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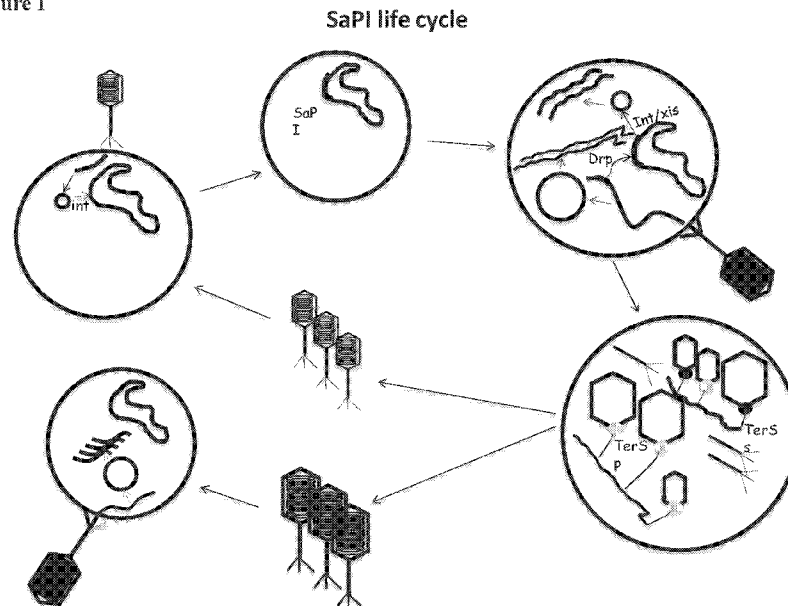
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ING OR DISRUPTING BACTERIAL GENES INVOLVED IN VIRULENCE OR VIABILITY

Figure 1



(57) Abstract: Provided are modified *Staphylococcus aureus* pathogenicity islands of a variety of types and origins. The pathogenicity island are characterized as having a polynucleotide comprising a bacterial pathogenicity island nucleotide sequence (a "B-PINS") that contains one or more modifications ("modified B-PINS"), that include i) a deletion or disruption of at least one virulence determinant of the B- PINS; and ii) an insertion of at least one cargo sequence. The polynucleotide are capable of being packaged within a bacterium into a phage- like particle that comprises a bacteriophage capsid, tail and tail fiber proteins in the form of an antibacterial drone ("ABD"). The ABD is capable of infecting bacteria such that at least one cargo sequence is introduced into bacteria infected by the ABD. Pharmaceutical and other compositions the ABDs are also included. Bacteria that make the ABDs are provided, as are isolated

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COMPOSITIONS AND METHODS FOR NON-ANTIBIOTIC TREATING OF BACTERIAL INFECTIONS BY BLOCKING OR DISRUPTING BACTERIAL GENES INVOLVED IN VIRULENCE OR VIABILITY

CROSS REFERENCE TO RELATED APPLICATIONS

5 This application claims priority to U.S. provisional application serial no. 62/506,546, filed May 15, 2017, and to U.S. provisional application serial no. 62/543,343, filed August 9, 2017, the disclosures of each of which are incorporated herein by reference.

FIELD

10 The present disclosure relates generally to approaches for attenuating virulence, inhibiting growth of and/or killing bacteria in an infection site as well as in vitro, and more particularly to engineered particles comprising modified bacterial DNA islands.

BACKGROUND

Antibiotic resistance is one of the world's most pressing public health problems. Illnesses that were once easily treatable with antibiotics are becoming more difficult to cure and more expensive to treat. Each year in the United States alone, at least 2 million people become infected with bacteria that are resistant to antibiotics. Genotypic as well as phenotypic antibiotic resistance can arise in a wide variety of bacteria. Of particular concern is that *Staphylococcus aureus* and other staphylococci continue to cause life-threatening infections affecting any bodily organ and, during the past 15 years have become a major cause of community-acquired infections, as well as continuing to be the scourge of the hospital environment. Staphylococci have become increasingly resistant to antibiotics, especially to β -lactams and glycopeptides, and their infections are now, in many cases, totally untreatable. Thus there is an ongoing need for improved compositions and methods for treating bacterial infections. The present disclosure is pertinent to these needs.

25 SUMMARY

The present disclosure provides compositions and methods for converting bacterial DNA islands into what is referred to herein from time to time herein as "Anti-bacterial Drones" (ABDs), and includes the ABDs themselves, compositions comprising them, and methods of using them. Thus, in embodiments the disclosure provides non-antibiotic and non-phage compositions, and methods of treating bacterial infections using them.

30 In embodiments compositions and methods that involve modified bacterial chromosomal islands are provided. Particular aspects of this disclosure are based on the

highly mobile phage-inducible staphylococcal pathogenicity islands (SaPIs) and on similar elements from other bacteria known generally as phage-inducible chromosomal islands (PICIs). SaPIs and certain other mobilizable bacterial chromosomal islands are known in the art and are described in, for example, Novick RP, Ram G. *The floating (pathogenicity)*

5 *island: a genomic dessert*. Trends in genetics. 2016;32(2):114-126.

doi:10.1016/j.tig.2015.11.005, the entire disclosure of which is incorporated herein by reference.

The SaPIs are ~15kb genetic elements inserted in the staphylococcal chromosome at specific sites. There, they reside quietly, under the control of a SaPI-coded repressor, and
10 replicate along with the chromosomal DNA. Certain bacteriophages, known as “helper phages”, counter the repressor, de-repress the SaPI and induce the island to excise from the chromosome and to replicate autonomously. The replicated SaPI DNA is packaged efficiently in capsids composed entirely of phage virion proteins. Infectious phage-like particles (consisting of capsids + replicated SaPI DNA, tail and tail fibers) are formed and then
15 released from the bacterial cell upon phage-induced lysis and are transferred at very high frequencies (depicted in the schematic of Figure 1). Most SaPIs encode their own terminase small subunit (TerS), which directs exclusive packaging of the SaPI genome (instead of the phage genome) and most SaPIs encode capsid morphogenesis functions (CpmAB or Ccm), which remodel the phage capsids to accommodate the smaller SaPI genome (depicted in the
20 schematic of Figure 2).

SaPI genomes have a well-conserved modular organization where genes are grouped into functional modules: integration-excision, regulation, replication, packaging and phage-interference, and accessory genes (depicted schematically in Figure 3A). Additional annotation of SaPI2 and non-limiting illustrations of SaPI derivatives referred to as
25 antibacterial drones (ABDs) is provided in Figure 4.

The SaPIs contain three types of genes: those critical for their distinctive lifestyle; those involved in phage-interference (which may also be important for their lifestyle); and those encoding toxins and other factors that contribute to the virulence and adaptability of the organism, but are irrelevant to the lifestyle of the SaPIs. These genes are referred to as
30 accessory genes. They are the cargo of the island and are replicated and transferred along with the rest of the island. However, regulation of accessory gene expression is independent of the rest of the island and is dependent only on the activity of the specific accessory gene promoter(s). Therefore, when the SaPI resides in the chromosome and most of the SaPI genes are repressed, the accessory genes will usually be expressed.

In certain aspects this disclosure couples the promiscuous mobility of the SaPIs with recombinant DNA methodology to introduce a wide variety of antibacterial cargoes that can attenuate the virulence of, inhibit the growth of, or kill infecting bacteria, or modify non-pathogenic bacteria as described herein.

5 In various and non-limiting embodiments, the present disclosure provides for modifying any naturally occurring phage-packageable and mobilizable bacterial chromosomal island, which can further comprise detoxifying the island as described further below, optionally deleting genes that determine small-size capsids to increase the island's packaging capacity. These modifications enable an island, such as SaPI2 to carry, package
10 and safely transfer more large segments of polynucleotides, such as up to 30 kb of genetically designed cargo.

The disclosure includes designing and constructing DNA cargo modules which encode antibacterial agent(s) and/or other agents that facilitate and/or improve and/or alter the function of the ABDs, and affect cells into which they are introduced. The disclosure includes
15 inserting one or more anti-bacterial cargo modules into the modified island to create previously unavailable DNA islands (ABD-islands) that have the ability to kill or attenuate or otherwise modify any bacterial cell that is infected by it. The disclosure thus provides for exploiting the packaging system and high frequency transfer mechanism of the naturally occurring island to package and disseminate the re-purposed island DNA (ABD-DNA). The
20 ABD-DNA is packaged in infectious phage-like particles (ABD-particles), which are released from the cell upon phage-induced lysis, or by other mechanisms, such as enzyme-mediated cell lysis. The disclosure includes customizing and optimizing ABD-particle producing bacterial strains, and includes such strains themselves.

In certain aspects the invention includes introducing by any suitable approach the
25 ABDs into bacterial cells such that the cargo is expressed or otherwise affects function of the bacterial host. Depending on the cargo, ABD may alter, kill, weaken or disarm the targeted bacteria or the surrounding bacteria, or may deliver a drug or other substance to a particular locale as further described below. ABD can then proliferate throughout the bacterial population either spontaneously, or by design. ABDs have been constructed to treat
30 staphylococcal infections and can be considered alternatives or adjuncts to conventional antibiotics, and are expected to be suitable for targeting a wide variety of other pathogenic or otherwise unwanted bacteria.

The disclosure includes all modifications that are described herein, and those that are depicted in the figures. In certain and non-limiting embodiments, modifications to

prototypical SaPI, SaPI2, are as depicted in Figure 3A and 3B, and or deleting or modifying capsid morphogenesis genes to allow for cargo of up to ~30 kb. Additional modifications to the SaPI genome using SaPI2, other SaPIs or a combination thereof include modifications that increase the probability of induction and consequent spread, or to inhibit and/or prevent packaging of resident SaPIs (or parts of them), or to reduce unintended consequences of mis-packaging by ABD during production and subsequently in vivo use.

Embodiments of the disclosure include at least two types of DNA cargo modules, which can be characterized by the type of anti-bacterial agents they encode – i) those that kill the infecting bacteria and, in some cases induce the SOS response and consequently induce prophages and the island, and ii) those that disarm or attenuate virulence.

The disclosure demonstrates prophylactic and therapeutic utility for specific embodiments of the invention, which can be readily extended to the other embodiments that are described herein by the skilled artisan when given the benefit of the present description. In particular, in vitro results presented herein show that both killing and disarming ABD-particles are effective against a derivative of a prototypical lab strain, *Staphylococcus aureus* NCTC 8325 and against an important clinical strain USA300. Typical results are shown in Figures 7 (killing) and 8 (disarming). Furthermore, in vivo results show that representative killing ABD-particles targeting *S. aureus* are not toxic to C57-bl6 mice, do not elicit an immediate immune response and can find staphylococci in the infected mouse, can inject their ABD-DNA into these Staphylococcal cells, express the ABD cargo genes, express the ABD lifestyle genes, can integrate the ABD-DNA into the recipient cell, can treat an infection, and can prevent an infection from developing. In particular embodiments, it is demonstrated that killing ABD-particles targeting a chromosomal gene of *Listeria monocytogenes* are also effective against that organism. Killing of staphylococci by ABD2009 is shown in Figure 12. ABD2009 is effective against *S. aureus* RN4220 (A), but not against RN4220 containing the lysostaphin immunity gene (B). Blockage of subcutaneous (SC) abscess formation is shown in Figures 13 and 14, and 15. Treatment of an SC abscess is shown in Figure 15. Rescue by ABD2003 of mice given a lethal IP dose of staphylococci is shown in Figure 16.

In view of the description provided herein, it will be apparent the disclosure provides in various embodiments: a polynucleotide comprising a bacterial pathogenicity island nucleotide sequence (referred to herein as a “B-PINS”) comprising one or more modifications (referred to herein as a “modified B-PINS”), the one or more modifications including but not necessarily limited to a B-PINS comprising: i) a deletion or disruption of at least one

virulence determinant of the B- PINS; and ii) an insertion of at least one cargo sequence into the B-PINS. In embodiments, the polynucleotide comprising the modified B-PINS is capable of being packaged within a bacterium into a phage-like particle that comprises or consists of bacteriophage capsid, tail and tail fiber proteins that is referred to herein as an antibacterial drone (“ABD”). The ABD is capable of infecting bacteria such that at least one cargo sequence is introduced into bacteria infected by the ABD. In non-limiting embodiments, one or more modifications of a virulence determinant in a B-PINS comprises a deletion of all or substantially all of the virulence determinants in the B-PINS. In embodiments, at least one cargo sequence comprises a polynucleotide sequence encoding an anti-bacterial agent that is functional against a target in at least some bacteria in a bacterial population. In embodiments, between 80-100% of the bacteria are killed.

In embodiments, the disclosure provides polynucleotides, and ABDs containing them, that include a DNA sequence or encode an RNA that comprises specificity for a target that is an essential gene, or an RNA encoded by an essential gene, or a variable gene, or an RNA encoded by a variable gene. In embodiments, the ABDs include a sequence encoding a protein that has specificity for a target and can participate in and/or cause its cleavage and/or inactivation. In embodiments, the ABCs include a sequence encoding a toxin, which may or may not be an excreted toxin, that is cytostatic against bacteria, or a non-toxin protein that inhibits growth of bacteria in a bacterial population, or inhibits formation of and/or kills persister bacteria and/or dormant viable but non-culturable (VBNC) bacteria, such toxin capable of killing bacteria that have not been infected by the ABD, and/or can kill bacteria that do harbor or are otherwise infected by the ABD. In embodiments, the toxin is lysostaphin. In embodiments, the ABDs comprise a sequence encoding an anti-sense RNA, or a Clustered Regularly Interspaced Short Palindromic repeats (CRISPR) guide RNA targeted to a sequence in a bacterium in a bacterial population. In embodiments, the ABDs comprise a sequence encoding a CRISPR-associated nuclease including a Cas9 nuclease, a Cpf1 nuclease, or a dCas9. In embodiments, a target of a component of the CRISPR system is a bacterial chromosome or a bacterial plasmid. In embodiments, a polynucleotide in the ABD comprises a deletion of SaPI genes *cpmA* and/or *B*. Pharmaceutical compositions comprising ABDs of this disclosure, including mixtures of distinct types of ABDs that are differentiated from one another at least by the polynucleotide they include, are provided. Methods of killing bacteria or otherwise limiting the growth of bacteria, or changing a phenotype of bacteria, are provided by introducing ABDs into bacteria. The bacteria may be in an individual, or present on or impregnated in a surface, such as a surface of an inanimate object, which may be any of

a variety of objects, devices and the like, including but not limited to medical devices, surgical implants, and the like. Methods of producing ABDs by engineering bacteria to produce them are included in the disclosure, as are methods of separating ABDs from the bacteria, the engineered and infected bacteria, and the cell culture media comprising the bacteria and/or secreted ABDs. Isolated and/or purified ABDs are also included. In specific and non-limiting embodiments, an ABD or polynucleotide of this disclosure comprises a modified *Staphylococcus aureus* pathogenicity island (SaPI), which may be any of a SaPI, SaPI1, SaPI2, SaPIbov1, or SaPIbov2. Also provided are libraries of distinct ABDs.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Phage and SaPI replication cycles. SaPI particles and DNA are shown in black.

Figure 2 Phage and SaPI DNA packaging. Phage genome, top left, encodes TerS and TerL, procapsids, and tails; SaPI genome, top right encodes TerS and modifies procapsid size. Phage and SaPI terminases package both phage and SaPI DNAs into procapsids of both sizes, resulting in both SaPI and phage particles of both sizes.

Figure 3. SaPI2, SaPIbov2 and a hybrid between them A. SaPI2 genome organization. B. ABD2001. C. SaPI2 with regulatory region replaced by that of SaPIbov2. D. SaPIbov2

Figure 4. ABD constructs. From *attL* to *tetM* is the ABD backbone. Black boxes represent the cloning site. Gray rectangles between cloning sites represent different modules that have been or will be added to the backbone. dr: direct repeat; sp: spacer; cr: crRNA leader; tracr: tracr RNA.

Figure 5. Schematic representation of ABD production and function.

Figure 6. CRISPR/Cas9 system. A. Simplified diagram of CRISPR locus. cr RNA is transcribed from one repeat and adjacent spacer and a second small RNA, tracr RNA, is transcribed separately. **B.** crRNA binds to the protospacer (recognition sequence) in the target DNA and tracr RNA binds jointly to crRNA and to Cas9, forming the complex that induces local melting of the DNA; Cas9 then cleaves both strands of the DNA at a pre-determined point. dCas9 (not shown) is a derivative of Cas9 lacking Cas9's nuclease function. It binds to the target DNA by the same mechanism, but instead of cleaving the target DNA it remains bound and blocks function of the targeted gene or regulatory element.

Figure 7. Plating tests to demonstrate ABD antibacterial activities in vitro. A. Killing of *S. aureus* by ABD2003 and of *L. monocytogenes* by ABD2004. Suitable

dilutions of ABD2002, 2003 or 2004 particle preparations were mixed with RN1, RN1 Δ *agr*, or *L. monocytogenes* SK1442, plated on TSB with 5 μ g/ml tetracycline (Tc5), and incubated at 37°C for 48 h. **B. Inhibition of hemolytic activity by ABD2006.** Suitable dilutions of ABD2005 or 2006 particle preparations were mixed with RN1 or USA300 LAC, plated on sheep blood agar plates supplemented with Tc5 and incubated at 37°C for 48 h.

Figure 8. inhibition by ABD2006 (CRISPR/dcas9, with *agr*P₂P₃ spacer), of *agr*-P₃lux reporter. Strains with integrated ABDs 2001, 2005 and 2006 and a control strain without any ABD were incubated with shaking at 37°C. Two 100 μ l samples were withdrawn at each time point and assayed for growth (OD at 600 nm) and Relative Luciferase Units (RLU) in a Molecular Devices luminometer. Graphs show averages of experiments performed in triplicate with error bars representing standard deviations.

Figure 9. The *agr* regulatory circuit. The *agr* locus, widely conserved among Gram-positive bacteria, consists of 2 transcription units driven by promoters P₂ & P₃. The P₂ operon encodes AgrB, a trans-membrane protein that processes the AgrD peptide to form a 7-9 amino acid peptide (the AIP) that is the activating ligand for AgrC, the receptor-histidine kinase component of the two-component signaling module, of which AgrA is the response regulator. Binding of the AIP to an extracellular loop of AgrC causes autophosphorylation of a histidine residue in the cytoplasmic domain of the receptor. The phosphate is then transferred to AgrA, activating its transcriptional regulatory function. AgrA~P binds to P₂, completing a positive feedback loop. It also binds to P₃, whose transcript is the regulatory RNA, RNAIII, which regulates indirectly the transcription of most virulence genes and directly the translation of a few key genes. RNAIII governs the production of most virulence proteins. AgrA~P separately activates transcription of a set of genes encoding virulence peptides known as phenol-soluble modulins. The *agr* system occurs as 4 allelic forms in *S. aureus*, such that interactions between one AIP and the signaling module of another allelic form are usually cross-inhibitory. Inhibition of *agrI* by AIP-II is shown.

Figure 10. Hybrid auto-regulatory circuit combining *S. warneri agrBD*, *B. subtilis comA* and *B. subtilis* -*S. warneri comP-agrC* hybrid. In the hybrid, driven by the comQ promoter, AgrB & D combine to produce an inhibitory AIP which blocks *agr* activation in target bacteria. ComA & P are a two-component signaling module from *B. subtilis*, parallel to *agrA* and C, in which phosphorylated ComA activates PcomQ, establishing an autoinduction circuit. ComQ promoter (PcomQ) drives the hybrid locus, inducing the expression of *S. warneri* AIP, which binds to the N-terminal moiety of the

ComP-AgrC hybrid, activating phosphorylation of ComA, which up-regulates comQ. The *S. warneri* AIP inhibits the *agr* system in *S. aureus* strains of all 4 allelic types, and thus blocks virulence.

Figure 11. Method of allelic replacement using pMAD.

Figure 12. Killing of staphylococci by ABD2009. *S. aureus* RN4220 (A) and RN4220 containing the lysostaphin immunity gene, *lif* (B) were infected with particles of ABD2009 (see Table 3), which contains the lysostaphin gene cloned to ABD2001, at a multiplicity of 3, then diluted and plated on tetracycline-containing agar to select for ABD transductants. Plates were incubated overnight at 37C and then held at room temperature for an additional 3 days. The same number of colonies appeared initially on each plate; however, during the subsequent 3 days, those on the RN4220 plate slowly dissolved whereas those on the *lif* plate remained intact. The 4220 plating bacteria, which were sensitive to lysostaphin, but grew very slowly on the Tc plates, showed halos of lysostaphin lysis surrounding the dissolving colonies in plate A. This result shows that the production of lysostaphin was slow enough to allow the initial growth of the colonies, which then underwent lytic suicide as they aged.

Figure 13. Blockage of subcutaneous (SC) abscess formation by ABD2003 (SaPI2 containing CRISPR/cas9 with an *agrA* spacer). Bacteria, 4×10^8 , were injected into the SC space of hairless mice through a 27-gauge teflon cannula, followed by 1.2×10^9 ABD2002 or 2003 particles, through the same cannula. Bacteria were imaged in the in vivo imaging system (IVIS) immediately and after 24 and 48 h. In panel (A) is shown the IVIS images for luciferase activity (Top 3 rows) and photographs of the abscesses of the same mice (bottom row). In panel (B) is shown a quantitative analysis of the luciferase signals. Error bars represent standard errors. $**P=.01$; $*P=.05$, determined by the one-tailed Fisher's exact test. Luciferase signals were quantitated using Living Image software (Perkin-Elmer, Inc.).

Figure 14. Blockage of abscess formation by an *agr*-inhibiting ABD. Hairless mice were infected with 4×10^8 RN1 cells, in 50 μ l PBS, through a teflon cannula, followed immediately by 4×10^9 ABD particles in 50 μ l PBS, either ABD2005 (non-targeting) or ABD2006 (targeting the *agrP₂P₃* promoter region), as indicated. Mice were imaged in the IVIS immediately and after 18 and 42 h. The 42h images are shown.

Figure 15. Treatment of an SC murine abscess by IP administration of ABD particles. Mice were injected SC with 4×10^8 organisms, strain RN1 containing an *agrP₃::lux* fusion, followed immediately by 8.8×10^9 ABD particles IP. IP treatment with ABD particles

at the same dose was repeated 1h later. Mice were imaged in the IVIS immediately after the first ABD injection, and again after 24 and 48 h. Panel A – IVIS images and abscess photographs; panel B - quantitative analysis of luciferase signals. Each bar represents the average of the luciferase signals for the five mice in each group at the three time points shown. Error bars represent standard deviations. Significance was evaluated by the one-tailed Fisher's exact test; *P=.05. Abscesses at 48 h are the prominent white areas in the mouse flanks – present in all 5 of the ABD2002 mice but in only one of the ABD2003 mice. The difference in abscess formation is significant at the 5% level, using a one-tailed Fisher's exact test.

Figure 16. Rescue by ABD2003 of mice given a lethal IP dose of staphylococci.

Groups of 5 mice were infected IP with 5×10^9 cells (in 50 μ l PBS) of RN1. This was followed immediately by IP injection of different numbers of ABD2003 particles in 250 μ l PBS. Mice were monitored for 48h. In panel (A) is shown the time course of mouse deaths; In panel (B) is a graphical representation of the final results, in which the groups of mice were pooled and statistics calculated on the pooled groups. Error bars represent standard deviations for each set of 3 pools; *P=.01; **P=.004, calculated by the one-tailed Fisher's exact test.

Figure 17. Examples of suitable cargo sequences and their sequence contexts are provided. *com* sequences are black on a white background. *agr* sequences are white on a black background. Figure 17 provides SEQ ID NO:1.

Figure 18. SaPI2 representative sequences to illustrate incorporation of CRISPR/Cas9 segment into an ABD of this disclosure. Interpretation of the sequences is aided by the schematic genetic element maps of SaPI2 with deletions as indicated (the sequence includes precise locations which are enlarged and italicized). The deletion from nucleotides 8136-9210 removes the 3 genes, *ptiB*, *cpmA* and *cpmB*; the sequence from 10982-14209 removes the virulence genes, *tst* and *eta*. The second deletion is the site into which the *tetM* gene and the CRISPR/cas9 module were inserted, resulting in ABD2002, as in the diagram. The CRISPR/cas9 segment contains the CRISPR array, the *cas9* gene and the *tracr* RNA gene. The *tracr* RNA pairs with the spacer RNA (crRNA) to form the guide RNA complex, which binds to the Cas9 protein and directs it to the spacer-determined target site. Figure 18 provides SEQ ID NO:2.

Figure 19. Sequences and diagram illustrating representative SaPI2 CRISPR/cas9 construct, related to Figure 18. Color of sequence is as designated in the legend above the

diagram. Figure 19 provides SEQ ID NO:3.

Figure 20. Sequences and diagram illustrating representative lysostaphin gene construct, related to ABD2009. Figure 20 provides SEQ ID NO:5.

DETAILED DESCRIPTION

5 Unless defined otherwise herein, all technical and scientific terms used in this disclosure have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains.

Every numerical range given throughout this specification includes its upper and lower values, as well as every narrower numerical range that falls within it, as if such
10 narrower numerical ranges were all expressly written herein.

The disclosure includes all polynucleotide and amino acid sequences described herein. Each RNA sequence includes its DNA equivalent, and each DNA sequence includes its RNA equivalent. Complementary and anti-parallel polynucleotide sequences are included. Every DNA and RNA sequence encoding polypeptides disclosed herein is encompassed by
15 this disclosure. Amino acids of all protein sequences and all polynucleotide sequences encoding them are also included. Sequences of from 80-99.99% identical to any sequence (amino acids and nucleotide sequences) of this disclosure are included. In some embodiments a cargo module may be referred to herein as a module.

The disclosure includes polynucleotides comprising ABDs of this disclosure. In
20 certain approaches of this disclosure expression vectors, such as plasmids, are used to produce one or more than one construct and/or component of the ABDs, and any of their cloning steps or intermediates. A variety of suitable expression vectors known in the art can be adapted to produce the ABDs of this disclosure.

In one aspect the disclosure includes a kit comprising one or more expression
25 vector(s) that encode one or more ABD components. The expression vector in certain approaches includes a cloning site, such as a poly-cloning site, such that any desirable cargo gene can be cloned into the cloning site to be expressed in any target cell into which the ABD is introduced. The kit can further comprise one or more containers, printed material providing instructions as to how to use make and/or use the expression vector to produce ABDs, and
30 reagents for introducing the expression vector into cells. The kits may further comprise one or more bacterial strains for use in producing the ABDs. The bacterial strains may be provided in a composition wherein growth of the bacteria is restricted, such as a frozen culture with one or more cryoprotectants, such as glycerol.

