CodonCode Aligner Version 1.2 Released

CodonCode Corporation has released CodonCode Aligner version 1.2, a new version of its DNA sequence assembly and contig editing software. New in CodonCode Aligner 1.2 is the ability to identify heterozygous point mutations in sequence trace data.

With the new ability to find heterozygous point mutations, CodonCode Aligner offers a complete set of tools for the analysis of heterozygous mutations in sequence traces. Functions to find and analyze heterozygous insertions and deletions have already been part of CodonCode Aligner since version 1.1. CodonCode Aligner's algorithms for detecting heterozygous point mutations evaluate aligned sequence traces for both secondary peaks and the characteristic drop in peak intensities, thereby achieving a higher sensitivity and accuracy compared to simpler algorithms that are still widely used.

The new functions for mutation detection were showcased by CodonCode Corporation at the Annual Clinical Genetics Meeting 2004, held by the American College of Medical Genetics in Orlando, Florida, from March 4-7, 2004. The new mutation detection functions in CodonCode Aligner were very well received by scientists and medical researchers from leading laboratories.

CodonCode Aligner is an easy-to-learn, easy-to-use program for sequence assembly, contig editing, and mutation detection. Aligner provides support for base calling, quality-based end clipping, vector trimming, sequence assembly and alignments, and fast navigation with user-definable criteria. CodonCode Aligner is available for Mac OS X and Microsoft Windows. Free demo and time-limited trial versions are available at www.codoncode.com/aligner/.

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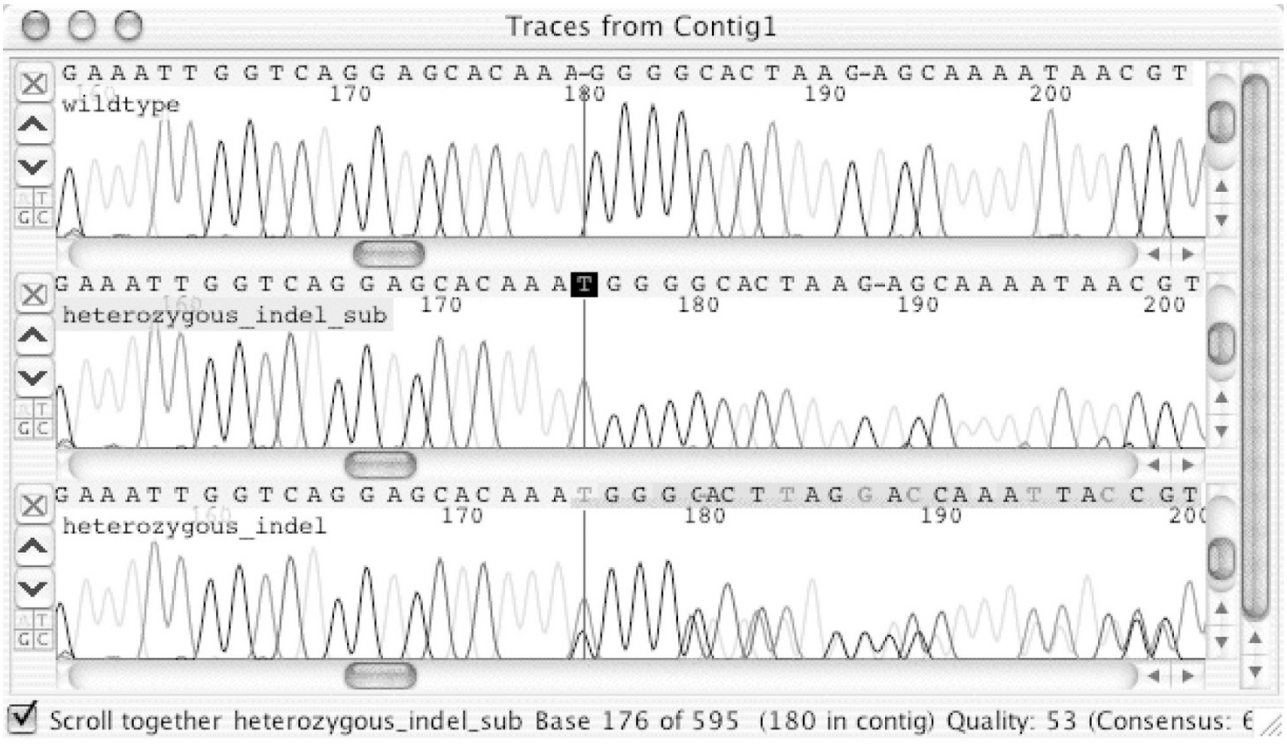

Example of analyzing a heterozygous insertion with CodonCode Aligner. By subtracting the "wild type" trace (at the top) from the heterozygous trace (in the middle), the heterozygous one base insertion becomes clearly visible.

