WHAT IS CLAIMED IS:

1. A method for modifying the genetic material of a cell, comprising:

(a) providing a cell containing a target DNA sequence; and

(b) introducing a transcription activator-like (TAL) effector -DNA modifying enzyme into the cell, the TAL effector-DNA modifying enzyme comprising:

(i) a DNA modifying enzyme domain that can modify double stranded DNA, and

(ii) a TAL effector domain comprising a plurality of TAL effector repeat sequences that, in combination, bind to a specific nucleotide sequence in the target DNA sequence,

such that the TAL effector-DNA modifying enzyme modifies the target DNA within or adjacent to the specific nucleotide sequence in the cell or progeny thereof.

2. The method of claim 1, further comprising providing to the cell a nucleic acid comprising a sequence homologous to at least a portion of the target DNA sequence, such that homologous recombination occurs between the target DNA sequence and the nucleic acid.

3. The method of claim 1, wherein the cell is a eukaryotic cell.

4. The method of claim 1, wherein the cell is a mammalian cell.

5. The method of claim 1, wherein the cell is a plant cell.

6. The method of claim 1, wherein the cell is a prokaryotic cell.

7. The method of claim 1, wherein the target DNA is chromosomal DNA.

8. The method of claim 1, wherein the introducing comprises transfecting the cell with a vector encoding the TAL effector-DNA modifying enzyme.

9. The method of claim 1, wherein the introducing comprises mechanically injecting the TAL effector-DNA modifying enzyme into the cell as a protein.

10. The method of claim 1, wherein the introducing comprises delivering the TAL effector-DNA modifying enzyme into the cell as a protein by means of the bacterial type III secretion system.

11. The method of claim 1, wherein the introducing comprises introducing the TAL effector-DNA modifying enzyme into the cell as a protein by electroporation.

12. The method of claim 1, wherein the DNA modifying enzyme domain is an endonuclease.

13. The method of claim 12, wherein the endonuclease is a type II restriction endonuclease.

14. The method of claim 13, wherein the type II restriction endonuclease is *Fok*I.

15. The method of claim 1, wherein the TAL effector domain that binds to a specific nucleotide sequence within the target DNA comprises 10 or more DNA binding repeats, more preferably 15 or more DNA binding repeats.

16. The method of claim 15, wherein each DNA binding repeat comprises a repeat variable-diresidue (RVD) that determines recognition of a base pair in the target DNA sequence, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA sequence, and wherein the RVD comprises one or more of:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T, wherein * represents a gap in the second position of the RVD;

HG for recognizing T;

H* for recognizing T, wherein * represents a gap in the second position of the RVD;

IG for recognizing T;

NK for recognizing G;

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A; and

YG for recognizing T.

17. The method of claim 16, wherein each DNA binding repeat comprises a RVD that determines recognition of a base pair in the target DNA sequence, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA sequence, and wherein the RVD comprises one or more of:

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A;

YG for recognizing T; and

NK for recognizing G,

and one or more of:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T, wherein * represents a gap in the second position of the RVD;

HG for recognizing T;

H* for recognizing T, wherein * represents a gap in the second position of the

RVD; and

IG for recognizing T.

18. A method for generating a nucleic acid encoding a TAL effector specific for a selected nucleotide sequence, comprising:

(1) linearizing a starter plasmid with *Psp*XI, the starter plasmid comprising a nucleotide sequence that encodes a first TAL effector DNA binding repeat domain having a repeat variable-diresidue (RVD) specific for the first nucleotide of the selected nucleotide sequence, wherein the first TAL effector DNA binding repeat domain has a unique *Psp*XI site at its 3' end;

(2) ligating into the starter plasmid *Psp*XI site a DNA module encoding one or more TAL effector DNA binding repeat domains that have RVDs specific for the next nucleotide(s) of the selected nucleotide sequence, wherein the DNA module has *Xho*I sticky ends; and

(3) repeating steps (1) and (2) until the nucleic acid encodes a TAL effector capable of binding to the selected nucleotide sequence.

19. The method of claim 18, further comprising, after the ligating, determining the orientation of the DNA module in the *Psp*XI site.