Methods of making ABDs are included and generally comprise introducing one or more polynucleotide encoding at least some portion of an ABD into suitable cells that comprise resident phages or prophages and/or other suitable genetic elements and/or proteins, allowing replication of the polynucleotides such that ABDs are formed, harvesting the ABDs from the cells, the cell cultures, or the culture supernatants, and optionally separating the ABDs from the cells, cell culture, cell culture supernatant, etc. Cells and cell cultures that harbor polynucleotides comprising the ABDs are included, as are isolated and/or purified ABDs. The ABDs can be purified to any desired degree of purity using standard approaches, such as density gradient separation or commercially available kits used to purify infectious particles made by bacteria.

In certain aspects the disclosure includes a pharmaceutical formulation comprising ABDs as described herein. The form of pharmaceutical preparation is not particularly limited, but generally comprises ABDs and at least one inactive ingredient. In certain embodiments suitable pharmaceutical compositions can be prepared by mixing any one type of ABD, or combination of distinct ABDs, with a pharmaceutically-acceptable carrier, diluent or excipient, and suitable such components are well known in the art. Some examples of such carriers, diluents and excipients can be found in: Remington: The Science and Practice of Pharmacy (2005) 21st Edition, Philadelphia, PA. Lippincott Williams & Wilkins.

In another aspect the disclosure comprises delivering to bacteria a cargo via ABDs of this disclosure. The method generally comprises adding a preparation of ABDs of this disclosure to one or more bacterial cells, allowing attachment of ABDs to the cells, such as via a surface receptor, whereby the nucleic acids contained by the ABDs enter the cells. Subsequent to ABD nucleic acid entry the expression of the cargo occurs.

Administration of formulations comprising the ABDs as described herein can be performed using any suitable route of administration, which include but are not necessarily limited to intradermal, transdermal, intravenous, topical, intramuscular, intraperitoneal, intravenous, subcutaneous, oral, and intranasal routes. In certain aspects the disclosure includes providing the ABDs in the form of creams, aqueous solutions, suspensions or dispersions, oils, balms, foams, lotions, gels, cream gels, hydrogels, liniments, serums, films, ointments, sprays or aerosols, other forms of coating, or any multiple emulsions, slurries or tinctures. Compositions comprising ABDs may also be used to treat inanimate objects, such as medical devices, or implements used in food handling. In embodiments, the device is an implantable medical device or other implanted surgical object, whether permanent or

temporarily implanted, including but not necessarily limited to an indwelling catheter or surgical implant of any kind.

It will be recognized by those of skill in the art that the form and character of the particular dosing regimen employed in the method of this disclosure will be dictated by the route of administration and other well-known variables, such as the age, sex, health and size of the individual, the type and severity of bacterial infection, or risk of bacterial infection, and other factors that will be apparent to the skilled artisan given the benefit of the present disclosure.

The compositions can be administered to humans, and are also suitable for use in a veterinary context and accordingly can be given to non-human animals, including but not limited to non-human mammals, and avian animals, and/or to any eukaryotic organism, including plants, wherein targeting of bacteria would be desirable.

In embodiments the ABDs are introduced into a subject as a component of a pharmaceutical composition. In certain aspects, the ABDs can be administered using any suitable route and method which may in part be dictated by the type of cargo that is encoded in the ABD, and the subject to which the ABDs are administered, the type and severity of the bacterial infection, its location, and other factors that will be apparent to those skilled in the art. In embodiments, the amount of ABDs is an effective amount such that the cargo achieves a desired result. The desired result can comprise a prophylactic effect or a therapeutic effect.

In this regard, the type of cargo that the ABDs encode is not particularly limited and non-limiting illustrations are described further below.

This disclosure is considered to be suitable for targeting any microorganism that is susceptible to infection by any ABD described herein. In present embodiments the bacteria that are targeted by ABDs of this disclosure are Gram-positive. In alternative embodiments the bacteria that are targeted by ABDs of this disclosure may be Gram-negative. In embodiments the bacteria are resistant to one or more antibiotics and the ABDs kill or reduce the growth of the antibiotic-resistant bacteria, and/or the ABDs sensitize the bacteria to an antibiotic by, for example, use of cargo that targets an antibiotic resistance gene, which may be present on a chromosome or a plasmid. The disclosure is thus suitable for targeting bacterial chromosomes or episomal elements. In certain approaches the present disclosure can comprise use of a composition comprising ABDs as the only antimicrobial agent in the composition, or the composition can also comprise other antimicrobial agents. In embodiments, the disclosure encompasses using ABDs in the same composition as at least one other antimicrobial compound, or in concurrent or sequential, distinct administrations

wherein ABDs are administered separately from at least one other antimicrobial compound, examples of which include but are not limited to any known antimicrobial compound and/or compounds that interfere with, for example, bacterial quorum sensing. In various embodiments, the ABDs can be used with antibiotics that are members of classes such as aminoglycosides, beta lactams (with or without beta lactamase inhibitor such as clavulanic acid), macrolides, glycopeptides, polypeptides, cephalosporins, lincosamides, ketolides, rifampicin, polyketides, carbapenem, pleuromutilin, quinolones, streptogramins, oxazolidinones, lipopeptides, etc.

In embodiments, the method of this disclosure is used to reduce or eradicate bacterial cells. A reduction can be determined by comparing bacteria treated with ABDs to any suitable control. Eradication can comprise killing all bacterial cells as determined using any suitable measurement of bacteria. The bacteria can be present in an infection, which may be systemic, or localized to any particular system, organ or tissue, including but not limited to a wound. The bacteria may also be present in a biological or non-biologic liquid, or on an inanimate surface, or a food product. In non-limiting examples the surface can be a non-porous surface, a surface in a hospital, or a surface that is used for food processing or preparation.

Embodiments of this disclosure may be used to reduce or eradicate persister bacteria and/or dormant viable but non-culturable (VBNC) bacteria, and/or small-colony variant (SCV) bacteria. Such cells include but are not necessarily limited to mid-stationary phase or late-stationary phase cells. Such cells include pathogenic bacteria that neither grow nor die in the presence of conventional microbicidal antibiotics. In embodiments, persister cells and SCVs contribute to the recalcitrance of clinical infections. In embodiments, the bacteria are present in a biofilm. In embodiments, the disclosure inhibits formation of a biofilm, and may promote biofilm dispersal.

In certain embodiments, the method of the disclosure results in eradication of a bacterial population from an infection, such as from an infection of an organ, tissue, skin, or biological fluid from an individual, or from the surface of an inanimate object, including but not necessarily limited to medical devices, such as implantable or implanted medical devices, and/or any medical device that may stay in contact with the skin or be fully or partially present within the body of an individual for a period of time during which the surface of the device may be susceptible to biofilm formation. In embodiments, the method of this disclosure is used to reduce or eradicate bacteria that are present in anaerobic conditions. Thus, the disclosure in various implementations provides flexible approaches for a) killing b)

attenuating virulence and c) inhibiting growth of a wide variety of bacteria in diverse environments, as well as for modifying non-pathogenic bacteria so that they have at least one intended characteristic/comprise/express a cargo as described herein.

In embodiments, disarming means reducing the capability of bacteria to cause damage to a host, such as by reducing or eliminating the capacity to produce toxins. In embodiments, attenuating means weakening the organism, such as by slowing or blocking its growth, or its ability to penetrate cells.

As discussed briefly above, the SaPIs are embedded in the staphylococcal chromosome at any of 5 different attachment sites that are similar in structure, but not sequence, to prophage attachment sites. The SaPIs are maintained in a quiescent state by a repressor. They are induced by certain staphylococcal bacteriophages (helper phages) to excise from the bacterial chromosome and replicate their DNA extensively within the bacterial cell. One key function of the helper phage is to counteract the SaPI repressor which enables the excision and replication of the SaPI. The inducing phage is meanwhile replicating alongside the SaPI and synthesizing the virion proteins that form the phage particle. The SaPI encodes 2 proteins, CpmA & B that direct the formation from the virion proteins of small-sized phage particle-like capsids into which their DNA is packaged. SaPIs and phages each encode sequence-specific terminase small subunit (TerS) enzymes that recognize specific packaging sequences (*pac* sites) in the DNA that are required for insertion of DNA into a phage precursor particle. The SaPI and phage TerS enzymes recognize different *pac* sites specific for their respective genomes, and do not cross-react. The resulting SaPI particles are released in very large numbers by phage-induced cellular lysis and, as they behave like phage particles, can usually infect any *S. aureus* bacteria with which they come in contact. For most *S. aureus* strains, phages and phage-like particles adsorb non-specifically to the ribitol-containing cell wall teichoic acid (WTA), enabling them to inject their DNA. Nevertheless, there is wide strain-specific variability in the host range of staphylococcal phages, which is normally determined by the ability to form plaques. By this criterion, host range is determined by intracellular factors rather than by adsorption specificity. These factors include phage inhibitors, restriction-modification systems, prophage immunity and the presence or absence of host functions required for phage reproduction. Consequently, limitations of phage host range, according to plaque-forming ability, do not generally affect the ability of a SaPI to enter and become established in a new cell.

In order to enable the production of large numbers of SaPI particles uncontaminated by co-produced infective bacteriophage particles, we have deleted the helper phage's TerS

gene. This mutant phage can form normal (empty) phage heads (procapsids) but cannot package phage DNA and therefore can exist only as a lysogen. As with WT lysogens, this mutant one can be induced by DNA damage (UV radiation or mitomycin C treatment – the so-called SOS response) to go through the phage lytic cycle, producing a crop of empty

5 procapsids and phage tails. If, however, there is a co-resident SaPI, then all of the released particles, of both SaPI and phage sizes, will contain SaPI DNA which is packaged by means of the SaPI TerS. In the several embodiments of this invention, we have deleted SaPI genes *cpmA* & *B* responsible for the formation of small particles so that SaPI DNA is always packaged in phage-sized particles. Up to about 42 kb of SaPI DNA can be packaged in these

10 particles. This means that approximately 30 kb of additional DNA can be inserted into the 13 kb modified SaPI genome. Following infection of new bacterial cells, the SaPI DNA is integrated into the new cell's chromosome and propagated thenceforth. Large numbers of particles for testing are produced by transfer to a strain containing the mutant helper phage described above, inducing the helper phage by mitomycin C and allowing the culture to

15 undergo phage-induced lysis. As described above, the resulting lysate will contain only the engineered SaPI2 particles plus very rare particles containing mis-packaged host or helper phage DNA. This scheme is diagrammed in Figure 5. These particles are concentrated by polyethylene glycol (PEG) precipitation, purified by density gradient centrifugation, dialyzed, filtered, enumerated and then used to infect any desired staphylococcal strain, including any

20 strain that has caused an infection within the tissues of an animal or human. This strategy can be applied to the curing of a staphylococcal infection, which was demonstrated in an animal model, non-toxicity for mice given an intraperitoneal dose of 3×10^{11} particles is also demonstrated. Such results are expected to be applicable to any mammal, including but not limited to humans, and other animals that are susceptible to bacterial infections.

25 In various and non-limiting embodiments, the present disclosure provides the following composition and methods, some of which are demonstrated in the application, and others of which can be predicted from what is demonstrated and described herein.

In one embodiment, the disclosure provides for modifying any naturally occurring phage-packageable and mobilizable bacterial chromosomal island, which can further

30 comprise detoxifying the island (e.g., deleting and/or disrupting virulence determinants, preferably deleting all virulence determinants, other non-essential genes and optionally other accessory genes that makeup the island's natural cargo), and deleting the genes that determine small-size capsids, if any, thereby increasing the island's packaging capacity. These modifications enable an island such as SaPI2 to carry, package and safely transfer

more than 30 kb of genetically designed cargo.

The disclosure includes designing and constructing DNA cargo modules. These cargo modules comprise DNA sequences encoding antibacterial agent(s). These cargo modules may also encode any other agents that facilitate and/or improve and/or alter the function of the
5 ABDs. Numerous specific examples of DNA cargo modules are discussed below, and others will be apparent to those skilled in the art when given the benefit of the present description. The disclosure includes inserting one or more anti-bacterial cargo modules into the modified island to create a novel DNA island (ABD-island) that has the ability to kill or attenuate any bacterial cell that is infected by it.

10 The disclosure provides for exploiting the packaging system and high frequency transfer mechanism of the naturally occurring island to package and disseminate the re-purposed island DNA (ABD-DNA). The ABD-DNA is packaged in infectious phage-like particles (ABD-particles), which are released from the cell upon phage-induced lysis, or by other mechanisms, such as enzyme-mediated cell lysis. The disclosure includes customizing
15 and optimizing ABD-particle producing bacterial strains, and includes such strains themselves.

In embodiments, the disclosure facilitates producing large quantities of ABD particles, which can be purified to any desired degree of purity. The particles can be included in a variety of compositions, including but not limited to pharmaceutical compositions.

20 In certain aspects the invention includes introducing by any suitable approach the ABDs into bacterial cells such that the cargo is expressed or otherwise affects function of the bacterial host. In embodiments, ABDs are introduced into bacteria and affect one or more properties of the bacteria. In embodiments, such effects are realized without integration of the ABD or any segment of its DNA content into the host chromosome; in other embodiments,
25 the effects are realized subsequent to integration into the host chromosome.

Depending on the cargo, ABD may kill, weaken or disarm the targeted bacteria or the surrounding bacteria (or may deliver a drug or other substance to a particular locale). ABD can then spread throughout the bacterial population either spontaneously or by design. ABDs have been constructed to treat staphylococcal infections and can be considered alternatives or
30 adjuncts to conventional antibiotics. Implicit in their design and construction is applicability to a wide variety of other pathogenic bacteria.

With respect to designing and constructing the genetic content of ABDs of this disclosure, the invention includes all modifications that are described herein, and those that are depicted in the figures. In certain and non-limiting embodiments, modifications to

prototypical SaPI, SaPI2, are as depicted in Figure 3A and 3B. In representative examples, the disclosure comprises deleting or modifying all virulence determinants to make the island inert (i.e., “detoxifying” the SaPI).

Modifications also comprise deleting or modifying capsid morphogenesis genes, *cpmAB*, to allow for cargo of up to ~30 kb. Additional modifications to the SaPI genome using SaPI2, other SaPIs or a combination thereof include the following: To increase the probability of induction and consequent spread, the disclosure includes converting ABD into an auto-inducing island by incorporating the phage-determined de-repressor gene expressed from an SOS-inducible promoter. This would result in helper phage independent induction owing to stochastic SOS activity. In an approach the disclosure includes ABDs that, like the SaPIs, do not induce resident prophages, but if an endogenous prophage undergoes spontaneous induction (as often occurs in vivo), embodiments of the disclosure take advantage of it, even if the endogenous prophage is not a helper phage. In one approach, if the ABD is derived from SaPI2, the disclosure includes cloning *dut*. If the ABD is derived from SaPIbov2 or has a SaPIbov2 regulatory module, the disclosure includes cloning the SaPIbov2 de-repressor, gp15, from phage 80α. The advantage of using the SaPIbov2 repressor and cognate de-repressor is that induction of ABD is very unlikely to inadvertently induce SaPIs resident in human-adapted staphylococci. In general, the disclosure includes use of a SaPI repressor that is not known to occur in the resident SaPIs of the infecting (or otherwise targeted) bacteria. Methods for determining unique repressor sites (e.g., sites that are orthogonal to the targeted bacterial genome) are known in the art, and include, for example, sequencing and analysis of the whole or partial genomes of any bacterial sample of interest.

To inhibit and/or prevent packaging of resident SaPIs (or parts of them) by ABD *terS*, the disclosure provides for use of the bov2 *terS* and *pac* sites. Again, a general principle is: use a SaPI *terS* (and *pac* site) that is not known to occur in the resident SaPIs of the infecting bacteria. The disclosure provides for use of SaPIbov2 regulatory module, *terS* and *pac* site, and SaPI2 replication module, integration/*xis* and phage interference genes (Figure 3C).

To reduce unintended consequences of mis-packaging by ABD during production and subsequently in vivo use, the disclosure provides for use of a *cos terS*, in lieu of a *pac terS*. The *pac terS* packages more efficiently and gives higher titers. Therefore, those skilled in the art can determine, depending on any particular situation, which *terS* is preferable, and one skilled in the art could make a suitable selection given the benefit of the present disclosure.

The disclosure includes at least two types of DNA cargo modules, which can be characterized by the type of anti-bacterial agents they encode: i) those that kill the infecting bacteria and, in some cases induce the SOS response and consequently induce prophages and the island, and ii) those that disarm or attenuate virulence.

5 Cargo destined to kill infecting bacteria in embodiments can disseminate the island (and other islands). For example, and as described more fully below, if cargo designed to kill bacteria in a bacterial infection damages the DNA of the bacterium it will trigger the so-called SOS response, which will induce endogenous prophages. If an endogenous prophage is a helper for either a resident SaPI or SaPI-like element, or for the incoming ABD, then the
10 resident SaPI and/or the incoming ABD will also be induced and will spread to other neighboring cells when the first cell lyses. In embodiments, the incoming ABD may contain *dut*, the gene encoding the SaPI2 repressor. This will cause the incoming ABD to replicate following entry and to be packaged if an endogenous prophage is induced. It will also induce any endogenous SaPI that is sensitive to it.

15 The disclosure includes different approaches (using cargo of the same type) to effect similar results. These include, for example, targeting all the bacteria in the population using any suitable agent, such as DNA encoding anti-sense RNAs targeting expression of essential genes. An anti-sense RNA can be expressed from the same promoter as the sense RNA (the target) so both sense and anti-sense can be expressed at the same time, alternatively, the
20 antisense could be expressed from a strong constitutive promoter. In embodiments, the cargo comprises genes encoding a toxin that acts within the bacterial cell (such as the toxin of a toxin, anti-toxin module). These genes can be expressed from constitutive promoters or from promoters induced within the infected host such as temperature-sensitive promoters. In embodiments, the cargo comprises genes encoding a toxin that is secreted and acts outside
25 the cell (ex. lysostaphin). Production of these toxins would affect not only the bacterial cell that has been infected by ABD, but also neighboring cells.) These genes can also be expressed from constitutive promoters or from promoters induced within the infected cell. In alternative embodiments, the cargo can comprise a CRISPR-Cas9 system configured with spacers targeting highly conserved constant chromosomal genes or plasmids or other mobile
30 elements containing, for example, antibiotic resistance genes. In Figure 6 is a diagram of the CRISPR system.

With respect to cargo that is intended to disarm, attenuate virulence, or weaken the infecting bacteria, those skilled in the art will recognize from the specification that the specific cargo will depend on the type of infection, and may take into account the genotype of

the strain. The disclosure provides for use of modules to target all the cells in a population, or a subset of particular cells.

For targeting ABD-infected bacteria only, the disclosure includes using as cargo DNA encoding anti-sense RNAs targeting staphylococcal virulence genes (genes encoding toxins, enzymes, adhesins, proteins involved in immune evasion, proteins involved in the production of surface capsular polysaccharides). The cargo can also comprise DNA encoding anti-sense RNAs targeting genes encoding regulators of virulence, and/or genes required for biofilm formation, such as the intercellular adhesion (*ica*) operon (see Table 1 for a list of genes referred to in the disclosure) which is repressed by IcaR.

Table 1. Bacterial and SaPI genes described herein.

Bacterial and SaPI genes		
Gene	Locus tag, ID or ref.	Description or function
<i>agrA</i>	SAOUHSC_02265	<i>Agr</i> response regulator
<i>agrB</i>	SAOUHSC_02261	<i>AgrD</i> processing enzyme
<i>agrC</i>	SAOUHSC_02264	<i>Agr</i> signal receptor-histidine kinase
<i>agrD</i>	SAOUHSC_02262	<i>Agr</i> autoinducing peptide precursor
<i>blaZ</i>	ID: 2610354	β -lactamase
<i>comA</i>	BSU31680	Competence signal receptor
<i>comP</i>	BSU31690	Competence response regulator
<i>comQ</i>	BSU31710	Competence processing enzyme
<i>comX</i>	BSU31700	Competence peptide
<i>covA</i>	Microbiol Mol Biol Rev 63: 174	Streptococcal global virulence regulator
<i>cpmA</i>	Virology 432:277, 2012	SaPI capsid morphogenesis
<i>cpmB</i>	Virology 432:277, 2012	SaPI capsid morphogenesis
<i>dnaA</i>	BSU00010	Chromosomal replication initiator
<i>dut</i>	SA80_28	dUTPase
<i>eta</i>	pETB_p07	Exfoliative toxin
<i>fib</i>	SAOUHSC_01114	Fibrinogen binding protein
<i>fnbA</i>	SAOUHSC_02802	Fibronectin binding protein
<i>fnbB</i>	SAOUHSC_02803	Fibronectin binding protein
<i>gelE</i>	J. Bacteriol. 189:1358	Gelatinase
<i>ghoT</i>	ECK4122	Membranolytic toxin
<i>icaR</i>	SAOUHSC_03001	Repressor of <i>ica</i> operon
<i>int</i>	SA1810	integrase
<i>lsp</i>		lysostaphin
<i>llo</i>	lmo0202	listeriolysin
<i>mecA</i>	NI36_00210	Methicillin resistance PBP-2A
<i>pezT</i>	STH8232_0686	Inhibitor of cell wall synthesis
<i>pri</i>		DNA primase

<i>ptiA</i>	Novick&Ram TIG op. cit.	SaPI Phage interference protein
<i>ptiB</i>	Novick&Ram TIG op. cit.	SaPI Phage interference protein
<i>ptiM</i>	Novick&Ram TIG op. cit.	SaPI Phage interference modulator
<i>rep</i>	pSK1_p03	Replication initiation
<i>rsbW</i>	USA300HOU_2060	Inhibitor of sigmaB function
<i>saeR</i>	SAOUHSC_00715	Response regulator of <i>sae</i> signaling system
<i>spa</i>	SAOUHSC_00069	Staphylococcal protein A
<i>srtA</i>	SAR2608	sortase
<i>tarFIJLS</i>	SA40_0212	Teichoic acid synthesis operon
<i>terL</i>	PI31_gp44	Terminase large subunit
<i>terS</i>	phiJB_ORF42	Terminase small subunit
<i>tst</i>	SA1819	Toxic shock syndrome toxin-1
<i>uvrB</i>	SAA6008_00773	DNA damage repair
<i>wzg</i>	INV104_02980	Pneumococcal capsule regulator
<i>xis</i>	80α_gp02	Phage or SaPI excision

This gene, the product of which interferes with biofilm formation, can be expressed from a strong constitutive promoter, as one example. The cargo can comprise genes required for producing an inhibitory peptide that can block the activation of the staphylococcal global regulator of virulence, *agr*, and consequently, can block production of most staphylococcal toxins. These genes can be expressed from a quorum-sensing promoter, for example, In embodiments, the cargo can comprise a CRISPR/dCas9 with spacers targeting promoters of global regulators of virulence or of biofilm formation, thereby inhibiting their expression without modifying the chromosome. Thus, it will be apparent that for targeting ABD-infected bacteria only, in embodiments, the cargo is suitable for affecting the expression/production/activity of any one or combination of: virulence determinants and regulators, biofilm determinants and regulators, sensors to different environmental cues, genes that affect metabolism, and genes that affect antibiotic resistance, or resistance to other agents. Thus, in embodiments, the disclosure comprises sensitizing bacteria to one or more agents.

For targeting ABD-infected bacteria and bacteria surrounding ABD-infected bacteria, in embodiments, genes required for producing an *agr*-inhibitory peptide can be added, as described above. In embodiments, cargo modules can be grouped by mechanism of action. In embodiments, cargo can be adapted to produce antisense RNA used to target any one or combination of: *secY* (killing), *agrA*, *saeR*, *spa*, *fnbA*, or *fnbB*. In embodiments, cargo can be adapted to produce toxins without anti-toxins, including but not limited to *pezT* (killing), *ghoT* (killing). In embodiments, cargo can be adapted to target Staphylococcal regulators,

such as *agrA*, or to produce quorum sensing inhibitors, or to include one or more systems and spacers for CRISPR/Cas9 (killing), or for CRISPR/dCas9 inhibition of gene expression. In an embodiment, the disclosure comprises cargo adapted to express an extracellular-acting toxin or enzyme without an immunity gene, such as Lysostaphin (for killing).

5 In embodiments, the disclosure includes inserting two or more cargo modules into the basic modified SaPI2 and into each variant. With these embodiments, a pathogenic island can be converted into a therapeutic island.

It should be recognized that each type of ABD (killing or disarming) may have at least 2 cargo modules of the same type to reduce the probability of resistance or of a single
10 inactivating mutation. When the ABD particles are administered with an antibiotic, the ABD can carry cargo that targets the appropriate antibiotic resistance gene, in addition to its regular killing or disarming cargo. Thus, the disclosure in embodiments also comprises targeting specific bacteria with specific variable genes (such as cell capsule variants, antibiotic resistance genes, etc.) including by using elements such as: DNA encoding anti-sense RNAs
15 targeting highly conserved variable genes; CRISPR-Cas9 with spacers targeting highly conserved variable genes; and CRISPR-dCas9 with spacers targeting the promoters of highly conserved virulence genes or genes regulating virulence.

In certain implementations, the disclosure comprises exploiting the natural packaging system and high frequency transfer of the SaPIs. In certain examples, the disclosure
20 accordingly includes creating (customizing and optimizing) ABD-particle producing strains by, for instance, customizing the particle-producing strains for the basic ABD or for variants. A lysogenic strain with a mutant prophage ($\Delta terS$) will ensure that there is a high titer of ABD particles and no viable phage particles. Depending on which variant of SaPI is used, the phage will be a helper phage or need not be. In other implementations, a modified prophage
25 ($\Delta terS$) (helper and non) will be used that produces particles with different receptor specificity for treating infections caused by the atypical *S. aureus* strains of the ST395 lineage. In certain implementations, the producing strains will be customized for the specific antibacterial modules. For example, for ABDs with killing modules the particle-producing strain would be made insensitive to the killing.

30 In embodiments, the disclosure comprises producing large quantities of purified ABD-particles. In embodiments, the disclosure comprises delivering ABD-particles in vivo to the infecting bacteria and consequently treating the infection.

The disclosure demonstrates prophylactic and therapeutic utility for specific

embodiments of the invention, which can be readily extended to the other embodiments that are described herein by the skilled artisan when given the benefit of the present description. In particular, in vitro results presented herein show that both killing and disarming ABD-particles are effective against a derivative of a prototypical lab strain, *Staphylococcus aureus* NCTC 8325 and against an important clinical strain USA300. Typical results are shown in Figures 7 (killing) and 8 (disarming). Furthermore, in vivo results show that representative killing ABD-particles targeting *S. aureus* are not toxic to C57-bl6 mice, do not elicit an immediate immune response and can find staphylococci in the infected mouse, can inject their ABD-DNA into these Staphylococcal cells, express the ABD cargo genes, express the ABD lifestyle genes, can integrate the ABD-DNA into the recipient cell, can treat an infection, and can prevent an infection from developing. The disclosure also demonstrates that killing ABD-particles targeting a chromosomal gene of *Listeria monocytogenes* are effective against that organism.

