



(51) International Patent Classification:

C12N 9/22 (2006.01)

C12N 15/90 (2006.01)

C12N 15/10 (2006.01)

(21) International Application Number:

PCT/US2023/061500

(22) International Filing Date:

27 January 2023 (27.01.2023)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/304,565

28 January 2022 (28.01.2022)

US

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(81) Designated States (unless otherwise indicated, for every

kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CV, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IQ, IR, IS, IT, JM, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every

kind of regional protection available): ARIPO (BW, CV, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, ME, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))
- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))
- of inventorship (Rule 4.17(iv))

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(54) Title: SERINE RECOMBINASE SYSTEMS FOR SITE-SPECIFIC GENE EDITING

(57) Abstract: The present disclosure provides engineered large serine recombinases and systems containing the recombinases for gene editing.



WO 2023/147507 A1

SERINE RECOMBINASE SYSTEMS FOR SITE-SPECIFIC GENE EDITING

CROSS REFERENCE TO RELATED APPLICATIONS

[1] The present application claims priority from U.S. Provisional Application 63/304,565, filed January 28, 2022, the content of which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[2] The instant application contains a Sequence Listing that has been submitted electronically in XML format. The Sequence Listing is hereby incorporated by reference in its entirety. The XML copy, created on January 26, 2023, is named 025297.WO043.xml and is 361,227 bytes in size.

BACKGROUND OF THE INVENTION

[3] Large serine recombinases (LSRs) are a family of enzymes encoded by temperate phages. These enzymes can precisely cut and recombine DNA in a site-specific manner, moving DNA elements into and out of bacterial chromosomes between short DNA attachment sites in the phage (attP) and in the host bacteria (attB) (Duyne and Rutherford, *Crit Rev Biochem Mol Biol.* (2013) 48(5):476-91; Smith, *Microbiol Spectr.* (2015) 3(4):doi10.1128/microbiolspec). The highly directional and controlled process of DNA recombination mediated by LSRs render them a potential tool in genetic engineering and gene therapy where site-specific DNA integration, excision, inversion, or cassette exchange in a genome is desired.

[4] Bxb1 recombinase, also known as Bxb1 integrase, is an LSR encoded by phage Bxb1 that facilitates integration of the phage DNA into the *Mycobacterium smegmatis* genome (Russell et al., *Biotechniques* (2018) 40(4): doi.org/10.2144/000112150). The recombinase contains an N-terminal catalytic domain similar to that of smaller resolvases/invertases and a larger C-terminal domain responsible for coordination of activities unique to LSRs. This C-terminal domain is further divided into a recombinase domain (RD) and a Zinc ribbon domain (ZD) that contains a coiled-coil (CC) motif (Rutherford et al., *Nucleic Acids Res.* (2013) 41(17):8341-56). During recombination events, the ZD and RD domains of a Bxb1 recombinase

dimer bind to an attachment site (attB or attP) on a double-stranded DNA segment, while the ZD and RD domains of another Bxb1 recombinase dimer bind to the other attachment site (attP or attB) on another double-stranded DNA segment. The subsequent complexing of the two dimers leads to the formation of a Bxb1 recombinase tetramer and brings together the attP and attB sites on the two DNA segments. Serine residues at the tetramer's active sites form covalent bonds at those center dinucleotide base pairs and cleave the double-stranded DNA. This cleavage makes the center dinucleotides into 3' overhangs. The resulting protein/DNA complex is rotated and the previously separate DNA molecules or segments are ligated if the center dinucleotides at the attB and attP sequences are identical. This process produces attachment R (attR) and attachment (attL) sites that are no longer substrates for the recombinase without the presence of additional co-factors.

[5] Despite the precision of gene editing afforded by large serine recombinases, their utility as a genetic engineering and therapeutic tool has been limited by the rarity of their binding sites in the human genome, including in therapeutically relevant genes. Thus, there remains a need for new recombinases that can recognize a variety of DNA attachment sites and realize the therapeutic potential of this category of enzymes.

SUMMARY OF THE INVENTION

[6] The present disclosure provides large serine recombinase variants that have altered DNA target specificity compared to their wildtype counterparts. In one aspect, the disclosure provides a non-naturally occurring variant of Bxb1 recombinase with altered DNA target specificity relative to wildtype Bxb1 recombinase (e.g., SEQ ID NO: 1), comprising one or more amino acid mutations (e.g., substitutions, deletions, or insertions) within a ZD or a RD.

[7] In some embodiments, 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). In further embodiments, 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.

[8] In some embodiments, the Bxb1 recombinase variant mediates increased transgene insertion at an endogenous target site in a eukaryotic genome, relative to wild-type Bxb1 recombinase.

[9] In other aspects, the present disclosure provides a non-naturally occurring variant of ϕ C31 integrase, Pa557 recombinase, or Pa570 recombinase, comprising one or more amino acid mutations (e.g., substitutions, deletions, or insertions) that produce altered DNA target specificity relative to the wildtype counterpart.

[10] In some embodiments, the ϕ C31 integrase variants comprise one or more amino acid mutations at one or more of positions 273, 275, 279, 375, 376, 377, 379, and 386 (numbering according to SEQ ID NO: 77). In further embodiments, the one or more amino acid mutations are selected from D273, A275, R279, K375, R376, G377, E379, and R386.

[11] In some embodiments, the Pa557 recombinase variants comprise one or more amino acid mutations at one or more of positions 236, 238, 242, 327, 328, 329, 331, and 338

(numbering according to SEQ ID NO: 78). In further embodiments, the one or more amino acid mutations are selected from G236, A238, A242, R327, T328, G329, G331, and R338.

[12] In some embodiments, the Pa570 recombinase variants comprise one or more amino acid mutations at one or more of positions 243, 245, 249, 333, 334, 335, 337, and 344

(numbering according to SEQ ID NO: 79). In further embodiments, the one or more amino acid mutations are selected from E243, S245, K249, I333, N334, P335, I337, and Q344.

[13] In some embodiments, the DNA target is specific to a particular allele of a gene.

[14] In some embodiments, the DNA target is in a cell, such as a eukaryotic cell, e.g., a mammalian cell (e.g., a human cell).

[15] Also provided herein are nucleic acid molecules encoding the recombinase variants herein and expression vectors comprising the coding sequences. The vector may be, e.g., a

plasmid or a viral vector (e.g., an adeno-associated viral vector, an adenoviral vector, or a lentiviral vector).

[16] The present disclosure also provides a system for editing DNA in a cell, comprising the recombinase variant, the nucleic acid molecule, or the vector herein. In some embodiments, the system further comprises donor DNA, such as a circularized DNA or a linear DNA. IN further embodiments, the donor DNA comprises a sequence selected from SED ID NOs: 80-81 and 134-136 and the sequences found in Tables 3, 4 and 5. The donor DNA may be delivered through, e.g., a plasmid or viral vector.

[17] The editing by the system herein may comprise integration of DNA into the genome of the cell, excision or inversion of DNA in the genome of the cell, or a chromosomal translocation in the genome of the cell. In some embodiments, the editing occurs at a genomic region comprising a sequence selected from SED ID NOs: 80-81 and 134-136 and the sequences found in Tables 3, 4 and 5.

[18] In another aspect, the present disclosure provides a method of editing the genome of a cell, the method comprising providing to the cell the gene editing system herein. In some embodiments, more than one genomic region is edited. The editing method may result in excising DNA from the genome, inverting DNA in the genome, chromosomal swap, recombinase-mediated cassette exchange (RMCE), and/or integrating donor DNA into the genome.

[19] Provided herein are also cells comprising the present system, cells edited by the present methods, or descendent cells thereof. The cells may be eukaryotic cells (e.g., mammalian such as human cells).

[20] In another aspect, the present disclosure provides a method of treating a disease in a subject in need thereof, comprising administering the edited cells to the subject. Also included are cells for use in treating a disease in a subject in need thereof, and use of the cells in the manufacture of a medicament for treating a disease in a subject in need thereof.

[21] Other features, objectives, and advantages of the invention are apparent in the detailed description that follows. It should be understood, however, that the detailed description, while indicating embodiments and aspects of the invention, is given by way of illustration only, not limitation. Various changes and modification within the scope of the invention will become apparent to those skilled in the art from the detailed description.

BRIEF DESCRIPTION OF THE FIGURES

[22] **FIG. 1** is a schematic illustrating (A) the structure of Bxb1 recombinase and (B) its mechanism of action as a tetramer on bound attB and attP sites (B. NTD: catalytic N-Terminal domain (NTD); α E: conserved alpha helix; CTD: C-terminal domain; RD: recombinase domain; CC: a coiled-coil motif; and ZD: Zinc ribbon domain (ZD)). The numbers underneath the protein structure in (A) indicate the approximate distance, from the N-terminus of the protein: of the C-terminal border of the NTD (~150 amino acids), the N-terminal border of the CTD (300 amino acids), and the C-terminus of the CTD (600 amino acids).

10 [23] **FIG. 2** is a schematic illustrating the nucleotide numbering system for attB and attP sequences, including the nucleotides bound by the ZD and RD domains of Bxb1 recombinase. The attP sequence shown is identical to the wildtype sequence (SEQ ID NO: 3), while the attB sequence was edited to be more symmetric compared to the wildtype attB site (SEQ ID NO: 80).

[24] **FIGs. 3A-E** are a panel of schematics illustrating recombinase-mediated (A) integration, (B) excision, (C) inversion, (D) chromosome swap, and (E) cassette exchange. For recombinase-mediate cassette exchange (RMCE), the donor DNA can be circular (illustrated) or linear (not illustrated).

[25] **FIG. 4** is a schematic illustrating the plasmid-based recombination assay used with NGS to determine the DNA sequence specificity of mutant Bxb1 recombinase variants. One plasmid is shown in light gray and the other in black. White and dark gray boxes indicate attB and attP sites, respectively. P1 and P2 refer to primer binding locations. Shown at bottom are the products resulting from successful integration events.

20 [26] **FIG. 5** is a schematic illustrating the chromosomal recombination assay in human K562 cells. Bxb1 facilitates the targeted integration (TI) of a donor plasmid into a chromosomal Bxb1 attB pseudo-site (an endogenous human sequence with some homology to the natural Bxb1 attB target site). White and dark gray boxes indicate attB and attP sites, respectively. F-Primer and R-Primer refer to primer binding locations used for a PCR-based NGS assay to quantify TI events. Shown at bottom is the product resulting from a successful TI event.

25 [27] **FIGs. 6A-C** illustrate the alteration of the target site preference of Bxb1 variant S231F. (A) Target preference shift for Bxb1 variant S231F obtained from the plasmid-based experimental system shown in **FIG. 4**. S231F shows improved targeting of both C and T vs.

wild-type (WT) Bxb1 at position 10. (B) Endogenous human Bxb1 target sites s5-8 (SEQ ID NOs: 141 and 264), s5-1 (SEQ ID NOs: 137 and 265), s5-11 (SEQ ID NOs: 143 and 266), and s1-41 (SEQ ID NOs: 161 and 267) with both strands of DNA shown, center dinucleotide shaded gray, RD motifs underlined and base at position 10 of both left and right half site shown in bold.

Changes from the A base preferred by WT Bxb1 are indicated by arrows. (C) Targeted integration (TI) values (percent of endogenous alleles containing targeted integration) at these endogenous sites in human cells for either a 50% mixture of the S231F Bxb1 variant and WT Bxb1 or 100% WT Bxb1. Any changes at position 10 of the target site relative to the preferred target of WT Bxb1 are indicated in the second column. Multiple replicates of the WT Bxb1 were performed. Data for WT Bxb1 is the mean value of all replicates +/- the standard deviation. The last column shows the ratio of TI with the S231F variant to TI with WT Bxb1. The increased TI activity for the S231F variant at endogenous sites s5-1, s5-11, and s1-41 is consistent with both the target preference changes observed in the plasmid-based experimental system and the targeting rules shown in Table 1.

[28] FIG. 7 is a list of Bxb1 variants that improve targeted integration (TI) activity vs. wild-type (WT) Bxb1 at endogenous human target sites consistent with the alterations in DNA target sequence shown in **Table 1**. Variants that gave TI values at least 3 standard deviations above the mean value for WT Bxb1 at the same target in a side-by-side experiment were considered to be improved vs. WT Bxb1. TI and variant/WT data is presented as in **FIG. 6C**.

Sequence alterations at these sites that match alterations in **Table 1** are shown in the second, third, and fourth column, where the second column shows the relevant position in the target site of the alteration, the third column shows the alterations at the given position in the left half-site of the target site listed in the first column, and the fourth column shows the alteration in the target site at the relevant position of the right half-site. If the base at the indicated position of the indicated half-site matches the target preferences of WT Bxb1 (e.g. A at position 10, C at position 9, or A at position 7), then the base is indicated as “WT Bxb1.”

[29] FIGs. 8A-C illustrates alterations in target site preference of Bxb1 variants F314G and G316Y. (A) Target preference specificity shift for Bxb1 variant F314G at position 19 (left panel) and target preference specificity shift for Bxb1 variant G316Y at position 21 (right panel) obtained from the plasmid-based experimental system shown in **FIG. 4**. The bases are numbered according to the scheme shown in **FIG. 2**. Note that these endogenous human target sites all

resemble attB sites. Because attP sites have five bases inserted relative to attB sequences and those inserted bases are at positions 13-17 if present, the base labeled as position 18 is adjacent to the base labeled as position 12. (B) The symmetric attB site (SEQ ID NOs: 268 and 269) used in the plasmid-based experiment system shown in **FIG. 4** compared with endogenous human Bxb1 target sites s5-16 (SEQ ID NOs: 146 and 270) and s3-28 (SEQ ID NOs: 163 and 271). The center dinucleotide is shaded in gray and the ZD motifs in each half-site are underlined. Note that the ZD motif in the left half-site of site s5-16 diverges so much from the ZD motif used in the plasmid-based system that it likely represents a distinct sequence motif and cannot be treated as the same ZD sequence motif characterized in the plasmid-based system; thus, it likely does not follow the same target preference rules shown in **Table 1**. Site s5-16 has a ZD motif similar to the ZD motif in the plasmid-based system in the right half-site; the T in position 19 in the right half-site of this site is shown in bold and indicated by an arrow. Both half-sites of s3-28 contain a ZD motif that resembles the ZD motif used in the plasmid based system and thus ZD motifs in both half-sites are underlined. The G at position 21 of the right half-site is shown in bold and indicated by an arrow. (C) Comparison of targeted integration (TI) data in human cells at the endogenous human target site s5-16 with a 50% mixture of Bxb1 variant F314G and wild-type (WT) Bxb1 vs. 100% WT Bxb1 (top panel), and comparison of TI data in human cells at the endogenous human target site s3-28 with a 50% mixture of Bxb1 variant G316Y and WT Bxb1 vs. 100% WT Bxb1 (bottom panel). Target alterations and TI data is displayed as in **FIG. 6C**.

FIG. 9 is a list of Bxb1 variants that improve targeted integration (TI) activity vs. wild-type (WT) Bxb1 at the indicated endogenous human target sites. Bases that match the target preferences of WT Bxb1 (e.g., G at position 19) are indicated with "WT Bxb1." Half-sites with ZD domains that diverge so much from the ZD motif characterized in the plasmid system that they likely represent different sequence motifs are indicated by a blank space in the entry for the relevant half-site. Data is presented as in **FIGs. 6C, 7, and 8C**.

FIG. 10 is a list of Bxb1 variants that improve targeted integration (TI) activity vs. wild-type (WT) Bxb1 at the indicated endogenous human target sites, with alterations at position 21, 22, 23, or 24 in the ZD motif of one or both half-sites. Target site alterations and data are displayed as in **FIG. 9**. Target sequence preference for WT Bxb1 is T at positions 21 and 22, and G at positions 23 and 24.

[32] FIG. 11 shows data demonstrating improvement in targeted integration (TI) activity with the D257K Bxb1 variant at a variety of different endogenous human target sites. D257K improved TI activity vs. wild-type (WT) Bxb1 both as a 50% mixture with WT Bxb1 and as 100% D257K variant without any WT Bxb1. In these examples, 100% D257K variant has higher activity than either 50% D257K or 100% WT Bxb1. Thus, D257K appears to represent a Bxb1 variant that can increase activity at most or all endogenous target sites regardless of the exact target site alterations vs. the preferred target site for WT Bxb1.

DETAILED DESCRIPTION OF THE INVENTION

[33] The present disclosure provides large serine recombinase variants, such as Bxb1 recombinase variants and orthologous recombinase variants, and systems comprising said variants for gene editing. These recombinase variants have altered DNA target sequences compared to their wildtype counterparts and can be used to target endogenous DNA sequences within the genome of organisms of interest, including humans. These enzymes can integrate donor DNA into the genome or excise or invert a target genomic sequence. Thus, they can be used to integrate therapeutic genes into the genome or to repair or remove pathogenic genes from the genome, to achieve therapeutic effects.

[34] The present gene editing systems comprising the recombinase variants are advantageous over other gene editing systems in several important ways. First, the present systems avoid undesired changes to the genome. The most widely used gene editing systems are CRISPR/Cas (clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein (Cas)) systems, zinc-finger nuclease (ZFN) systems, and transcription activator-like effector nuclease (TALEN) systems. Those systems depend upon the activity of nucleases and DNA repair mechanisms, such as homologous recombination and non-homologous end joining, which are error prone and may introduce insertions or deletions (indels) and/or translocations. By having both the cutting and ligating functions, the present recombinases cleave DNA and ligate its breaks at a highly precise, site-specific manner, avoiding the introduction of harmful indels into the genome. Second, there is no inherent size limit to the DNA that can be integrated into a host genome using the present editing systems. Third, the recombination generated by the present systems is not easily reversible without an accessory protein called recombination directionality factor (RDF); thus, the gene edits are stable

and heritable. In sum, the present recombinase variants can be used to stably and precisely remove DNA from, integrate large synthetic and/or exogenous donor DNA into, or invert a segment of, a host genome at sites that are specifically recognized by the present recombinase variants.

5

I. Variant Serine Recombinase Systems

[35] Provided in the present disclosure are systems for gene editing comprising large serine recombinase variants, such as Bxb1 recombinase variants or orthologous recombinase variants, and optionally donor DNA to be integrated into a host genome at target sites. Also provided are expression constructs for delivering any of the above components, as well as methods for gene editing using one or more of the above components. Each component of the present gene editing system is further described in detail below.

10

A. Large Serine Recombinase Variants with Altered DNA Target Sequences

[36] As used herein, the term “recombinase” refers to a protein that catalyzes recombination. The term “recombination” refers to the excision, inversion, integration, chromosomal swap, RMCE, or rearrangement of DNA in a target DNA sequence, such as a host genome. The terms “large serine recombinase” and “serine recombinase” refer to a family of recombinase proteins that induce double-stranded DNA breaks and utilize serine residues in their active sites to bind separate DNA segments during recombination.

15

[37] The term “Bxb1 recombinase” as used herein, refers to a serine recombinase, with an exemplary amino acid sequence shown below:

20

Wildtype Bxb1	
	10 20 30 40 50
25	MRALVVIRLS RVTDATTSPE RQLESCQQLC AQRGWDVVG V AEDLDVSGAV
	60 70 80 90 100
	DPFDRKRRPN LARWLAFEEQ PFDVIVAYRV DRLTRSIRHL QQLVHWAEDH
	110 120 130 140 150
	KKLVVSATEA HFDTTTTFAA VVIALMGTVA QMELEAIKER NRSAAHFNIR
30	160 170 180 190 200
	AGKYRGS LPP WGYPTRVDG EWRLVPDPVQ RERILEVYHR VVDNHEPLHL
	210 220 230 240 250
	VAHDLNRRGV LSPKDYFAQL QGREPQGREW SATALKRSMI SEAMLGYATL
	260 270 280 290 300
35	NGKTVRDDD G APLVRAEPIL TREQLEALRA ELVKTSRAKP AVSTPSLLLR
	310 320 330 340 350

VLFCAVCGEP AYKFAGGGRK HPRYRCRSMG FPKHCGNGTV AMAEWDAFCE
 360 370 380 390 400
 EQVLDLLGDA ERLEKVVWAG SDSAVELAEV NAELVDLTSL IGSPAYRAGS
 410 420 430 440 450
 5 PQREALDARI AALAARQEEL EGLEARPSGW EWRETGQRFG DWWREQDTAA
 460 470 480 490 500
 KNTWLRSMNV RLTFDVRGGL TRTIDFGDLQ EYEQHLRLGS VVERLHTGMS
 (SEQ ID NO: 1)

[38] The domain structure of Bxb1 recombinase and its mechanism of action are illustrated in FIG. 1. The following sequences are the attB and attP sites recognized by wildtype Bxb1 recombinase, where the center dinucleotides are italicized and in boldface, the single-underlined regions are recognized by the ZD domains, and the double-underlined regions are recognized by the RD domains:

Wildtype attB

GGCTTGTCGACGACGGCG**GT**CTCCGTCGTCCAGGATCAT (SEQ ID NO: 2)

Wildtype attP

GGTTTGTCTGGTCAACCACCGCG**GT**CTCAGTGGTGTACGGTACAAACC (SEQ ID NO: 3)

[39] To simplify the search for Bxb1 recombinase variants with altered target DNA specificity, a more symmetric version of the attB target site may be used, with an exemplary nucleotide sequence shown below (SEQ ID NO: 80; *see also* FIG. 2). The center dinucleotides are italicized and bold, the single-underlined regions are recognized by the ZD domains, and the double-underlined regions are recognized by the RD binding domains:

Symmetric attB

GGTTTGTCGACGACGGCG**GT**CTCCGTCGTCCAACAAACC (SEQ ID NO: 80)

However, the variants identified through this attB sequence will not be limited to recognizing symmetric attB sequences.

[40] The present disclosure provides variants of the above SEQ ID NO: 1 that have altered DNA recognition sequences. As used herein, the term “Bxb1 recombinase variant(s),” “variant Bxb1 recombinase(s),” “Bxb1 variant(s),” or “variant Bxb1” refers to Bxb1 recombinases with one or more amino acid mutations (e.g., substitutions, insertions, and/or deletions) that alter the

DNA targeting specificity of the variant relative to the wildtype (WT) Bxb1 recombinase. The term “orthologous recombinase variant(s)” or “orthologous serine recombinase variant(s)” as used herein refers to orthologous serine recombinases with one or more amino acid mutations that alter the DNA targeting specificity of the variants relative to their WT counterparts.

5 [41] Serine recombinases, including the present recombinase variants, comprise a catalytic NTD and a CTD involved in sequence-specific DNA recognition. The CTD is further divided into a RD and a ZD containing a CC motif (**FIG. 1**). The NTD domain may approximately correspond to amino acids 1-145 (numbering according to SEQ ID NO: 1) in wildtype Bxb1 recombinase or the functionally analogous sequence in Bxb1 recombinase variants, or the
10 functionally analogous sequence in orthologous serine recombinase(s) and their variants. The term “functionally analogous sequence” refers to a sequence of amino acid residues or a protein domain having the same or substantially the same biological function. The RD domain may approximately correspond to amino acids 140-287 (numbering according to SEQ ID NO: 1) in wildtype Bxb1 recombinase or the functionally analogous sequence in Bxb1 recombinase
15 variants, or the functionally analogous sequence in orthologous serine recombinase(s) and their variants. The ZD domain may approximately correspond to amino acids 302-500 (numbering according to SEQ ID NO: 1) in wildtype Bxb1 recombinase or the functionally analogous sequences in Bxb1 recombinase variants, or the functionally analogous sequence(s) in orthologous serine recombinase(s) and their variants. The coiled-coil (CC) motif may
20 approximately correspond to that found within the ZD domain in wildtype Bxb1 recombinase or the functionally analogous sequences in Bxb1 recombinase variants, or the functionally analogous sequence(s) in orthologous serine recombinase(s) and their variants.

[42] In some embodiments, the provided recombinase variants may comprise the amino acid sequence GSGSGSHHHHHGSGPKKKRKV (SEQ ID NO: 249) at the C terminus end, or
25 analogous linkers, His tags, and/or nuclear localization sequences. In some embodiments, the provided recombinase variants comprise a nuclear localization signal at the N- or C-terminal ends.

[43] In some embodiments, the present Bxb1 recombinase variants may comprise mutations within the ZD domain or RD domain amino acid sequences. For example,
30 substitutions in the ZD domain can be made at one or more of amino acids 311-335. Substitutions for the RD domain can be made at one or more of amino acids 137 to 160, 195-

201, 229-239, 249-252, and 284-287. The region between the ZD and RD is thought to function as a linker between these domains so substitutions to this linker region can be made at one or more of amino acids 288-301. In some embodiments, the present recombinase variants may comprise one or more mutations at the following amino acid locations: 147, 148, 149, 154, 155,
 5 156, 158, 197, 198, 230, 231, 232, 233, 237, 257, 309, 312, 314, 315, 316, 318, 323, 324, 325, 326, and 335. Unless otherwise indicated, the amino acid positions in Bxb1 recombinase in the present disclosure are numbered in accordance with SEQ ID NO: 1.

[44] In further embodiments, the Bxb1 variant ZD domain may comprise one or more of the following amino acid substitutions:

- 10 F314: to A, C, D, E, G, H, I, L, N, Q, S, T, V, W, or Y;
 A315: to F, G, H, I, M, N, S, T, W, or Y;
 G316: to A, C, D, E, F, H, I, K, L, M, P, Q, R, S, T, V, W, or Y;
 G318: to I, K, R, or W;
 R323: to G or K; and
 15 R325: to D, E, K, L, M, N, Q, S, or W.

[45] In further embodiments, the Bxb1 variant RD domain may comprise any one or more of the following amino acid mutations:

- F147: to A, K, or R;
 N148: to Q or T;
 20 L158: to D, N, S, T, or W;
 P197: to H, R, or T;
 S231: to F, G, H, K, R, V, or Y;
 T233: to F, H, K, R, W, or Y; and
 R237: to A, C, D, E, F, G, H, I, K, L, M, N, P, Q, S, T, V, W, or Y.

25 **[46]** In some embodiments, the present recombinase variants may comprise mutations within the NTD domain or CC coiled motif amino acid sequences.

[47] The effects of exemplary single amino acid substitutions of Bxb1 recombinase (SEQ ID NO: 1) on the recombinase's recognition site are shown in **Table 1** and **Table 2** below. In these tables, "WT Nt" refers to the nucleotide in the wildtype attB or attP site (e.g., SEQ ID
 30 NOs: 2 and 3). **Table 1** shows the results of saturation mutagenesis studies at amino acids 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 (see Example 3 below). In the table, “new Nt” refers to the nucleotide for which the Bxb1 recombinase mutation produces at least a 3-fold change in the nucleotide preference of the wildtype Bxb1 recombinase or shifts the preferred nucleotide of the wildtype Bxb1 recombinase to a different nucleotide. For example, at nucleotide 6 of the WT attB or attP site, when the Bxb1 recombinase variant has a F147A, N148T, L158W, T233F, or T233Y substitution, the Bxb1 recombinase variant has at least a 3-fold higher binding affinity for nucleotide A compared to the wildtype Bxb1 recombinase.

Table 1. Bxb1 Recombinase Mutants with Altered DNA Target Sequences

Pos.*	WT Nt	New Nt	Mutants
6	C	A	F147A, N148T, L158W, T233F, T233Y
		G	F147A, F147R, N148Q, N148T, P197H
7	A	C	F147K, F147R, N148Q, N148T, L158D, L158N, L158S, L158T, T233F, T233Y
9	C	A	N148T, R237A, R237C, R237F, R237G, R237H, R237I, R237K, R237L, R237M, R237N, R237Q, R237S, R237V, R237W, R237Y
		G	F147A, F147R, N148T, P197H, P197R, P197T, R237A, R237C, R237D, R237E, R237F, R237G, R237H, R237I, R237M, R237N, R237P, R237Q, R237S, R237T, R237V, R237W, R237Y
		T	R237A, R237C, R237H, R237M, R237N, R237S, R237T, R237V
10	A	C	F147A, F147R, N148Q, N148T, S231F, S231G, S231H, S231K, S231R, S231V, S231Y, T233H, T233K, T233W
		G	T233R
		T	N148Q, N148T, P197H, S231F, S231G, S231R, S231V, T233F, T233W, T233Y
18	T	A	R325W
		C	R325K

Pos.*	WT Nt	New Nt	Mutants
19	G	A	F314D, F314Q, A315T
		C	F314L, A315F, A315I, A315M, A315T, A315W, A315Y, G318R, R325K
		T	F314A, F314C, F314G, F314N, F314Q, F314S, F314T, A315F, A315I, A315S, A315W, A315Y, G318R
20	T	A	G318R, R325K, R325W
		C	A315F, A315G, A315W, A315Y, R325D, R325E, R325K, R325L, R325M, R325N, R325Q, R325S
		G	F314D, F314N, F314S, F314T, A315T, G318K, G318R
21	T	A	F314D, F314I, F314L, A315F, A315W, A315Y
		C	F314D, F314E, R323G, R325W
		G	F314A, F314C, F314H, F314N, F314S, F314T, F314V, F314W, G316F, G316H, G316K, G316P, G316Y
22	T	A	F314T, A315F, A315W, A315Y, G316C, G316S, G318I
		G	F314D, F314T, F314Y, A315F, A315H, A315N, A315W, A315Y, G316A, G316H, G316Q, G316R, G316S, R323K
23	G	A	A315F, A315H, A315W, A315Y, G316T, G316V, G316W, G318I, G318K, G318R
		C	A315F, A315H, A315N, A315Y, G316A, G316C, G316D, G316E, G316F, G316H, G316I, G316L, G316M, G316Q, G316S, G316T, G316V, G316W, G316Y
		T	G316C, G316I, G316V, G316H
24	G	C	A315F, A315Y, G316W, G318W

*Nucleotide position in the recombinase recognition site corresponding to that in **FIG. 2**.

