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(54) **NOVEL CELL LINE SCREENING METHOD**

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(52) **U.S. Cl.**  
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435/7.92; 506/7; 435/7.21

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(57) **ABSTRACT**

(21) Appl. No.: **14/092,786**

The invention provides a novel cell line development method useful to screen for recombinant protein production. The method utilizes a membrane-anchored reporter or an intracellular reporter residing in the expression vector for a gene of interest to facilitate initial cell selection by FACS or MACS. A switching mechanism can be used to delete the reporter from the chromosome by providing an appropriate DNA recombinase, which turns the selected cells into production cells that secrete the protein of interest without co-expression of the reporter.

(22) Filed: **Nov. 27, 2013**

**Related U.S. Application Data**

(60) Provisional application No. 61/732,156, filed on Nov. 30, 2012.

Figure 1A

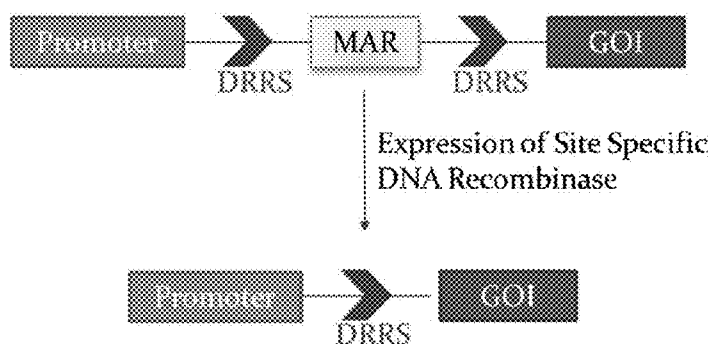


Figure 1B

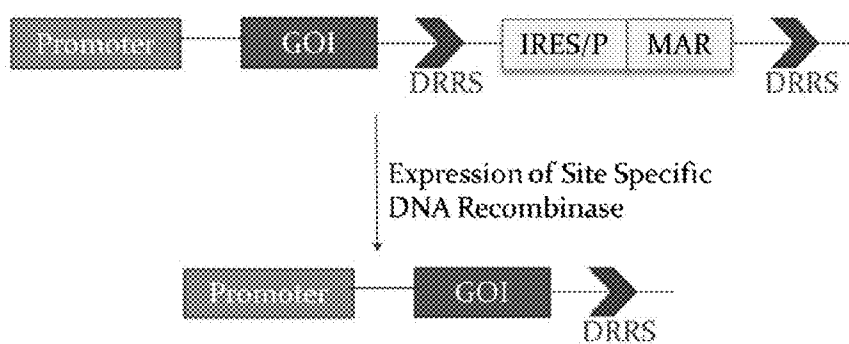


Figure 1C

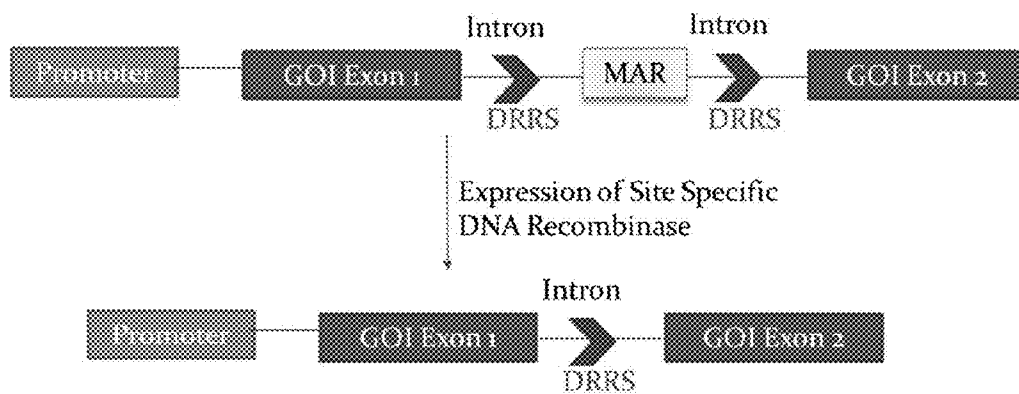


Figure 2

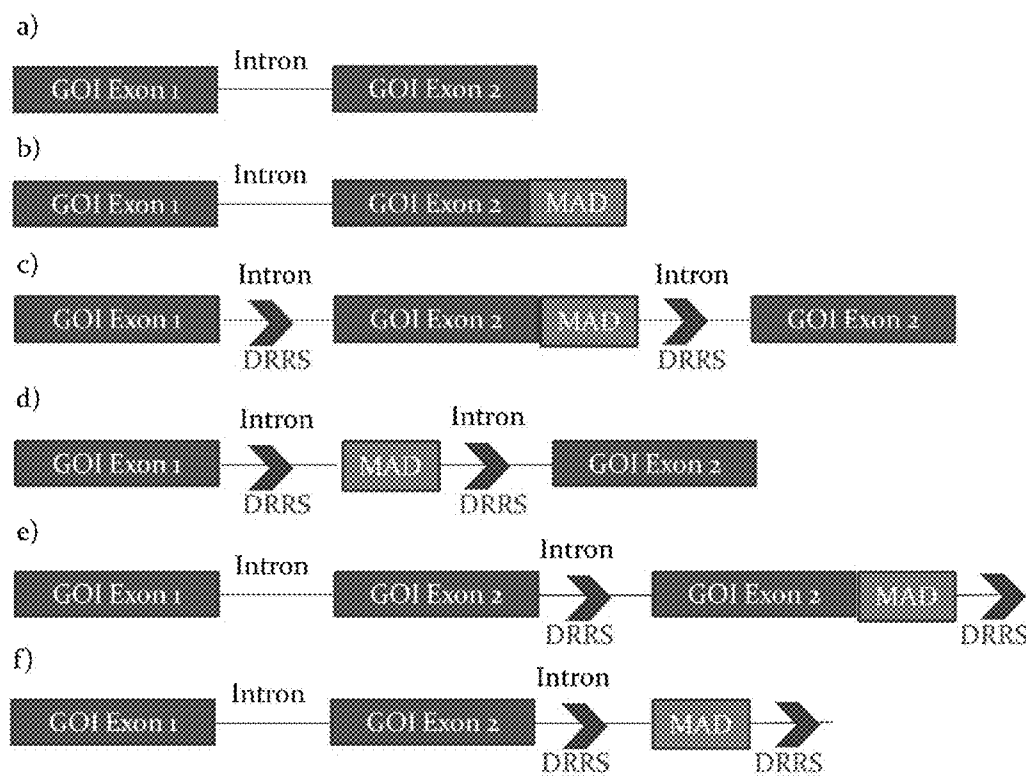


Figure 3A

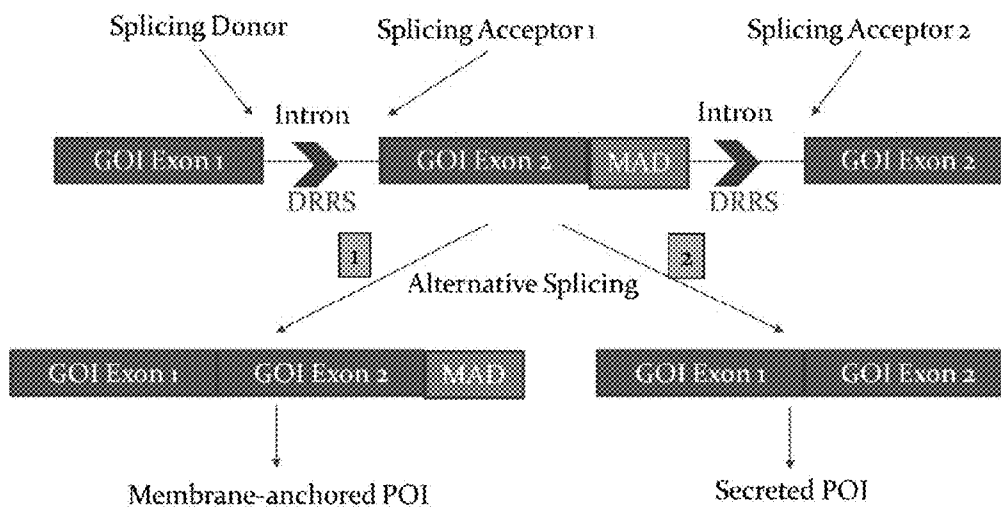


Figure 3B

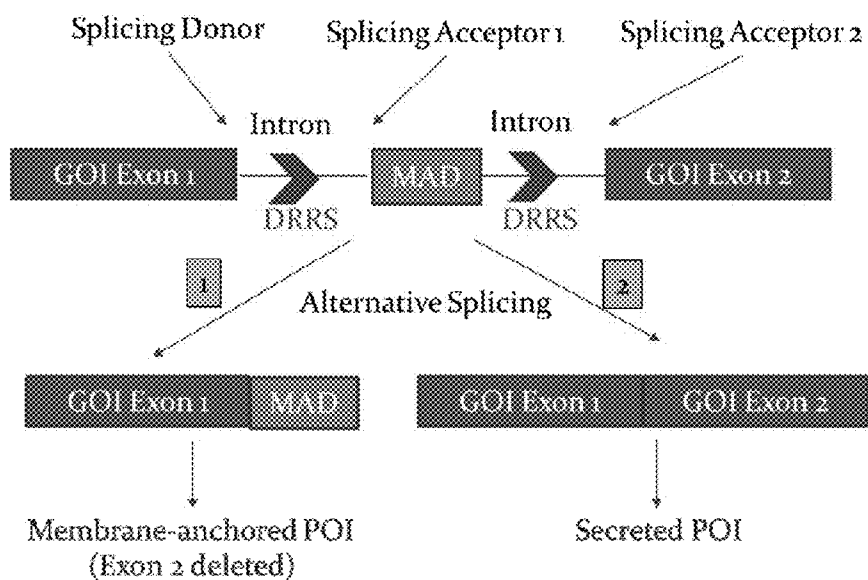


Figure 3C

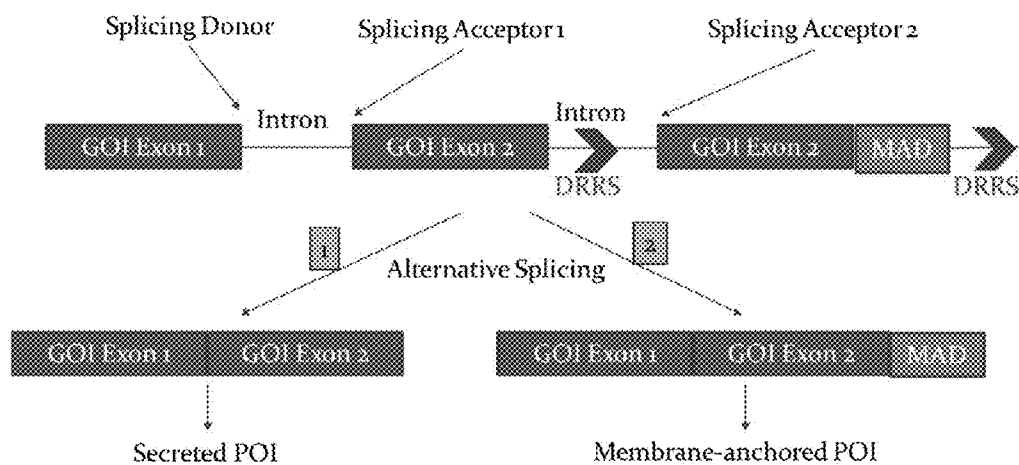


Figure 3D

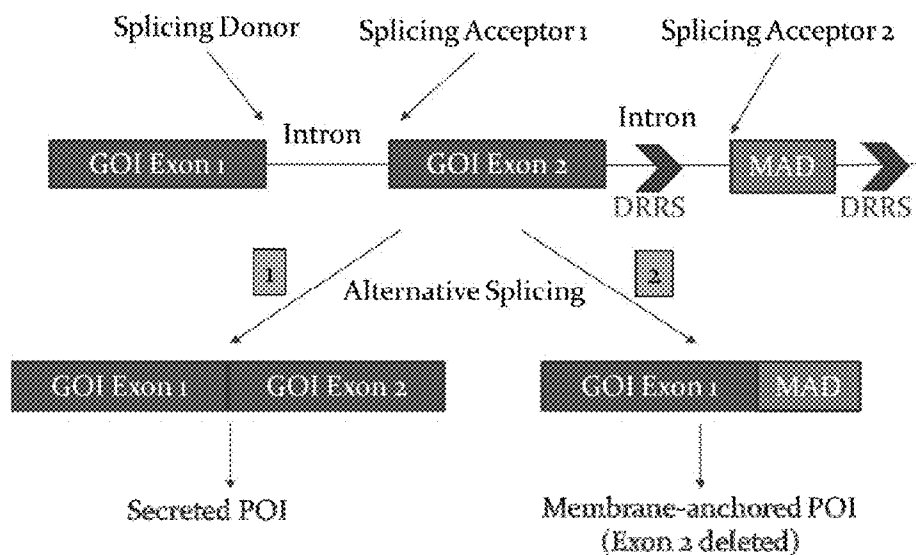


Figure 4A

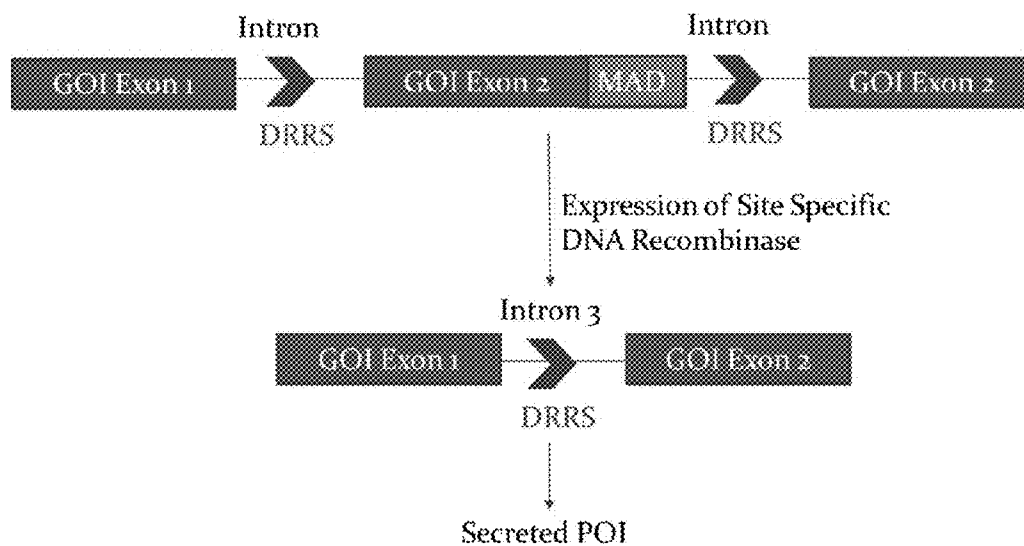


Figure 4B

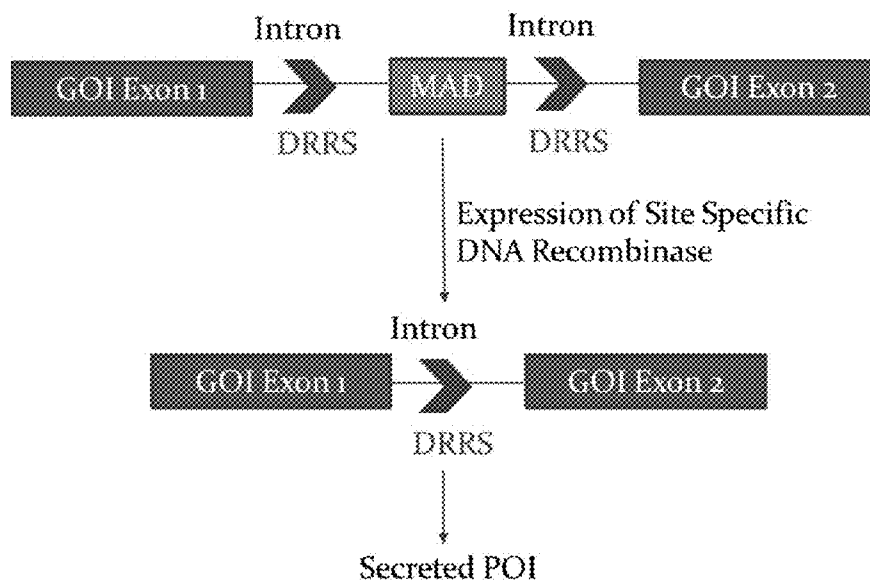


Figure 4C

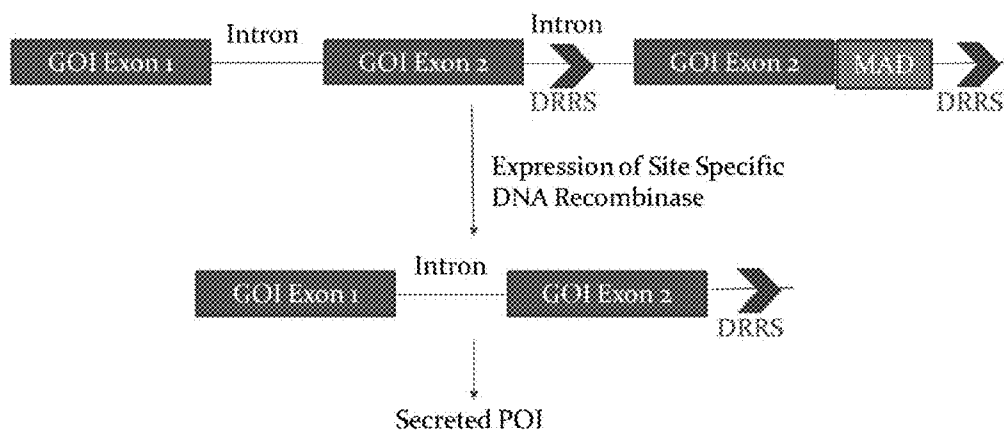


Figure 4D

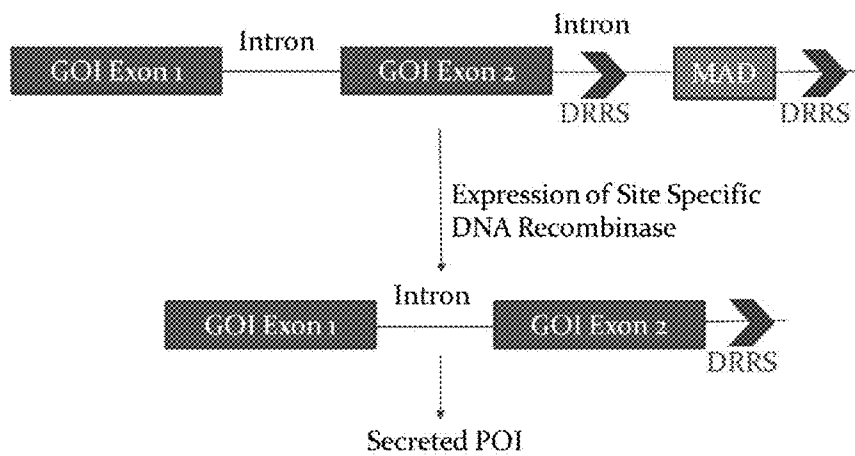


Figure 5

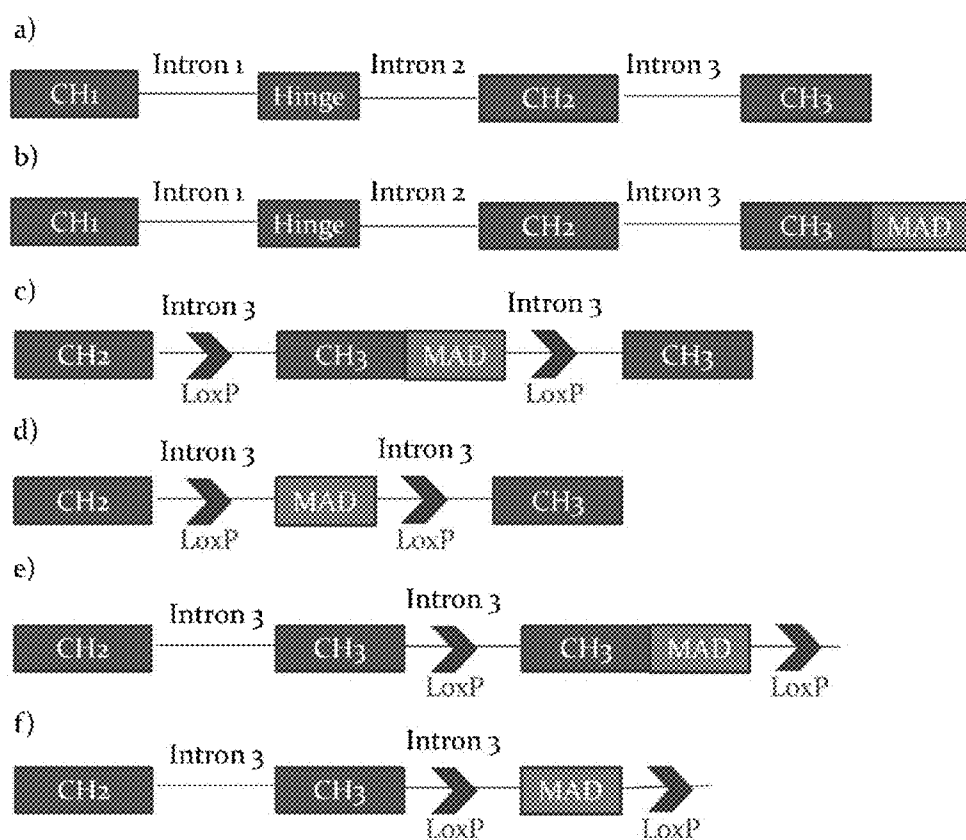




Figure 6A

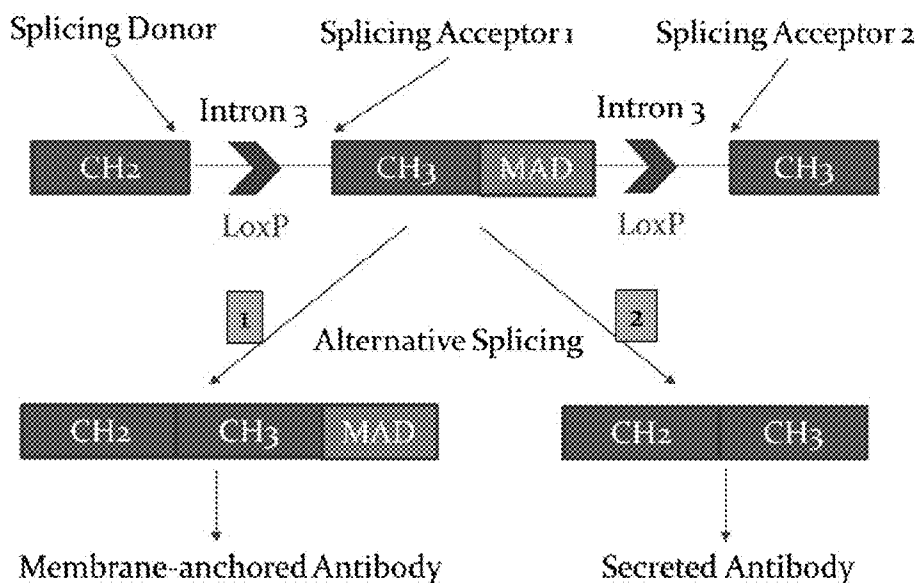


Figure 6B

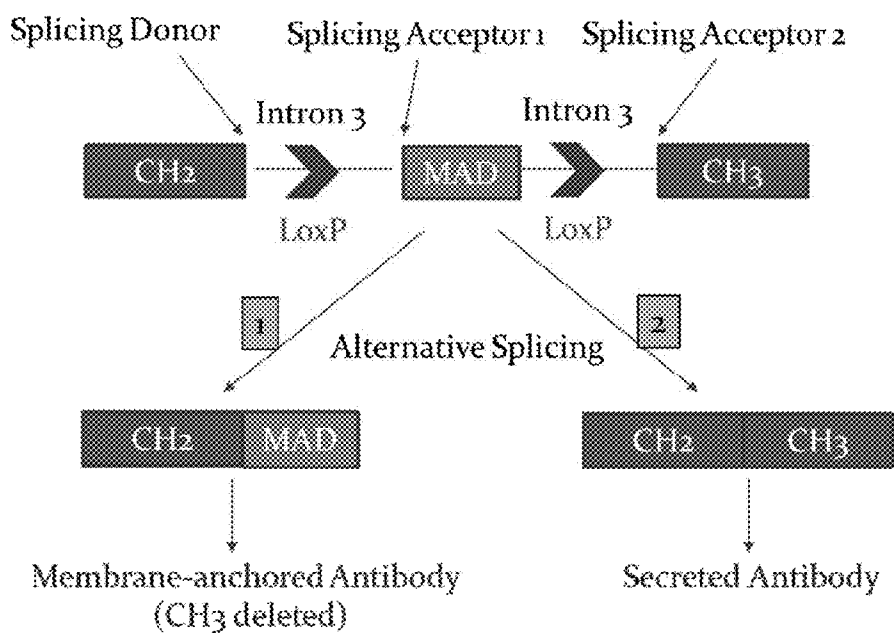


Figure 7A

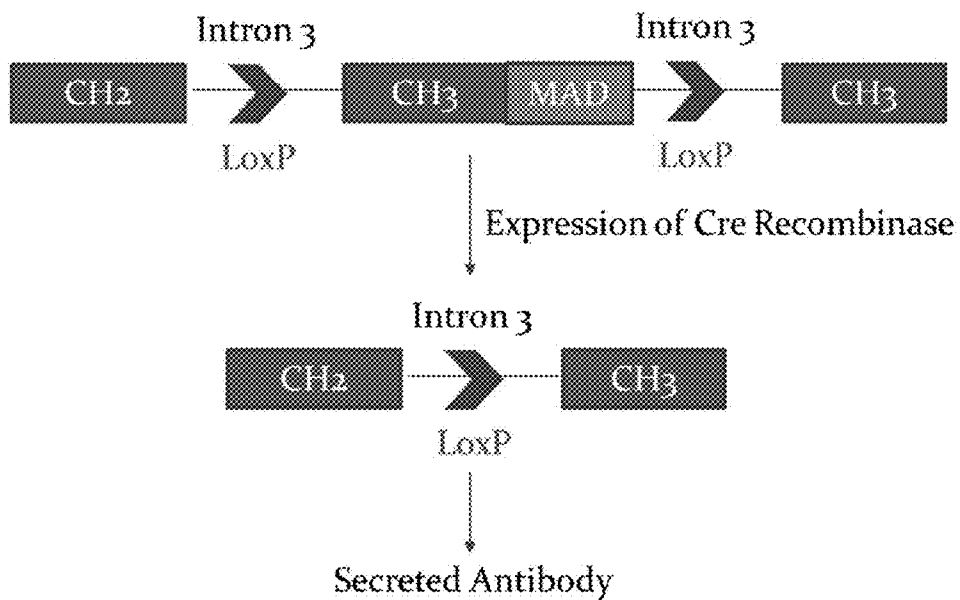


Figure 7B

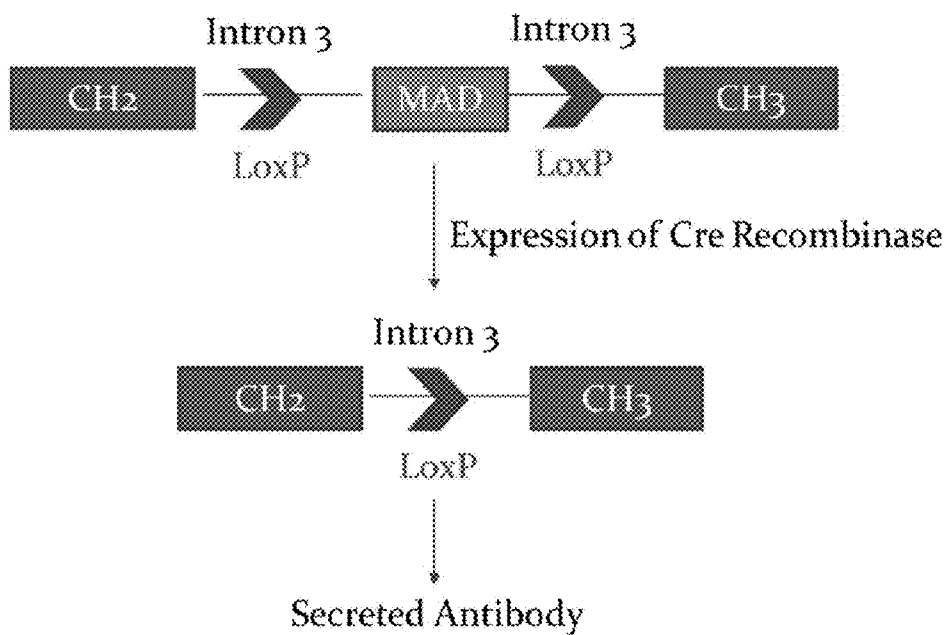


