Overview of the cDNA evaluation system

cDNA sequences

cDNA evaluation system
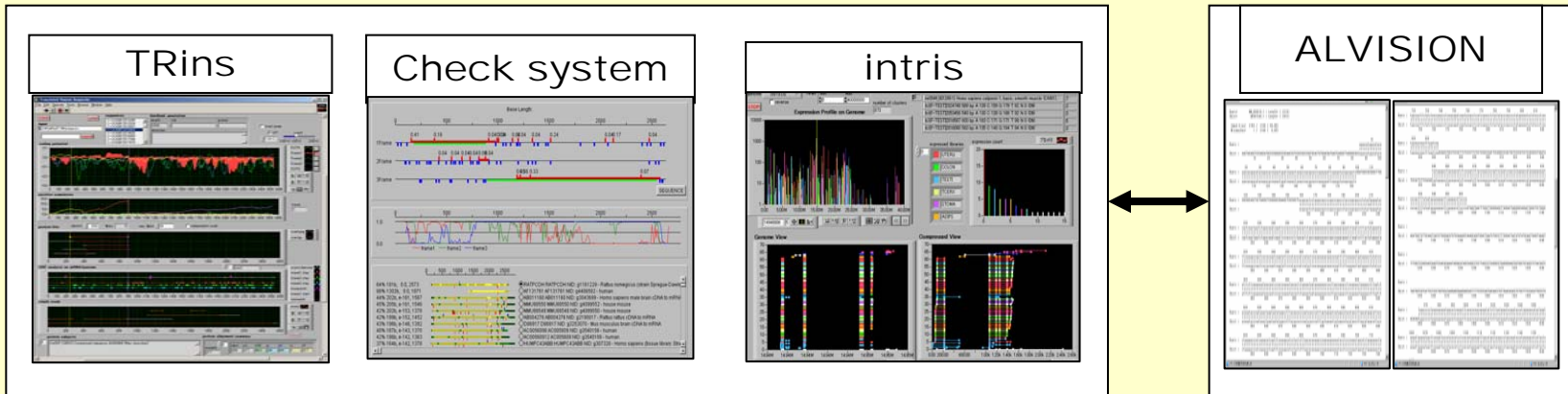
Check List

●**cDNA reliability check**
    ·**Immature, Frame-shift, Truncate, Amino-acid substitution**
●**Splicing variants detection**
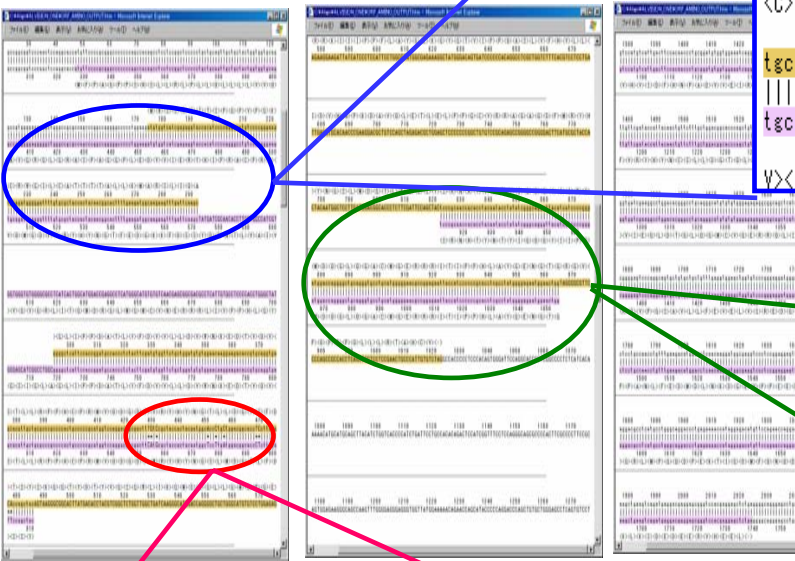●**Transcription start site check**

Graphical check

Sequence level check

| TRins |
| Check system |
| intris |

ALVISION

Judgment where the sequence should be extended

Amino-acid sequences are different among queries, though those nucleotide sequences are the same.