[48] In some embodiments, the Bxb1 recombinase variant may comprise two or more substitutions, e.g., those shown in **Table 1** above. Such a variant may have a higher binding affinity to a target sequence that contains two or more nucleotide differences from the WT attB or attP recognition sequence. For example, a Bxb1 recombinase variant that comprises

mutations R237K and T233R will have a higher binding affinity to the target sequence that comprises A at position 9 and G at position 10. Some of the single substitutions will produce increases in binding affinities at multiple nucleotide positions. By way of example, a Bxb1 recombinase variant that comprises the mutation F147R will have a higher binding affinity to the target sequence that comprises G at position 6, C at position 7, G at position 9, and C at position 10. Some of the substitutions will produce increases in binding affinities for multiple nucleotides at a single position. For example, a Bxb1 recombinase variant that comprises the mutation R237V will have higher binding affinities to the target sequences that comprise A, G, or T at position 9.

[49] In certain embodiments, the Bxb1 recombinase variants may comprise one or more substitutions, e.g., those shown in **Table 2** below. Shown in **Table 2** are the two Bxb1 recombinase mutations that produce in the targeted DNA binding sequence the greatest increase in binding affinity for A, C, G, or T at the indicated nucleotide position (position numbers according to **FIG. 2**). For example, while the mutations F147A, N148T, L158W, T233F, and T233Y produce a Bxb1 recombinase variant with increased binding affinity to the target sequence that comprises A at position 6, T233F and N148T produce the greatest increase in affinity. The underlined mutations produce Bxb1 recombinase variants that recognize a target sequence comprising a new preferred nucleotide at the indicated position. For example, Bxb1 recombinase variants with a T233R mutation preferentially recognize sequences with a G at position 10, while the wildtype Bxb1 recombinase preferentially recognizes sequences with an A at position 10.

Table 2. Bxb1 Recombinase Mutants with Particular Increases in Binding Affinity

Domain	Pos.*	WT Nt	A	C	G	T
RD	6	C	T233F, N148T	WT Bxb1	N148T, F147R	
	7	A	WT Bxb1	N148T, T233Y		
	9	C	<u>R237G/K</u>	WT Bxb1	<u>R237D/E</u>	<u>R237A/T</u>
	10	A	WT Bxb1	S231R/Y	<u>T233R</u>	T233Y, S231R

ZD	18	T	<u>R325W</u>	<u>R325K</u>		WT Bxb1
	19	G	<u>F314D/Q</u>	<u>R325K,</u> <u>F314L</u>	WT Bxb1	F314G/S
	20	T	R325K, G318R	<u>R325Q/M</u>	F314T/D	WT Bxb1
	21	T	<u>F314L/I</u>	F314E/D	<u>F314N/V</u>	WT Bxb1
	22	T	G316C/S		<u>F314Y,</u> <u>G316R</u>	WT Bxb1
	23	G	G316W, A315Y	<u>G316Y/D</u>	WT Bxb1	<u>G316C/I</u>
	24	G		G318W, G316W	WT Bxb1	<u>G316H</u>

*Nucleotide position in the recombinase recognition site corresponding to that in **FIG. 2**.

[50] In some aspects of the present disclosure, a recombinase orthologous to the Bxb1 recombinase may also be used. In some embodiments, the orthologous serine recombinase is ϕ C31 integrase, comprising an exemplary amino acid sequence below:

Wildtype ϕ C31

	10	20	30	40	50
	MDTYAGAYDR	QSRERENSSA	ASPATQRSAN	EDKAADLQRE	VERDGGFRFR
10	60	70	80	90	100
	VGHFSEAPGT	SAFGTAERPE	FERILNECRA	GRLNMIIVYD	VSRFSRLKVM
	110	120	130	140	150
	DAIPIVSELL	ALGVTIVSTQ	EGVFRQGNVM	DLIHLIMRLD	ASHKESSLKS
	160	170	180	190	200
15	AKILDTKNLQ	RELGGYVGGK	APYGFELVSE	TKEITRNGRM	VNVVINKLAH
	210	220	230	240	250
	STTPLTGPF	FEPDVIRWWW	REIKTHKHL	FKPGSQAAIH	PGSITGLCKR
	260	270	280	290	300
	MDADAVPTRG	ETIGKKTASS	AWDPATVMRI	LRDPRIAGFA	AEVIYKKKPD
20	310	320	330	340	350
	GTPTTKIEGY	RIQRDPITLR	PVELDCGPII	EPAEWYELQA	WLDGRGRGKG
	360	370	380	390	400
	LSRGQAILSA	MDKLYCECGA	VMTSKRGEES	IKDSYRCRRR	KVVDPSAPGQ
	410	420	430	440	450
25	HEGTCNVSMA	ALDKFVAERI	FNKIRHAEGD	EETLALLWEA	ARRFGKLTEA
	460	470	480	490	500

PEKSGERANL VAERADALNA LEELYEDRAA GAYDGPVGRK HFRKQQAALT
 510 520 530 540 550
 LRQQGAEEERL AELEAAEAPK LPLDQWFPED ADADPTGPKS WWGRASVDDK
 560 570 580 590 600
 5 RVFVGLFVVDK IVVTKSTTGR GQGTPIEKRA SITWAKPPTD DDEDDAQDGT
 EDVAA (SEQ ID NO: 77)

[51] In some embodiments, the orthologous serine recombinase is Pa557 recombinase,
 10 comprising an exemplary amino acid sequence below:

Wildtype Pa557

	10	20	30	40	50
15	MNMHSPTVTT	RAALYLRVST	ARQAEHDISI	PDQKRQGEAY	CEQRGFQLVE
	60	70	80	90	100
	TYVEPGATAT	NDKRPEFQRM	IEAGTSKPAP	FDIVVVHSFS	RFFRDHFEME
	110	120	130	140	150
	FYVRKLAKNG	VKLVSITQEM	GDDPMHQMMR	QIMALFDEYQ	SKENAKHVLR
	160	170	180	190	200
20	AMNENARQGF	WNGARPPIGY	RIVAAEQRGS	KTKKKLEIDP	LHADTVRLIY
	210	220	230	240	250
	RLFLEGDGTR	GAMGVKAIAT	YLNERRFFTR	DGGRWGLAQI	HAILTRTTYI
	260	270	280	290	300
	GEHRFNTRSH	KDREKKPESE	IAIMAVPPLI	EREIYDAVQA	RLKSRNPMVT
25	310	320	330	340	350
	PARVSSGPTL	LTGICFCAKC	GGAMTLRTGQ	GSTGATYRYY	TCSTKARQ GK
	360	370	380	390	400
	TGCKGRTIPM	DKLDHLVADH	IGDRLLQPKR	LETVLASVID	RRQERAERRR
	410	420	430	440	450
30	EHLAELNRRI	TEADQRLGRL	FDAIEAGMVD	KDDAMAKERM	VSLKALRDQA
	460	470	480	490	500
	AADAERTQLA	LDSSGNQGV S	PDMLKGFARK	ARERIRLDDG	GYRRDHLRAL
	510	520	530	540	550
	AQRVEVADDE	VRIMGSKSEL	LRTLVAASSV	ETAAFGVQSS	VLKWRTQEDS
35					
	NLRPLGS (SEQ ID NO: 78)				

[52] In some embodiments, the orthologous serine recombinase is Pa570 recombinase,
 comprising an exemplary amino acid sequence below:

40

Wildtype Pa570

	10	20	30	40	50
	MARLISYLRM	STSEQLRGFS	LERQRKLIAD	FAAKNGLSVE	EENTLEDIGR
	60	70	80	90	100
45	SSFSDDAQQK	ELTRFFENLN	AGKYEPGDVF	ALENIDRLTR	RGPVDAILKV

	110	120	130	140	150
	NQIISKGLKL	AIISGNEQRI	IEDVNDVFTI	INLSIDASRA	NKESKNKSDK
	160	170	180	190	200
5	GLSNWQEKRN	LASTYKIAMT	AQAPAWLDTE	IFYIFDEEEKK	KNTKRRKYVL
	210	220	230	240	250
	NEEKAEAVRL	IFDLYSNGNG	ALKIKNILNE	RNIPTFKGAP	YWEPSIITKI
	260	270	280	290	300
	LKNPATFGLY	QPKKQGTGKR	DLIAAGEPIN	DYFPPVITRD	LFEQCEHIRE
	310	320	330	340	350
10	GNSTRKGRKG	KLFTNLFTGL	LTCSKCGGPV	HLINPGIDKR	NKVQKSIYYL
	360	370	380	390	400
	VCKRAKFTKE	CTTKRVRYDD	FEIALLKAIQ	EINLADILNE	NNPLEILVKK
	410	420	430	440	450
15	QRSKETEINK	KRKLIENFQR	QFLENDGDLP	SFMISQAKDA	EISIKELEED
	460	470	480	490	500
	QREIASEIAQ	LNIYNSNVDN	AIEELKENAD	YGTRSKINLL	FHEIKNISL
	510	520	530	540	550
	DTENQFYTVR	FKNGVMRVIT	AAGFIATTEE	QTQADINAIL	QSIEGPRIPR
	560	570			
20	EIATDAEKLI	EYLKAREVIE	(SEQ ID NO: 79)		

[53] In some embodiments, the orthologous serine recombinase is LI Integrase, comprising an exemplary amino acid sequence below:

25	Wildtype LI				
	10	20	30	40	50
	MKAAIYIRVS	TQEQVENYSI	QAQTEKLTAL	CRSKDWDVYD	TFIDGGYSGS
	60	70	80	90	100
30	NMNRPALNEM	LSKLHEIDAV	VVYRLDRLSR	SQKDTITLIE	EYFLKNNVEF
	110	120	130	140	150
	VSLSETLDTS	SPFGRAMIGI	LSVFAQLERE	TIRDRMVMGK	IKRIEAGLPL
	160	170	180	190	200
	TTAKGRFTGY	DVIDTKLYIN	EEEAKQLRLI	YDIFEEEQSI	TFLQKRLKKL
	210	220	230	240	250
35	GFKVRTYNRY	NNWLTNDLYC	GYVSYKDKVH	VKGIHEPIIS	EEQFYRVQEI
	260	270	280	290	300
	FSRMGKNPNM	NKESASLLNN	LVVCSKCGLG	FVHRRKDTVS	RGKKYHYRYY
	310	320	330	340	350
	SCKTYKHTHE	LEKCGNKIWR	ADKLEELIID	RVNNYSFASR	NIDKEDELDS
40	360	370	380	390	400
	LNEKLKIEHA	KKKRLFDLYI	NGSYEVSELD	SMMNDIDAQI	NYEEAQIEAN
	410	420	430	440	450
	EELKKNKKIQ	ENLADLATVD	FNSLEFREKQ	LYLKSLINKI	YIDGEQVTIE
45	WL (SEQ ID NO: 131)				

[54] In some embodiments, the orthologous serine recombinase is A118 Integrase, comprising an exemplary amino acid sequence below:

Wildtype A118

5	10	20	30	40	50
	MKAAIYIRVS	TQEQVENYSI	QAQTEKLTAL	CRSKDWDVYD	IFIDGGYSGS
	60	70	80	90	100
	NMNRPALNEM	LSKLHEIDAV	VVYRLDRLSR	SQRDTITLIE	EYFLKNNVEF
	110	120	130	140	150
10	VSLSETLDTS	SPFGRAMIGI	LSVFAQLERE	TIRDRMVMGK	IKRIEAGLPL
	160	170	180	190	200
	TTAKGRTPGY	DVIDTKLYIN	EEEAKQLQLI	YDIFEEEQSI	TFLQKRLKKL
	210	220	230	240	250
	GFKVRTYNRY	NNWLTNDLYC	GYVSYKDKVH	VKGIHEPIIS	EEQFYRVQEI
15	260	270	280	290	300
	FTRMGKNPNM	NRDSASLLNN	LVVCSKCGLG	FVHRRKDTMS	RGKKYHYRYY
	310	320	330	340	350
	SCKTYKHTHE	LEKCGNKIWR	ADKLEELIIN	RVNNYSFASR	NVDKEDELDS
	360	370	380	390	400
20	LNEKLKIEHA	KKKRLFDLYI	NGSYEVSELD	SMMNDIDAQI	NYYESQIEAN
	410	420	430	440	450
	EELKKNKKIQ	ENLADLATVD	FDSLEFREKQ	LYLKSLINKI	YIDGGEQVTIE
	WL (SEQ ID NO: 132)				

25

[55] In some embodiments, the orthologous serine recombinase is TP901 recombinase, comprising an exemplary amino acid sequence below:

Wildtype TP901

30	10	20	30	40	50
	MTKKVAIYTR	VSTTNQAEEG	FSIDEQIDRL	TKYAEAMGWQ	VSDTYTDAGF
	60	70	80	90	100
	SGAKLERPAM	QRLINDIENK	AFDTVLVYKL	DRLSRSVRDT	LYLVKDVFTK
	110	120	130	140	150
35	NKIDFISLNE	SIDTSSAMGS	LFLTILSAIN	EFERENIKER	MTMGKLGRAK
	160	170	180	190	200
	SGKSMMWTKT	AFGYHHNRKT	GILEIVPLQA	TIVEQIFTDY	LSGISLTKLR
	210	220	230	240	250
	DKLNESEGHIG	KDIPWSYRTL	RQTLNPNVYC	GYIKFKDSL	EGMHKPIIPY
40	260	270	280	290	300
	ETYLKVQKEL	EERQQQTYER	NNNRPFPQAK	YMLSGMARCG	YCGAPLKIVL
	310	320	330	340	350
	GHKRKDGSR	MKYHCANRFP	RKTKGITVYN	DNKKCDSTY	DLSNLENTVI
	360	370	380	390	400
45	DNLIGFQENN	DSLLKIINGN	NQPILDTSSF	KKQISQIDKK	IQKNSDLYLN

```

          410          420          430          440          450
DFITMDELKD RTDSLQAEKK LLKAKISENK FNDSTDVFEL VKTQLGSIPI
          460          470          480
NELSYDNKKK IVNNLVSKVD VTADNVDIIF KFQLA (SEQ ID NO: 133)

```

5

[56] An alignment of some of the above orthologous recombinases can be found in Figure 3 of Rutherford et al., *supra*.

[57] In some embodiments, the orthologous recombinase variant may comprise mutations within the ZD or RD. In some embodiments, the orthologous recombinase variant may comprise mutations within the NTD domain or CC coiled motif amino acid sequences. In some
 10 embodiments, the orthologous recombinase may comprise one or more mutations at positions that correspond to residues S231, T233, R237, F314, A315, G316, G318, and R325 of Bxb1 recombinase. For example, the ϕ C31 integrase variant may comprise one or more mutations at amino acid positions D273, A275, R279, K375, R376, G377, E379, and R386 (numbering
 15 according to SEQ ID NO: 77); the Pa557 recombinase variant may comprise one or more mutations at amino acid positions G236, A238, A242, R327, T328, G329, G331, and R338 (numbering according to SEQ ID NO: 78); and the Pa570 recombinase variant may comprise one or more mutations at amino acid positions E243, S245, K249, I333, N334, P335, I337, and Q344 (numbering according to SEQ ID NO: 79).

20 [58] In some embodiments, the system comprises a mixture of different Bxb1 recombinase variants and/or other orthologous serine recombinase variants, and/or the nucleic acids that encode them, as well as any associated donor DNA molecules.

[59] In some embodiments, the Bxb1 recombinase variant mediates increased transgene insertion at an endogenous target site in a eukaryotic genome, relative to wild-type Bxb1
 25 recombinase. In some embodiments, the Bxb1 recombinase variant increases transgene insertion at least 1-, 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 11-, 12-, 13-, 14-, 15-, 16-, 17-, 18-, 19-, or 20-fold, relative to wild-type Bxb1 recombinase.

B. Recombinase Variant Recognition Sites

[60] The present recombinase variants are collectively more versatile than their WT
 30 counterparts in that the variants can bind a wider repertoire of DNA recognition sites. The table below (**Table 3**) shows attB-like sequences that may be more efficiently bound by one or mixtures of the variants herein than by wildtype Bxb1 recombinase. The sequences in the table

below are SEQ ID NOs: 83 to 130, in the order of appearance. In the table, underlined nucleotides are center dinucleotides; “hg38 coordinates” refer to positions according to the Genome Reference Consortium Human Build 38 standard; and boldfaced and italicized nucleotides indicate mismatches to the consensus attB sequences below (for sites 1-14, this is SEQ ID NO: 82 (*see Examples*); for sites 15-24, this is SEQ ID NO: 134; for sites 25-36, this is SEQ ID NO: 135; and for sites 37-48, this is SEQ ID NO: 136):

5' -GGTTTGTNNACNACNGNNNNNNCNGTNGTNAGGATCNN (SEQ ID NO: 134)

5' -NNGATCCTGACGACNGNNNNNNCNGTNGTNACAAACC (SEQ ID NO: 135)

5' -NNGATCCTGACGACNGNNNNNNCNGTNGTNAGGATCNN (SEQ ID NO: 136)

Table 3. Endogenous Human Binding Sites for Wildtype Bxb1 Recombinase

SEQ ID NO	#	hg38 coordinates		Endogenous Human Sequence
83	1	chr18	23228819	<i>TGCTT</i> GTTG <i>CCT</i> ACAGCCTCTGCAG <i>AA</i> GTTCACAAAC <i>T</i>
84	2	chr21	39796718	GG <i>G</i> TTGTTGACTACAGATTGC <i>ACT</i> <i>ATT</i> <i>TT</i> GCAGAAACC
85	3	chr5	130870404	<i>TAG</i> TTGTAGACCACAGAAATTTCTG <i>CT</i> GTTCA <i>GAA</i> AC <i>T</i>
86	4	chr10	114431581	G <i>T</i> TTTGTGGACAA <i>TGG</i> TTTCCTCTG <i>CT</i> GTAA <i>GAA</i> AC <i>G</i>
87	5	chr4	78331600	GG <i>G</i> TTG <i>GT</i> GC <i>AA</i> <i>TGG</i> AGATCTCAGTGGTGA <i>AAA</i> <i>TCA</i>
88	6	chr3	21564386	<i>AG</i> CTTGTTTACA <i>TG</i> TGAATTTTCTGTAGTAAACA <i>CCA</i>
89	7	chr17	37733272	<i>TG</i> TTTGTAC <i>TCT</i> ACCGAAGATTCC <i>AT</i> AGTTAAACA <i>CCA</i>
90	8	chr7	37683631	<i>TAT</i> TT <i>CT</i> TGACAA <i>TTGG</i> CCTCTCTGTAGTTT <i>GCA</i> ACC <i>T</i>
91	9	chr9	94861248	GGTTTG <i>AGG</i> <i>GCAG</i> CAGCAGCTG <i>CT</i> GTCA <i>CCAA</i> ACA
92	10	chrX	50461727	G <i>T</i> TTTGTTC <i>ACT</i> <i>GTAGA</i> ATCCTCAGTGGTTAG <i>GCACA</i> AT
93	11	chr1	203596869	<i>CTCT</i> TGATGACT <i>GCAG</i> AGTATTCC <i>ATT</i> GTTGACAA <i>ATC</i>
94	12	chr5	35969016	<i>TG</i> TTT <i>CTCA</i> ACTACAGCATGAGCTGTGGTTGAC <i>AGTAA</i>
95	13	chr1	183975066	GATTTG <i>GATA</i> CA <i>CCT</i> GAGATGACAGTTGTCA <i>AGAAA</i> <i>TC</i>
96	14	chr6	120401383	<i>ATT</i> <i>GT</i> TTAACTACTGAGTTTTCAGTAGTTAA <i>AAAGC</i> <i>T</i>
97	15	chr2	131113644	GG <i>CT</i> <i>TTT</i> CA <i>TT</i> ACAGAACACCCAGTTGTCAG <i>TAT</i> CAG
98	16	chr18	68095661	<i>TTAT</i> TGTTGACAACTGATATTTC <i>AC</i> GGTGAG <i>AAT</i> CCC

SEQ ID NO	#	hg38 coordinates		Endogenous Human Sequence
99	17	chr10	95438042	GG G TT TT TAA A CACTGACTTGCCTG G TGTGAGGATCCA
100	18	chr11	93987223	A ATTTG C TGACAACAGGTGCTTCTGTGGTTAGGA G TGG
101	19	chr18	38351472	GG C TT TT AGACT G ATGAGTGATCAGTC TT CAGGATCCC
102	20	chr6	84802299	A TAGTGT TT TACC TC AGAA A GATCTGTGGTAAGGA C CAA
103	21	chrX	54472830	GGT G TGAGGACAA G AGAGTGAGCAGTAGTCA A GAG C TC
104	22	chr3	138022040	T GT A TGTGGACCA T AGGAAAAGCTG G AGTCAGGA G CTC
105	23	chr7	125717751	T GTTTGTGGAG G GA G TGATGGCTCAGTGGTA T GGATCTA
106	24	chr6	29957229	G C TTT TT TGACC TC GGCCTCCGCT C AGGTCAGGA C CAG
107	25	chr2	118918350	CTGAT A CTT G CAACTGAACACACTGTAGTCCACA C ACC
108	26	chr1	218729444	GAGATC TT G G CAA T AGGA A CCTCAG CT GT C AG C AA G CA
109	27	chr12	82686460	GAG TT TG TGACAACCGAAGCTGCAG C AGTCG C AAACC
110	28	chr1	12564817	TTG CT TCT CACC G TAGATGACCCT CT TGTCCACAAACC
111	29	chr14	33253493	CAG CT CCTCACA A CTGATTTCCCA A TGGTA A TC A G C T
112	30	chr5	168835161	GAGATCCTAG CC CACAGGCGGGCCC A GGGTTG G CAAACC
113	31	chr1	205211683	TGG CT CC CA ACC T CCGTCACTGCCGTTG CA AA C AAACC
114	32	chr17	51831373	AG AT TCCTGACTACAGTGGATGCTGTTGTTT G CA A TT C
115	33	chr7	73438826	CAG CT CCTGA AC ACAGCAGTCCCAG G TGTTGA AA A G CC
116	34	chr8	138569746	TTG G TC TT TACA A CTGGGGCTACTGTGGTGGTA TA TC G
117	35	chr7	26280167	CAG G TCCTGACC TC AGAGCCAGCTG GA ATGAA AA AACC
118	36	chr18	64064874	CAGAT G CTC T CCACAGGGTCTGCTG C AGTTTACA A TC C
119	37	chr15	26397212	ATGATCCTCACTACAGCTATGGCA A TTGTA TT GATCCT
120	38	chr11	121591710	GTG CT CCTAACAG G CAGGCGGAACAG A GGTGAGGATCCT
121	39	chr1	84080800	AAGATCCTGACC T CCGA A GAAGCTG G AGTT A AGATCAT
122	40	chr6	124844046	ATG G TCCCAG C TACTGGGGAGGCTG A GGTGAGGATCGC
123	41	chr3	194380608	TTG CT CCTCACAG G CAGAGGACTCTG A AG A CAGGA G CAT
124	42	chr21	38902753	TGGATC TT CACTA T GGCACTCCCA TT GGTA T GGATCTC

SEQ ID NO	#	hg38 coordinates		Endogenous Human Sequence
125	43	chr18	33954365	CAGATC T ATACG G CTGACTACACAGTGGTGAG AA CCAT
126	44	chr14	42626161	ATGATCCTCACAG G CAGATATATCTGTT CT CA AG AT TTA
127	45	chr10	27365656	ATGATC TT GACAACAGGGAGT G CTG GG TT C TG GA AC AT
128	46	chr4	9830819	CTGAT G CTGACCACAGCAA AT TGCTG CC AA CAGGATCCC
129	47	chr12	69787548	ATGATCCTAACT CT TGCTTTATCT ACT GTGA AA ATCAT
130	48	chr11	97082317	TTG G TCCTG GAT CCTGAGGTTGCTGTGGTGA AG ATCCC

[61] A wildtype Bxb1 recombinase or an ortholog thereof may be engineered as described above by, e.g., adopting the amino acid substitutions shown in **Tables 1** and **2**, such that the engineered protein can now bind with high affinity to these endogenous genomic target sites in human cells.

C. Donor DNA with Engineered attB or attP Sequences.

[62] The provided recombinase variants can integrate donor DNA (e.g., circularized donor DNA) into a host genome if the donor and host DNA include wildtype or variant attB and/or attP sequences. The present disclosure provides nucleic acid molecules comprising the variant attB and attP sequences recognized by the provided recombinase variants.

[63] In some embodiments, the attB sequences described herein comprise any one of the sequences of SEQ ID NOs: 83-130, as shown in **Table 3**. In some embodiments, the attB sequences described herein comprise any one of the sequences of SEQ ID NOs: 4-40, as shown in **Table 4**. In some embodiments, the attP sequences described herein comprise any one of the sequences of SEQ ID NOs: 41-76, as shown in **Table 5**. In some embodiments, the attB or attP sequences may comprise a sequence selected from SEQ ID NOs: 80-82 and 134-136.

D. Recombination Events

[64] Bxb1 recombinase can generate a range of dimers that recognize and specifically bind DNA recognition attB and attP sites. When the attB and attP sites are present in the same cell, a pair of Bxb1 recombinase dimers that bind the attB and attP sites form a tetramer, bringing together the DNA segments containing the attB and attP sites and initiating DNA recombination. When the DNA segments are on the same DNA molecule (e.g., chromosome), this recombination event can lead to DNA inversion or deletion. When the DNA segments are on

different DNA molecules, this recombination event may lead to DNA integration or cassette exchange. The present recombinase variants contain mutations that enable them to catalyze the recombination between variant attB and attP sequences, greatly expanding the repertoire of recognizable endogenous sites and increasing the versatility of the enzymes.

5 [65] The present recombinase variants can produce recombination events of interest, such as integration, inversion, excision, chromosome swap, and RMCE. **FIG. 3A** illustrates integration mediated by the recombinase variants of the present disclosure. Integration requires the presence of donor DNA with an attachment site that is compatible to the attachment site of the target DNA. **FIG. 3B** illustrates excision mediated by the recombinase variants of the present disclosure. Excision requires two complementary attachment sites similarly orientated on the same DNA molecule. **FIG. 3C** illustrates inversion mediated by the recombinase variants of the present disclosure. Inversion requires two complementary attachment sites oppositely orientated on the same DNA molecule. **FIG. 3D** illustrates chromosome swap mediated by the recombinase variants of the present disclosure. Chromosome swap requires two complementary attachment sites similarly orientated on two separate linear DNA molecules. **FIG. 3E** illustrates RMCE mediated by the recombinase variants of the present disclosure. RMCE requires donor and target DNA molecules each contain two complementary attachment sites that are not cross-compatible. For example, a donor DNA molecule containing gene X flanked by two different attB sites and a target DNA molecule containing gene Y flanked by two different attP sites where the compatible attachment sites upstream of gene X and Y are complementary and the compatible attachment sites downstream of genes X and Y are complementary, but the upstream and downstream sites are not cross-compatible. Cross-compatibility can be avoided, for example, by using different center dinucleotides in the upstream and downstream attachment sites. This system allows genes X and Y to be exchanged in the presence of the recombinase variants of the present disclosure. Only in the presence of the appropriate RDF can serine recombinases bind to attR and attL sites and mediate the reverse recombination event.

II. Delivery of Variant Recombinase Systems

30 [66] The Bxb1 recombinase variants or orthologous recombinase variants of the present disclosure may be introduced to target cells as a protein, through a variety of methods (e.g., electroporation, lipid nanoparticles, cationic or anionic liposomes, or a nuclear localization signal

(e.g., in combination with liposomes)). In some embodiments, a provided recombinase variant is introduced to target cells through a nucleic acid molecule encoding it, for example, a DNA plasmid or mRNA. The nucleic acid molecule may be in a nucleic acid expression vector, which may include expression control sequences such as promoters, enhancers, transcription signal sequences, and transcription termination sequences that allow expression of the coding sequence for the provided recombinase variants. "Delivery of a system" as described herein may refer to either delivery of a system comprising a Bxb1 recombinase variant or orthologous recombinase variant as described herein or delivery of nucleic acid molecules encoding said system of a provided recombinase variant or vectors or expression constructs comprising said nucleic acid molecules.

