What is claimed is:

1. A chimeric polypeptide comprising:

a) a recombinase, a transcription factor or nuclease; and

b) a transcription activator-like effector (TALE) protein.

2. The chimeric protein of claim 1, wherein the TALE protein is truncated.

3. The chimeric protein of claim 2, wherein the TALE protein comprises a C-terminal or N-terminal truncation.

4. The chimeric protein of claim 3, wherein the TALE protein comprises a C-terminal truncation.

5. The chimeric protein of claim 1, wherein the TALE protein is selected from the group consisting of: AcrXa7, Tal1c, and PthXo1.

6. The chimeric protein of claim 1, wherein the TALE protein comprises an amino acid sequence as set forth in SEQ ID NO: 2.

7. The chimeric protein of claim 6, wherein the TALE protein comprises a C-terminal truncation.

8. The chimeric protein of claim 7, wherein the TALE protein is truncated between amino acid residues 27 and 268, 92 and 134, 120 and 129, 74 and 147, or 87 and 120.

9. The chimeric protein of claim 8, wherein the TALE protein is truncated at amino acid residue 28, 74, 87, 92, 95, 120, 124, 128, 129, 147 and 150.

10. The chimeric protein of claim 1, wherein the recombinase is selected from the group consisting of:

(a) Tn3, also known as EcoTn3; Hin, also known as StyHin; Gin, also known as MuGin; Sin; Beta; Pin; Min; Din; Cin; EcoTn21; SfaTn917; BmeTn5083; Bme53; Cpe; SauSK1; SauSK41; SauTn552; Ran; Aac; Lla; pMER05; Mlo92; Mlo90; Rrh; Pje; Req; PpsTn5501; Pae; Xan; ISXc5; Spy; RhizY4cG; SarpNL1; SsolSC1904a; SsolSC1904b; SsolSC1913; Aam606; MjaM0014; Pab; HpylS607; MtulS_Y349; MtuRv2792c; MtuRv2979c; MtuRv3828c; MtuRv0921; MceRv0921; TnpX; TndX; WwK; lactococcal phage TP901-1 serine recombinase; *S. pyogenes* phage ϕ370.1 serine recombinase; *S. pyogenes* phage ϕFC1 serine recombinase; *Listeria* phage A118 serine recombinase; *S. coelicolor* chromosome SC3C8.24 serine recombinase; *S. coelicolor* chromosome SC2E1.37 serine recombinase; *S. coelicolor* chromosome SCD78.04c serine recombinase; *S. coelicolor* chromosome SC8F4.15c serine recombinase; *S. coelicolor* chromosome SCD12A.23 serine recombinase; *S. coelicolor* chromosome SCH10.38c serine recombinase; *S. coelicolor*

chromosome SCC88.14 serine recombinase; *Streptomyces* phage ϕC31 serine recombinase; *Streptomyces* phage R4 serine recombinase; *Bacillus* phage ϕ105 serine recombinase; *Bacillus* phage SPBc2 serine recombinase; *Bacillus* prophage SKIN serine recombinase; *S. aureus ccrA* serine recombinase; *S. aureus ccrB* serine recombinase; *M. tuberculosis* phage Bxb1 serine recombinase; *M. tuberculosis* prophage ϕRV1 serine recombinase; YBCK_ECOLI; Y4bA; Bja; Spn; Cac 1956; and Cac 1954; and

(b) muteins of recombinases of (a).

11. The chimeric protein of claim 10, wherein the recombinase is selected from the group consisting of Gin, Hin, Tn3, Sin, Beta, Pin. Min, Din, and Cin and muteins of Gin, muteins of Hin, muteins of Sin, muteins of Beta, muteins of Pin, muteins of Min, muteins of Din, muteins of Cin, muteins of Tn3.

12. The chimeric protein of claim 10, wherein the recombinase is Gin.

13. The chimeric protein of claim 1, wherein the recombinase is Gin and the TALE protein is AcrXa7.

14. An isolated nucleic acid molecule encoding the chimeric protein of any of claims 1-13.

15. An expression cassette comprising the nucleic acid molecule of claim 14.

16. A vector comprising the expression cassette of claim 15.

17. A host cell transformed or transfected with the nucleic acid molecule of claim 14 or the vector of claim 16.

18. A method for site-specific recombination comprising:

(a) providing a DNA sequence comprising at least two binding sites for specifically interacting with the chimeric protein of claim 1; and

(b) reacting the DNA sequence with the chimeric protein, wherein the chimeric protein catalyzes a site-specific recombination event in which both strands of the DNA sequence are cleaved between the two sites specifically interacting with the chimeric protein.

