Claims:

1. A polynucleotide comprising at least two consecutive transcription termination signals, characterized in that said consecutive transcription termination signals comprise at least a first and a second transcription termination signal that are at most 1000 nucleotides apart, and at least one of the termination signal has or encodes a RNA hairpin structure, said hairpin structure comprising a stem of at least 12 internal base pairs ~~with at least 75% G or C nucleic acids and a base pair content of the stem of at least 90%~~ and wherein said hairpin structure is defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least 60%,
X is a nucleotide sequence of 4 nucleotides in length,
X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and
Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z.

2. The polynucleotide of claim 1 comprising a third transcription termination signal, optionally comprising or encoding a RNA hairpin structure, said third transcription termination signal being at most 1000 nucleotides apart from the first or second transcription termination signal.

3. The polynucleotide according to claim 1 or 2, ~~characterized in that said hairpin structure is defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least 75%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, and
Z is a nucleotide sequence with at least 90% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z~~wherein the hairpin structure with a stem of at least 12 internal base pairs of the at least one termination signal having or encoding a RNA hairpin structure has at least 70% G or C nucleic acids.

~~4. The polynucleotide of claim 3, characterized in that X has 3, 4, 5, 6, 7, 8 or 9 nucleotides in length.~~

~~5~~4. The polynucleotide of ~~claim 3 or 4~~any one of claims 1 to 3, characterized in that X comprises or consists of the sequence U/T-NCG ~~U/T-NNG, with N being any nucleotide selected from U(T), A, C, G~~.

~~5~~6. The polynucleotide of any one of claims 1 to ~~4~~5, characterized in that X comprises or consists of the sequence ~~wherein the sequence U/T-NNG is U/T-NCG or~~ U/T-U/T-CG.

~~7~~6. The polynucleotide of any one of claims 1 to ~~6~~5, characterized in that said first, second and/or third transcription termination signal comprises said hairpin structures as defined in any one of claims ~~3 to 5~~

1, 3 or 4 to 5.

78. The polynucleotide of any one of claims 1 to 6, characterized in that said first, second and/or third transcription termination signal comprises said hairpin structures as defined in any one of claims 1, 3 or 4 to 5~~The polynucleotide of claim 7~~, wherein at least one of the transcription termination signals comprises a hairpin structure as defined in claims 4 or 5~~5 or 6~~ and at least a further transcription termination signal comprises a hairpin structure of claim ~~3~~1, with Y, X and Z being selected independently.

~~9~~8. The polynucleotide according to any one of claims 1 to ~~8~~7 wherein at least one of said terminator signals is a class II terminator.

~~10~~9. The polynucleotide according any one of claims 1 to ~~9~~8, characterized in that at least one transcription termination signal comprises a A/T(U)-rich region of at least 4 nucleotides in length comprising at least 75% A or T(U).

~~11~~10. The polynucleotide according to claim ~~10~~9, wherein said A/T(U)-rich region is downstream of a hairpin.

~~12~~11. The polynucleotide according to claim ~~11~~10, wherein said A/T(U)-rich region is not more than~~t~~ 20 nucleotides apart from said hairpin.

~~13~~12. The polynucleotide according any one of claims ~~3~~1 to ~~12~~11, characterized in that Y is of 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length.

~~14~~13. The polynucleotide according any one of claims ~~3~~1 to ~~13~~12, characterized in that Y and Z are of m nucleotides in length, Y consists of the nucleotides y_1 to y_m and Z consists of the nucleotides z_1 to z_m, the hairpin consists of the sequence $y_m y_{m-1} y_{m-2} \ldots y_8 y_7 y_6 y_5 y_4 y_3 y_2 y_1$-X-$z_1 z_2 z_3 z_4 z_5 z_6 z_7 z_8 \ldots z_{m-1} z_m$, wherein z_1 is complementary to y_1 and z_m is complementary to y_m.

~~15~~14. The polynucleotide according to any one of claims ~~3~~ 1 to ~~14~~13, characterized in that Y and Z are at least ~~95~~90% complementary.

~~16~~15. The polynucleotide of claim ~~15~~14, characterized in that Y and Z are at least 95% complementary, or 100% complementary.

