1

N NN N NAN TTN NA A GCTTGTATTAA GTAGAGTAGCTTACATCGACCTGAATAGCATTGTCTTTCCCAAAAATTTTAAATCTCTGACAATGA

91

AACGTGTAAGTAAAATCAAGTGGTGGAACATCGAGGAAAATATACTAAAGGAACTAAAAGTCGATAAGAGAACTTTTAAATCGTTGTACATAAAGGAAGA

191

TGATAGTAAATTCACAAAATTTTTTAATTTACGACACACAAGAATAAAAGAGCTTGACAAAAGTGAAATTAATCAAATAACATACCTTCGATGTCAAGCAAT

293

AGTTTGGCTATCTTTTCGGACTTTGAACCATATCAAGCTACAAAATGTATCTGAAGTTTTTAACAATATCATCGTACCTAGAGCATTGTTCGATAGTAAACG

395

AGTAGAGATTTATCGATGTGAAAAAATCTCTCAGGTTTTGGTAATATAAAAATGTGGAAAACCGGCGGTATTTTAGAATTCGAGCTCGTTTTCGACACTGGA

CTF13 Stop codon

497

TGGCGGCGTTAGTATCGAATCGACAGCAGTATAGCGACCAGCATTCACATACGATTGACGCATGATATTACTTTCTGCGCACTTAACTTCGCATCTGGGCA

598

GATGATGTCGAGGCGAAAAAAAATATAAATCACGCTAACATTTGATTAAAATAGAACAACTACAATATAAAAAAACTATACAAATGACAAGTTCTTGAAAA

699

NNNNAATCTNTTTTATTGTCNGNTACTGATTTANAAAAACTCATCGAGCNTCGAANGANNNNNGAATTGTGCNNNNNANNNNNTAAANANNNNNNNNNN

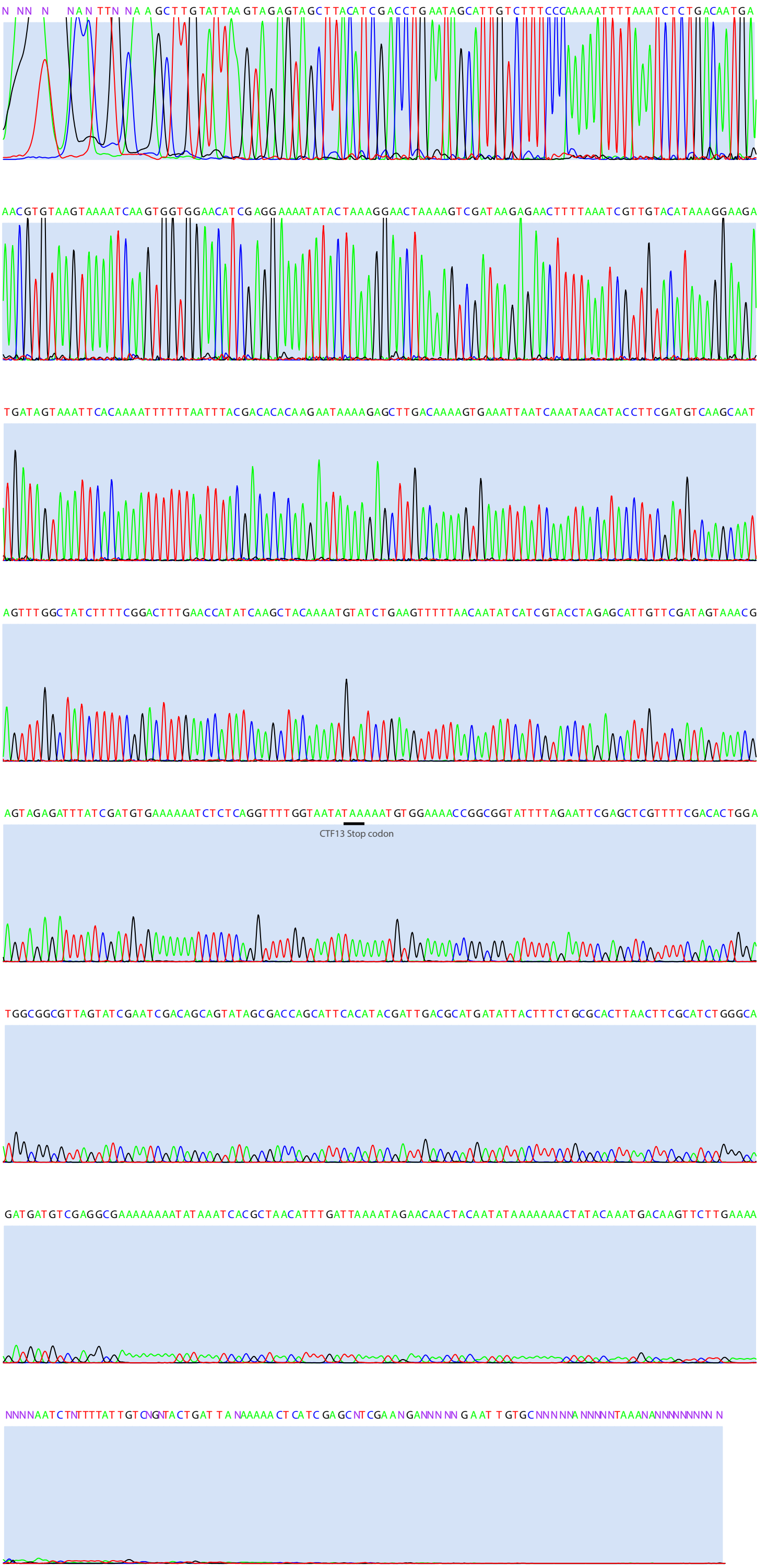

Figure S5. Sanger sequence read for the complete *CTF13* 3′ RACE PCR product in the *sno1Δ* strain. Full length *CTF13* mRNA 3′ RACE Sanger sequencing read from the *sno1Δ* strain. Highlighted TAA denotes the *CTF13* ORF stop codon. Purple "N" denote poor quality base calls.