<M><W><S><S><R><G><T><T><S><P><G><P><Y><P><G><K>
```
        130      140      150      160      170      180      190      200      210      220
gccgtgggggaggggggctggsgccgcgccagcccggccgggggcccccctggaaatgtggtcatcgagaggtaccacatcccaggggcctgtccccgggaag
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
gccgtgggggaggggggctggsgccgcgccagcccggccgggggcccccctggaagatgtggtcatcgagaggtaccacatcccaggggcctgtccccgggaag
        410      420      430      440      450      460      470      480      490      500
```
<A><V><G><R><G><L><G><R><A><S><P><A><G><G><P><L><E><D><V><V><I><E><R><Y><H><I><P><R><A><C><P><R><E><

<C><R><W><G><I><L><C><A><T><T><T><T><A><L><L><K><M><A><R><S><L><I><Q><A
```
        230      240      250      260      270      280      290
tgcagatgggggattttgtgcgctaccactacaacggcacttttgaagatggcaagaagtttgattcaagc
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
tgcagatgggggattttgtgcgctaccactacaacggcacttttgaagatggcaagaagtttgattcaagcTATGATCGCAACACCTTGGTGGCCATCGT
        510      520      530      540      550      560      570      580      590      600
```
Y><Q><M><G><D><F><V><R><Y><H><Y><N><G><T><F><E><D><G><K><K><F><D><S><S><Y><D><R><N><T><L><V><A><I><V

ORF of one strand indicated by yellow is terminated by a splicing variant.

>><Y><N><G><S><L><M><D><G><T><L><F><D><S><S><Y><S><R><N><H><T><Y><N><T><Y><I><G><Q><G><Y><I><I><P><G>
```
        780      790      800      810      820      830      840      850      860      870
CTACAATGGCTCCTTGATGGACGGCACCCTCTTCGATTCCAGCTACtcccgcaaccacacctacaatacctatatcgggcagggttacatcatcccgggg
                                                ||||||||||||||||||||||||||||||||||||||||||||||||
                                                tcccgcaaccacacctacaatacctatatcgggcagggttacatcatcccgggg
                                                920      930      940      950      960
```
<S><R><N><H><T><Y><N><T><Y><I><G><Q><G><Y><I><I><P><G>

<M><D><Q><G><L><Q><G><A><C><M><G><E><R><R><R><I><T><I><P><P><H><L><A><Y><G><E><N><G><T><G><R><G><V><
```
        880      890      900      910      920      930      940      950      960      970
atggaccaggggctgcagggtgcctgcatggggggaacgccggagaattaccatcccccccgcacctcgcctatggggagaatggaactggTAGGGGCGTTC
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
atggaccaggggctgcagggtgcctgcatggggggaacgccggagaattaccatcccccccgcacctcgcctatggggagaatggaactgg
        970      980      990      1000     1010     1020     1030     1040     1050
```
<M><D><Q><G><L><Q><G><A><C><M><G><E><R><R><R><I><T><I><P><P><H><L><A><Y><G><E><N><G><T><G

P><Q><P><P><P><Q><L><L><L><R><T><A><H><C><V><<->
```
        980      990      1000     1010     1020     1030     1040     1050     1060     1070
CCCAGCCGCCACCTCAGCTCCTCCTCCGAACTGCCCATTGTGTCTAGgcccaccccctcccacagtgggattccaggcaccgctcggcccctctcatcaca
```

Nucleotide substitutions occur

<D><F><V><R><Y><H><Y><N><G><T><L><L><D><G><T><S><F><D
```
        430      440      450      460      470
gacttTGtCcgctaccactacaatggcAccCtgCtggacggcaccTCcttcga
        |||||**|*||*||||||||||||||||||*||*||*|||||||||**||||||
gacttCAtGcgctaccactacaatggcTccTtgAtggacggcaccCTcttcga
        850      860      870      880      890      900
```
<D><F><M><R><Y><H><Y><N><G><S><L><M><D><G><T><L><F><D

An Example of ALVISION Analysis