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(52) **U.S. Cl.**

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(57)

ABSTRACT

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Related U.S. Application Data

(63) Continuation of application No. 15/329,651, filed on Jan. 27, 2017, now Pat. No. 10,240,146, filed as application No. PCT/US2015/042559 on Jul. 29, 2015.

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Publication Classification

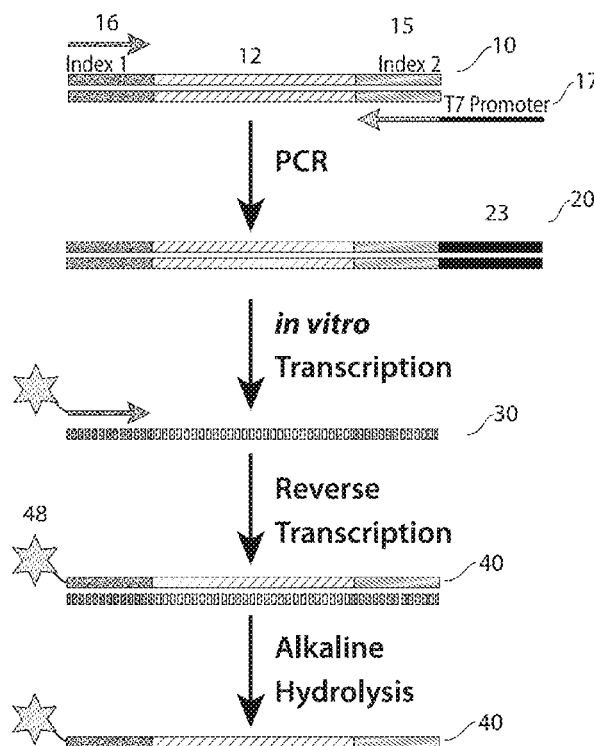
(51) **Int. Cl.**

C12N 15/10 (2006.01)

C12Q 1/6837 (2006.01)

The present invention generally relates to systems and methods for producing nucleic acids. In some aspects, relatively large quantities of oligonucleotides can be produced, and in some cases, the oligonucleotides may have a variety of different sequences and/or lengths. For instance, a relatively small quantity of oligonucleotides may be amplified to produce a large amount of nucleotides. In one set of embodiments, oligonucleotides may be amplified using PCR, then transcribed to produce RNA. The RNA may then be reverse transcribed to produce DNA, and optionally, the RNA may be selectively degraded or removed, relative to the DNA. In one set of embodiments, the oligonucleotides may be chemically modified. These modifications may include, but are not limited to, the adding of fluorescent dyes or other signaling entities.

Specification includes a Sequence Listing.



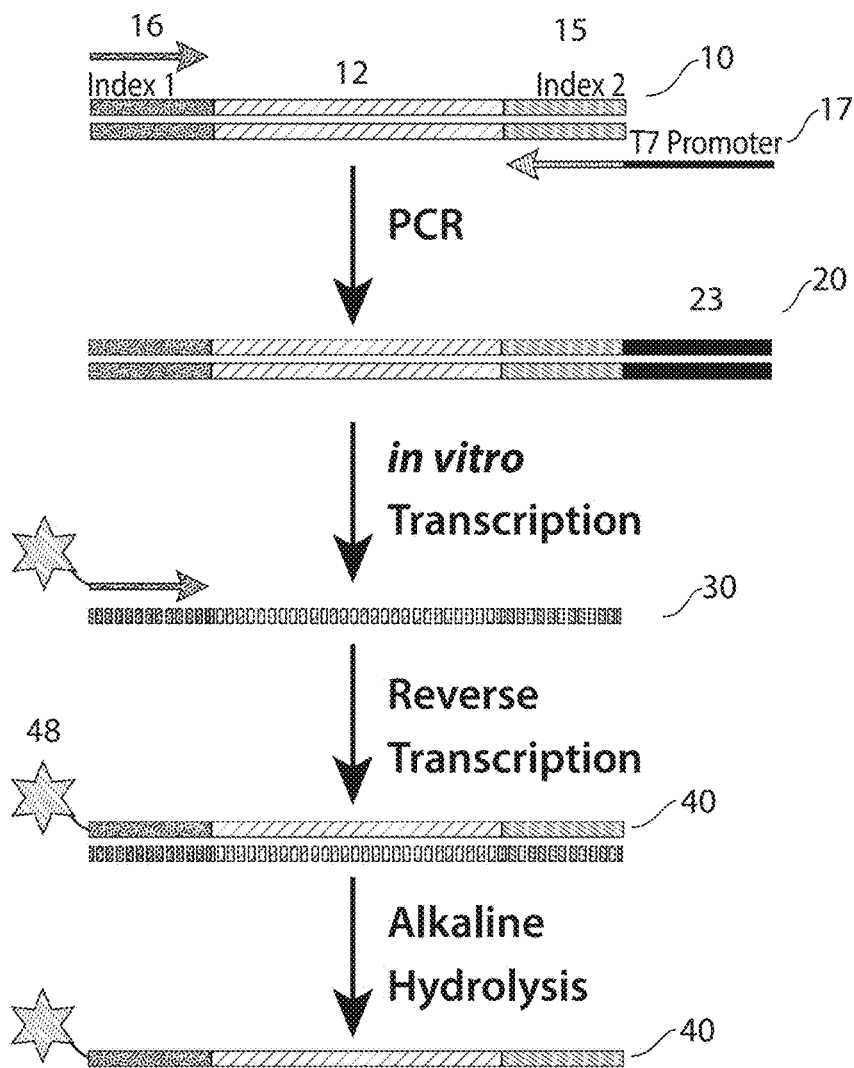


FIG. 1

ACAACCGCGTGTTACAAGGCCAGGCATCCGAGAGGTCTGGGAATGCC
 AGCAGCTCTACAAGTGC GGCCATTGGTTCA TTGCGCTTCTCCGAAAC
 ATTAGC (SEQ ID NO: 3)

FIG. 2

>bc25mer_8982-20 CGGTAGGACCCTACACATCC	>bc25mer_69827-20 GTGCGATTGTCACATGTGCT	>bc25mer_218789-20 GACCCGGGAGTTATGATACG
>bc25mer_37497-20 TGTGGCGCCTAACCATACAC	>bc25mer_85616-20 GGCTTGCTCTCAATTATCCG	>bc25mer_235702-20 CTCGGGTAGGCTATCTCCAA
>bc25mer_48272-20 GACACCGAGCTAGAAATTCGG	>bc25mer_90788-20 CCCACGTGACTTGACTTCTC	>bc25mer_239358-20 CTGCAGGTGCTCTAGATGGA
>bc25mer_96434-20 TGTCTTGGGTCTCTTACGG	>bc25mer_108211-20 CCTCTACATGCTCCGGATCC	>bc25mer_5878-20 GTCCAGGCTCGTCTTCTCGA
>bc25mer_135960-20 TATCACGTGAGGCTCCGTGT	>bc25mer_113656-20 GAATAGTAACCCGGTCGCAA	>bc25mer_9018-20 CTTACCTGAGCGCAGTTCGA
>bc25mer_217459-20 GTCTACGGATCCTTGCGTGT	>bc25mer_121326-20 TGGGCCACTAGTCTTCGCTA	>bc25mer_9904-20 GTTGTTCGATCCCTCCACCA
>bc25mer_5177-20 ACGGGTACATTGGATCCACT	>bc25mer_123881-20 CGGCACGTACCCTTTACAGG	>bc25mer_10475-20 CGGCAGAGGATAATCCTAGC
>bc25mer_7835-20 AAGACGTGGTCCACCTGAT	>bc25mer_138428-20 GATCAGTGAGCCTACCAAG	>bc25mer_11594-20 GGGAGTCCGGATGTTAGTGC
>bc25mer_13747-20 TGCCAGGTCCACTACTTGGG	>bc25mer_140203-20 TGGTATGTGAGCTCTTTGGG	>bc25mer_12189-20 CGCATCTATGCTCCGCTTAC
>bc25mer_14156-20 GACCCGAAGGAGAATGCAAA	>bc25mer_159878-20 AGAGTCACGCATACTTGGGA	>bc25mer_14363-20 AACGCGCTACCCAATTCTAG
>bc25mer_14649-20 ATGTGCTCTCTCAGGGCTTT	>bc25mer_163235-20 GGGTCAGGCGTCATAGATTG	>bc25mer_16178-20 TACTGGACGATTCCTCGACTG
>bc25mer_16849-20 AAGGGCGAAGCACTCTCTT	>bc25mer_184954-20 AGAATGTGGAGGACATGTGG	>bc25mer_17067-20 AGCGTCGTACCCAGTTAAGC
>bc25mer_25227-20 TGGTCCCGCATTTGTACCTT	>bc25mer_188166-20 TCGGACTGTGAGACATTTCC	>bc25mer_18548-20 GAGATTCACGCCCTCATGAG
>bc25mer_45585-20 AAGTCCGTCTGCTAAGCCAT	>bc25mer_192833-20 ATCAAATGCCTCGGTCTGTTG	>bc25mer_20080-20 CCGCTAGCGTTACCTCTACC
>bc25mer_46295-20 CTCCAGAGTCTCGGCATGA	>bc25mer_193757-20 GCAATGCTATGCTGGGACAA	>bc25mer_20601-20 CCACACCGTATGCATTTCTG
>bc25mer_46396-20 TCTAACGAGCTCCGTGGTTG	>bc25mer_199694-20 ATGGAGGCGGTTCTCTGACA	>bc25mer_26252-20 CCTTAGCGCACAAAGAGACG
>bc25mer_55377-20 CCTGGGCAGGAAACAACACT	>bc25mer_200273-20 GCAGATGGGTGCATTCATTC	>bc25mer_28353-20 GTCCTGATGGCTTTCTCAGC
>bc25mer_57092-20 GCGCACACCTTAGTCATAGC	>bc25mer_208214-20 TATGCACTCTGCGGATGACC	>bc25mer_30927-20 GGTCGTCGGTAGATCATTGC

FIG. 3A

>bc25mer_32240-20 AGAGCCGGTATGATCCATCG	>bc25mer_65782-20 TCTCCGAAGATCCGATATCG	>bc25mer_96522-20 GGCGTTCATCGAAACTCTA
>bc25mer_32875-20 CCGGACGAAGGTTGATATCC	>bc25mer_66426-20 GATGCAGGGCCTAATTAACG	>bc25mer_96896-20 GGCCATCGACTTAGATTCCA
>bc25mer_39270-20 ACCCGGTACCTGTTATCACG	>bc25mer_68963-20 TGACGCGGCTAAATACTGAC	>bc25mer_97519-20 GGTGCTCCTGCCATTATAGG
>bc25mer_40398-20 ATCCCGTCTCGTTCTATGGG	>bc25mer_70828-20 GCAATGCACGCTCTCCTAGT	>bc25mer_100107-20 TGTCGACGTGCGGAAAGTAG
>bc25mer_41429-20 CAGGTGAGGGTCTCTCCTTC	>bc25mer_71011-20 TGGCGTCAGATGGATTAGGA	>bc25mer_100109-20 GCCGCACGAGTATGCTACTG
>bc25mer_42283-20 CCTTATGGAAACGTGATGCC	>bc25mer_71626-20 GTTGGCGGGAGACTAAGAAG	>bc25mer_100502-20 TGCTGCCGCTTACTACTGCT
>bc25mer_43506-20 GGCTGGGCATACATAGACCT	>bc25mer_72701-20 TCGCGTCTCGTCTTCTACC	>bc25mer_102626-20 TAGCACTCTTCTGGCCATCG
>bc25mer_45853-20 AGTGGCGGCTATTACCGGAT	>bc25mer_79345-20 CGGTCACGTCGGAAATAACC	>bc25mer_103544-20 CGGTAATCGGTTCCACCAGTG
>bc25mer_47706-20 TGATAACGTCGCTCGTTGA	>bc25mer_79641-20 ATTAACGGGCCAGGTTACTG	>bc25mer_108258-20 TTTAGTGCTGGCTCCGTTG
>bc25mer_54028-20 TACATCGTTGAGGCCCGTTT	>bc25mer_81698-20 ATTGTATGGAGGCGCCCTAT	>bc25mer_109838-20 GGAGTTACAGCCACTTTCGG
>bc25mer_54772-20 CGTTGTGGCATCAGCTAGAG	>bc25mer_82313-20 GCCAGCTTCCAAGATTCAG	>bc25mer_114408-20 GTGTGGACGGAACCTGACAA
>bc25mer_55112-20 ACTGGCCACACACTTACCT	>bc25mer_83004-20 ACAACCGCGTGTACAAGGC	>bc25mer_115589-20 CACACGTGGAATTGTTCTGC
>bc25mer_57695-20 ATCGGGTCACGGAATATGAC	>bc25mer_83517-20 GCTAATGTTCCGGAGAAGC	>bc25mer_116534-20 CTTGTACATGGAGGGCGACT
>bc25mer_58256-20 CGTAGGTTACAGATTTGCG	>bc25mer_83687-20 GAAGTATCCGGCATCACAGC	>bc25mer_116605-20 AATCCGGTGTACAGGTTCCC
>bc25mer_59008-20 TAGGGCACGAGAAGGTATCC	>bc25mer_85062-20 TCGTTACGGACTTTCACGAC	>bc25mer_121894-20 AGGTGCGACGATATACACCA
>bc25mer_61977-20 ACTAGCTTGATCGCCGGAT	>bc25mer_87436-20 GCCATTCTGACATACCCAGA	>bc25mer_123748-20 ACTGCATATGACCGCTGCAA
>bc25mer_63426-20 CGGCGGTTTGATATTCGAAG	>bc25mer_90109-20 GTATTTGAACCGGCCAGCTG	>bc25mer_125347-20 CCTTCCATTAGCCGAGATCA
>bc25mer_63840-20 GCCGAGTGTATGAGCAAG	>bc25mer_95782-20 GGTTGTGGCCATATCCAAT	>bc25mer_125541-20 GACGCGAGGAGTGATCGACT

FIG. 3B

>bc25mer_126017-20 CGACCCCTCACACATTTGGGT	>bc25mer_149885-20 AAGCGGTCGTGGTTTATACC	>bc25mer_175501-20 GCAGTGCGGGTAGATACGCT
>bc25mer_126439-20 CGCTCCCGTATTCTTCTGTG	>bc25mer_150249-20 GCCACCTTGATGGTATCGA	>bc25mer_180358-20 AGGCGTGGGTAGCAACGTAT
>bc25mer_128324-20 CAGGGATAGTCAGGCCAGTG	>bc25mer_150996-20 TAATGCTTAGGCCCGTCGGT	>bc25mer_180797-20 GCTCATTGGACTTTCTCCCA
>bc25mer_130576-20 CGTAATGAGTGCTTCGCCAT	>bc25mer_153952-20 GACGCGACGGATTATTTAGG	>bc25mer_181432-20 AAGGACCACGTATCTGCATG
>bc25mer_132438-20 CTCGTCTCGTGGAACACATG	>bc25mer_156264-20 GGTCGCGCCCATATATAAGG	>bc25mer_181702-20 ATCTGATAGTGCCGCGACGT
>bc25mer_133420-20 TATGCTGGGCAGTAATCAGG	>bc25mer_156364-20 TGACTACGGTTGGGTGCATC	>bc25mer_182418-20 TGACCTGCACGGATAGTAGG
>bc25mer_133575-20 GCATCTCGTAGCATCCTGCT	>bc25mer_157007-20 TCAGGCGCTCATTGTATGTC	>bc25mer_182774-20 GTTATTCGCAGTCCTTGGGT
>bc25mer_134218-20 AGTATGGTACCGGGAACAGC	>bc25mer_160860-20 GTAGATACTCCCGGCCGAA	>bc25mer_183321-20 GTGCAGGTGCTTAAATCCG
>bc25mer_136989-20 ACCATTCTCGCAACTCGCTA	>bc25mer_161471-20 GCAGCACTTAGGGCAGCATC	>bc25mer_188636-20 CGCGGGTGTAAATAAGGAC
>bc25mer_137798-20 CGTGGGCGAAGTACTTGGTC	>bc25mer_163904-20 CGCGGGAACCATATTAGGAA	>bc25mer_189039-20 GCGAGGCGTGSTAATAGTCA
>bc25mer_138338-20 CCGGACGCTTCGATAATGC	>bc25mer_164195-20 GATCCATGGCCAGTTCGTAT	>bc25mer_190422-20 CAAGGCGCAAACATAGACAG
>bc25mer_139329-20 TGATGCTCTTTCAGTTCGG	>bc25mer_164787-20 GTGCGCAAAGGACTTAGTG	>bc25mer_191525-20 GGAACAAGGGCGTCTATGTC
>bc25mer_139807-20 ATGCCGGTCATAACAGTGTC	>bc25mer_166664-20 GATCCCGCTATTCACCGATT	>bc25mer_193359-20 GCAGTGCGGATAAGCTACAC
>bc25mer_140760-20 TGGTGGCTCGTTATCACAAG	>bc25mer_167568-20 GCATAGATGGTTCACCCGTA	>bc25mer_193734-20 AGAGATGCGTGTAGGCGATT
>bc25mer_141708-20 TCTGAAGCGTGGCCATTACC	>bc25mer_169085-20 GTCTATAAGCCGCGCTGCAA	>bc25mer_194512-20 CCCTTTCGAGCTAAGTTTGG
>bc25mer_141799-20 CATATGCCGGACATTCAGCT	>bc25mer_170764-20 GCGGAGTATGCCATCATGAG	>bc25mer_196660-20 CCTTAAGCAACCCGTCGATG
>bc25mer_142929-20 ACTAATGGTCTGCGGCATA	>bc25mer_171455-20 TGCCGCGATCATCTACTATG	>bc25mer_197001-20 TTGCTCGTGACTGAACAACG
>bc25mer_146048-20 GGTGCCGTGTTGCATGTAAG	>bc25mer_174112-20 GACCGGGTATTCGACGTCAT	>bc25mer_197794-20 GGTCGTGCGTATAAGCCTCA

FIG. 3C

>bc25mer_198508-20 CGGATGGTCTTCGTTAAACC	>bc25mer_213506-20 GGTTGCGTGCCACTTAAAGC	>bc25mer_229488-20 CAGCCGGGCCATAATAGTTG
>bc25mer_198891-20 GGCACGGTGGCTAGTAACGA	>bc25mer_216161-20 GGAGGTTGCGTTGTACTGCA	>bc25mer_229709-20 TGCGGTGGACCTATTATCCT
>bc25mer_200581-20 GCCGGCCCAACTGATAGTAG	>bc25mer_216486-20 GTTGTCGTCTCCATCGGTT	>bc25mer_229929-20 CCTGCGTTAGGCAATCCATC
>bc25mer_200721-20 TCGACTTCGGTCACCTTTCC	>bc25mer_218887-20 GGGACGGAACTACACATGTG	>bc25mer_230898-20 GTGGGCTCTTCGAAGTAACC
>bc25mer_206382-20 CGGGTCGATACTTTCCTCGT	>bc25mer_221408-20 GATCCATCTGATTGAGGGT	>bc25mer_233755-20 GCCGTGGACCACTAAAGTTC
>bc25mer_207645-20 GTGCCGTGTGAATATCCGA	>bc25mer_222754-20 CTTCATGGTACCGGTTGAGA	>bc25mer_234401-20 GCTTAAGTCATGGGCGCATC
>bc25mer_210956-20 CGCGCCTGGAATAACTCCTA	>bc25mer_223329-20 TCGGTCGGCTGTAAGGATAC	>bc25mer_236515-20 ACAGGTAGTCCGCGCACT
>bc25mer_210958-20 GTCAGGGAACCGTTTCTTCA	>bc25mer_224422-20 ATTGCACGAGGTCAGAGTCG	>bc25mer_237582-20 GGCGTGGCATTAGACTACC
>bc25mer_210961-20 CTTGTCATGTACCCGAATGG	>bc25mer_225143-20 GCTTAGATCCGCTCGCTACG	>bc25mer_238816-20 ACTACGGCCAACAACCAACA
>bc25mer_211638-20 CGACCTGGCTACGTAGAACC	>bc25mer_227128-20 CGGCTGGCCTACTGTAGAGA	>bc25mer_238839-20 GTTGACAAGGCTCTGTACGG
>bc25mer_211770-20 CTAGCTAAAGGGCCGTGCGT	>bc25mer_227360-20 GCAACATGACCTGTCATCGC	>bc25mer_239304-20 TTGTTCTCTTGCCGGTCGAT
>bc25mer_213351-20 AAGTATTAGCGCGGCAACGT	>bc25mer_228435-20 GGCCGCACGATATATTGAC	>bc25mer_239849-20 GTTGATCGTAGCCAATTCGG

FIG. 3D

Exp-1_acnB-73_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCAGCTCTACAAGTGCGGC CATTGGTT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-191_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTTCGCGATAGCAGCCAGGA AGCCTGCTT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-671_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGCGGAAACCTTTCTGTT GCAGAGCTT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2404_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCAGTTCCGCAGAAGCCAG GAAGACATT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1307_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTGTGGCAGAAAGACTGCA TCACCAGGT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-779_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCGCGTTTGTTCGGCACAT GTGGAATAT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1343_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTGCGTGTTACGTCAACTG GCTTCGGAT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1961_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCTGCATCGGCTTCCAGCA GCTCAGGAT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2131_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAGCACGGAAGTGACCGAT GTTGGTCAT
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2039_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCCGGGTCGTTCCGGAGCAC ACAGGATTG
CATTGC GCTTCTCCGGAAACATTAGC

FIG. 4A

Exp-1_acnB-2262_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACGCGCACCCTCTTACCG AAGACGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2542_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGGCTTTCTCGGTGTAAGT AGAAAGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2369_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGTACCCAGACGGTTCGGGA AGTTACGGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1811_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTTGTTTCTGCTTGTGTTAC AACCAGCGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-428_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCCGCCAGGACTGCATAA CCTGCTTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-744_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCATAAACACAGAACGGAG TTAGTGGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-393_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGTTGCCTGCTTTCGCTTTC TCTTCTACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-530_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGTGCCGGAGAAAGGTCAT CGGTGTTAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1378_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGCCACGGTTCATAATGAA GTCCGGCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2170_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTCCGCAACTGACCTTTATG CGCATCCAG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4B

Exp-1_acnB-943_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGTTCGCCGGTTTCGTGGTT ACGCACTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1881_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGCCGTAACCTTCGCGATC ATCCACTTC
CATTGC GCTTCTCCGGAAACATTAGC

Exp-1_acnB-634_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTGATCGGACCAACAACACC AGGCTGGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1224_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGTGGTGTCTGGGAACCT ACAGAAGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1768_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGACGCATCGGTTAGCTCAA GGCCTGCTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2473_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTACCTGCGCCACGTAGGT CTGGTACTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1005_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACGGCCACCAGCACGCACT TCATCAATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-352_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGAACATCAGCAGCGTGTG AGAAAGTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2002_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AATATCCGCCAGATCGATGTC GATCACTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2088_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACACTTCGTGATCTTCTCA CCCTGTACC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4C

Exp-1_acnB-1681_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTGCCTTTCTTCTCAACGGT CAGCAGACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1916_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATGCCCTGAATACGACGTT CCAGGGTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1478_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAAACGGGTATGGGAGTCAC CACCGGTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-706_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAAGAACCCGTACCCACAAC GTCACCGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-897_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTCAATCACGTCGCCCATG TTCAGGTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1515_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCAGACCAGAACCCGCCGGG AAAGAGATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1581_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGAAGCGCACCAGAACGGAT TCCGGCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2226_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTTCTTCGGTCAACTGTGCG GCGTCCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-2297_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTTACCCATACACAGGGAAC AGCCAGGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1733_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAGATCCGGCAGACCTTCAA TTTCCAGGA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4D

Exp-1_acnB-305_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTTTGCCATCATCCAGCG CGTCGATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1266_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCAGGCACGCCAGGTCTTTC AGTTCATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1040_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTTGGTGGTCAGGCCACGCC CGATAATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1646_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGATCGCATAACGCGGAATAG CGTGTACCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-848_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTGCACCCGCGTCTTCCA TCGTGTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1436_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGCAGCATAACGGTTCAGCC AGGAGTGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_acnB-1105_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTCTCAGCGACATCTTTCGC CTGACGGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-646_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTTTCAAGGTCGCCCGCCAG TTTCTGTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1951_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGGTGCTGGAACCCCGGC ATAGAAGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1354_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTCCCGTTGATACCAACAGC ATAACCTGT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4E

Exp-1_bamA-686_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGAAACGGGCATAACCGCGAT CCAGATAGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1189_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGAACACGTTGGGTATCGGT ATCGACAGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1410_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGGTGAAGTACGGGTTGGTT ACCGACAGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-857_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAGCTACCCGGCTCGATCT TAGTCAGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1490_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTTGGTATAGTCGGACAGGT CGGCGTCAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-85_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCACACGCTGAAGGCCTTC GAAATGAAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-564_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGAATGAGAGATCAGTTCG TCGGTGGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-508_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGCTGGATTTCAGCTGACAC ACCTTCCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-967_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCGGCATCGTTAATTCGGG CATCGACTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1989_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTGCTTTCGGACCAATGGTA TTGGACTGG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4F

Exp-1_bamA-1224_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCTTGTAGACGACATCAACC TGGTCCGGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1787_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATCCGATCCAGGAATGGTCA CTTTACCGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-50_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCACTACGAACCCTTCAGCAC CGTATACGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1101_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCCATGCACCTTCCATCTGA CGCATTTCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1560_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCAGACCTGCACGCAGCGAG TTATATTCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-2382_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACTGGAAGTGTCTGCCTTG TCTCCATCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-145_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTTCATCATTAAACCGTGTC GCCTGTGCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1700_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCCAACCATAGTTGAACGTGA AGTCGTCCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-2299_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATTGTAATGCGATACCCGC AGACATACG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-611_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATTTACGATCGCCTACCACGT TCCACCACG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4G

Exp-1_bamA-2229_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGCTGGAATCCAGTTTGTA TCCCAAACG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-423_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGCTGGCGCTATATTTACCG ACGCTGTAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-2095_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGCCTACAGCATCATCCGA TTTACACAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-721_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTGGCGTCAGACTGACCTG GGTAGAGTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-2059_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGCCGTCCTGAGTCGCACA TTCGTAATC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1857_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAACCCATTTGTGATCGTCA TCGATCGGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1630_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCCATAGAGTACAGATAACG CCACATCGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1260_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACCAAAGTTGAAGCTACCG GTGTTGCGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-1445_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATAGAAGAGACGACCACCGA GGCTTACGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_bamA-892_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCATCTTCCATCTTGGTAC TTTGGTGCC CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4H