SaPI genomes have a well-conserved modular organization. Genes are grouped into functional modules that mediate integration-excision, regulation, replication, packaging and phage-interference, and accessory genes (Figure 3a). The model system in the demonstrations of this disclosure is based on the well characterized SaPI, SaPI2, and its helper phage, 80α. It is readily applicable to other SaPIs or SaPI-like elements in staphylococci or other bacteria, given the benefit of the present disclosure. However, it is expected that any SaPI can be adapted for use in embodiments of the invention. In this regard, non-limiting examples of specific SaPI sequences are given in the following Table 2. The table provides in the left column a GenBank accession number that pertains to the genome of each bacterial strain or to the sequence of the SaPI itself. The genome of strain NY940 has not been sequenced. Bacterial strain names are provided in the “Strain” column. All nucleotide and amino acid sequences that are indexed in the NCBI database for the accession numbers given in Table 2 are incorporated herein by reference as they exist on the date of this application or patent. Table 2 includes the *att* site type and its sequence. The SaPI coordinates for SaPI sequences when present in bacterial chromosomes are given by flanking nucleotide position in the bacterial genome as indicated for the 5’ and 3’ positions. The approximate sizes of the elements are given (those smaller than 12 kb are defective), as are the names of the particular SaPIs that have been published. Those lacking names have been identified by genome examination.

Table 2 - SaPI Examples

Accession #	Strain	Att site	Att site sq	SEQ ID	SaPI coordinates (5'-3')		Size, Kb	SaPI
<u>CP012409.1</u> **	Tager 104	I	AAAGAAGAACAATA ATAT	6	1196124	1211879	15.8	
<u>CP010942.1</u> **	949-S8-S. <i>epidermidis</i>	I	AAAGAAGAACAATA ATAT	7	2243432	2251563	8.1	
AY954948.1	NY940	I	AAAGAAGAACAATA ATAT	8			15.6	SaPI 1028
<u>BX571856.1</u> **	MRSA252	I	AAAGAAGAACAATA ATAT	9			15.1	SaPI4
<u>AF217235.1</u> *	RF122	II	TAATTATTCCCACT CAAT	10			15.8	bov1
<u>AY220730.1</u> *	V 329	II	TAATTATTCCCACT CAAT	11			27	bov2
<u>CP019945.1</u> **	BA01611	II	TAATTATTCCCACT CAAT	12	467996	481943	14.0	
<u>CP014791.1</u> **	MCRF184	II	TAATTATTCCCACT CAAT	13	391487	396451	5.0	
<u>HM228919.1</u> *	JP5338	II	TAATTATTCCCACT CAAT	14			13.5	SaPIbov5
<u>BA000033.2</u> **	MW2	III	TCCCGCCGTCTCCA T	15	2088648	2100838	14.4	SaPI MW2
<u>BA000017.4</u> **	MU50	III	TCCCGCCGTCTCCA T	16			14.4	SaPI m4
<u>AP006716.1</u> **	JCSC1435 <i>S. haemolyticus</i>	III					16.6	ShPI2
<u>KT845956.1</u> *	4s-13 S. <i>epidermidis</i>	III	TCCCGCCGTCTCCA T	17	79	21426	21.3	Double SaPI
<u>LT615218.1</u> *	AUS0325	III	TCCCGCCGTCTCCA T	18	794655	846139	51.5	Triple SaPI
<u>U93688.2</u> *	RN4282	IV	TTATTTAGCAGGAA TAA	19			15.2	SaPI1
<u>CP000046.1</u> **	COL	IV	TTATTTAGCAGGAA TAA	20			15.6	SaPI3
<u>CP015447.1</u> **	M92	IV	TTATTTAGCAGGAA TAA	21	911782	926360	14.6	
<u>CP019590.1</u> **	C2406	IV	TTATTTAGCAGGAA TAA	22	901697	915669	14.0	
<u>CP020619.1</u> **	JE2	IV	TTATTTAGCAGGAA TAA	23	896724	910696	14.0	
<u>CP013182.1</u> **	SA40TW	IV	TTATTTAGCAGGAA TAA	24	850818	866767	15.9	
<u>CP017094.1</u> **	2148.CO1	IV	TTATTTAGCAGGAA TAA	25	1966279	1980248	14.0	
<u>CP012120.1</u> **	USA300	IV	TTATTTAGCAGGAA TAA	26			14.0	SaPI5
<u>CP016855.1</u> **	5118.N	IV	TTATTTAGCAGGAA TAA	27	897139	911106	14.0	
<u>AB690438.1</u> *	PM1	IV	TTATTTAGCAGGAA TAA	28			12.1	SaPIPM1
<u>BA000018.3</u> **	N315	V	TTTTACATCATTCT GGCAT	29				SaPIN1
<u>AJ938182.1</u> *	RF122	V	TTTTACATCATTCT GGCAT	30	2011992	2038438	26.5	SaPI122

AB716351.1 *	#10	V	TTTTACATCATTCT GGCAT	31	2046958	2031831	15.1	
CP015447.1 **	M92	V	TTTTACATCATTCT GGCAT	32	2161986	2158884	3.1	SaPI6Δ
CP019590.1 **	C2406	V	TTTTACATCATTCT GGCAT	33	2143261	2146401	3.1	SaPI6Δ
CP012120.1 **	USA300	V	TTTTACATCATTCT GGCAT	34	2184162	2187302	3.1	SaPI6Δ
CP019563.1 **	SR434	V	TTTTACATCATTCT GGCAT	35	2805478	12419	16.1	
EF010993.1*	RN3984	V	TTTTACATCATTCT GGCAT	36			14.7	SaPI2
AM292600.1	CS6- EEFIC	V	TTTTACATCATTCCA GGCAT	37			20.7	SaPIfusB
AP008934	15305 <i>S. saprophyti cus</i>	VI	CGAGGGGACTAAT AAGT	38			17.0	SsPI15305

*SaPI sequence; **whole genome sequence.

It is considered, and without intending to be limited by any particular theory, that ABD's exhibit two forms of tropism, one towards a specific pathogen and the other towards a specific infection. The first form is determined by ABD-particle adsorption specificity. Since ABD-particles are composed entirely of virion proteins, they have the same cell-surface specificity as the helper phage particles. Thus, to change the specificity of the ABD particle, the helper phage can be changed. While all presently known helper phages have been shown to adsorb to the bacterial cell walls via teichoic acid (WTA), different phages recognize different WTA structures. For example, most *S. aureus* strains produce a WTA that contains repeating ribitol-phosphate units decorated with N-acetyl-D-glucosamine residues. Phages 80α and Φ11 recognize this structure and therefore, when they are used as helper phages, the ABD particles will target most *S. aureus* strains and are expected to effectively treat (kill) infections caused by these strains. However, *S. aureus* strains of clade ST395 produce an atypical WTA consisting of a glycerophosphate polymer modified with N-acetyl-D-galactosamine residues. To treat infections caused by these strains, the disclosure includes using a suitable helper phage such as Φ187, which recognizes this WTA structure. In embodiments, the disclosure comprises modifying or otherwise adapting compositions to tailor the cellular tropism of the modified SaPIs, which may be provided as ABDs. To expand the ABD host range to include ST395 strains, the present disclosure includes using an available hybrid host strain, PS187-H, which contains the glycerol-WTA for phages such as 187 as well as the ribitol WTA receptors for 80α and other phages of its type. This strain will be lysogenized by phage 187 ΔterS. An ABD can be introduced by transfer via phage 80α.

Since phage 187 is not a helper phage for SaPI2-based ABDs, the ABD will contain *dut* driven by the SOS-inducible *uvrB* promoter. Growth in the presence of mitomycin C will then induce both the prophage and the ABD and the resulting ABD particles will be specific for ST395 strains. The disclosure includes broadening the ABD system to other species, such as by modifying existing ABDs to infect these other organisms, using this same strategy. In general, the disclosure includes adapting the ADBs using genes from streptococci, which are closely related to staphylococci, by cloning the gene(s) for streptococcal phage receptor specificity into a standard *S. aureus* host strain, then lysogenizing this strain with a streptococcal phage, deleting its *terS* gene and introducing an ABD of this disclosure to provide a strain that will produce ABD particles specific for streptococci. Alternatively, the tail fiber genes from a suitable streptococcus phage can be cloned into a helper phage, followed by introduction of an ABD, and induction of the phage and ABD using a suitable reagent such as mitomycin, thereby producing particles that are specific for the streptococcus.

Modifications of these approaches will be apparent to those skilled in the art, given the benefit of the present disclosure. In embodiments, the disclosure comprises testing a sample of bacteria to determine helper phages which the bacteria contain, and selecting and/or generating suitable ABDs such that the bacteria can be effectively targeted based on a tropism designed to enable infection and killing and/or modifying of such bacteria.

In embodiments, the disclosure includes tailoring the ABDs toward specific infections. A plurality of distinct ABDs is described herein, wherein members of the plurality have distinct genetic elements relative to one another. Thus, in embodiments the disclosure includes a library of distinct ABDs. In embodiment, the members of the library differ from one another in their genetic content. For example, a first member of the library can comprise any genetic modification as described herein, whereas a second member of the library may comprise a different genetic modification, or different combinations of genetic elements. The ABDs can be, for example, held in separate containers, and for example indexed using any suitable indicators, including but not limited to text, numerical, and machine readable indicators, such as bar codes. Providing a library of ABDs facilitates rapid selection of a suitable ABD to, for example, target a specific type infection that an individual may have. Thus, in one embodiment, an individual is diagnosed with an infection by a particular type or class of bacteria, and a ready-made preparation of ABDs made according to this disclosure can be selected and administered to the individual. The ABDs may be stored in any suitable form, such as lyophilized, or frozen, and may be ready for, for instance, reconstitution into a pharmaceutical formulation.

The ability to target a wide diversity of bacteria, including but not limited to, via accounting for tropism as discussed above, imparts on the disclosure a powerful approach to modifying bacterial chromosomes using the ABDs that are described herein. In this regard it is established in the art that SaPI lifestyle includes integration of the SaPI in to the host chromosome, and it was expected that this property of SaPIs would be essential for a wide variety of implementations of this disclosure. However, in arriving at the present invention certain unexpected properties of ABDs in connection with their infectivity and killing activity came to light.

To use an ABD effectively, one must determine the number of ABD particles in the preparation. In the present disclosure, an unexpectedly high level of bacterial killing by the ABD with a CRISPR-Cas9 cargo module was observed. We had predicted that the Killing Units, measured by infecting a population of bacteria that have been treated with ultra-sound to disrupt clumps, then determining the fraction of surviving bacteria by plating for colony counts, would be equal to the Transfer Units, measured by colony formation on selective media, if the killing were very efficient and fewer, if less efficient. Enumeration of sub-microscopic particles, such as phage, SaPI, ABD particles, etc., is done microbiologically by counting the particles based on some specific property. In the case of a phage, this would be the ability of a single particle to form a plaque. A plaque is a circular clearing zone within a lawn of bacteria growing on an agar plate. The individual phage particle adsorbs to the surface of the bacterial cell and injects its DNA, which replicates within the cell, produces progeny particles and lyses the cell. The new particles infect surrounding cells, creating a zone of lysis, which is seen as a plaque. For a SaPI or ABD particle, this would be the ability to infect a bacterial cell and enable it to form a colony on an agar plate containing an antibiotic to which the SaPI or ABD confers resistance. In the disclosure, tetracycline (Tc) resistance, determined by the *tetM* gene, is used. A series of dilutions is prepared and a measured sample of each is mixed with a suitable number of Tc-sensitive bacteria – *e. g.* 10^8 – and the mixture spread on an agar plate containing a suitable concentration of Tc. Only cells infected by an ABD particle can grow and produce colonies on the plate. Counting the colonies and multiplying by the dilution factor gives the number of particles in the preparation, the titer of transducing units (TU). With an ABD containing a CRISPR/cas9 module with a spacer targeting a bacterial chromosomal gene, it was assumed that each cell infected by such a particle would be killed by a CRISPR-induced DSB in the chromosomal DNA. In an experimental test of this, a known number of ABD particles was mixed with twice the number of staphylococcal bacteria. Because of the random nature of the infection

events, it was expected that about 39% of the bacteria (rather than 50%) should have been killed by the CRISPR, because 11% would have been infected by 2 or more particles. Much to our surprise, however, over 95% of the bacteria were killed. To achieve this killing frequency, one would have had to use a ratio of 5 particles per bacterial cell. In other words, the particle titer determined by measuring the formation of Tc-resistant colonies (using bacteria that were resistant to CRISPR killing) was about 10-fold lower than the particle titer measured by CRISPR killing. To confirm this, we performed a second test in which we used a ratio of 1:20 transducing particles to bacteria. If the killing and transducing titers were equal, a barely measurable 5% of the bacteria would have been killed. Instead, about 40% were killed, the expectation for a 1:2 ratio rather than a 1:20 ratio. The number of killing units (KU) is thus about 10x that of the TU. Without intending to be constrained by any particular theory, it is considered that the explanation for this disparity is that an incoming ABD DNA molecule, which is linear, must undergo two specific and possibly inefficient steps before the bacterium can grow on a Tc-containing plate: it must first form a closed DNA loop, which requires the action of a specific, possibly inefficient enzyme, and it must then integrate into the host cell's chromosome, via this closed loop, to be propagated. To kill a cell, however, the incoming DNA need not form a loop or integrate; it must simply express its CRISPR/cas9 module, which requires only a linear template. The implication of these results is that some 90% of infecting ABD particles never become stably established in a targeted bacterial cell. Among the genes that would be immediately expressed following entry of the ABD DNA is *stl*, which encodes the master repressor. Consequently the incoming DNA would be repressed and would probably not replicate, so that during division of the infected cell, it would be inherited by only one of the daughter cells. This means that the antibacterial cargo must complete its intended effect before the first cell division. Thus, there may be 2 types of ABD cargo – those that complete their antibacterial function before the first cell division, and those that do not. Of the latter, only those ABDs that become established by integration will be able to perform their inhibitory function, and, consequently, dosing must be based on the TU titer rather than on the KU titer. Therefore, in embodiments in which the ABD disarms rather than kills the targeted bacteria, it will either be able to replicate, by incorporating the *B. subtilis* phage 29 replication system, which uses a linear template, or will block the cell division mechanism of the targeted bacteria. Alternatively, it may be that the infecting bacteria multiply very slowly, so that neither of these approaches will be necessary.

The Cas9-induced double-stranded break induces the SOS response and consequently induces prophages before cell death is finalized. If a resident prophage is a helper phage (or any phage that can package the ABD genome), then the ABD (and consequently the killing) will spread to adjacent cells. Thus, the ABD killing zone can be considered analogous to a phage plaque. Accordingly, in embodiments, the disclosure comprises determining a number of Transfer Units in order to kill a known or estimated bacterial population. In embodiments, the disclosure comprises using standardized amounts of TUs for killing any particular bacterial population, which may be correlated with parameters that can be calculated by known approaches, such as the type or severity of infection. Thus, in embodiments, the disclosure includes providing pre-determined amounts of ABDs to kill and/or modify bacteria. In embodiments, the disclosure further includes testing a sample of the bacteria to determine any one or combination of characteristic of the bacteria, such as type of bacteria, severity of infection, pathogenicity/virulence of the bacteria, resistance to one or more antibiotics, the location of the infection, genetic components of the bacteria that can be targeted for killing or modification and/or for sensitizing the bacteria to a conventional anti-microbial agent(s), the amount of bacteria in an infection, and other parameters that will be apparent from this disclosure.

In one aspect the disclosure accordingly relates to attenuation of virulence of bacteria, and further comprises not only attenuating virulence of the ABD-infected cells, but also of the surrounding cells, thereby amplifying the attenuating effect. In an embodiment this aspect comprises attenuating a population of *S. aureus*, but similar approaches can be adapted for other bacterial types as described further below and as will otherwise be apparent to those skilled in the art given the benefit of the present disclosure.

In embodiments, the disclosure comprises use of ABDs to affect bacteria into which the ABDs are introduced, and also to affect bacteria that may be near and/or in fluid communication with the ABD-infected bacteria, but may not necessarily be infected themselves. In one implementation ABDs are designed to cause infected bacteria to secrete an inhibitor of one or more quorum-sensing (QS) genes and/or QS modulating proteins. For example, in embodiments, and as discussed further below, a cell infected by an ABD produced according to this disclosure can be modified to secrete an inhibitor of the accessory gene regulator (*agr*), the global regulator of staphylococcal virulence. *agr* is an autoinducing QS system that coordinates the expression of over 50 genes (encoding toxins, degradative enzymes, immune evasion factors, adhesins and other exoproteins) in response to bacterial cell density, discovered and characterized in the inventors' laboratory. Figure 9 provides an

illustration that is related to this embodiment. The complex *agr* locus has two major transcriptional units driven by the *agr*-inducible promoters, P₂ and P₃. The P₂ operon includes four genes, *agrB*, *D*, *C* and *A* and encodes a typical QS system. *agrD* encodes the precursor of an extracellular QS signaling peptide, the auto-inducing peptide (AIP). AgrB is required for processing and secretion of the AIP, which is the ligand of AgrC. AgrC and A form a classical two component system (TCS), with C the histidine kinase sensor (the detector of the QS signal) and A its cognate response regulator (the activator of the QS system). At a high cell density (the quorum), the AIP accumulates in the extracellular environment, binds the N-terminal trans-membrane domain of AgrC, C autophosphorylates, transfers a phosphate group to A, which then activates (up-regulates) transcription from P₂. Consequently, the P₂ operon is considered to be doubly autocatalytic, a key feature of all QS systems. AgrA~P also activates the divergent *agr* promoter, P₃, as well as the promoters of two operons that encode the important toxins, phenol-soluble modulins α and β . However, it is not AgrA, but the *agrP*₃ transcript, RNAIII, that is the major effector of global gene regulation in the *agr* system. While the basic architecture, regulatory circuitry and sequences of *agrA* and the 3' end of *agrC* are highly conserved among the staphylococci, *agrB*, *D* and the 5' end of *C* are variable. Allelic variations in these *agr* genes have resulted in the emergence of four QS specificity groups (with different AIPs and different corresponding AIP receptors) in *S. aureus*. Strains within a group (with homologous *agr* loci) cross-activate, but strains from different groups (with heterologous loci) exhibit strong mutual cross-inhibition. The other, non-aureus staphylococcal species appear to possess unique species-specific *agr* loci (some with more than one allelic variant). Several of these interfere with at least one of the *S. aureus* QS groups. The AIP (YSPCTNFF; SEQ ID NO:4) produced by *S. warneri* strains RN833 and SG1 has been shown to interfere with all four *S. aureus* QS groups (although, *S. warneri* is indifferent to the *aureus* AIPs). An *agr*-parallel QS system is found in *Bacillus subtilis*, where it controls competence rather than virulence. Moreover, this *com* locus is exactly analogous to the *agr* P₂ operon. It consists of four genes, *comQ*, *X*, *P* and *A*. *comX* encodes the precursor of the AIP; *Q* is required for its processing and secretion; *C* encodes the detector, *A* the activator of the *com* promoter and the locus is autoinduced. There even exist *com* allelic variants and *com* QS specificity groups. Thus, in embodiments, ABDs of this disclosure are engineered to produce a cargo that is a hybrid of *com/agr* QS operon as illustrated in Figure 10, comprising or consisting of the *B. subtilis* *com* promoter, the *S. warneri* *agr* variable region, including *agrB*, *D* and the 5' moiety of *C*, and the *B. subtilis*

com conserved region, including the 3' moiety of *comP* and the entire *comA*. The composite locus creates a fusion histidine kinase with the N-terminal transmembrane sensor domain of AgrC and the C-terminal cytosolic domain of ComP. This fusion protein is designed to detect the *agrD*-encoded AIP and to activate the *comA*-encoded response regulator. Therefore, the AIP will not only inhibit the four *S. aureus agr* groups, but also serve as the effector of a positive feedback loop, activating the hybrid locus, maximizing the production of the AIP (and minimizing the cost of producing it).

Since the QS promoters have a very low basal level (prior to activation), the disclosure further comprises insertion of a second promoter downstream of the *com* promoter and upstream of the *agrB* Shine-Dalgarno (ribosomal binding site). For this second promoter, suitable choices include but are not necessarily limited to the following: *Pcad*, which has a high basal level, *agrP₁*, which is induced in vivo, or the promoter used to express CRISPR-Cas9 in other cargo modules. Non-limiting examples of suitable cargo sequences and their sequence contexts are shown in Figure 17 (SEQ ID NO:1).

In order to implement this approach, modifications (deletions, insertions and nucleotide changes) to SaPIs, basic Drones or ABDs can be made when the elements are integrated in the chromosome and standard allelic replacement vectors (pMAD, pKOR1 or pIMAY) are used to make these modifications. To streamline the process and facilitate cloning, the disclosure includes inserting all single modules between the *terS* and *tetM* (using the same Left and Right Flanking regions) and introducing a novel multiple cloning site (MCS) between the two flanks creating an off-the-shelf user-friendly vector, pMAD-FL-MCS-FR.

In an embodiment the disclosure includes constructing a hybrid (a tripartite) locus. This approach uses restriction enzymes and conventional cloning methodology, instead of Gibson Cloning. This approach facilitates rapid modifications of any of the module's three parts individually. The *Pcom* part can be amplified from *B. subtilis* 168 genomic DNA with the primer pair Pcom-PstIF and Pcom-EcoRIR, the *agr* variable region from *S. warneri* SG1 genomic DNA with the primer pair agrv-EcoRIF and agrv-KpnIR and the *com* conserved region from *B. subtilis* 168 genomic DNA with the primer pair comc-KpnIF and comc-XhoIR. Restriction sites (PstI, EcoRI, KpnI and XhoI) can be incorporated in the appropriate PCR primers and the purified amplicons digested with restriction enzymes EcoRI and KpnI. The restricted PCR products can be ligated and the ligated DNA used as a template to be amplified using the outer primers, Pcom-PstIF and comc-XhoIR. This PCR product covering the entire hybrid locus can be purified and cloned into pUC18 at the HincII site of the

polylinker (by blunt ligation). The insert can be sequenced and for verification and subcloned into the allelic replacement vector pMAD-FL-MCS-RL using restriction enzymes PstI and XhoI which are novel in the MCS.

As discussed above, aspects of this disclosure include an approximately 15 kb DNA molecule that is a derivative of staphylococcal pathogenicity island SaPI2 with the following modifications: the native virulence genes of the island, *tst* (encoding toxic shock syndrome toxin-1) and *eta* encoding exfoliative toxin A), have been replaced by a DNA segment containing the *tetM* gene for tetracycline resistance; in some embodiments, the capsid morphogenesis genes (*cpmA* & *cpmB*), and the phage interference gene, *ptiB*, have been replaced by a DNA segment containing the SaPI2 derepressor gene, *dut*. In embodiments, all or substantially all of the *tst* and *eta* genes have been replaced. In embodiments, all or substantially all of the *cpmA* & *cpmB* and *ptiB*, have been replaced. This SaPI2 derivative is used in the following embodiments, and is diagrammed in Figures 3B & 4 to illustrate what is referred to herein as the “basic SaPI2 derivative”.

An embodiment by which the basic SaPI2 derivative can block the expression of virulence by an infecting organism, (see Figure 10) includes three insertions: an autoinduction circuit comprising *S. warneri agrB* & *agrD* plus *B. subtilis comA* & a *comP-agrC* hybrid, driven by *B. subtilis* promoter, *PcomQ* which will produce an auto-inducing peptide (AIP) that inhibits activation of the virulence-controlling *agr* locus, the 3' segment of RNAIII, an antisense RNA targeting *spa* (the gene for staphylococcal protein A) which will enhance the anti-virulence activity of the inhibitory AIP, and an anti-sense RNA against *agrA*, which will block expression of certain other virulence genes.

In a separate embodiment designed to block biofilm formation, *rsbW*, a protein that blocks the activity of sigmaB plus the gene for IcaR, the repressor of the *ica* operon, will both be inserted into the basic SaPI2 derivative. This modification of the basic SaPI2 derivative is expected to be useful in the treatment of foreign body infections.

In a further embodiment, designed to kill the infecting bacteria, the genes encoding the secreted proteins, PezA, which blocks the synthesis of the staphylococcal cell wall, GhoT, a membrane poison, or lysostaphin, or any combination of the three, can be inserted into the basic SaPI2 derivative. PezA or GhoT will not only kill the infecting staphylococci but will also activate the bacterial SOS response, which will induce resident staphylococcal prophages as well as the SaPI-carried *dut* gene. Lysostaphin, a powerful staphylolytic enzyme, will destroy not only the ABD-infected staphylococci but also any surrounding bacteria that have not been directly infected.

The Dut protein, dUTPase, will derepress SaPI2 replication enabling SaPI packaging by any resident prophage, and spread of the SaPI to any residual staphylococci in the animal. In a further embodiment, an antisense RNA complementary to the translational start of the *secY* gene will be inserted. This will also kill the target organism by blocking expression of the essential *secY* gene. These 3 insertions will effectively eliminate the occurrence of mutants resistant to the ABD.

In a further embodiment, an ABD can be used as a probiotic agent, separately from an anti-infective ABD.

In an embodiment, an ABD expressing a secreted antibacterial protein can be inserted into a non-pathogenic bacterium that is co-resident within the body, and wherein a pathogenic bacterium that the non-pathogenic bacterium will kill or inhibit may also be present. An example comprises arming a probiotic lactobacillus with an ABD that expresses a bacteriocin that kills enterocolitis-causing *Clostridium difficile* in the large intestine.

In another approach the basic SaPI2 derivative is modified by the insertion of a CRISPR/Cas9 cassette. This cassette contains a spacer specific for a bacterial gene or other bacterial sequence and will kill the target organism by introducing a double-strand break in its DNA.

A variation of this embodiment is the insertion of a CRISPR/dcas9 cassette into the basic SaPI2 derivative containing one or more spacers specific for the regulatory regions of bacterial genes required for growth, viability, or the expression of virulence genes.

The disclosure, as illustrated in part by the figures, includes derivatives of the CRISPR/cas9-containing molecule in which the spacer has been replaced by a new spacer specific for the *agrA* gene of *S. aureus*, which is highly conserved among all staphylococci and several other Gram-positive species, or by a new spacer targeting the *mecA* gene, which is required for methicillin resistance in MRSA and is present only in MRSA strains. Other examples include but are not limited to replacement of the spacer with any gene present in some but not other strains.

Embodiments of this disclosure, as illustrated in part by the figures, relate to derivatives of the CRISPR/dcas9-containing derivatives of the basic SaPI2 derivative wherein the CRISPR array contains spacers derived from any bacterial or inserted element sequences, including but not limited to spacers which will block the expression of host virulence genes, biofilm genes or regulatory genes. One example is a spacer targeting *S. aureus* gene *agrA*. Another example is three spacers targeting *S. aureus* genes *Pica*, *Psrt* & *PfnbA*, respectively. A third example includes 3 spacers targeting *S. aureus* promoters *agr-p2-p3*, *Pspa* & *PfnbA*,

respectively.

