What is claimed is:

1. ABxb1 integrase comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the Bxb1 integrase comprises one or more mutations or mutation combinations selected from Table 1, Table 13, Table 17, and Table 20 compared to wild-type Bxb1 integrase.

2. The Bxb1 integrase of claim 1, comprising an amino acid sequence that is at least 98% identical to the amino acid sequence of SEQ ID NO: 1, or comprising an amino acid sequence that is at least 99% identical to the amino acid sequence of SEQ ID NO: 1.

3. The Bxb1 integrase of claim 1 or 2, wherein the one or more mutations or mutation combinations is at position 4, 5, 18, 24, 34, 36, 40, 42, 46, 51, 61, 62, 63, 67, 69, 79, 85, 87, 88, 89, 90, 92, 95, 99, 100, 105, 106, 110, 111, 119, 122, 130, 133, 137, 140, 145, 153, 156, 160, 164, 166, 174, 175, 178, 179, 181, 187, 189, 191, 203, 209, 218, 223, 229, 231, 239, 248, 251, 254, 261, 264, 268, 272, 278, 280, 281, 282, 283, 285, 287, 288, 292, 295, 302, 306, 307, 311, 313, 319, 321, 328, 331, 332, 333, 334, 347, 353, 355, 359, 360, 361, 362, 369, 370, 375, 380, 388, 397, 398, 405, 409, 411, 414, 415, 416, 419, 425, 428, 434, 435, 444, 453, 461, 463, 466, 468, 476, 479, 480, 483, 484, 487, 488, 489, 494, 496, and/or 499, or optionally wherein the one or more mutations or mutation combinations are selected from mutations at the following positions: L4, G34, D36, E42, R57, L61, F67, V74, V76, D99, H100, H111, A145, T166, V168, V187, H189, M239, N251, T254, L263, V264, R272, P332, A341, V353, D355, D359, V366, A369, V380, T388, A398, R409, A414, R416, R426, R444, E445, Q480, Q484, L488, and M499.

4. The Bxb1 integrase of any one of claims 1-3, wherein the one or more mutations or mutation combinations comprise L4I, V5V, S18S, E24E, G34D, D36A, V40I, V40A, V40V, E42K, V46V, D51D, D51N, L61F, A62A, R63K, F67S, E69A, E69E, R79R, R85R, I87L, I87V, R88R, H89G, L90L, Q92H, Q92Q, H95Y, D99N, H100N, V105A, S106S, A110A, H111P, A119S, V122M, A130A, E133E, I137I, R140R, A145T, K153K, G156G, P160P, L164L, T166I, L174L, V175V, P178P, V179A, V179I, R181K, V187I, V187V, H189N, Q191Q, H203Y, G209G, A218A, R223R, E229K, S231S, M239I, A248T, N251K, N251N, T254S, A261T, V264A, P268P, R272Q, L278L, A280T, A280A, E281E,

L282L, V283V, T285A, R287R, A288V, A288T, P292P, P295P, L302L, V306V, C307C, A311V, K313R, K313K, R319K, R319G, H321P, H321N, S328S, F331S, P332H, K333K, H334R, A347E, V353I, D355N, D359N, D359D, A360T, E361E, R362K, A369P, A369E, A369T, A369S, G370G, V375V, V380I, T388M, R397R, A398S, A405A, R409H, A411V, A414A, A414V, A415S, R416K, E419E, A425T, A425A, S428S, E434G, T435T, R444L, T453I, R461R, T463I, V466M, V466V, G468D, G468G, F476F, L479I, Q480STOP, E483E, Q484K, R487R, del L488, G489G, R494S, R494R, H496N, and/or M499T, or optionally wherein the one or more mutations or mutation combinations are selected from the following mutations: L4I, G34D, D36A/D36N, E42K, R57K, L61F, F67S, V74I, V76I, H89G, D99N, H100N, H111P, V122M, A145T, T166I, V168I, V175A, V179A/V179I, V187I, H189N/H189Y, E229K, M239I, A248T, N251K, T254S, A261S/A261T, L263I, V264A, R272Q, R287H, A288V, K313R, R319G/R319K, P332H, H334R, A341D, A347E, V353I, D355N, D359A/D359N, A360V, V366I, A369E/A369P/A369S/A369T, V380I, T388M, A398S, R409H, A414V, A415S, R416K, A425T, R426K, R444L, E445Q, T453I, V466L, Q480STOP, Q484K, delL488frameshift, R494S, H496N, and M499T.

