What is Claimed:

1. A method of synthesizing a DNA molecule having a desired sequence comprising:

a) annealing at least two oligonucleotides to an anchor strand so that the at least two oligonucleotides annealed to the anchor strand abut one another on the anchor strand;

wherein the at least two oligonucleotides each comprise a universal primer binding site on a 3' or 5' end, and a variable sequence on the opposing 5' or 3' end, and a conserved flanking sequence in between the universal primer binding site and the variable sequence; and

wherein the anchor strand comprises conserved flanking sequences complementary to those on the at least two oligonucleotides, and further comprises at least one variable sequence, wherein at least a portion of the at least one variable sequence on the anchor strand is complementary to at least a portion of the variable sequences on the at least two oligonucleotides;

b) ligating the at least two oligonucleotides annealed to the anchor strand to produce a first dsDNA molecule;

c) performing an amplification step on the first dsDNA molecule having a desired sequence and comprising, a conserved flanking sequence inside each of the 3' and 5' ends, and a variable sequence inside the conserved flanking sequences;

d) contacting the first dsDNA molecule with a restriction endonuclease to produce first dsDNA fragments comprising 3' and/or 5' overhang sequences comprising a portion of the variable sequence from the first dsDNA molecule.

2. The method of claim 1 further comprising providing at least one additional dsDNA fragment comprising a 3' and/or 5' overhang sequence that is at least partially complementary to an overhang sequence of at least one of the first dsDNA fragments;

annealing the first dsDNA fragments and at least one additional dsDNA fragment by the 3' and/or 5' overhang sequences; and

ligating the annealed dsDNA fragments to produce a second dsDNA molecule comprising a conserved flanking sequence inside each of the 3' and 5' ends, and a variable sequence inside

the 3’ and 5’ conserved flanking sequences that is longer than the variable sequence on the first dsDNA molecule; and

optionally wherein the at least one additional dsDNA fragment is the product of a parallel DNA synthesis reaction.

3. The method of claim 2 further comprising contacting the at least one second dsDNA molecule with a restriction endonuclease to produce a plurality of second dsDNA fragments comprising 3’ and/or 5’ overhang sequences and a conserved flanking sequence inside each of the 3’ or 5’ ends;

providing at least one additional dsDNA fragment comprising a 3’ and/or 5’ overhang sequence that is at least partially complementary to an overhang sequence of at least one of the second dsDNA fragments;

annealing the plurality of second dsDNA fragments to the one or more additional dsDNA fragment(s) by the 3’ and/or 5’ overhang sequence(s); and

performing a step of ligation to produce a third dsDNA molecule comprising a conserved flanking sequence on the 3’ and 5’ ends, and a variable sequence inside the conserved flanking sequences that is longer than the variable sequence of the second dsDNA molecule;

optionally wherein the at least one additional dsDNA fragment is the product of a parallel DNA synthesis reaction.

4. The method of claim 3 further comprising reacting the at least one third dsDNA molecule with a restriction endonuclease to produce a plurality of third dsDNA fragments comprising 3’ and/or 5’ overhang sequences and a conserved flanking sequence inside each of the 3’ or 5’ ends;

providing at least one additional dsDNA fragment comprising a 3’ and/or 5’ overhang sequence that is at least partially complementary to an overhang sequence of at least one of the third dsDNA fragments;

annealing the plurality of third dsDNA fragments to the one or more additional dsDNA fragment(s) by the 3’ and/or 5’ overhang sequence(s); and

performing a step of ligation to produce a fourth dsDNA molecule comprising a conserved flanking sequence on the 3’ and 5’ ends, and a variable sequence inside the conserved flanking sequences that is longer than the variable sequence of the third dsDNA molecule;

optionally wherein the at least one additional dsDNA fragment is the product of a parallel DNA synthesis reaction.

5. The method of claim 1 wherein step a) further comprises

annealing at least two paired oligonucleotides to a paired anchor strand so that the at least two paired oligonucleotides bound to the paired anchor strand abut one another on the paired anchor strand, wherein the at least two paired oligonucleotides comprise a universal primer binding site on a 3’ or 5’ end, and a variable sequence on the opposing 5’ or 3’ end, and a conserved flanking sequence in between the universal primer binding site and the variable sequence;

and wherein the paired anchor strand comprises conserved flanking sequences complementary to those on the at least two paired oligonucleotides, and further comprises at least one variable sequence, and wherein a portion of the variable sequence on the paired anchor strand overlaps with a portion of the variable sequence on the first anchor strand,

d) ligating the at least two paired oligonucleotides annealed to the anchor strand;

e) performing an amplification step to produce a paired dsDNA molecule of desired sequence and comprising a universal primer binding site at a 3’ and 5’ end, a conserved flanking sequence inside each of the 3’ and 5’ ends, and a variable sequence inside the conserved flanking sequences that partially overlaps with the variable sequence of the first dsDNA molecule.

6. The method of claim 5 further comprising contacting the first dsDNA molecule and the paired dsDNA molecule with a restriction endonuclease to produce at least one dsDNA fragment and at least one paired dsDNA fragment, each comprising at least one 3’ and/or 5’ overhang sequence; and wherein at least a portion of a 3’ or 5’ overhang sequence from the first dsDNA fragment is complementary to at least a portion of a 5’ or 3’ overhang sequence from the paired dsDNA fragment,

annealing the at least one first and paired dsDNA fragments by their complementary overhang sequences and performing a step of ligation to produce a second dsDNA molecule comprising a conserved flanking sequence inside each of the 3’ and 5’ ends, and a variable sequence inside the 3’ and 5’ conserved flanking sequences that is longer than the variable sequence on the respective first dsDNA molecules.