~~17~~16. The polynucleotide according any one of claims ~~3~~ 1 to ~~16~~15, characterized in that in the hairpin, between nucleotides of Y and Z, at most 3, 2 or 1 G-U complementarities are adjacent to another G-U complementarity.

~~18~~17. The polynucleotide according to claim 16, wherein the hairpin is without adjacent G-U complementaries.

~~19~~18. The polynucleotide according any one of claims 1 to ~~18~~ 17 being DNA, encoding the termination signals as defined in any one of claims 1 to ~~15~~17; or RNA comprising the termination signals as defined in claims 1 to 15.

~~20~~19. A polynucleotide according to any one of claims 1 to ~~19~~ 18 having a size of at most 10000 nucleotides in length.

~~21~~20. A polynucleotide according to any one of claims 1 to ~~20~~19, characterized in that the polynucleotide comprises one or more restriction sites flanking said transcription termination signals and/or a cloning site upstream of the transcription termination signals, or a coding sequence upstream of the transcription termination signals.

~~22~~21. A polynucleotide according to any one of claims 1 to 20, characterized in that the polynucleotide comprises one or more restriction sites flanking said transcription termination signals and/or a cloning site upstream of the transcription termination signals, or a coding sequence upstream of the transcription termination signals~~The polynucleotide according to claim 21, wherein the coding sequence is further~~, further operatively linked to a promoter.

~~23~~22. A polynucleotide according to any one of claims 1 to ~~22~~ 21 comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least ~~75~~60%, X is a nucleotide sequence of ~~3 to 9~~4 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and
Z is a nucleotide sequence with at least ~~90~~80% complementarity to Y,
the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a class II termination signal.

~~24~~23. A polynucleotide according to any one of claims 1 to ~~23~~ 22

(i) comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 14 nucleotides in length and with a G/C content of at least ~~75~~60%,

X is a nucleotide sequence of 3 to 9 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and

Z is a nucleotide sequence with at least ~~90~~80% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,

X is a nucleotide sequence of 3 to 9 nucleotides in length, and

Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z; with the first and second terminator being at most 1000 nucleotides apart to provide a concerted termination by the first and second termination signal, wherein Y, X, and Z of the first and second terminator can be selected independently~~.~~; or

~~25. A polynucleotide according to any one of claims 1 to 23~~

(ii) comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least ~~75~~60%,

X is a nucleotide sequence of 3 to 9 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and Z is a nucleotide sequence with at least ~~90~~80% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a class II termination signal~~.~~; or

~~26. A polynucleotide according to any one of claims 1 to 23~~ (iii) comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least ~~75~~60%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and Z is a nucleotide sequence with at least 90% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a third terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

with the first, second and third terminator being at most 1000 nucleotides apart to provide a concerted termination by the first, second and third termination signal, wherein Y, X, and Z of the first, second or third terminator can be selected can be selected independently~~.~~; or

~~27. A polynucleotide according to any one of claims 1 to 23~~ (iv) comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence

of at least 12 nucleotides in length and with a G/C content of at least ~~75~~60%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and Z is a nucleotide sequence with at least ~~90~~80% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a class II termination signal;

a third terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,X is a nucleotide sequence of 3 to 9 nucleotides in length, and
Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z; with the first, second and third terminator being at most 1000 nucleotides apart to provide a concerted termination by the first, second and third termination signal, wherein Y, X, and Z of the first or third terminator and the consensus and T-rich sequence of the class II termination signal can be selected independently~~.~~;or

~~28. A polynucleotide according to any one of claims 1 to 23~~ (v) comprising a first terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least ~~75~~60%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, X comprises or consists of the sequence U/T-NNG, with N being any nucleotide selected from U(T), A, C, G, and Z is a nucleotide sequence with at least ~~90~~80% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z;

a second terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,X is a nucleotide sequence of 3 to 9 nucleotides in length, and
Z is a nucleotide sequence with at least 70% complementarity to

Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z and a class II termination signal adjacent to the hairpin structure;

a third terminator signal comprising a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with a G/C content of at least 40%,X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least 70% complementarity to Y, the complementary nucleotides of Z being base paired with the nucleotides of Y, and X being a loop with no base pairing to Y or Z; with the first, second and third terminator being at most 1000 nucleotides apart to provide a concerted termination by the first, second and third termination signal, wherein Y, X, and Z of the first, second or third terminator and the consensus and T-rich sequence of the class II termination signal can be selected independently.

