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 ~~60~~75% G or C nucleic acids and a base pair content of the stem of at least 90%.

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 ~~60~~75%,
X is a nucleotide sequence of 3 to 9 nucleotides in length, and
Z is a nucleotide sequence with at least ~~70~~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.

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

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

6. The polynucleotide of claim 5, wherein the sequence U/T-NNG is U/T-NCG or U/T-U/T-CG.

~~6~~7. The polynucleotide of any one of claims 1 to ~~5~~6, 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~~, preferably at least one of the tran-~~

~~scription termination signals comprises a hairpin structure as defined in claim 5 and at least a further transcription termination signal comprises a hairpin structure of claim 3, with Y, X and Z being selected independently~~.

8. The polynucleotide of claim 7, wherein at least one of the transcription termination signals comprises a hairpin structure as defined in claim 5 or 6 and at least a further transcription termination signal comprises a hairpin structure of claim 3, with Y, X and Z being selected independently.

~~7~~9. The polynucleotide according to any one of claims 1 to ~~6~~8 wherein at least one of said terminator signals is a class II terminator.

~~8. A polynucleotide comprising at least one transcription termination signal comprising a hairpin structure having the sequence Y-U/T-NNG-Z,~~
~~wherein Y is a nucleotide sequence of at least 12 nucleotides in length and with a G/C content of at least 60%,~~
~~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 sequence U/T-NNG being a loop with no base pairing to Y or Z, with N being any nucleotide selected from T(U), A, C, G; preferably the sequence U/T-NNG is U/T-U/T-CG.~~

~~9~~10. The polynucleotide according any one of claims 1 to ~~8~~9, 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)~~, wherein preferably said A/T(U)-rich region is downstream of a hairpin, in particular preferred not more that 20 nucleotides apart from said hairpin~~.

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

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

~~10~~13. The polynucleotide according any one of claims 3 to ~~9~~12, 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.

~~11~~14. The polynucleotide according any one of claims 3 to ~~10~~13, 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 ymym-1y_{m-2}...$y_8y_7y_6y_5y_4y_3y_2y_1$-X-$z_1z_2z_3z_4z_5z_6z_7z_8$...$z_{m-1}z_m$, wherein z_1 is complementary to y_1 and z_m is complementary to y_m.

~~12~~15. The polynucleotide according to any one of claims 3 to ~~11~~14, characterized in that Y and Z are ~~at least 80% complementary, preferably~~ at least ~~90~~95% complementary~~, in particular preferred 100% complementary, most preferred with at least 70% G-C or A-T(U) complementarity~~.

16. The polynucleotide of claim 15, characterized in that Y and Z are 100% complementary.

~~13~~17. The polynucleotide according any one of claims 3 to ~~12~~16, 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~~, preferably the hairpin being without adjacent G-U complementaries~~.

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

~~14~~19. The polynucleotide according any one of claims 1 to ~~13~~18 being DNA, encoding the termination signals as defined in any one of claims 1 to ~~12~~15; or RNA comprising the termination signals as defined in claims 1 to ~~12~~15.

~~15~~20. A polynucleotide according to any one of claims 1 to ~~14~~19 having a size of at most 10000 nucleotides in length.

~~16~~21. A polynucleotide according to any one of claims 1 to ~~15~~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~~, preferably further operatively linked to a promoter~~.

22. The polynucleotide according to claim 21, wherein the coding sequence is further operatively linked to a promoter.

~~17~~23. A polynucleotide according to any one of claims 1 to ~~16~~22 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 ~~60~~75%, ~~preferably at least 65%,~~
X is a nucleotide sequence of 3 to 9 nucleotides in length, and
Z is a nucleotide sequence with at least ~~80~~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 class II termination signal~~, preferably comprising the consensus sequence TCTGTT, especially preferred comprising a sequence of at least 20 nucleotides in length with a T content of at least 40%~~.