20. The method of claim 18, comprising repeating steps (1) and (2) from one to 30 times.

21. A method for generating a nucleic acid encoding a transcription activator-like effector endonuclease (TALEN), comprising:

(a) identifying a first unique nucleotide sequence in the genome of a cell; and

(b) synthesizing a nucleic acid encoding a TALEN that comprises (i) a plurality of DNA binding repeats that, in combination, bind to the first unique nucleotide sequence, and (ii) an endonuclease that generates a double-stranded break at a second nucleotide sequence within or adjacent to the first nucleotide sequence, wherein each DNA binding repeat comprises a RVD that determines recognition of a base pair in the target DNA, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA, and wherein the TALEN comprises one or more of the following RVDs:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T;

HG for recognizing T;

H* for recognizing T;

IG for recognizing T;

NK for recognizing G;

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A; and

YG for recognizing T.

22. The method of claim 21, wherein the TALEN comprises one or more of the following RVDs:

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A;

YG for recognizing T;and

NK for recognizing G,

and one or more of:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T;

HG for recognizing T;

H* for recognizing T; and

IG for recognizing T.

23. The method of claim 21, wherein the first nucleotide sequence meets at least one of the following criteria:

i) is a minimum of 15 bases long and is oriented from 5' to 3' with a T immediately preceding the site at the 5' end;

ii) does not have a T in the first (5') position or an A in the second position;

iii) ends in T at the last (3') position and does not have a G at the next to last position; and

iv) has a base composition of 0-63% A, 11-63% C, 0-25% G, and 2-42% T.

24. The method of claim 23, comprising identifying a first nucleotide sequence and a second nucleotide sequence in the genome of the cell, wherein the first and second nucleotide sequences meet at least one of the criteria set forth in claim 23, and are separated by 15-18 bp.

25. The method of claim 24, wherein the endonuclease generates a double-stranded break between the first and second nucleotide sequences.

26. A TALEN comprising an endonuclease domain and a TAL effector DNA binding domain specific for a target DNA, wherein the DNA binding domain comprises a plurality of DNA binding repeats, each repeat comprising a RVD that determines recognition of a base pair in the target DNA, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA, and wherein the TALEN comprises one or more of the following RVDs:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T;

HG for recognizing T;

H* for recognizing T;

IG for recognizing T;

NK for recognizing G;

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A; and

YG for recognizing T.

27. The TALEN of claim 26, wherein the TALEN comprises one or more of the following RVDs:

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G;

NA for recognizing G;

SN for recognizing G or A;

YG for recognizing T; and

NK for recognizing G,

and at least one or more of :

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G or A;

NS for recognizing A or C or G or T;

N* for recognizing C or T;

HG for recognizing T;

H* for recognizing T; and

IG for recognizing T.

28. The TALEN of claim 26, wherein the endonuclease domain is from a type II restriction endonuclease.

29. The TALEN of claim 28, wherein the type II restriction endonuclease is *Fok*I.

30. A TALEN comprising an endonuclease domain and a TAL effector domain, wherein the amino acid sequence of said TALEN is selected from the group consisting of SEQ ID NO:33 to SEQ ID NO:55, SEQ ID NO:72, and SEQ ID NO:73.

31. A method for generating an animal, comprising:

providing a eukaryotic cell comprising a target DNA sequence into which it is desired to introduce a genetic modification;

generating a double-stranded break within the target DNA sequence with a TALEN comprising an endonuclease domain and a TAL effector domain that binds to the target DNA sequence; and

generating an animal from the cell or progeny thereof in which a double-stranded break has occurred.

32. The method of claim 31, further comprising:

introducing into the cell an exogenous nucleic acid comprising a sequence homologous to at least a portion of the target DNA, wherein the introducing is under conditions that permit homologous recombination to occur between the exogenous nucleic acid and the target DNA sequence in the cell or progeny thereof; and

generating an animal from the cell or progeny thereof in which homologous recombination has occurred.