Figure 8A

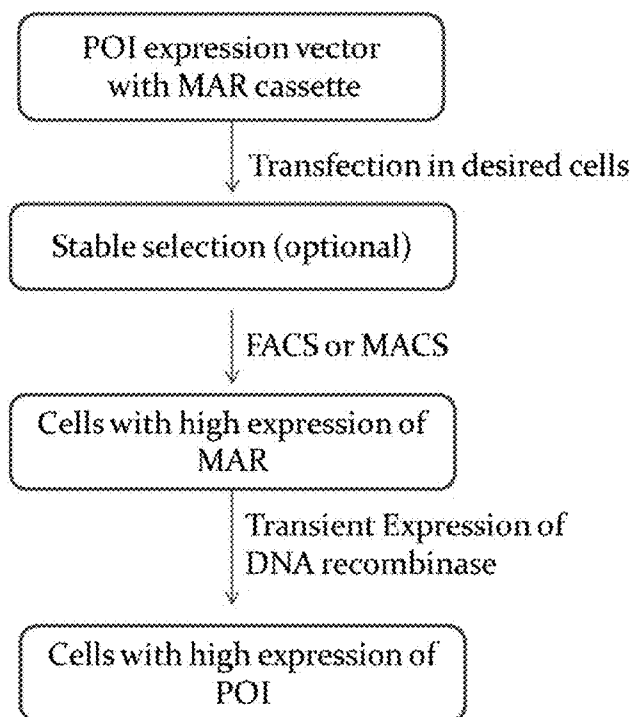


Figure 8B

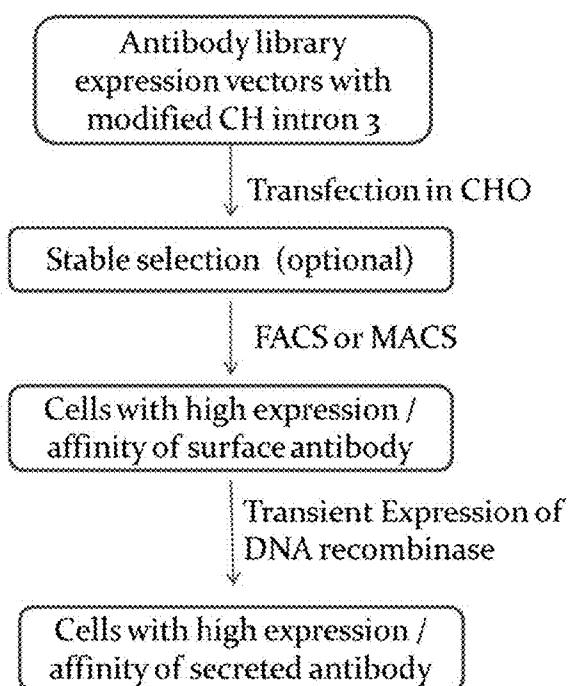


Figure 9A

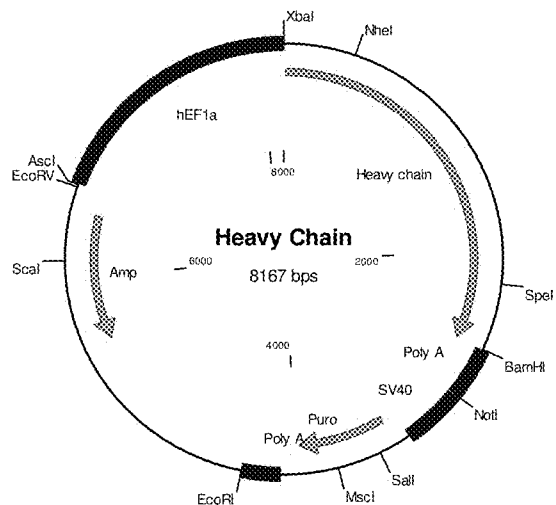


Figure 9B

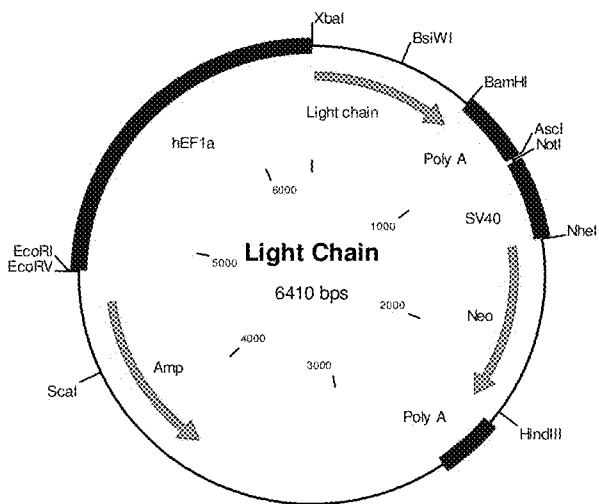


Figure 9C

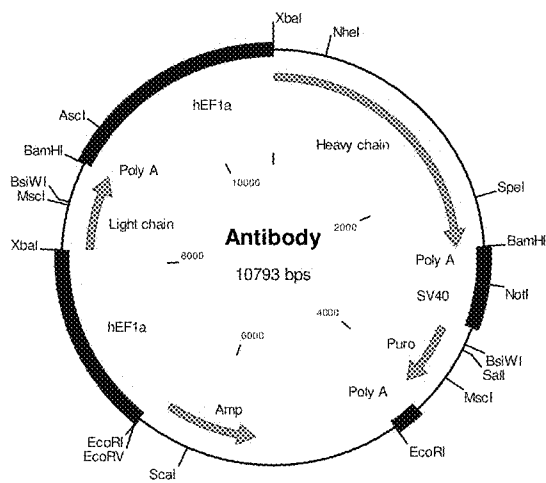


Figure 10A

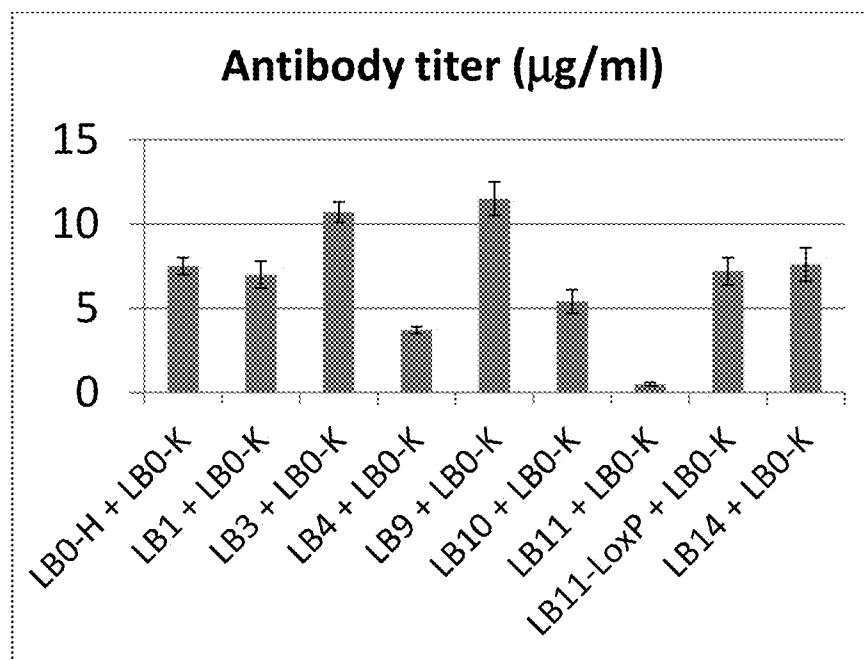


Figure 10B

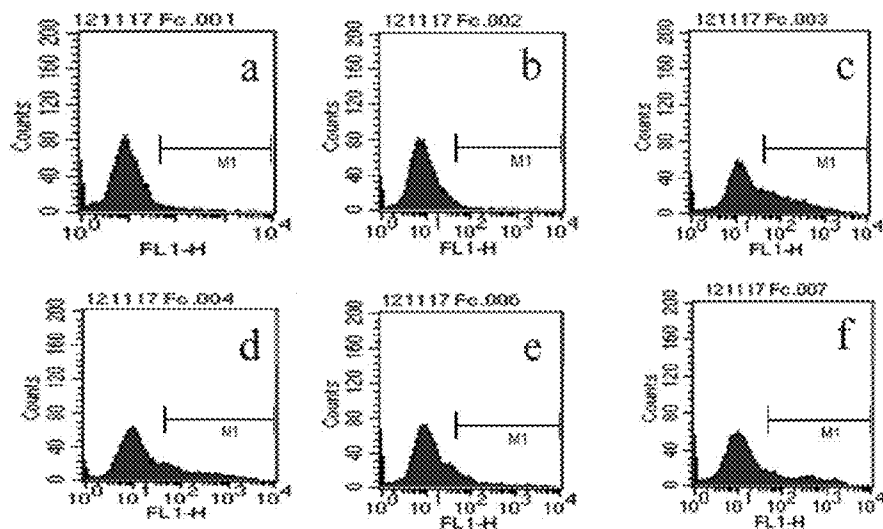


Figure 11A

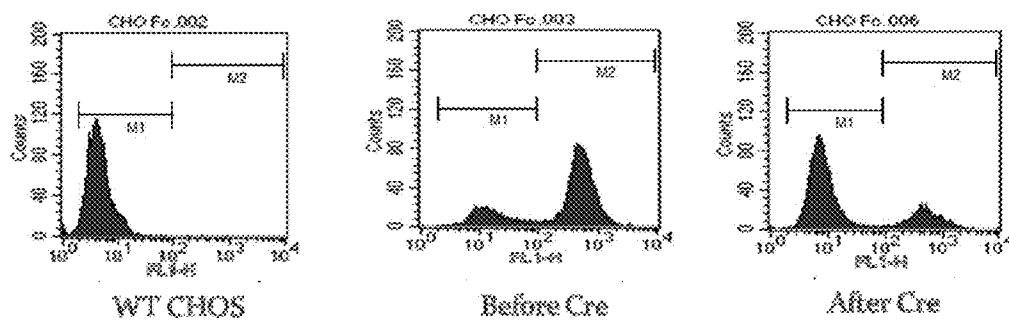


Figure 11B

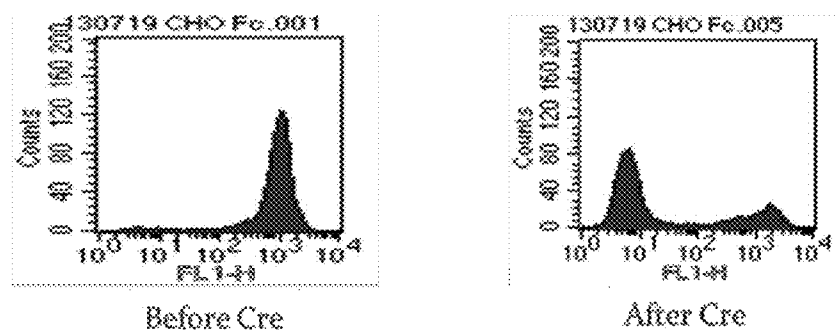


Figure 12A

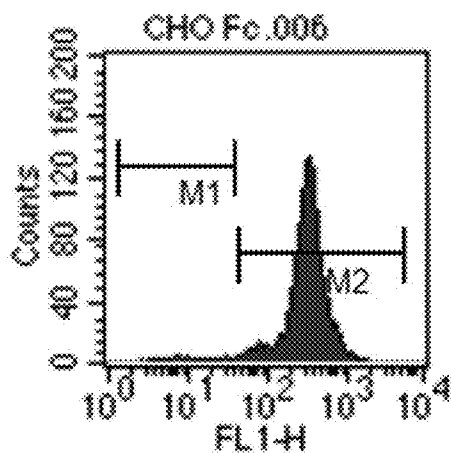


Figure 12B

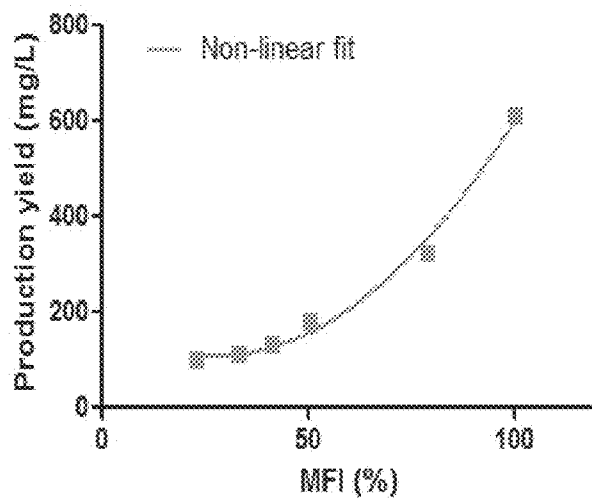


Figure 13

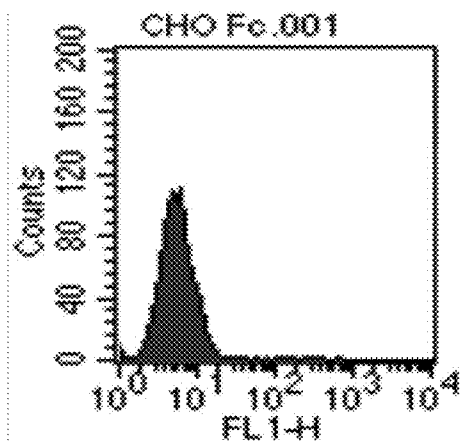
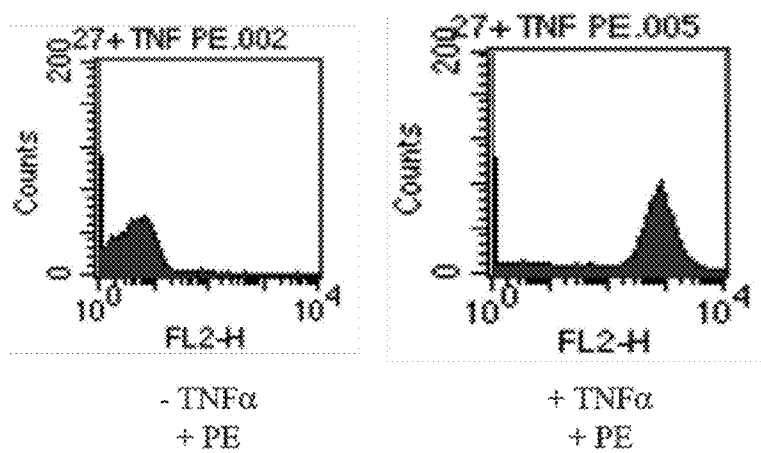


Figure 14





## NOVEL CELL LINE SCREENING METHOD

### CROSS-REFERENCE TO RELATED APPLICATIONS

**[0001]** This application claims the priority benefit of U.S. provisional application No. 61/732,156, filed Nov. 30, 2012, which is expressly incorporated by reference herein in its entirety.

