

What is claimed is:

1. A non-naturally occurring variant of Bxb1 recombinase with altered DNA target specificity relative to wildtype Bxb1 recombinase, comprising one or more amino acid mutations within a zinc ribbon domain (ZD) or a recombinase domain (RD).
2. The Bxb1 recombinase variant of claim 1, wherein the one or more amino acid mutations occur at one or more of positions 147, 148, 149, 154, 155, 156, 158, 197, 198, 230, 231, 232, 233, 237, 257, 309, 312, 314, 315, 316, 318, 323, 324, 325, 326, and 335 (numbering according to SEQ ID NO: 1).
3. The Bxb1 recombinase variant of claim 1, wherein the one or more amino acid mutations are selected from F314A, F314C, F314D, F314E, F314G, F314H, F314I, F314L, F314N, F314Q, F314S, F314T, F314V, F314W, F314Y, A315F, A315G, A315H, A315I, A315M, A315N, A315S, A315T, A315W, A315Y, G316A, G316C, G316D, G316E, G316F, G316H, G316I, G316K, G316L, G316M, G316P, G316Q, G316R, G316S, G316T, G316V, G316W, G316Y, G318I, G318K, G318R, G318W, R323G, R323K, R325D, R325E, R325K, R325L, R325M, R325N, R325Q, R325S, R325W, F147A, F147K, F147R, N148Q, N148T, L158D, L158N, L158S, L158T, L158W, P197H, P197R, P197T, S231F, S231G, S231H, S231K, S231R, S231V, S231Y, T233F, T233H, T233K, T233R, T233W, T233Y, R237A, R237C, R237D, R237E, R237F, R237G, R237H, R237I, R237K, R237L, R237M, R237N, R237P, R237Q, R237S, R237T, R237V, R237W, R237Y, and D257K (numbering according to SEQ ID NO: 1).
4. A non-naturally occurring variant of ϕ C31 integrase, Pa557 recombinase, or Pa570 recombinase, comprising one or more amino acid mutations that produce altered DNA target specificity relative to the wildtype counterpart.
5. The ϕ C31 integrase variant of claim 4, wherein the one or more amino acid mutations occur at one or more of positions 273, 275, 279, 375, 376, 377, 379, and 386 (numbering according to SEQ ID NO: 77).

6. The ϕ C31 integrase variant of claim 5, wherein the one or more amino acid mutations are selected from D273, A275, R279, K375, R376, G377, E379, and R386 (numbering according to SEQ ID NO: 77).
7. The Pa557 recombinase variant of claim 4, wherein the one or more amino acid mutations occur at one or more of positions 236, 238, 242, 327, 328, 329, 331, and 338 (numbering according to SEQ ID NO: 78).
8. The Pa557 recombinase variant of claim 7, wherein the one or more amino acid mutations are selected from G236, A238, A242, R327, T328, G329, G331, and R338 (numbering according to SEQ ID NO: 78).
9. The Pa570 recombinase variant of claim 4, wherein the one or more amino acid mutations occur at one or more of positions 243, 245, 249, 333, 334, 335, 337, and 344 (numbering according to SEQ ID NO: 79).
10. The Pa570 recombinase variant of claim 9, wherein the one or more amino acid mutations are selected from E243, S245, K249, I333, N334, P335, I337, and Q344 (numbering according to SEQ ID NO: 79).
11. The recombinase variant of any one of claims 1-10, wherein the DNA target is specific to a particular allele of a gene.
12. A nucleic acid molecule encoding the recombinase variant of claim 1.
13. A vector comprising the nucleic acid molecule of claim 12.
14. The vector of claim 13, wherein the vector is a plasmid or a viral vector, optionally selected from an adeno-associated viral vector, an adenoviral vector, or a lentiviral vector.
15. A system for editing DNA in a cell, comprising the recombinase variant of claim 1.

16. A method of editing the genome of a cell, the method comprising providing to the cell the system of claim 15.
17. A cell comprising the system of claim 15, or a descendent thereof.
18. A cell edited by the method of claim 16, or a descendent thereof.
19. The cell or descendent of claim 18 for use in treating a disease in a subject in need thereof.
20. Use of the cell or descendent of claim 18 in the manufacture of a medicament for treating a disease in a subject in need thereof.