SAPI: A Semi-Automated Polymorphism Identification System

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Single nucleotide polymorphisms (SNPs) are the most frequent form of DNA sequence variation in the human genome. The identification and typing of these variations plays a central role in analysing the relationships between genome structure and function, and in understanding the allelic variation within and among populations.

SAPI is an application that assists biologists in identifying and utilising SNPs. It has been designed specifically as a system to generate, track and manipulate data about SNPs. SAPI's front-end consists of a user-friendly web based system that allows scientists easy access and use. Underlying the system is an oracle database for automatic storage from the application.

SAPI aids the identification of SNPs from in-house sequencing projects using data assembled with Phrap or from public ESTs.

Potential SNPs are identified within a contig and can be displayed in a number of ways such as highlighted on individual trace files or labelled on the contig. SNPs can then be manually annotated as good, bad or unsure based on the traces.

Additional functionality includes the ability to design primers and order these from the in-house oligo ordering system as well as view RFLP sites etc