19. The method of claim 18, wherein the site-specific recombination event is an inversion.

20. The method of claim 18, wherein the site-specific recombination event is an integration.

21. The method of claim 18, wherein the site-specific recombination event is a resolution.

22. A method for gene therapy comprising administering to a subject a composition comprising a nucleic acid molecule encoding the chimeric protein of claim 1, wherein upon

expression of the nucleic acid molecule, a gene present in the genome of the subject is specifically removed or inactivated.

23. The method of claim 22, further comprising administering to the subject a nucleic acid molecule comprising a functional replacement of the gene.

24. A pharmaceutical composition comprising:

a) the chimeric protein of claim 1; and

b) a pharmaceutically acceptable carrier.

25. A pharmaceutical composition comprising:

a) a nucleic acid molecule encoding the chimeric protein of claim 1; and

b) a pharmaceutically acceptable carrier.

26. A transgenic organism produced by an act of recombination catalyzed by the chimeric protein of claim 1.

27. A method for gene therapy comprising administering to a subject a cell comprising a nucleic acid molecule having the DNA sequence generated by the method of any of claims 18-21.

28. A method for modifying a genome of an organism, comprising modifying the genome of the organism by performing site-specific recombination on a nucleic acid molecule of the genome using the method of any of claims 18-22.

29. The method of claim 28, wherein the organism is a prokaryote, bacterium, virus or eukaryote.

30. A method of generating a transcription activator-like effector (TALE) protein binding domain which specifically binds a desired nucleotide, comprising:

a) randomizing the amino acid sequence of the TALE protein binding domain by mutating an amino acid residue within a variable di-residue (RVD), or within 1 to 2 amino acid residues N-terminal or C-terminal of the RVD;

b) selecting for the randomized TALE protein binding domain of (a), wherein the TALE protein binding domain specifically binds to the desired nucleotide.

31. An isolated protein comprising a transcription activator-like effector (TALE) protein binding domain generated by the method of claim 30.

32. The isolated protein of claim 31, wherein the protein comprises from 1 to 40 TALE protein binding domains.

33. The isolated protein of claim 32, wherein the protein specifically binds a target nucleotide sequence.

34. The isolated protein of claim 33, wherein the protein comprises nuclease or recombinase activity.

35. The isolated protein of claim 33, wherein the protein regulates gene expression.

36. An isolated nucleic acid molecule encoding a protein comprising the TALE protein binding domain of any of claims 31-35.

37. An expression cassette comprising the nucleic acid molecule of claim 36.

38. A vector comprising the expression cassette of claim 37.

39. A host cell transformed or transfected with the nucleic acid molecule of claim 37 or the vector of claim 38.

40. An isolated polypeptide comprising a *Xanthamonus* derived transcription activator-like effector (TALE) protein, the TALE protein having an N-terminal domain (NTD) comprising an amino acid sequence as set forth in SEQ ID NO: 3 (VGKQWSGARAL) having one or more mutations or deletions selected from: Q is Y, Q is S, Q is R, W is R, W is G, W is deleted, S is R, S is H, S is A, S is N, and S is T.

41. The polypeptide of claim 40, wherein the NTD comprises an amino acid sequence selected from: VGKYRGARAL (SEQ ID NO: 4), VGKSRSGARAL (SEQ ID NO: 5), VGKYHGARAL (SEQ ID NO: 6), and VGKRGAGARAL (SEQ ID NO: 7).

42. An isolated polypeptide comprising a *Ralstonia* derived transcription activator-like effector (TALE) protein, the TALE protein having an N-terminal domain (NTD) comprising an amino acid sequence as set forth in SEQ ID NO: 8 ($IVDIAR_1QR_2SGDLA$) having one or more mutations or deletions selected from: R_1 is K, Q is Y, Q is S, Q is R, R_2 is W, R_2 is G, R_2 is deleted, S is R, S is H, S is A, S is N, and S is T.

