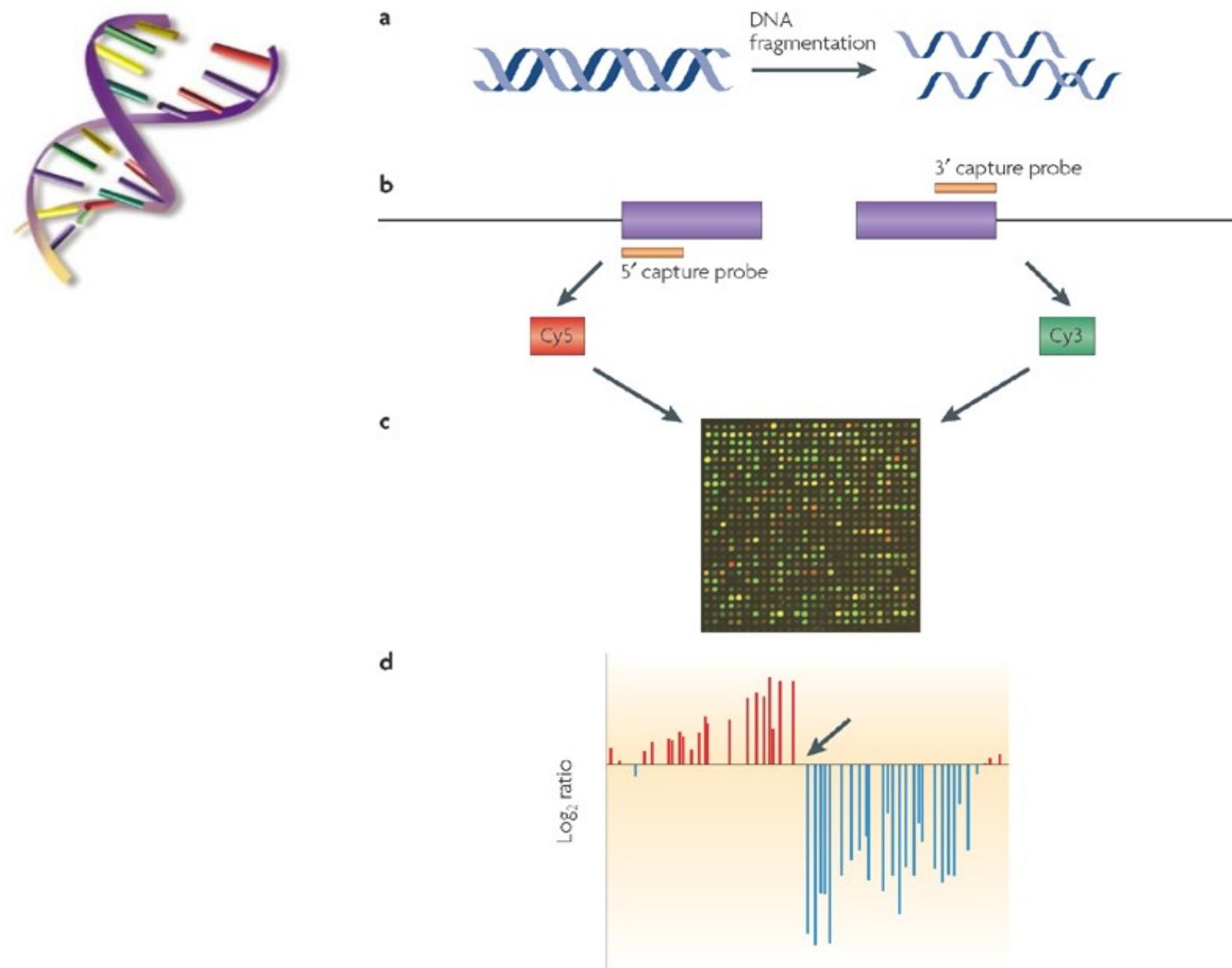
# Comparing whole genomes using DNA microarrays

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**Abstract** | The rapid accumulation of complete genomic sequences offers the opportunity to carry out an analysis of inter- and intra-individual genome variation within a species on a routine basis. Sequencing whole genomes requires resources that are currently beyond those of a single laboratory and therefore it is not a practical approach for resequencing hundreds of individual genomes. DNA microarrays present an alternative way to study differences between closely related genomes. Advances in microarray-based approaches have enabled the main forms of genomic variation (amplifications, deletions, insertions, rearrangements and base-pair changes) to be detected using techniques that are readily performed in individual laboratories using simple experimental approaches.









# Software for analyzing and visualizing microarray data for genome comparisons

Software	Website	Use	Variant class	Examples	Refs
Java TreeView	<a href="http://jtreeview.sourceforge.net">http://jtreeview.sourceforge.net</a>	Visualization	Structural	See FIG. 1	110
Integrated Genome Browser	<a href="http://www.affymetrix.com/support/developer/tools/download_igb.affx">http://www.affymetrix.com/support/developer/tools/download_igb.affx</a>	Visualization	Structural and SNP	See FIG. 2	-
MeV	<a href="http://www.tm4.org/mev.html">http://www.tm4.org/mev.html</a>	Data analysis and visualization	Structural	-	111
Bioconductor	<a href="http://www.bioconductor.org">http://www.bioconductor.org</a>	Data analysis and visualization	Structural and SNP	-	112
SNPScanner	<a href="http://genomics-pubs.princeton.edu/SNPscanner">http://genomics-pubs.princeton.edu/SNPscanner</a>	SNP detection	SNP	See FIG. 2	31