Exp-1_bamA-1029_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGATCTTACGCACGTAGAAA CGGTTACCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1066_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGACGGCATCTTTCGAGGT ATCGTTACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1154_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAAGCCCAGACGATTCAGAC GCTCCTTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1751_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGACACGTGAACCATCTGTCG GGAAGTAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-15_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCTAAACAGCAGCGACGCT ATGAGCAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1595_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAGGCTGCATGTTGGACAGGG AGTTATGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1525_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGGAAGCCCAACGTCACGTC TGTACCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-2024_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGATCATAATTACTGGCCT GATGCGGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1665_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAGCTGTTATCCTGATCAGAG GTGCTCGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-234_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCTGAACCAGAAGGGTATCA CCATCACGA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4I

Exp-1_bamA-1911_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCATCTCTTTGCCGCTAAA CCATCACCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-1318_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTTATCCTGCTGCACACC AGCCTGGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-932_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGATAGGCATAACCATAGC GACCGAGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-803_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAAGTTGCCGCTCACTTCAA CGCCAGAAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_bamA-199_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGAACATCCTCAAAGTTGCC GGTAGCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-721_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTGGGCTTGCACGTTCAA CCAGTCACT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-764_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGTGAAAGCGCATTACAGA GCTGTTGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-418_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGCGCTTCAATTGCGCGTA CTGATCCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-143_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCTTGTGGAGGATAGTCGG AATAGCTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-637_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGAATTTGGTCCGGTCCGCC TGTAATGAC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4J

Exp-1_btuF-595_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAGCGTGCTAACACCTGTT CCGGCTAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-240_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATTACCTCCACGCCAGGCA ATCACCAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_btuF-87_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAAAGGCAAGTTCAGTGTTG CCGGGAGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-349_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATATCGCGGATATGCAGCAG CCAGTTGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-202_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTTCAGGTCAGTGTGAAT GACCAGGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-167_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATTACGGTGAACAAAGAGTT CGCCCGGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-630_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGTGGTTGGCGTGTTCAGC TTGAGGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-132_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGTTAAACGTTCTGCAGGA ACGCGACTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-434_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGTTCCATGACGTTTCAGTT CACACAAGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_can-237_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGAGTACATCCACTGCATAC TGAACCACG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4K

Exp-1_can-480_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTTCCACGCTGATTGCATA ATGGTGGAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_can-595_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCGTGACGGTAACGTTGCTC AAGGGTTTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_can-279_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCCGCAACCGTAGTGGCCA CAGATAATA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_can-559_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTGGCGGTAACATCCAGATC ACGCAGCAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-414_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAATGATTCTCGTCATAGTGC CAGGCCCGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-37_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGAAACAACGCCGCGATGAC GACGGGTAT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-87_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAGCATGCAGACCACCAGC GTTACAATG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-319_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAGTTACGCCAGATTGCTGC GGAACCTGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-247_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAAGCCCAAGTGAGATTTC AACCAGCGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_cdsA-809_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTAACAACAAGCAAGCAAAGA CCGGTACCG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4L

Exp-1_cdsA-449_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGATCATGACATAGAGCAGCC ATATTGCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-749_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACCACCGTGTCTGGAATTA AATGACCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-490_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTTGCCAAACATATATGCGCC GGAGTCAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-575_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCTGCAGTAGCGAGTCCAC CGATAAAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-700_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGCTTAAACATACTCTCGGT CAGATCGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-179_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATCAGCGCCAACAATAACC CGCATAACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-618_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGACGTCGAGATTCGCCAC ATGCCATAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-282_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCACCAGCAATAGCGCGACA ATCCACCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_cdsA-665_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGAGGCTAACGCTGCGACAA TAGAGCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-653_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAACGCGACCGTAGTGGATTT CGCCGGTTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4M

Exp-1_dapD-93_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGAATCCAGCAGGGCGATC ACCTGATTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-384_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTGCCTTCATCAACATATGCG CCGATGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-148_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAACCACTGATGCGTCACCCA CTGACCGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-51_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTAACGGTGTCTGCATTGGCT GCGTGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-724_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACCGCACAGTAGAGGCTGTA TTTGCCATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-794_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGTCGATGGTACGCAGCAGTT CGTTAATGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-613_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AATACGGGTGCTCTGACCAAT GTATACGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-540_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTTCAGAGCGCGCGCCGATG AAGCAATTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-348_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGGCATCAGCACGGTGTTA CGGGCAATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_dapD-257_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCGTCGTAGTCGGCGAATT TCATCGGCA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4N

Exp-1_dapD-292_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGCACAACGCGGAAGCCTTC TTTCTGGAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_dapD-419_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACAAGAACCGACGGTCGCCC AGGTATCAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-302_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTAAACCGGCACCTTGCC ATAGAAGTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-95_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTCGACAGGATACGCGTCAA TACCGCCTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-814_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTGTGGCTGGTCATACCCGG TGAGGTATT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-766_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGTCCATCGCTGTCCAGCAT AACGTCAAT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-614_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGCCTCATAATCATAGAAGG TTCCGGACG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-726_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTTTGCAACCTAACGTCGTC CATGCTTTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-168_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCGACCGTGTAGCGGATA AACACTTTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ddIB-435_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACATTCCCACTGGAACCT TCGCGGCTC CATTGC
GCTTCTCCGAAACATTAGC

FIG. 40

Exp-1_ddlB-559_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCTTCACCGAGTATCGCAAC CGTGA ACTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-394_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACCGGCAAACCCAGAGCAGA AATTTCTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-691_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAATGCCTGCAAATTGGCCTC TTGTGACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-259_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCCATTGAAAGCGCAGATGC CATCACTCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-891_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGTCCGCCAGTTCCAGAATT CGTACTACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-133_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCCATCGACTTCAGTTGCGT CACGTGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-55_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCTAACACCGCTGCGCCAGA ATTCAGAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ddlB-224_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTATAAGGCAAGCCCATCA GCTCGAGCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1219_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGTTGTTCACTACCACGCC CTGATCTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-703_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTCAGGTTAACCGCGCACC ACCGGAGTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4P

Exp-1_degP-1114_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCAGTTCAGGTTACGTT AACCTGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-948_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGCGGAGGAATTAGGCAGA ACCTGGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-13_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTCAGAGCCAGTGCCTCAG TGCTAATGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1184_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTTGCTCATCTCAGCGCCTT CAATGCCGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1359_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGAATGTTGAGTGCCAGCACA GACGGTTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-319_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGGAACCCAGCGCCATGAA TTTCTGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1149_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATGGAGCTGGAATCAACCTGA TTCTGGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-852_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATAATACCCAGTCCACCGCT TTCACCTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1015_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCAAAGCTGCTGATCGGCTT ACCGTTTCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-904_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGGGCGTCAACTTTCATCGC TTTCGCCAG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4Q

Exp-1_degP-86_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATCTGCTGGGCTGTCGTTG CTGAAGAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-603_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCGCAGAGACAATCCCGGAA GTTACCGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-481_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGGTCTGGATTGATCAG CGCGATATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-741_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTGCGAGGATCGCGGTGTTG ATACCGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1394_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTGCATTAACAGGTAGATGG TGCTGTCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-371_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAACAACGTGGTTGTTGGTGA CGACATAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-411_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCCATCGCTCAGTTGAACT TTAATGACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-141_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTTAATGCTGACCACTGAA GGCATCACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-1294_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACTGCCTGCTGGTTCGCGCC AATAATCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_degP-528_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGCGCAGTGCATCAGAATCC GCCATCTTA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4R

Exp-1_degP-565_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCAAACGGGTTACCAATCGC TACGGTGTA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-177_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCATACGCGCGTATTAACG GTTGTGCTA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-1076_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTAAGCCCAGGGTCAGTT TGCTGCCTA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-446_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGATCTTTGCCAACCATCT TCGCGTCGA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-258_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGCAGAACGGAGAGCTCTGG AACGGAGAA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-223_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGGCAGAACGGAGAATCATC ACCGAAGAA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_degP-48_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGTTGCAGAGAGCGGAGAT AACGCCAAA CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_erpA-158_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGATGGTCATATCGCCTTCGT TCACCTGAT CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_erpA-63_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGATTCGGGTTATCTTCGTCA GCGATCAGG CATTGC
GCTTCTCCGGAACATTAGC

Exp-1_erpA-314_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGATACTAAAGGAAGAACCGC AACCGCAGG CATTGC
GCTTCTCCGGAACATTAGC

FIG. 4S

Exp-1_erpA-28_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACTTTGTTGGCTGCTGCGTC GGTAAGCTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_erpA-238_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCTTCGGTATAATCAACGGA ACCGCCGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_erpA-277_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGTTCGGGTTGGTCACGAT GAAACGAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_erpA-123_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAGGTGAAACCATACTGGAAG CCGCTGCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-409_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCCTGCAACTTCAGGCCATT CAGATAGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-599_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGTCTGGAACAGGCTGTCAG TACCGGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-529_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTGACCATATTCAACAGGCC GCCAGGACT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1514_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCACCACGCCAGGTAACT GTTTGTCAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1253_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTCGTAACCAAACCAGGCGT TGATGTCAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-490_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTAAAGCACGGAAACCGGGCC ACGCATAAT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4T

Exp-1_fhuA-176_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTAGCAGACTGTCGCGCCG CAATAGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1471_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTCCCGCAACGCGGTTAAG AGATTCTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1799_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTTTTGCTTCGATTCTA CGCCACGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1183_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCGATATCGCCAGTGGCAA CTTGCTCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1100_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACGTGCCAGATAATGGCCTT TATCCGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1029_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGGAGCAGACGCCGTAACCA TAAACGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1871_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGTAGTATCGGTGGTGTATT CCGCATCGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1218_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACGCATAAAGTCGACACCG GTCAGCAGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-264_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACTTCGGCTGATGCAGCGCC ATCTCTTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1323_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGGATCTTTGGCATTGAAG TCGAAATCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4U

Exp-1_fhuA-2129_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGATCGAACAGGTTGTAA CATGCAGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-873_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCATTAAGTCTGTCCGCAGA CGTTACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-455_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGTTCAGCATATACGGT CAATGACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1693_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACACGGCACCAGTAACTAC AATCGGACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1435_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTCATAACGACCGCCTAG GGTGACCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1600_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCATCCTTCCCAACTTGCGA AGAAGGTTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-118_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAGGTGCAGCGGTAACGGT GATAGTGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-939_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AATTCGTGATCGAAGCTGTAG CCGACCATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-2167_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAAGCAGCCATAAGTGTTAAA GCAGCTGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-2029_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCCCACCTTAAAGGAGTTAGC CGGATCACC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4V

Exp-1_fhuA-2215_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTAGAAACGGAAGGTTGCGGT TGCAACGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1288_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCGGATTGTACAGATTGAG CAGTGGCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-734_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAGGTGAACGCCGGTGCAA TAGCATAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-664_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAAGACCGGTCAGGCGATA AGAGTAAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1399_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCCCACTGCGCCTGATCCTG AACATAAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-2084_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATGCCGACTCGCGCCAGAT CATAACGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-309_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTACCAACAGAGACACCCGGC GTGTAGCTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-358_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAAAGCCGCGAATGATCAG GTGGTCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-564_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGAACCTTTTCAGCGGTTTCG GTGGTCGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-47_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTAACCGCTGTGGCTACTA CAACTGCGA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4W

Exp-1_fhuA-82_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTTCAACCGCTGCCTGTGC ATAAACAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-796_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGGTTTCCGGCTCGTTCTG GAAGTAAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-699_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCTTCTGACCCTTTCTGCTGG GCATTGGCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-980_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCAAAGCGCAGGTTCTGAC GCACAGTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1764_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTCGCCACCTTCAACCGAG AAGAAGGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuA-1966_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCGTCAGACCTGAAAGCGG ACCGTCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-257_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAGGAAGCTGCTGCGGCAAAT AAGCCACTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-536_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGACAGCACATCAACCTGGT GGGCGATAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-133_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAGCAGAGTGATTACCAGA ACCGTTGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-720_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCATCGGGATGCCATAAATC ATTTGAGG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4X

Exp-1_fhuC-221_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAAACGCTTTGCTGCTCCAGC TTTCCAGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-639_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCGCAGGGCGACCAGATAA TCACAGTAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-310_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACGGGTAACGACCAATCGC CACCAGTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-500_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGAGGTCGGTTCGTCGAGCA ACAGACAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-95_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACCGGTCACCTTTCCCGGCAG GAAAGGTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-578_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAATGACCGTCAGGCCACGCT CCTGACTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-45_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTGCGCCCGGGCACACGAAAG GAGATATTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-431_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGTTCCGCCAGAGAGAC TATCGACCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_fhuC-680_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATAATTTCCGCAGGCGTTC CCTGAGCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-321_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGTGCGGAACGGTCAGGCGT TCAGTATTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4Y

Exp-1_folk-16_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGAGAGGCCAGATTGCTGCC TATGGCAAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-281_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACCAAACAGCATGATGTCGA GATCCAGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-391_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCAGGAAACACCAACTCCGG CGCGATTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-148_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGGCTGCGTTAAGTAATC GGGTTGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-80_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTAAGAATGTGGCTTTCAG GGATATCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-183_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGTAGCTTTCAGGTGCAAGA GAGGTTTCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-356_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGCCACAGCATAAATCCAC GATTCTTCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_folk-230_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTTGCGGACGCGACCTTGCT GCAATTCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-866_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTCGATCACCTCTGCCAGTG TCTGACGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-608_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCGATATCGACGACGAGA CACCCAGTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4Z

Exp-1_ftsA-721_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCGTGCCAAAGGCGTAAGC GATATCACT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-43_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACTAAAGCGGCAACCTTCGC GGTACCAAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-429_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCACGCCCGAAAGTCCTACC GGATTCTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-475_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCATATCGTTGTGACATGT GATCAGGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-264_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCACCATACCAATTCATTC TGGCAGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-117_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTTATCCATACCACGCGAC GGGCAGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-393_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCCTGATAGTCAATCGCATACTCTTGCGGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-679_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAGCATAAGGAATTACCTT AGTGTGGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-1136_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTCTTTCCCATAGTGAAGCA ATCCCACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsA-1095_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACGGCTCCTGAGCATAATCC GTTAAACCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AA

Exp-1_ftsA-82_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAATGATATTGACCATAACC GTCGGGCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-526_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGTTGGTCAACTTTCAGCCC ACAACGTTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-196_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGACAATCTGCCATCAATTC TGCCTGGTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-907_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATCTCTTCGTTGACCAGGTT GAGCAGCTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-768_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCAGCGCACAAACCGTGGCGA ACTTTAATC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-562_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAATACCGAATAACTTGATGC CAGTCCGGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-1040_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCACTTGCGTATGAAACACGC GCTGAGCAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-1221_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAGCCA ACTATTGAGTCGC TTGATCCAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-998_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTGATCTGCGCTGCGCCAC CGGTTAATA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsA-161_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGTTGTACGCACTTGACCA CGGATTCGA CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AB

Exp-1_ftsQ-423_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTCTGGCGGCACGCTGAAG GTATTCCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-464_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCCGGGCCATACAGCATTG GAAGCACCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-500_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTTCGCGATAGCCCTGCAACA CTTCATTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-773_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTGCTGAGTAGATTCCTCTG GCGGCAAGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-216_I1-bc25mer_83004-20_I2-bc25mer_83517-20

ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAATGCCAGGATCGACTGC CGGATATCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-290_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAATCCACGGCAGGCGTTGTT CTATTTGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-251_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTTGACATCTGGGTCATAA AGGTACCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-589_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGTTATTCAGCGTCAACTG CCAGGAACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-47_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGACGCGTTCATTATTGC GGCGAGAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-554_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTCATCGCCGCTTCCTTCA GAGTAAATC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AC

Exp-1_ftsQ-702_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTAGCTAATCCGTTTGCCA TCGGTTTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-388_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCTACCATATGTTGATCATT CCACCGCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-329_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAATTCATCAGGCCACTGCT TTCTGACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-738_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCCTACTGCCGCTCCAGAG TCATAACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-181_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTGTGTAATGGCGTTCACC GGTC AACAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsQ-12_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCTTCTTCGCTGTTTCGCGTG TTCAGAGCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-829_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCAAATGCACGGATGGTGTT ACCTACCGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-552_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCACAGCGCCTTTCAGTACA TCGTTCGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-864_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAGAAGTACCGATAACCACA GTCGCGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-969_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCTGAACCTGCTTATTGGTC ACCAGAGTG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AD

Exp-1_ftsZ-899_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTTACGCGCAGCTCGTCAT TCATATCCG CATTGC GCT-
TCTCCGAAACATTAGC

Exp-1_ftsZ-505_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGGAGATACCGCGGCCAG AACTTTCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-742_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGCCAGACAGGTCGATATC TTCCAGCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-781_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGTCGAAGCCCGCCGTGAT GTTAACCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-934_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGACGTTTGCCATGCCGAT ACCTGTCCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-706_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAGATAGCCATTTTCAGCAGC TTCTTCCGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-291_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACCACCCATACCCGCAGCA ATAAAGACC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-326_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTAGCGACGACTGGTGCTG CACCTGTAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-182_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCGCCAGTCCTTTGGTGA TACCGCTAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_ftsZ-1069_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAGTTTGCGGCGCATTGTC ATTCACGAC CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AE

Exp-1_ftsZ-622_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATTACGGTTCGTACGTCTGC AAAGTCCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-587_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAAACCGGACGAGTAATCA GTTCAGCGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-377_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGAAAGGCTTAGTGACGACAG CAACGGTCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-27_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGACGCCGATGACTTTAATC ACCGCGTCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-1004_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATCCCATGCTGCTGGTAGC GATCCATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-470_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTCGTTCCGGATAGTGATCA GAGAGTCCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-118_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCGCTTGTCATCGGTATT TACCGCGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ftsZ-77_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCATGCGCTCGCGACCA TGTGTTCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-965_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACCCGTTTGGTGTCTGGCA TATTGCTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-820_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCACTCCGGCGAAGCGGT TTCTGCTTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AF

Exp-1_gcd-1189_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGTGCCAGGAGTTTGCGA GTTAAAGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-785_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATGATAAGAGACACCACGGC AGGTTACGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1154_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTGTTTCGTCAGACGGGATTG CGTTCGGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1502_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGAACCACCAGTTCGCCAT TACGACGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-368_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCGCTAATCAGCAGTGCGA CCACCAGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1447_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCGAGCGTAAATAACTGG CACTTTCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-644_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCACTTTAATCGGCGTCA CTCATTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1975_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCTGGCTGTTTACATGGCAG ACCAAATGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-877_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AATCGCAATCAGTCGACCATC ATTGACCGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-930_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGAGCACGCCTTTATTGGCG AAGGTTTCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AG

Exp-1_gcd-1616_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACATATCCGCACCGCTCAAAT CTTTCGTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-542_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTATCGGCGTTAATTTGTT TCAGCGGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-23_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGGCTGTTAGCGTGACGAGTA ATCGTCGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2325_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGTCGCCCATCTTCGTACCA AATGAACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-126_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGAGCATCACAAGGCCAGCG ATAGGGTAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-403_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCGGATCGTTAAATCCGGC CCAGGTCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-679_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGCGCTGGTGAGCGGTACA CAGGTAAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1729_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTACCCGGGAAGACCAGCGT ACCCTGTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1000_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGGTGATAATCGGTGGCGA AGTCGGTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1387_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGTGCCGGAAGATCCATGTC CCACAGGTC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AH

Exp-1_gcd-1240_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTACGCCCCATCGGCAGATA GACCAGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-728_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGATCGTAATGCCATTTCT CTTTGCCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2362_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTA CTTCACATCATCCGGCAG CGCATAAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1352_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAACGGTCTGGTAGCTCCACG CCAGTTTCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2290_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCTGCGGAGATCACACATA CTGCTTACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2159_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCGTAGCGGCGATAAACA GCACGTTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2255_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTT CATAGGTCATTGGCGTAG CCTGACCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1789_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCAATCGCCACTTCACGATT TGGATCAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-247_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGAGTCAGCGCCAGAAGTC GAAACCAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1940_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAACGGGTTGAGCGTGACAC CATA CGGTA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AI

Exp-1_gcd-2194_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGTTGCTCATGTTGTAAGC GCGCAGGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-603_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGATCGTTCGGCTGCTTACA TCGCCAGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-76_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACCAGCCAGCCTCCGCCAAT GAGTAGATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1682_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCCTTCATAGCGCATCTGGT GGAACATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-507_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTGACCTTCCTGATTACGA CCATAGGCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2048_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGCGGCGTACCAATACGTT TCTTCCACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1839_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGGACCACGCGGGATCAGT TTCGAAACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-2113_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCGCCAGCATCGGCATACC CATATTGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-298_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACAAACGGCAGGATCAGCCA GATGCCGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_gcd-1066_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATCACGCCAGACGTTTCGCG GGTTGAGAA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AJ

Exp-1_guaC-112_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGCCGACCAGCTCTGACC TGAATGTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-407_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCTTCGCAACGAACTGCA CGAAGTGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-148_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTGCCTACGGTGTCCATATT TGCGGCGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-458_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCAGTCACTACGTTACCAG CACAAATGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-351_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAAACGAAGTTTAATGCCGGG TTCAGGTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-760_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAATTTCTCGCGTTCTCCTC AACGATGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-39_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAGTGGAGCGTTTAGGGCGG ATGAGAACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-641_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGTGCAGCCACCATCGCTGA CGATCATT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-499_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACGATATCGGCACCTGAGAG GATAAGCTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-989_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTGTTCTGCACACGAATAA ACGTGGTGC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AK

Exp-1_guaC-74_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATTGACGTTCCAGTTCAACAT CGGAACGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-541_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGCGAGTTGTACAAACAGA ACCTGGGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-811_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAACGTGACGTTTCATCGC AGACTCGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-598_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAGCATCGGCACATTCGAT TACCGCAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_guaC-302_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAAATCCGCATCAGACGTAC CGGTAGAAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-416_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCAGTCAGCGTGACCATGGT AACACCCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-298_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCATATCCATGGTCGGGAC CAGTTCGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-996_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTCTTCTGCCGTTCCAGC AGACCTTCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-250_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACTTCCATTTCCGTTGGTGC ACCAAAGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-628_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAACTCTGGCAGCGGCGGAAC ACAGTTCAT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AL

Exp-1_hemL-961_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTGTTGTCAGCTCATCCAG CGTTTCGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-1211_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATTGATATCTTCCATGCTGT GCGCCACGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-708_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTACGCGAAACCGGTCATC ACTTCATCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-120_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGCCATCAACATCGTACAGA TAAGCGCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-762_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGAGGCAGGTTAAATCTGGC ACTACGCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-547_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCAAATGCGGCGGTACAGA AGCCAGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-1249_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAACTTCGAAACACCCGACG TGCAGCATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-1113_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTTAAAGCGTTCCACGTCA CAGGCCATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-500_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGTATATTTGGCGAAATCTG CCGGAACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hemL-333_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCATGGTCGCTTCAGTGCCG GAGTTCACC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AM

Exp-1_hemL-830_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGCGCATCCATTACATCAC GACGACCAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-1171_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTTCAAACGCTGACGGTGC CAGGTAAAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-923_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTGCGGACTTCATTACAGAC AGGCGAAAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-888_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCATCGCAATCGGGTTACCG GAAAGCGTA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-1040_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACCGAACATGCCGCAACGT GGTAAACGA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-452_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTAACGTGAGTGCGCCAGAAC CGGCTTTCA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hemL-593_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCACCGGCTCGACGATAA TACAGGCAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hpt-483_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGATATACGGCAGATGACGG TAACGCTGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hpt-80_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATATCGCTGCCGCTGTCTT TGTAACGCT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_hpt-330_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTTCGCGCAGGCTTAAGATC TCACGCACT CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AN

Exp-1_hpt-153_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCATGAGATACCTGAACTTCA CGGCACAGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-365_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTTATCCAGCAGCGTACAAA TCGCCAGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-400_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAATTCTACCGGGACGTTTAC TTCACGACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-271_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTTCAACAATCAGCACGTC CTTGCCACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-189_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTACCGTAGCTGGAGGCG GTCATAAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-447_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAATGCCGTAACCCACCACA AACTCATCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-115_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAACATAAATGAGCCACGCAG CAGACCCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_hpt-41_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGACCCAGTTCGGCGATAC GCGCTTTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-376_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTATTCCCGGCTGTTAGCGC TTCAGATTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-339_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTCTTGCAAACGCGAGTTA AAGCGACTG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4A0

Exp-1_ispU-304_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAATAATACGCAGACGCAC GTTATGTTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-180_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAGGCATACAGCGTTAACGCC TCAATACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-411_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACCGTAGTTCGCCGCAATA TTCAGCGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-486_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTGATCTGTTGCAGGTTT CCTTGCTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-106_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCTTTATGCCAAAGGCACG AATCTTCCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-446_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTTGCCTGACTCCCTGGA CTATATCCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-655_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCTTGTTTCATCGAAATCGGG CCAGAGAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-257_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTATCGAGCGCCACACAA ACAGTTCCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_ispU-706_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGCCGAAACGACGCTCTCG ATTAGCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-389_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATGCGTAGCGCCAGGTACA GGCTTTCTT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AP

Exp-1_map-151_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAGGCAGGCAGAAACCGCGTG TTGTTCAAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-301_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAGGTATCGCCGTGGAAACC ATCTTTGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-766_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTATTCGTCGTGCGAGATTAT CGCCGGGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-79_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGCCCGGTTAACATACGG TTCGATCAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-187_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGAGATGCAAACGGATTTCCG ATAGCCGTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-114_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAATCATTACAGATGCGATCC AGCTCGCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-247_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGCCATCTTTCAGCAGCTT AGCATCGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-597_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGTTGACCATTGGCTCGATG GTGAACGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-639_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGTCCAGCCATCTTTCATG GTGCGGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-731_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCCTTGCGTAGCGTCAGAA TTTCGCAGC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AQ

Exp-1_map-481_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCCGCAATATTCACGAACGAC GGAGAAGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-516_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCGGTTCTTCATGGAAGCCG CGACCAATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-562_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGTTTCAGTACGACGTTGGT TTCACGGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-446_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCGACAAATTTCTGAATCG CCGCACCGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_map-338_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCATGATGGTCGGCTTAC CGACGATAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1945_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCTGCGGGAAGCTCTGATA CAGCACTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-146_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTACGCCCTTTGCCTTTGC CCTTACCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1588_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCAATTGGCGCATCCGCAAT CCACGTATT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1167_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCGGACGGGCACTCAACATG TCATAGAGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1001_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCTTAGCTCTTCTACCGGGC GACCAAAGT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AR

