

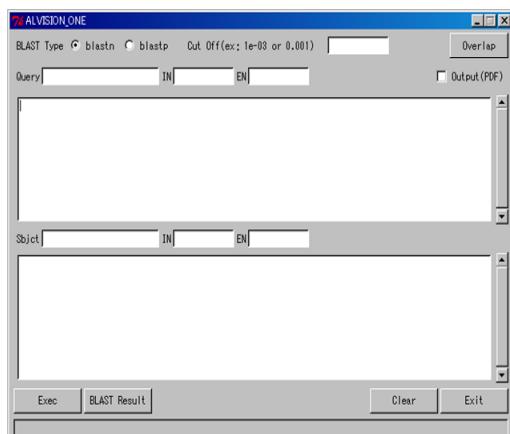
ALVISION

Global Viewer of Local Alignments

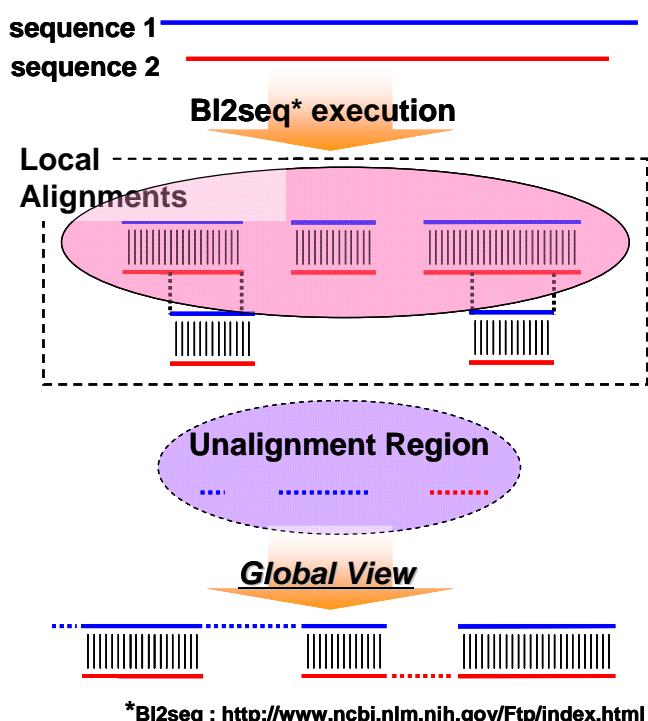
A newly developed sequence level checking tool, ALVISION, aligns two cDNA sequences that are splicing variants to each other, allowing large gaps. Figure 1 shows an overview of ALVISION. For given two DNAs or two amino acids sequences, ALVISION executes BLAST (bl2seq). After removing redundancy based on a simple rule from local alignments obtained by a BLAST calculation, a global alignment is built by assembling those local alignments. These graphical and sequence level checking tools help us to find the splicing variants and clone problems efficiently.

Jun-ichi Yamamoto, Naoto Hatano, Kenji Araki, Hiroshi Makita, Kouichi Kimura, Ai Wakamatsu, Shizuko Ishii, Tetsuo Nishikawa, Takao Isogai.
A cDNA Evaluation System for Highly Efficient Sequencing of Splicing Variant cDNAs.
Genome Informatics, 14: 430-431 (2003).

Main Window of ALVISION



Overview of ALVISION



*BL2seq : <http://www.ncbi.nlm.nih.gov/Ftp/index.html>

Figure 1. About ALVISION

An example of ALVISION analysis are shown in Figure 2.

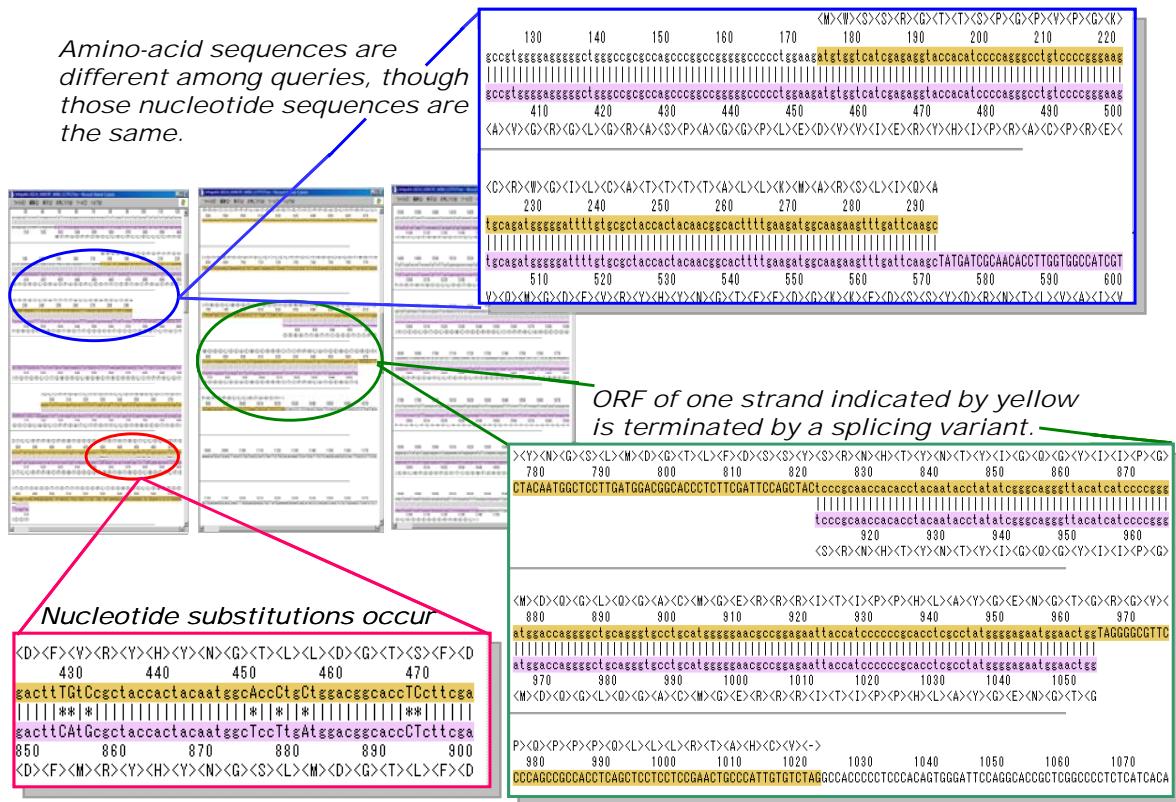


Figure 2. An Example of ALVISION Analysis