[67] In some embodiments, the promoter on the vector for directing a provided recombinase variant's expression is a constitutively active promoter or an inducible promoter. Suitable promoters include, without limitation, a Rous sarcoma virus (RSV) long terminal repeat (LTR) promoter (optionally with an RSV enhancer), a cytomegalovirus (CMV) promoter (optionally with a CMV enhancer), a CMV immediate early promoter, a simian virus 40 (SV40) promoter, a dihydrofolate reductase (DHFR) promoter, a β -actin promoter, a phosphoglycerate kinase (PGK) promoter, an EFl α promoter, a Moloney murine leukemia virus (MoMLV) LTR, a creatine kinase-based (CK6) promoter, a transthyretin promoter (TTR), a thymidine kinase (TK) promoter, a tetracycline responsive promoter (TRE), a hepatitis B Virus (HBV) promoter, a human α 1-antitrypsin (hAAT) promoter, chimeric liver-specific promoters (LSPs), an E2 factor (E2F) promoter, the human telomerase reverse transcriptase (hTERT) promoter, a CMV enhancer/chicken β -actin/rabbit β -globin promoter (CAG promoter; Niwa et al., *Gene* (1991) 108(2):193-9), and an RU-486-responsive promoter. In addition, the promoter may include one or more self-regulating elements whereby a provided recombinase variant can bind to and repress its own expression level to a preset threshold.

[68] Any method of introducing the nucleotide sequence into a cell may be employed, including but not limited to, electroporation, calcium phosphate precipitation, microinjection, cationic or anionic liposomes, liposomes in combination with a nuclear localization signal, naturally occurring liposomes (e.g., exosomes), or viral transduction. In certain embodiments, the nucleotide sequence is in the form of mRNA and is delivered to a cell via electroporation.

[69] For *in vivo* delivery of an expression vector, viral transduction may be used. A variety of viral vectors known in the art may be adapted by one of skill in the art for use in the present disclosure, for example, vaccinia vectors, adenoviral vectors, lentiviral vectors, poxviral vectors, adeno-associated viral (AAV) vectors, retroviral vectors, and hybrid viral vectors. In some embodiments, the viral vector used herein is a recombinant AAV (rAAV) vector. Any suitable AAV serotype may be used. For example, the AAV may be AAV1, AAV2, AAV3, AAV3b, AAV4, AAV5, AAV6, AAV7, AAV8, AAV8.2, AAV9, AAV.PHP.B, AAV.PHP.eB, or AAVrh10, or of a novel serotype or a pseudotype such as AAV2/8, AAV2/5, AAV2/6, AAV2/9, or AAV2/6/9. In some embodiments, the expression vector is an AAV viral vector and is introduced to the target human cell by a recombinant AAV virion whose genome comprises the construct, including having the AAV Inverted Terminal Repeat (ITR) sequences on both ends to allow the production of the AAV virion in a production system such as an insect cell/baculovirus production system or a mammalian cell production system. The AAV may be engineered such that its capsid proteins have reduced immunogenicity or enhanced transduction ability in humans. Viral vectors described herein may be produced using methods known in the art. Any suitable permissive or packaging cell type may be employed to produce the viral particles. For example, mammalian (e.g., 293) or insect (e.g., sf9) cells may be used as the packaging cell line.

[70] Any type of cell may be targeted for the gene editing methods described herein. For example, the cells may be eukaryotic or prokaryotic. In some embodiments, the cells are mammalian (e.g., human) cells or plant cells. Human cells may include, for example, T cells, Natural Killer (NK) cells, NK T cells, alpha-beta T cells, gamma-delta T-cells, cytotoxic T lymphocytes (CTL), regulatory T cells, B cells, human embryonic stem cells, tumor-infiltrating lymphocytes (TIL) or a pluripotent stem cell from which lymphoid cells may be differentiated (e.g., an induced pluripotent stem cell (iPSC)). In some embodiments, the systems can be used to modify pluripotent stem cells prior to their differentiation into multiple cell types. For example, a lymphoid cell precursor may be modified prior to differentiation into lymphoid cell types such as regulatory T cells, effector T cells, natural killer cells, etc. Systems of the present disclosure comprising more than one Bxb1 recombinase variant or orthologous recombinase variant, in particular, can be used to prepare cells with multiple integrated, excised, or inverted

genes at once, including pluripotent cells. In some embodiments, systems containing more than one of the provided recombinase variants may be used to prepare, e.g., allogeneic T cells.

[71] For agricultural applications, any method for introduction of proteins or nucleic acid molecules to a plant cell is also contemplated, such as *Agrobacterium tumefaciens*-mediated T-DNA delivery.

III. Therapeutic Applications

[72] The present disclosure provides methods of integrating, excising, and inverting a gene or sequence of DNA in cellular DNA, comprising delivering a Bxb1 recombinase variant or orthologous recombinase variant system described herein to a cell (e.g., from a patient). The cell may be within a patient (*in vivo* treatment), or a method as described herein may be performed on a cell removed from a patient and then the edited cell delivered to the patient (*ex vivo* treatment). In some embodiments, the cells are further manipulated *ex vivo* prior to use as a treatment. The term “treating” encompasses alleviation of symptoms, prevention of onset of symptoms, slowing of disease progression, improvement of quality of life, and increased survival. In some embodiments, a patient treated by the methods described herein is a mammal, e.g., a human.

[73] In some embodiments, the methods of the present disclosure are used to insert or excise a gene or regulatory sequence associated with a disease towards restoring normal gene expression or activity. In some embodiments, the methods of the present disclosure may target a particular allele of a gene, e.g., a wild-type or mutated allele. In certain embodiments, the allele may be associated with cancer.

[74] In some embodiments, the patient has cancer. In certain embodiments, the cell from the patient is further modified before or after gene editing to provide resistance to a chemotherapeutic agent. The patient may then be treated with the chemotherapeutic agent, which in some embodiments may result in greater survival of edited over unedited cells.

[75] In some embodiments, the patient has an autoimmune disorder.

[76] In some embodiments, the patient has an autosomal dominant disease, such as autosomal dominant polycystic kidney disease.

[77] In some embodiments, the patient has a neuro-developmental disorder.

[78] In some embodiments, the patient has a mitochondrial disorder.

[79] In some embodiments, the patient has sickle cell disease, hemophilia (e.g., hemophilia A, B, or C), cystic fibrosis, phenylketonuria, Tay-Sachs, prion disease, color blindness, a lysosomal storage disease (e.g., Fabry disease), Friedreich's ataxia, prostate cancer, beta thalassemia, Huntington's disease, renal transplant, inflammatory bowel disease, multiple sclerosis, amyotrophic lateral sclerosis, or frontotemporal dementia.

[80] The present disclosure further provides a pharmaceutical composition comprising elements of the gene editing system described herein, such as a Bxb1 recombinase variant or orthologous recombinase variant, or nucleotide sequences encoding said elements (e.g., in viral or non-viral vectors as described herein). The pharmaceutical composition may further comprise a pharmaceutically acceptable carrier such as water, saline (e.g., phosphate-buffered saline), dextrose, glycerol, sucrose, lactose, gelatin, dextran, albumin, or pectin. In addition, the composition may contain auxiliary substances, such as, wetting or emulsifying agents, pH-buffering agents, stabilizing agents, or other reagents that enhance the effectiveness of the pharmaceutical composition. The pharmaceutical composition may contain delivery vehicles such as liposomes, nanocapsules, microparticles, microspheres, lipid particles, and vesicles.

[81] In some embodiments, the provided recombinase variants described herein may be used in a method of treatment described herein, may be for use in a treatment described herein, or may be used in the manufacture of a medicament for a treatment described herein.

[82] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present disclosure. In case of conflict, the present specification, including definitions, will control. Generally, nomenclature used in connection with, and techniques of neurology, medicine, medicinal and pharmaceutical chemistry, and cell biology described herein are those well-known and commonly used in the art. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Throughout this specification and embodiments, the words "have" and "comprise," or variations such as

“has,” “having,” “comprises,” or “comprising,” will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. All publications and other references mentioned herein are incorporated by reference in their entirety. Although a number of documents are cited herein, this citation does not constitute an admission that any of these documents forms part of the common general knowledge in the art. As used herein, the term “approximately” or “about” as applied to one or more values of interest refers to a value that is similar to a stated reference value. In certain embodiments, the term refers to a range of values that fall within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context.

[83] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLES

Example 1: attB and attP Plasmid Variants

[84] The following are the wildtype Bxb1 recombinase consensus target sequences (the underlined sequence 5'-GGTTTGT is the ZD domain binding site, the underlined sequence 5'-ACNACNG is the RD domain binding site, and the center dinucleotide position is shown as XX in bold):

attP Consensus:

5' -GGTTTGTNNNNNNNACNACNGNN**XX**NNCNGTNGTNNNNNNNACAAACC
CCAAACANNNNNNNNTGNTGNCNN**XX**NNGNCANCANNNNNNNNNNTGTTTGG-5' (SEQ ID
NO: 81)

attB Consensus:

5' -GGTTTGTNNACNACNGNN**XX**NNCNGTNGTNNACAAACC
CCAAACANNTGNTGNCNN**XX**NNGNCANCANNTGTTTGG-5' (SEQ ID NO: 82)

[85] To simplify searching for Bxb1 recombinase variants with altered target DNA specificity, a more symmetric version of the Bxb1 attB target site was created (**Table 4**; see SEQ

ID NO: 2 for the wildtype attB site). This facilitated the creation of symmetric mutations to both halves of the attB target site. As the wildtype attP site is already palindromic at the ZD and RD domain binding sites (see SEQ ID NO: 3), a palindromic version did not have to be created. As with the attB plasmid variants, the individual nucleotides of the binding domains were mutated to produce a construct with each nucleotide available (**Table 5**), as shown in bold for mutations at positions 9 and 10 below (outer and inner underlined sequences are bound by ZD and RD domains, respectively; center dinucleotides are italicized). “SEQ” in the tables refer to SEQ ID NOs.

10 Mutations at position 10:

		SEQ ID NO
15	attB	<u>GGTTTGT</u> <u>CGACGACGGCGGTCTCCGTCGTCAACAAACC</u> 80
		<u>GGTTTGT</u> <u>CG</u> <u>CCGACGGCGGTCTCCGTCG</u> <u>G</u> <u>CAACAAACC</u> 252
		<u>GGTTTGT</u> <u>CG</u> <u>GCGACGGCGGTCTCCGTCG</u> <u>C</u> <u>CAACAAACC</u> 253
		<u>GGTTTGT</u> <u>CG</u> <u>TCGACGGCGGTCTCCGTCG</u> <u>A</u> <u>CAACAAACC</u> 254
20	attP	<u>GGTTTGTCTGGTCA</u> <u>ACCACCGCGGTCTCAGTGGTGTACGGT</u> <u>ACAAACC</u> 3
		<u>GGTTTGTCTGGTCA</u> <u>CCCACCGCGGTCTCAGTGG</u> <u>G</u> <u>GTACGGT</u> <u>ACAAACC</u> 255
		<u>GGTTTGTCTGGTCA</u> <u>GCCACCGCGGTCTCAGTGG</u> <u>C</u> <u>GTACGGT</u> <u>ACAAACC</u> 256
		<u>GGTTTGTCTGGTCA</u> <u>TCCACCGCGGTCTCAGTGG</u> <u>A</u> <u>GTACGGT</u> <u>ACAAACC</u> 257

Mutations at position 9:

25	attB	<u>GGTTTGT</u> <u>CGACGACGGCGGTCTCCGTCGTCAACAAACC</u> 80
		<u>GGTTTGT</u> <u>CGA</u> <u>AGACGGCGGTCTCCGTCT</u> <u>T</u> <u>CAACAAACC</u> 258
		<u>GGTTTGT</u> <u>CGA</u> <u>GGACGGCGGTCTCCGTCT</u> <u>C</u> <u>CAACAAACC</u> 259
		<u>GGTTTGT</u> <u>CGA</u> <u>TGACGGCGGTCTCCGTCA</u> <u>T</u> <u>CAACAAACC</u> 260
30	attP	<u>GGTTTGTCTGGTCA</u> <u>ACCACCGCGGTCTCAGTGGTGTACGGT</u> <u>ACAAACC</u> 3
		<u>GGTTTGTCTGGTCA</u> <u>ACACCGCGGTCTCAGTGT</u> <u>T</u> <u>GTACGGT</u> <u>ACAAACC</u> 261
		<u>GGTTTGTCTGGTCA</u> <u>AGCACCGCGGTCTCAGTG</u> <u>C</u> <u>TGTACGGT</u> <u>ACAAACC</u> 262
		<u>GGTTTGTCTGGTCA</u> <u>ATCACCGCGGTCTCAGTGA</u> <u>T</u> <u>GTACGGT</u> <u>ACAAACC</u> 263

Table 4. Variant attB Sequences

SEQ	Description	Sequence
4	Bxb1_AttB_P alindrome	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTCTC GACGACGGCGGTCTCCGTCGTCAACAAACCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG

SEQ	Description	Sequence
5	Bxb1_AttB_t GTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAtGTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAACaCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
6	Bxb1_AttB_c GTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAcGTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAACgCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
7	Bxb1_AttB_a GTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAaGTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAACtCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
8	Bxb1_AttB_G tTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGtTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAAaCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
9	Bxb1_AttB_G cTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGcTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAAgCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
10	Bxb1_AttB_G aTTTGTGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGaTTTGTCTC GACGACGGCGGTCTCCGTCTGCTCAACAAAtCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
11	Bxb1_AttB_G GgTTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGgTTGTC GACGACGGCGGTCTCCGTCTGCTCAACAAcCCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
12	Bxb1_AttB_G GaTTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGaTTGTC GACGACGGCGGTCTCCGTCTGCTCAACAAAtCCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
13	Bxb1_AttB_G GcTTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGcTTGTC GACGACGGCGGTCTCCGTCTGCTCAACAAgCCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
14	Bxb1_AttB_G GTgTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTgTGTC GACGACGGCGGTCTCCGTCTGCTCAACAcACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
15	Bxb1_AttB_G GTaTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTaTGTC GACGACGGCGGTCTCCGTCTGCTCAACAtACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
16	Bxb1_AttB_G GTcTGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTcTGTC GACGACGGCGGTCTCCGTCTGCTCAACAgACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
17	Bxb1_AttB_G GTTgGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTgGTC GACGACGGCGGTCTCCGTCTGCTCAACcAACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
18	Bxb1_AttB_G GTTaGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTaGTC GACGACGGCGGTCTCCGTCTGCTCAACtAACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
19	Bxb1_AttB_G GTTcGTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTcGTC GACGACGGCGGTCTCCGTCTGCTCAACgAACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
20	Bxb1_AttB_G GTTTtTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTtTC GACGACGGCGGTCTCCGTCTGCTCAAAaAAACCCCGGCAGATAAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG

SEQ	Description	Sequence
21	Bxb1_AttB_G GTTTcTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTcTC GACGACGGCGGTCTCCGTCTGCTCAAgAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
22	Bxb1_AttB_G GTTTaTCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTaTC GACGACGGCGGTCTCCGTCTGCTCAAtAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
23	Bxb1_AttB_G GTTTGgCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGgC GACGACGGCGGTCTCCGTCTGCTCAcCAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
24	Bxb1_AttB_G GTTTGaCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGaC GACGACGGCGGTCTCCGTCTGCTCaTCAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
25	Bxb1_AttB_G GTTTGcCGACG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGcC GACGACGGCGGTCTCCGTCTGCTCAgCAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
26	Bxb1_AttB_G GTTTGTCGtCG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GtCGACGGCGGTCTCCGTCTGcCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
27	Bxb1_AttB_G GTTTGTCGgCG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GgCGACGGCGGTCTCCGTCTGcCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
28	Bxb1_AttB_G GTTTGTCGcCG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GcCGACGGCGGTCTCCGTCTGgCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
29	Bxb1_AttB_G GTTTGTCGAgG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GAgGACGGCGGTCTCCGTCTcTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
30	Bxb1_AttB_G GTTTGTCGAtG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GAtGACGGCGGTCTCCGTCTaTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
31	Bxb1_AttB_G GTTTGTCGAaG ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GAaGACGGCGGTCTCCGTCTtTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
32	Bxb1_AttB_G GTTTGTCGACt ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GACtACGGCGGTCTCCGTaGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
33	Bxb1_AttB_G GTTTGTCGACc ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GACcACGGCGGTCTCCGTgGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
34	Bxb1_AttB_G GTTTGTCGACa ACGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GACaACGGCGGTCTCCGTtGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
35	Bxb1_AttB_G GTTTGTCGACG tCGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GACGtCGGCGGTCTCCGCaCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
36	Bxb1_AttB_G GTTTGTCGACG gCGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTC GACGgCGGCGGTCTCCGcCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG

SEQ	Description	Sequence
37	Bxb1_AttB_G GTTTGTGACG cCGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTCTC GACGcCGGCGGTCTCCGgCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
38	Bxb1_AttB_G GTTTGTGACG AgGGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTCTC GACGAgGGGCGGTCTCCcTCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
39	Bxb1_AttB_G GTTTGTGACG AtGGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTCTC GACGAtGGGCGGTCTCCaTCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG
40	Bxb1_AttB_G GTTTGTGACG AaGGGCGGT	ATGCTTCTCTGCATCCGTCTGCTAAATCCGCGTGATAGGGGAGGTTTGTCTC GACGAaGGGCGGTCTCctTCGTCAACAAACCCCGGCAGATAAAAGTACCCA GAACCAGAGCCTACAATACCGGCCCTGGGAATATAAG

Table 5. Variant attP Sequences

SEQ	Description	Sequence
41	AttP_TCCAC	GGTTTGTCTGGTCATCCACCGCGGTCTCAGTGGAGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
42	AttP_CCCAC	GGTTTGTCTGGTCACCCACCGCGGTCTCAGTGGGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
43	AttP_GCCAG	GGTTTGTCTGGTCAGCCACCGCGGTCTCAGTGGCGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
44	AttP_AACAC	GGTTTGTCTGGTCAAACACCGCGGTCTCAGTGTTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
45	AttP_ATCAC	GGTTTGTCTGGTCAATCACCAGCGGTCTCAGTGATGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
46	AttP_AGCAC	GGTTTGTCTGGTCAAGCACCAGCGGTCTCAGTGCTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
47	AttP_ACTAC	GGTTTGTCTGGTCAACTACCGCGGTCTCAGTAGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
48	AttP_ACAAC	GGTTTGTCTGGTCAACAACCGCGGTCTCAGTTGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
49	AttP_ACGAC	GGTTTGTCTGGTCAACGACCGCGGTCTCAGTCGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
50	AttP_ACCTC	GGTTTGTCTGGTCAACCTCCGCGGTCTCAGAGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG

SEQ	Description	Sequence
51	AttP_ACCCC	GGTTTGTCTGGTCAACCCCCGCGGTCTCAGGGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
52	AttP_ACCGC	GGTTTGTCTGGTCAACCGCCGCGGTCTCAGCGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
53	AttP_ACCAG	GGTTTGTCTGGTCAACCAGCGCGGTCTCACTGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
54	AttP_ACCAT	GGTTTGTCTGGTCAACCATCGCGGTCTCAATGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
55	AttP_ACCAA	GGTTTGTCTGGTCAACCAACGCGGTCTCATTGGTGTACGGTACAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
56	AttP_CGTTTGT	CGTTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAACG CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
57	AttP_TGTTTGT	TGTTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAACA CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
58	AttP_AGTTTGT	AGTTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAACT CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
59	AttP_GCTTTGT	GCTTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAAGC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
60	AttP_GTTTTGT	GTTTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAAAC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
61	AttP_GATTTGT	GATTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAATC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
62	AttP_GGATTGT	GGATTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAATCC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
63	AttP_GGCTTGT	GGCTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAAGCC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
64	AttP_GGGTTGT	GGGTTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAACCC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
65	AttP_GGTCTGT	GGTCTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACAGACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
66	AttP_GGTGTGT	GGTGTGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACACACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG

SEQ	Description	Sequence
67	AttP_GGTATGT	GGTATGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACATACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
68	AttP_GGTTAGT	GGTTAGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACTAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
69	AttP_GGTTTCGT	GGTTTCGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACGAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
70	AttP_GGTTGGT	GGTTGGTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTACCAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
71	AttP_GGTTTTT	GGTTTTTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTAAAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
72	AttP_GGTTTAT	GGTTTATCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTATAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
73	AttP_GGTTTCT	GGTTTCTCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTAGAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
74	AttP_GGTTTGA	GGTTTGA CTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTTCAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
75	AttP_GGTTTGC	GGTTTGCCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTGCAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG
76	AttP_GGTTTGG	GGTTTGGCTGGTCAACCACCGCGGTCTCAGTGGTGTACGGTCCAAACC CAATAAAAGTACCCAGAACCAGAGCCTACAATACCGGCCCTGGGAATA TAAG

Example 2: Initial Serine Scan Screen

[86] Individual constructs with serine scan mutations were generated from a pVax vector that expresses Bxb1 recombinase driven by a CMV promoter. The Bxb1 recombinase construct included the amino acid sequence GSGSGSHHHHHGSGPKKKRKV (SEQ ID NO: 249) at the C terminal end. Individual constructs matching SEQ ID NOs: 2-76 were generated in a non-expression plasmid. Sets of constructs were pooled together such that all four bases at a specific site were in equal concentration (e.g., plasmids with attP SEQ ID NOs: 3, 41, 42, and 43 were pooled together and SEQ ID NOs: 3, 44, 45, and 46 were pooled together; plasmids with attB SEQ ID NOs: 4, 5, 6, and 7 were pooled together and SEQ ID NOs: 4, 8, 9, and 10 were pooled together).

[87] K562 cells were transfected following the manufacturer's protocol. 2E5 cells were transfected with 200ng of Bxb1 expression plasmid, 20ng total of attB plasmid, and 1600ng total of attP plasmid. The attB plasmids had 5ng each of pooled nucleotide mutants at a specific site. For example, when testing base 24 (**FIG. 2**), SEQ ID NOs: 4, 5, 6, and 7 were pooled, such that 5ng of each were delivered in 20ng of total attB plasmid. In that same well, SEQ ID NOs: 3, 56, 57, and 58 were pooled, such that 400ng of each were delivered in 1600ng total of attP plasmid.

[88] Individual expression plasmids with the mutations M244S, L245S, G246S, Y247S, A248S, L250S, N251S, G252S, K253S, T254S, V255S, R256S, D257S, D258S, D259S, G260S, A262S, K284S, T285S, S286A, R287S, A288S, K289S, P290S, A291S, V292S, S293A, T294S, P295S, S296A, L297S, L298S, L299S, R300S, V301S, A311S, Y312S, K313S, F314S, A315S, G316S, G317S, G318S, R319S, K320S, H321S, P322S, R323S, Y324S, R325S, C326S, R327S, S328A, M329S, G330S, F331S, P332S, K333S, H334S, C335S, E445S, Q446S, D447S, A449S, A450S, K451S, Y452S, T453S, W454S, L455S, R456S, M458S, N459S, and V460S were transfected across libraries for all seven nucleotides thought to be recognized by the ZD domains.

[89] Individual expression plasmids with the mutations I137S, K138S, E139S, R140S, N141S, R142S, S143A, A144S, A145S, H146S, F147S, N148S, I149S, R150S, A151S, G152S, K153S, Y154S, R155S, G156S, S157A, L158S, P159S, P160S, H195S, E196S, P197S, L198S, H199S, L200S, V201S, E229S, W230S, S231A, A232S, T233S, A234S, L235S, K236S, R237S, S238A, M239S, M244S, L245S, G246S, Y247S, A248S, T249S, L250S, N251S, G252S, K253S, T254S, V255S, R256S, D257S, D258S, D259S, G260S, A262S, K284S, T285S, S286A, R287S, A288S, K289S, P290S, A291S, V292S, S293A, T294S, P295S, S296A, L297S, L298S, L299S, R300S, V301S, A311S, Y312S, K313S, F314S, A315S, G316S, G317S, G318S, R319S, K320S, H321S, P322S, R323S, Y324S, R325S, C326S, R327S, S328A, M329S, G330S, F331S, P332S, K333S, H334S, and C335S were transfected across nucleotide mutant libraries spanning the five bases thought to be recognized by the RD domain (see **FIG. 2**).

[90] Transfected cells were harvested after three days of incubation at 37°C using QuickExtract™ by Lucigen (Cat No: QE09050) following the manufacturer's protocol. A polymerase chain reaction (PCR) was performed on the extracted DNA using Invitrogen's Accuprimer™ Taq DNA Polymerase, high fidelity (cat no: 12346094), as shown in **Table 6** below.

Table 6. NGS PCR1 Setup

Reagent	1x (μl)	MM (μl)
10x AccuPrime™ Buffer II	2.5	275
10 μM fw oligo	1	110
10 μM rev oligo	1	110
AccuPrime™ Taq (HiFi)	0.2	22
H ₂ O	17.3	1903
gDNA	3	
Total	25	2420
Rxns: 110	Aliquot 22.0 μl of MM	
	Add 3.0 μl of gDNA	

- 5 [91] The PCR was performed using the primers shown in **Table 7** below, where P1 and P2 refer to primers 1 and 2, respectively.

Table 7. NGS PCR1 primers

	SEQ ID NO	
P1	250	ACACGACGCTCTTCCGATCTNNNNATGCTTCTCTGCATCCGTCT
P2	251	GACGTGTGCTCTTCCGATCTAGGGAATAGATGACATCAAAGAGAA

- 10 [92] The PCR was performed using the temperature cycling protocol in **Table 8** below. The format of the time is minutes:seconds.

Table 8. NGS PCR1 Program

Temperature	Time	
95 °C	5:00	
95 °C	0:30	30x
55 °C	0:30	
68 °C	0:40	
68 °C	10:00	
4 °C	∞	

[93] The product of next generation sequencing (NGS) PCR1 was used as the template for NGS PCR2, as shown in **Table 9** below.

Table 9. NGS PCR2 Setup

Reagent	1x (μl)	MM (μl)
2x Phusion™ HiFi PCR MM w/ HF buffer	10	1100
10 μM fw oligo (N5xx)	1	110
10 μM rev oligo (Index)	1	
H ₂ O	6.5	715
gDNA	1.5	
Total	20	1925
Rxns: 110	Aliquot 17.5 μl of MM	
	Add 1 μl of Index oligo	
	Add 1.5 μl of PCR #1	

5

[94] The PCR was performed using the temperature cycling protocol in **Table 10** below. The format of the time is minutes:seconds.

Table 10. NGS PCR2 Program

Temperature	Time	
98 °C	0:30	
98 °C	0:10	12x
60 °C	0:30	
72 °C	0:40	
72 °C	10:00	
4 °C	∞	

10

[95] The primers used are universal primers that add on the required DNA sequences for Illumina Sequencing machines. NGS PCR2 products were purified and sequenced on Illumina Sequencing machines.

[96] Sequences were analyzed for changes in specificity at the nucleotide sites that were pooled together. For example, for the samples tested with nucleotide 21, integration events that differed from the percentages seen by wild-type Bxb1 recombinase were examined and documented (**FIG. 4**).

15

Example 3: Saturation Mutagenesis of Identified Residues

[97] Saturation mutagenesis was performed at amino acids that showed a different integration profile during the serine scan of Example 2. These differences ranged from eliminating integration, relaxing specificity, increasing specificity, or changing specificity. Sites selected for saturation mutagenesis included F147, N148, I149, Y154, R155, G156, L158, P197, L198, W230, S231, A232, T233, R237, D257, E309, Y312, F314, A315, G316, G318, R323, Y324, R325, C326, and C335. K562 transfections and NGS analysis were performed in the same manner described in Example 2 (**FIG. 4**).

[98] A summary of the results of saturation mutagenesis in the RD domain of Bxb1 recombinase is shown in **Table 11** below. “Specificity shift” refers to as the largest shift towards a non-WT nucleotide for a given mutant at a given position. For example, if WT Bxb1 recombinase has the following preference at position 9: 4.5% A, 85.6% C, 1.0% G, and 8.9% T, and if the R237A mutant has the following preferences at position 9: 23.6% A, 1.9% C, 17.1% G, and 57.4% T, then the largest shift towards a non-WT nucleotide is for T (57.4% - 8.9% = 48.5% change); R237A has a specificity shift at position 9 of 48.5%. The “average % specificity shift” is the average of the specificity shift for all mutants at a given amino acid position. “%TI” refers to the percent of successful targeted integration; it is calculated as the percent of sequence reads that had a sequence consistent with integration of the donor sequence, over the total sequence reads. In %TI for mutant a class (e.g., R237X) is the average for %TI for all members of that class (e.g., the average %TI for R237A, R237C, R237D, etc.) WT is the average of four replicates. In tables 11 and 12 below, “%TI” for a mutant class (e.g., R237X) is the average %TI for all members of that class (e.g., the average %TI for R237A, R237C, R237D, etc.), and WT is the average of four replicates.

Table 11. Bxb1 RD Domain Saturation Mutagenesis Results

	Interesting Mutants	%TI	Average % Specificity Shift				
			A	C	N	A	C
WT	NA	77.4	0.0	0.0	0.0	0.0	0.0
F147X	3	33.1	8.4	10.7	4.6	9.4	18.9
N148X	2	61.8	2.5	2.7	1.1	2.7	4.5
I149X	0	8.4	0.0	0.0	0.0	0.0	0.0
Y154X	0	8.3	0.0	0.0	0.0	0.0	0.0
R155X	0	15.7	0.0	0.0	0.0	0.0	0.3

G156X	0	0.1	0.0	0.0	0.0	0.0	0.0
L158X	5	50.6	0.0	0.0	5.3	9.4	5.3
P197X	3	76.8	2.2	2.3	0.7	1.9	2.5
L198X	0	59.6	0.0	0.0	0.0	0.0	0.0
W230X	0	39.5	0.4	0.0	1.0	0.0	0.0
S231X	7	50.2	11.4	0.0	0.0	0.0	0.0
A232X	0	70.9	0.2	0.0	0.9	0.5	1.3
T233X	6	64.4	8.8	2.1	0.0	2.4	5.1
R237X	19	28.4	0.0	47.6	0.0	0.0	0.0
D257X	0	74.5	5.4	3.9	3.3	4.1	6.1

[99] A summary of the results of saturation mutagenesis in the ZD domains of Bxb1 recombinase is shown in **Table 12** below.