In a further embodiment, all of the above derivatives of the basic SaPI2 derivative can be inserted into the genomic DNA of a derivative of *S. aureus* strain RN450 lysogenic for a derivative of bacteriophage 80 α with a deletion of its small terminase subunit (*terS*) gene. In

5 an alternative embodiment, all of the above derivatives of the basic SaPI2 derivative can be inserted into the genomic DNA of a derivative of *S. aureus* strain RN450 containing a part of the 80 α prophage consisting of the SaPI2 de-repressor, the virion genes and the lysins, the first two being driven by the strong but inducible *Ptet* promoter, and the lysin genes driven by the inducible *Pbla* promoter. In further embodiments, all of the above derivatives of the basic
10 SaPI2 derivative can be inserted into any staphylococcal strain or any bacterial strain.

An aspect of this disclosure is the use of any molecule derived from any SaPI-like element in bacteria by the insertion of cloned bacterial or bacteriophage genes or any CRISPR array packaged in a bacteriophage-like particle and directed toward disrupting a bacterial infection.

15 An alternative approach comprises use of the basic SaPI2 derivative, modified by the insertion of a CRISPR/cas9 module with a conserved chromosomal gene-specific spacer, as an anti-staphylococcal or antibacterial gene drive. In this embodiment, the CRISPR/cas9 – containing molecule can be inserted into the chromosome of an attenuated *S. aureus* strain with deletions of its *agr*, *spa*, *hla* and *sae* genes and containing prophage 80 α .

20 In further embodiments, the ABD system can be modified to enable it to be used therapeutically against infections with other Gram-positive bacteria. Those skilled in the art, given the benefit of this disclosure, will recognize that these illustrative examples include a multitude of variations. For example, in embodiments the CRISPR/cas9 modules can contain spacers targeting the conserved *dnaA* or any other conserved gene of any of the following
25 organisms: *L. monocytogenes*, *E. faecalis*, *S. pyogenes*, *S. pneumoniae*, and *C. difficile*.

A variant of this embodiment can utilize a CRISPR/dcas9 module with different spacers, each targeting a gene essential for the virulence of each of the same 5 organisms, specifically, spacers targeting the *P_{llo}* promoter of *L. monocytogenes*, the *P_{gelE}* promoter of *E. faecalis*, *P_{covA}* promoter of *S. pyogenes*, the *P_{wzg}* promoter of *S. pneumoniae*, or the *P_{txa}* promoter of
30 *C. difficile*.

It is considered that these embodiments can be extended to include any members of the entire pathobiological bacterial spectrum. In particular, for each bacterial pathogen to be targeted, an attenuated or non-pathogenic bacterial strain can be developed, containing a

CRISPR/Cas9 derivative with one or more spacers targeting one or more genes or other sequences of the targeted bacterial species. These embodiments can utilize any SaPI or SaPI-like element in bacteria, or derivative thereof coupled with any prophage or prophage derivative.

5 In one embodiment, a solution is provided containing SaPI2 particles harboring *S. warneri agrB*, *agrD*, and the 5' half of *agrC*, *B. subtilis comA* and the 3' half of *comP*, *rsbW*, the anti-*spa* segment of RNAIII, anti-sense *agrA* and *secY* have been inserted (ABD2012 – see Table 3). The *S. warneri* AIP inhibits activation of the *agr* locus in all known staphylococci. Expression of *agrB* & *D* will be driven by an autoinduction circuit composed
10 of the *B. subtilis ComAP* signal transduction module driven by the *comQ* promoter. This construct is designed to sharply attenuate the virulence of infecting *S. aureus* bacteria. 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans. In this formulation, *rsbW* will block SigB function and thus prevent biofilm formation. *AgrB* & *D* will combine to produce and secrete an inhibitory AIP that will block the expression of the
15 endogenous *agr* locus in the infecting bacteria and in any neighboring bacteria that have not been infected by the SaPI; anti-*Pspa* RNAIII will block translation of staphylococcal protein A. Anti-*agrA* will block expression of the phenol-soluble modulins. Anti-*secY* will block expression of *secY*, essential for protein secretion and for viability. This combination will severely attenuate the virulence of the infecting bacteria. Resident prophages, induced
20 spontaneously will package the ABD DNA, enabling its spread to any bacteria that were not infected by the initial dose of ABDs.

In another embodiment, a solution is provided containing SaPI2 particles carrying genes for the anti-staphylococcal toxins PezT and GhoT, 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans. This formulation is designed to
25 block the growth and likely kill the infecting organisms by interfering with cell wall synthesis and by disrupting the integrity of the bacterial cytoplasmic membrane.

In another embodiment, a solution is provided containing SaPI2 particles carrying the gene for the secreted staphylolytic enzyme, lysostaphin, 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans or the bovine udder. This
30 formulation is intended destroy the infecting organisms by degrading their cell walls.

In another embodiment, a solution is provided containing SaPI2::CRISPR/Cas9(*agrA*-spacer) particles. This formulation is designed to kill the targeted organisms by introducing a DSB in the chromosomal DNA. The DSB will induce resident prophages, which will package the SaPI and lyse the bacterium, enabling the SaPI to spread to any bacteria not originally

infected by it.

In another embodiment, a solution is provided of SaPI2::CRISPR/dCas9(*agr*-P₂P₃; *Pspa PfnbA* spacers) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. This formulation is designed to disarm the organism by blocking the expression of the key virulence genes up-regulated by *agr* and the expression of *spa* and *fnbA*, virulence genes that are down-regulated by *agr*.

In another embodiment, a solution is provided of SaPI2::CRISPR/dCas9(*Pica*, *PfnbA* and *Psrt* spacers) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. This embodiment is designed for the blockage of biofilm formation by staphylococci.

In another embodiment, a solution is provided containing a mixture of two or more types of the particles described in the first 3 embodiments above, 10¹⁰/ml each, in sterile buffered saline for IV injection in mice or 3x10¹²/ml each for IV injection in humans.

Exemplary embodiments are directed toward infections by other Gram-positive bacteria. In one embodiment, a solution is provided of SaPI2::CRISPR/Cas9(DnaA spacer) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. In this embodiment, for treatment of *Listeria* infections, the DnaA spacer is from *L. monocytogenes* and this formulation is designed to kill the organism by introducing a chromosomal DSB.

In another embodiment, a solution is provided of SaPI2::CRISPR/dCas9(*Pilo* spacer) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans.

In another embodiment, a solution is provided of EfCIV583::CRISPR/Cas9(DnaA spacer) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. In this embodiment, the dnaA spacer is from *Enterococcus faecalis* and the CRISPR-containing particles are targeted at infecting *E. faecalis* or *E. faecium* and administering a lethal DSB.

In another embodiment, a solution is provided of EfCIV583::CRISPR/dCas9(*PgelE* spacer) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. In this embodiment, the spacer targets the *E. faecalis gelE* promoter, required for virulence, and attenuates *E. faecalis* or *E. faecium* infections.

In another embodiment, a solution is provided of SpnCI-ST556::CRISPR/Cas9(DnaA spacer) particles, 10¹⁰/ml in sterile buffered saline for IV injection in mice or 3x10¹² for IV injection in humans. In this embodiment, the CRISPR-containing particles are targeted at

infecting *Streptococcus pneumoniae*, and administering a lethal DSB.

In another embodiment, a solution is provided of SpnCI-ST556::CRISPR/dCas9(Pwzg spacer) particles, 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans. The Pwzg spacer corresponds to a motif in the promoter of a gene that is required for capsule biosynthesis and is conserved throughout the pneumococci; in this embodiment, the CRISPR-containing particles are thus targeted to capsular synthesis by any infecting *Streptococcus pneumoniae*. This will render the organism avirulent and cure the infection.

In another embodiment, a solution is provided of SpyCI-NZ131::CRISPR/Cas9(DnaA spacer) particles, 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans. In this embodiment, the CRISPR-containing particles are targeted at infecting *Streptococcus pyogenes* and administering a lethal DSB.

In another embodiment, a solution is provided of SpyCI-NZ131::CRISPR/dCas9(PcovA spacer) particles, 10^{10} /ml in sterile buffered saline for IV injection in mice or 3×10^{12} for IV injection in humans. In this embodiment, the CRISPR-containing particles are targeted at infecting *Streptococcus pyogenes* and attenuating virulence of the organism.

Additional aspects of this disclosure relate at least in part to the properties of many of the SaPIs to carry the genes for superantigen toxins and other virulence factors. For example, SaPIs are the only known reservoir of the gene for toxic shock syndrome toxin (TSST-1), which they disseminate widely among *S. aureus* strains, and therefore are of considerable clinical interest. For the purposes of this disclosure, which in certain embodiments relates to SaPI2, the TSST-1 gene, as well as the SaPI2-carried gene for exfoliatin, the scalded skin syndrome toxin, have been deleted. The disarmed SaPI2 can be engineered to carry the SaPI2 anti-repressor, *dut*, which will facilitate spread of the SaPI among infecting bacteria, and therapeutic genes described below. Diagrams of the SaPI2 genome and its derivatives are presented in Figure 4 and Table 3. Other aspects of the disclosure include using and/or modifying any one or combination of the following genetic elements to, for example, modify a SaPI2 genome to replace toxin genes. The sequences of each of these genes is well known in the art and can be readily accessed by the skilled artisan.

Dut encodes the phage dUTPase, a dual function protein that, in addition to its classical enzymatic activity, doubles as the anti-repressor protein for SaPI2, and several other SaPIs. In this system *dut* is driven by *PuvrB*, an SOS-inducible promoter. *Dut* will be expressed following spontaneous SOS induction, resulting in autonomous replication of the

island. Virtually all staphylococci are lysogenic, many carrying several prophages. Although the prophage state is stable and long-lasting, individual cells undergo spontaneous prophage induction in vitro at frequencies of 10^{-3} - 10^{-5} /per cell generation and these frequencies are probably greater in vivo. Any prophage undergoing spontaneous induction will package a de-
 5 repressed SaPI, such as SaPI2, whether or not it is a SaPI2 helper, as well as its own genome, and will release SaPI2 as well as infective phage particles following lysis of that cell. (The infective phage particles will be non-functional since the neighboring cells will be immune as lysogens). This will enable SaPI2 to spread to any other staphylococci that were not initially infected by SaPI2, and repeat the process.

10 Among the therapeutic genes that can be inserted into the SaPI2 genome in place of the toxin genes are the AIP-producing *agrB* & *D* genes and the anti-*spa* segment of RNAIII.

AgrB & *D* combine to produce the thiolactone-containing autoinducing peptide molecule that is the activating ligand for the *agr* signal transduction - quorum-sensing system. The *agr* locus is conserved throughout the staphylococci and the AIPs produced by most non-aureus
 15 staphylococci are potent inhibitors of *agr* expression in *S. aureus*. One of these, produced by *S. warneri*, is a universal inhibitor of all four known *S. aureus agr* alleles and will be incorporated in the ABD system. *S. warneri AgrB&D* will be driven by an autoinducing circuit involving the *B. subtilis comAP* locus (see Figure 10) and in this invention will generate and secrete the inhibitory *S. warneri* AIP, which will diffuse and block the
 20 expression of the *agr* locus belonging to any infecting *S. aureus*, including not only that being targeted by the ABD, but any other *S. aureus* bacteria in the animal.

Anti-*spa* segment of RNAIII. RNAIII is a regulatory RNA molecule that is the effector molecule of the staphylococcal *agr* quorum sensing system, which regulates staphylococcal virulence. RNAIII carries out most of the regulatory function of the *agr*
 25 system. It contains several stem-loops that are designed to pair with the translation-initiation signals of the virulence genes that it regulates, thus blocking their translation. During the exponential phase of growth, it down-regulates many of genes that are required for the establishment of an infection, including the adhesins and anti-immunity genes, especially *spa* (staphylococcal protein A), specifically down-regulated by the 3' stem-loop of RNAIII.
 30 Protein A protects the organism from opsonization and therefore has a major role in the initiation of infection.

Anti-sense RNA against *agrA*. Since *agrA* has its own promoter which is activated in vivo, and since AgrA directly activates certain virulence genes, blocking overall *agr* expression by an inhibitory AIP will not be sufficient to fully attenuate virulence.

Accordingly, an anti-sense RNA directed against *agrA* translational start can be included.

Anti-sense RNA against *secY*. *SecY* is an essential gene for which antisense RNA against its translational start has been shown to effectively inhibit cell growth.

RsbW. RsbW blocks the function of the alternative RNA-polymerase sigma subunit, sigB, which is involved in many stress-induced gene functions in staphylococci, especially including biofilm formation. As biofilm formation is an important aspect of staphylococcal infections, especially those involving surgical implants, blockage of biofilm formation is an important aspect of anti-staphylococcal therapy.

IcaR. IcaR is the repressor of the staphylococcal *ica* locus, which contains several genes involved in the synthesis of the intracellular adhesin that is required for biofilm formation. Blockage of this locus by the ABD-carried repressor will prevent biofilm formation.

PezT and GhoT. PezT and GhoT are the toxin components of bacterial toxin-antitoxin (TA) systems, which act by blocking cell wall synthesis and by disrupting the bacterial cellular membrane potential, respectively. Either will kill or strongly inhibit any infecting staphylococcus. Production of ABDs containing these toxins can be achieved by equipping the ABD-producing strain with the respective antitoxins. Those skilled in the art will recognize that the foregoing represent non-limiting examples, but the possible alternatives are limited only by the size of the DNA to be packaged by the SaPI system.

CRISPR/Cas9. A highly versatile gene editing system known as the CRISPR/Cas9 system has recently been developed and is now in worldwide use, largely for modifying human, plant, or animal genes. CRISPR stands for clustered regularly interspaced short palindromic repeats and Cas9 stands for CRISPR-associated protein 9, a key component of the type II CRISPR system. The system was originally discovered as an adaptive immune system for bacteria and archaea. Its function is well known. Briefly, when foreign DNA, *e. g.*, DNA of a bacterial virus enters the bacterial cell, a short segment of that DNA is incorporated into the CRISPR array as a new spacer. This process is diagrammed in Figure 6. Although most of the phage-infected cells are killed in a natural setting, a few survive, containing the phage DNA segment in their spacer array. If that cell or any of its descendants is then infected by the same or a closely related bacteriophage, the spacer in the cell's CRISPR array specific for that phage plus the adjacent upstream repeat is transcribed into a small RNA molecule which is paired with another small RNA and the complex then binds to both the Cas9 protein and also to the corresponding segment of the phage DNA. This brings the Cas9 protein into direct contact with the targeted phage DNA where it introduces a double-stranded cut into the phage genome, effectively destroying the phage DNA.

Once this mechanism was determined, it became evident that any DNA segment could be introduced by recombinant DNA methods as a spacer in the CRISPR array, enabling the CRISPR to target and cut any arbitrarily chosen DNA. In addition to introducing SaPI2-linked genes that impact the spread of SaPI2 and the virulence or survival of the organism, we have engineered CRISPR/Cas9 functionality into SaPI2. In most bacteria or any bacterial DNA element, a double-stranded cut is lethal. Thus, in some of the embodiments of this disclosure, a DNA segment corresponding to a bacterial gene is incorporated into a CRISPR array. This array is then cloned by recombinant DNA methods into SaPI2 or a similar mobile element. Any bacterial cell infected by a SaPI containing a CRISPR/Cas9 segment with a spacer corresponding to any chromosomal gene will suffer a lethal DSB in the targeted gene. This DSB will activate the SOS response, inducing any resident prophages. The *dut* gene carried by the SaPI may also be induced so that the SaPI DNA will replicate, will be encapsidated by an induced prophage, and thus enabled to spread to any other infecting cells.

In certain non-limiting approaches, SaPI2 representative sequences depicted in Figure 18 (SEQ ID NO:2) and Figure 19 (SEQ ID NO:3) provide non-limiting illustrations of sequences that show incorporation of CRISPR/Cas9 segment into an ABD of this disclosure. Interpretation of the sequences is aided by the schematic genetic element maps of SaPI2 with deletions as indicated by comparison of Figures 18 and 19 (sequences show certain annotated and precise locations which are enlarged and italicized). Color coding of sequences is as described in the figure descriptions and in the figures. The deletion from nucleotides 8136-9210 removes the 3 genes, *ptiB*, *cpmA* and *cpmB*; that from 10982-14209 removes the virulence genes, *tst* and *eta*. The second deletion is the site into which the *tetM* gene and the CRISPR/cas9 module were inserted, resulting in ABD2002, as in the diagram of Figure 18. The CRISPR/cas9 segment contains the CRISPR array, the *cas9* gene and the *tracr* RNA gene. The *tracr* RNA pairs with the spacer RNA (crRNA) to form the guide RNA complex, which binds to the Cas9 protein and directs it to the spacer-determined target site.

An alternative strategy to CRISPR/Cas9 killing involves a modified CRISPR/Cas9 system in which the nuclease activity of Cas9 has been eliminated by mutation. This Cas9 derivative, known as dCas9, retains its full ability to bind tightly to any DNA to which it is targeted by a spacer-coded RNA. This tightly bound dCas9 can block expression of the targeted gene, whether it is bound to the coding sequence or to the 5' regulatory region of the gene. In these embodiments, the cell is not killed but can be strongly attenuated for virulence by dCas9 binding to virulence genes or their regulators. In some of the embodiments, the dCas9 is targeted to several different genes simultaneously by having corresponding spacer

constructs in its CRISPR array. In one embodiment, these several genes are involved in virulence; in another, they are involved in biofilm formation. A variety of combinations is included by the disclosure: two different CRISPR arrays on separate SaPI derivatives can simply be mixed for administration, or they can both be present on a single SaPI, or they can all be present in a single CRISPR array.

Among the therapeutic genes that have been inserted into the SaPI2 genome as spacers in the CRISPR array are the following:

AgrA. The *agr* system is a widespread global genetic regulatory system in Gram-positive bacteria, first discovered in *S. aureus* and extensively characterized in that species – see Figure 9 for a genetic diagram. The *agr* locus contains a 2-component signal transduction circuit, of which AgrC is the receptor and AgrA the response regulator, which is activated by a small peptide (AIP) processed from AgrD by AgrB. AgrA binds to and activates its own promoter, P₂, setting up a positive feedback loop, and also to the adjacent and divergent promoter, P₃, whose transcript, RNAIII, is a regulatory RNA that is the primary effector molecule of the regulatory system. AgrA is absolutely conserved within the staphylococci so that its use as a spacer enables the CRISPR/Cas9-mediated killing of any staphylococcal strain or species.

lsp. The gene for lysostaphin, a powerful lytic enzyme that destroys staphylococcal cells by degrading the cell wall. This is envisioned especially for bovine mastitis, which is largely intractable because it responds poorly to antibiotics.

fib. The gene for staphylococcal fibrinogen binding protein, a highly conserved but non-essential gene whose incorporation as a spacer in the ABD CRISPR/cas9 array will enable killing of virtually all *S. aureus*. The incorporation of 2 separate spacers in the array will largely eliminate the problem of CRISPR resistance.

P₂-P₃. The intergenic region between *agrB* and RNAIII (see Figure 9), containing the *agr* promoters P₂ and P₃, is used as a binding target for dCas9, which thus blocks expression of the entire *agr* regulon, including many virulence genes. This attenuates staphylococcal virulence by about 100-fold.

P_{spa} is the protein A promoter. Targeting of P_{spa} by dCas9 blocks transcription of *spa*.

P_{fnbA} is the fibronectin binding protein A (FnbA) promoter. Targeting of P_{fnbA} by dCas9 blocks transcription of *fnbA*. FnbA is a major staphylococcal adhesin having a key role in the localization and stabilization of the organism during the establishment of an infection, and serves as the primary adhesin for biofilm formation.

Pica is the promoter for the intercellular adhesin (*ica*) gene. Ica is the intercellular polysaccharide adhesin, also known as “slime”, which is required for biofilm formation. The formation of a robust biofilm requires FnbA to enable adhesion to the substrate plus Ica to enable the massive buildup of structured cellular layers and protect the cells from host immunity and many antibiotics.

Psrt is the sortase promoter. Targeting of *Psrt* by dCas9 blocks transcription of *srt*. Since sortase is the major enzyme that anchors outer surface bacterial proteins to the peptidoglycan of the bacterial cell wall, bacteria lacking sortase are deprived of their outer surface proteins, which causes them to be seriously compromised in their ability to initiate and sustain an infection and to resist innate immunity.

The above genes are exemplary – many other genes could be used and are encompassed by this disclosure. A few non-limiting examples of genes that would act against other Gram-positive bacteria are listed below.

DnaA is the universal initiator for bacterial chromosome replication and is a target for a DSB-inducing spacer.

Pilo is the promoter of the gene for listeriolysin O, a lytic enzyme that enables *L. monocytogenes* to spread between cells. Blocking this promoter will prevent *llo* expression, which will abrogate a *L. monocytogenes* infection.

PcovA is the promoter for *covA*, a global regulator of *S. pyogenes* virulence. Blocking this promoter will prevent *covA* expression, which will sharply attenuate an infection.

PgelE is the promoter for *gelE*, which encodes a gelatinase enzyme that is necessary for enterococcal virulence.

Pwzg is the promoter for the pneumococcal capsule regulatory gene, *wzg*, and has a motif absolutely conserved among the pathogenic pneumococci. Blockage of the expression of this gene prevents capsule formation and renders the organism totally avirulent.

Helper phage modification. In order to enhance the production of infectious SaPI2 particles, we have modified the helper phage 80α as follows: i) deletion of the terminase small subunit (*terS*) gene, which will eliminate its ability to package its own (phage) DNA so that only SaPI-containing particles are produced, generally at a frequency of $>10^9$ /ml of culture; ii) an alternative strategy involves a major deletion of helper prophage genes so that the prophage element contains only the SaPI de-repressor gene, *dut*, the entire set of virion genes and the lysins. To maximize SaPI particle production, the *dut* and virion modules are driven by the strong but inducible Ptet promoter, and the lysin genes driven by the inducible

Pbla promoter – which will enable lysis to be delayed until the cell is filled with SaPI particles. With this alternative, no phage DNA is produced at all. Modifications to enable adsorption and gene expression in diverse bacterial hosts will permit the SaPI strategy to be applicable to diverse bacterial pathogens.

5 **Spread of the SaPI2 particles.** With respect to the staphylococci, all known clinical isolates are lysogenic and most carry 2 or more prophages. All known functional prophages undergo spontaneous induction owing to stochastic triggering of the SOS (DNA damage) response. This occurs in ~1 in 1,000 or 10,000 cells so that any culture contains considerable numbers of free phage particles. In addition, a CRISPR-induced DSB is will induce the SOS
10 response to DNA damage, which will increase the induction of resident prophages. A SaPI infecting a strain that is lysogenic for a helper phage will then be spread to neighboring cells as a consequence of spontaneous or induced prophage induction with the concomitant production of SaPI particles. Since the primary role of a helper phage is to relieve repression of the SaPI, it follows that if a SaPI is spontaneously de-repressed, it can be packaged and
15 transferred by any co-resident phage, whether or not it is a helper. This will apply to any incoming SaPI2 of this invention since it will carry the antirepressor gene, *dut*.

It will be recognized from the foregoing, but without intending to be bound by any particular theory, that it is considered that the present SaPI-based approach has the following advantages over phage-based approaches: i) phages have a very limited capacity for genome
20 expansion (about 3 kb for coliphage λ), whereas the present modified SaPI2 genome can be expanded by ~30 kb – which is sufficient room for a wide variety of additions; ii) SaPIs intrinsically have a much greater host range than phages, which would be of concern for many types of phage therapy; iii) with SaPIs, there are a wide variety of options for interfering with a bacterial infection; with phages, options are limited to direct killing of the
25 bacteria, which is highly selective for resistance. iv) A version of the ABD, ABD2002, can be adapted to provide an autoinduction circuit that produces an inhibitory AIP that will block the virulence of any *S. aureus* bacteria present in an infected animal.

Table 3. Representative ABDs

SaPIs and ABDs	Size, Kb	Deletions	Insertions	Function
Demonstrated				
SaPI2 (WT)	15.7			
ABD2001	12.5	<i>cpmA&B tst eta</i>	<i>tetM</i>	ABD backbone
ABD2002	17.6	<i>cpmA&B tst eta</i>	<i>tetM CRISPR/cas9/non-targeting</i>	Generic CRISPR/cas9
ABD2003	17.6	<i>cpmA&B tst eta</i>	<i>tetM CRISPR/cas9/agrA</i>	Causes lethal double-strand

				break (DSB) in <i>agrA</i>
ABD2004	17.6	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/cas9/hly</i>	Causes lethal DSB in <i>hly</i> (listeriolysin O)
ABD2005	17.6	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/dcas9/ non-targeting</i>	Generic CRISPR/dcas9
ABD2006	17.6	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/dcas9/agrP₂P₃</i>	Blocks virulence by inhibiting expression of <i>agr</i> locus
ABD2007	17.7	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/cas9/fib</i>	Causes lethal double-strand break (DSB) in <i>fib</i>
ABD2008	17.8	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/cas9/agrA/fib</i>	Causes lethal double-strand break (DSB) in <i>agrA</i> and <i>fib</i>
ABD2009	14.0	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM lsp</i>	Secretes lysostaphin, lyses ABD-infected and surrounding uninfected
Included				
ABD2010	19.0	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM CRISPR/cas9/agr; lsp</i>	Causes lethal double-strand break (DSB) in <i>agrA</i> ; lyses all cells
ABD2011	14.5	<i>cpmA</i> & <i>B tst eta</i>	<i>dut* tetM</i>	replicates autonomously
ABD2012	18.3	<i>cpmA</i> & <i>B tst eta</i>	<i>dut tetM, hybrid agr-com, anti-spa RNAIII, anti-agrA, anti-secY</i>	replicates autonomously; blocks <i>agr</i> , <i>spa</i> , PSMs, <i>secY</i> expression
ABD2013	14.9	<i>cpmA</i> & <i>B tst eta</i>	<i>dut tetM rsbW icaR</i>	replicates autonomously; blocks biofilm formation
ABD2014	16.2	<i>cpmA</i> & <i>B tst eta</i>	<i>tetM pezT ghoT</i>	Kills ABD-infected staphylococci

*Constructs made both with and without *dut* are included in the disclosure.

The following Example 1 is intended to illustrate, but not limit the invention.

5

Example 1

Material and methods for construction of the ABDs

Standard bacteriologic methods are adapted for use in this disclosure. Bacteria are
 10 cultured on trypticase-soy (TSB) agar with erythromycin, tetracycline or chloramphenicol,
 each at 5 µg/ml, as needed, or in TSB broth. Phages and SaPIs are enumerated by dilution
 and plating for plaque or colony formation, respectively, with suitable indicator strains, as
 discussed above. Phage or SaPI lysates are prepared by mitomycin C (2µg/ml) induction in
 CY broth with slow shaking at 32°C. Lysates are centrifuged at 10,000 rpm for 10 min,
 15 treated with DNAase and RNAase for 3 h at 37°C, then filter-sterilized with a 0.22
 µ Millipore filter. Lysates are concentrated by precipitation with PEG-8000 (10%) + NaCl
 (0.5M) for 18 h at 4°C, then centrifuged at 9,000 rpm for 15', and resuspended in 1/100

volume of phosphate-buffered saline (PBS). Particles are further purified by centrifugation through a CsCl step gradient followed by dialysis against phage buffer.