43. The polypeptide of claim 42, wherein the NTD comprises an amino acid sequence selected from: IVDIARQWSGDLA (SEQ ID NO: 9), IVDIARYRGDLA (SEQ ID NO: 10), IVDIARSRSGDLA (SEQ ID NO: 11), IVDIARYHGDLA (SEQ ID NO: 12), and IVDIARRGAGDLA (SEQ ID NO: 13).

44. The polypeptide of any of claims 40-43 further comprising a recombinase domain or a nuclease domain.

45. An isolated nucleic acid molecule encoding the polypeptide of any of claims 40-44.

46. An expression cassette comprising the nucleic acid molecule of claim 45.

47. A vector comprising the expression cassette of claim 46.

48. A host cell transformed or transfected with the nucleic acid molecule of claim 45 or the vector of claim 47.

49. A method of generating a transcription activator-like effector (TALE) protein N-terminal domain (NTD), comprising:

a) randomizing an amino acid sequence of the NTD by mutating or deleting one or more amino acid residues within the NTD, wherein the amino acid sequence is SEQ ID NO: 14 (VGKXXXGAR) or SEQ ID NO: 15 (VDIAXXXXGDLA); and

b) selecting for the randomized TALE protein NTD of (a), wherein the TALE protein NTD specifically binds to a desired nucleotide or exhibits enhanced activity.

50. A method of generating a plurality of zinc finger recombinase (ZFRs) proteins having catalytic specificity greater than the corresponding wild type recombinase comprising:

a) performing random mutagenesis on a recombinase catalytic domain at positions equivalent to Gin Ile120, Thr123, Leu127, Ile136 and Gly137 or a combination thereof, mutating the DNA at positions 2 and 3 for each amino acid;

b) fusing the recombinase catalytic domain of a) with a plurality of zinc finger binding domains to form ZFRs, and

c) enriching for ZFRs of b) having catalytic specificity greater than the corresponding wild type recombinase.

51. The method of claim 50, wherein the ZFRs have increased catalytic activity on DNA targets selected from GC, GT, CA, TT and AC.

52. The method of claim 50, wherein the recombinase catalytic domain is mutagenized at Ile136 and/or Gly137.

53. The method of claim 50, wherein the ZFRs have increased target specificity at chromosomes 1, 2, 4, 6, 7, 11, 13, and/or X.

54. The method of claim 50, wherein the ZFRs are in a vector.

55. The method of claim 50, wherein the recombinase catalytic domain is from a recombinase selected from the group consisting of:

a) Tn3, also known as EcoTn3; Hin, also known as StyHin; Gin, also known as MuGin; Sin; Beta; Pin; Min; Din; Cin; EcoTn21; SfaTn917; BmeTn5083; Bme53; Cpe; SauSK1; SauSK41; SauTn552; Ran; Aac; Lla; pMER05; Mlo92; Mlo90; Rrh; Pje; Req; PpsTn5501; Pac; Xan; ISXc5; Spy; RhizY4cG; SarpNL1; SsolSC1904a; SsolSC1904b; SsolSC1913; Aam606; MjaM0014; Pab; HpylS607; MtulS_Y349; MtuRv2792c; MtuRv2979c; MtuRv3828c; MtuRv0921; MceRv0921; TnpX; TndX; WwK; lactococcal phage TP901-1 serine recombinase; *S. pyogenes* phage ϕ370.1 serine recombinase; *S. pyogenes* phage ϕFC1 serine recombinase; *Listeria* phage A118 serine recombinase; *S.*

coelicolor chromosome SC3C8.24 serine recombinase; *S. coelicolor* chromosome SC2E1.37 serine recombinase; *S. coelicolor* chromosome SCD78.04c serine recombinase; *S. coelicolor* chromosome SC8F4.15c serine recombinase; *S. coelicolor* chromosome SCD12A.23 serine recombinase; *S. coelicolor* chromosome SCH10.38c serine recombinase; *S. coelicolor* chromosome SCC88.14 serine recombinase; *Streptomyces* phage ϕC31 serine recombinase; *Streptomyces* phage R4 serine recombinase; *Bacillus* phage ϕ105 serine recombinase; *Bacillus* phage SPBc2 serine recombinase; *Bacillus* prophage SKIN serine recombinase; *S. aureus ccrA* serine recombinase; *S. aureus ccrB* serine recombinase; *M. tuberculosis* phage Bxb1 serine recombinase; *M. tuberculosis* prophage ϕRV1 serine recombinase; YBCK_ECOLI; Y4bA; Bja; Spn; Cac 1956; and Cac 1954; and

b) muteins of a).