33. The method of claim 31, wherein the animal is a mammal.

34. The method of claim 31, wherein the genetic modification comprises a substitution, an insertion, or a deletion.

35. A method for generating a plant, comprising:

providing a plant cell comprising a target DNA sequence into which it is desired to introduce a preselected genetic modification;

generating a double-stranded break within the target DNA sequence with a TALEN comprising an endonuclease domain and a TAL effector domain that binds to the target DNA sequence; and

generating a plant from the cell or progeny thereof in which a double-stranded break has occurred.

36. The method of claim 35, further comprising:

introducing into the plant cell an exogenous nucleic acid comprising a sequence homologous to at least a portion of the target DNA sequence, wherein the introducing is under conditions that permit homologous recombination to occur between the exogenous nucleic acid and the target DNA sequence in the cell or progeny thereof; and

generating a plant from the cell or progeny thereof in which homologous recombination has occurred.

37. A method for targeted genetic recombination in a cell, comprising:

introducing into the cell a nucleic acid encoding a TAL effector endonuclease targeted to a selected DNA target sequence;

inducing expression of the TAL effector endonuclease within the cell; and

identifying a cell in which the selected DNA target sequence exhibits a mutation.

38. The method of claim 37, wherein the mutation is selected from the group consisting of deletion of genetic material, insertion of genetic material, and both deletion and insertion of genetic material.

39. The method of claim 37, further comprising introducing donor DNA into the cell.

40. The method of claim 37, wherein the cell is an insect cell, a plant cell, a fish cell, or a mammalian cell.

41. A method for generating a TAL effector having enhanced targeting capacity for a target DNA, said method comprising generating a nucleic acid encoding a TAL effector that comprises DNA binding domain having a plurality of DNA binding repeats, wherein each repeat comprises a RVD that determines recognition of a base pair in the target DNA, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA,
wherein said generating comprises incorporating a nucleic acid encoding a variant 0th DNA binding repeat sequence with specificity for A, C, or G, thus eliminating the requirement for T at position -1 of the binding site.

42. A method for generating a TAL effector having enhanced targeting capacity for a target DNA, said method comprising generating a nucleic acid encoding a TAL effector that comprises DNA binding domain having a plurality of DNA binding repeats, wherein each repeat comprises a RVD that determines recognition of a base pair in the target DNA, wherein each DNA binding repeat is responsible for recognizing one base pair in the target DNA,
wherein said generating comprises incorporating one or more nucleic acids encoding TAL effector DNA binding domains that contain RVDs having enhanced specificity for G, and wherein said RVDs are selected from the group consisting of RN, R*, NG, NH, KN, K*, NA, NT, DN, D*, NL, NM, EN, E*, NV, NC, QN, Q*, NR, NP, HN, H*, NK, NY, SN, S*, ND, NW, TN, T*, NE, NF, YN, Y*, and NQ, wherein * indicates a gap at the second position of the RVD.

43. A method for producing a polypeptide that selectively recognizes at least one base pair in a target DNA sequence, the method comprising synthesizing a polypeptide comprising a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a transcription activator-like (TAL) effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in the target DNA sequence, wherein the repeat unit is responsible for the recognition of one base pair in the DNA sequence, and wherein the hypervariable region comprises a member selected from the group consisting of:

(a) HD for recognition of C/G;

(b) NI for recognition of A/T;

(c) NG for recognition of T/A;

(d) NS for recognition of C/G or A/T or T/A or G/C;

(e) NN for recognition of G/C or A/T;

(f) NG for recognition of T/A;

(g) N for recognition of C/G;

(h) HG for recognition of C/G or T/A;

(i) H for recognition of T/A; and

(j) NK for recognition of G/C.