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Table 12. Bxb1 ZD Domain Saturation Mutagenesis Results

Substitutions	Interesting Mutants	%TI	Average % Specificity Shift						
			G	G	T	T	T	G	T
WT	NA	82.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
E309X	0	79.9	1.0	0.5	0.2	0.7	1.4	0.5	4.0
Y312X	0	25.5	0.0	0.0	0.1	0.8	0.6	0.8	8.3
F314X	15	35.7	1.4	1.2	18.5	59.8	7.5	13.8	8.7
A315X	18	82.6	4.6	5.5	8.3	6.7	1.1	2.8	5.1
G316X	4	67.0	5.0	25.8	11.8	24.9	0.1	0.2	0.0
G318X	2	79.1	7.7	2.4	3.9	4.7	2.5	0.6	1.2
R323X	2	8.2	4.3	4.5	5.2	3.6	0.2	0.6	0.0
Y324X	0	41.0	2.5	0.0	0.0	0.0	0.0	0.0	0.0
R325X	9	6.5	0.0	0.0	0.4	0.4	30.4	4.6	19.1
C326X	0	3.3	0.5	0.0	8.2	0.0	0.0	0.0	0.0
C335X	0	5.9	0.3	0.0	7.9	10.2	0.0	0.0	0.0

Detailed results for S231F at position 10 and WT Bxb1 from a side-by-side experiment are shown in **FIG. 6A**, and detailed results for F314G and G316Y at positions 19 and 21, respectively, are shown in **FIG. 8A**.

10

Example 4: Bxb1-Mediated Targeted Integration at Endogenous Sites in Human Cells

[100] The performance of Bxb1 variants was characterized at a panel of endogenous Bxb1 sites where wild-type Bxb1 enables detectable integration activity (**FIG. 5**).

[101] Bxb1 recombinase pseudo-attB target sequences in the human genome are shown in **Table 13** below; the pseudo-attB site is flanked by five nucleotides on the 5' and 3' end, and the center dinucleotide position is shown in bold.

5

Table 13. Endogenous Bxb1 Pseudo-attB Target Sequences

SEQ	Site	Bxb1 Target
137	s5-1	CCATTCCCTTCTTCTACACAGCG TT CTCAATTGGGTAAGCATCAAAAT
138	s5-2	TTTAGTTGCTCCTGACAGCAGTG GG AGCTATTGTCTAAGAGATACAAA
139	s5-4	GGAGTTGAGTCCTGACTGCAGC CA TGCAGGTGAGGAAGCAGTAGAAG
140	s5-6	TACTGGGGATTCCCATAACCGTG CA CTCAGCTGCGGGAAGGCAGGAGA
141	s5-8	GAGTAGTGTATCTGACACCAGC CA CTCTGGTGTGAGAATCTTGGGTT
142	s5-10	ATAGTGAACTTACAACACAGAG TT TCCAGTTGTTCAATCTCTCTTGT
143	s5-11	TTGAAGCCCCTTCTCCTACAGAG CA AGCAGCAGGGTAAATTCTGTATT
144	s5-14	TGGTGCAATCTTGGCTCACTGCA AC CTCTGCAGTTGAAGCAATTCTCC
145	s5-15	ATTTGTGGTACTATACTACAGAG AA TGCTGATGTTAAAGAGCTAATTT
146	s5-16	GCACTCCAGCCTGGGCAACAGAG CA CTCTGTTGTCAAAAAAAAAAAAAA
147	s5-17	ACACCTGGATCTCCACCCCTGTG TT TGCTGTTGTCTAAGTTTTACATT
148	s5-18	CCGTCATGTTCCCTACACAGCT AA CCCAAGTCTTCAAACTCACTTAA
149	s5-19	GGCCTCCTGCTTGCTCAGCTGAG AC GGCAGAGGCTGAAGCTGCACGGG
150	s5-21	CTTCCTTCTTTTAAACCACTGAT CA TGCAGAAGTATAAGCTCACCACT
151	s5-24	GTGGCAGAAATAGTACAACAGCT AA CGCAGATGTTAAAAATCAAATGG
152	s1-1	CAGTGTGCTTGTGCTACAGCC TC TGCAGAAGTTCACAACTTGCAC
153	s1-5	ATTAGGGGTTGGTGGCAATGGAG AT CTCAGTGGTGAAAAATCACTTCT
154	s1-10	ATGTGGTTTTGTTCACTGTAGAA TC CTCAGTGGTTAGCACAAATGTTAA
155	s1-11	CATTTCTCTTGATGACTGCAGAG TA TTCCATTGTTGACAAATCCATTT
156	s1-17	GCTATGGGTTTTTAAACACTGAC TT GCCTGGTGTGAGGATCCATGCTT
157	s1-25	GTGTTCTGATACTTGCAACTGA AC CACTGTAGTCCACACACCACTAT
158	s1-28	GGGGGTTGCTTCTCACCGTAGAT GA CCCTCTTGTCCACAAACCACAAC
159	s1-31	CAGCCTGGCTCCCAACCTCCGTC AC TGCCGTTGCAAACAAACCAACC
160	s1-39	TTTCAAAGATCCTGACCTCCGA GA AGCTGGAGTTGAGATCATACTGT
161	s1-41	CGAGCTTGCTCCTCACAGCAGAG GA CTCTGAAGACAGGAGCATCATGA
162	s1-43	CCTTGACAGATCTATACGGCTGAC TA CACAGTGGTGAGAACCATAGTCT
163	s3-28	ACCTTTGTTTGGCCCCAACTGCC TC TGCCACTGTGACACACTTGGGA
164	s3-41	GATGCATGATTCTAGGCACTGGG AA CACAGTGGTGATCAAACCAGTCA

[102] Individual donor constructs were generated by cloning the target site-specific sequences shown in **Table 14** below into a standard plasmid DNA backbone. Each donor DNA

sequence consists of a Bxb1 attP sequence with the target site matching the center dinucleotide, and a target site-specific primer binding site. The attP sequence and primer binding sites are flanking additional genomic sequences that were partially randomized to form a tag sequence to detect targeted integration events through next generation sequencing.

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Table 14. Target Site-Specific Donor Sequences

SEQ	Site	Donor
165	s5-1	GGTTTGTCTGGTCAACCACCGCGTTCTCAGTGGTGTACGGTACAAAC CTTCGTTTCAACTGACCAATTCACCTCCAAATGTAACA
166	s5-2	GGTTTGTCTGGTCAACCACCGCGGGCTCAGTGGTGTACGGTACAAAC CAAGAGGAAAAGTATACCTGCAGCAAGTGATAT
167	s5-4	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CATTGCTGCCGTCTGTCCCCTTCCCATCCCTTCTGACATGT
168	s5-6	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CAGCCCGAACTTAGCTTCCCTCATCGCCTA
169	s5-8	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CATATCGTTTGCTACTCAAACGTGTGGTCCT
170	s5-10	GGTTTGTCTGGTCAACCACCGCGTTCTCAGTGGTGTACGGTACAAAC CTATCTTCCTTTTCTGTGGAAGGGAAAACCTT
171	s5-11	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CAAGCAGCTCGGAGCCTCTCTGTCACTTGCTCTTTAGA
172	s5-14	GGTTTGTCTGGTCAACCACCGCGACCTCAGTGGTGTACGGTACAAAC CGCCTGTCACCTCCTGAGTACCTGGGATTACAGGCGCACAACTACT TCT
173	s5-15	GGTTTGTCTGGTCAACCACCGCGAACTCAGTGGTGTACGGTACAAAC CTCAGGAGGTGTTTTTCTTCCCTTTTGAAATCAGATAGCAGGAAA
174	s5-16	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CAAGAGCACAGTGATTATGATTATTGTTTCTGAGTGATGGCA
175	s5-17	GGTTTGTCTGGTCAACCACCGCGTTCTCAGTGGTGTACGGTACAAAC CTAATGTCCGCACTTCCCTAAGTTTTGGTTTCCAGAGCCACTAGTAA
176	s5-18	GGTTTGTCTGGTCAACCACCGCGAACTCAGTGGTGTACGGTACAAAC CTCTATTCGCACTCAGGGAGGCCTTCCCTGATCTCCAGGGCCAGATT AAGTA
177	s5-19	GGTTTGTCTGGTCAACCACCGCGACCTCAGTGGTGTACGGTACAAAC CCGGCCAGTCAGTCACTGTCAGGTGAGCACCCGCGAGGGTCCCCGGGG AGGTACGGGTGAC
178	s5-21	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CACCTTCACGTCCTAACCAGACCATGAGCTCCAGGGGTAAAATC
179	s5-24	GGTTTGTCTGGTCAACCACCGCGAACTCAGTGGTGTACGGTACAAAC CCATGTAAAACAGCTTATTGCCAACAGAGTTATGGA
180	s1-1	GGTTTGTCTGGTCAACCACCGCGTCCTCAGTGGTGTACGGTACAAAC CAGAATCAGGATAAGGCTCCTCTAGGTACATGTGGCTAAGCTGC

181	s1-5	GGTTTGTCTGGTCAACCACCGCGATCTCAGTGGTGTACGGTACAAAC CGGTCCCTCCATCAAGCGCTGAGGCACAGTGAATGTACTCAGAGGG
182	s1-10	GGTTTGTCTGGTCAACCACCGCGTCCTCAGTGGTGTACGGTACAAAC CACACAATAGCGACATGGAGCAGGTATCAGTTTACGTTT
183	s1-11	GGTTTGTCTGGTCAACCACCGCGTACTCAGTGGTGTACGGTACAAAC CAACCACCTGATTGTGATGGATGTTTAGGTTGTTTCCAATCTTTTGC TATTAAAAAGAATGTGACAGTGAGAACTTTGTGTATAGTGTCAATT TGCAC
184	s1-17	GGTTTGTCTGGTCAACCACCGCGTTCTCAGTGGTGTACGGTACAAAC CAGCATCTTTCAAATAGCACCTCATTTTATCCTGAAGACCCAG
185	s1-25	GGTTTGTCTGGTCAACCACCGCGCACTCAGTGGTGTACGGTACAAAC CCAAAACCTGGTAGAATCTCAGTGACCTTAAAGATTGCCTGGG
186	s1-28	GGTTTGTCTGGTCAACCACCGCGGACTCAGTGGTGTACGGTACAAAC CCATCTCCCTTTTTCCGTGCTGATTAGGACTGGGGCAGTGGGGTTTCG TGTATTTGTGACCTGG
187	s1-31	GGTTTGTCTGGTCAACCACCGCGACCTCAGTGGTGTACGGTACAAAC CGCAGTGTCCACCTGGCGGAACCTTTCTCTCCACTATCCA
188	s1-39	GGTTTGTCTGGTCAACCACCGCGGACTCAGTGGTGTACGGTACAAAC CTAGTAAATAGGATCAAAGGAATAGAGTCTGATGCC
189	s1-41	GGTTTGTCTGGTCAACCACCGCGGACTCAGTGGTGTACGGTACAAAC CCTGTGACTACATTTAGTGAGCAGGTGGAATGAACAA
190	s1-43	GGTTTGTCTGGTCAACCACCGCGTACTCAGTGGTGTACGGTACAAAC CGGATAAGTTTCAGTAAAGGGACTACTGCAGGATTTGGTGGTA
191	s3-28	GGTTTGTCTGGTCAACCACCGCGTCCTCAGTGGTGTACGGTACAAAC CTGCGTTGTCTGAGCTCCTCAGCACTCCCTCCCCAACTTCCTAT
192	s3-41	GGTTTGTCTGGTCAACCACCGCGAACTCAGTGGTGTACGGTACAAAC CAGTCACCAATCTGGAGGGGATGAGGTGAGGGAGGGATAGACAATA

[103] K562 cells were transfected following the manufacturer's protocol. 2E5 cells were transfected with 200ng of total Bxb1 expression plasmid (200ng of one Bxb1 expression plasmid, or 100ng of a Bxb1 variant expression plasmid mixed with 100ng of a WT Bxb1 expression plasmid), and 1600ng total of the target site-specific attP donor plasmid. In most experiments, TI activity data for Bxb1 variants was obtained with a mixture of 50% Bxb1 variant expression plasmid and 50% WT Bxb1 expression plasmid. One exception was the data shown in the left panel of **FIG. 11**, which used 100% (200 ng) Bxb1 D257K expression plasmid or 100% WT Bxb1 expression plasmid. In addition, except for experiments involving the D257K Bxb1 variant, a 50% mixture of Bxb1 variant and WT Bxb1 was used. This is because Bxb1 variants with altered target preferences generally only show improved targeting to half-sites with the alterations shown in **Table 1**, and may target the attP site in the donor and/or the other half-site more poorly than WT Bxb1. A 50% mixture of variant Bxb1 and WT Bxb1 should allow the

Bxb1 variant to bind its preferred half-site and allow the WT Bxb1 to bind the donor and the half-site not preferred by the Bxb1 variant.

[104] Transfected cells were harvested after three days of incubation at 37°C using QuickExtract™ by Lucigen (Cat No: QE09050) following the manufacturer's protocol. A polymerase chain reaction (PCR) was performed on the extracted DNA using Invitrogen's Accuprimer™ Taq DNA Polymerase, high fidelity (cat no: 12346094), as shown in **Table 6**.

[105] The target site-specific PCR was performed using the forward primers shown in **Table 15**.

Table 15. Target Site-Specific Forward Primer Sequences

SEQ	Site	F-primer
193	s5-1	ACACGACGCTCTTCCGATCTNNNNTTCTTTCATTTCTGTTGAGGGTC
194	s5-2	ACACGACGCTCTTCCGATCTNNNNACCCTGTGTTAGAAAGCAGTAAC
195	s5-4	ACACGACGCTCTTCCGATCTNNNNATGTGTTTGAAGCTGAGCATAG
196	s5-6	ACACGACGCTCTTCCGATCTNNNNCGATGTGTTCTCCATGAAGCA
197	s5-8	ACACGACGCTCTTCCGATCTNNNNGCATAGCTGAGTAATACATTGCATG
198	s5-10	ACACGACGCTCTTCCGATCTNNNNATGGGCAGCATTTCATTAAGTAAAT
199	s5-11	ACACGACGCTCTTCCGATCTNNNNCAATTAGTTGGCTGTATAATTTGG
200	s5-14	ACACGACGCTCTTCCGATCTNNNNATTTACATTGATTGATTTTCTTGTT
201	s5-15	ACACGACGCTCTTCCGATCTNNNNACTGCCACCTACATTCAACAAAT
202	s5-16	ACACGACGCTCTTCCGATCTNNNNAGAGGGCTGAGGTTGCAATG
203	s5-17	ACACGACGCTCTTCCGATCTNNNNTGCAGATAATTCTTATGCAAAACAGA AC
204	s5-18	ACACGACGCTCTTCCGATCTNNNNGCAGAAAGTTAGTATGACACAGAC
205	s5-19	ACACGACGCTCTTCCGATCTNNNNGACCAGACAGTTCCAGATACATTCCA
206	s5-21	ACACGACGCTCTTCCGATCTNNNNTTACTCTCTCTCCTAGACTCAAGC
207	s5-24	ACACGACGCTCTTCCGATCTNNNNTGCTAGTATTTGTCTGCACTTTCT
208	s1-1	ACACGACGCTCTTCCGATCTNNNNCGTGGGCCAGTTTTAAATGTCA
209	s1-5	ACACGACGCTCTTCCGATCTNNNNGCTGAACATTAGCTCCATATAT
210	s1-10	ACACGACGCTCTTCCGATCTNNNNAGTCTCTCATTTACCAGTTTGCTT
211	s1-11	ACACGACGCTCTTCCGATCTNNNNGGATTATCCCATATCCAGACATA
212	s1-17	ACACGACGCTCTTCCGATCTNNNNAGCCCAGAGTTAACCAAGCTAC
213	s1-25	ACACGACGCTCTTCCGATCTNNNNTACAACTAAAGCACCAATGGCTC
214	s1-28	ACACGACGCTCTTCCGATCTNNNNGTGAGAAGTCCCAGATGTGCT
215	s1-31	ACACGACGCTCTTCCGATCTNNNNGGAATCCGCCTCCTGACG
216	s1-39	ACACGACGCTCTTCCGATCTNNNNTGATGTTAGAGATCAGCCTGTAC
217	s1-41	ACACGACGCTCTTCCGATCTNNNNAGCCATTTCTTCTAGCAAATT
218	s1-43	ACACGACGCTCTTCCGATCTNNNNCAATACAGGCACAATCCCCTTATT

219	s3-28	ACACGACGCTCTTCCGATCTNNNTGAAGGGAAAGGTCTGGCTTTA
220	s3-41	ACACGACGCTCTTCCGATCTNNNCAGCAGTCGATGTGGGAAC

The target site-specific PCR was performed using the reverse primers shown in **Table 16** below.

Table 16. Target Site-Specific Reverse Primer Sequences

SEQ	Site	R-primer
221	s5-1	GACGTGTGCTCTTCCGATCTTGTTACATTTGGAGTGAATTGGTCA
222	s5-2	GACGTGTGCTCTTCCGATCTATATCACTTGCTGCAGGTATACTTTT
223	s5-4	GACGTGTGCTCTTCCGATCTACATGTCAGAAGGGATGGGAAG
224	s5-6	GACGTGTGCTCTTCCGATCTTAGGCGATGAGGGAAGCTAAGT
225	s5-8	GACGTGTGCTCTTCCGATCTAGGACCACACAGTTTGAGTAGC
226	s5-10	GACGTGTGCTCTTCCGATCTAAGTTTTCCCTCCACAGAAA
227	s5-11	GACGTGTGCTCTTCCGATCTTCTAAAGAGCAAGTGACAGAGAGG
228	s5-14	GACGTGTGCTCTTCCGATCTAGAGTAGTGTTGTGCGCCTG
229	s5-15	GACGTGTGCTCTTCCGATCTTTTCCCTGCTATCTGATTTCAAAGGA
230	s5-16	GACGTGTGCTCTTCCGATCTTGCCATCACTCAGAAACAATAATCA
231	s5-17	GACGTGTGCTCTTCCGATCTTTACTAGTGGCTCTGGAAACCA
232	s5-18	GACGTGTGCTCTTCCGATCTTACTTAATCTGGCCCTGGAGATC
233	s5-19	GACGTGTGCTCTTCCGATCTGTACCCGTACCTCCCCG
234	s5-21	GACGTGTGCTCTTCCGATCTGATTTTACCCCTGGAGCTCATG
235	s5-24	GACGTGTGCTCTTCCGATCTTCCATAACTCTGTTGGCAATAAG
236	s1-1	GACGTGTGCTCTTCCGATCTGCAGCTTAGCCACATGTACCTA
237	s1-5	GACGTGTGCTCTTCCGATCTCCCTCTGAGTACATTCACTG
238	s1-10	GACGTGTGCTCTTCCGATCTAAACGTAACTGATACCTGCTCC
239	s1-11	GACGTGTGCTCTTCCGATCTGTGCAAAATGACACTATACACAAAG
240	s1-17	GACGTGTGCTCTTCCGATCTCTGGGTCTTCAGGATAAAATGAGG
241	s1-25	GACGTGTGCTCTTCCGATCTCCCAGGCAATCTTTAAGGTCAC
242	s1-28	GACGTGTGCTCTTCCGATCTCCAGGTCACAAATACACGAAC
243	s1-31	GACGTGTGCTCTTCCGATCTTGGATAGTGGAGAGAAAGGTTCC
244	s1-39	GACGTGTGCTCTTCCGATCTGGCATCAGACTCTATTCCCTT
245	s1-41	GACGTGTGCTCTTCCGATCTTTGTTCAATCCACCTGCTCACT
246	s1-43	GACGTGTGCTCTTCCGATCTTACCACCAAATCCTGCAGTAGT
247	s3-28	GACGTGTGCTCTTCCGATCTATAGGAAGTTGGGGAGGGAGTG
248	s3-41	GACGTGTGCTCTTCCGATCTTATTGTCTATCCCTCCCTCACCT

- 5 [106] The PCR was performed using the temperature cycling protocol in **Table 8**; the format of the time is minutes:seconds. The product of next generation sequencing (NGS) PCR1 was used as the template for NGS PCR2, as shown in **Table 9**. The PCR was performed using the

temperature cycling protocol in **Table 10**; the format of the time is minutes:seconds. The primers used are universal primers that add on the required DNA sequences for Illumina Sequencing machines. NGS PCR2 products were purified and sequenced on Illumina Sequencing machines. See also Miller et al., *Nat Biotechnol.* (2019) 37(8):945-52 for further description of this sequencing-based assay.

[107] In one example experiment, the target preference shift for Bxb1 variant S231F in position 10 was determined. The S231F variant demonstrated improved targeting of C and T bases, relative to the WT Bxb1 recombinase (**FIG. 6A**), resulting in improved targeted integration at the endogenous human target sites s5-1, s5-11, and s1-41 (**FIGs. 6B-C**). The target preference shifts for different Bxb1 variants at positions that bind the RD domain (e.g., positions 7, 9, and 10) are shown in **FIG. 7**.

[108] In other example experiments, the target preference shifts for Bxb1 variants F314G and G316Y at positions 19 and 21, respectively, were determined. The F314G variant demonstrated improved targeting of T at position 19, relative to the WT Bxb1, and the G316Y variant demonstrated improved targeting of G at position 21, relative to WT Bxb1 (**FIG. 8A**). The F314G and G316Y variants were found to have improved targeted integration at the s5-16 and s3-28 endogenous human target sites, respectively (**FIGs. 8B-C**). The target preference shifts for various Bxb1 variants at positions that bind the ZD domain (e.g., positions 19, 21, 22, 23, and 24) are shown in **FIGs. 9 and 10**.

[109] The Bxb1 variants described here may also demonstrate improved targeted integration at a variety of different endogenous human target sites, relative to WT Bxb1. For example, the D257K Bxb1 variant demonstrated improved targeted integration at human target sites including s1-10, s1-39, s3-28, s3-41, s5-10, s5-11, s5-14, s5-15, s5-16, and s5-17 (**FIG. 11**).

LIST OF SEQUENCES

[110] Sequences disclosed herein are listed in the table below (SEQ: SEQ ID NO).

SEQ	Description
1	Wildtype Bxb1 recombinase exemplary amino acid sequence
2	Wildtype attB sequence
3	Wildtype attP sequence
4-40	Variant attB sequences in Table 4
41-76	Variant attP sequences in Table 5
77	Wildtype ϕ C31 integrase exemplary amino acid sequence
78	Wildtype Pa557 recombinase exemplary amino acid sequence
79	Wildtype Pa570 recombinase exemplary amino acid sequence
80	Symmetric attB sequence
81	Consensus attP sequence
82	Consensus attB sequence
83-130	Endogenous human attP- and attB-like sequences in Table 3
131	Wildtype LI integrase exemplary amino acid sequence
132	Wildtype A118 integrase exemplary amino acid sequence
133	Wildtype TP901 recombinase exemplary amino acid sequence
134	Consensus attB sequence
135	Consensus attB sequence
136	Consensus attB sequence
137-164	Endogenous Bxb1 pseudo-attB target sequences
165-192	Target site-specific donor sequences
193-220	Target site-specific forward primer sequences
221-248	Target site-specific reverse primer sequences
249	Bxb1 recombinase construct C terminal end amino acid sequence
250-251	NGS PCR1 primers in Table 7
252-254	Symmetric attB sequences with mutations at position 10
255-257	attP sequences with mutations at position 10
258-260	Symmetric attB sequences with mutations at position 9
261-263	attP sequences with mutations with mutations at position 9
264-267	Endogenous Bxb1 pseudo-attB target sequences
268-269	Symmetric attB sequences
270-271	Endogenous Bxb1 pseudo-attB target sequences

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. The recombinase variant of any one of claims 1-11, wherein the DNA target is in a cell.
13. The recombinase variant of claim 12, wherein the cell is a eukaryotic cell, optionally a mammalian cell, further optionally a human cell.
14. A nucleic acid molecule encoding the recombinase variant of any one of claims 1-13.
15. A vector comprising the nucleic acid molecule of claim 14.

16. The vector of claim 15, 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.
17. A system for editing DNA in a cell, comprising the recombinase variant of any one of claims 1-13, the nucleic acid molecule of claim 14, or the vector of claim 15 or 16.
18. The system of claim 17, further comprising donor DNA, optionally wherein the donor DNA is circularized or linear.
19. The system of claim 18, wherein the donor DNA comprises a sequence selected from SED ID NOs: 80-81 and 134-136 and the sequences found in Tables 3, 4 and 5.
20. The system of claim 18 or 19, wherein the donor DNA is delivered through a plasmid or viral vector.
21. The system of any one of claims 17-20, wherein the editing comprises integration of DNA into the genome of the cell.
22. The system of any one of claims 17-20, wherein the editing comprises excision or inversion of DNA in the genome of the cell.
23. The system of any one of claims 17-20, wherein the editing comprises a chromosomal translocation in the genome of the cell.
24. The system of any one of claims 17-23, wherein the editing occurs at a genomic region comprising a sequence selected from SED ID NOs: 80-81 and 134-136 and the sequences found in Tables 3, 4 and 5.
25. A method of editing the genome of a cell, the method comprising providing to the cell the system of any one of claims 17-24.
26. The method of claim 26, wherein more than one genomic region is edited.

27. The method of claims 25 or 26, wherein the editing results in excising DNA from the genome, inverting DNA in the genome, chromosomal swap, recombinase-mediated cassette exchange (RMCE), and/or integrating donor DNA into the genome.
28. A cell comprising the system of any one of claims 17-24, or a descendent thereof.
29. A cell edited by the method of any one of claims 25-27, or a descendent thereof.
30. The cell or descendent of claim 28 or 29, wherein the cell is a eukaryotic cell, optionally a mammalian cell, further optionally a human cell.
31. A method of treating a disease in a subject in need thereof, comprising administering the cell or descendent of claim 30 to the subject.
32. The cell or descendent of claim 30 for use in treating a disease in a subject in need thereof.
33. Use of the cell or descendent of claim 30 in the manufacture of a medicament for treating a disease in a subject in need thereof.
34. The Bxb1 recombinase variant of claim 3, wherein the variant mediates increased transgene insertion at an endogenous target site in a eukaryotic genome, relative to wild-type Bxb1 recombinase.