For gene cloning and allelic replacement, genes to be cloned are identified from publicly available databases or are independently identified, then isolated by polymerase chain reaction (PCR) and the products gel-purified and redissolved in Tris/EDTA (TE) buffer. They are then cloned to a shuttle vector in *E. coli* and used for further constructions. Modifications of the basic SaPI2 genome have been made using an allelic replacement scheme that makes use of a plasmid known as pMAD (Arnaud, *et al.*, App. Env. Microbiol. 70:6887 (2004), commercially available from Addgene) which is outlined in Figure 11. In the illustration, the relevant region of SaPI2 containing the *tst* and *eta* genes, shown in yellow, are replaced by the tetracycline resistance (TcR) gene, *tetM*, shown in dark blue. To perform such a replacement, PCR is used to prepare a ~1kb segment from each side of the gene region to be replaced, including at the ends of each of the two segments restriction enzyme sites that match those in the multicloning site (MCS) of the pMAD plasmid. These flanking sequences (FR & FL) are then cloned to pMAD followed by cloning between them the gene (*tetM*) that is to replace the SaPI2 *tst* and *eta* genes. pMAD has a thermosensitive replicon so that when introduced into the organism where the replacement is to be made, and required to grow and express its erythromycin resistance (EmR) at the restrictive temperature (42°C), it can survive only by undergoing a recombinational event (crossover) involving either of the flanking sequences. This results in the insertion of the entire plasmid along with *tetM*, FR and FL. The resulting colonies will be not only EmR but also blue on an X-gal plate owing to the expression of the plasmid-carried β -galactosidase gene. The configuration with the integrated plasmid, shown in Figure 11B is genetically unstable owing to the duplicated flanking sequences (FR and FL), and can undergo a second recombinational crossover. This can involve either the green FR segments (red dotted line), or the blue FL segments (solid black line). The former will simply restore the original configuration, whereas the latter will substitute *tetM* for the *tst/eta* region. When the resulting culture is plated on tetracycline-containing medium at the restrictive temperature, only bacteria containing *tetM* in place of the *tst/eta* region will be able to grow and these will be white on X-gal, having lost the entire pMAD plasmid, with its β -galactosidase gene.

This approach has been used for SaPI2 modifications disclosed herein and can be adapted for all modifications that are contemplated by this disclosure. In some cases, a new gene can be inserted at a specific site in SaPI2 but will not replace any resident gene. In such

instances, the 1 kb region on either side of the target site will be cloned to pMAD adjacent to one another, but separated by a restriction site into which will secondarily be cloned the gene to be inserted.

Studies with mice described herein revealed that an IP dose of 10^{11} of the SaPI2 particles containing the CRISPR/dCas9 construct had no visible ill effects, nor did a similar dose of the SaPI2 particles containing the *hla* gene, which encodes α -hemolysin, a toxin with μ g lethality. Mice were observed for 7 days following the SaPI injections. In order to avoid the presence of an antibiotic resistance gene (*tetM*) in the SaPI2 derivatives, we plan to prepare derivatives similar to those shown in Figure 4 in which an arsenate resistance cassette has replaced *tetM*.

We have demonstrated that the constructs illustrated in Figure 4 and Table 3 (ABD2003 and ABD2006) with a CRISPR/Cas9 spacer targeting *agrA* or CRISPR/dCas9 with a spacer targeting *agrP₂P₃*, either kills a staphylococcus or blocks its expression of *agr*, respectively, in vitro (Figures 7 & 8); we have also demonstrated that ABD2009, in which the lysostaphin gene has been cloned to the basic SaPI2 backbone, kills staphylococci by lysis (Figure 12); either ABD2003 or ABD2006 prevents the development of a murine staphylococcal subcutaneous abscess when injected immediately after inoculation of the subcutaneous tissue with a virulent staphylococcus (Figures 13 & 14), or when injected intraperitoneally (Figure 15). Additionally, the CRISPR/cas9/*agrA* construct rescues mice given a lethal IP dose of staphylococci (Figure 16). In these tests, the infecting bacteria are tagged with a luciferase gene that generates a light signal that is imaged with an in vivo imaging system (IVIS) (Perkin-Elmer) camera. Thus, the disclosure provides demonstrations of both prophylaxis and therapy using representative ABDs that were made and used according to the instant description. The skilled artisan will accordingly be able to adapt these demonstrations to make and use any embodiment of the invention that is described herein, given the benefit of the present disclosure.

While the disclosure has been particularly shown and described with reference to specific embodiments, it should be understood by those having skill in the art that various changes in form and detail may be made therein without departing from the spirit and scope of the present disclosure as disclosed herein.

What is claimed is:

1. A polynucleotide comprising a bacterial pathogenicity island nucleotide sequence (B-PINS) comprising one or more modifications (a modified B-PINS),
5 wherein the one or more modifications comprise:
 - i) a deletion or disruption of at least one virulence determinant of the B- PINS; and
 - ii) an insertion of at least one cargo sequence into the B-PINS;wherein the polynucleotide comprising the modified B-PINS is capable of being packaged within a bacterium into a phage-like particle that comprises or consists of
10 bacteriophage capsid, tail and tail fiber proteins, and wherein the phage-like particle (an antibacterial drone “ABD”) is capable of infecting bacteria such that the at least one cargo sequence is introduced into bacteria infected by the ABD.
2. The polynucleotide of claim 1, wherein the one or more modifications of i) comprises
15 a deletion of all or substantially all of the virulence determinants in the B-PINS.
3. The polynucleotide of claim 1, wherein the at least one cargo sequence comprises a polynucleotide sequence encoding an anti-bacterial agent that is functional against a target in at least some bacteria in a bacterial population.
20
4. The polynucleotide of claim 3, wherein the anti-bacterial agent comprises one or a combination of:
 - a) a sequence encoding an RNA or DNA polynucleotide that comprises specificity for the target, wherein the target comprises an essential gene or an RNA encoded by an essential
25 gene or a variable gene or an RNA encoded by a variable gene;
 - b) a sequence encoding a protein that has specificity for the target and can participate in and/or cause its cleavage and/or inactivation; or
 - c) a sequence encoding a toxin that is cytostatic against bacteria, or a non-toxin protein that inhibits growth of bacteria in the bacterial population or inhibits formation of
30 and/or kills persister bacteria and/or dormant viable but non-culturable (VBNC) bacteria.
5. The polynucleotide of claim 4, wherein a) comprises an anti-sense RNA.
6. The polynucleotide of claim 4, wherein b) comprises a Clustered Regularly

Interspaced Short Palindromic repeats (CRISPR) guide RNA targeted to a sequence in the bacteria in the bacterial population.

7. The polynucleotide of claim 4, wherein the encoded protein of b) comprises a
5 CRISPR-associated nuclease including but not limited to a Cas9 nuclease or a Cpf1 nuclease, or a dCas9.

8. The polynucleotide of claim 4, wherein the toxin of c) comprises a toxin that kills
bacteria that have been infected by the ABD.

10 9. The polynucleotide of claim 8, wherein the toxin comprises lysostaphin.

10. The polynucleotide of claim 4, wherein the toxin of c) comprises a toxin that is
secreted by the bacteria and which is bactericidal against the bacteria and bacteria that are
15 uninfected by the ABD.

11. The polynucleotide of claim 4, wherein the target is comprised by a bacterial
chromosome or a bacterial plasmid.

20 12. The polynucleotide of claim 10, wherein the target confers antibiotic resistance.

13. An ABD of any one of claims 1–12, wherein the polynucleotide in the ABD further
comprises a deletion of SaPI genes *cpmA* and/or *B*.

25 14. A pharmaceutical composition comprising an ABD of claim 13.

15. A method comprising administering a pharmaceutical or other composition
comprising ABDs of claim 13 to an individual in need thereof, wherein subsequent to the
administration bacteria in the individual are killed or exhibit reduced virulence.

30 16. The method of claim 15, wherein prior to the administering, the method further
comprises determining a characteristic of bacteria in the individual, and wherein the ABD is
designed to comprise a cargo that has specificity for the characteristic.

17. The method of claim 16, wherein the characteristic comprises a nucleotide sequence in the bacteria.

18. The method of claim 17, wherein the nucleotide sequence comprises a sequence that
5 can be recognized by a CRISPR system.

19. The method of claim 15, wherein the ABD comprises a sequence encoding a toxin that is cytostatic against bacteria, wherein the toxin is optionally lysostaphin.

10 20. A method for producing an ABD of claim 13 comprising growing bacterial cells comprising a polynucleotide comprising a bacterial pathogenicity island nucleotide sequence (B-PINS) comprising one or more modifications (a modified B-PINS),

wherein the one or more modifications comprise:

i) a deletion or disruption of at least one virulence determinant of the B- PINS; and

15 ii) an insertion of at least one cargo sequence into the B-PINS;

wherein the polynucleotide comprising the modified B-PINS is packaged within the bacteria to thereby produce the ABD.

21. The method of claim 20, further comprising separating the ABD from the bacteria.

20 22. A bacterial population comprising bacteria which comprise a polynucleotide of claim 1.

23. The bacterial population of claim 22, wherein the population comprises a single
25 distinct bacterial strain.

24. Cell culture media comprising the bacterial population of claim 22.

25. A bacterial population comprising ABDs of claim 13.

30 26. A method comprising infecting a population of bacteria of with one or more ABDs of claim 13, thereby producing a gene drive effect whereby the cargo sequence carried by the one or more ABDs is disseminated to a plurality of bacteria in the population.

27. A method comprising determining a target sequence in bacteria in a sample, generating or selecting an ABD of claim 13, and contacting the source of the sample with a plurality of the generated or selected ABD.
- 5 28. A B-PINS of any one of claims 1–12, wherein the B-PINS comprises a modified *Staphylococcus aureus* pathogenicity island (SaPI).
29. The B-PINS of claim 28, wherein the SaPI is SaPI1, SaPI2, SaPIbov1, or SaPIbov2.
- 10 30. A library of distinct ABDs of any one of claims 1–12, wherein ABDs in the library comprise distinct nucleic acid sequences encoding distinct cargo.

SaPI life cycle

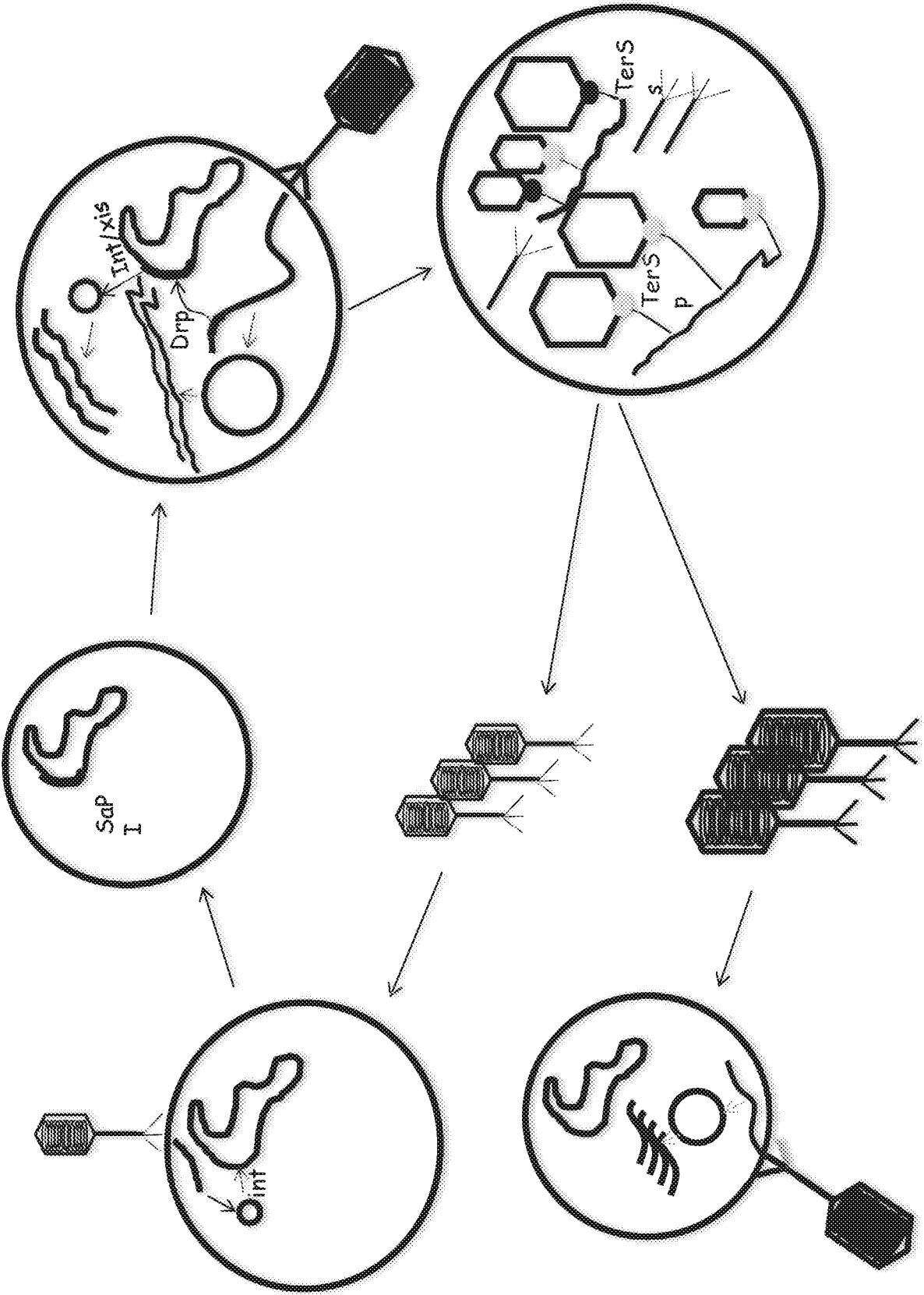


Figure 1

Figure 2

Packaging of phage and SaPI DNA

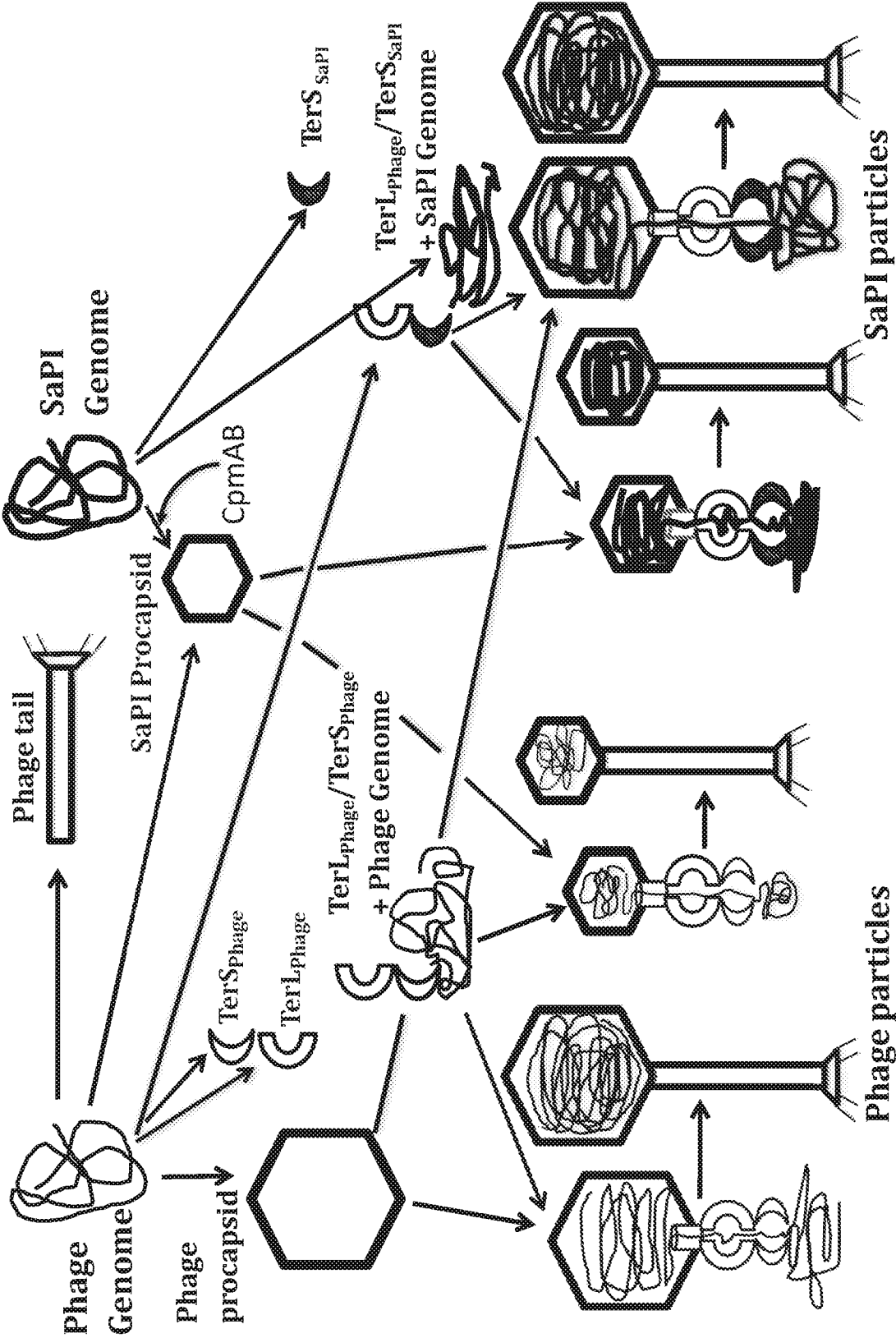


Figure 3

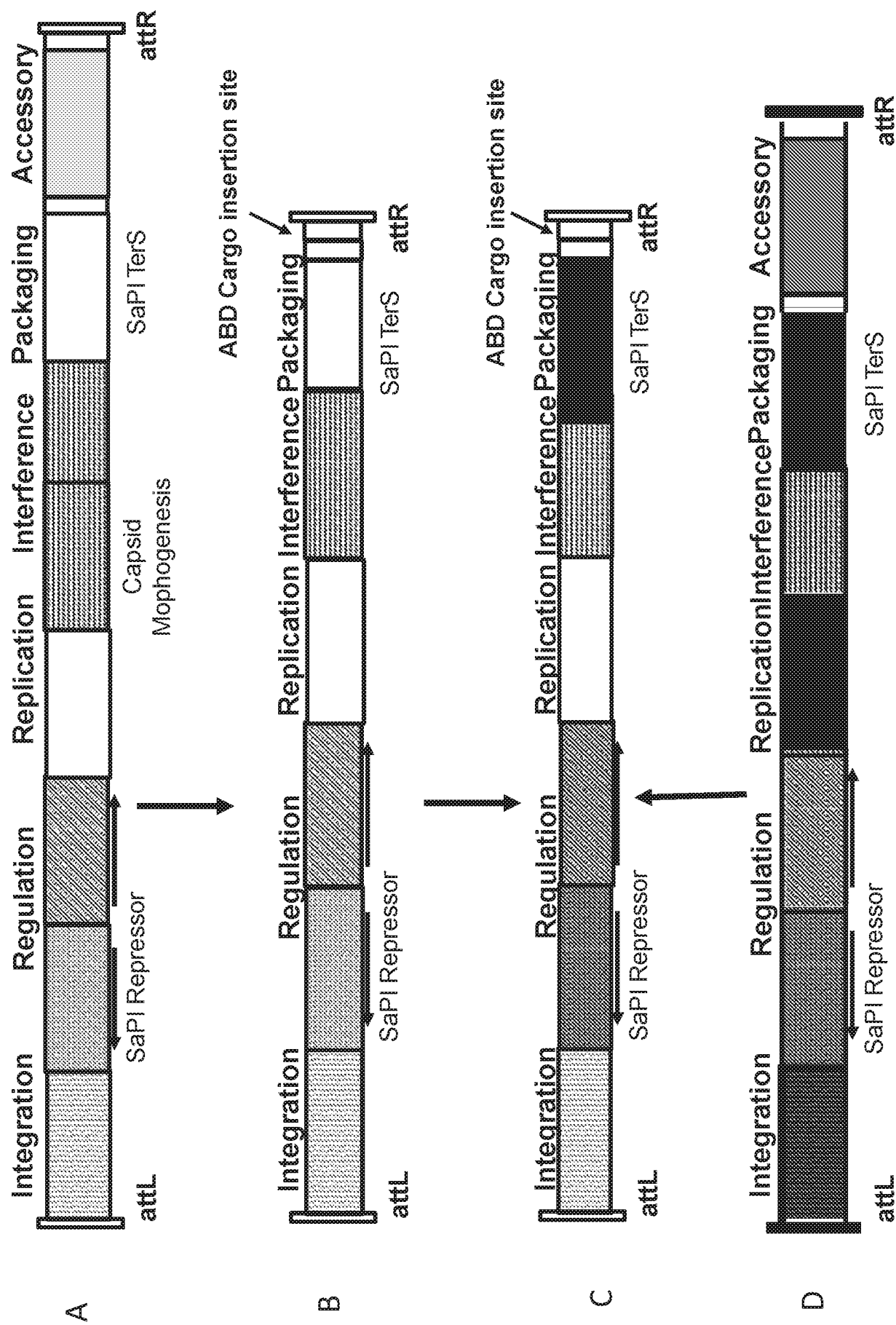


Figure 4

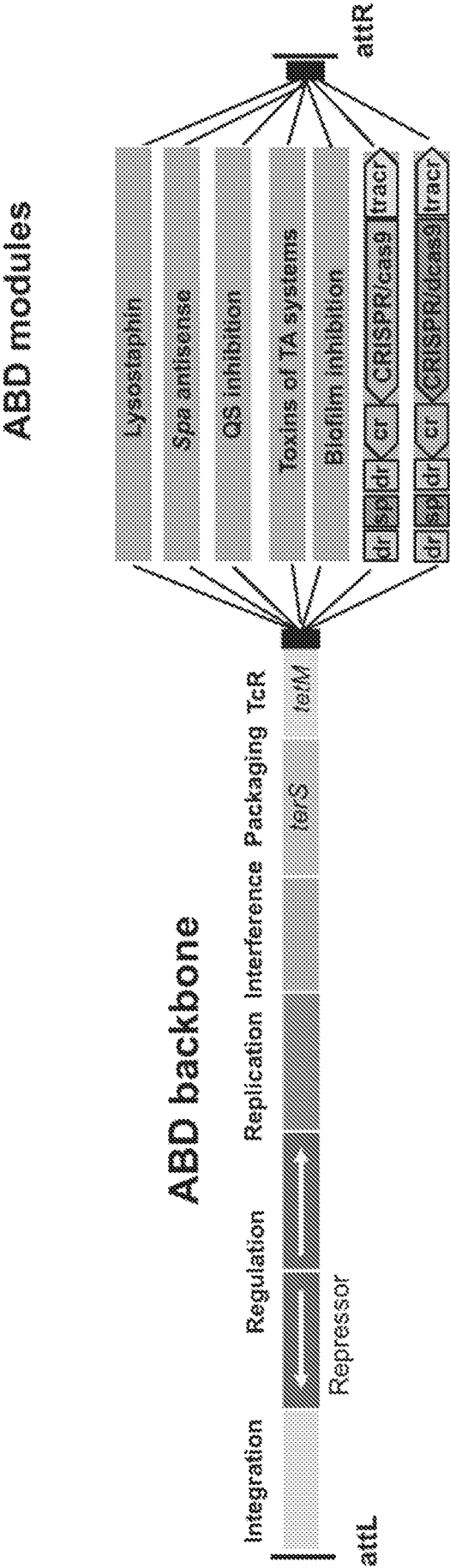


Figure 5

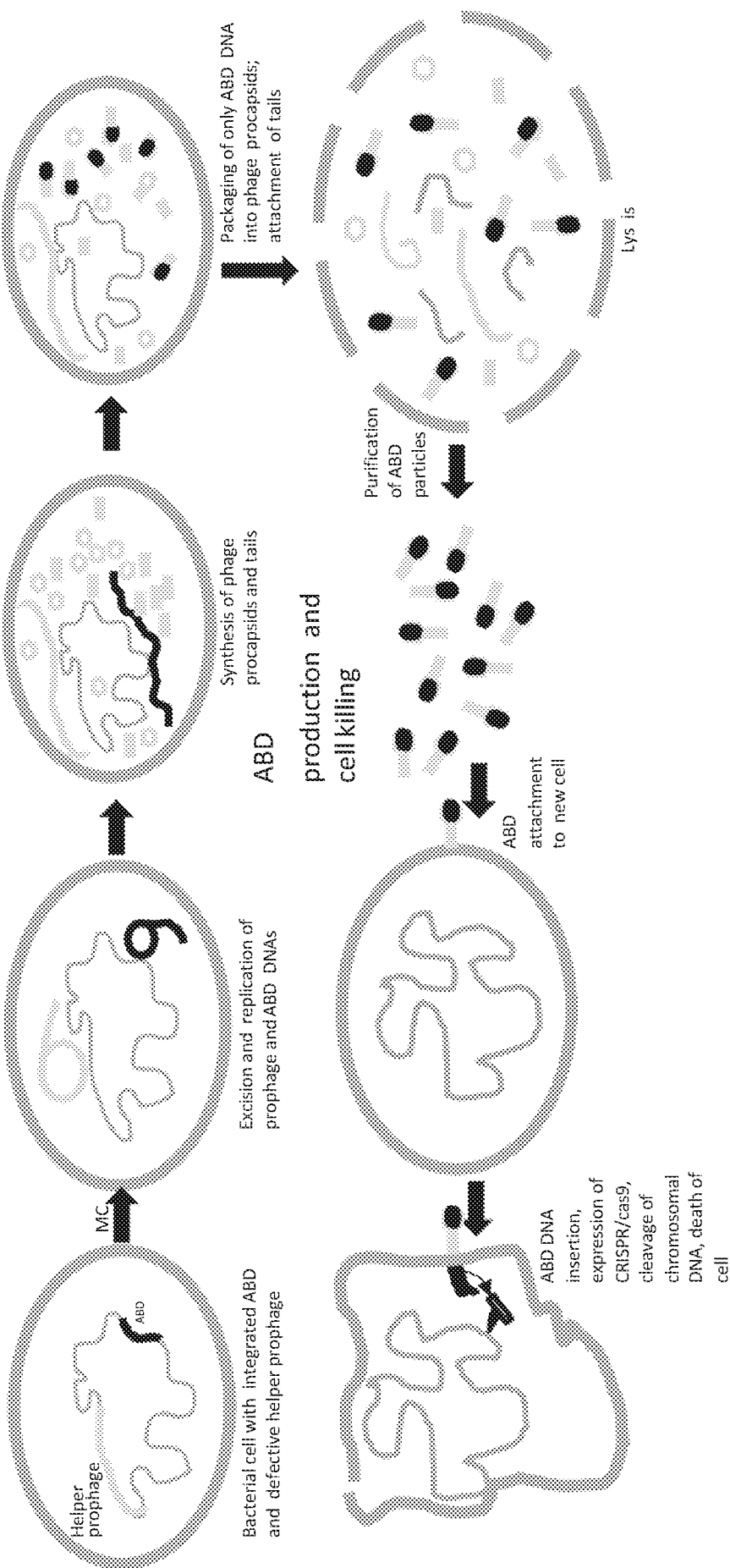
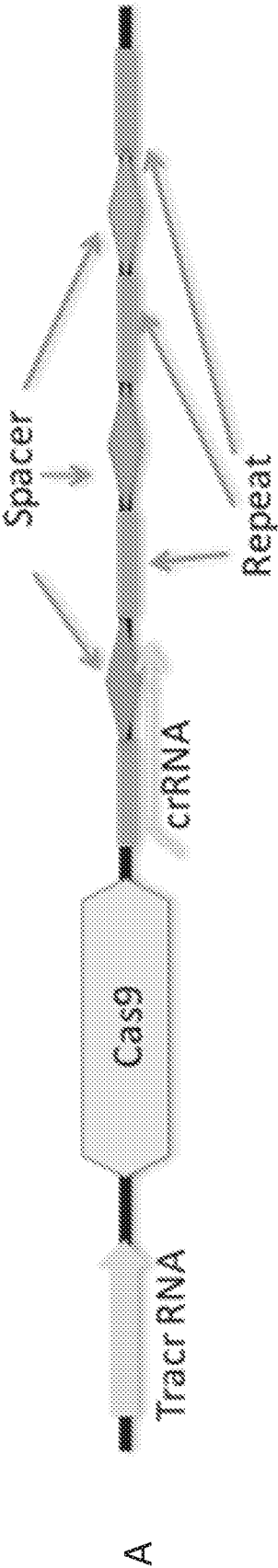


