-continued

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(2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTAGAATTA TGAAAAAAAA CATCGCATTT CTTCTTGCAT CTATGTTCGT          50

TTTTTCTATT GCTACAAACG CGTATGCM                                  78


(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTAGAATTA TGAAAAAAAA CATTGCCTTT CTTCTTGCAT CTATGTTCGT          50

TTTTTCTATT GCTACAAACG CGTATGCM                                  78


(2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCTAGAATTA TGAAGAAAAA CATCGCTTTT CTTCTTGCAT CTATGTTCGT          50

TTTTTCTATT GCTACAAACG CGTATGCM                                  78


(2) INFORMATION FOR SEQ ID NO:22:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 78 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTAGAATTA TGAAAAAGAA CATAGCGTTT CTTCTTGCAT CTATGTTCGT          50

TTTTTCTATT GCTACAAACG CGTATGCM                                  78


(2) INFORMATION FOR SEQ ID NO:23:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 90 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCTAGAGGTT GAGGTGATTT TATGAAAAAA AACATCGCAT TTCTTCTTGC          50

ATCTATGTTC GTTTTTTCTA TTGCTACAAA CGCGTATGCM                     90
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What is claimed is:

1. A method of optimizing secretion of a heterologous polypeptide of interest in a cell comprising comparing the levels of expression of the polypeptide under control of a set of nucleic acid variants of a translation initiation region, wherein the set of variants represents a range of translational