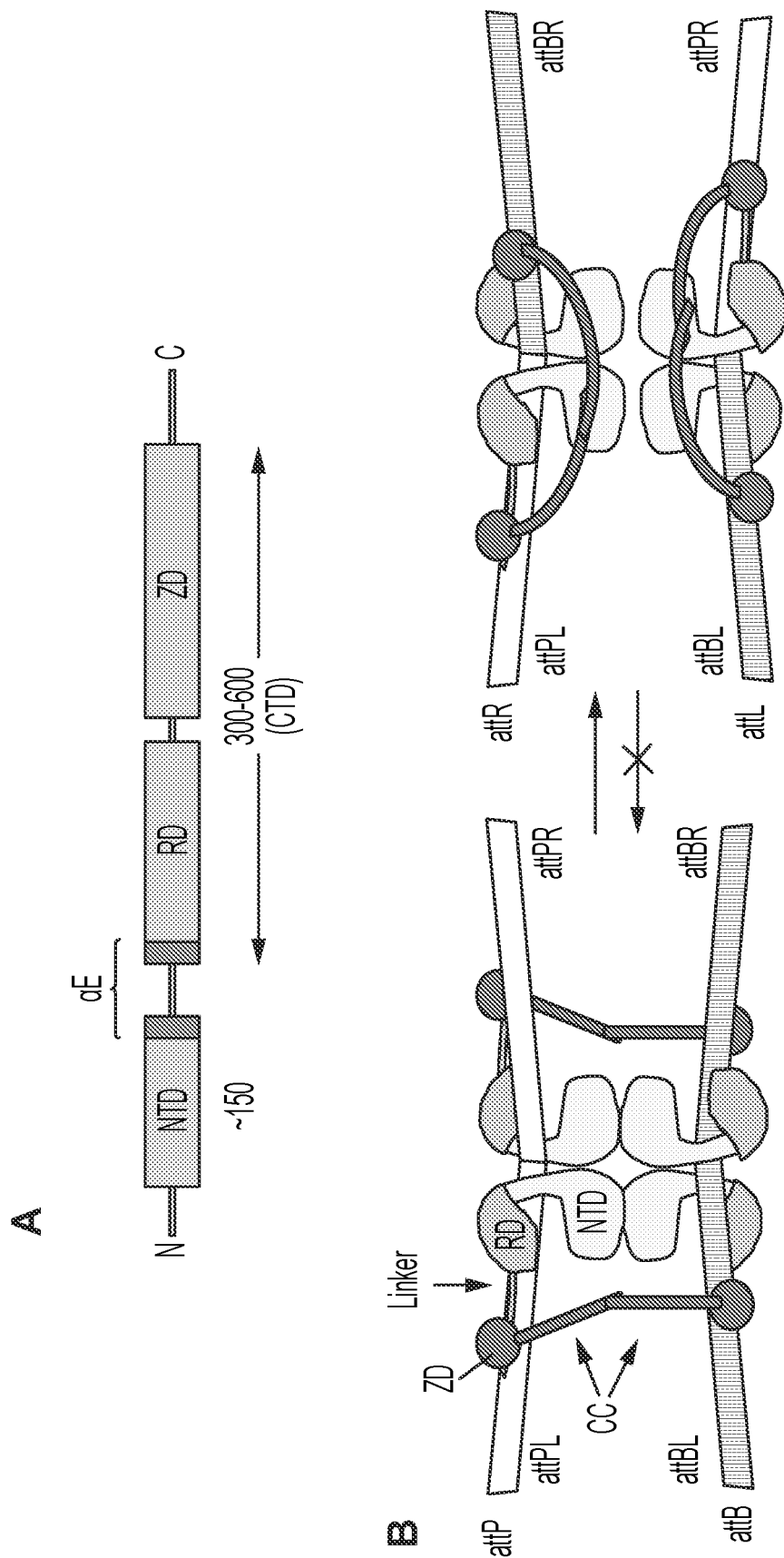


FIG. 1

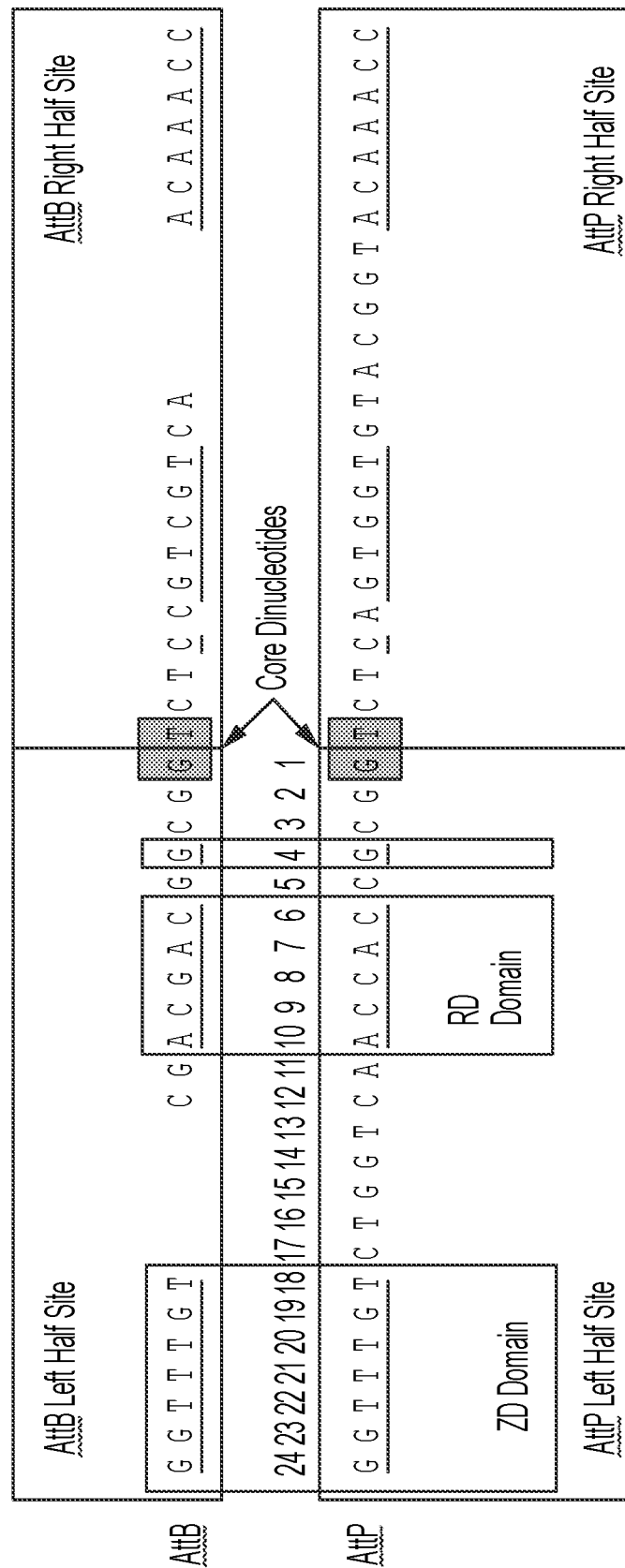
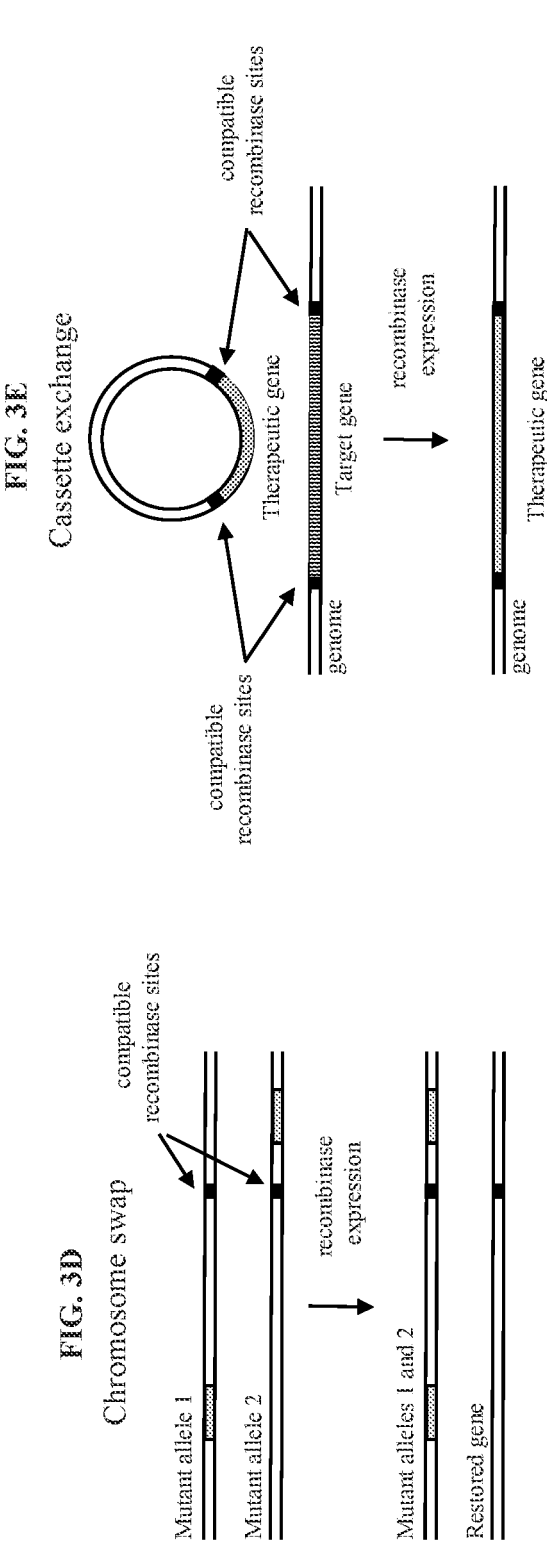
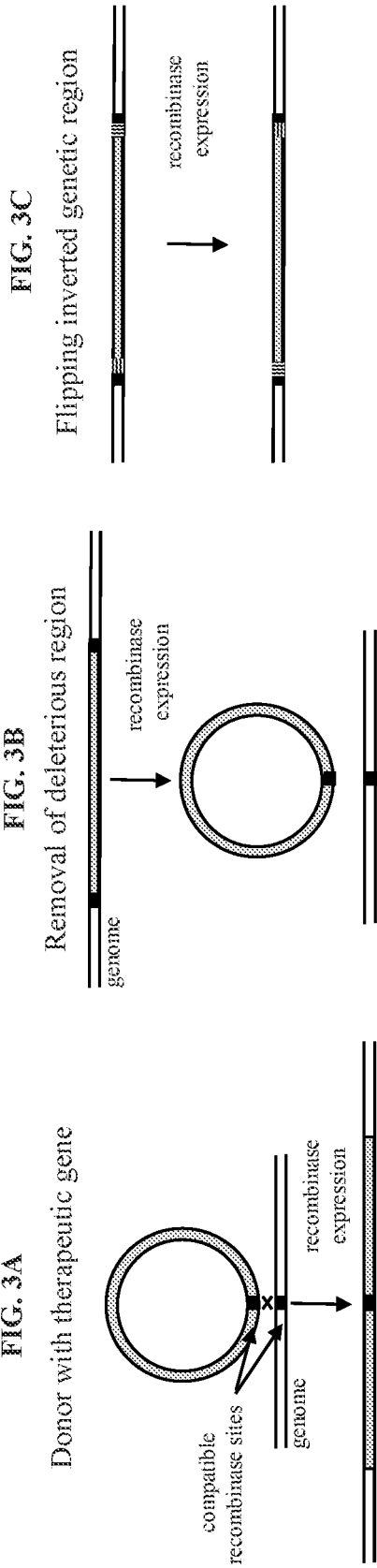


FIG. 2



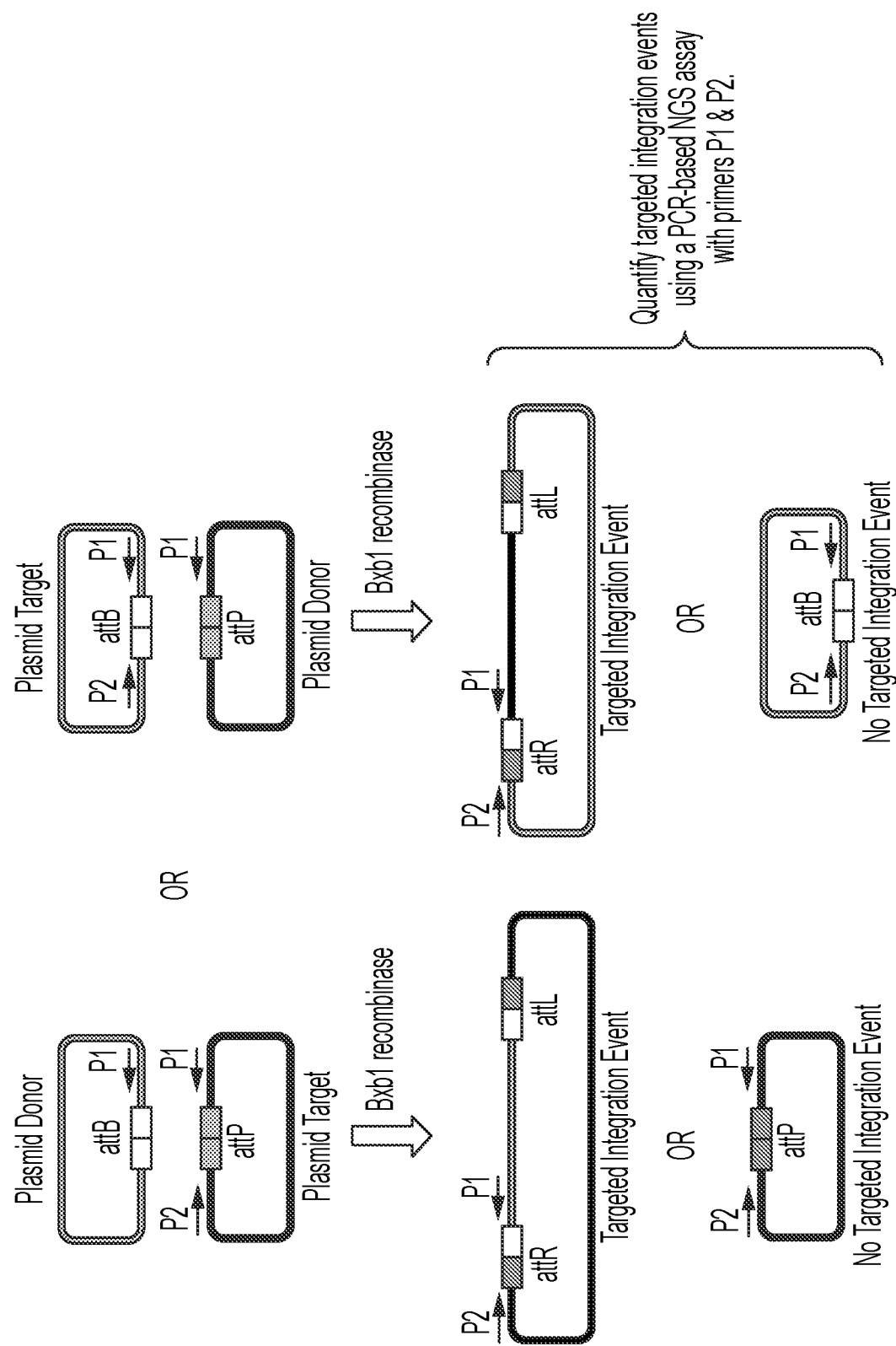


FIG. 4

5/11

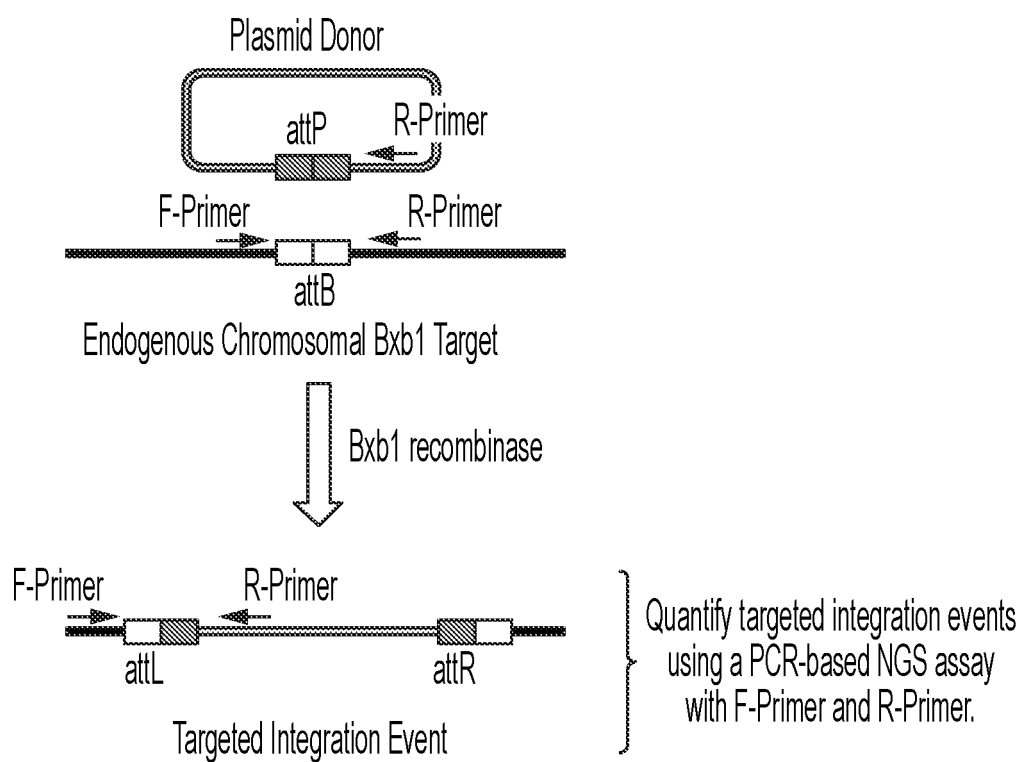


FIG. 5

FIG. 6A

position 10 (A in wt Bxb1 target)			
	%A	%C	%G
WT	85.1	0.8	10.0
S231F	62.7	12.1	5.2

FIG. 6B

	Left half-site	Right half-site
s5-8	5' --GAGTAGTGTATCTGACACACAGCACTCTCTGGTGCAGAAATCTTGGGTTCTCATCACATAGACTGTGGTCGTGAGACCAAGTCTTAGAACCCAA-5'	
s5-1	5' --CCATTCCCTTCTTCTACACAGCGTTCTCAATTGGTAAGCATCAAAATGGTAAGGAAGAAGATGGTGTCGCAAGAGTTAACCATTTCGTAGTTTA-5'	
s5-11	5' --TTGAAGCCCTTCTCCTACAGAGCAAGCAGCAGGGTAAATCTGTATTAACTTCGGGGAAGAGGATGTCTCTTCGTCGCCATTAAAGACATAA-5'	
s1-41	5' --CGAGCTTGCTCCTCACAGCAGAGCACTCTGAAGACAGGAGCATCATGAGCTCGAACGAGGAGTGTCTCTCGAGACTTCTGTCTCGTAGTACT-5'	

FIG. 6C

site	Mutations at Position 10	%targeted integration S231F wt Bxb1	S231F / wt
s5-8	None- matches wt Bxb1	6.95	1.00
s5-1	C in right halfsite	13.18	2.10
s5-11	C in both halvesites	9.46	5.95
s1-41	T in right halvesites	19.40	7.92

7/11

site	position	mutations in halfsites		Bxb1 variant	%TI		variant/wt
		left	right		variant	wt Bxb1	
s5-4	7	G	C	L158D	0.35	0.26 +/- 0.02	1.33
s5-4	7	G	C	T233F	0.66	0.26 +/- 0.02	2.51
s5-4	7	G	C	T233Y	0.88	0.26 +/- 0.02	3.34
s5-18	9	wt Bxb1	A	R237A	0.78	0.25 +/- 0.06	3.15
s5-18	9	wt Bxb1	A	R237C	0.51	0.25 +/- 0.06	2.06
s5-18	9	wt Bxb1	A	R237K	0.59	0.25 +/- 0.06	2.38
s5-18	9	wt Bxb1	A	R237N	0.57	0.25 +/- 0.06	2.30
s5-6	9	T	wt Bxb1	R237N	0.79	0.26 +/- 0.13	3.04
s3-28	10	C	wt Bxb1	N148T	0.41	0.25 +/- 0.05	1.62
s5-4	10	wt Bxb1	T	P197H	0.58	0.26 +/- 0.02	2.20
s3-28	10	C	wt Bxb1	S231F	0.42	0.25 +/- 0.05	1.66
s5-1	10	wt Bxb1	C	S231F	13.18	6.27 +/- 1.88	2.10
s5-11	10	C	C	S231F	9.46	1.59 +/- 0.82	5.95
s5-4	10	wt Bxb1	T	S231F	1.60	0.26 +/- 0.02	6.08
s5-19	10	T	G	S231F	23.59	2.11 +/- 0.56	11.18
s1-41	10	wt Bxb1	T	S231F	19.40	2.45 +/- 0.89	7.92
s5-4	10	wt Bxb1	T	S231G	0.76	0.26 +/- 0.02	2.89
s5-4	10	wt Bxb1	T	S231R	0.43	0.26 +/- 0.02	1.63
s1-41	10	wt Bxb1	T	S231R	5.77	2.45 +/- 0.89	2.36
s5-11	10	C	C	S231Y	6.00	1.59 +/- 0.82	3.77
s3-28	10	C	wt Bxb1	S231V	0.40	0.25 +/- 0.05	1.58
s5-4	10	wt Bxb1	T	S231V	0.57	0.26 +/- 0.02	2.16
s5-4	10	wt Bxb1	T	T233F	0.66	0.26 +/- 0.02	2.51
s1-1	10	C	wt Bxb1	T233K	0.10	0.04 +/- 0.02	2.43
s1-5	10	G	wt Bxb1	T233R	0.09	0.03 +/- 0.02	2.94
s3-28	10	C	wt Bxb1	T233W	0.39	0.25 +/- 0.05	1.54
s5-4	10	wt Bxb1	T	T233W	1.55	0.26 +/- 0.02	5.89
s5-19	10	T	G	T233W	5.21	2.11 +/- 0.56	2.47
s5-4	10	wt Bxb1	T	T233Y	0.88	0.26 +/- 0.02	3.34

FIG. 7

FIG. 8A

position 19 (G in wt Bxb1 target)				position 21 (T in wt Bxb1 target)				
	%A	%C	%G	%T	%A	%C	%G	%T
WT	0.8	1.8	96.5	1.0	2.2	0.1	12.5	85.2
F314G	0.7	5.3	73.7	20.3	4.8	0.2	78.5	16.6

FIG. 8B

		Left half-site		Right half-site	
Symmetric	5'-GGTTTGTGCGACGACGGCGCTCTCCGTCGTCAACAAACC				
AttB site	CCAAACAGCTGCTGCCGCCGAGGAGGCAGCAGTTGTTTGG-5'				
s5-16	5'-GCACTCCAGCCTGGGCAACAGAGCACTCTGTGTGTCAAAAA				
	CGTGAGGTGGACCCGTTGTCTCCGAGAGACAAACAGTTT			Position 19 T	
s3-28	5'-ACCTTTGTGTGGCCCAACTGCCCTGTGCCACTGTCGACACACTTGGGA				
	TGGAAACAAACCGGGTTGACGGAGACGGTGACAGCTGTGTGAACCCCT-5'			Position 21 G	

FIG. 8C

site	Mutations at Position 19	%targeted integration F314G	wt Bxb1	F314G / wt
s5-16	T in right half-site	3.11	1.09 +/- 0.28	2.85

site	Mutations at Position 21	%targeted integration G316Y	wt Bxb1	G316Y / wt
s3-28	G in right half-site	0.45	0.25 +/- 0.05	1.78

9/11

site	position	mutations in halvesites		Bxb1 variant	%TI		variant/wt
		left	right		variant	wt Bxb1	
s5-24	19		T	F314A	0.21	0.12 +/- 0.03	1.75
s5-6	19		T	F314C	0.66	0.26 +/- 0.13	2.54
s5-16	19		T	F314C	2.21	1.09 +/- 0.28	2.03
s1-5	19	wt Bxb1	T	F314C	0.15	0.03 +/- 0.02	4.97
s5-6	19		T	F314G	1.84	0.26 +/- 0.13	7.08
s5-16	19		T	F314G	3.11	1.09 +/- 0.28	2.85
s5-21	19	T		F314N	1.74	0.85 +/- 0.15	2.04
s5-21	19	T		F314Q	1.78	0.85 +/- 0.15	2.09
s5-6	19		T	F314Q	0.71	0.26 +/- 0.13	2.73
s5-16	19		T	F314Q	3.21	1.09 +/- 0.28	2.94
s1-5	19	wt Bxb1	T	F314Q	0.12	0.03 +/- 0.02	4.19
s5-6	19		T	F314S	2.03	0.26 +/- 0.13	7.81
s1-5	19	wt Bxb1	T	F314S	0.14	0.03 +/- 0.02	4.66
s5-6	19		T	F314T	2.40	0.26 +/- 0.13	9.23
s5-16	19		T	F314T	2.27	1.09 +/- 0.28	2.08
s1-5	19	wt Bxb1	T	A315F	0.12	0.03 +/- 0.02	3.92
s5-6	19		T	A315I	0.85	0.26 +/- 0.13	3.27
s1-5	19	wt Bxb1	T	A315I	0.11	0.03 +/- 0.02	3.61
s5-16	19		T	A315S	2.79	1.09 +/- 0.28	2.56
s1-5	19	wt Bxb1	T	A315S	0.08	0.03 +/- 0.02	2.60
s5-24	19		T	A315W	0.24	0.12 +/- 0.03	2.00
s5-16	19		T	A315Y	2.11	1.09 +/- 0.28	1.94
s5-16	19		T	G318R	2.17	1.09 +/- 0.28	1.99

FIG. 9

10/11

site	position	mutations in halfsites		Bxb1 variant	%TI		variant/wt
		left	right		variant	wt Bxb1	
s5-6	21		C	F314E	1.06	0.26 +/- 0.13	4.08
s3-28	21	wt Bxb1	G	G316Y	0.45	0.25 +/- 0.05	1.78
s1-5	22	G	A	A315F	0.12	0.03 +/- 0.02	3.92
s1-5	22	G	A	A315H	0.16	0.03 +/- 0.02	5.27
s1-5	22	G	A	A315N	0.13	0.03 +/- 0.02	4.32
s5-24	22		A	A315W	0.24	0.12 +/- 0.03	2.00
s1-5	22	G	A	G316A	0.11	0.03 +/- 0.02	3.82
s1-5	22	G	A	G316C	0.14	0.03 +/- 0.02	4.86
s1-11	23	T	A	A315F	0.11	0.04 +/- 0.01	3.19
s1-11	23	T	A	A315H	0.35	0.04 +/- 0.01	9.87
s1-11	23	T	A	A315W	0.12	0.04 +/- 0.01	3.30
s1-11	23	T	A	A315Y	0.30	0.04 +/- 0.01	8.28
s5-21	23	T		G316C	1.47	0.85 +/- 0.15	1.72
s1-10	23	T	T	G316C	1.57	0.49 +/- 0.15	3.20
s1-11	23	T	A	G316C	0.08	0.04 +/- 0.01	2.35
s1-11	23	T	A	G316T	0.18	0.04 +/- 0.01	4.98
s1-11	24	C	wt Bxb1	A315F	0.11	0.04 +/- 0.01	3.19
s1-11	24	C	wt Bxb1	A315Y	0.30	0.04 +/- 0.01	8.28

FIG. 10

Site	100% variant		50% variant + 50% wt	
	D257K	wt Bxb1	D257K	D257K/wt
s1-10	1.37	0.35 +/- 0.04	0.96	0.49 +/- 0.15
s1-39	6.70	0.48 +/- 0.09	2.10	0.64 +/- 0.16
s3-28	1.94	0.38 +/- 0.19	0.46	0.25 +/- 0.05
s3-41	2.66	0.41 +/- 0.04	1.29	0.32 +/- 0.17
s5-10	2.06	0.28 +/- 0.03	1.51	0.39 +/- 0.12
s5-11	10.03	1.11 +/- 0.41	1.67	1.59 +/- 0.82
s5-14	2.78	0.29 +/- 0.10	0.70	0.36 +/- 0.24
s5-15	3.38	0.72 +/- 0.25	1.07	1.49 +/- 0.61
s5-16	5.79	1.33 +/- 0.63	2.38	1.09 +/- 0.28
s5-17	2.55	1.23 +/- 0.42	1.32	1.13 +/- 0.68

Site	100% variant		50% variant + 50% wt	
	D257K	wt Bxb1	D257K	D257K/wt
s1-10	1.37	0.35 +/- 0.04	0.96	0.49 +/- 0.15
s1-39	6.70	0.48 +/- 0.09	2.10	0.64 +/- 0.16
s3-28	1.94	0.38 +/- 0.19	0.46	0.25 +/- 0.05
s3-41	2.66	0.41 +/- 0.04	1.29	0.32 +/- 0.17
s5-10	2.06	0.28 +/- 0.03	1.51	0.39 +/- 0.12
s5-11	10.03	1.11 +/- 0.41	1.67	1.59 +/- 0.82
s5-14	2.78	0.29 +/- 0.10	0.70	0.36 +/- 0.24
s5-15	3.38	0.72 +/- 0.25	1.07	1.49 +/- 0.61
s5-16	5.79	1.33 +/- 0.63	2.38	1.09 +/- 0.28
s5-17	2.55	1.23 +/- 0.42	1.32	1.13 +/- 0.68

FIG. 11

Sequence Listing

1	Sequence Listing Information	
1-1	File Name	025297.WO043.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.2.0
1-5	Production Date	2023-01-26
1-6	Original free text language code	
1-7	Non English free text language code	
2	General Information	
2-1	Current application: IP Office	
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	025297.WO043
2-5	Earliest priority application: IP Office	
2-6	Earliest priority application: Application number	
2-7	Earliest priority application: Filing date	
2-8en	Applicant name	SANGAMO THERAPEUTICS, INC.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	ARANGUNDY, Sebastian
2-9	Inventor name: Name Latin	
2-10en	Invention title	SERINE RECOMBINASE SYSTEMS FOR SITE-SPECIFIC GENE EDITING
2-11	Sequence Total Quantity	271

