CLAIMS

1. A variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand, or of a functional fragment of such a polymerase, said variant comprising a~~t least one~~ substitution ~~of~~ at residue E457~~in at least one position selected from the group consisting of Q455, F334, K338, H342, D343, V344, D345, F346, A397, D399, D434, A446, L447, L448, G449, R458, R461, N474, D501, Y502, I503~~, or a functionally equivalent residue, the position~~s indicated being determined by alignment with SEQ ID No. 1, said variant having at least 70% identity with the sequence according to SEQ ID No. 1 and being able to incorporate a modified nucleotide.

2. The variant of a DNA polymerase of the polX family according to claim 1, ~~said variant comprising at least one~~wherein said substitution at~~of the~~ residue E457 is selected from E457G/N/S/T~~at the position Q455~~.

~~2.~~3. The variant of a DNA polymerase of the polX family according to claim 1 or 2, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of T331, G332, G333, F334, R336, K338, H342, D343, V344, D345, F346, A397, D399, D434, V436, A446, L447, L448, G449, W450, G452, R454, Q455, F456, R458, R461, N474, E491, D501, Y502, I503, P505, R508, N509 and A510, or a functionally equivalent residue, in which at least one mutation consists of a substitution, a deletion or an addition of one or more amino acid residues, the positions indicated being determined by alignment with SEQ ID No. 1.

~~3.~~ The variant of a DNA polymerase of the polX family according to any one of the preceding claim~~s 1 or 2~~, said variant being capable of synthesizing a DNA strand and/or an RNA strand and/or ~~.~~

4. ~~The variant of a DNA polymerase of the polX family according to any one of previous claims,~~ said variant being a variant of Pol IV, Pol μ, or of the terminal deoxyribonucleotidyl transferase (TdT).

5. The variant of a DNA polymerase of the polX family according to any one of the preceding claims, ~~and~~ having at least ~~60% identity with the sequence according to SEQ ID No. 1, preferably at least 70%,~~ 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity with the sequence according to SEQ ID No. 1.

6. The variant according to any one of the preceding claims, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of R336 and R454, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1, and/or said variant comprising a combination of substitutions selected from R336G-E457N; R336N-E457N; R336N-R454A-E457N; R336N-E457N; R336N-R454A-E457G; R336N-E457G; R336G-R454A-E457N; R336G-E457N, the positions indicated being determined by alignment with SEQ ID No. 1.

~~5.~~7. The variant according to claim 6, comprising mutations of residues at each one of positions R336, R454 and E457.

~~6.~~8. The variant of a DNA polymerase of the polX family according to any one of the preceding claims, said variant having at least one~~a~~ mutation of a residue in at least one semi-conserved sequence region

(i) $X_1X_2GGFR_1R_2GKX_3X_4$ (SEQ ID No. 4),

in which

X_1 represents a residue selected from M, I, V, L
X_2 represents a residue selected from T, A, M, Q
X_3 represents a residue selected from M, K, E, Q, L, S, P, R, D
X_4 represents a residue selected from T, I, M, F, K, V, Y, E, Q, H, S, R, D

(ii) $X_1X_2LGX_3X_4GSR_1X_5X_6ER_2$ (SEQ ID No. 5)

in which

X_1 represents a residue selected from A, C, G, S
X_2 represents a residue selected from L, T, R
X_3 represents a residue selected from W, Y
X_4 represents a residue selected from T, S, I
X_5 represents a residue selected from Q, L, H, F, Y, N, E, D or ∅
X_6 represents a residue selected from F, Y

(iii) LX1YX2X3PX4X5RNA (SEQ ID No. 6)

X_1 represents a residue selected from D, E, S, P, A, K
X_2 represents a residue selected from I, L, M, V, A, T
X_3 represents a residue selected from E, Q, P, Y, L, K, G, N
X_4 represents a residue selected from W, S, V, E, R, Q, T, C, K, H
X_5 represents a residue selected from E, Q, D, H, L.

