Sanger sequencing electropherogram alignment (two sequence reads compared across positions 1–805).

```
Position 1:
Top:    T CG C  AGT CG TGCTA TG G  AACT GA G C ATG AGAT GA GG AGG ATCA CAGG TAGG TT GAGG AG AAG AGGA TCA CACT TG CCCCT CTATGG TAATAA GCCT C
Bottom: T CG A  AGT AG AGCCA TG G  AACT GC G C ACG ACAT TA GTTGAAGCT CATTC AGGTT GAGG AAA AAG AGGA TA AATTG TG CCC CRTGRKRA TTCACGA GTGTC

Position 100:
Top:    G GATTCTCTC TGGGACT GG GTGATGCACA TTTGCTCCAC AAC TCGCTCCAT CATC TTGATGTCA GTTTCG GTG AAGTT CTCCC CCTT GGTGGT GGTGGTG
Bottom: G CGAGCT CACGACYAGAGG TMGCSGCAGA TTAGAAGWYT GAT TTMWTGGGT CTTC TSTTGGTCS MSGAAA GAGAGGRS KTCCC CCAAGTCTAG GGGCGASW

Position 200:
Top:    ACTG TGTGT TGCTTGACTGTG ATGTT GACAC AGT CATGCA CAAAGGTA ATC TGGTTATTATACT GATC CACTGGCCTGTAGTACACTTGG TTGGGGTAACG
Bottom: GCTG SCCGT RATMAGAKTGCG ATGMS CTCCC KTT CTCCWT CAYYTCCG TTCTGGTTATTATACT GATC CACTGGCCTGTAGTACACTTGG TTGGGGTAACG

Position 301:
Top:    GT ACA TG TTTTCACG ATAGTAACG GTCCTCA TAGTCATTGCC AAAATGTATAA GAGGCCTGCTCATGGCACTTCCCAGCATGTAGCCACCGAGG CCCCCTA
Bottom: GT ACA TG TTTTCACG ATAGTAACG GTCCTCA TAGTCATTGCC AAAATGTATAA GAGGCCTGCTCATGGCACTTCCCAGCATGTAGCCACCGAGG CCCCCTA

Position 402:
Top:    CCACTGC TCCAGCTG CAGCAGCTC CTGCCACATGCTTCATG TTGGTTTTTGGTTTACTGGGCTTGTTCCACTGACTGTGGGTACCACCTTGACCCCAGCCT
Bottom: CCACTGC TCCAGCTG CAGCAGCTC CTGCCACATGCTTCATG TTGGTTTTTGGATTACTGGGCTTGTTCCACTGACTGTGGGTACCACCTTGACCCCAGCCT

Position 503:
Top:    CC ACCACCATG TGGCTGTCCCCAGCCACCACCATGGGGCTGACCCCAGCCACCTCCATGAGGTTGGCCCCAGCCACCTCCATGGGGCTGACCCCAGCCAC
Bottom: CC ACCACCATG TGGCTGTCCCCAGCCACCACCATGGGGCTGACCCCAGCCACCTCCATGAGGTTGGCCCCAGCCACCTCCATGGGGCTGACCCCAGCCAC

Position 603:
Top:    CCCCTCCCTGAGGTGGATAGCGGTTGCCTCCAGGACTTCCCTGTCCCGGGTATCGGCTCCCCCCAGTGTTCCATCCTCCTCCAAGTTTTGGTCGCTTC
Bottom: CCCCTCCCTGAGGTGGATAGCGGTTGCCTCCAGGACTTCCCTGTCCCGGGTATCGGCTCCCCCCAGTGTTCCATCCTCCTCCACGTTTTGGTCGCTTC

Position 701:
Top:    TTGCAGAGGCCGACGTCACTCCACATGGTCACTAAGAGAACTAGGATCCAGCTGCCTATGTGGCATTGCACCATGATGACTTATCTGCAAAATAAATGGGG
Bottom: TTGCAGAGGCCGACGTCACTCCACATGGACACTAAGAGAACTAGGATCCAGTTGCCTATGTGGCGTTGCACCATAATGACTTATTTGCAAAATAAATGGGG

Position 802:
Top:    GG TG TA
Bottom: GG TA TA
```