### SEQUENCE LISTING

**[0002]** The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Nov. 27, 2013, is named 34166-00003\_SL.txt and is 32,799 bytes in size.

**[0003]** The present technology pertains to cell line development and protein production, and more specifically to a switch mechanism that converts cells that express a membrane-anchored reporter (MAR) into production cells that secrete a protein of interest (POI) into culture media.

### BACKGROUND

**[0004]** Recombinant therapeutic proteins are widely used to treat numerous human diseases from cancer to infertility. They include various blood-clotting factors, insulin, growth hormones, enzymes, Fc fusion proteins, monoclonal antibodies and other proteins (Scott C., *Bioprocess Int.* 10(6): S72-S78, 2012). Many recombinant therapeutic proteins are manufactured using mammalian host cells because of the need for correct folding and post-translational modification including glycosylation. Among them, therapeutic antibodies represent one of the largest sectors of protein therapeutics with a global market of approximately \$50 billion in 2011 for approximately 30 approved antibody therapeutics.

**[0005]** The predominant therapeutic antibodies come from antibody discovery programs that belong to four categories: chimeric antibodies, humanized antibodies, fully human antibodies from synthetic human antibody libraries selected with various display systems, and fully human antibodies from transgenic animals bearing human immunoglobulin genes (Chames P. et al, *Br J Pharmacol.* 157(2): 220-233, 2009). Chimeric antibodies containing human constant regions and non-human variable regions pose an immunogenicity risk in the human body and as a result have lost favor to humanized or fully human antibodies in terms of therapeutic applications. Humanized antibodies contain 90-95% human residues and 5-10% non-human residues that are essential for antigen interaction, whereas fully human antibodies contain 100% human residues. Both humanized and fully human antibodies have enjoyed great success in therapeutic applications to treat various diseases.

**[0006]** Development of a therapeutic antibody often takes 10-15 years including antibody discovery, engineering, production cell line development, manufacturing process development, and clinical studies. Among these tasks, antibody discovery may take 6-18 months and production cell line development may require an additional 6-10 months. One of the biggest problems with current antibody discovery methodologies is that they do not utilize the format of the final antibody product which is commonly a full-length human IgG. The selected antibodies are typically murine antibodies or fragments of human antibodies such as scFv or Fab, that require reformatting into the final IgG format before produc-

tion cell line development. Reformatting sometimes leads to unexpected problems in downstream process development, including loss of activity, low expression level, aggregation, insolubility, and/or instability. Therefore further antibody engineering and optimization may be required, resulting in loss of valuable time and increased cost.

**[0007]** Cell line development is a critical part of the process to obtain production cell lines for any therapeutic protein including antibodies. Production cell lines should be highly productive, stable, and have correct product quality attributes including biological activity, protein sequence homogeneity, glycosylation profile, charge variants, oxidation, deamination and low levels of aggregation. CHO cells are the most popular mammalian cells for production of therapeutic proteins. Other mammalian cells like NS0 or SP2/0 cells have also been used to produce biological therapeutics (Jayapal K R, et al., *Chemical Engineering Progress*, 103: 40-47, 2007; Li F, et al., *MAbs.* 2(5): 466-477, 2010). Conventional cell line development utilizes gene amplification systems by incorporating Dihydrofolate Reductase (DHFR) or Glutamine Synthetase (GS) as selection markers. Typically up to 1000 clones are screened in a cell line development program by limiting dilution cloning in 96-well tissue culture plates. Obtaining a highly productive cell line requires gene amplification by adding selection pressure after stable transfection using, for example, Methotrexate (MTX) in the DHFR system, or Methionine Sulphoximine (MSX) in the GS system. In most cases, productivity is often the only selection criteria until a very late stage in the process when only a handful of clones are assessed for the other quality attributes important for large scale manufacturing, resulting in increased project risk and complex issues regarding downstream development.

**[0008]** The process of selecting a cell population of interest for use as a recombinant protein production cell line may involve expression of a cell surface or intracellular reporter molecule. High level of expression of intracellular reporters such as GFP have been shown to be cytotoxic (Liu H S, et al., *Biochem Biophys Res Commun*, 260: 712-717, 1999; Wallace L M, et al., *Molecular Therapy Nucleic Acids.* 2, e86, 2013), however, the cytotoxicity of a reporter is minimized by cell surface display.

**[0009]** Display techniques have been developed for high-throughput screening of proteins, such as antibodies. Antibody display systems have been successfully applied to screen, select and characterize antibody fragments. These systems typically rely on phage display, *E. coli* display or yeast display. Each display system has its strengths and weaknesses, however, in general these systems lack post-translational modification functions or exhibit different post-translational modification functions from mammalian cells and tend to display small antibody fragments instead of full-length IgGs. Thus, characterization of the biological activities and further development of the isolated antibody fragments often requires conversion to whole immunoglobulins and expression in mammalian cells for proper folding and post-translational processing. This conversion process may produce antibodies with binding characteristics unlike those selected for in the initial screen.

**[0010]** There is a need for improved processes for selection of recombinant protein producing cell lines (such as antibody-producing cell lines), wherein the selection process facilitates rapid cell line selection based on quality attributes other than productivity. The present invention provides

improved compositions and methods for screening and selection of cell lines for recombinant protein production.

#### SUMMARY OF THE INVENTION

**[0011]** Additional features and advantages of the disclosure will be set forth in the description which follows, and in part will be obvious from the description, or can be learned by practice of the herein disclosed principles. The features and advantages of the disclosure can be realized and obtained by means of the disclosure and examples provided herein. These and other features of the invention will become more fully apparent from the following description and appended claims, or can be learned by the practice of the principles set forth herein.

**[0012]** The present invention relates to a switch mechanism that may turn off expression of a reporter (e.g., a cell surface or intracellular reporter) after selection of a subpopulation of cells providing for optimal expression of a POI. The reporter can be GFP or any other molecule detectable by FACS, MACS, or any other analytic method effective to detect the reporter. Expression of the reporter is functionally linked to expression of a POI such that the reporter is a surrogate for POI expression. The above-mentioned switch mechanism maybe used to turn cells displaying a cell surface membrane anchored reporter (MAR) or intracellular reporter into production cells secreting a POI. Disclosed are a series of molecular designs which incorporate sequences of MAR flanked by site-specific DNA recombinase recognition sequences (DRRS) inserted into an expression vector for a gene of interest (GOI). The reporter cassette could reside between the promoter and the GOI or downstream of the GOI following an internal ribosome entry site (IRES) or another promoter. In both cases, reporter expression will be first allowed to facilitate cell selection by FACS or MACS and then eliminated by transient expression or direct provision of an appropriate site-specific DNA recombinase to the cells in order to switch the cells to produce the POI without co-expression of the reporter.

**[0013]** Alternatively, the reporter cassette could reside in the middle of an intron sequence of the GOI to create alternative splicing leading to expression of the reporter. After transient expression or direct provision of an appropriate site-specific DNA recombinase protein, the reporter cassette is deleted from the intron enabling optimal expression and secretion of the POI without co-expression of the reporter.

#### BRIEF DESCRIPTION OF THE DRAWINGS

**[0014]** In order to describe the manner in which the above-recited and other advantages and features of the disclosure can be obtained, a more particular description of the principles briefly described above will be rendered by reference to specific embodiments thereof which are illustrated in the appended drawings. Understanding that these drawings depict only exemplary embodiments of the disclosure and are not therefore to be considered to be limiting of its scope, the principles herein are described and explained with additional specificity and detail through the use of the accompanying drawings.

**[0015]** FIGS. 1A-C are schematic drawings of exemplary MAR cassettes containing expression vectors and the switch mechanism that deletes the MAR. The MAR resides before

the GOI (in A), or after the GOI following an IRES or another promoter (in B), or in the middle of an intron of the GOI (in C).

**[0016]** FIGS. 2A-F are schematic drawings of exemplary molecular structures of a model GOI, including A) a wild-type genomic sequence with one intron and two exons; B) the exon 2 fused with a membrane association domain (MAD); C) insertion of Exon 2-MAD flanked by site specific DNA recombinase recognition sequences (DRRS) in the intron; D) insertion of MAD flanked by DRRS into the intron; E) insertion of Exon 2-MAD flanked by site specific DNA recombinase recognition sequences (DRRS) downstream of Exon 2 and F) insertion of MAD flanked by DRRS downstream of Exon 2.

**[0017]** FIGS. 3A and B are schematic drawings of two alternative RNA splicing events of the molecular design in FIG. 2C (3A), FIG. 2D (3B), FIG. 2E (3C) and FIG. 2F (3D).

**[0018]** FIG. 4A-D are schematic drawings of DNA recombination in the presence of an appropriate site specific DNA recombinase of the molecular design in FIG. 2C (4A), FIG. 2D (4B), FIG. 2E (4C) and FIG. 2F (4D).

**[0019]** FIGS. 5A-F are schematic drawings of exemplary antibody heavy chain genomic sequences. A) Wild-type heavy chain constant region, including four exons (CH1, Hinge, CH2, and CH3) and three introns (Intron 1-3); B) The heavy chain fused with a MAD; C) Insertion of CH3-MAD flanked by LoxP sequences into the Intron 3; D) Insertion of MAD flanked by LoxP sequences into the Intron 3; E) Insertion of CH3-MAD flanked by LoxP sequences downstream of CH3; and F) Insertion of MAD flanked by LoxP sequences downstream of CH3. Regions before CH2 are present but not shown in C)-F).

**[0020]** FIGS. 6A and B are schematic drawings of two alternative RNA splicing events of the molecular designs in FIG. 5C (6A) and FIG. 5D (6B). Regions before CH2 are not shown.

**[0021]** FIGS. 7A and B are schematic drawings of DNA recombination in the presence of Cre recombinase of the molecular designs in FIG. 5C (7A) and FIG. 5D (7B). Regions before CH2 are not shown.

**[0022]** FIGS. 8A and B are flow charts of an antibody cell line development process (8A) and an antibody library screening process (8B).

**[0023]** FIGS. 9A-C are plasmid maps of an antibody heavy chain expression vector (9A), an antibody light chain expression vector (9B) and an antibody heavy and light chain expression vector (9C).

**[0024]** FIG. 10A shows Rituxan levels in culture media 2 days after transfection of 293F cells with Rituxan expression vectors.

**[0025]** FIG. 10B shows FACS plots indicating cell surface Rituxan expression 2 days after transfection of 293F cells with Rituxan expression vectors.

**[0026]** FIG. 11A shows that membrane-anchored antibody expression was switched off by transient transfection of a Cre expression vector ("After Cre").

**[0027]** FIG. 11B shows that membrane-anchored antibody expression was switched off by treatment of cells with recombinant Cre ("After Cre").

**[0028]** FIG. 12A shows that cell surface antibody of a CHOS cell line that expresses both membrane-anchored Humira and secreted Humira via alternative splicing.

**[0029]** FIG. 12B shows that the membrane antibody expression correlates strongly with the secreted antibody lev-

els in cells that express both membrane-anchored Humira and secreted Humira via alternative splicing.

**[0030]** FIG. 13 shows lack of surface antibody on a Humira expressing cell line after switching off membrane anchorage.

**[0031]** FIG. 14 shows that a CHOS cell line expressing membrane-anchored Humira stained positively after binding with biotinylated TNF $\alpha$  and streptavidin Phycoerythrin conjugates.

#### DETAILED DESCRIPTION OF THE INVENTION

**[0032]** Provided herein are compositions, methods and systems for improved selection of production cells that secrete a protein of interest (POI) into culture media.

**[0033]** The invention is not limited to the specific compositions, devices, methodology, systems, kits or medical conditions described herein, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention.

**[0034]** The present invention concerns a switch mechanism that can be used to turn cells expressing a membrane-anchored reporter (MAR) or an intracellular reporter into production cells secreting a protein of interest (POI) into culture media, e.g., an antibody or any other protein. The MAR can be any molecule including a membrane-anchored POI, a membrane-anchored GFP, or any other membrane associated molecule which can be detected or selected using high throughput methodologies such as fluorescence-activated cell sorting (FACS) or magnetic-activated cell sorting (MACS), or any other analytic method effective to detect expression of the reporter molecule. The method allows for initial screening or selection of desired cells using methodologies such as FACS or MACS by detecting a reporter molecule, followed by application of a molecular switch that transforms the cells such that they secrete the POI without co-expression of the reporter molecule for production purposes.

**[0035]** Various embodiments of the disclosure are discussed in detail below. While specific embodiments are discussed, it should be understood that this is done for illustration purposes only. A person skilled in the relevant art will recognize that other configurations may be used without departing from the spirit and scope of the disclosure.

#### DEFINITIONS

**[0036]** It must be noted that as used herein and in the appended claims, the singular forms “a”, “and”, and “the” include plural references unless the context clearly dictates otherwise.

**[0037]** Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

**[0038]** The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such a disclosure by virtue of prior invention.

**[0039]** As used herein, the term “membrane-anchored reporter” or “MAR” is used with reference to any membrane molecule or a non-membrane molecule fused with a membrane association domain (MAD).

**[0040]** As used herein, the term “membrane association domain” or “MAD” is used with reference to a protein domain associated with a membrane, which could be a GPI anchor signal sequence (GASS), a transmembrane domain, or any molecule that binds to a cell membrane or a membrane protein e.g., an Ab, GFP, and the like. In one aspect of the invention a host cell is characterized by the expression of a cell surface membrane anchored reporter fused to a POI wherein expression of the reporter is detected by FACS, MACS or any technique that can detect cell surface expression of a POI. Expression of the cell surface membrane anchored reporter fused to a POI is detected following transfection with a DNA construct such as shown in FIGS. 3A-D, 6A and B.