3-1	Sequences	
3-1-1	Sequence Number [ID]	1
3-1-2	Molecule Type	AA
3-1-3	Length	500
3-1-4	Features Location/ Qualifiers	REGION 1..500 note=Synthetic: Wildtype Bxb1 source 1..500 mol_type=protein organism=synthetic construct
3-1-5	NonEnglishQualifier Value Residues	MRALVVIRLS RVTDATTSPE RQLESCQQLC AQRGWDVVG V AEDLDVSGAV DPFDRKRRPN 60 LARWLAFEEQ PFDVIVAYRV DRLTRSIRHL QQLVHWAEDH KKLVSATEA HFDTTTPFAA 120 VVIALMGTV A QMELEAIKER NRSAAHFNIR AGKYRGS LPP WGYLPTRVDG EWRLVPDPVQ 180 RERILEVYHR VVDNHEPLHL VAHDLNRRGV LSPKDYFAQL QGREPQGREW SATALKRSMI 240 SEAMLGYATL NGKTVRDDDG APLVRAEPIL TREQLEALRA ELVKTSRAKP AVSTPSLLLR 300 VLFCAVCGEP AYKFAGGGRK HPRYRCRSMG FPKHCGNGTV AMAEWDAFCE EQVLDLLGDA 360 ERLEKVVWAG SDSAVELAEV NAELVDLTSL IGSPAYRAGS PQREALDARI AALAAARQEEL 420 EGLEARPSGW EWRETGQRF G DWWREQDTAA KNTWL RSMNV RLTFDVRGGL TRTIDFGDLQ 480 EYEQHLRLGS VVERLHTGMS 500
3-2	Sequences	
3-2-1	Sequence Number [ID]	2
3-2-2	Molecule Type	DNA
3-2-3	Length	38
3-2-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Wildtype attB source 1..38 mol_type=other DNA organism=synthetic construct
3-2-5	NonEnglishQualifier Value Residues	ggcttgctcga cgacggcggt ctccgctgctc aggatcat 38
3-3	Sequences	
3-3-1	Sequence Number [ID]	3
3-3-2	Molecule Type	DNA
3-3-3	Length	48
3-3-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: Wildtype attP source 1..48 mol_type=other DNA organism=synthetic construct
3-3-5	NonEnglishQualifier Value Residues	ggtttgctctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaacc 48
3-4	Sequences	
3-4-1	Sequence Number [ID]	4
3-4-2	Molecule Type	DNA
3-4-3	Length	137
3-4-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-4-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgacggcg 60 gtctccgtcg tcaacaacc ccggcagata aaagtacc ca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-5	Sequences	
3-5-1	Sequence Number [ID]	5
3-5-2	Molecule Type	DNA
3-5-3	Length	137
3-5-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-5-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gatgtttgtc gacgacggcg 60 gtctccgtcg tcaacaaaca ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-6	Sequences	
3-6-1	Sequence Number [ID]	6
3-6-2	Molecule Type	DNA
3-6-3	Length	137
3-6-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-6-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gacgtttgtc gacgacggcg 60 gtctccgtcg tcaacaaacg ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-7	Sequences	
3-7-1	Sequence Number [ID]	7
3-7-2	Molecule Type	DNA
3-7-3	Length	137
3-7-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-7-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaagtttgtc gacgacggcg 60 gtctccgtcg tcaacaaact ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-8	Sequences	
3-8-1	Sequence Number [ID]	8
3-8-2	Molecule Type	DNA
3-8-3	Length	137
3-8-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-8-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gagttttgtc gacgacggcg 60 gtctccgtcg tcaacaaaac ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-9	Sequences	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	DNA
3-9-3	Length	137
3-9-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-9-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gagctttgtc gacgacggcg 60 gtctccgtcg tcaacaaagc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-10	Sequences	
3-10-1	Sequence Number [ID]	10
3-10-2	Molecule Type	DNA
3-10-3	Length	137
3-10-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-10-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gagatttgtc gacgacggcg 60 gtctccgtcg tcaacaatc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-11	Sequences	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	DNA
3-11-3	Length	137
3-11-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-11-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttgtc gacgacggcg 60 gtctccgtcg tcaacaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-12	Sequences	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	DNA
3-12-3	Length	137
3-12-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-12-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttgtc gacgacggcg 60 gtctccgtcg tcaacaatcc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-13	Sequences	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	DNA
3-13-3	Length	137
3-13-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-13-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttgtc gacgacggcg 60 gtctccgtcg tcaacaagcc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-14	Sequences	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	DNA
3-14-3	Length	137
3-14-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-14-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttgtc gacgacggcg 60 gtctccgtcg tcaacacacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-15	Sequences	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	DNA
3-15-3	Length	137
3-15-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-15-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtatgtc gacgacggcg 60 gtctccgtcg tcaacatacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-16	Sequences	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	DNA
3-16-3	Length	137
3-16-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-16-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtctgtc gacgacggcg 60 gtctccgtcg tcaacagacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-17	Sequences	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	DNA
3-17-3	Length	137
3-17-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-17-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttggtc gacgacggcg 60 gtctccgtcg tcaaccaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-18	Sequences	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	DNA
3-18-3	Length	137
3-18-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-18-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttagtc gacgacggcg 60 gtctccgtcg tcaactaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-19	Sequences	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	DNA
3-19-3	Length	137
3-19-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-19-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggttcgtc gacgacggcg 60 gtctccgtcg tcaacgaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-20	Sequences	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	DNA
3-20-3	Length	137
3-20-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-20-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttttc gacgacggcg 60 gtctccgtcg tcaaaaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-21	Sequences	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	DNA
3-21-3	Length	137
3-21-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-21-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttctc gacgacggcg 60 gtctccgtcg tcaagaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-22	Sequences	
3-22-1	Sequence Number [ID]	22
3-22-2	Molecule Type	DNA
3-22-3	Length	137
3-22-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-22-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttatc gacgacggcg 60 gtctccgtcg tcaataaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-23	Sequences	
3-23-1	Sequence Number [ID]	23
3-23-2	Molecule Type	DNA
3-23-3	Length	137
3-23-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-23-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttggc gacgacggcg 60 gtctccgtcg tcaccaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-24	Sequences	
3-24-1	Sequence Number [ID]	24
3-24-2	Molecule Type	DNA
3-24-3	Length	137
3-24-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-24-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgac gacgacggcg 60 gtctccgtcg tcatcaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-25	Sequences	
3-25-1	Sequence Number [ID]	25
3-25-2	Molecule Type	DNA
3-25-3	Length	137
3-25-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-25-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgcc gacgacggcg 60 gtctccgtcg tcagcaaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-26	Sequences	
3-26-1	Sequence Number [ID]	26
3-26-2	Molecule Type	DNA
3-26-3	Length	137
3-26-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-26-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gtcgacggcg 60 gtctccgtcg acaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-27	Sequences	
3-27-1	Sequence Number [ID]	27
3-27-2	Molecule Type	DNA
3-27-3	Length	137
3-27-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-27-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc ggcgacggcg 60 gtctccgtcg ccaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-28	Sequences	
3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	DNA
3-28-3	Length	137
3-28-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-28-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gccgacggcg 60 gtctccgtcg gcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-29	Sequences	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	DNA
3-29-3	Length	137
3-29-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-29-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gaggacggcg 60 gtctccgtcc tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-30	Sequences	
3-30-1	Sequence Number [ID]	30
3-30-2	Molecule Type	DNA
3-30-3	Length	137
3-30-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-30-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gatgacggcg 60 gtctccgtca tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-31	Sequences	
3-31-1	Sequence Number [ID]	31
3-31-2	Molecule Type	DNA
3-31-3	Length	137
3-31-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-31-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gaagacggcg 60 gtctccgtct tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-32	Sequences	
3-32-1	Sequence Number [ID]	32
3-32-2	Molecule Type	DNA
3-32-3	Length	137
3-32-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-32-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gactacggcg 60 gtctccgtag tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-33	Sequences	
3-33-1	Sequence Number [ID]	33
3-33-2	Molecule Type	DNA
3-33-3	Length	137
3-33-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-33-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gaccacggcg 60 gtctccgtgg tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-34	Sequences	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	DNA
3-34-3	Length	137
3-34-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-34-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacaacggcg 60 gtctccgttg tcaacaacc ccggcagata aaagtaccca gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-35	Sequences	
3-35-1	Sequence Number [ID]	35
3-35-2	Molecule Type	DNA
3-35-3	Length	137
3-35-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-35-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgtcggcg 60 gtctccgacg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-36	Sequences	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	DNA
3-36-3	Length	137
3-36-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-36-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacggcggcg 60 gtctccgccg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-37	Sequences	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	DNA
3-37-3	Length	137
3-37-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-37-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgccggcg 60 gtctccggcg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-38	Sequences	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	DNA
3-38-3	Length	137
3-38-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-38-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgagggcg 60 gtctccctcg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-39	Sequences	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	DNA
3-39-3	Length	137
3-39-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
3-39-5	NonEnglishQualifier Value Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgatggcg 60 gtctccatcg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-40	Sequences	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	DNA
3-40-3	Length	137
3-40-4	Features Location/ Qualifiers	misc_feature 1..137 note=Synthetic: Variant attB sequence source 1..137 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-40-5	Residues	atgcttctct gcatccgtct gctaaatccg cgtgataggg gaggtttgtc gacgaaggcg 60 gtctccttcg tcaacaaacc ccggcagata aaagtaccga gaaccagagc ctacaatacc 120 ggccctggga atataag 137
3-41	Sequences	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	DNA
3-41-3	Length	100
3-41-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-41-5	Residues	ggtttgtctg gtcattccacc gcggtctcag tggagtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-42	Sequences	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	DNA
3-42-3	Length	100
3-42-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-42-5	Residues	ggtttgtctg gtcaccacc gcggtctcag tggggtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-43	Sequences	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	DNA
3-43-3	Length	100
3-43-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-43-5	Residues	ggtttgtctg gtcagccacc gcggtctcag tggcgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-44	Sequences	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	DNA
3-44-3	Length	100
3-44-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-44-5	Residues	ggtttgtctg gtcaaaccacc gcggtctcag tgttgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-45	Sequences	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	DNA
3-45-3	Length	100
3-45-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-45-5	Residues	ggtttgtctg gtcaatcacc gcggtctcag tgatgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-46	Sequences	
3-46-1	Sequence Number [ID]	46

3-46-2	Molecule Type	DNA
3-46-3	Length	100
3-46-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-46-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaagcacc gcggtctcag tgctgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-47	Sequences	
3-47-1	Sequence Number [ID]	47
3-47-2	Molecule Type	DNA
3-47-3	Length	100
3-47-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-47-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaactacc gcggtctcag tagtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-48	Sequences	
3-48-1	Sequence Number [ID]	48
3-48-2	Molecule Type	DNA
3-48-3	Length	100
3-48-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-48-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaacaacc gcggtctcag ttgtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-49	Sequences	
3-49-1	Sequence Number [ID]	49
3-49-2	Molecule Type	DNA
3-49-3	Length	100
3-49-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-49-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaacgacc gcggtctcag tcgtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-50	Sequences	
3-50-1	Sequence Number [ID]	50
3-50-2	Molecule Type	DNA
3-50-3	Length	100
3-50-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-50-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaacctcc gcggtctcag aggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-51	Sequences	
3-51-1	Sequence Number [ID]	51
3-51-2	Molecule Type	DNA
3-51-3	Length	100
3-51-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100

3-51-5	NonEnglishQualifier Value Residues	mol_type=other DNA organism=synthetic construct ggtttgtctg gtcaaccccc gcggtctcag ggggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-52	Sequences	
3-52-1	Sequence Number [ID]	52
3-52-2	Molecule Type	DNA
3-52-3	Length	100
3-52-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-52-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccgcc gcggtctcag cgggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-53	Sequences	
3-53-1	Sequence Number [ID]	53
3-53-2	Molecule Type	DNA
3-53-3	Length	100
3-53-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-53-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccagc gcggtctcac tgggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-54	Sequences	
3-54-1	Sequence Number [ID]	54
3-54-2	Molecule Type	DNA
3-54-3	Length	100
3-54-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-54-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccatc gcggtctcaa tgggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-55	Sequences	
3-55-1	Sequence Number [ID]	55
3-55-2	Molecule Type	DNA
3-55-3	Length	100
3-55-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-55-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccaac gcggtctcat tgggtgtacgg tacaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-56	Sequences	
3-56-1	Sequence Number [ID]	56
3-56-2	Molecule Type	DNA
3-56-3	Length	100
3-56-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-56-5	NonEnglishQualifier Value Residues	cgtttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaacgca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100

3-57	Sequences	
3-57-1	Sequence Number [ID]	57
3-57-2	Molecule Type	DNA
3-57-3	Length	100
3-57-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-57-5	NonEnglishQualifier Value Residues	tgtttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaacaca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-58	Sequences	
3-58-1	Sequence Number [ID]	58
3-58-2	Molecule Type	DNA
3-58-3	Length	100
3-58-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-58-5	NonEnglishQualifier Value Residues	agtttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaactca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-59	Sequences	
3-59-1	Sequence Number [ID]	59
3-59-2	Molecule Type	DNA
3-59-3	Length	100
3-59-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-59-5	NonEnglishQualifier Value Residues	gctttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaagcca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-60	Sequences	
3-60-1	Sequence Number [ID]	60
3-60-2	Molecule Type	DNA
3-60-3	Length	100
3-60-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-60-5	NonEnglishQualifier Value Residues	gttttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaaacca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-61	Sequences	
3-61-1	Sequence Number [ID]	61
3-61-2	Molecule Type	DNA
3-61-3	Length	100
3-61-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-61-5	NonEnglishQualifier Value Residues	gatttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaaatcca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-62	Sequences	
3-62-1	Sequence Number [ID]	62
3-62-2	Molecule Type	DNA
3-62-3	Length	100

3-62-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-62-5	NonEnglishQualifier Value Residues	ggattgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaatccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-63	Sequences	
3-63-1	Sequence Number [ID]	63
3-63-2	Molecule Type	DNA
3-63-3	Length	100
3-63-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-63-5	NonEnglishQualifier Value Residues	ggcttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaagccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-64	Sequences	
3-64-1	Sequence Number [ID]	64
3-64-2	Molecule Type	DNA
3-64-3	Length	100
3-64-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-64-5	NonEnglishQualifier Value Residues	gggttgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacaacccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-65	Sequences	
3-65-1	Sequence Number [ID]	65
3-65-2	Molecule Type	DNA
3-65-3	Length	100
3-65-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-65-5	NonEnglishQualifier Value Residues	ggtctgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacagacca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-66	Sequences	
3-66-1	Sequence Number [ID]	66
3-66-2	Molecule Type	DNA
3-66-3	Length	100
3-66-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-66-5	NonEnglishQualifier Value Residues	ggtgtgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacacacca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-67	Sequences	
3-67-1	Sequence Number [ID]	67
3-67-2	Molecule Type	DNA
3-67-3	Length	100
3-67-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct

3-67-5	NonEnglishQualifier Value Residues	ggatatgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacataccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-68	Sequences	
3-68-1	Sequence Number [ID]	68
3-68-2	Molecule Type	DNA
3-68-3	Length	100
3-68-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-68-5	NonEnglishQualifier Value Residues	ggttagtctg gtcaaccacc gcggtctcag tgggtgtacgg tactaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-69	Sequences	
3-69-1	Sequence Number [ID]	69
3-69-2	Molecule Type	DNA
3-69-3	Length	100
3-69-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-69-5	NonEnglishQualifier Value Residues	ggttcgtctg gtcaaccacc gcggtctcag tgggtgtacgg tacgaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-70	Sequences	
3-70-1	Sequence Number [ID]	70
3-70-2	Molecule Type	DNA
3-70-3	Length	100
3-70-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-70-5	NonEnglishQualifier Value Residues	ggttggctg gtcaaccacc gcggtctcag tgggtgtacgg taccaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-71	Sequences	
3-71-1	Sequence Number [ID]	71
3-71-2	Molecule Type	DNA
3-71-3	Length	100
3-71-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-71-5	NonEnglishQualifier Value Residues	ggtttttctg gtcaaccacc gcggtctcag tgggtgtacgg taaaaacca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-72	Sequences	
3-72-1	Sequence Number [ID]	72
3-72-2	Molecule Type	DNA
3-72-3	Length	100
3-72-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-72-5	NonEnglishQualifier Value Residues	ggtttatctg gtcaaccacc gcggtctcag tgggtgtacgg tataaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-73	Sequences	
3-73-1	Sequence Number [ID]	73

3-73-2	Molecule Type	DNA
3-73-3	Length	100
3-73-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-73-5	NonEnglishQualifier Value Residues	ggtttctctg gtcaaccacc gcggtctcag tgggtgtacgg tagaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-74	Sequences	
3-74-1	Sequence Number [ID]	74
3-74-2	Molecule Type	DNA
3-74-3	Length	100
3-74-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-74-5	NonEnglishQualifier Value Residues	ggtttgactg gtcaaccacc gcggtctcag tgggtgtacgg ttcaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-75	Sequences	
3-75-1	Sequence Number [ID]	75
3-75-2	Molecule Type	DNA
3-75-3	Length	100
3-75-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-75-5	NonEnglishQualifier Value Residues	ggtttgccctg gtcaaccacc gcggtctcag tgggtgtacgg tgcaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-76	Sequences	
3-76-1	Sequence Number [ID]	76
3-76-2	Molecule Type	DNA
3-76-3	Length	100
3-76-4	Features Location/ Qualifiers	misc_feature 1..100 note=Synthetic: Variant attP sequence source 1..100 mol_type=other DNA organism=synthetic construct
3-76-5	NonEnglishQualifier Value Residues	ggtttggtctg gtcaaccacc gcggtctcag tgggtgtacgg tccaaaccca ataaaagtac 60 ccagaaccag agcctacaat accggccctg ggaatataag 100
3-77	Sequences	
3-77-1	Sequence Number [ID]	77
3-77-2	Molecule Type	AA
3-77-3	Length	605
3-77-4	Features Location/ Qualifiers	REGION 1..605 note=Synthetic: Wildtype phi-C31 source 1..605 mol_type=protein organism=synthetic construct
3-77-5	NonEnglishQualifier Value Residues	MDTYAGAYDR QSRERENSSA ASPATQRSAN EDKAADLQRE VERDGGFRFRF VGHFSEAPGT 60 SAFGTAERPE FERILNECRA GRLNMIIVYD VSRFSRLKVM DAIPIVSELL ALGVTIVSTQ 120 EGVFRQGNVM DLIHLIMRLD ASHKESLKS AKILDTKNLQ RELGGYVGGK APYGFELVSE 180 TKEITRNGRM VNVVINKLAH STPLTGPF EFPDVIRWW REIKTHKHL FKPQSQAIIH 240 PGSITGLCKR MDADAVPTRG ETIGKKTASS AWDPATVMRI LRDPRIAGFA AEVIYKKKPD 300 GTPTTKIEGY RIQRDPITLR PVELDCGPII EPAEWYELQA WLDGRGRGKG LSRGQAII SA 360 MDKLYCEGA VMTSKRGEES IKDSYRCRRR KVVDPSPAPGQ HEGTCNV SMA ALDKFVAERI 420 FNKIRHAEGD EETLALLWEA ARRFGLTEA PEKSGERANL VAERADALNA LEELYEDRAA 480 GAYDGPVGRK HFRKQQAALT LRQQGAERL AELEAAEAPK LPLDQWFPED ADADPTGPKS 540

		WWGRASVDDK RVFVGLFVDK IIVTKSTTGR GQGTPIEKRA SITWAKPPTD DDEDDAQDGT 600 EDVAA 605
3-78	Sequences	
3-78-1	Sequence Number [ID]	78
3-78-2	Molecule Type	AA
3-78-3	Length	557
3-78-4	Features Location/ Qualifiers	REGION 1..557 note=Synthetic: Wildtype Pa557 source 1..557 mol_type=protein organism=synthetic construct
3-78-5	NonEnglishQualifier Value Residues	MNMHSPTVTT RAALYLRVST ARQAEHDISI PDQKRQGEAY CEQRGFQLVE TYVEPGATAT 60 NDKRPEFQRM IEAGTSKPAP FDIVVHSFS RFFRDHFEME FYVRKLAKNG VKLVSITQEM 120 GDDPMHQMMR QIMALFDEYQ SKENAKHVLR AMNENARQGF WNGARPPIGY RIVAAEQRGS 180 KTKKKLEIDP LHADTVRLIY RLFLEGDGTR GAMGVKAIAT YLNERRFFTR DGGRWGLAQI 240 HAILTRTTYI GEHRFNTRSH KDREKKPESE IAIMAVPPLI EREIYDAVQA RLKSRNPMVT 300 PARVSSGPTL LTGICFCAKC GGAMTLRTGQ GSTGATYRYY TCSTKARQGK TGCKGRTIPM 360 DKLDHLVADH IGDRLQLPKR LETVLASVID RRQERAERRR EHIAELNRRRI TEADQRLGRL 420 FDAIEAGMVD KDDAMAKERM VSLKALRDQA AADAERTQLA LDSSGNQGVGS PDMLKGFARK 480 ARERIRLDDG GYRRDHLRAL AQRVEVADDE VRIMGSKSEL LRTLVAASSV ETAAFGVQSS 540 VLKWRTQEDS NLRPLGS 557
3-79	Sequences	
3-79-1	Sequence Number [ID]	79
3-79-2	Molecule Type	AA
3-79-3	Length	570
3-79-4	Features Location/ Qualifiers	REGION 1..570 note=Synthetic: Wildtype Pa570 source 1..570 mol_type=protein organism=synthetic construct
3-79-5	NonEnglishQualifier Value Residues	MARLISYLRM STSEQLRGFS LERQRKLIAD FAAKNGLSVE EENTLEDIGR SSFSDDAQQK 60 ELTRFFENLN AGKYEPGDVF ALENIDRLTR RGPVDAILKV NQIISKGLKL AIISGNEQRI 120 IEDVNDVFTI INLSIDASRA NKESKNKSDK GLSNWQEKRN LASTYKIAMT AQAPAWLDTE 180 IFYIFDEEKK KNTKRRKYVL NEEKAEAVRL IFDLYSNGNG ALKIKNILNE RNIPTFKGAP 240 YWEPSIITKI LKNPATFGLY QPKKQGTGKR DLIAAGEPIN DYFPPVITRD LFEQCEHIRE 300 GNSTRKGRKG KLFTNLFTGL LTCSKCGGPV HLINPGIDKR NKVQKSIYYL VCKRAKFTKE 360 CTTKRVRYDD FEIALLKAIQ EINLADILNE NNPLEILVKK QRSKETEINK KRKLIENFQR 420 QFLENDGDLP SFMISQAKDA EISIKLEED QREIASEIAQ LNIYNSNVDN AIEELKENAD 480 YGTRSKINLL FHEIKNISL DTENQFYTVR FKNGVMRVIT AAGFIATTEE QTQADINAIL 540 QSIEGPRIPR EIATDAEKLI EYLKAREVIE 570
3-80	Sequences	
3-80-1	Sequence Number [ID]	80
3-80-2	Molecule Type	DNA
3-80-3	Length	38
3-80-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Symmetric attB source 1..38 mol_type=other DNA organism=synthetic construct
3-80-5	NonEnglishQualifier Value Residues	ggtttgctga cgacggcggt ctccgtcgtc aacaaacc 38
3-81	Sequences	
3-81-1	Sequence Number [ID]	81
3-81-2	Molecule Type	DNA
3-81-3	Length	48
3-81-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP Consensus source 1..48 mol_type=other DNA organism=synthetic construct
3-81-5	NonEnglishQualifier Value Residues	ggtttgtnnn nnnnacnacn gnnnnnncng tngtnnnnnn nacaacc 48
3-82	Sequences	

3-82-1	Sequence Number [ID]	82	
3-82-2	Molecule Type	DNA	
3-82-3	Length	38	
3-82-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB Consensus source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-82-5	Residues	ggtttgtnna cnacngnnnn nncngtngtn nacaaacc	38
3-83	Sequences		
3-83-1	Sequence Number [ID]	83	
3-83-2	Molecule Type	DNA	
3-83-3	Length	38	
3-83-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr18 - 23228819 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-83-5	Residues	tgcttggtgc ctacagcctc tgcagaagtt cacaaact	38
3-84	Sequences		
3-84-1	Sequence Number [ID]	84	
3-84-2	Molecule Type	DNA	
3-84-3	Length	38	
3-84-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr21 - 39796718 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-84-5	Residues	gggttggtga ctacagattg cactattttg cagaaacc	38
3-85	Sequences		
3-85-1	Sequence Number [ID]	85	
3-85-2	Molecule Type	DNA	
3-85-3	Length	38	
3-85-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr5 - 130870404 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-85-5	Residues	tagttgtaga ccacagaaat ttctgctggt cagaaact	38
3-86	Sequences		
3-86-1	Sequence Number [ID]	86	
3-86-2	Molecule Type	DNA	
3-86-3	Length	38	
3-86-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr10 - 114431581 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-86-5	Residues	gttttggtga caatggttc ctctgctgta aagaaacg	38
3-87	Sequences		
3-87-1	Sequence Number [ID]	87	
3-87-2	Molecule Type	DNA	
3-87-3	Length	38	
3-87-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr4 - 78331600 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-87-5	Residues	gggttggtgg caatggagat ctcaagtgtg aaaaatca	38

3-88	Sequences		
3-88-1	Sequence Number [ID]	88	
3-88-2	Molecule Type	DNA	
3-88-3	Length	38	
3-88-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr3 - 21564386 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-88-5	Residues	agcttgttta catgtgaatt ttctgtagta aacaacca	38
3-89	Sequences		
3-89-1	Sequence Number [ID]	89	
3-89-2	Molecule Type	DNA	
3-89-3	Length	38	
3-89-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr17 - 37733272 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-89-5	Residues	tgtttgtact ctaccgaaga ttccatagtt aacaacca	38
3-90	Sequences		
3-90-1	Sequence Number [ID]	90	
3-90-2	Molecule Type	DNA	
3-90-3	Length	38	
3-90-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr7 - 37683631 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-90-5	Residues	tatttcttga caattggcct ctctgtagtt tgcaacct	38
3-91	Sequences		
3-91-1	Sequence Number [ID]	91	
3-91-2	Molecule Type	DNA	
3-91-3	Length	38	
3-91-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr9 - 94861248 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-91-5	Residues	ggtttgaggg cagcagcagc agctgctgtc accaaaca	38
3-92	Sequences		
3-92-1	Sequence Number [ID]	92	
3-92-2	Molecule Type	DNA	
3-92-3	Length	38	
3-92-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chrX - 50461727 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-92-5	Residues	gttttgttca ctgtagaatc ctcagtggtt agcacaat	38
3-93	Sequences		
3-93-1	Sequence Number [ID]	93	
3-93-2	Molecule Type	DNA	
3-93-3	Length	38	
3-93-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 203596869 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		

3-93-5	Residues	ctcttgatga ctgcagagta ttccattggt gacaaatc	38
3-94	Sequences		
3-94-1	Sequence Number [ID]	94	
3-94-2	Molecule Type	DNA	
3-94-3	Length	38	
3-94-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr5 - 35969016 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-94-5	Residues	tgtttctcaa ctacagcatg agctgtgggt gacagtaa	38
3-95	Sequences		
3-95-1	Sequence Number [ID]	95	
3-95-2	Molecule Type	DNA	
3-95-3	Length	38	
3-95-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 183975066 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-95-5	Residues	gatttgata cacctgagat gacagttgtc aagaaatc	38
3-96	Sequences		
3-96-1	Sequence Number [ID]	96	
3-96-2	Molecule Type	DNA	
3-96-3	Length	38	
3-96-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr6 - 120401383 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-96-5	Residues	atttgtttaa ctactgagtt ttcagtagtt aaaaagct	38
3-97	Sequences		
3-97-1	Sequence Number [ID]	97	
3-97-2	Molecule Type	DNA	
3-97-3	Length	38	
3-97-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr2 - 131113644 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-97-5	Residues	ggctttttca ttacagaaca cccagttgtc agtatcag	38
3-98	Sequences		
3-98-1	Sequence Number [ID]	98	
3-98-2	Molecule Type	DNA	
3-98-3	Length	38	
3-98-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr18 - 68095661 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-98-5	Residues	ttattgttga caactgatat ttccacggtg agaatccc	38
3-99	Sequences		
3-99-1	Sequence Number [ID]	99	
3-99-2	Molecule Type	DNA	
3-99-3	Length	38	
3-99-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr10 - 95438042 source 1..38 mol_type=other DNA organism=synthetic construct	