5. The Bxb1 integrase of any one of claims 1-4, wherein the one or more mutations are at a position selected from I87, Q91, H95, and E98, and wherein

the mutation at position I87 comprises a mutation selected from I87D, I87K, I87H, I87Y, I87L, I87A, and I87S,

the mutation at position Q91 comprises a mutation selected from Q91E, Q91K, Q91Y, Q91L, Q91A, and Q91S,

the mutation at position H95 comprises a mutation selected from H95D, H95K, H95L, H95A, and H95S, and

the mutation at position E98 comprises a mutation selected from E98D, E98K, E98H, E98Y, E98L, E98A, and E98S.

6. The Bxb1 integrase of any one of claims 1-5, wherein one or more of the following amino acids relative to SEQ ID NO: 1 are not mutated: V5, S18, E24, V40, V46, D51, A62, E69, R79, R85, R88, L90, Q92, H100, S106, A110, A130, E133, I137, R140, K153, G156, P160, L164, L174, V175, P178, R181, V187, Q191, G209, A218, R223, S231, N251, P268, R272, L278, A280, E281, L282, V283,

R287, P292, P295, L302, V306, C307, K313, S328, K333, D359, E361, G370, V375, L387, R397, A405, A414, E419, A425, S428, T435, R461, V466, G468, F476, E483, R487, G489, and R494.

7. The Bxb1 integrase of claim 1, wherein the Bxb1 integrase comprises:

an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 1; and

one or more amino acid mutations at positions selected from L4, E42, R57, R63, V76, H111, V122, V187, R319, A341, D359, A369, A398, R416, A425, L479, and M499, relative to SEQ ID NO: 1.

8. The Bxb1 integrase of claim 7, comprising an amino acid sequence that is at least 98% identical to the amino acid sequence of SEQ ID NO: 1, or comprising an amino acid sequence that is at least 99% identical to the amino acid sequence of SEQ ID NO: 1.

9. The Bxb1 integrase of claim 7 or 8, further comprising one or more amino acid mutations selected from L4I, E42K, R57K, R63K, V76I, H111P, V122M, V187I, R319K, A341D, D359A, A369P, A398S, R416K, A425T, L479I, and M499T, relative to SEQ ID NO: 1.

10. The Bxb1 integrase of any one of claims 7-9, further comprising further comprising one or more amino acid mutations selected from D36N, V40A, A49S, V74I, I87L or I87A or I87S, H89G, V175A, V179A, R287H, A288V, T453I, and H496N, and/or further comprising one or more amino acid mutations selected from V40I, D45G, I75V, H95Y, A119S, A280T, A311V, E434G, and V466M.

11. The Bxb1 integrase of any one of claims 7-10, wherein one or more of the following amino acids relative to SEQ ID NO: 1 are not mutated: A62, H100, G209, P295, L302, C307, L387, E419, S428, E483, and R487.

12. The Bxb1 integrase of any one of claims 7-11, comprising the mutation V122M and/or the mutation A369P.

13. The Bxb1 integrase of any one of claims 7-12, further comprising:

a combination of amino acid mutations selected from:

A119S, A369P, and E434G;

A288V, A311V, A398S, R416K, T453I, H496N, and E42K,

A369P and E434G;

A49S, A369P, and E434G;

A49S, I87L, A369P, and E434G;

A49S, V122M, A369P, and E434G;

D36N, A369P, and E434G;

D36N, I87L, A369P, and E434G;

D36N, V122M, A369P, and E434G;

D45G, A369P, and E434G;