44. A polypeptide produced by the method of claim 43.

45. A DNA comprising a coding sequence for the polypeptide produced by the method of claim 43.

46. An expression cassette comprising a promoter operably linked to the DNA of claim 45.

47. A non-human host cell comprising the expression cassette of claim 46.

48. A transformed, non-human organism comprising the expression cassette of claim 46.

49. A method for selectively recognizing a base pair in a DNA sequence by a polypeptide, the method comprising constructing a polypeptide comprising a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a TAL effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in the DNA sequence, wherein the repeat unit is responsible for the recognition of one base pair in the DNA sequence, and wherein the hypervariable region comprises a member selected from the group consisting of:

(a) HD for recognition of C/G;

(b) NI for recognition of A/T;

(c) NG for recognition of T/A;

(d) NS for recognition of C/G or A/T or T/A or G/C;

(e) NN for recognition of G/C or A/T;

(f) IG for recognition of T/A;

(g) N for recognition of C/G;

(h) HG for recognition of C/G or T/A;

(i) H for recognition of T/A; and

(j) NK for recognition of G/C .

50. A method of modulating expression of a target gene in a cell, wherein cells are provided which contain a polypeptide wherein the polypeptide comprises a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a TAL effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in a DNA sequence, wherein the repeat unit is responsible for the recognition of one base pair in the DNA sequence, and wherein the hypervariable region comprises a member selected from the group consisting of:

(a) HD for recognition of C/G;

(b) NI for recognition of A/T;

(c) NG for recognition of T/A;

(d) NS for recognition of C/G or A/T or T/A or G/C;

(e) NN for recognition of G/C or A/T;

(f) IG for recognition of T/A;

(g) N for recognition of C/G;

(h) HG for recognition of C/G or T/A;

(i) H for recognition of T/A; and

(j) NK for recognition of G/C .

51. A polypeptide comprising a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a TAL effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in a DNA sequence, wherein the repeat unit is responsible for the recognition of one base pair in the DNA sequence, and wherein the hypervariable region comprises a member selected from the group consisting of:

(a) HD for recognition of C/G;

(b) NI for recognition of A/T;

(c) NG for recognition of T/A;

(d) NS for recognition of C/G or A/T or T/A or G/C;

(e) NN for recognition of G/C or A/T;

(f) IG for recognition of T/A;

(g) N for recognition of C/G;

(h) HG for recognition of C/G or T/A;

(i) H for recognition of T/A; and

(j) NK for recognition of G/C .

52. A DNA comprising a coding sequence for the polypeptide of claim 51.

53. A DNA which is modified to include a base pair located in a target DNA sequence so that the base pair can be specifically recognized by a polypeptide comprising a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a TAL effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in the DNA sequence, wherein the repeat unit is responsible for the recognition of one base pair in the DNA sequence, and wherein, to receive a selective and determined recognition by the hypervariable region, the base pair is selected from the group consisting of:

(a) C/G for recognition by HD;

(b) A/T for recognition by NI;

(c) T/A for recognition by NG;

(d) CT or A/T or T/A or G/C for recognition by NS;

(e) G/C or A/T for recognition by NN;

(f) T/A for recognition by IG;

(g) C/G or T/A for recognition by N;

(h) T/A for recognition by HG;

(i) T/A for recognition by H; and

(j) G/C for recognition by NK.

54. A vector comprising the DNA of claim 53.

55. A non-human host cell comprising the DNA of claim 53.

56. A transformed, non-human organism comprising the DNA of claim 53.

57. A method for producing a DNA comprising a target DNA sequence that is selectively recognized by a polypeptide comprising a repeat domain, wherein the repeat domain comprises at least one repeat unit derived from a TAL effector, wherein the repeat unit comprises a hypervariable region which determines recognition of a base pair in the target DNA sequence, and wherein the repeat unit is responsible for the recognition of one base pair in the target DNA sequence, the method comprising synthesizing a DNA comprising a base pair that is capable of being recognized by the repeat unit, wherein the base pair is selected from the group consisting of:

(a) C/G for recognition by HD;

(b) A/T for recognition by NI;

(c) T/A for recognition by NG;

(d) CT or A/T or T/A or G/C for recognition by NS;

(e) G/C or A/T for recognition by NN;

(f) T/A for recognition by IG;

(g) C/G or T/A for recognition by N;

(h) T/A for recognition by HG;

(i) T/A for recognition by H; and

(j) G/C for recognition by NK.