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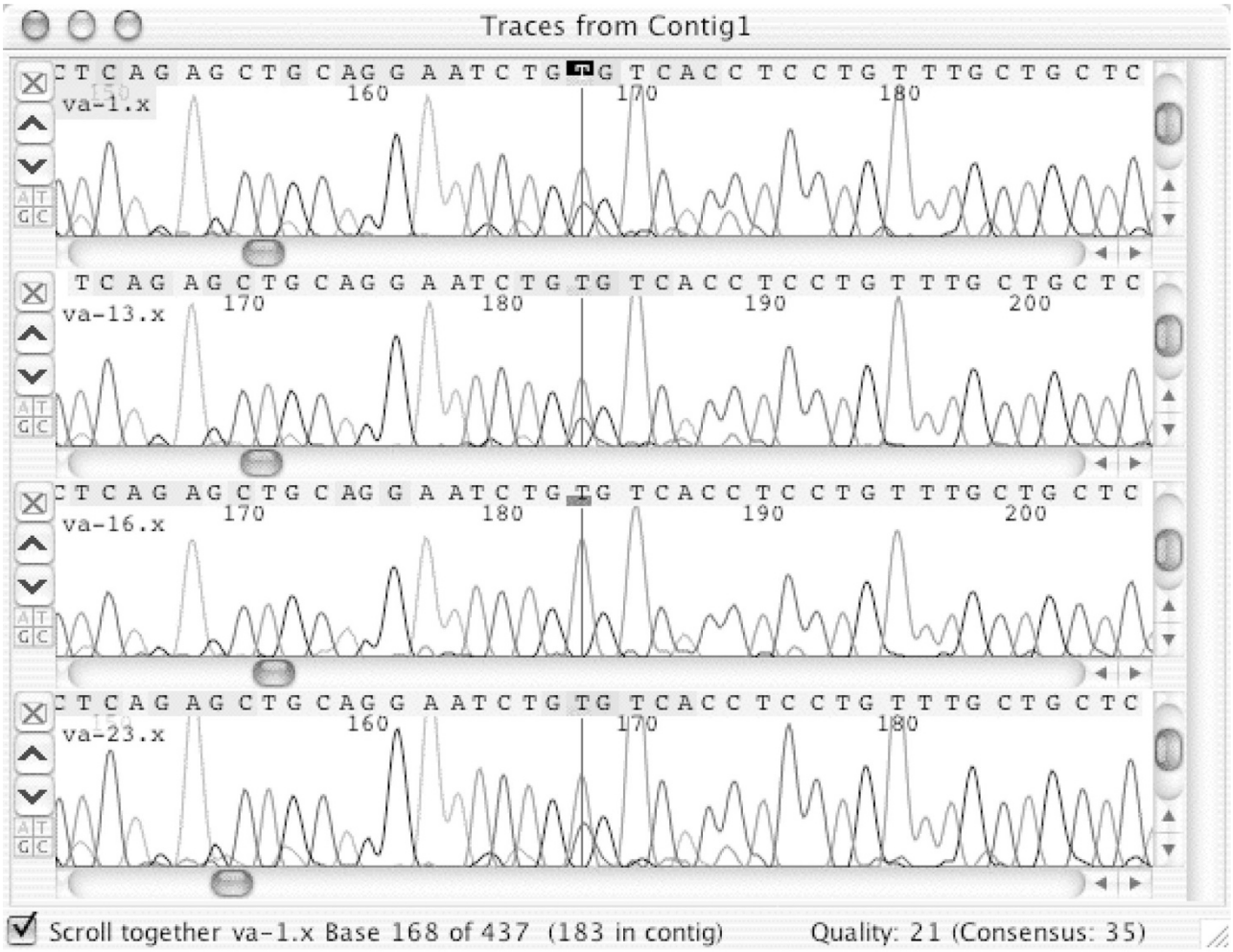

Example of heterozygous point mutations identified with CodonCode Aligner. Pink boxes at the cursor position indicate heterozygousC-T base calls, the blue box indicates a homozygous T.

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