Exp-1_mrcB-861_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATGATCAGCGCCATGTAAGCT TCGTTCGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1670_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACCAGCATCACTCTGCCGC TTTCGCTAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-944_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGATTCGTTGTCGCCGCTCT GACCGAGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2181_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGGCACCATACAGTTTGGTC GGCTGGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1036_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTTCACCATACCGACTAACAG CGCCTGCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-446_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGGACGGCGAATCATCTCAA TGCTGTTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1635_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTCATCATTCTGCGGTGAC CAGACCTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1710_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGATTTACCGTCGGCACGTTT ATCGAACGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-325_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTCATGTCTGGCTCAAGATT GACCATTCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1457_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAACTGCGGCTCAGAACCTC CGACCATCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AS

Exp-1_mrcB-896_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTCAAGAATACGGTCTTTGC TGTAACGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2493_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACATATCCTTGATCCAACCG GCTACACCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-826_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTAAGAACGCTCGCTGGA GAGGAACAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-582_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATGGTGATCAGACGCGGATCA AGACGGAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-617_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAAACAGACGCTGCTCACCGT TTGGCGAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-363_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCGCCTCCAGCAGCTTACC ATCTCGTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-19_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTCGGTTTCCCTTTGCGTCC AATTGGCTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2425_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCTGTTGCTGCGGCTGAGA AGACTGATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-541_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGGTTGTTCTCCATATTGAC GATCGTCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1543_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCTGGCTTAAGGCCGTCAG ATAAGTCGC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AT

Exp-1_mrcB-234_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGAGATAAACGCCGTAAATG GCGATCAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1128_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATAATCTGTTGCTGTTGCAGC AGACGCAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-678_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGACGGTCTTCTGTCCGAGC AAAGTATCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1377_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGCTCAACTTACGCTGTTTC TTCAGTGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-784_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGTTGCGTCAGCGTACTCGC ACCCTGTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2244_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAAGATTCAGCGGCGTTGGC GTCTGGTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-736_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTTGCCAGCACCGCACGTCC GATTGAGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2117_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCCGTCATGCCCGCAAACC AGGTATCTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2012_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGTTGTACCACCTGCTGCA TGGTCCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-282_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGGCAGTTGCCAGACCTTG CCATCAATA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AU

Exp-1_mrcB-2286_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTCGTAGTCCACGCCATA TCTGCAATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1422_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACTTCACCACTAAAGCGGTCG ACGACCACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1766_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTACGCCAGTTAATCCAGG TCTCCGTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1241_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGCAGCTCCTGACGCACCA GTTGCATAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-1315_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCCTGGGCCACCGAGTCAA GGTAGTGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-481_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCACCTGTCCTTCTTTACT GTCCGGGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mrcB-2321_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAAGATACGCATGCCACCGC TGCAAACAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mtn-253_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCGTCCGAGACAACGATATC GCCCACTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mtn-323_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCGGACAGCCTGGTAACT GACCGTATT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_mtn-366_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGCCTCAGCGGCAGCGATC AGTTTATCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AV

Exp-1_mtn-67_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCGCAACCGCCGAGACTGAT AGTTTGACG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-634_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCAGGCTGGACTGTTTAGC GGCAACAGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-183_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCACATCTGGCTTGCAGTGT TCCAACAGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-448_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCAGACCAACAGAACCGTT GATGAAAGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-594_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGAAGCTAAGATGAGACTGT TGATCGGCC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-669_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGCCATGTGCAAGTTTCTGC ACCAGTGAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-559_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAGATGGCGGTACGACAAC AAACGGGAC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-102_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAACCTCGTTCCATTCACT TGGCCGGTA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-512_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATGGGCGATTGCCGTCGCTT CCATCTCTA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-137_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCAGCGACTTTACCGATGC CCGATTCA CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AW

Exp-1_mtn-413_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTAACAAATCAGGCCACGTA CAGCGTTAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_mtn-288_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAAATGCCGTGACATCCGCG TCGTGATAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-1430_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTCCGGAGTTGCGGCTTCA GTTTGATTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-282_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAATACGCGCTTCATGAGCG GCGACAATT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-1064_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTAATGGTGGCGTCCACTT CCGTCGGGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-698_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCGCGTAACAATTCGCGGA TCACCGGAT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-741_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGGCATCTTCGCTGAAGCCG TAAGTCGTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-550_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTGACAATCGCCACCATCGG TTGCAGATG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-597_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCTCAAAGTCGCCCTGGTAG GTATCCATG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-402_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTCTGCGTAGATGCTGGAA ACCATCGCG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AX

Exp-1_murC-911_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGCCTCGTCGTCATGCCCT CTCCGTAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-156_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCATTAAGTCTGCGTGACC GGATTTGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-106_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGATAACCTTCATTGGCCAG AACTTCGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-994_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCATTCCTGGCTCCAGCGG GAATTCACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-191_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGGCGATGGTTGAAATAA TCGTCGCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-776_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGGCCAATCTGCTGATAAT CTTCTACAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-1268_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGTCCACGAATTGTGCGAC ACAGCGAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-247_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTATCGGCAGAAATCGCGCT GGAAACAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-1337_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTTAATACCGGTGCCAGCA TCTCGGCTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_murC-321_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCATTAAGTCTAGCCAGCATT TCGGCACGA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4AY

Exp-1_murC-1214_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCGCCAGCCGGATACACTT CCAGCATCA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-515_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGATGCATCACTCTCATCTG CTTCGGCAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_murC-1179_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTATCAACCTGCGTCAGCACA TTGGCGAAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-616_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCACGAGGATCTGCCCGTC AGTGACGTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-578_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAATGCCAATAACCGGGATCG CCAGTGCTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-304_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACCATGTTAGCACCCGGCACG CATAACCGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-62_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGCGAAGCTATAGTCATAAG CGGTGATGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-653_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGGAATGTGACCCCGGTAA TACCAAAGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-8_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTA CTCTGCAGTAAGGAGA TGGTGGTCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_panB-762_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGGAACTGTGTTCTTCGCC GGATAAACG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4AZ

Exp-1_panB-490_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCAGCTTCTAAGGCTAATGC ATCGCTGAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-727_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCCACTTCAGCCATATACTG CCGCACAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-386_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACCTAAGTGACCACATACAG GAACGGCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-351_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCAGCATTGTACGGTTTCT ACCAGCCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-180_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTGTGGTAGGCGATATCG GCAACGGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-242_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATA CGCCATAAACGGCAGGT CAGCCAGCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panB-113_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGCGAATCGCCCACCAGCA TGACGTTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-775_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGGCGGCTACCAGAATTAC TGCCCGTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-406_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATGTCCGGCTGGACCAGGTT GAACAGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-37_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTGCCTTCCATACGCAGGCG GCGAATTTG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BA

Exp-1_panC-226_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTTTGTAGCTTCTCGCA GTCCTCTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-297_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTAAGTGTGGTTCAGTA CCGTTCGGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-565_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGTTGTCCGCCGTCAGATA ACCGTTACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-76_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGTGCAGGTTACCCATGGT AGGCACCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-523_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGACCGTCTTTGGCGCGCAT AATTGGCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-111_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGGCTTTGGCTTCGTCGACC AGCTTCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-2_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGCAGCGGCAGGGTTTCGA TAATTAACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panC-332_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACCTCCAGCATGGTCGAAA GGCCAGGAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-26_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCATGAGTCACTTTCACGC GGTGGAGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-274_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGGTGCGAGCTTCTTCATC TGGCATGGT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BB

Exp-1_panD-156_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCCGATGGCATAAGTGGAG AAACGCTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-63_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCCTGGTCAATGGCGCAAGAA CCTTCATAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-352_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAAGCAACCTGTACCGGAAT CGTTTCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-239_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGCTGGCGATGATGACAATAT CGCCGACAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_panD-204_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGTGGGCCGCCGACCGTTA ACAGAAATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-1007_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAAAGCGTCGTGATAGTCA GGCCGCTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-652_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTTTCCGGGCTGATGCGCAT ACCCAATTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-1102_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCAACTGCCAGATATCGCG GGTTAATGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-920_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAACGCCGGTTCACGCGCA TATCGTTAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-1314_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGGTGACGGTTCATCC AGCTCGTTG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BC

Exp-1_pcnB-960_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGTCTCCAGCAGTGGGTAC CAGAACATG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-478_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACAGGCTGTTGATAGTGAA ATCGCGGCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-728_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTAAAGCGATTCTTCAAACA GGCGTGCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-767_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAGCTTATAGGTTTCGTAAC CGTAGCCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-268_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTTACGGAACAGTTTGCG CACCTGCTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-569_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTTCCGGTTACCAATCAGAC GGATAACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-1176_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCATAAGCCGCACGGAACCTTA GGATGCTCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-533_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCAGATCCTTCATGCCGCAA CGTAATCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-371_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGTCGCTGACGTTACCTTCGT GGTGTCCAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pcnB-336_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCGCAACTTCGATAATCTCC GGGCCAAAC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BD

Exp-1_pcnB-168_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAACCAGCCAGGCTTCGTAT CCCGCTTTCATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pcnB-604_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCAGCATACGTACCGGATC TTCACGGTA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pcnB-1137_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATGCGGTTTACCCTGACGA CGGGACATA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pcnB-885_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGTATCGGTATTCTTCAGC ACCTGTTCA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pcnB-1211_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTACGCTCAACTTCAGCTC GCAAGGCCA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pcnB-824_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTGAAGTAGCGGTAATGG TCGGGAACA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pyrH-497_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGATCAGCGTAAACACGC CGTCAACTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pyrH-350_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAACAGGCTGATAGCTTCTG CCCAGCTGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pyrH-551_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGCACTTCGCTGTAAGTCA GTTGCTCGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_pyrH-462_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTTCAGCACCATCGGCT TCAATTTTCG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4BE

Exp-1_pyrH-139_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCAATCACCAACCAACCTG AATACCCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-91_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCCTGAGCCATACGATCCAG TATGCTTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-618_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAATCGGTAATTTATGGTCA CGAGCCAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-315_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGCACACGCCATTCAATGGA ATAGCGGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-42_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTGCCCTGCAGAGCTTCGCCA CTCAACTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-425_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGGCAAGCTGCTGAGTCGG TGGTAAAGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_pyrH-390_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTACCTGTACCGGCGGAGAGG ATCACCACA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-723_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATCGACTTTAACGATCCTG TCGCCTGCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-959_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCGACGATGGCGTTGAACG GCCCATACT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-1068_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGGCGATAGAGATCGGCCA CTGAGGTTG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BF

Exp-1_rseP-565_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGTAAATCGAGCTTTACATC CCGCCGTTG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-64_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGGGCAACCCAGAAATGACC AAATTCATG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-758_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATCACAAGGTCACCCACT GCGTTAAGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-245_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATTATTGAAGGCATGGTGGC GGAGTTCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-866_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCGCTTACCATTACCCGGT TACTCTCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-793_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAACGCTAAGGATTTACCCGG GTTATCCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-650_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTACAGGTTCAATTTGCG GCCCACGAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-1138_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTTCACGCTAATAAGCGCAAG AAACGGCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-172_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCCAACGGGATCAGGGCGAT AACATATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-913_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCATCTGGCAAAGGAATGAC TTTCGGCTC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BG

Exp-1_rseP-481_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACCAACTGCAAACGCACGGC ATCCCAATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-530_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCCAAATGGCGCTACTGTAA TGGTGGTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-1286_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTAACAGCACCAGCAGAATCG AGCCAATGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-1008_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCAGCATACTGACCGTCAGC TTCATCAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-25_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAGTACACCCAGTGCAACGAT GAACGAAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-423_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGTTCCGTACCTGGTGCAATT TGTGCTTCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-600_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCGGATCTTCTTTATCAGGC TCAAACGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-387_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCGAATTGGCTGCTATTTTCG CCAACCACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-134_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTATCAGTTCGCCGCCAGA GCGCCTTAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_rseP-99_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTATTGAGAAACGCTCAACG CGAACACCA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BH

Exp-1_rseP-299_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGAAGTTTGCAACCGGACCTG CGGCAATAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-907_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCGTTACGTGGTGCATCAG CATGATGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1073_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTCTGGATCTGCACACCTT CTTTCGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-77_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATCTCCGTTCCATGGCAT TGATGATGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1859_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTTGGCAATCGCTTTAGTCA CCCACGGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1760_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACGCATCAGCGCATCTTCCA TCGACAGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2308_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGGTGCTCTTTCCACAGGGA GTCAAGCGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2184_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTCACGCAGCGTCTCTTCA TGCAGTTCT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1703_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GACGACCAGAACGACCGCGCA ACTGGTTAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1535_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCTGCCAGCTACCACCGA GCACAATAT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BI

Exp-1_secA-1666_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGGGATTCGTGACGCTCGGT ACCGATGAT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-2631_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGGGCAAGGATCGTTACGT CCTACTTTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-2078_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATCCCACATTTCTTCCAGCG ACTGTGGTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-610_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGAGTCCACTTCGTCCACCAG CGCATAGTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-247_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATAACCGCCGAGTAAGTGAAC GTCGAAGTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-1348_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATGGAGATAGTACCCACCAG CACCGGCTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-2427_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCAACGACTCCAGCATCGCT GCAAACATG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-681_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTATACATTTCCGAGCTGTCT TCTGCCGGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-351_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCACGCCTTTACCGGTTAGT GCGTTCAGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secA-2500_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGTTGTTCCAGCTCCTCAAC CTCTTCAGG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4BJ

Exp-1_secA-540_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGTCGCGCAGGTAGTCAAAG CCGTATTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1121_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAGACGGAAGTAGTTCTGGA AGGTGATCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2148_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTATCCAGCCACTCGGCAATT GGCAAATCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-575_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACGCTGTACACGTTCTCAG GGCTGAACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1435_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTTCGTTGGCGTGGAATTT GGCGTTCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-454_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATGCCCGGCAGGTTGATACC GACAGTCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1267_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTTCAGTCATGTAGACCAG GTCCGGCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-853_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCATCCATGATGCCCTCTTT CACCAGCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-955_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACGATGTAGTCGACGTCACG GGTAACAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-763_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGAGAAGTGGCCTTCGCCCTG GAAGGTTTC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BK

Exp-1_secA-1500_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACGACCCGCCATATTGGTC GCGATAGTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2343_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGGTGGATACCCTGACGCAGA TAGTCCATC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1907_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGTTGCTTACGAATGTCGA AGTTACGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2221_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTTACGCTGATACACTTCGAT GGACTGCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1970_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAGTTCGTTACGCTGGGAGT AAATGGCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1821_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTTCGCTGGCTTCATACCC AGTTTACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-505_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGTACCGTAAGTGATGTCAGC TGCGTAAGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1626_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGCTTCCAGTACCGCATCG TGACGTACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1392_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATACCGGCTTTGGTCAGTTCG TTTGACACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2005_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTGTTAATGTTTCGCTCAC ATCGCTGAC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BL

Exp-1_secA-1231_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGAATCATTGGACGGTTGGT CGGAACAAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-282_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTACGCATTTCCGGCGATGCAG CGTTCGTTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-212_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACCAAAGACGCGCTTACTTG CCTCACGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2535_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGCATTTGCGCTAAACGCTCG GCTTCCATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2273_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATGACGCCTTTCTCGAAGT GACGCATCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-386_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CACGTTGCGCCAGGTAGTCGT TGACGGTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-2570_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCTGCAGAGTCGTCATCCT GATGGCTAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secA-1007_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGCATGGTACGACCGGTGT GTTCGTCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secM-45_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCATCCCTAATAAGAGATGC GGCCAGAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_secM-346_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGCGCGCTGAGCGTATCCAG TAATGCAAG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BM

Exp-1_secM-174_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCGCTTCCAGCAAGGCCAAT TGACCAAAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secM-81_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGTTGCTGAGCGCAGGCAA CCTAAACTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secM-209_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AATCAACGGAATAGTTTGAAT TCGGGCGGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_secM-311_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCCTGAAGAGGCAAAGATT CTTCAGCAA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-215_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGAATAGTGACGCTGGCAC CCTGTGGTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-407_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGAGAAATCACGCCGAGG TAGAGACTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-689_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCTGTCGGTTAAGTCTTCCG GTTTGGTGT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-724_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCTTTCCACAGCGCAGCGGT AATTTCTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-759_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTGGCATATTGCGCCCGTAA TAAATCTCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speD-593_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGACGTTACATCCACCATGT CATAACGCG CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4BN

Exp-1_speD-139_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACAGGTTTCTGACAGGATTTC GGTCAGACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-371_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGCGCGAAGGTACATAAAC CGCCTTCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-301_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCAAGATGGGCAACGACCGT TTCTGGCAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-250_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCGATGAGTTTCGGGTCAAC CGGTTCTTC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-85_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATAAGCAATATAACCGTCGCG CTCTTCGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-442_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTCAAGCTGGTGGATCAGGTA ATTCAGCGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speD-477_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGCGCACGCGATAATCAATG GTTACGATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speE-622_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCAACGTCGCTGAAGTAATG GCTGAGTTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speE-367_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGATCGTCGTAGCTACCGGC GTTATGGTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speE-159_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TAGATAAACTCGTCGCGCTCG GTGGTTTGT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4B0

Exp-1_speE-194_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGGCCAGTAGCGGAACATGGG TCATCATCT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-229_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGCCGATAATCAGCACATG TTTCGCGTG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-462_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGATAGGATCGGTGCAGTCG GAGATAATG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-729_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCGCCTGAATAATTTCCGTT GAGAGATGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-783_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCCGTATGGATTGCCGATTG TAATAACGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-332_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATACTGACGGCAGAACGATA CGACACCCG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-122_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CATCCAGCGCCATTACGCGAC CAAATGCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-406_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AACGAAATTGACGCCATCGTC GATCACCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-37_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCTACCGCAAAGTACTGCC AAAGTGGTC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_speE-666_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCATGATACCGCCGTAATAG GTCGGGATC CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4BP

Exp-1_speE-542_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTGCGACGAAGATACCGCCAG GATTCAGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_speE-824_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAGCCAGTGCCTTGCAGAT ACTGAGGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-248_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAATGCCGCTGAGATCGCGGT AGCTGTCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-80_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCGTTAAATCGGCCATAT CTTCGGCTT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-21_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CAGACGGCCATCAGGCTGCCG AATAACACT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-315_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGACGTAGGCAAGCAGGCTT AAGGAATCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-203_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTCGAAGGTGTCGTAATTAC TGAGGTCCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacC-149_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCAGTGCGCGACGAATTTGCC CGTTAGGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-506_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGACTGGCGAATTAATCCA GCACCATGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-117_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCACTGACATTACGGAAGAAA TGCAGCGCG CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BQ

Exp-1_yacF-715_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTAGCAACAGGCCAGTTCGAA ATCCAGACG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-613_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTGCGGATAAAGCTGTGAATC GAGCGACAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-210_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACGCCAATCCAGGTCTGGAGT TTACGTTGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-245_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTAATGCTTCAATACGGCTCT GGTCCACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-385_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGTAGGTAATCAAAGCTGCA ACAGCCGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-175_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GTCAAGTTCTTTCAACAGCTC AGTGCGGAC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-305_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GAAATTGCCGATACGCGGCG CGGAAATTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-461_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGGGTTCAGGCTGGCAATCC AGGTTTCTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacF-349_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCTCAGTCGCTGACGCACCAG AGCAATCAA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yacG-10_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCCGCAGGTTGGGCAATTAC CGTAATAGT CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BR

Exp-1_yacG-169_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCACTGCTTTGGTTCTTCGCT CCAGTCATC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacG-101_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTTCAGCAGCCCATTCTCCGA GGTCGATCA CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-284_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTCAACGCCGCATAGCGACA GGCTTTCTT CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-191_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCATCACCTTTCACCGTCCA TCCACAGGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-110_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGCTGCTTGTCCACTTCAT CAAGCAAGG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-145_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTTGCCAGGACCGTTCGCT ACCTTTCAG CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-226_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCATCGCCAGCGAATTCCAG TTGATTGGC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-333_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACTTCTGCTGCACGAAATTG CGGTAAGCC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-69_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTCACCTTTCATTAACCAG TGCCCCGACC CATTGC
GCTTCTCCGAAACATTAGC

Exp-1_yacL-27_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATGGACATACGCACCTTTACC ACTCCGGTA CATTGC
GCTTCTCCGAAACATTAGC

FIG. 4BS

Exp-1_yadG-726_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AGTCGATACTGATAGCCATCG AGCTTCGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-761_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCAGCACTTCACTTCCAGCG TCGCGGTAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-575_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATTTCTGCTTCTTCCAGGT AGTGTGTGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-870_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACCAGTGAAACAACAGCTCT TCCAGACGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-281_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCCTGATTCACCACAATTT GCTGCACGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-393_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ATCCC GCCAGATAACATACGC GCACGTTTCG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-227_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCTGCGCACCAGTCCCAACT GACGTTTAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-428_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCATTAACGCACGGGCAATCA TTAAACGGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-497_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC ACATTGAGCGGCGAAGTTCAA TATCCACGC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-182_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTACAAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCTCGAGATCGTAACCAAATA CGCTGACCC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BT

Exp-1_yadG-316_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GATGTACGCTTCTTTGCGCTC CACGCCGTA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-685_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGGTGCGAGATCGAGAATAAA GGTTCCTCGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-617_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCACCAGCTCACCGTGTGAA TAATGCCGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadG-66_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TCACCCGCTTCGACCTGCAA TCTATCCCA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-217_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGATGACGCAACGTTGGCGTA GGCATTGGT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-742_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TTAGCTACGCAAACACGTCC ACGTTGGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-53_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GCGTCTGCACCCAGATACGCA TAAAGCGAT CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-88_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC AAAGTAAAGGGTCATGGTGAT GACTGGCGG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-463_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC GGCAAACACACCGTTCAGCAA ACCCGCAAG CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-519_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGTTACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TACGTGAGTGGCGTTAACACA AAGGTTGGC CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BU

Exp-1_yadH-151_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CTGCATATAGCTGAAGCCATG CATATCGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-599_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATAAACGATTGGGTT CAGGT GCGACAGCC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-297_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TATCCGGCAATAATGACGTGA GTCGGAACC CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-419_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CCGTGAGCACCAGCGTTAAGG CAACGAATA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-653_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC TGACCAGCGGAACATCATTGA TACCGAGGA CATTGC
GCTTCTCCGGAAACATTAGC

Exp-1_yadH-688_I1-bc25mer_83004-20_I2-bc25mer_83517-20
ACAACCGCGTGT TACAAGGC CAGGCATCCGAGAGGTCTGG
GAATGC CGCCACAATAAAGACCACCAG TACGCCAAA CATTGC
GCTTCTCCGGAAACATTAGC

FIG. 4BV

PROBE LIBRARY CONSTRUCTION

RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Ser. No. 15/329,651, filed Jan. 27, 2017, entitled “Probe Library Construction,” by Zhuang, et al., which is a national stage filing of International Patent Application Serial No. PCT/US2015/042559, filed Jul. 29, 2015, entitled “Probe Library Construction,” by Zhuang, et al., which claims the benefit of U.S. Provisional Patent Application Ser. No. 62/050,636, filed Sep. 15, 2014, entitled “Probe Library Construction,” by Zhuang, et al.; U.S. Provisional Patent Application Ser. No. 62/031,062, filed Jul. 30, 2014, entitled “Systems and Methods for Determining Nucleic Acids,” by Zhuang, et al.; and U.S. Provisional Patent Application Ser. No. 62/142,653, filed Apr. 3, 2015, entitled “Systems and Methods for Determining Nucleic Acids,” by Zhuang, et al. Each of the above is incorporated herein by reference.

GOVERNMENT FUNDING

[0002] This invention was made with government support under Grant No. GM096450 awarded by the National Institutes of Health. The government has certain rights in the invention.

FIELD

[0003] The present invention generally relates to systems and methods for producing nucleic acids.

BACKGROUND

[0004] Custom-synthesized, oligonucleotide probes have emerged as a powerful tool for the identification and isolation of specific nucleic acid targets via hybridization. Applications for such hybridization probe sets range from next generation sequencing—where such probes are used to enrich or deplete samples for specific nucleic acid targets—to imaging of fixed samples—where fluorescently labeled hybridization probes allow the direct measurement of the number and spatial organization of the targeted species.

[0005] There are now a wide range of commercial sources for such probes. Such probes are often made by synthesizing each oligonucleotide member using standard solid phase synthesis methods. Unfortunately, this limits both the number of probes within a single set and the number of unique sets, due to the requirement that each oligonucleotide member must be individually and separately synthesized.

[0006] Recent advances in array-based synthesis of oligonucleotides by several companies have reduced the cost of producing oligonucleotides. However, these approaches also result in 1000-fold less oligonucleotide probes than is required for a single hybridization reaction, thus limiting their usefulness. Accordingly, improvements in oligonucleotide production are needed.

SUMMARY

[0007] The present invention generally relates to systems and methods for producing nucleic acids. The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles.

[0008] In one aspect, the present invention is generally directed to a method. The method, in accordance with one set of embodiments, includes amplifying at least some of a plurality of oligonucleotides using real-time PCR to produce amplified oligonucleotides, transcribing in vitro at least some of the amplified oligonucleotides to produce RNA, reverse transcribing the RNA to produce transcribed DNA, and selectively degrading the RNA relative to the transcribed DNA.

[0009] In another set of embodiments, the method includes simultaneously amplifying at least some of a plurality of oligonucleotides in a common solution using PCR to produce amplified oligonucleotides, transcribing in vitro at least some of the amplified oligonucleotides to produce RNA, reverse transcribing the RNA to produce transcribed DNA, and selectively degrading the RNA relative to the transcribed DNA.

[0010] In yet another set of embodiments, the method includes acts of providing a plurality of oligonucleotides having an average length of between 10 and 200 nucleotides and including at least 100 unique oligonucleotide sequences, producing amplified oligonucleotides comprising one of the plurality of oligonucleotides and a promoter using real-time PCR, transcribing at least some of the amplified oligonucleotides to produce RNA using an RNA polymerase, reverse transcribing the RNA to produce DNA using a primer comprising a signaling entity, and chemically reducing the RNA.

