

A hand holding a black marker against a blue background. The hand is positioned vertically, with the marker held between the thumb and index finger. The background is a gradient of blue, with a darker blue at the top and a lighter blue at the bottom. The text is overlaid on the right side of the image.

RIPSEQ
MIXED

Detect
InDel / Copy Variants
directly from your
sequencing
chromatograms

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RipSeq® Mixed is an online application able to read and interpret mixed sequencing chromatograms through the use of advanced algorithms. The RipSeq Mixed module can automatically handle and identify **InDel / Copy Variants** in DNA sequences obtained from pure bacterial isolates.

Almost all bacterial species have more than one copy of the 16S rRNA gene. They are placed in different parts of the genome, and are not necessarily 100% identical. Because they are all amplified simultaneously in the 16S PCR, variations in base compositions will create ambiguity in the resulting chromatograms.

If a proportion of the 16S rRNA gene copies have an insertion or a deletion compared to the rest of the gene copies, this will create ambiguity not only in that

particular position, but in the entire remaining chromatogram. This phenomenon is known as an indel, and creates a false impression of a mixed sample. The complexity of the chromatogram might be further increased because an indel copy variant often contains more than a single insertion/deletion.

With RipSeq Mixed, you can identify indel copy variants directly after 16S DNA sequencing of your samples, whether the sample is from pure culture or clinical material. Below you will find a typical chromatogram of an indel copy variant (Figure 1). RipSeq Mixed is capable of identifying the bacteria (Figure 2) as well as presenting a detailed view of the basecalling and the exact position of the indel occurrence (Figure 3). The RipSeq Mixed module is easily accessible, being based on a user-friendly and easily understood web-based interface.

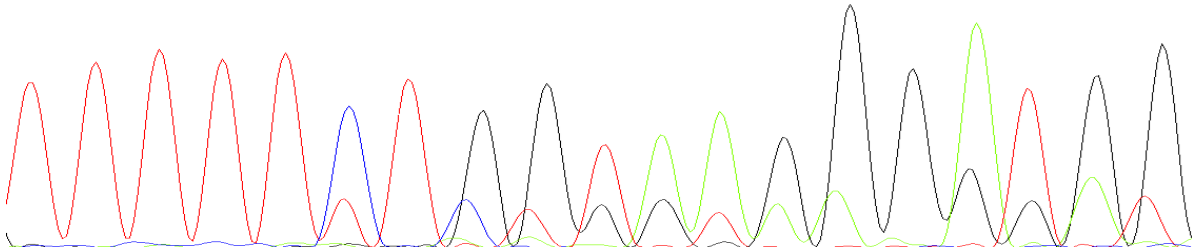


Figure 1: A typical sequencing chromatogram containing an indel copy variant.

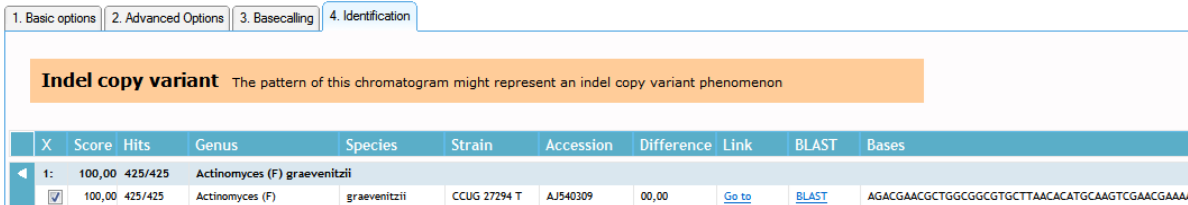


Figure 2: Presentation of the identified bacteria in RipSeq Mixed. copy variant.

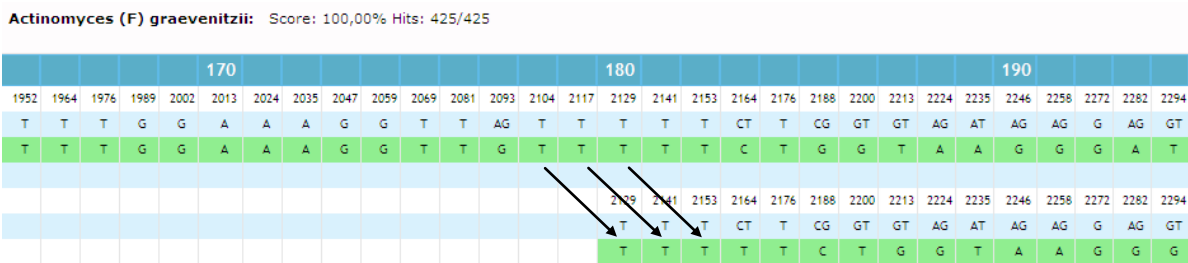


Figure 3: Visual presentation showing the position of the indel that causes the Copy Variant (2 positions offset).

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