7. The method of claim 6 further comprising contacting the at least one second dsDNA molecule and an at least one paired second dsDNA molecule with a restriction endonuclease to produce a plurality of second dsDNA fragments and paired second dsDNA fragments, each comprising a 3’ and/or 5’ overhang sequence(s), wherein at least two of the plurality comprise, a conserved flanking sequence inside each of the 3’ or 5’ ends; and wherein at least a portion of the 3’ or 5’ overhang sequence from a second dsDNA fragment is complementary to at least a portion of the 5’ or 3’ overhang sequence from a paired second dsDNA fragment,

annealing the second and paired second dsDNA fragments by their complementary overhang sequences; and

performing a step of ligation to produce a third dsDNA molecule comprising a conserved flanking sequence inside each of the 3’ and 5’ ends, and a variable sequence inside the 3’ and 5’ conserved flanking sequences that is longer than the variable sequence on the second dsDNA molecules.

8. The method of claim 7 further comprising contacting the at least one third dsDNA molecule and an at least one paired third dsDNA molecule with a restriction endonuclease to produce a plurality of third dsDNA fragments and paired third dsDNA fragments, each comprising a 3’ and/or 5’ overhang sequence(s), wherein at least two of the plurality comprise, a conserved flanking sequence inside each of the 3’ or 5’ ends; and wherein at least a portion of the 3’ or 5’ overhang sequence from a third dsDNA fragment is complementary to at least a portion of the 5’ or 3’ overhang sequence from a paired third dsDNA fragment,

annealing the third and paired third dsDNA fragments by their complementary overhang sequences; and performing a step of ligation to produce a fourth dsDNA molecule comprising a conserved flanking sequence inside each of the 3’ and 5’ ends, and a variable sequence inside the

3’ and 5’ conserved flanking sequences that is longer than the variable sequence on the third dsDNA molecule.

9. The method of any one of claims 1-8 wherein the first dsDNA molecule comprises a variable sequence of 8-12 base pairs; or wherein the paired dsDNA molecule comprises a variable sequence of 8-12 base pairs; or

the method of any one of claims 2-4 or 6-8 wherein the second dsDNA molecule comprises a variable sequence of 14-18 base pairs; or

the method of any one of claims 3-4 or 7-8 wherein the third dsDNA molecule comprises a variable sequence of 24-32 base pairs; or

the method of claim 8 wherein the fourth dsDNA molecule comprises a variable sequence of 90-110 base pairs; or

the method of any one of claims 1-8 wherein the at least two oligonucleotides have a variable sequence of 4-6 nucleotides.

10. The method of any one of claims 1-9 wherein the anchor strands comprise the sequences complementary to the conserved flanking sequences on the at least two oligonucleotides on the 3’ and 5’ ends.

11. The method of any one of claims 1-10 wherein the amplification step is performed by the polymerase chain reaction (PCR).

12. The method of any one of claims 1-12 wherein the variable sequence is equal to the lengths of the variable sequences on the at least two oligonucleotides; or

wherein the anchor strand comprises a variable sequence present in between the two sequences complementary to the conserved flanking sequences on the at least two oligonucleotides; or

wherein the at least two oligonucleotides bound to the anchor strand abut one another on the anchor strand at their variable sequences; or

wherein the portion of the variable sequence on the anchor strand that is complementary to the conserved flanking sequence on the at least two oligonucleotides comprises 2-6 nucleotides; or

13. The method of any one of claims 1-12 wherein the at least two oligonucleotides and anchor strand further comprise a recognition site for a restriction endonuclease, optionally wherein the restriction endonuclease is a Type IIS endonuclease.

14. The method of any one of claims 2-4 wherein the at least one additional dsDNA fragment is from a parallel synthesis reaction.

15. The method of any one of claims 1-14 wherein the anchor strands comprise 4-6 degenerate nucleotides.

16. The method of claim 15 wherein the degenerate nucleotides comprise a universal or randomized base.

17. A composition comprising at least two oligonucleotides, each comprising a universal primer binding site on a 3' or 5' end, and a variable sequence on the opposing 5' or 3' end, and a conserved flanking sequence in between the universal primer binding site and the variable sequence; and

wherein an anchor strand comprising sequences complementary to the conserved flanking sequences on the at least two oligonucleotides, and further comprising at least one variable sequence, wherein at least a portion of the at least one variable sequence on the anchor strand is complementary to at least a portion of the variable sequences on the at least two oligonucleotides.

18. The composition of claim 17 wherein the anchor strand comprises sequences complementary to the conserved flanking sequences on the at least two oligonucleotides at its 3' and 5' ends.

19. The composition of any one of claims 17-18 wherein the anchor strand comprises the variable sequence in between the two sequences complementary to the conserved flanking sequence.

20. A method of storing data in a DNA sequence comprising:

determining a sequence of DNA that encodes a non-genetic message according to a coding scheme that translates the non-genetic message from a reference language into a DNA sequence and vice versa;

synthesizing the sequence of DNA that encodes the non-genetic message according to the method of any one of claims 1-16; and

thereby store data in a DNA sequence.

21. A method of synthesizing a DNA sequence encoding a guide RNA comprising:

determining a sequence of DNA that encodes a guide RNA;

synthesizing the sequence of DNA that encodes the guide RNA according to any one of claims 1-16.