Figure 6



B

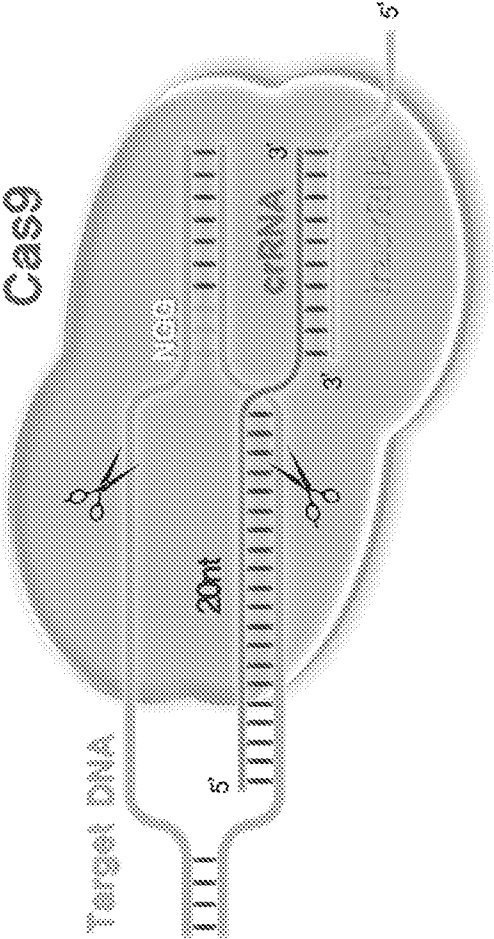


Figure 7

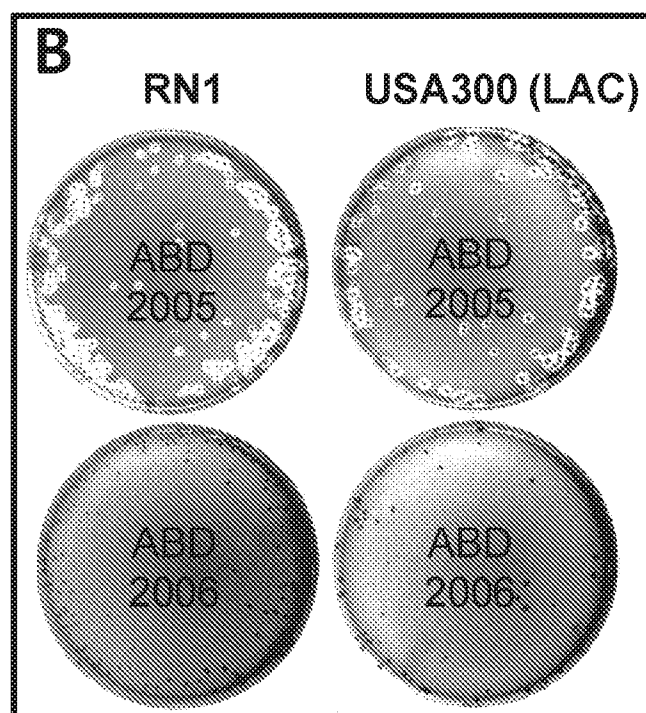
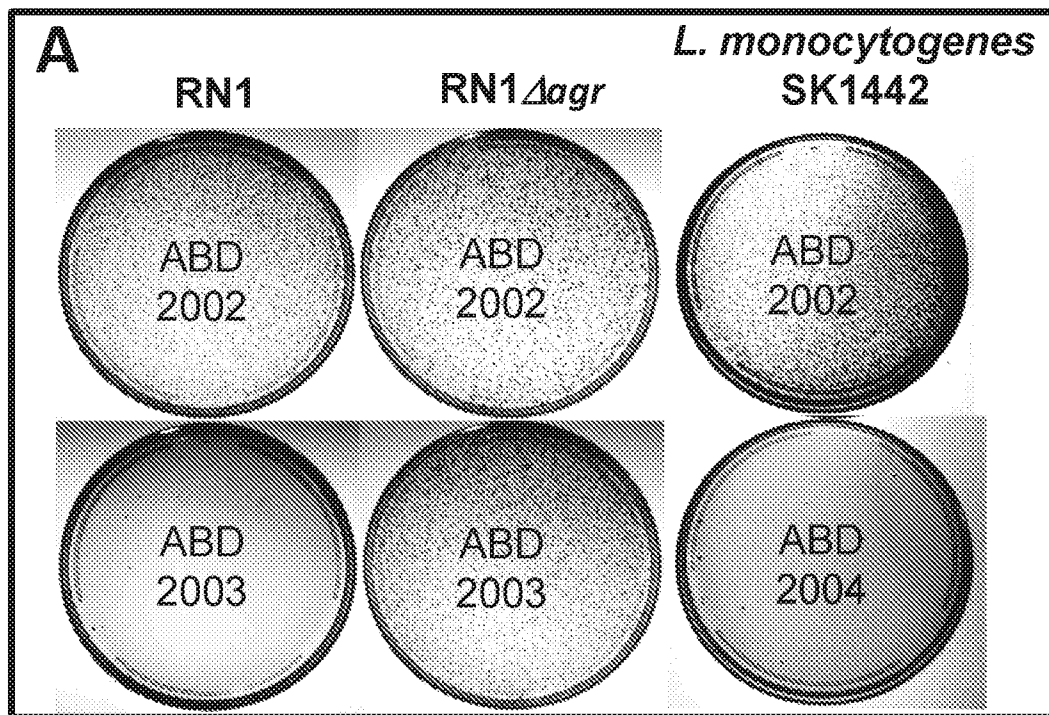


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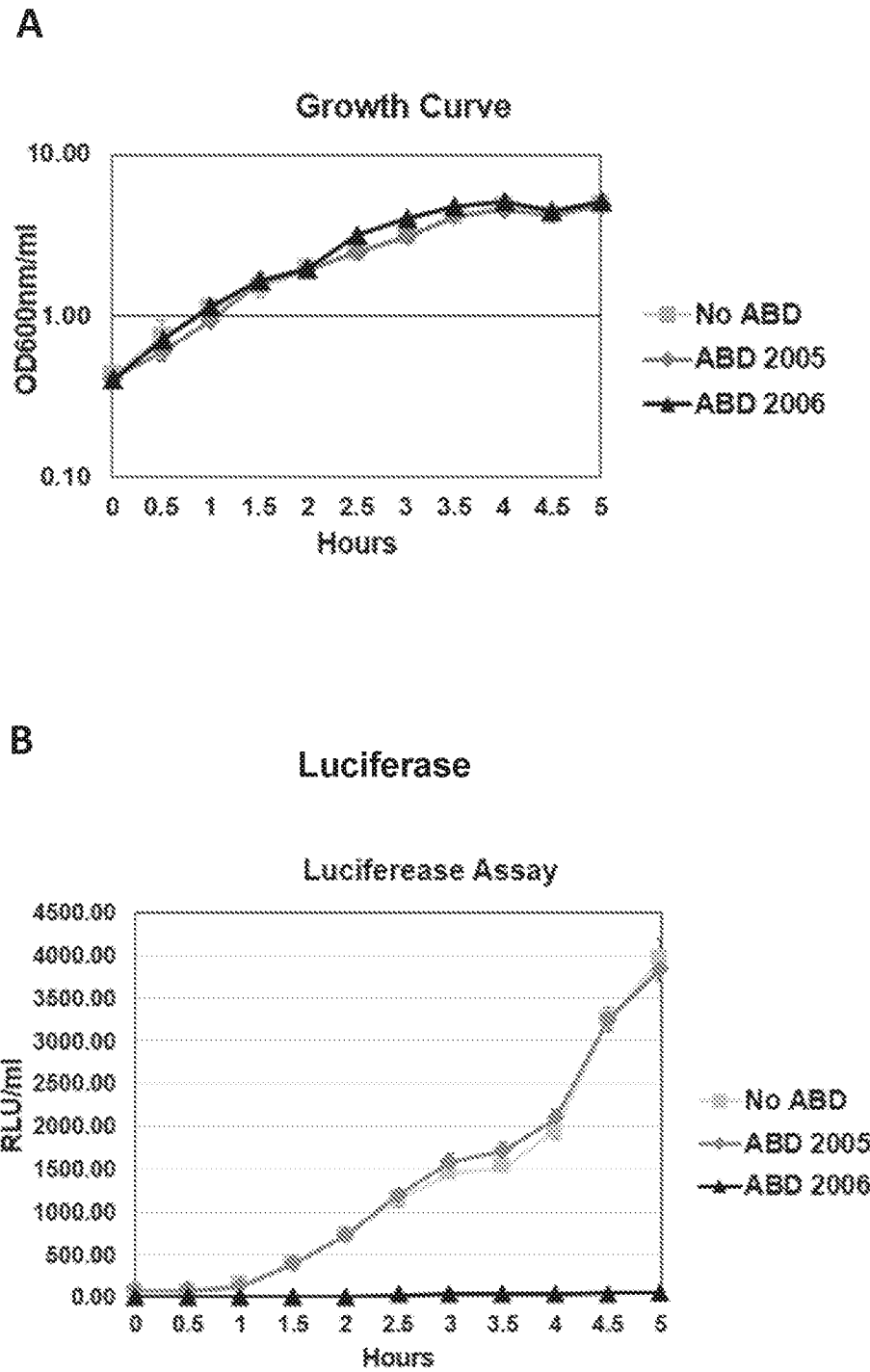


Figure 9

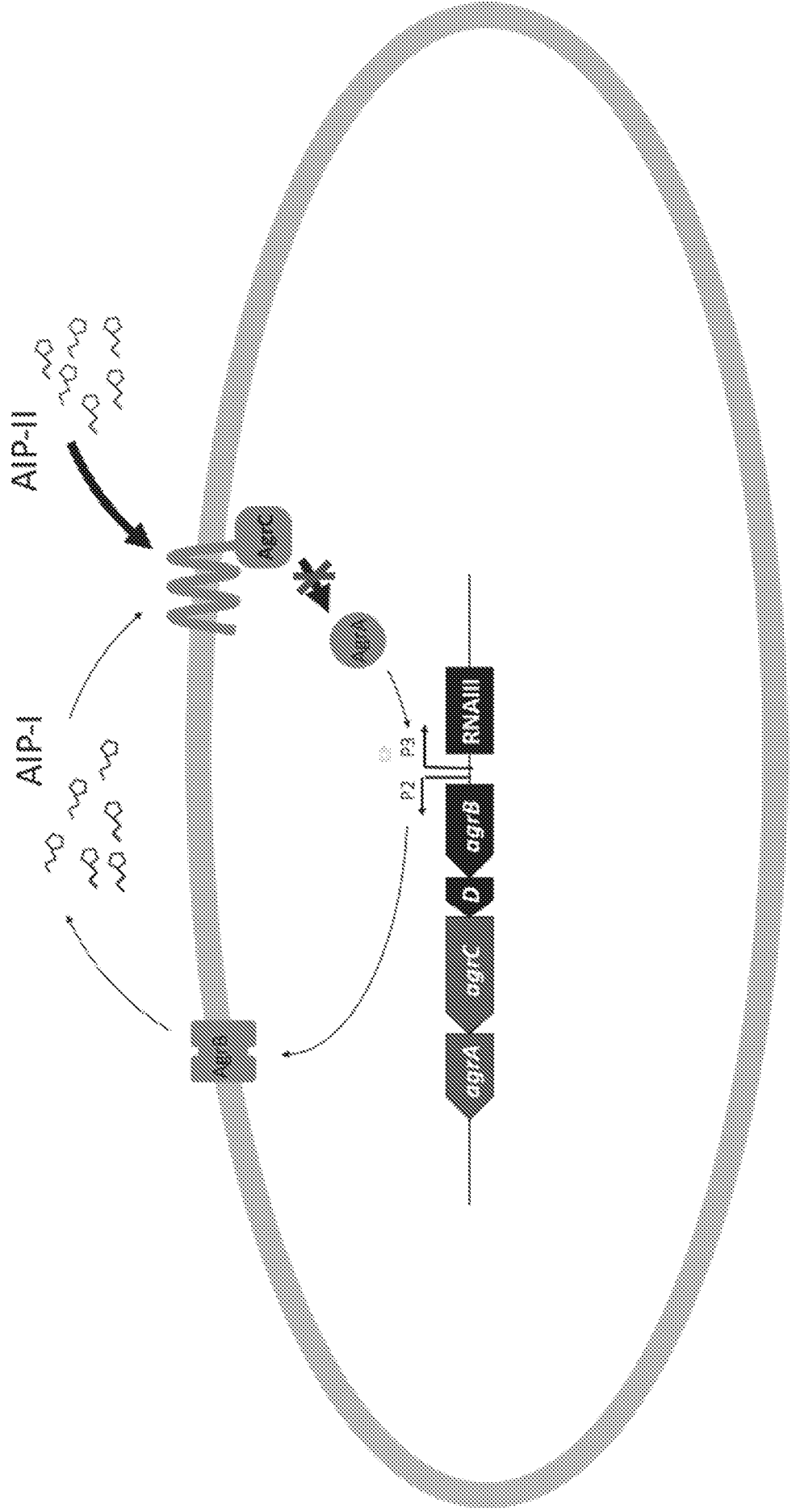


Figure 10

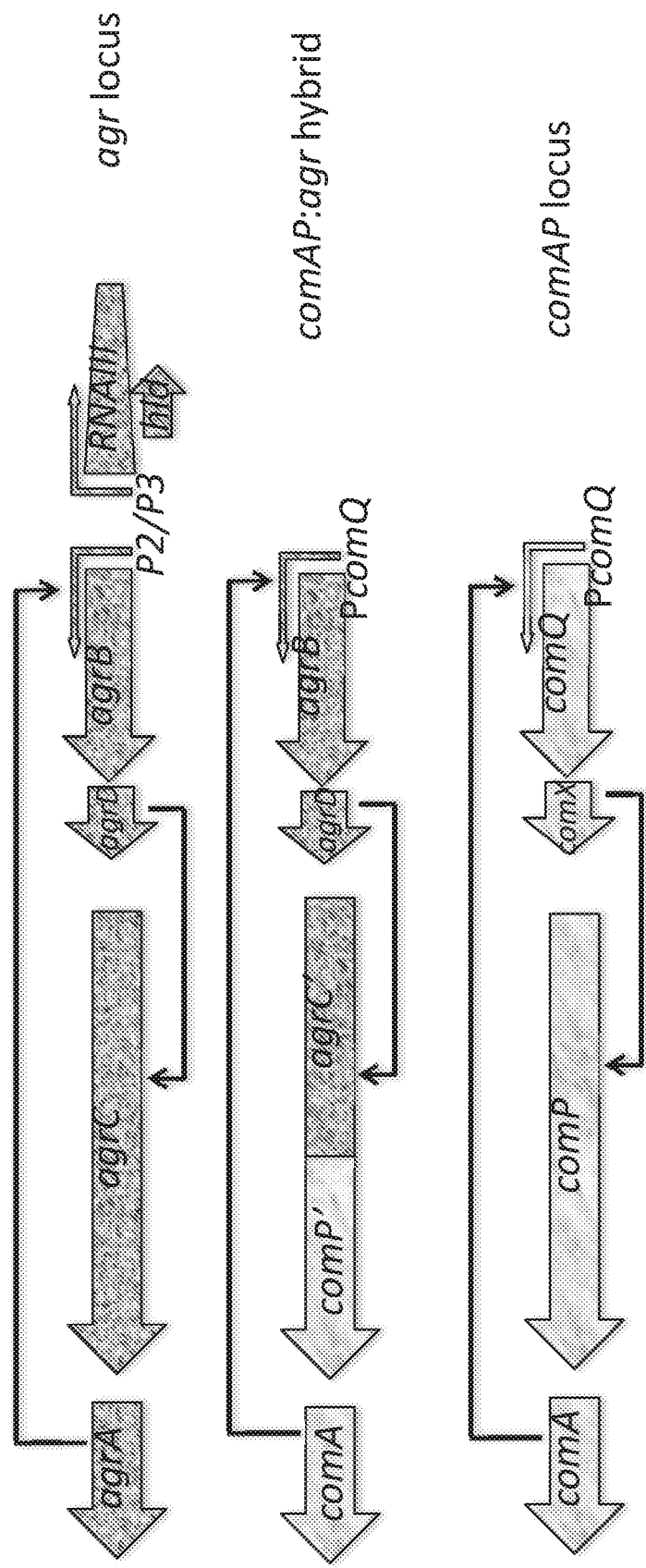


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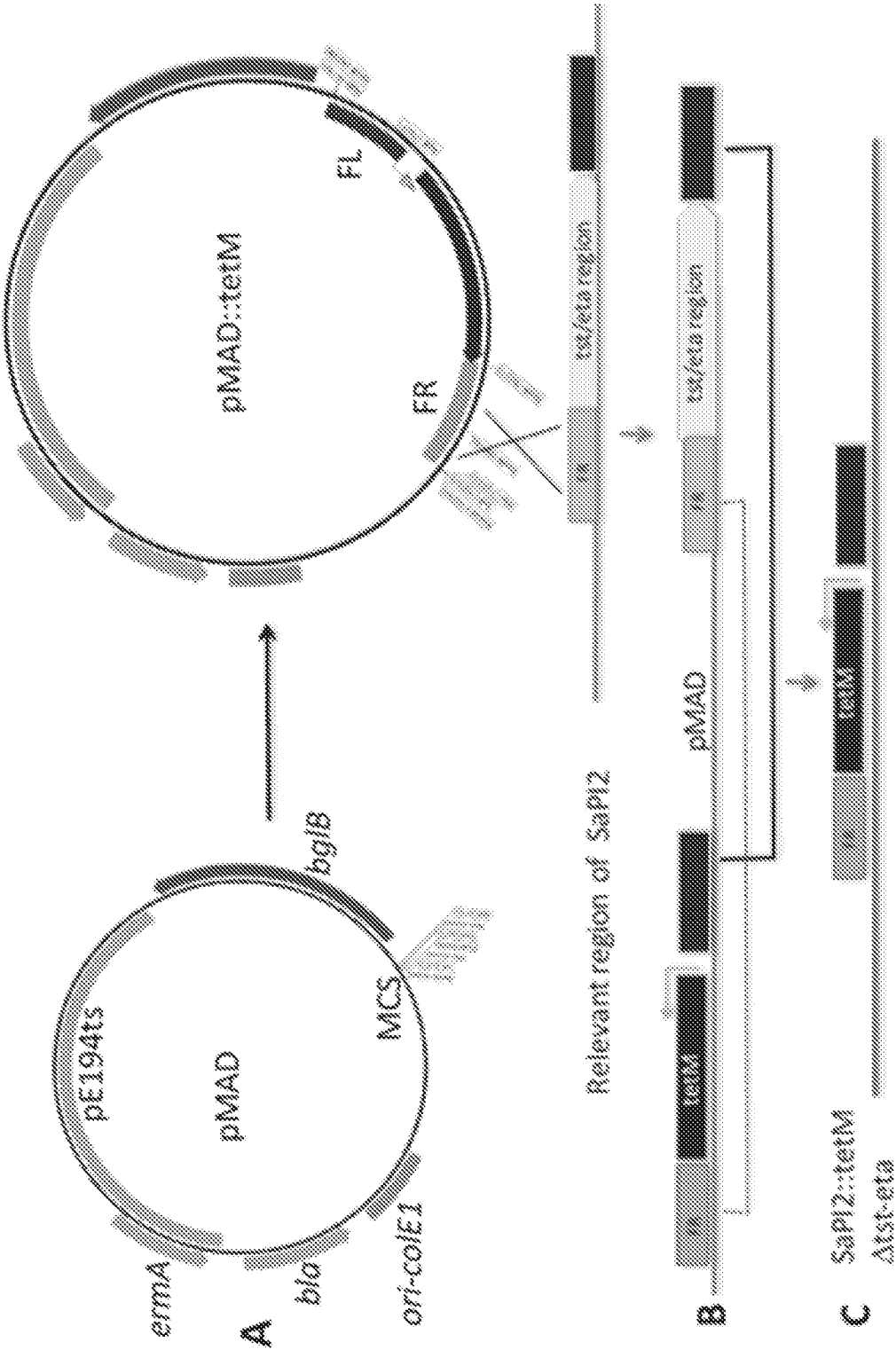


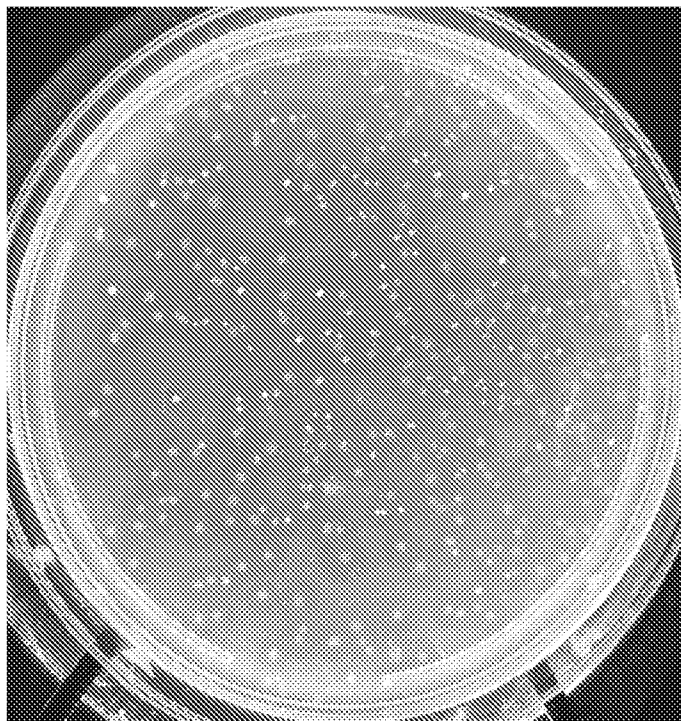
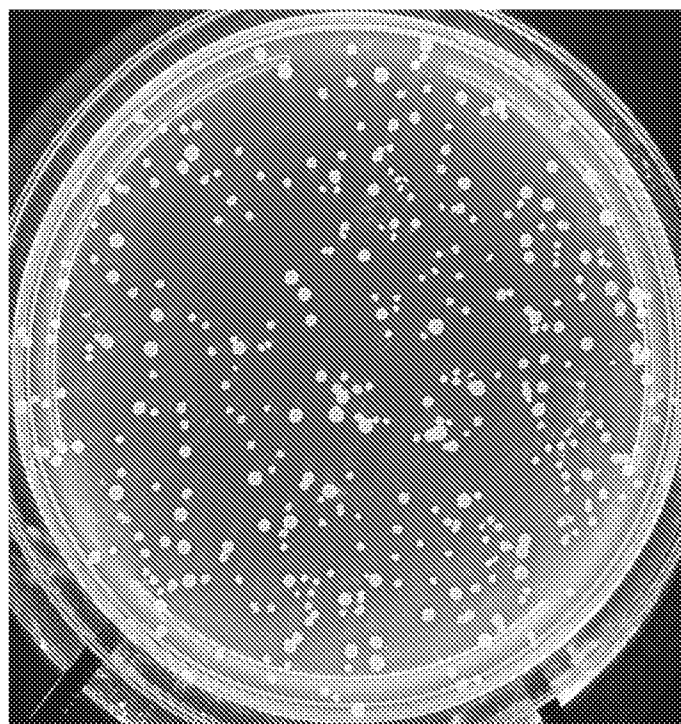
Figure 12**A****B**