[0011] The method, in still another set of embodiments, includes acts of providing a plurality of oligonucleotides having an average length of between 10 and 200 nucleotides and including at least 100 unique oligonucleotide sequences, producing amplified oligonucleotides in a common solution comprising one of the plurality of oligonucleotides and a promoter using PCR, transcribing at least some of the amplified oligonucleotides to produce RNA using an RNA polymerase, reverse transcribing the RNA to produce DNA using a primer comprising a signaling entity, and chemically reducing the RNA.

[0012] In another aspect, the present invention encompasses methods of making one or more of the embodiments described herein, such as oligonucleotides, including but not limited to modified oligonucleotides such as those described herein (e.g., labeled with a signaling entity). In still another aspect, the present invention encompasses methods of using one or more of the embodiments described herein, for example, such as oligonucleotides, including but not limited to modified oligonucleotides such as those described herein (e.g., labeled with a signaling entity).

[0013] Other advantages and novel features of the present invention will become apparent from the following detailed description of various non-limiting embodiments of the invention when considered in conjunction with the accompanying figures. In cases where the present specification and a document incorporated by reference include conflicting and/or inconsistent disclosure, the present specification shall control. If two or more documents incorporated by reference include conflicting and/or inconsistent disclosure with respect to each other, then the document having the later effective date shall control.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] Non-limiting embodiments of the present invention will be described by way of example with reference to the

accompanying figures, which are schematic and are not intended to be drawn to scale. In the figures, each identical or nearly identical component illustrated is typically represented by a single numeral. For purposes of clarity, not every component is labeled in every figure, nor is every component of each embodiment of the invention shown where illustration is not necessary to allow those of ordinary skill in the art to understand the invention. In the figures:

[0015] FIG. 1 illustrates the production of DNA probes, in accordance with one set of embodiments; and

[0016] FIG. 2 illustrates a template molecule (SEQ ID NO: 3) produced in accordance with one embodiment of the invention;

[0017] FIGS. 3A-3D list optimized primers from the *E. coli* transcriptome, in another embodiment of the invention (the sequences, from top to bottom and left to right, by page, correspond to SEQ ID NOs: 4-57, 58-111, 112-165, and 166-201); and

[0018] FIGS. 4A-4BV show various probes in accordance with yet another embodiment of the invention. The sequences in FIGS. 4A-4BV, from top to bottom and left to right, by page, correspond to SEQ ID NOs: 202-221, 222-243, 244-265, 266-287, 288-309, 310-331, 332-353, 354-375, 376-397, 398-419, 420-441, 442-463, 464-485, 486-507, 508-529, 530-551, 552-573, 574-595, 596-617, 618-639, 640-661, 662-683, 684-705, 706-727, 728-749, 750-771, 772-793, 794-815, 816-837, 838-859, 860-881, 882-903, 904-925, and 926-937.

DETAILED DESCRIPTION

[0019] The present invention generally relates to systems and methods for producing nucleic acids. In some aspects, relatively large quantities of oligonucleotides can be produced, and in some cases, the oligonucleotides may have a variety of different sequences and/or lengths. For instance, a relatively small quantity of oligonucleotides may be amplified to produce a large amount of nucleotides. In one set of embodiments, oligonucleotides may be amplified using PCR, then transcribed to produce RNA. The RNA may then be reverse transcribed to produce DNA, and optionally, the RNA may be selectively degraded or removed, relative to the DNA. In one set of embodiments, the oligonucleotides may be chemically modified. These modifications may include, but are not limited to, the adding of fluorescent dyes or other signaling entities.

[0020] U.S. Provisional Patent Application Ser. No. 62/031,062, filed Jul. 30, 2014, entitled "Systems and Methods for Determining Nucleic Acids," by Zhuang, et al. is incorporated herein by reference in its entirety.

[0021] In one aspect, the present invention is generally directed to in vitro methods of amplifying a plurality of oligonucleotides. In some cases, relatively large numbers of unique oligonucleotides within a plurality of oligonucleotides may be amplified. For instance, a plurality of oligonucleotides to be amplified may include 10, 100, 1,000, or more unique sequences.

[0022] In addition, in some embodiments, the oligonucleotides may be amplified without selective amplification of some oligonucleotides over others, e.g., due to competitive effects.

[0023] Although some drift may occur, it is desired that the relative ratios of the oligonucleotides within a plurality of oligonucleotides stay substantially the same after amplification, at least for some applications. However, in many

amplification techniques, due to differences in binding or affinity of different oligonucleotides, some oligonucleotides may be amplified to a greater degree than others, and thus, specific techniques need to be utilized to reduce or eliminate this problem, for example, by separately amplifying each of the oligonucleotides before combining them together to form the plurality of oligonucleotides. In contrast, as is discussed herein, in certain embodiments, a plurality of oligonucleotides can be amplified without causing substantial alterations or changes in the ratios of the oligonucleotides, without requiring separation of the oligonucleotides, separate growth of the oligonucleotides, or other cumbersome techniques.

[0024] Referring now to FIG. 1, one example of an embodiment of the invention is now illustrated. In this figure, a plurality of oligonucleotides **10** is provided. This may include 1, 10, 100, 1,000, 10,000, 100,000, or any other suitable number of unique oligonucleotide sequences. Of course, more than one copy of any particular unique oligonucleotide may also be present as well within the plurality of oligonucleotides. The unique oligonucleotides may have the same or different lengths. In some cases, the plurality of oligonucleotides have an overall average length (number average or arithmetic mean) of less than 200 nt (nucleotides), although longer average lengths are also possible in some embodiments.

[0025] The plurality of oligonucleotides **10** may initially be amplified, using PCR (polymerase chain reaction) or another suitable oligonucleotide amplification method, to produce a plurality of amplified oligonucleotides **20**. In some cases, PCR may be used to generate thousands to millions of copies per oligonucleotide within the plurality of oligonucleotides. In some embodiments, the plurality of oligonucleotides may be amplified while still contained in a common solution, for instance, without requiring separation of the oligonucleotides prior to amplification, e.g., as is required in certain techniques such as emulsion PCR.

[0026] Within a common solution, while it is possible that different oligonucleotides of the plurality of oligonucleotides may be amplified at different rates (e.g., leading to non-uniform amplification of the plurality of oligonucleotides, and the potential loss of complexity or species within the plurality of oligonucleotides during amplification), in certain embodiments, this can be reduced or minimized through the use of various oligonucleotide structures and/or through the use of certain types of PCR techniques, as is discussed herein.

[0027] As an example, in one set of embodiments, the plurality of oligonucleotides may all be chosen to minimize competitive effects, e.g., as caused by differences in binding or affinity of the oligonucleotides to reagents within the common solution or the preferential enzymatic amplification of some sequence features. For example, in one set of embodiments, the plurality of oligonucleotides may be chosen to have similar lengths and/or sequences.

[0028] As is shown in FIG. 1, the plurality of oligonucleotides may each contain one or more index regions **15**, **16** on one or both ends of the oligonucleotides that can be recognized by certain reagents. In some cases, the oligonucleotides of the plurality of oligonucleotides may have one or more index regions to which suitable primers can interact with in order to allow PCR or other amplification to occur. In some embodiments, these index regions can be used to

selectively produce DNA probes only from subset of the plurality of oligonucleotides **10**.

[0029] These index regions can also be used in some instances to add additional sequences to that of the plurality of oligonucleotides, e.g., as is shown in FIG. 1, oligonucleotide **11** may include an index region **15**, to which a sequence **17** containing a T7 promoter can bind and be introduced into the amplified oligonucleotides (e.g., as region **23**). Various sequences may thus be applied to the plurality of oligonucleotides that include a portion able to bind an index region. In some cases, if substantially all of the plurality of oligonucleotides contain similar or identical index regions, the relative affinities or binding to the index regions of the oligonucleotides by enzymes such as polymerases may be substantially similar or identical, which may allow for relatively uniform amplification to occur. The plurality of oligonucleotides may also contain other different regions that can be varied to produce a plurality of unique oligonucleotides, e.g., region **12**. These regions can vary in terms of length and/or sequence, etc.

[0030] In some embodiments, the amount of amplification that occurs may be carefully controlled by monitoring the PCR amplification reaction, e.g., using techniques such as real-time PCR. This may occur, for example, using oligonucleotides having common index regions, substantially similar lengths and/or sequences, etc., including those previously discussed, or with other suitable pluralities of oligonucleotides. For instance, in some embodiments, the PCR reaction may be monitored by illuminating the solution containing the oligonucleotides with suitable light and determining the amount of fluorescence that is present, which can be related to the DNA present within the sample. Techniques for monitoring PCR reactions, such as real-time PCR methodologies, are known to those of ordinary skill in the art. The PCR reaction can also be controlled, in some embodiments, by controlling the amount and/or concentration of nucleotides and/or cofactors that are present.

[0031] After amplification, the plurality of amplified oligonucleotides **20** may be transcribed to produce a plurality of RNAs **30**, as is shown in the example of FIG. 1. This may be performed, for example, by exposing the amplified oligonucleotides to a suitable RNA polymerase, such as T7 RNA polymerase, that can transcribe the oligonucleotides to produce corresponding RNA. The amount of RNA production can be controlled in some embodiments by controlling the amount and/or concentration of nucleotides and/or cofactors that are present as well as the duration of the in vitro transcription reaction.

[0032] The plurality of RNAs **30**, may then be used to produce additional amounts of DNA **40**, e.g., by using reverse transcription. For example a suitable enzyme, such as reverse transcriptase, may be used to perform the reverse transcription. In some cases, primers may be used to facilitate transcription, and in some embodiments, the primers may also be used to attach additional entities to the DNA. For example, signaling entities may be attached, as is shown with signaling entity **48** in FIG. 1. Alternatively, additional nucleic acid sequences can also be attached, which can serve to recruit additional oligonucleotides via Watson-Crick base-pairing. The amount of DNA that is produced can be controlled, for example, by controlling the amount and/or concentration of nucleotides and/or cofactors that are present as well as the duration and temperature of the reverse transcription reaction.

[0033] In some embodiments, multiple copies of DNA may be produced from each RNA molecule. In addition, optionally, the RNA may then be removed or selectively degraded, relative to the DNA, for example, through alkaline hydrolysis, enzymatic digestion, or other techniques.

[0034] Accordingly, in certain aspects, the present invention is generally directed to systems and methods of amplifying a plurality of oligonucleotides. In one set of embodiments, relatively large quantities or masses of oligonucleotides can be produced as is discussed herein, e.g., at least about 10^{-3} pmol, at least about 10^{-2} pmol, at least about 10^{-1} pmol, at least about 10^0 pmol, at least about 10^1 pmol, at least about 10^2 pmol, at least about 10^3 pmol, etc. In addition, in some embodiments, the plurality of oligonucleotides may be substantially diverse. For example, the plurality of oligonucleotides may include at least about 10^1 , at least about 10^2 , at least about 10^3 , at least about 10^4 , at least about 10^5 , or at least about 10^6 unique sequences of oligonucleotides, even after amplification to the amounts discussed above. (It should also be noted that a plurality or population of oligonucleotides may include more than one copy of a given unique oligonucleotide sequence.) In contrast, certain prior art techniques are able to amplify large numbers of unique oligonucleotides, but to only small quantities or masses (e.g., to amounts of around 10^{-3} pmol or less), or are able to produce large quantities or masses of oligonucleotides, but only for 1 or a few unique sequences (e.g., less than 10 sequences).

[0035] As discussed, in certain embodiments, a plurality of oligonucleotides, which may include a plurality of unique sequences of oligonucleotides such as those described above, may be amplified without substantial selective amplification of some oligonucleotide sequences over others, e.g., due to competitive effects, unlike in many prior art techniques. Although some drift may occur during the amplification process, the drift may be relatively small. For example, in certain embodiments, the ratios or percentages of a representative unique oligonucleotide sequence, relative to the starting overall population, on the average, may change upon amplification by no more than about 10%, no more than about 8%, no more than about 6%, no more than about 5%, no more than about 4%, no more than about 3%, no more than about 2%, no more than about 1%, etc., relative to the starting ratio or percentage of the oligonucleotide sequence, prior to amplification. However, it should be noted that the oligonucleotide sequence itself, prior to any amplification, may also exhibit some variability, which is not included in the above numbers.

[0036] The unique oligonucleotides within a plurality of oligonucleotides may have the same or different lengths. If more than one unique oligonucleotide is present, then the unique oligonucleotides may independently have the same or different lengths. For example, in some cases, a plurality of oligonucleotides may have an average length (number average) of at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 50, at least 60, at least 65, at least 75, at least 100, at least 125, at least 150, at least 175, at least 200, at least 250, at least 300, at least 350, at least 400, or at least 450 nucleotides. In some cases, the average length may be no more than 500, no more than 450, no more than 400, no more than 350, no more than 300, no more than 250, no more than 200, no more than 175, no more than 150, no more than 125, no more than 100, be no more than 75, no more than 60, no more than 65, no more

than 60, no more than 55, no more than 50, no more than 45, no more than 40, no more than 35, no more than 30, no more than 20, or no more than 10 nucleotides. Combinations of any of these are also possible, e.g., the average length may be between 10 and 30 nucleotides, between 20 and 40 nucleotides, between 5 and 50 nucleotides, between 10 and 200 nucleotides, or between 25 and 35 nucleotides, between 10 and 300 nucleotides, etc.

[0037] In one set of embodiments, any suitable technique may be used to amplify the plurality of oligonucleotides. In some cases, for each oligonucleotide to be amplified, at least about 100, at least about 300, at least about 500, at least about 1,000, at least about 3,000, at least about 5,000, at least about 10,000, at least about 30,000, at least about 50,000 at least about 100,000, at least about 300,000, at least about 500,000, at least about 1,000,000 copies, at least about 3,000,000 copies, at least about 5,000,000 copies, at least about 10,000,000 copies, at least about 30,000,000 copies, at least about 50,000,000 copies, or at least about 100,000,000 copies of the oligonucleotide may be produced using any of the amplification techniques discussed herein (e.g., including PCR amplification, in vitro transcription etc.). As discussed, in some cases, the amplification may occur without substantial selective amplification of some oligonucleotide sequences over others.

[0038] Any suitable technique may be used to generate the plurality of oligonucleotides. For example, the plurality of oligonucleotides may be synthetically produced, grown within a cell, grown on a substrate (e.g., in an array), or the like. Techniques for producing oligonucleotides are known to those of ordinary skill in the art. The plurality of oligonucleotides may also be computationally designed in some embodiments.

[0039] In one embodiment, the oligonucleotides may be amplified using PCR (polymerase chain reaction). In some cases, the oligonucleotides may be amplified while contained in a common liquid or solution. This is to be contrasted with certain PCR techniques, such as emulsion PCR or digital PCR, which requires separation of the oligonucleotides, e.g., into separate compartments or droplets, prior to amplification so as to prevent relatively selective amplification of certain oligonucleotides from occurring. However, surprisingly, it has been found that such separation is not required, and other techniques (such as is described herein) may be used to prevent or reduce selective amplification while keeping the oligonucleotides together within a common solution.

[0040] As mentioned, in some cases, by using certain oligonucleotide structures and/or certain types of PCR techniques, the amount of selective amplification that may occur may be reduced or eliminated. For instance, in one set of embodiments, oligonucleotides are chosen to minimize competitive effects. For instance, the oligonucleotides may have substantially the same lengths, and/or share identical or similar portions or regions.

[0041] For example, in one set of embodiments, the oligonucleotides may have a distribution of lengths such that no more than about 10%, no more than about 5%, no more than about 3%, or no more than about 1% of the oligonucleotides has a length that is less than about 80% or greater than about 120%, less than about 90% or greater than about 110%, or less than about 95% or greater than about 105% of the overall average length of the plurality of nucleotides.

[0042] In another set of embodiments the oligonucleotides may share one or more regions, such as index regions, that are identical or substantially similar. The oligonucleotides sharing index or other regions may have substantially the same lengths, as discussed above, or different lengths. In some embodiments, the oligonucleotides may comprise at least two index regions that each are identical or substantially similar, surrounding a variable region having different nucleotide sequences, and optionally, different lengths. For example, the oligonucleotides may include, in sequence, a first region that is identical or substantially similar to the other oligonucleotides, a second region that is not identical, and optionally, a third region that is identical or substantially similar to the other oligonucleotides. In some embodiments, competition of oligonucleotides may be controlled by using oligonucleotides selected to reduce amplification bias. For instance, in some cases, groups of oligonucleotides that have similar compositions may be amplified together.

[0043] In some cases, the index regions may have a length of greater than 5, 7, 10, 12, 14, 16, 18, or 20 nucleotides, and/or have a length of less than 30, 28, 25, 22, 20, 18, 16, 14, 12, or 10 nucleotides. For instance, the regions that are identical or substantially similar may have a length of between 18 and 22 nucleotides. The regions may be identical, or differ by no more than 1, 2, 3, 4, or 5 nucleotides (consecutively or non-consecutively) within the region.

[0044] In certain embodiments, primer sequences may be added to facilitate the PCR reaction. For example, the primer sequence may include sequences substantially complementary to a region within the oligonucleotides, e.g., an index region. A variety of such sequences suitable for PCR or in vitro transcription may be readily obtained commercially.

[0045] In some embodiments, the primer sequence may also include other sequences, e.g., promoter sequences or other sequences that may be added to the oligonucleotide during PCR amplification, such as is shown in FIG. 1 with a T7 promoter. Accordingly, oligonucleotides comprising the original sequence and one or more promoter sequences may be produced in certain cases. Besides the T7 promoter, other suitable promoters that may be used include, but are not limited to, T3 promoters or SP6 promoters. Such promoters may be useful, for example, to facilitate transcription to produce RNA, as is discussed in more detail below. In addition, in some embodiments, more than one promoter may be added.

[0046] In one set of embodiments, more than one sequence containing a PCR primer may be used, e.g., to amplify different subsets of the plurality of oligonucleotides. If more than one primer-containing sequence is used, the PCR primers contained on each of them may be the same or different. Examples of suitable PCR primers include those described herein. Thus, for example, in one set of embodiments, for example, the plurality of oligonucleotides may include different subpools having different index regions or other regions as discussed above, which may be selectively amplified through the use of an appropriate sequence including a PCR primer. Any suitable number of subpools may be created for a plurality of oligonucleotides. For example, at least 1, 2, 4, 10, 20, 96, 100, or 192 subpools of the plurality of oligonucleotides may be selective amplified, through the use of specific PCR primers.

[0047] Thus, in some cases, the oligonucleotides may be formed into "pools" or groups or sets of oligonucleotides within the plurality of oligonucleotides that share one or

more common features, such as an index region or other identical sequence. For instance, the common feature in a group or set of oligonucleotides may have an identical sequence of nucleotides of at least 5, 7, 10, 12, 14, 16, 18, or 20 nucleotides, and/or less than 30, 28, 25, 22, 20, 18, 16, 14, 12, or 10 nucleotides. For instance, the common region that is identical or substantially similar in a group of oligonucleotides may have a length of between 18 and 22 nucleotides. The common regions may be identical, or differ by no more than 1, 2, 3, 4, or 5 nucleotides (consecutively or non-consecutively) within the region. In some embodiments, each group or pool may contain two (or more) unique index regions that are not used in any other pool, e.g., to reduce the contamination of off-target amplified products from the amplification products of another.

[0048] In certain embodiments, PCR amplification may be monitored, and controlled to reduce or minimize selective amplification. For example, in one set of embodiments, real-time PCR techniques may be used. In some embodiments, the extent of the PCR reaction may be monitored or controlled, for example, by illuminating the solution containing the oligonucleotides with suitable light and determining the amount of fluorescence that is present to monitor the PCR reaction. Accordingly, for example, the reaction conditions may be controlled such that the oligonucleotides react in conditions that minimize the amount of selective amplification, for example, by providing an excess of nucleotides, ions (e.g., Mg^{2+}), enzyme, etc. Once the oligonucleotide concentrations have reached the point where competitive effects may start to occur, the reaction may be stopped before significant selective amplification begins.

[0049] After amplification as discussed above, the amplified oligonucleotides may then be transcribed to produce RNA. Further amplification may also occur in this step. For instance, in some cases, each oligonucleotide can be used to produce, on the average, at least about 50, at least about 100, at least about 300, at least about 500, at least about 1,000, at least about 3,000, at least about 5,000, at least about 10,000, at least about 30,000, at least about 50,000 at least about 100,000, at least about 300,000, at least about 500,000 or at least about 1,000,000 transcribed RNA molecules. In some cases, the mass of RNA that is produced may be at least about 10, at least about 20, at least about 30, at least about 50, at least about 100, at least about 200, at least about 300, or at least about 500 times the mass of the oligonucleotides. Thus, for example, one microgram of oligonucleotides may be converted into at least 10 micrograms, at least 30 micrograms, or at least 100 micrograms of RNA.

[0050] In one set of embodiments, transcription may occur in vitro by exposing the amplified oligonucleotides to a suitable RNA polymerase. A variety of RNA polymerases are available commercially, including T7, T3, or SP6 RNA polymerases. Other non-limiting examples of RNA polymerases include RNA polymerase I, RNA polymerase II, RNA polymerase III, RNA polymerase IV, or RNA polymerase V. The RNA polymerase may arise from any suitable source, e.g., bacteria, viruses, or eukaryotes. In some embodiments, more than one RNA polymerase may be used. In addition, as previously discussed, in some embodiments, the amplified oligonucleotides may include promoter sequences, such as one or more of T7, T3, or SP6 promoter sequences, that can be used to facilitate the transcription

process. Those of ordinary skill in the art will be aware of suitable conditions for causing transcription in vitro using RNA polymerases.

[0051] In some embodiments, the total amplification bias may be reduced by changing the relative amount of amplification produced by the PCR and the in vitro transcription. For example, the PCR can be used to produce smaller amounts of DNA than are typically produced in a PCR, to reduce the amplification bias of this process. However, this reduced yield can be compensated in some cases by increasing the duration of the in vitro transcription reaction.

[0052] The RNA may, in turn, be reverse transcribed to produce DNA. In one set of embodiments, reverse transcription may occur by exposing the RNA to a suitable reverse transcriptase enzyme. In some cases, the reverse transcriptase may be a viral reverse transcriptase, e.g., M-MLV reverse transcriptase, AMV reverse transcriptase, or the like. A variety of reverse transcriptase enzymes are commercially available. Those of ordinary skill in the art will be aware of suitable conditions for causing reverse transcription to occur.

[0053] In certain embodiments, reverse transcription may be facilitated through the use of primer-containing sequences, e.g., containing primers for reverse transcription. In some cases, the primer-containing sequences may contain other sequences or entities as well, although this is not necessarily a requirement. The primer-containing sequences may be added at any suitable point, e.g., just before starting transcription reaction. Suitable transcription primers for conducting reverse transcription may be obtained commercially.

[0054] In one set of embodiments, the primer-containing sequence may be incorporated into the DNA during production of the DNA by the reverse transcriptase. In some cases, the primer-containing sequence may contain other entities, and/or sequences suitable for attaching other entities (e.g., on the 5' or 3' ends, internally, etc.). For instance, the primer-containing sequence may contain a non-nucleic acid moiety, such as a digoxigenin moiety, a biotin moiety, etc. located on the 5' end, the 3' end, internally, or the like. In some cases, the signaling entity that can be subsequently detected or determined may be introduced to the DNA. For instance, the signaling entity may be fluorescent, or a specific nucleotide sequence that can be determined, e.g., enzymatically. Examples of signaling entities are discussed in more detail below.

[0055] In some cases, the RNA may be purified prior to reverse transcription. However, it should be noted that purification is not required, and in other embodiments, the RNA may be reverse transcribed to form DNA without any intermediate purification steps. If the RNA is purified, it may be purified using any suitable technique, e.g., by passing the RNA over a suitable column to remove oligonucleotides.

[0056] Optionally, in some embodiments, the RNA may be separated from the DNA or the DNA may be purified in some fashion. For example, the RNA may be selectively degraded, relative to the DNA. In one set of embodiments, the RNA may be degraded relative to the DNA by alkaline hydrolysis. For instance, the pH of the solution may be raised to at least about 8, at least about 9, at least about 10, etc. Any suitable alkaline may be used to raise the pH. In some cases, after degradation of the RNA, the pH may also be lowered, e.g., to about 7, to about 7.4, to physiological conditions, or the like. In some cases, techniques such as

enzymatic degradation can be used to selectively degrade RNA, relative to DNA. The DNA may also be purified using techniques such as column purification, ethanol precipitation, and/or solid-phase reversible immobilization techniques. In addition, in some cases, the DNA may be concentrated, e.g., through evaporation techniques.

[0057] In addition, techniques such as those described above may be scaled-up or “numbered-up” to produce larger quantities of material. For example, a process may be repeated using multi-well techniques or by simultaneously running multiple reactions in parallel, etc. to produce larger quantities or masses of oligonucleotides. As a non-limiting example, in one embodiment, processes such as those discussed herein may be performed using multiple wells of a microtiter plate (e.g., having 96, 384, 1536, wells, etc.) to increase output.

[0058] The DNA may be used for a variety of purposes, in different embodiments of the invention. For example, in certain embodiments, the DNA may be hybridized to nucleic acid species in liquid samples, e.g., extracted from a variety of biological sources, including human. In some cases, the DNA may be used to physically separate one set of nucleic acids from another, or as primers for PCR or reverse transcription.

[0059] In addition, as previously discussed, in certain aspects, signaling entities are incorporated into DNA in some embodiments. The signaling entities may be determined for a variety of purposes. For example, the DNA that is produced may be used as a biological probe, and the signaling entities may be determined in some fashion, e.g., quantitatively or qualitatively, to determine a characteristic or feature of the probe. Examples include, but are not limited to, the position of the probe, the activity of the probe, the concentration of the probe, or the like.

[0060] In some cases, signaling entities within a sample may be determined, e.g., spatially, using a variety of techniques. In some embodiments, the signaling entities may be fluorescent, and techniques for determining fluorescence within a sample, such as fluorescence microscopy or confocal microscopy, may be used to spatially identify the positions of signaling entities within a cell. In some cases, the positions of the entities within the sample may be determined in two or even three dimensions.

[0061] In some embodiments, the spatial positions of the signaling entities may be determined at relatively high resolutions. For instance, the positions may be determined at spatial resolutions of better than about 100 micrometers, better than about 30 micrometers, better than about 10 micrometers, better than about 3 micrometers, better than about 1 micrometer, better than about 800 nm, better than about 600 nm, better than about 500 nm, better than about 400 nm, better than about 300 nm, better than about 200 nm, better than about 100 nm, better than about 90 nm, better than about 80 nm, better than about 70 nm, better than about 60 nm, better than about 50 nm, better than about 40 nm, better than about 30 nm, better than about 20 nm, or better than about 10 nm, etc.

