CLAIMS

1. A recombinant altered DNA polymerase comprising an amino acid sequence that is at least 90% identical to the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the DNA polymerase comprises at least one amino acid substitution mutation at the following positions:

a) the position functionally equivalent to Thr349 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the substitution mutation is a mutation to Lys, Asn or Ser;

b) the position functionally equivalent to Ala281 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the substitution mutation is a mutation to Phe;

c) the position functionally equivalent to Phe283 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the substitution mutation is a mutation to Ser;

d) the position functionally equivalent to Trp397 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the substitution mutation is a mutation to Cys; and

e) the position functionally equivalent to His633 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the substitution mutation is a mutation to Thr.

2. The recombinant DNA polymerase of claim 1, wherein the polymerase has an amino acid substitution mutation at only one of the positions (a) to (e).

3. The polymerase of claim 1, wherein the polymerase comprises substitution mutations at at least two, at at least three, at at least four, or at five of the substitution mutations at each of the positions (a) to (e).

4. The polymerase of claims 1 to 3, wherein the polymerase comprises the substitution mutation at the position functionally equivalent to Thr349, wherein the substitution at the position functionally equivalent to Thr349 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Lys, Asn or Ser, and

wherein the further comprises one or more amino acid substitution mutations at positions functionally equivalent to amino acids Met129, Asp141, Glu143, Cys223, Leu408, Tyr409, Pro410, Ala485, Tyr497, Arg247, Glu599, and His633 in the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein:

(f) the substitution mutation at the position functionally equivalent to Met129 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ala; and/or

(g) the substitution mutation at the position functionally equivalent to Asp141 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ala; and/or

(h) the substitution mutation at the position functionally equivalent to Glu143 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ala; and/or

(i) the substitution mutation at the position functionally equivalent to Cys223 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ser; and/or

(j) the substitution mutation at the position functionally equivalent to Leu408 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ala; and/or

(k) the substitution mutation at the position functionally equivalent to Tyr409 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ala; and/or

(l) the substitution mutation at the position functionally equivalent to Pro410 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Ile; and/or

(m) the substitution mutation at the position functionally equivalent to Ala485 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Val; and/or

(n) the substitution mutation at the position functionally equivalent to Tyr497 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Gly; and/or

(o) the substitution mutation at the position functionally equivalent to Arg247 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Tyr; and/or

(p) the substitution mutation at the position functionally equivalent to Glu599 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Asp; and/or

(q) the substitution mutation at the position functionally equivalent to His633 of the 9°N DNA polymerase amino acid sequence SEQ ID NO:1 is a mutation to Gly.

5. A DNA polymerase comprising the amino acid sequence of any one of SEQ ID NOs:9-11 and 13 to 16.