3-99-5	NonEnglishQualifier Value Residues	gggtttttaa acactgactt gcctggtgtg aggatcca	38
3-100	Sequences		
3-100-1	Sequence Number [ID]	100	
3-100-2	Molecule Type	DNA	
3-100-3	Length	38	
3-100-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr11 - 93987223 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-100-5	Residues	aatttgctga caacagggtgc ttctgtgggtt aggagtgg	38
3-101	Sequences		
3-101-1	Sequence Number [ID]	101	
3-101-2	Molecule Type	DNA	
3-101-3	Length	38	
3-101-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr18 - 38351472 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-101-5	Residues	ggctttttaga ctgatgagtg atcagtccttc aggatccc	38
3-102	Sequences		
3-102-1	Sequence Number [ID]	102	
3-102-2	Molecule Type	DNA	
3-102-3	Length	38	
3-102-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr6 - 84802299 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-102-5	Residues	atagtgttta cctcagaaag atctgtggta aggaccaa	38
3-103	Sequences		
3-103-1	Sequence Number [ID]	103	
3-103-2	Molecule Type	DNA	
3-103-3	Length	38	
3-103-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chrX - 54472830 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-103-5	Residues	ggtgtgagga caagagagtg agcagtagtc aagagctc	38
3-104	Sequences		
3-104-1	Sequence Number [ID]	104	
3-104-2	Molecule Type	DNA	
3-104-3	Length	38	
3-104-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr3 - 138022040 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-104-5	Residues	tgtatgtgga ccataggaaa agctggagtc aggagctc	38
3-105	Sequences		
3-105-1	Sequence Number [ID]	105	
3-105-2	Molecule Type	DNA	
3-105-3	Length	38	
3-105-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr7 - 125717751 source 1..38 mol_type=other DNA	

		organism=synthetic construct	
3-105-5	NonEnglishQualifier Value Residues	tgtttgtgga ggagtgatgg ctcagtggtgaggatctga	38
3-106	Sequences		
3-106-1	Sequence Number [ID]	106	
3-106-2	Molecule Type	DNA	
3-106-3	Length	38	
3-106-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr6 - 29957229 source 1..38 mol_type=other DNA organism=synthetic construct	
3-106-5	NonEnglishQualifier Value Residues	gcttttttga cctcggcctc cgctcaggtc aggaccag	38
3-107	Sequences		
3-107-1	Sequence Number [ID]	107	
3-107-2	Molecule Type	DNA	
3-107-3	Length	38	
3-107-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr2 - 118918350 source 1..38 mol_type=other DNA organism=synthetic construct	
3-107-5	NonEnglishQualifier Value Residues	ctgatacttg caactgaaca cactgtagtc cacacacc	38
3-108	Sequences		
3-108-1	Sequence Number [ID]	108	
3-108-2	Molecule Type	DNA	
3-108-3	Length	38	
3-108-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 218729444 source 1..38 mol_type=other DNA organism=synthetic construct	
3-108-5	NonEnglishQualifier Value Residues	gagatcttgg caataggaac ctcagctgtc agcaagca	38
3-109	Sequences		
3-109-1	Sequence Number [ID]	109	
3-109-2	Molecule Type	DNA	
3-109-3	Length	38	
3-109-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr12 - 82686460 source 1..38 mol_type=other DNA organism=synthetic construct	
3-109-5	NonEnglishQualifier Value Residues	gagtttgtga caaccgaagc tgcagcagtc gccaaacc	38
3-110	Sequences		
3-110-1	Sequence Number [ID]	110	
3-110-2	Molecule Type	DNA	
3-110-3	Length	38	
3-110-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 12564817 source 1..38 mol_type=other DNA organism=synthetic construct	
3-110-5	NonEnglishQualifier Value Residues	ttgcttctca ccgtagatga ccctcttgtc cacaaacc	38
3-111	Sequences		
3-111-1	Sequence Number [ID]	111	
3-111-2	Molecule Type	DNA	
3-111-3	Length	38	
3-111-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr14 - 33253493 source 1..38	

		mol_type=other DNA organism=synthetic construct	
3-111-5	NonEnglishQualifier Value Residues	cagctcctca caactgattt cccaatggta atcaagct	38
3-112	Sequences		
3-112-1	Sequence Number [ID]	112	
3-112-2	Molecule Type	DNA	
3-112-3	Length	38	
3-112-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr5 - 168835161 source 1..38 mol_type=other DNA organism=synthetic construct	
3-112-5	NonEnglishQualifier Value Residues	gagatcctag ccacaggcgg gcccaggggtt ggcaaacc	38
3-113	Sequences		
3-113-1	Sequence Number [ID]	113	
3-113-2	Molecule Type	DNA	
3-113-3	Length	38	
3-113-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 205211683 source 1..38 mol_type=other DNA organism=synthetic construct	
3-113-5	NonEnglishQualifier Value Residues	tggtcccaa cctccgtcac tgccgttgca aacaaacc	38
3-114	Sequences		
3-114-1	Sequence Number [ID]	114	
3-114-2	Molecule Type	DNA	
3-114-3	Length	38	
3-114-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr17 - 51831373 source 1..38 mol_type=other DNA organism=synthetic construct	
3-114-5	NonEnglishQualifier Value Residues	agattcctga ctacagtga tgctgttggt tgcaattc	38
3-115	Sequences		
3-115-1	Sequence Number [ID]	115	
3-115-2	Molecule Type	DNA	
3-115-3	Length	38	
3-115-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr7 - 73438826 source 1..38 mol_type=other DNA organism=synthetic construct	
3-115-5	NonEnglishQualifier Value Residues	cagctcctga acacagcagt cccaggtggt gaaaagcc	38
3-116	Sequences		
3-116-1	Sequence Number [ID]	116	
3-116-2	Molecule Type	DNA	
3-116-3	Length	38	
3-116-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr8 - 138569746 source 1..38 mol_type=other DNA organism=synthetic construct	
3-116-5	NonEnglishQualifier Value Residues	ttggtcttta caactggggc tactgtgggtg gataatcg	38
3-117	Sequences		
3-117-1	Sequence Number [ID]	117	
3-117-2	Molecule Type	DNA	
3-117-3	Length	38	
3-117-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr7 - 26280167	

		source 1..38 mol_type=other DNA organism=synthetic construct	
3-117-5	NonEnglishQualifier Value Residues	caggtcctga cctcagagcc agctggaatg aaaaaacc	38
3-118	Sequences		
3-118-1	Sequence Number [ID]	118	
3-118-2	Molecule Type	DNA	
3-118-3	Length	38	
3-118-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr18 - 64064874 source 1..38 mol_type=other DNA organism=synthetic construct	
3-118-5	NonEnglishQualifier Value Residues	cagatgctct ccacagggtc tgctgcagtt tacaatcc	38
3-119	Sequences		
3-119-1	Sequence Number [ID]	119	
3-119-2	Molecule Type	DNA	
3-119-3	Length	38	
3-119-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr15 - 26397212 source 1..38 mol_type=other DNA organism=synthetic construct	
3-119-5	NonEnglishQualifier Value Residues	atgacctca ctacagctat ggcaattgta ttgacct	38
3-120	Sequences		
3-120-1	Sequence Number [ID]	120	
3-120-2	Molecule Type	DNA	
3-120-3	Length	38	
3-120-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr11 - 121591710 source 1..38 mol_type=other DNA organism=synthetic construct	
3-120-5	NonEnglishQualifier Value Residues	gtgctcctaa cagcaggcgg aacagagggtg aggatcct	38
3-121	Sequences		
3-121-1	Sequence Number [ID]	121	
3-121-2	Molecule Type	DNA	
3-121-3	Length	38	
3-121-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr1 - 84080800 source 1..38 mol_type=other DNA organism=synthetic construct	
3-121-5	NonEnglishQualifier Value Residues	aagatcctga cctccgaaga agctggagtt gagatcat	38
3-122	Sequences		
3-122-1	Sequence Number [ID]	122	
3-122-2	Molecule Type	DNA	
3-122-3	Length	38	
3-122-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr6 - 124844046 source 1..38 mol_type=other DNA organism=synthetic construct	
3-122-5	NonEnglishQualifier Value Residues	atggtccag ctactgggga ggctgaggtg aggatcgc	38
3-123	Sequences		
3-123-1	Sequence Number [ID]	123	
3-123-2	Molecule Type	DNA	
3-123-3	Length	38	

3-123-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr3 - 194380608 source 1..38 mol_type=other DNA organism=synthetic construct	
3-123-5	NonEnglishQualifier Value Residues	ttgctcctca cagcagagga ctctgaagac aggagcat	38
3-124	Sequences		
3-124-1	Sequence Number [ID]	124	
3-124-2	Molecule Type	DNA	
3-124-3	Length	38	
3-124-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr21 - 38902753 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-124-5	Residues	tggatcttca ctatggcact ccatttggtg tggatctc	38
3-125	Sequences		
3-125-1	Sequence Number [ID]	125	
3-125-2	Molecule Type	DNA	
3-125-3	Length	38	
3-125-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr18 - 33954365 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-125-5	Residues	cagatctata cggctgacta cacagtgggtg agaaccat	38
3-126	Sequences		
3-126-1	Sequence Number [ID]	126	
3-126-2	Molecule Type	DNA	
3-126-3	Length	38	
3-126-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr14 - 42626161 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-126-5	Residues	atgatcctca cagcagatat atctgttctc aagattta	38
3-127	Sequences		
3-127-1	Sequence Number [ID]	127	
3-127-2	Molecule Type	DNA	
3-127-3	Length	38	
3-127-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr10 - 27365656 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-127-5	Residues	atgatcttga caacagggag tgctgggttc tggaacat	38
3-128	Sequences		
3-128-1	Sequence Number [ID]	128	
3-128-2	Molecule Type	DNA	
3-128-3	Length	38	
3-128-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr4 - 9830819 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-128-5	Residues	ctgatgctga ccacagcaaa tgctgccaac aggatccc	38
3-129	Sequences		
3-129-1	Sequence Number [ID]	129	
3-129-2	Molecule Type	DNA	

3-129-3	Length	38
3-129-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr12 - 69787548 source 1..38 mol_type=other DNA organism=synthetic construct
3-129-5	NonEnglishQualifier Value Residues	atgatcctaa ctcttgcttt atctactgtg aaaatcat 38
3-130	Sequences	
3-130-1	Sequence Number [ID]	130
3-130-2	Molecule Type	DNA
3-130-3	Length	38
3-130-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: chr11 - 97082317 source 1..38 mol_type=other DNA organism=synthetic construct
3-130-5	NonEnglishQualifier Value Residues	ttggtcctgg atcctgaggt tgctgtggtg aagatccc 38
3-131	Sequences	
3-131-1	Sequence Number [ID]	131
3-131-2	Molecule Type	AA
3-131-3	Length	452
3-131-4	Features Location/ Qualifiers	REGION 1..452 note=Synthetic: Wildtype LI source 1..452 mol_type=protein organism=synthetic construct
3-131-5	NonEnglishQualifier Value Residues	MKAAIYIRVS TQEQVENYSI QAQTEKLTAL CRSKDWDVYD TFIDGGYSGS NMNRPALNEM 60 LSKLHEIDAV VVYRLDRLSR SQKDTITLIE EYFLKNNVEF VSLSETLDTS SPFGGRAMIGI 120 LSVFAQLERE TIRDRMVMGK IKRIEAGLPL TTAKGRTFGY DVIDTKLYIN EEEAKQLRLI 180 YDIFEEEQSI TFLQKRLKKL GFKVRTYNRY NNWLTNDLYC GYVSYKDKVH VKGIHEPIIS 240 EEQFYRVQEI FSRMGKNPNM NKESASLLNN LVVCSKCGLG FVHRRKDTVS RGKKYHYRYY 300 SCKTYKTHE LEKCGNKIWR ADKLEELIID RVNNYSFASR NIDKEDELD LNEKLKIEHA 360 KKKRLFDLYI NGSYEVSELD SMMNDIDAQI NYEAEQIEAN EELKKNKKIQ ENLADLATVD 420 FNSLEFREKQ LYLSLINKI YIDGEQVTIE WL 452
3-132	Sequences	
3-132-1	Sequence Number [ID]	132
3-132-2	Molecule Type	AA
3-132-3	Length	452
3-132-4	Features Location/ Qualifiers	REGION 1..452 note=Synthetic: Wildtype A118 source 1..452 mol_type=protein organism=synthetic construct
3-132-5	NonEnglishQualifier Value Residues	MKAAIYIRVS TQEQVENYSI QAQTEKLTAL CRSKDWDVYD IFIDGGYSGS NMNRPALNEM 60 LSKLHEIDAV VVYRLDRLSR SQRDTITLIE EYFLKNNVEF VSLSETLDTS SPFGGRAMIGI 120 LSVFAQLERE TIRDRMVMGK IKRIEAGLPL TTAKGRTFGY DVIDTKLYIN EEEAKQLQLI 180 YDIFEEEQSI TFLQKRLKKL GFKVRTYNRY NNWLTNDLYC GYVSYKDKVH VKGIHEPIIS 240 EEQFYRVQEI FTRMGKNPNM NRDSASLLNN LVVCSKCGLG FVHRRKDTMS RGKKYHYRYY 300 SCKTYKTHE LEKCGNKIWR ADKLEELIIN RVNNYSFASR NVDKEDELD LNEKLKIEHA 360 KKKRLFDLYI NGSYEVSELD SMMNDIDAQI NYYESQIEAN EELKKNKKIQ ENLADLATVD 420 FDSLEFREKQ LYLSLINKI YIDGEQVTIE WL 452
3-133	Sequences	
3-133-1	Sequence Number [ID]	133
3-133-2	Molecule Type	AA
3-133-3	Length	485
3-133-4	Features Location/ Qualifiers	REGION 1..485 note=Synthetic: Wildtype TP901 source 1..485 mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	

3-133-5	Residues	MTKKVAIYTR VSTTNQAEFG FSIDEQIDRL TKYAEAMGWQ VSDTYTDAGF SGAKLERPAM 60 QRLINDIENK AFDTVLVYKL DRLSRVSRDT LYLVKDVFTK NKIDFISLNE SIDTSSAMGS 120 LFLTILSAIN EFERENIKER MTMGKLGRAK SGKSMWTKT AFGYYHNRKT GILEIVPLQA 180 TIVEQIFTDY LSGISLTKLR DKLNESGHIG KDIPWSYRTL RQTLDNPVYC GYIKFKDSL 240 EGMHKPIIPY ETYLVQKEL EERQQQTYER NNNPRPFQAK YMLSGMARCG YCGAPLKIVL 300 GHKRKDGSRM MKYHCANRFP RKTGKITVYN DNKKCDSGTY DLSNLENTVI DNLIGFQENN 360 DSLLKIINGN NQPILDTSSF KKQISQIDKK IQKNSDLYLN DFITMDELKD RTDSLQAEKK 420 LLKAKISENK FNDSTDVFEL VKTQLGSIPI NELSYDNKKK IVNNLVSKVD VTADNVDIIF 480 KFQLA 485
3-134	Sequences	
3-134-1	Sequence Number [ID]	134
3-134-2	Molecule Type	DNA
3-134-3	Length	38
3-134-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Consensus attB sequence source 1..38 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-134-5	Residues	ggtttgtnna cnacngnnnn nncngtngtn aggatcnn 38
3-135	Sequences	
3-135-1	Sequence Number [ID]	135
3-135-2	Molecule Type	DNA
3-135-3	Length	38
3-135-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Consensus attB sequence source 1..38 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-135-5	Residues	nngatcctga cgacngnnnn nncngtngtn nacaacc 38
3-136	Sequences	
3-136-1	Sequence Number [ID]	136
3-136-2	Molecule Type	DNA
3-136-3	Length	38
3-136-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Consensus attB sequence source 1..38 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-136-5	Residues	nngatcctga cgacngnnnn nncngtngtn aggatcnn 38
3-137	Sequences	
3-137-1	Sequence Number [ID]	137
3-137-2	Molecule Type	DNA
3-137-3	Length	48
3-137-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-1 source 1..48 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-137-5	Residues	ccattccttc ttctaccaca gcgttctcaa ttgggtaagc atcaaaat 48
3-138	Sequences	
3-138-1	Sequence Number [ID]	138
3-138-2	Molecule Type	DNA
3-138-3	Length	48
3-138-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-2 source 1..48 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-138-5	Residues	ttagttgct cctgacagca gtgggagcta ttgtctaaga gatacaaa 48
3-139	Sequences	

3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	DNA	
3-139-3	Length	48	
3-139-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-4 source 1..48 mol_type=other DNA organism=synthetic construct	
3-139-5	NonEnglishQualifier Value Residues	ggagttgagt cctgactgca gcacatgcag gtgaggaagc agtagaag	48
3-140	Sequences		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	DNA	
3-140-3	Length	48	
3-140-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-6 source 1..48 mol_type=other DNA organism=synthetic construct	
3-140-5	NonEnglishQualifier Value Residues	tactggggat tcccataacc gtgcactcag ctgcggaag gcaggaga	48
3-141	Sequences		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	DNA	
3-141-3	Length	48	
3-141-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-8 source 1..48 mol_type=other DNA organism=synthetic construct	
3-141-5	NonEnglishQualifier Value Residues	gagtagtgta tctgacacca gcacactctg gtgtcagaat cttggggt	48
3-142	Sequences		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	DNA	
3-142-3	Length	48	
3-142-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-10 source 1..48 mol_type=other DNA organism=synthetic construct	
3-142-5	NonEnglishQualifier Value Residues	atagtgaaac ttacaacaca gagtttccag ttgttcaatc tctcttgt	48
3-143	Sequences		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	DNA	
3-143-3	Length	48	
3-143-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-11 source 1..48 mol_type=other DNA organism=synthetic construct	
3-143-5	NonEnglishQualifier Value Residues	ttgaagcccc ttctctaca gagcaagcag cagggtaaat tctgtatt	48
3-144	Sequences		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	DNA	
3-144-3	Length	48	
3-144-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-14 source 1..48 mol_type=other DNA organism=synthetic construct	
3-144-5	NonEnglishQualifier Value Residues	tggtgcaatc ttggctcact gcaacctctg cagttgaagc aattctcc	48

3-145	Sequences		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	DNA	
3-145-3	Length	48	
3-145-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-15 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-145-5	Residues	atttgtggta ctatactaca gagaatgctg atgttaaaga gctaattt	48
3-146	Sequences		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	DNA	
3-146-3	Length	48	
3-146-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-16 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-146-5	Residues	gcactccagc ctgggcaaca gacactctg ttgtcaaaaa aaaaaaaaa	48
3-147	Sequences		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	DNA	
3-147-3	Length	48	
3-147-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-17 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-147-5	Residues	acacctggat ctccaccct gtgtttgctg ttgtctaagt ttacatt	48
3-148	Sequences		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	DNA	
3-148-3	Length	48	
3-148-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-18 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-148-5	Residues	cctgcatgtt cctcaccaca gctaaccag tcttcaaac tcacttaa	48
3-149	Sequences		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	DNA	
3-149-3	Length	48	
3-149-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-19 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-149-5	Residues	ggcctcctgc ttgctcagct gagacggcag aggctgaagc tgcacggg	48
3-150	Sequences		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	DNA	
3-150-3	Length	48	
3-150-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-21 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		

3-150-5	Residues	cttccttctt ttaaaccact gatcatgcag aagtataagc tcaccagt	48
3-151	Sequences		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	DNA	
3-151-3	Length	48	
3-151-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-24 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-151-5	Residues	gtggcagaaa tagtacaaca gctaacgcag atgttaaaaa tcaaattgg	48
3-152	Sequences		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	DNA	
3-152-3	Length	48	
3-152-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-1 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-152-5	Residues	cagtgtgctt gttgcctaca gcctctgcag aagttcacia acttgcac	48
3-153	Sequences		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	DNA	
3-153-3	Length	48	
3-153-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-5 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-153-5	Residues	attaggggtt ggtggcaatg gagatctcag tggtgaaaaa tcacttct	48
3-154	Sequences		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	DNA	
3-154-3	Length	48	
3-154-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-10 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-154-5	Residues	atgtggtttt gttcactgta gaatcctcag tggtagcac aatgttaa	48
3-155	Sequences		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	DNA	
3-155-3	Length	48	
3-155-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-11 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-155-5	Residues	catttctctt gatgactgca gagtattcca ttgttgacaa atccattt	48
3-156	Sequences		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	DNA	
3-156-3	Length	48	
3-156-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-17 source 1..48 mol_type=other DNA organism=synthetic construct	

3-156-5	NonEnglishQualifier Value Residues	gctatggggtt tttaaacact gacttgacctg gtgtgaggat ccatgctt	48
3-157	Sequences		
3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	DNA	
3-157-3	Length	48	
3-157-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-25 source 1..48 mol_type=other DNA organism=synthetic construct	
3-157-5	NonEnglishQualifier Value Residues	gtgttctgat acttgcaact gaacacactg tagtccacac accactat	48
3-158	Sequences		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	DNA	
3-158-3	Length	48	
3-158-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-28 source 1..48 mol_type=other DNA organism=synthetic construct	
3-158-5	NonEnglishQualifier Value Residues	gggggttgct tctcaccgta gatgaccctc ttgtccacaa accacaac	48
3-159	Sequences		
3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	DNA	
3-159-3	Length	48	
3-159-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-31 source 1..48 mol_type=other DNA organism=synthetic construct	
3-159-5	NonEnglishQualifier Value Residues	cagcctggct cccaacctcc gtcactgccg ttgcaaacaa accaaacc	48
3-160	Sequences		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	DNA	
3-160-3	Length	48	
3-160-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-39 source 1..48 mol_type=other DNA organism=synthetic construct	
3-160-5	NonEnglishQualifier Value Residues	tttcaaagat cctgacctcc gaagaagctg gagttgagat catactgt	48
3-161	Sequences		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	DNA	
3-161-3	Length	48	
3-161-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-41 source 1..48 mol_type=other DNA organism=synthetic construct	
3-161-5	NonEnglishQualifier Value Residues	cgagcttgct cctcacagca gaggactctg aagacaggag catcatga	48
3-162	Sequences		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	DNA	
3-162-3	Length	48	
3-162-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-43 source 1..48 mol_type=other DNA	

		organism=synthetic construct	
3-162-5	NonEnglishQualifier Value Residues	ccttgcagat ctatacggct gactacacag tggtgagaac catagtct	48
3-163	Sequences		
3-163-1	Sequence Number [ID]	163	
3-163-2	Molecule Type	DNA	
3-163-3	Length	48	
3-163-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s3-28 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-163-5	Residues	acctttgttt ggccccaact gcctctgcc a ctgtcgacac acttgga	48
3-164	Sequences		
3-164-1	Sequence Number [ID]	164	
3-164-2	Molecule Type	DNA	
3-164-3	Length	48	
3-164-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s3-41 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-164-5	Residues	gatgcatgat tctaggcact gggaacacag tggatgatcaa accagtca	48
3-165	Sequences		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	DNA	
3-165-3	Length	84	
3-165-4	Features Location/ Qualifiers	misc_feature 1..84 note=Synthetic: s5-1 source 1..84 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-165-5	Residues	ggtttgtctg gtcaaccacc gcgttctcag tgggtgtacgg taaaacctt cgtttcaact 60 gaccaattca ctccaaatgt aaca	84
3-166	Sequences		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	DNA	
3-166-3	Length	80	
3-166-4	Features Location/ Qualifiers	misc_feature 1..80 note=Synthetic: s5-2 source 1..80 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-166-5	Residues	ggtttgtctg gtcaaccacc gcgggctcag tgggtgtacgg taaaaccaa gaggaagt 60 atacctgcag caagtatat	80
3-167	Sequences		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	DNA	
3-167-3	Length	88	
3-167-4	Features Location/ Qualifiers	misc_feature 1..88 note=Synthetic: s5-4 source 1..88 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-167-5	Residues	ggtttgtctg gtcaaccacc gcgcactcag tgggtgtacgg taaaacctat tgctgccgtc 60 tgtcccttc ccatcccttc tgacatgt	88
3-168	Sequences		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	DNA	
3-168-3	Length	77	

3-168-4	Features Location/ Qualifiers	misc_feature 1..77 note=Synthetic: s5-6 source 1..77 mol_type=other DNA organism=synthetic construct
3-168-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccag cccgaactta 60 gcttcctca tcgccta 77
3-169	Sequences	
3-169-1	Sequence Number [ID]	169
3-169-2	Molecule Type	DNA
3-169-3	Length	79
3-169-4	Features Location/ Qualifiers	misc_feature 1..79 note=Synthetic: s5-8 source 1..79 mol_type=other DNA organism=synthetic construct
3-169-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccat atcgtttgct 60 actcaaactg tgtggtcct 79
3-170	Sequences	
3-170-1	Sequence Number [ID]	170
3-170-2	Molecule Type	DNA
3-170-3	Length	78
3-170-4	Features Location/ Qualifiers	misc_feature 1..78 note=Synthetic: s5-10 source 1..78 mol_type=other DNA organism=synthetic construct
3-170-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgttctcag tgggtgtacgg tacaaaccta tcttcctttt 60 ctgtggaagg gaaaactt 78
3-171	Sequences	
3-171-1	Sequence Number [ID]	171
3-171-2	Molecule Type	DNA
3-171-3	Length	85
3-171-4	Features Location/ Qualifiers	misc_feature 1..85 note=Synthetic: s5-11 source 1..85 mol_type=other DNA organism=synthetic construct
3-171-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccaa gcagctcgga 60 gcctctctgt cacttgctct ttaga 85
3-172	Sequences	
3-172-1	Sequence Number [ID]	172
3-172-2	Molecule Type	DNA
3-172-3	Length	97
3-172-4	Features Location/ Qualifiers	misc_feature 1..97 note=Synthetic: s5-14 source 1..97 mol_type=other DNA organism=synthetic construct
3-172-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgacctcag tgggtgtacgg tacaaaccgc ctgtcacctc 60 ctgagtacct gggattacag gcgcacaaca ctactct 97
3-173	Sequences	
3-173-1	Sequence Number [ID]	173
3-173-2	Molecule Type	DNA
3-173-3	Length	92
3-173-4	Features Location/ Qualifiers	misc_feature 1..92 note=Synthetic: s5-15 source 1..92 mol_type=other DNA organism=synthetic construct

3-173-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgaactcag tgggtgtacgg tacaaacctc aggaggtggt 60 tttccttcct tttgaaatca gatagcagga aa 92
3-174	Sequences	
3-174-1	Sequence Number [ID]	174
3-174-2	Molecule Type	DNA
3-174-3	Length	89
3-174-4	Features Location/ Qualifiers	misc_feature 1..89 note=Synthetic: s5-16 source 1..89 mol_type=other DNA organism=synthetic construct
3-174-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccaa gagcacagtg 60 attatgatta ttgtttctga gtgatggca 89
3-175	Sequences	
3-175-1	Sequence Number [ID]	175
3-175-2	Molecule Type	DNA
3-175-3	Length	93
3-175-4	Features Location/ Qualifiers	misc_feature 1..93 note=Synthetic: s5-17 source 1..93 mol_type=other DNA organism=synthetic construct
3-175-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgttctcag tgggtgtacgg tacaaacctc atgtccgcac 60 ttcctaagtt ttggtttcca gagccactag taa 93
3-176	Sequences	
3-176-1	Sequence Number [ID]	176
3-176-2	Molecule Type	DNA
3-176-3	Length	99
3-176-4	Features Location/ Qualifiers	misc_feature 1..99 note=Synthetic: s5-18 source 1..99 mol_type=other DNA organism=synthetic construct
3-176-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgaactcag tgggtgtacgg tacaaacctc tattcgcaact 60 cagggaggcc ttccctgac tccagggcca gattaagta 99
3-177	Sequences	
3-177-1	Sequence Number [ID]	177
3-177-2	Molecule Type	DNA
3-177-3	Length	107
3-177-4	Features Location/ Qualifiers	misc_feature 1..107 note=Synthetic: s5-19 source 1..107 mol_type=other DNA organism=synthetic construct
3-177-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgacctcag tgggtgtacgg tacaaaccgg gccagtcagt 60 cactgtcagg tgagcaccgg cgaggggtccc ggggaggtac ggggtgac 107
3-178	Sequences	
3-178-1	Sequence Number [ID]	178
3-178-2	Molecule Type	DNA
3-178-3	Length	91
3-178-4	Features Location/ Qualifiers	misc_feature 1..91 note=Synthetic: s5-21 source 1..91 mol_type=other DNA organism=synthetic construct
3-178-5	NonEnglishQualifier Value Residues	ggtttgctcg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccac cttcacgtcc 60 taaccagacc atgagctcca ggggtaaaat c 91
3-179	Sequences	
3-179-1	Sequence Number [ID]	179

3-179-2	Molecule Type	DNA
3-179-3	Length	84
3-179-4	Features Location/ Qualifiers	misc_feature 1..84 note=Synthetic: s5-24 source 1..84 mol_type=other DNA organism=synthetic construct
3-179-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgaactcag tgggtgtacgg tacaaaccca tgtaaaacca 60 gcttattgcc aacagagtta tgga 84
3-180	Sequences	
3-180-1	Sequence Number [ID]	180
3-180-2	Molecule Type	DNA
3-180-3	Length	91
3-180-4	Features Location/ Qualifiers	misc_feature 1..91 note=Synthetic: s1-1 source 1..91 mol_type=other DNA organism=synthetic construct
3-180-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgtcctcag tgggtgtacgg tacaaaccag aatcaggata 60 aggctcctct aggtacatgt ggctaagctg c 91
3-181	Sequences	
3-181-1	Sequence Number [ID]	181
3-181-2	Molecule Type	DNA
3-181-3	Length	92
3-181-4	Features Location/ Qualifiers	misc_feature 1..92 note=Synthetic: s1-5 source 1..92 mol_type=other DNA organism=synthetic construct
3-181-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgatctcag tgggtgtacgg tacaaaccgg tcctccatca 60 agcgctgagg cacagtgaat gtactcagag gg 92
3-182	Sequences	
3-182-1	Sequence Number [ID]	182
3-182-2	Molecule Type	DNA
3-182-3	Length	86
3-182-4	Features Location/ Qualifiers	misc_feature 1..86 note=Synthetic: s1-10 source 1..86 mol_type=other DNA organism=synthetic construct
3-182-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgtcctcag tgggtgtacgg tacaaaccac acaatagcga 60 catggagcag gtatcagttt acgttt 86
3-183	Sequences	
3-183-1	Sequence Number [ID]	183
3-183-2	Molecule Type	DNA
3-183-3	Length	146
3-183-4	Features Location/ Qualifiers	misc_feature 1..146 note=Synthetic: s1-11 source 1..146 mol_type=other DNA organism=synthetic construct
3-183-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgtactcag tgggtgtacgg tacaaaccaa ccacctgatt 60 gtgatggatg tttaggttgt ttccaatcct ttgctattaa aaagaatgtg acagtgagaa 120 actttgtgta tagtgcatt ttgcac 146
3-184	Sequences	
3-184-1	Sequence Number [ID]	184
3-184-2	Molecule Type	DNA
3-184-3	Length	90
3-184-4	Features Location/ Qualifiers	misc_feature 1..90 note=Synthetic: s1-17