Figure 13

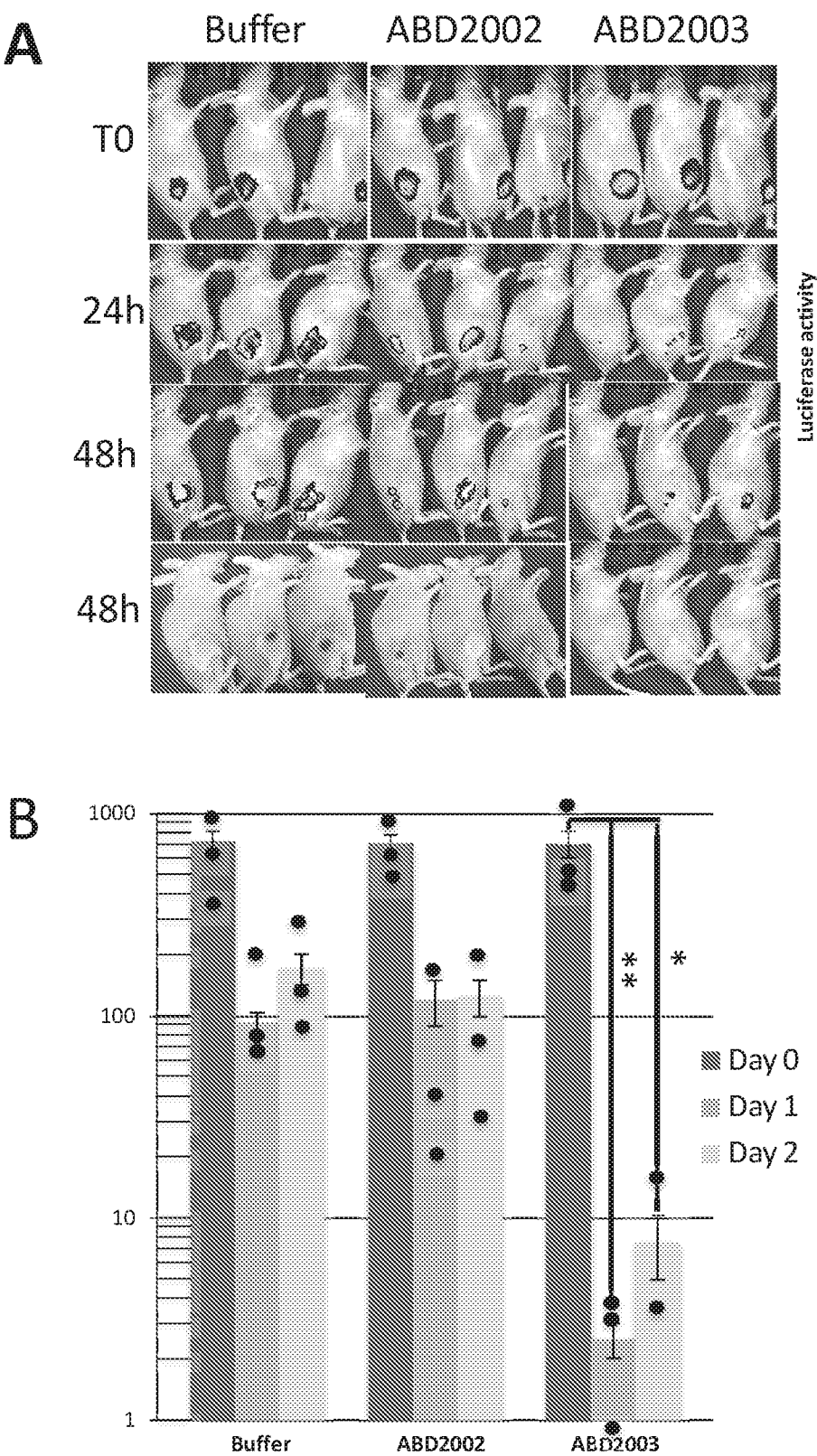


Figure 14

Buffer

ABD2005

ABD2006

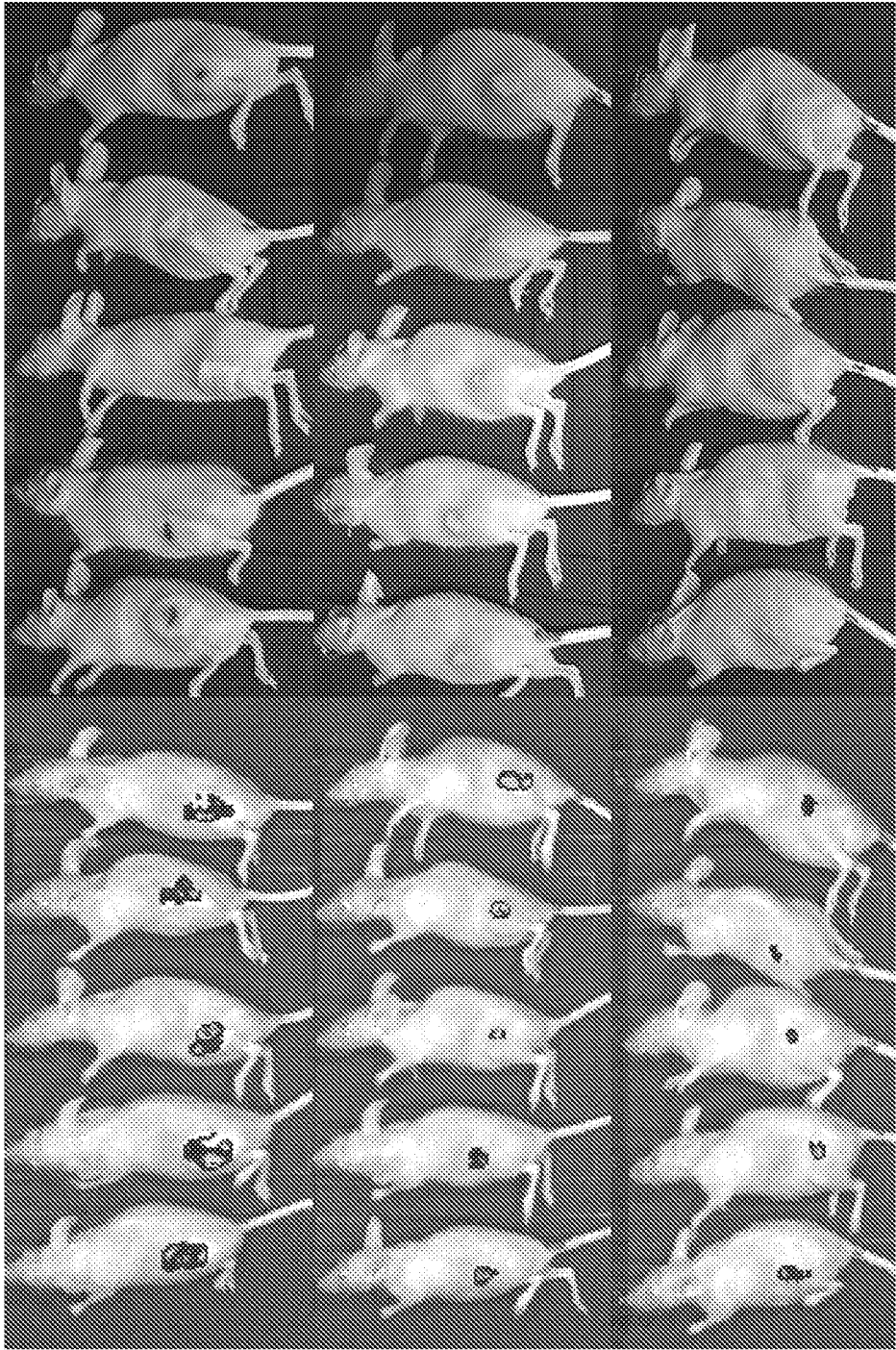


Figure 15

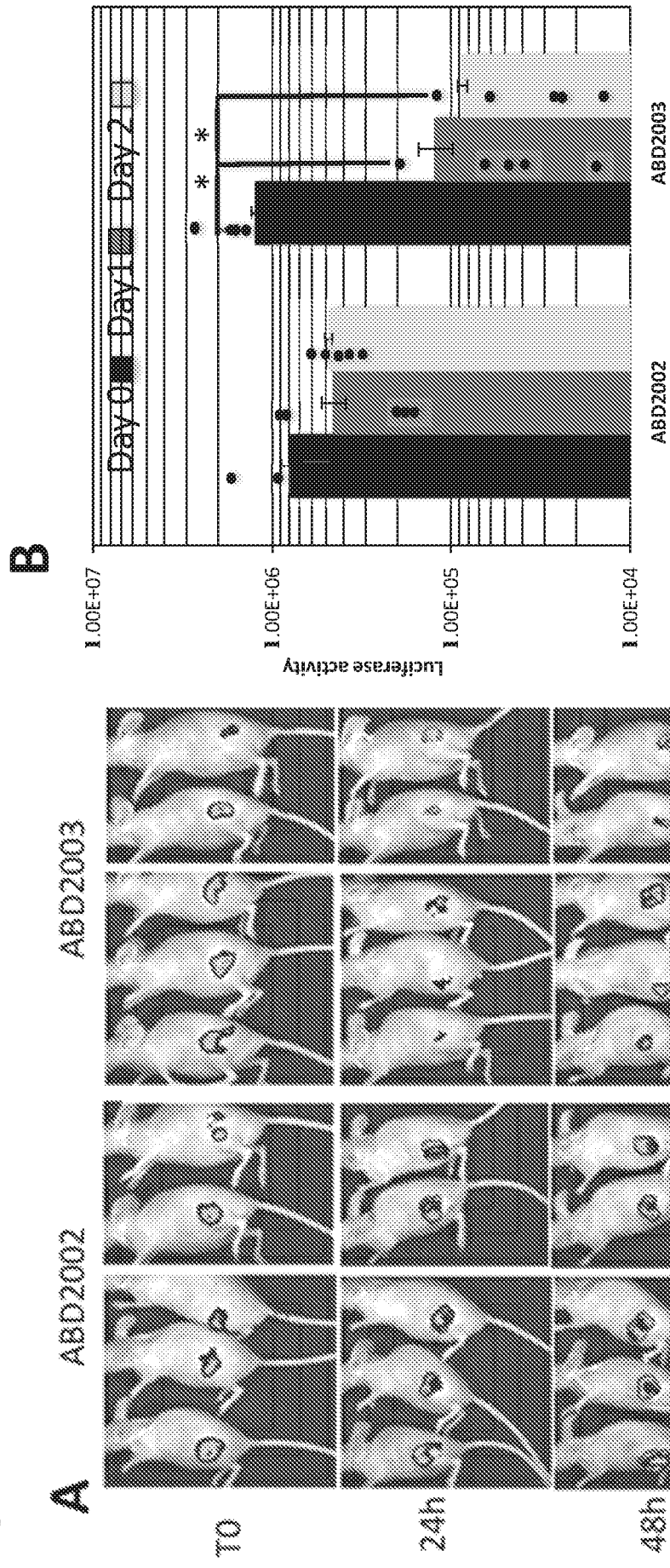


Figure 16

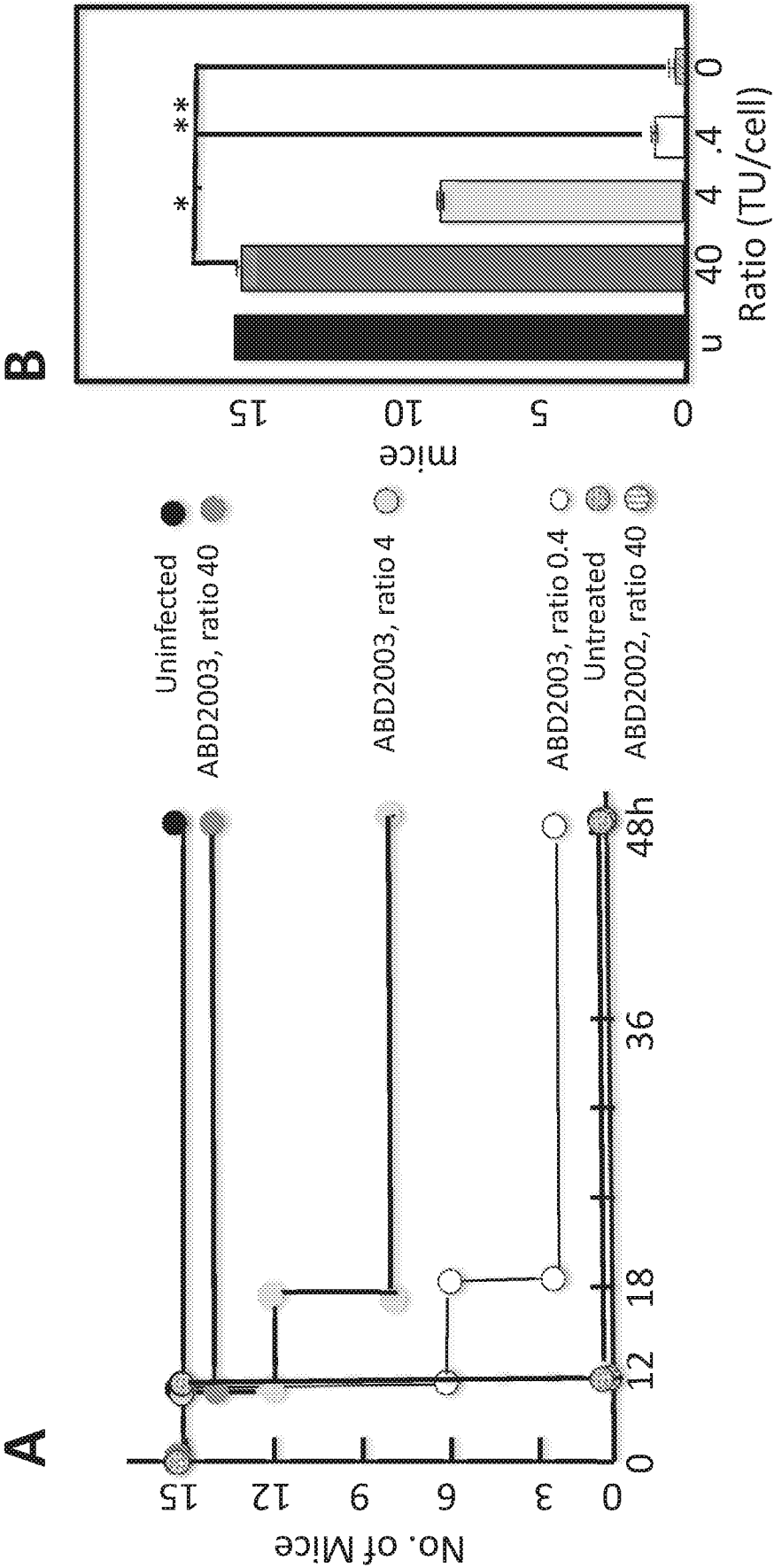


Figure 17

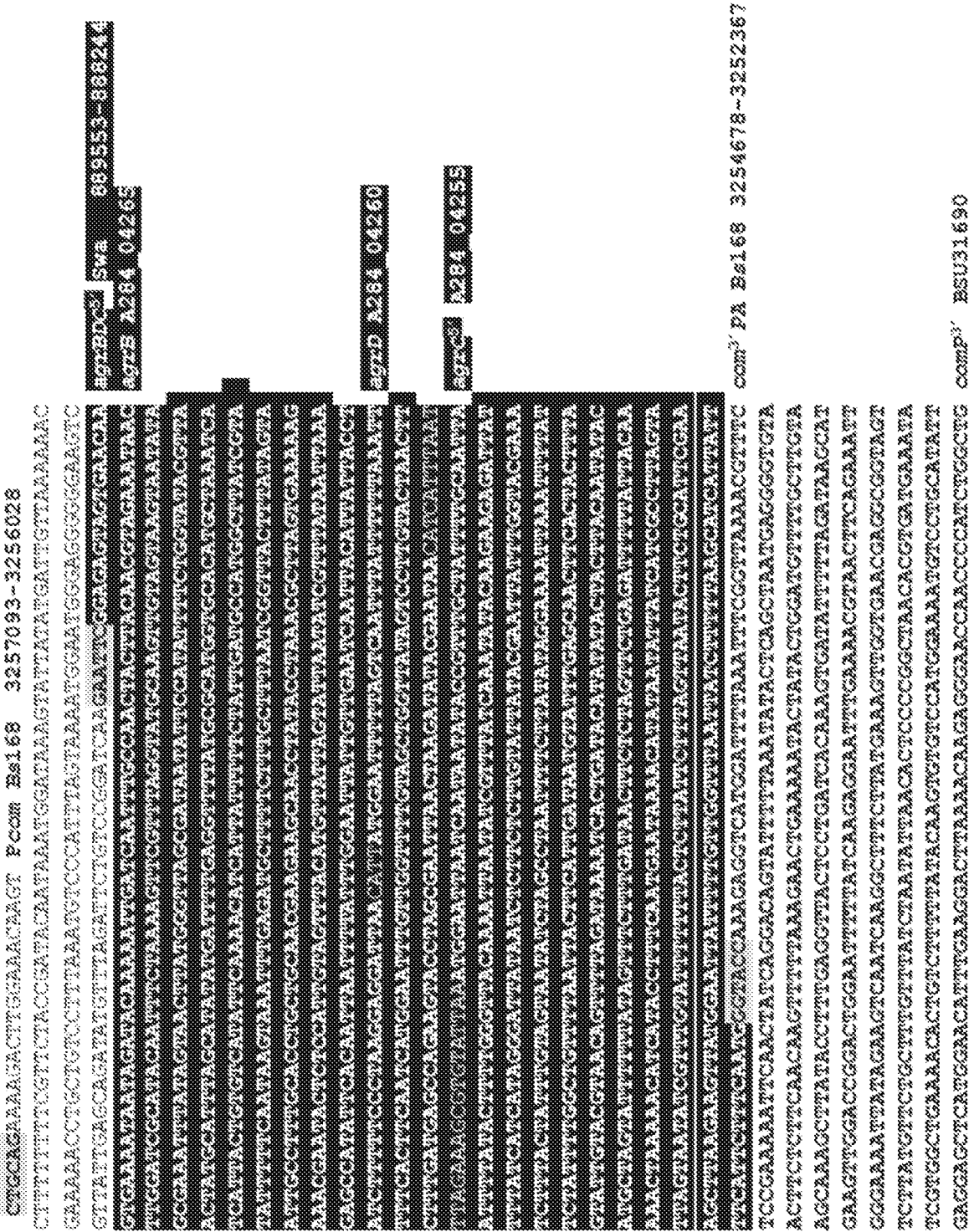


Figure 17, continued

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SEQ ID NO:1

com sequences are black on a white background.
agr sequences are white on a black background.

Figure 18

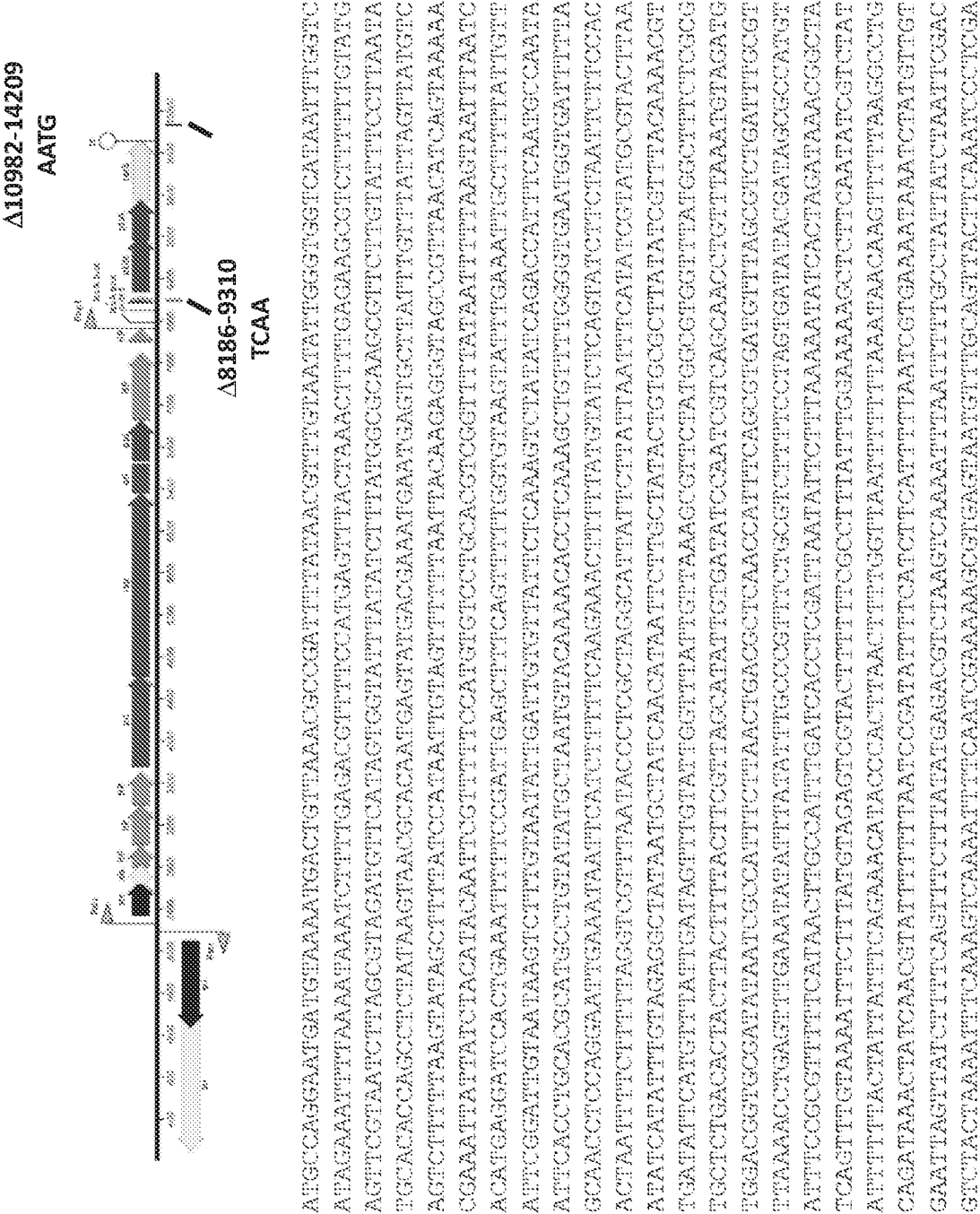


Figure 18, continued

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Figure 18, continued

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Figure 18, continued

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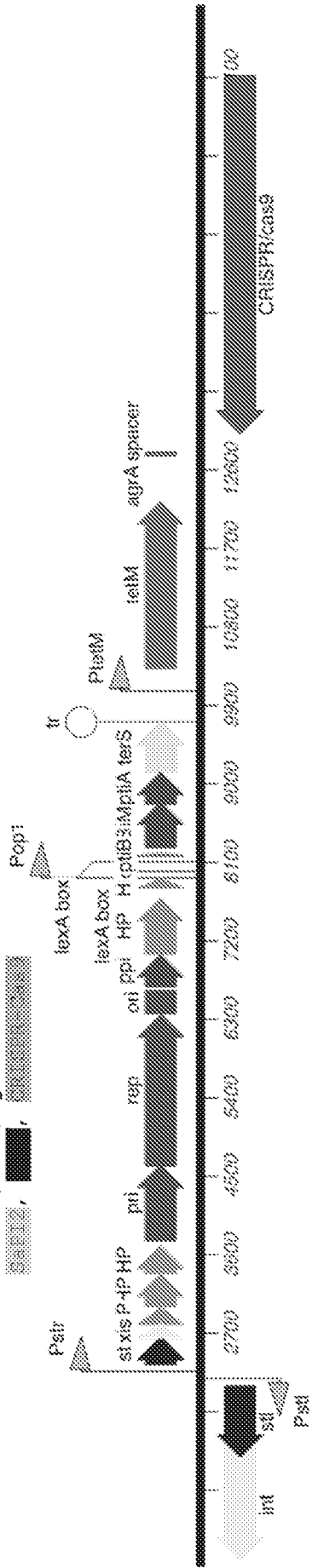
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SEQ ID NO:2

Figure 19

ABD2003: Sapi2 with deletions of *ptiB*, *cpmAB*, *tst*, & *eta*, insertions of *tetM* and CRISPR/*cas9/agrA*



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Figure 19, continued

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CTCTACATAAAATTTTCAAAAGTCAAAATTTTCAATCCAAAAGCGTCAGTAATCTTTCCAGTTACTTCAAAATCCCTCGA
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Figure 19, continued