[0062] There are a variety of techniques able to determine or image the spatial positions of entities optically, e.g., using fluorescence microscopy. In some cases, the spatial positions may be determined at super resolutions, or at resolutions better than the wavelength of light. Non-limiting examples include STORM (stochastic optical reconstruction microscopy), STED (stimulated emission depletion microscopy),

NSOM (Near-field Scanning Optical Microscopy), 4Pi microscopy, SIM (Structured Illumination Microscopy), SMI (Spatially Modulated Illumination) microscopy, RESOLFT (Reversible Saturable Optically Linear Fluorescence Transition Microscopy), GSD (Ground State Depletion Microscopy), SSIM (Saturated Structured-Illumination Microscopy), SPDM (Spectral Precision Distance Microscopy), Photo-Activated Localization Microscopy (PALM), Fluorescence Photoactivation Localization Microscopy (FPALM), LIMON (3D Light Microscopical Nanosizing Microscopy), Super-resolution optical fluctuation imaging (SOFI), or the like. See, e.g., U.S. Pat. No. 7,838,302, issued Nov. 23, 2010, entitled “Sub-Diffraction Limit Image Resolution and Other Imaging Techniques,” by Zhuang, et al.; U.S. Pat. No. 8,564,792, issued Oct. 22, 2013, entitled “Sub-diffraction Limit Image Resolution in Three Dimensions,” by Zhuang, et al.; or Int. Pat. Apl. Pub. No. WO 2013/090360, published Jun. 20, 2013, entitled “High Resolution Dual-Objective Microscopy,” by Zhuang, et al., each incorporated herein by reference in their entireties.

[0063] In addition, the signaling entity may be inactivated in some cases. For example, in some embodiments, a first secondary nucleic acid probe containing a signaling entity may be applied to a sample that can recognize a first read sequence, then the first secondary nucleic acid probe can be inactivated before a second secondary nucleic acid probe is applied to the sample. If multiple signaling entities are used, the same or different techniques may be used to inactivate the signaling entities, and some or all of the multiple signaling entities may be inactivated, e.g., sequentially or simultaneously.

[0064] Inactivation may be caused by removal of the signaling entity (e.g., from the sample, or from the nucleic acid probe, etc.), and/or by chemically altering the signaling entity in some fashion, e.g., by photobleaching the signaling entity, bleaching or chemically altering the structure of the signaling entity, etc.). For instance, in one set of embodiments, a fluorescent signaling entity may be inactivated by chemical or optical techniques such as oxidation, photobleaching, chemically bleaching, stringent washing or enzymatic digestion or reaction by exposure to an enzyme, dissociating the signaling entity from other components (e.g., a probe), chemical reaction of the signaling entity (e.g., to a reactant able to alter the structure of the signaling entity) or the like.

[0065] In some embodiments, various nucleic acid probes (including primary and/or secondary nucleic acid probes) may include one or more signaling entities. If more than one nucleic acid probe is used, the signaling entities may each by the same or different. In certain embodiments, a signaling entity is any entity able to emit light. For instance, in one embodiment, the signaling entity is fluorescent. In other embodiments, the signaling entity may be phosphorescent, radioactive, absorptive, etc. In some cases, the signaling entity is any entity that can be determined within a sample at relatively high resolutions, e.g., at resolutions better than the wavelength of visible light. The signaling entity may be, for example, a dye, a small molecule, a peptide or protein, or the like. The signaling entity may be a single molecule in some cases. If multiple secondary nucleic acid probes are used, the nucleic acid probes may comprise the same or different signaling entities.

[0066] Non-limiting examples of signaling entities include fluorescent entities (fluorophores) or phosphorescent enti-

ties, for example, cyanine dyes (e.g., Cy2, Cy3, Cy3B, Cy5, Cy5.5, Cy7, etc.), Alexa Fluor dyes, Atto dyes, photoswitchable dyes, photoactivatable dyes, fluorescent dyes, metal nanoparticles, semiconductor nanoparticles or “quantum dots”, fluorescent proteins such as GFP (Green Fluorescent Protein), or photoactivatable fluorescent proteins, such as PAGFP, PSCFP, PSCFP2, Dendra, Dendra2, EosFP, tdEos, mEos2, mEos3, PAmCherry, PAtagRFP, mMaple, mMaple2, and mMaple3. Other suitable signaling entities are known to those of ordinary skill in the art. See, e.g., U.S. Pat. No. 7,838,302 or U.S. Pat. Apl. Ser. No. 61/979,436, each incorporated herein by reference in its entirety.

[0067] As used herein, the term “light” generally refers to electromagnetic radiation, having any suitable wavelength (or equivalently, frequency). For instance, in some embodiments, the light may include wavelengths in the optical or visual range (for example, having a wavelength of between about 400 nm and about 700 nm, i.e., “visible light”), infrared wavelengths (for example, having a wavelength of between about 300 micrometers and 700 nm), ultraviolet wavelengths (for example, having a wavelength of between about 400 nm and about 10 nm), or the like. In certain cases, as discussed in detail below, more than one entity may be used, i.e., entities that are chemically different or distinct, for example, structurally. However, in other cases, the entities may be chemically identical or at least substantially chemically identical.

[0068] In one set of embodiments, the signaling entity is “switchable,” i.e., the entity can be switched between two or more states, at least one of which emits light having a desired wavelength. In the other state(s), the entity may emit no light, or emit light at a different wavelength. For instance, an entity may be “activated” to a first state able to produce light having a desired wavelength, and “deactivated” to a second state not able to emit light of the same wavelength. An entity is “photoactivatable” if it can be activated by incident light of a suitable wavelength. As a non-limiting example, Cy5, can be switched between a fluorescent and a dark state in a controlled and reversible manner by light of different wavelengths, i.e., 633 nm (or 642 nm, 647 nm, 656 nm) red light can switch or deactivate Cy5 to a stable dark state, while 405 nm green light can switch or activate the Cy5 back to the fluorescent state. In some cases, the entity can be reversibly switched between the two or more states, e.g., upon exposure to the proper stimuli. For example, a first stimuli (e.g., a first wavelength of light) may be used to activate the switchable entity, while a second stimuli (e.g., a second wavelength of light) may be used to deactivate the switchable entity, for instance, to a non-emitting state. Any suitable method may be used to activate the entity. For example, in one embodiment, incident light of a suitable wavelength may be used to activate the entity to emit light, i.e., the entity is “photoswitchable.” Thus, the photoswitchable entity can be switched between different light-emitting or non-emitting states by incident light, e.g., of different wavelengths. The light may be monochromatic (e.g., produced using a laser) or polychromatic. In another embodiment, the entity may be activated upon stimulation by electric field and/or magnetic field. In other embodiments, the entity may be activated upon exposure to a suitable chemical environment, e.g., by adjusting the pH, or inducing a reversible chemical reaction involving the entity, etc. Similarly, any suitable method may be used to deactivate the entity, and the methods of activating and deactivating the

entity need not be the same. For instance, the entity may be deactivated upon exposure to incident light of a suitable wavelength, or the entity may be deactivated by waiting a sufficient time.

[0069] Typically, a “switchable” entity can be identified by one of ordinary skill in the art by determining conditions under which an entity in a first state can emit light when exposed to an excitation wavelength, switching the entity from the first state to the second state, e.g., upon exposure to light of a switching wavelength, then showing that the entity, while in the second state can no longer emit light (or emits light at a much reduced intensity) when exposed to the excitation wavelength.

[0070] In one set of embodiments, as discussed, a switchable entity may be switched upon exposure to light. In some cases, the light used to activate the switchable entity may come from an external source, e.g., a light source such as a laser light source, another light-emitting entity proximate the switchable entity, etc. The second, light emitting entity, in some cases, may be a fluorescent entity, and in certain embodiments, the second, light-emitting entity may itself also be a switchable entity.

[0071] In some embodiments, the switchable entity includes a first, light-emitting portion (e.g., a fluorophore), and a second portion that activates or “switches” the first portion. For example, upon exposure to light, the second portion of the switchable entity may activate the first portion, causing the first portion to emit light. Examples of activator portions include, but are not limited to, Alexa Fluor 405 (Invitrogen), Alexa Fluor 488 (Invitrogen), Cy2 (GE Healthcare), Cy3 (GE Healthcare), Cy3B (GE Healthcare), Cy3.5 (GE Healthcare), or other suitable dyes. Examples of light-emitting portions include, but are not limited to, Cy5, Cy5.5 (GE Healthcare), Cy7 (GE Healthcare), Alexa Fluor 647 (Invitrogen), Alexa Fluor 680 (Invitrogen), Alexa Fluor 700 (Invitrogen), Alexa Fluor 750 (Invitrogen), Alexa Fluor 790 (Invitrogen), DiD, DiR, YOYO-3 (Invitrogen), YO-PRO-3 (Invitrogen), TOT-3 (Invitrogen), TO-PRO-3 (Invitrogen) or other suitable dyes. These may be linked together, e.g., covalently, for example, directly, or through a linker, e.g., forming compounds such as, but not limited to, Cy5-Alexa Fluor 405, Cy5-Alexa Fluor 488, Cy5-Cy2, Cy5-Cy3, Cy5-Cy3.5, Cy5.5-Alexa Fluor 405, Cy5.5-Alexa Fluor 488, Cy5.5-Cy2, Cy5.5-Cy3, Cy5.5-Cy3.5, Cy7-Alexa Fluor 405, Cy7-Alexa Fluor 488, Cy7-Cy2, Cy7-Cy3, Cy7-Cy3.5, Alexa Fluor 647-Alexa Fluor 405, Alexa Fluor 647-Alexa Fluor 488, Alexa Fluor 647-Cy2, Alexa Fluor 647-Cy3, Alexa Fluor 647-Cy3.5, Alexa Fluor 750-Alexa Fluor 405, Alexa Fluor 750-Alexa Fluor 488, Alexa Fluor 750-Cy2, Alexa Fluor 750-Cy3, or Alexa Fluor 750-Cy3.5. Those of ordinary skill in the art will be aware of the structures of these and other compounds, many of which are available commercially. The portions may be linked via a covalent bond, or by a linker, such as those described in detail below. Other light-emitting or activator portions may include portions having two quaternized nitrogen atoms joined by a polymethine chain, where each nitrogen is independently part of a heteroaromatic moiety, such as pyrrole, imidazole, thiazole, pyridine, quinoine, indole, benzothiazole, etc., or part of a nonaromatic amine. In some cases, there may be 5, 6, 7, 8, 9, or more carbon atoms between the two nitrogen atoms.

[0072] In certain cases, the light-emitting portion and the activator portions, when isolated from each other, may each

be fluorophores, i.e., entities that can emit light of a certain, emission wavelength when exposed to a stimulus, for example, an excitation wavelength. However, when a switchable entity is formed that comprises the first fluorophore and the second fluorophore, the first fluorophore forms a first, light-emitting portion and the second fluorophore forms an activator portion that switches that activates or “switches” the first portion in response to a stimulus. For example, the switchable entity may comprise a first fluorophore directly bonded to the second fluorophore, or the first and second entity may be connected via a linker or a common entity. Whether a pair of light-emitting portion and activator portion produces a suitable switchable entity can be tested by methods known to those of ordinary skills in the art. For example, light of various wavelength can be used to stimulate the pair and emission light from the light-emitting portion can be measured to determined wither the pair makes a suitable switch.

[0073] As a non-limiting example, Cy3 and Cy5 may be linked together to form such an entity. In this example, Cy3 is an activator portion that is able to activate Cy5, the light-emission portion. Thus, light at or near the absorption maximum (e.g., near 532 nm light for Cy3) of the activation or second portion of the entity may cause that portion to activate the first, light-emitting portion, thereby causing the first portion to emit light (e.g., near 647 nm for Cy5). See, e.g., U.S. Pat. No. 7,838,302, incorporated herein by reference in its entirety. In some cases, the first, light-emitting portion can subsequently be deactivated by any suitable technique (e.g., by directing 647 nm red light to the Cy5 portion of the molecule).

[0074] Other non-limiting examples of potentially suitable activator portions include 1,5 IAEDANS, 1,8-ANS, 4-Methylumbelliferone, 5-carboxy-2,7-dichlorofluorescein, 5-Carboxyfluorescein (5-FAM), 5-Carboxynaphthofluorescein, 5-Carboxytetramethylrhodamine (5-TAMRA), 5-FAM (5-Carboxyfluorescein), 5-HAT (Hydroxy Tryptamine), 5-Hydroxy Tryptamine (HAT), 5-ROX (carboxy-X-rhodamine), 5-TAMRA (5-Carboxytetramethylrhodamine), 6-Carboxyrhodamine 6G, 6-CR 6G, 6-JOE, 7-Amino-4-methylcoumarin, 7-Aminoactinomycin D (7-AAD), 7-Hydroxy-4-methylcoumarin, 9-Amino-6-chloro-2-methoxyacridine, AB Q, Acid Fuchsin, ACMA (9-Amino-6-chloro-2-methoxyacridine), Acridine Orange, Acridine Red, Acridine Yellow, Acriflavin, Acriflavin Feulgen SITSAs, Alexa Fluor 350, Alexa Fluor 405, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 500, Alexa Fluor 514, Alexa Fluor 532, Alexa Fluor 546, Alexa Fluor 555, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 610, Alexa Fluor 633, Alexa Fluor 635, Alizarin Complexon, Alizarin Red, AMC, AMCA-S, AMCA (Aminomethylcoumarin), AMCA-X, Aminoactinomycin D, Aminocoumarin, Aminomethylcoumarin (AMCA), Anilin Blue, Anthrocyll stearate, APTRA-BTC, APTS, Astrazon Brilliant Red 4G, Astrazon Orange R, Astrazon Red 6B, Astrazon Yellow 7 GLL, Atabrine, ATTO 390, ATTO 425, ATTO 465, ATTO 488, ATTO 495, ATTO 520, ATTO 532, ATTO 550, ATTO 565, ATTO 590, ATTO 594, ATTO 610, ATTO 611X, ATTO 620, ATTO 633, ATTO 635, ATTO 647, ATTO 647N, ATTO 655, ATTO 680, ATTO 700, ATTO 725, ATTO 740, ATTO-TAG CBQCA, ATTO-TAG FQ, Auramine, Aurophosphine G, Aurophosphine, BAO 9 (Bisaminophenylloxadiazole), BCECF (high pH), BCECF (low pH), Berberine Sulphate, Bimane, Bisbenzamide, Bisbenzimidazole (Hoechst), bis-BTC, Blancophor FFG,

Blancophor SV, BOBO-1, BOBO-3, Bodipy 492/515, Bodipy 493/503, Bodipy 500/510, Bodipy 505/515, Bodipy 530/550, Bodipy 542/563, Bodipy 558/568, Bodipy 564/570, Bodipy 576/589, Bodipy 581/591, Bodipy 630/650-X, Bodipy 650/665-X, Bodipy 665/676, Bodipy Fl, Bodipy FL ATP, Bodipy Fl-Ceramide, Bodipy R6G, Bodipy TMR, Bodipy TMR-X conjugate, Bodipy TMR-X, SE, Bodipy TR, Bodipy TR ATP, Bodipy TR-X SE, BO-PRO-1, BO-PRO-3, Brilliant Sulphoflavin FF, BTC, BTC-5N, Calcein, Calcein Blue, Calcium Crimson, Calcium Green, Calcium Green-1 Ca²⁺ Dye, Calcium Green-2 Ca²⁺, Calcium Green-5N Ca²⁺, Calcium Green-C18 Ca²⁺, Calcium Orange, Calcofluor White, Carboxy-X-rhodamine (5-ROX), Cascade Blue, Cascade Yellow, Catecholamine, CCF2 (GeneBlazer), CFDA, Chromomycin A, Chromomycin A, CL-NERF, CMFDA, Coumarin Phalloidin, CPM Methylcoumarin, CTC, CTC Formazan, Cy2, Cy3.1 8, Cy3.5, Cy3, Cy5.1 8, cyclic AMP Fluoresensor (FiCRhR), Dabcyl, Dansyl, Dansyl Amine, Dansyl Cadaverine, Dansyl Chloride, Dansyl DHPE, Dansyl fluoride, DAPI, Dapoxyl, Dapoxyl 2, Dapoxyl 3' DCFDA, DCFH (Dichlorodihydrofluorescein Diacetate), DDAO, DHR (Dihydrohodamine 123), Di-4-ANEPPS, Di-8-ANEPPS (non-ratio), DiA (4-Di-16-ASP), Dichlorodihydrofluorescein Diacetate (DCFH), DiD—Lipophilic Tracer, DiD (DiIC18(5)), DIDS, Dihydrohodamine 123 (DHR), DiI (DiIC18(3)), Dinitrophenol, DiO (DiOC18(3)), DiR, DiR (DiIC18(7)), DM-NERF (high pH), DNP, Dopamine, DTAF, DY-630-NHS, DY-635-NHS, DyLight 405, DyLight 488, DyLight 549, DyLight 633, DyLight 649, DyLight 680, DyLight 800, ELF 97, Eosin, Erythrosin, Erythrosin ITC, Ethidium Bromide, Ethidium homodimer-1 (EthD-1), Euchrysin, EukoLight, Europium (III) chloride, Fast Blue, FDA, Feulgen (Pararosaniline), FIF (Formaldehyd Induced Fluorescence), FITC, Flazo Orange, Fluo-3, Fluo-4, Fluorescein (FITC), Fluorescein Diacetate, Fluoro-Emerald, Fluoro-Gold (Hydroxystilbamidine), Fluor-Ruby, FluorX, FM 1-43, FM 4-46, Fura Red (high pH), Fura Red/Fluo-3, Fura-2, Fura-2/BCECF, Genacryl Brilliant Red B, Genacryl Brilliant Yellow 10GF, Genacryl Pink 3G, Genacryl Yellow SGF, GeneBlazer (CCF2), Gloxalic Acid, Granular blue, Haematoporphyrin, Hoechst 33258, Hoechst 33342, Hoechst 34580, HPTS, Hydroxycoumarin, Hydroxystilbamidine (FluoroGold), Hydroxytryptamine, Indo-1, high calcium, Indo-1, low calcium, Indodicarbocyanine (DiD), Indotricarbocyanine (DiR), Intrawhite Cf, JC-1, JO-JO-1, JO-PRO-1, LaserPro, Laurodan, LDS 751 (DNA), LDS 751 (RNA), Leucophor PAF, Leucophor SF, Leucophor WS, Lissamine Rhodamine, Lissamine Rhodamine B, Calcein/Ethidium homodimer, LOLO-1, LO-PRO-1, Lucifer Yellow, Lyso Tracker Blue, Lyso Tracker Blue-White, Lyso Tracker Green, Lyso Tracker Red, Lyso Tracker Yellow, LysoSensor Blue, LysoSensor Green, LysoSensor Yellow/Blue, Mag Green, Magdala Red (Phloxin B), Mag-Fura Red, Mag-Fura-2, Mag-Fura-5, Mag-Indo-1, Magnesium Green, Magnesium Orange, Malachite Green, Marina Blue, Maxilon Brilliant Flavin 10 GFF, Maxilon Brilliant Flavin 8 GFF, Merocyanin, Methoxycoumarin, Mitotracker Green FM, Mitotracker Orange, Mitotracker Red, Mitracyclin, Monobromobimane, Monobromobimane (mBBr-GSH), Monochlorobimane, MPS (Methyl Green Pyronine Stilbene), NBD, NBD Amine, Nile Red, Nitrobenzoxadidole, Noradrenaline, Nuclear Fast Red, Nuclear Yellow, Nylosan Brilliant lavin EBG, Oregon Green, Oregon Green 488-X, Oregon Green, Oregon Green 488, Oregon Green 500,

Oregon Green 514, Pacific Blue, Pararosanine (Feulgen), PBF1, Phloxin B (Magdala Red), Phorwite AR, Phorwite BKL, Phorwite Rev, Phorwite RPA, Phosphine 3R, PKH26 (Sigma), PKH67, PMIA, Pontochrome Blue Black, POPO-1, POPO-3, PO-PRO-1, PO-PRO-3, Primuline, Procion Yellow, Propidium Iodid (PI), PyMPO, Pyrene, Pyronine, Pyronine B, Pyrozal Brilliant Flavin 7GF, QSY 7, Quinacrine Mustard, Resorufin, RH 414, Rhod-2, Rhodamine, Rhodamine 110, Rhodamine 123, Rhodamine 5 GLD, Rhodamine 6G, Rhodamine B, Rhodamine B 200, Rhodamine B extra, Rhodamine BB, Rhodamine BG, Rhodamine Green, Rhodamine Phallicidine, Rhodamine Phalloidine, Rhodamine Red, Rhodamine WT, Rose Bengal, S65A, S65C, S65L, S65T, SBFI, Serotonin, Sevron Brilliant Red 2B, Sevron Brilliant Red 4G, Sevron Brilliant Red B, Sevron Orange, Sevron Yellow L, SITS, SITS (Primuline), SITS (Stilbene Isothiosulphonic Acid), SNAFL calcein, SNAFL-1, SNAFL-2, SNARF calcein, SNARF1, Sodium Green, SpectrumAqua, SpectrumGreen, SpectrumOrange, Spectrum Red, SPQ (6-methoxy-N-(3-sulfopropyl)quinolinium), Stilbene, Sulphorhodamine B can C, Sulphorhodamine Extra, SYTO 11, SYTO 12, SYTO 13, SYTO 14, SYTO 15, SYTO 16, SYTO 17, SYTO 18, SYTO 20, SYTO 21, SYTO 22, SYTO 23, SYTO 24, SYTO 25, SYTO 40, SYTO 41, SYTO 42, SYTO 43, SYTO 44, SYTO 45, SYTO 59, SYTO 60, SYTO 61, SYTO 62, SYTO 63, SYTO 64, SYTO 80, SYTO 81, SYTO 82, SYTO 83, SYTO 84, SYTO 85, SYTOX Blue, SYTOX Green, SYTOX Orange, Tetracycline, Tetramethylrhodamine (TAMRA), Texas Red, Texas Red-X conjugate, Thiadicarbocyanine (DiSC3), Thiazine Red R, Thiazole Orange, Thioflavin 5, Thioflavin S, Thioflavin TCN, Thiolyte, Thiozole Orange, Tinopol CBS (Calcofluor White), TMR, TO-PRO-1, TO-PRO-3, TO-PRO-5, TOTO-1, TOTO-3, TRITC (tetramethylrhodamine isothiocyanate), True Blue, TruRed, Ultralite, Uranine B, Uvitex SFC, WW 781, X-Rhodamine, XRITC, Xylene Orange, Y66F, Y66H, Y66W, YO-PRO-1, YO-PRO-3, YOYO-1, YOYO-3, SYBR Green, Thiazole orange (interchelating dyes), or combinations thereof.

[0075] In some aspects, the nucleotides can be used to study a sample, such as a biological sample. For instance, the nucleotides may be used to determine nucleic acids within a cell or other sample. The sample may include a cell culture, a suspension of cells, a biological tissue, a biopsy, an organism, or the like. The sample may also be cell-free but nevertheless contain nucleic acids. If the sample contains a cell, the cell may be a human cell, or any other suitable cell, e.g., a mammalian cell, a fish cell, an insect cell, a plant cell, or the like. More than one cell may be present in some cases.

[0076] The nucleic acids to be determined may be, for example, DNA, RNA, or other nucleic acids that are present within a cell (or other sample). The nucleic acids may be endogenous to the cell, or added to the cell. For instance, the nucleic acid may be viral, or artificially created. In some cases, the nucleic acid to be determined may be expressed by the cell. The nucleic acid is RNA in some embodiments. The RNA may be coding and/or non-coding RNA. Non-limiting examples of RNA that may be studied within the cell include mRNA, siRNA, rRNA, miRNA, tRNA, lncRNA, snoRNAs, snRNAs, exRNAs, piRNAs, or the like. In some embodiments, for example, at least some of the plurality of oligonucleotides are complementary to a portion of a specific chromosome sequence, e.g., of a human chromosome.

[0077] In some cases, a significant portion of the nucleic acid within the cell may be studied. For instance, in some cases, enough of the RNA present within a cell may be determined so as to produce a partial or complete transcriptome of the cell. In some cases, at least 4 types of mRNAs are determined within a cell, and in some cases, at least 3, at least 4, at least 7, at least 8, at least 12, at least 14, at least 15, at least 16, at least 22, at least 30, at least 31, at least 32, at least 50, at least 63, at least 64, at least 72, at least 75, at least 100, at least 127, at least 128, at least 140, at least 255, at least 256, at least 500, at least 1,000, at least 1,500, at least 2,000, at least 2,500, at least 3,000, at least 4,000, at least 5,000, at least 7,500, at least 10,000, at least 12,000, at least 15,000, at least 20,000, at least 25,000, at least 30,000, at least 40,000, at least 50,000, at least 75,000, or at least 100,000 types of mRNAs may be determined within a cell.

[0078] In some cases, the transcriptome of a cell may be determined. It should be understood that the transcriptome generally encompasses all RNA molecules produced within a cell, not just mRNA. Thus, for instance, the transcriptome may also include rRNA, tRNA, etc. In some embodiments, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or 100% of the transcriptome of a cell may be determined.

[0079] The determination of one or more nucleic acids within the cell or other sample may be qualitative and/or quantitative. In addition, the determination may also be spatial, e.g., the position of the nucleic acid within the cell or other sample may be determined in two or three dimensions. In some embodiments, the positions, number, and/or concentrations of nucleic acids within the cell (or other sample) may be determined.

[0080] One non-limiting example of such a system may be found in U.S. Provisional Patent Application Ser. No. 62/031,062, filed Jul. 30, 2014, entitled "Systems and Methods for Determining Nucleic Acids," by Zhuang, et al. incorporated herein by reference in its entirety.

[0081] The following documents are each incorporated herein by reference in their entireties: U.S. Pat. No. 7,838,302, issued Nov. 23, 2010, entitled "Sub-Diffraction Limit Image Resolution and Other Imaging Techniques," by Zhuang, et al.; U.S. Pat. No. 8,564,792, issued Oct. 22, 2013, entitled "Sub-diffraction Limit Image Resolution in Three Dimensions," by Zhuang, et al.; and Int. Pat. Apl. Pub. No. WO 2013/090360, published Jun. 20, 2013, entitled "High Resolution Dual-Objective Microscopy," by Zhuang, et al. In addition, incorporated herein by reference in their entireties are U.S. Provisional Patent Application Ser. No. 62/031,062, filed Jul. 30, 2014, entitled "Systems and Methods for Determining Nucleic Acids," by Zhuang, et al.; U.S. Provisional Patent Application Ser. No. 62/050,636, filed Sep. 15, 2014, entitled "Probe Library Construction," by Zhuang, et al.; U.S. Provisional Patent Application Ser. No. 62/142,653, filed Apr. 3, 2015, entitled "Systems and Methods for Determining Nucleic Acids," by Zhuang, et al.; and a PCT application filed on even date herewith, entitled "Systems and Methods for Determining Nucleic Acids," by Zhuang, et al.

