CLAIMS

1. A composition comprising:

CRISPR complex components comprising:

I. CRISPR-Cas system polynucleotide sequence(s) which comprise(s):

(a) an engineered guide sequence comprised of RNA and capable of hybridizing to a target sequence in a polynucleotide locus,

(b) a tracr mate sequence comprised of RNA, and

(c) a tracrRNA sequence comprised of RNA, and

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

II. a Type II Cas9 protein,

in which the tracr mate sequence hybridizes to the tracrRNA sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to a target sequence,

in which the CRISPR complex comprises the Type II Cas9 protein complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracrRNA sequence, and

in which the Type II Cas9 protein is or comprises a *Staphylococcus aureus* Cas9 (SaCas9).

2. A composition according to Claim 1, in which the CRISPR-Cas system polynucleotide sequence is a chimeric RNA (chiRNA).

3. A composition according to Claim 2, comprising a pair of chiRNAs.

4. A composition according to Claim 3, comprising two pairs of chiRNAs.

5. A composition according to any preceding claim, comprising a vector system comprising one or more vectors, and in which polynucleotide sequences comprising or encoding said components I and II are located on the same or different vectors of the system.

6. A composition according to Claim 5, in which the one or more vectors comprise one or more viral vectors.

7. A composition according to Claim 6, in which the one or more viral vectors comprise one or more retrovirus, lentivirus, adenovirus, adeno-associated virus or herpes simplex virus vectors.

8. A composition according to any of Claims 1 to 4, comprising a nanoparticle, liposome, exosome, yeast system or microvesicle.

9. A composition according to any preceding claim, including one or more functional domains.

10. A composition according to Claim 9, in which the one or more functional domain comprises a transcriptional activator domain.

11. A composition according to Claim 9, in which the functional domain comprises VP64 or KRAB, SID or SID4X, or a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome, a light inducible/controllable domain or a chemically inducible/controllable domain.

12. A composition according to any of Claims 5 to 11, in which the vector composition comprises a single vector.

13. A composition according to any of Claims 5 to 12, in which the cell is a eukaryotic cell.

14. A composition according to any of Claims 5 to 13, in which the polynucleotide sequence encoding the Type II Cas9 protein is codon optimized for expression in a eukaryotic cell.

15. A composition according to any of Claims 5 to 14, in which the polynucleotide sequences comprising or encoding said CRISPR complex components comprises a tissue-specific promoter.

16. A composition according to Claim 15, in which the tissue-specific promoter directs expression of said CRISPR complex components in muscle, neuron, bone, skin, blood, liver, pancreas, or lymphocytes.

17. A composition according to any preceding claim, in which the guide sequence is capable of hybridizing to a target sequence in a eukaryotic cell.

18. A composition according to any preceding claim, in which the tracrRNA sequence is 30 or more nucleotides in length.

19. A composition according to Claim 18, in which the tracrRNA is 50 or more nucleotides in length.

20. A composition according to any preceding claim, in which the Type II Cas9 protein further comprises one or more nuclear localization sequences (NLSs).

21. An *ex vivo* or *in vitro* host cell or cell line comprising the composition according to any preceding claim, or progeny thereof, in which the host cell or cell line is not a human germ line cell.

22. An *ex vivo* or *in vitro* host cell, cell line or progeny thereof according to Claim 21, which is a stem cell or stem cell line.

23. A method of modifying an organism by manipulation of one or more target sequences at genomic loci of interest comprising delivering to the organism a composition according to any of Claims 1 to 20, in which the organism is a non-animal organism.

24. An *ex vivo* method of modifying a cell of an organism by manipulation of one or more target sequences at genomic loci of interest comprising delivering to the cell a composition according to any of Claims 1 to 20, in which the method does not comprise a process for modifying the germ line genetic identity of a human being.

25. A method according to Claim 23 or 24, in which the organism is a plant or algae.

26. Use of a composition according to any of Claims 1 to 20 in *ex vivo* gene or genome editing, in which the use does not comprise a process for modifying the germ line genetic identity of a human being.