**[0041]** As used herein, the term “protein of interest” or “POI” is used with reference to a protein having desired characteristics that may be selected using the method of the invention. A “protein of interest” (POI) includes full length proteins, polypeptides, and fragments thereof, peptides, all of which can be expressed in the selected host cell. Exemplary POIs are antibodies, enzymes, cytokines, adhesion molecules, receptors, derivatives and any other polypeptides that can be expressed using the methods described herein. In another aspect of the invention, the protein of interest is recovered from the culture medium as a secreted polypeptide. In general, the protein of interest is produced in the culture media at a level of at least 100 mg/L, at least 150 mg/L, at least 200 mg/L, at least 300 mg/L, at least 500 mg/L, at least, or at least 1000 mg/L, e.g., 100-150 mg/L, 150-200 mg/L, 200-250 mg/L, 250-300 mg/L, 300-500 mg/L, or 500-1000 mg/L. In some cases, the POI, e.g., an enzyme, may be biologically active a low concentration. In such cases, production at a level below 100 mg/L in the culture media will satisfy commercial production requirements. In general, methods teaching a skilled person how to purify a protein expressed by host cells are well known in the art.

**[0042]** As used herein, the term “gene of interest” or “GOP” is used with reference to a polynucleotide sequence of any length that encodes a “protein of interest” (POI). The selected sequence can be full length or a truncated gene, a fusion or tagged gene, and can be a cDNA, a genomic DNA, or a DNA fragment, preferably, a cDNA. It can be the native sequence, i.e. naturally occurring form(s), or can be mutated or otherwise modified as desired.

**[0043]** The term “host cells” or “expression host cells” as used herein refers to any cell line that will effectively produce a POI with correct folding and post-translational modification including glycosylation as required for biological activity. Exemplary host cells include Chinese Hamster Ovary (CHO) cells, e.g., CHOS (Invitrogen), NSO, Sp2/0, CHO derived mutant cell or derivatives or progenies of any of such cells. Other mammalian cells, including but not limited to human, mice, rat, monkey, and rodent cells, and eukaryotic cells, including but not limited to yeast, insect, plant and avian cells, can also be used in the meaning of this invention, as appropriate for the production of a particular POI.

**[0044]** As used herein, the term “magnetic-activated cell sorting” or “MACS” is used with reference to a method for separation of various cell populations depending on their surface antigens (CD molecules). The term MACS is a registered trademark of Miltenyi Biotec and the method is marketed by the company as MACS Technology.

**[0045]** As used herein, the term “DNA recombinase recognition sequence” or “DRRS” is used with reference to a

sequence that facilitates the rearrangement of DNA segment by the activity of a site-specific recombinase which recognizes and binds to short DNA sequences resulting in cleavage of the DNA backbone such that two DNA sequences are exchanged, followed by rejoining of the DNA strands.

**[0046]** As used herein, the term “GPI anchored signal sequence” or “GASS” is used with reference to a glycolipid that can be attached to the C-terminus of a protein during posttranslational modification. It is composed of a phosphatidylinositol group linked through a carbohydrate-containing linker (glucosamine and mannose glycosidically bound to the inositol residue) to the C-terminal amino acid of a mature protein. The hydrophobic phosphatidyl-inositol group anchors the protein to the cell membrane.

**[0047]** The term “productivity” or “specific productivity” describes the quantity of a specific protein (e.g., a POI) which is produced by a defined number of cells within a defined time. One exemplary way to measure “productivity” is to seed cells into fresh culture medium at defined densities. After a defined time, e.g. after 24, 48 or 72 hours, a sample of the cell culture fluid is taken and subjected to ELISA measurement to determine the titer of the protein of interest. The productivity can be reported as mg/L of culture media. In the context of industrial manufacturing, the specific productivity is usually expressed as amount of protein in picogram produced per cell and day (“pg/cell/day”).

**[0048]** The term “biological activity” describes and quantifies the biological functions of the protein within the cell or in in vitro assays.

#### DESCRIPTION

**[0049]** The present invention relates to a series of molecular designs incorporating sequences of a membrane-anchored reporter (MAR) or an intracellular reporter flanked by site specific DNA recombinase recognition sequences (DRRS) inserted into an expression vector for the GOI. The reporter cassette could reside between the promoter and the GOI (FIG. 1A), or after the GOI following an IRES or another promoter (FIG. 1B), or in the middle of an intron of the GOI (FIG. 1C). The reporter is first expressed allowing cell selection e.g., by FACS or MACS, and then deleted by transient expression or direct provision of an appropriate site-specific DNA recombinase to switch the cells to secretion of the POI without co-expression of the reporter. The MAR needs to be detected or selected using high throughput methodologies such as FACS or MACS, and could be any membrane protein or non-membrane protein fused with a membrane association domain (MAD), which could be a GPI anchor signal sequence (GASS), or a transmembrane domain, or any peptide that binds to a cell surface protein. For example, the MAR could be membrane-anchored GFP or membrane-anchored POI. One of the advantages of using a membrane anchored reporter protein instead of an intracellular reporter protein is to avoid any potential cellular toxicity after accumulation of high concentrations of the reporter protein. SEQ ID NO: 1 shows the nucleotide sequence of GFP fused to the IL2 signal peptide at the N-terminus and DAF GASS at the C-terminus. Any GFP variants or other fluorescence proteins, functional signal peptides or membrane association domains can be used here.

**[0050]** After being transfected with reporter-containing expression vectors, the host cells such as CHO cells can be allowed to grow in the presence of appropriate antibiotics for selection of stable cells with the expression vector integrated

into the chromosome. Alternatively, the transfected cells can be selected directly for the reporter expression by FACS or MACS for 1-2 weeks until the reporter expression is stable. The advantage of not using antibiotics is for better health of the cells and potentially less gene-silencing of the expression cassette (Kaufman W L, et al., *Nucleic Acids Res.*, 36(17), e111, 2008). Desired cells with high expression levels of the reporter or other properties (such as stability, protein sequence homogeneity, proper glycosylation profile, proper charge variants, and acceptable aggregate levels), can then be selected with FACS or MACS or another analytic technique. Subsequently the reporter cassette can be deleted by providing an appropriate site-specific DNA recombinase to switch the selected cells into production cells that produce the POI. The DNA recombinase can be supplied to the cells by transient transfection with an expression vector, or by direct provision of the DNA recombinase protein to the culture media, or by any other means.

**[0051]** The present invention also provides a series of molecular designs to modify the intron sequence of a GOI. FIG. 2A shows the genomic sequence of a model secreted GOI containing two exons and an intron. It would be anchored on cell surface if fused with a MAD, which could be a GASS, or a transmembrane domain, or any peptide that binds to a cell surface protein (FIG. 2B). In order to create an alternative splicing site, the DNA sequence of GOI Exon 2 fused with MAD flanked by DRRS can be inserted into the Intron (FIG. 2C), MAD flanked by DRRS can be inserted into the Intron (FIG. 2D), the DNA sequence of GOI Exon 2 fused with MAD flanked by DRRS can be inserted downstream of Exon 2 (FIG. 2E), or MAD flanked by DRRS can be inserted downstream of Exon 2 (FIG. 2F).

**[0052]** The mRNA may contain an unaltered splicing donor or any functional splicing donor for the Intron and two splicing acceptors shown in FIG. 3A. The two splicing acceptors may be identical to the splicing acceptor in the wild type GOI mRNA or any functional splicing acceptor. This exemplary alternative splicing would lead to membrane-anchored POI using the acceptor 1 or secreted POI using the acceptor 2 (FIG. 3A). If only secreted POI is desired, appropriate site-specific DNA recombinase recognizing the DRRS can be transiently expressed in the cell and the sequence between the DRRS deleted as shown in FIG. 4A.

**[0053]** Another way to manipulate the Intron is to insert a MAD sequence flanked by DRRS directly (FIG. 2D). Alternative splicing shown in FIG. 3B would lead to either membrane-anchored POI with Exon 2 deleted or secreted POI. When an appropriate site-specific DNA recombinase is supplied, the sequence between DRRS is deleted and all the expressed POI is secreted (FIG. 4B).

**[0054]** Yet another way to manipulate the Intron is to insert Exon-2-MAD flanked by site specific DNA recombinase recognition sequences (DRRS) downstream of Exon 2 (FIG. 2E). Alternative splicing shown in FIG. 3C would lead to either membrane-anchored POI with Exon-1 and Exon-2 fused to MAD, or secreted POI with Exon1 and Exon2. When an appropriate site-specific DNA recombinase is supplied, the sequence between DRRS is deleted and all the expressed POI is secreted (FIG. 4C).

**[0055]** A further way to manipulate the Intron is to insert a MAD sequence flanked by DRRS downstream of Exon 2 (FIG. 2F). Alternative splicing shown in FIG. 3D would lead to either membrane-anchored POI with Exon 2 deleted, or secreted POI with Exon1 and Exon2. When an appropriate

site-specific DNA recombinase is supplied, the MAD sequence between DRRS is deleted and all the expressed POI is secreted (FIG. 4D).

**[0056]** FIGS. 5-7 describe how the above-mentioned intron modifying designs are applied to manipulate a human immunoglobulin gamma genomic sequence. The genomic structure of the wild-type human antibody IgG1 heavy chain constant region contains four exons and three introns as shown in FIG. 5A. The DNA sequence is shown in SEQ ID NO: 3. FIG. 5B shows a membrane-anchored antibody heavy chain prepared by fusing with a MAD. It has been reported that membrane-anchored antibodies can be constructed by fusing a GASS or a transmembrane domain (TM) at the C-terminus of the heavy chain (Zhou C, et al., *MAbs*, 2:508-518, 2010; Bowers P M, et al. *Proc Natl Acad Sci USA*, 108(51):20455-20460, 2011; Li. F, et al., *Appl Microbiol Biotechnol.*, 96(5):1233-41 2012). The GASS of human DAF is shown in SEQ ID NO: 4 (nucleotide) and SEQ ID NO: 5 (amino acid), respectively. Any other GASS or TM or any peptide that binds to a cell surface protein can also be used for membrane anchoring. In order to create an alternative splicing site, the DNA sequence for CH3-MAD flanked by DRRS can be inserted into Intron 3 (FIG. 5C), or into the other two introns; the DNA sequence for MAD flanked by DRRS can be inserted into Intron 3 (FIG. 5D), the DNA sequence for CH3-MAD flanked by LoxP sequences may be inserted downstream of Exon 3 (FIG. 5E) or the DNA sequence for MAD flanked by LoxP sequences may be inserted downstream of Exon 3 (FIG. 5F).

**[0057]** One commonly used recognition sequence for DNA recombinase Cre is LoxP the sequence of which is shown in SEQ ID NO: 8. Similarly, any other LoxP variant sequences or recognition sequences for other site specific DNA recombinases can be used here, for example, an FRT sequence (DRRS for FLP), or an attB or attP (DRRS for  $\phi$ C31 integrase (Wang Y, et al., *Plant Cell Rep.*; 30(3):267-85, 2011) or a specific DNA recognition sequence for any other tyrosine recombinase or serine recombinase. The mRNA may have an unaltered splicing donor for the Intron 3 and two identical splicing acceptors as shown in FIG. 6A.

**[0058]** The alternative splicing would lead to membrane-anchored antibody using the acceptor 1 or secreted antibody using the acceptor 2. If only secreted antibody is desired, DNA recombinase Cre can be transiently expressed in the cell or supplied in the culture media and the sequence between the two LoxP sites will be deleted as shown in FIG. 7A.

**[0059]** For example, if one were to manipulate Intron 3 is to insert a DNA sequence for MAD flanked by LoxP sites directly (FIG. 5D), alternative splicing shown in FIG. 6B would give membrane-anchored antibody with CH3 deleted or secreted antibody. When DNA recombinase Cre is expressed, the sequence between LoxP sites is deleted and all the expressed antibody is secreted (FIG. 7B). Similarly, the MAD flanked by LoxP sites can also be inserted into the other two introns to create alternative splicing.

**[0060]** FIG. 8A illustrates an exemplary cell line development process utilizing the MAR cassette and the switching mechanism. Expression vector of the GOI is modified with the MAR cassette as shown in FIG. 1. It could carry a selection marker gene. If the POI contains more than one subunit, they may be cloned into the same vector or into separate expression vectors. The expression vector or vectors are transfected into desired cells. After 1-2 weeks allowing stable integration into the chromosome, with or without antibiotic selection, the cells are analyzed and selected for high expres-

sion of the MAR by any high throughput cell selection or enrichment methodology, such as FACS or MACS. In one approach, the selected cells are transfected transiently with an expression vector for an appropriate DNA recombinase to induce site-specific DNA recombination. Deletion of the MAR cassette results in cells that produce the POI. Following single cell sorting or limiting dilution cloning into 96-well plates, clones are screened for the POI expression levels in the culture media and/or other desired product quality attributes. Selected clones are expanded and cryopreserved.

**[0061]** In one application of the invention, an human immunoglobulin gamma expression vector comprising a membrane association domain (MAD) flanked by site specific DNA recombinase recognition sequences (DRRS) can be inserted into the intron region between CH<sub>2</sub> and CH<sub>3</sub> sequences. The MAD can be a GPI anchored signal sequence (GASS) or a transmembrane domain or a peptide that binds to any cell surface protein. Alternative splicing results in a portion of expressed antibodies to be membrane-anchored and thus readily detected by fluorescence-labeled antigen or secondary antibody. After selection of cells with high expression levels of membrane-anchored antibodies by FACS, the cells may then be switched into production cells secreting the antibody into culture media by transient expression of an appropriate site-specific DNA recombinase in order to delete the sequences responsible for membrane association in the intron. The switch mechanism can be used for cell line development with greatly reduced time and cost, and can be used for production of antibody or any other recombinant protein.

**[0062]** Library display techniques have been developed for high-throughput screening of proteins having desired characteristics. WO 2010/022961 discloses a method for generating or selecting a eukaryotic host cell expressing a desired level of a polypeptide of interest from a population of host cells by use of a fusion polypeptide including an immunoglobulin transmembrane anchor such that the fusion polypeptide is being displayed on the surface of the host cell.

**[0063]** Bowers P M, et al. (*Proc Natl Acad Sci USA*. 108 (51):20455-60, 2011) disclose a method for the isolation of human antibodies using a library screening method based on initial selection of well-expressed human IgM antibodies with high binding affinity by FACS, followed by activation-induced cytidine deaminase (AID) directed in vitro somatic hypermutation (SHM) in vitro and selection of high-affinity antibodies using the same library screening method.

**[0064]** DuBridge et al. U.S. Pat. No. 7,947,495, disclose dual display vector compositions and methods which provide for expression of secreted and membrane-bound forms of an immunoglobulin based on splice sites and recombinase recognition sites, allowing for simultaneous expression of transcripts for a membrane-bound immunoglobulin and a secreted form of the same immunoglobulin in a single host cell.

