# CLAIMS

What is claimed is:

1. A recombinant DNA polymerase comprising an amino acid sequence that is at least 80% identical to the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the recombinant DNA polymerase comprises an amino acid substitution mutation at a position functionally equivalent to Tyr497 and at least one amino acid substitution mutation at a position functionally equivalent to Phe152, Val278, Met329, Val471, Thr514, Leu631, or Glu734 in the 9°N DNA polymerase amino acid sequence, wherein the amino acid substitution mutation at a position functionally equivalent to Tyr497 comprises a mutation to Gly, Ile, Leu, Met, Pro, Val, Ser, Asn, Gln, or Thr.

2. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Tyr497 comprises a mutation to Gly.

3. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Phe152 comprises a mutation to a non-polar, hydrophobic, or uncharged amino acid.

4. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Phe152 comprises a mutation to Gly.

5. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Val278 comprises a mutation to a non-polar or hydrophobic amino acid.

6. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Val278 comprises a mutation to Leu.

7. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Met329 comprises a mutation to a polar amino acid.

8. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Met329 comprises a mutation to His.

9. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Val471 comprises a mutation to a polar or uncharged amino acid.

10. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Val471 comprises a mutation to Ser.

11. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Thr514 comprises a mutation to a non-polar or hydrophobic amino acid.

12. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Thr514 comprises a mutation to Ala.

13. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Leu631 comprises a mutation to a non-polar or hydrophobic amino acid.

14. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Leu631 comprises a mutation to Met.

15. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Glu734 comprises a mutation to a polar amino acid.

16. The polymerase of claim 1, wherein the substitution mutation at the position functionally equivalent to Glu734 comprises a mutation to Arg.

17. The polymerase of claim 1, wherein the polymerase comprises at least two amino acid substitution mutations at positions functionally equivalent to an amino acid selected from Phe152, Val278, Met329, Val471, Thr514, Leu631, and Glu734 in the 9°N DNA polymerase amino acid sequence.

18. The polymerase of claim 1, wherein the polymerase further comprises amino acid substitution mutations at positions functionally equivalent to amino acids Met129, Asp141, Glu143, Cys223, Leu408, Tyr409, Pro410, and Ala485 in the 9°N DNA polymerase amino acid sequence.

19. A recombinant DNA polymerase comprising an amino acid sequence that is at least 80% identical to the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the recombinant DNA polymerase comprises an amino acid substitution mutation at position functionally equivalent to Tyr497 and at least one amino acid substitution mutation at a position functionally equivalent to Lys620 or Val661 in the 9°N DNA polymerase amino acid sequence, wherein the amino acid substitution mutation at a position functionally equivalent to Tyr497 comprises a mutation to Gly, Ile, Leu, Met, Pro, Val, Ser, Asn, Gln, or Thr.

20. The polymerase of claim 19, wherein the substitution mutation at the position functionally equivalent to Lys620 comprises a mutation to a polar amino acid.

21. The polymerase of claim 19, wherein the substitution mutation at the position functionally equivalent to Lys620 comprises a mutation to Arg.

22. The polymerase of claim 19, wherein the substitution mutation at the position functionally equivalent to Val661 comprises a mutation to a polar amino acid.

23. The polymerase of claim 19, wherein the substitution mutation at the position functionally equivalent to Val661 comprises a mutation to Asp.

24. The polymerase of claim 19, wherein the polymerase comprises at least two amino acid substitution mutations at positions functionally equivalent to an amino acid selected from Arg247, Glu599, Lys620, His633, and Val661 in the 9°N DNA polymerase amino acid sequence.

25. The polymerase of claim 19, wherein the polymerase further comprises amino acid substitution mutations at positions functionally equivalent to amino acids Met129, Asp141, Glu143, Cys223, Leu408, Tyr409, Pro410, and Ala485 in the 9°N DNA polymerase amino acid sequence.

26. A recombinant DNA polymerase comprising an amino acid sequence that is at least 80% identical to the 9°N DNA polymerase amino acid sequence SEQ ID NO:1, wherein the recombinant DNA polymerase comprises (i) an amino acid substitution mutation at position functionally equivalent to Tyr497; (ii) at least one amino acid substitution mutation at a position functionally equivalent to Phe152, Val278, Met329, Val471, Thr514, Leu631, or Glu734 in the 9°N DNA polymerase amino acid sequence, and (iii) at least one amino acid substitution mutation at a position functionally equivalent to Arg247, Glu599, Lys620, His633, or Val661 in the 9°N DNA polymerase amino acid sequence, wherein the amino acid substitution mutation at a position functionally equivalent to Tyr497 comprises a mutation to Gly, Ile, Leu, Met, Pro, Val, Ser, Asn, Gln, or Thr.

27. The polymerase of claim 26, wherein the polymerase comprises at least two amino acid substitution mutations at positions functionally equivalent to an amino acid selected from Phe152, Val278, Met329, Val471, Thr514, Leu631, and Glu734 in the 9°N DNA polymerase amino acid sequence.

28. The polymerase of claim 26, wherein the polymerase comprises at least two amino acid substitution mutations at positions functionally equivalent to an amino acid selected from Arg247, Glu599, Lys620, His633, or Val661 in the 9°N DNA polymerase amino acid sequence.

29. The polymerase of claim 26, wherein the polymerase further comprises amino acid substitution mutations at positions functionally equivalent to amino acids Met129, Asp141, Glu143, Cys223, Leu408, Tyr409, Pro410, and Ala485 in the 9°N DNA polymerase amino acid sequence.

30. The polymerase of claim 19, wherein the substitution mutation at the position functionally equivalent to Tyr497 comprises a mutation to Gly.

31. The polymerase of claim 26, wherein the substitution mutation at the position functionally equivalent to Tyr497 comprises a mutation to Gly.