WHAT IS CLAIMED IS:

1. A method for modifying the genetic material of a cell, comprising:

(a) providing a cell containing a target DNA sequence; and

(b) introducing into the cell a vector encoding a transcription activator-like (TAL) effector endonuclease, the TAL effector endonuclease comprising:

(i) an endonuclease domain that can cleave double stranded DNA, wherein the endonuclease domain is from a type II restriction endonuclease, and

(ii) a TAL effector domain comprising a plurality of TAL effector repeat sequences that, in combination, bind to a specific nucleotide sequence in the target DNA sequence,

such that the TAL effector endonuclease cleaves the target DNA sequence within or adjacent to the specific nucleotide sequence in the cell or progeny thereof.

2. The method of claim 1, further comprising providing to the cell a nucleic acid comprising a sequence homologous to at least a portion of the target DNA sequence, such that homologous recombination occurs between the target DNA sequence and the nucleic acid.

3. The method of claim 1 or claim 2, wherein the cell is a mammalian cell.

4. The method of claim 1 or claim 2, wherein the cell is a plant cell.

5. The method of any one of claims 1 to 4, wherein the introducing comprises transfecting the cell with a vector encoding the TAL effector endonuclease.

6. The method of any one of claims 1 to 5, wherein the type II restriction endonuclease is *Fok*I.

7. The method of any one of claims 1 to 6, wherein the TAL effector domain that binds to a specific nucleotide sequence within the target DNA sequence comprises 10 or more TAL effector repeat sequences, more preferably 15 or more TAL effector repeat sequences.

8. The method of claim 7, wherein each TAL effector repeat sequence comprises a repeat variable-diresidue (RVD) that determines recognition of a base pair in the target DNA sequence, wherein each TAL effector repeat sequence is responsible for recognizing one base pair in the target DNA sequence, and wherein the RVD comprises one or more of:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G;

NS for recognizing A;

HG for recognizing T;

IG for recognizing T;

NK for recognizing G;

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G; and

NA for recognizing G.

9. A method for generating a nucleic acid encoding a TAL effector endonuclease, said method comprising:

(a) identifying a first unique nucleotide sequence in the genome of a cell; and

(b) synthesizing a nucleic acid encoding a TAL effector endonuclease that comprises (i) a plurality of TAL effector repeat sequences that, in combination, bind to the first unique nucleotide sequence, and (ii) an endonuclease that generates a double-stranded break within or adjacent to the first nucleotide sequence, wherein each TAL effector repeat sequence comprises a RVD that determines recognition of a base pair in the target DNA, wherein each TAL effector repeat sequence is responsible for recognizing one base pair in the target DNA, and wherein the TAL effector endonuclease comprises one or more of the following RVDs:

HD for recognizing C;

NG for recognizing T;

NI for recognizing A;

NN for recognizing G;

NS for recognizing A;

HG for recognizing T;

IG for recognizing T;

NK for recognizing G;

HA for recognizing C;

ND for recognizing C;

HI for recognizing C;

HN for recognizing G; and

NA for recognizing G.

10. The method of claim 9, wherein the first nucleotide sequence meets at least one of the following criteria:

i) is a minimum of 15 bases long and is oriented from 5' to 3' with a T immediately preceding the site at the 5' end;

ii) does not have a T in the first (5') position or an A in the second position;

iii) ends in T at the last (3') position and does not have a G at the next to last position; and

iv) has a base composition of 0-63% A, 11-63% C, 0-25% G, and 2-42% T.

11. The method of claim 9 or claim 10, further comprising identifying a-second nucleotide sequence in the genome of the cell, wherein the first and second nucleotide sequences are separated by 15-18 bp.

12. The method of any one of claims 9 to 11, wherein the endonuclease generates a double-stranded break between the first and second nucleotide sequences.

13. A TAL effector endonuclease monomer comprising an endonuclease domain and a TAL effector DNA binding domain specific for a target DNA, wherein the endonuclease domain is from a type II restriction endonuclease, wherein the DNA binding domain comprises a plurality of TAL effector repeat sequences, each TAL effector repeat sequence comprising a RVD that determines recognition of a base pair in

the target DNA, and wherein each TAL effector repeat sequence is responsible for recognizing one base pair in the target DNA.