**[0065]** Beerli, R., et al., (*PNAS*, vol. 105 (38), 14336-14341, 2008) describe a technology for the rapid isolation of fully human mAbs by isolation of antigen-specific B cells from human peripheral blood mononuclear cells (PBMC) and generation of recombinant, antigen-specific single-chain Fv (scFv) libraries which are screened by mammalian cell surface display using a Sindbis virus expression system, which is followed by isolation of fully human high-affinity antibodies following a single round of selection. Another display system used to screen, select and characterize antibody fragments based on display of full-length functional antibodies on the

surface of mammalian cells relies on recombinase-mediated DNA integration coupled with high throughput FACS screening for selection of antibodies with very high antigen binding affinities is disclosed by Zhou et al. (mAbs 2:5, 508-518; 2010).

**[0066]** Mammalian cell based immunoglobulin libraries that rely on use of “removable-tether display vectors,” or “transmembrane display vectors,” which can be used for the expression of cell surface-bound immunoglobulins for affinity-based screening and the expression of secreted immunoglobulin are disclosed by Akamatsu et al., U.S. Pat. No. 8,163,546. In these “removable-tether display vectors”, the polynucleotide encoding the cell surface tether domain is flanked by a first and a second restriction endonuclease site.

**[0067]** The invention disclosed herein provides improved libraries and screening methods for selecting a POI with desired characteristics.

**[0068]** FIG. 8B illustrates an exemplary antibody library screening process utilizing alternative splicing and the switching mechanism. In one exemplary approach, a library of VH sequences can be cloned into an expression vector with modified Intron 3 as shown in FIG. 5C or 5D. A library of light chain sequences may be cloned into the same expression vector or into a separate vector. Expression of the antibody library vectors will result in an expression library of membrane-anchored antibodies. After transfection into CHO cells or other expression host cells, cells expressing antigen binding antibodies may be sorted or selected by FACS or MACS. Multiple rounds of sorting or selection may be performed under different stringent conditions to isolate production cells for antibodies with the best affinity for the antigen. The antibody sequences can be obtained from the selected cells by PCR or RT-PCR. The selected cells may be turned into production cells by expression of an appropriate site specific DNA recombinase to delete the MAD sequence. Similar designs may be applied to any engineered libraries of antibody or any other proteins. See, Example 8.

## EXAMPLES

### Example 1

#### Expression of Rituxan from Expression Vector Containing a LoxP Site in the 3<sup>rd</sup> Intron of the Heavy Chain Genomic Sequence

**[0069]** The Rituxan heavy chain variable sequence (VH) was gene synthesized and cloned into a mammalian expression vector containing the human IgG1 heavy chain constant region genomic sequence between restriction sites Xba I and Nhe I, to make vector LB0-H. The Rituxan VH sequence including signal peptide is shown in SEQ ID NO: 9. Expression of the antibody heavy chain was under the control of an EF1 $\alpha$  promoter. The vector carries a Puromycin resistance gene for stable cell selection and an Ampicillin resistance gene for *E. coli* propagation. The plasmid map is shown in FIG. 9A.

**[0070]** The Rituxan light chain cDNA was gene synthesized and cloned into a separate mammalian expression vector between restriction sites Xba I and BamH I to make vector LB0-K. The sequence of the light chain is shown in SEQ ID NO: 11. Expression of the antibody light chain was under the control of an EF1 $\alpha$  promoter. It carries a Neomycin resistance

gene for stable cell selection and an Ampicillin resistance gene for *E. coli* propagation. The plasmid map is shown in FIG. 9B.

**[0071]** A LoxP site was inserted into the middle of the 3<sup>rd</sup> intron of Rituxan gamma genomic sequence in LB0-H by Bridge PCR to make vector LB 1. The sequence of the heavy chain constant region is shown in SEQ ID NO: 13.

**[0072]** To express Rituxan, 293F cells (Invitrogen Inc.) were co-transfected with LB0-H or LB1, together with LB0-K. Transfection conditions were optimized with Freestyle Max transfection reagent (Invitrogen) and a GFP expression vector. 30  $\mu$ g of DNA and 37.5  $\mu$ l of Freestyle Max were used to transfect 30 ml of cells ( $1 \times 10^6$  cells/ml). The cells were typically diluted 3 times the next day and subjected to flow cytometric analysis for GFP expression after one more day of culturing. Transfection efficiencies were determined to be ~80% for 293F cells under these conditions. To assess Rituxan expression, antibody levels in media were determined by dilution ELISA in which Rituxan was captured with goat anti-human IgG Fc (100 ng/well, Bethyl) and detected with the goat anti-human Kappa antibody HRP conjugates (1:10, 000 dilution, Bethyl).

**[0073]** Human IgG antibody (2  $\mu$ g/ml of IgG, Sigma) was used as the standard for IgG quantitation. The expression levels are shown in FIG. 10A. LB1-transfected cells produced a similar amount of antibody as the wild-type control LB0-H, suggesting that the LoxP sequence inserted in the middle of the intron between CH2 and CH3 did not affect antibody expression levels. The heavy chain constant regions in both transfected cells were amplified by RT-PCR and sequenced. The RNA splicing was found to be identical with or without a LoxP site inside of the gamma chain intron.

### Example 2

#### Expression of Rituxan Anchored on Cell Surface

**[0074]** The human IgG1 CH3 sequence fused with the DAF GPI anchor signal sequence (SEQ ID NO: 4) or the PDGFR TM domain sequence (SEQ ID NO: 6) followed by LoxP and intron 3 sequences were synthesized and inserted into the 3<sup>rd</sup> intron in LB1 to make vector LB3 or LB4, respectively, as shown in FIG. 5C. The sequences of the heavy chain constant region of LB3 and LB4 are shown in SEQ ID NO: 14 and SEQ ID NO: 15, respectively. The light chain expression cassette in LB0-K was digested with restriction enzymes EcoR V and Asc I. The DNA fragment of 2625 bp was then cloned into LB4 between EcoR V and Asc I to make Rituxan expression vector LB37. The plasmid map is shown in FIG. 9C. To assess Rituxan expression, 293F cells were co-transfected with heavy chain vectors LB3, or LB4, together with the light chain vector LB0-K using Freestyle Max transfection reagent.

**[0075]** The antibody titers in media were determined by dilution ELISA in which Rituxan was captured with goat anti-human IgG Fc (100 ng/well, Bethyl) and detected with the goat anti-human Kappa antibody HRP conjugates (1:10, 000 dilution, Bethyl). Human IgG antibody (2  $\mu$ g/ml of IgG, Sigma) was used as the standard for IgG quantitation. The expression levels are shown in FIG. 10A. Vectors employing the modified intron demonstrate robust expression of Rituxan ranging from 4-10  $\mu$ g/ml in culture media after 2 days when cell densities are typically about  $1 \times 10^6$  cells/ml. LB1-transfected cells produced a similar amount of antibody as the wild-type control LB0-H, suggesting that the LoxP sequence

inserted in the middle of the intron between CH2 and CH3 did not affect antibody expression levels. LB3 secreted 2-3 times more antibody into the media than LB4, consistent with the fact that GPI-linked membrane anchorage is not 100%. This result has been reproduced in 3 independent experiments.

**[0076]** The transfected 293F cells were also labeled with goat anti-human Fc antibody FITC conjugate (1:1,000 dilution, Bethyl) and subjected to flow cytometric analysis. 293F cells transfected with the wild-type CH3 exon vector (LB0-H, FIG. 10B.a) or LoxP modified CH3 exon vector (LB1, FIG. 10B.b) did not show cell surface antibody expression, whereas 293F cells transfected with alternatively spliced CH3-GASS vector (LB3, FIG. 10B.c) or CH3-TM vector (LB4, FIG. 10B.d) exhibited cell surface antibodies in 20-30% of the cells (Table 1).

TABLE 1

| Cell Surface Antibody Expression for Cells Transfected with Various Constructs. |        |
|---------------------------------------------------------------------------------|--------|
| Transfection                                                                    | M1 (%) |
| LB0-H + LB0-K                                                                   | 1.8    |
| LB1 + LB0-K                                                                     | 1.1    |
| LB3 + LB0-K                                                                     | 27.9   |
| LB4 + LB0-K                                                                     | 20.1   |
| LB9 + LB0-K                                                                     | 8.3    |
| LB10 + LB0-K                                                                    | 16.5   |

## Example 3

## Expression of CH3 Deleted Rituxan Anchored on Cell Surface

**[0077]** The DAF GPI anchor signal sequence or the PDGFR TM domain sequence followed by LoxP and intron3 sequences were synthesized and inserted into the 3<sup>rd</sup> intron in LB 1 to make vector LB9 or LB 10, respectively, as shown in Figure D. The sequences of the heavy chain constant region of LB9 and LB10 are shown in SEQ ID NO: 16 and SEQ ID NO: 17, respectively.

**[0078]** 293F cells were co-transfected with LB9 or LB 10, together with LB0-K using Freestyle Max transfection reagent. After 2 days the antibody levels in the media were assayed by ELISA similarly as described in Example 1. LB9-transfected cells secreted more antibodies into media than LB10-transfected cells (FIG. 10A), consistent with the result described in Example 2. The transfected 293F cells were also labeled with goat anti-human Fc antibody FITC conjugate (1:1,000 dilution, Bethyl) and subjected to flow cytometric analysis. 293F cells transfected with alternatively spliced vectors LB3 (FIG. 10B.e) or LB4 (FIG. 10B.f) exhibited cell surface expression of antibody in 8-20% of the cells (Table 1).

## Example 4

## Expression of Membrane-Anchored GFP Upstream of the Rituxan Heavy Chain

**[0079]** The membrane-anchored GFP (SEQ ID NO: 1) carrying a Kosak consensus sequence was flanked by two LoxP sites, and inserted between the EF1 $\alpha$  promoter and the Rituxan gamma sequence in the vector LB0-H to make vector LB11, as described in FIG. 1A. The sequence between the 2 LoxP sites was deleted in LB 11 and only one LoxP site remained to make vector LB11-LoxP. 293F cells were co-

transfected with LB0-H, LB11, or LB11-LoxP, together with LB0-K using Freestyle Max transfection reagent. After 2 days, antibody levels were assayed by ELISA as described in Example 1. LB11-transfected cells produced less than 10% of relative to LB0-H-transfected cells (FIG. 10A), suggesting that the presence of the GFP cassette upstream of the Rituxan heavy chain gene greatly diminished expression of Rituxan. After removal of the GFP cassette, LB11-LoxP produced Rituxan at a similar level to LB0-H (FIG. 10A). Expression of GFP in LB11-transfected cells was confirmed by flow cytometric analysis.

## Example 5

## Expression of Membrane-Anchored GFP Downstream of the Rituxan Heavy Chain

**[0080]** An IRES sequence (SEQ ID NO: 18) was fused with the membrane-anchored GFP (SEQ ID NO: 1) carrying a Kosak consensus sequence. A LoxP site was then added at both N- and C-terminals. The whole sequence was inserted downstream of the Rituxan gamma stop codon and before the poly A signal in the vector LB0-H to make vector LB14, as described in FIG. 1B. 293F cells were co-transfected with LB14 and LB0-K using Freestyle Max transfection reagent. After 2 days, the antibody level in the media was assayed by ELISA as described in Example 1, and was shown in FIG. 10A. Expression of GFP in LB11-transfected cells was confirmed by flow cytometric analysis.

## Example 6

## Switching Off the Membrane-Anchored Antibody by Providing Cre

**[0081]** A Cre Expression Vector LB30 Was Constructed. The Cre cDNA Was Human Codon optimized and fused with a peptide of MPKKKRRK (SEQ ID NO: 19) at the N-terminus for nuclear localization. Expression of Cre was driven by a human EF1 $\alpha$  promoter.

**[0082]** The 293F cells were transfected with LB37 linearized with restriction enzyme Asc I using Freestyle Max transfection reagent, and cultured in the presence of 1  $\mu$ g/ml of Puromycin and 400  $\mu$ g/ml of G418. After selection for approximately 2 weeks, the stable pool was transiently transfected with the Cre expression vector LB30. After one more week of culture, the cells were labeled with goat anti-human Fc antibody FITC conjugate (1:1,000 dilution, Bethyl) and subjected to flow cytometric analysis to assess cell surface Rituxan expression. Most of the cells lost membrane-anchored antibody after Cre transfection as shown in FIG. 11A ("After Cre").

**[0083]** Switching off the membrane-anchored antibody was also achieved by providing recombinant Cre in the cell culture. A cell line expressing membrane-anchored antibody cloned from the stable pool described above was treated with 1  $\mu$ M of recombinant Cre fused with TAT-NLS for nuclear localization (Excellgen, Inc.) for 2 hours. After one additional week of culture, the cells were assessed for cell surface antibody expression, as described above. Most of the cells lost membrane-anchored antibody as shown in FIG. 11B ("After Cre").

## Example 7

## Screening of Highly Productive Humira Production Cell Lines

**[0084]** The variable sequence of Humira light chain (SEQ ID NO: 20) was gene synthesized and cloned into LB0-K between restriction sites Xba I and BsiW I to make vector LB42. The variable sequence of Humira heavy chain (SEQ ID NO: 22) was gene synthesized and cloned into LB4 between restriction sites XbaI and Nhe I to make vector LB25. The light chain expression cassette in LB42 was digested with restriction enzymes EcoR V and Asc I. the DNA fragment of 2641 bp was then cloned into LB25 between EcoR V and Asc I to make Humira expression vector LB29.

**[0085]** CHOS cells (Invitrogen, Inc.) were cultured in Freestyle CHO media (Invitrogen, Inc.).  $1 \times 10^8$  CHOS cells were transfected with LB29 linearized with restriction enzyme Asc I using Freestyle Max transfection reagent, and then selected with 10 ug/ml of Puromycin for 2 weeks.  $1 \times 10^7$  stable cells were labeled with goat anti-human Fc antibody FITC conjugate (1:1,000 dilution, Bethyl) and subjected to FACS sorting. The 0.01% of the cells with the highest expression of cell surface antibodies were sorted into five 96-well plates. Approximately 100 colonies grew out after 2-3 weeks. The culture media was screened for expression of Humira by ELISA as described in Example 1. The 24 highest expressing clones were picked, expanded, and cryopreserved. Six clones with different levels of antibody expression were picked for cell surface antibody assessment. They were labeled with goat anti-human Fc antibody FITC conjugate (1:1,000 dilution, Bethyl) and subjected to flow cytometric analysis to confirm membrane-anchored antibody expression (FIG. 12A). They were also subjected to 30 ml of shaking culture. The antibody production in the culture media was assessed by ELISA as described in Example 1 after 7-day non-fed batch culture. Higher membrane antibody expression was found to be strongly correlated with increased, secreted antibody production (FIG. 12B). The 0.01% of stable cells transfected with linearized LB29 having the highest expression of cell surface antibodies was also sorted into a pool. After culturing for a week, the selected pool was transiently transfected with the Cre expression vector described in Example 6 with Neon Transfection System (Invitrogen, Inc.). After one more week of culturing, the cells were cloned into ten 96-well plates by limiting dilution. Approximately 200 colonies grew out after 2-3 weeks. The culture media was screened for expression of

Humira by ELISA as described in Example 1. The 24 clones having the highest level of antibody in the media were picked and expanded to a 24-well plate. After 3 days of culturing, the culture media was screened again for expression of Humira. The 12 clones having the highest level of antibody in the media were picked, expanded, and cryopreserved. The cells were confirmed to lack of membrane-anchored antibody (FIG. 13A). The antibody production in culture media was assessed after 7-day non-fed batch culture in a 30 ml of shaking culture. Antibody yields of the 5 clones having the highest level of antibody in the media are shown in Table 2.