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Figure 19, continued

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Figure 19, continued

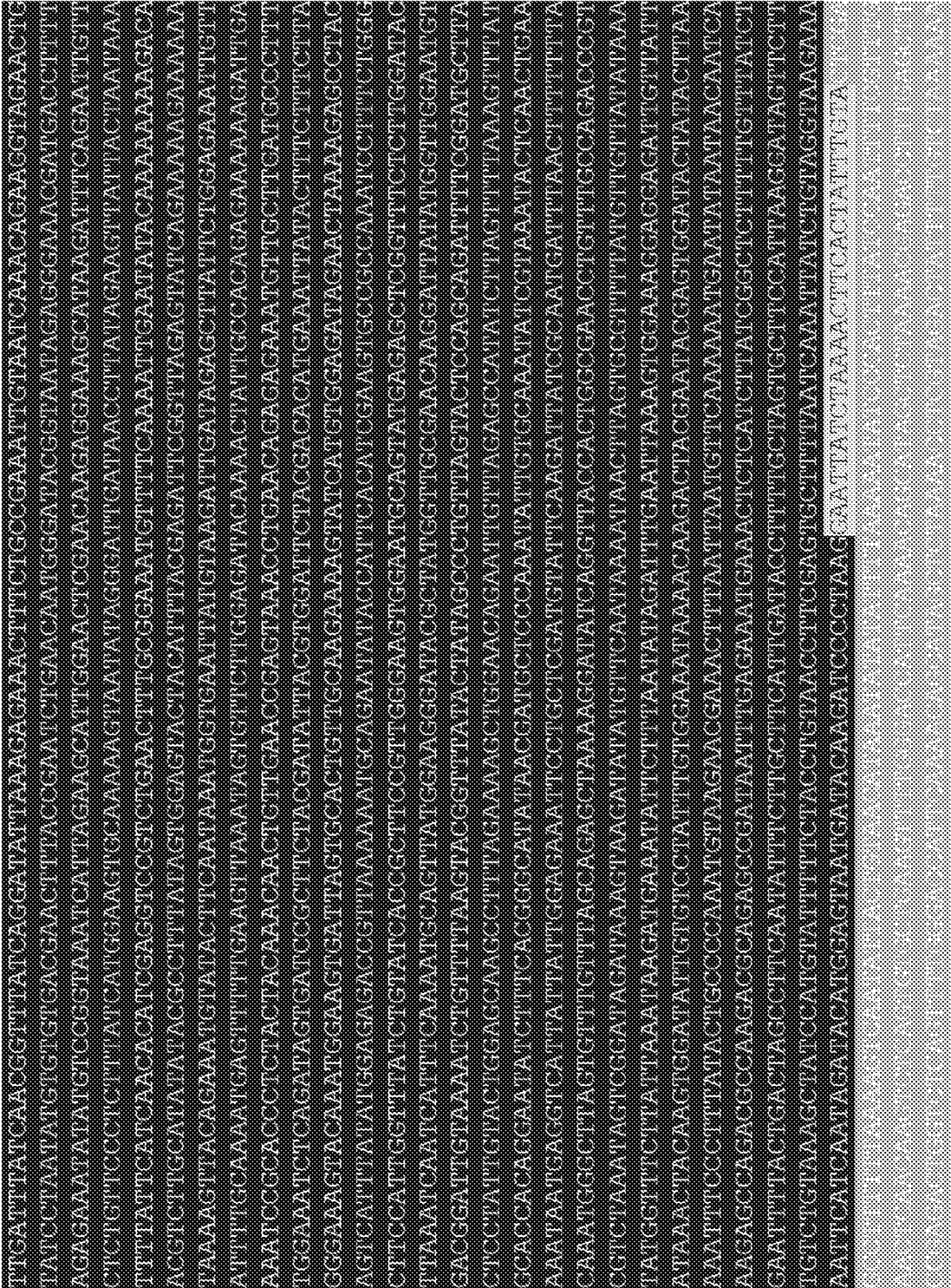


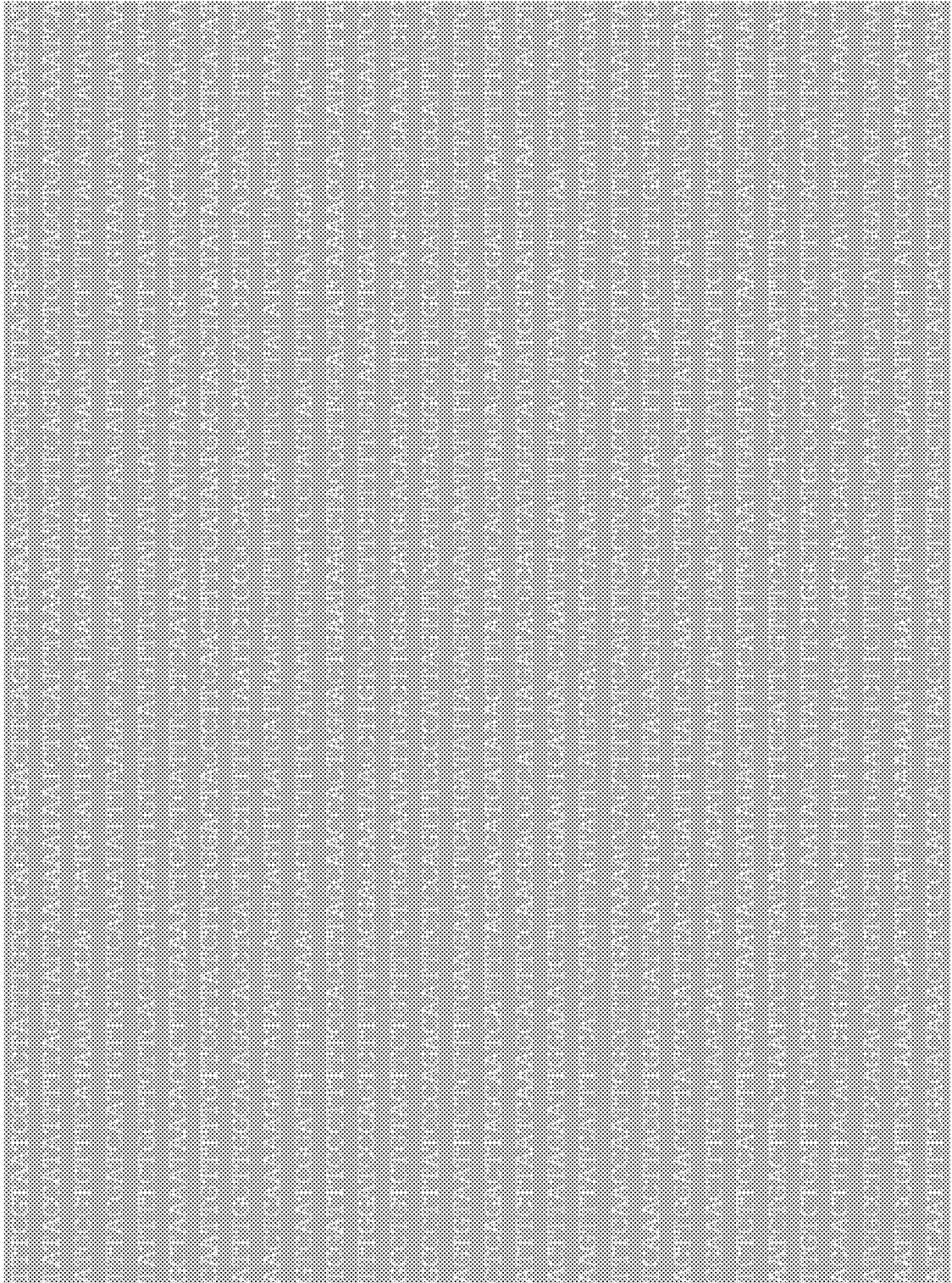
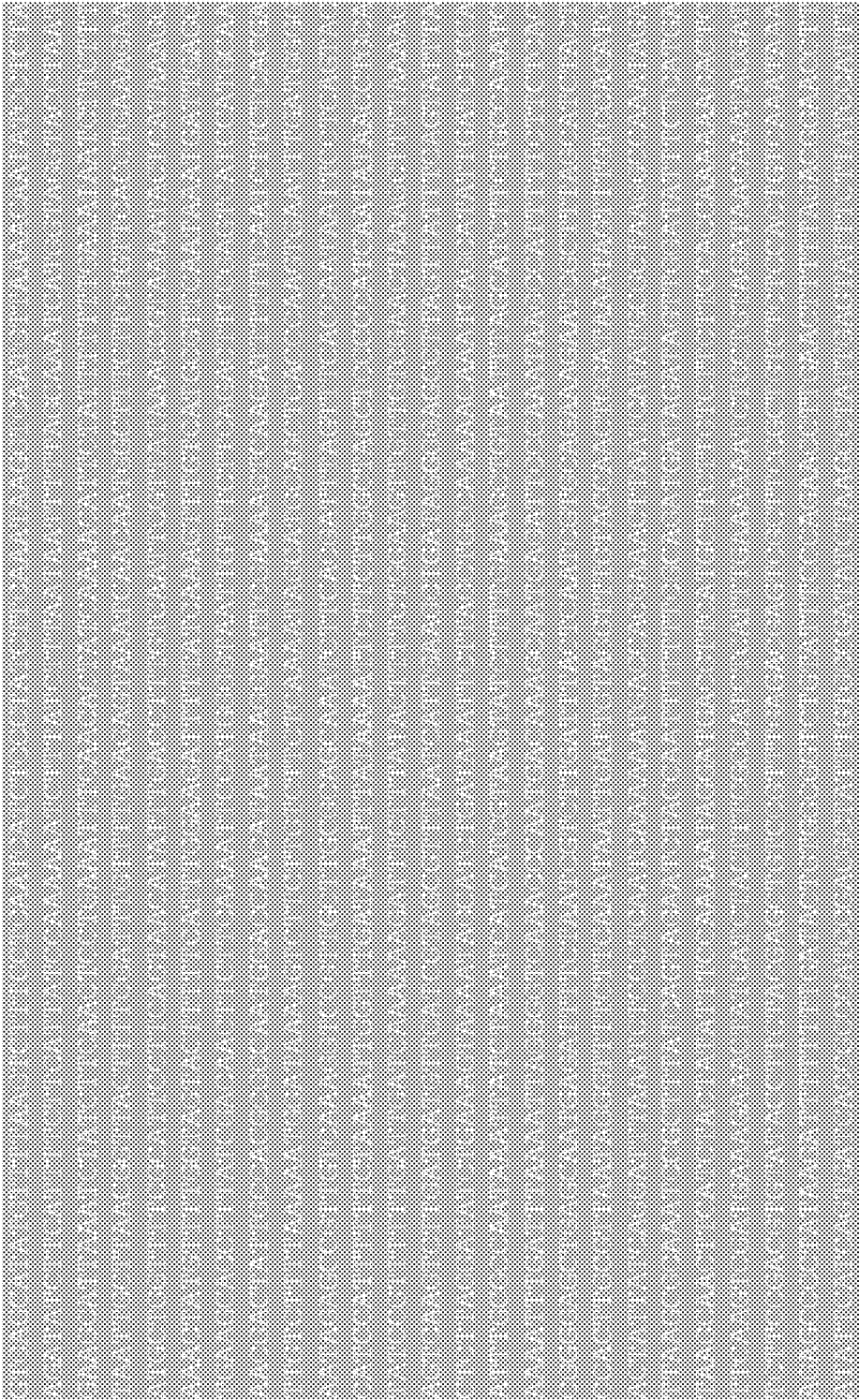
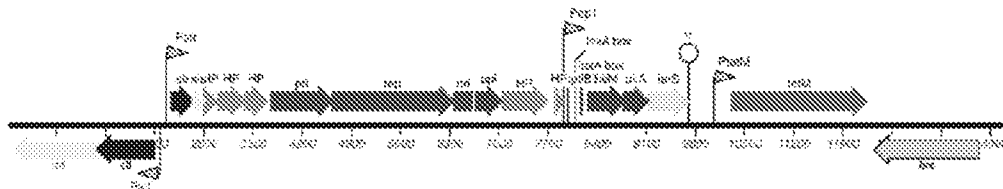
Figure 19, continued

Figure 19, continued



ABD2009 SaPI2, tetM



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Figure 20, continued

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Figure 20, continued

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Figure 20, continued

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TCAAAGCTATATATAAACGTTGATTATTTATGTATATTAGGTCAAACGTGTACACGA
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TTAATTAAAGGTGAAAAAGATCGCTTGCAAAAAAAGGTGAGTCACAAAAACATTA
AGTATAGAGGATTTGCTATAAACAAAGAAATGCTTGAAGAATTAGGATTTGATTTT
CTCGAATTCTCATAATCCTTATTCAGATTATTAAATAGTTCCCAAAGTTCCCGAT
AAGTTCCCGCGAAAAACATACAAACGGGAACCTATAAGACTACTTTAACCACAAGC
AATTAAAGTTAATAGTTCCCGAAGTTCCCAATAAATAATATTATTATTATTATT
TGAAAACGAACAAATGTTGTTAGCTTTATACCATATATGATAGAAAATTTTTAAC
GGGTACAACGGGAACCTAAGTTTATTTAAAGTTTATATATCAATGGTTTGACTAGT
TCCCGATAAGTATTTTAAAGTCGGGAATTCAACGGGGACTAGTTCCCATTTAAAAA
TATTGGAGGTAACACATGGATAAAGAGCAACTTAAAAAGTATATATACGATTATG
TAAAAGAATATAAGGAGATACCGATATATCAGTTAGAAGATTTGTTTAAAGAAAT
GAATCACGACTATATAGGGAGAACCAGTGTACACACGATAAGGATGAGAATATT
GTGTTTTTGGAGTGGATGGAACAAAATTACAATGTTTGCGCTGATTGAATTAGTTA
AAAGTGAACAACCTTGATTTAGTGTATAGAGGTAGTTTGTGAATCGGTTATTGTGTT
GGATGGTAGAGTTCCCTAACTTACCATTAGCAATTTGTTATCCAGAAGATGGACAA
CAAACGGACGTGCCCTCATGGGTGCCTATGSTATTAAGAATAAATAAAGAGGAGA
AAATCAAATGAACATAGAACTATCGTAAACCAATTTGAAACACGAGCAGGCACG
TTACTAAGGTACTACACAGCATTATTAGAACATACTAAAGTCAACCATGTTGCT
TTAAGTTATACAATGATCCATTTGATATGGCATACTGATGATGAATGGGAAGTT
ATTCGGTCATGTATATATTAAAGATTGTAAAGTAAGGCAATCATTGGAATTAGCG
TCACCTAAGCACACTGAGGGGCTTATAAGAAGTATAGAAGGTCATTATGTACGTT
ATGAATTACATGACGGTAAACAGCTTCTATTAGTGATATGATGGCCAGTCAATT

Figure 20, continued

ATTGGAAGATGAGTATTTTATGTATGGATTACAAACATATGCAGAATCAAATAAT
AGTGATGTGTTTGAGTACCTAGAAAAATGGATTGATACCGATACACTTGAGGGCA
TTCAATCGAGTAATACTGATGTGATAGCGAATATTGAAATGTTGTATCAGTTAGC
TACAGGAATCAATGAACCAGCACCAGAGTTAGTTGAGGGGTTGAGATTAGTAACT
GAGTTTGTACAAGATGAGAATGCGACACAAGAGGATTACAAGGCTTTAGAGCATA
AGTTAACTGAGTTGAAGTCATCTTATTACAGTTTGAATAAGTAATTAAATATGGA
GTCTCACSTGGTGTGTGGCTCCTAATATAAAAAGTATAAGGTATAGAAGTTTTAAA
ATGTAAAGGTTGCAACAATAGTGAGTTAATAGATAGGTAGGCGAAATTCAAAAAA
GTGTGAAATGTTGATATTGAGCTGTTTTATGGCTTTGAAAATAATAAGGTTATAT
AAAGGTGTTAGCTTTTAACATCGGAAGGTATACAGTCTTTGAGAATTGAAAAAAT
GGCAAGATTTGTGCAAGGTGTGAGAACTTTGTTAACGCTAATACAAGCTAAAGTT
TGTGTTTTTGGCATAGGCCTAAAAGTTAAGTTTGTTCGCTGTTTGTTCGTGTTAT
TTTATCGAACTTAAGTTCTATATTAGGTTAATGTGAAAAGCCTAACGTTAAGTTT
ATAACATGATTTTATAAGTGTTATATATGATAAGCTAAACAATTGATAAAACGCG
CTATAAAGCGAACGTAAGTTTGTTTTAGACCTGTAAAAATGGTATAATTTAGGTA
TGAAATAAATTAAAAGAAAGAGGTGTAGAAATGCAAAGTATCAATTTAGCTAAGCA
AAACAGGATTATTAAATAGCAATGATTGCCTATCCAATTCGGGTAGGCTCTGTTT
ATAGGGGTGAATAAATGAAACTGCTTAAAACGAAGAATTGTTTATATTATCGTAA
TGGCGACAATAAACTATCTGAGTATCAACTATTAAAGCAATTTAACCAGCATT
ATTAATAAAAAAATTAAAGATGTGTGAATTCCAAATTGAAAGTATGTACCATATGA
GTGCGTCGACCACAACATGTGATGAAATAATGGGGTTCGTGTCTGTCTCATATCC
GATTGAAAAATTAGTTATCAAAATTATTGAAACAAAAGCAGGGTTACAAAACATAT
AAAAATAGATCTATAAATAATATGGCGTTGTTGAAAAAGGTACTAAATCATTATA
CAGAAAAAGAGCAGAAGCAAGTTGTAAAATATATGCGTTCAAATGGACGATATAA
GCCTTACAACGTCATTGAACGCTTACAAGTTGATTGTTATCAAGCAAGTATTAAA
CAACGTTTCAGAACGTCAAAAACAAAGAAATACAGCAATTGAAAACAGTAAGATTG
CACGAGTAAATGCATATCACCAATCTTCATATGTAAAAGTGGTGTAAACAATGGAT
AAAAAGCAAATAAAAGACTTCGTTTGTGATTATCATAAGCGAACTAGAAGTGATG
TGTTGATAGATGATGAAATAAATACCGATGAATTCTTTTCAATAGGTGATGAAAA
TTCTAATGAATGGATGGCAGACGATAACATTGATGATCATATTGTAAAGAATCAC
TTAGAAATGATTGTTGACCAAGTAGCTAATGACAAAGAGTTTTATATTTTCGATT
CTTTAATACAAGGACGTAGTTTTAAAGATATTAGCAATGTCTTAGAGTGTTCAGA
ACAATCTGTAAGATTATGGTATGAAACCTTATTAGATAAAATTGTGGAGGTGATA
GAATGAGTGAGTTAACGGCAAACAAGCGCGTTTTGTGAATGAGTATATAAGAAC
ACTTAATGTAACACAAAGTGCCATAAAAGCAGGCTATAGCGCAAATAGTGCACAT

Figure 20, continued

GTGACAGGATGTAGGTTATTAAAGAAGCCACACATCAAGCAATATATACAAGAAC
AAAAAGATAAGATTATAGATGAGAATGTATTAACCGCABAAGAGTTACTACATGT
GCTTACGAATGCGGCAGTCGGTGATGAGACAGAAACGAAAGAAGTTGTAGTCAAG
CGAGGGGAATATAAAGAGAATCCACAAAGTGGCAAAGTACAGCTAGTCTATAACG
AACATGTTGAACTGATAGAGGTACCAATAAAAACCTAGTGATCGTTTAAAAGCTCG
TGATATGTTGGGTAATPACCATAAGTTATTTACAGATAAGCATGATATTAACGGG
AATGTGCCTATATTCATTAATAATTGGTGAATGGGATGGCGATGATGAAGATTTAG
ATAAGACGGTACAAGAGGTATCTAACGCTAATCCTAATCATACTGTGATTGTGGA
TGATATACCGTTAGAGGATTGATTACAGTAAAAACGATTATCATATTGAGTTAGT
CAGCATTAAGTTTACTAATTCACCCTAGCTTTATATTAAGCCTTATAAAGATAAA
AGGGAGAACGCTTATTATAATTAACGGACTCCCTTTATTAATAATTATTACAGAA
AAAGTGGTAAATTAATTAATTTCTGCTTCTATAGTTTTTATTTCAATCAATATTTA
TAGCTGGTTTTTTCAGTATTGTATTCAAACTTTTTAGATAAATCACTTTGATATGT
GGATCCGTCATTCATTGTTATTTTCCAATAACCACCCGTTTTATCGCTTGAACGA
TATAATCCATGTATTTGAGTTAGCTGATGACGAATTTCAAAGTCTAAAGTTGATA
TAGCTAATTGTTTTTTATCGAACTTTGGCCAATACTTTAAGGGGCTATCTTTACC
ATGAACCTTAACCTTTTAAAGGTAGTTCTATTGGAGTAGCTAATTTTTTCACTATTT
GTAACGCCACTTATTTGGAAATGGATATAAGTTCCCTTCGCTAGTATGTTGGCTTT
TTTTAGTTCTTTTTGTGTTTAAAGTCAACTTTTTCCCTTTTGTAAAAGCAGGGCT
ATAATAAGGACTCGEAAAAATTATAAGGCTGATGCTGCCATCTGTGTTTTTTATA
CGCATAGATCCTAAGACCGGATCAAGAAACAAAGGCCAACCCMAATCTCGCAATTTG
AGTTGATATTAGAAAAACAAGATAAATTGGAAGATTGTAAAAATAACAAATATTTGGT
ACATGATTACAGATACTTTGTAATCATGTACTCTTTTTTGATAAAAAAATTGGAGAT
TCCTTTACAAATATGCTCTTACGTGCTATTAATTTAAGTGACTATTTAAAAGGAGT
TAATAAATATGCGGCAAGGTATTTCTTAAATAAACTGTCAATTTGATAGCGGGAAC
AAATAATTAGATGTCCTTTTTTAGGAGGGCTTAGTTTTTTGTACCCAGTTTAAGA
ATACCTTTATCATGTGATTCTAAAGTATCCAGAGAATATCTGTATGCTTTGTATA
CCTATGGTTATGCATAAAAAATCCAGTGATAAAAGTATTTATCACTGGGATTTTT
ATGCCCTTTTGGGTTTTTGAATGEAGGAAAAATCACATGAAAAATTATTAATATTGG
AGTTTTTAGCTCATGTTGATGCAGGAAAAACTACCTTAACAGAAAGCTTATTATAT
AACAGTGGAGCGATTACAGAATTAGGAAGCGTGGACAAAGGTACAACGAGGACGG
ATAATAACGCTTTTAGAACGTCAGAGAGGAATTACAATTCAGACAGGAATAACCTC
TTTTCACTGGGAAAAATACGAAGGTGAACATCATAGACACGCCAGGACATATGGAT
TTCTTAGCAGAAGTATATCGTTCATTATCAGTTTTAGATGGGGCAATTCTACTGA
TTTCTGCAAAAGATGGCGTACAAGCACAACTCGTATATTAATTTCAATGCACTTAG

Figure 20, continued

GAAAATGGGGATTCCCACAAATCTTTTATCAATAAGATTGACCAAAAATGGAAATT
GATTTATCAACGGTTTATCAGGATATTAAAGAGAAACTTTCTGCCGAAATTGTAA
TCAAACAGAAGGTAGAACTGTATCCTAATATGTGTGTGACGAACTTTACCGAATC
TGAACAATGGGATACGGTAATAGAGGGAAACGATGACCTTTTAGAGAAATATATG
TCCGGTAAATCATTAGAAGCATTGGAACTCGAACAAGAGGAAAGCATAAGATTTC
AGAATTGTTCTCTGTTCCCTCTTTATCATGGAAGTGCAAAAAGTAATATAGGGAT
TGATAACCTTATAGAAGTTATTACTAATAAATTTTATTTCATCAACACATCGAGGT
CCGTCTGAACTTTGCCGAAATGTTTTCAAATTTGAATATACAAAAAAGACAAC
GTCTTGCAATATATACGCCTTTATAGTGGAGTACTACATTTACGAGATTCGGTTAG
AGTATCAGAAAAAGAAAAAATAAAAGTTACAGAAATGTATACTTCAATAAATGGT
GAATTATGTAAGATTGATAGAGCTTATTCTGGAGAAATGTTATTTTGCAAAATG
AGTTTTTGAAAGTTAAATAGTGTTCTTGGAGATACAAAACCTATTECCACAGAGAAA
AAAGATTGAAAATCCGCACCCTCTACTACAAACAACCTGTTGAACCGAGTAAACCT
GAACAGAGAGAAATGTTGCTTGATGCCCTTTTGGAAATCTCAGATAGTGATCCGC
TTCTACGATATTACGTGGATTCTACGACACATGAAATTTATACTTTCTTTCTTAGG
GAAAGTACAAATGGAAGTGATTAGTGCACCTGTTGCAAGAAAAGTATCATGTGGAG
ATAGAACTAAAAGAGCCTACAGTCATTTATATGGAGAGACCGTTAAAAAATGCAG
AATATACCATTCACATCGAAGTGCCGCCAAATCCTTTCTGGGGCTTCCATTGGTTT
ATCTGTATCACCGCTTCCGTGGGGAAGTGAATGCAGTATGAGAGCTCGGTTCCT
CTTGGATACTTAAATCAATCAATTTCAAATGCGAGTTATGGAAGGGATACGCTATG
GTTGGCAACAAGGATTATATGCTTGGAAATGTGACGGATTGTAAAATCTGTTTAA
GTACGGTTTATACATATAGCCCTGTTAGTACTCCAGCAGATTTCGGGATGCTTACT
CCTATTTGTACTGGAGCAAGCCTTTAGAAAAGCTGGAACAGAATTGTTAGAGCCAT
ATCTTAGTTTTAAAGTTTATGCACCACAGGAATATCTTTCACGGGCATATAACGA
TGCTCCCAAATATTGTGCAAATATCGTAAATACTCAACTGAAAAATAATGAGGTC
ATTATTATTGGAGAAATTCCTGCTCGATGTATTCAAGATTATCGCAATGATTTAA
CTTTTTTTTACAAATGGGCTTAGTGTTTGTTTAGCAGAGCTAAAAGGATATCAGGT
TACCACCTGGCGAACCTGTTTGCCAGACCCGTCGTCCTAAATAGTCGGATAGATAAA
GTAAGATATATGTTCAATAAAAATAACTTAGTGCGTTTTATGTTGTTATATAAATA
TGGTTTTCTTATTAAATAAGATGAAATATTCTTTAATATAGATTTGAATTAAGTG
GAAAGGAGGAGATTGTTATTATAAACTACAAGTGGATATTGTGTCCTATTGTGG
AAATAAAAACAAGACTACGAATACGACTGGATACTATACTTAAAAATTTCCCTTTA
TACTGCCCCAAATGTAAGAACGAAACTTTAATTAATGTTCAAAAAATGAATATAA
TAACAATCAAAGAGCCAGACGCCAAGACGCAGAGCCGATAATTTGAGAAATGAAA
CTCTCATCTTATCGGCTCTTTTGTGTTATCTGAATTTTACTGACTAGCCTTCMA

[illegible]

Figure 20, continued

CTGCTTAAGTCAATATGCAATCAATTTTAAGAAATAGGTTTTTTTGGAAATT
CAAAATTAACATTCAGAGTTCCGCAATAAGCATTATATTGCAATGAAAAAG
CATTATATGGATAATCATATCTATCATTGCAAATATACTTATAGAGATTTATGTG
TGTGATAATTGGTGGTCATAAATTGGTCATAATGAAATAAAAAAACTAAAAAAT
TGAATGCATAAAGAATACACGATGCTGATTTAATAGGATTTTTGTATATGATTTA
TATCTATTTCACTGCCCCTTAATGCCAGGAATGATGTAAAAT

SEQ ID NO:5

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2018/032754

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12N 7/01; C12N 9/22; C12N 15/113; C12N 15/74 (2018.01)

CPC - C12N 9/22; C12N 15/113; C12N 15/74; C12N 2310/20; C12N 2795/10311; C12N 2795/10323; C12N 2795/10341; C12N 2795/10352 (2018.05)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 435/5; 435/6.1; 435/36; 435/320.1; 514044R (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2014/160418 A2 (GENEWEAVE BIOSCIENCES, INC.) 02 October 2014 (02.10.2014) entire document	1-30
Y	WO 2014/124226 A1 (THE ROCKEFELLER UNIVERSITY) 14 August 2014 (14.08.2014) entire document	1-30
Y	VIPRA et al. "Antistaphylococcal activity of bacteriophage derived chimeric protein P128," BMC Microbiol, 22 March 2012 (22.03.2012), Vol. 12, No. 41, Pgs. 1-9. entire document	4-12, 19
Y	DAMLE et al. "The roles of SaPI1 proteins gp7 (CpmA) and gp6 (CpmB) in capsid size determination and helper phage interference," Virology, 17 June 2012 (17.06.2012), Vol. 432, No. 2, Pgs. 277-282. entire document	13-21, 25-27
Y	CHEN et al. "Pathogenicity island-directed transfer of unlinked chromosomal virulence genes," Mol Cell, 11 December 2014 (11.12.2014), Vol. 57, No. 1, Pgs. 138-149. entire document	26
A	VERCOE et al. "Cytotoxic chromosomal targeting by CRISPR/Cas systems can reshape bacterial genomes and expel or remodel pathogenicity islands," PLoS Genet, 18 April 2013 (18.04.2013), Vol. 9, No. 4, e1003454, Pgs. 1-13. entire document	1-30
A	SANTIAGO et al. "A new platform for ultra-high density Staphylococcus aureus transposon libraries," BMC Genomics, 29 March 2015 (29.03.2015), Vol. 16, No. 252, Pgs. 1-18. entire document	1-30



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

05 July 2018

Date of mailing of the international search report

09 AUG 2018

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PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2018/032754

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KIM et al. "Identification of an Antimicrobial Agent Effective against Methicillin-Resistant Staphylococcus aureus Persists Using a Fluorescence-Based Screening Strategy," PLoS One, 03 June 2015 (03.06.2015), Vol. 10, No. 6, e0127640, Pgs. 1-15. entire document	1-30
A	PARK et al. "Genetic engineering of a temperate phage-based delivery system for CRISPR/Cas9 antimicrobials against Staphylococcus aureus," Sci Rep, 21 March 2017 (21.03.2017), Vol. 21, No. 7, Pgs. 1-13. entire document	1-30