

A) ...TGAGACGAACTGATCGGAAGAGCACA
 ...TCTTAGTGCAAAGATCGGAAGAGCGT

TGAG - template sequence
 GATC - adapter sequence
 GATC - adapter contamination
 GA-TC - gap (indel)
 GAAGC - mismatch
 ACGCT - trimmed sequence

B) GATCGGAA-GAGCACACGTCTGAACTCCAGTCAC
 ...TGAGACGAACTGAGCGGAAAGAGCACA
 AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
 ...TCTTAGTGCAAAGATCGG-AGACCGT
 TTGCACTAAGATTCGTGAGACGAACTGATCGGAAGAGCACA
 ACGCTCTTCCGATCTTTGCACTAAGAACGT CAGACGAACT

C) 1/5 bp match, adapters found in overhangs (poor match)
 TTGCACTAAGATTCGTGAGACGAACTGATCGGAAGAGCACA
 ACGCTCTTCCGATCTTTGCACTAAGAACGT CAGACGAACT

9/34 bp match, adapters not found in overhangs (poor match)
 TTGCACTAAGATTCGTGAGACGAACTGATCGGAAGAGCACA
 ACGCTCTTCCGATCTTTGCACTAAGAACGT CAGACGAACT

23/25 bp match, adapters found in overhangs (best match)
 TTGCACTAAGATTCGTGAGACGAACTGATCGGAAGAGCACA
 ACGCTCTTCCGATCTTTGCACTAAGAACGT CAGACGAACT

D) GATCGGAAGAGCACACGTCTGAACTCCAGTCAC
~~GATCGGAAGAGCTCACGTCTGAAGGCCAGTCACAAAAAAAAACNNNANC...~~
~~AGATCGGAAGAGCGTC-TGTAGGGATAGAGTGTAAAAAAAAAANNNTC...~~
 AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

Discarded Read Pair