56. The method of claim 6, wherein the recombinase catalytic domain is from a mutein of Gin, Hin, Sin, Bcta, Pin, Min, Din, Cin, or Tn3.

57. A chimeric polypeptide generated by the method of claim 50.

58. The chimeric polypeptide of claim 57, wherein the recombinase catalytic domain is selected from the group consisting of:

a) Tn3, also known as EcoTn3; Hin, also known as StyHin; Gin, also known as MuGin; Sin; Beta; Pin; Min; Din; Cin; EcoTn21; SfaTn917; BmeTn5083; Bme53; Cpe; SauSK1; SauSK41; SauTn552; Ran; Aac; Lla; pMER05; Mlo92; Mlo90; Rrh; Pje; Req; PpsTn5501; Pae; Xan; ISXc5; Spy; RhizY4cG; SarpNL1; SsolSC1904a; SsolSC1904b; SsolSC1913; Aam606; MjaM0014; Pab; HpylS607; MtulS_Y349; MtuRv2792c; MtuRv2979c; MtuRv3828c; MtuRv0921; MceRv0921; TnpX; TndX; WwK; lactococcal phage TP901-1 serine recombinase; *S. pyogenes* phage ϕ370.1 serine recombinase; *S. pyogenes* phage ϕFC1 serine recombinase; *Listeria* phage A118 serine recombinase; *S. coelicolor* chromosome SC3C8.24 serine recombinase; *S. coelicolor* chromosome SC2E1.37 serine recombinase; *S. coelicolor* chromosome SCD78.04c serine recombinase; *S. coelicolor* chromosome SC8F4.15c serine recombinase; *S. coelicolor* chromosome SCD12A.23 serine recombinase; *S. coelicolor* chromosome SCH10.38c serine recombinase; *S. coelicolor* chromosome SCC88.14 serine recombinase; *Streptomyces* phage ϕC31 serine recombinase; *Streptomyces* phage R4 serine recombinase; *Bacillus* phage ϕ105 serine recombinase; *Bacillus* phage SPBc2 serine recombinase; *Bacillus* prophage SKIN serine recombinase; *S. aureus ccrA* serine recombinase; *S. aureus ccrB* serine recombinase; *M. tuberculosis* phage Bxb1 serine recombinase; *M. tuberculosis* prophage ϕRV1 serine recombinase;

YBCK_ECOLI; Y4bA; Bja; Spn; Cac 1956; and Cac 1954; and

b) muteins of a).

59. The method of claim 9, wherein the recombinase catalytic domain is from a mutein of Gin, Hin, Sin, Beta, Pin, Min, Din, Cin, or Tn3.

60. An isolated nucleic acid molecule encoding the polypeptide of claim 57.

61. An expression cassette comprising the nucleic acid molecule of claim 60.

62. A vector comprising the expression cassette of claim 61.

63. An isolated host cell containing the vector of claim 62.

64. A method for site-specific integration into a DNA sequence comprising:

contacting the DNA sequence with a chimeric polypeptide of claim 57, wherein the chimeric polypeptide catalyzes site-specific integration.

65. A method for gene therapy comprising administering to a subject a composition comprising a nucleic acid molecule encoding the chimeric polypeptide of claim 57, wherein upon expression of the nucleic acid molecule, a gene present in the genome of the subject is specifically removed or inactivated.

66. The method of claim 65, further comprising administering to the subject a nucleic acid molecule comprising a functional replacement of the gene.

67. A pharmaceutical composition comprising:

a) the chimeric polypeptide of claim 57; and

b) a pharmaceutically acceptable carrier.

68. A pharmaceutical composition comprising:

a) a nucleic acid molecule encoding the chimeric polypeptide of claim 57; and

b) a pharmaceutically acceptable carrier.

69. A transgenic organism produced by recombination catalyzed by the chimeric polypeptide of claim 57.

CLAIMS

1. An invention not claimed in any divisional application.