TABLE 2

| Humira Antibody Production In Culture Media. |                              |              |
|----------------------------------------------|------------------------------|--------------|
| Clone                                        | Peak cell density (cells/ml) | Yield (mg/L) |
| 61.7B11                                      | $4.1 \times 10^6$            | 282          |
| 61.13C9                                      | $4.8 \times 10^6$            | 320          |
| 61.14E8                                      | $4.9 \times 10^6$            | 154          |
| 61.14F6                                      | $5.3 \times 10^6$            | 390          |
| 61.15G6                                      | $5.2 \times 10^6$            | 752          |

## Example 8

## A Model Screening of Antibody Library

**[0086]** One cell line selected in Example 7 and designated #27 expresses membrane-anchored Humira. Cells from cell line #27 were treated with  $1 \mu\text{g/ml}$  of biotinylated human TNF $\alpha$  (ACRO Biosystems, Inc.) for 30 min. After washing once with PBS, the cells were labeled with streptavidin Phycoerythrin conjugate (VectorLabs, Inc.) for 30 min. After washing twice with PBS, the cells were subjected to flow cytometric analysis and exhibited positive binding of TNF $\alpha$  on cell surface Humira (FIG. 14). The cell line #27 was spiked at a ratio of 1:1000 into a stable pool of CHOS cells transfected with Rituxan expression vector LB37. After binding with biotinylated TNF $\alpha$  and then streptavidin Phycoerythrin conjugates, the cells were subjected to FACS sorting. 1000 positive cells were sorted into a pool. After culturing for 2 weeks, the antibody sequence in the FACS positive cells was amplified by RT-PCR and confirmed to be the Humira antibody sequence.

## SEQUENCE LISTING

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<210> SEQ ID NO 1

<211> LENGTH: 906

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

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-continued

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<400> SEQUENCE: 2

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Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 35          40          45
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 50          55          60
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 65          70          75          80
Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 85          90          95
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
100         105         110
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
115         120         125
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
130         135         140
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
145         150         155         160
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
165         170         175
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
180         185         190
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile

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| 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asp | Gly | Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ala | Leu | Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Glu | Phe | Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Tyr | Lys | Ser | Gly | His | Glu | Thr | Thr | Pro | Asn | Lys | Gly | Ser | Gly | Thr | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ser | Gly | Thr | Thr | Arg | Leu | Leu | Ser | Gly | His | Thr | Cys | Phe | Thr | Leu | Thr |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Leu | Leu | Gly | Thr | Leu | Val | Thr | Met | Gly | Leu | Leu | Thr |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |

&lt;210&gt; SEQ ID NO 3

&lt;211&gt; LENGTH: 1596

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 3

```

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc   60
acagcggccc tgggctgect ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg   120
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtccctcagga   180
ctctactccc tcagcagcgt ggtgaccgtg cctccagca gcttgggcac ccagacctac   240
atctgaacg tgaatcacia gcccagcaac accaagggtg acaagaaagt tggtagagag   300
ccagcacagg gagggagggt gtctgctgga agccaggctc agcgcctctg cctggacgca   360
tcccggctat gcagccccag tccagggcag caaggcaggc cccgtctgcc tcttcaccgc   420
gaggcctctg cccgccccac tcatgctcag ggagagggtc ttctggettt tccccaggc   480
tctgggcagg cacaggctag gtgcccctaa cccaggccct gcacacaaag gggcagggtg   540
tgggctcaga cctgccaaaga gccatcccg ggaggacct gccctgacc taagcccacc   600
ccaaaggcca aactctccac tccctcagct cggcacactt ctctcctccc agattccagt   660
aactcccaat cttctctctg cagagcccaa atcttgtgac aaaactcaca catgcccacc   720
gtgccagggt aagccagccc aggcctcgcc ctccagctca aggcgggaca ggtgccctag   780
agtagcctgc atccagggac aggccccagc cgggtgctga cacgtccaacc tccatctctt   840
cctcagcacc tgaactcctg gggggaccgt cagtcttctt cttcccccca aaaccaagg   900
acaccctcat gatctccccg acccctgagg tcacatgctg ggtggtggac gtgagccacg   960
aagaccctga ggtcaagttc aactggtagc tggacggcgt ggagggtgcat aatgccaaaga  1020
caaagccgcy ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc  1080
tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc  1140
cagcccccat cgagaaaaacc atctccaaag ccaaagggtg gaccctgtgg gtgcyagggc  1200
cacatggaca gaggccggct cggccccccc tctgccctga gagtgaccgc tgtaccaacc  1260
tctgtcccta cagggcagcc ccgagaacca caggtgtaca cctgtcccc atccccggat  1320
gagctgacca agaaccagggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  1380
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc  1440
gtgtgggact ccgacggctc cttcttctct tacagcaagc tcaccgtgga caagagcagg  1500

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tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1560
acgcagaaga gcctctccct gtctccgggt aatga 1596

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<210> SEQ ID NO 4
<211> LENGTH: 123
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 4
catgaaacaa ccccaataa aggaagtgga accacttcag gtactaccg tcttctatct 60
gggcacacgt gtttcacgtt gacaggtttg cttgggacgc tagtaacat gggcttgctg 120
act 123

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<210> SEQ ID NO 5
<211> LENGTH: 41
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 5
His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr
1 5 10 15
Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly
20 25 30
Thr Leu Val Thr Met Gly Leu Leu Thr
35 40

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<210> SEQ ID NO 6
<211> LENGTH: 147
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Platelet derived growth
factor receptor transmembrane domain polynucleotide

```

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<400> SEQUENCE: 6
gctgtgggccc aggacacgca ggaggtcatc gtggtgccac actccttgcc ctttaagggtg 60
gtggtgatct cagccatcct ggccctgggtg gtgctcacca tcactcctc tatcctcctc 120
atcatgcttt ggcagaagaa gccacgt 147

```

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<210> SEQ ID NO 7
<211> LENGTH: 49
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Platelet derived growth
factor receptor transmembrane domain polypeptide

```

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<400> SEQUENCE: 7
Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
1 5 10 15
Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
20 25 30
Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
35 40 45

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Arg

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<210> SEQ ID NO 8

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<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: LoxP
        oligonucleotide

<400> SEQUENCE: 8
ataacttcgt atagcataca ttatacgaag ttat                               34

<210> SEQ ID NO 9
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
        polynucleotide

<400> SEQUENCE: 9
atgtatctgg gattgaattg cgtcattatc gtgtttctgc tcaaggggtg gcaaagtcag   60
gtccagctgc agcagccagg cgcagagctg gttaagccag gagcctcagt gaaaatgagc   120
tgcaaagcct ctggctacac ctttaccagc tataacatgc attgggtgaa acagacaccc   180
ggcagagggc tggaatggat cggagccata taccccggga acggggacac ctctataac   240
cagaagtcca agggaaagcg cacactcact gctgacaagt ccagtagcac cgcttacatg   300
caactttcaa gcttgacatc agaggattct gcagtttact actgtgcccg gtctacttac   360
tatggcggcg attggtatct caatgtatgg ggtgctggca caacagtcac tgtgagcgca   420
gct                                                                    423

<210> SEQ ID NO 10
<211> LENGTH: 141
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
        polypeptide

<400> SEQUENCE: 10
Met Tyr Leu Gly Leu Asn Cys Val Ile Ile Val Phe Leu Leu Lys Gly
 1           5           10           15
Val Gln Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20           25           30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35           40           45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50           55           60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65           70           75           80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85           90           95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100          105          110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115          120          125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala
130          135          140

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<210> SEQ ID NO 11
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
        polynucleotide

<400> SEQUENCE: 11

atgaaactcc cagtcaggct gctggtgctt atgttctgga taccgccag ttcattcag    60
attgtcttga gccagctctc cgccattttg tctgcctccc ctggggagaa agtaaccatg   120
acttgtcgcg catcctcaag cgtgagttac atccactggt ttcagcagaa gcctggcagc   180
tcaccaaacg cctggatcta tgctaactcc aacctcgctt ccggagtgcc tgtgcggttt   240
tctgggtccg gtagtggtag cagctactca ctgactatct caagagtga ggctgaagat   300
gccgcaacct attactgcca acagtggaca agtaatccac caacattcgg tggcggcact   360
aaactggaga tcaaactgtac ggtggctgca ccatctgtct tcattctccc gccatctgat   420
gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga   480
gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt   540
gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcacctc gacgctgagc   600
aaagcagact acgagaaaca caaagtctac gcctgcgaag tcaccatca gggcctgagc   660
tcgcccgtca caaagagctt caacagggga gagtgt                                696

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<210> SEQ ID NO 12
<211> LENGTH: 232
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
        polypeptide

<400> SEQUENCE: 12

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
 1          5          10          15

Ser Ser Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala
 20          25          30

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
 35          40          45

Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro
 50          55          60

Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe
 65          70          75          80

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val
 85          90          95

Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
100          105          110

Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
115          120          125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
130          135          140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145          150          155          160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165          170          175

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Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
                   180                                  185                                  190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
                   195                                  200                                  205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
                   210                                  215                                  220

Lys Ser Phe Asn Arg Gly Glu Cys  
                   225                                  230

<210> SEQ ID NO 13  
 <211> LENGTH: 1631  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
                                   polynucleotide

<400> SEQUENCE: 13

```

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc      60
acagggccc tgggtgcct ggtcaaggac tacttccccg aaccgggtgac ggtgtcgtgg      120
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      180
ctctactccc tcagcagcgt ggtgaccgtg cctccagca gcttgggcac ccagacctac      240
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tggtgagagg      300
ccagcacagg gaggagggt gtctgtgga agccaggctc agcgtcctg cctggacgca      360
tcccggctat gcagcccag tcaggggcag caaggcaggc cccgtctgcc tcttcaaccg      420
gaggcctctg cccgcccac tcatgctcag ggagagggtc ttctgggttt tccccagge      480
tctgggcagg cacaggctag gtgccctaa cccaggccct gcacacaaag gggcaggtgc      540
tgggtcaga cctgccaaga gccatatccg ggaggacct gccctgacc taagcccacc      600
ccaaaggcca aactctccac tccctcagct cggacacct ctctcctccc agattccagt      660
aactcccaat cttctctctg cagagcccaa atcttgtgac aaaactcaca catgcccacc      720
gtgcccaggt aagccagccc aggcctcgcc ctccagctca aggcgggaca ggtgccctag      780
agtagcctgc atccagggac aggccccagc cgggtgctga cacgtccacc tccatctctt      840
cctcagcacc tgaactcctg gggggaccgt cagtcttctt cttcccccca aaaccaagg      900
acaccctcat gatctcccgg acccctgagg tcacatgctg ggtgggtggac gtgagccaag      960
aagaccctga ggtcaagttc aactggtacg tggacggcgt ggagggtgcat aatgccaaga     1020
caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc     1080
tgaccaggga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc     1140
cagcccccat cgagaaaacc atctccaaag ccaaagggtg gaccctgggg gtgcgagggc     1200
cacatggaca gaggccggct cggccccata acttcgtata gcatacatta tacgaagtta     1260
taccctctgc cctgagagtg acccgtgtac caacctctgt ccctacaggg cagccccgag     1320
aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac caggtcagcc     1380
tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg gagagcaatg     1440
ggcagccgga gaacaactac aagaccagc ctcccgtgct ggactccgac ggtccttct     1500
tctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac gtcttctcat     1560
gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc tccctgtctc     1620

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cgggtaaatg a 1631

<210> SEQ ID NO 14  
<211> LENGTH: 2170  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 14

agcaccaagg gccatcgggt cttccccctg gcaccctect ccaagagcac ctctgggggc 60  
acagcggccc tgggtcgcct ggtcaaggac tacttccccg aaccgggtgac ggtgtcgtgg 120  
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtctcagga 180  
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 240  
atctgcaacg tgaatcacia gccacgcaac accaaggtgg acaagaaagt tggtgagagg 300  
ccagcacagg gagggagggt gtctgctgga agccaggctc agcgtctctg cctggacgca 360  
tcccggctat gcagccccag tccagggcag caaggcaggc cccgtctgcc tcttcacccg 420  
gaggcctctg cccgccccac tcatgtctag ggagagggtc ttctggcttt tccccaggc 480  
tctgggcagg cacaggctag gtgccctaa cccaggcctt gcacacaaag gggcagggtc 540  
tgggtcaga cctgccaaga gccatattcg ggaggacct gccctgacc taagcccacc 600  
ccaaaggcca aactctccac tccctcagct cggacacctt ctctcctccc agattccagt 660  
aactcccaat cttctctctg cagagcccaa atcttgtgac aaaactcaca catgcccacc 720  
gtgcccaggt aagccagccc aggcctcgcc ctccagctca aggcgggaca ggtgccctag 780  
agtagcctgc atccagggac aggccccagc cgggtgctga cacgtccacc tccatctctt 840  
cctcagcacc tgaactcctg gggggaccgt cagtcttctt cttcccccca aaacccaagg 900  
acaccctcat gatctcccgg acccctgagg tcacatgctt ggtggtggac gtgagccaag 960  
aagaccctga ggtcaagttc aactggtacg tggacggcgt ggagggtgat aatgccaaga 1020  
caaagccgcy ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc 1080  
tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc 1140  
cagcccccat cgagaaaacc atctccaaag ccaaaggtgg gaccctggg gtgcgagggc 1200  
cacatggaca gaggcgggct cggccccata acttcgtata gcatacatta tacgaagtta 1260  
taccctctgc cctgagagtg accgctgtac caacctctgt ccctacaggg cagccccgag 1320  
aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac caggtcagcc 1380  
tgacctgctt ggtcaaaagg ttctatccca cgcacatcgc cgtggagtgg gagagcaatg 1440  
ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac ggtctcttct 1500  
tcctctacag caagctcacc gtggacaaga gcagggtgca gcaggggaac gtcttctcat 1560  
gctccgtgat gcatgagget ctgcacaacc actacagca gaagagcctc tcctgtctc 1620  
cgggtaaatc cggacatgaa acaaccccaa ataaaggaag tggaaacctc tcaggtacta 1680  
cccgtcttct atctgggac acgtgtttca cgttgacagg tttgcttggg acgctagtaa 1740  
ccatgggctt gctgacttaa actagtataa cttcgtatag catacattat acgaagtatt 1800  
accctctgcc ctgagagtga ccgctgtacc aacctctgtc cctacagggc agccccgaga 1860  
accacaggtg tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct 1920

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gacctgcctg gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg 1980
gcagccggag aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt 2040
cctctacagc aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg 2100
ctccgtgatg catgaggctc tgcacaacca ctacacgcag aagagcctct cctgtctctc 2160
gggtaaatga 2170

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&lt;210&gt; SEQ ID NO 15

&lt;211&gt; LENGTH: 2194

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 15

