>Seq1

GATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq2 (Del1)

GATCAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq3 (Del2)

GATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGATCTGATACTCTAGATCTAGCTATA

>Seq4 (Ins1)

GATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTCAGATCTAGCTATA

>Seq5 (Ins2)

GATACAGACTTTCGAGGAGAGATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq6 (InDel1)

GATACAGACTTTCAGGAAGGATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq7 (InDel2)

GATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGCATCTGATACTCTAGATCTAGCTATA

>Seq8 (Circ1)

TCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATAGATACAGACTTTCGAGGAGGA

>Seq9 (Circ2)

TCTCGATACTCTAGATCTAGCTATAGATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGA

>Seq10 (Long5Ext)

AGCTAGCACTCGATCGAGCCGATGCATCAGAAGCTAGCTCGCTAAGCTCAGACTATAGCTAGGATACAGACT

>Seq11 (Short5Ext)

CTCTAACTAGCATATAGCTCGAGAGAGATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTCTCTAGAGA

>Seq12 (Long3Ext)

TACTCTAGATCTAGCTATAAACTAACTCATGGACTACGATCGGCTCGCCCCCTAAATCGCTAATCGATTGAT

>Seq13 (Short3Ext)

CTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATAATATTTCGTTAGGGGATCGCTATAG

>Seq14 (LargeDel)

GATACAGACTTTCGCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq15 (2LargeDel)

GATACAGACTCTCTATATCGGCTCTCTCTAGAGATCATCTAGCTATA

>Seq16 (LargeIns)

GATACAGACTTTCGAGGAGGACATCGATATTCGATCATCTCTATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq17 (2LargeIns)

GATACAGACTTTCGAGGAGGACTGCTAGCATAGCATCATCTCTATATCGGCTCTCTCTAGACAAAATTAGGGGGATCTCGATACTCTAGATCTAGCTATA

>Seq18 (LargeInDel1)

GATACAGACTTTCGAGGTTTTCCTAGAGAATATCGGCTCTCTCTAGAGATCTCGATACTCTAGATCTAGCTATA

>Seq18 (LargeInDel2)

GATACAGACTTTCGAGGAGGATCTCTATATCGGCTCTACTCGCAGATATTTTCAAAAGCTATATTCTAGCTATA

>Seq19 (Random1)

GGGATTTTTCAATATCGGCTCTATATAATATCGCGAGAGATCTCAGATGGGGTATTTTAACCCAAGAGCTCCCA

>Seq20 (Random2)

TTATATATAAAGCACCCCTAGGGAAATATCATGAGAGATCCCTATGATCCCTACCCTAAAAGGATCTATCCTACG

Sequencing reads alignment mode:

Assumes that the template sequence is identical and that differences are the result of read errors or differing read windows.

Algo:

1. Slide one against the other, scoring each round. Retain the maximum scoring match (or multiple?)

* Scoring:
  + Goal: a perfect end match should override a spotty but lengthier match.
    - What about a lengthy deletion? Circular matching?
  + 1 point for every matched nt.
  + 1 extra point for every matched nucleotide between it and a gap
  + Gap penalty will be assessed relative to the length of the match+gaps length
* Example:

ACGTCGTGTACG

TGTACGGAGATC Score = 1+6+2+5+3+4+4+3+5+2+6+1=7\*6=42

* + So a perfect match will have a score = n(n+1)

ACGTCGTGTAC-G

TGTACCGAGATC Score = 6\*5+1=31