~~7.~~9. The variant of a DNA polymerase of the polX family according to claim ~~6~~8, said variant having

- at least one substitution of a residue in at least one position R_1, R_2 and/or K of the semi-conserved sequence region SEQ ID No. 4; and/or
- at least one substitution of a residue in at least one position S, R1 and/or E of the semi-conserved sequence region SEQ ID No. 5; and/or
- a deletion of the residue in position X_1 and/or at least one substitution in the positions R and/or N of the semi-conserved sequence region SEQ ID No. 6.

10. The variant according to any one of the preceding claims, said variant comprising a substitution of a residue in at least one position selected from the group consisting of R336, K338, H342, A397, S453, R454, R461, N474, D501, Y502, I503, R508 and N509, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

11. The variant according to claim 10, comprising a substitution of a residue in at least one position selected from the group consisting of R336, A397, R454, R461, N474, D501, Y502 and I503, or a functionally equivalent residue.

12. The variant according to claim 10 or 11, wherein the substitutions in positions R336, K338, H342, A397, S453, R454, E457, R461, N474, D501, Y502, I503, R508 and N509 are selected from the group consisting of R336K/H/N/G/D, K338A/C/G/S/T/N, H342A/C/G/S/T.N, A397R/H/K/D/E, S453A/C/G/S/T, R454F/Y/W/A, E457G/N/S/T, N474S/T/N/Q, D501A/G/X, Y502A/G/X, I503A/G/X, R508A/C/G/S/T, N509A/C/G/S/T.

~~8.~~13. The variant according to any one of the preceding claims, in which the variant comprises or has a substitution, deletion, combinations of substitutions and/or of deletions listed in table 1, the positions indicated being determined by alignment with SEQ ID No. 1.

~~9.~~14. The variant of a DNA polymerase of the polX family according to any one of the preceding claims, said variant being a variant of the TdT of sequence SEQ ID No. 1 and comprising moreover a substitution of the residues between the positions C378 to L406, or the functionally equivalent residues, with the residues H363 to C390 of the polymerase Polμ of sequence SEQ ID No. 2, or the functionally equivalent residues.

~~10.~~15. An isolated nucleic acid coding for a variant of a DNA polymerase of the polX family according to any one of claims 1 to 14~~8~~.

~~11.~~16. An expression cassette of a nucleic acid according to claim 15~~9~~.

~~12.~~17. A vector comprising a nucleic acid according to claim 15~~9~~ or an expression cassette according to claim 16~~0~~.

~~13.~~18. A host cell comprising a nucleic acid according to claim ~~9~~15 or an expression cassette according to claim 1~~0~~6 or a vector according to claim 1~~1~~7.

~~14.~~19. Use of a nucleic acid according to claim 1~~2~~5, of an expression cassette according to claim 1~~6~~0, of a vector according to claim 1~~1~~7 or of a cell according to claim 1~~2~~8, for producing a variant of a DNA polymerase of the polX family according to any one of claims 1-14~~8~~.

~~15.~~20. A method for producing a variant of a DNA polymerase of the polX family according to any one of claims 1-~~8~~14, according to which a host cell according to claim 1~~8~~2 is cultured under culture conditions enabling the expression of the nucleic acid coding for said variant, and optionally said variant thus expressed is recovered from the culture medium or from said host cells.

~~16.~~21. Use of a variant of a DNA polymerase of the polX family according to any one of claims 1-~~8~~14, for synthesizing a nucleic acid molecule without a template strand, from 3'-OH modified nucleotides.

~~17. The use according to claim 15, for synthesizing a DNA strand or an RNA strand.~~

~~18.~~22. A method for the enzymatic synthesis of a nucleic acid molecule without a template strand, according to which a primer strand is brought in contact with at least one nucleotide, preferably a 3'-OH modified nucleotide, in the presence of a variant of a DNA polymerase of the polX family according to any one of claims 1-14~~8~~.

~~19.~~23. A kit for the enzymatic synthesis of a nucleic acid molecule without a template strand, comprising at least one variant of a DNA polymerase of the polX family according to any one of claims 1-~~8~~14, nucleotides, preferably 3'-OH modified nucleotides, and optionally at least one nucleotide primer.