CLAIMS:

1. A composition comprising:

a first engineered Class 1 Type I CRISPR-Cas effector complex comprising,

a first Cas5 subunit protein and a first Cas7 subunit protein,

a first fusion protein comprising a first Cas8 subunit protein and a first FokI, wherein the N-terminus of the first Cas8 subunit protein or the C-terminus of the first Cas8 subunit protein is covalently connected by a first linker polypeptide to the C-terminus or N-terminus of the first FokI, and wherein the first linker polypeptide has a length of between 17 amino acids and 20 amino acids, and

a first guide polynucleotide comprising a first spacer capable of binding a first nucleic acid target sequence; and

a second engineered Class 1 Type I CRISPR-Cas effector complex comprising,

a second Cas5 subunit protein and a second Cas7 subunit protein,

a second fusion protein comprising a second Cas8 subunit protein and a second FokI, wherein the N-terminus of the second Cas8 subunit protein or the C-terminus of the second Cas8 subunit protein is covalently connected by a second linker polypeptide to the C-terminus or N-terminus, respectively, of the second FokI, and wherein the second linker polypeptide has a length of between 17 amino acids and 20 amino acids, and

a second guide polynucleotide comprising a second spacer capable of binding a second nucleic acid target sequence, wherein a protospacer adjacent motif (PAM) of the second nucleic acid target sequence and a PAM of the first nucleic acid target sequence have an interspacer distance between 29 base pairs and 34 base pairs.

2. The composition of claim 1, wherein the first linker polypeptide and the second linker polypeptide are of the same length.

3. The composition of any one of the preceding claims, wherein the first FokI and the second FokI are monomeric subunits capable of associating to form a homodimer.

4. The composition of claim 1 or claim 2, wherein the first FokI and the second FokI are distinct monomeric subunits capable of associating to form a heterodimer.

5. The composition of any one of the preceding claims, wherein the N-terminus of the first Cas8 subunit protein is covalently connected by the first linker polypeptide to the C-terminus of the first FokI, and/or the C-terminus of the first Cas8 subunit protein is covalently connected by a first linker polypeptide to the N-terminus of the first FokI.

6. The composition of any one of the preceding claims, wherein the N-terminus of the second Cas8 subunit protein is covalently connected by the second linker polypeptide to the C-terminus of the second FokI, and/or the C-terminus of the second Cas8 subunit protein is covalently connected by a second linker polypeptide to the N-terminus of the second FokI.

7. The composition of any one of the preceding claims, wherein the first Cas8 subunit protein and the second Cas8 subunit protein each comprise identical amino acid sequences.

8. The composition of any one of the preceding claims, wherein the first Cse2 subunit protein and the second Cse2 subunit protein each comprises identical amino acid sequences, the first Cas5 subunit protein and the second Cas5 subunit protein each comprises identical amino acid sequences, the first Cas6 subunit protein and the second Cas6 subunit protein each comprises identical amino acid sequences, and the first Cas7 subunit protein and the second Cas7 subunit protein each comprises identical amino acid sequences.

9. The composition of any one of the preceding claims, wherein the first guide polynucleotide comprises RNA, and/or the second guide polynucleotide comprises RNA.

10. The composition of any one of the preceding claims, wherein genomic DNA comprises the PAM of the second nucleic acid target sequence and the PAM of the first nucleic acid target sequence.

11. The composition of any one of the preceding claims, wherein the first engineered Class 1 Type I CRISPR-Cas effector complex is based on Type I CRISPR-Cas effector complexes of one or more organisms selected from the group consisting of *Salmonella enterica*, *Geothermobacter sp*. (strain EPR-M), *Methanocella arvoryzae* MRE50, *Streptococcus thermophilus*, *Pseudomonas sp*. S-6-2, and *Escherichia coli*.

12. The composition of any one of the preceding claims, wherein the second engineered Class 1 Type I CRISPR-Cas effector complex is based on Type I CRISPR-Cas effector complexes of one or more organisms selected from the group consisting of *Salmonella enterica*, *Geothermobacter sp*. (strain EPR-M), *Methanocella arvoryzae* MRE50, *Streptococcus thermophilus*, *Pseudomonas sp*. S-6-2, and *Escherichia coli*.

13. A host cell comprising: the composition of any one of the preceding claims.

14. The host cell of claim 13, wherein the cell is a eukaryotic cell.

15. One or more nucleic acid sequences encoding the first Cse2 subunit protein, the first Cas5 subunit protein, the first Cas6 subunit protein, the first Cas7 subunit protein, the first fusion protein, and the first guide polynucleotide of any one of claims 1 to 12; and/or one or more nucleic acid sequences encoding the second Cse2 subunit protein, the second Cas5 subunit protein, the second Cas6 subunit protein, the second Cas7 subunit protein, the second fusion protein, and the second guide polynucleotide of any one of claims 1 to 12.

16. A method of cutting a polynucleotide comprising a first nucleic acid target sequence and a second nucleic acid target sequence in a host cell or a biochemical reaction, the method comprising:

introducing the composition any one of claims 1 to 12 into a host cell or a

biochemical reaction, thereby facilitating contact of the first engineered Class 1 Type I CRISPR-Cas effector complex with the first nucleic acid target sequence and contact of the engineered second Class 1 Type I CRISPR-Cas effector complex with the second nucleic acid target sequence, resulting in cutting of the first nucleic acid target sequence by the first engineered Class 1 Type I CRISPR-Cas effector complex and cutting of the second nucleic acid target sequence by the second engineered Class 1 Type I CRISPR-Cas effector complex;

optionally wherein the method is in the host cell and the host cell is a human cell outside of a human body.

17. The method of claim 16, wherein the host cell further comprises a donor polynucleotide and at least a portion of the donor polynucleotide is integrated in the dsDNA.