E42K, H95Y, A369P, and E434G;

E42K, V76I, and I87L;

H111P and E434G

H95, V122M and A369P;

H95Y and A341D;

H95Y and A369P;

H95Y and K313R;

H95Y and V122M;

H95Y, A369P, A425T, and E434G;

H95Y, A369P, and E434G;

H95Y, A369P, E434G, and L479I;

H95Y, A369P, E434G, and V466M;

H95Y, R319K, A369P, and E434G;

H95Y, V122M and E434G;

H95Y, V179A, A369P, and E434G;

I75V and V76I;

I87L and A341D;

I87L and A369P;

I87L and A425T;

I 87L and D359A;

I87L and L479I;

I87L and L4I;

I87L and R319K;

I87L and V122M;

I87L, A341D, A369P, and E434G;

I87L, A341D, and R287H;

I87L, A369P, A425T, and E434G;

I87L, A369P, and E434G;

I87L, A369P, E434G, and R319K;

I87L, D359A, A369P, and E434G;

I87L, H95Y, A369P and E434G;

I87L, H95Y, and A369P;

I87L, H95Y, V122M, and E434G;

I87L, R287H, A369P, and E434G;

I87L, R287H, A369P, E434G, and A341D;

I87L, R57K, and R63K;

I87L, V122, A369P, and E434G;

I87L, V122M, and A369P;

I87L, V122M, and E434G;

I87L, V175A, and D359A;

L4I and V76I;

L4I, H95Y, A369P, and E434G;

L4I, I87L, A369P, and E434G;

L4I, V122M, A369P, and E434G;

R57K, I87L, A369P, and E434G;

R57K, R63K and H95Y;

R57K, R63K, I87L, A369P, and E434G;

R57K, R63K, V122M, A369P, and E434G;

R63K and I87L;

R63K and V122M;

R63K, A119S, and M499T;

R63K, I87L, A369P, and E434G;
R63K, I87V, and N194D;
R63K, V122M, A369P, and E434G;
R63K, V122M, R319K, and V40I;
V122M and A369P;
V122M and E434G;
V122M, A369P, A425T, and E434G;
V122M, A369P, and E434G;
V122M, A369P, E434G, and A341D;
V122M, A369P, E434G, and R319K;
V122M, A369P, E434G, and V175A;
V122M, D359A, A369P, and E434G;
V122M, R287H, A341D, A369P, and E434G;
V122M, R287H, A369P, and E434G;
V122M, V175A, D359A, A369P, and E434G;
V40A, R63K, and H89G;
V40I, H95Y, A369P, and E434G;
V74I and V76I;
V74I, I75V, and V76I;
V76I and A119S;
V76I and A369P;
V76I and V122M;
V76I, A369P, and E434G;
V76I, I87L, and K313R; and
V76I, V122M, and A369P.

14. The Bxb1 integrase of any one of claims 7-13, wherein the Bxb1 integrase comprises an amino acid sequence that is at least 98% identical to the amino acid sequence of SEQ ID NO: 1 and having the amino acid mutations I87L, A369P, and E434G; the amino acid mutations V122M, A369P, and E434G; or the amino acid mutations H95Y, A369P, and E434G.

15. An isolated nucleic acid encoding the Bxb1 integrase of any one of claims 1-14.

16. A vector comprising the isolated nucleic acid of claim 15.

17. A cell comprising the Bxb1 integrase of any one of claims 1-14, the isolated nucleic acid of claim 16 or the vector of claim 17.

18. A method of altering the sequence of a genome of a cell comprising contacting a cell with the Bxb1 integrase of any one of claims 1-14, or the nucleic acid of claim 15, or the vector of claim 16, wherein the cell comprises in its genome at least one integrase recognition sequence recognized by the Bxb1 integrase so that the Bxb1 integrase binds to the integrase recognition sequence and alters the sequence of the genome of the cell.

19. The method of claim 18, wherein the insertion comprises integration of an exogenous nucleic acid sequence into the genome of the cell at a safe harbor locus.