~~29~~24. The polynucleotide according to any one of claims 22, 23(ii), 23(iv) and 23(v), ~~23, 25, 27 and 28~~ wherein the class II termination signal comprises the consensus sequence TCTGTT.

~~30~~25. The polynucleotide according to any one of claims 22, 23(ii), 23(iv) and 23(v), ~~23, 25, 27 and 28~~ wherein the class II termination signal comprises a sequence of at least 20 nucleotides in length with a T content of at least 40%.

~~31~~26. The polynucleotide according to any one of claims 23(i), 23(iii) and 23(v), ~~24, 26 and 28~~ wherein the second terminator signal comprises a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with ~~has~~ a G/C content of at least 50%.

~~32~~27. The polynucleotide according to any one of claims 23(i), 23(iii) and 23(v)~~31~~, wherein the second terminator signal comprises a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with ~~has~~ a G/C content of at least 60%.

~~33~~28. The polynucleotide according to any one of claims 23(iii), 23(iv) and 23(v), ~~26, 27 and 28~~ wherein the third terminator signal comprises a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with ~~has~~ a G/C content of at least 50%.

~~34~~29. The polynucleotide according to any one of claims 23(iii), 23(iv) and 23(v)~~33~~, wherein the third terminator signal comprises a hairpin structure defined by a sequence Y-X-Z, wherein Y is a nucleotide sequence of at least 8 nucleotides in length and with ~~has~~ a G/C content of at least 60%.

30. The polynucleotide according to claim 23, wherein:

- Y, X, and Z of the first and second terminator of claim 23(i) can be selected independently, and are as defined in claims 1, 3 to 5 and 12 to 17; or
- Y, X, and Z of the first, second and third terminator of claim 23(iii) can be selected independently, and are as defined in claims 1, 3 to 5 and 12 to 17; or
- Y, X, and Z of the first or third terminator and the consensus and T-rich sequence of the class II termination signal of claim 23(iv) can be selected independently, and are as defined in claims 1, 3 to 5 and 12 to 17; or
- Y, X, and Z of the first, second or third terminator and the consensus and T-rich sequence of the class II termination signal of claim 23(v) can be selected independently, and are as defined in claims 1, 3 to 5 and 12 to 17.

31. A polynucleotide according to any one of claims 1 to 30, wherein at least one of the termination signals comprises a sequence selected from SEQ ID NO: 4, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18 or SEQ ID NO: 19.

~~35~~32. An expression cassette comprising a polynucleotide sequence according to any one of claims 1 to ~~34~~ 31 and a coding sequence, wherein the sequence is operatively positioned for termination of the coding sequence.

~~36~~33. A vector comprising a polynucleotide as defined in any one of claims 1 to ~~34~~ 31 or the expression cassette according to claim ~~35~~32.

~~37~~34. The vector according to claim ~~36~~ 33, wherein the vector is~~being~~ a plasmid.

~~38~~35. A cell comprising a polynucleotide molecule with a gene operatively linked to the transcription termination signals of the polynucleotide according to any one of claims 1 to ~~34~~ 31~~or the vector of claim 36 or 37~~.

36. The cell according to claim 35 comprising a polynucleotide molecule with a gene operatively linked to the transcription termination signals of the polynucleotide according to any one of claims 1 to 34, in a vector.

~~39~~37. The cell according to claim ~~38~~ 35, wherein said cell comprises the T7 RNA polymerase or a polynucleotide encoding the T7 RNA polymerase.

~~40~~38. A method of producing a gene product, comprising providing a cell according to any one of claims 35 to 37~~38 or 39~~ and cultivating said cell under conditions allowing expression of said gene.

~~41~~39. An in vitro method of producing a mRNA, comprising providing a polynucleotide according to any one of claims 1 to ~~34~~ 31 and a coding sequence upstream of said transcription termination signal and contacting said polynucleotide with the T7 RNA polymerase.