```

agcaccaagg gcccatcggt cttccccctg gcacctcct ccaagagcac ctctgggggc 60
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccgggtgac ggtgtcgtgg 120
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtccctcagga 180
ctctactccc tcagcagcgt ggtgaccgtg cctccagca gcttgggcac ccagacctac 240
atctgcaacg tgaatcacia gcccagcaac accaagggtg acaagaaagt tggtgagagg 300
ccagcacagg gagggagggt gtctgctgga agccaggctc agcgcctctg cctggacgca 360
tcccggctat gcagccccag tccagggcag caaggcaggc cccgtctgcc tcttcaccgg 420
gaggcctctg cccgccccac tcatgctcag ggagagggtc ttctggcttt tccccaggc 480
tctgggcagg cacaggctag gtgccoctaa cccaggcctt gcacacaaag gggcagggtg 540
tgggctcaga cctgccaaaga gccatctccg ggaggacctt gccctgacc taagcccacc 600
ccaaaggcca aactctccac tccctcagct cggacacctt ctctcctccc agattccagt 660
aactcccaat cttctctctg cagagcccaa atcttgtgac aaaactcaca catgccacc 720
gtgcccagggt aagccagccc aggcctcgcc ctccagctca aggcgggaca ggtgccctag 780
agtagcctgc atccagggac aggccccagc cgggtgctga cacgtccacc tccatctctt 840
cctcagcacc tgaactcctg gggggaccgt cagtcttctt cttcccccca aaaccaagg 900
acaccctcat gatctcccgg acccctgagg tcacatgctg ggtggtggac gtgagccacg 960
aagacctga ggtcaagttc aactggtagc tggacggcgt ggagggtgcat aatgccaaga 1020
caaagccgcy ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc 1080
tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc 1140
cagcccccat cgagaaaaacc atctccaaag ccaaagggtg gacccgtggg gtgcygagggc 1200
cacatggaca gagggccggt cggccccata acttcgtata gcatacatta tacgaagtta 1260
taccctctgc cctgagagtg accgctgtac caacctctgt ccctacaggg cagccccgag 1320
aaccacagggt gtacaccctg ccccatccc gggatgagct gaccaagaac caggtcagcc 1380
tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg gagagcaatg 1440
ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac ggtccttct 1500
tcctctacag caagctcacc gtggacaaga gcagggtgca gcaggggaac gtcttctcat 1560
gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc tccctgtctc 1620
cgggtaaatc cggagctgtg ggccaggaca cgcaggaggt catcgtggtg ccacactcct 1680

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tgccctttaa ggtggtggtg atctcagcca tcttggccct ggtggtgctc accatcatct 1740
cccttatcat cctcatcatg ctttggcaga agaagccacg ttaaactagt ataacttcgt 1800
atagcataca ttatacgaag ttataccctc tgccctgaga gtgaccgctg taccaacctc 1860
tgtccctaca gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga 1920
gctgaccaag aaccaggtea gcctgacctg cctggtcaaa ggcttctatc ccagcgacat 1980
cgccgtggag tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt 2040
gctggactcc gaaggctcct tcttccteta cagcaagctc accgtggaca agagcagggtg 2100
gcagcagggg aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac 2160
gcagaagagc ctctccctgt ctccgggtaa atga 2194

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&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 1876

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 16

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aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 180
ctctactccc tcagcagcgt ggtgacctg cctccagca gcttgggcac ccagacctac 240
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gaggcctctg cccgccccac tcatgctcag ggagagggtc ttctgggttt tccccaggc 480
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tgggctcaga cctgccaaga gccatctccg ggaggacct gccctgacc taagcccacc 600
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taccctctgc cctgagagtg accgctgtac caacctctgt ccctacaggg cagccccgag 1320
aaccacaggt gtacacctcc ggacatgaaa caaccccaaa taaaggaagt ggaaccactt 1380
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cgctagtaac catgggcttg ctgacttaaa ctagtataac ttcgtatagc atacattata 1500
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cctgtctccg ggtaaa 1876

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&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 1900

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

&lt;400&gt; SEQUENCE: 17

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ctctactccc tcagcagcgt ggtgaccgtg cctccagca gcttgggcac ccagacctac 240
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gaggcctctg cccgccccac tcatgctcag ggagagggtc ttctggcttt tccccaggc 480
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tgggctcaga cctgccaaga gccatctccg ggaggacct gccctgacc taagcccacc 600
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cacactcctt gccctttaag gtggtggtga tctcagccat cctggccctg gtggtgctca 1440
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taacttcgta tagcatacat tatacgaagt tataccctct gccctgagag tgaccgctgt 1560
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ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gctttctatcc 1680
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gagcagggtg cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa 1860
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<210> SEQ ID NO 18
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Internal
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<400> SEQUENCE: 18

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tcctccccc cccctaacy ttactggccg aagccgcttg gaataaggcc ggtgtgcggt 60
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tggccctgtc ttcttgacga gcattcctag gggcttttcc cctctcgcca aaggaatgca 180
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gaaggatgcc cagaaggtac cccattgtat gggatctgat ctggggcctc ggtacacatg 480
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<210> SEQ ID NO 19
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 19

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Met Pro Lys Lys Lys Arg Lys
1 5

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<210> SEQ ID NO 20
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 20

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atggacatga gggccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtgaca tccagatgac ccagttccca tctccctgt ctgcatctgt aggggacaga 120
gtcacatca cttgtcgggc aagtcagggc atcagaaatt acttagcctg gtatcagcaa 180

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aaaccagggg aagcccctaa gctcctgata tatgctgcat ccactttgca atcaggggtc 240
ccatctcggg tcaagtggcag tggatctggg acagatttca ctctcaccat cagcagccta 300
cagctgaag atgttgcaac ttattactgt caaaggtata accgtgcacc gtatactttt 360
ggccagggga ccaaggtgga aatcaaa 387

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<210> SEQ ID NO 21
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

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<400> SEQUENCE: 21

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1           5           10           15
Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
      20           25           30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
      35           40           45
Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
      50           55           60
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 65           70           75           80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
      85           90           95
Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg
      100          105          110
Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
      115          120          125

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Lys

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<210> SEQ ID NO 22
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 22

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tgtcgggect ctggattcac ctttgatgat tatgccatgc actgggtccg gcaagctcca 180
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gactctgtgg agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatctg 300
caaatgaaca gtctgagagc tgaggatacg gccgtatatt actgtgcgaa agtctcgtac 360
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gct 423

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<210> SEQ ID NO 23
<211> LENGTH: 141
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 23

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1             5             10             15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
      20             25             30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      35             40             45

Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50             55             60

Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala
65             70             75             80

Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
      85             90             95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
      100            105            110

Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp
      115            120            125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
      130            135            140

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What is claimed is:

1. A DNA construct comprising (a) promoter; (b) a gene of interest (GOI); and (c) a reporter gene flanked by a DNA recombinase recognition sequence (DRRS).

2. The DNA construct of claim 1, wherein the DRSS is selected from the group consisting of an FRT sequence (DRRS for flippase or FLP), an LoxP (DRRS for Cre), and an attB or attP (DRRS for  $\phi$ C31 integrase).

3. The DNA construct of claim 1, further comprising an IRES upstream of the reporter gene.

4. The DNA construct of claim 1, wherein the reporter gene encodes a membrane anchored reporter (MAR) molecule, wherein the MAR is any molecule that can be detected on the cell surface.

5. The DNA construct of claim 4, wherein the MAR is selected from the group consisting of membrane-anchored GFP, and a membrane-anchored protein of interest.

6. The DNA construct of claim 1, wherein the reporter gene encodes an intracellular reporter molecule.

7. The DNA construct of claim 1, wherein the gene of interest has two or more exons and one or more introns.

8. The DNA construct of claim 7, wherein an intron of the gene of the interest comprises a splice acceptor sequence followed by a membrane association sequence.

9. The DNA construct of claim 8, wherein a splice acceptor sequence provides a means for alternative splicing wherein the expressed protein of interest can be membrane associated or secreted.

10. The DNA construct of claim 1, wherein the gene of interest encodes a recombinant protein.

11. The DNA construct of claim 10, wherein the gene of interest encodes an antibody.

12. The DNA construct of claim 11, wherein the gene of the interest encoding said antibody comprises a splice acceptor sequence in the third intron of the antibody gamma constant region coding sequence.

13. An expression vector for delivering a gene of interest into a host cell, comprising the DNA construct of claim 1.

14. A cell comprising the DNA construct of claim 1.

15. A cell culture comprising the cell of claim 14.

16. The cell culture of claim 15, wherein a site specific DNA recombinase is added to the culture media.

17. The cell culture of claim 16, wherein the site specific DNA recombinase is provided by transfection of an expression vector encoding the DNA recombinase into the cells of the cell culture.

18. The cell culture of claim 16, wherein the sequence encoding said reporter is deleted in the cells of the cell culture.

19. The cell culture of claim 18, wherein the gene of interest is expressed and the corresponding protein of interest (POI) is secreted into the cell culture media.

20. A DNA construct comprising (a) promoter; (b) a library containing a plurality of genes of interest; and (c) a reporter gene flanked by a DNA recombinase recognition sequence (DRRS).

21. The DNA construct of claim 20, wherein the genes of interest in the library comprise an intron with a splice acceptor sequence followed by a membrane association sequence.

22. The DNA construct of claim 21, wherein the splice acceptor sequence provides a means for alternative splicing wherein the expressed genes of interest can encode membrane associated or secreted proteins of interest.

23. The DNA construct of claim 20, wherein the library is an antibody library.

24. The DNA construct of claim 23, wherein the antibody library is an affinity maturation library.

25. A cell library comprising the DNA construct of claim 24.
26. A cell culture comprising the cell library of claim 25.
27. A cell line screening method comprising,
- providing host cells transfected with a DNA construct according to claim 1;
  - culturing the transfected cells wherein the reporter protein is expressed and a protein of interest may also be secreted into the cell culture media;
  - screening the transfected host cells and selecting host cells expressing a reporter molecule;
  - exposing the selected cells to a DNA recombinase, wherein following such exposure the cells no longer express the reporter protein; and
  - screening for cells that secrete a protein of interest into the cell culture media.
28. The cell line screening method of claim 27, wherein the reporter molecule is a membrane anchored reporter (MAR).
29. The cell line screening method of claim 27, wherein the reporter molecule is an intracellular reporter.
30. The cell line screening method of claim 27, wherein the DNA construct comprises a DRSS selected from the group consisting of an FRT sequence (DRRS for flippase or FLP), a LoxP (DRRS for Cre), and an attB or attP (DRRS for  $\phi$ C31 integrase).
31. The cell line screening method of claim 28, wherein the MAR is any protein that can be detected on the cell surface.
32. The cell line screening method of claim 31, wherein the MAR is detected on the cell surface by FACS or MACS.
33. The cell line screening method of claim 27, wherein the gene of interest encoded by the DNA construct has two or more exons and one or more introns.
34. The cell line screening method of claim 33, wherein an intron of the gene of the interest comprises a splice acceptor sequence followed by a membrane association sequence.
35. The cell line screening method of claim 27, wherein the transfected host cell is exposed to a site specific DNA recombinase.
36. The cell line screening method of claim 27, wherein the protein of interest is an antibody.
37. A cell line screening method comprising the steps of:
- providing host cells in culture media;
  - transfecting the host cells with a DNA construct according to claim 20;
  - screening the transfected host cells and selecting host cells expressing a reporter molecule;
  - exposing the selected host cells to a DNA recombinase;
  - culturing the host cells in cell culture media; and
  - screening the cell culture media for a protein of interest with a desired property.
38. The cell line screening method of claim 37, wherein the reporter molecule is a membrane anchored reporter (MAR).
39. The cell line screening method of claim 37, wherein the reporter molecule is an intracellular reporter.
40. The cell line screening method of claim 37, wherein the DNA construct comprises a DRSS selected from the group consisting of an FRT sequence (DRRS for flippase or FLP), an LoxP (DRRS for Cre), an attB or attP (DRRS for  $\phi$ C31 integrase).
41. The cell line screening method of claim 38, wherein the MAR is any protein that can be detected on the cell surface.
42. The cell line screening method of claim 41, wherein the MAR is detected on the cell surface by FACS or MACS.
43. The cell line screening method of claim 37, wherein the gene of interest encoded by the DNA construct has two or more exons and one or more introns.
44. The cell line screening method of claim 43, wherein an intron of the gene of the interest comprises a splice acceptor sequence followed by a membrane association sequence.
45. The cell line screening method of claim 37, wherein the transfected host cell is exposed to a site specific DNA recombinase.
46. The cell line screening method of claim 37, wherein the protein of interest is an antibody.
47. A method of screening a cell library screening for a protein of interest comprising switching a cell having a membrane anchored reporter protein into a cell that secretes a protein of interest into culture media, comprising:
- providing host cells in culture media;
  - transfecting the host cells with a DNA construct according to claim 20 to generate a cell library expressing a library of membrane-anchored protein of interest;
  - screening the cell library and selecting host cells expressing a membrane-anchored protein of interest with a desired property;
  - exposing the selected host cells to a DNA recombinase;
  - screening the cell culture media for the protein of interest for the protein of interest with desired property; and
48. The screening method of claim 47, wherein the library is an antibody library.
49. The screening method of claim 47, wherein the desired property is binding of an antigen.
50. The screening method of claim 47, wherein the desired property is bioactivity.

\* \* \* \* \*