[0082] The following examples are intended to illustrate certain embodiments of the present invention, but do not exemplify the full scope of the invention.

EXAMPLE 1

[0083] This example illustrates high-throughput hybridization construction of DNA probes, according to certain embodiments of the invention.

[0084] Overview. This protocol uses complex libraries of oligonucleotides as templates for the enzymatic construction of large quantities of single-stranded DNA molecules that can be chemically labeled and which are designed to be hybridized to specific sets of nucleic acid targets that can vary significantly in complexity, i.e. the number of unique target sequences. The use of this protocol involves several basic steps: 1) computational design and optimization of a set of oligonucleotide sequences that will serve as the hybridization regions on the sample of interest; 2) computational design and optimization of a large set of short oligonucleotide sequences to serve as highly specific PCR primers; 3) computational construction of the template molecules; 4) synthesis of the template molecules to create the template library; 5) selection of a sub-set of in vitro template molecules from a template library via PCR; 6) in-vitro-transcription-based amplification of the in vitro template molecules into RNA, which serves as the final template for the hybridization probes; 7) reverse transcription of the RNA back into DNA using chemically-modified primers; 8) removal of the RNA via alkaline hydrolysis; and 9) purification of the chemically-modified ssDNA molecules, called probes in this example. These steps are discussed in detail below.

[0085] Construction of Probes. Selection of Hybridization Regions. The software OligoArray 2.0 was used to design a large set of potential hybridization regions in the *E. coli* transcriptome in this example. Briefly, this software selects hybridization regions that lie within user-specified ranges for length and melting temperature. This software also screens for off-target hybridization as well as potential secondary structure. This software was used to generate hybridization regions of 30-nt length, a melting-temperature range of 80-85° C., a GC content of between 50-60%, and a secondary structure melting threshold and cross-hybridization-melting temperature of 75° C. using all annotated, transcribed mRNAs in *E. coli* (K-12 mg1655; NC90013.2).

[0086] Design of Hundreds of Orthogonal Primers. The general hybridization probe set may require far fewer unique sequences than is provided in the complex sets of oligonucleotides typically generated by array-based synthesis—the oligopool. To exploit this disparity in complexity and significantly lower the cost per experiment, this example uses a method to embed a large number of unique template sets within a single oligopool. Briefly, each template molecule was flanked by a unique pair of PCR primers common only to the template molecules for all probes within a given set. To facilitate the embedding of hundreds of unique probe template sets within a single oligopool, a protocol was created for constructing hundreds of orthogonal PCR primers.

[0087] Specifically, the protocol starts by truncating the members of an existing library of 240,000, semi-orthogonal, 25-mer oligonucleotides to 20-nt length and selecting oligos on parameters optimal for PCR: a narrow range of predicted melting-temperature (65-70° C.) and GC content (50-60%); the absence of contiguous runs of the same base longer than 4, i.e. AAAA; and the presence of a 3' GC-clamp, i.e. 2-3 G/C within the final 5 nt. BLAST was then run with these optimized primers against all annotated RNAs in the *E. coli*

transcriptome as well as the T7 promoter (TAATACGACT-CACTATAGGG) (SEQ ID NO. 1) and a common priming region (P9: CAGGCATCCGAGAGGTCTGG) (SEQ ID NO. 2) and potential primers with hits to the transcriptome with 12-nt or longer of homology, or with a hit of any length within 3-nt of the 3' end of the potential primer, were removed. Finally, the remaining primers were screened for homology to each other, again using BLAST. Any primer with longer than 11-nt of homology or with any homology within 3-nt of the 3' end of another primer was removed. These cuts reduced the original 240,000 oligos to 198 highly optimized primers for the *E. coli* transcriptome. The final set of 198 primers are listed in FIGS. 3A-3D.

[0088] If required, more primers could be generated using established techniques to create a larger set of initial oligonucleotides, or by relaxing the stringency of the cuts described above. Finally, by changing the transcriptome used to screen the primers, this approach can also be generalized to the generation of optimal index primers for any organism.

[0089] Template Construction. To design the template libraries used to create our probe sets, the desired RNA targets were first selected to be stained simultaneously. Individual template molecules were designed by concatenating the following sequences: i) the first of two unique primers for the appropriate mRNA group, ii) the common primer P9, iii) the site for the nicking enzyme Nb.BsmI, iv) the reverse complement of the hybridization region to the target, v) the reverse complement of the nicking enzyme Nb.BsrDI, and vi) the reverse complement of the second unique primer for the given mRNA group. FIG. 2 demonstrates this organization. Multiple probe template sets were combined into large oligopools and these pools were synthesized via CustomArray.

[0090] FIG. 2 shows an example template sequence containing a probe the mRNA, acnB. Underlined at the beginning is the sequence of the first primer, not underlined is the common P9 priming site, then underlined is the Nb.BsmI site, not underlined is the reverse complement to the hybridization region for acnB, next underlined is the reverse complement of the Nb.BsrDI site, and the final not underlined portion is the second unique primer. This template is one of 736 used to create probes to stain all mRNAs expressed in the copy number range of 1-10 per cell transcribed from the *E. coli* genomic locus corresponding to base pairs 1-100 kb. See FIGS. 4A-4BV for the sequences of the 736 probes.

[0091] Index PCR. The template for specific probe sets were selected from the complex oligopool via limited-cycle PCR. 0.5 to 1 ng of the complex oligopool was combined with 0.5 micromolar of each primer. The forward primer matched the priming sequence for the desired sub set while the reverse primer was a 5'concatenation of this sequence with the T7 promoter. To avoid the generation of G-quadruplets, which can be difficult to synthesize, the terminal Gs required in the T7 promoter were generated from Gs located at the 5' of the priming region where appropriate. All primers were synthesized by IDT. A 50 microliter reaction volume was amplified either using the KAPA real-time library amplification kit (KAPA Biosystems; KK2701) or via a homemade qPCR mix which included 0.8x EvaGreen (Biotium; 31000-T) and the hot-start Phusion polymerase (New England Biolabs; M0535S). Amplification was followed in real time using Agilent's MX300P or Biorad's CFX Con-

nect. Individual samples were removed before the plateau in amplification, often at concentrations about 10-fold lower than would correspond to this plateau, to minimize distortion of template abundance due to over-amplification. Individual templates were purified with columns according to the manufacturer's instructions (Zymo DNA Clean and Concentrator; D4003) and eluted in RNase-free deionized water.

[0092] Amplification via in vitro transcription. The template was then amplified via in vitro transcription. Briefly, 0.5 to 1 micrograms of template DNA was amplified into 100 to 200 micrograms of RNA in a single 20-30 microliter reaction with a high yield RNA polymerase (New England Biolabs; E2040S). Reactions were supplemented with 1× RNase inhibitor (Promega RNasin; N2611). Amplification was typically run for 2 to 4 hours at 37° C. to maximize the yield. The RNA was not purified after the reaction and was either stored at -80° C. or immediately converted into DNA as described below.

[0093] Reverse Transcription. 1-2 nmol of fluorescently-labeled ssDNA probe was created from the above in vitro transcription reactions using the reverse transcriptase Maxima H-(Thermo Scientific; EP0751). This enzyme was used because of its higher processivity and temperature resistance, which allowed the conversion of large quantities of RNA into DNA within small volumes at temperatures that disfavor secondary structure formation. The unpurified RNA created above was supplemented with 1.6 mM of each dNTP, 1-2 nmol of fluorescently labeled P9 primer, 300 units of Maxima H-, 60 units of RNasin, and a final 1× concentration of the Maxima RT buffer. The final 75 microliter volume was incubated at 50° C. for 60 minutes.

[0094] Strand Selection and Purification. The template RNA in the reaction above was then removed from the DNA via alkaline hydrolysis. 75 microliters of a solution of 0.25 M EDTA and 0.5 N NaOH was added to each reverse transcription reaction, and the sample was incubated at 95° C. for 10 minutes. The reaction was immediately neutralized by purifying the ssDNA probe with a modified version of the Zymo Oligo Clean and Concentrator protocol. Specifically, the 5-microgram capacity column was replaced with a 100-microgram capacity DNA column as appropriate. The remainder of the protocol was run according to the manufacturer's instructions. Probe was eluted in 100 microliter RNase-free deionized water and evaporated in a vacuum concentrator. The final pellet was resuspend in 10 microliter RNase-free water and stored at -20° C. Denaturing polyacrylamid gel electrophoresis and absorption spectroscopy revealed that this protocol typically produces 90-100% incorporate of the fluorescent primer into full length probe and 60-75% recovery of the total fluorescent probe. Thus, without exceeding a 150-microliter reaction volume, this protocol can be used to create ~2 nmol of fluorescent probe. The small reaction volumes were conducive to the use of high-throughput fluid handling techniques and significantly lower the cost of this reaction as compared to alternative approaches. Thus, 24-96 probes could be constructed in parallel, with minimal hands-on time, across two days, for a final cost of ~\$14 per 2 nmol of each probe set.

[0095] While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the

advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the present invention. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the teachings of the present invention is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, the invention may be practiced otherwise than as specifically described and claimed. The present invention is directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the scope of the present invention.

[0096] All definitions, as defined and used herein, should be understood to control over dictionary definitions, definitions in documents incorporated by reference, and/or ordinary meanings of the defined terms.

[0097] The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

[0098] The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, i.e., elements that are conjunctively present in some cases and disjunctively present in other cases. Multiple elements listed with "and/or" should be construed in the same fashion, i.e., "one or more" of the elements so conjoined. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, a reference to "A and/or B", when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A only (optionally including elements other than B); in another embodiment, to B only (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

[0099] As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in a list, "or" or "and/or" shall be interpreted as being inclusive, i.e., the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as "only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of exactly one element of a number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (i.e. "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or

“exactly one of,” “Consisting essentially of,” when used in the claims, shall have its ordinary meaning as used in the field of patent law.

[0100] As used herein in the specification and in the claims, the phrase “at least one,” in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements. This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase “at least one” refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, “at least one of A and B” (or, equivalently, “at least one of A or B,” or, equivalently “at least one of A and/or B”) can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodi-

ment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

[0101] It should also be understood that, unless clearly indicated to the contrary, in any methods claimed herein that include more than one step or act, the order of the steps or acts of the method is not necessarily limited to the order in which the steps or acts of the method are recited.

[0102] In the claims, as well as in the specification above, all transitional phrases such as “comprising,” “including,” “carrying,” “having,” “containing,” “involving,” “holding,” “composed of,” and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases “consisting of” and “consisting essentially of” shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

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attaacgggc caggttactg 20

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attgtatgga ggcgccctat 20

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acaaccgcgt gttacaaggc 20

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gaagtatccg gcatcacagc 20

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gtatttgaac cggccagctg 20

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ggttggtgggc catatccaat 20

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ggcgttccat cgaaactcta 20

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ggccatcgac ttagattcca 20

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ggtgctcctg ccattatagg 20

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tgtcgacgtg cggaaagtag 20

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tgctgcccgt tactactgct 20

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actgcatatg accgctgcaa 20

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<400> SEQUENCE: 111

gacgcgagga gtgatcgact 20

<210> SEQ ID NO 112
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 113

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<400> SEQUENCE: 115

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<400> SEQUENCE: 116

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<400> SEQUENCE: 117

tatgctgggc agtaatcagg 20

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gcattctgta gcattctgct 20

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<400> SEQUENCE: 119

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accattctcg caactcgcta 20

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cgtgggagaa gtacttggtc 20

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ccggacgtct tcgataatgc 20

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<400> SEQUENCE: 123

tgatgctctt tgcagttcgg 20

<210> SEQ ID NO 124
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<212> TYPE: DNA
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<400> SEQUENCE: 124

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<210> SEQ ID NO 125
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<400> SEQUENCE: 125

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catatgccgg acattcagct 20

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<212> TYPE: DNA
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<400> SEQUENCE: 128

actaatggtc ctgcggcata 20

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ggtgccgtgt tgcattgaag 20

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aagcggctgt ggtttatacc 20

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<212> TYPE: DNA
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<220> FEATURE:
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gccaccttgt atggtatcga 20

<210> SEQ ID NO 132
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<212> TYPE: DNA
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<400> SEQUENCE: 132

taatgcttag gcccgtegg 20

<210> SEQ ID NO 133
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<212> TYPE: DNA
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<400> SEQUENCE: 133

gacgcgacgg attatttag 20

<210> SEQ ID NO 134
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 134

ggtcgcgcc atatataagg 20

<210> SEQ ID NO 135
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 135

tgactacggt tgggtgcac 20

<210> SEQ ID NO 136
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 136

tcaggcctc attgtatg 20

<210> SEQ ID NO 137
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 137

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gtagatactc cggcccga 20

<210> SEQ ID NO 138
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 138

gcagcactta gggcagcatc 20

<210> SEQ ID NO 139
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<212> TYPE: DNA
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<220> FEATURE:
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cgcggaacc atattaggaa 20

<210> SEQ ID NO 140
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<400> SEQUENCE: 140

gatccatggc cagttcgtat 20

<210> SEQ ID NO 141
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 141

gtgccc aaa ggacttagtg 20

<210> SEQ ID NO 142
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 142

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<210> SEQ ID NO 143
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<212> TYPE: DNA
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 144

gtctataagc cgcgctgcaa 20

<210> SEQ ID NO 145
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<212> TYPE: DNA
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<400> SEQUENCE: 145

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<210> SEQ ID NO 146
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 146

tgccgcgatc atctactatg 20

<210> SEQ ID NO 147
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 147

gaccgggtat tcgacgtcat 20

<210> SEQ ID NO 148
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 148

gcagtgcggg tagatacgct 20

<210> SEQ ID NO 149
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 149

aggcgtgggt agcaacgtat 20

<210> SEQ ID NO 150
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 150

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<210> SEQ ID NO 151
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 151

aaggaccacg tatctgcatg 20

<210> SEQ ID NO 152
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<212> TYPE: DNA
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<400> SEQUENCE: 152

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<210> SEQ ID NO 153
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 153

tgacctgcac ggatagtagg 20

<210> SEQ ID NO 154
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 154

gttattcgca gtccttgggt 20

<210> SEQ ID NO 155
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 155

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<210> SEQ ID NO 156
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

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cgcggtgtt aaataaggac 20

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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 157

gcgaggcgtg gtaatagtca 20

<210> SEQ ID NO 158
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caaggcgcaa acatagacag 20

<210> SEQ ID NO 159
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<212> TYPE: DNA
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ggaacaaggg cgtctatgtc 20

<210> SEQ ID NO 160
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<212> TYPE: DNA
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<400> SEQUENCE: 160

gcagtgcgga taagctacac 20

<210> SEQ ID NO 161
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 161

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<210> SEQ ID NO 162
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<212> TYPE: DNA
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<400> SEQUENCE: 162

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<210> SEQ ID NO 163
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 163

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<210> SEQ ID NO 164
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 164

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<210> SEQ ID NO 165
<211> LENGTH: 20
<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 165

ggtcgtgcgt ataagcctca 20

<210> SEQ ID NO 166
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 166

cggatggtct tcgtttaacc 20

<210> SEQ ID NO 167
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 167

ggcacggtgg ctagtaacga 20

<210> SEQ ID NO 168
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 168

gccggcccaa ctgatagtag 20

<210> SEQ ID NO 169
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 169

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<210> SEQ ID NO 170
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<400> SEQUENCE: 170

cgggtcgata ctttcctcgt 20

<210> SEQ ID NO 171
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<210> SEQ ID NO 172
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<400> SEQUENCE: 173

gtcaggaac cgtttcttca 20

<210> SEQ ID NO 174
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 174

cttgtcatgt acccgaatgg 20

<210> SEQ ID NO 175
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 175

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cgacctggct acgtagaacc 20

<210> SEQ ID NO 176
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 176

ctagctaaag ggccgtgcgt 20

<210> SEQ ID NO 177
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<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 177

aagtattagc gcggaacgt 20

<210> SEQ ID NO 178
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 178

ggttgcgtgc cacttaaagc 20

<210> SEQ ID NO 179
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 179

ggaggttcgg ttgtactgca 20

<210> SEQ ID NO 180
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 180

gttgcgtcc tccatcggtt 20

<210> SEQ ID NO 181
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 181

gggacggaac tacacatgtg 20

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<210> SEQ ID NO 182
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 182

gatccatcct gattgagggt 20

<210> SEQ ID NO 183
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 183

cttcattgta ccggttgaga 20

<210> SEQ ID NO 184
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 184

tcggtcggct gtaaggatac 20

<210> SEQ ID NO 185
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 185

attgcacgag gtcagagtcg 20

<210> SEQ ID NO 186
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 186

gcttagatcc gctcgctacg 20

<210> SEQ ID NO 187
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 187

cggtggcct actgtagaga 20

<210> SEQ ID NO 188
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 188

gcaacatgac ctgtcatcgc 20

<210> SEQ ID NO 189
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 189

ggccgcacga tatatttgac 20

<210> SEQ ID NO 190
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 190

cagccgggcc ataatagtgtg 20

<210> SEQ ID NO 191
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 191

tgccgtggac ctattatcct 20

<210> SEQ ID NO 192
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 192

cctgcgttag gcaatccatc 20

<210> SEQ ID NO 193
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 193

gtgggctctt cgaagtaacc 20

<210> SEQ ID NO 194
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 194

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gccgtggacc actaaagtcc 20

<210> SEQ ID NO 195
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 195

gettaagtca tggg'gcac 20

<210> SEQ ID NO 196
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 196

acaggttagt tccgcgca 20

<210> SEQ ID NO 197
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 197

ggcgtggcat ttagactacc 20

<210> SEQ ID NO 198
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 198

actacggcca acaaccaaca 20

<210> SEQ ID NO 199
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 199

gttgacaagg ctctgtacgg 20

<210> SEQ ID NO 200
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 200

ttgttctctt gccggtcgat 20

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<210> SEQ ID NO 201
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 201

gttgatcgta gccaatcgg 20

<210> SEQ ID NO 202
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 202

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagc agctctacaa 60

gtgcggccat ttggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 203
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 203

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttt cgcgatagca 60

gccaggaagc ctgcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 204
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 204

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag cgggaaacct 60

ttctgttgca gagcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 205
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 205

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcc agttccgcag 60

aagccaggaa gacattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 206
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 206

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggt gtggcagaaa 60

gactgcatca ccaggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 207

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 207

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ggcacatgtg gaatatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 208

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 208

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggtg cgtgttcacg 60

tcaactggct tcggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 209

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 209

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatc tgcacggct 60

tccagcagct caggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 210

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 210

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca gcacggaagt 60

gaccgatggt ggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 211

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 211

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccate cgggtcgttc 60

ggagcacaca ggattgatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 212
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 212

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatac gcgcaccact 60
cttaccgaag acgctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 213
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 213

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatcg gctttctcgg 60
tgtagtgaga aagctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 214
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 214

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccagt acccagacgg 60
ttcgggaagt tacgggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 215
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 215

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccttt gttcagcttg 60
atggtacaac cagcggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 216
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 216

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccatc cgcccaggac 60
tgcataacct gcttcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 217
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 217

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccc taaaccacag 60

aacggagtta gtggcgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 218

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 218

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctcgt tgectgcttt 60

cgctttctct tctacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 219

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 219

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgg tgccggagaa 60

aggtcatcgg tgtagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 220

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 220

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taatgaagtc cggcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 221

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 221

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ctttatgcgc atccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 222

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 222

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cggtggttac cacttcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 223
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 223

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgc cgtaaccttc 60

cgcgatcadc cacttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 224
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 224

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttg atcgaccaa 60

caacaccagg ctggtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 225
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 225

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgg tgggtgctctg 60

ggaacctaca gaagtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 226
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 226

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc gcatcgggta 60

gctcaaaggc ctgctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 227
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 227

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatct acctgcgcca 60

cgtaggtctg gtactccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 228
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 228

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatac ggccaccagc 60
acgcacttca tcaatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 229
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 229

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcg aacatcagca 60
gcggtgagaga aagtgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 230
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 230

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaata tccgccagat 60
cgatgtcgat cactgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 231
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 231

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaca cttcgtcgat 60
cttctcacc cgtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 232
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 232

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttg cttttcttct 60
caacggtcag cagaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 233
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 233

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccatt gccttgaata 60

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cgacgttcca ggtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 234
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 234

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggaa acgggtatgg 60

gagtcaccac cgtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 235
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 235

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgaa gaaccctac 60

ccacaacgtc accgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 236
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 236

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt caatcacgtc 60

gcccattgtc aggttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 237
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 237

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacca gaccagaacc 60

cgccgggaaa gagatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 238
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 238

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttga agegcaccag 60

aacggattcc ggcatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 239
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 239

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctt ctcgggtcaa 60
ctgtgcgggc tccatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 240
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 240

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtt acccatacac 60
agggaacagc caggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 241
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 241

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcag atccggcaga 60
ccttcaattt ccaggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 242
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 242

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag tttggcatca 60
tccagcgcgt cgatcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 243
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 243

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccc ggcacgccag 60
gtctttcagt tcatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 244
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 244

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acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgccttt ggtggtcagg 60

ccacgcccga taatcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 245
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 245

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgctgat cgcatacagc 60

ggaatagcgt gtaccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 246
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 246

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgcag tgcaccgcg 60

tcttccatcg tgtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 247
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 247

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgcag cagcatacgg 60

ttcagccagg agtgaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 248
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 248

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgctc tcagcgacat 60

ctttcgctg acggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 249
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 249

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcggtt tcaaggtcgc 60

ccgccagttt ctgtttcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 250
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 250

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccacg gtgctggaac 60
cacgggcata gaagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 251
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 251

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgc cgttgatac 60
caacagcata acctgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 252
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 252

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgaa acgggcataa 60
ccgcatcca gatagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 253
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 253

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgga acacgttggg 60
tatcggatc gacagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 254
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 254

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacgg tgaagtacgg 60
gttggttacc gacagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 255
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 255

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacag ctcaccggc 60
tcgatcttag tcagctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 256

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 256

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctggt ggtatagtcg 60
gacaggtcgg cgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 257

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 257

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcggcg acacgctgaa 60
ggccttcgaa atgaatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 258

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 258

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgga aatgagagat 60
cagttcgtcg gtggtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 259

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 259

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttgc tggatttcag 60
ctgacacacc ttctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 260

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 260

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgtcg gcatcgtaa 60
tttcgggcat cgactgcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 261
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 261
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcactg ctttcggacc 60
aatggtattg gactggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 262
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 262
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacct tgtagacgac 60
atcaacctgg tccgggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 263
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 263
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctatc cgatccagga 60
atggtcactt taccggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 264
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 264
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcac tacgaacct 60
tcagcacctg ataccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 265
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 265
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagcc atgcaccttc 60
catctgacgc atttcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 266
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 266

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccc gacctgcacg 60
cagcgagtta tattcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 267
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 267

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaact ggaactgttc 60
tgccttgtct ccatcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 268
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 268

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatct tcatcattaa 60
cgtgtgcgcc tgtgcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 269
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 269

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcca accatagttg 60
aacgtgaagt cgtccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 270
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 270

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac tgtaatgcga 60
taccgcaga catacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 271
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 271

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcattt acgatcgctt 60

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accacgttcc accacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 272
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 272

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggc tggaatccca 60

gtttgtatcc caaacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 273
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 273

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgc tggcgctata 60

tttaccgacg ctgtagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 274
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 274

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaccg cctacagcat 60

catccgattt acacagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 275
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 275

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatct ggcgtcagac 60

tgacctgggt agagtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 276
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 276

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcg ccgctctgag 60

tcgcacattc gtaatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 277
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 277

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacaa cccatttgtg 60
atcgctcatcg atcggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 278
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 278

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaccc atagagtaca 60
gataacgcca catcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 279
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 279

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatac caaagttgaa 60
gctaccgggtg ttgcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 280
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 280

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctata gaagagacga 60
ccaccgaggc ttacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 281
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 281

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtca tcttccatct 60
tggtcacttt ggtgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 282
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 282

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgga ttttacgcac 60

gtagaaacgg ttacccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 283
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 283

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg acggcatctt 60

tcgaggtatc gttacccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 284
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 284

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagaa gcccagacga 60

ttcagacgct ccttaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 285
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 285

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgac acgtgaacca 60

tctgtcggga agtaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 286
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 286

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc taaacagcag 60

cgacgctatg agcaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 287
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 287

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgagg ctgcatgttg 60

gacagggagt tatgtacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 288
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 288

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggg aagccaacg 60
tcacgtctgt accatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 289
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 289

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggg atcataatta 60
ctggcctgat gcgggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 290
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 290

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaagc tgttatctcg 60
atcagaggtg ctcggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 291
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 291

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacct gaaccagaag 60
ggtatcacca tcacgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 292
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 292

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca tctctttgcc 60
gcctaaacca tcaccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 293
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 293

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccag ttatcctgct 60
gcacaccagc ctggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 294

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 294

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgagg ataggcataa 60
ccatagcgac cgagaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 295

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 295

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaag gttgccgctc 60
acttcaacgc cagaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 296

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 296

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcga acatcctcaa 60
agttgccggt agcaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 297

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 297

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt gggcttgac 60
gttcaaacca gtcactcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 298

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 298

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctg tgaagcgca 60
ttacagagct gttgtgcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 299
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 299

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttgc gctttcaatt 60

gcgcgtactg atccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 300
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 300

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcgc ttgtggagga 60

tagtcggaat agctgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 301
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 301

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagga atttggctccg 60

gtccgcctgt aatgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 302
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 302

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgag cgtgctaaca 60

cctgttcgcg gctaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 303
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 303

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcat tacctccacg 60

ccaggcaatc accagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 304
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 304

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcaa aggcaagttc 60
agtgttgcg ggagaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 305
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 305

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgata tcgcgatat 60
gcagcagcca gttgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 306
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 306

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag ttcaggtcag 60
tgtgaatgac caggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 307
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 307

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatt acggtgaaca 60
aagagttcgc cgggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 308
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 308

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttgt ggttggcgtg 60
tttcagcttg aggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 309
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 309

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccg ttaacggttc 60

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tgcaggaacg cgactgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 310
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 310

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctg ttccatgacg 60

ttcagttcac acaaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 311
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 311

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcga gtacatccac 60

tgcatactga accacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 312
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 312