~~18~~24. A polynucleotide according to any one of claims 1 to ~~17~~ 23 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 ~~60~~75%, ~~preferably at least 65%,~~ 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;

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%, ~~preferably at least 50%, especially at least 60%,~~ 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~~, in particular as defined in claims 4, 5, 10 to 13~~.

~~19~~25. A polynucleotide according to any one of claims 1 to ~~17~~23 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 ~~60~~75%, ~~preferably at least 65%,~~ X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least ~~80~~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 class II termination signal~~, preferably comprising the consensus sequence TCTGTT, es-~~

~~pecially preferred comprising a sequence of at least 20 nucleotides in length with a T content of at least 40%~~.

~~20~~26. A polynucleotide according to any one of claims 1 to ~~17~~23 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 ~~60~~75%, ~~preferably at least 65%,~~ X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least ~~80~~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%, ~~preferably at least 50%, especially at least 60%,~~ 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%, ~~preferably at least 50%, especially at least 60%,~~ 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~~, in particular as defined in claims 4, 5, 10 to 13~~.

~~21~~27. A polynucleotide according to any one of claims 1 to ~~17~~23 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 ~~60~~75%, ~~preferably at least 65%,~~
X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least ~~80~~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 class II termination signal~~, preferably comprising the consensus sequence TCTGTT, especially preferred comprising a sequence of at least 20 nucleotides in length with a T content of at least 40%~~;

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%, ~~preferably at least 50%, especially at least 60%,~~
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~~, in particular as defined in claims 4, 5, 10 to 13~~.

~~22~~28. A polynucleotide according to any one of claims 1 to ~~17~~23 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 ~~60~~75%, ~~preferably at least 65%,~~
X is a nucleotide sequence of 3 to 9 nucleotides in length, and Z is a nucleotide sequence with at least ~~80~~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%, ~~preferably at least 50%, especially at least 60%,~~
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~~, preferably comprising the consensus sequence TCTGTT, especially preferred comprising a sequence of at least 20 nucleotides in length with a T content of at least 40%~~;

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%,~~ preferably at least 50%, especially at least 60%,~~ 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~~, in particular as defined in claims 4, 5, 10 to 13~~.

29. The polynucleotide according to claim 23, 25, 27 and 28 wherein the class II termination signal comprises the consensus sequence TCTGTT.

30. The polynucleotide according to claim 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. The polynucleotide according to claim 24, 26 and 28 wherein the second terminator signal has a G/C content of at least 50%.

32. The polynucleotide according to claim 31, wherein the second terminator signal has a G/C content of at least 60%.

33. The polynucleotide according to claim 26, 27 and 28 wherein the third terminator signal has a G/C content of at least 50%.

34. The polynucleotide according to claim 33, wherein the third terminator signal has a G/C content of at least 60%.

~~23~~35. An expression cassette comprising a polynucleotide sequence according to any one of claims 1 to ~~22~~ 34 and a coding sequence, wherein the sequence is operatively positioned for termination of the coding sequence.

~~24~~36. A vector comprising a polynucleotide as defined in any one of claims 1 to ~~22~~ 34 or the expression cassette according to claim ~~18~~35~~, the vector preferably being a plasmid~~.

37. The vector according to claim 36 being a plasmid.

~~25~~38. 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 ~~22, preferably in a~~34 or the vector of claim 36 or 37.

~~26~~39. The cell according to claim ~~25~~ 38 said cell comprises the T7 RNA polymerase or a polynucleotide encoding the T7 RNA polymerase.

~~27~~40. A method of producing a gene product, comprising providing a cell according to claim ~~25~~38 or ~~26~~39 and cultivating said cell under conditions allowing expression of said gene.

~~28~~41. An in vitro method of producing a mRNA, comprising providing a polynucleotide according to any one of claims 1 to ~~22~~34 and a coding sequence upstream of said transcription termination signal and contacting said polynucleotide with the T7 RNA polymerase.