>sequence1 - no errors

CATACTACGATCAGATCGACTGACTCGTACATGCAGTGATGTACGAATGCATGCATCGATCGATCGAAATGATAGCATGACTCAGACTGATCAGATCGA

>sequence2 - two point errors apart (25:T>A, 65:C>T)

CATACTACGATCAGATCGACTGACaCGTACATGCAGTGATGTACGAATGCATGCATCGATCGATtGAAATGATAGCATGACTCAGACTGATCAGATCGA

>sequence3 - one insertion error (34:A)

CATACTACGATCAGATCGACTGACTCGTACATGaCAGTGATGTACGAATGCATGCATCGATCGATCGAAATGATAGCATGACTCAGACTGATCAGATCGA

>sequence4 - one deletion error (34:C)

CATACTACGATCAGATCGACTGACTCGTACATG|AGTGATGTACGAATGCATGCATCGATCGATCGAAATGATAGCATGACTCAGACTGATCAGATCGA

>sequence5 - one homopolymer insertion error (69:A)

CATACTACGATCAGATCGACTGACTCGTACATGCAGTGATGTACGAATGCATGCATCGATCGATCGAAaATGATAGCATGACTCAGACTGATCAGATCGA

>sequence6 - one homopolymer deletion error (68:A)

CATACTACGATCAGATCGACTGACTCGTACATGCAGTGATGTACGAATGCATGCATCGATCGATCG|AATGATAGCATGACTCAGACTGATCAGATCGA

>sequence7 - two point errors overlapping (25:T>A, 35:C>T)

CATACTACGATCAGATCGACTGACaCGTACATGCtGTGATGTACGAATGCATGCATCGATCGATCGAAATGATAGCATGACTCAGACTGATCAGATCGA

>sequence8 - one point error masked by other region (25:T>A, 35:C>T)

CATACTACGATCAGATCGACTGACTCGTACATGCAGTGATGTACGAATGCATGCATCGATCGATCGAAATGcTAGCATGACTCAGACTGATCAGATCGA

>sequence9 - one point error masked by same kmers elsewhere (50:C>T)

CATACTACGATCAGATCGACTGACTCGTACATGCAGTGATGTACGAATGtATGCATCGATCGATCGAAATGATAGCATGACTCAGACTGATCAGATCGA

A = errors

A = affected kmers (missing)

A = affected kmers (edge missing)