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgt tccacgctga 60

ttgcataatg gtggagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 313
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 313

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccccg tgacggtaac 60

ggtgctcaag ggtttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 314
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 314

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc cgcaaccgta 60

gtggccacag ataatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 315
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 315

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtg gcgtaacat 60
ccagatcacg cagcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 316
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 316

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctaata gattctcgtc 60
atagtgccag gcccgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 317
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 317

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaga aacaaccgccg 60
cgatgacgac gggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 318
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 318

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcca gcatgcagac 60
caccagcgtt acaatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 319
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 319

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagag ttaccgacaga 60
ttgctgcgga acctggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 320
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 320

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgaa gcccaaagtg 60

agatttcaac cagcggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 321
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 321

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgtaa caacaagcaa 60

gcaaagaccg gtaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 322
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 322

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcggat catgacatag 60

agcagccata ttgcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 323
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 323

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctacc accgtgtcct 60

ggaattaaat gaccgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 324
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 324

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctttg ccaaacatat 60

atgcgccgga gtcagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 325
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 325

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccg tgcagtagcg 60

agtccaccga taaagccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 326
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 326

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacgc ttaaacatac 60
tctcggtcag atcgcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 327
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 327

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcat cagcgccaac 60
aataaccgcg ataacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 328
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 328

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcca cgtcgagatt 60
cgcccacatg ccataacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 329
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 329

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagca ccagcaatag 60
cgcgacaatc caccaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 330
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 330

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcctga ggctaacgct 60
gcgacaatag agcaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 331
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 331

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaac gcgaccgtag 60
tggatttcgc cggtttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 332

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 332

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgg aatccagcag 60
ggcgatcacc tgatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 333

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 333

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtgc cttcatcaac 60
atatgcgccg atgttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 334

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 334

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaac cactgatgcg 60
tcaccactg accgtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 335

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 335

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtaa cgggtgctgc 60
attggctggc gtgatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 336

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 336

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacc gcacagtaga 60
ggctgtatgt gccatccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 337
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 337

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagtc gatggtacgc 60

agcagttcgt taatgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 338
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 338

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaata cgggtgctct 60

gaccaatgta tacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 339
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 339

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcactt cagagcgcgc 60

gccgatgaag caattacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 340
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 340

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgacg gcatcagcac 60

ggtgttacgg gcaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 341
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 341

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccttc gtcgtagtcg 60

gcgaatttca tcggcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 342
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 342

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggc acaaccgcga 60
agccttcttt ctggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 343
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 343

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaca agaaccgcgc 60
gtcggcccagg tatcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 344
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 344

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgg taaaccggca 60
ccttgccata gaagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 345
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 345

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctc gacaggatac 60
gcgtcaatac cgccttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 346
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 346

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctg tggctgggtca 60
taccgggtga ggtattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 347
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 347

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgt ccatcgctgt 60

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ccagcataac gtcaatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 348
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 348

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgc ctcaataca 60

tagaaggttc cggacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 349
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 349

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccctt tgcaacctaa 60

cgctgtccat gctttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 350
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 350

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc gaccgtgtag 60

cgcgataaac actttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 351
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 351

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaca ttcccacact 60

ggaaccttcg cggctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 352
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 352

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttct tcaccgagta 60

tcgcaaccgt gaactccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 353
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 353

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacc ggcaaaccca 60
gagcagaaat ttctgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 354
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 354

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctaata gcctgcaaat 60
tggcctcttg tgacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 355
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 355

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcc attgaaagcg 60
cagatgccaat cactcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 356
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 356

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctagt ccgccagttc 60
cagaattcgt actaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 357
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 357

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgccc atcgacttca 60
gttgcgtcac gtcgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 358
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 358

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccgt aacaccgctg 60

cgccagaatt cagagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 359
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 359

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccgt ataaggcaag 60

cccatcagct cgagcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 360
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 360

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccacg ttgttacta 60

ccacgcctg atctttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 361
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 361

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccgt aggttaacca 60

gcgaccacc ggagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 362
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 362

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccgt agttccaggt 60

tcacgttaac ctgcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 363
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 363

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccgt cggaggaatt 60

aggcagaacc tggcttcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 364
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 364

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcactc agagccagtg 60
cactcagtgc taatgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 365
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 365

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctggt gctcatctca 60
gcgcttcaa tgccgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 366
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 366

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgaa tgttgagtgc 60
cagcacagac ggtttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 367
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 367

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgccg gaaccagcg 60
ccatgaattt ctgttgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 368
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 368

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatgg agctggaatc 60
aacctgattc tggtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 369
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 369

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcataa taccagctc 60
accgcgttcc acctggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 370

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 370

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcggca aagctgctga 60
tcggcttacc gttcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 371

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 371

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcctgg gcgtcaactt 60
tcacgcgttt cgccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 372

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 372

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgcat ctgctgggct 60
gtcgctgctg aagaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 373

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 373

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcagcg cagagacaat 60
cccgaagt accgtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 374

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 374

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccggg ttctggattt 60
ggatcagcgc gatatccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 375
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 375

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtg cgaggatcgc 60
ggtgttgata ccgatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 376
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 376

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcactg cattaacagg 60
tagatggtgc tgcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 377
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 377

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaac aacgtggttg 60
ttggtgacga catagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 378
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 378

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggc catcgctcag 60
ttgaacttta atgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 379
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 379

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt taatgctgac 60
cactgaaggc atcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 380
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 380

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccact gcctgctggt 60
tcgcgccaat aatcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 381
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 381

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgc gcagtgcac 60
agaatccgcc atcttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 382
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 382

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacca aacgggttac 60
caatcgctac ggtgtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 383
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 383

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggca tacgcggcgt 60
attaacgggtt gtgctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 384
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 384

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag taagcccagg 60
gtcagtttgc tgcttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 385
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 385

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggcg atctttgcc 60

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accatcttcg cgtcgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 386
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 386

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggc agaacggaga 60

gctctggaac ggagaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 387
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 387

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgg cagaacggag 60

aatcatcacc gaagaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 388
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 388

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgccg ttgcagagag 60

cgagataac gccaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 389
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 389

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgat ggtcatatcg 60

ccttcgttca cctgatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 390
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 390

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagat tcgggttatc 60

ttcgtcagcg atcaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 391
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 391

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagat actaaaggaa 60
gaaccgcaac cgcaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 392
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 392

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaact ttgttgctg 60
ctgcgtcggg aaactccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 393
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 393

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacct tcggtataat 60
caacggaaacc gccgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 394
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 394

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcg ttcgggttgg 60
tcacgatgaa acgagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 395
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 395

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaagg tgaaccata 60
ctggaagccg ctgcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 396
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 396

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acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgcc tgcaacttca 60

ggccattcag atagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 397

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 397

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgccagt ctggaacagg 60

ctgtcagtac cggcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 398

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 398

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgctg accatattca 60

acaggccgcc aggactcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 399

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 399

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgccacc accacgccag 60

gtaaactggt tgtcatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 400

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 400

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgccgctc gtaaccaaac 60

caggcggtga tgtcatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 401

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 401

acaaccgctg gttacaaggc caggcatccg agaggtctgg gaatgcgtaa agcacggaaa 60

ccgggccacg cataatcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 402
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 402

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccggt agcagactgt 60
cgcgccgcaa tagttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 403
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 403

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgctc ccggcaacgc 60
ggttaagaga ttcttgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 404
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 404

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgcc tttcgettcg 60
atttctacgc cacgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 405
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 405

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgctcg atatcgccag 60
tggcaaaactt gctctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 406
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 406

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctacg tgccagataa 60
tggcctttat ccgctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 407
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 407

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgg agcagacgcc 60
gtaaccataa acgctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 408

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 408

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagg agtatcgggtg 60
gtgtattccg catcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 409

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 409

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatac gcataaagtc 60
gacaccggtc agcaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 410

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 410

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgact tcggctgatg 60
cagcgccatc tcttcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 411

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 411

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgccg gatccttggc 60
attgaagtcg aaatcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 412

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 412

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacg atcgaacagg 60
ttgttaacat gcagcgcatc gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 413
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 413

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctcat taaagtctgt 60

cggcagacgc ttaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 414
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 414

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcg ttccagcata 60

tacgggtcaa tgaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 415
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 415

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatac acggcaccag 60

taactacaat cggacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 416
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 416

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccag tcataacgac 60

cgcttagggt gaccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 417
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 417

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacca tccttcccaa 60

cttgcaaga aggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 418
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 418

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca ggtgcagcgg 60
taacggtgat agtgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 419
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 419

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaatt cgtgatcgaa 60
gctgtagccg accatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 420
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 420

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaag cagccataag 60
tgtaaagca gctggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 421
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 421

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctccc actttaaagg 60
agttagccgg atcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 422
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 422

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttag aaacggaagg 60
ttgcggttgc aacgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 423
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 423

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacc ggattgtaca 60

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gattgagcag tggcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 424
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 424

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcca ggtgaacgcc 60

ggtgcaatag cataaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 425
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 425

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccga agaccgggtca 60

ggcgataaga gtaaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 426
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 426

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaccc cactgcccct 60

gatcctgaac ataaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 427
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 427

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac gccgactcgc 60

gccagatcat aacgtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 428
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 428

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtac caacagagac 60

accggcgctg tagctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 429
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 429

acaaccgcgt gttacaagc cagcatccg agaggtctgg gaatgccga aagccgcaa 60
tgatcagggtg gtcatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 430
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 430

acaaccgcgt gttacaagc cagcatccg agaggtctgg gaatgctgaa cttctttcag 60
cggttcgggtg gtcggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 431
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 431

acaaccgcgt gttacaagc cagcatccg agaggtctgg gaatgccgct aaccgctgtg 60
gctactacaa ctggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 432
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 432

acaaccgcgt gttacaagc cagcatccg agaggtctgg gaatgccggt tcaaccgctg 60
cctgtgcata aacagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 433
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 433

acaaccgcgt gttacaagc cagcatccg agaggtctgg gaatgcaccg gttccggct 60
cgttctggaa gtaagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 434
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 434

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acaaccgct gttacaaggc caggcacccg agaggtctgg gaatgctctt ctgacccttt 60

ctgctgggca ttggcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 435

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 435

acaaccgct gttacaaggc caggcacccg agaggtctgg gaatgccagc aaagcgcagg 60

ttctgacgca cagtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 436

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 436

acaaccgct gttacaaggc caggcacccg agaggtctgg gaatgcatct cgccaccttc 60

aaccgagaag aaggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 437

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 437

acaaccgct gttacaaggc caggcacccg agaggtctgg gaatgccagc gtcagacctg 60

aaagcggacc gtcaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 438

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 438

acaaccgct gttacaaggc caggcacccg agaggtctgg gaatgcgagg aagctgctgc 60

ggcaataag ccacttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 439

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 439

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acctggtggg cgatatcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 440
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 440

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgagc agagtggatt 60
taccagaacc gttgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 441
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 441

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccc tcgggatgcc 60
ataaatcatt tcgaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 442
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 442

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccc cgctttgctg 60
ctccagcttt ccagcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 443
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 443

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgc gcagggcgac 60
cagataatca cagtagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 444
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 444

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccac gggtaacgac 60
caatgcccac cagttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 445
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 445

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccga ggtcggttcg 60
tcgagcaaca gacaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 446

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 446

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgacc ggtaactttc 60
ccggcaggaa aggttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 447

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 447

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccaat gaccgtcagg 60
ccacgctcct gacttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 448

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 448

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgac gcccgggcac 60
acgaaaggag atattacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 449

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 449

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgacg ttcgccgcca 60
gagagactat cgaccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 450

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 450

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcat aatttccgca 60
ggcgcttcct gagcaacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 451
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 451
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctagt gcggaacggt 60
caggcggttca gtatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 452
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 452
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgga gaggccagat 60
tgctgcctat ggcaatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 453
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 453
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctacc aacagcagt 60
atgtcgagat ccagcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 454
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 454
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatca ggaaacacca 60
actccggcgc gatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 455
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 455
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacg gctgcgttta 60
agtaatcggg ttgatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 456
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 456

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggt aagaatgtgg 60
ctttcagggg tategccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 457
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 457

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagta gctcttcagg 60
tgcaagagag gtttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 458
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 458

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgagg ccacagcata 60
aatccacgat tcttcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 459
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 459

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttt gcggacgcga 60
ccttgctgca attcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 460
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 460

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctc gatcacctct 60
gccagtgtct gacgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 461
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 461

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacc gatatcgacg 60

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acgcagacac ccagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 462
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 462

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggc gtgccaaagg 60

cgtaagcgat atcactcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 463
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 463

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgtact aaagcggcaa 60

ccttcgcggt accaatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 464
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 464

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca cgcccgaag 60

tctaccgga ttcttgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 465
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 465

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcc atatcgttgt 60

gacatgtgat caggtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 466
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 466

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca ccataccaat 60

ttcattctgg cagctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 467
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 467

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctt tatccatacc 60
acgcgacggg cagctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 468
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 468

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcct gatagtcaat 60
cgcatactct tgcgggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 469
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 469

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcca gcataaggaa 60
ttaccttagt gtggcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 470
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 470

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcactc tttcccatag 60
tgaagcaatc ccaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 471
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 471

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctacg gctcctgagc 60
ataatccggt aaaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 472
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 472

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acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgcgcca atgatattga 60

ccataccgtc gggcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 473
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 473

acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgccagt tggccaactt 60

tcagcccaca acgttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 474
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 474

acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgcctga caatctgcca 60

tcaattctgc ctggtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 475
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 475

acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgctatc tcttctgtga 60

ccaggttgag cagctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 476
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 476

acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgcccc ggcgacaacc 60

gtggcgaact ttaatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 477
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 477

acaaccgcgt gttacaaggg cagggatccg agaggtctgg gaatgccaat accgaataac 60

ttgatgccag tccggccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 478
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 478

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcac ttgcgtatga 60
aacacgcgct gagcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 479
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 479

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccga gccaaactatt 60
gagtcgcttg atccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 480
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 480

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccttc gatctcgcgt 60
gcccaccgg ttaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 481
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 481

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgc ttgtacgcac 60
ttgaccacgg attcgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 482
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 482

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgt ctggcggcac 60
gctgaaggta tttctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 483
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 483

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccttc cgggccatac 60

agcattggaa gcacctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 484

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 484

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tgcaaacatt cattggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 485

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 485

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tcctctggcg gcaaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 486

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 486

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cgactgccgg atatcgcat gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 487

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 487

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cgttgttcta tttggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 488

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 488

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgtt gacatcctgg 60

gtcataaagg taccgcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 489
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 489

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcg ttattcagcg 60

tcaactgccca ggaacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 490
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 490

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag acgcgttcca 60

ttattgcggc gagaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 491
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 491

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggt catcgccgct 60

tccttcagag taaatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 492
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 492

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt agctaaccg 60

tttgccatcg gtttgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 493
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 493

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctct accatatggt 60

gatcattcca ccgcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 494
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 494

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcaa ttcacaggc 60
cactgctttc tgacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 495
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 495

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagc ctactgccgc 60
tccagagtca taacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 496
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 496

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt gtgtaatggc 60
gttcaccggt caacaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 497
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 497

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctctt cttoctgtt 60
tcgctgttc agagcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 498
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 498

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagca aatgcacgga 60
tggtgttaac taccgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 499
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 499

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgca cagcgccttt 60

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cagtacatcg ttcgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 500
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 500

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagag aagtaccgat 60

aaccacagtc gcgttgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 501
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 501

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgct gaacctgctt 60

attggtcacc agagtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 502
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 502

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgt tacgcgcagc 60

tcgtcattca taccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 503
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 503

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg gagataaccgc 60

ggcccagaac tttcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 504
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 504

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcg ccagacaggt 60

cgatatcttc cagcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 505
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 505

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg tcgaagcccg 60
ccgtgatggt aaccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 506
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 506

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagga cgtttgtcca 60
tgccgatacc tgtegccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 507
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 507

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagag atagccattt 60
cagcagcttc ttecgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 508
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 508

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac cacccatacc 60
cgcagcaata aagaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 509
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 509

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttc agcgacgact 60
ggtgctgcac ctgtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 510
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 510

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgcg gcccgctcct 60

ttggtgatac cgctaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 511
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 511

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgca gtttgccgcg 60

cattgtcatt cagcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 512
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 512

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccatt acggtgcgta 60

cgtctgcaaa gtccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 513
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 513

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctcaa acccgagcga 60

gtaatcagtt cagcgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 514
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 514

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctgaa aggcttagtg 60

acgacagcaa cggtcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 515
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 515

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgca cgcgatgac 60

tttaatcacc gcgtcacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 516
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 516
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccat cccatgctgc 60
tggtagcgat ccatcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 517
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 517
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgtc gttcgggata 60
gtgatcagag agtccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 518
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 518
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccagc gcttgtgcat 60
cggatattac cgcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 519
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 519
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccttc aatgcgctcg 60
cgcacatgt gttcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 520
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 520
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgacc cggtttggtg 60
tctggcatat tgctttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 521
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 521

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatc acttccggcg 60
aagcggtttc tgctttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 522

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 522

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggt gccaggagt 60
ttggcgagtt aaaggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 523

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 523

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatg ataagagaca 60
ccacggcagg ttacgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 524

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 524

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgtg ttcgtcagac 60
gggattgcgt tcggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 525

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 525

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggg aaccaccagt 60
tcgccattac gacgatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 526

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 526

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacc gctaatacagc 60
agtgcgacca ccagtgcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 527
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 527

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcc ggagcgtaaa 60
taactggcac tttctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 528
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 528

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcc cactttaatc 60
ggcgtcactt cattggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 529
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 529

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgct ggctgtttac 60
atggcagacc aaatggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 530
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 530

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaatc gcaatcagtc 60
gaccatcatt gaccggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 531
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 531

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttga gcacgccttt 60
attggcgaag gtttcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 532
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 532

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacat atccgcaccg 60
ctcaaatctt tcgtcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 533
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 533

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgtt atccgcgtta 60
atctgtttca gcggcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 534
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 534

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgggc tgtagcgtg 60
acgagtaatc gtcgcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 535
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 535

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctagt cgccatctt 60
cgtaccaaat gaaccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 536
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 536

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccga gcatcacaag 60
gccagcgata ggtagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 537
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 537

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc ggatcgtaa 60

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atccggccca ggtcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 538
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 538

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg cgctgggtgag 60

cggtacacag gtaaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 539
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 539

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgta cccgggaaga 60

ccagcgtacc ctgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 540
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 540

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcg gtgataatcg 60

gtggcgaagt cggttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 541
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 541

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgt gccggaagat 60

ccatgtccca caggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 542
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 542

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtc acgcccacg 60

gcagatagac cagatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 543
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 543

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg atcgtaatgc 60
catttctctt tgccgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 544
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 544

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttac ttcacatcat 60
cgggcagcgc ataagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 545
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 545

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaac ggtctggtag 60
ctccacgcca gtttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 546
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 546

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt gcggagatca 60
ccacatactg cttaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 547
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 547

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc cgtagcggcg 60
ataaacagca cgttaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 548
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 548

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttc ataggtcatt 60

ggcgtagcct gaccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 549

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 549

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cacgatttgg atcaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 550

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 550

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccga gtcagcggcc 60

agaagtggaa accaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 551

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 551

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gtgacacat acggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 552

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 552

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tgtaagcgcg caggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 553

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 553

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggat cgttcggctg 60

cttcacatcg ccaggtacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 554
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 554

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgacc agccagcctc 60
cgccaatgag tagatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 555
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 555

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgcc ttcatagcgc 60
atctggtgga acatcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 556
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 556

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgtt gaccttctcg 60
attacgacca taggcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 557
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 557

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccctg cggcgtacca 60
atacgtttct tccacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 558
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 558

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccag gaccacgcgg 60
gatcagtttc gaaacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 559
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 559

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccccg cccagcatcg 60
gcatacccat attgaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 560

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 560

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaca aacggcagga 60
tcagccagat gccgaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 561

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 561

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgatc acgccagacg 60
tttcgcggtg tgagaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 562

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 562

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacg ccggaccagc 60
tctgacctga atgtttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 563

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 563

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcgc tttcgcaacg 60
aactgcacga agtgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 564

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 564

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgtg cctacggtgt 60
ccatatttgc ggcgatcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 565
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 565
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacc agtcaactacg 60
ttaccagcac aaatggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 566
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 566
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaaa cgaagtttaa 60
tgccgggttc aggtcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 567
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 567
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaat ttctcgcctg 60
tctctcaac gatcgcgatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 568
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 568
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagag tggagcgttt 60
agggcggatg agaacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 569
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 569
acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggt gcagccacca 60
tcgctgacga tcattccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 570
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 570

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacg atatcggcac 60
ctgagaggat aagctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 571
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 571

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttg ttctgcaca 60
cgaataaacg tgggtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 572
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 572

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcattg acgttccagt 60
tcaacatcgg aacggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 573
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 573

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgacg cgagttgtac 60
aaacagaacc tgggcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 574
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 574

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccga acgtgacgtt 60
tcacgcaga ctcggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 575
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 575

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca gcatcggcac 60

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attcgattac cgcagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 576
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 576

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgaa atccgcatca 60

gacgtaccgg tagaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 577
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 577

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgca gtcagcgtga 60

ccatggtaac acccttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 578
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 578

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacc atatccatgg 60

tgggaccag ttcggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 579
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 579

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt cttctgccgc 60

ttccagcaga ccttctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 580
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 580

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccact tccatttcgg 60

ttggtgcacc aaagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 581
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 581

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgaac tctggcagcg 60
gcggaacaca gttcatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 582
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 582

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt gttgtcagct 60
catccagcgt ttcgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 583
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 583

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctatt gatattctcc 60
atgctgtgcg ccacggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 584
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 584

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcta cgcggaaacc 60
ggtcatcact tcatcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 585
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 585

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttgc catcaacatc 60
gtacagataa gcgccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 586
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 586

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccga ggcaggtaa 60

atctggcaact acgcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 587
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 587

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcctca aatgcggcgc 60

gtacagaagc cagatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 588
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 588

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccaac ttcgcaaaca 60

cccgcagtgc agcatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 589
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 589

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgct taaagcgctc 60

cacgtcacag gccatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 590
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 590

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcaggc atatttgccg 60

aaatctgccg gaacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 591
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 591

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcctca tggctccttc 60

agtgccggag ttcaccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 592
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 592

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccag cgcatccatt 60
acatcacgac gaccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 593
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 593

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgct tcaaaccgctg 60
acggtgccag gtaaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 594
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 594

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgctg cgcgacttca 60
ttcagacagg cgaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 595
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 595

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcca tcgcaatcgg 60
gttaccggaa agcgtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 596
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 596

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctacc gaacatgccg 60
ccaacgtggt taacgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 597
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 597

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctaa cgtgagtgcg 60
ccagaaccgg ctttcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 598

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 598

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc caccggtcgc 60
acgataatac aggcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 599

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 599

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccga tatacggcag 60
atgacggtaa cgctgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 600

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 600

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccat atcgctgccg 60
ctgtctttgt aacgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 601

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 601

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtt cgcgcaggct 60
taagatctca cgcactcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 602

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 602

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcat gagatacctg 60
aacttcacgg cacaggcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 603
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 603

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgttt atccagcagc 60

gtacaaatcg ccagcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 604
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 604

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaaat tctaccggga 60

cgttcacttc acgacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 605
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 605

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatct tcaacaatca 60

gcacgtcctt gccacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 606
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 606

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcg taccgtagct 60

ggaggcggtc ataaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 607
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 607

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctcaa tgccgtaacc 60

caccacaaac tcatcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 608
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 608

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac ataatgagc 60
cacgcagcag acccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 609
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 609

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac acccagttcg 60
gcgatacgcg cttaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 610
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 610

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac ttcccggctg 60
ttagcgttcc agatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 611
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 611

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac cttgcaaacg 60
cgagttaaag cgactgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 612
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 612

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac ataatacgca 60
gacgcacggt atgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 613
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 613

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaaac catacagcgt 60

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taacgcctca ataccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 614
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 614

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac cgtagtctgc 60

cgcaatattc agcgtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 615
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 615

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatct gatctggttg 60

caggtttcct tgctgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 616
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 616

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgt ttatgcccac 60

aggcagcaat cttccccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 617
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 617

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag ttgcttgact 60

ccctggacta tatccccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 618
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 618

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctctt tgttcatcga 60

aatcggggcca gagaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 619
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 619

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgct atcgagcgcc 60
cacacaaaca gttccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 620
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 620

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgccc ccgaaacgac 60
gctctcgatt agcaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 621
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 621

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccat gcgtagcgcc 60
aggtacaggc tttcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 622
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 622

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgagg caggcagaaa 60
ccgcgtgttg ttcattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 623
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 623

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgag gtatcgccgt 60
ggaaaccatc tttgatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 624
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 624

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttat tcgctgtgcg 60

agattatcgc cgggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 625

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 625

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttat cccggtttaa 60

catcgggttc gatcatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 626

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 626

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagag atgcaaacgg 60

atttcggata gccgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 627

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 627

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctaat cattacagat 60

gcgatccagc tcgccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 628

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 628

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcg ccatctttca 60

gcagcttagc atcgtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 629

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 629

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgct tgaccattgg 60

ctcgatggtg aacgtccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 630
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 630

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaccg tccagccatc 60
tttcatggtg cggatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 631
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 631

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccatc cttgcgtagc 60
gtcagaatth cgcagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 632
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 632

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctccg caatattcac 60
gaacgacgga gaagcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 633
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 633

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgcg gttcttcatg 60
gaagccgcga ccaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 634
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 634

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaggc ttcagtacga 60
cgttggtttc acgggacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 635
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 635

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttc gacaaatttc 60
tgaatcgccg caccgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 636

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 636

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc catgatggtc 60
ggcttaccga cgataacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 637

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 637

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc tgegggaagc 60
tctgatacag cactttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 638

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 638

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt acgccctttg 60
cctttgcctt taccttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 639

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 639

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccgc attggcgcat 60
ccgcaatcca cgtattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 640

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 640

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagcg gacgggcact 60
caacatgtca tagagtcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 641
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 641

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgt tagctcttct 60

accggggcgc caaagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 642
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 642

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatga tcagcggcat 60

gtaagcttcg ttcgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 643
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 643

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccac cagcctcact 60

ctgcccgttt cgctatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 644
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 644