14. The TAL effector endonuclease monomer of claim 13, wherein the type II restriction endonuclease is *Fok*I.

15. The TAL effector endonuclease monomer of claim 14, wherein said monomer functions as a dimer with another monomer across a bipartite recognition site with a spacer, allowing *Fok*I to dimerize and create a double-strand break in said target DNA within said spacer.

16. The TAL effector endonuclease monomer of claim 13, wherein the TAL effector endonuclease monomer comprises one or more of the following RVDs:

HD for recognizing C;
NG for recognizing T;
NI for recognizing A;
NN for recognizing G;
NS for recognizing A;
HG for recognizing T;
IG for recognizing T;
NK for recognizing G;
HA for recognizing C;
ND for recognizing C;
HI for recognizing C;
HN for recognizing G; and
NA for recognizing G.

17. The TAL effector endonuclease monomer of claim 13, wherein the amino acid sequence of said TAL effector endonuclease has at least 95% identity to a sequence selected from SEQ ID NO:33 to SEQ ID NO:55, SEQ ID NO:72, and SEQ ID NO:73.

18. A method for generating non-human animal, comprising:

i) providing a eukaryotic cell comprising a target DNA sequence into which it is

desired to introduce a genetic modification, wherein the cell comprises a nucleic acid encoding a TAL effector endonuclease according to any one of claims 13 to 17;

ii) generating a double-stranded break within the target DNA sequence with the TAL effector endonuclease; and

iii) generating non-human animal from the cell or progeny thereof in which a double-stranded break has occurred.

19. The method of claim 18, further comprising:

introducing into the cell an exogenous nucleic acid comprising a sequence homologous to at least a portion of the target DNA, wherein the introducing is under conditions that permit homologous recombination to occur between the exogenous nucleic acid and the target DNA sequence in the cell or progeny thereof; and

generating non-human animal from the cell or progeny thereof in which homologous recombination has occurred.

20. A method for generating a plant, comprising:

i) providing a plant cell comprising a target DNA sequence into which it is desired to introduce a preselected genetic modification, wherein the plant cell comprises a nucleic acid encoding a TAL effector endonuclease according to any one of claims 13 to 17;

ii) generating a double-stranded break within the target DNA sequence with the TAL effector endonuclease; and

iii) generating a plant from the cell or progeny thereof in which a double-stranded break has occurred.

21. The method of claim 20, further comprising:

introducing into the plant cell an exogenous nucleic acid comprising a sequence homologous to at least a portion of the target DNA sequence, wherein the introducing is under conditions that permit homologous recombination to occur between the exogenous nucleic acid and the target DNA sequence in the cell or progeny thereof; and

generating a plant from the cell or progeny thereof in which homologous recombination has occurred.

22. A method for targeted genetic recombination in a cell, comprising:

i) introducing into the cell a nucleic acid encoding a TAL effector endonuclease according to any one of claims 13 to 17, wherein said TAL effector endonuclease is targeted to a selected DNA target sequence;

ii) inducing expression of the TAL effector endonuclease within the cell; and

iii) identifying a cell in which the selected DNA target sequence exhibits a mutation.

23. The method of claim 22, wherein the mutation is selected from the group consisting of deletion of genetic material, insertion of genetic material, and both deletion and insertion of genetic material.

24. The method of claim 22, further comprising introducing donor DNA into the cell.

25. The method of any one of claims 22 to 24, wherein the cell is an insect cell, a plant cell, a fish cell, or a mammalian cell.

26. A nucleic acid encoding a TAL effector endonuclease comprising (i) an endonuclease domain that can cleave double stranded DNA, wherein the endonuclease domain is from a type II restriction endonuclease, and (ii) a TAL effector domain comprising a plurality of TAL effector repeat sequences that, in combination, bind to a selected target DNA sequence.

27. The nucleic acid of claim 26, wherein said endonuclease domain is from *Fok*I.

28. An expression cassette comprising a promoter operably linked to the nucleic acid of claim 26 or claim 27.

29. A host cell comprising the expression cassette of claim 28.