3-184-5	NonEnglishQualifier Value Residues	source 1..90 mol_type=other DNA organism=synthetic construct ggtttgtctg gtcaaccacc gcgttctcag tgggtgtacgg tacaaaccag catctttcaa 60 atagcacctc attttatcct gaagaccag 90
3-185	Sequences	
3-185-1	Sequence Number [ID]	185
3-185-2	Molecule Type	DNA
3-185-3	Length	89
3-185-4	Features Location/ Qualifiers	misc_feature 1..89 note=Synthetic: s1-25 source 1..89 mol_type=other DNA organism=synthetic construct
3-185-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgcactcag tgggtgtacgg tacaaaccga aaactggtag 60 aatctcagtg accttaaaga ttgcctggg 89
3-186	Sequences	
3-186-1	Sequence Number [ID]	186
3-186-2	Molecule Type	DNA
3-186-3	Length	110
3-186-4	Features Location/ Qualifiers	misc_feature 1..110 note=Synthetic: s1-28 source 1..110 mol_type=other DNA organism=synthetic construct
3-186-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcggactcag tgggtgtacgg tacaaaccga tctccctttt 60 tccgtgctga ttaggactgg ggcagtgagg ttcgtgtatt tgtgacctgg 110
3-187	Sequences	
3-187-1	Sequence Number [ID]	187
3-187-2	Molecule Type	DNA
3-187-3	Length	87
3-187-4	Features Location/ Qualifiers	misc_feature 1..87 note=Synthetic: s1-31 source 1..87 mol_type=other DNA organism=synthetic construct
3-187-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcgacctcag tgggtgtacgg tacaaaccgc agtgtccacc 60 tggcggaacc tttctctcca ctatcca 87
3-188	Sequences	
3-188-1	Sequence Number [ID]	188
3-188-2	Molecule Type	DNA
3-188-3	Length	83
3-188-4	Features Location/ Qualifiers	misc_feature 1..83 note=Synthetic: s1-39 source 1..83 mol_type=other DNA organism=synthetic construct
3-188-5	NonEnglishQualifier Value Residues	ggtttgtctg gtcaaccacc gcggactcag tgggtgtacgg tacaaacctg gtaaataagga 60 tcaaaggaat agagtctgat gcc 83
3-189	Sequences	
3-189-1	Sequence Number [ID]	189
3-189-2	Molecule Type	DNA
3-189-3	Length	84
3-189-4	Features Location/ Qualifiers	misc_feature 1..84 note=Synthetic: s1-41 source 1..84 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	

3-189-5	Residues	ggtttgctcg gtcaaccacc gcggactcag tgggtgtacgg tacaaaccct gtgactacat 60 ttagtgagca ggtggaatga acaa 84
3-190	Sequences	
3-190-1	Sequence Number [ID]	190
3-190-2	Molecule Type	DNA
3-190-3	Length	90
3-190-4	Features Location/ Qualifiers	misc_feature 1..90 note=Synthetic: s1-43 source 1..90 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-190-5	Residues	ggtttgctcg gtcaaccacc gcgtactcag tgggtgtacgg tacaaaccgg ataagtttca 60 gtaaagggac tactgcagga ttggtggta 90
3-191	Sequences	
3-191-1	Sequence Number [ID]	191
3-191-2	Molecule Type	DNA
3-191-3	Length	91
3-191-4	Features Location/ Qualifiers	misc_feature 1..91 note=Synthetic: s3-28 source 1..91 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-191-5	Residues	ggtttgctcg gtcaaccacc gcgtcctcag tgggtgtacgg tacaaacctg cgttgtctga 60 gctcctcagc actccctccc caacttccta t 91
3-192	Sequences	
3-192-1	Sequence Number [ID]	192
3-192-2	Molecule Type	DNA
3-192-3	Length	93
3-192-4	Features Location/ Qualifiers	misc_feature 1..93 note=Synthetic: s3-41 source 1..93 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-192-5	Residues	ggtttgctcg gtcaaccacc gcgaactcag tgggtgtacgg tacaaaccag tcaccaatct 60 ggaggggatg aggtgagga gggatagaca ata 93
3-193	Sequences	
3-193-1	Sequence Number [ID]	193
3-193-2	Molecule Type	DNA
3-193-3	Length	47
3-193-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s5-1 source 1..47 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-193-5	Residues	acacgacgct cttccgatct nnnnttcttt catttcgtgt gagggtc 47
3-194	Sequences	
3-194-1	Sequence Number [ID]	194
3-194-2	Molecule Type	DNA
3-194-3	Length	46
3-194-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s5-2 source 1..46 mol_type=other DNA organism=synthetic construct
	NonEnglishQualifier Value	
3-194-5	Residues	acacgacgct cttccgatct nnnnaccctg tgtagaagc agtaac 46
3-195	Sequences	
3-195-1	Sequence Number [ID]	195
3-195-2	Molecule Type	DNA
3-195-3	Length	47

3-195-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s5-4 source 1..47 mol_type=other DNA organism=synthetic construct	
3-195-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnatgtgt ttggaagctg agcatag	47
3-196	Sequences		
3-196-1	Sequence Number [ID]	196	
3-196-2	Molecule Type	DNA	
3-196-3	Length	46	
3-196-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s5-6 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-196-5	Residues	acacgacgct cttccgatct nnnncgatgt gttcctccat gaagca	46
3-197	Sequences		
3-197-1	Sequence Number [ID]	197	
3-197-2	Molecule Type	DNA	
3-197-3	Length	49	
3-197-4	Features Location/ Qualifiers	misc_feature 1..49 note=Synthetic: s5-8 source 1..49 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-197-5	Residues	acacgacgct cttccgatct nnnngcatag ctgagtaata cattgcatg	49
3-198	Sequences		
3-198-1	Sequence Number [ID]	198	
3-198-2	Molecule Type	DNA	
3-198-3	Length	48	
3-198-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-10 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-198-5	Residues	acacgacgct cttccgatct nnnnatgggc agcattcatt aagtaaat	48
3-199	Sequences		
3-199-1	Sequence Number [ID]	199	
3-199-2	Molecule Type	DNA	
3-199-3	Length	48	
3-199-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-11 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-199-5	Residues	acacgacgct cttccgatct nnnncaatta gttggctgta taatttgg	48
3-200	Sequences		
3-200-1	Sequence Number [ID]	200	
3-200-2	Molecule Type	DNA	
3-200-3	Length	50	
3-200-4	Features Location/ Qualifiers	misc_feature 1..50 note=Synthetic: s5-14 source 1..50 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-200-5	Residues	acacgacgct cttccgatct nnnnatttca cattgattga ttttcttggt	50
3-201	Sequences		
3-201-1	Sequence Number [ID]	201	
3-201-2	Molecule Type	DNA	

3-201-3	Length	47	
3-201-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s5-15 source 1..47 mol_type=other DNA organism=synthetic construct	
3-201-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnactgcc acctacattc aacaaat	47
3-202	Sequences		
3-202-1	Sequence Number [ID]	202	
3-202-2	Molecule Type	DNA	
3-202-3	Length	44	
3-202-4	Features Location/ Qualifiers	misc_feature 1..44 note=Synthetic: s5-16 source 1..44 mol_type=other DNA organism=synthetic construct	
3-202-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnagaggg ctgaggttgc aatg	44
3-203	Sequences		
3-203-1	Sequence Number [ID]	203	
3-203-2	Molecule Type	DNA	
3-203-3	Length	52	
3-203-4	Features Location/ Qualifiers	misc_feature 1..52 note=Synthetic: s5-17 source 1..52 mol_type=other DNA organism=synthetic construct	
3-203-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnntgcaga taattcttat gcaaaacaga ac	52
3-204	Sequences		
3-204-1	Sequence Number [ID]	204	
3-204-2	Molecule Type	DNA	
3-204-3	Length	48	
3-204-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-18 source 1..48 mol_type=other DNA organism=synthetic construct	
3-204-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnngcagaa agttagtatg acacagac	48
3-205	Sequences		
3-205-1	Sequence Number [ID]	205	
3-205-2	Molecule Type	DNA	
3-205-3	Length	50	
3-205-4	Features Location/ Qualifiers	misc_feature 1..50 note=Synthetic: s5-19 source 1..50 mol_type=other DNA organism=synthetic construct	
3-205-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnngaccag acagttccag atacattcca	50
3-206	Sequences		
3-206-1	Sequence Number [ID]	206	
3-206-2	Molecule Type	DNA	
3-206-3	Length	48	
3-206-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-21 source 1..48 mol_type=other DNA organism=synthetic construct	
3-206-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnttactc tctctcctag actcaagc	48
3-207	Sequences		
3-207-1	Sequence Number [ID]	207	

3-207-2	Molecule Type	DNA	
3-207-3	Length	48	
3-207-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-24 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-207-5	Residues	acacgacgct cttccgatct nnnntgctag tatttgctcg cactttct	48
3-208	Sequences		
3-208-1	Sequence Number [ID]	208	
3-208-2	Molecule Type	DNA	
3-208-3	Length	46	
3-208-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s1-1 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-208-5	Residues	acacgacgct cttccgatct nnnncgtggg ccagttttaa atgtca	46
3-209	Sequences		
3-209-1	Sequence Number [ID]	209	
3-209-2	Molecule Type	DNA	
3-209-3	Length	46	
3-209-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s1-5 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-209-5	Residues	acacgacgct cttccgatct nnnngctgaa cattagctcc atatat	46
3-210	Sequences		
3-210-1	Sequence Number [ID]	210	
3-210-2	Molecule Type	DNA	
3-210-3	Length	49	
3-210-4	Features Location/ Qualifiers	misc_feature 1..49 note=Synthetic: s1-10 source 1..49 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-210-5	Residues	acacgacgct cttccgatct nnnnagctctc tcatttacca gttttgctt	49
3-211	Sequences		
3-211-1	Sequence Number [ID]	211	
3-211-2	Molecule Type	DNA	
3-211-3	Length	47	
3-211-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s1-11 source 1..47 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-211-5	Residues	acacgacgct cttccgatct nnnnggatta tcccatatcc agacata	47
3-212	Sequences		
3-212-1	Sequence Number [ID]	212	
3-212-2	Molecule Type	DNA	
3-212-3	Length	46	
3-212-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s1-17 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-212-5	Residues	acacgacgct cttccgatct nnnnagccca gagttaacca agctac	46
3-213	Sequences		

3-213-1	Sequence Number [ID]	213	
3-213-2	Molecule Type	DNA	
3-213-3	Length	47	
3-213-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s1-25 source 1..47 mol_type=other DNA organism=synthetic construct	
3-213-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnntacaac taaagcacca atggctc	47
3-214	Sequences		
3-214-1	Sequence Number [ID]	214	
3-214-2	Molecule Type	DNA	
3-214-3	Length	45	
3-214-4	Features Location/ Qualifiers	misc_feature 1..45 note=Synthetic: s1-28 source 1..45 mol_type=other DNA organism=synthetic construct	
3-214-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnngtcaga agtcccagat gtgct	45
3-215	Sequences		
3-215-1	Sequence Number [ID]	215	
3-215-2	Molecule Type	DNA	
3-215-3	Length	42	
3-215-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s1-31 source 1..42 mol_type=other DNA organism=synthetic construct	
3-215-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnggaatc cgcctcctga cg	42
3-216	Sequences		
3-216-1	Sequence Number [ID]	216	
3-216-2	Molecule Type	DNA	
3-216-3	Length	47	
3-216-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s1-39 source 1..47 mol_type=other DNA organism=synthetic construct	
3-216-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnntgatgt tagagatcag cctgtac	47
3-217	Sequences		
3-217-1	Sequence Number [ID]	217	
3-217-2	Molecule Type	DNA	
3-217-3	Length	47	
3-217-4	Features Location/ Qualifiers	misc_feature 1..47 note=Synthetic: s1-41 source 1..47 mol_type=other DNA organism=synthetic construct	
3-217-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnnagccat ttccttccta gcaaatt	47
3-218	Sequences		
3-218-1	Sequence Number [ID]	218	
3-218-2	Molecule Type	DNA	
3-218-3	Length	48	
3-218-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-43 source 1..48 mol_type=other DNA organism=synthetic construct	
3-218-5	NonEnglishQualifier Value Residues	acacgacgct cttccgatct nnnncaatac aggcacaatc cccttatt	48

3-219	Sequences		
3-219-1	Sequence Number [ID]	219	
3-219-2	Molecule Type	DNA	
3-219-3	Length	46	
3-219-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s3-28 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-219-5	Residues	acacgacgct cttccgatct nnnntgaagg gaaaggctctg gcttta	46
3-220	Sequences		
3-220-1	Sequence Number [ID]	220	
3-220-2	Molecule Type	DNA	
3-220-3	Length	43	
3-220-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s3-41 source 1..43 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-220-5	Residues	acacgacgct cttccgatct nnnncagcag tcgatgtggg aac	43
3-221	Sequences		
3-221-1	Sequence Number [ID]	221	
3-221-2	Molecule Type	DNA	
3-221-3	Length	45	
3-221-4	Features Location/ Qualifiers	misc_feature 1..45 note=Synthetic: s5-1 source 1..45 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-221-5	Residues	gacgtgtgct cttccgatct tgttacattt ggagtgaatt ggtca	45
3-222	Sequences		
3-222-1	Sequence Number [ID]	222	
3-222-2	Molecule Type	DNA	
3-222-3	Length	46	
3-222-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s5-2 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-222-5	Residues	gacgtgtgct cttccgatct atatcacttg ctgcaggat actttt	46
3-223	Sequences		
3-223-1	Sequence Number [ID]	223	
3-223-2	Molecule Type	DNA	
3-223-3	Length	42	
3-223-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s5-4 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-223-5	Residues	gacgtgtgct cttccgatct acatgtcaga agggatggga ag	42
3-224	Sequences		
3-224-1	Sequence Number [ID]	224	
3-224-2	Molecule Type	DNA	
3-224-3	Length	42	
3-224-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s5-6 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		

3-224-5	Residues	gacgtgtgct cttccgatct taggcgatga gggaagctaa gt	42
3-225	Sequences		
3-225-1	Sequence Number [ID]	225	
3-225-2	Molecule Type	DNA	
3-225-3	Length	42	
3-225-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s5-8 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-225-5	Residues	gacgtgtgct cttccgatct aggaccacac agtttgagta gc	42
3-226	Sequences		
3-226-1	Sequence Number [ID]	226	
3-226-2	Molecule Type	DNA	
3-226-3	Length	41	
3-226-4	Features Location/ Qualifiers	misc_feature 1..41 note=Synthetic: s5-10 source 1..41 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-226-5	Residues	gacgtgtgct cttccgatct aagttttccc ttccacagaa a	41
3-227	Sequences		
3-227-1	Sequence Number [ID]	227	
3-227-2	Molecule Type	DNA	
3-227-3	Length	44	
3-227-4	Features Location/ Qualifiers	misc_feature 1..44 note=Synthetic: s5-11 source 1..44 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-227-5	Residues	gacgtgtgct cttccgatct tctaaagagc aagtgacaga gagg	44
3-228	Sequences		
3-228-1	Sequence Number [ID]	228	
3-228-2	Molecule Type	DNA	
3-228-3	Length	40	
3-228-4	Features Location/ Qualifiers	misc_feature 1..40 note=Synthetic: s5-14 source 1..40 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-228-5	Residues	gacgtgtgct cttccgatct agagtagtgt tgtgcgcctg	40
3-229	Sequences		
3-229-1	Sequence Number [ID]	229	
3-229-2	Molecule Type	DNA	
3-229-3	Length	46	
3-229-4	Features Location/ Qualifiers	misc_feature 1..46 note=Synthetic: s5-15 source 1..46 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-229-5	Residues	gacgtgtgct cttccgatct tttcctgcta tctgatttca aaagga	46
3-230	Sequences		
3-230-1	Sequence Number [ID]	230	
3-230-2	Molecule Type	DNA	
3-230-3	Length	45	
3-230-4	Features Location/ Qualifiers	misc_feature 1..45 note=Synthetic: s5-16 source 1..45 mol_type=other DNA organism=synthetic construct	

3-230-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct tgccatcact cagaaacaat aatca	45
3-231	Sequences		
3-231-1	Sequence Number [ID]	231	
3-231-2	Molecule Type	DNA	
3-231-3	Length	42	
3-231-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s5-17 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-231-5	Residues	gacgtgtgct cttccgatct ttactagtgg ctctggaaac ca	42
3-232	Sequences		
3-232-1	Sequence Number [ID]	232	
3-232-2	Molecule Type	DNA	
3-232-3	Length	43	
3-232-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s5-18 source 1..43 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-232-5	Residues	gacgtgtgct cttccgatct tacttaatct ggccctggag atc	43
3-233	Sequences		
3-233-1	Sequence Number [ID]	233	
3-233-2	Molecule Type	DNA	
3-233-3	Length	38	
3-233-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: s5-19 source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-233-5	Residues	gacgtgtgct cttccgatct gtcacccgta cctccccg	38
3-234	Sequences		
3-234-1	Sequence Number [ID]	234	
3-234-2	Molecule Type	DNA	
3-234-3	Length	42	
3-234-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s5-21 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-234-5	Residues	gacgtgtgct cttccgatct gattttaccc ctggagctca tg	42
3-235	Sequences		
3-235-1	Sequence Number [ID]	235	
3-235-2	Molecule Type	DNA	
3-235-3	Length	43	
3-235-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s5-24 source 1..43 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-235-5	Residues	gacgtgtgct cttccgatct tccataactc tgttggcaat aag	43
3-236	Sequences		
3-236-1	Sequence Number [ID]	236	
3-236-2	Molecule Type	DNA	
3-236-3	Length	42	
3-236-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s1-1 source 1..42 mol_type=other DNA	

	NonEnglishQualifier Value	organism=synthetic construct	
3-236-5	Residues	gacgtgtgct cttccgatct gcagcttagc cacatgtacc ta	42
3-237	Sequences		
3-237-1	Sequence Number [ID]	237	
3-237-2	Molecule Type	DNA	
3-237-3	Length	40	
3-237-4	Features Location/ Qualifiers	misc_feature 1..40 note=Synthetic: s1-5 source 1..40 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-237-5	Residues	gacgtgtgct cttccgatct ccctctgagt acattcactg	40
3-238	Sequences		
3-238-1	Sequence Number [ID]	238	
3-238-2	Molecule Type	DNA	
3-238-3	Length	43	
3-238-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s1-10 source 1..43 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-238-5	Residues	gacgtgtgct cttccgatct aaacgtaaac tgatacctgc tcc	43
3-239	Sequences		
3-239-1	Sequence Number [ID]	239	
3-239-2	Molecule Type	DNA	
3-239-3	Length	45	
3-239-4	Features Location/ Qualifiers	misc_feature 1..45 note=Synthetic: s1-11 source 1..45 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-239-5	Residues	gacgtgtgct cttccgatct gtgcaaaatg acactataca caaag	45
3-240	Sequences		
3-240-1	Sequence Number [ID]	240	
3-240-2	Molecule Type	DNA	
3-240-3	Length	44	
3-240-4	Features Location/ Qualifiers	misc_feature 1..44 note=Synthetic: s1-17 source 1..44 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-240-5	Residues	gacgtgtgct cttccgatct ctgggtcttc aggataaaat gagg	44
3-241	Sequences		
3-241-1	Sequence Number [ID]	241	
3-241-2	Molecule Type	DNA	
3-241-3	Length	42	
3-241-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s1-25 source 1..42 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-241-5	Residues	gacgtgtgct cttccgatct cccaggcaat ctttaaggtc ac	42
3-242	Sequences		
3-242-1	Sequence Number [ID]	242	
3-242-2	Molecule Type	DNA	
3-242-3	Length	41	
3-242-4	Features Location/ Qualifiers	misc_feature 1..41 note=Synthetic: s1-28 source 1..41	

		mol_type=other DNA organism=synthetic construct	
3-242-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct ccaggtcaca aatacacgaa c	41
3-243	Sequences		
3-243-1	Sequence Number [ID]	243	
3-243-2	Molecule Type	DNA	
3-243-3	Length	43	
3-243-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s1-31 source 1..43 mol_type=other DNA organism=synthetic construct	
3-243-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct tggatagtgagg agagaaaggt tcc	43
3-244	Sequences		
3-244-1	Sequence Number [ID]	244	
3-244-2	Molecule Type	DNA	
3-244-3	Length	40	
3-244-4	Features Location/ Qualifiers	misc_feature 1..40 note=Synthetic: s1-39 source 1..40 mol_type=other DNA organism=synthetic construct	
3-244-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct ggcacacagac tctattcctt	40
3-245	Sequences		
3-245-1	Sequence Number [ID]	245	
3-245-2	Molecule Type	DNA	
3-245-3	Length	42	
3-245-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s1-41 source 1..42 mol_type=other DNA organism=synthetic construct	
3-245-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct ttgttcattc cacctgctca ct	42
3-246	Sequences		
3-246-1	Sequence Number [ID]	246	
3-246-2	Molecule Type	DNA	
3-246-3	Length	42	
3-246-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s1-43 source 1..42 mol_type=other DNA organism=synthetic construct	
3-246-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct taccacaaaa tcctgcagta gt	42
3-247	Sequences		
3-247-1	Sequence Number [ID]	247	
3-247-2	Molecule Type	DNA	
3-247-3	Length	42	
3-247-4	Features Location/ Qualifiers	misc_feature 1..42 note=Synthetic: s3-28 source 1..42 mol_type=other DNA organism=synthetic construct	
3-247-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct ataggaaggt ggggagggag tg	42
3-248	Sequences		
3-248-1	Sequence Number [ID]	248	
3-248-2	Molecule Type	DNA	
3-248-3	Length	43	
3-248-4	Features Location/ Qualifiers	misc_feature 1..43 note=Synthetic: s3-41	

		source 1..43 mol_type=other DNA organism=synthetic construct	
3-248-5	NonEnglishQualifier Value Residues	gacgtgtgct cttccgatct tattgtctat ccctccctca cct	43
3-249	Sequences		
3-249-1	Sequence Number [ID]	249	
3-249-2	Molecule Type	AA	
3-249-3	Length	22	
3-249-4	Features Location/ Qualifiers	REGION 1..22 note=Synthetic: Bxb1 recombinase construct C terminal end amino acid sequence source 1..22 mol_type=protein organism=synthetic construct	
	NonEnglishQualifier Value		
3-249-5	Residues	GSGSGSHHHH HHGSGPKKKR KV	22
3-250	Sequences		
3-250-1	Sequence Number [ID]	250	
3-250-2	Molecule Type	DNA	
3-250-3	Length	44	
3-250-4	Features Location/ Qualifiers	misc_feature 1..44 note=Synthetic: P1 source 1..44 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-250-5	Residues	acacgacgct cttccgatct nnnnatgctt ctctgcatcc gtct	44
3-251	Sequences		
3-251-1	Sequence Number [ID]	251	
3-251-2	Molecule Type	DNA	
3-251-3	Length	45	
3-251-4	Features Location/ Qualifiers	misc_feature 1..45 note=Synthetic: P2 source 1..45 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-251-5	Residues	gacgtgtgct cttccgatct agggaataga tgacatcaaa gagaa	45
3-252	Sequences		
3-252-1	Sequence Number [ID]	252	
3-252-2	Molecule Type	DNA	
3-252-3	Length	38	
3-252-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-252-5	Residues	ggtttgtcgc cgacggcggt ctccgtcggc aacaaacc	38
3-253	Sequences		
3-253-1	Sequence Number [ID]	253	
3-253-2	Molecule Type	DNA	
3-253-3	Length	38	
3-253-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-253-5	Residues	ggtttgtcgg cgacggcggt ctccgtcgcc aacaaacc	38
3-254	Sequences		
3-254-1	Sequence Number [ID]	254	
3-254-2	Molecule Type	DNA	
3-254-3	Length	38	

3-254-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
3-254-5	NonEnglishQualifier Value Residues	ggtttgtcgt cgacggcggg ctccgtcgac aacaaacc	38
3-255	Sequences		
3-255-1	Sequence Number [ID]	255	
3-255-2	Molecule Type	DNA	
3-255-3	Length	48	
3-255-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-255-5	Residues	ggtttgctctg gtcaccacc gcggtctcag tggggtacgg tacaaacc	48
3-256	Sequences		
3-256-1	Sequence Number [ID]	256	
3-256-2	Molecule Type	DNA	
3-256-3	Length	48	
3-256-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-256-5	Residues	ggtttgctctg gtcagccacc gcggtctcag tggcgtacgg tacaaacc	48
3-257	Sequences		
3-257-1	Sequence Number [ID]	257	
3-257-2	Molecule Type	DNA	
3-257-3	Length	48	
3-257-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-257-5	Residues	ggtttgctctg gtcattccacc gcggtctcag tggagtacgg tacaaacc	48
3-258	Sequences		
3-258-1	Sequence Number [ID]	258	
3-258-2	Molecule Type	DNA	
3-258-3	Length	38	
3-258-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-258-5	Residues	ggtttgtcga agacggcggg ctccgtcttc aacaaacc	38
3-259	Sequences		
3-259-1	Sequence Number [ID]	259	
3-259-2	Molecule Type	DNA	
3-259-3	Length	38	
3-259-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-259-5	Residues	ggtttgtcga ggacggcggg ctccgtcctc aacaaacc	38
3-260	Sequences		
3-260-1	Sequence Number [ID]	260	
3-260-2	Molecule Type	DNA	

3-260-3	Length	38	
3-260-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: attB source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-260-5	Residues	ggtttgtcga tgacggcggc ctccgtcatc aacaaacc	38
3-261	Sequences		
3-261-1	Sequence Number [ID]	261	
3-261-2	Molecule Type	DNA	
3-261-3	Length	48	
3-261-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-261-5	Residues	ggtttgctctg gtcaaacacc gcggtctcag tgttgtagcg tacaaccc	48
3-262	Sequences		
3-262-1	Sequence Number [ID]	262	
3-262-2	Molecule Type	DNA	
3-262-3	Length	48	
3-262-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-262-5	Residues	ggtttgctctg gtcaagcacc gcggtctcag tgctgtacgg tacaaccc	48
3-263	Sequences		
3-263-1	Sequence Number [ID]	263	
3-263-2	Molecule Type	DNA	
3-263-3	Length	48	
3-263-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: attP source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-263-5	Residues	ggtttgctctg gtcaatcacc gcggtctcag tgatgtacgg tacaaccc	48
3-264	Sequences		
3-264-1	Sequence Number [ID]	264	
3-264-2	Molecule Type	DNA	
3-264-3	Length	48	
3-264-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-8 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-264-5	Residues	aaccaagat tctgacacca gagtgtgctg gtgtcagata cactactc	48
3-265	Sequences		
3-265-1	Sequence Number [ID]	265	
3-265-2	Molecule Type	DNA	
3-265-3	Length	48	
3-265-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-1 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-265-5	Residues	at ttgatgc ttaccaatt gagaacgctg tggtagaaga aggaatgg	48
3-266	Sequences		
3-266-1	Sequence Number [ID]	266	

3-266-2	Molecule Type	DNA	
3-266-3	Length	48	
3-266-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-11 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-266-5	Residues	aatacagaat ttaccctgct gcttgctctg taggagaagg ggcttcaa	48
3-267	Sequences		
3-267-1	Sequence Number [ID]	267	
3-267-2	Molecule Type	DNA	
3-267-3	Length	48	
3-267-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s1-41 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-267-5	Residues	tcatgatgct cctgtcttca gagtcctctg ctgtgaggag caagctcg	48
3-268	Sequences		
3-268-1	Sequence Number [ID]	268	
3-268-2	Molecule Type	DNA	
3-268-3	Length	38	
3-268-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Symmetric AttB site source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-268-5	Residues	ggtttgtcga cgacggcggg ctccgctcgtc aacaaacc	38
3-269	Sequences		
3-269-1	Sequence Number [ID]	269	
3-269-2	Molecule Type	DNA	
3-269-3	Length	38	
3-269-4	Features Location/ Qualifiers	misc_feature 1..38 note=Synthetic: Symmetric AttB site source 1..38 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-269-5	Residues	ggtttgttga cgacggagac cgccgctcgtc gacaaacc	38
3-270	Sequences		
3-270-1	Sequence Number [ID]	270	
3-270-2	Molecule Type	DNA	
3-270-3	Length	48	
3-270-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s5-16 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-270-5	Residues	ttttttttt ttgacaaca gagtgtctctg ttgccaggc tggagtgc	48
3-271	Sequences		
3-271-1	Sequence Number [ID]	271	
3-271-2	Molecule Type	DNA	
3-271-3	Length	48	
3-271-4	Features Location/ Qualifiers	misc_feature 1..48 note=Synthetic: s3-28 source 1..48 mol_type=other DNA organism=synthetic construct	
	NonEnglishQualifier Value		
3-271-5	Residues	tccaagtgt gtcgacagtg gcagaggcag ttggggccaa acaaaggt	48