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgt ttggttgcg 60

ccgctctgac cgagatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 645
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 645

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcctgg caccatacag 60

tttggtcggc tggttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 646
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 646

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctttc accataaccga 60
ctaacagcgc ctgctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 647
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 647

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgg acggcgaatc 60
atctcaatgc tgttggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 648
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 648

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggt catcattctg 60
cggtgaccag acctggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 649
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 649

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagat ttaccgtcgg 60
cacgttcac gaacggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 650
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 650

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtc atgtctgget 60
caagattgac cattcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 651
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 651

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaaa ctgctgctca 60

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gaacctccga ccatcgcat ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 652
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 652

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcgctc aagaatcgg 60

tctttgctgt aacgcgcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 653
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 653

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcaaca tacccttgat 60

ccaaccggct acaccgcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 654
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 654

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgccag taagaacgct 60

cgctggagag gaacagcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 655
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 655

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcatgg tgatcagacg 60

cggatcaaga cggagcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 656
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 656

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcaaaa cagacgctgc 60

tcaccgtttg gcgaagcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 657
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 657

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgctcg cctccagcag 60
cttcaccatc tcgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 658
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 658

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgctcg ggtttccctt 60
tgctccaat tggtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 659
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 659

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgctcg tttgtctgctg 60
gctgagaaga ctgatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 660
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 660

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgctcg ttgttctcca 60
tattgacgat cgtcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 661
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 661

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgctcg tggttaagg 60
ccgtcagata agtcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 662
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 662

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcga gataaacgcc 60

gtaaattggcg atcagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 663
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 663

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcataa tctgttgctg 60

ttgcagcaga cgcagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 664
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 664

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgac ggtcttctgt 60

cgccagcaaa gtatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 665
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 665

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgc tcaacttacg 60

ctgtttcttc agtgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 666
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 666

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgt tgcgtcagcg 60

tactcgcacc ctgtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 667
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 667

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacaa gattcagcgg 60

cgttggcgtc tggttacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 668
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 668

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgttt gccagcaccg 60
cacgtccgat tgagtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 669
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 669

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgcc gtcaatgccc 60
gcaaaccagg tatctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 670
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 670

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcg ttgtaccacc 60
tgctgcatgg tccatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 671
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 671

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcag gcagttgcca 60
gaccttgcca tcaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 672
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 672

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccgct cgtagtcac 60
gcccatatct gcaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 673
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 673

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcactt caccactaaa 60
gcggtcgcag accacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 674

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 674

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtac gccagttta 60
atccaggtct cgtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 675

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 675

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctg cagctcctga 60
cgcaccagtt gcataacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 676

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 676

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtcc tgggccaccg 60
agtcaaagggt agtgaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 677

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 677

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcgc acctgtcctt 60
ctttactgtc cgggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 678

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 678

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcaa gatacgcgatg 60
ccaccgctgc aaacaacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 679
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 679

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg tccgagacaa 60
cgatategcc cactttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 680
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 680

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc cggacagcct 60
ggtaactgac cgtattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 681
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 681

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg cctcagcggc 60
agcgatcagt ttatcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 682
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 682

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg caaccgccga 60
gactgatagt ttgacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 683
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 683

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatc aggctggact 60
gtttagcggc aacagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 684
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 684

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatca catctggctt 60
gcagtgttcc aacagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 685
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 685

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcc agaccaacag 60
aacggttgat gaaagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 686
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 686

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcga agctaagatg 60
agactgttga tcggcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 687
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 687

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctagc catgtgcaag 60
tttctgcacc agtgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 688
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 688

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggag atggcgcgta 60
cgacaacaaa cgggaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 689
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 689

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcaa cctcggttcc 60

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attcagttgg ccggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 690
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 690

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgccatg ggcgattgcc 60

gtcgccttcca tctctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 691
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 691

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcccgc agcgacttta 60

ccgatgcccg atttcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 692
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 692

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcccgt aacaatcagg 60

ccacgtacag cgtaaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 693
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 693

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgcccga atgcccgtgac 60

atcccgcgtc tgataacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 694
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 694

acaaccgct gttacaaggc caggcatccg agaggtctgg gaatgccctc cggagtttgc 60

ggcttcagtt tgatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 695
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 695

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggaa tacgcgcttc 60
atgagcggcg acaattcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 696
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 696

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttt aatggtggcg 60
tccacttccg tcgggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 697
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 697

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctcg cggtacaat 60
tcgcggtatca ccggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 698
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 698

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgg catcttcgct 60
gaagccgtaa gtcgtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 699
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 699

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtg acaatcgcca 60
ccatcggttg cagatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 700
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 700

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttct caaagtgcgc 60

ctggttaggta tccatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 701
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 701

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgctt ctgcgtagat 60

gctggaaacc atcgcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 702
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 702

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctagc ctgcgctgca 60

atgcctcttt cgttagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 703
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 703

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttca ttaactgctg 60

cgtgaccgga tttggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 704
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 704

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcctga taaccttcat 60

tggccagaac ttcggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 705
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 705

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcacca tteactgget 60

ccagcgggaa ttcaccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 706
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 706

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccg gcatggttg 60
aaataaatcg tcgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 707
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 707

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccg gccaatctgc 60
tgataatctt ctacaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 708
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 708

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccg tccacgaatt 60
gtgacacaca gcgaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 709
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 709

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctta tcggcagaaa 60
tcgctctgga acaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 710
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 710

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgg taataccggt 60
gccagcatct cggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 711
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 711

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccga ttaactcagc 60
cagcatttcg gcacgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 712

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 712

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttc gccagccgga 60
tacacttcca gcacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 713

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 713

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacga tgcacactc 60
tcacttgctt cggcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 714

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 714

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtat caacctgcgt 60
cagcacattg gcgaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 715

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 715

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatc acgaggatct 60
gcccgtcagt gacgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 716

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 716

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaat gccataacc 60
gggatcgcca gtgcttcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 717
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 717

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgacc atgttagcac 60

cggcagcgcatt aaccgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 718
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 718

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctggc gaagctatag 60

tcataagcgg tgatggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 719
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 719

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctagg aatgtgaccg 60

ccggtaatc caaaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 720
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 720

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgta cttctgcagt 60

aaggagatgg tggctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 721
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 721

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgga aactgtgttc 60

ttcgccccga taaacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 722
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 722

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagca gtttctaagg 60
ctaattgcatc gctgagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 723
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 723

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctcc acttcagcca 60
tatactgccg cacagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 724
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 724

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacc taagtgacca 60
catacaggaa cggcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 725
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 725

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtca gcatttgtagc 60
ggtttctacc agccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 726
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 726

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag tgtggttaggc 60
gatatcggca acggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 727
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 727

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccata cgccataaac 60

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ggcaggtcag ccagcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 728
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 728

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag cgaatcgccc 60

accagcatga cgtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 729
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 729

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag gcggtacca 60

gaattactgc cgtttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 730
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 730

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgatg tccggetgga 60

ccaggttgaa cagcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 731
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 731

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttg cttccatac 60

gcaggcggcg aatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 732
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 732

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt ttgttagct 60

tctcgcagtc ctctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 733
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 733

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt aagtgtgggt 60
ttcagtaccg ttcgggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 734
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 734

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcgt tgttccgccg 60
tcagataacc gttacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 735
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 735

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacgt tgcaggttac 60
ccatggtagg caccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 736
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 736

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaga ccgtctttgg 60
cgcgcataat tggcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 737
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 737

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggg ctttggttc 60
gtcgaccagc ttcatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 738
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 738

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgcag cagcggcagg 60

gtttcgataa ttaacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 739

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 739

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gtcgaaggc caggaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 740

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 740

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccgc atgagtcact 60

ttcacgcggt ggagttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 741

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 741

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccg gtgcgagctt 60

cttcatctgg catggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 742

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 742

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgccg cgatggcata 60

agtggagaaa cgcttgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 743

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 743

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctcct ggtcaatggc 60

gcaagaacct tcatagcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 744
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 744

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctcaa gcaacctgta 60
ccggaatcgc ttctgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 745
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 745

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagct ggcgatgatg 60
acaatatcgc cgacaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 746
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 746

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccagt gggccgcccg 60
accgttaaca gaaatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 747
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 747

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgaa agcgtcgtga 60
taggtcaggc cgctttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 748
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 748

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcggtt tccgggctga 60
tgccataacc caatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 749
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 749

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcctgc aactgccaga 60
tatcgcggtg taatgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 750

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 750

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcggaa cgccgggttc 60
acgcgcatat cgttatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 751

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 751

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgcg gtgacgggtc 60
ttcatccagc tcgttgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 752

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 752

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgccg tctccagcag 60
tgggtaccag aacatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 753

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 753

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcatac aggctgttga 60
tagtgaaatc gcggcgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 754

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 754

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgttt aagcgattct 60
tcaaacaggc gtgccgcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 755
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 755

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacag cttataggtt 60

tcgtaaccgt agcccgcaatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 756
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 756

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag ttacggaaca 60

gtttgcgcaac ctgctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 757
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 757

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcc cgggttacca 60

atcagacgga taacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 758
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 758

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcat aagccgcacg 60

gaacttagga tgetcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 759
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 759

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcag atccttcatg 60

ccgccaacgt aatcaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 760
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 760

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcggtc gctgacgtta 60
ccttcgtggt gtccaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 761
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 761

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtcg caacttcgat 60
aatctccggg ccaaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 762
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 762

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac ccagccaggc 60
ttcgtatccc gctttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 763
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 763

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctc agcatacgta 60
ccggatcttc acggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 764
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 764

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatg cgcgtttacc 60
ctgacgacgg gacatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 765
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 765

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgct taccggtatt 60

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cttcagcacc tggtcacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 766
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 766

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgtt acgctcaact 60

tcagctcgca aggccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 767
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 767

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgtt gaagtagcgg 60

gtaatggtcg ggaacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 768
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 768

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgg atcagcggtta 60

aacacgccgt caacttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 769
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 769

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcaa caggctgata 60

gcttctgccc agctgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 770
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 770

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccag cacttcgctg 60

taagtcagtt gctcgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 771
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 771

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt tcagcaccac 60
atcggcttca atttcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 772
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 772

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacca atcaccacac 60
caactgaat acccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 773
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 773

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcc tgagccatac 60
gatccagtat gcttgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 774
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 774

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgaa tcggtaat 60
atggtcacga gccagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 775
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 775

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctcgc acagccatt 60
caatggaata gcggaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 776
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 776

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtgc cctgcagagc 60

ttcgccactc aacttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 777

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 777

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag gcaagctgct 60

gagtcggtgg taaagacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 778

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 778

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttac ctgtaccggc 60

ggagaggatc accacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 779

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 779

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac cgactttaac 60

gatcctgtcg cctgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 780

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 780

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccttc gacgatggcg 60

ttgaacggcc catactcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 781

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 781

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttgg cgatagagat 60

cgcccaactg aggttgcatc gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 782
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 782

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacgt aaatcgagct 60
ttacatcccg ccgttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 783
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 783

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccg gcaaccacaga 60
aatgacacaaa ttcattgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 784
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 784

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgcat cacaaaggtc 60
accactgcg ttaaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 785
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 785

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctatt attgaaggca 60
tgggtggcgga gttccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 786
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 786

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctcgc ttaccatta 60
cccggtttac tctccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 787
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 787

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctaac gctaaggatt 60
taccggggtt atcccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 788

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 788

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccag tacaggttca 60
atctggggcc cagcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 789

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 789

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttc acgctaataa 60
gcgcaagaaa cggcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 790

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 790

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccc aacgggatca 60
ggcgataac atattccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 791

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 791

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcctca tctggcaaag 60
gaatgacttt cggctccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 792

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 792

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcgacc aactgcaaac 60
gcacggcatc ccaatccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 793
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 793
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgcc aaatggcgct 60
actgtaatgg tgggtgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 794
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 794
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttaa cagcaccagc 60
agaatcgagc caatgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 795
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 795
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcccc gcatactgac 60
cgtcagcttc atcagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 796
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 796
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcaagt acaccagtg 60
caacgatgaa cgaagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 797
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 797
acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagtt ccgtacctgg 60
tgcaatttgt gcttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 798
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 798

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaccg gatcttcttt 60
atcagggtca aacgcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 799
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 799

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcg aattggctgc 60
tatttcgcca accaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 800
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 800

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt atcagttcgc 60
cgccagagcg ccttaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 801
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 801

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccta ttgagaaacg 60
ctcaacgcga acaccacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 802
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 802

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgaa gtttgcaacc 60
ggacctgcgg caataacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 803
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 803

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgcc gttacgtggt 60

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gcacacagcat gatgttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 804
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 804

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgtt ctggatctgc 60

acaccttctt tcgcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 805
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 805

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccat ctccggttcc 60

atggcattga tgatgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 806
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 806

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgtt ggcaatcgct 60

ttagtcaccc acgggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 807
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 807

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctacg catcagcgca 60

tcttccatcg acaggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 808
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 808

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagg tgctctttcc 60

acagggagtc aagcgtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 809
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 809

acaaccgct gttacaaggc cagcatccg agaggtctgg gaatgccgt caccgagct 60
ctcttcctgc agttctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 810
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 810

acaaccgct gttacaaggc cagcatccg agaggtctgg gaatgccg accagaacga 60
ccgcgcaact ggttatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 811
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 811

acaaccgct gttacaaggc cagcatccg agaggtctgg gaatgcctgc ctgccagcta 60
ccaccgagca caatatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 812
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 812

acaaccgct gttacaaggc cagcatccg agaggtctgg gaatgcacgg gattcgtgac 60
gctcgggtacc gatgatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 813
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 813

acaaccgct gttacaaggc cagcatccg agaggtctgg gaatgccacg ggcaaggatc 60
gttacgtcct actttgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 814
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 814

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctatc ccacatttct 60

tccagcgact gtggtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 815
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 815

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctggg tccacttcgt 60

ccaccagcgc atagtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 816
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 816

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccata ccgccgagta 60

actgaacgtc gaagtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 817
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 817

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctatg gagatagtac 60

ccaccagcac cggctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 818
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 818

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttca acgactccag 60

catcgctgca aacatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 819
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 819

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttat acatttccga 60

gctgtcttct gccgggcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 820
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 820

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgctgca cgcctttacc 60
ggttagtgcg ttcaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 821
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 821

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcctgt tgttccagct 60
cctcaacctc ttcaggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 822
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 822

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttgt cgcgcaggta 60
gtcaaagccg tattcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 823
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 823

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacag acggaagtag 60
ttctggaagg tgategcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 824
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 824

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttat ccagccactc 60
ggcaattggc aaatcgcatc gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 825
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 825

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctacg ctgtacacgt 60
tcttcagggc tgaacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 826

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 826

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgct tcgttggcgt 60
ggaatttggc gttcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 827

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 827

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatg cccggcaggt 60
tgataccgac agtcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 828

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 828

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgct tcagtcatgt 60
agaccaggtc cggcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 829

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 829

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttca tccatgatgc 60
cctctttcac cagcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 830

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 830

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacg atgtagtcca 60
cgtcacgggt aaacagcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 831
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 831

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgag aagtggcctt 60
gcgccctggaa gggttccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 832
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 832

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccac gaccgcctt 60
attggtcgcg atagtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 833
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 833

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaggt ggataccctg 60
acgcagatag tccatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 834
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 834

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcag ttgcttacga 60
atgtcgaagt tacggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 835
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 835

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttta cgctgatata 60
cttcgatgga ctgcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 836
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 836

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacag ttcgttacgc 60
tgggagtaaa tggcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 837
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 837

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctt cgcttgctt 60
catacccagt ttacgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 838
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 838

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgta ccgtaagtga 60
tgtcagctgc gtaagccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 839
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 839

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctg cttocagtac 60
cgcatcgtga cgtaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 840
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 840

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatac cggcttttgg 60
cagttcgctt gacaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 841
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 841

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgctg ttaatggttt 60

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cgctcacatc gctgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 842
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 842

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacga atcattggac 60

ggttggtcgg aacaaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 843
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 843

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtac gcatttggc 60

gatgcagcgt tcgttacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 844
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 844

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctacc aaagacgcgc 60

ttacttgct cagctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 845
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 845

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgca tttgcgctaa 60

acgctcggct tccatacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 846
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 846

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcat gacgcctttc 60

tcgaagtgac gcacacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 847
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 847

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccacg ttgcgccagg 60
tagtcggtga cggtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 848
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 848

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccggc tgcagagtcg 60
tcacctgat ggctaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 849
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 849

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctg catggtacga 60
cgggtgtggt cgtaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 850
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 850

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacca tcctaataa 60
gagatgcggc cagaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 851
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 851

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccagc gcgctgagcg 60
tatccagtaa tgcaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 852
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 852

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acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg cttocagcaa 60

ggccaattga ccaaagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 853
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 853

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg tgctgagcgc 60

aggcaaacct aaactccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 854
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 854

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaatc aacggaatag 60

ttcgaattcg ggcggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 855
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 855

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg ctgaagagggc 60

aaagattctt cagcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 856
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 856

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccag aatagtgacg 60

ctggcacctc gtggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 857
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 857

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttcg agaaatcagc 60

ccgcaggtag agacttcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 858
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 858

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgccgct gtcggttaag 60
tcttcgggtt tgggtgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 859
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 859

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcttct ttccacagcg 60
cagcggtaat ttctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 860
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 860

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcgctg gcatattgcg 60
cccgtataaa atctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 861
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 861

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcagac gttcacatcc 60
accatgtcat acagcgcat gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 862
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 862

acaaccgcgt gttacaaggc cagggatccg agaggtctgg gaatgcacag gtttctgaca 60
ggatttcggt cagacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 863
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 863

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgc gcggaaggta 60
cataaaccgc cttcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 864

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 864

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatca agatgggcaa 60
cgaccgtttc tggcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 865

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 865

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgtcg atgagtttcg 60
ggtcaaccgg ttcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 866

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 866

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcataa gcaatataac 60
cgtcgcgctc ttcggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 867

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 867

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctca agctggtgga 60
tcaggttaatt cagcgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 868

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 868

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgc gcacgcgata 60
atcaatggtt acgatacatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 869
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 869

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcca acgtcgctga 60
agtaatggct gagtttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 870
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 870

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccgga tcgtcgtagc 60
taccggcggt atggttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 871
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 871

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctaga taaactcgtc 60
gcgctcggtg gtttgctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 872
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 872

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgggc cagtagcgga 60
acatgggtca tcatttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 873
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 873

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgccg ccgataatca 60
gcacatgttt cgctgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 874
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 874

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccga taggatcgg 60
gcagtcggag ataatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 875
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 875

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccg cctgaataat 60
ttcggttgag agatggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 876
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 876

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgccg tatggattgc 60
cggattgtaa taacggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 877
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 877

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgata ctgacggcag 60
aacgatacga caccgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 878
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 878

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccatc cagcgcatt 60
acgcgaccaa atgcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 879
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 879

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaacg aaattgacgc 60

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catcgtcgat caccagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 880
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 880

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatct accgcaaagt 60

actgcccaaa ctggtccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 881
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 881

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgca tgataccgcc 60

gtaataggtc gggatccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 882
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 882

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgca gacgaagata 60

ccgccaggat tcaggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 883
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 883

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcaagc cagtgcgtct 60

tgcagatact gaggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 884
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 884

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaat gccgctgaga 60

tcgcggtagc tgttctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 885
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 885

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc cgttaaatcg 60
gccatatctt cggcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 886
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 886

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccaga cggccatcag 60
gctgccaat aacctcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 887
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 887

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttga cgtaggcaag 60
caggcttaag gaatgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 888
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 888

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctgtc gaaggtgctc 60
taattactga ggtccccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 889
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 889

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccag tgcgcgacga 60
attgcccgt taggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 890
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 890

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acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccga ctggcgaatt 60

aatccagca ccatggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 891
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 891

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctcac tgacattacg 60

gaagaaatgc agcgcgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 892
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 892

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttag caacaggcca 60

gttcgaaatc cagacgcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 893
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 893

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttgc ggataaagct 60

gtgaatcgag cgacagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 894
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 894

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcacgc caatccaggt 60

ctggagtta cgttgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 895
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 895

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcttaa tgettcaata 60

cggtctctgg ccacgccatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 896
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 896

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctgta ggtaaatcaa 60
agctgcaaca gccgccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 897
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 897

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctgca agttctttca 60
acagctcagt gccgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 898
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 898

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctgaa ttgcccgata 60
cgcgcgccgg aaattacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 899
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 899

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctgct gttcaggctg 60
gcaatccagg tttctacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 900
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 900

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctctc agtcgctgac 60
gcaccagagc aatcaacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 901
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 901

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgccccg caggttgggc 60

aattcaccgt aatagtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 902

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 902

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgctcac tgctttggtt 60

cttcgctcca gtcacccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 903

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 903

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tctccgaggt cgatcacatt gcgcttctcc ggaaacatta gc 102

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<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 904

acaaccgcgt gttacaaggc caggcacccg agaggtctgg gaatgcccct aacgcccgat 60

agcgacaggc tttcttcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 905

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 905

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ccgtccatcc acagggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 906

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 906

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acttcatcaa gcaaggcatt gcgcttctcc ggaaacatta gc 102

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<210> SEQ ID NO 907
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 907

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcccg tgcaggacc 60
gttcgctacc tttcagcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 908
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 908

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttca tcgccagcga 60
attccagttg attggccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 909
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 909

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctact tctgctgcac 60
gaaattgcgg taagcccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 910
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 910

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcttca cctcttcatt 60
aaaccagtgc ccgaccatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 911
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 911

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatgg acatacgcac 60
ctttaccact ccggtacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 912
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 912

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcagtc gatactgata 60
gccatcgagc ttcggtcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 913
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 913

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgag cacttcaact 60
tccagcgtcg cggatcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 914
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 914

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcat tctgcttct 60
tccaggtagt gtgtggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 915
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 915

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacca gtgaaacaaa 60
cagctcttcc agacggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 916
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 916

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcctgc ctgattcacc 60
acaatttgct gcacggcatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 917
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 917

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcatcc cgccagataa 60

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catacgcgca cgttcgcat ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 918
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 918

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgccctg cggcaccagt 60

cccaactgac gtttagcatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 919
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 919

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgcat taacgcacgg 60

gcaatcatta aacggccatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 920
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 920

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcacat tgagcggcga 60

agttcaatat ccacgccatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 921
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 921

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgctctc gagatcgtaa 60

ccaaatacgc tgacccatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 922
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 922

acaaccgcgt gttacaaggc caggcatccg agaggtctgg gaatgcgatg tacgcttctt 60

tgcgctccac gccgtacatt ggccttctcc ggaaacatta gc 102

<210> SEQ ID NO 923
<211> LENGTH: 102

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 923

acaaccgcgt gttacaagc caggcatccg agaggtctgg gaatgccggt gcgagatcga 60
gaataaaggt ttccgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 924
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 924

acaaccgcgt gttacaagc caggcatccg agaggtctgg gaatgccac cagctcaccg 60
tgttgaataa tgccgacatt gcgcttctcc ggaaacatta gc 102

<210> SEQ ID NO 925
<211> LENGTH: 102
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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1-72. (canceled)

73. A method, comprising:

simultaneously amplifying at least some of a plurality of oligonucleotides in a common solution using PCR to produce amplified oligonucleotides;

transcribing in vitro at least some of the amplified oligonucleotides to produce RNA;

reverse transcribing the RNA to produce transcribed DNA; and

selectively degrading the RNA relative to the transcribed DNA.

74. The method of claim **73**, wherein the plurality of oligonucleotides have an average length of between 10 and 200 nucleotides.

75. The method of claim **73**, wherein the plurality of oligonucleotides includes at least 10 unique oligonucleotide sequences.

76-79. (canceled)

80. The method of claim **73**, wherein amplifying at least some of the plurality of oligonucleotides comprises exposing at least some of the plurality of oligonucleotides to primer-containing sequences.

81. (canceled)

82. The method of claim **80**, wherein at least some of the amplified oligonucleotides contain a promoter.

83-85. (canceled)

86. The method of claim **73**, wherein at least some of the plurality of oligonucleotides comprise at least a first set of oligonucleotides having a first common index region, and a

second set of oligonucleotides having a second common index region distinguishable from the first common index region.

87. The method of claim **86**, comprising amplifying the first set of oligonucleotides but not the second set of oligonucleotides.

88. The method of claim **86**, wherein the plurality of oligonucleotides comprises at least 2 sets of oligonucleotides having distinguishable common index regions.

89-95. (canceled)

96. The method of claim **73**, wherein transcribing at least some of the amplified oligonucleotides comprises a mass of RNA that is at least 100-fold greater than the mass of amplified oligonucleotides.

97. The method of claim **73**, wherein transcribing at least some of the amplified oligonucleotides comprises exposing the amplified oligonucleotides to an RNA polymerase.

98-102. (canceled)

103. The method of claim **73**, wherein transcribing at least some of amplified oligonucleotides to produce RNA comprises producing, on average, at least 10 RNA copies of each of the amplified oligonucleotides.

104-106. (canceled)

107. The method of claim **73**, wherein reverse transcribing the RNA comprises exposing the RNA to a reverse transcriptase.

108. (canceled)

109. The method of claim **73**, wherein reverse transcribing the RNA to produce transcribed DNA occurs without first purifying the RNA from components used to produce the RNA.

110. The method of claim **73**, further comprising purifying the RNA from components used to produce the RNA prior to reverse transcribing the RNA to produce transcribed DNA.

111. The method of claim **73**, wherein reverse transcribing the RNA to produce transcribed DNA comprises reverse transcribing the RNA to produce transcribed DNA using a sequence containing a transcription primer.

112. The method of claim **111**, wherein the sequence containing a transcription primer is incorporated into the transcribed DNA.

113-122. (canceled)

123. The method of claim **73**, wherein selectively degrading the RNA relative to the transcribed DNA comprises chemically reducing the RNA.

124-126. (canceled)

127. The method of claim **73**, wherein the transcribed DNA is substantially single-stranded.

128-140. (canceled)

141. The method of any one of claim **73**, wherein each oligonucleotide of a subset of the oligonucleotides comprises an index portion that is identical.

142. (canceled)

143. The method of claim **73**, wherein the plurality of oligonucleotides has a distribution of lengths such that no more than 10% of the oligonucleotides has a length that is less than 80% or greater than 120% of the overall average length of the plurality of nucleotides.

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